SI Table S1. Quantitative protein and peptide data of the 11 time-course groups (n=5/group)

Time point 0.5 hour

Accession number	**Protein DESCRIPTION**	**Protein Ratio (0.5h)**	**P-value (0.5h)**	**Peptide number (0.5h)**
Accession number	Peptide sequence	Peptide Ratio (0.5h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**1.315815199**	**0.00988**	**2**
A0JPJ7	IGIVGLPNVGK	1.405806436	2	2.652685404
A0JPJ7	YLEANMTQSALPK	1.315701829	2	2.78365469
A0JPM9	**EIF3J Eukaryotic translation initiation factor 3 subunit J**	**1.12065691**	**0.82792**	**2**
A0JPM9	EEAEVKPEVKISEK	1.062914851	2	2.334575653
A0JPM9	RLEEPEESK	1.130084442	2	2.49113059
A0JPQ8	**ALKMO Alkylglycerol monooxygenase**	**1.370471014**	**0.00368**	**2**
A0JPQ8	LDDILTSMSAGVVSR	1.710010531	2	2.827005386
A0JPQ8	SITHLASGSWK	1.355726197	2	2.418783665
A1A5P5	**ARMC9 LisH domain_containing protein ARMC9**	**1.012220178**	**0.9997**	**2**
A1A5P5	CFIKEGNAEMIR+Oxidation(10)	1.012287997	2	2.713591814
A1A5P5	LYLAQNTKVLRMLEGR+Oxidation(12)	1.004945665	2	2.306550741
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.038965396**	**0.98707**	**2**
A2ADY9	IDFSSIAVPGTSNPQQR	0.927131523	2	2.561553717
A2ADY9	VLVEQQQDR	1.041071237	2	2.768367529
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**1.055581849**	**0.72712**	**2**
A2AF47	NLLMCYLYIVK	1.055834256	2	2.494649887
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(1)	0.850277362	3	3.358799696
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.610215595**	**0.00138**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(14)	0.189192761	2	2.829661608
A2AGT5	IGSKENTKEGLAELYEYK	0.614038165	2	2.466874123
A2AJL3	**FGGY FGGY carbohydrate kinase domain_containing protein**	**1.16276762**	**0.01654**	**2**
A2AJL3	GHGLTCEGQPVTSR	1.349709508	2	3.664535046
A2AJL3	MSKVGKVVFPEHADK	1.049487927	2	2.385738134
A2AL36	**CNTRL Centriolin**	**1.172972236**	**0.42268**	**3**
A2AL36	NQDKLNK	1.160877877	1	2.169896126
A2AL36	EQQLDIMNR+Oxidation(7)	1.194066064	2	2.332228422
A2AL36	LQDEKETLLQR	1.304018757	2	2.407828331
A2AQP0	**MYH7B Myosin_7B**	**0.788335546**	**0.71305**	**6**
A2AQP0	AITDAAMMAEELKK	0.755192068	2	3.50283885
A2AQP0	DIDDLELTLAK	0.605824665	2	3.550842762
A2AQP0	EQDTSAHLER	0.987867134	2	2.382186174
A2AQP0	KDIDDLELTLAK	0.955224027	2	2.325482607
A2AQP0	SIQELEK	1.026368908	2	2.399574995
A2AQP0	VGNEYVTK	0.88629975	2	2.621120691
A2ASS6	**TITIN Titin**	**1.080968309**	**0.1702**	**11**

A2ASS6	TFLQDQLVSLQVLK	0.950749933	1	1.93290627
A2ASS6	AENRFGIGPPAETIQRTTAR	0.826908809	2	2.674449682
A2ASS6	DVLEEPEIDLDVALR	0.804856236	2	2.820721626
A2ASS6	KDLNMVVSAARISCGGAIR	0.927074184	2	2.307215214
A2ASS6	KGDGTQLACKVTGTPPIK	0.442644734	2	2.727824926
A2ASS6	SSVSLSWSRPKDDGGSR	1.006707428	2	2.343025684
A2ASS6	TCEIEIGQLK	1.126747516	2	2.455161333
A2ASS6	VGDDAWIKDTTGTALR	1.131864	2	2.499356985
A2ASS6	VKNAMPEDIDEYAVEIEGK+Oxidation(5)	4.470479804	2	2.342764378
A2ASS6	VMKLTTGEEYQFRIK+Oxidation(2)	1.206652504	2	2.345289707
A2ASS6	YDGGHKLTGYIVEK	0.551149212	2	2.302132607
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.148662426**	**1**	**9**
A2VCW9	AGGILQEDITEACLILGVK	1.196496165	2	2.619549751
A2VCW9	AQEANMSLLDEVLK	1.064174381	2	3.045842648
A2VCW9	GAQEVFNELPCEYVEPHELK	1.070314865	2	4.684628487
A2VCW9	KYDINTVNVTVGK	1.1452932	2	3.977996826
A2VCW9	REDVNAWER	1.187291608	2	2.788863897
A2VCW9	SSVVPVEGCPELPHK	0.984896366	2	3.071965933
A2VCW9	YDINTVNVTVGK	0.982003502	2	2.778713942
A2VCW9	KTDGVYDPVEYEKYPER	1.143690468	3	3.688358784
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	1.027365179	3	3.672071695
A3KMP2	**TTC38 Tetratricopeptide repeat protein 38**	**1.193346476**	**0.15206**	**2**
A3KMP2	DVGLPLCQALLEAENGNPDR	1.199728175	2	2.392767429
A3KMP2	VLELLLPIR	0.827878469	2	2.722713709
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.008284748**	**0.01073**	**11**
A7VJC2	NYYEQWGK	0.969327487	1	2.369861841
A7VJC2	EESGKPGAHVTVK	1.09431043	2	3.260646582
A7VJC2	GGGGNFGPGPGSNFR	1.126209151	2	3.142210484
A7VJC2	GGNFGFGDSR	1.064224507	2	2.876637459
A7VJC2	IDTIEIITDR	1.022690428	2	3.887227297
A7VJC2	LFIGGLSFETTEESLR	1.348370676	2	4.544666767
A7VJC2	LTDCVVMR	1.17576985	2	2.64514327
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	1.118034706	2	5.964814186
A7VJC2	QEMQEVQSSR	1.009424694	2	3.077036619
A7VJC2	QEMQEVQSSR+Oxidation(3)	1.454998232	2	2.563605547
A7VJC2	YHTINGHNAEVR	1.365446233	2	3.866345644
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.118559462**	**0.87172**	**2**
B0BN93	GSIDEVDKR	1.127265554	2	2.482929468
B0BN93	SAWGQQPDLAANEAQLLR	1.076886764	2	3.321202517
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.083868712**	**0.9999**	**8**
B0BNE5	AFNGYLGPDQSK	1.00416869	2	3.686881542

B0BNE5	AYDATCLVK	1.081487653	2	2.403613806
B0BNE5	FAIYLPPQAESAK	1.045494249	2	2.586284637
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.111794954	2	5.641798496
B0BNE5	SVSAFAPICNPVLCPWGK	0.98349855	2	4.66455555
B0BNE5	VFEHSSVELK	1.069165544	2	2.565324783
B0BNE5	MYSYVTEELPQLINANFPVDPQR	0.986580355	3	5.166892529
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.177114046	3	5.446433544
B0BNN3	**CAH1 Carbonic anhydrase 1**	**1.04007202**	**0.97396**	**3**
B0BNN3	ADGLAIIGVLMK	0.752056186	2	2.847889185
B0BNN3	VLDALSSVK	1.037709874	2	2.403592587
B0BNN3	HDSSLKPVSVSYNPATAK	1.050064806	3	4.797493935
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.053639878**	**0.05972**	**2**
B0K020	HNEETGDNVGPLIIK	1.080300497	2	5.714765072
B0K020	VVHAFDMEDLGDK	1.087160048	2	3.651798964
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**0.966955027**	**0.38102**	**3**
B2GV24	QLVSQNK	0.452671297	1	1.919166803
B2GV24	TYDLPGDFLTQALTQR	1.226002944	2	2.737926483
B2GV24	VNIVDLQQVINVDLTHIENR	1.024285649	3	4.159801483
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**1.398674553**	**0.00011**	**2**
B2RX88	SISSVNVDQVRMRNEDR	1.439127914	2	2.558050156
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(12)	1.560779148	2	2.558271646
B2RY56	**RBM25 RNA_binding protein 25**	**0.764257816**	**0.73931**	**2**
B2RY56	FEDEDSDDVPRKR	0.718114528	2	2.333686113
B2RY56	LLIYETEAK	1.015932755	2	2.499816656
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.977945116**	**0.86884**	**4**
B2RYW9	ATDVMAYVAGFTVAHDVSAR	1.222841506	2	3.059402227
B2RYW9	KGDEVQCEIEELGVIINK	0.965474158	2	5.327217102
B2RYW9	TFDTFCPLGPALVTK	0.84188831	2	5.067196846
B2RYW9	VNGEIVQSSNTNQMVFK	0.801949518	2	4.388745308
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**1.148588349**	**0.0687**	**2**
B2RZ78	GDFDESLNYPEQK	1.14556445	2	3.319764853
B2RZ78	IQHILCTGNLCTK	1.307255095	2	3.306453943
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.164576498**	**0.64944**	**4**
B3DMA2	AVLTVTQYR	1.173905812	2	2.304055214
B3DMA2	NLPDSDNEECLVHGDFK	1.039295686	2	3.593083382
B3DMA2	RGQEVLTR	0.532494084	2	2.713801146
B3DMA2	SGQSNPTFFLQK	1.046478726	2	2.943371058
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.242430384**	**0.01196**	**4**
B5DFC8	GCILTLVER	1.112476461	2	2.392477751
B5DFC8	GTEITHAVVIK	1.246962659	2	2.461471319

B5DFC8	SEQDQAENEGEDSAVLMER	2.429500905	2	4.687895298
B5DFC8	TEPTAQQNLALQLAEK	1.195895126	2	4.75485754
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**0.759395376**	**0.00106**	**2**
D3ZTX0	SVIDYQTHFR	1.695068319	2	2.590851068
D3ZTX0	VSALTQMESACVSIHEALK	0.516780011	2	2.475839376
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.027268514**	**0.96045**	**3**
D3ZW55	IDLPEYQGEPDEISIQK	0.9785072	2	4.306489944
D3ZW55	LQEYFGVTDGAGDH	0.862232433	2	3.208432674
D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.015767506	3	4.228414536
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**0.982609638**	**0.1901**	**2**
D3ZZL9	IEDLEQEMKIQK	0.538646442	2	2.435746193
D3ZZL9	MLQETVTKEAELR+Oxidation(1)	1.147339339	2	2.374644756
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.235665848**	**0.03644**	**2**
D4A4T9	KEEDSDEIKIGTSCK	1.685960769	2	2.594999075
D4A4T9	LSSGNEEDKKEEDSDEIK	1.231131041	3	4.351505756
E9Q557	**DESP Desmoplakin**	**1.111024562**	**0.98065**	**2**
E9Q557	KQVQTSQKNTLR	1.124915163	1	1.99945426
E9Q557	SQCTQVVQER	1.030879929	2	2.79091239
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**1.25547674**	**0.07174**	**2**
O08550	HAAVALGQARAMVPEDVPR	1.226129237	2	2.401769876
O08550	RGEEGTERMVQALTELLR	1.255628962	2	2.83263135
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.402483228**	**0.06194**	**9**
O08557	GAEILADTFK	1.175689927	1	2.139324903
O08557	DYAVSTVPVADSLHLK	1.080853681	2	3.469610453
O08557	LKDHLLIPVSNSEMEK	1.194686794	2	3.511649609
O08557	LTVPDDMAANCIYLNIPSK	1.244304489	2	3.429961443
O08557	SFCSMAGPNLIAIGSSESAQK	1.054505439	2	4.64247942
O08557	SQGEEVDFAR	1.128132026	2	2.422720671
O08557	VDGLLTCCSVFINK	0.873831689	2	3.436801195
O08557	GAEILADTFKDYAVSTVPVADSLHLK	1.213656406	3	3.507713556
O08557	LQLNIVEMKDENATLDGGDVLFTGR	1.454836969	3	3.402597666
O08583	**THOC4 THO complex subunit 4**	**1.102239253**	**0.64635**	**2**
O08583	QQLSAEELDAQLDAYNAR	1.01969946	2	2.902570248
O08583	SLGTADVHFER	1.109656533	2	2.398238659
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**0.897829566**	**3.4E-15**	**11**
O08601	NALLPEGIPLLLK	1.645786539	1	2.748514414
O08601	EFYSYENEPVGIENLK	0.912611565	2	4.645369053
O08601	GCPSLAEHWKSIR	1.40258143	2	4.021571636
O08601	GHTTGLSLNNER	1.505922499	2	2.6936059
O08601	MLSASGDPVSVVK	1.241121923	2	3.71732688

O08601	NILLSIGELPK	1.245345857	2	4.036984444
O08601	SDSSIILQER	1.356468907	2	2.403862476
O08601	SGSSSAYTGYVER	1.285284847	2	3.72904706
O08601	SNLNIFQYIGK	1.40453061	2	3.088437796
O08601	VKEFYSYENEPVGIENLK	1.315066169	2	3.447844744
O08601	REEILQILK	1.196248391	3	3.394383907
O08795	**GLU2B Glucosidase 2 subunit beta**	**0.859171733**	**2.6E-07**	**6**
O08795	ETVVTSTTEPSR	0.693991615	2	2.959150553
O08795	KLWEEQQAAAK	1.103979872	2	3.431666374
O08795	LWEEQQAAAK	0.893613482	2	2.322457075
O08795	MPPYDEETQAIIDAAQEAR	0.92924588	2	5.391526222
O08795	SLEDQVETLR	0.910196023	2	3.431058645
O08795	YEQGTGCWQGPNR	0.995512338	2	3.907977343
O08874	**PKN2 Serine/threonine_protein kinase N2**	**1.292875046**	**0.5501**	**3**
O08874	QLDIELK	1.330289853	1	2.359610558
O08874	ATSVALPGWSPSENRSSFMSR	1.020504982	2	2.339031458
O08874	YSLEQRLNELPKNHPK	0.83246165	2	2.401260853
O08949	**TF2AA Transcription initiation factor IIA subunit 1**	**1.188832759**	**0.31777**	**2**
O08949	DGIMNLNGRDYIFSK+Oxidation(4)	1.238135624	2	2.59036684
O08949	MANSANTNTVPK	0.820005922	2	2.564783812
O09158	**CP3AP Cytochrome P450 3A25**	**0.786720521**	**0.11199**	**2**
O09158	DVEINGVFIPK	0.547302647	2	2.472405195
O09158	VDFLQLMMNTQNSK	0.79296395	2	2.606653452
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.291874985**	**9.9E-20**	**13**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.323195875	2	6.022236347
O09171	AGPWTPEAAVEHPEAVR	0.819874414	2	5.192662239
O09171	AGSNVMQTFTFYASEDKLENR	0.819018339	2	4.68469286
O09171	GAAELMQQK	1.202421033	2	3.500292778
O09171	GAAELMQQK+Oxidation(6)	1.362426167	2	2.782459259
O09171	IFHQQLEVFMK	1.376112632	2	2.882479668
O09171	QGFIDLPEFPFGLEPR	1.124513801	2	5.17962122
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.239878003	2	6.10487318
O09171	VNEAACDIAR	1.268996074	2	3.986949444
O09171	KEYWQNLR	1.32158986	3	3.425658703
O09171	LNAGEVVIGDGGFVFALEK	1.321525334	3	5.90617466
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.239612031	3	6.454136372
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(10)	1.471874359	3	6.185049534
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.033365517**	**0.27849**	**9**
O09173	CFYNSDGDFLIVPQK	2.096925753	2	4.164485455
O09173	FSVDVFEETR	1.03335707	2	3.827785015
O09173	LLIYTEFGK	1.785687383	2	2.516003132
O09173	NCMSEFMGLIK	0.943564961	2	3.119481087

O09173	QDVSPFNVVAWHGNYTPYK	1.11193741	2	3.498546124
O09173	SLRPGVAIADFVIFPPR	1.083909923	2	3.731158972
O09173	YISGFGNECASEDPR	1.953898747	2	3.84489727
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.321286521	3	5.27784729
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.109859811	3	3.422561407
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.070043069**	**6.4E-09**	**17**
O35077	ELHSILQHK	0.874838602	1	2.705610275
O35077	ANTIGISLIK	1.093599685	2	3.11797452
O35077	FCETTIGCK	1.034894522	2	2.711673737
O35077	FCETTIGCKDPAQGQLLK	1.148111011	2	5.040987492
O35077	GIDEGPNGLK	1.097511406	2	2.730050802
O35077	ITVVQEVDTVEICGALK	0.985410398	2	4.912765026
O35077	IVGSNASQLAHFDPR	2.469519107	2	3.084201336
O35077	KLTEIINTQHENVK	1.190333731	2	5.200676441
O35077	LTEIINTQHENVK	1.096919753	2	4.374824524
O35077	NIVAVGAGFCDGLGFGDNTK	0.972501741	2	4.861309528
O35077	SIEQLEK	1.026368908	2	2.465974331
O35077	VCIVGSGNWGSAIAK	1.252932713	2	4.577895641
O35077	VTMWVFEEDIGGR	1.363130727	2	3.334704876
O35077	GLVDKFPLFTAVYK	0.983800572	3	3.962428093
O35077	ICDQLKGHLK	1.170613793	3	3.337562323
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	0.960180697	3	4.643340588
O35077	VCYEGQPVGEFICCLQNHPEHM	1.009449193	3	4.406251907
O35078	**OXDA D_amino_acid oxidase**	**1.255083234**	**0.77425**	**2**
O35078	GQIIQVEAPWIK	1.034996615	2	3.030266047
O35078	SCCQLEPTLK	1.487269299	2	2.745720387
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**1.090401192**	**0.49012**	**3**
O35094	KLEESDALQEAR	1.090643249	2	3.410974503
O35094	TEMSEVLTEILR	0.781855598	2	2.501097441
O35094	VTDLLGGLFSK	1.106694834	2	3.512970209
O35142	**COPB2 Coatomer subunit beta_**	**1.146914031**	**4.1E-05**	**5**
O35142	AAESLADPTEYENLFPGLK	1.148050831	2	4.130021095
O35142	FELALQLGELK	1.147030433	2	2.952200651
O35142	GSNNVALGYDEGSIIVK	1.173307219	2	3.468582392
O35142	HSEVQQANLK	0.735620047	2	3.725630522
O35142	TFEVCDLPVR	1.135036965	2	2.622041941
O35180	**SH3G3 Endophilin_A3**	**1.193918262**	**0.3197**	**2**
O35180	AVAEILSK	1.233803843	1	1.94412601
O35180	QSTEILQELQNK	1.124915163	1	2.029147863
O35244	**PRDX6 Peroxiredoxin_6**	**1.04810079**	**0.94615**	**9**
O35244	NFDEILR	1.074227625	1	2.377286673
O35244	DINAYNGAAPTEK	0.9932294	2	3.968900442

O35244	DLAILLGMLDPAEKDEK	1.012013569	2	3.54870677
O35244	GESVMVLPTLPEEEAK	0.887966812	2	3.068173647
O35244	KGESVMVLPTLPEEEAK	1.037599701	2	5.048854828
O35244	LIALSIDSVEDHFAWSK	1.317841269	2	4.417764187
O35244	LSILYPATTGR	1.588613371	2	3.006505966
O35244	VVDSLQLTASNPVATPVDWK	1.078360729	2	6.051705837
O35244	VVFIFGPDKK	1.140895368	2	2.492742538
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.847192164**	**0.50599**	**2**
O35469	DLGYEPLVSWEEAK	0.782514198	2	4.267533779
O35469	TSEWIGTLVEQHR	1.24553296	2	3.51987648
O35509	**RB11B Ras_related protein Rab_11B**	**0.997127687**	**0.84537**	**5**
O35509	NEFNLESK	1.104118771	1	2.101644278
O35509	AQIWDTAGQER	1.007383273	2	2.342137337
O35509	GAVGALLVYDIAK	0.973923961	2	3.515868425
O35509	HLTYENVER	1.286561028	2	2.543623209
O35509	VVLIGDSGVGK	1.122947152	2	2.603195429
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.128753964**	**9.7E-06**	**7**
O35567	ALFEEVPELLTEAEK	1.067642143	2	2.83424902
O35567	DGQVIGIGAGQQSR	0.921880002	2	3.000334501
O35567	EVSDGIVAPGYEEEALK	1.145347112	2	3.593898296
O35567	HVSPAGAAVGVPLSEDEAR	1.366003867	2	5.438792706
O35567	MSSFGDFVALSDVCDVPTAK	1.305164844	2	3.935188293
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.037359777	2	5.37996006
O35567	YTQSNSVCYAK	1.091247243	2	2.805931568
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.125148244**	**0.73381**	**2**
O35660	RYAMGDAPDYDR	1.21043435	2	3.906485796
O35660	YAMGDAPDYDR+Oxidation(3)	1.098243494	2	2.823656797
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.768884636**	**0.99699**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	0.946155723	2	3.846392632
O35760	NCHLNENIDK	0.706395148	2	2.999662399
O35760	NVTLNPDPNEIK	0.832470424	2	2.822279692
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	1.028068379	3	5.499254704
O35763	**MOES Moesin**	**0.99710329**	**0.34677**	**5**
O35763	ALTSELANAR	1.095553456	2	2.601706028
O35763	AQMVQEDLEK	0.92645744	2	2.36089468
O35763	AQQELEEQTR	0.787281048	2	3.201079845
O35763	IQVWHEEHR	1.208103205	2	2.4082129
O35763	TQEQLASEMAELTAR	0.997697413	2	3.232579947
O35783	**CALU Calumenin**	**1.055042262**	**0.82382**	**2**
O35783	HLVYESDQDKDGK	0.973419572	2	4.475465775
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.185620754	3	4.94550848
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.109603522**	**0.40752**	**3**

O35796	AEEQEPELTSTPNFVVEVTK	1.158394263	2	4.669938087
O35796	AFVEFLTDEIKEEK	0.859042726	2	2.830543518
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.302125109	3	5.091276169
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**0.87639389**	**1.4E-09**	**8**
O35814	ALDLDSSCK	1.162914819	1	2.113708735
O35814	ALSAGNIDDALQCYSEAIK	0.842323437	2	5.0334692
O35814	AMADPEVQQIMSDPAMR	0.867294347	2	4.239911079
O35814	DCEECIQLEPTFIK	0.972400671	2	3.949631214
O35814	ELIEQLQNKPSDLGTK	0.712401849	2	4.105322838
O35814	LDPQNHVLYSNR	1.497205565	2	3.123892069
O35814	LMDVGLIAIR	1.010263124	2	3.372227669
O35814	TVDLKPDWGK	1.080773632	2	2.448185682
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.757205914**	**8.9E-10**	**9**
O35826	EVGAFGTPVINLGTR	1.116583752	2	2.756300926
O35826	ILLAGCPSYDK	2.62221061	2	2.402135134
O35826	LIQEWNSVDLR	1.471415758	2	2.369228363
O35826	MIEQDDFDINTR	1.582048967	2	2.472289562
O35826	SIDLQEPLQK	1.605257674	2	2.535382032
O35826	TLVLFPNIDAGSK	1.640008139	2	2.313866377
O35826	VNPQEGVVLHSTK	1.459104614	2	2.343410254
O35826	ILHIEGGEVSGTIDDSIR	1.71682997	3	4.064212799
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.915496597	3	5.795366764
O35867	**NEB1 Neurabin_1**	**1.149104744**	**0.27283**	**2**
O35867	DSNSRPSSNKQATDTEEPEK	1.187000696	2	2.365522623
O35867	EKAGEAEPQDEWGGSKSNR	0.654316614	2	2.341050625
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.810449555**	**2.7E-10**	**6**
O35913	EGLQENVDGTENAK	0.60418995	2	3.444642544
O35913	ILAGIPAPIYFGALIDR	1.16215173	2	2.427643061
O35913	LYLGLPAALR	2.374134862	2	2.636874199
O35913	SLSGTYMNSMLTQIER	0.832989382	2	4.215642452
O35913	SQTLNPTQDPSECVK	0.874153602	2	4.295593262
O35913	TFQFPGDIESSK	0.556737846	2	2.498107195
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.439052482**	**0.61861**	**6**
O35952	HVEPGNTAVQEK	1.087946855	1	3.957814693
O35952	ALLEVLGR	1.035028035	2	2.844345808
O35952	FYEGTADEMYK	1.501773786	2	2.756554127
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.135653	2	4.058031082
O35952	TVQQHAGETDPVTTMR	1.073945542	2	5.594100952
O35952	LTTVLTTHHHWDHAGGNEK	1.562984554	3	3.722848415
O35987	**NSF1C NSFL1 cofactor p47**	**1.046837458**	**0.54907**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.03994172	2	5.063035011

O35987	LGAAPEEESAYVAGER	0.993960087	2	4.04073
O35987	LGSTAPQVLNTSSPAQQAENEAK	1.882332962	2	3.868021488
O35987	SYQDPSNAQFLESIR	1.036505858	2	4.747212887
O35987	TGFSLDNGDLR	1.124299453	2	2.703923941
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.193143981**	**0.00036**	**2**
O54975	GSLTFEPLTLVPIQTK	1.316732781	2	3.941550255
O54975	IENVVLVVPAK	1.211787022	2	3.244685411
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**0.917662023**	**6.1E-07**	**3**
O55012	ATTLSNAVSSLASTGLSLTK	1.520318909	2	4.145849228
O55012	ITAAQHSVTGSAVSK	1.44164671	2	4.28246069
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	0.859378936	3	4.636709213
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.132228203**	**0.07402**	**4**
O55096	AGLLALEFYTPETANWR	1.129152488	2	4.286039829
O55096	LASVLNTEPALDSELTSK	2.312392181	2	3.780650616
O55096	SYEFQGNHFQVTR	1.128051466	2	3.823973417
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.075270187	3	4.272258282
O55125	**NIPS1 Protein NipSnap homolog 1**	**1.051767418**	**0.3433**	**4**
O55125	AGPNIYELR	1.020786626	2	3.018843412
O55125	FSGGYPALMDCMNK	1.021730643	2	2.978015423
O55125	GWDENVYYTVPLVR	0.633145678	2	3.475094318
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.548064663	3	4.732031345
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.071458374**	**0.99914**	**6**
O55171	ADAGGELDLAR	1.122029562	2	2.949822664
O55171	DGLLDVVEALQSPLVDKK	1.073857694	2	4.547800541
O55171	GGELGLAMASFLK	1.097430213	2	3.554387569
O55171	IEYFEEAVNYLR	1.10375954	2	3.315134525
O55171	SCWDEPLSITVR	1.027201155	2	3.910436153
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.040607727	3	4.010867119
O70127	**ABCBB Bile salt export pump**	**1.119144161**	**0.88029**	**4**
O70127	AGQITSEALSNIR	0.917478275	2	3.349183798
O70127	ILLLDEATSALDTESEK	1.17522311	2	4.49362278
O70127	ILLLDMATSALDNESEAR	0.625849887	2	3.979476452
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.034072615	3	3.506204844
O70133	**DHX9 ATP_dependent RNA helicase A**	**1.048676454**	**0.00835**	**3**
O70133	ELDALDANDELTPLGR	0.78839257	2	2.481321335
O70133	KMTPAYEIRAVGNK	1.063560161	2	2.406519651
O70133	TTQVPQYILDDFIQNDR	1.392913763	2	3.379849195
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**0.852164401**	**0.50029**	**2**
O70173	FLGHAQTFGGIKR	1.075051793	1	1.990355134
O70173	WTFSHPLEALGLLTSR	0.675487609	2	2.348977089
O70196	**PPCE Prolyl endopeptidase**	**1.450188706**	**2.2E-11**	**2**

O70196	SDGTETSTNLHQK	1.450813717	2	3.228951693
O70196	VFLDPNTLSDDGTVALR	1.452772671	2	3.717586279
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.067950359**	**0.02005**	**14**
O70199	EADLVFISVNTPTK	0.94541935	2	3.176719904
O70199	EQIVVDLSHPGVSADDQVSR	1.020087611	2	5.84453392
O70199	FSLQDPPNKKPK	0.979751899	2	2.466976166
O70199	IIDSLFNTVTDK	1.620979695	2	2.55908823
O70199	IIDSLFNTVTDKK	1.414202847	2	3.175640583
O70199	ILTTNTWSSELSK	1.535953758	2	3.217821836
O70199	INAWNSPTLPIYEPGLK	1.53727738	2	4.287862778
O70199	NLFFSTNIDDAIR	0.828396467	2	3.17403841
O70199	VLDGLHNELQTIGFQIETIGK	1.037425274	2	5.184099674
O70199	VLIGGDETPEGQR	1.197243784	2	3.841752768
O70199	VTVVDVNEAR	1.104876417	2	3.446736336
O70199	YWQQVIDMNDYQR	0.947866961	2	4.499551773
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.317065507	3	6.623196125
O70199	VLDGLHNELQTIGFQIETIGKK	0.912160665	3	3.364318848
O70251	**EF1B Elongation factor 1_beta**	**1.153208081**	**0.69889**	**4**
O70251	SIQADGLVWGSSK	1.161506503	2	4.078268051
O70251	SSILLDVKPWDDETDMTK	0.994685656	2	4.491770744
O70251	TPAGLQVLNDYLADK	1.197970285	2	4.135920048
O70251	SSILLDVKPWDDETDMTKLEECVR	1.079313587	3	5.005930901
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.166907892**	**6.9E-09**	**16**
O70351	GGIVGMTLPIAR	0.99752082	2	3.586050749
O70351	GLVAVITGGASGLGLSTAK	1.065734919	2	4.469354153
O70351	IDVAVNCAGIAVAIK	1.16480889	2	4.580410004
O70351	KLGGNCIFAPANVTSEK	1.34944922	2	4.976331234
O70351	KNQVHTLEDFQR	1.196484029	2	4.033670425
O70351	LGGNCIFAPANVTSEK	1.386136358	2	3.379862547
O70351	LVAGVMGQNEPDQGGQR	1.551249416	2	5.50302124
O70351	LVGQGATAVLLDVPNSEGETEAK	2.048671209	2	5.300712109
O70351	NFLASQVPFPSR	1.055029043	2	4.511791706
O70351	NQVHTLEDFQR	1.218974287	2	3.662584782
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.181268192	2	6.089731216
O70351	VINVNLIGTFNVIR	1.232649465	2	4.142115593
O70351	VVTIAPGLFATPLLTTLPDK	1.249205597	2	4.873594761
O70351	GVIINTASVAAFEGQVGQAAYSASK	0.584128899	3	3.997257233
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.068195994	3	5.53706646
O70351	LVGQGATAVLLDVPNSEGETEAKK	1.509050117	3	3.665767908
O70456	**1433S 14_3_3 protein sigma**	**1.447040724**	**0.00028**	**3**
O70456	VLSSIEQK	1.447367681	1	2.196409464
O70456	DSTLIMQLLR	1.058048697	2	3.697201252
O70456	NLLSVAYK	1.054074732	2	2.309886932

O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.125567177**	**0.05988**	**8**
O88428	GCTVWLTGLSGAGK	1.138945177	2	3.52943635
O88428	GFTGIDSDYEKPETPECVLK	1.25023126	2	4.953738213
O88428	GIHELFVPENK	1.147317047	2	3.036515951
O88428	KDLYEPTHGGK	1.057396679	2	2.65147543
O88428	NLGFSAGDREENIR	1.055409378	2	3.350319386
O88428	STNVVYQAHHVSR	1.142826162	2	2.904532194
O88428	VLSMAPGLTSVEIIPFR	1.482890113	2	3.412371635
O88428	IHESAGLPFFEIFVDAPLNICESR	0.750837828	3	4.041903973
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.054674747**	**9.2E-09**	**17**
O88600	AESEEMETSQAGSK	1.316843924	2	4.372684956
O88600	AFSDPFVEAEK	1.04574518	2	2.856027365
O88600	AGGIETIANEYSDR	0.792107757	2	3.283239841
O88600	FQESEERPK	1.282593534	2	2.710899115
O88600	FVSEDDRNNFTLK	1.393834824	2	2.878988743
O88600	GCALQCAILSPAFK	1.216619061	2	3.70980835
O88600	LEDTENWLYEDGEDQPK	1.476084555	2	4.365236282
O88600	MIMQDKLEK+Oxidation(1)	1.09668952	2	2.363325357
O88600	NFTTEQVTAMLLSK	1.104753022	2	3.315846205
O88600	SNLAYDIVQLPTGLTGIK	1.590636857	2	4.916441917
O88600	SVMDATQIAGLNCLR	1.092135969	2	2.59881258
O88600	TSTVDLPIESQLLWQLDR	1.194835717	2	3.862757683
O88600	VLATAFDTTLGGR	1.214185083	2	3.786184788
O88600	WNSPAEEGSSDCEVFPK	1.280709869	2	4.043489456
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	1.12534742	3	5.96833849
O88600	MQVDQEEPHTEEQQPQTPAENK	0.869152133	3	5.138442993
O88600	NKEDQYEHLDAADMTK	1.026184595	3	3.990259409
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.193201433**	**7.3E-06**	**21**
O88618	AFAACLGAIK	1.269829185	2	2.514373779
O88618	AGEYEALPEK	1.140449561	2	2.580494404
O88618	ALLDAAAFYCDK	1.458563414	2	3.888640881
O88618	ALLDAAAFYCDKEK	1.363446106	2	3.691847086
O88618	GVSMDECVLCAK	1.139397589	2	3.87451601
O88618	IIEYLVPDSGPEQSLLDASLR	1.168619708	2	5.580385208
O88618	ISSLLQEAK	1.565868264	2	2.541893005
O88618	KVQGIGWYLEEK	1.274286764	2	2.787406683
O88618	LAEELNVPVYLYGEAAQMPSR	1.142818715	2	4.737108231
O88618	LFVLEEEHR	1.371497934	2	2.92692852
O88618	LGLDSLAPFDPK	1.273673691	2	3.60929203
O88618	LIPPFHAASAQLTSLVDADAR	1.670213067	2	3.824771643
O88618	MGALDVCPFIPVR	1.096095841	2	4.078537464
O88618	MGALDVCPFIPVR+Oxidation(1)	1.194723383	2	2.807260513

O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.188199084	2	3.702193975
O88618	TCALQEGLR	1.38959046	2	3.176256657
O88618	TQAALVLGSLEAR	1.154311656	2	4.782528877
O88618	TVYTFVGQPECVVEGALSAAR	0.964814316	2	4.350530148
O88618	VQGIGWYLEEK	1.254660847	2	3.240135908
O88618	EAQELNLPVVGSQLVGLVPLK	1.109920353	3	4.431312561
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.55781825	3	4.034054279
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.217458292**	**0.01822**	**5**
O88637	HKGPPVFTQEER	1.265195019	2	2.99806428
O88637	TEIVPDRDGSDPYEEPK	1.151735971	2	2.944588661
O88637	TQGVSTTDLVGR	1.157571423	2	3.277355194
O88637	AHHSSQEMSSEYR	1.362764392	3	3.399446487
O88637	HNCDFCVHGNDITLTVDGR	1.047350319	3	4.30518198
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**1.374042167**	**0.47576**	**2**
O88656	ASSEGGAATGAGLDSLHK	1.091835667	2	4.152938366
O88656	NSVSQISVLSGGK	2.342397505	2	2.922357798
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**0.912474118**	**0.95752**	**2**
O88696	GQATDIAIQAEEIMK	1.034270849	2	2.553423643
O88696	VLVHPPQDGEDEPELVQK	0.912464805	3	3.972308159
O88735	**MAP7 Ensconsin**	**1.128902469**	**0.32252**	**2**
O88735	KTTEQRNGDIAK	1.190094022	2	2.507984638
O88735	TSAGTTDPEEATR	0.907920168	2	2.385059357
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.173004731**	**0.273**	**2**
O88761	DTSEDIEELVEPVAAHGPK	1.165327996	2	5.098733425
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.175439554	2	3.757750511
O88767	**PARK7 Protein DJ_1**	**0.980476934**	**0.89518**	**8**
O88767	ALVILAK	0.93737361	2	2.305561781
O88767	DVVICPDTSLEEAK	0.873023805	2	3.664283037
O88767	GAEEMETVIPVDIMR	0.991509148	2	3.481728315
O88767	GLIAAICAGPTALLAHEVGFGCK	0.983717736	2	4.359347343
O88767	VEKDGLILTSR	0.963178949	2	2.338358402
O88767	VTVAGLAGKDPVQCSR	1.21469905	2	4.362809181
O88767	KGLIAAICAGPTALLAHEVGFGCK	1.083214073	3	5.502694607
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	0.931026541	3	5.622874737
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**0.986955597**	**0.22727**	**3**
O88794	KKNEELGQLYR	1.371014845	2	2.376026392
O88794	SSQIGAVVSR	0.73364704	2	2.485803604
O88794	GLATGDSPLGPMTHHGEEDWVYER	1.022514637	3	3.564765453
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.0705182**	**0.1076**	**16**
O88813	AILEDLQK	1.141921685	1	2.208765745
O88813	FFQTQIK	1.026402581	1	1.933111548
O88813	ADISVVICDTPQK	1.096832745	2	3.111206293

O88813	AEYLGSCLLHK	1.236329119	2	2.499963999
O88813	FLLNLAIISK	1.301120487	2	2.986961603
O88813	GLAVSDNGPCLGYR	1.01200377	2	2.528308868
O88813	GSFEELCQNQCVK	1.055856562	2	4.732886314
O88813	IGFFQGDIR	1.731453505	2	3.331885576
O88813	LMITGAAPISTPVLTFFR	1.277106089	2	3.051851273
O88813	LVQGVIFSCGGK	1.19180791	2	2.888515949
O88813	SFLIGVVVPDPESLPSFAAK	1.21811974	2	3.605300665
O88813	SIFVHPEPFSIENGLLTPTLK	1.657606609	2	2.852311611
O88813	TVILMDPFDDDLMK	1.033445575	2	3.288805246
O88813	GAMLTHQNIVSNMAAFLK	1.004043845	3	3.643492937
O88813	SRPILQVFVHGESLR	1.028468223	3	3.534984589
O88813	TQEVLDKDGWLHTGDIGR	1.012901749	3	3.791064501
O88867	**KMO Kynurenine 3_monooxygenase**	**1.084396196**	**0.99968**	**5**
O88867	AVGLEDQIVSK	1.054363238	2	2.307790756
O88867	DFFLLPAQPMISVK	1.233418557	2	2.510764837
O88867	DITCDLIVGCDGAYSTVR	1.100465474	2	2.574083567
O88867	FNNDLSVCLPEFSR	1.01944602	2	3.96233511
O88867	NFPDAIPLMGEQALMR	0.969513331	2	3.578394413
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.111973557**	**0.65526**	**2**
O88941	ALESHAAAFK	1.127354132	2	2.454850435
O88941	MDPSLFPPVPLFSGVPSR	1.103408069	2	3.09273839
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.160992847**	**0.70973**	**4**
O88986	ALDLLMESNAIIQSMAAK+Oxidation(6)	1.38339901	2	2.522479773
O88986	GTDELLGVMDQVTIINSTLGK	1.022978314	2	2.616819859
O88986	MEAAGFTVSGADHPICPVMLGDAR+Oxidation(1)	1.052182874	2	2.623003721
O88986	VQISAVHSEEDIDR	1.250941088	2	4.038550377
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.138084336**	**9.9E-20**	**9**
O88989	EKMDLTAKELTEEK+Oxidation(3)	1.4029254	2	2.385555983
O88989	ELTEEKETAFEFLSSA	1.237725641	2	3.732053518
O88989	EVGVYEALKDDSWLK	0.715206286	2	3.829363585
O88989	FVEGLPINDFSR	0.986658702	2	3.44061923
O88989	GEFITTVQQR	1.179825095	2	3.874038935
O88989	LGVTADDVK	1.252904646	2	2.842994928
O88989	NVIIWGNHSSTQYPDVNHAK	1.271093873	2	5.666488647
O88989	VIVVGNPANTNCLTASK	1.212403213	2	5.565514088
O88989	DLDVAVLVGSMPR	0.903895893	3	3.854241133
O88990	**ACTN3 Alpha_actinin_3**	**0.989304828**	**0.9993**	**4**
O88990	ALDFIASK	1.055047173	2	2.622205973
O88990	CQLEINFNTLQTK	0.993342296	2	3.582752943
O88990	FAIQDISVEETSAK	1.043013922	2	3.919304609
O88990	HEAFESDLAAHQDR	0.893737442	3	3.957798719

O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**1.052379861**	**0.98589**	**6**
O88994	QLQQVGTVSK	1.096202741	1	2.284577608
O88994	CVLTTVDPDTGIIDR	1.009311931	2	4.195524216
O88994	GVSVCETECTDMGLR	1.018170396	2	3.428885937
O88994	RQLQQVGTVSK	1.032765084	2	3.281895161
O88994	SLYQSSPLFGMYFSVEK	1.477957413	2	3.726329327
O88994	LYPSESYLQNYEVAYPDCSPIHLISEASLVDLNTR	1.190767856	3	3.743320704
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.068982908**	**8.8E-07**	**7**
O89000	EGGADGVTATNTVSGLMGLK	1.012877335	2	3.347672701
O89000	GAVIVLGAGDTAFDCATSALR	1.38041058	2	4.819698334
O89000	GMGLACGQDPELVR	1.080651449	2	3.310385466
O89000	LENNFDDIK	1.019149576	2	2.655248404
O89000	QEYVGGLSTSEIPQFR	1.295453306	2	3.574075222
O89000	TEQDETGNWVEDEEQIVR	1.245818471	2	5.078963757
O89000	TFSLDKDIVTNVSPR	1.159817999	2	2.831040382
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.004346174**	**0.78623**	**2**
O89032	DDSDINTSKTGEVSKR	0.849576685	2	2.515427828
O89032	FPIEGGQKDPK	1.051565435	2	2.345448971
O89046	**COR1B Coronin_1B**	**0.530552994**	**0.01116**	**4**
O89046	KCEPIVMTVPR	0.676319813	2	2.601777077
O89046	NDQCYEDIR	0.146578374	2	2.824823141
O89046	NVLSDSKPAGYSR	1.22301876	2	2.927918911
O89046	SGVSTATAITDIPSGNLAGSGEAGK	1.130036697	2	4.232242107
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**0.986403416**	**0.92599**	**7**
O89049	IEQIEAGTPGR	1.125086622	2	2.984171152
O89049	IEQIEAGTPGRLK	1.161673665	2	2.361508608
O89049	LELTPVAIQAGR	1.03841026	2	2.811136246
O89049	STNSEETIEDEFNTVLLAVGR	1.067720885	2	2.323794603
O89049	VMVLDFVTPTPLGTR	1.027791558	2	2.785917997
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.532718482	2	2.405636787
O89049	WGLGGTCVNVGCIPK	1.07926168	2	3.565220356
P00173	**CYB5 Cytochrome b5**	**1.045119325**	**0.9877**	**6**
P00173	VYDLTK	1.122824885	1	1.969877243
P00173	EQAGGDATENFEDVGHSTDAR	1.101211877	2	5.446107864
P00173	FLEEHPGGEEVLR	1.06807341	2	4.166350365
P00173	STWVILHHK	1.230164841	2	2.913404942
P00173	TYIIGELHPDDR	0.99374542	2	4.062681675
P00173	YYTLEEIQK	1.043029987	2	2.887542486
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.005888634**	**0.91776**	**7**
P00388	GMSADPEEYDLADLSSLPEIDK	1.142723463	2	5.095649242
P00388	RSDEDYLYR	0.975173941	2	2.843274117
P00388	SYENQKPPFDAK	1.005396049	2	3.2051301

P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	0.872423622	3	4.305461407
P00388	LIHEGGAHIYVCGDAR	1.314563772	3	3.844526529
P00388	TNVLYELAQYASEPSEQEHLHK	0.843415222	3	3.614204884
P00388	VHPNSVHICAVAVEYEAK	1.077480384	3	3.569468498
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.034709472**	**0.99823**	**3**
P00406	ILYMMDEINNPVLTVK	0.988557935	2	3.601320982
P00406	LLEVDNR	1.077699381	2	2.528322935
P00406	VVLPMELPIR	1.014007416	2	2.517837524
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.249320859**	**0.98197**	**19**
P00481	QSDLDILAK	1.05174755	1	1.964445233
P00481	GEYLPLLQGK	1.102092986	2	3.0811553
P00481	GGNVLITDTWISMGQEDEK	1.0250244	2	5.548265934
P00481	GGNVLITDTWISMGQEDEKK	1.024000723	2	4.82241869
P00481	GYEPDPNIVK	1.077737678	2	2.582421303
P00481	LQAFQGYQVTMK	1.878171662	2	4.246646404
P00481	LQAFQGYQVTMK+Oxidation(11)	1.565886068	2	2.322446585
P00481	LSMTNDPLEAAR	1.29018101	2	2.910248756
P00481	QKGEYLPLLQGK	1.237463704	2	3.666311979
P00481	SLGMIFEK	1.116724229	2	2.391788483
P00481	SLGMIFEK+Oxidation(4)	0.899821997	2	2.397035122
P00481	SLVFPEAENR	1.050783137	2	2.674598455
P00481	SLVFPEAENRK	1.170409047	2	2.883150101
P00481	VLSSMTDAVLAR	1.251011408	2	3.833729982
P00481	VLSSMTDAVLAR+Oxidation(5)	1.14555884	2	2.686970949
P00481	YGKPVQSQVQLK	0.892741765	2	2.794847965
P00481	FGMHLQAATPK	1.220699592	3	3.646673918
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.393431137	3	4.473722458
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.384814531	3	7.252273083
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.568317339**	**0.00156**	**2**
P00502	FIQSPEDLEK	0.622446398	2	2.770030022
P00502	WLLAAAGVEFDEK	0.498796539	2	4.530766964
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.117538423**	**4.5E-06**	**19**
P00507	KQWLQEVK	1.24235527	1	2.394308805
P00507	QWLQEVK	1.3397754	1	2.061826468
P00507	ASAELALGENSEVLK	1.166672361	2	4.63685751
P00507	DAGMQLQGYR	0.458112277	2	2.809578657
P00507	DDNGKPYVLPSVR	0.980335141	2	3.283000469
P00507	EYLPIGGLADFCK	0.877988847	2	2.619502306
P00507	FVTVQTISGTGALR	1.237511728	2	4.803735733
P00507	ISVAGVTSGNVGYLAHAIHQVTK	1.521048523	2	2.675931931
P00507	KMNLGVGAYR	1.161528485	2	2.545520306
P00507	MNLGVGAYR	1.309066959	2	3.010416746
P00507	NLDKEYLPIGGLADFCK	1.122449801	2	5.871150494

P00507	NMGLYGER	1.123275791	2	2.636112928
P00507	TCGFDFSGALEDISK	1.108527144	2	5.022319317
P00507	VGAFTVVCK	1.184967635	2	3.345834494
P00507	VGASFLQR	1.466069893	2	3.112003326
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.224683457	3	5.266993046
P00507	HFIEQGINVCLCQSYAK	1.224956726	3	5.263133049
P00507	ILIRPLYSNPPLNGAR	2.869399583	3	3.353263378
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	0.915846282	3	4.523588181
P00564	**KCRM Creatine kinase M_type**	**0.630904694**	**0.00373**	**7**
P00564	GGDDLDPNYVLSSR	0.606516181	2	4.649000168
P00564	GQSIDDMIPAQK	0.450488201	2	2.96390152
P00564	GTGGVDTAAVGAVFDISNADR	0.571419841	2	5.905533791
P00564	LGSSEVEQVQLVVDGVK	0.551706564	2	4.613338947
P00564	LSVEALNSLTGEFK	0.653696312	2	4.163503647
P00564	RGTGGVDTAAVGAVFDISNADR	0.386626542	2	4.330402374
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	0.597766191	3	6.314071655
P00787	**CATB Cathepsin B**	**1.354124765**	**9.9E-20**	**3**
P00787	GENHCGIESEIVAGIPR	1.354885631	2	4.860041618
P00787	MCEAGYSTSYKEDK	1.073142186	2	3.92348814
P00787	HEAGDVMGGHAIR	1.171832129	3	3.965120792
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.380489483**	**9.9E-20**	**18**
P00884	ELSEIAQR	0.407830038	1	1.935182571
P00884	GIVVGIK	1.402928907	1	1.913529992
P00884	ALQASALAAWGGK	1.472391299	2	4.771947384
P00884	ATQEAFMK	1.195671467	2	2.684629679
P00884	ETTIQGLDGLSER	0.835929168	2	3.892059803
P00884	FPALTSEQK	1.200752697	2	2.364191294
P00884	GILAADESVGTMGNR	1.210144113	2	5.668917179
P00884	GILAADESVGTMGNR+Oxidation(12)	1.299306654	2	5.025375843
P00884	IKVENTEENR	1.251354727	2	2.6895051
P00884	IKVENTEENRR	1.568095285	2	2.777957439
P00884	ISDQCPSSLAIQENANALAR	1.38142032	2	6.619446754
P00884	KELSEIAQR	1.306718836	2	2.615085125
P00884	LDQGGAPLAGTNK	1.277308996	2	4.578846931
P00884	YTPEQVAMATVTALHR	1.324920157	2	4.813942909
P00884	YTPEQVAMATVTALHR+Oxidation(8)	1.355662436	2	3.666167736
P00884	KYTPEQVAMATVTALHR	1.358483207	3	6.198992729
P00884	KYTPEQVAMATVTALHR+Oxidation(9)	1.329488682	3	3.544509649
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	0.87654109	3	5.149598122
P01026	**CO3 Complement C3**	**1.211184613**	**2.5E-12**	**17**
P01026	ACEPGVDYVYK	1.091999379	2	2.944654703
P01026	ADIGCTPGSGK	1.217400845	2	2.792225361
P01026	AFYEHAPK	1.259440388	2	2.356638432

P01026	EYVLPSFEVLVEPTEK	1.167194518	2	3.434158802
P01026	IFTVDNNLLPVGK	1.269662345	2	3.388560057
P01026	IGLQEVEVK	1.135712305	2	2.590595484
P01026	NEQVEIRAVLFNYR	1.171403251	2	2.314445019
P01026	QNEGFSLTAK	1.127791377	2	2.383964777
P01026	SDVDEDIIPEEDIISR	0.975268189	2	4.571992397
P01026	SGSDEVQAGQER	1.31471639	2	4.130421162
P01026	TNQGLQTDQR	1.095957125	2	2.85435462
P01026	TVLTGATGHLNR	1.246266583	2	2.951196671
P01026	TVVIVIETPDGVPIKR	1.157978489	2	3.000169039
P01026	VLIEDGSGEAVLSR	1.236719514	2	3.827539206
P01026	RVPVVTQGSDAQALTQDDGVAK	1.239118332	3	5.303939819
P01026	TNQGLQTDQREDPECAKPAAR	1.32308041	3	4.071914196
P01026	VELKPGDNLNVNFHLR	1.037227669	3	4.008153915
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.744285078**	**1**	**9**
P01946	FLASVSTVLTSK	0.637902154	2	4.05183506
P01946	IGGHGGEYGEEALQR	0.766819808	2	4.977880001
P01946	LRVDPVNFK	0.860015815	2	2.538651943
P01946	MFAAFPTTK	0.571101784	2	3.093313217
P01946	MFAAFPTTK+Oxidation(1)	0.754462667	2	2.654871702
P01946	TYFSHIDVSPGSAQVK	0.666323824	2	5.215978146
P01946	AADHVEDLPGALSTLSDLHAHK	0.772370756	3	7.673351288
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.660336774	4	5.808580399
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.816299016	4	6.229043961
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.603577299**	**1**	**4**
P02089	GTFASLSELHCDK	0.767987886	2	3.688642263
P02089	LHVDPENFR	0.728339163	2	2.75852704
P02089	YFDSFGDLSSASAIMGNPK	0.652667467	2	6.615319729
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(15)	0.608369755	2	4.957607269
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.758574544**	**1**	**9**
P02091	EFTPCAQAAFQK	0.626606948	2	3.126243353
P02091	GTFAHLSELHCDK	0.744971218	2	4.473133087
P02091	KVINAFNDGLK	0.706426871	2	3.701747179
P02091	LLGNMIVIVLGHHLGK	0.962582923	2	3.3463974
P02091	VINAFNDGLK	0.71954057	2	3.00209403
P02091	VNPDDVGGEALGR	0.627036339	2	4.293959141
P02091	VVAGVASALAHK	0.788361725	2	3.822754622
P02091	GTFAHLSELHCDKLHVDPENFR	0.767383294	3	4.592807293
P02091	LLGNMIVIVLGHHLGKEFTPCAQAAFQK	0.648752566	3	5.415453434
P02401	**RLA2 60S acidic ribosomal protein P2**	**0.946931937**	**1.8E-14**	**7**
P02401	VISELNGK	1.307087985	1	2.064009905
P02401	ILDSVGIEADDER	1.106321954	2	4.60929203
P02401	ILDSVGIEADDERLNK	1.375225343	2	3.196656704

P02401	KILDSVGIEADDER	0.61631914	2	3.942422867
P02401	NIEDVIAQGVGK	1.012520137	2	4.772317886
P02401	YVASYLLAALGGNSNPSAK	1.300307634	2	5.79398632
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.394562738	3	6.558177471
P02564	**MYH7 Myosin_7**	**0.657591345**	**0.19818**	**25**
P02564	ANDDLKENIAIVER	0.564869266	2	3.362997055
P02564	DLEEATLQHEATAAALR	1.0982568	2	5.402421951
P02564	EQYEEETEAK	0.671678323	2	2.504103661
P02564	GTLEDQIIQANPALEAFGNAK	0.7245935	2	5.170654297
P02564	IEDEQALGSQLQK	0.546875442	2	4.073475361
P02564	IEELEEELEAER	0.381833356	2	4.111586571
P02564	ILNPAAIPEGQFIDSR	1.052455554	2	3.354573011
P02564	KLAEQELIETSER	0.819967667	2	3.976933956
P02564	KMEGDLNEMEIQLSHANR+Oxidation(2)	1.024797881	2	2.501081228
P02564	KVQHELDEAEER	1.248986437	2	2.791472197
P02564	LDEAEQIALK	0.589820464	2	3.369658709
P02564	LELDDVTSNMEQIIK	1.030330487	2	3.493429899
P02564	LQDAEEAVEAVNAK	0.565062758	2	4.711004734
P02564	LQNEIEDLMVDVER	0.822019119	2	3.445061207
P02564	MDADLSQLQTEVEEAVQECR	0.875544183	2	4.805260658
P02564	NLQEEISDLTEQLGSTGK	0.728725144	2	5.673125744
P02564	NLTEEMAGLDEIIVK	1.072320671	2	3.139538288
P02564	NNLLQAELEELR	0.631979351	2	2.861516237
P02564	QAEEAEEQANTNLSK	0.967143159	2	4.78076458
P02564	QKYEESQSELESSQK	1.157284001	2	2.95824337
P02564	TLEDQMNEHR	0.733129014	2	2.593061209
P02564	VQLLHSQNTSLINQK	0.649955503	2	3.847197294
P02564	VVDSLQTSLDAETR	0.673692777	2	2.727909327
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.524549134	3	5.485077381
P02564	QLEAEKLELQSALEEAEASLEHEEGK	0.530538303	3	4.503925323
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**0.515090209**	**0.00112**	**8**
P02600	ALGTNPTNAEVK	0.475423112	2	3.224626541
P02600	ALGTNPTNAEVKK	0.485657528	2	2.720016956
P02600	DQGGYEDFVEGLR	0.413358314	2	3.587915659
P02600	IEFEQFLPMMQAISNNK	1.052606097	2	2.736751795
P02600	ITLSQVGDVLR	0.591606596	2	3.089337349
P02600	KIEFEQFLPMMQAISNNK	0.666226416	2	5.458103657
P02600	VLGNPSNEEMNAK	0.419097318	2	3.849383593
P02600	VLGNPSNEEMNAK+Oxidation(10)	0.855528682	2	2.573149681
P02625	**PRVA Parvalbumin alpha**	**0.750835726**	**0.31735**	**4**
P02625	AIGAFTAADSFDHKK	0.218047624	2	3.911603212
P02625	SGFIEEDELGSILK	1.009790686	2	2.851767778
P02625	TLMAAGDKDGDGK	0.85860526	2	3.179671288

P02625	TLMAAGDKDGDGK+Oxidation(3)	0.317242421	2	3.359597206
P02650	**APOE Apolipoprotein E**	**1.311608661**	**0.6047**	**13**
P02650	ELEEQLGPVAEETR	0.971810118	2	4.331418037
P02650	GRLEEVGNQAR	1.12246003	2	3.700950384
P02650	GWFEPLVEDMQR	1.201401613	2	3.239335775
P02650	LEEVGNQAR	1.049550946	2	2.56681776
P02650	LGADMEDLR	1.104729784	2	3.03110671
P02650	LGPLVEQGR	1.18814855	2	2.309450865
P02650	LQAEIFQAR	1.369995936	2	2.711163044
P02650	MEEQTQQIR	0.759033101	2	3.238872528
P02650	MEEQTQQIR+Oxidation(1)	1.172441212	2	2.876990795
P02650	NEVNTMLGQSTEELR	1.035038613	2	4.490174294
P02650	SKMEEQTQQIR	1.090242481	2	3.2987957
P02650	SKMEEQTQQIR+Oxidation(3)	1.528990168	2	3.560912132
P02650	TANLGAGAAQPLR	0.974673889	2	2.37243557
P02680	**FIBG Fibrinogen gamma chain**	**1.184636828**	**0.91405**	**3**
P02680	VGPESDKYR	1.162196203	2	2.592888117
P02680	YEALLLTHESSIR	1.106709534	2	3.71654582
P02680	YLQDIYTSNK	1.078174337	2	2.785181999
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.080191951**	**9.9E-20**	**13**
P02692	MVTTFK	1.180588936	1	1.913039923
P02692	MVTTFK+Oxidation(1)	1.465288859	1	2.022849083
P02692	AMGLPEDLIQK	1.145505835	2	3.633579254
P02692	AMGLPEDLIQK+Oxidation(2)	1.266888278	2	3.373602867
P02692	GVSEIVHEGK	1.192246681	2	3.492818117
P02692	GVSEIVHEGKK	1.215989028	2	3.327571154
P02692	SVTEFNGDTITNTMTLGDIVYK	1.247193376	2	5.653516293
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(14)	1.076583906	2	5.642945766
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.366411255	2	3.735480309
P02692	YQVQSQENFEPFMK	1.247666649	2	6.053904533
P02692	YQVQSQENFEPFMK+Oxidation(13)	1.359652031	2	5.280806541
P02692	VIHNEFTLGEECELETMTGEK	1.240152039	3	6.306419849
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(17)	1.271776045	3	5.510181904
P02696	**RET1 Retinol_binding protein 1**	**1.195343103**	**0.99866**	**8**
P02696	ALDVNVALR	1.085862948	2	3.277495623
P02696	CMTTVSWDGDKLQCVQK	1.072905199	2	4.543385029
P02696	EFEEDLTGIDDR	0.966497599	2	2.343901157
P02696	EFEEDLTGIDDRK	1.04065049	2	2.752989054
P02696	GWTQWIEGDELHLEMR	1.075061789	2	4.309483051
P02696	MLSNENFEEYLR	1.10852486	2	3.630520821
P02696	MLSNENFEEYLR+Oxidation(1)	1.427743388	2	2.969955683
P02696	NYIMDFQVGKEFEEDLTGIDDRK	1.135349408	3	3.465123177
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.032277483**	**0.9487**	**6**

P02706	LVESQLEK	1.015507205	1	2.067113876
P02706	QLVSDVR	0.452671297	1	2.070900679
P02706	SLSCQMAALR	0.923197654	2	3.051878691
P02706	WVCETELGK	1.008541784	2	2.362579584
P02706	WVDGTDYETGFK	1.050998173	2	3.464968681
P02706	DYQDFQHLDNENDHHQLQR	1.173156747	3	3.414072037
P02770	**ALBU Serum albumin**	**1.251425171**	**1**	**27**
P02770	SIHTLFGDK	0.514475916	1	2.283918619
P02770	AADKDNCFATEGPNLVAR	0.770237081	2	4.928193569
P02770	AETFTFHSDICTLPDKEK	1.193869577	2	3.745814562
P02770	CCSGSLVER	0.736407423	2	3.231502295
P02770	CCTLPEAQR	0.895371044	2	2.773377895
P02770	DLGEQHFK	0.7582788	2	2.309936047
P02770	DNCFATEGPNLVAR	0.629476222	2	3.363330841
P02770	DNYGELADCCAK	0.174535981	2	3.366791725
P02770	ECCHGDLLECADDR	0.91596082	2	3.936957836
P02770	ECCHGDLLECADDRAELAK	1.069564073	2	5.328629017
P02770	GLVLIAFSQYLQK	0.97503866	2	4.08360672
P02770	KYEATLEK	1.091602341	2	2.693745852
P02770	LQACCDKPVLQK	1.173216048	2	4.277095318
P02770	LRDNYGELADCCAK	0.375980221	2	3.34416151
P02770	LVQEVTDFAK	1.113955797	2	3.708904505
P02770	QEPERNECFLQHK	0.231377929	2	2.355108976
P02770	TCVADENAENCDK	1.013594602	2	4.645998478
P02770	TNCELYEK	1.089449344	2	2.821719646
P02770	TVMGDFAQFVDK	0.701924264	2	4.271928787
P02770	YMCENQATISSK	1.026436545	2	4.414502621
P02770	YMCENQATISSK+Oxidation(2)	0.988624156	2	3.68944335
P02770	YNEVLTQCCTESDK	0.847958769	2	5.734190464
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	0.943675023	3	5.322396278
P02770	FKDLGEQHFK	1.124087356	3	4.180323124
P02770	INKECCHGDLLECADDRAELAK	1.156711545	3	5.444173336
P02770	KQTALAELVK	1.111171881	3	4.126062393
P02770	RHPDYSVSLLLR	1.124569026	3	4.809328079
P02803	**MT1 Metallothionein_1**	**1.115660231**	**0.63007**	**2**
P04041	**GPX1 Glutathione peroxidase 1**	**1.103298015**	**0.00096**	**10**
P04041	FLVGPDGVPVR	1.039460243	2	3.246809483
P04041	FLVGPDGVPVRR	1.237142116	2	2.319866896
P04041	GLVVLGFPCNQFGHQENGK	1.300606658	2	4.285676956
P04041	NALPAPSDDPTALMTDPK	0.994902074	2	3.474921227
P04041	NDISWNFEK	1.03850122	2	2.904446125
P04041	NEEILNSLK	1.046113352	2	2.541545153
P04041	YIIWSPVCR	1.086119585	2	2.936386824

P04041	YVRPGGGFEPNFTLFEK	1.272024374	2	4.581185818
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.975957461	3	4.329761028
P04041	TIDIEPDIEALLSK	1.269373932	3	4.279593945
P04167	**CP2B2 Cytochrome P450 2B2**	**1.063281012**	**0.9998**	**2**
P04167	GTIAVIEPIFK	1.104070483	2	2.560103416
P04167	NLQEILDYIGHIVEK	1.063279543	2	4.228871822
P04176	**PH4H Phenylalanine_4_hydroxylase**	**0.937537473**	**6.3E-07**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	0.664512609	2	4.140900135
P04176	LRPVAGLLSSR	3.20996589	2	2.711697578
P04176	NDIGATVHELSR	1.12991262	2	3.75592804
P04176	QFADIAYNYR	0.870283808	2	2.815701008
P04176	SFAQFSQEIGLASLGAPDEYIEK	0.704954797	2	4.825675011
P04176	VEVLDNTQQLK	0.99015647	2	3.84534359
P04176	VEYTEEEK	1.011297439	2	2.696576834
P04176	VEYTEEEKQTWGTVFR	1.11278363	2	4.336387634
P04176	EDNIPQLEDVSQFLQTCTGFR	0.950378335	3	4.727074146
P04176	FANQILSYGAELDADHPGFK	0.598734663	3	3.979325771
P04176	FANQILSYGAELDADHPGFKDPVYR	0.849419906	3	5.362295151
P04176	ILADSINSEVGILCNALQK	1.245975797	3	6.608252525
P04176	LNKDEYEFFTYLDKR	2.947870696	3	3.605403185
P04176	TACQEYSVTEFQPLYYVAESFSDAK	0.689789147	3	3.692085981
P04176	THACYEHNHIFPLLEK	1.206492276	3	4.730014801
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.019314913	3	5.301527023
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.646576773**	**1.6E-05**	**9**
P04182	AFYNNVLGEYEEYITK	0.6374993	2	4.485980988
P04182	GIYMWDVEGR	0.775769464	2	2.718210936
P04182	GLLNAIVIR	0.651878438	2	3.141702414
P04182	HQVLFIADEIQTGLAR	0.465140923	2	4.04962492
P04182	IIEAMKSQVDK	0.826793359	2	2.332972288
P04182	KTEQGPPSSEYIFER	0.744418093	2	3.922631025
P04182	TEQGPPSSEYIFER	0.637218944	2	4.121782303
P04182	VLPMNTGVEAGETACK	0.674235425	2	3.984940052
P04182	WLAVDHENVRPDIVLLGK	0.407961262	2	4.935504913
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.217203735**	**0.64316**	**4**
P04256	EDSQRPGAHLTVK	1.110551149	2	3.220856905
P04256	IEVIEIMTDR	1.109826916	2	3.135530233
P04256	NQGGYGGSSSSSSYGSGR	1.182740332	2	4.731561184
P04256	YHTVNGHNCEVR	1.263368261	2	3.317225933
P04276	**VTDB Vitamin D_binding protein**	**1.245975973**	**9.9E-20**	**2**
P04276	SCESDAPFPVHPGTSECCTK	1.369275257	2	4.741000652
P04276	YCSSQIDAEMR	0.930636291	2	2.875705004
P04355	**MT2 Metallothionein_2**	**1.086785687**	**0.3197**	**2**
P04462	**MYH8 Myosin_8 (Fragment)**	**0.716677171**	**0.33934**	**3**

P04462	LQHELEEAEER	0.691988434	2	3.649016142
P04462	RAALQAEIEELR	0.505889478	2	3.875791788
P04462	KLQHELEEAEER	0.633278158	3	3.893842459
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**0.548578003**	**0.2343**	**7**
P04466	AAAEGSSNVFSMFDQTQIQEFK	0.809587482	2	4.493775845
P04466	GADPEDVITGAFK	0.774778398	2	3.849882364
P04466	KQFLEELLTTQCDR	0.749920015	2	4.107820034
P04466	NICYVITHGDAKDQE	0.459996564	2	4.703526497
P04466	NMWAAFPPDVGGNVDYK	0.475450733	2	3.095844746
P04466	QFLEELLTTQCDR	0.62734394	2	3.777317047
P04466	LKGADPEDVITGAFK	0.712503121	3	4.462659359
P04550	**PTMS Parathymosin**	**0.92474017**	**1.1E-12**	**4**
P04550	SVEAAAELSAK	0.834999105	2	3.644512892
P04550	TAEEEDEADPK	0.864635517	2	3.32467556
P04550	TAEEEDEADPKR	1.172091225	2	3.700356007
P04550	RTAEEEDEADPKR	1.090210001	3	4.034061432
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**0.935916353**	**9.9E-20**	**16**
P04636	EGVIECSFVQSK	0.506119646	1	3.036523104
P04636	AGAGSATLSMAYAGAR	1.013022436	2	4.657131672
P04636	ANTFVAELK	1.107787353	2	2.778107643
P04636	ETECTYFSTPLLLGK	0.387408366	2	3.503462315
P04636	FVFSLVDAMNGK	1.192528529	2	4.426695824
P04636	GCDVVVIPAGVPR	1.08844629	2	4.370471001
P04636	GYLGPEQLPDCLK	1.09262132	2	4.126103401
P04636	IFGVTTLDIVR	1.397644158	2	3.60158062
P04636	IQEAGTEVVK	1.05959094	2	2.880748272
P04636	MIAEAIPELK	0.905070301	2	3.211016655
P04636	MIAEAIPELK+Oxidation(1)	1.33580916	2	2.539983034
P04636	TIIPLISQCTPK	1.045307628	2	3.511655331
P04636	VAVLGASGGIGQPLSLLLK	0.981110586	2	6.118106365
P04636	VDFPQDQLATLTGR	1.071322075	2	4.869530678
P04636	VNVPVIGGHAGK	1.050838653	2	3.210429192
P04636	LTLYDIAHTPGVAADLSHIETR	1.290802284	3	7.018770218
P04639	**APOA1 Apolipoprotein A_I**	**0.927719214**	**1**	**6**
P04639	AKPALDDLGQGLMPVLEAWK	1.004097593	2	3.742036819
P04639	LQEQLGPVTQEFWANLEK	1.002559275	2	4.89842701
P04639	NEMNKDLENVK	1.047590612	2	3.4349823
P04639	QLNLNLLDNWDTLGSTVGR	0.852118563	2	4.502742767
P04639	VKDFATVYVDAVK	1.143778999	2	3.111225128
P04639	WNEEVEAYR	0.897651633	2	2.370805979
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.036845798**	**4E-10**	**22**
P04642	NVNIFK	1.198959336	1	2.087940931

P04642	DLADELALVDVIEDK	1.08301851	2	5.479312897
P04642	DLADELALVDVIEDKLK	1.369467798	2	4.615240097
P04642	DQLIVNLLK	0.886385821	2	2.945695877
P04642	DQLIVNLLKEEQVPQNK	1.199687124	2	4.867084026
P04642	EDVFLSVPCILGQNGISDVVK	1.124801154	2	4.798501492
P04642	FIIPNVVK	1.107478758	2	2.394251108
P04642	GEMMDLQHGSLFLK	1.268245514	2	3.855429649
P04642	GEMMDLQHGSLFLK+Oxidation(3)	1.368909505	2	3.452834368
P04642	GEMMDLQHGSLFLK+Oxidation(4)	1.364676234	2	3.147318602
P04642	KSADTLWGIQK	1.172786851	2	3.09570241
P04642	LKGEMMDLQHGSLFLK	1.336645435	2	3.999520063
P04642	LLIVSNPVDILTYVAWK	1.308397954	2	4.876182556
P04642	QVVDSAYEVIK	1.102782304	2	3.119016409
P04642	RVHPISTMIK	1.022188096	2	2.372539759
P04642	SADTLWGIQK	1.122018735	2	3.940787554
P04642	SLNPQLGTDADK	0.938588084	2	2.674868107
P04642	SLNPQLGTDADKEQWK	1.09051496	2	4.840538979
P04642	SLNPQLGTDADKEQWKDVHK	1.281692959	2	4.680558205
P04642	VTLTPDEEAR	1.103414475	2	2.928517342
P04642	GLYGIKEDVFLSVPCILGQNGISDVVK	1.684702313	3	3.354486704
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.720537067	3	5.727637768
P04644	**RS17 40S ribosomal protein S17**	**1.195611068**	**1.2E-05**	**4**
P04644	DNYVPEVSALDQEIIEVDPDTK	1.04192164	2	4.33566761
P04644	LGNDFHTNK	1.202883584	2	2.923883677
P04644	LLDFGSLSNLQVTQPTVGMNFK	1.462003044	2	4.119847298
P04644	VCEEIAIIPSK	1.019111041	2	3.114224672
P04692	**TPM1 Tropomyosin alpha_1 chain**	**0.792348045**	**0.26906**	**10**
P04692	AISEELDHALNDMTSI	0.596156402	2	2.627863169
P04692	AQKDEEKMEIQEIQLK	0.82169778	2	3.851212263
P04692	GTEDELDKYSEALK	1.17039542	2	2.308058023
P04692	KLVIIESDLER	0.767737808	2	3.653575182
P04692	LDKENALDR	0.84612377	2	2.389130354
P04692	LKGTEDELDK	0.64839868	2	2.621469021
P04692	LVIIESDLER	0.707298989	2	3.233721972
P04692	MEIQEIQLK	0.934506283	2	2.850198507
P04692	QLEDELVSLQK	0.692850341	2	2.487179518
P04692	SIDDLEDELYAQK	0.431961006	2	3.702502012
P04694	**ATTY Tyrosine aminotransferase**	**1.078463412**	**0.54647**	**2**
P04762	**CATA Catalase**	**5.829707923**	**2.4E-13**	**30**
P04762	DYPLIPVGK	0.780643024	1	2.529969692
P04762	DAMLFPSFIHSQK	0.598281163	2	2.354496956
P04762	DAQLFIQR	0.479471306	2	3.089246988
P04762	EAETFPFNPFDLTK	0.807356087	2	4.349022865

P04762	FNSANEDNVTQVR	0.906977176	2	4.709765911
P04762	FSTVAGESGSADTVR	0.890307101	2	5.190100193
P04762	FSTVAGESGSADTVRDPR	0.953186828	2	2.966955423
P04762	GAGAFGYFEVTHDITR	0.973752909	2	5.118216038
P04762	GPLLVQDVVFTDEMAHFDR	1.050191151	2	5.71143198
P04762	HMNGYGSHTFK+Oxidation(2)	1.053803259	2	2.76322937
P04762	LAQEDPDYGLR	1.223435999	2	2.639903784
P04762	LFAYPDTHR	1.233747997	2	2.876427174
P04762	LGPNYLQIPVNCPYR	1.169157433	2	4.395477295
P04762	LNIMTAGPR	1.038499739	2	3.16048336
P04762	LVNANGEAVYCK	1.264272	2	4.050684452
P04762	NAIHTYVQAGSHIAAK	1.050274962	2	5.337962627
P04762	NFTDVHPDYGAR	0.932045154	2	4.083245277
P04762	NLPVEEAGR	0.939210422	2	2.383164167
P04762	RFNSANEDNVTQVR	1.023678389	2	5.180953979
P04762	VFEHIGK	0.997638009	2	2.443536043
P04762	VFEHIGKR	0.907399159	2	2.391176224
P04762	VLNEEER	1.023921698	2	2.863687515
P04762	VQALLDQYNSQKPK	0.996539389	2	5.120443821
P04762	VWPHKDYPLIPVGK	1.037206207	2	3.852797747
P04762	FYTEDGNWDLVGNNTPIFFIR	1.558867267	3	6.274604797
P04762	HMNGYGSHTFK	0.863942967	3	4.200131893
P04762	LCENIANHLK	1.129418096	3	4.051400661
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	0.362276503	3	6.38896513
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK+Oxidation(19)	0.573918435	3	3.917787075
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	0.957371023	4	5.17080307
P04764	**ENOA Alpha_enolase**	**0.990729975**	**0.99863**	**17**
P04764	AGYTDQVVIGMDVAASEFYR	0.861664533	2	5.546107769
P04764	DATNVGDEGGFAPNILENK	0.885288955	2	5.442581654
P04764	DYPVVSIEDPFDQDDWDAWQK	0.995230076	2	4.741069317
P04764	FTATAGIQVVGDDLTVTNPK	0.807375211	2	5.175417423
P04764	GNPTVEVDLYTAK	1.265926136	2	4.058582783
P04764	IDQLMIEMDGTENK	0.905299639	2	4.64170599
P04764	IEEELGSK	1.13629022	2	2.400004625
P04764	IGAEVYHNLK	1.178254078	2	3.321850538
P04764	KLNVVEQEK	1.044095896	2	2.353833437
P04764	LNVVEQEK	1.082990107	2	2.733103514
P04764	SCNCLLLK	1.209693688	2	3.057877779
P04764	VNQIGSVTESLQACK	1.03014398	2	5.182933331
P04764	YITPDQLADLYK	1.083301195	2	3.319537878
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.034837253	3	6.571229458
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.148725578	3	6.04055357

P04764	LNVVEQEKIDQLMIEMDGTENK	1.134792869	3	4.596259594
P04764	SFIKDYPVVSIEDPFDQDDWDAWQK	0.960659449	3	4.354124546
P04785	**PDIA1 Protein disulfide_isomerase**	**1.22208234**	**9.9E-20**	**24**
P04785	SVSDYDGK	1.572140279	1	2.259652615
P04785	DHENIVIAK	1.018585127	2	2.916556597
P04785	HNQLPLVIEFTEQTAPK	1.188146192	2	5.613448143
P04785	ILEFFGLK	1.192762032	2	3.144329309
P04785	ILFIFIDSDHTDNQR	1.250690456	2	3.840448856
P04785	ITQFCHHFLEGK	0.879710232	2	3.08998704
P04785	LITLEEEMTK	1.078938469	2	3.710759163
P04785	LKAEGSEIR	1.355077264	2	2.426496029
P04785	LLDFIK	1.160584159	2	2.413236618
P04785	MDSTANEVEAVK	1.036812967	2	4.234432697
P04785	MDSTANEVEAVK+Oxidation(1)	1.176345336	2	3.730894804
P04785	NFEEVAFDEK	1.124208788	2	3.200937033
P04785	NFEEVAFDEKK	1.163695321	2	4.047382355
P04785	NNFEGEITK	1.148116387	2	2.55672431
P04785	THILLFLPK	1.094639187	2	2.982904911
P04785	TVIDYNGER	1.10190824	2	2.66856885
P04785	VDATEESDLAQQYGVR	0.911635256	2	5.429687977
P04785	YQLDKDGVVLFK	1.208447627	2	3.839205742
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(6)	1.753960703	3	3.873647928
P04785	LGETYKDHENIVIAK	1.298960881	3	5.082270622
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.004684179	3	6.293552399
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.16523621	3	6.733226299
P04785	YKPESDELTAEK	1.161324124	3	4.453520298
P04785	IKPHLMSQELPEDWDKQPVK	1.432116987	4	5.603489399
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.194696928**	**9.9E-20**	**13**
P04797	GAAQNIIPASTGAAK	1.252221938	2	4.138769627
P04797	IVSNASCTTNCLAPLAK	1.368743936	2	4.965082169
P04797	LISWYDNEYGYSNR	2.032232492	2	4.337045193
P04797	VIISAPSADAPMFVMGVNHEK	1.237685047	2	4.294912815
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(12)	1.427016623	2	3.850122452
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(15)	1.427016623	2	3.524465799
P04797	VPTPNVSVVDLTCR	1.365375505	2	2.608547926
P04797	VVDLMAYMASK	0.738270132	2	4.433794022
P04797	WGDAGAEYVVESTGVFTTMEK	1.055339627	2	5.23757267
P04797	LVINGKPITIFQER	1.330987018	3	3.569601297
P04797	RVIISAPSADAPMFVMGVNHEK	1.091747407	3	5.469033718
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.226268604	3	7.705269814
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(13)	1.371494817	4	4.664880753
P04799	**CP1A2 Cytochrome P450 1A2**	**0.977621958**	**0.00029**	**6**
P04799	DFVENVTSGNAVDFFPVLR	0.962372182	2	3.217481613

P04799	FLTNDNTAIDK	1.176977624	2	3.067927599
P04799	IGSTPVVVLSGLNTIK	1.242207921	2	2.417352676
P04799	NSIQDITGALFK	0.779738452	2	3.12713027
P04799	SMTFNPDSGPVWAAR	3.578599941	2	3.310022593
P04799	TVQEHYQDFNK	1.05821668	2	3.426420689
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.820877047**	**9.9E-20**	**10**
P04903	YDLYGK	0.815494531	1	2.010271311
P04903	YLPAFEK	0.887117537	1	2.038910866
P04903	DGNLMFDQVPMVEIDGMK	0.658659911	2	4.884653568
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(11)	0.752798144	2	4.611674786
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(17)	0.778195782	2	3.445337534
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(5)	0.741150509	2	4.233358383
P04903	KDGNLMFDQVPMVEIDGMK	0.785079905	2	4.921662807
P04903	LIQSPEDLEK	1.466628279	2	3.06853056
P04903	LKKDGNLMFDQVPMVEIDGMK	1.688266582	2	3.187908888
P04903	WLLAAAGVEFEEK	0.960067673	2	4.388711452
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.972534967**	**9.9E-11**	**8**
P04904	LRNDGSLMFQQVPMVEIDGMK	1.658050503	2	4.665158272
P04904	NDGSLMFQQVPMVEIDGMK	1.050944552	2	5.374155045
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(12)	1.055404201	2	4.44112587
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(18)	1.068574308	2	4.106361866
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(6)	1.047830471	2	4.02233696
P04904	SHGQDYLVGNR	0.95102551	2	3.922860861
P04904	WLLAAAGVEFEEQFLK	1.252634848	2	6.153484344
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	0.742470012	4	6.987894058
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.173855183**	**9.9E-20**	**15**
P04905	ADIVENQVMDNR	1.081128004	2	4.18138361
P04905	ADIVENQVMDNR+Oxidation(9)	1.149291785	2	3.738868713
P04905	CLDAFPNLKDFLAR	1.110247007	2	3.249734879
P04905	FKLGLDFPNLPYLIDGSR	1.406454805	2	4.553408623
P04905	IRADIVENQVMDNR	1.485025099	2	3.982368231
P04905	ITQSNAIMR	1.266229002	2	3.106966019
P04905	ITQSNAIMR+Oxidation(8)	1.472577182	2	2.830822229
P04905	LGLDFPNLPYLIDGSR	1.172711946	2	4.746170521
P04905	MQLIMLCYNPDFEK	1.189851362	2	4.408873558
P04905	YLSTPIFSK	1.051019802	2	2.598889351
P04905	HHLCGETEEER	1.219189546	3	3.782840729
P04905	KHHLCGETEEER	0.759430984	3	4.457825661
P04905	KITQSNAIMR	1.104725742	3	3.827308655
P04905	KITQSNAIMR+Oxidation(9)	1.262746484	3	3.44760251
P04905	VTYVDFLAYDILDQYHIFEPK	1.024936458	3	3.633151531
P04906	**GSTP1 Glutathione S_transferase P**	**0.876496358**	**0.55039**	**2**
P04906	STCLYGQLPK	1.108190087	1	1.921939492

P04906	EAALVDMVNDGVEDLR	0.879266803	2	4.656117439
P04937	**FINC Fibronectin**	**1.149352945**	**0.02844**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	1.535401943	2	4.756765842
P04937	SSPVVIDASTAIDAPSNLR	1.159876328	2	4.494763374
P04937	SYTITGLQPGTDYK	0.795508424	2	2.577772856
P04937	VVTPLSPPTNLHLEANPDTGVLTVSWER	1.120695314	3	4.162885666
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**0.67153936**	**0.32924**	**8**
P05065	ALANSLACQGK	0.69882468	2	2.442160845
P05065	FSNEEIAMATVTALR	0.786233531	2	3.896584272
P05065	FSNEEIAMATVTALRR	0.541672786	2	2.387432337
P05065	GILAADESTGSIAK	0.713383664	2	3.969165087
P05065	GVVPLAGTNGETTTQGLDGLSER	0.737013285	2	5.52686882
P05065	IGEHTPSSLAIMENANVLAR	0.453846495	2	4.820976257
P05065	LQSIGTENTEENR	0.936869503	2	3.612361193
P05065	RLQSIGTENTEENR	0.760936138	2	2.784571171
P05178	**CP2C6 Cytochrome P450 2C6**	**0.958589458**	**0.99997**	**8**
P05178	EALIDHGEEFAER	0.940814693	2	2.971801043
P05178	FIDLIPTNLPHAVTCDIK	0.942205158	2	3.99672389
P05178	GTTIITSLSSVLHDSK	0.90700786	2	3.675725937
P05178	MCAGEGLAR	0.884634366	2	2.615818501
P05178	NITQSLTSFSK	0.907179905	2	3.079434633
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	1.084996099	2	2.546616554
P05178	FDYKDQDFLNLMEK	1.014425613	3	4.924890995
P05178	GTTIITSLSSVLHDSKEFPDPEIFDPGHFLDGNGK	0.795140967	4	4.778802872
P05179	**CP2C7 Cytochrome P450 2C7**	**1.314327581**	**0.68909**	**8**
P05179	ACVGEGLAR	1.063993063	2	3.019695044
P05179	HMPYTDAMIHEVQR	0.956675019	2	4.155092716
P05179	IEEHQESLDVTNPR	1.234778526	2	4.848712921
P05179	KIEEHQESLDVTNPR	1.352997303	2	4.980474472
P05179	VLTSLTSVLHDSK	1.863516234	2	3.404206753
P05179	FINFVPTNLPHAVTCDIK	1.200561088	3	3.533191919
P05179	KLPPGPTPLPIIGNFLQIDVK	1.064383349	3	5.984199047
P05179	TYGPVFTLYLGSQPTVILHGYEAIK	1.174205999	3	3.444455862
P05182	**CP2E1 Cytochrome P450 2E1**	**1.144808379**	**0.95494**	**12**
P05182	AKEHLQSLDINCAR	1.185116724	2	4.489892483
P05182	DIDLSPVTVGFGSIPPQFK	0.794285775	2	3.340556145
P05182	DTVFQGYVIPK	2.023123514	2	2.357030392
P05182	DVTDCLLIEMEKEK	0.809889256	2	3.295629263
P05182	EHLQSLDINCAR	0.917211009	2	2.483947039
P05182	FGPVFTLHLGSR	1.22792046	2	2.509732485
P05182	FINLVPSNLPHEATR	1.194668506	2	3.880681753
P05182	FKPEHFLNENGK	1.052259366	2	3.245394707
P05182	FSLSILR	1.226673869	2	2.387015104

P05182	GTVVIPTLDSLLYDSHEFPDPEK	1.07318386	2	4.707065582
P05182	LDMPYMDAVVHEIQR	1.004356965	2	3.1217978
P05182	YGLLILMK	1.261198094	2	3.161237717
P05183	**CP3A2 Cytochrome P450 3A2**	**1.846496338**	**7.5E-12**	**12**
P05183	DIELDGLFIPK	0.409329389	2	3.563749313
P05183	EMFPIIEQYGDILVK	0.864525728	2	3.763849974
P05183	KLQEEIDGALPSK	0.933358406	2	3.570443153
P05183	LKEMFPIIEQYGDILVK	2.128551709	2	3.266082764
P05183	LQEEIDGALPSK	0.927654582	2	4.094852924
P05183	QAILEPEKPIVLK	0.911261295	2	3.29446888
P05183	QEAETGKPVTMK	0.822468684	2	3.42798543
P05183	QEAETGKPVTMK+Oxidation(11)	1.028601755	2	3.183372498
P05183	VDFLQLMLNAHNNSK	1.104360389	2	4.094488144
P05183	YLKQEAETGKPVTMK	1.001909334	2	3.789287806
P05183	KDIELDGLFIPK	0.867394539	3	3.739842176
P05183	VDFLQLMLNAHNNSKDEVSHK	1.529526125	3	3.491888762
P05197	**EF2 Elongation factor 2**	**1.235515557**	**9.9E-20**	**27**
P05197	YFDPANGK	1.245994792	1	2.046126842
P05197	ALLELQLEPEELYQTFQR	1.409932484	2	5.28370285
P05197	AYLPVNESFGFTADLR	0.82415192	2	4.521506786
P05197	CELLYEGPPDDEAAMGIK	1.093433179	2	4.252473831
P05197	CLYASVLTAQPR	0.775930887	2	2.616899967
P05197	DLEEDHACIPIKK	1.162668509	2	3.385225534
P05197	EGIPALDNFLDKL	0.982423607	2	3.43691206
P05197	ETVSEESNVLCLSK	0.691682284	2	4.32697916
P05197	GEGQLGAAER	1.180984129	2	3.659483671
P05197	GHVFEESQVAGTPMFVVK	1.028205555	2	6.091641426
P05197	IWCFGPDGTGPNILTDITK	1.664333606	2	5.1323843
P05197	KIWCFGPDGTGPNILTDITK	1.16431318	2	4.752459526
P05197	KVEDMMK+Oxidation(5)Oxidation(6)	1.754153896	2	2.310080051
P05197	KVEDMMK+Oxidation(6)	1.323020472	2	2.390286207
P05197	NMSVIAHVDHGK	0.989320993	2	3.875102997
P05197	NMSVIAHVDHGK+Oxidation(2)	1.594053699	2	3.524287701
P05197	STLTDSLVCK	1.13030658	2	3.126808882
P05197	TFCQLILDPIFK	1.100852733	2	4.197811127
P05197	TGTITTFEHAHNMR	1.075549515	2	3.984627962
P05197	VFDAIMNFR	1.103566317	2	2.682761908
P05197	VFSGVVSTGLK	1.214691285	2	2.996866941
P05197	YEWDVAEAR	1.060363612	2	2.977055073
P05197	ARPFPDGLAEDIDKGEVSAR	1.250757962	3	5.691037178
P05197	LDSEDKDKEGKPLLK	1.378229072	3	3.968532085
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	1.175315913	3	5.066856384
P05197	WLPAGDALLQMITIHLPSPVTAQK	0.993055241	3	3.56220746

P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.521619819	3	5.757658958
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.22408903**	**1**	**11**
P05369	ALYEELDLR	0.990882073	2	3.110642672
P05369	EVLEYNTVGGK	0.961642013	2	3.002253294
P05369	GLTVVQTFQELVEPR	0.958241365	2	3.999997377
P05369	IKEVLEYNTVGGK	1.13852147	2	4.472659111
P05369	QILEENYGQK	0.835587752	2	2.422171116
P05369	QILEENYGQKDPEK	1.118611675	2	3.624308586
P05369	QNFIQHFSQIVK	0.801940491	2	2.483190536
P05369	SLIEQCSAPLPPSIFLELANK	0.930485695	2	5.199175835
P05369	VGTDIQDNK	1.117569414	2	3.767540693
P05369	VLTEDELGHPEK	1.065754878	2	2.521546602
P05369	VLTEDELGHPEKGDAITR	1.245759143	2	4.737894058
P05426	**RL7 60S ribosomal protein L7**	**1.454304925**	**8.9E-08**	**6**
P05426	AGNFYVPAEPK	1.164631581	2	2.989900589
P05426	IVEPYIAWGYPNLK	1.166001507	2	3.631530046
P05426	KKVPAVPETLK	1.224602283	2	3.000320435
P05426	TTHFVEGGDAGNR	1.13158602	2	2.748411417
P05426	TTHFVEGGDAGNREDQINR	1.215730019	2	4.435407162
P05426	FGIICMEDLIHEIYTVGK	1.37685175	3	4.352676868
P05544	**SPA3L Serine protease inhibitor A3L**	**0.90486334**	**0.91845**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	1.258468683	2	2.810756683
P05544	DSTMEEILEGLK	0.801985322	2	2.887428522
P05544	IAELFSDLEER	1.109070449	2	2.553490639
P05544	MQQVESSLQPETLK	0.899429486	2	4.153573036
P05544	MQQVESSLQPETLKK	0.838111188	2	3.304696798
P05544	VFSQQADLSR	1.266083359	2	2.933134794
P05545	**SPA3K Serine protease inhibitor A3K**	**1.005113854**	**0.69167**	**5**
P05545	AVLDVDETGTEGAAATAVTAALK	0.946344678	2	6.174769878
P05545	FSISTDYNLEEVLPELGIR	1.113272286	2	3.910863638
P05545	IAELFSELDER	1.04246531	2	3.013139009
P05545	IFSQQADLSR	1.320262309	2	2.4812181
P05545	NLHVSQVVHK	1.288875313	2	2.619493246
P05765	**RS21 40S ribosomal protein S21**	**1.063406685**	**0.38577**	**3**
P05765	DHASIQMNVAEVDR	0.787299415	2	3.687282562
P05765	MGESDDSILR	0.995600167	2	3.009903431
P05765	TYGICGAIR	1.144119341	2	2.440311193
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**1.164021513**	**0.89793**	**9**
P06214	AGADIIITYFAPQLLK	0.885251649	2	4.470230103
P06214	AGAFDLR	1.086043189	2	2.577320576
P06214	AGCQVVAPSDMMDGR	1.434112006	2	3.912256479
P06214	CVLIFGVPSR	1.540869382	2	2.482594967
P06214	DEQGSAADSEDSPTIEAVR	0.952884641	2	5.917180061

P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.880976789	2	3.900589228
P06214	TAVLESMTAFR	1.060971864	2	3.213579178
P06214	VPKDEQGSAADSEDSPTIEAVR	1.084980105	2	5.983965874
P06214	YGVNQLEEMLRPLVEAGLR	1.147469221	3	4.29485178
P06302	**PTMA Prothymosin alpha**	**1.152691217**	**2.1E-14**	**3**
P06302	VAEDDEDDDVETK	1.054489217	2	4.316760063
P06302	VAEDDEDDDVETKK	1.244560642	2	4.581508636
P06302	RVAEDDEDDDVETKK	1.288426318	3	5.832990646
P06399	**FIBA Fibrinogen alpha chain**	**0.977539614**	**0.99956**	**9**
P06399	AQQIQVLQK	1.17412981	1	2.08348608
P06399	GDFANANNFDNTFGQVSEDLR	1.064859711	2	4.997902393
P06399	GDKELLIGNEK	1.223966957	2	2.775907516
P06399	GLIDEANQDFTNR	1.047347082	2	3.030899763
P06399	MADEAASEAHQEGDTR	0.948761856	2	3.846734047
P06399	SQLQEGPPEWK	1.039796159	2	2.908297539
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.853051456	3	4.41502142
P06399	GDFANANNFDNTFGQVSEDLRR	0.989992729	3	3.414928436
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	0.932503034	3	3.480721235
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.060935057**	**0.39712**	**6**
P06685	AVAGDASESALLK	1.021437598	2	3.630400658
P06685	AVFQANQENLPILK	1.131259346	2	2.681112051
P06685	LNIPVNQVNPR	1.25025127	2	3.137957335
P06685	MSINAEDVVVGDLVEVK	0.859917661	2	3.510727406
P06685	YEPAAVSEHGDKK	1.230168172	2	3.36372757
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.222130928	3	3.351732254
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.067839315**	**0.99986**	**3**
P06687	DGPNALTPPPTTPEWVK	1.081852939	2	2.970988035
P06687	GVGIISEGNETVEDIAAR	1.06705186	2	4.467101574
P06687	QGAIVAVTGDGVNDSPALK	1.123995993	2	5.045359612
P06757	**ADH1 Alcohol dehydrogenase 1**	**1.065888419**	**0.98657**	**19**
P06757	GAIFGGFK	1.080391685	2	2.69597578
P06757	GALLDGTSR	1.125749311	2	2.796796083
P06757	HPESNLCCQTK	1.452691445	2	3.244339705
P06757	IDAAAPLDK	1.010360029	2	2.974300385
P06757	IIAVDINKDK	1.24187763	2	2.896382809
P06757	INEAFDLLR	1.083068517	2	3.711343288
P06757	LVADFMAK	1.199396054	2	2.403615952
P06757	MVATGVCR	1.082459846	2	2.607994318
P06757	MVATGVCR+Oxidation(1)	1.274045524	2	2.526633739
P06757	VCLIGCGFSTGYGSAVQVAK	1.246508397	2	6.477605343
P06757	VIPLFSPQCGK	0.95066231	2	2.598103762
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.146846787	3	5.60936594

P06757	FPLEPLITHVLPFEK	1.191249846	3	4.682451248
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.608824459	3	5.403717995
P06757	ICKHPESNLCCQTK	0.917127241	3	3.88413763
P06757	IDAAAPLDKVCLIGCGFSTGYGSAVQVAK	1.27597992	3	3.317619801
P06757	KFPLEPLITHVLPFEK	1.126781681	3	4.526114941
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.127325057	3	5.261638641
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	0.9649248	4	7.900928497
P06761	**GRP78 78 kDa glucose_regulated protein**	**0.986487496**	**9.9E-20**	**28**
P06761	DAGTIAGLNVMR	0.754576774	2	3.328724146
P06761	DNHLLGTFDLTGIPPAPR	0.724489592	2	4.77969265
P06761	ELEEIVQPIISK	0.975692559	2	4.04531765
P06761	FEELNMDLFR	1.018944071	2	3.538638353
P06761	IEIESFFEGEDFSETLTR	1.010228071	2	5.730442524
P06761	IEWLESHQDADIEDFK	1.087472733	2	5.681033611
P06761	IINEPTAAAIAYGLDKR	1.393290639	2	4.428890705
P06761	ITITNDQNR	1.217103509	2	2.676016569
P06761	ITPSYVAFTPEGER	1.244147686	2	4.055995941
P06761	KKELEEIVQPIISK	1.164727674	2	5.423585892
P06761	KSDIDEIVLVGGSTR	1.122785357	2	5.167689323
P06761	KSQIFSTASDNQPTVTIK	1.170859557	2	5.328254223
P06761	LYGSGGPPPTGEEDTSEKDEL	1.566084215	2	5.497441769
P06761	MKETAEAYLGK	1.046164268	2	3.375916958
P06761	MKETAEAYLGK+Oxidation(1)	1.194265595	2	2.931211233
P06761	NELESYAYSLK	1.367987728	2	3.591028452
P06761	NQLTSNPENTVFDAK	1.042506768	2	5.289854527
P06761	SDIDEIVLVGGSTR	0.962073818	2	3.450711966
P06761	SQIFSTASDNQPTVTIK	0.996103595	2	5.446584225
P06761	TFAPEEISAMVLTK	1.021594324	2	4.756736279
P06761	TKPYIQVDIGGGQTK	1.183351917	2	4.351467133
P06761	TWNDPSVQQDIK	1.084248947	2	4.165688992
P06761	VLEDSDLK	1.171718808	2	2.346911907
P06761	VLEDSDLKK	1.238001908	2	2.455084324
P06761	VTHAVVTVPAYFNDAQR	1.403330702	2	5.049962997
P06761	VYEGERPLTK	1.186640751	2	2.908306599
P06761	AKFEELNMDLFR	1.205568477	3	4.639408112
P06761	IEWLESHQDADIEDFKAK	1.249957951	3	4.597001553
P06766	**DPOLB DNA polymerase beta**	**1.139963091**	**0.31831**	**2**
P06766	EEMLQMQDIVLNEVKK+Oxidation(6)	1.138400941	2	2.327768326
P06766	QDDTSSSINFLTR	1.187532268	2	2.398083687
P06866	**HPT Haptoglobin**	**0.738992385**	**1.7E-08**	**6**
P06866	NQLVEIEK	0.773456456	1	2.251029253
P06866	SVVDIGLIK	0.757959724	1	1.920938969
P06866	ATDLKDWVQETMAK	0.903264946	2	2.709246635

P06866	GAVSPVGVQPILNK	0.640872696	2	3.59387517
P06866	LQTEGDGIYTLNSEK	0.67540843	2	4.378346443
P06866	YVMLPVADQEK	0.534495755	2	2.596458435
P07150	**ANXA1 Annexin A1**	**1.107458952**	**0.00011**	**2**
P07150	GLGTDEDTLIEILTTR	1.582507644	2	4.49952507
P07150	GGPGSAVSPYPSFNPSSDVAALHK	1.011936613	3	3.940739393
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.118120282**	**9.9E-20**	**14**
P07153	ASSFVLALEPELESR	1.254430616	2	3.959182978
P07153	AVTSEIAVLQSR	1.19355757	2	3.694245338
P07153	FVDHVFDEQVIDSLTVK	1.164720325	2	4.495520592
P07153	GEDEEDNNLEVR	1.184843609	2	3.777470827
P07153	HFDETVNR	1.186549708	2	2.790056229
P07153	LKTEGSDLCDR	1.363131828	2	2.959554911
P07153	NIQVDSPYDISR	1.212268483	2	3.653958797
P07153	SEDILDYGPFK	1.038050708	2	3.62311697
P07153	TEGSDLCDR	1.166305576	2	2.414081812
P07153	TVDLSSHLAK	1.348259392	2	2.409823179
P07153	VHYENNSPFLTITSMTR	1.201249579	2	3.341266632
P07153	VTAEVVLAHPGGGSTAR	1.256340184	2	4.480870724
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.124253583	3	4.673970699
P07153	NLVEQHIQDIVVHYTFNK	1.070474662	3	4.465881824
P07323	**ENOG Gamma_enolase**	**0.941801014**	**0.03771**	**4**
P07323	AAVPSGASTGIYEALELR	1.280339465	2	5.223526955
P07323	FGANAILGVSLAVCK	0.834202549	2	3.771245003
P07323	GNPTVEVDLHTAK	0.439594787	2	2.952318668
P07323	SGETEDTFIADLVVGLCTGQIK	1.08393976	2	4.977723122
P07335	**KCRB Creatine kinase B_type**	**1.280849009**	**0.00301**	**3**
P07335	FCTGLTQIETLFK	1.448534101	2	3.016513109
P07335	LGFSEVELVQMVVDGVK	0.854031149	2	2.682432652
P07335	TDLNPDNLQGGDDLDPNYVLSSR	1.052182874	2	2.890532017
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**0.963240352**	**0.42551**	**3**
P07340	AYGENIGYSEK	1.167239188	2	2.532585859
P07340	VAPPGLTQIPQIQK	1.035320656	2	2.692167521
P07340	YNPNVLPVQCTGK	0.861720956	2	2.48489213
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.021074519**	**1**	**12**
P07379	TVIITQEQR	0.954823407	1	1.913128734
P07379	AINPENGFFGVAPGTSVK	0.904912435	2	4.277411461
P07379	FLWPGFGENSR	0.993430821	2	2.546698809
P07379	GLGDVNVEELFGISK	1.067599066	2	3.705416679
P07379	IGIELTDSPYVVASMR	1.003229226	2	4.205003738
P07379	MGTSVLEALGDGEFIK	1.004489143	2	3.86515522

P07379	VECVGDDIAWMK	0.884741413	2	3.510163307
P07379	VIQGSLDSLPQEVR	0.975800885	2	3.711210728
P07379	YLAAAFPSACGK	1.004803727	2	2.941397667
P07379	YLEDQVNADLPYEIER	1.046197988	2	4.789985657
P07379	EEGWLAEHMLILGITNPEGK	0.922610636	3	3.773885012
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	0.729088829	3	4.274688244
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**0.899748502**	**1E-15**	**5**
P07632	DGVANVSIEDR	0.547407729	2	2.830558538
P07632	GDGPVQGVIHFEQK	0.904628463	2	3.887235403
P07632	HVGDLGNVAAGK	0.909196583	2	3.980212927
P07632	QDDLGKGGNEESTK	1.330806417	2	3.611913919
P07632	VISLSGEHSIIGR	0.99446338	2	3.121565104
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**1.300030727**	**0.2937**	**10**
P07633	AFDNDVDALCNLR	1.300365427	2	3.648095608
P07633	AYNMLDIIHAVIDER	1.138624305	2	4.191164494
P07633	GFVDDIIQPSSTR	1.067167305	2	3.091489553
P07633	HLLGDTNYAWPTAEIAVMGAK	0.745350015	2	5.72321701
P07633	ICCDLEVLASK	1.269950178	2	3.539125443
P07633	IMDQAITVGAPVIGLNDSGGAR	1.34494105	2	5.038619518
P07633	IQEGVESLAGYADIFLR	1.071048007	2	4.423560619
P07633	LVPELDTVVPLESSK	1.048345868	2	3.573656797
P07633	SVTNEDVTQEQLGGAK	1.050954404	2	5.233456135
P07633	TVGIVGNQPNVASGCLDINSSVK	1.090484236	2	5.049739361
P07687	**HYEP Epoxide hydrolase 1**	**0.842230625**	**8.7E-07**	**25**
P07687	IIPLLTDPK	1.596255475	1	1.97014153
P07687	DIELLYPYK	0.764741529	2	3.032964706
P07687	EDESIRPFK	0.958751311	2	2.713902712
P07687	ENLGQGIMVHK	0.861976421	2	2.961742163
P07687	FHYGFNSNYMK	0.982532489	2	2.654889345
P07687	FLGYTEKDIELLYPYK	1.243310054	2	4.867154121
P07687	FVSLAELQ	1.052537191	2	2.455443621
P07687	GGHFAAFEEPK	1.146155036	2	3.325154781
P07687	GLHLNMAFISR	1.294636981	2	2.881347895
P07687	GLNSVATAR	1.252668585	2	2.454266548
P07687	KFVSLAELQ	1.38935344	2	2.448912144
P07687	LLAQDIR	1.376618375	2	2.438859224
P07687	QVEILNQYPHFK	1.256137464	2	3.556695938
P07687	VETSDEEIK	0.920715051	2	2.488401413
P07687	VETSDEEIKDLHQR	1.030028341	2	4.86286211
P07687	VFVPTGFSAFPSELLHAPEK	1.390658304	2	5.122310162
P07687	DKEETLPLGDGWWGPGSKPSAK	1.104050775	3	4.930778503
P07687	EDESIRPFKVETSDEEIKDLHQR	0.95794826	3	6.37014246

P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.425418745	3	6.128227711
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.254113735	3	4.070290565
P07687	IEGLDIHFIHVKPPQLPSGR	1.337445556	3	4.309512615
P07687	KQVEILNQYPHFK	1.279356287	3	5.452825546
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.078108957	3	6.293729305
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSKK	1.474545257	3	5.167556763
P07687	TKIEGLDIHFIHVKPPQLPSGR	1.158768495	3	4.199641705
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**0.973192151**	**9.9E-20**	**98**
P07756	DELGLNK	1.072562342	1	2.243742466
P07756	DILNMDK	0.649364144	1	1.927698255
P07756	EIEYEVVR	0.617966697	1	2.06334424
P07756	ETLMDLGTK	0.628334977	1	2.359094143
P07756	EVEMDAVGK	0.389896156	1	2.222835302
P07756	QNLIAEVSTK	0.968430434	1	2.534120798
P07756	SFPFVSK	1.056426408	1	1.916057587
P07756	YMESDGIK	1.061268285	1	2.14819026
P07756	YMESDGIK+Oxidation(2)	1.195449367	1	2.300519466
P07756	AADTIGYPVMIR	1.123628995	2	3.932675838
P07756	AADTIGYPVMIR+Oxidation(10)	1.214424698	2	3.365308285
P07756	AFAISGPFNVQFLVK	0.983198094	2	5.021260262
P07756	AFAMTNQILVER	1.12912667	2	4.378676891
P07756	AFAMTNQILVER+Oxidation(4)	1.061008237	2	3.79375577
P07756	ALENNMSLDEIVK	1.017713507	2	4.758444309
P07756	ALENNMSLDEIVK+Oxidation(6)	0.983807033	2	3.962586164
P07756	AMLSTGFK	1.026863993	2	2.531510353
P07756	AQTAHIVLEDGTK	0.743171897	2	4.476671696
P07756	ATGYPLAFIAAK	1.164765245	2	3.104708672
P07756	CLGLTEAQTR	1.06618632	2	3.604779482
P07756	DGSIDLVINLPNNNTK	0.691335959	2	5.539203167
P07756	EPLFGISTGNIITGLAAGAK	1.161728589	2	5.324253082
P07756	FLEEATR	1.0336015	2	2.477151155
P07756	FLGVAEQLHNEGFK	1.057529001	2	4.884843349
P07756	GILIGIQQSFRPR	1.004039306	2	2.477206945
P07756	GLNSESVTEETLR	0.82161176	2	4.868316174
P07756	GNDVLVIECNLR	1.091411427	2	4.349513054
P07756	GQILTMANPIIGNGGAPDTTAR	0.873054969	2	6.45637846
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(6)	0.817589326	2	4.893274784
P07756	GQNQPVLNITNR	0.994302602	2	4.299999714
P07756	GTTITSVLPKPALVASR	1.035650759	2	3.651688099
P07756	HLPTLEQPIIPSDYVAIK	0.678433767	2	5.15389061
P07756	IALGIPLPEIK	1.49646311	2	2.975263834
P07756	IAPSFAVESMEDALK	1.616633135	2	5.284111977

P07756	IAPSFAVESMEDALK+Oxidation(10)	1.20915521	2	3.455365658
P07756	IEFEGQSVDFVDPNK	0.956715133	2	5.557072639
P07756	IMGTSPLQIDR	1.668603263	2	3.054864168
P07756	IMGTSPLQIDR+Oxidation(2)	1.753506698	2	3.093187809
P07756	IMGTSPLQIDRAEDR	0.869498901	2	2.44207859
P07756	KELSEPSSTR	0.859148215	2	2.739980221
P07756	KEPLFGISTGNIITGLAAGAK	0.949515766	2	5.468696594
P07756	KTVVVNCNPETVSTDFDECDK	0.300483392	2	5.12185955
P07756	LFAEAVQK	1.052459106	2	3.42457366
P07756	LTSIDKWFLYK	1.297703372	2	2.480920792
P07756	LYFEELSLER	0.570447136	2	3.46032238
P07756	MRDILNMDK	0.944154576	2	3.037030458
P07756	MRDILNMDK+Oxidation(1)	1.254715864	2	2.748796701
P07756	QLFSDKLNEINEK	1.021411801	2	3.851453066
P07756	RFLEEATR	1.000965189	2	2.994326115
P07756	RTAVDSGIALLTNFQVTK	0.96045973	2	4.754297733
P07756	SAYALGGLGSGICPNK	1.146645691	2	4.958547592
P07756	SIFSAVLDELK	0.838742641	2	3.928220987
P07756	SLGQWLQEEK	1.049738834	2	4.186653137
P07756	SLGQWLQEEKVPAIYGVDTR	0.985800324	2	3.937293768
P07756	SVGEVMAIGR	0.964552942	2	3.590549231
P07756	SVGEVMAIGR+Oxidation(6)	1.002717432	2	3.098220825
P07756	TFEESFQK	0.975672537	2	2.540362597
P07756	TLGVDFIDVATK	1.010949257	2	4.181095123
P07756	TSACFEPSLDYMVTK	0.899518833	2	4.72636795
P07756	TSACFEPSLDYMVTK+Oxidation(12)	0.871764485	2	3.560952187
P07756	TSINVVR	1.03593717	2	2.439437866
P07756	TVLMNPNIASVQTNEVGLK	1.032116073	2	6.626826763
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(4)	1.073361447	2	5.957698345
P07756	TVVVNCNPETVSTDFDECDK	0.31484475	2	5.625226498
P07756	VLGTSVESIMATEDR	1.100962079	2	4.901515007
P07756	VLGTSVESIMATEDR+Oxidation(10)	1.069232469	2	4.221991539
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	0.985891788	2	5.814639091
P07756	VMIGESVDEK	0.917238431	2	3.569792509
P07756	VMIGESVDEK+Oxidation(2)	0.899699272	2	3.009068966
P07756	VSQEHPVVLTK	1.002950806	2	3.982559919
P07756	VVAVDCGIK	1.064809203	2	2.592153311
P07756	AERPDGLILGMGGQTALNCGVELFK	1.036505958	3	6.726362228
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(11)	0.742253448	3	6.184842587
P07756	CEMASTGEVACFGEGIHTAFLK	0.961194416	3	4.784420967
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(3)	1.002525555	3	4.702718735
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	1.095772643	3	6.446156979

P07756	FVHDNYVIR	1.251792311	3	3.529940844
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.149500954	3	6.114260197
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(16)	1.013433385	3	5.750696659
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.971091611	3	4.843554974
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(6)	1.039705143	3	3.432430267
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	0.318472678	3	6.451427937
P07756	HLGIVGECNIQFALHPTSMEYCIIEVNAR	0.950125762	3	4.849568844
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	1.011325615	3	5.149014473
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.193100401	3	6.074044228
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	1.024445948	3	3.784959078
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	0.967766672	3	5.127151489
P07756	LRDADPILR	1.13378774	3	3.514882565
P07756	MCHPSVDGFTPR	0.970604505	3	5.048313618
P07756	MCHPSVDGFTPR+Oxidation(1)	1.165663598	3	4.331572056
P07756	QADAVYFLPITPQFVTEVIK	0.200324115	3	4.411620617
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	1.00568507	3	3.359024048
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.117392319	3	4.971365929
P07756	SIFSAVLDELKVAQAPWK	0.660791816	3	3.444389343
P07756	TAVDSGIALLTNFQVTK	1.17240412	3	6.386646748
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	0.666041245	3	6.006108284
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	0.98003324	3	7.590694427
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(23)	0.967676247	3	7.040621281
P07824	**ARGI1 Arginase_1**	**1.236224034**	**6.2E-11**	**15**
P07824	YFSMTEVDK	1.084622948	1	2.248888969
P07824	ANEQLAAVVAETQK	1.120702932	2	5.359277248
P07824	DHGDLAFVDVPNDSPFQIVK	0.993179439	2	6.239706516
P07824	DIVYIGLR	1.047884496	2	2.710651875
P07824	DVDPGEHYIIK	0.717682671	2	3.293957472
P07824	EGNHKPETDYLKPPK	1.036228006	2	2.707977057
P07824	TGLLSGLDIMEVNPTLGK	1.179321975	2	5.726959705
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(10)	0.845890538	2	2.671370983
P07824	TVNTAVALTLSCFGTK	1.145130817	2	4.25558567
P07824	VMEETFSYLLGR	1.003731359	2	3.827658176
P07824	YFSMTEVDKLGIGK+Oxidation(4)	1.056769463	2	2.588949442
P07824	GKFPDVPGFSWVTPCISAK	1.324723069	3	4.657401085
P07824	LKETEYNVR	1.277272419	3	3.710442781
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.236265463	3	4.50948143
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.293977016	4	4.623486042
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.988318681**	**2.5E-09**	**16**
P07871	AEELGLPILGVLR	1.031457179	2	4.41574955
P07871	AEIVPVTTTVLDDK	0.89278978	2	4.625771046

P07871	AEIVPVTTTVLDDKGDR	1.001476151	2	3.946777582
P07871	AEIVPVTTTVLDDKGDRK	1.018816317	2	4.380599499
P07871	DCLIPMGITSENVAER	0.534110596	2	3.771882296
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.99902	2	6.220921993
P07871	IAQFLSGIPETVPLSAVNR	1.348451982	2	4.105624199
P07871	QCSSGLQAVANIAGGIR	0.869498901	2	4.907503128
P07871	QDAFALASQQK	0.852896873	2	3.939664841
P07871	QKQDAFALASQQK	0.995305441	2	3.971053362
P07871	QVVTLLNELK	1.054111739	2	2.479454994
P07871	SKAEELGLPILGVLR	1.014149938	2	4.039048672
P07871	TITVSQDEGVRPSTTMEGLAK	0.971301669	2	4.34833622
P07871	VNPLGGAIALGHPLGCTGAR	1.223603238	2	5.203404427
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.859027828	3	5.14951992
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	1.007243983	3	4.820228577
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.86720898**	**1.3E-06**	**20**
P07872	IYDQVR	1.101686972	1	1.994236827
P07872	LVEIAAK	1.203411414	1	2.080260277
P07872	AFTTWTANAGIEECR	1.187491762	2	4.057673931
P07872	EIENLILNDPDFQHEDYNFLTR	1.30982479	2	4.400592804
P07872	EIGTHKPLPGITVGDIGPK	0.978623994	2	4.045987606
P07872	EVAWNLTSVDLVR	0.674022546	2	2.868701696
P07872	EYGISDPEEIMWFK	0.686074716	2	3.573589087
P07872	FGYEEMDNGYLK	0.96608596	2	3.020596266
P07872	GGDFLEGSIITGAQLSQVNAR	0.973295454	2	5.995479107
P07872	GLETTATYDPK	0.983568722	2	3.502531528
P07872	NLCLLYSLYGISQK	0.789035824	2	3.247888327
P07872	QSEPEPQILDFQTQQYK	1.056483844	2	4.868469715
P07872	SFLVGNAAQSLSK	1.101734699	2	3.768397093
P07872	SKEVAWNLTSVDLVR	1.118057231	2	3.376637459
P07872	TQEFILNSPTVTSIK	0.937593367	2	4.342841148
P07872	YDGNVYENLFEWAK	1.099679013	2	5.441574574
P07872	ASATFNPELITHILDGSPENTR	0.711704947	3	4.578322411
P07872	ASEAHCHYVVVK	1.148769318	3	4.015044689
P07872	INESIGQGDLSELPELHALTAGLK	1.054423411	3	5.29580307
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	0.840906681	4	4.972455025
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.96398301**	**0.99957**	**4**
P07895	AIWNVINWENVSQR	1.011544216	2	3.766192198
P07895	GDVTTQVALQPALK	0.874633954	2	3.37852025
P07895	HHATYVNNLNVTEEK	1.007164487	2	4.732997894
P07895	NVRPDYLK	0.897097757	2	2.437200785
P07896	**ECHP Peroxisomal bifunctional enzyme**	**1.092906249**	**0.93047**	**21**
P07896	GGPMFYAASVGLPTVLEK	0.661681233	2	3.987511873
P07896	GQGLTGPSLPPGTPVR	0.942592184	2	4.23901701

P07896	GWYQYDKPLGR	1.060939501	2	3.079889536
P07896	IGVVVGNCYGFVGNR	1.411733923	2	3.294219971
P07896	IIDKPIEPR	1.149819252	2	2.584297657
P07896	KGQGLTGPSLPPGTPVR	1.016442567	2	4.66442585
P07896	KQYPGVLAPETCVR	1.200895035	2	4.063900471
P07896	LCNPPVNAVSPTVIR	1.478001555	2	4.772686958
P07896	LGILDAVVK	1.092024887	2	2.912793636
P07896	LLEVIPSR	0.943739475	2	2.410527468
P07896	QNPDIPQLEPSDYLR	0.884195762	2	3.963437796
P07896	QYPGVLAPETCVR	0.992945866	2	2.970385075
P07896	TASAQPVSSVGVLGLGTMGR	1.058195353	2	5.141682625
P07896	TISKEEILER	1.19793934	2	2.964619637
P07896	VGISVVAVESDPK	1.012011414	2	4.197182655
P07896	VGLPEVTLGILPGAR	1.178565694	2	3.445039034
P07896	VSDLAGLDVGWK	1.020709498	2	4.500705242
P07896	YLSADEALR	1.124756122	2	3.116860867
P07896	YSPLGDMLCEAGR	1.000772846	2	3.861076593
P07896	YSSPTTIATVMSLSK	1.146442513	2	3.230472803
P07896	IFNKPVPSLPNMDSVFAEAIAK	1.711029679	3	3.99486661
P07943	**ALDR Aldose reductase**	**1.21718416**	**0.563**	**2**
P07943	AIGVSNFNPLQIER	1.248164319	2	3.075436831
P07943	HIDCAQVYQNEK	1.205588944	2	3.928550482
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.242855726**	**9.9E-20**	**6**
P08009	LCYNPDFEK	2.464641675	1	2.267436743
P08009	LLLEYTDSSYEEK	1.293689086	2	4.917578697
P08009	LLLEYTDSSYEEKR	1.340612975	2	4.132488251
P08009	NQVFEATCLDAFPNLK	0.782801903	2	4.254366398
P08009	SQWLNEK	1.136011648	2	2.684843779
P08009	YTMGDAPDFDR	0.879915612	2	2.371947527
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**0.976103054**	**0.05484**	**14**
P08010	FLSKPIFAK	1.720161709	1	2.193525791
P08010	ITYVDFLVYDVLDQHR	1.964190494	2	5.224453449
P08010	KPEYLEGLPEK	1.244442699	2	3.197163582
P08010	KYSMGDAPDYDR	1.085011187	2	3.437572241
P08010	LFLEYTDTSYEDK	1.244712792	2	5.490555286
P08010	LFLEYTDTSYEDKK	1.033739327	2	4.784173965
P08010	LQLAMVCYSPDFER	1.163641963	2	4.155865669
P08010	LQLAMVCYSPDFER+Oxidation(5)	2.01030636	2	3.643967152
P08010	VDVLENQAMDTR	1.129959969	2	4.63296175
P08010	VDVLENQAMDTR+Oxidation(9)	1.217956946	2	3.741384268
P08010	YSMGDAPDYDR	1.094357633	2	3.545629501
P08010	YSMGDAPDYDR+Oxidation(3)	1.283728315	2	2.65854001
P08010	IRVDVLENQAMDTR	1.437965288	3	4.548021793

P08010	KKPEYLEGLPEK	1.077479552	3	4.34089756
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**1.042359828**	**0.00177**	**6**
P08011	IYHTIAYLTPLPQPNR	0.83367355	2	5.113888741
P08011	MMFLSSATAFQR	1.277107408	2	4.029896736
P08011	MMFLSSATAFQR+Oxidation(1)	1.210011208	2	3.099094391
P08011	MMFLSSATAFQR+Oxidation(2)	1.216416933	2	3.458062649
P08011	VFANPEDCAGFGK	1.137844939	2	4.789256096
P08011	VFANPEDCAGFGKGENAK	1.096322371	2	4.781914711
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**1.050491115**	**0.60882**	**2**
P08032	ADVVESWIGEK	1.204451484	2	3.061196566
P08032	IEDLGDSMEEALILDIK	1.050445664	2	2.495487452
P08081	**CLCA Clathrin light chain A**	**0.974329007**	**0.93447**	**2**
P08081	LEALDANSR	0.971379093	2	2.478680372
P08081	WREEQTER	1.069331586	2	2.366039515
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.152685209**	**9.5E-10**	**4**
P08461	DVPLGTPLCIIVEK	0.960956388	2	3.875911951
P08461	DVPVGSIICITVEKPQDIEAFK	1.316200326	2	3.459570885
P08461	GLETIASDVVSLASK	1.197112168	2	4.112021446
P08461	VAPTPAGVFIDIPISNIR	1.331816301	2	4.599755287
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.923255527**	**2.3E-05**	**8**
P08503	AFTGFIVEADTPGIHIGK	1.101353669	2	4.244825363
P08503	EEIIPVAPDYDK	0.843296581	2	3.552479029
P08503	IYQIYEGTAQIQR	1.135272038	2	4.513210297
P08503	KGDEYVINGQK	1.03730592	2	4.226099014
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	0.195974587	2	4.603645802
P08503	QEPGLGFSFELTEQQK	0.755992199	2	3.734213829
P08503	SGEYPFPLIK	0.969325756	2	2.653902769
P08503	TRPTVAAGAVGLAQR	1.16277751	2	4.213721752
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.295350183**	**4.9E-13**	**10**
P08541	DELQNHFIK	1.275806356	2	2.789991617
P08541	LLDVWTYELPR	1.741366114	2	3.645707369
P08541	NVMLLSTIHHDQPMKPLDR	1.228434237	2	4.157388687
P08541	VEIWLIR	1.350467851	2	2.892772675
P08541	VLVWPMDFSHWMNIK	1.480041578	2	3.505607843
P08541	FEIFSTSISKDELQNHFIK	1.233931477	3	3.502398729
P08541	FILPPSYVPVILSGLAGK	1.392062802	3	5.590003014
P08541	GHEVTVLKPSAYFFLDPK	1.624147301	3	4.69409132
P08541	HKEWDTFYSEILGRPTTVDETMSK	0.783804766	3	4.326952457
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(3)	1.390923355	3	3.391382694
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.213340622**	**0.7888**	**6**
P08542	EIINNPFYK	0.858376348	1	2.213383436

P08542	FETFPTSVSKDELENYFIK	1.107854305	2	4.172694206
P08542	KWDPFYSEILGRPTTLAETMGK	1.132122809	2	4.497436047
P08542	LVDVWTYELQR	1.25075948	2	3.256995678
P08542	WDPFYSEILGRPTTLAETMGK	1.288483405	2	4.008360386
P08542	NAVWLSTIHHDQPMKPLDK	1.154109771	3	3.716145992
P08683	**CP2CB Cytochrome P450 2C11**	**1.318985382**	**0.99988**	**16**
P08683	FNENFR	1.088989938	1	2.018418789
P08683	NYVLEK	1.236263133	1	1.938961744
P08683	EALVDLGEEFSGR	0.96145275	2	3.620311975
P08683	EHQESLDKDNPR	1.034558817	2	4.219596863
P08683	FDPGHFLDER	1.113596454	2	2.664953709
P08683	ICAGEALAR	1.212076486	2	2.782515287
P08683	LPPGPTPLPIIGNTLQIYMK	0.940909974	2	3.81854248
P08683	SQMPYTDAVVHEIQR	0.9480653	2	4.658567905
P08683	VQEEIER	1.100513315	2	2.642582178
P08683	YGLLLLLK	1.475153485	2	3.454749346
P08683	YIDLVPTNLPHLVTR	1.09988993	2	3.558331013
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	0.910905798	3	5.474644661
P08683	FDYKDPTFLNLMHR	1.295296777	3	4.908605099
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.089463609	3	5.433080673
P08683	LFSSPWLQVCNTFPAIIDYFPGSHNQVLK	1.240584209	3	4.237119675
P08683	VKEHQESLDKDNPR	1.234196583	3	4.938120842
P09006	**SPA3N Serine protease inhibitor A3N**	**1.235042902**	**0.98957**	**2**
P09034	**ASSY Argininosuccinate synthase**	**1.125168839**	**0.80859**	**14**
P09034	APNTPDVLEIEFK	1.132809438	2	2.772825956
P09034	DGTTHSTSLDLFMYLNEVAGK	2.632628845	2	5.055802345
P09034	EFVEEFIWPAVQSSALYEDR	1.581335068	2	5.674581528
P09034	FAELVYTGFWHSPECEFVR	0.447173505	2	4.370034218
P09034	FELTCYSLAPQIK	0.678967838	2	4.236130714
P09034	GRNDLMEYAK	0.948863022	2	2.93580389
P09034	IDIVENR	1.104522535	2	2.551079512
P09034	KVFIEDVSK	1.10521527	2	2.764323235
P09034	NDLMEYAK	0.887157073	2	2.663493395
P09034	TQDPAKAPNTPDVLEIEFK	1.14074271	2	4.801448345
P09034	VFIEDVSK	1.024149865	2	2.582131863
P09034	EQGYDVIAYLANIGQK	0.806871246	3	3.762732029
P09034	SPWSMDENLMHISYEAGILENPK	1.010365217	3	4.854954243
P09034	TQDPAKAPNTPDVLEIEFKK	1.080459339	3	4.208372593
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.040258856**	**0.69567**	**5**
P09041	VDFNVPMK	1.0342891	1	2.212665796
P09041	FHVEEEGK	1.050572166	2	2.686316967
P09041	FHVEEEGKGK	1.014720472	2	2.81999898
P09041	LGDVYVNDAFGTAHR	1.143821548	2	4.003675461

P09041	VSHVSTGGGASLELLEGK	1.079101947	2	5.295320034
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.281317251**	**0.00171**	**3**
P09117	VLAAVYK	1.359182595	2	2.67524457
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	0.719060077	3	5.820940971
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	0.808701198	3	5.020802498
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.890431322**	**0.11868**	**2**
P09139	LLLGPGPSNLAPR	2.521416435	2	2.553364277
P09139	VLNAPPGISLISFNDK	1.704770486	2	2.637414217
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**1.224249509**	**0.17976**	**2**
P09456	**KAP0 cAMP_dependent protein kinase type I_alpha regulatory subunit**	**1.096277509**	**0.98087**	**2**
P09456	LTVADALEPVQFEDGQK	1.184677973	2	4.177518368
P09456	SENEEFVEVGR	1.014282609	2	2.318448544
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.062932914**	**0.00047**	**11**
P09495	EDKYEEEIK	0.47041845	1	2.21056509
P09495	EENVGLHQTLDQTLNELNCI	1.791827593	2	4.836336136
P09495	IQALQQQADDAEDR	1.393373496	2	4.660092831
P09495	IQLVEEELDR	0.892101661	2	3.430251598
P09495	IQLVEEELDRAQER	0.946722647	2	3.119031668
P09495	KLVILEGELER	0.699445791	2	2.958195925
P09495	LEEAEKAADESER	0.754701703	2	4.061527729
P09495	LVILEGELER	0.826844371	2	3.336939335
P09495	MEIQEMQLK	0.550212281	2	2.518589258
P09495	RIQLVEEELDR	0.870858591	2	2.712732792
P09495	YSEKEDKYEEEIK	1.274339649	2	4.544022083
P09527	**RAB7A Ras_related protein Rab_7a**	**0.982849785**	**0.96577**	**7**
P09527	ATIGADFLTK	1.076922457	2	2.354333162
P09527	DPENFPFVVLGNK	0.944938242	2	3.264183998
P09527	GADCCVLVFDVTAPNTFK	1.143079246	2	4.194108009
P09527	TSLMNQYVNK	1.049143907	2	2.638431787
P09527	TSLMNQYVNKK	1.036797666	2	2.326337099
P09527	VIILGDSGVGK	1.169119314	2	2.362135649
P09527	TLDSWRDEFLIQASPR	1.055976933	3	3.834145308
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**0.92832429**	**0.99735**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	0.987750768	2	3.58598876
P09605	LSEMTEQDQQR	0.928302516	2	3.349126101
P09606	**GLNA Glutamine synthetase**	**1.326142183**	**0.06972**	**8**
P09606	CIEEAIDK	1.143023784	2	2.322644949
P09606	LTGFHETSNINDFSAGVANR	1.414030314	2	5.877891064
P09606	MGDHLWVAR	1.131946443	2	3.001159906
P09606	QMYMNLPQGEK	1.093104651	2	2.5490098
P09606	TCLLNETGDEPFQYK	1.117303714	2	5.436609745
P09606	TCLLNETGDEPFQYKN	1.857432678	2	5.199202061

P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.305924779	3	4.982322693
P09606	RLTGFHETSNINDFSAGVANR	1.097653363	3	5.439883709
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**0.998033356**	**0.16497**	**2**
P09626	VDNSSLTGESEPQTR	0.992614408	2	4.37604475
P09626	VIMVTGDHPITAK	1.585091466	2	2.927926779
P09739	**TNNT3 Troponin T_ fast skeletal muscle**	**1.031859969**	**0.30344**	**3**
P09739	ELWDTLYQLETDKFEFGEK	0.848107373	2	3.999119759
P09739	KEEEELIALK	1.055559084	2	2.329298019
P09739	KKEEEELIALK	0.685603818	3	3.674286366
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.118647372**	**0.55838**	**23**
P09811	DLSQLTK	0.968008571	1	2.043612719
P09811	IFVDIEK	1.254755622	1	1.956813574
P09811	VDDVAALDK	1.027470348	1	1.958987355
P09811	DFSELEPDKFQNK	0.821371883	2	3.328881979
P09811	EGWQVEEADDWLR	0.91277418	2	3.569577694
P09811	GIVGVENVAELK	0.915018792	2	3.228814602
P09811	GIVGVENVAELKK	1.160694433	2	3.401254416
P09811	HLQIIYEINQK	1.009897265	2	3.870623112
P09811	LVIDQIDNGFFSPNQPDLFK	1.190962881	2	4.902861595
P09811	LVTSVAEVVNNDPMVGSK	1.301906023	2	4.281748772
P09811	MSLIEEEGGKR	1.331749226	2	2.793661833
P09811	TFAYTNHTVLPEALER	1.209797455	2	4.448800564
P09811	VFADYEAYVK	1.083974469	2	2.750363111
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.159498434	2	6.078500748
P09811	VLYPNDNFFEGK	1.072079545	2	2.907433033
P09811	VSQLYMNQK	1.065750443	2	2.601977587
P09811	WLLLCNPGLADLIAEK	1.008181477	2	4.710886955
P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	0.850019119	2	2.92583704
P09811	YEYGIFNQK	1.12385032	2	2.326445818
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.222605093	3	5.589896202
P09811	INMAHLCIVGCHAVNGVAK	1.425550254	3	4.179925442
P09811	LHSFVGDDIFLR	3.687260394	3	3.321690321
P09811	VDDVAALDKK	1.163418632	3	3.303032398
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**1.080969928**	**0.67454**	**2**
P09812	NLAENISR	1.070023181	1	2.753947258
P09812	VIFLENYR	1.653358143	2	2.457214117
P09838	**TDT DNA nucleotidylexotransferase**	**1.043813886**	**0.95833**	**2**
P09838	KMMLDNHALYDRTK+Oxidation(2)	1.043813886	2	2.34814477
P09838	KMMLDNHALYDRTK+Oxidation(3)	1.043813886	2	2.400234699
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**0.988673504**	**0.99998**	**8**
P09875	FDGKKPDTLGSNTR	1.261836319	2	2.707607031
P09875	FSGGLPLPPSYVPVVLSELSDR	1.048659077	2	3.897190332
P09875	IILNELAQR	1.274639326	2	2.408900499

P09875	SDLEYSFAK	0.959048737	2	2.648369312
P09875	SWSQFYSDVLGRPTTLTEMMGK	1.017265885	2	3.871595144
P09875	VDFSILSTTGLLTALK	1.104665199	2	4.370866299
P09875	VFNEYSDVVENLCK	1.008112314	2	2.885116577
P09875	ANVVASALAQIPQK	0.947204732	3	4.334767342
P09895	**RL5 60S ribosomal protein L5**	**1.103754866**	**0.01027**	**6**
P09895	GAVDGGLSIPHSTK	1.15315258	2	4.977292061
P09895	HIMGQNVADYMR	0.985632115	2	3.22737956
P09895	NNVTPDMMEEMYK	1.006282702	2	3.035978317
P09895	RFPGYDSESK	1.070516723	2	2.607470989
P09895	YLMEEDEDAYKK	1.187740128	2	3.473121405
P09895	IEGDMIVCAAYAHELPK	1.013546016	3	3.387053013
P0C0S7	**H2AZ Histone H2A.Z**	**1.109688331**	**0.99983**	**2**
P0C0S7	GDEELDSLIK	0.973359146	1	2.196940899
P0C0S7	ATIAGGGVIPHIHK	1.109065409	2	3.704195023
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**1.014575196**	**0.52392**	**20**
P0C2X9	AIEAAVLAR	1.03451175	2	2.933066845
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.855286728	2	5.257025719
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	1.341879416	2	2.974384785
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.703291791	2	5.221261501
P0C2X9	EEIFGPVLTVYVYPDEK	0.958451058	2	4.393566132
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	0.716945211	2	4.445161819
P0C2X9	KEWDLKPVADR	1.005725675	2	3.593531847
P0C2X9	LLEEHSR	0.831282216	2	2.371658087
P0C2X9	LYVPQSLWPQIK	3.388540923	2	3.569741011
P0C2X9	NAAGNFYINDK	1.360545053	2	2.468804598
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.157997159	2	5.692126751
P0C2X9	SAFEYGGQK	1.12986388	2	2.903755665
P0C2X9	STGSVVGQQPFGGAR	1.003702557	2	4.229782104
P0C2X9	TIVQEATR	1.072534721	2	2.543223381
P0C2X9	VANEPILAFTQGSPER	1.051095264	2	5.336018085
P0C2X9	VGNPAEDFGTFFSAVIDAK	0.860002747	2	4.828312874
P0C2X9	YQLSPFNHGHK	1.16838065	2	2.9401052
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	0.93259409	3	3.723867893
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.886266372	3	5.979300022
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	0.721248566	3	3.378230095
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.156519194**	**1E-07**	**4**
P0C5H9	DRDVTFSPATIEEELIK	1.102449089	2	4.972234726
P0C5H9	DVTFSPATIEEELIK	1.011146922	2	2.989422321
P0C5H9	ILDDWGEMCK	1.144453402	2	3.160619736
P0C5H9	IINEVSKPLAHHIPVEK	1.277132853	3	4.259290695
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.105469096**	**0.24539**	**2**

P0C6F1	EKVEVMSLELEDAK+Oxidation(6)	1.104994437	2	2.68745923
P0C6F1	TMPLISDLR+Oxidation(2)	1.113992701	2	2.306237221
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.112266896**	**9.9E-20**	**10**
P10111	EGMSIVEAMER	0.662506534	2	3.195190191
P10111	FEDENFILK	1.140430423	2	3.217045784
P10111	IIPGFMCQGGDFTR	1.53894246	2	2.886377811
P10111	KITISDCGQL	1.277803669	2	3.483732462
P10111	SIYGEKFEDENFILK	1.189059585	2	4.674582481
P10111	TEWLDGK	1.027940427	2	2.383071184
P10111	VCFELFADK	1.339953627	2	3.364836931
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.008219	3	6.275004864
P10111	VCFELFADKVPK	1.321383778	3	3.717035055
P10111	VKEGMSIVEAMER	1.23081188	3	3.443871737
P10536	**RAB1B Ras_related protein Rab_1B**	**1.068582929**	**0.12198**	**3**
P10536	MGPGAASGGERPNLK	1.293609473	2	3.894422293
P10536	NATNVEQAFMTMAAEIK+Oxidation(10)	0.954225117	2	4.160442352
P10536	NATNVEQAFMTMAAEIK+Oxidation(12)	0.954382032	2	3.801312923
P10633	**CP2D1 Cytochrome P450 2D1**	**1.246278402**	**0.17342**	**4**
P10633	SQGVILASYGPEWR	0.642553611	2	3.994930029
P10633	TFMALLDNLLAENR	1.460191086	2	3.691400766
P10633	YGDVFSLQK	0.941338815	2	2.522557735
P10633	GTTLIINLSSVLKDETVWEKPHR	1.057205154	3	3.959924936
P10634	**CP2DQ Cytochrome P450 2D26**	**1.145686051**	**0.0251**	**20**
P10634	ACLGEPLAR	0.822810154	2	2.751560926
P10634	DMTDAFLAEMQK	0.590455433	2	2.544116735
P10634	EAEHPFNPSILLSK	0.720940472	2	2.485780716
P10634	FADIVPTNIPHMTSR	1.229641643	2	2.594512463
P10634	FADIVPTNIPHMTSRDIK	1.446085382	2	2.410597086
P10634	FEYEDPFFNR	0.884543657	2	2.380530596
P10634	FHPEHFLDAQGNFVK	0.975826243	2	4.687509537
P10634	FQGFLIPK	0.85841349	2	2.480246544
P10634	GNPESSFNDENLR	1.016070939	2	4.353241444
P10634	GTTLIPNLSSVLK	0.935214814	2	2.522253513
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.126897009	2	4.660493851
P10634	GVVLAPYGPEWR	0.997177663	2	3.276290417
P10634	LNSFIALVDK	1.64701411	2	2.821019888
P10634	RFEYEDPFFNR	1.079500544	2	3.535578966
P10634	RVHEEIDEVIGQVR	1.055080209	2	4.150885105
P10634	SLEQWVTEEAGHLCDTFAK	1.085733419	2	5.27866745
P10634	SWDPAQPPR	0.924347637	2	2.652755976
P10634	VHEEIDEVIGQVR	0.962665483	2	4.940594196
P10634	AVSNVIASLVYAR	1.022013991	3	4.389504433
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	0.807858357	3	5.411210537

P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.068222923**	**3.2E-12**	**28**
P10719	ILQDYK	1.233507774	1	2.085426807
P10719	AHGGYSVFAGVGER	0.977164639	2	3.98884058
P10719	AIAELGIYPAVDPLDSTSR	0.958155478	2	4.928899765
P10719	EGNDLYHEMIESGVINLK	0.86858182	2	5.368168354
P10719	FLSQPFQVAEVFTGHMGK	1.216468257	2	4.758239269
P10719	FTQAGSEVSALLGR	1.120919884	2	4.798026085
P10719	IGLFGGAGVGK	1.505730651	2	3.324647188
P10719	IMDPNIVGSEHYDVAR	1.104932297	2	4.641401768
P10719	IMDPNIVGSEHYDVAR+Oxidation(2)	1.237771207	2	3.975841284
P10719	IMNVIGEPIDER	1.561897131	2	4.037744045
P10719	IMNVIGEPIDER+Oxidation(2)	1.650457157	2	3.335940123
P10719	IPSAVGYQPTLATDMGTMQER	1.565061217	2	4.889055729
P10719	LVLEVAQHLGESTVR	1.325329788	2	4.844874382
P10719	TIAMDGTEGLVR	1.008280042	2	3.642417669
P10719	TIAMDGTEGLVR+Oxidation(4)	1.214519446	2	2.711362839
P10719	TREGNDLYHEMIESGVINLK	1.074520336	2	6.040424347
P10719	TVLIMELINNVAK	0.820991483	2	5.063540936
P10719	TVLIMELINNVAK+Oxidation(5)	0.882984164	2	2.787698746
P10719	VALTGLTVAEYFR	1.633399305	2	4.106044769
P10719	VALVYGQMNEPPGAR	1.010842559	2	3.550090075
P10719	VLDSGAPIK	1.076449804	2	3.032022953
P10719	VVDLLAPYAK	1.186399413	2	3.234768629
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	1.125589448	3	4.984230518
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	1.186967404	3	3.719862223
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	0.73642682	3	4.875733376
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.23413412	3	5.341989994
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(11)	0.9899915	3	3.781440258
P10719	VLDSGAPIKIPVGPETLGR	1.035881836	3	4.454595089
P10760	**SAHH Adenosylhomocysteinase**	**1.101554282**	**9.9E-20**	**16**
P10760	SKFDNLYGCR	1.19982286	1	3.197076797
P10760	AGIPVFAWK	1.102747606	2	2.72345233
P10760	ALDIAENEMPGLMR	1.06438973	2	3.189830542
P10760	ATDVMIAGK	1.040776179	2	2.777018547
P10760	DGPLNMILDDGGDLTNLIHTK	1.21007634	2	5.570093632
P10760	FDNLYGCR	1.194141986	2	2.764606237
P10760	GETDEEYLWCIEQTLHFK	1.347857062	2	4.330360889
P10760	GISEETTTGVHNLYK	1.105456248	2	4.260594368
P10760	IILLAEGR	1.486505237	2	2.717395306
P10760	KLDEAVAEAHLGK	1.167771838	2	4.782101631
P10760	LDEAVAEAHLGK	1.118314778	2	3.355521202
P10760	VAVVAGYGDVGK	1.373772929	2	4.158931255
P10760	VNIKPQVDR	1.233659326	2	2.815467358

P10760	WLNENAVEK	1.134806867	2	2.723619699
P10760	WSSCNIFSTQDHAAAAIAK	1.437184078	2	5.017638206
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(6)	0.95025849	3	3.368877411
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**1.085632661**	**0.21722**	**2**
P10818	HEEHERPEFVAYPHLR	1.015605502	3	3.825531483
P10818	SRHEEHERPEFVAYPHLR	1.109655719	3	3.952997446
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**1.330164842**	**9.9E-20**	**26**
P10860	ALASLMTYK	1.052850663	2	3.454084873
P10860	CAVVDVPFGGAK	1.145005197	2	3.288215399
P10860	CVGVGESDGSIWNPDGIDPK	1.082176937	2	5.305278301
P10860	DDGSWEVIEGYR	0.636622865	2	3.950361013
P10860	DIVHSGLAYTMER	0.661318835	2	3.381713867
P10860	DSNYHLLMSVQESLER	0.911458189	2	4.173229694
P10860	GASIVEDKLVEDLK	1.472566563	2	3.683504343
P10860	GFIGPGIDVPAPDMSTGER	1.106629049	2	5.171654701
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(14)	1.068002775	2	4.548741817
P10860	HGGTIPVVPTAEFQDR	1.138512646	2	4.675029278
P10860	IIAEGANGPTTPEADK	1.05053605	2	5.367348194
P10860	IIAEGANGPTTPEADKIFLER	1.195727852	2	4.975968361
P10860	KGFIGPGIDVPAPDMSTGER	1.114875913	2	5.035651684
P10860	MVEGFFDR	1.143524231	2	3.028182983
P10860	MVEGFFDR+Oxidation(1)	1.280938375	2	2.470053196
P10860	NLNHVSYGR	1.190776962	2	2.369826794
P10860	NYTDNELEK	1.116725724	2	2.496811867
P10860	RDDGSWEVIEGYR	1.210345513	2	3.616101742
P10860	RFTMELAK	1.269978614	2	2.471533537
P10860	TAAYVNAIEK	1.24565475	2	3.414144993
P10860	TFVVQGFGNVGLHSMR	1.2871201	2	4.527501106
P10860	YNLGLDLR	1.125111899	2	3.25063467
P10860	YSTDVSVDEVK	1.039853298	2	3.373617172
P10860	IIKPCNHVLSLSFPIR	1.188679216	3	3.517613173
P10860	LQHGSILGFPK	1.617020136	3	3.390925407
P10860	VYEGSILEADCDILIPAASEK	1.087394676	3	5.838824749
P10867	**GGLO L_gulonolactone oxidase**	**1.100654186**	**0.24365**	**5**
P10867	GDDILLSPCFQR	0.932252398	2	3.107581615
P10867	LDPTGMFLNSYLEK	0.9273902	2	4.134648323
P10867	LDYWLAYETIMK	1.065746473	2	4.068061352
P10867	TYGCSPEVYYQPTSVEEVR	0.878191042	2	4.987960815
P10867	VVAHYPVEVR	1.220826494	2	2.48660183
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.096438596**	**0.52285**	**6**
P10868	ENICTEVMALVPPADCR	0.821100646	2	3.075416088
P10868	LQNWALK	1.101125311	2	2.451489925

P10868	WETPYMHSLAAAAASR	1.387614388	2	2.887610912
P10868	YYAFPQMITPLVTK	0.819408211	2	3.851308823
P10868	EHWIIECNDGVFQR	0.890471518	3	3.37182641
P10868	YTDITAMFEETQVPALLEAGFQR	1.154638995	3	6.898396492
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.048626183**	**0.22105**	**4**
P10888	DYPLPDVAHVK	0.826229294	2	2.705712795
P10888	IQFNESFAEMNK	1.183236502	2	3.8960042
P10888	SEDYALPSYVDR	1.014826581	2	3.979999304
P10888	VNPIQGFSAK	1.208552626	2	2.318281174
P10959	**EST2 Liver carboxylesterase 1**	**0.971455027**	**0.18539**	**2**
P10959	AISESGVVLTTNLDKK	0.768777045	2	3.52784586
P10959	EGASEEETNLSKLVMK	1.304804422	2	2.326089859
P11030	**ACBP Acyl_CoA_binding protein**	**1.14509099**	**0.8364**	**4**
P11030	WDSWNK	0.94669814	1	1.946791053
P11030	QATVGDVNTDRPGLLDLK	1.257132898	2	3.390898466
P11030	TQPTDEEMLFIYSHFK	1.54667975	2	4.342547417
P11030	TYVEKVEELK	1.096950372	2	2.831024408
P11232	**THIO Thioredoxin**	**1.109327394**	**9.9E-20**	**2**
P11232	EAFQEALAAAGDK	0.557253809	2	4.800396442
P11232	VGEFSGANK	1.110170099	2	3.073779106
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**1.076240655**	**0.27328**	**6**
P11240	GMNTLVGYDLVPEPK	1.034525618	2	4.410397053
P11240	IIDAALR	1.10267327	2	2.332580805
P11240	LNDFASAVR	1.066534449	2	3.336289644
P11240	RLNDFASAVR	1.342409464	2	2.420677423
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.458827367	3	6.863557816
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.423105261	3	7.046726227
P11348	**DHPR Dihydropteridine reductase**	**1.14957946**	**0.9565**	**10**
P11348	NCDLMWK	1.109695585	1	2.315269232
P11348	AALDGTPGMIGYGMAK	1.372220021	2	3.796345472
P11348	EGGLLTLAGAK	1.070983808	2	2.767081976
P11348	GAVHQLCQSLAGK	1.294873483	2	3.839771271
P11348	MTDSFTEQADQVTAEVGK	0.88060778	2	5.769455433
P11348	MTDSFTEQADQVTAEVGK+Oxidation(1)	1.239240466	2	4.853416443
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.165804176	2	5.299614429
P11348	QSIWTSTISSHLATK	1.216093944	2	3.606249332
P11348	RPNSGSLIQVVTTDGK	0.67613325	2	3.765700579
P11348	VDAILCVAGGWAGGNAK	1.144791743	2	4.200397491
P11442	**CLH Clathrin heavy chain 1**	**1.175811093**	**8.1E-11**	**40**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	0.652413615	2	5.466551781
P11442	AFMTADLPNELIELLEK	1.157233969	2	4.172587872
P11442	AHIAQLCEK	1.639534448	2	2.588712454

P11442	ALEHFTDLYDIK	1.190848795	2	3.3691504
P11442	CNEPAVWSQLAK	1.03257661	2	2.672060728
P11442	EDKLECSEELGDLVK	0.967435325	2	2.98283577
P11442	FNALFAQGNYSEAAK	0.941962917	2	4.278571606
P11442	GQCDLELINVCNENSLFK	1.012493691	2	4.904414177
P11442	GQFSTDELVAEVEK	1.330772651	2	3.851697922
P11442	GQFSTDELVAEVEKR	1.074015581	2	3.521629572
P11442	HELIEFR	1.017853437	2	2.629707336
P11442	HSSLAGCQIINYR	1.100015992	2	3.143580437
P11442	IHEGCEEPATHNALAK	1.187765909	2	5.160325527
P11442	ISGETIFVTAPHEATAGIIGVNR	1.175192131	2	5.499844074
P11442	IVLDNSVFSEHR	1.556425354	2	2.813750029
P11442	IYIDSNNNPER	1.053212566	2	3.07195282
P11442	KFNALFAQGNYSEAAK	1.185117223	2	3.62978673
P11442	LAELEEFINGPNNAHIQQVGDR	1.043080598	2	5.22302866
P11442	LECSEELGDLVK	1.320169589	2	3.013247728
P11442	LHIIEVGTPPTGNQPFPK	1.139161234	2	4.128503323
P11442	LLYNNVSNFGR	1.172336297	2	2.777089834
P11442	LPVVIGGLLDVDCSEDVIK	1.124232287	2	5.113552094
P11442	LTDQLPLIIVCDR	1.015574076	2	3.229765415
P11442	NLQNLLILTAIK	1.229907792	2	4.343196869
P11442	NNLAGAEELFAR	0.957934338	2	3.782678604
P11442	SVDPTLALSVYLR	0.968357708	2	2.64977622
P11442	SVNESLNNLFITEEDYQALR	1.09289619	2	4.644442558
P11442	TLQIFNIEMK	1.021634892	2	2.796615839
P11442	TSIDAYDNFDNISLAQR	1.011081907	2	4.987639904
P11442	VDKLDASESLR	1.182215206	2	2.533713102
P11442	VGEQAQVVIIDMNDPSNPIR	1.0032315	2	5.296023846
P11442	VIQCFAETGQVQK	1.301127546	2	4.75095129
P11442	VSQPIEGHAASFAQFK	1.086763599	2	4.136192799
P11442	WLLLTGISAQQNR	1.21362539	2	2.634001732
P11442	YESLELCRPVLQQGR	0.970862501	2	3.210555077
P11442	KDPELWGSVLLESNPYR	1.130043694	3	3.484855413
P11442	KFDVNTSAVQVLIEHIGNLDR	1.135139195	3	5.905497551
P11442	LLEMNLMHAPQVADAILGNQMFTHYDR	1.041338099	3	3.95717907
P11442	NNRPSEGPLQTR	1.103007108	3	3.933251619
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.035463557	3	5.842098236
P11497	**ACACA Acetyl_CoA carboxylase 1**	**0.881869058**	**0.55637**	**3**
P11497	ECSQPVMVYIPPQAELR+Oxidation(7)	0.88182268	2	2.439479113
P11497	LPELLLK	0.913707801	2	2.492558002
P11497	TLRDPSLPLLELQDIMTSVSGR	1.284313439	3	3.969368696
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.87746502**	**0.27734**	**5**

P11507	DIVPGDIVEIAVGDKVPADIR	1.060874763	2	3.685843229
P11507	IRDEMVATEQER	1.021568153	2	3.193726301
P11507	KSEIGIAMGSGTAVAK	0.799926643	2	3.186424255
P11507	TASEMVLADDNFSTIVAAVEEGR	1.147644498	2	2.869868279
P11507	VDQSILTGESVSVIK	0.794582581	2	4.111185551
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.158765174**	**9.9E-20**	**25**
P11598	DGEEAGAYDGPR	0.74014958	2	3.445865393
P11598	DLLTAYYDVDYEK	0.920916216	2	3.668124437
P11598	DPNIVIAK	1.447107565	2	2.377151012
P11598	EATNPPIIQEEKPK	0.906533143	2	3.648104191
P11598	EYDDNGEGITIFRPLHLANK	0.979209926	2	3.987533569
P11598	FISDKDASVVGFFR	1.350618604	2	4.558806419
P11598	FLQEYFDGNLK	1.04220807	2	3.72903657
P11598	FLQEYFDGNLKR	1.418196292	2	3.707463026
P11598	FVMQEEFSR	1.289563388	2	2.989457846
P11598	GFPTIYFSPANK	0.892978032	2	2.797986746
P11598	IFRDGEEAGAYDGPR	1.191203639	2	4.139390469
P11598	KQAGPASVPLR	1.264470634	2	2.412615776
P11598	LAPEYEAAATR	1.121989043	2	2.875238895
P11598	LNFAVASR	1.709092732	2	2.667378664
P11598	MDATANDVPSPYEVK	1.198268308	2	4.330312252
P11598	MDATANDVPSPYEVK+Oxidation(1)	1.234506422	2	3.988277674
P11598	RLAPEYEAAATR	1.132887888	2	3.350922108
P11598	SEPIPETNEGPVK	1.103410039	2	2.954803228
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.139023265	2	5.975343227
P11598	VDCTANTNTCNK	1.204727102	2	4.460864544
P11598	YGVSGYPTLK	1.09125184	2	2.893121004
P11598	EYDDNGEGITIFRPLHLANKFEDK	1.152696435	3	3.809692621
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.115746429	3	5.281380177
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.177899548	3	4.451574326
P11598	LSKDPNIVIAK	1.273148326	3	4.333740234
P11608	**ATP8 ATP synthase protein 8**	**1.125861262**	**0.85935**	**2**
P11608	ISSQTFPAPPSPK	1.14310629	2	2.375633478
P11608	TNNPWESK	1.080236822	2	2.359498739
P11711	**CP2A1 Cytochrome P450 2A1**	**0.996189614**	**0.99987**	**5**
P11711	GEQATYNTLFK	0.942345563	2	3.128634453
P11711	GTDVFPILGSLMTDPK	1.016012976	2	3.473768711
P11711	ILEEAGYLIK	1.120139064	2	2.78407979
P11711	TVSNVISSIVFGER	1.140398654	2	3.170994759
P11711	VHEEIEQVIGR	0.948402742	2	3.420905352
P11714	**CP2D9 Cytochrome P450 2D9**	**1.177216464**	**0.04303**	**2**
P11714	GNPESSFNDENLLMVVR	1.03078707	2	2.579715252
P11714	VQQEIDEVIGQVR	1.191103349	2	4.621613503

P11862	**GAS2 Growth arrest_specific protein 2**	**1.074378482**	**0.92481**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.437941621	2	3.909667253
P11862	LDNGALLCQLAATVQEK	1.059428502	2	3.902297735
P11862	YGVEPPGLIK	1.084797626	2	2.523393393
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**1.021048513**	**9.9E-20**	**24**
P11884	DGMTIAKEEIFGPVMQILK	1.003296404	2	3.823958874
P11884	EEIFGPVMQILK	0.771276444	2	3.910346746
P11884	ELGEYGLQAYTEVK	0.677769933	2	4.570565224
P11884	GYFIQPTVFGDVK	0.825981932	2	3.924601316
P11884	LGPALATGNVVVMK	1.308724653	2	4.067557335
P11884	LGPALATGNVVVMK+Oxidation(13)	1.437479151	2	3.59059
P11884	LLCGGGAAADR	1.597346982	2	3.784983635
P11884	RVTLELGGK	1.115203927	2	2.784054041
P11884	TEQGPQVDETQFK	1.020940136	2	4.543169975
P11884	TEQGPQVDETQFKK	1.178759221	2	3.850818396
P11884	TFPTVNPSTGEVICQVAEGNK	0.649126236	2	5.299621105
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.994338144	2	4.290913105
P11884	TFVQEDVYDEFVER	1.165154638	2	5.23867321
P11884	TIEEVVGR	1.015989095	2	3.024271965
P11884	TIPIDGDFFSYTR	0.916907949	2	2.511714458
P11884	VAEQTPLTALYVANLIK	1.457232617	2	5.490668774
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.044316066	2	5.785320282
P11884	VTLELGGK	1.117310053	2	2.304816723
P11884	VVGNPFDSR	1.020836536	2	3.042837143
P11884	YGLAAAVFTK	1.128757249	2	3.872758627
P11884	YYAGWADK	1.063632173	2	2.550104141
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.908685622	3	4.206560612
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	1.019056803	3	4.131679058
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.079125717	3	3.803150177
P11915	**NLTP Non_specific lipid_transfer protein**	**0.99348808**	**0.01483**	**22**
P11915	ADCTITMADSDLLALMTGK	1.324680299	2	5.335825443
P11915	ADCTITMADSDLLALMTGK+Oxidation(7)	1.003491554	2	3.626098871
P11915	ANLIFK	1.08345928	2	2.392467737
P11915	AVEIVAQEMVTDMPSTFEEK	1.162225142	2	4.339728355
P11915	GSVLPDSDKK	1.058791085	2	2.781841993
P11915	HIDVLINK	1.092966102	2	2.868802786
P11915	IGGIFAFK	2.202191959	2	2.428835869
P11915	KADCTITMADSDLLALMTGK	1.22984606	2	4.259275913
P11915	KLEEEGEEFVK	1.037028881	2	4.324304104
P11915	LEEEGEEFVK	1.250109494	2	3.029355049
P11915	LEEEGEEFVKK	1.116736689	2	3.687112331
P11915	LQSLQLQPDK	1.453001191	2	3.298052549
P11915	MGFPEAASSFR	1.252909438	2	2.920224667

P11915	MNPQSAFFQGK	1.015372712	2	3.19330883
P11915	MNPQSAFFQGK+Oxidation(1)	0.221307236	2	2.576643467
P11915	THQISAAPTSSAGDGFK	1.384763446	2	4.49084425
P11915	WVINPSGGLISK	1.152845285	2	2.891032457
P11915	YGMSACPFAPQLFGSAGK	0.843366259	2	4.384728909
P11915	HGLQSKAVEIVAQEMVTDMPSTFEEKSVIK+Oxidation(15)Oxidation(19)	0.942958667	3	3.384591579
P11915	HSVNNPYSQFQDEYSLDEIMK	1.06251929	3	5.664580345
P11915	KLEEEGEEFVKK	1.111177407	3	4.748982906
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.363783916	3	5.530677795
P11960	**ODBA 2_oxoisovalerate dehydrogenase subunit alpha_ mitochondrial (Fragment)**	**1.035627151**	**0.73007**	**10**
P11960	TDLVFGQYR	1.055283813	1	1.982256174
P11960	AVAENQPFLIEAMTYR	1.097588976	2	3.791732311
P11960	HFVTISSPLATQIPQAVGAAYAAK	0.841597869	2	4.131171703
P11960	NNGYAISTPTSEQYR	1.034319718	2	3.977689266
P11960	QGQIINPSEDPHLPQEEVLK	1.03693031	2	2.520677328
P11960	QYLLNQGWWDEEQEK	0.826439105	2	3.593105078
P11960	SVDEVNYWDK	1.106089229	2	2.465878725
P11960	VMEAFEQAER	1.009541543	2	3.618213177
P11960	HLQTYGEHYPLDHFDK	0.880070332	3	3.415318966
P11960	IGHHSTSDDSSAYR	1.537761566	3	4.056050777
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**0.91883621**	**0.90927**	**3**
P11980	GVNLPGAAVDLPAVSEK	1.048521522	2	3.856466055
P11980	NTGIICTIGPASR	0.926232788	2	3.630494833
P11980	AEGSDVANAVLDGADCIMLSGETAK	0.780213237	3	3.648101091
P12001	**RL18 60S ribosomal protein L18**	**1.147985097**	**4.5E-08**	**5**
P12001	GTVLLSGPR	1.101125932	2	2.697547674
P12001	ILTFDQLALESPK	1.454793325	2	4.8977561
P12001	TAVVVGTITDDVR	1.20299334	2	4.058363914
P12001	TNSTFNQVVLK	1.028227586	2	3.064238071
P12001	TNRPPLSLSR	1.152309834	3	3.376418829
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**0.947367268**	**0.99985**	**9**
P12007	AQEIDQSNDFK	0.74230498	2	3.557794809
P12007	FVQENLAPK	1.050340507	2	2.849884748
P12007	FWITNGPDADVLVVYAK	1.182931338	2	4.609944344
P12007	GSNTCELVFEDCK	0.954815208	2	4.24366188
P12007	GVYVLMSGLDLER	0.9875435	2	3.72927022
P12007	IGQFQLMQGK	1.458842374	2	2.668593407
P12007	LYEIGGGTSEVR	1.11523244	2	2.830498934
P12007	TDLTAVPASR	1.091523145	2	2.851703882
P12007	GSNTCELVFEDCKVPAANILSQESK	1.167104955	3	5.398565769
P12346	**TRFE Serotransferrin**	**1.095200911**	**0.00108**	**19**
P12346	ADRDQYELLCLDNTR	1.291368777	2	4.336149693

P12346	ASDSSINWNNLK	1.244067159	2	3.187478304
P12346	DFQLFGSPLGK	0.728801199	2	2.982681751
P12346	DLKQEDFQLLCPDGTK	1.096147401	2	5.024483204
P12346	EGVCPEGSIDSAPVK	0.648148618	2	3.848221779
P12346	FDEFFSQGCAPGYK	1.14846357	2	4.540841103
P12346	GDKDCTGNFCLFR	1.010334489	2	3.440336943
P12346	GTDFQLNQLQGK	1.091221947	2	3.193485498
P12346	GYYAVAVVK	1.084265762	2	2.388500929
P12346	HQTVLENTNGK	0.884611965	2	3.042891502
P12346	HTTIFEVLPQK	1.121292742	2	3.47261858
P12346	KGTDFQLNQLQGK	1.154135731	2	4.154240608
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.184250728	2	4.733694077
P12346	QEDFQLLCPDGTK	1.105043727	2	3.61021471
P12346	SKDFQLFGSPLGK	0.841975908	2	3.31851697
P12346	VSTVLTAQK	1.211859133	2	2.766580343
P12346	WCALSHQER	1.794423649	2	3.146803856
P12346	WCAVSEHENTK	1.169315951	2	3.791657448
P12346	NGDGKEDLIWEILK	1.095512421	3	3.520635605
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.414248914**	**0.10819**	**2**
P12368	NLDQEQLSQVLDAMFEK	1.426839685	2	4.761984825
P12368	SVGQYDNRGSFGELALMYNTPR	1.199327556	2	2.389774799
P12711	**ADHX Alcohol dehydrogenase class_3**	**0.920499284**	**0.00532**	**10**
P12711	AFDLMHSGNSIR	0.646574677	2	3.118848801
P12711	AGDTVIPLYIPQCGECK	1.00228778	2	3.064471483
P12711	AKEFGATECINPQDFSK	1.070180445	2	4.767474174
P12711	EFGATECINPQDFSK	0.821007241	2	4.629048824
P12711	IIGIDINK	1.189891688	2	2.42186451
P12711	IIGIDINKDK	1.267625265	2	2.416529655
P12711	VCLLGCGISTGYGAAVNTAK	1.419956049	2	5.676909924
P12711	VDEFVTGNLSFDQINK	0.924611711	2	4.955120564
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	1.311518384	2	4.091789722
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.170511658	3	5.930791378
P12749	**RL26 60S ribosomal protein L26**	**1.116409314**	**3.5E-08**	**5**
P12749	FNPFVTSDR	1.04676185	2	2.600344658
P12749	KDDEVQVVR	1.282145551	2	3.160134315
P12749	KIMSSPLSKELR+Oxidation(3)	1.421728035	2	2.473786592
P12749	YKEETIEK	1.160534281	2	2.895754576
P12749	HFNAPSHIR	1.122336347	3	3.972728252
P12785	**FAS Fatty acid synthase**	**1.243960938**	**9.4E-06**	**41**
P12785	ACIDTALENLSTLK	1.56417687	2	3.928814888
P12785	AGSDTELAAPK	1.193308264	2	3.488818407
P12785	ALIAEATK	1.320623284	2	2.314914227

P12785	DANLPAGSMAAVGLSWEECK	0.710241322	2	4.293672562
P12785	DGGFLLMHTVLK	0.944302338	2	2.546758652
P12785	DHKDNLEFFLTNLGK	1.896316945	2	2.368258238
P12785	EEEPEAMLPGAQPTLISAISK	1.146046183	2	4.049019814
P12785	EQGVTFPSGEAQEQLIR	1.272619486	2	4.398286343
P12785	FDASFFGVHPK	1.329496165	2	3.405438423
P12785	FVFTPHVEPECLSESAILQK	1.063546502	2	4.369114876
P12785	GLESIINIIHSSLAEPR	1.355913805	2	4.624364853
P12785	GNAGQSNYGFANSTMER	1.211387985	2	4.485902309
P12785	GVDLVLNSLAEEK	1.095662163	2	3.340507984
P12785	LFDHPEVPIPAESESVSR	1.155932366	2	4.393259048
P12785	LTPGCEAEAEAEAICFFIK	1.342601028	2	4.666091442
P12785	MTVPGLEDLPQHGLPR	1.234006175	2	3.495958328
P12785	QAQLNLSILLVNPEGPTLTR	1.325677224	2	4.358307362
P12785	QQEQLVPTLEK	0.732686868	2	2.625486135
P12785	RQQEQLVPTLEK	0.940803734	2	2.987709761
P12785	SDEALKPLGVK	1.247554054	2	2.991137028
P12785	SFDDSGNGYCR	1.447393216	2	3.034501076
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.248643078	2	5.562194824
P12785	SNMGHPEPASGLAALTK	1.057837232	2	3.191679716
P12785	TGGTYGEDLGADYNLSQVCDGK	1.135317432	2	4.865222454
P12785	TMEAVQGLLEQGR	1.007252313	2	3.568962336
P12785	VGDPQELNGITR	1.458319736	2	2.737977505
P12785	VHLTGIDINPNALFPPVEFPVPR	1.212409433	2	5.232684135
P12785	VLEALLPLK	1.25969231	2	2.625289679
P12785	VLESDLVMNVYR	1.130777335	2	3.043799639
P12785	VTAIYIDPATHLQK	1.315734782	2	3.558335543
P12785	VYATILNAGTNTDGCK	1.064519158	2	4.898737907
P12785	VYMLEGDTQVADVTTSR	0.580769918	2	4.839961052
P12785	VYQWEDPDSK	0.995232341	2	3.317261934
P12785	WLSTSIPEAQWQSSLAR	1.106184598	2	3.535788298
P12785	YNGTLNLDR	1.129660204	2	2.583141088
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.179880671	3	3.442133188
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	1.535351282	3	5.904062271
P12785	LLLPEDPLISGLLNSQALK	1.892257096	3	5.125070572
P12785	LSPQDKPIFLPVEDTSFQWVDSLK	0.909184462	3	3.913658381
P12785	SLSLSLEETPVVFENVTFHQATILPR	1.131853281	3	4.131784439
P12785	VSVHIIEGDHR	1.504731451	3	3.474067211
P12791	**CP2BA Cytochrome P450 2B10**	**1.096852639**	**0.99999**	**2**
P12791	IQEEAQCLVEELR	1.006527101	2	4.581433773
P12791	IQEEAQCLVEELRK	1.211122627	2	3.824499607
P12847	**MYH3 Myosin_3**	**0.607935079**	**0.20992**	**6**
P12847	EQYEEEQEGK	1.254755898	2	3.069120169

P12847	GQEDLKEQLAIVER	1.807317308	2	3.983333826
P12847	GTLEDQIISANPLLEAFGNAK	0.791186531	2	3.287407637
P12847	IEAQNQPFDAK	0.540008648	2	2.378525972
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(1)	0.688411372	2	4.399733543
P12847	MKGTLEDQIISANPLLEAFGNAK	0.475753572	3	6.98020792
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.441597273**	**9.9E-20**	**19**
P12928	AETSDVANAVLDGADCIMLSGETAK	1.19472441	2	5.517800808
P12928	CCAAAIIVLTK	1.166409907	2	2.865659952
P12928	EATESFATSPLSYRPVAIALDTK	1.031657414	2	3.888613939
P12928	EPPEAIWADDVDR	1.184504747	2	2.464012623
P12928	GDLGIEIPAEK	1.221309865	2	3.134979248
P12928	GSFPVEAVMMQHAIAR	1.230231735	2	3.236725092
P12928	GSQVLVTVDPK	1.190706836	2	2.86613965
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.399590479	2	5.25019598
P12928	IGPEGLVTEVEHGGILGSR	1.457437162	2	5.284585953
P12928	IYIDDGLISLVVQK	1.515440869	2	4.519283295
P12928	RVQFGIESGK	1.307189389	2	2.461746693
P12928	STSIIATIGPASR	1.197737955	2	3.324488401
P12928	TGVLQGGPESEVEIVK	0.870488803	2	4.457147121
P12928	TVWVDYHNITR	1.331907885	2	2.330378532
P12928	VQFGIESGK	1.245879644	2	2.833667517
P12928	CNLAGKPVVCATQMLESMITK	1.281659719	3	4.838200569
P12928	KFDEILEVSDGIMVAR	0.171004922	3	4.172465801
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.513692094	3	4.803504467
P12928	LNFSHGSHEYHAESIANIR	1.878661901	3	5.138937473
P12938	**CP2D3 Cytochrome P450 2D3**	**0.882456911**	**0.99109**	**7**
P12938	DLTDAFLAEIEK	0.867271324	2	3.862091303
P12938	FDYGDPDFIK	0.958175194	2	2.921566725
P12938	GNPESSFNDANLR	0.908014024	2	3.935704708
P12938	RFDYGDPDFIK	1.074684433	2	3.120231867
P12938	TFLTMVDNLVTEHK	1.176134827	2	3.09592104
P12938	AVQELLVTCGEDTADRPEMPIFQHIGYGHK	0.72951195	3	3.730769873
P12938	TWDPDQPPRDLTDAFLAEIEK	1.039878947	3	4.041320801
P12939	**CP2DA Cytochrome P450 2D10**	**1.335918929**	**6.4E-14**	**9**
P12939	ALCNVIASLIFAR	1.768776753	2	2.544020176
P12939	FEYEDPYLIR	1.264220249	2	2.848116875
P12939	FGDIAPLNLPR	1.543459861	2	3.447325706
P12939	ITSCDIEVQDFVIPK	1.714133306	2	4.18802309
P12939	NLTDAFLAEVEK	1.199044697	2	4.046593189
P12939	RFEYEDPYLIR	1.439720085	2	2.978718042
P12939	TFMAFLDNLLAENR	1.565971032	2	3.068898201
P12939	TTWDPAQPPR	1.250153439	2	2.36779356
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.425546493	3	5.331332207

P13084	**NPM Nucleophosmin**	**1.328978993**	**1.2E-05**	**2**
P13084	MTDQEAIQDLWQWR	1.183186442	2	2.841659784
P13084	VDNDENEHQLSLR	1.504467321	2	3.887588978
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.098441719**	**0.00611**	**5**
P13086	MGHAGAIIAGGK	1.068967666	1	2.840764761
P13086	NIYIDK	1.214429725	1	1.98727262
P13086	HLGLPVFNTVK	1.045458668	2	2.377262115
P13086	LIGPNCPGIINPGECK	1.685960769	2	4.877100468
P13086	QGTFHSQQALEYGTK	1.13402621	2	2.78468442
P13107	**CP2B3 Cytochrome P450 2B3**	**0.959952916**	**0.17685**	**7**
P13107	SFIQLQEK	1.247955074	1	2.353750706
P13107	ATLDPNAPR	1.103261446	2	2.630428314
P13107	EVLDYIDHSVENHR	1.031187259	2	4.078854084
P13107	FSDVSPMGLPCR	0.792944784	2	3.293252945
P13107	MCLGEGIAR	1.081722415	2	2.82668829
P13107	QSVEDQIKEEAK	0.959864664	2	2.585967064
P13107	GIIAVLQPIMQEYGVSFVNEER	1.463040257	3	6.340869904
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.17055993**	**0.34985**	**4**
P13221	ITWSNPPAQGAR	1.218962857	2	3.196347475
P13221	NLDYVATSINEAVTK	1.095779949	2	3.999975681
P13221	SCASQLVLGDNSPALR	1.342086147	2	4.521241188
P13221	TDDSQPWVLPVVR	0.961904468	2	2.886639118
P13255	**GNMT Glycine N_methyltransferase**	**0.990579988**	**0.08056**	**6**
P13255	AHMVTLDYTVQVPGAGR	1.067738907	2	5.19588089
P13255	AWLLGLLR	1.211168678	2	2.784122944
P13255	DITTSVLTVNNK	0.933027755	2	3.516041994
P13255	NYDYILSTGCAPPGK	0.967175557	2	4.805923462
P13255	SDLTKDITTSVLTVNNK	1.647969903	2	2.746668577
P13255	SLGVAAEGIPDQYADGEAAR	1.001492465	2	5.511157513
P13383	**NUCL Nucleolin**	**0.97057439**	**0.5919**	**6**
P13383	NDLAAVDVR	1.038638539	1	1.905761719
P13383	GFGFVDFNSEEDAK	0.958147867	2	3.344038725
P13383	GSPNARSQPSKTLFVK	1.049507529	2	2.3621068
P13383	SEADAEKNLEEK	0.667173774	2	2.568212509
P13383	TLVLSNLSYSATEETLQEVFEK	1.15139143	2	2.766373634
P13383	NLSFNITEDELKEVFEDAVEIR	0.651969701	3	3.436611176
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**1.055761921**	**1E-09**	**22**
P13437	AANEAGYFNEEMAPIEVK	0.911784886	2	5.136263847
P13437	AANEAGYFNEEMAPIEVK+Oxidation(12)	1.098108713	2	4.87476778
P13437	DAEVVLCGGTESMSQSPYSVR	0.609332454	2	4.566064835
P13437	DFTATDLTEFAAR	0.683463894	2	3.467659235
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(2)	1.055837076	2	3.430994034

P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.891117485	2	5.777636051
P13437	FGLDLK	1.089234059	2	2.336063147
P13437	GVFIVAAK	1.092054935	2	2.521404505
P13437	HNFTPLAR	1.226745375	2	2.330615759
P13437	ITAHLVHELR	2.033718395	2	3.306064606
P13437	LCGSGFQSIVSGCQEICSK	2.052694487	2	5.547416687
P13437	LEDTLWAGLTDQHVK	1.057166361	2	5.247082233
P13437	RTPFGAYGGLLK	1.522901262	2	3.035877943
P13437	SLDLDPSK	1.056473105	2	2.620229244
P13437	TNVSGGAIALGHPLGGSGSR	1.072352848	2	5.854893208
P13437	VGVPTETGALTLNR	1.17918478	2	3.683221579
P13437	YAVGSACIGGGQGISLIIQNTA	0.882679718	2	4.308791161
P13437	DMDLIDVNEAFAPQFLAVQK	1.56889776	3	6.969806671
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	1.047320165	3	4.983426571
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	1.05336633	3	6.662649155
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.195684088	3	5.078184128
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	1.144652205	3	4.208768845
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.214561867**	**9.9E-20**	**8**
P13444	FVIGGPQGDAGVTGR	1.186060076	2	4.565331936
P13444	HIGYDDSAK	1.178329356	2	2.797793388
P13444	SEFPWEVPK	1.130740098	2	2.319064617
P13444	SGVLPWLRPDSK	1.350277358	2	2.969911337
P13444	TQVTVQYVQDNGAVIPVR	1.370007853	2	4.342388153
P13444	ICDQISDAVLDAHLK	1.286183102	3	5.633167744
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.416080241	3	6.753329754
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.306429811	3	5.493741512
P13471	**RS14 40S ribosomal protein S14**	**1.104088902**	**2.9E-10**	**2**
P13471	ADRDESSPYAAMLAAQDVAQR	0.690400603	2	5.436663628
P13471	IEDVTPIPSDSTR	1.142007128	2	3.936299324
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.794926799**	**0.78613**	**20**
P13601	ANNTPYGLAAGVFTK	0.565634226	2	3.937418938
P13601	EEIFGPVQQIMK	0.753063574	2	3.529680967
P13601	EMGEQGVYEYTELK	0.593063655	2	3.678078175
P13601	GFFVQPTVFSNVTDEMR	0.974412908	2	4.179467201
P13601	IFINNEWHNSLNGK	1.078224827	2	4.032707691
P13601	ILDLIESGK	0.8259371	2	3.220338106
P13601	ILDLIESGKK	0.968592588	2	2.951691628
P13601	LFVEESIYDEFVR	0.704150123	2	4.186003685
P13601	VLLATMESMNAGK	0.660063488	2	4.074687958
P13601	VSFTGSTEVGK	0.602876279	2	3.186300755
P13601	YVLGNPLDSGISQGPQIDK	0.62414293	2	4.610680103
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.684206885	2	4.245731831

P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	0.629967307	3	3.78903985
P13601	FPVINPATEEVICHVEEGDK	0.577250237	3	3.749338865
P13601	IAKEEIFGPVQQIMK	1.167418246	3	3.472584009
P13601	IHGQTIPSDGDVFTYTR	1.037714969	3	4.462311268
P13601	KFPVINPATEEVICHVEEGDK	1.141947159	3	3.368245363
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	1.232788765	3	5.277019024
P13601	FPVINPATEEVICHVEEGDKADVDK	1.025139568	4	5.193379879
P13601	KFPVINPATEEVICHVEEGDKADVDK	1.305196666	4	4.826226711
P13697	**MAOX NADP_dependent malic enzyme**	**1.101380598**	**0.99537**	**5**
P13697	AECSAEECYK	0.986475079	2	3.05233717
P13697	AIFASGSPFDPVTLPDGR	1.256002814	2	4.804337978
P13697	GHIASVLNAWPEDVVK	1.111592734	2	4.057563782
P13697	HINDSVFLTTAEVISQQVSDK	0.937097055	2	5.886251926
P13697	ILGLGDLGCNGMGIPVGK	1.161111873	2	2.683139086
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.11904223**	**4E-12**	**13**
P13803	AAVDAGFVPNDMQVGQTGK	1.105375215	2	4.542864799
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(12)	1.51773564	2	3.714374304
P13803	GLLPEELTPLILETQK	1.172390234	2	4.893165112
P13803	GTSFEAAAASGGSASSEK	1.210497488	2	5.160123825
P13803	LGGEVSCLVAGTK	1.119064427	2	4.749477386
P13803	LLYDLADQLHAAVGASR	1.388701291	2	4.933016777
P13803	LNVAPVSDIIEIK	1.293993421	2	4.127431393
P13803	QFSYTHICAGASAFGK	1.019429771	2	3.129345894
P13803	TIYAGNALCTVK	1.082415175	2	3.704957008
P13803	VLVAQHDAYK	1.177778811	2	3.320490837
P13803	VVQDLCK	1.094344478	2	2.801054478
P13803	SDRPELTGAK	1.111614096	3	3.448247194
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.970730026	3	6.951367855
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.194105142**	**0.00126**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.408601139	2	5.135836601
P13832	FTDEEVDELYR	1.145225154	2	3.442534924
P13832	GNFNYIEFTR	1.219677396	2	2.719451904
P14046	**A1I3 Alpha_1_inhibitor 3**	**1.139809069**	**0.9912**	**6**
P14046	FSIDTNGISDYSLNIK	1.085027336	2	2.458673716
P14046	GMYESLPVVAVK	1.047376922	2	3.289045095
P14046	ISLCHGNPTFSSETK	1.870988488	2	3.861707687
P14046	LVDIKGDPIPNEQVLIK	1.164097071	2	3.415861368
P14046	QQNSYGGFSSTQDTVVALDALSK	1.29892697	2	4.394548893
P14046	QSPGPCGSEVATVPETGR	1.09641479	2	3.350817204
P14141	**CAH3 Carbonic anhydrase 3**	**1.069457318**	**7.8E-16**	**16**
P14141	EPMTVSSDQMAK	1.758937769	1	2.974419355
P14141	EAPFNHFDPSCLFPACR	0.627261019	2	4.424545288

P14141	EKGEFQILLDALDK	0.847580649	2	4.52233696
P14141	EKGEFQILLDALDKIK	1.157004031	2	3.574609995
P14141	GDNQSPIELHTK	1.019681141	2	3.648750067
P14141	GEFQILLDALDK	1.091210683	2	4.758408546
P14141	GEFQILLDALDKIK	1.33100132	2	3.672061205
P14141	GGPLSGPYR	1.091882359	2	2.800245762
P14141	QFHLHWGSSDDHGSEHTVDGVK	1.075999293	2	4.729166985
P14141	VVFDDTFDR	1.030681602	2	3.430849791
P14141	YAAELHLVHWNPK	1.060364738	2	4.41928196
P14141	EWGYASHNGPEHWHELYPIAK	0.699318699	3	5.032088757
P14141	GKEAPFNHFDPSCLFPACR	1.028799759	3	4.452027321
P14141	HDPSLQPWSVSYDPGSAK	1.064244894	3	4.839396
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.809944394	3	6.016844273
P14141	YNTFGEALKQPDGIAVVGIFLK	0.967025723	3	5.935792446
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.126996414**	**0.80204**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	1.201895645	2	4.989021301
P14173	ALIPTTAPQEPETYEDIIR	1.059486335	2	3.832613468
P14173	GSNQLNETLLQR	1.304018757	2	3.0522089
P14173	HSHQDSGLITDYR	1.126996203	2	3.465000629
P14173	LVAYTSDQAHSSVER	1.627750564	2	4.516513824
P14173	MLELPEAFLAGR	1.074314473	2	2.621317148
P14173	TDLTEAFNMDPVYLR	0.953261352	2	3.707056999
P14173	TVESAHVQLAWEHIR	1.042946708	3	4.505698681
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.153348219**	**0.04084**	**15**
P14408	YYGAQTVR	1.178402771	1	1.923023582
P14408	AAAEVNQEYGLDPK	1.229999394	2	4.014422894
P14408	AIEMLGGELGSK	1.15228144	2	3.920088291
P14408	IEYDTFGELK	1.144642121	2	3.156110525
P14408	IEYDTFGELKVPTDK	0.958956387	2	3.47807312
P14408	IYELAAGGTAVGTGLNTR	1.213260108	2	5.473001003
P14408	SGLGELILPENEPGSSIMPGK	1.058917613	2	4.798383236
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(18)	0.961651579	2	3.278529882
P14408	SKEFAQVIK	1.144465611	2	2.323045015
P14408	TAIELGYLTAEQFDEWVKPK	1.307276378	2	4.899390697
P14408	KTAIELGYLTAEQFDEWVKPK	1.188064064	3	4.735435486
P14408	LMNESLMLVTALNPHIGYDK	1.643553182	3	5.38368082
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.963460273	3	6.588690758
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.14301468	3	5.033370495
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	0.772707081	3	6.408947468
P14480	**FIBB Fibrinogen beta chain**	**1.042770578**	**0.99937**	**7**
P14480	DNENVINEYSSILEDQK	0.989867247	2	3.271347523
P14480	GFGNIATNEDTK	1.116169632	2	3.037185669
P14480	GFGNIATNEDTKK	1.079732717	2	3.165142298

P14480	LYIDETVNDNIPLNLR	1.118178442	2	3.265820742
P14480	TENGGWTVIQNR	0.856023304	2	2.786273479
P14480	YCGLPGEYWLGNDK	0.83611653	2	3.273317099
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.001788098	3	4.990393162
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**1.255446321**	**0.80572**	**10**
P14604	AFAAGADIK	1.014475741	2	3.045915842
P14604	AQFGQPEILLGTIPGAGGTQR	0.979862932	2	5.695135593
P14604	ESVNAAFEMTLTEGNKLEK	0.628610525	2	3.735871315
P14604	FLSHWDHITR	1.02999998	2	3.135186195
P14604	IFPVETLVEEAIQCAEK	1.245201515	2	5.532610893
P14604	LFYSTFATDDR	1.046979791	2	2.520432234
P14604	NSSVGLIQLNRPK	1.085689339	2	3.452644348
P14604	SLAMEMVLTGDR	0.916106622	2	3.654171705
P14604	SLAMEMVLTGDRISAQDAK+Oxidation(4)Oxidation(6)	0.948655013	2	2.357272387
P14604	TFQDCYSGK	1.103413945	2	2.564814568
P14668	**ANXA5 Annexin A5**	**1.223169841**	**0.00072**	**3**
P14668	ETSGNLENLLLAVVK	1.088693816	2	2.515480518
P14668	GLGTDEDSILNLLTAR	1.54469047	2	4.530513287
P14668	GTVTDFSGFDGR	1.052567338	2	2.954829693
P14669	**ANXA3 Annexin A3**	**1.138216865**	**0.02817**	**8**
P14669	GMGTDEDTLIEILTTR	1.142700341	2	4.289757729
P14669	GTINNYPGFNPSVDAEAIR	1.01969946	2	3.626094103
P14669	KDAQTLYDAGEK	1.448834777	2	2.943830729
P14669	KDAQTLYDAGEKK	1.096425781	2	3.331220388
P14669	QYQEAYEQALK	1.080258379	2	3.018727541
P14669	SEIDLLDIR	1.235496443	2	2.684845448
P14669	TLINILTER	1.388967593	2	2.944310427
P14669	WGTDEDKFTEILCLR	1.218940791	2	3.559969902
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.099566445**	**0.80008**	**3**
P14685	AIQLEYSEAR	0.993630655	2	2.71694994
P14685	LQLDSPEDAEFIVAK	1.100321297	2	3.893123865
P14685	SVFPEQANNNEWAR	1.057921912	2	2.530438662
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.092932022**	**0.15792**	**3**
P14740	LGTLEVEDQIEAAR	1.043997844	2	3.940571547
P14740	VLEDNSALDK	1.186048225	2	3.042428493
P14740	YMGLPTPEDNLDHYR	1.40945254	2	2.467093706
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.061124826**	**0.9983**	**11**
P14882	FLSDVYPDGFK	1.132216418	2	3.007523298
P14882	FSSQEAASSFGDDR	1.009525576	2	3.795495749
P14882	HGNALWLNER	0.884163521	2	2.935956955
P14882	HIEIQVLGDK	1.064031103	2	2.363935947
P14882	MADEAVCVGPAPTSK	1.038894056	2	4.183652878

P14882	SYLNMDAIMEAIKK	0.934638916	2	2.417435884
P14882	TGAQAVHPGYGFLSENK	1.068017208	2	3.527343035
P14882	TVAIHSDVDASSVHVK	1.015072979	2	3.482520342
P14882	VVEEAPSIFLDPETR	1.187387102	2	4.093249798
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	1.282025882	3	5.781293392
P14882	LQVEHPVTECITGLDLVQEMILVAK	1.146141671	3	4.070876598
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**1.20354758**	**1.1E-10**	**2**
P14942	YFPVFEK	1.175759898	1	1.912090898
P14942	KPPPDGHYVDVVR	1.204445822	2	2.90515399
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.045352237**	**0.9952**	**4**
P15083	EIQNAGDQAQENR	1.008278844	2	3.868920565
P15083	FSVLITGLR	1.222567881	2	2.614567757
P15083	GVTGGSVAIVCPYNPK	1.055199556	2	4.069482803
P15083	SSVTFECDLGR	1.083655823	2	2.63517952
P15149	**CP2A2 Cytochrome P450 2A2**	**1.110306056**	**0.9996**	**11**
P15149	DVYSSITQLSER	0.738269453	2	2.905100107
P15149	FSNLAPLGIPR	1.181793293	2	3.210529089
P15149	GELPTFNILFK	1.034561976	2	2.392362118
P15149	GTDVFPIIGSLMTEPK	1.092145079	2	4.162041664
P15149	GYGFSLSNVEQAK	1.024212347	2	3.403674603
P15149	IVVLYGYDAVK	1.864128757	2	2.67362833
P15149	NFIDSFLIR	1.148159735	2	2.964167833
P15149	TLQGTCGAPIDPSIYLSK	0.995953477	2	4.677064896
P15149	TVSNVINSIVFGNR	0.896567162	2	3.091063023
P15149	DVQECILEEAGYLIK	0.927124715	3	3.621809959
P15149	FKFPMNLEDINEYPSPIGFTR	1.047213338	3	4.651076317
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.083220963**	**4.7E-06**	**2**
P15178	FQTEIQTVNK	1.081863207	2	2.556355476
P15178	QMVKFAANINK+Oxidation(2)	1.291955913	2	2.804523706
P15429	**ENOB Beta_enolase**	**0.625151224**	**0.00198**	**5**
P15429	IEEALGDK	0.428336371	1	2.316432476
P15429	TAIQAAGYPDK	0.461295955	2	2.440401077
P15429	VNQIGSVTESIQACK	1.03014398	2	5.182933331
P15429	DATNVGDEGGFAPNILENNEALELLK	0.494834242	3	5.529212475
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	0.488861322	3	4.766695976
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.08646854**	**9.9E-20**	**22**
P15650	LDSASASMAK	1.100261071	1	2.331483126
P15650	SGSDWILNGSK	1.135717011	1	2.275664806
P15650	AFVDSCLQLHETK	1.263273068	2	4.089658737
P15650	AQDTAELFFEDVR	1.293284205	2	4.876450062
P15650	CIGAIAMTEPGAGSDLQGVR	0.902482571	2	5.275468826
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(7)	1.054278322	2	5.18063736

P15650	EQIEQFIPQMTAGK	0.507550657	2	4.397865772
P15650	FFQEEVIPYHEEWEK	1.142685805	2	4.990666389
P15650	GFYYLMQELPQER	1.116444414	2	4.287563801
P15650	IFSSEHDIFR	1.093086744	2	2.933987617
P15650	KFFQEEVIPYHEEWEK	1.215182292	2	5.197075844
P15650	KLTDIGIR	1.135362828	2	2.430160761
P15650	LDSASASMAK+Oxidation(8)	1.131670061	2	2.528651714
P15650	LPASALLGEENK	0.944623256	2	2.677301884
P15650	LTDIGIR	1.107578453	2	2.3446455
P15650	QGLLGINIAEK	0.991994336	2	3.253712177
P15650	RLDSASASMAK	1.088206895	2	3.5289042
P15650	RLDSASASMAK+Oxidation(9)	1.300262895	2	3.076704264
P15650	TNICVTR	1.082318322	2	2.50199151
P15650	VQPIYGGTNEIMK	1.010288553	2	3.427618265
P15650	VQPIYGGTNEIMK+Oxidation(12)	1.093059047	2	2.700313568
P15650	AQDTAELFFEDVRLPASALLGEENK	1.179854574	3	5.305358887
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.138441139**	**0.00218**	**9**
P15651	ASSTANLIFEDCR	1.2285357	2	3.20798564
P15651	EEGDSWVLNGTK	0.97598442	2	2.963784933
P15651	ELVPIAAQLDK	0.692307847	2	2.476452589
P15651	ELVPIAAQLDKEHLFPTSQVK	0.451174035	2	4.688177109
P15651	GISAFLVPMPTPGLTLGK	0.782451328	2	3.053979397
P15651	IGCFALSEPGNGSDAGAASTTAR	1.621039415	2	5.861381531
P15651	ITEIYEGTSEIQR	1.022551399	2	4.978203297
P15651	IGIASQALGIAQASLDCAVK	1.482068775	3	4.720147133
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.181279877	3	3.340387583
P15684	**AMPN Aminopeptidase N**	**1.215680925**	**0.00476**	**4**
P15684	ALGDTPAPNIDTTELVER	1.294541767	2	4.177735329
P15684	AQIIHDSFNLASAGK	1.362087805	2	3.2882061
P15684	LRSALACSNEVWILNR	1.118178442	2	2.349259853
P15684	VVATTQMQAADAR	1.215556728	2	3.786349297
P15709	**ST2A1 Bile salt sulfotransferase**	**1.14315403**	**0.99977**	**2**
P15709	NHFTVSQAEAFDK	1.173443666	2	4.03877449
P15709	SIFTGIGLMR	0.786955749	2	2.69509387
P15919	**RAG1 V(D)J recombination_activating protein 1**	**1.053626809**	**0.37761**	**2**
P15919	EEGGDVKAVCLTLFLLALR	1.09839117	2	2.56061244
P15919	SQDLDDYLNGPFTVVVK	0.737470061	2	2.572839499
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.088794793**	**0.00031**	**3**
P15978	GYEQHAYDGR	2.929945392	2	2.811419725
P15978	VEHEGLPEPLSQR	1.123991952	2	3.126129389
P15978	YDSDAENPR	1.380757589	2	2.471601725
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.014356119**	**6.2E-06**	**24**

P15999	GYLDKLEPSK	1.148171151	1	3.006398201
P15999	AVDSLVPIGR	1.062152365	2	3.628524303
P15999	EVAAFAQFGSDLDAATQQLLSR	1.026892197	2	6.790812969
P15999	GMSLNLEPDNVGVVVFGNDK	1.227723999	2	5.74031496
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(2)	0.968206573	2	4.28827858
P15999	ILGADTSVDLEETGR	1.089503744	2	5.062841415
P15999	LELAQYR	1.092781916	2	2.725661278
P15999	LKEIVTNFLAGFEP	1.343782135	2	3.05903101
P15999	LTDADAMK	0.94720507	2	2.553508043
P15999	LYCIYVAIGQK	0.979046817	2	2.712709427
P15999	NVQAEEMVEFSSGLK	0.584151158	2	4.338400841
P15999	RLTDADAMK	1.046826711	2	2.600925922
P15999	RLTDADAMK+Oxidation(8)	1.170687759	2	2.326205492
P15999	RTGAIVDVPVGDELLGR	1.046421818	2	3.914255857
P15999	STVAQLVK	1.057748284	2	2.395340204
P15999	TGAIVDVPVGDELLGR	1.051277027	2	4.720200062
P15999	TGTAEMSSILEER	0.860350296	2	4.486801624
P15999	TGTAEMSSILEER+Oxidation(6)	0.852557918	2	3.154788017
P15999	TSIAIDTIINQK	1.023159043	2	4.67326498
P15999	VLSIGDGIAR	0.923275836	2	3.161044121
P15999	VVDALGNAIDGK	1.133200791	2	4.481194973
P15999	FESAFLSHVVSQHQSLLGNIR	1.183411565	3	6.095953465
P15999	GIRPAINVGLSVSR	1.158826389	3	3.862540722
P15999	QGQYSPMAIEEQVAVIYAGVR	0.57183957	3	5.253682137
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**0.978562692**	**0.98252**	**8**
P16036	EEGLNAFYK	1.004651382	1	2.404520512
P16036	FGFYEVFK	1.19925978	1	2.25841713
P16036	ALYSNILGEENTYLWR	0.881154542	2	3.17017436
P16036	GIFNGFSITLK	1.187187496	2	3.335949898
P16036	GSTASQVLQR	1.126699889	2	3.301098108
P16036	GWAPTLIGYSMQGLCK	0.966948068	2	2.958094835
P16036	IQTQPGYANTLR	1.207800525	2	3.773623943
P16036	MYKEEGLNAFYK	1.010794081	3	3.467235565
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.180451577**	**9.9E-20**	**28**
P16086	ALINADELANDVAGAEALLDR	1.051035859	2	4.863788605
P16086	ALSSEGKPYVTK	1.267691626	2	2.920911789
P16086	DLASVQALLR	1.284850618	2	2.958594799
P16086	DLSSVQTLLTK	0.950251007	2	2.537048817
P16086	GVIDMGNSLIER	0.94128498	2	2.956037998
P16086	HQAFEAELSANQSR	0.975972597	2	4.123606682
P16086	LFGAAEVQR	1.1666711	2	2.511528969
P16086	LGDSHDLQR	1.217883896	2	3.157053709
P16086	LGESQTLQQFSR	1.092815454	2	3.434172153

P16086	LIQEQHPEEELIK	1.223149048	2	3.554828882
P16086	LQQSHPLSANQIQVK	1.398263412	2	4.242005348
P16086	LQTASDESYKDPTNIQSK	1.318427934	2	4.511181831
P16086	LQVASDENYKDPTNLQGK	1.139014555	2	5.532623768
P16086	LSDDNTIGQEEIQQR	1.230690861	2	3.277731895
P16086	MTLVASEDYGDTLAAIQGLLK	0.903698824	2	4.370153427
P16086	NQALNTDNYGHDLASVQALQR	1.238252453	2	5.753691673
P16086	QFQDAGHFDAENIKK	1.142423952	2	2.556478262
P16086	REELITNWEQIR	1.258839371	2	4.118757248
P16086	SQLLGSAHEVQR	0.658620816	2	3.229640007
P16086	SSLSSAQADFNQLAELDR	1.217868973	2	5.209545612
P16086	TATDEAYKDPSNLQGK	1.129757856	2	3.677365303
P16086	TKQEEVNAAWQR	1.173216048	2	2.93573451
P16086	VLETAEDIQER	0.783019084	2	3.489853859
P16086	VNDVCTNGQDLIK	1.379012635	2	3.201797247
P16086	VNSLGETAQR	1.35203986	2	2.688143253
P16086	HQALQAEIAGHEPR	1.172227789	3	4.148955822
P16086	HQLLEADISAHEDR	1.142515683	3	3.788481474
P16086	KFEEFQTDLAAHEER	1.042657151	3	5.316686153
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.029206489**	**0.9991**	**9**
P16232	EECALEIIK	0.980444602	1	2.013290405
P16232	FVVEAGK	0.973849948	1	1.919831753
P16232	KDEVYYDK	1.093606479	1	2.73098731
P16232	ETSGIILSQAAPK	0.979300193	2	3.505043983
P16232	FALDGFFSTIR	1.015705756	2	2.430719376
P16232	IMEFLSLR	1.921727875	2	2.510408878
P16232	MGAHVVLTAR	1.28766236	2	2.878896952
P16232	MTQPLIASYSASK	0.89324538	2	3.396929741
P16232	SSWTPLLLGNPGR	0.989791008	2	3.651449919
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.261248068**	**6.8E-05**	**5**
P16290	HYGGLTGLNK	1.06251823	1	3.137686014
P16290	AMEAVAAQGK	1.066349219	2	2.593196392
P16290	AMEAVAAQGK+Oxidation(2)	1.347895854	2	2.436759472
P16290	HGESSWNQENR	0.583104146	2	3.62318182
P16290	VLIAAHGNSLR	1.273064917	2	2.673626184
P16303	**CES3 Carboxylesterase 3**	**0.845424904**	**0.08739**	**18**
P16303	FAPPQPAEPWNFVK	1.408375486	1	2.470395565
P16303	MIPVVAEK	0.895013987	1	1.950248718
P16303	AKEAAEEPSHWK	0.955140034	2	4.024044991
P16303	DGASEEETNLSK	0.810242465	2	4.112846375
P16303	EAAEEPSHWK	0.795992169	2	2.784585953
P16303	ENIPLQFSEDCLYLNVYTPADLTK	0.477789004	2	4.283071041

P16303	IGASTQAAQR	0.403812038	2	3.301632881
P16303	LDLLGNPK	0.957788813	2	2.333940029
P16303	QKTEDELLETSLK	1.005251939	2	3.603182316
P16303	SFNTVPYIVGINK	0.762765928	2	2.897765636
P16303	TEDELLETSLK	0.918457765	2	3.591706753
P16303	TTTSAVMVHCLR	1.12982366	2	3.062420607
P16303	TVIGDHGDELFSVFGSPFLK	1.035023135	2	5.394604206
P16303	YFGGTDDPAK	0.943850465	2	3.246355534
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	1.002666565	3	5.558481693
P16303	ESYPFLPTVIDGVVLPK	0.780491128	3	4.110737801
P16303	QEFGWIIPTLMGYPLSEGK	0.649115784	3	4.091054916
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	0.77570101	3	3.745062113
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.001893469**	**0.99627**	**5**
P16332	GDVGMAGVAIDTVEDTK	0.99619622	2	3.463490725
P16332	IDSGSEVIVGVNK	1.083510534	2	4.019878387
P16332	NTQIIIQEESGIPK	0.977043881	2	3.023189783
P16332	TGLQAGLTIDEFAPR	0.967755386	2	3.659989595
P16332	EVAQQAVDADVHAVGVSTLAAGHK	1.107364622	3	3.412843704
P16409	**MYL3 Myosin light chain 3**	**0.72622825**	**0.36871**	**10**
P16409	LTEDEVEK	0.553376445	1	2.196972609
P16409	AAPAPAAAPAAAPEPERPK	0.654166516	2	4.032061577
P16409	ALGQNPTQAEVLR	0.704097595	2	4.40128994
P16409	DTGTYEDFVEGLR	0.834500385	2	2.981570005
P16409	EGNGTVMGAELR	0.943398104	2	2.530056477
P16409	IEFTPEQIEEFK	0.807355745	2	2.332529068
P16409	LMAGQEDSNGCINYEAFVK	1.150542304	2	4.926936626
P16409	NKDTGTYEDFVEGLR	0.885307562	2	4.188948154
P16409	VFDKEGNGTVMGAELR	1.080596942	2	3.972046852
P16409	MMDFETFLPMLQHISK	0.838246429	3	4.022271633
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.014299002**	**0.34634**	**18**
P16617	IQLINNMLDK+Oxidation(7)	2.083180582	1	2.027346134
P16617	AHSSMVGVNLPQK+Oxidation(5)	1.048182284	2	2.463469982
P16617	GCITIIGGGDTATCCAK	0.970430614	2	5.537135124
P16617	IQLINNMLDK	0.946214498	2	2.794849634
P16617	ITLPVDFVTADK	1.094916976	2	2.330098152
P16617	ITLPVDFVTADKFDENAK	1.590615217	2	5.184028149
P16617	QIVWNGPVGVFEWEAFAR	1.063099278	2	4.124938488
P16617	SLMDEVVK	0.953634396	2	2.313436508
P16617	TGQATVASGIPAGWMGLDCGTESSK	0.887682467	2	4.703309536
P16617	VLNNMEIGTSLYDEEGAK	1.133946512	2	5.210412025
P16617	VLPGVDALSNV	1.216693849	2	2.758839607
P16617	YSLEPVAAELK	1.064231145	2	3.145616055
P16617	AHSSMVGVNLPQK	1.006158279	3	3.777389765

P16617	ALESPERPFLAILGGAK	0.752640729	3	4.597068787
P16617	DCVGSEVENACANPAAGTVILLENLR	1.126599622	3	6.364088058
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.084943744	3	4.217716694
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.063627855	3	4.661272526
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.041897127	4	5.281949043
P16638	**ACLY ATP_citrate synthase**	**0.874235183**	**8.2E-06**	**21**
P16638	AFDSGIIPMEFVNK	1.212029305	2	4.110857487
P16638	DEPSVAAMVYPFTGDHK	0.85777162	2	2.638434172
P16638	EAYPEEAYIADLDAK	1.157332308	2	3.065079212
P16638	EEADEYVDIGALNGVFVLGR	1.121816265	2	4.199786186
P16638	FGGALDAAAK	1.257776957	2	2.861598253
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.078027979	2	3.810249805
P16638	GVTIIGPATVGGIKPGCFK	1.205785469	2	3.628886938
P16638	HLLVHAPEDKK	1.496965538	2	3.363459349
P16638	IGNTGGMLDNILASK	1.631881931	2	3.206224203
P16638	LGLVGVNLSLDGVK	2.367189293	2	2.316249609
P16638	RGGPNYQEGLR	1.358645793	2	3.218430996
P16638	SAYDSTMETMNYAQIR	1.251342109	2	4.117153645
P16638	SGGMSNELNNIISR	0.973570754	2	3.74579978
P16638	TIAIIAEGIPEALTR	1.109500498	2	4.067539215
P16638	TTDGVYEGVAIGGDR	1.158806145	2	2.871428013
P16638	VDATADYICK	1.474465985	2	2.550135136
P16638	WGDIEFPPPFGR	1.133578981	2	3.832359076
P16638	YICTTSAIQNR	1.10649471	2	2.883973122
P16638	DLVSSLTSGLLTIGDR	0.709425477	3	3.922989368
P16638	QHFPATPLLDYALEVEK	0.985400763	3	4.242563248
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	0.990414943	3	3.62030077
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**1.05396737**	**0.33596**	**9**
P16970	ITEDTVEFGS	0.951465376	1	1.902376175
P16970	DQVIYPDGKEDQK	0.718846644	2	3.243852139
P16970	EGGWDSVQDWMDVLSGGEK	1.001933183	2	4.382962227
P16970	GYLDNVQLGHILER	0.892501374	2	3.42316246
P16970	ITELMQVLK	0.988596643	2	2.522975445
P16970	SGANVLICGPNGCGK	0.977888839	2	3.303839922
P16970	FDHVPLATPNGDILIQDLSFEVR	1.265759053	3	3.856988907
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.84566826	3	5.151042938
P16970	HLHSTHSELLEDYYQSGR	1.097894418	3	5.330324173
P17077	**RL9 60S ribosomal protein L9**	**0.993167006**	**0.00147**	**7**
P17077	GTVQQPDE	1.362233153	1	2.182544708
P17077	FLDGIYVSEK	0.955271993	2	3.05948925
P17077	KFLDGIYVSEK	1.11046958	2	2.971188307
P17077	TGVACSVSQAQK	1.060516488	2	3.259533644
P17077	TICSHVQNMIK	1.245030334	2	3.68726325

P17077	TILSNQTVDIPENVDITLK	0.913823136	2	4.836412907
P17077	DFNHINVELSLLGK	0.750527643	3	3.51505518
P17078	**RL35 60S ribosomal protein L35**	**1.105264079**	**0.02774**	**2**
P17078	QLDDLKVELSQLR	1.133185448	2	2.493783712
P17078	VLTVINQTQK	1.170596709	2	3.02412653
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.136658397**	**0.54774**	**4**
P17178	DHESTEGPGTGQDRPR	1.282784807	2	2.7344172
P17178	TNVNLASAPLLEQVMR	1.136623228	2	4.198735237
P17178	VGCLEPSIPEDTATFIR	1.24629935	2	3.420549631
P17178	YEVVLSPGMGEVK	1.318101736	2	3.26356411
P17209	**MYL4 Myosin light chain 4**	**0.581985245**	**0.37964**	**2**
P17209	HVLATLGEK	0.556071812	1	2.569966793
P17209	ITYGQCGDVLR	0.896082903	2	2.47546792
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.876416963**	**0.99998**	**11**
P17425	ITASLCDLK	0.960214403	1	1.95508039
P17425	ASAELFNQK	0.65408636	2	2.569483757
P17425	LEDTYFDRDVEK	0.724454301	2	2.995756865
P17425	MFLNDFLNDQNR	0.769714121	2	2.86577177
P17425	MGFCTDREDINSLCLTVVQK	0.802227829	2	4.548354149
P17425	NSIYSGLEAFGDVK	0.872063475	2	2.776197672
P17425	NSLSYDCIGR	0.627626689	2	2.860199213
P17425	TCVAPDVFAENMK	0.754582482	2	3.616374731
P17425	VTQDATPGSALDK	0.973753805	2	3.618481874
P17425	YTIGLGQAR	0.775029778	2	2.785285234
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	0.701622326	3	5.31103611
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.064849278**	**0.83959**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(7)	1.242090366	2	3.552829027
P17426	NADVELQQR	1.031030623	2	2.505679131
P17426	VGGYILGEFGNLIAGDPR	1.257758741	2	4.169583797
P17475	**A1AT Alpha_1_antiproteinase**	**0.858837973**	**0.85364**	**4**
P17475	VINDYVEK	1.024375375	1	2.290829182
P17475	MQHLEQTLTK	0.79138721	2	2.68606925
P17475	TLLSSLGITR	0.845325887	2	2.903346777
P17475	VFNNDADLSGITEDAPLK	0.92147296	2	5.212237835
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.284418236**	**9.9E-20**	**15**
P17764	EEQDKYAIGSYTR	1.067922868	2	3.394931793
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	0.841016702	2	4.530545235
P17764	EVYMGNVIQGGEGQAPTR	0.910435959	2	5.247784615
P17764	FANEITPITISVK	1.016030992	2	3.977552652
P17764	GKPDVVVKEDEEYK	1.068812275	2	3.683993101
P17764	GKPDVVVKEDEEYKR	1.321630332	2	4.612516403
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.978271396	2	5.234680653

P17764	IHMGNCAENTAK	1.574312565	2	3.404375315
P17764	IHMGNCAENTAK+Oxidation(3)	2.222837692	2	3.495884657
P17764	LEDLIVK	1.253944782	2	2.429467678
P17764	LGTIAIQGAIEK	1.748215074	2	3.304086924
P17764	QATLGAGLPIATPCTTVNK	1.174234371	2	5.10218811
P17764	QGEFGLASICNGGGGASAVLIEK	1.091211813	2	4.734839439
P17764	TPIGSFLGSLASQPATK	1.43666426	2	4.210940361
P17764	VNVHGGAVSLGHPIGMSGAR	1.254939388	2	5.732958317
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.110176795**	**1**	**3**
P17879	TTPSYVAFTDTER	1.024258735	2	3.598173857
P17879	VEIIANDQGNR	0.995426191	2	3.667200565
P17879	QTQTFTTYSDNQPGVLIQVYEGER	0.864050715	3	5.333651066
P17988	**ST1A1 Sulfotransferase 1A1**	**1.083833825**	**0.10432**	**6**
P17988	CPGVPSGLETLEETPAPR	1.135765547	2	4.495327473
P17988	FDAHYAK	1.199188555	2	2.356271982
P17988	NTFTVAQNER	1.049225742	2	2.988041162
P17988	SLPEETVDSIVHHTSFK	1.183074374	2	4.522598743
P17988	THLPLSLLPQSLLDQK	1.337899723	2	5.007662773
P17988	YFAETIGPLQNFTAWPDDLLISTYPK	0.981199576	3	4.152879715
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.285092937**	**1.1E-10**	**27**
P18163	TMYDGFQR	1.139756168	1	1.913467407
P18163	AELSVIFADKPEK	1.285306623	2	3.565847635
P18163	AILEDMVK	1.028050903	2	2.472254753
P18163	ALEDLGR	1.070955432	2	2.461280823
P18163	ALKPPCDLSMQSVEVTGTTEGVR	1.173489409	2	4.554934502
P18163	CGVEIIGLK	1.037027741	2	2.704549789
P18163	GAMVTHQNIMNDCSGFIK	1.610423177	2	5.332997799
P18163	GFQGSFEELCR	1.225341575	2	3.392648697
P18163	GIAVHPELFSIDNGLLTPTLK	1.272642112	2	5.727280617
P18163	GIQVSNDGPCLGSR	1.064070838	2	4.485711098
P18163	IENIYLR	1.058223385	2	2.964355707
P18163	IFGQANTSVK	1.253270075	2	2.60531497
P18163	IIVIMDSYDNDLVER	1.268246953	2	4.929255962
P18163	LLLEGVENK	1.190521285	2	3.183618069
P18163	LLMDDLK	1.128929978	2	2.4259305
P18163	LVDVEDMNYQAAK	0.845504427	2	4.577793121
P18163	LVDVEDMNYQAAK+Oxidation(7)	0.651832294	2	2.762492418
P18163	NAGLKPFEQVK	1.118093473	2	4.004687309
P18163	QVAEMAECIGSALIQK	0.941384706	2	5.252670288
P18163	SAVLEDDKLLLYYYDDVR	0.757475983	2	4.234344959
P18163	SQIDELYSTIK	0.827490978	2	3.766600132
P18163	SQIDELYSTIKI	0.953141905	2	3.116420746
P18163	TAEALDKDGWLHTGDIGK	1.239300471	2	5.354172707

P18163	VLQPTIFPVVPR	1.154261308	2	3.676960468
P18163	WLLDFASK	1.094111163	2	2.612455606
P18163	LMITGAAPVSATVLTFLR	1.72057009	3	4.144877911
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	0.592794612	3	6.187456131
P18297	**SPRE Sepiapterin reductase**	**1.089176495**	**0.09564**	**5**
P18297	LLLINNAGTLGDVSK	2.024439921	2	3.029378653
P18297	LNSEGELVDCGTSAQK	1.068212973	2	4.952135086
P18297	TVVNISSLCALQPFK	0.809902162	2	3.131248713
P18297	VLSYAPGPLDTNMQQLAR	1.159131693	2	2.744343996
P18297	ALAPQLAGLLSPGSVLLLSAR	1.232078042	3	3.9368155
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.520178849**	**3.1E-08**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.576838819	2	5.64404583
P18298	YLDEDTIYHLQPSGR	1.120770779	2	4.389833927
P18298	KIIVDTYGGWGAHGGGAFSGK	1.182710044	3	3.423740864
P18418	**CALR Calreticulin**	**1.084427414**	**9.9E-20**	**17**
P18418	FYGDQEK	1.347291461	1	2.02837038
P18418	FYGDQEKDK	1.279280253	1	2.819950581
P18418	QIDNPDYK	1.332780026	1	1.952384233
P18418	VHVIFNYK	1.123910365	1	2.344139814
P18418	DMHGDSEYNIMFGPDICGPGTK	0.913457611	2	6.195069313
P18418	FYALSAR	1.370902545	2	2.328241825
P18418	GQTLVVQFTVK	1.004567816	2	3.816910028
P18418	HEQNIDCGGGYVK	1.216078418	2	4.373522282
P18418	IDNSQVESGSLEDDWDFLPPK	0.856541194	2	5.51749754
P18418	IDNSQVESGSLEDDWDFLPPKK	0.972761648	2	5.049960136
P18418	IKDPDAAKPEDWDER	1.271744803	2	4.368840694
P18418	LFPGGLDQK	1.58277014	2	2.339840889
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	1.272735488	3	6.03648901
P18418	CKDDEFTHLYTLIVRPDNTYEVK	0.85778062	3	5.412304878
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.085943558	3	5.700286865
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.205614188	3	5.494481564
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.196981866	4	4.665221214
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.165939722**	**0.1224**	**2**
P18420	AQPSQAADEPAEK	1.167640267	2	3.606403112
P18420	IHQIEYAMEAVK	1.036953194	2	2.300308466
P18421	**PSB1 Proteasome subunit beta type_1**	**1.253490124**	**0.00266**	**2**
P18421	AGGSASAMLQPLLDNQVGFK	1.288844901	2	4.796003342
P18421	NMQNVEHVPLTLDR	1.061050693	2	3.781368017
P18422	**PSA3 Proteasome subunit alpha type_3**	**1.264807142**	**0.0022**	**3**
P18422	DGVVFGVEKLVLSK	1.781867526	1	1.945633531
P18422	AVENSSTAIGIR	1.265239028	2	3.310664892
P18422	HVGMAVAGLLADAR	1.101328619	3	3.609472036

P18437	**HMGN2 Non_histone chromosomal protein HMG_17**	**0.924254481**	**0.94653**	**2**
P18437	DANNPAEDGDAK	1.178966807	2	3.327004671
P18437	DANNPAEDGDAKTDQAQK	0.924205848	2	4.887946129
P18445	**RL27A 60S ribosomal protein L27a**	**1.071967772**	**0.08396**	**3**
P18445	NGVAPIIDVVR	1.290034148	1	2.507063866
P18445	NQSFCPTVNLDK	1.138458748	2	3.203341484
P18445	RNQSFCPTVNLDK	1.18760872	2	3.123755217
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**1.042224024**	**0.61294**	**5**
P18484	FFQPTEMASQDFFQR	1.242090366	2	3.986418486
P18484	ILVAGDTMDSVK	1.339106333	2	2.438645363
P18484	NNGVLFENQLLQIGLK	0.886003087	2	2.552242756
P18484	YGGTFQNVSVK	0.993368346	2	2.485367298
P18484	IIGFGSALLEEVDPNPANFVGAGIIHTK	1.419011999	3	3.39960289
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.136756051**	**0.18027**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	0.468211746	2	3.329761028
P18596	SLPSVETLGCTSVICSDK	0.987127534	2	4.277377605
P18596	TGTLTTNQMSVCR	1.208773904	2	2.864724398
P18596	VGEATETALTCLVEK	1.041684706	2	4.972034454
P18757	**CGL Cystathionine gamma_lyase**	**1.08689477**	**0.99927**	**15**
P18757	AGDEVICMDEVYGGTNR	0.869553098	2	5.772587299
P18757	ATLGISDTLIR	0.947668224	2	3.569734335
P18757	AVAALDGAK	0.949932205	2	2.445112228
P18757	FLQNSLGAVPSPFDCYLCCR	1.430518306	2	3.619330168
P18757	LLEAAITPQTK	1.003431775	2	3.613528013
P18757	LVWIETPTNPTLK	1.168520938	2	3.802896023
P18757	QCTGCPGMVSFYIK	1.088572517	2	3.827675819
P18757	QDSPGQSSGFVYSR	0.783597425	2	3.896388769
P18757	RVASEFGLK	1.088231162	2	2.650898218
P18757	VIYPGLPSHPQHELAK	1.043388902	2	4.188634396
P18757	AVVLPISLATTFK	0.877852323	3	4.987933636
P18757	GTLQHAQVFLK	0.903362591	3	3.31622386
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.347510383	3	3.798883438
P18757	LSVGLEDEKDLLEDLGQALK	1.105467297	3	6.644096851
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	2.047484114	4	5.756370544
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.262708399**	**9.4E-10**	**10**
P18886	ATNLTVSAVR	1.272822977	2	3.514708519
P18886	ELHAHLLAQDK	0.348076862	2	3.467175961
P18886	LIFDGNEETLK	1.304716327	2	3.249944687
P18886	QYGQTVATYESCSTAAFK	1.161340487	2	4.033313274
P18886	SEYNDQLTR	1.067088384	2	2.482808828
P18886	TETIRPASIFTK	1.390770222	2	3.071148396
P18886	TLQAGLLEPEVFHLNPSK	4.30805384	2	4.059551716

P18886	TLSIDSIQFQR	1.164586735	2	3.398393154
P18886	YILSDSSPVPEFPVAYLTSENR	1.229180381	2	5.211328983
P18886	YLNAQKPLLDDSQFR	1.257140382	2	4.710803509
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.120497089**	**9.9E-20**	**16**
P19112	AGGTGEMTQLLNSLCTAIK	1.160872981	2	5.396643162
P19112	APVIMGSTEDVQEFLEIYNK	1.364476845	2	4.337750912
P19112	DFDPAINEYIQR	0.467611846	2	3.57267189
P19112	GNIYSINEGYAK	1.041492124	2	3.942631483
P19112	KGNIYSINEGYAK	1.130271993	2	4.215837479
P19112	KLDILSNDLVINMLK	1.169660564	2	5.060664654
P19112	LDILSNDLVINMLK	1.316622321	2	4.852484703
P19112	LLYECNPIAYVMEK	1.393473519	2	4.364347935
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.166046007	2	5.899817467
P19112	SRPSLPLPQSR	1.100079057	2	3.302189589
P19112	TLVYGGIFLYPANK	0.697829417	2	3.983035564
P19112	TSANEPSEKDALQPGR	1.171941382	2	4.455714226
P19112	AGGLATTGNEDILDIVPTEIHQK	1.140114932	3	6.215169907
P19112	APVIMGSTEDVQEFLEIYNKDK	1.201043587	3	3.445442915
P19112	KTSANEPSEKDALQPGR	1.229903459	3	3.87502408
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.313984189	3	6.003943443
P19225	**CP270 Cytochrome P450 2C70**	**1.22993687**	**0.06589**	**12**
P19225	FSLMVLRSMGMGK+Oxidation(4)	1.316029468	1	1.972090364
P19225	IQEEITR	1.320473629	1	2.117668152
P19225	EALIDRGEEFSDK	1.062791874	2	2.498483181
P19225	FDPGHFLDEK	1.216912376	2	2.666654587
P19225	FILMEINR	1.238222279	2	2.378604174
P19225	IQEEVVYLLEALR	0.840416569	2	3.859040737
P19225	KLPPGPTPLPIFGNILQVGVK	1.42784205	2	2.42874527
P19225	LPPGPTPLPIFGNILQVGVK	1.14522851	2	4.151506424
P19225	YIDFVPIPLPR	1.100142582	2	3.110712051
P19225	ASLNLSNPQDFIDYFLIK	0.953615477	3	4.099287987
P19225	GTSVMACLTSALHDDKEFPNPEK	1.170068697	3	4.1864748
P19225	TNGSPCDPSFLLACVPCNVISSVIFQHR	1.104421114	3	3.462341309
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**0.948768931**	**0.83889**	**5**
P19234	DIEEIIDELR	0.887246259	2	3.639214039
P19234	DTPENNPDTPFDFTPENYER	0.780578959	2	4.876343727
P19234	FCCEPAGGLTSLTEPPK	1.048489529	2	3.294402838
P19234	FCCEPAGGLTSLTEPPKGPGFGVQAGL	1.159509122	2	3.0144701
P19234	YHIQVCTTTPCMLR	1.111573793	2	3.324624538
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.048578079**	**0.97714**	**8**
P19468	ASGELMTVAR	1.10855175	2	2.337459087
P19468	CNQIANELCECPELLGSGFR	1.016287646	2	5.084675312

P19468	DKNTPSPFVETFPEDEEASK	0.785539488	2	3.589823008
P19468	NTPSPFVETFPEDEEASK	0.956145668	2	4.229588985
P19468	SLFFPDEAINK	1.149758584	2	2.477593422
P19468	SRYDSIDSYLSK	0.955406487	2	2.925888777
P19468	VQLLLNGGDVLETLQEK	1.198623985	2	4.990014076
P19468	WGVISASVDDR	1.037123838	2	3.067216635
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**0.920340319**	**1**	**8**
P19488	AEMWLIR	1.073550813	2	2.89594698
P19488	FETFPTSVSKDELEK	0.971994713	2	4.031106472
P19488	GAAVTLNIR	0.801976823	2	2.597839594
P19488	GHEVTVLKPSAYYVLDPK	1.165626933	2	4.443253517
P19488	NWDPFYTEILGRPTTLAETMGK	1.132122809	2	5.319781303
P19488	SDLFNALK	1.002264626	2	2.945985556
P19488	TILDELVQR	1.006442554	2	3.530071735
P19488	ANAIAWALAQIPQK	1.101003287	3	6.591358185
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.071774818**	**0.99904**	**6**
P19511	HVIQSISAQQEK	1.079302855	2	4.001601696
P19511	HYLFDVQR	1.064157992	2	2.695663929
P19511	LNEEKIAQLEEIK	0.99489552	2	2.5854671
P19511	HVIQSISAQQEKETIAK	1.107768791	3	4.501843929
P19511	LDYHISVQDMMR	1.157264581	3	3.869146824
P19511	YGASIGEFIDKLNEEK	1.156030541	3	3.600708485
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.139029569**	**0.35688**	**13**
P19643	YVISAIPPVLGMK	1.351326044	1	2.854526997
P19643	FIGGSGQVSER	1.231833699	2	3.463067532
P19643	IISTTNGGQER	1.529773708	2	2.862328768
P19643	KFIGGSGQVSER	0.994782565	2	3.265601873
P19643	KLCELYAK	1.732083214	2	2.350284338
P19643	LLHDCGLSVVVLEAR	1.831314205	2	3.763983011
P19643	TLNHEIYEAK	1.205357008	2	2.550701857
P19643	TMDEMGQEIPSDAPWK	1.018275328	2	4.525197983
P19643	TYTIRNKNVK	0.881670626	2	2.411031246
P19643	VLNSQEALQPVHYEEK	1.226334967	2	4.529945374
P19643	YVDLGGSYVGPTQNR	1.172748603	2	5.032373428
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	0.888166016	3	4.80675745
P19643	LERPVIHIDQTGENVVVK	1.123351006	3	5.532964706
P19804	**NDKB Nucleoside diphosphate kinase B**	**0.787527028**	**9.9E-20**	**9**
P19804	DRPFFPGLVK	0.642296388	2	2.379807711
P19804	EIGLWFKPEELIDYK	1.039241243	2	4.233841419
P19804	GDFCIQVGR	1.219745243	2	3.28501296
P19804	NIIHGSDSVESAEK	1.189295357	2	4.039561749
P19804	TFIAIKPDGVQR	1.258186683	2	2.980665207
P19804	VMLGETNPADSKPGTIR	1.277472606	2	4.470665932

P19804	VMLGETNPADSKPGTIR+Oxidation(2)	1.405057271	2	4.252462387
P19804	YMNSGPVVAMVWEGLNVVK	1.289731506	2	5.272873402
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.202185471	4	5.651983261
P19944	**RLA1 60S acidic ribosomal protein P1**	**0.950274943**	**0.98684**	**2**
P19944	INALIK	1.114727607	2	2.421574354
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	0.99356303	4	5.808135033
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.198707701**	**9.9E-20**	**9**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.093101312	2	5.896059036
P19945	CFIVGADNVGSK	1.06413373	2	3.659412861
P19945	GHLENNPALEK	1.205588418	2	3.633954287
P19945	GTIEILSDVQLIK	1.172853814	2	3.110620737
P19945	IIQLLDDYPK	1.815064312	2	3.463037014
P19945	TSFFQALGITTK	1.231626206	2	4.034369946
P19945	VLALSVETDYTFPLAEK	1.301760722	2	4.494778156
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.16808214	3	5.121566772
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.092214851	3	3.64301753
P20059	**HEMO Hemopexin**	**1.094284411**	**0.99997**	**6**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	0.973034345	2	4.752447128
P20059	FNPVTGEVPPR	0.904523097	2	2.551001787
P20059	GECQSEGVLFFQGNR	1.075263942	2	3.925517082
P20059	SGAQATWAELSWPHEK	0.854903119	2	3.418834686
P20059	VDGALCLEK	0.89709421	2	2.433994293
P20059	LFQEEFPGIPYPPDAAVECHR	0.906019395	3	4.466547012
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**0.972694134**	**0.97917**	**8**
P20070	DILLRPELEELR	0.892608102	2	2.526962757
P20070	MSQYLENMNIGDTIEFR	0.911902724	2	5.306854248
P20070	SSPAITLENPDIK	0.983734601	2	3.596059084
P20070	SSPAITLENPDIKYPLR	1.135398149	2	3.961005688
P20070	SVGMIAGGTGITPMLQVIR	0.985648748	2	4.632184505
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(14)	1.323494258	2	2.322671413
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	0.920886665	3	5.687831879
P20070	LIDKEIISHDTR	1.097960163	3	3.750200272
P20280	**RL21 60S ribosomal protein L21**	**1.317190924**	**9.9E-20**	**4**
P20280	KGDIVDIK	1.357997583	1	2.090175629
P20280	HGVVPLATYMR	1.286603416	2	2.50098896
P20280	TNGKEPELLEPIPYEFMA	0.774148042	2	3.427423239
P20280	VYNVTQHAVGIIVNK	1.303284322	2	4.139404297
P20651	**PP2BB Serine/threonine_protein phosphatase 2B catalytic subunit beta isoform**	**1.851567259**	**0.21672**	**2**
P20651	VVKAVPFPPTHR	1.852090481	1	1.953714013
P20651	GLTPTGMLPSGVLAGGR	1.150294196	2	2.425142765
P20673	**ARLY Argininosuccinate lyase**	**0.871997755**	**0.82834**	**16**
P20673	HLWNVDLQGSK	0.940536073	1	3.375018835

P20673	AEAECEVLFPGYTHLQR	1.286348845	2	4.162320137
P20673	AEMQQILQGLDK	0.989606791	2	4.469894886
P20673	EFNFVQLSDAYSTGSSLMPQK	0.985812012	2	5.133170605
P20673	FNSSIAYDR	1.067539553	2	2.437246323
P20673	INVLPLGSGAIAGNPLGVDR	0.690295588	2	5.656494141
P20673	KNPDSLELIR	0.962692755	2	2.380158186
P20673	LKELIGEAAGK	1.183807636	2	3.19137311
P20673	LYPNDEDIHTANER	0.974589861	2	3.873672724
P20673	MAEDLILYGTK	1.123456291	2	3.945381403
P20673	MAEDLILYGTK+Oxidation(1)	1.163192803	2	2.368430376
P20673	NDQVVTDLR	1.007192989	2	3.147680044
P20673	SRNDQVVTDLR	1.05596496	2	3.060928345
P20673	VAEEWAQGIFK	1.114571381	2	3.44796896
P20673	VLIEAMVDR	1.125698259	2	2.591138601
P20673	VLIEAMVDRAEAECEVLFPGYTHLQR	1.294309746	3	4.70818615
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.06145986**	**0.12277**	**5**
P20788	EIDQEAAVEVSQLR	0.787817635	2	3.543031216
P20788	ESLSGQAATRPLVATVGLNVPASVR	0.561567222	2	2.771337509
P20788	SGPFAPVLSATSR	1.001230926	2	2.879316092
P20788	EIDQEAAVEVSQLRDPQHDLER	0.940985703	3	3.434633017
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.152940716	3	5.112568855
P20801	**TNNC2 Troponin C_ skeletal muscle**	**0.576953815**	**0.47181**	**3**
P20801	GKSEEELAECFR	0.568123734	2	3.391043663
P20801	NADGYIDAEELAEIFR	0.87020894	2	4.783592224
P20801	SEEELAECFR	0.478438508	2	3.263453245
P20812	**CP2A3 Cytochrome P450 2A3**	**1.067012062**	**0.90728**	**2**
P20812	ELQGLEDFITKKVEQNQR	1.068812514	2	2.471184254
P20812	YGPVFTIHLGPR	0.96959614	2	3.04289341
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.060588699**	**0.98872**	**3**
P20814	FDYEDKDFLNLIEK	1.076814912	2	2.324587822
P20814	GTAVLTSLTSVLHDSK	1.049383029	2	3.269942045
P20814	IKEHEESLDVSNPR	1.060673648	3	3.592621326
P20817	**CP4AE Cytochrome P450 4A14**	**1.385514891**	**0.99758**	**6**
P20817	ACQIAHEHTDGVIK	1.082720469	2	4.265432835
P20817	AQLQNEEELQK	1.087431043	2	3.313856602
P20817	AVEDLNNLTFFR	1.067558932	2	3.608228445
P20817	HLDFLDILLFAK	1.427534311	2	4.209019661
P20817	MRKAQLQNEEELQK+Oxidation(1)	1.285441991	2	3.088461637
P20817	VLLYDPDYVK	1.190741805	2	2.528860569
P20852	**CP2A5 Cytochrome P450 2A5**	**1.540529557**	**0.51416**	**2**
P20852	DFIDSFLIR	1.558911918	2	2.940039873
P20852	EALVDQAEEFSGR	0.865858019	2	2.868562698

P21213	**HUTH Histidine ammonia_lyase**	**1.484340256**	**3.3E-11**	**15**
P21213	NSATIPESDDL	0.938302497	1	1.961559653
P21213	ALDYLAIGVHELAAISER	1.397661081	2	4.520086288
P21213	DIITTELNSATDNPMVFASR	1.244843215	2	4.475279808
P21213	EGLALINGTQMITSLGCEAVER	1.398747382	2	3.245096445
P21213	GETISGGNFHGEYPAK	0.988576198	2	4.027246952
P21213	GEWLAVPCQDGK	1.559366048	2	3.044139624
P21213	GYSGISLETLK	1.435692563	2	2.356289387
P21213	LQELQVNLVR	1.651435781	2	3.279755831
P21213	NKPDNGGFTSVDEVR	1.549298915	2	3.709554195
P21213	SHSSGVGKPLSPER	1.48517702	2	4.068227291
P21213	TVVYGITTGFGK	1.377583852	2	3.621262074
P21213	VQDAYTLR	1.11099876	2	2.57219243
P21213	VWEVAAPYIEK	1.220874197	2	2.58398962
P21213	YIALDGDSLSTEDLVNLGK	1.211894085	2	5.302823067
P21213	SLLDSDHHPSEIAESHR	1.257786618	3	4.608310699
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.164059573**	**0.47866**	**10**
P21396	NLPSVPGLLK	1.104997006	1	1.925306082
P21396	DVPAIEITHTFLER	0.963403878	2	3.57749033
P21396	FVGGSGQVSEQIMGLLGDK	0.938896174	2	3.117954969
P21396	IFSVTNGGQER	1.172312038	2	2.486310959
P21396	INVLVLEAR	1.415893005	2	3.137600899
P21396	KDIWVEEPESK	1.113768926	2	3.859616995
P21396	KICELYAK	1.732083214	2	2.350284338
P21396	VLGSQEALYPVHYEEK	1.030486097	2	3.609202623
P21396	WVDVGGAYVGPTQNR	1.114928349	2	4.343579769
P21396	YVISAIPPILTAK	1.215621252	2	3.121562958
P21531	**RL3 60S ribosomal protein L3**	**1.079891155**	**0.00208**	**8**
P21531	FIDTTSK	1.03162493	1	2.027659655
P21531	AHLMEIQVNGGTVAEK	1.082722772	2	5.251093864
P21531	HGSLGFLPR	1.305907585	2	3.033504963
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	0.989030867	2	5.06789732
P21531	NNASTDYDLSDK	1.141082799	2	3.377257824
P21531	TVFAEHISDECK	1.112439811	2	3.782171965
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	0.859157253	3	5.406507492
P21531	SINPLGGFVHYGEVTNDFIMLK	0.97463622	3	3.383485317
P21533	**RL6 60S ribosomal protein L6**	**1.235882921**	**2.8E-07**	**9**
P21533	FVIATSTK	1.427023406	1	2.226892471
P21533	YYPTEDVPR	1.136795114	1	1.966498375
P21533	AVDSQILPK	1.075779149	2	2.468883514
P21533	HLTDAYFK	1.082718096	2	2.383720398
P21533	HQEGEIFDTEK	1.091016576	2	3.296468973
P21533	HQEGEIFDTEKEK	1.215380712	2	4.127365589

P21533	QLGSGLLLVTGPLALNR	1.355998595	2	5.174674988
P21533	SSITPGTVLIILTGR	1.142772078	2	4.2042346
P21533	HQEGEIFDTEKEKYEITEQR	1.110029522	3	4.734498978
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.106366423**	**0.0027**	**5**
P21571	FEVLDKPQS	0.919242498	1	2.008687735
P21571	LASGGPVDTGPEYQQEVDR	1.57142046	2	5.288843632
P21571	GEMDKFPTFNFEDPK	0.847050636	3	3.486589432
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.01037514	3	3.968932152
P21571	LASGGPVDTGPEYQQEVDRELFK	2.181233562	3	3.446192265
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.099679013**	**0.99289**	**2**
P21643	YNHVCMVHRMLGSK+Oxidation(10)	1.099679013	2	2.462922096
P21643	YNHVCMVHRMLGSK+Oxidation(6)	1.099679013	2	2.302551985
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.595952586**	**0.02146**	**4**
P21670	ATCIGNNSAAAVSMLK	2.40185741	2	3.310961962
P21670	LLDEVFFSEK	1.601965409	2	3.123696089
P21670	LNEDMACSVAGITSDANVLTNELR	1.623118972	2	5.077010155
P21670	YLLQYQEPIPCEQLVTALCDIK	1.164440429	2	4.041108608
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.037435191**	**1**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	1.051767747	3	5.458117962
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(23)	0.944102408	3	4.449806213
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.003374437**	**0.66157**	**5**
P21913	CGPMVLDALIK	1.035437002	2	2.728055
P21913	CGPMVLDALIKIK	0.808337535	2	2.442568064
P21913	CHTIMNCTQTCPK	0.918261397	2	3.994816065
P21913	IKNEIDSTLTFR	1.309178005	2	3.416602135
P21913	RIDTDLGK	1.131174302	2	2.568562746
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.054101262**	**0.9074**	**5**
P21981	CDLEIQANGR	1.056469647	2	2.920935631
P21981	DHHTADLCQEK	0.392003414	2	2.843559504
P21981	SEGTYCCGPVSVR	1.216666272	2	3.71941781
P21981	VDLFPTDIGLHK	0.985867194	2	2.730942726
P21981	YSGCLTESNLIK	1.038495797	2	2.696643353
P22734	**COMT Catechol O_methyltransferase**	**0.740818953**	**7.7E-05**	**12**
P22734	EWAMNVGDAK	0.325379899	1	2.504380703
P22734	AIYQGPSSPDKS	0.723364339	2	3.350111485
P22734	GQIMDAVIR	0.736219989	2	3.378092051
P22734	GSSSFECTHYSSYLEYMK	0.124677414	2	4.331179619
P22734	KGTVLLADNVIVPGTPDFLAYVR	0.847725826	2	4.543992043
P22734	KYDVDTLDMVFLDHWK	0.773250124	2	4.997812271
P22734	VTILNGASQDLIPQLK	0.750198574	2	4.416718006
P22734	YDVDTLDMVFLDHWK	0.879759523	2	4.055151939
P22734	YLPDTLLLEK	0.784386346	2	3.094539881

P22734	GTVLLADNVIVPGTPDFLAYVR	0.869402091	3	5.05449152
P22734	LLTMEMNPDYAAITQQMLNFAGLQDK	0.958786118	3	3.867681026
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	0.793428286	3	6.630687714
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.05981916**	**0.9988**	**4**
P22789	ETLQNVCNK	0.797779691	2	2.344160795
P22789	KLEPDELDLVLK	1.067711006	2	3.728842974
P22789	LEPDELDLVLK	0.935632041	2	2.338692188
P22789	NHFTVAQAEAFDK	1.706664955	2	3.394924641
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.124006763**	**1.2E-12**	**23**
P22791	TDTWPK	1.274859407	1	1.929580688
P22791	ASLDMFNK	1.058937581	2	2.752293587
P22791	ASLDMFNKK	1.192937913	2	2.931014776
P22791	GLKLEETYTNK	1.193562427	2	2.761961699
P22791	IGAFSYGSGLAASFFSFR	1.197332478	2	4.387377262
P22791	LEETYTNK	1.172956308	2	3.408850431
P22791	LEETYTNKDVDK	1.263426026	2	4.274282455
P22791	LEVGTETIIDK	1.084690912	2	3.800287485
P22791	LMFNDFLSSSSDK	2.335985079	2	3.794752359
P22791	LMFNDFLSSSSDK+Oxidation(2)	2.247177496	2	4.066440582
P22791	LMFNDFLSSSSDKQNNLYK	2.475554491	2	4.732571125
P22791	LSIQCYLR	2.542093846	2	2.454970121
P22791	LVSSVSDLPK	1.376402187	2	3.711685896
P22791	MGFCSVQEDINSLCLTVVQR	1.011419733	2	4.268334389
P22791	MSPEEFTEIMNQR	1.028286381	2	4.773990154
P22791	MSPEEFTEIMNQR+Oxidation(1)	1.136649403	2	3.849300623
P22791	MSPEEFTEIMNQR+Oxidation(10)	0.996137138	2	3.529051304
P22791	VNFSPPGDTSNLFPGTWYLER	1.379681342	2	4.877635002
P22791	YTVGLGQTR	1.111359022	2	3.416113853
P22791	DVGILALEVYFPAQYVDQTDLEK	1.219094743	3	6.246345997
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.000617673	3	6.929349422
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(4)	1.084352917	3	5.631859303
P22791	TKLPWDAVGR	1.197945319	3	4.031892776
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.108480906**	**0.96063**	**9**
P22985	TNLPSNTAFR	1.075007984	1	2.181307793
P22985	DPPANVQLFQEVPK	1.11755642	2	3.662600517
P22985	LDPTFASATLLFQK	1.101366238	2	3.793518543
P22985	NQPEPTVEEIENAFQGNLCR	1.393257568	2	4.857160568
P22985	QLFQLDSPATPEK	1.104950503	2	3.226982117
P22985	TLLRPEEILLSIEIPYSK	1.266160408	2	2.72729969
P22985	DEVTCVGHIIGAVVADTPEHAQR	1.203145163	3	4.507471085
P22985	SVASIGGNIITASPISDLNPVFMASGAK	0.950408082	3	5.8927145
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.192853498	3	4.833966255

P23358	**RL12 60S ribosomal protein L12**	**1.259348249**	**3.9E-09**	**5**
P23358	CTGGEVGATSALAPK	1.313699731	2	4.303649902
P23358	EILGTAQSVGCNVDGR	0.769758701	2	4.312339306
P23358	HNGNITFDEIVNIAR	1.040224888	2	3.944396257
P23358	HPHDIIDDINSGAVECPAS	1.173566837	2	4.502219677
P23358	QAQIEVVPSASALIIK	1.294495475	2	3.617325783
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.229126465**	**2.9E-06**	**9**
P23457	MLDYCK	1.129541814	1	1.985561609
P23457	ELTQVFEFQLASEDMK	0.833075445	2	4.593788624
P23457	HFDSAYLYEVEEEVGQAIR	0.887217452	2	6.112951756
P23457	LLFETVDICDTWEAMEK	2.047946456	2	4.613921642
P23457	SIGVSNFNCR	1.156923448	2	3.188670635
P23457	SKDIILVSYCTLGSSR	1.118682511	2	4.45343399
P23457	VALNDGNFIPVLGFGTTVPEK	1.512259884	2	4.724995136
P23457	YFDDHPNHPFTDE	1.482390608	2	3.732545614
P23457	YKPVCNQVECHLYLNQSK	0.995824467	2	4.63280344
P23514	**COPB Coatomer subunit beta**	**1.205771386**	**0.0137**	**6**
P23514	EAGELKPEEEITVGPVQK	1.207390777	2	3.67300272
P23514	TNNVSEHEDTDKYR	1.282324197	2	4.598968983
P23514	VLQDLVMDILR	1.032084853	2	3.207043886
P23514	VLSECSPLMNDIFNK	1.306849274	2	2.609308481
P23514	YEAAGTLVTLSSAPTAIK	1.097279952	2	4.522890091
P23514	NFENLIPDAPELIHDFLVNEK	1.101542423	3	4.226730347
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.873964471**	**4.4E-07**	**8**
P23965	ALQLGTLFPPAEALK	1.13493368	2	5.436872482
P23965	ATADNLIK	1.086181011	2	2.689707518
P23965	DNYVNTIGHR	0.839551943	2	2.784561634
P23965	QREADIQNFTSFISR	1.231522759	2	2.913761854
P23965	SLHVYLEK	1.243166642	2	2.370505095
P23965	VGLVDEVVPEDQVHSK	1.156621715	2	4.881798744
P23965	WFTIPDHSR	1.113283056	2	2.632999659
P23965	GVILTSERPGIFSAGLDLMEMYGR	1.267871842	3	5.42027998
P24049	**RL17 60S ribosomal protein L17**	**1.031051838**	**0.99967**	**3**
P24049	YSLDPENPTK	1.009407599	1	2.738854647
P24049	EQIVPKPEEEVAQK	0.984288197	2	3.791962624
P24049	GLDVDSLVIEHIQVNK	1.068396168	2	4.904154778
P24050	**RS5 40S ribosomal protein S5**	**1.241322784**	**0.70503**	**2**
P24050	VNQAIWLLCTGAR	1.271255692	2	2.909425735
P24050	WSTDDVQINDISLQDYIAVK	1.090681527	2	4.333250523
P24063	**ITAL Integrin alpha_L**	**1.059355315**	**0.87471**	**2**
P24063	ASEAQVLVKVDLIHEK	1.060079671	2	2.320819855
P24063	DFEKILEFMK	1.061022396	3	3.681478739
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.010489497**	**0.2404**	**5**

P24090	LGGEEVSVACK	0.99581124	2	3.456698895
P24090	VGQPGDAGAAGPVAPLCPGR	1.113744199	2	5.126104355
P24090	ELACDDPETEHVALIAVDYLNK	1.443696833	3	4.167754173
P24090	HAFSPVASVESASGEVLHSPK	0.929480392	3	5.920415401
P24090	VLHAQCHSTPDSAEDVRK	1.200689375	3	3.749132395
P24268	**CATD Cathepsin D**	**1.256093252**	**0.01502**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.263689475	2	3.365305185
P24268	DPTGQPGGELMLGGTDSR	1.094398811	2	4.575200558
P24268	GGCEAIVDTGTSLLVGPVDEVK	1.222579311	2	3.223855972
P24268	LGGQNYELHPEK	1.442190452	2	2.474981308
P24329	**THTR Thiosulfate sulfurtransferase**	**1.068975294**	**0.00229**	**11**
P24329	EGHPVTSEPSRPEPAVFK	0.744576406	2	4.871678829
P24329	FQLVDSR	1.058141045	2	2.304784298
P24329	GSVNVPFMNFLTEDGFEK	1.076700012	2	3.499294758
P24329	HVPGASFFDIEECR	1.180585666	2	4.056631088
P24329	KVDLSQPLIATCR	1.081871078	2	4.631714344
P24329	RFQLVDSR	1.086542951	2	2.335967064
P24329	TVSVLNGGFR	1.036444234	2	3.104261637
P24329	TYEQVLENLQSK	1.074692008	2	4.998729229
P24329	VDLSQPLIATCR	1.099474826	2	4.002289772
P24329	VLDASWYSPGTR	0.960876897	2	3.778036594
P24329	YLGTQPEPDAVGLDSGHIR	1.089321645	2	4.756073952
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.213888157**	**0.05593**	**9**
P24368	DVIIVDCGK	1.125060348	1	1.945339799
P24368	DKPLKDVIIVDCGK	1.009272956	2	3.907006502
P24368	DTNGSQFFITTVK	1.018168968	2	3.903661966
P24368	HYGPGWVSMANAGK	0.74208759	2	3.989025116
P24368	IEVEKPFAIAK	1.121338546	2	3.208997965
P24368	IEVEKPFAIAKE	1.26888628	2	3.531745911
P24368	TVDNFVALATGEK	1.208302322	2	3.361536741
P24368	VLEGMDVVR	1.141193129	2	2.910602331
P24368	VYFDFQIGDEPVGR	1.093618054	2	3.968120813
P24457	**CP2DB Cytochrome P450 2D11**	**1.121699172**	**0.97955**	**2**
P24457	RFSVSTLR	1.139402902	2	2.552740335
P24457	SLEEWVTK	1.120379526	2	2.437288761
P24470	**CP2CN Cytochrome P450 2C23**	**1.036989168**	**0.00421**	**11**
P24470	ACVGESLAR	1.222583551	2	2.456404448
P24470	EALLQQGDEFLGR	0.972427629	2	2.466630697
P24470	FGLLLLMK	1.986821409	2	3.153158665
P24470	GTTVLPMLSSVMLDQK	0.990330852	2	3.841703653
P24470	GYGLIFSNGER	1.121754711	2	3.526362658
P24470	IEEEKDNLK	1.250759962	2	2.817461252
P24470	LPPGPTPLPIIGNLLQLNLK	1.09468495	2	4.21538496

P24470	TFLNLMDLLNK	1.349491785	2	3.80478406
P24470	YITLLPSSLPHAVVQDTK	0.908531868	2	3.944270611
P24470	DLDIKPITTGIINLPPPYK	1.003197507	3	4.331919193
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	0.997604933	3	4.288266659
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.88790189**	**0.6116**	**8**
P24473	AGMATAQAQHLLNK	1.011580157	2	4.151591778
P24473	DEDITESQNILSAAEK	0.851467653	2	5.096897125
P24473	DSGNQPPAMVPHK	0.955919588	2	2.601180077
P24473	FLTAVSMEQPEMLEK	0.890537184	2	5.052872181
P24473	MELLAYLLGEK	1.126392	2	3.983911037
P24473	QLFQVPMSVPK	0.784598546	2	2.664340496
P24473	YGAFGLPTTVAHVDGK	0.708893317	2	3.908105373
P24473	IWSRDEDITESQNILSAAEK	1.126308544	3	3.696666479
P25093	**FAAA Fumarylacetoacetase**	**1.179380118**	**8.9E-16**	**15**
P25093	HLFTGPVLSK	1.084693085	1	2.765454531
P25093	AIDVGQGQTR	1.070327669	2	3.394204617
P25093	AQEHIFGMVLMNDWSAR	1.026430172	2	3.629671574
P25093	ASLQNLLSASQAQLR	1.10395385	2	4.883368015
P25093	ASLQNLLSASQAQLRDDK	1.230729627	2	3.945441008
P25093	ASSVVVSGTPIR	1.093126449	2	3.669288158
P25093	DIQQWEYVPLGPFLGK	0.685331039	2	4.596293449
P25093	FGEPIPISK	1.016621821	2	2.820636511
P25093	GEGMSQAATICR	1.237285262	2	3.64031148
P25093	GEGMSQAATICR+Oxidation(4)	1.857382191	2	3.114842415
P25093	HQHVFDETTLNSFMGLGQAAWK	1.230725899	2	5.369887352
P25093	IGVAIGDQILDLSVIK	1.754293108	2	5.240512371
P25093	TFLLDGDEVIITGHCQGDGYR	1.161119005	2	5.223490238
P25093	VGFGQCAGK	1.379175631	2	2.715004206
P25093	GKENALLPNWLHLPVGYHGR	1.253603931	3	4.552680016
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.129590512**	**0.99931**	**7**
P25113	ALPFWNEEIVPQIK	1.223158607	2	3.504539967
P25113	FSGWYDADLSPAGHEEAK	1.069909013	2	5.050189018
P25113	HGESAWNLENR	1.127510089	2	4.107781887
P25113	SYDVPPPPMEPDHPFYSNISK	0.928655941	2	4.433281898
P25113	YADLTEDQLPSCESLK	1.011949937	2	5.598347664
P25113	YADLTEDQLPSCESLKDTIAR	1.119972843	2	5.375968933
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	1.176510019	3	4.064957142
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.168230011**	**9.9E-20**	**13**
P25235	EDQVIQLMNTIFSK	1.011272852	2	3.433978796
P25235	FPEEEAPSTVLSQNLFTPK	1.266760164	2	4.208042622
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.243495037	2	4.760773659
P25235	KNFESLSEAFSVASAAAALSQNR	1.486002324	2	5.59980154

P25235	LQVSSVLSQPLAQAAVK	1.579471699	2	5.728624821
P25235	NFESLSEAFSVASAAAALSQNR	1.218648891	2	3.129725695
P25235	TGQEVVFVAEPDNK	0.573643167	2	3.858957291
P25235	YIANTVELR	1.049551273	2	2.658235312
P25235	EETVLATVQALHTASHLSQQADLR	1.144338252	3	4.829692364
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.15496367	3	4.440647602
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.427846446	3	5.588846684
P25235	NIVEEIEDLVAR	1.145479743	3	4.325499535
P25235	YHVPVVVVPEGSASDTQEQAILR	1.056926659	3	5.76707077
P25318	**CO8A2 Collagen alpha_2(VIII) chain**	**1.011362528**	**0.54206**	**2**
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(10)	1.034958873	2	2.381000519
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(13)	1.131567944	2	2.491301537
P25977	**UBF1 Nucleolar transcription factor 1**	**1.188833457**	**0.80461**	**2**
P25977	AKYAKLHPEMSNLDLTK	1.093389538	2	2.554172277
P25977	ALKAMEMTWNNMEKK+Oxidation(12)	1.193678047	2	2.326903582
P26039	**TLN1 Talin_1**	**1.230295923**	**1.9E-11**	**23**
P26039	ADAEGESDLENSRK	1.007713523	2	3.609754562
P26039	AGALQCSPSDVYTK	1.446715045	2	2.829824686
P26039	AQEACGPLEMDSALSVVQNLEK	1.013833617	2	4.08805418
P26039	ASAGPQPLLVQSCK	1.051241099	2	2.370123625
P26039	AVAEQIPLLVQGVR	1.111504676	2	2.921387672
P26039	EAAEGLRMATNAAAQNAIKK	1.293043503	2	2.443385363
P26039	EADESLNFEEQILEAAK	0.837919264	2	4.337168217
P26039	GLAGAVSELLR	1.202753156	2	3.249569178
P26039	GVGAAATAVTQALNELLQHVK	1.261071161	2	3.837661743
P26039	ILAQATSDLVNAIK	2.140871615	2	3.531150341
P26039	LGAASLGAEDPETQVVLINAVK	1.944575161	2	4.704748631
P26039	LLGEIAQGNENYAGIAAR	1.049130184	2	4.408174515
P26039	LNEAAAGLNQAATELVQASR	1.122951738	2	5.413677692
P26039	NCGQMSEIEAK	0.933362058	2	3.073689222
P26039	SNTSPEELGPLANQLTSDYGR	1.331727879	2	3.715160131
P26039	TMLESAGGLIQTAR	0.8449146	2	2.516405106
P26039	VGAIPANALDDGQWSQGLISAAR	1.116111852	2	4.738274574
P26039	VLGEAMTGISQNAK	1.230309801	2	3.271969795
P26039	VLVQNAAGSQEK	1.235855044	2	3.164654732
P26039	VSQMAQYFEPLTLAAVGAASK	1.077256368	2	3.112826824
P26039	VVAPTISSPVCQEQLVEAGR	1.221055939	2	5.1501441
P26039	MVAAATNNLCEAANAAVQGHASQEK	1.439714297	3	3.660537958
P26039	TEDSGLQTQVIAAATQCALSTSQLVACTK	1.040572234	3	4.324841022
P26043	**RADI Radixin**	**1.115254859**	**9.7E-13**	**13**
P26043	AFAAQEDLEK	1.078443827	2	3.217357397
P26043	ALELEQER	1.131409592	2	2.523349285

P26043	AQKELEEQTR	0.787281048	2	2.639369488
P26043	IQNWHEEHR	1.264873857	2	2.787378788
P26043	KEEEATEWQHK	1.131361277	2	2.924817324
P26043	KKEEEATEWQHK	1.29123272	2	4.34168005
P26043	KTQNDVLHAENVK	1.215824992	2	5.154298782
P26043	NQEQLAAELAEFTAK	0.981705075	2	5.276311398
P26043	QLQALSSELAQAR	0.946550145	2	4.362291336
P26043	RKPDTIEVQQMK	1.172099972	2	3.403125525
P26043	TQNDVLHAENVK	0.965265402	2	3.902241707
P26043	FFPEDVSEELIQEITQR	1.15784755	3	4.2845788
P26043	GTELWLGVDALGLNIYEHDDKLTPK	1.29755384	3	3.466474533
P26231	**CTNA1 Catenin alpha_1**	**1.457965911**	**0.0678**	**5**
P26231	LIEVANLACSISNNEEGVK	1.133374897	2	5.879324913
P26231	LLEPLVTQVTTLVNTNSK	1.232296171	2	4.158715248
P26231	QIIVDPLSFSEER	1.086200296	2	2.367936611
P26231	SAAGEFADDPCSSVK	1.465394724	2	2.962716818
P26231	TIADHCPDSACK	5.087837831	2	3.30973196
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.142127945**	**0.00454**	**8**
P26284	AILAELTGR	1.155264393	2	2.622756004
P26284	LEEGPPVTTVLTR	1.153862872	2	3.559135675
P26284	MVNSNLASVEELKEIDVEVR	1.320547839	2	4.344293594
P26284	NFYGGNGIVGAQVPLGAGIALACK	1.60941771	2	3.740194798
P26284	RGDFIPGLR	1.283670012	2	2.387872458
P26284	TREEIQEVR	1.15724352	2	3.061421156
P26284	VDGMDILCVR	1.139162637	2	2.574897528
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	0.914328012	3	7.260267735
P26453	**BASI Basigin**	**1.261492497**	**0.01545**	**8**
P26453	GNINVEGPPR	1.104947948	2	3.359060526
P26453	KSEHASEGEFVK	1.081400208	2	3.346899033
P26453	SGEYSCIFLPEPVGR	1.002758341	2	3.934657574
P26453	VLQEDTLPDLQMK	1.13053384	2	4.011968613
P26453	YTVDADDR	1.083003796	2	2.415110111
P26453	RKPDQTLDEDDPGAAPLK	1.212420028	3	4.269199371
P26453	SEASHPPVDEWVWFK	0.927241572	3	3.369357347
P26453	SEHASEGEFVK	1.254322005	3	3.60509944
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**1.081403041**	**0.74175**	**2**
P26516	SVVALHNLINNK	1.108313515	2	2.800028086
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	1.012717791	3	3.714164257
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**1.13887923**	**0.04087**	**8**
P26772	VLLPEYGGTK	1.17934074	1	2.010956287
P26772	GGEIQPVSVK	0.960325815	2	3.605909348
P26772	GGIMLPEK	0.915623463	2	2.532717943

P26772	GGIMLPEK+Oxidation(4)	1.014250718	2	2.708327293
P26772	GKGGEIQPVSVK	1.205277802	2	3.539177418
P26772	KFLPLFDR	1.355760099	2	2.376558304
P26772	VLQATVVAVGSGGK	1.063899752	2	5.282898426
P26772	VVLDDKDYFLFR	1.007353694	2	3.474089861
P27139	**CAH2 Carbonic anhydrase 2**	**1.046894773**	**0.99923**	**4**
P27139	AVQHPDGLAVLGIFLK	0.939879208	2	3.813611746
P27139	IGPASQGLQK	0.892641349	2	3.402122021
P27139	ITEALHSIK	0.888378375	2	2.352903843
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	1.028531332	3	3.603748322
P27321	**ICAL Calpastatin**	**1.168223892**	**0.80287**	**3**
P27321	FQDAPSADGESVAGGVTVATASDK	0.709929575	2	5.307972908
P27321	KGSDEVTASSAATGTSPR	1.185364937	2	4.722723484
P27321	SQSSEPPVIHEK	1.119231168	2	2.641834021
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**1.1829074**	**0.49404**	**7**
P27364	QTILDVNVK	1.233554878	1	2.210381031
P27364	AVLAANGSILK	1.231546788	2	2.934461117
P27364	ETILNDREEEHR	1.031056679	2	2.962894678
P27364	GDIVDAQFLR	1.120519214	2	3.351875782
P27364	IVQMLVQEK	1.676796411	2	3.132189274
P27364	NGGTFHTCALR	1.220717675	2	2.554223776
P27364	SQSIQGQFYYISDDTPHQSYDDLNYTLSK	0.773403974	3	4.178978443
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.198705195**	**0.00026**	**6**
P27605	DLNHVCVISESGK	0.910376339	2	3.489212275
P27605	FFADLLDYIK	1.433381825	2	3.370615482
P27605	NVLIVEDIIDTGK	1.150651692	2	3.913418293
P27605	SYCNDQSTGDIK	1.295134245	2	3.903835773
P27605	VIGGDDLSTLTGK	0.130023181	2	3.995244503
P27605	SVGYRPDFVGFEIPDK	1.063973078	3	3.591121674
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.174056941**	**8E-14**	**16**
P27653	ASQAPSSFQLLYDLK	1.258883078	2	4.298936844
P27653	AYTEEDLDLVEK	0.905095322	2	3.343456268
P27653	IFHELTQTDK	1.328830049	2	2.660971642
P27653	IYGADDIELLPEAQNK	1.079133999	2	5.272947788
P27653	KITIGQAPTEK	0.960880583	2	3.127436876
P27653	KVVGDVAYDEAK	1.364594536	2	3.743204117
P27653	LDIDPETITWQR	1.113982651	2	3.843300581
P27653	MHGGGPTVTAGLPLPK	1.197695679	2	2.6892941
P27653	QGFGNLPICMAK	1.153987903	2	3.621730804
P27653	TDPAALTDDEINR	1.061896424	2	4.367473602
P27653	THLSLSHNPEQK	1.332414989	2	3.834512949
P27653	VVGDVAYDEAK	1.174791651	2	3.676102161

P27653	YVVVTGITPTPLGEGK	1.20826697	2	4.841324329
P27653	CTHWAEGGQGALALAQAVQR	1.173727323	3	3.661638021
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.219141585	3	4.27814436
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.168901425	3	4.746803284
P27661	**H2AX Histone H2A.x**	**1.037094453**	**0.01269**	**3**
P27661	AGLQFPVGR	1.038718111	2	3.043129444
P27661	HLQLAIR	1.313960234	2	2.730419874
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.309279572	2	5.250966072
P27867	**DHSO Sorbitol dehydrogenase**	**1.052832986**	**9.9E-20**	**15**
P27867	HSADFCYK	1.190946476	1	2.891199589
P27867	AKEVGADFTIQVAK	1.216156671	2	2.821359634
P27867	AMGASQVVVIDLSASR	0.943211284	2	4.743847847
P27867	EVGADFTIQVAK	0.736901244	2	3.142116785
P27867	GENLSLVVHGPGDIR	1.076207014	2	3.756174088
P27867	IGDFVVK	0.984916194	2	2.63384366
P27867	LENYPIPELGPNDVLLK	0.99706793	2	4.999317646
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.466802419	2	4.73684454
P27867	TLNVKPLVTHR	1.244647285	2	3.083122015
P27867	VAIEPGVPR	1.310427244	2	2.314198732
P27867	VAIEPGVPREIDEFCKIGR	0.826908809	2	2.494354248
P27867	YCNTWPMAVSMLASK	1.088496472	2	3.396667004
P27867	YNLTPSIFFCATPPDDGNLCR	0.693826233	2	4.076542377
P27867	MHSVGICGSDVHYWEHGR+Oxidation(1)	1.380151076	3	4.054058075
P27867	VLVCGAGPIGIVTLLVAK	2.030818558	3	5.478995323
P27952	**RS2 40S ribosomal protein S2**	**1.137194887**	**0.0273**	**5**
P27952	AEDKEWIPVTK	1.131983275	2	3.553625822
P27952	AFVAIGDYNGHVGLGVK	1.285332173	2	3.70253849
P27952	GCTATLGNFAK	1.184371349	2	2.798514128
P27952	GTGIVSAPVPK	1.143094065	2	2.849607468
P27952	TYSYLTPDLWK	1.14840185	2	2.451853991
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.102859083**	**1.4E-06**	**27**
P28037	ADPLGLEAEK	1.121974746	1	1.928585172
P28037	NIQLEDGK	1.144605536	1	2.244835377
P28037	TDVAAPFGGFK	1.111962136	1	2.047585249
P28037	ANATEFGLASGVFTR	1.040795936	2	4.538104057
P28037	AVQMGMSSVFFNK	1.101067042	2	4.078591347
P28037	DLGEAALNEYLR	0.601010999	2	3.671352386
P28037	DTNHGPQNHEAHLR	1.152344941	2	3.629118681
P28037	ECEVLPDDTVSTLYNR	1.143323435	2	3.817711115
P28037	EESFGPIMIISR	0.654632109	2	2.834797144
P28037	EGHEVVGVFTIPDKDGK	0.972654722	2	4.639080048
P28037	GNDKVPGAWTEACGQK	1.027452034	2	4.010484695

P28037	GQALPEVVAK	1.060742071	2	2.626609802
P28037	GSASSDLELTEAELATAEAVR	0.983342919	2	6.67671299
P28037	GVVNILPGSGSLVGQR	1.050354138	2	4.788880348
P28037	IGFTGSTEVGK	1.442954594	2	2.582347155
P28037	ILPNVPEVEDSTDFFK	1.324891214	2	3.405344248
P28037	INWDQPAEAIHNWIR	1.146697925	2	3.833553314
P28037	KIGFTGSTEVGK	1.152092595	2	2.731748819
P28037	KLVEYCQR	1.575180332	2	2.667683363
P28037	LFVEESIHNQFVQK	1.032091533	2	4.796468258
P28037	LIAEGTAPR	1.206175648	2	3.634975195
P28037	LSDHPDVR	1.285076528	2	2.380564451
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.194958701	2	4.159995079
P28037	THVGMSIQTFR	1.240052043	2	2.927773952
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	0.833376657	2	5.122963428
P28037	VVEEVEK	1.082538576	2	2.437713385
P28037	KEGHEVVGVFTIPDKDGK	1.022922695	3	4.494100094
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.018151611**	**1.6E-08**	**11**
P28480	NADELVK	1.41622257	1	1.933566093
P28480	AFHNEAQVNPER	0.913133372	2	3.415516376
P28480	FATEAAITILR	1.267543656	2	3.101143837
P28480	HGGYENAVHSGALDD	1.022952686	2	4.177913666
P28480	ICDDELILIK	1.104799984	2	3.469373941
P28480	LLEVEHPAAK	1.36686088	2	2.682475328
P28480	MLVDDIGDVTITNDGATILK	1.223034315	2	3.565364122
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.421863948	2	4.569278717
P28480	SQNVMAAASIANIVK	0.990771487	2	4.773455143
P28480	SSLGPVGLDK	0.976462432	2	2.77135253
P28480	YINENLIINTDELGR	1.078960268	2	4.642449856
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.858518567**	**0.99749**	**3**
P28492	ATGLQTSDPR	0.936680309	2	2.473162651
P28492	FVIPDFEEFTGHVDR	0.903782067	2	2.994664192
P28492	SNPDLWGVSLCTVDGQR	0.857284841	2	3.63273859
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**0.850075933**	**0.93385**	**2**
P28650	LDILDVLSEIK	0.966990536	2	3.129473686
P28650	VVDLLATDADIVSR	0.885450365	2	2.673437357
P29117	**PPIF Peptidyl_prolyl cis_trans isomerase F_ mitochondrial**	**0.966850518**	**0.8795**	**2**
P29117	GANSSSQNPLVYLDVGADGQPLGR	1.051468229	2	4.019591808
P29117	KIVITDCGQLS	0.920096305	2	2.48963666
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.131628831**	**0.79679**	**15**
P29147	YEMHPLGVK	1.123364173	1	2.412760973
P29147	AVLVTGCDSGFGFSLAK	0.893506765	2	5.88231802
P29147	FGVEAFSDCLR	1.224495627	2	3.725776196

P29147	GFLVFAGCLLK	0.865835189	2	2.976827383
P29147	KMWDELPEVVR	1.110909547	2	3.399260044
P29147	MQVMTHFPGAISDK	1.143719198	2	4.512424946
P29147	MQVMTHFPGAISDK+Oxidation(1)	1.445299867	2	3.432653904
P29147	MQVMTHFPGAISDK+Oxidation(4)	1.429466264	2	3.715347767
P29147	MWDELPEVVR	0.990937739	2	3.260728836
P29147	MWDELPEVVR+Oxidation(1)	1.036502804	2	3.50850749
P29147	TIQLNVCNSEEVEK	0.931542763	2	4.40609026
P29147	VSVVEPGNFIAATSLYSPER	0.994918547	2	6.01061964
P29147	VVNISSMLGR	1.160418864	2	3.870239496
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.440321807	3	6.257657528
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(1)	1.097519845	3	4.50835228
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**1.191652172**	**0.51691**	**6**
P29266	DLGLAQDSATSTK	0.763547117	2	3.945106506
P29266	EAGEQVASSPADVAEK	0.84573427	2	4.807677269
P29266	GSLLIDSSTIDPSVSK	0.895853108	2	4.648542881
P29266	HGYPLILYDVFPDVCK	1.203573216	2	4.874583721
P29266	KGSLLIDSSTIDPSVSK	1.017534016	2	4.046681404
P29266	MGAVFMDAPVSGGVGAAR	1.161482456	2	5.024012566
P29314	**RS9 40S ribosomal protein S9**	**1.277262384**	**0.00012**	**8**
P29314	IGVLDEGK	1.139047	2	2.310127974
P29314	KGQGGAGAGDDEEED	1.8647191	2	4.33377409
P29314	KQVVNIPSFIVR	1.051871317	2	2.514836311
P29314	LDYILGLK	0.9912682	2	2.74566865
P29314	LFEGNALLR	1.442318534	2	2.656370878
P29314	QVVNIPSFIVR	1.298076226	2	3.01960659
P29314	RLQTQVFK	1.263877653	2	2.310749531
P29314	SRLDQELK	1.253370275	3	3.388149738
P29315	**RINI Ribonuclease inhibitor**	**0.943120018**	**0.07895**	**8**
P29315	ASLQELDLGSNK	0.366961379	2	2.969290972
P29315	LDDCGLTEVR	0.927280956	2	3.182410479
P29315	LENCGITSANCK	1.071569426	2	3.32412672
P29315	LGNTGIAALCSGLLLPSCR	1.191483854	2	2.72560215
P29315	LSLQNCSLTEAGCGVLPDVLR	1.270256635	2	2.912808418
P29315	SAIQANPALTELSLR	1.150294196	2	4.496706486
P29315	TCSLTAASCPHFCSVLTK	1.008392556	2	2.92780304
P29315	TNELGDAGVGLVLQGLQNPTCK	1.165166669	2	5.291962147
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.129057386**	**0.00651**	**11**
P29410	AMVASGSELGK	0.970198401	2	2.812905073
P29410	AMVASGSELGKK	1.221125327	2	2.848814964
P29410	AVLLGPPGAGK	1.052878312	2	2.854625463
P29410	EAMKDDITGEPLIR	1.030137336	2	2.322304487

P29410	LEAYHTQTTPLVEYYR	1.233328741	2	5.380480289
P29410	LVSDEMVVELIEK	0.943122702	2	4.149550915
P29410	NGFLLDGFPR	0.936097429	2	2.643473148
P29410	NLETPSCK	1.109177053	2	2.36560297
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.02019772	3	4.690304756
P29410	SYHEEFNPPK	1.129913427	3	3.517333746
P29410	TRLEAYHTQTTPLVEYYR	1.146539746	3	3.462128639
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**0.98957067**	**0.85595**	**6**
P29411	AYEAQTEPVLQYYQK	0.944797369	2	3.617428541
P29411	EDDKPETVIK	1.064046002	2	2.51937294
P29411	NLTQCSWLLDGFPR	1.086500754	2	2.644672155
P29411	TVGIDDLTGEPLIQR	0.906231324	2	3.966644287
P29411	VYNIEFNPPK	1.061288167	2	2.803151131
P29411	VYQIDTVINLNVPFEVIK	1.164340717	2	4.404606819
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**1.083741756**	**9.9E-20**	**2**
P29419	ELAEAEDVSIFK	0.680985346	1	3.055395126
P29419	YSALILGMAYGAK	1.064771816	2	3.894043207
P29994	**ITPR1 Inositol 1_4_5_trisphosphate receptor type 1**	**1.121033871**	**0.8356**	**3**
P29994	AKDDLEMSAVITIMQPILR+Oxidation(7)Oxidation(14)	1.064728745	2	2.680905581
P29994	CVVQPEAGDLNNPPKK	1.092838694	2	2.337486029
P29994	EGASNLVIDLIMNASSDR	1.168896482	2	2.430640221
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.089266965**	**0.94632**	**3**
P30009	AEDGAAPSPSSETPK	1.089617408	2	3.674095154
P30009	EAEAAEPEQPEQPEQPAAEEPR	1.059675927	2	3.863767147
P30009	GEAAAERPGEAAVASSPSK	0.869048281	2	3.488724232
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.061470179**	**0.89126**	**3**
P30349	GSPMEISLPIALSK	1.181541333	2	2.444993973
P30349	SSALQWLTPEQTSGK	1.107645777	2	3.378072977
P30349	SLSNVIAHEISHSWTGNLVTNK	1.05668762	3	3.511677742
P30427	**PLEC Plectin**	**0.950971007**	**0.0091**	**4**
P30427	LLDPEDVDVPQPDEK	0.885356388	2	3.591024637
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(1)	1.219725509	2	2.420744181
P30427	REEAAVDAQQQK	1.639445519	2	3.53455472
P30427	VLALPEPSPAAPTLR	0.917922763	2	2.433952332
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.187250299**	**0.9283**	**8**
P30713	AQVHEYLGWHADNIR	1.181098901	2	5.108009338
P30713	GQHLSEQFSQVNCLK	1.18257653	2	4.877961636
P30713	GTFGVLLWTK	1.667119584	2	2.501968861
P30713	NSMVLALQR	0.976992024	2	2.781214714
P30713	VLGPLIGVQVPEEK	1.118148631	2	3.932375431
P30713	YQVADHWYPADLQAR	1.184047327	2	5.113251686
P30713	ERVEAFLGAELCQEAHNPIMSVLGQAAK	0.878616588	3	4.814851284
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.913330991	3	4.59752512

P30835	**K6PL 6_phosphofructokinase_ liver type**	**0.934781612**	**0.52555**	**2**
P30835	NEWGSLLEELVK	0.960840431	2	2.56702733
P30835	VFANAPDSACVIGLR	0.568266223	2	2.774189711
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.052647408**	**0.77392**	**8**
P30839	EKDILAAIAADLSK	0.803574819	2	4.254760742
P30839	FDHILYTGNTAVGK	0.83735353	2	4.193453789
P30839	LQQLEALR	1.274424397	2	2.585543633
P30839	NVEEAINFINDR	1.244592962	2	3.807792902
P30839	VMQEEIFGPILPIVSVK	1.03470654	2	4.646743774
P30839	VMQEEIFGPILPIVSVK+Oxidation(2)	1.064941243	2	4.134921074
P30839	YIAPTILTDVDPNSK	1.037718033	2	4.147580147
P30839	HLTPVTLELGGK	1.044891583	3	3.768920898
P30904	**MIF Macrophage migration inhibitory factor**	**1.147305685**	**0.65672**	**2**
P30904	LHISPDR	1.097235269	1	1.973350763
P30904	LLCGLLSDR	1.681723282	2	2.798320532
P31000	**VIME Vimentin**	**1.09274932**	**0.27924**	**13**
P31000	DGQVINETSQHHDDLE	0.898026853	2	3.233851433
P31000	KLLEGEESR	1.146796945	2	2.800938606
P31000	KVESLQEEIAFLK	1.149306113	2	3.861921787
P31000	LGDLYEEEMR	1.262119786	2	3.092240572
P31000	LLEGEESR	1.06315547	2	2.810749769
P31000	LQDEIQNMKEEMAR	1.104271267	2	3.826996803
P31000	NLQEAEEWYK	1.054513689	2	3.09701252
P31000	QDVDNASLAR	1.232433665	2	2.91217351
P31000	QVQSLTCEVDALK	1.128489527	2	3.419394493
P31000	RQVDQLTNDK	1.141266819	2	3.132071018
P31000	TNEKVELQELNDR	1.187617205	2	3.628848553
P31000	VELQELNDR	1.054851666	2	2.656137705
P31000	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	1.122027205	4	5.039466858
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**0.761010766**	**3.7E-08**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.04811948	2	6.294384003
P31044	LYTLVLTDPDAPSR	1.265658723	2	4.429330826
P31044	VDYGGVTVDELGK	0.995520332	2	5.04155159
P31044	YHLGAPVAGTCFQAEWDDSVPK	0.314371111	2	5.391111374
P31044	YVWLVYEQEQPLNCDEPILSNK	1.259252365	2	5.25710535
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.832232517	3	5.126684189
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.231018092**	**0.9663**	**21**
P31210	DIEALNK	1.061932988	1	2.463108063
P31210	DELLTSLGK	1.203552901	2	2.715799809
P31210	EEMKDIEALNK	0.906187147	2	3.679901123
P31210	ENFQIFDFSLTK	1.224915199	2	2.850292444
P31210	GLVVIPK	1.313443967	2	2.388926268
P31210	HIDGAYVYR	1.462046213	2	2.907973766

P31210	LWSTDHDPEMVRPALER	1.666636718	2	2.356253147
P31210	NEHEVGEAIR	1.255684151	2	3.076349258
P31210	NPLWVNVSSPPLLK	1.704307606	2	4.128967762
P31210	QLEVILNKPGLK	1.457278757	2	3.593202829
P31210	REEIFYCGK	0.592935948	2	2.792121887
P31210	SLGVSNFNR	0.980649346	2	2.398679256
P31210	SNLCATWEALEACK	1.162143088	2	4.607090473
P31210	SNLCATWEALEACKDAGLVK	1.346882893	2	4.80440855
P31210	TAIDEGYR	1.295610722	2	2.898334503
P31210	TQAQIVLR	1.228781518	2	2.912289143
P31210	YKPVTNQVECHPYFTQTK	1.172342338	2	5.614727974
P31210	FVEMLMWSDHPEYPFHDEY	0.998818497	3	3.872775316
P31210	IKENFQIFDFSLTK	2.19301021	3	4.121700764
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.52536437	3	5.820475101
P31210	RQLEVILNKPGLK	1.279805075	3	4.249275208
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.350960562**	**0.18106**	**2**
P31230	KEIEELK	1.320473629	1	1.949190736
P31230	TVVSGLVNHVPLEQMQNR	1.414834224	3	3.44866848
P31232	**TAGL Transgelin**	**1.388791625**	**0.05162**	**2**
P31232	KYDEELEER	1.392440213	2	2.586951733
P31232	TVMALGSLAVTK	1.112260078	2	2.819388866
P31254	**UBA1Y Ubiquitin_like modifier_activating enzyme 1 Y**	**1.065196776**	**0.87087**	**2**
P31254	YDGQVAVFGSDLQEK	1.06275495	2	4.524292469
P31254	YFLVGAGAIGCELLK	1.16759792	2	2.765663862
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.011187845**	**0.9713**	**9**
P31399	ANVDKPGLVDDFK	1.017862031	2	3.908787966
P31399	KYPYWPHQPIENL	1.362166715	2	2.846992493
P31399	NCAQFVTGSQAR	0.865649082	2	3.866711617
P31399	NMIPFDQMTIDDLNEVFPETK	1.035918933	2	5.288871765
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(2)	0.918080592	2	3.133387566
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(8)	0.918080592	2	2.311555624
P31399	SWNETFHTR	1.084633556	2	2.717628479
P31399	TIDWVSFVEIMPQNQK	1.172898931	2	3.284012556
P31399	YTALVDAEEKEDVK	0.979446074	2	3.565298319
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.161122217**	**0.99422**	**4**
P32089	FIHDQTSSNPK	1.097347372	1	3.749800444
P32089	GLSSLLYGSIPK	1.011715889	2	3.822352409
P32089	NTLDCGVQILK	1.071180567	2	3.799686909
P32089	TQLQLDER	1.079435717	2	2.609786272
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**0.939438346**	**0.7528**	**3**
P32198	ELEQQMQQILDDPSEPQPGEAK	0.798189973	2	4.06369257
P32198	LLGSTIPLCSAQWER	0.942259338	2	3.010069609

P32198	MTALAQDFAVNLGPK	0.957278086	2	4.235921383
P32232	**CBS Cystathionine beta_synthase**	**1.187727533**	**0.01141**	**8**
P32232	FDSPESHVGVAWR	1.140547198	2	3.291404724
P32232	NASNPLAHYDDTAEEILQQCDGK	1.303575806	2	5.56080246
P32232	SNDDDSFAFAR	1.152235526	2	3.056133747
P32232	VDMLVASAGTGGTITGIAR	1.042867669	2	4.605305195
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.09443645	3	5.325117588
P32232	LKNEIPNSHILDQYR	1.837620665	3	3.551264286
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.032157312	3	4.199677467
P32232	VRPSDEVCK	1.245939277	3	3.60828495
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.050095346**	**0.00163**	**11**
P32551	AVAFQNPQTR	1.106599506	2	3.432546139
P32551	AVAQGNLSSADVQAAK	1.028521152	2	5.082112789
P32551	GNNTTSLLSQSVAK	0.951027746	2	3.972553253
P32551	IIENLHDVAYK	1.191733234	2	4.046308041
P32551	NALANPLYCPDYR	1.005404015	2	3.373339891
P32551	RGNNTTSLLSQSVAK	0.974493202	2	2.787323713
P32551	RWEVAALR	1.329539449	2	2.76017499
P32551	SMTASGNLGHTPFLDEL	0.993721722	2	3.147227287
P32551	TSAPGGVPLQPQELEFTK	1.039551282	2	3.826017857
P32551	YENYNYLGTSHLLR	1.740264551	2	4.069802284
P32551	ITSEELHYFVQNHFTSAR	1.820936082	3	3.473325014
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.263650692**	**2.8E-06**	**19**
P32755	ILVDYDEK	1.148182816	1	1.986255288
P32755	AFEEEQALR	1.131240477	2	3.375731707
P32755	DIAFEVEDCEHIVQK	1.225833473	2	3.998969555
P32755	ENMDVLEELK	0.772410404	2	2.669015646
P32755	FAVLQTYGDTTHTLVEK	1.302653813	2	5.14359808
P32755	FLPGFEAPTYK	1.200986841	2	2.562648773
P32755	FWSVDDTQVHTEYSSLR	0.732928702	2	5.678789616
P32755	GMEFLAVPSSYYR	1.04750359	2	2.628211975
P32755	GNLTDLETNGVR	1.125284575	2	3.676733017
P32755	IVFVLCSALNPWNK	1.613613182	2	2.53188777
P32755	MGFEPLAYK	1.583498486	2	2.602234125
P32755	SIVVANYEESIK	1.131779641	2	4.067883968
P32755	SQIQEYVDYNGGAGVQHIALR	1.212154831	2	5.592956543
P32755	TEDIITTIR	1.135443598	2	3.342715979
P32755	FLHFHSVTFWVGNAK	1.019165585	3	3.466375113
P32755	HGDGVKDIAFEVEDCEHIVQK	1.392280361	3	4.850141048
P32755	HNHQGFGAGNFNSLFK	1.240177702	3	4.690702438
P32755	IVREPWVEEDKFGK	1.440798316	3	4.353768826
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.245606831	3	7.422192097

P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.131702443**	**0.99449**	**2**
P33124	ALRPTIFPVVPR	1.143695877	2	3.25879097
P33124	IENIYIR	1.058223385	2	2.964355707
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.066336844**	**9.9E-20**	**27**
P34058	ADLINNLGTIAK	1.041609106	2	4.223329544
P34058	EDQTEYLEER	0.91014811	2	3.492019653
P34058	EGLELPEDEEEK	0.931733777	2	2.460272551
P34058	EGLELPEDEEEKKK	1.139767951	2	3.149965763
P34058	ELISNASDALDK	0.765819987	2	3.706088543
P34058	GFEVVYMTEPIDEYCVQQLK	0.757229535	2	3.425091267
P34058	GVVDSEDLPLNISR	1.092206737	2	4.869516373
P34058	HFSVEGQLEFR	1.049754744	2	2.943310976
P34058	HLEINPDHPIVETLR	1.059494957	2	4.457112789
P34058	HSQFIGYPITLYLEK	1.428328222	2	3.947757483
P34058	IDIIPNPQER	1.021326365	2	2.919069052
P34058	KHLEINPDHPIVETLR	1.148842243	2	4.891440392
P34058	LGIHEDSTNR	1.183894437	2	3.041154861
P34058	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	1.500422063	2	4.512372017
P34058	NPDDITQEEYGEFYK	1.023580594	2	4.608767986
P34058	RAPFDLFENK	1.264826221	2	3.024918079
P34058	SIYYITGESK	1.230888897	2	2.629929304
P34058	SLTNDWEDHLAVK	1.196314696	2	4.325899601
P34058	TLTLVDTGIGMTK	1.031348469	2	4.342950344
P34058	TLTLVDTGIGMTK+Oxidation(11)	1.068426249	2	3.389466763
P34058	VFIMDSCDELIPEYLNFIR	1.530856735	2	2.481673002
P34058	YESLTDPSK	1.122465392	2	2.918346167
P34058	YESLTDPSKLDSGK	1.441116818	2	3.458040953
P34058	YHTSQSGDEMTSLSEYVSR	1.123286803	2	5.499484062
P34058	YIDQEELNK	1.09515611	2	3.489870787
P34058	GEKEEEDKEDEEKPK	1.498993815	3	4.104837418
P34058	VILHLKEDQTEYLEER	1.44658924	3	4.544484615
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.31589476**	**1.6E-15**	**2**
P34064	AIGSASEGAQSSLQEVYHK	1.3145924	2	4.512516975
P34064	LNATNIELATVQPGQNFHMFTK	1.760917167	3	3.392017841
P34067	**PSB4 Proteasome subunit beta type_4**	**1.360346948**	**0.00012**	**4**
P34067	FDCGVVIAADMLGSYGSLAR	0.9285797	2	3.93522954
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.169594675	2	4.030925274
P34067	TQNPMVTGTSVLGVK	1.068695468	2	2.366650343
P34067	VNDSTMLGASGDYADFQYLK	1.378362243	2	5.345889091
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.085178929**	**1**	**2**
P35171	GGTSDALLYR	1.037203171	2	3.244963408
P35171	LFQEDNGMPVHLK	1.079496134	2	3.695898771

P35213	**1433B 14_3_3 protein beta/alpha**	**1.001467236**	**0.09549**	**7**
P35213	AVTEQGHELSNEER	0.751758975	2	4.483836174
P35213	QTTVSNSQQAYQEAFEISK	1.321706357	2	5.435275555
P35213	TAFDEAIAELDTLNEESYK	1.226890258	2	4.911929607
P35213	YDDMAAAMK	0.781944808	2	2.659874678
P35213	YLILNATHAESK	1.297417204	2	3.539207458
P35213	YLSEVASGDNK	1.129609217	2	3.142864466
P35213	EKIEAELQDICSDVLELLDK	1.247671782	3	5.31281805
P35278	**RAB5C Ras_related protein Rab_5C**	**1.021984976**	**0.83155**	**3**
P35278	FEIWDTAGQER	0.726410697	2	2.834126234
P35278	GVDLQESNPASR	1.023088635	2	3.208179951
P35278	NEPQNAAGAPGR	1.047979974	2	3.106112957
P35427	**RL13A 60S ribosomal protein L13a**	**1.178002328**	**0.03897**	**3**
P35427	CEGINISGNFYR	1.162576466	2	2.960158587
P35427	VLDGIPPPYDK	1.186782757	2	2.661778927
P35427	YQAVTATLEEK	1.18435022	2	3.202342749
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**1.017901116**	**0.99037**	**2**
P35434	AQSELSGAADEAAR	1.063831124	2	4.661328793
P35434	IEANEALVK	1.04027738	2	2.540045977
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.08299561**	**1.1E-16**	**6**
P35435	NASDMIDK	1.230868194	1	2.124659538
P35435	THSDQFLVSFK	1.217238882	1	2.872419119
P35435	GLCGAIHSSVAK	1.249417718	2	3.606096268
P35435	HLIIGVSSDR	1.128522225	2	3.234421015
P35435	NDMAALTAAGK	1.052100741	2	3.769015789
P35435	VYGTGSLALYEK	1.517089365	2	3.454094172
P35559	**IDE Insulin_degrading enzyme**	**1.48576899**	**0.01625**	**2**
P35559	YTLETRPNQEGIDVR	1.582381664	2	2.513833761
P35559	SNPGHYLGHLIGHEGPGSLLSELK	1.32048861	3	3.76112628
P35565	**CALX Calnexin**	**1.112365809**	**0.99787**	**9**
P35565	GSLSGWILSK	0.925162028	2	2.357779503
P35565	NKGDEEEEEEKLEEK	1.015190166	2	5.183688164
P35565	SDTSTPPSPK	0.918409522	2	2.880451918
P35565	TSELNLDQFHDK	1.086058383	2	3.784151077
P35565	VVDDWANDGWGLK	0.778262915	2	3.710409164
P35565	VVDDWANDGWGLKK	1.257526409	2	3.291986227
P35565	WEVDEMKETK	1.12512914	2	2.558961153
P35565	KIPNPDFFEDLEPFR	1.080881318	3	4.962648392
P35565	TDAPQPDVKDEEGKEEEK	1.158812662	3	4.066793919
P35704	**PRDX2 Peroxiredoxin_2**	**1.133770457**	**1**	**4**
P35704	EGGLGPLNIPLLADVTK	1.059364564	2	3.49646759
P35704	KEGGLGPLNIPLLADVTK	0.993149983	2	4.739411354
P35704	QITVNDLPVGR	1.058583851	2	3.233533144

P35704	SLSQNYGVLK	1.08558534	2	2.556364298
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.98889801**	**0.97685**	**4**
P35738	MNLFQSITSALDNSLAK	1.041216025	2	3.392501354
P35738	SGDLFNCGSLTIR	1.035511947	2	3.538057089
P35738	GLLLSCIEDKNPCIFFEPK	1.178616575	3	4.013040066
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	1.099048215	3	5.853898525
P35815	**PPM1B Protein phosphatase 1B**	**0.937012974**	**0.9588**	**3**
P35815	ILSAENIPNLPPGGGLAGK	1.121812966	2	2.508383751
P35815	IQNAGGSVMIQR	1.024600923	2	2.323540688
P35815	SGFALEPSVENVK	0.912779984	2	2.306948662
P36201	**CRIP2 Cysteine_rich protein 2**	**1.023347469**	**0.65857**	**3**
P36201	ASSVTTFTGEPNMCPR	0.345713405	2	3.658021212
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.020504982	2	4.872480869
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.041565998	3	5.919444084
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**0.870710858**	**0.9746**	**9**
P36365	AILTQWDR	0.642205769	1	2.030872822
P36365	FTEHVEEGR	1.026410968	2	3.382514715
P36365	NLLPTPVVSWLISK	1.010234549	2	2.581128836
P36365	SCDLGGLWR	0.997077122	2	2.696571827
P36365	VAIVGAGVSGLASIK	1.306489716	2	3.072285891
P36365	VEDGQASLYK	0.999031337	2	3.18401742
P36365	VLVVGMGNSGTDIAVEASHLAK	1.013718274	2	5.218905449
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.41142694	3	3.982517481
P36365	TQLREPVLNDELPGR	0.993658003	3	4.011910439
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.163202263**	**0.22256**	**8**
P36511	FVTFPTSFSSHDLENFFTR	1.200926327	2	4.574592113
P36511	IILEELVQK	1.093816674	2	3.368931055
P36511	ANIIAWALAQIPQK	1.091924561	3	5.925393105
P36511	GHEVTVLRPSAFVFLDPK	1.125016745	3	3.646332026
P36511	NAMWLSTIHHDQPTKPLDR	1.219566761	3	3.445832253
P36511	NAMWLSTIHHDQPTKPLDR+Oxidation(3)	1.911775739	3	3.308521271
P36511	SDLLNALEEVIDNPFYK	1.15608665	3	5.302687645
P36511	TLGRPTTLAEIMGK	1.350134281	3	3.580854416
P36972	**APT Adenine phosphoribosyltransferase**	**1.159906511**	**0.72768**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	1.091851774	2	4.203484535
P36972	IDYIAGLDSR	1.021926477	2	2.472723007
P36972	SFPDFPIPGVLFR	1.166700237	2	3.073006392
P37397	**CNN3 Calponin_3**	**0.859694352**	**0.8285**	**4**
P37397	AGQSVIGLQMGTNK	0.992340126	2	2.725144863
P37397	LTLQPVDNSTISLQMGTNK	1.397519991	2	3.424619436
P37397	VNESSLNWPQLENIGNFIK	0.944216399	2	3.901625395
P37397	YDQQAEEDLR	0.855716872	2	2.897398472

P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.003140038**	**0.89943**	**5**
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.794579389	2	3.562012196
P38650	ILDDDTIITTLENLK	1.043080651	2	2.616546631
P38650	VQGLTVEQAEAVAR	1.090656067	2	2.969914913
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	0.961790596	3	5.071119785
P38650	VTDFGDKVEDPTFLNQLQSGVNR	1.007396712	3	3.665153503
P38652	**PGM1 Phosphoglucomutase_1**	**1.03141766**	**0.21465**	**18**
P38652	KQRVEDILK	1.279898839	1	2.018953323
P38652	QQFDLENK	1.067044441	1	2.095968723
P38652	SFVGKQFSANDK	0.760894729	1	1.924017429
P38652	ADNFEYSDPVDGSISK	1.008691924	2	4.926165104
P38652	AIGGIILTASHNPGGPNGDFGIK	1.27978021	2	5.632178783
P38652	FFGNLMDASK	1.118222986	2	2.591431379
P38652	FNISNGGPAPEAITDK	1.051160633	2	4.26755476
P38652	IDAMHGVVGPYVK	0.793558105	2	2.966551781
P38652	INQDPQVMLAPLISIALK	1.064142532	2	3.585681677
P38652	LSGTGSAGATIR	1.43564662	2	3.472823381
P38652	LVIGQNGILSTPAVSCIIR	1.792775232	2	4.770109653
P38652	NIFDFNALK	1.115398173	2	2.483455896
P38652	QEATLVVGGDGR	1.157126309	2	3.700804234
P38652	SGEHDFGAAFDGDGDR	1.041481181	2	4.364538193
P38652	TIEEYAICPDLK	0.809590006	2	3.755599737
P38652	TQAYPDQKPGTSGLR	1.196908756	2	3.456156969
P38652	YDYEEVEAEGANK	0.971759525	2	5.317848206
P38652	ILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMK	0.855934665	3	3.370280981
P38656	**LA Lupus La protein homolog**	**1.167122544**	**0.10347**	**2**
P38656	ITDDQQESLNK	1.167243092	2	4.127904892
P38656	LDEGWVPLETMIK	1.095707483	2	2.782540083
P38659	**PDIA4 Protein disulfide_isomerase A4**	**1.112500237**	**9.9E-20**	**20**
P38659	TFDAIVMDPK	1.055123768	1	2.00869298
P38659	DLGLSESGEDVNAAILDESGKK	1.140538084	2	5.145179272
P38659	DNDPPIAVAK	0.943414138	2	2.554540634
P38659	EVSQPDWTPPPEVTLTLTK	0.995650317	2	3.575316191
P38659	FDVSGYPTIK	1.096142344	2	2.969977856
P38659	FDVSGYPTLK	1.096142344	2	2.969977856
P38659	FIDEHATK	1.12722439	2	2.772375107
P38659	GQAVDYDGSR	1.17055432	2	2.482684135
P38659	GRPFDYNGPR	1.270861431	2	2.641290665
P38659	IDATSASMLASK	1.173687036	2	4.090368748
P38659	KGQAVDYDGSR	1.596249796	2	2.968010426
P38659	MDATANDITNDR	0.890454865	2	3.637084484
P38659	MHVMDVQGSTEASAIK	1.176457841	2	4.43625927

P38659	RFDVSGYPTLK	1.168299329	2	3.185270309
P38659	RSPPIPLAK	1.561928257	2	2.885532618
P38659	TQEEIVAK	1.138992524	2	2.326618195
P38659	VDATEQTDLAK	1.132795321	2	3.584650755
P38659	VEGFPTIYFAPSGDK	0.714814476	2	3.254150391
P38659	YGIVDYMVEQSGPPSK	1.104620588	2	3.456413507
P38659	MHVMDVQGSTEASAIKDYVVK	1.12950078	3	3.88319087
P38718	**BR44 Brain protein 44**	**1.060759011**	**0.05169**	**3**
P38718	LMDKVELLLPK	0.635154714	2	2.721551895
P38718	LRPLYNHPAGPR	2.001221646	2	2.46547699
P38718	YSLVIIPK	1.040641998	2	2.350928307
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.951004805**	**0.99288**	**7**
P38918	FFGNPFSQLYMDR	1.596627352	2	2.52821207
P38918	FYAFNPLAGGLLTGR	1.184399916	2	4.753445148
P38918	MDVTSSSASVR	0.883390478	2	3.776616335
P38918	QVETELFPCLR	0.933635383	2	2.559310675
P38918	RMDVTSSSASVR	1.003811368	2	3.756806374
P38918	TTYGPTAPSMISAAVR	0.94783577	2	3.759147406
P38918	GHTEIDTAFVYANGQSETILGDLGLGLGR	0.928584822	3	4.962246418
P38983	**RSSA 40S ribosomal protein SA**	**1.077617613**	**0.00558**	**6**
P38983	SDGIYIINLK	0.966844175	1	2.120496035
P38983	AIVAIENPADVSVISSR	1.070606298	2	4.776054859
P38983	FTPGTFTNQIQAAFR	1.070238977	2	4.529576302
P38983	YVDIAIPCNNK	1.129132727	2	3.15111208
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.26989659	3	6.091676712
P38983	FLAAGTHLGGTNLDFQMEQYIYK	0.927274689	3	4.056909084
P39032	**RL36 60S ribosomal protein L36**	**1.12968257**	**0.00013**	**2**
P39032	EELSNVLAAMRKAAAK+Oxidation(10)	0.688717642	2	2.325865507
P39032	KREELSNVLAAMR	1.141223267	3	3.301331997
P40112	**PSB3 Proteasome subunit beta type_3**	**1.194273205**	**0.98298**	**2**
P40112	FGIQAQMVTTDFQK	0.957503202	2	3.986826181
P40112	FGPYYTEPVIAGLDPK	1.186348382	2	3.052815437
P40307	**PSB2 Proteasome subunit beta type_2**	**1.301717405**	**0.00141**	**3**
P40307	FILNLPTFSVR	1.743772318	2	2.856540918
P40307	NGYELSPTAAANFTR	1.344108762	2	4.037248611
P40307	VIDKDGIHNLENITFTK	1.145538312	2	4.036499977
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.104306922**	**0.53525**	**5**
P41034	AECPELSADLHPR	1.073359893	2	3.09518075
P41034	AIFDLEGWQISHAFQITPSVAK	0.836684773	2	4.322775841
P41034	AQEEGVPETPQPLTDAFLLR	1.294328957	2	4.185168743
P41034	QLNEQPDHSPLVQPGLAELR	1.061453956	3	3.641489267
P41034	GIHLINEPVIFHAVFSMIKPFLTEK	1.044161729	4	4.895967484
P41123	**RL13 60S ribosomal protein L13**	**1.129710175**	**0.44065**	**5**

P41123	AITEEEKNFK	1.249513922	2	2.455186844
P41123	LATQLTGPVMPIR	1.471200464	2	2.778961182
P41123	STESLQANVQR	1.151585079	2	4.003963947
P41123	TIGISVDPR	1.079971335	2	2.308715105
P41123	VDTWFNQPAR	1.018931445	2	3.151993752
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.0496959**	**0.04528**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.111443446	2	4.658724785
P41498	IELLGSYDPQK	1.744235404	2	3.662454128
P41498	LVTDENVSDNWR	1.016005587	2	3.689095497
P41542	**USO1 General vesicular transport factor p115**	**1.071389527**	**0.0001**	**11**
P41542	AWFEVGDENPGWSAQK	1.694806814	2	4.025725842
P41542	IVAFENAFER	1.283766727	2	2.642039061
P41542	LQTENSELQQR	1.053713814	2	3.055716038
P41542	LREEIEELR	1.355726197	2	2.621761322
P41542	QLGPPVQQIILVSPMGVSK	1.054057183	2	4.268157959
P41542	SQLCSQSLEITR	1.026854201	2	2.94369173
P41542	SVPVEGESELVTAAK	1.017385314	2	3.374811411
P41542	TLEQHDNIVTHYK	1.138980461	2	3.806278706
P41542	VLVSPTNPPGATSSCQK	1.284430622	2	3.872002125
P41542	AETLAKSVPVEGESELVTAAK	1.030262618	3	3.323758602
P41542	CQNEQLQTAVTQQASQIQQHK	1.11630421	3	3.847817183
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**1.505201989**	**9.9E-20**	**18**
P41562	GWPLYLSTK	2.04869625	1	1.90683496
P41562	ATDFVVPGPGK	1.12361562	2	3.383036613
P41562	CATITPDEK	1.27331143	2	2.92148304
P41562	CATITPDEKR	1.206217753	2	2.502599001
P41562	GQETSTNPIASIFAWSR	1.23895894	2	5.309575081
P41562	IHGGSVVEMQGDEMTR	1.322233627	2	5.1817379
P41562	IIWELIK	1.185784475	2	2.345202684
P41562	LIDDMVAQAMK	1.117542325	2	4.494102955
P41562	LILPYVELDLHSYDLGIENR	2.770295738	2	5.197762489
P41562	LVTGWVKPIIIGR	1.670058327	2	3.351747751
P41562	SDYLNTFEFMDK	1.320850273	2	4.437115669
P41562	SEGGFIWACK	1.175922952	2	3.51202178
P41562	SIEDFAHSSFQMALSK	1.119936638	2	4.939804554
P41562	TVEAEAAHGTVTR	1.216975548	2	3.941995859
P41562	VEITYTPK	1.122107745	2	2.739459038
P41562	FKDIFQEIYDK	1.130189701	3	4.606517792
P41562	KIHGGSVVEMQGDEMTR	1.178412502	3	3.318214655
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.022506545	3	3.615740061
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.2929392**	**1.3E-15**	**5**
P42123	DYSVTANSK	0.866902708	2	2.821960449

P42123	IVADKDYSVTANSK	0.725434432	2	2.783463001
P42123	LIAPVADDETAVPNNK	1.118944018	2	2.584647655
P42123	SLADELALVDVLEDK	1.369457191	2	2.950399637
P42123	VIGSGCNLDSAR	1.272022818	2	3.804280758
P42930	**HSPB1 Heat shock protein beta_1**	**0.991587503**	**0.66199**	**2**
P42930	AQIGGPESEQSGAK	0.446463592	2	3.890389204
P42930	VSLDVNHFAPEELTVK	0.996843653	2	3.43201828
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.215991679**	**2.7E-07**	**9**
P42932	AIAGTGANVIVTGGK	1.330420831	2	3.833057165
P42932	ELEVQHPAAK	1.249595666	2	2.984286785
P42932	GEENLMDAQVK	1.049143124	2	3.569110155
P42932	GSTDNLMDDIER	0.799442855	2	2.926175833
P42932	HEKEDGAISTIVLR	1.043396789	2	2.788162708
P42932	LFVTNDAATILR	1.748331967	2	2.998513222
P42932	LYSVHQEGNK	1.222584576	2	2.677674532
P42932	NVGLDIEAEVPAVK	0.992822642	2	3.687562704
P42932	QITSYGETCPGLEQYAIK	1.246468737	2	4.844157219
P43244	**MATR3 Matrin_3**	**1.287785624**	**0.02145**	**3**
P43244	ITPENLPQILLQLK	1.229535067	2	3.578965902
P43244	TENPAEGKEQEEK	1.199227784	2	3.314584494
P43244	YQLLQLVEPFGVISNHLILNK	1.779341814	3	4.061010361
P43274	**H14 Histone H1.4**	**1.215361389**	**9.9E-20**	**3**
P43274	ALAAAGYDVEK	1.188473991	2	3.692065001
P43274	SGVSLAALK	0.955823119	2	3.140358686
P43274	SGVSLAALKK	1.108916871	2	2.47759223
P43276	**H15 Histone H1.5**	**1.364704583**	**9.9E-20**	**2**
P43276	ALAAGGYDVEK	1.388207255	2	2.774060965
P43276	ATGPPVSELITK	1.126181598	2	2.967749834
P43278	**H10 Histone H1.0**	**0.90135335**	**0.94898**	**2**
P43278	VGENADSQIK	1.115954972	2	3.431298971
P43278	YSDMIVAAIQAEK	0.829607679	2	4.261011124
P43424	**GALT Galactose_1_phosphate uridylyltransferase**	**1.041964859**	**0.05909**	**2**
P43424	HDPLNPLCPGATR	1.182673701	2	2.87984395
P43424	YNPLQDEWVLVSAHR	0.876307022	2	2.439340115
P45591	**COF2 Cofilin_2**	**1.108198938**	**0.86357**	**4**
P45591	KEDLVFIFWAPESAPLK	1.108658911	2	3.911050558
P45591	MASGVTVNDEVIK	1.057762906	2	2.483415604
P45591	QILVGDIGDTVEDPYTSFVK	1.095979703	2	5.174490452
P45591	HEWQVNGLDDIKDR	0.94595299	3	4.206285477
P45592	**COF1 Cofilin_1**	**1.25870089**	**9.9E-20**	**4**
P45592	HELQANCYEEVK	1.281729401	2	3.319258213
P45592	LGGSAVISLEGKPL	1.918698606	2	2.431261778
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.364604353	2	5.019269466

P45592	HELQANCYEEVKDR	1.268444019	3	5.493163586
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.179527043**	**0.19334**	**3**
P45878	GWDQGLLGMCEGEK	1.17830993	2	2.832413912
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	0.996903094	2	3.705191851
P45878	LVIPSELGYGER	1.64341981	2	2.401523352
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.063500215**	**8.7E-05**	**20**
P45953	AMVENGGLVTSNPLR	0.892692164	2	2.740113497
P45953	AMVENGGLVTSNPLRV	1.336717472	2	4.140826702
P45953	ASNTSEVYFDGVK	1.195566858	2	3.509231329
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	0.94314265	2	4.655416489
P45953	ENMASLQSNPQQQELFR	1.213894222	2	3.892059326
P45953	FFEEVNDPAK	0.775599841	2	2.708445549
P45953	GIVNEQFLLQR	1.11525746	2	3.219193935
P45953	IFEGTNDILR	1.206342567	2	3.003589869
P45953	IFGSEAAWK	0.708863655	2	2.654495955
P45953	IHNFGVIQEK	1.45598919	2	2.314133644
P45953	LFVALQGCMDK	1.107153405	2	2.483862162
P45953	NDSLEKVEEDTLQGLK	1.006826517	2	3.594150543
P45953	NPLGNVGLLIGEASK	1.224553449	2	2.682408571
P45953	SFGGVTHGLPEK	1.179911666	2	2.71756506
P45953	SFGGVTHGLPEKK	1.249881059	2	2.384603024
P45953	SLSEGYPTAQHEK	1.197462776	2	3.347725391
P45953	TGIGSGLSLSGIVHPELSR	1.070790493	2	4.321165085
P45953	VEEDTLQGLK	0.955135095	2	2.588833094
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.072821005	3	4.563464642
P45953	SGELAVQALEQFATVVEAK	1.000205426	3	4.955094337
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.032901356**	**0.99776**	**4**
P46418	AILNYIATK	0.867363733	2	3.372720003
P46418	SDGSLMFEQVPMVEIDGMK	0.973476078	2	3.545745373
P46418	SHGQDYLVGNK	1.085057936	2	3.569638252
P46418	VSNLPTVK	1.092704249	2	2.859722376
P46425	**GSTP2 Glutathione S_transferase P 2**	**1.085975723**	**0.98119**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	1.101352294	2	4.461594105
P46425	FEDGDLTLYQSNAILR	0.860958501	2	4.537661076
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.107356444**	**5.2E-11**	**25**
P46462	AIANECQANFISIK	1.328570163	2	2.494134188
P46462	EAVCIVLSDDTCSDEK	1.130752003	2	3.747733831
P46462	EDEEESLNEVGYDDIGGCR	1.083229013	2	4.849054337
P46462	ELQELVQYPVEHPDK	1.045039491	2	4.625997543
P46462	ETVVEVPQVTWEDIGGLEDVK	1.032402121	2	3.100064039
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.110317478	2	4.122541904
P46462	EVDIGIPDATGR	0.63644902	2	3.1448071

P46462	GDDLSTAILK	0.880800212	2	2.972871304
P46462	GGNIGDGGGAADR	1.118180026	2	3.201267958
P46462	GILLYGPPGTGK	0.947543865	2	3.575330496
P46462	IVSQLLTLMDGLK	2.428646054	2	4.220181465
P46462	KYEMFAQTLQQSR	1.052642626	2	3.045798063
P46462	LAGESESNLRKAFEEAEK	1.023950347	2	2.42502141
P46462	LDQLIYIPLPDEK	1.0805802	2	4.847033501
P46462	LEILQIHTK	1.086698581	2	2.912633896
P46462	LGDVISIQPCPDVK	1.128190847	2	4.46848774
P46462	LIVDEAINEDNSVVSLSQPK	1.111816151	2	5.328796864
P46462	MDELQLFR	0.845071777	2	3.199991703
P46462	MTNGFSGADLTEICQR	1.021533275	2	4.517092228
P46462	QTNPSAMEVEEDDPVPEIR	0.966899371	2	4.611572266
P46462	RSVSDNDIR	1.395856096	2	2.658648968
P46462	WALSQSNPSALR	1.143507344	2	2.599133492
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.355302425	3	6.792405128
P46462	NAPAIIFIDELDAIAPK	1.415358095	3	5.109483719
P46462	NVFIIGATNRPDIIDPAILRPGR	1.077588707	3	4.199270248
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**1.426556183**	**0.39684**	**3**
P46664	FIEDELQIPVK	1.013778539	2	3.165514231
P46664	VGIGAFPTEQDNEIGELLQTR	1.448152763	2	4.304396629
P46664	VVDLLAQDADIVCR	1.102860347	2	3.09315753
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.203783005**	**0.31555**	**3**
P46720	GIGETPIVPLGISYIEDFAK	1.207139987	2	3.589865923
P46720	GVQHQLHVESK	0.886165366	2	3.238781214
P46720	SENSPLYIGILEMGK	0.911604381	2	3.218569994
P46844	**BIEA Biliverdin reductase A**	**1.015867245**	**0.99976**	**3**
P46844	FGVVVVGVGR	1.026818299	2	2.475596666
P46844	LLDQVSAEDLAAEK	0.866966062	2	3.807953835
P46844	MTVQLETQNK	1.05425142	2	2.814459324
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.179592657**	**0.2301**	**6**
P46953	AQGSVALSVTQDPACK	1.024178822	2	4.411123276
P46953	ASFQPPVCNK	1.101089333	2	2.673982859
P46953	DLGTQLAPIIQEFFHSEQYR	1.013802731	2	3.165488243
P46953	QDVDVWLWQLEGSSK	1.392952308	2	3.309269428
P46953	YYVGDTEDVLFEK	1.166825858	2	4.052299023
P46953	TGKPNPDQLLK	1.163214054	3	3.593695402
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.305143713**	**0.00043**	**4**
P46978	FGQVYTEAK	1.231354379	2	2.602279425
P46978	FYSLLDPSYAK	1.165797797	2	3.093926668
P46978	VGQAMASTEEK	1.453695029	2	3.204134226
P46978	VGQAMASTEEK+Oxidation(5)	1.71542878	2	2.622654915

P47198	**RL22 60S ribosomal protein L22**	**1.150643135**	**6.4E-05**	**2**
P47198	AGNLGGGVVTIER	1.145888694	2	3.16187501
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.566668428	3	4.872404575
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.384677035**	**9.9E-20**	**4**
P47875	GFGFGQGAGALVHSE	1.107968835	2	3.079694748
P47875	GLESTTLADKDGEIYCK	1.39610164	2	4.980594635
P47875	NLDSTTVAVHGEEIYCK	0.955343017	2	4.353924751
P47875	HEEAPGHRPTTNPNASK	1.525462789	3	3.497723103
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**0.974324812**	**0.74836**	**3**
P47942	GLYDGPVCEVSVTPK	0.969693936	2	3.581647396
P47942	QIGENLIVPGGVK	1.019414057	2	2.439012289
P47942	SITIANQTNCPLYVTK	1.423724683	2	3.289038897
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.142303725**	**0.71967**	**2**
P48004	NYTDDAIETDDLTIK	0.974845324	2	4.706778049
P48004	YVAEIEKEKEENEK	1.161659995	2	4.028362274
P48037	**ANXA6 Annexin A6**	**1.149775174**	**9.9E-20**	**17**
P48037	ALLALCGGED	1.42420528	1	2.190618992
P48037	GELSGDFEK	1.222982183	1	2.069562435
P48037	AANDFNPDADAK	1.21972326	2	2.905189276
P48037	AINEAYKEDYHK	1.308997253	2	3.384114504
P48037	ALIEILATR	1.255196315	2	3.495878696
P48037	DLESDIIGDTSGHFQK	1.011286763	2	4.260920048
P48037	GFGSDKESILELITSR	0.941323181	2	4.132144451
P48037	GSVHDFADFDANQDAEALYTAMK	0.495391796	2	6.128281116
P48037	QRQEICQSYK	1.306970609	2	3.276952744
P48037	SEIDLLNIR	1.531013314	2	3.112278461
P48037	SLEDALSSDTSGHFK	1.134293112	2	3.288510323
P48037	TNEQIHQLVAAYK	1.324640569	2	3.872861385
P48037	TNYDIEHVIK	1.077477434	2	3.238611937
P48037	TTGKPIEASIR	1.323999735	2	2.503026962
P48037	WGTDEAQFIYILGNR	1.838920266	2	2.347768068
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.075489957	3	5.089622021
P48037	GIGTDEATIIDIITQR	1.080391482	3	4.102993011
P48500	**TPIS Triosephosphate isomerase**	**1.212924092**	**1.2E-15**	**12**
P48500	FFVGGNWK	1.264627359	1	1.992959619
P48500	CNVSEGVAQCTR	1.119534422	2	3.832330942
P48500	DLGATWVVLGHSER	0.72379007	2	4.006038666
P48500	HIFGESDELIGQK	1.072143174	2	4.002853394
P48500	IIYGGSVTGATCK	1.51432115	2	4.168003559
P48500	KFFVGGNWKMNGR	0.961232731	2	2.310231924
P48500	LPADTEVVCAPPTAYIDFAR	0.300766871	2	4.472621918
P48500	RHIFGESDELIGQK	1.11553044	2	4.29209137
P48500	TATPQQAQEVHEK	1.213594707	2	3.633104801

P48500	VNHALSEGLGVIACIGEK	1.155347048	2	5.179026127
P48500	VVLAYEPVWAIGTGK	1.047353104	2	4.134837151
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.028637538	4	5.37005806
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.947409844**	**0.6879**	**6**
P48508	EFPDVLECTMSHAVEK	0.874303192	2	3.768867731
P48508	INPDEREEMK	1.1620082	2	2.472528458
P48508	LFIVGSNSSSSTR	1.118856868	2	3.510997057
P48508	QFDIQLLTHNDPK	1.347381612	2	2.612658024
P48508	TLNEWSSQISPDLVR	0.810787865	2	4.629065037
P48508	ASTLHLQTGNLLNWGR	1.325635142	3	3.838911533
P48675	**DESM Desmin**	**0.846997255**	**0.25238**	**3**
P48675	FLEQQNAALAAEVNR	0.904002127	2	4.231886864
P48675	HQIQSYTCEIDALK	1.824250125	2	3.552767992
P48675	VSDLTQAANK	0.836961288	2	2.850980997
P48679	**LMNA Prelamin_A/C**	**0.977755741**	**0.46722**	**14**
P48679	AQHEDQVEQYK	1.309805119	2	2.699162006
P48679	AQHEDQVEQYKK	1.182157736	2	4.380353928
P48679	IDSLSAQLSQLQK	0.983110882	2	3.041064978
P48679	ITESEEVVSR	0.996059988	2	2.832991838
P48679	LQEKEDLQELNDR	1.140582427	2	4.027468204
P48679	MQQQLDEYQELLDIK	1.188238015	2	4.884830475
P48679	NSNLVGAAHEELQQSR	0.949299254	2	4.609542847
P48679	SGAQASSTPLSPTR	0.97869107	2	3.623058081
P48679	SLETENAGLR	1.44515394	2	2.628831625
P48679	SVGGSGGGSFGDNLVTR	0.999248265	2	3.432418346
P48679	TALINATGEEVAMR	1.030663586	2	2.847514391
P48679	TVLCGTCGQPADK	0.947523098	2	2.83457613
P48679	VAVEEVDEEGK	0.900321884	2	3.037405729
P48679	VAVEEVDEEGKFVR	0.997519295	2	2.940264702
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**0.954612228**	**7.2E-14**	**27**
P48721	VINEPTAAALAYGLDK	1.449462188	1	3.381241798
P48721	AQFEGIVTDLIK	1.096893699	2	3.839066982
P48721	ASNGDAWVEAHGK	1.265524002	2	3.659946203
P48721	DAGQISGLNVLR	1.066076428	2	3.503056765
P48721	EEISKMRELLAR	1.094034948	2	2.437199593
P48721	EQQIVIQSSGGLSK	0.930810316	2	3.712967396
P48721	EQQIVIQSSGGLSKDDIENMVK	0.945011436	2	4.768486023
P48721	GAVVGIDLGTTNSCVAVMEGK	0.908556867	2	5.069857121
P48721	LFEMAYK	1.02092578	2	2.352840424
P48721	LLGQFTLIGIPPAPR	1.853224717	2	3.368118286
P48721	MEEFKDQLPADECNK	0.93467941	2	4.553418636
P48721	MEEFKDQLPADECNK+Oxidation(1)	1.413451942	2	3.967645407
P48721	MKETAENYLGHTAK	0.989124519	2	4.216881275

P48721	NAVITVPAYFNDSQR	1.11704278	2	3.157208443
P48721	QAVTNPNNTFYATK	0.956497122	2	3.418057919
P48721	RYDDPEVQK	1.082264044	2	2.951504707
P48721	RYDDPEVQKDTK	1.399395966	2	3.756350517
P48721	SDIGEVILVGGMTR	1.107814203	2	4.035479546
P48721	SQVFSTAADGQTQVEIK	0.458981519	2	5.313323498
P48721	STNGDTFLGGEDFDQALLR	1.212896897	2	5.319878578
P48721	TTPSVVAFTPDGER	1.030580811	2	3.550759554
P48721	VEAVNMAEGIIHDTETK	1.142150641	2	4.38138485
P48721	VLENAEGAR	1.126896877	2	3.13884902
P48721	VQQTVQDLFGR	1.064386552	2	3.490255356
P48721	YDDPEVQKDTK	1.095920364	2	2.927332401
P48721	ERVEAVNMAEGIIHDTETK	1.022058645	3	5.587630749
P48721	MKETAENYLGHTAK+Oxidation(1)	1.602511416	3	3.373778105
P48998	**INVO Involucrin**	**1.060998019**	**0.93603**	**2**
P48998	HKLENLTQKEK	1.077434343	1	1.965730667
P48998	ELLDQRLDQELVNK	1.060995709	2	2.420773745
P49025	**CTRO Citron Rho_interacting kinase**	**0.96492917**	**0.8132**	**2**
P49025	LLMIAGEERALCLVDVK+Oxidation(3)	0.864574925	2	2.325179338
P49025	LMMNQLEEDLVSARR+Oxidation(2)	1.045474467	2	2.352519274
P49134	**ITB1 Integrin beta_1**	**0.99231736**	**0.96781**	**4**
P49134	CNCQSHGIPASPK	1.147794777	2	3.204071522
P49134	FCECDNFNCDR	0.983736506	2	3.459947586
P49134	GICECGACK	0.994501737	2	2.318189621
P49134	WDTGENPIYK	1.131550691	2	2.384713888
P49242	**RS3A 40S ribosomal protein S3a**	**0.989362277**	**2.4E-11**	**10**
P49242	ADGYEPPVQESV	1.013347466	1	2.009725809
P49242	ACQSIYPLHDVFVR	1.38015979	2	3.778867722
P49242	EVQTNDLKEVVNK	0.913117869	2	2.331767559
P49242	LIPDSIGKDIEK	1.479854389	2	2.907618999
P49242	LITEDVQGK	1.244003584	2	2.358298779
P49242	LMELHGEGGSSGK	1.202367807	2	3.234148741
P49242	LMELHGEGGSSGK+Oxidation(2)	1.269710699	2	3.103387594
P49242	NCLTNFHGMDLTR	1.195068888	2	4.157990932
P49242	TTDGYLLR	1.133768782	2	2.991350412
P49242	VFEVSLADLQNDEVAFR	1.019974797	2	4.789309978
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**1.018443313**	**0.46793**	**5**
P49432	EAINQGMDEELERDEK	1.061878316	2	2.84861517
P49432	ILEDNSIPQVK	1.001433752	2	3.461088657
P49432	IMEGPAFNFLDAPAVR	1.024837502	2	4.558763027
P49432	TIRPMDIEAIEASVMK	2.405487838	2	3.426910162
P49432	VFLLGEEVAQYDGAYK	0.920036432	2	3.501980543

P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.771622038**	**2.1E-12**	**10**
P49889	CKEDALFNR	1.062675692	2	2.375930786
P49889	FEEHYQQQMK	1.091485291	2	2.954859018
P49889	FMEGQVPYGSWYDHVK	0.792094021	2	4.335290432
P49889	IIQHTSFQEMK	1.899490585	2	3.216384649
P49889	NEDLINGIK	0.96444413	2	2.915210009
P49889	NNPCTNYSMLPETMIDLK	0.738914739	2	4.364925385
P49889	NNPCTNYSMLPETMIDLK+Oxidation(14)	0.770295822	2	3.112719536
P49889	NNPCTNYSMLPETMIDLK+Oxidation(9)	0.770295822	2	4.146317005
P49889	SGSTWISEIVDMIYK	1.263299125	2	4.754103661
P49889	LIEFLERDPSAELVDR	1.030064697	3	4.730216503
P50137	**TKT Transketolase**	**0.992521985**	**0.99928**	**20**
P50137	AVELAANTK	1.065464492	1	1.971679568
P50137	GITGIEDK	1.005803076	1	2.426312447
P50137	HQPTAIIAK	0.906154352	2	2.513094902
P50137	IIALDGDTK	1.015705316	2	2.668824911
P50137	ISSDLDGHPVPK	0.990278868	2	3.352298975
P50137	KISSDLDGHPVPK	1.035971388	2	4.050012112
P50137	LDNLVAIFDINR	0.894802285	2	4.753306866
P50137	LGQSDPAPLQHQVDVYQK	1.174963656	2	3.742672205
P50137	MFGIDKDAIVQAVK	0.958674358	2	4.381688118
P50137	NSTFSELFK	0.868344489	2	2.45201087
P50137	SVPMSTVFYPSDGVATEK	0.848492495	2	4.690301895
P50137	VLDPFTIKPLDK	1.343247023	2	3.49276638
P50137	VLDPFTIKPLDKK	1.121966181	2	2.438898087
P50137	ILATPPQEDAPSVDIANIR	1.159733904	3	4.92330265
P50137	ILTVEDHYYEGGIGEAVSAVVVGEPGVTVTR	2.434805423	3	3.821249008
P50137	NMAEQIIQEIYSQVQSK	0.932743147	3	6.513892174
P50137	SGKPAELLK	0.934244634	3	3.427255154
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	0.980211514	3	5.446114063
P50137	TSRPENAIIYSNNEDFQVGQAK	0.898821573	3	5.596367359
P50137	SKDDQVTVIGAGVTLHEALAAAEMLKK	1.20499387	4	5.550498009
P50169	**RDH3 Retinol dehydrogenase 3**	**1.040865017**	**6.5E-05**	**9**
P50169	FQDSYMK	1.100929346	1	1.935591459
P50169	GLWGLVNNAGISVPVGPNEWMR	1.046670041	2	3.56431222
P50169	KLWDQTTEEVK	1.463956285	2	2.557690144
P50169	LWDQTTEEVK	1.032132286	2	3.599947453
P50169	LWDQTTEEVKEIYGEK	1.064483493	2	4.993239403
P50169	MSLVGGGYCISK	1.183242802	2	3.909941435
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.311910211	3	5.483289242
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(2)	1.241021763	3	4.308114052
P50169	KLWDQTTEEVKEIYGEK	1.019029781	3	4.301816463
P50237	**ST1C1 Sulfotransferase 1C1**	**1.033419852**	**0.69022**	**9**

P50237	AGTTWTQEIVDMIQNDGDVQK	1.007383847	2	5.6509161
P50237	DISEEVLNK	0.813744685	2	2.627704144
P50237	DLHLGEQDLQPETR	0.897973867	2	3.95352149
P50237	FLEKDISEEVLNK	1.147339339	2	3.409332752
P50237	IWNFQAKPDDLLIATYAK	1.290701735	2	4.465745449
P50237	MKDLHLGEQDLQPETR	0.920718717	2	4.920691013
P50237	MLPDPGTLGEYIEQFK+Oxidation(1)	1.116777466	2	3.070204496
P50237	VLWGSWYDHVK	1.486121748	2	3.183143854
P50237	MLPDPGTLGEYIEQFK	1.115726058	3	4.675834179
P50289	**ASPX Acrosomal protein SP_10**	**0.937807102**	**0.4238**	**2**
P50289	MQIMCCRNEPLCNK	0.934770703	2	2.348809719
P50289	MQIMCCRNEPLCNK+Oxidation(1)	1.215694598	2	2.391864061
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**1.075478432**	**0.02457**	**7**
P50398	FDLGQDVIDFTGHALALYR	0.847836291	2	2.744448423
P50398	FQLLEGPPESMGR	1.037575463	2	3.684373856
P50398	KQNDVFGEADQ	0.912734004	2	3.312532663
P50398	NPYYGGESSSITPLEELYK	1.327428132	2	5.890672207
P50398	QLICDPSYIPDR	1.131589133	2	2.894898891
P50398	TDDYLDQPCLETINR	0.857826176	2	4.675558567
P50398	TFEGVDPQTTSMR	0.96202825	2	3.223177195
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.152394272**	**0.0611**	**10**
P50399	DWNVDLIPK	1.01573452	2	2.353840351
P50399	EIRPALELLEPIEQK	1.043834513	2	3.498961687
P50399	FDLGQDVIDFTGHSLALYR	1.182132266	2	4.4165802
P50399	FVSISDLFVPK	1.155683694	2	3.510244846
P50399	MTGSEFDFEEMKR	1.13724167	2	2.732398033
P50399	NTNDANSCQIIIPQNQVNR	1.255503967	2	4.028598309
P50399	TDDYLDQPCCETINR	1.09419523	2	4.681679726
P50399	VICILSHPIK	1.421338112	2	2.510890722
P50399	AYDATTHFETTCDDIKDIYK	0.93638306	3	5.151251316
P50399	VLHMDQNPYYGGESASITPLEDLYK	1.047140344	3	4.653731823
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.305741589**	**2.5E-07**	**8**
P50431	GLLEEDFQK	1.166970069	1	2.300783634
P50431	ALSDALTELGYK	1.16143318	2	4.362866879
P50431	AVLEALGSCLNNK	1.345240526	2	4.139972687
P50431	IMGLDLPDGGHLTHGFMTDK	1.054505439	2	2.845616102
P50431	IYQLQVLANCR	1.3123966	2	2.571626663
P50431	LIIAGTSCYSR	1.690175296	2	2.363415718
P50431	VLEACSIACNK	1.288793316	2	3.999352455
P50431	YSEGYPGQR	1.099888771	2	2.441403866
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**1.127281706**	**9.9E-20**	**14**
P50475	SVLGDADQK	1.53594469	1	2.282062054
P50475	ASEWVQQVSGLMDGK	1.020348272	2	4.042644024

P50475	AVFDETYPDPVR	1.304407243	2	2.996023893
P50475	EIADLGEVLATAVIPQWQK	0.872462807	2	3.148565769
P50475	GLEATDDSPK	1.248523823	2	2.671415091
P50475	ITCLCQVPQNAANR	1.363479423	2	4.130670547
P50475	IVAVTGAEAQK	1.347673152	2	2.45564723
P50475	MSNYDTDLFVPYFEAIQK	0.834345007	2	3.443878174
P50475	NSSHAGAFVIVTEEAIAK	1.128594818	2	3.782939434
P50475	QIWQNLGLDEAK	1.080759602	2	2.825498581
P50475	RIVAVTGAEAQK	1.120294986	2	3.122610331
P50475	TITVALADGGRPDNTGR	1.2063144	2	2.760581493
P50475	VDDSSEDKTEFTVK	1.284022698	2	4.013429165
P50475	VGAEDTDGIDMAYR	1.115166042	2	3.332469702
P50503	**F10A1 Hsc70_interacting protein**	**1.305256009**	**9.9E-20**	**5**
P50503	AIDLFTDAIK	1.210756403	2	2.533326149
P50503	AIEINPDSAQPYK	1.090080805	2	2.804926157
P50503	GAAIDALNDGELQK	1.252973632	2	3.311888218
P50503	KGAAIDALNDGELQK	1.568694049	2	4.767714977
P50503	LDYDEDASAMLR	1.070894691	2	3.282337666
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**1.015780272**	**0.40983**	**10**
P50554	GTFCSFDTPDEAIR	1.257895513	2	3.183335304
P50554	IDIPSFDWPIAPFPR	1.221477598	2	3.651266813
P50554	IFNTWLGDPSK	1.125817411	2	2.336909056
P50554	TLLTGLLDLQAQYPQFVSR	1.191639239	2	4.235865593
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.252213026	2	4.270765305
P50554	VDFEFDYDGPLMK	0.745614122	2	3.722331047
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.240555646	3	4.99710083
P50554	MLDLYSQISSVPIGYNHPALAK	0.831513662	3	3.481969118
P50554	NLLLAEVINIIK	0.838476558	3	5.310154438
P50554	REDLLNNVAHAGK	0.981722902	3	3.761541843
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.030900704**	**0.47582**	**2**
P50580	HELLQPFNVLYEK	1.302817066	2	2.409907341
P50580	TIIQNPTDQQK	1.0241189	2	2.757921219
P50878	**RL4 60S ribosomal protein L4**	**1.108699904**	**0.0001**	**10**
P50878	NIPGITLLNVSK	1.150413617	1	2.375369072
P50878	NVTLPAVFK	0.849361989	1	2.225018501
P50878	FCIWTESAFR	1.266072789	2	2.453387737
P50878	KLDELYGTWR	1.106351801	2	3.094302893
P50878	LEAAAAALAAK	1.305527508	2	2.34503293
P50878	RGPCIIYNEDNGIIK	1.388264882	2	2.956162214
P50878	SGQGAFGNMCR	1.101583097	2	2.776360512
P50878	SNYNLPMHK	1.058615996	2	2.418854237
P50878	YAICSALAASALPALVMSK	1.223304677	2	3.681823254

P50878	KLEAAAAALAAK	1.264742441	3	3.786335945
P50904	**RASA1 Ras GTPase_activating protein 1**	**0.922142801**	**0.71645**	**3**
P50904	LESLLLCTLNDR	1.218377896	1	1.902323246
P50904	IMESKQSCELSPSK+Oxidation(2)	0.69991909	2	2.501337767
P50904	YYNSIGDIIDHYRK	1.020769842	2	2.429328918
P51538	**CP3A9 Cytochrome P450 3A9**	**1.213116187**	**0.92994**	**2**
P51538	GFWEFDKYCHK	0.999859849	1	2.230127811
P51538	EMFPIINQYTDMLVR	1.14433249	2	2.530366898
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.087024277**	**5.5E-08**	**8**
P51635	QLDALNK	1.215271098	1	1.989902377
P51635	ALEALVAK	1.130795826	2	2.85836792
P51635	GLEVTAYSPLGSSDR	1.086004474	2	4.150090218
P51635	HIDCASVYGNETEIGEALK	1.158800444	2	5.872045994
P51635	ILQNIQVFDFTFSPEEMK	3.837295645	2	4.523253918
P51635	HHPEDVEPAVR	1.194045623	3	3.763026476
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.957442178	3	6.803411961
P51635	HPDEPVLLEEPVVLALAEK	1.679487218	3	5.668543816
P51647	**AL1A1 Retinal dehydrogenase 1**	**1.015758815**	**2.8E-08**	**17**
P51647	YCAGWADK	1.360863441	1	2.248506308
P51647	ANNTTYGLAAGVFTK	1.107059032	2	4.531414032
P51647	ELGEHGLYEYTELK	1.093528065	2	3.456165552
P51647	IFINNEWHDSVSGK	1.949878381	2	4.598176479
P51647	IFVEESVYDEFVR	1.243419823	2	4.496495724
P51647	IHGQTIPSDGDIFTFTR	2.064500102	2	4.356768608
P51647	LLLATIEAINGGK	13.1930495	2	4.730998516
P51647	VFANAYLSDLGGSIK	1.796666045	2	4.644490242
P51647	YVLGNPLTQGINQGPQIDK	1.462105766	2	5.060204029
P51647	YVLGNPLTQGINQGPQIDKEQHDK	1.164313407	2	3.766478539
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	1.222356005	3	3.56138134
P51647	FPVLNPATEEVICHVEEGDK	0.577250237	3	3.749338865
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	1.744710445	3	4.749162197
P51647	KFPVLNPATEEVICHVEEGDK	1.141947159	3	3.368245363
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	1.418315959	3	3.838535547
P51647	FPVLNPATEEVICHVEEGDKADVDK	1.025139568	4	5.193379879
P51647	KFPVLNPATEEVICHVEEGDKADVDK	1.305196666	4	4.826226711
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.912589777**	**0.99978**	**9**
P51650	EVGEVLCTDPLVSK	0.744769514	2	4.143151283
P51650	GIHDSFVTK	1.059991698	2	2.301894903
P51650	HQSGGNFFEPTLLSNVTR	0.965526604	2	3.936876297
P51650	IITAESGKPLK	1.040099993	2	2.618567944
P51650	ILLHHAANSVK	1.521466038	2	2.428305626
P51650	LGTVADCGVPEAR	1.118315713	2	3.269433022

P51650	VGNGFEEGTTQGPLINEK	0.860754438	2	4.881690025
P51650	WLPTPATFPVYDPASGAK	0.869501857	2	3.038829803
P51650	YGIDEYLEVK	0.999817121	2	2.5931952
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**1.16029934**	**0.4266**	**3**
P51863	LYPEGLAQLAR	1.134452871	1	1.901862025
P51863	ADDYEQVK	1.177513893	2	2.385859728
P51863	LHLQSTDYGNFLANEASPLTVSVIDDK	1.445113158	3	3.606918335
P51869	**CP4F4 Cytochrome P450 4F4**	**1.736326429**	**0.00257**	**4**
P51869	ALPSQHEDDILK	1.050068256	2	2.878508806
P51869	NISLMTLDSLQK	1.053459762	2	3.6509552
P51869	TLDFIDVLLLTK	1.890187196	2	3.800179243
P51869	WQDLASGGSAR	1.000385906	2	2.497128248
P51886	**LUM Lumican**	**0.953407361**	**0.99861**	**4**
P51886	LDGNPLTQSSLPPDMYECLR	0.881188583	2	2.644064188
P51886	NNQIDHIDEK	0.938238465	2	3.330487728
P51886	SIPTVNENLENYYLEVNK	0.960875131	2	4.131548405
P51886	SLQDLQLANNK	1.11211847	2	2.963608503
P52296	**IMB1 Importin subunit beta_1**	**1.233639607**	**0.01389**	**4**
P52296	AAVENLPTFLVELSR	1.262981754	2	3.26080966
P52296	TVSPDRLELEAAQK	1.240151616	2	3.324921846
P52296	VLANPGNSQVAR	1.164345223	2	3.516394854
P52296	VQHQDALQISDVVMASLLR	1.060846603	2	2.473317385
P52303	**AP1B1 AP_1 complex subunit beta_1**	**0.869072505**	**0.63041**	**2**
P52303	NINLIVQK	0.854208119	1	2.026650667
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.037623888	3	4.775326252
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**1.305758876**	**9.8E-14**	**2**
P52504	IIACDGGGGALGHPK	1.165241841	2	3.521810055
P52504	VYINLDKETK	1.51913804	2	2.98061204
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.136451172**	**0.89725**	**5**
P52555	FDTQYPYGEK	1.18692745	2	2.545891523
P52555	ILDQGEDFPASELAR	1.190250793	2	4.638560295
P52555	QGQDGLSGVK	0.948369152	2	2.661386013
P52555	SLNILTAFR	1.285073186	2	2.529396057
P52555	GQGVYLGMPGCLPAYDALAGQFIEASSR	1.235077794	3	4.141711712
P52631	**STAT3 Signal transducer and activator of transcription 3**	**1.018641562**	**0.69845**	**2**
P52759	**UK114 Ribonuclease UK114**	**1.038458906**	**0.91827**	**6**
P52759	IEIEAIAVQGPFTTAGL	1.055668791	1	3.552279949
P52759	AAGCDFTNVVK	2.354883794	2	3.342602968
P52759	AAYQVAALPK	1.15448498	2	2.465381145
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	0.807576745	2	4.433669567
P52759	TTVLLADINDFGTVNEIYK	1.020647397	2	5.159482002
P52759	TYFQGNLPAR	0.993675649	2	2.594797611

P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.129057356**	**0.06182**	**2**
P52845	CKEDAIFNR	1.062675692	2	2.375930786
P52845	SGSTWIGEIVDMIYK	1.306602794	2	2.932119846
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.192597304**	**9.9E-20**	**8**
P52847	NYFTMTQSEK	1.076850605	1	2.768094063
P52847	DNPLVNYTHLPTEIMDHSK	1.213083252	2	4.060273647
P52847	FLAGNVAYGSWFDHVK	0.687956211	2	3.63775897
P52847	IVHHTSFEVMK	1.684515956	2	2.872457743
P52847	SGVELLKK	1.438291968	2	2.362816572
P52847	TLDEHTLER	1.20353762	2	2.863834143
P52847	IEEFQSRPCDIVIPTYPK	1.251921707	3	4.521101475
P52847	THLPIDLLPK	1.145535522	3	3.624888659
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**0.962615193**	**1.7E-07**	**38**
P52873	ADEAYLIGR	0.996560253	1	2.10107708
P52873	DAHQSLLATR	0.718453996	1	3.271965027
P52873	FLYECPWR	0.998821172	1	2.140245676
P52873	ADFAQACQDAGVR	1.041542404	2	4.643203735
P52873	AEAEAQAEELSFPR	0.978367818	2	4.691789627
P52873	AGTHILCIK	1.451138655	2	2.84563899
P52873	ALAVSDLNR	1.091287569	2	2.754179001
P52873	AYSEALAAFGNGALFVEK	1.162150339	2	3.714300632
P52873	AYVEANQMLGDLIK	0.791154377	2	4.687201977
P52873	DFTATFGPLDSLNTR	0.606987103	2	3.752676964
P52873	DMAGLLKPAACTMLVSSLR	0.937470921	2	3.689877033
P52873	ENGVDAVHPGYGFLSER	0.870272405	2	3.155660152
P52873	FIGPSPEVVR	1.114632126	2	2.322738886
P52873	GANAVGYTNYPDNVVFK	1.531914446	2	4.463457108
P52873	GLAPVQAYLHIPDIIK	1.396515037	2	3.157716036
P52873	GQIGAPMPGK	0.888280434	2	2.433309078
P52873	GTPLDTEVPLER	1.044675622	2	3.714527607
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.372860235	2	5.680670261
P52873	HYFIEVNSR	1.286507455	2	2.488399744
P52873	IAEEFEVELER	0.890778674	2	3.192231178
P52873	IEGRPGASLPPLNLK	1.023867972	2	3.535955429
P52873	INGCAIQCR	1.500998629	2	2.957741499
P52873	IVGDLAQFMVQNGLSR	1.195555252	2	2.880027533
P52873	LDNASAFQGAVISPHYDSLLVK	1.030464643	2	5.776531219
P52873	NHQGLLLMDTTFR	0.926272659	2	2.906809568
P52873	QKADEAYLIGR	1.117796451	2	2.343159914
P52873	QVFFELNGQLR	0.956556255	2	3.047743082
P52873	QVGYENAGTVEFLVDK	0.991378909	2	3.914651394
P52873	SGEGMGIR	0.948498664	2	2.614797592
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.261482227	2	4.566065788

P52873	TVAVYSEQDTGQMHR	1.07238027	2	4.563057899
P52873	VFDYSEYWEGAR	1.081712436	2	4.310987949
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.106889327	2	4.313866138
P52873	VVEIAPATHLDPQLR	1.158402887	2	4.472713947
P52873	VVHSYEELEENYTR	1.136063207	2	5.249162197
P52873	HIEVQILGDQYGNILHLYER	1.277241778	3	6.67320776
P52873	YSLEYYMGLAEELVR	1.108223147	3	4.917481422
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	0.946418478	4	6.3476367
P52925	**HMGB2 High mobility group protein B2**	**1.203740545**	**0.42552**	**2**
P52925	KHPDSSVNFAEFSK	1.081242168	2	2.84177947
P52925	SEHPGLSIGDTAK	1.244882255	2	3.07004261
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.342787539**	**0.17034**	**4**
P53395	LSEVVGSGK	1.131453449	1	1.929826975
P53395	LREELKPVALAR	1.345852025	2	2.685581446
P53395	LSDIGEGIR	0.965169278	2	2.473059177
P53395	SYLENPAFMLLDLK	1.824407607	2	4.334559441
P53987	**MOT1 Monocarboxylate transporter 1**	**1.066429755**	**0.00261**	**4**
P53987	DGKEDETSTDVDEKPK	1.412284213	2	5.042818069
P53987	ETQSPAPLQNSSGDPAEEESPV	1.138871131	2	5.292596817
P53987	SDANTDLIGGSPK	1.02479536	2	3.90022707
P53987	DGKEDETSTDVDEKPKK	1.577706325	3	4.942588329
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**1.016841573**	**0.39066**	**2**
P54313	ACGDSTLTQITAGLDPVGR	1.077633265	2	4.456865311
P54313	TFVSGACDASIK	0.937812774	2	3.037605762
P54319	**PLAP Phospholipase A_2_activating protein**	**1.072867394**	**0.99302**	**3**
P54319	IGDVVGSSGANQQTSGK	1.036010574	2	4.497104645
P54319	TGDLGDINAEQLPGR	1.09013104	2	3.354496002
P54319	YVPGTSGPSNTVQTADPFTGAGR	1.048746566	2	3.92414403
P54822	**PUR8 Adenylosuccinate lyase**	**0.984078564**	**0.91199**	**2**
P54822	VLSQQAAAVVK	1.154644483	2	2.838360786
P54822	KVDIEVLSVLASLGASVHK	0.965560664	3	3.857550621
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.087740542**	**0.62723**	**5**
P54921	AIDIYEQVGTSAMDSPLLK	0.970320379	2	4.51538229
P54921	HDAATCFVDAGNAFK	1.412167442	2	2.994300127
P54921	IEEACEIYAR	0.743287341	2	2.463450193
P54921	NSQSFFSGLFGGSSK	1.024672864	2	3.1457901
P54921	TIQGDEEDLR	1.147258511	2	2.407578468
P55006	**RDH7 Retinol dehydrogenase 7**	**1.149043153**	**0.00226**	**11**
P55006	LETVILDVTK	0.919728693	2	3.662212133
P55006	TESIVAATQWVK	1.038812534	2	3.97608614
P55006	TNVTNMER	1.053980629	2	2.762046576

P55006	TNVTNMER+Oxidation(6)	1.455403284	2	2.503949642
P55006	VAIIEPGGFK	1.48522194	2	2.301734447
P55006	VLAACLTEK	1.217697915	2	3.140192509
P55006	VVNIASTMGR	1.188067348	2	3.489846945
P55006	VVNIASTMGR+Oxidation(8)	1.154406085	2	2.73594594
P55006	YGVEAFSDSLR	1.208711396	2	3.756338835
P55006	YVFITGCDSGFGNLLAR	1.094914105	2	4.420186043
P55006	TSDRLETVILDVTK	1.036295528	3	4.585410595
P55007	**BART1 Protein BART_1**	**1.362964165**	**0.44519**	**2**
P55007	MILMYEEKNKNTR+Oxidation(1)	1.078224827	2	2.363380432
P55007	YNSDEDLQSKLESSR	1.365215322	2	2.54420352
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.298630326**	**0.14241**	**3**
P55051	LTDSQNFDEYMK	1.309961182	2	3.92359519
P55051	QVGNVTKPTVIISQEGGK	1.400676721	2	3.4454844
P55051	WDGKETNCVR	1.580397902	2	2.560559988
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.239199318**	**0.17208**	**6**
P55053	FDETTADGR	1.166394148	2	2.589968204
P55053	LVESHGFEDYMK	1.455291473	2	3.358900309
P55053	MVVECVMNNAICTR	1.192822245	2	3.365865231
P55053	TETVCTFTDGALVQHQK	1.24852506	2	4.533274651
P55053	KTETVCTFTDGALVQHQK	1.380409253	3	5.675509453
P55053	MGAMAKPDCIITLDGNNLTVK	1.248448592	3	3.665053368
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**0.996896131**	**0.89869**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.0983617	2	3.72413826
P55159	IFFYDSENPPGSEVLR	1.1545398	2	5.995079517
P55159	IQSILSEDPK	1.161180597	2	3.134261608
P55159	VVADGFDFANGIGISLDGK	0.952162231	2	4.81074667
P55159	YVYIAELLAHK	1.268841858	2	2.966114759
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	0.716500061	3	4.455825329
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	1.063243044	3	6.174095154
P55260	**ANXA4 Annexin A4**	**0.979025109**	**1**	**3**
P55260	AEIDMLDIPANFK	1.031676851	1	2.318104267
P55260	GAGTDEGCLIEILASR	1.119214052	2	3.73858285
P55260	GLGTDEDAIIGVLACR	0.944647351	2	3.908058882
P55770	**NH2L1 NHP2_like protein 1**	**1.145588384**	**0.47124**	**2**
P55770	LLDLVQQSCNYK	1.186060493	2	3.802531242
P55770	QQIQSIQQSIER	1.091236893	2	2.895318508
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.126000509**	**0.00449**	**3**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.109721106	2	4.331850529
P56399	IFQNAPTDPTQDFSTQVAK	1.461893768	2	4.504079342
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	0.918985024	3	4.418961048
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.159912654**	**0.23724**	**4**

P56522	AVPTGDVEDLPCGLLLSSVGYK	3.295354022	2	2.934486389
P56522	NVINTFTQTAR	1.664402749	2	2.850655556
P56522	TATEKPGVEEAAR	0.981678932	2	3.077511311
P56522	TDITEVALGVLR	0.889744419	2	3.435468197
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.115626501**	**0.05154**	**13**
P56574	ATDFVVDR	1.130319508	2	2.391165257
P56574	DLAGCIHGLSNVK	1.042181572	2	3.736787796
P56574	DQTNDQVTIDSALATQK	0.65653866	2	3.919327259
P56574	FKDIFQEIFDK	1.072953387	2	3.514017582
P56574	GKLDGNQDLIR	1.253782362	2	3.351620436
P56574	LDGNQDLIR	1.144967972	2	2.449467182
P56574	LIDDMVAQVLK	1.183609006	2	4.125781059
P56574	LNEHFLNTTDFLDTIK	1.441944691	2	4.427992344
P56574	NILGGTVFR	1.087136841	2	2.705949306
P56574	SSGGFVWACK	1.264013927	2	2.857958555
P56574	TIEAEAAHGTVTR	1.032627193	2	3.87384963
P56574	VCVQTVESGAMTK	1.312723462	2	3.692461014
P56574	IKVEKPVVEMDGDEMTR	1.573767798	3	3.418231487
P56593	**CP2AC Cytochrome P450 2A12**	**0.928424883**	**0.99905**	**3**
P56593	MLQGTCGAPIDPTIYLSK	0.867515309	2	4.733406544
P56593	NRQPQYEDHMK	1.045312652	3	3.458683491
P56593	NRQPQYEDHMK+Oxidation(10)	1.141187833	3	3.418986559
P56656	**CP239 Cytochrome P450 2C39**	**1.085449961**	**0.99699**	**5**
P56656	NYLIPK	0.861634255	1	2.044853449
P56656	EHQESLDVTNPR	0.895796508	2	3.698302984
P56656	IKEHQESLDVTNPR	1.126208613	2	5.02221632
P56656	VCAGEGLAR	1.063993063	2	2.361390352
P56656	VQEEIDHVIGR	1.017749338	2	3.433795691
P56812	**PDCD5 Programmed cell death protein 5**	**1.137784527**	**0.05351**	**3**
P56812	HGDPGDAAQQEAK	1.18829724	2	4.202708244
P56812	NSILAQVLDQSAR	1.068429454	2	3.112371445
P56812	VSEQGLIEILEK	0.88943325	2	3.075420856
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.858019078**	**0.19268**	**7**
P57093	NLVSDDDIQR	0.818887579	1	2.529603958
P57093	YCALPQIVK	0.990046115	1	2.069173098
P57093	AISCHYGSSDCK	0.729747209	2	3.477989674
P57093	EVKPPGMTVMKDVAIAKQGYAPSER	1.034765539	2	2.377455711
P57093	IQDFQQNEELFR	1.292774269	2	3.234589338
P57093	KFYEENGFLVIK	0.980423426	2	3.151189089
P57093	NNGCLVVLPGTHK	0.852052659	2	2.417842865
P57113	**MAAI Maleylacetoacetate isomerase**	**1.225429535**	**9.9E-20**	**11**
P57113	AITSGFNALEK	1.18385461	2	2.859687567

P57113	ALLALEAFQVSHPCR	1.312026124	2	4.332039356
P57113	DGGQQFSEEFQTLNPMK	0.870847274	2	5.029709816
P57113	FKVDLSPYPTISHINK	1.203567135	2	4.823620319
P57113	GIDYEIVPINLIK	1.021440448	2	4.109237194
P57113	MISDLIASGIQPLQNLSVLK	1.411389738	2	5.598331451
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(1)	1.342756704	2	5.422665119
P57113	QVGQENQMPWAQK	1.023019521	2	3.942327976
P57113	VDLSPYPTISHINK	1.123701322	2	3.746309996
P57113	YCVGDEVSMADVCLAPQVANAER	0.98296277	3	5.941504955
P57113	IDGITIGQSLAILEYLEETRPIPR	1.071260063	4	4.879099846
P57722	**PCBP3 Poly(rC)_binding protein 3**	**0.949489204**	**0.99842**	**2**
P57722	ESTGAQVQVAGDMLPNSTER	0.931672244	2	5.430318832
P57722	INISEGNCPER	1.111127007	2	3.442995787
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**1.043688419**	**0.81652**	**2**
P58321	WLPLEANPEVTNQFLK	1.147307065	2	4.061931133
P58321	VTHETSAHEGQTEAPSIDEK	1.015981751	3	5.063393116
P58751	**RELN Reelin**	**1.143968341**	**0.96282**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**0.677555747**	**0.02727**	**11**
P58775	AISEELDNALNDITSL	0.588563232	2	3.54075098
P58775	ATDAEADVASLNR	0.424194848	2	3.656267643
P58775	DAQEKLEQAEK	0.696415805	2	2.849157095
P58775	KATDAEADVASLNR	0.566816493	2	3.375598192
P58775	LDKENAIDR	0.84612377	2	2.389130354
P58775	LKGTEDEVEK	0.64839868	2	2.75252533
P58775	MELQEMQLK	0.550212281	2	2.518589258
P58775	QLEEEQQALQK	0.539968629	2	3.31009078
P58775	SLEAQADKYSTK	1.229626345	2	2.872665882
P58775	TIDDLEDEVYAQK	0.454331111	2	3.957789898
P58775	YSESVKDAQEK	0.396611473	2	3.010276794
P59242	**CING Cingulin**	**1.020103057**	**0.88803**	**2**
P59242	LGQEQQALNR	1.177730088	2	2.516333818
P59242	LQGLEQEAENK	1.006968098	2	2.978303909
P59470	**RPC2 DNA_directed RNA polymerase III subunit RPC2**	**0.668839958**	**0.00539**	**2**
P59470	MPIMLRSSNCVLTGK+Oxidation(1)	0.678123288	2	2.537024736
P59470	NAKCTLKR	0.526861122	2	2.326963425
P59759	**MKL2 MKL/myocardin_like protein 2**	**1.057752739**	**0.83093**	**2**
P59759	LVEVLK	1.153617879	1	2.017632723
P59759	QIEELK	0.782262199	1	2.062122107
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.142467718**	**0.14479**	**3**
P59999	ELLLQPVTISR	0.786182772	2	2.45137763
P59999	HNKPEVEVR	0.946532092	2	2.524792194
P59999	VLIEGSINSVR	1.171931914	2	2.9430902

P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.193903431**	**0.51245**	**6**
P60335	AITIAGVPQSVTECVK	1.115490536	2	3.287467718
P60335	IITLTGPTNAIFK	1.653033446	2	2.960630894
P60335	LVVPATQCGSLIGK	1.474471067	2	3.035526514
P60335	QICLVMLETLSQSPQGR	1.281654791	2	2.430150032
P60335	VMTIPYQPMPASSPVICAGGQDR	1.252626806	2	4.05454731
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	1.278930269	4	5.644421101
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.235702843**	**5.2E-08**	**5**
P60843	ATQALVLAPTR	1.371894092	1	2.167750835
P60843	GFKDQIYDIFQK	1.055905471	2	3.442202091
P60843	KEELTLEGIR	1.405317855	2	2.367393732
P60843	LQMEAPHIIVGTPGR	1.413069117	2	3.495971441
P60843	KGVAINMVTEEDKR	1.077303387	3	3.942266226
P60868	**RS20 40S ribosomal protein S20**	**1.332087735**	**8.5E-15**	**2**
P60868	LIDLHSPSEIVK	1.451731446	2	2.907347918
P60868	DTGKTPVEPEVAIHR	1.066291549	3	3.936476469
P60892	**PRPS1 Ribose_phosphate pyrophosphokinase 1**	**0.999279546**	**0.59818**	**2**
P60892	FSNQETCVEIGESVR	0.98002976	2	2.774755955
P60892	NCTIVSPDAGGAK	1.773087882	2	2.313577175
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.551578244**	**4.7E-05**	**4**
P60901	AINQGGLTSVAVR	1.27529903	2	3.953048229
P60901	GKDCAVIVTQK	2.182034628	2	3.163130522
P60901	ITENIGCVMTGMTADSR	1.562028578	2	4.387292385
P60901	LLDSSTVTHLFK	1.604601599	2	2.923425674
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.342613457**	**0.00044**	**2**
P61087	GEIAGPPDTPYEGGR	1.34349543	2	2.988562822
P61087	VDLVDENFTELR	1.128704663	2	2.572960377
P61107	**RAB14 Ras_related protein Rab_14**	**1.695699614**	**0.20038**	**4**
P61107	NLTNPNTVIILIGNK	0.99549558	2	3.784221649
P61107	SCLLHQFTEK	1.131024585	2	3.061702728
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	1.066624752	3	3.804285288
P61107	TGENVEDAFLEAAKK	1.299144582	3	3.693715572
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.202907636**	**0.0402**	**2**
P61222	NTVANSPQTLLAGMNK	1.088057303	2	2.904885054
P61222	NVEDLSGGELQR	1.239223201	2	2.625719309
P61314	**RL15 60S ribosomal protein L15**	**1.170954533**	**0.22573**	**5**
P61314	GATYGKPVHHGVNQLK	1.152881322	2	4.465008736
P61314	SLQSVAEER	1.180831053	2	2.88703537
P61314	VLNSYWVGEDSTYK	1.188689167	2	4.038472652
P61314	YIQELWR	1.147488141	2	2.482518196
P61314	FFEVILIDPFHK	1.220365035	3	3.867430687
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.248034775**	**6.6E-07**	**4**
P61459	AVGWNELEGR	1.103971133	2	2.997452736

P61459	VHITLSTHECAGLSER	1.852434909	2	3.742439747
P61459	LDHHPEWFNVYNK	1.293182975	3	5.124075413
P61459	LSAEERDQLLPNLR	1.218732815	3	4.099134445
P61589	**RHOA Transforming protein RhoA**	**1.498886488**	**6E-15**	**6**
P61589	HFCPNVPIILVGNK	2.11377854	2	3.164068222
P61589	IGAFGYMECSAK	1.567368213	2	3.002639055
P61589	KKLVIVGDGACGK	1.105065212	2	2.428843498
P61589	MKQEPVKPEEGR+Oxidation(1)	1.611905989	2	3.501302481
P61589	HFCPNVPIILVGNKK	1.188254392	3	3.940511703
P61589	MKQEPVKPEEGR	1.007308989	3	3.501685619
P61751	**ARF4 ADP_ribosylation factor 4**	**1.049657438**	**0.3635**	**5**
P61751	ILMVGLDAAGK	1.924461437	2	2.459672451
P61751	IQEGAAVLQK	1.107558417	2	2.562535763
P61751	NICFTVWDVGGQDK	0.930460942	2	4.031912327
P61751	QDLPNAMAISEMTDK	1.187920834	2	3.462885141
P61751	LGEIVTTIPTIGFNVETVEYK	1.154160097	3	4.575340271
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.194375466**	**0.2548**	**2**
P61805	ADFQGISPER	1.248930087	1	1.953309774
P61805	FLEEYLSSTPQR	1.194200157	2	3.740853786
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.016920146**	**0.96967**	**3**
P61924	AILILDNDGDR	0.85574477	2	2.901428938
P61924	GEDVPLTEQTVSQVLQSAK	1.068089529	2	5.139336586
P61924	YYDDTYPSVK	1.070523091	2	2.47498107
P61972	**NTF2 Nuclear transport factor 2**	**1.071163465**	**0.95132**	**2**
P61972	NINDAWVCTNDMFR	0.874666276	2	3.042766571
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	1.072824897	3	5.419419289
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.190521404**	**0.86438**	**11**
P61980	GSDFDCELR	0.884756148	2	2.460565805
P61980	GSYGDLGGPIITTQVTIPK	0.99508419	2	4.680757046
P61980	IDEPLEGSEDR	0.97240887	2	3.372882366
P61980	IILDLISESPIK	1.146370775	2	3.927420616
P61980	LFQECCPHSTDR	1.232209722	2	3.559969664
P61980	LLIHQSLAGGIIGVK	2.182312836	2	2.587921858
P61980	NTDEMVELR	0.898821308	2	2.427403927
P61980	RSRNTDEMVELR	0.894277161	2	2.325223923
P61980	TDYNASVSVPDSSGPER	0.918540042	2	4.652390957
P61980	VVLIGGKPDR	1.222874957	2	2.535669804
P61980	IITITGTQDQIQNAQYLLQNSVK	1.05567024	3	6.684838772
P61983	**1433G 14_3_3 protein gamma**	**1.050923728**	**3.7E-05**	**4**
P61983	AYSEAHEISK	1.23532012	2	3.352713346
P61983	NVTELNEPLSNEER	1.03236056	2	4.760193348
P61983	TAFDDAIAELDTLNEDSYK	0.99667585	2	5.55698204

P61983	YLAEVATGEK	0.979861655	2	2.731076956
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**1.056311981**	**0.97876**	**4**
P62076	CIGKPGGSLDNSEQK	1.047162772	2	4.235889912
P62076	KCIGKPGGSLDNSEQK	1.132372786	2	4.305035591
P62076	VQIAVANAQELLQR	1.086813263	2	4.409189224
P62076	YMDAWNTVSR	1.022510348	2	3.098544359
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**1.034558347**	**0.98946**	**2**
P62078	FIDTTLAITGR	0.934397012	2	2.565805435
P62078	TENCLSSCVDR	1.034847499	2	2.323645115
P62083	**RS7 40S ribosomal protein S7**	**1.108471794**	**1.3E-08**	**5**
P62083	AIIIFVPVPQLK	1.172868668	2	3.749596357
P62083	KAIIIFVPVPQLK	1.262445453	2	3.626477003
P62083	LDGSRLIK	1.213427555	2	2.332994461
P62083	TLTAVHDAILEDLVFPSEIVGK	1.240943007	2	5.056869984
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.449063945	3	5.023117065
P62161	**CALM Calmodulin**	**1.129919433**	**0.00242**	**4**
P62161	DGNGYISAAELR	0.832967552	2	2.666472912
P62161	EADIDGDGQVNYEEFVQMMTAK	1.279707332	2	4.89699316
P62161	EAFSLFDKDGDGTITTK	0.878908742	2	4.333684444
P62161	VFDKDGNGYISAAELR	1.131876359	2	4.356308937
P62193	**PRS4 26S protease regulatory subunit 4**	**0.91750476**	**0.42768**	**4**
P62193	APQETYADIGGLDNQIQEIK	0.722173295	2	4.97511816
P62193	AVANQTSATFLR	1.100006884	2	2.602229357
P62193	NQEQMKPLEEK	1.306530171	2	2.913417101
P62193	TMLELLNQLDGFDSR	1.112839541	2	3.999098301
P62198	**PRS8 26S protease regulatory subunit 8**	**1.193058405**	**0.05507**	**4**
P62198	LEGGSGGDSEVQR	1.190831968	2	3.533853054
P62198	TMLELLNQLDGFEATK	1.374336429	2	3.368898153
P62198	VPDSTYEMIGGLDKQIK	1.188238015	2	2.336406946
P62198	EVIELPVKHPELFEALGIAQPK	1.183386583	3	3.903122902
P62243	**RS8 40S ribosomal protein S8**	**1.177252114**	**4.1E-11**	**8**
P62243	ADGYVLEGK	1.079563498	2	2.380846024
P62243	IIDVVYNASNNELVR	0.702066317	2	4.16358614
P62243	ISSLLEEQFQQGK	1.396111012	2	3.990936279
P62243	KYELGRPAANTK	1.240236016	2	3.752409458
P62243	LDVGNFSWGSECCTR	1.469686897	2	3.908139944
P62243	LTPEEEEILNK	1.068008479	2	3.248128891
P62243	NCIVLIDSTPYR	1.396343647	2	3.332680941
P62243	YELGRPAANTK	1.557845222	2	3.228212833
P62246	**RS15A 40S ribosomal protein S15a**	**1.214166405**	**7.3E-10**	**3**
P62246	HGYIGEFEIIDDHR	1.231750923	2	4.239281178
P62246	MNVLADALK	1.068778505	2	2.780020952

P62246	WQNNLLPSR	1.250768732	2	2.672238111
P62250	**RS16 40S ribosomal protein S16**	**1.012018259**	**0.70439**	**5**
P62250	ALVAYYQK	1.138260773	1	2.388912678
P62250	GGGHVAQIYAIR	0.846596624	2	2.643356562
P62250	LLEPVLLLGK	1.157762333	2	2.723938704
P62250	TLLVADPR	1.190793937	2	2.452762842
P62250	VNGRPLEMIEPR	1.087207371	2	2.609104156
P62260	**1433E 14_3_3 protein epsilon**	**1.281204867**	**1.4E-09**	**7**
P62260	AAFDDAIAELDTLSEESYK	1.270303015	2	6.160812855
P62260	HLIPAANTGESK	1.249260272	2	3.506571293
P62260	IISSIEQK	1.363573503	2	2.794229984
P62260	LICCDILDVLDK	1.761975586	2	4.062607765
P62260	YDEMVESMK	0.831765892	2	2.484943867
P62260	YLAEFATGNDR	0.840032977	2	2.796429157
P62260	YLAEFATGNDRK	1.329629265	2	2.720851183
P62271	**RS18 40S ribosomal protein S18**	**1.131195786**	**9.9E-20**	**4**
P62271	LREDLER	1.401804742	1	2.005393267
P62271	AGELTEDEVER	1.199570924	2	3.483625174
P62271	VLNTNIDGR	1.108228677	2	3.03602457
P62271	YSQVLANGLDNK	1.271283563	2	3.774343252
P62278	**RS13 40S ribosomal protein S13**	**1.432198716**	**2.6E-10**	**4**
P62278	LILIESR	1.294381715	1	1.935991764
P62278	GLAPDLPEDLYHLIK	1.417462927	2	2.97082305
P62278	GLTPSQIGVILR	1.032850041	2	2.760576487
P62278	KGLTPSQIGVILR	1.107035608	3	3.671672106
P62329	**TYB4 Thymosin beta_4**	**1.173558342**	**0.00024**	**4**
P62329	ETIEQEKQAGES	1.059930912	2	3.080891132
P62329	KTETQEKNPLPSK	1.257379998	2	3.459882259
P62329	NPLPSKETIEQEK	1.214218686	2	3.007745028
P62329	TETQEKNPLPSK	1.166021152	2	3.795808077
P62332	**ARF6 ADP_ribosylation factor 6**	**0.753435615**	**0.38742**	**2**
P62332	FNVWDVGGQDK	0.753473237	2	3.002868414
P62332	LGQSVTTIPTVGFNVETVTYK	0.69198963	2	2.409654379
P62334	**PRS10 26S protease regulatory subunit 10B**	**0.974188711**	**0.20194**	**6**
P62334	ALQSVGQIVGEVLK	1.064978997	2	2.41708827
P62334	AVASQLDCNFLK	0.907761404	2	2.440780401
P62334	EVIELPLTNPELFQR	0.815634174	2	3.207231522
P62334	GCLLYGPPGTGK	0.766780372	2	2.512974024
P62334	HGEIDYEAIVK	0.991103641	2	3.752446651
P62334	IHIDLPNEQAR	1.277750734	2	2.353969574
P62425	**RL7A 60S ribosomal protein L7a**	**1.189120495**	**9.9E-20**	**10**
P62425	HWGGNVLGPK	1.324217761	1	2.684365034
P62425	VAPAPAVVK	1.299622276	1	1.972314119

P62425	AGVNTVTTLVENK	1.202413451	2	3.858448982
P62425	AGVNTVTTLVENKK	1.262208231	2	2.843029737
P62425	KVVNPLFEK	1.496226435	2	2.342804193
P62425	NFGIGQDIQPK	1.031923991	2	3.164599657
P62425	TCTTVAFTQVNSEDK	1.006007293	2	3.736149311
P62425	TCTTVAFTQVNSEDKGALAK	1.265339758	2	4.067199707
P62425	VPPAINQFTQALDR	1.056318008	2	3.407683849
P62425	LKVPPAINQFTQALDR	1.461390939	3	4.654883862
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.096222346**	**9.9E-20**	**15**
P62630	YEEIVK	1.275582042	1	1.988847494
P62630	MDSTEPPYSQK	0.833974203	2	3.665522814
P62630	MDSTEPPYSQK+Oxidation(1)	0.902864519	2	3.271005869
P62630	RYEEIVK	0.934100594	2	2.66200304
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.152832302	2	5.60172224
P62630	YYVTIIDAPGHR	1.117773759	2	3.511394262
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.272212109	3	5.221583843
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.067601124	3	6.271458626
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.17106787	3	5.211957932
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(15)	1.135791065	3	3.791638136
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(9)	1.0540959	3	3.425503016
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(10)	1.076435692	3	4.639975071
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.395377905	4	5.938967228
P62630	RGNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	0.788203586	5	4.639298916
P62630	GNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.137179506	6	4.526237965
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.200764835**	**9.9E-20**	**6**
P62632	EHALLAYTLGVK	0.991932703	1	3.590357065
P62632	QLIVGVNK	1.245912586	1	2.520667553
P62632	IGGIGTVPVGR	1.442093193	2	3.635869265
P62632	STTTGHLIYK	1.234294035	2	3.145236254
P62632	THINIVVIGHVDSGK	1.193361326	2	5.64054203
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.10132991	3	5.858225822
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.115229893**	**0.89776**	**2**
P62634	CGETGHVAINCSK	1.183255829	2	4.475936413
P62634	CYSCGEFGHIQK	1.07368535	2	3.115870953
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.233134575**	**0.00158**	**5**
P62703	FDTGNLCMVTGGANLGR	1.191500332	2	5.072371483
P62703	GIPHLVTHDAR	1.416781271	2	2.359055281
P62703	LSNIFVIGK	1.86634029	2	3.209797382
P62703	TDITYPAGFMDVISIDK	1.143515899	2	5.146757126
P62703	VNDTIQIDLETGK	1.243148706	2	4.45044899
P62752	**RL23A 60S ribosomal protein L23a**	**1.136013645**	**7.1E-10**	**6**
P62752	LYDIDVAK	1.088069188	1	1.972061753

P62752	LAPDYDALDVANK	1.13200337	2	3.747881174
P62752	LDHYAIIK	1.123316289	2	2.644943953
P62752	NKLDHYAIIK	1.4848726	2	2.76412034
P62752	VNTLIRPDGEK	1.158450055	2	3.23205781
P62752	VNTLIRPDGEKK	1.380840032	2	2.912998676
P62755	**RS6 40S ribosomal protein S6**	**1.225042613**	**0.00388**	**4**
P62755	DIPGLTDTTVPR	0.774703425	2	2.660520792
P62755	LIEVDDER	1.137868424	2	2.764392138
P62755	LNISFPATGCQK	1.50453078	2	3.245526552
P62755	NKEEAAEYAK	1.292658821	2	2.511170149
P62775	**MTPN Myotrophin**	**1.099648455**	**0.04532**	**2**
P62775	NGDLDEVKDYVAK	1.110627131	2	3.240452766
P62775	GADINAPDKHHITPLLSAVYEGHVSCVK	1.026754827	4	5.225226879
P62804	**H4 Histone H4**	**0.802987183**	**9.9E-20**	**8**
P62804	DAVTYTEHAK	0.533439364	2	2.881001234
P62804	DNIQGITKPAIR	0.79387868	2	3.415593147
P62804	ISGLIYEETR	1.282626211	2	3.644930124
P62804	KTVTAMDVVYALK	0.335847047	2	2.499256611
P62804	RISGLIYEETR	1.181902275	2	2.306322336
P62804	TVTAMDVVYALK	0.735767035	2	4.044817448
P62804	TVTAMDVVYALK+Oxidation(5)	0.786421049	2	2.853513002
P62804	VFLENVIR	1.105606309	2	3.265380383
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**1.186373429**	**0.34819**	**2**
P62815	AVVQVFEGTSGIDAK	1.186403712	2	3.282146692
P62815	NFITQGPYENR	1.181050739	2	2.480132103
P62832	**RL23 60S ribosomal protein L23**	**1.276302124**	**0.02333**	**2**
P62832	GSAITGPVAK	1.016190239	2	2.788820982
P62832	ISLGLPVGAVINCADNTGAK	1.61587768	2	4.777138233
P62845	**RS15 40S ribosomal protein S15**	**0.822889196**	**0.54037**	**2**
P62845	DMIILPEMVGSMVGVYNGK	0.841817472	2	3.109612226
P62845	TFNQVEIKPEMIGHYLGEFSITYKPVK	0.821825944	4	5.100975513
P62853	**RS25 40S ribosomal protein S25**	**2.06058117**	**9.5E-12**	**2**
P62853	GGDAPAAGEDA	2.097707114	1	2.201814413
P62853	LNNLVLFDK	1.462000285	2	2.867256641
P62856	**RS26 40S ribosomal protein S26**	**1.21471945**	**0.19616**	**2**
P62856	DISEASVFDAYVLPK	0.943215492	2	3.033699989
P62856	NIVEAAAVR	1.147510037	2	3.048341036
P62859	**RS28 40S ribosomal protein S28**	**0.748712133**	**3.2E-09**	**2**
P62859	EGDVLTLLESER	0.749478045	2	3.79795146
P62859	VEFMDDTSR	1.013879202	2	2.328010321
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.141105012**	**0.70984**	**2**
P62870	ADDTFEALR	1.103798787	2	2.620431185

P62870	TLGECGFTSQTARPQAPATVGLAFR	1.085585417	3	4.408924103
P62890	**RL30 60S ribosomal protein L30**	**1.182381889**	**1E-08**	**3**
P62890	LVILANNCPALR	1.099546376	2	3.067088604
P62890	TGVHHYSGNNIELGTACGK	1.291376507	2	5.709477901
P62890	VCTLAIIDPGDSDIIR	1.891624638	2	4.131717205
P62898	**CYC Cytochrome c_ somatic**	**1.084773617**	**0.86267**	**6**
P62898	ADLIAYLK	0.991412812	2	2.889705658
P62898	GITWGEDTLMEYLENPK	1.11498437	2	5.227754116
P62898	GITWGEDTLMEYLENPKK	1.220137792	2	4.654350281
P62898	KTGQAAGFSYTDANK	1.175251247	2	3.947921753
P62898	TGPNLHGLFGR	1.087706495	2	3.380541801
P62898	TGQAAGFSYTDANK	1.041555286	2	4.323997498
P62902	**RL31 60S ribosomal protein L31**	**0.995073437**	**0.96617**	**3**
P62902	NLQTVNVDEN	0.821820981	1	2.421167374
P62902	LYTLVTYVPVTTFK	0.980852756	2	3.199885845
P62902	SAINEVVTR	1.150354905	2	2.562259197
P62907	**RL10A 60S ribosomal protein L10a**	**1.119797965**	**0.03111**	**6**
P62907	ILGPGLNK	1.945390751	1	1.932412982
P62907	AVDIPHMDIEALK	1.01413478	2	2.690131903
P62907	FSVCVLGDQQHCDEAK	1.164701116	2	4.402685642
P62907	KYDAFLASESLIK	1.102881716	2	3.316598892
P62907	VLCLAVAVGHVK	1.022285859	2	3.225061178
P62907	YDAFLASESLIK	0.832827493	2	3.114611387
P62909	**RS3 40S ribosomal protein S3**	**1.320981688**	**1.3E-06**	**10**
P62909	ELTAVVQK	1.062001219	1	2.098902941
P62909	AELNEFLTR	1.095284003	2	2.623243093
P62909	DEILPTTPISEQK	1.401201023	2	3.058280706
P62909	ELAEDGYSGVEVR	1.049148834	2	3.326314926
P62909	FGFPEGSVELYAEK	1.17194183	2	3.931038857
P62909	GCEVVVSGK	1.402551359	2	2.581297159
P62909	GGKPEPPAMPQPVPTA	1.247353147	2	4.047960281
P62909	GLCAIAQAESLR	1.364333737	2	3.247208595
P62909	TEIIILATR	1.334227175	2	3.153639555
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.037368278	3	5.17329073
P62912	**RL32 60S ribosomal protein L32**	**1.060247016**	**9.9E-20**	**2**
P62912	GQILMPNIGYGSNK	1.051608239	2	2.664583206
P62912	SYCAEIAHNVSSK	1.250222329	2	4.278460503
P62914	**RL11 60S ribosomal protein L11**	**1.144597191**	**0.99584**	**2**
P62914	VLEQLTGQTPVFSK	0.995207445	2	4.056946754
P62914	YDGIILPGK	1.081637923	2	3.270677567
P62919	**RL8 60S ribosomal protein L8**	**1.120308161**	**2.4E-07**	**3**
P62919	ASGNYATVISHNPETK	1.144650558	2	4.49216938
P62919	AVVGVVAGGGR	1.211436607	2	3.347933292

P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.042846804	3	5.439704418
P62944	**AP2B1 AP_2 complex subunit beta**	**1.152517223**	**0.32545**	**2**
P62944	LQNNNVYTIAK	1.027392256	2	3.000480652
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.366526199	3	3.64915657
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.969506155**	**0.99998**	**7**
P62959	AQVAQPGGDTIFGK	0.997908509	2	4.968637943
P62959	CAADLGLK	1.050753247	2	2.507773638
P62959	IIFEDDR	1.096842309	2	2.650553703
P62959	CLAFHDISPQAPTHFLVIPK	0.92758206	3	3.708772898
P62959	HISQISVADDDDESLLGHLMIVGK	0.89593975	3	7.645215034
P62959	KHISQISVADDDDESLLGHLMIVGK	1.053882893	3	5.090732574
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.946947499	3	4.085944176
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.196793458**	**0.3102**	**4**
P62961	GAEAANVTGPGGVPVQGSK	0.907829967	2	4.989742279
P62961	NEGSESAPEGQAQQR	0.649159222	2	5.129517078
P62961	EDGNEEDKENQGDETQGQQPPQR	1.080314666	3	5.004816055
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.007217669	4	5.46954155
P62963	**PROF1 Profilin_1**	**1.227171622**	**0.00036**	**5**
P62963	DSLLQDGEFTMDLR	0.717576047	2	3.887597084
P62963	DSPSVWAAVPGK	1.051930277	2	2.9324615
P62963	SSFFVNGLTLGGQK	1.268497064	2	3.927990675
P62963	STGGAPTFNVTVTMTAK	1.068217423	2	3.295814753
P62963	TFVSITPAEVGVLVGK	1.171037213	2	5.099938393
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.196791721**	**9.9E-20**	**22**
P63018	DAGTIAGLNVLR	0.650958239	2	3.425006628
P63018	FDDAVVQSDMK	0.989536832	2	3.268348694
P63018	FEELNADLFR	0.989197602	2	3.151538134
P63018	FELTGIPPAPR	0.968887708	2	2.716971159
P63018	IINEPTAAAIAYGLDK	1.202566533	2	5.532402039
P63018	IINEPTAAAIAYGLDKK	1.524789529	2	4.171666145
P63018	LLQDFFNGK	1.469310151	2	2.707604885
P63018	MKEIAEAYLGK	1.155800779	2	3.440849543
P63018	MVNHFIAEFK	1.119818108	2	3.179060936
P63018	NQTAEKEEFEHQQK	1.196821765	2	5.2484622
P63018	NQVAMNPTNTVFDAK	1.044941651	2	5.075264931
P63018	NQVAMNPTNTVFDAK+Oxidation(5)	1.135923519	2	4.231907845
P63018	NSLESYAFNMK	1.387758588	2	3.934849501
P63018	RFDDAVVQSDMK	1.068702805	2	3.436346531
P63018	SFYPEEVSSMVLTK	1.089867838	2	5.203951836
P63018	SINPDEAVAYGAAVQAAILSGDK	0.605524131	2	6.262359619
P63018	SQIHDIVLVGGSTR	1.039986959	2	4.868242264
P63018	STAGDTHLGGEDFDNR	1.02447531	2	4.310505867

P63018	VCNPIITK	1.187268558	2	2.434274912
P63018	VQVEYKGETK	1.238569496	2	2.474661589
P63018	ARFEELNADLFR	1.301915281	3	3.889532566
P63018	TVTNAVVTVPAYFNDSQR	1.157174392	3	4.394991398
P63025	**VAMP3 Vesicle_associated membrane protein 3**	**0.797899831**	**0.55198**	**2**
P63025	ADALQAGASQFETSAAK	0.788052881	2	4.679193497
P63025	LQQTQNQVDEVVDIMR	0.947486057	2	3.611054659
P63029	**TCTP Translationally_controlled tumor protein**	**0.768464185**	**1.5E-09**	**4**
P63029	DLISHDELFSDIYK	0.754815919	2	3.976761103
P63029	EIADGLCLEVEGK	1.023448783	2	2.829034805
P63029	GKLEEQKPER	1.642550464	2	3.412974358
P63029	VKPFMTGAAEQIK	1.20508384	2	2.513881922
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.199375863**	**0.54207**	**5**
P63036	QISQAYEVLADSK	1.086309293	2	2.579585791
P63036	TIVITSHPGQIVK	1.097567393	2	3.485225916
P63036	VNFPENGFLSPDK	1.094355998	2	3.141109705
P63036	HYNGEAYEDDEHHPR	1.216720311	3	4.967424393
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	0.959014194	3	4.167887211
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.034689891**	**2.8E-07**	**35**
P63039	DDAMLLKGK	0.456769473	1	1.921868324
P63039	DIGNIISDAMK	0.8803889	1	2.051076174
P63039	GIIDPTK	1.130818235	1	1.947704434
P63039	AAVEEGIVLGGGCALLR	1.045301493	2	5.708492279
P63039	CEFQDAYVLLSEK	1.407211897	2	4.536536694
P63039	CIPALDSLKPANEDQK	1.074907324	2	3.924773693
P63039	DDAMLLKGKGDK+Oxidation(4)	1.079773292	2	2.331838846
P63039	GVMLAVDAVIAELK	0.998613931	2	2.362944365
P63039	GVMLAVDAVIAELKK	1.280703734	2	4.570212364
P63039	GYISPYFINTSK	1.043151157	2	2.742613077
P63039	IGIEIIK	1.143030774	2	2.814539671
P63039	IQEITEQLDITTSEYEK	0.987357712	2	6.087544918
P63039	IQEITEQLDITTSEYEKEK	1.126902528	2	5.133924484
P63039	ISSVQSIVPALEIANAHR	1.458699144	2	4.472651482
P63039	KPLVIIAEDVDGEALSTLVLNR	1.226172958	2	6.099022388
P63039	LSDGVAVLK	1.16266278	2	2.994213343
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.227760607	2	6.496946335
P63039	NAGVEGSLIVEK	1.118773603	2	3.509324312
P63039	QSKPVTTPEEIAQVATISANGDK	1.037693531	2	3.550752401
P63039	TLNDELEIIEGMK	1.090558349	2	4.848937988
P63039	TLNDELEIIEGMK+Oxidation(12)	0.932632399	2	2.747194529
P63039	TVIIEQSWGSPK	1.01628098	2	4.281285763
P63039	VGEVIVTK	1.12613828	2	3.094950676
P63039	VGEVIVTKDDAMLLK	1.170807855	2	3.788001299

P63039	VGGTSDVEVNEK	1.213831274	2	3.918417454
P63039	VGGTSDVEVNEKK	1.235220206	2	3.734411716
P63039	VGLQVVAVK	1.20545601	2	3.261184216
P63039	VTDALNATR	1.087115891	2	3.522561073
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(18)	1.050552398	3	4.406934738
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(3)	1.089481884	3	3.754022121
P63039	DMAIATGGAVFGEEGLNLNLEDVQAHDLGK	0.92012012	3	4.107060909
P63039	ILQSSSEVGYDAMLGDFVNMVEK	2.333223613	3	6.146465302
P63039	KISSVQSIVPALEIANAHR	1.451240509	3	3.924005032
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.11684251	3	4.936254025
P63039	RGVMLAVDAVIAELKK	1.120851206	3	5.896333218
P63102	**1433Z 14_3_3 protein zeta/delta**	**1.103650311**	**1.4E-15**	**8**
P63102	DICNDVLSLLEK	1.244471382	2	3.92897439
P63102	FLIPNASQPESK	1.076143561	2	3.474337578
P63102	GIVDQSQQAYQEAFEISK	0.964429379	2	5.745241165
P63102	KGIVDQSQQAYQEAFEISK	1.695348047	2	5.040278435
P63102	SVTEQGAELSNEER	0.734585109	2	5.100693703
P63102	TAFDEAIAELDTLSEESYK	1.384816839	2	5.837608814
P63102	YDDMAACMK	0.833177642	2	2.596227646
P63102	YLAEVAAGDDKK	1.291955913	2	3.724322081
P63159	**HMGB1 High mobility group protein B1**	**1.041747593**	**0.17591**	**5**
P63159	GEHPGLSIGDVAK	1.039909116	2	3.15639925
P63159	IKGEHPGLSIGDVAK	1.398756061	2	3.871833086
P63159	KHPDASVNFSEFSK	1.096215605	3	4.10919714
P63159	KLGEMWNNTAADDKQPYEK	0.848695971	3	4.314481735
P63159	LGEMWNNTAADDKQPYEK	0.975551205	3	3.596772432
P63174	**RL38 60S ribosomal protein L38**	**1.041108351**	**5.9E-05**	**3**
P63174	IEEIKDFLLTAR	1.12890267	2	3.039553404
P63174	KIEEIKDFLLTAR	1.247436502	2	4.592374325
P63174	YLYTLVITDKEK	1.037237445	2	2.707944393
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.087882373**	**6.2E-14**	**13**
P63245	DETNYGIPQR	0.823794961	2	3.008755445
P63245	DGQAMLWDLNEGK	0.754954713	2	3.366820097
P63245	FSPNSSNPIIVSCGWDK	1.276418935	2	4.269349098
P63245	HLYTLDGGDIINALCFSPNR	1.606327052	2	5.606865406
P63245	IIVDELKQEVISTSSK	1.330241979	2	4.129142284
P63245	LWDLTTGTTTR	1.159936955	2	2.955522537
P63245	LWNTLGVCK	1.945923099	2	2.328050375
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.079607608	2	4.724562168
P63245	VWNLANCK	0.920238058	2	2.677676439
P63245	VWQVTIGTR	0.790943822	2	2.90550971
P63245	YTVQDESHSEWVSCVR	1.253143266	2	3.309490681

P63245	YWLCAATGPSIK	1.4108188	2	3.15877223
P63245	GHNGWVTQIATTPQFPDMILSASR	0.83524393	3	4.288396835
P63259	**ACTG Actin_ cytoplasmic 2**	**1.125695699**	**9.9E-20**	**8**
P63259	DLYANTVLSGGTTMYPGIADR	0.835098047	2	5.769021034
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.725873099	2	4.350805283
P63259	GYSFTTTAER	1.134644939	2	3.370332718
P63259	KDLYANTVLSGGTTMYPGIADR	1.070714213	2	6.162316322
P63259	LCYVALDFEQEMATAASSSSLEK	2.14813767	2	5.209465027
P63259	VAPEEHPVLLTEAPLNPK	1.272255473	2	4.642065048
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.102478604	3	5.741781712
P63259	QEYDESGPSIVHR	1.060637587	3	3.517314434
P63269	**ACTH Actin_ gamma_enteric smooth muscle**	**1.222123243**	**0.61125**	**2**
P63269	DLYANNVLSGGTTMYPGIADR	1.152578578	2	3.436091185
P63269	KDLYANNVLSGGTTMYPGIADR	1.326451031	2	5.080255032
P63324	**RS12 40S ribosomal protein S12**	**1.246662692**	**0.06754**	**3**
P63324	KVVGCSCVVVK	1.223093864	2	2.629013777
P63324	LGEWVGLCK	1.24935305	2	3.14660573
P63324	VVGCSCVVVK	1.145856148	2	3.031853914
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**1.009328627**	**0.99006**	**2**
P63331	YSFLQFDPAPR	1.004174531	2	3.261454821
P63331	GAGYTFGQDISETFNHANGLTLVSR	1.033358221	3	3.332388639
P67779	**PHB Prohibitin**	**0.892757892**	**0.98511**	**10**
P67779	NVPVITGSK	1.004240676	1	2.470448017
P67779	AAELIANSLATAGDGLIELR	0.999629297	2	5.350703239
P67779	AAIISAEGDSK	1.142356423	2	2.403121471
P67779	DLQNVNITLR	0.932202002	2	3.784236193
P67779	FDAGELITQR	1.071713223	2	3.746639967
P67779	IYTSIGEDYDER	1.559331971	2	3.40908742
P67779	KLEAAEDIAYQLSR	0.89151599	2	4.912333488
P67779	QVSDDLTER	0.938414273	2	2.6317451
P67779	VLPSITTEILK	1.004469537	2	2.519778013
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.02652339	3	5.326686382
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.231894069**	**5.5E-12**	**4**
P68037	ADLAEEYSK	0.860948144	2	2.58318162
P68037	GQVCLPVISAENWKPATK	1.018044764	2	3.266385078
P68037	IEINFPAEYPFKPPK	1.353673811	2	3.694463015
P68037	TDQVIQSLIALVNDPQPEHPLR	1.202428603	2	4.870034218
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.147851001**	**0.24322**	**5**
P68101	AGLNCSTETMPIK	1.108461936	2	2.860800982
P68101	TEGLSVLNQAMAVIK	1.173987462	2	3.80155921
P68101	VVTDTDETELAR	1.146900316	2	3.165407181
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.981867851	3	4.206168652

P68101	HVAEVLEYTKDEQLESLFQR	0.979770173	3	3.539818525
P68136	**ACTS Actin_ alpha skeletal muscle**	**0.714829699**	**9.9E-20**	**16**
P68136	EITALAPSTMK	0.759520193	1	2.949130297
P68136	AGFAGDDAPR	1.24535447	2	3.363376856
P68136	AVFPSIVGRPR	1.115660682	2	2.951979399
P68136	DLYANNVMSGGTTMYPGIADR	0.506586113	2	3.726366282
P68136	DSYVGDEAQSK	0.331020514	2	3.055640697
P68136	DSYVGDEAQSKR	1.729650898	2	2.466546297
P68136	EITALAPSTMK+Oxidation(10)	0.839038976	2	2.766232967
P68136	GYSFVTTAER	0.595120799	2	3.80149889
P68136	KDLYANNVMSGGTTMYPGIADR	0.568381325	2	5.20123291
P68136	QEYDEAGPSIVHR	0.418906743	2	3.148323774
P68136	VAPEEHPTLLTEAPLNPK	0.627394598	2	4.536060333
P68136	YPIEHGIITNWDDMEK	1.276756028	2	4.545828342
P68136	CPETLFQPSFIGMESAGIHETTYNSIMK	0.361069306	3	4.20481348
P68136	IWHHTFYNELR	1.174066788	3	3.712670803
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	0.482996535	3	6.719168663
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(29)	0.763819248	3	5.513119698
P68255	**1433T 14_3_3 protein theta**	**1.238502517**	**0.0007**	**5**
P68255	VISSIEQK	1.447367681	1	2.196409464
P68255	AVTEQGAELSNEER	0.684950012	2	4.628492355
P68255	SICTTVLELLDK	1.193929523	2	2.770486593
P68255	TAFDEAIAELDTLNEDSYK	1.19948733	2	4.521142006
P68255	YLIANATNPESK	1.141545575	2	3.574478388
P68511	**1433F 14_3_3 protein eta**	**1.024584884**	**1**	**2**
P68511	AVTELNEPLSNEDR	1.03462494	2	4.846217632
P68511	NSVVEASEAAYK	0.9987231	2	3.173925161
P69527	**AMPO Aminopeptidase O**	**1.020009714**	**0.0845**	**2**
P69527	LQQLAHRCFELVK	0.870488803	2	2.365371943
P69527	WHRLQDELQNSPEGMQVLRPNK	1.300660704	2	2.493444204
P69897	**TBB5 Tubulin beta_5 chain**	**0.770103942**	**0.14264**	**4**
P69897	ALTVPELTQQVFDAK	1.005250417	2	3.419495583
P69897	ISVYYNEATGGK	1.02769059	2	2.888415813
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.086017363	2	5.224981308
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	0.781508143	3	5.777481556
P70372	**ELAV1 ELAV_like protein 1**	**1.099279321**	**0.93626**	**3**
P70372	SLFSSIGEVESAK	1.101867848	2	3.415598154
P70372	TNLIVNYLPQNMTQEELR	1.095983513	2	4.159861088
P70372	VLVDQTTGLSR	1.095617223	2	2.562122583
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.165385647**	**0.8641**	**2**
P70470	ASFSQGPINSANR	1.35583939	2	2.895800829
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.108962711	3	3.973758936
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.953729357**	**0.00399**	**12**

P70473	ADVLLEPFR	0.999264737	2	3.54111743
P70473	DYGFSQEEIHQLHSDR	0.904705656	2	5.006958008
P70473	GQNLLDGGAPFYTTYK	0.751701286	2	5.220074654
P70473	LGSVNHPSHLAR	2.023007613	2	2.914581299
P70473	LQLGPETLR	1.040681538	2	2.41605401
P70473	LSGFGQSGIFSK	2.520062651	2	2.778597832
P70473	TQAMGLWAQPR	0.899447011	2	3.512560844
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	1.077473423	3	5.555346012
P70473	GLGLESEELPSQMSIEDWPEMK	1.055110249	3	4.662271976
P70473	GSFITDEEQHACPRPAPQLSR	1.024081336	3	3.624453545
P70473	RDPSVGEHTVEVLK	0.9645083	3	4.365359306
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	1.174377726	4	5.758040428
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**0.786353483**	**0.37822**	**2**
P70552	VLGNNFYEYYVNDPPR	1.222281235	2	3.969724655
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.710584965	3	4.796403408
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**1.217977049**	**0.74863**	**9**
P70580	RYDGVQDPR	1.188994591	1	2.181524277
P70580	EGEEPTVYSDDEEPKDEAAR	0.787242695	2	4.385364532
P70580	FYGPEGPYGVFAGR	0.975858247	2	4.09911871
P70580	GDQPGASGDNDDDEPPPLPR	1.068993282	2	5.144382954
P70580	KFYGPEGPYGVFAGR	1.030642781	2	3.817750216
P70580	YDGVQDPR	0.982521869	2	3.019557953
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	1.226894367	3	5.462334156
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.301243601	3	5.176754951
P70580	LLKEGEEPTVYSDDEEPKDEAAR	0.765626078	3	5.170353889
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.09251149**	**1**	**10**
P70584	ASSTCQLTFENVK	0.98307196	2	2.872116089
P70584	FAQEQIAPLVSTMDENSK	1.023950347	2	4.305191517
P70584	IGTIYEGTSNIQLNTIAK	0.927542768	2	4.55360508
P70584	KFAQEQIAPLVSTMDENSK	0.934090341	2	5.426749229
P70584	SGNYYVINGSK	1.073097748	2	2.618046999
P70584	SVIQGLFQQGMMGIEVEAK	0.976965813	2	4.48707819
P70584	VDASVALLCDIQNTVINK	0.898434418	2	4.913732529
P70584	YYASEVAGLTTSK	1.063280412	2	4.060379505
P70584	ASSTCQLTFENVKVPETSVLGK	1.10417342	3	3.612604856
P70584	IFDFQGLQHQVAHVATQLEAAR	1.183379693	3	6.069091797
P70615	**LMNB1 Lamin_B1**	**1.109646923**	**0.60064**	**3**
P70615	ALYETELADAR	1.058349068	2	3.241983414
P70615	LSSEMNTSTVNSAR	1.11439925	2	2.989428282
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.098320072	3	3.796171188
P70619	**GSHR Glutathione reductase (Fragment)**	**0.879408594**	**0.76678**	**2**

P70619	ALLTPVAIAAGR	0.879290225	2	2.726614952
P70619	LNNIYQNNLTK	1.10798663	2	3.053934813
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**0.828614534**	**0.00024**	**2**
P70694	REDIFYTSK	0.788817828	2	3.060360432
P70694	SIGVSNFNR	0.980649346	2	2.398679256
P70712	**KYNU Kynureninase**	**1.205589034**	**5.8E-05**	**8**
P70712	IATELNCDPTDER	1.587874049	2	3.631254435
P70712	IGAYGHEVGK	1.282642139	2	2.841657639
P70712	LLTAILDSTERN	1.601759976	2	3.540504217
P70712	MEDILEVIEK	1.048780646	2	2.618864775
P70712	SILLTGYLEYLLK	1.201782111	2	3.106482267
P70712	TYLEEELDKWAK	0.644375157	2	2.954217911
P70712	VAPVPLYNSFHDVYK	0.838749042	2	3.420878172
P70712	YLNSGAGGLAGAFIHEK	1.254924404	2	4.454124451
P80067	**CATC Dipeptidyl peptidase 1**	**1.181714744**	**0.00325**	**5**
P80067	NQESCGSCYSFASLGMLEAR	0.946205032	2	4.877143383
P80067	NSWGSQWGESGYFR	0.961018128	2	3.031618834
P80067	RGTDECAIESIAMAAIPIPK	1.1529645	2	4.460057735
P80067	GTDECAIESIAMAAIPIPK	1.176997382	3	4.697886944
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.36101079	3	5.56243515
P80254	**DOPD D_dopachrome decarboxylase**	**0.858760711**	**0.81654**	**4**
P80254	FFPLEPWQIGK	0.863041305	2	3.027359724
P80254	FLTEELSLDQDR	0.868408512	2	3.730730057
P80254	LCAATATILDKPEDR	1.864358448	2	4.233145714
P80254	STEPCAHLLISSIGVVGTAEQNR	0.806152627	2	5.400578499
P80299	**HYES Epoxide hydrolase 2**	**1.222450889**	**0.00025**	**2**
P80299	ATEMGGILVGTPEDPK	1.375634387	2	3.029355049
P80299	TEIQNPSVTSK	1.149956511	2	2.925995111
P80313	**TCPH T_complex protein 1 subunit eta**	**1.144507417**	**0.00268**	**4**
P80313	ATISNDGATILK	1.144156482	2	2.837523937
P80313	GGAEQFMEETER	1.209617389	2	2.504128218
P80313	QLCDNAGFDATNILNK	1.296746762	2	3.52347517
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.285096465	2	5.069993973
P80317	**TCPZ T_complex protein 1 subunit zeta**	**0.928318233**	**0.68032**	**9**
P80317	ALQFLEQVK	1.238220153	2	2.511016846
P80317	AQAALAVNISAAR	0.99445104	2	3.070793867
P80317	GIDPFSLDALAK	1.376846176	2	2.797105789
P80317	HKSETDTSLIR	1.10667278	2	2.676139116
P80317	TEVNSGFFYK	1.137481813	2	2.522156
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.000346537	2	4.962697506
P80317	VLAQNSGFDLQETLVK	0.920155023	2	3.464996815
P80317	DGNVLLHEMQIQHPTASLIAK	1.036665154	3	4.781133175
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.112920845	3	5.038513184

P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.854620904**	**0.40203**	**5**
P81155	LTFDTTFSPNTGK	0.890744482	2	2.610927582
P81155	LTFDTTFSPNTGKK	1.075386217	2	2.868081331
P81155	SCSGVEFSTSGSSNTDTGK	0.548938927	2	2.416996717
P81155	VNNSSLIGVGYTQTLRPGVK	0.656266106	2	3.61387682
P81155	YQLDPTASISAK	1.008878237	2	2.948932409
P82995	**HS90A Heat shock protein HSP 90_alpha**	**0.98591535**	**1.7E-07**	**14**
P82995	FYEQFSK	1.109102803	1	2.046714306
P82995	ELHINLIPNKQDR	0.935695904	2	2.977379322
P82995	ELISNSSDALDK	0.897011924	2	2.705179214
P82995	HIYFITGETK	1.038969685	2	2.96289587
P82995	HSQFIGYPITLFVEK	2.14855625	2	3.710536242
P82995	NPDDITNEEYGEFYK	0.957242553	2	5.073233128
P82995	RAPFDLFENR	1.350299242	2	2.364841461
P82995	SLTNDWEEHLAVK	1.045663953	2	4.164336681
P82995	TLTIVDTGIGMTK	1.031348469	2	4.342950344
P82995	TLTIVDTGIGMTK+Oxidation(11)	1.068426249	2	3.389466763
P82995	YYTSASGDEMVSLK	1.02511405	2	3.424346685
P82995	HGLEVIYMIEPIDEYCVQQLK	1.041836676	3	5.55117178
P82995	HLEINPDHSIIETLR	1.083800449	3	4.288922787
P82995	LGIHEDSQNR	1.328859369	3	3.471329689
P83732	**RL24 60S ribosomal protein L24**	**1.119382862**	**0.99972**	**2**
P83732	AITGASLADIMAK	1.120735408	2	4.67363739
P83732	VELCSFSGYK	1.030717195	2	2.370834827
P83868	**TEBP Prostaglandin E synthase 3**	**1.45413899**	**0.12916**	**2**
P83868	LTFSCLGGSDNFK	1.444450199	2	2.768555164
P83868	HLNEIDLFHCIDPNDSK	1.533332692	3	3.304775476
P83883	**RL36A 60S ribosomal protein L36a**	**1.372084883**	**0.00095**	**2**
P83883	HFELGGDK	1.385620697	1	2.383584261
P83883	LECVEPNCR	1.300516591	2	2.340214729
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.136135171**	**0.03466**	**2**
P83941	AMLSGPGQFAENETNEVNFR	1.32006104	2	5.018530369
P83941	TYGGCEGPDAMYVK	1.175436488	2	3.788761139
P84082	**ARF2 ADP_ribosylation factor 2**	**0.953020222**	**0.99999**	**2**
P84082	NISFTVWDVGGQDK	0.834382858	2	4.525797367
P84082	QDLPNAMNAAEITDK	1.06922074	2	3.861403942
P84083	**ARF5 ADP_ribosylation factor 5**	**1.095456936**	**0.30916**	**2**
P84083	DAVLLVFANK	1.057738442	2	2.487585545
P84083	VQESADELQK	1.199080807	2	2.937437057
P84100	**RL19 60S ribosomal protein L19**	**1.241540623**	**0.00031**	**2**
P84100	LLADQAEAR	1.296770165	2	3.441292763
P84100	VWLDPNETNEIANANSR	1.091923582	2	5.813951492

P84245	**H33 Histone H3.3**	**1.116327211**	**0.1765**	**4**
P84245	RVTIMPKDIQLAR+Oxidation(5)	1.261550549	2	2.921031713
P84245	STELLIR	1.112410016	2	2.513198376
P84245	YRPGTVALR	1.09594384	2	2.360016346
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.104571871	3	5.967076778
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.028014487**	**0.62651**	**4**
P84817	FQSEQAAGSVSK	0.98084659	2	2.976790905
P84817	GIVLLEELLPK	1.233674193	2	2.317269802
P84817	GLLQTEPQNNQAK	1.027986198	2	3.585855722
P84817	KFQSEQAAGSVSK	1.067697511	2	4.055670738
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.881714839**	**0.99548**	**16**
P85834	AEAGDNLGALVR	1.012259709	2	3.74795413
P85834	DLEKPFLLPVESVYSIPGR	1.226713913	2	3.918323278
P85834	GDECELLGHNK	1.04599607	2	2.590711355
P85834	GEETPVIVGSALCALEQR	0.917852316	2	4.593341351
P85834	GITINAAHVEYSTAAR	0.971758441	2	3.013216019
P85834	GTVVTGTLER	1.01663913	2	2.874448776
P85834	HYAHTDCPGHADYVK	0.824452692	2	4.196345329
P85834	KYEEIDNAPEER	1.094061426	2	3.57918644
P85834	LLDAVDTYIPVPTR	1.006040329	2	3.923561811
P85834	QIGVEHVVVYVNK	0.887141492	2	2.858068705
P85834	TIGTGLVTDVPAMTEEDK	0.859948899	2	4.126779079
P85834	TIGTGLVTDVPAMTEEDKNIK	1.141481631	2	4.706573009
P85834	TVVTGIEMFHK	0.896989947	2	2.451441526
P85834	YEEIDNAPEER	1.094196558	2	3.185129404
P85834	DKPHVNVGTIGHVDHGK	0.945992889	3	3.480632067
P85834	KGDECELLGHNK	1.099125213	3	3.93868351
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.003027742**	**3.2E-15**	**10**
P85968	YGPSLMPGGNK	1.163999393	1	2.200737238
P85968	AGQAVDDFIEK	1.22308592	2	2.926632643
P85968	CLSSLKEER	1.313856531	2	2.403604507
P85968	FQDTDGKELLPK	1.263895333	2	3.130638361
P85968	GILFVGSGVSGGEEGAR	1.011887786	2	5.049153805
P85968	HEMLPANLIQAQR	0.992131682	2	3.254577875
P85968	LVPLLDTGDIIIDGGNSEYR	1.960957464	2	5.557896137
P85968	NPELQNLLLDDFFK	1.591864153	2	4.765734196
P85968	SAVDDCQDSWR	0.708275638	2	2.947916508
P85968	VGTGEPCCDWVGDEGAGHFVK	1.118608056	3	4.549165249
P85971	**6PGL 6_phosphogluconolactonase**	**1.104715927**	**0.96171**	**5**
P85971	DLPAATAPAGPASFAR	0.912964903	2	2.414294958
P85971	ILEDQESALPAAMVQPR	1.144735486	2	4.168530941
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.074298527	2	4.99045372

P85971	TGALCWFLDEAAAR	1.109365528	2	3.796179295
P85971	WTLGFCDER	1.120856212	2	2.307162285
P85972	**VINC Vinculin**	**1.073260571**	**0.71275**	**12**
P85972	AIPDLTAPVAAVQAAVSNLVR	1.055505021	2	3.352092505
P85972	AQQVSQGLDVLTAK	0.990091409	2	4.467333794
P85972	AVAGNISDPGLQK	1.012331936	2	3.382884026
P85972	GQGASPVAMQK	1.325373393	2	3.000859499
P85972	MLGQMTDQVADLR	1.189598566	2	2.513656616
P85972	NRNFTVGKMSAEINEIIR+Oxidation(9)	1.08949061	2	2.730239868
P85972	QVATALQNLQTK	1.084805737	2	3.721686602
P85972	SLLDASEEAIKK	1.165513395	2	2.633711815
P85972	STVEGIQASVK	1.059503295	2	2.303559303
P85972	VLQLTSWDEDAWASK	1.3198038	2	3.668216705
P85972	WIDNPTVDDR	0.993207502	2	3.180115223
P85972	TNISDEESEQATEMLVHNAQNLMQSVK	0.887311524	3	4.044253826
P85973	**PNPH Purine nucleoside phosphorylase**	**0.987171235**	**0.04788**	**12**
P85973	ASHQEVLEAGK	1.117242078	2	3.421037912
P85973	DHINLPGFCGQNPLR	0.8816483	2	4.103766441
P85973	ELQEGTYIMSAGPTFETVAESCLLR	0.783833104	2	5.054265976
P85973	FEVGDIMLIR	0.869178667	2	3.609839916
P85973	MLGADAVGMSTVPEVIVAR	1.124358515	2	6.070861816
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(1)	1.220630284	2	5.118424416
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(9)	1.210369613	2	3.744544983
P85973	VFGFSLITNK	1.141888276	2	2.816716671
P85973	VFHLLGVDTLVVTNAAGGLNPK	1.250720251	2	5.835546017
P85973	VVMDYNNLEK	1.101766125	2	2.606795549
P85973	HRPQVAVICGSGLGGLTAK	1.015423725	3	6.297535419
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.75919929	3	4.737533092
P86048	**RL10L 60S ribosomal protein L10_like**	**1.266925052**	**2.8E-07**	**4**
P86048	GAFGKPQGTVAR	1.27987658	2	3.043518543
P86048	VHIGQVIMSIR	1.318356567	2	2.824522495
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.215648953	3	5.037976742
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	0.966128775	3	5.803258896
P86252	**PURA Transcriptional activator protein Pur_alpha (Fragments)**	**1.115824359**	**0.5756**	**2**
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	1.190142116	2	4.17131567
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	1.127815255	3	5.066577435
P97310	**MCM2 DNA replication licensing factor MCM2**	**0.82760674**	**0.38363**	**4**
P97310	EAGRGLGRMR	1.176746401	2	2.547754049
P97310	HIESMIRMAEAHARMHLR	0.799657917	2	2.667583704
P97310	LNQMDQDKVAR+Oxidation(4)	0.692861589	2	2.57703948
P97310	MITGLSKDQQIGEK+Oxidation(1)	0.749740275	2	2.460684776
P97323	**F16P3 Fructose_1_6_bisphosphatase isozyme 3 (Fragment)**	**1.053538361**	**0.83208**	**2**

P97323	GNIYSLNEGYAK	1.041492124	2	3.942631483
P97323	KGNIYSLNEGYAK	1.130271993	2	4.215837479
P97384	**ANX11 Annexin A11**	**1.021022247**	**0.27788**	**2**
P97384	GFGTDEQAIIDCLGSR	0.937677805	2	4.242279053
P97384	SELDLLDIR	1.235496443	2	2.684845448
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.039137504**	**0.36052**	**8**
P97519	GFEEAVAAGAK	1.054885734	2	3.20173192
P97519	GYVSCALGCPYEGK	1.187344437	2	3.726517677
P97519	KNVNCSIEESFQR	1.092406496	2	3.561650276
P97519	LIDMLSEAGLPVIEATSFVSPK	1.303613547	2	4.858964443
P97519	LLEAGDFICQALNR	1.165612225	2	4.500074863
P97519	NVNCSIEESFQR	1.033813399	2	3.446860552
P97519	WVPQMADHSDVLK	0.441897966	2	3.013937473
P97519	GASGNLATEDLVYMLTGLGIHTGVNLQK	0.903637148	3	3.892085791
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**1.259342975**	**0.70967**	**5**
P97521	CLLQIQASSGK	1.112160891	2	3.105041981
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.452621736	2	3.791845322
P97521	LYQEFGIR	1.216678819	2	2.355670452
P97521	SVHDLSVPR	1.14674298	2	2.542304516
P97521	YSGTLDCAK	1.209854213	2	2.517919064
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.237585836**	**9.4E-08**	**15**
P97524	ALHDHLGLR	1.678953407	2	2.416388988
P97524	GEVGLLICK	1.163945437	2	2.617999077
P97524	IQDTIEITGTFK	1.021242547	2	2.50409317
P97524	ITELTPFFGYAGGK	0.613113321	2	2.308541298
P97524	MKENYEFNGK	0.909032087	2	3.256679296
P97524	SEVTFTTPAVYIYTSGTTGLPK	0.360175189	2	2.650690317
P97524	SLLHCFQCCGAK	1.237801578	2	3.29537487
P97524	TILHVFLEQAR	1.176190413	2	2.96387434
P97524	TYVPMTEDIYNAIIDK	1.006228815	2	4.046018124
P97524	VLLASPELHEAVEEVLPTLK	1.318171046	2	3.867323875
P97524	VTLMEEGFNPSVIK	0.744004716	2	3.676892519
P97524	YDVEKDEPVR	1.3019188	2	2.835950851
P97524	YLCNTPQKPNDR	1.255339705	2	3.040333509
P97524	YNATVIQYIGELLR	1.407813763	2	2.753760099
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	0.815033492	3	5.789157867
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.15174893**	**0.43862**	**8**
P97532	AFGHHSVSLLDGGFR	1.303157359	2	3.449926853
P97532	ALVSAQWVAEALK	0.936052322	2	3.786030769
P97532	AQPEHVISQGR	1.121898425	2	2.79148984
P97532	FQGTQPEPR	1.045768519	2	2.943843842
P97532	LLDASWYLPK	1.483400653	2	3.912312508

P97532	THEDILENLDAR	1.078966524	2	3.375565767
P97532	YWLSQNLPISSGK	0.993070158	2	3.603411674
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.16309959	3	6.766563416
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.122929157**	**0.49132**	**5**
P97536	EGPAVVGQFIQDVK	1.051190716	2	2.758027554
P97536	ITSEALLVTQQLVK	1.266980584	2	2.347746134
P97536	LGTLSALDILIK	1.850380755	2	2.534323215
P97536	LTLIDPETLLPR	1.429957695	2	2.680687428
P97536	TYIQCIAAISR	1.119284285	2	2.985819817
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.082014686**	**0.65253**	**18**
P97562	ATASCTYEGENTVLYLQVAR	0.855084249	2	4.605514526
P97562	ATFADFCAQGAEICR	0.940994345	2	5.037241936
P97562	CSAQTAADFR	1.05003967	2	2.437994242
P97562	DFSLLPELHALSTGMK	0.930293017	2	2.608090878
P97562	EAFLDLLPLIR	0.795717864	2	2.711181879
P97562	ILEYQTQQQK	1.148526252	2	3.91689992
P97562	KVESIIQSDPVFNLK	1.046969328	2	4.949226379
P97562	LGTPQSNYLGMLVTR	1.760917167	2	3.515344143
P97562	LTNILDGGLPNTVLR	1.2381837	2	4.250740528
P97562	MGLEHIDNGFLQLNHVR	1.191565918	2	4.42318821
P97562	SLEDHTPLPGITVGDIGPK	0.96479171	2	4.551180363
P97562	SLGSDEQIAK	1.085064288	2	2.849404812
P97562	VESIIQSDPVFNLK	0.830889255	2	4.571508884
P97562	VLDGNVNLSLHGVAMNAIR	1.08650571	2	5.008135796
P97562	DAILLTDAFDFSDHCLNSALGCYDGHVYER	1.033767284	3	4.045087814
P97562	LCDLYALHGVLTNSGDFLHDGFLSGAQVDMAR	1.801156567	3	5.698264122
P97562	LDKEPEIQR	1.125015539	3	3.549217463
P97562	SGVDQHDAWNQTTVIHLQAAK	1.025816757	3	6.266915321
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**0.933666411**	**0.02232**	**3**
P97576	ALADTENLR	1.079435717	2	2.306185007
P97576	DLLEVADILEK	0.858938319	2	2.432030201
P97576	EEVSNNNPHLK	0.933924554	2	3.284099102
P97584	**PTGR1 Prostaglandin reductase 1**	**1.103649423**	**0.98332**	**5**
P97584	ALTDLMNWVSEGK	1.214568223	2	3.672785521
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.203479591	2	4.741648674
P97584	HFEGFPTDSNFELR	1.023285385	2	3.899152994
P97584	TGPCPPGPSPEVIIYQQLR	0.748352602	2	4.044153214
P97584	YHEYITEGFEK	1.077623364	2	2.927996874
P97608	**OPLA 5_oxoprolinase**	**1.173895427**	**0.84959**	**4**
P97608	AGDFGAAFVER	1.139745443	2	2.43717885
P97608	GSILDPSPEAAVVGGNVLTSQR	1.232871616	2	5.046818256
P97608	LLSEDPANYADAPTEGIR	0.941932391	2	3.844626904

P97608	TGDLLEIQQPVDLEALR	1.063879976	2	4.889736176
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.515918347**	**0.01622**	**8**
P97612	EVEQLMTPQK	0.623702782	2	2.323554277
P97612	GTNCVTSYLTDCETQLSQAPR	0.927109596	2	4.567977905
P97612	GYFGDIWDIILK	1.53425406	2	3.401735067
P97612	LQHEIEMYR	1.110341752	2	2.376777172
P97612	LQSGELSPEAVFFTYLGK	1.665936998	2	4.523787498
P97612	NSVGLPVAVQCVALPWQEELCLR	1.297379905	2	4.155115128
P97612	QGLLYGVPVSLK	0.810406866	2	2.74480772
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.147655487	3	4.691340923
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.206198197**	**0.1881**	**3**
P97700	AVVVNAAQLASYSQSK	1.108165617	2	4.738537312
P97700	LGIYTVLFER	2.635926219	2	3.058425426
P97700	LTGADGTPPGFLLK	1.2845451	2	2.820734024
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**1.112169274**	**7.3E-05**	**24**
P97852	AAVAVPSRPPDAVLR	1.277808995	2	2.327848434
P97852	AVANYDSVEAGEK	1.152044931	2	3.856596708
P97852	AYALAFAER	1.250245149	2	3.063968658
P97852	DTTSLNQAALYR	0.703817677	2	2.658269644
P97852	FVYEGSADFSCLPTFGVIVAQK	0.998042412	2	4.825916767
P97852	GALVVVNDLGGDFK	0.988737171	2	3.658643007
P97852	GNIMLSQKLQMILK+Oxidation(4)Oxidation(11)	1.009068797	2	2.33970809
P97852	GSSAADKVVEEIR	1.130929692	2	3.151083469
P97852	HVLQQFADNDVSR	1.050209187	2	4.615936756
P97852	IDVVVNNAGILR	1.023297355	2	3.654800415
P97852	ISDEDWDIIQR	0.85830352	2	3.376808643
P97852	KNNIHCNTIAPNAGSR	1.196097004	2	4.782763004
P97852	LGLLGLANTLVIEGR	1.971161288	2	3.407360315
P97852	LNPQNAFFSGR	1.291456109	2	2.830401421
P97852	NGSGEVYQGPAK	1.012207589	2	3.515029669
P97852	NNIHCNTIAPNAGSR	1.026731226	2	4.626990318
P97852	SIQESTGGIIEVLHK	1.201604637	2	4.167755604
P97852	SLMSGGLAEVPGLSINFAK	1.073640216	2	4.597380161
P97852	SLMSGGLAEVPGLSINFAK+Oxidation(3)	0.852132201	2	3.525694847
P97852	VLHGEQYLELYKPLPR	1.110254558	2	4.917131424
P97852	VNAVFEWHITK	1.355234954	2	3.193546295
P97852	VVLVTGAGGGLGR	1.089324376	2	4.554958344
P97852	ICDFSNASKPK	1.313974489	3	3.791045904
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	1.180552674	3	6.135745525
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.091318161**	**0.56784**	**3**
Q00438	KLPSDVTEGEVISLGLPFGK	1.066254284	2	2.657301903
Q00438	NNQFQALLQYADPVSAQHAK	1.097108811	2	5.142713547

Q00438	NFQNIFPPSATLHLSNIPPSVSEDDLK	1.607097488	3	3.816119432
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.45030438**	**0.16492**	**4**
Q00PI9	EEAQPIVTKYK	1.169358685	1	1.949212432
Q00PI9	AVEEQGDDQDSEK	1.452763566	2	3.800951004
Q00PI9	DLLVQQASQCLSK	1.079034493	2	2.37082696
Q00PI9	SGDETPGSEAPGDK	1.037540366	2	2.68726778
Q01177	**PLMN Plasminogen**	**1.173592967**	**0.39863**	**3**
Q01177	ILGSDVQQIAVTK	1.152886499	2	3.400075197
Q01177	LVLEPNDADIALLK	1.268503428	2	2.649971962
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	1.092053554	3	4.977295876
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.024371046**	**0.94631**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.166860096	2	6.39428997
Q01205	NDVITVQTPAFAESVTEGDVR	0.904961437	2	5.497101307
Q01205	NVETMNYADIER	0.977551838	2	3.519267559
Q01205	VEGGTPLFTLR	1.020167796	2	3.307943106
Q01405	**SC23A Protein transport protein Sec23A**	**1.013702965**	**6E-08**	**4**
Q01405	AETEEGPDVLR	0.989249909	2	3.17017293
Q01405	AVLNPLCQVDYR	1.21896638	2	2.801267862
Q01405	YIDTEHGGSQAR	1.329166186	2	3.424380302
Q01405	HLLQAPVDDAQEILHSR	1.067060015	3	4.534856796
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**1.015840381**	**0.21358**	**29**
Q02253	NHGVVMPDANK	0.975552574	1	3.280660152
Q02253	AEMEAAVAACK	1.072865662	2	3.905119896
Q02253	AEMEAAVAACK+Oxidation(3)	1.092013073	2	2.863432169
Q02253	AEMEAAVAACKR	1.246911497	2	3.216963768
Q02253	AFPAWADTSILSR	1.110873966	2	4.202379704
Q02253	AISFVGSNQAGEYIFER	0.908487439	2	5.484769344
Q02253	CMALSTAVLVGEAK	1.120049079	2	4.563595772
Q02253	CMALSTAVLVGEAK+Oxidation(2)	1.147225244	2	2.773892879
Q02253	EEDATLSSPAVVMPTMGR	0.8404729	2	4.908480167
Q02253	ENTLNQLVGAAFGAAGQR	0.831302632	2	5.017956257
Q02253	GDTNFYGK	0.900152947	2	2.395291328
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.115941731	2	5.907081604
Q02253	GYENGNFVGPTIISNVKPSMTCYK	0.740766194	2	3.429329872
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.141038925	2	5.57311058
Q02253	KWLPELVER	0.925467747	2	2.324751854
Q02253	LITLEQGK	1.175848603	2	2.898320913
Q02253	NHGVVMPDANK+Oxidation(6)	1.222284204	2	3.113446474
Q02253	QGIQFYTQLK	0.897548667	2	2.854214668
Q02253	SDKWIDIHNPATNEVVGR	1.167814241	2	5.592189789

Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.880910358	2	5.416849613
Q02253	TLADAEGDVFR	1.056755947	2	3.570842266
Q02253	VCNLIDSGAK	1.053624723	2	3.471072435
Q02253	VNAGDQPGADLGPLITPQAK	1.033259794	2	5.999648094
Q02253	WIDIHNPATNEVVGR	1.043717546	2	5.108803272
Q02253	WLPELVER	0.959210544	2	2.314651251
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.413518636	3	4.821789265
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	1.053710533	3	6.381165981
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(6)	1.025411445	3	4.817329407
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.01672512	3	4.637993336
Q02769	**FDFT Squalene synthase**	**0.769271477**	**0.88136**	**3**
Q02769	TQSLPNCQLISR	0.58281497	2	2.597066164
Q02769	VVLEDFPTISLEFR	0.895611999	2	3.91082406
Q02769	KLEDFVKPENVDVAVK	0.7690246	3	4.24852562
Q02974	**KHK Ketohexokinase**	**1.153443262**	**0.74331**	**9**
Q02974	FGCQVAGK	1.037665524	2	2.878886223
Q02974	GGNASNSCTVLSLLGAR	1.109085312	2	4.660804272
Q02974	GNSMQEALR	1.063663524	2	3.18398118
Q02974	IEQYNATQPLQQK	1.07996088	2	4.771267891
Q02974	TIILYDTNLPDVSAK	1.138093147	2	4.822946072
Q02974	VSVEIEKPR	1.226519469	2	2.41057539
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.171734435	3	5.863091469
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.10237602	3	5.307177544
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.272842648	3	6.365031242
Q03248	**BUP1 Beta_ureidopropionase**	**1.08033804**	**9.9E-20**	**13**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.061128558	2	6.299263477
Q03248	ELAEAVKPNYSPNIVK	1.003731124	2	4.328555107
Q03248	HLPPDDLSQVK	1.219144517	2	2.306904316
Q03248	KHNMVVISPILER+Oxidation(4)	1.068681723	2	2.782516956
Q03248	NAAIANHCFTCALNR	1.492810472	2	4.71797657
Q03248	VGQEHYPNEFTSGDGK	1.208078499	2	4.405058384
Q03248	EKLPWTEFAESAEDGLTTR	0.92139841	3	5.011903763
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	1.084921189	3	3.435462236
Q03248	HNMVVISPILER	1.247465183	3	3.437039375
Q03248	IPLPTSAPVAEQVSALHK	1.757509293	3	5.066462517
Q03248	KHNMVVISPILER	1.13533867	3	3.525016546
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.284618917	3	4.806408405
Q03248	VGQEHYPNEFTSGDGKK	1.370184227	3	5.190376759
Q03336	**RGN Regucalcin**	**1.392058655**	**9.9E-20**	**19**
Q03336	CGESPVWEEASK	1.188582914	2	4.566966057
Q03336	CLLFVDIPSK	1.659975319	2	3.268264055
Q03336	DEQIPDGMCIDVEGK	1.208677804	2	4.634918213
Q03336	DYSEMYVTCAR	0.491975117	2	2.501927614

Q03336	FNDGKVDPAGR	1.210047029	2	2.716225624
Q03336	GIAPYSYAG	1.32025062	2	2.538486004
Q03336	HQGSLYSLFPDHSVK	1.243653959	2	4.597604752
Q03336	IECVLR	1.111450682	2	2.418573618
Q03336	LWVACYNGGR	1.250867461	2	3.10249567
Q03336	MEKDEQIPDGMCIDVEGK	1.215948474	2	5.297059059
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(1)	1.460811595	2	4.622582912
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(11)	1.481507906	2	2.715712309
Q03336	QSGGYVATIGTK	1.062784086	2	2.776037931
Q03336	VGVDAPVSSVALR	1.318644302	2	3.715521812
Q03336	YFAGTMAEETAPAVLER	1.148196703	2	5.825893402
Q03336	YFAGTMAEETAPAVLER+Oxidation(6)	1.222394588	2	5.420331478
Q03336	YFDQVDISNGLDWSLDHK	1.100050919	2	4.528508186
Q03336	FCALNWEDQSVFILAMVDEDKK	2.281988713	3	4.193659306
Q03336	KYFDQVDISNGLDWSLDHK	1.051948312	3	5.205665112
Q03410	**SYCP1 Synaptonemal complex protein 1**	**1.062833127**	**0.7397**	**4**
Q03410	LQDENLK	1.160877877	1	1.988655686
Q03410	NIEELHQENKALK	1.107568808	1	1.908851027
Q03410	ATVDEAVKLQKEIDLR	0.675487609	2	2.366490841
Q03410	ISEEKLLGEVEK	0.955224027	2	2.308815956
Q03626	**MUG1 Murinoglobulin_1**	**1.274033432**	**0.75168**	**7**
Q03626	EESSCIHSSCTAER	1.031081121	2	4.145668983
Q03626	GGEFEMMPLGVNK	0.836151545	2	3.150003672
Q03626	VQTVPLTCNNPK	1.178582799	2	2.77076292
Q03626	VYHKEESSCIHSSCTAER	1.176212461	2	5.465482712
Q03626	ESVVFVQTDKPVYKPGQSVK	0.828893969	3	3.46966958
Q03626	LTAQPAPSPEDLALSMGTIK	1.290838747	3	3.951302528
Q03626	NLHPLNELFPLAYIEDPK	1.284715315	3	4.114753246
Q04462	**SYVC Valyl_tRNA synthetase**	**1.078500758**	**0.05378**	**3**
Q04462	ADFPAGIPECGTDALR	0.747113226	2	2.404207945
Q04462	ALNPLEEWLR	1.162871007	2	2.301828861
Q04462	SVTQQPGSEITAPQK	1.078399328	2	3.893895388
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**1.128532965**	**0.22364**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(1)	1.160696572	2	2.608152151
Q05144	YLECSALTQR	1.035300345	2	3.000401258
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.17250621**	**0.00012**	**8**
Q06647	YATALYSAASK	0.23488364	1	2.120351315
Q06647	FSPLTANLMNLLAENGR	1.223486767	2	3.964576244
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.187281138	2	5.331629276
Q06647	GQILNLEVK	1.128236567	2	2.664919853
Q06647	TDPSIMGGMIVR	0.998344259	2	3.26981473
Q06647	TVLNSFLSK	1.12470393	2	2.754984856
Q06647	VSLAVLNPYIK	1.475583634	2	3.671344042

Q06647	LGNTQGVISAFSTIMSVHR	1.156204098	3	4.719233513
Q07071	**GCKR Glucokinase regulatory protein**	**1.434970211**	**9.9E-20**	**12**
Q07071	AAPISCHVQVAHEK	1.449921423	2	4.803567886
Q07071	GFLIGDHSDMFNQK	1.21263003	2	2.56756711
Q07071	GLGQKPLYTYLIAGGDR	1.038672763	2	2.608589172
Q07071	LLGQCDAEIFQEEGQIVPTYQR	2.106475221	2	4.956361294
Q07071	LYSESVLTTMLQVAGK	1.368003815	2	3.297308445
Q07071	QEAFVLNPAIGPEGLSGSSR	1.101848944	2	4.249424458
Q07071	TVDQGVVSSQR	1.294788657	2	3.654975891
Q07071	VIPTALLSLLLR	1.651804163	2	3.409047127
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.313657931	2	5.236416817
Q07071	WVLNTVSTGAHVLLGK	1.461700902	2	3.437934637
Q07071	CQNIQALVHSTVGQSLPAPLKK	1.322800988	3	4.859113216
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	0.854289406	3	4.010899067
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.977221486**	**0.99893**	**8**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.95032244	2	5.173858643
Q07116	HEVTVTLQCAGNR	1.480011154	2	3.095987082
Q07116	MSPPLEASDPYSNDPMR	0.757893483	2	3.938340664
Q07116	NHLPVPNLDPDTYR	1.00844114	2	2.798040867
Q07116	VSVESEESYSHWQR	0.970247621	2	4.036505699
Q07116	VVVPGVVGAR	1.000514414	2	2.746874571
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	0.834489018	3	4.505449295
Q07116	INSQRPFNAEPPPELLTESYITPNPIFFTR	1.479640188	3	4.477169514
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.165602658**	**0.24798**	**2**
Q07205	AMGPLVLTEVLFDEK	1.223502854	2	3.549428701
Q07205	TVIVNMVDVAK	1.136587899	2	2.350655079
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**1.015742632**	**0.98858**	**14**
Q07523	EDAELAMK	0.924305819	1	1.941813111
Q07523	ALKEEKPTQSVPVSFPK	1.051954174	2	4.623281956
Q07523	ALVITIDTPVLGNR	0.972135124	2	4.009721756
Q07523	ASFCWNDLSLLQSITR	1.557699795	2	4.589102745
Q07523	CMTLSGCQSVAEISPDLIQFSR	1.057571383	2	3.548344374
Q07523	EEKPTQSVPVSFPK	0.889551282	2	2.944642067
Q07523	EVLDILTAELHR	0.844495964	2	3.173909903
Q07523	NQLNLEANILLK	0.814429163	2	3.619381666
Q07523	QLDEVSASIDALR	0.952885852	2	3.119019747
Q07523	TGTDVLK	0.82864591	2	2.31738615
Q07523	TSWDFIEGEADDGITYSENIAAFK	0.564508438	2	4.451080322
Q07523	GEDGVKEVLDILTAELHR	1.376175919	3	5.545389652
Q07523	HNVQGIVVSNHGGR	0.931441455	3	6.222715378
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	0.840079629	3	3.771000385
Q07936	**ANXA2 Annexin A2**	**1.094851516**	**0.42852**	**4**
Q07936	AEDGSVIDYELIDQDAR	1.117562048	2	3.901085615

Q07936	GLGTDEDSLIEIICSR	1.10293055	2	3.975583553
Q07936	GVDEVTIVNILTNR	0.870871019	2	3.825793028
Q07936	TNQELQEINR	1.095763914	2	3.107836723
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.225493334**	**3.7E-06**	**2**
Q07984	FFDEESYSLLR	1.209262744	2	3.12842536
Q07984	NNEDVSIIPPLFTVSVDHR	1.225251622	2	4.276744366
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**1.030362768**	**0.00349**	**9**
Q08163	ALLVTASQCQQPAGNK	0.922766069	2	4.224589348
Q08163	AYLSIWTELQAYIK	0.890074727	2	2.301376104
Q08163	LSDLLAPISEQIQEVITFR	1.012700291	2	4.004083633
Q08163	NSLDCEIVSAK	1.072611131	2	2.351902485
Q08163	SALFAQINQGESITHALK	1.125009531	2	4.564942837
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.229950549	2	4.07185173
Q08163	VENQENVSNLVIDDTELK	1.213586282	2	5.129750252
Q08163	ELSGLPSGPSVGSGPPPPPPGPPPPPVPTSSGSDDSASR	1.241992484	3	4.706572533
Q08163	LEAVSHTSDMHCGYGDSPSK	0.962584524	3	5.015257359
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**0.849749823**	**0.1751**	**3**
Q08415	ILVLNTPNNPLGK	2.222007915	2	3.386118174
Q08415	LGASNDWQLDPAELASK	1.004341611	2	3.980907679
Q08415	EQQHFGQPSSYFLQLPQAMELNR	0.90963948	3	4.848612309
Q09073	**ADT2 ADP/ATP translocase 2**	**1.069613946**	**9.9E-20**	**7**
Q09073	DFLAGGVAAAISK	0.632236899	2	5.010077953
Q09073	GLGDCLVK	1.157623412	2	2.875092506
Q09073	GMGGAFVLVLYDEIKK	1.328712209	2	3.61510396
Q09073	GTDIMYTGTLDCWR	0.677283791	2	3.55932641
Q09073	KGTDIMYTGTLDCWR	0.93319217	2	4.031659603
Q09073	LLLQVQHASK	2.012983927	2	2.741006613
Q09073	QIFLGGVDKR	1.203726578	2	2.3789258
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**1.034422711**	**0.77805**	**9**
Q0D2L3	SVDEGLLDSK	0.919242498	1	1.926742435
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	0.767391392	2	3.893678665
Q0D2L3	SVDEGLLDSKR	1.061253941	2	3.079544783
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.205808563	2	5.178209305
Q0D2L3	VVLAEDCWMK	1.598017137	2	2.405902386
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.614461119	3	3.395273209
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	1.021659233	3	3.474751711
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	0.79435864	3	4.771517277
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	1.275817726	3	5.759459496
Q0VAV2	**EXPH5 Exophilin_5**	**1.234992863**	**0.35925**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(2)	1.249433392	2	2.528829813
Q0VAV2	SLSDQDPGQEQREEK	1.234973957	2	2.304531574
Q0VGK3	**GLCTK Glycerate kinase**	**1.14347158**	**0.9057**	**6**

Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	1.13608855	2	4.849723816
Q0VGK3	GATIQELNTIR	1.113545187	2	2.868217468
Q0VGK3	QLFDSAVGAVQPGPMLQR	0.994849304	2	4.805804253
Q0VGK3	VAAACLTSSTAERPLEEEAK	1.087864063	2	3.201857567
Q0VGK3	ADSDPHGPHTCGHVLNVIIGSNSLALAEAQR	1.100574249	3	4.82085371
Q0VGK3	LHQLAAELQLPDLQLEEALEAVAK	1.565467573	3	3.610090494
Q0ZHH6	**ATLA3 Atlastin_3**	**1.10068041**	**0.00116**	**8**
Q0ZHH6	ALASVLLQDHIR	1.406644686	2	2.655458689
Q0ZHH6	EHQHEEIQNVR	0.819094522	2	3.605910063
Q0ZHH6	EQLQTLIPYVLNPSK	0.825048441	2	3.26649189
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	2.95543129	2	2.358603239
Q0ZHH6	IYQGEDLPHPK	1.123045775	2	2.788579464
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(3)	1.125997913	2	2.489993811
Q0ZHH6	YQQELEEEITELYENFCK	1.542190455	2	5.327203751
Q0ZHH6	YSGQYLELGGAIDSGAAYVLEQASSHIGNSTQAAVR	1.280072726	3	3.365163565
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**1.090455676**	**0.93393**	**2**
Q10728	QEEKKESEVSR	0.840307896	2	2.339062214
Q10728	SLLEMEKRER+Oxidation(5)	1.081315861	2	2.400444508
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.975096954**	**0.69363**	**25**
Q10758	QIHEEEIR	1.040614224	1	2.316265821
Q10758	QLEALGQEK	0.961014747	1	2.150196552
Q10758	AEAETMYQIK	1.046719899	2	3.122698784
Q10758	AQYEEIANR	0.991995137	2	3.166008234
Q10758	ATLEAAIADAEQR	0.94076691	2	4.706914902
Q10758	DVDEAYMNKVELESR	1.74602193	2	3.563874483
Q10758	ELQSQISDTSVVLSMDNSR	0.589992557	2	5.96615839
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	1.005659249	2	4.748090744
Q10758	KDVDEAYMNK	0.975278284	2	2.576738119
Q10758	LEGLTDEINFLR	1.012576889	2	4.051198006
Q10758	LESGMQNMSIHTK	0.953285868	2	4.181872368
Q10758	LEVDPNIQAVR	0.940707493	2	3.830272913
Q10758	LEVELGNMQGLVEDFK	1.090956518	2	4.968849182
Q10758	LQAEIDALK	1.043962825	2	2.975306273
Q10758	LVSESSDIMSK	1.139070537	2	3.332324743
Q10758	SKTEISEMNR	0.80544933	2	3.083977222
Q10758	SKTEISEMNR+Oxidation(8)	1.46273039	2	3.093940973
Q10758	SLDMDSIIAEVR	0.907140516	2	4.939464569
Q10758	SNMDNMFESYINNLR	1.176552418	2	4.055940628
Q10758	SRAEAETMYQIK	1.056427969	2	3.441725969
Q10758	TEISEMNR	0.926173205	2	2.444743872
Q10758	TEMENEFVLIK	0.96770091	2	3.651865482
Q10758	TEMENEFVLIK+Oxidation(3)	0.995496404	2	2.408712387
Q10758	WSLLQQQK	0.951837145	2	2.934141159

Q10758	YEELQTLAGK	0.984598385	2	3.562259912
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**1.081534956**	**0.99977**	**6**
Q14DH7	CVPGYNVMILDDNMQK	0.806823531	2	2.63263154
Q14DH7	STLSALVNGKPYK	0.99660776	2	2.450207949
Q14DH7	THFAASVADPER	0.87531511	2	3.674227238
Q14DH7	VDDVINVAGHR	1.006496503	2	3.745274544
Q14DH7	VLAEHGVAALFTAPTAIR	0.931356887	2	4.45122385
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.112109014	2	2.912098885
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.947282828**	**1.5E-06**	**10**
Q1HCL7	ASYYEISVDDGPWEK	1.063007251	2	2.527392864
Q1HCL7	LKPVIGVNTDPER	1.493747891	2	2.88496089
Q1HCL7	NVEHIIDSLRDEGIEVR	1.314408638	2	3.455521584
Q1HCL7	QGNLTLPLNK	1.078908783	2	2.338242054
Q1HCL7	REYDEETVR	1.477389359	2	2.448055744
Q1HCL7	SEASGPQLLPVR	0.924269093	2	2.951103449
Q1HCL7	SSGLNLCTGTGSK	0.99695408	2	3.854199171
Q1HCL7	VTNEYNESLLYSPEEPK	1.213558682	2	4.46385479
Q1HCL7	YTHSFPEALQK	1.202771158	2	2.598319054
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.106061654	3	4.710017681
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.151093137**	**0.41535**	**3**
Q1JU68	LLDMDGIIVEK	1.256174474	2	2.555736303
Q1JU68	NQLTAMSSVLAK	1.133807507	2	2.650067568
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	0.894142741	3	3.442136526
Q29RW1	**MYH4 Myosin_4**	**0.463092673**	**0.01231**	**14**
Q29RW1	LQDLVDKLQTK	1.145643385	1	1.938905001
Q29RW1	ANLMQAEIEELR	0.765341045	2	3.010677099
Q29RW1	ELENEVENEQKR	0.257936782	2	2.98761797
Q29RW1	LAQESTMDIENDKQQLDEK	0.28644068	2	4.940879345
Q29RW1	LQDAEEHVEAVNSK	0.300859101	2	4.562023163
Q29RW1	MEGDLNEMEIQLNHANR	0.635823233	2	4.341679096
Q29RW1	NAYEESLDQLETLK	0.572972141	2	4.578883648
Q29RW1	NAYEESLDQLETLKR	0.541672786	2	4.054221153
Q29RW1	SELQASLEEAEASLEHEEGK	0.258565246	2	5.287261486
Q29RW1	SNAACAALDKK	0.81226443	2	2.451460123
Q29RW1	TEGGATVTVK	0.507510221	2	2.691892147
Q29RW1	TKLEQQVDDLEGSLEQEK	1.191813155	2	5.655308247
Q29RW1	TKLEQQVDDLEGSLEQEKK	0.475567271	3	5.108285427
Q29RW1	VRELENEVENEQKR	0.511770184	3	3.707527399
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**1.120315117**	**0.47658**	**3**
Q2EMV9	LQEELTR	1.320473629	1	2.117668152
Q2EMV9	LIISEVLK	1.185784475	2	2.5172019
Q2EMV9	VLVEFEKESLNIAGK	0.876719856	2	2.586992979

Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.2859189**	**2.8E-08**	**8**
Q2V057	ASIYGQFVAGETAEEVR	1.068854897	2	4.22115469
Q2V057	EDCTQPDYEATSR	1.001813046	2	3.542513371
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.515794073	2	4.807704926
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.293269013	2	5.75995779
Q2V057	REQALLSQELWR	1.343016454	2	3.095223427
Q2V057	SIPYGCLEEVIPYLIR	1.2759654	2	4.115543365
Q2V057	TSEAWYEGNLSAMLHCVDLSR	0.731898014	2	2.629750252
Q2V057	SVTQLHGKEDCTQPDYEATSR	0.958058318	3	4.610406399
Q32LZ8	**PLPL5 Patatin_like phospholipase domain_containing protein 5**	**1.081627399**	**0.86723**	**2**
Q32LZ8	NFIVTDFATR	0.973810287	1	1.901532173
Q32LZ8	FYGSSSGALNAMAIVFGK	1.081852939	2	2.411370039
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.411598749**	**7.6E-08**	**2**
Q3B7D0	HCDDSYTPQDK	1.412168263	2	3.406932354
Q3B7D0	TCAEAVVPSYVPIVK	1.403254128	2	2.684961081
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.074589026**	**0.72435**	**4**
Q3B7U9	SCSQVLEHQPDNIK	1.135639748	2	4.176351547
Q3B7U9	TAEDGPDLEMLSGQER	0.96886415	2	4.123155594
Q3B7U9	VDMTCEEEEELLQLK	1.191264058	2	4.140001774
Q3B7U9	VLAQQGEYSEAIPILR	1.067659707	2	3.776660442
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**1.101937033**	**0.84404**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	1.057430709	2	4.667364597
Q3B8Q2	GIYAYGFEKPSAIQQRAIK	1.080207025	2	2.40851593
Q3KR86	**IMMT Mitochondrial inner membrane protein (Fragment)**	**1.049607339**	**7.7E-10**	**9**
Q3KR86	AVDEAADALLK	1.405015128	2	2.542653322
Q3KR86	EIAGATPYITAAEEK	0.592443592	2	3.04442668
Q3KR86	GIEQAVQSHAVAEEEAR	1.238548094	2	4.86500597
Q3KR86	QTITAQNAAVQAVK	1.192891449	2	4.237040997
Q3KR86	SEIQAEQDR	1.201104988	2	2.799418688
Q3KR86	SLEDALNQTATVTR	1.175682825	2	3.984568834
Q3KR86	TSSAEMPTIPLGSAVEAIR	1.154261857	2	3.845381021
Q3KR86	VVSQYHELVVQAR	1.470647596	2	3.563866138
Q3KR86	YSTSSSSGVTAGK	0.994079569	2	2.774996281
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.183667233**	**0.29933**	**2**
Q3KRD8	HGLLVPNNTTDQELQHIR	1.028829927	3	5.102761745
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.16144133	3	4.402582645
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.623184747**	**0.54674**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.172777182	2	2.664327621
Q3KRE0	ISVLEALR	1.965300822	2	2.626279831
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**0.74735101**	**0.74728**	**3**
Q3KRE8	ALTVPELTQQMFDSK	0.947887914	2	2.752089024

Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.886568181	3	4.383858204
Q3KRE8	FWEVISDEHGIDPTGSYHGDSDLQLER	0.744439786	3	3.37130785
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**0.783939891**	**0.75159**	**3**
Q3MIB4	MEIIQVPGYTQEEK	0.918958117	2	2.499184608
Q3MIB4	TVGVNNPVFLLDEVDK	0.745580031	2	2.616867304
Q3MIB4	GTSLQSTILGVIPNTPDPASDSQDLPPLHR	1.016537606	3	3.59310627
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**1.08882067**	**0.87209**	**7**
Q3MIE0	DGQEGIEAFIQK	0.618938408	2	3.417719364
Q3MIE0	SDILHEAESEDLK	1.144857717	2	3.463267565
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.038064146	2	4.171805382
Q3MIE0	VALEMLFTGEPISAQEALR	0.849318513	2	4.062315941
Q3MIE0	VIIISAEGPVFSSGHDLK	1.116855231	2	4.334732056
Q3MIE0	VVPEEQLEEEATR	1.069977696	2	3.763500929
Q3MIE0	SDILHEAESEDLKVIIISAEGPVFSSGHDLK	0.956590047	4	5.75890255
Q3MIF4	**XYLB Xylulose kinase**	**0.956264965**	**0.90409**	**6**
Q3MIF4	FNADNMEVSAFPGDVEIR	1.062616773	2	4.337610245
Q3MIF4	IRDESASCSWNK	1.121925845	2	4.087095261
Q3MIF4	LGSPVPSCSVVGAISSYYVQR	1.54297367	2	3.257169008
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	0.282825152	2	4.227624893
Q3MIF4	VVAFTGDNPASLAGMR	1.2497052	2	3.913111448
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	0.976255149	2	5.158540726
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**0.978370067**	**0.71298**	**4**
Q3T1J1	EDLRLPEGDLGK	0.964924925	2	2.821481466
Q3T1J1	EDLRLPEGDLGKEIEQK	1.112245166	2	4.517254829
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.20896479	2	5.084915638
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.510912905	3	3.634307384
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**0.941325478**	**0.59766**	**3**
Q3T1K5	FTVTPSTTQVVGILK	1.153602868	2	3.827370405
Q3T1K5	LLLNNDNLLR	0.968596099	2	2.635862827
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.138025857	3	3.989356279
Q3TVW5	**TCHP Trichoplein keratin filament_binding protein**	**1.255671788**	**0.01018**	**2**
Q3TVW5	RTQEIQEELEVDGRILQALLEK	1.471594768	2	2.683987617
Q3TVW5	TELGRFLKHQYNAQLNR	1.255628962	2	2.914061546
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**1.197125649**	**0.00554**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	0.890537184	2	2.444278479
Q3U0J8	QIELDLLRTLPNNK	1.331804144	2	2.758384466
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.139999939**	**0.37687**	**2**
Q3UHR0	ACEERLGLPGRELLLQDNK	1.136970013	2	2.408666372
Q3UHR0	IESLWESWGSNMVVKVK	1.231957854	2	2.354676485
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.095399115**	**0.02081**	**3**
Q3ULJ0	GIDEGPDGLK	1.14097197	2	2.506152391

Q3ULJ0	LGLMEMIAFAK	1.779219504	2	3.947365284
Q3ULJ0	LTDIINNDHENVKYLPGHK	1.809168415	2	2.455640554
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**0.841383117**	**3.3E-07**	**16**
Q3UQ44	ALVGSENPPLTVIR	1.246755248	2	3.895332813
Q3UQ44	AWVNQLETQTGEASK	1.030931643	2	4.791055202
Q3UQ44	GVLLGIDDLQTNQFK	1.11403878	2	4.589389324
Q3UQ44	HTDNTVQWLR	1.154896275	2	3.332205296
Q3UQ44	LGIAPQIQDLLGK	1.836792428	2	2.945426226
Q3UQ44	LPYDVTTEQALTYPEVK	1.339381212	2	4.570028782
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.607640597	2	2.41396904
Q3UQ44	LSAEEMDER	1.043970098	2	2.901484251
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.179506726	2	5.312180519
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.653447805	2	5.106618404
Q3UQ44	TLDTLLLPTANIR	0.996994845	2	2.596486807
Q3UQ44	TLEQTGHVSSK	0.705117522	2	3.100010395
Q3UQ44	VDFTEEEISNMR	0.992820557	2	2.921215773
Q3UQ44	VDQVQDIVTGNPTVIK	1.177702842	2	5.247410774
Q3UQ44	YQDILNEIAK	1.034317792	2	2.431580067
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.624630972	3	4.694124699
Q3UVR3	**TTBK2 Tau_tubulin kinase 2**	**1.128732039**	**0.72911**	**2**
Q3UVR3	NLADLR	1.126265328	1	1.902606368
Q3UVR3	YKVLGSSNSDSDLFSR	1.121198539	2	2.526452541
Q3V0K9	**PLSI Plastin_1**	**1.138697025**	**0.18361**	**3**
Q3V0K9	AYFHLLNQIAPK	1.188066518	2	2.847847939
Q3V0K9	KIENCNYAVELGK	0.838260898	2	3.674270391
Q3V0K9	QFVTPADVVSGNPK	0.925270342	2	3.325225115
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.091659002**	**0.91627**	**2**
Q3V132	GNLANVIR	1.089173105	2	2.666749954
Q3V132	YFPTQALNFAFK	1.332789033	2	3.396478653
Q497B0	**NIT2 Omega_amidase NIT2**	**1.079258536**	**0.1436**	**17**
Q497B0	ADLYSVESK	1.177165961	2	2.91508317
Q497B0	AGTEETILYSDIDLK	0.884319479	2	3.963971138
Q497B0	AGTEETILYSDIDLKK	0.91285219	2	3.524597645
Q497B0	AVDNQVYVATASPAR	0.880108245	2	4.872796535
Q497B0	AVDNQVYVATASPARDEK	1.010019616	2	3.64772439
Q497B0	ENSIYLIGGSIPEEDDGK	0.70146154	2	3.638831854
Q497B0	FAELAQIYAR	1.191873351	2	3.518334627
Q497B0	IHLFDIDVPGK	1.109846409	2	2.790529966
Q497B0	LALIQLQVSSIK	1.595317111	2	3.068480253
Q497B0	LYNTCAVFGPDGNLLVK	1.157328733	2	3.972441912
Q497B0	TLSPGDSFSTFDTPYCR	1.061252982	2	4.52126646
Q497B0	VGLGICYDMR	1.262812908	2	2.55745697
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.946961764	3	5.48963356

Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.154347874	3	5.170785904
Q497B0	GCQLLVYPGAFNMTTGPAHWELLQR	1.236963716	3	3.535847902
Q497B0	KIHLFDIDVPGK	1.375381001	3	4.549983501
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.005706009	3	5.281800747
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**1.138813521**	**0.95059**	**5**
Q498D5	GQLQILEK	1.072942208	1	1.946201086
Q498D5	AYGDMYDLSTNTQEK	0.885733951	2	3.508284569
Q498D5	FCNLALLLPIVTK	1.134419855	2	2.726423502
Q498D5	LNELLTNVEELKEEIK	1.187963464	2	3.098065615
Q498D5	ALNTHIEDLKLDVLLQK	0.947940956	3	3.440882683
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.293835357**	**0.65017**	**8**
Q499N5	GATLSHHNIVNNSNLIGQR	1.213638637	2	4.611359119
Q499N5	GGENIYPAELEDFFHK	1.231204614	2	3.322753191
Q499N5	GGVIAGSLAPPELIR	1.237501971	2	2.890384674
Q499N5	GYCVMQGYWGEPQK	0.8999575	2	2.887845993
Q499N5	TFETVGQDR	1.09901907	2	2.650983572
Q499N5	TGDIASMDEQGFCR	1.103438605	2	3.746155262
Q499N5	TVGECLDATAQR	1.291810818	2	2.994221687
Q499N5	YIVFVEGYPLTVSGK	1.320348713	2	4.522711754
Q4AEF8	**COPG Coatomer subunit gamma**	**1.136012107**	**0.08555**	**5**
Q4AEF8	ALQQYTLEPSEKPFDLK	1.134367439	2	3.346613407
Q4AEF8	FGAQNEEMLPSILVLLK	1.200007871	2	3.968838453
Q4AEF8	SSPEPVALTESETEYVIR	1.179593351	2	4.712357044
Q4AEF8	TLEEAVGNIVK	1.062537359	2	2.346026897
Q4AEF8	VVLEHEEVR	1.499015275	2	2.306049109
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.100182773**	**0.87568**	**5**
Q4FZT0	SELGKLSLDKVFR	1.361943722	1	2.066349745
Q4FZT0	AEQINQAAGEASAVLAK	1.118004503	2	4.790539742
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.263050665	2	4.837722778
Q4FZT0	ATVLESEGTR	1.104473361	2	2.656892061
Q4FZT0	ILEPGLNVLIPVLDR	1.011720138	2	2.880103111
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.121227479**	**0.09646**	**5**
Q4FZT9	FGGSGSQVDSAR	1.130838455	2	3.629247665
Q4FZT9	SETELKDTYAR	1.209702184	2	2.710785866
Q4FZT9	SSTTSMTSVPKPLK	1.000585582	2	2.905899525
Q4FZT9	TPVQSQQPSATAPSGADEK	1.143173154	2	4.444346428
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.911289421	3	4.482903004
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.39304784**	**0.00041**	**4**
Q4FZX7	GDAGSADVQDLEK	1.224803289	2	3.497640848
Q4FZX7	GNSLTLIDLPGHESLR	1.167517949	2	2.962847233
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.395471062	2	4.960078716

Q4FZX7	VGDGAGGAFQPYLDSLR	1.121141609	2	2.407241821
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**0.918756907**	**0.71388**	**3**
Q4G061	AEEEGGSDGSAAEAEPR	0.894582835	2	4.543288231
Q4G061	GTQGVVTNFEIFR	1.091242633	2	2.330028772
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	1.806082194	3	4.589909077
Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**0.933401788**	**0.41076**	**2**
Q4KLF8	ALAAGGVGSIVR	1.149212305	2	2.317006588
Q4KLF8	QGNMTAALQAALK	0.887002244	2	2.519743681
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.277083155**	**1.1E-06**	**16**
Q4KLP0	SSLYSSDIGK	1.028334577	1	2.095977068
Q4KLP0	ARPSVDHGLAR	1.324514624	2	2.520576239
Q4KLP0	LEELCPFPLDSLQQEMGK	1.349117664	2	5.122525215
Q4KLP0	LLLESQEFDHFLATK	1.353913578	2	3.835387945
Q4KLP0	LVTVYCEHGHK	1.218360757	2	2.831177235
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	1.317314755	2	3.016624212
Q4KLP0	SVEVPEELQLHSHLLK	1.261151972	2	2.703264713
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.205649742	2	4.991351128
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.238108999	3	3.674619436
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.185236182	3	4.30594635
Q4KLP0	LSAYGGITDIIIGMPHR	2.194688294	3	3.533017635
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.166472901	3	3.515598297
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.070655247	3	4.998397827
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.376292224	3	3.831418991
Q4KLP0	YGGEGAESMMGFFHELLK	1.130484611	3	4.243721008
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.086214571	3	4.337694168
Q4KLZ6	**DHAK Bifunctional ATP_dependent dihydroxyacetone kinase/FAD_AMP lyase (cyclizing)**	**1.005782249**	**0.32128**	**13**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.131314724	2	4.605414867
Q4KLZ6	AILEVLQTK	1.222356457	2	2.876458168
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.27489989	2	3.260283709
Q4KLZ6	AVAQAGTAGTLLIVK	1.364505939	2	4.424355984
Q4KLZ6	EGPTPASPAQVLSK	1.136890868	2	3.303151608
Q4KLZ6	ISTTLIGLEEHLNALDR	2.677474366	2	4.154751778
Q4KLZ6	LIDAETNAK	1.143551011	2	3.056431532
Q4KLZ6	LSVLLLEK	1.733889416	2	2.683353662
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	0.879242774	2	4.596370697
Q4KLZ6	TMLDSLWAAAQELQAWK	0.89081189	2	4.305660248
Q4KLZ6	VAGALAEEGMGLEEITK	1.29408573	2	3.657215118
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.102687785	3	5.096961021
Q4KLZ6	RGLCGTILIHK	0.909817476	3	3.407773495
Q4KM35	**PSB10 Proteasome subunit beta type_10**	**1.314373148**	**0.01975**	**2**
Q4KM35	ALSSPIEPVQR	1.250254635	2	2.373132944

Q4KM35	FAPGTTPVQTQEVR	1.314887578	2	2.843578577
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.296164067**	**1.2E-08**	**3**
Q4KM49	QVEPLDPPAGSAPGER	1.087567254	2	2.578236103
Q4KM49	TVVSGLVQFVPK	1.125792744	2	3.293801785
Q4KM49	VDAQFGGIDQR	1.306735805	2	3.361602783
Q4KM62	**PALMD Palmdelphin**	**1.398772839**	**0.08269**	**2**
Q4KM62	TGESVVLSSIPLPSDDFK	0.877648773	2	3.401993752
Q4KM62	VEKEEIPEESIEDIYANIPDLPSSYIPSR	1.399398714	3	3.426925659
Q4KM73	**KCY UMP_CMP kinase**	**1.164955738**	**0.00079**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.127071723	2	4.92602396
Q4KM73	IVPVEITISLLK	1.037886947	2	3.041659832
Q4KM73	KNPDSQYGELIEK	1.167119787	2	4.293810844
Q4KM73	NQDNLQGWNK	1.02930325	2	2.940244913
Q4KM73	SVDEVFGDVMK	0.976649942	2	3.166023016
Q4KM73	YGYTHLSAGELLR	1.151714697	3	3.614707708
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**0.898067553**	**0.20692**	**4**
Q4KM74	DLQQYQSQAK	0.88606264	2	3.392679214
Q4KM74	GEALSALDSK	1.202942115	2	2.416548967
Q4KM74	IMVANIEEVLQR	1.319497039	2	2.705671549
Q4KM74	NLGSINTELQDVQR	1.068892608	2	4.165977955
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.068470174**	**0.999**	**4**
Q4KMA2	IDIDPEETVK	1.059435707	1	2.633613348
Q4KMA2	NFVVVMVTKPK	1.067524479	2	3.460596085
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.08889861	2	3.847612619
Q4KMA2	ESQAVVDPPPQAVSTGTPQSPAVAAAAATTTATTTTTSGGHPLEFLR	1.035169097	3	3.946579218
Q4QQV3	**F162A Protein FAM162A**	**1.120823834**	**0.60884**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	1.089471878	2	3.452002764
Q4QQV3	RHESLTSLNLER	1.127566735	2	2.759135485
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**1.068624975**	**0.97076**	**2**
Q4QQW3	HLETAEILGANIR	1.068563986	2	3.278478861
Q4QQW3	IQDAGPVLADALR	1.057306564	2	2.48977828
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**0.976588879**	**6.6E-08**	**5**
Q4QRB4	AILVDLEPGTMDSVR	1.130479082	2	4.561449528
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(11)	1.1402093	2	2.63351965
Q4QRB4	EIVHIQAGQCGNQIGAK	0.760685124	2	5.107461452
Q4QRB4	IMNTFSVVPSPK	1.059044705	2	3.44654727
Q4QRB4	ISEQFTAMFR	1.141019306	2	3.359265089
Q4V7C7	**ARP3 Actin_related protein 3**	**1.066101**	**0.95173**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	1.116983472	2	4.828017235
Q4V7C7	KDYEEIGPSICR	1.045851646	2	3.903962851
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	0.974631482	2	3.456576347
Q4V7C7	LSEELSGGR	1.157907301	2	2.778646946

Q4V7C7	NIVLSGGSTMFR	1.070630456	2	2.664943457
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	0.857660728	2	4.597793579
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**1.13271486**	**0.89027**	**5**
Q4V8K1	QVFVCGNDSK	1.12005364	2	2.558608055
Q4V8K1	TCADEFPLTVDSSEK	1.159710656	2	4.465877056
Q4V8K1	TLGLTPLDQGSLVAAK	1.147555101	2	3.375766993
Q4V8K1	VLIDVSNNQK	1.071615286	2	2.314770699
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	0.887338162	3	3.309345961
Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**0.912985523**	**0.53889**	**2**
Q501J6	ELAQQVQQVADDYGK	1.084132133	2	2.677911043
Q501J6	VLEEANQAINPK	0.912720857	2	2.711358786
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**1.25472378**	**0.00117**	**5**
Q505J8	LQQVQAGQAEK	1.255049888	2	2.952146292
Q505J8	SIPLEGLVQSELMQLPSGK	1.192739557	2	2.766185284
Q505J8	SLQALGEVIEAELR	1.564200306	2	3.893519163
Q505J8	VVDSIEDEVQR	1.141536077	2	2.844742775
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	1.051066477	3	5.149074554
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**1.095714506**	**0.34511**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	1.093686244	2	4.080215454
Q561R9	ILIDTGEPSVPEYISCLK	1.145801262	2	3.521716118
Q561R9	NISNDATYCIK	0.935421456	2	2.724781513
Q561R9	NNREEQIITVFR	0.87072599	2	2.779378653
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.37592442**	**0.804**	**5**
Q561S0	VITVDGNICSGK	0.978356935	2	3.128950357
Q561S0	VVEDIEYLNYNK	1.240116662	2	3.566642284
Q561S0	YAPGYNADVGDK	1.26669953	2	2.750463963
Q561S0	YGLLASILGDK	1.028763073	2	2.957306147
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	1.598447922	3	3.698609591
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.842728638**	**0.9519**	**7**
Q562C4	VLQEVQR	0.893858948	1	2.015970707
Q562C4	AQFSEVQLEWQPPPFK	0.869719804	2	4.814002037
Q562C4	FIVAYGENMK	0.852518524	2	2.348133087
Q562C4	GTSNEVTLLELGCGTGANFQFYPPGCK	0.434972381	2	4.044890881
Q562C4	HIGDGCHLTR	0.902894269	2	2.757642984
Q562C4	KVLQEVQR	1.053848642	2	2.523785353
Q562C4	VTCVDPNPNFEK	0.718323396	2	3.720582962
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**0.886049522**	**0.29043**	**10**
Q58FK9	AIILNTPHNPIGK	1.232062964	2	3.296651602
Q58FK9	DSTLDAAEEIFR	0.617884258	2	2.998790979
Q58FK9	IEGLDQNVWVEFTK	1.104251706	2	4.550024986
Q58FK9	LGWSIGPGHLIK	2.143334827	2	2.435388327
Q58FK9	MDDPECYFNSLPK	0.891776754	2	4.117753983

Q58FK9	RIEGLDQNVWVEFTK	1.141166499	2	3.917770863
Q58FK9	RMDDPECYFNSLPK	1.027413873	2	2.352519274
Q58FK9	SDEPYDYK	1.266391607	2	2.481590271
Q58FK9	WTSSDWTFNPQELESK	1.084668705	2	5.183171749
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.473169153	3	5.672567844
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.12625547**	**0.02091**	**2**
Q5BJQ0	AVLDSSPFLSEANAER	0.879742084	2	4.587979794
Q5BJQ0	TLNNDLGPHWR	1.214259706	2	3.012342691
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**1.027069126**	**0.94706**	**23**
Q5BJY9	AQIFANSVDNAR	0.959389347	2	3.817731619
Q5BJY9	AQYEQLAQK	1.033709497	2	3.29735446
Q5BJY9	IREYLEK	1.104628259	2	2.365219355
Q5BJY9	KVVDDTNITR	1.039034408	2	2.940171957
Q5BJY9	LEAEIATYR	0.907432817	2	3.23043704
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.880388904	2	5.300693035
Q5BJY9	LQLETEIEALKEELLFMK	1.835050445	2	4.957084656
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.868311253	2	6.53033638
Q5BJY9	NQNINLENNLGEVEAR	0.97883643	2	5.602835655
Q5BJY9	QSVESDIHGLR	0.971158944	2	3.315738201
Q5BJY9	QSVESDIHGLRK	1.086837213	2	2.690906048
Q5BJY9	QTQEYEALLNIK	1.133896139	2	3.535063028
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	1.01969946	2	5.729651451
Q5BJY9	TLQTLEIDLDSMK	1.05539472	2	4.226108551
Q5BJY9	VKLEAEIATYR	0.990719323	2	2.603852034
Q5BJY9	VKYETELAMR	1.089632842	2	2.630768299
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.584011192	2	5.605264664
Q5BJY9	VVDDTNITR	1.056070786	2	3.359093666
Q5BJY9	YWSQQIEESTTVVTTK	1.298673253	2	4.325231552
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	0.898957081	3	4.301848888
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	1.005205206	3	5.704818726
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	1.051061717	3	4.825302124
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.075921194	3	5.259335041
Q5BK17	**IYD1 Iodotyrosine dehalogenase 1**	**1.134849872**	**0.32307**	**2**
Q5BK17	FISSEPVPMEVIDNVIK	1.06393338	2	3.265035868
Q5BK17	LLVLLPVGYPSR	2.001944361	2	2.634382963
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.137154844**	**0.01422**	**5**
Q5BK63	AVQHSNVVINLIGR	1.074175805	2	2.548207521
Q5BK63	LFGLSPFEPWTTK	1.869945601	2	2.586514711
Q5BK63	NFDFEDVFVNIPR	1.297572721	2	3.954186678
Q5BK63	WLSSEIEETKPAK	1.462866461	2	3.10594511
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.259087445	3	5.358795643
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**1.027858094**	**0.99979**	**3**

Q5BK81	DVPYPPPLPPAVEAIQK	0.943400221	2	3.243910074
Q5BK81	TGNVAEQLR	1.012202704	2	2.334260464
Q5BK81	VEEVSLPDTINEGQVR	1.056498177	2	3.804463148
Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**0.793831542**	**0.56919**	**2**
Q5BQE6	NIMINLMDILEVDTKK+Oxidation(3)Oxidation(7)	0.91404926	2	2.413469553
Q5BQE6	QLGCQDAFPEVYDK	0.793142881	2	3.76182723
Q5DU56	**NLRC3 Protein NLRC3**	**1.00117102**	**0.44401**	**2**
Q5DU56	LTGLALGHLYR	1.748215074	2	2.402391911
Q5DU56	TLEILDLR	0.974495917	2	2.334411144
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.170237494**	**0.72933**	**2**
Q5EB77	NDIVNMLVGNK	1.108959252	2	3.277287722
Q5EB77	TCDGVQCAFEELVEK	1.208528317	2	3.738393307
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.116693645**	**0.57967**	**2**
Q5FVM4	MEELHNQEVQK	1.081773715	2	3.262027979
Q5FVM4	RMEELHNQEVQK	1.119815721	3	4.003191948
Q5FVQ4	**MLEC Malectin**	**1.268893076**	**3.4E-07**	**2**
Q5FVQ4	STPEDQILYQTER	0.902419414	2	3.977519035
Q5FVQ4	KEEEEEEEYDEGSNLKR	1.373262775	3	6.081984997
Q5FVR2	**TYPH Thymidine phosphorylase**	**1.037499971**	**0.21341**	**4**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(11)	1.236857863	2	2.60545969
Q5FVR2	DVTATVDSVPLITASILSK	0.924488217	2	3.639132261
Q5FVR2	KQEELLSPADGIVECVR	1.168817859	2	4.528800488
Q5FVR2	VHLDGPALSSQQR	1.246049919	2	2.400645971
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.492567437**	**0.43481**	**4**
Q5FVR5	DEKENLFQSK	0.893346646	2	2.79954958
Q5FVR5	ILFIVGENDQCLASK	1.5671573	2	3.746778011
Q5FVR5	IQQPGIGVISVSK	1.468063892	2	2.761187792
Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	1.336257364	3	3.809499979
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**1.074292449**	**1**	**2**
Q5FW57	AIDQEMFK	1.00533918	2	2.705004692
Q5FW57	SSQMLQMLESSLR	1.082166044	2	3.87968564
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**0.941153582**	**0.6582**	**2**
Q5HZV9	AIENIDTLTNLESLFLGK	0.980300202	2	3.13882494
Q5HZV9	ELDLYDNQIKK	0.440736541	2	2.378619432
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**1.039334582**	**0.9802**	**2**
Q5HZY2	IDRPEAISEER	1.035584224	2	2.926367998
Q5HZY2	LLESKEELDSLMTDETIANVPILILGNK	1.09963546	3	4.26350832
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.981728291**	**0.24606**	**6**
Q5I0C3	HAPLVEFEEEV	0.975900465	2	2.873004913
Q5I0C3	IIEEAPAPGIDPEVR	1.134771311	2	3.694898605
Q5I0C3	SEKEFQEQLESAR	1.147906174	2	3.553263187

Q5I0C3	VFFSEGAQANR	1.294706893	2	2.525081635
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	1.075560491	2	5.093858242
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	1.077628393	3	6.018025398
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**1.103557371**	**0.5716**	**2**
Q5I0D1	ESQSILTPLVSLDTPGK	1.104513102	2	3.505735397
Q5I0D1	HEEFEEGCK	1.086344376	2	2.648400784
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**1.11169989**	**0.98954**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	1.040841493	2	2.65226078
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.086307145	2	3.795943975
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.207004075**	**0.04936**	**2**
Q5I0D7	GVNTDSGNVCR	1.207005849	2	2.721880674
Q5I0D7	YAVDDVQYADEIASVLTSR	1.169769633	2	4.208346844
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.177909769**	**0.92956**	**2**
Q5I0E7	QLVEQVEQIQK	1.179192392	2	4.045115471
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.084916112	3	3.607738018
Q5I0G4	**SYG Glycyl_tRNA synthetase (Fragment)**	**1.214597541**	**0.49117**	**5**
Q5I0G4	AEVSELPSVVR	1.052637926	2	3.23682332
Q5I0G4	LGDAVEQGVINNSVLGYFIGR	1.23545557	2	3.04629755
Q5I0G4	TLHVEEVVPSVIEPSFGLGR	1.378363133	2	4.123369694
Q5I0G4	TVNVVQFEPNK	0.392990985	2	2.478611469
Q5I0G4	VDDSSGSIGR	1.086472222	2	2.618674517
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**1.180312918**	**0.0043**	**7**
Q5I0H9	DKNQDLCQQESVK	0.932884691	2	4.207155704
Q5I0H9	GPPLWEEDPGAK	1.285072915	2	2.829642057
Q5I0H9	GQGTICWVDCGDAESR	1.227391091	2	4.205665112
Q5I0H9	NGEQQAVPALR	1.20644297	2	2.817538023
Q5I0H9	NQDLCQQESVK	1.125591423	2	2.642869473
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	0.489021018	3	4.962248802
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.537102337	3	4.51512289
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.146084342**	**1.8E-09**	**5**
Q5I0J9	IIHESGVQILR	1.069768171	2	2.631151199
Q5I0J9	LDAAGGLQSLR	1.201882429	2	3.741920471
Q5I0J9	LEGPLAAAHSSGPR	1.202145721	2	3.582673788
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.418122301	2	3.886192799
Q5I0J9	HANLLVGSPSALADQTTER	1.109607755	3	5.100832462
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.249985005**	**2.2E-07**	**3**
Q5I0M2	DNHVVAAGSMEK	1.059948579	2	2.937930584
Q5I0M2	LYAEGDIPVPHAR	1.208881632	2	3.322430611
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.385365681	3	5.670990944
Q5M7U6	**ARP2 Actin_related protein 2**	**1.055421637**	**0.33134**	**6**
Q5M7U6	GYAFNHSADFETVR	1.208316517	2	3.593050003

Q5M7U6	HLWDYTFGPEK	1.166204927	2	3.391563177
Q5M7U6	ILLTEPPMNPTK	0.908064441	2	3.059725761
Q5M7U6	LCYVGYNIEQEQK	0.720496021	2	3.312533855
Q5M7U6	SMLEVNYPMENGIVR	1.064193997	2	4.464024544
Q5M7U6	VVVCDNGTGFVK	1.054358823	2	2.951761723
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.97079953**	**0.92392**	**9**
Q5M7W5	AAVGLTGNDIATPPNK	1.13563099	2	3.333067894
Q5M7W5	ATSPSTLVSTGSSSR	0.96625937	2	3.387913704
Q5M7W5	EAETALPIEMDLAPPEDVALPK	1.320743728	2	2.483345509
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	1.018184168	2	4.325022697
Q5M7W5	NTAPPTEEETVPGK	0.950660439	2	2.525020123
Q5M7W5	NTTPTGATPPAGMASTR	1.093960664	2	2.40905571
Q5M7W5	STLPVDEGSPLEK	0.918862116	2	2.350764036
Q5M7W5	VGSLDNVGHLPAGGTVK	0.965042622	2	2.803241014
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.064492965	2	4.667416096
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.700251356**	**9.9E-20**	**6**
Q5M875	ALTAELDTLGK	1.50037355	2	3.513955593
Q5M875	IQNIQFEAIVGHR	1.713625287	2	3.683205128
Q5M875	NSGHIVTVASVCGHR	1.628551116	2	4.211539268
Q5M875	SLIDGILTNK	1.303268233	2	2.977232456
Q5M875	SVAGQTVLITGAGHGIGR	1.717853341	2	3.985351086
Q5M875	TSCLCPVFVNTGFTK	1.556790058	2	4.150798798
Q5M9G3	**CAPR1 Caprin_1**	**1.267075382**	**6.5E-07**	**3**
Q5M9G3	LNQDQLDAVSK	1.296873032	2	3.150937319
Q5M9G3	YQEVTNNLEFAK	1.026095817	2	2.591183186
Q5M9G3	SSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMK	0.932457203	3	4.989726067
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.098023361**	**0.00032**	**2**
Q5M9I5	EEEEEELVDPLTTVR	1.085944592	2	3.332681417
Q5M9I5	SQTEEDCTEELFDFLHAR	2.102408018	2	5.020609379
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.253826802**	**1.1E-05**	**10**
Q5PPL3	AVLDANDPK	1.126510093	1	1.976686597
Q5PPL3	GYAVNVFDVR	1.263612995	1	2.030426502
Q5PPL3	AVLDANDPKK	1.499684026	2	2.478002787
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	1.267472241	2	4.346493244
Q5PPL3	GQVTGTDLINEVSK	1.034482497	2	4.07318306
Q5PPL3	GVSTVFHCASPPSNSNNK	1.122519279	2	4.780426979
Q5PPL3	ILTGLNYEAPK	1.391748559	2	3.420877695
Q5PPL3	KGQVTGTDLINEVSK	1.139589682	2	4.50861454
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.584341152	2	4.710452557
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.08060572	3	3.882331848
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.383410772**	**2.5E-05**	**5**
Q5PQT3	AIQNLASIHSLQVK	1.470808204	2	3.95813489

Q5PQT3	KLFPSLLDTK	1.459123377	2	2.467707396
Q5PQT3	LSSLDVTHAALVNK	1.718934103	2	3.467075586
Q5PQT3	QHLQIQSSQSHLNK	1.253911725	2	3.50531292
Q5PQT3	NFPSSCVLGPEGTPASWTLMDQTGEMR	0.855579485	3	4.036950111
Q5QNV8	**CQ066 Uncharacterized protein C17orf66 homolog**	**1.102246782**	**0.53515**	**2**
Q5QNV8	LEAPAFSFYFSKPK	0.994858819	2	2.369113922
Q5QNV8	YFKDSAQMPNLHVSISK+Oxidation(8)	1.186177151	2	2.412693739
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.051683702**	**0.12508**	**5**
Q5RJR8	ATVLDLSCNK	1.169316816	2	2.396241188
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	0.959639512	2	5.826883793
Q5RJR8	HHEILQWVLQTDSQQ	1.094720775	2	3.441896439
Q5RJR8	LDGNELDLSLSDLNEVPVK	0.860274773	2	4.329481125
Q5RJR8	LQQLPADFGR	1.947168197	2	2.320665359
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.09242059**	**0.42073**	**3**
Q5RKI0	YAPSGFYIASGDISGK	1.123377861	2	4.160158634
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	0.993973564	3	5.274300098
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	0.649126236	3	3.737568617
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.117022729**	**2.8E-09**	**5**
Q5RKI1	ELAQQIQK	1.139452591	1	2.174785376
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.007748331	2	4.738516331
Q5RKI1	GYDVIAQAQSGTGK	1.199479325	2	5.208706856
Q5RKI1	MFVLDEADEMLSR	1.038706459	2	4.724527836
Q5RKI1	VLITTDLLAR	1.269305294	2	2.416933537
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.070226158**	**0.38476**	**11**
Q5SGE0	AALDLEQVPSELAVTR	1.237813421	2	3.873970747
Q5SGE0	CIANNQVETLEK	1.208039451	2	3.062364817
Q5SGE0	HCVTMDTPAEK	1.31261423	2	3.191393852
Q5SGE0	HDNAEDALNLK	1.059197857	2	3.737994909
Q5SGE0	LKAEGHPVGDPLK	1.658165337	2	2.434809685
Q5SGE0	MEGANIQPNR	1.140820805	2	2.596491575
Q5SGE0	SCGSLLPELSLAER	1.078655724	2	2.495158434
Q5SGE0	SSLSSSSPSAGDTVTEK	1.068535234	2	4.365277767
Q5SGE0	SYVADKDVASAK	1.067484797	2	3.387579679
Q5SGE0	TLLELIPELR	1.207310387	2	2.494793415
Q5SGE0	VQDAINILK	1.085970978	2	2.305063725
Q5SVT3	**ETAA1 Ewing_s tumor_associated antigen 1 homolog**	**1.084442319**	**0.34177**	**2**
Q5SVT3	ELMKLAQQFDK+Oxidation(3)	0.96138284	2	2.508353949
Q5SVT3	NHDFIQMTSKMGHLDNHK+Oxidation(7)Oxidation(11)	3.814094161	2	2.48525095
Q5SX40	**MYH1 Myosin_1**	**0.617812541**	**6.5E-12**	**75**
Q5SX40	EQYEEEQEAK	0.166984659	1	3.023170233
Q5SX40	QLEEEIK	1.320473629	1	2.075603485
Q5SX40	SSVFVVDAK	0.436249419	1	2.314751625

Q5SX40	TNAACAALDK	0.622058474	1	1.930557489
Q5SX40	YETDAIQR	0.218447792	1	2.088631153
Q5SX40	AAYLQNLNSADLLK	0.596893085	2	3.600010395
Q5SX40	ADIAESQVNK	0.54390154	2	3.398128033
Q5SX40	AEDEEEINAELTAK	0.551156848	2	3.953575134
Q5SX40	AGLLGLLEEMR	0.693915601	2	3.888468981
Q5SX40	AGLLGLLEEMRDDK	0.930899446	2	3.381224632
Q5SX40	ANLLQAEIEELR	0.502709126	2	4.009237289
Q5SX40	ANSEVAQWR	0.503093783	2	2.323421955
Q5SX40	DLEEATLQHEATAATLR	0.517675891	2	4.936537743
Q5SX40	DTQLHLDDALR	0.426390409	2	2.930723906
Q5SX40	EEQAEPDGTEVADK	0.506437172	2	3.146573544
Q5SX40	ELEGEVENEQK	0.475453484	2	2.963731527
Q5SX40	ELEGEVENEQKR	0.431248117	2	3.183594465
Q5SX40	ELTYQTEEDRK	0.913133372	2	3.142572403
Q5SX40	ENQSILITGESGAGK	0.562074982	2	3.678750277
Q5SX40	GQEDLKEQLAMVER	0.701313849	2	4.081747532
Q5SX40	GQTVQQVYNSVGALAK	0.495334524	2	3.015706301
Q5SX40	GSSFQTVSALFR	0.915063692	2	2.545173645
Q5SX40	HADSVAELGEQIDNLQR	0.474530419	2	5.889241695
Q5SX40	IAEKDEEIDQLKR	1.258839371	2	2.435076237
Q5SX40	IAEQELLDASER	0.484942741	2	3.608406067
Q5SX40	IEAQNKPFDAK	0.560030839	2	2.790340662
Q5SX40	IEDEQALGMQLQK	0.434304431	2	4.429235458
Q5SX40	IEELEEEIEAER	0.381833356	2	4.111586571
Q5SX40	IKLEQQVDDLEGSLEQEK	0.635922969	2	5.079025269
Q5SX40	INQQLDTK	0.979223369	2	2.36048913
Q5SX40	IQHELEEAEER	0.691988434	2	3.649016142
Q5SX40	IQLELNQVK	0.741598298	2	2.908679962
Q5SX40	KIAEQELLDASER	0.611857489	2	4.152240753
Q5SX40	KLEDECSELK	0.562458274	2	2.954327106
Q5SX40	KLETDISQIQGEMEDIVQEAR	0.580885803	2	5.37808609
Q5SX40	LAQESTMDVENDKQQLDEK	0.24135456	2	4.567634106
Q5SX40	LDEAEQLALK	0.589820464	2	3.369658709
Q5SX40	LEDECSELKK	0.59256354	2	3.100575209
Q5SX40	LEEAGGATSAQIEMNK	0.902659729	2	4.744553566
Q5SX40	LEQQVDDLEGSLEQEK	0.5450527	2	5.578268528
Q5SX40	LEQQVDDLEGSLEQEKK	0.838380929	2	4.823029041
Q5SX40	LETDISQIQGEMEDIVQEAR	0.510067669	2	5.121719837
Q5SX40	LINELTAQR	0.574034257	2	2.95327282
Q5SX40	LQDAEEHVEAVNAK	0.414622616	2	4.577136993
Q5SX40	LQDLVDK	0.609187767	2	2.361414194
Q5SX40	LQNEVEDLMIDVER	0.592049322	2	4.472345352

Q5SX40	LQTESGEYSR	0.45151683	2	2.667229891
Q5SX40	MEIDDLASNMEVISK	0.522112799	2	4.394586563
Q5SX40	MEIDDLASNMEVISKSKGNLEK	0.980370687	2	2.430502176
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(1)	0.688411372	2	4.399733543
Q5SX40	NDLQLQVQSEADSLADAEER	0.606707268	2	5.579258442
Q5SX40	NKDPLNETVVGLYQK	0.460203481	2	4.54413271
Q5SX40	NLQQEISDLTEQIAEGGK	0.480247074	2	5.916985512
Q5SX40	NLQQEISDLTEQIAEGGKR	0.59388238	2	4.432350636
Q5SX40	NLTEEMAGLDETIAK	0.502614693	2	5.154585361
Q5SX40	QAEEAEEQSNVNLAK	0.516940583	2	4.427749157
Q5SX40	QKYEETHAELEASQK	0.577442097	2	4.03924799
Q5SX40	QLDEKDSLVSQLSR	0.885963741	2	2.813599348
Q5SX40	QREEQAEPDGTEVADK	0.522023118	2	4.337385178
Q5SX40	SELQAALEEAEASLEHEEGK	0.57141676	2	5.433350563
Q5SX40	TKYETDAIQR	0.610927149	2	3.315425873
Q5SX40	TLEDQVSELK	0.589763659	2	3.179094791
Q5SX40	VKELTYQTEEDRK	1.243069743	2	2.62993288
Q5SX40	VLNASAIPEGQFIDSK	0.504163087	2	4.488241673
Q5SX40	VQLLHTQNTSLINTK	0.453524501	2	4.899279594
Q5SX40	YEETHAELEASQK	0.495411906	2	4.437749386
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	0.533039209	3	6.559906006
Q5SX40	IKLEQQVDDLEGSLEQEKK	0.71320896	3	5.007100582
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	0.462163964	3	4.190873623
Q5SX40	KIQHELEEAEER	0.633278158	3	3.893842459
Q5SX40	KKLETDISQIQGEMEDIVQEAR	0.792500399	3	5.14356041
Q5SX40	KLEDECSELKK	0.477038262	3	4.052670956
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	0.479971791	3	6.60423851
Q5SX40	TNAACAALDKK	0.518895252	3	3.431129932
Q5SX40	VRELEGEVENEQKR	0.687949575	3	3.662515163
Q5TKR9	**KAT6A Histone acetyltransferase KAT6A**	**1.090113217**	**0.56845**	**2**
Q5TKR9	ENKDQDSSSLIESEKKPEVK	0.925426642	2	2.386845112
Q5TKR9	KGYGRFLIDFSYLLSK	1.484331953	2	2.301556826
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.189852418**	**0.00016**	**5**
Q5U206	DTDSEEEIR	0.923322732	2	2.416905165
Q5U206	KMKDTDSEEEIR	1.23501912	2	2.625957727
Q5U206	KMKDTDSEEEIR+Oxidation(2)	1.421294749	2	2.482021809
Q5U206	MKDTDSEEEIR+Oxidation(1)	1.34155275	2	3.440978527
Q5U206	MKDTDSEEEIR	1.051996461	3	4.169401646
Q5U211	**SNX3 Sorting nexin_3**	**1.0044227**	**0.99371**	**2**
Q5U211	GDDGIFDDNFIEER	0.97509745	2	2.869857788
Q5U211	YSDFEWLR	1.053108699	2	2.540637016
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.232675588**	**3.1E-05**	**4**

Q5U2Q7	GFGGIGGILR	1.122975577	2	2.973564148
Q5U2Q7	LSVLGAITSVQQR	1.668434528	2	2.441142082
Q5U2Q7	YFDEISQDTGK	1.05853338	2	2.788476229
Q5U2Q7	YVLHCQGTEEEK	1.40884589	2	3.964041471
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**1.110859006**	**0.99989**	**2**
Q5U2U0	QQAEVEK	1.096364138	1	2.019519329
Q5U2U0	SGESNTHQDIEEKDR	0.940243834	3	3.689881563
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.144136897**	**7.5E-10**	**12**
Q5U300	AENYDISPADR	0.820192441	2	2.444752693
Q5U300	DNPGVVTCLDEAR	0.812059484	2	2.350698709
Q5U300	FEVQGLQPNGEEMTLK	1.013536933	2	2.795833349
Q5U300	FEVQGLQPNGEEMTLK+Oxidation(13)	1.072648265	2	2.438231707
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.262416026	2	5.608586311
Q5U300	LDQPMTEIVSR	1.05841983	2	3.124912977
Q5U300	NEEDATELVTLAQAVNAR	1.194537905	2	5.293211937
Q5U300	NFPNAIEHTLQWAR	1.041919917	2	3.560248137
Q5U300	SLPASLAEPDFVMTDFAK	1.075229911	2	4.069308281
Q5U300	SPPAVQQDNVDEDLIR	1.135794748	2	4.87026453
Q5U300	VVQGHQQLDSYK	1.53018031	2	3.31052804
Q5U300	AAVASLLQSVQVPEFTPK	1.234118711	3	3.422892809
Q5U312	**RAI14 Ankycorbin**	**1.076170544**	**0.71404**	**2**
Q5U312	MHLLYAVQGQMDEDVQKVLK	1.08392435	2	2.340395689
Q5U312	QDLQRALEESK	1.075850633	2	2.439958096
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**1.023487304**	**0.77677**	**2**
Q5U4E6	EFNTQLAQK	1.017274419	2	2.348141909
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(17)	1.131599801	2	2.413443089
Q5XFW8	**SEC13 Protein SEC13 homolog**	**0.97661358**	**0.22884**	**2**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	0.93581355	2	3.583430529
Q5XFW8	LEAHSDWVR	1.413153419	2	2.696453333
Q5XFX0	**TAGL2 Transgelin_2**	**1.047307863**	**0.92943**	**5**
Q5XFX0	DDGLFSGDPNWFPK	0.500455551	2	3.427964449
Q5XFX0	NFSDNQLQEGK	1.054469414	2	3.249543428
Q5XFX0	NVIGLQMGTNR	1.036204262	2	2.775540829
Q5XFX0	TLMNLGGLAVAR	1.042065745	2	3.406979561
Q5XFX0	YGINTTDIFQTVDLWEGK	1.334423639	2	5.0701828
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.099451699**	**2.9E-06**	**11**
Q5XHY5	AEHDSILAEK	1.399205247	2	2.656368971
Q5XHY5	FLGDIEIWNQAEK	0.993508478	2	3.460999489
Q5XHY5	FMVDIDLDPGCTLNK	1.089153313	2	2.4584167
Q5XHY5	FNLTYVSHDGDDK	1.085051951	2	2.677567005
Q5XHY5	GFQEVVTPNIFNSR	1.158162048	2	3.556724072
Q5XHY5	LKAEHDSILAEK	1.0863266	2	3.36677289

Q5XHY5	QLENSLNEFGEK	1.039492796	2	2.901065588
Q5XHY5	QVMVVPVGPTCDEYAQK	1.271958132	2	3.096116304
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.329021047	2	4.006989956
Q5XHY5	VVWDLDRPLETDCTLELLK	1.831340105	2	3.972016096
Q5XHY5	WELNPGDGAFYGPK	1.153486602	2	3.724630356
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.102420598**	**0.00431**	**13**
Q5XHZ0	AFLEALQHQAETSSR	1.160503164	2	4.50467968
Q5XHZ0	AQLLQPTLEINPR	1.184236521	2	3.079290628
Q5XHZ0	EGIVTTAEQDIKEDIAK	0.853890246	2	2.399739265
Q5XHZ0	ELISNASDALEK	0.966481427	2	2.953892231
Q5XHZ0	FEDTSPAGER	0.886017725	2	2.895195246
Q5XHZ0	GTITIQDTGIGMTK	0.960774945	2	2.883798838
Q5XHZ0	GVVDSEDIPLNLSR	1.092206737	2	4.869516373
Q5XHZ0	HLAEHSPYYEAMK	1.211302088	2	3.008198738
Q5XHZ0	SDCKDFANESR	1.106680993	2	2.897912264
Q5XHZ0	YESSALPAGQLTSLSDYASR	1.205395005	2	5.453862667
Q5XHZ0	YIAQAYDKPR	1.269368725	2	2.806532621
Q5XHZ0	LDTHPAMVTVLEMGAAR	0.961709196	3	4.040245533
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	0.984180821	3	4.308713913
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.10462715**	**0.99998**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	1.137091542	2	4.776508331
Q5XI22	HGSNLEAMSK	1.150911027	2	2.444938898
Q5XI22	HGSNLEAMSK+Oxidation(8)	0.922738558	2	3.269510508
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	1.05856286	2	5.249322414
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	0.866630452	2	5.35949707
Q5XI22	VNIDGGAIALGHPLGASGCR	1.095472186	2	5.387734413
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	1.196341761	3	5.158839226
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	1.130869667	3	3.882935286
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	0.890133549	3	4.653283119
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**0.920691193**	**0.00133**	**2**
Q5XI29	QNLSQFEAQAR	0.86291701	2	2.372994661
Q5XI29	SIGVYDVVELK	0.835150406	2	2.58266449
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**0.991594968**	**0.6258**	**6**
Q5XI32	GCWDSIHVVEVQEK	1.327251441	2	3.209188223
Q5XI32	KLEVEANNAFDQYR	1.082662114	2	4.140471935
Q5XI32	LEVEANNAFDQYR	0.933729193	2	3.576242924
Q5XI32	LVEDMENK	1.084182274	2	2.756031513
Q5XI32	NDLVEALK	1.004035035	2	2.575969934
Q5XI32	SGSGTMNLGGSLTR	1.066452628	2	3.255939007
Q5XI41	**TRAM1 Translocating chain_associated membrane protein 1**	**0.947182211**	**0.99106**	**2**
Q5XI41	EHSAFQAPPVK	0.940251083	2	2.350444078
Q5XI41	LDFSTGNFNVLAVR	1.047547222	2	3.066029787

Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.435076091**	**0.61558**	**3**
Q5XI60	ALDIAAGITR	1.061839414	2	2.564697504
Q5XI60	HHVALDSAASQLSGR	1.448836814	2	4.519289494
Q5XI60	NVATDALGALEAR	1.259647465	2	4.045724392
Q5XI72	**IF4H Eukaryotic translation initiation factor 4H**	**1.127717534**	**0.48164**	**2**
Q5XI72	EALTYDGALLGDRSLR	1.301540973	2	2.601260424
Q5XI72	SLRVDIAEGRK	0.970031971	2	2.436845779
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.106668174**	**0.21917**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.193341235	2	4.116736889
Q5XI73	IDKTDYMVGSYGPR	1.107300667	2	4.006309986
Q5XI73	SIQEIQELDKDDESLR	1.089269646	2	5.290998936
Q5XI73	SIQEIQELDKDDESLRK	1.095800784	2	4.151248455
Q5XI73	VAVSADPNVPNVIVTR	1.246220718	2	4.108188629
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	1.899043489	3	3.450900793
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**0.932140027**	**0.96843**	**13**
Q5XI78	FGLEGCEVLIPALK	0.995663505	2	2.964377165
Q5XI78	ICEEAFTR	1.003904207	2	2.41024375
Q5XI78	IEQLSPFPFDLLLK	1.071896167	2	3.37631321
Q5XI78	LEAADEGSGDMK	1.02587153	2	2.893482208
Q5XI78	LNVLANVIR	1.353004896	2	2.531419516
Q5XI78	NITLSLVANPSHLEAADPVVMGK	0.843618692	2	4.911587715
Q5XI78	NTNAGAPPGTAYQSPLSLSR	1.137158617	2	3.81319356
Q5XI78	SWDIFFR	0.976870505	2	2.337411165
Q5XI78	VIPEDGPAAQNPDK	0.926824664	2	2.702236176
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.167037009	3	5.040868759
Q5XI78	HHVLHDQNVDK	0.590031472	3	3.372943163
Q5XI78	SSLATMAHAQSLVEAQPNVDK	0.554822897	3	3.906039953
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	0.789428142	3	4.370318413
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**1.139416332**	**0.96783**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	1.315677475	2	3.647271395
Q5XI95	IIAVDINK	1.209247457	2	2.788011074
Q5XI95	MVATGVCGTDIK	1.014317144	2	2.684589148
Q5XI95	NNICTEIR	1.083747725	2	2.409723759
Q5XI95	TVGATDCVDPR	1.098483096	2	2.972200394
Q5XIA0	**DZI1L Zinc finger protein DZIP1L**	**1.062312549**	**0.8398**	**2**
Q5XIA0	EVCNHCRQPVDPVLLK	1.062322399	2	2.368977785
Q5XIA0	GQQELGRQADELK	1.062312079	2	2.443547249
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.110943949**	**0.99993**	**6**
Q5XIC0	ATQQDFENAMNQVK	0.941155253	2	4.523313522
Q5XIC0	GILVTSEGGITK	1.050955501	2	3.42509079
Q5XIC0	LHAVNEEECTTLR	1.089349472	2	4.136922359
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.892894638	2	5.114122868
Q5XIC0	WDAWNALGSLPK	1.126397986	2	3.436161041

Q5XIC0	WLSEECINAIMSFVTR	0.870323069	2	2.360720634
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.164775571**	**0.08663**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	1.548399771	2	2.617502213
Q5XIC1	VEGTPNDPNPNDPR	0.658905892	2	2.602965117
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.18118514**	**0.61119**	**7**
Q5XIE6	AGIATHFVDSEK	0.708304415	2	3.238562584
Q5XIE6	AVLIDKDQTPK	1.179298695	2	2.972886801
Q5XIE6	GCAGVITLNRPK	1.014725372	2	2.686513901
Q5XIE6	HTETAEVLLER	1.098555951	2	2.575521708
Q5XIE6	INSCFSANTVEQILENLR	1.08949061	2	4.727361679
Q5XIE6	QDGSPFAMEQIK	1.171324912	2	2.56450963
Q5XIE6	LHVLEEELLALK	1.186971753	3	4.61975193
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.132542109**	**0.80544**	**2**
Q5XIF3	HGWSYDVEGR	1.111503618	2	2.699670553
Q5XIF3	LDVTPLTGVPEEHIK	1.153597955	2	3.45411396
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**0.979458309**	**0.91582**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	0.946252012	2	4.140595913
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.028618575	2	5.47256279
Q5XIF6	DVNAAIAAIK	0.876636619	2	2.904357433
Q5XIF6	SIQFVDWCPTGFK	1.063585504	2	4.451962948
Q5XIF6	TIGGGDDSFTTFFCETGAGK	0.78841158	2	4.260843277
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.092416414**	**0.76067**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	1.172812501	2	3.766812325
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.043462586	2	5.155099869
Q5XIH7	**PHB2 Prohibitin_2**	**1.018453017**	**0.03947**	**10**
Q5XIH7	AQVSLLIR	1.244709068	2	2.34243083
Q5XIH7	DLQMVNISLR	0.723417619	2	3.089460373
Q5XIH7	FNASQLITQR	1.049292537	2	3.761054277
Q5XIH7	IVQAEGEAEAAK	1.058361871	2	3.871401548
Q5XIH7	IYLTADNLVLNLQDESFTR	2.016769811	2	4.736650944
Q5XIH7	LGLDYEER	1.180347307	2	2.304040194
Q5XIH7	LLLGAGAVAYGVR	3.370458279	2	3.473404408
Q5XIH7	VLPSIVNEVLK	0.904010008	2	2.730412722
Q5XIH7	VLSRPNAQELPSMYQR	1.179829251	2	4.583477497
Q5XIH7	IGGVQQDTILAEGLHFR	1.364807042	3	4.201953888
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.202193327**	**0.00595**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	1.067126114	2	4.206585884
Q5XIM9	GATQQILDEAER	1.184934851	2	3.968919039
Q5XIM9	GSGNLEAIHVIK	1.155960397	2	2.64897275
Q5XIM9	HGINCFINR	1.276389995	2	2.617143393
Q5XIM9	LGGSLADSYLDEGFLLDK	1.381923683	2	4.147614956

Q5XIM9	SLHDALCVLAQTVK	1.688514845	2	3.571403027
Q5XIM9	VAEIEHAEKEK	1.590087287	2	2.448612213
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.203961016	2	4.745425701
Q5XIM9	LGGSLADSYLDEGFLLDKK	1.099606509	3	3.313374996
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.030629095**	**0.81736**	**10**
Q5XIN6	AAEVEGEQVDNK	1.127542706	2	4.090139866
Q5XIN6	AMYLPDTLSPADQLK	1.52383221	2	2.315105677
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.902891441	2	4.612581253
Q5XIN6	FLQDTIEEMALK	1.193595226	2	2.910087824
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.059197297	2	3.955680132
Q5XIN6	LEEGGPVYSPPAQVVVK	0.986585152	2	2.781867027
Q5XIN6	LLELQSIGTNNFLR	1.025276221	2	3.352968693
Q5XIN6	STLQTLPEIVAK	1.050297093	2	2.385340929
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	1.067539892	3	4.759286404
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.225910671	3	4.837278366
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**1.134991697**	**0.04806**	**7**
Q5XIT9	AATGEEVSAEDLGGADLHCR	1.19205197	2	5.007183075
Q5XIT9	ALYGDTLVTGFAR	1.147326955	2	3.111362457
Q5XIT9	AQEIALQNR	0.831605742	2	2.566584587
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.162908265	2	4.940058708
Q5XIT9	LWDDGIIDPVDTR	1.08841213	2	3.15926218
Q5XIT9	LYGEEEVPAGGIITGIGR	1.075832186	2	4.553246498
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.213730328	3	4.910382271
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.153211206**	**0.53264**	**5**
Q5XIU9	GLATFCLDK	1.085540886	1	1.957779408
Q5XIU9	VFDVTK	1.212500858	1	2.0025599
Q5XIU9	FYGPAGPYGIFAGR	1.126476206	2	2.888855696
Q5XIU9	GGDGSPGGAGATAAR	1.116379257	2	3.209258795
Q5XIU9	GLCSGPGAGEESPAATLPR	1.118072509	2	4.802998543
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**1.005776054**	**3.3E-06**	**6**
Q60587	AMDSDWFAQNYMGR	0.964253605	2	3.214321613
Q60587	AQDEGHLSDIVPFK	1.238179196	2	3.329460859
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	1.038360176	2	5.268391609
Q60587	DNGIRPSSLEQMAK	1.010121633	2	3.615104198
Q60587	DQLLLGPTYATPK	0.67356696	2	3.727067232
Q60587	NIVVVEGVR	1.077652029	2	3.009549379
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.169796126**	**0.76917**	**5**
Q60759	DILGGNGISDEYHVIR	0.764585341	2	3.224007845
Q60759	DIVYEMGELGVLGPTIK	1.204227087	2	3.029067993
Q60759	GYGCAGVSSVAYGLLTR	0.942259338	2	3.981208324
Q60759	SMMSVQSSLVMHPIYTYGSEEQR	1.096128026	3	3.839382172

Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.1468126	4	5.464575291
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**0.853372844**	**1**	**2**
Q60817	IEDLSQQAQLAAAEK	1.035405973	2	4.552981377
Q60817	NILFVITKPDVYK	0.988401546	2	3.547375917
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.951890333**	**0.99468**	**3**
Q61029	SELVANNVTLPAGEQR	0.912062298	2	4.079693317
Q61029	SSTPLPTVSSSAENTR	0.991948396	2	2.9060812
Q61029	YGVNPGPIVGTTR	1.094994437	2	3.07916069
Q61043	**NIN Ninein**	**0.791095526**	**0.64533**	**2**
Q61043	ERATAAAMKQEQEILER	0.794761065	2	2.335002422
Q61043	LQEENSILR	0.66225603	2	2.403963327
Q61233	**PLSL Plastin_2**	**1.018647073**	**0.99968**	**2**
Q61233	ALENDPDCR	0.993617662	2	2.519220591
Q61233	MINLSVPDTIDER	1.027065669	2	3.581685543
Q61301	**CTNA2 Catenin alpha_2**	**1.131847415**	**0.06972**	**2**
Q61301	LLEPLVTQVTTLVNTSNK	1.232296171	2	4.043756008
Q61301	TSVQTEDDQLIAGQSAR	1.0451857	2	4.621164799
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.999076383**	**0.99903**	**5**
Q61335	AENEALAMQK	1.035459279	2	3.055585384
Q61335	LKDELASTK	0.872379252	2	2.622096539
Q61335	YMEENDQLK	1.054731038	2	2.410335064
Q61335	YMEENDQLKK	0.957034248	2	2.565962553
Q61335	KYMEENDQLKK+Oxidation(3)	1.050287907	3	3.365251541
Q61599	**GDIR2 Rho GDP_dissociation inhibitor 2**	**1.129967761**	**0.1352**	**2**
Q61599	TLLGDVPVVADPTVPNVTVTR	1.024741615	2	4.638727665
Q61599	ATFMVGSYGPRPEEYEFLTPVEEAPK	1.661595475	3	3.62484026
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**0.99618345**	**0.98849**	**3**
Q61656	ELAQQVQQVAAEYCR	0.898563433	2	2.663357496
Q61656	GDGPICLVLAPTR	1.011773881	2	3.425886393
Q61656	MLDMGFEPQIR	0.917716807	2	3.380897045
Q61830	**MRC1 Macrophage mannose receptor 1**	**1.16006822**	**0.4006**	**3**
Q61830	KMDPQPK+Oxidation(2)	1.160877877	1	1.915970087
Q61830	LKLPWHEAETYCK	1.098950819	2	2.302882671
Q61830	TGVAGGLWDVLSCEEK	1.21358273	2	3.16429615
Q61941	**NNTM NAD(P) transhydrogenase_ mitochondrial**	**1.17510732**	**0.9955**	**11**
Q61941	EANSIVITPGYGLCAAK	1.144485584	2	3.640205622
Q61941	FFTGQITAAGK	1.177736991	2	2.432063341
Q61941	GITHIGYTDLPSR	1.053183682	2	3.553814173
Q61941	ILIVGGGVAGLASAGAAK	1.423041437	2	4.577931881
Q61941	KTTVLAMDQVPR	0.979982476	2	3.498476505
Q61941	MATQASTLYSNNITK	0.876341129	2	4.33093214
Q61941	QGFNVVVESGAGEASK	0.937944714	2	3.865109921

Q61941	SAPLLLPGR	1.65176437	2	2.34673357
Q61941	SLGAEPLEVDLK	1.181637509	2	3.06028986
Q61941	TTVLAMDQVPR	1.168318422	2	2.755830288
Q61941	VTIAQGYDALSSMANISGYK	1.125699195	2	5.380628109
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**1.182200685**	**0.56575**	**2**
Q61990	AITIAGIPQSIIECVK	1.182181738	2	2.332728863
Q61990	IITLAGPTNAIFK	1.210574162	2	2.730564594
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.216821039**	**7E-12**	**4**
Q62095	SFLLDLLNATGK	1.307808992	2	3.900295734
Q62095	VGNLGLATSFFNER	1.587001585	2	2.774291754
Q62095	VGSTSENITQK	1.186455828	2	2.935770273
Q62095	HVINFDLPSDIEEYVHR	1.411176032	3	4.260271549
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.1739265**	**3.7E-12**	**17**
Q62261	LISDINK	0.741404923	1	1.950804472
Q62261	ALVADSHPESER	1.100736899	2	3.275490284
Q62261	EGMQLISEKPETEAVVK	0.964332832	2	2.82314539
Q62261	EGMQLISEKPETEAVVKEK	1.258467416	2	2.388931513
Q62261	EIEELQSQAQALSQEGK	1.518117828	2	2.821334839
Q62261	FESLEPEMNNQASR	1.06887036	2	3.53976655
Q62261	HDTSASTQSTPASSR	1.528985586	2	2.796015739
Q62261	LLDPEDISVDHPDEK	1.282570061	2	3.356891155
Q62261	LTTLELLEVR	1.804962165	2	2.565802574
Q62261	LVSDGNINSDR	1.215943475	2	2.82438612
Q62261	LVSQDNFGFDLPAVEAATK	0.917967065	2	3.907705545
Q62261	SQNIITDSSSLNAEAIR	1.416388197	2	4.990614414
Q62261	TLETPAAQMEGFLNR	1.906899139	2	2.652644157
Q62261	TQTAIASEDMPNTLTEAEK	1.155781506	2	5.539876461
Q62261	VIESTQDLGNDLAGVMALQR	0.224792418	2	3.834308863
Q62261	HQILEQAVEDYAETVHQLSK	1.013513424	3	6.188471794
Q62261	LEDLEVIQHR	0.852423282	3	3.358629942
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**0.87084605**	**0.17269**	**3**
Q62425	FYSVNVDYSK	1.062451728	1	2.602736235
Q62425	KNNPEPWNK	1.108290657	2	2.566680193
Q62425	LGPNEQYK	1.099521758	2	2.344420671
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.157847211**	**0.99293**	**5**
Q62452	AMEIAEALGR	0.959927166	2	3.624193907
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(11)	1.047131737	2	3.569714546
Q62452	WLPQNDLLGHPK	1.111532363	2	3.349861145
Q62452	YTGTRPSNLAK	1.025227117	2	2.981249332
Q62452	GAGVTLNVLEMTADDLENALK	1.014145444	3	5.889406681
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.095046827**	**0.90295**	**6**
Q62465	ACGLNFADLMGR	1.340170723	2	2.804127216

Q62465	GVDIVMDPLGGSDTAK	1.106521155	2	4.182638645
Q62465	IDSVWPFEK	1.117152142	2	2.359446764
Q62465	TVENVTVFGTASASK	1.052075755	2	3.25393343
Q62465	VLLVPGPEKET	1.136212673	2	2.705144644
Q62465	VVTYGMANLLTGPK	1.060457454	2	2.539130926
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.210587385**	**0.03101**	**2**
Q62636	INVNEIFYDLVR	1.449742361	2	3.974482536
Q62636	LVVLGSGGVGK	1.071888289	2	2.551850319
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**1.018436937**	**0.88488**	**6**
Q62651	EVDVGLAADVGTLQR	0.740670281	2	3.360381126
Q62651	HVLHVQLNRPEK	1.152878084	2	3.43016696
Q62651	MMADEALDSGLVSR	1.055992298	2	3.351325035
Q62651	SLVNELTFTAR	1.008908593	2	3.5063622
Q62651	YCTQDAFFQVK	2.132415883	2	2.714946747
Q62651	RIPEEVSDHNYESIQVTSAQK	0.98615841	3	6.449939728
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**0.921322249**	**0.76633**	**5**
Q62730	AVLVTGADSGFGHALAK	0.864596437	2	4.189218044
Q62730	EIQENYGQEYVHTQK	0.749839021	2	4.520549774
Q62730	LSVLQMDVTKPEQIK	1.182743999	2	3.635671854
Q62730	VVTIHPGGFQTNIVGSQDSWDK	0.806803529	2	5.586349487
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.899237855	3	4.227124691
Q62736	**CALD1 Non_muscle caldesmon**	**0.840446708**	**2.2E-16**	**11**
Q62736	EEIERR	0.653322416	1	1.903689504
Q62736	ASGDKEAEGAPQVEAGK	1.230742524	2	4.617053032
Q62736	EFDPTITDGSLSVPSR	0.837773683	2	3.188447714
Q62736	GGNLGENQIKDEK	1.137572079	2	3.314880848
Q62736	LEQYTNAIEGTK	1.177776309	2	3.591938257
Q62736	NDDDEEEAAR	4.40885659	2	2.714674473
Q62736	RGETESEEFEK	1.228376736	2	2.935166121
Q62736	RRGETESEEFEK	1.435056788	2	3.227398634
Q62736	VLEEEEQR	1.19180108	2	2.494880915
Q62736	ASGDKEAEGAPQVEAGKR	1.306933687	3	3.80129981
Q62736	MQNNSAENETAEGEEKGESR	0.830571159	3	4.60929966
Q62745	**CD81 CD81 antigen**	**1.099087946**	**0.55614**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.188675696	2	2.900876522
Q62745	QFYDQALQQAVMDDDANNAK	1.041853022	2	4.603666306
Q62769	**UN13B Protein unc_13 homolog B**	**1.077327062**	**0.95154**	**2**
Q62769	SNDEVAREFVK	1.081060307	1	2.040540218
Q62769	DHMVREETRNLTPK	1.069637724	2	2.525531292
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.285955988**	**0.46503**	**5**
Q62785	ANEEDEQEEGGDGASGDPK	0.918336315	2	4.618529797
Q62785	GVEGLIDIENPNR	0.984919147	2	2.349184752

Q62785	KVTQLDLDGPK	0.774300892	2	2.468475103
Q62785	YMKMHLAGKTEQAK	1.104994437	2	2.437740326
Q62785	ANEEDEQEEGGDGASGDPKK	1.351533211	3	3.306435347
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.158616455**	**1.8E-10**	**2**
Q62789	IILDELVQR	1.417463745	2	3.632585764
Q62789	WIPQNDLLGHPK	1.111532363	2	3.349861145
Q62812	**MYH9 Myosin_9**	**1.051377298**	**9.9E-20**	**61**
Q62812	CQYLQAEK	1.374561066	1	1.930441737
Q62812	EEILAQAK	1.096833332	1	2.235195875
Q62812	ADFCIIHYAGK	0.842302439	2	2.697236538
Q62812	ALEEAMEQK	1.206908505	2	2.726024866
Q62812	ALELDSNLYR	1.218046956	2	3.554942846
Q62812	ALEQQVEEMK	0.815556147	2	3.012245178
Q62812	ANLQIDQINTDLNLER	1.274886241	2	4.797300339
Q62812	ASIAALEAK	1.202688013	2	2.336327076
Q62812	ASREEILAQAK	0.754983876	2	3.121592522
Q62812	DLEAHIDTANK	0.830766753	2	3.638653755
Q62812	DLQGRDEQSEEK	1.173379875	2	3.215069532
Q62812	ELEDATETADAMNR	1.015965091	2	4.239623547
Q62812	ELETQISELQEDLESER	1.030387883	2	4.973768234
Q62812	HEAMITDLEER	1.180061422	2	3.434575081
Q62812	HEDELLAK	1.293000256	2	3.225544214
Q62812	HSQAVEELAEQLEQTK	1.185295251	2	4.910439968
Q62812	IIGLDQVAGMSETALPGAFK	1.446084563	2	5.89154768
Q62812	IRELETQISELQEDLESER	1.191044131	2	5.164258957
Q62812	KEEELQAALAR	1.196867208	2	3.276796103
Q62812	KKVEAQLQELQVK	1.26980592	2	4.72319603
Q62812	KLEEDQIIMEDQNCK	1.074932843	2	5.685668468
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.192557776	2	5.746975899
Q62812	KQELEEICHDLEAR	1.150578746	2	4.544197559
Q62812	KVEAQLQELQVK	1.27861851	2	3.943715572
Q62812	LEEDQIIMEDQNCK	1.24950925	2	3.328718424
Q62812	LEGDSTDLSDQIAELQAQIAELK	1.150308716	2	4.971636295
Q62812	LEVNLQAMK	1.243353784	2	2.677559376
Q62812	LQEMESAVK	1.040721972	2	2.417757988
Q62812	LQQELDDLLVDLDHQR	0.910763964	2	4.713189602
Q62812	LQVELDSVTGLLNQSDSK	1.144328116	2	5.706380367
Q62812	LTEMETMQSQLMAEK	1.112495873	2	4.405055046
Q62812	MEDGVGCLETAEEAK	0.823816967	2	4.594924927
Q62812	MQQNIQELEEQLEEEESAR	1.003666552	2	5.940896988
Q62812	NAEQFKDQADK	1.513057896	2	3.643934965
Q62812	NLPIYSEEIVDMYK	1.358450375	2	3.280553102
Q62812	NMDPLNDNIATLLHQSSDK	1.227187802	2	5.059238911

Q62812	NTDQASMPDNTAAQK	1.073030279	2	5.31372261
Q62812	NTDQASMPDNTAAQK+Oxidation(7)	1.420808628	2	4.89611578
Q62812	QIATLHAQVTDMK	0.726426029	2	2.362208366
Q62812	QLEEAEEEAQR	1.099910455	2	3.495079517
Q62812	QSVSNLEK	1.125418986	2	2.401685953
Q62812	QTLENERGELANEVK	1.207552282	2	3.404907465
Q62812	RGDMPFVVTR	1.124072213	2	2.630325079
Q62812	RQLEEAEEEAQR	1.295416397	2	4.263204098
Q62812	SMEAEMIQLQEELAAAER	1.045265089	2	4.524121284
Q62812	TDLLLEPYNK	1.294006649	2	2.681063414
Q62812	TELEDTLDSTAAQQELR	1.018093805	2	5.48874712
Q62812	THEAQIQEMR	1.155407074	2	3.475738764
Q62812	TQLEELEDELQATEDAK	1.064390347	2	6.67947197
Q62812	VAEFTTDLMEEEEK	1.141287526	2	4.222003937
Q62812	VEAQLQELQVK	1.468716755	2	3.675487995
Q62812	VEDMAELTCLNEASVLHNLK	1.284101788	2	4.317490101
Q62812	VISGVLQLGNIVFK	1.251181678	2	3.653894186
Q62812	VSHLLGINVTDFTR	1.30051776	2	3.692348957
Q62812	YEILTPNSIPK	1.043528758	2	3.248054028
Q62812	DFSALESQLQDTQELLQEENR	1.115422348	3	6.353455067
Q62812	HSQAVEELAEQLEQTKR	1.169396924	3	5.717298031
Q62812	LDPHLVLDQLR	1.393330506	3	3.410103559
Q62812	NKHEAMITDLEER	1.245332359	3	3.668581963
Q62812	QAQQERDELADEIANSSGK	1.155095757	3	4.15320015
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.089463829	3	5.664568901
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**0.995859057**	**0.10731**	**8**
Q62826	VGSEIER	1.064499058	1	1.963758111
Q62826	ADILEDKDGK	1.209860099	2	2.677770615
Q62826	AFITNIPFDVK	0.974170291	2	3.136331797
Q62826	GIGMGNLGPAGMGMEGIGFGINK	1.141145782	2	4.880948544
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.075398209	2	4.889839172
Q62826	INEILSNALK	1.157194634	2	2.345985651
Q62826	MGANNLERMGLERMGANSLER	1.043331239	2	2.40319252
Q62826	MGPVMDRMATGLER+Oxidation(1)Oxidation(5)Oxidation(8)	1.003202624	2	2.576577663
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.379695794**	**0.03415**	**2**
Q62871	ADAEEEAATR	1.442742563	2	2.630241156
Q62871	SVSTPSEAGSQDSGDGAVGSR	1.344344139	2	5.35132122
Q62902	**LMAN1 Protein ERGIC_53**	**1.122745716**	**6.8E-05**	**5**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.117551908	2	4.28385973
Q62902	GHPDLQGQPADDIFESIGDR	0.99809441	2	5.221512794
Q62902	YQEEFEHFQQELDK	1.215694598	2	5.12994194
Q62902	YVSSLTEEISR	1.213750633	2	2.651608467

Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.407297367	3	4.137228966
Q62910	**SYNJ1 Synaptojanin_1**	**0.365725508**	**0.10672**	**2**
Q62910	MLIQLPSASQSK+Oxidation(1)	0.399018789	2	2.316416979
Q62910	NQTLTDWLLDAPK	0.306490031	2	2.489532232
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.942270632**	**1**	**2**
Q62967	GLQVAPVLLSDELK	0.933961363	2	3.370207548
Q62967	VYGVEGDLSEVAR	1.006078661	2	3.287140846
Q63041	**A1M Alpha_1_macroglobulin**	**1.218818638**	**0.96871**	**13**
Q63041	AEDITHNGIVYTPK	1.024873109	2	3.351067066
Q63041	AEQGAYLGPLPYK	0.924821186	2	3.04494977
Q63041	DLSSSDLTTASK	0.601178226	2	2.513082743
Q63041	DTVVKPVIVEPEGIEK	0.787282669	2	3.032286167
Q63041	GSIFNSGSHVLPLEQGK	1.143697133	2	4.036331177
Q63041	HSQGNTWLTAFVLK	0.915857019	2	2.356443405
Q63041	IKEDGTGIELTGTGSCEIANTLSK	1.182704353	2	3.89410615
Q63041	KLQDQSNIQR	1.149988612	2	2.47674799
Q63041	LIVYTILPNEELIADVQK	1.474913552	2	4.530250549
Q63041	LQDQSNIQR	0.998134373	2	2.799537182
Q63041	QDLNDNDAYSVFQSIGLK	0.847961959	2	2.663622856
Q63041	YNILPEAEGEAPFTLK	0.947332752	2	4.227367401
Q63041	YVVLVPSELYAGVPEK	0.763311876	2	3.212722063
Q63060	**GLPK Glycerol kinase**	**1.334081757**	**9.9E-20**	**11**
Q63060	AVLGPLVGAVDQGTSSTR	1.031492884	2	5.486318111
Q63060	CVFSEHGLLTTVAYK	1.248511032	2	4.279586315
Q63060	DCGIPLSHLQVDGGMTSNK	0.863696753	2	4.20494175
Q63060	EILQSVYECIEK	0.958617049	2	3.849361658
Q63060	FEPQINAEESEIR	1.24999898	2	3.58185482
Q63060	KVQEAVEENR	1.497059718	2	3.560523748
Q63060	LGQLNIDISNIK	2.24542752	2	3.327306986
Q63060	NTYGTGCFLLCNTGHK	1.364296499	2	3.939956188
Q63060	VQEAVEENR	1.150911027	2	3.373373747
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.25340323	3	4.299882889
Q63060	TAELLSHHQVEIK	1.60157258	3	3.769693613
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**0.95728868**	**0.91041**	**10**
Q63081	GESPVDYDGGR	1.105413332	2	2.916925669
Q63081	GSFSEQGINEFLR	1.040646998	2	4.108110428
Q63081	GSTAPVGGGSFPNITPR	1.106287417	2	4.826847553
Q63081	HQSLGGQYGVQGFPTIK	1.133176358	2	5.030941486
Q63081	NLEPEWAAAATEVK	1.089149156	2	4.19713974
Q63081	NSYLEVLLK	1.055763423	2	2.982584476
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.171797307	2	5.073419094
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.135878315	3	6.054111958
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.991908036	3	5.39329195

Q63081	TGEAIVDAALSALR	1.033324162	3	4.717514038
Q63108	**EST3 Liver carboxylesterase 3**	**0.990484311**	**0.94743**	**4**
Q63108	GGTSKEEINLSK	1.118260358	2	3.727011681
Q63108	LDPMTATSLLK	0.916297196	2	2.443587303
Q63108	QKTEEELLETTLK	0.942620735	2	3.445750475
Q63108	SSFLLNLPEEAIPVAVEK	1.11380739	2	4.76671648
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.058910057**	**2.6E-09**	**4**
Q63120	NIQVQNMKNK	1.042759178	1	1.901636481
Q63120	ACALLPDLEILPGGDMAEIGEK	1.469507057	2	4.246836662
Q63120	YFAWEPSFQEQVQGIR	1.437751006	2	4.454555511
Q63120	YLGGDDLDTSAIR	0.511845749	2	2.568296432
Q63150	**DPYS Dihydropyrimidinase**	**0.956749339**	**0.77266**	**9**
Q63150	ALGKDDFTK	1.065396812	2	2.642771006
Q63150	DQTCTPIPVKR	0.902401453	2	2.496285439
Q63150	EIGAIAQVHAENGDLIAEGAK	1.0858343	2	5.153172016
Q63150	FVAVTSTNAAK	1.023865847	2	2.97909832
Q63150	GSSLIEAFETWR	1.118894917	2	3.184033155
Q63150	VVNDDFSQVADVLVEDGVVR	1.069070852	2	5.937115669
Q63150	VVYEAGVFDVTAGHGK	1.1636923	2	4.235015392
Q63150	VVYGEPIAAGLGTDGTQYWNK	0.944633295	2	5.366512299
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	1.052743826	3	3.717774868
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.124420354**	**2E-11**	**18**
Q63270	NCDEFLVK	1.310389529	1	2.239323139
Q63270	NQDLEFER	1.11820516	1	2.658351898
Q63270	SWNALAAPSEK	1.098079338	1	2.300641298
Q63270	AVEAGLNVKPYVK	1.242143819	2	2.67434144
Q63270	DFSDSSQDPDFTQVVELDLK	0.770152087	2	4.954069138
Q63270	FVEFFGPGVAQLSIADR	1.088606544	2	5.336707115
Q63270	GFQVAPDHHNDHK	1.400090214	2	3.448931694
Q63270	IIPPGSGIIHQVNLEYLAR	1.702603465	2	3.466883183
Q63270	NDIENILNWSIMQHK	1.223594557	2	3.17455554
Q63270	SIEVPFKPAR	1.109076322	2	2.500580549
Q63270	TSLSPGSGVVTYYLR	1.165304749	2	3.135689259
Q63270	VILQDFTGVPAVVDFAAMR	0.924973387	2	4.651241302
Q63270	YQQAGLPLIVLAGK	1.116518476	2	3.757121801
Q63270	IDFEKEPLGVNAQGQQVFLK	1.115788409	3	4.994035244
Q63270	KNDIENILNWSIMQHK	1.157714255	3	4.087688446
Q63270	QAPQTVHLPSGETLDVFDAAER	1.3253802	3	3.655105352
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.453586057	3	4.968088627
Q63270	SPPFFESLTLDLQPPK	0.971596643	3	3.593346834
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.011659878**	**0.02254**	**17**
Q63276	AHGHFLFVVGEDDKNLNSK	1.503149107	2	6.101480007

Q63276	ASEVGEVDLER	1.022811374	2	3.940260172
Q63276	DDKGNLFNSQAFYR	1.22978803	2	3.530853748
Q63276	GNLFNSQAFYR	0.99514255	2	3.188331604
Q63276	LTAVPLSALVDEPVHIR	0.451354822	2	3.872433186
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	0.70588591	2	4.647769451
Q63276	QHLNPGFNSQL	1.323476452	2	3.526279688
Q63276	TFEETADKDSK	1.025521201	2	3.750548124
Q63276	VDLEYFEEGVEFLLR	1.157537315	2	4.404406548
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.381801208	2	5.603541374
Q63276	VISSSLDSLILER	1.033363017	2	4.403005123
Q63276	WYVAPGVTR	1.030206534	2	2.64707303
Q63276	YCFPIEK	0.971986802	2	2.631840944
Q63276	LCHPYFPVEGK	1.73744131	3	3.466310263
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	0.89605487	3	4.230904102
Q63276	QITATVLINGPNFVSSNPHVYR	1.081188025	3	4.943460464
Q63276	VTGLTPFQVVCLQASLK	1.120187542	3	4.145860195
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.042145066**	**1**	**28**
Q63342	IHYDSIK	1.220231992	1	2.104641199
Q63342	DGLLFGPYESQEK	0.478652401	2	2.606134653
Q63342	EGQESPPSPPEWK	0.731026199	2	2.495781422
Q63342	GGYDVEIR	1.07049369	2	2.435756683
Q63342	GQDSTQLLDHLCANVIPK	1.346754123	2	4.15152216
Q63342	IHELFPLLNMDK	1.045846002	2	2.591301441
Q63342	IMNAGQEEGIDNFGTYALNALR	0.925061193	2	4.847625256
Q63342	ISDIPVTAIR	1.108522392	2	2.757280827
Q63342	ITEHVEAAMEMVPVLK	0.83953834	2	4.025818348
Q63342	LEEETGQVVGFHQPGSIR	1.020986064	2	4.966467381
Q63342	LNKPADFTGK	1.508713781	2	2.655618668
Q63342	LTSEDLSDDVFK	1.179647827	2	3.837613344
Q63342	LVCLTLATDDVDPEGNESVWYK	3.270743776	2	2.872274399
Q63342	NITDELGVLGVAGPYAR	1.115426864	2	5.004398346
Q63342	REDSAALYER	0.961130972	2	3.035499811
Q63342	TNWHATEQYIIEPEK	0.769912937	2	4.165535927
Q63342	VGFTNISHMLTPR	1.272801404	2	3.22311306
Q63342	VGVIDLSPFGK	1.09055118	2	3.227581263
Q63342	VIGNTTSGSYSYSIQK	1.016920296	2	4.547920227
Q63342	WIEEAAVR	1.08753606	2	2.603426933
Q63342	WTTTQYTEAK	1.135144699	2	2.898115158
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	0.992436247	3	4.58571291
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.300716497	3	4.582043171
Q63342	ELFESDLDRITEHVEAAMEMVPVLK	1.113967851	3	4.647511005
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.071234297	3	7.514883518

Q63342	NYPATIIQEPLVLTEPTR	1.08415669	3	4.927755833
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.007324937	3	5.881083012
Q63342	YLSDWILHGEPPFDLIELDPNR	1.152184055	3	4.706014633
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.094325549**	**0.05937**	**8**
Q63347	ALDEGDIALLK	1.181803069	2	2.793187141
Q63347	ESDTGLAPPALWDLAADK	1.075036472	2	2.47637248
Q63347	FDDGAGGDNEVQR	1.120220559	2	4.210432529
Q63347	FVVDLSDQVAPTDIEEGMR	1.28191981	2	3.377626181
Q63347	IINADSEDPK	1.285625444	2	2.835820436
Q63347	QTLQSEQPLQVAR	1.114051181	2	4.129840851
Q63347	QVEDDIQQLLK	0.910265244	2	2.745229244
Q63347	TMLELINQLDGFDPR	1.2637415	2	3.182103872
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**0.92203474**	**0.53441**	**4**
Q63362	YTEQITSEK	1.156881951	1	2.144310236
Q63362	KLENLLQGGEVEEVILQAEK	0.840964551	2	6.272477627
Q63362	LENLLQGGEVEEVILQAEK	0.968666594	2	2.576205492
Q63362	TTGLVGLAVCDTPHER	0.977136012	2	4.149106026
Q63377	**AT1B3 Sodium/potassium_transporting ATPase subunit beta_3**	**1.015915686**	**0.64045**	**2**
Q63377	EENIANIVTYPDDGLIDLK	0.922651767	2	4.445621967
Q63377	LFIYNPTSGEFLGR	1.19165988	2	2.521842957
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**1.184028678**	**0.17685**	**2**
Q63413	GLAITFVSDENDAK	0.333627839	2	2.777574539
Q63413	NCPHIVVGTPGR	1.184121577	2	2.843339443
Q63429	**UBC Polyubiquitin_C**	**1.011903822**	**1**	**2**
Q63429	TITLEVEPSDTIENVK	1.035134313	2	4.819263935
Q63429	TLSDYNIQK	0.988533302	2	2.858415842
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.160052341**	**0.12488**	**12**
Q63448	ADWLDSEAPLAAYR	0.877302784	2	4.197645187
Q63448	EIHALASAGKPLASWTAQR	0.988191971	2	4.542737961
Q63448	FHEHTHSSSVPPSLR	1.160877877	2	2.737631559
Q63448	GGYISGEQTGK	1.245235662	2	3.061327934
Q63448	LGASLGSLSSGR	1.298617281	2	2.564835548
Q63448	NLWAAVLQQSGVLER	1.072669319	2	4.019648075
Q63448	RDSVLWSDIPK	1.628248546	2	2.301288366
Q63448	TIFLDLIELQR	1.487308066	2	3.553589106
Q63448	TVNFLEAYPGILGQK	1.16864707	2	5.401540756
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.599195841	3	4.07204628
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.154264306	3	4.74618578
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.12258511	3	4.77525568
Q63507	**RL14 60S ribosomal protein L14**	**1.473190729**	**0.0316**	**2**
Q63507	CMQLTDFILK	1.471729998	2	2.391203165
Q63507	LVAIVDVIDQNR	1.45860092	2	4.491383076

Q63520	**SYCP3 Synaptonemal complex protein 3**	**0.789160387**	**0.00911**	**2**
Q63520	KVMMETQQQEMANVR	0.789160387	2	2.686218977
Q63520	VMMETQQQEMANVRK	0.789160387	2	2.542192459
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.225812157**	**0.1914**	**3**
Q63524	HEQEYMEVR	1.11781717	2	3.392907381
Q63524	HEQEYMEVR+Oxidation(6)	1.256078346	2	2.49630928
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.117347566	3	4.960169315
Q63525	**NUDC Nuclear migration protein nudC**	**1.119416797**	**3.2E-05**	**4**
Q63525	GQAPVIDGELYNEVK	1.168630393	2	3.240917206
Q63525	LSDLDSETR	1.119415306	2	2.32303524
Q63525	LVTSDPEINTK	1.455883359	2	2.900334358
Q63525	WTQTLSELDLAVPFR	1.066916271	2	2.614911079
Q63556	**SPA3M Serine protease inhibitor A3M (Fragment)**	**0.899354808**	**0.96223**	**2**
Q63556	MQQVEASLQPETLK+Oxidation(1)	0.899429486	2	3.406789064
Q63556	MQQVEASLQPETLKK+Oxidation(1)	0.840821347	2	2.816839218
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.016899569**	**0.27754**	**7**
Q63569	CTDDFNGAQCK	1.210224932	2	3.485991478
Q63569	DSYLILETLPTEYDSR	1.222871249	2	2.466905594
Q63569	MATVWDEAEQDGIGEEVLK	0.908237686	2	3.195255756
Q63569	MNVSPDVNYEELAR	1.125858652	2	3.379712343
Q63569	QTYFLPVIGLVDAEK	0.644560296	2	2.426525831
Q63569	TMLELLNQLDGFQPNTQVK	0.938805472	2	3.714195251
Q63569	AMEVDERPTEQYSDIGGLDK	0.771275761	3	4.717461586
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.02480655**	**0.98307**	**4**
Q63570	FDAQTGADR	1.099139469	2	2.513715506
Q63570	KDEQEHEFYK	1.118817887	2	3.098102331
Q63570	RFDAQTGADR	1.042193193	2	2.650105476
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.015223547	3	5.848505974
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.371128097**	**8.5E-12**	**4**
Q63584	NYEEIAK	1.343790094	1	2.171534777
Q63584	ITDSAGHILYAK	1.385189816	2	3.673077583
Q63584	LEDLSESIVNDFAYMK	1.224914856	2	4.589953899
Q63584	RLEDLSESIVNDFAYMK	1.080604792	2	4.302197456
Q63598	**PLST Plastin_3**	**1.078122017**	**1.5E-05**	**12**
Q63598	AESMLQQADK	0.973070834	2	3.143989563
Q63598	ATDDIIVNWVNGTLSEAGK	1.179217355	2	5.045184612
Q63598	HVIPMNPNTDDLFK	1.032105617	2	3.019182205
Q63598	IDINMSGFNETDDLKR	1.090720669	2	4.2491045
Q63598	INNFSADIK	1.118403809	2	2.494403124
Q63598	KLENCNYAVELGK	0.838260898	2	3.674270391
Q63598	NEALAALLR	1.038651038	2	2.601296663
Q63598	VDLNSNGFICDYELHELFK	1.254224778	2	4.113369942

Q63598	VYALPEDLVEVKPK	1.150325348	2	2.743694782
Q63598	YTLNVMEDLGEGQK	0.87219881	2	3.881883144
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	0.829131356	3	3.488801956
Q63598	YPALTKPENQDIDWTLLEGETR	0.812425355	3	5.238245487
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.10764519**	**0.00221**	**8**
Q63610	AREQAEAEVASLNR	1.716761244	2	2.897412777
Q63610	EQAEAEVASLNR	0.654645845	2	2.577198029
Q63610	IQVLQQQADDAEER	1.20402928	2	5.086588383
Q63610	KIQVLQQQADDAEER	1.0435641	2	4.864339828
Q63610	LVIIEGDLER	1.050200061	2	2.755397797
Q63610	MELQEIQLK	0.934506283	2	2.850198507
Q63610	YSQKEDKYEEEIK	0.963957641	2	4.639174461
Q63610	KLVIIEGDLER	0.968671929	3	3.847391605
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.122060322**	**0.00042**	**11**
Q63617	GQAGPEGVPPAPEEEKK	0.788949764	2	3.50480032
Q63617	LIPEMDQIFTDVEMTTLEK	1.441709181	2	4.675857544
Q63617	LYQPEYQEVSTEEQR	1.195000603	2	4.930164814
Q63617	NINADEAAAMGAVYQAAALSK	0.858917693	2	5.194873333
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.23941461	2	3.869139194
Q63617	TLGGLEMELR	1.122174664	2	2.595779419
Q63617	VAIVKPGVPMEIVLNK	1.37273572	2	2.657951117
Q63617	VEFEELCADLFDR	1.498776757	2	3.590438843
Q63617	VESVFETLVEDSPEEESTLTK	0.772549246	2	3.813996792
Q63617	VLQLINDNTATALSYGVFR	1.262969293	2	5.275783539
Q63617	EGETPDEKESGDKSEAQKPNEK	1.588653509	3	3.545764685
Q63716	**PRDX1 Peroxiredoxin_1**	**1.11394246**	**4.5E-06**	**15**
Q63716	DISLSDYK	0.671509703	1	1.936965227
Q63716	ADEGISFR	1.111907886	2	3.150327206
Q63716	ATAVMPDGQFK	1.119766033	2	2.850000381
Q63716	ATAVMPDGQFK+Oxidation(5)	1.223293833	2	2.337226152
Q63716	KQGGLGPMNIPLVSDPK	1.054113186	2	3.983803749
Q63716	LVQAFQFTDK	2.621910665	2	3.372455359
Q63716	QGGLGPMNIPLVSDPK	1.34277668	2	3.171905279
Q63716	QGGLGPMNIPLVSDPK+Oxidation(7)	1.225551126	2	2.783349752
Q63716	QITINDLPVGR	1.076485199	2	3.339039803
Q63716	RTIAQDYGVLK	1.177995117	2	2.69777751
Q63716	SVDEILR	1.156416917	2	2.489869833
Q63716	TIAQDYGVLK	1.089932782	2	3.460532904
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.102786492	3	6.329619408
Q63716	KQGGLGPMNIPLVSDPKR	0.982823581	3	4.042648315
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.482087534	3	3.91787982
Q63755	**PRDM2 PR domain zinc finger protein 2**	**0.890548701**	**0.66401**	**2**
Q63755	LSFNVELGKMSPNK	0.749740275	2	2.423091888

Q63755	VKAAAATPFQGPFLKE	0.914973819	2	2.301956654
Q63768	**CRK Adapter molecule crk**	**1.090657229**	**0.44106**	**2**
Q63768	IGDQEFDSLPALLEFYK	1.054559336	2	3.627699375
Q63768	VPNAYDKTALALEVGELVK	1.454947515	2	2.908525944
Q63797	**PSME1 Proteasome activator complex subunit 1**	**1.182593736**	**0.7889**	**8**
Q63797	ISELDAFLKEPALNEANLSNLK	0.870267187	2	5.269669533
Q63797	LEGFQTQISK	1.146047404	2	2.62213254
Q63797	QLVHELDEAEYQEIR	1.164782261	2	4.385774612
Q63797	TENLLGSYFPK	1.017155495	2	3.335464239
Q63797	VDVFREDLCSK	1.182967509	2	2.76590538
Q63797	VFELMTSLHTK	1.174231204	2	2.524885654
Q63797	KGDEDDKGPPCGPVNCNEK	1.015730181	3	5.036543369
Q63797	KISELDAFLKEPALNEANLSNLK	1.088596731	3	6.288860321
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.101657396**	**0.16635**	**4**
Q63798	AFYAELHHIISSNLEK	1.159805371	2	3.725074291
Q63798	IEDGNDFGVAIQEK	1.105162573	2	4.526755333
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.731803033	2	4.521368504
Q63798	TKVEAFQTAISK	1.167344971	2	3.447448254
Q63836	**SBP2 Selenium_binding protein 2**	**0.822094361**	**0.20655**	**4**
Q63836	EGSVMLQVDVDTVNGGLK	1.19682043	2	2.562051773
Q63836	GGSVQVLEDQELTCQPEPLVVK	0.888370201	2	5.190620899
Q63836	IYVVDVGSEPR	0.778323481	2	3.773953199
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.016043696	3	4.190232754
Q63862	**MYH11 Myosin_11 (Fragments)**	**0.767932417**	**0.19423**	**2**
Q63862	LQQELDDLVVDLDNQR	0.639612116	2	4.292026043
Q63862	SLEAELMQLQEDLAAAER	1.110583443	2	2.922306538
Q63945	**SET Protein SET**	**1.118045157**	**0.03481**	**2**
Q63945	IDFYFDENPYFENK	1.314680614	2	3.594690084
Q63945	VEVTEFEDIK	1.038120566	2	2.615303755
Q63965	**SFXN1 Sideroflexin_1**	**1.064563749**	**0.12797**	**4**
Q63965	NILLTNEQLENAR	1.006063384	2	4.501932621
Q63965	QGIVPAGLTENELWR	1.043202285	2	2.696221828
Q63965	WDQSTFIGR	0.94697168	2	2.364945889
Q63965	YAYDSAFHPDTGEK	1.255868064	2	4.298267365
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**1.266593133**	**9.9E-20**	**17**
Q64057	DYEETIGK	0.718798127	1	2.055888176
Q64057	AWNIWADIPAPK	1.241479645	2	3.797827244
Q64057	EDNEGVFNGSWGGR	0.667672012	2	3.486234903
Q64057	FKNEEEVFEWNNEVK	1.200382875	2	5.802443981
Q64057	GAPTTSLVSIAVTK	1.105402646	2	4.918702602
Q64057	GEVITTYCPANNEPIAR	1.044479428	2	5.399247169
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.947148315	2	5.85716629

Q64057	LFLHESIHDEVVDR	1.348962907	2	3.966860056
Q64057	NEEEVFEWNNEVK	0.914128872	2	4.560766697
Q64057	QAVSMFVQAVEEAK	0.91873841	2	2.80875349
Q64057	QGLSSSIFTK	1.061165479	2	2.374955893
Q64057	QVALMVQER	1.057797469	2	2.427427769
Q64057	STCTINYSTALPLAQGIK	0.489021018	2	4.965934277
Q64057	VNLLSFTGSTQVGK	1.611717985	2	4.751021385
Q64057	VGNPWDPNILYGPLHTK	1.52285417	3	3.684678316
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.022515099	3	6.065776348
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(2)	1.069606907	3	6.038885117
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**1.024491702**	**0.90828**	**2**
Q640L5	NEKIRSLESNINTEHEK	1.024176538	2	2.378394127
Q640L5	TELEKTTNSVKELER	1.078960268	2	2.333319902
Q64119	**MYL6 Myosin light polypeptide 6**	**1.185556604**	**2E-06**	**7**
Q64119	DQGTYEDYVEGLR	0.789900513	2	3.218517542
Q64119	EGNGTVMGAEIR	0.943398104	2	2.530056477
Q64119	HVLVTLGEK	1.237456509	2	2.56329608
Q64119	ILYSQCGDVMR	1.886204197	2	3.139659643
Q64119	NKDQGTYEDYVEGLR	1.151192809	2	4.282741547
Q64119	VFDKEGNGTVMGAEIR	1.080596942	2	3.972046852
Q64119	VLDFEHFLPMLQTVAK	1.090819617	2	4.96607542
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**1.333590118**	**1.7E-11**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.432633661	2	5.248878956
Q64122	LNGTDPEDVIR	1.281245182	2	2.784110785
Q64176	**EST22 Liver carboxylesterase 22**	**1.080448512**	**0.13512**	**4**
Q64176	AISESGVALTAGLVK	1.048291663	2	4.875881195
Q64176	EGYLQIGATTQQAQK	1.104994437	2	4.296083927
Q64176	LGIWGFFSTGDEHSR	1.304448105	2	3.131472826
Q64176	NFNTVPYIVGINK	0.651881396	2	3.444725752
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.338310606**	**0.00185**	**7**
Q641Y0	ELGSECGIEFDEEK	1.037967093	2	3.694343805
Q641Y0	NTLLIAGLQAR	1.247093039	2	3.797177553
Q641Y0	TADDPSLSLIK	1.162002941	2	2.336344481
Q641Y0	TLVLLDNLNVR	1.344192339	2	3.935337782
Q641Y0	WVPFDGDDIQLEFVR	1.327630831	2	3.336732864
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.163849543	3	6.137796879
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	1.414233991	4	5.120691776
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.027637301**	**0.07422**	**5**
Q641Y2	GSGIQWDLR	1.09398417	2	2.710246086
Q641Y2	IDEVEEMLTNNR	1.08448092	2	3.49955821
Q641Y2	IIEQCLNK	1.413310421	2	2.896279573
Q641Y2	LYTEGYQVPPGATYTAIEAPK	1.591668006	2	2.756647825

Q641Y2	TQPYDVYDQVEFDVPIGSR	1.028367167	2	4.249838829
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.118525032**	**0.93737**	**3**
Q64232	HYEVEIR	0.969282598	2	2.328707218
Q64232	LCFLDKVEPQATISEIK	1.088363408	2	4.541799068
Q64232	SLKDEDVLQK	1.111236283	2	3.004000425
Q64240	**AMBP Protein AMBP**	**1.193052139**	**0.47631**	**3**
Q64240	AFAELWAFDAAQGK	1.129228356	2	2.770967484
Q64240	AVLPQENEGSGSEPLITGTLK	1.194804042	2	4.795111656
Q64240	TIAACNLPIVQGPCR	1.136332463	2	3.96865654
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.22648134**	**0.72272**	**17**
Q64380	AIDSLSIEK	0.952857448	2	2.555262804
Q64380	AYGIESHVLSPAETK	1.043844798	2	4.293030739
Q64380	DGTMDPAGTCTTLTR	0.573318303	2	4.047020912
Q64380	DLYPLMNVDDLYGTLYVPR	1.024265502	2	3.49597168
Q64380	FHHSLTDHPR	1.221696674	2	2.554536343
Q64380	FYLLGADAR	1.154212532	2	2.545306683
Q64380	HGLVNAGYR	1.08666748	2	2.352528572
Q64380	IEGIQNMPNVR	1.01294952	2	2.839958429
Q64380	LGVGGVVLLER	2.430351918	2	3.151747942
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.873305879	2	4.28136301
Q64380	NYSVVFPHDEPLAGR	0.936445486	2	3.879293203
Q64380	SDDSPLEAGLAFTCK	1.117833332	2	4.659955978
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	1.183865505	3	5.026329041
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	1.122083199	3	4.51250124
Q64380	RDPLHEELLGQGCVFQER	1.201471282	3	5.265172005
Q64380	STVCGPESFTPDHKPLMGEAPELR	1.092885792	3	4.865081787
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	1.043021851	3	5.117280483
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.050270186**	**0.01326**	**25**
Q64428	ALMGLYNGQVLCK	1.173382055	2	3.277787685
Q64428	DSIFSNLIGQLDYK	0.661834621	2	2.540228844
Q64428	DTTASAVAVGLK	0.98980627	2	3.771733284
Q64428	FGELALTK	1.045304999	2	2.686711788
Q64428	FGGGSVELLK	1.069522395	2	3.296212673
Q64428	FVDLYGAQK	1.171005831	2	3.178231955
Q64428	GFYIYQSGSK	1.202631629	2	3.035098314
Q64428	ILQEGVDPK	1.113559428	2	3.150660515
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.586014648	2	4.280008316
Q64428	KYESAYGTQFTPCQLLR	0.972821911	2	4.433245659
Q64428	MGLVDQLVDPLGPGIK	1.063585385	2	4.825469017
Q64428	MGLVDQLVDPLGPGIK+Oxidation(1)	1.052781821	2	2.451394796
Q64428	MQLLEIITTDK	1.095288058	2	4.020749092
Q64428	MVGVPAAFDMMLTGR	1.080139458	2	3.235998154

Q64428	NLNSEIDNILVNLR	1.14474664	2	4.788310051
Q64428	TGLEQGNDAGYLAESEK	1.0372805	2	5.136666775
Q64428	YESAYGTQFTPCQLLR	1.024775143	2	4.413252354
Q64428	ADMVIEAVFEDLAVK	0.959243727	3	4.758580685
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.762120233	3	6.849063396
Q64428	EVQSEFVEVMNEIWANDQIR	1.070650505	3	3.322697401
Q64428	LPAKPEVSSDEDIQYR	1.159009035	3	3.848047733
Q64428	TIEYLEEVAVNFAK	1.016029946	3	4.148970127
Q64428	TVLGVPEVLLGILPGAGGTQR	1.210363701	3	5.002803326
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	1.054037329	3	5.991014481
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.165838918	4	5.037264347
Q64458	**CP2CT Cytochrome P450 2C29**	**1.163362269**	**0.97387**	**5**
Q64458	IKEHKESLDVTNPR	1.059212563	2	5.02221632
Q64458	VQEEAQCLVEELR	1.259500425	2	4.275462151
Q64458	VQEEAQCLVEELRK	1.343833892	2	3.72656846
Q64458	VQEEIDR	1.044630516	2	2.495527506
Q64458	LPPGPTPLPIIGNFLQIDVK	1.131806777	3	4.371341705
Q64481	**CP3AG Cytochrome P450 3A16**	**0.919618307**	**0.99999**	**2**
Q64481	GSIDPYVYLPFGNGPR	0.83524393	2	3.943891525
Q64481	VLQNFSFQPCK	1.039950073	2	2.609072685
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.008782945**	**1**	**4**
Q64550	GHEVVVIAPEASIHIK	0.893017318	2	4.664513111
Q64550	NMIIALTENFLCR	1.121584424	2	4.659689903
Q64550	SVFDQDPFLLR	1.131908148	2	3.410800219
Q64550	VVYSPYGSLATEILQK	1.012563329	2	4.55074501
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.003692446**	**0.99974**	**16**
Q64563	AAVDCTVVGWGSCTVVGAK	1.833374963	2	4.181503296
Q64563	ALGATDCLNPR	0.98019705	2	3.008248568
Q64563	IIAIDINSEKFPK	1.043743346	2	2.650220156
Q64563	INDAIDLMNQGK	1.055790133	2	4.349094868
Q64563	LCLSPLTNLCGK	2.249460673	2	2.319315434
Q64563	SVDSVPNLVTDYK	0.903418465	2	3.25919795
Q64563	TDSPLCIEEIEVSPPK	0.976655137	2	4.232413769
Q64563	VCLIGCGFTSGYGAAINTAK	1.525114248	2	5.574826241
Q64563	VDDEANLER	1.006876896	2	2.675382853
Q64563	VDEMNISTVDMILGR	0.983566878	2	3.387874842
Q64563	VIATCVCPTDINATNPK	1.22711428	2	4.222022533
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	0.995654495	3	5.840706825
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	0.902376056	3	5.560966015
Q64563	FDLDLLVTHALPFDK	1.180361328	3	3.320618391
Q64563	KFDLDLLVTHALPFDK	0.976264676	3	5.691926479
Q64563	KFDLDLLVTHALPFDKINDAIDLMNQGK	0.766525432	3	4.682949543

Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**1.037666363**	**0.69018**	**15**
Q64565	YIEQFK	1.255602735	1	2.050944805
Q64565	AYSNHTDIISFR	1.234320187	2	3.354557514
Q64565	GGNFSQTFR	1.17350168	2	2.412196398
Q64565	GGVCIADEVQTGFGR	1.0626236	2	4.314655781
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.065441525	2	3.196557522
Q64565	GLMVGIEMVQDK	0.918574194	2	3.762531042
Q64565	HNMPPCDFSPEK	1.034377416	2	3.320510387
Q64565	LRDEFDIVGDVR	1.061932615	2	2.635327101
Q64565	LSALLPEPLK	2.331966523	2	2.584724665
Q64565	NSQEVGTYMLLK	1.095126919	2	2.375362396
Q64565	SALTQHMER	1.318129336	2	2.714660168
Q64565	TEVNQIHEDCK	1.17099139	2	3.269109249
Q64565	TEVNQIHEDCKDMGLLVGR	1.05445752	2	5.223378181
Q64565	VIFLVNSGSEANDLAMVMAR	1.545246507	2	5.690999031
Q64565	YLDFFSGIVTVGVGHCHPK	0.907514713	2	2.782546997
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**0.541240453**	**0.0316**	**4**
Q64578	DIVPGDIVEVAVGDKVPADIR	0.468211746	2	3.329761028
Q64578	IGIFSENEEVADR	0.818891295	2	2.899600983
Q64578	VGEATETALTTLVEK	0.540016708	2	4.032546043
Q64578	YGPNELPAEEGK	0.784531014	2	2.542826176
Q64581	**CP3AI Cytochrome P450 3A18**	**1.052373937**	**0.8837**	**3**
Q64581	KLQNEIDR	0.95996849	2	2.358011007
Q64581	LAVIGVLQNFNIQPCEK	1.868613755	2	4.049885273
Q64581	NPEYWLEPEEFNPER	1.020983043	2	4.248091698
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.842748152**	**0.00035**	**9**
Q64591	NIDVLK	0.946204682	1	2.057032824
Q64591	ATAEEITSK	1.562808566	2	2.938466072
Q64591	EEWDVIEGLIR	0.621825298	2	3.724044561
Q64591	FFPPILKPMLPPNAFQGK	1.138000339	2	3.905992031
Q64591	FNIIQPGPIK	0.875132915	2	3.115134001
Q64591	VAFITGGGTGLGK	1.020641869	2	2.911386728
Q64591	DPDMVHNTVLELIK	0.65749461	3	4.292530537
Q64591	VTKEEWDVIEGLIR	0.889920962	3	5.016978264
Q64591	CDVRDPDMVHNTVLELIK	0.980351111	4	4.551716328
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.257767113**	**0.05606**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.281521719	2	5.288329124
Q64602	DIISLAPGSPNPK	0.923862883	2	3.079529285
Q64602	EILLVPGNSFFVDNSAPSSFFR	0.874066846	2	2.32144928
Q64602	FLYTIPNGNNPTGNSLTGDR	1.252608377	2	4.142947674
Q64602	SAVFTVENGSTIR	0.968599764	2	3.860829115

Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.349409059	3	6.373969555
Q64602	VLSQWKPEDSKDPTKR	2.118751524	3	3.946004629
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**0.985235647**	**0.99906**	**11**
Q64611	YLVEEIK	1.220418199	1	2.297017574
Q64611	AQGGQGLEWR	1.266923469	2	3.030952215
Q64611	CHGSQASYLFQQDK	0.972283683	2	5.261312485
Q64611	FFNQLFSGLDPHALAGR	0.942681393	2	4.701593876
Q64611	FYNVALDTGDK	1.080135594	2	3.088741779
Q64611	GAAFLGLGTDSVR	1.300502316	2	3.448966503
Q64611	IDQAFALTR	1.033425334	2	3.189400673
Q64611	LLAAGLQCSALLLR	4.761453016	2	3.303945541
Q64611	QLLDLELQSQGESR	0.877061866	2	4.094171047
Q64611	TLDGDPVAVEALLR	1.03198309	2	5.039214134
Q64611	VCEWKEPEELK	1.133682467	3	3.801840544
Q64633	**UD17 UDP_glucuronosyltransferase 1_7**	**0.98362834**	**0.96105**	**2**
Q64633	QSSFDAVFLDPFDVCGLTVAK	0.983716594	2	2.383490562
Q64633	TYSVSHTQEDLNR	0.930769348	2	3.272384167
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**1.191108051**	**0.12196**	**2**
Q64638	VVFETGNYVK	1.47968001	1	1.962199211
Q64638	TFLETSEILK	0.958814325	2	2.406353951
Q64640	**ADK Adenosine kinase**	**1.06183804**	**0.99444**	**11**
Q64640	AATFFGCIGIDK	0.921065938	2	3.082792997
Q64640	FGEILK	1.057661774	2	2.383528471
Q64640	HKELFDELVK	0.899075828	2	2.750713825
Q64640	HLDLENNWMLVEK	1.076094844	2	3.595920324
Q64640	SLVANLAAANCYK	1.113612753	2	4.354123592
Q64640	VEYHAGGSTQNSMK	1.04896697	2	3.819094181
Q64640	VEYHAGGSTQNSMK+Oxidation(13)	1.050552314	2	3.618259192
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.142286259	3	7.148843765
Q64640	AGHYAASVIIR	1.137923189	3	3.322164536
Q64640	FKVEYHAGGSTQNSMK	1.13031699	3	3.44434762
Q64640	YSLKPNDQILAEDK	1.101399373	3	4.234285355
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**1.041946764**	**0.99911**	**8**
Q64654	EPAEDILQTLLDSTYK	1.025398092	2	3.467680931
Q64654	GVAYDVPNAVFLEQK	1.099454646	2	4.034034729
Q64654	NEDLNAEEVYGR	0.881075904	2	3.822248936
Q64654	SGLNIAHFK	0.980554126	2	2.86670208
Q64654	TFTYLLGSDAAALLFNSK	0.839568683	2	2.932697535
Q64654	TVCGEDLPPLTYEQLK	0.771915314	2	4.126359463
Q64654	YGPVFSFTMVGK	0.888941231	2	2.729981899
Q64654	YLQDNPASGEK	0.870553319	2	2.847353697
Q64737	**PUR2 Trifunctional purine biosynthetic protein adenosine_3**	**0.945435637**	**0.94099**	**2**

Q64737	DSGVDIAAGNMLVKK+Oxidation(11)	0.94541935	2	2.307566166
Q64737	FGDPECQVILPLLK	0.979452856	2	2.453150272
Q65CL1	**CTNA3 Catenin alpha_3**	**1.202923903**	**0.6821**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(1)	1.212029305	2	2.600138664
Q65CL1	NLMNAVVQTVK	0.898295196	2	3.155761719
Q65Z40	**WAPL Wings apart_like protein homolog**	**0.874572035**	**0.3447**	**3**
Q65Z40	EKSISRIPEDNANK	0.879831884	2	2.678282738
Q65Z40	LGQKRPNFKPDIQEIPK	1.275523795	2	2.913098097
Q65Z40	TESPSESCPVKGSVR	0.947475781	2	2.524430037
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.326051566**	**0.00525**	**3**
Q66H12	CNINCEEDPK	1.041632597	2	2.401847839
Q66H12	INQDPLGIQGR	1.128609568	2	2.451294661
Q66H12	TISPQNIDILQNPLLIK	1.341854745	2	3.881380081
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**0.885784441**	**0.4289**	**2**
Q66H15	AIPGEAGDAAMLSSLPQEGQEK	1.393633309	2	4.198450089
Q66H15	AYSDMTELTEEESEKK	0.854259144	2	2.533581495
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**1.006898387**	**0.97619**	**2**
Q66H45	LQGDVAGALEDLER	0.998676174	2	3.658977032
Q66H45	RDFEQAAR	1.044711574	2	2.304555893
Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**1.041544468**	**0.94444**	**2**
Q66H71	LTEQAVEAINK	1.039699666	2	3.691011667
Q66H71	SIDEDDDYFNLTK	1.361340878	2	2.835181952
Q66H80	**COPD Coatomer subunit delta**	**1.26772285**	**0.01626**	**5**
Q66H80	GVQLQTHPNVDKK	1.27801845	2	3.166584253
Q66H80	LFTAESLIGLK	1.402993813	2	2.904071808
Q66H80	NSNILEDLETLR	1.083595177	2	2.906677008
Q66H80	NTLEWCLPVIDAK	1.010984497	2	3.299034595
Q66H80	VAPAPARPSGPSK	1.172917157	2	2.498586416
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.097995436**	**0.79731**	**5**
Q66HA8	AGGIETIANEFSDR	1.062700169	2	2.842128277
Q66HA8	FVVQNVSAQK	1.112471388	2	2.683887243
Q66HA8	LKETAENNLK	1.241592755	2	2.398279428
Q66HA8	NQQITHANNTVSSFK	1.110375195	2	4.482751369
Q66HA8	SVLDAAQIVGLNCLR	1.0896257	2	2.719074488
Q66HD0	**ENPL Endoplasmin**	**1.005193719**	**9.9E-20**	**32**
Q66HD0	EVEEDEYK	0.865214102	1	2.38898325
Q66HD0	YNDTFWK	1.150619272	1	2.193241358
Q66HD0	DISTNYYASQK	0.337330142	2	3.067604542
Q66HD0	EATEKEFEPLLNWMK	1.023554061	2	3.138513088
Q66HD0	EEASDYLELDTIK	1.156734673	2	4.280916214
Q66HD0	EEEAIQLDGLNASQIR	1.141216582	2	4.547014713
Q66HD0	EFEPLLNWMK	1.000640921	2	2.315117359

Q66HD0	GLFDEYGSK	1.14801781	2	2.344799995
Q66HD0	GVVDSDDLPLNVSR	1.127194922	2	4.812913418
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGK	0.488153492	2	3.721064091
Q66HD0	KEAESSPFVER	1.13523106	2	3.605721951
Q66HD0	LGVIEDHSNR	1.387663362	2	3.331030369
Q66HD0	LIINSLYK	1.943995398	2	2.426030397
Q66HD0	LISLTDENALAGNEELTVK	1.454947515	2	5.851543903
Q66HD0	LTESPCALVASQYGWSGNMER	1.124744363	2	5.566545486
Q66HD0	MKEKQDK	0.989060093	2	2.330203533
Q66HD0	NLLHVTDTGVGMTR+Oxidation(12)	1.293109561	2	2.987621784
Q66HD0	SGTSEFLNK	1.153719466	2	3.10225749
Q66HD0	SGYLLPDTK	1.081330194	2	3.169315338
Q66HD0	SILFVPTSAPR	0.93667129	2	3.474208593
Q66HD0	TDDEVVQR	1.09283856	2	2.947075367
Q66HD0	TETVEEPLEEDETAQEEK	0.776108087	2	5.18552494
Q66HD0	TFEINPR	1.130905553	2	2.725261211
Q66HD0	VFITDDFHDMMPK	1.062812927	2	4.02559042
Q66HD0	FQSSHHSTDITSLDQYVER	1.208556585	3	6.205788612
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	0.526328379	3	4.024006844
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	0.674037529	3	4.419525146
Q66HD0	NLLHVTDTGVGMTR	1.13213477	3	4.034244537
Q66HD0	RVFITDDFHDMMPK	1.30565016	3	3.335545301
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	1.20392669	3	5.351276875
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.212688852	3	4.027099609
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	0.554365116	5	6.45001173
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.007385384**	**0.30275**	**12**
Q66HF1	GWNILTNSEK	1.170003295	1	2.146276951
Q66HF1	ALSEIAGITLPYDTLDQVR	1.188736784	2	3.979142189
Q66HF1	DDGAAILAAVSSIAQK	1.017746027	2	4.337766171
Q66HF1	FASEIAGVDDLGTTGR	1.21263003	2	3.477347136
Q66HF1	GLLTYTSWEDALSR	0.960293681	2	3.383852482
Q66HF1	ILQDIASGNHEFSK	1.307345497	2	4.155754566
Q66HF1	LGEVSPNLVR	1.148548399	2	3.160465717
Q66HF1	LVDQEFLADPLVPPQLTIK	1.033931249	2	3.285637856
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.793206425	2	4.637685299
Q66HF1	YDHLGDSPK	0.965293825	2	2.555663109
Q66HF1	DCFIVYQGHHGDVGAPIADVILPGAAYTEK	0.965991418	3	4.199045658
Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	1.018032081	3	4.519767761
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**0.853959284**	**1.7E-11**	**11**
Q66HF8	ADVDLAVR	1.251876484	2	2.357654095
Q66HF8	EEIFGPVQPLFK	0.771916264	2	3.219243288
Q66HF8	LAPALATGNTVVMK	2.035210138	2	3.287401676

Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.498663269	2	4.636391163
Q66HF8	TFVEESIYHEFLER	1.197421217	2	3.81672883
Q66HF8	VAEQTPLSALYLASLIK	1.213893067	2	3.178241968
Q66HF8	VGNPFELDTQQGPQVDK	1.258518989	2	3.041733027
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.992289169	2	4.471832275
Q66HF8	YGLAAAVFTR	1.229646918	2	3.856504679
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	1.366037315	3	3.854003668
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.779221	3	4.504412651
Q66HG4	**GALM Aldose 1_epimerase**	**1.019878384**	**1**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	1.045804008	2	4.706767559
Q66HG4	TVFGELPSGGGAVEK	1.039271807	2	3.668407679
Q66HG4	VSPDGEEGYPGELK	0.987202504	2	3.785018206
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.165421334**	**1.8E-06**	**21**
Q66X93	ADDADEFGYSR	2.185021864	2	2.783961773
Q66X93	ALLLPDHYLVTVMLSGIK	1.222472178	2	3.328964949
Q66X93	DTNGENIAESLVAEGLASR	0.998233646	2	5.023663521
Q66X93	ETDGSETPEPFAAEAK	0.81325791	2	3.693834782
Q66X93	FVDGEWYR	0.997306465	2	2.319098473
Q66X93	GDVGLGLVK	1.050241697	2	2.707770109
Q66X93	LEGDNIQDK	1.137290906	2	2.708917141
Q66X93	LSECEEQAK	2.251580046	2	2.607335567
Q66X93	MVLSGCAIIVR	1.269033694	2	2.371476889
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.470628964	2	5.427797318
Q66X93	SAYYKPLLSAEEAAK	1.257728432	2	2.522879362
Q66X93	SSHYDELLAAEAR	1.2710539	2	3.74548173
Q66X93	TCATVTIGGINIAEALVSK	1.256230735	2	3.926304817
Q66X93	TDAVDSVVR	0.986679451	2	2.655802727
Q66X93	VITEYLNAQESAK	1.0919313	2	3.786048174
Q66X93	VMQVLNADAIVVK	1.504941232	2	3.98234129
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.02986085	3	5.562504292
Q66X93	HFVDSHHQKPVNAIIEHVR	1.113591714	3	4.868802547
Q66X93	SDISSHPPVEGAYAPR	1.098919248	3	4.613807201
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.075566859	3	5.063763618
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.836609851	3	4.577794552
Q67FY2	**BCL9L B_cell CLL/lymphoma 9_like protein**	**0.769320621**	**0.53699**	**2**
Q67FY2	EAGTPSLDSEAKEVAPR	0.976681583	2	2.451547146
Q67FY2	NLVGSEGLSKEQLEHRER	0.742690372	2	2.353882313
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**1.064556897**	**0.93221**	**8**
Q68FP2	YVYVADVTAK	1.085748906	1	2.892066717
Q68FP2	HNNWDLTPVK	0.957696173	2	3.308071375
Q68FP2	IFLMDLNEPYPK	1.292468773	2	3.059904099
Q68FP2	IQDPLSDNPR	0.99818902	2	2.878886938

Q68FP2	LLIYNPEDPPGSEVLR	1.431975044	2	4.306882381
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.133942705	2	4.954349518
Q68FP2	VVAQGFSSANGITVSLDQK	1.13538634	2	4.176673889
Q68FP2	LVALTVLGASLALLGER	1.515684223	3	4.015354633
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.365773143**	**1.9E-05**	**5**
Q68FQ0	GSNDMQYQHVIETLIGK	1.261045497	2	3.559807062
Q68FQ0	HKLDVTSVEDYK	1.405413554	2	3.157534838
Q68FQ0	SLHDALCVIR	1.238623684	2	2.990057945
Q68FQ0	WVGGPEIELIAIATGGR	1.410480376	2	3.885253191
Q68FQ0	ETGANLAICQWGFDDEANHLLLQNGLPAVR	1.02946574	3	3.709010124
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.29197713**	**1.8E-15**	**8**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.303251597	2	5.338454247
Q68FR6	ALIAAQYSGAQIR	0.895592096	2	4.230010986
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	1.587125757	2	3.763025284
Q68FR6	ILGLLDTHLK	1.721804944	2	2.64118433
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.113781468	2	4.26509428
Q68FR6	KLDPGSEETQTLVR	1.208064044	2	3.912443161
Q68FR6	LDPGSEETQTLVR	1.012915855	2	2.938840151
Q68FR6	STFVLDEFKR	1.087493682	2	2.711997509
Q68FR9	**EF1D Elongation factor 1_delta**	**1.191203495**	**0.00048**	**6**
Q68FR9	ATAPQTQHVSPMR	1.161036337	2	3.055468559
Q68FR9	FYEQMNGPVTAGSR	0.989036834	2	4.219642639
Q68FR9	GVVQDLQQAISK	1.17341439	2	3.426027536
Q68FR9	SIQLDGLVWGASK	1.129935468	2	2.788300276
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.180431318	2	5.316636562
Q68FR9	SSILLDVKPWDDETDMAQLETCVR	1.064756321	3	3.340085745
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.022973772**	**0.00689**	**18**
Q68FS4	GLVLGIYSK	1.24838866	1	2.034808397
Q68FS4	ADMGGAATICSAIVSAAK	1.222064684	2	5.388221264
Q68FS4	DKDDDVPQFTSAGENFNK	0.913439412	2	5.099095821
Q68FS4	GITFDSGGISIK	1.025979396	2	3.242561817
Q68FS4	GVLFASGQNLAR	0.914997795	2	3.615752935
Q68FS4	LFEASVETGDR	1.140042295	2	3.505314589
Q68FS4	LHGSGDLEAWEK	1.571794996	2	3.57463026
Q68FS4	LNLPINIIGLAPLCENMPSGK	2.539950301	2	4.828619957
Q68FS4	QLMESPANEMTPTR	1.027937263	2	3.387782812
Q68FS4	QVIDCQLADVNNLGK	1.126222879	2	4.933416367
Q68FS4	SAGACTAAAFLR	1.417836245	2	3.690693378
Q68FS4	SAGVDDQENWHEGK	1.249233307	2	3.927734137
Q68FS4	SWIEEQEMGSFLSVAK	1.19260655	2	5.508905411
Q68FS4	TFYGLHQDFPSVVVVGLGK	0.851139929	2	4.902935028
Q68FS4	TIQVDNTDAEGR	1.069723665	2	4.194920063
Q68FS4	TLIEFLLR	1.141987167	2	2.696519136

Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	0.814835208	3	5.98961401
Q68FS4	WAHLDIAGVMTNKDEIPYLR	1.054511149	3	3.456581354
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.213563718**	**0.03939**	**3**
Q68FT1	INDAMNMGHTAK+Oxidation(5)Oxidation(7)	1.558862119	2	2.795644522
Q68FT1	LNHVLEEEQK	1.229070806	3	3.335385799
Q68FT1	YTDQSGEEEEDYESEEQIQHR	1.108974862	3	4.67617321
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**1.014602123**	**1**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	1.106225303	2	3.651364803
Q68FT3	ISQLDTQSPVTK	1.052415905	2	3.548380375
Q68FT3	SLLLGTDVAENQK	0.912889594	2	2.883433819
Q68FT3	TLGAQLPQYYEVLTAPISK	1.011752229	2	4.771354675
Q68FT3	VFDCIEAYAPGFK	0.872022782	2	2.332330942
Q68FT3	VLDQWFESEPLK	0.920426596	2	3.202563286
Q68FT3	VQGVVLQGGEEVR	0.979822429	2	3.370826483
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.098927391**	**0.00059**	**11**
Q68FT5	AGADVLQTFTFSAAEDR	0.949745974	2	3.843240023
Q68FT5	AGANIIGVNCR	1.183485257	2	3.220835209
Q68FT5	AIAEELAPER	1.149349248	2	3.816420555
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.346039888	2	3.899584293
Q68FT5	FGPWTSLQTMK	0.930049882	2	3.088423729
Q68FT5	GGFVDLPEYPFGLEPR	1.182522164	2	4.072601795
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.086451315	2	5.360916615
Q68FT5	YIGGCCGFEPYHIR	2.262760251	2	4.624770641
Q68FT5	AGLWTPEAVVEYPSAVR	0.904721872	3	3.752787828
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.121551862	3	4.681605339
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	1.636826566	3	3.472177029
Q68FT9	**SCLY Selenocysteine lyase**	**1.311010462**	**0.10785**	**5**
Q68FT9	AEVDLIVQDLK	0.952902575	2	3.723337412
Q68FT9	CFHEQQTLQGR	1.377389686	2	2.759497166
Q68FT9	VLVHTDAAQALGK	0.961829836	2	3.036961079
Q68FT9	RVDVEDLGVDFLTIVGHK	1.361870482	3	5.925532341
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	1.200299478	3	3.613837719
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**1.029627513**	**9.8E-07**	**12**
Q68FU3	AGDLGVDLTSK	1.067392239	2	3.727008104
Q68FU3	EIIAVSCGPPQCQETIR	0.863534442	2	4.861820698
Q68FU3	GIHVEVPGAEAENLGPLQVAR	1.343150347	2	5.739820004
Q68FU3	HSMNPFCEIAVEEAVR	1.017771867	2	5.694419384
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(3)	1.268233084	2	4.289790154
Q68FU3	RVIDFAVK	1.203000844	2	2.382764339
Q68FU3	SGVVTDGVK	0.955560739	2	2.888639688
Q68FU3	VDLLFLGK	0.923912091	2	2.982012272

Q68FU3	VETTEDLVAK	1.009836749	2	3.335743427
Q68FU3	VIDFAVK	1.037370257	2	2.353140593
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	0.940622192	3	6.307808399
Q68FU3	VSVISVEEPPQR	1.114454677	3	3.412222862
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.022687141**	**0.99751**	**9**
Q68FY0	IEEVDAQMVR	0.974776535	2	3.687473059
Q68FY0	LCTSATESEVTR	1.148744638	2	3.173052788
Q68FY0	NALISHLDGTTPVCEDIGR	1.136431379	2	4.70270586
Q68FY0	NNGAGYFLEHLAFK	1.138605224	2	3.425251722
Q68FY0	RIPLAEWESR	1.137973505	2	2.780925751
Q68FY0	TDLTDYLSR	1.088327136	2	2.665097713
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.038167009	2	5.116642952
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	0.928394999	3	5.880926609
Q68FY0	VVELLADIVQNISLEDSQIEK	0.991780363	3	5.734788895
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**1.281055487**	**0.99968**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	1.054122798	2	4.68219614
Q68G31	GESGGQTTPYDFYSR	1.237868892	2	4.278223038
Q68G31	LQPTDSFSQSSCFGLR	1.021056011	2	3.488534451
Q68G31	NVNSTLTFVTLSGELK	1.008254343	2	3.790798426
Q68G31	VNTEPLPGIEK	1.036379693	2	3.031413078
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	0.962836195	3	3.697976828
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.175510229	3	5.739984512
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.513245314**	**0.01123**	**2**
Q69Z23	YFIDLLMEK	1.710789932	1	2.153031588
Q69Z23	GDPTRAEDQVLMRALR	0.675487609	2	2.332085133
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.154648473**	**0.04741**	**2**
Q6A0A9	SQGGVQPIPSQGGK	1.094680392	2	3.141606808
Q6A0A9	VEGSSTASSGSQLAEGK	1.156024443	2	4.299808979
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.330554787**	**7.1E-06**	**4**
Q6AXM8	FQEEENSLLHLK	1.312031933	2	3.43415761
Q6AXM8	LFVYDPNHPPSSEVLR	1.132908018	2	2.501709223
Q6AXM8	LVAEGFDSANGINISPDKK	1.3335177	2	3.657101393
Q6AXM8	VLQLGTLVDNLSIDPSSGDIWVGCHPNGQK	1.013134747	3	4.429273129
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**1.025541842**	**0.84292**	**3**
Q6AXS5	EETQPPVALKK	0.835803531	2	2.742065907
Q6AXS5	FDQLFDDESDPFEVLK	0.945287281	2	5.205064774
Q6AXS5	SAAQAAAQTNSNAAGK	1.025658281	2	5.098505497
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.944020686**	**0.89251**	**2**
Q6AXY0	YFPAFEK	1.09367481	1	1.911069512
Q6AXY0	FLQPGSQR	0.919118237	2	2.512714624
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**0.923043635**	**0.9426**	**5**

Q6AY09	ATENDIYNFFSPLNPMR	0.877346728	2	4.018090725
Q6AY09	GLPWSCSAEEVMR	0.884807221	2	3.10272646
Q6AY09	HTGPNSPDTANDGFVR	0.915869129	2	4.194076061
Q6AY09	STGEAFVQFASQEIAEK	1.000178699	2	4.290854931
Q6AY09	STGEAFVQFASQEIAEKALKK	1.018295514	2	2.546010494
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**0.969832733**	**0.75924**	**2**
Q6AY20	HTLAGNFNPVSEER	0.957691485	2	4.300218105
Q6AY20	SCDLVGEKDKESK	1.200484519	2	3.720636606
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.013906259**	**0.49908**	**6**
Q6AY30	LQQVLEK	1.317522817	1	2.067964554
Q6AY30	ATLVLNCVGPYR	0.981399904	2	2.56127286
Q6AY30	GGGVFTPGAAFSR	1.005438303	2	2.364259958
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.111315092	2	3.253741741
Q6AY30	SVSNLKPVPVIGSK	1.078119821	2	3.613881111
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.175265868	3	5.312945366
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.136941098**	**2.9E-11**	**9**
Q6AY56	EDAANNYAR	1.058889246	1	2.073451042
Q6AY56	AFVHWYVGEGMEEGEFSEAR	1.07619074	2	4.602024555
Q6AY56	AVCMLSNTTAIAEAWAR	1.023365702	2	4.625179291
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.290463184	2	5.410570145
Q6AY56	LISQIVSSITASLR	1.737487384	2	3.6666224
Q6AY56	NLDIERPTYTNLNR	1.131864	2	3.58130765
Q6AY56	QLFHPEQLITGK	1.085514725	2	2.851508379
Q6AY56	TIQFVDWCPTGFK	0.981926736	2	3.881794214
Q6AY56	VGINYQPPTVVPGGDLAK	1.161291517	2	4.843519688
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.906658569**	**0.98347**	**2**
Q6AY80	NDVTGALSNPEVFK	0.977912314	2	3.415158272
Q6AY80	VLAPQISFGPEVSSEEQR	0.893616257	2	3.378974915
Q6AYH5	**DCTN2 Dynactin subunit 2**	**0.923836586**	**0.38907**	**3**
Q6AYH5	ASVEDADTQNK	0.876374151	2	3.222342014
Q6AYH5	LLGPDAAINLADPDGALAK	1.676652035	2	2.925565958
Q6AYH5	WSPVASTLPELVQR	1.368981471	2	2.570433378
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.904620908**	**0.56289**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	0.837570939	2	4.398078918
Q6AYQ8	SFTSSCPVSAFVPK	0.971638447	2	4.085939884
Q6AYQ8	NLHHEVELGVLLGR	1.026947178	3	4.438677311
Q6AYR8	**SCRN2 Secernin_2**	**1.04442928**	**0.99975**	**3**
Q6AYR8	GHQAALGLMDEQEQAQLR	1.005211983	2	3.872862577
Q6AYR8	QEQQSLEQEGLEALR	1.092151387	2	4.02417469
Q6AYR8	TTASMVSVLPQDPTKPCVHFLTATPDPSR	1.008058041	3	3.571760416
Q6AYS7	**ACY1A Aminoacylase_1A**	**1.033531988**	**0.01342**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	0.989283596	2	3.459307194

Q6AYS7	ICTVQPNPDYGSAVTFLEER	2.324416105	2	4.425976276
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.849690697**	**0.9779**	**3**
Q6AYS8	ALTDELAALGCTGVR	1.086279546	2	2.361281395
Q6AYS8	SVAGEIVLITGAGHGIGR	0.982580526	2	4.276732922
Q6AYS8	NPSTNLGPTLEPEEVVEHLMHGILTNQK	1.059477999	3	3.6643641
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.851209332**	**0.83423**	**3**
Q6AYT9	AFIVLSPAYVSHDPEALTR	1.125012302	2	4.691833019
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.716959406	2	3.378476858
Q6AYT9	NDDVINSSSYR	0.938219074	2	3.305897474
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.151426089**	**0.00029**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	1.065841498	2	5.301738739
Q6AYZ1	DVNAAIATIK	1.022765815	2	3.295983553
Q6AYZ1	IHFPLATYAPVISAEK	1.683032309	2	3.901093006
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.245889936	2	5.561451912
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.228957585	2	4.75199604
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	0.860355931	3	4.255541801
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**0.977939878**	**1**	**7**
Q6DGG1	AVAIDLPGLGR	0.964523704	2	3.478761435
Q6DGG1	FSSETWQNLGTLHR	1.020718409	2	3.571706533
Q6DGG1	FSVLLLHGIR	1.172439797	2	3.01432538
Q6DGG1	GYVPVAPICTDK	0.997033543	2	2.542141914
Q6DGG1	INAADYAR	1.049313927	2	2.401296616
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	0.980995534	2	4.966036797
Q6DGG1	VLVMEGAGHPCYLDKPDEWHTGLLDFLQELA	0.932497432	3	3.891675234
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**1.056343671**	**0.99048**	**2**
Q6EDY6	ELMESIK+Oxidation(3)	1.054072132	1	2.192120552
Q6EDY6	IENYLLR	1.058223385	2	2.503957272
Q6GQT9	**NOMO1 Nodal modulator 1**	**1.089854998**	**0.79014**	**2**
Q6GQT9	SSIDSEPALVLGPLK	1.099304897	2	2.697806358
Q6GQT9	VQVVVPEAETR	1.113181422	2	2.843816996
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**1.165251624**	**0.61973**	**2**
Q6I7R3	GLGSTVQEIDLTGVK	1.089584954	2	3.855787992
Q6I7R3	ILGIPVIITEQYPK	1.529252426	2	3.272509575
Q6IE52	**MUG2 Murinoglobulin_2**	**1.178256123**	**0.99999**	**13**
Q6IE52	NLYPLKELVQDPK	1.124271794	1	2.149428606
Q6IE52	AHFSVMGDILSSAIK	1.028988151	2	3.643508673
Q6IE52	HGIPFFVK	1.982168453	2	2.814110518
Q6IE52	HTSSWLVTPK	1.057378758	2	2.625513554
Q6IE52	LPSSEEEESLDINIEGAK	1.202783561	2	5.402191162
Q6IE52	MLIYTILPDGEVIADSVK	1.057015854	2	4.316309929
Q6IE52	MLSGFIPLKPTVK	1.077824935	2	2.855487347
Q6IE52	QLSFSLSAEPIQGPYK	0.911321956	2	4.320585728

Q6IE52	VKTVPLTCNNPK	1.230058406	2	2.77076292
Q6IE52	VLIVEPEGIKK	1.049373137	2	2.372513294
Q6IE52	VTASPQSLCGLR	1.135784508	2	2.595253229
Q6IE52	YMVLVPSQLYTETPEK	0.973874396	2	4.060165405
Q6IE52	VHLSFSPSQSLPASQTHMR	1.08837082	3	3.559564352
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.013069825**	**0.90964**	**2**
Q6IFX1	**K1C24 Keratin_ type I cytoskeletal 24**	**1.135168843**	**0.10983**	**2**
Q6IFX1	LLNDMR	1.100640582	1	1.920396566
Q6IFX1	QEAEKQFNER	1.13523106	2	2.562886238
Q6IG00	**K2C4 Keratin_ type II cytoskeletal 4**	**1.103812032**	**0.44143**	**3**
Q6IG00	LMQDSVEDFK+Oxidation(2)	1.172854939	1	2.075060368
Q6IG00	NLDLDGIIAEVR	0.839570973	2	3.267659426
Q6IG00	WNLLQQQTTTTSPR	1.001640681	2	4.362920761
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**0.955094865**	**0.99902**	**4**
Q6IRK9	IVVYNQPYTDYGK	0.900815539	2	2.406757832
Q6IRK9	TYPDTDSFNTVAEITGSK	0.934368519	2	4.464190006
Q6IRK9	VGAVASLIR	1.113993134	2	2.455492258
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.932267094	3	5.616140842
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**1.096795778**	**0.90629**	**4**
Q6MGB5	AGVIGLTQTAAR	1.144131289	2	3.02583313
Q6MGB5	GSIINISSIVGK	1.281044711	2	2.792261124
Q6MGB5	LAAEGAAVAACDLDGAAAQDTVR	0.918976384	2	3.852378845
Q6MGB5	VGNIGQTNYASSK	1.087857512	2	2.855432749
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.039364058**	**0.12454**	**2**
Q6NSR8	TVEINNTDAEGR	1.038081797	2	3.024205446
Q6NSR8	HNSPSAAHFITR	1.181917706	3	4.136219025
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**0.864394055**	**0.39254**	**4**
Q6NYB7	EFADSLGIPFLETSAK	0.754411471	2	3.033235073
Q6NYB7	MGPGATAGGAEK	0.921611196	2	3.545272112
Q6NYB7	MGPGATAGGAEK+Oxidation(1)	1.279225874	2	2.442881107
Q6NYB7	NATNVEQSFMTMAAEIK	0.954225117	2	4.544320107
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**0.964384734**	**0.12498**	**6**
Q6NZJ6	GLPLVDDGGWNTVPISK	1.126742413	2	3.385184288
Q6NZJ6	IHNAENIQPGEQK	0.975210294	2	4.045236111
Q6NZJ6	KVEYTLGEESEAPGQR	1.067923567	2	4.602254868
Q6NZJ6	LKEELEEAR	1.111382671	2	2.672970533
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.253834983	3	3.356858015
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	1.06120978	3	5.343784332
Q6P0K8	**PLAK Junction plakoglobin**	**0.986726646**	**0.66333**	**4**
Q6P0K8	LLNDEDPVVVTK	1.219995386	2	2.745243311
Q6P0K8	TMQNTSDLDTAR	0.856279374	2	2.955661774
Q6P0K8	MEEIVEGCTGALHILAR	1.314822022	3	3.30865097

Q6P0K8	NLALCPANHAPLQEAAVIPR	0.927260998	3	3.95562458
Q6P2K6	**P4R3A Serine/threonine_protein phosphatase 4 regulatory subunit 3A**	**1.125662363**	**0.90997**	**3**
Q6P2K6	ESEEKEVLLK	1.025990097	1	2.026123047
Q6P2K6	FKEVIPISDPELK	1.133787079	1	2.01321435
Q6P2K6	LDSMRSILR	1.107210995	1	2.024996281
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.344257359**	**0.00715**	**12**
Q6P502	AMTGVEQWPYR	1.153538045	2	2.570135832
Q6P502	AVAQALEVIPR	1.305400193	2	2.852933645
Q6P502	DMMLNIINSSITTK	0.61994406	2	2.348280668
Q6P502	EIQVQHPAAK	0.99890527	2	3.12741065
Q6P502	IVLLDSSLEYK	1.453662618	2	2.460586786
Q6P502	KGESQTDIEITR	1.155407317	2	2.902511835
Q6P502	NLQDAMQVCR	1.195539141	2	3.172851086
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	1.39508836	2	4.088465691
Q6P502	TAVETAVLLLR	1.223861124	2	2.80806303
Q6P502	TLIQNCGASTIR	1.232446496	2	3.094666481
Q6P502	WSSLACNIALDAVK	1.183604379	2	3.63206625
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.770037509	3	4.28635788
Q6P6M7	**SPCS O_phosphoseryl_tRNA(Sec) selenium transferase**	**0.996388294**	**0.75405**	**4**
Q6P6M7	EMFVYLSTQLKK+Oxidation(2)	0.456887753	2	2.957832575
Q6P6M7	KEMFVYLSTQLKK	1.062914851	2	2.546669006
Q6P6M7	SGDISAVQPK	0.999600144	2	2.593178034
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	0.867751188	2	3.661745071
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**1.019853738**	**1.2E-15**	**10**
Q6P6R2	ALTGGIAHLFK	1.309764134	2	2.356988668
Q6P6R2	IDVSVEAASGGK	1.096217457	2	3.216104269
Q6P6R2	NETLGGTCLNVGCIPSK	1.104333337	2	5.259196281
Q6P6R2	NQVTATTADGSTQVIGTK	1.115200155	2	5.374361515
Q6P6R2	TNADTDGMVK	1.065352794	2	2.872279882
Q6P6R2	TNADTDGMVK+Oxidation(8)	1.62064465	2	2.688243866
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.272854453	3	4.43587923
Q6P6R2	RPFTQNLGLEELGIELDPK	1.091185209	3	3.740945339
Q6P6R2	SEEQLKEEGVEFK	0.922003901	3	3.894545078
Q6P6R2	VCHAHPTLSEAFR	1.372280822	3	3.787272215
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**1.047933921**	**0.57613**	**4**
Q6P6S9	AQTLLLEVEEIFK	1.235192093	2	2.985926151
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.48825639	2	4.117293835
Q6P6S9	QGAETVQELLEVAK	0.853883564	2	3.082659006
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	1.133081218	3	4.701375008
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.131294495**	**0.00034**	**9**
Q6P6V0	DVMPEVNKVLDK+Oxidation(3)	1.606619687	2	2.369725704
Q6P6V0	HFVALSTNTDK	1.204152106	2	3.167718887

Q6P6V0	ILLANFLAQTEALMK	1.315975959	2	3.134547472
Q6P6V0	TFTTQETITNAETAK	1.112614503	2	5.133061409
Q6P6V0	VFEGNRPTNSIVFTK	1.271934525	2	3.255814075
Q6P6V0	VWFVSNIDGTHIAK	0.234530719	2	3.588757753
Q6P6V0	AITDIINIGIGGSDLGPLMVTEALKPYSK	0.939708066	3	3.808739185
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.129018588	3	4.835181236
Q6P6V0	TLANLNPESSLFIIASK	1.224459588	3	5.021155357
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.104843448**	**0.79792**	**5**
Q6P7Q4	FEELGVK	1.139436137	1	1.94432199
Q6P7Q4	DFLLQQTMLR	0.939504968	2	3.258581161
Q6P7Q4	GFGHIGIAVPDVYEACK	1.415856057	2	3.715379715
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.124374566	2	5.804505348
Q6P7Q4	VLGLTLLQK	1.147491873	2	2.722939968
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.258632768**	**0.39557**	**3**
Q6P7R8	LGEWAVVTGGTDGIGK	1.199757254	2	4.123653412
Q6P7R8	LININVLSICK	3.350235871	2	2.644697905
Q6P7R8	TIAVDFSLDDIYDK	0.938807362	2	2.969437599
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.222096953**	**1.6E-11**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	0.981874603	2	4.731951714
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(11)	1.131931766	2	2.518610954
Q6P9T8	EIVHLQAGQCGNQIGAK	0.760685124	2	5.107461452
Q6P9T8	EVDEQMLNVQNK	0.885334775	2	4.198689461
Q6P9T8	INVYYNEATGGK	0.987973849	2	3.652630568
Q6P9T8	LHFFMPGFAPLTSR	2.269687277	2	2.988349676
Q6P9T8	MSATFIGNSTAIQELFK	1.424117279	2	4.366367817
Q6P9T8	TAVCDIPPR	0.420488502	2	2.388725996
Q6P9T8	YLTVAAVFR	1.105392387	2	2.710983992
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.85858937	3	5.55760622
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	0.706687901	3	5.468779564
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.172628298	3	5.75967741
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	0.755103876	3	3.942024469
Q6PA06	**ATLA2 Atlastin_2**	**1.220633748**	**0.36149**	**4**
Q6PA06	AGLTDQVSHHAR	1.600310869	2	3.084488153
Q6PA06	NLVPLLLAPENLVEK	1.068778363	2	2.820347309
Q6PA06	QNQHEELQNVR	1.081769651	2	2.867370129
Q6PA06	SMLQATAEANNLAAVAGAR	1.335678791	2	3.217149258
Q6PCM2	**INT6 Integrator complex subunit 6**	**0.878041426**	**0.00617**	**2**
Q6PCM2	MLIEQLENFLDEIHRR+Oxidation(1)	0.614038165	2	2.508454561
Q6PCM2	NPFFLEPAIIITITDGSK	1.909394316	2	2.349538326
Q6PDV7	**RL10 60S ribosomal protein L10**	**1.205396021**	**0.59134**	**2**
Q6PDV7	FNADEFEDMVAEK	1.139603801	2	3.733217239
Q6PDV7	FNADEFEDMVAEKR	1.034612864	2	2.650208712
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.122804264**	**0.04554**	**4**

Q6PEC1	AEDGENYAIKK	1.151659101	2	2.573964596
Q6PEC1	LEAAYTDLR	0.888863032	2	2.846982241
Q6PEC1	RLEAAYTDLR	1.134592868	2	2.472072601
Q6PEC1	QILESEKDLEEAEEYKEAR	0.91205896	3	4.098305702
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.100911027**	**0.90198**	**3**
Q6PEC4	NDFTEEEEAQVR	1.092911531	2	3.18561244
Q6PEC4	RTDDIPVWDQEFLK	1.053774531	2	3.103571177
Q6PEC4	TDDIPVWDQEFLK	1.335293372	2	2.709439754
Q6PGB8	**SMCA1 Probable global transcription activator SNF2L1**	**1.057292472**	**0.93534**	**2**
Q6PGB8	EMDPEYEEKMVNMPLK+Oxidation(13)	1.026322528	2	2.410116673
Q6PGB8	IKTDVEKSLPPK	1.068055621	2	2.320291281
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**0.939052392**	**0.64771**	**6**
Q6Q0N1	AVFQYIDENQDR	1.317674448	2	3.251579762
Q6Q0N1	EGGSIPVTLTFQEATGK	0.959894781	2	2.753709555
Q6Q0N1	LGGSVELVDIGK	1.458744569	2	2.389075279
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	0.468766488	2	3.422594786
Q6Q0N1	MTEAAAADVQR	1.123760931	2	2.587192774
Q6Q0N1	TGQEIPVNLR	1.031378274	2	2.495492458
Q6RT24	**CENPE Centromere_associated protein E**	**1.082528164**	**0.90594**	**2**
Q6RT24	DLLQKVQDEK	1.086858551	2	2.381723404
Q6RT24	MELENVNMKLQEK	0.997519295	2	2.403448105
Q6RUV5	**RAC1 Ras_related C3 botulinum toxin substrate 1**	**1.130222819**	**0.19265**	**2**
Q6RUV5	HHCPNTPIILVGTK	1.121175813	2	3.115976572
Q6RUV5	LTPITYPQGLAMAK	1.300698181	2	2.985276699
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**1.225281117**	**0.83195**	**2**
Q6SKG1	FDSTSILQTLSK	1.190943177	2	3.143416405
Q6SKG1	TGTVLIPGTTQLTQK	1.255354296	2	2.523626089
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.143343649**	**0.00258**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.100939028	2	4.739874363
Q6TUG0	FQMTQEVVCDECPNVK	1.16129433	2	5.050189495
Q6TUG0	KGEGLPNFDNNNIK	1.255452773	2	3.319294214
Q6TUG0	TLEVEIEPGVR	1.138615069	2	3.033923626
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.055808706**	**0.42139**	**17**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.329952763	2	4.500598431
Q6UPE1	ALNEGGLQSIPK	1.060343093	2	3.480325937
Q6UPE1	ASCDAQTYGIGLK	0.974877452	2	3.826020002
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	0.887144411	2	4.657173634
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.376699774	2	4.884549618
Q6UPE1	GAPLNTPVTEDR	1.025097824	2	3.476269007
Q6UPE1	GIATNDVGIQK	1.039495959	2	3.5613451
Q6UPE1	HHPSIRPTLEGGK	0.977537453	2	2.317771673

Q6UPE1	LQINAQNCVHCK	1.314015747	2	3.507416487
Q6UPE1	LTFPGGLLIGCSPGFMNVPK	1.355388004	2	3.468096972
Q6UPE1	NLSIYDGPEQR	0.994874804	2	2.628942728
Q6UPE1	QLTSENLQSK	0.950402862	2	2.322185993
Q6UPE1	SGSLAAEAIFK	1.118389559	2	3.291090965
Q6UPE1	TAGLHVTEYEDNLK	0.822333175	2	3.694874525
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	1.116597869	2	4.520920753
Q6UPE1	VDHTVGWPLDR	1.052351185	2	2.491892815
Q6UPE1	VTIFAEGCHGHLAK	1.263005468	2	3.792708874
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**1.137080789**	**0.00661**	**7**
Q6URK4	EDSVKPGAHLTVK	1.06538928	2	3.697330475
Q6URK4	GFAFVTFDDHDTVDK	1.061587236	2	3.847793341
Q6URK4	IETIEVMEDR	1.035237491	2	3.36210537
Q6URK4	IFVGGIKEDTEEYNLR	1.966612062	2	4.263820648
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	0.830671458	2	4.6206007
Q6URK4	WGTLTDCVVMR	0.987551707	2	3.020562172
Q6URK4	YHTINGHNCEVK	1.289591606	2	3.574862957
Q6URW6	**MYH14 Myosin_14**	**1.192547277**	**2.2E-16**	**4**
Q6URW6	FDQLLAEEK	1.005683669	1	2.019554377
Q6URW6	EDQSILCTGESGAGK	1.007571375	2	4.611320972
Q6URW6	KFDQLLAEEK	1.283844063	2	3.167654276
Q6URW6	QLLQANPILEAFGNAK	1.229941708	2	4.591949463
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.956292052**	**1**	**4**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.94649426	2	3.831031084
Q6XQN1	LDSGDLLQQAK	0.955908522	2	3.643898964
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.313820475	2	5.467859745
Q6XQN1	QLQNPAVYQVALSEK	1.080438029	2	3.153610706
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.187849014**	**0.03435**	**2**
Q6ZPJ3	FRTTDIVIR	0.816280245	2	2.5243752
Q6ZPJ3	NCAQGEGSMAKKVK	1.333733932	2	2.903820515
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.211236908**	**0.43013**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	1.088239775	2	2.7353127
Q70FJ1	HEAEITNYKIKLEMLEK+Oxidation(14)	1.331256446	2	2.517131567
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.150929498**	**0.91428**	**4**
Q711G3	DCGTDVLDLWTLMQK	1.282142681	2	4.218900204
Q711G3	DVEETKPELSLLGDGDH	0.981782836	2	3.641267061
Q711G3	LNVAVGEYAK	1.206197116	2	2.557029009
Q711G3	VILITPPPLCEAAWEK	1.181653096	2	2.830877781
Q71LX4	**TLN2 Talin_2**	**0.926488476**	**0.99531**	**4**
Q71LX4	NCGEMSEIEAK	1.002113785	2	2.427862644
Q71LX4	QEDVIATANLSR	0.860367837	2	3.116561174
Q71LX4	QELTVFQSKDIPEK	1.075297604	2	2.325152397
Q71LX4	QVAASTAQLLVACK	1.076840898	2	3.261856556

Q71TY3	**RS27 40S ribosomal protein S27**	**1.252648256**	**3.2E-11**	**3**
Q71TY3	DLLHPSPEEEK	0.764413846	2	2.798995018
Q71TY3	LTEGCSFR	1.33742028	2	2.317952871
Q71TY3	LVQSPNSYFMDVK	1.422975824	2	2.880159855
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.265838176**	**0.01354**	**6**
Q75Q39	GLELISKAIEIDNK	1.426851576	2	2.332773209
Q75Q39	NADLSTFYQNR	1.301727307	2	2.897637844
Q75Q39	NREPLMPSPQFIK	0.99489552	2	2.320943594
Q75Q39	SDEDKDKEGEALEVK	1.269981758	2	3.907357693
Q75Q39	SYFSSFTDDIISQPMLK	0.928882297	2	2.939303637
Q75Q39	YEQAIQCYTEAISLCPTEK	0.960242415	2	3.671491385
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.218055759**	**0.00043**	**7**
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.049762974	2	4.674767494
Q76MZ3	LNIISNLDCVNEVIGIR	1.178700272	2	3.941186428
Q76MZ3	LTQDQDVDVK	1.106330227	2	3.179389954
Q76MZ3	NLCSDDTPMVR	1.03112769	2	2.44692111
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.277716006	3	5.721029758
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	1.02843252	3	5.080785751
Q76MZ3	QLSQSLLPAIVELAEDAK	1.288195934	3	4.244922638
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**1.050202967**	**0.5425**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	0.711228961	2	5.526954174
Q78P75	NFGSYVTHETK	0.95426377	2	2.499804258
Q78P75	YNPTWHCIVGR	1.25534578	2	2.944176912
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**1.048413871**	**0.19916**	**5**
Q791V5	EEGIVGFFAGLIPR	1.124181326	2	3.325727701
Q791V5	GLFTGLTPR	1.037314053	2	2.571585655
Q791V5	LCSGVLGTVVHGK	1.871848702	2	3.094375849
Q791V5	VLIQVGYEPLPPTIGR	1.053830335	2	4.332697392
Q791V5	YCGLCDSIVTIYR	1.219267604	2	2.846269608
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.123628988**	**7.2E-06**	**3**
Q794E4	ATENDIYNFFSPLNPVR	1.121954717	2	4.220320225
Q794E4	HSGPNSADSANDGFVR	1.036323612	2	3.753245115
Q794E4	VHIEIGPDGR	1.135683854	2	2.955318689
Q7M0E3	**DEST Destrin**	**1.234847013**	**4E-12**	**3**
Q7M0E3	HEYQANGPEDLNR	1.235313632	2	4.6347785
Q7M0E3	HFVGMLPEK	0.950050161	2	2.40531826
Q7M0E3	HFVGMLPEKDCR	1.13616345	2	2.646548748
Q7TMA5	**APOB Apolipoprotein B_100**	**1.059815116**	**0.99186**	**8**
Q7TMA5	GFEPTLEALFGK	1.058735923	2	2.363183975
Q7TMA5	GIISLLEAMK	0.872799068	2	2.437071085
Q7TMA5	IEGNLVFDPSSYLPK	1.06319424	2	3.419215918
Q7TMA5	IEIDIPLPLGGK	0.962764425	2	2.823627949

Q7TMA5	ITDNDVLIALDSAK	0.846920853	2	2.793828487
Q7TMA5	LSISEQNAQR	1.020113239	2	2.40176177
Q7TMA5	TILFDTFVNDVAPVEK	1.129311063	2	2.722047567
Q7TMA5	NFVASHIANILNSEELYVQDLK	0.951018884	3	3.41705513
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.313145944**	**0.93413**	**4**
Q7TNG8	AVVGSPHVSTASAVR	1.259418577	2	3.146075726
Q7TNG8	AYSTDVCVPISR	1.126056537	2	3.791149378
Q7TNG8	GSQGGLSQDFVEALK	1.182941575	2	3.08360076
Q7TNG8	QLLQEEVGPVGVETMR	1.198621687	2	3.475400925
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.290547468**	**0.40129**	**3**
Q7TP47	AGPIWDLR	1.293558417	2	2.408130169
Q7TP47	DLFEDELVPLFEK	1.386251636	2	2.788420916
Q7TP47	NLANTVTEEILEK	0.928524505	2	2.810117722
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.559246508**	**0.01628**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	0.980798722	2	3.277083397
Q7TP48	LENGEIETIAR	1.103012211	2	3.23254323
Q7TP48	LLLSSETPIEGK	1.72375263	2	3.056897879
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	0.982357286	3	4.214074612
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.178787349**	**1E-10**	**7**
Q7TP52	NLIEWLNK	1.129984806	1	2.293941498
Q7TP52	AGVSVYGIIR	1.385528196	2	2.79576993
Q7TP52	EDCSPADKPYIEEAR	1.054394661	2	3.508070946
Q7TP52	LDYGGMGQEVQVEHIK	1.101541078	2	4.555503368
Q7TP52	LKEHCIVNYQVK	1.429875829	2	4.148532867
Q7TP52	TFSGQTHGFVHR	1.263506737	2	3.412432432
Q7TP52	KREDCSPADKPYIEEAR	1.066308975	3	3.780951023
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.022080828**	**1.1E-12**	**7**
Q7TPB1	ALIAGGGAPEIELALR	1.249011114	2	3.731241465
Q7TPB1	AQDIEAGDGTTSVVIIAGSLLDSCTK	0.691212212	2	4.788865566
Q7TPB1	GDVTITNDGATILK	1.001680565	2	2.894594669
Q7TPB1	GLEILTDMSRPVQLSDR	1.183049007	2	2.506119013
Q7TPB1	LVIEEAER	1.210180865	2	2.356992006
Q7TPB1	SIHDALCVIR	1.238623684	2	2.990057945
Q7TPB1	VIDPATATSVDLR	1.253017405	2	4.016985893
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.193553141**	**0.21731**	**2**
Q7TPJ0	GEDFPANNIVK	1.15504458	2	2.939582348
Q7TPJ0	GTEDFIVESLDASFR	1.056627905	2	4.090071201
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**1.234215524**	**0.34278**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(1)	1.234215524	2	2.503757238
Q7TQ20	MMEEVEKLCDR+Oxidation(2)	1.234215524	2	2.406287432
Q7TQ94	**NIT1 Nitrilase homolog 1**	**1.212458798**	**0.37597**	**2**
Q7TQ94	GQDWEQTQK	1.307444529	2	2.381137371

Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.185682093	3	3.546572924
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.322376038**	**0.04241**	**3**
Q7TQM4	AIWEAVQAYPK	1.147099949	2	2.963289976
Q7TQM4	QDRPLPSTASDSTR	1.175673289	2	3.422183752
Q7TQM4	TQCLEQAQR	1.523957763	2	2.952393055
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.88587572**	**0.95115**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(2)	0.937761308	3	3.613743305
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(6)	0.774849117	3	3.527656555
Q7TSQ1	**CL18A C_type lectin domain family 18 member A**	**1.345528633**	**0.11524**	**2**
Q7TSQ1	MKCQGKGGVLAQIESQK	1.366003867	2	2.322629929
Q7TSQ1	QANDSAGALPVAGKPEPMAR+Oxidation(18)	1.106539442	2	2.778123379
Q80SY4	**MIB1 E3 ubiquitin_protein ligase MIB1**	**0.9421611**	**0.88044**	**2**
Q80SY4	LDIQDKDGDTPLHEALR	0.933464957	2	2.40635705
Q80SY4	NTLIMGLGTQGAEKK	1.046822666	2	2.505900145
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.129780078**	**1**	**13**
Q80W21	KISDYMK	1.109826416	1	1.954682946
Q80W21	CLDAFPNLK	1.092289559	2	3.112538576
Q80W21	CLDAFPNLKDFIAR	1.110247007	2	3.249734879
Q80W21	HNLCGETEEER	1.059964586	2	3.946029425
Q80W21	IRVDILENQLMDNR	1.219977058	2	2.938523293
Q80W21	ITQSNAILR	1.396125732	2	3.077727079
Q80W21	LFLEYTDSSYEEK	1.239462917	2	3.995661736
Q80W21	LKPGYLEQLPGMMR	1.389273828	2	3.294069767
Q80W21	LYSEFLGK	1.167655878	2	2.460704565
Q80W21	VDILENQLMDNR	0.921658171	2	3.505652428
Q80W21	FKLGLDFPNLPYLIDGSHK	1.148508192	3	4.908658028
Q80W21	KHNLCGETEEER	1.147712962	3	4.116714478
Q80W21	LGLDFPNLPYLIDGSHK	1.247001653	3	4.791420937
Q80WE4	**KI20B Kinesin_like protein KIF20B**	**1.145335193**	**0.24699**	**2**
Q80WE4	IKDLEVIVETQKDECK	1.184984326	2	2.399355888
Q80WE4	KEEDCAELKEK	0.440736541	2	2.346516609
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**0.897648629**	**0.20298**	**2**
Q80WS3	TNIIPVLEDAR	0.81365321	2	2.423078537
Q80WS3	DHAVVVGVYRPPPK	0.92973647	3	3.407886744
Q80X90	**FLNB Filamin_B**	**1.249959659**	**0.82977**	**6**
Q80X90	GAGIGGLGITVEGPSESK	1.110701649	2	3.622593641
Q80X90	IEYDDQNDGSCDVK	0.866693614	2	4.030610561
Q80X90	IGNLQTDLSDGLR	1.252647932	2	2.66318059
Q80X90	VDIQTEDLEDGTCK	1.03139333	2	3.975257158
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.088187263	2	4.933664799
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.168071459	2	3.096527815
Q80XB4	**NRAP Nebulin_related_anchoring protein**	**1.454270567**	**0.15748**	**2**

Q80XB4	EAFERMKGQMLGSR+Oxidation(10)	1.171223179	2	2.376036406
Q80XB4	GRSQFHSRADQPGFLQAK	1.454947515	2	2.649783611
Q80XC3	**US6NL USP6 N_terminal_like protein**	**1.079518638**	**0.95798**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	1.089129216	2	2.542774916
Q80XC3	SVDEGSKNLK	0.983485952	2	2.380831003
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**1.135326028**	**0.04761**	**2**
Q80XI3	EFEKDKADDDVFEK	0.511081384	2	2.600506306
Q80XI3	NHDEESLECLCR	1.265539683	2	3.172860384
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**1.046343794**	**0.99991**	**2**
Q80Y84	CDIGLLGLK	1.042905974	2	2.305757046
Q80Y84	ETAAAMATLGEARLR	1.010129804	2	2.410491228
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.057510921**	**0.62016**	**3**
Q80Z25	MIEESLK+Oxidation(1)	1.060280934	1	1.9516325
Q80Z25	ELEQEAERLEK	1.306530171	2	2.559172869
Q80Z25	RMIEESLK+Oxidation(2)	0.957589135	2	2.386195183
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.364036059**	**4.5E-09**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.078509975	2	3.877110004
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.385216005	2	4.487816811
Q80Z29	YLLETSGNLDGLEYK	1.036427476	2	4.070201874
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.450097653	5	4.654572487
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.079408728**	**0.52542**	**3**
Q811D2	AQEDFDK	0.818024358	1	1.94186604
Q811D2	SNLEEEARDLK	1.419619317	1	1.924129844
Q811D2	RSADQLSEKTMEQLR+Oxidation(11)	1.128939104	2	2.318179369
Q811L6	**MAST4 Microtubule_associated serine/threonine_protein kinase 4**	**0.513616789**	**0.20839**	**2**
Q811L6	FPKATAQMEERLK+Oxidation(8)	0.791154377	2	2.338645458
Q811L6	SGHFENTSAELPSVGSLLK	0.502357927	2	2.398220062
Q811Q2	**CLIC6 Chloride intracellular channel protein 6**	**1.199633536**	**0.30686**	**2**
Q811Q2	AGSDGESIGNCPFSQR	1.214767859	2	3.728628159
Q811Q2	FLDGDELTLADCNLLPK	0.799322118	2	2.310149193
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.069080028**	**0.00963**	**5**
Q811X6	EMKSLEQSGSLK+Oxidation(2)	1.008030879	1	1.967831016
Q811X6	IVDDQVILSSSSSCLLPSK	1.34103396	2	4.541796684
Q811X6	LVEEGIVSPNDLDLVMSDGLGMR	1.193734111	2	3.446676254
Q811X6	LYDIEQQQITNALESIR	1.295503636	2	4.84074688
Q811X6	TFGPVPEFSGDTVEK	1.064528692	2	3.023160696
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.061527102**	**9.9E-20**	**10**
Q8BFZ3	DLTDYLMK	0.506369559	1	2.300020695
Q8BFZ3	CDVDIRK	1.153105492	2	2.499210596
Q8BFZ3	HQGVMVGMGQK+Oxidation(8)	1.071946081	2	2.82784462
Q8BFZ3	SYELPDGQVITIGNER	0.846122627	2	5.148619175
Q8BFZ3	HQGVMVGMGQK	1.005630804	3	3.946663618

Q8BFZ3	HQGVMVGMGQK+Oxidation(5)	1.085051248	3	3.874840021
Q8BFZ3	HQGVMVGMGQK+Oxidation(5)Oxidation(8)	1.354988062	3	3.585509777
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	0.995580936	3	6.918212891
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(6)	1.011728957	3	5.718425751
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.269159085	3	3.993017435
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**0.988566384**	**0.9998**	**3**
Q8BG32	LYDNLLEQNLIR	1.092806333	2	2.852474928
Q8BG32	TTANAIYCPPK	0.851354161	2	3.142029762
Q8BG32	VQIEHISSLIK	1.003505625	2	2.851612329
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**0.852460721**	**0.5002**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.762212751	2	3.163911819
Q8BGT5	VLCIINPGNPTGQVQSR	1.115505531	2	4.748867512
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.199509439**	**0.0003**	**4**
Q8BGY2	EDLKLPEGELGK	1.198012728	2	2.428681374
Q8BGY2	YEDICPSTHNMDVPNIK	1.159843835	2	4.094659805
Q8BGY2	KYEDICPSTHNMDVPNIK	1.131414213	3	4.731079578
Q8BGY2	VHLVGIDIFTGK	1.273325563	3	3.658273458
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.178520217**	**5.9E-06**	**9**
Q8BH00	ELNLPFGGMK	0.907978369	1	2.377738714
Q8BH00	LSLELGGK	1.118570859	1	1.911461353
Q8BH00	ELLMLENFIGGK	0.673123636	2	3.913826942
Q8BH00	ILCGEGVDQLSLPLR	1.209903191	2	4.685049057
Q8BH00	ITQLSAPHCK	1.302323839	2	3.117837429
Q8BH00	KLSLELGGK	1.370360397	2	2.404917955
Q8BH00	NPAIIFEDANLEECIPATVR	1.202899964	2	4.449766636
Q8BH00	SSFANQGEICLCTSR	1.141811578	2	4.162261963
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.215443612	3	5.112445831
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**0.999114174**	**0.13388**	**7**
Q8BHN3	AEKDEPGAWEETFK	1.037979989	2	4.243261814
Q8BHN3	MLDYLQGSGETPQTDIR	1.053664285	2	5.495077133
Q8BHN3	REPWLLASQYQDAIR	1.043595426	2	2.882961035
Q8BHN3	SGGIERPFVLSR	1.20169112	2	2.587230682
Q8BHN3	VTEGGEPYR	0.80673816	2	2.370399714
Q8BHN3	VVIMGAGKPAAVVLQTK	1.109340305	3	3.32273531
Q8BHN3	THSDSKPYGPTSVGLDFSLPGMEHVYGIPEHADSLR	1.215148155	4	5.020823956
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**1.025893221**	**0.99787**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.031676851	1	2.15258503
Q8BIJ6	SCQTALAEILDVLVR	1.049822371	3	3.820162296
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.038687811**	**1**	**9**
Q8BJ64	ADSAYHPSCTCK	1.054270888	2	3.808933496
Q8BJ64	AEVQTLVSR	1.1503535	2	2.756081581
Q8BJ64	ELQPGSHVQSDK	0.925111282	2	3.154007912

Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.932736531	2	3.969662428
Q8BJ64	GGDGPLHVSR	1.096766097	2	2.453290939
Q8BJ64	VIGVENLR	1.041638154	2	2.726027012
Q8BJ64	VLLLEAGPK	1.14071071	2	2.668742657
Q8BJ64	TNHPLHQAFLQAAR	0.957805779	3	4.560591221
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	0.758773454	5	5.505509377
Q8BL66	**EEA1 Early endosome antigen 1**	**1.29378715**	**0.02286**	**2**
Q8BL66	AAVLDLEK	1.294880708	1	1.983706236
Q8BL66	IQAGEGETAVLNQLQEK	1.27199042	2	3.320890665
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**1.043879357**	**0.76919**	**3**
Q8BP47	KEDGTFYEFGDDIPEAPER	1.196123404	2	3.954987764
Q8BP47	LMTDTINEPILLCR	1.03934673	2	3.188336134
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.060277678	2	2.697900295
Q8BTM8	**FLNA Filamin_A**	**1.07001713**	**0.73128**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	1.26945721	2	3.074577332
Q8BTM8	ANLPQSFQVDTSK	0.922616316	2	2.573916912
Q8BTM8	GAGTGGLGLAVEGPSEAK	1.038604439	2	3.530128956
Q8BTM8	GLVEPVDVVDNADGTQTVNYVPSR	1.131662609	2	5.516614437
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	1.121047072	3	4.895051479
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.102948982**	**0.00013**	**2**
Q8BTZ7	IGQNCSIGPNVSLGPGVVVEDGVCIR	0.942222914	2	2.741019011
Q8BTZ7	HHGQEGSILVTK	1.348756796	3	3.570860147
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.145506305**	**0.78672**	**4**
Q8BU33	AAVETLGVPCFLGGMSR	0.927650644	2	3.287715197
Q8BU33	LPNSLMGR+Oxidation(6)	1.095254876	2	2.348659277
Q8BU33	LTGTVGVAAVTAGPGLTNTVTAVK	1.396056268	2	3.158547878
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.889741869	2	4.930418015
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.124276926**	**0.8774**	**2**
Q8BWQ1	ADIWLIR	1.123812861	1	1.957116008
Q8BWQ1	IHHDQPVKPLDR	1.204734469	3	3.758649349
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**0.963659152**	**0.31911**	**2**
Q8BX70	ENALSELDVPFKVK	0.830889255	2	3.04153204
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(20)	1.011087037	2	2.480703354
Q8BZ81	**LRRT3 Leucine_rich repeat transmembrane neuronal protein 3**	**1.090577925**	**0.86392**	**2**
Q8BZ81	GLRENTIICASPK	0.899323897	1	1.943642139
Q8BZ81	YPASMKQLQQR+Oxidation(5)	1.090890988	2	2.583102226
Q8BZN6	**DOC10 Dedicator of cytokinesis protein 10**	**1.009266358**	**0.58069**	**2**
Q8BZN6	IIQDSNKVNPK	0.99445104	2	2.585124016
Q8BZN6	LTQMEASALLYFFMRK+Oxidation(14)	1.191884425	2	2.382379532
Q8C547	**HTR5B HEAT repeat_containing protein 5B**	**1.359639869**	**0.18527**	**2**
Q8C547	MVVSIAEDLLR+Oxidation(1)	1.403732073	2	2.309351206

Q8C547	SAESQGRSEILMSLQK	1.213260108	2	2.330236912
Q8C7R4	**UBA6 Ubiquitin_like modifier_activating enzyme 6**	**1.047326141**	**0.99483**	**2**
Q8C7R4	GMVTVTDPDLIEK+Oxidation(2)	0.982351175	1	1.991837859
Q8C7R4	NFALLGVGTGREK	1.060941013	2	2.418986797
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.212181359**	**0.11882**	**2**
Q8C7X2	FNVEDGEIVQQVR	1.489877128	2	4.066555977
Q8C7X2	VMGDRSVLYK+Oxidation(2)	0.986244851	2	2.539273977
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.325966157**	**3E-07**	**4**
Q8CC88	FLPSLAQSALEK	1.007233776	2	2.512056112
Q8CC88	HQATGELDDAK	1.33802724	2	3.080752611
Q8CC88	LQLTDEQLQNR	1.031953864	2	2.387462378
Q8CC88	VSSDQLSSENLTSAVGQK	0.885763304	2	3.705358744
Q8CCF0	**PRP31 U4/U6 small nuclear ribonucleoprotein Prp31**	**1.119656517**	**0.86124**	**2**
Q8CCF0	YFSSMAEFLKVK	1.119878911	1	2.052215338
Q8CCF0	ERLGLTEIR	1.110586575	2	2.479750395
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**0.89249396**	**0.01217**	**2**
Q8CDI6	EKVANMEVALDK+Oxidation(6)	1.057762906	2	2.618868828
Q8CDI6	ELDDRNMEVQRLEALLK	0.614038165	2	2.359146357
Q8CDI7	**CC150 Coiled_coil domain_containing protein 150**	**1.202783563**	**0.89962**	**2**
Q8CDI7	EDNRKLAMSLEQALQTNGHLQSK	99999.89988	2	2.347748518
Q8CDI7	MNIFHLQTEKESNPQK+Oxidation(1)	1.202783561	2	2.589575529
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**0.922371791**	**0.95488**	**2**
Q8CDM4	MEEESIDLIIK	0.906187147	2	2.309832573
Q8CDM4	VTCQHKMEEESIDLIIK	0.949455022	2	2.512662411
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.172909395**	**0.14631**	**3**
Q8CFN2	DDPSTIEK	1.228197068	1	2.090017557
Q8CFN2	YVECSALTQK	1.205103207	2	3.128201485
Q8CFN2	NVFDEAILAALEPPEPK	1.172351877	3	4.855863094
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.082859554**	**0.74964**	**9**
Q8CG45	EHHFEAIALVEK	0.861256981	2	2.937575579
Q8CG45	FFGNSWSETYR	1.27545543	2	2.62629509
Q8CG45	FYAYNPLAGGLLTGK	1.434679567	2	4.113083363
Q8CG45	MDASASAATVR	1.049741667	2	3.43906188
Q8CG45	RMDASASAATVR	1.060516488	2	2.906724691
Q8CG45	TTYGTSAPSMTSAALR	1.106142262	2	3.989971161
Q8CG45	WMYHHSQLQGTR	1.379907969	2	3.13119626
Q8CG45	AVSGAPLRPGTVLGTMEMGR	1.15337543	3	3.49970293
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.176674042	3	5.482962608
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.25430377**	**0.39582**	**2**
Q8CG48	EEKLLEK	1.320473629	1	1.982037425
Q8CG48	KIKALNCEIEELER	1.210204744	2	2.40289402
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.153866599**	**1.6E-06**	**8**

Q8CGC7	AIQGATSHHLGQNFSK	1.296962476	2	4.540873051
Q8CGC7	DQDVEPGAPSMGAK	0.926400873	2	2.986260891
Q8CGC7	GDVSISVEEGKENLLR	1.156011129	2	3.491641283
Q8CGC7	GSQFGQSCCLR	0.989018352	2	2.796952724
Q8CGC7	KEENLAEWYSQVITK	0.90560529	2	3.838823795
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.418361248	2	4.330032825
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.15392563	2	4.680173397
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.732218862	2	3.193164825
Q8CGN4	**BCOR BCL_6 corepressor**	**1.305960525**	**0.30005**	**2**
Q8CGN4	FLTDYLNDLQGR	1.42219392	1	2.167698622
Q8CGN4	KQTQPSCTPASRLPAK	1.143697133	2	2.32960701
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.020304194**	**0.07558**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(11)	1.229892188	2	2.621778011
Q8CHB8	ISSATTGGQKPNTLPQK	1.007910411	2	2.328954697
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.059699328**	**0.00012**	**7**
Q8CHM7	DTSKPCLINIMIEPQSTR	0.686362398	2	3.215198755
Q8CHM7	GVVPDNHPNCVGAAR	1.192887853	2	3.441797733
Q8CHM7	GYFVQTPEELQDSLR	1.113916131	2	3.481383801
Q8CHM7	LVELCNLPFLPTPMGK	1.623161724	2	4.402967453
Q8CHM7	NCFIVSEGANTMDIGR	1.20477682	2	4.699247837
Q8CHM7	NQEAMGAFQEFPQVEACR	1.100177039	2	6.068603992
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	0.702347777	3	4.66683054
Q8CIB5	**FERM2 Fermitin family homolog 2**	**1.096589138**	**0.35955**	**2**
Q8CIB5	GCEVTPDVNISGQK	1.073695454	2	2.926573515
Q8CIB5	TSTILGDITSIPELADYIK	1.152946469	2	3.637227058
Q8CIE6	**COPA Coatomer subunit alpha**	**1.082307157**	**0.27827**	**11**
Q8CIE6	ASNLENSTYDLYTIPK	1.107261427	2	3.157133341
Q8CIE6	DADSQNPDAPEGK	0.816150206	2	3.849972963
Q8CIE6	GITGVDLFGTTDAVVK	0.981362537	2	3.815433264
Q8CIE6	KKNLSPGAVESDVR	1.034040247	2	2.343878031
Q8CIE6	LLELGPKPEVAQQTR	1.056013282	2	2.579835176
Q8CIE6	QQPLFVSGGDDYK	1.17743858	2	2.396327496
Q8CIE6	SILLSVPLLVVDNK	1.111610684	2	3.048382282
Q8CIE6	SSGLTAVWVAR	1.46300234	2	2.664338112
Q8CIE6	TLDLPIYVTR	1.051293939	2	2.400628567
Q8CIE6	GTSPTQIWCNNSQLPVDHILAGSFETAMR	1.140673596	3	3.891744137
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.108582313	3	3.653582096
Q8CJF7	**ELYS Protein ELYS**	**1.0046196**	**0.22754**	**2**
Q8CJF7	QNSNRVNIEELLK	0.99489552	2	2.661190033
Q8CJF7	SVENGQSTEILDDLK	1.160696572	2	2.635882616
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.040349369**	**0.6484**	**3**
Q8JZN5	GIILVGNEEQK	1.074251803	2	2.717178583

Q8JZN5	GSNTCEVHFENTR	1.163629096	2	4.031219959
Q8JZN5	SGNVTTVMETIGR	0.82291626	2	3.405417204
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.209181711**	**0.22249**	**16**
Q8K009	KVSLELGGK	1.40819567	1	2.130205393
Q8K009	NLQFEDGK	1.22370939	1	2.044054985
Q8K009	YFAGWCDK	1.217634825	1	2.091299772
Q8K009	AGFSVFWADDGLDTGPILLQR	0.869412163	2	4.641120911
Q8K009	AMVEAVQLIADGK	1.148026871	2	3.956334829
Q8K009	ANNTEYGLASGVFTR	1.148422369	2	4.432839394
Q8K009	DLGEEALNEYLK	1.439477388	2	3.651471853
Q8K009	EESFGPIMVISK	0.862088897	2	2.831002951
Q8K009	FLFPEGIK	0.972556774	2	2.316706657
Q8K009	FQNGDIDGVLQR	1.174491606	2	2.858817101
Q8K009	GVINIIPGSGGVAGQR	1.16175567	2	3.81226778
Q8K009	HGSIIYHPSLLPR	1.182238383	2	4.396770477
Q8K009	KLGFTGSTSVGK	0.906614249	2	2.43472743
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.205021425	2	4.036365986
Q8K009	SCDVKPNDTVDSLYNR	1.210321537	2	3.917734146
Q8K009	VVGVFTVPDKDGK	1.271928933	2	3.325073242
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.393206353**	**0.00041**	**5**
Q8K442	GQITAILGHSGAGK	1.5737335	2	3.442412138
Q8K442	LTGVCPQCNVQFDFLTVR	1.398347212	2	3.274153709
Q8K442	NTQNILVQNLSGGQK	1.062914851	2	2.943261862
Q8K442	STLLNVLSGLCVPTK	1.418495548	2	3.239352465
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	1.308457658	3	4.260466099
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.876611613**	**0.9703**	**10**
Q8K4C0	CCLEEGLEPVCFER	1.006953503	2	4.231117249
Q8K4C0	EYKNPVEFTGK	0.811503517	2	2.373410463
Q8K4C0	FDHEMFGLKPK	0.908853781	2	3.185684204
Q8K4C0	GYPIDILLSSR	1.160804081	2	3.058079958
Q8K4C0	HSALGQHPTINDDLPNR	1.021225935	2	4.504080772
Q8K4C0	IAVIGSGASGLTCIK	1.913382367	2	3.711714029
Q8K4C0	KLPSQSEMMAEINK	0.866318021	2	4.170432091
Q8K4C0	KTILTTEDR	0.96596677	2	2.700097561
Q8K4C0	SDDIGGLWR	0.879061683	2	2.928570032
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	1.078745156	3	4.590936184
Q8K4G6	**MACD1 MACRO domain_containing protein 1 (Fragment)**	**1.071280387**	**0.89647**	**3**
Q8K4G6	AAGSLLTDECR	0.925761968	2	3.069678783
Q8K4G6	SCYLSSLDLLLEHR	1.080904487	2	3.064972639
Q8K4G6	HVIHTVGPIAVGQPTASQAAELR	1.148334124	3	5.096166611
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.079233979**	**0.96269**	**3**

Q8K4T4	EVLNLTK	1.108543529	1	2.056444883
Q8K4T4	IEELEETNKSLQK	1.046822666	2	2.409121752
Q8K4T4	SSIISSDGGKGPSEDAKK	1.105573205	2	2.44810009
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.034668321**	**0.83304**	**3**
Q8K4Z3	GNPSGIQPDLLISLTAPK	1.042066825	2	3.731160641
Q8K4Z3	LFGYQPTIYYPK	1.625080452	2	2.39132905
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.031225718	2	5.523769379
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**0.915155025**	**0.98216**	**4**
Q8K586	FNVWDTAGQEK	1.128130998	2	3.267007828
Q8K586	LVLVGDGGTGK	1.218213261	2	2.375268698
Q8K586	NLQYYDISAK	1.081227073	2	2.772548199
Q8K586	VCENIPIVLCGNK	0.913117869	2	4.064858437
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.882910342**	**0.50212**	**2**
Q8QZY1	VFSDEVQQQAQLSTIR	0.828769242	2	4.1369133
Q8QZY1	VYEIQDIYENSWTK	1.012717791	2	3.812175512
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.108152576**	**0.62783**	**4**
Q8R081	SDALETLGFLNHYQMK	1.178377088	2	3.645467758
Q8R081	SSSGLLEWDSK	0.936478974	2	2.736476898
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	1.359347292	3	4.673249245
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	1.127540871	3	7.076634407
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.107711743**	**0.81626**	**5**
Q8R0F9	FDNTYSLLHTK	1.181050739	2	3.201810598
Q8R0F9	GSSHQVENEILFPGCVLR	1.084754842	2	5.200308323
Q8R0F9	VCEMLLHECELQSQK	1.220478862	2	4.935697079
Q8R0F9	VGYTAEVLLPDK	0.813448471	2	2.596436262
Q8R0F9	VGYTAEVLLPDKACEEK	0.91404926	2	2.411343336
Q8R164	**BPHL Valacyclovir hydrolase**	**1.016412615**	**0.91094**	**3**
Q8R164	FTLVAWDPR	1.325522238	2	2.514173031
Q8R164	QVSLLGWSDGGITALIAAAK	1.192589307	2	3.941599846
Q8R164	TDFAPQLQSLNK	1.014976523	2	3.803179264
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**1.091914882**	**0.96611**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	0.974285934	2	3.580742836
Q8R1V4	QLLDQVEQIQK	1.179192392	2	3.405798912
Q8R2H4	**KLH12 Kelch_like protein 12**	**0.534262819**	**0.13396**	**2**
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(15)	0.534262819	2	2.39592433
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(3)	0.534262819	2	2.655059099
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**0.931912295**	**0.54686**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	0.629142627	2	3.692912817
Q8R3Q6	NCIAQTSAVVK	0.970239754	2	3.003870726
Q8R491	**EHD3 EH domain_containing protein 3**	**1.123974134**	**0.7576**	**3**
Q8R491	ADQIETQQLMR	1.145666797	2	3.081978321

Q8R491	LFEAEEQDLFK	0.976069702	2	3.372247696
Q8R491	MQDQLQAQDFSK	1.161434616	2	3.641734838
Q8R508	**FAT3 Protocadherin Fat 3**	**1.252916006**	**0.01417**	**2**
Q8R508	FFIDPK	1.254241492	2	2.331485271
Q8R508	QVSYHITGGNPR	0.768152491	2	2.582986593
Q8R5M4	**OPTN Optineurin**	**1.124332681**	**0.87894**	**2**
Q8R5M4	NSATPSELNEK	1.174403119	1	2.187112331
Q8R5M4	LELQVESMRSEIK+Oxidation(8)	1.066780458	2	2.41690731
Q8VBU2	**NDRG2 Protein NDRG2**	**0.93483075**	**0.73148**	**3**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.928258313	2	5.835636616
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.713457493	2	4.723073959
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.01859176	2	4.637427807
Q8VC12	**HUTU Urocanate hydratase**	**1.355291154**	**0.60642**	**6**
Q8VC12	HQLVVGSQAR	1.257893657	2	2.916214228
Q8VC12	LLALEFAQELR	1.903746155	2	4.30324173
Q8VC12	LVITNGMVIPNYSSR	1.465332093	2	3.599220514
Q8VC12	MMLSWDVSNGVAR	1.115851924	2	2.468038797
Q8VC12	VAIAVAINQAIASGK	1.431430304	2	2.667102814
Q8VC12	VFVTSGLGGMSGAQAK	1.314644521	2	4.463918209
Q8VC28	**AK1CD Aldo_keto reductase family 1 member C13**	**0.756994983**	**0.16005**	**2**
Q8VC28	ILNKPGLK	1.998435055	1	2.030481577
Q8VC28	YKEWVDQNSPVLLNDPVLCDVAK	0.747843904	3	4.417491436
Q8VCD5	**MED17 Mediator of RNA polymerase II transcription subunit 17**	**1.088880049**	**0.0517**	**2**
Q8VCD5	EIFAQLSREAVQIK	0.950749933	1	2.096586704
Q8VCD5	MELLMSALSPCLL+Oxidation(1)Oxidation(5)	1.92544266	2	2.556518793
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**1.173691503**	**0.0969**	**3**
Q8VDC1	GLELQVMQLQQEK	1.321614737	2	2.39601469
Q8VDC1	MEEALASLAQELQDSK	1.105573205	2	2.407505512
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(1)	1.139293321	2	2.350479603
Q8VDD9	**PHIP PH_interacting protein**	**1.29165686**	**0.76239**	**2**
Q8VDD9	EDLLQK	0.865144607	1	1.963890433
Q8VDD9	MELREQELMKIVGIK	1.293953516	2	2.444310665
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**1.050253893**	**0.73593**	**2**
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.990921055**	**0.79293**	**3**
Q8VED5	YEDEINK	1.422677948	1	2.178145885
Q8VED5	NKYEDEINK	1.015026592	2	2.381468534
Q8VED5	NKYEDEINKR	0.983642487	3	3.442986727
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.106029547**	**5.8E-05**	**10**
Q8VEK3	GGYSNRGNYNRGGMPNR	1.304138943	2	2.353109837
Q8VEK3	LLEQYKEESK	0.789575586	2	3.074449301
Q8VEK3	LLEQYKEESKK	1.149182358	2	3.736121893
Q8VEK3	NFILDQTNVSAAAQR	1.160696572	2	5.071896076

Q8VEK3	TCNCETEDYGEK	1.376518432	2	3.351394892
Q8VEK3	VSELKEELK	1.193618709	2	2.657158852
Q8VEK3	VSELKEELKK	1.176789082	2	2.541083097
Q8VEK3	YNILGTNTIMDK	1.030628716	2	3.314326763
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.001365256	3	4.94856596
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.13721982	3	5.04553318
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.893094069**	**0.112**	**9**
Q8VHE9	ATVQSVLLDSAGR	0.875617471	2	3.010750532
Q8VHE9	FLPLPLTQLLNK	1.029395043	2	2.661053419
Q8VHE9	GATYGADHDLAR	0.802039377	2	3.111813784
Q8VHE9	NLYSDLQALGSK	0.785733166	2	3.701475859
Q8VHE9	RPPEPLVTDK	0.888146263	2	3.01343441
Q8VHE9	VESVTGGSPLTNQYYLAAHR	0.428338855	2	4.077107906
Q8VHE9	VLVLEQHTK	0.841591488	2	2.30949378
Q8VHE9	VVAHGVSHAILLK	0.798042843	2	2.823715925
Q8VHE9	RPPEPLVTDKEAR	1.051200117	3	3.893317938
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**1.206730531**	**0.97779**	**4**
Q8VHF5	ALGVLAQLIWSR	1.021771134	2	2.74878788
Q8VHF5	GLVYETSVLDPDEGIR	1.088239775	2	3.507694006
Q8VHF5	GYSIPECQK	1.08770465	2	2.507483244
Q8VHF5	IVPNILLEQGK	1.235910103	2	2.561623335
Q8VHN7	**GPR98 G_protein coupled receptor 98**	**1.028314553**	**0.78837**	**2**
Q8VHN7	FIVEEPEFNSVR	0.861705494	2	2.304203272
Q8VHN7	ITMVASDAPYGR	1.063568672	2	2.640762568
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.134298344**	**0.06206**	**2**
Q8VHT6	SLQNVHEEVISR	1.126368336	2	3.298285723
Q8VHT6	TSADLQTNACVTPAK	1.211923237	2	3.977719545
Q8VHX6	**FLNC Filamin_C**	**1.113512377**	**0.50633**	**2**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.113889136	2	3.876795769
Q8VHX6	IECDDKGDGSCDVR	0.446958651	2	3.602124214
Q8VI04	**ASGL1 L_asparaginase**	**0.998407926**	**0.97684**	**3**
Q8VI04	GLGGLILINK	1.070747465	2	2.432905436
Q8VI04	GNLAYATSTGGIVNK	0.965138351	2	4.068856239
Q8VI04	TVDEAATLALDYMK	1.076788797	2	2.609549522
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.056972703**	**2.8E-05**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.331948387	2	4.57313633
Q8VID1	LAEDGAHVVISSR	0.669793517	2	3.70780015
Q8VID1	NFAAELAPK	0.927226839	2	2.326081514
Q8VID1	VNCLAPGLIK	0.663374437	2	2.489539146
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.750528528**	**0.03261**	**10**
Q8VIF7	QYDISNPK	0.804097567	1	1.992500424
Q8VIF7	CGPGYATPLEAMK	0.721851316	2	3.124633312

Q8VIF7	FLHDPDATQGFVGCALSSNIQR	0.977437788	2	4.826551914
Q8VIF7	GGFVLLDGETFEVK	0.867060984	2	4.277728558
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.783424565	2	3.900733709
Q8VIF7	HEIIQTLQMK	0.791343477	2	2.714158058
Q8VIF7	HNIMVSTEWAAPNVFK	0.740592944	2	4.73441267
Q8VIF7	LTGQIFLGGSIVK	0.900810414	2	3.471406698
Q8VIF7	NEGGTWSVEK	0.754765862	2	2.534460545
Q8VIF7	NTGIEAPDYLATVDVDPK	0.735870915	2	4.629254818
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.002758904**	**0.96939**	**2**
Q8VIJ6	FGQGGAGPVGGQGPR	1.022851991	2	3.313546658
Q8VIJ6	YGEPGEVFINK	0.941219274	2	2.328407526
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**1.064177083**	**0.10932**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	1.363486398	2	5.457888603
Q91VA0	AILPFDLQIIDEK	1.058052694	2	4.200493813
Q91VA0	GNILPPNTEGYIGIR	0.979566542	2	3.162102461
Q91VA0	HNQGLAFR	1.041612401	2	2.533815622
Q91VA0	KVEFVSELPK	1.006574534	3	3.407253265
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.980460209**	**1**	**2**
Q91VM9	IIAINVNDPEAEK	1.00156704	2	2.974803448
Q91VM9	MEIATEEPLNPIK	0.921293691	2	4.087888241
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**1.164360836**	**0.92231**	**3**
Q91W43	EMLQALGLASIDELIEK	0.894375016	2	2.484267235
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	1.257730009	2	4.244522095
Q91W43	VSFQPNSGAQGEYAGLATIR	1.196308314	2	5.061907768
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.084342398**	**0.94157**	**2**
Q91W90	SFEDTIAQGITFVK	1.049528619	2	2.667158365
Q91W90	VDCTQHYAVCSEHQVR	1.084442645	3	4.735944748
Q91X77	**CY250 Cytochrome P450 2C50**	**1.152408469**	**0.24359**	**4**
Q91X77	NFLLEK	1.228280829	1	2.086547375
Q91X77	EHEESLDVTIPR	0.895796508	2	2.460468769
Q91X77	IKEHEESLDVTIPR	1.17536802	2	3.751028299
Q91X77	YALLLLLK	1.372638356	2	2.684285879
Q91X78	**ERLN1 Erlin_1**	**1.428532437**	**0.00012**	**2**
Q91X78	ISEIEDAAFLAR	1.07372323	2	2.796798706
Q91X78	SVQTTLQTDEVK	1.480894192	2	2.931272268
Q91Y81	**SEPT2 Septin_2**	**1.142758334**	**0.67632**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	1.201150193	2	3.161390305
Q91Y81	ILDEIEEHSIK	0.713396943	2	2.896253586
Q91Y81	LTVVDTPGYGDAINSR	1.12687825	2	3.923052788
Q91Y81	STLINSLFLTDLYPER	1.155781671	2	2.758109093
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.001510529**	**0.99234**	**8**

Q91YT0	GAGAYICGEETALIESIEGK	1.009544593	2	4.396888733
Q91YT0	GEFYNEASNLQVAIR	1.056596692	2	3.404612064
Q91YT0	GGAGFPTGLK	1.14129073	2	2.338701248
Q91YT0	KTSFGSLKDEDR	1.209941431	2	2.848312616
Q91YT0	LVEGCLVGGR	1.001470085	2	2.796410084
Q91YT0	YLVVNADEGEPGTCK	1.004099172	2	5.211250782
Q91YT0	GDARPAEIDSLWEISK	1.005916549	3	3.708158255
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.303719493	3	4.732461929
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.083596113**	**0.01058**	**6**
Q91Z53	LLDAAGANLR	1.178419102	2	2.515960217
Q91Z53	NCVILPHIGSATYK	1.00E+00	2	3.583428144
Q91Z53	NTMSLLAANNLLAGLR	0.915475174	2	4.772294044
Q91Z53	RLPEAIEEVK	1.097273696	2	2.784994602
Q91Z53	VISTLSVGVDHLALDEIK	1.580246744	2	4.130730629
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.172260047	3	6.913645267
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**1.060439006**	**9.9E-20**	**16**
Q91ZJ5	EFPTVPLVK	1.200994307	1	2.04294157
Q91ZJ5	FVQDLSK	1.508113461	1	1.936302423
Q91ZJ5	GGTLTQYEGK	1.34222195	2	2.670147181
Q91ZJ5	GLPDNISSVLNK	1.170339067	2	3.306905508
Q91ZJ5	GTVIIIANHGDR	1.279045122	2	3.097029448
Q91ZJ5	IDIPPGAVLENK	1.330081321	2	3.029579639
Q91ZJ5	LNGGLGTSMGCK	1.740952554	2	3.251587868
Q91ZJ5	LQEQNAIDMEIIVNPK	1.052876137	2	4.192785263
Q91ZJ5	LVEIAQVPK	1.272815289	2	2.461324692
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.51309597	2	5.086017132
Q91ZJ5	SFENSLGINVPR	1.064537261	2	3.459330082
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	1.239074452	2	5.411497593
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.271477228	2	4.537339687
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	1.178725624	3	4.976561069
Q91ZJ5	IQRPPEDSIQPYEK	1.383689285	3	4.587617397
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	1.109081486	3	4.566628933
Q91ZU6	**DYST Dystonin**	**1.140756127**	**0.63908**	**4**
Q91ZU6	LQVEQNK	1.330289853	1	1.925152898
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(1)	1.107086993	2	2.51303339
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(2)	1.107086993	2	2.513103724
Q91ZU6	SAETNIDQDITNLK	1.24999898	2	2.432936192
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**1.38372663**	**0.15242**	**2**
Q91ZV0	CGDLECETLISRVLALR	1.481900679	2	2.469432592
Q91ZV0	KMLDQDDIVENDK+Oxidation(2)	1.194856285	2	2.419124365
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**0.955377778**	**0.86216**	**3**
Q91ZX7	GCHVNECLSR	0.887991219	2	2.679976463

Q91ZX7	MYDAQQQQVGTNK	0.955503756	2	4.094335556
Q91ZX7	VFFTDYGQIPK	1.103812764	2	2.672917366
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**0.939146953**	**0.42369**	**2**
Q920A6	DLDTVASDMMVLLK	1.136123254	2	2.389456749
Q920A6	GLAEVSDIAEQVLNAVNK	1.111641378	3	5.861097336
Q920B9	**SP16H FACT complex subunit SPT16**	**1.263591647**	**0.11396**	**2**
Q920B9	EMKIYIDK+Oxidation(2)	1.238655201	1	1.911048412
Q920B9	ICDVYNSVMDVVKK	1.342300752	2	2.329063177
Q920D2	**DYR Dihydrofolate reductase**	**1.19386026**	**0.00067**	**4**
Q920D2	LIEQPELASK	1.211878978	1	2.02802515
Q920D2	IMQEFESDTFFPEIDLEK	1.344906502	2	5.029399872
Q920D2	LLPEYPGVLSEIQEEK	1.398123344	2	3.776790857
Q920D2	NGDLPWPLLR	1.163034127	2	2.825037479
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.992894287**	**0.06357**	**3**
Q920F5	EIAEVTGDPVHESLK	1.093975486	2	2.982332945
Q920F5	ISECEAVHPVK	0.722373819	2	3.234783649
Q920F5	WLLGLLNVQGK	1.566087245	2	2.366596699
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.053854869**	**0.46984**	**2**
Q920J4	IDQYQGADAVGLEEK	1.064262507	2	4.54865551
Q920J4	AGCECLNESDEHGFDNCLR	1.159015305	3	3.794691801
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.084785848**	**0.98625**	**20**
Q920L2	ACALSIAESCRPGDK	1.02662989	2	2.354421616
Q920L2	ANAGEESVMNLDK	1.009170719	2	3.65202117
Q920L2	GEGGILINSQGER	1.116336665	2	3.502244473
Q920L2	GVIALCIEDGSIHR	0.977829773	2	4.024643421
Q920L2	HTLSYVDTK	1.058301978	2	2.742524147
Q920L2	IDEYDYSKPIEGQQK	1.007466581	2	4.463561535
Q920L2	KHTLSYVDTK	1.503686687	2	2.328847647
Q920L2	LGANSLLDLVVFGR	1.568838402	2	2.361578465
Q920L2	NTIIATGGYGR	0.973628208	2	2.438231468
Q920L2	SMQSHAAVFR	1.048340169	2	2.302069426
Q920L2	TGHSLLHTLYGR	1.281010564	2	3.006803989
Q920L2	TLNEADCATVPPAIR	1.039473571	2	3.936993837
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.225886973	2	5.820820332
Q920L2	VGSVLQEGCEK	1.095044047	2	3.678835869
Q920L2	VSQLYGDLQHLK	1.175255946	2	3.481491327
Q920L2	VTLDYRPVIDK	1.021908352	2	3.133111715
Q920L2	ACALSIAESCRPGDKVPPIK	1.321467683	3	3.344251156
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	0.981287857	3	4.669754982
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.15170358	3	6.509884357
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.960377421	3	4.427851677
Q920P0	**DCXR L_xylulose reductase**	**1.283483633**	**0.81959**	**7**

Q920P0	AVVQVSQIVAR	1.077572551	1	2.460403442
Q920P0	SSMTTGSALPVDGGFLAT	1.12047455	1	2.555672646
Q920P0	ALTNHTVYCSTK	0.600540947	2	3.549277306
Q920P0	GVPGAIVNVSSQASQR	1.063543905	2	5.619990349
Q920P0	STVLALQAAGAQVVAVSR	1.02820691	2	3.790534973
Q920P0	TREDLDSLVR	1.133619241	2	2.938616037
Q920P0	VNAVNPTVVMTPMGR	0.679882326	2	3.288023233
Q920P6	**ADA Adenosine deaminase**	**2.005609096**	**0.03104**	**2**
Q920P6	FKDDQANYSLNSDDPLIFK	2.040879778	2	2.660372734
Q920P6	TVHAGEVGSAEVVR	1.915801231	2	3.456770897
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.09820979**	**0.8173**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	1.105505562	2	4.178931713
Q921F2	GISVHISNAEPK	1.111214601	2	2.521897316
Q921F2	KDLKTGHSK	0.960670278	2	2.472450256
Q921F2	TSDLIVLGLPWK	1.051770847	2	2.813910007
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.022996671**	**0.05809**	**7**
Q922F4	ALTVPELTQQMFDAK	0.951042493	2	4.0499897
Q922F4	GHYTEGAELVDSVLDVVR	1.01827926	2	6.77488327
Q922F4	IREEYPDR	0.908544484	2	2.853942394
Q922F4	MASTFIGNSTAIQELFK	1.424117279	2	4.438858509
Q922F4	NMMAACDPR	0.939128438	2	2.514367104
Q922F4	NSSYFVEWIPNNVK	1.006751238	2	4.701595306
Q922F4	YLTVATVFRGPMSMK+Oxidation(14)	1.957826905	2	2.31305337
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.196645226**	**0.00076**	**2**
Q922J3	EMETMQAKLMK+Oxidation(5)	1.169823336	2	2.639829397
Q922J3	HEEILQNLQKMLADTEDK	0.932736531	2	2.419271708
Q923D2	**BLVRB Flavin reductase (NADPH)**	**1.133993241**	**1.4E-06**	**3**
Q923D2	LQDVTDDHIR	1.146774813	2	3.305094242
Q923D2	TGLTTLAQAVQAGYEVTVLVR	1.055428164	3	4.01170826
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.791900448	3	4.08564949
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**1.034416933**	**0.51001**	**2**
Q923J6	LEFLTNLDIK	0.625137707	1	2.013311386
Q923J6	MSDPNKTAITAEKEALNLK	1.046129987	2	2.465999603
Q923K9	**A1CF APOBEC1 complementation factor**	**1.115169427**	**0.87278**	**2**
Q923K9	LAPQILEEICQK	1.299899185	2	2.429979324
Q923K9	TGYSLVQENGQR	1.063406473	2	2.771718264
Q923V8	**SEP15 15 kDa selenoprotein**	**1.072017925**	**0.31973**	**2**
Q923V8	GCCQEEAQFETK	0.955957641	2	4.15205574
Q923V8	LLDDNGNIAEELSILK	1.337793281	2	3.655009508
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**0.7916597**	**0.315**	**4**
Q924C3	ELESPAAASLLAPMDLGEEPLEK	1.127566111	2	3.416186571

Q924C3	SGTYFWPGSDVEIDGILPDIYK	0.731862849	2	3.698600054
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	0.767039159	2	3.250379801
Q924C3	AEYLHTWGGLLPVISK	1.006983535	3	3.693504333
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.085757451**	**0.99999**	**7**
Q924S5	AQSVLEEDHYGMEDVK	1.106735772	2	3.971151352
Q924S5	FSVGGMTDVAEIK	1.073248846	2	2.875715733
Q924S5	HVMDVVDEELSK	1.078557857	2	3.824842215
Q924S5	MEMINVSGYVAQEK	0.941471834	2	3.779714346
Q924S5	QLEVEPEGLEPEAENK	1.069006931	2	4.163259506
Q924S5	TENPLVLIDEVDK	1.114001311	2	2.475800991
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	0.940899504	3	6.393419743
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**1.157489297**	**0.54945**	**3**
Q924W5	ELDMKEKELQEK	1.141304684	2	2.60380888
Q924W5	MEEQQVRLNDAEKK	0.985116509	2	2.387438297
Q924W5	TKEQINQGEERLTELK	1.243718316	2	2.561676025
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.105630948**	**0.09739**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	1.051876562	2	4.11878109
Q99020	FGEVVDCTIK	1.118985908	2	2.500708342
Q99020	IFVGGLNPEATEEK	1.69855029	2	3.753350496
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.151846442**	**0.0078**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.573402015	2	3.021803379
Q99JI4	RLDEELEDAEK	1.133117411	2	2.918748617
Q99JI4	VNEIVETNRPDSK	1.215460998	2	3.332903624
Q99JW2	**ACY1 Aminoacylase_1**	**1.042362612**	**0.99734**	**2**
Q99JW2	FIEDTAAEK	1.077236427	2	2.630792618
Q99JW2	SVSIQYLEAVR	1.009982362	2	2.395458221
Q99K43	**PRC1 Protein regulator of cytokinesis 1**	**1.673946499**	**0.00033**	**2**
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(1)	1.673946499	2	2.368153572
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(6)	1.673946499	2	2.368328571
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**1.163458717**	**0.07937**	**2**
Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(14)	1.163334437	2	2.517407179
Q99KK9	YDLTVPFARYLAMNKLK+Oxidation(13)	1.217624458	2	2.596557617
Q99KW3	**TARA TRIO and F_actin_binding protein**	**1.014069113**	**0.6514**	**2**
Q99KW3	AYQEELSRELSK	1.053379539	1	2.030693769
Q99KW3	SEREIEQLK	0.925607516	1	1.971695542
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.782693706**	**0.8727**	**2**
Q99L04	ATAQEAQSLGGR	0.970964461	2	3.340855837
Q99L04	CVPVVCDSSQESEVK	0.706103143	2	4.446412086
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.053665689**	**1**	**4**
Q99LF4	GLGHQVATDALVAMEK	0.997637868	2	2.309446573
Q99LF4	NLDFQDVLDK	0.98570138	2	2.88338542

Q99LF4	NVTDVVNTCHDAGISK	1.054476964	2	4.276314735
Q99LF4	TNLDESDVQPVK	1.05418244	2	3.692002773
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.244576355**	**0.07157**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(12)	1.244576355	2	2.330037355
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(6)	1.244576355	2	2.317301512
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**1.081108244**	**0.70217**	**2**
Q99M87	AQGLYETINVTIPAGIQTDQK	1.009612381	2	2.410283089
Q99M87	GSIITNPCVVCR	1.135046139	2	2.598234892
Q99ML9	**RN111 E3 ubiquitin_protein ligase Arkadia**	**1.562204207**	**0.0399**	**2**
Q99ML9	LHPHEVMQRMEVQR+Oxidation(7)	1.21214341	2	2.412626028
Q99ML9	DMTGNQQEQEKSGVVRK	1.589888634	3	3.623355865
Q99MN1	**SYK Lysyl_tRNA synthetase**	**1.229085248**	**0.03862**	**4**
Q99MN1	MATLQESEVKVDGEQKLSK+Oxidation(1)	0.934090341	2	2.338323355
Q99MN1	RGDIIGVEGNPGK	1.248373942	2	3.326686621
Q99MN1	SEEEFVHINNK	1.206260668	2	3.514252186
Q99MN1	YLDLILNDFVR	1.20711695	2	2.691838503
Q99MQ1	**BICC1 Protein bicaudal C homolog 1**	**1.128906125**	**0.58157**	**2**
Q99MQ1	EAKEMIMSVLDTK	1.200484519	2	2.398347378
Q99MQ1	QYLMGCLPLVLMFDMK+Oxidation(15)	1.092399208	2	2.301759481
Q99MS0	**S14L2 SEC14_like protein 2**	**1.315064531**	**0.69063**	**4**
Q99MS0	AGEMTEVLPNQR	1.068210441	2	3.826982498
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	1.582237044	2	3.860684633
Q99MS0	DQVKQQYEHSVQISR	0.976474979	2	2.384320974
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.204220224	2	4.780360222
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.983717954**	**0.23559**	**5**
Q99MZ8	TGDTGMLPANYVEAI	2.085234369	1	2.430654287
Q99MZ8	GFSVVADTPELQR	0.990023556	2	3.588947058
Q99MZ8	QQSELQSQVR	1.010811493	2	2.520248413
Q99MZ8	QSFTMVADTPENLR	0.830465764	2	3.175507784
Q99MZ8	TQDQISNIK	1.047791719	2	2.869517326
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**1.058047022**	**0.26958**	**5**
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.842594116	2	6.942374229
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.103893421	2	4.848217964
Q99PF5	IGQQPQQPGAPPQQDYTK	1.114106144	2	4.054358006
Q99PF5	IINDLLQSLR	1.203498575	2	2.572946072
Q99PF5	SVSLTGAPESVQK	1.015897848	2	2.550324678
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.24415595**	**1.6E-14**	**18**
Q99PL5	IQEELEK	1.320473629	1	2.312760353
Q99PL5	AENSQLTER	1.05562957	2	2.38333416
Q99PL5	DALNQATSQVESK	0.682217856	2	3.31478858
Q99PL5	EAEETQNSLQAECDQYR	1.230668564	2	5.641663551
Q99PL5	EHTSHLEAELEK	0.857366922	2	3.359024525

Q99PL5	GELESSDQVR	1.112365779	2	3.198652267
Q99PL5	HMAAASAECQNYAK	1.056543255	2	4.309083939
Q99PL5	HMAAASAECQNYAK+Oxidation(2)	1.552745897	2	3.958441496
Q99PL5	LKELESQVSCLEK	1.15811233	2	4.080004215
Q99PL5	LLATEQEDAAVAK	1.299260768	2	3.992249966
Q99PL5	LQQENSILR	0.734473167	2	2.611452579
Q99PL5	QLHLAEAQTK	1.13918985	2	2.351928473
Q99PL5	RLEEVTR	0.962950166	2	2.443027973
Q99PL5	TGVIQDTWHK	1.0671231	2	2.319155216
Q99PL5	TILAETEGMLK	1.082755174	2	3.165858269
Q99PL5	TLQEQLENGPNTQLAR	1.230983434	2	5.044582367
Q99PL5	TLVSTVGSMVFSEGEAQR	1.054399968	2	4.283988476
Q99PL5	VEPAVSSIVNSIQVLASK	1.21051671	2	4.011188507
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**1.101541078**	**0.78039**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(10)	1.101541078	2	2.693808079
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(11)	1.101541078	2	2.650903225
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.081233665**	**0.99947**	**2**
Q9CPQ1	FGVAEPR	1.103592791	2	2.432296038
Q9CPQ1	NYDSMKDFEEMR	0.913617908	2	3.796538591
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.165344312**	**0.78481**	**2**
Q9CRB9	VAEELALEQAK	1.032833704	2	3.439563274
Q9CRB9	YEYHPVCADLQTK	1.117451897	2	3.678458452
Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**1.199294682**	**0.04663**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.173987462	2	2.667444944
Q9CTN4	LKDSGDVSDIIEK	1.238964526	2	2.478770018
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.930294472**	**0.99719**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	0.913990049	2	4.378838062
Q9CW42	GLSVSEAECTAMGLR	0.935742999	2	3.179822922
Q9CW42	LQQVGTVAQLWIYPIK	0.864998854	2	3.339229107
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**0.984277119**	**0.5596**	**3**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.074634235	2	4.261363983
Q9CWH6	ALLEVVQSGGK	1.647413585	2	2.945260048
Q9CWH6	LTVEDPVTVEYITR	1.218017829	2	4.007008076
Q9CWK8	**SNX2 Sorting nexin_2**	**1.341765986**	**0.20936**	**3**
Q9CWK8	ALSQLAEVEEK	1.031042845	2	2.372405767
Q9CWK8	AVNTQALSGAGILR	1.214295633	2	3.517492056
Q9CWK8	QQQFENLDQQLR	1.630659029	2	2.513881683
Q9CXD6	**CC90A Coiled_coil domain_containing protein 90A_ mitochondrial**	**1.169002382**	**0.01292**	**2**
Q9CXD6	MLELRTEIVSLHAQQDR	1.78230575	2	2.683454752
Q9CXD6	VRTDTKLNFNLEK	1.066780458	2	2.484920502
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**1.159215956**	**0.2662**	**2**

Q9CYW4	LEDILTGLGLR	1.112829988	2	3.744465828
Q9CYW4	RLEDILTGLGLR	0.835987811	2	3.288958311
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.151832667**	**0.35354**	**2**
Q9CZY3	LLEELEEGQK	1.177915798	2	2.811604023
Q9CZY3	VNMSGVSSSNGVVDPR	1.119990441	2	3.019990444
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**0.875041853**	**0.0224**	**3**
Q9D024	ERIMNEEDPEKQR	1.111654126	2	2.585873365
Q9D024	IMQEEGQPLKLPDTK	0.674532714	2	2.899211168
Q9D024	RLEEAALR	1.073854434	2	2.618826866
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.091994633**	**0.00068**	**5**
Q9D0M3	GLLSSLDHTSIR	1.184706713	2	2.776491404
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.073659359	2	5.265496254
Q9D0M3	HLVGVCYTEEEAK	0.905263262	2	3.935879707
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	1.134998491	3	4.274136543
Q9D0M3	LSDYFPKPYPNPEAAR	1.275286722	3	3.413618326
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.084804922**	**0.10029**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.81084129	2	2.944493532
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.310415766	2	5.235791206
Q9D0S9	SLPADILYEDQQCLVFR	1.087262745	2	4.47976923
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.115438501**	**0.60154**	**5**
Q9D172	NLSTFAVDGK	1.16860043	1	2.920947552
Q9D172	NVLAESAR	1.18573871	1	2.007691145
Q9D172	GVEVTVGHEQEEGGK	1.009175697	2	3.793674469
Q9D172	GVTEAHVDQK	0.728226929	2	2.827171803
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.576604672	2	4.33207655
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.130820795**	**5.2E-05**	**4**
Q9D1Q6	NIIGYFEQK	1.093797898	1	2.474280596
Q9D1Q6	MNPAVFLSLADLR+Oxidation(1)	1.082150296	2	2.369707823
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.220390273	2	5.437285423
Q9D1Q6	VDCDQHSDIAQR	1.244990707	2	3.54489994
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.265024333**	**9.9E-20**	**5**
Q9D2U9	AMGIMNSFVNDIFER	1.323612054	2	5.177259445
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)	1.296518444	2	4.357598782
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)Oxidation(5)	1.046174993	2	3.088084221
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(5)	1.296869345	2	3.887322664
Q9D2U9	LLLPGELAK	1.361866756	2	2.417346954
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.02074738**	**0.99804**	**2**
Q9D6M3	GAAVNLTLVTPEK	1.040878395	2	2.770613909
Q9D6M3	GVNEDTYSGFLDCAR	0.8999575	2	4.650985241
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.113574495**	**1.3E-10**	**10**
Q9D6Y9	CVAYAESHDQALVGDK	1.154492316	2	4.957682133
Q9D6Y9	GTHDLWDSR	1.18614856	2	2.36400485

Q9D6Y9	HFTSNVLPR	1.239991775	2	2.453317881
Q9D6Y9	IVLDSDAAEYGGHQR	1.115250948	2	4.491281509
Q9D6Y9	IYESHVGISSHEGK	1.360878081	2	4.531390667
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	0.401214393	2	3.804407597
Q9D6Y9	QFNLTDDDLLR	0.920502142	2	2.754038811
Q9D6Y9	RQFNLTDDDLLR	0.977363646	2	2.864859819
Q9D6Y9	WELYIPPK	1.2594803	2	2.385748386
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	0.881057619	3	3.911939859
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.072494258**	**0.91683**	**2**
Q9D6Z1	ELNEEKLEK	1.106599506	2	2.464313269
Q9D6Z1	IDCFSEVPTSVFGEK	1.001615001	2	2.752813339
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.301249227**	**0.7118**	**4**
Q9D7B6	AVIFEDCAVPVANR	0.818265676	2	3.361348629
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	1.303371966	2	4.9260149
Q9D7B6	IGTEGQGFLIAMK	1.126229061	2	2.980456352
Q9D7B6	VHQILEGSNEVMR	1.180424178	2	2.91190505
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**0.925354803**	**0.92671**	**2**
Q9D7X8	ISDEMEDIIK	0.886863908	2	2.734996796
Q9D7X8	SNISSLDEQEGVK	1.029872906	2	3.743230104
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.455596462**	**0.00491**	**5**
Q9D819	YVANLFPYK	1.144001392	1	2.131053686
Q9D819	GISCMNTTVSESPFK	0.981802762	2	4.744656086
Q9D819	GQYISPFHDVPIYADK	1.269542215	2	3.941816568
Q9D819	VLGILAMIDEGETDWK	1.844921625	2	4.29685688
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.337802202	3	4.98183012
Q9D855	**QCR7 Cytochrome b_c1 complex subunit 7**	**1.104162496**	**0.37399**	**2**
Q9D855	RLPEDLYNDR	1.113425798	2	2.544440508
Q9D855	YEEDKFYLEPYLK	1.090183001	2	4.624572277
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**0.935478906**	**0.79804**	**3**
Q9D880	TIALNQVEDVR	0.91654218	2	3.127310514
Q9D880	TVLEHYALEDDPLEAFK	1.149138261	2	4.925953865
Q9D880	VLLDLSAFLK	1.289926378	2	2.553409338
Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**1.2029095**	**0.36538**	**2**
Q9D8W5	MVQQCCTYVEEITDLPVK	1.486201872	2	4.889622688
Q9D8W5	WSTLVEDYGVELR	0.915643979	2	3.08286643
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**0.997432167**	**0.52947**	**2**
Q9DB15	NYVQGINLVQAK	0.996554207	2	2.781139851
Q9DB15	SEALAGAPLDNAPK	1.891356476	2	3.19210124
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.093730476**	**0.8402**	**2**
Q9DBH5	WSELAGCTADFR	1.04826695	2	3.283900261
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	1.205629886	3	3.841823339

Q9DCJ5	**NDUA8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8**	**1.07059282**	**0.78548**	**2**
Q9DCJ5	ARPEPNPVIEGDLKPAK	0.910990385	3	4.665341854
Q9DCJ5	TDRPLPENPYHSR	1.035942208	3	3.894039869
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**0.945610519**	**0.99984**	**3**
Q9DCM0	SLLPGCQSVISR	0.932830214	2	3.073825121
Q9DCM0	TDFQQGCAK	0.968654655	2	2.91068387
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.216088641	3	4.187090874
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.247919956**	**0.00043**	**3**
Q9DCS9	AYDLVVDWPVTLVR	1.287053314	2	4.403495789
Q9DCS9	RVPDITECK	1.145155762	2	2.326785088
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.012173674	2	2.973173141
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.230618027**	**0.42934**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.216378718	2	2.833332062
Q9DCT2	ILTDYGFEGHPFR	0.879975012	2	2.892276525
Q9DCT2	KFDLNSPWEAFPAYR	0.974452372	2	3.658503294
Q9DCT2	SLADLTAVDVPTR	1.148614643	2	2.736535549
Q9DCT2	VVAEPVELAQEFR	1.02183304	2	3.649208784
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.13883559**	**0.02463**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.225345252	2	5.446032047
Q9DCU9	LIEPNTAVTR	1.104016233	2	3.190212488
Q9DCU9	TMDWFGYYGGPCR	1.138835933	2	3.536493778
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**0.986012157**	**0.81797**	**9**
Q9EP89	EVWSEGLGYADVENR	0.975908288	2	3.020353317
Q9EP89	FENSIESLR	0.962704708	2	2.97218442
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	1.499219437	2	5.522389412
Q9EP89	IKDEVGAPGIVVGVSVDGK	1.17780568	2	4.163432121
Q9EP89	KNDFEQGELYLK	1.187532268	2	4.194926739
Q9EP89	LVNTPYVDNSYK	1.631031013	2	2.577412844
Q9EP89	WAGGGFLSTVGDLLK	1.143360885	2	4.632734299
Q9EP89	LDLDLPVQHYVPEFPEK	0.942818839	3	3.688930988
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.242024064	3	3.801635027
Q9EPH2	**MRP MARCKS_related protein**	**1.032214026**	**0.10764**	**2**
Q9EPH2	AAATPESQEPQAK	1.381307677	2	2.667475939
Q9EPH2	GDVTAEEAAGASPAK	1.025424121	2	3.050321341
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.154862248**	**0.54632**	**7**
Q9EPH8	ALDTMNFDVIK	1.12754191	2	3.105648518
Q9EPH8	GFGFVCFSSPEEATK	1.661326923	2	2.655185223
Q9EPH8	GFGFVSFER	1.233407452	2	2.50764823
Q9EPH8	KEFSPFGTITSAK	1.028318047	2	3.188788652
Q9EPH8	SLGYAYVNFQQPADAER	1.069474432	2	3.363800287

Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	0.925194215	3	4.733613491
Q9EPH8	SKVDEAVAVLQAHQAK	1.077856414	3	4.314959526
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**2.262349119**	**9.9E-20**	**13**
Q9EQ76	NNEVTLYK	1.305124422	1	2.003182173
Q9EQ76	ASIYQSVFTNSSK	1.595183406	2	2.784206152
Q9EQ76	GTCILPSVNDMMDDIDEK	2.20214081	2	3.925513506
Q9EQ76	ILCGTVSIKPNVK	1.785156344	2	2.914944887
Q9EQ76	KEPVFNDELPAR	1.19833442	2	3.049708128
Q9EQ76	LQEYITSFATEK	2.265943312	2	3.329575777
Q9EQ76	NNLPTAISDWWYMK	1.432792561	2	3.015808105
Q9EQ76	SCLEEGLEPTCFER	1.520654968	2	4.387738228
Q9EQ76	SDDVGGLWK	2.050134708	2	2.835040808
Q9EQ76	VAVIGAGVSGLAAIR	1.274873308	2	3.93653512
Q9EQ76	VWNDGYPWDMVVITR	1.565145826	2	3.861160994
Q9EQ76	YIQFETLVTR	2.997640495	2	2.854773045
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.175502796	3	4.001115799
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.311480624**	**1.7E-06**	**3**
Q9EQH3	IREDLPNLESSEETEQINK	1.026859142	2	5.099476337
Q9EQH3	LNLEHIATSSAVSK	1.354889266	2	4.035788059
Q9EQH3	VLETTVEIFNK	1.095675061	2	2.959443808
Q9EQS0	**TALDO Transaldolase**	**1.075680694**	**0.03145**	**7**
Q9EQS0	VSTEVDAR	1.329615825	1	1.981729388
Q9EQS0	ALAGCDFLTISPK	1.319493252	2	2.935023546
Q9EQS0	ILDWHVANTDKK	1.221076244	2	3.2501719
Q9EQS0	LGGPQEEQIK	1.291586773	2	2.679030895
Q9EQS0	LSSTWEGIQAGK	0.547472618	2	2.714589119
Q9EQS0	SYEPQEDPGVK	1.085676803	2	2.909102201
Q9EQS0	WLHNEDQMAVEK	1.039348889	2	3.690667152
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**1.145682983**	**0.79395**	**2**
Q9EQW7	DETIAVPLEENSALPK	1.069637724	2	2.663294554
Q9EQW7	VTQWAEER	1.180831053	2	2.452829361
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.168056701**	**4.6E-12**	**3**
Q9EQX9	LELFLPEEYPMAAPK	0.944465642	2	3.857037067
Q9EQX9	SNEAQAIETAR	1.22927667	2	3.276730299
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	0.795901122	3	3.996587992
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.057593432**	**0.57233**	**17**
Q9ER34	FNPETDFLTGK	1.018867212	1	2.288868189
Q9ER34	ADIANLAEEFK	0.890536137	2	2.438708067
Q9ER34	CTTDHISAAGPWLK	1.140573024	2	3.906744003
Q9ER34	DINQEVYNFLATAGAK	0.99252196	2	4.154200077
Q9ER34	FKLEAPDADELPR	1.150309553	2	3.696936369
Q9ER34	GHLDNISNNLLIGAINIENGK	1.104368904	2	5.612960815

Q9ER34	IVYGHLDDPANQEIER	1.248205143	2	4.731932163
Q9ER34	LTGTLSGWTSPK	1.45017587	2	3.116814613
Q9ER34	NAVTQEFGPVPDTAR	0.937123056	2	4.156704903
Q9ER34	QGLLPLTFADPSDYNK	0.83225385	2	3.570981264
Q9ER34	SDFDPGQDTYQHPPK	0.985860769	2	2.913554668
Q9ER34	SQFTITPGSEQIR	1.007388613	2	3.565665007
Q9ER34	VDVSPTSQR	0.948369152	2	2.521443844
Q9ER34	VGLIGSCTNSSYEDMGR	1.279624522	2	4.231098175
Q9ER34	WVVIGDENYGEGSSR	1.033735171	2	4.202404022
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	1.283673394	3	4.097528934
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	0.986228822	3	4.214668274
Q9ER72	**SYCC Cysteinyl_tRNA synthetase_ cytoplasmic**	**1.35821399**	**0.17419**	**2**
Q9ER72	LSETTDPDKR	1.396279365	2	2.430091858
Q9ER72	QMLERIQNSVK+Oxidation(2)	1.021168933	2	2.469664574
Q9ERK4	**XPO2 Exportin_2**	**1.049960536**	**0.52303**	**3**
Q9ERK4	IIIPEIQK	1.361866756	2	2.398523808
Q9ERK4	LLQTDDEEEAGLLELLK	1.04965903	2	2.384386539
Q9ERK4	SNNVNEFPVLK	1.404641879	2	2.499286652
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**1.633575845**	**0.23361**	**3**
Q9ES21	HFDSQVIIYGK	1.115472706	2	2.455652237
Q9ES21	LSNTSPEFQEMSLLER	2.301929914	2	3.600185871
Q9ES21	TQLGLVMDGFNSLLR	1.172043705	2	3.98378706
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.198179109**	**6.1E-15**	**12**
Q9ES38	ACQAAWALK	1.322576866	2	2.73195982
Q9ES38	ADVWENFQQR	1.243686733	2	3.064492941
Q9ES38	EGFDVGVIADPLYILDNK	1.125186326	2	4.912632942
Q9ES38	GATAILVLPSK	1.312744133	2	2.929193735
Q9ES38	IQDSLEITNTYK	1.200511419	2	3.650266171
Q9ES38	LKEATIQEDK	1.389792752	2	2.806114912
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.485356138	2	4.229716301
Q9ES38	SISALSVFLGLAK	1.340278475	2	3.198299646
Q9ES38	SLMPDVYQAVCEGTWK	1.016724921	2	3.916050911
Q9ES38	YLCNVPGQPEDK	1.137752329	2	3.486678839
Q9ES38	YLCNVPGQPEDKK	1.491214808	2	3.756635189
Q9ES38	QGFCIPVETGKPGLLLTK	1.101220648	3	3.662816048
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.879909399**	**0.56647**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.862128596	2	3.790046215
Q9EST6	SLDLFGCEVTNR	1.086676322	2	2.744765282
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.310774067**	**0.29663**	**3**
Q9ESW0	QGQGQLVTCSGAFK	0.945057442	2	2.359763861
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.29987516	3	5.727999687
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.24473229	3	5.986730576

Q9HB97	**PARVA Alpha_parvin**	**1.088423071**	**0.27572**	**4**
Q9HB97	DLAEDLYDGQVLQK	1.158162048	2	2.359844685
Q9HB97	LNVAEVTQSEIAQK	1.088247425	2	3.146553993
Q9HB97	QIQEEITGNTEALSGR	1.331807808	2	3.167425156
Q9HB97	VLIDWINDVLVGER	0.999617042	2	3.237922668
Q9JHL4	**DBNL Drebrin_like protein**	**1.081425743**	**0.61209**	**4**
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**1.362560919**	**9.8E-05**	**2**
Q9JHZ9	AYEQLGYR	1.343785747	2	2.550028801
Q9JHZ9	HLEGLLPVGMPTADTQR	1.438763388	2	3.794389486
Q9JI57	**GT2D1 General transcription factor II_I repeat domain_containing protein 1**	**1.01223477**	**0.99494**	**2**
Q9JI57	EMEDINTLRECVQILFNSR	1.02026845	2	2.322575808
Q9JI57	GTQPTTEGQAHPLVLPTR	1.011678279	2	2.379821062
Q9JI85	**NUCB2 Nucleobindin_2**	**1.064689363**	**0.25952**	**5**
Q9JI85	TRLDELK	1.623952689	1	2.028229952
Q9JI85	FQQGIAPSGPAGELK	1.175113312	2	2.663860798
Q9JI85	LSQELDLVSHK	1.457654207	2	2.758491755
Q9JI85	QEYQQAVQQLEQK	1.04617795	2	4.300695419
Q9JI85	VHNVEPVESAR	1.097079142	2	2.89632535
Q9JI91	**ACTN2 Alpha_actinin_2**	**1.077233173**	**0.45365**	**8**
Q9JI91	ACLISMGYDLGEAEFAR	1.082750308	2	4.420625687
Q9JI91	GYEEWLLNEIR	1.438595064	2	2.850530863
Q9JI91	HRPDLIDYSK	1.066611456	2	2.417123318
Q9JI91	HTNYTMEHIR	1.098742187	2	2.806650877
Q9JI91	KHEAFESDLAAHQDR	1.101905853	2	5.297757626
Q9JI91	MLDAEDIVNTPKPDER	0.849099489	2	3.088994741
Q9JI91	QSILAIQNEVEK	0.800244107	2	2.842998505
Q9JI91	TINEVETQILTR	0.773214208	2	3.164352655
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.012951083**	**5.7E-06**	**9**
Q9JJ19	AVDPDSPAEASGLR	1.005859218	2	3.248405457
Q9JJ19	IVEVNGVCMEGK	0.960713962	2	3.674657345
Q9JJ19	LLVVDPETDEQLK	0.983478872	2	2.689920187
Q9JJ19	LLVVDPETDEQLKK	1.444810063	2	2.86783123
Q9JJ19	LVEPGSPAEK	1.183835684	2	2.56203723
Q9JJ19	LVEVNGENVEK	1.014343466	2	2.882863283
Q9JJ19	SEHTEPPAAADTK	0.693595564	2	3.206414461
Q9JJ19	SEHTEPPAAADTKK	1.035444434	3	4.611467838
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	0.617904541	3	3.914588451
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.013446688**	**0.14658**	**3**
Q9JJ54	FGDVVDCTLK	0.985560333	2	2.722913504
Q9JJ54	IFVGGLSPDTPEEK	1.364312865	2	3.913995743
Q9JJ54	IDASKNEEDEGHSNSSPR	1.171610898	3	3.897474289

Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.085709279**	**0.9208**	**3**
Q9JJ79	ASDLKDLNSR	1.082377661	2	2.352930784
Q9JJ79	DQIEVMKGNVKSR	1.012173291	2	2.366572618
Q9JJ79	NCLEEWTKAAGLEK	1.091596899	2	2.372308016
Q9JJM9	**SEPT5 Septin_5**	**1.082553174**	**0.18694**	**2**
Q9JJM9	LIRMKDEELR	1.903746155	2	2.481617451
Q9JJM9	MQEMLQKMK+Oxidation(4)	0.615586995	2	2.417910814
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.014656426**	**0.9972**	**2**
Q9JJU8	GDYDAFFEAR	1.048101297	2	2.544910192
Q9JJU8	QQDVLCFLEANK	1.013880202	2	2.88103199
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.183963782**	**2E-06**	**4**
Q9JK38	GRVEDVVVSDECR	1.111166287	2	3.459815979
Q9JK38	ITLECLPQNVGFYK	1.496753324	2	3.747694016
Q9JK38	VEDVVVSDECR	1.191905538	2	3.7012043
Q9JK38	VLGQLTETGVVSPEQFMK	1.211183875	2	4.539330006
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.245626071**	**0.76969**	**8**
Q9JLA3	EGETYYDVVAVVDPVTR	0.959830491	2	2.60989213
Q9JLA3	IVPEWQDYDQEIK	1.077559389	2	3.562581539
Q9JLA3	LNIQPSETDYAVDIR	1.223842247	2	4.133049488
Q9JLA3	VEEDVASDLVMK	1.118542361	2	3.258431673
Q9JLA3	YVLEPEISFTADNSFAK	1.104145781	2	3.722279549
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	0.568306733	3	3.918198347
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.141493191	3	6.133787632
Q9JLA3	LGIEGLSLHNILK	1.59341832	3	3.886561632
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**0.918235852**	**0.00039**	**17**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.333531059	2	4.441753864
Q9JLJ3	ANDTTFGLAAGVFTR	1.024749549	2	4.90164423
Q9JLJ3	CQVLLEAAR	1.225349265	2	3.037918329
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.084873223	2	4.690720558
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.156990463	2	4.654038906
Q9JLJ3	EVNLAVENAK	0.896049957	2	2.976658821
Q9JLJ3	GALLANFLTQGQVCCNGTR	0.954299925	2	5.349894524
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.17295208	2	4.583210468
Q9JLJ3	IGDPLLEDTR	1.202866907	2	3.927162886
Q9JLJ3	MGPLINAPHLER	1.28140107	2	3.495093107
Q9JLJ3	MGPLINAPHLER+Oxidation(1)	1.3776815	2	3.016052961
Q9JLJ3	RDEIAIMETINNGK	1.05306108	2	5.45677042
Q9JLJ3	VEPVDASGTEK	1.203747474	2	2.323982239
Q9JLJ3	VSFTGSVPTGMK	1.200148822	2	3.368051291
Q9JLJ3	VSFTGSVPTGMK+Oxidation(11)	1.298966494	2	2.814189911
Q9JLJ3	VTIEYYSQLK	1.15007905	2	3.192930937

Q9JLJ3	GIKPITLELGGK	1.125076298	3	3.921104193
Q9JLT0	**MYH10 Myosin_10**	**1.279541654**	**1.9E-10**	**3**
Q9JLT0	DEELLKVKEK	1.134452871	1	2.14849782
Q9JLT0	AGVLAHLEEER	1.415941507	2	3.516296864
Q9JLT0	DAAGLESQLQDTQELLQEETR	0.670334725	2	3.746877909
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**1.084452693**	**0.28276**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	1.215360202	2	5.805500031
Q9JLZ3	SEVPGIFCAGADLK	1.066678629	2	3.259103298
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	1.100116906	3	4.581832409
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**1.148117869**	**0.43022**	**13**
Q9JM53	DGEQHEDLNEVAK	0.853057662	2	3.926563025
Q9JM53	ILPEYLSNWTMEK	1.188601367	2	2.61017561
Q9JM53	KSQASGIEVIQLFPEK	1.030232106	2	3.647904158
Q9JM53	KVETDHIVTAVGLEPNVELAK	1.174710723	2	6.325231075
Q9JM53	LNDGSQITFEK	1.176977624	2	3.578783989
Q9JM53	SATEQSGTGIR	0.819553064	2	3.854152918
Q9JM53	SITVIGGGFLGSELACALGR	1.029655972	2	3.413947105
Q9JM53	SQASGIEVIQLFPEK	0.947905819	2	4.256615162
Q9JM53	TGGLEIDSDFGGFR	1.133486354	2	3.816315413
Q9JM53	VETDHIVTAVGLEPNVELAK	1.060020242	2	6.018784046
Q9JM53	VMPNAIVQSVGVSGGK	1.266117326	2	4.523158073
Q9JM53	VNAELQAR	1.054084696	2	2.374446869
Q9JM53	VLIVSEDPELPYMRPPLSK	0.789225282	3	3.706329107
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**1.044677435**	**0.89199**	**2**
Q9JMA1	CTESEEEEVTK	1.028858773	2	3.644242048
Q9JMA1	EKESVNAKVLK	1.183609006	2	2.559516668
Q9JMB7	**PIWL1 Piwi_like protein 1**	**0.953948896**	**0.72943**	**2**
Q9JMB7	ELIGLIVLTKYNNK	1.047272163	2	2.42495203
Q9JMB7	SQELQISAGFQELSLAERGGRR	0.647581091	2	2.340773582
Q9JMD3	**PCTL PCTP_like protein**	**1.21889155**	**4.2E-07**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.114177962	2	4.544362545
Q9JMD3	ESVQVPDDQDFR	0.542492588	2	2.671562195
Q9JMD3	SSQFLAPK	1.047591138	2	2.346596479
Q9JMD3	WDSNVIETFDIAR	1.203085741	2	4.122594357
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.219325013	3	4.43348074
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(1)	1.245906141	3	3.570852995
Q9JMK8	**VPS54 Vacuolar protein sorting_associated protein 54**	**1.283738047**	**0.64672**	**2**
Q9JMK8	DKIAQIDK	1.3397754	1	1.933704972
Q9JMK8	STSLLGALQSQANK	0.989967483	2	2.353252888
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.201225188**	**7.7E-10**	**5**
Q9QVC8	ALELDSNNEK	1.021240527	2	2.415370941
Q9QVC8	GEPNNVAGNQAQVK	1.024202857	2	3.892968416

Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.076726338	2	3.300282001
Q9QVC8	VLQLYPSNK	1.404077579	2	2.517601252
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	1.20197179	3	6.195102215
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.098341862**	**0.37142**	**2**
Q9QWN8	IIGTQEQLNQR	1.309613319	2	2.459606647
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	1.092569696	3	3.960112095
Q9QX79	**FETUB Fetuin_B**	**1.195574941**	**0.20018**	**3**
Q9QX79	IFYETVHGQCK	1.260798509	2	2.884487629
Q9QX79	NTAPTSSPSITAPR	1.114772535	2	3.307208061
Q9QX79	GSIQHLPEQEEPEDSKGK	0.9036012	3	3.921628475
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**1.104130864**	**0.73523**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	0.887757902	2	3.753323793
Q9QXG4	IGPIATPDYIQNAPGLPK	1.228532767	2	2.878663778
Q9QXK2	**RAD18 E3 ubiquitin_protein ligase RAD18**	**1.095697177**	**0.32522**	**2**
Q9QXK2	SAAEIVQEIESMEK	1.107568808	1	2.090774298
Q9QXK2	TVYNLLSDR	0.388777069	2	2.341837645
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**1.255429619**	**0.30315**	**2**
Q9QXK3	SIATLAITTLLK	1.184731218	2	3.025342464
Q9QXK3	SSEPVQLTEAETEYFVR	1.329447558	2	3.84454751
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.19198529**	**9.9E-20**	**28**
Q9QXQ0	NFITAEELR	1.22852318	1	2.142407894
Q9QXQ0	ACLISLGYDVENDR	1.10475239	2	3.960352898
Q9QXQ0	AGTQIENIDEDFR	1.063602597	2	2.836354017
Q9QXQ0	AGTQIENIDEDFRDGLK	1.29952537	2	4.472687721
Q9QXQ0	DDPVTNLNNAFEVAEK	0.394023762	2	3.639472008
Q9QXQ0	ETTDTDTADQVIASFK	0.892271768	2	4.884986401
Q9QXQ0	HRDYETATLSDIK	1.366958371	2	4.041306019
Q9QXQ0	HTNYTMEHLR	1.098742187	2	2.806650877
Q9QXQ0	ICDQWDNLGSLTHSR	1.190287607	2	4.033131599
Q9QXQ0	ISIEMNGTLEDQLSHLK	0.935345892	2	2.834712982
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.363438804	2	4.471069813
Q9QXQ0	LVSIGAEEIVDGNAK	1.395863187	2	3.682148218
Q9QXQ0	MAPYQGPDAAPGALDYK	1.206375962	2	4.320530415
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(1)	1.136745818	2	3.093882561
Q9QXQ0	MLDAEDIVNTARPDEK	1.260643976	2	4.050361156
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(1)	1.002450507	2	2.640120029
Q9QXQ0	QLETIDQLHLEYAK	1.105267866	2	3.101920128
Q9QXQ0	TINEVENQILTR	0.726793172	2	3.366102457
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	1.420273205	2	5.000962257
Q9QXQ0	VGWEQLLTTIAR	1.276257751	2	4.240642071
Q9QXQ0	VLAGDKNFITAEELR	0.987880547	2	3.774789095
Q9QXQ0	VLAVNQENEHLMEDYER	1.196861783	2	5.552915573
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.081239939	3	3.313280344

Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.145357809	3	3.709055662
Q9QXQ0	HRPELIEYDK	1.066436936	3	4.724974155
Q9QXQ0	KDDPVTNLNNAFEVAEK	1.052767141	3	4.932396412
Q9QXQ0	RDHALLEEQSK	1.27973913	3	4.180046082
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.205183921	3	3.648904562
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.123406756**	**0.59887**	**4**
Q9QXT0	ALVDELEWEIAR	0.886673459	2	3.776273727
Q9QXT0	INPDGSQSVVEVPYAR	1.128873349	2	3.74830389
Q9QXT0	TDLCDHALHR	1.176297415	2	3.067386866
Q9QXT0	RTDLCDHALHR	1.120888959	3	3.354558706
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.073885419**	**9.5E-11**	**18**
Q9QXX4	DVEVTKEEFALAAQK	0.849460922	2	4.085061073
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.309911424	2	6.553933144
Q9QXX4	FGLYLPLFKPSASTSK	1.11923091	2	2.605918407
Q9QXX4	GLLPQLLGVAPEK	1.236268988	2	3.181954384
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.286373782	2	5.390130997
Q9QXX4	ILREEGPK	1.279700203	2	2.405819178
Q9QXX4	ITLPAPNPDHVGGYK	1.424448331	2	2.416774273
Q9QXX4	KDVEVTKEEFALAAQK	1.113576943	2	5.515861988
Q9QXX4	LQVAGEITTGPR	1.244901717	2	3.705809355
Q9QXX4	LTVNDFVR	1.311445986	2	2.561140537
Q9QXX4	NGEFFMSPHDFVTR	0.85390248	2	4.00643301
Q9QXX4	SSPQFGVTLLTYELLQR	1.423238967	2	4.538599491
Q9QXX4	STGSFVGELMYK	1.033866616	2	3.085702419
Q9QXX4	TVELLSGVVDQTK	1.212542272	2	3.96633482
Q9QXX4	YEGFFGLYR	1.01869167	2	2.719932318
Q9QXX4	YLNIFGESQPNPK	1.061325343	2	4.329919815
Q9QXX4	ASGDAARPFLLQLAESAYR	1.06598428	3	3.320191145
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.006375553	3	6.070115089
Q9QXY2	**SRCN1 SRC kinase signaling inhibitor 1**	**1.011489557**	**0.79817**	**2**
Q9QXY2	DINRLLEETQAELLK	1.463326322	2	2.413820744
Q9QXY2	IIAELESGGGSVPPMK	0.896224129	2	2.436297178
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.914332479**	**0.94085**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	0.877312032	2	4.05963707
Q9QYU4	SLGMAVEDLVAAK	0.794859778	2	3.623161554
Q9QYU4	SSSLLIPPLEAALANFSK	0.900520634	2	3.137943983
Q9QYU4	RAPAFLSADEVQDHLR	1.24701662	3	5.07879734
Q9QZ76	**MYG Myoglobin**	**0.669572287**	**0.68037**	**7**
Q9QZ76	GQHAAEIQPLAQSHATK	0.57355462	2	4.568988323
Q9QZ76	HGCTVLTALGTILK	0.675998992	2	3.512140512
Q9QZ76	YSGDFGADAQGAMSK	0.477771326	2	4.03223753
Q9QZ76	HGCTVLTALGTILKK	0.828715762	3	3.701293468

Q9QZ76	KGQHAAEIQPLAQSHATK	0.158294434	3	4.783436775
Q9QZ76	KKGQHAAEIQPLAQSHATK	0.605592951	3	4.597335815
Q9QZ76	VEGDLAGHGQEVLISLFK	0.57029744	3	4.345952988
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.011261797**	**0.84838**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	0.916009591	2	3.469152212
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.203669585	2	2.506603956
Q9QZA2	FYNELTEILVR	0.889652926	2	2.706029654
Q9QZA2	LLDEEEATDNDLR	1.117752188	2	3.674225569
Q9QZA2	NIQVSHQEFSK	1.075850633	2	3.378335238
Q9QZA2	NLATAYDNFVELVANLK	1.067999675	2	4.433708668
Q9QZA2	STAVVEQGGIQTVDQLIK	1.012797743	2	4.446197987
Q9QZA2	TMQGSEVVNVLK	1.015611717	2	3.343164444
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.041153094**	**2.5E-05**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	1.138809477	2	4.952244282
Q9QZD8	LFSGATMASSR	0.825685309	2	2.63167119
Q9QZD8	MTGMALQVVR	1.018184931	2	2.667765856
Q9QZD8	NYSHALDGLYR	1.029730034	2	2.923059702
Q9QZD8	VHLQTQQEVK	1.24317769	2	2.852312326
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.33264287	2	5.691683769
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	0.998815859	3	3.804111242
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.077936668**	**1**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.055746138	2	4.183673859
Q9QZH8	WFLQEDILEK	1.106656287	2	3.320789576
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.148582881**	**0.40561**	**5**
Q9QZU7	IDANNVAYTTGK	0.825312265	2	3.308521509
Q9QZU7	IIELDDKGQVVR	1.122840163	2	2.53600359
Q9QZU7	LLLEALDVNIR	2.261325124	2	2.836933374
Q9QZU7	MNPGDVITFDNWR	0.933564153	2	2.72871685
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.18145391	2	4.476000309
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.987761311**	**0.14261**	**10**
Q9R063	ETDLLLDDSLVSLFGNR	1.091192152	2	4.488534927
Q9R063	GVLFGVPGAFTPGCSK	0.919850914	2	4.538834572
Q9R063	KGVLFGVPGAFTPGCSK	0.974546394	2	3.501199484
Q9R063	KVNLAELFK	0.929395565	2	2.304795265
Q9R063	VGDTIPSVEVFEGEPGK	0.923684325	2	4.477273941
Q9R063	VGDTIPSVEVFEGEPGKK	1.101521418	2	3.900148392
Q9R063	VNLAELFK	0.93982547	2	2.722461939
Q9R063	VQLLADPTGAFGK	1.107783361	2	3.710577488
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	1.741056211	3	4.357468605
Q9R063	THLPGFVEQAGALK	0.967053343	3	4.343317986
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**1.076055343**	**0.94357**	**2**
Q9R064	ADTSSLTVDVMSPASK	1.069068843	2	3.47929287
Q9R064	LYVYNTDTDNCR	1.587874049	2	2.797038317

Q9R0N0	**GALK1 Galactokinase**	**1.27394657**	**0.0007**	**4**
Q9R0N0	RQCEEVAQALGK	1.182988113	2	2.857145548
Q9R0N0	SLETSLVPLSDPK	1.33869336	2	3.356185198
Q9R0N0	TDGLVSLLTTSK	1.445430674	2	3.431886911
Q9R0N0	VEELLAEAR	1.271095061	2	3.042392492
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.221102383**	**0.34645**	**6**
Q9R0T3	AEPSVAEYTVR	1.227383243	2	2.829093456
Q9R0T3	ICSEVLQLEPDNVNALK	0.882040535	2	5.562837124
Q9R0T3	LIGSAEELIR	1.44980039	2	2.860871077
Q9R0T3	LKNDNTEAFYK	1.51726407	2	2.819411993
Q9R0T3	SNPSENEEKEAQSQLVK	1.07891626	2	5.091547966
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	1.202362073	3	5.408206463
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.15347175**	**0.92052**	**3**
Q9R112	EGNALFTFPNTPVK	0.903264954	2	3.046411753
Q9R112	STLSVIPSGVQWIQDR	1.065435027	2	2.795131445
Q9R112	VGAENVAIVEPSER	1.175499742	2	2.844654083
Q9R1M5	**NALP5 NACHT_ LRR and PYD domains_containing protein 5**	**1.051333861**	**0.92432**	**2**
Q9R1M5	SLDLGNNALGDK	1.06326788	1	1.919072747
Q9R1M5	KMTSPENDSKSIQK	0.98251797	2	2.39211154
Q9R1T3	**CATZ Cathepsin Z**	**1.121713539**	**0.20335**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.121609796	2	4.191784382
Q9R1T3	VGDYGSLSGR	1.235873455	2	2.454202652
Q9R1T4	**SEPT6 Septin_6**	**1.038148622**	**0.12288**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(2)	1.293017618	1	1.997941136
Q9R1T4	STLMDTLFNTK	0.757488091	2	2.442177534
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**0.907708833**	**0.99982**	**4**
Q9R1Z0	LCQNNFALGYK	1.165265801	2	2.835753202
Q9R1Z0	LTVDTIFVPNTGK	1.06548351	2	2.588443279
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.885650057	2	4.152097702
Q9R1Z0	WNTDNTLGTEISWENK	0.986877203	2	3.084305048
Q9R257	**HEBP1 Heme_binding protein 1**	**1.31637179**	**0.07731**	**2**
Q9R257	EAMPKIMKYVGGTNDK+Oxidation(3)	1.153521797	2	2.323169231
Q9R257	NSLFGSVETWPWQVLSTGGK	1.320251673	2	2.474430084
Q9WTT6	**GUAD Guanine deaminase**	**1.113583244**	**8E-13**	**9**
Q9WTT6	AVMVSNVLLINK	0.924655298	2	2.853058338
Q9WTT6	EIGNFEVGKDFDALLINPR	1.186487223	2	4.545716286
Q9WTT6	ETTEESVKETER	0.881296527	2	3.414883137
Q9WTT6	FQSTDVAEEVYTR	1.07429828	2	3.482673645
Q9WTT6	FSLSCTETLMSELGNIAK	1.501969545	2	4.78656292
Q9WTT6	IVFLEESSQQEK	1.217423461	2	4.163647175
Q9WTT6	NYTDVYDKNNLLTNK	1.539776395	2	4.503720284

Q9WTT6	VCMDLNNTVPEYK	1.319531855	2	3.137197256
Q9WTT6	THDLYIQSHISENREEIEAVK	1.492844067	3	4.066703796
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**1.288049703**	**0.00166**	**9**
Q9WU19	AIFVTVDTPYLGNR	1.224848065	2	3.741362095
Q9WU19	GVQDVLEILK	0.925199848	2	3.609725475
Q9WU19	GVQDVLEILKEEFR	1.489398751	2	4.380950451
Q9WU19	MKNFETNDLAFSPK+Oxidation(1)	0.981802762	2	2.675359488
Q9WU19	NFETNDLAFSPK	1.123706969	2	3.404445648
Q9WU19	NVADIDLSTSVLGQR	0.962064947	2	5.091208935
Q9WU19	VEVFLDGGVR	1.239377952	2	2.643554688
Q9WU19	AVFVGRPIIWGLAFQGEK	1.067747837	3	4.126003265
Q9WU19	HGVDGILVSNHGAR	1.023421658	3	4.840137005
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**1.153393062**	**0.04799**	**2**
Q9WU49	HETWSGHVISS	1.240608708	2	2.958870411
Q9WU49	LQAVEVVITHLAPGTK	1.146091615	2	4.45315218
Q9WU65	**GLPK2 Glycerol kinase 2**	**1.064461083**	**0.44487**	**2**
Q9WU65	GIICGLTQFTNK	1.043077722	2	3.564902544
Q9WU65	LAEVNIDISNIK	2.039353783	2	2.338747978
Q9WU82	**CTNB1 Catenin beta_1**	**1.14826083**	**0.46509**	**3**
Q9WU82	HQEAEMAQNAVR	1.09841888	2	3.347616911
Q9WU82	LLNDEDQVVVNK	0.361190176	2	3.114640951
Q9WU82	TMQNTNDVETAR	1.151980062	2	3.577583313
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.06816346**	**0.95068**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.150727924	2	3.788460016
Q9WUC4	VCIESEHSSDILLATLNK	1.069006172	2	5.880673885
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**0.874804425**	**0.91514**	**2**
Q9WUH4	AIVAGDQNVEYK	0.874900891	2	2.392768383
Q9WUH4	FCANTCVECR	0.874789947	2	2.780707836
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**0.970366714**	**0.98216**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7)	0.970366714	2	2.309640169
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(8)	0.970366714	2	2.36095643
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**1.122025122**	**0.03302**	**4**
Q9WUS0	GVLHQFSGTETNR	1.166984906	2	3.456543446
Q9WUS0	TLVQAEALDR	1.087837477	2	2.636130095
Q9WUS0	YKDAAKPVIELYK	1.002158207	2	3.924734116
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.67650421	3	5.468357563
Q9WVA1	**TIM8A Mitochondrial import inner membrane translocase subunit Tim8 A**	**1.077814768**	**0.78712**	**2**
Q9WVA1	AEACFVNCVER	1.219270298	2	2.460909843
Q9WVA1	SKPVFSESLSD	1.076637206	2	2.911373615
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.714702368**	**0.35398**	**2**
Q9WVF7	AANMPDSELFELISENR	0.792556856	2	2.432553768
Q9WVF7	MAWQWRGEFMPASR+Oxidation(1)Oxidation(10)	0.521519839	2	2.373280764

Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**1.072514361**	**0.57626**	**13**
Q9WVK3	AGVYNLTK	0.967496568	2	2.722889423
Q9WVK3	ASQPPSSSTQVTAIQCNIR	1.154639906	2	5.527894497
Q9WVK3	ELLHLGCNVVIASR	0.792555733	2	4.050622463
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.26703533	2	5.459639549
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(13)	1.245916852	2	3.557024002
Q9WVK3	LTAAVDELR	1.266386626	2	2.789311409
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.869605986	2	5.074594021
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.893872797	2	5.953708172
Q9WVK3	TMALTWASSGVR	0.878089598	2	3.744310141
Q9WVK3	TMALTWASSGVR+Oxidation(2)	1.285072915	2	2.30107522
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.057733713	3	7.082596779
Q9WVK3	KEEEVNNLVK	1.067907255	3	3.926213026
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	0.967808881	3	4.067037582
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.025897719**	**6.4E-10**	**14**
Q9WVK7	LVEVIK	1.153617879	1	2.017632723
Q9WVK7	AADEFVEK	1.121142897	2	3.025589466
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	0.934437002	2	5.716365814
Q9WVK7	GDASKEDIDTAMK	1.03599484	2	3.92681694
Q9WVK7	GDASKEDIDTAMK+Oxidation(12)	1.352214769	2	3.188327074
Q9WVK7	KGIEESLK	1.217210214	2	2.544475555
Q9WVK7	LKNELFQR	1.421849188	2	2.544277906
Q9WVK7	LLVPYLIEAIR	1.816105629	2	2.671334743
Q9WVK7	TFESLVDFCK	1.2543281	2	3.589492559
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	1.04732192	3	5.605311394
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(22)	1.000955301	3	3.715282917
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(9)	1.000955301	3	3.986675978
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	1.076559464	3	7.799145699
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	1.044840621	3	6.464444637
Q9WVL6	**EXTL3 Exostosin_like 3**	**1.500548015**	**0.00119**	**2**
Q9WVL6	QDLLQLK	0.663728394	1	2.155037165
Q9WVL6	QELNSEIAKLNLK	1.719634952	2	2.571891069
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.410286507**	**1.7E-10**	**2**
Q9Z0N2	IVLTNPVCTEVGEK	1.42276481	2	2.453890324
Q9Z0N2	VGQEIEVRPGIVSK	1.409302279	2	3.562809467
Q9Z0U5	**ADO Aldehyde oxidase**	**1.065542172**	**0.99977**	**16**
Q9Z0U5	DLEPLILTIEEAIQHK	0.891731398	2	3.005634546
Q9Z0U5	EFQPLDPTQELIFPPELMR	1.168694606	2	3.071500301
Q9Z0U5	ELSILYGGVGPTTIGAK	0.876719856	2	3.813266516
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	1.127891727	2	4.808963299
Q9Z0U5	GYESNINWEK	0.97260177	2	2.963125229

Q9Z0U5	HIQDIVAATLK	1.121038548	2	2.605260134
Q9Z0U5	KLECGNVDEAFK	1.017946543	2	3.600631952
Q9Z0U5	LVLDEVTLAGSAPGGK	1.107165565	2	4.281523705
Q9Z0U5	MTWISPVTLEELVEAK	1.278057142	2	3.710557699
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	1.190304431	2	4.059614658
Q9Z0U5	NMASLGGHIVSR	1.085615116	2	3.288194895
Q9Z0U5	QQNALAIVNSGMR	1.282129453	2	2.582466602
Q9Z0U5	RLEPIISK	1.118865599	2	2.359570742
Q9Z0U5	VVENNVDPEMMLLPYLR	1.586794322	2	3.466851711
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	1.416672339	3	5.119720459
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	1.070020107	3	3.982263088
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**1.095200139**	**0.05006**	**5**
Q9Z0V5	GLFIIDDK	1.086803163	2	3.052164078
Q9Z0V5	QITLNDLPVGR	1.076485199	2	3.339039803
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.331095001	3	4.244266987
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	1.024145882	3	3.821614504
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	0.650632186	3	6.412078381
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.976064701**	**1**	**5**
Q9Z0V6	GLFIIDPNGVIK	0.973147436	2	3.406084061
Q9Z0V6	GTAVVNGEFK	1.018242164	2	2.610221148
Q9Z0V6	NGGLGHMNITLLSDLTK	0.911317261	2	2.593870878
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	1.057570324	3	6.427451134
Q9Z0V6	ANEFHDVNCEVVAVSVDSHFSHLAWINTPR	0.974628336	4	4.532271862
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.129823407**	**0.28271**	**2**
Q9Z0W7	FLDGDEMTLADCNLLPK	0.911062533	2	4.164153099
Q9Z0W7	NSRPEANEALER	1.131221634	3	3.489917278
Q9Z122	**FADS2 Fatty acid desaturase 2**	**1.019499352**	**0.98312**	**2**
Q9Z122	HGIEYQEKPLLR	1.1565878	2	3.534074306
Q9Z122	AFHLDLDFVGK	1.01871729	3	3.767548323
Q9Z1A6	**VIGLN Vigilin**	**1.079833853**	**1.3E-15**	**21**
Q9Z1A6	LQDLELK	1.330289853	1	2.451515436
Q9Z1A6	ANSFTVSSVSAPSWLHR	1.114645876	2	3.255950689
Q9Z1A6	ASVITQVFHVPLEER	0.628591852	2	3.427108288
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.078801056	2	3.321467876
Q9Z1A6	ELQAEQEDR	0.712673973	2	2.375046968
Q9Z1A6	GNSLQEILER	1.225494753	2	2.651376963
Q9Z1A6	IDLPAENSNSETIVITGK	1.133220775	2	5.229811192
Q9Z1A6	IEGDPQGVQQAK	1.166678488	2	3.704582214
Q9Z1A6	IIFPAAEDKDQDLITIIGK	0.959930475	2	2.981565952
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.019999911	2	4.564909458
Q9Z1A6	LGQALTEVYAK	1.273309905	2	3.361284971
Q9Z1A6	LQTQASATVPIPK	1.33412707	2	3.628298044

Q9Z1A6	LVGEIMQETGTR	1.139058552	2	3.694584608
Q9Z1A6	MDYVEINIDHK	1.090280489	2	2.910159588
Q9Z1A6	MVADLVENSYSISVPIFK	0.896434787	2	3.773902416
Q9Z1A6	RCDIIVISGR	1.078287245	2	3.221526146
Q9Z1A6	TEIVFTGEKEQLAQAVAR	0.516065802	2	4.404613972
Q9Z1A6	TKDLIIEQR	1.160089732	2	2.790896416
Q9Z1A6	HEVLLISAEQDKR	0.908812352	3	4.395677567
Q9Z1A6	TGAHLELSLAK	1.206176762	3	3.393668175
Q9Z1A6	VKELQAEQEDR	1.283295995	3	4.044124603
Q9Z1J8	**S14L3 SEC14_like protein 3**	**1.625990376**	**0.00554**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	1.282242554	2	2.848772287
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.692218776	2	4.349563122
Q9Z1J8	GSSHQVEYEILFPGCVLR	1.272714404	2	4.860179901
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.023362269**	**0.13884**	**5**
Q9Z1P2	DYETATLSEIK	1.217369092	1	2.015165329
Q9Z1P2	GISQEQMNEFR	1.248221263	2	2.588960886
Q9Z1P2	ICDQWDNLGALTQK	1.13161602	2	3.458558321
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	0.971675239	2	4.600465775
Q9Z1P2	MVSDINNAWGCLEQAEK	0.392521575	2	4.027552128
Q9Z1W6	**LYRIC Protein LYRIC**	**1.078958759**	**1**	**4**
Q9Z1W6	SWQDELAQQAEEGSAR	0.968341521	2	5.553553581
Q9Z1W6	TELGLDLGLEPK	0.967595292	2	3.326608419
Q9Z1W6	TLPPAISAEPSVTLSK	0.938430147	2	3.165914297
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.033669482	3	3.901822805
Q9Z1Y3	**CADH2 Cadherin_2**	**0.855245837**	**0.17018**	**5**
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	1.301624566	2	3.723932981
Q9Z1Y3	IDPVNGQITTIAVLDR	0.766122696	2	3.497877836
Q9Z1Y3	FAILTDPNSNDGLVTVVKPIDFETNR	0.979236341	3	4.273710251
Q9Z1Y3	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	1.182854146	3	5.947423458
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	0.694929359	3	3.826067924
Q9Z221	**PMFBP Polyamine_modulated factor 1_binding protein 1**	**1.114441051**	**0.64492**	**2**
Q9Z221	DHLHNVMAHLQQENK+Oxidation(7)	1.059327754	2	2.537157536
Q9Z221	ELTNSLSKLQDELAETK	1.24652446	2	2.316555023
Q9Z269	**VAPB Vesicle_associated membrane protein_associated protein B**	**1.123424844**	**0.18736**	**2**
Q9Z269	VEQVLSLEPQHELK	1.123224107	2	3.813992739
Q9Z269	TEAPVAAKPLTSPLDDAEVKK	1.133014665	3	3.400276184
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.00280037**	**0.96621**	**3**
Q9Z270	FKGPFTDVVTTNLK	1.046506963	2	2.992416382
Q9Z270	HEQILVLDPPSDLK	0.996296858	2	3.923573256
Q9Z270	QDGPLPKPHSVSLNDTETR	0.878346951	3	3.794166565
Q9Z277	**BAZ1B Tyrosine_protein kinase BAZ1B**	**1.111488185**	**0.2799**	**2**

Q9Z277	IHPLEKVDEEAVEK	1.104994437	2	2.454237223
Q9Z277	IHPLEKVDEEAVEKK	1.213260108	2	2.46698904
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.860583932**	**0.44186**	**9**
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	0.505798276	2	4.810449123
Q9Z2I8	INFDDNAEFR	0.775213757	2	3.21979785
Q9Z2I8	LEGTNVQEAQNILK	0.99489552	2	4.87168932
Q9Z2I8	SENEPIENEAAR	0.825088061	2	4.080607414
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.966705735	2	6.245894432
Q9Z2I8	SSGLPITSAVDLEDAAK	0.994067265	2	4.83935976
Q9Z2I8	SSGLPITSAVDLEDAAKK	1.040474022	2	3.120940924
Q9Z2I8	VMVAEALDISR	1.040224271	2	3.220794439
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.833311017	3	4.332261562
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.276597502**	**0.12133**	**7**
Q9Z2I9	AVSSQMIGQK	1.085235919	2	2.494864941
Q9Z2I9	ICNQVLVCER	1.526103592	2	2.888119698
Q9Z2I9	ILACDDLDEAAK	1.13798447	2	2.953155518
Q9Z2I9	INFDSNSAYR	1.235979281	2	3.09645915
Q9Z2I9	MGFPSNIVDSAAENMIK	1.061225658	2	3.883609533
Q9Z2I9	SSDEAYAIAK	1.136238849	2	3.454493761
Q9Z2I9	VQAILVNIFGGIMR	1.218077028	2	4.227815151
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.016569765**	**0.99874**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	0.977895311	2	4.250332355
Q9Z2L0	KLETAVNLAWTAGNSNTR	0.964690772	2	5.898197651
Q9Z2L0	LETAVNLAWTAGNSNTR	0.829352706	2	2.65625
Q9Z2L0	LTFDSSFSPNTGK	1.261809886	2	3.89905405
Q9Z2L0	LTFDSSFSPNTGKK	1.231804565	2	3.216537952
Q9Z2L0	LTLSALLDGK	2.032878561	2	2.35033536
Q9Z2L0	SENGLEFTSSGSANTETTK	0.92014646	2	4.559126854
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	0.950828511	2	5.313694
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	0.898360172	2	4.377214909
Q9Z2L0	VTQSNFAVGYK	1.165303855	2	3.179372549
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.038833724	2	4.8481493
Q9Z2L0	WTEYGLTFTEK	0.89306184	2	2.681206226
Q9Z2L0	YQVDPDACFSAK	0.858912005	2	3.312426329
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**1.000939355**	**0.72213**	**4**
Q9Z2M4	GQVLQLHAGAAK	1.28509449	2	3.425955057
Q9Z2M4	HLAVEWGPQNIR	0.979509222	2	3.114251852
Q9Z2M4	TVVDIDTLGTFNVSR	0.880490416	2	2.839390278
Q9Z2M4	VNSLAPGAISGTEGLR	1.039704296	2	2.9476192
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.006118488**	**0.12617**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	0.77075844	2	3.565805435

Q9Z2Q1	AVQLTQALDTNTVGALLAEK	0.94633661	2	5.501294613
Q9Z2Q1	CLSSATDPQTK	1.262186091	2	2.889880657
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.088155783	2	3.753166437
Q9Z2Q1	IIAGDKEVVIAQK	1.275640762	2	2.469168425
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.341482637	2	5.133758068
Q9Z2Q1	QVQHILASASPSGR	1.323565531	2	2.428299904
Q9Z2Q1	RQPVFISQVVTEK	1.477262951	2	2.53900075
Q9Z2Q1	SSYEGQPLPK	1.036672277	2	2.353846073
Q9Z2Q1	TQPPEDISCIAWNR	0.997559407	2	3.585420132
Q9Z2Q1	TTFEDLIQR	0.994190633	2	2.683398724
Q9Z2Q1	VNFEEDSR	1.151646325	2	2.56008482
Q9Z2Q1	VYSIMGGSIDGLR	1.126797259	2	2.372255564
Q9Z2Q1	RQPVFISQVVTEKDFLSR	0.937311643	3	3.538206577
Q9Z2U2	**ZN292 Zinc finger protein 292**	**1.100882834**	**0.12263**	**3**
Q9Z2U2	KGQKSNNLNTPNHGK	1.375374317	2	2.579275608
Q9Z2U2	KLEVLSNNPDRTVLK	1.181994961	2	2.400108337
Q9Z2U2	LINEDSTNAENQGNTTLK	1.062671154	2	2.965633631
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.074299633**	**0.99297**	**2**
Q9Z2Z8	AIECSYTSADGLK	0.977743467	2	3.628277779
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.13026621	2	5.312107563
Q9Z311	**MECR Trans_2_enoyl_CoA reductase_ mitochondrial**	**0.79348937**	**0.51591**	**2**
Q9Z311	DIPLQSAATLGVNPCTAYR	0.963635109	2	2.431901217
Q9Z311	LKDLGADYVLTEEELR	0.792701401	2	2.611778736
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.084335328**	**0.0005**	**5**
Q9Z339	GSAPPGPVPEGQIR	1.02266319	2	3.62902832
Q9Z339	LEALELNECIDHTPK	1.331568352	2	4.226669788
Q9Z339	LEEAMANKR	1.069182468	2	2.617623091
Q9Z339	LEEAMANKR+Oxidation(5)	1.620200596	2	2.533723354
Q9Z339	NPFGLVPVLENTQGHLITESVITCEYLDEAYPEKK	1.215614606	3	4.782817364

Time point 1.0 hour

Accession number	**Protein DESCRIPTION**	**Protein Ratio (1.0 h)**	**P-value (1.0 h)**	**Peptide number (1.0 h)**
Accession number	Peptide sequence	Peptide Ratio (1.0 h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**1.282611221**	**0.004731**	**2**
A0JPJ7	IGIVGLPNVGK	1.464409671	2	2.6526854
A0JPJ7	YLEANMTQSALPK	1.281359995	2	2.7836547
A0JPM9	**EIF3J Eukaryotic translation initiation factor 3 subunit J**	**1.067056765**	**0.8616943**	**2**
A0JPM9	EEAEVKPEVKISEK	1.077357415	2	2.3345757
A0JPM9	RLEEPEESK	1.052579615	2	2.4911306
A0JPQ8	**ALKMO Alkylglycerol monooxygenase**	**1.253052124**	**0.113226**	**2**
A0JPQ8	LDDILTSMSAGVVSR	1.629109884	2	2.8270054
A0JPQ8	SITHLASGSWK	1.232822255	2	2.4187837
A1A5P5	**ARMC9 LisH domain_containing protein ARMC9**	**0.945666029**	**0.7844031**	**2**
A1A5P5	CFIKEGNAEMIR+Oxidation(10)	0.939484672	2	2.7135918
A1A5P5	LYLAQNTKVLRMLEGR+Oxidation(12)	1.11351373	2	2.3065507
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**0.939627673**	**0.7269738**	**2**
A2ADY9	IDFSSIAVPGTSNPQQR	0.673248458	2	2.5615537
A2ADY9	VLVEQQQDR	0.939765462	2	2.7683675
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**0.993723478**	**0.4100011**	**2**
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(1)	0.715729158	3	3.3587997
A2AF47	NLLMCYLYIVK	1.049503803	2	2.4946499
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.123256905**	**0.0005366**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(14)	0.082994717	2	2.8296616
A2AGT5	IGSKENTKEGLAELYEYK	0.626211916	2	2.4668741
A2AJL3	**FGGY FGGY carbohydrate kinase domain_containing protein**	**0.975832067**	**0.9566252**	**2**
A2AJL3	GHGLTCEGQPVTSR	1.130402696	2	3.664535
A2AJL3	MSKVGKVVFPEHADK	0.982435139	2	2.3857381
A2AL36	**CNTRL Centriolin**	**1.213590124**	**0.551845**	**3**
A2AL36	EQQLDIMNR+Oxidation(7)	1.102825911	2	2.3322284
A2AL36	LQDEKETLLQR	1.244693268	2	2.4078283
A2AL36	NQDKLNK	1.066883444	1	2.1698961
A2AQP0	**MYH7B Myosin_7B**	**0.958701021**	**0.9993568**	**6**
A2AQP0	AITDAAMMAEELKK	0.997241393	2	3.5028389
A2AQP0	DIDDLELTLAK	0.801403416	2	3.5508428
A2AQP0	EQDTSAHLER	1.02127588	2	2.3821862
A2AQP0	KDIDDLELTLAK	0.933129524	2	2.3254826
A2AQP0	SIQELEK	0.963509147	2	2.399575
A2AQP0	VGNEYVTK	0.983275318	2	2.6211207
A2ASS6	**TITIN Titin**	**1.120042001**	**0.1456303**	**11**
A2ASS6	AENRFGIGPPAETIQRTTAR	0.868440118	2	2.6744497
A2ASS6	DVLEEPEIDLDVALR	1.006548773	2	2.8207216
A2ASS6	KDLNMVVSAARISCGGAIR	1.066454313	2	2.3072152
A2ASS6	KGDGTQLACKVTGTPPIK	0.492943185	2	2.7278249
A2ASS6	SSVSLSWSRPKDDGGSR	0.783433844	2	2.3430257
A2ASS6	TCEIEIGQLK	1.106520863	2	2.4551613
A2ASS6	TFLQDQLVSLQVLK	0.912101245	1	1.9329063
A2ASS6	VGDDAWIKDTTGTALR	1.165331893	2	2.499357
A2ASS6	VKNAMPEDIDEYAVEIEGK+Oxidation(5)	1.221749158	2	2.3427644
A2ASS6	VMKLTTGEEYQFRIK+Oxidation(2)	1.203847282	2	2.3452897
A2ASS6	YDGGHKLTGYIVEK	1.313683895	2	2.3021326

A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**0.88114129**	**0.4087608**	**9**
A2VCW9	AGGILQEDITEACLILGVK	1.053240699	2	2.6195498
A2VCW9	AQEANMSLLDEVLK	0.821384724	2	3.0458426
A2VCW9	GAQEVFNELPCEYVEPHELK	0.79082896	2	4.6846285
A2VCW9	KTDGVYDPVEYEKYPER	0.801797854	3	3.6883588
A2VCW9	KYDINTVNVTVGK	0.876688128	2	3.9779968
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	0.914070509	3	3.6720717
A2VCW9	REDVNAWER	0.788441982	2	2.7888639
A2VCW9	SSVVPVEGCPELPHK	0.857181847	2	3.0719659
A2VCW9	YDINTVNVTVGK	0.776544163	2	2.7787139
A3KMP2	**TTC38 Tetratricopeptide repeat protein 38**	**1.221616706**	**0.0772782**	**2**
A3KMP2	DVGLPLCQALLEAENGNPDR	1.232064174	2	2.3927674
A3KMP2	VLELLLPIR	0.790766402	2	2.7227137
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**0.966637719**	**0.0296529**	**11**
A7VJC2	EESGKPGAHVTVK	0.711043518	2	3.2606466
A7VJC2	GGGGNFGPGPGSNFR	1.027358664	2	3.1422105
A7VJC2	GGNFGFGDSR	0.912970257	2	2.8766375
A7VJC2	IDTIEIITDR	0.962352809	2	3.8872273
A7VJC2	LFIGGLSFETTEESLR	1.278573557	2	4.5446668
A7VJC2	LTDCVVMR	1.015508941	2	2.6451433
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	0.944421089	2	5.9648142
A7VJC2	NYYEQWGK	1.075423937	1	2.3698618
A7VJC2	QEMQEVQSSR	0.915627463	2	3.0770366
A7VJC2	QEMQEVQSSR+Oxidation(3)	1.444753931	2	2.5636055
A7VJC2	YHTINGHNAEVR	1.243223546	2	3.8663456
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.035979839**	**0.9980742**	**2**
B0BN93	GSIDEVDKR	0.978659239	2	2.4829295
B0BN93	SAWGQQPDLAANEAQLLR	1.044086716	2	3.3212025
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.110346573**	**0.8476847**	**8**
B0BNE5	AFNGYLGPDQSK	0.959827584	2	3.6868815
B0BNE5	AYDATCLVK	1.003641979	2	2.4036138
B0BNE5	FAIYLPPQAESAK	1.019299363	2	2.5862846
B0BNE5	MYSYVTEELPQLINANFPVDPQR	1.141834292	3	5.1668925
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.08246856	2	5.6417985
B0BNE5	SVSAFAPICNPVLCPWGK	1.115899034	2	4.6645556
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.369214986	3	5.4464335
B0BNE5	VFEHSSVELK	1.081269569	2	2.5653248
B0BNN3	**CAH1 Carbonic anhydrase 1**	**1.11014163**	**0.9315382**	**3**
B0BNN3	ADGLAIIGVLMK	0.760479005	2	2.8478892
B0BNN3	HDSSLKPVSVSYNPATAK	1.090772253	3	4.7974939
B0BNN3	VLDALSSVK	0.920372846	2	2.4035926
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.232795386**	**1.896E-11**	**2**
B0K020	HNEETGDNVGPLIIK	1.205610379	2	5.7147651
B0K020	VVHAFDMEDLGDK	1.066976665	2	3.651799
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.06516362**	**0.6367753**	**3**
B2GV24	QLVSQNK	0.339738457	1	1.9191668
B2GV24	TYDLPGDFLTQALTQR	1.075478525	2	2.7379265
B2GV24	VNIVDLQQVINVDLTHIENR	1.055590347	3	4.1598015
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**1.212899951**	**0.0795735**	**2**
B2RX88	SISSVNVDQVRMRNEDR	1.134722285	2	2.5580502
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(12)	1.411395828	2	2.5582716
B2RY56	**RBM25 RNA_binding protein 25**	**1.022208214**	**0.3547781**	**2**
B2RY56	FEDEDSDDVPRKR	0.604899039	2	2.3336861

B2RY56	LLIYETEAK	1.038108419	2	2.4998167
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.974683087**	**0.9789159**	**4**
B2RYW9	ATDVMAYVAGFTVAHDVSAR	1.110236912	2	3.0594022
B2RYW9	KGDEVQCEIEELGVIINK	1.091545494	2	5.3272171
B2RYW9	TFDTFCPLGPALVTK	0.862861991	2	5.0671968
B2RYW9	VNGEIVQSSNTNQMVFK	0.822220256	2	4.3887453
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**1.062754852**	**0.4581708**	**2**
B2RZ78	GDFDESLNYPEQK	1.061985332	2	3.3197649
B2RZ78	IQHILCTGNLCTK	1.354639593	2	3.3064539
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**0.945604862**	**0.7098812**	**4**
B3DMA2	AVLTVTQYR	0.946201703	2	2.3040552
B3DMA2	NLPDSDNEECLVHGDFK	0.954751667	2	3.5930834
B3DMA2	RGQEVLTR	0.363291701	2	2.7138011
B3DMA2	SGQSNPTFFLQK	1.004463696	2	2.9433711
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.098734265**	**0.1526584**	**4**
B5DFC8	GCILTLVER	1.070544639	2	2.3924778
B5DFC8	GTEITHAVVIK	1.089766327	2	2.4614713
B5DFC8	SEQDQAENEGEDSAVLMER	2.717056051	2	4.6878953
B5DFC8	TEPTAQQNLALQLAEK	1.140701801	2	4.7548575
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.281102755**	**2.621E-09**	**2**
D3ZTX0	SVIDYQTHFR	1.272173706	2	2.5908511
D3ZTX0	VSALTQMESACVSIHEALK	0.396514444	2	2.4758394
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.0548415**	**0.9999997**	**3**
D3ZW55	IDLPEYQGEPDEISIQK	0.925931645	2	4.3064899
D3ZW55	KLEEVIQILGDKFPCTLVAQK	0.95802878	3	4.2284145
D3ZW55	LQEYFGVTDGAGDH	0.976431985	2	3.2084327
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.303207296**	**0.0563265**	**2**
D3ZZL9	IEDLEQEMKIQK	0.94424965	2	2.4357462
D3ZZL9	MLQETVTKEAELR+Oxidation(1)	1.305076038	2	2.3746448
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.220481082**	**0.0034934**	**2**
D4A4T9	KEEDSDEIKIGTSCK	1.468711755	2	2.5949991
D4A4T9	LSSGNEEDKKEEDSDEIK	1.210432222	3	4.3515058
E9Q557	**DESP Desmoplakin**	**1.223796824**	**0.7054989**	**2**
E9Q557	KQVQTSQKNTLR	1.230242974	1	1.9994543
E9Q557	SQCTQVVQER	1.0566009	2	2.7909124
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**1.414482882**	**0.0623595**	**2**
O08550	HAAVALGQARAMVPEDVPR	0.961665636	2	2.4017699
O08550	RGEEGTERMVQALTELLR	1.419869512	2	2.8326314
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.132835627**	**0.0943715**	**9**
O08557	DYAVSTVPVADSLHLK	1.004435998	2	3.4696105
O08557	GAEILADTFK	1.051825212	1	2.1393249
O08557	GAEILADTFKDYAVSTVPVADSLHLK	1.373418153	3	3.5077136
O08557	LKDHLLIPVSNSEMEK	1.075023049	2	3.5116496
O08557	LQLNIVEMKDENATLDGGDVLFTGR	1.626443612	3	3.4025977
O08557	LTVPDDMAANCIYLNIPSK	1.182083724	2	3.4299614
O08557	SFCSMAGPNLIAIGSSESAQK	0.908755041	2	4.6424794
O08557	SQGEEVDFAR	1.032167729	2	2.4227207
O08557	VDGLLTCCSVFINK	0.87485947	2	3.4368012
O08583	**THOC4 THO complex subunit 4**	**1.164923652**	**0.4258407**	**2**
O08583	QQLSAEELDAQLDAYNAR	0.954287751	2	2.9025702
O08583	SLGTADVHFER	1.164946157	2	2.3982387

O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.286993018**	**0.0371156**	**11**
O08601	EFYSYENEPVGIENLK	1.015697157	2	4.6453691
O08601	GCPSLAEHWKSIR	1.315057742	2	4.0215716
O08601	GHTTGLSLNNER	1.325730342	2	2.6936059
O08601	MLSASGDPVSVVK	0.950189746	2	3.7173269
O08601	NALLPEGIPLLLK	1.423738745	1	2.7485144
O08601	NILLSIGELPK	1.150956111	2	4.0369844
O08601	REEILQILK	1.041824867	3	3.3943839
O08601	SDSSIILQER	1.208029623	2	2.4038625
O08601	SGSSSAYTGYVER	1.09083354	2	3.7290471
O08601	SNLNIFQYIGK	1.253577936	2	3.0884378
O08601	VKEFYSYENEPVGIENLK	1.160753474	2	3.4478447
O08795	**GLU2B Glucosidase 2 subunit beta**	**0.925393201**	**0.9860837**	**6**
O08795	ETVVTSTTEPSR	0.891485513	2	2.9591506
O08795	KLWEEQQAAAK	0.940034623	2	3.4316664
O08795	LWEEQQAAAK	1.300341843	2	2.3224571
O08795	MPPYDEETQAIIDAAQEAR	0.949872806	2	5.3915262
O08795	SLEDQVETLR	0.93426207	2	3.4310586
O08795	YEQGTGCWQGPNR	0.942867512	2	3.9079773
O08874	**PKN2 Serine/threonine_protein kinase N2**	**1.470142682**	**0.0001243**	**3**
O08874	ATSVALPGWSPSENRSSFMSR	1.145321821	2	2.3390315
O08874	QLDIELK	1.471399488	1	2.3596106
O08874	YSLEQRLNELPKNHPK	0.872793142	2	2.4012609
O08949	**TF2AA Transcription initiation factor IIA subunit 1**	**1.210041922**	**0.1214202**	**2**
O08949	DGIMNLNGRDYIFSK+Oxidation(4)	1.256176388	2	2.5903668
O08949	MANSANTNTVPK	0.714468313	2	2.5647838
O09158	**CP3AP Cytochrome P450 3A25**	**0.733453558**	**0.4044045**	**2**
O09158	DVEINGVFIPK	0.66862191	2	2.4724052
O09158	VDFLQLMMNTQNSK	0.982644127	2	2.6066535
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.291750216**	**9.9E-20**	**13**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.209315016	2	6.0222363
O09171	AGPWTPEAAVEHPEAVR	1.112997313	2	5.1926622
O09171	AGSNVMQTFTFYASEDKLENR	1.388096701	2	4.6846929
O09171	GAAELMQQK	1.178735963	2	3.5002928
O09171	GAAELMQQK+Oxidation(6)	1.367596747	2	2.7824593
O09171	IFHQQLEVFMK	1.3024421	2	2.8824797
O09171	KEYWQNLR	1.208476315	3	3.4256587
O09171	LNAGEVVIGDGGFVFALEK	1.80659963	3	5.9061747
O09171	QGFIDLPEFPFGLEPR	1.144189688	2	5.1796212
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.332705554	2	6.1048732
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.222329426	3	6.4541364
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(10)	1.588592225	3	6.1850495
O09171	VNEAACDIAR	1.2167606	2	3.9869494
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.017636178**	**0.0002014**	**9**
O09173	CFYNSDGDFLIVPQK	1.458942203	2	4.1644855
O09173	FSVDVFEETR	1.031924784	2	3.827785
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.299298501	3	5.2778473
O09173	LLIYTEFGK	1.305483938	2	2.5160031
O09173	NCMSEFMGLIK	0.998643684	2	3.1194811
O09173	QDVSPFNVVAWHGNYTPYK	0.925217818	2	3.4985461
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.055550778	3	3.4225614
O09173	SLRPGVAIADFVIFPPR	1.23802189	2	3.731159
O09173	YISGFGNECASEDPR	1.048544099	2	3.8448973
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.068876072**	**4.879E-11**	**17**

O35077	ANTIGISLIK	1.025143892	2	3.1179745
O35077	ELHSILQHK	0.800835128	1	2.7056103
O35077	FCETTIGCK	0.906307403	2	2.7116737
O35077	FCETTIGCKDPAQGQLLK	1.055544662	2	5.0409875
O35077	GIDEGPNGLK	0.954349408	2	2.7300508
O35077	GLVDKFPLFTAVYK	1.201026043	3	3.9624281
O35077	ICDQLKGHLK	1.206757935	3	3.3375623
O35077	ITVVQEVDTVEICGALK	0.942597829	2	4.912765
O35077	IVGSNASQLAHFDPR	2.160697912	2	3.0842013
O35077	KLTEIINTQHENVK	1.094855439	2	5.2006764
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	1.135973908	3	4.6433406
O35077	LTEIINTQHENVK	1.022303504	2	4.3748245
O35077	NIVAVGAGFCDGLGFGDNTK	0.956875928	2	4.8613095
O35077	SIEQLEK	0.963509147	2	2.4659743
O35077	VCIVGSGNWGSAIAK	1.022367558	2	4.5778956
O35077	VCYEGQPVGEFICCLQNHPEHM	1.177024315	3	4.4062519
O35077	VTMWVFEEDIGGR	1.231721275	2	3.3347049
O35078	**OXDA D_amino_acid oxidase**	**1.223574431**	**0.969439**	**2**
O35078	GQIIQVEAPWIK	1.181981041	2	3.030266
O35078	SCCQLEPTLK	1.243901821	2	2.7457204
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.958408394**	**0.9100133**	**3**
O35094	KLEESDALQEAR	1.023918186	2	3.4109745
O35094	TEMSEVLTEILR	0.841097126	2	2.5010974
O35094	VTDLLGGLFSK	0.956635432	2	3.5129702
O35142	**COPB2 Coatomer subunit beta_**	**1.044041676**	**0.0009015**	**5**
O35142	AAESLADPTEYENLFPGLK	1.18855318	2	4.1300211
O35142	FELALQLGELK	1.171702758	2	2.9522007
O35142	GSNNVALGYDEGSIIVK	1.071591618	2	3.4685824
O35142	HSEVQQANLK	0.574011099	2	3.7256305
O35142	TFEVCDLPVR	0.94045816	2	2.6220419
O35180	**SH3G3 Endophilin_A3**	**1.247285192**	**0.1629548**	**2**
O35180	AVAEILSK	1.265484099	1	1.944126
O35180	QSTEILQELQNK	1.230242974	1	2.0291479
O35244	**PRDX6 Peroxiredoxin_6**	**1.014736545**	**0.9003**	**9**
O35244	DINAYNGAAPTEK	1.029547947	2	3.9689004
O35244	DLAILLGMLDPAEKDEK	1.074150248	2	3.5487068
O35244	GESVMVLPTLPEEEAK	0.901261946	2	3.0681736
O35244	KGESVMVLPTLPEEEAK	1.029436441	2	5.0488548
O35244	LIALSIDSVEDHFAWSK	1.176792345	2	4.4177642
O35244	LSILYPATTGR	1.318825073	2	3.006506
O35244	NFDEILR	1.004905616	1	2.3772867
O35244	VVDSLQLTASNPVATPVDWK	1.079512348	2	6.0517058
O35244	VVFIFGPDKK	1.161336409	2	2.4927425
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**1.099338424**	**0.9999575**	**2**
O35469	DLGYEPLVSWEEAK	0.895925732	2	4.2675338
O35469	TSEWIGTLVEQHR	1.093385897	2	3.5198765
O35509	**RB11B Ras_related protein Rab_11B**	**1.051195587**	**0.9084564**	**5**
O35509	AQIWDTAGQER	0.86140828	2	2.3421373
O35509	GAVGALLVYDIAK	1.054707737	2	3.5158684
O35509	HLTYENVER	1.14672827	2	2.5436232
O35509	NEFNLESK	1.025325023	1	2.1016443
O35509	VVLIGDSGVGK	1.099732622	2	2.6031954
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.055682977**	**0.0004264**	**7**
O35567	ALFEEVPELLTEAEK	0.992064381	2	2.834249
O35567	DGQVIGIGAGQQSR	0.919978928	2	3.0003345

O35567	EVSDGIVAPGYEEEALK	1.046067345	2	3.5938983
O35567	HVSPAGAAVGVPLSEDEAR	1.223481716	2	5.4387927
O35567	MSSFGDFVALSDVCDVPTAK	1.35982339	2	3.9351883
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.278869419	2	5.3799601
O35567	YTQSNSVCYAK	1.217037719	2	2.8059316
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.129938382**	**0.9990024**	**2**
O35660	RYAMGDAPDYDR	1.12978154	2	3.9064858
O35660	YAMGDAPDYDR+Oxidation(3)	1.042887627	2	2.8236568
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.795874346**	**0.7913543**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	1.246943903	2	3.8463926
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	1.139293546	3	5.4992547
O35760	NCHLNENIDK	0.641691339	2	2.9996624
O35760	NVTLNPDPNEIK	0.63595974	2	2.8222797
O35763	**MOES Moesin**	**1.028703847**	**0.9889003**	**5**
O35763	ALTSELANAR	1.030281352	2	2.601706
O35763	AQMVQEDLEK	0.973843149	2	2.3608947
O35763	AQQELEEQTR	0.935697339	2	3.2010798
O35763	IQVWHEEHR	1.164563824	2	2.4082129
O35763	TQEQLASEMAELTAR	1.020187881	2	3.2325799
O35783	**CALU Calumenin**	**1.028694013**	**0.9999121**	**2**
O35783	HLVYESDQDKDGK	1.062999837	2	4.4754658
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.040193653	3	4.9455085
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**0.964709999**	**0.0021156**	**3**
O35796	AEEQEPELTSTPNFVVEVTK	0.999167136	2	4.6699381
O35796	AFVEFLTDEIKEEK	0.636943472	2	2.8305435
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.52222989	3	5.0912762
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.012224335**	**0.0232522**	**8**
O35814	ALDLDSSCK	1.016860928	1	2.1137087
O35814	ALSAGNIDDALQCYSEAIK	0.909810688	2	5.0334692
O35814	AMADPEVQQIMSDPAMR	0.705085121	2	4.2399111
O35814	DCEECIQLEPTFIK	1.01483195	2	3.9496312
O35814	ELIEQLQNKPSDLGTK	0.835761522	2	4.1053228
O35814	LDPQNHVLYSNR	2.391650758	2	3.1238921
O35814	LMDVGLIAIR	1.085444012	2	3.3722277
O35814	TVDLKPDWGK	0.95234151	2	2.4481857
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.291528693**	**0.0019671**	**9**
O35826	EVGAFGTPVINLGTR	1.00415075	2	2.7563009
O35826	ILHIEGGEVSGTIDDSIR	1.183248088	3	4.0642128
O35826	ILLAGCPSYDK	1.390332457	2	2.4021351
O35826	LIQEWNSVDLR	1.364800549	2	2.3692284
O35826	MIEQDDFDINTR	1.291509868	2	2.4722896
O35826	SIDLQEPLQK	1.294660406	2	2.535382
O35826	TLVLFPNIDAGSK	1.391552833	2	2.3138664
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.335897776	3	5.7953668
O35826	VNPQEGVVLHSTK	1.738794293	2	2.3434103
O35867	**NEB1 Neurabin_1**	**1.205028726**	**0.1395959**	**2**
O35867	DSNSRPSSNKQATDTEEPEK	1.35023384	2	2.3655226
O35867	EKAGEAEPQDEWGGSKSNR	0.719233223	2	2.3410506
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**1.107415464**	**0.1197147**	**6**
O35913	EGLQENVDGTENAK	0.91795639	2	3.4446425
O35913	ILAGIPAPIYFGALIDR	1.557504653	2	2.4276431
O35913	LYLGLPAALR	1.771738093	2	2.6368742
O35913	SLSGTYMNSMLTQIER	0.991858671	2	4.2156425
O35913	SQTLNPTQDPSECVK	1.117526508	2	4.2955933

O35913	TFQFPGDIESSK	1.063760062	2	2.4981072
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.034431189**	**0.13903**	**6**
O35952	ALLEVLGR	0.94667816	2	2.8443458
O35952	FYEGTADEMYK	0.911811231	2	2.7565541
O35952	HVEPGNTAVQEK	0.973429668	1	3.9578147
O35952	LTTVLTTHHHWDHAGGNEK	1.549244378	3	3.7228484
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.155282608	2	4.0580311
O35952	TVQQHAGETDPVTTMR	0.994869854	2	5.594101
O35987	**NSF1C NSFL1 cofactor p47**	**1.117400141**	**2.526E-09**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.17674427	2	5.063035
O35987	LGAAPEEESAYVAGER	0.944354481	2	4.04073
O35987	LGSTAPQVLNTSSPAQQAENEAK	1.856353117	2	3.8680215
O35987	SYQDPSNAQFLESIR	1.066635951	2	4.7472129
O35987	TGFSLDNGDLR	1.975565588	2	2.7039239
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.230862314**	**0.0117296**	**2**
O54975	GSLTFEPLTLVPIQTK	1.251313388	2	3.9415503
O54975	IENVVLVVPAK	1.030011208	2	3.2446854
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.020073867**	**9.9E-20**	**3**
O55012	ATTLSNAVSSLASTGLSLTK	1.110764397	2	4.1458492
O55012	ITAAQHSVTGSAVSK	1.467212882	2	4.2824607
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	0.817332455	3	4.6367092
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.014972097**	**0.0308218**	**4**
O55096	AGLLALEFYTPETANWR	1.209345428	2	4.2860398
O55096	LASVLNTEPALDSELTSK	1.694226419	2	3.7806506
O55096	SYEFQGNHFQVTR	1.198380945	2	3.8239734
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	0.922065327	3	4.2722583
O55125	**NIPS1 Protein NipSnap homolog 1**	**0.996646856**	**0.0003758**	**4**
O55125	AGPNIYELR	1.038937674	2	3.0188434
O55125	FSGGYPALMDCMNK	0.913074964	2	2.9780154
O55125	GWDENVYYTVPLVR	1.019449064	2	3.4750943
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.606258068	3	4.7320313
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**0.900925119**	**0.999255**	**6**
O55171	ADAGGELDLAR	0.89891313	2	2.9498227
O55171	DGLLDVVEALQSPLVDKK	1.031829095	2	4.5478005
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.030838955	3	4.0108671
O55171	GGELGLAMASFLK	0.989154224	2	3.5543876
O55171	IEYFEEAVNYLR	0.990169015	2	3.3151345
O55171	SCWDEPLSITVR	0.861595511	2	3.9104362
O70127	**ABCBB Bile salt export pump**	**0.960640093**	**0.9914903**	**4**
O70127	AGQITSEALSNIR	0.919159141	2	3.3491838
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.09172149	3	3.5062048
O70127	ILLLDEATSALDTESEK	1.034084996	2	4.4936228
O70127	ILLLDMATSALDNESEAR	0.833214842	2	3.9794765
O70133	**DHX9 ATP_dependent RNA helicase A**	**1.243349273**	**0.0060483**	**3**
O70133	ELDALDANDELTPLGR	0.847545343	2	2.4813213
O70133	KMTPAYEIRAVGNK	1.171901379	2	2.4065197
O70133	TTQVPQYILDDFIQNDR	1.456336174	2	3.3798492
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**0.936259274**	**0.2103762**	**2**
O70173	FLGHAQTFGGIKR	0.512916578	1	1.9903551
O70173	WTFSHPLEALGLLTSR	1.409506882	2	2.3489771
O70196	**PPCE Prolyl endopeptidase**	**1.29358916**	**1.935E-11**	**2**
O70196	SDGTETSTNLHQK	1.278113932	2	3.2289517
O70196	VFLDPNTLSDDGTVALR	1.533188506	2	3.7175863

O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.030415726**	**9E-11**	**14**
O70199	EADLVFISVNTPTK	1.160020985	2	3.1767199
O70199	EQIVVDLSHPGVSADDQVSR	1.085107218	2	5.8445339
O70199	FSLQDPPNKKPK	0.935457241	2	2.4669762
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.506903864	3	6.6231961
O70199	IIDSLFNTVTDK	1.320141514	2	2.5590882
O70199	IIDSLFNTVTDKK	1.408035466	2	3.1756406
O70199	ILTTNTWSSELSK	1.475199696	2	3.2178218
O70199	INAWNSPTLPIYEPGLK	1.682921418	2	4.2878628
O70199	NLFFSTNIDDAIR	1.02880933	2	3.1740384
O70199	VLDGLHNELQTIGFQIETIGK	0.993190293	2	5.1840997
O70199	VLDGLHNELQTIGFQIETIGKK	0.950278971	3	3.3643188
O70199	VLIGGDETPEGQR	1.168812701	2	3.8417528
O70199	VTVVDVNEAR	1.074185733	2	3.4467363
O70199	YWQQVIDMNDYQR	0.945072158	2	4.4995518
O70251	**EF1B Elongation factor 1_beta**	**1.219222948**	**0.9728134**	**4**
O70251	SIQADGLVWGSSK	1.127653777	2	4.0782681
O70251	SSILLDVKPWDDETDMTK	0.959037512	2	4.4917707
O70251	SSILLDVKPWDDETDMTKLEECVR	1.062949742	3	5.0059309
O70251	TPAGLQVLNDYLADK	1.208665523	2	4.13592
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**0.997067889**	**9.9E-20**	**16**
O70351	GGIVGMTLPIAR	0.934763209	2	3.5860507
O70351	GLVAVITGGASGLGLSTAK	1.016353365	2	4.4693542
O70351	GVIINTASVAAFEGQVGQAAYSASK	0.952851037	3	3.9972572
O70351	IDVAVNCAGIAVAIK	1.00757107	2	4.58041
O70351	KLGGNCIFAPANVTSEK	1.218873434	2	4.9763312
O70351	KNQVHTLEDFQR	1.108610794	2	4.0336704
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.329800401	3	5.5370665
O70351	LGGNCIFAPANVTSEK	1.239062245	2	3.3798625
O70351	LVAGVMGQNEPDQGGQR	1.2323601	2	5.5030212
O70351	LVGQGATAVLLDVPNSEGETEAK	1.836878359	2	5.3007121
O70351	LVGQGATAVLLDVPNSEGETEAKK	1.285752701	3	3.6657679
O70351	NFLASQVPFPSR	0.998417032	2	4.5117917
O70351	NQVHTLEDFQR	1.142137414	2	3.6625848
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.116772658	2	6.0897312
O70351	VINVNLIGTFNVIR	1.212079085	2	4.1421156
O70351	VVTIAPGLFATPLLTTLPDK	1.265450652	2	4.8735948
O70456	**1433S 14_3_3 protein sigma**	**1.232069819**	**0.059484**	**3**
O70456	DSTLIMQLLR	1.137962828	2	3.6972013
O70456	NLLSVAYK	1.072515932	2	2.3098869
O70456	VLSSIEQK	1.240017053	1	2.1964095
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.318440112**	**9.9E-20**	**8**
O88428	GCTVWLTGLSGAGK	1.269967009	2	3.5294364
O88428	GFTGIDSDYEKPETPECVLK	1.375643524	2	4.9537382
O88428	GIHELFVPENK	1.33228414	2	3.036516
O88428	IHESAGLPFFEIFVDAPLNICESR	1.396642338	3	4.041904
O88428	KDLYEPTHGGK	1.145477362	2	2.6514754
O88428	NLGFSAGDREENIR	1.188517134	2	3.3503194
O88428	STNVVYQAHHVSR	1.298796521	2	2.9045322
O88428	VLSMAPGLTSVEIIPFR	1.673880897	2	3.4123716
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.310409116**	**6.622E-07**	**17**
O88600	AESEEMETSQAGSK	1.038278582	2	4.372685
O88600	AFSDPFVEAEK	1.001812928	2	2.8560274
O88600	AGGIETIANEYSDR	0.985060871	2	3.2832398
O88600	FQESEERPK	1.239450374	2	2.7108991
O88600	FVSEDDRNNFTLK	1.432834347	2	2.8789887

O88600	GCALQCAILSPAFK	1.191363108	2	3.7098084
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	1.330799675	3	5.9683385
O88600	LEDTENWLYEDGEDQPK	1.484104659	2	4.3652363
O88600	MIMQDKLEK+Oxidation(1)	1.069337008	2	2.3633254
O88600	MQVDQEEPHTEEQQPQTPAENK	1.027997659	3	5.138443
O88600	NFTTEQVTAMLLSK	1.169367357	2	3.3158462
O88600	NKEDQYEHLDAADMTK	0.960223841	3	3.9902594
O88600	SNLAYDIVQLPTGLTGIK	1.344529326	2	4.9164419
O88600	SVMDATQIAGLNCLR	0.958969289	2	2.5988126
O88600	TSTVDLPIESQLLWQLDR	1.29807379	2	3.8627577
O88600	VLATAFDTTLGGR	1.116583366	2	3.7861848
O88600	WNSPAEEGSSDCEVFPK	1.133548517	2	4.0434895
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.138471014**	**3.387E-12**	**21**
O88618	AFAACLGAIK	1.129617463	2	2.5143738
O88618	AGEYEALPEK	1.017482631	2	2.5804944
O88618	ALLDAAAFYCDK	1.195902897	2	3.8886409
O88618	ALLDAAAFYCDKEK	1.358977337	2	3.6918471
O88618	EAQELNLPVVGSQLVGLVPLK	1.117935383	3	4.4313126
O88618	GVSMDECVLCAK	1.055879159	2	3.874516
O88618	IIEYLVPDSGPEQSLLDASLR	1.207594263	2	5.5803852
O88618	ISSLLQEAK	1.148513737	2	2.541893
O88618	KVQGIGWYLEEK	1.069986145	2	2.7874067
O88618	LAEELNVPVYLYGEAAQMPSR	1.28438263	2	4.7371082
O88618	LFVLEEEHR	1.209285126	2	2.9269285
O88618	LGLDSLAPFDPK	1.090944548	2	3.609292
O88618	LIPPFHAASAQLTSLVDADAR	1.309213581	2	3.8247716
O88618	MGALDVCPFIPVR	0.867445171	2	4.0785375
O88618	MGALDVCPFIPVR+Oxidation(1)	1.002021342	2	2.8072605
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.818581697	3	4.0340543
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.035647027	2	3.702194
O88618	TCALQEGLR	1.093840554	2	3.1762567
O88618	TQAALVLGSLEAR	1.025264606	2	4.7825289
O88618	TVYTFVGQPECVVEGALSAAR	1.250368076	2	4.3505301
O88618	VQGIGWYLEEK	1.018410621	2	3.2401359
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.122334787**	**0.3183231**	**5**
O88637	AHHSSQEMSSEYR	1.356577242	3	3.3994465
O88637	HKGPPVFTQEER	1.11892014	2	2.9980643
O88637	HNCDFCVHGNDITLTVDGR	1.190417087	3	4.305182
O88637	TEIVPDRDGSDPYEEPK	1.13771546	2	2.9445887
O88637	TQGVSTTDLVGR	1.0527415	2	3.2773552
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**1.044101137**	**0.7523517**	**2**
O88656	ASSEGGAATGAGLDSLHK	1.044387119	2	4.1529384
O88656	NSVSQISVLSGGK	0.528281236	2	2.9223578
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**0.882437305**	**0.8308269**	**2**
O88696	GQATDIAIQAEEIMK	0.911340308	2	2.5534236
O88696	VLVHPPQDGEDEPELVQK	0.881859144	3	3.9723082
O88735	**MAP7 Ensconsin**	**1.08559926**	**0.8749385**	**2**
O88735	KTTEQRNGDIAK	1.030165519	2	2.5079846
O88735	TSAGTTDPEEATR	1.109720504	2	2.3850594
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.141076465**	**0.1748922**	**2**
O88761	DTSEDIEELVEPVAAHGPK	1.20766321	2	5.0987334
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.108589059	2	3.7577505
O88767	**PARK7 Protein DJ_1**	**0.891312591**	**0.9991503**	**8**
O88767	ALVILAK	0.811232677	2	2.3055618
O88767	DVVICPDTSLEEAK	0.885446894	2	3.664283

O88767	GAEEMETVIPVDIMR	0.935018371	2	3.4817283
O88767	GLIAAICAGPTALLAHEVGFGCK	1.054797568	2	4.3593473
O88767	KGLIAAICAGPTALLAHEVGFGCK	0.900321155	3	5.5026946
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	0.99524374	3	5.6228747
O88767	VEKDGLILTSR	1.060771348	2	2.3383584
O88767	VTVAGLAGKDPVQCSR	1.077694063	2	4.3628092
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**0.962343993**	**0.3029304**	**3**
O88794	GLATGDSPLGPMTHHGEEDWVYER	0.964610867	3	3.5647655
O88794	KKNEELGQLYR	1.200382445	2	2.3760264
O88794	SSQIGAVVSR	0.77464173	2	2.4858036
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**0.885875797**	**0.4289245**	**16**
O88813	ADISVVICDTPQK	0.84961075	2	3.1112063
O88813	AEYLGSCLLHK	1.411184376	2	2.499964
O88813	AILEDLQK	1.041015062	1	2.2087657
O88813	FFQTQIK	0.887907361	1	1.9331115
O88813	FLLNLAIISK	1.218637817	2	2.9869616
O88813	GAMLTHQNIVSNMAAFLK	1.062785559	3	3.6434929
O88813	GLAVSDNGPCLGYR	0.91756668	2	2.5283089
O88813	GSFEELCQNQCVK	0.956938693	2	4.7328863
O88813	IGFFQGDIR	1.327084703	2	3.3318856
O88813	LMITGAAPISTPVLTFFR	1.03838115	2	3.0518513
O88813	LVQGVIFSCGGK	1.103401879	2	2.8885159
O88813	SFLIGVVVPDPESLPSFAAK	1.088698403	2	3.6053007
O88813	SIFVHPEPFSIENGLLTPTLK	1.619848519	2	2.8523116
O88813	SRPILQVFVHGESLR	0.788629404	3	3.5349846
O88813	TQEVLDKDGWLHTGDIGR	0.862999442	3	3.7910645
O88813	TVILMDPFDDDLMK	0.900172434	2	3.2888052
O88867	**KMO Kynurenine 3_monooxygenase**	**1.09499776**	**0.7551097**	**5**
O88867	AVGLEDQIVSK	0.982109202	2	2.3077908
O88867	DFFLLPAQPMISVK	1.371613934	2	2.5107648
O88867	DITCDLIVGCDGAYSTVR	1.488993568	2	2.5740836
O88867	FNNDLSVCLPEFSR	1.097504423	2	3.9623351
O88867	NFPDAIPLMGEQALMR	1.241009199	2	3.5783944
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.016604114**	**0.9932552**	**2**
O88941	ALESHAAAFK	1.016468077	2	2.4548504
O88941	MDPSLFPPVPLFSGVPSR	1.088536429	2	3.0927384
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.026047041**	**0.042342**	**4**
O88986	ALDLLMESNAIIQSMAAK+Oxidation(6)	1.893827801	2	2.5224798
O88986	GTDELLGVMDQVTIINSTLGK	1.030019942	2	2.6168199
O88986	MEAAGFTVSGADHPICPVMLGDAR+Oxidation(1)	0.743434356	2	2.6230037
O88986	VQISAVHSEEDIDR	1.139923747	2	4.0385504
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.06096253**	**1.374E-12**	**9**
O88989	DLDVAVLVGSMPR	0.803153662	3	3.8542411
O88989	EKMDLTAKELTEEK+Oxidation(3)	1.305982278	2	2.385556
O88989	ELTEEKETAFEFLSSA	1.4445332	2	3.7320535
O88989	EVGVYEALKDDSWLK	0.770666537	2	3.8293636
O88989	FVEGLPINDFSR	1.017931885	2	3.4406192
O88989	GEFITTVQQR	1.061721992	2	3.8740389
O88989	LGVTADDVK	1.067511837	2	2.8429949
O88989	NVIIWGNHSSTQYPDVNHAK	1.112842614	2	5.6664886
O88989	VIVVGNPANTNCLTASK	1.102923636	2	5.5655141
O88990	**ACTN3 Alpha_actinin_3**	**1.133448477**	**0.9846544**	**4**
O88990	ALDFIASK	1.084444316	2	2.622206
O88990	CQLEINFNTLQTK	1.219705191	2	3.5827529
O88990	FAIQDISVEETSAK	1.00894181	2	3.9193046
O88990	HEAFESDLAAHQDR	0.968072609	3	3.9577987

O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.995378244**	**0.994761**	**6**
O88994	CVLTTVDPDTGIIDR	0.840218942	2	4.1955242
O88994	GVSVCETECTDMGLR	0.94155543	2	3.4288859
O88994	LYPSESYLQNYEVAYPDCSPIHLISEASLVDLNTR	1.32001196	3	3.7433207
O88994	QLQQVGTVSK	0.961714597	1	2.2845776
O88994	RQLQQVGTVSK	0.846056072	2	3.2818952
O88994	SLYQSSPLFGMYFSVEK	0.998996734	2	3.7263293
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.281433326**	**0.0002146**	**7**
O89000	EGGADGVTATNTVSGLMGLK	1.081395153	2	3.3476727
O89000	GAVIVLGAGDTAFDCATSALR	1.089937855	2	4.8196983
O89000	GMGLACGQDPELVR	1.002564448	2	3.3103855
O89000	LENNFDDIK	0.922371432	2	2.6552484
O89000	QEYVGGLSTSEIPQFR	1.397078873	2	3.5740752
O89000	TEQDETGNWVEDEEQIVR	1.04311645	2	5.0789638
O89000	TFSLDKDIVTNVSPR	1.014424252	2	2.8310404
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.103686784**	**0.9870073**	**2**
O89032	DDSDINTSKTGEVSKR	1.113467215	2	2.5154278
O89032	FPIEGGQKDPK	1.003508173	2	2.345449
O89046	**COR1B Coronin_1B**	**1.026350082**	**0.9431831**	**4**
O89046	KCEPIVMTVPR	0.741707512	2	2.6017771
O89046	NDQCYEDIR	1.041295092	2	2.8248231
O89046	NVLSDSKPAGYSR	1.033651103	2	2.9279189
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.990148394	2	4.2322421
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**0.931491475**	**0.7918589**	**7**
O89049	IEQIEAGTPGR	1.076804533	2	2.9841712
O89049	IEQIEAGTPGRLK	0.659257349	2	2.3615086
O89049	LELTPVAIQAGR	1.03237763	2	2.8111362
O89049	STNSEETIEDEFNTVLLAVGR	1.365714147	2	2.3237946
O89049	VMVLDFVTPTPLGTR	1.049038116	2	2.785918
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.627696967	2	2.4056368
O89049	WGLGGTCVNVGCIPK	0.91050662	2	3.5652204
P00173	**CYB5 Cytochrome b5**	**1.083553255**	**1.017E-05**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	1.205570491	2	5.4461079
P00173	FLEEHPGGEEVLR	1.107261366	2	4.1663504
P00173	STWVILHHK	1.299724991	2	2.9134049
P00173	TYIIGELHPDDR	1.10947825	2	4.0626817
P00173	VYDLTK	1.165558501	1	1.9698772
P00173	YYTLEEIQK	1.125660292	2	2.8875425
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.141244806**	**6.803E-05**	**7**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.144815742	3	4.3054614
P00388	GMSADPEEYDLADLSSLPEIDK	1.433639373	2	5.0956492
P00388	LIHEGGAHIYVCGDAR	1.366561061	3	3.8445265
P00388	RSDEDYLYR	1.024623507	2	2.8432741
P00388	SYENQKPPFDAK	1.113927215	2	3.2051301
P00388	TNVLYELAQYASEPSEQEHLHK	1.317041673	3	3.6142049
P00388	VHPNSVHICAVAVEYEAK	1.1579099	3	3.5694685
P00406	**COX2 Cytochrome c oxidase subunit 2**	**0.990614851**	**0.9527314**	**3**
P00406	ILYMMDEINNPVLTVK	0.823314038	2	3.601321
P00406	LLEVDNR	1.039640143	2	2.5283229
P00406	VVLPMELPIR	0.936205047	2	2.5178375
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.189090815**	**1.961E-13**	**19**
P00481	FGMHLQAATPK	1.011427877	3	3.6466739
P00481	GEYLPLLQGK	0.998494619	2	3.0811553
P00481	GGNVLITDTWISMGQEDEK	1.137682684	2	5.5482659
P00481	GGNVLITDTWISMGQEDEKK	1.082448961	2	4.8224187
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.394291067	3	4.4737225

P00481	GYEPDPNIVK	0.987425137	2	2.5824213
P00481	LQAFQGYQVTMK	1.548335378	2	4.2466464
P00481	LQAFQGYQVTMK+Oxidation(11)	1.477219692	2	2.3224466
P00481	LSMTNDPLEAAR	0.942938309	2	2.9102488
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.421067953	3	7.2522731
P00481	QKGEYLPLLQGK	1.192346333	2	3.666312
P00481	QSDLDILAK	1.074160198	1	1.9644452
P00481	SLGMIFEK	0.909779851	2	2.3917885
P00481	SLGMIFEK+Oxidation(4)	0.87770619	2	2.3970351
P00481	SLVFPEAENR	0.97249245	2	2.6745985
P00481	SLVFPEAENRK	1.248890714	2	2.8831501
P00481	VLSSMTDAVLAR	1.073461335	2	3.83373
P00481	VLSSMTDAVLAR+Oxidation(5)	1.136298213	2	2.6869709
P00481	YGKPVQSQVQLK	0.657442096	2	2.794848
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.993631704**	**1**	**2**
P00502	FIQSPEDLEK	1.105804638	2	2.77003
P00502	WLLAAAGVEFDEK	1.010386969	2	4.530767
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.064752752**	**5.056E-07**	**19**
P00507	ASAELALGENSEVLK	1.169242732	2	4.6368575
P00507	DAGMQLQGYR	0.457097334	2	2.8095787
P00507	DDNGKPYVLPSVR	1.04032596	2	3.2830005
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.480823468	3	5.266993
P00507	EYLPIGGLADFCK	1.000842646	2	2.6195023
P00507	FVTVQTISGTGALR	1.170135276	2	4.8037357
P00507	HFIEQGINVCLCQSYAK	1.139963548	3	5.263133
P00507	ILIRPLYSNPPLNGAR	1.63196202	3	3.3532634
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.331824801	3	4.5235882
P00507	ISVAGVTSGNVGYLAHAIHQVTK	1.794592683	2	2.6759319
P00507	KMNLGVGAYR	0.844309014	2	2.5455203
P00507	KQWLQEVK	1.169282277	1	2.3943088
P00507	MNLGVGAYR	1.026609258	2	3.0104167
P00507	NLDKEYLPIGGLADFCK	1.086290387	2	5.8711505
P00507	NMGLYGER	0.952531694	2	2.6361129
P00507	QWLQEVK	1.198550731	1	2.0618265
P00507	TCGFDFSGALEDISK	1.148607917	2	5.0223193
P00507	VGAFTVVCK	1.024255662	2	3.3458345
P00507	VGASFLQR	1.208110633	2	3.1120033
P00564	**KCRM Creatine kinase M_type**	**0.868882495**	**1**	**7**
P00564	GGDDLDPNYVLSSR	0.766245	2	4.6490002
P00564	GQSIDDMIPAQK	0.960226032	2	2.9639015
P00564	GTGGVDTAAVGAVFDISNADR	0.993804186	2	5.9055338
P00564	LGSSEVEQVQLVVDGVK	1.088862491	2	4.6133389
P00564	LSVEALNSLTGEFK	1.096615121	2	4.1635036
P00564	RGTGGVDTAAVGAVFDISNADR	1.021411542	2	4.3304024
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	1.275677563	3	6.3140717
P00787	**CATB Cathepsin B**	**1.200977059**	**2.985E-07**	**3**
P00787	GENHCGIESEIVAGIPR	1.216276213	2	4.8600416
P00787	HEAGDVMGGHAIR	1.073801274	3	3.9651208
P00787	MCEAGYSTSYKEDK	1.043557879	2	3.9234881
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.858687202**	**9.9E-20**	**18**
P00884	ALQASALAAWGGK	1.188203072	2	4.7719474
P00884	ATQEAFMK	0.948202575	2	2.6846297
P00884	ELSEIAQR	0.686553288	1	1.9351826
P00884	ETTIQGLDGLSER	0.882341643	2	3.8920598
P00884	FPALTSEQK	0.950339527	2	2.3641913
P00884	GILAADESVGTMGNR	1.019908157	2	5.6689172
P00884	GILAADESVGTMGNR+Oxidation(12)	1.146109716	2	5.0253758

P00884	GIVVGIK	1.139840031	1	1.91353
P00884	IKVENTEENR	1.022865424	2	2.6895051
P00884	IKVENTEENRR	1.288225124	2	2.7779574
P00884	ISDQCPSSLAIQENANALAR	1.219298154	2	6.6194468
P00884	KELSEIAQR	1.027324844	2	2.6150851
P00884	KYTPEQVAMATVTALHR	1.17394211	3	6.1989927
P00884	KYTPEQVAMATVTALHR+Oxidation(9)	1.225453146	3	3.5445096
P00884	LDQGGAPLAGTNK	1.039588117	2	4.5788469
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.37866634	3	5.1495981
P00884	YTPEQVAMATVTALHR	1.128876222	2	4.8139429
P00884	YTPEQVAMATVTALHR+Oxidation(8)	1.333929194	2	3.6661677
P01026	**CO3 Complement C3**	**1.01973457**	**0.752711**	**17**
P01026	ACEPGVDYVYK	1.110219756	2	2.9446547
P01026	ADIGCTPGSGK	1.068271965	2	2.7922254
P01026	AFYEHAPK	1.12614691	2	2.3566384
P01026	EYVLPSFEVLVEPTEK	1.11492648	2	3.4341588
P01026	IFTVDNNLLPVGK	1.237157272	2	3.3885601
P01026	IGLQEVEVK	1.043355836	2	2.5905955
P01026	NEQVEIRAVLFNYR	1.008104112	2	2.314445
P01026	QNEGFSLTAK	1.016036835	2	2.3839648
P01026	RVPVVTQGSDAQALTQDDGVAK	1.177843308	3	5.3039398
P01026	SDVDEDIIPEEDIISR	0.908159778	2	4.5719924
P01026	SGSDEVQAGQER	1.150940652	2	4.1304212
P01026	TNQGLQTDQR	0.823790186	2	2.8543546
P01026	TNQGLQTDQREDPECAKPAAR	1.053778304	3	4.0719142
P01026	TVLTGATGHLNR	1.25751116	2	2.9511967
P01026	TVVIVIETPDGVPIKR	1.098183553	2	3.000169
P01026	VELKPGDNLNVNFHLR	1.050171585	3	4.0081539
P01026	VLIEDGSGEAVLSR	1.185369986	2	3.8275392
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.833246767**	**1**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.846039507	3	7.6733513
P01946	FLASVSTVLTSK	0.672946468	2	4.0518351
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.661690079	4	5.8085804
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.908878648	4	6.229044
P01946	IGGHGGEYGEEALQR	0.820336423	2	4.97788
P01946	LRVDPVNFK	1.145039078	2	2.5386519
P01946	MFAAFPTTK	0.621548836	2	3.0933132
P01946	MFAAFPTTK+Oxidation(1)	0.873012608	2	2.6548717
P01946	TYFSHIDVSPGSAQVK	0.788758253	2	5.2159781
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.809072598**	**1**	**4**
P02089	GTFASLSELHCDK	0.967807981	2	3.6886423
P02089	LHVDPENFR	0.78200589	2	2.758527
P02089	YFDSFGDLSSASAIMGNPK	0.728077384	2	6.6153197
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(15)	0.685969062	2	4.9576073
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.890990492**	**1**	**9**
P02091	EFTPCAQAAFQK	0.744111797	2	3.1262434
P02091	GTFAHLSELHCDK	0.775157229	2	4.4731331
P02091	GTFAHLSELHCDKLHVDPENFR	0.941432356	3	4.5928073
P02091	KVINAFNDGLK	0.743056261	2	3.7017472
P02091	LLGNMIVIVLGHHLGK	0.998553428	2	3.3463974
P02091	LLGNMIVIVLGHHLGKEFTPCAQAAFQK	0.618057247	3	5.4154534
P02091	VINAFNDGLK	0.784318557	2	3.002094
P02091	VNPDDVGGEALGR	0.646164964	2	4.2939591
P02091	VVAGVASALAHK	0.891287096	2	3.8227546
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.264520656**	**9.9E-20**	**7**
P02401	ILDSVGIEADDER	1.018620367	2	4.609292
P02401	ILDSVGIEADDERLNK	1.478399347	2	3.1966567

P02401	KILDSVGIEADDER	0.930102748	2	3.9424229
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.415089331	3	6.5581775
P02401	NIEDVIAQGVGK	0.984043258	2	4.7723179
P02401	VISELNGK	1.189183417	1	2.0640099
P02401	YVASYLLAALGGNSNPSAK	1.434309842	2	5.7939863
P02564	**MYH7 Myosin_7**	**1.206711037**	**1**	**25**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.911886488	3	5.4850774
P02564	ANDDLKENIAIVER	0.725482148	2	3.3629971
P02564	DLEEATLQHEATAAALR	1.267695428	2	5.402422
P02564	EQYEEETEAK	1.060202548	2	2.5041037
P02564	GTLEDQIIQANPALEAFGNAK	1.110575858	2	5.1706543
P02564	IEDEQALGSQLQK	0.814275377	2	4.0734754
P02564	IEELEEELEAER	0.836288687	2	4.1115866
P02564	ILNPAAIPEGQFIDSR	1.191246503	2	3.354573
P02564	KLAEQELIETSER	1.074250074	2	3.976934
P02564	KMEGDLNEMEIQLSHANR+Oxidation(2)	1.10318448	2	2.5010812
P02564	KVQHELDEAEER	1.258818727	2	2.7914722
P02564	LDEAEQIALK	1.053051161	2	3.3696587
P02564	LELDDVTSNMEQIIK	1.107424957	2	3.4934299
P02564	LQDAEEAVEAVNAK	0.885256634	2	4.7110047
P02564	LQNEIEDLMVDVER	1.191139635	2	3.4450612
P02564	MDADLSQLQTEVEEAVQECR	1.128533264	2	4.8052607
P02564	NLQEEISDLTEQLGSTGK	1.029583532	2	5.6731257
P02564	NLTEEMAGLDEIIVK	1.060391412	2	3.1395383
P02564	NNLLQAELEELR	0.896438421	2	2.8615162
P02564	QAEEAEEQANTNLSK	1.005114208	2	4.7807646
P02564	QKYEESQSELESSQK	1.238641854	2	2.9582434
P02564	QLEAEKLELQSALEEAEASLEHEEGK	0.864369022	3	4.5039253
P02564	TLEDQMNEHR	0.898849309	2	2.5930612
P02564	VQLLHSQNTSLINQK	1.082499827	2	3.8471973
P02564	VVDSLQTSLDAETR	0.941309884	2	2.7279093
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**0.944726677**	**0.9986639**	**8**
P02600	ALGTNPTNAEVK	0.984915782	2	3.2246265
P02600	ALGTNPTNAEVKK	1.198130194	2	2.720017
P02600	DQGGYEDFVEGLR	0.453595211	2	3.5879157
P02600	IEFEQFLPMMQAISNNK	0.72696944	2	2.7367518
P02600	ITLSQVGDVLR	0.883888083	2	3.0893373
P02600	KIEFEQFLPMMQAISNNK	0.946437882	2	5.4581037
P02600	VLGNPSNEEMNAK	1.012331624	2	3.8493836
P02600	VLGNPSNEEMNAK+Oxidation(10)	1.166699211	2	2.5731497
P02625	**PRVA Parvalbumin alpha**	**1.308282867**	**0.6519958**	**4**
P02625	AIGAFTAADSFDHKK	1.133934372	2	3.9116032
P02625	SGFIEEDELGSILK	1.136549828	2	2.8517678
P02625	TLMAAGDKDGDGK	1.30817467	2	3.1796713
P02625	TLMAAGDKDGDGK+Oxidation(3)	1.66373016	2	3.3595972
P02650	**APOE Apolipoprotein E**	**1.10247069**	**0.0001675**	**13**
P02650	ELEEQLGPVAEETR	1.187023356	2	4.331418
P02650	GRLEEVGNQAR	1.142529393	2	3.7009504
P02650	GWFEPLVEDMQR	1.236827756	2	3.2393358
P02650	LEEVGNQAR	0.990508131	2	2.5668178
P02650	LGADMEDLR	1.197977017	2	3.0311067
P02650	LGPLVEQGR	1.090200086	2	2.3094509
P02650	LQAEIFQAR	1.465001376	2	2.711163
P02650	MEEQTQQIR	1.136642848	2	3.2388725
P02650	MEEQTQQIR+Oxidation(1)	1.168274422	2	2.8769908
P02650	NEVNTMLGQSTEELR	1.066044406	2	4.4901743
P02650	SKMEEQTQQIR	1.20965784	2	3.2987957

P02650	SKMEEQTQQIR+Oxidation(3)	1.711520265	2	3.5609121
P02650	TANLGAGAAQPLR	0.851718485	2	2.3724356
P02680	**FIBG Fibrinogen gamma chain**	**1.078733804**	**0.9980565**	**3**
P02680	VGPESDKYR	1.051316472	2	2.5928881
P02680	YEALLLTHESSIR	1.140074286	2	3.7165458
P02680	YLQDIYTSNK	1.018823648	2	2.785182
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.135985026**	**9.9E-20**	**13**
P02692	AMGLPEDLIQK	0.986832225	2	3.6335793
P02692	AMGLPEDLIQK+Oxidation(2)	1.136794638	2	3.3736029
P02692	GVSEIVHEGK	0.949999153	2	3.4928181
P02692	GVSEIVHEGKK	1.038074047	2	3.3275712
P02692	MVTTFK	0.873012666	1	1.9130399
P02692	MVTTFK+Oxidation(1)	1.100016647	1	2.0228491
P02692	SVTEFNGDTITNTMTLGDIVYK	1.204267837	2	5.6535163
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(14)	1.009578815	2	5.6429458
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.302065375	2	3.7354803
P02692	VIHNEFTLGEECELETMTGEK	1.066392376	3	6.3064198
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(17)	1.17118256	3	5.5101819
P02692	YQVQSQENFEPFMK	1.138079962	2	6.0539045
P02692	YQVQSQENFEPFMK+Oxidation(13)	1.150098895	2	5.2808065
P02696	**RET1 Retinol_binding protein 1**	**1.139802383**	**0.2488333**	**8**
P02696	ALDVNVALR	1.085350411	2	3.2774956
P02696	CMTTVSWDGDKLQCVQK	1.097536297	2	4.543385
P02696	EFEEDLTGIDDR	1.20602911	2	2.3439012
P02696	EFEEDLTGIDDRK	1.315605854	2	2.7529891
P02696	GWTQWIEGDELHLEMR	1.114059768	2	4.3094831
P02696	MLSNENFEEYLR	1.356032159	2	3.6305208
P02696	MLSNENFEEYLR+Oxidation(1)	1.899095667	2	2.9699557
P02696	NYIMDFQVGKEFEEDLTGIDDRK	1.221576464	3	3.4651232
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**0.947169545**	**0.5405579**	**6**
P02706	DYQDFQHLDNENDHHQLQR	1.31862867	3	3.414072
P02706	LVESQLEK	1.059806703	1	2.0671139
P02706	QLVSDVR	0.339738457	1	2.0709007
P02706	SLSCQMAALR	0.829541119	2	3.0518787
P02706	WVCETELGK	0.995967141	2	2.3625796
P02706	WVDGTDYETGFK	1.027054773	2	3.4649687
P02770	**ALBU Serum albumin**	**0.953699398**	**1**	**27**
P02770	AADKDNCFATEGPNLVAR	0.711393681	2	4.9281936
P02770	AETFTFHSDICTLPDKEK	1.398653399	2	3.7458146
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.29508197	3	5.3223963
P02770	CCSGSLVER	0.702288894	2	3.2315023
P02770	CCTLPEAQR	0.924322202	2	2.7733779
P02770	DLGEQHFK	0.840342949	2	2.309936
P02770	DNCFATEGPNLVAR	0.59880318	2	3.3633308
P02770	DNYGELADCCAK	0.283041754	2	3.3667917
P02770	ECCHGDLLECADDR	0.972833772	2	3.9369578
P02770	ECCHGDLLECADDRAELAK	1.265834801	2	5.328629
P02770	FKDLGEQHFK	1.158160479	3	4.1803231
P02770	GLVLIAFSQYLQK	1.571200837	2	4.0836067
P02770	INKECCHGDLLECADDRAELAK	1.288956263	3	5.4441733
P02770	KQTALAELVK	1.133475662	3	4.1260624
P02770	KYEATLEK	1.079363042	2	2.6937459
P02770	LQACCDKPVLQK	1.282782955	2	4.2770953
P02770	LRDNYGELADCCAK	0.493771416	2	3.3441615
P02770	LVQEVTDFAK	1.11937817	2	3.7089045
P02770	QEPERNECFLQHK	0.313422768	2	2.355109
P02770	RHPDYSVSLLLR	1.29667264	3	4.8093281

P02770	SIHTLFGDK	0.618280622	1	2.2839186
P02770	TCVADENAENCDK	0.987653359	2	4.6459985
P02770	TNCELYEK	0.891325842	2	2.8217196
P02770	TVMGDFAQFVDK	0.793124809	2	4.2719288
P02770	YMCENQATISSK	0.947049798	2	4.4145026
P02770	YMCENQATISSK+Oxidation(2)	0.967232049	2	3.6894434
P02770	YNEVLTQCCTESDK	0.85045188	2	5.7341905
P02803	**MT1 Metallothionein_1**	**1.074014593**	**0.4187868**	**2**
P04041	**GPX1 Glutathione peroxidase 1**	**1.175558037**	**7.235E-08**	**10**
P04041	FLVGPDGVPVR	0.884603845	2	3.2468095
P04041	FLVGPDGVPVRR	1.005401564	2	2.3198669
P04041	GLVVLGFPCNQFGHQENGK	1.137319294	2	4.285677
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.897015758	3	4.329761
P04041	NALPAPSDDPTALMTDPK	0.926827401	2	3.4749212
P04041	NDISWNFEK	0.860390817	2	2.9044461
P04041	NEEILNSLK	0.913262544	2	2.5415452
P04041	TIDIEPDIEALLSK	1.144111938	3	4.2795939
P04041	YIIWSPVCR	0.86463434	2	2.9363868
P04041	YVRPGGGFEPNFTLFEK	1.225712265	2	4.5811858
P04167	**CP2B2 Cytochrome P450 2B2**	**0.696527077**	**0.2735377**	**2**
P04167	GTIAVIEPIFK	0.57908014	2	2.5601034
P04167	NLQEILDYIGHIVEK	0.712269483	2	4.2288718
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.122173794**	**9.9E-20**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	0.587220896	2	4.1409001
P04176	EDNIPQLEDVSQFLQTCTGFR	1.122851338	3	4.7270741
P04176	FANQILSYGAELDADHPGFK	1.309722265	3	3.9793258
P04176	FANQILSYGAELDADHPGFKDPVYR	1.262333175	3	5.3622952
P04176	ILADSINSEVGILCNALQK	1.322604732	3	6.6082525
P04176	LNKDEYEFFTYLDKR	3.914555938	3	3.6054032
P04176	LRPVAGLLSSR	3.021006192	2	2.7116976
P04176	NDIGATVHELSR	1.148329255	2	3.755928
P04176	QFADIAYNYR	1.050115643	2	2.815701
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.302546234	2	4.825675
P04176	TACQEYSVTEFQPLYYVAESFSDAK	1.734836125	3	3.692086
P04176	THACYEHNHIFPLLEK	1.307186894	3	4.7300148
P04176	VEVLDNTQQLK	1.015604533	2	3.8453436
P04176	VEYTEEEK	1.084056198	2	2.6965768
P04176	VEYTEEEKQTWGTVFR	1.206728648	2	4.3363876
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.290203618	3	5.301527
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**1.480347556**	**0.2338167**	**9**
P04182	AFYNNVLGEYEEYITK	1.331058844	2	4.485981
P04182	GIYMWDVEGR	1.077738907	2	2.7182109
P04182	GLLNAIVIR	1.427872426	2	3.1417024
P04182	HQVLFIADEIQTGLAR	1.468050119	2	4.0496249
P04182	IIEAMKSQVDK	0.790962517	2	2.3329723
P04182	KTEQGPPSSEYIFER	1.385380937	2	3.922631
P04182	TEQGPPSSEYIFER	1.178782134	2	4.1217823
P04182	VLPMNTGVEAGETACK	2.002769727	2	3.9849401
P04182	WLAVDHENVRPDIVLLGK	1.301261227	2	4.9355049
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.355823834**	**0.8730367**	**4**
P04256	EDSQRPGAHLTVK	1.123772964	2	3.2208569
P04256	IEVIEIMTDR	1.011264528	2	3.1355302
P04256	NQGGYGGSSSSSSYGSGR	1.058653555	2	4.7315612
P04256	YHTVNGHNCEVR	1.517271524	2	3.3172259
P04276	**VTDB Vitamin D_binding protein**	**1.214643063**	**0.0001013**	**2**
P04276	SCESDAPFPVHPGTSECCTK	1.214730093	2	4.7410007
P04276	YCSSQIDAEMR	1.027061563	2	2.875705

P04355	**MT2 Metallothionein_2**	**1.205335827**	**0.752912**	**2**
P04462	**MYH8 Myosin_8 (Fragment)**	**0.936236038**	**1**	**3**
P04462	KLQHELEEAEER	1.071480511	3	3.8938425
P04462	LQHELEEAEER	0.896071077	2	3.6490161
P04462	RAALQAEIEELR	0.955864171	2	3.8757918
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**1.068208089**	**0.9996565**	**7**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.183250541	2	4.4937758
P04466	GADPEDVITGAFK	0.838308413	2	3.8498824
P04466	KQFLEELLTTQCDR	1.279338666	2	4.10782
P04466	LKGADPEDVITGAFK	1.321380142	3	4.4626594
P04466	NICYVITHGDAKDQE	1.029352311	2	4.7035265
P04466	NMWAAFPPDVGGNVDYK	0.933018763	2	3.0958447
P04466	QFLEELLTTQCDR	0.953573703	2	3.777317
P04550	**PTMS Parathymosin**	**1.087070079**	**1.419E-05**	**4**
P04550	RTAEEEDEADPKR	1.101584517	3	4.0340614
P04550	SVEAAAELSAK	1.039043405	2	3.6445129
P04550	TAEEEDEADPK	0.896768328	2	3.3246756
P04550	TAEEEDEADPKR	1.189031313	2	3.700356
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**0.889194747**	**9.9E-20**	**16**
P04636	AGAGSATLSMAYAGAR	1.053305124	2	4.6571317
P04636	ANTFVAELK	0.997308122	2	2.7781076
P04636	EGVIECSFVQSK	0.717100616	1	3.0365231
P04636	ETECTYFSTPLLLGK	0.793008244	2	3.5034623
P04636	FVFSLVDAMNGK	1.139543272	2	4.4266958
P04636	GCDVVVIPAGVPR	0.984808284	2	4.370471
P04636	GYLGPEQLPDCLK	1.018487333	2	4.1261034
P04636	IFGVTTLDIVR	1.487860532	2	3.6015806
P04636	IQEAGTEVVK	0.951601107	2	2.8807483
P04636	LTLYDIAHTPGVAADLSHIETR	1.281340797	3	7.0187702
P04636	MIAEAIPELK	0.83453473	2	3.2110167
P04636	MIAEAIPELK+Oxidation(1)	1.474575834	2	2.539983
P04636	TIIPLISQCTPK	0.998753541	2	3.5116553
P04636	VAVLGASGGIGQPLSLLLK	1.420423092	2	6.1181064
P04636	VDFPQDQLATLTGR	0.978366615	2	4.8695307
P04636	VNVPVIGGHAGK	1.073155411	2	3.2104292
P04639	**APOA1 Apolipoprotein A_I**	**1.02687771**	**0.5895147**	**6**
P04639	AKPALDDLGQGLMPVLEAWK	1.007083926	2	3.7420368
P04639	LQEQLGPVTQEFWANLEK	1.414402423	2	4.898427
P04639	NEMNKDLENVK	1.26432789	2	3.4349823
P04639	QLNLNLLDNWDTLGSTVGR	1.066442641	2	4.5027428
P04639	VKDFATVYVDAVK	1.361322658	2	3.1112251
P04639	WNEEVEAYR	1.021014713	2	2.370806
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.006370934**	**1.884E-10**	**22**
P04642	DLADELALVDVIEDK	1.139214536	2	5.4793129
P04642	DLADELALVDVIEDKLK	1.492624562	2	4.6152401
P04642	DQLIVNLLK	0.857298395	2	2.9456959
P04642	DQLIVNLLKEEQVPQNK	1.07345204	2	4.867084
P04642	EDVFLSVPCILGQNGISDVVK	1.131738719	2	4.7985015
P04642	FIIPNVVK	0.994995522	2	2.3942511
P04642	GEMMDLQHGSLFLK	1.049336932	2	3.8554296
P04642	GEMMDLQHGSLFLK+Oxidation(3)	1.267803043	2	3.4528344
P04642	GEMMDLQHGSLFLK+Oxidation(4)	1.279641532	2	3.1473186
P04642	GLYGIKEDVFLSVPCILGQNGISDVVK	1.192171772	3	3.3544867
P04642	KSADTLWGIQK	1.034902283	2	3.0957024
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.252346639	3	5.7276378
P04642	LKGEMMDLQHGSLFLK	1.148357647	2	3.9995201

P04642	LLIVSNPVDILTYVAWK	1.125611077	2	4.8761826
P04642	NVNIFK	1.04207547	1	2.0879409
P04642	QVVDSAYEVIK	0.96704588	2	3.1190164
P04642	RVHPISTMIK	0.825753196	2	2.3725398
P04642	SADTLWGIQK	0.930416049	2	3.9407876
P04642	SLNPQLGTDADK	0.830098952	2	2.6748681
P04642	SLNPQLGTDADKEQWK	0.996539131	2	4.840539
P04642	SLNPQLGTDADKEQWKDVHK	1.263235365	2	4.6805582
P04642	VTLTPDEEAR	0.924306217	2	2.9285173
P04644	**RS17 40S ribosomal protein S17**	**1.050526561**	**1.622E-08**	**4**
P04644	DNYVPEVSALDQEIIEVDPDTK	1.025462549	2	4.3356676
P04644	LGNDFHTNK	0.984175068	2	2.9238837
P04644	LLDFGSLSNLQVTQPTVGMNFK	1.61974853	2	4.1198473
P04644	VCEEIAIIPSK	0.992458774	2	3.1142247
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.088148804**	**0.9999999**	**10**
P04692	AISEELDHALNDMTSI	1.007800218	2	2.6278632
P04692	AQKDEEKMEIQEIQLK	0.959126794	2	3.8512123
P04692	GTEDELDKYSEALK	1.084536603	2	2.308058
P04692	KLVIIESDLER	0.977557937	2	3.6535752
P04692	LDKENALDR	0.992999877	2	2.3891304
P04692	LKGTEDELDK	1.140311825	2	2.621469
P04692	LVIIESDLER	1.002924663	2	3.233722
P04692	MEIQEIQLK	0.885497282	2	2.8501985
P04692	QLEDELVSLQK	0.892084195	2	2.4871795
P04692	SIDDLEDELYAQK	1.009780627	2	3.702502
P04694	**ATTY Tyrosine aminotransferase**	**0.860668908**	**0.4321365**	**2**
P04762	**CATA Catalase**	**1.134130102**	**9.9E-20**	**30**
P04762	DAMLFPSFIHSQK	0.778342109	2	2.354497
P04762	DAQLFIQR	0.902930979	2	3.089247
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	1.06799584	4	5.1708031
P04762	DYPLIPVGK	1.036612673	1	2.5299697
P04762	EAETFPFNPFDLTK	1.190028199	2	4.3490229
P04762	FNSANEDNVTQVR	1.026066164	2	4.7097659
P04762	FSTVAGESGSADTVR	1.032310611	2	5.1901002
P04762	FSTVAGESGSADTVRDPR	1.139638872	2	2.9669554
P04762	FYTEDGNWDLVGNNTPIFFIR	2.3027948	3	6.2746048
P04762	GAGAFGYFEVTHDITR	1.118004801	2	5.118216
P04762	GPLLVQDVVFTDEMAHFDR	1.414335103	2	5.711432
P04762	HMNGYGSHTFK	1.149892012	3	4.2001319
P04762	HMNGYGSHTFK+Oxidation(2)	1.198346511	2	2.7632294
P04762	LAQEDPDYGLR	1.303612141	2	2.6399038
P04762	LCENIANHLK	1.17502088	3	4.0514007
P04762	LFAYPDTHR	1.465039263	2	2.8764272
P04762	LGPNYLQIPVNCPYR	1.379355543	2	4.3954773
P04762	LNIMTAGPR	1.112878034	2	3.1604834
P04762	LVNANGEAVYCK	1.31883807	2	4.0506845
P04762	NAIHTYVQAGSHIAAK	1.074121714	2	5.3379626
P04762	NFTDVHPDYGAR	1.046900521	2	4.0832453
P04762	NLPVEEAGR	1.079712764	2	2.3831642
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	1.240285986	3	6.3889651
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK+Oxidation(19)	1.570805484	3	3.9177871
P04762	RFNSANEDNVTQVR	1.214267801	2	5.180954
P04762	VFEHIGK	1.003976746	2	2.443536
P04762	VFEHIGKR	1.159288802	2	2.3911762
P04762	VLNEEER	1.04857421	2	2.8636875
P04762	VQALLDQYNSQKPK	1.076702397	2	5.1204438

P04762	VWPHKDYPLIPVGK	1.299411931	2	3.8527977
P04764	**ENOA Alpha_enolase**	**0.971246781**	**0.9957392**	**17**
P04764	AGYTDQVVIGMDVAASEFYR	0.884680201	2	5.5461078
P04764	DATNVGDEGGFAPNILENK	0.867633898	2	5.4425817
P04764	DYPVVSIEDPFDQDDWDAWQK	1.081061877	2	4.7410693
P04764	FTATAGIQVVGDDLTVTNPK	0.98668878	2	5.1754174
P04764	GNPTVEVDLYTAK	1.334250034	2	4.0585828
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.147593572	3	6.5712295
P04764	IDQLMIEMDGTENK	0.83122884	2	4.641706
P04764	IEEELGSK	1.015127544	2	2.4000046
P04764	IGAEVYHNLK	1.210321853	2	3.3218505
P04764	KLNVVEQEK	0.769272868	2	2.3538334
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.010905659	3	6.0405536
P04764	LNVVEQEK	1.01148275	2	2.7331035
P04764	LNVVEQEKIDQLMIEMDGTENK	0.860612632	3	4.5962596
P04764	SCNCLLLK	1.117122625	2	3.0578778
P04764	SFIKDYPVVSIEDPFDQDDWDAWQK	1.021788264	3	4.3541245
P04764	VNQIGSVTESLQACK	1.025145059	2	5.1829333
P04764	YITPDQLADLYK	1.043271168	2	3.3195379
P04785	**PDIA1 Protein disulfide_isomerase**	**1.142236347**	**9.9E-20**	**24**
P04785	DHENIVIAK	0.957989273	2	2.9165566
P04785	HNQLPLVIEFTEQTAPK	1.233325901	2	5.6134481
P04785	IKPHLMSQELPEDWDKQPVK	1.558668311	4	5.6034894
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(6)	2.125646868	3	3.8736479
P04785	ILEFFGLK	1.318556993	2	3.1443293
P04785	ILFIFIDSDHTDNQR	1.322471293	2	3.8404489
P04785	ITQFCHHFLEGK	1.23048485	2	3.089987
P04785	LGETYKDHENIVIAK	1.231583636	3	5.0822706
P04785	LITLEEEMTK	1.025053646	2	3.7107592
P04785	LKAEGSEIR	1.188117593	2	2.426496
P04785	LLDFIK	1.114097692	2	2.4132366
P04785	MDSTANEVEAVK	0.954689685	2	4.2344327
P04785	MDSTANEVEAVK+Oxidation(1)	1.247304461	2	3.7308948
P04785	NFEEVAFDEK	1.061861975	2	3.200937
P04785	NFEEVAFDEKK	1.141971779	2	4.0473824
P04785	NNFEGEITK	1.05743235	2	2.5567243
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.378460081	3	6.2935524
P04785	SVSDYDGK	1.765531956	1	2.2596526
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.2675069	3	6.7332263
P04785	THILLFLPK	1.175079988	2	2.9829049
P04785	TVIDYNGER	1.088367162	2	2.6685689
P04785	VDATEESDLAQQYGVR	0.789004209	2	5.429688
P04785	YKPESDELTAEK	1.099179727	3	4.4535203
P04785	YQLDKDGVVLFK	1.217809474	2	3.8392057
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.20349934**	**9.9E-20**	**13**
P04797	GAAQNIIPASTGAAK	1.076352321	2	4.1387696
P04797	IVSNASCTTNCLAPLAK	1.257668463	2	4.9650822
P04797	LISWYDNEYGYSNR	1.785194584	2	4.3370452
P04797	LVINGKPITIFQER	1.323922702	3	3.5696013
P04797	RVIISAPSADAPMFVMGVNHEK	0.995299913	3	5.4690337
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.101613	3	7.7052698
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(13)	1.445765868	4	4.6648808
P04797	VIISAPSADAPMFVMGVNHEK	0.98617112	2	4.2949128
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(12)	1.321138553	2	3.8501225
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(15)	1.321138553	2	3.5244658
P04797	VPTPNVSVVDLTCR	0.982390694	2	2.6085479
P04797	VVDLMAYMASK	1.352388326	2	4.433794

P04797	WGDAGAEYVVESTGVFTTMEK	1.256513097	2	5.2375727
P04799	**CP1A2 Cytochrome P450 1A2**	**1.188767551**	**0.0966398**	**6**
P04799	DFVENVTSGNAVDFFPVLR	1.109200316	2	3.2174816
P04799	FLTNDNTAIDK	1.053742218	2	3.0679276
P04799	IGSTPVVVLSGLNTIK	1.539714876	2	2.4173527
P04799	NSIQDITGALFK	0.87490918	2	3.1271303
P04799	SMTFNPDSGPVWAAR	3.830047208	2	3.3100226
P04799	TVQEHYQDFNK	1.087521243	2	3.4264207
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.853347463**	**0.0002301**	**10**
P04903	DGNLMFDQVPMVEIDGMK	0.891077822	2	4.8846536
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(11)	1.164232182	2	4.6116748
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(17)	1.276751443	2	3.4453375
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(5)	1.131561002	2	4.2333584
P04903	KDGNLMFDQVPMVEIDGMK	1.013486332	2	4.9216628
P04903	LIQSPEDLEK	1.054619647	2	3.0685306
P04903	LKKDGNLMFDQVPMVEIDGMK	1.84222987	2	3.1879089
P04903	WLLAAAGVEFEEK	0.705642417	2	4.3887115
P04903	YDLYGK	1.071810866	1	2.0102713
P04903	YLPAFEK	1.160674924	1	2.0389109
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**1.22876295**	**9.9E-20**	**8**
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	1.636802334	4	6.9878941
P04904	LRNDGSLMFQQVPMVEIDGMK	1.823015398	2	4.6651583
P04904	NDGSLMFQQVPMVEIDGMK	1.179796717	2	5.374155
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(12)	1.241983184	2	4.4411259
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(18)	1.268375993	2	4.1063619
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(6)	1.236231365	2	4.022337
P04904	SHGQDYLVGNR	1.071771821	2	3.9228609
P04904	WLLAAAGVEFEEQFLK	1.516926174	2	6.1534843
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.27804727**	**9.9E-20**	**15**
P04905	ADIVENQVMDNR	1.095962008	2	4.1813836
P04905	ADIVENQVMDNR+Oxidation(9)	1.203355001	2	3.7388687
P04905	CLDAFPNLKDFLAR	1.295384337	2	3.2497349
P04905	FKLGLDFPNLPYLIDGSR	1.166124503	2	4.5534086
P04905	HHLCGETEEER	1.170789725	3	3.7828407
P04905	IRADIVENQVMDNR	1.543120825	2	3.9823682
P04905	ITQSNAIMR	1.104916983	2	3.106966
P04905	ITQSNAIMR+Oxidation(8)	1.330111291	2	2.8308222
P04905	KHHLCGETEEER	0.71921247	3	4.4578257
P04905	KITQSNAIMR	0.731021102	3	3.8273087
P04905	KITQSNAIMR+Oxidation(9)	1.110194219	3	3.4476025
P04905	LGLDFPNLPYLIDGSR	0.965582103	2	4.7461705
P04905	MQLIMLCYNPDFEK	1.47268119	2	4.4088736
P04905	VTYVDFLAYDILDQYHIFEPK	2.984649536	3	3.6331515
P04905	YLSTPIFSK	1.037643926	2	2.5988894
P04906	**GSTP1 Glutathione S_transferase P**	**1.048298097**	**0.3231937**	**2**
P04906	EAALVDMVNDGVEDLR	0.983214048	2	4.6561174
P04906	STCLYGQLPK	1.240908158	1	1.9219395
P04937	**FINC Fibronectin**	**1.321202386**	**0.075778**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	1.430343872	2	4.7567658
P04937	SSPVVIDASTAIDAPSNLR	1.040243617	2	4.4947634
P04937	SYTITGLQPGTDYK	1.077706221	2	2.5777729
P04937	VVTPLSPPTNLHLEANPDTGVLTVSWER	1.075975605	3	4.1628857
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.025960884**	**1**	**8**
P05065	ALANSLACQGK	1.135796688	2	2.4421608
P05065	FSNEEIAMATVTALR	1.020300456	2	3.8965843
P05065	FSNEEIAMATVTALRR	0.903549725	2	2.3874323
P05065	GILAADESTGSIAK	1.017949901	2	3.9691651

P05065	GVVPLAGTNGETTTQGLDGLSER	1.269190014	2	5.5268688
P05065	IGEHTPSSLAIMENANVLAR	0.908421992	2	4.8209763
P05065	LQSIGTENTEENR	1.023851477	2	3.6123612
P05065	RLQSIGTENTEENR	1.271369887	2	2.7845712
P05178	**CP2C6 Cytochrome P450 2C6**	**0.892940729**	**0.7183337**	**8**
P05178	EALIDHGEEFAER	1.196443748	2	2.971801
P05178	FDYKDQDFLNLMEK	1.300168709	3	4.924891
P05178	FIDLIPTNLPHAVTCDIK	1.091051953	2	3.9967239
P05178	GTTIITSLSSVLHDSK	1.050847911	2	3.6757259
P05178	GTTIITSLSSVLHDSKEFPDPEIFDPGHFLDGNGK	0.570882403	4	4.7788029
P05178	MCAGEGLAR	0.848439187	2	2.6158185
P05178	NITQSLTSFSK	0.914350589	2	3.0794346
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	1.270720752	2	2.5466166
P05179	**CP2C7 Cytochrome P450 2C7**	**1.176129571**	**0.0692781**	**8**
P05179	ACVGEGLAR	1.016446791	2	3.019695
P05179	FINFVPTNLPHAVTCDIK	1.202301751	3	3.5331919
P05179	HMPYTDAMIHEVQR	0.799077298	2	4.1550927
P05179	IEEHQESLDVTNPR	1.072378757	2	4.8487129
P05179	KIEEHQESLDVTNPR	1.276988993	2	4.9804745
P05179	KLPPGPTPLPIIGNFLQIDVK	1.27609824	3	5.984199
P05179	TYGPVFTLYLGSQPTVILHGYEAIK	1.019991994	3	3.4444559
P05179	VLTSLTSVLHDSK	1.615763495	2	3.4042068
P05182	**CP2E1 Cytochrome P450 2E1**	**1.24813172**	**0.0332875**	**12**
P05182	AKEHLQSLDINCAR	1.317964021	2	4.4898925
P05182	DIDLSPVTVGFGSIPPQFK	0.860394607	2	3.3405561
P05182	DTVFQGYVIPK	1.460635891	2	2.3570304
P05182	DVTDCLLIEMEKEK	0.967590279	2	3.2956293
P05182	EHLQSLDINCAR	0.926980221	2	2.483947
P05182	FGPVFTLHLGSR	1.237264614	2	2.5097325
P05182	FINLVPSNLPHEATR	1.251918927	2	3.8806818
P05182	FKPEHFLNENGK	1.14361774	2	3.2453947
P05182	FSLSILR	1.133627124	2	2.3870151
P05182	GTVVIPTLDSLLYDSHEFPDPEK	1.161530607	2	4.7070656
P05182	LDMPYMDAVVHEIQR	1.182012178	2	3.1217978
P05182	YGLLILMK	1.165316685	2	3.1612377
P05183	**CP3A2 Cytochrome P450 3A2**	**1.328616233**	**5.86E-12**	**12**
P05183	DIELDGLFIPK	0.853462051	2	3.5637493
P05183	EMFPIIEQYGDILVK	1.302122107	2	3.76385
P05183	KDIELDGLFIPK	1.228832484	3	3.7398422
P05183	KLQEEIDGALPSK	1.079701284	2	3.5704432
P05183	LKEMFPIIEQYGDILVK	1.289253033	2	3.2660828
P05183	LQEEIDGALPSK	1.240056314	2	4.0948529
P05183	QAILEPEKPIVLK	1.264401982	2	3.2944689
P05183	QEAETGKPVTMK	1.106725471	2	3.4279854
P05183	QEAETGKPVTMK+Oxidation(11)	2.272346503	2	3.1833725
P05183	VDFLQLMLNAHNNSK	1.299083449	2	4.0944881
P05183	VDFLQLMLNAHNNSKDEVSHK	1.58872172	3	3.4918888
P05183	YLKQEAETGKPVTMK	1.602189004	2	3.7892878
P05197	**EF2 Elongation factor 2**	**1.272348054**	**9.9E-20**	**27**
P05197	ALLELQLEPEELYQTFQR	1.796917078	2	5.2837029
P05197	ARPFPDGLAEDIDKGEVSAR	1.223512515	3	5.6910372
P05197	AYLPVNESFGFTADLR	0.964400703	2	4.5215068
P05197	CELLYEGPPDDEAAMGIK	1.365478747	2	4.2524738
P05197	CLYASVLTAQPR	0.9426149	2	2.6169
P05197	DLEEDHACIPIKK	1.27935721	2	3.3852255
P05197	EGIPALDNFLDKL	1.602094039	2	3.4369121
P05197	ETVSEESNVLCLSK	0.930832053	2	4.3269792

P05197	GEGQLGAAER	1.036239489	2	3.6594837
P05197	GHVFEESQVAGTPMFVVK	1.154467853	2	6.0916414
P05197	IWCFGPDGTGPNILTDITK	1.807892968	2	5.1323843
P05197	KIWCFGPDGTGPNILTDITK	1.105962279	2	4.7524595
P05197	KVEDMMK+Oxidation(5)Oxidation(6)	1.647348838	2	2.3100801
P05197	KVEDMMK+Oxidation(6)	1.193106414	2	2.3902862
P05197	LDSEDKDKEGKPLLK	1.4044622	3	3.9685321
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	1.196038763	3	5.0668564
P05197	NMSVIAHVDHGK	1.016900709	2	3.875103
P05197	NMSVIAHVDHGK+Oxidation(2)	1.361625829	2	3.5242877
P05197	STLTDSLVCK	1.05995948	2	3.1268089
P05197	TFCQLILDPIFK	1.272725804	2	4.1978111
P05197	TGTITTFEHAHNMR	0.789506688	2	3.984628
P05197	VFDAIMNFR	1.174040704	2	2.6827619
P05197	VFSGVVSTGLK	1.196282256	2	2.9968669
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.304916599	3	3.5622075
P05197	YEWDVAEAR	1.05034788	2	2.9770551
P05197	YFDPANGK	1.242553443	1	2.0461268
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.846905497	3	5.757659
P05369	**FPPS Farnesyl pyrophosphate synthase**	**0.973179352**	**0.9999995**	**11**
P05369	ALYEELDLR	0.925134801	2	3.1106427
P05369	EVLEYNTVGGK	1.535084381	2	3.0022533
P05369	GLTVVQTFQELVEPR	0.984355068	2	3.9999974
P05369	IKEVLEYNTVGGK	1.037595943	2	4.4726591
P05369	QILEENYGQK	0.697613459	2	2.4221711
P05369	QILEENYGQKDPEK	0.942157026	2	3.6243086
P05369	QNFIQHFSQIVK	1.107487862	2	2.4831905
P05369	SLIEQCSAPLPPSIFLELANK	1.080443506	2	5.1991758
P05369	VGTDIQDNK	0.882736781	2	3.7675407
P05369	VLTEDELGHPEK	0.881502651	2	2.5215466
P05369	VLTEDELGHPEKGDAITR	0.923029027	2	4.7378941
P05426	**RL7 60S ribosomal protein L7**	**1.170653906**	**1.11E-15**	**6**
P05426	AGNFYVPAEPK	1.065143577	2	2.9899006
P05426	FGIICMEDLIHEIYTVGK	1.454749574	3	4.3526769
P05426	IVEPYIAWGYPNLK	1.409633166	2	3.63153
P05426	KKVPAVPETLK	1.159422585	2	3.0003204
P05426	TTHFVEGGDAGNR	1.186937397	2	2.7484114
P05426	TTHFVEGGDAGNREDQINR	1.150304632	2	4.4354072
P05544	**SPA3L Serine protease inhibitor A3L**	**1.274296428**	**0.2535105**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	1.412773899	2	2.8107567
P05544	DSTMEEILEGLK	0.806379711	2	2.8874285
P05544	IAELFSDLEER	1.317193382	2	2.5534906
P05544	MQQVESSLQPETLK	1.162655478	2	4.153573
P05544	MQQVESSLQPETLKK	1.022717751	2	3.3046968
P05544	VFSQQADLSR	1.208859235	2	2.9331348
P05545	**SPA3K Serine protease inhibitor A3K**	**0.945349672**	**0.0125547**	**5**
P05545	AVLDVDETGTEGAAATAVTAALK	1.073543266	2	6.1747699
P05545	FSISTDYNLEEVLPELGIR	1.307234236	2	3.9108636
P05545	IAELFSELDER	0.946494822	2	3.013139
P05545	IFSQQADLSR	1.407512564	2	2.4812181
P05545	NLHVSQVVHK	1.112554584	2	2.6194932
P05765	**RS21 40S ribosomal protein S21**	**0.868751414**	**0.8253413**	**3**
P05765	DHASIQMNVAEVDR	0.819717357	2	3.6872826
P05765	MGESDDSILR	0.882709423	2	3.0099034
P05765	TYGICGAIR	1.053373019	2	2.4403112
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**1.026904335**	**0.9481123**	**9**
P06214	AGADIIITYFAPQLLK	1.346282257	2	4.4702301

P06214	AGAFDLR	0.928565047	2	2.5773206
P06214	AGCQVVAPSDMMDGR	0.863093626	2	3.9122565
P06214	CVLIFGVPSR	0.88674471	2	2.482595
P06214	DEQGSAADSEDSPTIEAVR	0.835036279	2	5.9171801
P06214	DIQEGADILMVKPGLPYLDMVQEVK	1.202421929	2	3.9005892
P06214	TAVLESMTAFR	0.845387044	2	3.2135792
P06214	VPKDEQGSAADSEDSPTIEAVR	0.998190672	2	5.9839659
P06214	YGVNQLEEMLRPLVEAGLR	1.043145035	3	4.2948518
P06302	**PTMA Prothymosin alpha**	**1.213481246**	**3.907E-07**	**3**
P06302	RVAEDDEDDDVETKK	1.246013945	3	5.8329906
P06302	VAEDDEDDDVETK	1.022577415	2	4.3167601
P06302	VAEDDEDDDVETKK	1.213013515	2	4.5815086
P06399	**FIBA Fibrinogen alpha chain**	**1.011823688**	**0.999739**	**9**
P06399	AQQIQVLQK	1.089154474	1	2.0834861
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.809694698	3	4.4150214
P06399	GDFANANNFDNTFGQVSEDLR	1.02115901	2	4.9979024
P06399	GDFANANNFDNTFGQVSEDLRR	0.882332472	3	3.4149284
P06399	GDKELLIGNEK	1.122760667	2	2.7759075
P06399	GLIDEANQDFTNR	1.001745195	2	3.0308998
P06399	MADEAASEAHQEGDTR	1.120813774	2	3.846734
P06399	SQLQEGPPEWK	1.071909794	2	2.9082975
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	0.923430347	3	3.4807212
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.129517501**	**0.0195885**	**6**
P06685	AVAGDASESALLK	1.004651917	2	3.6304007
P06685	AVFQANQENLPILK	1.099663332	2	2.6811121
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.705847246	3	3.3517323
P06685	LNIPVNQVNPR	1.170597545	2	3.1379573
P06685	MSINAEDVVVGDLVEVK	0.909899609	2	3.5107274
P06685	YEPAAVSEHGDKK	1.207424733	2	3.3637276
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.14053942**	**0.98536**	**3**
P06687	DGPNALTPPPTTPEWVK	0.974156424	2	2.970988
P06687	GVGIISEGNETVEDIAAR	1.007833629	2	4.4671016
P06687	QGAIVAVTGDGVNDSPALK	1.159301691	2	5.0453596
P06757	**ADH1 Alcohol dehydrogenase 1**	**0.926899201**	**1**	**19**
P06757	AAVLWEPHKPFTIEDIEVAPPK	0.989503374	3	5.6093659
P06757	FPLEPLITHVLPFEK	1.119891207	3	4.6824512
P06757	GAIFGGFK	0.867638595	2	2.6959758
P06757	GALLDGTSR	0.836206671	2	2.7967961
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.669873664	3	5.403718
P06757	HPESNLCCQTK	1.212201024	2	3.2443397
P06757	ICKHPESNLCCQTK	0.91900127	3	3.8841376
P06757	IDAAAPLDK	0.858122701	2	2.9743004
P06757	IDAAAPLDKVCLIGCGFSTGYGSAVQVAK	1.019697028	3	3.3176198
P06757	IIAVDINKDK	1.011912111	2	2.8963828
P06757	INEAFDLLR	0.916490493	2	3.7113433
P06757	KFPLEPLITHVLPFEK	0.947044445	3	4.5261149
P06757	LVADFMAK	0.975645813	2	2.403616
P06757	MVATGVCR	0.768362522	2	2.6079943
P06757	MVATGVCR+Oxidation(1)	0.982298237	2	2.5266337
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	0.967095206	4	7.9009285
P06757	VCLIGCGFSTGYGSAVQVAK	1.005618239	2	6.4776053
P06757	VIPLFSPQCGK	1.005399486	2	2.5981038
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	0.875139402	3	5.2616386
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.113988783**	**9.9E-20**	**28**
P06761	AKFEELNMDLFR	1.109701646	3	4.6394081

P06761	DAGTIAGLNVMR	0.859506262	2	3.3287241
P06761	DNHLLGTFDLTGIPPAPR	0.752339906	2	4.7796927
P06761	ELEEIVQPIISK	0.928291823	2	4.0453177
P06761	FEELNMDLFR	0.996342478	2	3.5386384
P06761	IEIESFFEGEDFSETLTR	1.096460543	2	5.7304425
P06761	IEWLESHQDADIEDFK	0.968119759	2	5.6810336
P06761	IEWLESHQDADIEDFKAK	1.284401268	3	4.5970016
P06761	IINEPTAAAIAYGLDKR	1.644952677	2	4.4288907
P06761	ITITNDQNR	1.032544271	2	2.6760166
P06761	ITPSYVAFTPEGER	1.208178796	2	4.0559959
P06761	KKELEEIVQPIISK	1.138032217	2	5.4235859
P06761	KSDIDEIVLVGGSTR	1.126687025	2	5.1676893
P06761	KSQIFSTASDNQPTVTIK	1.285317266	2	5.3282542
P06761	LYGSGGPPPTGEEDTSEKDEL	1.395350379	2	5.4974418
P06761	MKETAEAYLGK	1.031128579	2	3.375917
P06761	MKETAEAYLGK+Oxidation(1)	1.36892039	2	2.9312112
P06761	NELESYAYSLK	1.431054803	2	3.5910285
P06761	NQLTSNPENTVFDAK	1.034710629	2	5.2898545
P06761	SDIDEIVLVGGSTR	1.04011641	2	3.450712
P06761	SQIFSTASDNQPTVTIK	1.020155632	2	5.4465842
P06761	TFAPEEISAMVLTK	1.142058287	2	4.7567363
P06761	TKPYIQVDIGGGQTK	1.194297409	2	4.3514671
P06761	TWNDPSVQQDIK	1.07650637	2	4.165689
P06761	VLEDSDLK	1.126124042	2	2.3469119
P06761	VLEDSDLKK	1.182223204	2	2.4550843
P06761	VTHAVVTVPAYFNDAQR	1.350772709	2	5.049963
P06761	VYEGERPLTK	1.106455032	2	2.9083066
P06766	**DPOLB DNA polymerase beta**	**1.205335827**	**0.2287417**	**2**
P06766	EEMLQMQDIVLNEVKK+Oxidation(6)	1.205366598	2	2.3277683
P06766	QDDTSSSINFLTR	0.986752622	2	2.3980837
P06866	**HPT Haptoglobin**	**0.948088808**	**0.9265279**	**6**
P06866	ATDLKDWVQETMAK	1.052571981	2	2.7092466
P06866	GAVSPVGVQPILNK	0.909249721	2	3.5938752
P06866	LQTEGDGIYTLNSEK	0.931937886	2	4.3783464
P06866	NQLVEIEK	0.917110603	1	2.2510293
P06866	SVVDIGLIK	0.950542031	1	1.920939
P06866	YVMLPVADQEK	0.662173301	2	2.5964584
P07150	**ANXA1 Annexin A1**	**1.052921853**	**0.0011076**	**2**
P07150	GGPGSAVSPYPSFNPSSDVAALHK	0.830565289	3	3.9407394
P07150	GLGTDEDTLIEILTTR	1.549331701	2	4.4995251
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.129621612**	**9.9E-20**	**14**
P07153	ASSFVLALEPELESR	1.25726184	2	3.959183
P07153	AVTSEIAVLQSR	1.025377432	2	3.6942453
P07153	FVDHVFDEQVIDSLTVK	1.246331607	2	4.4955206
P07153	GEDEEDNNLEVR	1.068844831	2	3.7774708
P07153	HFDETVNR	0.975543682	2	2.7900562
P07153	ISIVVETVYTHVLHPYPTQITQSEK	0.91742583	3	4.6739707
P07153	LKTEGSDLCDR	1.381013554	2	2.9595549
P07153	NIQVDSPYDISR	1.165367744	2	3.6539588
P07153	NLVEQHIQDIVVHYTFNK	1.243853545	3	4.4658818
P07153	SEDILDYGPFK	1.025809122	2	3.623117
P07153	TEGSDLCDR	0.930747724	2	2.4140818
P07153	TVDLSSHLAK	1.227563375	2	2.4098232
P07153	VHYENNSPFLTITSMTR	1.883040535	2	3.3412666
P07153	VTAEVVLAHPGGGSTAR	1.20834944	2	4.4808707
P07323	**ENOG Gamma_enolase**	**1.004503425**	**0.4865367**	**4**

P07323	AAVPSGASTGIYEALELR	1.221532193	2	5.223527
P07323	FGANAILGVSLAVCK	0.873785961	2	3.771245
P07323	GNPTVEVDLHTAK	0.939623726	2	2.9523187
P07323	SGETEDTFIADLVVGLCTGQIK	1.205979267	2	4.9777231
P07335	**KCRB Creatine kinase B_type**	**0.974866015**	**0.1260848**	**3**
P07335	FCTGLTQIETLFK	1.228719461	2	3.0165131
P07335	LGFSEVELVQMVVDGVK	1.089346847	2	2.6824327
P07335	TDLNPDNLQGGDDLDPNYVLSSR	0.743434356	2	2.890532
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**0.984568446**	**0.9881677**	**3**
P07340	AYGENIGYSEK	0.99118749	2	2.5325859
P07340	VAPPGLTQIPQIQK	0.996076387	2	2.6921675
P07340	YNPNVLPVQCTGK	0.91687999	2	2.4848921
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**0.978695825**	**0.9929748**	**12**
P07379	AINPENGFFGVAPGTSVK	1.034815263	2	4.2774115
P07379	EEGWLAEHMLILGITNPEGK	0.910351238	3	3.773885
P07379	FLWPGFGENSR	1.078251983	2	2.5466988
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	0.976447769	3	4.2746882
P07379	GLGDVNVEELFGISK	1.358097859	2	3.7054167
P07379	IGIELTDSPYVVASMR	1.240628009	2	4.2050037
P07379	MGTSVLEALGDGEFIK	1.186029909	2	3.8651552
P07379	TVIITQEQR	1.185681587	1	1.9131287
P07379	VECVGDDIAWMK	1.022993989	2	3.5101633
P07379	VIQGSLDSLPQEVR	1.212495242	2	3.7112107
P07379	YLAAAFPSACGK	0.931627623	2	2.9413977
P07379	YLEDQVNADLPYEIER	0.872772874	2	4.7899857
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**0.964778734**	**1.196E-07**	**5**
P07632	DGVANVSIEDR	0.698111348	2	2.8305585
P07632	GDGPVQGVIHFEQK	0.986869672	2	3.8872354
P07632	HVGDLGNVAAGK	0.919451273	2	3.9802129
P07632	QDDLGKGGNEESTK	1.607076895	2	3.6119139
P07632	VISLSGEHSIIGR	1.01706013	2	3.1215651
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.999128045**	**0.9530243**	**10**
P07633	AFDNDVDALCNLR	1.176629247	2	3.6480956
P07633	AYNMLDIIHAVIDER	1.157350704	2	4.1911645
P07633	GFVDDIIQPSSTR	0.979210538	2	3.0914896
P07633	HLLGDTNYAWPTAEIAVMGAK	1.034827048	2	5.723217
P07633	ICCDLEVLASK	1.188508595	2	3.5391254
P07633	IMDQAITVGAPVIGLNDSGGAR	1.131144026	2	5.0386195
P07633	IQEGVESLAGYADIFLR	1.159096435	2	4.4235606
P07633	LVPELDTVVPLESSK	0.930229024	2	3.5736568
P07633	SVTNEDVTQEQLGGAK	0.935802851	2	5.2334561
P07633	TVGIVGNQPNVASGCLDINSSVK	0.939311404	2	5.0497394
P07687	**HYEP Epoxide hydrolase 1**	**1.449719039**	**9.9E-20**	**25**
P07687	DIELLYPYK	0.908054396	2	3.0329647
P07687	DKEETLPLGDGWWGPGSKPSAK	1.44077772	3	4.9307785
P07687	EDESIRPFK	1.171515822	2	2.7139027
P07687	EDESIRPFKVETSDEEIKDLHQR	1.51801132	3	6.3701425
P07687	ENLGQGIMVHK	0.981064993	2	2.9617422
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.740536993	3	6.1282277
P07687	FHYGFNSNYMK	1.117285653	2	2.6548893
P07687	FLGYTEKDIELLYPYK	1.446847746	2	4.8671541
P07687	FVSLAELQ	1.145750987	2	2.4554436
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.466232126	3	4.0702906
P07687	GGHFAAFEEPK	1.150467816	2	3.3251548

P07687	GLHLNMAFISR	1.403368622	2	2.8813479
P07687	GLNSVATAR	1.073288185	2	2.4542665
P07687	IEGLDIHFIHVKPPQLPSGR	1.411103766	3	4.3095126
P07687	IIPLLTDPK	1.610899969	1	1.9701415
P07687	KFVSLAELQ	1.359486924	2	2.4489121
P07687	KQVEILNQYPHFK	1.261631034	3	5.4528255
P07687	LLAQDIR	1.371306521	2	2.4388592
P07687	QVEILNQYPHFK	1.342499109	2	3.5566959
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.225444483	3	6.2937293
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSKK	1.452628088	3	5.1675568
P07687	TKIEGLDIHFIHVKPPQLPSGR	1.118925799	3	4.1996417
P07687	VETSDEEIK	0.919770625	2	2.4884014
P07687	VETSDEEIKDLHQR	1.373115806	2	4.8628621
P07687	VFVPTGFSAFPSELLHAPEK	1.867724626	2	5.1223102
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.077081604**	**9.9E-20**	**98**
P07756	AADTIGYPVMIR	0.955655342	2	3.9326758
P07756	AADTIGYPVMIR+Oxidation(10)	1.114102119	2	3.3653083
P07756	AERPDGLILGMGGQTALNCGVELFK	1.121249282	3	6.7263622
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(11)	0.828633123	3	6.1848426
P07756	AFAISGPFNVQFLVK	1.230842057	2	5.0212603
P07756	AFAMTNQILVER	1.082674024	2	4.3786769
P07756	AFAMTNQILVER+Oxidation(4)	1.151219865	2	3.7937558
P07756	ALENNMSLDEIVK	1.043264842	2	4.7584443
P07756	ALENNMSLDEIVK+Oxidation(6)	1.014107031	2	3.9625862
P07756	AMLSTGFK	0.877608003	2	2.5315104
P07756	AQTAHIVLEDGTK	0.812213263	2	4.4766717
P07756	ATGYPLAFIAAK	1.299005735	2	3.1047087
P07756	CEMASTGEVACFGEGIHTAFLK	0.996686216	3	4.784421
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(3)	1.04618811	3	4.7027187
P07756	CLGLTEAQTR	1.000830888	2	3.6047795
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	1.170814813	3	6.446157
P07756	DELGLNK	1.065151672	1	2.2437425
P07756	DGSIDLVINLPNNNTK	0.795527165	2	5.5392032
P07756	DILNMDK	0.711673575	1	1.9276983
P07756	EIEYEVVR	0.774368589	1	2.0633442
P07756	EPLFGISTGNIITGLAAGAK	1.008196181	2	5.3242531
P07756	ETLMDLGTK	0.746944479	1	2.3590941
P07756	EVEMDAVGK	0.574897898	1	2.2228353
P07756	FLEEATR	0.989315251	2	2.4771512
P07756	FLGVAEQLHNEGFK	1.072677357	2	4.8848433
P07756	FVHDNYVIR	1.073821016	3	3.5299408
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.265552738	3	6.1142602
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(16)	1.295532547	3	5.7506967
P07756	GILIGIQQSFRPR	1.017879824	2	2.4772069
P07756	GLNSESVTEETLR	0.977882881	2	4.8683162
P07756	GNDVLVIECNLR	1.075166675	2	4.3495131
P07756	GQILTMANPIIGNGGAPDTTAR	0.928837205	2	6.4563785
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(6)	0.965528743	2	4.8932748
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	1.067330501	3	4.843555
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(6)	0.818569612	3	3.4324303
P07756	GQNQPVLNITNR	0.991646501	2	4.2999997
P07756	GTTITSVLPKPALVASR	1.049353907	2	3.6516881
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	0.985935508	3	6.4514279

P07756	HLGIVGECNIQFALHPTSMEYCIIEVNAR	1.111254478	3	4.8495688
P07756	HLPTLEQPIIPSDYVAIK	1.015912303	2	5.1538906
P07756	IALGIPLPEIK	0.985979941	2	2.9752638
P07756	IAPSFAVESMEDALK	1.703144594	2	5.284112
P07756	IAPSFAVESMEDALK+Oxidation(10)	1.256733476	2	3.4553657
P07756	IEFEGQSVDFVDPNK	0.920641633	2	5.5570726
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	1.039180362	3	5.1490145
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.214791484	3	6.0740442
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	1.10008543	3	3.7849591
P07756	IMGTSPLQIDR	1.461149193	2	3.0548642
P07756	IMGTSPLQIDR+Oxidation(2)	1.693402938	2	3.0931878
P07756	IMGTSPLQIDRAEDR	0.698698456	2	2.4420786
P07756	KELSEPSSTR	0.743012471	2	2.7399802
P07756	KEPLFGISTGNIITGLAAGAK	0.976850433	2	5.4686966
P07756	KTVVVNCNPETVSTDFDECDK	0.157318746	2	5.1218596
P07756	LFAEAVQK	1.055639256	2	3.4245737
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.308620729	3	5.1271515
P07756	LRDADPILR	1.142506262	3	3.5148826
P07756	LTSIDKWFLYK	1.122222345	2	2.4809208
P07756	LYFEELSLER	1.492237906	2	3.4603224
P07756	MCHPSVDGFTPR	0.915850084	3	5.0483136
P07756	MCHPSVDGFTPR+Oxidation(1)	1.220973938	3	4.3315721
P07756	MRDILNMDK	0.859916954	2	3.0370305
P07756	MRDILNMDK+Oxidation(1)	1.384721826	2	2.7487967
P07756	QADAVYFLPITPQFVTEVIK	1.208722028	3	4.4116206
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	1.944661767	3	3.359024
P07756	QLFSDKLNEINEK	1.087464943	2	3.8514531
P07756	QNLIAEVSTK	0.958168877	1	2.5341208
P07756	RFLEEATR	0.977125985	2	2.9943261
P07756	RTAVDSGIALLTNFQVTK	1.144686206	2	4.7542977
P07756	SAYALGGLGSGICPNK	1.030783056	2	4.9585476
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.115866665	3	4.9713659
P07756	SFPFVSK	1.029061176	1	1.9160576
P07756	SIFSAVLDELK	1.044301838	2	3.928221
P07756	SIFSAVLDELKVAQAPWK	0.727780897	3	3.4443893
P07756	SLGQWLQEEK	1.03218583	2	4.1866531
P07756	SLGQWLQEEKVPAIYGVDTR	1.121218864	2	3.9372938
P07756	SVGEVMAIGR	0.929227635	2	3.5905492
P07756	SVGEVMAIGR+Oxidation(6)	1.064258521	2	3.0982208
P07756	TAVDSGIALLTNFQVTK	1.351464742	3	6.3866467
P07756	TFEESFQK	0.939473577	2	2.5403626
P07756	TLGVDFIDVATK	1.002943296	2	4.1810951
P07756	TSACFEPSLDYMVTK	0.962407904	2	4.726368
P07756	TSACFEPSLDYMVTK+Oxidation(12)	1.133563053	2	3.5609522
P07756	TSINVVR	0.922879788	2	2.4394379
P07756	TVLMNPNIASVQTNEVGLK	0.952757782	2	6.6268268
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(4)	1.133652222	2	5.9576983
P07756	TVVVNCNPETVSTDFDECDK	0.258269399	2	5.6252265
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	2.093014891	3	6.0061083
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	1.163891368	3	7.5906944
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(23)	1.175694451	3	7.0406213
P07756	VLGTSVESIMATEDR	1.143291552	2	4.901515
P07756	VLGTSVESIMATEDR+Oxidation(10)	1.111873018	2	4.2219915
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.001589523	2	5.8146391
P07756	VMIGESVDEK	0.867067022	2	3.5697925
P07756	VMIGESVDEK+Oxidation(2)	1.042288577	2	3.009069

P07756	VSQEHPVVLTK	1.010733973	2	3.9825599
P07756	VVAVDCGIK	0.93216067	2	2.5921533
P07756	YMESDGIK	0.948659158	1	2.1481903
P07756	YMESDGIK+Oxidation(2)	1.137989946	1	2.3005195
P07824	**ARGI1 Arginase_1**	**0.995133943**	**0.2842236**	**15**
P07824	ANEQLAAVVAETQK	0.994879223	2	5.3592772
P07824	DHGDLAFVDVPNDSPFQIVK	0.977657495	2	6.2397065
P07824	DIVYIGLR	0.895346689	2	2.7106519
P07824	DVDPGEHYIIK	0.869107883	2	3.2939575
P07824	EGNHKPETDYLKPPK	0.954862959	2	2.7079771
P07824	GKFPDVPGFSWVTPCISAK	1.114225226	3	4.6574011
P07824	LKETEYNVR	1.116557091	3	3.7104428
P07824	NGTISVVLGGDHSMAIGSISGHAR	0.958982865	3	4.5094814
P07824	TGLLSGLDIMEVNPTLGK	1.118680136	2	5.7269597
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(10)	0.753744978	2	2.671371
P07824	TVNTAVALTLSCFGTK	1.022583747	2	4.2555857
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.293065122	4	4.623486
P07824	VMEETFSYLLGR	1.396785387	2	3.8276582
P07824	YFSMTEVDK	0.997038364	1	2.248889
P07824	YFSMTEVDKLGIGK+Oxidation(4)	0.958476399	2	2.5889494
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.898243065**	**9.9E-20**	**16**
P07871	AEELGLPILGVLR	0.980457216	2	4.4157496
P07871	AEIVPVTTTVLDDK	0.845781537	2	4.625771
P07871	AEIVPVTTTVLDDKGDR	0.855391349	2	3.9467776
P07871	AEIVPVTTTVLDDKGDRK	0.995780898	2	4.3805995
P07871	DCLIPMGITSENVAER	0.687865036	2	3.7718823
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	1.012790922	2	6.220922
P07871	IAQFLSGIPETVPLSAVNR	1.675134244	2	4.1056242
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.62508639	3	5.1495199
P07871	QCSSGLQAVANIAGGIR	0.698698456	2	4.9075031
P07871	QDAFALASQQK	0.808992255	2	3.9396648
P07871	QKQDAFALASQQK	0.891830684	2	3.9710534
P07871	QVVTLLNELK	1.107348578	2	2.479455
P07871	SKAEELGLPILGVLR	0.941905791	2	4.0390487
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.900851548	3	4.8202286
P07871	TITVSQDEGVRPSTTMEGLAK	0.891124054	2	4.3483362
P07871	VNPLGGAIALGHPLGCTGAR	1.11095215	2	5.2034044
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**1.0265755**	**0.0001217**	**20**
P07872	AFTTWTANAGIEECR	1.134202639	2	4.0576739
P07872	ASATFNPELITHILDGSPENTR	0.815716801	3	4.5783224
P07872	ASEAHCHYVVVK	1.011766253	3	4.0150447
P07872	EIENLILNDPDFQHEDYNFLTR	1.599870469	2	4.4005928
P07872	EIGTHKPLPGITVGDIGPK	0.988905863	2	4.0459876
P07872	EVAWNLTSVDLVR	0.705503858	2	2.8687017
P07872	EYGISDPEEIMWFK	0.771386621	2	3.5735891
P07872	FGYEEMDNGYLK	0.863568576	2	3.0205963
P07872	GGDFLEGSIITGAQLSQVNAR	0.998989515	2	5.9954791
P07872	GLETTATYDPK	0.890359515	2	3.5025315
P07872	INESIGQGDLSELPELHALTAGLK	1.066764456	3	5.2958031
P07872	IYDQVR	1.021957964	1	1.9942368
P07872	LVEIAAK	1.147761463	1	2.0802603
P07872	NLCLLYSLYGISQK	1.124437578	2	3.2478883
P07872	QSEPEPQILDFQTQQYK	0.985808055	2	4.8684697
P07872	SFLVGNAAQSLSK	0.989651328	2	3.7683971
P07872	SKEVAWNLTSVDLVR	1.07910141	2	3.3766375
P07872	TQEFILNSPTVTSIK	0.966903558	2	4.3428411
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	0.940200533	4	4.972455

P07872	YDGNVYENLFEWAK	1.686960676	2	5.4415746
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**1.06569606**	**0.4295503**	**4**
P07895	AIWNVINWENVSQR	1.216052155	2	3.7661922
P07895	GDVTTQVALQPALK	0.914211301	2	3.3785203
P07895	HHATYVNNLNVTEEK	1.005404713	2	4.7329979
P07895	NVRPDYLK	0.964826997	2	2.4372008
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.971680172**	**0.0986079**	**21**
P07896	GGPMFYAASVGLPTVLEK	1.591009594	2	3.9875119
P07896	GQGLTGPSLPPGTPVR	0.947823466	2	4.239017
P07896	GWYQYDKPLGR	1.066390307	2	3.0798895
P07896	IFNKPVPSLPNMDSVFAEAIAK	1.543001213	3	3.9948666
P07896	IGVVVGNCYGFVGNR	1.197555031	2	3.29422
P07896	IIDKPIEPR	1.194986712	2	2.5842977
P07896	KGQGLTGPSLPPGTPVR	1.021224505	2	4.6644259
P07896	KQYPGVLAPETCVR	0.967699837	2	4.0639005
P07896	LCNPPVNAVSPTVIR	1.407062556	2	4.772687
P07896	LGILDAVVK	1.044891327	2	2.9127936
P07896	LLEVIPSR	0.83708647	2	2.4105275
P07896	QNPDIPQLEPSDYLR	0.860732531	2	3.9634378
P07896	QYPGVLAPETCVR	0.895195133	2	2.9703851
P07896	TASAQPVSSVGVLGLGTMGR	0.968455413	2	5.1416826
P07896	TISKEEILER	1.158239901	2	2.9646196
P07896	VGISVVAVESDPK	0.919190221	2	4.1971827
P07896	VGLPEVTLGILPGAR	1.031835391	2	3.445039
P07896	VSDLAGLDVGWK	0.966799175	2	4.5007052
P07896	YLSADEALR	1.017939193	2	3.1168609
P07896	YSPLGDMLCEAGR	0.962815856	2	3.8610766
P07896	YSSPTTIATVMSLSK	0.996098263	2	3.2304728
P07943	**ALDR Aldose reductase**	**1.145505082**	**0.1442545**	**2**
P07943	AIGVSNFNPLQIER	1.099715774	2	3.0754368
P07943	HIDCAQVYQNEK	1.34479071	2	3.9285505
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.473938919**	**9.9E-20**	**6**
P08009	LCYNPDFEK	2.422426889	1	2.2674367
P08009	LLLEYTDSSYEEK	1.259518755	2	4.9175787
P08009	LLLEYTDSSYEEKR	1.362455705	2	4.1324883
P08009	NQVFEATCLDAFPNLK	1.160827669	2	4.2543664
P08009	SQWLNEK	1.04485204	2	2.6848438
P08009	YTMGDAPDFDR	0.945928726	2	2.3719475
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.285377789**	**9.9E-20**	**14**
P08010	FLSKPIFAK	1.685086042	1	2.1935258
P08010	IRVDVLENQAMDTR	1.452487923	3	4.5480218
P08010	ITYVDFLVYDVLDQHR	3.332139462	2	5.2244534
P08010	KKPEYLEGLPEK	1.142177576	3	4.3408976
P08010	KPEYLEGLPEK	1.361961174	2	3.1971636
P08010	KYSMGDAPDYDR	1.281395739	2	3.4375722
P08010	LFLEYTDTSYEDK	1.252581296	2	5.4905553
P08010	LFLEYTDTSYEDKK	1.214266622	2	4.784174
P08010	LQLAMVCYSPDFER	1.250393072	2	4.1558657
P08010	LQLAMVCYSPDFER+Oxidation(5)	1.931057644	2	3.6439672
P08010	VDVLENQAMDTR	1.133204161	2	4.6329618
P08010	VDVLENQAMDTR+Oxidation(9)	1.258991049	2	3.7413843
P08010	YSMGDAPDYDR	1.035084566	2	3.5456295
P08010	YSMGDAPDYDR+Oxidation(3)	1.072485552	2	2.65854
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**1.026094876**	**1.113E-09**	**6**
P08011	IYHTIAYLTPLPQPNR	1.16451218	2	5.1138887
P08011	MMFLSSATAFQR	1.123589504	2	4.0298967
P08011	MMFLSSATAFQR+Oxidation(1)	1.275653768	2	3.0990944

P08011	MMFLSSATAFQR+Oxidation(2)	1.280657883	2	3.4580626
P08011	VFANPEDCAGFGK	1.107743074	2	4.7892561
P08011	VFANPEDCAGFGKGENAK	1.210671629	2	4.7819147
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**0.942707909**	**0.4676204**	**2**
P08032	ADVVESWIGEK	1.09047113	2	3.0611966
P08032	IEDLGDSMEEALILDIK	0.579663675	2	2.4954875
P08081	**CLCA Clathrin light chain A**	**1.031594381**	**0.7460679**	**2**
P08081	LEALDANSR	1.012112852	2	2.4786804
P08081	WREEQTER	1.149516292	2	2.3660395
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.292227231**	**5.551E-16**	**4**
P08461	DVPLGTPLCIIVEK	0.974204027	2	3.875912
P08461	DVPVGSIICITVEKPQDIEAFK	0.92433806	2	3.4595709
P08461	GLETIASDVVSLASK	1.150236032	2	4.1120214
P08461	VAPTPAGVFIDIPISNIR	1.452716947	2	4.5997553
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.993670775**	**0.9623649**	**8**
P08503	AFTGFIVEADTPGIHIGK	1.153986163	2	4.2448254
P08503	EEIIPVAPDYDK	0.985219906	2	3.552479
P08503	IYQIYEGTAQIQR	1.086723561	2	4.5132103
P08503	KGDEYVINGQK	1.041377364	2	4.226099
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	0.758942228	2	4.6036458
P08503	QEPGLGFSFELTEQQK	0.909946878	2	3.7342138
P08503	SGEYPFPLIK	0.89653673	2	2.6539028
P08503	TRPTVAAGAVGLAQR	1.128998891	2	4.2137218
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.04008528**	**0.9489424**	**10**
P08541	DELQNHFIK	0.945577689	2	2.7899916
P08541	FEIFSTSISKDELQNHFIK	1.146099247	3	3.5023987
P08541	FILPPSYVPVILSGLAGK	1.113366867	3	5.590003
P08541	GHEVTVLKPSAYFFLDPK	1.326195708	3	4.6940913
P08541	HKEWDTFYSEILGRPTTVDETMSK	0.647782577	3	4.3269525
P08541	LLDVWTYELPR	1.315195677	2	3.6457074
P08541	NVMLLSTIHHDQPMKPLDR	1.133036087	2	4.1573887
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(3)	1.544085038	3	3.3913827
P08541	VEIWLIR	1.011300516	2	2.8927727
P08541	VLVWPMDFSHWMNIK	1.136015938	2	3.5056078
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.434195712**	**2.331E-14**	**6**
P08542	EIINNPFYK	1.066148217	1	2.2133834
P08542	FETFPTSVSKDELENYFIK	1.425056432	2	4.1726942
P08542	KWDPFYSEILGRPTTLAETMGK	1.191231502	2	4.497436
P08542	LVDVWTYELQR	1.458269107	2	3.2569957
P08542	NAVWLSTIHHDQPMKPLDK	1.189437478	3	3.716146
P08542	WDPFYSEILGRPTTLAETMGK	1.532750932	2	4.0083604
P08683	**CP2CB Cytochrome P450 2C11**	**1.24123214**	**9.9E-20**	**16**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	1.131515056	3	5.4746447
P08683	EALVDLGEEFSGR	1.102924206	2	3.620312
P08683	EHQESLDKDNPR	1.660736485	2	4.2195969
P08683	FDPGHFLDER	1.291803481	2	2.6649537
P08683	FDYKDPTFLNLMHR	1.502958905	3	4.9086051
P08683	FNENFR	1.219376624	1	2.0184188
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.386808548	3	5.4330807
P08683	ICAGEALAR	1.19097914	2	2.7825153
P08683	LFSSPWLQVCNTFPAIIDYFPGSHNQVLK	1.190625573	3	4.2371197
P08683	LPPGPTPLPIIGNTLQIYMK	1.259788187	2	3.8185425
P08683	NYVLEK	1.334058483	1	1.9389617
P08683	SQMPYTDAVVHEIQR	1.083063575	2	4.6585679

P08683	VKEHQESLDKDNPR	1.453375893	3	4.9381208
P08683	VQEEIER	1.042671514	2	2.6425822
P08683	YGLLLLLK	1.915349276	2	3.4547493
P08683	YIDLVPTNLPHLVTR	1.300538719	2	3.558331
P09006	**SPA3N Serine protease inhibitor A3N**	**1.032009804**	**0.6554818**	**2**
P09034	**ASSY Argininosuccinate synthase**	**1.110185503**	**2.454E-13**	**14**
P09034	APNTPDVLEIEFK	0.980456487	2	2.772826
P09034	DGTTHSTSLDLFMYLNEVAGK	3.130309672	2	5.0558023
P09034	EFVEEFIWPAVQSSALYEDR	2.479505327	2	5.6745815
P09034	EQGYDVIAYLANIGQK	1.18346528	3	3.762732
P09034	FAELVYTGFWHSPECEFVR	1.21308811	2	4.3700342
P09034	FELTCYSLAPQIK	1.462048733	2	4.2361307
P09034	GRNDLMEYAK	0.89044449	2	2.9358039
P09034	IDIVENR	0.933525856	2	2.5510795
P09034	KVFIEDVSK	1.063627112	2	2.7643232
P09034	NDLMEYAK	0.826262124	2	2.6634934
P09034	SPWSMDENLMHISYEAGILENPK	1.231994235	3	4.8549542
P09034	TQDPAKAPNTPDVLEIEFK	1.104620934	2	4.8014483
P09034	TQDPAKAPNTPDVLEIEFKK	1.171930723	3	4.2083726
P09034	VFIEDVSK	1.059263556	2	2.5821319
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.057613708**	**0.0022583**	**5**
P09041	FHVEEEGK	1.051511057	2	2.686317
P09041	FHVEEEGKGK	0.871440436	2	2.819999
P09041	LGDVYVNDAFGTAHR	1.168066973	2	4.0036755
P09041	VDFNVPMK	1.085176555	1	2.2126658
P09041	VSHVSTGGGASLELLEGK	1.126287196	2	5.29532
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.134812202**	**0.7881111**	**3**
P09117	VLAAVYK	1.124188396	2	2.6752446
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	0.929082399	3	5.820941
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.09813877	3	5.0208025
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.381280101**	**0.1094228**	**2**
P09139	LLLGPGPSNLAPR	1.391239538	2	2.5533643
P09139	VLNAPPGISLISFNDK	1.220869442	2	2.6374142
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**1.142026505**	**0.0324456**	**2**
P09456	**KAP0 cAMP_dependent protein kinase type I_alpha regulatory subunit**	**1.385830036**	**7.652E-11**	**2**
P09456	LTVADALEPVQFEDGQK	1.435936648	2	4.1775184
P09456	SENEEFVEVGR	1.183964756	2	2.3184485
P09495	**TPM4 Tropomyosin alpha_4 chain**	**0.950633946**	**5.019E-10**	**11**
P09495	EDKYEEEIK	0.809418273	1	2.2105651
P09495	EENVGLHQTLDQTLNELNCI	2.443186831	2	4.8363361
P09495	IQALQQQADDAEDR	1.200341391	2	4.6600928
P09495	IQLVEEELDR	0.903941374	2	3.4302516
P09495	IQLVEEELDRAQER	1.095023976	2	3.1190317
P09495	KLVILEGELER	0.8162977	2	2.9581959
P09495	LEEAEKAADESER	0.990932199	2	4.0615277
P09495	LVILEGELER	0.910873809	2	3.3369393
P09495	MEIQEMQLK	0.523812834	2	2.5185893
P09495	RIQLVEEELDR	1.031456752	2	2.7127328
P09495	YSEKEDKYEEEIK	1.059781367	2	4.5440221
P09527	**RAB7A Ras_related protein Rab_7a**	**1.087275942**	**0.7514482**	**7**
P09527	ATIGADFLTK	1.037001625	2	2.3543332
P09527	DPENFPFVVLGNK	0.871687774	2	3.264184
P09527	GADCCVLVFDVTAPNTFK	1.240193613	2	4.194108
P09527	TLDSWRDEFLIQASPR	1.048357233	3	3.8341453
P09527	TSLMNQYVNK	0.992063379	2	2.6384318

P09527	TSLMNQYVNKK	0.934447673	2	2.3263371
P09527	VIILGDSGVGK	1.200336667	2	2.3621356
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.001911666**	**0.9904764**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	1.062345726	2	3.5859888
P09605	LSEMTEQDQQR	0.969423104	2	3.3491261
P09606	**GLNA Glutamine synthetase**	**1.334645413**	**9.9E-20**	**8**
P09606	CIEEAIDK	1.106673225	2	2.3226449
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.475528915	3	4.9823227
P09606	LTGFHETSNINDFSAGVANR	1.496766396	2	5.8778911
P09606	MGDHLWVAR	1.108401679	2	3.0011599
P09606	QMYMNLPQGEK	1.164961769	2	2.5490098
P09606	RLTGFHETSNINDFSAGVANR	1.191450159	3	5.4398837
P09606	TCLLNETGDEPFQYK	1.360042643	2	5.4366097
P09606	TCLLNETGDEPFQYKN	2.625043755	2	5.1992021
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**1.256882608**	**0.2611093**	**2**
P09626	VDNSSLTGESEPQTR	1.015016667	2	4.3760448
P09626	VIMVTGDHPITAK	1.340223523	2	2.9279268
P09739	**TNNT3 Troponin T_ fast skeletal muscle**	**0.986131913**	**0.7618502**	**3**
P09739	ELWDTLYQLETDKFEFGEK	1.590012326	2	3.9991198
P09739	KEEEELIALK	1.002349247	2	2.329298
P09739	KKEEEELIALK	0.906288701	3	3.6742864
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.206130563**	**4.918E-05**	**23**
P09811	DFSELEPDKFQNK	0.93413418	2	3.328882
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.473043747	3	5.5898962
P09811	DLSQLTK	1.003727705	1	2.0436127
P09811	EGWQVEEADDWLR	0.935803691	2	3.5695777
P09811	GIVGVENVAELK	0.887204189	2	3.2288146
P09811	GIVGVENVAELKK	1.373596583	2	3.4012544
P09811	HLQIIYEINQK	0.978887565	2	3.8706231
P09811	IFVDIEK	1.142914609	1	1.9568136
P09811	INMAHLCIVGCHAVNGVAK	1.310227669	3	4.1799254
P09811	LHSFVGDDIFLR	2.044534546	3	3.3216903
P09811	LVIDQIDNGFFSPNQPDLFK	1.284416421	2	4.9028616
P09811	LVTSVAEVVNNDPMVGSK	1.050793529	2	4.2817488
P09811	MSLIEEEGGKR	1.173412528	2	2.7936618
P09811	TFAYTNHTVLPEALER	1.165925191	2	4.4488006
P09811	VDDVAALDK	1.012683254	1	1.9589874
P09811	VDDVAALDKK	1.088982586	3	3.3030324
P09811	VFADYEAYVK	1.107633709	2	2.7503631
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.088440113	2	6.0785007
P09811	VLYPNDNFFEGK	1.029688566	2	2.907433
P09811	VSQLYMNQK	0.436038311	2	2.6019776
P09811	WLLLCNPGLADLIAEK	1.3518264	2	4.710887
P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	1.577739863	2	2.925837
P09811	YEYGIFNQK	1.043824731	2	2.3264458
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**1.074158609**	**0.9673796**	**2**
P09812	NLAENISR	1.070758969	1	2.7539473
P09812	VIFLENYR	1.188670194	2	2.4572141
P09838	**TDT DNA nucleotidylexotransferase**	**1.215579015**	**0.1014342**	**2**
P09838	KMMLDNHALYDRTK+Oxidation(2)	1.215579015	2	2.3481448
P09838	KMMLDNHALYDRTK+Oxidation(3)	1.215579015	2	2.4002347
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.269880142**	**0.9174917**	**8**
P09875	ANVVASALAQIPQK	1.04922458	3	4.3347673
P09875	FDGKKPDTLGSNTR	1.435292013	2	2.707607
P09875	FSGGLPLPPSYVPVVLSELSDR	1.046273709	2	3.8971903
P09875	IILNELAQR	1.460523145	2	2.4089005
P09875	SDLEYSFAK	1.097248135	2	2.6483693

P09875	SWSQFYSDVLGRPTTLTEMMGK	1.07882805	2	3.8715951
P09875	VDFSILSTTGLLTALK	1.261796288	2	4.3708663
P09875	VFNEYSDVVENLCK	0.776252612	2	2.8851166
P09895	**RL5 60S ribosomal protein L5**	**1.086595882**	**0.1121142**	**6**
P09895	GAVDGGLSIPHSTK	1.150959153	2	4.9772921
P09895	HIMGQNVADYMR	0.869013459	2	3.2273796
P09895	IEGDMIVCAAYAHELPK	1.109791543	3	3.387053
P09895	NNVTPDMMEEMYK	0.942411362	2	3.0359783
P09895	RFPGYDSESK	1.10063119	2	2.607471
P09895	YLMEEDEDAYKK	1.094705938	2	3.4731214
P0C0S7	**H2AZ Histone H2A.Z**	**1.09265894**	**7.807E-06**	**2**
P0C0S7	ATIAGGGVIPHIHK	1.230218546	2	3.704195
P0C0S7	GDEELDSLIK	1.005701009	1	2.1969409
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.98988927**	**6.067E-08**	**20**
P0C2X9	AIEAAVLAR	0.991429755	2	2.9330668
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.966260847	2	5.2570257
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	1.677727712	2	2.9743848
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.683743499	2	5.2212615
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	1.238237479	3	3.7238679
P0C2X9	EEIFGPVLTVYVYPDEK	1.111977919	2	4.3935661
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	0.79453044	2	4.4451618
P0C2X9	KEWDLKPVADR	0.982453745	2	3.5935318
P0C2X9	LLEEHSR	0.674454328	2	2.3716581
P0C2X9	LYVPQSLWPQIK	1.926992402	2	3.569741
P0C2X9	NAAGNFYINDK	1.123118606	2	2.4688046
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.116250962	2	5.6921268
P0C2X9	SAFEYGGQK	1.041799901	2	2.9037557
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.941162076	3	5.9793
P0C2X9	STGSVVGQQPFGGAR	1.00536423	2	4.2297821
P0C2X9	TIVQEATR	0.920062938	2	2.5432234
P0C2X9	VANEPILAFTQGSPER	0.992477264	2	5.3360181
P0C2X9	VGNPAEDFGTFFSAVIDAK	1.150095868	2	4.8283129
P0C2X9	YQLSPFNHGHK	1.242926499	2	2.9401052
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	0.9119118	3	3.3782301
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.205735122**	**9.9E-20**	**4**
P0C5H9	DRDVTFSPATIEEELIK	1.184537802	2	4.9722347
P0C5H9	DVTFSPATIEEELIK	1.067641202	2	2.9894223
P0C5H9	IINEVSKPLAHHIPVEK	1.327015901	3	4.2592907
P0C5H9	ILDDWGEMCK	1.119952286	2	3.1606197
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.184183416**	**0.0057001**	**2**
P0C6F1	EKVEVMSLELEDAK+Oxidation(6)	1.234301759	2	2.6874592
P0C6F1	TMPLISDLR+Oxidation(2)	1.122477464	2	2.3062372
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.177019588**	**9.9E-20**	**10**
P10111	EGMSIVEAMER	0.796291329	2	3.1951902
P10111	FEDENFILK	1.100924725	2	3.2170458
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.115364698	3	6.2750049
P10111	IIPGFMCQGGDFTR	1.366200839	2	2.8863778
P10111	KITISDCGQL	1.298744072	2	3.4837325
P10111	SIYGEKFEDENFILK	1.233187389	2	4.6745825
P10111	TEWLDGK	0.98962615	2	2.3830712
P10111	VCFELFADK	1.352284611	2	3.3648369
P10111	VCFELFADKVPK	1.357810721	3	3.7170351
P10111	VKEGMSIVEAMER	1.093220788	3	3.4438717
P10536	**RAB1B Ras_related protein Rab_1B**	**1.189129607**	**0.0399452**	**3**
P10536	MGPGAASGGERPNLK	1.170245337	2	3.8944223

P10536	NATNVEQAFMTMAAEIK+Oxidation(10)	1.2173956	2	4.1604424
P10536	NATNVEQAFMTMAAEIK+Oxidation(12)	1.217443473	2	3.8013129
P10633	**CP2D1 Cytochrome P450 2D1**	**1.16327605**	**8.105E-09**	**4**
P10633	GTTLIINLSSVLKDETVWEKPHR	1.082531936	3	3.9599249
P10633	SQGVILASYGPEWR	0.737002717	2	3.99493
P10633	TFMALLDNLLAENR	1.731136019	2	3.6914008
P10633	YGDVFSLQK	1.173564503	2	2.5225577
P10634	**CP2DQ Cytochrome P450 2D26**	**1.3633255**	**0.0182104**	**20**
P10634	ACLGEPLAR	0.813782865	2	2.7515609
P10634	AVSNVIASLVYAR	1.194817399	3	4.3895044
P10634	DMTDAFLAEMQK	0.985577706	2	2.5441167
P10634	EAEHPFNPSILLSK	1.048393262	2	2.4857807
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.155344538	3	5.4112105
P10634	FADIVPTNIPHMTSR	1.313076956	2	2.5945125
P10634	FADIVPTNIPHMTSRDIK	0.894113188	2	2.4105971
P10634	FEYEDPFFNR	0.984615343	2	2.3805306
P10634	FHPEHFLDAQGNFVK	1.084239467	2	4.6875095
P10634	FQGFLIPK	0.97724214	2	2.4802465
P10634	GNPESSFNDENLR	1.170949651	2	4.3532414
P10634	GTTLIPNLSSVLK	0.978604699	2	2.5222535
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.287148809	2	4.6604939
P10634	GVVLAPYGPEWR	1.022244886	2	3.2762904
P10634	LNSFIALVDK	1.629838884	2	2.8210199
P10634	RFEYEDPFFNR	1.230536204	2	3.535579
P10634	RVHEEIDEVIGQVR	1.259589896	2	4.1508851
P10634	SLEQWVTEEAGHLCDTFAK	1.237350364	2	5.2786675
P10634	SWDPAQPPR	0.968436654	2	2.652756
P10634	VHEEIDEVIGQVR	1.041400701	2	4.9405942
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.06070827**	**9.9E-20**	**28**
P10719	AHGGYSVFAGVGER	1.099667598	2	3.9888406
P10719	AIAELGIYPAVDPLDSTSR	0.980797564	2	4.9288998
P10719	EGNDLYHEMIESGVINLK	0.900055681	2	5.3681684
P10719	FLSQPFQVAEVFTGHMGK	1.344649025	2	4.7582393
P10719	FTQAGSEVSALLGR	1.00064327	2	4.7980261
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	2.424437762	3	4.9842305
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	2.056112936	3	3.7198622
P10719	IGLFGGAGVGK	1.333995205	2	3.3246472
P10719	ILQDYK	1.186523624	1	2.0854268
P10719	IMDPNIVGSEHYDVAR	1.082272768	2	4.6414018
P10719	IMDPNIVGSEHYDVAR+Oxidation(2)	1.320908073	2	3.9758413
P10719	IMNVIGEPIDER	1.413539444	2	4.037744
P10719	IMNVIGEPIDER+Oxidation(2)	1.639055089	2	3.3359401
P10719	IPSAVGYQPTLATDMGTMQER	1.100907719	2	4.8890557
P10719	LVLEVAQHLGESTVR	1.245862665	2	4.8448744
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	1.130693147	3	4.8757334
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.311264223	3	5.34199
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(11)	1.036177492	3	3.7814403
P10719	TIAMDGTEGLVR	0.9538721	2	3.6424177
P10719	TIAMDGTEGLVR+Oxidation(4)	1.260216931	2	2.7113628
P10719	TREGNDLYHEMIESGVINLK	1.147415464	2	6.0404243
P10719	TVLIMELINNVAK	1.028975851	2	5.0635409
P10719	TVLIMELINNVAK+Oxidation(5)	1.101305252	2	2.7876987
P10719	VALTGLTVAEYFR	1.345192953	2	4.1060448
P10719	VALVYGQMNEPPGAR	0.96726506	2	3.5500901
P10719	VLDSGAPIK	0.976935624	2	3.032023
P10719	VLDSGAPIKIPVGPETLGR	0.917051904	3	4.4545951
P10719	VVDLLAPYAK	1.14716928	2	3.2347686

P10760	**SAHH Adenosylhomocysteinase**	**1.086222986**	**9.9E-20**	**16**
P10760	AGIPVFAWK	0.98283854	2	2.7234523
P10760	ALDIAENEMPGLMR	1.003142847	2	3.1898305
P10760	ATDVMIAGK	0.90883639	2	2.7770185
P10760	DGPLNMILDDGGDLTNLIHTK	1.280989986	2	5.5700936
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(6)	0.950843981	3	3.3688774
P10760	FDNLYGCR	1.101260985	2	2.7646062
P10760	GETDEEYLWCIEQTLHFK	1.463269682	2	4.3303609
P10760	GISEETTTGVHNLYK	1.076475838	2	4.2605944
P10760	IILLAEGR	1.363077448	2	2.7173953
P10760	KLDEAVAEAHLGK	1.126215877	2	4.7821016
P10760	LDEAVAEAHLGK	1.061112796	2	3.3555212
P10760	SKFDNLYGCR	1.145716381	1	3.1970768
P10760	VAVVAGYGDVGK	1.167017388	2	4.1589313
P10760	VNIKPQVDR	1.145711107	2	2.8154674
P10760	WLNENAVEK	1.073257517	2	2.7236197
P10760	WSSCNIFSTQDHAAAAIAK	1.293656261	2	5.0176382
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**1.149149411**	**0.0864578**	**2**
P10818	HEEHERPEFVAYPHLR	1.095426457	3	3.8255315
P10818	SRHEEHERPEFVAYPHLR	1.156452367	3	3.9529974
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**1.046427168**	**1.424E-11**	**26**
P10860	ALASLMTYK	0.983679692	2	3.4540849
P10860	CAVVDVPFGGAK	1.060006208	2	3.2882154
P10860	CVGVGESDGSIWNPDGIDPK	0.94634857	2	5.3052783
P10860	DDGSWEVIEGYR	0.776228077	2	3.950361
P10860	DIVHSGLAYTMER	0.796687765	2	3.3817139
P10860	DSNYHLLMSVQESLER	1.016963502	2	4.1732297
P10860	GASIVEDKLVEDLK	1.323320844	2	3.6835043
P10860	GFIGPGIDVPAPDMSTGER	0.981369512	2	5.1716547
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(14)	0.989082274	2	4.5487418
P10860	HGGTIPVVPTAEFQDR	1.040559064	2	4.6750293
P10860	IIAEGANGPTTPEADK	0.943905296	2	5.3673482
P10860	IIAEGANGPTTPEADKIFLER	1.100992495	2	4.9759684
P10860	IIKPCNHVLSLSFPIR	1.101767418	3	3.5176132
P10860	KGFIGPGIDVPAPDMSTGER	0.919159455	2	5.0356517
P10860	LQHGSILGFPK	1.414371997	3	3.3909254
P10860	MVEGFFDR	0.886221688	2	3.028183
P10860	MVEGFFDR+Oxidation(1)	1.119114306	2	2.4700532
P10860	NLNHVSYGR	0.975299277	2	2.3698268
P10860	NYTDNELEK	0.990216412	2	2.4968119
P10860	RDDGSWEVIEGYR	0.943671654	2	3.6161017
P10860	RFTMELAK	1.103844966	2	2.4715335
P10860	TAAYVNAIEK	1.008723203	2	3.414145
P10860	TFVVQGFGNVGLHSMR	1.071945828	2	4.5275011
P10860	VYEGSILEADCDILIPAASEK	1.173044145	3	5.8388247
P10860	YNLGLDLR	0.992584923	2	3.2506347
P10860	YSTDVSVDEVK	1.032592487	2	3.3736172
P10867	**GGLO L_gulonolactone oxidase**	**1.284302415**	**0.1567014**	**5**
P10867	GDDILLSPCFQR	0.968908545	2	3.1075816
P10867	LDPTGMFLNSYLEK	1.183320551	2	4.1346483
P10867	LDYWLAYETIMK	1.272871017	2	4.0680614
P10867	TYGCSPEVYYQPTSVEEVR	1.1111722	2	4.9879608
P10867	VVAHYPVEVR	1.291345455	2	2.4866018
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.292541372**	**7.287E-05**	**6**
P10868	EHWIIECNDGVFQR	1.032060424	3	3.3718264
P10868	ENICTEVMALVPPADCR	1.071333686	2	3.0754161

P10868	LQNWALK	1.565201888	2	2.4514899
P10868	WETPYMHSLAAAAASR	1.590520082	2	2.8876109
P10868	YTDITAMFEETQVPALLEAGFQR	1.364805782	3	6.8983965
P10868	YYAFPQMITPLVTK	1.441889588	2	3.8513088
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.152053451**	**0.2971721**	**4**
P10888	DYPLPDVAHVK	0.877187958	2	2.7057128
P10888	IQFNESFAEMNK	1.192773511	2	3.8960042
P10888	SEDYALPSYVDR	0.971097197	2	3.9799993
P10888	VNPIQGFSAK	1.234500153	2	2.3182812
P10959	**EST2 Liver carboxylesterase 1**	**0.928077571**	**0.3605693**	**2**
P10959	AISESGVVLTTNLDKK	0.925983883	2	3.5278459
P10959	EGASEEETNLSKLVMK	1.362188226	2	2.3260899
P11030	**ACBP Acyl_CoA_binding protein**	**0.920736223**	**0.3461337**	**4**
P11030	QATVGDVNTDRPGLLDLK	1.060811127	2	3.3908985
P11030	TQPTDEEMLFIYSHFK	2.657878901	2	4.3425474
P11030	TYVEKVEELK	0.987435704	2	2.8310244
P11030	WDSWNK	0.875144874	1	1.9467911
P11232	**THIO Thioredoxin**	**0.869426461**	**0.0038334**	**2**
P11232	EAFQEALAAAGDK	0.797039517	2	4.8003964
P11232	VGEFSGANK	1.029101294	2	3.0737791
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**0.966847249**	**1.491E-13**	**6**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.185422633	3	6.8635578
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.934972708	3	7.0467262
P11240	GMNTLVGYDLVPEPK	0.964995806	2	4.4103971
P11240	IIDAALR	1.03602289	2	2.3325808
P11240	LNDFASAVR	0.987789221	2	3.3362896
P11240	RLNDFASAVR	1.29505204	2	2.4206774
P11348	**DHPR Dihydropteridine reductase**	**1.168961664**	**0.0297192**	**10**
P11348	AALDGTPGMIGYGMAK	0.965075003	2	3.7963455
P11348	EGGLLTLAGAK	0.994426234	2	2.767082
P11348	GAVHQLCQSLAGK	1.212335557	2	3.8397713
P11348	MTDSFTEQADQVTAEVGK	0.825444322	2	5.7694554
P11348	MTDSFTEQADQVTAEVGK+Oxidation(1)	1.233680315	2	4.8534164
P11348	NCDLMWK	0.987175434	1	2.3152692
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.172619898	2	5.2996144
P11348	QSIWTSTISSHLATK	1.13443854	2	3.6062493
P11348	RPNSGSLIQVVTTDGK	0.56084699	2	3.7657006
P11348	VDAILCVAGGWAGGNAK	0.983024787	2	4.2003975
P11442	**CLH Clathrin heavy chain 1**	**1.172090375**	**9.9E-20**	**40**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	0.883917777	2	5.4665518
P11442	AFMTADLPNELIELLEK	1.260277298	2	4.1725879
P11442	AHIAQLCEK	1.484565437	2	2.5887125
P11442	ALEHFTDLYDIK	1.275990278	2	3.3691504
P11442	CNEPAVWSQLAK	1.029477221	2	2.6720607
P11442	EDKLECSEELGDLVK	0.834325169	2	2.9828358
P11442	FNALFAQGNYSEAAK	0.824176605	2	4.2785716
P11442	GQCDLELINVCNENSLFK	1.210758371	2	4.9044142
P11442	GQFSTDELVAEVEK	1.195628236	2	3.8516979
P11442	GQFSTDELVAEVEKR	1.110782601	2	3.5216296
P11442	HELIEFR	1.041562054	2	2.6297073
P11442	HSSLAGCQIINYR	1.147293549	2	3.1435804
P11442	IHEGCEEPATHNALAK	1.185359188	2	5.1603255
P11442	ISGETIFVTAPHEATAGIIGVNR	1.200707856	2	5.4998441
P11442	IVLDNSVFSEHR	1.414995951	2	2.81375
P11442	IYIDSNNNPER	0.883895626	2	3.0719528

P11442	KDPELWGSVLLESNPYR	1.175112698	3	3.4848554
P11442	KFDVNTSAVQVLIEHIGNLDR	1.136685289	3	5.9054976
P11442	KFNALFAQGNYSEAAK	1.210938146	2	3.6297867
P11442	LAELEEFINGPNNAHIQQVGDR	1.007175939	2	5.2230287
P11442	LECSEELGDLVK	1.106042053	2	3.0132477
P11442	LHIIEVGTPPTGNQPFPK	1.185148128	2	4.1285033
P11442	LLEMNLMHAPQVADAILGNQMFTHYDR	0.993295664	3	3.9571791
P11442	LLYNNVSNFGR	1.290615427	2	2.7770898
P11442	LPVVIGGLLDVDCSEDVIK	1.10685623	2	5.1135521
P11442	LTDQLPLIIVCDR	0.971665901	2	3.2297654
P11442	NLQNLLILTAIK	1.271890276	2	4.3431969
P11442	NNLAGAEELFAR	1.124412063	2	3.7826786
P11442	NNRPSEGPLQTR	1.08103224	3	3.9332516
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.223806064	3	5.8420982
P11442	SVDPTLALSVYLR	1.081810122	2	2.6497762
P11442	SVNESLNNLFITEEDYQALR	1.426325705	2	4.6444426
P11442	TLQIFNIEMK	1.139100567	2	2.7966158
P11442	TSIDAYDNFDNISLAQR	1.161753961	2	4.9876399
P11442	VDKLDASESLR	0.939318469	2	2.5337131
P11442	VGEQAQVVIIDMNDPSNPIR	0.975221073	2	5.2960238
P11442	VIQCFAETGQVQK	1.057082444	2	4.7509513
P11442	VSQPIEGHAASFAQFK	1.149568573	2	4.1361928
P11442	WLLLTGISAQQNR	1.206160938	2	2.6340017
P11442	YESLELCRPVLQQGR	0.830924211	2	3.2105551
P11497	**ACACA Acetyl_CoA carboxylase 1**	**0.898487876**	**0.4421476**	**3**
P11497	ECSQPVMVYIPPQAELR+Oxidation(7)	0.884686585	2	2.4394791
P11497	LPELLLK	1.286072936	2	2.492558
P11497	TLRDPSLPLLELQDIMTSVSGR	1.016774777	3	3.9693687
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**1.041816724**	**0.5446349**	**5**
P11507	DIVPGDIVEIAVGDKVPADIR	1.142303017	2	3.6858432
P11507	IRDEMVATEQER	1.02852788	2	3.1937263
P11507	KSEIGIAMGSGTAVAK	0.862094596	2	3.1864243
P11507	TASEMVLADDNFSTIVAAVEEGR	1.617581955	2	2.8698683
P11507	VDQSILTGESVSVIK	0.979141206	2	4.1111856
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.041523845**	**9.9E-20**	**25**
P11598	DGEEAGAYDGPR	0.950918592	2	3.4458654
P11598	DLLTAYYDVDYEK	1.050089692	2	3.6681244
P11598	DPNIVIAK	1.052218896	2	2.377151
P11598	EATNPPIIQEEKPK	0.97509035	2	3.6481042
P11598	EYDDNGEGITIFRPLHLANK	1.056876913	2	3.9875336
P11598	EYDDNGEGITIFRPLHLANKFEDK	0.859571719	3	3.8096926
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.10976055	3	5.2813802
P11598	FISDKDASVVGFFR	1.283835071	2	4.5588064
P11598	FLQEYFDGNLK	1.030387972	2	3.7290366
P11598	FLQEYFDGNLKR	1.336692948	2	3.707463
P11598	FVMQEEFSR	1.124094218	2	2.9894578
P11598	GFPTIYFSPANK	0.968172025	2	2.7979867
P11598	IFRDGEEAGAYDGPR	1.214457531	2	4.1393905
P11598	KQAGPASVPLR	1.049610858	2	2.4126158
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.237240512	3	4.4515743
P11598	LAPEYEAAATR	1.103627318	2	2.8752389
P11598	LNFAVASR	1.539380145	2	2.6673787
P11598	LSKDPNIVIAK	1.224111549	3	4.3337402
P11598	MDATANDVPSPYEVK	1.219299509	2	4.3303123
P11598	MDATANDVPSPYEVK+Oxidation(1)	1.28323817	2	3.9882777
P11598	RLAPEYEAAATR	0.8337862	2	3.3509221

P11598	SEPIPETNEGPVK	1.106086225	2	2.9548032
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.194447282	2	5.9753432
P11598	VDCTANTNTCNK	1.210384713	2	4.4608645
P11598	YGVSGYPTLK	1.042122761	2	2.893121
P11608	**ATP8 ATP synthase protein 8**	**1.110496898**	**0.5010009**	**2**
P11608	ISSQTFPAPPSPK	1.173949365	2	2.3756335
P11608	TNNPWESK	0.8803161	2	2.3594987
P11711	**CP2A1 Cytochrome P450 2A1**	**1.077046252**	**0.6030909**	**5**
P11711	GEQATYNTLFK	1.176844697	2	3.1286345
P11711	GTDVFPILGSLMTDPK	1.061294938	2	3.4737687
P11711	ILEEAGYLIK	1.089690187	2	2.7840798
P11711	TVSNVISSIVFGER	1.031285146	2	3.1709948
P11711	VHEEIEQVIGR	1.036276932	2	3.4209054
P11714	**CP2D9 Cytochrome P450 2D9**	**1.223328486**	**0.0067447**	**2**
P11714	GNPESSFNDENLLMVVR	1.08207428	2	2.5797153
P11714	VQQEIDEVIGQVR	1.224586816	2	4.6216135
P11862	**GAS2 Growth arrest_specific protein 2**	**1.055996367**	**0.9869501**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.127865518	2	3.9096673
P11862	LDNGALLCQLAATVQEK	1.083092095	2	3.9022977
P11862	YGVEPPGLIK	1.020391243	2	2.5233934
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**0.969555255**	**9.9E-20**	**24**
P11884	DGMTIAKEEIFGPVMQILK	1.132294237	2	3.8239589
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.433648441	3	4.2065606
P11884	EEIFGPVMQILK	0.839191969	2	3.9103467
P11884	ELGEYGLQAYTEVK	0.837812712	2	4.5705652
P11884	GYFIQPTVFGDVK	1.062538517	2	3.9246013
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.952917251	3	4.1316791
P11884	LGPALATGNVVVMK	1.191578724	2	4.0675573
P11884	LGPALATGNVVVMK+Oxidation(13)	1.408404933	2	3.59059
P11884	LLCGGGAAADR	1.414557606	2	3.7849836
P11884	RVTLELGGK	0.840033709	2	2.784054
P11884	TEQGPQVDETQFK	0.979707412	2	4.54317
P11884	TEQGPQVDETQFKK	1.186223534	2	3.8508184
P11884	TFPTVNPSTGEVICQVAEGNK	0.73805856	2	5.2996211
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.971711648	2	4.2909131
P11884	TFVQEDVYDEFVER	1.333632089	2	5.2386732
P11884	TIEEVVGR	0.946319186	2	3.024272
P11884	TIPIDGDFFSYTR	1.43340992	2	2.5117145
P11884	VAEQTPLTALYVANLIK	1.66946469	2	5.4906688
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.015647894	2	5.7853203
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.000833513	3	3.8031502
P11884	VTLELGGK	0.99159815	2	2.3048167
P11884	VVGNPFDSR	0.968714257	2	3.0428371
P11884	YGLAAAVFTK	1.025636262	2	3.8727586
P11884	YYAGWADK	0.891955096	2	2.5501041
P11915	**NLTP Non_specific lipid_transfer protein**	**0.985459502**	**6.958E-08**	**22**
P11915	ADCTITMADSDLLALMTGK	1.386730146	2	5.3358254
P11915	ADCTITMADSDLLALMTGK+Oxidation(7)	1.373822334	2	3.6260989
P11915	ANLIFK	0.965054322	2	2.3924677
P11915	AVEIVAQEMVTDMPSTFEEK	1.004568839	2	4.3397284
P11915	GSVLPDSDKK	0.892747244	2	2.781842
P11915	HGLQSKAVEIVAQEMVTDMPSTFEEKSVIK+Oxidation(15)Oxidation(19)	1.255905527	3	3.3845916
P11915	HIDVLINK	0.812373186	2	2.8688028
P11915	HSVNNPYSQFQDEYSLDEIMK	0.965503615	3	5.6645803
P11915	IGGIFAFK	1.28099976	2	2.4288359
P11915	KADCTITMADSDLLALMTGK	1.418989169	2	4.2592759

P11915	KLEEEGEEFVK	0.986983524	2	4.3243041
P11915	KLEEEGEEFVKK	1.020819995	3	4.7489829
P11915	LEEEGEEFVK	1.130139217	2	3.029355
P11915	LEEEGEEFVKK	0.985158213	2	3.6871123
P11915	LQSLQLQPDK	1.38292825	2	3.2980525
P11915	MGFPEAASSFR	0.808974546	2	2.9202247
P11915	MNPQSAFFQGK	0.92941872	2	3.1933088
P11915	MNPQSAFFQGK+Oxidation(1)	0.353790292	2	2.5766435
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.318413743	3	5.5306778
P11915	THQISAAPTSSAGDGFK	1.033416258	2	4.4908443
P11915	WVINPSGGLISK	0.872216143	2	2.8910325
P11915	YGMSACPFAPQLFGSAGK	0.919245431	2	4.3847289
P11960	**ODBA 2_oxoisovalerate dehydrogenase subunit alpha_ mitochondrial (Fragment)**	**0.915492611**	**0.2445898**	**10**
P11960	AVAENQPFLIEAMTYR	1.468518416	2	3.7917323
P11960	HFVTISSPLATQIPQAVGAAYAAK	0.986972937	2	4.1311717
P11960	HLQTYGEHYPLDHFDK	0.91580948	3	3.415319
P11960	IGHHSTSDDSSAYR	1.424578454	3	4.0560508
P11960	NNGYAISTPTSEQYR	1.007614165	2	3.9776893
P11960	QGQIINPSEDPHLPQEEVLK	0.99264848	2	2.5206773
P11960	QYLLNQGWWDEEQEK	0.849770091	2	3.5931051
P11960	SVDEVNYWDK	1.197892855	2	2.4658787
P11960	TDLVFGQYR	0.94928201	1	1.9822562
P11960	VMEAFEQAER	0.770968098	2	3.6182132
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.010889134**	**0.5963242**	**3**
P11980	AEGSDVANAVLDGADCIMLSGETAK	1.075991386	3	3.6481011
P11980	GVNLPGAAVDLPAVSEK	1.200523628	2	3.8564661
P11980	NTGIICTIGPASR	0.936330877	2	3.6304948
P12001	**RL18 60S ribosomal protein L18**	**1.492266872**	**9.9E-20**	**5**
P12001	GTVLLSGPR	1.347038405	2	2.6975477
P12001	ILTFDQLALESPK	1.493516554	2	4.8977561
P12001	TAVVVGTITDDVR	1.175413228	2	4.0583639
P12001	TNRPPLSLSR	1.075889802	3	3.3764188
P12001	TNSTFNQVVLK	1.152302804	2	3.0642381
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.001795002**	**0.560411**	**9**
P12007	AQEIDQSNDFK	0.437772199	2	3.5577948
P12007	FVQENLAPK	0.935803704	2	2.8498847
P12007	FWITNGPDADVLVVYAK	1.303875389	2	4.6099443
P12007	GSNTCELVFEDCK	0.90803506	2	4.2436619
P12007	GSNTCELVFEDCKVPAANILSQESK	1.144802107	3	5.3985658
P12007	GVYVLMSGLDLER	1.108546936	2	3.7292702
P12007	IGQFQLMQGK	1.09848927	2	2.6685934
P12007	LYEIGGGTSEVR	1.107105632	2	2.8304989
P12007	TDLTAVPASR	1.032239278	2	2.8517039
P12346	**TRFE Serotransferrin**	**1.038380932**	**0.0402809**	**19**
P12346	ADRDQYELLCLDNTR	1.38533584	2	4.3361497
P12346	ASDSSINWNNLK	1.067476615	2	3.1874783
P12346	DFQLFGSPLGK	0.882878745	2	2.9826818
P12346	DLKQEDFQLLCPDGTK	0.921288049	2	5.0244832
P12346	EGVCPEGSIDSAPVK	0.814924074	2	3.8482218
P12346	FDEFFSQGCAPGYK	1.0536061	2	4.5408411
P12346	GDKDCTGNFCLFR	0.927261821	2	3.4403369
P12346	GTDFQLNQLQGK	1.027841949	2	3.1934855
P12346	GYYAVAVVK	1.023298577	2	2.3885009
P12346	HQTVLENTNGK	0.557908952	2	3.0428915
P12346	HTTIFEVLPQK	1.03968704	2	3.4726186
P12346	KGTDFQLNQLQGK	1.035724282	2	4.1542406

P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.274017132	2	4.7336941
P12346	NGDGKEDLIWEILK	0.978028159	3	3.5206356
P12346	QEDFQLLCPDGTK	0.941259634	2	3.6102147
P12346	SKDFQLFGSPLGK	1.062133855	2	3.318517
P12346	VSTVLTAQK	0.978562684	2	2.7665803
P12346	WCALSHQER	1.413382532	2	3.1468039
P12346	WCAVSEHENTK	1.001966932	2	3.7916574
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.109813907**	**0.8332758**	**2**
P12368	NLDQEQLSQVLDAMFEK	1.175799657	2	4.7619848
P12368	SVGQYDNRGSFGELALMYNTPR	1.077376044	2	2.3897748
P12711	**ADHX Alcohol dehydrogenase class_3**	**1.043146914**	**0.0202066**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.112424734	3	5.9307914
P12711	AFDLMHSGNSIR	0.649807028	2	3.1188488
P12711	AGDTVIPLYIPQCGECK	1.011688615	2	3.0644715
P12711	AKEFGATECINPQDFSK	0.955243211	2	4.7674742
P12711	EFGATECINPQDFSK	0.924013626	2	4.6290488
P12711	IIGIDINK	0.982774605	2	2.4218645
P12711	IIGIDINKDK	1.030967046	2	2.4165297
P12711	VCLLGCGISTGYGAAVNTAK	1.411282023	2	5.6769099
P12711	VDEFVTGNLSFDQINK	0.851217694	2	4.9551206
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	1.401003978	2	4.0917897
P12749	**RL26 60S ribosomal protein L26**	**1.071127561**	**0.3785667**	**5**
P12749	FNPFVTSDR	0.965058687	2	2.6003447
P12749	HFNAPSHIR	0.961591894	3	3.9727283
P12749	KDDEVQVVR	1.136253394	2	3.1601343
P12749	KIMSSPLSKELR+Oxidation(3)	1.436121707	2	2.4737866
P12749	YKEETIEK	0.994315319	2	2.8957546
P12785	**FAS Fatty acid synthase**	**1.037059603**	**0.6967094**	**41**
P12785	ACIDTALENLSTLK	1.179091149	2	3.9288149
P12785	AGSDTELAAPK	0.956706557	2	3.4888184
P12785	ALIAEATK	0.933355127	2	2.3149142
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.198311091	3	3.4421332
P12785	DANLPAGSMAAVGLSWEECK	0.7115954	2	4.2936726
P12785	DGGFLLMHTVLK	0.934021413	2	2.5467587
P12785	DHKDNLEFFLTNLGK	1.613643781	2	2.3682582
P12785	EEEPEAMLPGAQPTLISAISK	1.095689509	2	4.0490198
P12785	EQGVTFPSGEAQEQLIR	0.994477184	2	4.3982863
P12785	FDASFFGVHPK	1.166310721	2	3.4054384
P12785	FVFTPHVEPECLSESAILQK	0.835521739	2	4.3691149
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	1.790344772	3	5.9040623
P12785	GLESIINIIHSSLAEPR	1.224955323	2	4.6243649
P12785	GNAGQSNYGFANSTMER	1.009634794	2	4.4859023
P12785	GVDLVLNSLAEEK	1.038035508	2	3.340508
P12785	LFDHPEVPIPAESESVSR	0.970871946	2	4.393259
P12785	LLLPEDPLISGLLNSQALK	1.500684548	3	5.1250706
P12785	LSPQDKPIFLPVEDTSFQWVDSLK	0.828702545	3	3.9136584
P12785	LTPGCEAEAEAEAICFFIK	1.67605961	2	4.6660914
P12785	MTVPGLEDLPQHGLPR	1.153305241	2	3.4959583
P12785	QAQLNLSILLVNPEGPTLTR	1.046604608	2	4.3583074
P12785	QQEQLVPTLEK	0.722785089	2	2.6254861
P12785	RQQEQLVPTLEK	0.889541849	2	2.9877098
P12785	SDEALKPLGVK	1.131235267	2	2.991137
P12785	SFDDSGNGYCR	1.253967766	2	3.0345011
P12785	SLSLSLEETPVVFENVTFHQATILPR	1.395098365	3	4.1317844
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.109454266	2	5.5621948
P12785	SNMGHPEPASGLAALTK	0.963990359	2	3.1916797

P12785	TGGTYGEDLGADYNLSQVCDGK	0.905375171	2	4.8652225
P12785	TMEAVQGLLEQGR	0.772859399	2	3.5689623
P12785	VGDPQELNGITR	1.42260904	2	2.7379775
P12785	VHLTGIDINPNALFPPVEFPVPR	0.985019782	2	5.2326841
P12785	VLEALLPLK	0.966538811	2	2.6252897
P12785	VLESDLVMNVYR	0.923791578	2	3.0437996
P12785	VSVHIIEGDHR	1.14996173	3	3.4740672
P12785	VTAIYIDPATHLQK	1.028736601	2	3.5583355
P12785	VYATILNAGTNTDGCK	1.134178411	2	4.8987379
P12785	VYMLEGDTQVADVTTSR	0.721547927	2	4.8399611
P12785	VYQWEDPDSK	0.823929963	2	3.3172619
P12785	WLSTSIPEAQWQSSLAR	1.18004283	2	3.5357883
P12785	YNGTLNLDR	0.982362649	2	2.5831411
P12791	**CP2BA Cytochrome P450 2B10**	**1.346756375**	**0.072944**	**2**
P12791	IQEEAQCLVEELR	1.029004174	2	4.5814338
P12791	IQEEAQCLVEELRK	1.352725247	2	3.8244996
P12847	**MYH3 Myosin_3**	**1.245433402**	**0.9905646**	**6**
P12847	EQYEEEQEGK	0.594229652	2	3.0691202
P12847	GQEDLKEQLAIVER	1.560955528	2	3.9833338
P12847	GTLEDQIISANPLLEAFGNAK	1.153351611	2	3.2874076
P12847	IEAQNQPFDAK	0.769586352	2	2.378526
P12847	MKGTLEDQIISANPLLEAFGNAK	1.111906908	3	6.9802079
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(1)	1.11970286	2	4.3997335
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.087381711**	**0.9944923**	**19**
P12928	AETSDVANAVLDGADCIMLSGETAK	1.014625449	2	5.5178008
P12928	CCAAAIIVLTK	0.941997227	2	2.86566
P12928	CNLAGKPVVCATQMLESMITK	1.100344235	3	4.8382006
P12928	EATESFATSPLSYRPVAIALDTK	1.029203314	2	3.8886139
P12928	EPPEAIWADDVDR	0.922170826	2	2.4640126
P12928	GDLGIEIPAEK	1.05450527	2	3.1349792
P12928	GSFPVEAVMMQHAIAR	1.042836987	2	3.2367251
P12928	GSQVLVTVDPK	0.915275676	2	2.8661397
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.137462419	2	5.250196
P12928	IGPEGLVTEVEHGGILGSR	1.14090488	2	5.284586
P12928	IYIDDGLISLVVQK	1.227255507	2	4.5192833
P12928	KFDEILEVSDGIMVAR	0.791173148	3	4.1724658
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.116642454	3	4.8035045
P12928	LNFSHGSHEYHAESIANIR	1.815186921	3	5.1389375
P12928	RVQFGIESGK	1.387344423	2	2.4617467
P12928	STSIIATIGPASR	1.028699794	2	3.3244884
P12928	TGVLQGGPESEVEIVK	0.95381157	2	4.4571471
P12928	TVWVDYHNITR	1.308485606	2	2.3303785
P12928	VQFGIESGK	0.933550901	2	2.8336675
P12938	**CP2D3 Cytochrome P450 2D3**	**1.108375869**	**0.1753848**	**7**
P12938	AVQELLVTCGEDTADRPEMPIFQHIGYGHK	0.983590009	3	3.7307699
P12938	DLTDAFLAEIEK	1.352782128	2	3.8620913
P12938	FDYGDPDFIK	1.030733563	2	2.9215667
P12938	GNPESSFNDANLR	1.026605953	2	3.9357047
P12938	RFDYGDPDFIK	1.175184755	2	3.1202319
P12938	TFLTMVDNLVTEHK	1.129363463	2	3.095921
P12938	TWDPDQPPRDLTDAFLAEIEK	1.528252794	3	4.0413208
P12939	**CP2DA Cytochrome P450 2D10**	**1.397311676**	**9.9E-20**	**9**
P12939	ALCNVIASLIFAR	1.532568543	2	2.5440202
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.70032985	3	5.3313322
P12939	FEYEDPYLIR	1.298146123	2	2.8481169
P12939	FGDIAPLNLPR	1.652095532	2	3.4473257
P12939	ITSCDIEVQDFVIPK	1.720382867	2	4.1880231

P12939	NLTDAFLAEVEK	1.43767822	2	4.0465932
P12939	RFEYEDPYLIR	1.572010935	2	2.978718
P12939	TFMAFLDNLLAENR	1.960620598	2	3.0688982
P12939	TTWDPAQPPR	1.285270236	2	2.3677936
P13084	**NPM Nucleophosmin**	**1.498006997**	**1.276E-10**	**2**
P13084	MTDQEAIQDLWQWR	1.29040237	2	2.8416598
P13084	VDNDENEHQLSLR	1.569693955	2	3.887589
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.139339139**	**3.886E-15**	**5**
P13086	HLGLPVFNTVK	1.097040459	2	2.3772621
P13086	LIGPNCPGIINPGECK	1.468711755	2	4.8771005
P13086	MGHAGAIIAGGK	0.783506515	1	2.8407648
P13086	NIYIDK	1.050240488	1	1.9872726
P13086	QGTFHSQQALEYGTK	1.138950657	2	2.7846844
P13107	**CP2B3 Cytochrome P450 2B3**	**1.815598944**	**9.178E-06**	**7**
P13107	ATLDPNAPR	1.155669512	2	2.6304283
P13107	EVLDYIDHSVENHR	1.170574827	2	4.0788541
P13107	FSDVSPMGLPCR	1.230151451	2	3.2932529
P13107	GIIAVLQPIMQEYGVSFVNEER	1.82872971	3	6.3408699
P13107	MCLGEGIAR	1.113255657	2	2.8266883
P13107	QSVEDQIKEEAK	1.24156894	2	2.5859671
P13107	SFIQLQEK	1.37685108	1	2.3537507
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.144170023**	**0.6343867**	**4**
P13221	ITWSNPPAQGAR	1.144129421	2	3.1963475
P13221	NLDYVATSINEAVTK	1.07888244	2	3.9999757
P13221	SCASQLVLGDNSPALR	1.239735614	2	4.5212412
P13221	TDDSQPWVLPVVR	0.766526869	2	2.8866391
P13255	**GNMT Glycine N_methyltransferase**	**1.253307173**	**2.478E-08**	**6**
P13255	AHMVTLDYTVQVPGAGR	1.383350613	2	5.1958809
P13255	AWLLGLLR	1.572753146	2	2.7841229
P13255	DITTSVLTVNNK	1.251913178	2	3.516042
P13255	NYDYILSTGCAPPGK	1.209632543	2	4.8059235
P13255	SDLTKDITTSVLTVNNK	1.544217271	2	2.7466686
P13255	SLGVAAEGIPDQYADGEAAR	1.246763515	2	5.5111575
P13383	**NUCL Nucleolin**	**1.006429042**	**0.083321**	**6**
P13383	GFGFVDFNSEEDAK	0.643868773	2	3.3440387
P13383	GSPNARSQPSKTLFVK	1.22504047	2	2.3621068
P13383	NDLAAVDVR	1.129121877	1	1.9057617
P13383	NLSFNITEDELKEVFEDAVEIR	0.751744373	3	3.4366112
P13383	SEADAEKNLEEK	1.108855264	2	2.5682125
P13383	TLVLSNLSYSATEETLQEVFEK	1.278427224	2	2.7663736
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**1.192827961**	**5.347E-13**	**22**
P13437	AANEAGYFNEEMAPIEVK	0.409837487	2	5.1362638
P13437	AANEAGYFNEEMAPIEVK+Oxidation(12)	0.967597423	2	4.8747678
P13437	DAEVVLCGGTESMSQSPYSVR	0.809375281	2	4.5660648
P13437	DFTATDLTEFAAR	0.930126654	2	3.4676592
P13437	DMDLIDVNEAFAPQFLAVQK	1.837973232	3	6.9698067
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(2)	1.122568871	2	3.430994
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.732316655	2	5.7776361
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	0.814052624	3	4.9834266
P13437	FGLDLK	0.847774316	2	2.3360631
P13437	GVFIVAAK	0.880496527	2	2.5214045
P13437	HNFTPLAR	0.95013196	2	2.3306158
P13437	ITAHLVHELR	1.254624415	2	3.3060646
P13437	LCGSGFQSIVSGCQEICSK	1.442382622	2	5.5474167
P13437	LEDTLWAGLTDQHVK	0.830728556	2	5.2470822
P13437	RTPFGAYGGLLK	1.150538954	2	3.0358779

P13437	SLDLDPSK	0.835202003	2	2.6202292
P13437	TNVSGGAIALGHPLGGSGSR	0.887778996	2	5.8548932
P13437	VGVPTETGALTLNR	0.928543278	2	3.6832216
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	1.035013357	3	6.6626492
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.020788441	3	5.0781841
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	1.114675626	3	4.2087688
P13437	YAVGSACIGGGQGISLIIQNTA	0.808136953	2	4.3087912
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**0.96218223**	**2.497E-11**	**8**
P13444	FVIGGPQGDAGVTGR	1.009871509	2	4.5653319
P13444	HIGYDDSAK	0.965386629	2	2.7977934
P13444	ICDQISDAVLDAHLK	1.059470821	3	5.6331677
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.570936264	3	6.7533298
P13444	SEFPWEVPK	0.925953071	2	2.3190646
P13444	SGVLPWLRPDSK	1.075286749	2	2.9699113
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.301659409	3	5.4937415
P13444	TQVTVQYVQDNGAVIPVR	1.082630539	2	4.3423882
P13471	**RS14 40S ribosomal protein S14**	**1.184721547**	**1.201E-05**	**2**
P13471	ADRDESSPYAAMLAAQDVAQR	1.195069881	2	5.4366636
P13471	IEDVTPIPSDSTR	1.120191291	2	3.9362993
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.847875957**	**0.0009993**	**20**
P13601	ANNTPYGLAAGVFTK	0.729568078	2	3.9374189
P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	0.600238736	3	3.7890399
P13601	EEIFGPVQQIMK	0.614991262	2	3.529681
P13601	EMGEQGVYEYTELK	0.667745923	2	3.6780782
P13601	FPVINPATEEVICHVEEGDK	0.737576093	3	3.7493389
P13601	FPVINPATEEVICHVEEGDKADVDK	0.852635397	4	5.1933799
P13601	GFFVQPTVFSNVTDEMR	1.28992495	2	4.1794672
P13601	IAKEEIFGPVQQIMK	0.923914799	3	3.472584
P13601	IFINNEWHNSLNGK	0.989505894	2	4.0327077
P13601	IHGQTIPSDGDVFTYTR	0.985077941	3	4.4623113
P13601	ILDLIESGK	0.64127202	2	3.2203381
P13601	ILDLIESGKK	0.741706471	2	2.9516916
P13601	KFPVINPATEEVICHVEEGDK	0.867732548	3	3.3682454
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.900697503	4	4.8262267
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	0.825912671	3	5.277019
P13601	LFVEESIYDEFVR	0.678818972	2	4.1860037
P13601	VLLATMESMNAGK	0.556893077	2	4.074688
P13601	VSFTGSTEVGK	0.581409242	2	3.1863008
P13601	YVLGNPLDSGISQGPQIDK	0.691234012	2	4.6106801
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.684928973	2	4.2457318
P13697	**MAOX NADP_dependent malic enzyme**	**1.177497594**	**0.6883647**	**5**
P13697	AECSAEECYK	1.138789948	2	3.0523372
P13697	AIFASGSPFDPVTLPDGR	1.326701576	2	4.804338
P13697	GHIASVLNAWPEDVVK	1.161877476	2	4.0575638
P13697	HINDSVFLTTAEVISQQVSDK	1.26053583	2	5.8862519
P13697	ILGLGDLGCNGMGIPVGK	1.081418978	2	2.6831391
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.13007068**	**9.9E-20**	**13**
P13803	AAVDAGFVPNDMQVGQTGK	1.040405252	2	4.5428648
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(12)	1.562090609	2	3.7143743
P13803	GLLPEELTPLILETQK	1.185017095	2	4.8931651
P13803	GTSFEAAAASGGSASSEK	1.044591089	2	5.1601238
P13803	LGGEVSCLVAGTK	1.044147689	2	4.7494774
P13803	LLYDLADQLHAAVGASR	1.443563939	2	4.9330168
P13803	LNVAPVSDIIEIK	1.432746012	2	4.1274314
P13803	QFSYTHICAGASAFGK	0.961835103	2	3.1293459

P13803	SDRPELTGAK	0.992839586	3	3.4482472
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	1.081279595	3	6.9513679
P13803	TIYAGNALCTVK	1.050991711	2	3.704957
P13803	VLVAQHDAYK	1.051478544	2	3.3204908
P13803	VVQDLCK	0.938699675	2	2.8010545
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.152534732**	**1.082E-09**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.656874378	2	5.1358366
P13832	FTDEEVDELYR	1.110076968	2	3.4425349
P13832	GNFNYIEFTR	1.226061782	2	2.7194519
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.978625946**	**0.9972214**	**6**
P14046	FSIDTNGISDYSLNIK	1.053049347	2	2.4586737
P14046	GMYESLPVVAVK	0.880613227	2	3.2890451
P14046	ISLCHGNPTFSSETK	1.576140556	2	3.8617077
P14046	LVDIKGDPIPNEQVLIK	1.112816096	2	3.4158614
P14046	QQNSYGGFSSTQDTVVALDALSK	1.232914435	2	4.3945489
P14046	QSPGPCGSEVATVPETGR	0.764047251	2	3.3508172
P14141	**CAH3 Carbonic anhydrase 3**	**1.257975282**	**1.743E-14**	**16**
P14141	EAPFNHFDPSCLFPACR	0.971840425	2	4.4245453
P14141	EKGEFQILLDALDK	1.106661866	2	4.522337
P14141	EKGEFQILLDALDKIK	1.399667663	2	3.57461
P14141	EPMTVSSDQMAK	1.463507052	1	2.9744194
P14141	EWGYASHNGPEHWHELYPIAK	0.991463335	3	5.0320888
P14141	GDNQSPIELHTK	1.140989239	2	3.6487501
P14141	GEFQILLDALDK	1.338702913	2	4.7584085
P14141	GEFQILLDALDKIK	1.655208307	2	3.6720612
P14141	GGPLSGPYR	1.117967473	2	2.8002458
P14141	GKEAPFNHFDPSCLFPACR	1.353018648	3	4.4520273
P14141	HDPSLQPWSVSYDPGSAK	1.238856824	3	4.839396
P14141	QFHLHWGSSDDHGSEHTVDGVK	1.347633816	2	4.729167
P14141	SLFASAENEPPVPLVGNWRPPQPIK	1.185816095	3	6.0168443
P14141	VVFDDTFDR	1.152086847	2	3.4308498
P14141	YAAELHLVHWNPK	1.11700607	2	4.419282
P14141	YNTFGEALKQPDGIAVVGIFLK	1.16123745	3	5.9357924
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.233854653**	**0.0414698**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	1.276759988	2	4.9890213
P14173	ALIPTTAPQEPETYEDIIR	1.09411192	2	3.8326135
P14173	GSNQLNETLLQR	1.244693268	2	3.0522089
P14173	HSHQDSGLITDYR	1.194991561	2	3.4650006
P14173	LVAYTSDQAHSSVER	1.421269142	2	4.5165138
P14173	MLELPEAFLAGR	1.123618614	2	2.6213171
P14173	TDLTEAFNMDPVYLR	1.210314071	2	3.707057
P14173	TVESAHVQLAWEHIR	1.149980819	3	4.5056987
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.139984362**	**0.0078276**	**15**
P14408	AAAEVNQEYGLDPK	0.904958751	2	4.0144229
P14408	AIEMLGGELGSK	0.96896216	2	3.9200883
P14408	IEYDTFGELK	0.973348341	2	3.1561105
P14408	IEYDTFGELKVPTDK	0.956036527	2	3.4780731
P14408	IYELAAGGTAVGTGLNTR	1.084018733	2	5.473001
P14408	KTAIELGYLTAEQFDEWVKPK	1.040917205	3	4.7354355
P14408	LMNESLMLVTALNPHIGYDK	1.562697727	3	5.3836808
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.983026223	3	6.5886908
P14408	SGLGELILPENEPGSSIMPGK	0.975473122	2	4.7983832
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(18)	1.085865638	2	3.2785299
P14408	SKEFAQVIK	1.066190215	2	2.323045
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.034452747	3	5.0333705
P14408	TAIELGYLTAEQFDEWVKPK	1.23857725	2	4.8993907
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	0.78417292	3	6.4089475

P14408	YYGAQTVR	1.030338978	1	1.9230236
P14480	**FIBB Fibrinogen beta chain**	**1.018224882**	**0.9814619**	**7**
P14480	DNENVINEYSSILEDQK	1.096511699	2	3.2713475
P14480	GFGNIATNEDTK	1.038811521	2	3.0371857
P14480	GFGNIATNEDTKK	1.018783961	2	3.1651423
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	0.904985567	3	4.9903932
P14480	LYIDETVNDNIPLNLR	1.124096702	2	3.2658207
P14480	TENGGWTVIQNR	0.800151272	2	2.7862735
P14480	YCGLPGEYWLGNDK	0.920979006	2	3.2733171
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.971607699**	**5.546E-09**	**10**
P14604	AFAAGADIK	1.023229168	2	3.0459158
P14604	AQFGQPEILLGTIPGAGGTQR	1.06178743	2	5.6951356
P14604	ESVNAAFEMTLTEGNKLEK	0.765306613	2	3.7358713
P14604	FLSHWDHITR	1.110476228	2	3.1351862
P14604	IFPVETLVEEAIQCAEK	1.161222236	2	5.5326109
P14604	LFYSTFATDDR	1.396997062	2	2.5204322
P14604	NSSVGLIQLNRPK	1.110312516	2	3.4526443
P14604	SLAMEMVLTGDR	0.898700545	2	3.6541717
P14604	SLAMEMVLTGDRISAQDAK+Oxidation(4)Oxidation(6)	1.150181781	2	2.3572724
P14604	TFQDCYSGK	0.992066738	2	2.5648146
P14668	**ANXA5 Annexin A5**	**1.110041561**	**2.214E-09**	**3**
P14668	ETSGNLENLLLAVVK	0.963407786	2	2.5154805
P14668	GLGTDEDSILNLLTAR	1.755157511	2	4.5305133
P14668	GTVTDFSGFDGR	0.926133379	2	2.9548297
P14669	**ANXA3 Annexin A3**	**1.181072905**	**0.0028907**	**8**
P14669	GMGTDEDTLIEILTTR	1.295299413	2	4.2897577
P14669	GTINNYPGFNPSVDAEAIR	0.954287751	2	3.6260941
P14669	KDAQTLYDAGEK	1.232155893	2	2.9438307
P14669	KDAQTLYDAGEKK	1.057707793	2	3.3312204
P14669	QYQEAYEQALK	1.012934802	2	3.0187275
P14669	SEIDLLDIR	1.044832936	2	2.6848454
P14669	TLINILTER	1.32483063	2	2.9443104
P14669	WGTDEDKFTEILCLR	1.752193223	2	3.5599699
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.066505676**	**0.9678652**	**3**
P14685	AIQLEYSEAR	1.001425632	2	2.7169499
P14685	LQLDSPEDAEFIVAK	1.086411577	2	3.8931239
P14685	SVFPEQANNNEWAR	0.955291351	2	2.5304387
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.269315922**	**0.2862723**	**3**
P14740	LGTLEVEDQIEAAR	0.984438365	2	3.9405715
P14740	VLEDNSALDK	1.279017159	2	3.0424285
P14740	YMGLPTPEDNLDHYR	0.989961113	2	2.4670937
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**0.851998971**	**0.6506413**	**11**
P14882	FLSDVYPDGFK	0.945085866	2	3.0075233
P14882	FSSQEAASSFGDDR	0.897684092	2	3.7954957
P14882	HGNALWLNER	0.802786003	2	2.935957
P14882	HIEIQVLGDK	0.874056391	2	2.3639359
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	1.164889898	3	5.7812934
P14882	LQVEHPVTECITGLDLVQEMILVAK	1.226714697	3	4.0708766
P14882	MADEAVCVGPAPTSK	0.839749239	2	4.1836529
P14882	SYLNMDAIMEAIKK	0.805091256	2	2.4174359
P14882	TGAQAVHPGYGFLSENK	1.005355419	2	3.527343
P14882	TVAIHSDVDASSVHVK	0.883636018	2	3.4825203
P14882	VVEEAPSIFLDPETR	0.996520136	2	4.0932498
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**1.103203871**	**0.000887**	**2**
P14942	KPPPDGHYVDVVR	1.10354991	2	2.905154

P14942	YFPVFEK	1.048661519	1	1.9120909
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.164155074**	**0.270522**	**4**
P15083	EIQNAGDQAQENR	1.223579237	2	3.8689206
P15083	FSVLITGLR	1.09033784	2	2.6145678
P15083	GVTGGSVAIVCPYNPK	1.120147137	2	4.0694828
P15083	SSVTFECDLGR	1.120339566	2	2.6351795
P15149	**CP2A2 Cytochrome P450 2A2**	**1.19394453**	**5.184E-05**	**11**
P15149	DVQECILEEAGYLIK	1.006825471	3	3.62181
P15149	DVYSSITQLSER	0.92434704	2	2.9051001
P15149	FKFPMNLEDINEYPSPIGFTR	1.037076393	3	4.6510763
P15149	FSNLAPLGIPR	1.22468119	2	3.2105291
P15149	GELPTFNILFK	1.327070952	2	2.3923621
P15149	GTDVFPIIGSLMTEPK	1.211241366	2	4.1620417
P15149	GYGFSLSNVEQAK	1.044648583	2	3.4036746
P15149	IVVLYGYDAVK	1.345816984	2	2.6736283
P15149	NFIDSFLIR	1.398891809	2	2.9641678
P15149	TLQGTCGAPIDPSIYLSK	1.327170938	2	4.6770649
P15149	TVSNVINSIVFGNR	1.009812524	2	3.091063
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.269187535**	**9.9E-20**	**2**
P15178	FQTEIQTVNK	1.077480363	2	2.5563555
P15178	QMVKFAANINK+Oxidation(2)	1.28606324	2	2.8045237
P15429	**ENOB Beta_enolase**	**1.173358463**	**0.9999887**	**5**
P15429	DATNVGDEGGFAPNILENNEALELLK	0.864595785	3	5.5292125
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	1.096552676	3	4.766696
P15429	IEEALGDK	1.144211394	1	2.3164325
P15429	TAIQAAGYPDK	0.88786141	2	2.4404011
P15429	VNQIGSVTESIQACK	1.025145059	2	5.1829333
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.134845701**	**9.9E-20**	**22**
P15650	AFVDSCLQLHETK	1.243890336	2	4.0896587
P15650	AQDTAELFFEDVR	1.609470142	2	4.8764501
P15650	AQDTAELFFEDVRLPASALLGEENK	1.261527333	3	5.3053589
P15650	CIGAIAMTEPGAGSDLQGVR	0.854313765	2	5.2754688
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(7)	1.181578715	2	5.1806374
P15650	EQIEQFIPQMTAGK	0.668035517	2	4.3978658
P15650	FFQEEVIPYHEEWEK	1.973852953	2	4.9906664
P15650	GFYYLMQELPQER	1.698801363	2	4.2875638
P15650	IFSSEHDIFR	1.245704186	2	2.9339876
P15650	KFFQEEVIPYHEEWEK	1.743025613	2	5.1970758
P15650	KLTDIGIR	1.050316968	2	2.4301608
P15650	LDSASASMAK	1.029308924	1	2.3314831
P15650	LDSASASMAK+Oxidation(8)	1.214057472	2	2.5286517
P15650	LPASALLGEENK	0.964253471	2	2.6773019
P15650	LTDIGIR	1.020338035	2	2.3446455
P15650	QGLLGINIAEK	0.924237295	2	3.2537122
P15650	RLDSASASMAK	0.951969948	2	3.5289042
P15650	RLDSASASMAK+Oxidation(9)	1.121607922	2	3.0767043
P15650	SGSDWILNGSK	0.98339442	1	2.2756648
P15650	TNICVTR	0.87031946	2	2.5019915
P15650	VQPIYGGTNEIMK	0.965626338	2	3.4276183
P15650	VQPIYGGTNEIMK+Oxidation(12)	1.148687146	2	2.7003136
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.864102548**	**2.22E-16**	**9**
P15651	ASSTANLIFEDCR	0.930852795	2	3.2079856
P15651	EEGDSWVLNGTK	0.853031874	2	2.9637849
P15651	ELVPIAAQLDK	0.691943652	2	2.4764526
P15651	ELVPIAAQLDKEHLFPTSQVK	0.204240224	2	4.6881771

P15651	GISAFLVPMPTPGLTLGK	0.786813748	2	3.0539794
P15651	IGCFALSEPGNGSDAGAASTTAR	1.302385002	2	5.8613815
P15651	IGIASQALGIAQASLDCAVK	1.201052491	3	4.7201471
P15651	ITEIYEGTSEIQR	0.886443305	2	4.9782033
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.148263915	3	3.3403876
P15684	**AMPN Aminopeptidase N**	**1.10122621**	**0.0681096**	**4**
P15684	ALGDTPAPNIDTTELVER	1.270679295	2	4.1777353
P15684	AQIIHDSFNLASAGK	1.099262361	2	3.2882061
P15684	LRSALACSNEVWILNR	1.124096702	2	2.3492599
P15684	VVATTQMQAADAR	1.057938983	2	3.7863493
P15709	**ST2A1 Bile salt sulfotransferase**	**0.992517082**	**0.999426**	**2**
P15709	NHFTVSQAEAFDK	0.867345654	2	4.0387745
P15709	SIFTGIGLMR	0.774742759	2	2.6950939
P15919	**RAG1 V(D)J recombination_activating protein 1**	**0.881045422**	**0.1725257**	**2**
P15919	EEGGDVKAVCLTLFLLALR	0.917907885	2	2.5606124
P15919	SQDLDDYLNGPFTVVVK	0.626387826	2	2.5728395
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.121625912**	**3.208E-05**	**3**
P15978	GYEQHAYDGR	3.915510857	2	2.8114197
P15978	VEHEGLPEPLSQR	1.023604085	2	3.1261294
P15978	YDSDAENPR	1.895488685	2	2.4716017
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**0.984770683**	**0.0002267**	**24**
P15999	AVDSLVPIGR	0.997344046	2	3.6285243
P15999	EVAAFAQFGSDLDAATQQLLSR	1.185060167	2	6.790813
P15999	FESAFLSHVVSQHQSLLGNIR	1.21101623	3	6.0959535
P15999	GIRPAINVGLSVSR	1.017323561	3	3.8625407
P15999	GMSLNLEPDNVGVVVFGNDK	1.261691001	2	5.740315
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(2)	1.020413245	2	4.2882786
P15999	GYLDKLEPSK	1.082891125	1	3.0063982
P15999	ILGADTSVDLEETGR	1.048553181	2	5.0628414
P15999	LELAQYR	1.001696549	2	2.7256613
P15999	LKEIVTNFLAGFEP	1.985791198	2	3.059031
P15999	LTDADAMK	0.766012514	2	2.553508
P15999	LYCIYVAIGQK	1.088423578	2	2.7127094
P15999	NVQAEEMVEFSSGLK	1.031693997	2	4.3384008
P15999	QGQYSPMAIEEQVAVIYAGVR	1.158066815	3	5.2536821
P15999	RLTDADAMK	0.876193373	2	2.6009259
P15999	RLTDADAMK+Oxidation(8)	1.047081682	2	2.3262055
P15999	RTGAIVDVPVGDELLGR	0.956650436	2	3.9142559
P15999	STVAQLVK	0.927518818	2	2.3953402
P15999	TGAIVDVPVGDELLGR	1.040538488	2	4.7202001
P15999	TGTAEMSSILEER	0.824476369	2	4.4868016
P15999	TGTAEMSSILEER+Oxidation(6)	0.774558233	2	3.154788
P15999	TSIAIDTIINQK	0.946344177	2	4.673265
P15999	VLSIGDGIAR	0.908781088	2	3.1610441
P15999	VVDALGNAIDGK	1.058223591	2	4.481195
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**0.994340423**	**0.8856219**	**8**
P16036	ALYSNILGEENTYLWR	1.316010251	2	3.1701744
P16036	EEGLNAFYK	0.988063465	1	2.4045205
P16036	FGFYEVFK	1.143452054	1	2.2584171
P16036	GIFNGFSITLK	1.138622085	2	3.3359499
P16036	GSTASQVLQR	0.995785149	2	3.3010981
P16036	GWAPTLIGYSMQGLCK	1.149287274	2	2.9580948
P16036	IQTQPGYANTLR	1.130743174	2	3.7736239
P16036	MYKEEGLNAFYK	0.945405676	3	3.4672356
P16086	**SPTA2 Spectrin alpha chain_ brain**	**0.972781482**	**9.9E-20**	**28**
P16086	ALINADELANDVAGAEALLDR	1.067463446	2	4.8637886

P16086	ALSSEGKPYVTK	1.153979012	2	2.9209118
P16086	DLASVQALLR	1.051865479	2	2.9585948
P16086	DLSSVQTLLTK	1.198282996	2	2.5370488
P16086	GVIDMGNSLIER	0.862107235	2	2.956038
P16086	HQAFEAELSANQSR	1.122983747	2	4.1236067
P16086	HQALQAEIAGHEPR	1.077528072	3	4.1489558
P16086	HQLLEADISAHEDR	1.214863647	3	3.7884815
P16086	KFEEFQTDLAAHEER	1.018595346	3	5.3166862
P16086	LFGAAEVQR	1.111331309	2	2.511529
P16086	LGDSHDLQR	1.157535583	2	3.1570537
P16086	LGESQTLQQFSR	1.050827511	2	3.4341722
P16086	LIQEQHPEEELIK	1.332794921	2	3.5548289
P16086	LQQSHPLSANQIQVK	1.360029737	2	4.2420053
P16086	LQTASDESYKDPTNIQSK	1.141958503	2	4.5111818
P16086	LQVASDENYKDPTNLQGK	1.134220286	2	5.5326238
P16086	LSDDNTIGQEEIQQR	1.128292384	2	3.2777319
P16086	MTLVASEDYGDTLAAIQGLLK	0.97984441	2	4.3701534
P16086	NQALNTDNYGHDLASVQALQR	1.228680501	2	5.7536917
P16086	QFQDAGHFDAENIKK	1.05288917	2	2.5564783
P16086	REELITNWEQIR	1.282581668	2	4.1187572
P16086	SQLLGSAHEVQR	0.693388387	2	3.22964
P16086	SSLSSAQADFNQLAELDR	1.190984412	2	5.2095456
P16086	TATDEAYKDPSNLQGK	1.035105481	2	3.6773653
P16086	TKQEEVNAAWQR	1.282782955	2	2.9357345
P16086	VLETAEDIQER	0.761635081	2	3.4898539
P16086	VNDVCTNGQDLIK	1.238989721	2	3.2017972
P16086	VNSLGETAQR	1.19216509	2	2.6881433
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.037125321**	**0.9199111**	**9**
P16232	EECALEIIK	0.934095039	1	2.0132904
P16232	ETSGIILSQAAPK	1.058136316	2	3.505044
P16232	FALDGFFSTIR	1.075575715	2	2.4307194
P16232	FVVEAGK	0.957056215	1	1.9198318
P16232	IMEFLSLR	2.476489726	2	2.5104089
P16232	KDEVYYDK	0.998068589	1	2.7309873
P16232	MGAHVVLTAR	1.158468062	2	2.878897
P16232	MTQPLIASYSASK	0.922331609	2	3.3969297
P16232	SSWTPLLLGNPGR	1.011830582	2	3.6514499
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.181533327**	**0.2342197**	**5**
P16290	AMEAVAAQGK	0.920573445	2	2.5931964
P16290	AMEAVAAQGK+Oxidation(2)	1.237039662	2	2.4367595
P16290	HGESSWNQENR	1.181358203	2	3.6231818
P16290	HYGGLTGLNK	1.041578658	1	3.137686
P16290	VLIAAHGNSLR	1.196934606	2	2.6736262
P16303	**CES3 Carboxylesterase 3**	**0.99370373**	**0.0035745**	**18**
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	1.083917321	3	5.5584817
P16303	AKEAAEEPSHWK	1.124919574	2	4.024045
P16303	DGASEEETNLSK	0.916375041	2	4.1128464
P16303	EAAEEPSHWK	1.025529414	2	2.784586
P16303	ENIPLQFSEDCLYLNVYTPADLTK	1.334518836	2	4.283071
P16303	ESYPFLPTVIDGVVLPK	0.949714645	3	4.1107378
P16303	FAPPQPAEPWNFVK	1.642135168	1	2.4703956
P16303	IGASTQAAQR	0.374396668	2	3.3016329
P16303	LDLLGNPK	1.055156894	2	2.33394
P16303	MIPVVAEK	0.958690321	1	1.9502487
P16303	QEFGWIIPTLMGYPLSEGK	1.185103004	3	4.0910549
P16303	QKTEDELLETSLK	1.049456137	2	3.6031823

P16303	SFNTVPYIVGINK	1.077090585	2	2.8977656
P16303	TEDELLETSLK	0.940585766	2	3.5917068
P16303	TTTSAVMVHCLR	1.11557159	2	3.0624206
P16303	TVIGDHGDELFSVFGSPFLK	1.669060566	2	5.3946042
P16303	YFGGTDDPAK	0.959864821	2	3.2463555
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	0.995040013	3	3.7450621
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**0.875383235**	**0.7949572**	**5**
P16332	EVAQQAVDADVHAVGVSTLAAGHK	1.10603358	3	3.4128437
P16332	GDVGMAGVAIDTVEDTK	1.026111695	2	3.4634907
P16332	IDSGSEVIVGVNK	0.994087955	2	4.0198784
P16332	NTQIIIQEESGIPK	1.04380799	2	3.0231898
P16332	TGLQAGLTIDEFAPR	0.86511341	2	3.6599896
P16409	**MYL3 Myosin light chain 3**	**0.99911607**	**0.9936242**	**10**
P16409	AAPAPAAAPAAAPEPERPK	0.928950141	2	4.0320616
P16409	ALGQNPTQAEVLR	0.900128032	2	4.4012899
P16409	DTGTYEDFVEGLR	1.193091928	2	2.98157
P16409	EGNGTVMGAELR	0.980549563	2	2.5300565
P16409	IEFTPEQIEEFK	0.761467654	2	2.3325291
P16409	LMAGQEDSNGCINYEAFVK	1.137742758	2	4.9269366
P16409	LTEDEVEK	0.788266619	1	2.1969726
P16409	MMDFETFLPMLQHISK	1.147626067	3	4.0222716
P16409	NKDTGTYEDFVEGLR	0.934423129	2	4.1889482
P16409	VFDKEGNGTVMGAELR	1.210810587	2	3.9720469
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.210903849**	**9.9E-20**	**18**
P16617	AHSSMVGVNLPQK	1.001818793	3	3.7773898
P16617	AHSSMVGVNLPQK+Oxidation(5)	1.263175672	2	2.46347
P16617	ALESPERPFLAILGGAK	1.257709716	3	4.5970688
P16617	DCVGSEVENACANPAAGTVILLENLR	1.406909918	3	6.3640881
P16617	GCITIIGGGDTATCCAK	1.047312929	2	5.5371351
P16617	IQLINNMLDK	0.915860153	2	2.7948496
P16617	IQLINNMLDK+Oxidation(7)	2.13473727	1	2.0273461
P16617	ITLPVDFVTADK	1.128893618	2	2.3300982
P16617	ITLPVDFVTADKFDENAK	1.863494533	2	5.1840281
P16617	QIVWNGPVGVFEWEAFAR	1.451152047	2	4.1249385
P16617	SLMDEVVK	0.959918157	2	2.3134365
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.231508651	4	5.281949
P16617	TGQATVASGIPAGWMGLDCGTESSK	0.936612826	2	4.7033095
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.112371727	3	4.2177167
P16617	VLNNMEIGTSLYDEEGAK	1.138812983	2	5.210412
P16617	VLPGVDALSNV	1.308525153	2	2.7588396
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.007287253	3	4.6612725
P16617	YSLEPVAAELK	1.083504849	2	3.1456161
P16638	**ACLY ATP_citrate synthase**	**1.079301693**	**0.1012934**	**21**
P16638	AFDSGIIPMEFVNK	1.204780892	2	4.1108575
P16638	DEPSVAAMVYPFTGDHK	0.917090002	2	2.6384342
P16638	DLVSSLTSGLLTIGDR	0.764312314	3	3.9229894
P16638	EAYPEEAYIADLDAK	1.120565612	2	3.0650792
P16638	EEADEYVDIGALNGVFVLGR	1.38677118	2	4.1997862
P16638	FGGALDAAAK	1.048353982	2	2.8615983
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.25152876	2	3.8102498
P16638	GVTIIGPATVGGIKPGCFK	0.967362976	2	3.6288869
P16638	HLLVHAPEDKK	1.266890858	2	3.3634593
P16638	IGNTGGMLDNILASK	1.562928081	2	3.2062242
P16638	LGLVGVNLSLDGVK	1.88399305	2	2.3162496
P16638	QHFPATPLLDYALEVEK	1.104569917	3	4.2425632
P16638	RGGPNYQEGLR	1.124289229	2	3.218431
P16638	SAYDSTMETMNYAQIR	1.09240202	2	4.1171536

P16638	SGGMSNELNNIISR	0.962756769	2	3.7457998
P16638	TIAIIAEGIPEALTR	1.038960884	2	4.0675392
P16638	TTDGVYEGVAIGGDR	1.004171547	2	2.871428
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	1.069772773	3	3.6203008
P16638	VDATADYICK	1.047923098	2	2.5501351
P16638	WGDIEFPPPFGR	1.012688555	2	3.8323591
P16638	YICTTSAIQNR	0.964331092	2	2.8839731
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**1.00208546**	**0.8716084**	**9**
P16970	DQVIYPDGKEDQK	0.778243019	2	3.2438521
P16970	EGGWDSVQDWMDVLSGGEK	1.136594013	2	4.3829622
P16970	FDHVPLATPNGDILIQDLSFEVR	1.180044847	3	3.8569889
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.768771171	3	5.1510429
P16970	GYLDNVQLGHILER	1.035726148	2	3.4231625
P16970	HLHSTHSELLEDYYQSGR	1.072748546	3	5.3303242
P16970	ITEDTVEFGS	1.015040865	1	1.9023762
P16970	ITELMQVLK	1.014242826	2	2.5229754
P16970	SGANVLICGPNGCGK	1.05646281	2	3.3038399
P17077	**RL9 60S ribosomal protein L9**	**1.113828261**	**0.0428265**	**7**
P17077	DFNHINVELSLLGK	0.839045023	3	3.5150552
P17077	FLDGIYVSEK	0.955724467	2	3.0594893
P17077	GTVQQPDE	1.278826674	1	2.1825447
P17077	KFLDGIYVSEK	1.14490117	2	2.9711883
P17077	TGVACSVSQAQK	1.011655345	2	3.2595336
P17077	TICSHVQNMIK	1.063434963	2	3.6872633
P17077	TILSNQTVDIPENVDITLK	1.019342265	2	4.8364129
P17078	**RL35 60S ribosomal protein L35**	**1.1178292**	**0.8544552**	**2**
P17078	QLDDLKVELSQLR	1.119504532	2	2.4937837
P17078	VLTVINQTQK	1.070655809	2	3.0241265
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.044907658**	**0.0236879**	**4**
P17178	DHESTEGPGTGQDRPR	1.251329608	2	2.7344172
P17178	TNVNLASAPLLEQVMR	1.061874553	2	4.1987352
P17178	VGCLEPSIPEDTATFIR	1.35169934	2	3.4205496
P17178	YEVVLSPGMGEVK	0.895205343	2	3.2635641
P17209	**MYL4 Myosin light chain 4**	**0.99493086**	**0.9114634**	**2**
P17209	HVLATLGEK	0.940837376	1	2.5699668
P17209	ITYGQCGDVLR	1.161026453	2	2.4754679
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.694705741**	**0.9995524**	**11**
P17425	ASAELFNQK	0.738560422	2	2.5694838
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	0.692483644	3	5.3110361
P17425	ITASLCDLK	0.911974705	1	1.9550804
P17425	LEDTYFDRDVEK	0.720459987	2	2.9957569
P17425	MFLNDFLNDQNR	0.745620036	2	2.8657718
P17425	MGFCTDREDINSLCLTVVQK	0.73421962	2	4.5483541
P17425	NSIYSGLEAFGDVK	0.891193602	2	2.7761977
P17425	NSLSYDCIGR	0.577847521	2	2.8601992
P17425	TCVAPDVFAENMK	0.795744828	2	3.6163747
P17425	VTQDATPGSALDK	0.968432034	2	3.6184819
P17425	YTIGLGQAR	0.737537726	2	2.7852852
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**0.920847892**	**0.0445655**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(7)	1.396532546	2	3.552829
P17426	NADVELQQR	0.919581361	2	2.5056791
P17426	VGGYILGEFGNLIAGDPR	1.40561143	2	4.1695838
P17475	**A1AT Alpha_1_antiproteinase**	**1.037880908**	**0.9978445**	**4**
P17475	MQHLEQTLTK	0.84647822	2	2.6860693
P17475	TLLSSLGITR	1.014821541	2	2.9033468
P17475	VFNNDADLSGITEDAPLK	1.060769573	2	5.2122378

P17475	VINDYVEK	0.955163756	1	2.2908292
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.13493303**	**9.9E-20**	**15**
P17764	EEQDKYAIGSYTR	0.928367943	2	3.3949318
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.219665156	2	4.5305452
P17764	EVYMGNVIQGGEGQAPTR	0.77027746	2	5.2477846
P17764	FANEITPITISVK	0.825613861	2	3.9775527
P17764	GKPDVVVKEDEEYK	1.100253425	2	3.6839931
P17764	GKPDVVVKEDEEYKR	1.006529375	2	4.6125164
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.522154645	2	5.2346807
P17764	IHMGNCAENTAK	1.329446435	2	3.4043753
P17764	IHMGNCAENTAK+Oxidation(3)	1.603624909	2	3.4958847
P17764	LEDLIVK	0.976313254	2	2.4294677
P17764	LGTIAIQGAIEK	1.45484934	2	3.3040869
P17764	QATLGAGLPIATPCTTVNK	0.951187142	2	5.1021881
P17764	QGEFGLASICNGGGGASAVLIEK	1.006282388	2	4.7348394
P17764	TPIGSFLGSLASQPATK	0.979130982	2	4.2109404
P17764	VNVHGGAVSLGHPIGMSGAR	0.996679172	2	5.7329583
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.122821587**	**0.9999999**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.095783915	3	5.3336511
P17879	TTPSYVAFTDTER	1.147824419	2	3.5981739
P17879	VEIIANDQGNR	1.019468796	2	3.6672006
P17988	**ST1A1 Sulfotransferase 1A1**	**1.222756204**	**2.571E-05**	**6**
P17988	CPGVPSGLETLEETPAPR	1.130176317	2	4.4953275
P17988	FDAHYAK	0.920057712	2	2.356272
P17988	NTFTVAQNER	0.893689851	2	2.9880412
P17988	SLPEETVDSIVHHTSFK	1.25253681	2	4.5225987
P17988	THLPLSLLPQSLLDQK	1.455186072	2	5.0076628
P17988	YFAETIGPLQNFTAWPDDLLISTYPK	1.339142236	3	4.1528797
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**0.963230069**	**7.772E-16**	**27**
P18163	AELSVIFADKPEK	1.14710303	2	3.5658476
P18163	AILEDMVK	0.92825807	2	2.4722548
P18163	ALEDLGR	0.940799091	2	2.4612808
P18163	ALKPPCDLSMQSVEVTGTTEGVR	1.049509281	2	4.5549345
P18163	CGVEIIGLK	0.92096864	2	2.7045498
P18163	GAMVTHQNIMNDCSGFIK	1.512557909	2	5.3329978
P18163	GFQGSFEELCR	1.052957084	2	3.3926487
P18163	GIAVHPELFSIDNGLLTPTLK	1.220275642	2	5.7272806
P18163	GIQVSNDGPCLGSR	0.980896668	2	4.4857111
P18163	IENIYLR	0.992523271	2	2.9643557
P18163	IFGQANTSVK	1.133539424	2	2.605315
P18163	IIVIMDSYDNDLVER	1.299910577	2	4.929256
P18163	LLLEGVENK	1.109025116	2	3.1836181
P18163	LLMDDLK	0.933447172	2	2.4259305
P18163	LMITGAAPVSATVLTFLR	1.550770193	3	4.1448779
P18163	LVDVEDMNYQAAK	1.119782897	2	4.5777931
P18163	LVDVEDMNYQAAK+Oxidation(7)	0.981938916	2	2.7624924
P18163	NAGLKPFEQVK	0.983684286	2	4.0046873
P18163	QVAEMAECIGSALIQK	1.010981092	2	5.2526703
P18163	SAVLEDDKLLLYYDDVR	2.417038961	2	4.234345
P18163	SQIDELYSTIK	1.077029135	2	3.7666001
P18163	SQIDELYSTIKI	1.279992683	2	3.1164207
P18163	TAEALDKDGWLHTGDIGK	1.036974571	2	5.3541727
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	1.343291512	3	6.1874561
P18163	TMYDGFQR	1.014701485	1	1.9134674
P18163	VLQPTIFPVVPR	1.088764116	2	3.6769605
P18163	WLLDFASK	1.03331795	2	2.6124556
P18297	**SPRE Sepiapterin reductase**	**0.949341581**	**0.0184348**	**5**

P18297	ALAPQLAGLLSPGSVLLLSAR	1.257323522	3	3.9368155
P18297	LLLINNAGTLGDVSK	1.469610288	2	3.0293787
P18297	LNSEGELVDCGTSAQK	0.948225943	2	4.9521351
P18297	TVVNISSLCALQPFK	1.084468643	2	3.1312487
P18297	VLSYAPGPLDTNMQQLAR	1.168610391	2	2.744344
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.257013909**	**0.1676444**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.258587766	2	5.6440458
P18298	KIIVDTYGGWGAHGGGAFSGK	0.953052743	3	3.4237409
P18298	YLDEDTIYHLQPSGR	1.100334868	2	4.3898339
P18418	**CALR Calreticulin**	**1.220932865**	**9.9E-20**	**17**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	1.304447033	3	6.036489
P18418	CKDDEFTHLYTLIVRPDNTYEVK	1.220054523	3	5.4123049
P18418	DMHGDSEYNIMFGPDICGPGTK	1.003912439	2	6.1950693
P18418	FYALSAR	1.528866851	2	2.3282418
P18418	FYGDQEK	1.124669994	1	2.0283704
P18418	FYGDQEKDK	1.204311135	1	2.8199506
P18418	GQTLVVQFTVK	1.05715565	2	3.81691
P18418	HEQNIDCGGGYVK	1.113076332	2	4.3735223
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.158492952	4	4.6652212
P18418	IDNSQVESGSLEDDWDFLPPK	1.296539443	2	5.5174975
P18418	IDNSQVESGSLEDDWDFLPPKK	1.299838892	2	5.0499601
P18418	IKDPDAAKPEDWDER	1.202954031	2	4.3688407
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.033691038	3	5.7002869
P18418	LFPGGLDQK	1.41139828	2	2.3398409
P18418	QIDNPDYK	1.25249152	1	1.9523842
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.659730765	3	5.4944816
P18418	VHVIFNYK	1.239133601	1	2.3441398
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.084370345**	**0.9895174**	**2**
P18420	AQPSQAADEPAEK	1.086401323	2	3.6064031
P18420	IHQIEYAMEAVK	1.009177502	2	2.3003085
P18421	**PSB1 Proteasome subunit beta type_1**	**1.230845563**	**1.019E-13**	**2**
P18421	AGGSASAMLQPLLDNQVGFK	1.302725054	2	4.7960033
P18421	NMQNVEHVPLTLDR	1.013002688	2	3.781368
P18422	**PSA3 Proteasome subunit alpha type_3**	**1.127233106**	**0.1140642**	**3**
P18422	AVENSSTAIGIR	1.127389725	2	3.3106649
P18422	DGVVFGVEKLVLSK	2.370689986	1	1.9456335
P18422	HVGMAVAGLLADAR	0.874644728	3	3.609472
P18437	**HMGN2 Non_histone chromosomal protein HMG_17**	**1.074014593**	**0.0011467**	**2**
P18437	DANNPAEDGDAK	1.488274722	2	3.3270047
P18437	DANNPAEDGDAKTDQAQK	1.06032037	2	4.8879461
P18445	**RL27A 60S ribosomal protein L27a**	**1.128145103**	**0.9516388**	**3**
P18445	NGVAPIIDVVR	1.102219713	1	2.5070639
P18445	NQSFCPTVNLDK	1.086493261	2	3.2033415
P18445	RNQSFCPTVNLDK	1.130718801	2	3.1237552
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**1.021893094**	**0.1497284**	**5**
P18484	FFQPTEMASQDFFQR	1.396532546	2	3.9864185
P18484	IIGFGSALLEEVDPNPANFVGAGIIHTK	1.155242463	3	3.3996029
P18484	ILVAGDTMDSVK	1.389131333	2	2.4386454
P18484	NNGVLFENQLLQIGLK	0.986845448	2	2.5522428
P18484	YGGTFQNVSVK	0.877376257	2	2.4853673
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.123807113**	**0.9795799**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	1.460984156	2	3.329761
P18596	SLPSVETLGCTSVICSDK	1.096646853	2	4.2773776
P18596	TGTLTTNQMSVCR	1.116353755	2	2.8647244
P18596	VGEATETALTCLVEK	1.121434254	2	4.9720345

P18757	**CGL Cystathionine gamma_lyase**	**1.076506834**	**2.887E-15**	**15**
P18757	AGDEVICMDEVYGGTNR	0.874181748	2	5.7725873
P18757	ATLGISDTLIR	0.973394626	2	3.5697343
P18757	AVAALDGAK	0.95224727	2	2.4451122
P18757	AVVLPISLATTFK	0.969872527	3	4.9879336
P18757	FLQNSLGAVPSPFDCYLCCR	2.001574691	2	3.6193302
P18757	GTLQHAQVFLK	1.045713036	3	3.3162239
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.655429811	3	3.7988834
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	2.158359657	4	5.7563705
P18757	LLEAAITPQTK	1.021319131	2	3.613528
P18757	LSVGLEDEKDLLEDLGQALK	1.176384707	3	6.6440969
P18757	LVWIETPTNPTLK	1.11695541	2	3.802896
P18757	QCTGCPGMVSFYIK	1.240435112	2	3.8276758
P18757	QDSPGQSSGFVYSR	0.975180546	2	3.8963888
P18757	RVASEFGLK	1.050493406	2	2.6508982
P18757	VIYPGLPSHPQHELAK	1.137602915	2	4.1886344
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.071122422**	**0.9902441**	**10**
P18886	ATNLTVSAVR	1.03682552	2	3.5147085
P18886	ELHAHLLAQDK	1.016843729	2	3.467176
P18886	LIFDGNEETLK	1.077116106	2	3.2499447
P18886	QYGQTVATYESCSTAAFK	1.087010775	2	4.0333133
P18886	SEYNDQLTR	0.796893111	2	2.4828088
P18886	TETIRPASIFTK	1.033445799	2	3.0711484
P18886	TLQAGLLEPEVFHLNPSK	10.63019844	2	4.0595517
P18886	TLSIDSIQFQR	0.9343207	2	3.3983932
P18886	YILSDSSPVPEFPVAYLTSENR	1.263139375	2	5.211329
P18886	YLNAQKPLLDDSQFR	0.956902028	2	4.7108035
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.020482161**	**0.0016275**	**16**
P19112	AGGLATTGNEDILDIVPTEIHQK	0.993214215	3	6.2151699
P19112	AGGTGEMTQLLNSLCTAIK	1.070866823	2	5.3966432
P19112	APVIMGSTEDVQEFLEIYNK	1.301427189	2	4.3377509
P19112	APVIMGSTEDVQEFLEIYNKDK	1.247683653	3	3.4454429
P19112	DFDPAINEYIQR	0.621121096	2	3.5726719
P19112	GNIYSINEGYAK	1.013183874	2	3.9426315
P19112	KGNIYSINEGYAK	0.994636502	2	4.2158375
P19112	KLDILSNDLVINMLK	1.055012691	2	5.0606647
P19112	KTSANEPSEKDALQPGR	0.998239757	3	3.8750241
P19112	LDILSNDLVINMLK	1.128309386	2	4.8524847
P19112	LLYECNPIAYVMEK	1.43148501	2	4.3643479
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.032801836	2	5.8998175
P19112	SRPSLPLPQSR	1.011485078	2	3.3021896
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.160943497	3	6.0039434
P19112	TLVYGGIFLYPANK	0.752490238	2	3.9830356
P19112	TSANEPSEKDALQPGR	1.024098172	2	4.4557142
P19225	**CP270 Cytochrome P450 2C70**	**1.166738415**	**0.0051449**	**12**
P19225	ASLNLSNPQDFIDYFLIK	1.445465368	3	4.099288
P19225	EALIDRGEEFSDK	1.23119103	2	2.4984832
P19225	FDPGHFLDEK	1.273523294	2	2.6666546
P19225	FILMEINR	1.252932172	2	2.3786042
P19225	FSLMVLRSMGMGK+Oxidation(4)	1.126174389	1	1.9720904
P19225	GTSVMACLTSALHDDKEFPNPEK	1.155323397	3	4.1864748
P19225	IQEEITR	1.162721296	1	2.1176682
P19225	IQEEVVYLLEALR	2.024132962	2	3.8590407
P19225	KLPPGPTPLPIFGNILQVGVK	1.26059519	2	2.4287453
P19225	LPPGPTPLPIFGNILQVGVK	1.216313902	2	4.1515064
P19225	TNGSPCDPSFLLACVPCNVISSVIFQHR	1.286043812	3	3.4623413

P19225	YIDFVPIPLPR	1.057505522	2	3.1107121
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.11611721**	**0.9924874**	**5**
P19234	DIEEIIDELR	1.039068882	2	3.639214
P19234	DTPENNPDTPFDFTPENYER	0.874996379	2	4.8763437
P19234	FCCEPAGGLTSLTEPPK	1.008264542	2	3.2944028
P19234	FCCEPAGGLTSLTEPPKGPGFGVQAGL	1.189768479	2	3.0144701
P19234	YHIQVCTTTPCMLR	1.090909266	2	3.3246245
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**0.821918453**	**0.9999998**	**8**
P19468	ASGELMTVAR	1.006158312	2	2.3374591
P19468	CNQIANELCECPELLGSGFR	1.033251448	2	5.0846753
P19468	DKNTPSPFVETFPEDEEASK	0.974163746	2	3.589823
P19468	NTPSPFVETFPEDEEASK	0.992690871	2	4.229589
P19468	SLFFPDEAINK	0.916026871	2	2.4775934
P19468	SRYDSIDSYLSK	0.81936009	2	2.9258888
P19468	VQLLLNGGDVLETLQEK	1.048660799	2	4.9900141
P19468	WGVISASVDDR	1.018548797	2	3.0672166
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.0393782**	**0.2065883**	**8**
P19488	AEMWLIR	1.06694245	2	2.895947
P19488	ANAIAWALAQIPQK	1.068550408	3	6.5913582
P19488	FETFPTSVSKDELEK	0.857727162	2	4.0311065
P19488	GAAVTLNIR	0.811913621	2	2.5978396
P19488	GHEVTVLKPSAYYVLDPK	1.334717287	2	4.4432535
P19488	NWDPFYTEILGRPTTLAETMGK	1.191231502	2	5.3197813
P19488	SDLFNALK	1.29766689	2	2.9459856
P19488	TILDELVQR	0.966556623	2	3.5300717
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.041715105**	**0.7935245**	**6**
P19511	HVIQSISAQQEK	0.981278284	2	4.0016017
P19511	HVIQSISAQQEKETIAK	1.098295853	3	4.5018439
P19511	HYLFDVQR	1.031214798	2	2.6956639
P19511	LDYHISVQDMMR	0.983907117	3	3.8691468
P19511	LNEEKIAQLEEIK	0.975087276	2	2.5854671
P19511	YGASIGEFIDKLNEEK	1.18010988	3	3.6007085
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.260830901**	**1.013E-11**	**13**
P19643	FIGGSGQVSER	1.207013975	2	3.4630675
P19643	IISTTNGGQER	1.353168703	2	2.8623288
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.041651836	3	4.8067575
P19643	KFIGGSGQVSER	0.815344379	2	3.2656019
P19643	KLCELYAK	1.551969943	2	2.3502843
P19643	LERPVIHIDQTGENVVVK	1.192995559	3	5.5329647
P19643	LLHDCGLSVVVLEAR	1.429522818	2	3.763983
P19643	TLNHEIYEAK	1.282985585	2	2.5507019
P19643	TMDEMGQEIPSDAPWK	1.005103852	2	4.525198
P19643	TYTIRNKNVK	1.005112381	2	2.4110312
P19643	VLNSQEALQPVHYEEK	1.243552011	2	4.5299454
P19643	YVDLGGSYVGPTQNR	1.166875085	2	5.0323734
P19643	YVISAIPPVLGMK	1.176490778	1	2.854527
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.415044724**	**9.9E-20**	**9**
P19804	DRPFFPGLVK	0.764523219	2	2.3798077
P19804	EIGLWFKPEELIDYK	1.030846135	2	4.2338414
P19804	GDFCIQVGR	1.078296986	2	3.285013
P19804	NIIHGSDSVESAEK	1.086539364	2	4.0395617
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.403383759	4	5.6519833
P19804	TFIAIKPDGVQR	1.110637201	2	2.9806652
P19804	VMLGETNPADSKPGTIR	1.056792154	2	4.4706659
P19804	VMLGETNPADSKPGTIR+Oxidation(2)	1.496084543	2	4.2524624
P19804	YMNSGPVVAMVWEGLNVVK	1.410232324	2	5.2728734

P19944	**RLA1 60S acidic ribosomal protein P1**	**0.761712561**	**0.6124653**	**2**
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.084802947	4	5.808135
P19944	INALIK	0.760761097	2	2.4215744
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.096316256**	**9.9E-20**	**9**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.147392177	2	5.896059
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.142516052	3	5.1215668
P19945	CFIVGADNVGSK	1.106220459	2	3.6594129
P19945	GHLENNPALEK	1.123940764	2	3.6339543
P19945	GTIEILSDVQLIK	1.244552816	2	3.1106207
P19945	IIQLLDDYPK	1.886785304	2	3.463037
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.072177437	3	3.6430175
P19945	TSFFQALGITTK	1.177164632	2	4.0343699
P19945	VLALSVETDYTFPLAEK	1.333366553	2	4.4947782
P20059	**HEMO Hemopexin**	**1.416372211**	**0.2706646**	**6**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.323652667	2	4.7524471
P20059	FNPVTGEVPPR	0.970566844	2	2.5510018
P20059	GECQSEGVLFFQGNR	1.539810001	2	3.9255171
P20059	LFQEEFPGIPYPPDAAVECHR	1.132977917	3	4.466547
P20059	SGAQATWAELSWPHEK	0.949514634	2	3.4188347
P20059	VDGALCLEK	1.053978068	2	2.4339943
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.035332933**	**8.882E-16**	**8**
P20070	DILLRPELEELR	1.091286617	2	2.5269628
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	1.099557277	3	5.6878319
P20070	LIDKEIISHDTR	1.354402494	3	3.7502003
P20070	MSQYLENMNIGDTIEFR	1.09323285	2	5.3068542
P20070	SSPAITLENPDIK	1.056274655	2	3.5960591
P20070	SSPAITLENPDIKYPLR	1.278047517	2	3.9610057
P20070	SVGMIAGGTGITPMLQVIR	1.139331393	2	4.6321845
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(14)	1.52045649	2	2.3226714
P20280	**RL21 60S ribosomal protein L21**	**1.262533581**	**2.39E-11**	**4**
P20280	HGVVPLATYMR	1.384729276	2	2.500989
P20280	KGDIVDIK	1.125017989	1	2.0901756
P20280	TNGKEPELLEPIPYEFMA	0.651674673	2	3.4274232
P20280	VYNVTQHAVGIIVNK	1.308432689	2	4.1394043
P20651	**PP2BB Serine/threonine_protein phosphatase 2B catalytic subunit beta isoform**	**1.219004437**	**0.4100556**	**2**
P20651	GLTPTGMLPSGVLAGGR	1.2269218	2	2.4251428
P20651	VVKAVPFPPTHR	1.210856117	1	1.953714
P20673	**ARLY Argininosuccinate lyase**	**1.219204709**	**0.0389949**	**16**
P20673	AEAECEVLFPGYTHLQR	1.202451827	2	4.1623201
P20673	AEMQQILQGLDK	1.012887342	2	4.4698949
P20673	EFNFVQLSDAYSTGSSLMPQK	1.220314769	2	5.1331706
P20673	FNSSIAYDR	0.978195834	2	2.4372463
P20673	HLWNVDLQGSK	0.941750852	1	3.3750188
P20673	INVLPLGSGAIAGNPLGVDR	0.911543528	2	5.6564941
P20673	KNPDSLELIR	0.894523443	2	2.3801582
P20673	LKELIGEAAGK	1.135939297	2	3.1913731
P20673	LYPNDEDIHTANER	0.993591436	2	3.8736727
P20673	MAEDLILYGTK	0.95746185	2	3.9453814
P20673	MAEDLILYGTK+Oxidation(1)	0.966880095	2	2.3684304
P20673	NDQVVTDLR	0.959221175	2	3.14768
P20673	SRNDQVVTDLR	1.118203933	2	3.0609283
P20673	VAEEWAQGIFK	0.960108695	2	3.447969
P20673	VLIEAMVDR	0.989748157	2	2.5911386
P20673	VLIEAMVDRAEAECEVLFPGYTHLQR	1.23777798	3	4.7081862

P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**0.966691088**	**2.353E-10**	**5**
P20788	EIDQEAAVEVSQLR	0.894997079	2	3.5430312
P20788	EIDQEAAVEVSQLRDPQHDLER	1.151082297	3	3.434633
P20788	ESLSGQAATRPLVATVGLNVPASVR	0.71637133	2	2.7713375
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.287044279	3	5.1125689
P20788	SGPFAPVLSATSR	0.961062755	2	2.8793161
P20801	**TNNC2 Troponin C_ skeletal muscle**	**0.787396808**	**0.3396953**	**3**
P20801	GKSEEELAECFR	0.984746486	2	3.3910437
P20801	NADGYIDAEELAEIFR	1.589751902	2	4.7835922
P20801	SEEELAECFR	0.480404369	2	3.2634532
P20812	**CP2A3 Cytochrome P450 2A3**	**1.3635893**	**0.0042364**	**2**
P20812	ELQGLEDFITKKVEQNQR	1.347979183	2	2.4711843
P20812	YGPVFTIHLGPR	1.64935303	2	3.0428934
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.227647716**	**0.1213548**	**3**
P20814	FDYEDKDFLNLIEK	1.186628948	2	2.3245878
P20814	GTAVLTSLTSVLHDSK	1.231860851	2	3.269942
P20814	IKEHEESLDVSNPR	1.190658548	3	3.5926213
P20817	**CP4AE Cytochrome P450 4A14**	**1.079274158**	**1.776E-15**	**6**
P20817	ACQIAHEHTDGVIK	1.054770055	2	4.2654328
P20817	AQLQNEEELQK	1.134980308	2	3.3138566
P20817	AVEDLNNLTFFR	1.153771238	2	3.6082284
P20817	HLDFLDILLFAK	1.217490359	2	4.2090197
P20817	MRKAQLQNEEELQK+Oxidation(1)	1.276562433	2	3.0884616
P20817	VLLYDPDYVK	1.228266712	2	2.5288606
P20852	**CP2A5 Cytochrome P450 2A5**	**1.230075876**	**4.164E-08**	**2**
P20852	DFIDSFLIR	2.385626213	2	2.9400399
P20852	EALVDQAEEFSGR	1.207747328	2	2.8685627
P21213	**HUTH Histidine ammonia_lyase**	**1.1684594**	**3.741E-09**	**15**
P21213	ALDYLAIGVHELAAISER	1.491121551	2	4.5200863
P21213	DIITTELNSATDNPMVFASR	1.408769255	2	4.4752798
P21213	EGLALINGTQMITSLGCEAVER	0.884303431	2	3.2450964
P21213	GETISGGNFHGEYPAK	0.703396217	2	4.027247
P21213	GEWLAVPCQDGK	0.945640435	2	3.0441396
P21213	GYSGISLETLK	0.840084109	2	2.3562894
P21213	LQELQVNLVR	0.899426922	2	3.2797558
P21213	NKPDNGGFTSVDEVR	0.881048199	2	3.7095542
P21213	NSATIPESDDL	0.637965761	1	1.9615597
P21213	SHSSGVGKPLSPER	0.817458255	2	4.0682273
P21213	SLLDSDHHPSEIAESHR	0.794661988	3	4.6083107
P21213	TVVYGITTGFGK	0.918568855	2	3.6212621
P21213	VQDAYTLR	0.753712115	2	2.5721924
P21213	VWEVAAPYIEK	0.839062463	2	2.5839896
P21213	YIALDGDSLSTEDLVNLGK	1.30889325	2	5.3028231
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.0734472**	**0.9142688**	**10**
P21396	DVPAIEITHTFLER	1.056694998	2	3.5774903
P21396	FVGGSGQVSEQIMGLLGDK	1.062066076	2	3.117955
P21396	IFSVTNGGQER	1.04756694	2	2.486311
P21396	INVLVLEAR	1.232924071	2	3.1376009
P21396	KDIWVEEPESK	1.073735475	2	3.859617
P21396	KICELYAK	1.551969943	2	2.3502843
P21396	NLPSVPGLLK	0.867956428	1	1.9253061
P21396	VLGSQEALYPVHYEEK	1.022962883	2	3.6092026
P21396	WVDVGGAYVGPTQNR	1.053382998	2	4.3435798
P21396	YVISAIPPILTAK	1.142414371	2	3.121563
P21531	**RL3 60S ribosomal protein L3**	**1.058873711**	**0.0039067**	**8**
P21531	AHLMEIQVNGGTVAEK	1.055376441	2	5.2510939

P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	0.935760167	3	5.4065075
P21531	FIDTTSK	0.864755211	1	2.0276597
P21531	HGSLGFLPR	1.176889122	2	3.033505
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.145308034	2	5.0678973
P21531	NNASTDYDLSDK	1.074613484	2	3.3772578
P21531	SINPLGGFVHYGEVTNDFIMLK	1.237443047	3	3.3834853
P21531	TVFAEHISDECK	1.14933107	2	3.782172
P21533	**RL6 60S ribosomal protein L6**	**1.372439165**	**7.099E-08**	**9**
P21533	AVDSQILPK	1.008442948	2	2.4688835
P21533	FVIATSTK	1.214833463	1	2.2268925
P21533	HLTDAYFK	1.009868462	2	2.3837204
P21533	HQEGEIFDTEK	0.997866871	2	3.296469
P21533	HQEGEIFDTEKEK	1.108040325	2	4.1273656
P21533	HQEGEIFDTEKEKYEITEQR	1.248141141	3	4.734499
P21533	QLGSGLLLVTGPLALNR	1.395900096	2	5.174675
P21533	SSITPGTVLIILTGR	1.251024632	2	4.2042346
P21533	YYPTEDVPR	1.163301411	1	1.9664984
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**0.952275101**	**9.9E-20**	**5**
P21571	FEVLDKPQS	0.922198954	1	2.0086877
P21571	GEMDKFPTFNFEDPK	0.864997954	3	3.4865894
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.074222667	3	3.9689322
P21571	LASGGPVDTGPEYQQEVDR	1.574757461	2	5.2888436
P21571	LASGGPVDTGPEYQQEVDRELFK	2.25389268	3	3.4461923
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.686960676**	**0.4073189**	**2**
P21643	YNHVCMVHRMLGSK+Oxidation(10)	1.686960676	2	2.4629221
P21643	YNHVCMVHRMLGSK+Oxidation(6)	1.686960676	2	2.302552
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.346965112**	**0.4568171**	**4**
P21670	ATCIGNNSAAAVSMLK	1.157434152	2	3.310962
P21670	LLDEVFFSEK	1.347042101	2	3.1236961
P21670	LNEDMACSVAGITSDANVLTNELR	1.249258153	2	5.0770102
P21670	YLLQYQEPIPCEQLVTALCDIK	0.993977275	2	4.0411086
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.092305847**	**0.9998474**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	1.032789554	3	5.458118
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(23)	0.934510622	3	4.4498062
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.045625284**	**0.5570939**	**5**
P21913	CGPMVLDALIK	1.046129372	2	2.728055
P21913	CGPMVLDALIKIK	1.006946529	2	2.4425681
P21913	CHTIMNCTQTCPK	0.930664348	2	3.9948161
P21913	IKNEIDSTLTFR	1.386188967	2	3.4166021
P21913	RIDTDLGK	0.998384788	2	2.5685627
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**0.91203767**	**0.7883708**	**5**
P21981	CDLEIQANGR	0.917956074	2	2.9209356
P21981	DHHTADLCQEK	0.43965843	2	2.8435595
P21981	SEGTYCCGPVSVR	0.912202172	2	3.7194178
P21981	VDLFPTDIGLHK	1.01904698	2	2.7309427
P21981	YSGCLTESNLIK	0.84349839	2	2.6966434
P22734	**COMT Catechol O_methyltransferase**	**1.26259384**	**2.408E-12**	**12**
P22734	AIYQGPSSPDKS	0.96919576	2	3.3501115
P22734	EWAMNVGDAK	0.726721512	1	2.5043807
P22734	GQIMDAVIR	0.96392397	2	3.3780921
P22734	GSSSFECTHYSSYLEYMK	2.656068297	2	4.3311796
P22734	GTVLLADNVIVPGTPDFLAYVR	1.770989841	3	5.0544915
P22734	KGTVLLADNVIVPGTPDFLAYVR	1.446054433	2	4.543992
P22734	KYDVDTLDMVFLDHWK	1.571729538	2	4.9978123
P22734	LLTMEMNPDYAAITQQMLNFAGLQDK	1.616333488	3	3.867681

P22734	VTILNGASQDLIPQLK	1.042352255	2	4.416718
P22734	YDVDTLDMVFLDHWK	2.193009766	2	4.0551519
P22734	YLPDTLLLEK	1.057131712	2	3.0945399
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.297245745	3	6.6306877
P22789	**ST2A2 Alcohol sulfotransferase A**	**0.721429244**	**0.0042392**	**4**
P22789	ETLQNVCNK	0.722896392	2	2.3441608
P22789	KLEPDELDLVLK	0.694124358	2	3.728843
P22789	LEPDELDLVLK	0.660880249	2	2.3386922
P22789	NHFTVAQAEAFDK	0.522015035	2	3.3949246
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.15362652**	**9.9E-20**	**23**
P22791	ASLDMFNK	0.882238857	2	2.7522936
P22791	ASLDMFNKK	1.029186277	2	2.9310148
P22791	DVGILALEVYFPAQYVDQTDLEK	1.383957411	3	6.246346
P22791	GLKLEETYTNK	0.914264637	2	2.7619617
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.031722958	3	6.9293494
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(4)	1.146567438	3	5.6318593
P22791	IGAFSYGSGLAASFFSFR	1.296027354	2	4.3873773
P22791	LEETYTNK	1.016221878	2	3.4088504
P22791	LEETYTNKDVDK	1.060217084	2	4.2742825
P22791	LEVGTETIIDK	0.941259781	2	3.8002875
P22791	LMFNDFLSSSSDK	1.613368704	2	3.7947524
P22791	LMFNDFLSSSSDK+Oxidation(2)	1.802457214	2	4.0664406
P22791	LMFNDFLSSSSDKQNNLYK	1.915169724	2	4.7325711
P22791	LSIQCYLR	1.720850839	2	2.4549701
P22791	LVSSVSDLPK	1.242675687	2	3.7116859
P22791	MGFCSVQEDINSLCLTVVQR	1.231847403	2	4.2683344
P22791	MSPEEFTEIMNQR	0.96240649	2	4.7739902
P22791	MSPEEFTEIMNQR+Oxidation(1)	1.056918583	2	3.8493006
P22791	MSPEEFTEIMNQR+Oxidation(10)	0.965713861	2	3.5290513
P22791	TDTWPK	0.855514833	1	1.9295807
P22791	TKLPWDAVGR	0.999405904	3	4.0318928
P22791	VNFSPPGDTSNLFPGTWYLER	1.473649499	2	4.877635
P22791	YTVGLGQTR	0.960011419	2	3.4161139
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.181275807**	**0.7545602**	**9**
P22985	DEVTCVGHIIGAVVADTPEHAQR	0.924266527	3	4.5074711
P22985	DPPANVQLFQEVPK	1.148147003	2	3.6626005
P22985	LDPTFASATLLFQK	1.251303958	2	3.7935185
P22985	NQPEPTVEEIENAFQGNLCR	0.946977081	2	4.8571606
P22985	QLFQLDSPATPEK	1.149633556	2	3.2269821
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.169959877	3	5.8927145
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.137225524	3	4.8339663
P22985	TLLRPEEILLSIEIPYSK	1.242269629	2	2.7272997
P22985	TNLPSNTAFR	1.208640236	1	2.1813078
P23358	**RL12 60S ribosomal protein L12**	**1.211749487**	**0.0699774**	**5**
P23358	CTGGEVGATSALAPK	1.104024603	2	4.3036499
P23358	EILGTAQSVGCNVDGR	0.8567744	2	4.3123393
P23358	HNGNITFDEIVNIAR	0.997250824	2	3.9443963
P23358	HPHDIIDDINSGAVECPAS	1.095024758	2	4.5022197
P23358	QAQIEVVPSASALIIK	1.212373653	2	3.6173258
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.068244918**	**0.0013363**	**9**
P23457	ELTQVFEFQLASEDMK	1.178786901	2	4.5937886
P23457	HFDSAYLYEVEEEVGQAIR	1.53234222	2	6.1129518
P23457	LLFETVDICDTWEAMEK	2.027067848	2	4.6139216
P23457	MLDYCK	1.055346173	1	1.9855616
P23457	SIGVSNFNCR	1.044567821	2	3.1886706
P23457	SKDIILVSYCTLGSSR	1.382583652	2	4.453434

P23457	VALNDGNFIPVLGFGTTVPEK	1.185636881	2	4.7249951
P23457	YFDDHPNHPFTDE	1.194556634	2	3.7325456
P23457	YKPVCNQVECHLYLNQSK	1.071624176	2	4.6328034
P23514	**COPB Coatomer subunit beta**	**1.270916185**	**5.076E-05**	**6**
P23514	EAGELKPEEEITVGPVQK	1.116599254	2	3.6730027
P23514	NFENLIPDAPELIHDFLVNEK	1.253951061	3	4.2267303
P23514	TNNVSEHEDTDKYR	1.386190144	2	4.598969
P23514	VLQDLVMDILR	1.115503417	2	3.2070439
P23514	VLSECSPLMNDIFNK	1.416306783	2	2.6093085
P23514	YEAAGTLVTLSSAPTAIK	0.993343152	2	4.5228901
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.997212066**	**0.0217708**	**8**
P23965	ALQLGTLFPPAEALK	0.982978274	2	5.4368725
P23965	ATADNLIK	0.889346852	2	2.6897075
P23965	DNYVNTIGHR	0.840812691	2	2.7845616
P23965	GVILTSERPGIFSAGLDLMEMYGR	1.571106578	3	5.42028
P23965	QREADIQNFTSFISR	1.15003153	2	2.9137619
P23965	SLHVYLEK	0.994011849	2	2.3705051
P23965	VGLVDEVVPEDQVHSK	0.979004281	2	4.8817987
P23965	WFTIPDHSR	0.892134639	2	2.6329997
P24049	**RL17 60S ribosomal protein L17**	**1.013273319**	**1**	**3**
P24049	EQIVPKPEEEVAQK	1.026241996	2	3.7919626
P24049	GLDVDSLVIEHIQVNK	1.002238317	2	4.9041548
P24049	YSLDPENPTK	1.005959527	1	2.7388546
P24050	**RS5 40S ribosomal protein S5**	**1.202077286**	**0.1945447**	**2**
P24050	VNQAIWLLCTGAR	1.35367823	2	2.9094257
P24050	WSTDDVQINDISLQDYIAVK	1.135351073	2	4.3332505
P24063	**ITAL Integrin alpha_L**	**1.129139748**	**0.7624887**	**2**
P24063	ASEAQVLVKVDLIHEK	0.99161243	2	2.3208199
P24063	DFEKILEFMK	1.059014919	3	3.6814787
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.516641644**	**0.4191768**	**5**
P24090	ELACDDPETEHVALIAVDYLNK	1.722519197	3	4.1677542
P24090	HAFSPVASVESASGEVLHSPK	1.18596961	3	5.9204154
P24090	LGGEEVSVACK	1.011074662	2	3.4566989
P24090	VGQPGDAGAAGPVAPLCPGR	1.16139285	2	5.1261044
P24090	VLHAQCHSTPDSAEDVRK	1.214920695	3	3.7491324
P24268	**CATD Cathepsin D**	**1.109844125**	**0.0007287**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.021361674	2	3.3653052
P24268	DPTGQPGGELMLGGTDSR	0.976076097	2	4.5752006
P24268	GGCEAIVDTGTSLLVGPVDEVK	1.357164477	2	3.223856
P24268	LGGQNYELHPEK	1.456585168	2	2.4749813
P24329	**THTR Thiosulfate sulfurtransferase**	**1.029868608**	**0.6347546**	**11**
P24329	EGHPVTSEPSRPEPAVFK	0.962230025	2	4.8716788
P24329	FQLVDSR	1.020789517	2	2.3047843
P24329	GSVNVPFMNFLTEDGFEK	1.833887763	2	3.4992948
P24329	HVPGASFFDIEECR	1.249065894	2	4.0566311
P24329	KVDLSQPLIATCR	1.036289268	2	4.6317143
P24329	RFQLVDSR	0.954365249	2	2.3359671
P24329	TVSVLNGGFR	1.018601974	2	3.1042616
P24329	TYEQVLENLQSK	1.008171353	2	4.9987292
P24329	VDLSQPLIATCR	1.028219644	2	4.0022898
P24329	VLDASWYSPGTR	0.905242824	2	3.7780366
P24329	YLGTQPEPDAVGLDSGHIR	1.055551472	2	4.756074
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.085339877**	**0.5744912**	**9**
P24368	DKPLKDVIIVDCGK	0.98547871	2	3.9070065
P24368	DTNGSQFFITTVK	1.063534358	2	3.903662
P24368	DVIIVDCGK	1.007795945	1	1.9453398
P24368	HYGPGWVSMANAGK	0.800520041	2	3.9890251

P24368	IEVEKPFAIAK	1.027784442	2	3.208998
P24368	IEVEKPFAIAKE	1.219892199	2	3.5317459
P24368	TVDNFVALATGEK	1.116076861	2	3.3615367
P24368	VLEGMDVVR	1.010707764	2	2.9106023
P24368	VYFDFQIGDEPVGR	1.075368508	2	3.9681208
P24457	**CP2DB Cytochrome P450 2D11**	**1.07196168**	**0.9685225**	**2**
P24457	RFSVSTLR	1.152345096	2	2.5527403
P24457	SLEEWVTK	1.071038535	2	2.4372888
P24470	**CP2CN Cytochrome P450 2C23**	**1.062927272**	**0.0018366**	**11**
P24470	ACVGESLAR	1.049392734	2	2.4564044
P24470	DLDIKPITTGIINLPPPYK	1.025740849	3	4.3319192
P24470	EALLQQGDEFLGR	0.994075324	2	2.4666307
P24470	FGLLLLMK	2.022800635	2	3.1531587
P24470	GTTVLPMLSSVMLDQK	0.891424375	2	3.8417037
P24470	GYGLIFSNGER	1.132561123	2	3.5263627
P24470	IEEEKDNLK	1.168903557	2	2.8174613
P24470	LPPGPTPLPIIGNLLQLNLK	1.024985096	2	4.215385
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	1.007019623	3	4.2882667
P24470	TFLNLMDLLNK	1.294532007	2	3.8047841
P24470	YITLLPSSLPHAVVQDTK	0.85560713	2	3.9442706
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.972698769**	**0.0670047**	**8**
P24473	AGMATAQAQHLLNK	0.863483082	2	4.1515918
P24473	DEDITESQNILSAAEK	1.003989099	2	5.0968971
P24473	DSGNQPPAMVPHK	1.018425824	2	2.6011801
P24473	FLTAVSMEQPEMLEK	0.821088156	2	5.0528722
P24473	IWSRDEDITESQNILSAAEK	1.314716619	3	3.6966665
P24473	MELLAYLLGEK	1.455083713	2	3.983911
P24473	QLFQVPMSVPK	0.932668339	2	2.6643405
P24473	YGAFGLPTTVAHVDGK	1.01878247	2	3.9081054
P25093	**FAAA Fumarylacetoacetase**	**0.986899436**	**9.9E-20**	**15**
P25093	AIDVGQGQTR	0.971851433	2	3.3942046
P25093	AQEHIFGMVLMNDWSAR	1.300960987	2	3.6296716
P25093	ASLQNLLSASQAQLR	1.111541442	2	4.883368
P25093	ASLQNLLSASQAQLRDDK	1.185745252	2	3.945441
P25093	ASSVVVSGTPIR	1.027478255	2	3.6692882
P25093	DIQQWEYVPLGPFLGK	0.850382507	2	4.5962934
P25093	FGEPIPISK	0.943080857	2	2.8206365
P25093	GEGMSQAATICR	0.863590199	2	3.6403115
P25093	GEGMSQAATICR+Oxidation(4)	1.352095998	2	3.1148424
P25093	GKENALLPNWLHLPVGYHGR	1.322845698	3	4.55268
P25093	HLFTGPVLSK	1.101231042	1	2.7654545
P25093	HQHVFDETTLNSFMGLGQAAWK	1.428704134	2	5.3698874
P25093	IGVAIGDQILDLSVIK	1.796374598	2	5.2405124
P25093	TFLLDGDEVIITGHCQGDGYR	0.897248955	2	5.2234902
P25093	VGFGQCAGK	0.874728337	2	2.7150042
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.11584623**	**0.9888027**	**7**
P25113	ALPFWNEEIVPQIK	1.24478961	2	3.50454
P25113	FSGWYDADLSPAGHEEAK	1.022971626	2	5.050189
P25113	HGESAWNLENR	1.02366107	2	4.1077819
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	1.228740574	3	4.0649571
P25113	SYDVPPPPMEPDHPFYSNISK	0.969534757	2	4.4332819
P25113	YADLTEDQLPSCESLK	0.946514206	2	5.5983477
P25113	YADLTEDQLPSCESLKDTIAR	1.119224194	2	5.3759689
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.414980597**	**9.9E-20**	**13**
P25235	EDQVIQLMNTIFSK	1.104276794	2	3.4339788
P25235	EETVLATVQALHTASHLSQQADLR	1.052346425	3	4.8296924

P25235	FPEEEAPSTVLSQNLFTPK	1.237925268	2	4.2080426
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.150335946	2	4.7607737
P25235	KNFESLSEAFSVASAAAALSQNR	1.36079972	2	5.5998015
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.394527347	3	4.4406476
P25235	LQVSSVLSQPLAQAAVK	1.453249419	2	5.7286248
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.585844913	3	5.5888467
P25235	NFESLSEAFSVASAAAALSQNR	1.156314368	2	3.1297257
P25235	NIVEEIEDLVAR	1.172922062	3	4.3254995
P25235	TGQEVVFVAEPDNK	1.354585565	2	3.8589573
P25235	YHVPVVVVPEGSASDTQEQAILR	1.260496708	3	5.7670708
P25235	YIANTVELR	1.013247837	2	2.6582353
P25318	**CO8A2 Collagen alpha_2(VIII) chain**	**1.181358606**	**0.4311805**	**2**
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(10)	1.183036181	2	2.3810005
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(13)	1.190171472	2	2.4913015
P25977	**UBF1 Nucleolar transcription factor 1**	**1.120887606**	**0.8740282**	**2**
P25977	AKYAKLHPEMSNLDLTK	1.058542565	2	2.5541723
P25977	ALKAMEMTWNNMEKK+Oxidation(12)	1.175570263	2	2.3269036
P26039	**TLN1 Talin_1**	**1.129935534**	**1.11E-16**	**23**
P26039	ADAEGESDLENSRK	1.100669406	2	3.6097546
P26039	AGALQCSPSDVYTK	1.258606437	2	2.8298247
P26039	AQEACGPLEMDSALSVVQNLEK	1.09475436	2	4.0880542
P26039	ASAGPQPLLVQSCK	0.975111459	2	2.3701236
P26039	AVAEQIPLLVQGVR	1.085201027	2	2.9213877
P26039	EAAEGLRMATNAAAQNAIKK	1.39919965	2	2.4433854
P26039	EADESLNFEEQILEAAK	0.828169609	2	4.3371682
P26039	GLAGAVSELLR	1.09490122	2	3.2495692
P26039	GVGAAATAVTQALNELLQHVK	1.322662433	2	3.8376617
P26039	ILAQATSDLVNAIK	1.901331926	2	3.5311503
P26039	LGAASLGAEDPETQVVLINAVK	2.207274419	2	4.7047486
P26039	LLGEIAQGNENYAGIAAR	1.014943614	2	4.4081745
P26039	LNEAAAGLNQAATELVQASR	1.144792665	2	5.4136777
P26039	MVAAATNNLCEAANAAVQGHASQEK	1.256602138	3	3.660538
P26039	NCGQMSEIEAK	0.860826719	2	3.0736892
P26039	SNTSPEELGPLANQLTSDYGR	1.164567884	2	3.7151601
P26039	TEDSGLQTQVIAAATQCALSTSQLVACTK	1.01842093	3	4.324841
P26039	TMLESAGGLIQTAR	0.918761796	2	2.5164051
P26039	VGAIPANALDDGQWSQGLISAAR	0.995846154	2	4.7382746
P26039	VLGEAMTGISQNAK	1.274217939	2	3.2719698
P26039	VLVQNAAGSQEK	1.099512631	2	3.1646547
P26039	VSQMAQYFEPLTLAAVGAASK	2.231007779	2	3.1128268
P26039	VVAPTISSPVCQEQLVEAGR	1.087242498	2	5.1501441
P26043	**RADI Radixin**	**1.112131811**	**9.9E-20**	**13**
P26043	AFAAQEDLEK	1.343171964	2	3.2173574
P26043	ALELEQER	1.107369825	2	2.5233493
P26043	AQKELEEQTR	0.935697339	2	2.6393695
P26043	FFPEDVSEELIQEITQR	1.363797578	3	4.2845788
P26043	GTELWLGVDALGLNIYEHDDKLTPK	1.358506298	3	3.4664745
P26043	IQNWHEEHR	1.403485576	2	2.7873788
P26043	KEEEATEWQHK	1.081288379	2	2.9248173
P26043	KKEEEATEWQHK	1.21686412	2	4.3416801
P26043	KTQNDVLHAENVK	1.147677078	2	5.1542988
P26043	NQEQLAAELAEFTAK	1.204485355	2	5.2763114
P26043	QLQALSSELAQAR	1.055467987	2	4.3622913
P26043	RKPDTIEVQQMK	1.07452815	2	3.4031255
P26043	TQNDVLHAENVK	1.066093767	2	3.9022417

P26231	**CTNA1 Catenin alpha_1**	**1.281631336**	**6.775E-07**	**5**
P26231	LIEVANLACSISNNEEGVK	1.215729798	2	5.8793249
P26231	LLEPLVTQVTTLVNTNSK	1.330301933	2	4.1587152
P26231	QIIVDPLSFSEER	1.143343548	2	2.3679366
P26231	SAAGEFADDPCSSVK	1.33684186	2	2.9627168
P26231	TIADHCPDSACK	2.828313813	2	3.309732
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.035723561**	**0.9753541**	**8**
P26284	AILAELTGR	0.923138418	2	2.622756
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	1.036472233	3	7.2602677
P26284	LEEGPPVTTVLTR	1.016500895	2	3.5591357
P26284	MVNSNLASVEELKEIDVEVR	1.201159812	2	4.3442936
P26284	NFYGGNGIVGAQVPLGAGIALACK	1.101781348	2	3.7401948
P26284	RGDFIPGLR	1.151028447	2	2.3878725
P26284	TREEIQEVR	0.969188066	2	3.0614212
P26284	VDGMDILCVR	0.737418421	2	2.5748975
P26453	**BASI Basigin**	**1.09189141**	**0.4901788**	**8**
P26453	GNINVEGPPR	1.001215846	2	3.3590605
P26453	KSEHASEGEFVK	1.106948218	2	3.346899
P26453	RKPDQTLDEDDPGAAPLK	1.222184293	3	4.2691994
P26453	SEASHPPVDEWVWFK	1.04264074	3	3.3693573
P26453	SEHASEGEFVK	1.07544671	3	3.6050994
P26453	SGEYSCIFLPEPVGR	0.935160452	2	3.9346576
P26453	VLQEDTLPDLQMK	1.113751022	2	4.0119686
P26453	YTVDADDR	0.963981769	2	2.4151101
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**1.239297473**	**0.0991936**	**2**
P26516	SVVALHNLINNK	1.278166851	2	2.8000281
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	1.082983543	3	3.7141643
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.930187105**	**0.852787**	**8**
P26772	GGEIQPVSVK	0.868835035	2	3.6059093
P26772	GGIMLPEK	0.795047606	2	2.5327179
P26772	GGIMLPEK+Oxidation(4)	0.898003232	2	2.7083273
P26772	GKGGEIQPVSVK	1.013965129	2	3.5391774
P26772	KFLPLFDR	1.149965761	2	2.3765583
P26772	VLLPEYGGTK	1.045086376	1	2.0109563
P26772	VLQATVVAVGSGGK	0.932957407	2	5.2828984
P26772	VVLDDKDYFLFR	0.941717911	2	3.4740899
P27139	**CAH2 Carbonic anhydrase 2**	**0.951142685**	**0.9839263**	**4**
P27139	AVQHPDGLAVLGIFLK	0.903418549	2	3.8136117
P27139	IGPASQGLQK	0.891522026	2	3.402122
P27139	ITEALHSIK	0.912029638	2	2.3529038
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	1.205610829	3	3.6037483
P27321	**ICAL Calpastatin**	**1.089489399**	**0.8666288**	**3**
P27321	FQDAPSADGESVAGGVTVATASDK	0.766023238	2	5.3079729
P27321	KGSDEVTASSAATGTSPR	0.980309222	2	4.7227235
P27321	SQSSEPPVIHEK	1.090297984	2	2.641834
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**1.086131478**	**0.9984246**	**7**
P27364	AVLAANGSILK	1.050016206	2	2.9344611
P27364	ETILNDREEEHR	1.080162154	2	2.9628947
P27364	GDIVDAQFLR	1.015990842	2	3.3518758
P27364	IVQMLVQEK	1.233483034	2	3.1321893
P27364	NGGTFHTCALR	1.029523444	2	2.5542238
P27364	QTILDVNVK	1.059940325	1	2.210381
P27364	SQSIQGQFYYISDDTPHQSYDDLNYTLSK	1.685315067	3	4.1789784
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.043619021**	**0.9023261**	**6**

P27605	DLNHVCVISESGK	0.945657392	2	3.4892123
P27605	FFADLLDYIK	1.22082625	2	3.3706155
P27605	NVLIVEDIIDTGK	1.053928457	2	3.9134183
P27605	SVGYRPDFVGFEIPDK	0.843261377	3	3.5911217
P27605	SYCNDQSTGDIK	1.095008617	2	3.9038358
P27605	VIGGDDLSTLTGK	0.792428558	2	3.9952445
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.16734052**	**9.9E-20**	**16**
P27653	ASQAPSSFQLLYDLK	1.794871769	2	4.2989368
P27653	AYTEEDLDLVEK	0.744815964	2	3.3434563
P27653	CTHWAEGGQGALALAQAVQR	1.181566707	3	3.661638
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.243646355	3	4.2781444
P27653	IFHELTQTDK	1.287720322	2	2.6609716
P27653	IYGADDIELLPEAQNK	1.19001466	2	5.2729478
P27653	KITIGQAPTEK	1.08532262	2	3.1274369
P27653	KVVGDVAYDEAK	1.324651614	2	3.7432041
P27653	LDIDPETITWQR	1.071205866	2	3.8433006
P27653	MHGGGPTVTAGLPLPK	1.128321337	2	2.6892941
P27653	QGFGNLPICMAK	1.026905361	2	3.6217308
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.085096007	3	4.7468033
P27653	TDPAALTDDEINR	1.051658015	2	4.3674736
P27653	THLSLSHNPEQK	1.209945902	2	3.8345129
P27653	VVGDVAYDEAK	1.1797158	2	3.6761022
P27653	YVVVTGITPTPLGEGK	1.234798276	2	4.8413243
P27661	**H2AX Histone H2A.x**	**1.316541888**	**0.005442**	**3**
P27661	AGLQFPVGR	0.935346338	2	3.0431294
P27661	HLQLAIR	1.171245374	2	2.7304199
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.337219228	2	5.2509661
P27867	**DHSO Sorbitol dehydrogenase**	**1.11309243**	**9.9E-20**	**15**
P27867	AKEVGADFTIQVAK	1.191530893	2	2.8213596
P27867	AMGASQVVVIDLSASR	0.924265629	2	4.7438478
P27867	EVGADFTIQVAK	0.896923332	2	3.1421168
P27867	GENLSLVVHGPGDIR	1.108862294	2	3.7561741
P27867	HSADFCYK	1.116075393	1	2.8911996
P27867	IGDFVVK	1.039988414	2	2.6338437
P27867	LENYPIPELGPNDVLLK	1.045557102	2	4.9993176
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.62636271	2	4.7368445
P27867	MHSVGICGSDVHYWEHGR+Oxidation(1)	1.642513213	3	4.0540581
P27867	TLNVKPLVTHR	1.181194222	2	3.083122
P27867	VAIEPGVPR	1.047501988	2	2.3141987
P27867	VAIEPGVPREIDEFCKIGR	0.868440118	2	2.4943542
P27867	VLVCGAGPIGIVTLLVAK	2.291619439	3	5.4789953
P27867	YCNTWPMAVSMLASK	1.309286561	2	3.396667
P27867	YNLTPSIFFCATPPDDGNLCR	1.992781416	2	4.0765424
P27952	**RS2 40S ribosomal protein S2**	**1.113687461**	**0.8931338**	**5**
P27952	AEDKEWIPVTK	1.040281719	2	3.5536258
P27952	AFVAIGDYNGHVGLGVK	1.25238167	2	3.7025385
P27952	GCTATLGNFAK	1.136545116	2	2.7985141
P27952	GTGIVSAPVPK	1.040629025	2	2.8496075
P27952	TYSYLTPDLWK	1.262827651	2	2.451854
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.40150214**	**9.9E-20**	**27**
P28037	ADPLGLEAEK	1.25088125	1	1.9285852
P28037	ANATEFGLASGVFTR	1.100184861	2	4.5381041
P28037	AVQMGMSSVFFNK	1.041701607	2	4.0785913
P28037	DLGEAALNEYLR	0.720186983	2	3.6713524
P28037	DTNHGPQNHEAHLR	1.206112178	2	3.6291187
P28037	ECEVLPDDTVSTLYNR	1.892868405	2	3.8177111

P28037	EESFGPIMIISR	0.925266156	2	2.8347971
P28037	EGHEVVGVFTIPDKDGK	1.242220042	2	4.63908
P28037	GNDKVPGAWTEACGQK	1.15962831	2	4.0104847
P28037	GQALPEVVAK	1.116231543	2	2.6266098
P28037	GSASSDLELTEAELATAEAVR	1.160121262	2	6.676713
P28037	GVVNILPGSGSLVGQR	1.104231488	2	4.7888803
P28037	IGFTGSTEVGK	1.503494327	2	2.5823472
P28037	ILPNVPEVEDSTDFFK	1.56931085	2	3.4053442
P28037	INWDQPAEAIHNWIR	1.384262171	2	3.8335533
P28037	KEGHEVVGVFTIPDKDGK	1.163516081	3	4.4941001
P28037	KIGFTGSTEVGK	1.157485478	2	2.7317488
P28037	KLVEYCQR	1.653458252	2	2.6676834
P28037	LFVEESIHNQFVQK	1.192318405	2	4.7964683
P28037	LIAEGTAPR	1.334291538	2	3.6349752
P28037	LSDHPDVR	1.287358244	2	2.3805645
P28037	NIQLEDGK	1.272093893	1	2.2448354
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.388463121	2	4.1599951
P28037	TDVAAPFGGFK	1.319571567	1	2.0475852
P28037	THVGMSIQTFR	1.414983419	2	2.927774
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	1.075090977	2	5.1229634
P28037	VVEEVEK	1.200504484	2	2.4377134
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.175393141**	**1.766E-06**	**11**
P28480	AFHNEAQVNPER	1.046943417	2	3.4155164
P28480	FATEAAITILR	1.036332576	2	3.1011438
P28480	HGGYENAVHSGALDD	1.088141626	2	4.1779137
P28480	ICDDELILIK	1.113558296	2	3.4693739
P28480	LLEVEHPAAK	1.175553628	2	2.6824753
P28480	MLVDDIGDVTITNDGATILK	1.265155136	2	3.5653641
P28480	NADELVK	1.264685259	1	1.9335661
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.347954855	2	4.5692787
P28480	SQNVMAAASIANIVK	0.939860147	2	4.7734551
P28480	SSLGPVGLDK	0.937920549	2	2.7713525
P28480	YINENLIINTDELGR	1.066807757	2	4.6424499
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.913168173**	**0.7980306**	**3**
P28492	ATGLQTSDPR	0.83750297	2	2.4731627
P28492	FVIPDFEEFTGHVDR	0.815143993	2	2.9946642
P28492	SNPDLWGVSLCTVDGQR	1.021108867	2	3.6327386
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**0.899385822**	**0.3596445**	**2**
P28650	LDILDVLSEIK	1.371860414	2	3.1294737
P28650	VVDLLATDADIVSR	0.868360584	2	2.6734374
P29117	**PPIF Peptidyl_prolyl cis_trans isomerase F_ mitochondrial**	**1.072499746**	**0.0752912**	**2**
P29117	GANSSSQNPLVYLDVGADGQPLGR	1.239794423	2	4.0195918
P29117	KIVITDCGQLS	1.044829803	2	2.4896367
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.170124573**	**1.162E-07**	**15**
P29147	AVLVTGCDSGFGFSLAK	1.007767684	2	5.882318
P29147	FGVEAFSDCLR	1.316141571	2	3.7257762
P29147	GFLVFAGCLLK	1.041743763	2	2.9768274
P29147	KMWDELPEVVR	1.066322656	2	3.39926
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.453350532	3	6.2576575
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(1)	0.969552322	3	4.5083523
P29147	MQVMTHFPGAISDK	0.857628594	2	4.5124249
P29147	MQVMTHFPGAISDK+Oxidation(1)	1.245279151	2	3.4326539
P29147	MQVMTHFPGAISDK+Oxidation(4)	1.243942848	2	3.7153478
P29147	MWDELPEVVR	1.039135646	2	3.2607288
P29147	MWDELPEVVR+Oxidation(1)	1.029589209	2	3.5085075

P29147	TIQLNVCNSEEVEK	1.034642557	2	4.4060903
P29147	VSVVEPGNFIAATSLYSPER	1.135319924	2	6.0106196
P29147	VVNISSMLGR	1.07025927	2	3.8702395
P29147	YEMHPLGVK	1.092026238	1	2.412761
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**1.052580663**	**9.513E-11**	**6**
P29266	DLGLAQDSATSTK	0.798824329	2	3.9451065
P29266	EAGEQVASSPADVAEK	0.854922745	2	4.8076773
P29266	GSLLIDSSTIDPSVSK	0.947236289	2	4.6485429
P29266	HGYPLILYDVFPDVCK	1.428822501	2	4.8745837
P29266	KGSLLIDSSTIDPSVSK	1.028637097	2	4.0466814
P29266	MGAVFMDAPVSGGVGAAR	0.897134927	2	5.0240126
P29314	**RS9 40S ribosomal protein S9**	**1.364732415**	**3.038E-13**	**8**
P29314	IGVLDEGK	1.018381652	2	2.310128
P29314	KGQGGAGAGDDEEED	2.393454306	2	4.3337741
P29314	KQVVNIPSFIVR	1.03397751	2	2.5148363
P29314	LDYILGLK	0.953352252	2	2.7456687
P29314	LFEGNALLR	1.340825701	2	2.6563709
P29314	QVVNIPSFIVR	1.15596427	2	3.0196066
P29314	RLQTQVFK	1.043653606	2	2.3107495
P29314	SRLDQELK	1.067749892	3	3.3881497
P29315	**RINI Ribonuclease inhibitor**	**0.8552067**	**4.072E-09**	**8**
P29315	ASLQELDLGSNK	0.480417226	2	2.969291
P29315	LDDCGLTEVR	0.846723146	2	3.1824105
P29315	LENCGITSANCK	1.227365413	2	3.3241267
P29315	LGNTGIAALCSGLLLPSCR	1.427628456	2	2.7256022
P29315	LSLQNCSLTEAGCGVLPDVLR	1.12485378	2	2.9128084
P29315	SAIQANPALTELSLR	1.2269218	2	4.4967065
P29315	TCSLTAASCPHFCSVLTK	0.938274381	2	2.927803
P29315	TNELGDAGVGLVLQGLQNPTCK	1.181415432	2	5.2919621
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.081709279**	**1.053E-08**	**11**
P29410	AMVASGSELGK	0.907986433	2	2.8129051
P29410	AMVASGSELGKK	1.065675457	2	2.848815
P29410	AVLLGPPGAGK	0.926550586	2	2.8546255
P29410	EAMKDDITGEPLIR	1.043802142	2	2.3223045
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.29053182	3	4.6903048
P29410	LEAYHTQTTPLVEYYR	1.358100413	2	5.3804803
P29410	LVSDEMVVELIEK	1.067823764	2	4.1495509
P29410	NGFLLDGFPR	0.909648249	2	2.6434731
P29410	NLETPSCK	0.951359687	2	2.365603
P29410	SYHEEFNPPK	1.10884603	3	3.5173337
P29410	TRLEAYHTQTTPLVEYYR	1.152604997	3	3.4621286
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**1.072367597**	**0.8718745**	**6**
P29411	AYEAQTEPVLQYYQK	1.081843015	2	3.6174285
P29411	EDDKPETVIK	1.003122365	2	2.5193729
P29411	NLTQCSWLLDGFPR	0.886406321	2	2.6446722
P29411	TVGIDDLTGEPLIQR	0.812919161	2	3.9666443
P29411	VYNIEFNPPK	1.148462437	2	2.8031511
P29411	VYQIDTVINLNVPFEVIK	0.943695304	2	4.4046068
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**0.894724689**	**1.214E-06**	**2**
P29419	ELAEAEDVSIFK	0.817575927	1	3.0553951
P29419	YSALILGMAYGAK	0.955020718	2	3.8940432
P29994	**ITPR1 Inositol 1_4_5_trisphosphate receptor type 1**	**0.983618153**	**0.0500434**	**3**
P29994	AKDDLEMSAVITIMQPILR+Oxidation(7)Oxidation(14)	1.444439527	2	2.6809056
P29994	CVVQPEAGDLNNPPKK	0.908398212	2	2.337486
P29994	EGASNLVIDLIMNASSDR	1.053054914	2	2.4306402
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.082592021**	**0.8333118**	**3**

P30009	AEDGAAPSPSSETPK	1.036951303	2	3.6740952
P30009	EAEAAEPEQPEQPEQPAAEEPR	1.042941327	2	3.8637671
P30009	GEAAAERPGEAAVASSPSK	1.278665341	2	3.4887242
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.012027939**	**0.9998233**	**3**
P30349	GSPMEISLPIALSK	1.003194726	2	2.444994
P30349	SLSNVIAHEISHSWTGNLVTNK	0.979051887	3	3.5116777
P30349	SSALQWLTPEQTSGK	1.030909755	2	3.378073
P30427	**PLEC Plectin**	**0.922825995**	**0.7556308**	**4**
P30427	LLDPEDVDVPQPDEK	0.915926193	2	3.5910246
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(1)	1.189840323	2	2.4207442
P30427	REEAAVDAQQQK	1.141641986	2	3.5345547
P30427	VLALPEPSPAAPTLR	0.888881545	2	2.4339523
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.344633509**	**0.0094673**	**8**
P30713	AQVHEYLGWHADNIR	1.330029823	2	5.1080093
P30713	ERVEAFLGAELCQEAHNPIMSVLGQAAK	0.986465888	3	4.8148513
P30713	GQHLSEQFSQVNCLK	1.388731329	2	4.8779616
P30713	GTFGVLLWTK	1.824373827	2	2.5019689
P30713	NSMVLALQR	0.963626226	2	2.7812147
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.914533165	3	4.5975251
P30713	VLGPLIGVQVPEEK	1.135703298	2	3.9323754
P30713	YQVADHWYPADLQAR	1.182828588	2	5.1132517
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.155847355**	**0.3557933**	**2**
P30835	NEWGSLLEELVK	1.156003767	2	2.5670273
P30835	VFANAPDSACVIGLR	0.534852313	2	2.7741897
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.22468673**	**3.776E-09**	**8**
P30839	EKDILAAIAADLSK	1.03734826	2	4.2547607
P30839	FDHILYTGNTAVGK	1.19752108	2	4.1934538
P30839	HLTPVTLELGGK	1.10278358	3	3.7689209
P30839	LQQLEALR	1.326893374	2	2.5855436
P30839	NVEEAINFINDR	1.39366673	2	3.8077929
P30839	VMQEEIFGPILPIVSVK	1.124497489	2	4.6467438
P30839	VMQEEIFGPILPIVSVK+Oxidation(2)	1.237782801	2	4.1349211
P30839	YIAPTILTDVDPNSK	1.151715208	2	4.1475801
P30904	**MIF Macrophage migration inhibitory factor**	**1.433829234**	**2.191E-08**	**2**
P30904	LHISPDR	1.347568336	1	1.9733508
P30904	LLCGLLSDR	1.786856351	2	2.7983205
P31000	**VIME Vimentin**	**1.028508333**	**0.9739099**	**13**
P31000	DGQVINETSQHHDDLE	0.861482904	2	3.2338514
P31000	KLLEGEESR	1.051946404	2	2.8009386
P31000	KVESLQEEIAFLK	1.040838043	2	3.8619218
P31000	LGDLYEEEMR	1.078520914	2	3.0922406
P31000	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	1.133755388	4	5.0394669
P31000	LLEGEESR	0.981660218	2	2.8107498
P31000	LQDEIQNMKEEMAR	1.211725044	2	3.8269968
P31000	NLQEAEEWYK	1.009309949	2	3.0970125
P31000	QDVDNASLAR	1.155383653	2	2.9121735
P31000	QVQSLTCEVDALK	1.138920653	2	3.4193945
P31000	RQVDQLTNDK	1.048403543	2	3.132071
P31000	TNEKVELQELNDR	1.033500908	2	3.6288486
P31000	VELQELNDR	1.217723018	2	2.6561377
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**1.016321472**	**2.21E-08**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.05617709	2	6.294384
P31044	LYTLVLTDPDAPSR	1.451176294	2	4.4293308
P31044	VDYGGVTVDELGK	1.05178304	2	5.0415516
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.898924142	3	5.1266842
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.021054261	2	5.3911114
P31044	YVWLVYEQEQPLNCDEPILSNK	1.434073022	2	5.2571054

P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.595518692**	**2.22E-16**	**21**
P31210	DELLTSLGK	1.38357289	2	2.7157998
P31210	DIEALNK	1.419085091	1	2.4631081
P31210	EEMKDIEALNK	1.120870547	2	3.6799011
P31210	ENFQIFDFSLTK	1.442901182	2	2.8502924
P31210	FVEMLMWSDHPEYPFHDEY	1.599715827	3	3.8727753
P31210	GLVVIPK	1.393402123	2	2.3889263
P31210	HIDGAYVYR	1.468433871	2	2.9079738
P31210	IKENFQIFDFSLTK	2.678638915	3	4.1217008
P31210	LWSTDHDPEMVRPALER	1.69063223	2	2.3562531
P31210	NEHEVGEAIR	1.322224877	2	3.0763493
P31210	NPLWVNVSSPPLLK	1.501088293	2	4.1289678
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.48688473	3	5.8204751
P31210	QLEVILNKPGLK	1.567767955	2	3.5932028
P31210	REEIFYCGK	1.660813861	2	2.7921219
P31210	RQLEVILNKPGLK	1.322698981	3	4.2492752
P31210	SLGVSNFNR	0.930369089	2	2.3986793
P31210	SNLCATWEALEACK	1.169754556	2	4.6070905
P31210	SNLCATWEALEACKDAGLVK	1.569744614	2	4.8044086
P31210	TAIDEGYR	1.188827498	2	2.8983345
P31210	TQAQIVLR	1.21373792	2	2.9122891
P31210	YKPVTNQVECHPYFTQTK	1.410347148	2	5.614728
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.155172663**	**0.5271169**	**2**
P31230	KEIEELK	1.162721296	1	1.9491907
P31230	TVVSGLVNHVPLEQMQNR	1.134413108	3	3.4486685
P31232	**TAGL Transgelin**	**1.205893818**	**0.4816868**	**2**
P31232	KYDEELEER	1.335552164	2	2.5869517
P31232	TVMALGSLAVTK	1.060249665	2	2.8193889
P31254	**UBA1Y Ubiquitin_like modifier_activating enzyme 1 Y**	**1.173404988**	**0.5530779**	**2**
P31254	YDGQVAVFGSDLQEK	1.183416134	2	4.5242925
P31254	YFLVGAGAIGCELLK	0.982636592	2	2.7656639
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.188302638**	**6.442E-05**	**9**
P31399	ANVDKPGLVDDFK	1.087487457	2	3.908788
P31399	KYPYWPHQPIENL	1.258472531	2	2.8469925
P31399	NCAQFVTGSQAR	0.757652669	2	3.8667116
P31399	NMIPFDQMTIDDLNEVFPETK	1.303352991	2	5.2888718
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(2)	1.217988602	2	3.1333876
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(8)	1.217988602	2	2.3115556
P31399	SWNETFHTR	1.080387607	2	2.7176285
P31399	TIDWVSFVEIMPQNQK	1.570589037	2	3.2840126
P31399	YTALVDAEEKEDVK	0.983490962	2	3.5652983
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.315366665**	**0.0011773**	**4**
P32089	FIHDQTSSNPK	1.210863286	1	3.7498004
P32089	GLSSLLYGSIPK	1.053243656	2	3.8223524
P32089	NTLDCGVQILK	1.093383257	2	3.7996869
P32089	TQLQLDER	1.08929156	2	2.6097863
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.183161212**	**0.7660886**	**3**
P32198	ELEQQMQQILDDPSEPQPGEAK	1.063114663	2	4.0636926
P32198	LLGSTIPLCSAQWER	1.033169214	2	3.0100696
P32198	MTALAQDFAVNLGPK	1.189628224	2	4.2359214
P32232	**CBS Cystathionine beta_synthase**	**1.074660748**	**0.0409356**	**8**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.128303731	3	5.3251176
P32232	FDSPESHVGVAWR	1.064614261	2	3.2914047
P32232	LKNEIPNSHILDQYR	1.760804016	3	3.5512643
P32232	NASNPLAHYDDTAEEILQQCDGK	1.193771324	2	5.5608025

P32232	SNDDDSFAFAR	1.10134611	2	3.0561337
P32232	VDMLVASAGTGGTITGIAR	0.875167565	2	4.6053052
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.23697885	3	4.1996775
P32232	VRPSDEVCK	1.081325264	3	3.608285
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**0.996351874**	**0.0348029**	**11**
P32551	AVAFQNPQTR	1.127010608	2	3.4325461
P32551	AVAQGNLSSADVQAAK	0.94563208	2	5.0821128
P32551	GNNTTSLLSQSVAK	1.026577268	2	3.9725533
P32551	IIENLHDVAYK	1.195493916	2	4.046308
P32551	ITSEELHYFVQNHFTSAR	1.092000331	3	3.473325
P32551	NALANPLYCPDYR	0.931863474	2	3.3733399
P32551	RGNNTTSLLSQSVAK	1.016920955	2	2.7873237
P32551	RWEVAALR	1.183644014	2	2.760175
P32551	SMTASGNLGHTPFLDEL	1.131297576	2	3.1472273
P32551	TSAPGGVPLQPQELEFTK	0.930386215	2	3.8260179
P32551	YENYNYLGTSHLLR	1.748797702	2	4.0698023
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.192681655**	**9.9E-20**	**19**
P32755	AFEEEQALR	1.126436801	2	3.3757317
P32755	DIAFEVEDCEHIVQK	1.318745967	2	3.9989696
P32755	ENMDVLEELK	0.998526506	2	2.6690156
P32755	FAVLQTYGDTTHTLVEK	1.406239801	2	5.1435981
P32755	FLHFHSVTFWVGNAK	0.844136791	3	3.4663751
P32755	FLPGFEAPTYK	1.169556788	2	2.5626488
P32755	FWSVDDTQVHTEYSSLR	1.286162241	2	5.6787896
P32755	GMEFLAVPSSYYR	1.355456396	2	2.628212
P32755	GNLTDLETNGVR	1.234656687	2	3.676733
P32755	HGDGVKDIAFEVEDCEHIVQK	1.313212745	3	4.850141
P32755	HNHQGFGAGNFNSLFK	1.265222093	3	4.6907024
P32755	ILVDYDEK	1.207975736	1	1.9862553
P32755	IVFVLCSALNPWNK	1.467188582	2	2.5318878
P32755	IVREPWVEEDKFGK	1.507809339	3	4.3537688
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.482297827	3	7.4221921
P32755	MGFEPLAYK	1.678668662	2	2.6022341
P32755	SIVVANYEESIK	1.128289112	2	4.067884
P32755	SQIQEYVDYNGGAGVQHIALR	1.281406108	2	5.5929565
P32755	TEDIITTIR	1.148240248	2	3.342716
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.037217578**	**1**	**2**
P33124	ALRPTIFPVVPR	1.072574847	2	3.258791
P33124	IENIYIR	0.992523271	2	2.9643557
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.178709526**	**9.9E-20**	**27**
P34058	ADLINNLGTIAK	1.01955214	2	4.2233295
P34058	EDQTEYLEER	0.932213063	2	3.4920197
P34058	EGLELPEDEEEK	0.979143309	2	2.4602726
P34058	EGLELPEDEEEKKK	1.19127502	2	3.1499658
P34058	ELISNASDALDK	0.884261929	2	3.7060885
P34058	GEKEEEDKEDEEKPK	0.4649926	3	4.1048374
P34058	GFEVVYMTEPIDEYCVQQLK	1.117486331	2	3.4250913
P34058	GVVDSEDLPLNISR	1.161577589	2	4.8695164
P34058	HFSVEGQLEFR	1.115045529	2	2.943311
P34058	HLEINPDHPIVETLR	1.106524446	2	4.4571128
P34058	HSQFIGYPITLYLEK	3.135153588	2	3.9477575
P34058	IDIIPNPQER	1.020593537	2	2.9190691
P34058	KHLEINPDHPIVETLR	1.195054467	2	4.8914404
P34058	LGIHEDSTNR	1.139008943	2	3.0411549
P34058	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	1.948619119	2	4.512372
P34058	NPDDITQEEYGEFYK	1.209669905	2	4.608768

P34058	RAPFDLFENK	1.219919319	2	3.0249181
P34058	SIYYITGESK	1.208707313	2	2.6299293
P34058	SLTNDWEDHLAVK	1.247765499	2	4.3258996
P34058	TLTLVDTGIGMTK	0.985614068	2	4.3429503
P34058	TLTLVDTGIGMTK+Oxidation(11)	1.223860152	2	3.3894668
P34058	VFIMDSCDELIPEYLNFIR	1.613113989	2	2.481673
P34058	VILHLKEDQTEYLEER	1.478532639	3	4.5444846
P34058	YESLTDPSK	1.096556802	2	2.9183462
P34058	YESLTDPSKLDSGK	1.330291834	2	3.458041
P34058	YHTSQSGDEMTSLSEYVSR	1.148124217	2	5.4994841
P34058	YIDQEELNK	1.068068145	2	3.4898708
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.349356262**	**5.218E-14**	**2**
P34064	AIGSASEGAQSSLQEVYHK	1.251594185	2	4.512517
P34064	LNATNIELATVQPGQNFHMFTK	1.680257951	3	3.3920178
P34067	**PSB4 Proteasome subunit beta type_4**	**1.287825334**	**0.0005278**	**4**
P34067	FDCGVVIAADMLGSYGSLAR	0.745517372	2	3.9352295
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.134521413	2	4.0309253
P34067	TQNPMVTGTSVLGVK	0.941953655	2	2.3666503
P34067	VNDSTMLGASGDYADFQYLK	1.35481768	2	5.3458891
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**0.982519847**	**0.9960404**	**2**
P35171	GGTSDALLYR	1.102920299	2	3.2449634
P35171	LFQEDNGMPVHLK	1.033970211	2	3.6958988
P35213	**1433B 14_3_3 protein beta/alpha**	**1.131531205**	**0.0040335**	**7**
P35213	AVTEQGHELSNEER	1.00227434	2	4.4838362
P35213	EKIEAELQDICSDVLELLDK	1.25823225	3	5.3128181
P35213	QTTVSNSQQAYQEAFEISK	1.214087263	2	5.4352756
P35213	TAFDEAIAELDTLNEESYK	1.361630494	2	4.9119296
P35213	YDDMAAAMK	0.631475899	2	2.6598747
P35213	YLILNATHAESK	1.358440487	2	3.5392075
P35213	YLSEVASGDNK	1.101075782	2	3.1428645
P35278	**RAB5C Ras_related protein Rab_5C**	**1.118180961**	**0.0095149**	**3**
P35278	FEIWDTAGQER	0.670222898	2	2.8341262
P35278	GVDLQESNPASR	1.118335722	2	3.20818
P35278	NEPQNAAGAPGR	0.984438726	2	3.106113
P35427	**RL13A 60S ribosomal protein L13a**	**1.259335176**	**0.0157617**	**3**
P35427	CEGINISGNFYR	1.193864264	2	2.9601586
P35427	VLDGIPPPYDK	1.253231683	2	2.6617789
P35427	YQAVTATLEEK	1.163614232	2	3.2023427
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**0.95091058**	**0.914465**	**2**
P35434	AQSELSGAADEAAR	0.946949607	2	4.6613288
P35434	IEANEALVK	0.915311537	2	2.540046
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.139027113**	**1.032E-05**	**6**
P35435	GLCGAIHSSVAK	1.116073415	2	3.6060963
P35435	HLIIGVSSDR	1.023338265	2	3.234421
P35435	NASDMIDK	0.922895472	1	2.1246595
P35435	NDMAALTAAGK	0.906732133	2	3.7690158
P35435	THSDQFLVSFK	1.121051454	1	2.8724191
P35435	VYGTGSLALYEK	1.478815729	2	3.4540942
P35559	**IDE Insulin_degrading enzyme**	**1.382583982**	**0.0337298**	**2**
P35559	SNPGHYLGHLIGHEGPGSLLSELK	1.235797126	3	3.7611263
P35559	YTLETRPNQEGIDVR	1.511846942	2	2.5138338
P35565	**CALX Calnexin**	**1.136233081**	**9.572E-13**	**9**
P35565	GSLSGWILSK	0.88829082	2	2.3577795
P35565	KIPNPDFFEDLEPFR	1.248743919	3	4.9626484
P35565	NKGDEEEEEEKLEEK	1.060251084	2	5.1836882
P35565	SDTSTPPSPK	0.883412527	2	2.8804519

P35565	TDAPQPDVKDEEGKEEEK	1.16201134	3	4.0667939
P35565	TSELNLDQFHDK	1.178962981	2	3.7841511
P35565	VVDDWANDGWGLK	0.827596965	2	3.7104092
P35565	VVDDWANDGWGLKK	0.724938911	2	3.2919862
P35565	WEVDEMKETK	1.067105254	2	2.5589612
P35704	**PRDX2 Peroxiredoxin_2**	**1.083052932**	**0.9999999**	**4**
P35704	EGGLGPLNIPLLADVTK	1.05040461	2	3.4964676
P35704	KEGGLGPLNIPLLADVTK	1.109627788	2	4.7394114
P35704	QITVNDLPVGR	1.010077224	2	3.2335331
P35704	SLSQNYGVLK	1.044893686	2	2.5563643
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.953391925**	**0.7471209**	**4**
P35738	GLLLSCIEDKNPCIFFEPK	1.109814942	3	4.0130401
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	1.047295713	3	5.8538985
P35738	MNLFQSITSALDNSLAK	1.182411664	2	3.3925014
P35738	SGDLFNCGSLTIR	0.881836441	2	3.5380571
P35815	**PPM1B Protein phosphatase 1B**	**1.04809771**	**0.9092232**	**3**
P35815	ILSAENIPNLPPGGGLAGK	1.009488931	2	2.5083838
P35815	IQNAGGSVMIQR	1.063652589	2	2.3235407
P35815	SGFALEPSVENVK	0.900104936	2	2.3069487
P36201	**CRIP2 Cysteine_rich protein 2**	**1.131522565**	**0.9995892**	**3**
P36201	ASSVTTFTGEPNMCPR	1.065721764	2	3.6580212
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.01086321	3	5.9194441
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.145321821	2	4.8724809
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**1.280388811**	**9.9E-20**	**9**
P36365	AILTQWDR	0.965141326	1	2.0308728
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.739693584	3	3.9825175
P36365	FTEHVEEGR	1.214369314	2	3.3825147
P36365	NLLPTPVVSWLISK	1.346509649	2	2.5811288
P36365	SCDLGGLWR	1.108180809	2	2.6965718
P36365	TQLREPVLNDELPGR	1.174677659	3	4.0119104
P36365	VAIVGAGVSGLASIK	1.035662717	2	3.0722859
P36365	VEDGQASLYK	1.181784907	2	3.1840174
P36365	VLVVGMGNSGTDIAVEASHLAK	1.431016238	2	5.2189054
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.280759439**	**9.9E-20**	**8**
P36511	ANIIAWALAQIPQK	1.329118071	3	5.9253931
P36511	FVTFPTSFSSHDLENFFTR	1.78000529	2	4.5745921
P36511	GHEVTVLRPSAFVFLDPK	1.991654892	3	3.646332
P36511	IILEELVQK	1.159902899	2	3.3689311
P36511	NAMWLSTIHHDQPTKPLDR	1.554670791	3	3.4458323
P36511	NAMWLSTIHHDQPTKPLDR+Oxidation(3)	2.413429425	3	3.3085213
P36511	SDLLNALEEVIDNPFYK	1.491265701	3	5.3026876
P36511	TLGRPTTLAEIMGK	1.593014582	3	3.5808544
P36972	**APT Adenine phosphoribosyltransferase**	**1.173308588**	**0.0999455**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	1.241600891	2	4.2034845
P36972	IDYIAGLDSR	0.956706765	2	2.472723
P36972	SFPDFPIPGVLFR	1.163676613	2	3.0730064
P37397	**CNN3 Calponin_3**	**1.027354339**	**0.2522131**	**4**
P37397	AGQSVIGLQMGTNK	0.982675453	2	2.7251449
P37397	LTLQPVDNSTISLQMGTNK	1.374293375	2	3.4246194
P37397	VNESSLNWPQLENIGNFIK	1.039341789	2	3.9016254
P37397	YDQQAEEDLR	0.818036868	2	2.8973985
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.035485011**	**0.6046362**	**5**
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.245072349	2	3.5620122
P38650	ILDDDTIITTLENLK	1.237040764	2	2.6165466
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	1.025108137	3	5.0711198

P38650	VQGLTVEQAEAVAR	0.999473735	2	2.9699149
P38650	VTDFGDKVEDPTFLNQLQSGVNR	1.117252326	3	3.6651535
P38652	**PGM1 Phosphoglucomutase_1**	**1.007241762**	**5.474E-06**	**18**
P38652	ADNFEYSDPVDGSISK	0.968026071	2	4.9261651
P38652	AIGGIILTASHNPGGPNGDFGIK	1.18183005	2	5.6321788
P38652	FFGNLMDASK	1.055760133	2	2.5914314
P38652	FNISNGGPAPEAITDK	1.133516881	2	4.2675548
P38652	IDAMHGVVGPYVK	0.75692871	2	2.9665518
P38652	ILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMK	1.675415155	3	3.370281
P38652	INQDPQVMLAPLISIALK	1.275541042	2	3.5856817
P38652	KQRVEDILK	1.042469897	1	2.0189533
P38652	LSGTGSAGATIR	1.39626133	2	3.4728234
P38652	LVIGQNGILSTPAVSCIIR	1.584326419	2	4.7701097
P38652	NIFDFNALK	1.05950793	2	2.4834559
P38652	QEATLVVGGDGR	1.097054833	2	3.7008042
P38652	QQFDLENK	1.030823084	1	2.0959687
P38652	SFVGKQFSANDK	0.799766674	1	1.9240174
P38652	SGEHDFGAAFDGDGDR	1.03829652	2	4.3645382
P38652	TIEEYAICPDLK	0.918459178	2	3.7555997
P38652	TQAYPDQKPGTSGLR	1.196448874	2	3.456157
P38652	YDYEEVEAEGANK	0.807564568	2	5.3178482
P38656	**LA Lupus La protein homolog**	**1.150910534**	**0.0454026**	**2**
P38656	ITDDQQESLNK	1.151766771	2	4.1279049
P38656	LDEGWVPLETMIK	1.080372543	2	2.7825401
P38659	**PDIA4 Protein disulfide_isomerase A4**	**0.9459077**	**0.0085168**	**20**
P38659	DLGLSESGEDVNAAILDESGKK	1.138745328	2	5.1451793
P38659	DNDPPIAVAK	0.887297153	2	2.5545406
P38659	EVSQPDWTPPPEVTLTLTK	1.221692686	2	3.5753162
P38659	FDVSGYPTIK	0.99306649	2	2.9699779
P38659	FDVSGYPTLK	0.99306649	2	2.9699779
P38659	FIDEHATK	1.047714491	2	2.7723751
P38659	GQAVDYDGSR	1.05448302	2	2.4826841
P38659	GRPFDYNGPR	1.210421753	2	2.6412907
P38659	IDATSASMLASK	1.126929929	2	4.0903687
P38659	KGQAVDYDGSR	1.189673734	2	2.9680104
P38659	MDATANDITNDR	0.867801075	2	3.6370845
P38659	MHVMDVQGSTEASAIK	1.039328249	2	4.4362593
P38659	MHVMDVQGSTEASAIKDYVVK	1.083173513	3	3.8831909
P38659	RFDVSGYPTLK	0.927391371	2	3.1852703
P38659	RSPPIPLAK	1.234745048	2	2.8855326
P38659	TFDAIVMDPK	1.011723924	1	2.008693
P38659	TQEEIVAK	1.032950698	2	2.3266182
P38659	VDATEQTDLAK	1.065348856	2	3.5846508
P38659	VEGFPTIYFAPSGDK	1.16495585	2	3.2541504
P38659	YGIVDYMVEQSGPPSK	1.155421843	2	3.4564135
P38718	**BR44 Brain protein 44**	**1.148980413**	**0.0090233**	**3**
P38718	LMDKVELLLPK	0.685836721	2	2.7215519
P38718	LRPLYNHPAGPR	1.85863721	2	2.465477
P38718	YSLVIIPK	1.090212037	2	2.3509283
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**1.112524002**	**0.2598255**	**7**
P38918	FFGNPFSQLYMDR	2.005330884	2	2.5282121
P38918	FYAFNPLAGGLLTGR	1.645902969	2	4.7534451
P38918	GHTEIDTAFVYANGQSETILGDLGLGLGR	1.186880902	3	4.9622464
P38918	MDVTSSSASVR	1.080025446	2	3.7766163
P38918	QVETELFPCLR	1.135412646	2	2.5593107
P38918	RMDVTSSSASVR	1.123668375	2	3.7568064
P38918	TTYGPTAPSMISAAVR	1.136442051	2	3.7591474

P38983	**RSSA 40S ribosomal protein SA**	**1.138668948**	**8.193E-14**	**6**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.526424368	3	6.0916767
P38983	AIVAIENPADVSVISSR	1.033485723	2	4.7760549
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.25825513	3	4.0569091
P38983	FTPGTFTNQIQAAFR	1.066008708	2	4.5295763
P38983	SDGIYIINLK	1.12585573	1	2.120496
P38983	YVDIAIPCNNK	1.081365766	2	3.1511121
P39032	**RL36 60S ribosomal protein L36**	**1.1216257**	**0.0152214**	**2**
P39032	EELSNVLAAMRKAAAK+Oxidation(10)	0.693328435	2	2.3258655
P39032	KREELSNVLAAMR	1.142763828	3	3.301332
P40112	**PSB3 Proteasome subunit beta type_3**	**1.073315151**	**0.9935545**	**2**
P40112	FGIQAQMVTTDFQK	0.920878859	2	3.9868262
P40112	FGPYYTEPVIAGLDPK	1.143959289	2	3.0528154
P40307	**PSB2 Proteasome subunit beta type_2**	**1.221038143**	**1.259E-06**	**3**
P40307	FILNLPTFSVR	1.57832208	2	2.8565409
P40307	NGYELSPTAAANFTR	1.225097375	2	4.0372486
P40307	VIDKDGIHNLENITFTK	1.057297397	2	4.0365
P41034	**TTPA Alpha_tocopherol transfer protein**	**0.956641477**	**8.199E-09**	**5**
P41034	AECPELSADLHPR	1.003658665	2	3.0951808
P41034	AIFDLEGWQISHAFQITPSVAK	0.692476762	2	4.3227758
P41034	AQEEGVPETPQPLTDAFLLR	1.521455504	2	4.1851687
P41034	GIHLINEPVIFHAVFSMIKPFLTEK	1.534289196	4	4.8959675
P41034	QLNEQPDHSPLVQPGLAELR	1.123918093	3	3.6414893
P41123	**RL13 60S ribosomal protein L13**	**0.946385281**	**0.0333041**	**5**
P41123	AITEEEKNFK	1.233219978	2	2.4551868
P41123	LATQLTGPVMPIR	1.174868849	2	2.7789612
P41123	STESLQANVQR	1.053374322	2	4.0039639
P41123	TIGISVDPR	1.001099954	2	2.3087151
P41123	VDTWFNQPAR	1.043079449	2	3.1519938
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.09161182**	**0.5654463**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.098179499	2	4.6587248
P41498	IELLGSYDPQK	1.300442008	2	3.6624541
P41498	LVTDENVSDNWR	1.021704822	2	3.6890955
P41542	**USO1 General vesicular transport factor p115**	**1.166892526**	**0.0064392**	**11**
P41542	AETLAKSVPVEGESELVTAAK	1.01838479	3	3.3237586
P41542	AWFEVGDENPGWSAQK	1.327533678	2	4.0257258
P41542	CQNEQLQTAVTQQASQIQQHK	1.01771681	3	3.8478172
P41542	IVAFENAFER	1.099219939	2	2.6420391
P41542	LQTENSELQQR	1.115991316	2	3.055716
P41542	LREEIEELR	1.232822255	2	2.6217613
P41542	QLGPPVQQIILVSPMGVSK	1.213465534	2	4.268158
P41542	SQLCSQSLEITR	1.10781093	2	2.9436917
P41542	SVPVEGESELVTAAK	1.111963462	2	3.3748114
P41542	TLEQHDNIVTHYK	1.318648211	2	3.8062787
P41542	VLVSPTNPPGATSSCQK	1.101659252	2	3.8720021
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**1.093884874**	**9.9E-20**	**18**
P41562	ATDFVVPGPGK	1.013479198	2	3.3830366
P41562	CATITPDEK	0.985856041	2	2.921483
P41562	CATITPDEKR	1.095557537	2	2.502599
P41562	FKDIFQEIYDK	1.049638981	3	4.6065178
P41562	GQETSTNPIASIFAWSR	1.479246424	2	5.3095751
P41562	GWPLYLSTK	2.14306447	1	1.906835
P41562	IHGGSVVEMQGDEMTR	1.120857875	2	5.1817379
P41562	IIWELIK	1.113023624	2	2.3452027
P41562	KIHGGSVVEMQGDEMTR	1.068076295	3	3.3182147
P41562	LIDDMVAQAMK	0.950277131	2	4.494103

P41562	LILPYVELDLHSYDLGIENR	2.349322267	2	5.1977625
P41562	LVTGWVKPIIIGR	1.316776831	2	3.3517478
P41562	SDYLNTFEFMDK	1.447115685	2	4.4371157
P41562	SEGGFIWACK	1.112697218	2	3.5120218
P41562	SIEDFAHSSFQMALSK	1.094951476	2	4.9398046
P41562	TVEAEAAHGTVTR	1.113139358	2	3.9419959
P41562	VEITYTPK	0.981868116	2	2.739459
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.08581182	3	3.6157401
P42123	**LDHB L_lactate dehydrogenase B chain**	**0.822692054**	**0.5876882**	**5**
P42123	DYSVTANSK	0.814469172	2	2.8219604
P42123	IVADKDYSVTANSK	1.233137813	2	2.783463
P42123	LIAPVADDETAVPNNK	1.236088113	2	2.5846477
P42123	SLADELALVDVLEDK	1.482371113	2	2.9503996
P42123	VIGSGCNLDSAR	1.080321778	2	3.8042808
P42930	**HSPB1 Heat shock protein beta_1**	**0.852207067**	**0.8968793**	**2**
P42930	AQIGGPESEQSGAK	0.991939911	2	3.8903892
P42930	VSLDVNHFAPEELTVK	0.850063891	2	3.4320183
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.192989986**	**0.0020623**	**9**
P42932	AIAGTGANVIVTGGK	1.075891117	2	3.8330572
P42932	ELEVQHPAAK	1.074970623	2	2.9842868
P42932	GEENLMDAQVK	0.977807508	2	3.5691102
P42932	GSTDNLMDDIER	0.951485608	2	2.9261758
P42932	HEKEDGAISTIVLR	1.360170789	2	2.7881627
P42932	LFVTNDAATILR	1.418285076	2	2.9985132
P42932	LYSVHQEGNK	1.21229214	2	2.6776745
P42932	NVGLDIEAEVPAVK	0.894809072	2	3.6875627
P42932	QITSYGETCPGLEQYAIK	1.223379208	2	4.8441572
P43244	**MATR3 Matrin_3**	**1.465092954**	**9.9E-20**	**3**
P43244	ITPENLPQILLQLK	1.333923207	2	3.5789659
P43244	TENPAEGKEQEEK	1.466686813	2	3.3145845
P43244	YQLLQLVEPFGVISNHLILNK	1.672803926	3	4.0610104
P43274	**H14 Histone H1.4**	**1.106335065**	**8.982E-11**	**3**
P43274	ALAAAGYDVEK	1.116051503	2	3.692065
P43274	SGVSLAALK	0.911180125	2	3.1403587
P43274	SGVSLAALKK	1.045747972	2	2.4775922
P43276	**H15 Histone H1.5**	**1.2464578**	**3.138E-06**	**2**
P43276	ALAAGGYDVEK	1.311008635	2	2.774061
P43276	ATGPPVSELITK	1.017555131	2	2.9677498
P43278	**H10 Histone H1.0**	**0.884240306**	**0.9638246**	**2**
P43278	VGENADSQIK	0.957529769	2	3.431299
P43278	YSDMIVAAIQAEK	0.851299479	2	4.2610111
P43424	**GALT Galactose_1_phosphate uridylyltransferase**	**1.104249564**	**0.0614608**	**2**
P43424	HDPLNPLCPGATR	1.130213448	2	2.879844
P43424	YNPLQDEWVLVSAHR	0.814005513	2	2.4393401
P45591	**COF2 Cofilin_2**	**0.992750139**	**0.9587831**	**4**
P45591	HEWQVNGLDDIKDR	1.038563344	3	4.2062855
P45591	KEDLVFIFWAPESAPLK	1.062844395	2	3.9110506
P45591	MASGVTVNDEVIK	0.989403614	2	2.4834156
P45591	QILVGDIGDTVEDPYTSFVK	1.146277701	2	5.1744905
P45592	**COF1 Cofilin_1**	**1.208025051**	**9.9E-20**	**4**
P45592	HELQANCYEEVK	1.097981827	2	3.3192582
P45592	HELQANCYEEVKDR	1.179917599	3	5.4931636
P45592	LGGSAVISLEGKPL	1.516880635	2	2.4312618
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.272636527	2	5.0192695
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.925307154**	**7.843E-05**	**3**
P45878	GWDQGLLGMCEGEK	1.105043153	2	2.8324139
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	1.604481449	2	3.7051919

P45878	LVIPSELGYGER	1.653711425	2	2.4015234
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.068779274**	**0.1794215**	**20**
P45953	AMVENGGLVTSNPLR	0.850571722	2	2.7401135
P45953	AMVENGGLVTSNPLRV	1.264206609	2	4.1408267
P45953	ASNTSEVYFDGVK	1.061349635	2	3.5092313
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	0.935151072	2	4.6554165
P45953	ENMASLQSNPQQQELFR	1.104343302	2	3.8920593
P45953	FFEEVNDPAK	0.893067839	2	2.7084455
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.041689984	3	4.5634646
P45953	GIVNEQFLLQR	1.136658909	2	3.2191939
P45953	IFEGTNDILR	1.079816169	2	3.0035899
P45953	IFGSEAAWK	0.822517742	2	2.654496
P45953	IHNFGVIQEK	1.2902198	2	2.3141336
P45953	LFVALQGCMDK	1.012925399	2	2.4838622
P45953	NDSLEKVEEDTLQGLK	0.93637392	2	3.5941505
P45953	NPLGNVGLLIGEASK	1.081836086	2	2.6824086
P45953	SFGGVTHGLPEK	1.087934133	2	2.7175651
P45953	SFGGVTHGLPEKK	1.155219013	2	2.384603
P45953	SGELAVQALEQFATVVEAK	1.038526699	3	4.9550943
P45953	SLSEGYPTAQHEK	1.087278741	2	3.3477254
P45953	TGIGSGLSLSGIVHPELSR	0.985621209	2	4.3211651
P45953	VEEDTLQGLK	0.766363029	2	2.5888331
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.016130936**	**0.999998**	**4**
P46418	AILNYIATK	1.082948482	2	3.37272
P46418	SDGSLMFEQVPMVEIDGMK	1.01899965	2	3.5457454
P46418	SHGQDYLVGNK	1.030456007	2	3.5696383
P46418	VSNLPTVK	1.042794806	2	2.8597224
P46425	**GSTP2 Glutathione S_transferase P 2**	**1.175760792**	**0.9643056**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	1.120139307	2	4.4615941
P46425	FEDGDLTLYQSNAILR	1.141524192	2	4.5376611
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.03177839**	**9.9E-20**	**25**
P46462	AIANECQANFISIK	1.32962922	2	2.4941342
P46462	EAVCIVLSDDTCSDEK	1.075413948	2	3.7477338
P46462	EDEEESLNEVGYDDIGGCR	1.13758243	2	4.8490543
P46462	ELQELVQYPVEHPDK	1.114004834	2	4.6259975
P46462	ETVVEVPQVTWEDIGGLEDVK	0.847241384	2	3.100064
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.286976149	2	4.1225419
P46462	EVDIGIPDATGR	0.826707347	2	3.1448071
P46462	GDDLSTAILK	0.847688299	2	2.9728713
P46462	GGNIGDGGGAADR	1.133039101	2	3.201268
P46462	GILLYGPPGTGK	1.026453362	2	3.5753305
P46462	IVSQLLTLMDGLK	2.142418013	2	4.2201815
P46462	KYEMFAQTLQQSR	1.340146136	2	3.0457981
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.456243524	3	6.7924051
P46462	LAGESESNLRKAFEEAEK	0.97965986	2	2.4250214
P46462	LDQLIYIPLPDEK	1.148338802	2	4.8470335
P46462	LEILQIHTK	1.065642679	2	2.9126339
P46462	LGDVISIQPCPDVK	1.100488782	2	4.4684877
P46462	LIVDEAINEDNSVVSLSQPK	1.132964193	2	5.3287969
P46462	MDELQLFR	0.833750121	2	3.1999917
P46462	MTNGFSGADLTEICQR	1.042437798	2	4.5170922
P46462	NAPAIIFIDELDAIAPK	1.833219509	3	5.1094837
P46462	NVFIIGATNRPDIIDPAILRPGR	1.057778884	3	4.1992702
P46462	QTNPSAMEVEEDDPVPEIR	1.030437265	2	4.6115723
P46462	RSVSDNDIR	1.318782435	2	2.658649
P46462	WALSQSNPSALR	0.905165938	2	2.5991335

P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**1.225467573**	**0.0250031**	**3**
P46664	FIEDELQIPVK	1.191469229	2	3.1655142
P46664	VGIGAFPTEQDNEIGELLQTR	1.335905303	2	4.3043966
P46664	VVDLLAQDADIVCR	1.156418552	2	3.0931575
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.056160927**	**9.961E-07**	**3**
P46720	GIGETPIVPLGISYIEDFAK	1.521731488	2	3.5898659
P46720	GVQHQLHVESK	1.021141395	2	3.2387812
P46720	SENSPLYIGILEMGK	1.241913344	2	3.21857
P46844	**BIEA Biliverdin reductase A**	**0.978511811**	**0.9858334**	**3**
P46844	FGVVVVGVGR	1.104375887	2	2.4755967
P46844	LLDQVSAEDLAAEK	1.058589375	2	3.8079538
P46844	MTVQLETQNK	0.976903547	2	2.8144593
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.008845919**	**0.7540645**	**6**
P46953	AQGSVALSVTQDPACK	0.193379659	2	4.4111233
P46953	ASFQPPVCNK	0.85961268	2	2.6739829
P46953	DLGTQLAPIIQEFFHSEQYR	0.941741731	2	3.1654882
P46953	QDVDVWLWQLEGSSK	1.477654477	2	3.3092694
P46953	TGKPNPDQLLK	1.024976619	3	3.5936954
P46953	YYVGDTEDVLFEK	1.208885395	2	4.052299
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.090340989**	**0.011832**	**4**
P46978	FGQVYTEAK	1.033419909	2	2.6022794
P46978	FYSLLDPSYAK	1.078247719	2	3.0939267
P46978	VGQAMASTEEK	1.0774878	2	3.2041342
P46978	VGQAMASTEEK+Oxidation(5)	1.629318749	2	2.6226549
P47198	**RL22 60S ribosomal protein L22**	**1.100240556**	**1.989E-06**	**2**
P47198	AGNLGGGVVTIER	1.071230885	2	3.161875
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.896057638	3	4.8724046
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.365514152**	**9.9E-20**	**4**
P47875	GFGFGQGAGALVHSE	1.101436852	2	3.0796947
P47875	GLESTTLADKDGEIYCK	1.532824674	2	4.9805946
P47875	HEEAPGHRPTTNPNASK	1.636135631	3	3.4977231
P47875	NLDSTTVAVHGEEIYCK	0.966065745	2	4.3539248
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.012877558**	**0.7064435**	**3**
P47942	GLYDGPVCEVSVTPK	1.01275931	2	3.5816474
P47942	QIGENLIVPGGVK	1.143860527	2	2.4390123
P47942	SITIANQTNCPLYVTK	1.188137469	2	3.2890389
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.013185884**	**0.9946927**	**2**
P48004	NYTDDAIETDDLTIK	0.92787288	2	4.706778
P48004	YVAEIEKEKEENEK	1.017806067	2	4.0283623
P48037	**ANXA6 Annexin A6**	**1.176187976**	**1.114E-08**	**17**
P48037	AANDFNPDADAK	1.113962338	2	2.9051893
P48037	AINEAYKEDYHK	1.151825452	2	3.3841145
P48037	ALIEILATR	1.064806116	2	3.4958787
P48037	ALLALCGGED	1.302298328	1	2.190619
P48037	DLESDIIGDTSGHFQK	0.987501959	2	4.26092
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.035432285	3	5.089622
P48037	GELSGDFEK	1.074508386	1	2.0695624
P48037	GFGSDKESILELITSR	0.935621295	2	4.1321445
P48037	GIGTDEATIIDIITQR	0.941664973	3	4.102993
P48037	GSVHDFADFDANQDAEALYTAMK	1.138458197	2	6.1282811
P48037	QRQEICQSYK	1.051528407	2	3.2769527
P48037	SEIDLLNIR	1.364818611	2	3.1122785
P48037	SLEDALSSDTSGHFK	1.061383064	2	3.2885103
P48037	TNEQIHQLVAAYK	1.244219557	2	3.8728614
P48037	TNYDIEHVIK	0.948496715	2	3.2386119

P48037	TTGKPIEASIR	1.149185926	2	2.503027
P48037	WGTDEAQFIYILGNR	2.019506395	2	2.3477681
P48500	**TPIS Triosephosphate isomerase**	**0.909885099**	**9.9E-20**	**12**
P48500	CNVSEGVAQCTR	0.966285031	2	3.8323309
P48500	DLGATWVVLGHSER	0.819938579	2	4.0060387
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.074535883	4	5.3700581
P48500	FFVGGNWK	1.103065845	1	1.9929596
P48500	HIFGESDELIGQK	1.037158699	2	4.0028534
P48500	IIYGGSVTGATCK	1.435106679	2	4.1680036
P48500	KFFVGGNWKMNGR	0.995355787	2	2.3102319
P48500	LPADTEVVCAPPTAYIDFAR	0.180105506	2	4.4726219
P48500	RHIFGESDELIGQK	1.055050629	2	4.2920914
P48500	TATPQQAQEVHEK	1.200266383	2	3.6331048
P48500	VNHALSEGLGVIACIGEK	1.007148003	2	5.1790261
P48500	VVLAYEPVWAIGTGK	0.995115586	2	4.1348372
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.981661003**	**0.9964004**	**6**
P48508	ASTLHLQTGNLLNWGR	1.167883852	3	3.8389115
P48508	EFPDVLECTMSHAVEK	0.933683791	2	3.7688677
P48508	INPDEREEMK	1.071676873	2	2.4725285
P48508	LFIVGSNSSSSTR	0.813094364	2	3.5109971
P48508	QFDIQLLTHNDPK	1.282661742	2	2.612658
P48508	TLNEWSSQISPDLVR	1.085330281	2	4.629065
P48675	**DESM Desmin**	**0.948633818**	**0.6945858**	**3**
P48675	FLEQQNAALAAEVNR	1.22079853	2	4.2318869
P48675	HQIQSYTCEIDALK	1.342805925	2	3.552768
P48675	VSDLTQAANK	0.936883724	2	2.850981
P48679	**LMNA Prelamin_A/C**	**1.007785942**	**2.036E-10**	**14**
P48679	AQHEDQVEQYK	1.205305526	2	2.699162
P48679	AQHEDQVEQYKK	1.259516823	2	4.3803539
P48679	IDSLSAQLSQLQK	0.874297593	2	3.041065
P48679	ITESEEVVSR	0.997715462	2	2.8329918
P48679	LQEKEDLQELNDR	1.171162252	2	4.0274682
P48679	MQQQLDEYQELLDIK	1.478167196	2	4.8848305
P48679	NSNLVGAAHEELQQSR	0.934384248	2	4.6095428
P48679	SGAQASSTPLSPTR	1.00446379	2	3.6230581
P48679	SLETENAGLR	1.048258897	2	2.6288316
P48679	SVGGSGGGSFGDNLVTR	0.911457342	2	3.4324183
P48679	TALINATGEEVAMR	0.96804929	2	2.8475144
P48679	TVLCGTCGQPADK	0.97299118	2	2.8345761
P48679	VAVEEVDEEGK	0.833502961	2	3.0374057
P48679	VAVEEVDEEGKFVR	1.144387314	2	2.9402647
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.055381162**	**9.9E-20**	**27**
P48721	AQFEGIVTDLIK	1.024145852	2	3.839067
P48721	ASNGDAWVEAHGK	1.046467426	2	3.6599462
P48721	DAGQISGLNVLR	1.078035488	2	3.5030568
P48721	EEISKMRELLAR	0.86281341	2	2.4371996
P48721	EQQIVIQSSGGLSK	0.84866558	2	3.7129674
P48721	EQQIVIQSSGGLSKDDIENMVK	0.950246152	2	4.768486
P48721	ERVEAVNMAEGIIHDTETK	0.998570342	3	5.5876307
P48721	GAVVGIDLGTTNSCVAVMEGK	0.838491954	2	5.0698571
P48721	LFEMAYK	0.977052359	2	2.3528404
P48721	LLGQFTLIGIPPAPR	2.026206533	2	3.3681183
P48721	MEEFKDQLPADECNK	0.914638415	2	4.5534186
P48721	MEEFKDQLPADECNK+Oxidation(1)	1.435901056	2	3.9676454
P48721	MKETAENYLGHTAK	0.937946455	2	4.2168813
P48721	MKETAENYLGHTAK+Oxidation(1)	1.475328841	3	3.3737781
P48721	NAVITVPAYFNDSQR	1.123919461	2	3.1572084

P48721	QAVTNPNNTFYATK	1.05360121	2	3.4180579
P48721	RYDDPEVQK	0.981831063	2	2.9515047
P48721	RYDDPEVQKDTK	1.348175656	2	3.7563505
P48721	SDIGEVILVGGMTR	0.978638309	2	4.0354795
P48721	SQVFSTAADGQTQVEIK	1.175530769	2	5.3133235
P48721	STNGDTFLGGEDFDQALLR	1.145719675	2	5.3198786
P48721	TTPSVVAFTPDGER	0.955075681	2	3.5507596
P48721	VEAVNMAEGIIHDTETK	1.121138298	2	4.3813849
P48721	VINEPTAAALAYGLDK	1.53370718	1	3.3812418
P48721	VLENAEGAR	0.993968148	2	3.138849
P48721	VQQTVQDLFGR	1.000809619	2	3.4902554
P48721	YDDPEVQKDTK	1.144218045	2	2.9273324
P48998	**INVO Involucrin**	**1.021408127**	**0.9654486**	**2**
P48998	ELLDQRLDQELVNK	1.021276207	2	2.4207737
P48998	HKLENLTQKEK	1.059553074	1	1.9657307
P49025	**CTRO Citron Rho_interacting kinase**	**1.038524518**	**0.6400014**	**2**
P49025	LLMIAGEERALCLVDVK+Oxidation(3)	1.056807073	2	2.3251793
P49025	LMMNQLEEDLVSARR+Oxidation(2)	0.871928789	2	2.3525193
P49134	**ITB1 Integrin beta_1**	**0.806709057**	**0.6978152**	**4**
P49134	CNCQSHGIPASPK	1.106277616	2	3.2040715
P49134	FCECDNFNCDR	0.898796065	2	3.4599476
P49134	GICECGACK	0.805578539	2	2.3181896
P49134	WDTGENPIYK	0.842240464	2	2.3847139
P49242	**RS3A 40S ribosomal protein S3a**	**1.048764311**	**9.9E-20**	**10**
P49242	ACQSIYPLHDVFVR	1.349860958	2	3.7788677
P49242	ADGYEPPVQESV	1.037013145	1	2.0097258
P49242	EVQTNDLKEVVNK	1.042382393	2	2.3317676
P49242	LIPDSIGKDIEK	1.475329451	2	2.907619
P49242	LITEDVQGK	1.139493035	2	2.3582988
P49242	LMELHGEGGSSGK	1.046989086	2	3.2341487
P49242	LMELHGEGGSSGK+Oxidation(2)	1.17536713	2	3.1033876
P49242	NCLTNFHGMDLTR	1.150666454	2	4.1579909
P49242	TTDGYLLR	1.074464811	2	2.9913504
P49242	VFEVSLADLQNDEVAFR	1.175513878	2	4.78931
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.944614336**	**0.0990228**	**5**
P49432	EAINQGMDEELERDEK	0.971181721	2	2.8486152
P49432	ILEDNSIPQVK	0.919628433	2	3.4610887
P49432	IMEGPAFNFLDAPAVR	1.056794383	2	4.558763
P49432	TIRPMDIEAIEASVMK	2.489888793	2	3.4269102
P49432	VFLLGEEVAQYDGAYK	1.132387865	2	3.5019805
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.978175495**	**0.0109701**	**10**
P49889	CKEDALFNR	1.206994377	2	2.3759308
P49889	FEEHYQQQMK	1.254346579	2	2.954859
P49889	FMEGQVPYGSWYDHVK	1.176190753	2	4.3352904
P49889	IIQHTSFQEMK	1.146636039	2	3.2163846
P49889	LIEFLERDPSAELVDR	1.139284788	3	4.7302165
P49889	NEDLINGIK	0.959206464	2	2.91521
P49889	NNPCTNYSMLPETMIDLK	1.16856466	2	4.3649254
P49889	NNPCTNYSMLPETMIDLK+Oxidation(14)	1.103130985	2	3.1127195
P49889	NNPCTNYSMLPETMIDLK+Oxidation(9)	1.103130985	2	4.146317
P49889	SGSTWISEIVDMIYK	2.073290529	2	4.7541037
P50137	**TKT Transketolase**	**1.13007746**	**1.469E-08**	**20**
P50137	AVELAANTK	0.852573982	1	1.9716796
P50137	GITGIEDK	0.897363278	1	2.4263124
P50137	HQPTAIIAK	0.649609077	2	2.5130949
P50137	IIALDGDTK	0.943832735	2	2.6688249

P50137	ILATPPQEDAPSVDIANIR	0.942722143	3	4.9233027
P50137	ILTVEDHYYEGGIGEAVSAVVVGEPGVTVTR	2.924251514	3	3.821249
P50137	ISSDLDGHPVPK	0.900907979	2	3.352299
P50137	KISSDLDGHPVPK	0.957799969	2	4.0500121
P50137	LDNLVAIFDINR	0.81806111	2	4.7533069
P50137	LGQSDPAPLQHQVDVYQK	1.071823299	2	3.7426722
P50137	MFGIDKDAIVQAVK	0.736101593	2	4.3816881
P50137	NMAEQIIQEIYSQVQSK	0.941800736	3	6.5138922
P50137	NSTFSELFK	0.754657096	2	2.4520109
P50137	SGKPAELLK	0.725591557	3	3.4272552
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	0.873114427	3	5.4461141
P50137	SKDDQVTVIGAGVTLHEALAAAEMLKK	1.012498871	4	5.550498
P50137	SVPMSTVFYPSDGVATEK	0.80020795	2	4.6903019
P50137	TSRPENAIIYSNNEDFQVGQAK	0.869351181	3	5.5963674
P50137	VLDPFTIKPLDK	1.144179016	2	3.4927664
P50137	VLDPFTIKPLDKK	0.918733906	2	2.4388981
P50169	**RDH3 Retinol dehydrogenase 3**	**1.070066014**	**4.052E-14**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.437743334	3	5.4832892
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(2)	1.172104909	3	4.3081141
P50169	FQDSYMK	1.059179079	1	1.9355915
P50169	GLWGLVNNAGISVPVGPNEWMR	1.00686804	2	3.5643122
P50169	KLWDQTTEEVK	1.444734132	2	2.5576901
P50169	KLWDQTTEEVKEIYGEK	1.100926604	3	4.3018165
P50169	LWDQTTEEVK	1.039193019	2	3.5999475
P50169	LWDQTTEEVKEIYGEK	1.231829501	2	4.9932394
P50169	MSLVGGGYCISK	1.070788343	2	3.9099414
P50237	**ST1C1 Sulfotransferase 1C1**	**1.092821616**	**1.4E-12**	**9**
P50237	AGTTWTQEIVDMIQNDGDVQK	1.204952807	2	5.6509161
P50237	DISEEVLNK	0.940183226	2	2.6277041
P50237	DLHLGEQDLQPETR	1.066391547	2	3.9535215
P50237	FLEKDISEEVLNK	1.305076038	2	3.4093328
P50237	IWNFQAKPDDLLIATYAK	1.39988195	2	4.4657454
P50237	MKDLHLGEQDLQPETR	1.021865534	2	4.920691
P50237	MLPDPGTLGEYIEQFK	1.363905254	3	4.6758342
P50237	MLPDPGTLGEYIEQFK+Oxidation(1)	1.312066658	2	3.0702045
P50237	VLWGSWYDHVK	1.299725528	2	3.1831439
P50289	**ASPX Acrosomal protein SP_10**	**1.025891779**	**0.7378636**	**2**
P50289	MQIMCCRNEPLCNK	0.919694029	2	2.3488097
P50289	MQIMCCRNEPLCNK+Oxidation(1)	1.133671266	2	2.3918641
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**1.111167108**	**0.676396**	**7**
P50398	FDLGQDVIDFTGHALALYR	0.884394732	2	2.7444484
P50398	FQLLEGPPESMGR	0.948924045	2	3.6843739
P50398	KQNDVFGEADQ	0.97854885	2	3.3125327
P50398	NPYYGGESSSITPLEELYK	1.236515847	2	5.8906722
P50398	QLICDPSYIPDR	1.229348045	2	2.8948989
P50398	TDDYLDQPCLETINR	0.978306498	2	4.6755586
P50398	TFEGVDPQTTSMR	0.871067525	2	3.2231772
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.201811306**	**0.0015835**	**10**
P50399	AYDATTHFETTCDDIKDIYK	0.988753403	3	5.1512513
P50399	DWNVDLIPK	1.124718615	2	2.3538404
P50399	EIRPALELLEPIEQK	1.002436419	2	3.4989617
P50399	FDLGQDVIDFTGHSLALYR	1.494772961	2	4.4165802
P50399	FVSISDLFVPK	1.230723397	2	3.5102448
P50399	MTGSEFDFEEMKR	1.198549192	2	2.732398
P50399	NTNDANSCQIIIPQNQVNR	1.251369151	2	4.0285983
P50399	TDDYLDQPCCETINR	1.207607957	2	4.6816797
P50399	VICILSHPIK	1.030785916	2	2.5108907

P50399	VLHMDQNPYYGGESASITPLEDLYK	1.153353339	3	4.6537318
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.069267776**	**0.135806**	**8**
P50431	ALSDALTELGYK	1.14267423	2	4.3628669
P50431	AVLEALGSCLNNK	1.21313233	2	4.1399727
P50431	GLLEEDFQK	1.099088053	1	2.3007836
P50431	IMGLDLPDGGHLTHGFMTDK	0.908755041	2	2.8456161
P50431	IYQLQVLANCR	1.184099524	2	2.5716267
P50431	LIIAGTSCYSR	1.586066376	2	2.3634157
P50431	VLEACSIACNK	1.119263561	2	3.9993525
P50431	YSEGYPGQR	0.974596685	2	2.4414039
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**1.153049312**	**9.9E-20**	**14**
P50475	ASEWVQQVSGLMDGK	1.037952564	2	4.042644
P50475	AVFDETYPDPVR	1.168480939	2	2.9960239
P50475	EIADLGEVLATAVIPQWQK	1.055486778	2	3.1485658
P50475	GLEATDDSPK	1.081417708	2	2.6714151
P50475	ITCLCQVPQNAANR	1.300418022	2	4.1306705
P50475	IVAVTGAEAQK	1.261364935	2	2.4556472
P50475	MSNYDTDLFVPYFEAIQK	1.495576184	2	3.4438782
P50475	NSSHAGAFVIVTEEAIAK	1.193022925	2	3.7829394
P50475	QIWQNLGLDEAK	1.227676853	2	2.8254986
P50475	RIVAVTGAEAQK	1.018177814	2	3.1226103
P50475	SVLGDADQK	1.591005684	1	2.2820621
P50475	TITVALADGGRPDNTGR	1.19622876	2	2.7605815
P50475	VDDSSEDKTEFTVK	1.229231532	2	4.0134292
P50475	VGAEDTDGIDMAYR	1.043474909	2	3.3324697
P50503	**F10A1 Hsc70_interacting protein**	**1.284439506**	**1.028E-08**	**5**
P50503	AIDLFTDAIK	1.225066716	2	2.5333261
P50503	AIEINPDSAQPYK	1.231118249	2	2.8049262
P50503	GAAIDALNDGELQK	1.22011173	2	3.3118882
P50503	KGAAIDALNDGELQK	1.351634859	2	4.767715
P50503	LDYDEDASAMLR	1.080772292	2	3.2823377
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**0.980702087**	**0.2005077**	**10**
P50554	GTFCSFDTPDEAIR	1.036577837	2	3.1833353
P50554	IDIPSFDWPIAPFPR	1.16815004	2	3.6512668
P50554	IFNTWLGDPSK	0.961519967	2	2.3369091
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.106343856	3	4.9971008
P50554	MLDLYSQISSVPIGYNHPALAK	1.020975263	3	3.4819691
P50554	NLLLAEVINIIK	1.01972511	3	5.3101544
P50554	REDLLNNVAHAGK	1.032371591	3	3.7615418
P50554	TLLTGLLDLQAQYPQFVSR	1.399814352	2	4.2358656
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	0.991089605	2	4.2707653
P50554	VDFEFDYDGPLMK	0.77577827	2	3.722331
P50580	**PA2G4 Proliferation_associated protein 2G4**	**0.982399246**	**0.0150526**	**2**
P50580	HELLQPFNVLYEK	2.057960046	2	2.4099073
P50580	TIIQNPTDQQK	0.980134715	2	2.7579212
P50878	**RL4 60S ribosomal protein L4**	**1.133424533**	**0.0404791**	**10**
P50878	FCIWTESAFR	0.940451604	2	2.4533877
P50878	KLDELYGTWR	1.127745846	2	3.0943029
P50878	KLEAAAAALAAK	1.191532935	3	3.7863359
P50878	LEAAAAALAAK	1.201866038	2	2.3450329
P50878	NIPGITLLNVSK	1.191537981	1	2.3753691
P50878	NVTLPAVFK	0.990364706	1	2.2250185
P50878	RGPCIIYNEDNGIIK	1.153481153	2	2.9561622
P50878	SGQGAFGNMCR	0.877850432	2	2.7763605
P50878	SNYNLPMHK	1.077213069	2	2.4188542
P50878	YAICSALAASALPALVMSK	1.640749321	2	3.6818233

P50904	**RASA1 Ras GTPase_activating protein 1**	**0.996812202**	**0.8249905**	**3**
P50904	IMESKQSCELSPSK+Oxidation(2)	0.784810894	2	2.5013378
P50904	LESLLLCTLNDR	0.725229788	1	1.9023232
P50904	YYNSIGDIIDHYRK	1.001697848	2	2.4293289
P51538	**CP3A9 Cytochrome P450 3A9**	**0.998814205**	**0.0037588**	**2**
P51538	EMFPIINQYTDMLVR	1.284813931	2	2.5303669
P51538	GFWEFDKYCHK	0.773015442	1	2.2301278
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.040704162**	**1.155E-14**	**8**
P51635	ALEALVAK	1.017992929	2	2.8583679
P51635	GLEVTAYSPLGSSDR	1.043743562	2	4.1500902
P51635	HHPEDVEPAVR	1.078549894	3	3.7630265
P51635	HIDCASVYGNETEIGEALK	0.954661365	2	5.872046
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.761773627	3	6.803412
P51635	HPDEPVLLEEPVVLALAEK	2.099108407	3	5.6685438
P51635	ILQNIQVFDFTFSPEEMK	2.660819195	2	4.5232539
P51635	QLDALNK	1.081401933	1	1.9899024
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.845637917**	**0.4038139**	**17**
P51647	ANNTTYGLAAGVFTK	0.783591876	2	4.531414
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.989306804	3	3.5613813
P51647	ELGEHGLYEYTELK	0.779929721	2	3.4561656
P51647	FPVLNPATEEVICHVEEGDK	0.737576093	3	3.7493389
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.852635397	4	5.1933799
P51647	IFINNEWHDSVSGK	1.101319685	2	4.5981765
P51647	IFVEESVYDEFVR	0.800691854	2	4.4964957
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	1.155066991	3	4.7491622
P51647	IHGQTIPSDGDIFTFTR	1.385440604	2	4.3567686
P51647	KFPVLNPATEEVICHVEEGDK	0.867732548	3	3.3682454
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.900697503	4	4.8262267
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	0.962745749	3	3.8385355
P51647	LLLATIEAINGGK	2.427652131	2	4.7309985
P51647	VFANAYLSDLGGSIK	0.872303451	2	4.6444902
P51647	YCAGWADK	0.890684385	1	2.2485063
P51647	YVLGNPLTQGINQGPQIDK	0.767084405	2	5.060204
P51647	YVLGNPLTQGINQGPQIDKEQHDK	1.129484805	2	3.7664785
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.907640423**	**0.9965396**	**9**
P51650	EVGEVLCTDPLVSK	0.795885976	2	4.1431513
P51650	GIHDSFVTK	1.017924143	2	2.3018949
P51650	HQSGGNFFEPTLLSNVTR	1.016186267	2	3.9368763
P51650	IITAESGKPLK	1.088301626	2	2.6185679
P51650	ILLHHAANSVK	1.271703734	2	2.4283056
P51650	LGTVADCGVPEAR	0.692463467	2	3.269433
P51650	VGNGFEEGTTQGPLINEK	0.873756496	2	4.88169
P51650	WLPTPATFPVYDPASGAK	0.925171261	2	3.0388298
P51650	YGIDEYLEVK	0.97494947	2	2.5931952
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**1.106184605**	**0.7144331**	**3**
P51863	ADDYEQVK	1.138158548	2	2.3858597
P51863	LHLQSTDYGNFLANEASPLTVSVIDDK	1.327702663	3	3.6069183
P51863	LYPEGLAQLAR	1.072753063	1	1.901862
P51869	**CP4F4 Cytochrome P450 4F4**	**1.204714545**	**1.11E-16**	**4**
P51869	ALPSQHEDDILK	1.220555711	2	2.8785088
P51869	NISLMTLDSLQK	1.058019067	2	3.6509552
P51869	TLDFIDVLLLTK	2.184786884	2	3.8001792
P51869	WQDLASGGSAR	0.940670217	2	2.4971282
P51886	**LUM Lumican**	**0.889479469**	**0.1605535**	**4**
P51886	LDGNPLTQSSLPPDMYECLR	0.767367563	2	2.6440642
P51886	NNQIDHIDEK	1.165048519	2	3.3304877

P51886	SIPTVNENLENYYLEVNK	1.348841187	2	4.1315484
P51886	SLQDLQLANNK	0.818826848	2	2.9636085
P52296	**IMB1 Importin subunit beta_1**	**1.103483648**	**0.0216844**	**4**
P52296	AAVENLPTFLVELSR	1.378361871	2	3.2608097
P52296	TVSPDRLELEAAQK	1.036896022	2	3.3249218
P52296	VLANPGNSQVAR	1.098743451	2	3.5163949
P52296	VQHQDALQISDVVMASLLR	1.320875594	2	2.4733174
P52303	**AP1B1 AP_1 complex subunit beta_1**	**0.882151668**	**0.1766628**	**2**
P52303	NINLIVQK	0.800656942	1	2.0266507
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.099051634	3	4.7753263
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**1.175225195**	**9.9E-20**	**2**
P52504	IIACDGGGGALGHPK	1.152469637	2	3.5218101
P52504	VYINLDKETK	1.474147069	2	2.980612
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**0.979872358**	**0.4326043**	**5**
P52555	FDTQYPYGEK	0.995439769	2	2.5458915
P52555	GQGVYLGMPGCLPAYDALAGQFIEASSR	1.508061617	3	4.1417117
P52555	ILDQGEDFPASELAR	1.086711415	2	4.6385603
P52555	QGQDGLSGVK	0.893111761	2	2.661386
P52555	SLNILTAFR	1.273464495	2	2.5293961
P52631	**STAT3 Signal transducer and activator of transcription 3**	**1.142556624**	**0.7664655**	**2**
P52759	**UK114 Ribonuclease UK114**	**1.194364167**	**0.0529708**	**6**
P52759	AAGCDFTNVVK	0.957989401	2	3.342603
P52759	AAYQVAALPK	1.044513462	2	2.4653811
P52759	IEIEAIAVQGPFTTAGL	1.213908058	1	3.5522799
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	0.803334629	2	4.4336696
P52759	TTVLLADINDFGTVNEIYK	1.236366349	2	5.159482
P52759	TYFQGNLPAR	1.0643645	2	2.5947976
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.21526882**	**0.7683882**	**2**
P52845	CKEDAIFNR	1.206994377	2	2.3759308
P52845	SGSTWIGEIVDMIYK	1.216752987	2	2.9321198
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.060950518**	**0.2505128**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	1.054054005	2	4.0602736
P52847	FLAGNVAYGSWFDHVK	0.428630345	2	3.637759
P52847	IEEFQSRPCDIVIPTYPK	1.051339927	3	4.5211015
P52847	IVHHTSFEVMK	2.065575555	2	2.8724577
P52847	NYFTMTQSEK	0.988247956	1	2.7680941
P52847	SGVELLKK	1.09421875	2	2.3628166
P52847	THLPIDLLPK	0.960907287	3	3.6248887
P52847	TLDEHTLER	1.076041474	2	2.8638341
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.295606443**	**5.551E-15**	**38**
P52873	ADEAYLIGR	1.071955909	1	2.1010771
P52873	ADFAQACQDAGVR	0.997809893	2	4.6432037
P52873	AEAEAQAEELSFPR	1.110244188	2	4.6917896
P52873	AGTHILCIK	1.42529322	2	2.845639
P52873	ALAVSDLNR	1.162978473	2	2.754179
P52873	AYSEALAAFGNGALFVEK	1.39124165	2	3.7143006
P52873	AYVEANQMLGDLIK	0.791366402	2	4.687202
P52873	DAHQSLLATR	0.947350495	1	3.271965
P52873	DFTATFGPLDSLNTR	0.808583846	2	3.752677
P52873	DMAGLLKPAACTMLVSSLR	0.924868339	2	3.689877
P52873	ENGVDAVHPGYGFLSER	1.277931372	2	3.1556602
P52873	FIGPSPEVVR	1.074112788	2	2.3227389
P52873	FLYECPWR	1.033729704	1	2.1402457
P52873	GANAVGYTNYPDNVVFK	1.13646565	2	4.4634571
P52873	GLAPVQAYLHIPDIIK	1.227619473	2	3.157716

P52873	GQIGAPMPGK	0.736192644	2	2.4333091
P52873	GTPLDTEVPLER	1.048564872	2	3.7145276
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.675631996	2	5.6806703
P52873	HIEVQILGDQYGNILHLYER	1.435768131	3	6.6732078
P52873	HYFIEVNSR	1.244471685	2	2.4883997
P52873	IAEEFEVELER	0.976444642	2	3.1922312
P52873	IEGRPGASLPPLNLK	1.183288784	2	3.5359554
P52873	INGCAIQCR	1.135419473	2	2.9577415
P52873	IVGDLAQFMVQNGLSR	1.352805759	2	2.8800275
P52873	LDNASAFQGAVISPHYDSLLVK	1.072578651	2	5.7765312
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	0.99864373	4	6.3476367
P52873	NHQGLLLMDTTFR	1.097540672	2	2.9068096
P52873	QKADEAYLIGR	1.070236382	2	2.3431599
P52873	QVFFELNGQLR	0.942465951	2	3.0477431
P52873	QVGYENAGTVEFLVDK	1.113612548	2	3.9146514
P52873	SGEGMGIR	0.867560944	2	2.6147976
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.425288911	2	4.5660658
P52873	TVAVYSEQDTGQMHR	1.202530742	2	4.5630579
P52873	VFDYSEYWEGAR	1.128241642	2	4.3109879
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.194894512	2	4.3138661
P52873	VVEIAPATHLDPQLR	1.126246027	2	4.4727139
P52873	VVHSYEELEENYTR	1.186607072	2	5.2491622
P52873	YSLEYYMGLAEELVR	1.18469028	3	4.9174814
P52925	**HMGB2 High mobility group protein B2**	**1.158447667**	**0.0055074**	**2**
P52925	KHPDSSVNFAEFSK	1.25681253	2	2.8417795
P52925	SEHPGLSIGDTAK	1.154730178	2	3.0700426
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**0.812844134**	**5.931E-11**	**4**
P53395	LREELKPVALAR	1.333631348	2	2.6855814
P53395	LSDIGEGIR	0.774537279	2	2.4730592
P53395	LSEVVGSGK	1.00781756	1	1.929827
P53395	SYLENPAFMLLDLK	2.424924476	2	4.3345594
P53987	**MOT1 Monocarboxylate transporter 1**	**1.059852393**	**0.662334**	**4**
P53987	DGKEDETSTDVDEKPK	1.096051858	2	5.0428181
P53987	DGKEDETSTDVDEKPKK	1.352532051	3	4.9425883
P53987	ETQSPAPLQNSSGDPAEEESPV	1.096475094	2	5.2925968
P53987	SDANTDLIGGSPK	0.906186417	2	3.9002271
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**0.944461797**	**0.5785908**	**2**
P54313	ACGDSTLTQITAGLDPVGR	0.983041022	2	4.4568653
P54313	TFVSGACDASIK	0.921605874	2	3.0376058
P54319	**PLAP Phospholipase A_2_activating protein**	**1.037497074**	**0.9554391**	**3**
P54319	IGDVVGSSGANQQTSGK	1.056484421	2	4.4971046
P54319	TGDLGDINAEQLPGR	1.017003036	2	3.354496
P54319	YVPGTSGPSNTVQTADPFTGAGR	1.059152701	2	3.924144
P54822	**PUR8 Adenylosuccinate lyase**	**1.149272675**	**0.1874731**	**2**
P54822	KVDIEVLSVLASLGASVHK	1.266129214	3	3.8575506
P54822	VLSQQAAAVVK	1.125245857	2	2.8383608
P54921	**SNAA Alpha_soluble NSF attachment protein**	**0.963550898**	**0.3641891**	**5**
P54921	AIDIYEQVGTSAMDSPLLK	1.078421065	2	4.5153823
P54921	HDAATCFVDAGNAFK	1.345090577	2	2.9943001
P54921	IEEACEIYAR	0.641331496	2	2.4634502
P54921	NSQSFFSGLFGGSSK	1.05009353	2	3.1457901
P54921	TIQGDEEDLR	1.086580856	2	2.4075785
P55006	**RDH7 Retinol dehydrogenase 7**	**1.076470044**	**8.159E-09**	**11**
P55006	LETVILDVTK	1.023487801	2	3.6622121

P55006	TESIVAATQWVK	1.035879689	2	3.9760861
P55006	TNVTNMER	0.948645398	2	2.7620466
P55006	TNVTNMER+Oxidation(6)	1.456446867	2	2.5039496
P55006	TSDRLETVILDVTK	1.128449585	3	4.5854106
P55006	VAIIEPGGFK	1.214453676	2	2.3017344
P55006	VLAACLTEK	1.227591312	2	3.1401925
P55006	VVNIASTMGR	1.131378475	2	3.4898469
P55006	VVNIASTMGR+Oxidation(8)	1.093586547	2	2.7359459
P55006	YGVEAFSDSLR	1.385608677	2	3.7563388
P55006	YVFITGCDSGFGNLLAR	1.429182906	2	4.420186
P55007	**BART1 Protein BART_1**	**1.235651146**	**0.537719**	**2**
P55007	MILMYEEKNKNTR+Oxidation(1)	0.989505894	2	2.3633804
P55007	YNSDEDLQSKLESSR	1.370870744	2	2.5442035
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.154240124**	**0.9998401**	**3**
P55051	LTDSQNFDEYMK	1.079361772	2	3.9235952
P55051	QVGNVTKPTVIISQEGGK	1.23347248	2	3.4454844
P55051	WDGKETNCVR	1.136761098	2	2.56056
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**0.891323483**	**0.0217587**	**6**
P55053	FDETTADGR	0.707479132	2	2.5899682
P55053	KTETVCTFTDGALVQHQK	0.863641494	3	5.6755095
P55053	LVESHGFEDYMK	1.024730797	2	3.3589003
P55053	MGAMAKPDCIITLDGNNLTVK	0.769128755	3	3.6650534
P55053	MVVECVMNNAICTR	0.678235696	2	3.3658652
P55053	TETVCTFTDGALVQHQK	0.781695312	2	4.5332747
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.312308471**	**9.9E-20**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.04325986	2	3.7241383
P55159	IFFYDSENPPGSEVLR	1.295286428	2	5.9950795
P55159	IQSILSEDPK	1.382492748	2	3.1342616
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.821572324	3	4.4558253
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	1.41998095	3	6.1740952
P55159	VVADGFDFANGIGISLDGK	1.192788187	2	4.8107467
P55159	YVYIAELLAHK	1.383497734	2	2.9661148
P55260	**ANXA4 Annexin A4**	**1.017801231**	**0.9961462**	**3**
P55260	AEIDMLDIPANFK	1.017683817	1	2.3181043
P55260	GAGTDEGCLIEILASR	1.168453258	2	3.7385829
P55260	GLGTDEDAIIGVLACR	0.944876229	2	3.9080589
P55770	**NH2L1 NHP2_like protein 1**	**1.144684416**	**0.1673296**	**2**
P55770	LLDLVQQSCNYK	1.175305404	2	3.8025312
P55770	QQIQSIQQSIER	1.179973914	2	2.8953185
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.096598872**	**0.0122152**	**3**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.08588248	2	4.3318505
P56399	IFQNAPTDPTQDFSTQVAK	1.32886725	2	4.5040793
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.04371594	3	4.418961
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.067729908**	**0.7483977**	**4**
P56522	AVPTGDVEDLPCGLLLSSVGYK	2.67747589	2	2.9344864
P56522	NVINTFTQTAR	1.068315673	2	2.8506556
P56522	TATEKPGVEEAAR	0.940190592	2	3.0775113
P56522	TDITEVALGVLR	0.876876091	2	3.4354682
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**0.945485772**	**0.7139088**	**13**
P56574	ATDFVVDR	0.948897545	2	2.3911653
P56574	DLAGCIHGLSNVK	0.851604384	2	3.7367878
P56574	DQTNDQVTIDSALATQK	0.552718783	2	3.9193273
P56574	FKDIFQEIFDK	0.929494415	2	3.5140176
P56574	GKLDGNQDLIR	1.133642867	2	3.3516204
P56574	IKVEKPVVEMDGDEMTR	1.246317035	3	3.4182315

P56574	LDGNQDLIR	0.80956464	2	2.4494672
P56574	LIDDMVAQVLK	1.00507454	2	4.1257811
P56574	LNEHFLNTTDFLDTIK	1.204486547	2	4.4279923
P56574	NILGGTVFR	0.992515912	2	2.7059493
P56574	SSGGFVWACK	1.082073223	2	2.8579586
P56574	TIEAEAAHGTVTR	0.881816338	2	3.8738496
P56574	VCVQTVESGAMTK	0.945570984	2	3.692461
P56593	**CP2AC Cytochrome P450 2A12**	**1.152510346**	**0.0722322**	**3**
P56593	MLQGTCGAPIDPTIYLSK	1.067570324	2	4.7334065
P56593	NRQPQYEDHMK	1.412415969	3	3.4586835
P56593	NRQPQYEDHMK+Oxidation(10)	1.314374711	3	3.4189866
P56656	**CP239 Cytochrome P450 2C39**	**1.184566413**	**0.9275284**	**5**
P56656	EHQESLDVTNPR	0.918687564	2	3.698303
P56656	IKEHQESLDVTNPR	1.022609556	2	5.0222163
P56656	NYLIPK	0.970892074	1	2.0448534
P56656	VCAGEGLAR	1.016446791	2	2.3613904
P56656	VQEEIDHVIGR	1.210616356	2	3.4337957
P56812	**PDCD5 Programmed cell death protein 5**	**1.096208068**	**0.8111545**	**3**
P56812	HGDPGDAAQQEAK	1.107113362	2	4.2027082
P56812	NSILAQVLDQSAR	0.873521304	2	3.1123714
P56812	VSEQGLIEILEK	1.039847858	2	3.0754209
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.903316955**	**0.8931412**	**7**
P57093	AISCHYGSSDCK	0.857388837	2	3.4779897
P57093	EVKPPGMTVMKDVAIAKQGYAPSER	1.148648172	2	2.3774557
P57093	IQDFQQNEELFR	1.281051194	2	3.2345893
P57093	KFYEENGFLVIK	1.038703795	2	3.1511891
P57093	NLVSDDDIQR	0.922890848	1	2.529604
P57093	NNGCLVVLPGTHK	1.086988745	2	2.4178429
P57093	YCALPQIVK	1.170200471	1	2.0691731
P57113	**MAAI Maleylacetoacetate isomerase**	**1.060055298**	**9.9E-20**	**11**
P57113	AITSGFNALEK	1.073563417	2	2.8596876
P57113	ALLALEAFQVSHPCR	1.242327832	2	4.3320394
P57113	DGGQQFSEEFQTLNPMK	0.974217024	2	5.0297098
P57113	FKVDLSPYPTISHINK	1.161794942	2	4.8236203
P57113	GIDYEIVPINLIK	1.137669304	2	4.1092372
P57113	IDGITIGQSLAILEYLEETRPIPR	1.305708284	4	4.8790998
P57113	MISDLIASGIQPLQNLSVLK	1.424598305	2	5.5983315
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(1)	1.353029419	2	5.4226651
P57113	QVGQENQMPWAQK	0.836123845	2	3.942328
P57113	VDLSPYPTISHINK	1.015695445	2	3.74631
P57113	YCVGDEVSMADVCLAPQVANAER	1.061804711	3	5.941505
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.054884099**	**0.9453524**	**2**
P57722	ESTGAQVQVAGDMLPNSTER	0.878876251	2	5.4303188
P57722	INISEGNCPER	1.068390785	2	3.4429958
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**1.063060194**	**0.9994635**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	1.038350936	3	5.0633931
P58321	WLPLEANPEVTNQFLK	1.100159585	2	4.0619311
P58751	**RELN Reelin**	**1.176129669**	**0.7628198**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**1.13699149**	**0.7221722**	**11**
P58775	AISEELDNALNDITSL	1.28235461	2	3.540751
P58775	ATDAEADVASLNR	0.901306721	2	3.6562676
P58775	DAQEKLEQAEK	0.809877284	2	2.8491571
P58775	KATDAEADVASLNR	0.761953298	2	3.3755982
P58775	LDKENAIDR	0.992999877	2	2.3891304
P58775	LKGTEDEVEK	1.140311825	2	2.7525253
P58775	MELQEMQLK	0.523812834	2	2.5185893

P58775	QLEEEQQALQK	0.984101853	2	3.3100908
P58775	SLEAQADKYSTK	1.191712293	2	2.8726659
P58775	TIDDLEDEVYAQK	0.184378529	2	3.9577899
P58775	YSESVKDAQEK	0.21385161	2	3.0102768
P59242	**CING Cingulin**	**1.191025479**	**0.4485071**	**2**
P59242	LGQEQQALNR	1.191726902	2	2.5163338
P59242	LQGLEQEAENK	1.055911761	2	2.9783039
P59470	**RPC2 DNA_directed RNA polymerase III subunit RPC2**	**0.926215939**	**0.7711596**	**2**
P59470	MPIMLRSSNCVLTGK+Oxidation(1)	1.053972731	2	2.5370247
P59470	NAKCTLKR	0.88471441	2	2.3269634
P59759	**MKL2 MKL/myocardin_like protein 2**	**1.060976982**	**0.9591282**	**2**
P59759	LVEVLK	1.22196091	1	2.0176327
P59759	QIEELK	0.984981218	1	2.0621221
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.098693408**	**0.3678892**	**3**
P59999	ELLLQPVTISR	0.900944121	2	2.4513776
P59999	HNKPEVEVR	0.780139316	2	2.5247922
P59999	VLIEGSINSVR	1.101408094	2	2.9430902
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.147796822**	**2.862E-07**	**6**
P60335	AITIAGVPQSVTECVK	1.050678349	2	3.2874677
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	1.408679833	4	5.6444211
P60335	IITLTGPTNAIFK	1.494342936	2	2.9606309
P60335	LVVPATQCGSLIGK	1.550837523	2	3.0355265
P60335	QICLVMLETLSQSPQGR	1.446436917	2	2.43015
P60335	VMTIPYQPMPASSPVICAGGQDR	1.18661287	2	4.0545473
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.069145825**	**3.345E-05**	**5**
P60843	ATQALVLAPTR	1.314999377	1	2.1677508
P60843	GFKDQIYDIFQK	0.923118412	2	3.4422021
P60843	KEELTLEGIR	1.200272426	2	2.3673937
P60843	KGVAINMVTEEDKR	1.049091425	3	3.9422662
P60843	LQMEAPHIIVGTPGR	1.288057217	2	3.4959714
P60868	**RS20 40S ribosomal protein S20**	**1.343960868**	**2.346E-13**	**2**
P60868	DTGKTPVEPEVAIHR	1.028455747	3	3.9364765
P60868	LIDLHSPSEIVK	1.4112121	2	2.9073479
P60892	**PRPS1 Ribose_phosphate pyrophosphokinase 1**	**1.062234687**	**0.9209906**	**2**
P60892	FSNQETCVEIGESVR	1.091704308	2	2.774756
P60892	NCTIVSPDAGGAK	1.000137151	2	2.3135772
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.241599908**	**1.064E-07**	**4**
P60901	AINQGGLTSVAVR	1.246070062	2	3.9530482
P60901	GKDCAVIVTQK	1.097271447	2	3.1631305
P60901	ITENIGCVMTGMTADSR	0.781635943	2	4.3872924
P60901	LLDSSTVTHLFK	1.490763268	2	2.9234257
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.203058245**	**0.1074748**	**2**
P61087	GEIAGPPDTPYEGGR	1.204192522	2	2.9885628
P61087	VDLVDENFTELR	1.084093464	2	2.5729604
P61107	**RAB14 Ras_related protein Rab_14**	**1.227247211**	**0.0016523**	**4**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	1.28453601	3	3.8042853
P61107	NLTNPNTVIILIGNK	1.242075248	2	3.7842216
P61107	SCLLHQFTEK	1.176164873	2	3.0617027
P61107	TGENVEDAFLEAAKK	1.314871305	3	3.6937156
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.241414333**	**0.1129436**	**2**
P61222	NTVANSPQTLLAGMNK	1.242664113	2	2.9048851
P61222	NVEDLSGGELQR	1.161564055	2	2.6257193
P61314	**RL15 60S ribosomal protein L15**	**1.325639949**	**1.716E-08**	**5**
P61314	FFEVILIDPFHK	1.223860215	3	3.8674307
P61314	GATYGKPVHHGVNQLK	1.388215447	2	4.4650087
P61314	SLQSVAEER	1.058465472	2	2.8870354
P61314	VLNSYWVGEDSTYK	1.124613934	2	4.0384727

P61314	YIQELWR	0.955505084	2	2.4825182
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**0.984759303**	**0.5039939**	**4**
P61459	AVGWNELEGR	0.924757445	2	2.9974527
P61459	LDHHPEWFNVYNK	1.207157777	3	5.1240754
P61459	LSAEERDQLLPNLR	1.00779995	3	4.0991344
P61459	VHITLSTHECAGLSER	1.611072339	2	3.7424397
P61589	**RHOA Transforming protein RhoA**	**1.445933017**	**5.124E-12**	**6**
P61589	HFCPNVPIILVGNK	1.935703899	2	3.1640682
P61589	HFCPNVPIILVGNKK	1.114300956	3	3.9405117
P61589	IGAFGYMECSAK	1.521859401	2	3.0026391
P61589	KKLVIVGDGACGK	0.877632239	2	2.4288435
P61589	MKQEPVKPEEGR	1.143521221	3	3.5016856
P61589	MKQEPVKPEEGR+Oxidation(1)	1.444607635	2	3.5013025
P61751	**ARF4 ADP_ribosylation factor 4**	**1.07970205**	**1.291E-06**	**5**
P61751	ILMVGLDAAGK	1.368514683	2	2.4596725
P61751	IQEGAAVLQK	1.059230816	2	2.5625358
P61751	LGEIVTTIPTIGFNVETVEYK	1.428938426	3	4.5753403
P61751	NICFTVWDVGGQDK	1.213710953	2	4.0319123
P61751	QDLPNAMAISEMTDK	1.249545557	2	3.4628851
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.000328523**	**0.761471**	**2**
P61805	ADFQGISPER	1.101794329	1	1.9533098
P61805	FLEEYLSSTPQR	0.999270252	2	3.7408538
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.039887327**	**0.9999824**	**3**
P61924	AILILDNDGDR	0.990830048	2	2.9014289
P61924	GEDVPLTEQTVSQVLQSAK	1.054236945	2	5.1393366
P61924	YYDDTYPSVK	0.977250999	2	2.4749811
P61972	**NTF2 Nuclear transport factor 2**	**1.183831557**	**0.3007314**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	1.197546043	3	5.4194193
P61972	NINDAWVCTNDMFR	1.306074132	2	3.0427666
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.044616297**	**5.436E-06**	**11**
P61980	GSDFDCELR	0.936718487	2	2.4605658
P61980	GSYGDLGGPIITTQVTIPK	0.970863573	2	4.680757
P61980	IDEPLEGSEDR	0.932049902	2	3.3728824
P61980	IILDLISESPIK	1.271131267	2	3.9274206
P61980	IITITGTQDQIQNAQYLLQNSVK	1.164989596	3	6.6848388
P61980	LFQECCPHSTDR	1.210708006	2	3.5599697
P61980	LLIHQSLAGGIIGVK	1.967298829	2	2.5879219
P61980	NTDEMVELR	0.882533596	2	2.4274039
P61980	RSRNTDEMVELR	0.888092965	2	2.3252239
P61980	TDYNASVSVPDSSGPER	0.99870274	2	4.652391
P61980	VVLIGGKPDR	1.117049698	2	2.5356698
P61983	**1433G 14_3_3 protein gamma**	**1.029514383**	**0.0005005**	**4**
P61983	AYSEAHEISK	1.206059981	2	3.3527133
P61983	NVTELNEPLSNEER	0.956873705	2	4.7601933
P61983	TAFDDAIAELDTLNEDSYK	1.015362215	2	5.556982
P61983	YLAEVATGEK	0.862701773	2	2.731077
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.912462513**	**0.5392002**	**4**
P62076	CIGKPGGSLDNSEQK	0.934525853	2	4.2358899
P62076	KCIGKPGGSLDNSEQK	0.970430142	2	4.3050356
P62076	VQIAVANAQELLQR	0.924840514	2	4.4091892
P62076	YMDAWNTVSR	0.75880915	2	3.0985444
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**0.883160312**	**0.5825454**	**2**
P62078	FIDTTLAITGR	0.883802859	2	2.5658054
P62078	TENCLSSCVDR	0.797870655	2	2.3236451

P62083	**RS7 40S ribosomal protein S7**	**1.134081329**	**9.9E-20**	**5**
P62083	AIIIFVPVPQLK	1.09429215	2	3.7495964
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.627864043	3	5.0231171
P62083	KAIIIFVPVPQLK	1.235274517	2	3.626477
P62083	LDGSRLIK	1.022919875	2	2.3329945
P62083	TLTAVHDAILEDLVFPSEIVGK	1.380352652	2	5.05687
P62161	**CALM Calmodulin**	**1.125698886**	**8.926E-13**	**4**
P62161	DGNGYISAAELR	0.838166946	2	2.6664729
P62161	EADIDGDGQVNYEEFVQMMTAK	2.074730015	2	4.8969932
P62161	EAFSLFDKDGDGTITTK	1.105880821	2	4.3336844
P62161	VFDKDGNGYISAAELR	1.134058593	2	4.3563089
P62193	**PRS4 26S protease regulatory subunit 4**	**1.035220483**	**0.5688233**	**4**
P62193	APQETYADIGGLDNQIQEIK	1.028050467	2	4.9751182
P62193	AVANQTSATFLR	1.069677698	2	2.6022294
P62193	NQEQMKPLEEK	1.166547269	2	2.9134171
P62193	TMLELLNQLDGFDSR	1.172569242	2	3.9990983
P62198	**PRS8 26S protease regulatory subunit 8**	**1.173684198**	**0.0082827**	**4**
P62198	EVIELPVKHPELFEALGIAQPK	1.106439671	3	3.9031229
P62198	LEGGSGGDSEVQR	1.174866469	2	3.5338531
P62198	TMLELLNQLDGFEATK	1.381705096	2	3.3688982
P62198	VPDSTYEMIGGLDKQIK	1.478167196	2	2.3364069
P62243	**RS8 40S ribosomal protein S8**	**1.034964746**	**0.9713571**	**8**
P62243	ADGYVLEGK	0.935297931	2	2.380846
P62243	IIDVVYNASNNELVR	1.056678132	2	4.1635861
P62243	ISSLLEEQFQQGK	1.237913049	2	3.9909363
P62243	KYELGRPAANTK	1.139494787	2	3.7524095
P62243	LDVGNFSWGSECCTR	1.181985022	2	3.9081399
P62243	LTPEEEEILNK	1.075659083	2	3.2481289
P62243	NCIVLIDSTPYR	1.169919325	2	3.3326809
P62243	YELGRPAANTK	1.022606954	2	3.2282128
P62246	**RS15A 40S ribosomal protein S15a**	**1.109817797**	**0.0001791**	**3**
P62246	HGYIGEFEIIDDHR	1.174167732	2	4.2392812
P62246	MNVLADALK	0.962883102	2	2.780021
P62246	WQNNLLPSR	1.272604802	2	2.6722381
P62250	**RS16 40S ribosomal protein S16**	**1.085562631**	**0.3134755**	**5**
P62250	ALVAYYQK	1.097568687	1	2.3889127
P62250	GGGHVAQIYAIR	0.900475899	2	2.6433566
P62250	LLEPVLLLGK	1.269163074	2	2.7239387
P62250	TLLVADPR	1.082901597	2	2.4527628
P62250	VNGRPLEMIEPR	1.110666841	2	2.6091042
P62260	**1433E 14_3_3 protein epsilon**	**1.19706238**	**2.677E-13**	**7**
P62260	AAFDDAIAELDTLSEESYK	1.423975739	2	6.1608129
P62260	HLIPAANTGESK	1.040886608	2	3.5065713
P62260	IISSIEQK	1.159418015	2	2.79423
P62260	LICCDILDVLDK	2.225035468	2	4.0626078
P62260	YDEMVESMK	0.609155229	2	2.4849439
P62260	YLAEFATGNDR	0.720437103	2	2.7964292
P62260	YLAEFATGNDRK	1.124174485	2	2.7208512
P62271	**RS18 40S ribosomal protein S18**	**1.080763556**	**4.963E-09**	**4**
P62271	AGELTEDEVER	1.131264804	2	3.4836252
P62271	LREDLER	1.193054462	1	2.0053933
P62271	VLNTNIDGR	1.029899366	2	3.0360246
P62271	YSQVLANGLDNK	1.216794574	2	3.7743433
P62278	**RS13 40S ribosomal protein S13**	**1.47239667**	**5.156E-12**	**4**
P62278	GLAPDLPEDLYHLIK	1.488607165	2	2.9708231
P62278	GLTPSQIGVILR	0.996535681	2	2.7605765
P62278	KGLTPSQIGVILR	0.925460298	3	3.6716721

P62278	LILIESR	1.257654397	1	1.9359918
P62329	**TYB4 Thymosin beta_4**	**1.177974337**	**9.9E-20**	**4**
P62329	ETIEQEKQAGES	1.227172324	2	3.0808911
P62329	KTETQEKNPLPSK	1.19354658	2	3.4598823
P62329	NPLPSKETIEQEK	1.146164844	2	3.007745
P62329	TETQEKNPLPSK	1.191095242	2	3.7958081
P62332	**ARF6 ADP_ribosylation factor 6**	**0.640022701**	**0.0383086**	**2**
P62332	FNVWDVGGQDK	0.548723703	2	3.0028684
P62332	LGQSVTTIPTVGFNVETVTYK	0.994929983	2	2.4096544
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.00225624**	**0.1891681**	**6**
P62334	ALQSVGQIVGEVLK	1.018225881	2	2.4170883
P62334	AVASQLDCNFLK	0.788278727	2	2.4407804
P62334	EVIELPLTNPELFQR	0.895870073	2	3.2072315
P62334	GCLLYGPPGTGK	0.762038428	2	2.512974
P62334	HGEIDYEAIVK	1.005207091	2	3.7524467
P62334	IHIDLPNEQAR	1.272406749	2	2.3539696
P62425	**RL7A 60S ribosomal protein L7a**	**1.581981053**	**3.828E-11**	**10**
P62425	AGVNTVTTLVENK	1.119865565	2	3.858449
P62425	AGVNTVTTLVENKK	1.079585563	2	2.8430297
P62425	HWGGNVLGPK	1.252279387	1	2.684365
P62425	KVVNPLFEK	1.419878081	2	2.3428042
P62425	LKVPPAINQFTQALDR	1.505926002	3	4.6548839
P62425	NFGIGQDIQPK	0.996448848	2	3.1645997
P62425	TCTTVAFTQVNSEDK	1.354003993	2	3.7361493
P62425	TCTTVAFTQVNSEDKGALAK	1.177643224	2	4.0671997
P62425	VAPAPAVVK	1.172988097	1	1.9723141
P62425	VPPAINQFTQALDR	1.119296441	2	3.4076838
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.104791074**	**9.9E-20**	**15**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.251793636	3	5.2215838
P62630	GNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.258021244	6	4.526238
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.347066046	4	5.9389672
P62630	MDSTEPPYSQK	1.049653774	2	3.6655228
P62630	MDSTEPPYSQK+Oxidation(1)	1.224716246	2	3.2710059
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.082362525	3	6.2714586
P62630	RGNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.112815894	5	4.6392989
P62630	RYEEIVK	1.071113542	2	2.662003
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.216721437	3	5.2119579
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(15)	1.158670644	3	3.7916381
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(9)	1.146789513	3	3.425503
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.090001267	2	5.6017222
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(10)	1.042900718	3	4.6399751
P62630	YEEIVK	1.060590512	1	1.9888475
P62630	YYVTIIDAPGHR	1.103255216	2	3.5113943
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.017722912**	**0.0025799**	**6**
P62632	EHALLAYTLGVK	1.204461395	1	3.5903571
P62632	IGGIGTVPVGR	1.248516341	2	3.6358693
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.075252565	3	5.8582258
P62632	QLIVGVNK	1.144848301	1	2.5206676
P62632	STTTGHLIYK	1.026472715	2	3.1452363
P62632	THINIVVIGHVDSGK	1.064733234	2	5.640542
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.010907752**	**0.9993516**	**2**
P62634	CGETGHVAINCSK	0.991889851	2	4.4759364
P62634	CYSCGEFGHIQK	1.068109181	2	3.115871
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.265884576**	**9.9E-20**	**5**
P62703	FDTGNLCMVTGGANLGR	1.121134954	2	5.0723715

P62703	GIPHLVTHDAR	1.372945688	2	2.3590553
P62703	LSNIFVIGK	1.512031487	2	3.2097974
P62703	TDITYPAGFMDVISIDK	1.309818923	2	5.1467571
P62703	VNDTIQIDLETGK	1.165363929	2	4.450449
P62752	**RL23A 60S ribosomal protein L23a**	**1.219341891**	**9.9E-20**	**6**
P62752	LAPDYDALDVANK	1.034534289	2	3.7478812
P62752	LDHYAIIK	1.111138524	2	2.644944
P62752	LYDIDVAK	1.06264466	1	1.9720618
P62752	NKLDHYAIIK	1.358287471	2	2.7641203
P62752	VNTLIRPDGEK	1.127534949	2	3.2320578
P62752	VNTLIRPDGEKK	1.349529406	2	2.9129987
P62755	**RS6 40S ribosomal protein S6**	**1.271051048**	**0.0290562**	**4**
P62755	DIPGLTDTTVPR	0.810078555	2	2.6605208
P62755	LIEVDDER	1.032914936	2	2.7643921
P62755	LNISFPATGCQK	1.287489401	2	3.2455266
P62755	NKEEAAEYAK	1.113799942	2	2.5111701
P62775	**MTPN Myotrophin**	**1.049016873**	**0.9838522**	**2**
P62775	GADINAPDKHHITPLLSAVYEGHVSCVK	1.059115762	4	5.2252269
P62775	NGDLDEVKDYVAK	1.04900446	2	3.2404528
P62804	**H4 Histone H4**	**1.164325332**	**2.261E-07**	**8**
P62804	DAVTYTEHAK	0.776071308	2	2.8810012
P62804	DNIQGITKPAIR	0.88546258	2	3.4155931
P62804	ISGLIYEETR	1.256365887	2	3.6449301
P62804	KTVTAMDVVYALK	1.067555256	2	2.4992566
P62804	RISGLIYEETR	1.177629576	2	2.3063223
P62804	TVTAMDVVYALK	1.094156224	2	4.0448174
P62804	TVTAMDVVYALK+Oxidation(5)	1.24789357	2	2.853513
P62804	VFLENVIR	1.051612765	2	3.2653804
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**1.108279416**	**0.6543848**	**2**
P62815	AVVQVFEGTSGIDAK	1.063032894	2	3.2821467
P62815	NFITQGPYENR	1.208437828	2	2.4801321
P62832	**RL23 60S ribosomal protein L23**	**1.002200791**	**9.9E-20**	**2**
P62832	GSAITGPVAK	0.811279691	2	2.788821
P62832	ISLGLPVGAVINCADNTGAK	1.607411079	2	4.7771382
P62845	**RS15 40S ribosomal protein S15**	**1.067907496**	**0.9982872**	**2**
P62845	DMIILPEMVGSMVGVYNGK	0.922493047	2	3.1096122
P62845	TFNQVEIKPEMIGHYLGEFSITYKPVK	1.045708076	4	5.1009755
P62853	**RS25 40S ribosomal protein S25**	**1.50816482**	**9.9E-20**	**2**
P62853	GGDAPAAGEDA	2.137721721	1	2.2018144
P62853	LNNLVLFDK	1.380492419	2	2.8672566
P62856	**RS26 40S ribosomal protein S26**	**1.03144391**	**0.4870869**	**2**
P62856	DISEASVFDAYVLPK	1.009288232	2	3.0337
P62856	NIVEAAAVR	1.129613641	2	3.048341
P62859	**RS28 40S ribosomal protein S28**	**1.075665882**	**0.9826673**	**2**
P62859	EGDVLTLLESER	1.005458161	2	3.7979515
P62859	VEFMDDTSR	0.939803213	2	2.3280103
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.159162769**	**0.7397561**	**2**
P62870	ADDTFEALR	1.103336386	2	2.6204312
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.120778623	3	4.4089241
P62890	**RL30 60S ribosomal protein L30**	**1.048612842**	**1.811E-06**	**3**
P62890	LVILANNCPALR	0.909474837	2	3.0670886
P62890	TGVHHYSGNNIELGTACGK	1.053307635	2	5.7094779
P62890	VCTLAIIDPGDSDIIR	1.741954822	2	4.1317172
P62898	**CYC Cytochrome c_ somatic**	**1.02574126**	**1.336E-11**	**6**
P62898	ADLIAYLK	0.978121682	2	2.8897057
P62898	GITWGEDTLMEYLENPK	1.315371084	2	5.2277541
P62898	GITWGEDTLMEYLENPKK	1.453328938	2	4.6543503

P62898	KTGQAAGFSYTDANK	1.188912813	2	3.9479218
P62898	TGPNLHGLFGR	1.036174351	2	3.3805418
P62898	TGQAAGFSYTDANK	1.018546982	2	4.3239975
P62902	**RL31 60S ribosomal protein L31**	**1.021472574**	**0.9807122**	**3**
P62902	LYTLVTYVPVTTFK	1.254763579	2	3.1998858
P62902	NLQTVNVDEN	1.033739165	1	2.4211674
P62902	SAINEVVTR	0.953503606	2	2.5622592
P62907	**RL10A 60S ribosomal protein L10a**	**1.108034671**	**1.632E-05**	**6**
P62907	AVDIPHMDIEALK	1.066206266	2	2.6901319
P62907	FSVCVLGDQQHCDEAK	1.217773361	2	4.4026856
P62907	ILGPGLNK	1.671594489	1	1.932413
P62907	KYDAFLASESLIK	1.082985545	2	3.3165989
P62907	VLCLAVAVGHVK	0.696755994	2	3.2250612
P62907	YDAFLASESLIK	0.908723713	2	3.1146114
P62909	**RS3 40S ribosomal protein S3**	**1.224779382**	**0.0008023**	**10**
P62909	AELNEFLTR	1.08355645	2	2.6232431
P62909	DEILPTTPISEQK	1.259339197	2	3.0582807
P62909	ELAEDGYSGVEVR	0.950532804	2	3.3263149
P62909	ELTAVVQK	1.018834504	1	2.0989029
P62909	FGFPEGSVELYAEK	1.739743211	2	3.9310389
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.132739071	3	5.1732907
P62909	GCEVVVSGK	1.083369926	2	2.5812972
P62909	GGKPEPPAMPQPVPTA	1.217369035	2	4.0479603
P62909	GLCAIAQAESLR	1.146163786	2	3.2472086
P62909	TEIIILATR	1.262423181	2	3.1536396
P62912	**RL32 60S ribosomal protein L32**	**1.257930863**	**9.9E-20**	**2**
P62912	GQILMPNIGYGSNK	1.021971152	2	2.6645832
P62912	SYCAEIAHNVSSK	1.2604263	2	4.2784605
P62914	**RL11 60S ribosomal protein L11**	**0.995566139**	**0.9999996**	**2**
P62914	VLEQLTGQTPVFSK	1.006109586	2	4.0569468
P62914	YDGIILPGK	0.992816717	2	3.2706776
P62919	**RL8 60S ribosomal protein L8**	**1.106868159**	**0.001854**	**3**
P62919	ASGNYATVISHNPETK	1.174865014	2	4.4921694
P62919	AVVGVVAGGGR	1.112241065	2	3.3479333
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.035376611	3	5.4397044
P62944	**AP2B1 AP_2 complex subunit beta**	**1.643812338**	**0.0118433**	**2**
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.536690274	3	3.6491566
P62944	LQNNNVYTIAK	1.139695741	2	3.0004807
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.99042522**	**0.9999059**	**7**
P62959	AQVAQPGGDTIFGK	0.99615895	2	4.9686379
P62959	CAADLGLK	0.856670486	2	2.5077736
P62959	CLAFHDISPQAPTHFLVIPK	0.951217663	3	3.7087729
P62959	HISQISVADDDDESLLGHLMIVGK	0.898524874	3	7.645215
P62959	IIFEDDR	1.084078658	2	2.6505537
P62959	KHISQISVADDDDESLLGHLMIVGK	1.052837649	3	5.0907326
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.985558854	3	4.0859442
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**0.981669036**	**0.9999984**	**4**
P62961	EDGNEEDKENQGDETQGQQPPQR	0.992556561	3	5.0048161
P62961	GAEAANVTGPGGVPVQGSK	0.930363602	2	4.9897423
P62961	NEGSESAPEGQAQQR	0.847043668	2	5.1295171
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	0.975590914	4	5.4695416
P62963	**PROF1 Profilin_1**	**1.174886974**	**0.3688024**	**5**
P62963	DSLLQDGEFTMDLR	0.823821774	2	3.8875971
P62963	DSPSVWAAVPGK	1.194628825	2	2.9324615
P62963	SSFFVNGLTLGGQK	1.208673604	2	3.9279907
P62963	STGGAPTFNVTVTMTAK	1.048500634	2	3.2958148
P62963	TFVSITPAEVGVLVGK	1.141728382	2	5.0999384

P63018	**HSP7C Heat shock cognate 71 kDa protein**	**0.981044629**	**9.9E-20**	**22**
P63018	ARFEELNADLFR	1.352121372	3	3.8895326
P63018	DAGTIAGLNVLR	0.734738687	2	3.4250066
P63018	FDDAVVQSDMK	0.993411509	2	3.2683487
P63018	FEELNADLFR	0.934937433	2	3.1515381
P63018	FELTGIPPAPR	1.035746161	2	2.7169712
P63018	IINEPTAAAIAYGLDK	1.232821556	2	5.532402
P63018	IINEPTAAAIAYGLDKK	1.892881616	2	4.1716661
P63018	LLQDFFNGK	1.422914218	2	2.7076049
P63018	MKEIAEAYLGK	1.115034839	2	3.4408495
P63018	MVNHFIAEFK	1.179667829	2	3.1790609
P63018	NQTAEKEEFEHQQK	1.190734263	2	5.2484622
P63018	NQVAMNPTNTVFDAK	1.032945645	2	5.0752649
P63018	NQVAMNPTNTVFDAK+Oxidation(5)	1.386417845	2	4.2319078
P63018	NSLESYAFNMK	1.508568266	2	3.9348495
P63018	RFDDAVVQSDMK	1.025300699	2	3.4363465
P63018	SFYPEEVSSMVLTK	1.102662011	2	5.2039518
P63018	SINPDEAVAYGAAVQAAILSGDK	1.296808402	2	6.2623596
P63018	SQIHDIVLVGGSTR	1.085110085	2	4.8682423
P63018	STAGDTHLGGEDFDNR	1.002949975	2	4.3105059
P63018	TVTNAVVTVPAYFNDSQR	1.189568068	3	4.3949914
P63018	VCNPIITK	1.080677864	2	2.4342749
P63018	VQVEYKGETK	1.366058334	2	2.4746616
P63025	**VAMP3 Vesicle_associated membrane protein 3**	**0.693006258**	**0.0038581**	**2**
P63025	ADALQAGASQFETSAAK	0.681347713	2	4.6791935
P63025	LQQTQNQVDEVVDIMR	0.915654699	2	3.6110547
P63029	**TCTP Translationally_controlled tumor protein**	**1.058793769**	**0.9999997**	**4**
P63029	DLISHDELFSDIYK	0.957060841	2	3.9767611
P63029	EIADGLCLEVEGK	0.98172353	2	2.8290348
P63029	GKLEEQKPER	1.151775084	2	3.4129744
P63029	VKPFMTGAAEQIK	1.004382813	2	2.5138819
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.216369789**	**2.461E-09**	**5**
P63036	HYNGEAYEDDEHHPR	1.32936869	3	4.9674244
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.295167349	3	4.1678872
P63036	QISQAYEVLADSK	1.124475943	2	2.5795858
P63036	TIVITSHPGQIVK	1.059567828	2	3.4852259
P63036	VNFPENGFLSPDK	1.009151045	2	3.1411097
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.026833811**	**9.9E-20**	**35**
P63039	AAVEEGIVLGGGCALLR	0.960018687	2	5.7084923
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(18)	1.016687362	3	4.4069347
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(3)	1.054039949	3	3.7540221
P63039	CEFQDAYVLLSEK	1.802843555	2	4.5365367
P63039	CIPALDSLKPANEDQK	1.051357534	2	3.9247737
P63039	DDAMLLKGK	0.918820038	1	1.9218683
P63039	DDAMLLKGKGDK+Oxidation(4)	1.033087197	2	2.3318388
P63039	DIGNIISDAMK	0.849326857	1	2.0510762
P63039	DMAIATGGAVFGEEGLNLNLEDVQAHDLGK	0.917961847	3	4.1070609
P63039	GIIDPTK	1.012644959	1	1.9477044
P63039	GVMLAVDAVIAELK	0.913418771	2	2.3629444
P63039	GVMLAVDAVIAELKK	1.090128115	2	4.5702124
P63039	GYISPYFINTSK	1.258672061	2	2.7426131
P63039	IGIEIIK	1.030113604	2	2.8145397
P63039	ILQSSSEVGYDAMLGDFVNMVEK	2.364107557	3	6.1464653
P63039	IQEITEQLDITTSEYEK	0.923678867	2	6.0875449
P63039	IQEITEQLDITTSEYEKEK	1.035588941	2	5.1339245
P63039	ISSVQSIVPALEIANAHR	1.360114668	2	4.4726515
P63039	KISSVQSIVPALEIANAHR	1.492746171	3	3.924005

P63039	KPLVIIAEDVDGEALSTLVLNR	1.102675346	2	6.0990224
P63039	LSDGVAVLK	1.01070722	2	2.9942133
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.118608281	2	6.4969463
P63039	NAGVEGSLIVEK	0.968593695	2	3.5093243
P63039	QSKPVTTPEEIAQVATISANGDK	1.008735384	2	3.5507524
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.049464215	3	4.936254
P63039	RGVMLAVDAVIAELKK	1.025185687	3	5.8963332
P63039	TLNDELEIIEGMK	0.99521003	2	4.848938
P63039	TLNDELEIIEGMK+Oxidation(12)	0.888935611	2	2.7471945
P63039	TVIIEQSWGSPK	0.906654234	2	4.2812858
P63039	VGEVIVTK	0.948349095	2	3.0949507
P63039	VGEVIVTKDDAMLLK	1.117675808	2	3.7880013
P63039	VGGTSDVEVNEK	0.972217248	2	3.9184175
P63039	VGGTSDVEVNEKK	1.105188625	2	3.7344117
P63039	VGLQVVAVK	0.987392879	2	3.2611842
P63039	VTDALNATR	0.984728914	2	3.5225611
P63102	**1433Z 14_3_3 protein zeta/delta**	**1.284005365**	**9.9E-20**	**8**
P63102	DICNDVLSLLEK	1.587820877	2	3.9289744
P63102	FLIPNASQPESK	1.063147774	2	3.4743376
P63102	GIVDQSQQAYQEAFEISK	1.046658824	2	5.7452412
P63102	KGIVDQSQQAYQEAFEISK	1.569680417	2	5.0402784
P63102	SVTEQGAELSNEER	1.049361127	2	5.1006937
P63102	TAFDEAIAELDTLSEESYK	1.710854922	2	5.8376088
P63102	YDDMAACMK	0.76846491	2	2.5962276
P63102	YLAEVAAGDDKK	1.28606324	2	3.7243221
P63159	**HMGB1 High mobility group protein B1**	**1.155509839**	**9.9E-20**	**5**
P63159	GEHPGLSIGDVAK	1.07903703	2	3.1563993
P63159	IKGEHPGLSIGDVAK	1.562010398	2	3.8718331
P63159	KHPDASVNFSEFSK	1.260420703	3	4.1091971
P63159	KLGEMWNNTAADDKQPYEK	0.961629518	3	4.3144817
P63159	LGEMWNNTAADDKQPYEK	0.888069587	3	3.5967724
P63174	**RL38 60S ribosomal protein L38**	**1.240106452**	**4.782E-06**	**3**
P63174	IEEIKDFLLTAR	0.888175012	2	3.0395534
P63174	KIEEIKDFLLTAR	1.248023009	2	4.5923743
P63174	YLYTLVITDKEK	1.23679629	2	2.7079444
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.285679395**	**2.718E-12**	**13**
P63245	DETNYGIPQR	0.844175936	2	3.0087554
P63245	DGQAMLWDLNEGK	0.939454303	2	3.3668201
P63245	FSPNSSNPIIVSCGWDK	1.089470188	2	4.2693491
P63245	GHNGWVTQIATTPQFPDMILSASR	1.313705225	3	4.2883968
P63245	HLYTLDGGDIINALCFSPNR	1.376266902	2	5.6068654
P63245	IIVDELKQEVISTSSK	1.300356146	2	4.1291423
P63245	LWDLTTGTTTR	1.004905466	2	2.9555225
P63245	LWNTLGVCK	1.357655892	2	2.3280504
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.104869115	2	4.7245622
P63245	VWNLANCK	0.826718099	2	2.6776764
P63245	VWQVTIGTR	0.687900686	2	2.9055097
P63245	YTVQDESHSEWVSCVR	1.153130347	2	3.3094907
P63245	YWLCAATGPSIK	1.351853657	2	3.1587722
P63259	**ACTG Actin_ cytoplasmic 2**	**1.098042342**	**9.9E-20**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.803646094	3	5.7417817
P63259	DLYANTVLSGGTTMYPGIADR	0.946523364	2	5.769021
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.808950054	2	4.3508053
P63259	GYSFTTTAER	1.07990828	2	3.3703327
P63259	KDLYANTVLSGGTTMYPGIADR	0.967103293	2	6.1623163
P63259	LCYVALDFEQEMATAASSSSLEK	2.285763569	2	5.209465

P63259	QEYDESGPSIVHR	1.048630267	3	3.5173144
P63259	VAPEEHPVLLTEAPLNPK	1.294041923	2	4.642065
P63269	**ACTH Actin_ gamma_enteric smooth muscle**	**0.72617463**	**0.4112287**	**2**
P63269	DLYANNVLSGGTTMYPGIADR	0.76043507	2	3.4360912
P63269	KDLYANNVLSGGTTMYPGIADR	0.707261784	2	5.080255
P63324	**RS12 40S ribosomal protein S12**	**1.046550504**	**0.3651088**	**3**
P63324	KVVGCSCVVVK	0.951467836	2	2.6290138
P63324	LGEWVGLCK	1.16458733	2	3.1466057
P63324	VVGCSCVVVK	1.007184376	2	3.0318539
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**0.94140351**	**0.9480321**	**2**
P63331	GAGYTFGQDISETFNHANGLTLVSR	0.92336997	3	3.3323886
P63331	YSFLQFDPAPR	0.966562785	2	3.2614548
P67779	**PHB Prohibitin**	**0.833804052**	**0.0025647**	**10**
P67779	AAELIANSLATAGDGLIELR	0.881539123	2	5.3507032
P67779	AAIISAEGDSK	0.767447446	2	2.4031215
P67779	DLQNVNITLR	0.825895852	2	3.7842362
P67779	FDAGELITQR	0.92631448	2	3.74664
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.092203352	3	5.3266864
P67779	IYTSIGEDYDER	1.306070389	2	3.4090874
P67779	KLEAAEDIAYQLSR	0.92111836	2	4.9123335
P67779	NVPVITGSK	0.822102103	1	2.470448
P67779	QVSDDLTER	0.910131903	2	2.6317451
P67779	VLPSITTEILK	0.867142665	2	2.519778
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.21599766**	**0.001988**	**4**
P68037	ADLAEEYSK	0.892443881	2	2.5831816
P68037	GQVCLPVISAENWKPATK	0.830905351	2	3.2663851
P68037	IEINFPAEYPFKPPK	1.224284414	2	3.694463
P68037	TDQVIQSLIALVNDPQPEHPLR	1.211961894	2	4.8700342
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.010613815**	**0.9992475**	**5**
P68101	AGLNCSTETMPIK	1.050055885	2	2.860801
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.817202049	3	4.2061687
P68101	HVAEVLEYTKDEQLESLFQR	1.0043235	3	3.5398185
P68101	TEGLSVLNQAMAVIK	1.07399803	2	3.8015592
P68101	VVTDTDETELAR	1.020638194	2	3.1654072
P68136	**ACTS Actin_ alpha skeletal muscle**	**0.915472093**	**5.922E-06**	**16**
P68136	AGFAGDDAPR	0.995697625	2	3.3633769
P68136	AVFPSIVGRPR	1.074145814	2	2.9519794
P68136	CPETLFQPSFIGMESAGIHETTYNSIMK	0.816960256	3	4.2048135
P68136	DLYANNVMSGGTTMYPGIADR	0.661750803	2	3.7263663
P68136	DSYVGDEAQSK	0.651668329	2	3.0556407
P68136	DSYVGDEAQSKR	0.89910707	2	2.4665463
P68136	EITALAPSTMK	0.882976992	1	2.9491303
P68136	EITALAPSTMK+Oxidation(10)	0.918357929	2	2.766233
P68136	GYSFVTTAER	0.927647541	2	3.8014989
P68136	IWHHTFYNELR	1.646294415	3	3.7126708
P68136	KDLYANNVMSGGTTMYPGIADR	0.854895526	2	5.2012329
P68136	QEYDEAGPSIVHR	0.879555803	2	3.1483238
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	1.18939632	3	6.7191687
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(29)	1.190475869	3	5.5131197
P68136	VAPEEHPTLLTEAPLNPK	1.099835234	2	4.5360603
P68136	YPIEHGIITNWDDMEK	1.099042327	2	4.5458283
P68255	**1433T 14_3_3 protein theta**	**1.032121796**	**0.1272415**	**5**
P68255	AVTEQGAELSNEER	0.855776925	2	4.6284924
P68255	SICTTVLELLDK	1.073060498	2	2.7704866
P68255	TAFDEAIAELDTLNEDSYK	1.32110901	2	4.521142

P68255	VISSIEQK	1.240017053	1	2.1964095
P68255	YLIANATNPESK	0.939078346	2	3.5744784
P68511	**1433F 14_3_3 protein eta**	**1.158269297**	**0.4944032**	**2**
P68511	AVTELNEPLSNEDR	1.155881776	2	4.8462176
P68511	NSVVEASEAAYK	1.13662354	2	3.1739252
P69527	**AMPO Aminopeptidase O**	**1.334919219**	**0.0276389**	**2**
P69527	LQQLAHRCFELVK	0.95381157	2	2.3653719
P69527	WHRLQDELQNSPEGMQVLRPNK	1.430161146	2	2.4934442
P69897	**TBB5 Tubulin beta_5 chain**	**1.150357731**	**1.123E-07**	**4**
P69897	ALTVPELTQQVFDAK	1.159971853	2	3.4194956
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	0.87903047	3	5.7774816
P69897	ISVYYNEATGGK	1.130744812	2	2.8884158
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.318648657	2	5.2249813
P70372	**ELAV1 ELAV_like protein 1**	**1.028836849**	**0.9370979**	**3**
P70372	SLFSSIGEVESAK	0.971030121	2	3.4155982
P70372	TNLIVNYLPQNMTQEELR	1.028971137	2	4.1598611
P70372	VLVDQTTGLSR	1.073500501	2	2.5621226
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.316482453**	**0.2712092**	**2**
P70470	ASFSQGPINSANR	1.248910964	2	2.8958008
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.318324061	3	3.9737589
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**1.397043801**	**9.9E-20**	**12**
P70473	ADVLLEPFR	1.060792352	2	3.5411174
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	1.276740962	3	5.555346
P70473	DYGFSQEEIHQLHSDR	1.135898033	2	5.006958
P70473	GLGLESEELPSQMSIEDWPEMK	1.2779261	3	4.662272
P70473	GQNLLDGGAPFYTTYK	1.028505173	2	5.2200747
P70473	GSFITDEEQHACPRPAPQLSR	1.171145643	3	3.6244535
P70473	LGSVNHPSHLAR	1.94420004	2	2.9145813
P70473	LQLGPETLR	1.03994825	2	2.416054
P70473	LSGFGQSGIFSK	1.663126279	2	2.7785978
P70473	RDPSVGEHTVEVLK	1.065993157	3	4.3653593
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	1.364787168	4	5.7580404
P70473	TQAMGLWAQPR	0.865417854	2	3.5125608
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**0.885322874**	**0.026417**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.827242108	3	4.7964034
P70552	VLGNNFYEYYVNDPPR	1.366110776	2	3.9697247
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.986392837**	**0.0003373**	**9**
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	1.536106397	3	5.4623342
P70580	EGEEPTVYSDDEEPKDEAAR	0.953804378	2	4.3853645
P70580	FYGPEGPYGVFAGR	1.015548194	2	4.0991187
P70580	GDQPGASGDNDDDEPPPLPR	1.174175375	2	5.144383
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.099677535	3	5.176755
P70580	KFYGPEGPYGVFAGR	1.217053341	2	3.8177502
P70580	LLKEGEEPTVYSDDEEPKDEAAR	1.087998797	3	5.1703539
P70580	RYDGVQDPR	1.24728451	1	2.1815243
P70580	YDGVQDPR	0.927666207	2	3.019558
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.133111217**	**0.5553834**	**10**
P70584	ASSTCQLTFENVK	0.97690478	2	2.8721161
P70584	ASSTCQLTFENVKVPETSVLGK	1.133732985	3	3.6126049
P70584	FAQEQIAPLVSTMDENSK	0.97965986	2	4.3051915
P70584	IFDFQGLQHQVAHVATQLEAAR	1.176729166	3	6.0690918
P70584	IGTIYEGTSNIQLNTIAK	0.992500318	2	4.5536051
P70584	KFAQEQIAPLVSTMDENSK	0.954952284	2	5.4267492
P70584	SGNYYVINGSK	0.968892084	2	2.618047

P70584	SVIQGLFQQGMMGIEVEAK	0.928839422	2	4.4870782
P70584	VDASVALLCDIQNTVINK	1.146059733	2	4.9137325
P70584	YYASEVAGLTTSK	1.071041774	2	4.0603795
P70615	**LMNB1 Lamin_B1**	**1.159626652**	**0.1209243**	**3**
P70615	ALYETELADAR	1.020974441	2	3.2419834
P70615	LSSEMNTSTVNSAR	1.032593949	2	2.9894283
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.284225774	3	3.7961712
P70619	**GSHR Glutathione reductase (Fragment)**	**1.15362194**	**0.7499379**	**2**
P70619	ALLTPVAIAAGR	1.01576828	2	2.726615
P70619	LNNIYQNNLTK	1.195908012	2	3.0539348
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**1.095541584**	**0.9143047**	**2**
P70694	REDIFYTSK	1.088317316	2	3.0603604
P70694	SIGVSNFNR	0.930369089	2	2.3986793
P70712	**KYNU Kynureninase**	**1.103518227**	**1.368E-06**	**8**
P70712	IATELNCDPTDER	2.063266437	2	3.6312544
P70712	IGAYGHEVGK	1.254978647	2	2.8416576
P70712	LLTAILDSTERN	1.58694896	2	3.5405042
P70712	MEDILEVIEK	1.02843715	2	2.6188648
P70712	SILLTGYLEYLLK	1.564994999	2	3.1064823
P70712	TYLEEELDKWAK	0.82846084	2	2.9542179
P70712	VAPVPLYNSFHDVYK	0.613200386	2	3.4208782
P70712	YLNSGAGGLAGAFIHEK	1.226435415	2	4.4541245
P80067	**CATC Dipeptidyl peptidase 1**	**1.294879115**	**2.918E-05**	**5**
P80067	GTDECAIESIAMAAIPIPK	1.199532897	3	4.6978869
P80067	NQESCGSCYSFASLGMLEAR	1.026785096	2	4.8771434
P80067	NSWGSQWGESGYFR	1.00518147	2	3.0316188
P80067	RGTDECAIESIAMAAIPIPK	1.191618934	2	4.4600577
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.245513711	3	5.5624352
P80254	**DOPD D_dopachrome decarboxylase**	**1.626650996**	**0.0323566**	**4**
P80254	FFPLEPWQIGK	1.563284352	2	3.0273597
P80254	FLTEELSLDQDR	1.587690945	2	3.7307301
P80254	LCAATATILDKPEDR	3.309104291	2	4.2331457
P80254	STEPCAHLLISSIGVVGTAEQNR	1.543463727	2	5.4005785
P80299	**HYES Epoxide hydrolase 2**	**1.259001005**	**0.1265742**	**2**
P80299	ATEMGGILVGTPEDPK	1.39033027	2	3.029355
P80299	TEIQNPSVTSK	0.891568328	2	2.9259951
P80313	**TCPH T_complex protein 1 subunit eta**	**1.134541213**	**8.64E-05**	**4**
P80313	ATISNDGATILK	1.067701174	2	2.8375239
P80313	GGAEQFMEETER	1.161395081	2	2.5041282
P80313	QLCDNAGFDATNILNK	0.946535754	2	3.5234752
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.404869734	2	5.069994
P80317	**TCPZ T_complex protein 1 subunit zeta**	**0.92037883**	**0.826503**	**9**
P80317	ALQFLEQVK	1.201501797	2	2.5110168
P80317	AQAALAVNISAAR	0.899922528	2	3.0707939
P80317	DGNVLLHEMQIQHPTASLIAK	1.147590155	3	4.7811332
P80317	GIDPFSLDALAK	1.37583938	2	2.7971058
P80317	HKSETDTSLIR	1.101032358	2	2.6761391
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.155349633	3	5.0385132
P80317	TEVNSGFFYK	1.074176324	2	2.522156
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.018718497	2	4.9626975
P80317	VLAQNSGFDLQETLVK	1.060492116	2	3.4649968
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.929931684**	**0.9588435**	**5**
P81155	LTFDTTFSPNTGK	0.968770047	2	2.6109276
P81155	LTFDTTFSPNTGKK	1.039398459	2	2.8680813
P81155	SCSGVEFSTSGSSNTDTGK	0.750185751	2	2.4169967
P81155	VNNSSLIGVGYTQTLRPGVK	1.041980775	2	3.6138768

P81155	YQLDPTASISAK	0.946567526	2	2.9489324
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.17517464**	**3.963E-14**	**14**
P82995	ELHINLIPNKQDR	0.911854945	2	2.9773793
P82995	ELISNSSDALDK	0.949394108	2	2.7051792
P82995	FYEQFSK	1.131141351	1	2.0467143
P82995	HGLEVIYMIEPIDEYCVQQLK	1.213473704	3	5.5511718
P82995	HIYFITGETK	1.047177515	2	2.9628959
P82995	HLEINPDHSIIETLR	1.116171944	3	4.2889228
P82995	HSQFIGYPITLFVEK	3.476649886	2	3.7105362
P82995	LGIHEDSQNR	1.262761051	3	3.4713297
P82995	NPDDITNEEYGEFYK	1.01794841	2	5.0732331
P82995	RAPFDLFENR	1.366148011	2	2.3648415
P82995	SLTNDWEEHLAVK	1.030024211	2	4.1643367
P82995	TLTIVDTGIGMTK	0.985614068	2	4.3429503
P82995	TLTIVDTGIGMTK+Oxidation(11)	1.223860152	2	3.3894668
P82995	YYTSASGDEMVSLK	1.073566937	2	3.4243467
P83732	**RL24 60S ribosomal protein L24**	**1.076067485**	**0.9981371**	**2**
P83732	AITGASLADIMAK	1.07636136	2	4.6736374
P83732	VELCSFSGYK	1.063770465	2	2.3708348
P83868	**TEBP Prostaglandin E synthase 3**	**1.218651078**	**0.1454499**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.696631203	3	3.3047755
P83868	LTFSCLGGSDNFK	1.21673141	2	2.7685552
P83883	**RL36A 60S ribosomal protein L36a**	**1.237644968**	**0.0005785**	**2**
P83883	HFELGGDK	1.279408048	1	2.3835843
P83883	LECVEPNCR	1.227550674	2	2.3402147
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.153315431**	**0.9964775**	**2**
P83941	AMLSGPGQFAENETNEVNFR	1.096385459	2	5.0185304
P83941	TYGGCEGPDAMYVK	1.123221847	2	3.7887611
P84082	**ARF2 ADP_ribosylation factor 2**	**1.125925976**	**0.9999253**	**2**
P84082	NISFTVWDVGGQDK	0.800385835	2	4.5257974
P84082	QDLPNAMNAAEITDK	1.149679664	2	3.8614039
P84083	**ARF5 ADP_ribosylation factor 5**	**1.16554971**	**0.4751581**	**2**
P84083	DAVLLVFANK	1.174985081	2	2.4875855
P84083	VQESADELQK	1.161296974	2	2.9374371
P84100	**RL19 60S ribosomal protein L19**	**1.289238165**	**0.0013175**	**2**
P84100	LLADQAEAR	1.240135612	2	3.4412928
P84100	VWLDPNETNEIANANSR	0.998601185	2	5.8139515
P84245	**H33 Histone H3.3**	**1.088898282**	**2.46E-07**	**4**
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.515856595	3	5.9670768
P84245	RVTIMPKDIQLAR+Oxidation(5)	1.264053156	2	2.9210317
P84245	STELLIR	1.086442764	2	2.5131984
P84245	YRPGTVALR	1.075252263	2	2.3600163
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.147004009**	**0.4080784**	**4**
P84817	FQSEQAAGSVSK	0.925902056	2	2.9767909
P84817	GIVLLEELLPK	1.303621769	2	2.3172698
P84817	GLLQTEPQNNQAK	1.077854211	2	3.5858557
P84817	KFQSEQAAGSVSK	0.999303354	2	4.0556707
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.903902512**	**0.3901839**	**16**
P85834	AEAGDNLGALVR	0.89991319	2	3.7479541
P85834	DKPHVNVGTIGHVDHGK	0.952548317	3	3.4806321
P85834	DLEKPFLLPVESVYSIPGR	1.296758778	2	3.9183233
P85834	GDECELLGHNK	0.936307387	2	2.5907114
P85834	GEETPVIVGSALCALEQR	0.974070554	2	4.5933414
P85834	GITINAAHVEYSTAAR	1.250414642	2	3.013216
P85834	GTVVTGTLER	0.858215433	2	2.8744488
P85834	HYAHTDCPGHADYVK	0.975946204	2	4.1963453
P85834	KGDECELLGHNK	0.817182999	3	3.9386835

P85834	KYEEIDNAPEER	0.873918778	2	3.5791864
P85834	LLDAVDTYIPVPTR	0.940767765	2	3.9235618
P85834	QIGVEHVVVYVNK	0.763600747	2	2.8580687
P85834	TIGTGLVTDVPAMTEEDK	0.712910771	2	4.1267791
P85834	TIGTGLVTDVPAMTEEDKNIK	0.947730793	2	4.706573
P85834	TVVTGIEMFHK	0.814641473	2	2.4514415
P85834	YEEIDNAPEER	0.895030049	2	3.1851294
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.114327662**	**5.551E-15**	**10**
P85968	AGQAVDDFIEK	1.077997958	2	2.9266326
P85968	CLSSLKEER	1.19030795	2	2.4036045
P85968	FQDTDGKELLPK	1.198244373	2	3.1306384
P85968	GILFVGSGVSGGEEGAR	1.122444879	2	5.0491538
P85968	HEMLPANLIQAQR	1.06443237	2	3.2545779
P85968	LVPLLDTGDIIIDGGNSEYR	1.806368474	2	5.5578961
P85968	NPELQNLLLDDFFK	1.460964479	2	4.7657342
P85968	SAVDDCQDSWR	0.52698355	2	2.9479165
P85968	VGTGEPCCDWVGDEGAGHFVK	1.082980353	3	4.5491652
P85968	YGPSLMPGGNK	0.948221177	1	2.2007372
P85971	**6PGL 6_phosphogluconolactonase**	**1.381338825**	**0.2282776**	**5**
P85971	DLPAATAPAGPASFAR	0.887527086	2	2.414295
P85971	ILEDQESALPAAMVQPR	1.009203344	2	4.1685309
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.335186087	2	4.9904537
P85971	TGALCWFLDEAAAR	1.133323156	2	3.7961793
P85971	WTLGFCDER	1.088702648	2	2.3071623
P85972	**VINC Vinculin**	**0.854313529**	**0.7750318**	**12**
P85972	AIPDLTAPVAAVQAAVSNLVR	0.968971285	2	3.3520925
P85972	AQQVSQGLDVLTAK	0.853444889	2	4.4673338
P85972	AVAGNISDPGLQK	0.837887172	2	3.382884
P85972	GQGASPVAMQK	0.919304727	2	3.0008595
P85972	MLGQMTDQVADLR	1.000415864	2	2.5136566
P85972	NRNFTVGKMSAEINEIIR+Oxidation(9)	1.039838711	2	2.7302399
P85972	QVATALQNLQTK	1.052844346	2	3.7216866
P85972	SLLDASEEAIKK	1.300783011	2	2.6337118
P85972	STVEGIQASVK	0.966468254	2	2.3035593
P85972	TNISDEESEQATEMLVHNAQNLMQSVK	0.973277752	3	4.0442538
P85972	VLQLTSWDEDAWASK	1.447031488	2	3.6682167
P85972	WIDNPTVDDR	0.931623269	2	3.1801152
P85973	**PNPH Purine nucleoside phosphorylase**	**1.411895858**	**3.223E-07**	**12**
P85973	ASHQEVLEAGK	1.058376757	2	3.4210379
P85973	DHINLPGFCGQNPLR	0.996523057	2	4.1037664
P85973	ELQEGTYIMSAGPTFETVAESCLLR	1.046321559	2	5.054266
P85973	FEVGDIMLIR	1.066166674	2	3.6098399
P85973	HRPQVAVICGSGLGGLTAK	1.085093556	3	6.2975354
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.826390837	3	4.7375331
P85973	MLGADAVGMSTVPEVIVAR	1.267075121	2	6.0708618
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(1)	1.279894077	2	5.1184244
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(9)	1.264175762	2	3.744545
P85973	VFGFSLITNK	1.331058306	2	2.8167167
P85973	VFHLLGVDTLVVTNAAGGLNPK	1.367478575	2	5.835546
P85973	VVMDYNNLEK	1.135306483	2	2.6067955
P86048	**RL10L 60S ribosomal protein L10_like**	**1.463269625**	**0.0015074**	**4**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.356727611	3	5.0379767
P86048	GAFGKPQGTVAR	1.143727642	2	3.0435185
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.279161984	3	5.8032589
P86048	VHIGQVIMSIR	1.296902083	2	2.8245225

P86252	**PURA Transcriptional activator protein Pur_alpha (Fragments)**	**1.310506383**	**5.056E-05**	**2**
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	1.213315034	2	4.1713157
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	1.296951323	3	5.0665774
P97310	**MCM2 DNA replication licensing factor MCM2**	**0.890986943**	**0.2009834**	**4**
P97310	EAGRGLGRMR	1.042431493	2	2.547754
P97310	HIESMIRMAEAHARMHLR	0.759887416	2	2.6675837
P97310	LNQMDQDKVAR+Oxidation(4)	0.596743378	2	2.5770395
P97310	MITGLSKDQQIGEK+Oxidation(1)	0.778983709	2	2.4606848
P97323	**F16P3 Fructose_1_6_bisphosphatase isozyme 3 (Fragment)**	**1.020469306**	**1**	**2**
P97323	GNIYSLNEGYAK	1.013183874	2	3.9426315
P97323	KGNIYSLNEGYAK	0.994636502	2	4.2158375
P97384	**ANX11 Annexin A11**	**1.147440361**	**0.6273466**	**2**
P97384	GFGTDEQAIIDCLGSR	0.890213463	2	4.2422791
P97384	SELDLLDIR	1.044832936	2	2.6848454
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.268961988**	**0.1897487**	**8**
P97519	GASGNLATEDLVYMLTGLGIHTGVNLQK	1.268968351	3	3.8920858
P97519	GFEEAVAAGAK	0.893903021	2	3.2017319
P97519	GYVSCALGCPYEGK	1.082271749	2	3.7265177
P97519	KNVNCSIEESFQR	0.938315123	2	3.5616503
P97519	LIDMLSEAGLPVIEATSFVSPK	1.477892587	2	4.8589644
P97519	LLEAGDFICQALNR	1.180640262	2	4.5000749
P97519	NVNCSIEESFQR	0.897016165	2	3.4468606
P97519	WVPQMADHSDVLK	0.616292227	2	3.0139375
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**0.98980755**	**0.9884229**	**5**
P97521	CLLQIQASSGK	0.927378921	2	3.105042
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.2383871	2	3.7918453
P97521	LYQEFGIR	1.098209416	2	2.3556705
P97521	SVHDLSVPR	1.143618952	2	2.5423045
P97521	YSGTLDCAK	0.96751598	2	2.5179191
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**0.975121061**	**9.659E-15**	**15**
P97524	ALHDHLGLR	1.279137809	2	2.416389
P97524	GEVGLLICK	1.161997376	2	2.6179991
P97524	IQDTIEITGTFK	1.036449209	2	2.5040932
P97524	ITELTPFFGYAGGK	0.197182055	2	2.3085413
P97524	MKENYEFNGK	0.965699543	2	3.2566793
P97524	SEVTFTTPAVYIYTSGTTGLPK	0.500479959	2	2.6506903
P97524	SLLHCFQCCGAK	1.693333146	2	3.2953749
P97524	TILHVFLEQAR	1.098494923	2	2.9638743
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	0.713712802	3	5.7891579
P97524	TYVPMTEDIYNAIIDK	1.055314948	2	4.0460181
P97524	VLLASPELHEAVEEVLPTLK	1.270614464	2	3.8673239
P97524	VTLMEEGFNPSVIK	0.696807945	2	3.6768925
P97524	YDVEKDEPVR	1.316786628	2	2.8359509
P97524	YLCNTPQKPNDR	1.338462012	2	3.0403335
P97524	YNATVIQYIGELLR	1.704444595	2	2.7537601
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.00532321**	**3.331E-16**	**8**
P97532	AFGHHSVSLLDGGFR	1.392483956	2	3.4499269
P97532	ALVSAQWVAEALK	0.917067148	2	3.7860308
P97532	AQPEHVISQGR	1.015417223	2	2.7914898
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.737826866	3	6.7665634
P97532	FQGTQPEPR	0.953349573	2	2.9438438
P97532	LLDASWYLPK	1.311759751	2	3.9123125
P97532	THEDILENLDAR	0.995435656	2	3.3755658

P97532	YWLSQNLPISSGK	0.851275639	2	3.6034117
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.14234072**	**0.0629709**	**5**
P97536	EGPAVVGQFIQDVK	0.812214561	2	2.7580276
P97536	ITSEALLVTQQLVK	1.107216083	2	2.3477461
P97536	LGTLSALDILIK	1.532342098	2	2.5343232
P97536	LTLIDPETLLPR	1.324545796	2	2.6806874
P97536	TYIQCIAAISR	1.136650415	2	2.9858198
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.233674272**	**9.9E-20**	**18**
P97562	ATASCTYEGENTVLYLQVAR	1.798397846	2	4.6055145
P97562	ATFADFCAQGAEICR	1.213802553	2	5.0372419
P97562	CSAQTAADFR	0.930361484	2	2.4379942
P97562	DAILLTDAFDFSDHCLNSALGCYDGHVYER	1.457674484	3	4.0450878
P97562	DFSLLPELHALSTGMK	0.860786504	2	2.6080909
P97562	EAFLDLLPLIR	1.026786317	2	2.7111819
P97562	ILEYQTQQQK	1.224929056	2	3.9168999
P97562	KVESIIQSDPVFNLK	1.229430283	2	4.9492264
P97562	LCDLYALHGVLTNSGDFLHDGFLSGAQVDMAR	1.84685428	3	5.6982641
P97562	LDKEPEIQR	1.175911274	3	3.5492175
P97562	LGTPQSNYLGMLVTR	1.680257951	2	3.5153441
P97562	LTNILDGGLPNTVLR	1.406123712	2	4.2507405
P97562	MGLEHIDNGFLQLNHVR	1.374614365	2	4.4231882
P97562	SGVDQHDAWNQTTVIHLQAAK	1.193268742	3	6.2669153
P97562	SLEDHTPLPGITVGDIGPK	1.072262827	2	4.5511804
P97562	SLGSDEQIAK	1.157405172	2	2.8494048
P97562	VESIIQSDPVFNLK	1.071201677	2	4.5715089
P97562	VLDGNVNLSLHGVAMNAIR	1.101226145	2	5.0081358
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.048547135**	**0.6053961**	**3**
P97576	ALADTENLR	1.08929156	2	2.306185
P97576	DLLEVADILEK	1.048395589	2	2.4320302
P97576	EEVSNNNPHLK	1.049620772	2	3.2840991
P97584	**PTGR1 Prostaglandin reductase 1**	**1.103662839**	**0.9699983**	**5**
P97584	ALTDLMNWVSEGK	1.142004501	2	3.6727855
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.130046351	2	4.7416487
P97584	HFEGFPTDSNFELR	0.952184214	2	3.899153
P97584	TGPCPPGPSPEVIIYQQLR	1.059708258	2	4.0441532
P97584	YHEYITEGFEK	1.057509053	2	2.9279969
P97608	**OPLA 5_oxoprolinase**	**1.256797873**	**0.0047185**	**4**
P97608	AGDFGAAFVER	1.12252075	2	2.4371789
P97608	GSILDPSPEAAVVGGNVLTSQR	1.281111069	2	5.0468183
P97608	LLSEDPANYADAPTEGIR	1.128538601	2	3.8446269
P97608	TGDLLEIQQPVDLEALR	1.21071693	2	4.8897362
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.269469204**	**9.9E-20**	**8**
P97612	EVEQLMTPQK	0.592679819	2	2.3235543
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.070009241	3	4.6913409
P97612	GTNCVTSYLTDCETQLSQAPR	1.05418182	2	4.5679779
P97612	GYFGDIWDIILK	1.929461804	2	3.4017351
P97612	LQHEIEMYR	0.953692132	2	2.3767772
P97612	LQSGELSPEAVFFTYLGK	2.081927917	2	4.5237875
P97612	NSVGLPVAVQCVALPWQEELCLR	1.668088718	2	4.1551151
P97612	QGLLYGVPVSLK	0.933673209	2	2.7448077
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.040990739**	**8.928E-07**	**3**
P97700	AVVVNAAQLASYSQSK	1.020369212	2	4.7385373
P97700	LGIYTVLFER	2.464161388	2	3.0584254
P97700	LTGADGTPPGFLLK	1.090337887	2	2.820734
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**1.126859793**	**9.9E-20**	**24**

P97852	AAVAVPSRPPDAVLR	1.256643048	2	2.3278484
P97852	AVANYDSVEAGEK	1.169632834	2	3.8565967
P97852	AYALAFAER	1.390808354	2	3.0639687
P97852	DTTSLNQAALYR	0.86128781	2	2.6582696
P97852	FVYEGSADFSCLPTFGVIVAQK	0.925069611	2	4.8259168
P97852	GALVVVNDLGGDFK	0.979947861	2	3.658643
P97852	GNIMLSQKLQMILK+Oxidation(4)Oxidation(11)	1.308454081	2	2.3397081
P97852	GSSAADKVVEEIR	1.213643025	2	3.1510835
P97852	HVLQQFADNDVSR	1.102575079	2	4.6159368
P97852	ICDFSNASKPK	1.444127198	3	3.7910459
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	1.177289156	3	6.1357455
P97852	IDVVVNNAGILR	1.094199903	2	3.6548004
P97852	ISDEDWDIIQR	0.936863275	2	3.3768086
P97852	KNNIHCNTIAPNAGSR	1.102637598	2	4.782763
P97852	LGLLGLANTLVIEGR	1.660945396	2	3.4073603
P97852	LNPQNAFFSGR	1.353126981	2	2.8304014
P97852	NGSGEVYQGPAK	1.245675223	2	3.5150297
P97852	NNIHCNTIAPNAGSR	1.066986511	2	4.6269903
P97852	SIQESTGGIIEVLHK	1.291189334	2	4.1677556
P97852	SLMSGGLAEVPGLSINFAK	1.09023349	2	4.5973802
P97852	SLMSGGLAEVPGLSINFAK+Oxidation(3)	0.831454783	2	3.5256948
P97852	VLHGEQYLELYKPLPR	1.268883171	2	4.9171314
P97852	VNAVFEWHITK	1.344292589	2	3.1935463
P97852	VVLVTGAGGGLGR	1.115671999	2	4.5549583
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.332120056**	**5.458E-09**	**3**
Q00438	KLPSDVTEGEVISLGLPFGK	1.168715279	2	2.6573019
Q00438	NFQNIFPPSATLHLSNIPPSVSEDDLK	1.810999886	3	3.8161194
Q00438	NNQFQALLQYADPVSAQHAK	1.338109534	2	5.1427135
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.377654022**	**0.5170388**	**4**
Q00PI9	AVEEQGDDQDSEK	1.380428877	2	3.800951
Q00PI9	DLLVQQASQCLSK	1.491404259	2	2.370827
Q00PI9	EEAQPIVTKYK	1.007557093	1	1.9492124
Q00PI9	SGDETPGSEAPGDK	1.23921447	2	2.6872678
Q01177	**PLMN Plasminogen**	**1.356384663**	**0.1334826**	**3**
Q01177	ILGSDVQQIAVTK	1.174130873	2	3.4000752
Q01177	LVLEPNDADIALLK	1.445947235	2	2.649972
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	1.213826596	3	4.9772959
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.047455583**	**0.9998367**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.148750983	2	6.39429
Q01205	NDVITVQTPAFAESVTEGDVR	0.936291037	2	5.4971013
Q01205	NVETMNYADIER	1.086604617	2	3.5192676
Q01205	VEGGTPLFTLR	0.973138815	2	3.3079431
Q01405	**SC23A Protein transport protein Sec23A**	**1.001734493**	**0.0047645**	**4**
Q01405	AETEEGPDVLR	1.000950462	2	3.1701729
Q01405	AVLNPLCQVDYR	1.150512774	2	2.8012679
Q01405	HLLQAPVDDAQEILHSR	1.133830741	3	4.5348568
Q01405	YIDTEHGGSQAR	1.206784959	2	3.4243803
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**1.028262407**	**0.0003629**	**29**
Q02253	AEMEAAVAACK	1.008000789	2	3.9051199
Q02253	AEMEAAVAACK+Oxidation(3)	1.307392442	2	2.8634322
Q02253	AEMEAAVAACKR	1.135537382	2	3.2169638
Q02253	AFPAWADTSILSR	1.170334925	2	4.2023797
Q02253	AISFVGSNQAGEYIFER	1.137865665	2	5.4847693

Q02253	CMALSTAVLVGEAK	0.994437803	2	4.5635958
Q02253	CMALSTAVLVGEAK+Oxidation(2)	1.062026592	2	2.7738929
Q02253	EEDATLSSPAVVMPTMGR	0.789767133	2	4.9084802
Q02253	ENTLNQLVGAAFGAAGQR	0.914983944	2	5.0179563
Q02253	GDTNFYGK	0.964939255	2	2.3952913
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.222705851	2	5.9070816
Q02253	GYENGNFVGPTIISNVKPSMTCYK	1.108367975	2	3.4293299
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.301747374	2	5.5731106
Q02253	KWLPELVER	0.839928687	2	2.3247519
Q02253	LITLEQGK	1.123381166	2	2.8983209
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.471108206	3	4.8217893
Q02253	NHGVVMPDANK	0.92582944	1	3.2806602
Q02253	NHGVVMPDANK+Oxidation(6)	1.288102529	2	3.1134465
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	1.111905644	3	6.381166
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(6)	1.104285102	3	4.8173294
Q02253	QGIQFYTQLK	1.222643191	2	2.8542147
Q02253	SDKWIDIHNPATNEVVGR	1.079830529	2	5.5921898
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.905285883	2	5.4168496
Q02253	TLADAEGDVFR	1.045178146	2	3.5708423
Q02253	VCNLIDSGAK	1.055831486	2	3.4710724
Q02253	VNAGDQPGADLGPLITPQAK	1.003015308	2	5.9996481
Q02253	WIDIHNPATNEVVGR	0.982844997	2	5.1088033
Q02253	WLPELVER	0.984320904	2	2.3146513
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.204098203	3	4.6379933
Q02769	**FDFT Squalene synthase**	**0.912974358**	**0.9835911**	**3**
Q02769	KLEDFVKPENVDVAVK	0.890579669	3	4.2485256
Q02769	TQSLPNCQLISR	0.680965535	2	2.5970662
Q02769	VVLEDFPTISLEFR	1.14215085	2	3.9108241
Q02974	**KHK Ketohexokinase**	**1.187018254**	**8.862E-05**	**9**
Q02974	FGCQVAGK	0.793753068	2	2.8788862
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.175693797	3	5.8630915
Q02974	GGNASNSCTVLSLLGAR	1.11712931	2	4.6608043
Q02974	GNSMQEALR	0.882916343	2	3.1839812
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.067962624	3	5.3071775
Q02974	IEQYNATQPLQQK	1.078506555	2	4.7712679
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.364731229	3	6.3650312
Q02974	TIILYDTNLPDVSAK	1.051953661	2	4.8229461
Q02974	VSVEIEKPR	1.352240654	2	2.4105754
Q03248	**BUP1 Beta_ureidopropionase**	**1.327357427**	**9.9E-20**	**13**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.155065919	2	6.2992635
Q03248	EKLPWTEFAESAEDGLTTR	0.934556377	3	5.0119038
Q03248	ELAEAVKPNYSPNIVK	1.115176395	2	4.3285551
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	1.105223124	3	3.4354622
Q03248	HLPPDDLSQVK	1.065653074	2	2.3069043
Q03248	HNMVVISPILER	1.093530063	3	3.4370394
Q03248	IPLPTSAPVAEQVSALHK	1.314650135	3	5.0664625
Q03248	KHNMVVISPILER	1.074440368	3	3.5250165
Q03248	KHNMVVISPILER+Oxidation(4)	1.139469329	2	2.782517
Q03248	NAAIANHCFTCALNR	1.373941043	2	4.7179766
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.511419337	3	4.8064084
Q03248	VGQEHYPNEFTSGDGK	1.194311109	2	4.4050584
Q03248	VGQEHYPNEFTSGDGKK	1.24839871	3	5.1903768
Q03336	**RGN Regucalcin**	**1.111475893**	**9.9E-20**	**19**
Q03336	CGESPVWEEASK	1.109909302	2	4.5669661
Q03336	CLLFVDIPSK	1.626964687	2	3.2682641
Q03336	DEQIPDGMCIDVEGK	0.791421221	2	4.6349182
Q03336	DYSEMYVTCAR	0.684507348	2	2.5019276

Q03336	FCALNWEDQSVFILAMVDEDKK	3.161940284	3	4.1936593
Q03336	FNDGKVDPAGR	1.144730211	2	2.7162256
Q03336	GIAPYSYAG	1.870277613	2	2.538486
Q03336	HQGSLYSLFPDHSVK	1.639684937	2	4.5976048
Q03336	IECVLR	1.004923564	2	2.4185736
Q03336	KYFDQVDISNGLDWSLDHK	0.994581048	3	5.2056651
Q03336	LWVACYNGGR	1.110017691	2	3.1024957
Q03336	MEKDEQIPDGMCIDVEGK	1.09436664	2	5.2970591
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(1)	1.273533598	2	4.6225829
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(11)	1.331371066	2	2.7157123
Q03336	QSGGYVATIGTK	0.993626411	2	2.7760379
Q03336	VGVDAPVSSVALR	1.162665104	2	3.7155218
Q03336	YFAGTMAEETAPAVLER	1.126290337	2	5.8258934
Q03336	YFAGTMAEETAPAVLER+Oxidation(6)	1.234646674	2	5.4203315
Q03336	YFDQVDISNGLDWSLDHK	1.052413628	2	4.5285082
Q03410	**SYCP1 Synaptonemal complex protein 1**	**0.970651663**	**0.7775538**	**4**
Q03410	ATVDEAVKLQKEIDLR	1.409506882	2	2.3664908
Q03410	ISEEKLLGEVEK	0.933129524	2	2.308816
Q03410	LQDENLK	1.066883444	1	1.9886557
Q03410	NIEELHQENKALK	1.100059948	1	1.908851
Q03626	**MUG1 Murinoglobulin_1**	**1.201702373**	**5.965E-05**	**7**
Q03626	EESSCIHSSCTAER	1.069221745	2	4.145669
Q03626	ESVVFVQTDKPVYKPGQSVK	0.713890495	3	3.4696696
Q03626	GGEFEMMPLGVNK	0.918800904	2	3.1500037
Q03626	LTAQPAPSPEDLALSMGTIK	1.433018665	3	3.9513025
Q03626	NLHPLNELFPLAYIEDPK	1.611578959	3	4.1147532
Q03626	VQTVPLTCNNPK	1.13708333	2	2.7707629
Q03626	VYHKEESSCIHSSCTAER	0.814435712	2	5.4654827
Q04462	**SYVC Valyl_tRNA synthetase**	**1.160914053**	**0.0863643**	**3**
Q04462	ADFPAGIPECGTDALR	0.863149615	2	2.4042079
Q04462	ALNPLEEWLR	1.161046607	2	2.3018289
Q04462	SVTQQPGSEITAPQK	0.991540379	2	3.8938954
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**0.947203878**	**0.4410485**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(1)	1.146104747	2	2.6081522
Q05144	YLECSALTQR	1.037018187	2	3.0004013
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.032074093**	**0.0001322**	**8**
Q06647	FSPLTANLMNLLAENGR	1.343590268	2	3.9645762
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.188786818	2	5.3316293
Q06647	GQILNLEVK	1.11883274	2	2.6649199
Q06647	LGNTQGVISAFSTIMSVHR	1.276031927	3	4.7192335
Q06647	TDPSIMGGMIVR	0.858048943	2	3.2698147
Q06647	TVLNSFLSK	0.975169293	2	2.7549849
Q06647	VSLAVLNPYIK	0.967995133	2	3.671344
Q06647	YATALYSAASK	1.09275903	1	2.1203513
Q07071	**GCKR Glucokinase regulatory protein**	**1.059930346**	**0.0004064**	**12**
Q07071	AAPISCHVQVAHEK	1.074611196	2	4.8035679
Q07071	CQNIQALVHSTVGQSLPAPLKK	1.05526543	3	4.8591132
Q07071	GFLIGDHSDMFNQK	1.125321535	2	2.5675671
Q07071	GLGQKPLYTYLIAGGDR	1.111905032	2	2.6085892
Q07071	LLGQCDAEIFQEEGQIVPTYQR	1.719969539	2	4.9563613
Q07071	LYSESVLTTMLQVAGK	1.141936539	2	3.2973084
Q07071	QEAFVLNPAIGPEGLSGSSR	0.985618638	2	4.2494245
Q07071	TVDQGVVSSQR	1.028885447	2	3.6549759
Q07071	VIPTALLSLLLR	2.202556886	2	3.4090471
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.175394623	2	5.2364168
Q07071	WVLNTVSTGAHVLLGK	1.052602726	2	3.4379346
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.086396516	3	4.0108991

Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.931542183**	**0.2667247**	**8**
Q07116	AVDDSYNVQPDTVAPIWNLR	1.021899913	2	5.1738586
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	0.932491089	3	4.5054493
Q07116	HEVTVTLQCAGNR	1.144364152	2	3.0959871
Q07116	INSQRPFNAEPPPELLTESYITPNPIFFTR	1.703994821	3	4.4771695
Q07116	MSPPLEASDPYSNDPMR	0.531969286	2	3.9383407
Q07116	NHLPVPNLDPDTYR	1.020798555	2	2.7980409
Q07116	VSVESEESYSHWQR	1.036384359	2	4.0365057
Q07116	VVVPGVVGAR	0.900819595	2	2.7468746
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.297371325**	**0.0305496**	**2**
Q07205	AMGPLVLTEVLFDEK	1.474574817	2	3.5494287
Q07205	TVIVNMVDVAK	0.940721479	2	2.3506551
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**1.003327653**	**0.0023168**	**14**
Q07523	ALKEEKPTQSVPVSFPK	1.169487399	2	4.623282
Q07523	ALVITIDTPVLGNR	1.04803372	2	4.0097218
Q07523	ASFCWNDLSLLQSITR	1.601002034	2	4.5891027
Q07523	CMTLSGCQSVAEISPDLIQFSR	1.309554117	2	3.5483444
Q07523	EDAELAMK	1.072352167	1	1.9418131
Q07523	EEKPTQSVPVSFPK	0.968276201	2	2.9446421
Q07523	EVLDILTAELHR	1.039298605	2	3.1739099
Q07523	GEDGVKEVLDILTAELHR	1.551487251	3	5.5453897
Q07523	HNVQGIVVSNHGGR	1.057463554	3	6.2227154
Q07523	NQLNLEANILLK	1.043873002	2	3.6193817
Q07523	QLDEVSASIDALR	1.143580591	2	3.1190197
Q07523	TGTDVLK	0.832790973	2	2.3173862
Q07523	TSWDFIEGEADDGITYSENIAAFK	1.127752378	2	4.4510803
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	1.413389596	3	3.7710004
Q07936	**ANXA2 Annexin A2**	**1.071150457**	**0.9820729**	**4**
Q07936	AEDGSVIDYELIDQDAR	1.037658346	2	3.9010856
Q07936	GLGTDEDSLIEIICSR	1.026729289	2	3.9755836
Q07936	GVDEVTIVNILTNR	0.883956267	2	3.825793
Q07936	TNQELQEINR	1.105925346	2	3.1078367
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.176050194**	**1.695E-06**	**2**
Q07984	FFDEESYSLLR	1.19627126	2	3.1284254
Q07984	NNEDVSIIPPLFTVSVDHR	1.195881836	2	4.2767444
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**1.000321228**	**0.7347801**	**9**
Q08163	ALLVTASQCQQPAGNK	0.989959079	2	4.2245893
Q08163	AYLSIWTELQAYIK	0.864934783	2	2.3013761
Q08163	ELSGLPSGPSVGSGPPPPPPGPPPPPVPTSSGSDDSASR	1.021846978	3	4.7065725
Q08163	LEAVSHTSDMHCGYGDSPSK	0.965034	3	5.0152574
Q08163	LSDLLAPISEQIQEVITFR	1.006616947	2	4.0040836
Q08163	NSLDCEIVSAK	0.848894935	2	2.3519025
Q08163	SALFAQINQGESITHALK	1.124488861	2	4.5649428
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.037899221	2	4.0718517
Q08163	VENQENVSNLVIDDTELK	1.184372204	2	5.1297503
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.125435025**	**2.68E-08**	**3**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	1.064936076	3	4.8486123
Q08415	ILVLNTPNNPLGK	2.100664013	2	3.3861182
Q08415	LGASNDWQLDPAELASK	0.817631529	2	3.9809077
Q09073	**ADT2 ADP/ATP translocase 2**	**0.848360181**	**9.9E-20**	**7**
Q09073	DFLAGGVAAAISK	0.687403275	2	5.010078
Q09073	GLGDCLVK	0.99535403	2	2.8750925
Q09073	GMGGAFVLVLYDEIKK	1.389959888	2	3.615104
Q09073	GTDIMYTGTLDCWR	0.95679043	2	3.5593264
Q09073	KGTDIMYTGTLDCWR	1.036802847	2	4.0316596
Q09073	LLLQVQHASK	1.860811728	2	2.7410066

Q09073	QIFLGGVDKR	1.210095792	2	2.3789258
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.973792172**	**0.9868545**	**9**
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.260602442	3	3.3952732
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	1.017726409	2	3.8936787
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	0.995387477	3	3.4747517
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	0.876491525	3	4.7715173
Q0D2L3	SVDEGLLDSK	0.922198954	1	1.9267424
Q0D2L3	SVDEGLLDSKR	0.974995085	2	3.0795448
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.243862935	2	5.1782093
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	1.258378962	3	5.7594595
Q0D2L3	VVLAEDCWMK	1.054816783	2	2.4059024
Q0VAV2	**EXPH5 Exophilin_5**	**1.253321245**	**0.0238421**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(2)	1.246177239	2	2.5288298
Q0VAV2	SLSDQDPGQEQREEK	1.259104555	2	2.3045316
Q0VGK3	**GLCTK Glycerate kinase**	**1.001495623**	**0.1171887**	**6**
Q0VGK3	ADSDPHGPHTCGHVLNVIIGSNSLALAEAQR	1.026365367	3	4.8208537
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	1.015129949	2	4.8497238
Q0VGK3	GATIQELNTIR	1.012159942	2	2.8682175
Q0VGK3	LHQLAAELQLPDLQLEEALEAVAK	1.65145101	3	3.6100905
Q0VGK3	QLFDSAVGAVQPGPMLQR	0.996610936	2	4.8058043
Q0VGK3	VAAACLTSSTAERPLEEEAK	1.352037725	2	3.2018576
Q0ZHH6	**ATLA3 Atlastin_3**	**0.935552372**	**2.431E-14**	**8**
Q0ZHH6	ALASVLLQDHIR	1.377770022	2	2.6554587
Q0ZHH6	EHQHEEIQNVR	1.045658017	2	3.6059101
Q0ZHH6	EQLQTLIPYVLNPSK	1.215070877	2	3.2664919
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	2.908165959	2	2.3586032
Q0ZHH6	IYQGEDLPHPK	1.167921247	2	2.7885795
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(3)	0.993451256	2	2.4899938
Q0ZHH6	YQQELEEEITELYENFCK	2.266557871	2	5.3272038
Q0ZHH6	YSGQYLELGGAIDSGAAYVLEQASSHIGNSTQAAVR	1.269667721	3	3.3651636
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**1.243450155**	**0.2209137**	**2**
Q10728	QEEKKESEVSR	1.054119854	2	2.3390622
Q10728	SLLEMEKRER+Oxidation(5)	1.23111936	2	2.4004445
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.985163159**	**0.217173**	**25**
Q10758	AEAETMYQIK	1.041194291	2	3.1226988
Q10758	AQYEEIANR	0.910568492	2	3.1660082
Q10758	ATLEAAIADAEQR	0.948513181	2	4.7069149
Q10758	DVDEAYMNKVELESR	2.772159376	2	3.5638745
Q10758	ELQSQISDTSVVLSMDNSR	0.872992995	2	5.9661584
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	0.991075194	2	4.7480907
Q10758	KDVDEAYMNK	1.060931202	2	2.5767381
Q10758	LEGLTDEINFLR	1.04475854	2	4.051198
Q10758	LESGMQNMSIHTK	1.048361599	2	4.1818724
Q10758	LEVDPNIQAVR	0.899682334	2	3.8302729
Q10758	LEVELGNMQGLVEDFK	1.063922279	2	4.9688492
Q10758	LQAEIDALK	1.073289897	2	2.9753063
Q10758	LVSESSDIMSK	0.889083796	2	3.3323247
Q10758	QIHEEEIR	0.981800967	1	2.3162658
Q10758	QLEALGQEK	0.937126865	1	2.1501966
Q10758	SKTEISEMNR	0.966784465	2	3.0839772
Q10758	SKTEISEMNR+Oxidation(8)	1.417701457	2	3.093941
Q10758	SLDMDSIIAEVR	0.946202798	2	4.9394646
Q10758	SNMDNMFESYINNLR	1.368112322	2	4.0559406
Q10758	SRAEAETMYQIK	1.193725677	2	3.441726
Q10758	TEISEMNR	0.866719209	2	2.4447439
Q10758	TEMENEFVLIK	0.998216767	2	3.6518655
Q10758	TEMENEFVLIK+Oxidation(3)	1.095614265	2	2.4087124

Q10758	WSLLQQQK	0.933277429	2	2.9341412
Q10758	YEELQTLAGK	1.056466013	2	3.5622599
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**1.066977261**	**0.9904211**	**6**
Q14DH7	CVPGYNVMILDDNMQK	1.014164428	2	2.6326315
Q14DH7	STLSALVNGKPYK	1.179957018	2	2.4502079
Q14DH7	THFAASVADPER	1.107841276	2	3.6742272
Q14DH7	VDDVINVAGHR	1.050141404	2	3.7452745
Q14DH7	VLAEHGVAALFTAPTAIR	1.202227057	2	4.4512239
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.112398596	2	2.9120989
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**1.064670762**	**9.9E-20**	**10**
Q1HCL7	ASYYEISVDDGPWEK	0.838193928	2	2.5273929
Q1HCL7	LKPVIGVNTDPER	1.552622651	2	2.8849609
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.007131739	3	4.7100177
Q1HCL7	NVEHIIDSLRDEGIEVR	1.377152043	2	3.4555216
Q1HCL7	QGNLTLPLNK	0.962018469	2	2.3382421
Q1HCL7	REYDEETVR	1.026228518	2	2.4480557
Q1HCL7	SEASGPQLLPVR	0.870383274	2	2.9511034
Q1HCL7	SSGLNLCTGTGSK	0.915368123	2	3.8541992
Q1HCL7	VTNEYNESLLYSPEEPK	1.238972549	2	4.4638548
Q1HCL7	YTHSFPEALQK	1.008720785	2	2.5983191
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.114255841**	**0.9539656**	**3**
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	1.022327993	3	3.4421365
Q1JU68	LLDMDGIIVEK	1.022482353	2	2.5557363
Q1JU68	NQLTAMSSVLAK	1.118155929	2	2.6500676
Q29RW1	**MYH4 Myosin_4**	**0.969765305**	**0.9982488**	**14**
Q29RW1	ANLMQAEIEELR	1.403027699	2	3.0106771
Q29RW1	ELENEVENEQKR	2.539262311	2	2.987618
Q29RW1	LAQESTMDIENDKQQLDEK	3.238416479	2	4.9408793
Q29RW1	LQDAEEHVEAVNSK	2.989636951	2	4.5620232
Q29RW1	LQDLVDKLQTK	1.044070603	1	1.938905
Q29RW1	MEGDLNEMEIQLNHANR	1.144252947	2	4.3416791
Q29RW1	NAYEESLDQLETLK	0.784268793	2	4.5788836
Q29RW1	NAYEESLDQLETLKR	0.903549725	2	4.0542212
Q29RW1	SELQASLEEAEASLEHEEGK	1.227193555	2	5.2872615
Q29RW1	SNAACAALDKK	0.755328174	2	2.4514601
Q29RW1	TEGGATVTVK	1.029254373	2	2.6918921
Q29RW1	TKLEQQVDDLEGSLEQEK	0.727193041	2	5.6553082
Q29RW1	TKLEQQVDDLEGSLEQEKK	2.007400973	3	5.1082854
Q29RW1	VRELENEVENEQKR	1.816489115	3	3.7075274
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**1.146176966**	**0.6541089**	**3**
Q2EMV9	LIISEVLK	1.113023624	2	2.5172019
Q2EMV9	LQEELTR	1.162721296	1	2.1176682
Q2EMV9	VLVEFEKESLNIAGK	1.250231706	2	2.586993
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**0.88936366**	**0.0008454**	**8**
Q2V057	ASIYGQFVAGETAEEVR	0.9805181	2	4.2211547
Q2V057	EDCTQPDYEATSR	0.900679137	2	3.5425134
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.18761921	2	4.8077049
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.129998781	2	5.7599578
Q2V057	REQALLSQELWR	1.066055996	2	3.0952234
Q2V057	SIPYGCLEEVIPYLIR	1.53223335	2	4.1155434
Q2V057	SVTQLHGKEDCTQPDYEATSR	0.885257535	3	4.6104064
Q2V057	TSEAWYEGNLSAMLHCVDLSR	0.788038489	2	2.6297503
Q32LZ8	**PLPL5 Patatin_like phospholipase domain_containing protein 5**	**0.90804083**	**0.7917798**	**2**
Q32LZ8	FYGSSSGALNAMAIVFGK	0.974156424	2	2.41137

Q32LZ8	NFIVTDFATR	0.897573297	1	1.9015322
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**0.997880914**	**0.9094454**	**2**
Q3B7D0	HCDDSYTPQDK	1.010908171	2	3.4069324
Q3B7D0	TCAEAVVPSYVPIVK	0.851343865	2	2.6849611
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.089088321**	**0.062101**	**4**
Q3B7U9	SCSQVLEHQPDNIK	1.062211396	2	4.1763515
Q3B7U9	TAEDGPDLEMLSGQER	1.029967482	2	4.1231556
Q3B7U9	VDMTCEEEEELLQLK	1.419450274	2	4.1400018
Q3B7U9	VLAQQGEYSEAIPILR	1.020496407	2	3.7766604
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**1.13439289**	**0.8292281**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	1.110354912	2	4.6673646
Q3B8Q2	GIYAYGFEKPSAIQQRAIK	1.084765234	2	2.4085159
Q3KR86	**IMMT Mitochondrial inner membrane protein (Fragment)**	**0.93805892**	**0.6433813**	**9**
Q3KR86	AVDEAADALLK	1.237877451	2	2.5426533
Q3KR86	EIAGATPYITAAEEK	0.802691478	2	3.0444267
Q3KR86	GIEQAVQSHAVAEEEAR	1.013815532	2	4.865006
Q3KR86	QTITAQNAAVQAVK	0.919195422	2	4.237041
Q3KR86	SEIQAEQDR	0.908350754	2	2.7994187
Q3KR86	SLEDALNQTATVTR	0.965919083	2	3.9845688
Q3KR86	TSSAEMPTIPLGSAVEAIR	0.963441324	2	3.845381
Q3KR86	VVSQYHELVVQAR	1.154287514	2	3.5638661
Q3KR86	YSTSSSSGVTAGK	0.701363881	2	2.7749963
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.237329037**	**0.3775787**	**2**
Q3KRD8	HGLLVPNNTTDQELQHIR	1.105309557	3	5.1027617
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.069437774	3	4.4025826
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.039366139**	**0.9314445**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.080528389	2	2.6643276
Q3KRE0	ISVLEALR	1.011513233	2	2.6262798
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**0.916975158**	**0.4401772**	**3**
Q3KRE8	ALTVPELTQQMFDSK	1.028507583	2	2.752089
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.75399939	3	4.3838582
Q3KRE8	FWEVISDEHGIDPTGSYHGDSDLQLER	0.825852849	3	3.3713079
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**1.04061766**	**0.7025315**	**3**
Q3MIB4	GTSLQSTILGVIPNTPDPASDSQDLPPLHR	1.185462986	3	3.5931063
Q3MIB4	MEIIQVPGYTQEEK	1.12647967	2	2.4991846
Q3MIB4	TVGVNNPVFLLDEVDK	0.981101037	2	2.6168673
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**1.030593795**	**0.6863988**	**7**
Q3MIE0	DGQEGIEAFIQK	0.6050882	2	3.4177194
Q3MIE0	SDILHEAESEDLK	0.992396859	2	3.4632676
Q3MIE0	SDILHEAESEDLKVIIISAEGPVFSSGHDLK	1.014292413	4	5.7589026
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.07871996	2	4.1718054
Q3MIE0	VALEMLFTGEPISAQEALR	1.185900238	2	4.0623159
Q3MIE0	VIIISAEGPVFSSGHDLK	0.995038508	2	4.3347321
Q3MIE0	VVPEEQLEEEATR	0.954755081	2	3.7635009
Q3MIF4	**XYLB Xylulose kinase**	**1.265450517**	**0.3799393**	**6**
Q3MIF4	FNADNMEVSAFPGDVEIR	1.138883185	2	4.3376102
Q3MIF4	IRDESASCSWNK	1.029829276	2	4.0870953
Q3MIF4	LGSPVPSCSVVGAISSYYVQR	1.571891692	2	3.257169
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	1.0223649	2	4.2276249
Q3MIF4	VVAFTGDNPASLAGMR	1.026793309	2	3.9131114
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	1.277330937	2	5.1585407
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.133512564**	**0.0149564**	**4**
Q3T1J1	EDLRLPEGDLGK	1.103465003	2	2.8214815

Q3T1J1	EDLRLPEGDLGKEIEQK	1.162175998	2	4.5172548
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.369802032	2	5.0849156
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.386534239	3	3.6343074
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.094945366**	**0.2462911**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.225507812	3	3.9893563
Q3T1K5	FTVTPSTTQVVGILK	1.095081695	2	3.8273704
Q3T1K5	LLLNNDNLLR	1.029589936	2	2.6358628
Q3TVW5	**TCHP Trichoplein keratin filament_binding protein**	**1.41987659**	**0.0001508**	**2**
Q3TVW5	RTQEIQEELEVDGRILQALLEK	1.478632967	2	2.6839876
Q3TVW5	TELGRFLKHQYNAQLNR	1.419869512	2	2.9140615
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**0.881658868**	**0.0112474**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	0.821088156	2	2.4442785
Q3U0J8	QIELDLLRTLPNNK	1.244818828	2	2.7583845
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.121461178**	**0.4488634**	**2**
Q3UHR0	ACEERLGLPGRELLLQDNK	1.109653082	2	2.4086664
Q3UHR0	IESLWESWGSNMVVKVK	1.233050795	2	2.3546765
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.004332283**	**0.0152644**	**3**
Q3ULJ0	GIDEGPDGLK	0.985989465	2	2.5061524
Q3ULJ0	LGLMEMIAFAK	1.57360647	2	3.9473653
Q3ULJ0	LTDIINNDHENVKYLPGHK	0.964076589	2	2.4556406
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.036209407**	**4.976E-12**	**16**
Q3UQ44	ALVGSENPPLTVIR	1.299862547	2	3.8953328
Q3UQ44	AWVNQLETQTGEASK	0.990884684	2	4.7910552
Q3UQ44	GVLLGIDDLQTNQFK	0.994344729	2	4.5893893
Q3UQ44	HTDNTVQWLR	1.091468642	2	3.3322053
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	2.142408876	3	4.6941247
Q3UQ44	LGIAPQIQDLLGK	1.668796312	2	2.9454262
Q3UQ44	LPYDVTTEQALTYPEVK	1.107950764	2	4.5700288
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.481036511	2	2.413969
Q3UQ44	LSAEEMDER	0.951094426	2	2.9014843
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.126393	2	5.3121805
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.327823957	2	5.1066184
Q3UQ44	TLDTLLLPTANIR	1.02003419	2	2.5964868
Q3UQ44	TLEQTGHVSSK	0.583423959	2	3.1000104
Q3UQ44	VDFTEEEISNMR	0.963605992	2	2.9212158
Q3UQ44	VDQVQDIVTGNPTVIK	1.124994853	2	5.2474108
Q3UQ44	YQDILNEIAK	0.978065901	2	2.4315801
Q3UVR3	**TTBK2 Tau_tubulin kinase 2**	**0.938177051**	**0.9429084**	**2**
Q3UVR3	NLADLR	1.063559111	1	1.9026064
Q3UVR3	YKVLGSSNSDSDLFSR	0.971733516	2	2.5264525
Q3V0K9	**PLSI Plastin_1**	**1.177862943**	**0.4159551**	**3**
Q3V0K9	AYFHLLNQIAPK	1.147594428	2	2.8478479
Q3V0K9	KIENCNYAVELGK	1.163308073	2	3.6742704
Q3V0K9	QFVTPADVVSGNPK	1.017666173	2	3.3252251
Q3V132	**ADT4 ADP/ATP translocase 4**	**0.984750658**	**0.259632**	**2**
Q3V132	GNLANVIR	0.982138189	2	2.66675
Q3V132	YFPTQALNFAFK	1.590392314	2	3.3964787
Q497B0	**NIT2 Omega_amidase NIT2**	**1.058206654**	**6.106E-15**	**17**
Q497B0	ADLYSVESK	1.297508335	2	2.9150832
Q497B0	AGTEETILYSDIDLK	1.624797941	2	3.9639711
Q497B0	AGTEETILYSDIDLKK	1.27197314	2	3.5245976
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.992930851	3	5.4896336
Q497B0	AVDNQVYVATASPAR	1.235765157	2	4.8727965
Q497B0	AVDNQVYVATASPARDEK	1.38566777	2	3.6477244
Q497B0	ENSIYLIGGSIPEEDDGK	0.834976793	2	3.6388319

Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.394982884	3	5.1707859
Q497B0	FAELAQIYAR	1.032144621	2	3.5183346
Q497B0	GCQLLVYPGAFNMTTGPAHWELLQR	1.099648982	3	3.5358479
Q497B0	IHLFDIDVPGK	0.944006936	2	2.79053
Q497B0	KIHLFDIDVPGK	1.390101526	3	4.5499835
Q497B0	LALIQLQVSSIK	1.366464677	2	3.0684803
Q497B0	LYNTCAVFGPDGNLLVK	1.082376302	2	3.9724419
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.242490821	3	5.2818007
Q497B0	TLSPGDSFSTFDTPYCR	1.372029749	2	4.5212665
Q497B0	VGLGICYDMR	1.084111344	2	2.557457
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**1.074839655**	**0.472881**	**5**
Q498D5	ALNTHIEDLKLDVLLQK	0.686215329	3	3.4408827
Q498D5	AYGDMYDLSTNTQEK	0.568571208	2	3.5082846
Q498D5	FCNLALLLPIVTK	1.077053624	2	2.7264235
Q498D5	GQLQILEK	1.081745775	1	1.9462011
Q498D5	LNELLTNVEELKEEIK	1.104381621	2	3.0980656
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.28301827**	**0.0005789**	**8**
Q499N5	GATLSHHNIVNNSNLIGQR	1.275079889	2	4.6113591
Q499N5	GGENIYPAELEDFFHK	1.335019747	2	3.3227532
Q499N5	GGVIAGSLAPPELIR	1.361310034	2	2.8903847
Q499N5	GYCVMQGYWGEPQK	0.949890947	2	2.887846
Q499N5	TFETVGQDR	1.318874213	2	2.6509836
Q499N5	TGDIASMDEQGFCR	1.26315947	2	3.7461553
Q499N5	TVGECLDATAQR	1.319926455	2	2.9942217
Q499N5	YIVFVEGYPLTVSGK	1.554322761	2	4.5227118
Q4AEF8	**COPG Coatomer subunit gamma**	**1.338725119**	**0.1645636**	**5**
Q4AEF8	ALQQYTLEPSEKPFDLK	1.210008228	2	3.3466134
Q4AEF8	FGAQNEEMLPSILVLLK	1.166607481	2	3.9688385
Q4AEF8	SSPEPVALTESETEYVIR	1.153406648	2	4.712357
Q4AEF8	TLEEAVGNIVK	1.05652674	2	2.3460269
Q4AEF8	VVLEHEEVR	1.34604724	2	2.3060491
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.057174112**	**0.6577873**	**5**
Q4FZT0	AEQINQAAGEASAVLAK	0.997426783	2	4.7905397
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.14005138	2	4.8377228
Q4FZT0	ATVLESEGTR	1.041646642	2	2.6568921
Q4FZT0	ILEPGLNVLIPVLDR	1.075878986	2	2.8801031
Q4FZT0	SELGKLSLDKVFR	5.976501015	1	2.0663497
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.037928735**	**0.2210994**	**5**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.830100154	3	4.482903
Q4FZT9	FGGSGSQVDSAR	1.10793378	2	3.6292477
Q4FZT9	SETELKDTYAR	1.037929034	2	2.7107859
Q4FZT9	SSTTSMTSVPKPLK	0.939950753	2	2.9058995
Q4FZT9	TPVQSQQPSATAPSGADEK	1.121449121	2	4.4443464
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.131118109**	**0.5380341**	**4**
Q4FZX7	GDAGSADVQDLEK	1.081735674	2	3.4976408
Q4FZX7	GNSLTLIDLPGHESLR	1.192190919	2	2.9628472
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.132023372	2	4.9600787
Q4FZX7	VGDGAGGAFQPYLDSLR	1.415854021	2	2.4072418
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.080120861**	**0.7764192**	**3**
Q4G061	AEEEGGSDGSAAEAEPR	0.753526755	2	4.5432882
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	1.420091314	3	4.5899091
Q4G061	GTQGVVTNFEIFR	0.967921688	2	2.3300288
Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**0.927708083**	**0.3806499**	**2**

Q4KLF8	ALAAGGVGSIVR	1.22650679	2	2.3170066
Q4KLF8	QGNMTAALQAALK	0.920169232	2	2.5197437
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.169398658**	**1.887E-14**	**16**
Q4KLP0	ARPSVDHGLAR	1.112605933	2	2.5205762
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.018687702	3	3.6746194
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.165622766	3	4.3059464
Q4KLP0	LEELCPFPLDSLQQEMGK	1.408274586	2	5.1225252
Q4KLP0	LLLESQEFDHFLATK	1.41727565	2	3.8353879
Q4KLP0	LSAYGGITDIIIGMPHR	1.612939502	3	3.5330176
Q4KLP0	LVTVYCEHGHK	1.119358476	2	2.8311772
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	1.218062714	2	3.0166242
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.26429325	3	3.5155983
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.21638365	3	4.9983978
Q4KLP0	SSLYSSDIGK	1.130254299	1	2.0959771
Q4KLP0	SVEVPEELQLHSHLLK	1.265454766	2	2.7032647
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.298869146	3	3.831419
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.217604018	2	4.9913511
Q4KLP0	YGGEGAESMMGFFHELLK	1.039544721	3	4.243721
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.126992178	3	4.3376942
Q4KLZ6	**DHAK Bifunctional ATP_dependent dihydroxyacetone kinase/FAD_AMP lyase (cyclizing)**	**0.97696822**	**0.8011021**	**13**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	0.911631665	2	4.6054149
Q4KLZ6	AILEVLQTK	0.893930176	2	2.8764582
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.103339156	2	3.2602837
Q4KLZ6	AVAQAGTAGTLLIVK	1.059985969	2	4.424356
Q4KLZ6	EGPTPASPAQVLSK	0.929832629	2	3.3031516
Q4KLZ6	ISTTLIGLEEHLNALDR	1.922424771	2	4.1547518
Q4KLZ6	LIDAETNAK	0.85008635	2	3.0564315
Q4KLZ6	LSVLLLEK	1.269120458	2	2.6833537
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	1.221911481	2	4.5963707
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	0.982502461	3	5.096961
Q4KLZ6	RGLCGTILIHK	0.830978286	3	3.4077735
Q4KLZ6	TMLDSLWAAAQELQAWK	0.991181587	2	4.3056602
Q4KLZ6	VAGALAEEGMGLEEITK	0.826273726	2	3.6572151
Q4KM35	**PSB10 Proteasome subunit beta type_10**	**1.371198459**	**4.128E-06**	**2**
Q4KM35	ALSSPIEPVQR	1.330053711	2	2.3731329
Q4KM35	FAPGTTPVQTQEVR	1.383998436	2	2.8435786
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.091427003**	**0.9775504**	**3**
Q4KM49	QVEPLDPPAGSAPGER	1.107497305	2	2.5782361
Q4KM49	TVVSGLVQFVPK	0.977740175	2	3.2938018
Q4KM49	VDAQFGGIDQR	1.097175903	2	3.3616028
Q4KM62	**PALMD Palmdelphin**	**1.255153903**	**0.0190269**	**2**
Q4KM62	TGESVVLSSIPLPSDDFK	0.939600968	2	3.4019938
Q4KM62	VEKEEIPEESIEDIYANIPDLPSSYIPSR	1.52794296	3	3.4269257
Q4KM73	**KCY UMP_CMP kinase**	**1.024827925**	**2.85E-07**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.32851822	2	4.926024
Q4KM73	IVPVEITISLLK	1.067938575	2	3.0416598
Q4KM73	KNPDSQYGELIEK	1.140386197	2	4.2938108
Q4KM73	NQDNLQGWNK	1.086426697	2	2.9402449
Q4KM73	SVDEVFGDVMK	0.937244976	2	3.166023
Q4KM73	YGYTHLSAGELLR	1.152549238	3	3.6147077
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.079868676**	**0.3361452**	**4**
Q4KM74	DLQQYQSQAK	1.047366909	2	3.3926792
Q4KM74	GEALSALDSK	1.152966706	2	2.416549
Q4KM74	IMVANIEEVLQR	1.349653699	2	2.7056715
Q4KM74	NLGSINTELQDVQR	1.14163536	2	4.165978

Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.040958132**	**0.7870583**	**4**
Q4KMA2	ESQAVVDPPPQAVSTGTPQSPAVAAAAATTTATTTTTSGGHPLEFLR	1.19798611	3	3.9465792
Q4KMA2	IDIDPEETVK	1.083835196	1	2.6336133
Q4KMA2	NFVVVMVTKPK	1.000610711	2	3.4605961
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.1308742	2	3.8476126
Q4QQV3	**F162A Protein FAM162A**	**1.213319491**	**0.1261519**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	1.350094674	2	3.4520028
Q4QQV3	RHESLTSLNLER	1.155161603	2	2.7591355
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.985051205**	**0.9767968**	**2**
Q4QQW3	HLETAEILGANIR	0.990027936	2	3.2784789
Q4QQW3	IQDAGPVLADALR	0.95781711	2	2.4897783
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**0.88508266**	**0.4638358**	**5**
Q4QRB4	AILVDLEPGTMDSVR	0.978882509	2	4.5614495
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(11)	1.059491835	2	2.6335197
Q4QRB4	EIVHIQAGQCGNQIGAK	0.855006919	2	5.1074615
Q4QRB4	IMNTFSVVPSPK	1.16119707	2	3.4465473
Q4QRB4	ISEQFTAMFR	1.085839656	2	3.3592651
Q4V7C7	**ARP3 Actin_related protein 3**	**1.139334845**	**0.9658275**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	0.969724595	2	4.8280172
Q4V7C7	KDYEEIGPSICR	1.01284185	2	3.9039629
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.084843759	2	3.4565763
Q4V7C7	LSEELSGGR	1.108749568	2	2.7786469
Q4V7C7	NIVLSGGSTMFR	0.984876916	2	2.6649435
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1.08041243	2	4.5977936
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**0.992530952**	**0.9851715**	**5**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	0.994064622	3	3.309346
Q4V8K1	QVFVCGNDSK	1.108446564	2	2.5586081
Q4V8K1	TCADEFPLTVDSSEK	1.021421223	2	4.4658771
Q4V8K1	TLGLTPLDQGSLVAAK	1.089884548	2	3.375767
Q4V8K1	VLIDVSNNQK	0.918167743	2	2.3147707
Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**0.928818753**	**0.9135214**	**2**
Q501J6	ELAQQVQQVADDYGK	1.077359321	2	2.677911
Q501J6	VLEEANQAINPK	0.926100764	2	2.7113588
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.984953459**	**3.893E-08**	**5**
Q505J8	LQQVQAGQAEK	1.292524426	2	2.9521463
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	1.017642319	3	5.1490746
Q505J8	SIPLEGLVQSELMQLPSGK	1.18760463	2	2.7661853
Q505J8	SLQALGEVIEAELR	0.954819705	2	3.8935192
Q505J8	VVDSIEDEVQR	1.195039115	2	2.8447428
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**1.092713678**	**0.9711122**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	1.121877025	2	4.0802155
Q561R9	ILIDTGEPSVPEYISCLK	1.070124017	2	3.5217161
Q561R9	NISNDATYCIK	1.098603949	2	2.7247815
Q561R9	NNREEQIITVFR	1.095131932	2	2.7793787
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.215997816**	**0.0296927**	**5**
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	1.574857658	3	3.6986096
Q561S0	VITVDGNICSGK	0.905193365	2	3.1289504
Q561S0	VVEDIEYLNYNK	1.693446043	2	3.5666423
Q561S0	YAPGYNADVGDK	1.123518187	2	2.750464
Q561S0	YGLLASILGDK	1.092583499	2	2.9573061
Q562C4	**MET7B Methyltransferase_like protein 7B**	**1.221768199**	**0.0032413**	**7**
Q562C4	AQFSEVQLEWQPPPFK	1.666395814	2	4.814002
Q562C4	FIVAYGENMK	1.240824161	2	2.3481331
Q562C4	GTSNEVTLLELGCGTGANFQFYPPGCK	1.231869357	2	4.0448909

Q562C4	HIGDGCHLTR	1.53607186	2	2.757643
Q562C4	KVLQEVQR	1.408197376	2	2.5237854
Q562C4	VLQEVQR	1.286546456	1	2.0159707
Q562C4	VTCVDPNPNFEK	0.982754752	2	3.720583
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.175342897**	**0.2182075**	**10**
Q58FK9	AIILNTPHNPIGK	1.081504219	2	3.2966516
Q58FK9	DSTLDAAEEIFR	0.716671234	2	2.998791
Q58FK9	IEGLDQNVWVEFTK	1.204137149	2	4.550025
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.634113048	3	5.6725678
Q58FK9	LGWSIGPGHLIK	1.588037711	2	2.4353883
Q58FK9	MDDPECYFNSLPK	0.931502656	2	4.117754
Q58FK9	RIEGLDQNVWVEFTK	1.135821834	2	3.9177709
Q58FK9	RMDDPECYFNSLPK	0.969861684	2	2.3525193
Q58FK9	SDEPYDYK	1.225671845	2	2.4815903
Q58FK9	WTSSDWTFNPQELESK	1.105711433	2	5.1831717
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.154565678**	**0.3241624**	**2**
Q5BJQ0	AVLDSSPFLSEANAER	1.028632553	2	4.5879798
Q5BJQ0	TLNNDLGPHWR	1.160628928	2	3.0123427
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**1.012913744**	**2.896E-06**	**23**
Q5BJY9	AQIFANSVDNAR	1.09919252	2	3.8177316
Q5BJY9	AQYEQLAQK	1.013847143	2	3.2973545
Q5BJY9	IREYLEK	1.054786789	2	2.3652194
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	0.755320986	3	4.3018489
Q5BJY9	KVVDDTNITR	1.016769597	2	2.940172
Q5BJY9	LEAEIATYR	0.952679695	2	3.230437
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.904645296	2	5.300693
Q5BJY9	LQLETEIEALKEELLFMK	2.738400508	2	4.9570847
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.902578258	2	6.5303364
Q5BJY9	NQNINLENNLGEVEAR	0.972506534	2	5.6028357
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	0.985393674	3	5.7048187
Q5BJY9	QSVESDIHGLR	1.092480536	2	3.3157382
Q5BJY9	QSVESDIHGLRK	1.109387205	2	2.690906
Q5BJY9	QTQEYEALLNIK	1.205940145	2	3.535063
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.954287751	2	5.7296515
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	1.021518652	3	4.8253021
Q5BJY9	TLQTLEIDLDSMK	1.084353288	2	4.2261086
Q5BJY9	VKLEAEIATYR	0.995934923	2	2.603852
Q5BJY9	VKYETELAMR	1.030142221	2	2.6307683
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.191630267	3	5.259335
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.942825829	2	5.6052647
Q5BJY9	VVDDTNITR	1.026314031	2	3.3590937
Q5BJY9	YWSQQIEESTTVVTTK	1.047381055	2	4.3252316
Q5BK17	**IYD1 Iodotyrosine dehalogenase 1**	**1.075535787**	**0.4621634**	**2**
Q5BK17	FISSEPVPMEVIDNVIK	1.085868503	2	3.2650359
Q5BK17	LLVLLPVGYPSR	1.450769107	2	2.634383
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.456810987**	**9.9E-20**	**5**
Q5BK63	AVQHSNVVINLIGR	1.10970209	2	2.5482075
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.624614566	3	5.3587956
Q5BK63	LFGLSPFEPWTTK	1.485781839	2	2.5865147
Q5BK63	NFDFEDVFVNIPR	1.715693989	2	3.9541867
Q5BK63	WLSSEIEETKPAK	1.390133818	2	3.1059451
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**1.026068239**	**0.9999917**	**3**
Q5BK81	DVPYPPPLPPAVEAIQK	1.023266209	2	3.2439101
Q5BK81	TGNVAEQLR	1.057591204	2	2.3342605
Q5BK81	VEEVSLPDTINEGQVR	1.039114432	2	3.8044631

Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**0.844710841**	**0.9364985**	**2**
Q5BQE6	NIMINLMDILEVDTKK+Oxidation(3)Oxidation(7)	0.980956128	2	2.4134696
Q5BQE6	QLGCQDAFPEVYDK	0.831888135	2	3.7618272
Q5DU56	**NLRC3 Protein NLRC3**	**1.447529429**	**0.0935945**	**2**
Q5DU56	LTGLALGHLYR	1.45484934	2	2.4023919
Q5DU56	TLEILDLR	0.988832702	2	2.3344111
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.150073692**	**0.0987228**	**2**
Q5EB77	NDIVNMLVGNK	1.000668803	2	3.2772877
Q5EB77	TCDGVQCAFEELVEK	1.310873563	2	3.7383933
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**0.982792623**	**0.3834348**	**2**
Q5FVM4	MEELHNQEVQK	1.12060991	2	3.262028
Q5FVM4	RMEELHNQEVQK	0.970303064	3	4.0031919
Q5FVQ4	**MLEC Malectin**	**1.246026287**	**8.105E-15**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	1.25526224	3	6.081985
Q5FVQ4	STPEDQILYQTER	1.113138024	2	3.977519
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.950456013**	**0.9336219**	**4**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(11)	0.885640397	2	2.6054597
Q5FVR2	DVTATVDSVPLITASILSK	0.974137253	2	3.6391323
Q5FVR2	KQEELLSPADGIVECVR	1.057277945	2	4.5288005
Q5FVR2	VHLDGPALSSQQR	1.111177377	2	2.400646
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.762014125**	**0.0399349**	**4**
Q5FVR5	DEKENLFQSK	0.768242158	2	2.7995496
Q5FVR5	ILFIVGENDQCLASK	1.356158689	2	3.746778
Q5FVR5	IQQPGIGVISVSK	1.258647745	2	2.7611878
Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	1.832233121	3	3.8095
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.903235881**	**0.920479**	**2**
Q5FW57	AIDQEMFK	0.85768787	2	2.7050047
Q5FW57	SSQMLQMLESSLR	0.940529121	2	3.8796856
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**0.963381258**	**0.4101564**	**2**
Q5HZV9	AIENIDTLTNLESLFLGK	0.80811757	2	3.1388249
Q5HZV9	ELDLYDNQIKK	1.244798177	2	2.3786194
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**1.065087056**	**0.9976674**	**2**
Q5HZY2	IDRPEAISEER	1.065120696	2	2.926368
Q5HZY2	LLESKEELDSLMTDETIANVPILILGNK	1.042448128	3	4.2635083
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.977090976**	**0.3683969**	**6**
Q5I0C3	HAPLVEFEEEEV	0.888832522	2	2.8730049
Q5I0C3	IIEEAPAPGIDPEVR	0.947551606	2	3.6948986
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	0.941222519	3	6.0180254
Q5I0C3	SEKEFQEQLESAR	0.95576561	2	3.5532632
Q5I0C3	VFFSEGAQANR	1.162481563	2	2.5250816
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	1.010798767	2	5.0938582
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**1.024916543**	**0.9999997**	**2**
Q5I0D1	ESQSILTPLVSLDTPGK	1.025012686	2	3.5057354
Q5I0D1	HEEFEEGCK	1.018537561	2	2.6484008
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**1.042441527**	**0.9556009**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	0.899366916	2	2.6522608
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.068663206	2	3.795944
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.107460657**	**0.2097808**	**2**
Q5I0D7	GVNTDSGNVCR	1.100278264	2	2.7218807
Q5I0D7	YAVDDVQYADEIASVLTSR	1.294790759	2	4.2083468
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.186548645**	**0.7473762**	**2**
Q5I0E7	QLVEQVEQIQK	1.185201104	2	4.0451155

Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.227966581	3	3.607738
Q5I0G4	**SYG Glycyl_tRNA synthetase (Fragment)**	**0.96000312**	**0.9246731**	**5**
Q5I0G4	AEVSELPSVVR	0.9599957	2	3.2368233
Q5I0G4	LGDAVEQGVINNSVLGYFIGR	1.230710348	2	3.0462976
Q5I0G4	TLHVEEVVPSVIEPSFGLGR	1.10316334	2	4.1233697
Q5I0G4	TVNVVQFEPNK	0.100962617	2	2.4786115
Q5I0G4	VDDSSGSIGR	0.887415822	2	2.6186745
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**0.986721342**	**0.2006217**	**7**
Q5I0H9	DKNQDLCQQESVK	0.979979869	2	4.2071557
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	0.859104893	3	4.9622488
Q5I0H9	GPPLWEEDPGAK	1.077888731	2	2.8296421
Q5I0H9	GQGTICWVDCGDAESR	0.901024467	2	4.2056651
Q5I0H9	NGEQQAVPALR	1.067070582	2	2.817538
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.887248548	3	4.5151229
Q5I0H9	NQDLCQQESVK	0.97677844	2	2.6428695
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.177683268**	**3.856E-13**	**5**
Q5I0J9	HANLLVGSPSALADQTTER	1.012312389	3	5.1008325
Q5I0J9	IIHESGVQILR	1.139770468	2	2.6311512
Q5I0J9	LDAAGGLQSLR	1.136123447	2	3.7419205
Q5I0J9	LEGPLAAAHSSGPR	1.205302568	2	3.5826738
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.666568856	2	3.8861928
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.045986652**	**1.785E-12**	**3**
Q5I0M2	DNHVVAAGSMEK	0.863577453	2	2.9379306
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.381455357	3	5.6709909
Q5I0M2	LYAEGDIPVPHAR	1.171433149	2	3.3224306
Q5M7U6	**ARP2 Actin_related protein 2**	**1.143118982**	**0.3714715**	**6**
Q5M7U6	GYAFNHSADFETVR	1.242758565	2	3.59305
Q5M7U6	HLWDYTFGPEK	1.14449818	2	3.3915632
Q5M7U6	ILLTEPPMNPTK	0.857661747	2	3.0597258
Q5M7U6	LCYVGYNIEQEQK	0.772801876	2	3.3125339
Q5M7U6	SMLEVNYPMENGIVR	0.955920205	2	4.4640245
Q5M7U6	VVVCDNGTGFVK	1.109841417	2	2.9517617
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.966201144**	**0.3709795**	**9**
Q5M7W5	AAVGLTGNDIATPPNK	1.038403721	2	3.3330679
Q5M7W5	ATSPSTLVSTGSSSR	0.949415464	2	3.3879137
Q5M7W5	EAETALPIEMDLAPPEDVALPK	1.410179352	2	2.4833455
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	1.293954132	2	4.3250227
Q5M7W5	NTAPPTEEETVPGK	1.030676682	2	2.5250201
Q5M7W5	NTTPTGATPPAGMASTR	1.113874617	2	2.4090557
Q5M7W5	STLPVDEGSPLEK	0.893441776	2	2.350764
Q5M7W5	VGSLDNVGHLPAGGTVK	0.906039492	2	2.803241
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.127140585	2	4.6674161
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.017865286**	**0.9981365**	**6**
Q5M875	ALTAELDTLGK	1.091660678	2	3.5139556
Q5M875	IQNIQFEAIVGHR	1.106892663	2	3.6832051
Q5M875	NSGHIVTVASVCGHR	1.090477728	2	4.2115393
Q5M875	SLIDGILTNK	0.993780524	2	2.9772325
Q5M875	SVAGQTVLITGAGHGIGR	1.148751179	2	3.9853511
Q5M875	TSCLCPVFVNTGFTK	0.854280295	2	4.1507988
Q5M9G3	**CAPR1 Caprin_1**	**1.248870665**	**1.356E-10**	**3**
Q5M9G3	LNQDQLDAVSK	1.249445983	2	3.1509373
Q5M9G3	SSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMK	0.920789139	3	4.9897261
Q5M9G3	YQEVTNNLEFAK	1.148622953	2	2.5911832
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.082115994**	**3.846E-11**	**2**
Q5M9I5	EEEEEELVDPLTTVR	1.074174584	2	3.3326814

Q5M9I5	SQTEEDCTEELFDFLHAR	2.505850328	2	5.0206094
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.290097122**	**0.1825553**	**10**
Q5PPL3	AVLDANDPK	0.995044029	1	1.9766866
Q5PPL3	AVLDANDPKK	1.157476408	2	2.4780028
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	1.225265332	2	4.3464932
Q5PPL3	GQVTGTDLINEVSK	0.977941481	2	4.0731831
Q5PPL3	GVSTVFHCASPPSNSNNK	1.159547289	2	4.780427
Q5PPL3	GYAVNVFDVR	1.178436457	1	2.0304265
Q5PPL3	ILTGLNYEAPK	1.309495572	2	3.4208777
Q5PPL3	KGQVTGTDLINEVSK	0.942987007	2	4.5086145
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.207250475	3	3.8823318
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.276729127	2	4.7104526
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.238044093**	**0.0017833**	**5**
Q5PQT3	AIQNLASIHSLQVK	1.252032764	2	3.9581349
Q5PQT3	KLFPSLLDTK	1.036595072	2	2.4677074
Q5PQT3	LSSLDVTHAALVNK	1.693538303	2	3.4670756
Q5PQT3	NFPSSCVLGPEGTPASWTLMDQTGEMR	0.700513354	3	4.0369501
Q5PQT3	QHLQIQSSQSHLNK	1.010336751	2	3.5053129
Q5QNV8	**CQ066 Uncharacterized protein C17orf66 homolog**	**1.074889586**	**0.0197753**	**2**
Q5QNV8	LEAPAFSFYFSKPK	1.074640426	2	2.3691139
Q5QNV8	YFKDSAQMPNLHVSISK+Oxidation(8)	1.52499424	2	2.4126937
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.011773148**	**0.4502701**	**5**
Q5RJR8	ATVLDLSCNK	1.136096305	2	2.3962412
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	1.085067299	2	5.8268838
Q5RJR8	HHEILQWVLQTDSQQ	0.88803838	2	3.4418964
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.042983253	2	4.3294811
Q5RJR8	LQQLPADFGR	1.634710048	2	2.3206654
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.05744247**	**0.6475045**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.039369341	3	5.2743001
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	0.73805856	3	3.7375686
Q5RKI0	YAPSGFYIASGDISGK	1.098078272	2	4.1601586
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.071794868**	**0.5634065**	**5**
Q5RKI1	ELAQQIQK	1.138944922	1	2.1747854
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.128623589	2	4.7385163
Q5RKI1	GYDVIAQAQSGTGK	1.080441213	2	5.2087069
Q5RKI1	MFVLDEADEMLSR	1.028616353	2	4.7245278
Q5RKI1	VLITTDLLAR	1.131895383	2	2.4169335
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**0.966344224**	**0.1478131**	**11**
Q5SGE0	AALDLEQVPSELAVTR	0.692872588	2	3.8739707
Q5SGE0	CIANNQVETLEK	0.991140419	2	3.0623648
Q5SGE0	HCVTMDTPAEK	1.067637783	2	3.1913939
Q5SGE0	HDNAEDALNLK	1.560100417	2	3.7379949
Q5SGE0	LKAEGHPVGDPLK	1.208464416	2	2.4348097
Q5SGE0	MEGANIQPNR	0.977438238	2	2.5964916
Q5SGE0	SCGSLLPELSLAER	0.840892849	2	2.4951584
Q5SGE0	SSLSSSSPSAGDTVTEK	0.930952314	2	4.3652778
Q5SGE0	SYVADKDVASAK	0.939086678	2	3.3875797
Q5SGE0	TLLELIPELR	1.022386818	2	2.4947934
Q5SGE0	VQDAINILK	0.89814123	2	2.3050637
Q5SVT3	**ETAA1 Ewing_s tumor_associated antigen 1 homolog**	**0.89234928**	**0.0494533**	**2**
Q5SVT3	ELMKLAQQFDK+Oxidation(3)	0.885900788	2	2.5083539
Q5SVT3	NHDFIQMTSKMGHLDNHK+Oxidation(7)Oxidation(11)	3.640736968	2	2.485251
Q5SX40	**MYH1 Myosin_1**	**0.721808174**	**1**	**75**
Q5SX40	AAYLQNLNSADLLK	0.811312406	2	3.6000104
Q5SX40	ADIAESQVNK	0.907857362	2	3.398128

Q5SX40	AEDEEEINAELTAK	0.954443832	2	3.9535751
Q5SX40	AGLLGLLEEMR	1.035495172	2	3.888469
Q5SX40	AGLLGLLEEMRDDK	1.058752436	2	3.3812246
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	1.043318171	3	6.559906
Q5SX40	ANLLQAEIEELR	0.940482747	2	4.0092373
Q5SX40	ANSEVAQWR	0.640664484	2	2.323422
Q5SX40	DLEEATLQHEATAATLR	0.79133235	2	4.9365377
Q5SX40	DTQLHLDDALR	0.75945362	2	2.9307239
Q5SX40	EEQAEPDGTEVADK	0.956002554	2	3.1465735
Q5SX40	ELEGEVENEQK	0.611606785	2	2.9637315
Q5SX40	ELEGEVENEQKR	0.754171231	2	3.1835945
Q5SX40	ELTYQTEEDRK	1.046943417	2	3.1425724
Q5SX40	ENQSILITGESGAGK	0.878454633	2	3.6787503
Q5SX40	EQYEEEQEAK	0.950370777	1	3.0231702
Q5SX40	GQEDLKEQLAMVER	0.905489496	2	4.0817475
Q5SX40	GQTVQQVYNSVGALAK	2.569249767	2	3.0157063
Q5SX40	GSSFQTVSALFR	0.675692328	2	2.5451736
Q5SX40	HADSVAELGEQIDNLQR	0.938990326	2	5.8892417
Q5SX40	IAEKDEEIDQLKR	1.282581668	2	2.4350762
Q5SX40	IAEQELLDASER	0.855550716	2	3.6084061
Q5SX40	IEAQNKPFDAK	0.79546111	2	2.7903407
Q5SX40	IEDEQALGMQLQK	0.96472219	2	4.4292355
Q5SX40	IEELEEEIEAER	0.836288687	2	4.1115866
Q5SX40	IKLEQQVDDLEGSLEQEK	1.167486059	2	5.0790253
Q5SX40	IKLEQQVDDLEGSLEQEKK	1.043444632	3	5.0071006
Q5SX40	INQQLDTK	1.024165113	2	2.3604891
Q5SX40	IQHELEEAEER	0.896071077	2	3.6490161
Q5SX40	IQLELNQVK	0.960843805	2	2.90868
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	1.224981329	3	4.1908736
Q5SX40	KIAEQELLDASER	0.996654858	2	4.1522408
Q5SX40	KIQHELEEAEER	1.071480511	3	3.8938425
Q5SX40	KKLETDISQIQGEMEDIVQEAR	1.16595699	3	5.1435604
Q5SX40	KLEDECSELK	0.991694346	2	2.9543271
Q5SX40	KLEDECSELKK	1.109252306	3	4.052671
Q5SX40	KLETDISQIQGEMEDIVQEAR	1.067980352	2	5.3780861
Q5SX40	LAQESTMDVENDKQQLDEK	1.003378724	2	4.5676341
Q5SX40	LDEAEQLALK	1.053051161	2	3.3696587
Q5SX40	LEDECSELKK	1.059311559	2	3.1005752
Q5SX40	LEEAGGATSAQIEMNK	1.019508222	2	4.7445536
Q5SX40	LEQQVDDLEGSLEQEK	0.721715641	2	5.5782685
Q5SX40	LEQQVDDLEGSLEQEKK	1.268283214	2	4.823029
Q5SX40	LETDISQIQGEMEDIVQEAR	0.851257682	2	5.1217198
Q5SX40	LINELTAQR	0.976966344	2	2.9532728
Q5SX40	LQDAEEHVEAVNAK	1.022933444	2	4.577137
Q5SX40	LQDLVDK	0.968286455	2	2.3614142
Q5SX40	LQNEVEDLMIDVER	1.222228859	2	4.4723454
Q5SX40	LQTESGEYSR	0.861615107	2	2.6672299
Q5SX40	MEIDDLASNMEVISK	0.912758422	2	4.3945866
Q5SX40	MEIDDLASNMEVISKSKGNLEK	0.834394274	2	2.4305022
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	1.121931533	3	6.6042385
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(1)	1.11970286	2	4.3997335
Q5SX40	NDLQLQVQSEADSLADAEER	0.596683739	2	5.5792584
Q5SX40	NKDPLNETVVGLYQK	0.879464522	2	4.5441327
Q5SX40	NLQQEISDLTEQIAEGGK	0.924530457	2	5.9169855
Q5SX40	NLQQEISDLTEQIAEGGKR	0.964589903	2	4.4323506
Q5SX40	NLTEEMAGLDETIAK	0.892800285	2	5.1545854
Q5SX40	QAEEAEEQSNVNLAK	0.886568657	2	4.4277492

Q5SX40	QKYEETHAELEASQK	1.065428699	2	4.039248
Q5SX40	QLDEKDSLVSQLSR	1.282553611	2	2.8135993
Q5SX40	QLEEEIK	1.162721296	1	2.0756035
Q5SX40	QREEQAEPDGTEVADK	1.08219736	2	4.3373852
Q5SX40	SELQAALEEAEASLEHEEGK	0.877987831	2	5.4333506
Q5SX40	SSVFVVDAK	0.922944386	1	2.3147516
Q5SX40	TKYETDAIQR	0.990080544	2	3.3154259
Q5SX40	TLEDQVSELK	0.913716899	2	3.1790948
Q5SX40	TNAACAALDK	1.110858696	1	1.9305575
Q5SX40	TNAACAALDKK	0.938552561	3	3.4311299
Q5SX40	VKELTYQTEEDRK	0.879649653	2	2.6299329
Q5SX40	VLNASAIPEGQFIDSK	1.148391889	2	4.4882417
Q5SX40	VQLLHTQNTSLINTK	1.040169142	2	4.8992796
Q5SX40	VRELEGEVENEQKR	0.972783202	3	3.6625152
Q5SX40	YEETHAELEASQK	0.856199787	2	4.4377494
Q5SX40	YETDAIQR	0.771107783	1	2.0886312
Q5TKR9	**KAT6A Histone acetyltransferase KAT6A**	**1.129174412**	**0.1415794**	**2**
Q5TKR9	ENKDQDSSSLIESEKKPEVK	1.045992816	2	2.3868451
Q5TKR9	KGYGRFLIDFSYLLSK	1.645453568	2	2.3015568
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.223472986**	**0.0001718**	**5**
Q5U206	DTDSEEEIR	1.028511094	2	2.4169052
Q5U206	KMKDTDSEEEIR	1.21806248	2	2.6259577
Q5U206	KMKDTDSEEEIR+Oxidation(2)	1.333657502	2	2.4820218
Q5U206	MKDTDSEEEIR	0.982783674	3	4.1694016
Q5U206	MKDTDSEEEIR+Oxidation(1)	1.34817744	2	3.4409785
Q5U211	**SNX3 Sorting nexin_3**	**0.988524135**	**0.3081064**	**2**
Q5U211	GDDGIFDDNFIEER	1.410458548	2	2.8698578
Q5U211	YSDFEWLR	0.927232228	2	2.540637
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.055570344**	**7.398E-05**	**4**
Q5U2Q7	GFGGIGGILR	0.995448947	2	2.9735641
Q5U2Q7	LSVLGAITSVQQR	1.300590876	2	2.4411421
Q5U2Q7	YFDEISQDTGK	1.071327501	2	2.7884762
Q5U2Q7	YVLHCQGTEEEK	1.301724265	2	3.9640415
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**1.405265917**	**0.2841349**	**2**
Q5U2U0	QQAEVEK	1.21131269	1	2.0195193
Q5U2U0	SGESNTHQDIEEKDR	1.171714698	3	3.6898816
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.132545222**	**4.441E-16**	**12**
Q5U300	AAVASLLQSVQVPEFTPK	1.226428864	3	3.4228928
Q5U300	AENYDISPADR	0.851016041	2	2.4447527
Q5U300	DNPGVVTCLDEAR	0.912729876	2	2.3506987
Q5U300	FEVQGLQPNGEEMTLK	1.032148294	2	2.7958333
Q5U300	FEVQGLQPNGEEMTLK+Oxidation(13)	1.137056773	2	2.4382317
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.316733304	2	5.6085863
Q5U300	LDQPMTEIVSR	0.91011164	2	3.124913
Q5U300	NEEDATELVTLAQAVNAR	1.186935526	2	5.2932119
Q5U300	NFPNAIEHTLQWAR	0.945008666	2	3.5602481
Q5U300	SLPASLAEPDFVMTDFAK	1.210886969	2	4.0693083
Q5U300	SPPAVQQDNVDEDLIR	1.037240476	2	4.8702645
Q5U300	VVQGHQQLDSYK	1.38374439	2	3.310528
Q5U312	**RAI14 Ankycorbin**	**1.083336421**	**0.7130426**	**2**
Q5U312	MHLLYAVQGQMDEDVQKVLK	1.123430425	2	2.3403957
Q5U312	QDLQRALEESK	1.081662182	2	2.4399581
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**1.020794756**	**0.6429093**	**2**
Q5U4E6	EFNTQLAQK	0.996442259	2	2.3481419
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(17)	1.209978097	2	2.4134431
Q5XFW8	**SEC13 Protein SEC13 homolog**	**1.105917901**	**0.6764547**	**2**

Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	1.098054486	2	3.5834305
Q5XFW8	LEAHSDWVR	1.138442722	2	2.6964533
Q5XFX0	**TAGL2 Transgelin_2**	**0.987261118**	**0.0023124**	**5**
Q5XFX0	DDGLFSGDPNWFPK	0.530570006	2	3.4279644
Q5XFX0	NFSDNQLQEGK	1.046020236	2	3.2495434
Q5XFX0	NVIGLQMGTNR	0.881143451	2	2.7755408
Q5XFX0	TLMNLGGLAVAR	0.879922209	2	3.4069796
Q5XFX0	YGINTTDIFQTVDLWEGK	1.531319253	2	5.0701828
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.015074448**	**5.498E-06**	**11**
Q5XHY5	AEHDSILAEK	0.953348286	2	2.656369
Q5XHY5	FLGDIEIWNQAEK	1.011388568	2	3.4609995
Q5XHY5	FMVDIDLDPGCTLNK	1.350798143	2	2.4584167
Q5XHY5	FNLTYVSHDGDDK	1.101658374	2	2.677567
Q5XHY5	GFQEVVTPNIFNSR	1.015929512	2	3.5567241
Q5XHY5	LKAEHDSILAEK	0.690328772	2	3.3667729
Q5XHY5	QLENSLNEFGEK	0.895164121	2	2.9010656
Q5XHY5	QVMVVPVGPTCDEYAQK	1.110058047	2	3.0961163
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.258362317	2	4.00699
Q5XHY5	VVWDLDRPLETDCTLELLK	2.035290607	2	3.9720161
Q5XHY5	WELNPGDGAFYGPK	0.872988067	2	3.7246304
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.256870394**	**0.0001573**	**13**
Q5XHZ0	AFLEALQHQAETSSR	1.118787979	2	4.5046797
Q5XHZ0	AQLLQPTLEINPR	1.188135487	2	3.0792906
Q5XHZ0	EGIVTTAEQDIKEDIAK	0.661032644	2	2.3997393
Q5XHZ0	ELISNASDALEK	1.062348917	2	2.9538922
Q5XHZ0	FEDTSPAGER	0.869360278	2	2.8951952
Q5XHZ0	GTITIQDTGIGMTK	0.981954478	2	2.8837988
Q5XHZ0	GVVDSEDIPLNLSR	1.161577589	2	4.8695164
Q5XHZ0	HLAEHSPYYEAMK	1.277263678	2	3.0081987
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.036424173	3	4.0402455
Q5XHZ0	SDCKDFANESR	1.110898376	2	2.8979123
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	0.932432306	3	4.3087139
Q5XHZ0	YESSALPAGQLTSLSDYASR	1.223053791	2	5.4538627
Q5XHZ0	YIAQAYDKPR	1.234452957	2	2.8065326
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.092763838**	**0.9575124**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	1.086469602	2	4.7765083
Q5XI22	HGSNLEAMSK	0.925228764	2	2.4449389
Q5XI22	HGSNLEAMSK+Oxidation(8)	0.674722624	2	3.2695105
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	1.448120636	3	5.1588392
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	1.211400087	3	3.8829353
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	0.919580043	3	4.6532831
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	1.071324659	2	5.2493224
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	1.088409247	2	5.3594971
Q5XI22	VNIDGGAIALGHPLGASGCR	1.052350466	2	5.3877344
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**1.021383383**	**0.8712307**	**2**
Q5XI29	QNLSQFEAQAR	0.925981248	2	2.3729947
Q5XI29	SIGVYDVVELK	1.021427218	2	2.5826645
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.058985894**	**0.0990773**	**6**
Q5XI32	GCWDSIHVVEVQEK	1.430907476	2	3.2091882
Q5XI32	KLEVEANNAFDQYR	1.059170522	2	4.1404719
Q5XI32	LEVEANNAFDQYR	0.777600054	2	3.5762429
Q5XI32	LVEDMENK	1.022423903	2	2.7560315
Q5XI32	NDLVEALK	0.925689716	2	2.5759699
Q5XI32	SGSGTMNLGGSLTR	1.065010578	2	3.255939
Q5XI41	**TRAM1 Translocating chain_associated membrane protein 1**	**1.068385678**	**0.9912859**	**2**

Q5XI41	EHSAFQAPPVK	1.06920234	2	2.3504441
Q5XI41	LDFSTGNFNVLAVR	1.061965577	2	3.0660298
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.119941239**	**0.9999775**	**3**
Q5XI60	ALDIAAGITR	0.934135952	2	2.5646975
Q5XI60	HHVALDSAASQLSGR	1.128610402	2	4.5192895
Q5XI60	NVATDALGALEAR	1.105958207	2	4.0457244
Q5XI72	**IF4H Eukaryotic translation initiation factor 4H**	**0.946056686**	**0.8596743**	**2**
Q5XI72	EALTYDGALLGDRSLR	0.898241895	2	2.6012604
Q5XI72	SLRVDIAEGRK	0.952849905	2	2.4368458
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.096496015**	**0.2145044**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.207261543	2	4.1167369
Q5XI73	IDKTDYMVGSYGPR	1.086365437	2	4.00631
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	1.519733063	3	3.4509008
Q5XI73	SIQEIQELDKDDESLR	1.05098262	2	5.2909989
Q5XI73	SIQEIQELDKDDESLRK	0.921909494	2	4.1512485
Q5XI73	VAVSADPNVPNVIVTR	1.144429756	2	4.1081886
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**0.958095144**	**0.4779858**	**13**
Q5XI78	FGLEGCEVLIPALK	1.038744265	2	2.9643772
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.149270657	3	5.0408688
Q5XI78	HHVLHDQNVDK	0.507461629	3	3.3729432
Q5XI78	ICEEAFTR	0.890734848	2	2.4102438
Q5XI78	IEQLSPFPFDLLLK	1.201819304	2	3.3763132
Q5XI78	LEAADEGSGDMK	0.918804785	2	2.8934822
Q5XI78	LNVLANVIR	1.164815293	2	2.5314195
Q5XI78	NITLSLVANPSHLEAADPVVMGK	0.988576379	2	4.9115877
Q5XI78	NTNAGAPPGTAYQSPLSLSR	1.113096199	2	3.8131936
Q5XI78	SSLATMAHAQSLVEAQPNVDK	0.436355399	3	3.90604
Q5XI78	SWDIFFR	0.856877405	2	2.3374112
Q5XI78	VIPEDGPAAQNPDK	0.854152138	2	2.7022362
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	0.912412109	3	4.3703184
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**1.020043903**	**0.9999586**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	1.074482013	2	3.6472714
Q5XI95	IIAVDINK	0.989557308	2	2.7880111
Q5XI95	MVATGVCGTDIK	0.975855122	2	2.6845891
Q5XI95	NNICTEIR	0.896474401	2	2.4097238
Q5XI95	TVGATDCVDPR	0.869055179	2	2.9722004
Q5XIA0	**DZI1L Zinc finger protein DZIP1L**	**0.930664708**	**0.816247**	**2**
Q5XIA0	EVCNHCRQPVDPVLLK	1.0607312	2	2.3689778
Q5XIA0	GQQELGRQADELK	0.927259621	2	2.4435472
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.054591085**	**9.978E-05**	**6**
Q5XIC0	ATQQDFENAMNQVK	0.824765917	2	4.5233135
Q5XIC0	GILVTSEGGITK	0.977850864	2	3.4250908
Q5XIC0	LHAVNEEECTTLR	1.047628296	2	4.1369224
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.767494875	2	5.1141229
Q5XIC0	WDAWNALGSLPK	1.464943086	2	3.436161
Q5XIC0	WLSEECINAIMSFVTR	0.914479539	2	2.3607206
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.302625815**	**0.1328038**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	1.48884422	2	2.6175022
Q5XIC1	VEGTPNDPNPNDPR	0.65830146	2	2.6029651
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.060533697**	**0.8559982**	**7**
Q5XIE6	AGIATHFVDSEK	0.674777104	2	3.2385626
Q5XIE6	AVLIDKDQTPK	1.104632607	2	2.9728868
Q5XIE6	GCAGVITLNRPK	1.063093636	2	2.6865139
Q5XIE6	HTETAEVLLER	0.938866833	2	2.5755217
Q5XIE6	INSCFSANTVEQILENLR	1.039838711	2	4.7273617

Q5XIE6	LHVLEEELLALK	1.150542697	3	4.6197519
Q5XIE6	QDGSPFAMEQIK	1.11962046	2	2.5645096
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.050317133**	**0.9930039**	**2**
Q5XIF3	HGWSYDVEGR	1.00151346	2	2.6996706
Q5XIF3	LDVTPLTGVPEEHIK	1.079142328	2	3.454114
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.030564763**	**0.0127753**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	0.936795321	2	4.1405959
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.103667113	2	5.4725628
Q5XIF6	DVNAAIAAIK	0.859046617	2	2.9043574
Q5XIF6	SIQFVDWCPTGFK	1.080170709	2	4.4519629
Q5XIF6	TIGGGDDSFTTFFCETGAGK	2.200254119	2	4.2608433
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**0.919228689**	**0.9984843**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	0.943331221	2	3.7668123
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	0.917137459	2	5.1550999
Q5XIH7	**PHB2 Prohibitin_2**	**0.929997311**	**9.567E-10**	**10**
Q5XIH7	AQVSLLIR	0.999901188	2	2.3424308
Q5XIH7	DLQMVNISLR	0.719466437	2	3.0894604
Q5XIH7	FNASQLITQR	0.869584005	2	3.7610543
Q5XIH7	IGGVQQDTILAEGLHFR	1.025610119	3	4.2019539
Q5XIH7	IVQAEGEAEAAK	0.85336298	2	3.8714015
Q5XIH7	IYLTADNLVLNLQDESFTR	1.753391014	2	4.7366509
Q5XIH7	LGLDYEER	0.969263071	2	2.3040402
Q5XIH7	LLLGAGAVAYGVR	2.190670126	2	3.4734044
Q5XIH7	VLPSIVNEVLK	0.920725596	2	2.7304127
Q5XIH7	VLSRPNAQELPSMYQR	1.122095164	2	4.5834775
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.129815997**	**1.898E-09**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	1.152398569	2	4.2065859
Q5XIM9	GATQQILDEAER	1.136510048	2	3.968919
Q5XIM9	GSGNLEAIHVIK	1.254077349	2	2.6489728
Q5XIM9	HGINCFINR	1.060093924	2	2.6171434
Q5XIM9	LGGSLADSYLDEGFLLDK	1.255465308	2	4.147615
Q5XIM9	LGGSLADSYLDEGFLLDKK	1.221383398	3	3.313375
Q5XIM9	SLHDALCVLAQTVK	0.74872371	2	3.571403
Q5XIM9	VAEIEHAEKEK	1.667266275	2	2.4486122
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.347669773	2	4.7454257
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.082988154**	**0.6487959**	**10**
Q5XIN6	AAEVEGEQVDNK	1.170376398	2	4.0901399
Q5XIN6	AMYLPDTLSPADQLK	1.06270974	2	2.3151057
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	1.029558328	2	4.6125813
Q5XIN6	FLQDTIEEMALK	1.192774283	2	2.9100878
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.195855211	2	3.9556801
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	1.110526984	3	4.7592864
Q5XIN6	LEEGGPVYSPPAQVVVK	0.990745906	2	2.781867
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.439636592	3	4.8372784
Q5XIN6	LLELQSIGTNNFLR	0.951972077	2	3.3529687
Q5XIN6	STLQTLPEIVAK	1.092984216	2	2.3853409
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**1.032168503**	**0.0775443**	**7**
Q5XIT9	AATGEEVSAEDLGGADLHCR	1.055182512	2	5.0071831
Q5XIT9	ALYGDTLVTGFAR	0.992220986	2	3.1113625
Q5XIT9	AQEIALQNR	0.843906739	2	2.5665846
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.410873242	3	4.9103823
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.011009056	2	4.9400587
Q5XIT9	LWDDGIIDPVDTR	1.150298138	2	3.1592622
Q5XIT9	LYGEEEVPAGGIITGIGR	0.96642271	2	4.5532465

Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.15344856**	**0.2557549**	**5**
Q5XIU9	FYGPAGPYGIFAGR	1.294746082	2	2.8888557
Q5XIU9	GGDGSPGGAGATAAR	1.090660932	2	3.2092588
Q5XIU9	GLATFCLDK	1.439423497	1	1.9577794
Q5XIU9	GLCSGPGAGEESPAATLPR	1.0136701	2	4.8029985
Q5XIU9	VFDVTK	1.174143347	1	2.0025599
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**1.097537868**	**0.9831598**	**6**
Q60587	AMDSDWFAQNYMGR	1.043050902	2	3.2143216
Q60587	AQDEGHLSDIVPFK	1.086605488	2	3.3294609
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.869874558	2	5.2683916
Q60587	DNGIRPSSLEQMAK	0.876626856	2	3.6151042
Q60587	DQLLLGPTYATPK	0.850795587	2	3.7270672
Q60587	NIVVVEGVR	0.925669505	2	3.0095494
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.162957003**	**0.6914153**	**5**
Q60759	DILGGNGISDEYHVIR	0.820303995	2	3.2240078
Q60759	DIVYEMGELGVLGPTIK	1.284172475	2	3.029068
Q60759	GYGCAGVSSVAYGLLTR	1.033169214	2	3.9812083
Q60759	HAMNLEAVNTYEGTHDIHALILGR	0.986730427	4	5.4645753
Q60759	SMMSVQSSLVMHPIYTYGSEEQR	0.944966571	3	3.8393822
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**0.974389662**	**0.4544764**	**2**
Q60817	IEDLSQQAQLAAAEK	0.974385494	2	4.5529814
Q60817	NILFVITKPDVYK	1.248315686	2	3.5473759
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.999994502**	**0.994696**	**3**
Q61029	SELVANNVTLPAGEQR	1.010163436	2	4.0796933
Q61029	SSTPLPTVSSSAENTR	0.999932841	2	2.9060812
Q61029	YGVNPGPIVGTTR	1.107645804	2	3.0791607
Q61043	**NIN Ninein**	**1.064984504**	**0.9053833**	**2**
Q61043	ERATAAAMKQEQEILER	1.06864258	2	2.3350024
Q61043	LQEENSILR	0.799890383	2	2.4039633
Q61233	**PLSL Plastin_2**	**1.013241645**	**0.9755713**	**2**
Q61233	ALENDPDCR	1.048121747	2	2.5192206
Q61233	MINLSVPDTIDER	1.013209504	2	3.5816855
Q61301	**CTNA2 Catenin alpha_2**	**1.179701022**	**4.494E-07**	**2**
Q61301	LLEPLVTQVTTLVNTSNK	1.330301933	2	4.043756
Q61301	TSVQTEDDQLIAGQSAR	1.123361844	2	4.6211648
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.966826555**	**0.8536183**	**5**
Q61335	AENEALAMQK	0.966529161	2	3.0555854
Q61335	KYMEENDQLKK+Oxidation(3)	1.086145884	3	3.3652515
Q61335	LKDELASTK	0.755093418	2	2.6220965
Q61335	YMEENDQLK	1.034094039	2	2.4103351
Q61335	YMEENDQLKK	1.009697339	2	2.5659626
Q61599	**GDIR2 Rho GDP_dissociation inhibitor 2**	**1.017097545**	**0.8780173**	**2**
Q61599	ATFMVGSYGPRPEEYEFLTPVEEAPK	1.204302067	3	3.6248403
Q61599	TLLGDVPVVADPTVPNVTVTR	0.965365764	2	4.6387277
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**0.856119684**	**0.4065185**	**3**
Q61656	ELAQQVQQVAAEYCR	0.687557829	2	2.6633575
Q61656	GDGPICLVLAPTR	0.947078084	2	3.4258864
Q61656	MLDMGFEPQIR	0.792374929	2	3.380897
Q61830	**MRC1 Macrophage mannose receptor 1**	**1.126234657**	**0.2483314**	**3**
Q61830	KMDPQPK+Oxidation(2)	1.066883444	1	1.9159701
Q61830	LKLPWHEAETYCK	1.092107012	2	2.3028827
Q61830	TGVAGGLWDVLSCEEK	1.289060084	2	3.1642962
Q61941	**NNTM NAD(P) transhydrogenase_ mitochondrial**	**0.95587109**	**0.5756294**	**11**

Q61941	EANSIVITPGYGLCAAK	0.860876067	2	3.6402056
Q61941	FFTGQITAAGK	0.992461693	2	2.4320633
Q61941	GITHIGYTDLPSR	1.041712973	2	3.5538142
Q61941	ILIVGGGVAGLASAGAAK	1.14593177	2	4.5779319
Q61941	KTTVLAMDQVPR	1.05912369	2	3.4984765
Q61941	MATQASTLYSNNITK	1.01587723	2	4.3309321
Q61941	QGFNVVVESGAGEASK	0.878877937	2	3.8651099
Q61941	SAPLLLPGR	1.390511478	2	2.3467336
Q61941	SLGAEPLEVDLK	1.076893883	2	3.0602899
Q61941	TTVLAMDQVPR	1.063457537	2	2.7558303
Q61941	VTIAQGYDALSSMANISGYK	1.192636343	2	5.3806281
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**1.469360972**	**0.0302106**	**2**
Q61990	AITIAGIPQSIIECVK	1.065272738	2	2.3327289
Q61990	IITLAGPTNAIFK	1.488237826	2	2.7305646
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.174279458**	**1.11E-16**	**4**
Q62095	HVINFDLPSDIEEYVHR	1.643942936	3	4.2602715
Q62095	SFLLDLLNATGK	1.382498312	2	3.9002957
Q62095	VGNLGLATSFFNER	1.363747816	2	2.7742918
Q62095	VGSTSENITQK	1.129759295	2	2.9357703
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.184712898**	**4.552E-15**	**17**
Q62261	ALVADSHPESER	1.133859196	2	3.2754903
Q62261	EGMQLISEKPETEAVVK	1.050028082	2	2.8231454
Q62261	EGMQLISEKPETEAVVKEK	1.256062565	2	2.3889315
Q62261	EIEELQSQAQALSQEGK	1.478872664	2	2.8213348
Q62261	FESLEPEMNNQASR	1.108963175	2	3.5397666
Q62261	HDTSASTQSTPASSR	1.428965944	2	2.7960157
Q62261	HQILEQAVEDYAETVHQLSK	1.16030519	3	6.1884718
Q62261	LEDLEVIQHR	1.008695346	3	3.3586299
Q62261	LISDINK	1.509044672	1	1.9508045
Q62261	LLDPEDISVDHPDEK	1.21547075	2	3.3568912
Q62261	LTTLELLEVR	1.678980025	2	2.5658026
Q62261	LVSDGNINSDR	1.131395354	2	2.8243861
Q62261	LVSQDNFGFDLPAVEAATK	1.10537152	2	3.9077055
Q62261	SQNIITDSSSLNAEAIR	1.298010772	2	4.9906144
Q62261	TLETPAAQMEGFLNR	2.34001437	2	2.6526442
Q62261	TQTAIASEDMPNTLTEAEK	1.075350964	2	5.5398765
Q62261	VIESTQDLGNDLAGVMALQR	0.114089998	2	3.8343089
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**0.983717757**	**0.9626096**	**3**
Q62425	FYSVNVDYSK	1.199573981	1	2.6027362
Q62425	KNNPEPWNK	0.843184809	2	2.5666802
Q62425	LGPNEQYK	0.944347353	2	2.3444207
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.097787319**	**0.6255215**	**5**
Q62452	AMEIAEALGR	0.905662059	2	3.6241939
Q62452	GAGVTLNVLEMTADDLENALK	1.128122074	3	5.8894067
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(11)	1.563037631	2	3.5697145
Q62452	WLPQNDLLGHPK	1.10349416	2	3.3498611
Q62452	YTGTRPSNLAK	0.9372215	2	2.9812493
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.003367577**	**0.9961193**	**6**
Q62465	ACGLNFADLMGR	1.152138217	2	2.8041272
Q62465	GVDIVMDPLGGSDTAK	0.935859382	2	4.1826386
Q62465	IDSVWPFEK	0.980463798	2	2.3594468
Q62465	TVENVTVFGTASASK	1.146820875	2	3.2539334
Q62465	VLLVPGPEKET	0.921228492	2	2.7051446
Q62465	VVTYGMANLLTGPK	1.027471893	2	2.5391309
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.030755702**	**3.662E-09**	**2**

Q62636	INVNEIFYDLVR	1.681431152	2	3.9744825
Q62636	LVVLGSGGVGK	0.89302738	2	2.5518503
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.948699939**	**0.9983059**	**6**
Q62651	EVDVGLAADVGTLQR	0.844874667	2	3.3603811
Q62651	HVLHVQLNRPEK	0.870579503	2	3.430167
Q62651	MMADEALDSGLVSR	0.975241484	2	3.351325
Q62651	RIPEEVSDHNYESIQVTSAQK	0.90771621	3	6.4499397
Q62651	SLVNELTFTAR	0.954923689	2	3.5063622
Q62651	YCTQDAFFQVK	0.95084541	2	2.7149467
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**1.674353805**	**0.305299**	**5**
Q62730	AVLVTGADSGFGHALAK	1.249804379	2	4.189218
Q62730	EIQENYGQEYVHTQK	1.114689652	2	4.5205498
Q62730	LSVLQMDVTKPEQIK	2.067453724	2	3.6356719
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.738858862	3	4.2271247
Q62730	VVTIHPGGFQTNIVGSQDSWDK	1.11990299	2	5.5863495
Q62736	**CALD1 Non_muscle caldesmon**	**0.882212801**	**0.0014119**	**11**
Q62736	ASGDKEAEGAPQVEAGK	1.030511528	2	4.617053
Q62736	ASGDKEAEGAPQVEAGKR	1.052601389	3	3.8012998
Q62736	EEIERR	0.894280738	1	1.9036895
Q62736	EFDPTITDGSLSVPSR	0.881109994	2	3.1884477
Q62736	GGNLGENQIKDEK	0.994115439	2	3.3148808
Q62736	LEQYTNAIEGTK	1.035777594	2	3.5919383
Q62736	MQNNSAENETAEGEEKGESR	0.876263794	3	4.6092997
Q62736	NDDDEEEAAR	5.808626621	2	2.7146745
Q62736	RGETESEEFEK	1.083134902	2	2.9351661
Q62736	RRGETESEEFEK	1.311470766	2	3.2273986
Q62736	VLEEEEQR	1.08253698	2	2.4948809
Q62745	**CD81 CD81 antigen**	**1.031564335**	**0.9933646**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.110512208	2	2.9008765
Q62745	QFYDQALQQAVMDDDANNAK	1.006064349	2	4.6036663
Q62769	**UN13B Protein unc_13 homolog B**	**0.849770013**	**0.7627983**	**2**
Q62769	DHMVREETRNLTPK	0.829869049	2	2.5255313
Q62769	SNDEVAREFVK	1.008433538	1	2.0405402
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.255907253**	**0.1695373**	**5**
Q62785	ANEEDEQEEGGDGASGDPK	0.904645859	2	4.6185298
Q62785	ANEEDEQEEGGDGASGDPKK	1.531884885	3	3.3064353
Q62785	GVEGLIDIENPNR	0.985595586	2	2.3491848
Q62785	KVTQLDLDGPK	0.835430349	2	2.4684751
Q62785	YMKMHLAGKTEQAK	1.234301759	2	2.4377403
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.107220388**	**0.9999995**	**2**
Q62789	IILDELVQR	1.006589489	2	3.6325858
Q62789	WIPQNDLLGHPK	1.10349416	2	3.3498611
Q62812	**MYH9 Myosin_9**	**1.031333781**	**9.9E-20**	**61**
Q62812	ADFCIIHYAGK	1.185512128	2	2.6972365
Q62812	ALEEAMEQK	1.090314648	2	2.7260249
Q62812	ALELDSNLYR	1.257042371	2	3.5549428
Q62812	ALEQQVEEMK	0.641345254	2	3.0122452
Q62812	ANLQIDQINTDLNLER	1.291584228	2	4.7973003
Q62812	ASIAALEAK	1.036550073	2	2.3363271
Q62812	ASREEILAQAK	0.797454368	2	3.1215925
Q62812	CQYLQAEK	1.307612405	1	1.9304417
Q62812	DFSALESQLQDTQELLQEENR	1.173350431	3	6.3534551
Q62812	DLEAHIDTANK	0.866415365	2	3.6386538
Q62812	DLQGRDEQSEEK	1.436506841	2	3.2150695
Q62812	EEILAQAK	1.053467489	1	2.2351959
Q62812	ELEDATETADAMNR	0.748112862	2	4.2396235

Q62812	ELETQISELQEDLESER	1.014709016	2	4.9737682
Q62812	HEAMITDLEER	1.124669343	2	3.4345751
Q62812	HEDELLAK	1.164982386	2	3.2255442
Q62812	HSQAVEELAEQLEQTK	1.164731855	2	4.91044
Q62812	HSQAVEELAEQLEQTKR	1.121430649	3	5.717298
Q62812	IIGLDQVAGMSETALPGAFK	1.424591986	2	5.8915477
Q62812	IRELETQISELQEDLESER	1.198466806	2	5.164259
Q62812	KEEELQAALAR	1.174977952	2	3.2767961
Q62812	KKVEAQLQELQVK	1.186822467	2	4.723196
Q62812	KLEEDQIIMEDQNCK	1.038598993	2	5.6856685
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.150448372	2	5.7469759
Q62812	KQELEEICHDLEAR	1.14572499	2	4.5441976
Q62812	KVEAQLQELQVK	1.18673233	2	3.9437156
Q62812	LDPHLVLDQLR	1.437668259	3	3.4101036
Q62812	LEEDQIIMEDQNCK	1.137150585	2	3.3287184
Q62812	LEGDSTDLSDQIAELQAQIAELK	1.006070827	2	4.9716363
Q62812	LEVNLQAMK	1.185515078	2	2.6775594
Q62812	LQEMESAVK	0.932945934	2	2.417758
Q62812	LQQELDDLLVDLDHQR	0.942572321	2	4.7131896
Q62812	LQVELDSVTGLLNQSDSK	1.206973967	2	5.7063804
Q62812	LTEMETMQSQLMAEK	1.024374548	2	4.405055
Q62812	MEDGVGCLETAEEAK	0.839064029	2	4.5949249
Q62812	MQQNIQELEEQLEEEESAR	0.964028508	2	5.940897
Q62812	NAEQFKDQADK	1.313672225	2	3.643935
Q62812	NKHEAMITDLEER	1.067151741	3	3.668582
Q62812	NLPIYSEEIVDMYK	1.247797264	2	3.2805531
Q62812	NMDPLNDNIATLLHQSSDK	1.200663669	2	5.0592389
Q62812	NTDQASMPDNTAAQK	1.000013819	2	5.3137226
Q62812	NTDQASMPDNTAAQK+Oxidation(7)	1.487110111	2	4.8961158
Q62812	QAQQERDELADEIANSSGK	1.067544546	3	4.1532002
Q62812	QIATLHAQVTDMK	0.594514866	2	2.3622084
Q62812	QLEEAEEEAQR	1.22727403	2	3.4950795
Q62812	QSVSNLEK	1.034934483	2	2.401686
Q62812	QTLENERGELANEVK	1.148445565	2	3.4049075
Q62812	RGDMPFVVTR	0.981834163	2	2.6303251
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.05746945	3	5.6645689
Q62812	RQLEEAEEEAQR	1.260656377	2	4.2632041
Q62812	SMEAEMIQLQEELAAAER	0.9840666	2	4.5241213
Q62812	TDLLLEPYNK	1.238030205	2	2.6810634
Q62812	TELEDTLDSTAAQQELR	0.964762873	2	5.4887471
Q62812	THEAQIQEMR	1.192570498	2	3.4757388
Q62812	TQLEELEDELQATEDAK	1.049342744	2	6.679472
Q62812	VAEFTTDLMEEEEK	1.187629095	2	4.2220039
Q62812	VEAQLQELQVK	1.243093486	2	3.675488
Q62812	VEDMAELTCLNEASVLHNLK	1.366292479	2	4.3174901
Q62812	VISGVLQLGNIVFK	1.047592767	2	3.6538942
Q62812	VSHLLGINVTDFTR	1.251328257	2	3.692349
Q62812	YEILTPNSIPK	1.104300611	2	3.248054
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.137721859**	**0.7192763**	**8**
Q62826	ADILEDKDGK	1.0832586	2	2.6777706
Q62826	AFITNIPFDVK	0.745923012	2	3.1363318
Q62826	GIGMGNLGPAGMGMEGIGFGINK	1.008771069	2	4.8809485
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.1599352	2	4.8898392
Q62826	INEILSNALK	1.111694627	2	2.3459857
Q62826	MGANNLERMGLERMGANSLER	1.314126024	2	2.4031925
Q62826	MGPVMDRMATGLER+Oxidation(1)Oxidation(5)Oxidation(8)	0.921641091	2	2.5765777

Q62826	VGSEIER	0.98457347	1	1.9637581
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.415760975**	**0.0007267**	**2**
Q62871	ADAEEEAATR	1.459906268	2	2.6302412
Q62871	SVSTPSEAGSQDSGDGAVGSR	1.400214618	2	5.3513212
Q62902	**LMAN1 Protein ERGIC_53**	**1.103587783**	**0.0005169**	**5**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.096166997	2	4.2838597
Q62902	GHPDLQGQPADDIFESIGDR	0.990841896	2	5.2215128
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.355292715	3	4.137229
Q62902	YQEEFEHFQQELDK	1.133671266	2	5.1299419
Q62902	YVSSLTEEISR	1.254805012	2	2.6516085
Q62910	**SYNJ1 Synaptojanin_1**	**0.703913289**	**0.290025**	**2**
Q62910	MLIQLPSASQSK+Oxidation(1)	0.81535313	2	2.316417
Q62910	NQTLTDWLLDAPK	0.213296869	2	2.4895322
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.987547383**	**0.9949903**	**2**
Q62967	GLQVAPVLLSDELK	0.987563567	2	3.3702075
Q62967	VYGVEGDLSEVAR	0.890763987	2	3.2871408
Q63041	**A1M Alpha_1_macroglobulin**	**1.081793911**	**0.6107794**	**13**
Q63041	AEDITHNGIVYTPK	1.035604991	2	3.3510671
Q63041	AEQGAYLGPLPYK	1.037286911	2	3.0449498
Q63041	DLSSSDLTTASK	0.671069804	2	2.5130827
Q63041	DTVVKPVIVEPEGIEK	0.943132743	2	3.0322862
Q63041	GSIFNSGSHVLPLEQGK	1.216436352	2	4.0363312
Q63041	HSQGNTWLTAFVLK	1.269673342	2	2.3564434
Q63041	IKEDGTGIELTGTGSCEIANTLSK	0.978188233	2	3.8941062
Q63041	KLQDQSNIQR	1.177382073	2	2.476748
Q63041	LIVYTILPNEELIADVQK	1.515591698	2	4.5302505
Q63041	LQDQSNIQR	0.933718756	2	2.7995372
Q63041	QDLNDNDAYSVFQSIGLK	0.855517709	2	2.6636229
Q63041	YNILPEAEGEAPFTLK	1.097810029	2	4.2273674
Q63041	YVVLVPSELYAGVPEK	0.866983928	2	3.2127221
Q63060	**GLPK Glycerol kinase**	**1.102334242**	**7.669E-11**	**11**
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.066982642	3	4.2998829
Q63060	AVLGPLVGAVDQGTSSTR	1.030233085	2	5.4863181
Q63060	CVFSEHGLLTTVAYK	1.277239328	2	4.2795863
Q63060	DCGIPLSHLQVDGGMTSNK	1.153063419	2	4.2049418
Q63060	EILQSVYECIEK	1.070534939	2	3.8493617
Q63060	FEPQINAEESEIR	1.076026181	2	3.5818548
Q63060	KVQEAVEENR	1.247867891	2	3.5605237
Q63060	LGQLNIDISNIK	1.387225606	2	3.327307
Q63060	NTYGTGCFLLCNTGHK	1.262015659	2	3.9399562
Q63060	TAELLSHHQVEIK	1.45384445	3	3.7696936
Q63060	VQEAVEENR	0.925228764	2	3.3733737
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**1.148305861**	**4.411E-10**	**10**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.714891295	3	6.054112
Q63081	GESPVDYDGGR	1.096810321	2	2.9169257
Q63081	GSFSEQGINEFLR	0.957081795	2	4.1081104
Q63081	GSTAPVGGGSFPNITPR	1.113279565	2	4.8268476
Q63081	HQSLGGQYGVQGFPTIK	1.08772497	2	5.0309415
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.790364122	3	5.393292
Q63081	NLEPEWAAAATEVK	1.046620305	2	4.1971397
Q63081	NSYLEVLLK	1.014773191	2	2.9825845
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.225321144	2	5.0734191
Q63081	TGEAIVDAALSALR	1.015263958	3	4.717514
Q63108	**EST3 Liver carboxylesterase 3**	**1.307980581**	**2.328E-09**	**4**
Q63108	GGTSKEEINLSK	1.203367072	2	3.7270117
Q63108	LDPMTATSLLK	0.932088085	2	2.4435873
Q63108	QKTEEELLETTLK	1.023633541	2	3.4457505

Q63108	SSFLLNLPEEAIPVAVEK	1.351946887	2	4.7667165
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.14991983**	**0.3204095**	**4**
Q63120	ACALLPDLEILPGGDMAEIGEK	1.266031361	2	4.2468367
Q63120	NIQVQNMKNK	1.004593634	1	1.9016365
Q63120	YFAWEPSFQEQVQGIR	1.18828264	2	4.4545555
Q63120	YLGGDDLDTSAIR	0.451816154	2	2.5682964
Q63150	**DPYS Dihydropyrimidinase**	**1.049682409**	**7.772E-16**	**9**
Q63150	ALGKDDFTK	1.121040684	2	2.642771
Q63150	DQTCTPIPVKR	1.048633219	2	2.4962854
Q63150	EIGAIAQVHAENGDLIAEGAK	1.144632477	2	5.153172
Q63150	FVAVTSTNAAK	1.009124827	2	2.9790983
Q63150	GSSLIEAFETWR	1.329048402	2	3.1840332
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	0.944108777	3	3.7177749
Q63150	VVNDDFSQVADVLVEDGVVR	1.343329542	2	5.9371157
Q63150	VVYEAGVFDVTAGHGK	1.15506738	2	4.2350154
Q63150	VVYGEPIAAGLGTDGTQYWNK	0.999133653	2	5.3665123
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.062380387**	**7.514E-10**	**18**
Q63270	AVEAGLNVKPYVK	1.138292761	2	2.6743414
Q63270	DFSDSSQDPDFTQVVELDLK	1.594404316	2	4.9540691
Q63270	FVEFFGPGVAQLSIADR	1.436049364	2	5.3367071
Q63270	GFQVAPDHHNDHK	1.220537093	2	3.4489317
Q63270	IDFEKEPLGVNAQGQQVFLK	1.015657737	3	4.9940352
Q63270	IIPPGSGIIHQVNLEYLAR	1.536837003	2	3.4668832
Q63270	KNDIENILNWSIMQHK	1.070020437	3	4.0876884
Q63270	NCDEFLVK	1.195329886	1	2.2393231
Q63270	NDIENILNWSIMQHK	1.246424478	2	3.1745555
Q63270	NQDLEFER	1.036017045	1	2.6583519
Q63270	QAPQTVHLPSGETLDVFDAAER	1.13565594	3	3.6551054
Q63270	SIEVPFKPAR	1.129320124	2	2.5005805
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.580539411	3	4.9680886
Q63270	SPPFFESLTLDLQPPK	0.95601205	3	3.5933468
Q63270	SWNALAAPSEK	1.058409268	1	2.3006413
Q63270	TSLSPGSGVVTYYLR	1.250297098	2	3.1356893
Q63270	VILQDFTGVPAVVDFAAMR	1.485945868	2	4.6512413
Q63270	YQQAGLPLIVLAGK	1.111916632	2	3.7571218
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.301204764**	**9.9E-20**	**17**
Q63276	AHGHFLFVVGEDDKNLNSK	1.691851456	2	6.10148
Q63276	ASEVGEVDLER	1.136909988	2	3.9402602
Q63276	DDKGNLFNSQAFYR	1.386002742	2	3.5308537
Q63276	GNLFNSQAFYR	1.285350252	2	3.1883316
Q63276	LCHPYFPVEGK	1.946846725	3	3.4663103
Q63276	LTAVPLSALVDEPVHIR	2.434313628	2	3.8724332
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	1.104043165	3	4.2309041
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.420453031	2	4.6477695
Q63276	QHLNPGFNSQL	1.465775974	2	3.5262797
Q63276	QITATVLINGPNFVSSNPHVYR	1.368448582	3	4.9434605
Q63276	TFEETADKDSK	1.114048402	2	3.7505481
Q63276	VDLEYFEEGVEFLLR	2.316291768	2	4.4044065
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	2.130482403	2	5.6035414
Q63276	VISSSLDSLILER	0.46141977	2	4.4030051
Q63276	VTGLTPFQVVCLQASLK	1.492562587	3	4.1458602
Q63276	WYVAPGVTR	1.111919852	2	2.647073
Q63276	YCFPIEK	1.113395641	2	2.6318409
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.233714752**	**0.5124166**	**28**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.073276891	3	4.5857129

Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.298766805	3	4.5820432
Q63342	DGLLFGPYESQEK	0.807212063	2	2.6061347
Q63342	EGQESPPSPPEWK	0.726839594	2	2.4957814
Q63342	ELFESDLDRITEHVEAAMEMVPVLK	1.247579075	3	4.647511
Q63342	GGYDVEIR	0.97449274	2	2.4357567
Q63342	GQDSTQLLDHLCANVIPK	1.0679357	2	4.1515222
Q63342	IHELFPLLNMDK	0.951538062	2	2.5913014
Q63342	IHYDSIK	1.115509363	1	2.1046412
Q63342	IMNAGQEEGIDNFGTYALNALR	0.743366559	2	4.8476253
Q63342	ISDIPVTAIR	1.063191752	2	2.7572808
Q63342	ITEHVEAAMEMVPVLK	0.724244157	2	4.0258183
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	0.804978619	3	7.5148835
Q63342	LEEETGQVVGFHQPGSIR	1.130676249	2	4.9664674
Q63342	LNKPADFTGK	1.469995458	2	2.6556187
Q63342	LTSEDLSDDVFK	1.110876588	2	3.8376133
Q63342	LVCLTLATDDVDPEGNESVWYK	2.377674677	2	2.8722744
Q63342	NITDELGVLGVAGPYAR	1.175176532	2	5.0043983
Q63342	NYPATIIQEPLVLTEPTR	1.236123776	3	4.9277558
Q63342	REDSAALYER	0.675686694	2	3.0354998
Q63342	TNWHATEQYIIEPEK	0.991517449	2	4.1655359
Q63342	VGFTNISHMLTPR	1.15284125	2	3.2231131
Q63342	VGVIDLSPFGK	1.045279048	2	3.2275813
Q63342	VIGNTTSGSYSYSIQK	1.125292845	2	4.5479202
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.147311498	3	5.881083
Q63342	WIEEAAVR	0.952518048	2	2.6034269
Q63342	WTTTQYTEAK	1.133487616	2	2.8981152
Q63342	YLSDWILHGEPPFDLIELDPNR	1.515261607	3	4.7060146
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.11399831**	**0.2264906**	**8**
Q63347	ALDEGDIALLK	1.137962817	2	2.7931871
Q63347	ESDTGLAPPALWDLAADK	0.871454714	2	2.4763725
Q63347	FDDGAGGDNEVQR	1.08065595	2	4.2104325
Q63347	FVVDLSDQVAPTDIEEGMR	1.135276462	2	3.3776262
Q63347	IINADSEDPK	1.082260228	2	2.8358204
Q63347	QTLQSEQPLQVAR	1.379472344	2	4.1298409
Q63347	QVEDDIQQLLK	0.860879268	2	2.7452292
Q63347	TMLELINQLDGFDPR	1.109368567	2	3.1821039
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.126152359**	**0.0841757**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.146496462	2	6.2724776
Q63362	LENLLQGGEVEEVILQAEK	1.046281165	2	2.5762055
Q63362	TTGLVGLAVCDTPHER	1.164130937	2	4.149106
Q63362	YTEQITSEK	1.275575391	1	2.1443102
Q63377	**AT1B3 Sodium/potassium_transporting ATPase subunit beta_3**	**1.18104137**	**0.4523655**	**2**
Q63377	EENIANIVTYPDDGLIDLK	1.196905184	2	4.445622
Q63377	LFIYNPTSGEFLGR	1.16094049	2	2.521843
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**0.954416866**	**0.6797776**	**2**
Q63413	GLAITFVSDENDAK	0.437871653	2	2.7775745
Q63413	NCPHIVVGTPGR	0.955394644	2	2.8433394
Q63429	**UBC Polyubiquitin_C**	**0.964076636**	**0.9999986**	**2**
Q63429	TITLEVEPSDTIENVK	1.007612937	2	4.8192639
Q63429	TLSDYNIQK	0.963792207	2	2.8584158
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.179894714**	**9.9E-20**	**12**
Q63448	ADWLDSEAPLAAYR	1.064389604	2	4.1976452
Q63448	EIHALASAGKPLASWTAQR	1.224436634	2	4.542738
Q63448	FHEHTHSSSVPPSLR	1.066883444	2	2.7376316
Q63448	GGYISGEQTGK	1.2936191	2	3.0613279

Q63448	LGASLGSLSSGR	1.090560194	2	2.5648355
Q63448	NLWAAVLQQSGVLER	1.139098114	2	4.0196481
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.623336588	3	4.0720463
Q63448	RDSVLWSDIPK	1.801311105	2	2.3012884
Q63448	TIFLDLIELQR	2.211534736	2	3.5535891
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.404324178	3	4.7461858
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.314710809	3	4.7752557
Q63448	TVNFLEAYPGILGQK	1.417890564	2	5.4015408
Q63507	**RL14 60S ribosomal protein L14**	**1.306461005**	**0.0038642**	**2**
Q63507	CMQLTDFILK	1.779108964	2	2.3912032
Q63507	LVAIVDVIDQNR	1.320900063	2	4.4913831
Q63520	**SYCP3 Synaptonemal complex protein 3**	**0.865914237**	**0.2325195**	**2**
Q63520	KVMMETQQQEMANVR	0.865914237	2	2.686219
Q63520	VMMETQQQEMANVRK	0.865914237	2	2.5421925
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.238524061**	**0.0625355**	**3**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	0.885239219	3	4.9601693
Q63524	HEQEYMEVR	1.171985285	2	3.3929074
Q63524	HEQEYMEVR+Oxidation(6)	1.291978953	2	2.4963093
Q63525	**NUDC Nuclear migration protein nudC**	**1.028379606**	**4.187E-07**	**4**
Q63525	GQAPVIDGELYNEVK	1.315404131	2	3.2409172
Q63525	LSDLDSETR	0.92133738	2	2.3230352
Q63525	LVTSDPEINTK	1.247962367	2	2.9003344
Q63525	WTQTLSELDLAVPFR	1.027499005	2	2.6149111
Q63556	**SPA3M Serine protease inhibitor A3M (Fragment)**	**1.176197224**	**0.5244227**	**2**
Q63556	MQQVEASLQPETLK+Oxidation(1)	1.162655478	2	3.4067891
Q63556	MQQVEASLQPETLKK+Oxidation(1)	1.02745635	2	2.8168392
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.020032177**	**0.5289573**	**7**
Q63569	AMEVDERPTEQYSDIGGLDK	0.934128812	3	4.7174616
Q63569	CTDDFNGAQCK	1.39358245	2	3.4859915
Q63569	DSYLILETLPTEYDSR	1.240806458	2	2.4669056
Q63569	MATVWDEAEQDGIGEEVLK	1.016577016	2	3.1952558
Q63569	MNVSPDVNYEELAR	1.090227305	2	3.3797123
Q63569	QTYFLPVIGLVDAEK	1.076932627	2	2.4265258
Q63569	TMLELLNQLDGFQPNTQVK	0.731978856	2	3.7141953
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.021008198**	**0.0004574**	**4**
Q63570	FDAQTGADR	1.057224192	2	2.5137155
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.831175636	3	5.848506
Q63570	KDEQEHEFYK	0.891620852	2	3.0981023
Q63570	RFDAQTGADR	0.998395691	2	2.6501055
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.421902344**	**3.419E-11**	**4**
Q63584	ITDSAGHILYAK	1.421965157	2	3.6730776
Q63584	LEDLSESIVNDFAYMK	1.49455806	2	4.5899539
Q63584	NYEEIAK	1.138371965	1	2.1715348
Q63584	RLEDLSESIVNDFAYMK	1.195912697	2	4.3021975
Q63598	**PLST Plastin_3**	**1.236893815**	**0.0104495**	**12**
Q63598	AESMLQQADK	0.970015852	2	3.1439896
Q63598	ATDDIIVNWVNGTLSEAGK	1.136872083	2	5.0451846
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	1.014735745	3	3.488802
Q63598	HVIPMNPNTDDLFK	1.038522657	2	3.0191822
Q63598	IDINMSGFNETDDLKR	1.141972544	2	4.2491045
Q63598	INNFSADIK	1.123994106	2	2.4944031
Q63598	KLENCNYAVELGK	1.163308073	2	3.6742704
Q63598	NEALAALLR	1.11056408	2	2.6012967
Q63598	VDLNSNGFICDYELHELFK	1.262637346	2	4.1133699
Q63598	VYALPEDLVEVKPK	1.288878584	2	2.7436948

Q63598	YPALTKPENQDIDWTLLEGETR	0.951194576	3	5.2382455
Q63598	YTLNVMEDLGEGQK	1.141944259	2	3.8818831
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.113175876**	**0.0025057**	**8**
Q63610	AREQAEAEVASLNR	1.823902454	2	2.8974128
Q63610	EQAEAEVASLNR	0.890398613	2	2.577198
Q63610	IQVLQQQADDAEER	1.20366432	2	5.0865884
Q63610	KIQVLQQQADDAEER	1.004793037	2	4.8643398
Q63610	KLVIIEGDLER	1.003408475	3	3.8473916
Q63610	LVIIEGDLER	0.984969651	2	2.7553978
Q63610	MELQEIQLK	0.885497282	2	2.8501985
Q63610	YSQKEDKYEEEIK	1.078694978	2	4.6391745
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.068218152**	**1.798E-07**	**11**
Q63617	EGETPDEKESGDKSEAQKPNEK	1.538081322	3	3.5457647
Q63617	GQAGPEGVPPAPEEEKK	0.87686624	2	3.5048003
Q63617	LIPEMDQIFTDVEMTTLEK	1.577631222	2	4.6758575
Q63617	LYQPEYQEVSTEEQR	1.065818238	2	4.9301648
Q63617	NINADEAAAMGAVYQAAALSK	1.127315177	2	5.1948733
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.242430464	2	3.8691392
Q63617	TLGGLEMELR	1.161451387	2	2.5957794
Q63617	VAIVKPGVPMEIVLNK	1.061308866	2	2.6579511
Q63617	VEFEELCADLFDR	1.752017583	2	3.5904388
Q63617	VESVFETLVEDSPEEESTLTK	1.01531051	2	3.8139968
Q63617	VLQLINDNTATALSYGVFR	1.27983123	2	5.2757835
Q63716	**PRDX1 Peroxiredoxin_1**	**1.092782949**	**7.803E-11**	**15**
Q63716	ADEGISFR	1.012361573	2	3.1503272
Q63716	ATAVMPDGQFK	1.011301664	2	2.8500004
Q63716	ATAVMPDGQFK+Oxidation(5)	1.204065253	2	2.3372262
Q63716	DISLSDYK	0.808740193	1	1.9369652
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.060704182	3	6.3296194
Q63716	KQGGLGPMNIPLVSDPK	1.087170388	2	3.9838037
Q63716	KQGGLGPMNIPLVSDPKR	0.88073121	3	4.0426483
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.556899121	3	3.9178798
Q63716	LVQAFQFTDK	2.356488011	2	3.3724554
Q63716	QGGLGPMNIPLVSDPK	0.899918307	2	3.1719053
Q63716	QGGLGPMNIPLVSDPK+Oxidation(7)	1.429165113	2	2.7833498
Q63716	QITINDLPVGR	1.079327457	2	3.3390398
Q63716	RTIAQDYGVLK	1.09938434	2	2.6977775
Q63716	SVDEILR	1.086354173	2	2.4898698
Q63716	TIAQDYGVLK	1.053153959	2	3.4605329
Q63755	**PRDM2 PR domain zinc finger protein 2**	**0.889385657**	**0.7268903**	**2**
Q63755	LSFNVELGKMSPNK	0.778983709	2	2.4230919
Q63755	VKAAAATPFQGPFLKE	0.903952168	2	2.3019567
Q63768	**CRK Adapter molecule crk**	**0.923456197**	**0.384703**	**2**
Q63768	IGDQEFDSLPALLEFYK	0.942737686	2	3.6276994
Q63768	VPNAYDKTALALEVGELVK	1.310068063	2	2.9085259
Q63797	**PSME1 Proteasome activator complex subunit 1**	**1.013280863**	**0.5729325**	**8**
Q63797	ISELDAFLKEPALNEANLSNLK	0.954729262	2	5.2696695
Q63797	KGDEDDKGPPCGPVNCNEK	1.002608594	3	5.0365434
Q63797	KISELDAFLKEPALNEANLSNLK	1.085393906	3	6.2888603
Q63797	LEGFQTQISK	1.206279822	2	2.6221325
Q63797	QLVHELDEAEYQEIR	1.092499302	2	4.3857746
Q63797	TENLLGSYFPK	0.977633868	2	3.3354642
Q63797	VDVFREDLCSK	1.135611423	2	2.7659054
Q63797	VFELMTSLHTK	1.350830623	2	2.5248857
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.098429651**	**0.1211081**	**4**
Q63798	AFYAELHHIISSNLEK	1.119294767	2	3.7250743
Q63798	IEDGNDFGVAIQEK	1.051549863	2	4.5267553

Q63798	KIISLSQLLQEDSLNVADLSSLR	2.757643946	2	4.5213685
Q63798	TKVEAFQTAISK	1.187775205	2	3.4474483
Q63836	**SBP2 Selenium_binding protein 2**	**0.819165446**	**0.0623499**	**4**
Q63836	EGSVMLQVDVDTVNGGLK	1.461658887	2	2.5620518
Q63836	GGSVQVLEDQELTCQPEPLVVK	0.905155075	2	5.1906209
Q63836	IYVVDVGSEPR	0.760583057	2	3.7739532
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.033975951	3	4.1902328
Q63862	**MYH11 Myosin_11 (Fragments)**	**0.876357245**	**0.0520475**	**2**
Q63862	LQQELDDLVVDLDNQR	0.476666017	2	4.292026
Q63862	SLEAELMQLQEDLAAAER	1.154968183	2	2.9223065
Q63945	**SET Protein SET**	**1.143046185**	**4.201E-06**	**2**
Q63945	IDFYFDENPYFENK	1.543001724	2	3.5946901
Q63945	VEVTEFEDIK	0.993459412	2	2.6153038
Q63965	**SFXN1 Sideroflexin_1**	**1.027020727**	**0.9946348**	**4**
Q63965	NILLTNEQLENAR	0.873539893	2	4.5019326
Q63965	QGIVPAGLTENELWR	0.998902457	2	2.6962218
Q63965	WDQSTFIGR	0.813600099	2	2.3649459
Q63965	YAYDSAFHPDTGEK	1.043622868	2	4.2982674
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**0.93916466**	**2.018E-08**	**17**
Q64057	AWNIWADIPAPK	0.951303618	2	3.7978272
Q64057	DYEETIGK	0.640471981	1	2.0558882
Q64057	EDNEGVFNGSWGGR	0.667853257	2	3.4862349
Q64057	FKNEEEVFEWNNEVK	0.936360453	2	5.802444
Q64057	GAPTTSLVSIAVTK	0.925173316	2	4.9187026
Q64057	GEVITTYCPANNEPIAR	0.911347368	2	5.3992472
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.86204101	2	5.8571663
Q64057	LFLHESIHDEVVDR	1.270137058	2	3.9668601
Q64057	NEEEVFEWNNEVK	0.76403017	2	4.5607667
Q64057	QAVSMFVQAVEEAK	0.773822255	2	2.8087535
Q64057	QGLSSSIFTK	0.762294277	2	2.3749559
Q64057	QVALMVQER	0.886159886	2	2.4274278
Q64057	STCTINYSTALPLAQGIK	0.859104893	2	4.9659343
Q64057	VGNPWDPNILYGPLHTK	1.35449424	3	3.6846783
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	0.865786518	3	6.0657763
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(2)	1.041524036	3	6.0388851
Q64057	VNLLSFTGSTQVGK	1.433952119	2	4.7510214
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**1.053594074**	**0.8607859**	**2**
Q640L5	NEKIRSLESNINTEHEK	1.051857932	2	2.3783941
Q640L5	TELEKTTNSVKELER	1.066807757	2	2.3333199
Q64119	**MYL6 Myosin light polypeptide 6**	**1.16693375**	**2.357E-13**	**7**
Q64119	DQGTYEDYVEGLR	0.94348454	2	3.2185175
Q64119	EGNGTVMGAEIR	0.980549563	2	2.5300565
Q64119	HVLVTLGEK	1.176892237	2	2.5632961
Q64119	ILYSQCGDVMR	2.039233405	2	3.1396596
Q64119	NKDQGTYEDYVEGLR	1.112867818	2	4.2827415
Q64119	VFDKEGNGTVMGAEIR	1.210810587	2	3.9720469
Q64119	VLDFEHFLPMLQTVAK	1.121985374	2	4.9660754
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**1.276052667**	**4.075E-06**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.279231158	2	5.248879
Q64122	LNGTDPEDVIR	1.224251157	2	2.7841108
Q64176	**EST22 Liver carboxylesterase 22**	**1.23555121**	**7.62E-09**	**4**
Q64176	AISESGVALTAGLVK	1.085563196	2	4.8758812
Q64176	EGYLQIGATTQQAQK	1.234301759	2	4.2960839
Q64176	LGIWGFFSTGDEHSR	1.441783943	2	3.1314728
Q64176	NFNTVPYIVGINK	1.198658718	2	3.4447258

Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.235263454**	**9.9E-20**	**7**
Q641Y0	ELGSECGIEFDEEK	1.237576131	2	3.6943438
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	1.692452714	4	5.1206918
Q641Y0	NTLLIAGLQAR	1.12403761	2	3.7971776
Q641Y0	TADDPSLSLIK	1.031929598	2	2.3363445
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.220359451	3	6.1377969
Q641Y0	TLVLLDNLNVR	1.293073918	2	3.9353378
Q641Y0	WVPFDGDDIQLEFVR	1.6891111	2	3.3367329
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.303551387**	**0.000102**	**5**
Q641Y2	GSGIQWDLR	0.995739899	2	2.7102461
Q641Y2	IDEVEEMLTNNR	1.121772544	2	3.4995582
Q641Y2	IIEQCLNK	1.290383996	2	2.8962796
Q641Y2	LYTEGYQVPPGATYTAIEAPK	1.650525655	2	2.7566478
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.378867244	2	4.2498388
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.14236035**	**0.004**	**3**
Q64232	HYEVEIR	0.887724535	2	2.3287072
Q64232	LCFLDKVEPQATISEIK	1.158798833	2	4.5417991
Q64232	SLKDEDVLQK	1.181448624	2	3.0040004
Q64240	**AMBP Protein AMBP**	**1.015640825**	**0.7947292**	**3**
Q64240	AFAELWAFDAAQGK	1.430061893	2	2.7709675
Q64240	AVLPQENEGSGSEPLITGTLK	0.985525955	2	4.7951117
Q64240	TIAACNLPIVQGPCR	1.018430454	2	3.9686565
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**0.973688725**	**0.0022073**	**17**
Q64380	AIDSLSIEK	0.848758668	2	2.5552628
Q64380	AYGIESHVLSPAETK	0.968393977	2	4.2930307
Q64380	DGTMDPAGTCTTLTR	0.739387475	2	4.0470209
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	1.499396548	3	5.026329
Q64380	DLYPLMNVDDLYGTLYVPR	1.243857679	2	3.4959717
Q64380	FHHSLTDHPR	1.208447856	2	2.5545363
Q64380	FYLLGADAR	0.871907894	2	2.5453067
Q64380	HGLVNAGYR	0.842978988	2	2.3525286
Q64380	IEGIQNMPNVR	0.860679993	2	2.8399584
Q64380	LGVGGVVLLER	1.489429322	2	3.1517479
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.769486836	2	4.281363
Q64380	NYSVVFPHDEPLAGR	0.948947329	2	3.8792932
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.827102642	3	4.5125012
Q64380	RDPLHEELLGQGCVFQER	1.020992813	3	5.265172
Q64380	SDDSPLEAGLAFTCK	0.94091559	2	4.659956
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.961313191	3	4.8650818
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.793257936	3	5.1172805
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.317067344**	**0.0018596**	**25**
Q64428	ADMVIEAVFEDLAVK	1.134097532	3	4.7585807
Q64428	ALMGLYNGQVLCK	0.94849478	2	3.2777877
Q64428	DSIFSNLIGQLDYK	0.879688349	2	2.5402288
Q64428	DTTASAVAVGLK	0.916438811	2	3.7717333
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.877773321	3	6.8490634
Q64428	EVQSEFVEVMNEIWANDQIR	1.03547487	3	3.3226974
Q64428	FGELALTK	0.925106746	2	2.6867118
Q64428	FGGGSVELLK	0.890009957	2	3.2962127
Q64428	FVDLYGAQK	1.031822154	2	3.178232
Q64428	GFYIYQSGSK	1.001367455	2	3.0350983
Q64428	ILQEGVDPK	0.926556776	2	3.1506605
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.358466115	4	5.0372643
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.454020202	2	4.2800083

Q64428	KYESAYGTQFTPCQLLR	0.917288888	2	4.4332457
Q64428	LPAKPEVSSDEDIQYR	0.960377026	3	3.8480477
Q64428	MGLVDQLVDPLGPGIK	0.926557509	2	4.825469
Q64428	MGLVDQLVDPLGPGIK+Oxidation(1)	1.095310011	2	2.4513948
Q64428	MQLLEIITTDK	0.947832207	2	4.0207491
Q64428	MVGVPAAFDMMLTGR	1.063453138	2	3.2359982
Q64428	NLNSEIDNILVNLR	1.15180772	2	4.7883101
Q64428	TGLEQGNDAGYLAESEK	1.019667416	2	5.1366668
Q64428	TIEYLEEVAVNFAK	1.020776757	3	4.1489701
Q64428	TVLGVPEVLLGILPGAGGTQR	1.238670032	3	5.0028033
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.888660535	3	5.9910145
Q64428	YESAYGTQFTPCQLLR	0.971351354	2	4.4132524
Q64458	**CP2CT Cytochrome P450 2C29**	**1.258309876**	**0.9453032**	**5**
Q64458	IKEHKESLDVTNPR	1.020813495	2	5.0222163
Q64458	LPPGPTPLPIIGNFLQIDVK	1.146498617	3	4.3713417
Q64458	VQEEAQCLVEELR	1.194889857	2	4.2754622
Q64458	VQEEAQCLVEELRK	1.155741751	2	3.7265685
Q64458	VQEEIDR	0.946095231	2	2.4955275
Q64481	**CP3AG Cytochrome P450 3A16**	**1.314747126**	**0.800765**	**2**
Q64481	GSIDPYVYLPFGNGPR	1.313705225	2	3.9438915
Q64481	VLQNFSFQPCK	1.327481952	2	2.6090727
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**0.967780028**	**0.6607695**	**4**
Q64550	GHEVVVIAPEASIHIK	0.865501255	2	4.6645131
Q64550	NMIIALTENFLCR	1.275392943	2	4.6596899
Q64550	SVFDQDPFLLR	1.172352774	2	3.4108002
Q64550	VVYSPYGSLATEILQK	1.182688493	2	4.550745
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.4951663**	**0.033105**	**16**
Q64563	AAVDCTVVGWGSCTVVGAK	1.262188791	2	4.1815033
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.445271891	3	5.8407068
Q64563	ALGATDCLNPR	1.245823964	2	3.0082486
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	1.287064286	3	5.560966
Q64563	FDLDLLVTHALPFDK	1.335274651	3	3.3206184
Q64563	IIAIDINSEKFPK	1.331094491	2	2.6502202
Q64563	INDAIDLMNQGK	1.246594441	2	4.3490949
Q64563	KFDLDLLVTHALPFDK	1.363404123	3	5.6919265
Q64563	KFDLDLLVTHALPFDKINDAIDLMNQGK	0.978921459	3	4.6829495
Q64563	LCLSPLTNLCGK	2.189000239	2	2.3193154
Q64563	SVDSVPNLVTDYK	1.490728984	2	3.259198
Q64563	TDSPLCIEEIEVSPPK	1.228625788	2	4.2324138
Q64563	VCLIGCGFTSGYGAAINTAK	1.3538816	2	5.5748262
Q64563	VDDEANLER	1.976548084	2	2.6753829
Q64563	VDEMNISTVDMILGR	1.323504476	2	3.3878748
Q64563	VIATCVCPTDINATNPK	1.500727844	2	4.2220225
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**0.958121458**	**0.1939892**	**15**
Q64565	AYSNHTDIISFR	1.033400729	2	3.3545575
Q64565	GGNFSQTFR	0.889087359	2	2.4121964
Q64565	GGVCIADEVQTGFGR	0.86804749	2	4.3146558
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.061471642	2	3.1965575
Q64565	GLMVGIEMVQDK	0.773108329	2	3.762531
Q64565	HNMPPCDFSPEK	0.872693388	2	3.3205104
Q64565	LRDEFDIVGDVR	1.080360642	2	2.6353271
Q64565	LSALLPEPLK	1.522684724	2	2.5847247
Q64565	NSQEVGTYMLLK	1.181910408	2	2.3753624
Q64565	SALTQHMER	0.933972085	2	2.7146602
Q64565	TEVNQIHEDCK	0.95628221	2	3.2691092
Q64565	TEVNQIHEDCKDMGLLVGR	0.881527576	2	5.2233782

Q64565	VIFLVNSGSEANDLAMVMAR	1.364616693	2	5.690999
Q64565	YIEQFK	1.051453503	1	2.0509448
Q64565	YLDFFSGIVTVGVGHCHPK	1.152485728	2	2.782547
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**1.436742471**	**0.988913**	**4**
Q64578	DIVPGDIVEVAVGDKVPADIR	1.460984156	2	3.329761
Q64578	IGIFSENEEVADR	1.28929126	2	2.899601
Q64578	VGEATETALTTLVEK	1.0649561	2	4.032546
Q64578	YGPNELPAEEGK	0.949369088	2	2.5428262
Q64581	**CP3AI Cytochrome P450 3A18**	**1.013777522**	**0.1225016**	**3**
Q64581	KLQNEIDR	1.012101655	2	2.358011
Q64581	LAVIGVLQNFNIQPCEK	1.635383855	2	4.0498853
Q64581	NPEYWLEPEEFNPER	0.961757038	2	4.2480917
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.91471756**	**0.0624012**	**9**
Q64591	ATAEEITSK	1.034242725	2	2.9384661
Q64591	CDVRDPDMVHNTVLELIK	0.849644452	4	4.5517163
Q64591	DPDMVHNTVLELIK	0.648489231	3	4.2925305
Q64591	EEWDVIEGLIR	0.651839549	2	3.7240446
Q64591	FFPPILKPMLPPNAFQGK	1.18864259	2	3.905992
Q64591	FNIIQPGPIK	0.833848383	2	3.115134
Q64591	NIDVLK	0.862058014	1	2.0570328
Q64591	VAFITGGGTGLGK	0.849005698	2	2.9113867
Q64591	VTKEEWDVIEGLIR	0.89190881	3	5.0169783
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**0.907517898**	**2.232E-06**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.272016454	2	5.2883291
Q64602	DIISLAPGSPNPK	0.905122847	2	3.0795293
Q64602	EILLVPGNSFFVDNSAPSSFFR	1.141671955	2	2.3214493
Q64602	FLYTIPNGNNPTGNSLTGDR	1.050477143	2	4.1429477
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.277275241	3	6.3739696
Q64602	SAVFTVENGSTIR	0.807722795	2	3.8608291
Q64602	VLSQWKPEDSKDPTKR	1.217665048	3	3.9460046
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**0.928305174**	**0.9824936**	**11**
Q64611	AQGGQGLEWR	1.017173892	2	3.0309522
Q64611	CHGSQASYLFQQDK	1.156033019	2	5.2613125
Q64611	FFNQLFSGLDPHALAGR	1.063864354	2	4.7015939
Q64611	FYNVALDTGDK	0.965781453	2	3.0887418
Q64611	GAAFLGLGTDSVR	1.168298997	2	3.4489665
Q64611	IDQAFALTR	1.016064856	2	3.1894007
Q64611	LLAAGLQCSALLLR	2.603869698	2	3.3039455
Q64611	QLLDLELQSQGESR	0.806842597	2	4.094171
Q64611	TLDGDPVAVEALLR	0.910701788	2	5.0392141
Q64611	VCEWKEPEELK	1.024719994	3	3.8018405
Q64611	YLVEEIK	1.090584894	1	2.2970176
Q64633	**UD17 UDP_glucuronosyltransferase 1_7**	**1.003214323**	**0.9527639**	**2**
Q64633	QSSFDAVFLDPFDVCGLTVAK	0.958961857	2	2.3834906
Q64633	TYSVSHTQEDLNR	1.040540687	2	3.2723842
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**1.169855207**	**0.6007782**	**2**
Q64638	TFLETSEILK	1.071907682	2	2.406354
Q64638	VVFETGNYVK	1.170043249	1	1.9621992
Q64640	**ADK Adenosine kinase**	**1.187021115**	**4.62E-06**	**11**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.154664519	3	7.1488438
Q64640	AATFFGCIGIDK	0.688255604	2	3.082793
Q64640	AGHYAASVIIR	1.053669329	3	3.3221645
Q64640	FGEILK	0.991064157	2	2.3835285
Q64640	FKVEYHAGGSTQNSMK	1.119575768	3	3.4443476
Q64640	HKELFDELVK	0.861465529	2	2.7507138

Q64640	HLDLENNWMLVEK	1.23102575	2	3.5959203
Q64640	SLVANLAAANCYK	1.102334809	2	4.3541236
Q64640	VEYHAGGSTQNSMK	1.042252226	2	3.8190942
Q64640	VEYHAGGSTQNSMK+Oxidation(13)	0.955892042	2	3.6182592
Q64640	YSLKPNDQILAEDK	1.151541504	3	4.2342854
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.907657717**	**0.9999949**	**8**
Q64654	EPAEDILQTLLDSTYK	1.041197798	2	3.4676809
Q64654	GVAYDVPNAVFLEQK	0.96888262	2	4.0340347
Q64654	NEDLNAEEVYGR	0.960474648	2	3.8222489
Q64654	SGLNIAHFK	0.944694383	2	2.8667021
Q64654	TFTYLLGSDAAALLFNSK	1.080584785	2	2.9326975
Q64654	TVCGEDLPPLTYEQLK	0.813632471	2	4.1263595
Q64654	YGPVFSFTMVGK	0.856334565	2	2.7299819
Q64654	YLQDNPASGEK	0.821050228	2	2.8473537
Q64737	**PUR2 Trifunctional purine biosynthetic protein adenosine_3**	**1.042616545**	**0.8472233**	**2**
Q64737	DSGVDIAAGNMLVKK+Oxidation(11)	1.160020985	2	2.3075662
Q64737	FGDPECQVILPLLK	1.042026303	2	2.4531503
Q65CL1	**CTNA3 Catenin alpha_3**	**1.203793282**	**0.7432678**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(1)	1.204780892	2	2.6001387
Q65CL1	NLMNAVVQTVK	1.091963955	2	3.1557617
Q65Z40	**WAPL Wings apart_like protein homolog**	**1.022500088**	**0.9924886**	**3**
Q65Z40	EKSISRIPEDNANK	1.109038205	2	2.6782827
Q65Z40	LGQKRPNFKPDIQEIPK	1.091010936	2	2.9130981
Q65Z40	TESPSESCPVKGSVR	0.937052304	2	2.52443
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.251044723**	**0.0812064**	**3**
Q66H12	CNINCEEDPK	0.892419946	2	2.4018478
Q66H12	INQDPLGIQGR	1.040895547	2	2.4512947
Q66H12	TISPQNIDILQNPLLIK	1.265414443	2	3.8813801
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**1.225879677**	**0.459101**	**2**
Q66H15	AIPGEAGDAAMLSSLPQEGQEK	1.383159354	2	4.1984501
Q66H15	AYSDMTELTEEESEKK	1.225158175	2	2.5335815
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**0.81418019**	**0.3112322**	**2**
Q66H45	LQGDVAGALEDLER	0.931989219	2	3.658977
Q66H45	RDFEQAAR	0.784685806	2	2.3045559
Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**1.115761525**	**0.4601146**	**2**
Q66H71	LTEQAVEAINK	1.115163543	2	3.6910117
Q66H71	SIDEDDDYFNLTK	1.972888668	2	2.835182
Q66H80	**COPD Coatomer subunit delta**	**1.221558725**	**3.419E-05**	**5**
Q66H80	GVQLQTHPNVDKK	1.202218381	2	3.1665843
Q66H80	LFTAESLIGLK	1.428276572	2	2.9040718
Q66H80	NSNILEDLETLR	1.160085182	2	2.906677
Q66H80	NTLEWCLPVIDAK	0.991031453	2	3.2990346
Q66H80	VAPAPARPSGPSK	1.194539711	2	2.4985864
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.122132789**	**0.7814712**	**5**
Q66HA8	AGGIETIANEFSDR	0.978906084	2	2.8421283
Q66HA8	FVVQNVSAQK	1.003851807	2	2.6838872
Q66HA8	LKETAENNLK	1.267465798	2	2.3982794
Q66HA8	NQQITHANNTVSSFK	1.158023743	2	4.4827514
Q66HA8	SVLDAAQIVGLNCLR	1.028202756	2	2.7190745
Q66HD0	**ENPL Endoplasmin**	**1.069249414**	**9.9E-20**	**32**
Q66HD0	DISTNYYASQK	0.88963018	2	3.0676045
Q66HD0	EATEKEFEPLLNWMK	1.078534032	2	3.1385131
Q66HD0	EEASDYLELDTIK	1.241144787	2	4.2809162
Q66HD0	EEEAIQLDGLNASQIR	0.784016715	2	4.5470147
Q66HD0	EFEPLLNWMK	1.004820105	2	2.3151174

Q66HD0	EVEEDEYK	1.020941149	1	2.3889833
Q66HD0	FQSSHHSTDITSLDQYVER	1.228108043	3	6.2057886
Q66HD0	GLFDEYGSK	1.097404504	2	2.3448
Q66HD0	GVVDSDDLPLNVSR	1.113844137	2	4.8129134
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGK	1.40902242	2	3.7210641
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	1.584903236	3	4.0240068
Q66HD0	KEAESSPFVER	1.212143488	2	3.605722
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	1.435288065	3	4.4195251
Q66HD0	LGVIEDHSNR	1.254733295	2	3.3310304
Q66HD0	LIINSLYK	1.518905542	2	2.4260304
Q66HD0	LISLTDENALAGNEELTVK	1.310068063	2	5.8515439
Q66HD0	LTESPCALVASQYGWSGNMER	1.08793067	2	5.5665455
Q66HD0	MKEKQDK	0.892421417	2	2.3302035
Q66HD0	NLLHVTDTGVGMTR	1.078995171	3	4.0342445
Q66HD0	NLLHVTDTGVGMTR+Oxidation(12)	1.3992181	2	2.9876218
Q66HD0	RVFITDDFHDMMPK	1.18056737	3	3.3355453
Q66HD0	SGTSEFLNK	1.048530935	2	3.1022575
Q66HD0	SGYLLPDTK	1.050472892	2	3.1693153
Q66HD0	SILFVPTSAPR	1.086293935	2	3.4742086
Q66HD0	TDDEVVQR	1.031280157	2	2.9470754
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	1.026872914	3	5.3512769
Q66HD0	TETVEEPLEEDETAQEEK	0.589552915	2	5.1855249
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	0.288391877	5	6.4500117
Q66HD0	TFEINPR	1.049738295	2	2.7252612
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.269821272	3	4.0270996
Q66HD0	VFITDDFHDMMPK	0.992194204	2	4.0255904
Q66HD0	YNDTFWK	1.124136418	1	2.1932414
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.008169061**	**1.224E-08**	**12**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.358010921	2	3.9791422
Q66HF1	DCFIVYQGHHGDVGAPIADVILPGAAYTEK	1.18325864	3	4.1990457
Q66HF1	DDGAAILAAVSSIAQK	1.03171207	2	4.3377662
Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	1.123489431	3	4.5197678
Q66HF1	FASEIAGVDDLGTTGR	1.125321535	2	3.4773471
Q66HF1	GLLTYTSWEDALSR	0.999570359	2	3.3838525
Q66HF1	GWNILTNSEK	1.121938655	1	2.146277
Q66HF1	ILQDIASGNHEFSK	1.344115111	2	4.1557546
Q66HF1	LGEVSPNLVR	1.127161718	2	3.1604657
Q66HF1	LVDQEFLADPLVPPQLTIK	1.130159471	2	3.2856379
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.919369621	2	4.6376853
Q66HF1	YDHLGDSPK	0.871744665	2	2.5556631
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.021838943**	**0.018053**	**11**
Q66HF8	ADVDLAVR	1.06001525	2	2.3576541
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	0.89843289	3	3.8540037
Q66HF8	EEIFGPVQPLFK	0.840974996	2	3.2192433
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.009568164	3	4.5044127
Q66HF8	LAPALATGNTVVMK	1.29617081	2	3.2874017
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	0.835161646	2	4.6363912
Q66HF8	TFVEESIYHEFLER	0.896430559	2	3.8167288
Q66HF8	VAEQTPLSALYLASLIK	1.293256282	2	3.178242
Q66HF8	VGNPFELDTQQGPQVDK	1.321334754	2	3.041733
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	0.975477368	2	4.4718323
Q66HF8	YGLAAAVFTR	0.930458088	2	3.8565047
Q66HG4	**GALM Aldose 1_epimerase**	**0.906542372**	**0.00293**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	0.958988929	2	4.7067676
Q66HG4	TVFGELPSGGGAVEK	0.907443781	2	3.6684077
Q66HG4	VSPDGEEGYPGELK	0.884169235	2	3.7850182

Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.002578635**	**8.771E-15**	**21**
Q66X93	ADDADEFGYSR	1.360155347	2	2.7839618
Q66X93	ALLLPDHYLVTVMLSGIK	1.130113575	2	3.3289649
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.231988487	3	5.5625043
Q66X93	DTNGENIAESLVAEGLASR	1.066285633	2	5.0236635
Q66X93	ETDGSETPEPFAAEAK	1.048184366	2	3.6938348
Q66X93	FVDGEWYR	1.026603929	2	2.3190985
Q66X93	GDVGLGLVK	0.948789113	2	2.7077701
Q66X93	HFVDSHHQKPVNAIIEHVR	1.220755819	3	4.8688025
Q66X93	LEGDNIQDK	1.064593483	2	2.7089171
Q66X93	LSECEEQAK	2.707835596	2	2.6073356
Q66X93	MVLSGCAIIVR	1.14136309	2	2.3714769
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.156130808	2	5.4277973
Q66X93	SAYYKPLLSAEEAAK	1.204625359	2	2.5228794
Q66X93	SDISSHPPVEGAYAPR	0.998767311	3	4.6138072
Q66X93	SSHYDELLAAEAR	1.30152364	2	3.7454817
Q66X93	TCATVTIGGINIAEALVSK	1.331561437	2	3.9263048
Q66X93	TDAVDSVVR	0.642832254	2	2.6558027
Q66X93	VITEYLNAQESAK	1.206621335	2	3.7860482
Q66X93	VMQVLNADAIVVK	1.318374506	2	3.9823413
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.06949001	3	5.0637636
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.760335323	3	4.5777946
Q67FY2	**BCL9L B_cell CLL/lymphoma 9_like protein**	**0.784874791**	**0.1656904**	**2**
Q67FY2	EAGTPSLDSEAKEVAPR	0.78581372	2	2.4515471
Q67FY2	NLVGSEGLSKEQLEHRER	0.68018844	2	2.3538823
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**1.20221963**	**3.442E-15**	**8**
Q68FP2	HNNWDLTPVK	1.098241254	2	3.3080714
Q68FP2	IFLMDLNEPYPK	1.453333475	2	3.0599041
Q68FP2	IQDPLSDNPR	1.078029733	2	2.8788869
Q68FP2	LLIYNPEDPPGSEVLR	1.706155166	2	4.3068824
Q68FP2	LVALTVLGASLALLGER	1.413528951	3	4.0153546
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.463939448	2	4.9543495
Q68FP2	VVAQGFSSANGITVSLDQK	1.134099797	2	4.1766739
Q68FP2	YVYVADVTAK	1.129699804	1	2.8920667
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.250719515**	**0.0002983**	**5**
Q68FQ0	ETGANLAICQWGFDDEANHLLLQNGLPAVR	0.971283264	3	3.7090101
Q68FQ0	GSNDMQYQHVIETLIGK	1.057204267	2	3.5598071
Q68FQ0	HKLDVTSVEDYK	1.19093125	2	3.1575348
Q68FQ0	SLHDALCVIR	1.273978182	2	2.9900579
Q68FQ0	WVGGPEIELIAIATGGR	1.488384803	2	3.8852532
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.258575553**	**9.9E-20**	**8**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.231510544	2	5.3384542
Q68FR6	ALIAAQYSGAQIR	1.108442818	2	4.230011
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	1.990468488	2	3.7630253
Q68FR6	ILGLLDTHLK	1.59224757	2	2.6411843
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.134477423	2	4.2650943
Q68FR6	KLDPGSEETQTLVR	1.258588655	2	3.9124432
Q68FR6	LDPGSEETQTLVR	1.061197205	2	2.9388402
Q68FR6	STFVLDEFKR	1.032536793	2	2.7119975
Q68FR9	**EF1D Elongation factor 1_delta**	**1.149083047**	**8.794E-05**	**6**
Q68FR9	ATAPQTQHVSPMR	1.005602906	2	3.0554686
Q68FR9	FYEQMNGPVTAGSR	0.968004048	2	4.2196426
Q68FR9	GVVQDLQQAISK	1.0468292	2	3.4260275
Q68FR9	SIQLDGLVWGASK	1.030551525	2	2.7883003
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.201036203	2	5.3166366
Q68FR9	SSILLDVKPWDDETDMAQLETCVR	1.229540233	3	3.3400857

Q68FS4	**AMPL Cytosol aminopeptidase**	**0.936221847**	**4.76E-13**	**18**
Q68FS4	ADMGGAATICSAIVSAAK	0.993732955	2	5.3882213
Q68FS4	DKDDDVPQFTSAGENFNK	0.92528115	2	5.0990958
Q68FS4	GITFDSGGISIK	1.098463823	2	3.2425618
Q68FS4	GLVLGIYSK	1.17843388	1	2.0348084
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.477217274	3	5.989614
Q68FS4	GVLFASGQNLAR	0.999355887	2	3.6157529
Q68FS4	LFEASVETGDR	1.058720962	2	3.5053146
Q68FS4	LHGSGDLEAWEK	1.379331658	2	3.5746303
Q68FS4	LNLPINIIGLAPLCENMPSGK	2.776462162	2	4.82862
Q68FS4	QLMESPANEMTPTR	0.89735243	2	3.3877828
Q68FS4	QVIDCQLADVNNLGK	1.07402712	2	4.9334164
Q68FS4	SAGACTAAAFLR	1.148623613	2	3.6906934
Q68FS4	SAGVDDQENWHEGK	0.938932101	2	3.9277341
Q68FS4	SWIEEQEMGSFLSVAK	1.182991577	2	5.5089054
Q68FS4	TFYGLHQDFPSVVVVGLGK	0.94851487	2	4.902935
Q68FS4	TIQVDNTDAEGR	1.01324621	2	4.1949201
Q68FS4	TLIEFLLR	1.210234975	2	2.6965191
Q68FS4	WAHLDIAGVMTNKDEIPYLR	1.080231263	3	3.4565814
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.076445749**	**0.1056723**	**3**
Q68FT1	INDAMNMGHTAK+Oxidation(5)Oxidation(7)	1.860492181	2	2.7956445
Q68FT1	LNHVLEEEQK	1.067487833	3	3.3353858
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.749349564	3	4.6761732
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.936452747**	**0.9711012**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	0.889783309	2	3.6513648
Q68FT3	ISQLDTQSPVTK	1.029994342	2	3.5483804
Q68FT3	SLLLGTDVAENQK	0.8786873	2	2.8834338
Q68FT3	TLGAQLPQYYEVLTAPISK	1.158551031	2	4.7713547
Q68FT3	VFDCIEAYAPGFK	0.701776383	2	2.3323309
Q68FT3	VLDQWFESEPLK	1.08027118	2	3.2025633
Q68FT3	VQGVVLQGGEEVR	0.878444399	2	3.3708265
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.090165701**	**9.9E-20**	**11**
Q68FT5	AGADVLQTFTFSAAEDR	1.309585177	2	3.84324
Q68FT5	AGANIIGVNCR	1.136719983	2	3.2208352
Q68FT5	AGLWTPEAVVEYPSAVR	1.083417722	3	3.7527878
Q68FT5	AIAEELAPER	1.184744386	2	3.8164206
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	0.973207583	3	4.6816053
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.302643597	2	3.8995843
Q68FT5	FGPWTSLQTMK	0.924780886	2	3.0884237
Q68FT5	GGFVDLPEYPFGLEPR	1.138781873	2	4.0726018
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.106486547	2	5.3609166
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	1.705167588	3	3.472177
Q68FT5	YIGGCCGFEPYHIR	3.074568348	2	4.6247706
Q68FT9	**SCLY Selenocysteine lyase**	**1.011389503**	**4.723E-11**	**5**
Q68FT9	AEVDLIVQDLK	0.949357841	2	3.7233374
Q68FT9	CFHEQQTLQGR	1.318858748	2	2.7594972
Q68FT9	RVDVEDLGVDFLTIVGHK	2.047820729	3	5.9255323
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	1.30963002	3	3.6138377
Q68FT9	VLVHTDAAQALGK	1.00497175	2	3.0369611
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**1.034181479**	**2.22E-16**	**12**
Q68FU3	AGDLGVDLTSK	0.943450081	2	3.7270081
Q68FU3	EIIAVSCGPPQCQETIR	0.876853035	2	4.8618207
Q68FU3	GIHVEVPGAEAENLGPLQVAR	0.546823802	2	5.73982
Q68FU3	HSMNPFCEIAVEEAVR	1.026108468	2	5.6944194

Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(3)	1.521178042	2	4.2897902
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	0.975273934	3	6.3078084
Q68FU3	RVIDFAVK	1.11890303	2	2.3827643
Q68FU3	SGVVTDGVK	0.756854313	2	2.8886397
Q68FU3	VDLLFLGK	1.039175438	2	2.9820123
Q68FU3	VETTEDLVAK	0.928298898	2	3.3357434
Q68FU3	VIDFAVK	0.999155193	2	2.3531406
Q68FU3	VSVISVEEPPQR	1.035264523	3	3.4122229
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**0.969477372**	**0.9999562**	**9**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.02798641	3	5.8809266
Q68FY0	IEEVDAQMVR	0.977366464	2	3.6874731
Q68FY0	LCTSATESEVTR	1.1003658	2	3.1730528
Q68FY0	NALISHLDGTTPVCEDIGR	1.064892745	2	4.7027059
Q68FY0	NNGAGYFLEHLAFK	1.125058118	2	3.4252517
Q68FY0	RIPLAEWESR	1.092709737	2	2.7809258
Q68FY0	TDLTDYLSR	1.050291868	2	2.6650977
Q68FY0	VVELLADIVQNISLEDSQIEK	0.964191584	3	5.7347889
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.154084959	2	5.116643
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**1.170823312**	**2.296E-12**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	1.083976602	2	4.6821961
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	1.04823229	3	3.6979768
Q68G31	GESGGQTTPYDFYSR	1.673065059	2	4.278223
Q68G31	LQPTDSFSQSSCFGLR	1.112602722	2	3.4885345
Q68G31	NVNSTLTFVTLSGELK	1.229875319	2	3.7907984
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.222568019	3	5.7399845
Q68G31	VNTEPLPGIEK	1.089681997	2	3.0314131
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.068983414**	**0.528378**	**2**
Q69Z23	GDPTRAEDQVLMRALR	1.409506882	2	2.3320851
Q69Z23	YFIDLLMEK	1.068780002	1	2.1530316
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.104460535**	**0.0382458**	**2**
Q6A0A9	SQGGVQPIPSQGGK	0.918540854	2	3.1416068
Q6A0A9	VEGSSTASSGSQLAEGK	1.107857512	2	4.299809
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.314253531**	**5.486E-10**	**4**
Q6AXM8	FQEEENSLLHLK	1.397108131	2	3.4341576
Q6AXM8	LFVYDPNHPPSSEVLR	1.248927786	2	2.5017092
Q6AXM8	LVAEGFDSANGINISPDKK	1.313402887	2	3.6571014
Q6AXM8	VLQLGTLVDNLSIDPSSGDIWVGCHPNGQK	1.28171997	3	4.4292731
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**1.012416679**	**0.9998954**	**3**
Q6AXS5	EETQPPVALKK	0.943598412	2	2.7420659
Q6AXS5	FDQLFDDESDPFEVLK	0.992222811	2	5.2050648
Q6AXS5	SAAQAAAQTNSNAAGK	0.991258999	2	5.0985055
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**1.000033106**	**0.8764477**	**2**
Q6AXY0	FLQPGSQR	0.985500647	2	2.5127146
Q6AXY0	YFPAFEK	1.09844537	1	1.9110695
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.036784426**	**0.5099049**	**5**
Q6AY09	ATENDIYNFFSPLNPMR	1.230680608	2	4.0180907
Q6AY09	GLPWSCSAEEVMR	0.807211206	2	3.1027265
Q6AY09	HTGPNSPDTANDGFVR	1.032130317	2	4.1940761
Q6AY09	STGEAFVQFASQEIAEK	1.403519814	2	4.2908549
Q6AY09	STGEAFVQFASQEIAEKALKK	1.104536096	2	2.5460105
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**0.968927448**	**0.2265363**	**2**
Q6AY20	HTLAGNFNPVSEER	0.968776895	2	4.3002181

Q6AY20	SCDLVGEKDKESK	1.257375492	2	3.7206366
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.103949395**	**0.0754905**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.3627871	3	5.3129454
Q6AY30	ATLVLNCVGPYR	0.994119546	2	2.5612729
Q6AY30	GGGVFTPGAAFSR	1.023905672	2	2.36426
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.183997992	2	3.2537417
Q6AY30	LQQVLEK	1.253295802	1	2.0679646
Q6AY30	SVSNLKPVPVIGSK	1.090932665	2	3.6138811
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.187071162**	**9.9E-20**	**9**
Q6AY56	AFVHWYVGEGMEEGEFSEAR	1.515636753	2	4.6020246
Q6AY56	AVCMLSNTTAIAEAWAR	1.072757634	2	4.6251793
Q6AY56	EDAANNYAR	1.095950142	1	2.073451
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.438375268	2	5.4105701
Q6AY56	LISQIVSSITASLR	1.430279437	2	3.6666224
Q6AY56	NLDIERPTYTNLNR	1.165331893	2	3.5813077
Q6AY56	QLFHPEQLITGK	1.157613776	2	2.8515084
Q6AY56	TIQFVDWCPTGFK	1.101829149	2	3.8817942
Q6AY56	VGINYQPPTVVPGGDLAK	1.091288247	2	4.8435197
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.930090416**	**0.9132444**	**2**
Q6AY80	NDVTGALSNPEVFK	0.925238804	2	3.4151583
Q6AY80	VLAPQISFGPEVSSEEQR	0.871851888	2	3.3789749
Q6AYH5	**DCTN2 Dynactin subunit 2**	**1.149663048**	**0.1809188**	**3**
Q6AYH5	ASVEDADTQNK	1.119783556	2	3.222342
Q6AYH5	LLGPDAAINLADPDGALAK	1.727896041	2	2.925566
Q6AYH5	WSPVASTLPELVQR	1.072998907	2	2.5704334
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.914103576**	**1**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	1.04924403	2	4.3980789
Q6AYQ8	NLHHEVELGVLLGR	0.976984621	3	4.4386773
Q6AYQ8	SFTSSCPVSAFVPK	0.883150003	2	4.0859399
Q6AYR8	**SCRN2 Secernin_2**	**1.004698225**	**0.5664104**	**3**
Q6AYR8	GHQAALGLMDEQEQAQLR	1.010520544	2	3.8728626
Q6AYR8	QEQQSLEQEGLEALR	0.995091094	2	4.0241747
Q6AYR8	TTASMVSVLPQDPTKPCVHFLTATPDPSR	1.428123156	3	3.5717604
Q6AYS7	**ACY1A Aminoacylase_1A**	**1.390622487**	**2.331E-15**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	1.213023499	2	3.4593072
Q6AYS7	ICTVQPNPDYGSAVTFLEER	2.820259344	2	4.4259763
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.924750599**	**0.9646387**	**3**
Q6AYS8	ALTDELAALGCTGVR	1.021069226	2	2.3612814
Q6AYS8	NPSTNLGPTLEPEEVVEHLMHGILTNQK	1.080717491	3	3.6643641
Q6AYS8	SVAGEIVLITGAGHGIGR	0.93033325	2	4.2767329
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**1.393729878**	**0.5507546**	**3**
Q6AYT9	AFIVLSPAYVSHDPEALTR	1.309573142	2	4.691833
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	1.125465787	2	3.3784769
Q6AYT9	NDDVINSSSYR	1.225832006	2	3.3058975
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.340671539**	**9.9E-20**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	1.120011128	2	5.3017387
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	0.922226106	3	4.2555418
Q6AYZ1	DVNAAIATIK	1.017661046	2	3.2959836
Q6AYZ1	IHFPLATYAPVISAEK	1.671618396	2	3.901093
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.980126311	2	5.5614519
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.082272921	2	4.751996
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.150339278**	**0.8136104**	**7**
Q6DGG1	AVAIDLPGLGR	0.929451411	2	3.4787614
Q6DGG1	FSSETWQNLGTLHR	1.110280506	2	3.5717065
Q6DGG1	FSVLLLHGIR	1.024850614	2	3.0143254

Q6DGG1	GYVPVAPICTDK	1.040777806	2	2.5421419
Q6DGG1	INAADYAR	0.994613269	2	2.4012966
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	0.984812863	2	4.9660368
Q6DGG1	VLVMEGAGHPCYLDKPDEWHTGLLDFLQELA	2.28605131	3	3.8916752
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.9955653**	**0.999998**	**2**
Q6EDY6	ELMESIK+Oxidation(3)	1.013116918	1	2.1921206
Q6EDY6	IENYLLR	0.992523271	2	2.5039573
Q6GQT9	**NOMO1 Nodal modulator 1**	**1.104656711**	**0.5675845**	**2**
Q6GQT9	SSIDSEPALVLGPLK	1.142165488	2	2.6978064
Q6GQT9	VQVVVPEAETR	1.010431143	2	2.843817
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**1.122568045**	**0.0076526**	**2**
Q6I7R3	GLGSTVQEIDLTGVK	1.028139615	2	3.855788
Q6I7R3	ILGIPVIITEQYPK	1.517267995	2	3.2725096
Q6IE52	**MUG2 Murinoglobulin_2**	**1.096862304**	**0.9674516**	**13**
Q6IE52	AHFSVMGDILSSAIK	1.183286418	2	3.6435087
Q6IE52	HGIPFFVK	3.443513239	2	2.8141105
Q6IE52	HTSSWLVTPK	0.976054922	2	2.6255136
Q6IE52	LPSSEEEESLDINIEGAK	1.252288021	2	5.4021912
Q6IE52	MLIYTILPDGEVIADSVK	1.149696244	2	4.3163099
Q6IE52	MLSGFIPLKPTVK	1.009548961	2	2.8554873
Q6IE52	NLYPLKELVQDPK	1.143595831	1	2.1494286
Q6IE52	QLSFSLSAEPIQGPYK	1.038819579	2	4.3205857
Q6IE52	VHLSFSPSQSLPASQTHMR	1.056859543	3	3.5595644
Q6IE52	VKTVPLTCNNPK	1.172568623	2	2.7707629
Q6IE52	VLIVEPEGIKK	1.200602925	2	2.3725133
Q6IE52	VTASPQSLCGLR	1.240438004	2	2.5952532
Q6IE52	YMVLVPSQLYTETPEK	1.132601882	2	4.0601654
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.093333561**	**0.6398857**	**2**
Q6IFX1	**K1C24 Keratin_ type I cytoskeletal 24**	**1.161817358**	**0.0022475**	**2**
Q6IFX1	LLNDMR	0.890652439	1	1.9203966
Q6IFX1	QEAEKQFNER	1.212143488	2	2.5628862
Q6IG00	**K2C4 Keratin_ type II cytoskeletal 4**	**1.154847398**	**0.5127044**	**3**
Q6IG00	LMQDSVEDFK+Oxidation(2)	1.13785138	1	2.0750604
Q6IG00	NLDLDGIIAEVR	0.902352886	2	3.2676594
Q6IG00	WNLLQQQTTTTSPR	1.410120691	2	4.3629208
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**1.028018305**	**0.6464886**	**4**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.970329576	3	5.6161408
Q6IRK9	IVVYNQPYTDYGK	1.641446092	2	2.4067578
Q6IRK9	TYPDTDSFNTVAEITGSK	0.803915797	2	4.46419
Q6IRK9	VGAVASLIR	1.019678639	2	2.4554923
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.866389931**	**0.4353467**	**4**
Q6MGB5	AGVIGLTQTAAR	1.05064874	2	3.0258331
Q6MGB5	GSIINISSIVGK	2.050812443	2	2.7922611
Q6MGB5	LAAEGAAVAACDLDGAAAQDTVR	0.828743248	2	3.8523788
Q6MGB5	VGNIGQTNYASSK	1.118092921	2	2.8554327
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**0.979691961**	**0.5135217**	**2**
Q6NSR8	HNSPSAAHFITR	0.967155904	3	4.136219
Q6NSR8	TVEINNTDAEGR	0.820502898	2	3.0242054
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.073208402**	**0.4706117**	**4**
Q6NYB7	EFADSLGIPFLETSAK	0.970122819	2	3.0332351
Q6NYB7	MGPGATAGGAEK	0.841297209	2	3.5452721
Q6NYB7	MGPGATAGGAEK+Oxidation(1)	1.420083764	2	2.4428811
Q6NYB7	NATNVEQSFMTMAAEIK	1.2173956	2	4.5443201
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.099923807**	**0.3287398**	**6**
Q6NZJ6	GLPLVDDGGWNTVPISK	1.019716721	2	3.3851843
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.017656097	3	3.356858

Q6NZJ6	IHNAENIQPGEQK	0.955844489	2	4.0452361
Q6NZJ6	KVEYTLGEESEAPGQR	1.312208558	2	4.6022549
Q6NZJ6	LKEELEEAR	1.062964257	2	2.6729705
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	1.097635123	3	5.3437843
Q6P0K8	**PLAK Junction plakoglobin**	**1.029546264**	**0.9956387**	**4**
Q6P0K8	LLNDEDPVVVTK	1.053044122	2	2.7452433
Q6P0K8	MEEIVEGCTGALHILAR	1.07626392	3	3.308651
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.006353912	3	3.9556246
Q6P0K8	TMQNTSDLDTAR	0.94190208	2	2.9556618
Q6P2K6	**P4R3A Serine/threonine_protein phosphatase 4 regulatory subunit 3A**	**0.967537976**	**0.9745716**	**3**
Q6P2K6	ESEEKEVLLK	0.854986076	1	2.026123
Q6P2K6	FKEVIPISDPELK	1.1042854	1	2.0132144
Q6P2K6	LDSMRSILR	0.932100038	1	2.0249963
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**0.987275647**	**0.0264209**	**12**
Q6P502	AMTGVEQWPYR	1.169588155	2	2.5701358
Q6P502	AVAQALEVIPR	1.077697405	2	2.8529336
Q6P502	DMMLNIINSSITTK	0.501717785	2	2.3482807
Q6P502	EIQVQHPAAK	0.912836117	2	3.1274107
Q6P502	IVLLDSSLEYK	1.403183989	2	2.4605868
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.395926753	3	4.2863579
Q6P502	KGESQTDIEITR	1.037634333	2	2.9025118
Q6P502	NLQDAMQVCR	0.985405109	2	3.1728511
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	1.593505072	2	4.0884657
Q6P502	TAVETAVLLLR	1.302723554	2	2.808063
Q6P502	TLIQNCGASTIR	1.020613618	2	3.0946665
Q6P502	WSSLACNIALDAVK	1.112544151	2	3.6320663
Q6P6M7	**SPCS O_phosphoseryl_tRNA(Sec) selenium transferase**	**1.08441563**	**0.9486736**	**4**
Q6P6M7	EMFVYLSTQLKK+Oxidation(2)	0.959343122	2	2.9578326
Q6P6M7	KEMFVYLSTQLKK	1.077357415	2	2.546669
Q6P6M7	SGDISAVQPK	1.089395386	2	2.593178
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	1.192704311	2	3.6617451
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**1.262507253**	**9.9E-20**	**10**
Q6P6R2	ALTGGIAHLFK	1.167505238	2	2.3569887
Q6P6R2	IDVSVEAASGGK	0.956240626	2	3.2161043
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.48646265	3	4.4358792
Q6P6R2	NETLGGTCLNVGCIPSK	1.093014124	2	5.2591963
Q6P6R2	NQVTATTADGSTQVIGTK	1.028085693	2	5.3743615
Q6P6R2	RPFTQNLGLEELGIELDPK	1.052565166	3	3.7409453
Q6P6R2	SEEQLKEEGVEFK	1.041680402	3	3.8945451
Q6P6R2	TNADTDGMVK	0.956422036	2	2.8722799
Q6P6R2	TNADTDGMVK+Oxidation(8)	1.683653636	2	2.6882439
Q6P6R2	VCHAHPTLSEAFR	1.304111506	3	3.7872722
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**1.011300856**	**0.0627277**	**4**
Q6P6S9	AQTLLLEVEEIFK	1.411688397	2	2.9859262
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	1.010949155	2	4.1172938
Q6P6S9	QGAETVQELLEVAK	1.146891348	2	3.082659
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	1.35185051	3	4.701375
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.099538134**	**5.789E-05**	**9**
Q6P6V0	AITDIINIGIGGSDLGPLMVTEALKPYSK	1.055957138	3	3.8087392
Q6P6V0	DVMPEVNKVLDK+Oxidation(3)	1.079512889	2	2.3697257
Q6P6V0	HFVALSTNTDK	1.04077448	2	3.1677189
Q6P6V0	ILLANFLAQTEALMK	0.930348541	2	3.1345475
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.088975942	3	4.8351812
Q6P6V0	TFTTQETITNAETAK	1.10280566	2	5.1330614
Q6P6V0	TLANLNPESSLFIIASK	1.30340954	3	5.0211554

Q6P6V0	VFEGNRPTNSIVFTK	1.323349038	2	3.2558141
Q6P6V0	VWFVSNIDGTHIAK	0.182298027	2	3.5887578
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.127649237**	**1.256E-08**	**5**
Q6P7Q4	DFLLQQTMLR	0.818991728	2	3.2585812
Q6P7Q4	FEELGVK	1.158442557	1	1.944322
Q6P7Q4	GFGHIGIAVPDVYEACK	1.168088465	2	3.7153797
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.525384099	2	5.8045053
Q6P7Q4	VLGLTLLQK	1.182502301	2	2.72294
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.090409249**	**0.096911**	**3**
Q6P7R8	LGEWAVVTGGTDGIGK	1.09075783	2	4.1236534
Q6P7R8	LININVLSICK	2.564689281	2	2.6446979
Q6P7R8	TIAVDFSLDDIYDK	0.896421388	2	2.9694376
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.05520721**	**5.865E-10**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	0.961239892	2	4.7319517
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(11)	1.365514915	2	2.518611
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.029784793	3	5.5576062
Q6P9T8	EIVHLQAGQCGNQIGAK	0.855006919	2	5.1074615
Q6P9T8	EVDEQMLNVQNK	1.103768031	2	4.1986895
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	0.861251943	3	5.4687796
Q6P9T8	INVYYNEATGGK	1.25020745	2	3.6526306
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.256877745	3	5.7596774
Q6P9T8	LHFFMPGFAPLTSR	1.635920587	2	2.9883497
Q6P9T8	MSATFIGNSTAIQELFK	1.506448143	2	4.3663678
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	0.814017411	3	3.9420245
Q6P9T8	TAVCDIPPR	0.360211999	2	2.388726
Q6P9T8	YLTVAAVFR	1.05730931	2	2.710984
Q6PA06	**ATLA2 Atlastin_2**	**1.201470083**	**0.8733496**	**4**
Q6PA06	AGLTDQVSHHAR	1.259155068	2	3.0844882
Q6PA06	NLVPLLLAPENLVEK	1.083380944	2	2.8203473
Q6PA06	QNQHEELQNVR	0.976898731	2	2.8673701
Q6PA06	SMLQATAEANNLAAVAGAR	1.055235508	2	3.2171493
Q6PCM2	**INT6 Integrator complex subunit 6**	**0.690290408**	**0.0021681**	**2**
Q6PCM2	MLIEQLENFLDEIHRR+Oxidation(1)	0.626211916	2	2.5084546
Q6PCM2	NPFFLEPAIIITITDGSK	1.936134996	2	2.3495383
Q6PDV7	**RL10 60S ribosomal protein L10**	**1.092384113**	**0.7186562**	**2**
Q6PDV7	FNADEFEDMVAEK	1.165953406	2	3.7332172
Q6PDV7	FNADEFEDMVAEKR	0.904417988	2	2.6502087
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.083147923**	**0.444607**	**4**
Q6PEC1	AEDGENYAIKK	1.251079381	2	2.5739646
Q6PEC1	LEAAYTDLR	0.84850472	2	2.8469822
Q6PEC1	QILESEKDLEEAEEYKEAR	1.099897355	3	4.0983057
Q6PEC1	RLEAAYTDLR	1.12623305	2	2.4720726
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.248595335**	**0.2706691**	**3**
Q6PEC4	NDFTEEEEAQVR	1.202427559	2	3.1856124
Q6PEC4	RTDDIPVWDQEFLK	1.123877231	2	3.1035712
Q6PEC4	TDDIPVWDQEFLK	1.47131567	2	2.7094398
Q6PGB8	**SMCA1 Probable global transcription activator SNF2L1**	**1.053234731**	**0.9134721**	**2**
Q6PGB8	EMDPEYEEKMVNMPLK+Oxidation(13)	0.925670083	2	2.4101167
Q6PGB8	IKTDVEKSLPPK	1.057272179	2	2.3202913
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.062551537**	**0.0739734**	**6**
Q6Q0N1	AVFQYIDENQDR	2.192149583	2	3.2515798
Q6Q0N1	EGGSIPVTLTFQEATGK	0.988020749	2	2.7537096
Q6Q0N1	LGGSVELVDIGK	1.335376435	2	2.3890753
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	0.270944461	2	3.4225948
Q6Q0N1	MTEAAAADVQR	1.061564533	2	2.5871928
Q6Q0N1	TGQEIPVNLR	1.004718891	2	2.4954925
Q6RT24	**CENPE Centromere_associated protein E**	**1.000882301**	**0.7018898**	**2**

Q6RT24	DLLQKVQDEK	0.947632281	2	2.3817234
Q6RT24	MELENVNMKLQEK	1.144387314	2	2.4034481
Q6RUV5	**RAC1 Ras_related C3 botulinum toxin substrate 1**	**0.942899218**	**0.9061824**	**2**
Q6RUV5	HHCPNTPIILVGTK	0.942519421	2	3.1159766
Q6RUV5	LTPITYPQGLAMAK	1.149415566	2	2.9852767
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.932853428**	**0.982197**	**2**
Q6SKG1	FDSTSILQTLSK	0.931564302	2	3.1434164
Q6SKG1	TGTVLIPGTTQLTQK	1.053586779	2	2.5236261
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.239018588**	**5.41E-09**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.11815962	2	4.7398744
Q6TUG0	FQMTQEVVCDECPNVK	1.140926016	2	5.0501895
Q6TUG0	KGEGLPNFDNNNIK	1.224941606	2	3.3192942
Q6TUG0	TLEVEIEPGVR	1.247883463	2	3.0339236
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.188547153**	**0.0013587**	**17**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.123305943	2	4.5005984
Q6UPE1	ALNEGGLQSIPK	0.985793985	2	3.4803259
Q6UPE1	ASCDAQTYGIGLK	0.962589944	2	3.82602
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	0.900540867	2	4.6571736
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.358645037	2	4.8845496
Q6UPE1	GAPLNTPVTEDR	1.011125432	2	3.476269
Q6UPE1	GIATNDVGIQK	0.954448015	2	3.5613451
Q6UPE1	HHPSIRPTLEGGK	0.92741472	2	2.3177717
Q6UPE1	LQINAQNCVHCK	1.298708522	2	3.5074165
Q6UPE1	LTFPGGLLIGCSPGFMNVPK	1.396990001	2	3.468097
Q6UPE1	NLSIYDGPEQR	0.987050373	2	2.6289427
Q6UPE1	QLTSENLQSK	0.734557195	2	2.322186
Q6UPE1	SGSLAAEAIFK	1.066765542	2	3.291091
Q6UPE1	TAGLHVTEYEDNLK	0.74684008	2	3.6948745
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	1.129149813	2	4.5209208
Q6UPE1	VDHTVGWPLDR	1.01784644	2	2.4918928
Q6UPE1	VTIFAEGCHGHLAK	1.154109703	2	3.7927089
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**1.011669912**	**9.9E-20**	**7**
Q6URK4	EDSVKPGAHLTVK	1.262686769	2	3.6973305
Q6URK4	GFAFVTFDDHDTVDK	1.050212001	2	3.8477933
Q6URK4	IETIEVMEDR	1.038064874	2	3.3621054
Q6URK4	IFVGGIKEDTEEYNLR	1.95730098	2	4.2638206
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	0.739756051	2	4.6206007
Q6URK4	WGTLTDCVVMR	0.974138322	2	3.0205622
Q6URK4	YHTINGHNCEVK	1.464405873	2	3.574863
Q6URW6	**MYH14 Myosin_14**	**1.097752745**	**9.9E-20**	**4**
Q6URW6	EDQSILCTGESGAGK	1.06544023	2	4.611321
Q6URW6	FDQLLAEEK	1.126955756	1	2.0195544
Q6URW6	KFDQLLAEEK	1.222940652	2	3.1676543
Q6URW6	QLLQANPILEAFGNAK	1.282804204	2	4.5919495
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.907089828**	**0.3601682**	**4**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.608372049	2	3.8310311
Q6XQN1	LDSGDLLQQAK	0.855742147	2	3.643899
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.196718735	2	5.4678597
Q6XQN1	QLQNPAVYQVALSEK	1.163852161	2	3.1536107
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**0.970877117**	**0.2204134**	**2**
Q6ZPJ3	FRTTDIVIR	0.744750495	2	2.5243752
Q6ZPJ3	NCAQGEGSMAKKVK	1.046033848	2	2.9038205
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.160142019**	**0.1586349**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	1.094782122	2	2.7353127
Q70FJ1	HEAEITNYKIKLEMLEK+Oxidation(14)	1.417696543	2	2.5171316

Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.061769857**	**0.0349901**	**4**
Q711G3	DCGTDVLDLWTLMQK	1.422313168	2	4.2189002
Q711G3	DVEETKPELSLLGDGDH	0.938571235	2	3.6412671
Q711G3	LNVAVGEYAK	1.199501014	2	2.557029
Q711G3	VILITPPPLCEAAWEK	1.239587343	2	2.8308778
Q71LX4	**TLN2 Talin_2**	**0.864696549**	**0.8078478**	**4**
Q71LX4	NCGEMSEIEAK	1.475120473	2	2.4278626
Q71LX4	QEDVIATANLSR	0.68271311	2	3.1165612
Q71LX4	QELTVFQSKDIPEK	1.218190078	2	2.3251524
Q71LX4	QVAASTAQLLVACK	1.051697888	2	3.2618566
Q71TY3	**RS27 40S ribosomal protein S27**	**1.208336591**	**0.3165594**	**3**
Q71TY3	DLLHPSPEEEK	0.883875333	2	2.798995
Q71TY3	LTEGCSFR	1.10791183	2	2.3179529
Q71TY3	LVQSPNSYFMDVK	1.209992505	2	2.8801599
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.151319738**	**0.3076286**	**6**
Q75Q39	GLELISKAIEIDNK	1.124985458	2	2.3327732
Q75Q39	NADLSTFYQNR	1.181928069	2	2.8976378
Q75Q39	NREPLMPSPQFIK	0.975087276	2	2.3209436
Q75Q39	SDEDKDKEGEALEVK	1.108306913	2	3.9073577
Q75Q39	SYFSSFTDDIISQPMLK	0.887729223	2	2.9393036
Q75Q39	YEQAIQCYTEAISLCPTEK	1.030517019	2	3.6714914
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.321368137**	**9.055E-12**	**7**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.251739683	3	5.7210298
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	1.199421656	3	5.0807858
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.22559638	2	4.6747675
Q76MZ3	LNIISNLDCVNEVIGIR	1.003765097	2	3.9411864
Q76MZ3	LTQDQDVDVK	1.039869388	2	3.17939
Q76MZ3	NLCSDDTPMVR	0.971601839	2	2.4469211
Q76MZ3	QLSQSLLPAIVELAEDAK	1.477010134	3	4.2449226
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**1.000026578**	**0.8843046**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	0.723058164	2	5.5269542
Q78P75	NFGSYVTHETK	0.95835637	2	2.4998043
Q78P75	YNPTWHCIVGR	1.05022883	2	2.9441769
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**1.418480078**	**1.261E-11**	**5**
Q791V5	EEGIVGFFAGLIPR	1.331868796	2	3.3257277
Q791V5	GLFTGLTPR	1.007028515	2	2.5715857
Q791V5	LCSGVLGTVVHGK	1.728975881	2	3.0943758
Q791V5	VLIQVGYEPLPPTIGR	1.069262541	2	4.3326974
Q791V5	YCGLCDSIVTIYR	1.169648164	2	2.8462696
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**0.97710014**	**0.4706859**	**3**
Q794E4	ATENDIYNFFSPLNPVR	1.266468209	2	4.2203202
Q794E4	HSGPNSADSANDGFVR	1.007580576	2	3.7532451
Q794E4	VHIEIGPDGR	1.054395758	2	2.9553187
Q7M0E3	**DEST Destrin**	**1.126941105**	**0.0083107**	**3**
Q7M0E3	HEYQANGPEDLNR	1.127086081	2	4.6347785
Q7M0E3	HFVGMLPEK	0.870673332	2	2.4053183
Q7M0E3	HFVGMLPEKDCR	1.2451959	2	2.6465487
Q7TMA5	**APOB Apolipoprotein B_100**	**1.157746175**	**0.6093418**	**8**
Q7TMA5	GFEPTLEALFGK	0.992842521	2	2.363184
Q7TMA5	GIISLLEAMK	0.823171483	2	2.4370711
Q7TMA5	IEGNLVFDPSSYLPK	1.16158527	2	3.4192159
Q7TMA5	IEIDIPLPLGGK	1.182082472	2	2.8236279
Q7TMA5	ITDNDVLIALDSAK	0.818099966	2	2.7938285
Q7TMA5	LSISEQNAQR	1.136336501	2	2.4017618
Q7TMA5	NFVASHIANILNSEELYVQDLK	1.004237422	3	3.4170551

Q7TMA5	TILFDTFVNDVAPVEK	1.112120936	2	2.7220476
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.121671734**	**0.9963472**	**4**
Q7TNG8	AVVGSPHVSTASAVR	1.11046281	2	3.1460757
Q7TNG8	AYSTDVCVPISR	1.103401774	2	3.7911494
Q7TNG8	GSQGGLSQDFVEALK	1.126131723	2	3.0836008
Q7TNG8	QLLQEEVGPVGVETMR	0.917095163	2	3.4754009
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.150963029**	**0.0779757**	**3**
Q7TP47	AGPIWDLR	1.203930218	2	2.4081302
Q7TP47	DLFEDELVPLFEK	1.618968685	2	2.7884209
Q7TP47	NLANTVTEEILEK	0.880572307	2	2.8101177
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.263066524**	**7.588E-07**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	1.355705136	2	3.2770834
Q7TP48	LENGEIETIAR	1.141483972	2	3.2325432
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	1.187979978	3	4.2140746
Q7TP48	LLLSSETPIEGK	1.648332087	2	3.0568979
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.051186026**	**0.2913683**	**7**
Q7TP52	AGVSVYGIIR	1.109595182	2	2.7957699
Q7TP52	EDCSPADKPYIEEAR	1.001423118	2	3.5080709
Q7TP52	KREDCSPADKPYIEEAR	1.000266731	3	3.780951
Q7TP52	LDYGGMGQEVQVEHIK	1.045430749	2	4.5555034
Q7TP52	LKEHCIVNYQVK	1.337808924	2	4.1485329
Q7TP52	NLIEWLNK	0.988244939	1	2.2939415
Q7TP52	TFSGQTHGFVHR	1.201655723	2	3.4124324
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.137518491**	**1.849E-05**	**7**
Q7TPB1	ALIAGGGAPEIELALR	1.247897802	2	3.7312415
Q7TPB1	AQDIEAGDGTTSVVIIAGSLLDSCTK	0.717967441	2	4.7888656
Q7TPB1	GDVTITNDGATILK	0.89003149	2	2.8945947
Q7TPB1	GLEILTDMSRPVQLSDR	0.954888891	2	2.506119
Q7TPB1	LVIEEAER	1.079917957	2	2.356992
Q7TPB1	SIHDALCVIR	1.273978182	2	2.9900579
Q7TPB1	VIDPATATSVDLR	1.159657289	2	4.0169859
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.057771738**	**0.7509621**	**2**
Q7TPJ0	GEDFPANNIVK	1.090529577	2	2.9395823
Q7TPJ0	GTEDFIVESLDASFR	1.136830605	2	4.0900712
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**1.026921177**	**0.9994514**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(1)	1.026921177	2	2.5037572
Q7TQ20	MMEEVEKLCDR+Oxidation(2)	1.026921177	2	2.4062874
Q7TQ94	**NIT1 Nitrilase homolog 1**	**1.44170396**	**0.3277174**	**2**
Q7TQ94	GQDWEQTQK	1.231036008	2	2.3811374
Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.227294692	3	3.5465729
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.133999136**	**0.6120254**	**3**
Q7TQM4	AIWEAVQAYPK	0.883665947	2	2.96329
Q7TQM4	QDRPLPSTASDSTR	1.043985123	2	3.4221838
Q7TQM4	TQCLEQAQR	1.260463725	2	2.9523931
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.905063053**	**0.956998**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(2)	0.737795896	3	3.6137433
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(6)	1.174073267	3	3.5276566
Q7TSQ1	**CL18A C_type lectin domain family 18 member A**	**1.180027564**	**0.0987944**	**2**
Q7TSQ1	MKCQGKGGVLAQIESQK	1.223481716	2	2.3226299
Q7TSQ1	QANDSAGALPVAGKPEPMAR+Oxidation(18)	1.167258326	2	2.7781234
Q80SY4	**MIB1 E3 ubiquitin_protein ligase MIB1**	**0.96591299**	**0.9203051**	**2**
Q80SY4	LDIQDKDGDTPLHEALR	0.941777436	2	2.4063571
Q80SY4	NTLIMGLGTQGAEKK	1.037073365	2	2.5059001
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.16795774**	**9.9E-20**	**13**
Q80W21	CLDAFPNLK	1.083046963	2	3.1125386

Q80W21	CLDAFPNLKDFIAR	1.295384337	2	3.2497349
Q80W21	FKLGLDFPNLPYLIDGSHK	1.364328225	3	4.908658
Q80W21	HNLCGETEEER	1.132696108	2	3.9460294
Q80W21	IRVDILENQLMDNR	1.27667805	2	2.9385233
Q80W21	ITQSNAILR	1.328052187	2	3.0777271
Q80W21	KHNLCGETEEER	1.233381244	3	4.1167145
Q80W21	KISDYMK	1.105921573	1	1.9546829
Q80W21	LFLEYTDSSYEEK	1.229330506	2	3.9956617
Q80W21	LGLDFPNLPYLIDGSHK	1.398256251	3	4.7914209
Q80W21	LKPGYLEQLPGMMR	1.165669745	2	3.2940698
Q80W21	LYSEFLGK	1.240461146	2	2.4607046
Q80W21	VDILENQLMDNR	0.752121561	2	3.5056524
Q80WE4	**KI20B Kinesin_like protein KIF20B**	**1.248822649**	**0.1989124**	**2**
Q80WE4	IKDLEVIVETQKDECK	1.262594729	2	2.3993559
Q80WE4	KEEDCAELKEK	1.244798177	2	2.3465166
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**0.873414391**	**0.4955114**	**2**
Q80WS3	DHAVVVGVYRPPPK	0.866886963	3	3.4078867
Q80WS3	TNIIPVLEDAR	0.874743354	2	2.4230785
Q80X90	**FLNB Filamin_B**	**1.070142333**	**0.3912912**	**6**
Q80X90	GAGIGGLGITVEGPSESK	1.152249038	2	3.6225936
Q80X90	IEYDDQNDGSCDVK	0.748378937	2	4.0306106
Q80X90	IGNLQTDLSDGLR	1.057529979	2	2.6631806
Q80X90	VDIQTEDLEDGTCK	0.855321018	2	3.9752572
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.012846843	2	4.9336648
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.19653415	2	3.0965278
Q80XB4	**NRAP Nebulin_related_anchoring protein**	**1.226372287**	**0.1566431**	**2**
Q80XB4	EAFERMKGQMLGSR+Oxidation(10)	1.201009434	2	2.3760364
Q80XB4	GRSQFHSRADQPGFLQAK	1.310068063	2	2.6497836
Q80XC3	**US6NL USP6 N_terminal_like protein**	**0.956370614**	**0.6589976**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	1.195991158	2	2.5427749
Q80XC3	SVDEGSKNLK	0.956328084	2	2.380831
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**1.204224888**	**0.4764016**	**2**
Q80XI3	EFEKDKADDDVFEK	1.034232062	2	2.6005063
Q80XI3	NHDEESLECLCR	1.211223423	2	3.1728604
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**1.298621191**	**0.8129729**	**2**
Q80Y84	CDIGLLGLK	0.993568648	2	2.305757
Q80Y84	ETAAAMATLGEARLR	1.382413313	2	2.4104912
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**0.986363714**	**0.9129679**	**3**
Q80Z25	ELEQEAERLEK	1.166547269	2	2.5591729
Q80Z25	MIEESLK+Oxidation(1)	1.017188923	1	1.9516325
Q80Z25	RMIEESLK+Oxidation(2)	0.926831252	2	2.3861952
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.20222989**	**1.389E-08**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	0.957274081	2	3.87711
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.466094142	5	4.6545725
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.29744969	2	4.4878168
Q80Z29	YLLETSGNLDGLEYK	1.038568715	2	4.0702019
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.052368245**	**0.3240885**	**3**
Q811D2	AQEDFDK	0.71327778	1	1.941866
Q811D2	RSADQLSEKTMEQLR+Oxidation(11)	1.077551113	2	2.3181794
Q811D2	SNLEEEARDLK	1.51553958	1	1.9241298
Q811L6	**MAST4 Microtubule_associated serine/threonine_protein kinase 4**	**0.83229663**	**0.6802318**	**2**
Q811L6	FPKATAQMEERLK+Oxidation(8)	0.791366402	2	2.3386455
Q811L6	SGHFENTSAELPSVGSLLK	1.162272885	2	2.3982201
Q811Q2	**CLIC6 Chloride intracellular channel protein 6**	**0.958513196**	**0.0411825**	**2**

Q811Q2	AGSDGESIGNCPFSQR	1.275977089	2	3.7286282
Q811Q2	FLDGDELTLADCNLLPK	0.577202101	2	2.3101492
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.04692661**	**0.9358714**	**5**
Q811X6	EMKSLEQSGSLK+Oxidation(2)	0.995106433	1	1.967831
Q811X6	IVDDQVILSSSSSCLLPSK	1.074020569	2	4.5417967
Q811X6	LVEEGIVSPNDLDLVMSDGLGMR	0.814605825	2	3.4466763
Q811X6	LYDIEQQQITNALESIR	1.22703424	2	4.8407469
Q811X6	TFGPVPEFSGDTVEK	0.836787129	2	3.0231607
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**0.983768737**	**9.9E-20**	**10**
Q8BFZ3	CDVDIRK	0.990772302	2	2.4992106
Q8BFZ3	DLTDYLMK	0.636404339	1	2.3000207
Q8BFZ3	HQGVMVGMGQK	0.85801351	3	3.9466636
Q8BFZ3	HQGVMVGMGQK+Oxidation(5)	1.10851791	3	3.87484
Q8BFZ3	HQGVMVGMGQK+Oxidation(5)Oxidation(8)	1.35294037	3	3.5855098
Q8BFZ3	HQGVMVGMGQK+Oxidation(8)	1.091647916	2	2.8278446
Q8BFZ3	SYELPDGQVITIGNER	0.954458964	2	5.1486192
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.171153995	3	6.9182129
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(6)	1.240994172	3	5.7184258
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.292521996	3	3.9930174
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**1.224517316**	**0.9698389**	**3**
Q8BG32	LYDNLLEQNLIR	1.08302033	2	2.8524749
Q8BG32	TTANAIYCPPK	0.774231938	2	3.1420298
Q8BG32	VQIEHISSLIK	1.220090718	2	2.8516123
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**1.124103152**	**0.508162**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.777904476	2	3.1639118
Q8BGT5	VLCIINPGNPTGQVQSR	1.131716259	2	4.7488675
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.120235797**	**0.0018969**	**4**
Q8BGY2	EDLKLPEGELGK	1.189151032	2	2.4286814
Q8BGY2	KYEDICPSTHNMDVPNIK	1.093033342	3	4.7310796
Q8BGY2	VHLVGIDIFTGK	1.217939425	3	3.6582735
Q8BGY2	YEDICPSTHNMDVPNIK	1.052908003	2	4.0946598
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.087588207**	**3.478E-11**	**9**
Q8BH00	ELLMLENFIGGK	0.913812453	2	3.9138269
Q8BH00	ELNLPFGGMK	0.888616022	1	2.3777387
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.072558647	3	5.1124458
Q8BH00	ILCGEGVDQLSLPLR	1.251002659	2	4.6850491
Q8BH00	ITQLSAPHCK	1.349143259	2	3.1178374
Q8BH00	KLSLELGGK	1.211426696	2	2.404918
Q8BH00	LSLELGGK	0.993617104	1	1.9114614
Q8BH00	NPAIIFEDANLEECIPATVR	1.071265049	2	4.4497666
Q8BH00	SSFANQGEICLCTSR	1.011952581	2	4.162262
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.098162023**	**0.0010888**	**7**
Q8BHN3	AEKDEPGAWEETFK	1.088310195	2	4.2432618
Q8BHN3	MLDYLQGSGETPQTDIR	1.095181943	2	5.4950771
Q8BHN3	REPWLLASQYQDAIR	1.140645221	2	2.882961
Q8BHN3	SGGIERPFVLSR	1.337640758	2	2.5872307
Q8BHN3	THSDSKPYGPTSVGLDFSLPGMEHVYGIPEHADSLR	1.228953626	4	5.020824
Q8BHN3	VTEGGEPYR	0.700344334	2	2.3703997
Q8BHN3	VVIMGAGKPAAVVLQTK	1.065111688	3	3.3227353
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**1.118719705**	**0.9991358**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.017683817	1	2.152585
Q8BIJ6	SCQTALAEILDVLVR	1.072689578	3	3.8201623
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.041810478**	**1**	**9**
Q8BJ64	ADSAYHPSCTCK	1.032187488	2	3.8089335
Q8BJ64	AEVQTLVSR	1.144403132	2	2.7560816
Q8BJ64	ELQPGSHVQSDK	0.974942516	2	3.1540079

Q8BJ64	ELQPGSHVQSDKEIDAFVR	1.078665526	2	3.9696624
Q8BJ64	GGDGPLHVSR	1.058885212	2	2.4532909
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.197367714	5	5.5055094
Q8BJ64	TNHPLHQAFLQAAR	1.028812803	3	4.5605912
Q8BJ64	VIGVENLR	1.002309947	2	2.726027
Q8BJ64	VLLLEAGPK	1.079919563	2	2.6687427
Q8BL66	**EEA1 Early endosome antigen 1**	**1.022553773**	**0.7872394**	**2**
Q8BL66	AAVLDLEK	0.926934442	1	1.9837062
Q8BL66	IQAGEGETAVLNQLQEK	1.041366681	2	3.3208907
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**1.024837537**	**0.9999972**	**3**
Q8BP47	KEDGTFYEFGDDIPEAPER	0.987437226	2	3.9549878
Q8BP47	LMTDTINEPILLCR	1.015457375	2	3.1883361
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.018744047	2	2.6979003
Q8BTM8	**FLNA Filamin_A**	**0.945008027**	**0.9740865**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	1.061518552	2	3.0745773
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	1.062049732	3	4.8950515
Q8BTM8	ANLPQSFQVDTSK	0.944994323	2	2.5739169
Q8BTM8	GAGTGGLGLAVEGPSEAK	0.99051768	2	3.530129
Q8BTM8	GLVEPVDVVDNADGTQTVNYVPSR	0.655698069	2	5.5166144
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.146181987**	**0.8120959**	**2**
Q8BTZ7	HHGQEGSILVTK	1.13747527	3	3.5708601
Q8BTZ7	IGQNCSIGPNVSLGPGVVVEDGVCIR	1.045965459	2	2.741019
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.12561164**	**0.2862477**	**4**
Q8BU33	AAVETLGVPCFLGGMSR	0.716646339	2	3.2877152
Q8BU33	LPNSLMGR+Oxidation(6)	1.120610604	2	2.3486593
Q8BU33	LTGTVGVAAVTAGPGLTNTVTAVK	1.257921007	2	3.1585479
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	1.078355226	2	4.930418
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.107777383**	**0.0004817**	**2**
Q8BWQ1	ADIWLIR	1.069204141	1	1.957116
Q8BWQ1	IHHDQPVKPLDR	1.319673392	3	3.7586493
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**1.157435744**	**0.5262562**	**2**
Q8BX70	ENALSELDVPFKVK	1.071201677	2	3.041532
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(20)	1.133847006	2	2.4807034
Q8BZ81	**LRRT3 Leucine_rich repeat transmembrane neuronal protein 3**	**0.995268415**	**0.9102668**	**2**
Q8BZ81	GLRENTIICASPK	0.887528222	1	1.9436421
Q8BZ81	YPASMKQLQQR+Oxidation(5)	0.995269087	2	2.5831022
Q8BZN6	**DOC10 Dedicator of cytokinesis protein 10**	**0.900846143**	**0.6126224**	**2**
Q8BZN6	IIQDSNKVNPK	0.899922528	2	2.585124
Q8BZN6	LTQMEASALLYFFMRK+Oxidation(14)	1.118544273	2	2.3823795
Q8C547	**HTR5B HEAT repeat_containing protein 5B**	**1.093755937**	**0.0984127**	**2**
Q8C547	MVVSIAEDLLR+Oxidation(1)	1.493087167	2	2.3093512
Q8C547	SAESQGRSEILMSLQK	1.084018733	2	2.3302369
Q8C7R4	**UBA6 Ubiquitin_like modifier_activating enzyme 6**	**1.245838562**	**0.2701685**	**2**
Q8C7R4	GMVTVTDPDLIEK+Oxidation(2)	0.628306605	1	1.9918379
Q8C7R4	NFALLGVGTGREK	1.25313421	2	2.4189868
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.325821612**	**0.0296084**	**2**
Q8C7X2	FNVEDGEIVQQVR	1.300454205	2	4.066556
Q8C7X2	VMGDRSVLYK+Oxidation(2)	1.326412938	2	2.539274
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.164918037**	**0.1029958**	**4**
Q8CC88	FLPSLAQSALEK	1.025861663	2	2.5120561
Q8CC88	HQATGELDDAK	1.167825673	2	3.0807526
Q8CC88	LQLTDEQLQNR	1.050323534	2	2.3874624
Q8CC88	VSSDQLSSENLTSAVGQK	1.071423828	2	3.7053587
Q8CCF0	**PRP31 U4/U6 small nuclear ribonucleoprotein Prp31**	**1.109139887**	**0.8097948**	**2**

Q8CCF0	ERLGLTEIR	1.061343483	2	2.4797504
Q8CCF0	YFSSMAEFLKVK	1.177269082	1	2.0522153
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**0.989360871**	**0.0141412**	**2**
Q8CDI6	EKVANMEVALDK+Oxidation(6)	0.989403614	2	2.6188688
Q8CDI6	ELDDRNMEVQRLEALLK	0.626211916	2	2.3591464
Q8CDI7	**CC150 Coiled_coil domain_containing protein 150**	**1.252288346**	**0.797425**	**2**
Q8CDI7	EDNRKLAMSLEQALQTNGHLQSK	99999.9	2	2.3477485
Q8CDI7	MNIFHLQTEKESNPQK+Oxidation(1)	1.252288021	2	2.5895755
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**1.104930282**	**0.9342718**	**2**
Q8CDM4	MEEESIDLIIK	1.120870547	2	2.3098326
Q8CDM4	VTCQHKMEEESIDLIIK	1.090860685	2	2.5126624
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.213270386**	**0.2568036**	**3**
Q8CFN2	DDPSTIEK	1.209663377	1	2.0900176
Q8CFN2	NVFDEAILAALEPPEPK	1.258175377	3	4.8558631
Q8CFN2	YVECSALTQK	1.138178022	2	3.1282015
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.169138142**	**0.0424938**	**9**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	1.081798297	3	3.4997029
Q8CG45	EHHFEAIALVEK	1.007486384	2	2.9375756
Q8CG45	FFGNSWSETYR	1.311792301	2	2.6262951
Q8CG45	FYAYNPLAGGLLTGK	1.497645726	2	4.1130834
Q8CG45	MDASASAATVR	0.953563509	2	3.4390619
Q8CG45	RMDASASAATVR	1.011655345	2	2.9067247
Q8CG45	TTYGTSAPSMTSAALR	1.175519527	2	3.9899712
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.617750521	3	5.4829626
Q8CG45	WMYHHSQLQGTR	1.398730768	2	3.1311963
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.295093489**	**0.4809205**	**2**
Q8CG48	EEKLLEK	1.162721296	1	1.9820374
Q8CG48	KIKALNCEIEELER	1.231150022	2	2.402894
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**0.818062674**	**1.443E-15**	**8**
Q8CGC7	AIQGATSHHLGQNFSK	1.357603904	2	4.5408731
Q8CGC7	DQDVEPGAPSMGAK	0.817338675	2	2.9862609
Q8CGC7	GDVSISVEEGKENLLR	1.173477467	2	3.4916413
Q8CGC7	GSQFGQSCCLR	1.078544402	2	2.7969527
Q8CGC7	KEENLAEWYSQVITK	0.933119891	2	3.8388238
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.294417133	2	4.3300328
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.085854049	2	4.6801734
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.674297114	2	3.1931648
Q8CGN4	**BCOR BCL_6 corepressor**	**1.272426989**	**0.1219185**	**2**
Q8CGN4	FLTDYLNDLQGR	1.307026851	1	2.1676986
Q8CGN4	KQTQPSCTPASRLPAK	1.216436352	2	2.329607
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.215423709**	**0.0739793**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(11)	1.145208072	2	2.621778
Q8CHB8	ISSATTGGQKPNTLPQK	1.402973422	2	2.3289547
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.807057929**	**4.369E-06**	**7**
Q8CHM7	DTSKPCLINIMIEPQSTR	0.718980298	2	3.2151988
Q8CHM7	GVVPDNHPNCVGAAR	1.215142469	2	3.4417977
Q8CHM7	GYFVQTPEELQDSLR	1.096891917	2	3.4813838
Q8CHM7	LVELCNLPFLPTPMGK	1.854350492	2	4.4029675
Q8CHM7	NCFIVSEGANTMDIGR	1.236071348	2	4.6992478
Q8CHM7	NQEAMGAFQEFPQVEACR	1.063221325	2	6.068604
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	0.526414574	3	4.6668305
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.865009959**	**0.003254**	**2**
Q8CIB5	GCEVTPDVNISGQK	1.101933927	2	2.9265735
Q8CIB5	TSTILGDITSIPELADYIK	1.216333685	2	3.6372271
Q8CIE6	**COPA Coatomer subunit alpha**	**0.952079876**	**0.7613379**	**11**
Q8CIE6	ASNLENSTYDLYTIPK	1.272951424	2	3.1571333

Q8CIE6	DADSQNPDAPEGK	0.947590353	2	3.849973
Q8CIE6	GITGVDLFGTTDAVVK	0.995434789	2	3.8154333
Q8CIE6	GTSPTQIWCNNSQLPVDHILAGSFETAMR	1.155234571	3	3.8917441
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.100243039	3	3.6535821
Q8CIE6	KKNLSPGAVESDVR	0.825256378	2	2.343878
Q8CIE6	LLELGPKPEVAQQTR	1.346766615	2	2.5798352
Q8CIE6	QQPLFVSGGDDYK	0.998018509	2	2.3963275
Q8CIE6	SILLSVPLLVVDNK	1.26289583	2	3.0483823
Q8CIE6	SSGLTAVWVAR	1.313145514	2	2.6643381
Q8CIE6	TLDLPIYVTR	1.044044375	2	2.4006286
Q8CJF7	**ELYS Protein ELYS**	**1.056478181**	**0.442756**	**2**
Q8CJF7	QNSNRVNIEELLK	0.975087276	2	2.66119
Q8CJF7	SVENGQSTEILDDLK	1.146104747	2	2.6358826
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**0.993619613**	**0.9868357**	**3**
Q8JZN5	GIILVGNEEQK	0.999596266	2	2.7171786
Q8JZN5	GSNTCEVHFENTR	1.072644879	2	4.03122
Q8JZN5	SGNVTTVMETIGR	0.958610576	2	3.4054172
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.084448576**	**0.0284571**	**16**
Q8K009	AGFSVFWADDGLDTGPILLQR	1.12363274	2	4.6411209
Q8K009	AMVEAVQLIADGK	0.885756343	2	3.9563348
Q8K009	ANNTEYGLASGVFTR	0.935065711	2	4.4328394
Q8K009	DLGEEALNEYLK	1.68333773	2	3.6514719
Q8K009	EESFGPIMVISK	0.883991591	2	2.831003
Q8K009	FLFPEGIK	0.988857892	2	2.3167067
Q8K009	FQNGDIDGVLQR	0.902228839	2	2.8588171
Q8K009	GVINIIPGSGGVAGQR	0.967344416	2	3.8122678
Q8K009	HGSIIYHPSLLPR	1.300311398	2	4.3967705
Q8K009	KLGFTGSTSVGK	0.644295578	2	2.4347274
Q8K009	KVSLELGGK	1.537677322	1	2.1302054
Q8K009	NLQFEDGK	0.996436332	1	2.044055
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.140902521	2	4.036366
Q8K009	SCDVKPNDTVDSLYNR	0.961536096	2	3.9177341
Q8K009	VVGVFTVPDKDGK	1.015460287	2	3.3250732
Q8K009	YFAGWCDK	1.220696731	1	2.0912998
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**0.939023509**	**0.8229481**	**5**
Q8K442	GQITAILGHSGAGK	0.987481421	2	3.4424121
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	0.863843782	3	4.2604661
Q8K442	LTGVCPQCNVQFDFLTVR	1.223680937	2	3.2741537
Q8K442	NTQNILVQNLSGGQK	1.077357415	2	2.9432619
Q8K442	STLLNVLSGLCVPTK	0.990011383	2	3.2393525
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.975286586**	**0.3328159**	**10**
Q8K4C0	CCLEEGLEPVCFER	0.949550296	2	4.2311172
Q8K4C0	EYKNPVEFTGK	0.936185516	2	2.3734105
Q8K4C0	FDHEMFGLKPK	1.101542149	2	3.1856842
Q8K4C0	GYPIDILLSSR	1.254490303	2	3.05808
Q8K4C0	HSALGQHPTINDDLPNR	1.0117609	2	4.5040808
Q8K4C0	IAVIGSGASGLTCIK	1.617158084	2	3.711714
Q8K4C0	KLPSQSEMMAEINK	0.967056394	2	4.1704321
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.943899968	3	4.5909362
Q8K4C0	KTILTTEDR	1.002781974	2	2.7000976
Q8K4C0	SDDIGGLWR	0.939336242	2	2.92857
Q8K4G6	**MACD1 MACRO domain_containing protein 1 (Fragment)**	**0.994607812**	**0.0164927**	**3**

Q8K4G6	AAGSLLTDECR	0.647456009	2	3.0696788
Q8K4G6	HVIHTVGPIAVGQPTASQAAELR	0.994570756	3	5.0961666
Q8K4G6	SCYLSSLDLLLEHR	1.123246657	2	3.0649726
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.345264564**	**0.1105216**	**3**
Q8K4T4	EVLNLTK	1.368210661	1	2.0564449
Q8K4T4	IEELEETNKSLQK	1.037073365	2	2.4091218
Q8K4T4	SSIISSDGGKGPSEDAKK	1.413800425	2	2.4481001
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**0.936708031**	**0.2506864**	**3**
Q8K4Z3	GNPSGIQPDLLISLTAPK	1.156521672	2	3.7311606
Q8K4Z3	LFGYQPTIYYPK	1.543257526	2	2.3913291
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	0.928025751	2	5.5237694
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.090937245**	**0.9232093**	**4**
Q8K586	FNVWDTAGQEK	1.053858088	2	3.2670078
Q8K586	LVLVGDGGTGK	1.171619535	2	2.3752687
Q8K586	NLQYYDISAK	1.211027701	2	2.7725482
Q8K586	VCENIPIVLCGNK	1.042382393	2	4.0648584
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.880891473**	**0.6173687**	**2**
Q8QZY1	VFSDEVQQQAQLSTIR	0.866352303	2	4.1369133
Q8QZY1	VYEIQDIYENSWTK	1.082983543	2	3.8121755
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.045904967**	**0.0624948**	**4**
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	1.064665631	3	4.6732492
Q8R081	SDALETLGFLNHYQMK	1.136766603	2	3.6454678
Q8R081	SSSGLLEWDSK	0.957168307	2	2.7364769
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	1.245393912	3	7.0766344
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.232475002**	**0.3103821**	**5**
Q8R0F9	FDNTYSLLHTK	1.208437828	2	3.2018106
Q8R0F9	GSSHQVENEILFPGCVLR	0.890845811	2	5.2003083
Q8R0F9	VCEMLLHECELQSQK	1.316657294	2	4.9356971
Q8R0F9	VGYTAEVLLPDK	0.797392053	2	2.5964363
Q8R0F9	VGYTAEVLLPDKACEEK	0.980956128	2	2.4113433
Q8R164	**BPHL Valacyclovir hydrolase**	**1.152971197**	**0.9024161**	**3**
Q8R164	FTLVAWDPR	1.133313869	2	2.514173
Q8R164	QVSLLGWSDGGITALIAAAK	1.142433388	2	3.9415998
Q8R164	TDFAPQLQSLNK	0.95733799	2	3.8031793
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**1.163453599**	**0.9383064**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	0.911013585	2	3.5807428
Q8R1V4	QLLDQVEQIQK	1.185201104	2	3.4057989
Q8R2H4	**KLH12 Kelch_like protein 12**	**0.404061504**	**0.0263236**	**2**
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(15)	0.404061504	2	2.3959243
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(3)	0.404061504	2	2.6550591
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**0.858528417**	**0.487762**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	0.821959842	2	3.6929128
Q8R3Q6	NCIAQTSAVVK	0.858813464	2	3.0038707
Q8R491	**EHD3 EH domain_containing protein 3**	**1.006788924**	**0.9527801**	**3**
Q8R491	ADQIETQQLMR	1.07636216	2	3.0819783
Q8R491	LFEAEEQDLFK	0.85507842	2	3.3722477
Q8R491	MQDQLQAQDFSK	1.047157509	2	3.6417348
Q8R508	**FAT3 Protocadherin Fat 3**	**0.895441478**	**0.2899356**	**2**
Q8R508	FFIDPK	0.844014331	2	2.3314853
Q8R508	QVSYHITGGNPR	0.897255386	2	2.5829866
Q8R5M4	**OPTN Optineurin**	**1.034514364**	**0.6969779**	**2**
Q8R5M4	LELQVESMRSEIK+Oxidation(8)	1.12191168	2	2.4169073
Q8R5M4	NSATPSELNEK	0.814061526	1	2.1871123
Q8VBU2	**NDRG2 Protein NDRG2**	**1.193950419**	**0.0871794**	**3**

Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	1.171827233	2	5.8356366
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.884445667	2	4.723074
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.378703837	2	4.6374278
Q8VC12	**HUTU Urocanate hydratase**	**0.992829093**	**3.596E-10**	**6**
Q8VC12	HQLVVGSQAR	0.899788058	2	2.9162142
Q8VC12	LLALEFAQELR	1.582800225	2	4.3032417
Q8VC12	LVITNGMVIPNYSSR	1.028334236	2	3.5992205
Q8VC12	MMLSWDVSNGVAR	0.844962118	2	2.4680388
Q8VC12	VAIAVAINQAIASGK	0.874865199	2	2.6671028
Q8VC12	VFVTSGLGGMSGAQAK	0.913845949	2	4.4639182
Q8VC28	**AK1CD Aldo_keto reductase family 1 member C13**	**1.499493563**	**0.0172655**	**2**
Q8VC28	ILNKPGLK	1.361141056	1	2.0304816
Q8VC28	YKEWVDQNSPVLLNDPVLCDVAK	1.504118627	3	4.4174914
Q8VCD5	**MED17 Mediator of RNA polymerase II transcription subunit 17**	**0.919132637**	**0.9312625**	**2**
Q8VCD5	EIFAQLSREAVQIK	0.912101245	1	2.0965867
Q8VCD5	MELLMSALSPCLL+Oxidation(1)Oxidation(5)	0.962400416	2	2.5565188
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**1.114932905**	**0.1206467**	**3**
Q8VDC1	GLELQVMQLQQEK	1.231557155	2	2.3960147
Q8VDC1	MEEALASLAQELQDSK	1.413800425	2	2.4075055
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(1)	1.051594547	2	2.3504796
Q8VDD9	**PHIP PH_interacting protein**	**0.532064309**	**0.2026016**	**2**
Q8VDD9	EDLLQK	0.597410951	1	1.9638904
Q8VDD9	MELREQELMKIVGIK	0.531131229	2	2.4443107
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**1.041117441**	**0.5926424**	**2**
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.994320439**	**0.9712071**	**3**
Q8VED5	NKYEDEINK	1.044613708	2	2.3814685
Q8VED5	NKYEDEINKR	0.984828655	3	3.4429867
Q8VED5	YEDEINK	1.173983408	1	2.1781459
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.120514825**	**0.2165993**	**10**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.098391749	3	4.948566
Q8VEK3	GGYSNRGNYNRGGMPNR	1.623405226	2	2.3531098
Q8VEK3	LLEQYKEESK	0.734485916	2	3.0744493
Q8VEK3	LLEQYKEESKK	1.152560684	2	3.7361219
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.108873989	3	5.0455332
Q8VEK3	NFILDQTNVSAAAQR	1.146104747	2	5.0718961
Q8VEK3	TCNCETEDYGEK	1.204359279	2	3.3513949
Q8VEK3	VSELKEELK	1.096176419	2	2.6571589
Q8VEK3	VSELKEELKK	1.143078583	2	2.5410831
Q8VEK3	YNILGTNTIMDK	1.037214163	2	3.3143268
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**1.546715639**	**0.0740386**	**9**
Q8VHE9	ATVQSVLLDSAGR	1.160193304	2	3.0107505
Q8VHE9	FLPLPLTQLLNK	1.824404977	2	2.6610534
Q8VHE9	GATYGADHDLAR	1.161012326	2	3.1118138
Q8VHE9	NLYSDLQALGSK	1.114333416	2	3.7014759
Q8VHE9	RPPEPLVTDK	1.286581691	2	3.0134344
Q8VHE9	RPPEPLVTDKEAR	1.197861094	3	3.8933179
Q8VHE9	VESVTGGSPLTNQYYLAAHR	1.295547267	2	4.0771079
Q8VHE9	VLVLEQHTK	1.203683288	2	2.3094938
Q8VHE9	VVAHGVSHAILLK	1.089501612	2	2.8237159
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**1.022746002**	**0.9556749**	**4**
Q8VHF5	ALGVLAQLIWSR	0.976662006	2	2.7487879
Q8VHF5	GLVYETSVLDPDEGIR	1.094782122	2	3.507694
Q8VHF5	GYSIPECQK	1.073672133	2	2.5074832
Q8VHF5	IVPNILLEQGK	1.241829861	2	2.5616233
Q8VHN7	**GPR98 G_protein coupled receptor 98**	**1.024474296**	**0.6303125**	**2**

Q8VHN7	FIVEEPEFNSVR	1.595585754	2	2.3042033
Q8VHN7	ITMVASDAPYGR	1.02268786	2	2.6407626
Q8VHT6	**AS3MT Arsenite methyltransferase**	**0.999509394**	**1**	**2**
Q8VHT6	SLQNVHEEVISR	0.986886326	2	3.2982857
Q8VHT6	TSADLQTNACVTPAK	1.029222361	2	3.9777195
Q8VHX6	**FLNC Filamin_C**	**1.06047646**	**0.8854124**	**2**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.061806595	2	3.8767958
Q8VHX6	IECDDKGDGSCDVR	0.698543484	2	3.6021242
Q8VI04	**ASGL1 L_asparaginase**	**0.980042584**	**0.8660032**	**3**
Q8VI04	GLGGLILINK	1.050947694	2	2.4329054
Q8VI04	GNLAYATSTGGIVNK	0.974860526	2	4.0688562
Q8VI04	TVDEAATLALDYMK	1.139295017	2	2.6095495
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.065240439**	**0.9360822**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.141837358	2	4.5731363
Q8VID1	LAEDGAHVVISSR	1.024503727	2	3.7078002
Q8VID1	NFAAELAPK	0.869006383	2	2.3260815
Q8VID1	VNCLAPGLIK	0.894134148	2	2.4895391
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.798829983**	**0.0297288**	**10**
Q8VIF7	CGPGYATPLEAMK	0.697548222	2	3.1246333
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	0.830538315	2	4.8265519
Q8VIF7	GGFVLLDGETFEVK	0.851846968	2	4.2777286
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.982447964	2	3.9007337
Q8VIF7	HEIIQTLQMK	0.82233819	2	2.7141581
Q8VIF7	HNIMVSTEWAAPNVFK	0.655232613	2	4.7344127
Q8VIF7	LTGQIFLGGSIVK	0.910256443	2	3.4714067
Q8VIF7	NEGGTWSVEK	0.717286529	2	2.5344605
Q8VIF7	NTGIEAPDYLATVDVDPK	0.774811161	2	4.6292548
Q8VIF7	QYDISNPK	0.929128527	1	1.9925004
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**0.958011723**	**0.8684058**	**2**
Q8VIJ6	FGQGGAGPVGGQGPR	0.963752153	2	3.3135467
Q8VIJ6	YGEPGEVFINK	1.131941153	2	2.3284075
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**1.006865202**	**0.9998031**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	1.439319696	2	5.4578886
Q91VA0	AILPFDLQIIDEK	1.072565412	2	4.2004938
Q91VA0	GNILPPNTEGYIGIR	1.019690629	2	3.1621025
Q91VA0	HNQGLAFR	0.874412447	2	2.5338156
Q91VA0	KVEFVSELPK	0.984036804	3	3.4072533
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.837605453**	**0.882766**	**2**
Q91VM9	IIAINVNDPEAEK	0.884104698	2	2.9748034
Q91VM9	MEIATEEPLNPIK	0.789518961	2	4.0878882
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.881196511**	**0.9298269**	**3**
Q91W43	EMLQALGLASIDELIEK	0.823939483	2	2.4842672
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	1.087469288	2	4.2445221
Q91W43	VSFQPNSGAQGEYAGLATIR	0.880946272	2	5.0619078
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.125682516**	**0.6711742**	**2**
Q91W90	SFEDTIAQGITFVK	1.040714703	2	2.6671584
Q91W90	VDCTQHYAVCSEHQVR	1.126805629	3	4.7359447
Q91X77	**CY250 Cytochrome P450 2C50**	**1.035490071**	**0.9849448**	**4**
Q91X77	EHEESLDVTIPR	0.918687564	2	2.4604688
Q91X77	IKEHEESLDVTIPR	1.023457014	2	3.7510283
Q91X77	NFLLEK	1.119967469	1	2.0865474
Q91X77	YALLLLLK	1.274741998	2	2.6842859
Q91X78	**ERLN1 Erlin_1**	**1.027835157**	**0.0719891**	**2**
Q91X78	ISEIEDAAFLAR	0.92811894	2	2.7967987

Q91X78	SVQTTLQTDEVK	1.376694175	2	2.9312723
Q91Y81	**SEPT2 Septin_2**	**1.118189669**	**0.5674749**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	0.950264171	2	3.1613903
Q91Y81	ILDEIEEHSIK	0.835447108	2	2.8962536
Q91Y81	LTVVDTPGYGDAINSR	1.149660852	2	3.9230528
Q91Y81	STLINSLFLTDLYPER	1.155711292	2	2.7581091
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**0.919294979**	**0.3956687**	**8**
Q91YT0	GAGAYICGEETALIESIEGK	1.142069508	2	4.3968887
Q91YT0	GDARPAEIDSLWEISK	0.978033071	3	3.7081583
Q91YT0	GEFYNEASNLQVAIR	1.076268404	2	3.4046121
Q91YT0	GGAGFPTGLK	1.086952697	2	2.3387012
Q91YT0	KTSFGSLKDEDR	1.232384977	2	2.8483126
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.361585225	3	4.7324619
Q91YT0	LVEGCLVGGR	0.917431063	2	2.7964101
Q91YT0	YLVVNADEGEPGTCK	1.113102751	2	5.2112508
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.255342918**	**9.9E-20**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.366763755	3	6.9136453
Q91Z53	LLDAAGANLR	1.258495755	2	2.5159602
Q91Z53	NCVILPHIGSATYK	1.09496404	2	3.5834281
Q91Z53	NTMSLLAANNLLAGLR	0.9220346	2	4.772294
Q91Z53	RLPEAIEEVK	1.119490384	2	2.7849946
Q91Z53	VISTLSVGVDHLALDEIK	1.66117654	2	4.1307306
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**1.099322511**	**1.11E-16**	**16**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	1.155600917	3	4.9765611
Q91ZJ5	EFPTVPLVK	1.097099253	1	2.0429416
Q91ZJ5	FVQDLSK	1.157941222	1	1.9363024
Q91ZJ5	GGTLTQYEGK	1.071974562	2	2.6701472
Q91ZJ5	GLPDNISSVLNK	1.037820696	2	3.3069055
Q91ZJ5	GTVIIIANHGDR	1.110129961	2	3.0970294
Q91ZJ5	IDIPPGAVLENK	1.12761745	2	3.0295796
Q91ZJ5	IQRPPEDSIQPYEK	1.207421543	3	4.5876174
Q91ZJ5	LNGGLGTSMGCK	1.2439691	2	3.2515879
Q91ZJ5	LQEQNAIDMEIIVNPK	0.978525599	2	4.1927853
Q91ZJ5	LVEIAQVPK	1.101811748	2	2.4613247
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.372573677	2	5.0860171
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	1.114568963	3	4.5666289
Q91ZJ5	SFENSLGINVPR	1.062959457	2	3.4593301
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	1.005168007	2	5.4114976
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.397246475	2	4.5373397
Q91ZU6	**DYST Dystonin**	**1.468563185**	**0.0130153**	**4**
Q91ZU6	LQVEQNK	1.471399488	1	1.9251529
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(1)	1.586678495	2	2.5130334
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(2)	1.586678495	2	2.5131037
Q91ZU6	SAETNIDQDITNLK	1.076026181	2	2.4329362
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**1.151649369**	**0.6022527**	**2**
Q91ZV0	CGDLECETLISRVLALR	1.150473372	2	2.4694326
Q91ZV0	KMLDQDDIVENDK+Oxidation(2)	1.149697474	2	2.4191244
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**0.965709772**	**0.9942598**	**3**
Q91ZX7	GCHVNECLSR	0.926251592	2	2.6799765
Q91ZX7	MYDAQQQQVGTNK	0.966298934	2	4.0943356
Q91ZX7	VFFTDYGQIPK	0.93235577	2	2.6729174
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.231223109**	**0.0133801**	**2**
Q920A6	DLDTVASDMMVLLK	1.213973006	2	2.3894567
Q920A6	GLAEVSDIAEQVLNAVNK	1.188666141	3	5.8610973

Q920B9	**SP16H FACT complex subunit SPT16**	**1.151993737**	**0.4857485**	**2**
Q920B9	EMKIYIDK+Oxidation(2)	1.151651891	1	1.9110484
Q920B9	ICDVYNSVMDVVKK	1.352106561	2	2.3290632
Q920D2	**DYR Dihydrofolate reductase**	**1.33694936**	**2.15E-09**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	1.536395277	2	5.0293999
Q920D2	LIEQPELASK	1.240358621	1	2.0280252
Q920D2	LLPEYPGVLSEIQEEK	1.504635794	2	3.7767909
Q920D2	NGDLPWPLLR	1.160271657	2	2.8250375
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**1.040929411**	**0.1493404**	**3**
Q920F5	EIAEVTGDPVHESLK	1.153339508	2	2.9823329
Q920F5	ISECEAVHPVK	0.985195111	2	3.2347836
Q920F5	WLLGLLNVQGK	1.593266982	2	2.3665967
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.223359768**	**0.0245109**	**2**
Q920J4	AGCECLNESDEHGFDNCLR	1.02149911	3	3.7946918
Q920J4	IDQYQGADAVGLEEK	1.183239139	2	4.5486555
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.035560957**	**0.4097617**	**20**
Q920L2	ACALSIAESCRPGDK	0.997065762	2	2.3544216
Q920L2	ACALSIAESCRPGDKVPPIK	1.449281777	3	3.3442512
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.178799712	3	4.669755
Q920L2	ANAGEESVMNLDK	1.004921132	2	3.6520212
Q920L2	GEGGILINSQGER	1.05943498	2	3.5022445
Q920L2	GVIALCIEDGSIHR	0.960886839	2	4.0246434
Q920L2	HTLSYVDTK	1.023615414	2	2.7425241
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.132149837	3	6.5098844
Q920L2	IDEYDYSKPIEGQQK	0.985463684	2	4.4635615
Q920L2	KHTLSYVDTK	1.329144903	2	2.3288476
Q920L2	LGANSLLDLVVFGR	1.480935355	2	2.3615785
Q920L2	NTIIATGGYGR	0.886095267	2	2.4382315
Q920L2	SMQSHAAVFR	0.912783084	2	2.3020694
Q920L2	TGHSLLHTLYGR	0.963845913	2	3.006804
Q920L2	TLNEADCATVPPAIR	0.973436061	2	3.9369938
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.19929619	2	5.8208203
Q920L2	VGSVLQEGCEK	1.033928917	2	3.6788359
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.958701256	3	4.4278517
Q920L2	VSQLYGDLQHLK	1.226447179	2	3.4814913
Q920L2	VTLDYRPVIDK	1.04946376	2	3.1331117
Q920P0	**DCXR L_xylulose reductase**	**1.161185897**	**0.5848289**	**7**
Q920P0	ALTNHTVYCSTK	0.914858508	2	3.5492773
Q920P0	AVVQVSQIVAR	1.065616595	1	2.4604034
Q920P0	GVPGAIVNVSSQASQR	1.078734267	2	5.6199903
Q920P0	SSMTTGSALPVDGGFLAT	1.211196005	1	2.5556726
Q920P0	STVLALQAAGAQVVAVSR	1.296217138	2	3.790535
Q920P0	TREDLDSLVR	1.168983373	2	2.938616
Q920P0	VNAVNPTVVMTPMGR	0.617008451	2	3.2880232
Q920P6	**ADA Adenosine deaminase**	**1.894937739**	**0.122463**	**2**
Q920P6	FKDDQANYSLNSDDPLIFK	1.321284902	2	2.6603727
Q920P6	TVHAGEVGSAEVVR	2.256560462	2	3.4567709
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.015035587**	**0.3000175**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	1.090774859	2	4.1789317
Q921F2	GISVHISNAEPK	1.100951091	2	2.5218973
Q921F2	KDLKTGHSK	0.868974137	2	2.4724503
Q921F2	TSDLIVLGLPWK	1.071611118	2	2.81391
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.167875055**	**4.036E-08**	**7**
Q922F4	ALTVPELTQQMFDAK	1.187267007	2	4.0499897
Q922F4	GHYTEGAELVDSVLDVVR	1.071583546	2	6.7748833
Q922F4	IREEYPDR	0.88210723	2	2.8539424

Q922F4	MASTFIGNSTAIQELFK	1.506448143	2	4.4388585
Q922F4	NMMAACDPR	0.930278934	2	2.5143671
Q922F4	NSSYFVEWIPNNVK	1.198814227	2	4.7015953
Q922F4	YLTVATVFRGPMSMK+Oxidation(14)	1.181155215	2	2.3130534
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.13580296**	**0.0034582**	**2**
Q922J3	EMETMQAKLMK+Oxidation(5)	1.151119951	2	2.6398294
Q922J3	HEEILQNLQKMLADTEDK	1.078665526	2	2.4192717
Q923D2	**BLVRB Flavin reductase (NADPH)**	**1.107689993**	**0.006845**	**3**
Q923D2	LQDVTDDHIR	1.124931666	2	3.3050942
Q923D2	TGLTTLAQAVQAGYEVTVLVR	1.078796462	3	4.0117083
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.97507388	3	4.0856495
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**1.091964594**	**0.8350369**	**2**
Q923J6	LEFLTNLDIK	1.080855115	1	2.0133114
Q923J6	MSDPNKTAITAEKEALNLK	1.094651066	2	2.4659996
Q923K9	**A1CF APOBEC1 complementation factor**	**1.129413389**	**0.1170429**	**2**
Q923K9	LAPQILEEICQK	1.299287821	2	2.4299793
Q923K9	TGYSLVQENGQR	0.933568254	2	2.7717183
Q923V8	**SEP15 15 kDa selenoprotein**	**1.099052698**	**0.7004351**	**2**
Q923V8	GCCQEEAQFETK	1.088577488	2	4.1520557
Q923V8	LLDDNGNIAEELSILK	1.226541763	2	3.6550095
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**1.07501261**	**0.9991947**	**4**
Q924C3	AEYLHTWGGLLPVISK	1.034079843	3	3.6935043
Q924C3	ELESPAAASLLAPMDLGEEPLEK	1.064398502	2	3.4161866
Q924C3	SGTYFWPGSDVEIDGILPDIYK	0.890874835	2	3.6986001
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	1.117285541	2	3.2503798
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.018900216**	**0.2074624**	**7**
Q924S5	AQSVLEEDHYGMEDVK	0.966075804	2	3.9711514
Q924S5	FSVGGMTDVAEIK	0.977771271	2	2.8757157
Q924S5	HVMDVVDEELSK	1.039615572	2	3.8248422
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.316495426	3	6.3934197
Q924S5	MEMINVSGYVAQEK	0.855451662	2	3.7797143
Q924S5	QLEVEPEGLEPEAENK	0.954479242	2	4.1632595
Q924S5	TENPLVLIDEVDK	1.002944482	2	2.475801
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**1.194083061**	**0.0733597**	**3**
Q924W5	ELDMKEKELQEK	1.071355334	2	2.6038089
Q924W5	MEEQQVRLNDAEKK	1.124246102	2	2.3874383
Q924W5	TKEQINQGEERLTELK	1.352087719	2	2.561676
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.079987668**	**9.9E-20**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	1.5207327	2	4.1187811
Q99020	FGEVVDCTIK	1.051031492	2	2.5007083
Q99020	IFVGGLNPEATEEK	1.788005233	2	3.7533505
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.105433715**	**0.0166294**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.670507378	2	3.0218034
Q99JI4	RLDEELEDAEK	1.118859894	2	2.9187486
Q99JI4	VNEIVETNRPDSK	1.09242274	2	3.3329036
Q99JW2	**ACY1 Aminoacylase_1**	**0.977651336**	**0.9863656**	**2**
Q99JW2	FIEDTAAEK	0.968666914	2	2.6307926
Q99JW2	SVSIQYLEAVR	1.04272877	2	2.3954582
Q99K43	**PRC1 Protein regulator of cytokinesis 1**	**1.619196072**	**0.0189247**	**2**
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(1)	1.619196072	2	2.3681536
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(6)	1.619196072	2	2.3683286
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**1.303412583**	**0.001073**	**2**

Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(14)	1.500862433	2	2.5174072
Q99KK9	YDLTVPFARYLAMNKLK+Oxidation(13)	1.186818077	2	2.5965576
Q99KW3	**TARA TRIO and F_actin_binding protein**	**0.975936301**	**0.7886815**	**2**
Q99KW3	AYQEELSRELSK	1.104812993	1	2.0306938
Q99KW3	SEREIEQLK	0.9087764	1	1.9716955
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.863228973**	**0.6285428**	**2**
Q99L04	ATAQEAQSLGGR	0.94243256	2	3.3408558
Q99L04	CVPVVCDSSQESEVK	0.60818857	2	4.4464121
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**0.823832018**	**0.2616855**	**4**
Q99LF4	GLGHQVATDALVAMEK	0.985712113	2	2.3094466
Q99LF4	NLDFQDVLDK	0.798622843	2	2.8833854
Q99LF4	NVTDVVNTCHDAGISK	0.978825264	2	4.2763147
Q99LF4	TNLDESDVQPVK	1.005509792	2	3.6920028
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.039874617**	**0.8965107**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(12)	1.039874617	2	2.3300374
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(6)	1.039874617	2	2.3173015
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**1.019998668**	**0.8535158**	**2**
Q99M87	AQGLYETINVTIPAGIQTDQK	0.898635768	2	2.4102831
Q99M87	GSIITNPCVVCR	1.020581931	2	2.5982349
Q99ML9	**RN111 E3 ubiquitin_protein ligase Arkadia**	**1.389645106**	**0.0165496**	**2**
Q99ML9	DMTGNQQEQEKSGVVRK	1.582221409	3	3.6233559
Q99ML9	LHPHEVMQRMEVQR+Oxidation(7)	1.301283792	2	2.412626
Q99MN1	**SYK Lysyl_tRNA synthetase**	**1.216445649**	**0.0543525**	**4**
Q99MN1	MATLQESEVKVDGEQKLSK+Oxidation(1)	0.954952284	2	2.3383234
Q99MN1	RGDIIGVEGNPGK	1.192893607	2	3.3266866
Q99MN1	SEEEFVHINNK	1.068026372	2	3.5142522
Q99MN1	YLDLILNDFVR	1.392380573	2	2.6918385
Q99MQ1	**BICC1 Protein bicaudal C homolog 1**	**1.078631005**	**0.5122634**	**2**
Q99MQ1	EAKEMIMSVLDTK	1.257375492	2	2.3983474
Q99MQ1	QYLMGCLPLVLMFDMK+Oxidation(15)	0.97438512	2	2.3017595
Q99MS0	**S14L2 SEC14_like protein 2**	**1.084960968**	**0.5699321**	**4**
Q99MS0	AGEMTEVLPNQR	0.96054478	2	3.8269825
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	1.726118467	2	3.8606846
Q99MS0	DQVKQQYEHSVQISR	0.90922439	2	2.384321
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.149490331	2	4.7803602
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.984566529**	**0.012493**	**5**
Q99MZ8	GFSVVADTPELQR	1.041930677	2	3.5889471
Q99MZ8	QQSELQSQVR	0.917466252	2	2.5202484
Q99MZ8	QSFTMVADTPENLR	0.941375686	2	3.1755078
Q99MZ8	TGDTGMLPANYVEAI	2.517430229	1	2.4306543
Q99MZ8	TQDQISNIK	0.979182518	2	2.8695173
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**1.081986693**	**0.0128362**	**5**
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.839393316	2	6.9423742
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.092649973	2	4.848218
Q99PF5	IGQQPQQPGAPPQQDYTK	1.113114598	2	4.054358
Q99PF5	IINDLLQSLR	1.218561044	2	2.5729461
Q99PF5	SVSLTGAPESVQK	0.942982736	2	2.5503247
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.306834342**	**9.9E-20**	**18**
Q99PL5	AENSQLTER	0.854770169	2	2.3833342
Q99PL5	DALNQATSQVESK	0.758641466	2	3.3147886
Q99PL5	EAEETQNSLQAECDQYR	1.328925338	2	5.6416636
Q99PL5	EHTSHLEAELEK	1.047978798	2	3.3590245
Q99PL5	GELESSDQVR	0.905293949	2	3.1986523
Q99PL5	HMAAASAECQNYAK	0.962002721	2	4.3090839
Q99PL5	HMAAASAECQNYAK+Oxidation(2)	1.34765623	2	3.9584415

Q99PL5	IQEELEK	1.162721296	1	2.3127604
Q99PL5	LKELESQVSCLEK	1.084381944	2	4.0800042
Q99PL5	LLATEQEDAAVAK	1.23152852	2	3.99225
Q99PL5	LQQENSILR	0.95938078	2	2.6114526
Q99PL5	QLHLAEAQTK	1.037769377	2	2.3519285
Q99PL5	RLEEVTR	0.645784599	2	2.443028
Q99PL5	TGVIQDTWHK	0.945229242	2	2.3191552
Q99PL5	TILAETEGMLK	1.064685233	2	3.1658583
Q99PL5	TLQEQLENGPNTQLAR	1.148436364	2	5.0445824
Q99PL5	TLVSTVGSMVFSEGEAQR	1.134315291	2	4.2839885
Q99PL5	VEPAVSSIVNSIQVLASK	1.464117483	2	4.0111885
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**1.045430749**	**1**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(10)	1.045430749	2	2.6938081
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(11)	1.045430749	2	2.6509032
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**0.97923654**	**1**	**2**
Q9CPQ1	FGVAEPR	0.994867735	2	2.432296
Q9CPQ1	NYDSMKDFEEMR	0.979748869	2	3.7965386
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**0.928993324**	**0.0038375**	**2**
Q9CRB9	VAEELALEQAK	0.844690663	2	3.4395633
Q9CRB9	YEYHPVCADLQTK	0.94480756	2	3.6784585
Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**1.095424301**	**0.0764379**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.07399803	2	2.6674449
Q9CTN4	LKDSGDVSDIIEK	1.582082052	2	2.47877
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**1.188197636**	**0.9977283**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	1.016015243	2	4.3788381
Q9CW42	GLSVSEAECTAMGLR	0.964229742	2	3.1798229
Q9CW42	LQQVGTVAQLWIYPIK	0.829296376	2	3.3392291
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.225521332**	**0.1693685**	**3**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.137700085	2	4.261364
Q9CWH6	ALLEVVQSGGK	1.656639161	2	2.94526
Q9CWH6	LTVEDPVTVEYITR	1.177171348	2	4.0070081
Q9CWK8	**SNX2 Sorting nexin_2**	**0.921092366**	**0.9967254**	**3**
Q9CWK8	ALSQLAEVEEK	1.043541626	2	2.3724058
Q9CWK8	AVNTQALSGAGILR	1.10315279	2	3.5174921
Q9CWK8	QQQFENLDQQLR	0.907075763	2	2.5138817
Q9CXD6	**CC90A Coiled_coil domain_containing protein 90A_ mitochondrial**	**1.132122009**	**0.007305**	**2**
Q9CXD6	MLELRTEIVSLHAQQDR	1.673412279	2	2.6834548
Q9CXD6	VRTDTKLNFNLEK	1.12191168	2	2.4849205
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.986224252**	**0.9962905**	**2**
Q9CYW4	LEDILTGLGLR	0.991019506	2	3.7444658
Q9CYW4	RLEDILTGLGLR	0.799503949	2	3.2889583
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.006351165**	**0.8479664**	**2**
Q9CZY3	LLEELEEGQK	1.009721152	2	2.811604
Q9CZY3	VNMSGVSSSNGVVDPR	1.1705118	2	3.0199904
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**1.221213384**	**0.0380571**	**3**
Q9D024	ERIMNEEDPEKQR	1.677365011	2	2.5858734
Q9D024	IMQEEGQPLKLPDTK	0.767512597	2	2.8992112
Q9D024	RLEEAALR	1.029750386	2	2.6188269
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.155403156**	**0.0027521**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	0.998254017	3	4.2741365
Q9D0M3	GLLSSLDHTSIR	1.076950012	2	2.7764914
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.441634894	2	5.2654963
Q9D0M3	HLVGVCYTEEEAK	1.033700017	2	3.9358797

Q9D0M3	LSDYFPKPYPNPEAAR	1.156762938	3	3.4136183
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**0.954946886**	**8.282E-14**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.895854507	2	2.9444935
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.453796949	2	5.2357912
Q9D0S9	SLPADILYEDQQCLVFR	1.304006001	2	4.4797692
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**0.845785085**	**0.0071208**	**5**
Q9D172	GVEVTVGHEQEEGGK	0.949026185	2	3.7936745
Q9D172	GVTEAHVDQK	0.579854656	2	2.8271718
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.385240129	2	4.3320766
Q9D172	NLSTFAVDGK	1.161173845	1	2.9209476
Q9D172	NVLAESAR	0.996324071	1	2.0076911
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.064258617**	**0.061235**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(1)	1.032638694	2	2.3697078
Q9D1Q6	NIIGYFEQK	1.06169301	1	2.4742806
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.168193634	2	5.4372854
Q9D1Q6	VDCDQHSDIAQR	1.160027291	2	3.5448999
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.220737667**	**9.9E-20**	**5**
Q9D2U9	AMGIMNSFVNDIFER	1.352867198	2	5.1772594
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)	1.475522054	2	4.3575988
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)Oxidation(5)	1.36819455	2	3.0880842
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(5)	1.485231158	2	3.8873227
Q9D2U9	LLLPGELAK	1.307656024	2	2.417347
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**0.984047323**	**1**	**2**
Q9D6M3	GAAVNLTLVTPEK	1.014818932	2	2.7706139
Q9D6M3	GVNEDTYSGFLDCAR	0.949890947	2	4.6509852
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.086678463**	**0.4643344**	**10**
Q9D6Y9	CVAYAESHDQALVGDK	1.166884396	2	4.9576821
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	1.075889065	3	3.9119399
Q9D6Y9	GTHDLWDSR	1.047649318	2	2.3640049
Q9D6Y9	HFTSNVLPR	1.057948535	2	2.4533179
Q9D6Y9	IVLDSDAAEYGGHQR	1.118300844	2	4.4912815
Q9D6Y9	IYESHVGISSHEGK	1.191535539	2	4.5313907
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.056042617	2	3.8044076
Q9D6Y9	QFNLTDDDLLR	0.7916887	2	2.7540388
Q9D6Y9	RQFNLTDDDLLR	1.019272211	2	2.8648598
Q9D6Y9	WELYIPPK	1.151422865	2	2.3857484
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.116791037**	**0.8900348**	**2**
Q9D6Z1	ELNEEKLEK	1.127010608	2	2.4643133
Q9D6Z1	IDCFSEVPTSVFGEK	0.941523016	2	2.7528133
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.068424215**	**0.2724248**	**4**
Q9D7B6	AVIFEDCAVPVANR	0.907933574	2	3.3613486
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	1.309420909	2	4.9260149
Q9D7B6	IGTEGQGFLIAMK	1.239005165	2	2.9804564
Q9D7B6	VHQILEGSNEVMR	1.273522965	2	2.9119051
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**1.15993137**	**0.9989631**	**2**
Q9D7X8	ISDEMEDIIK	0.961529509	2	2.7349968
Q9D7X8	SNISSLDEQEGVK	1.035207623	2	3.7432301
Q9D819	**IPYR Inorganic pyrophosphatase**	**0.913909329**	**9.9E-20**	**5**
Q9D819	GISCMNTTVSESPFK	0.913442465	2	4.7446561
Q9D819	GQYISPFHDVPIYADK	1.65131366	2	3.9418166
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.007145473	3	4.9818301
Q9D819	VLGILAMIDEGETDWK	2.100432404	2	4.2968569
Q9D819	YVANLFPYK	0.984055967	1	2.1310537
Q9D855	**QCR7 Cytochrome b_c1 complex subunit 7**	**1.01315246**	**0.9946549**	**2**
Q9D855	RLPEDLYNDR	1.003909488	2	2.5444405

Q9D855	YEEDKFYLEPYLK	1.114353948	2	4.6245723
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**0.990473006**	**0.0158016**	**3**
Q9D880	TIALNQVEDVR	0.911274608	2	3.1273105
Q9D880	TVLEHYALEDDPLEAFK	1.288822088	2	4.9259539
Q9D880	VLLDLSAFLK	1.153303002	2	2.5534093
Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**1.22921082**	**0.7766758**	**2**
Q9D8W5	MVQQCCTYVEEITDLPVK	1.331555957	2	4.8896227
Q9D8W5	WSTLVEDYGVELR	1.038921995	2	3.0828664
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**0.886218823**	**0.6496437**	**2**
Q9DB15	NYVQGINLVQAK	0.886664845	2	2.7811399
Q9DB15	SEALAGAPLDNAPK	0.744951578	2	3.1921012
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.029473302**	**0.9295992**	**2**
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	1.124047054	3	3.8418233
Q9DBH5	WSELAGCTADFR	0.955731507	2	3.2839003
Q9DCJ5	**NDUA8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8**	**1.05971843**	**0.9762917**	**2**
Q9DCJ5	ARPEPNPVIEGDLKPAK	1.025329834	3	4.6653419
Q9DCJ5	TDRPLPENPYHSR	1.071623176	3	3.8940399
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**0.864520132**	**0.8465656**	**3**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.169928755	3	4.1870909
Q9DCM0	SLLPGCQSVISR	0.866268111	2	3.0738251
Q9DCM0	TDFQQGCAK	0.837051686	2	2.9106839
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.200202036**	**4.947E-06**	**3**
Q9DCS9	AYDLVVDWPVTLVR	1.282142079	2	4.4034958
Q9DCS9	RVPDITECK	1.179591726	2	2.3267851
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.41118718	2	2.9731731
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.459437113**	**1.785E-05**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.255652715	2	2.8333321
Q9DCT2	ILTDYGFEGHPFR	0.842833975	2	2.8922765
Q9DCT2	KFDLNSPWEAFPAYR	1.289043919	2	3.6585033
Q9DCT2	SLADLTAVDVPTR	1.162149013	2	2.7365355
Q9DCT2	VVAEPVELAQEFR	1.226888945	2	3.6492088
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.115265154**	**9.032E-13**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.179757208	2	5.446032
Q9DCU9	LIEPNTAVTR	1.097256558	2	3.1902125
Q9DCU9	TMDWFGYYGGPCR	1.20717054	2	3.5364938
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.010430354**	**0.8137214**	**9**
Q9EP89	EVWSEGLGYADVENR	0.726991328	2	3.0203533
Q9EP89	FENSIESLR	0.856679552	2	2.9721844
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	1.453154316	2	5.5223894
Q9EP89	IKDEVGAPGIVVGVSVDGK	0.980633783	2	4.1634321
Q9EP89	KNDFEQGELYLK	0.986752622	2	4.1949267
Q9EP89	LDLDLPVQHYVPEFPEK	1.104598292	3	3.688931
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.19438106	3	3.801635
Q9EP89	LVNTPYVDNSYK	1.324201032	2	2.5774128
Q9EP89	WAGGGFLSTVGDLLK	0.922958263	2	4.6327343
Q9EPH2	**MRP MARCKS_related protein**	**0.945837196**	**0.7860252**	**2**
Q9EPH2	AAATPESQEPQAK	1.071829037	2	2.6674759
Q9EPH2	GDVTAEEAAGASPAK	0.945745366	2	3.0503213
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.121514936**	**0.0459304**	**7**
Q9EPH8	ALDTMNFDVIK	0.987614366	2	3.1056485

Q9EPH8	GFGFVCFSSPEEATK	1.220330059	2	2.6551852
Q9EPH8	GFGFVSFER	1.204816214	2	2.5076482
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	1.128431123	3	4.7336135
Q9EPH8	KEFSPFGTITSAK	0.984167165	2	3.1887887
Q9EPH8	SKVDEAVAVLQAHQAK	1.083693024	3	4.3149595
Q9EPH8	SLGYAYVNFQQPADAER	1.132532258	2	3.3638003
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**3.149761066**	**9.9E-20**	**13**
Q9EQ76	ASIYQSVFTNSSK	1.944036486	2	2.7842062
Q9EQ76	GTCILPSVNDMMDDIDEK	2.253752567	2	3.9255135
Q9EQ76	ILCGTVSIKPNVK	1.901432316	2	2.9149449
Q9EQ76	KEPVFNDELPAR	1.152675664	2	3.0497081
Q9EQ76	LQEYITSFATEK	2.691759206	2	3.3295758
Q9EQ76	NNEVTLYK	2.044676018	1	2.0031822
Q9EQ76	NNLPTAISDWWYMK	1.696326729	2	3.0158081
Q9EQ76	SCLEEGLEPTCFER	1.476218902	2	4.3877382
Q9EQ76	SDDVGGLWK	2.15452802	2	2.8350408
Q9EQ76	VAVIGAGVSGLAAIR	1.025557411	2	3.9365351
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.192851979	3	4.0011158
Q9EQ76	VWNDGYPWDMVVITR	1.700439095	2	3.861161
Q9EQ76	YIQFETLVTR	3.098635734	2	2.854773
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.19725564**	**6.007E-06**	**3**
Q9EQH3	IREDLPNLESSEETEQINK	1.209714395	2	5.0994763
Q9EQH3	LNLEHIATSSAVSK	1.32721192	2	4.0357881
Q9EQH3	VLETTVEIFNK	1.067889056	2	2.9594438
Q9EQS0	**TALDO Transaldolase**	**1.351572177**	**5.826E-08**	**7**
Q9EQS0	ALAGCDFLTISPK	1.28703545	2	2.9350235
Q9EQS0	ILDWHVANTDKK	1.367404396	2	3.2501719
Q9EQS0	LGGPQEEQIK	1.232278964	2	2.6790309
Q9EQS0	LSSTWEGIQAGK	0.527648503	2	2.7145891
Q9EQS0	SYEPQEDPGVK	1.147275084	2	2.9091022
Q9EQS0	VSTEVDAR	1.3825588	1	1.9817294
Q9EQS0	WLHNEDQMAVEK	1.061412153	2	3.6906672
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**0.829936881**	**0.7181647**	**2**
Q9EQW7	DETIAVPLEENSALPK	0.829869049	2	2.6632946
Q9EQW7	VTQWAEER	1.058465472	2	2.4528294
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.117140917**	**0.0001916**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.02872546	2	3.8570371
Q9EQX9	SNEAQAIETAR	1.146227652	2	3.2767303
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	0.985890173	3	3.996588
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.048814591**	**0.6473455**	**17**
Q9ER34	ADIANLAEEFK	1.009301143	2	2.4387081
Q9ER34	CTTDHISAAGPWLK	1.063448273	2	3.906744
Q9ER34	DINQEVYNFLATAGAK	0.882279315	2	4.1542001
Q9ER34	FKLEAPDADELPR	1.149792	2	3.6969364
Q9ER34	FNPETDFLTGK	0.986392794	1	2.2888682
Q9ER34	GHLDNISNNLLIGAINIENGK	1.131452628	2	5.6129608
Q9ER34	IVYGHLDDPANQEIER	1.239966887	2	4.7319322
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	1.335527308	3	4.0975289
Q9ER34	LTGTLSGWTSPK	1.336999994	2	3.1168146
Q9ER34	NAVTQEFGPVPDTAR	0.954936218	2	4.1567049
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	0.989187812	3	4.2146683
Q9ER34	QGLLPLTFADPSDYNK	1.05835886	2	3.5709813
Q9ER34	SDFDPGQDTYQHPPK	0.97021258	2	2.9135547
Q9ER34	SQFTITPGSEQIR	0.987219768	2	3.565665
Q9ER34	VDVSPTSQR	0.893111761	2	2.5214438
Q9ER34	VGLIGSCTNSSYEDMGR	1.181189831	2	4.2310982

Q9ER34	WVVIGDENYGEGSSR	1.049129545	2	4.202404
Q9ER72	**SYCC Cysteinyl_tRNA synthetase_ cytoplasmic**	**1.183568333**	**0.6171079**	**2**
Q9ER72	LSETTDPDKR	0.946456336	2	2.4300919
Q9ER72	QMLERIQNSVK+Oxidation(2)	1.247326988	2	2.4696646
Q9ERK4	**XPO2 Exportin_2**	**1.295185444**	**0.1861181**	**3**
Q9ERK4	IIIPEIQK	1.307656024	2	2.3985238
Q9ERK4	LLQTDDEEEAGLLELLK	1.030889353	2	2.3843865
Q9ERK4	SNNVNEFPVLK	1.406580544	2	2.4992867
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**1.225031944**	**0.0324213**	**3**
Q9ES21	HFDSQVIIYGK	1.131421092	2	2.4556522
Q9ES21	LSNTSPEFQEMSLLER	2.367651144	2	3.6001859
Q9ES21	TQLGLVMDGFNSLLR	1.16542318	2	3.9837871
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.293415838**	**0.0488048**	**12**
Q9ES38	ACQAAWALK	1.161110259	2	2.7319598
Q9ES38	ADVWENFQQR	1.127482307	2	3.0644929
Q9ES38	EGFDVGVIADPLYILDNK	1.347192319	2	4.9126329
Q9ES38	GATAILVLPSK	1.09684237	2	2.9291937
Q9ES38	IQDSLEITNTYK	0.864157892	2	3.6502662
Q9ES38	LKEATIQEDK	1.223765569	2	2.8061149
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.155972655	2	4.2297163
Q9ES38	QGFCIPVETGKPGLLLTK	0.926023118	3	3.662816
Q9ES38	SISALSVFLGLAK	1.603003885	2	3.1982996
Q9ES38	SLMPDVYQAVCEGTWK	1.111705928	2	3.9160509
Q9ES38	YLCNVPGQPEDK	1.11943886	2	3.4866788
Q9ES38	YLCNVPGQPEDKK	1.285030426	2	3.7566352
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.885533482**	**0.7060971**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.862822349	2	3.7900462
Q9EST6	SLDLFGCEVTNR	1.064796925	2	2.7447653
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.258802758**	**0.1978323**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.250085009	3	5.7279997
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.202654687	3	5.9867306
Q9ESW0	QGQGQLVTCSGAFK	1.005717515	2	2.3597639
Q9HB97	**PARVA Alpha_parvin**	**1.258654512**	**0.0997909**	**4**
Q9HB97	DLAEDLYDGQVLQK	1.015929512	2	2.3598447
Q9HB97	LNVAEVTQSEIAQK	0.996723386	2	3.146554
Q9HB97	QIQEEITGNTEALSGR	1.346544706	2	3.1674252
Q9HB97	VLIDWINDVLVGER	1.004157392	2	3.2379227
Q9JHL4	**DBNL Drebrin_like protein**	**1.11956214**	**0.5120904**	**2**
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**1.24367306**	**0.5237893**	**2**
Q9JHZ9	AYEQLGYR	1.28640778	2	2.5500288
Q9JHZ9	HLEGLLPVGMPTADTQR	1.242160659	2	3.7943895
Q9JI57	**GT2D1 General transcription factor II_I repeat domain_containing protein 1**	**1.013941721**	**0.8409157**	**2**
Q9JI57	EMEDINTLRECVQILFNSR	1.047531285	2	2.3225758
Q9JI57	GTQPTTEGQAHPLVLPTR	0.82026777	2	2.3798211
Q9JI85	**NUCB2 Nucleobindin_2**	**0.960502666**	**0.124123**	**5**
Q9JI85	FQQGIAPSGPAGELK	1.278278939	2	2.6638608
Q9JI85	LSQELDLVSHK	1.262900972	2	2.7584918
Q9JI85	QEYQQAVQQLEQK	0.960042542	2	4.3006954
Q9JI85	TRLDELK	0.973235989	1	2.02823
Q9JI85	VHNVEPVESAR	1.17645967	2	2.8963254
Q9JI91	**ACTN2 Alpha_actinin_2**	**0.988119876**	**0.0028977**	**8**
Q9JI91	ACLISMGYDLGEAEFAR	1.016677	2	4.4206257
Q9JI91	GYEEWLLNEIR	1.904767399	2	2.8505309
Q9JI91	HRPDLIDYSK	1.224927578	2	2.4171233

Q9JI91	HTNYTMEHIR	0.968679238	2	2.8066509
Q9JI91	KHEAFESDLAAHQDR	1.06231686	2	5.2977576
Q9JI91	MLDAEDIVNTPKPDER	0.910797397	2	3.0889947
Q9JI91	QSILAIQNEVEK	0.986159165	2	2.8429985
Q9JI91	TINEVETQILTR	0.983888412	2	3.1643527
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.041646412**	**2.144E-09**	**9**
Q9JJ19	AVDPDSPAEASGLR	1.232362984	2	3.2484055
Q9JJ19	IVEVNGVCMEGK	1.203404998	2	3.6746573
Q9JJ19	LLVVDPETDEQLK	1.431372119	2	2.6899202
Q9JJ19	LLVVDPETDEQLKK	1.485759415	2	2.8678312
Q9JJ19	LVEPGSPAEK	1.08057578	2	2.5620372
Q9JJ19	LVEVNGENVEK	1.140510582	2	2.8828633
Q9JJ19	SEHTEPPAAADTK	0.920963981	2	3.2064145
Q9JJ19	SEHTEPPAAADTKK	0.948765023	3	4.6114678
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	0.913395137	3	3.9145885
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.287293088**	**1.679E-09**	**3**
Q9JJ54	FGDVVDCTLK	1.137172594	2	2.7229135
Q9JJ54	IDASKNEEDEGHSNSSPR	1.354471379	3	3.8974743
Q9JJ54	IFVGGLSPDTPEEK	1.39296616	2	3.9139957
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**0.814953965**	**0.8539567**	**3**
Q9JJ79	ASDLKDLNSR	0.903482839	2	2.3529308
Q9JJ79	DQIEVMKGNVKSR	0.796381156	2	2.3665726
Q9JJ79	NCLEEWTKAAGLEK	1.053123184	2	2.372308
Q9JJM9	**SEPT5 Septin_5**	**1.103655724**	**0.0547288**	**2**
Q9JJM9	LIRMKDEELR	1.582800225	2	2.4816175
Q9JJM9	MQEMLQKMK+Oxidation(4)	0.798961464	2	2.4179108
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.033060013**	**0.1550391**	**2**
Q9JJU8	GDYDAFFEAR	1.394510773	2	2.5449102
Q9JJU8	QQDVLCFLEANK	1.033059726	2	2.881032
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.199211217**	**4.271E-07**	**4**
Q9JK38	GRVEDVVVSDECR	1.148166973	2	3.459816
Q9JK38	ITLECLPQNVGFYK	1.566297227	2	3.747694
Q9JK38	VEDVVVSDECR	1.1622654	2	3.7012043
Q9JK38	VLGQLTETGVVSPEQFMK	1.237868055	2	4.53933
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**0.991279521**	**0.0163591**	**8**
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	0.669318478	3	3.9181983
Q9JLA3	EGETYYDVVAVVDPVTR	0.819279869	2	2.6098921
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.370867555	3	6.1337876
Q9JLA3	IVPEWQDYDQEIK	1.002964236	2	3.5625815
Q9JLA3	LGIEGLSLHNILK	1.481520657	3	3.8865616
Q9JLA3	LNIQPSETDYAVDIR	1.15128854	2	4.1330495
Q9JLA3	VEEDVASDLVMK	0.937387833	2	3.2584317
Q9JLA3	YVLEPEISFTADNSFAK	0.940398274	2	3.7222795
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.030352987**	**1.109E-05**	**17**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.204113883	2	4.4417539
Q9JLJ3	ANDTTFGLAAGVFTR	1.055873683	2	4.9016442
Q9JLJ3	CQVLLEAAR	1.090490222	2	3.0379183
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.046997773	2	4.6907206
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.188770323	2	4.6540389
Q9JLJ3	EVNLAVENAK	0.875551521	2	2.9766588
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.177011152	2	5.3498945
Q9JLJ3	GIKPITLELGGK	1.114392148	3	3.9211042
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.176152346	2	4.5832105

Q9JLJ3	IGDPLLEDTR	1.11382704	2	3.9271629
Q9JLJ3	MGPLINAPHLER	1.121195254	2	3.4950931
Q9JLJ3	MGPLINAPHLER+Oxidation(1)	1.430069465	2	3.016053
Q9JLJ3	RDEIAIMETINNGK	0.956722249	2	5.4567704
Q9JLJ3	VEPVDASGTEK	1.165331727	2	2.3239822
Q9JLJ3	VSFTGSVPTGMK	1.094035987	2	3.3680513
Q9JLJ3	VSFTGSVPTGMK+Oxidation(11)	1.292055025	2	2.8141899
Q9JLJ3	VTIEYYSQLK	1.494265705	2	3.1929309
Q9JLT0	**MYH10 Myosin_10**	**1.377438974**	**9.9E-20**	**3**
Q9JLT0	AGVLAHLEEER	1.400381682	2	3.5162969
Q9JLT0	DAAGLESQLQDTQELLQEETR	0.782942361	2	3.7468779
Q9JLT0	DEELLKVKEK	1.072753063	1	2.1484978
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**1.256499926**	**0.0100696**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	1.226289147	2	5.8055
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	1.172766395	3	4.5818324
Q9JLZ3	SEVPGIFCAGADLK	1.220898847	2	3.2591033
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**1.057412131**	**0.7229941**	**13**
Q9JM53	DGEQHEDLNEVAK	0.852787898	2	3.926563
Q9JM53	ILPEYLSNWTMEK	1.239548819	2	2.6101756
Q9JM53	KSQASGIEVIQLFPEK	0.978009335	2	3.6479042
Q9JM53	KVETDHIVTAVGLEPNVELAK	1.131759667	2	6.3252311
Q9JM53	LNDGSQITFEK	1.053742218	2	3.578784
Q9JM53	SATEQSGTGIR	0.730709407	2	3.8541529
Q9JM53	SITVIGGGFLGSELACALGR	1.065956699	2	3.4139471
Q9JM53	SQASGIEVIQLFPEK	0.897586948	2	4.2566152
Q9JM53	TGGLEIDSDFGGFR	1.009451762	2	3.8163154
Q9JM53	VETDHIVTAVGLEPNVELAK	1.009257254	2	6.018784
Q9JM53	VLIVSEDPELPYMRPPLSK	1.23737735	3	3.7063291
Q9JM53	VMPNAIVQSVGVSGGK	1.091089362	2	4.5231581
Q9JM53	VNAELQAR	0.914195816	2	2.3744469
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**1.009751386**	**0.9999984**	**2**
Q9JMA1	CTESEEEEVTK	1.097566312	2	3.644242
Q9JMA1	EKESVNAKVLK	1.00507454	2	2.5595167
Q9JMB7	**PIWL1 Piwi_like protein 1**	**1.033349849**	**0.9648326**	**2**
Q9JMB7	ELIGLIVLTKYNNK	1.047705483	2	2.424952
Q9JMB7	SQELQISAGFQELSLAERGGRR	1.184211282	2	2.3407736
Q9JMD3	**PCTL PCTP_like protein**	**1.928226275**	**9.9E-20**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.142246866	2	4.5443625
Q9JMD3	ESVQVPDDQDFR	0.889171622	2	2.6715622
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.545383822	3	4.4334807
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(1)	1.403051221	3	3.570853
Q9JMD3	SSQFLAPK	0.987819785	2	2.3465965
Q9JMD3	WDSNVIETFDIAR	1.492766656	2	4.1225944
Q9JMK8	**VPS54 Vacuolar protein sorting_associated protein 54**	**0.98623925**	**0.8119953**	**2**
Q9JMK8	DKIAQIDK	1.198550731	1	1.933705
Q9JMK8	STSLLGALQSQANK	0.977280869	2	2.3532529
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.227952328**	**6.162E-14**	**5**
Q9QVC8	ALELDSNNEK	1.194476511	2	2.4153709
Q9QVC8	GEPNNVAGNQAQVK	1.101093491	2	3.8929684
Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.239584787	2	3.300282
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	1.35454988	3	6.1951022
Q9QVC8	VLQLYPSNK	1.4973259	2	2.5176013
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**0.880236019**	**0.0098974**	**2**
Q9QWN8	IIGTQEQLNQR	1.430748378	2	2.4596066
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	0.879518117	3	3.9601121
Q9QX79	**FETUB Fetuin_B**	**1.223117703**	**0.3643188**	**3**

Q9QX79	GSIQHLPEQEEPEDSKGK	1.228140162	3	3.9216285
Q9QX79	IFYETVHGQCK	1.140490885	2	2.8844876
Q9QX79	NTAPTSSPSITAPR	1.025465771	2	3.3072081
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**1.121895056**	**0.0225391**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	0.9136407	2	3.7533238
Q9QXG4	IGPIATPDYIQNAPGLPK	1.36390824	2	2.8786638
Q9QXK2	**RAD18 E3 ubiquitin_protein ligase RAD18**	**1.051439313**	**0.2924139**	**2**
Q9QXK2	SAAEIVQEIESMEK	1.100059948	1	2.0907743
Q9QXK2	TVYNLLSDR	0.308634029	2	2.3418376
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**1.089297184**	**0.8609404**	**2**
Q9QXK3	SIATLAITTLLK	0.97502421	2	3.0253425
Q9QXK3	SSEPVQLTEAETEYFVR	1.166374253	2	3.8445475
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.174945071**	**9.9E-20**	**28**
Q9QXQ0	ACLISLGYDVENDR	1.073718499	2	3.9603529
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.125256901	3	3.3132803
Q9QXQ0	AGTQIENIDEDFR	0.981614562	2	2.836354
Q9QXQ0	AGTQIENIDEDFRDGLK	1.376763711	2	4.4726877
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.217088477	3	3.7090557
Q9QXQ0	DDPVTNLNNAFEVAEK	0.581116634	2	3.639472
Q9QXQ0	ETTDTDTADQVIASFK	1.017091061	2	4.8849864
Q9QXQ0	HRDYETATLSDIK	1.43550488	2	4.041306
Q9QXQ0	HRPELIEYDK	1.110420057	3	4.7249742
Q9QXQ0	HTNYTMEHLR	0.968679238	2	2.8066509
Q9QXQ0	ICDQWDNLGSLTHSR	1.17826757	2	4.0331316
Q9QXQ0	ISIEMNGTLEDQLSHLK	0.82223275	2	2.834713
Q9QXQ0	KDDPVTNLNNAFEVAEK	1.015285434	3	4.9323964
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.476915068	2	4.4710698
Q9QXQ0	LVSIGAEEIVDGNAK	1.395116858	2	3.6821482
Q9QXQ0	MAPYQGPDAAPGALDYK	1.125574049	2	4.3205304
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(1)	1.529017938	2	3.0938826
Q9QXQ0	MLDAEDIVNTARPDEK	1.114131628	2	4.0503612
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(1)	1.048536095	2	2.64012
Q9QXQ0	NFITAEELR	1.102818937	1	2.1424079
Q9QXQ0	QLETIDQLHLEYAK	1.330359436	2	3.1019201
Q9QXQ0	RDHALLEEQSK	1.18368983	3	4.1800461
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.425782805	3	3.6489046
Q9QXQ0	TINEVENQILTR	0.665073978	2	3.3661025
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	1.638143741	2	5.0009623
Q9QXQ0	VGWEQLLTTIAR	1.261559605	2	4.2406421
Q9QXQ0	VLAGDKNFITAEELR	0.98651377	2	3.7747891
Q9QXQ0	VLAVNQENEHLMEDYER	1.188144995	2	5.5529156
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.115659016**	**0.9528238**	**4**
Q9QXT0	ALVDELEWEIAR	0.942568581	2	3.7762737
Q9QXT0	INPDGSQSVVEVPYAR	1.118823727	2	3.7483039
Q9QXT0	RTDLCDHALHR	1.146046568	3	3.3545587
Q9QXT0	TDLCDHALHR	1.060344081	2	3.0673869
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.47164793**	**9.9E-20**	**18**
Q9QXX4	ASGDAARPFLLQLAESAYR	1.426791074	3	3.3201911
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.052847549	3	6.0701151
Q9QXX4	DVEVTKEEFALAAQK	1.062512305	2	4.0850611
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.298326781	2	6.5539331
Q9QXX4	FGLYLPLFKPSASTSK	1.117618445	2	2.6059184
Q9QXX4	GLLPQLLGVAPEK	1.265115993	2	3.1819544
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.829909296	2	5.390131
Q9QXX4	ILREEGPK	1.1692527	2	2.4058192
Q9QXX4	ITLPAPNPDHVGGYK	1.375251105	2	2.4167743

Q9QXX4	KDVEVTKEEFALAAQK	1.216490311	2	5.515862
Q9QXX4	LQVAGEITTGPR	1.206375729	2	3.7058094
Q9QXX4	LTVNDFVR	1.270597566	2	2.5611405
Q9QXX4	NGEFFMSPHDFVTR	0.938758813	2	4.006433
Q9QXX4	SSPQFGVTLLTYELLQR	1.904514613	2	4.5385995
Q9QXX4	STGSFVGELMYK	0.991262709	2	3.0857024
Q9QXX4	TVELLSGVVDQTK	1.387993244	2	3.9663348
Q9QXX4	YEGFFGLYR	1.059295846	2	2.7199323
Q9QXX4	YLNIFGESQPNPK	1.066999502	2	4.3299198
Q9QXY2	**SRCN1 SRC kinase signaling inhibitor 1**	**0.840126671**	**0.3475586**	**2**
Q9QXY2	DINRLLEETQAELLK	1.998510313	2	2.4138207
Q9QXY2	IIAELESGGGSVPPMK	0.70290762	2	2.4362972
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**1.122103686**	**0.2182569**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	1.309391636	2	4.0596371
Q9QYU4	RAPAFLSADEVQDHLR	1.363615038	3	5.0787973
Q9QYU4	SLGMAVEDLVAAK	0.940729334	2	3.6231616
Q9QYU4	SSSLLIPPLEAALANFSK	1.137267586	2	3.137944
Q9QZ76	**MYG Myoglobin**	**0.602576714**	**0.9998865**	**7**
Q9QZ76	GQHAAEIQPLAQSHATK	0.47809472	2	4.5689883
Q9QZ76	HGCTVLTALGTILK	1.00802315	2	3.5121405
Q9QZ76	HGCTVLTALGTILKK	1.170530392	3	3.7012935
Q9QZ76	KGQHAAEIQPLAQSHATK	1.263960993	3	4.7834368
Q9QZ76	KKGQHAAEIQPLAQSHATK	1.55221367	3	4.5973358
Q9QZ76	VEGDLAGHGQEVLISLFK	1.166118851	3	4.345953
Q9QZ76	YSGDFGADAQGAMSK	0.757676327	2	4.0322375
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.127653361**	**0.4954517**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	1.049570625	2	3.4691522
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.262202136	2	2.506604
Q9QZA2	FYNELTEILVR	0.923519478	2	2.7060297
Q9QZA2	LLDEEEATDNDLR	1.101401121	2	3.6742256
Q9QZA2	NIQVSHQEFSK	1.081662182	2	3.3783352
Q9QZA2	NLATAYDNFVELVANLK	1.078008071	2	4.4337087
Q9QZA2	STAVVEQGGIQTVDQLIK	0.990900025	2	4.446198
Q9QZA2	TMQGSEVVNVLK	0.833934804	2	3.3431644
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.079223849**	**0.9011966**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	0.930797787	2	4.9522443
Q9QZD8	LFSGATMASSR	0.757258502	2	2.6316712
Q9QZD8	MTGMALQVVR	0.89009817	2	2.6677659
Q9QZD8	NYSHALDGLYR	1.07725843	2	2.9230597
Q9QZD8	VHLQTQQEVK	1.075496436	2	2.8523123
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.23600761	2	5.6916838
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	1.120020692	3	3.8041112
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.025289645**	**1**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	0.992036591	2	4.1836739
Q9QZH8	WFLQEDILEK	1.054932238	2	3.3207896
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.140497449**	**1.118E-06**	**5**
Q9QZU7	IDANNVAYTTGK	1.164230388	2	3.3085215
Q9QZU7	IIELDDKGQVVR	0.972388154	2	2.5360036
Q9QZU7	LLLEALDVNIR	1.83520911	2	2.8369334
Q9QZU7	MNPGDVITFDNWR	1.245874236	2	2.7287169
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.266815239	2	4.4760003
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**1.016642421**	**9.9E-20**	**10**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	2.550610248	3	4.3574686
Q9R063	ETDLLLDDSLVSLFGNR	1.570181099	2	4.4885349
Q9R063	GVLFGVPGAFTPGCSK	0.955190059	2	4.5388346
Q9R063	KGVLFGVPGAFTPGCSK	0.967364425	2	3.5011995
Q9R063	KVNLAELFK	0.801444747	2	2.3047953

Q9R063	THLPGFVEQAGALK	0.99565043	3	4.343318
Q9R063	VGDTIPSVEVFEGEPGK	0.953143646	2	4.4772739
Q9R063	VGDTIPSVEVFEGEPGKK	1.248232713	2	3.9001484
Q9R063	VNLAELFK	0.947726158	2	2.7224619
Q9R063	VQLLADPTGAFGK	1.144844957	2	3.7105775
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**1.058100534**	**0.4480298**	**2**
Q9R064	ADTSSLTVDVMSPASK	1.018186812	2	3.4792929
Q9R064	LYVYNTDTDNCR	2.063266437	2	2.7970383
Q9R0N0	**GALK1 Galactokinase**	**0.974774321**	**0.9993394**	**4**
Q9R0N0	RQCEEVAQALGK	0.965730924	2	2.8571455
Q9R0N0	SLETSLVPLSDPK	0.959650043	2	3.3561852
Q9R0N0	TDGLVSLLTTSK	1.181664548	2	3.4318869
Q9R0N0	VEELLAEAR	0.985697944	2	3.0423925
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.076405333**	**3.02E-05**	**6**
Q9R0T3	AEPSVAEYTVR	1.137879569	2	2.8290935
Q9R0T3	ICSEVLQLEPDNVNALK	0.748074951	2	5.5628371
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	1.126870482	3	5.4082065
Q9R0T3	LIGSAEELIR	1.399951916	2	2.8608711
Q9R0T3	LKNDNTEAFYK	1.534058268	2	2.819412
Q9R0T3	SNPSENEEKEAQSQLVK	1.079885507	2	5.091548
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**0.907895184**	**0.9870469**	**3**
Q9R112	EGNALFTFPNTPVK	1.095868282	2	3.0464118
Q9R112	STLSVIPSGVQWIQDR	0.973533061	2	2.7951314
Q9R112	VGAENVAIVEPSER	0.877094304	2	2.8446541
Q9R1M5	**NALP5 NACHT_ LRR and PYD domains_containing protein 5**	**1.01726681**	**0.9105521**	**2**
Q9R1M5	KMTSPENDSKSIQK	1.100546555	2	2.3921115
Q9R1M5	SLDLGNNALGDK	1.016863758	1	1.9190727
Q9R1T3	**CATZ Cathepsin Z**	**1.153160229**	**0.3198932**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.056728859	2	4.1917844
Q9R1T3	VGDYGSLSGR	1.195363772	2	2.4542027
Q9R1T4	**SEPT6 Septin_6**	**0.953278485**	**0.514439**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(2)	1.187284652	1	1.9979411
Q9R1T4	STLMDTLFNTK	0.904771848	2	2.4421775
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**0.94393818**	**0.9893984**	**4**
Q9R1Z0	LCQNNFALGYK	0.801087083	2	2.8357532
Q9R1Z0	LTVDTIFVPNTGK	0.980904579	2	2.5884433
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.942626094	2	4.1520977
Q9R1Z0	WNTDNTLGTEISWENK	0.999365942	2	3.084305
Q9R257	**HEBP1 Heme_binding protein 1**	**1.643673681**	**0.0273378**	**2**
Q9R257	EAMPKIMKYVGGTNDK+Oxidation(3)	1.121365835	2	2.3231692
Q9R257	NSLFGSVETWPWQVLSTGGK	1.677413475	2	2.4744301
Q9WTT6	**GUAD Guanine deaminase**	**1.026858003**	**0.7388861**	**9**
Q9WTT6	AVMVSNVLLINK	0.712207348	2	2.8530583
Q9WTT6	EIGNFEVGKDFDALLINPR	0.941735505	2	4.5457163
Q9WTT6	ETTEESVKETER	0.907444291	2	3.4148831
Q9WTT6	FQSTDVAEEVYTR	0.896143374	2	3.4826736
Q9WTT6	FSLSCTETLMSELGNIAK	1.153695571	2	4.7865629
Q9WTT6	IVFLEESSQQEK	0.999466025	2	4.1636472
Q9WTT6	NYTDVYDKNNLLTNK	1.143900416	2	4.5037203
Q9WTT6	THDLYIQSHISENREEIEAVK	1.265122351	3	4.0667038
Q9WTT6	VCMDLNNTVPEYK	1.161136134	2	3.1371973
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**1.041858773**	**5.551E-16**	**9**
Q9WU19	AIFVTVDTPYLGNR	1.53209378	2	3.7413621
Q9WU19	AVFVGRPIIWGLAFQGEK	1.213194888	3	4.1260033
Q9WU19	GVQDVLEILK	1.023846779	2	3.6097255

Q9WU19	GVQDVLEILKEEFR	1.559715576	2	4.3809505
Q9WU19	HGVDGILVSNHGAR	1.044823575	3	4.840137
Q9WU19	MKNFETNDLAFSPK+Oxidation(1)	0.913442465	2	2.6753595
Q9WU19	NFETNDLAFSPK	1.180234734	2	3.4044456
Q9WU19	NVADIDLSTSVLGQR	0.987742793	2	5.0912089
Q9WU19	VEVFLDGGVR	1.930639492	2	2.6435547
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**1.076521929**	**0.0007273**	**2**
Q9WU49	HETWSGHVISS	1.03725402	2	2.9588704
Q9WU49	LQAVEVVITHLAPGTK	1.23978268	2	4.4531522
Q9WU65	**GLPK2 Glycerol kinase 2**	**1.127685741**	**0.4087524**	**2**
Q9WU65	GIICGLTQFTNK	0.989853591	2	3.5649025
Q9WU65	LAEVNIDISNIK	1.347014564	2	2.338748
Q9WU82	**CTNB1 Catenin beta_1**	**1.181587278**	**0.0159934**	**3**
Q9WU82	HQEAEMAQNAVR	1.192864112	2	3.3476169
Q9WU82	LLNDEDQVVVNK	0.235131263	2	3.114641
Q9WU82	TMQNTNDVETAR	1.066978276	2	3.5775833
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.030665704**	**0.657052**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.202825147	2	3.78846
Q9WUC4	VCIESEHSSDILLATLNK	1.06235081	2	5.8806739
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**0.779928195**	**0.8792263**	**2**
Q9WUH4	AIVAGDQNVEYK	0.929495912	2	2.3927684
Q9WUH4	FCANTCVECR	0.770369781	2	2.7807078
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.111575068**	**0.7945547**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7)	1.111575068	2	2.3096402
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(8)	1.111575068	2	2.3609564
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**1.142343187**	**2.304E-05**	**4**
Q9WUS0	GVLHQFSGTETNR	1.013187038	2	3.4565434
Q9WUS0	TLVQAEALDR	1.035189865	2	2.6361301
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.882345192	3	5.4683576
Q9WUS0	YKDAAKPVIELYK	1.265101122	2	3.9247341
Q9WVA1	**TIM8A Mitochondrial import inner membrane translocase subunit Tim8 A**	**1.001397094**	**0.9816283**	**2**
Q9WVA1	AEACFVNCVER	1.07451466	2	2.4609098
Q9WVA1	SKPVFSESLSD	0.999690824	2	2.9113736
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.728125336**	**0.279115**	**2**
Q9WVF7	AANMPDSELFELISENR	0.63718343	2	2.4325538
Q9WVF7	MAWQWRGEFMPASR+Oxidation(1)Oxidation(10)	0.906134124	2	2.3732808
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**1.030853471**	**0.0003462**	**13**
Q9WVK3	AGVYNLTK	1.019223668	2	2.7228894
Q9WVK3	ASQPPSSSTQVTAIQCNIR	1.159314284	2	5.5278945
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.235625088	3	7.0825968
Q9WVK3	ELLHLGCNVVIASR	0.906508491	2	4.0506225
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.53833927	2	5.4596395
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(13)	1.605556926	2	3.557024
Q9WVK3	KEEEVNNLVK	1.007944846	3	3.926213
Q9WVK3	LTAAVDELR	1.233677382	2	2.7893114
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.961924579	2	5.074594
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	1.012852245	3	4.0670376
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	1.061661107	2	5.9537082
Q9WVK3	TMALTWASSGVR	0.95314479	2	3.7443101
Q9WVK3	TMALTWASSGVR+Oxidation(2)	1.077888731	2	2.3010752
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.044868965**	**1.399E-10**	**14**
Q9WVK7	AADEFVEK	1.029692413	2	3.0255895
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	0.903702752	2	5.7163658
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	1.022947648	3	5.6053114

Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(22)	0.952806088	3	3.7152829
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(9)	0.952806088	3	3.986676
Q9WVK7	GDASKEDIDTAMK	0.965735905	2	3.9268169
Q9WVK7	GDASKEDIDTAMK+Oxidation(12)	1.334323116	2	3.1883271
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.964287062	3	7.7991457
Q9WVK7	KGIEESLK	0.892201157	2	2.5444756
Q9WVK7	LKNELFQR	1.19424743	2	2.5442779
Q9WVK7	LLVPYLIEAIR	1.778954643	2	2.6713347
Q9WVK7	LVEVIK	1.22196091	1	2.0176327
Q9WVK7	TFESLVDFCK	0.913223163	2	3.5894926
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	1.192811863	3	6.4644446
Q9WVL6	**EXTL3 Exostosin_like 3**	**0.893872665**	**0.0481337**	**2**
Q9WVL6	QDLLQLK	0.505969605	1	2.1550372
Q9WVL6	QELNSEIAKLNLK	1.321060901	2	2.5718911
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.207716295**	**0.0289743**	**2**
Q9Z0N2	IVLTNPVCTEVGEK	1.266707074	2	2.4538903
Q9Z0N2	VGQEIEVRPGIVSK	1.139220417	2	3.5628095
Q9Z0U5	**ADO Aldehyde oxidase**	**1.448975154**	**0.1637439**	**16**
Q9Z0U5	DLEPLILTIEEAIQHK	0.947257233	2	3.0056345
Q9Z0U5	EFQPLDPTQELIFPPELMR	1.514807761	2	3.0715003
Q9Z0U5	ELSILYGGVGPTTIGAK	1.250231706	2	3.8132665
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	1.348661246	2	4.8089633
Q9Z0U5	GYESNINWEK	1.220618867	2	2.9631252
Q9Z0U5	HIQDIVAATLK	1.294728589	2	2.6052601
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	1.56008731	3	5.1197205
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	1.167358311	3	3.9822631
Q9Z0U5	KLECGNVDEAFK	1.150230519	2	3.600632
Q9Z0U5	LVLDEVTLAGSAPGGK	1.354328955	2	4.2815237
Q9Z0U5	MTWISPVTLEELVEAK	1.515076363	2	3.7105577
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	1.041804498	2	4.0596147
Q9Z0U5	NMASLGGHIVSR	1.100856461	2	3.2881949
Q9Z0U5	QQNALAIVNSGMR	1.417313365	2	2.5824666
Q9Z0U5	RLEPIISK	1.420467468	2	2.3595707
Q9Z0U5	VVENNVDPEMMLLPYLR	2.058365049	2	3.4668517
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**1.025464277**	**0.9818552**	**5**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.727478569	3	4.244267
Q9Z0V5	GLFIIDDK	1.043174003	2	3.0521641
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	0.893006051	3	3.8216145
Q9Z0V5	QITLNDLPVGR	1.079327457	2	3.3390398
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	0.956390568	3	6.4120784
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.977688553**	**0.9971028**	**5**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	0.997108905	3	6.4274511
Q9Z0V6	ANEFHDVNCEVVAVSVDSHFSHLAWINTPR	0.886128938	4	4.5322719
Q9Z0V6	GLFIIDPNGVIK	0.961595201	2	3.4060841
Q9Z0V6	GTAVVNGEFK	0.88236723	2	2.6102211
Q9Z0V6	NGGLGHMNITLLSDLTK	1.107530741	2	2.5938709
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.113781571**	**0.1283922**	**2**
Q9Z0W7	FLDGDEMTLADCNLLPK	0.986154453	2	4.1641531
Q9Z0W7	NSRPEANEALER	1.123922993	3	3.4899173
Q9Z122	**FADS2 Fatty acid desaturase 2**	**0.865439263**	**0.8521228**	**2**
Q9Z122	AFHLDLDFVGK	0.853241212	3	3.7675483
Q9Z122	HGIEYQEKPLLR	0.987028788	2	3.5340743
Q9Z1A6	**VIGLN Vigilin**	**1.387110705**	**5.092E-11**	**21**
Q9Z1A6	ANSFTVSSVSAPSWLHR	1.162025714	2	3.2559507

Q9Z1A6	ASVITQVFHVPLEER	1.023768619	2	3.4271083
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.315676417	2	3.3214679
Q9Z1A6	ELQAEQEDR	0.948589584	2	2.375047
Q9Z1A6	GNSLQEILER	1.105934283	2	2.651377
Q9Z1A6	HEVLLISAEQDKR	0.973808055	3	4.3956776
Q9Z1A6	IDLPAENSNSETIVITGK	1.0070608	2	5.2298112
Q9Z1A6	IEGDPQGVQQAK	1.078417468	2	3.7045822
Q9Z1A6	IIFPAAEDKDQDLITIIGK	1.233135469	2	2.981566
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.188832466	2	4.5649095
Q9Z1A6	LGQALTEVYAK	1.196355226	2	3.361285
Q9Z1A6	LQDLELK	1.471399488	1	2.4515154
Q9Z1A6	LQTQASATVPIPK	1.148982633	2	3.628298
Q9Z1A6	LVGEIMQETGTR	1.087915943	2	3.6945846
Q9Z1A6	MDYVEINIDHK	0.89504672	2	2.9101596
Q9Z1A6	MVADLVENSYSISVPIFK	0.885795573	2	3.7739024
Q9Z1A6	RCDIIVISGR	1.151886797	2	3.2215261
Q9Z1A6	TEIVFTGEKEQLAQAVAR	1.292916484	2	4.404614
Q9Z1A6	TGAHLELSLAK	1.016375645	3	3.3936682
Q9Z1A6	TKDLIIEQR	1.121141705	2	2.7908964
Q9Z1A6	VKELQAEQEDR	1.226675667	3	4.0441246
Q9Z1J8	**S14L3 SEC14_like protein 3**	**1.160831927**	**4.319E-08**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	1.482733538	2	2.8487723
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.718745916	2	4.3495631
Q9Z1J8	GSSHQVEYEILFPGCVLR	1.10400696	2	4.8601799
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.397891386**	**0.1606374**	**5**
Q9Z1P2	DYETATLSEIK	1.18451345	1	2.0151653
Q9Z1P2	GISQEQMNEFR	1.140730827	2	2.5889609
Q9Z1P2	ICDQWDNLGALTQK	1.349244356	2	3.4585583
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	1.086454287	2	4.6004658
Q9Z1P2	MVSDINNAWGCLEQAEK	0.752062407	2	4.0275521
Q9Z1W6	**LYRIC Protein LYRIC**	**1.012863603**	**0.7102529**	**4**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.081828508	3	3.9018228
Q9Z1W6	SWQDELAQQAEEGSAR	0.874688258	2	5.5535536
Q9Z1W6	TELGLDLGLEPK	1.156180655	2	3.3266084
Q9Z1W6	TLPPAISAEPSVTLSK	0.920742967	2	3.1659143
Q9Z1Y3	**CADH2 Cadherin_2**	**1.107320423**	**0.986656**	**5**
Q9Z1Y3	FAILTDPNSNDGLVTVVKPIDFETNR	1.123920187	3	4.2737103
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	1.193659495	2	3.723933
Q9Z1Y3	IDPVNGQITTIAVLDR	0.955220162	2	3.4978778
Q9Z1Y3	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	1.011503229	3	5.9474235
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	0.964845021	3	3.8260679
Q9Z221	**PMFBP Polyamine_modulated factor 1_binding protein 1**	**1.190188337**	**0.1704908**	**2**
Q9Z221	DHLHNVMAHLQQENK+Oxidation(7)	1.247616261	2	2.5371575
Q9Z221	ELTNSLSKLQDELAETK	0.933312866	2	2.316555
Q9Z269	**VAPB Vesicle_associated membrane protein_associated protein B**	**1.137501322**	**0.0124547**	**2**
Q9Z269	TEAPVAAKPLTSPLDDAEVKK	1.113804147	3	3.4002762
Q9Z269	VEQVLSLEPQHELK	1.158048865	2	3.8139927
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.042359855**	**0.7959035**	**3**
Q9Z270	FKGPFTDVVTTNLK	1.108702051	2	2.9924164
Q9Z270	HEQILVLDPPSDLK	1.019530769	2	3.9235733
Q9Z270	QDGPLPKPHSVSLNDTETR	1.081562344	3	3.7941666
Q9Z277	**BAZ1B Tyrosine_protein kinase BAZ1B**	**1.2172157**	**0.0373049**	**2**
Q9Z277	IHPLEKVDEEAVEK	1.234301759	2	2.4542372
Q9Z277	IHPLEKVDEEAVEKK	1.084018733	2	2.466989

Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.99669305**	**0.9990493**	**9**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.852223238	3	4.3322616
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.153219595	2	4.8104491
Q9Z2I8	INFDDNAEFR	0.91242475	2	3.2197979
Q9Z2I8	LEGTNVQEAQNILK	0.975087276	2	4.8716893
Q9Z2I8	SENEPIENEAAR	0.819677918	2	4.0806074
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	1.046551698	2	6.2458944
Q9Z2I8	SSGLPITSAVDLEDAAK	0.943519292	2	4.8393598
Q9Z2I8	SSGLPITSAVDLEDAAKK	1.027513408	2	3.1209409
Q9Z2I8	VMVAEALDISR	0.892209759	2	3.2207944
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.123198987**	**0.4084184**	**7**
Q9Z2I9	AVSSQMIGQK	0.940301629	2	2.4948649
Q9Z2I9	ICNQVLVCER	1.323544582	2	2.8881197
Q9Z2I9	ILACDDLDEAAK	1.092528847	2	2.9531555
Q9Z2I9	INFDSNSAYR	1.105063996	2	3.0964592
Q9Z2I9	MGFPSNIVDSAAENMIK	1.098465485	2	3.8836095
Q9Z2I9	SSDEAYAIAK	1.075866648	2	3.4544938
Q9Z2I9	VQAILVNIFGGIMR	1.188426836	2	4.2278152
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.160958586**	**0.040602**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	0.765121153	2	4.2503324
Q9Z2L0	KLETAVNLAWTAGNSNTR	0.88923175	2	5.8981977
Q9Z2L0	LETAVNLAWTAGNSNTR	0.658537444	2	2.65625
Q9Z2L0	LTFDSSFSPNTGK	1.121084014	2	3.8990541
Q9Z2L0	LTFDSSFSPNTGKK	1.272780805	2	3.216538
Q9Z2L0	LTLSALLDGK	1.477712463	2	2.3503354
Q9Z2L0	SENGLEFTSSGSANTETTK	1.057386466	2	4.5591269
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	0.988708167	2	5.313694
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	1.105168302	2	4.3772149
Q9Z2L0	VTQSNFAVGYK	1.153341705	2	3.1793725
Q9Z2L0	WNTDNTLGTEITVEDQLAR	0.856720514	2	4.8481493
Q9Z2L0	WTEYGLTFTEK	1.186016371	2	2.6812062
Q9Z2L0	YQVDPDACFSAK	1.107552297	2	3.3124263
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**1.180482776**	**9.005E-05**	**4**
Q9Z2M4	GQVLQLHAGAAK	1.275409849	2	3.4259551
Q9Z2M4	HLAVEWGPQNIR	1.130542408	2	3.1142519
Q9Z2M4	TVVDIDTLGTFNVSR	1.094995021	2	2.8393903
Q9Z2M4	VNSLAPGAISGTEGLR	1.143831397	2	2.9476192
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**0.950423773**	**0.0338736**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	0.826416693	2	3.5658054
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.186086445	2	5.5012946
Q9Z2Q1	CLSSATDPQTK	1.326363592	2	2.8898807
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.126390909	2	3.7531664
Q9Z2Q1	IIAGDKEVVIAQK	1.260324081	2	2.4691684
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.25194376	2	5.1337581
Q9Z2Q1	QVQHILASASPSGR	1.284454245	2	2.4282999
Q9Z2Q1	RQPVFISQVVTEK	1.484875178	2	2.5390008
Q9Z2Q1	RQPVFISQVVTEKDFLSR	0.842692633	3	3.5382066
Q9Z2Q1	SSYEGQPLPK	1.073503235	2	2.3538461
Q9Z2Q1	TQPPEDISCIAWNR	0.942337025	2	3.5854201
Q9Z2Q1	TTFEDLIQR	1.00006718	2	2.6833987
Q9Z2Q1	VNFEEDSR	0.999164117	2	2.5600848
Q9Z2Q1	VYSIMGGSIDGLR	1.026322677	2	2.3722556
Q9Z2U2	**ZN292 Zinc finger protein 292**	**1.110083441**	**0.6141092**	**3**
Q9Z2U2	KGQKSNNLNTPNHGK	1.134100459	2	2.5792756

Q9Z2U2	KLEVLSNNPDRTVLK	1.133968673	2	2.4001083
Q9Z2U2	LINEDSTNAENQGNTTLK	1.049695298	2	2.9656336
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.194671811**	**0.3716408**	**2**
Q9Z2Z8	AIECSYTSADGLK	1.178445921	2	3.6282778
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.212475737	2	5.3121076
Q9Z311	**MECR Trans_2_enoyl_CoA reductase_ mitochondrial**	**0.99190289**	**0.7325038**	**2**
Q9Z311	DIPLQSAATLGVNPCTAYR	1.169252017	2	2.4319012
Q9Z311	LKDLGADYVLTEEELR	0.953234578	2	2.6117787
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.191327881**	**2.789E-10**	**5**
Q9Z339	GSAPPGPVPEGQIR	1.020146367	2	3.6290283
Q9Z339	LEALELNECIDHTPK	1.316788587	2	4.2266698
Q9Z339	LEEAMANKR	1.111175361	2	2.6176231
Q9Z339	LEEAMANKR+Oxidation(5)	1.628432902	2	2.5337234
Q9Z339	NPFGLVPVLENTQGHLITESVITCEYLDEAYPEKK	1.177462611	3	4.7828174

Time point 2.0 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (2.0 h)**	**P-value (2.0 h)**	**Peptide number (2.0 h)**
Accession number	Peptide sequence	Peptide Ratio (2.0 h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**1.299273203**	**0.006487**	**2**
A0JPJ7	IGIVGLPNVGK	1.59432171	2	2.65269
A0JPJ7	YLEANMTQSALPK	1.291591456	2	2.78365
A0JPM9	**EIF3J Eukaryotic translation initiation factor 3 subunit J**	**1.120451294**	**0.402165**	**2**
A0JPM9	EEAEVKPEVKISEK	1.105832724	2	2.33458
A0JPM9	RLEEPEESK	1.164045769	2	2.49113
A0JPQ8	**ALKMO Alkylglycerol monooxygenase**	**1.12406748**	**0.292935**	**2**
A0JPQ8	LDDILTSMSAGVVSR	1.113012553	2	2.82701
A0JPQ8	SITHLASGSWK	1.137524644	2	2.41878
A1A5P5	**ARMC9 LisH domain_containing protein ARMC9**	**1.080271469**	**0.776731**	**2**
A1A5P5	CFIKEGNAEMIR+Oxidation(10)	1.080276047	2	2.71359
A1A5P5	LYLAQNTKVLRMLEGR+Oxidation(12)	1.076536161	2	2.30655
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.022857897**	**0.988501**	**2**
A2ADY9	IDFSSIAVPGTSNPQQR	0.933719311	2	2.56155
A2ADY9	VLVEQQQDR	1.022886122	2	2.76837
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**0.934614669**	**0.364298**	**2**
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(1)	0.69008108	3	3.3588
A2AF47	NLLMCYLYIVK	1.039319973	2	2.49465
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.180207624**	**0.000209**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(14)	0.174735754	2	2.82966
A2AGT5	IGSKENTKEGLAELYEYK	0.510272645	2	2.46687
A2AJL3	**FGGY FGGY carbohydrate kinase domain_containing protein**	**1.065107427**	**0.98662**	**2**
A2AJL3	GHGLTCEGQPVTSR	1.070439036	2	3.66454
A2AJL3	MSKVGKVVFPEHADK	0.980617128	2	2.38574
A2AL36	**CNTRL Centriolin**	**1.136769698**	**0.122834**	**3**
A2AL36	EQQLDIMNR+Oxidation(7)	1.143941188	2	2.33223
A2AL36	LQDEKETLLQR	1.398454865	2	2.40783
A2AL36	NQDKLNK	0.946805521	1	2.1699
A2AQP0	**MYH7B Myosin_7B**	**0.967952443**	**0.946315**	**6**
A2AQP0	AITDAAMMAEELKK	1.443431115	2	3.50284
A2AQP0	DIDDLELTLAK	0.898379464	2	3.55084
A2AQP0	EQDTSAHLER	0.959399233	2	2.38219
A2AQP0	KDIDDLELTLAK	0.9119632	2	2.32548
A2AQP0	SIQELEK	1.170826917	2	2.39957
A2AQP0	VGNEYVTK	1.202402124	2	2.62112
A2ASS6	**TITIN Titin**	**0.893400636**	**0.000156**	**11**
A2ASS6	AENRFGIGPPAETIQRTTAR	0.616705312	2	2.67445
A2ASS6	DVLEEPEIDLDVALR	0.915069341	2	2.82072
A2ASS6	KDLNMVVSAARISCGGAIR	0.859938674	2	2.30722
A2ASS6	KGDGTQLACKVTGTPPIK	0.67951183	2	2.72782
A2ASS6	SSVSLSWSRPKDDGGSR	0.811079652	2	2.34303
A2ASS6	TCEIEIGQLK	0.846115287	2	2.45516
A2ASS6	TFLQDQLVSLQVLK	0.866122213	1	1.93291
A2ASS6	VGDDAWIKDTTGTALR	1.228738573	2	2.49936
A2ASS6	VKNAMPEDIDEYAVEIEGK+Oxidation(5)	0.534713818	2	2.34276
A2ASS6	VMKLTTGEEYQFRIK+Oxidation(2)	1.119074364	2	2.34529
A2ASS6	YDGGHKLTGYIVEK	1.70593978	2	2.30213

A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**0.86446107**	**0.011263**	**9**
A2VCW9	AGGILQEDITEACLILGVK	0.999660528	2	2.61955
A2VCW9	AQEANMSLLDEVLK	0.844736414	2	3.04584
A2VCW9	GAQEVFNELPCEYVEPHELK	0.972004272	2	4.68463
A2VCW9	KTDGVYDPVEYEKYPER	0.920198938	3	3.68836
A2VCW9	KYDINTVNVTVGK	0.901279607	2	3.978
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	0.765750374	3	3.67207
A2VCW9	REDVNAWER	0.833227113	2	2.78886
A2VCW9	SSVVPVEGCPELPHK	0.87482965	2	3.07197
A2VCW9	YDINTVNVTVGK	0.767486865	2	2.77871
A3KMP2	**TTC38 Tetratricopeptide repeat protein 38**	**1.109826635**	**0.316209**	**2**
A3KMP2	DVGLPLCQALLEAENGNPDR	1.182243354	2	2.39277
A3KMP2	VLELLLPIR	0.867424022	2	2.72271
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.03090678**	**0.252702**	**11**
A7VJC2	EESGKPGAHVTVK	1.278264229	2	3.26065
A7VJC2	GGGGNFGPGPGSNFR	1.112915994	2	3.14221
A7VJC2	GGNFGFGDSR	1.068521488	2	2.87664
A7VJC2	IDTIEIITDR	1.042973251	2	3.88723
A7VJC2	LFIGGLSFETTEESLR	1.320401837	2	4.54467
A7VJC2	LTDCVVMR	1.227713317	2	2.64514
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	0.955596998	2	5.96481
A7VJC2	NYYEQWGK	1.008223061	1	2.36986
A7VJC2	QEMQEVQSSR	0.994190768	2	3.07704
A7VJC2	QEMQEVQSSR+Oxidation(3)	1.369192578	2	2.56361
A7VJC2	YHTINGHNAEVR	1.006085865	2	3.86635
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.035751077**	**0.998281**	**2**
B0BN93	GSIDEVDKR	0.987608993	2	2.48293
B0BN93	SAWGQQPDLAANEAQLLR	1.050455826	2	3.3212
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.083056369**	**0.879756**	**8**
B0BNE5	AFNGYLGPDQSK	1.136556669	2	3.68688
B0BNE5	AYDATCLVK	1.109954868	2	2.40361
B0BNE5	FAIYLPPQAESAK	1.149721228	2	2.58628
B0BNE5	MYSYVTEELPQLINANFPVDPQR	1.18601009	3	5.16689
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.051536805	2	5.6418
B0BNE5	SVSAFAPICNPVLCPWGK	1.111606855	2	4.66456
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.378334641	3	5.44643
B0BNE5	VFEHSSVELK	1.015878692	2	2.56532
B0BNN3	**CAH1 Carbonic anhydrase 1**	**1.029312072**	**0.915168**	**3**
B0BNN3	ADGLAIIGVLMK	0.798696567	2	2.84789
B0BNN3	HDSSLKPVSVSYNPATAK	1.038619799	3	4.79749
B0BNN3	VLDALSSVK	1.076600187	2	2.40359
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**0.940591829**	**0.999968**	**2**
B0K020	HNEETGDNVGPLIIK	0.926707666	2	5.71477
B0K020	VVHAFDMEDLGDK	0.98948212	2	3.6518
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.063481737**	**0.143598**	**3**
B2GV24	QLVSQNK	0.459636424	1	1.91917
B2GV24	TYDLPGDFLTQALTQR	1.301517309	2	2.73793
B2GV24	VNIVDLQQVINVDLTHIENR	1.06229318	3	4.1598
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**1.069687119**	**0.999765**	**2**
B2RX88	SISSVNVDQVRMRNEDR	1.07246905	2	2.55805
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(12)	1.075350547	2	2.55827
B2RY56	**RBM25 RNA_binding protein 25**	**1.025086338**	**0.298102**	**2**

B2RY56	FEDEDSDDVPRKR	0.608054536	2	2.33369
B2RY56	LLIYETEAK	1.095360917	2	2.49982
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**1.027179988**	**0.963528**	**4**
B2RYW9	ATDVMAYVAGFTVAHDVSAR	1.103667322	2	3.0594
B2RYW9	KGDEVQCEIEELGVIINK	1.105670875	2	5.32722
B2RYW9	TFDTFCPLGPALVTK	0.903642955	2	5.0672
B2RYW9	VNGEIVQSSNTNQMVFK	0.783970629	2	4.38875
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**1.057264434**	**0.892089**	**2**
B2RZ78	GDFDESLNYPEQK	1.052845681	2	3.31976
B2RZ78	IQHILCTGNLCTK	1.216876032	2	3.30645
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**0.957212123**	**0.643447**	**4**
B3DMA2	AVLTVTQYR	1.194836102	2	2.30406
B3DMA2	NLPDSDNEECLVHGDFK	0.932568338	2	3.59308
B3DMA2	RGQEVLTR	0.963838141	2	2.7138
B3DMA2	SGQSNPTFFLQK	0.884075535	2	2.94337
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.155837071**	**0.34612**	**4**
B5DFC8	GCILTLVER	1.122675138	2	2.39248
B5DFC8	GTEITHAVVIK	1.031266779	2	2.46147
B5DFC8	SEQDQAENEGEDSAVLMER	1.91249947	2	4.6879
B5DFC8	TEPTAQQNLALQLAEK	1.211713679	2	4.75486
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.145424784**	**4.79E-06**	**2**
D3ZTX0	SVIDYQTHFR	1.208791478	2	2.59085
D3ZTX0	VSALTQMESACVSIHEALK	0.386772844	2	2.47584
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.289591908**	**0.715715**	**3**
D3ZW55	IDLPEYQGEPDEISIQK	0.992372263	2	4.30649
D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.084732256	3	4.22841
D3ZW55	LQEYFGVTDGAGDH	1.123710618	2	3.20843
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**0.974438481**	**0.909665**	**2**
D3ZZL9	IEDLEQEMKIQK	0.872530608	2	2.43575
D3ZZL9	MLQETVTKEAELR+Oxidation(1)	1.022532576	2	2.37464
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.190773909**	**0.035017**	**2**
D4A4T9	KEEDSDEIKIGTSCK	1.363532774	2	2.595
D4A4T9	LSSGNEEDKKEEDSDEIK	1.186144356	3	4.35151
E9Q557	**DESP Desmoplakin**	**0.920393962**	**0.9237**	**2**
E9Q557	KQVQTSQKNTLR	0.968680301	1	1.99945
E9Q557	SQCTQVVQER	0.897874697	2	2.79091
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**1.175543292**	**0.06034**	**2**
O08550	HAAVALGQARAMVPEDVPR	1.174316959	2	2.40177
O08550	RGEEGTERMVQALTELLR	1.420795486	2	2.83263
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.152831123**	**0.872462**	**9**
O08557	DYAVSTVPVADSLHLK	1.029868253	2	3.46961
O08557	GAEILADTFK	0.989228236	1	2.13932
O08557	GAEILADTFKDYAVSTVPVADSLHLK	1.139250215	3	3.50771
O08557	LKDHLLIPVSNSEMEK	0.866922695	2	3.51165
O08557	LQLNIVEMKDENATLDGGDVLFTGR	1.669425123	3	3.4026
O08557	LTVPDDMAANCIYLNIPSK	1.026326272	2	3.42996
O08557	SFCSMAGPNLIAIGSSESAQK	0.866632889	2	4.64248
O08557	SQGEEVDFAR	0.869643723	2	2.42272
O08557	VDGLLTCCSVFINK	0.826400326	2	3.4368

O08583	**THOC4 THO complex subunit 4**	**0.970187859**	**0.124336**	**2**
O08583	QQLSAEELDAQLDAYNAR	0.921663452	2	2.90257
O08583	SLGTADVHFER	1.182534593	2	2.39824
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.253874752**	**2.65E-14**	**11**
O08601	EFYSYENEPVGIENLK	1.226016071	2	4.64537
O08601	GCPSLAEHWKSIR	1.357612303	2	4.02157
O08601	GHTTGLSLNNER	1.474194855	2	2.69361
O08601	MLSASGDPVSVVK	1.259405319	2	3.71733
O08601	NALLPEGIPLLLK	1.494676516	1	2.74851
O08601	NILLSIGELPK	1.263501586	2	4.03698
O08601	REEILQILK	1.102859784	3	3.39438
O08601	SDSSIILQER	1.20674992	2	2.40386
O08601	SGSSSAYTGYVER	1.202025704	2	3.72905
O08601	SNLNIFQYIGK	1.803849557	2	3.08844
O08601	VKEFYSYENEPVGIENLK	1.329306235	2	3.44784
O08795	**GLU2B Glucosidase 2 subunit beta**	**1.071959368**	**0.999998**	**6**
O08795	ETVVTSTTEPSR	1.074453823	2	2.95915
O08795	KLWEEQQAAAK	1.043166914	2	3.43167
O08795	LWEEQQAAAK	1.124556691	2	2.32246
O08795	MPPYDEETQAIIDAAQEAR	0.931619382	2	5.39153
O08795	SLEDQVETLR	0.994676294	2	3.43106
O08795	YEQGTGCWQGPNR	1.069083075	2	3.90798
O08874	**PKN2 Serine/threonine_protein kinase N2**	**1.200476072**	**0.142134**	**3**
O08874	ATSVALPGWSPSENRSSFMSR	1.139865254	2	2.33903
O08874	QLDIELK	1.225948415	1	2.35961
O08874	YSLEQRLNELPKNHPK	0.829262455	2	2.40126
O08949	**TF2AA Transcription initiation factor IIA subunit 1**	**1.112093251**	**0.593396**	**2**
O08949	DGIMNLNGRDYIFSK+Oxidation(4)	1.042077737	2	2.59037
O08949	MANSANTNTVPK	0.804931469	2	2.56478
O09158	**CP3AP Cytochrome P450 3A25**	**0.61304415**	**0.039817**	**2**
O09158	DVEINGVFIPK	0.541494073	2	2.47241
O09158	VDFLQLMMNTQNSK	0.624155763	2	2.60665
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.351161471**	**9.9E-20**	**13**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.308624891	2	6.02224
O09171	AGPWTPEAAVEHPEAVR	1.257556459	2	5.19266
O09171	AGSNVMQTFTFYASEDKLENR	3.909435861	2	4.68469
O09171	GAAELMQQK	1.300397932	2	3.50029
O09171	GAAELMQQK+Oxidation(6)	1.309982514	2	2.78246
O09171	IFHQQLEVFMK	1.269436424	2	2.88248
O09171	KEYWQNLR	1.215878227	3	3.42566
O09171	LNAGEVVIGDGGFVFALEK	1.635279558	3	5.90617
O09171	QGFIDLPEFPFGLEPR	1.170481034	2	5.17962
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.507681042	2	6.10487
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.249710381	3	6.45414
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(10)	1.518703705	3	6.18505
O09171	VNEAACDIAR	1.274906013	2	3.98695
O09173	**HGD Homogentisate 1_2_dioxygenase**	**0.904068021**	**0.180097**	**9**
O09173	CFYNSDGDFLIVPQK	1.685537429	2	4.16449
O09173	FSVDVFEETR	1.171048899	2	3.82779
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.074935591	3	5.27785
O09173	LLIYTEFGK	1.423261168	2	2.516
O09173	NCMSEFMGLIK	1.173601262	2	3.11948
O09173	QDVSPFNVVAWHGNYTPYK	0.95716258	2	3.49855
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.08064114	3	3.42256

O09173	SLRPGVAIADFVIFPPR	1.113421661	2	3.73116
O09173	YISGFGNECASEDPR	1.221497662	2	3.8449
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.435586128**	**9.71E-11**	**17**
O35077	ANTIGISLIK	1.184108972	2	3.11797
O35077	ELHSILQHK	1.201051679	1	2.70561
O35077	FCETTIGCK	1.185454774	2	2.71167
O35077	FCETTIGCKDPAQGQLLK	1.246721459	2	5.04099
O35077	GIDEGPNGLK	1.227782955	2	2.73005
O35077	GLVDKFPLFTAVYK	1.565599825	3	3.96243
O35077	ICDQLKGHLK	1.159077269	3	3.33756
O35077	ITVVQEVDTVEICGALK	0.979946757	2	4.91277
O35077	IVGSNASQLAHFDPR	2.336584452	2	3.0842
O35077	KLTEIINTQHENVK	1.179634452	2	5.20068
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	1.225605458	3	4.64334
O35077	LTEIINTQHENVK	1.151689454	2	4.37482
O35077	NIVAVGAGFCDGLGFGDNTK	1.218947116	2	4.86131
O35077	SIEQLEK	1.170826917	2	2.46597
O35077	VCIVGSGNWGSAIAK	1.205023264	2	4.5779
O35077	VCYEGQPVGEFICCLQNHPEHM	1.292595082	3	4.40625
O35077	VTMWVFEEDIGGR	1.838677664	2	3.3347
O35078	**OXDA D_amino_acid oxidase**	**1.486490863**	**0.038137**	**2**
O35078	GQIIQVEAPWIK	1.360964148	2	3.03027
O35078	SCCQLEPTLK	1.740775529	2	2.74572
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.968252157**	**0.892508**	**3**
O35094	KLEESDALQEAR	0.998675758	2	3.41097
O35094	TEMSEVLTEILR	0.828731908	2	2.5011
O35094	VTDLLGGLFSK	0.946562465	2	3.51297
O35142	**COPB2 Coatomer subunit beta_**	**1.27844565**	**6.28E-10**	**5**
O35142	AAESLADPTEYENLFPGLK	1.356263519	2	4.13002
O35142	FELALQLGELK	1.282627315	2	2.9522
O35142	GSNNVALGYDEGSIIVK	1.077242617	2	3.46858
O35142	HSEVQQANLK	0.943374949	2	3.72563
O35142	TFEVCDLPVR	1.01489142	2	2.62204
O35180	**SH3G3 Endophilin_A3**	**1.128107588**	**0.360376**	**2**
O35180	AVAEILSK	1.172720146	1	1.94413
O35180	QSTEILQELQNK	0.968680301	1	2.02915
O35244	**PRDX6 Peroxiredoxin_6**	**0.828357404**	**1.99E-05**	**9**
O35244	DINAYNGAAPTEK	0.950564734	2	3.9689
O35244	DLAILLGMLDPAEKDEK	1.042538337	2	3.54871
O35244	GESVMVLPTLPEEEAK	0.902066352	2	3.06817
O35244	KGESVMVLPTLPEEEAK	1.063373626	2	5.04885
O35244	LIALSIDSVEDHFAWSK	1.294370035	2	4.41776
O35244	LSILYPATTGR	1.449435245	2	3.00651
O35244	NFDEILR	1.080960584	1	2.37729
O35244	VVDSLQLTASNPVATPVDWK	1.117653933	2	6.05171
O35244	VVFIFGPDKK	1.438479967	2	2.49274
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.803731252**	**0.057416**	**2**
O35469	DLGYEPLVSWEEAK	0.81279166	2	4.26753
O35469	TSEWIGTLVEQHR	0.804859809	2	3.51988
O35509	**RB11B Ras_related protein Rab_11B**	**1.245616764**	**0.687516**	**5**
O35509	AQIWDTAGQER	0.984338971	2	2.34214
O35509	GAVGALLVYDIAK	1.060832406	2	3.51587
O35509	HLTYENVER	1.245656744	2	2.54362
O35509	NEFNLESK	1.031186983	1	2.10164

O35509	VVLIGDSGVGK	1.23911658	2	2.6032
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.131440657**	**0.095449**	**7**
O35567	ALFEEVPELLTEAEK	1.235790963	2	2.83425
O35567	DGQVIGIGAGQQSR	1.0317981	2	3.00033
O35567	EVSDGIVAPGYEEEALK	1.102501821	2	3.5939
O35567	HVSPAGAAVGVPLSEDEAR	1.320231987	2	5.43879
O35567	MSSFGDFVALSDVCDVPTAK	1.196446244	2	3.93519
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.168933932	2	5.37996
O35567	YTQSNSVCYAK	1.283079634	2	2.80593
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.181664813**	**0.364163**	**2**
O35660	RYAMGDAPDYDR	0.919564086	2	3.90649
O35660	YAMGDAPDYDR+Oxidation(3)	1.186890126	2	2.82366
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.468619625**	**0.132329**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	1.063236989	2	3.84639
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	0.627778819	3	5.49925
O35760	NCHLNENIDK	0.566069168	2	2.99966
O35760	NVTLNPDPNEIK	0.493867411	2	2.82228
O35763	**MOES Moesin**	**1.005238784**	**0.120123**	**5**
O35763	ALTSELANAR	1.0751182	2	2.60171
O35763	AQMVQEDLEK	0.786846182	2	2.36089
O35763	AQQELEEQTR	0.735033322	2	3.20108
O35763	IQVWHEEHR	0.940943515	2	2.40821
O35763	TQEQLASEMAELTAR	1.014065629	2	3.23258
O35783	**CALU Calumenin**	**0.807914845**	**0.568126**	**2**
O35783	HLVYESDQDKDGK	0.792423231	2	4.47547
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.195094782	3	4.94551
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**0.851717057**	**0.427431**	**3**
O35796	AEEQEPELTSTPNFVVEVTK	1.042837661	2	4.66994
O35796	AFVEFLTDEIKEEK	0.756026138	2	2.83054
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.305942001	3	5.09128
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.143686516**	**0.924955**	**8**
O35814	ALDLDSSCK	1.021789536	1	2.11371
O35814	ALSAGNIDDALQCYSEAIK	1.140487013	2	5.03347
O35814	AMADPEVQQIMSDPAMR	0.92141934	2	4.23991
O35814	DCEECIQLEPTFIK	1.204178123	2	3.94963
O35814	ELIEQLQNKPSDLGTK	0.988801255	2	4.10532
O35814	LDPQNHVLYSNR	3.614292973	2	3.12389
O35814	LMDVGLIAIR	1.032237332	2	3.37223
O35814	TVDLKPDWGK	1.00209521	2	2.44819
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.707828836**	**0.00077**	**9**
O35826	EVGAFGTPVINLGTR	1.123043762	2	2.7563
O35826	ILHIEGGEVSGTIDDSIR	1.793015803	3	4.06421
O35826	ILLAGCPSYDK	1.894333453	2	2.40214
O35826	LIQEWNSVDLR	1.273879792	2	2.36923
O35826	MIEQDDFDINTR	1.477519281	2	2.47229
O35826	SIDLQEPLQK	1.540637551	2	2.53538
O35826	TLVLFPNIDAGSK	1.529571078	2	2.31387
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.701395139	3	5.79537
O35826	VNPQEGVVLHSTK	1.602685429	2	2.34341
O35867	**NEB1 Neurabin_1**	**1.03316697**	**0.55088**	**2**
O35867	DSNSRPSSNKQATDTEEPEK	1.079822161	2	2.36552
O35867	EKAGEAEPQDEWGGSKSNR	0.708469233	2	2.34105
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.912065686**	**3.5E-08**	**6**

O35913	EGLQENVDGTENAK	0.760322776	2	3.44464
O35913	ILAGIPAPIYFGALIDR	1.222543885	2	2.42764
O35913	LYLGLPAALR	1.255355825	2	2.63687
O35913	SLSGTYMNSMLTQIER	0.721377195	2	4.21564
O35913	SQTLNPTQDPSECVK	0.820444838	2	4.29559
O35913	TFQFPGDIESSK	0.832555085	2	2.49811
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.06963209**	**0.695456**	**6**
O35952	ALLEVLGR	1.118127271	2	2.84435
O35952	FYEGTADEMYK	1.033623002	2	2.75655
O35952	HVEPGNTAVQEK	1.051600351	1	3.95781
O35952	LTTVLTTHHHWDHAGGNEK	1.504913632	3	3.72285
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.007441511	2	4.05803
O35952	TVQQHAGETDPVTTMR	1.073075752	2	5.5941
O35987	**NSF1C NSFL1 cofactor p47**	**1.00826086**	**0.462413**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.057634481	2	5.06304
O35987	LGAAPEEESAYVAGER	0.887584306	2	4.04073
O35987	LGSTAPQVLNTSSPAQQAENEAK	1.549359046	2	3.86802
O35987	SYQDPSNAQFLESIR	1.007636755	2	4.74721
O35987	TGFSLDNGDLR	1.09446029	2	2.70392
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.334627818**	**3.6E-07**	**2**
O54975	GSLTFEPLTLVPIQTK	1.388048431	2	3.94155
O54975	IENVVLVVPAK	1.126296468	2	3.24469
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.163337146**	**1.36E-13**	**3**
O55012	ATTLSNAVSSLASTGLSLTK	1.483890552	2	4.14585
O55012	ITAAQHSVTGSAVSK	1.478269305	2	4.28246
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	0.955667097	3	4.63671
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.15491581**	**0.000137**	**4**
O55096	AGLLALEFYTPETANWR	1.179853286	2	4.28604
O55096	LASVLNTEPALDSELTSK	2.220370699	2	3.78065
O55096	SYEFQGNHFQVTR	1.108113848	2	3.82397
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.075710959	3	4.27226
O55125	**NIPS1 Protein NipSnap homolog 1**	**0.924514203**	**0.114815**	**4**
O55125	AGPNIYELR	0.899954203	2	3.01884
O55125	FSGGYPALMDCMNK	0.824239504	2	2.97802
O55125	GWDENVYYTVPLVR	0.761006711	2	3.47509
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.35110978	3	4.73203
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.02933734**	**0.995959**	**6**
O55171	ADAGGELDLAR	0.810769718	2	2.94982
O55171	DGLLDVVEALQSPLVDKK	0.905769193	2	4.5478
O55171	DVQKPYVVELEVLDGHEPDGGQR	0.966679104	3	4.01087
O55171	GGELGLAMASFLK	0.947890901	2	3.55439
O55171	IEYFEEAVNYLR	1.099206583	2	3.31513
O55171	SCWDEPLSITVR	0.973368597	2	3.91044
O70127	**ABCBB Bile salt export pump**	**0.993918338**	**0.975544**	**4**
O70127	AGQITSEALSNIR	1.298820519	2	3.34918
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.208853838	3	3.5062
O70127	ILLLDEATSALDTESEK	1.040220176	2	4.49362
O70127	ILLLDMATSALDNESEAR	1.122101343	2	3.97948
O70133	**DHX9 ATP_dependent RNA helicase A**	**1.198048048**	**0.070659**	**3**
O70133	ELDALDANDELTPLGR	0.814161434	2	2.48132
O70133	KMTPAYEIRAVGNK	0.659912669	2	2.40652
O70133	TTQVPQYILDDFIQNDR	1.242050573	2	3.37985
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**1.687783803**	**0.19712**	**2**

O70173	FLGHAQTFGGIKR	1.280692475	1	1.99036
O70173	WTFSHPLEALGLLTSR	1.688146377	2	2.34898
O70196	**PPCE Prolyl endopeptidase**	**1.214104105**	**0.006323**	**2**
O70196	SDGTETSTNLHQK	1.210131981	2	3.22895
O70196	VFLDPNTLSDDGTVALR	1.29608107	2	3.71759
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.11232583**	**9.9E-20**	**14**
O70199	EADLVFISVNTPTK	1.461736457	2	3.17672
O70199	EQIVVDLSHPGVSADDQVSR	1.202889148	2	5.84453
O70199	FSLQDPPNKKPK	1.109335923	2	2.46698
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.536147816	3	6.6232
O70199	IIDSLFNTVTDK	2.091469359	2	2.55909
O70199	IIDSLFNTVTDKK	1.491963975	2	3.17564
O70199	ILTTNTWSSELSK	1.546250117	2	3.21782
O70199	INAWNSPTLPIYEPGLK	1.628065391	2	4.28786
O70199	NLFFSTNIDDAIR	1.178522209	2	3.17404
O70199	VLDGLHNELQTIGFQIETIGK	1.144287437	2	5.1841
O70199	VLDGLHNELQTIGFQIETIGKK	0.865412273	3	3.36432
O70199	VLIGGDETPEGQR	1.299531491	2	3.84175
O70199	VTVVDVNEAR	1.091876125	2	3.44674
O70199	YWQQVIDMNDYQR	1.102569645	2	4.49955
O70251	**EF1B Elongation factor 1_beta**	**1.059983972**	**2.27E-07**	**4**
O70251	SIQADGLVWGSSK	1.277614555	2	4.07827
O70251	SSILLDVKPWDDETDMTK	0.963561862	2	4.49177
O70251	SSILLDVKPWDDETDMTKLEECVR	1.123444185	3	5.00593
O70251	TPAGLQVLNDYLADK	1.228611876	2	4.13592
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.006474048**	**0.342985**	**16**
O70351	GGIVGMTLPIAR	0.865900136	2	3.58605
O70351	GLVAVITGGASGLGLSTAK	0.946751393	2	4.46935
O70351	GVIINTASVAAFEGQVGQAAYSASK	0.855984169	3	3.99726
O70351	IDVAVNCAGIAVAIK	1.020663278	2	4.58041
O70351	KLGGNCIFAPANVTSEK	1.124776001	2	4.97633
O70351	KNQVHTLEDFQR	1.045568929	2	4.03367
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.096832952	3	5.53707
O70351	LGGNCIFAPANVTSEK	1.193625469	2	3.37986
O70351	LVAGVMGQNEPDQGGQR	1.117161063	2	5.50302
O70351	LVGQGATAVLLDVPNSEGETEAK	1.304227819	2	5.30071
O70351	LVGQGATAVLLDVPNSEGETEAKK	1.194793089	3	3.66577
O70351	NFLASQVPFPSR	0.964220551	2	4.51179
O70351	NQVHTLEDFQR	0.947088335	2	3.66258
O70351	RLVGQGATAVLLDVPNSEGETEAK	0.976090001	2	6.08973
O70351	VINVNLIGTFNVIR	1.148367325	2	4.14212
O70351	VVTIAPGLFATPLLTTLPDK	0.99268964	2	4.87359
O70456	**1433S 14_3_3 protein sigma**	**1.403913647**	**6.93E-06**	**3**
O70456	DSTLIMQLLR	1.438785617	2	3.6972
O70456	NLLSVAYK	1.129108002	2	2.30989
O70456	VLSSIEQK	1.295756669	1	2.19641
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.387466453**	**9.9E-20**	**8**
O88428	GCTVWLTGLSGAGK	1.612284832	2	3.52944
O88428	GFTGIDSDYEKPETPECVLK	1.274570183	2	4.95374
O88428	GIHELFVPENK	1.332267882	2	3.03652
O88428	IHESAGLPFFEIFVDAPLNICESR	1.543464068	3	4.0419
O88428	KDLYEPTHGGK	1.308410539	2	2.65148
O88428	NLGFSAGDREENIR	1.246342793	2	3.35032
O88428	STNVVYQAHHVSR	1.114590056	2	2.90453
O88428	VLSMAPGLTSVEIIPFR	1.381668308	2	3.41237
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.14042576**	**1.07E-07**	**17**

O88600	AESEEMETSQAGSK	0.898264724	2	4.37268
O88600	AFSDPFVEAEK	1.094178349	2	2.85603
O88600	AGGIETIANEYSDR	1.336350387	2	3.28324
O88600	FQESEERPK	1.29878695	2	2.7109
O88600	FVSEDDRNNFTLK	1.451743091	2	2.87899
O88600	GCALQCAILSPAFK	1.151684372	2	3.70981
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	0.857796193	3	5.96834
O88600	LEDTENWLYEDGEDQPK	1.388489957	2	4.36524
O88600	MIMQDKLEK+Oxidation(1)	1.106301379	2	2.36333
O88600	MQVDQEEPHTEEQQPQTPAENK	1.056748074	3	5.13844
O88600	NFTTEQVTAMLLSK	1.205770822	2	3.31585
O88600	NKEDQYEHLDAADMTK	1.076993659	3	3.99026
O88600	SNLAYDIVQLPTGLTGIK	1.419390575	2	4.91644
O88600	SVMDATQIAGLNCLR	1.07614954	2	2.59881
O88600	TSTVDLPIESQLLWQLDR	1.116022743	2	3.86276
O88600	VLATAFDTTLGGR	1.149402432	2	3.78618
O88600	WNSPAEEGSSDCEVFPK	1.223635338	2	4.04349
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.355374849**	**9.9E-20**	**21**
O88618	AFAACLGAIK	1.265713708	2	2.51437
O88618	AGEYEALPEK	1.091914509	2	2.58049
O88618	ALLDAAAFYCDK	1.674282169	2	3.88864
O88618	ALLDAAAFYCDKEK	1.357846848	2	3.69185
O88618	EAQELNLPVVGSQLVGLVPLK	1.14056064	3	4.43131
O88618	GVSMDECVLCAK	1.140961688	2	3.87452
O88618	IIEYLVPDSGPEQSLLDASLR	1.469804858	2	5.58039
O88618	ISSLLQEAK	1.57914231	2	2.54189
O88618	KVQGIGWYLEEK	1.21565137	2	2.78741
O88618	LAEELNVPVYLYGEAAQMPSR	1.647370419	2	4.73711
O88618	LFVLEEEHR	1.414824722	2	2.92693
O88618	LGLDSLAPFDPK	1.36503627	2	3.60929
O88618	LIPPFHAASAQLTSLVDADAR	1.170171995	2	3.82477
O88618	MGALDVCPFIPVR	1.177157155	2	4.07854
O88618	MGALDVCPFIPVR+Oxidation(1)	1.013859644	2	2.80726
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.720729095	3	4.03405
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.166748392	2	3.70219
O88618	TCALQEGLR	1.281683149	2	3.17626
O88618	TQAALVLGSLEAR	1.201509817	2	4.78253
O88618	TVYTFVGQPECVVEGALSAAR	2.177933076	2	4.35053
O88618	VQGIGWYLEEK	1.335941362	2	3.24014
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.726117425**	**0.002834**	**5**
O88637	AHHSSQEMSSEYR	1.716696603	3	3.39945
O88637	HKGPPVFTQEER	1.044171858	2	2.99806
O88637	HNCDFCVHGNDITLTVDGR	1.158058858	3	4.30518
O88637	TEIVPDRDGSDPYEEPK	1.068873007	2	2.94459
O88637	TQGVSTTDLVGR	1.145654579	2	3.27736
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**1.038514625**	**0.786629**	**2**
O88656	ASSEGGAATGAGLDSLHK	1.038236736	2	4.15294
O88656	NSVSQISVLSGGK	1.591706052	2	2.92236
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**0.930316903**	**0.791421**	**2**
O88696	GQATDIAIQAEEIMK	0.939685778	2	2.55342
O88696	VLVHPPQDGEDEPELVQK	0.873900712	3	3.97231
O88735	**MAP7 Ensconsin**	**0.957941733**	**0.992187**	**2**
O88735	KTTEQRNGDIAK	0.955958936	2	2.50798
O88735	TSAGTTDPEEATR	0.976907685	2	2.38506

O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.124672068**	**0.996037**	**2**
O88761	DTSEDIEELVEPVAAHGPK	1.011646841	2	5.09873
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.130618651	2	3.75775
O88767	**PARK7 Protein DJ_1**	**1.096680263**	**0.999752**	**8**
O88767	ALVILAK	1.023112512	2	2.30556
O88767	DVVICPDTSLEEAK	1.090988786	2	3.66428
O88767	GAEEMETVIPVDIMR	1.116217556	2	3.48173
O88767	GLIAAICAGPTALLAHEVGFGCK	1.128258826	2	4.35935
O88767	KGLIAAICAGPTALLAHEVGFGCK	1.095095474	3	5.50269
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	1.025421668	3	5.62287
O88767	VEKDGLILTSR	1.216241238	2	2.33836
O88767	VTVAGLAGKDPVQCSR	1.083129182	2	4.36281
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**1.025213913**	**0.273878**	**3**
O88794	GLATGDSPLGPMTHHGEEDWVYER	0.891246559	3	3.56477
O88794	KKNEELGQLYR	1.184357061	2	2.37603
O88794	SSQIGAVVSR	0.953398383	2	2.4858
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**0.939891264**	**9.9E-20**	**16**
O88813	ADISVVICDTPQK	0.928032004	2	3.11121
O88813	AEYLGSCLLHK	1.037763647	2	2.49996
O88813	AILEDLQK	1.267342468	1	2.20877
O88813	FFQTQIK	1.098356641	1	1.93311
O88813	FLLNLAIISK	1.362524777	2	2.98696
O88813	GAMLTHQNIVSNMAAFLK	1.097034865	3	3.64349
O88813	GLAVSDNGPCLGYR	1.077622063	2	2.52831
O88813	GSFEELCQNQCVK	1.101745356	2	4.73289
O88813	IGFFQGDIR	1.551550284	2	3.33189
O88813	LMITGAAPISTPVLTFFR	1.341609388	2	3.05185
O88813	LVQGVIFSCGGK	1.053384804	2	2.88852
O88813	SFLIGVVVPDPESLPSFAAK	1.082324841	2	3.6053
O88813	SIFVHPEPFSIENGLLTPTLK	1.558259474	2	2.85231
O88813	SRPILQVFVHGESLR	0.805118132	3	3.53498
O88813	TQEVLDKDGWLHTGDIGR	1.115210111	3	3.79106
O88813	TVILMDPFDDDLMK	1.397016966	2	3.28881
O88867	**KMO Kynurenine 3_monooxygenase**	**1.048732455**	**0.952836**	**5**
O88867	AVGLEDQIVSK	0.953440583	2	2.30779
O88867	DFFLLPAQPMISVK	1.219058362	2	2.51076
O88867	DITCDLIVGCDGAYSTVR	1.119006587	2	2.57408
O88867	FNNDLSVCLPEFSR	1.016907589	2	3.96234
O88867	NFPDAIPLMGEQALMR	1.123385055	2	3.57839
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.103097262**	**0.973766**	**2**
O88941	ALESHAAAFK	0.952367661	2	2.45485
O88941	MDPSLFPPVPLFSGVPSR	1.109925633	2	3.09274
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.19596194**	**0.34264**	**4**
O88986	ALDLLMESNAIIQSMAAK+Oxidation(6)	1.914607336	2	2.52248
O88986	GTDELLGVMDQVTIINSTLGK	0.89689579	2	2.61682
O88986	MEAAGFTVSGADHPICPVMLGDAR+Oxidation(1)	0.839535766	2	2.623
O88986	VQISAVHSEEDIDR	1.022688253	2	4.03855
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.196267641**	**9.9E-20**	**9**
O88989	DLDVAVLVGSMPR	0.951303783	3	3.85424
O88989	EKMDLTAKELTEEK+Oxidation(3)	0.878860012	2	2.38556
O88989	ELTEEKETAFEFLSSA	1.630020714	2	3.73205
O88989	EVGVYEALKDDSWLK	1.026746468	2	3.82936
O88989	FVEGLPINDFSR	1.16822396	2	3.44062
O88989	GEFITTVQQR	1.157571224	2	3.87404
O88989	LGVTADDVK	1.243899825	2	2.84299

O88989	NVIIWGNHSSTQYPDVNHAK	1.21558085	2	5.66649
O88989	VIVVGNPANTNCLTASK	1.198382817	2	5.56551
O88990	**ACTN3 Alpha_actinin_3**	**1.290816921**	**0.045743**	**4**
O88990	ALDFIASK	1.213698441	2	2.62221
O88990	CQLEINFNTLQTK	1.450146621	2	3.58275
O88990	FAIQDISVEETSAK	1.415083048	2	3.9193
O88990	HEAFESDLAAHQDR	0.868776171	3	3.9578
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.894028728**	**0.944242**	**6**
O88994	CVLTTVDPDTGIIDR	0.803659425	2	4.19552
O88994	GVSVCETECTDMGLR	0.901758713	2	3.42889
O88994	LYPSESYLQNYEVAYPDCSPIHLISEASLVDLNTR	1.098532465	3	3.74332
O88994	QLQQVGTVSK	0.857627921	1	2.28458
O88994	RQLQQVGTVSK	0.801678769	2	3.2819
O88994	SLYQSSPLFGMYFSVEK	1.221345039	2	3.72633
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.246955021**	**0.082374**	**7**
O89000	EGGADGVTATNTVSGLMGLK	0.886014906	2	3.34767
O89000	GAVIVLGAGDTAFDCATSALR	1.167368339	2	4.8197
O89000	GMGLACGQDPELVR	1.083461836	2	3.31039
O89000	LENNFDDIK	1.049936479	2	2.65525
O89000	QEYVGGLSTSEIPQFR	1.247340134	2	3.57408
O89000	TEQDETGNWVEDEEQIVR	1.146804948	2	5.07896
O89000	TFSLDKDIVTNVSPR	0.950139357	2	2.83104
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.021453563**	**0.784803**	**2**
O89032	DDSDINTSKTGEVSKR	1.1563994	2	2.51543
O89032	FPIEGGQKDPK	0.94559231	2	2.34545
O89046	**COR1B Coronin_1B**	**0.93059835**	**0.97566**	**4**
O89046	KCEPIVMTVPR	0.819408773	2	2.60178
O89046	NDQCYEDIR	1.13195624	2	2.82482
O89046	NVLSDSKPAGYSR	0.952025496	2	2.92792
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.929760316	2	4.23224
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.503181873**	**0.387975**	**7**
O89049	IEQIEAGTPGR	1.368491553	2	2.98417
O89049	IEQIEAGTPGRLK	2.096338832	2	2.36151
O89049	LELTPVAIQAGR	1.087647058	2	2.81114
O89049	STNSEETIEDEFNTVLLAVGR	1.138640712	2	2.32379
O89049	VMVLDFVTPTPLGTR	1.22928449	2	2.78592
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.628768722	2	2.40564
O89049	WGLGGTCVNVGCIPK	1.074096446	2	3.56522
P00173	**CYB5 Cytochrome b5**	**1.027520099**	**0.999977**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	1.032101522	2	5.44611
P00173	FLEEHPGGEEVLR	0.925678673	2	4.16635
P00173	STWVILHHK	0.837418372	2	2.9134
P00173	TYIIGELHPDDR	0.957281457	2	4.06268
P00173	VYDLTK	0.96918874	1	1.96988
P00173	YYTLEEIQK	0.962558801	2	2.88754
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.182065794**	**3.55E-05**	**7**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.046990916	3	4.30546
P00388	GMSADPEEYDLADLSSLPEIDK	1.427576281	2	5.09565
P00388	LIHEGGAHIYVCGDAR	1.350290303	3	3.84453
P00388	RSDEDYLYR	0.915650857	2	2.84327
P00388	SYENQKPPFDAK	1.025342576	2	3.20513
P00388	TNVLYELAQYASEPSEQEHLHK	1.462231165	3	3.6142
P00388	VHPNSVHICAVAVEYEAK	1.183835337	3	3.56947
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.029501487**	**0.867575**	**3**
P00406	ILYMMDEINNPVLTVK	0.893664363	2	3.60132
P00406	LLEVDNR	1.133411795	2	2.52832

P00406	VVLPMELPIR	1.029397671	2	2.51784
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.220464972**	**5.53E-06**	**19**
P00481	FGMHLQAATPK	0.964128049	3	3.64667
P00481	GEYLPLLQGK	0.931389163	2	3.08116
P00481	GGNVLITDTWISMGQEDEK	1.188591335	2	5.54827
P00481	GGNVLITDTWISMGQEDEKK	1.132289368	2	4.82242
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.220890484	3	4.47372
P00481	GYEPDPNIVK	1.023719045	2	2.58242
P00481	LQAFQGYQVTMK	1.412746258	2	4.24665
P00481	LQAFQGYQVTMK+Oxidation(11)	1.435446073	2	2.32245
P00481	LSMTNDPLEAAR	1.200741821	2	2.91025
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.326609411	3	7.25227
P00481	QKGEYLPLLQGK	0.88090116	2	3.66631
P00481	QSDLDILAK	0.975827729	1	1.96445
P00481	SLGMIFEK	0.99511493	2	2.39179
P00481	SLGMIFEK+Oxidation(4)	0.983160036	2	2.39704
P00481	SLVFPEAENR	0.97314371	2	2.6746
P00481	SLVFPEAENRK	1.184650293	2	2.88315
P00481	VLSSMTDAVLAR	1.093882193	2	3.83373
P00481	VLSSMTDAVLAR+Oxidation(5)	1.170935078	2	2.68697
P00481	YGKPVQSQVQLK	0.552621747	2	2.79485
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.502530053**	**1.24E-14**	**2**
P00502	FIQSPEDLEK	0.430920142	2	2.77003
P00502	WLLAAAGVEFDEK	0.432136632	2	4.53077
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**0.947829047**	**0.041639**	**19**
P00507	ASAELALGENSEVLK	1.064543268	2	4.63686
P00507	DAGMQLQGYR	0.813845786	2	2.80958
P00507	DDNGKPYVLPSVR	0.866998119	2	3.283
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.371295114	3	5.26699
P00507	EYLPIGGLADFCK	1.098190402	2	2.6195
P00507	FVTVQTISGTGALR	1.034174327	2	4.80374
P00507	HFIEQGINVCLCQSYAK	1.11226786	3	5.26313
P00507	ILIRPLYSNPPLNGAR	1.622240886	3	3.35326
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.412191019	3	4.52359
P00507	ISVAGVTSGNVGYLAHAIHQVTK	1.430673798	2	2.67593
P00507	KMNLGVGAYR	0.999784503	2	2.54552
P00507	KQWLQEVK	0.941441346	1	2.39431
P00507	MNLGVGAYR	0.99105887	2	3.01042
P00507	NLDKEYLPIGGLADFCK	0.959292222	2	5.87115
P00507	NMGLYGER	1.030861913	2	2.63611
P00507	QWLQEVK	1.02844094	1	2.06183
P00507	TCGFDFSGALEDISK	1.049603253	2	5.02232
P00507	VGAFTVVCK	1.059914368	2	3.34583
P00507	VGASFLQR	1.336992421	2	3.112
P00564	**KCRM Creatine kinase M_type**	**1.271241482**	**1**	**7**
P00564	GGDDLDPNYVLSSR	0.865582809	2	4.649
P00564	GQSIDDMIPAQK	1.446373666	2	2.9639
P00564	GTGGVDTAAVGAVFDISNADR	1.144352801	2	5.90553
P00564	LGSSEVEQVQLVVDGVK	1.424679978	2	4.61334
P00564	LSVEALNSLTGEFK	1.345680707	2	4.1635
P00564	RGTGGVDTAAVGAVFDISNADR	1.012700278	2	4.3304
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	1.378728361	3	6.31407
P00787	**CATB Cathepsin B**	**1.220954338**	**1.06E-05**	**3**
P00787	GENHCGIESEIVAGIPR	1.222432687	2	4.86004
P00787	HEAGDVMGGHAIR	1.069558243	3	3.96512
P00787	MCEAGYSTSYKEDK	1.087911363	2	3.92349

P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.231845338**	**9.9E-20**	**18**
P00884	ALQASALAAWGGK	1.40475021	2	4.77195
P00884	ATQEAFMK	1.237831893	2	2.68463
P00884	ELSEIAQR	1.184706951	1	1.93518
P00884	ETTIQGLDGLSER	1.20008377	2	3.89206
P00884	FPALTSEQK	1.201154657	2	2.36419
P00884	GILAADESVGTMGNR	1.222376295	2	5.66892
P00884	GILAADESVGTMGNR+Oxidation(12)	1.391236226	2	5.02538
P00884	GIVVGIK	1.308058781	1	1.91353
P00884	IKVENTEENR	1.241998737	2	2.68951
P00884	IKVENTEENRR	1.502701228	2	2.77796
P00884	ISDQCPSSLAIQENANALAR	1.323586851	2	6.61945
P00884	KELSEIAQR	1.218263347	2	2.61509
P00884	KYTPEQVAMATVTALHR	1.149322546	3	6.19899
P00884	KYTPEQVAMATVTALHR+Oxidation(9)	1.364711648	3	3.54451
P00884	LDQGGAPLAGTNK	1.27949238	2	4.57885
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	2.043583505	3	5.1496
P00884	YTPEQVAMATVTALHR	1.155092514	2	4.81394
P00884	YTPEQVAMATVTALHR+Oxidation(8)	1.205056616	2	3.66617
P01026	**CO3 Complement C3**	**1.237910089**	**1.42E-05**	**17**
P01026	ACEPGVDYVYK	1.151207812	2	2.94465
P01026	ADIGCTPGSGK	1.236919052	2	2.79223
P01026	AFYEHAPK	1.051904146	2	2.35664
P01026	EYVLPSFEVLVEPTEK	1.05267	2	3.43416
P01026	IFTVDNNLLPVGK	1.345097742	2	3.38856
P01026	IGLQEVEVK	1.227118772	2	2.5906
P01026	NEQVEIRAVLFNYR	0.749442394	2	2.31445
P01026	QNEGFSLTAK	1.035391108	2	2.38396
P01026	RVPVVTQGSDAQALTQDDGVAK	1.299826907	3	5.30394
P01026	SDVDEDIIPEEDIISR	1.091641454	2	4.57199
P01026	SGSDEVQAGQER	1.229888322	2	4.13042
P01026	TNQGLQTDQR	1.08420318	2	2.85435
P01026	TNQGLQTDQREDPECAKPAAR	1.124687601	3	4.07191
P01026	TVLTGATGHLNR	1.2363546	2	2.9512
P01026	TVVIVIETPDGVPIKR	1.206868353	2	3.00017
P01026	VELKPGDNLNVNFHLR	1.194446218	3	4.00815
P01026	VLIEDGSGEAVLSR	1.349361239	2	3.82754
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.961586204**	**1**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.766307435	3	7.67335
P01946	FLASVSTVLTSK	0.770135602	2	4.05184
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.750046248	4	5.80858
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.826969426	4	6.22904
P01946	IGGHGGEYGEEALQR	0.821303731	2	4.97788
P01946	LRVDPVNFK	1.086977552	2	2.53865
P01946	MFAAFPTTK	0.742734566	2	3.09331
P01946	MFAAFPTTK+Oxidation(1)	0.786213092	2	2.65487
P01946	TYFSHIDVSPGSAQVK	1.006392371	2	5.21598
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.811670834**	**0.998238**	**4**
P02089	GTFASLSELHCDK	0.662157245	2	3.68864
P02089	LHVDPENFR	0.792187743	2	2.75853
P02089	YFDSFGDLSSASAIMGNPK	0.682078356	2	6.61532
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(15)	0.597221356	2	4.95761
P02091	**HBB1 Hemoglobin subunit beta_1**	**1.001246505**	**0.998047**	**9**
P02091	EFTPCAQAAFQK	0.752680276	2	3.12624
P02091	GTFAHLSELHCDK	0.835659036	2	4.47313
P02091	GTFAHLSELHCDKLHVDPENFR	0.705545072	3	4.59281
P02091	KVINAFNDGLK	0.771653794	2	3.70175

P02091	LLGNMIVIVLGHHLGK	0.822821326	2	3.3464
P02091	LLGNMIVIVLGHHLGKEFTPCAQAAFQK	0.543549912	3	5.41545
P02091	VINAFNDGLK	0.783191583	2	3.00209
P02091	VNPDDVGGEALGR	0.704082878	2	4.29396
P02091	VVAGVASALAHK	0.819297881	2	3.82275
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.075021674**	**9.9E-20**	**7**
P02401	ILDSVGIEADDER	1.13050418	2	4.60929
P02401	ILDSVGIEADDERLNK	1.222440672	2	3.19666
P02401	KILDSVGIEADDER	0.687710113	2	3.94242
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.330263212	3	6.55818
P02401	NIEDVIAQGVGK	1.063440615	2	4.77232
P02401	VISELNGK	1.284009091	1	2.06401
P02401	YVASYLLAALGGNSNPSAK	1.244933119	2	5.79399
P02564	**MYH7 Myosin_7**	**0.864494444**	**0.119923**	**25**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.466962578	3	5.48508
P02564	ANDDLKENIAIVER	0.563867733	2	3.363
P02564	DLEEATLQHEATAAALR	1.072296305	2	5.40242
P02564	EQYEEETEAK	0.774611143	2	2.5041
P02564	GTLEDQIIQANPALEAFGNAK	0.931226386	2	5.17065
P02564	IEDEQALGSQLQK	0.517375471	2	4.07348
P02564	IEELEEELEAER	0.801005113	2	4.11159
P02564	ILNPAAIPEGQFIDSR	0.691302682	2	3.35457
P02564	KLAEQELIETSER	0.797493597	2	3.97693
P02564	KMEGDLNEMEIQLSHANR+Oxidation(2)	1.605467446	2	2.50108
P02564	KVQHELDEAEER	1.086938742	2	2.79147
P02564	LDEAEQIALK	0.94057071	2	3.36966
P02564	LELDDVTSNMEQIIK	1.114220085	2	3.49343
P02564	LQDAEEAVEAVNAK	0.552274539	2	4.711
P02564	LQNEIEDLMVDVER	0.918592641	2	3.44506
P02564	MDADLSQLQTEVEEAVQECR	0.761572776	2	4.80526
P02564	NLQEEISDLTEQLGSTGK	0.739727286	2	5.67313
P02564	NLTEEMAGLDEIIVK	1.365564585	2	3.13954
P02564	NNLLQAELEELR	0.714671817	2	2.86152
P02564	QAEEAEEQANTNLSK	0.852529938	2	4.78076
P02564	QKYEESQSELESSQK	0.856123567	2	2.95824
P02564	QLEAEKLELQSALEEAEASLEHEEGK	0.64283911	3	4.50393
P02564	TLEDQMNEHR	0.752520327	2	2.59306
P02564	VQLLHSQNTSLINQK	0.545170104	2	3.8472
P02564	VVDSLQTSLDAETR	0.693986334	2	2.72791
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**1.057068693**	**0.996846**	**8**
P02600	ALGTNPTNAEVK	1.03784286	2	3.22463
P02600	ALGTNPTNAEVKK	0.928906689	2	2.72002
P02600	DQGGYEDFVEGLR	0.54152741	2	3.58792
P02600	IEFEQFLPMMQAISNNK	0.68336755	2	2.73675
P02600	ITLSQVGDVLR	1.0690889	2	3.08934
P02600	KIEFEQFLPMMQAISNNK	1.098751563	2	5.4581
P02600	VLGNPSNEEMNAK	1.02899738	2	3.84938
P02600	VLGNPSNEEMNAK+Oxidation(10)	1.122107116	2	2.57315
P02625	**PRVA Parvalbumin alpha**	**0.947142237**	**0.95131**	**4**
P02625	AIGAFTAADSFDHKK	0.589067644	2	3.9116
P02625	SGFIEEDELGSILK	1.135166616	2	2.85177
P02625	TLMAAGDKDGDGK	0.941644955	2	3.17967
P02625	TLMAAGDKDGDGK+Oxidation(3)	0.569829545	2	3.3596
P02650	**APOE Apolipoprotein E**	**1.141705239**	**0.10625**	**13**
P02650	ELEEQLGPVAEETR	1.175427268	2	4.33142
P02650	GRLEEVGNQAR	1.010962392	2	3.70095

P02650	GWFEPLVEDMQR	1.264061342	2	3.23934
P02650	LEEVGNQAR	0.993818474	2	2.56682
P02650	LGADMEDLR	1.113262426	2	3.03111
P02650	LGPLVEQGR	1.274468558	2	2.30945
P02650	LQAEIFQAR	1.586139652	2	2.71116
P02650	MEEQTQQIR	1.048936481	2	3.23887
P02650	MEEQTQQIR+Oxidation(1)	1.008599282	2	2.87699
P02650	NEVNTMLGQSTEELR	1.096315482	2	4.49017
P02650	SKMEEQTQQIR	1.017322505	2	3.2988
P02650	SKMEEQTQQIR+Oxidation(3)	1.463579884	2	3.56091
P02650	TANLGAGAAQPLR	0.977976604	2	2.37244
P02680	**FIBG Fibrinogen gamma chain**	**1.154387806**	**0.721419**	**3**
P02680	VGPESDKYR	1.083773858	2	2.59289
P02680	YEALLLTHESSIR	1.300682545	2	3.71655
P02680	YLQDIYTSNK	1.207203104	2	2.78518
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.408518169**	**9.9E-20**	**13**
P02692	AMGLPEDLIQK	1.114488825	2	3.63358
P02692	AMGLPEDLIQK+Oxidation(2)	1.201357732	2	3.3736
P02692	GVSEIVHEGK	1.059342419	2	3.49282
P02692	GVSEIVHEGKK	1.076976046	2	3.32757
P02692	MVTTFK	1.038339826	1	1.91304
P02692	MVTTFK+Oxidation(1)	1.254752833	1	2.02285
P02692	SVTEFNGDTITNTMTLGDIVYK	1.239257558	2	5.65352
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(14)	1.100010135	2	5.64295
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.287133915	2	3.73548
P02692	VIHNEFTLGEECELETMTGEK	1.145824734	3	6.30642
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(17)	1.206553565	3	5.51018
P02692	YQVQSQENFEPFMK	1.156955	2	6.0539
P02692	YQVQSQENFEPFMK+Oxidation(13)	1.254040312	2	5.28081
P02696	**RET1 Retinol_binding protein 1**	**1.362827484**	**8.99E-06**	**8**
P02696	ALDVNVALR	1.26451667	2	3.2775
P02696	CMTTVSWDGDKLQCVQK	1.562716526	2	4.54339
P02696	EFEEDLTGIDDR	1.218962272	2	2.3439
P02696	EFEEDLTGIDDRK	1.217305256	2	2.75299
P02696	GWTQWIEGDELHLEMR	1.221365629	2	4.30948
P02696	MLSNENFEEYLR	1.371217896	2	3.63052
P02696	MLSNENFEEYLR+Oxidation(1)	1.509677312	2	2.96996
P02696	NYIMDFQVGKEFEEDLTGIDDRK	1.344949726	3	3.46512
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.176413796**	**0.217159**	**6**
P02706	DYQDFQHLDNENDHHQLQR	1.249414481	3	3.41407
P02706	LVESQLEK	1.19534563	1	2.06711
P02706	QLVSDVR	0.459636424	1	2.0709
P02706	SLSCQMAALR	1.069903471	2	3.05188
P02706	WVCETELGK	1.164801177	2	2.36258
P02706	WVDGTDYETGFK	1.238982658	2	3.46497
P02770	**ALBU Serum albumin**	**1.178601003**	**0.922055**	**27**
P02770	AADKDNCFATEGPNLVAR	0.852279136	2	4.92819
P02770	AETFTFHSDICTLPDKEK	1.97297749	2	3.74581
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.686514837	3	5.3224
P02770	CCSGSLVER	0.877306734	2	3.2315
P02770	CCTLPEAQR	1.069820413	2	2.77338
P02770	DLGEQHFK	1.235843992	2	2.30994
P02770	DNCFATEGPNLVAR	0.895724927	2	3.36333
P02770	DNYGELADCCAK	0.218066021	2	3.36679
P02770	ECCHGDLLECADDR	1.253977864	2	3.93696
P02770	ECCHGDLLECADDRAELAK	1.278380238	2	5.32863
P02770	FKDLGEQHFK	1.221216568	3	4.18032

P02770	GLVLIAFSQYLQK	1.347446768	2	4.08361
P02770	INKECCHGDLLECADDRAELAK	1.229000279	3	5.44417
P02770	KQTALAELVK	1.149526432	3	4.12606
P02770	KYEATLEK	1.206043956	2	2.69375
P02770	LQACCDKPVLQK	1.380289493	2	4.2771
P02770	LRDNYGELADCCAK	0.341201	2	3.34416
P02770	LVQEVTDFAK	1.309490286	2	3.7089
P02770	QEPERNECFLQHK	0.373330287	2	2.35511
P02770	RHPDYSVSLLLR	1.264239547	3	4.80933
P02770	SIHTLFGDK	0.535791601	1	2.28392
P02770	TCVADENAENCDK	0.974418854	2	4.646
P02770	TNCELYEK	1.049481581	2	2.82172
P02770	TVMGDFAQFVDK	0.789931748	2	4.27193
P02770	YMCENQATISSK	1.19759097	2	4.4145
P02770	YMCENQATISSK+Oxidation(2)	1.077262192	2	3.68944
P02770	YNEVLTQCCTESDK	1.055433253	2	5.73419
P02803	**MT1 Metallothionein_1**	**1.227282968**	**0.167304**	**2**
P04041	**GPX1 Glutathione peroxidase 1**	**1.07571009**	**0.931005**	**10**
P04041	FLVGPDGVPVR	1.067959304	2	3.24681
P04041	FLVGPDGVPVRR	1.069965003	2	2.31987
P04041	GLVVLGFPCNQFGHQENGK	1.128727029	2	4.28568
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.963179449	3	4.32976
P04041	NALPAPSDDPTALMTDPK	1.00739837	2	3.47492
P04041	NDISWNFEK	1.059093103	2	2.90445
P04041	NEEILNSLK	1.103401583	2	2.54155
P04041	TIDIEPDIEALLSK	1.220690286	3	4.27959
P04041	YIIWSPVCR	1.041827611	2	2.93639
P04041	YVRPGGGFEPNFTLFEK	1.201470354	2	4.58119
P04167	**CP2B2 Cytochrome P450 2B2**	**0.686534934**	**0.123749**	**2**
P04167	GTIAVIEPIFK	0.761735326	2	2.5601
P04167	NLQEILDYIGHIVEK	0.684815842	2	4.22887
P04176	**PH4H Phenylalanine_4_hydroxylase**	**0.928374849**	**1.27E-14**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.296790324	2	4.1409
P04176	EDNIPQLEDVSQFLQTCTGFR	0.982879331	3	4.72707
P04176	FANQILSYGAELDADHPGFK	1.739137822	3	3.97933
P04176	FANQILSYGAELDADHPGFKDPVYR	1.221502243	3	5.3623
P04176	ILADSINSEVGILCNALQK	1.076842947	3	6.60825
P04176	LNKDEYEFFTYLDKR	4.096047861	3	3.6054
P04176	LRPVAGLLSSR	2.053183348	2	2.7117
P04176	NDIGATVHELSR	0.958969534	2	3.75593
P04176	QFADIAYNYR	0.895669155	2	2.8157
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.436440874	2	4.82568
P04176	TACQEYSVTEFQPLYYVAESFSDAK	3.838723176	3	3.69209
P04176	THACYEHNHIFPLLEK	1.008471754	3	4.73001
P04176	VEVLDNTQQLK	0.941109468	2	3.84534
P04176	VEYTEEEK	0.858312729	2	2.69658
P04176	VEYTEEEKQTWGTVFR	1.032077407	2	4.33639
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.005353642	3	5.30153
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.939526821**	**0.999999**	**9**
P04182	AFYNNVLGEYEEYITK	0.935363515	2	4.48598
P04182	GIYMWDVEGR	0.974579702	2	2.71821
P04182	GLLNAIVIR	0.984984372	2	3.1417
P04182	HQVLFIADEIQTGLAR	1.858480961	2	4.04962
P04182	IIEAMKSQVDK	0.940246391	2	2.33297
P04182	KTEQGPPSSEYIFER	1.094373768	2	3.92263
P04182	TEQGPPSSEYIFER	0.903312683	2	4.12178
P04182	VLPMNTGVEAGETACK	1.012400113	2	3.98494

P04182	WLAVDHENVRPDIVLLGK	0.837243137	2	4.9355
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.065175666**	**0.984128**	**4**
P04256	EDSQRPGAHLTVK	1.044066097	2	3.22086
P04256	IEVIEIMTDR	1.231626711	2	3.13553
P04256	NQGGYGGSSSSSYGSGR	1.098208639	2	4.73156
P04256	YHTVNGHNCEVR	1.304317528	2	3.31723
P04276	**VTDB Vitamin D_binding protein**	**1.34593568**	**8.47E-06**	**2**
P04276	SCESDAPFPVHPGTSECCTK	1.352378876	2	4.741
P04276	YCSSQIDAEMR	1.345818995	2	2.87571
P04355	**MT2 Metallothionein_2**	**1.4480128**	**0.862239**	**2**
P04462	**MYH8 Myosin_8 (Fragment)**	**0.84705101**	**0.890911**	**3**
P04462	KLQHELEEAEER	0.865634967	3	3.89384
P04462	LQHELEEAEER	0.781304514	2	3.64902
P04462	RAALQAEIEELR	1.898386546	2	3.87579
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**1.632448384**	**0.980103**	**7**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.420467631	2	4.49378
P04466	GADPEDVITGAFK	1.597904487	2	3.84988
P04466	KQFLEELLTTQCDR	1.195462824	2	4.10782
P04466	LKGADPEDVITGAFK	2.7010209	3	4.46266
P04466	NICYVITHGDAKDQE	1.646934929	2	4.70353
P04466	NMWAAFPPDVGGNVDYK	1.507513449	2	3.09584
P04466	QFLEELLTTQCDR	1.58781194	2	3.77732
P04550	**PTMS Parathymosin**	**0.909857573**	**0.664846**	**4**
P04550	RTAEEEDEADPKR	1.100919908	3	4.03406
P04550	SVEAAAELSAK	1.05549823	2	3.64451
P04550	TAEEEDEADPK	0.834475338	2	3.32468
P04550	TAEEEDEADPKR	1.123120466	2	3.70036
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.000297581**	**1.67E-09**	**16**
P04636	AGAGSATLSMAYAGAR	0.955376695	2	4.65713
P04636	ANTFVAELK	1.068516378	2	2.77811
P04636	EGVIECSFVQSK	0.954341578	1	3.03652
P04636	ETECTYFSTPLLLGK	1.162172861	2	3.50346
P04636	FVFSLVDAMNGK	1.210606805	2	4.4267
P04636	GCDVVVIPAGVPR	1.005916474	2	4.37047
P04636	GYLGPEQLPDCLK	0.999930167	2	4.1261
P04636	IFGVTTLDIVR	1.420965115	2	3.60158
P04636	IQEAGTEVVK	1.030258746	2	2.88075
P04636	LTLYDIAHTPGVAADLSHIETR	1.151746996	3	7.01877
P04636	MIAEAIPELK	0.992801511	2	3.21102
P04636	MIAEAIPELK+Oxidation(1)	1.288009297	2	2.53998
P04636	TIIPLISQCTPK	1.047023292	2	3.51166
P04636	VAVLGASGGIGQPLSLLLK	0.439838652	2	6.11811
P04636	VDFPQDQLATLTGR	0.917256738	2	4.86953
P04636	VNVPVIGGHAGK	0.96459857	2	3.21043
P04639	**APOA1 Apolipoprotein A_I**	**1.294178302**	**0.99889**	**6**
P04639	AKPALDDLGQGLMPVLEAWK	0.972566985	2	3.74204
P04639	LQEQLGPVTQEFWANLEK	1.295150755	2	4.89843
P04639	NEMNKDLENVK	1.083073184	2	3.43498
P04639	QLNLNLLDNWDTLGSTVGR	1.03428993	2	4.50274
P04639	VKDFATVYVDAVK	1.154826394	2	3.11123
P04639	WNEEVEAYR	0.919882746	2	2.37081
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.343158025**	**9.9E-20**	**22**
P04642	DLADELALVDVIEDK	1.33304895	2	5.47931
P04642	DLADELALVDVIEDKLK	1.39399826	2	4.61524
P04642	DQLIVNLLK	1.169480231	2	2.9457

P04642	DQLIVNLLKEEQVPQNK	1.309845398	2	4.86708
P04642	EDVFLSVPCILGQNGISDVVK	1.281442953	2	4.7985
P04642	FIIPNVVK	1.009623606	2	2.39425
P04642	GEMMDLQHGSLFLK	1.390190636	2	3.85543
P04642	GEMMDLQHGSLFLK+Oxidation(3)	1.525203123	2	3.45283
P04642	GEMMDLQHGSLFLK+Oxidation(4)	1.485163054	2	3.14732
P04642	GLYGIKEDVFLSVPCILGQNGISDVVK	1.284985958	3	3.35449
P04642	KSADTLWGIQK	1.318220032	2	3.0957
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.217841751	3	5.72764
P04642	LKGEMMDLQHGSLFLK	1.286958455	2	3.99952
P04642	LLIVSNPVDILTYVAWK	1.804345953	2	4.87618
P04642	NVNIFK	1.112451779	1	2.08794
P04642	QVVDSAYEVIK	1.168226448	2	3.11902
P04642	RVHPISTMIK	1.029299894	2	2.37254
P04642	SADTLWGIQK	1.13594217	2	3.94079
P04642	SLNPQLGTDADK	1.046452566	2	2.67487
P04642	SLNPQLGTDADKEQWK	1.117503921	2	4.84054
P04642	SLNPQLGTDADKEQWKDVHK	1.185160528	2	4.68056
P04642	VTLTPDEEAR	1.111305738	2	2.92852
P04644	**RS17 40S ribosomal protein S17**	**1.118232736**	**0.319967**	**4**
P04644	DNYVPEVSALDQEIIEVDPDTK	1.127318597	2	4.33567
P04644	LGNDFHTNK	1.131695788	2	2.92388
P04644	LLDFGSLSNLQVTQPTVGMNFK	1.238951528	2	4.11985
P04644	VCEEIAIIPSK	1.065763074	2	3.11422
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.366284916**	**0.987756**	**10**
P04692	AISEELDHALNDMTSI	2.53392642	2	2.62786
P04692	AQKDEEKMEIQEIQLK	0.983120866	2	3.85121
P04692	GTEDELDKYSEALK	1.059887502	2	2.30806
P04692	KLVIIESDLER	1.438893648	2	3.65358
P04692	LDKENALDR	0.950975587	2	2.38913
P04692	LKGTEDELDK	1.85086703	2	2.62147
P04692	LVIIESDLER	1.426628438	2	3.23372
P04692	MEIQEIQLK	1.049842476	2	2.8502
P04692	QLEDELVSLQK	2.061745395	2	2.48718
P04692	SIDDLEDELYAQK	3.093717782	2	3.7025
P04694	**ATTY Tyrosine aminotransferase**	**1.132647915**	**0.752136**	**2**
P04762	**CATA Catalase**	**0.974430306**	**9.9E-20**	**30**
P04762	DAMLFPSFIHSQK	0.928431996	2	2.3545
P04762	DAQLFIQR	1.003262807	2	3.08925
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	1.132920125	4	5.1708
P04762	DYPLIPVGK	0.963993426	1	2.52997
P04762	EAETFPFNPFDLTK	1.184017505	2	4.34902
P04762	FNSANEDNVTQVR	0.899260739	2	4.70977
P04762	FSTVAGESGSADTVR	0.94969414	2	5.1901
P04762	FSTVAGESGSADTVRDPR	0.93918022	2	2.96696
P04762	FYTEDGNWDLVGNNTPIFFIR	1.917539817	3	6.2746
P04762	GAGAFGYFEVTHDITR	1.036650073	2	5.11822
P04762	GPLLVQDVVFTDEMAHFDR	1.606374914	2	5.71143
P04762	HMNGYGSHTFK	0.941324298	3	4.20013
P04762	HMNGYGSHTFK+Oxidation(2)	1.126275373	2	2.76323
P04762	LAQEDPDYGLR	1.20942667	2	2.6399
P04762	LCENIANHLK	1.126024911	3	4.0514
P04762	LFAYPDTHR	1.282347991	2	2.87643
P04762	LGPNYLQIPVNCPYR	1.232832747	2	4.39548
P04762	LNIMTAGPR	1.094999347	2	3.16048
P04762	LVNANGEAVYCK	1.254724819	2	4.05068

P04762	NAIHTYVQAGSHIAAK	1.015021682	2	5.33796
P04762	NFTDVHPDYGAR	0.945867364	2	4.08325
P04762	NLPVEEAGR	0.953218416	2	2.38316
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	1.774642415	3	6.38897
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK+Oxidation(19)	1.564012586	3	3.91779
P04762	RFNSANEDNVTQVR	0.978139512	2	5.18095
P04762	VFEHIGK	0.966757615	2	2.44354
P04762	VFEHIGKR	0.805903609	2	2.39118
P04762	VLNEEER	1.0257644	2	2.86369
P04762	VQALLDQYNSQKPK	0.98591059	2	5.12044
P04762	VWPHKDYPLIPVGK	1.014954549	2	3.8528
P04764	**ENOA Alpha_enolase**	**1.112265578**	**8.56E-11**	**17**
P04764	AGYTDQVVIGMDVAASEFYR	1.181663693	2	5.54611
P04764	DATNVGDEGGFAPNILENK	1.190026027	2	5.44258
P04764	DYPVVSIEDPFDQDDWDAWQK	1.170242555	2	4.74107
P04764	FTATAGIQVVGDDLTVTNPK	1.252641966	2	5.17542
P04764	GNPTVEVDLYTAK	1.521784345	2	4.05858
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.2702819	3	6.57123
P04764	IDQLMIEMDGTENK	1.139021417	2	4.64171
P04764	IEEELGSK	1.168223574	2	2.4
P04764	IGAEVYHNLK	1.978295618	2	3.32185
P04764	KLNVVEQEK	1.049824478	2	2.35383
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.23618464	3	6.04055
P04764	LNVVEQEK	1.136675937	2	2.7331
P04764	LNVVEQEKIDQLMIEMDGTENK	0.990851792	3	4.59626
P04764	SCNCLLLK	1.306540152	2	3.05788
P04764	SFIKDYPVVSIEDPFDQDDWDAWQK	1.187248484	3	4.35412
P04764	VNQIGSVTESLQACK	1.149277108	2	5.18293
P04764	YITPDQLADLYK	1.164474496	2	3.31954
P04785	**PDIA1 Protein disulfide_isomerase**	**1.190832153**	**2.01E-08**	**24**
P04785	DHENIVIAK	1.031048413	2	2.91656
P04785	HNQLPLVIEFTEQTAPK	1.141242876	2	5.61345
P04785	IKPHLMSQELPEDWDKQPVK	1.362376379	4	5.60349
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(6)	1.647378171	3	3.87365
P04785	ILEFFGLK	1.387022093	2	3.14433
P04785	ILFIFIDSDHTDNQR	1.055307068	2	3.84045
P04785	ITQFCHHFLEGK	0.991107694	2	3.08999
P04785	LGETYKDHENIVIAK	1.087416622	3	5.08227
P04785	LITLEEEMTK	1.083787584	2	3.71076
P04785	LKAEGSEIR	1.212310926	2	2.4265
P04785	LLDFIK	1.18766573	2	2.41324
P04785	MDSTANEVEAVK	1.012030241	2	4.23443
P04785	MDSTANEVEAVK+Oxidation(1)	1.131186527	2	3.73089
P04785	NFEEVAFDEK	1.090830757	2	3.20094
P04785	NFEEVAFDEKK	1.127394311	2	4.04738
P04785	NNFEGEITK	1.087882074	2	2.55672
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.201222385	3	6.29355
P04785	SVSDYDGK	1.138198033	1	2.25965
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.010033172	3	6.73323
P04785	THILLFLPK	0.82304329	2	2.9829
P04785	TVIDYNGER	1.155422178	2	2.66857
P04785	VDATEESDLAQQYGVR	1.075579396	2	5.42969
P04785	YKPESDELTAEK	1.087258405	3	4.45352
P04785	YQLDKDGVVLFK	1.068974122	2	3.83921
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.442047286**	**9.9E-20**	**13**
P04797	GAAQNIIPASTGAAK	1.309430564	2	4.13877

P04797	IVSNASCTTNCLAPLAK	1.418137602	2	4.96508
P04797	LISWYDNEYGYSNR	2.221039739	2	4.33705
P04797	LVINGKPITIFQER	1.438850489	3	3.5696
P04797	RVIISAPSADAPMFVMGVNHEK	1.158416401	3	5.46903
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.245552219	3	7.70527
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(13)	1.547360528	4	4.66488
P04797	VIISAPSADAPMFVMGVNHEK	1.204360087	2	4.29491
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(12)	1.414461085	2	3.85012
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(15)	1.414461085	2	3.52447
P04797	VPTPNVSVVDLTCR	1.235124258	2	2.60855
P04797	VVDLMAYMASK	3.433572018	2	4.43379
P04797	WGDAGAEYVVESTGVFTTMEK	1.422723184	2	5.23757
P04799	**CP1A2 Cytochrome P450 1A2**	**1.094187767**	**0.019639**	**6**
P04799	DFVENVTSGNAVDFFPVLR	1.018016922	2	3.21748
P04799	FLTNDNTAIDK	1.148851107	2	3.06793
P04799	IGSTPVVVLSGLNTIK	2.097141447	2	2.41735
P04799	NSIQDITGALFK	0.996241155	2	3.12713
P04799	SMTFNPDSGPVWAAR	1.631931885	2	3.31002
P04799	TVQEHYQDFNK	1.0938811	2	3.42642
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.741838096**	**9.9E-20**	**10**
P04903	DGNLMFDQVPMVEIDGMK	0.68974409	2	4.88465
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(11)	0.768644682	2	4.61167
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(17)	0.760610232	2	3.44534
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(5)	0.77639773	2	4.23336
P04903	KDGNLMFDQVPMVEIDGMK	0.707982859	2	4.92166
P04903	LIQSPEDLEK	1.326901321	2	3.06853
P04903	LKKDGNLMFDQVPMVEIDGMK	1.512811991	2	3.18791
P04903	WLLAAAGVEFEEK	1.025950692	2	4.38871
P04903	YDLYGK	0.677792925	1	2.01027
P04903	YLPAFEK	0.682785147	1	2.03891
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**1.197573778**	**9.99E-16**	**8**
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	1.628211863	4	6.98789
P04904	LRNDGSLMFQQVPMVEIDGMK	1.491581511	2	4.66516
P04904	NDGSLMFQQVPMVEIDGMK	1.23258754	2	5.37416
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(12)	1.144775313	2	4.44113
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(18)	1.141817074	2	4.10636
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(6)	1.144452478	2	4.02234
P04904	SHGQDYLVGNR	0.873852945	2	3.92286
P04904	WLLAAAGVEFEEQFLK	1.272722784	2	6.15348
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**0.813179341**	**1.52E-05**	**15**
P04905	ADIVENQVMDNR	0.945380144	2	4.18138
P04905	ADIVENQVMDNR+Oxidation(9)	1.044505122	2	3.73887
P04905	CLDAFPNLKDFLAR	1.066248388	2	3.24973
P04905	FKLGLDFPNLPYLIDGSR	1.115894994	2	4.55341
P04905	HHLCGETEEER	1.136226113	3	3.78284
P04905	IRADIVENQVMDNR	1.145544567	2	3.98237
P04905	ITQSNAIMR	1.080841802	2	3.10697
P04905	ITQSNAIMR+Oxidation(8)	1.237876392	2	2.83082
P04905	KHHLCGETEEER	0.815038571	3	4.45783
P04905	KITQSNAIMR	0.940697104	3	3.82731
P04905	KITQSNAIMR+Oxidation(9)	1.011887542	3	3.4476
P04905	LGLDFPNLPYLIDGSR	1.127211868	2	4.74617
P04905	MQLIMLCYNPDFEK	1.84347163	2	4.40887
P04905	VTYVDFLAYDILDQYHIFEPK	7.55167032	3	3.63315
P04905	YLSTPIFSK	1.028524752	2	2.59889
P04906	**GSTP1 Glutathione S_transferase P**	**0.981497795**	**0.995216**	**2**
P04906	EAALVDMVNDGVEDLR	0.985662122	2	4.65612

P04906	STCLYGQLPK	0.990731007	1	1.92194
P04937	**FINC Fibronectin**	**1.121359262**	**0.827198**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	1.124493186	2	4.75677
P04937	SSPVVIDASTAIDAPSNLR	1.134231385	2	4.49476
P04937	SYTITGLQPGTDYK	0.897654784	2	2.57777
P04937	VVTPLSPPTNLHLEANPDTGVLTVSWER	1.16790544	3	4.16289
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.048357394**	**0.914228**	**8**
P05065	ALANSLACQGK	1.310248896	2	2.44216
P05065	FSNEEIAMATVTALR	1.471199407	2	3.89658
P05065	FSNEEIAMATVTALRR	0.771986703	2	2.38743
P05065	GILAADESTGSIAK	1.138001572	2	3.96917
P05065	GVVPLAGTNGETTTQGLDGLSER	1.433699622	2	5.52687
P05065	IGEHTPSSLAIMENANVLAR	0.833430783	2	4.82098
P05065	LQSIGTENTEENR	0.703812414	2	3.61236
P05065	RLQSIGTENTEENR	1.268913376	2	2.78457
P05178	**CP2C6 Cytochrome P450 2C6**	**0.775797436**	**6.4E-07**	**8**
P05178	EALIDHGEEFAER	0.779754675	2	2.9718
P05178	FDYKDQDFLNLMEK	0.913751924	3	4.92489
P05178	FIDLIPTNLPHAVTCDIK	0.646456164	2	3.99672
P05178	GTTIITSLSSVLHDSK	0.713283308	2	3.67573
P05178	GTTIITSLSSVLHDSKEFPDPEIFDPGHFLDGNGK	0.355057485	4	4.7788
P05178	MCAGEGLAR	0.698374928	2	2.61582
P05178	NITQSLTSFSK	0.721685296	2	3.07943
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	1.519181973	2	2.54662
P05179	**CP2C7 Cytochrome P450 2C7**	**2.053227957**	**1.11E-16**	**8**
P05179	ACVGEGLAR	2.051785252	2	3.0197
P05179	FINFVPTNLPHAVTCDIK	3.234510989	3	3.53319
P05179	HMPYTDAMIHEVQR	2.114077691	2	4.15509
P05179	IEEHQESLDVTNPR	2.407054825	2	4.84871
P05179	KIEEHQESLDVTNPR	3.143809333	2	4.98047
P05179	KLPPGPTPLPIIGNFLQIDVK	3.378903293	3	5.9842
P05179	TYGPVFTLYLGSQPTVILHGYEAIK	2.760659229	3	3.44446
P05179	VLTSLTSVLHDSK	4.341975384	2	3.40421
P05182	**CP2E1 Cytochrome P450 2E1**	**0.904475732**	**0.832559**	**12**
P05182	AKEHLQSLDINCAR	1.03289419	2	4.48989
P05182	DIDLSPVTVGFGSIPPQFK	0.859816551	2	3.34056
P05182	DTVFQGYVIPK	1.55907574	2	2.35703
P05182	DVTDCLLIEMEKEK	1.015543416	2	3.29563
P05182	EHLQSLDINCAR	1.145600512	2	2.48395
P05182	FGPVFTLHLGSR	1.04411169	2	2.50973
P05182	FINLVPSNLPHEATR	1.008430456	2	3.88068
P05182	FKPEHFLNENGK	1.140229568	2	3.24539
P05182	FSLSILR	1.041921419	2	2.38702
P05182	GTVVIPTLDSLLYDSHEFPDPEK	1.067482204	2	4.70707
P05182	LDMPYMDAVVHEIQR	1.244780817	2	3.1218
P05182	YGLLILMK	0.895505284	2	3.16124
P05183	**CP3A2 Cytochrome P450 3A2**	**1.032902139**	**0.665769**	**12**
P05183	DIELDGLFIPK	0.931925592	2	3.56375
P05183	EMFPIIEQYGDILVK	1.176492396	2	3.76385
P05183	KDIELDGLFIPK	0.919091829	3	3.73984
P05183	KLQEEIDGALPSK	1.004440207	2	3.57044
P05183	LKEMFPIIEQYGDILVK	1.22278288	2	3.26608
P05183	LQEEIDGALPSK	1.061035658	2	4.09485
P05183	QAILEPEKPIVLK	0.883623221	2	3.29447
P05183	QEAETGKPVTMK	0.740144422	2	3.42799
P05183	QEAETGKPVTMK+Oxidation(11)	1.320694517	2	3.18337
P05183	VDFLQLMLNAHNNSK	0.950079224	2	4.09449

P05183	VDFLQLMLNAHNNSKDEVSHK	1.029713777	3	3.49189
P05183	YLKQEAETGKPVTMK	1.208068131	2	3.78929
P05197	**EF2 Elongation factor 2**	**1.244156579**	**9.9E-20**	**27**
P05197	ALLELQLEPEELYQTFQR	1.597304764	2	5.2837
P05197	ARPFPDGLAEDIDKGEVSAR	1.192425142	3	5.69104
P05197	AYLPVNESFGFTADLR	1.108455217	2	4.52151
P05197	CELLYEGPPDDEAAMGIK	1.765460288	2	4.25247
P05197	CLYASVLTAQPR	1.455664899	2	2.6169
P05197	DLEEDHACIPIKK	1.047489969	2	3.38523
P05197	EGIPALDNFLDKL	1.669894953	2	3.43691
P05197	ETVSEESNVLCLSK	1.180839795	2	4.32698
P05197	GEGQLGAAER	1.163490744	2	3.65948
P05197	GHVFEESQVAGTPMFVVK	1.119954508	2	6.09164
P05197	IWCFGPDGTGPNILTDITK	1.585940504	2	5.13238
P05197	KIWCFGPDGTGPNILTDITK	1.194728996	2	4.75246
P05197	KVEDMMK+Oxidation(5)Oxidation(6)	1.282806591	2	2.31008
P05197	KVEDMMK+Oxidation(6)	1.255073541	2	2.39029
P05197	LDSEDKDKEGKPLLK	1.157507319	3	3.96853
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	1.277904858	3	5.06686
P05197	NMSVIAHVDHGK	1.06243128	2	3.8751
P05197	NMSVIAHVDHGK+Oxidation(2)	1.249813305	2	3.52429
P05197	STLTDSLVCK	1.144528644	2	3.12681
P05197	TFCQLILDPIFK	1.438083525	2	4.19781
P05197	TGTITTFEHAHNMR	1.071926902	2	3.98463
P05197	VFDAIMNFR	1.444202336	2	2.68276
P05197	VFSGVVSTGLK	1.242697949	2	2.99687
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.035829345	3	3.56221
P05197	YEWDVAEAR	1.113572739	2	2.97706
P05197	YFDPANGK	1.232662457	1	2.04613
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.439323839	3	5.75766
P05369	**FPPS Farnesyl pyrophosphate synthase**	**0.92231133**	**0.999992**	**11**
P05369	ALYEELDLR	1.001153681	2	3.11064
P05369	EVLEYNTVGGK	1.49565723	2	3.00225
P05369	GLTVVQTFQELVEPR	0.979914795	2	4
P05369	IKEVLEYNTVGGK	1.002993537	2	4.47266
P05369	QILEENYGQK	0.729880199	2	2.42217
P05369	QILEENYGQKDPEK	0.832199926	2	3.62431
P05369	QNFIQHFSQIVK	1.077531776	2	2.48319
P05369	SLIEQCSAPLPPSIFLELANK	0.835956747	2	5.19918
P05369	VGTDIQDNK	0.812442172	2	3.76754
P05369	VLTEDELGHPEK	0.759768655	2	2.52155
P05369	VLTEDELGHPEKGDAITR	0.795395391	2	4.73789
P05426	**RL7 60S ribosomal protein L7**	**1.286657149**	**8.65E-09**	**6**
P05426	AGNFYVPAEPK	1.21975564	2	2.9899
P05426	FGIICMEDLIHEIYTVGK	1.336675019	3	4.35268
P05426	IVEPYIAWGYPNLK	1.820641611	2	3.63153
P05426	KKVPAVPETLK	0.92095805	2	3.00032
P05426	TTHFVEGGDAGNR	1.042683598	2	2.74841
P05426	TTHFVEGGDAGNREDQINR	1.249574154	2	4.43541
P05544	**SPA3L Serine protease inhibitor A3L**	**1.361157042**	**0.000186**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	1.365427341	2	2.81076
P05544	DSTMEEILEGLK	1.334599692	2	2.88743
P05544	IAELFSDLEER	1.518022997	2	2.55349
P05544	MQQVESSLQPETLK	1.223550851	2	4.15357
P05544	MQQVESSLQPETLKK	1.306742921	2	3.3047
P05544	VFSQQADLSR	1.858792942	2	2.93313
P05545	**SPA3K Serine protease inhibitor A3K**	**1.69892585**	**0.000361**	**5**

P05545	AVLDVDETGTEGAAATAVTAALK	1.189058102	2	6.17477
P05545	FSISTDYNLEEVLPELGIR	1.193467019	2	3.91086
P05545	IAELFSELDER	1.224807077	2	3.01314
P05545	IFSQQADLSR	1.814460561	2	2.48122
P05545	NLHVSQVVHK	1.398884401	2	2.61949
P05765	**RS21 40S ribosomal protein S21**	**1.129985056**	**0.882488**	**3**
P05765	DHASIQMNVAEVDR	1.00868828	2	3.68728
P05765	MGESDDSILR	1.061019955	2	3.0099
P05765	TYGICGAIR	1.136159579	2	2.44031
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.967142954**	**0.443014**	**9**
P06214	AGADIIITYFAPQLLK	2.086275171	2	4.47023
P06214	AGAFDLR	0.935311659	2	2.57732
P06214	AGCQVVAPSDMMDGR	0.967155328	2	3.91226
P06214	CVLIFGVPSR	0.953149101	2	2.48259
P06214	DEQGSAADSEDSPTIEAVR	0.708644646	2	5.91718
P06214	DIQEGADILMVKPGLPYLDMVQEVK	1.0547132	2	3.90059
P06214	TAVLESMTAFR	0.931182314	2	3.21358
P06214	VPKDEQGSAADSEDSPTIEAVR	0.827006622	2	5.98397
P06214	YGVNQLEEMLRPLVEAGLR	0.883622213	3	4.29485
P06302	**PTMA Prothymosin alpha**	**1.427571584**	**6.66E-15**	**3**
P06302	RVAEDDEDDDVETKK	1.436640912	3	5.83299
P06302	VAEDDEDDDVETK	1.216427815	2	4.31676
P06302	VAEDDEDDDVETKK	1.383970818	2	4.58151
P06399	**FIBA Fibrinogen alpha chain**	**1.047766215**	**0.993504**	**9**
P06399	AQQIQVLQK	0.88149784	1	2.08349
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.939229903	3	4.41502
P06399	GDFANANNFDNTFGQVSEDLR	1.143096403	2	4.9979
P06399	GDFANANNFDNTFGQVSEDLRR	1.043216368	3	3.41493
P06399	GDKELLIGNEK	0.91000343	2	2.77591
P06399	GLIDEANQDFTNR	0.935050617	2	3.0309
P06399	MADEAASEAHQEGDTR	0.804880775	2	3.84673
P06399	SQLQEGPPEWK	1.334323449	2	2.9083
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	0.973164698	3	3.48072
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**0.888826487**	**0.182864**	**6**
P06685	AVAGDASESALLK	0.961060306	2	3.6304
P06685	AVFQANQENLPILK	1.188670568	2	2.68111
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.336171539	3	3.35173
P06685	LNIPVNQVNPR	1.158340243	2	3.13796
P06685	MSINAEDVVVGDLVEVK	0.708702534	2	3.51073
P06685	YEPAAVSEHGDKK	0.812458057	2	3.36373
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.042605025**	**1**	**3**
P06687	DGPNALTPPPTTPEWVK	1.032910077	2	2.97099
P06687	GVGIISEGNETVEDIAAR	1.064075195	2	4.4671
P06687	QGAIVAVTGDGVNDSPALK	1.050338803	2	5.04536
P06757	**ADH1 Alcohol dehydrogenase 1**	**0.703205225**	**0.651316**	**19**
P06757	AAVLWEPHKPFTIEDIEVAPPK	0.877184121	3	5.60937
P06757	FPLEPLITHVLPFEK	0.955878452	3	4.68245
P06757	GAIFGGFK	0.843944319	2	2.69598
P06757	GALLDGTSR	0.921062183	2	2.7968
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.932001859	3	5.40372
P06757	HPESNLCCQTK	0.879831355	2	3.24434
P06757	ICKHPESNLCCQTK	0.631638957	3	3.88414
P06757	IDAAAPLDK	0.843167401	2	2.9743
P06757	IDAAAPLDKVCLIGCGFSTGYGSAVQVAK	0.839756721	3	3.31762
P06757	IIAVDINKDK	0.888748962	2	2.89638

P06757	INEAFDLLR	0.893019986	2	3.71134
P06757	KFPLEPLITHVLPFEK	0.800394025	3	4.52611
P06757	LVADFMAK	0.997706522	2	2.40362
P06757	MVATGVCR	0.895740704	2	2.60799
P06757	MVATGVCR+Oxidation(1)	0.96021776	2	2.52663
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	0.964251595	4	7.90093
P06757	VCLIGCGFSTGYGSAVQVAK	0.863443574	2	6.47761
P06757	VIPLFSPQCGK	0.950908432	2	2.5981
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	0.723709239	3	5.26164
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.257946493**	**9.9E-20**	**28**
P06761	AKFEELNMDLFR	1.222036697	3	4.63941
P06761	DAGTIAGLNVMR	1.062624353	2	3.32872
P06761	DNHLLGTFDLTGIPPAPR	0.804628158	2	4.77969
P06761	ELEEIVQPIISK	1.094681661	2	4.04532
P06761	FEELNMDLFR	1.071348644	2	3.53864
P06761	IEIESFFEGEDFSETLTR	1.048023569	2	5.73044
P06761	IEWLESHQDADIEDFK	1.155459255	2	5.68103
P06761	IEWLESHQDADIEDFKAK	1.060922974	3	4.597
P06761	IINEPTAAAIAYGLDKR	1.087203261	2	4.42889
P06761	ITITNDQNR	1.214202815	2	2.67602
P06761	ITPSYVAFTPEGER	1.260880316	2	4.056
P06761	KKELEEIVQPIISK	1.120378627	2	5.42359
P06761	KSDIDEIVLVGGSTR	1.177142876	2	5.16769
P06761	KSQIFSTASDNQPTVTIK	1.385579972	2	5.32825
P06761	LYGSGGPPPTGEEDTSEKDEL	1.461442961	2	5.49744
P06761	MKETAEAYLGK	0.979700221	2	3.37592
P06761	MKETAEAYLGK+Oxidation(1)	1.022690026	2	2.93121
P06761	NELESYAYSLK	1.542937735	2	3.59103
P06761	NQLTSNPENTVFDAK	1.035711083	2	5.28985
P06761	SDIDEIVLVGGSTR	1.091728471	2	3.45071
P06761	SQIFSTASDNQPTVTIK	1.17394791	2	5.44658
P06761	TFAPEEISAMVLTK	1.126422748	2	4.75674
P06761	TKPYIQVDIGGGQTK	1.176770253	2	4.35147
P06761	TWNDPSVQQDIK	1.088908914	2	4.16569
P06761	VLEDSDLK	1.09370678	2	2.34691
P06761	VLEDSDLKK	1.128872882	2	2.45508
P06761	VTHAVVTVPAYFNDAQR	1.359317584	2	5.04996
P06761	VYEGERPLTK	1.058000492	2	2.90831
P06766	**DPOLB DNA polymerase beta**	**1.308844857**	**0.066424**	**2**
P06766	EEMLQMQDIVLNEVKK+Oxidation(6)	1.311700401	2	2.32777
P06766	QDDTSSSINFLTR	0.876027387	2	2.39808
P06866	**HPT Haptoglobin**	**1.031898633**	**0.869259**	**6**
P06866	ATDLKDWVQETMAK	1.058909854	2	2.70925
P06866	GAVSPVGVQPILNK	1.109250437	2	3.59388
P06866	LQTEGDGIYTLNSEK	1.187545502	2	4.37835
P06866	NQLVEIEK	1.143838795	1	2.25103
P06866	SVVDIGLIK	1.1079143	1	1.92094
P06866	YVMLPVADQEK	0.842687014	2	2.59646
P07150	**ANXA1 Annexin A1**	**1.732682695**	**1.28E-05**	**2**
P07150	GGPGSAVSPYPSFNPSSDVAALHK	1.546827496	3	3.94074
P07150	GLGTDEDTLIEILTTR	1.814066214	2	4.49953
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.050928711**	**2.31E-12**	**14**
P07153	ASSFVLALEPELESR	1.426416563	2	3.95918
P07153	AVTSEIAVLQSR	1.335049992	2	3.69425
P07153	FVDHVFDEQVIDSLTVK	1.1711137	2	4.49552

P07153	GEDEEDNNLEVR	1.062303047	2	3.77747
P07153	HFDETVNR	1.045468012	2	2.79006
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.062368216	3	4.67397
P07153	LKTEGSDLCDR	1.269092662	2	2.95955
P07153	NIQVDSPYDISR	1.214074125	2	3.65396
P07153	NLVEQHIQDIVVHYTFNK	1.372443535	3	4.46588
P07153	SEDILDYGPFK	1.051315406	2	3.62312
P07153	TEGSDLCDR	1.010913183	2	2.41408
P07153	TVDLSSHLAK	1.171356174	2	2.40982
P07153	VHYENNSPFLTITSMTR	1.529700386	2	3.34127
P07153	VTAEVVLAHPGGGSTAR	1.1120882	2	4.48087
P07323	**ENOG Gamma_enolase**	**1.323222568**	**0.081912**	**4**
P07323	AAVPSGASTGIYEALELR	1.35290335	2	5.22353
P07323	FGANAILGVSLAVCK	0.986078299	2	3.77125
P07323	GNPTVEVDLHTAK	1.065440437	2	2.95232
P07323	SGETEDTFIADLVVGLCTGQIK	1.190377286	2	4.97772
P07335	**KCRB Creatine kinase B_type**	**1.104718455**	**0.525342**	**3**
P07335	FCTGLTQIETLFK	1.256070631	2	3.01651
P07335	LGFSEVELVQMVVDGVK	1.104528666	2	2.68243
P07335	TDLNPDNLQGGDDLDPNYVLSSR	0.839535766	2	2.89053
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**0.848075054**	**0.517306**	**3**
P07340	AYGENIGYSEK	1.002270567	2	2.53259
P07340	VAPPGLTQIPQIQK	0.913326746	2	2.69217
P07340	YNPNVLPVQCTGK	0.806774955	2	2.48489
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.085228021**	**3.23E-05**	**12**
P07379	AINPENGFFGVAPGTSVK	1.292083794	2	4.27741
P07379	EEGWLAEHMLILGITNPEGK	1.253258589	3	3.77389
P07379	FLWPGFGENSR	1.223478411	2	2.5467
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	1.083392008	3	4.27469
P07379	GLGDVNVEELFGISK	1.599785303	2	3.70542
P07379	IGIELTDSPYVVASMR	1.447187995	2	4.205
P07379	MGTSVLEALGDGEFIK	1.344887339	2	3.86516
P07379	TVIITQEQR	1.279052581	1	1.91313
P07379	VECVGDDIAWMK	1.20842313	2	3.51016
P07379	VIQGSLDSLPQEVR	1.534924349	2	3.71121
P07379	YLAAAFPSACGK	1.081642761	2	2.9414
P07379	YLEDQVNADLPYEIER	1.03931527	2	4.78999
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.046117789**	**0.495738**	**5**
P07632	DGVANVSIEDR	0.912210274	2	2.83056
P07632	GDGPVQGVIHFEQK	1.03448115	2	3.88724
P07632	HVGDLGNVAAGK	1.039290933	2	3.98021
P07632	QDDLGKGGNEESTK	1.666703973	2	3.61191
P07632	VISLSGEHSIIGR	1.071141628	2	3.12157
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.923696325**	**0.413826**	**10**
P07633	AFDNDVDALCNLR	1.049548964	2	3.6481
P07633	AYNMLDIIHAVIDER	1.05977444	2	4.19116
P07633	GFVDDIIQPSSTR	0.933208673	2	3.09149
P07633	HLLGDTNYAWPTAEIAVMGAK	0.784302866	2	5.72322
P07633	ICCDLEVLASK	1.107045993	2	3.53913
P07633	IMDQAITVGAPVIGLNDSGGAR	1.028245795	2	5.03862
P07633	IQEGVESLAGYADIFLR	0.854833661	2	4.42356
P07633	LVPELDTVVPLESSK	0.844145082	2	3.57366
P07633	SVTNEDVTQEQLGGAK	0.85955901	2	5.23346
P07633	TVGIVGNQPNVASGCLDINSSVK	0.929927159	2	5.04974

P07687	**HYEP Epoxide hydrolase 1**	**1.181975341**	**1.28E-13**	**25**
P07687	DIELLYPYK	0.987171507	2	3.03296
P07687	DKEETLPLGDGWWGPGSKPSAK	1.281094131	3	4.93078
P07687	EDESIRPFK	1.036909135	2	2.7139
P07687	EDESIRPFKVETSDEEIKDLHQR	1.068459131	3	6.37014
P07687	ENLGQGIMVHK	1.025697875	2	2.96174
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.673291984	3	6.12823
P07687	FHYGFNSNYMK	0.942732605	2	2.65489
P07687	FLGYTEKDIELLYPYK	1.22119846	2	4.86715
P07687	FVSLAELQ	1.12109885	2	2.45544
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.28489906	3	4.07029
P07687	GGHFAAFEEPK	0.973645684	2	3.32515
P07687	GLHLNMAFISR	1.182081635	2	2.88135
P07687	GLNSVATAR	1.019844696	2	2.45427
P07687	IEGLDIHFIHVKPPQLPSGR	1.725057152	3	4.30951
P07687	IIPLLTDPK	1.203909054	1	1.97014
P07687	KFVSLAELQ	1.308100151	2	2.44891
P07687	KQVEILNQYPHFK	1.099760936	3	5.45283
P07687	LLAQDIR	1.283798581	2	2.43886
P07687	QVEILNQYPHFK	1.156424484	2	3.5567
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.075057583	3	6.29373
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSKK	1.153341161	3	5.16756
P07687	TKIEGLDIHFIHVKPPQLPSGR	1.243058102	3	4.19964
P07687	VETSDEEIK	0.996514524	2	2.4884
P07687	VETSDEEIKDLHQR	1.038547186	2	4.86286
P07687	VFVPTGFSAFPSELLHAPEK	1.577085332	2	5.12231
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**0.99428984**	**9.9E-20**	**98**
P07756	AADTIGYPVMIR	1.003427206	2	3.93268
P07756	AADTIGYPVMIR+Oxidation(10)	1.201864388	2	3.36531
P07756	AERPDGLILGMGGQTALNCGVELFK	1.002001164	3	6.72636
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(11)	0.85250502	3	6.18484
P07756	AFAISGPFNVQFLVK	0.799499755	2	5.02126
P07756	AFAMTNQILVER	1.040251164	2	4.37868
P07756	AFAMTNQILVER+Oxidation(4)	1.066744252	2	3.79376
P07756	ALENNMSLDEIVK	0.969163652	2	4.75844
P07756	ALENNMSLDEIVK+Oxidation(6)	1.064158329	2	3.96259
P07756	AMLSTGFK	0.896852357	2	2.53151
P07756	AQTAHIVLEDGTK	0.730440287	2	4.47667
P07756	ATGYPLAFIAAK	1.365475777	2	3.10471
P07756	CEMASTGEVACFGEGIHTAFLK	0.921560693	3	4.78442
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(3)	0.987592806	3	4.70272
P07756	CLGLTEAQTR	1.009919531	2	3.60478
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	1.097410393	3	6.44616
P07756	DELGLNK	1.051901204	1	2.24374
P07756	DGSIDLVINLPNNNTK	0.887675101	2	5.5392
P07756	DILNMDK	0.902143629	1	1.9277
P07756	EIEYEVVR	0.995586504	1	2.06334
P07756	EPLFGISTGNIITGLAAGAK	1.07594382	2	5.32425
P07756	ETLMDLGTK	0.949154037	1	2.35909
P07756	EVEMDAVGK	0.658062688	1	2.22284
P07756	FLEEATR	0.985296659	2	2.47715
P07756	FLGVAEQLHNEGFK	1.022327482	2	4.88484
P07756	FVHDNYVIR	1.146661811	3	3.52994
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.049886794	3	6.11426

P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(16)	1.078450941	3	5.7507
P07756	GILIGIQQSFRPR	0.903802488	2	2.47721
P07756	GLNSESVTEETLR	0.960834866	2	4.86832
P07756	GNDVLVIECNLR	1.02931232	2	4.34951
P07756	GQILTMANPIIGNGGAPDTTAR	0.874616018	2	6.45638
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(6)	0.858213908	2	4.89327
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.880672019	3	4.84355
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(6)	0.836310688	3	3.43243
P07756	GQNQPVLNITNR	0.955486493	2	4.3
P07756	GTTITSVLPKPALVASR	0.869665449	2	3.65169
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.47585438	3	6.45143
P07756	HLGIVGECNIQFALHPTSMEYCIIEVNAR	1.083978848	3	4.84957
P07756	HLPTLEQPIIPSDYVAIK	1.006101578	2	5.15389
P07756	IALGIPLPEIK	1.187386188	2	2.97526
P07756	IAPSFAVESMEDALK	1.299032886	2	5.28411
P07756	IAPSFAVESMEDALK+Oxidation(10)	1.224024995	2	3.45537
P07756	IEFEGQSVDFVDPNK	0.934737921	2	5.55707
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	0.965804615	3	5.14901
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.078503554	3	6.07404
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	0.917659952	3	3.78496
P07756	IMGTSPLQIDR	1.492827983	2	3.05486
P07756	IMGTSPLQIDR+Oxidation(2)	1.661117377	2	3.09319
P07756	IMGTSPLQIDRAEDR	0.896341565	2	2.44208
P07756	KELSEPSSTR	0.953259633	2	2.73998
P07756	KEPLFGISTGNIITGLAAGAK	0.880050441	2	5.4687
P07756	KTVVVNCNPETVSTDFDECDK	0.264383409	2	5.12186
P07756	LFAEAVQK	1.000933436	2	3.42457
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.229847932	3	5.12715
P07756	LRDADPILR	1.135226626	3	3.51488
P07756	LTSIDKWFLYK	1.134557889	2	2.48092
P07756	LYFEELSLER	1.842949776	2	3.46032
P07756	MCHPSVDGFTPR	0.937122629	3	5.04831
P07756	MCHPSVDGFTPR+Oxidation(1)	1.053653446	3	4.33157
P07756	MRDILNMDK	0.936923937	2	3.03703
P07756	MRDILNMDK+Oxidation(1)	1.146136654	2	2.7488
P07756	QADAVYFLPITPQFVTEVIK	0.846413929	3	4.41162
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	3.837226156	3	3.35902
P07756	QLFSDKLNEINEK	1.0966031	2	3.85145
P07756	QNLIAEVSTK	1.030400428	1	2.53412
P07756	RFLEEATR	1.093087515	2	2.99433
P07756	RTAVDSGIALLTNFQVTK	1.029765967	2	4.7543
P07756	SAYALGGLGSGICPNK	1.073380777	2	4.95855
P07756	SAYALGGLGSGICPNKETLMDLGTK	0.944460377	3	4.97137
P07756	SFPFVSK	0.985145882	1	1.91606
P07756	SIFSAVLDELK	0.971631852	2	3.92822
P07756	SIFSAVLDELKVAQAPWK	0.683253481	3	3.44439
P07756	SLGQWLQEEK	0.99578817	2	4.18665
P07756	SLGQWLQEEKVPAIYGVDTR	0.942098942	2	3.93729
P07756	SVGEVMAIGR	0.928242534	2	3.59055
P07756	SVGEVMAIGR+Oxidation(6)	0.973191126	2	3.09822
P07756	TAVDSGIALLTNFQVTK	1.16285482	3	6.38665
P07756	TFEESFQK	0.920982573	2	2.54036
P07756	TLGVDFIDVATK	0.967908841	2	4.1811
P07756	TSACFEPSLDYMVTK	0.799677953	2	4.72637
P07756	TSACFEPSLDYMVTK+Oxidation(12)	0.750920714	2	3.56095
P07756	TSINVVR	0.98915405	2	2.43944

P07756	TVLMNPNIASVQTNEVGLK	0.892485507	2	6.62683
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(4)	0.885412697	2	5.9577
P07756	TVVVNCNPETVSTDFDECDK	0.405320464	2	5.62523
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	1.806699496	3	6.00611
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	0.998850567	3	7.59069
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(23)	1.01570932	3	7.04062
P07756	VLGTSVESIMATEDR	1.037047863	2	4.90152
P07756	VLGTSVESIMATEDR+Oxidation(10)	1.109129808	2	4.22199
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.041637179	2	5.81464
P07756	VMIGESVDEK	0.826821475	2	3.56979
P07756	VMIGESVDEK+Oxidation(2)	0.94106722	2	3.00907
P07756	VSQEHPVVLTK	0.9164362	2	3.98256
P07756	VVAVDCGIK	0.929213788	2	2.59215
P07756	YMESDGIK	0.920981201	1	2.14819
P07756	YMESDGIK+Oxidation(2)	1.030056076	1	2.30052
P07824	**ARGI1 Arginase_1**	**1.204737467**	**4.31E-09**	**15**
P07824	ANEQLAAVVAETQK	1.20622791	2	5.35928
P07824	DHGDLAFVDVPNDSPFQIVK	1.306130504	2	6.23971
P07824	DIVYIGLR	0.859080758	2	2.71065
P07824	DVDPGEHYIIK	1.354667514	2	3.29396
P07824	EGNHKPETDYLKPPK	1.235906293	2	2.70798
P07824	GKFPDVPGFSWVTPCISAK	1.354158335	3	4.6574
P07824	LKETEYNVR	1.343817297	3	3.71044
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.18806855	3	4.50948
P07824	TGLLSGLDIMEVNPTLGK	1.392066253	2	5.72696
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(10)	0.779739589	2	2.67137
P07824	TVNTAVALTLSCFGTK	0.989421621	2	4.25559
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.52941877	4	4.62349
P07824	VMEETFSYLLGR	2.502128127	2	3.82766
P07824	YFSMTEVDK	1.384320996	1	2.24889
P07824	YFSMTEVDKLGIGK+Oxidation(4)	1.12206557	2	2.58895
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.887639207**	**0.00445**	**16**
P07871	AEELGLPILGVLR	0.91667472	2	4.41575
P07871	AEIVPVTTTVLDDK	0.857980407	2	4.62577
P07871	AEIVPVTTTVLDDKGDR	0.820423716	2	3.94678
P07871	AEIVPVTTTVLDDKGDRK	0.827464538	2	4.3806
P07871	DCLIPMGITSENVAER	0.846474189	2	3.77188
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.957472249	2	6.22092
P07871	IAQFLSGIPETVPLSAVNR	1.875302153	2	4.10562
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.701684559	3	5.14952
P07871	QCSSGLQAVANIAGGIR	0.896341565	2	4.9075
P07871	QDAFALASQQK	0.862759413	2	3.93966
P07871	QKQDAFALASQQK	0.850644106	2	3.97105
P07871	QVVTLLNELK	1.162155857	2	2.47945
P07871	SKAEELGLPILGVLR	0.828386871	2	4.03905
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.847767405	3	4.82023
P07871	TITVSQDEGVRPSTTMEGLAK	0.90467869	2	4.34834
P07871	VNPLGGAIALGHPLGCTGAR	0.899817558	2	5.2034
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.991616946**	**0.73088**	**20**
P07872	AFTTWTANAGIEECR	0.958755009	2	4.05767
P07872	ASATFNPELITHILDGSPENTR	0.888106769	3	4.57832
P07872	ASEAHCHYVVVK	0.91893664	3	4.01504
P07872	EIENLILNDPDFQHEDYNFLTR	1.55805084	2	4.40059
P07872	EIGTHKPLPGITVGDIGPK	0.958866051	2	4.04599
P07872	EVAWNLTSVDLVR	0.923210174	2	2.8687
P07872	EYGISDPEEIMWFK	1.064373596	2	3.57359

P07872	FGYEEMDNGYLK	0.887312535	2	3.0206
P07872	GGDFLEGSIITGAQLSQVNAR	0.891049157	2	5.99548
P07872	GLETTATYDPK	0.834249586	2	3.50253
P07872	INESIGQGDLSELPELHALTAGLK	0.986592587	3	5.2958
P07872	IYDQVR	0.93048712	1	1.99424
P07872	LVEIAAK	0.923436641	1	2.08026
P07872	NLCLLYSLYGISQK	1.376216272	2	3.24789
P07872	QSEPEPQILDFQTQQYK	1.036867899	2	4.86847
P07872	SFLVGNAAQSLSK	0.925702041	2	3.7684
P07872	SKEVAWNLTSVDLVR	0.872689796	2	3.37664
P07872	TQEFILNSPTVTSIK	0.87176166	2	4.34284
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	0.710951312	4	4.97246
P07872	YDGNVYENLFEWAK	1.422917812	2	5.44157
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.842337858**	**1.02E-09**	**4**
P07895	AIWNVINWENVSQR	1.058589983	2	3.76619
P07895	GDVTTQVALQPALK	0.751379906	2	3.37852
P07895	HHATYVNNLNVTEEK	1.006580957	2	4.733
P07895	NVRPDYLK	0.726666482	2	2.4372
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.920031476**	**0.020074**	**21**
P07896	GGPMFYAASVGLPTVLEK	1.56801815	2	3.98751
P07896	GQGLTGPSLPPGTPVR	0.781246961	2	4.23902
P07896	GWYQYDKPLGR	0.734871902	2	3.07989
P07896	IFNKPVPSLPNMDSVFAEAIAK	1.335848595	3	3.99487
P07896	IGVVVGNCYGFVGNR	1.20085691	2	3.29422
P07896	IIDKPIEPR	0.931610928	2	2.5843
P07896	KGQGLTGPSLPPGTPVR	0.825305823	2	4.66443
P07896	KQYPGVLAPETCVR	0.843854304	2	4.0639
P07896	LCNPPVNAVSPTVIR	1.240996179	2	4.77269
P07896	LGILDAVVK	1.034682041	2	2.91279
P07896	LLEVIPSR	0.937041273	2	2.41053
P07896	QNPDIPQLEPSDYLR	0.827414549	2	3.96344
P07896	QYPGVLAPETCVR	0.833128665	2	2.97039
P07896	TASAQPVSSVGVLGLGTMGR	0.910532158	2	5.14168
P07896	TISKEEILER	0.894502809	2	2.96462
P07896	VGISVVAVESDPK	0.914350684	2	4.19718
P07896	VGLPEVTLGILPGAR	1.002496722	2	3.44504
P07896	VSDLAGLDVGWK	0.902474775	2	4.50071
P07896	YLSADEALR	0.960383655	2	3.11686
P07896	YSPLGDMLCEAGR	0.828381454	2	3.86108
P07896	YSSPTTIATVMSLSK	0.967552365	2	3.23047
P07943	**ALDR Aldose reductase**	**1.481355575**	**0.111881**	**2**
P07943	AIGVSNFNPLQIER	1.100284098	2	3.07544
P07943	HIDCAQVYQNEK	1.481984382	2	3.92855
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.220440273**	**9.9E-20**	**6**
P08009	LCYNPDFEK	1.654565834	1	2.26744
P08009	LLLEYTDSSYEEK	1.163605321	2	4.91758
P08009	LLLEYTDSSYEEKR	1.227899305	2	4.13249
P08009	NQVFEATCLDAFPNLK	0.726858325	2	4.25437
P08009	SQWLNEK	1.044240911	2	2.68484
P08009	YTMGDAPDFDR	0.704924972	2	2.37195
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.083881592**	**9.9E-20**	**14**
P08010	FLSKPIFAK	1.232084934	1	2.19353
P08010	IRVDVLENQAMDTR	1.238469524	3	4.54802
P08010	ITYVDFLVYDVLDQHR	2.452180594	2	5.22445
P08010	KKPEYLEGLPEK	1.005553172	3	4.3409
P08010	KPEYLEGLPEK	0.908000821	2	3.19716
P08010	KYSMGDAPDYDR	1.137906866	2	3.43757

P08010	LFLEYTDTSYEDK	1.167519175	2	5.49056
P08010	LFLEYTDTSYEDKK	1.199771574	2	4.78417
P08010	LQLAMVCYSPDFER	1.603434525	2	4.15587
P08010	LQLAMVCYSPDFER+Oxidation(5)	1.604648508	2	3.64397
P08010	VDVLENQAMDTR	1.020298526	2	4.63296
P08010	VDVLENQAMDTR+Oxidation(9)	1.164967928	2	3.74138
P08010	YSMGDAPDYDR	1.186154711	2	3.54563
P08010	YSMGDAPDYDR+Oxidation(3)	1.517186386	2	2.65854
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**1.282941541**	**0.946611**	**6**
P08011	IYHTIAYLTPLPQPNR	0.873921167	2	5.11389
P08011	MMFLSSATAFQR	1.308873722	2	4.0299
P08011	MMFLSSATAFQR+Oxidation(1)	1.204993385	2	3.09909
P08011	MMFLSSATAFQR+Oxidation(2)	1.216161281	2	3.45806
P08011	VFANPEDCAGFGK	1.050803498	2	4.78926
P08011	VFANPEDCAGFGKGENAK	0.974522323	2	4.78191
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**1.229303934**	**0.592876**	**2**
P08032	ADVVESWIGEK	1.04632376	2	3.0612
P08032	IEDLGDSMEEALILDIK	1.499479668	2	2.49549
P08081	**CLCA Clathrin light chain A**	**1.068869561**	**0.842006**	**2**
P08081	LEALDANSR	1.070550875	2	2.47868
P08081	WREEQTER	1.055585206	2	2.36604
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.34579878**	**0.000809**	**4**
P08461	DVPLGTPLCIIVEK	1.252627779	2	3.87591
P08461	DVPVGSIICITVEKPQDIEAFK	1.01856551	2	3.45957
P08461	GLETIASDVVSLASK	1.224349802	2	4.11202
P08461	VAPTPAGVFIDIPISNIR	1.347475422	2	4.59976
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.016028097**	**0.999998**	**8**
P08503	AFTGFIVEADTPGIHIGK	1.05599226	2	4.24483
P08503	EEIIPVAPDYDK	0.988954181	2	3.55248
P08503	IYQIYEGTAQIQR	1.08506269	2	4.51321
P08503	KGDEYVINGQK	1.037321475	2	4.2261
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	1.762898374	2	4.60365
P08503	QEPGLGFSFELTEQQK	0.829307881	2	3.73421
P08503	SGEYPFPLIK	0.976423067	2	2.6539
P08503	TRPTVAAGAVGLAQR	1.049218537	2	4.21372
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.594482051**	**0.01629**	**10**
P08541	DELQNHFIK	1.326480628	2	2.78999
P08541	FEIFSTSISKDELQNHFIK	1.322068374	3	3.5024
P08541	FILPPSYVPVILSGLAGK	1.239113126	3	5.59
P08541	GHEVTVLKPSAYFFLDPK	2.02509448	3	4.69409
P08541	HKEWDTFYSEILGRPTTVDETMSK	0.840112805	3	4.32695
P08541	LLDVWTYELPR	1.911605497	2	3.64571
P08541	NVMLLSTIHHDQPMKPLDR	1.329451534	2	4.15739
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(3)	1.799198927	3	3.39138
P08541	VEIWLIR	1.189846777	2	2.89277
P08541	VLVWPMDFSHWMNIK	1.285546322	2	3.50561
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.17745292**	**1.74E-08**	**6**
P08542	EIINNPFYK	1.085314537	1	2.21338
P08542	FETFPTSVSKDELENYFIK	1.19553236	2	4.17269
P08542	KWDPFYSEILGRPTTLAETMGK	0.99325708	2	4.49744
P08542	LVDVWTYELQR	1.629741765	2	3.257
P08542	NAVWLSTIHHDQPMKPLDK	1.079135015	3	3.71615
P08542	WDPFYSEILGRPTTLAETMGK	1.459733763	2	4.00836
P08683	**CP2CB Cytochrome P450 2C11**	**1.213745728**	**1.35E-13**	**16**

P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	0.994472445	3	5.47464
P08683	EALVDLGEEFSGR	1.2682406	2	3.62031
P08683	EHQESLDKDNPR	1.291531	2	4.2196
P08683	FDPGHFLDER	1.231081848	2	2.66495
P08683	FDYKDPTFLNLMHR	1.394662291	3	4.90861
P08683	FNENFR	1.050223798	1	2.01842
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.204159888	3	5.43308
P08683	ICAGEALAR	1.15490238	2	2.78252
P08683	LFSSPWLQVCNTFPAIIDYFPGSHNQVLK	1.165275943	3	4.23712
P08683	LPPGPTPLPIIGNTLQIYMK	1.107005169	2	3.81854
P08683	NYVLEK	1.15539448	1	1.93896
P08683	SQMPYTDAVVHEIQR	1.005498061	2	4.65857
P08683	VKEHQESLDKDNPR	1.24250335	3	4.93812
P08683	VQEEIER	1.057434331	2	2.64258
P08683	YGLLLLLK	1.424409074	2	3.45475
P08683	YIDLVPTNLPHLVTR	1.093457463	2	3.55833
P09006	**SPA3N Serine protease inhibitor A3N**	**1.119346359**	**0.773565**	**2**
P09034	**ASSY Argininosuccinate synthase**	**4.095018612**	**9.99E-16**	**14**
P09034	APNTPDVLEIEFK	1.060417952	2	2.77283
P09034	DGTTHSTSLDLFMYLNEVAGK	4.580979682	2	5.0558
P09034	EFVEEFIWPAVQSSALYEDR	1.905078624	2	5.67458
P09034	EQGYDVIAYLANIGQK	2.780531008	3	3.76273
P09034	FAELVYTGFWHSPECEFVR	2.875374126	2	4.37003
P09034	FELTCYSLAPQIK	1.655997839	2	4.23613
P09034	GRNDLMEYAK	1.121095593	2	2.9358
P09034	IDIVENR	0.9857408	2	2.55108
P09034	KVFIEDVSK	1.077154679	2	2.76432
P09034	NDLMEYAK	0.982749854	2	2.66349
P09034	SPWSMDENLMHISYEAGILENPK	1.759567401	3	4.85495
P09034	TQDPAKAPNTPDVLEIEFK	1.02200164	2	4.80145
P09034	TQDPAKAPNTPDVLEIEFKK	0.968091861	3	4.20837
P09034	VFIEDVSK	1.044288535	2	2.58213
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.122658285**	**0.317862**	**5**
P09041	FHVEEEGK	1.040936009	2	2.68632
P09041	FHVEEEGKGK	1.224961302	2	2.82
P09041	LGDVYVNDAFGTAHR	1.138979495	2	4.00368
P09041	VDFNVPMK	0.949125091	1	2.21267
P09041	VSHVSTGGGASLELLEGK	1.16865732	2	5.29532
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.312811711**	**1.09E-05**	**3**
P09117	VLAAVYK	1.354185521	2	2.67524
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	1.220490571	3	5.82094
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.176337597	3	5.0208
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.435769783**	**0.009398**	**2**
P09139	LLLGPGPSNLAPR	1.338983178	2	2.55336
P09139	VLNAPPGISLISFNDK	1.47297227	2	2.63741
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**1.772647449**	**0.000323**	**2**
P09456	**KAP0 cAMP_dependent protein kinase type I_alpha regulatory subunit**	**1.25489374**	**0.025993**	**2**
P09456	LTVADALEPVQFEDGQK	1.266299214	2	4.17752
P09456	SENEEFVEVGR	1.184382994	2	2.31845
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.087726835**	**1.03E-13**	**11**
P09495	EDKYEEEIK	1.198100603	1	2.21057
P09495	EENVGLHQTLDQTLNELNCI	2.402627383	2	4.83634
P09495	IQALQQQADDAEDR	1.309034083	2	4.66009
P09495	IQLVEEELDR	1.257377761	2	3.43025

P09495	IQLVEEELDRAQER	1.259291951	2	3.11903
P09495	KLVILEGELER	1.517525701	2	2.9582
P09495	LEEAEKAADESER	0.964888111	2	4.06153
P09495	LVILEGELER	1.516773671	2	3.33694
P09495	MEIQEMQLK	1.049538992	2	2.51859
P09495	RIQLVEEELDR	1.17476042	2	2.71273
P09495	YSEKEDKYEEEIK	1.228785209	2	4.54402
P09527	**RAB7A Ras_related protein Rab_7a**	**1.183750886**	**0.886396**	**7**
P09527	ATIGADFLTK	1.275381233	2	2.35433
P09527	DPENFPFVVLGNK	1.259787766	2	3.26418
P09527	GADCCVLVFDVTAPNTFK	1.143982662	2	4.19411
P09527	TLDSWRDEFLIQASPR	1.085482185	3	3.83415
P09527	TSLMNQYVNK	1.006614876	2	2.63843
P09527	TSLMNQYVNKK	1.032328952	2	2.32634
P09527	VIILGDSGVGK	1.112530973	2	2.36214
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.027971077**	**0.996997**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	1.024672311	2	3.58599
P09605	LSEMTEQDQQR	1.057171818	2	3.34913
P09606	**GLNA Glutamine synthetase**	**0.909863959**	**0.002968**	**8**
P09606	CIEEAIDK	1.235731355	2	2.32264
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.1969853	3	4.98232
P09606	LTGFHETSNINDFSAGVANR	1.283534417	2	5.87789
P09606	MGDHLWVAR	0.908719169	2	3.00116
P09606	QMYMNLPQGEK	1.161864199	2	2.54901
P09606	RLTGFHETSNINDFSAGVANR	1.050322826	3	5.43988
P09606	TCLLNETGDEPFQYK	1.150805224	2	5.43661
P09606	TCLLNETGDEPFQYKN	1.914004088	2	5.1992
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**1.001228427**	**0.401947**	**2**
P09626	VDNSSLTGESEPQTR	0.932250658	2	4.37604
P09626	VIMVTGDHPITAK	1.179104108	2	2.92793
P09739	**TNNT3 Troponin T_ fast skeletal muscle**	**1.007206331**	**0.934966**	**3**
P09739	ELWDTLYQLETDKFEFGEK	1.591301863	2	3.99912
P09739	KEEEELIALK	0.988988907	2	2.3293
P09739	KKEEEELIALK	1.320065995	3	3.67429
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.390313118**	**2.33E-14**	**23**
P09811	DFSELEPDKFQNK	1.228756591	2	3.32888
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.27667154	3	5.5899
P09811	DLSQLTK	1.233957958	1	2.04361
P09811	EGWQVEEADDWLR	1.261810782	2	3.56958
P09811	GIVGVENVAELK	1.011275188	2	3.22881
P09811	GIVGVENVAELKK	1.612641062	2	3.40125
P09811	HLQIIYEINQK	1.113989723	2	3.87062
P09811	IFVDIEK	1.285022221	1	1.95681
P09811	INMAHLCIVGCHAVNGVAK	1.437462938	3	4.17993
P09811	LHSFVGDDIFLR	2.544386585	3	3.32169
P09811	LVIDQIDNGFFSPNQPDLFK	1.462257496	2	4.90286
P09811	LVTSVAEVVNNDPMVGSK	1.270396574	2	4.28175
P09811	MSLIEEEGGKR	1.103277908	2	2.79366
P09811	TFAYTNHTVLPEALER	1.285112028	2	4.4488
P09811	VDDVAALDK	1.098706868	1	1.95899
P09811	VDDVAALDKK	1.175992292	3	3.30303
P09811	VFADYEAYVK	1.385222157	2	2.75036
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.101363694	2	6.0785
P09811	VLYPNDNFFEGK	1.187370297	2	2.90743
P09811	VSQLYMNQK	0.805134636	2	2.60198
P09811	WLLLCNPGLADLIAEK	1.371330397	2	4.71089

P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	0.635788998	2	2.92584
P09811	YEYGIFNQK	1.167791657	2	2.32645
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**1.154549465**	**0.136266**	**2**
P09812	NLAENISR	1.154142808	1	2.75395
P09812	VIFLENYR	1.369504666	2	2.45721
P09838	**TDT DNA nucleotidylexotransferase**	**1.201232983**	**0.067304**	**2**
P09838	KMMLDNHALYDRTK+Oxidation(2)	1.201232983	2	2.34814
P09838	KMMLDNHALYDRTK+Oxidation(3)	1.201232983	2	2.40023
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.107794072**	**0.770479**	**8**
P09875	ANVVASALAQIPQK	1.137644675	3	4.33477
P09875	FDGKKPDTLGSNTR	1.044292017	2	2.70761
P09875	FSGGLPLPPSYVPVVLSELSDR	1.222950672	2	3.89719
P09875	IILNELAQR	1.677390179	2	2.4089
P09875	SDLEYSFAK	1.369764313	2	2.64837
P09875	SWSQFYSDVLGRPTTLTEMMGK	1.508658734	2	3.8716
P09875	VDFSILSTTGLLTALK	1.167498918	2	4.37087
P09875	VFNEYSDVVENLCK	0.942540646	2	2.88512
P09895	**RL5 60S ribosomal protein L5**	**1.050908887**	**2.64E-05**	**6**
P09895	GAVDGGLSIPHSTK	1.187253045	2	4.97729
P09895	HIMGQNVADYMR	1.043408674	2	3.22738
P09895	IEGDMIVCAAYAHELPK	1.409426079	3	3.38705
P09895	NNVTPDMMEEMYK	1.121020011	2	3.03598
P09895	RFPGYDSESK	1.165389118	2	2.60747
P09895	YLMEEDEDAYKK	1.144282284	2	3.47312
P0C0S7	**H2AZ Histone H2A.Z**	**0.983542254**	**1**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.977473594	2	3.7042
P0C0S7	GDEELDSLIK	1.047758561	1	2.19694
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**1.270828592**	**6.67E-11**	**20**
P0C2X9	AIEAAVLAR	0.948265404	2	2.93307
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.938055535	2	5.25703
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	1.907103556	2	2.97438
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.69789277	2	5.22126
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	1.146743877	3	3.72387
P0C2X9	EEIFGPVLTVYVYPDEK	1.819020445	2	4.39357
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	0.874087329	2	4.44516
P0C2X9	KEWDLKPVADR	0.806936811	2	3.59353
P0C2X9	LLEEHSR	0.898749612	2	2.37166
P0C2X9	LYVPQSLWPQIK	1.609067406	2	3.56974
P0C2X9	NAAGNFYINDK	1.264987744	2	2.4688
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.140498811	2	5.69213
P0C2X9	SAFEYGGQK	0.813240492	2	2.90376
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.978407689	3	5.9793
P0C2X9	STGSVVGQQPFGGAR	0.940902277	2	4.22978
P0C2X9	TIVQEATR	0.986604639	2	2.54322
P0C2X9	VANEPILAFTQGSPER	1.048676935	2	5.33602
P0C2X9	VGNPAEDFGTFFSAVIDAK	2.477559258	2	4.82831
P0C2X9	YQLSPFNHGHK	1.198529068	2	2.94011
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	0.962714625	3	3.37823
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.265994888**	**9.9E-20**	**4**
P0C5H9	DRDVTFSPATIEEELIK	1.300525067	2	4.97223
P0C5H9	DVTFSPATIEEELIK	1.043619088	2	2.98942
P0C5H9	IINEVSKPLAHHIPVEK	1.257670799	3	4.25929
P0C5H9	ILDDWGEMCK	1.245780152	2	3.16062
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.138156113**	**0.517801**	**2**

P0C6F1	EKVEVMSLELEDAK+Oxidation(6)	0.92206192	2	2.68746
P0C6F1	TMPLISDLR+Oxidation(2)	1.138216003	2	2.30624
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.164607259**	**9.9E-20**	**10**
P10111	EGMSIVEAMER	1.208874728	2	3.19519
P10111	FEDENFILK	1.17663584	2	3.21705
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.120389381	3	6.275
P10111	IIPGFMCQGGDFTR	1.351201082	2	2.88638
P10111	KITISDCGQL	1.359634343	2	3.48373
P10111	SIYGEKFEDENFILK	1.122821719	2	4.67458
P10111	TEWLDGK	1.051912833	2	2.38307
P10111	VCFELFADK	1.500393026	2	3.36484
P10111	VCFELFADKVPK	1.233588286	3	3.71704
P10111	VKEGMSIVEAMER	1.17338221	3	3.44387
P10536	**RAB1B Ras_related protein Rab_1B**	**1.29319239**	**0.461467**	**3**
P10536	MGPGAASGGERPNLK	1.104234816	2	3.89442
P10536	NATNVEQAFMTMAAEIK+Oxidation(10)	1.298100202	2	4.16044
P10536	NATNVEQAFMTMAAEIK+Oxidation(12)	1.298208196	2	3.80131
P10633	**CP2D1 Cytochrome P450 2D1**	**1.144260829**	**0.072812**	**4**
P10633	GTTLIINLSSVLKDETVWEKPHR	0.838473528	3	3.95992
P10633	SQGVILASYGPEWR	0.767098564	2	3.99493
P10633	TFMALLDNLLAENR	1.392944061	2	3.6914
P10633	YGDVFSLQK	0.794718642	2	2.52256
P10634	**CP2DQ Cytochrome P450 2D26**	**1.173390233**	**0.000131**	**20**
P10634	ACLGEPLAR	0.86260135	2	2.75156
P10634	AVSNVIASLVYAR	1.068980381	3	4.3895
P10634	DMTDAFLAEMQK	1.284977643	2	2.54412
P10634	EAEHPFNPSILLSK	1.238245761	2	2.48578
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.22636549	3	5.41121
P10634	FADIVPTNIPHMTSR	1.465218645	2	2.59451
P10634	FADIVPTNIPHMTSRDIK	0.872682537	2	2.4106
P10634	FEYEDPFFNR	1.133207085	2	2.38053
P10634	FHPEHFLDAQGNFVK	1.096275004	2	4.68751
P10634	FQGFLIPK	1.147515195	2	2.48025
P10634	GNPESSFNDENLR	1.120584873	2	4.35324
P10634	GTTLIPNLSSVLK	0.997816327	2	2.52225
P10634	GTTLIPNLSSVLKDETVWEKPLR	0.978131663	2	4.66049
P10634	GVVLAPYGPEWR	0.937468123	2	3.27629
P10634	LNSFIALVDK	1.996783021	2	2.82102
P10634	RFEYEDPFFNR	1.367922594	2	3.53558
P10634	RVHEEIDEVIGQVR	1.205543158	2	4.15089
P10634	SLEQWVTEEAGHLCDTFAK	1.296061085	2	5.27867
P10634	SWDPAQPPR	1.104158468	2	2.65276
P10634	VHEEIDEVIGQVR	1.174044823	2	4.94059
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.167803064**	**9.9E-20**	**28**
P10719	AHGGYSVFAGVGER	1.077582786	2	3.98884
P10719	AIAELGIYPAVDPLDSTSR	0.980061351	2	4.9289
P10719	EGNDLYHEMIESGVINLK	0.935396193	2	5.36817
P10719	FLSQPFQVAEVFTGHMGK	0.929959637	2	4.75824
P10719	FTQAGSEVSALLGR	0.989489502	2	4.79803
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	2.058885407	3	4.98423
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	4.301852115	3	3.71986
P10719	IGLFGGAGVGK	1.324805604	2	3.32465
P10719	ILQDYK	1.159012919	1	2.08543
P10719	IMDPNIVGSEHYDVAR	1.071793329	2	4.6414
P10719	IMDPNIVGSEHYDVAR+Oxidation(2)	1.165608647	2	3.97584
P10719	IMNVIGEPIDER	1.460047185	2	4.03774
P10719	IMNVIGEPIDER+Oxidation(2)	1.497661253	2	3.33594

P10719	IPSAVGYQPTLATDMGTMQER	1.338270924	2	4.88906
P10719	LVLEVAQHLGESTVR	1.141445299	2	4.84487
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	1.223204621	3	4.87573
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.133579352	3	5.34199
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(11)	0.973815574	3	3.78144
P10719	TIAMDGTEGLVR	0.979342383	2	3.64242
P10719	TIAMDGTEGLVR+Oxidation(4)	1.042295821	2	2.71136
P10719	TREGNDLYHEMIESGVINLK	1.01337871	2	6.04042
P10719	TVLIMELINNVAK	1.098315064	2	5.06354
P10719	TVLIMELINNVAK+Oxidation(5)	1.106188044	2	2.7877
P10719	VALTGLTVAEYFR	1.444368338	2	4.10604
P10719	VALVYGQMNEPPGAR	1.049916072	2	3.55009
P10719	VLDSGAPIK	0.990368303	2	3.03202
P10719	VLDSGAPIKIPVGPETLGR	0.950619572	3	4.4546
P10719	VVDLLAPYAK	1.050617489	2	3.23477
P10760	**SAHH Adenosylhomocysteinase**	**1.20213685**	**9.9E-20**	**16**
P10760	AGIPVFAWK	1.167622215	2	2.72345
P10760	ALDIAENEMPGLMR	1.185579958	2	3.18983
P10760	ATDVMIAGK	1.058593385	2	2.77702
P10760	DGPLNMILDDGGDLTNLIHTK	1.293208253	2	5.57009
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(6)	1.176595135	3	3.36888
P10760	FDNLYGCR	1.186283657	2	2.76461
P10760	GETDEEYLWCIEQTLHFK	1.564559835	2	4.33036
P10760	GISEETTTGVHNLYK	1.095774873	2	4.26059
P10760	IILLAEGR	1.496772014	2	2.7174
P10760	KLDEAVAEAHLGK	1.19074247	2	4.7821
P10760	LDEAVAEAHLGK	1.022319006	2	3.35552
P10760	SKFDNLYGCR	1.196605039	1	3.19708
P10760	VAVVAGYGDVGK	1.371933671	2	4.15893
P10760	VNIKPQVDR	1.247096638	2	2.81547
P10760	WLNENAVEK	1.213858269	2	2.72362
P10760	WSSCNIFSTQDHAAAAIAK	1.275458181	2	5.01764
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**0.976694562**	**0.708805**	**2**
P10818	HEEHERPEFVAYPHLR	0.977074845	3	3.82553
P10818	SRHEEHERPEFVAYPHLR	1.133789727	3	3.953
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**0.971500865**	**0.004711**	**26**
P10860	ALASLMTYK	1.031089696	2	3.45408
P10860	CAVVDVPFGGAK	1.056188059	2	3.28822
P10860	CVGVGESDGSIWNPDGIDPK	0.936331537	2	5.30528
P10860	DDGSWEVIEGYR	0.697329728	2	3.95036
P10860	DIVHSGLAYTMER	0.909897606	2	3.38171
P10860	DSNYHLLMSVQESLER	1.049969698	2	4.17323
P10860	GASIVEDKLVEDLK	1.089194171	2	3.6835
P10860	GFIGPGIDVPAPDMSTGER	0.872869564	2	5.17165
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(14)	0.926056454	2	4.54874
P10860	HGGTIPVVPTAEFQDR	1.008918227	2	4.67503
P10860	IIAEGANGPTTPEADK	0.903900325	2	5.36735
P10860	IIAEGANGPTTPEADKIFLER	0.949223025	2	4.97597
P10860	IIKPCNHVLSLSFPIR	1.055958906	3	3.51761
P10860	KGFIGPGIDVPAPDMSTGER	0.7674536	2	5.03565
P10860	LQHGSILGFPK	1.109783198	3	3.39093
P10860	MVEGFFDR	0.968533696	2	3.02818
P10860	MVEGFFDR+Oxidation(1)	1.049835157	2	2.47005
P10860	NLNHVSYGR	1.069657979	2	2.36983
P10860	NYTDNELEK	0.897055927	2	2.49681
P10860	RDDGSWEVIEGYR	0.939018511	2	3.6161

P10860	RFTMELAK	0.904828709	2	2.47153
P10860	TAAYVNAIEK	0.998521771	2	3.41414
P10860	TFVVQGFGNVGLHSMR	0.879264771	2	4.5275
P10860	VYEGSILEADCDILIPAASEK	0.906280888	3	5.83882
P10860	YNLGLDLR	0.95889661	2	3.25063
P10860	YSTDVSVDEVK	1.094117159	2	3.37362
P10867	**GGLO L_gulonolactone oxidase**	**1.055702023**	**0.997429**	**5**
P10867	GDDILLSPCFQR	0.92647118	2	3.10758
P10867	LDPTGMFLNSYLEK	0.954210418	2	4.13465
P10867	LDYWLAYETIMK	1.428056973	2	4.06806
P10867	TYGCSPEVYYQPTSVEEVR	0.875620926	2	4.98796
P10867	VVAHYPVEVR	1.061501792	2	2.4866
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.511827776**	**8.23E-05**	**6**
P10868	EHWIIECNDGVFQR	1.441829094	3	3.37183
P10868	ENICTEVMALVPPADCR	1.525340254	2	3.07542
P10868	LQNWALK	0.953230613	2	2.45149
P10868	WETPYMHSLAAAAASR	1.338560942	2	2.88761
P10868	YTDITAMFEETQVPALLEAGFQR	1.430160116	3	6.8984
P10868	YYAFPQMITPLVTK	2.531859313	2	3.85131
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.302534547**	**5.8E-05**	**4**
P10888	DYPLPDVAHVK	0.995222745	2	2.70571
P10888	IQFNESFAEMNK	1.281495553	2	3.896
P10888	SEDYALPSYVDR	1.120239216	2	3.98
P10888	VNPIQGFSAK	1.29319766	2	2.31828
P10959	**EST2 Liver carboxylesterase 1**	**1.002106424**	**0.176116**	**2**
P10959	AISESGVVLTTNLDKK	0.732268522	2	3.52785
P10959	EGASEEETNLSKLVMK	1.37137847	2	2.32609
P11030	**ACBP Acyl_CoA_binding protein**	**1.124231909**	**0.032639**	**4**
P11030	QATVGDVNTDRPGLLDLK	1.398075254	2	3.3909
P11030	TQPTDEEMLFIYSHFK	4.490522182	2	4.34255
P11030	TYVEKVEELK	1.107078324	2	2.83102
P11030	WDSWNK	1.045561468	1	1.94679
P11232	**THIO Thioredoxin**	**1.024395182**	**1**	**2**
P11232	EAFQEALAAAGDK	1.040325725	2	4.8004
P11232	VGEFSGANK	1.017792218	2	3.07378
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**1.082187877**	**0.00614**	**6**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.302103661	3	6.86356
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.569066923	3	7.04673
P11240	GMNTLVGYDLVPEPK	1.051544362	2	4.4104
P11240	IIDAALR	1.159982529	2	2.33258
P11240	LNDFASAVR	1.118834531	2	3.33629
P11240	RLNDFASAVR	1.122655408	2	2.42068
P11348	**DHPR Dihydropteridine reductase**	**1.199814159**	**0.444508**	**10**
P11348	AALDGTPGMIGYGMAK	1.18125442	2	3.79635
P11348	EGGLLTLAGAK	1.09638281	2	2.76708
P11348	GAVHQLCQSLAGK	1.204749146	2	3.83977
P11348	MTDSFTEQADQVTAEVGK	1.022802299	2	5.76946
P11348	MTDSFTEQADQVTAEVGK+Oxidation(1)	1.14655302	2	4.85342
P11348	NCDLMWK	1.000900129	1	2.31527
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.106698033	2	5.29961
P11348	QSIWTSTISSHLATK	1.150892598	2	3.60625
P11348	RPNSGSLIQVVTTDGK	0.587665891	2	3.7657
P11348	VDAILCVAGGWAGGNAK	1.068598387	2	4.2004
P11442	**CLH Clathrin heavy chain 1**	**1.12655846**	**7.23E-13**	**40**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	0.999391554	2	5.46655

P11442	AFMTADLPNELIELLEK	1.210604588	2	4.17259
P11442	AHIAQLCEK	1.449852166	2	2.58871
P11442	ALEHFTDLYDIK	1.281914712	2	3.36915
P11442	CNEPAVWSQLAK	1.188058834	2	2.67206
P11442	EDKLECSEELGDLVK	0.983663202	2	2.98284
P11442	FNALFAQGNYSEAAK	0.992763291	2	4.27857
P11442	GQCDLELINVCNENSLFK	1.159369173	2	4.90441
P11442	GQFSTDELVAEVEK	1.077797589	2	3.8517
P11442	GQFSTDELVAEVEKR	1.022836722	2	3.52163
P11442	HELIEFR	0.982811467	2	2.62971
P11442	HSSLAGCQIINYR	1.152420707	2	3.14358
P11442	IHEGCEEPATHNALAK	1.055545856	2	5.16033
P11442	ISGETIFVTAPHEATAGIIGVNR	1.307483352	2	5.49984
P11442	IVLDNSVFSEHR	1.202663858	2	2.81375
P11442	IYIDSNNNPER	1.067474272	2	3.07195
P11442	KDPELWGSVLLESNPYR	1.132766665	3	3.48486
P11442	KFDVNTSAVQVLIEHIGNLDR	1.162368841	3	5.9055
P11442	KFNALFAQGNYSEAAK	1.145643467	2	3.62979
P11442	LAELEEFINGPNNAHIQQVGDR	0.984333772	2	5.22303
P11442	LECSEELGDLVK	1.052001944	2	3.01325
P11442	LHIIEVGTPPTGNQPFPK	1.122614675	2	4.1285
P11442	LLEMNLMHAPQVADAILGNQMFTHYDR	0.87647524	3	3.95718
P11442	LLYNNVSNFGR	1.925179063	2	2.77709
P11442	LPVVIGGLLDVDCSEDVIK	0.978336968	2	5.11355
P11442	LTDQLPLIIVCDR	1.138231635	2	3.22977
P11442	NLQNLLILTAIK	1.246606744	2	4.3432
P11442	NNLAGAEELFAR	1.134357069	2	3.78268
P11442	NNRPSEGPLQTR	1.104545717	3	3.93325
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.00963042	3	5.8421
P11442	SVDPTLALSVYLR	0.991487027	2	2.64978
P11442	SVNESLNNLFITEEDYQALR	1.493632838	2	4.64444
P11442	TLQIFNIEMK	1.053164301	2	2.79662
P11442	TSIDAYDNFDNISLAQR	1.21545435	2	4.98764
P11442	VDKLDASESLR	1.35556071	2	2.53371
P11442	VGEQAQVVIIDMNDPSNPIR	0.893567783	2	5.29602
P11442	VIQCFAETGQVQK	1.031827176	2	4.75095
P11442	VSQPIEGHAASFAQFK	1.257396418	2	4.13619
P11442	WLLLTGISAQQNR	1.161162891	2	2.634
P11442	YESLELCRPVLQQGR	0.769451279	2	3.21056
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.104317619**	**0.18165**	**3**
P11497	ECSQPVMVYIPPQAELR+Oxidation(7)	0.864932924	2	2.43948
P11497	LPELLLK	1.148858604	2	2.49256
P11497	TLRDPSLPLLELQDIMTSVSGR	1.455229538	3	3.96937
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**1.185348226**	**0.816198**	**5**
P11507	DIVPGDIVEIAVGDKVPADIR	1.172064622	2	3.68584
P11507	IRDEMVATEQER	0.961871005	2	3.19373
P11507	KSEIGIAMGSGTAVAK	0.953851447	2	3.18642
P11507	TASEMVLADDNFSTIVAAVEEGR	1.331364319	2	2.86987
P11507	VDQSILTGESVSVIK	1.012293768	2	4.11119
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.043587995**	**1.11E-16**	**25**
P11598	DGEEAGAYDGPR	0.896941967	2	3.44587
P11598	DLLTAYYDVDYEK	1.01735807	2	3.66812
P11598	DPNIVIAK	1.268619006	2	2.37715
P11598	EATNPPIIQEEKPK	1.024985671	2	3.6481
P11598	EYDDNGEGITIFRPLHLANK	1.039781244	2	3.98753
P11598	EYDDNGEGITIFRPLHLANKFEDK	1.013367915	3	3.80969

P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.024357135	3	5.28138
P11598	FISDKDASVVGFFR	1.296690769	2	4.55881
P11598	FLQEYFDGNLK	0.971833706	2	3.72904
P11598	FLQEYFDGNLKR	1.245771965	2	3.70746
P11598	FVMQEEFSR	1.249415545	2	2.98946
P11598	GFPTIYFSPANK	1.17876248	2	2.79799
P11598	IFRDGEEAGAYDGPR	0.994245628	2	4.13939
P11598	KQAGPASVPLR	1.177320794	2	2.41262
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.176390885	3	4.45157
P11598	LAPEYEAAATR	1.03903225	2	2.87524
P11598	LNFAVASR	1.587838329	2	2.66738
P11598	LSKDPNIVIAK	1.195530978	3	4.33374
P11598	MDATANDVPSPYEVK	1.065221441	2	4.33031
P11598	MDATANDVPSPYEVK+Oxidation(1)	1.088481113	2	3.98828
P11598	RLAPEYEAAATR	0.62018506	2	3.35092
P11598	SEPIPETNEGPVK	1.126163734	2	2.9548
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.291646876	2	5.97534
P11598	VDCTANTNTCNK	1.119309793	2	4.46086
P11598	YGVSGYPTLK	1.094384035	2	2.89312
P11608	**ATP8 ATP synthase protein 8**	**1.111775945**	**0.397764**	**2**
P11608	ISSQTFPAPPSPK	1.238037211	2	2.37563
P11608	TNNPWESK	0.98183638	2	2.3595
P11711	**CP2A1 Cytochrome P450 2A1**	**1.085102134**	**0.81603**	**5**
P11711	GEQATYNTLFK	1.015062213	2	3.12863
P11711	GTDVFPILGSLMTDPK	1.125042409	2	3.47377
P11711	ILEEAGYLIK	1.272264029	2	2.78408
P11711	TVSNVISSIVFGER	1.033948326	2	3.17099
P11711	VHEEIEQVIGR	1.156559868	2	3.42091
P11714	**CP2D9 Cytochrome P450 2D9**	**0.972930936**	**0.996451**	**2**
P11714	GNPESSFNDENLLMVVR	1.024392767	2	2.57972
P11714	VQQEIDEVIGQVR	1.001944798	2	4.62161
P11862	**GAS2 Growth arrest_specific protein 2**	**1.138301114**	**0.558323**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.439603129	2	3.90967
P11862	LDNGALLCQLAATVQEK	1.088317556	2	3.9023
P11862	YGVEPPGLIK	1.126949131	2	2.52339
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**1.050254248**	**9.9E-20**	**24**
P11884	DGMTIAKEEIFGPVMQILK	1.037051639	2	3.82396
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.596327025	3	4.20656
P11884	EEIFGPVMQILK	0.956251256	2	3.91035
P11884	ELGEYGLQAYTEVK	1.020091576	2	4.57057
P11884	GYFIQPTVFGDVK	1.007771872	2	3.9246
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	1.017817429	3	4.13168
P11884	LGPALATGNVVVMK	1.134145174	2	4.06756
P11884	LGPALATGNVVVMK+Oxidation(13)	1.423711363	2	3.59059
P11884	LLCGGGAAADR	1.403084886	2	3.78498
P11884	RVTLELGGK	0.921098007	2	2.78405
P11884	TEQGPQVDETQFK	0.934047951	2	4.54317
P11884	TEQGPQVDETQFKK	0.961738705	2	3.85082
P11884	TFPTVNPSTGEVICQVAEGNK	0.719178138	2	5.29962
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.904821601	2	4.29091
P11884	TFVQEDVYDEFVER	1.139095043	2	5.23867
P11884	TIEEVVGR	0.936842595	2	3.02427
P11884	TIPIDGDFFSYTR	1.357649158	2	2.51171
P11884	VAEQTPLTALYVANLIK	1.9821413	2	5.49067
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.041731706	2	5.78532
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.021062051	3	3.80315
P11884	VTLELGGK	0.93961821	2	2.30482

P11884	VVGNPFDSR	1.026955481	2	3.04284
P11884	YGLAAAVFTK	0.995951334	2	3.87276
P11884	YYAGWADK	0.967510433	2	2.5501
P11915	**NLTP Non_specific lipid_transfer protein**	**1.07301436**	**1.3E-09**	**22**
P11915	ADCTITMADSDLLALMTGK	1.297631824	2	5.33583
P11915	ADCTITMADSDLLALMTGK+Oxidation(7)	0.839858338	2	3.6261
P11915	ANLIFK	1.048444801	2	2.39247
P11915	AVEIVAQEMVTDMPSTFEEK	1.349414033	2	4.33973
P11915	GSVLPDSDKK	1.02809161	2	2.78184
P11915	HGLQSKAVEIVAQEMVTDMPSTFEEKSVIK+Oxidation(15)Oxidation(19)	1.106086662	3	3.38459
P11915	HIDVLINK	1.08169896	2	2.8688
P11915	HSVNNPYSQFQDEYSLDEIMK	1.097398765	3	5.66458
P11915	IGGIFAFK	1.517305165	2	2.42884
P11915	KADCTITMADSDLLALMTGK	1.159811431	2	4.25928
P11915	KLEEEGEEFVK	0.982576965	2	4.3243
P11915	KLEEEGEEFVKK	1.020938417	3	4.74898
P11915	LEEEGEEFVK	0.932807253	2	3.02936
P11915	LEEEGEEFVKK	1.034490545	2	3.68711
P11915	LQSLQLQPDK	1.430237782	2	3.29805
P11915	MGFPEAASSFR	1.087049478	2	2.92022
P11915	MNPQSAFFQGK	1.108738661	2	3.19331
P11915	MNPQSAFFQGK+Oxidation(1)	0.73562861	2	2.57664
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.362627458	3	5.53068
P11915	THQISAAPTSSAGDGFK	1.0825754	2	4.49084
P11915	WVINPSGGLISK	1.111290702	2	2.89103
P11915	YGMSACPFAPQLFGSAGK	1.297535523	2	4.38473
P11960	**ODBA 2_oxoisovalerate dehydrogenase subunit alpha_ mitochondrial (Fragment)**	**0.894917966**	**3.99E-14**	**10**
P11960	AVAENQPFLIEAMTYR	0.812040529	2	3.79173
P11960	HFVTISSPLATQIPQAVGAAYAAK	0.7050185	2	4.13117
P11960	HLQTYGEHYPLDHFDK	0.654228653	3	3.41532
P11960	IGHHSTSDDSSAYR	0.723915404	3	4.05605
P11960	NNGYAISTPTSEQYR	0.623322454	2	3.97769
P11960	QGQIINPSEDPHLPQEEVLK	0.42234274	2	2.52068
P11960	QYLLNQGWWDEEQEK	0.840286114	2	3.59311
P11960	SVDEVNYWDK	0.798294173	2	2.46588
P11960	TDLVFGQYR	0.56699344	1	1.98226
P11960	VMEAFEQAER	0.619638051	2	3.61821
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.297678234**	**0.426951**	**3**
P11980	AEGSDVANAVLDGADCIMLSGETAK	1.465809848	3	3.6481
P11980	GVNLPGAAVDLPAVSEK	1.288788053	2	3.85647
P11980	NTGIICTIGPASR	1.279430508	2	3.63049
P12001	**RL18 60S ribosomal protein L18**	**1.146432502**	**9.9E-20**	**5**
P12001	GTVLLSGPR	1.298472476	2	2.69755
P12001	ILTFDQLALESPK	1.471101335	2	4.89776
P12001	TAVVVGTITDDVR	1.169283043	2	4.05836
P12001	TNRPPLSLSR	1.125022717	3	3.37642
P12001	TNSTFNQVVLK	1.02914174	2	3.06424
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.017500516**	**0.722722**	**9**
P12007	AQEIDQSNDFK	0.516840131	2	3.55779
P12007	FVQENLAPK	1.013359356	2	2.84988
P12007	FWITNGPDADVLVVYAK	1.349984145	2	4.60994
P12007	GSNTCELVFEDCK	1.05160531	2	4.24366
P12007	GSNTCELVFEDCKVPAANILSQESK	1.10123343	3	5.39857
P12007	GVYVLMSGLDLER	1.060533007	2	3.72927
P12007	IGQFQLMQGK	1.215526109	2	2.66859

P12007	LYEIGGGTSEVR	1.01112837	2	2.8305
P12007	TDLTAVPASR	0.985650752	2	2.8517
P12346	**TRFE Serotransferrin**	**0.924605527**	**1**	**19**
P12346	ADRDQYELLCLDNTR	1.070590672	2	4.33615
P12346	ASDSSINWNNLK	1.027322557	2	3.18748
P12346	DFQLFGSPLGK	1.020129535	2	2.98268
P12346	DLKQEDFQLLCPDGTK	0.820136882	2	5.02448
P12346	EGVCPEGSIDSAPVK	0.818634651	2	3.84822
P12346	FDEFFSQGCAPGYK	0.863792724	2	4.54084
P12346	GDKDCTGNFCLFR	0.921228111	2	3.44034
P12346	GTDFQLNQLQGK	0.922872492	2	3.19349
P12346	GYYAVAVVK	0.90293136	2	2.3885
P12346	HQTVLENTNGK	0.832610186	2	3.04289
P12346	HTTIFEVLPQK	0.986242631	2	3.47262
P12346	KGTDFQLNQLQGK	0.908884871	2	4.15424
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.188651907	2	4.73369
P12346	NGDGKEDLIWEILK	1.054378213	3	3.52064
P12346	QEDFQLLCPDGTK	0.855711779	2	3.61021
P12346	SKDFQLFGSPLGK	1.200790169	2	3.31852
P12346	VSTVLTAQK	1.037921378	2	2.76658
P12346	WCALSHQER	1.361782154	2	3.1468
P12346	WCAVSEHENTK	0.96840353	2	3.79166
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.245976343**	**0.81012**	**2**
P12368	NLDQEQLSQVLDAMFEK	1.202720556	2	4.76198
P12368	SVGQYDNRGSFGELALMYNTPR	1.08317274	2	2.38977
P12711	**ADHX Alcohol dehydrogenase class_3**	**1.098021165**	**0.756383**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.084700954	3	5.93079
P12711	AFDLMHSGNSIR	1.574768122	2	3.11885
P12711	AGDTVIPLYIPQCGECK	1.056373247	2	3.06447
P12711	AKEFGATECINPQDFSK	1.025584061	2	4.76747
P12711	EFGATECINPQDFSK	1.125672894	2	4.62905
P12711	IIGIDINK	0.906098273	2	2.42186
P12711	IIGIDINKDK	0.873737204	2	2.41653
P12711	VCLLGCGISTGYGAAVNTAK	1.484400125	2	5.67691
P12711	VDEFVTGNLSFDQINK	0.953927381	2	4.95512
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	0.978465608	2	4.09179
P12749	**RL26 60S ribosomal protein L26**	**1.041996072**	**0.013826**	**5**
P12749	FNPFVTSDR	1.019920543	2	2.60034
P12749	HFNAPSHIR	0.981078037	3	3.97273
P12749	KDDEVQVVR	1.182298382	2	3.16013
P12749	KIMSSPLSKELR+Oxidation(3)	2.0503358	2	2.47379
P12749	YKEETIEK	1.05354692	2	2.89575
P12785	**FAS Fatty acid synthase**	**1.564895524**	**9.9E-20**	**41**
P12785	ACIDTALENLSTLK	2.233086997	2	3.92881
P12785	AGSDTELAAPK	1.769345877	2	3.48882
P12785	ALIAEATK	1.784017816	2	2.31491
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	2.107099141	3	3.44213
P12785	DANLPAGSMAAVGLSWEECK	0.917929513	2	4.29367
P12785	DGGFLLMHTVLK	1.061234522	2	2.54676
P12785	DHKDNLEFFLTNLGK	1.480112952	2	2.36826
P12785	EEEPEAMLPGAQPTLISAISK	1.651624538	2	4.04902
P12785	EQGVTFPSGEAQEQLIR	1.930521446	2	4.39829
P12785	FDASFFGVHPK	1.734692356	2	3.40544
P12785	FVFTPHVEPECLSESAILQK	2.118505777	2	4.36911
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	2.036316769	3	5.90406
P12785	GLESIINIIHSSLAEPR	1.887839552	2	4.62436

P12785	GNAGQSNYGFANSTMER	1.893258345	2	4.4859
P12785	GVDLVLNSLAEEK	1.877070529	2	3.34051
P12785	LFDHPEVPIPAESESVSR	1.455214029	2	4.39326
P12785	LLLPEDPLISGLLNSQALK	2.506845909	3	5.12507
P12785	LSPQDKPIFLPVEDTSFQWVDSLK	1.146295525	3	3.91366
P12785	LTPGCEAEAEAEAICFFIK	2.200118527	2	4.66609
P12785	MTVPGLEDLPQHGLPR	1.527824526	2	3.49596
P12785	QAQLNLSILLVNPEGPTLTR	2.118659039	2	4.35831
P12785	QQEQLVPTLEK	1.796770964	2	2.62549
P12785	RQQEQLVPTLEK	2.00140561	2	2.98771
P12785	SDEALKPLGVK	1.425942777	2	2.99114
P12785	SFDDSGNGYCR	3.045507206	2	3.0345
P12785	SLSLSLEETPVVFENVTFHQATILPR	1.646374292	3	4.13178
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.692911983	2	5.56219
P12785	SNMGHPEPASGLAALTK	1.460826893	2	3.19168
P12785	TGGTYGEDLGADYNLSQVCDGK	1.259651305	2	4.86522
P12785	TMEAVQGLLEQGR	1.494546938	2	3.56896
P12785	VGDPQELNGITR	0.958508456	2	2.73798
P12785	VHLTGIDINPNALFPPVEFPVPR	1.695770953	2	5.23268
P12785	VLEALLPLK	2.128970349	2	2.62529
P12785	VLESDLVMNVYR	1.687312878	2	3.0438
P12785	VSVHIIEGDHR	1.947550838	3	3.47407
P12785	VTAIYIDPATHLQK	1.64953546	2	3.55834
P12785	VYATILNAGTNTDGCK	1.542948531	2	4.89874
P12785	VYMLEGDTQVADVTTSR	1.659762464	2	4.83996
P12785	VYQWEDPDSK	2.048414505	2	3.31726
P12785	WLSTSIPEAQWQSSLAR	0.793038707	2	3.53579
P12785	YNGTLNLDR	1.3698894	2	2.58314
P12791	**CP2BA Cytochrome P450 2B10**	**1.192887263**	**0.949612**	**2**
P12791	IQEEAQCLVEELR	0.956653637	2	4.58143
P12791	IQEEAQCLVEELRK	1.198029909	2	3.8245
P12847	**MYH3 Myosin_3**	**1.568623719**	**0.825362**	**6**
P12847	EQYEEEQEGK	10.59383857	2	3.06912
P12847	GQEDLKEQLAIVER	19.10183819	2	3.98333
P12847	GTLEDQIISANPLLEAFGNAK	0.868573723	2	3.28741
P12847	IEAQNQPFDAK	4.199196945	2	2.37853
P12847	MKGTLEDQIISANPLLEAFGNAK	1.667624723	3	6.98021
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(1)	1.139247244	2	4.39973
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.687139553**	**9.9E-20**	**19**
P12928	AETSDVANAVLDGADCIMLSGETAK	1.818724423	2	5.5178
P12928	CCAAAIIVLTK	1.092945084	2	2.86566
P12928	CNLAGKPVVCATQMLESMITK	1.682522431	3	4.8382
P12928	EATESFATSPLSYRPVAIALDTK	1.737813014	2	3.88861
P12928	EPPEAIWADDVDR	1.685742811	2	2.46401
P12928	GDLGIEIPAEK	1.605303871	2	3.13498
P12928	GSFPVEAVMMQHAIAR	1.466684892	2	3.23673
P12928	GSQVLVTVDPK	1.673745378	2	2.86614
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.764234683	2	5.2502
P12928	IGPEGLVTEVEHGGILGSR	1.724567833	2	5.28459
P12928	IYIDDGLISLVVQK	2.66755444	2	4.51928
P12928	KFDEILEVSDGIMVAR	0.12032842	3	4.17247
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.771712703	3	4.8035
P12928	LNFSHGSHEYHAESIANIR	3.420302713	3	5.13894
P12928	RVQFGIESGK	0.820821618	2	2.46175
P12928	STSIIATIGPASR	1.334504836	2	3.32449
P12928	TGVLQGGPESEVEIVK	1.655144691	2	4.45715
P12928	TVWVDYHNITR	1.953686506	2	2.33038

P12928	VQFGIESGK	1.944966282	2	2.83367
P12938	**CP2D3 Cytochrome P450 2D3**	**0.880835411**	**0.458045**	**7**
P12938	AVQELLVTCGEDTADRPEMPIFQHIGYGHK	0.712397665	3	3.73077
P12938	DLTDAFLAEIEK	1.190179465	2	3.86209
P12938	FDYGDPDFIK	0.839124829	2	2.92157
P12938	GNPESSFNDANLR	0.811051162	2	3.9357
P12938	RFDYGDPDFIK	1.009064768	2	3.12023
P12938	TFLTMVDNLVTEHK	0.957233282	2	3.09592
P12938	TWDPDQPPRDLTDAFLAEIEK	1.09308747	3	4.04132
P12939	**CP2DA Cytochrome P450 2D10**	**1.142392727**	**0.997969**	**9**
P12939	ALCNVIASLIFAR	1.060569327	2	2.54402
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.153669949	3	5.33133
P12939	FEYEDPYLIR	0.964318931	2	2.84812
P12939	FGDIAPLNLPR	1.173113284	2	3.44733
P12939	ITSCDIEVQDFVIPK	1.161761746	2	4.18802
P12939	NLTDAFLAEVEK	1.175764556	2	4.04659
P12939	RFEYEDPYLIR	1.269615328	2	2.97872
P12939	TFMAFLDNLLAENR	1.218741984	2	3.0689
P12939	TTWDPAQPPR	0.982404874	2	2.36779
P13084	**NPM Nucleophosmin**	**1.367417158**	**0.018722**	**2**
P13084	MTDQEAIQDLWQWR	1.329760722	2	2.84166
P13084	VDNDENEHQLSLR	1.369198356	2	3.88759
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.031540976**	**5.28E-09**	**5**
P13086	HLGLPVFNTVK	1.070893648	2	2.37726
P13086	LIGPNCPGIINPGECK	1.363532774	2	4.8771
P13086	MGHAGAIIAGGK	0.900751932	1	2.84076
P13086	NIYIDK	0.980952892	1	1.98727
P13086	QGTFHSQQALEYGTK	0.911805077	2	2.78468
P13107	**CP2B3 Cytochrome P450 2B3**	**1.349488469**	**9.9E-20**	**7**
P13107	ATLDPNAPR	1.32967306	2	2.63043
P13107	EVLDYIDHSVENHR	1.329654002	2	4.07885
P13107	FSDVSPMGLPCR	1.487950866	2	3.29325
P13107	GIIAVLQPIMQEYGVSFVNEER	2.119255666	3	6.34087
P13107	MCLGEGIAR	1.393131393	2	2.82669
P13107	QSVEDQIKEEAK	1.420344506	2	2.58597
P13107	SFIQLQEK	1.581323809	1	2.35375
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.192426855**	**0.988038**	**4**
P13221	ITWSNPPAQGAR	1.040761549	2	3.19635
P13221	NLDYVATSINEAVTK	1.01373208	2	3.99998
P13221	SCASQLVLGDNSPALR	1.230715287	2	4.52124
P13221	TDDSQPWVLPVVR	0.750603461	2	2.88664
P13255	**GNMT Glycine N_methyltransferase**	**0.919610532**	**0.999979**	**6**
P13255	AHMVTLDYTVQVPGAGR	0.966322317	2	5.19588
P13255	AWLLGLLR	1.00973	2	2.78412
P13255	DITTSVLTVNNK	0.92465194	2	3.51604
P13255	NYDYILSTGCAPPGK	0.897829647	2	4.80592
P13255	SDLTKDITTSVLTVNNK	1.232156217	2	2.74667
P13255	SLGVAAEGIPDQYADGEAAR	0.884787486	2	5.51116
P13383	**NUCL Nucleolin**	**1.159170435**	**0.006909**	**6**
P13383	GFGFVDFNSEEDAK	0.623016569	2	3.34404
P13383	GSPNARSQPSKTLFVK	1.075464201	2	2.36211
P13383	NDLAAVDVR	1.128062307	1	1.90576
P13383	NLSFNITEDELKEVFEDAVEIR	0.519616922	3	3.43661
P13383	SEADAEKNLEEK	1.264578643	2	2.56821
P13383	TLVLSNLSYSATEETLQEVFEK	1.598709348	2	2.76637
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.90943922**	**3.74E-06**	**22**

P13437	AANEAGYFNEEMAPIEVK	0.554562138	2	5.13626
P13437	AANEAGYFNEEMAPIEVK+Oxidation(12)	0.848942543	2	4.87477
P13437	DAEVVLCGGTESMSQSPYSVR	0.848411425	2	4.56606
P13437	DFTATDLTEFAAR	1.056733405	2	3.46766
P13437	DMDLIDVNEAFAPQFLAVQK	1.20097724	3	6.96981
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(2)	1.113709014	2	3.43099
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.695814833	2	5.77764
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	0.808501118	3	4.98343
P13437	FGLDLK	0.880438028	2	2.33606
P13437	GVFIVAAK	0.878667039	2	2.5214
P13437	HNFTPLAR	0.896165842	2	2.33062
P13437	ITAHLVHELR	1.289253497	2	3.30606
P13437	LCGSGFQSIVSGCQEICSK	1.352780829	2	5.54742
P13437	LEDTLWAGLTDQHVK	0.833500047	2	5.24708
P13437	RTPFGAYGGLLK	0.813573946	2	3.03588
P13437	SLDLDPSK	0.845300015	2	2.62023
P13437	TNVSGGAIALGHPLGGSGSR	0.850643591	2	5.85489
P13437	VGVPTETGALTLNR	0.847987276	2	3.68322
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	1.036795267	3	6.66265
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	0.812685605	3	5.07818
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	0.916844187	3	4.20877
P13437	YAVGSACIGGGQGISLIIQNTA	0.818809687	2	4.30879
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.136763731**	**4.76E-12**	**8**
P13444	FVIGGPQGDAGVTGR	1.093250665	2	4.56533
P13444	HIGYDDSAK	0.97692865	2	2.79779
P13444	ICDQISDAVLDAHLK	1.217281964	3	5.63317
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.335409197	3	6.75333
P13444	SEFPWEVPK	1.052008427	2	2.31906
P13444	SGVLPWLRPDSK	1.062035749	2	2.96991
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.414975469	3	5.49374
P13444	TQVTVQYVQDNGAVIPVR	1.268963587	2	4.34239
P13471	**RS14 40S ribosomal protein S14**	**1.08559835**	**0.364846**	**2**
P13471	ADRDESSPYAAMLAAQDVAQR	1.229919068	2	5.43666
P13471	IEDVTPIPSDSTR	1.062377019	2	3.9363
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.886484193**	**0.848953**	**20**
P13601	ANNTPYGLAAGVFTK	0.636735769	2	3.93742
P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	1.061665193	3	3.78904
P13601	EEIFGPVQQIMK	0.825637814	2	3.52968
P13601	EMGEQGVYEYTELK	0.953406925	2	3.67808
P13601	FPVINPATEEVICHVEEGDK	0.762110893	3	3.74934
P13601	FPVINPATEEVICHVEEGDKADVDK	0.929480434	4	5.19338
P13601	GFFVQPTVFSNVTDEMR	2.089383578	2	4.17947
P13601	IAKEEIFGPVQQIMK	0.565040384	3	3.47258
P13601	IFINNEWHNSLNGK	0.971166731	2	4.03271
P13601	IHGQTIPSDGDVFTYTR	0.977029833	3	4.46231
P13601	ILDLIESGK	0.792687635	2	3.22034
P13601	ILDLIESGKK	0.708666048	2	2.95169
P13601	KFPVINPATEEVICHVEEGDK	0.817609937	3	3.36825
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.909179354	4	4.82623
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	0.550002187	3	5.27702
P13601	LFVEESIYDEFVR	1.04422606	2	4.186
P13601	VLLATMESMNAGK	0.981970436	2	4.07469
P13601	VSFTGSTEVGK	0.783879465	2	3.1863
P13601	YVLGNPLDSGISQGPQIDK	0.868405231	2	4.61068
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.548183983	2	4.24573
P13697	**MAOX NADP_dependent malic enzyme**	**1.60916911**	**2.19E-07**	**5**

P13697	AECSAEECYK	1.667974394	2	3.05234
P13697	AIFASGSPFDPVTLPDGR	1.639385113	2	4.80434
P13697	GHIASVLNAWPEDVVK	1.404332857	2	4.05756
P13697	HINDSVFLTTAEVISQQVSDK	1.992880375	2	5.88625
P13697	ILGLGDLGCNGMGIPVGK	1.492239217	2	2.68314
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.025609099**	**4.55E-11**	**13**
P13803	AAVDAGFVPNDMQVGQTGK	0.951021107	2	4.54286
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(12)	0.949850462	2	3.71437
P13803	GLLPEELTPLILETQK	1.085106404	2	4.89317
P13803	GTSFEAAAASGGSASSEK	0.930891837	2	5.16012
P13803	LGGEVSCLVAGTK	1.005885487	2	4.74948
P13803	LLYDLADQLHAAVGASR	1.090631039	2	4.93302
P13803	LNVAPVSDIIEIK	1.463590259	2	4.12743
P13803	QFSYTHICAGASAFGK	1.0177972	2	3.12935
P13803	SDRPELTGAK	0.947675944	3	3.44825
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.845536153	3	6.95137
P13803	TIYAGNALCTVK	1.002490224	2	3.70496
P13803	VLVAQHDAYK	0.957226283	2	3.32049
P13803	VVQDLCK	1.015838965	2	2.80105
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.153984945**	**0.002971**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.696754776	2	5.13584
P13832	FTDEEVDELYR	0.90678314	2	3.44253
P13832	GNFNYIEFTR	1.276673975	2	2.71945
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.995892411**	**0.668977**	**6**
P14046	FSIDTNGISDYSLNIK	1.048892327	2	2.45867
P14046	GMYESLPVVAVK	0.82640547	2	3.28905
P14046	ISLCHGNPTFSSETK	1.868700864	2	3.86171
P14046	LVDIKGDPIPNEQVLIK	1.133072175	2	3.41586
P14046	QQNSYGGFSSTQDTVVALDALSK	1.267905517	2	4.39455
P14046	QSPGPCGSEVATVPETGR	0.763082188	2	3.35082
P14141	**CAH3 Carbonic anhydrase 3**	**0.914124698**	**0.016296**	**16**
P14141	EAPFNHFDPSCLFPACR	0.947841338	2	4.42455
P14141	EKGEFQILLDALDK	1.016366795	2	4.52234
P14141	EKGEFQILLDALDKIK	0.912528499	2	3.57461
P14141	EPMTVSSDQMAK	1.084889237	1	2.97442
P14141	EWGYASHNGPEHWHELYPIAK	0.918536613	3	5.03209
P14141	GDNQSPIELHTK	0.935017135	2	3.64875
P14141	GEFQILLDALDK	1.135629151	2	4.75841
P14141	GEFQILLDALDKIK	1.076817918	2	3.67206
P14141	GGPLSGPYR	0.974999861	2	2.80025
P14141	GKEAPFNHFDPSCLFPACR	0.870110261	3	4.45203
P14141	HDPSLQPWSVSYDPGSAK	1.068390659	3	4.8394
P14141	QFHLHWGSSDDHGSEHTVDGVK	0.975352415	2	4.72917
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.7391713	3	6.01684
P14141	VVFDDTFDR	0.961621047	2	3.43085
P14141	YAAELHLVHWNPK	1.135404247	2	4.41928
P14141	YNTFGEALKQPDGIAVVGIFLK	0.961744971	3	5.93579
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.182255019**	**6.82E-10**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	1.468823994	2	4.98902
P14173	ALIPTTAPQEPETYEDIIR	1.036030828	2	3.83261
P14173	GSNQLNETLLQR	1.398454865	2	3.05221
P14173	HSHQDSGLITDYR	1.178559515	2	3.465
P14173	LVAYTSDQAHSSVER	1.366874224	2	4.51651
P14173	MLELPEAFLAGR	1.303208907	2	2.62132
P14173	TDLTEAFNMDPVYLR	1.113730249	2	3.70706
P14173	TVESAHVQLAWEHIR	1.154020566	3	4.5057

P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.002640667**	**0.926875**	**15**
P14408	AAAEVNQEYGLDPK	1.063781815	2	4.01442
P14408	AIEMLGGELGSK	1.011765487	2	3.92009
P14408	IEYDTFGELK	1.020440081	2	3.15611
P14408	IEYDTFGELKVPTDK	0.882721884	2	3.47807
P14408	IYELAAGGTAVGTGLNTR	1.08744894	2	5.473
P14408	KTAIELGYLTAEQFDEWVKPK	0.973278183	3	4.73544
P14408	LMNESLMLVTALNPHIGYDK	1.342752459	3	5.38368
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.971160833	3	6.58869
P14408	SGLGELILPENEPGSSIMPGK	0.943260321	2	4.79838
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(18)	1.07362176	2	3.27853
P14408	SKEFAQVIK	1.005662719	2	2.32305
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.031556666	3	5.03337
P14408	TAIELGYLTAEQFDEWVKPK	1.193080054	2	4.89939
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.151030446	3	6.40895
P14408	YYGAQTVR	1.093459861	1	1.92302
P14480	**FIBB Fibrinogen beta chain**	**0.983236773**	**0.880504**	**7**
P14480	DNENVINEYSSILEDQK	1.136532265	2	3.27135
P14480	GFGNIATNEDTK	1.168956193	2	3.03719
P14480	GFGNIATNEDTKK	1.174338023	2	3.16514
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.226813309	3	4.99039
P14480	LYIDETVNDNIPLNLR	1.275860907	2	3.26582
P14480	TENGGWTVIQNR	0.768955723	2	2.78627
P14480	YCGLPGEYWLGNDK	1.176047132	2	3.27332
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.941146273**	**0.864793**	**10**
P14604	AFAAGADIK	0.933280053	2	3.04592
P14604	AQFGQPEILLGTIPGAGGTQR	0.904685734	2	5.69514
P14604	ESVNAAFEMTLTEGNKLEK	0.728243461	2	3.73587
P14604	FLSHWDHITR	0.927178706	2	3.13519
P14604	IFPVETLVEEAIQCAEK	1.039454704	2	5.53261
P14604	LFYSTFATDDR	1.553616561	2	2.52043
P14604	NSSVGLIQLNRPK	0.936309343	2	3.45264
P14604	SLAMEMVLTGDR	0.94238713	2	3.65417
P14604	SLAMEMVLTGDRISAQDAK+Oxidation(4)Oxidation(6)	1.334380175	2	2.35727
P14604	TFQDCYSGK	0.975910335	2	2.56481
P14668	**ANXA5 Annexin A5**	**1.337731551**	**0.00025**	**3**
P14668	ETSGNLENLLLAVVK	1.121697574	2	2.51548
P14668	GLGTDEDSILNLLTAR	1.545167058	2	4.53051
P14668	GTVTDFSGFDGR	1.247529572	2	2.95483
P14669	**ANXA3 Annexin A3**	**1.371029009**	**0.109566**	**8**
P14669	GMGTDEDTLIEILTTR	1.353476894	2	4.28976
P14669	GTINNYPGFNPSVDAEAIR	0.921663452	2	3.62609
P14669	KDAQTLYDAGEK	1.1037486	2	2.94383
P14669	KDAQTLYDAGEKK	1.196414683	2	3.33122
P14669	QYQEAYEQALK	1.120358735	2	3.01873
P14669	SEIDLLDIR	1.111004816	2	2.68485
P14669	TLINILTER	1.359368378	2	2.94431
P14669	WGTDEDKFTEILCLR	1.444692593	2	3.55997
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.097606304**	**0.459545**	**3**
P14685	AIQLEYSEAR	1.095229501	2	2.71695
P14685	LQLDSPEDAEFIVAK	1.094341363	2	3.89312
P14685	SVFPEQANNNEWAR	1.085154827	2	2.53044
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.213529161**	**0.236323**	**3**
P14740	LGTLEVEDQIEAAR	1.238144156	2	3.94057
P14740	VLEDNSALDK	1.104447735	2	3.04243
P14740	YMGLPTPEDNLDHYR	1.160400838	2	2.46709

P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**0.862183601**	**0.962886**	**11**
P14882	FLSDVYPDGFK	1.012168997	2	3.00752
P14882	FSSQEAASSFGDDR	1.039224136	2	3.7955
P14882	HGNALWLNER	0.976269039	2	2.93596
P14882	HIEIQVLGDK	0.854393891	2	2.36394
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	1.227109669	3	5.78129
P14882	LQVEHPVTECITGLDLVQEMILVAK	1.03313156	3	4.07088
P14882	MADEAVCVGPAPTSK	0.87179283	2	4.18365
P14882	SYLNMDAIMEAIKK	1.054320825	2	2.41744
P14882	TGAQAVHPGYGFLSENK	0.998147367	2	3.52734
P14882	TVAIHSDVDASSVHVK	0.756897989	2	3.48252
P14882	VVEEAPSIFLDPETR	0.857261385	2	4.09325
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**0.957972705**	**0.270721**	**2**
P14942	KPPPDGHYVDVVR	0.944568889	2	2.90515
P14942	YFPVFEK	1.132277174	1	1.91209
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.140481271**	**0.114559**	**4**
P15083	EIQNAGDQAQENR	1.116582434	2	3.86892
P15083	FSVLITGLR	1.166598269	2	2.61457
P15083	GVTGGSVAIVCPYNPK	1.288882566	2	4.06948
P15083	SSVTFECDLGR	1.198282374	2	2.63518
P15149	**CP2A2 Cytochrome P450 2A2**	**0.957158632**	**0.869626**	**11**
P15149	DVQECILEEAGYLIK	0.968456395	3	3.62181
P15149	DVYSSITQLSER	1.158683959	2	2.9051
P15149	FKFPMNLEDINEYPSPIGFTR	0.881663013	3	4.65108
P15149	FSNLAPLGIPR	1.176922252	2	3.21053
P15149	GELPTFNILFK	1.08078295	2	2.39236
P15149	GTDVFPIIGSLMTEPK	0.883170966	2	4.16204
P15149	GYGFSLSNVEQAK	1.064366858	2	3.40367
P15149	IVVLYGYDAVK	2.050164836	2	2.67363
P15149	NFIDSFLIR	1.322790981	2	2.96417
P15149	TLQGTCGAPIDPSIYLSK	0.977082351	2	4.67706
P15149	TVSNVINSIVFGNR	1.001621465	2	3.09106
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.156574255**	**8.22E-06**	**2**
P15178	FQTEIQTVNK	1.055323444	2	2.55636
P15178	QMVKFAANINK+Oxidation(2)	1.213868982	2	2.80452
P15429	**ENOB Beta_enolase**	**1.220030526**	**0.997173**	**5**
P15429	DATNVGDEGGFAPNILENNEALELLK	1.087096297	3	5.52921
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	1.421073234	3	4.7667
P15429	IEEALGDK	1.235829163	1	2.31643
P15429	TAIQAAGYPDK	1.404320073	2	2.4404
P15429	VNQIGSVTESIQACK	1.149277108	2	5.18293
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.080835371**	**3.33E-16**	**22**
P15650	AFVDSCLQLHETK	1.12467112	2	4.08966
P15650	AQDTAELFFEDVR	1.328579698	2	4.87645
P15650	AQDTAELFFEDVRLPASALLGEENK	1.103863925	3	5.30536
P15650	CIGAIAMTEPGAGSDLQGVR	0.979896297	2	5.27547
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(7)	1.546452435	2	5.18064
P15650	EQIEQFIPQMTAGK	0.92450639	2	4.39787
P15650	FFQEEVIPYHEEWEK	1.962186733	2	4.99067
P15650	GFYYLMQELPQER	1.73308401	2	4.28756
P15650	IFSSEHDIFR	1.263730277	2	2.93399
P15650	KFFQEEVIPYHEEWEK	1.912839568	2	5.19708
P15650	KLTDIGIR	1.02392241	2	2.43016
P15650	LDSASASMAK	0.921079017	1	2.33148
P15650	LDSASASMAK+Oxidation(8)	1.203411841	2	2.52865

P15650	LPASALLGEENK	0.908808674	2	2.6773
P15650	LTDIGIR	1.047508407	2	2.34465
P15650	QGLLGINIAEK	0.996869777	2	3.25371
P15650	RLDSASASMAK	1.04115629	2	3.5289
P15650	RLDSASASMAK+Oxidation(9)	1.131080517	2	3.0767
P15650	SGSDWILNGSK	1.141688923	1	2.27566
P15650	TNICVTR	1.057636857	2	2.50199
P15650	VQPIYGGTNEIMK	1.012430677	2	3.42762
P15650	VQPIYGGTNEIMK+Oxidation(12)	1.157875777	2	2.70031
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.016343427**	**2.31E-06**	**9**
P15651	ASSTANLIFEDCR	1.072648363	2	3.20799
P15651	EEGDSWVLNGTK	0.980106986	2	2.96378
P15651	ELVPIAAQLDK	0.852726427	2	2.47645
P15651	ELVPIAAQLDKEHLFPTSQVK	0.54530154	2	4.68818
P15651	GISAFLVPMPTPGLTLGK	0.289569386	2	3.05398
P15651	IGCFALSEPGNGSDAGAASTTAR	1.324931167	2	5.86138
P15651	IGIASQALGIAQASLDCAVK	1.289914653	3	4.72015
P15651	ITEIYEGTSEIQR	0.891344134	2	4.9782
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.003841315	3	3.34039
P15684	**AMPN Aminopeptidase N**	**0.945074833**	**0.050884**	**4**
P15684	ALGDTPAPNIDTTELVER	1.264308441	2	4.17774
P15684	AQIIHDSFNLASAGK	0.962745979	2	3.28821
P15684	LRSALACSNEVWILNR	1.275860907	2	2.34926
P15684	VVATTQMQAADAR	1.177765807	2	3.78635
P15709	**ST2A1 Bile salt sulfotransferase**	**2.334999371**	**0.107577**	**2**
P15709	NHFTVSQAEAFDK	2.271592746	2	4.03877
P15709	SIFTGIGLMR	1.603207633	2	2.69509
P15919	**RAG1 V(D)J recombination_activating protein 1**	**0.832831026**	**0.176212**	**2**
P15919	EEGGDVKAVCLTLFLLALR	0.980094201	2	2.56061
P15919	SQDLDDYLNGPFTVVVK	0.624281959	2	2.57284
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.71251795**	**0.1852**	**3**
P15978	GYEQHAYDGR	1.26938655	2	2.81142
P15978	VEHEGLPEPLSQR	0.924511703	2	3.12613
P15978	YDSDAENPR	1.516002321	2	2.4716
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.050755437**	**0.004058**	**24**
P15999	AVDSLVPIGR	1.0332997	2	3.62852
P15999	EVAAFAQFGSDLDAATQQLLSR	1.08688551	2	6.79081
P15999	FESAFLSHVVSQHQSLLGNIR	1.263968801	3	6.09595
P15999	GIRPAINVGLSVSR	0.930258037	3	3.86254
P15999	GMSLNLEPDNVGVVVFGNDK	1.166372758	2	5.74031
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(2)	0.974623932	2	4.28828
P15999	GYLDKLEPSK	1.009539919	1	3.0064
P15999	ILGADTSVDLEETGR	1.067380122	2	5.06284
P15999	LELAQYR	1.061281602	2	2.72566
P15999	LKEIVTNFLAGFEP	3.603040381	2	3.05903
P15999	LTDADAMK	0.897320545	2	2.55351
P15999	LYCIYVAIGQK	1.194131916	2	2.71271
P15999	NVQAEEMVEFSSGLK	1.421646922	2	4.3384
P15999	QGQYSPMAIEEQVAVIYAGVR	1.559884406	3	5.25368
P15999	RLTDADAMK	0.958698526	2	2.60093
P15999	RLTDADAMK+Oxidation(8)	1.056225505	2	2.32621
P15999	RTGAIVDVPVGDELLGR	0.927845401	2	3.91426
P15999	STVAQLVK	1.004364574	2	2.39534
P15999	TGAIVDVPVGDELLGR	0.984245704	2	4.7202
P15999	TGTAEMSSILEER	0.835837521	2	4.4868

P15999	TGTAEMSSILEER+Oxidation(6)	0.869909097	2	3.15479
P15999	TSIAIDTIINQK	0.899767592	2	4.67326
P15999	VLSIGDGIAR	0.953175679	2	3.16104
P15999	VVDALGNAIDGK	0.97393117	2	4.48119
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.016540731**	**0.998089**	**8**
P16036	ALYSNILGEENTYLWR	1.149157322	2	3.17017
P16036	EEGLNAFYK	0.99255653	1	2.40452
P16036	FGFYEVFK	1.032556763	1	2.25842
P16036	GIFNGFSITLK	1.005967945	2	3.33595
P16036	GSTASQVLQR	1.127699949	2	3.3011
P16036	GWAPTLIGYSMQGLCK	0.884674697	2	2.95809
P16036	IQTQPGYANTLR	1.116787614	2	3.77362
P16036	MYKEEGLNAFYK	0.967638201	3	3.46724
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.044803042**	**2.19E-13**	**28**
P16086	ALINADELANDVAGAEALLDR	1.066003693	2	4.86379
P16086	ALSSEGKPYVTK	1.250075278	2	2.92091
P16086	DLASVQALLR	1.03617726	2	2.95859
P16086	DLSSVQTLLTK	1.168517014	2	2.53705
P16086	GVIDMGNSLIER	0.96547818	2	2.95604
P16086	HQAFEAELSANQSR	0.779244029	2	4.12361
P16086	HQALQAEIAGHEPR	1.14714261	3	4.14896
P16086	HQLLEADISAHEDR	1.090541564	3	3.78848
P16086	KFEEFQTDLAAHEER	1.055966805	3	5.31669
P16086	LFGAAEVQR	1.146957575	2	2.51153
P16086	LGDSHDLQR	1.283388031	2	3.15705
P16086	LGESQTLQQFSR	1.095679486	2	3.43417
P16086	LIQEQHPEEELIK	1.217725973	2	3.55483
P16086	LQQSHPLSANQIQVK	1.242167217	2	4.24201
P16086	LQTASDESYKDPTNIQSK	1.142150224	2	4.51118
P16086	LQVASDENYKDPTNLQGK	1.116473611	2	5.53262
P16086	LSDDNTIGQEEIQQR	0.946951778	2	3.27773
P16086	MTLVASEDYGDTLAAIQGLLK	0.729711812	2	4.37015
P16086	NQALNTDNYGHDLASVQALQR	1.370804657	2	5.75369
P16086	QFQDAGHFDAENIKK	1.090777618	2	2.55648
P16086	REELITNWEQIR	1.250606495	2	4.11876
P16086	SQLLGSAHEVQR	0.588804428	2	3.22964
P16086	SSLSSAQADFNQLAELDR	1.036178508	2	5.20955
P16086	TATDEAYKDPSNLQGK	1.012063696	2	3.67737
P16086	TKQEEVNAAWQR	1.380289493	2	2.93573
P16086	VLETAEDIQER	1.006642793	2	3.48985
P16086	VNDVCTNGQDLIK	1.067779281	2	3.2018
P16086	VNSLGETAQR	1.182768135	2	2.68814
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**0.84787986**	**0.004281**	**9**
P16232	EECALEIIK	1.161693457	1	2.01329
P16232	ETSGIILSQAAPK	0.921769145	2	3.50504
P16232	FALDGFFSTIR	1.032897826	2	2.43072
P16232	FVVEAGK	0.63076368	1	1.91983
P16232	IMEFLSLR	2.170267573	2	2.51041
P16232	KDEVYYDK	0.730576843	1	2.73099
P16232	MGAHVVLTAR	0.971662105	2	2.8789
P16232	MTQPLIASYSASK	1.040374409	2	3.39693
P16232	SSWTPLLLGNPGR	0.70866861	2	3.65145
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.194005809**	**0.257207**	**5**
P16290	AMEAVAAQGK	1.141478081	2	2.5932
P16290	AMEAVAAQGK+Oxidation(2)	1.22032487	2	2.43676
P16290	HGESSWNQENR	1.03849052	2	3.62318

P16290	HYGGLTGLNK	1.157351842	1	3.13769
P16290	VLIAAHGNSLR	1.110246292	2	2.67363
P16303	**CES3 Carboxylesterase 3**	**0.823630715**	**1.55E-05**	**18**
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	1.008133331	3	5.55848
P16303	AKEAAEEPSHWK	0.813207563	2	4.02404
P16303	DGASEEETNLSK	0.876747877	2	4.11285
P16303	EAAEEPSHWK	0.955367105	2	2.78459
P16303	ENIPLQFSEDCLYLNVYTPADLTK	1.845826886	2	4.28307
P16303	ESYPFLPTVIDGVVLPK	0.819059429	3	4.11074
P16303	FAPPQPAEPWNFVK	0.996592616	1	2.4704
P16303	IGASTQAAQR	0.714762403	2	3.30163
P16303	LDLLGNPK	0.819439045	2	2.33394
P16303	MIPVVAEK	0.709885309	1	1.95025
P16303	QEFGWIIPTLMGYPLSEGK	1.12007126	3	4.09105
P16303	QKTEDELLETSLK	0.829639471	2	3.60318
P16303	SFNTVPYIVGINK	0.587218524	2	2.89777
P16303	TEDELLETSLK	0.782844439	2	3.59171
P16303	TTTSAVMVHCLR	0.731651771	2	3.06242
P16303	TVIGDHGDELFSVFGSPFLK	1.230864544	2	5.3946
P16303	YFGGTDDPAK	0.780375592	2	3.24636
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	1.040224666	3	3.74506
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**0.965232077**	**0.999986**	**5**
P16332	EVAQQAVDADVHAVGVSTLAAGHK	0.996088022	3	3.41284
P16332	GDVGMAGVAIDTVEDTK	1.036172572	2	3.46349
P16332	IDSGSEVIVGVNK	0.950878179	2	4.01988
P16332	NTQIIIQEESGIPK	1.128121037	2	3.02319
P16332	TGLQAGLTIDEFAPR	1.006584629	2	3.65999
P16409	**MYL3 Myosin light chain 3**	**1.152779354**	**0.259713**	**10**
P16409	AAPAPAAAPAAAPEPERPK	3.903099296	2	4.03206
P16409	ALGQNPTQAEVLR	0.701551965	2	4.40129
P16409	DTGTYEDFVEGLR	2.174029038	2	2.98157
P16409	EGNGTVMGAELR	1.215834104	2	2.53006
P16409	IEFTPEQIEEFK	1.567641569	2	2.33253
P16409	LMAGQEDSNGCINYEAFVK	2.71238204	2	4.92694
P16409	LTEDEVEK	3.041803335	1	2.19697
P16409	MMDFETFLPMLQHISK	1.790716229	3	4.02227
P16409	NKDTGTYEDFVEGLR	3.0801705	2	4.18895
P16409	VFDKEGNGTVMGAELR	1.37563337	2	3.97205
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.303181238**	**9.9E-20**	**18**
P16617	AHSSMVGVNLPQK	1.040658603	3	3.77739
P16617	AHSSMVGVNLPQK+Oxidation(5)	1.0388283	2	2.46347
P16617	ALESPERPFLAILGGAK	1.714689434	3	4.59707
P16617	DCVGSEVENACANPAAGTVILLENLR	1.284576018	3	6.36409
P16617	GCITIIGGGDTATCCAK	1.112670575	2	5.53714
P16617	IQLINNMLDK	1.070942067	2	2.79485
P16617	IQLINNMLDK+Oxidation(7)	2.06649008	1	2.02735
P16617	ITLPVDFVTADK	1.21297777	2	2.3301
P16617	ITLPVDFVTADKFDENAK	1.801516904	2	5.18403
P16617	QIVWNGPVGVFEWEAFAR	1.182416091	2	4.12494
P16617	SLMDEVVK	1.029434179	2	2.31344
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.295923304	4	5.28195
P16617	TGQATVASGIPAGWMGLDCGTESSK	0.991662178	2	4.70331
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.282665563	3	4.21772
P16617	VLNNMEIGTSLYDEEGAK	1.295249891	2	5.21041
P16617	VLPGVDALSNV	1.462440186	2	2.75884
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.024019114	3	4.66127
P16617	YSLEPVAAELK	1.098135757	2	3.14562

P16638	**ACLY ATP_citrate synthase**	**1.385769592**	**9.9E-20**	**21**
P16638	AFDSGIIPMEFVNK	1.667262441	2	4.11086
P16638	DEPSVAAMVYPFTGDHK	0.965646998	2	2.63843
P16638	DLVSSLTSGLLTIGDR	1.14856387	3	3.92299
P16638	EAYPEEAYIADLDAK	1.184025678	2	3.06508
P16638	EEADEYVDIGALNGVFVLGR	1.124574014	2	4.19979
P16638	FGGALDAAAK	1.400141867	2	2.8616
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.495693935	2	3.81025
P16638	GVTIIGPATVGGIKPGCFK	1.317677634	2	3.62889
P16638	HLLVHAPEDKK	1.60704062	2	3.36346
P16638	IGNTGGMLDNILASK	1.841396759	2	3.20622
P16638	LGLVGVNLSLDGVK	2.320396199	2	2.31625
P16638	QHFPATPLLDYALEVEK	1.190059939	3	4.24256
P16638	RGGPNYQEGLR	1.536139002	2	3.21843
P16638	SAYDSTMETMNYAQIR	1.57364734	2	4.11715
P16638	SGGMSNELNNIISR	1.230659525	2	3.7458
P16638	TIAIIAEGIPEALTR	1.574554539	2	4.06754
P16638	TTDGVYEGVAIGGDR	1.225813114	2	2.87143
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	1.407907983	3	3.6203
P16638	VDATADYICK	1.731062077	2	2.55014
P16638	WGDIEFPPPFGR	1.514377809	2	3.83236
P16638	YICTTSAIQNR	1.423743263	2	2.88397
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**1.043639908**	**0.851121**	**9**
P16970	DQVIYPDGKEDQK	1.342898218	2	3.24385
P16970	EGGWDSVQDWMDVLSGGEK	1.131763107	2	4.38296
P16970	FDHVPLATPNGDILIQDLSFEVR	1.23511958	3	3.85699
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.788836038	3	5.15104
P16970	GYLDNVQLGHILER	0.986504928	2	3.42316
P16970	HLHSTHSELLEDYYQSGR	1.032292329	3	5.33032
P16970	ITEDTVEFGS	0.892857081	1	1.90238
P16970	ITELMQVLK	1.01641464	2	2.52298
P16970	SGANVLICGPNGCGK	1.055244848	2	3.30384
P17077	**RL9 60S ribosomal protein L9**	**1.101335518**	**0.001355**	**7**
P17077	DFNHINVELSLLGK	1.095716201	3	3.51506
P17077	FLDGIYVSEK	1.055108291	2	3.05949
P17077	GTVQQPDE	1.275017061	1	2.18254
P17077	KFLDGIYVSEK	1.21880082	2	2.97119
P17077	TGVACSVSQAQK	1.117633779	2	3.25953
P17077	TICSHVQNMIK	1.073529954	2	3.68726
P17077	TILSNQTVDIPENVDITLK	0.919482718	2	4.83641
P17078	**RL35 60S ribosomal protein L35**	**1.174907466**	**0.08436**	**2**
P17078	QLDDLKVELSQLR	1.179341965	2	2.49378
P17078	VLTVINQTQK	1.161704453	2	3.02413
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.022395225**	**0.941126**	**4**
P17178	DHESTEGPGTGQDRPR	1.014132487	2	2.73442
P17178	TNVNLASAPLLEQVMR	1.08758239	2	4.19874
P17178	VGCLEPSIPEDTATFIR	1.260260165	2	3.42055
P17178	YEVVLSPGMGEVK	0.895225757	2	3.26356
P17209	**MYL4 Myosin light chain 4**	**1.08264697**	**0.731998**	**2**
P17209	HVLATLGEK	1.060568458	1	2.56997
P17209	ITYGQCGDVLR	3.404074621	2	2.47547
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.853688212**	**0.999999**	**11**
P17425	ASAELFNQK	0.674177614	2	2.56948
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	0.854042803	3	5.31104
P17425	ITASLCDLK	0.885066272	1	1.95508

P17425	LEDTYFDRDVEK	0.583261431	2	2.99576
P17425	MFLNDFLNDQNR	0.924852761	2	2.86577
P17425	MGFCTDREDINSLCLTVVQK	0.798939111	2	4.54835
P17425	NSIYSGLEAFGDVK	0.871408326	2	2.7762
P17425	NSLSYDCIGR	0.716867031	2	2.8602
P17425	TCVAPDVFAENMK	0.814455242	2	3.61637
P17425	VTQDATPGSALDK	0.971977406	2	3.61848
P17425	YTIGLGQAR	0.75759377	2	2.78529
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.237693765**	**0.253717**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(7)	1.321969734	2	3.55283
P17426	NADVELQQR	1.230170108	2	2.50568
P17426	VGGYILGEFGNLIAGDPR	1.281372728	2	4.16958
P17475	**A1AT Alpha_1_antiproteinase**	**1.568804136**	**0.000145**	**4**
P17475	MQHLEQTLTK	1.28640829	2	2.68607
P17475	TLLSSLGITR	1.559601011	2	2.90335
P17475	VFNNDADLSGITEDAPLK	1.650559426	2	5.21224
P17475	VINDYVEK	1.407517927	1	2.29083
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.098670074**	**9.9E-20**	**15**
P17764	EEQDKYAIGSYTR	0.96982164	2	3.39493
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.629551681	2	4.53055
P17764	EVYMGNVIQGGEGQAPTR	0.978069635	2	5.24778
P17764	FANEITPITISVK	1.076454165	2	3.97755
P17764	GKPDVVVKEDEEYK	0.920586541	2	3.68399
P17764	GKPDVVVKEDEEYKR	0.953860711	2	4.61252
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.58773076	2	5.23468
P17764	IHMGNCAENTAK	1.3745133	2	3.40438
P17764	IHMGNCAENTAK+Oxidation(3)	1.163271944	2	3.49588
P17764	LEDLIVK	1.00011171	2	2.42947
P17764	LGTIAIQGAIEK	1.449122125	2	3.30409
P17764	QATLGAGLPIATPCTTVNK	1.064756503	2	5.10219
P17764	QGEFGLASICNGGGGASAVLIEK	1.007065039	2	4.73484
P17764	TPIGSFLGSLASQPATK	1.137021858	2	4.21094
P17764	VNVHGGAVSLGHPIGMSGAR	1.075086596	2	5.73296
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.169993446**	**0.037118**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.301962205	3	5.33365
P17879	TTPSYVAFTDTER	1.246504959	2	3.59817
P17879	VEIIANDQGNR	1.123877182	2	3.6672
P17988	**ST1A1 Sulfotransferase 1A1**	**1.26763088**	**3.17E-11**	**6**
P17988	CPGVPSGLETLEETPAPR	1.343423329	2	4.49533
P17988	FDAHYAK	1.201450923	2	2.35627
P17988	NTFTVAQNER	1.134566867	2	2.98804
P17988	SLPEETVDSIVHHTSFK	1.26763752	2	4.5226
P17988	THLPLSLLPQSLLDQK	1.552140423	2	5.00766
P17988	YFAETIGPLQNFTAWPDDLLISTYPK	1.207197318	3	4.15288
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.060852815**	**9.9E-20**	**27**
P18163	AELSVIFADKPEK	1.37751982	2	3.56585
P18163	AILEDMVK	1.083596723	2	2.47225
P18163	ALEDLGR	1.095493925	2	2.46128
P18163	ALKPPCDLSMQSVEVTGTTEGVR	1.080373598	2	4.55493
P18163	CGVEIIGLK	1.204612029	2	2.70455
P18163	GAMVTHQNIMNDCSGFIK	1.39830126	2	5.333
P18163	GFQGSFEELCR	1.253860701	2	3.39265
P18163	GIAVHPELFSIDNGLLTPTLK	1.081346868	2	5.72728
P18163	GIQVSNDGPCLGSR	1.058105971	2	4.48571
P18163	IENIYLR	1.15866191	2	2.96436
P18163	IFGQANTSVK	1.167162364	2	2.60531
P18163	IIVIMDSYDNDLVER	1.377708392	2	4.92926

P18163	LLLEGVENK	1.264591099	2	3.18362
P18163	LLMDDLK	1.157354336	2	2.42593
P18163	LMITGAAPVSATVLTFLR	1.812740946	3	4.14488
P18163	LVDVEDMNYQAAK	1.413191479	2	4.57779
P18163	LVDVEDMNYQAAK+Oxidation(7)	1.283393868	2	2.76249
P18163	NAGLKPFEQVK	1.070711834	2	4.00469
P18163	QVAEMAECIGSALIQK	1.075502896	2	5.25267
P18163	SAVLEDDKLLLYYYDDVR	4.286920545	2	4.23434
P18163	SQIDELYSTIK	1.190071869	2	3.7666
P18163	SQIDELYSTIKI	1.378595527	2	3.11642
P18163	TAEALDKDGWLHTGDIGK	1.259143993	2	5.35417
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	4.371043352	3	6.18746
P18163	TMYDGFQR	1.08158009	1	1.91347
P18163	VLQPTIFPVVPR	1.168442047	2	3.67696
P18163	WLLDFASK	1.200015112	2	2.61246
P18297	**SPRE Sepiapterin reductase**	**1.178112206**	**0.000295**	**5**
P18297	ALAPQLAGLLSPGSVLLLSAR	0.971859419	3	3.93682
P18297	LLLINNAGTLGDVSK	1.805998263	2	3.02938
P18297	LNSEGELVDCGTSAQK	1.181105753	2	4.95214
P18297	TVVNISSLCALQPFK	1.096406503	2	3.13125
P18297	VLSYAPGPLDTNMQQLAR	1.250696278	2	2.74434
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.216259225**	**0.19591**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.250252492	2	5.64405
P18298	KIIVDTYGGWGAHGGGAFSGK	0.965949803	3	3.42374
P18298	YLDEDTIYHLQPSGR	1.128314946	2	4.38983
P18418	**CALR Calreticulin**	**1.355658869**	**9.9E-20**	**17**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	1.224504499	3	6.03649
P18418	CKDDEFTHLYTLIVRPDNTYEVK	1.351473871	3	5.4123
P18418	DMHGDSEYNIMFGPDICGPGTK	1.218428713	2	6.19507
P18418	FYALSAR	1.55684408	2	2.32824
P18418	FYGDQEK	1.111919594	1	2.02837
P18418	FYGDQEKDK	0.847802066	1	2.81995
P18418	GQTLVVQFTVK	1.043682055	2	3.81691
P18418	HEQNIDCGGGYVK	1.157994599	2	4.37352
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.004713415	4	4.66522
P18418	IDNSQVESGSLEDDWDFLPPK	1.380034249	2	5.5175
P18418	IDNSQVESGSLEDDWDFLPPKK	1.471870816	2	5.04996
P18418	IKDPDAAKPEDWDER	1.101860672	2	4.36884
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.03552376	3	5.70029
P18418	LFPGGLDQK	1.390930372	2	2.33984
P18418	QIDNPDYK	1.137515878	1	1.95238
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.354100195	3	5.49448
P18418	VHVIFNYK	1.435558901	1	2.34414
P18420	**PSA1 Proteasome subunit alpha type_1**	**0.90875513**	**0.957337**	**2**
P18420	AQPSQAADEPAEK	0.899235593	2	3.6064
P18420	IHQIEYAMEAVK	1.063696489	2	2.30031
P18421	**PSB1 Proteasome subunit beta type_1**	**1.291019215**	**9.12E-09**	**2**
P18421	AGGSASAMLQPLLDNQVGFK	1.408811805	2	4.796
P18421	NMQNVEHVPLTLDR	1.11223377	2	3.78137
P18422	**PSA3 Proteasome subunit alpha type_3**	**1.295094132**	**0.011165**	**3**
P18422	AVENSSTAIGIR	1.302955658	2	3.31066
P18422	DGVVFGVEKLVLSK	1.393145067	1	1.94563
P18422	HVGMAVAGLLADAR	1.144418152	3	3.60947
P18437	**HMGN2 Non_histone chromosomal protein HMG_17**	**1.25512643**	**0.007593**	**2**
P18437	DANNPAEDGDAK	1.446957788	2	3.327

P18437	DANNPAEDGDAKTDQAQK	0.916667584	2	4.88795
P18445	**RL27A 60S ribosomal protein L27a**	**1.105537248**	**0.481881**	**3**
P18445	NGVAPIIDVVR	1.171328069	1	2.50706
P18445	NQSFCPTVNLDK	1.106132472	2	3.20334
P18445	RNQSFCPTVNLDK	0.882123799	2	3.12376
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**1.356288305**	**0.036086**	**5**
P18484	FFQPTEMASQDFFQR	1.321969734	2	3.98642
P18484	IIGFGSALLEEVDPNPANFVGAGIIHTK	1.20251873	3	3.3996
P18484	ILVAGDTMDSVK	1.376392191	2	2.43865
P18484	NNGVLFENQLLQIGLK	1.126075678	2	2.55224
P18484	YGGTFQNVSVK	0.937768992	2	2.48537
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.139313775**	**0.178735**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	2.134966868	2	3.32976
P18596	SLPSVETLGCTSVICSDK	1.099681938	2	4.27738
P18596	TGTLTTNQMSVCR	1.180692172	2	2.86472
P18596	VGEATETALTCLVEK	1.059024417	2	4.97203
P18757	**CGL Cystathionine gamma_lyase**	**0.991296539**	**0.00071**	**15**
P18757	AGDEVICMDEVYGGTNR	0.925817058	2	5.77259
P18757	ATLGISDTLIR	0.924763218	2	3.56973
P18757	AVAALDGAK	0.900916875	2	2.44511
P18757	AVVLPISLATTFK	0.993710352	3	4.98793
P18757	FLQNSLGAVPSPFDCYLCCR	1.609343287	2	3.61933
P18757	GTLQHAQVFLK	0.886809505	3	3.31622
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.410692409	3	3.79888
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	1.782075217	4	5.75637
P18757	LLEAAITPQTK	0.954632245	2	3.61353
P18757	LSVGLEDEKDLLEDLGQALK	1.017719529	3	6.6441
P18757	LVWIETPTNPTLK	1.085792286	2	3.8029
P18757	QCTGCPGMVSFYIK	1.021683653	2	3.82768
P18757	QDSPGQSSGFVYSR	0.825204597	2	3.89639
P18757	RVASEFGLK	0.98314571	2	2.6509
P18757	VIYPGLPSHPQHELAK	1.028394711	2	4.18863
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.103533315**	**0.166741**	**10**
P18886	ATNLTVSAVR	1.136118659	2	3.51471
P18886	ELHAHLLAQDK	1.056454346	2	3.46718
P18886	LIFDGNEETLK	1.261391995	2	3.24994
P18886	QYGQTVATYESCSTAAFK	1.183769195	2	4.03331
P18886	SEYNDQLTR	2.01733312	2	2.48281
P18886	TETIRPASIFTK	0.973673319	2	3.07115
P18886	TLQAGLLEPEVFHLNPSK	0.68214162	2	4.05955
P18886	TLSIDSIQFQR	1.027870788	2	3.39839
P18886	YILSDSSPVPEFPVAYLTSENR	1.443649789	2	5.21133
P18886	YLNAQKPLLDDSQFR	1.096019787	2	4.7108
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.096674399**	**0.00014**	**16**
P19112	AGGLATTGNEDILDIVPTEIHQK	0.925465125	3	6.21517
P19112	AGGTGEMTQLLNSLCTAIK	1.132311551	2	5.39664
P19112	APVIMGSTEDVQEFLEIYNK	1.528710298	2	4.33775
P19112	APVIMGSTEDVQEFLEIYNKDK	1.317879356	3	3.44544
P19112	DFDPAINEYIQR	0.9218092	2	3.57267
P19112	GNIYSINEGYAK	0.916148676	2	3.94263
P19112	KGNIYSINEGYAK	0.84880973	2	4.21584
P19112	KLDILSNDLVINMLK	1.115793682	2	5.06066
P19112	KTSANEPSEKDALQPGR	1.063689517	3	3.87502
P19112	LDILSNDLVINMLK	1.040645419	2	4.85248
P19112	LLYECNPIAYVMEK	1.980151685	2	4.36435

P19112	QAGIAQLYGIAGSTNVTGDQVK	1.11854155	2	5.89982
P19112	SRPSLPLPQSR	0.847142827	2	3.30219
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.089206604	3	6.00394
P19112	TLVYGGIFLYPANK	0.66482492	2	3.98304
P19112	TSANEPSEKDALQPGR	0.975158472	2	4.45571
P19225	**CP270 Cytochrome P450 2C70**	**1.023937319**	**0.431074**	**12**
P19225	ASLNLSNPQDFIDYFLIK	1.10912343	3	4.09929
P19225	EALIDRGEEFSDK	1.210772017	2	2.49848
P19225	FDPGHFLDEK	1.099883154	2	2.66665
P19225	FILMEINR	1.254032241	2	2.3786
P19225	FSLMVLRSMGMGK+Oxidation(4)	1.576066173	1	1.97209
P19225	GTSVMACLTSALHDDKEFPNPEK	0.945169574	3	4.18647
P19225	IQEEITR	1.026942367	1	2.11767
P19225	IQEEVVYLLEALR	2.73363859	2	3.85904
P19225	KLPPGPTPLPIFGNILQVGVK	1.28194972	2	2.42875
P19225	LPPGPTPLPIFGNILQVGVK	0.968864346	2	4.15151
P19225	TNGSPCDPSFLLACVPCNVISSVIFQHR	1.113482107	3	3.46234
P19225	YIDFVPIPLPR	0.987285706	2	3.11071
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.142296214**	**0.041904**	**5**
P19234	DIEEIIDELR	1.352991102	2	3.63921
P19234	DTPENNPDTPFDFTPENYER	1.074222814	2	4.87634
P19234	FCCEPAGGLTSLTEPPK	1.021639816	2	3.2944
P19234	FCCEPAGGLTSLTEPPKGPGFGVQAGL	1.275016321	2	3.01447
P19234	YHIQVCTTTPCMLR	1.148397679	2	3.32462
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.078179783**	**0.999727**	**8**
P19468	ASGELMTVAR	1.03112372	2	2.33746
P19468	CNQIANELCECPELLGSGFR	1.122792607	2	5.08468
P19468	DKNTPSPFVETFPEDEEASK	0.877733185	2	3.58982
P19468	NTPSPFVETFPEDEEASK	1.056170684	2	4.22959
P19468	SLFFPDEAINK	1.083219262	2	2.47759
P19468	SRYDSIDSYLSK	0.933177355	2	2.92589
P19468	VQLLLNGGDVLETLQEK	1.221304015	2	4.99001
P19468	WGVISASVDDR	1.116550686	2	3.06722
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.143000742**	**0.1296**	**8**
P19488	AEMWLIR	1.1982088	2	2.89595
P19488	ANAIAWALAQIPQK	1.16997522	3	6.59136
P19488	FETFPTSVSKDELEK	1.016324379	2	4.03111
P19488	GAAVTLNIR	1.173120834	2	2.59784
P19488	GHEVTVLKPSAYYVLDPK	1.229285787	2	4.44325
P19488	NWDPFYTEILGRPTTLAETMGK	0.99325708	2	5.31978
P19488	SDLFNALK	1.303190272	2	2.94599
P19488	TILDELVQR	1.015556973	2	3.53007
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.084841558**	**0.000873**	**6**
P19511	HVIQSISAQQEK	1.028687607	2	4.0016
P19511	HVIQSISAQQEKETIAK	0.915726094	3	4.50184
P19511	HYLFDVQR	1.012387089	2	2.69566
P19511	LDYHISVQDMMR	1.113892545	3	3.86915
P19511	LNEEKIAQLEEIK	0.940251516	2	2.58547
P19511	YGASIGEFIDKLNEEK	1.271812247	3	3.60071
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.099992694**	**0.342321**	**13**
P19643	FIGGSGQVSER	1.160041629	2	3.46307
P19643	IISTTNGGQER	1.31090087	2	2.86233
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	0.8482076	3	4.80676
P19643	KFIGGSGQVSER	0.775992746	2	3.2656
P19643	KLCELYAK	0.908925496	2	2.35028
P19643	LERPVIHIDQTGENVVVK	1.128246078	3	5.53296

P19643	LLHDCGLSVVVLEAR	1.477873315	2	3.76398
P19643	TLNHEIYEAK	0.972338876	2	2.5507
P19643	TMDEMGQEIPSDAPWK	0.824903005	2	4.5252
P19643	TYTIRNKNVK	0.835463171	2	2.41103
P19643	VLNSQEALQPVHYEEK	1.049601563	2	4.52995
P19643	YVDLGGSYVGPTQNR	1.163299899	2	5.03237
P19643	YVISAIPPVLGMK	1.086140649	1	2.85453
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.143494327**	**1.11E-16**	**9**
P19804	DRPFFPGLVK	1.027310863	2	2.37981
P19804	EIGLWFKPEELIDYK	1.284569217	2	4.23384
P19804	GDFCIQVGR	1.179937908	2	3.28501
P19804	NIIHGSDSVESAEK	1.101136274	2	4.03956
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.323159403	4	5.65198
P19804	TFIAIKPDGVQR	1.136842214	2	2.98067
P19804	VMLGETNPADSKPGTIR	1.06228647	2	4.47067
P19804	VMLGETNPADSKPGTIR+Oxidation(2)	1.236897673	2	4.25246
P19804	YMNSGPVVAMVWEGLNVVK	1.284064564	2	5.27287
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.154816566**	**0.509037**	**2**
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.069648081	4	5.80814
P19944	INALIK	1.156800712	2	2.42157
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.143641611**	**9.9E-20**	**9**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.387314855	2	5.89606
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.103240884	3	5.12157
P19945	CFIVGADNVGSK	1.192284868	2	3.65941
P19945	GHLENNPALEK	1.134318631	2	3.63395
P19945	GTIEILSDVQLIK	1.321976583	2	3.11062
P19945	IIQLLDDYPK	1.948049738	2	3.46304
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.123993165	3	3.64302
P19945	TSFFQALGITTK	1.316521204	2	4.03437
P19945	VLALSVETDYTFPLAEK	1.411274888	2	4.49478
P20059	**HEMO Hemopexin**	**1.176036986**	**0.998821**	**6**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.125900794	2	4.75245
P20059	FNPVTGEVPPR	1.054505166	2	2.551
P20059	GECQSEGVLFFQGNR	1.282998731	2	3.92552
P20059	LFQEEFPGIPYPPDAAVECHR	1.138467416	3	4.46655
P20059	SGAQATWAELSWPHEK	0.896617153	2	3.41883
P20059	VDGALCLEK	1.124044677	2	2.43399
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.005137631**	**0.999996**	**8**
P20070	DILLRPELEELR	1.094490048	2	2.52696
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	0.966046564	3	5.68783
P20070	LIDKEIISHDTR	1.035225784	3	3.7502
P20070	MSQYLENMNIGDTIEFR	0.983833229	2	5.30685
P20070	SSPAITLENPDIK	0.989005257	2	3.59606
P20070	SSPAITLENPDIKYPLR	0.896662747	2	3.96101
P20070	SVGMIAGGTGITPMLQVIR	0.963150433	2	4.63218
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(14)	1.070590633	2	2.32267
P20280	**RL21 60S ribosomal protein L21**	**1.286734925**	**2.22E-16**	**4**
P20280	HGVVPLATYMR	1.157898919	2	2.50099
P20280	KGDIVDIK	1.214001449	1	2.09018
P20280	TNGKEPELLEPIPYEFMA	0.935460387	2	3.42742
P20280	VYNVTQHAVGIIVNK	1.28072883	2	4.1394
P20651	**PP2BB Serine/threonine_protein phosphatase 2B catalytic subunit beta isoform**	**1.33626745**	**0.180169**	**2**
P20651	GLTPTGMLPSGVLAGGR	1.296749136	2	2.42514
P20651	VVKAVPFPPTHR	2.030781692	1	1.95371
P20673	**ARLY Argininosuccinate lyase**	**0.989245698**	**5.84E-05**	**16**

P20673	AEAECEVLFPGYTHLQR	1.11071097	2	4.16232
P20673	AEMQQILQGLDK	0.879721758	2	4.46989
P20673	EFNFVQLSDAYSTGSSLMPQK	1.203821139	2	5.13317
P20673	FNSSIAYDR	0.773240277	2	2.43725
P20673	HLWNVDLQGSK	0.847953177	1	3.37502
P20673	INVLPLGSGAIAGNPLGVDR	0.819741804	2	5.65649
P20673	KNPDSLELIR	1.069781446	2	2.38016
P20673	LKELIGEAAGK	0.930816974	2	3.19137
P20673	LYPNDEDIHTANER	0.844798088	2	3.87367
P20673	MAEDLILYGTK	1.054171585	2	3.94538
P20673	MAEDLILYGTK+Oxidation(1)	1.064324012	2	2.36843
P20673	NDQVVTDLR	0.956999613	2	3.14768
P20673	SRNDQVVTDLR	1.131742778	2	3.06093
P20673	VAEEWAQGIFK	1.023430296	2	3.44797
P20673	VLIEAMVDR	1.018873152	2	2.59114
P20673	VLIEAMVDRAEAECEVLFPGYTHLQR	1.164426333	3	4.70819
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**0.955091401**	**0.097037**	**5**
P20788	EIDQEAAVEVSQLR	1.148066265	2	3.54303
P20788	EIDQEAAVEVSQLRDPQHDLER	1.094464396	3	3.43463
P20788	ESLSGQAATRPLVATVGLNVPASVR	0.606539451	2	2.77134
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.095242686	3	5.11257
P20788	SGPFAPVLSATSR	0.955487866	2	2.87932
P20801	**TNNC2 Troponin C_ skeletal muscle**	**1.419111959**	**0.678844**	**3**
P20801	GKSEEELAECFR	1.702841009	2	3.39104
P20801	NADGYIDAEELAEIFR	1.705748415	2	4.78359
P20801	SEEELAECFR	0.983922524	2	3.26345
P20812	**CP2A3 Cytochrome P450 2A3**	**0.891924835**	**0.085464**	**2**
P20812	ELQGLEDFITKKVEQNQR	1.441370307	2	2.47118
P20812	YGPVFTIHLGPR	0.883419027	2	3.04289
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.083679247**	**0.948663**	**3**
P20814	FDYEDKDFLNLIEK	1.172678656	2	2.32459
P20814	GTAVLTSLTSVLHDSK	1.009600166	2	3.26994
P20814	IKEHEESLDVSNPR	1.07966042	3	3.59262
P20817	**CP4AE Cytochrome P450 4A14**	**0.958141312**	**0.76382**	**6**
P20817	ACQIAHEHTDGVIK	0.717813246	2	4.26543
P20817	AQLQNEEELQK	0.797283791	2	3.31386
P20817	AVEDLNNLTFFR	0.968438786	2	3.60823
P20817	HLDFLDILLFAK	1.446816876	2	4.20902
P20817	MRKAQLQNEEELQK+Oxidation(1)	1.212702438	2	3.08846
P20817	VLLYDPDYVK	0.843909952	2	2.52886
P20852	**CP2A5 Cytochrome P450 2A5**	**1.165906787**	**0.043113**	**2**
P20852	DFIDSFLIR	1.289461043	2	2.94004
P20852	EALVDQAEEFSGR	1.165618056	2	2.86856
P21213	**HUTH Histidine ammonia_lyase**	**1.156803189**	**0.151618**	**15**
P21213	ALDYLAIGVHELAAISER	1.470763187	2	4.52009
P21213	DIITTELNSATDNPMVFASR	1.706014123	2	4.47528
P21213	EGLALINGTQMITSLGCEAVER	1.185114612	2	3.2451
P21213	GETISGGNFHGEYPAK	0.795125973	2	4.02725
P21213	GEWLAVPCQDGK	1.122409082	2	3.04414
P21213	GYSGISLETLK	1.003267357	2	2.35629
P21213	LQELQVNLVR	1.114895279	2	3.27976
P21213	NKPDNGGFTSVDEVR	1.075827473	2	3.70955
P21213	NSATIPESDDL	0.961520371	1	1.96156
P21213	SHSSGVGKPLSPER	1.074546036	2	4.06823
P21213	SLLDSDHHPSEIAESHR	0.96034423	3	4.60831
P21213	TVVYGITTGFGK	1.026232224	2	3.62126

P21213	VQDAYTLR	0.796691645	2	2.57219
P21213	VWEVAAPYIEK	1.016642074	2	2.58399
P21213	YIALDGDSLSTEDLVNLGK	0.951558605	2	5.30282
P21396	**AOFA Amine oxidase [flavin_containing] A**	**0.980947238**	**0.992073**	**10**
P21396	DVPAIEITHTFLER	1.072477957	2	3.57749
P21396	FVGGSGQVSEQIMGLLGDK	1.059410067	2	3.11795
P21396	IFSVTNGGQER	1.144991928	2	2.48631
P21396	INVLVLEAR	1.205756224	2	3.1376
P21396	KDIWVEEPESK	0.989589606	2	3.85962
P21396	KICELYAK	0.908925496	2	2.35028
P21396	NLPSVPGLLK	0.901139677	1	1.92531
P21396	VLGSQEALYPVHYEEK	0.951875128	2	3.6092
P21396	WVDVGGAYVGPTQNR	1.091476099	2	4.34358
P21396	YVISAIPPILTAK	1.138353744	2	3.12156
P21531	**RL3 60S ribosomal protein L3**	**1.17989249**	**0.974419**	**8**
P21531	AHLMEIQVNGGTVAEK	1.053158613	2	5.25109
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	0.859674269	3	5.40651
P21531	FIDTTSK	1.023517518	1	2.02766
P21531	HGSLGFLPR	1.013945343	2	3.0335
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.051343097	2	5.0679
P21531	NNASTDYDLSDK	1.186167019	2	3.37726
P21531	SINPLGGFVHYGEVTNDFIMLK	1.157508641	3	3.38349
P21531	TVFAEHISDECK	1.053156201	2	3.78217
P21533	**RL6 60S ribosomal protein L6**	**0.943490133**	**5.14E-11**	**9**
P21533	AVDSQILPK	1.140563083	2	2.46888
P21533	FVIATSTK	1.304568336	1	2.22689
P21533	HLTDAYFK	1.077346345	2	2.38372
P21533	HQEGEIFDTEK	0.922881795	2	3.29647
P21533	HQEGEIFDTEKEK	1.005613474	2	4.12737
P21533	HQEGEIFDTEKEKYEITEQR	0.981382906	3	4.7345
P21533	QLGSGLLLVTGPLALNR	1.548806319	2	5.17467
P21533	SSITPGTVLIILTGR	1.262210959	2	4.20423
P21533	YYPTEDVPR	1.110278998	1	1.9665
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.116110889**	**9.9E-20**	**5**
P21571	FEVLDKPQS	0.794876536	1	2.00869
P21571	GEMDKFPTFNFEDPK	1.063860032	3	3.48659
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.026206034	3	3.96893
P21571	LASGGPVDTGPEYQQEVDR	1.603719617	2	5.28884
P21571	LASGGPVDTGPEYQQEVDRELFK	2.027274844	3	3.44619
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.422917812**	**0.848326**	**2**
P21643	YNHVCMVHRMLGSK+Oxidation(10)	1.422917812	2	2.46292
P21643	YNHVCMVHRMLGSK+Oxidation(6)	1.422917812	2	2.30255
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.694021412**	**1.97E-05**	**4**
P21670	ATCIGNNSAAAVSMLK	1.487513005	2	3.31096
P21670	LLDEVFFSEK	1.696451849	2	3.1237
P21670	LNEDMACSVAGITSDANVLTNELR	1.804898133	2	5.07701
P21670	YLLQYQEPIPCEQLVTALCDIK	1.074725883	2	4.04111
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.092137857**	**1**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	1.022335699	3	5.45812
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(23)	0.990387058	3	4.44981
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.09457821**	**0.6504**	**5**
P21913	CGPMVLDALIK	1.140059174	2	2.72806
P21913	CGPMVLDALIKIK	1.068527098	2	2.44257
P21913	CHTIMNCTQTCPK	0.90650171	2	3.99482
P21913	IKNEIDSTLTFR	1.250383766	2	3.4166

P21913	RIDTDLGK	1.140393435	2	2.56856
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**0.931376213**	**0.999774**	**5**
P21981	CDLEIQANGR	0.953415876	2	2.92094
P21981	DHHTADLCQEK	0.608853303	2	2.84356
P21981	SEGTYCCGPVSVR	0.919707599	2	3.71942
P21981	VDLFPTDIGLHK	0.996917681	2	2.73094
P21981	YSGCLTESNLIK	0.948667759	2	2.69664
P22734	**COMT Catechol O_methyltransferase**	**1.395167636**	**0.001012**	**12**
P22734	AIYQGPSSPDKS	1.115666365	2	3.35011
P22734	EWAMNVGDAK	0.883856845	1	2.50438
P22734	GQIMDAVIR	1.00759069	2	3.37809
P22734	GSSSFECTHYSSYLEYMK	24.48319211	2	4.33118
P22734	GTVLLADNVIVPGTPDFLAYVR	1.647130554	3	5.05449
P22734	KGTVLLADNVIVPGTPDFLAYVR	1.405702981	2	4.54399
P22734	KYDVDTLDMVFLDHWK	1.456110063	2	4.99781
P22734	LLTMEMNPDYAAITQQMLNFAGLQDK	1.667496939	3	3.86768
P22734	VTILNGASQDLIPQLK	1.025630721	2	4.41672
P22734	YDVDTLDMVFLDHWK	1.946737641	2	4.05515
P22734	YLPDTLLLEK	1.073074564	2	3.09454
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.2198883	3	6.63069
P22789	**ST2A2 Alcohol sulfotransferase A**	**2.09529096**	**0.293592**	**4**
P22789	ETLQNVCNK	2.266819324	2	2.34416
P22789	KLEPDELDLVLK	1.429578611	2	3.72884
P22789	LEPDELDLVLK	1.831123085	2	2.33869
P22789	NHFTVAQAEAFDK	2.05150087	2	3.39492
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.047633384**	**9.9E-20**	**23**
P22791	ASLDMFNK	0.96037337	2	2.75229
P22791	ASLDMFNKK	0.974135643	2	2.93101
P22791	DVGILALEVYFPAQYVDQTDLEK	1.270209185	3	6.24635
P22791	GLKLEETYTNK	1.386180517	2	2.76196
P22791	GTHMENAYDFYKPNLASEYPLVDGK	0.922911922	3	6.92935
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(4)	0.965277187	3	5.63186
P22791	IGAFSYGSGLAASFFSFR	1.260767776	2	4.38738
P22791	LEETYTNK	1.008989683	2	3.40885
P22791	LEETYTNKDVDK	1.048710056	2	4.27428
P22791	LEVGTETIIDK	0.972460773	2	3.80029
P22791	LMFNDFLSSSSDK	1.776146697	2	3.79475
P22791	LMFNDFLSSSSDK+Oxidation(2)	1.858885441	2	4.06644
P22791	LMFNDFLSSSSDKQNNLYK	1.573219506	2	4.73257
P22791	LSIQCYLR	1.831071645	2	2.45497
P22791	LVSSVSDLPK	1.268226923	2	3.71169
P22791	MGFCSVQEDINSLCLTVVQR	1.224923027	2	4.26833
P22791	MSPEEFTEIMNQR	0.998095127	2	4.77399
P22791	MSPEEFTEIMNQR+Oxidation(1)	1.052092728	2	3.8493
P22791	MSPEEFTEIMNQR+Oxidation(10)	1.184768163	2	3.52905
P22791	TDTWPK	0.94595402	1	1.92958
P22791	TKLPWDAVGR	1.003838177	3	4.03189
P22791	VNFSPPGDTSNLFPGTWYLER	1.376969799	2	4.87764
P22791	YTVGLGQTR	1.001631002	2	3.41611
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.182040384**	**0.905345**	**9**
P22985	DEVTCVGHIIGAVVADTPEHAQR	0.883256889	3	4.50747
P22985	DPPANVQLFQEVPK	1.070427599	2	3.6626
P22985	LDPTFASATLLFQK	1.341998531	2	3.79352
P22985	NQPEPTVEEIENAFQGNLCR	1.044538964	2	4.85716
P22985	QLFQLDSPATPEK	1.182417688	2	3.22698

P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.07024561	3	5.89271
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.169213926	3	4.83397
P22985	TLLRPEEILLSIEIPYSK	1.090142162	2	2.7273
P22985	TNLPSNTAFR	1.182876452	1	2.18131
P23358	**RL12 60S ribosomal protein L12**	**1.11625442**	**1.43E-06**	**5**
P23358	CTGGEVGATSALAPK	1.332706306	2	4.30365
P23358	EILGTAQSVGCNVDGR	0.98964304	2	4.31234
P23358	HNGNITFDEIVNIAR	1.099364586	2	3.9444
P23358	HPHDIIDDINSGAVECPAS	1.325580824	2	4.50222
P23358	QAQIEVVPSASALIIK	1.410551595	2	3.61733
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.284407255**	**9.9E-20**	**9**
P23457	ELTQVFEFQLASEDMK	1.538880918	2	4.59379
P23457	HFDSAYLYEVEEEVGQAIR	3.382759607	2	6.11295
P23457	LLFETVDICDTWEAMEK	2.116501079	2	4.61392
P23457	MLDYCK	1.384950269	1	1.98556
P23457	SIGVSNFNCR	1.243291523	2	3.18867
P23457	SKDIILVSYCTLGSSR	2.886608331	2	4.45343
P23457	VALNDGNFIPVLGFGTTVPEK	1.596463437	2	4.725
P23457	YFDDHPNHPFTDE	1.76946568	2	3.73255
P23457	YKPVCNQVECHLYLNQSK	2.127994833	2	4.6328
P23514	**COPB Coatomer subunit beta**	**1.214993651**	**0.004836**	**6**
P23514	EAGELKPEEEITVGPVQK	1.258063353	2	3.673
P23514	NFENLIPDAPELIHDFLVNEK	1.226963196	3	4.22673
P23514	TNNVSEHEDTDKYR	1.011098946	2	4.59897
P23514	VLQDLVMDILR	1.128730038	2	3.20704
P23514	VLSECSPLMNDIFNK	1.356721508	2	2.60931
P23514	YEAAGTLVTLSSAPTAIK	1.295638873	2	4.52289
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.892428238**	**1.8E-08**	**8**
P23965	ALQLGTLFPPAEALK	0.902825449	2	5.43687
P23965	ATADNLIK	0.961229792	2	2.68971
P23965	DNYVNTIGHR	0.983769248	2	2.78456
P23965	GVILTSERPGIFSAGLDLMEMYGR	1.059282687	3	5.42028
P23965	QREADIQNFTSFISR	1.163941938	2	2.91376
P23965	SLHVYLEK	1.047082488	2	2.37051
P23965	VGLVDEVVPEDQVHSK	0.782213231	2	4.8818
P23965	WFTIPDHSR	0.730920528	2	2.633
P24049	**RL17 60S ribosomal protein L17**	**1.072515731**	**0.555138**	**3**
P24049	EQIVPKPEEEVAQK	1.099919969	2	3.79196
P24049	GLDVDSLVIEHIQVNK	1.062097819	2	4.90415
P24049	YSLDPENPTK	0.931729322	1	2.73885
P24050	**RS5 40S ribosomal protein S5**	**1.38614635**	**0.016379**	**2**
P24050	VNQAIWLLCTGAR	1.375227547	2	2.90943
P24050	WSTDDVQINDISLQDYIAVK	1.379502585	2	4.33325
P24063	**ITAL Integrin alpha_L**	**1.076957739**	**0.654213**	**2**
P24063	ASEAQVLVKVDLIHEK	1.054721549	2	2.32082
P24063	DFEKILEFMK	1.086853823	3	3.68148
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.027995718**	**0.159215**	**5**
P24090	ELACDDPETEHVALIAVDYLNK	1.840592918	3	4.16775
P24090	HAFSPVASVESASGEVLHSPK	1.12569042	3	5.92042
P24090	LGGEEVSVACK	1.007606251	2	3.4567
P24090	VGQPGDAGAAGPVAPLCPGR	1.073042381	2	5.1261
P24090	VLHAQCHSTPDSAEDVRK	1.09377059	3	3.74913
P24268	**CATD Cathepsin D**	**1.149261761**	**0.002107**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.265394325	2	3.36531
P24268	DPTGQPGGELMLGGTDSR	1.143726158	2	4.5752
P24268	GGCEAIVDTGTSLLVGPVDEVK	1.117966064	2	3.22386
P24268	LGGQNYELHPEK	1.812755383	2	2.47498

P24329	**THTR Thiosulfate sulfurtransferase**	**1.043411644**	**0.999993**	**11**
P24329	EGHPVTSEPSRPEPAVFK	0.925043531	2	4.87168
P24329	FQLVDSR	1.030275106	2	2.30478
P24329	GSVNVPFMNFLTEDGFEK	3.025992261	2	3.49929
P24329	HVPGASFFDIEECR	1.095526061	2	4.05663
P24329	KVDLSQPLIATCR	1.070982939	2	4.63171
P24329	RFQLVDSR	0.995612524	2	2.33597
P24329	TVSVLNGGFR	0.986787003	2	3.10426
P24329	TYEQVLENLQSK	0.992351177	2	4.99873
P24329	VDLSQPLIATCR	1.06019654	2	4.00229
P24329	VLDASWYSPGTR	1.071444331	2	3.77804
P24329	YLGTQPEPDAVGLDSGHIR	1.031344893	2	4.75607
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.077174071**	**0.702405**	**9**
P24368	DKPLKDVIIVDCGK	1.101465957	2	3.90701
P24368	DTNGSQFFITTVK	1.145872567	2	3.90366
P24368	DVIIVDCGK	1.025126159	1	1.94534
P24368	HYGPGWVSMANAGK	0.822498659	2	3.98903
P24368	IEVEKPFAIAK	1.08186435	2	3.209
P24368	IEVEKPFAIAKE	1.157522231	2	3.53175
P24368	TVDNFVALATGEK	1.185783963	2	3.36154
P24368	VLEGMDVVR	1.131614878	2	2.9106
P24368	VYFDFQIGDEPVGR	1.127625293	2	3.96812
P24457	**CP2DB Cytochrome P450 2D11**	**0.969260374**	**0.911197**	**2**
P24457	RFSVSTLR	1.203750813	2	2.55274
P24457	SLEEWVTK	0.966268811	2	2.43729
P24470	**CP2CN Cytochrome P450 2C23**	**1.059556939**	**0.000281**	**11**
P24470	ACVGESLAR	1.078108985	2	2.4564
P24470	DLDIKPITTGIINLPPPYK	1.02615065	3	4.33192
P24470	EALLQQGDEFLGR	1.042408135	2	2.46663
P24470	FGLLLLMK	1.346038025	2	3.15316
P24470	GTTVLPMLSSVMLDQK	0.906300807	2	3.8417
P24470	GYGLIFSNGER	1.041051474	2	3.52636
P24470	IEEEKDNLK	1.054451953	2	2.81746
P24470	LPPGPTPLPIIGNLLQLNLK	1.164853546	2	4.21538
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	0.907842	3	4.28827
P24470	TFLNLMDLLNK	1.145714852	2	3.80478
P24470	YITLLPSSLPHAVVQDTK	0.680916852	2	3.94427
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.884673846**	**1.13E-11**	**8**
P24473	AGMATAQAQHLLNK	0.79881956	2	4.15159
P24473	DEDITESQNILSAAEK	0.867590876	2	5.0969
P24473	DSGNQPPAMVPHK	0.859174678	2	2.60118
P24473	FLTAVSMEQPEMLEK	0.851313115	2	5.05287
P24473	IWSRDEDITESQNILSAAEK	1.123443493	3	3.69667
P24473	MELLAYLLGEK	1.523814547	2	3.98391
P24473	QLFQVPMSVPK	0.832968478	2	2.66434
P24473	YGAFGLPTTVAHVDGK	1.092910878	2	3.90811
P25093	**FAAA Fumarylacetoacetase**	**1.118760554**	**3.27E-10**	**15**
P25093	AIDVGQGQTR	1.041175805	2	3.3942
P25093	AQEHIFGMVLMNDWSAR	1.185888178	2	3.62967
P25093	ASLQNLLSASQAQLR	1.011435113	2	4.88337
P25093	ASLQNLLSASQAQLRDDK	1.066504278	2	3.94544
P25093	ASSVVVSGTPIR	1.063658594	2	3.66929
P25093	DIQQWEYVPLGPFLGK	0.96856476	2	4.59629
P25093	FGEPIPISK	0.971461654	2	2.82064
P25093	GEGMSQAATICR	1.069995136	2	3.64031
P25093	GEGMSQAATICR+Oxidation(4)	1.687545155	2	3.11484
P25093	GKENALLPNWLHLPVGYHGR	1.505174827	3	4.55268

P25093	HLFTGPVLSK	1.006841861	1	2.76545
P25093	HQHVFDETTLNSFMGLGQAAWK	1.251357641	2	5.36989
P25093	IGVAIGDQILDLSVIK	1.723321103	2	5.24051
P25093	TFLLDGDEVIITGHCQGDGYR	1.036209392	2	5.22349
P25093	VGFGQCAGK	1.143053479	2	2.715
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.11217112**	**0.365367**	**7**
P25113	ALPFWNEEIVPQIK	1.539732219	2	3.50454
P25113	FSGWYDADLSPAGHEEAK	1.0254575	2	5.05019
P25113	HGESAWNLENR	1.077083318	2	4.10778
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	1.257728226	3	4.06496
P25113	SYDVPPPPMEPDHPFYSNISK	1.097061041	2	4.43328
P25113	YADLTEDQLPSCESLK	1.069501979	2	5.59835
P25113	YADLTEDQLPSCESLKDTIAR	1.138651932	2	5.37597
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.238428235**	**9.9E-20**	**13**
P25235	EDQVIQLMNTIFSK	1.076124184	2	3.43398
P25235	EETVLATVQALHTASHLSQQADLR	1.181757553	3	4.82969
P25235	FPEEEAPSTVLSQNLFTPK	0.975265313	2	4.20804
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.205589996	2	4.76077
P25235	KNFESLSEAFSVASAAAALSQNR	1.18322229	2	5.5998
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.298674313	3	4.44065
P25235	LQVSSVLSQPLAQAAVK	1.326186515	2	5.72862
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.473048431	3	5.58885
P25235	NFESLSEAFSVASAAAALSQNR	1.086247906	2	3.12973
P25235	NIVEEIEDLVAR	1.260430729	3	4.3255
P25235	TGQEVVFVAEPDNK	2.376220175	2	3.85896
P25235	YHVPVVVVPEGSASDTQEQAILR	1.233020803	3	5.76707
P25235	YIANTVELR	1.149635498	2	2.65824
P25318	**CO8A2 Collagen alpha_2(VIII) chain**	**1.033684822**	**0.696752**	**2**
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(10)	1.022751422	2	2.381
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(6)Oxidation(13)	0.917507233	2	2.4913
P25977	**UBF1 Nucleolar transcription factor 1**	**1.300585292**	**0.551922**	**2**
P25977	AKYAKLHPEMSNLDLTK	1.066547889	2	2.55417
P25977	ALKAMEMTWNNMEKK+Oxidation(12)	1.331408682	2	2.3269
P26039	**TLN1 Talin_1**	**1.106721399**	**1.36E-11**	**23**
P26039	ADAEGESDLENSRK	0.923213288	2	3.60975
P26039	AGALQCSPSDVYTK	1.267529002	2	2.82982
P26039	AQEACGPLEMDSALSVVQNLEK	1.293538836	2	4.08805
P26039	ASAGPQPLLVQSCK	0.982937813	2	2.37012
P26039	AVAEQIPLLVQGVR	1.091378094	2	2.92139
P26039	EAAEGLRMATNAAAQNAIKK	1.139834045	2	2.44339
P26039	EADESLNFEEQILEAAK	0.88878493	2	4.33717
P26039	GLAGAVSELLR	1.139385956	2	3.24957
P26039	GVGAAATAVTQALNELLQHVK	1.194855766	2	3.83766
P26039	ILAQATSDLVNAIK	2.119304546	2	3.53115
P26039	LGAASLGAEDPETQVVLINAVK	1.919659092	2	4.70475
P26039	LLGEIAQGNENYAGIAAR	1.122373966	2	4.40817
P26039	LNEAAAGLNQAATELVQASR	1.08458351	2	5.41368
P26039	MVAAATNNLCEAANAAVQGHASQEK	1.319180263	3	3.66054
P26039	NCGQMSEIEAK	1.054888555	2	3.07369
P26039	SNTSPEELGPLANQLTSDYGR	1.157286	2	3.71516
P26039	TEDSGLQTQVIAAATQCALSTSQLVACTK	1.103721998	3	4.32484
P26039	TMLESAGGLIQTAR	1.148768416	2	2.51641
P26039	VGAIPANALDDGQWSQGLISAAR	1.256667027	2	4.73827
P26039	VLGEAMTGISQNAK	1.301431894	2	3.27197

P26039	VLVQNAAGSQEK	1.180877892	2	3.16465
P26039	VSQMAQYFEPLTLAAVGAASK	1.93157248	2	3.11283
P26039	VVAPTISSPVCQEQLVEAGR	1.196352148	2	5.15014
P26043	**RADI Radixin**	**1.294747285**	**4.63E-13**	**13**
P26043	AFAAQEDLEK	1.328623817	2	3.21736
P26043	ALELEQER	1.129826236	2	2.52335
P26043	AQKELEEQTR	0.735033322	2	2.63937
P26043	FFPEDVSEELIQEITQR	1.260815532	3	4.28458
P26043	GTELWLGVDALGLNIYEHDDKLTPK	1.390762447	3	3.46647
P26043	IQNWHEEHR	1.227471263	2	2.78738
P26043	KEEEATEWQHK	1.058854256	2	2.92482
P26043	KKEEEATEWQHK	1.436587765	2	4.34168
P26043	KTQNDVLHAENVK	1.106391967	2	5.1543
P26043	NQEQLAAELAEFTAK	1.229884389	2	5.27631
P26043	QLQALSSELAQAR	1.177147905	2	4.36229
P26043	RKPDTIEVQQMK	1.087476416	2	3.40313
P26043	TQNDVLHAENVK	1.044197825	2	3.90224
P26231	**CTNA1 Catenin alpha_1**	**1.135800272**	**0.168002**	**5**
P26231	LIEVANLACSISNNEEGVK	1.032080851	2	5.87932
P26231	LLEPLVTQVTTLVNTNSK	1.156930324	2	4.15872
P26231	QIIVDPLSFSEER	1.234977795	2	2.36794
P26231	SAAGEFADDPCSSVK	1.622701016	2	2.96272
P26231	TIADHCPDSACK	1.222500477	2	3.30973
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.048478996**	**0.79973**	**8**
P26284	AILAELTGR	1.069534564	2	2.62276
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	1.159747038	3	7.26027
P26284	LEEGPPVTTVLTR	1.059547554	2	3.55914
P26284	MVNSNLASVEELKEIDVEVR	1.161173933	2	4.34429
P26284	NFYGGNGIVGAQVPLGAGIALACK	1.35877264	2	3.74019
P26284	RGDFIPGLR	1.321909572	2	2.38787
P26284	TREEIQEVR	0.93920753	2	3.06142
P26284	VDGMDILCVR	0.915117334	2	2.5749
P26453	**BASI Basigin**	**1.217489888**	**0.355267**	**8**
P26453	GNINVEGPPR	1.097521755	2	3.35906
P26453	KSEHASEGEFVK	1.128967377	2	3.3469
P26453	RKPDQTLDEDDPGAAPLK	1.280281014	3	4.2692
P26453	SEASHPPVDEWVWFK	1.113980444	3	3.36936
P26453	SEHASEGEFVK	1.14413303	3	3.6051
P26453	SGEYSCIFLPEPVGR	1.003171821	2	3.93466
P26453	VLQEDTLPDLQMK	0.992214583	2	4.01197
P26453	YTVDADDR	1.084308539	2	2.41511
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**1.104210354**	**0.096704**	**2**
P26516	SVVALHNLINNK	1.238384991	2	2.80003
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	0.882283011	3	3.71416
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.929433244**	**0.999998**	**8**
P26772	GGEIQPVSVK	0.90548943	2	3.60591
P26772	GGIMLPEK	0.907313904	2	2.53272
P26772	GGIMLPEK+Oxidation(4)	0.976735307	2	2.70833
P26772	GKGGEIQPVSVK	0.947454691	2	3.53918
P26772	KFLPLFDR	0.947723892	2	2.37656
P26772	VLLPEYGGTK	0.996386625	1	2.01096
P26772	VLQATVVAVGSGGK	0.918057975	2	5.2829
P26772	VVLDDKDYFLFR	0.997355075	2	3.47409
P27139	**CAH2 Carbonic anhydrase 2**	**0.983671599**	**0.962341**	**4**
P27139	AVQHPDGLAVLGIFLK	0.974492669	2	3.81361

P27139	IGPASQGLQK	0.972056772	2	3.40212
P27139	ITEALHSIK	0.832915562	2	2.3529
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	1.219311253	3	3.60375
P27321	**ICAL Calpastatin**	**1.217054955**	**0.700167**	**3**
P27321	FQDAPSADGESVAGGVTVATASDK	1.256329976	2	5.30797
P27321	KGSDEVTASSAATGTSPR	1.22102683	2	4.72272
P27321	SQSSEPPVIHEK	0.843370318	2	2.64183
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.962164115**	**1.04E-06**	**7**
P27364	AVLAANGSILK	0.748612022	2	2.93446
P27364	ETILNDREEEHR	0.768627214	2	2.96289
P27364	GDIVDAQFLR	0.839915773	2	3.35188
P27364	IVQMLVQEK	1.022284956	2	3.13219
P27364	NGGTFHTCALR	0.864131016	2	2.55422
P27364	QTILDVNVK	0.77931018	1	2.21038
P27364	SQSIQGQFYYISDDTPHQSYDDLNYTLSK	2.140075198	3	4.17898
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.057288442**	**0.000107**	**6**
P27605	DLNHVCVISESGK	1.105747211	2	3.48921
P27605	FFADLLDYIK	1.638364993	2	3.37062
P27605	NVLIVEDIIDTGK	1.103106637	2	3.91342
P27605	SVGYRPDFVGFEIPDK	0.902868895	3	3.59112
P27605	SYCNDQSTGDIK	1.049109952	2	3.90384
P27605	VIGGDDLSTLTGK	0.950143286	2	3.99524
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.086143758**	**0.033336**	**16**
P27653	ASQAPSSFQLLYDLK	1.370154632	2	4.29894
P27653	AYTEEDLDLVEK	1.018201079	2	3.34346
P27653	CTHWAEGGQGALALAQAVQR	1.088284786	3	3.66164
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.095863747	3	4.27814
P27653	IFHELTQTDK	1.192095611	2	2.66097
P27653	IYGADDIELLPEAQNK	1.167668934	2	5.27295
P27653	KITIGQAPTEK	0.633845988	2	3.12744
P27653	KVVGDVAYDEAK	1.286168993	2	3.7432
P27653	LDIDPETITWQR	1.068005525	2	3.8433
P27653	MHGGGPTVTAGLPLPK	1.295374576	2	2.68929
P27653	QGFGNLPICMAK	1.059541327	2	3.62173
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.116772209	3	4.7468
P27653	TDPAALTDDEINR	1.08809052	2	4.36747
P27653	THLSLSHNPEQK	1.074607288	2	3.83451
P27653	VVGDVAYDEAK	0.971723098	2	3.6761
P27653	YVVVTGITPTPLGEGK	1.183800807	2	4.84132
P27661	**H2AX Histone H2A.x**	**1.110775535**	**0.952833**	**3**
P27661	AGLQFPVGR	1.06600857	2	3.04313
P27661	HLQLAIR	1.019469961	2	2.73042
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.118431371	2	5.25097
P27867	**DHSO Sorbitol dehydrogenase**	**1.184819172**	**2.36E-14**	**15**
P27867	AKEVGADFTIQVAK	1.144167969	2	2.82136
P27867	AMGASQVVVIDLSASR	1.108943776	2	4.74385
P27867	EVGADFTIQVAK	1.11252434	2	3.14212
P27867	GENLSLVVHGPGDIR	1.130306139	2	3.75617
P27867	HSADFCYK	1.168923058	1	2.8912
P27867	IGDFVVK	0.862837947	2	2.63384
P27867	LENYPIPELGPNDVLLK	1.125904527	2	4.99932
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.662314716	2	4.73684
P27867	MHSVGICGSDVHYWEHGR+Oxidation(1)	1.372444978	3	4.05406
P27867	TLNVKPLVTHR	1.117079509	2	3.08312
P27867	VAIEPGVPR	1.275042753	2	2.3142

P27867	VAIEPGVPREIDEFCKIGR	0.616705312	2	2.49435
P27867	VLVCGAGPIGIVTLLVAK	1.667152542	3	5.479
P27867	YCNTWPMAVSMLASK	1.301194573	2	3.39667
P27867	YNLTPSIFFCATPPDDGNLCR	16.42296732	2	4.07654
P27952	**RS2 40S ribosomal protein S2**	**1.193369009**	**0.400296**	**5**
P27952	AEDKEWIPVTK	1.08081333	2	3.55363
P27952	AFVAIGDYNGHVGLGVK	1.168966064	2	3.70254
P27952	GCTATLGNFAK	1.174448787	2	2.79851
P27952	GTGIVSAPVPK	1.157172356	2	2.84961
P27952	TYSYLTPDLWK	1.188439242	2	2.45185
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**0.952190347**	**0.659477**	**27**
P28037	ADPLGLEAEK	0.990109854	1	1.92859
P28037	ANATEFGLASGVFTR	0.994421494	2	4.5381
P28037	AVQMGMSSVFFNK	1.116804844	2	4.07859
P28037	DLGEAALNEYLR	0.876723775	2	3.67135
P28037	DTNHGPQNHEAHLR	1.269901066	2	3.62912
P28037	ECEVLPDDTVSTLYNR	1.389718758	2	3.81771
P28037	EESFGPIMIISR	0.996909501	2	2.8348
P28037	EGHEVVGVFTIPDKDGK	1.076477982	2	4.63908
P28037	GNDKVPGAWTEACGQK	0.872970369	2	4.01048
P28037	GQALPEVVAK	0.997034433	2	2.62661
P28037	GSASSDLELTEAELATAEAVR	0.852195796	2	6.67671
P28037	GVVNILPGSGSLVGQR	0.999057155	2	4.78888
P28037	IGFTGSTEVGK	1.179011335	2	2.58235
P28037	ILPNVPEVEDSTDFFK	1.305674878	2	3.40534
P28037	INWDQPAEAIHNWIR	1.102565558	2	3.83355
P28037	KEGHEVVGVFTIPDKDGK	1.025005391	3	4.4941
P28037	KIGFTGSTEVGK	0.949456232	2	2.73175
P28037	KLVEYCQR	1.389053879	2	2.66768
P28037	LFVEESIHNQFVQK	1.044389187	2	4.79647
P28037	LIAEGTAPR	1.099878392	2	3.63498
P28037	LSDHPDVR	1.034317009	2	2.38056
P28037	NIQLEDGK	1.026387137	1	2.24484
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.202899723	2	4.16
P28037	TDVAAPFGGFK	1.068185264	1	2.04759
P28037	THVGMSIQTFR	1.098553987	2	2.92777
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	0.983397086	2	5.12296
P28037	VVEEVEK	0.921917151	2	2.43771
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.160253858**	**0.034793**	**11**
P28480	AFHNEAQVNPER	1.25004615	2	3.41552
P28480	FATEAAITILR	1.213146068	2	3.10114
P28480	HGGYENAVHSGALDD	1.264565985	2	4.17791
P28480	ICDDELILIK	1.143456831	2	3.46937
P28480	LLEVEHPAAK	1.113353655	2	2.68248
P28480	MLVDDIGDVTITNDGATILK	1.175301033	2	3.56536
P28480	NADELVK	1.264350851	1	1.93357
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.368963407	2	4.56928
P28480	SQNVMAAASIANIVK	1.146691443	2	4.77346
P28480	SSLGPVGLDK	1.141630846	2	2.77135
P28480	YINENLIINTDELGR	1.153136765	2	4.64245
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**1.179795783**	**0.080946**	**3**
P28492	ATGLQTSDPR	0.666968101	2	2.47316
P28492	FVIPDFEEFTGHVDR	0.905695849	2	2.99466
P28492	SNPDLWGVSLCTVDGQR	1.224938113	2	3.63274
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**0.884113938**	**0.830117**	**2**
P28650	LDILDVLSEIK	1.070732993	2	3.12947

P28650	VVDLLATDADIVSR	0.859942082	2	2.67344
P29117	**PPIF Peptidyl_prolyl cis_trans isomerase F_ mitochondrial**	**1.136284138**	**0.197546**	**2**
P29117	GANSSSQNPLVYLDVGADGQPLGR	1.269857556	2	4.01959
P29117	KIVITDCGQLS	1.068935579	2	2.48964
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**0.999745606**	**0.41139**	**15**
P29147	AVLVTGCDSGFGFSLAK	0.841979272	2	5.88232
P29147	FGVEAFSDCLR	1.161458967	2	3.72578
P29147	GFLVFAGCLLK	0.964623795	2	2.97683
P29147	KMWDELPEVVR	1.033319508	2	3.39926
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.623867726	3	6.25766
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(1)	1.265334679	3	4.50835
P29147	MQVMTHFPGAISDK	1.05496428	2	4.51242
P29147	MQVMTHFPGAISDK+Oxidation(1)	1.401627479	2	3.43265
P29147	MQVMTHFPGAISDK+Oxidation(4)	1.336716556	2	3.71535
P29147	MWDELPEVVR	0.872674265	2	3.26073
P29147	MWDELPEVVR+Oxidation(1)	1.041214525	2	3.50851
P29147	TIQLNVCNSEEVEK	0.994625526	2	4.40609
P29147	VSVVEPGNFIAATSLYSPER	0.89296567	2	6.01062
P29147	VVNISSMLGR	1.082809066	2	3.87024
P29147	YEMHPLGVK	1.006928928	1	2.41276
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.902407138**	**0.995713**	**6**
P29266	DLGLAQDSATSTK	0.880380224	2	3.94511
P29266	EAGEQVASSPADVAEK	0.933472529	2	4.80768
P29266	GSLLIDSSTIDPSVSK	0.912767041	2	4.64854
P29266	HGYPLILYDVFPDVCK	1.174008874	2	4.87458
P29266	KGSLLIDSSTIDPSVSK	1.022233547	2	4.04668
P29266	MGAVFMDAPVSGGVGAAR	1.082359593	2	5.02401
P29314	**RS9 40S ribosomal protein S9**	**1.197033181**	**4.47E-06**	**8**
P29314	IGVLDEGK	1.208225678	2	2.31013
P29314	KGQGGAGAGDDEEED	1.104108336	2	4.33377
P29314	KQVVNIPSFIVR	1.165136024	2	2.51484
P29314	LDYILGLK	1.18166546	2	2.74567
P29314	LFEGNALLR	1.422845096	2	2.65637
P29314	QVVNIPSFIVR	1.227516535	2	3.01961
P29314	RLQTQVFK	1.215745515	2	2.31075
P29314	SRLDQELK	1.172030286	3	3.38815
P29315	**RINI Ribonuclease inhibitor**	**1.12266354**	**0.007218**	**8**
P29315	ASLQELDLGSNK	1.007856956	2	2.96929
P29315	LDDCGLTEVR	1.073067829	2	3.18241
P29315	LENCGITSANCK	1.149045211	2	3.32413
P29315	LGNTGIAALCSGLLLPSCR	1.266133026	2	2.7256
P29315	LSLQNCSLTEAGCGVLPDVLR	1.107813763	2	2.91281
P29315	SAIQANPALTELSLR	1.296749136	2	4.49671
P29315	TCSLTAASCPHFCSVLTK	1.143663787	2	2.9278
P29315	TNELGDAGVGLVLQGLQNPTCK	1.193454308	2	5.29196
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.119296811**	**0.786285**	**11**
P29410	AMVASGSELGK	1.0265753	2	2.81291
P29410	AMVASGSELGKK	1.036872137	2	2.84881
P29410	AVLLGPPGAGK	0.934185125	2	2.85463
P29410	EAMKDDITGEPLIR	1.100911001	2	2.3223
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.416434127	3	4.6903
P29410	LEAYHTQTTPLVEYYR	1.16640908	2	5.38048
P29410	LVSDEMVVELIEK	1.197225163	2	4.14955

P29410	NGFLLDGFPR	0.924418109	2	2.64347
P29410	NLETPSCK	1.018679276	2	2.3656
P29410	SYHEEFNPPK	0.959836958	3	3.51733
P29410	TRLEAYHTQTTPLVEYYR	1.090007664	3	3.46213
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**1.134021626**	**0.031084**	**6**
P29411	AYEAQTEPVLQYYQK	1.132713442	2	3.61743
P29411	EDDKPETVIK	0.927211415	2	2.51937
P29411	NLTQCSWLLDGFPR	1.030844338	2	2.64467
P29411	TVGIDDLTGEPLIQR	0.794017297	2	3.96664
P29411	VYNIEFNPPK	1.218578821	2	2.80315
P29411	VYQIDTVINLNVPFEVIK	0.951338769	2	4.40461
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**0.982232002**	**2.47E-07**	**2**
P29419	ELAEAEDVSIFK	0.887560999	1	3.0554
P29419	YSALILGMAYGAK	1.044322341	2	3.89404
P29994	**ITPR1 Inositol 1_4_5_trisphosphate receptor type 1**	**0.923595419**	**0.070258**	**3**
P29994	AKDDLEMSAVITIMQPILR+Oxidation(7)Oxidation(14)	1.404027945	2	2.68091
P29994	CVVQPEAGDLNNPPKK	0.810286927	2	2.33749
P29994	EGASNLVIDLIMNASSDR	1.11209638	2	2.43064
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.371734523**	**0.538062**	**3**
P30009	AEDGAAPSPSSETPK	1.393721032	2	3.6741
P30009	EAEAAEPEQPEQPEQPAAEEPR	1.241400213	2	3.86377
P30009	GEAAAERPGEAAVASSPSK	1.263302316	2	3.48872
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.098241146**	**0.811484**	**3**
P30349	GSPMEISLPIALSK	1.254658452	2	2.44499
P30349	SLSNVIAHEISHSWTGNLVTNK	1.007789545	3	3.51168
P30349	SSALQWLTPEQTSGK	1.093450628	2	3.37807
P30427	**PLEC Plectin**	**0.940512363**	**0.893235**	**4**
P30427	LLDPEDVDVPQPDEK	0.929918234	2	3.59102
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(1)	1.154557864	2	2.42074
P30427	REEAAVDAQQQK	1.109584556	2	3.53455
P30427	VLALPEPSPAAPTLR	0.8204653	2	2.43395
P30713	**GSTT2 Glutathione S_transferase theta_2**	**0.999613597**	**0.983011**	**8**
P30713	AQVHEYLGWHADNIR	1.109451146	2	5.10801
P30713	ERVEAFLGAELCQEAHNPIMSVLGQAAK	0.964528262	3	4.81485
P30713	GQHLSEQFSQVNCLK	1.021983083	2	4.87796
P30713	GTFGVLLWTK	1.306097821	2	2.50197
P30713	NSMVLALQR	0.98224987	2	2.78121
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.87501011	3	4.59753
P30713	VLGPLIGVQVPEEK	1.0427943	2	3.93238
P30713	YQVADHWYPADLQAR	1.125286443	2	5.11325
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.054458391**	**0.552856**	**2**
P30835	NEWGSLLEELVK	1.054506811	2	2.56703
P30835	VFANAPDSACVIGLR	0.594281007	2	2.77419
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.011509113**	**0.999037**	**8**
P30839	EKDILAAIAADLSK	0.974809943	2	4.25476
P30839	FDHILYTGNTAVGK	1.232713034	2	4.19345
P30839	HLTPVTLELGGK	1.061938636	3	3.76892
P30839	LQQLEALR	1.158471143	2	2.58554
P30839	NVEEAINFINDR	1.449812824	2	3.80779
P30839	VMQEEIFGPILPIVSVK	0.972747729	2	4.64674
P30839	VMQEEIFGPILPIVSVK+Oxidation(2)	1.010905994	2	4.13492
P30839	YIAPTILTDVDPNSK	1.110980315	2	4.14758
P30904	**MIF Macrophage migration inhibitory factor**	**1.247487259**	**7.3E-06**	**2**
P30904	LHISPDR	0.999701479	1	1.97335
P30904	LLCGLLSDR	1.504034713	2	2.79832

P31000	**VIME Vimentin**	**1.048200052**	**0.987634**	**13**
P31000	DGQVINETSQHHDDLE	1.071998725	2	3.23385
P31000	KLLEGEESR	0.976422965	2	2.80094
P31000	KVESLQEEIAFLK	1.260322672	2	3.86192
P31000	LGDLYEEEMR	1.324857107	2	3.09224
P31000	LHDEEIQELQAQIQEQHVQIDVDVSKPDLTAALR	1.366874845	4	5.03947
P31000	LLEGEESR	0.918880525	2	2.81075
P31000	LQDEIQNMKEEMAR	1.069939716	2	3.827
P31000	NLQEAEEWYK	1.236030945	2	3.09701
P31000	QDVDNASLAR	1.39257148	2	2.91217
P31000	QVQSLTCEVDALK	1.09402611	2	3.41939
P31000	RQVDQLTNDK	1.152089878	2	3.13207
P31000	TNEKVELQELNDR	1.001450013	2	3.62885
P31000	VELQELNDR	1.021139215	2	2.65614
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**1.901101197**	**7.29E-13**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.163719232	2	6.29438
P31044	LYTLVLTDPDAPSR	1.433173235	2	4.42933
P31044	VDYGGVTVDELGK	1.032619533	2	5.04155
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.932371712	3	5.12668
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.82488528	2	5.39111
P31044	YVWLVYEQEQPLNCDEPILSNK	1.853890769	2	5.25711
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.229133425**	**0.059062**	**21**
P31210	DELLTSLGK	1.181828727	2	2.7158
P31210	DIEALNK	1.106977948	1	2.46311
P31210	EEMKDIEALNK	1.145504612	2	3.6799
P31210	ENFQIFDFSLTK	1.526464836	2	2.85029
P31210	FVEMLMWSDHPEYPFHDEY	1.894709958	3	3.87278
P31210	GLVVIPK	1.10264745	2	2.38893
P31210	HIDGAYVYR	1.197025726	2	2.90797
P31210	IKENFQIFDFSLTK	2.067097632	3	4.1217
P31210	LWSTDHDPEMVRPALER	1.285321474	2	2.35625
P31210	NEHEVGEAIR	1.038085696	2	3.07635
P31210	NPLWVNVSSPPLLK	1.197233607	2	4.12897
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.257447696	3	5.82048
P31210	QLEVILNKPGLK	1.239672826	2	3.5932
P31210	REEIFYCGK	1.909994315	2	2.79212
P31210	RQLEVILNKPGLK	1.28538045	3	4.24928
P31210	SLGVSNFNR	1.286125533	2	2.39868
P31210	SNLCATWEALEACK	1.155557557	2	4.60709
P31210	SNLCATWEALEACKDAGLVK	1.126568192	2	4.80441
P31210	TAIDEGYR	1.085372684	2	2.89833
P31210	TQAQIVLR	1.082831328	2	2.91229
P31210	YKPVTNQVECHPYFTQTK	1.191871895	2	5.61473
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.026837915**	**0.962251**	**2**
P31230	KEIEELK	1.026942367	1	1.94919
P31230	TVVSGLVNHVPLEQMQNR	0.985996765	3	3.44867
P31232	**TAGL Transgelin**	**1.560898377**	**0.386224**	**2**
P31232	KYDEELEER	1.558431405	2	2.58695
P31232	TVMALGSLAVTK	1.612856015	2	2.81939
P31254	**UBA1Y Ubiquitin_like modifier_activating enzyme 1 Y**	**1.133080585**	**0.237979**	**2**
P31254	YDGQVAVFGSDLQEK	1.113745453	2	4.52429
P31254	YFLVGAGAIGCELLK	1.238254497	2	2.76566
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.161687642**	**0.013017**	**9**
P31399	ANVDKPGLVDDFK	1.079069519	2	3.90879

P31399	KYPYWPHQPIENL	1.156825226	2	2.84699
P31399	NCAQFVTGSQAR	1.016157855	2	3.86671
P31399	NMIPFDQMTIDDLNEVFPETK	1.106472346	2	5.28887
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(2)	1.166776116	2	3.13339
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(8)	1.166776116	2	2.31156
P31399	SWNETFHTR	1.000419655	2	2.71763
P31399	TIDWVSFVEIMPQNQK	1.607067813	2	3.28401
P31399	YTALVDAEEKEDVK	1.118476016	2	3.5653
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.066928651**	**1**	**4**
P32089	FIHDQTSSNPK	1.068975859	1	3.7498
P32089	GLSSLLYGSIPK	1.07289964	2	3.82235
P32089	NTLDCGVQILK	1.092265389	2	3.79969
P32089	TQLQLDER	1.024210192	2	2.60979
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.004158086**	**0.793359**	**3**
P32198	ELEQQMQQILDDPSEPQPGEAK	1.048372691	2	4.06369
P32198	LLGSTIPLCSAQWER	0.784255291	2	3.01007
P32198	MTALAQDFAVNLGPK	0.999862073	2	4.23592
P32232	**CBS Cystathionine beta_synthase**	**1.320107064**	**9.9E-20**	**8**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.268514549	3	5.32512
P32232	FDSPESHVGVAWR	1.043222565	2	3.2914
P32232	LKNEIPNSHILDQYR	2.011330809	3	3.55126
P32232	NASNPLAHYDDTAEEILQQCDGK	1.403221599	2	5.5608
P32232	SNDDDSFAFAR	1.229233655	2	3.05613
P32232	VDMLVASAGTGGTITGIAR	1.076316308	2	4.60531
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.417797359	3	4.19968
P32232	VRPSDEVCK	1.274585217	3	3.60828
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.049865339**	**0.007699**	**11**
P32551	AVAFQNPQTR	0.945050276	2	3.43255
P32551	AVAQGNLSSADVQAAK	0.992937225	2	5.08211
P32551	GNNTTSLLSQSVAK	0.977282257	2	3.97255
P32551	IIENLHDVAYK	1.099350088	2	4.04631
P32551	ITSEELHYFVQNHFTSAR	1.154587269	3	3.47333
P32551	NALANPLYCPDYR	1.254068718	2	3.37334
P32551	RGNNTTSLLSQSVAK	0.76233774	2	2.78732
P32551	RWEVAALR	1.107691727	2	2.76017
P32551	SMTASGNLGHTPFLDEL	1.251637965	2	3.14723
P32551	TSAPGGVPLQPQELEFTK	1.004549423	2	3.82602
P32551	YENYNYLGTSHLLR	1.901395593	2	4.0698
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.13762729**	**9.9E-20**	**19**
P32755	AFEEEQALR	1.122593093	2	3.37573
P32755	DIAFEVEDCEHIVQK	1.372644734	2	3.99897
P32755	ENMDVLEELK	1.234452701	2	2.66902
P32755	FAVLQTYGDTTHTLVEK	1.32582934	2	5.1436
P32755	FLHFHSVTFWVGNAK	1.042716398	3	3.46638
P32755	FLPGFEAPTYK	1.10387954	2	2.56265
P32755	FWSVDDTQVHTEYSSLR	1.725432779	2	5.67879
P32755	GMEFLAVPSSYYR	1.15333486	2	2.62821
P32755	GNLTDLETNGVR	1.225959586	2	3.67673
P32755	HGDGVKDIAFEVEDCEHIVQK	1.113773845	3	4.85014
P32755	HNHQGFGAGNFNSLFK	1.021575018	3	4.6907
P32755	ILVDYDEK	1.243653703	1	1.98626
P32755	IVFVLCSALNPWNK	1.567285982	2	2.53189
P32755	IVREPWVEEDKFGK	1.249062708	3	4.35377
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.480409031	3	7.42219

P32755	MGFEPLAYK	1.786935271	2	2.60223
P32755	SIVVANYEESIK	1.097686518	2	4.06788
P32755	SQIQEYVDYNGGAGVQHIALR	1.246716925	2	5.59296
P32755	TEDIITTIR	1.162157869	2	3.34272
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.139967057**	**0.305325**	**2**
P33124	ALRPTIFPVVPR	1.153799648	2	3.25879
P33124	IENIYIR	1.15866191	2	2.96436
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.12561883**	**9.9E-20**	**27**
P34058	ADLINNLGTIAK	1.059977448	2	4.22333
P34058	EDQTEYLEER	1.187735784	2	3.49202
P34058	EGLELPEDEEEK	1.110040209	2	2.46027
P34058	EGLELPEDEEEKKK	1.208407202	2	3.14997
P34058	ELISNASDALDK	1.029255379	2	3.70609
P34058	GEKEEEDKEDEEKPK	0.797563511	3	4.10484
P34058	GFEVVYMTEPIDEYCVQQLK	3.369092589	2	3.42509
P34058	GVVDSEDLPLNISR	1.112294501	2	4.86952
P34058	HFSVEGQLEFR	1.193507821	2	2.94331
P34058	HLEINPDHPIVETLR	1.100042118	2	4.45711
P34058	HSQFIGYPITLYLEK	4.348358069	2	3.94776
P34058	IDIIPNPQER	1.05147043	2	2.91907
P34058	KHLEINPDHPIVETLR	1.075336896	2	4.89144
P34058	LGIHEDSTNR	1.079247499	2	3.04115
P34058	LGLGIDEDEVTAEEPSAAVPDEIPPLEGDEDASR	1.196902138	2	4.51237
P34058	NPDDITQEEYGEFYK	1.376400983	2	4.60877
P34058	RAPFDLFENK	1.350127356	2	3.02492
P34058	SIYYITGESK	1.389487978	2	2.62993
P34058	SLTNDWEDHLAVK	1.223014481	2	4.3259
P34058	TLTLVDTGIGMTK	1.060784717	2	4.34295
P34058	TLTLVDTGIGMTK+Oxidation(11)	1.226849138	2	3.38947
P34058	VFIMDSCDELIPEYLNFIR	1.428340435	2	2.48167
P34058	VILHLKEDQTEYLEER	1.342514073	3	4.54448
P34058	YESLTDPSK	1.097710889	2	2.91835
P34058	YESLTDPSKLDSGK	1.092076408	2	3.45804
P34058	YHTSQSGDEMTSLSEYVSR	1.252039013	2	5.49948
P34058	YIDQEELNK	1.10344812	2	3.48987
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.208980299**	**1.77E-06**	**2**
P34064	AIGSASEGAQSSLQEVYHK	1.208893451	2	4.51252
P34064	LNATNIELATVQPGQNFHMFTK	1.535763653	3	3.39202
P34067	**PSB4 Proteasome subunit beta type_4**	**1.321849176**	**0.001897**	**4**
P34067	FDCGVVIAADMLGSYGSLAR	0.93487765	2	3.93523
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.171486425	2	4.03093
P34067	TQNPMVTGTSVLGVK	1.186934548	2	2.36665
P34067	VNDSTMLGASGDYADFQYLK	1.467166852	2	5.34589
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.291646566**	**8.77E-10**	**2**
P35171	GGTSDALLYR	1.290075124	2	3.24496
P35171	LFQEDNGMPVHLK	1.1334142	2	3.6959
P35213	**1433B 14_3_3 protein beta/alpha**	**1.107816073**	**2.27E-06**	**7**
P35213	AVTEQGHELSNEER	1.085356869	2	4.48384
P35213	EKIEAELQDICSDVLELLDK	1.294138429	3	5.31282
P35213	QTTVSNSQQAYQEAFEISK	1.177903881	2	5.43528
P35213	TAFDEAIAELDTLNEESYK	1.682647742	2	4.91193
P35213	YDDMAAAMK	1.080012007	2	2.65987
P35213	YLILNATHAESK	1.10583294	2	3.53921
P35213	YLSEVASGDNK	1.156549196	2	3.14286
P35278	**RAB5C Ras_related protein Rab_5C**	**1.042228436**	**0.592481**	**3**
P35278	FEIWDTAGQER	0.680897353	2	2.83413

P35278	GVDLQESNPASR	1.041332114	2	3.20818
P35278	NEPQNAAGAPGR	1.07873062	2	3.10611
P35427	**RL13A 60S ribosomal protein L13a**	**1.168513771**	**0.531058**	**3**
P35427	CEGINISGNFYR	1.215086642	2	2.96016
P35427	VLDGIPPPYDK	1.160498443	2	2.66178
P35427	YQAVTATLEEK	1.139071219	2	3.20234
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**0.996433441**	**0.979475**	**2**
P35434	AQSELSGAADEAAR	0.998048866	2	4.66133
P35434	IEANEALVK	0.945102025	2	2.54005
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.050181388**	**0.416758**	**6**
P35435	GLCGAIHSSVAK	1.070613361	2	3.6061
P35435	HLIIGVSSDR	1.015994435	2	3.23442
P35435	NASDMIDK	0.83239539	1	2.12466
P35435	NDMAALTAAGK	1.012502461	2	3.76902
P35435	THSDQFLVSFK	1.051712186	1	2.87242
P35435	VYGTGSLALYEK	1.384041976	2	3.45409
P35559	**IDE Insulin_degrading enzyme**	**1.247750448**	**0.228362**	**2**
P35559	SNPGHYLGHLIGHEGPGSLLSELK	1.24728621	3	3.76113
P35559	YTLETRPNQEGIDVR	1.270294442	2	2.51383
P35565	**CALX Calnexin**	**1.047069005**	**0.999623**	**9**
P35565	GSLSGWILSK	0.798197324	2	2.35778
P35565	KIPNPDFFEDLEPFR	1.099340296	3	4.96265
P35565	NKGDEEEEEKLEEK	0.979006842	2	5.18369
P35565	SDTSTPPSPK	0.901793572	2	2.88045
P35565	TDAPQPDVKDEEGKEEEK	0.974369826	3	4.06679
P35565	TSELNLDQFHDK	1.058283242	2	3.78415
P35565	VVDDWANDGWGLK	0.96802207	2	3.71041
P35565	VVDDWANDGWGLKK	0.748735374	2	3.29199
P35565	WEVDEMKETK	1.049524448	2	2.55896
P35704	**PRDX2 Peroxiredoxin_2**	**1.13825684**	**0.219209**	**4**
P35704	EGGLGPLNIPLLADVTK	1.12763325	2	3.49647
P35704	KEGGLGPLNIPLLADVTK	1.230877086	2	4.73941
P35704	QITVNDLPVGR	1.125967324	2	3.23353
P35704	SLSQNYGVLK	1.076087283	2	2.55636
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.835332098**	**0.034537**	**4**
P35738	GLLLSCIEDKNPCIFFEPK	0.776246499	3	4.01304
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	0.649389039	3	5.8539
P35738	MNLFQSITSALDNSLAK	1.021392326	2	3.3925
P35738	SGDLFNCGSLTIR	0.77875937	2	3.53806
P35815	**PPM1B Protein phosphatase 1B**	**0.863523064**	**0.638463**	**3**
P35815	ILSAENIPNLPPGGGLAGK	1.11093538	2	2.50838
P35815	IQNAGGSVMIQR	0.770927424	2	2.32354
P35815	SGFALEPSVENVK	1.036178907	2	2.30695
P36201	**CRIP2 Cysteine_rich protein 2**	**1.096026387**	**0.917698**	**3**
P36201	ASSVTTFTGEPNMCPR	1.710411444	2	3.65802
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	0.986171469	3	5.91944
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.139865254	2	4.87248
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**0.908625341**	**0.997163**	**9**
P36365	AILTQWDR	0.994495936	1	2.03087
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.333576521	3	3.98252
P36365	FTEHVEEGR	0.920071716	2	3.38251
P36365	NLLPTPVVSWLISK	1.083330766	2	2.58113
P36365	SCDLGGLWR	1.000798122	2	2.69657
P36365	TQLREPVLNDELPGR	0.879586501	3	4.01191
P36365	VAIVGAGVSGLASIK	0.99635904	2	3.07229

P36365	VEDGQASLYK	0.907124791	2	3.18402
P36365	VLVVGMGNSGTDIAVEASHLAK	0.996286014	2	5.21891
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.540478859**	**9.9E-20**	**8**
P36511	ANIIAWALAQIPQK	1.324104614	3	5.92539
P36511	FVTFPTSFSSHDLENFFTR	2.248836837	2	4.57459
P36511	GHEVTVLRPSAFVFLDPK	1.77626965	3	3.64633
P36511	IILEELVQK	1.316128501	2	3.36893
P36511	NAMWLSTIHHDQPTKPLDR	1.41951113	3	3.44583
P36511	NAMWLSTIHHDQPTKPLDR+Oxidation(3)	2.053808934	3	3.30852
P36511	SDLLNALEEVIDNPFYK	1.223848894	3	5.30269
P36511	TLGRPTTLAEIMGK	1.625938416	3	3.58085
P36972	**APT Adenine phosphoribosyltransferase**	**1.04517023**	**0.999589**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	1.082400923	2	4.20348
P36972	IDYIAGLDSR	0.989305626	2	2.47272
P36972	SFPDFPIPGVLFR	1.03815513	2	3.07301
P37397	**CNN3 Calponin_3**	**0.960040584**	**0.035678**	**4**
P37397	AGQSVIGLQMGTNK	0.956248476	2	2.72514
P37397	LTLQPVDNSTISLQMGTNK	1.251672937	2	3.42462
P37397	VNESSLNWPQLENIGNFIK	0.752871435	2	3.90163
P37397	YDQQAEEDLR	0.834953537	2	2.8974
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**0.928907009**	**0.982604**	**5**
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.001671843	2	3.56201
P38650	ILDDDTIITTLENLK	1.064300662	2	2.61655
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	0.832317045	3	5.07112
P38650	VQGLTVEQAEAVAR	0.983149985	2	2.96991
P38650	VTDFGDKVEDPTFLNQLQSGVNR	0.911067246	3	3.66515
P38652	**PGM1 Phosphoglucomutase_1**	**0.966252508**	**0.054188**	**18**
P38652	ADNFEYSDPVDGSISK	1.079542715	2	4.92617
P38652	AIGGIILTASHNPGGPNGDFGIK	1.071453551	2	5.63218
P38652	FFGNLMDASK	1.141201982	2	2.59143
P38652	FNISNGGPAPEAITDK	1.231523242	2	4.26755
P38652	IDAMHGVVGPYVK	0.831798849	2	2.96655
P38652	ILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMK	1.987647566	3	3.37028
P38652	INQDPQVMLAPLISIALK	1.165015488	2	3.58568
P38652	KQRVEDILK	0.866592948	1	2.01895
P38652	LSGTGSAGATIR	1.320363772	2	3.47282
P38652	LVIGQNGILSTPAVSCIIR	1.561955896	2	4.77011
P38652	NIFDFNALK	1.063866398	2	2.48346
P38652	QEATLVVGGDGR	1.079671464	2	3.7008
P38652	QQFDLENK	1.021154098	1	2.09597
P38652	SFVGKQFSANDK	0.769082315	1	1.92402
P38652	SGEHDFGAAFDGDGDR	0.963261924	2	4.36454
P38652	TIEEYAICPDLK	1.124505908	2	3.7556
P38652	TQAYPDQKPGTSGLR	1.129261354	2	3.45616
P38652	YDYEEVEAEGANK	1.008000811	2	5.31785
P38656	**LA Lupus La protein homolog**	**1.156313616**	**0.016722**	**2**
P38656	ITDDQQESLNK	1.1549451	2	4.1279
P38656	LDEGWVPLETMIK	1.280910544	2	2.78254
P38659	**PDIA4 Protein disulfide_isomerase A4**	**1.090207736**	**0.203048**	**20**
P38659	DLGLSESGEDVNAAILDESGKK	1.276244163	2	5.14518
P38659	DNDPPIAVAK	1.18118985	2	2.55454
P38659	EVSQPDWTPPPEVTLTLTK	1.088158429	2	3.57532
P38659	FDVSGYPTIK	1.110877033	2	2.96998
P38659	FDVSGYPTLK	1.110877033	2	2.96998
P38659	FIDEHATK	0.989633972	2	2.77238
P38659	GQAVDYDGSR	1.262133494	2	2.48268

P38659	GRPFDYNGPR	1.110368984	2	2.64129
P38659	IDATSASMLASK	1.225456884	2	4.09037
P38659	KGQAVDYDGSR	1.197453943	2	2.96801
P38659	MDATANDITNDR	1.086564326	2	3.63708
P38659	MHVMDVQGSTEASAIK	1.116383042	2	4.43626
P38659	MHVMDVQGSTEASAIKDYVVK	1.071912789	3	3.88319
P38659	RFDVSGYPTLK	1.158239072	2	3.18527
P38659	RSPPIPLAK	1.244280898	2	2.88553
P38659	TFDAIVMDPK	1.060504257	1	2.00869
P38659	TQEEIVAK	1.146271415	2	2.32662
P38659	VDATEQTDLAK	1.084911806	2	3.58465
P38659	VEGFPTIYFAPSGDK	2.506574048	2	3.25415
P38659	YGIVDYMVEQSGPPSK	1.647161736	2	3.45641
P38718	**BR44 Brain protein 44**	**1.053122084**	**0.131369**	**3**
P38718	LMDKVELLLPK	0.530963264	2	2.72155
P38718	LRPLYNHPAGPR	1.8380866	2	2.46548
P38718	YSLVIIPK	1.196756284	2	2.35093
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.913368607**	**0.988576**	**7**
P38918	FFGNPFSQLYMDR	1.47906177	2	2.52821
P38918	FYAFNPLAGGLLTGR	1.388774743	2	4.75345
P38918	GHTEIDTAFVYANGQSETILGDLGLGLGR	0.994391996	3	4.96225
P38918	MDVTSSSASVR	0.808603833	2	3.77662
P38918	QVETELFPCLR	0.940094281	2	2.55931
P38918	RMDVTSSSASVR	0.834293955	2	3.75681
P38918	TTYGPTAPSMISAAVR	0.972903027	2	3.75915
P38983	**RSSA 40S ribosomal protein SA**	**1.129730975**	**2.22E-16**	**6**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.469577647	3	6.09168
P38983	AIVAIENPADVSVISSR	1.130121496	2	4.77605
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.712489202	3	4.05691
P38983	FTPGTFTNQIQAAFR	1.057523787	2	4.52958
P38983	SDGIYIINLK	1.011665396	1	2.1205
P38983	YVDIAIPCNNK	1.16803336	2	3.15111
P39032	**RL36 60S ribosomal protein L36**	**1.125284475**	**0.386177**	**2**
P39032	EELSNVLAAMRKAAAK+Oxidation(10)	0.591320404	2	2.32587
P39032	KREELSNVLAAMR	1.044232792	3	3.30133
P40112	**PSB3 Proteasome subunit beta type_3**	**1.221023386**	**0.463869**	**2**
P40112	FGIQAQMVTTDFQK	1.028441008	2	3.98683
P40112	FGPYYTEPVIAGLDPK	1.290668061	2	3.05282
P40307	**PSB2 Proteasome subunit beta type_2**	**1.648974328**	**2.43E-08**	**3**
P40307	FILNLPTFSVR	1.721046027	2	2.85654
P40307	NGYELSPTAAANFTR	1.274508465	2	4.03725
P40307	VIDKDGIHNLENITFTK	1.23440175	2	4.0365
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.402117141**	**2.98E-07**	**5**
P41034	AECPELSADLHPR	1.124577239	2	3.09518
P41034	AIFDLEGWQISHAFQITPSVAK	0.935923768	2	4.32278
P41034	AQEEGVPETPQPLTDAFLLR	1.639396818	2	4.18517
P41034	GIHLINEPVIFHAVFSMIKPFLTEK	1.144254256	4	4.89597
P41034	QLNEQPDHSPLVQPGLAELR	1.277213337	3	3.64149
P41123	**RL13 60S ribosomal protein L13**	**1.178706502**	**0.289511**	**5**
P41123	AITEEEKNFK	1.22700905	2	2.45519
P41123	LATQLTGPVMPIR	1.139934836	2	2.77896
P41123	STESLQANVQR	1.103606027	2	4.00396
P41123	TIGISVDPR	1.131628444	2	2.30872
P41123	VDTWFNQPAR	1.155896928	2	3.15199
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.124595043**	**0.002214**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.046634526	2	4.65872

P41498	IELLGSYDPQK	1.324193365	2	3.66245
P41498	LVTDENVSDNWR	1.062039059	2	3.6891
P41542	**USO1 General vesicular transport factor p115**	**1.13269771**	**0.013518**	**11**
P41542	AETLAKSVPVEGESELVTAAK	0.843646452	3	3.32376
P41542	AWFEVGDENPGWSAQK	0.858354592	2	4.02573
P41542	CQNEQLQTAVTQQASQIQQHK	1.179306498	3	3.84782
P41542	IVAFENAFER	1.113805326	2	2.64204
P41542	LQTENSELQQR	1.191094951	2	3.05572
P41542	LREEIEELR	1.137524644	2	2.62176
P41542	QLGPPVQQIILVSPMGVSK	1.130147064	2	4.26816
P41542	SQLCSQSLEITR	1.142978949	2	2.94369
P41542	SVPVEGESELVTAAK	1.065153325	2	3.37481
P41542	TLEQHDNIVTHYK	1.072938004	2	3.80628
P41542	VLVSPTNPPGATSSCQK	1.184473128	2	3.872
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**1.450189819**	**9.9E-20**	**18**
P41562	ATDFVVPGPGK	1.183521371	2	3.38304
P41562	CATITPDEK	1.246564171	2	2.92148
P41562	CATITPDEKR	1.270988794	2	2.5026
P41562	FKDIFQEIYDK	1.12356282	3	4.60652
P41562	GQETSTNPIASIFAWSR	1.545091827	2	5.30958
P41562	GWPLYLSTK	2.83231715	1	1.90683
P41562	IHGGSVVEMQGDEMTR	1.216227081	2	5.18174
P41562	IIWELIK	1.248128873	2	2.3452
P41562	KIHGGSVVEMQGDEMTR	1.079270498	3	3.31821
P41562	LIDDMVAQAMK	1.126177407	2	4.4941
P41562	LILPYVELDLHSYDLGIENR	2.316265713	2	5.19776
P41562	LVTGWVKPIIIGR	1.441590065	2	3.35175
P41562	SDYLNTFEFMDK	1.449745484	2	4.43712
P41562	SEGGFIWACK	1.11998112	2	3.51202
P41562	SIEDFAHSSFQMALSK	1.08007681	2	4.9398
P41562	TVEAEAAHGTVTR	1.105122214	2	3.942
P41562	VEITYTPK	1.117901153	2	2.73946
P41562	VTYLVHDFEEGGGVAMGMYNQDK	0.932865839	3	3.61574
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.381035383**	**0.000167**	**5**
P42123	DYSVTANSK	1.113983785	2	2.82196
P42123	IVADKDYSVTANSK	3.81017732	2	2.78346
P42123	LIAPVADDETAVPNNK	1.294103212	2	2.58465
P42123	SLADELALVDVLEDK	1.262795241	2	2.9504
P42123	VIGSGCNLDSAR	1.233691782	2	3.80428
P42930	**HSPB1 Heat shock protein beta_1**	**3.79087099**	**0.330704**	**2**
P42930	AQIGGPESEQSGAK	5.477589883	2	3.89039
P42930	VSLDVNHFAPEELTVK	2.166285108	2	3.43202
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.261589722**	**2.22E-16**	**9**
P42932	AIAGTGANVIVTGGK	1.287349431	2	3.83306
P42932	ELEVQHPAAK	1.264275885	2	2.98429
P42932	GEENLMDAQVK	1.219035455	2	3.56911
P42932	GSTDNLMDDIER	1.12574128	2	2.92618
P42932	HEKEDGAISTIVLR	1.077010358	2	2.78816
P42932	LFVTNDAATILR	1.569234919	2	2.99851
P42932	LYSVHQEGNK	1.486665551	2	2.67767
P42932	NVGLDIEAEVPAVK	1.016198924	2	3.68756
P42932	QITSYGETCPGLEQYAIK	1.459038203	2	4.84416
P43244	**MATR3 Matrin_3**	**1.304250156**	**1.28E-06**	**3**
P43244	ITPENLPQILLQLK	1.177513333	2	3.57897
P43244	TENPAEGKEQEEK	1.360982223	2	3.31458
P43244	YQLLQLVEPFGVISNHLILNK	1.436330553	3	4.06101
P43274	**H14 Histone H1.4**	**1.024262216**	**0.999788**	**3**

P43274	ALAAAGYDVEK	1.074103722	2	3.69207
P43274	SGVSLAALK	0.991671714	2	3.14036
P43274	SGVSLAALKK	0.95018192	2	2.47759
P43276	**H15 Histone H1.5**	**1.411106086**	**2.37E-09**	**2**
P43276	ALAAGGYDVEK	1.584236977	2	2.77406
P43276	ATGPPVSELITK	1.409558703	2	2.96775
P43278	**H10 Histone H1.0**	**0.843543286**	**0.98779**	**2**
P43278	VGENADSQIK	1.029870753	2	3.4313
P43278	YSDMIVAAIQAEK	0.847225669	2	4.26101
P43424	**GALT Galactose_1_phosphate uridylyltransferase**	**1.021582879**	**0.12031**	**2**
P43424	HDPLNPLCPGATR	1.150609782	2	2.87984
P43424	YNPLQDEWVLVSAHR	0.925651795	2	2.43934
P45591	**COF2 Cofilin_2**	**1.279771715**	**0.244608**	**4**
P45591	HEWQVNGLDDIKDR	1.327851318	3	4.20629
P45591	KEDLVFIFWAPESAPLK	1.163764985	2	3.91105
P45591	MASGVTVNDEVIK	0.999891602	2	2.48342
P45591	QILVGDIGDTVEDPYTSFVK	1.292381511	2	5.17449
P45592	**COF1 Cofilin_1**	**1.202865106**	**0.000298**	**4**
P45592	HELQANCYEEVK	0.957427181	2	3.31926
P45592	HELQANCYEEVKDR	1.121687523	3	5.49316
P45592	LGGSAVISLEGKPL	1.726483799	2	2.43126
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.30026914	2	5.01927
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.216298675**	**0.006582**	**3**
P45878	GWDQGLLGMCEGEK	1.015859792	2	2.83241
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	1.301883072	2	3.70519
P45878	LVIPSELGYGER	1.42814268	2	2.40152
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.032003725**	**5.16E-07**	**20**
P45953	AMVENGGLVTSNPLR	1.027254517	2	2.74011
P45953	AMVENGGLVTSNPLRV	1.340316302	2	4.14083
P45953	ASNTSEVYFDGVK	1.147543263	2	3.50923
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.01720508	2	4.65542
P45953	ENMASLQSNPQQQELFR	1.286082562	2	3.89206
P45953	FFEEVNDPAK	0.769799451	2	2.70845
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.13733046	3	4.56346
P45953	GIVNEQFLLQR	1.255444515	2	3.21919
P45953	IFEGTNDILR	1.312130581	2	3.00359
P45953	IFGSEAAWK	1.107553809	2	2.6545
P45953	IHNFGVIQEK	1.372945117	2	2.31413
P45953	LFVALQGCMDK	1.142690286	2	2.48386
P45953	NDSLEKVEEDTLQGLK	1.170160275	2	3.59415
P45953	NPLGNVGLLIGEASK	1.232732113	2	2.68241
P45953	SFGGVTHGLPEK	1.060419235	2	2.71757
P45953	SFGGVTHGLPEKK	1.083680187	2	2.3846
P45953	SGELAVQALEQFATVVEAK	1.064464546	3	4.95509
P45953	SLSEGYPTAQHEK	1.147795081	2	3.34773
P45953	TGIGSGLSLSGIVHPELSR	1.015677808	2	4.32117
P45953	VEEDTLQGLK	0.909740091	2	2.58883
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.071431814**	**0.996887**	**4**
P46418	AILNYIATK	1.263236283	2	3.37272
P46418	SDGSLMFEQVPMVEIDGMK	0.915975579	2	3.54575
P46418	SHGQDYLVGNK	0.863890854	2	3.56964
P46418	VSNLPTVK	1.072934676	2	2.85972
P46425	**GSTP2 Glutathione S_transferase P 2**	**1.10187575**	**0.979315**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.994014616	2	4.46159
P46425	FEDGDLTLYQSNAILR	1.206706013	2	4.53766
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.105566967**	**9.53E-06**	**25**

P46462	AIANECQANFISIK	1.761188736	2	2.49413
P46462	EAVCIVLSDDTCSDEK	1.182180059	2	3.74773
P46462	EDEEESLNEVGYDDIGGCR	0.895691127	2	4.84905
P46462	ELQELVQYPVEHPDK	1.092989236	2	4.626
P46462	ETVVEVPQVTWEDIGGLEDVK	0.970099156	2	3.10006
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.035909319	2	4.12254
P46462	EVDIGIPDATGR	0.989441704	2	3.14481
P46462	GDDLSTAILK	0.898679053	2	2.97287
P46462	GGNIGDGGGAADR	1.084517849	2	3.20127
P46462	GILLYGPPGTGK	1.037136516	2	3.57533
P46462	IVSQLLTLMDGLK	1.953935842	2	4.22018
P46462	KYEMFAQTLQQSR	0.854241507	2	3.0458
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.462983526	3	6.79241
P46462	LAGESESNLRKAFEEAEK	0.880107187	2	2.42502
P46462	LDQLIYIPLPDEK	1.052699143	2	4.84703
P46462	LEILQIHTK	1.058703503	2	2.91263
P46462	LGDVISIQPCPDVK	1.111101521	2	4.46849
P46462	LIVDEAINEDNSVVSLSQPK	1.096221331	2	5.3288
P46462	MDELQLFR	0.945110319	2	3.19999
P46462	MTNGFSGADLTEICQR	1.070006945	2	4.51709
P46462	NAPAIIFIDELDAIAPK	1.426913956	3	5.10948
P46462	NVFIIGATNRPDIIDPAILRPGR	1.093268539	3	4.19927
P46462	QTNPSAMEVEEDDPVPEIR	1.038882832	2	4.61157
P46462	RSVSDNDIR	1.374885484	2	2.65865
P46462	WALSQSNPSALR	1.243161434	2	2.59913
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**1.363669927**	**0.005292**	**3**
P46664	FIEDELQIPVK	1.32216959	2	3.16551
P46664	VGIGAFPTEQDNEIGELLQTR	1.335479484	2	4.3044
P46664	VVDLLAQDADIVCR	1.26833541	2	3.09316
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.228806111**	**0.000986**	**3**
P46720	GIGETPIVPLGISYIEDFAK	1.231105923	2	3.58987
P46720	GVQHQLHVESK	1.073438477	2	3.23878
P46720	SENSPLYIGILEMGK	1.372188817	2	3.21857
P46844	**BIEA Biliverdin reductase A**	**0.926606819**	**0.994165**	**3**
P46844	FGVVVVGVGR	0.949917285	2	2.4756
P46844	LLDQVSAEDLAAEK	1.077122868	2	3.80795
P46844	MTVQLETQNK	0.924911263	2	2.81446
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.071228191**	**0.750885**	**6**
P46953	AQGSVALSVTQDPACK	1.015110019	2	4.41112
P46953	ASFQPPVCNK	1.029195422	2	2.67398
P46953	DLGTQLAPIIQEFFHSEQYR	0.965962576	2	3.16549
P46953	QDVDVWLWQLEGSSK	1.672210857	2	3.30927
P46953	TGKPNPDQLLK	1.087543424	3	3.5937
P46953	YYVGDTEDVLFEK	1.280365579	2	4.0523
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.230597537**	**0.065247**	**4**
P46978	FGQVYTEAK	1.363201926	2	2.60228
P46978	FYSLLDPSYAK	1.153388634	2	3.09393
P46978	VGQAMASTEEK	1.142046366	2	3.20413
P46978	VGQAMASTEEK+Oxidation(5)	1.462556936	2	2.62265
P47198	**RL22 60S ribosomal protein L22**	**1.159443976**	**3.15E-05**	**2**
P47198	AGNLGGGVVTIER	1.146687771	2	3.16188
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.849801734	3	4.8724
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.422017722**	**1.11E-16**	**4**
P47875	GFGFGQGAGALVHSE	1.362264351	2	3.07969

P47875	GLESTTLADKDGEIYCK	1.552707816	2	4.98059
P47875	HEEAPGHRPTTNPNASK	1.69472066	3	3.49772
P47875	NLDSTTVAVHGEEIYCK	1.069385876	2	4.35392
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.126775801**	**0.658484**	**3**
P47942	GLYDGPVCEVSVTPK	1.12063894	2	3.58165
P47942	QIGENLIVPGGVK	1.092854365	2	2.43901
P47942	SITIANQTNCPLYVTK	1.34610421	2	3.28904
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.114350285**	**0.818701**	**2**
P48004	NYTDDAIETDDLTIK	1.159398301	2	4.70678
P48004	YVAEIEKEKEENEK	0.934128561	2	4.02836
P48037	**ANXA6 Annexin A6**	**1.051931738**	**9.6E-05**	**17**
P48037	AANDFNPDADAK	1.04707511	2	2.90519
P48037	AINEAYKEDYHK	1.086318671	2	3.38411
P48037	ALIEILATR	1.10047556	2	3.49588
P48037	ALLALCGGED	1.219051353	1	2.19062
P48037	DLESDIIGDTSGHFQK	0.972745149	2	4.26092
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.074108991	3	5.08962
P48037	GELSGDFEK	0.951477838	1	2.06956
P48037	GFGSDKESILELITSR	0.993670182	2	4.13214
P48037	GIGTDEATIIDIITQR	1.022256433	3	4.10299
P48037	GSVHDFADFDANQDAEALYTAMK	1.525833253	2	6.12828
P48037	QRQEICQSYK	1.288731952	2	3.27695
P48037	SEIDLLNIR	1.341204774	2	3.11228
P48037	SLEDALSSDTSGHFK	0.975432003	2	3.28851
P48037	TNEQIHQLVAAYK	0.982182195	2	3.87286
P48037	TNYDIEHVIK	0.929398712	2	3.23861
P48037	TTGKPIEASIR	1.010115617	2	2.50303
P48037	WGTDEAQFIYILGNR	1.933834206	2	2.34777
P48500	**TPIS Triosephosphate isomerase**	**1.079260508**	**3.87E-13**	**12**
P48500	CNVSEGVAQCTR	1.167271714	2	3.83233
P48500	DLGATWVVLGHSER	1.10010673	2	4.00604
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.070368312	4	5.37006
P48500	FFVGGNWK	1.259955806	1	1.99296
P48500	HIFGESDELIGQK	1.171804257	2	4.00285
P48500	IIYGGSVTGATCK	1.515991275	2	4.168
P48500	KFFVGGNWKMNGR	0.962372103	2	2.31023
P48500	LPADTEVVCAPPTAYIDFAR	0.216473857	2	4.47262
P48500	RHIFGESDELIGQK	1.115909265	2	4.29209
P48500	TATPQQAQEVHEK	1.073214599	2	3.6331
P48500	VNHALSEGLGVIACIGEK	1.146797189	2	5.17903
P48500	VVLAYEPVWAIGTGK	1.119101843	2	4.13484
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.820948169**	**0.000393**	**6**
P48508	ASTLHLQTGNLLNWGR	1.093168447	3	3.83891
P48508	EFPDVLECTMSHAVEK	0.906715037	2	3.76887
P48508	INPDEREEMK	0.965694165	2	2.47253
P48508	LFIVGSNSSSSTR	0.832431224	2	3.511
P48508	QFDIQLLTHNDPK	1.288239968	2	2.61266
P48508	TLNEWSSQISPDLVR	0.665100417	2	4.62907
P48675	**DESM Desmin**	**1.776051528**	**0.454755**	**3**
P48675	FLEQQNAALAAEVNR	1.685506394	2	4.23189
P48675	HQIQSYTCEIDALK	1.898552324	2	3.55277
P48675	VSDLTQAANK	2.054639829	2	2.85098
P48679	**LMNA Prelamin_A/C**	**1.048240862**	**0.998623**	**14**
P48679	AQHEDQVEQYK	0.935216435	2	2.69916
P48679	AQHEDQVEQYKK	1.096297624	2	4.38035
P48679	IDSLSAQLSQLQK	0.874460851	2	3.04106

P48679	ITESEEVVSR	0.999726201	2	2.83299
P48679	LQEKEDLQELNDR	1.105227957	2	4.02747
P48679	MQQQLDEYQELLDIK	1.392297797	2	4.88483
P48679	NSNLVGAAHEELQQSR	0.932373445	2	4.60954
P48679	SGAQASSTPLSPTR	1.028044021	2	3.62306
P48679	SLETENAGLR	2.013119893	2	2.62883
P48679	SVGGSGGGSFGDNLVTR	1.075858862	2	3.43242
P48679	TALINATGEEVAMR	1.017325844	2	2.84751
P48679	TVLCGTCGQPADK	1.050194833	2	2.83458
P48679	VAVEEVDEEGK	0.936666184	2	3.03741
P48679	VAVEEVDEEGKFVR	1.133161829	2	2.94026
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.042849175**	**0.037949**	**27**
P48721	AQFEGIVTDLIK	0.979425478	2	3.83907
P48721	ASNGDAWVEAHGK	0.989642835	2	3.65995
P48721	DAGQISGLNVLR	1.07820811	2	3.50306
P48721	EEISKMRELLAR	1.176035907	2	2.4372
P48721	EQQIVIQSSGGLSK	0.921334725	2	3.71297
P48721	EQQIVIQSSGGLSKDDIENMVK	0.898482759	2	4.76849
P48721	ERVEAVNMAEGIIHDTETK	0.995778637	3	5.58763
P48721	GAVVGIDLGTTNSCVAVMEGK	0.928999913	2	5.06986
P48721	LFEMAYK	1.225466505	2	2.35284
P48721	LLGQFTLIGIPPAPR	1.6531627	2	3.36812
P48721	MEEFKDQLPADECNK	0.943636124	2	4.55342
P48721	MEEFKDQLPADECNK+Oxidation(1)	1.014197441	2	3.96765
P48721	MKETAENYLGHTAK	0.98061141	2	4.21688
P48721	MKETAENYLGHTAK+Oxidation(1)	1.09645264	3	3.37378
P48721	NAVITVPAYFNDSQR	1.120636313	2	3.15721
P48721	QAVTNPNNTFYATK	1.299405193	2	3.41806
P48721	RYDDPEVQK	1.008442742	2	2.9515
P48721	RYDDPEVQKDTK	1.082144586	2	3.75635
P48721	SDIGEVILVGGMTR	1.014211633	2	4.03548
P48721	SQVFSTAADGQTQVEIK	2.37641911	2	5.31332
P48721	STNGDTFLGGEDFDQALLR	1.163289247	2	5.31988
P48721	TTPSVVAFTPDGER	0.974561599	2	3.55076
P48721	VEAVNMAEGIIHDTETK	1.04151695	2	4.38138
P48721	VINEPTAAALAYGLDK	1.196545557	1	3.38124
P48721	VLENAEGAR	1.058116679	2	3.13885
P48721	VQQTVQDLFGR	1.025987081	2	3.49026
P48721	YDDPEVQKDTK	0.940855478	2	2.92733
P48998	**INVO Involucrin**	**1.109163632**	**0.490648**	**2**
P48998	ELLDQRLDQELVNK	1.136001189	2	2.42077
P48998	HKLENLTQKEK	0.908783418	1	1.96573
P49025	**CTRO Citron Rho_interacting kinase**	**1.053780778**	**0.683856**	**2**
P49025	LLMIAGEERALCLVDVK+Oxidation(3)	1.230506416	2	2.32518
P49025	LMMNQLEEDLVSARR+Oxidation(2)	0.962945792	2	2.35252
P49134	**ITB1 Integrin beta_1**	**0.961776005**	**0.784662**	**4**
P49134	CNCQSHGIPASPK	1.292915496	2	3.20407
P49134	FCECDNFNCDR	0.894874655	2	3.45995
P49134	GICECGACK	0.816123606	2	2.31819
P49134	WDTGENPIYK	1.007944778	2	2.38471
P49242	**RS3A 40S ribosomal protein S3a**	**1.219890922**	**4.1E-10**	**10**
P49242	ACQSIYPLHDVFVR	1.222422735	2	3.77887
P49242	ADGYEPPVQESV	1.079672017	1	2.00973
P49242	EVQTNDLKEVVNK	1.30942242	2	2.33177
P49242	LIPDSIGKDIEK	1.19025642	2	2.90762
P49242	LITEDVQGK	1.216174382	2	2.3583
P49242	LMELHGEGGSSGK	1.01707088	2	3.23415

P49242	LMELHGEGGSSGK+Oxidation(2)	1.008665468	2	3.10339
P49242	NCLTNFHGMDLTR	1.325370353	2	4.15799
P49242	TTDGYLLR	1.228991896	2	2.99135
P49242	VFEVSLADLQNDEVAFR	1.366023424	2	4.78931
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**1.070016592**	**0.93644**	**5**
P49432	EAINQGMDEELERDEK	0.976218532	2	2.84862
P49432	ILEDNSIPQVK	1.048397595	2	3.46109
P49432	IMEGPAFNFLDAPAVR	1.115252616	2	4.55876
P49432	TIRPMDIEAIEASVMK	1.301271422	2	3.42691
P49432	VFLLGEEVAQYDGAYK	0.905302756	2	3.50198
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**1.17913074**	**0.54655**	**10**
P49889	CKEDALFNR	2.569094029	2	2.37593
P49889	FEEHYQQQMK	0.966520938	2	2.95486
P49889	FMEGQVPYGSWYDHVK	1.31997834	2	4.33529
P49889	IIQHTSFQEMK	0.84371706	2	3.21638
P49889	LIEFLERDPSAELVDR	1.134138533	3	4.73022
P49889	NEDLINGIK	1.064621139	2	2.91521
P49889	NNPCTNYSMLPETMIDLK	1.394971301	2	4.36493
P49889	NNPCTNYSMLPETMIDLK+Oxidation(14)	1.01747146	2	3.11272
P49889	NNPCTNYSMLPETMIDLK+Oxidation(9)	1.01747146	2	4.14632
P49889	SGSTWISEIVDMIYK	1.547226949	2	4.7541
P50137	**TKT Transketolase**	**1.21621634**	**0.001149**	**20**
P50137	AVELAANTK	1.136536121	1	1.97168
P50137	GITGIEDK	1.029816485	1	2.42631
P50137	HQPTAIIAK	1.000689858	2	2.51309
P50137	IIALDGDTK	1.181541914	2	2.66882
P50137	ILATPPQEDAPSVDIANIR	1.312181505	3	4.9233
P50137	ILTVEDHYYEGGIGEAVSAVVVGEPGVTVTR	2.245600914	3	3.82125
P50137	ISSDLDGHPVPK	1.117083775	2	3.3523
P50137	KISSDLDGHPVPK	1.194747716	2	4.05001
P50137	LDNLVAIFDINR	1.185623134	2	4.75331
P50137	LGQSDPAPLQHQVDVYQK	1.374081149	2	3.74267
P50137	MFGIDKDAIVQAVK	1.068608833	2	4.38169
P50137	NMAEQIIQEIYSQVQSK	1.081004545	3	6.51389
P50137	NSTFSELFK	1.059803709	2	2.45201
P50137	SGKPAELLK	1.0280605	3	3.42726
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	1.102163429	3	5.44611
P50137	SKDDQVTVIGAGVTLHEALAAAEMLKK	1.070818635	4	5.5505
P50137	SVPMSTVFYPSDGVATEK	1.060472574	2	4.6903
P50137	TSRPENAIIYSNNEDFQVGQAK	1.24610672	3	5.59637
P50137	VLDPFTIKPLDK	1.222851318	2	3.49277
P50137	VLDPFTIKPLDKK	1.06271276	2	2.4389
P50169	**RDH3 Retinol dehydrogenase 3**	**1.190547151**	**5.88E-14**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.253757098	3	5.48329
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(2)	1.035099471	3	4.30811
P50169	FQDSYMK	1.073195868	1	1.93559
P50169	GLWGLVNNAGISVPVGPNEWMR	0.792196508	2	3.56431
P50169	KLWDQTTEEVK	1.085152797	2	2.55769
P50169	KLWDQTTEEVKEIYGEK	1.085012147	3	4.30182
P50169	LWDQTTEEVK	1.085541082	2	3.59995
P50169	LWDQTTEEVKEIYGEK	1.150031039	2	4.99324
P50169	MSLVGGGYCISK	1.227398069	2	3.90994
P50237	**ST1C1 Sulfotransferase 1C1**	**0.939262532**	**0.491228**	**9**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.921208762	2	5.65092
P50237	DISEEVLNK	0.824846029	2	2.6277

P50237	DLHLGEQDLQPETR	0.948326378	2	3.95352
P50237	FLEKDISEEVLNK	1.022532576	2	3.40933
P50237	IWNFQAKPDDLLIATYAK	0.731070496	2	4.46575
P50237	MKDLHLGEQDLQPETR	0.898492056	2	4.92069
P50237	MLPDPGTLGEYIEQFK	1.080371511	3	4.67583
P50237	MLPDPGTLGEYIEQFK+Oxidation(1)	1.202708971	2	3.0702
P50237	VLWGSWYDHVK	1.101868941	2	3.18314
P50289	**ASPX Acrosomal protein SP_10**	**0.943588027**	**0.356133**	**2**
P50289	MQIMCCRNEPLCNK	0.943376149	2	2.34881
P50289	MQIMCCRNEPLCNK+Oxidation(1)	1.270043832	2	2.39186
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**1.114458513**	**0.106608**	**7**
P50398	FDLGQDVIDFTGHALALYR	0.725356134	2	2.74445
P50398	FQLLEGPPESMGR	1.085782192	2	3.68437
P50398	KQNDVFGEADQ	1.062267471	2	3.31253
P50398	NPYYGGESSSITPLEELYK	1.299333761	2	5.89067
P50398	QLICDPSYIPDR	1.21242557	2	2.8949
P50398	TDDYLDQPCLETINR	1.045397631	2	4.67556
P50398	TFEGVDPQTTSMR	0.982630795	2	3.22318
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.221445015**	**0.001871**	**10**
P50399	AYDATTHFETTCDDIKDIYK	1.117689046	3	5.15125
P50399	DWNVDLIPK	1.368448346	2	2.35384
P50399	EIRPALELLEPIEQK	1.191017373	2	3.49896
P50399	FDLGQDVIDFTGHSLALYR	1.229625658	2	4.41658
P50399	FVSISDLFVPK	1.557075118	2	3.51024
P50399	MTGSEFDFEEMKR	1.204595356	2	2.7324
P50399	NTNDANSCQIIIPQNQVNR	1.255415767	2	4.0286
P50399	TDDYLDQPCCETINR	1.179174019	2	4.68168
P50399	VICILSHPIK	1.087475806	2	2.51089
P50399	VLHMDQNPYYGGESASITPLEDLYK	1.167624494	3	4.65373
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.200239998**	**9.56E-07**	**8**
P50431	ALSDALTELGYK	1.310856724	2	4.36287
P50431	AVLEALGSCLNNK	1.28200668	2	4.13997
P50431	GLLEEDFQK	1.181231555	1	2.30078
P50431	IMGLDLPDGGHLTHGFMTDK	0.866632889	2	2.84562
P50431	IYQLQVLANCR	1.166321133	2	2.57163
P50431	LIIAGTSCYSR	1.597009904	2	2.36342
P50431	VLEACSIACNK	1.209208591	2	3.99935
P50431	YSEGYPGQR	1.211644447	2	2.4414
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**1.060099847**	**0.140542**	**14**
P50475	ASEWVQQVSGLMDGK	0.97340874	2	4.04264
P50475	AVFDETYPDPVR	1.139942894	2	2.99602
P50475	EIADLGEVLATAVIPQWQK	1.083284284	2	3.14857
P50475	GLEATDDSPK	1.100912583	2	2.67142
P50475	ITCLCQVPQNAANR	1.182778062	2	4.13067
P50475	IVAVTGAEAQK	1.340183098	2	2.45565
P50475	MSNYDTDLFVPYFEAIQK	1.534702515	2	3.44388
P50475	NSSHAGAFVIVTEEAIAK	1.197996864	2	3.78294
P50475	QIWQNLGLDEAK	1.310553239	2	2.8255
P50475	RIVAVTGAEAQK	0.979133487	2	3.12261
P50475	SVLGDADQK	1.167179381	1	2.28206
P50475	TITVALADGGRPDNTGR	1.072694733	2	2.76058
P50475	VDDSSEDKTEFTVK	1.083185746	2	4.01343
P50475	VGAEDTDGIDMAYR	0.913557195	2	3.33247
P50503	**F10A1 Hsc70_interacting protein**	**1.271280987**	**3.34E-12**	**5**
P50503	AIDLFTDAIK	1.247615327	2	2.53333
P50503	AIEINPDSAQPYK	1.373241538	2	2.80493
P50503	GAAIDALNDGELQK	1.275908021	2	3.31189

P50503	KGAAIDALNDGELQK	1.473571542	2	4.76771
P50503	LDYDEDASAMLR	1.257198621	2	3.28234
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**0.990859937**	**0.997383**	**10**
P50554	GTFCSFDTPDEAIR	0.888412829	2	3.18334
P50554	IDIPSFDWPIAPFPR	1.00786199	2	3.65127
P50554	IFNTWLGDPSK	1.022111289	2	2.33691
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.327666849	3	4.9971
P50554	MLDLYSQISSVPIGYNHPALAK	1.202327633	3	3.48197
P50554	NLLLAEVINIIK	0.916087258	3	5.31015
P50554	REDLLNNVAHAGK	0.927950462	3	3.76154
P50554	TLLTGLLDLQAQYPQFVSR	1.139975679	2	4.23587
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	0.778400285	2	4.27077
P50554	VDFEFDYDGPLMK	0.98842347	2	3.72233
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.03597755**	**0.337576**	**2**
P50580	HELLQPFNVLYEK	1.522589345	2	2.40991
P50580	TIIQNPTDQQK	1.031852024	2	2.75792
P50878	**RL4 60S ribosomal protein L4**	**0.923040232**	**0.000286**	**10**
P50878	FCIWTESAFR	1.123973605	2	2.45339
P50878	KLDELYGTWR	1.189289683	2	3.0943
P50878	KLEAAAAALAAK	1.194023895	3	3.78634
P50878	LEAAAAALAAK	1.325967155	2	2.34503
P50878	NIPGITLLNVSK	1.256597785	1	2.37537
P50878	NVTLPAVFK	0.819274238	1	2.22502
P50878	RGPCIIYNEDNGIIK	1.441309998	2	2.95616
P50878	SGQGAFGNMCR	1.08429465	2	2.77636
P50878	SNYNLPMHK	0.977093125	2	2.41885
P50878	YAICSALAASALPALVMSK	1.526827204	2	3.68182
P50904	**RASA1 Ras GTPase_activating protein 1**	**0.808251849**	**0.531877**	**3**
P50904	IMESKQSCELSPSK+Oxidation(2)	0.675376035	2	2.50134
P50904	LESLLLCTLNDR	1.031191491	1	1.90232
P50904	YYNSIGDIIDHYRK	1.053950361	2	2.42933
P51538	**CP3A9 Cytochrome P450 3A9**	**1.141124193**	**0.715977**	**2**
P51538	EMFPIINQYTDMLVR	1.215534215	2	2.53037
P51538	GFWEFDKYCHK	1.002987422	1	2.23013
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**0.975190116**	**2.28E-13**	**8**
P51635	ALEALVAK	1.152390248	2	2.85837
P51635	GLEVTAYSPLGSSDR	0.995000925	2	4.15009
P51635	HHPEDVEPAVR	0.982338622	3	3.76303
P51635	HIDCASVYGNETEIGEALK	0.973083883	2	5.87205
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.890176088	3	6.80341
P51635	HPDEPVLLEEPVVLALAEK	1.969280623	3	5.66854
P51635	ILQNIQVFDFTFSPEEMK	2.502722481	2	4.52325
P51635	QLDALNK	1.198542194	1	1.9899
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.845609929**	**3.49E-11**	**17**
P51647	ANNTTYGLAAGVFTK	0.60191679	2	4.53141
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.983893606	3	3.56138
P51647	ELGEHGLYEYTELK	0.972651148	2	3.45617
P51647	FPVLNPATEEVICHVEEGDK	0.762110893	3	3.74934
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.929480434	4	5.19338
P51647	IFINNEWHDSVSGK	1.178024598	2	4.59818
P51647	IFVEESVYDEFVR	0.823231084	2	4.4965
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	1.170127131	3	4.74916
P51647	IHGQTIPSDGDIFTFTR	1.220020771	2	4.35677
P51647	KFPVLNPATEEVICHVEEGDK	0.817609937	3	3.36825
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.909179354	4	4.82623
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	0.876499191	3	3.83854

P51647	LLLATIEAINGGK	6.081524994	2	4.731
P51647	VFANAYLSDLGGSIK	1.142595274	2	4.64449
P51647	YCAGWADK	0.877233175	1	2.24851
P51647	YVLGNPLTQGINQGPQIDK	0.857530954	2	5.0602
P51647	YVLGNPLTQGINQGPQIDKEQHDK	1.23419724	2	3.76648
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.895038227**	**0.631761**	**9**
P51650	EVGEVLCTDPLVSK	1.421003518	2	4.14315
P51650	GIHDSFVTK	0.93020969	2	2.30189
P51650	HQSGGNFFEPTLLSNVTR	0.980202161	2	3.93688
P51650	IITAESGKPLK	0.863121393	2	2.61857
P51650	ILLHHAANSVK	1.02962984	2	2.42831
P51650	LGTVADCGVPEAR	0.666275702	2	3.26943
P51650	VGNGFEEGTTQGPLINEK	0.830550513	2	4.88169
P51650	WLPTPATFPVYDPASGAK	0.81162408	2	3.03883
P51650	YGIDEYLEVK	0.972131611	2	2.5932
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**1.062370687**	**0.532304**	**3**
P51863	ADDYEQVK	1.245463991	2	2.38586
P51863	LHLQSTDYGNFLANEASPLTVSVIDDK	1.110865105	3	3.60692
P51863	LYPEGLAQLAR	1.062226968	1	1.90186
P51869	**CP4F4 Cytochrome P450 4F4**	**1.230112532**	**9.96E-07**	**4**
P51869	ALPSQHEDDILK	1.17732208	2	2.87851
P51869	NISLMTLDSLQK	1.235036297	2	3.65096
P51869	TLDFIDVLLLTK	1.767047221	2	3.80018
P51869	WQDLASGGSAR	1.061757347	2	2.49713
P51886	**LUM Lumican**	**1.179336581**	**0.06038**	**4**
P51886	LDGNPLTQSSLPPDMYECLR	2.014385921	2	2.64406
P51886	NNQIDHIDEK	1.644061953	2	3.33049
P51886	SIPTVNENLENYYLEVNK	1.862543554	2	4.13155
P51886	SLQDLQLANNK	1.176777295	2	2.96361
P52296	**IMB1 Importin subunit beta_1**	**1.133318645**	**0.01513**	**4**
P52296	AAVENLPTFLVELSR	1.23368004	2	3.26081
P52296	TVSPDRLELEAAQK	1.081754797	2	3.32492
P52296	VLANPGNSQVAR	1.132976023	2	3.51639
P52296	VQHQDALQISDVVMASLLR	1.556095992	2	2.47332
P52303	**AP1B1 AP_1 complex subunit beta_1**	**0.969318779**	**0.929297**	**2**
P52303	NINLIVQK	0.948019757	1	2.02665
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.049718368	3	4.77533
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**1.11545096**	**5.04E-05**	**2**
P52504	IIACDGGGGALGHPK	1.11429268	2	3.52181
P52504	VYINLDKETK	1.354274773	2	2.98061
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.098001752**	**0.712091**	**5**
P52555	FDTQYPYGEK	1.085719236	2	2.54589
P52555	GQGVYLGMPGCLPAYDALAGQFIEASSR	1.646707626	3	4.14171
P52555	ILDQGEDFPASELAR	1.001296035	2	4.63856
P52555	QGQDGLSGVK	1.027292493	2	2.66139
P52555	SLNILTAFR	1.150466385	2	2.5294
P52631	**STAT3 Signal transducer and activator of transcription 3**	**1.089492616**	**0.950226**	**2**
P52759	**UK114 Ribonuclease UK114**	**1.560203723**	**0.000705**	**6**
P52759	AAGCDFTNVVK	1.744910462	2	3.3426
P52759	AAYQVAALPK	1.143788332	2	2.46538
P52759	IEIEAIAVQGPFTTAGL	1.24561615	1	3.55228
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.084745543	2	4.43367
P52759	TTVLLADINDFGTVNEIYK	1.448766055	2	5.15948
P52759	TYFQGNLPAR	1.204623978	2	2.5948

P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.706261865**	**0.079545**	**2**
P52845	CKEDAIFNR	2.569094029	2	2.37593
P52845	SGSTWIGEIVDMIYK	1.659208164	2	2.93212
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.018569429**	**0.575056**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	1.246837537	2	4.06027
P52847	FLAGNVAYGSWFDHVK	0.460343877	2	3.63776
P52847	IEEFQSRPCDIVIPTYPK	1.068465386	3	4.5211
P52847	IVHHTSFEVMK	1.693200774	2	2.87246
P52847	NYFTMTQSEK	1.006674129	1	2.76809
P52847	SGVELLKK	1.02175685	2	2.36282
P52847	THLPIDLLPK	1.002183596	3	3.62489
P52847	TLDEHTLER	1.099446925	2	2.86383
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.245830645**	**1.18E-05**	**38**
P52873	ADEAYLIGR	0.967407328	1	2.10108
P52873	ADFAQACQDAGVR	1.078098812	2	4.6432
P52873	AEAEAQAEELSFPR	1.114773914	2	4.69179
P52873	AGTHILCIK	1.564535396	2	2.84564
P52873	ALAVSDLNR	1.242772721	2	2.75418
P52873	AYSEALAAFGNGALFVEK	1.459750815	2	3.7143
P52873	AYVEANQMLGDLIK	0.893953926	2	4.6872
P52873	DAHQSLLATR	1.112453261	1	3.27197
P52873	DFTATFGPLDSLNTR	1.169582946	2	3.75268
P52873	DMAGLLKPAACTMLVSSLR	0.994865715	2	3.68988
P52873	ENGVDAVHPGYGFLSER	1.228836694	2	3.15566
P52873	FIGPSPEVVR	1.326114603	2	2.32274
P52873	FLYECPWR	1.073809723	1	2.14025
P52873	GANAVGYTNYPDNVVFK	1.847685415	2	4.46346
P52873	GLAPVQAYLHIPDIIK	2.251974025	2	3.15772
P52873	GQIGAPMPGK	0.871337679	2	2.43331
P52873	GTPLDTEVPLER	1.095003377	2	3.71453
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.516042147	2	5.68067
P52873	HIEVQILGDQYGNILHLYER	1.390178427	3	6.67321
P52873	HYFIEVNSR	1.312918606	2	2.4884
P52873	IAEEFEVELER	1.009872314	2	3.19223
P52873	IEGRPGASLPPLNLK	1.153965648	2	3.53596
P52873	INGCAIQCR	1.452020066	2	2.95774
P52873	IVGDLAQFMVQNGLSR	1.509185281	2	2.88003
P52873	LDNASAFQGAVISPHYDSLLVK	1.006794935	2	5.77653
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.107179029	4	6.34764
P52873	NHQGLLLMDTTFR	1.200634139	2	2.90681
P52873	QKADEAYLIGR	0.888381311	2	2.34316
P52873	QVFFELNGQLR	1.172995673	2	3.04774
P52873	QVGYENAGTVEFLVDK	1.303437364	2	3.91465
P52873	SGEGMGIR	0.894081481	2	2.6148
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.21361838	2	4.56607
P52873	TVAVYSEQDTGQMHR	1.237779999	2	4.56306
P52873	VFDYSEYWEGAR	1.245823005	2	4.31099
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.161435521	2	4.31387
P52873	VVEIAPATHLDPQLR	1.118366956	2	4.47271
P52873	VVHSYEELEENYTR	1.174804476	2	5.24916
P52873	YSLEYYMGLAEELVR	1.495372081	3	4.91748
P52925	**HMGB2 High mobility group protein B2**	**1.127820873**	**0.815631**	**2**
P52925	KHPDSSVNFAEFSK	1.155447783	2	2.84178
P52925	SEHPGLSIGDTAK	1.102188987	2	3.07004

P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.163052924**	**0.228195**	**4**
P53395	LREELKPVALAR	1.162501586	2	2.68558
P53395	LSDIGEGIR	1.086393604	2	2.47306
P53395	LSEVVGSGK	0.947089967	1	1.92983
P53395	SYLENPAFMLLDLK	1.579491829	2	4.33456
P53987	**MOT1 Monocarboxylate transporter 1**	**1.080524103**	**0.733581**	**4**
P53987	DGKEDETSTDVDEKPK	1.172180775	2	5.04282
P53987	DGKEDETSTDVDEKPKK	1.288181611	3	4.94259
P53987	ETQSPAPLQNSSGDPAEEESPV	1.095401766	2	5.2926
P53987	SDANTDLIGGSPK	1.086377562	2	3.90023
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**0.894658122**	**0.015306**	**2**
P54313	ACGDSTLTQITAGLDPVGR	0.881211127	2	4.45687
P54313	TFVSGACDASIK	1.004602833	2	3.03761
P54319	**PLAP Phospholipase A_2_activating protein**	**0.930655159**	**0.979862**	**3**
P54319	IGDVVGSSGANQQTSGK	0.984532993	2	4.4971
P54319	TGDLGDINAEQLPGR	0.899975415	2	3.3545
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.912008556	2	3.92414
P54822	**PUR8 Adenylosuccinate lyase**	**1.040290284**	**0.80961**	**2**
P54822	KVDIEVLSVLASLGASVHK	1.112974684	3	3.85755
P54822	VLSQQAAAVVK	1.074877585	2	2.83836
P54921	**SNAA Alpha_soluble NSF attachment protein**	**0.955771837**	**0.780611**	**5**
P54921	AIDIYEQVGTSAMDSPLLK	1.015428591	2	4.51538
P54921	HDAATCFVDAGNAFK	0.884443951	2	2.9943
P54921	IEEACEIYAR	0.869174269	2	2.46345
P54921	NSQSFFSGLFGGSSK	1.07918802	2	3.14579
P54921	TIQGDEEDLR	1.206395242	2	2.40758
P55006	**RDH7 Retinol dehydrogenase 7**	**1.068711967**	**6.98E-06**	**11**
P55006	LETVILDVTK	1.014925035	2	3.66221
P55006	TESIVAATQWVK	1.053988335	2	3.97609
P55006	TNVTNMER	1.072460262	2	2.76205
P55006	TNVTNMER+Oxidation(6)	1.315208737	2	2.50395
P55006	TSDRLETVILDVTK	1.073352136	3	4.58541
P55006	VAIIEPGGFK	1.508880417	2	2.30173
P55006	VLAACLTEK	1.211459593	2	3.14019
P55006	VVNIASTMGR	1.179720719	2	3.48985
P55006	VVNIASTMGR+Oxidation(8)	1.027416774	2	2.73595
P55006	YGVEAFSDSLR	1.279837084	2	3.75634
P55006	YVFITGCDSGFGNLLAR	1.450670867	2	4.42019
P55007	**BART1 Protein BART_1**	**1.173343085**	**0.629609**	**2**
P55007	MILMYEEKNKNTR+Oxidation(1)	0.971166731	2	2.36338
P55007	YNSDEDLQSKLESSR	1.361904368	2	2.5442
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.197697427**	**0.99996**	**3**
P55051	LTDSQNFDEYMK	1.204769277	2	3.9236
P55051	QVGNVTKPTVIISQEGGK	1.197666624	2	3.44548
P55051	WDGKETNCVR	1.014019382	2	2.56056
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.278070308**	**0.027071**	**6**
P55053	FDETTADGR	1.332049824	2	2.58997
P55053	KTETVCTFTDGALVQHQK	1.335432723	3	5.67551
P55053	LVESHGFEDYMK	1.718486495	2	3.3589
P55053	MGAMAKPDCIITLDGNNLTVK	1.381411824	3	3.66505
P55053	MVVECVMNNAICTR	1.345319002	2	3.36587
P55053	TETVCTFTDGALVQHQK	1.285716153	2	4.53327
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.155437589**	**3.81E-12**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.360593701	2	3.72414

P55159	IFFYDSENPPGSEVLR	1.211749659	2	5.99508
P55159	IQSILSEDPK	1.257176433	2	3.13426
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.984619258	3	4.45583
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	1.19364276	3	6.1741
P55159	VVADGFDFANGIGISLDGK	1.036575014	2	4.81075
P55159	YVYIAELLAHK	1.478831019	2	2.96611
P55260	**ANXA4 Annexin A4**	**0.901347726**	**0.786193**	**3**
P55260	AEIDMLDIPANFK	0.936512583	1	2.3181
P55260	GAGTDEGCLIEILASR	1.258290508	2	3.73858
P55260	GLGTDEDAIIGVLACR	0.867940295	2	3.90806
P55770	**NH2L1 NHP2_like protein 1**	**1.139932323**	**0.259907**	**2**
P55770	LLDLVQQSCNYK	1.24740717	2	3.80253
P55770	QQIQSIQQSIER	1.063744361	2	2.89532
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.254737088**	**0.015279**	**3**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.109843496	2	4.33185
P56399	IFQNAPTDPTQDFSTQVAK	1.395674945	2	4.50408
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.233819481	3	4.41896
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.100287766**	**0.670527**	**4**
P56522	AVPTGDVEDLPCGLLLSSVGYK	3.077366824	2	2.93449
P56522	NVINTFTQTAR	1.00533446	2	2.85066
P56522	TATEKPGVEEAAR	0.84088898	2	3.07751
P56522	TDITEVALGVLR	1.09778408	2	3.43547
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.074109058**	**0.000129**	**13**
P56574	ATDFVVDR	1.061696305	2	2.39117
P56574	DLAGCIHGLSNVK	1.05100758	2	3.73679
P56574	DQTNDQVTIDSALATQK	1.097150914	2	3.91933
P56574	FKDIFQEIFDK	1.001544082	2	3.51402
P56574	GKLDGNQDLIR	0.990916295	2	3.35162
P56574	IKVEKPVVEMDGDEMTR	1.299252287	3	3.41823
P56574	LDGNQDLIR	1.001082121	2	2.44947
P56574	LIDDMVAQVLK	1.112275191	2	4.12578
P56574	LNEHFLNTTDFLDTIK	1.33089563	2	4.42799
P56574	NILGGTVFR	1.080769968	2	2.70595
P56574	SSGGFVWACK	1.299021923	2	2.85796
P56574	TIEAEAAHGTVTR	0.888255333	2	3.87385
P56574	VCVQTVESGAMTK	1.07402331	2	3.69246
P56593	**CP2AC Cytochrome P450 2A12**	**1.186955438**	**0.729897**	**3**
P56593	MLQGTCGAPIDPTIYLSK	1.08154909	2	4.73341
P56593	NRQPQYEDHMK	1.268254912	3	3.45868
P56593	NRQPQYEDHMK+Oxidation(10)	1.072016172	3	3.41899
P56656	**CP239 Cytochrome P450 2C39**	**1.023106071**	**2.28E-08**	**5**
P56656	EHQESLDVTNPR	0.71710032	2	3.6983
P56656	IKEHQESLDVTNPR	0.809818255	2	5.02222
P56656	NYLIPK	1.749488261	1	2.04485
P56656	VCAGEGLAR	2.051785252	2	2.36139
P56656	VQEEIDHVIGR	1.252274258	2	3.4338
P56812	**PDCD5 Programmed cell death protein 5**	**0.951000552**	**0.996398**	**3**
P56812	HGDPGDAAQQEAK	0.942528855	2	4.20271
P56812	NSILAQVLDQSAR	0.982883805	2	3.11237
P56812	VSEQGLIEILEK	1.024425546	2	3.07542
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.916050535**	**0.002329**	**7**
P57093	AISCHYGSSDCK	0.682124727	2	3.47799
P57093	EVKPPGMTVMKDVAIAKQGYAPSER	1.112711381	2	2.37746
P57093	IQDFQQNEELFR	1.348592636	2	3.23459
P57093	KFYEENGFLVIK	0.846941712	2	3.15119

P57093	NLVSDDDIQR	0.795585263	1	2.5296
P57093	NNGCLVVLPGTHK	0.859955877	2	2.41784
P57093	YCALPQIVK	0.996415961	1	2.06917
P57113	**MAAI Maleylacetoacetate isomerase**	**1.150727564**	**0.015028**	**11**
P57113	AITSGFNALEK	1.234526125	2	2.85969
P57113	ALLALEAFQVSHPCR	1.038989739	2	4.33204
P57113	DGGQQFSEEFQTLNPMK	1.079859011	2	5.02971
P57113	FKVDLSPYPTISHINK	1.096983959	2	4.82362
P57113	GIDYEIVPINLIK	1.18791267	2	4.10924
P57113	IDGITIGQSLAILEYLEETRPIPR	1.228429521	4	4.8791
P57113	MISDLIASGIQPLQNLSVLK	1.227480244	2	5.59833
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(1)	1.153472021	2	5.42267
P57113	QVGQENQMPWAQK	1.111077343	2	3.94233
P57113	VDLSPYPTISHINK	1.088207979	2	3.74631
P57113	YCVGDEVSMADVCLAPQVANAER	1.002545713	3	5.9415
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.17660421**	**0.000919**	**2**
P57722	ESTGAQVQVAGDMLPNSTER	1.134003035	2	5.43032
P57722	INISEGNCPER	1.192671464	2	3.443
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**1.185646582**	**0.853522**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	1.092274447	3	5.06339
P58321	WLPLEANPEVTNQFLK	1.186486568	2	4.06193
P58751	**RELN Reelin**	**1.15192527**	**0.819837**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**1.743105882**	**0.996316**	**11**
P58775	AISEELDNALNDITSL	0.783593768	2	3.54075
P58775	ATDAEADVASLNR	1.399936132	2	3.65627
P58775	DAQEKLEQAEK	1.148628223	2	2.84916
P58775	KATDAEADVASLNR	1.480578713	2	3.3756
P58775	LDKENAIDR	0.950975587	2	2.38913
P58775	LKGTEDEVEK	1.85086703	2	2.75253
P58775	MELQEMQLK	1.049538992	2	2.51859
P58775	QLEEEQQALQK	1.677489653	2	3.31009
P58775	SLEAQADKYSTK	1.072770064	2	2.87267
P58775	TIDDLEDEVYAQK	1.437838079	2	3.95779
P58775	YSESVKDAQEK	0.438685272	2	3.01028
P59242	**CING Cingulin**	**1.140522335**	**0.007402**	**2**
P59242	LGQEQQALNR	1.325543609	2	2.51633
P59242	LQGLEQEAENK	1.060283926	2	2.9783
P59470	**RPC2 DNA_directed RNA polymerase III subunit RPC2**	**1.119728678**	**0.755683**	**2**
P59470	MPIMLRSSNCVLTGK+Oxidation(1)	1.563047623	2	2.53702
P59470	NAKCTLKR	1.032671742	2	2.32696
P59759	**MKL2 MKL/myocardin_like protein 2**	**1.154984542**	**0.989156**	**2**
P59759	LVEVLK	0.990257028	1	2.01763
P59759	QIEELK	1.167248682	1	2.06212
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.11761962**	**0.793089**	**3**
P59999	ELLLQPVTISR	0.922450798	2	2.45138
P59999	HNKPEVEVR	1.09965595	2	2.52479
P59999	VLIEGSINSVR	1.129358973	2	2.94309
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.304172926**	**7.08E-07**	**6**
P60335	AITIAGVPQSVTECVK	1.110899246	2	3.28747
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	1.42427747	4	5.64442
P60335	IITLTGPTNAIFK	1.649717671	2	2.96063
P60335	LVVPATQCGSLIGK	1.618756438	2	3.03553
P60335	QICLVMLETLSQSPQGR	1.911883366	2	2.43015
P60335	VMTIPYQPMPASSPVICAGGQDR	1.269822961	2	4.05455

P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.226951231**	**7.55E-10**	**5**
P60843	ATQALVLAPTR	1.232721889	1	2.16775
P60843	GFKDQIYDIFQK	0.991764989	2	3.4422
P60843	KEELTLEGIR	1.24862504	2	2.36739
P60843	KGVAINMVTEEDKR	1.162431859	3	3.94227
P60843	LQMEAPHIIVGTPGR	1.345873944	2	3.49597
P60868	**RS20 40S ribosomal protein S20**	**1.44964412**	**9.9E-20**	**2**
P60868	DTGKTPVEPEVAIHR	1.018350737	3	3.93648
P60868	LIDLHSPSEIVK	1.500510698	2	2.90735
P60892	**PRPS1 Ribose_phosphate pyrophosphokinase 1**	**1.090852743**	**0.762323**	**2**
P60892	FSNQETCVEIGESVR	1.051212936	2	2.77476
P60892	NCTIVSPDAGGAK	1.299914558	2	2.31358
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.38873042**	**3.91E-05**	**4**
P60901	AINQGGLTSVAVR	1.311731251	2	3.95305
P60901	GKDCAVIVTQK	1.495242579	2	3.16313
P60901	ITENIGCVMTGMTADSR	1.153117747	2	4.38729
P60901	LLDSSTVTHLFK	1.445434456	2	2.92343
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.144672276**	**0.547106**	**2**
P61087	GEIAGPPDTPYEGGR	1.136494541	2	2.98856
P61087	VDLVDENFTELR	1.168797082	2	2.57296
P61107	**RAB14 Ras_related protein Rab_14**	**1.195959154**	**0.855763**	**4**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	0.90029141	3	3.80429
P61107	NLTNPNTVIILIGNK	1.060028135	2	3.78422
P61107	SCLLHQFTEK	1.070724777	2	3.0617
P61107	TGENVEDAFLEAAKK	1.232786313	3	3.69372
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.193918806**	**0.514217**	**2**
P61222	NTVANSPQTLLAGMNK	1.208011555	2	2.90489
P61222	NVEDLSGGELQR	0.984173629	2	2.62572
P61314	**RL15 60S ribosomal protein L15**	**1.40922782**	**3.65E-07**	**5**
P61314	FFEVILIDPFHK	1.403431522	3	3.86743
P61314	GATYGKPVHHGVNQLK	0.821490051	2	4.46501
P61314	SLQSVAEER	1.194156021	2	2.88704
P61314	VLNSYWVGEDSTYK	1.300887094	2	4.03847
P61314	YIQELWR	1.230926949	2	2.48252
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.198657944**	**9.9E-20**	**4**
P61459	AVGWNELEGR	1.098957389	2	2.99745
P61459	LDHHPEWFNVYNK	1.336964439	3	5.12408
P61459	LSAEERDQLLPNLR	1.256042697	3	4.09913
P61459	VHITLSTHECAGLSER	1.761297821	2	3.74244
P61589	**RHOA Transforming protein RhoA**	**1.188595338**	**0.004902**	**6**
P61589	HFCPNVPIILVGNK	1.494180619	2	3.16407
P61589	HFCPNVPIILVGNKK	1.007793951	3	3.94051
P61589	IGAFGYMECSAK	1.711926818	2	3.00264
P61589	KKLVIVGDGACGK	0.913190729	2	2.42884
P61589	MKQEPVKPEEGR	1.072321819	3	3.50169
P61589	MKQEPVKPEEGR+Oxidation(1)	1.250555462	2	3.5013
P61751	**ARF4 ADP_ribosylation factor 4**	**1.323102591**	**4.64E-05**	**5**
P61751	ILMVGLDAAGK	1.451154536	2	2.45967
P61751	IQEGAAVLQK	1.153077681	2	2.56254
P61751	LGEIVTTIPTIGFNVETVEYK	1.26199487	3	4.57534
P61751	NICFTVWDVGGQDK	1.267192308	2	4.03191
P61751	QDLPNAMAISEMTDK	1.423695394	2	3.46289
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.278534666**	**0.332947**	**2**
P61805	ADFQGISPER	1.144428955	1	1.95331

P61805	FLEEYLSSTPQR	1.283207537	2	3.74085
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.188762445**	**0.720955**	**3**
P61924	AILILDNDGDR	1.276433485	2	2.90143
P61924	GEDVPLTEQTVSQVLQSAK	1.142049977	2	5.13934
P61924	YYDDTYPSVK	1.055492855	2	2.47498
P61972	**NTF2 Nuclear transport factor 2**	**1.10108893**	**0.762261**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	1.029963196	3	5.41942
P61972	NINDAWVCTNDMFR	1.074919325	2	3.04277
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.231026884**	**9.9E-20**	**11**
P61980	GSDFDCELR	1.231574626	2	2.46057
P61980	GSYGDLGGPIITTQVTIPK	0.914268853	2	4.68076
P61980	IDEPLEGSEDR	1.082432237	2	3.37288
P61980	IILDLISESPIK	1.477957295	2	3.92742
P61980	IITITGTQDQIQNAQYLLQNSVK	1.25194091	3	6.68484
P61980	LFQECCPHSTDR	1.244304382	2	3.55997
P61980	LLIHQSLAGGIIGVK	1.932746676	2	2.58792
P61980	NTDEMVELR	0.994642055	2	2.4274
P61980	RSRNTDEMVELR	0.987053629	2	2.32522
P61980	TDYNASVSVPDSSGPER	1.183496821	2	4.65239
P61980	VVLIGGKPDR	1.25015108	2	2.53567
P61983	**1433G 14_3_3 protein gamma**	**1.081423293**	**0.999963**	**4**
P61983	AYSEAHEISK	1.008211178	2	3.35271
P61983	NVTELNEPLSNEER	1.086434677	2	4.76019
P61983	TAFDDAIAELDTLNEDSYK	1.140280268	2	5.55698
P61983	YLAEVATGEK	0.908052763	2	2.73108
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.998499687**	**0.877702**	**4**
P62076	CIGKPGGSLDNSEQK	1.027100582	2	4.23589
P62076	KCIGKPGGSLDNSEQK	0.846882485	2	4.30504
P62076	VQIAVANAQELLQR	1.00566425	2	4.40919
P62076	YMDAWNTVSR	0.945732864	2	3.09854
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**1.043967197**	**0.932233**	**2**
P62078	FIDTTLAITGR	1.044583408	2	2.56581
P62078	TENCLSSCVDR	0.921172667	2	2.32365
P62083	**RS7 40S ribosomal protein S7**	**1.264499812**	**4.98E-06**	**5**
P62083	AIIIFVPVPQLK	1.155915996	2	3.7496
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.553335741	3	5.02312
P62083	KAIIIFVPVPQLK	1.103170556	2	3.62648
P62083	LDGSRLIK	1.096142838	2	2.33299
P62083	TLTAVHDAILEDLVFPSEIVGK	1.242569944	2	5.05687
P62161	**CALM Calmodulin**	**1.109222801**	**0.102832**	**4**
P62161	DGNGYISAAELR	0.990496021	2	2.66647
P62161	EADIDGDGQVNYEEFVQMMTAK	2.324412192	2	4.89699
P62161	EAFSLFDKDGDGTITTK	1.200938999	2	4.33368
P62161	VFDKDGNGYISAAELR	1.119689785	2	4.35631
P62193	**PRS4 26S protease regulatory subunit 4**	**1.002389643**	**0.872601**	**4**
P62193	APQETYADIGGLDNQIQEIK	1.254397914	2	4.97512
P62193	AVANQTSATFLR	1.097010623	2	2.60223
P62193	NQEQMKPLEEK	1.143267648	2	2.91342
P62193	TMLELLNQLDGFDSR	1.023261278	2	3.9991
P62198	**PRS8 26S protease regulatory subunit 8**	**1.141238794**	**0.051416**	**4**
P62198	EVIELPVKHPELFEALGIAQPK	1.261196664	3	3.90312
P62198	LEGGSGGDSEVQR	1.120943275	2	3.53385
P62198	TMLELLNQLDGFEATK	1.428342677	2	3.3689
P62198	VPDSTYEMIGGLDKQIK	1.392297797	2	2.33641

P62243	**RS8 40S ribosomal protein S8**	**1.292916573**	**0.00509**	**8**
P62243	ADGYVLEGK	1.090594687	2	2.38085
P62243	IIDVVYNASNNELVR	1.674584143	2	4.16359
P62243	ISSLLEEQFQQGK	1.475495169	2	3.99094
P62243	KYELGRPAANTK	0.968831744	2	3.75241
P62243	LDVGNFSWGSECCTR	1.213731224	2	3.90814
P62243	LTPEEEEILNK	1.08506936	2	3.24813
P62243	NCIVLIDSTPYR	0.995219355	2	3.33268
P62243	YELGRPAANTK	0.938155268	2	3.22821
P62246	**RS15A 40S ribosomal protein S15a**	**1.269291064**	**9.9E-20**	**3**
P62246	HGYIGEFEIIDDHR	1.284412784	2	4.23928
P62246	MNVLADALK	1.242158234	2	2.78002
P62246	WQNNLLPSR	1.471527881	2	2.67224
P62250	**RS16 40S ribosomal protein S16**	**1.251099536**	**0.007246**	**5**
P62250	ALVAYYQK	1.164214978	1	2.38891
P62250	GGGHVAQIYAIR	1.178417795	2	2.64336
P62250	LLEPVLLLGK	1.408049399	2	2.72394
P62250	TLLVADPR	1.200120764	2	2.45276
P62250	VNGRPLEMIEPR	1.090139134	2	2.6091
P62260	**1433E 14_3_3 protein epsilon**	**1.134610967**	**9.9E-20**	**7**
P62260	AAFDDAIAELDTLSEESYK	1.623120826	2	6.16081
P62260	HLIPAANTGESK	1.145309952	2	3.50657
P62260	IISSIEQK	1.285494094	2	2.79423
P62260	LICCDILDVLDK	2.271232589	2	4.06261
P62260	YDEMVESMK	1.097080038	2	2.48494
P62260	YLAEFATGNDR	0.909293327	2	2.79643
P62260	YLAEFATGNDRK	1.101495019	2	2.72085
P62271	**RS18 40S ribosomal protein S18**	**1.239812847**	**8.8E-11**	**4**
P62271	AGELTEDEVER	1.1071151	2	3.48363
P62271	LREDLER	1.215057988	1	2.00539
P62271	VLNTNIDGR	1.162484904	2	3.03602
P62271	YSQVLANGLDNK	1.352414544	2	3.77434
P62278	**RS13 40S ribosomal protein S13**	**1.139439807**	**1.01E-13**	**4**
P62278	GLAPDLPEDLYHLIK	1.475189316	2	2.97082
P62278	GLTPSQIGVILR	1.008858738	2	2.76058
P62278	KGLTPSQIGVILR	1.038968358	3	3.67167
P62278	LILIESR	1.256133132	1	1.93599
P62329	**TYB4 Thymosin beta_4**	**1.085150973**	**0.886836**	**4**
P62329	ETIEQEKQAGES	0.916048857	2	3.08089
P62329	KTETQEKNPLPSK	1.147034322	2	3.45988
P62329	NPLPSKETIEQEK	1.087122797	2	3.00775
P62329	TETQEKNPLPSK	1.122146742	2	3.79581
P62332	**ARF6 ADP_ribosylation factor 6**	**0.64178788**	**0.060369**	**2**
P62332	FNVWDVGGQDK	0.578386904	2	3.00287
P62332	LGQSVTTIPTVGFNVETVTYK	0.89699575	2	2.40965
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.072377032**	**0.233548**	**6**
P62334	ALQSVGQIVGEVLK	1.039406477	2	2.41709
P62334	AVASQLDCNFLK	1.010212713	2	2.44078
P62334	EVIELPLTNPELFQR	0.994804747	2	3.20723
P62334	GCLLYGPPGTGK	0.653119398	2	2.51297
P62334	HGEIDYEAIVK	1.060981281	2	3.75245
P62334	IHIDLPNEQAR	1.217841823	2	2.35397
P62425	**RL7A 60S ribosomal protein L7a**	**1.148143864**	**1.08E-12**	**10**
P62425	AGVNTVTTLVENK	1.214745437	2	3.85845
P62425	AGVNTVTTLVENKK	1.082027678	2	2.84303
P62425	HWGGNVLGPK	1.323940178	1	2.68437
P62425	KVVNPLFEK	1.366919166	2	2.3428

P62425	LKVPPAINQFTQALDR	1.377062122	3	4.65488
P62425	NFGIGQDIQPK	1.076715531	2	3.1646
P62425	TCTTVAFTQVNSEDK	1.08922659	2	3.73615
P62425	TCTTVAFTQVNSEDKGALAK	1.005263856	2	4.0672
P62425	VAPAPAVVK	1.128421957	1	1.97231
P62425	VPPAINQFTQALDR	1.050502551	2	3.40768
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.087496545**	**9.9E-20**	**15**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.339930975	3	5.22158
P62630	GNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.251468233	6	4.52624
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.346710763	4	5.93897
P62630	MDSTEPPYSQK	1.028422141	2	3.66552
P62630	MDSTEPPYSQK+Oxidation(1)	1.101839411	2	3.27101
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.226963507	3	6.27146
P62630	RGNVAGDSKNDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	0.993890982	5	4.6393
P62630	RYEEIVK	1.081660194	2	2.662
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.262084886	3	5.21196
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(15)	1.200747015	3	3.79164
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(9)	1.146035204	3	3.4255
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.107436708	2	5.60172
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(10)	1.058767119	3	4.63998
P62630	YEEIVK	1.188068267	1	1.98885
P62630	YYVTIIDAPGHR	1.240509573	2	3.51139
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.101387595**	**9.9E-20**	**6**
P62632	EHALLAYTLGVK	1.183785097	1	3.59036
P62632	IGGIGTVPVGR	1.362429721	2	3.63587
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.131337645	3	5.85823
P62632	QLIVGVNK	1.325664414	1	2.52067
P62632	STTTGHLIYK	1.15419542	2	3.14524
P62632	THINIVVIGHVDSGK	1.154448294	2	5.64054
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.168558776**	**0.366846**	**2**
P62634	CGETGHVAINCSK	1.091380797	2	4.47594
P62634	CYSCGEFGHIQK	1.203499705	2	3.11587
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.263593265**	**1.74E-12**	**5**
P62703	FDTGNLCMVTGGANLGR	1.102579482	2	5.07237
P62703	GIPHLVTHDAR	1.12233511	2	2.35906
P62703	LSNIFVIGK	1.621643379	2	3.2098
P62703	TDITYPAGFMDVISIDK	1.377099127	2	5.14676
P62703	VNDTIQIDLETGK	1.112648182	2	4.45045
P62752	**RL23A 60S ribosomal protein L23a**	**1.049670511**	**0.091111**	**6**
P62752	LAPDYDALDVANK	1.145809112	2	3.74788
P62752	LDHYAIIK	1.015879132	2	2.64494
P62752	LYDIDVAK	1.011369477	1	1.97206
P62752	NKLDHYAIIK	1.085906448	2	2.76412
P62752	VNTLIRPDGEK	1.089092522	2	3.23206
P62752	VNTLIRPDGEKK	1.306898218	2	2.913
P62755	**RS6 40S ribosomal protein S6**	**1.165955183**	**2.77E-05**	**4**
P62755	DIPGLTDTTVPR	1.101855312	2	2.66052
P62755	LIEVDDER	1.150027224	2	2.76439
P62755	LNISFPATGCQK	1.370203882	2	3.24553
P62755	NKEEAAEYAK	1.125466411	2	2.51117
P62775	**MTPN Myotrophin**	**0.996175864**	**0.943257**	**2**
P62775	GADINAPDKHHITPLLSAVYEGHVSCVK	1.086578024	4	5.22523
P62775	NGDLDEVKDYVAK	0.944180786	2	3.24045

P62804	**H4 Histone H4**	**1.13550279**	**0.000646**	**8**
P62804	DAVTYTEHAK	0.983268971	2	2.881
P62804	DNIQGITKPAIR	0.987722122	2	3.41559
P62804	ISGLIYEETR	1.368226453	2	3.64493
P62804	KTVTAMDVVYALK	0.955286571	2	2.49926
P62804	RISGLIYEETR	1.266294247	2	2.30632
P62804	TVTAMDVVYALK	1.019023277	2	4.04482
P62804	TVTAMDVVYALK+Oxidation(5)	1.051349677	2	2.85351
P62804	VFLENVIR	1.081386845	2	3.26538
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**1.081658268**	**0.766056**	**2**
P62815	AVVQVFEGTSGIDAK	1.132171828	2	3.28215
P62815	NFITQGPYENR	1.073003399	2	2.48013
P62832	**RL23 60S ribosomal protein L23**	**2.096169999**	**1.39E-13**	**2**
P62832	GSAITGPVAK	1.16606787	2	2.78882
P62832	ISLGLPVGAVINCADNTGAK	1.268262484	2	4.77714
P62845	**RS15 40S ribosomal protein S15**	**1.020462808**	**0.942106**	**2**
P62845	DMIILPEMVGSMVGVYNGK	1.172282941	2	3.10961
P62845	TFNQVEIKPEMIGHYLGEFSITYKPVK	0.977405839	4	5.10098
P62853	**RS25 40S ribosomal protein S25**	**1.818399769**	**9.36E-08**	**2**
P62853	GGDAPAAGEDA	1.872550294	1	2.20181
P62853	LNNLVLFDK	1.433059727	2	2.86726
P62856	**RS26 40S ribosomal protein S26**	**1.142690172**	**0.180557**	**2**
P62856	DISEASVFDAYVLPK	1.308890413	2	3.0337
P62856	NIVEAAAVR	1.149804551	2	3.04834
P62859	**RS28 40S ribosomal protein S28**	**1.088170249**	**0.788351**	**2**
P62859	EGDVLTLLESER	1.066003652	2	3.79795
P62859	VEFMDDTSR	1.240135072	2	2.32801
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.523530614**	**0.118736**	**2**
P62870	ADDTFEALR	1.344330706	2	2.62043
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.194557141	3	4.40892
P62890	**RL30 60S ribosomal protein L30**	**1.17778425**	**6.97E-05**	**3**
P62890	LVILANNCPALR	1.094240972	2	3.06709
P62890	TGVHHYSGNNIELGTACGK	1.169233173	2	5.70948
P62890	VCTLAIIDPGDSDIIR	1.472098429	2	4.13172
P62898	**CYC Cytochrome c_ somatic**	**1.018072626**	**0.001417**	**6**
P62898	ADLIAYLK	1.025432132	2	2.88971
P62898	GITWGEDTLMEYLENPK	1.143014099	2	5.22775
P62898	GITWGEDTLMEYLENPKK	1.345721562	2	4.65435
P62898	KTGQAAGFSYTDANK	1.201129356	2	3.94792
P62898	TGPNLHGLFGR	1.030933805	2	3.38054
P62898	TGQAAGFSYTDANK	1.046034351	2	4.324
P62902	**RL31 60S ribosomal protein L31**	**1.047049098**	**0.947743**	**3**
P62902	LYTLVTYVPVTTFK	1.9673063	2	3.19989
P62902	NLQTVNVDEN	1.298147336	1	2.42117
P62902	SAINEVVTR	1.04370109	2	2.56226
P62907	**RL10A 60S ribosomal protein L10a**	**1.17523922**	**0.00081**	**6**
P62907	AVDIPHMDIEALK	1.144889771	2	2.69013
P62907	FSVCVLGDQQHCDEAK	1.243098606	2	4.40269
P62907	ILGPGLNK	1.755329981	1	1.93241
P62907	KYDAFLASESLIK	1.11284461	2	3.3166
P62907	VLCLAVAVGHVK	1.337946882	2	3.22506
P62907	YDAFLASESLIK	1.06484194	2	3.11461
P62909	**RS3 40S ribosomal protein S3**	**1.187802578**	**1.43E-11**	**10**
P62909	AELNEFLTR	1.146986814	2	2.62324
P62909	DEILPTTPISEQK	1.260858373	2	3.05828

P62909	ELAEDGYSGVEVR	1.124940162	2	3.32631
P62909	ELTAVVQK	1.141901872	1	2.0989
P62909	FGFPEGSVELYAEK	1.99582163	2	3.93104
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.360003024	3	5.17329
P62909	GCEVVVSGK	1.248417768	2	2.5813
P62909	GGKPEPPAMPQPVPTA	1.25154697	2	4.04796
P62909	GLCAIAQAESLR	1.287999168	2	3.24721
P62909	TEIILATR	1.534277899	2	3.15364
P62912	**RL32 60S ribosomal protein L32**	**1.064152542**	**0.000166**	**2**
P62912	GQILMPNIGYGSNK	1.026068306	2	2.66458
P62912	SYCAEIAHNVSSK	1.209930164	2	4.27846
P62914	**RL11 60S ribosomal protein L11**	**1.107543904**	**0.716028**	**2**
P62914	VLEQLTGQTPVFSK	0.967011101	2	4.05695
P62914	YDGIILPGK	1.14534697	2	3.27068
P62919	**RL8 60S ribosomal protein L8**	**1.140159509**	**0.085278**	**3**
P62919	ASGNYATVISHNPETK	1.12050236	2	4.49217
P62919	AVVGVVAGGGR	1.143948635	2	3.34793
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.074281845	3	5.4397
P62944	**AP2B1 AP_2 complex subunit beta**	**1.244719313**	**0.11097**	**2**
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.3803475	3	3.64916
P62944	LQNNNVYTIAK	1.190604086	2	3.00048
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**1.13479056**	**0.591353**	**7**
P62959	AQVAQPGGDTIFGK	1.037946973	2	4.96864
P62959	CAADLGLK	1.131286902	2	2.50777
P62959	CLAFHDISPQAPTHFLVIPK	1.208425802	3	3.70877
P62959	HISQISVADDDDESLLGHLMIVGK	0.932663091	3	7.64522
P62959	IIFEDDR	1.22948185	2	2.65055
P62959	KHISQISVADDDDESLLGHLMIVGK	1.041302617	3	5.09073
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.867062136	3	4.08594
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.041537075**	**0.97376**	**4**
P62961	EDGNEEDKENQGDETQGQQPPQR	1.010768446	3	5.00482
P62961	GAEAANVTGPGGVPVQGSK	0.980621037	2	4.98974
P62961	NEGSESAPEGQAQQR	0.783837194	2	5.12952
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.052122649	4	5.46954
P62963	**PROF1 Profilin_1**	**1.264183337**	**0.001926**	**5**
P62963	DSLLQDGEFTMDLR	1.140735102	2	3.8876
P62963	DSPSVWAAVPGK	1.261975992	2	2.93246
P62963	SSFFVNGLTLGGQK	1.179567349	2	3.92799
P62963	STGGAPTFNVTVTMTAK	1.033580564	2	3.29581
P62963	TFVSITPAEVGVLVGK	1.207374263	2	5.09994
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.292777316**	**9.9E-20**	**22**
P63018	ARFEELNADLFR	1.239604697	3	3.88953
P63018	DAGTIAGLNVLR	1.084284241	2	3.42501
P63018	FDDAVVQSDMK	1.035864233	2	3.26835
P63018	FEELNADLFR	1.07086376	2	3.15154
P63018	FELTGIPPAPR	1.051517182	2	2.71697
P63018	IINEPTAAAIAYGLDK	1.235243827	2	5.5324
P63018	IINEPTAAAIAYGLDKK	1.312997254	2	4.17167
P63018	LLQDFFNGK	1.553909131	2	2.7076
P63018	MKEIAEAYLGK	1.084178283	2	3.44085
P63018	MVNHFIAEFK	1.544669665	2	3.17906
P63018	NQTAEKEEFEHQQK	1.200530238	2	5.24846
P63018	NQVAMNPTNTVFDAK	1.110696976	2	5.07526
P63018	NQVAMNPTNTVFDAK+Oxidation(5)	1.22058331	2	4.23191
P63018	NSLESYAFNMK	1.788788457	2	3.93485
P63018	RFDDAVVQSDMK	1.154985692	2	3.43635

P63018	SFYPEEVSSMVLTK	1.105329188	2	5.20395
P63018	SINPDEAVAYGAAVQAAILSGDK	1.599315288	2	6.26236
P63018	SQIHDIVLVGGSTR	1.104937277	2	4.86824
P63018	STAGDTHLGGEDFDNR	1.115040316	2	4.31051
P63018	TVTNAVVTVPAYFNDSQR	1.196359173	3	4.39499
P63018	VCNPIITK	1.219271195	2	2.43427
P63018	VQVEYKGETK	1.188153134	2	2.47466
P63025	**VAMP3 Vesicle_associated membrane protein 3**	**0.86023494**	**0.018388**	**2**
P63025	ADALQAGASQFETSAAK	0.724792315	2	4.67919
P63025	LQQTQNQVDEVVDIMR	1.445518723	2	3.61105
P63029	**TCTP Translationally_controlled tumor protein**	**1.15587109**	**0.942116**	**4**
P63029	DLISHDELFSDIYK	1.171793473	2	3.97676
P63029	EIADGLCLEVEGK	1.03620065	2	2.82903
P63029	GKLEEQKPER	1.159897128	2	3.41297
P63029	VKPFMTGAAEQIK	1.163390671	2	2.51388
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.299251995**	**0.002892**	**5**
P63036	HYNGEAYEDDEHHPR	1.190696045	3	4.96742
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.480205301	3	4.16789
P63036	QISQAYEVLADSK	1.281771505	2	2.57959
P63036	TIVITSHPGQIVK	1.089774094	2	3.48523
P63036	VNFPENGFLSPDK	1.182719006	2	3.14111
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.014189967**	**3.98E-09**	**35**
P63039	AAVEEGIVLGGGCALLR	0.980184367	2	5.70849
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(18)	0.906371252	3	4.40693
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(3)	0.984114953	3	3.75402
P63039	CEFQDAYVLLSEK	1.808521718	2	4.53654
P63039	CIPALDSLKPANEDQK	1.037176414	2	3.92477
P63039	DDAMLLKGK	0.99497997	1	1.92187
P63039	DDAMLLKGKGDK+Oxidation(4)	1.160537366	2	2.33184
P63039	DIGNIISDAMK	0.999733049	1	2.05108
P63039	DMAIATGGAVFGEEGLNLNLEDVQAHDLGK	0.963325595	3	4.10706
P63039	GIIDPTK	0.946060249	1	1.9477
P63039	GVMLAVDAVIAELK	0.928305267	2	2.36294
P63039	GVMLAVDAVIAELKK	1.032506639	2	4.57021
P63039	GYISPYFINTSK	0.733243688	2	2.74261
P63039	IGIEIIK	1.041552429	2	2.81454
P63039	ILQSSSEVGYDAMLGDFVNMVEK	2.084712302	3	6.14647
P63039	IQEITEQLDITTSEYEK	0.88599804	2	6.08754
P63039	IQEITEQLDITTSEYEKEK	0.987772488	2	5.13392
P63039	ISSVQSIVPALEIANAHR	1.214599013	2	4.47265
P63039	KISSVQSIVPALEIANAHR	1.648547144	3	3.92401
P63039	KPLVIIAEDVDGEALSTLVLNR	1.262377291	2	6.09902
P63039	LSDGVAVLK	1.091861095	2	2.99421
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.063397353	2	6.49695
P63039	NAGVEGSLIVEK	1.036632074	2	3.50932
P63039	QSKPVTTPEEIAQVATISANGDK	0.931305502	2	3.55075
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.087982733	3	4.93625
P63039	RGVMLAVDAVIAELKK	0.800289521	3	5.89633
P63039	TLNDELEIIEGMK	0.942492846	2	4.84894
P63039	TLNDELEIIEGMK+Oxidation(12)	0.920627044	2	2.74719
P63039	TVIIEQSWGSPK	0.95808114	2	4.28129
P63039	VGEVIVTK	0.992464431	2	3.09495
P63039	VGEVIVTKDDAMLLK	1.005649106	2	3.788
P63039	VGGTSDVEVNEK	0.968079594	2	3.91842
P63039	VGGTSDVEVNEKK	0.915696453	2	3.73441
P63039	VGLQVVAVK	1.02100758	2	3.26118
P63039	VTDALNATR	1.043102693	2	3.52256

P63102	**1433Z 14_3_3 protein zeta/delta**	**1.078899002**	**9.9E-20**	**8**
P63102	DICNDVLSLLEK	1.670939652	2	3.92897
P63102	FLIPNASQPESK	1.09724876	2	3.47434
P63102	GIVDQSQQAYQEAFEISK	1.042808923	2	5.74524
P63102	KGIVDQSQQAYQEAFEISK	1.113734743	2	5.04028
P63102	SVTEQGAELSNEER	1.076288077	2	5.10069
P63102	TAFDEAIAELDTLSEESYK	1.4819149	2	5.83761
P63102	YDDMAACMK	1.099821154	2	2.59623
P63102	YLAEVAAGDDKK	1.213868982	2	3.72432
P63159	**HMGB1 High mobility group protein B1**	**1.108535664**	**0.00249**	**5**
P63159	GEHPGLSIGDVAK	1.071227514	2	3.1564
P63159	IKGEHPGLSIGDVAK	1.397412339	2	3.87183
P63159	KHPDASVNFSEFSK	1.195579692	3	4.1092
P63159	KLGEMWNNTAADDKQPYEK	1.168940735	3	4.31448
P63159	LGEMWNNTAADDKQPYEK	1.134281755	3	3.59677
P63174	**RL38 60S ribosomal protein L38**	**1.102407391**	**0.154518**	**3**
P63174	IEEIKDFLLTAR	0.999630044	2	3.03955
P63174	KIEEIKDFLLTAR	1.175684281	2	4.59237
P63174	YLYTLVITDKEK	1.013828591	2	2.70794
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.286121324**	**2.16E-14**	**13**
P63245	DETNYGIPQR	1.166968968	2	3.00876
P63245	DGQAMLWDLNEGK	1.031634267	2	3.36682
P63245	FSPNSSNPIIVSCGWDK	1.274061894	2	4.26935
P63245	GHNGWVTQIATTPQFPDMILSASR	0.930016695	3	4.2884
P63245	HLYTLDGGDIINALCFSPNR	1.500829343	2	5.60687
P63245	IIVDELKQEVISTSSK	1.296106459	2	4.12914
P63245	LWDLTTGTTTR	1.131429265	2	2.95552
P63245	LWNTLGVCK	1.461016493	2	2.32805
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.072393083	2	4.72456
P63245	VWNLANCK	1.024143625	2	2.67768
P63245	VWQVTIGTR	0.803828522	2	2.90551
P63245	YTVQDESHSEWVSCVR	1.164975358	2	3.30949
P63245	YWLCAATGPSIK	1.025239602	2	3.15877
P63259	**ACTG Actin_ cytoplasmic 2**	**1.348284527**	**9.99E-16**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	2.588596178	3	5.74178
P63259	DLYANTVLSGGTTMYPGIADR	1.009314044	2	5.76902
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.871195797	2	4.35081
P63259	GYSFTTTAER	1.112440022	2	3.37033
P63259	KDLYANTVLSGGTTMYPGIADR	1.009398878	2	6.16232
P63259	LCYVALDFEQEMATAASSSSLEK	2.912073643	2	5.20947
P63259	QEYDESGPSIVHR	1.163665	3	3.51731
P63259	VAPEEHPVLLTEAPLNPK	1.250043641	2	4.64207
P63269	**ACTH Actin_ gamma_enteric smooth muscle**	**1.681045233**	**0.56855**	**2**
P63269	DLYANNVLSGGTTMYPGIADR	1.547293669	2	3.43609
P63269	KDLYANNVLSGGTTMYPGIADR	4.254378059	2	5.08026
P63324	**RS12 40S ribosomal protein S12**	**1.219347446**	**4.72E-12**	**3**
P63324	KVVGCSCVVVK	1.069644379	2	2.62901
P63324	LGEWVGLCK	1.293679374	2	3.14661
P63324	VVGCSCVVVK	1.139658641	2	3.03185
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**1.29482299**	**0.058553**	**2**
P63331	GAGYTFGQDISETFNHANGLTLVSR	1.035450174	3	3.33239
P63331	YSFLQFDPAPR	1.311650151	2	3.26145
P67779	**PHB Prohibitin**	**0.976641492**	**0.078012**	**10**
P67779	AAELIANSLATAGDGLIELR	0.990530748	2	5.3507
P67779	AAIISAEGDSK	1.134286787	2	2.40312

P67779	DLQNVNITLR	0.978849663	2	3.78424
P67779	FDAGELITQR	1.030185457	2	3.74664
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	0.63588999	3	5.32669
P67779	IYTSIGEDYDER	1.603037869	2	3.40909
P67779	KLEAAEDIAYQLSR	0.95982364	2	4.91233
P67779	NVPVITGSK	0.904689643	1	2.47045
P67779	QVSDDLTER	1.006376888	2	2.63175
P67779	VLPSITTEILK	0.979693742	2	2.51978
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.275542366**	**6.66E-16**	**4**
P68037	ADLAEEYSK	0.849307103	2	2.58318
P68037	GQVCLPVISAENWKPATK	0.971509239	2	3.26639
P68037	IEINFPAEYPFKPPK	1.301251089	2	3.69446
P68037	TDQVIQSLIALVNDPQPEHPLR	1.463081394	2	4.87003
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.095541325**	**0.059498**	**5**
P68101	AGLNCSTETMPIK	1.095730814	2	2.8608
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.935478596	3	4.20617
P68101	HVAEVLEYTKDEQLESLFQR	1.066688909	3	3.53982
P68101	TEGLSVLNQAMAVIK	1.197505916	2	3.80156
P68101	VVTDTDETELAR	1.169005223	2	3.16541
P68136	**ACTS Actin_ alpha skeletal muscle**	**1.24140935**	**0.913535**	**16**
P68136	AGFAGDDAPR	1.242805371	2	3.36338
P68136	AVFPSIVGRPR	1.038482416	2	2.95198
P68136	CPETLFQPSFIGMESAGIHETTYNSIMK	3.652996704	3	4.20481
P68136	DLYANNVMSGGTTMYPGIADR	1.062939755	2	3.72637
P68136	DSYVGDEAQSK	0.882674458	2	3.05564
P68136	DSYVGDEAQSKR	1.520891358	2	2.46655
P68136	EITALAPSTMK	1.080296774	1	2.94913
P68136	EITALAPSTMK+Oxidation(10)	1.05511408	2	2.76623
P68136	GYSFVTTAER	1.570524614	2	3.8015
P68136	IWHHTFYNELR	1.428699153	3	3.71267
P68136	KDLYANNVMSGGTTMYPGIADR	1.470899509	2	5.20123
P68136	QEYDEAGPSIVHR	1.559867972	2	3.14832
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	1.664286338	3	6.71917
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(29)	1.412080063	3	5.51312
P68136	VAPEEHPTLLTEAPLNPK	1.580132064	2	4.53606
P68136	YPIEHGIITNWDDMEK	1.295332082	2	4.54583
P68255	**1433T 14_3_3 protein theta**	**1.342402485**	**0.000619**	**5**
P68255	AVTEQGAELSNEER	1.074259236	2	4.62849
P68255	SICTTVLELLDK	1.236762899	2	2.77049
P68255	TAFDEAIAELDTLNEDSYK	1.381516915	2	4.52114
P68255	VISSIEQK	1.295756669	1	2.19641
P68255	YLIANATNPESK	1.096085031	2	3.57448
P68511	**1433F 14_3_3 protein eta**	**1.337109288**	**0.00017**	**2**
P68511	AVTELNEPLSNEDR	1.335098049	2	4.84622
P68511	NSVVEASEAAYK	1.149887883	2	3.17393
P69527	**AMPO Aminopeptidase O**	**1.143342398**	**0.207514**	**2**
P69527	LQQLAHRCFELVK	1.655144691	2	2.36537
P69527	WHRLQDELQNSPEGMQVLRPNK	1.109452532	2	2.49344
P69897	**TBB5 Tubulin beta_5 chain**	**1.47311081**	**1.53E-12**	**4**
P69897	ALTVPELTQQVFDAK	1.545658394	2	3.4195
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	1.241927399	3	5.77748
P69897	ISVYYNEATGGK	1.372895216	2	2.88842
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.499369408	2	5.22498
P70372	**ELAV1 ELAV_like protein 1**	**1.169085895**	**0.067698**	**3**
P70372	SLFSSIGEVESAK	1.095173825	2	3.4156

P70372	TNLIVNYLPQNMTQEELR	1.186701621	2	4.15986
P70372	VLVDQTTGLSR	1.102775956	2	2.56212
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.443668885**	**0.010873**	**2**
P70470	ASFSQGPINSANR	1.464008556	2	2.8958
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.440609875	3	3.97376
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.909301401**	**1.87E-13**	**12**
P70473	ADVLLEPFR	0.880947273	2	3.54112
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	0.991278378	3	5.55535
P70473	DYGFSQEEIHQLHSDR	0.95717537	2	5.00696
P70473	GLGLESEELPSQMSIEDWPEMK	1.007578865	3	4.66227
P70473	GQNLLDGGAPFYTTYK	0.647672989	2	5.22007
P70473	GSFITDEEQHACPRPAPQLSR	0.864073082	3	3.62445
P70473	LGSVNHPSHLAR	1.498139843	2	2.91458
P70473	LQLGPETLR	0.890725056	2	2.41605
P70473	LSGFGQSGIFSK	1.34896407	2	2.7786
P70473	RDPSVGEHTVEVLK	0.814164279	3	4.36536
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.92092394	4	5.75804
P70473	TQAMGLWAQPR	0.793575029	2	3.51256
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**1.110811917**	**0.039889**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.954371453	3	4.7964
P70552	VLGNNFYEYYVNDPPR	1.490080571	2	3.96972
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**1.096271286**	**0.426095**	**9**
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	1.36327259	3	5.46233
P70580	EGEEPTVYSDDEEPKDEAAR	0.901615891	2	4.38536
P70580	FYGPEGPYGVFAGR	1.011109506	2	4.09912
P70580	GDQPGASGDNDDDEPPPLPR	1.167261414	2	5.14438
P70580	IVRGDQPGASGDNDDDEPPPLPR	0.70825792	3	5.17675
P70580	KFYGPEGPYGVFAGR	0.959807381	2	3.81775
P70580	LLKEGEEPTVYSDDEEPKDEAAR	1.124795209	3	5.17035
P70580	RYDGVQDPR	0.991465857	1	2.18152
P70580	YDGVQDPR	1.004704877	2	3.01956
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.815405903**	**2.72E-07**	**10**
P70584	ASSTCQLTFENVK	0.843033959	2	2.87212
P70584	ASSTCQLTFENVKVPETSVLGK	0.793816325	3	3.6126
P70584	FAQEQIAPLVSTMDENSK	0.880107187	2	4.30519
P70584	IFDFQGLQHQVAHVATQLEAAR	0.903619379	3	6.06909
P70584	IGTIYEGTSNIQLNTIAK	0.785161546	2	4.55361
P70584	KFAQEQIAPLVSTMDENSK	0.773900478	2	5.42675
P70584	SGNYYVINGSK	0.823098437	2	2.61805
P70584	SVIQGLFQQGMMGIEVEAK	0.797376692	2	4.48708
P70584	VDASVALLCDIQNTVINK	1.053848493	2	4.91373
P70584	YYASEVAGLTTSK	0.841894006	2	4.06038
P70615	**LMNB1 Lamin_B1**	**1.088173913**	**0.272114**	**3**
P70615	ALYETELADAR	1.061837805	2	3.24198
P70615	LSSEMNTSTVNSAR	1.132144672	2	2.98943
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.188234263	3	3.79617
P70619	**GSHR Glutathione reductase (Fragment)**	**1.068753165**	**0.609431**	**2**
P70619	ALLTPVAIAAGR	0.8561289	2	2.72661
P70619	LNNIYQNNLTK	1.069549377	2	3.05393
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**1.319756031**	**0.033937**	**2**
P70694	REDIFYTSK	1.34396894	2	3.06036
P70694	SIGVSNFNR	1.286125533	2	2.39868
P70712	**KYNU Kynureninase**	**1.505685207**	**9.9E-20**	**8**
P70712	IATELNCDPTDER	1.536037109	2	3.63125

P70712	IGAYGHEVGK	1.623803317	2	2.84166
P70712	LLTAILDSTERN	1.959681951	2	3.5405
P70712	MEDILEVIEK	1.462477117	2	2.61886
P70712	SILLTGYLEYLLK	1.540309673	2	3.10648
P70712	TYLEEELDKWAK	0.753829609	2	2.95422
P70712	VAPVPLYNSFHDVYK	0.692188444	2	3.42088
P70712	YLNSGAGGLAGAFIHEK	1.508059677	2	4.45412
P80067	**CATC Dipeptidyl peptidase 1**	**1.307691016**	**0.00495**	**5**
P80067	GTDECAIESIAMAAIPIPK	1.069719483	3	4.69789
P80067	NQESCGSCYSFASLGMLEAR	1.34873644	2	4.87714
P80067	NSWGSQWGESGYFR	1.127531807	2	3.03162
P80067	RGTDECAIESIAMAAIPIPK	1.101193352	2	4.46006
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.362031005	3	5.56244
P80254	**DOPD D_dopachrome decarboxylase**	**1.106874751**	**0.085902**	**4**
P80254	FFPLEPWQIGK	0.919048694	2	3.02736
P80254	FLTEELSLDQDR	0.943269501	2	3.73073
P80254	LCAATATILDKPEDR	1.699942998	2	4.23315
P80254	STEPCAHLLISSIGVVGTAEQNR	0.925501783	2	5.40058
P80299	**HYES Epoxide hydrolase 2**	**1.306461711**	**0.195518**	**2**
P80299	ATEMGGILVGTPEDPK	1.353385655	2	3.02936
P80299	TEIQNPSVTSK	1.096748728	2	2.926
P80313	**TCPH T_complex protein 1 subunit eta**	**1.026756137**	**2.85E-05**	**4**
P80313	ATISNDGATILK	1.099830758	2	2.83752
P80313	GGAEQFMEETER	1.238575971	2	2.50413
P80313	QLCDNAGFDATNILNK	0.861787052	2	3.52348
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.346597044	2	5.06999
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.125873727**	**0.092055**	**9**
P80317	ALQFLEQVK	1.411263716	2	2.51102
P80317	AQAALAVNISAAR	1.050391325	2	3.07079
P80317	DGNVLLHEMQIQHPTASLIAK	1.214432801	3	4.78113
P80317	GIDPFSLDALAK	1.279168453	2	2.79711
P80317	HKSETDTSLIR	1.082563184	2	2.67614
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.120029101	3	5.03851
P80317	TEVNSGFFYK	1.232087044	2	2.52216
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.126056457	2	4.9627
P80317	VLAQNSGFDLQETLVK	1.052970059	2	3.465
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.990988623**	**0.006942**	**5**
P81155	LTFDTTFSPNTGK	1.525785068	2	2.61093
P81155	LTFDTTFSPNTGKK	1.049283477	2	2.86808
P81155	SCSGVEFSTSGSSNTDTGK	0.959788762	2	2.417
P81155	VNNSSLIGVGYTQTLRPGVK	0.51269105	2	3.61388
P81155	YQLDPTASISAK	1.047270349	2	2.94893
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.31028658**	**3.92E-10**	**14**
P82995	ELHINLIPNKQDR	1.125676385	2	2.97738
P82995	ELISNSSDALDK	0.968128477	2	2.70518
P82995	FYEQFSK	1.115200205	1	2.04671
P82995	HGLEVIYMIEPIDEYCVQQLK	1.304589381	3	5.55117
P82995	HIYFITGETK	1.424258787	2	2.9629
P82995	HLEINPDHSIIETLR	1.186474933	3	4.28892
P82995	HSQFIGYPITLFVEK	6.576263055	2	3.71054
P82995	LGIHEDSQNR	1.205612254	3	3.47133
P82995	NPDDITNEEYGEFYK	1.385077591	2	5.07323
P82995	RAPFDLFENR	1.243552163	2	2.36484
P82995	SLTNDWEEHLAVK	1.15840938	2	4.16434
P82995	TLTIVDTGIGMTK	1.060784717	2	4.34295
P82995	TLTIVDTGIGMTK+Oxidation(11)	1.226849138	2	3.38947

P82995	YYTSASGDEMVSLK	1.235977006	2	3.42435
P83732	**RL24 60S ribosomal protein L24**	**1.150890999**	**0.565838**	**2**
P83732	AITGASLADIMAK	1.115178459	2	4.67364
P83732	VELCSFSGYK	1.46194541	2	2.37083
P83868	**TEBP Prostaglandin E synthase 3**	**1.55202093**	**0.002387**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.992741176	3	3.30478
P83868	LTFSCLGGSDNFK	1.550877494	2	2.76856
P83883	**RL36A 60S ribosomal protein L36a**	**1.220190219**	**0.097475**	**2**
P83883	HFELGGDK	1.220078366	1	2.38358
P83883	LECVEPNCR	1.218358346	2	2.34021
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.310350362**	**0.010048**	**2**
P83941	AMLSGPGQFAENETNEVNFR	1.292798268	2	5.01853
P83941	TYGGCEGPDAMYVK	1.320785331	2	3.78876
P84082	**ARF2 ADP_ribosylation factor 2**	**1.050778992**	**0.543992**	**2**
P84082	NISFTVWDVGGQDK	1.019000883	2	4.5258
P84082	QDLPNAMNAAEITDK	1.32569207	2	3.8614
P84083	**ARF5 ADP_ribosylation factor 5**	**0.978880028**	**0.381391**	**2**
P84083	DAVLLVFANK	1.336713794	2	2.48759
P84083	VQESADELQK	1.031343806	2	2.93744
P84100	**RL19 60S ribosomal protein L19**	**1.098608576**	**2.67E-07**	**2**
P84100	LLADQAEAR	1.316714096	2	3.44129
P84100	VWLDPNETNEIANANSR	1.150823186	2	5.81395
P84245	**H33 Histone H3.3**	**1.062288841**	**0.127**	**4**
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.23728817	3	5.96708
P84245	RVTIMPKDIQLAR+Oxidation(5)	1.273090943	2	2.92103
P84245	STELLIR	1.05564038	2	2.5132
P84245	YRPGTVALR	1.019942844	2	2.36002
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.037701499**	**0.546541**	**4**
P84817	FQSEQAAGSVSK	0.95717053	2	2.97679
P84817	GIVLLEELLPK	1.102986446	2	2.31727
P84817	GLLQTEPQNNQAK	1.151145883	2	3.58586
P84817	KFQSEQAAGSVSK	1.009569914	2	4.05567
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**1.086314067**	**0.183886**	**16**
P85834	AEAGDNLGALVR	0.929281213	2	3.74795
P85834	DKPHVNVGTIGHVDHGK	0.836110982	3	3.48063
P85834	DLEKPFLLPVESVYSIPGR	1.379011271	2	3.91832
P85834	GDECELLGHNK	0.916041143	2	2.59071
P85834	GEETPVIVGSALCALEQR	1.089765147	2	4.59334
P85834	GITINAAHVEYSTAAR	3.554069861	2	3.01322
P85834	GTVVTGTLER	0.879532789	2	2.87445
P85834	HYAHTDCPGHADYVK	1.163321337	2	4.19635
P85834	KGDECELLGHNK	0.839190448	3	3.93868
P85834	KYEEIDNAPEER	0.920398912	2	3.57919
P85834	LLDAVDTYIPVPTR	0.891699467	2	3.92356
P85834	QIGVEHVVVYVNK	0.934615389	2	2.85807
P85834	TIGTGLVTDVPAMTEEDK	0.844162722	2	4.12678
P85834	TIGTGLVTDVPAMTEEDKNIK	0.8568085	2	4.70657
P85834	TVVTGIEMFHK	0.774539122	2	2.45144
P85834	YEEIDNAPEER	0.885030941	2	3.18513
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.303573281**	**9.9E-20**	**10**
P85968	AGQAVDDFIEK	1.345572387	2	2.92663
P85968	CLSSLKEER	1.482497581	2	2.4036
P85968	FQDTDGKELLPK	1.381392113	2	3.13064
P85968	GILFVGSGVSGGEEGAR	1.607728797	2	5.04915
P85968	HEMLPANLIQAQR	1.196038883	2	3.25458

P85968	LVPLLDTGDIIIDGGNSEYR	2.097067677	2	5.5579
P85968	NPELQNLLLDDFFK	1.530559836	2	4.76573
P85968	SAVDDCQDSWR	1.063870137	2	2.94792
P85968	VGTGEPCCDWVGDEGAGHFVK	1.315587122	3	4.54917
P85968	YGPSLMPGGNK	1.463108789	1	2.20074
P85971	**6PGL 6_phosphogluconolactonase**	**1.312321844**	**0.088767**	**5**
P85971	DLPAATAPAGPASFAR	1.171262307	2	2.41429
P85971	ILEDQESALPAAMVQPR	1.249841245	2	4.16853
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.190271055	2	4.99045
P85971	TGALCWFLDEAAAR	1.43179125	2	3.79618
P85971	WTLGFCDER	1.209580773	2	2.30716
P85972	**VINC Vinculin**	**1.018688896**	**0.846143**	**12**
P85972	AIPDLTAPVAAVQAAVSNLVR	1.082769948	2	3.35209
P85972	AQQVSQGLDVLTAK	0.99145778	2	4.46733
P85972	AVAGNISDPGLQK	0.995537311	2	3.38288
P85972	GQGASPVAMQK	0.864445548	2	3.00086
P85972	MLGQMTDQVADLR	1.225323582	2	2.51366
P85972	NRNFTVGKMSAEINEIIR+Oxidation(9)	1.051592845	2	2.73024
P85972	QVATALQNLQTK	1.150134593	2	3.72169
P85972	SLLDASEEAIKK	1.187504989	2	2.63371
P85972	STVEGIQASVK	1.083014328	2	2.30356
P85972	TNISDEESEQATEMLVHNAQNLMQSVK	1.11953256	3	4.04425
P85972	VLQLTSWDEDAWASK	1.515151213	2	3.66822
P85972	WIDNPTVDDR	1.026108221	2	3.18012
P85973	**PNPH Purine nucleoside phosphorylase**	**1.144303855**	**0.000776**	**12**
P85973	ASHQEVLEAGK	1.115420699	2	3.42104
P85973	DHINLPGFCGQNPLR	1.122081328	2	4.10377
P85973	ELQEGTYIMSAGPTFETVAESCLLR	1.077567495	2	5.05427
P85973	FEVGDIMLIR	1.141268281	2	3.60984
P85973	HRPQVAVICGSGLGGLTAK	1.058358401	3	6.29754
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.980524268	3	4.73753
P85973	MLGADAVGMSTVPEVIVAR	1.253131877	2	6.07086
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(1)	1.146393971	2	5.11842
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(9)	1.114778452	2	3.74454
P85973	VFGFSLITNK	1.215174183	2	2.81672
P85973	VFHLLGVDTLVVTNAAGGLNPK	1.268987475	2	5.83555
P85973	VVMDYNNLEK	1.100355531	2	2.6068
P86048	**RL10L 60S ribosomal protein L10_like**	**1.638591192**	**0.172223**	**4**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.3982182	3	5.03798
P86048	GAFGKPQGTVAR	1.165786482	2	3.04352
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.193688465	3	5.80326
P86048	VHIGQVIMSIR	1.244869943	2	2.82452
P86252	**PURA Transcriptional activator protein Pur_alpha (Fragments)**	**1.064327304**	**0.407195**	**2**
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	0.949489728	2	4.17132
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	1.20979872	3	5.06658
P97310	**MCM2 DNA replication licensing factor MCM2**	**0.720266133**	**0.117518**	**4**
P97310	EAGRGLGRMR	1.112631018	2	2.54775
P97310	HIESMIRMAEAHARMHLR	0.713814812	2	2.66758
P97310	LNQMDQDKVAR+Oxidation(4)	0.544119491	2	2.57704
P97310	MITGLSKDQQIGEK+Oxidation(1)	1.272184904	2	2.46068
P97323	**F16P3 Fructose_1_6_bisphosphatase isozyme 3 (Fragment)**	**0.887026076**	**0.188026**	**2**
P97323	GNIYSLNEGYAK	0.916148676	2	3.94263
P97323	KGNIYSLNEGYAK	0.84880973	2	4.21584
P97384	**ANX11 Annexin A11**	**1.023429215**	**0.950379**	**2**
P97384	GFGTDEQAIIDCLGSR	0.96192064	2	4.24228

P97384	SELDLLDIR	1.111004816	2	2.68485
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**0.890604226**	**0.367783**	**8**
P97519	GASGNLATEDLVYMLTGLGIHTGVNLQK	0.995949174	3	3.89209
P97519	GFEEAVAAGAK	0.994985468	2	3.20173
P97519	GYVSCALGCPYEGK	0.983084254	2	3.72652
P97519	KNVNCSIEESFQR	0.884719103	2	3.56165
P97519	LIDMLSEAGLPVIEATSFVSPK	1.372651424	2	4.85896
P97519	LLEAGDFICQALNR	1.218944485	2	4.50007
P97519	NVNCSIEESFQR	0.929285593	2	3.44686
P97519	WVPQMADHSDVLK	1.035851298	2	3.01394
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**1.098827119**	**0.999359**	**5**
P97521	CLLQIQASSGK	1.096962303	2	3.10504
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.013244767	2	3.79185
P97521	LYQEFGIR	1.12660541	2	2.35567
P97521	SVHDLSVPR	1.004643949	2	2.5423
P97521	YSGTLDCAK	1.000295694	2	2.51792
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.248810609**	**0.01028**	**15**
P97524	ALHDHLGLR	0.933122619	2	2.41639
P97524	GEVGLLICK	1.21878741	2	2.618
P97524	IQDTIEITGTFK	1.088805458	2	2.50409
P97524	ITELTPFFGYAGGK	0.429302341	2	2.30854
P97524	MKENYEFNGK	1.143504348	2	3.25668
P97524	SEVTFTTPAVYIYTSGTTGLPK	0.89408515	2	2.65069
P97524	SLLHCFQCCGAK	1.143439105	2	3.29537
P97524	TILHVFLEQAR	1.025619633	2	2.96387
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	1.07822962	3	5.78916
P97524	TYVPMTEDIYNAIIDK	1.149095806	2	4.04602
P97524	VLLASPELHEAVEEVLPTLK	1.363769309	2	3.86732
P97524	VTLMEEGFNPSVIK	1.205111716	2	3.67689
P97524	YDVEKDEPVR	1.262617733	2	2.83595
P97524	YLCNTPQKPNDR	1.219104714	2	3.04033
P97524	YNATVIQYIGELLR	1.671242004	2	2.75376
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.062246027**	**0.001896**	**8**
P97532	AFGHHSVSLLDGGFR	1.357132157	2	3.44993
P97532	ALVSAQWVAEALK	0.981871436	2	3.78603
P97532	AQPEHVISQGR	0.944364658	2	2.79149
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.456681247	3	6.76656
P97532	FQGTQPEPR	0.966581971	2	2.94384
P97532	LLDASWYLPK	1.235971978	2	3.91231
P97532	THEDILENLDAR	1.046491596	2	3.37557
P97532	YWLSQNLPISSGK	1.010469387	2	3.60341
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.34399522**	**0.000123**	**5**
P97536	EGPAVVGQFIQDVK	0.994303748	2	2.75803
P97536	ITSEALLVTQQLVK	1.21543026	2	2.34775
P97536	LGTLSALDILIK	1.689866082	2	2.53432
P97536	LTLIDPETLLPR	1.494342221	2	2.68069
P97536	TYIQCIAAISR	1.240046045	2	2.98582
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.278314753**	**8.83E-09**	**18**
P97562	ATASCTYEGENTVLYLQVAR	2.422090207	2	4.60551
P97562	ATFADFCAQGAEICR	1.329711393	2	5.03724
P97562	CSAQTAADFR	0.927807716	2	2.43799
P97562	DAILLTDAFDFSDHCLNSALGCYDGHVYER	1.298931227	3	4.04509
P97562	DFSLLPELHALSTGMK	0.960878045	2	2.60809
P97562	EAFLDLLPLIR	0.922923632	2	2.71118

P97562	ILEYQTQQQK	1.082562462	2	3.9169
P97562	KVESIIQSDPVFNLK	1.07139612	2	4.94923
P97562	LCDLYALHGVLTNSGDFLHDGFLSGAQVDMAR	1.79285437	3	5.69826
P97562	LDKEPEIQR	1.107034019	3	3.54922
P97562	LGTPQSNYLGMLVTR	1.535763653	2	3.51534
P97562	LTNILDGGLPNTVLR	1.32920945	2	4.25074
P97562	MGLEHIDNGFLQLNHVR	1.359124671	2	4.42319
P97562	SGVDQHDAWNQTTVIHLQAAK	1.070821145	3	6.26692
P97562	SLEDHTPLPGITVGDIGPK	1.074539188	2	4.55118
P97562	SLGSDEQIAK	1.148009336	2	2.8494
P97562	VESIIQSDPVFNLK	0.979673213	2	4.57151
P97562	VLDGNVNLSLHGVAMNAIR	0.895550169	2	5.00814
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.026386765**	**0.230743**	**3**
P97576	ALADTENLR	1.024210192	2	2.30619
P97576	DLLEVADILEK	1.166491288	2	2.43203
P97576	EEVSNNNPHLK	0.971843338	2	3.2841
P97584	**PTGR1 Prostaglandin reductase 1**	**1.264016851**	**0.722514**	**5**
P97584	ALTDLMNWVSEGK	1.208178662	2	3.67279
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.1688476	2	4.74165
P97584	HFEGFPTDSNFELR	0.849938919	2	3.89915
P97584	TGPCPPGPSPEVIIYQQLR	1.10123974	2	4.04415
P97584	YHEYITEGFEK	0.966945386	2	2.928
P97608	**OPLA 5_oxoprolinase**	**1.119915153**	**0.733694**	**4**
P97608	AGDFGAAFVER	1.085058713	2	2.43718
P97608	GSILDPSPEAAVVGGNVLTSQR	0.827954723	2	5.04682
P97608	LLSEDPANYADAPTEGIR	1.340113352	2	3.84463
P97608	TGDLLEIQQPVDLEALR	1.197281741	2	4.88974
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.197418278**	**0.002194**	**8**
P97612	EVEQLMTPQK	1.073183442	2	2.32355
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.111460763	3	4.69134
P97612	GTNCVTSYLTDCETQLSQAPR	1.229931236	2	4.56798
P97612	GYFGDIWDIILK	1.593645187	2	3.40174
P97612	LQHEIEMYR	1.062842666	2	2.37678
P97612	LQSGELSPEAVFFTYLGK	3.054078693	2	4.52379
P97612	NSVGLPVAVQCVALPWQEELCLR	1.318903821	2	4.15512
P97612	QGLLYGVPVSLK	0.960962687	2	2.74481
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.099278062**	**0.00355**	**3**
P97700	AVVVNAAQLASYSQSK	0.930024664	2	4.73854
P97700	LGIYTVLFER	1.897286694	2	3.05843
P97700	LTGADGTPPGFLLK	1.126928432	2	2.82073
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.964076782**	**0.997041**	**24**
P97852	AAVAVPSRPPDAVLR	1.0067777	2	2.32785
P97852	AVANYDSVEAGEK	1.035092721	2	3.8566
P97852	AYALAFAER	1.274104801	2	3.06397
P97852	DTTSLNQAALYR	0.92533796	2	2.65827
P97852	FVYEGSADFSCLPTFGVIVAQK	0.971376174	2	4.82592
P97852	GALVVVNDLGGDFK	1.096902954	2	3.65864
P97852	GNIMLSQKLQMILK+Oxidation(4)Oxidation(11)	0.94544163	2	2.33971
P97852	GSSAADKVVEEIR	0.910762824	2	3.15108
P97852	HVLQQFADNDVSR	0.959904296	2	4.61594
P97852	ICDFSNASKPK	1.148078814	3	3.79105
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	1.080785136	3	6.13575
P97852	IDVVVNNAGILR	0.980837255	2	3.6548
P97852	ISDEDWDIIQR	0.937190125	2	3.37681
P97852	KNNIHCNTIAPNAGSR	0.943019746	2	4.78276
P97852	LGLLGLANTLVIEGR	1.401589741	2	3.40736

P97852	LNPQNAFFSGR	1.228006294	2	2.8304
P97852	NGSGEVYQGPAK	0.964636198	2	3.51503
P97852	NNIHCNTIAPNAGSR	0.904188243	2	4.62699
P97852	SIQESTGGIIEVLHK	1.035454979	2	4.16776
P97852	SLMSGGLAEVPGLSINFAK	0.961792984	2	4.59738
P97852	SLMSGGLAEVPGLSINFAK+Oxidation(3)	1.051974025	2	3.52569
P97852	VLHGEQYLELYKPLPR	1.005300904	2	4.91713
P97852	VNAVFEWHITK	1.106342051	2	3.19355
P97852	VVLVTGAGGGLGR	0.981221499	2	4.55496
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.437355798**	**7.33E-13**	**3**
Q00438	KLPSDVTEGEVISLGLPFGK	0.965589642	2	2.6573
Q00438	NFQNIFPPSATLHLSNIPPSVSEDDLK	1.503894146	3	3.81612
Q00438	NNQFQALLQYADPVSAQHAK	1.446792467	2	5.14271
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.124020388**	**0.823789**	**4**
Q00PI9	AVEEQGDDQDSEK	1.124152951	2	3.80095
Q00PI9	DLLVQQASQCLSK	1.370865497	2	2.37083
Q00PI9	EEAQPIVTKYK	1.101789655	1	1.94921
Q00PI9	SGDETPGSEAPGDK	0.912839876	2	2.68727
Q01177	**PLMN Plasminogen**	**1.239758984**	**0.056086**	**3**
Q01177	ILGSDVQQIAVTK	1.246919757	2	3.40008
Q01177	LVLEPNDADIALLK	1.370122322	2	2.64997
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	1.102711478	3	4.9773
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.068936361**	**0.640327**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.122598985	2	6.39429
Q01205	NDVITVQTPAFAESVTEGDVR	1.035407122	2	5.4971
Q01205	NVETMNYADIER	1.425411147	2	3.51927
Q01205	VEGGTPLFTLR	1.022076132	2	3.30794
Q01405	**SC23A Protein transport protein Sec23A**	**1.274380708**	**4.85E-08**	**4**
Q01405	AETEEGPDVLR	1.142286933	2	3.17017
Q01405	AVLNPLCQVDYR	1.261131587	2	2.80127
Q01405	HLLQAPVDDAQEILHSR	1.188129975	3	4.53486
Q01405	YIDTEHGGSQAR	1.291803682	2	3.42438
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.917821521**	**0.998338**	**29**
Q02253	AEMEAAVAACK	0.899892116	2	3.90512
Q02253	AEMEAAVAACK+Oxidation(3)	1.306769006	2	2.86343
Q02253	AEMEAAVAACKR	0.976929006	2	3.21696
Q02253	AFPAWADTSILSR	1.099390114	2	4.20238
Q02253	AISFVGSNQAGEYIFER	1.065919793	2	5.48477
Q02253	CMALSTAVLVGEAK	0.928303847	2	4.5636
Q02253	CMALSTAVLVGEAK+Oxidation(2)	1.003751517	2	2.77389
Q02253	EEDATLSSPAVVMPTMGR	0.823612229	2	4.90848
Q02253	ENTLNQLVGAAFGAAGQR	0.924334191	2	5.01796
Q02253	GDTNFYGK	1.027717638	2	2.39529
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.14239377	2	5.90708
Q02253	GYENGNFVGPTIISNVKPSMTCYK	0.913631412	2	3.42933
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.051046553	2	5.57311
Q02253	KWLPELVER	0.968931328	2	2.32475
Q02253	LITLEQGK	1.041204264	2	2.89832
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.859133865	3	4.82179
Q02253	NHGVVMPDANK	0.841412378	1	3.28066
Q02253	NHGVVMPDANK+Oxidation(6)	1.008137022	2	3.11345
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	0.916663192	3	6.38117

Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(6)	0.934651913	3	4.81733
Q02253	QGIQFYTQLK	1.185223085	2	2.85421
Q02253	SDKWIDIHNPATNEVVGR	0.985375594	2	5.59219
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.829527221	2	5.41685
Q02253	TLADAEGDVFR	0.969726247	2	3.57084
Q02253	VCNLIDSGAK	0.944986271	2	3.47107
Q02253	VNAGDQPGADLGPLITPQAK	0.870734917	2	5.99965
Q02253	WIDIHNPATNEVVGR	0.974486194	2	5.1088
Q02253	WLPELVER	0.814182187	2	2.31465
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	0.94284401	3	4.63799
Q02769	**FDFT Squalene synthase**	**0.82427831**	**0.885526**	**3**
Q02769	KLEDFVKPENVDVAVK	0.777162463	3	4.24853
Q02769	TQSLPNCQLISR	0.576777814	2	2.59707
Q02769	VVLEDFPTISLEFR	1.099770839	2	3.91082
Q02974	**KHK Ketohexokinase**	**1.222238724**	**0.99842**	**9**
Q02974	FGCQVAGK	1.118551257	2	2.87889
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.228597699	3	5.86309
Q02974	GGNASNSCTVLSLLGAR	1.05010419	2	4.6608
Q02974	GNSMQEALR	1.056653598	2	3.18398
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.165457092	3	5.30718
Q02974	IEQYNATQPLQQK	1.235998558	2	4.77127
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.209361523	3	6.36503
Q02974	TIILYDTNLPDVSAK	1.085993515	2	4.82295
Q02974	VSVEIEKPR	1.164280738	2	2.41058
Q03248	**BUP1 Beta_ureidopropionase**	**1.040013534**	**9.9E-20**	**13**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.242826802	2	6.29926
Q03248	EKLPWTEFAESAEDGLTTR	1.104459768	3	5.0119
Q03248	ELAEAVKPNYSPNIVK	1.172925231	2	4.32856
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	1.020401854	3	3.43546
Q03248	HLPPDDLSQVK	1.084087606	2	2.3069
Q03248	HNMVVISPILER	1.129128236	3	3.43704
Q03248	IPLPTSAPVAEQVSALHK	1.484631768	3	5.06646
Q03248	KHNMVVISPILER	0.972175668	3	3.52502
Q03248	KHNMVVISPILER+Oxidation(4)	1.034496247	2	2.78252
Q03248	NAAIANHCFTCALNR	1.260299986	2	4.71798
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.615499205	3	4.80641
Q03248	VGQEHYPNEFTSGDGK	1.038158587	2	4.40506
Q03248	VGQEHYPNEFTSGDGKK	1.157505493	3	5.19038
Q03336	**RGN Regucalcin**	**1.142269931**	**9.9E-20**	**19**
Q03336	CGESPVWEEASK	1.261213827	2	4.56697
Q03336	CLLFVDIPSK	1.753792218	2	3.26826
Q03336	DEQIPDGMCIDVEGK	1.050977382	2	4.63492
Q03336	DYSEMYVTCAR	0.958673561	2	2.50193
Q03336	FCALNWEDQSVFILAMVDEDKK	3.172601391	3	4.19366
Q03336	FNDGKVDPAGR	1.026870124	2	2.71623
Q03336	GIAPYSYAG	2.583440778	2	2.53849
Q03336	HQGSLYSLFPDHSVK	1.162601126	2	4.5976
Q03336	IECVLR	1.078603424	2	2.41857
Q03336	KYFDQVDISNGLDWSLDHK	1.022286566	3	5.20567
Q03336	LWVACYNGGR	1.207721909	2	3.1025
Q03336	MEKDEQIPDGMCIDVEGK	1.298671562	2	5.29706
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(1)	1.363390866	2	4.62258
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(11)	1.36194456	2	2.71571
Q03336	QSGGYVATIGTK	1.067706843	2	2.77604
Q03336	VGVDAPVSSVALR	1.224693814	2	3.71552
Q03336	YFAGTMAEETAPAVLER	1.108122448	2	5.82589

Q03336	YFAGTMAEETAPAVLER+Oxidation(6)	1.143651675	2	5.42033
Q03336	YFDQVDISNGLDWSLDHK	1.050902002	2	4.52851
Q03410	**SYCP1 Synaptonemal complex protein 1**	**0.947214224**	**0.601665**	**4**
Q03410	ATVDEAVKLQKEIDLR	1.688146377	2	2.36649
Q03410	ISEEKLLGEVEK	0.9119632	2	2.30882
Q03410	LQDENLK	0.946805521	1	1.98866
Q03410	NIEELHQENKALK	1.058122015	1	1.90885
Q03626	**MUG1 Murinoglobulin_1**	**1.060301636**	**0.00537**	**7**
Q03626	EESSCIHSSCTAER	0.959648316	2	4.14567
Q03626	ESVVFVQTDKPVYKPGQSVK	1.210172819	3	3.46967
Q03626	GGEFEMMPLGVNK	0.798316317	2	3.15
Q03626	LTAQPAPSPEDLALSMGTIK	1.17533976	3	3.9513
Q03626	NLHPLNELFPLAYIEDPK	1.815815009	3	4.11475
Q03626	VQTVPLTCNNPK	1.048498822	2	2.77076
Q03626	VYHKEESSCIHSSCTAER	0.963923395	2	5.46548
Q04462	**SYVC Valyl_tRNA synthetase**	**1.037163732**	**0.333948**	**3**
Q04462	ADFPAGIPECGTDALR	0.927729334	2	2.40421
Q04462	ALNPLEEWLR	1.268512372	2	2.30183
Q04462	SVTQQPGSEITAPQK	1.040648516	2	3.8939
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**1.125193134**	**0.388616**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(1)	1.210174266	2	2.60815
Q05144	YLECSALTQR	1.10128853	2	3.0004
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.03855345**	**0.97864**	**8**
Q06647	FSPLTANLMNLLAENGR	1.29801048	2	3.96458
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.003120102	2	5.33163
Q06647	GQILNLEVK	1.109987483	2	2.66492
Q06647	LGNTQGVISAFSTIMSVHR	0.973459453	3	4.71923
Q06647	TDPSIMGGMIVR	0.979133484	2	3.26981
Q06647	TVLNSFLSK	1.067771879	2	2.75498
Q06647	VSLAVLNPYIK	1.037233233	2	3.67134
Q06647	YATALYSAASK	3.202639317	1	2.12035
Q07071	**GCKR Glucokinase regulatory protein**	**1.360419356**	**9.9E-20**	**12**
Q07071	AAPISCHVQVAHEK	1.344535366	2	4.80357
Q07071	CQNIQALVHSTVGQSLPAPLKK	1.642399093	3	4.85911
Q07071	GFLIGDHSDMFNQK	1.418831564	2	2.56757
Q07071	GLGQKPLYTYLIAGGDR	1.986030767	2	2.60859
Q07071	LLGQCDAEIFQEEGQIVPTYQR	2.462624061	2	4.95636
Q07071	LYSESVLTTMLQVAGK	1.484213214	2	3.29731
Q07071	QEAFVLNPAIGPEGLSGSSR	1.145395565	2	4.24942
Q07071	TVDQGVVSSQR	1.42680731	2	3.65498
Q07071	VIPTALLSLLLR	1.440262733	2	3.40905
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.382732044	2	5.23642
Q07071	WVLNTVSTGAHVLLGK	1.497048131	2	3.43793
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.723214738	3	4.0109
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.949793569**	**0.823725**	**8**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.863302709	2	5.17386
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	1.027874792	3	4.50545
Q07116	HEVTVTLQCAGNR	1.034758226	2	3.09599
Q07116	INSQRPFNAEPPPELLTESYITPNPIFFTR	1.502264643	3	4.47717
Q07116	MSPPLEASDPYSNDPMR	0.646160001	2	3.93834
Q07116	NHLPVPNLDPDTYR	0.983688073	2	2.79804
Q07116	VSVESEESYSHWQR	0.955455852	2	4.03651
Q07116	VVVPGVVGAR	0.878519074	2	2.74687
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.085347071**	**0.625744**	**2**
Q07205	AMGPLVLTEVLFDEK	1.113823814	2	3.54943
Q07205	TVIVNMVDVAK	1.064403564	2	2.35066
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**1.070865594**	**0.086142**	**14**

Q07523	ALKEEKPTQSVPVSFPK	0.986666525	2	4.62328
Q07523	ALVITIDTPVLGNR	1.001347779	2	4.00972
Q07523	ASFCWNDLSLLQSITR	1.498814083	2	4.5891
Q07523	CMTLSGCQSVAEISPDLIQFSR	1.134144102	2	3.54834
Q07523	EDAELAMK	1.022748673	1	1.94181
Q07523	EEKPTQSVPVSFPK	0.891248387	2	2.94464
Q07523	EVLDILTAELHR	1.157331237	2	3.17391
Q07523	GEDGVKEVLDILTAELHR	1.105865598	3	5.54539
Q07523	HNVQGIVVSNHGGR	0.97574736	3	6.22272
Q07523	NQLNLEANILLK	0.93019877	2	3.61938
Q07523	QLDEVSASIDALR	0.983921345	2	3.11902
Q07523	TGTDVLK	0.911926349	2	2.31739
Q07523	TSWDFIEGEADDGITYSENIAAFK	0.984352194	2	4.45108
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	1.684397747	3	3.771
Q07936	**ANXA2 Annexin A2**	**1.341397539**	**0.726133**	**4**
Q07936	AEDGSVIDYELIDQDAR	1.274199391	2	3.90109
Q07936	GLGTDEDSLIEIICSR	1.511412179	2	3.97558
Q07936	GVDEVTIVNILTNR	1.341686268	2	3.82579
Q07936	TNQELQEINR	1.255290012	2	3.10784
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.228748652**	**1.66E-09**	**2**
Q07984	FFDEESYSLLR	1.400769471	2	3.12843
Q07984	NNEDVSIIPPLFTVSVDHR	1.213374216	2	4.27674
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**0.995785524**	**0.410485**	**9**
Q08163	ALLVTASQCQQPAGNK	0.946171984	2	4.22459
Q08163	AYLSIWTELQAYIK	0.589671131	2	2.30138
Q08163	ELSGLPSGPSVGSGPPPPPPGPPPPPVPTSSGSDDSASR	1.141260654	3	4.70657
Q08163	LEAVSHTSDMHCGYGDSPSK	0.966839366	3	5.01526
Q08163	LSDLLAPISEQIQEVITFR	1.111498949	2	4.00408
Q08163	NSLDCEIVSAK	1.099894931	2	2.3519
Q08163	SALFAQINQGESITHALK	1.128997417	2	4.56494
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.142407332	2	4.07185
Q08163	VENQENVSNLVIDDTELK	1.226754092	2	5.12975
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.109979322**	**0.026563**	**3**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	0.918978818	3	4.84861
Q08415	ILVLNTPNNPLGK	1.673656358	2	3.38612
Q08415	LGASNDWQLDPAELASK	1.2393656	2	3.98091
Q09073	**ADT2 ADP/ATP translocase 2**	**1.102840099**	**0.000835**	**7**
Q09073	DFLAGGVAAAISK	0.929050349	2	5.01008
Q09073	GLGDCLVK	1.133653925	2	2.87509
Q09073	GMGGAFVLVLYDEIKK	1.180613782	2	3.6151
Q09073	GTDIMYTGTLDCWR	0.986008037	2	3.55933
Q09073	KGTDIMYTGTLDCWR	0.896410899	2	4.03166
Q09073	LLLQVQHASK	1.683789208	2	2.74101
Q09073	QIFLGGVDKR	1.284235604	2	2.37893
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.862549125**	**0.438372**	**9**
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.347152771	3	3.39527
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	0.809066864	2	3.89368
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	0.859766671	3	3.47475
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	0.888642651	3	4.77152
Q0D2L3	SVDEGLLDSK	0.794876536	1	1.92674
Q0D2L3	SVDEGLLDSKR	0.87891953	2	3.07954
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.179182674	2	5.17821
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	1.150567123	3	5.75946
Q0D2L3	VVLAEDCWMK	1.316266499	2	2.4059
Q0VAV2	**EXPH5 Exophilin_5**	**1.188523724**	**0.137239**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(2)	1.143699605	2	2.52883

Q0VAV2	SLSDQDPGQEQREEK	1.207732509	2	2.30453
Q0VGK3	**GLCTK Glycerate kinase**	**1.035388253**	**0.980714**	**6**
Q0VGK3	ADSDPHGPHTCGHVLNVIIGSNSLALAEAQR	0.964896144	3	4.82085
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	0.87967809	2	4.84972
Q0VGK3	GATIQELNTIR	1.096213499	2	2.86822
Q0VGK3	LHQLAAELQLPDLQLEEALEAVAK	1.272324586	3	3.61009
Q0VGK3	QLFDSAVGAVQPGPMLQR	1.102860749	2	4.8058
Q0VGK3	VAAACLTSSTAERPLEEEAK	1.141584471	2	3.20186
Q0ZHH6	**ATLA3 Atlastin_3**	**1.107823414**	**0.001715**	**8**
Q0ZHH6	ALASVLLQDHIR	1.255442956	2	2.65546
Q0ZHH6	EHQHEEIQNVR	1.069699755	2	3.60591
Q0ZHH6	EQLQTLIPYVLNPSK	1.229959766	2	3.26649
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	1.279894575	2	2.3586
Q0ZHH6	IYQGEDLPHPK	1.01154482	2	2.78858
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(3)	1.187411191	2	2.48999
Q0ZHH6	YQQELEEEITELYENFCK	1.711352417	2	5.3272
Q0ZHH6	YSGQYLELGGAIDSGAAYVLEQASSHIGNSTQAAVR	1.361278266	3	3.36516
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**1.089675134**	**0.963437**	**2**
Q10728	QEEKKESEVSR	1.134036498	2	2.33906
Q10728	SLLEMEKRER+Oxidation(5)	1.05130407	2	2.40044
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.927993704**	**1.03E-12**	**25**
Q10758	AEAETMYQIK	0.864517843	2	3.1227
Q10758	AQYEEIANR	0.877075669	2	3.16601
Q10758	ATLEAAIADAEQR	0.871592726	2	4.70691
Q10758	DVDEAYMNKVELESR	2.093787396	2	3.56387
Q10758	ELQSQISDTSVVLSMDNSR	0.983803497	2	5.96616
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	0.766360867	2	4.74809
Q10758	KDVDEAYMNK	0.850583854	2	2.57674
Q10758	LEGLTDEINFLR	0.960331625	2	4.0512
Q10758	LESGMQNMSIHTK	0.960729976	2	4.18187
Q10758	LEVDPNIQAVR	0.878114371	2	3.83027
Q10758	LEVELGNMQGLVEDFK	1.064935082	2	4.96885
Q10758	LQAEIDALK	1.007317805	2	2.97531
Q10758	LVSESSDIMSK	0.927044969	2	3.33232
Q10758	QIHEEEIR	0.827501016	1	2.31627
Q10758	QLEALGQEK	0.824027995	1	2.1502
Q10758	SKTEISEMNR	0.795662335	2	3.08398
Q10758	SKTEISEMNR+Oxidation(8)	1.077565876	2	3.09394
Q10758	SLDMDSIIAEVR	0.851369195	2	4.93946
Q10758	SNMDNMFESYINNLR	1.527726696	2	4.05594
Q10758	SRAEAETMYQIK	0.681752683	2	3.44173
Q10758	TEISEMNR	0.792804471	2	2.44474
Q10758	TEMENEFVLIK	0.955641039	2	3.65187
Q10758	TEMENEFVLIK+Oxidation(3)	1.018117476	2	2.40871
Q10758	WSLLQQQK	0.892020132	2	2.93414
Q10758	YEELQTLAGK	0.900993599	2	3.56226
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.905792012**	**0.295588**	**6**
Q14DH7	CVPGYNVMILDDNMQK	1.5566812	2	2.63263
Q14DH7	STLSALVNGKPYK	1.04221587	2	2.45021
Q14DH7	THFAASVADPER	1.097296186	2	3.67423
Q14DH7	VDDVINVAGHR	0.855808207	2	3.74527
Q14DH7	VLAEHGVAALFTAPTAIR	0.958809097	2	4.45122
Q14DH7	VTPTIEDPSIFGHIEEVLK	0.987926021	2	2.9121
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.928886565**	**2.29E-07**	**10**
Q1HCL7	ASYYEISVDDGPWEK	0.776157459	2	2.52739

Q1HCL7	LKPVIGVNTDPER	1.229573241	2	2.88496
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	0.78656244	3	4.71002
Q1HCL7	NVEHIIDSLRDEGIEVR	0.911886489	2	3.45552
Q1HCL7	QGNLTLPLNK	0.866622627	2	2.33824
Q1HCL7	REYDEETVR	0.898270062	2	2.44806
Q1HCL7	SEASGPQLLPVR	0.869714162	2	2.9511
Q1HCL7	SSGLNLCTGTGSK	0.812872462	2	3.8542
Q1HCL7	VTNEYNESLLYSPEEPK	0.956535663	2	4.46385
Q1HCL7	YTHSFPEALQK	1.094997253	2	2.59832
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.122761746**	**0.424962**	**3**
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	1.093859888	3	3.44214
Q1JU68	LLDMDGIIVEK	1.114972371	2	2.55574
Q1JU68	NQLTAMSSVLAK	1.153211806	2	2.65007
Q29RW1	**MYH4 Myosin_4**	**0.856152063**	**0.974105**	**14**
Q29RW1	ANLMQAEIEELR	1.05597971	2	3.01068
Q29RW1	ELENEVENEQKR	1.065463119	2	2.98762
Q29RW1	LAQESTMDIENDKQQLDEK	40.63178742	2	4.94088
Q29RW1	LQDAEEHVEAVNSK	1.19989154	2	4.56202
Q29RW1	LQDLVDKLQTK	1.051810331	1	1.93891
Q29RW1	MEGDLNEMEIQLNHANR	2.582484512	2	4.34168
Q29RW1	NAYEESLDQLETLK	0.843532304	2	4.57888
Q29RW1	NAYEESLDQLETLKR	0.771986703	2	4.05422
Q29RW1	SELQASLEEAEASLEHEEGK	0.712085006	2	5.28726
Q29RW1	SNAACAALDKK	0.799706941	2	2.45146
Q29RW1	TEGGATVTVK	0.878440995	2	2.69189
Q29RW1	TKLEQQVDDLEGSLEQEK	10.04324226	2	5.65531
Q29RW1	TKLEQQVDDLEGSLEQEKK	13.06683639	3	5.10829
Q29RW1	VRELENEVENEQKR	0.715722818	3	3.70753
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**1.027189051**	**0.443188**	**3**
Q2EMV9	LIISEVLK	1.248128873	2	2.5172
Q2EMV9	LQEELTR	1.026942367	1	2.11767
Q2EMV9	VLVEFEKESLNIAGK	1.302738956	2	2.58699
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.235409754**	**3.56E-07**	**8**
Q2V057	ASIYGQFVAGETAEEVR	1.211666704	2	4.22115
Q2V057	EDCTQPDYEATSR	1.164322114	2	3.54251
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.430313142	2	4.8077
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.326354163	2	5.75996
Q2V057	REQALLSQELWR	1.215482702	2	3.09522
Q2V057	SIPYGCLEEVIPYLIR	1.678044521	2	4.11554
Q2V057	SVTQLHGKEDCTQPDYEATSR	0.890410736	3	4.61041
Q2V057	TSEAWYEGNLSAMLHCVDLSR	1.209931082	2	2.62975
Q32LZ8	**PLPL5 Patatin_like phospholipase domain_containing protein 5**	**0.965747187**	**0.64608**	**2**
Q32LZ8	FYGSSSGALNAMAIVFGK	1.032910077	2	2.41137
Q32LZ8	NFIVTDFATR	0.849985397	1	1.90153
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.052397907**	**0.996988**	**2**
Q3B7D0	HCDDSYTPQDK	1.069057756	2	3.40693
Q3B7D0	TCAEAVVPSYVPIVK	1.036018145	2	2.68496
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.053701606**	**0.999987**	**4**
Q3B7U9	SCSQVLEHQPDNIK	0.930437634	2	4.17635
Q3B7U9	TAEDGPDLEMLSGQER	0.951742137	2	4.12316
Q3B7U9	VDMTCEEEEELLQLK	1.097810024	2	4.14
Q3B7U9	VLAQQGEYSEAIPILR	1.079315258	2	3.77666
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**1.113660006**	**0.661553**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	1.180822897	2	4.66736

Q3B8Q2	GIYAYGFEKPSAIQQRAIK	1.116959684	2	2.40852
Q3KR86	**IMMT Mitochondrial inner membrane protein (Fragment)**	**1.155280719**	**0.900507**	**9**
Q3KR86	AVDEAADALLK	1.29650876	2	2.54265
Q3KR86	EIAGATPYITAAEEK	0.907110211	2	3.04443
Q3KR86	GIEQAVQSHAVAEEEAR	1.105373323	2	4.86501
Q3KR86	QTITAQNAAVQAVK	1.167412423	2	4.23704
Q3KR86	SEIQAEQDR	1.109798785	2	2.79942
Q3KR86	SLEDALNQTATVTR	1.132834516	2	3.98457
Q3KR86	TSSAEMPTIPLGSAVEAIR	1.086359423	2	3.84538
Q3KR86	VVSQYHELVVQAR	1.226032522	2	3.56387
Q3KR86	YSTSSSSGVTAGK	0.845910749	2	2.775
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.300672301**	**0.08275**	**2**
Q3KRD8	HGLLVPNNTTDQELQHIR	1.141590653	3	5.10276
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.208616595	3	4.40258
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.766331068**	**0.404409**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.236473215	2	2.66433
Q3KRE0	ISVLEALR	1.79071844	2	2.62628
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**1.22243734**	**0.457166**	**3**
Q3KRE8	ALTVPELTQQMFDSK	1.289151045	2	2.75209
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.877260235	3	4.38386
Q3KRE8	FWEVISDEHGIDPTGSYHGDSDLQLER	1.208145546	3	3.37131
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**0.950376612**	**0.857371**	**3**
Q3MIB4	GTSLQSTILGVIPNTPDPASDSQDLPPLHR	1.094395161	3	3.59311
Q3MIB4	MEIIQVPGYTQEEK	0.98483631	2	2.49918
Q3MIB4	TVGVNNPVFLLDEVDK	0.839698242	2	2.61687
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**0.828582492**	**0.047497**	**7**
Q3MIE0	DGQEGIEAFIQK	0.652877486	2	3.41772
Q3MIE0	SDILHEAESEDLK	0.881062567	2	3.46327
Q3MIE0	SDILHEAESEDLKVIIISAEGPVFSSGHDLK	0.822475591	4	5.7589
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.043540704	2	4.17181
Q3MIE0	VALEMLFTGEPISAQEALR	1.396524262	2	4.06232
Q3MIE0	VIIISAEGPVFSSGHDLK	0.950309409	2	4.33473
Q3MIE0	VVPEEQLEEEATR	0.870537258	2	3.7635
Q3MIF4	**XYLB Xylulose kinase**	**1.268591769**	**0.173359**	**6**
Q3MIF4	FNADNMEVSAFPGDVEIR	1.127472791	2	4.33761
Q3MIF4	IRDESASCSWNK	1.15488004	2	4.0871
Q3MIF4	LGSPVPSCSVVGAISSYYVQR	1.466676773	2	3.25717
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	1.883982251	2	4.22762
Q3MIF4	VVAFTGDNPASLAGMR	1.375902208	2	3.91311
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	1.322313465	2	5.15854
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.16378253**	**1.07E-06**	**4**
Q3T1J1	EDLRLPEGDLGK	1.143741731	2	2.82148
Q3T1J1	EDLRLPEGDLGKEIEQK	1.19814935	2	4.51725
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.334078888	2	5.08492
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.454168056	3	3.63431
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.170477455**	**2.74E-06**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.214601806	3	3.98936
Q3T1K5	FTVTPSTTQVVGILK	1.222113341	2	3.82737
Q3T1K5	LLLNNDNLLR	1.092354147	2	2.63586
Q3TVW5	**TCHP Trichoplein keratin filament_binding protein**	**1.427516945**	**0.00047**	**2**
Q3TVW5	RTQEIQEELEVDGRILQALLEK	1.790037613	2	2.68399
Q3TVW5	TELGRFLKHQYNAQLNR	1.420795486	2	2.91406
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**1.185020898**	**0.318496**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	0.851313115	2	2.44428

Q3U0J8	QIELDLLRTLPNNK	1.250348167	2	2.75838
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.055232354**	**0.10196**	**2**
Q3UHR0	ACEERLGLPGRELLLQDNK	1.650320609	2	2.40867
Q3UHR0	IESLWESWGSNMVVKVK	0.988959153	2	2.35468
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.137356415**	**0.000271**	**3**
Q3ULJ0	GIDEGPDGLK	1.132504159	2	2.50615
Q3ULJ0	LGLMEMIAFAK	1.999230175	2	3.94737
Q3ULJ0	LTDIINNDHENVKYLPGHK	0.707932502	2	2.45564
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.448481837**	**1.06E-06**	**16**
Q3UQ44	ALVGSENPPLTVIR	1.170837281	2	3.89533
Q3UQ44	AWVNQLETQTGEASK	1.083604317	2	4.79106
Q3UQ44	GVLLGIDDLQTNQFK	1.095721857	2	4.58939
Q3UQ44	HTDNTVQWLR	1.133627713	2	3.33221
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	2.099468381	3	4.69412
Q3UQ44	LGIAPQIQDLLGK	1.843958462	2	2.94543
Q3UQ44	LPYDVTTEQALTYPEVK	1.448541011	2	4.57003
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.204478122	2	2.41397
Q3UQ44	LSAEEMDER	1.01661403	2	2.90148
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.1332485	2	5.31218
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.351537237	2	5.10662
Q3UQ44	TLDTLLLPTANIR	1.224029038	2	2.59649
Q3UQ44	TLEQTGHVSSK	0.91973545	2	3.10001
Q3UQ44	VDFTEEEISNMR	1.126808442	2	2.92122
Q3UQ44	VDQVQDIVTGNPTVIK	0.980742204	2	5.24741
Q3UQ44	YQDILNEIAK	1.014049026	2	2.43158
Q3UVR3	**TTBK2 Tau_tubulin kinase 2**	**0.926612437**	**0.875996**	**2**
Q3UVR3	NLADLR	0.913755364	1	1.90261
Q3UVR3	YKVLGSSNSDSDLFSR	1.096638106	2	2.52645
Q3V0K9	**PLSI Plastin_1**	**1.0845842**	**0.991998**	**3**
Q3V0K9	AYFHLLNQIAPK	1.154038707	2	2.84785
Q3V0K9	KIENCNYAVELGK	1.093554592	2	3.67427
Q3V0K9	QFVTPADVVSGNPK	1.023842777	2	3.32523
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.055589816**	**0.994613**	**2**
Q3V132	GNLANVIR	1.052505563	2	2.66675
Q3V132	YFPTQALNFAFK	1.22307579	2	3.39648
Q497B0	**NIT2 Omega_amidase NIT2**	**1.143463654**	**7E-07**	**17**
Q497B0	ADLYSVESK	1.299756715	2	2.91508
Q497B0	AGTEETILYSDIDLK	2.230201493	2	3.96397
Q497B0	AGTEETILYSDIDLKK	1.386312633	2	3.5246
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.937052568	3	5.48963
Q497B0	AVDNQVYVATASPAR	1.441734529	2	4.8728
Q497B0	AVDNQVYVATASPARDEK	1.222533593	2	3.64772
Q497B0	ENSIYLIGGSIPEEDDGK	0.848379136	2	3.63883
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.36029747	3	5.17079
Q497B0	FAELAQIYAR	1.182636669	2	3.51833
Q497B0	GCQLLVYPGAFNMTTGPAHWELLQR	1.256206274	3	3.53585
Q497B0	IHLFDIDVPGK	0.896942137	2	2.79053
Q497B0	KIHLFDIDVPGK	1.193351682	3	4.54998
Q497B0	LALIQLQVSSIK	1.546472976	2	3.06848
Q497B0	LYNTCAVFGPDGNLLVK	1.066269881	2	3.97244
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.125033025	3	5.2818
Q497B0	TLSPGDSFSTFDTPYCR	1.143268072	2	4.52127
Q497B0	VGLGICYDMR	1.134818167	2	2.55746
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**0.955334298**	**0.804846**	**5**

Q498D5	ALNTHIEDLKLDVLLQK	0.805060311	3	3.44088
Q498D5	AYGDMYDLSTNTQEK	0.834938363	2	3.50828
Q498D5	FCNLALLLPIVTK	0.976913138	2	2.72642
Q498D5	GQLQILEK	1.016368094	1	1.9462
Q498D5	LNELLTNVEELKEEIK	1.150722338	2	3.09807
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.367246049**	**0.000144**	**8**
Q499N5	GATLSHHNIVNNSNLIGQR	1.269313892	2	4.61136
Q499N5	GGENIYPAELEDFFHK	1.385648532	2	3.32275
Q499N5	GGVIAGSLAPPELIR	1.323929469	2	2.89038
Q499N5	GYCVMQGYWGEPQK	0.973213089	2	2.88785
Q499N5	TFETVGQDR	1.264665361	2	2.65098
Q499N5	TGDIASMDEQGFCR	1.235946389	2	3.74616
Q499N5	TVGECLDATAQR	1.330382345	2	2.99422
Q499N5	YIVFVEGYPLTVSGK	1.494819442	2	4.52271
Q4AEF8	**COPG Coatomer subunit gamma**	**1.330954991**	**0.053547**	**5**
Q4AEF8	ALQQYTLEPSEKPFDLK	0.956999924	2	3.34661
Q4AEF8	FGAQNEEMLPSILVLLK	1.349722224	2	3.96884
Q4AEF8	SSPEPVALTESETEYVIR	1.06055918	2	4.71236
Q4AEF8	TLEEAVGNIVK	1.15553002	2	2.34603
Q4AEF8	VVLEHEEVR	1.434926594	2	2.30605
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.153223513**	**0.753627**	**5**
Q4FZT0	AEQINQAAGEASAVLAK	1.109258866	2	4.79054
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.226234642	2	4.83772
Q4FZT0	ATVLESEGTR	1.15055898	2	2.65689
Q4FZT0	ILEPGLNVLIPVLDR	1.099631448	2	2.8801
Q4FZT0	SELGKLSLDKVFR	0.474547727	1	2.06635
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.134492566**	**0.085329**	**5**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.95829993	3	4.4829
Q4FZT9	FGGSGSQVDSAR	1.210084261	2	3.62925
Q4FZT9	SETELKDTYAR	0.897727256	2	2.71079
Q4FZT9	SSTTSMTSVPKPLK	0.980827951	2	2.9059
Q4FZT9	TPVQSQQPSATAPSGADEK	1.156694202	2	4.44435
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.482448199**	**7.97E-06**	**4**
Q4FZX7	GDAGSADVQDLEK	1.107509099	2	3.49764
Q4FZX7	GNSLTLIDLPGHESLR	1.356111851	2	2.96285
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.512587766	2	4.96008
Q4FZX7	VGDGAGGAFQPYLDSLR	1.451229309	2	2.40724
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.090051397**	**0.887008**	**3**
Q4G061	AEEEGGSDGSAAEAEPR	1.078365158	2	4.54329
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	1.59406999	3	4.58991
Q4G061	GTQGVVTNFEIFR	1.052001047	2	2.33003
Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**1.038801764**	**0.08774**	**2**
Q4KLF8	ALAAGGVGSIVR	1.256083946	2	2.31701
Q4KLF8	QGNMTAALQAALK	1.015982515	2	2.51974
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**0.986670282**	**0.043755**	**16**
Q4KLP0	ARPSVDHGLAR	0.946651421	2	2.52058
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.341335646	3	3.67462
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.099319382	3	4.30595
Q4KLP0	LEELCPFPLDSLQQEMGK	1.214841506	2	5.12253
Q4KLP0	LLLESQEFDHFLATK	1.281548632	2	3.83539
Q4KLP0	LSAYGGITDIIIGMPHR	1.444231268	3	3.53302

Q4KLP0	LVTVYCEHGHK	1.118316861	2	2.83118
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	1.487911668	2	3.01662
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.259198386	3	3.5156
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.131753224	3	4.9984
Q4KLP0	SSLYSSDIGK	1.111056013	1	2.09598
Q4KLP0	SVEVPEELQLHSHLLK	1.081627937	2	2.70326
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.060307087	3	3.83142
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.038754819	2	4.99135
Q4KLP0	YGGEGAESMMGFFHELLK	0.952436933	3	4.24372
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.155581861	3	4.33769
Q4KLZ6	**DHAK Bifunctional ATP_dependent dihydroxyacetone kinase/FAD_AMP lyase (cyclizing)**	**1.047376455**	**1.44E-05**	**13**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.157437401	2	4.60541
Q4KLZ6	AILEVLQTK	1.467350606	2	2.87646
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.30510744	2	3.26028
Q4KLZ6	AVAQAGTAGTLLIVK	1.498470729	2	4.42436
Q4KLZ6	EGPTPASPAQVLSK	1.32003216	2	3.30315
Q4KLZ6	ISTTLIGLEEHLNALDR	2.550057917	2	4.15475
Q4KLZ6	LIDAETNAK	1.285826016	2	3.05643
Q4KLZ6	LSVLLLEK	1.8680245	2	2.68335
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	0.846482295	2	4.59637
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.296672574	3	5.09696
Q4KLZ6	RGLCGTILIHK	1.249949621	3	3.40777
Q4KLZ6	TMLDSLWAAAQELQAWK	1.049692175	2	4.30566
Q4KLZ6	VAGALAEEGMGLEEITK	1.180462135	2	3.65722
Q4KM35	**PSB10 Proteasome subunit beta type_10**	**1.355321956**	**0.012185**	**2**
Q4KM35	ALSSPIEPVQR	1.269814084	2	2.37313
Q4KM35	FAPGTTPVQTQEVR	1.357678332	2	2.84358
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.178221559**	**0.15452**	**3**
Q4KM49	QVEPLDPPAGSAPGER	1.220474669	2	2.57824
Q4KM49	TVVSGLVQFVPK	1.143937673	2	3.2938
Q4KM49	VDAQFGGIDQR	1.177841596	2	3.3616
Q4KM62	**PALMD Palmdelphin**	**1.013523484**	**0.162922**	**2**
Q4KM62	TGESVVLSSIPLPSDDFK	1.005677759	2	3.40199
Q4KM62	VEKEEIPEESIEDIYANIPDLPSSYIPSR	1.282093072	3	3.42693
Q4KM73	**KCY UMP_CMP kinase**	**1.090058162**	**0.043077**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.377573001	2	4.92602
Q4KM73	IVPVEITISLLK	1.025044822	2	3.04166
Q4KM73	KNPDSQYGELIEK	1.100570925	2	4.29381
Q4KM73	NQDNLQGWNK	1.08722252	2	2.94024
Q4KM73	SVDEVFGDVMK	1.082959126	2	3.16602
Q4KM73	YGYTHLSAGELLR	1.323470592	3	3.61471
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.056767813**	**0.877716**	**4**
Q4KM74	DLQQYQSQAK	1.045788605	2	3.39268
Q4KM74	GEALSALDSK	1.08511414	2	2.41655
Q4KM74	IMVANIEEVLQR	1.198622678	2	2.70567
Q4KM74	NLGSINTELQDVQR	1.068699399	2	4.16598
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.062602296**	**0.991619**	**4**
Q4KMA2	ESQAVVDPPPQAVSTGTPQSPAVAAAAATTTATTTTTSGGHPLEFLR	1.039495945	3	3.94658
Q4KMA2	IDIDPEETVK	1.106684257	1	2.63361
Q4KMA2	NFVVVMVTKPK	0.937797438	2	3.4606
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.082906334	2	3.84761
Q4QQV3	**F162A Protein FAM162A**	**0.949056936**	**0.595904**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	1.15058062	2	3.452

Q4QQV3	RHESLTSLNLER	0.948045894	2	2.75914
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**1.134482748**	**0.893199**	**2**
Q4QQW3	HLETAEILGANIR	1.134496288	2	3.27848
Q4QQW3	IQDAGPVLADALR	0.997229246	2	2.48978
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.149560031**	**0.258105**	**5**
Q4QRB4	AILVDLEPGTMDSVR	1.160728086	2	4.56145
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(11)	1.174096056	2	2.63352
Q4QRB4	EIVHIQAGQCGNQIGAK	0.933240136	2	5.10746
Q4QRB4	IMNTFSVVPSPK	1.188284401	2	3.44655
Q4QRB4	ISEQFTAMFR	1.36496831	2	3.35927
Q4V7C7	**ARP3 Actin_related protein 3**	**1.065469519**	**0.458249**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	0.897194188	2	4.82802
Q4V7C7	KDYEEIGPSICR	0.992991031	2	3.90396
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.158180751	2	3.45658
Q4V7C7	LSEELSGGR	1.185985316	2	2.77865
Q4V7C7	NIVLSGGSTMFR	1.113980511	2	2.66494
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1.265779939	2	4.59779
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**1.075075491**	**0.935515**	**5**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	1.097660417	3	3.30935
Q4V8K1	QVFVCGNDSK	1.083831931	2	2.55861
Q4V8K1	TCADEFPLTVDSSEK	1.054341854	2	4.46588
Q4V8K1	TLGLTPLDQGSLVAAK	1.184959229	2	3.37577
Q4V8K1	VLIDVSNNQK	1.020718867	2	2.31477
Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**0.986458664**	**0.928971**	**2**
Q501J6	ELAQQVQQVADDYGK	1.108090565	2	2.67791
Q501J6	VLEEANQAINPK	0.980354788	2	2.71136
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**1.163747658**	**0.619517**	**5**
Q505J8	LQQVQAGQAEK	1.167488459	2	2.95215
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	1.082742986	3	5.14907
Q505J8	SIPLEGLVQSELMQLPSGK	0.894586105	2	2.76619
Q505J8	SLQALGEVIEAELR	0.909282777	2	3.89352
Q505J8	VVDSIEDEVQR	1.101680934	2	2.84474
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**1.13372386**	**0.755551**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	1.070605393	2	4.08022
Q561R9	ILIDTGEPSVPEYISCLK	1.169322008	2	3.52172
Q561R9	NISNDATYCIK	1.132092343	2	2.72478
Q561R9	NNREEQIITVFR	1.032272018	2	2.77938
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.248286468**	**0.011863**	**5**
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	1.835637225	3	3.69861
Q561S0	VITVDGNICSGK	0.963721377	2	3.12895
Q561S0	VVEDIEYLNYNK	1.818210373	2	3.56664
Q561S0	YAPGYNADVGDK	1.21419111	2	2.75046
Q561S0	YGLLASILGDK	0.962959252	2	2.95731
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.667220715**	**0.000866**	**7**
Q562C4	AQFSEVQLEWQPPPFK	0.689393815	2	4.814
Q562C4	FIVAYGENMK	0.666952881	2	2.34813
Q562C4	GTSNEVTLLELGCGTGANFQFYPPGCK	0.823794494	2	4.04489
Q562C4	HIGDGCHLTR	0.655539566	2	2.75764
Q562C4	KVLQEVQR	0.741846851	2	2.52379
Q562C4	VLQEVQR	0.639214219	1	2.01597
Q562C4	VTCVDPNPNFEK	0.662951409	2	3.72058
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.131255395**	**0.871139**	**10**
Q58FK9	AIILNTPHNPIGK	1.104503717	2	3.29665
Q58FK9	DSTLDAAEEIFR	1.11692175	2	2.99879

Q58FK9	IEGLDQNVWVEFTK	1.258077015	2	4.55002
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.349266797	3	5.67257
Q58FK9	LGWSIGPGHLIK	1.481196486	2	2.43539
Q58FK9	MDDPECYFNSLPK	0.971899572	2	4.11775
Q58FK9	RIEGLDQNVWVEFTK	1.062231912	2	3.91777
Q58FK9	RMDDPECYFNSLPK	1.074779536	2	2.35252
Q58FK9	SDEPYDYK	1.124947268	2	2.48159
Q58FK9	WTSSDWTFNPQELESK	1.23300502	2	5.18317
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.181418848**	**0.037284**	**2**
Q5BJQ0	AVLDSSPFLSEANAER	1.144477005	2	4.58798
Q5BJQ0	TLNNDLGPHWR	1.34981723	2	3.01234
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.912583532**	**0.014525**	**23**
Q5BJY9	AQIFANSVDNAR	0.873036089	2	3.81773
Q5BJY9	AQYEQLAQK	0.909587172	2	3.29735
Q5BJY9	IREYLEK	0.933184423	2	2.36522
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	0.805621959	3	4.30185
Q5BJY9	KVVDDTNITR	0.910515676	2	2.94017
Q5BJY9	LEAEIATYR	0.817487516	2	3.23044
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.763933193	2	5.30069
Q5BJY9	LQLETEIEALKEELLFMK	1.682212256	2	4.95708
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.809412994	2	6.53034
Q5BJY9	NQNINLENNLGEVEAR	0.920556231	2	5.60284
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	1.043308637	3	5.70482
Q5BJY9	QSVESDIHGLR	0.895216306	2	3.31574
Q5BJY9	QSVESDIHGLRK	0.979129517	2	2.69091
Q5BJY9	QTQEYEALLNIK	1.031013435	2	3.53506
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.921663452	2	5.72965
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	0.866884368	3	4.8253
Q5BJY9	TLQTLEIDLDSMK	0.948818795	2	4.22611
Q5BJY9	VKLEAEIATYR	0.824709546	2	2.60385
Q5BJY9	VKYETELAMR	0.842582893	2	2.63077
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.030094843	3	5.25934
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.629188806	2	5.60526
Q5BJY9	VVDDTNITR	0.928555154	2	3.35909
Q5BJY9	YWSQQIEESTTVVTTK	1.051962148	2	4.32523
Q5BK17	**IYD1 Iodotyrosine dehalogenase 1**	**1.263723455**	**0.250101**	**2**
Q5BK17	FISSEPVPMEVIDNVIK	1.120754541	2	3.26504
Q5BK17	LLVLLPVGYPSR	1.697855157	2	2.63438
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.159559815**	**1.08E-10**	**5**
Q5BK63	AVQHSNVVINLIGR	1.065014429	2	2.54821
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.515063763	3	5.3588
Q5BK63	LFGLSPFEPWTTK	1.607312191	2	2.58651
Q5BK63	NFDFEDVFVNIPR	1.362915644	2	3.95419
Q5BK63	WLSSEIEETKPAK	1.742699214	2	3.10595
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.99412822**	**0.913733**	**3**
Q5BK81	DVPYPPPLPPAVEAIQK	0.993451835	2	3.24391
Q5BK81	TGNVAEQLR	1.725062985	2	2.33426
Q5BK81	VEEVSLPDTINEGQVR	1.039756886	2	3.80446
Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**0.961770808**	**0.788512**	**2**
Q5BQE6	NIMINLMDILEVDTKK+Oxidation(3)Oxidation(7)	1.228205158	2	2.41347
Q5BQE6	QLGCQDAFPEVYDK	0.9615727	2	3.76183
Q5DU56	**NLRC3 Protein NLRC3**	**1.309358598**	**0.017387**	**2**
Q5DU56	LTGLALGHLYR	1.449122125	2	2.40239
Q5DU56	TLEILDLR	1.096691887	2	2.33441
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.249626333**	**0.760449**	**2**

Q5EB77	NDIVNMLVGNK	1.180430084	2	3.27729
Q5EB77	TCDGVQCAFEELVEK	1.279688245	2	3.73839
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.026199426**	**0.985374**	**2**
Q5FVM4	MEELHNQEVQK	1.021602411	2	3.26203
Q5FVM4	RMEELHNQEVQK	1.028157058	3	4.00319
Q5FVQ4	**MLEC Malectin**	**1.15966361**	**0.071019**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	1.234187716	3	6.08198
Q5FVQ4	STPEDQILYQTER	1.144488496	2	3.97752
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.980770506**	**0.313517**	**4**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(11)	0.90284578	2	2.60546
Q5FVR2	DVTATVDSVPLITASILSK	1.196277483	2	3.63913
Q5FVR2	KQEELLSPADGIVECVR	1.177930529	2	4.5288
Q5FVR2	VHLDGPALSSQQR	1.054288578	2	2.40065
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.782647732**	**6.29E-12**	**4**
Q5FVR5	DEKENLFQSK	1.0851031	2	2.79955
Q5FVR5	ILFIVGENDQCLASK	1.90658897	2	3.74678
Q5FVR5	IQQPGIGVISVSK	1.781180814	2	2.76119
Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	1.581318175	3	3.8095
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.988434853**	**0.990522**	**2**
Q5FW57	AIDQEMFK	0.923183858	2	2.705
Q5FW57	SSQMLQMLESSLR	1.030574188	2	3.87969
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**1.047950765**	**0.683144**	**2**
Q5HZV9	AIENIDTLTNLESLFLGK	0.944721526	2	3.13882
Q5HZV9	ELDLYDNQIKK	1.714694809	2	2.37862
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**1.068925079**	**0.984419**	**2**
Q5HZY2	IDRPEAISEER	1.068849743	2	2.92637
Q5HZY2	LLESKEELDSLMTDETIANVPILILGNK	1.060489794	3	4.26351
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**1.022674816**	**0.580527**	**6**
Q5I0C3	HAPLVEFEEEEV	0.870963168	2	2.873
Q5I0C3	IIEEAPAPGIDPEVR	0.890387172	2	3.6949
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	0.906061272	3	6.01803
Q5I0C3	SEKEFQEQLESAR	0.860543221	2	3.55326
Q5I0C3	VFFSEGAQANR	1.146103174	2	2.52508
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	0.899322401	2	5.09386
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.944207148**	**0.999977**	**2**
Q5I0D1	ESQSILTPLVSLDTPGK	1.025641063	2	3.50574
Q5I0D1	HEEFEEGCK	0.909758067	2	2.6484
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**1.298335502**	**0.04871**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	0.968161672	2	2.65226
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.28642761	2	3.79594
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.134482799**	**0.375356**	**2**
Q5I0D7	GVNTDSGNVCR	1.135754282	2	2.72188
Q5I0D7	YAVDDVQYADEIASVLTSR	1.040942209	2	4.20835
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.128857629**	**0.964871**	**2**
Q5I0E7	QLVEQVEQIQK	1.040735269	2	4.04512
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.15933545	3	3.60774
Q5I0G4	**SYG Glycyl_tRNA synthetase (Fragment)**	**1.098148134**	**0.781432**	**5**
Q5I0G4	AEVSELPSVVR	1.10608895	2	3.23682
Q5I0G4	LGDAVEQGVINNSVLGYFIGR	1.22843659	2	3.0463
Q5I0G4	TLHVEEVVPSVIEPSFGLGR	0.965804111	2	4.12337
Q5I0G4	TVNVVQFEPNK	1.104529119	2	2.47861
Q5I0G4	VDDSSGSIGR	1.090812022	2	2.61867

Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**1.000147546**	**0.879722**	**7**
Q5I0H9	DKNQDLCQQESVK	0.966058923	2	4.20716
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	1.655176597	3	4.96225
Q5I0H9	GPPLWEEDPGAK	0.974982528	2	2.82964
Q5I0H9	GQGTICWVDCGDAESR	1.022871315	2	4.20567
Q5I0H9	NGEQQAVPALR	0.984554505	2	2.81754
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.725807622	3	4.51512
Q5I0H9	NQDLCQQESVK	0.931491656	2	2.64287
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.40260161**	**0.00056**	**5**
Q5I0J9	HANLLVGSPSALADQTTER	1.15108331	3	5.10083
Q5I0J9	IIHESGVQILR	1.188235314	2	2.63115
Q5I0J9	LDAAGGLQSLR	1.228061416	2	3.74192
Q5I0J9	LEGPLAAAHSSGPR	1.172794038	2	3.58267
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.699630059	2	3.88619
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.379636764**	**1.66E-06**	**3**
Q5I0M2	DNHVVAAGSMEK	1.268766067	2	2.93793
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.340214436	3	5.67099
Q5I0M2	LYAEGDIPVPHAR	1.354447643	2	3.32243
Q5M7U6	**ARP2 Actin_related protein 2**	**1.050751619**	**0.925942**	**6**
Q5M7U6	GYAFNHSADFETVR	1.200351146	2	3.59305
Q5M7U6	HLWDYTFGPEK	1.190112906	2	3.39156
Q5M7U6	ILLTEPPMNPTK	0.879311399	2	3.05973
Q5M7U6	LCYVGYNIEQEQK	0.967831925	2	3.31253
Q5M7U6	SMLEVNYPMENGIVR	0.986478327	2	4.46402
Q5M7U6	VVVCDNGTGFVK	0.994975591	2	2.95176
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**1.005850684**	**0.935995**	**9**
Q5M7W5	AAVGLTGNDIATPPNK	1.14434722	2	3.33307
Q5M7W5	ATSPSTLVSTGSSSR	0.923540827	2	3.38791
Q5M7W5	EAETALPIEMDLAPPEDVALPK	1.198705425	2	2.48335
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	0.844873958	2	4.32502
Q5M7W5	NTAPPTEEETVPGK	0.973941646	2	2.52502
Q5M7W5	NTTPTGATPPAGMASTR	1.02852307	2	2.40906
Q5M7W5	STLPVDEGSPLEK	0.939537628	2	2.35076
Q5M7W5	VGSLDNVGHLPAGGTVK	0.961334145	2	2.80324
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.26940213	2	4.66742
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.310370216**	**6.06E-07**	**6**
Q5M875	ALTAELDTLGK	1.301966833	2	3.51396
Q5M875	IQNIQFEAIVGHR	1.866883416	2	3.68321
Q5M875	NSGHIVTVASVCGHR	1.316627053	2	4.21154
Q5M875	SLIDGILTNK	1.284409609	2	2.97723
Q5M875	SVAGQTVLITGAGHGIGR	1.357084204	2	3.98535
Q5M875	TSCLCPVFVNTGFTK	1.275179758	2	4.1508
Q5M9G3	**CAPR1 Caprin_1**	**1.271292108**	**2.24E-12**	**3**
Q5M9G3	LNQDQLDAVSK	1.271598216	2	3.15094
Q5M9G3	SSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMK	0.849266727	3	4.98973
Q5M9G3	YQEVTNNLEFAK	1.156520981	2	2.59118
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.06660963**	**5.25E-06**	**2**
Q5M9I5	EEEEEELVDPLTTVR	0.941510405	2	3.33268
Q5M9I5	SQTEEDCTEELFDFLHAR	2.56491061	2	5.02061
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.034581939**	**0.00399**	**10**
Q5PPL3	AVLDANDPK	0.971911948	1	1.97669
Q5PPL3	AVLDANDPKK	1.028489197	2	2.478
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	1.262944657	2	4.34649

Q5PPL3	GQVTGTDLINEVSK	0.948071742	2	4.07318
Q5PPL3	GVSTVFHCASPPSNSNNK	1.038548282	2	4.78043
Q5PPL3	GYAVNVFDVR	1.070172562	1	2.03043
Q5PPL3	ILTGLNYEAPK	1.381732698	2	3.42088
Q5PPL3	KGQVTGTDLINEVSK	1.02726207	2	4.50861
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.260336763	3	3.88233
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.427576977	2	4.71045
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**0.82715225**	**5.71E-05**	**5**
Q5PQT3	AIQNLASIHSLQVK	1.236372283	2	3.95813
Q5PQT3	KLFPSLLDTK	1.426925028	2	2.46771
Q5PQT3	LSSLDVTHAALVNK	1.820184317	2	3.46708
Q5PQT3	NFPSSCVLGPEGTPASWTLMDQTGEMR	0.706955901	3	4.03695
Q5PQT3	QHLQIQSSQSHLNK	1.092718232	2	3.50531
Q5QNV8	**CQ066 Uncharacterized protein C17orf66 homolog**	**1.023708498**	**0.159523**	**2**
Q5QNV8	LEAPAFSFYFSKPK	0.986563652	2	2.36911
Q5QNV8	YFKDSAQMPNLHVSISK+Oxidation(8)	1.334696344	2	2.41269
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.06534346**	**0.761061**	**5**
Q5RJR8	ATVLDLSCNK	1.04446932	2	2.39624
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	1.092366084	2	5.82688
Q5RJR8	HHEILQWVLQTDSQQ	1.123493187	2	3.4419
Q5RJR8	LDGNELDLSLSDLNEVPVK	0.996965154	2	4.32948
Q5RJR8	LQQLPADFGR	1.600709163	2	2.32067
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.054181506**	**0.645451**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.0377569	3	5.2743
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	0.719178138	3	3.73757
Q5RKI0	YAPSGFYIASGDISGK	1.078922535	2	4.16016
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.210034099**	**1.37E-13**	**5**
Q5RKI1	ELAQQIQK	1.264794739	1	2.17479
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.311598889	2	4.73852
Q5RKI1	GYDVIAQAQSGTGK	1.098410211	2	5.20871
Q5RKI1	MFVLDEADEMLSR	1.252012443	2	4.72453
Q5RKI1	VLITTDLLAR	1.40294292	2	2.41693
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.025866193**	**0.892854**	**11**
Q5SGE0	AALDLEQVPSELAVTR	0.910208368	2	3.87397
Q5SGE0	CIANNQVETLEK	1.312666936	2	3.06236
Q5SGE0	HCVTMDTPAEK	1.066008137	2	3.19139
Q5SGE0	HDNAEDALNLK	1.198564795	2	3.73799
Q5SGE0	LKAEGHPVGDPLK	1.258082235	2	2.43481
Q5SGE0	MEGANIQPNR	0.875662601	2	2.59649
Q5SGE0	SCGSLLPELSLAER	0.996140215	2	2.49516
Q5SGE0	SSLSSSSPSAGDTVTEK	0.985441677	2	4.36528
Q5SGE0	SYVADKDVASAK	0.95688676	2	3.38758
Q5SGE0	TLLELIPELR	1.175688068	2	2.49479
Q5SGE0	VQDAINILK	0.915056724	2	2.30506
Q5SVT3	**ETAA1 Ewing_s tumor_associated antigen 1 homolog**	**0.916638259**	**0.484698**	**2**
Q5SVT3	ELMKLAQQFDK+Oxidation(3)	0.913958572	2	2.50835
Q5SVT3	NHDFIQMTSKMGHLDNHK+Oxidation(7)Oxidation(11)	1.688695593	2	2.48525
Q5SX40	**MYH1 Myosin_1**	**0.836448589**	**1**	**75**
Q5SX40	AAYLQNLNSADLLK	0.711246643	2	3.60001
Q5SX40	ADIAESQVNK	1.408214784	2	3.39813
Q5SX40	AEDEEEINAELTAK	2.280340627	2	3.95358
Q5SX40	AGLLGLLEEMR	1.651767094	2	3.88847
Q5SX40	AGLLGLLEEMRDDK	1.023405665	2	3.38122
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	1.146311523	3	6.55991

Q5SX40	ANLLQAEIEELR	1.939298888	2	4.00924
Q5SX40	ANSEVAQWR	0.917714133	2	2.32342
Q5SX40	DLEEATLQHEATAATLR	0.693071745	2	4.93654
Q5SX40	DTQLHLDDALR	1.617976421	2	2.93072
Q5SX40	EEQAEPDGTEVADK	1.649747327	2	3.14657
Q5SX40	ELEGEVENEQK	2.168244147	2	2.96373
Q5SX40	ELEGEVENEQKR	2.270603158	2	3.18359
Q5SX40	ELTYQTEEDRK	1.25004615	2	3.14257
Q5SX40	ENQSILITGESGAGK	1.77516107	2	3.67875
Q5SX40	EQYEEEQEAK	0.678113855	1	3.02317
Q5SX40	GQEDLKEQLAMVER	0.935921229	2	4.08175
Q5SX40	GQTVQQVYNSVGALAK	1.435301976	2	3.01571
Q5SX40	GSSFQTVSALFR	0.799951293	2	2.54517
Q5SX40	HADSVAELGEQIDNLQR	0.758418792	2	5.88924
Q5SX40	IAEKDEEIDQLKR	1.250606495	2	2.43508
Q5SX40	IAEQELLDASER	2.055654352	2	3.60841
Q5SX40	IEAQNKPFDAK	4.338622873	2	2.79034
Q5SX40	IEDEQALGMQLQK	0.702499409	2	4.42924
Q5SX40	IEELEEEIEAER	0.801005113	2	4.11159
Q5SX40	IKLEQQVDDLEGSLEQEK	0.729034292	2	5.07903
Q5SX40	IKLEQQVDDLEGSLEQEKK	1.030014871	3	5.0071
Q5SX40	INQQLDTK	1.235558849	2	2.36049
Q5SX40	IQHELEEAEER	0.781304514	2	3.64902
Q5SX40	IQLELNQVK	1.542408598	2	2.90868
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	2.301269798	3	4.19087
Q5SX40	KIAEQELLDASER	2.124726496	2	4.15224
Q5SX40	KIQHELEEAEER	0.865634967	3	3.89384
Q5SX40	KKLETDISQIQGEMEDIVQEAR	0.928891217	3	5.14356
Q5SX40	KLEDECSELK	0.90643082	2	2.95433
Q5SX40	KLEDECSELKK	1.695889906	3	4.05267
Q5SX40	KLETDISQIQGEMEDIVQEAR	0.994611505	2	5.37809
Q5SX40	LAQESTMDVENDKQQLDEK	0.580210377	2	4.56763
Q5SX40	LDEAEQLALK	0.94057071	2	3.36966
Q5SX40	LEDECSELKK	1.463559221	2	3.10058
Q5SX40	LEEAGGATSAQIEMNK	1.030646404	2	4.74455
Q5SX40	LEQQVDDLEGSLEQEK	0.959151576	2	5.57827
Q5SX40	LEQQVDDLEGSLEQEKK	1.418556611	2	4.82303
Q5SX40	LETDISQIQGEMEDIVQEAR	0.816584304	2	5.12172
Q5SX40	LINELTAQR	2.619134008	2	2.95327
Q5SX40	LQDAEEHVEAVNAK	0.571033726	2	4.57714
Q5SX40	LQDLVDK	1.494976822	2	2.36141
Q5SX40	LQNEVEDLMIDVER	0.999052985	2	4.47235
Q5SX40	LQTESGEYSR	0.678369889	2	2.66723
Q5SX40	MEIDDLASNMEVISK	0.859754077	2	4.39459
Q5SX40	MEIDDLASNMEVISKSKGNLEK	0.99883164	2	2.4305
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	1.666653753	3	6.60424
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(1)	1.139247244	2	4.39973
Q5SX40	NDLQLQVQSEADSLADAEER	0.980995351	2	5.57926
Q5SX40	NKDPLNETVVGLYQK	0.640314361	2	4.54413
Q5SX40	NLQQEISDLTEQIAEGGK	1.341509435	2	5.91699
Q5SX40	NLQQEISDLTEQIAEGGKR	0.827761989	2	4.43235
Q5SX40	NLTEEMAGLDETIAK	2.306820853	2	5.15459
Q5SX40	QAEEAEEQSNVNLAK	2.065174711	2	4.42775
Q5SX40	QKYEETHAELEASQK	0.782010552	2	4.03925
Q5SX40	QLDEKDSLVSQLSR	1.09788632	2	2.8136
Q5SX40	QLEEEIK	1.026942367	1	2.0756
Q5SX40	QREEQAEPDGTEVADK	2.025607234	2	4.33739

Q5SX40	SELQAALEEAEASLEHEEGK	0.689744901	2	5.43335
Q5SX40	SSVFVVDAK	0.792959817	1	2.31475
Q5SX40	TKYETDAIQR	1.306776418	2	3.31543
Q5SX40	TLEDQVSELK	1.115147111	2	3.17909
Q5SX40	TNAACAALDK	1.908359996	1	1.93056
Q5SX40	TNAACAALDKK	1.930261918	3	3.43113
Q5SX40	VKELTYQTEEDRK	0.939542462	2	2.62993
Q5SX40	VLNASAIPEGQFIDSK	2.880104132	2	4.48824
Q5SX40	VQLLHTQNTSLINTK	1.883273789	2	4.89928
Q5SX40	VRELEGEVENEQKR	1.909509978	3	3.66252
Q5SX40	YEETHAELEASQK	0.716752139	2	4.43775
Q5SX40	YETDAIQR	0.96044056	1	2.08863
Q5TKR9	**KAT6A Histone acetyltransferase KAT6A**	**1.68986921**	**0.095008**	**2**
Q5TKR9	ENKDQDSSSLIESEKKPEVK	1.257371096	2	2.38685
Q5TKR9	KGYGRFLIDFSYLLSK	1.900900882	2	2.30156
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.092249942**	**2.67E-05**	**5**
Q5U206	DTDSEEEIR	1.153875174	2	2.41691
Q5U206	KMKDTDSEEEIR	1.201324688	2	2.62596
Q5U206	KMKDTDSEEEIR+Oxidation(2)	1.139492246	2	2.48202
Q5U206	MKDTDSEEEIR	1.019693407	3	4.1694
Q5U206	MKDTDSEEEIR+Oxidation(1)	1.132899561	2	3.44098
Q5U211	**SNX3 Sorting nexin_3**	**1.248693484**	**0.224391**	**2**
Q5U211	GDDGIFDDNFIEER	1.489916208	2	2.86986
Q5U211	YSDFEWLR	1.111057733	2	2.54064
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.157202479**	**0.374185**	**4**
Q5U2Q7	GFGGIGGILR	1.10658852	2	2.97356
Q5U2Q7	LSVLGAITSVQQR	1.634234053	2	2.44114
Q5U2Q7	YFDEISQDTGK	1.195899032	2	2.78848
Q5U2Q7	YVLHCQGTEEEK	1.141090501	2	3.96404
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**0.931025922**	**0.983936**	**2**
Q5U2U0	QQAEVEK	0.907587278	1	2.01952
Q5U2U0	SGESNTHQDIEEKDR	0.752322261	3	3.68988
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.132581691**	**9.41E-05**	**12**
Q5U300	AAVASLLQSVQVPEFTPK	1.142039345	3	3.42289
Q5U300	AENYDISPADR	0.978636341	2	2.44475
Q5U300	DNPGVVTCLDEAR	0.850836472	2	2.3507
Q5U300	FEVQGLQPNGEEMTLK	0.982568068	2	2.79583
Q5U300	FEVQGLQPNGEEMTLK+Oxidation(13)	1.18030153	2	2.43823
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.254619112	2	5.60859
Q5U300	LDQPMTEIVSR	1.02481345	2	3.12491
Q5U300	NEEDATELVTLAQAVNAR	0.935603078	2	5.29321
Q5U300	NFPNAIEHTLQWAR	0.983620108	2	3.56025
Q5U300	SLPASLAEPDFVMTDFAK	1.105303189	2	4.06931
Q5U300	SPPAVQQDNVDEDLIR	1.079848953	2	4.87026
Q5U300	VVQGHQQLDSYK	1.170501969	2	3.31053
Q5U312	**RAI14 Ankycorbin**	**1.214020984**	**0.256479**	**2**
Q5U312	MHLLYAVQGQMDEDVQKVLK	1.00577835	2	2.3404
Q5U312	QDLQRALEESK	1.215137396	2	2.43996
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**0.958767776**	**0.794084**	**2**
Q5U4E6	EFNTQLAQK	0.937333929	2	2.34814
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(17)	1.038456436	2	2.41344
Q5XFW8	**SEC13 Protein SEC13 homolog**	**1.076201038**	**0.956125**	**2**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	1.018128789	2	3.58343
Q5XFW8	LEAHSDWVR	1.062418127	2	2.69645
Q5XFX0	**TAGL2 Transgelin_2**	**0.913674828**	**0.987104**	**5**

Q5XFX0	DDGLFSGDPNWFPK	1.036816209	2	3.42796
Q5XFX0	NFSDNQLQEGK	1.000127838	2	3.24954
Q5XFX0	NVIGLQMGTNR	1.134226705	2	2.77554
Q5XFX0	TLMNLGGLAVAR	1.010226778	2	3.40698
Q5XFX0	YGINTTDIFQTVDLWEGK	1.18548695	2	5.07018
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.284822**	**1.31E-07**	**11**
Q5XHY5	AEHDSILAEK	1.540620479	2	2.65637
Q5XHY5	FLGDIEIWNQAEK	1.390042	2	3.461
Q5XHY5	FMVDIDLDPGCTLNK	1.588012641	2	2.45842
Q5XHY5	FNLTYVSHDGDDK	1.186966052	2	2.67757
Q5XHY5	GFQEVVTPNIFNSR	1.660273574	2	3.55672
Q5XHY5	LKAEHDSILAEK	1.015577852	2	3.36677
Q5XHY5	QLENSLNEFGEK	1.237548085	2	2.90107
Q5XHY5	QVMVVPVGPTCDEYAQK	1.39259927	2	3.09612
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.306119211	2	4.00699
Q5XHY5	VVWDLDRPLETDCTLELLK	2.322892827	2	3.97202
Q5XHY5	WELNPGDGAFYGPK	1.202839215	2	3.72463
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.014582165**	**0.21207**	**13**
Q5XHZ0	AFLEALQHQAETSSR	1.106959718	2	4.50468
Q5XHZ0	AQLLQPTLEINPR	1.226214572	2	3.07929
Q5XHZ0	EGIVTTAEQDIKEDIAK	0.591598219	2	2.39974
Q5XHZ0	ELISNASDALEK	1.054469118	2	2.95389
Q5XHZ0	FEDTSPAGER	1.080496788	2	2.8952
Q5XHZ0	GTITIQDTGIGMTK	1.027183656	2	2.8838
Q5XHZ0	GVVDSEDIPLNLSR	1.112294501	2	4.86952
Q5XHZ0	HLAEHSPYYEAMK	1.110539085	2	3.0082
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.075567432	3	4.04025
Q5XHZ0	SDCKDFANESR	0.870103232	2	2.89791
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	0.999408849	3	4.30871
Q5XHZ0	YESSALPAGQLTSLSDYASR	1.118153779	2	5.45386
Q5XHZ0	YIAQAYDKPR	1.253977942	2	2.80653
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.206932508**	**0.927139**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	0.911890189	2	4.77651
Q5XI22	HGSNLEAMSK	1.154449421	2	2.44494
Q5XI22	HGSNLEAMSK+Oxidation(8)	0.833455422	2	3.26951
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	1.281305629	3	5.15884
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	1.062004334	3	3.88294
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	0.873394596	3	4.65328
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	0.923916368	2	5.24932
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	1.337511474	2	5.3595
Q5XI22	VNIDGGAIALGHPLGASGCR	1.065481437	2	5.38773
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**0.96799803**	**0.961288**	**2**
Q5XI29	QNLSQFEAQAR	0.96029482	2	2.37299
Q5XI29	SIGVYDVVELK	0.968058379	2	2.58266
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.099053924**	**0.598185**	**6**
Q5XI32	GCWDSIHVVEVQEK	1.476898131	2	3.20919
Q5XI32	KLEVEANNAFDQYR	1.054021588	2	4.14047
Q5XI32	LEVEANNAFDQYR	0.900292988	2	3.57624
Q5XI32	LVEDMENK	1.266910618	2	2.75603
Q5XI32	NDLVEALK	1.052434236	2	2.57597
Q5XI32	SGSGTMNLGGSLTR	1.03368903	2	3.25594
Q5XI41	**TRAM1 Translocating chain_associated membrane protein 1**	**1.047975565**	**0.975463**	**2**
Q5XI41	EHSAFQAPPVK	1.07471524	2	2.35044
Q5XI41	LDFSTGNFNVLAVR	1.036490282	2	3.06603
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.176265138**	**0.82202**	**3**

Q5XI60	ALDIAAGITR	0.947360364	2	2.5647
Q5XI60	HHVALDSAASQLSGR	1.28251504	2	4.51929
Q5XI60	NVATDALGALEAR	1.067372197	2	4.04572
Q5XI72	**IF4H Eukaryotic translation initiation factor 4H**	**1.035685869**	**0.020228**	**2**
Q5XI72	EALTYDGALLGDRSLR	0.722011074	2	2.60126
Q5XI72	SLRVDIAEGRK	1.054383808	2	2.43685
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.071821568**	**0.889072**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.247551585	2	4.11674
Q5XI73	IDKTDYMVGSYGPR	1.030986209	2	4.00631
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	1.491716162	3	3.4509
Q5XI73	SIQEIQELDKDDESLR	1.046847973	2	5.291
Q5XI73	SIQEIQELDKDDESLRK	1.12173864	2	4.15125
Q5XI73	VAVSADPNVPNVIVTR	1.108523652	2	4.10819
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**1.168886384**	**0.140049**	**13**
Q5XI78	FGLEGCEVLIPALK	1.361403929	2	2.96438
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.33354975	3	5.04087
Q5XI78	HHVLHDQNVDK	0.896687153	3	3.37294
Q5XI78	ICEEAFTR	1.02963838	2	2.41024
Q5XI78	IEQLSPFPFDLLLK	1.121499539	2	3.37631
Q5XI78	LEAADEGSGDMK	1.112119982	2	2.89348
Q5XI78	LNVLANVIR	1.454274788	2	2.53142
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.247505223	2	4.91159
Q5XI78	NTNAGAPPGTAYQSPLSLSR	1.321969198	2	3.81319
Q5XI78	SSLATMAHAQSLVEAQPNVDK	1.303340902	3	3.90604
Q5XI78	SWDIFFR	1.285934178	2	2.33741
Q5XI78	VIPEDGPAAQNPDK	1.202373647	2	2.70224
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	0.933188832	3	4.37032
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**0.945548094**	**0.881787**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.856288005	2	3.64727
Q5XI95	IIAVDINK	0.900291726	2	2.78801
Q5XI95	MVATGVCGTDIK	0.83175473	2	2.68459
Q5XI95	NNICTEIR	1.024860371	2	2.40972
Q5XI95	TVGATDCVDPR	0.841280683	2	2.9722
Q5XIA0	**DZI1L Zinc finger protein DZIP1L**	**1.165116514**	**0.403226**	**2**
Q5XIA0	EVCNHCRQPVDPVLLK	1.139368701	2	2.36898
Q5XIA0	GQQELGRQADELK	1.166429424	2	2.44355
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**0.999057661**	**0.847367**	**6**
Q5XIC0	ATQQDFENAMNQVK	0.88986526	2	4.52331
Q5XIC0	GILVTSEGGITK	0.996306522	2	3.42509
Q5XIC0	LHAVNEEECTTLR	1.003982251	2	4.13692
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.930871096	2	5.11412
Q5XIC0	WDAWNALGSLPK	1.238934784	2	3.43616
Q5XIC0	WLSEECINAIMSFVTR	0.778850788	2	2.36072
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.240668125**	**0.232471**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	1.261882818	2	2.6175
Q5XIC1	VEGTPNDPNPNDPR	0.732574263	2	2.60297
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.058950521**	**0.372671**	**7**
Q5XIE6	AGIATHFVDSEK	0.6170223	2	3.23856
Q5XIE6	AVLIDKDQTPK	0.943163894	2	2.97289
Q5XIE6	GCAGVITLNRPK	0.701926353	2	2.68651
Q5XIE6	HTETAEVLLER	0.945289736	2	2.57552
Q5XIE6	INSCFSANTVEQILENLR	1.051592845	2	4.72736
Q5XIE6	LHVLEEELLALK	1.182024715	3	4.61975
Q5XIE6	QDGSPFAMEQIK	1.106675235	2	2.56451

Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.126222425**	**0.064564**	**2**
Q5XIF3	HGWSYDVEGR	1.125717942	2	2.69967
Q5XIF3	LDVTPLTGVPEEHIK	1.352308936	2	3.45411
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.162384994**	**0.000285**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	0.8917064	2	4.1406
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.221343141	2	5.47256
Q5XIF6	DVNAAIAAIK	0.993509466	2	2.90436
Q5XIF6	SIQFVDWCPTGFK	1.169407399	2	4.45196
Q5XIF6	TIGGGDDSFTTFFCETGAGK	5.365519689	2	4.26084
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.037671093**	**0.999803**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	1.089653294	2	3.76681
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	0.961436966	2	5.1551
Q5XIH7	**PHB2 Prohibitin_2**	**1.057925456**	**2.39E-05**	**10**
Q5XIH7	AQVSLLIR	1.070483801	2	2.34243
Q5XIH7	DLQMVNISLR	0.866902989	2	3.08946
Q5XIH7	FNASQLITQR	0.993892878	2	3.76105
Q5XIH7	IGGVQQDTILAEGLHFR	1.151676214	3	4.20195
Q5XIH7	IVQAEGEAEAAK	0.926902335	2	3.8714
Q5XIH7	IYLTADNLVLNLQDESFTR	1.673138049	2	4.73665
Q5XIH7	LGLDYEER	0.979904672	2	2.30404
Q5XIH7	LLLGAGAVAYGVR	2.160009074	2	3.4734
Q5XIH7	VLPSIVNEVLK	1.079281196	2	2.73041
Q5XIH7	VLSRPNAQELPSMYQR	0.921848553	2	4.58348
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.28758131**	**3.61E-07**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	1.239787763	2	4.20659
Q5XIM9	GATQQILDEAER	1.246356945	2	3.96892
Q5XIM9	GSGNLEAIHVIK	1.013651807	2	2.64897
Q5XIM9	HGINCFINR	0.892075564	2	2.61714
Q5XIM9	LGGSLADSYLDEGFLLDK	1.207948442	2	4.14761
Q5XIM9	LGGSLADSYLDEGFLLDKK	1.023919663	3	3.31337
Q5XIM9	SLHDALCVLAQTVK	1.221955211	2	3.5714
Q5XIM9	VAEIEHAEKEK	1.440373444	2	2.44861
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.237700449	2	4.74543
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.130643042**	**0.919621**	**10**
Q5XIN6	AAEVEGEQVDNK	1.145530007	2	4.09014
Q5XIN6	AMYLPDTLSPADQLK	0.902422747	2	2.31511
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	1.074519253	2	4.61258
Q5XIN6	FLQDTIEEMALK	1.162644569	2	2.91009
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.093101132	2	3.95568
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.978350264	3	4.75929
Q5XIN6	LEEGGPVYSPPAQVVVK	1.040120576	2	2.78187
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.32905149	3	4.83728
Q5XIN6	LLELQSIGTNNFLR	1.106546938	2	3.35297
Q5XIN6	STLQTLPEIVAK	1.077021549	2	2.38534
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**0.884843025**	**0.837511**	**7**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.946339615	2	5.00718
Q5XIT9	ALYGDTLVTGFAR	0.92769216	2	3.11136
Q5XIT9	AQEIALQNR	0.703133868	2	2.56658
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.082599515	3	4.91038
Q5XIT9	LGTQPDSGSSTYQENYEQMK	0.835774701	2	4.94006
Q5XIT9	LWDDGIIDPVDTR	1.003430624	2	3.15926
Q5XIT9	LYGEEEVPAGGIITGIGR	0.914502513	2	4.55325
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.046603794**	**0.90409**	**5**

Q5XIU9	FYGPAGPYGIFAGR	1.205352087	2	2.88886
Q5XIU9	GGDGSPGGAGATAAR	0.923031488	2	3.20926
Q5XIU9	GLATFCLDK	1.332899874	1	1.95778
Q5XIU9	GLCSGPGAGEESPAATLPR	1.0152424	2	4.803
Q5XIU9	VFDVTK	1.080452877	1	2.00256
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**0.916272607**	**0.991123**	**6**
Q60587	AMDSDWFAQNYMGR	1.047074627	2	3.21432
Q60587	AQDEGHLSDIVPFK	0.799921968	2	3.32946
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.906066703	2	5.26839
Q60587	DNGIRPSSLEQMAK	0.877370613	2	3.6151
Q60587	DQLLLGPTYATPK	0.971753819	2	3.72707
Q60587	NIVVVEGVR	0.95784383	2	3.00955
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**0.979086367**	**0.302821**	**5**
Q60759	DILGGNGISDEYHVIR	0.817190812	2	3.22401
Q60759	DIVYEMGELGVLGPTIK	0.987472804	2	3.02907
Q60759	GYGCAGVSSVAYGLLTR	0.784255291	2	3.98121
Q60759	HAMNLEAVNTYEGTHDIHALILGR	0.998924023	4	5.46458
Q60759	SMMSVQSSLVMHPIYTYGSEEQR	1.145164928	3	3.83938
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.121556311**	**0.994534**	**2**
Q60817	IEDLSQQAQLAAAEK	1.145369145	2	4.55298
Q60817	NILFVITKPDVYK	1.048760534	2	3.54738
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**1.076390483**	**0.573944**	**3**
Q61029	SELVANNVTLPAGEQR	1.182376843	2	4.07969
Q61029	SSTPLPTVSSSAENTR	1.059259653	2	2.90608
Q61029	YGVNPGPIVGTTR	1.115041876	2	3.07916
Q61043	**NIN Ninein**	**1.102877941**	**0.786701**	**2**
Q61043	ERATAAAMKQEQEILER	1.111655231	2	2.335
Q61043	LQEENSILR	0.718327998	2	2.40396
Q61233	**PLSL Plastin_2**	**1.059364007**	**0.985421**	**2**
Q61233	ALENDPDCR	1.048098032	2	2.51922
Q61233	MINLSVPDTIDER	1.060031582	2	3.58169
Q61301	**CTNA2 Catenin alpha_2**	**1.084549376**	**0.51265**	**2**
Q61301	LLEPLVTQVTTLVNTSNK	1.156930324	2	4.04376
Q61301	TSVQTEDDQLIAGQSAR	1.025739036	2	4.62116
Q61335	**BAP31 B_cell receptor_associated protein 31**	**1.109021278**	**0.956247**	**5**
Q61335	AENEALAMQK	1.045085725	2	3.05559
Q61335	KYMEENDQLKK+Oxidation(3)	1.12208871	3	3.36525
Q61335	LKDELASTK	0.811028565	2	2.6221
Q61335	YMEENDQLK	1.021713312	2	2.41034
Q61335	YMEENDQLKK	1.004176823	2	2.56596
Q61599	**GDIR2 Rho GDP_dissociation inhibitor 2**	**0.972666825**	**0.991636**	**2**
Q61599	ATFMVGSYGPRPEEYEFLTPVEEAPK	1.080274794	3	3.62484
Q61599	TLLGDVPVVADPTVPNVTVTR	0.972202883	2	4.63873
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**0.905787578**	**0.788335**	**3**
Q61656	ELAQQVQQVAAEYCR	0.795367328	2	2.66336
Q61656	GDGPICLVLAPTR	1.116038234	2	3.42589
Q61656	MLDMGFEPQIR	1.060579554	2	3.3809
Q61830	**MRC1 Macrophage mannose receptor 1**	**1.158039931**	**0.429759**	**3**
Q61830	KMDPQPK+Oxidation(2)	0.946805521	1	1.91597
Q61830	LKLPWHEAETYCK	1.09039277	2	2.30288
Q61830	TGVAGGLWDVLSCEEK	1.257500218	2	3.1643
Q61941	**NNTM NAD(P) transhydrogenase_ mitochondrial**	**1.087243698**	**0.824549**	**11**
Q61941	EANSIVITPGYGLCAAK	0.866338489	2	3.64021

Q61941	FFTGQITAAGK	1.150828966	2	2.43206
Q61941	GITHIGYTDLPSR	1.036368254	2	3.55381
Q61941	ILIVGGGVAGLASAGAAK	1.40216175	2	4.57793
Q61941	KTTVLAMDQVPR	0.931738705	2	3.49848
Q61941	MATQASTLYSNNITK	0.984144191	2	4.33093
Q61941	QGFNVVVESGAGEASK	1.037223125	2	3.86511
Q61941	SAPLLLPGR	1.424206093	2	2.34673
Q61941	SLGAEPLEVDLK	1.092138553	2	3.06029
Q61941	TTVLAMDQVPR	1.22993389	2	2.75583
Q61941	VTIAQGYDALSSMANISGYK	1.124859926	2	5.38063
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**1.501746211**	**0.053291**	**2**
Q61990	AITIAGIPQSIIECVK	1.216613056	2	2.33273
Q61990	IITLAGPTNAIFK	1.570360692	2	2.73056
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.109420811**	**9.36E-07**	**4**
Q62095	HVINFDLPSDIEEYVHR	1.50076933	3	4.26027
Q62095	SFLLDLLNATGK	1.247297658	2	3.9003
Q62095	VGNLGLATSFFNER	1.118621524	2	2.77429
Q62095	VGSTSENITQK	1.188043928	2	2.93577
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.109899702**	**4.26E-07**	**17**
Q62261	ALVADSHPESER	1.086250873	2	3.27549
Q62261	EGMQLISEKPETEAVVK	1.080075176	2	2.82315
Q62261	EGMQLISEKPETEAVVKEK	1.30647549	2	2.38893
Q62261	EIEELQSQAQALSQEGK	1.485810116	2	2.82133
Q62261	FESLEPEMNNQASR	1.140749985	2	3.53977
Q62261	HDTSASTQSTPASSR	0.848559674	2	2.79602
Q62261	HQILEQAVEDYAETVHQLSK	1.109720692	3	6.18847
Q62261	LEDLEVIQHR	0.987892702	3	3.35863
Q62261	LISDINK	1.000790567	1	1.9508
Q62261	LLDPEDISVDHPDEK	0.874510985	2	3.35689
Q62261	LTTLELLEVR	1.618008751	2	2.5658
Q62261	LVSDGNINSDR	1.228006676	2	2.82439
Q62261	LVSQDNFGFDLPAVEAATK	0.995289062	2	3.90771
Q62261	SQNIITDSSSLNAEAIR	1.164973289	2	4.99061
Q62261	TLETPAAQMEGFLNR	1.445812001	2	2.65264
Q62261	TQTAIASEDMPNTLTEAEK	1.136919833	2	5.53988
Q62261	VIESTQDLGNDLAGVMALQR	0.161399031	2	3.83431
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.311917017**	**0.940621**	**3**
Q62425	FYSVNVDYSK	1.373785264	1	2.60274
Q62425	KNNPEPWNK	1.123156235	2	2.56668
Q62425	LGPNEQYK	1.105712927	2	2.34442
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**0.868698594**	**0.000192**	**5**
Q62452	AMEIAEALGR	0.802144136	2	3.62419
Q62452	GAGVTLNVLEMTADDLENALK	0.827977631	3	5.88941
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(11)	1.141868852	2	3.56971
Q62452	WLPQNDLLGHPK	1.023054132	2	3.34986
Q62452	YTGTRPSNLAK	0.714934682	2	2.98125
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.078262133**	**0.999638**	**6**
Q62465	ACGLNFADLMGR	1.11228089	2	2.80413
Q62465	GVDIVMDPLGGSDTAK	0.956109147	2	4.18264
Q62465	IDSVWPFEK	0.970763776	2	2.35945
Q62465	TVENVTVFGTASASK	1.107383614	2	3.25393
Q62465	VLLVPGPEKET	0.873659488	2	2.70514
Q62465	VVTYGMANLLTGPK	0.962108984	2	2.53913
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.071781536**	**0.134838**	**2**
Q62636	INVNEIFYDLVR	2.028692108	2	3.97448

Q62636	LVVLGSGGVGK	1.009320554	2	2.55185
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.865066595**	**0.774785**	**6**
Q62651	EVDVGLAADVGTLQR	0.913746201	2	3.36038
Q62651	HVLHVQLNRPEK	0.850143141	2	3.43017
Q62651	MMADEALDSGLVSR	0.973924011	2	3.35133
Q62651	RIPEEVSDHNYESIQVTSAQK	0.796098431	3	6.44994
Q62651	SLVNELTFTAR	0.880528099	2	3.50636
Q62651	YCTQDAFFQVK	1.060305709	2	2.71495
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**1.424662034**	**0.024528**	**5**
Q62730	AVLVTGADSGFGHALAK	1.50175399	2	4.18922
Q62730	EIQENYGQEYVHTQK	1.436274794	2	4.52055
Q62730	LSVLQMDVTKPEQIK	2.004891786	2	3.63567
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	1.209575735	3	4.22712
Q62730	VVTIHPGGFQTNIVGSQDSWDK	1.440258141	2	5.58635
Q62736	**CALD1 Non_muscle caldesmon**	**1.054785866**	**8.17E-10**	**11**
Q62736	ASGDKEAEGAPQVEAGK	1.220943273	2	4.61705
Q62736	ASGDKEAEGAPQVEAGKR	1.145212142	3	3.8013
Q62736	EEIERR	0.833906239	1	1.90369
Q62736	EFDPTITDGSLSVPSR	1.102551426	2	3.18845
Q62736	GGNLGENQIKDEK	1.063329906	2	3.31488
Q62736	LEQYTNAIEGTK	1.046998397	2	3.59194
Q62736	MQNNSAENETAEGEEKGESR	1.030935942	3	4.6093
Q62736	NDDDEEEAAR	2.776727367	2	2.71467
Q62736	RGETESEEFEK	1.065386265	2	2.93517
Q62736	RRGETESEEFEK	1.512610382	2	3.2274
Q62736	VLEEEEQR	1.197190489	2	2.49488
Q62745	**CD81 CD81 antigen**	**1.098814995**	**0.999966**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.100282768	2	2.90088
Q62745	QFYDQALQQAVMDDDANNAK	1.057337748	2	4.60367
Q62769	**UN13B Protein unc_13 homolog B**	**1.04392894**	**0.92165**	**2**
Q62769	DHMVREETRNLTPK	0.841130121	2	2.52553
Q62769	SNDEVAREFVK	1.04804619	1	2.04054
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.05797514**	**0.267337**	**5**
Q62785	ANEEDEQEEGGDGASGDPK	0.974720161	2	4.61853
Q62785	ANEEDEQEEGGDGASGDPKK	1.315318098	3	3.30644
Q62785	GVEGLIDIENPNR	1.058384562	2	2.34918
Q62785	KVTQLDLDGPK	0.590530807	2	2.46848
Q62785	YMKMHLAGKTEQAK	0.92206192	2	2.43774
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.059979984**	**0.130176**	**2**
Q62789	IILDELVQR	1.249289831	2	3.63259
Q62789	WIPQNDLLGHPK	1.023054132	2	3.34986
Q62812	**MYH9 Myosin_9**	**1.167059968**	**9.9E-20**	**61**
Q62812	ADFCIIHYAGK	1.510474082	2	2.69724
Q62812	ALEEAMEQK	1.134101527	2	2.72602
Q62812	ALELDSNLYR	1.182725495	2	3.55494
Q62812	ALEQQVEEMK	1.113382196	2	3.01225
Q62812	ANLQIDQINTDLNLER	1.251710691	2	4.7973
Q62812	ASIAALEAK	1.257427132	2	2.33633
Q62812	ASREEILAQAK	1.006912462	2	3.12159
Q62812	CQYLQAEK	1.486478684	1	1.93044
Q62812	DFSALESQLQDTQELLQEENR	1.221171394	3	6.35346
Q62812	DLEAHIDTANK	0.9697551	2	3.63865
Q62812	DLQGRDEQSEEK	1.138787124	2	3.21507
Q62812	EEILAQAK	1.155072974	1	2.2352
Q62812	ELEDATETADAMNR	0.966503151	2	4.23962

Q62812	ELETQISELQEDLESER	1.11955758	2	4.97377
Q62812	HEAMITDLEER	1.182268289	2	3.43458
Q62812	HEDELLAK	1.213095124	2	3.22554
Q62812	HSQAVEELAEQLEQTK	1.091025972	2	4.91044
Q62812	HSQAVEELAEQLEQTKR	1.243008749	3	5.7173
Q62812	IIGLDQVAGMSETALPGAFK	1.301943857	2	5.89155
Q62812	IRELETQISELQEDLESER	1.262898959	2	5.16426
Q62812	KEEELQAALAR	1.219736206	2	3.2768
Q62812	KKVEAQLQELQVK	1.197477006	2	4.7232
Q62812	KLEEDQIIMEDQNCK	1.108127491	2	5.68567
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.170717096	2	5.74698
Q62812	KQELEEICHDLEAR	1.146423403	2	4.5442
Q62812	KVEAQLQELQVK	1.219983964	2	3.94372
Q62812	LDPHLVLDQLR	1.151080668	3	3.4101
Q62812	LEEDQIIMEDQNCK	0.937315621	2	3.32872
Q62812	LEGDSTDLSDQIAELQAQIAELK	0.907777136	2	4.97164
Q62812	LEVNLQAMK	1.155625547	2	2.67756
Q62812	LQEMESAVK	1.158857587	2	2.41776
Q62812	LQQELDDLLVDLDHQR	0.847973524	2	4.71319
Q62812	LQVELDSVTGLLNQSDSK	1.189426437	2	5.70638
Q62812	LTEMETMQSQLMAEK	1.224806574	2	4.40506
Q62812	MEDGVGCLETAEEAK	0.873353007	2	4.59492
Q62812	MQQNIQELEEQLEEEESAR	0.95928041	2	5.9409
Q62812	NAEQFKDQADK	1.328315768	2	3.64393
Q62812	NKHEAMITDLEER	1.134726157	3	3.66858
Q62812	NLPIYSEEIVDMYK	1.540729873	2	3.28055
Q62812	NMDPLNDNIATLLHQSSDK	1.180061839	2	5.05924
Q62812	NTDQASMPDNTAAQK	1.167304736	2	5.31372
Q62812	NTDQASMPDNTAAQK+Oxidation(7)	1.286492758	2	4.89612
Q62812	QAQQERDELADEIANSSGK	1.090700989	3	4.1532
Q62812	QIATLHAQVTDMK	0.707167431	2	2.36221
Q62812	QLEEAEEEAQR	1.324841813	2	3.49508
Q62812	QSVSNLEK	1.050968624	2	2.40169
Q62812	QTLENERGELANEVK	1.082457321	2	3.40491
Q62812	RGDMPFVVTR	1.054447258	2	2.63033
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.151810378	3	5.66457
Q62812	RQLEEAEEEAQR	1.158529272	2	4.2632
Q62812	SMEAEMIQLQEELAAAER	1.069104703	2	4.52412
Q62812	TDLLLEPYNK	1.236564841	2	2.68106
Q62812	TELEDTLDSTAAQQELR	0.846000934	2	5.48875
Q62812	THEAQIQEMR	1.140561158	2	3.47574
Q62812	TQLEELEDELQATEDAK	1.211772276	2	6.67947
Q62812	VAEFTTDLMEEEEK	1.315186455	2	4.222
Q62812	VEAQLQELQVK	1.111964434	2	3.67549
Q62812	VEDMAELTCLNEASVLHNLK	1.324162434	2	4.31749
Q62812	VISGVLQLGNIVFK	1.122469533	2	3.65389
Q62812	VSHLLGINVTDFTR	1.296805675	2	3.69235
Q62812	YEILTPNSIPK	1.049870182	2	3.24805
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.112869511**	**0.864335**	**8**
Q62826	ADILEDKDGK	1.016800761	2	2.67777
Q62826	AFITNIPFDVK	0.770180951	2	3.13633
Q62826	GIGMGNLGPAGMGMEGIGFGINK	1.162936395	2	4.88095
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.137627626	2	4.88984
Q62826	INEILSNALK	1.229178857	2	2.34599
Q62826	MGANNLERMGLERMGANSLER	0.924631215	2	2.40319

Q62826	MGPVMDRMATGLER+Oxidation(1)Oxidation(5)Oxidation(8)	0.991231757	2	2.57658
Q62826	VGSEIER	0.873569993	1	1.96376
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.214366385**	**0.136295**	**2**
Q62871	ADAEEEAATR	1.221634734	2	2.63024
Q62871	SVSTPSEAGSQDSGDGAVGSR	0.816363178	2	5.35132
Q62902	**LMAN1 Protein ERGIC_53**	**1.200564932**	**1.16E-12**	**5**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.181617965	2	4.28386
Q62902	GHPDLQGQPADDIFESIGDR	1.102534553	2	5.22151
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.571472653	3	4.13723
Q62902	YQEEFEHFQQELDK	1.270043832	2	5.12994
Q62902	YVSSLTEEISR	1.329124526	2	2.65161
Q62910	**SYNJ1 Synaptojanin_1**	**0.243229394**	**0.077296**	**2**
Q62910	MLIQLPSASQSK+Oxidation(1)	0.339157313	2	2.31642
Q62910	NQTLTDWLLDAPK	0.239642235	2	2.48953
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.97988915**	**0.999983**	**2**
Q62967	GLQVAPVLLSDELK	0.990213833	2	3.37021
Q62967	VYGVEGDLSEVAR	0.951498113	2	3.28714
Q63041	**A1M Alpha_1_macroglobulin**	**0.999790558**	**0.992165**	**13**
Q63041	AEDITHNGIVYTPK	0.960462889	2	3.35107
Q63041	AEQGAYLGPLPYK	0.980821071	2	3.04495
Q63041	DLSSSDLTTASK	0.708364112	2	2.51308
Q63041	DTVVKPVIVEPEGIEK	0.959546667	2	3.03229
Q63041	GSIFNSGSHVLPLEQGK	1.130443532	2	4.03633
Q63041	HSQGNTWLTAFVLK	1.020135251	2	2.35644
Q63041	IKEDGTGIELTGTGSCEIANTLSK	0.975985986	2	3.89411
Q63041	KLQDQSNIQR	1.076713087	2	2.47675
Q63041	LIVYTILPNEELIADVQK	1.402207934	2	4.53025
Q63041	LQDQSNIQR	0.887786982	2	2.79954
Q63041	QDLNDNDAYSVFQSIGLK	1.322689105	2	2.66362
Q63041	YNILPEAEGEAPFTLK	0.983219736	2	4.22737
Q63041	YVVLVPSELYAGVPEK	0.904672101	2	3.21272
Q63060	**GLPK Glycerol kinase**	**1.446832469**	**7.01E-09**	**11**
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.29257821	3	4.29988
Q63060	AVLGPLVGAVDQGTSSTR	1.127439232	2	5.48632
Q63060	CVFSEHGLLTTVAYK	1.385088406	2	4.27959
Q63060	DCGIPLSHLQVDGGMTSNK	1.553963396	2	4.20494
Q63060	EILQSVYECIEK	1.1960342	2	3.84936
Q63060	FEPQINAEESEIR	1.080160207	2	3.58185
Q63060	KVQEAVEENR	1.463941842	2	3.56052
Q63060	LGQLNIDISNIK	1.663963834	2	3.32731
Q63060	NTYGTGCFLLCNTGHK	1.327273834	2	3.93996
Q63060	TAELLSHHQVEIK	1.462971269	3	3.76969
Q63060	VQEAVEENR	1.154449421	2	3.37337
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**1.139378243**	**0.002265**	**10**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.353721201	3	6.05411
Q63081	GESPVDYDGGR	1.111609371	2	2.91693
Q63081	GSFSEQGINEFLR	1.086604081	2	4.10811
Q63081	GSTAPVGGGSFPNITPR	1.119325889	2	4.82685
Q63081	HQSLGGQYGVQGFPTIK	1.092772664	2	5.03094
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.799277192	3	5.39329
Q63081	NLEPEWAAAATEVK	1.037195399	2	4.19714
Q63081	NSYLEVLLK	1.096993683	2	2.98258
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.175856941	2	5.07342
Q63081	TGEAIVDAALSALR	1.060903049	3	4.71751
Q63108	**EST3 Liver carboxylesterase 3**	**1.040618233**	**0.043417**	**4**
Q63108	GGTSKEEINLSK	1.091420469	2	3.72701

Q63108	LDPMTATSLLK	0.900283891	2	2.44359
Q63108	QKTEEELLETTLK	0.979968267	2	3.44575
Q63108	SSFLLNLPEEAIPVAVEK	1.174147679	2	4.76672
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.299674574**	**0.041467**	**4**
Q63120	ACALLPDLEILPGGDMAEIGEK	1.176526229	2	4.24684
Q63120	NIQVQNMKNK	1.060370863	1	1.90164
Q63120	YFAWEPSFQEQVQGIR	1.342477939	2	4.45456
Q63120	YLGGDDLDTSAIR	0.542953416	2	2.5683
Q63150	**DPYS Dihydropyrimidinase**	**1.091044419**	**3.34E-10**	**9**
Q63150	ALGKDDFTK	1.144344506	2	2.64277
Q63150	DQTCTPIPVKR	1.013196389	2	2.49629
Q63150	EIGAIAQVHAENGDLIAEGAK	1.191147628	2	5.15317
Q63150	FVAVTSTNAAK	1.04509995	2	2.9791
Q63150	GSSLIEAFETWR	1.382931882	2	3.18403
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	1.021757013	3	3.71777
Q63150	VVNDDFSQVADVLVEDGVVR	1.428864442	2	5.93712
Q63150	VVYEAGVFDVTAGHGK	1.230779019	2	4.23502
Q63150	VVYGEPIAAGLGTDGTQYWNK	1.123679465	2	5.36651
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.070377073**	**2.22E-16**	**18**
Q63270	AVEAGLNVKPYVK	1.084767175	2	2.67434
Q63270	DFSDSSQDPDFTQVVELDLK	2.05206261	2	4.95407
Q63270	FVEFFGPGVAQLSIADR	1.830669396	2	5.33671
Q63270	GFQVAPDHHNDHK	1.299770599	2	3.44893
Q63270	IDFEKEPLGVNAQGQQVFLK	1.041908934	3	4.99404
Q63270	IIPPGSGIIHQVNLEYLAR	1.567212039	2	3.46688
Q63270	KNDIENILNWSIMQHK	1.161177125	3	4.08769
Q63270	NCDEFLVK	1.311828032	1	2.23932
Q63270	NDIENILNWSIMQHK	1.149924593	2	3.17456
Q63270	NQDLEFER	1.02688587	1	2.65835
Q63270	QAPQTVHLPSGETLDVFDAAER	0.987446709	3	3.65511
Q63270	SIEVPFKPAR	1.132809384	2	2.50058
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.444969421	3	4.96809
Q63270	SPPFFESLTLDLQPPK	1.120538298	3	3.59335
Q63270	SWNALAAPSEK	1.05930122	1	2.30064
Q63270	TSLSPGSGVVTYYLR	1.423628759	2	3.13569
Q63270	VILQDFTGVPAVVDFAAMR	1.643194277	2	4.65124
Q63270	YQQAGLPLIVLAGK	0.969212376	2	3.75712
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.025789484**	**0.118628**	**17**
Q63276	AHGHFLFVVGEDDKNLNSK	1.474132701	2	6.10148
Q63276	ASEVGEVDLER	0.95464642	2	3.94026
Q63276	DDKGNLFNSQAFYR	1.176253096	2	3.53085
Q63276	GNLFNSQAFYR	0.961925443	2	3.18833
Q63276	LCHPYFPVEGK	1.366554965	3	3.46631
Q63276	LTAVPLSALVDEPVHIR	2.930202007	2	3.87243
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	0.781539956	3	4.2309
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.151260839	2	4.64777
Q63276	QHLNPGFNSQL	1.195488981	2	3.52628
Q63276	QITATVLINGPNFVSSNPHVYR	1.022224313	3	4.94346
Q63276	TFEETADKDSK	0.849880424	2	3.75055
Q63276	VDLEYFEEGVEFLLR	1.141347015	2	4.40441
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.29052234	2	5.60354
Q63276	VISSSLDSLILER	1.262179607	2	4.40301
Q63276	VTGLTPFQVVCLQASLK	1.206274944	3	4.14586
Q63276	WYVAPGVTR	0.944258445	2	2.64707
Q63276	YCFPIEK	0.96059157	2	2.63184

Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**0.987692123**	**1**	**28**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.075829411	3	4.58571
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.085500102	3	4.58204
Q63342	DGLLFGPYESQEK	0.845286905	2	2.60613
Q63342	EGQESPPSPPEWK	0.851278972	2	2.49578
Q63342	ELFESDLDRITEHVEAAMEMVPVLK	1.072520626	3	4.64751
Q63342	GGYDVEIR	0.983068281	2	2.43576
Q63342	GQDSTQLLDHLCANVIPK	1.027194027	2	4.15152
Q63342	IHELFPLLNMDK	1.006272671	2	2.5913
Q63342	IHYDSIK	0.815492511	1	2.10464
Q63342	IMNAGQEEGIDNFGTYALNALR	0.922250513	2	4.84763
Q63342	ISDIPVTAIR	1.037892971	2	2.75728
Q63342	ITEHVEAAMEMVPVLK	0.832236821	2	4.02582
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.064452193	3	7.51488
Q63342	LEEETGQVVGFHQPGSIR	0.942630384	2	4.96647
Q63342	LNKPADFTGK	1.311359637	2	2.65562
Q63342	LTSEDLSDDVFK	1.006732728	2	3.83761
Q63342	LVCLTLATDDVDPEGNESVWYK	1.775253452	2	2.87227
Q63342	NITDELGVLGVAGPYAR	1.135928426	2	5.0044
Q63342	NYPATIIQEPLVLTEPTR	1.064657627	3	4.92776
Q63342	REDSAALYER	0.781739947	2	3.0355
Q63342	TNWHATEQYIIEPEK	0.960731119	2	4.16554
Q63342	VGFTNISHMLTPR	0.995091069	2	3.22311
Q63342	VGVIDLSPFGK	0.946968956	2	3.22758
Q63342	VIGNTTSGSYSYSIQK	0.98070681	2	4.54792
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.127943911	3	5.88108
Q63342	WIEEAAVR	1.063955551	2	2.60343
Q63342	WTTTQYTEAK	0.99188516	2	2.89812
Q63342	YLSDWILHGEPPFDLIELDPNR	1.179218292	3	4.70601
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.190634186**	**0.940462**	**8**
Q63347	ALDEGDIALLK	1.105308407	2	2.79319
Q63347	ESDTGLAPPALWDLAADK	0.965810826	2	2.47637
Q63347	FDDGAGGDNEVQR	1.103785344	2	4.21043
Q63347	FVVDLSDQVAPTDIEEGMR	0.928854757	2	3.37763
Q63347	IINADSEDPK	1.272899835	2	2.83582
Q63347	QTLQSEQPLQVAR	0.987441643	2	4.12984
Q63347	QVEDDIQQLLK	1.022133508	2	2.74523
Q63347	TMLELINQLDGFDPR	1.166524028	2	3.1821
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.088469739**	**0.401895**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.204518854	2	6.27248
Q63362	LENLLQGGEVEEVILQAEK	1.032404456	2	2.57621
Q63362	TTGLVGLAVCDTPHER	1.074081537	2	4.14911
Q63362	YTEQITSEK	1.345595938	1	2.14431
Q63377	**AT1B3 Sodium/potassium_transporting ATPase subunit beta_3**	**1.197701727**	**0.366387**	**2**
Q63377	EENIANIVTYPDDGLIDLK	1.195565529	2	4.44562
Q63377	LFIYNPTSGEFLGR	1.268337087	2	2.52184
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**0.953424788**	**0.972935**	**2**
Q63413	GLAITFVSDENDAK	1.044768312	2	2.77757
Q63413	NCPHIVVGTPGR	0.953386604	2	2.84334
Q63429	**UBC Polyubiquitin_C**	**1.073549407**	**0.99964**	**2**
Q63429	TITLEVEPSDTIENVK	1.090148044	2	4.81926
Q63429	TLSDYNIQK	1.064963205	2	2.85842
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.179551217**	**5.7E-05**	**12**
Q63448	ADWLDSEAPLAAYR	1.078245246	2	4.19765

Q63448	EIHALASAGKPLASWTAQR	1.101114496	2	4.54274
Q63448	FHEHTHSSSVPPSLR	0.946805521	2	2.73763
Q63448	GGYISGEQTGK	1.11152126	2	3.06133
Q63448	LGASLGSLSSGR	1.225869455	2	2.56484
Q63448	NLWAAVLQQSGVLER	1.17878425	2	4.01965
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.651407114	3	4.07205
Q63448	RDSVLWSDIPK	1.380573111	2	2.30129
Q63448	TIFLDLIELQR	1.823850061	2	3.55359
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.241211374	3	4.74619
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.203361611	3	4.77526
Q63448	TVNFLEAYPGILGQK	1.381402952	2	5.40154
Q63507	**RL14 60S ribosomal protein L14**	**1.726873185**	**3.95E-08**	**2**
Q63507	CMQLTDFILK	1.73371349	2	2.3912
Q63507	LVAIVDVIDQNR	1.536656383	2	4.49138
Q63520	**SYCP3 Synaptonemal complex protein 3**	**0.931269569**	**0.830941**	**2**
Q63520	KVMMETQQQEMANVR	0.931269569	2	2.68622
Q63520	VMMETQQQEMANVRK	0.931269569	2	2.54219
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.157630201**	**0.523747**	**3**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.128111643	3	4.96017
Q63524	HEQEYMEVR	1.295483812	2	3.39291
Q63524	HEQEYMEVR+Oxidation(6)	1.0114934	2	2.49631
Q63525	**NUDC Nuclear migration protein nudC**	**1.301963239**	**6.83E-05**	**4**
Q63525	GQAPVIDGELYNEVK	1.346683832	2	3.24092
Q63525	LSDLDSETR	1.043597146	2	2.32304
Q63525	LVTSDPEINTK	1.335792722	2	2.90033
Q63525	WTQTLSELDLAVPFR	1.043291961	2	2.61491
Q63556	**SPA3M Serine protease inhibitor A3M (Fragment)**	**1.292728419**	**0.341379**	**2**
Q63556	MQQVEASLQPETLK+Oxidation(1)	1.223550851	2	3.40679
Q63556	MQQVEASLQPETLKK+Oxidation(1)	1.311035645	2	2.81684
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.178630856**	**0.245856**	**7**
Q63569	AMEVDERPTEQYSDIGGLDK	1.022837943	3	4.71746
Q63569	CTDDFNGAQCK	1.459436753	2	3.48599
Q63569	DSYLILETLPTEYDSR	1.197397536	2	2.46691
Q63569	MATVWDEAEQDGIGEEVLK	1.007356465	2	3.19526
Q63569	MNVSPDVNYEELAR	1.100091159	2	3.37971
Q63569	QTYFLPVIGLVDAEK	1.143435113	2	2.42653
Q63569	TMLELLNQLDGFQPNTQVK	0.733560134	2	3.7142
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.025605139**	**0.201551**	**4**
Q63570	FDAQTGADR	0.964662051	2	2.51372
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.69139322	3	5.84851
Q63570	KDEQEHEFYK	0.942931895	2	3.0981
Q63570	RFDAQTGADR	1.025636265	2	2.65011
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.34196458**	**2.29E-11**	**4**
Q63584	ITDSAGHILYAK	1.347738148	2	3.67308
Q63584	LEDLSESIVNDFAYMK	1.372970455	2	4.58995
Q63584	NYEEIAK	1.141903181	1	2.17153
Q63584	RLEDLSESIVNDFAYMK	1.160419378	2	4.3022
Q63598	**PLST Plastin_3**	**1.180068351**	**0.081169**	**12**
Q63598	AESMLQQADK	1.109757716	2	3.14399
Q63598	ATDDIIVNWVNGTLSEAGK	1.126803526	2	5.04518
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	1.135810486	3	3.4888
Q63598	HVIPMNPNTDDLFK	1.066240679	2	3.01918
Q63598	IDINMSGFNETDDLKR	1.18466828	2	4.2491
Q63598	INNFSADIK	1.265348965	2	2.4944
Q63598	KLENCNYAVELGK	1.093554592	2	3.67427

Q63598	NEALAALLR	1.208324885	2	2.6013
Q63598	VDLNSNGFICDYELHELFK	1.247376229	2	4.11337
Q63598	VYALPEDLVEVKPK	1.146782354	2	2.74369
Q63598	YPALTKPENQDIDWTLLEGETR	0.936243043	3	5.23825
Q63598	YTLNVMEDLGEGQK	1.158212447	2	3.88188
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.102601102**	**0.240753**	**8**
Q63610	AREQAEAEVASLNR	1.482468594	2	2.89741
Q63610	EQAEAEVASLNR	1.013248476	2	2.5772
Q63610	IQVLQQQADDAEER	1.216782993	2	5.08659
Q63610	KIQVLQQQADDAEER	1.074089436	2	4.86434
Q63610	KLVIIEGDLER	1.042022071	3	3.84739
Q63610	LVIIEGDLER	1.013835005	2	2.7554
Q63610	MELQEIQLK	1.049842476	2	2.8502
Q63610	YSQKEDKYEEEIK	1.219290154	2	4.63917
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.234505595**	**7.64E-05**	**11**
Q63617	EGETPDEKESGDKSEAQKPNEK	1.424925688	3	3.54576
Q63617	GQAGPEGVPPAPEEEKK	0.819732188	2	3.5048
Q63617	LIPEMDQIFTDVEMTTLEK	1.228253951	2	4.67586
Q63617	LYQPEYQEVSTEEQR	1.199954046	2	4.93016
Q63617	NINADEAAAMGAVYQAAALSK	1.321853931	2	5.19487
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.179275763	2	3.86914
Q63617	TLGGLEMELR	1.181635996	2	2.59578
Q63617	VAIVKPGVPMEIVLNK	1.05175819	2	2.65795
Q63617	VEFEELCADLFDR	1.787403166	2	3.59044
Q63617	VESVFETLVEDSPEEESTLTK	1.055132544	2	3.814
Q63617	VLQLINDNTATALSYGVFR	1.422054717	2	5.27578
Q63716	**PRDX1 Peroxiredoxin_1**	**1.090924142**	**4.44E-16**	**15**
Q63716	ADEGISFR	1.077865998	2	3.15033
Q63716	ATAVMPDGQFK	1.104561977	2	2.85
Q63716	ATAVMPDGQFK+Oxidation(5)	1.249121986	2	2.33723
Q63716	DISLSDYK	0.964414712	1	1.93697
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.048372446	3	6.32962
Q63716	KQGGLGPMNIPLVSDPK	1.104013783	2	3.9838
Q63716	KQGGLGPMNIPLVSDPKR	1.064944809	3	4.04265
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.834717607	3	3.91788
Q63716	LVQAFQFTDK	2.543427821	2	3.37246
Q63716	QGGLGPMNIPLVSDPK	0.720144914	2	3.17191
Q63716	QGGLGPMNIPLVSDPK+Oxidation(7)	1.270033615	2	2.78335
Q63716	QITINDLPVGR	1.157600433	2	3.33904
Q63716	RTIAQDYGVLK	1.092513072	2	2.69778
Q63716	SVDEILR	1.099925735	2	2.48987
Q63716	TIAQDYGVLK	1.100896018	2	3.46053
Q63755	**PRDM2 PR domain zinc finger protein 2**	**0.762346848**	**0.258059**	**2**
Q63755	LSFNVELGKMSPNK	1.272184904	2	2.42309
Q63755	VKAAAATPFQGPFLKE	0.726127455	2	2.30196
Q63768	**CRK Adapter molecule crk**	**1.109904688**	**0.017862**	**2**
Q63768	IGDQEFDSLPALLEFYK	1.0227344	2	3.6277
Q63768	VPNAYDKTALALEVGELVK	1.452517783	2	2.90853
Q63797	**PSME1 Proteasome activator complex subunit 1**	**0.958482119**	**0.59173**	**8**
Q63797	ISELDAFLKEPALNEANLSNLK	0.936647056	2	5.26967
Q63797	KGDEDDKGPPCGPVNCNEK	0.917379289	3	5.03654
Q63797	KISELDAFLKEPALNEANLSNLK	1.119827779	3	6.28886
Q63797	LEGFQTQISK	1.117520158	2	2.62213
Q63797	QLVHELDEAEYQEIR	1.172843695	2	4.38577
Q63797	TENLLGSYFPK	1.063884069	2	3.33546
Q63797	VDVFREDLCSK	1.062743029	2	2.76591
Q63797	VFELMTSLHTK	0.962100219	2	2.52489

Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.185581646**	**0.030083**	**4**
Q63798	AFYAELHHIISSNLEK	1.123705462	2	3.72507
Q63798	IEDGNDFGVAIQEK	1.185780714	2	4.52676
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.631749813	2	4.52137
Q63798	TKVEAFQTAISK	0.961693738	2	3.44745
Q63836	**SBP2 Selenium_binding protein 2**	**0.905258598**	**0.236429**	**4**
Q63836	EGSVMLQVDVDTVNGGLK	0.949526661	2	2.56205
Q63836	GGSVQVLEDQELTCQPEPLVVK	0.935223264	2	5.19062
Q63836	IYVVDVGSEPR	0.793460548	2	3.77395
Q63836	LNPNFLVDFGKEPLGPALAHELR	0.939391027	3	4.19023
Q63862	**MYH11 Myosin_11 (Fragments)**	**1.193669189**	**0.51251**	**2**
Q63862	LQQELDDLVVDLDNQR	0.9493348	2	4.29203
Q63862	SLEAELMQLQEDLAAAER	1.193739903	2	2.92231
Q63945	**SET Protein SET**	**1.365670338**	**3.12E-05**	**2**
Q63945	IDFYFDENPYFENK	1.492517898	2	3.59469
Q63945	VEVTEFEDIK	1.135218751	2	2.6153
Q63965	**SFXN1 Sideroflexin_1**	**1.015271787**	**0.999956**	**4**
Q63965	NILLTNEQLENAR	0.999591032	2	4.50193
Q63965	QGIVPAGLTENELWR	1.009574571	2	2.69622
Q63965	WDQSTFIGR	1.082508801	2	2.36495
Q63965	YAYDSAFHPDTGEK	1.109812849	2	4.29827
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**1.131526788**	**2.21E-07**	**17**
Q64057	AWNIWADIPAPK	1.065907174	2	3.79783
Q64057	DYEETIGK	0.912621611	1	2.05589
Q64057	EDNEGVFNGSWGGR	0.802938443	2	3.48623
Q64057	FKNEEEVFEWNNEVK	1.128552367	2	5.80244
Q64057	GAPTTSLVSIAVTK	1.035823665	2	4.9187
Q64057	GEVITTYCPANNEPIAR	0.975229118	2	5.39925
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.914653172	2	5.85717
Q64057	LFLHESIHDEVVDR	1.319473259	2	3.96686
Q64057	NEEEVFEWNNEVK	0.884205527	2	4.56077
Q64057	QAVSMFVQAVEEAK	0.934900717	2	2.80875
Q64057	QGLSSSIFTK	1.058004629	2	2.37496
Q64057	QVALMVQER	1.033321972	2	2.42743
Q64057	STCTINYSTALPLAQGIK	1.655176597	2	4.96593
Q64057	VGNPWDPNILYGPLHTK	1.431580835	3	3.68468
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.00764355	3	6.06578
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(2)	1.133976701	3	6.03889
Q64057	VNLLSFTGSTQVGK	1.649237005	2	4.75102
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**0.927099163**	**0.624749**	**2**
Q640L5	NEKIRSLESNINTEHEK	0.92649315	2	2.37839
Q640L5	TELEKTTNSVKELER	1.153136765	2	2.33332
Q64119	**MYL6 Myosin light polypeptide 6**	**1.194887216**	**8.77E-15**	**7**
Q64119	DQGTYEDYVEGLR	0.797928497	2	3.21852
Q64119	EGNGTVMGAEIR	1.215834104	2	2.53006
Q64119	HVLVTLGEK	1.179987791	2	2.5633
Q64119	ILYSQCGDVMR	1.806312569	2	3.13966
Q64119	NKDQGTYEDYVEGLR	1.1723039	2	4.28274
Q64119	VFDKEGNGTVMGAEIR	1.37563337	2	3.97205
Q64119	VLDFEHFLPMLQTVAK	1.108040082	2	4.96608
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**1.481169635**	**6.28E-07**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.481197506	2	5.24888
Q64122	LNGTDPEDVIR	1.346048965	2	2.78411
Q64176	**EST22 Liver carboxylesterase 22**	**1.071253479**	**0.847076**	**4**
Q64176	AISESGVALTAGLVK	0.97923455	2	4.87588
Q64176	EGYLQIGATTQQAQK	0.92206192	2	4.29608

Q64176	LGIWGFFSTGDEHSR	1.505540379	2	3.13147
Q64176	NFNTVPYIVGINK	0.82666446	2	3.44473
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.325153981**	**0.000286**	**7**
Q641Y0	ELGSECGIEFDEEK	1.284306105	2	3.69434
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	1.570678586	4	5.12069
Q641Y0	NTLLIAGLQAR	1.167787338	2	3.79718
Q641Y0	TADDPSLSLIK	1.066133407	2	2.33634
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.271054969	3	6.1378
Q641Y0	TLVLLDNLNVR	1.152481443	2	3.93534
Q641Y0	WVPFDGDDIQLEFVR	1.585701299	2	3.33673
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.217171417**	**0.001529**	**5**
Q641Y2	GSGIQWDLR	1.190120346	2	2.71025
Q641Y2	IDEVEEMLTNNR	1.215956869	2	3.49956
Q641Y2	IIEQCLNK	1.460221863	2	2.89628
Q641Y2	LYTEGYQVPPGATYTAIEAPK	1.710641882	2	2.75665
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.200592659	2	4.24984
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.060899052**	**0.643501**	**3**
Q64232	HYEVEIR	0.875319876	2	2.32871
Q64232	LCFLDKVEPQATISEIK	1.184732652	2	4.5418
Q64232	SLKDEDVLQK	1.069057693	2	3.004
Q64240	**AMBP Protein AMBP**	**0.968781357**	**0.964126**	**3**
Q64240	AFAELWAFDAAQGK	1.262990611	2	2.77097
Q64240	AVLPQENEGSGSEPLITGTLK	0.938767936	2	4.79511
Q64240	TIAACNLPIVQGPCR	0.993787782	2	3.96866
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**0.878563878**	**3.36E-06**	**17**
Q64380	AIDSLSIEK	0.871430907	2	2.55526
Q64380	AYGIESHVLSPAETK	0.853509176	2	4.29303
Q64380	DGTMDPAGTCTTLTR	0.678166072	2	4.04702
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	1.191190383	3	5.02633
Q64380	DLYPLMNVDDLYGTLYVPR	1.172891832	2	3.49597
Q64380	FHHSLTDHPR	0.913708949	2	2.55454
Q64380	FYLLGADAR	0.928566191	2	2.54531
Q64380	HGLVNAGYR	0.856117593	2	2.35253
Q64380	IEGIQNMPNVR	0.848891619	2	2.83996
Q64380	LGVGGVVLLER	1.594289247	2	3.15175
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.948994957	2	4.28136
Q64380	NYSVVFPHDEPLAGR	0.865818727	2	3.87929
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.976770411	3	4.5125
Q64380	RDPLHEELLGQGCVFQER	0.945619922	3	5.26517
Q64380	SDDSPLEAGLAFTCK	0.797757555	2	4.65996
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.943372662	3	4.86508
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.86388327	3	5.11728
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.26769233**	**0.306128**	**25**
Q64428	ADMVIEAVFEDLAVK	1.013578579	3	4.75858
Q64428	ALMGLYNGQVLCK	0.897036113	2	3.27779
Q64428	DSIFSNLIGQLDYK	0.913141037	2	2.54023
Q64428	DTTASAVAVGLK	0.961415539	2	3.77173
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.892508235	3	6.84906
Q64428	EVQSEFVEVMNEIWANDQIR	1.080318222	3	3.3227
Q64428	FGELALTK	0.960562221	2	2.68671
Q64428	FGGGSVELLK	0.965687448	2	3.29621
Q64428	FVDLYGAQK	1.039318308	2	3.17823

Q64428	GFYIYQSGSK	1.287855981	2	3.0351
Q64428	ILQEGVDPK	0.980207224	2	3.15066
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	0.94742294	4	5.03726
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.2381174	2	4.28001
Q64428	KYESAYGTQFTPCQLLR	0.708533169	2	4.43325
Q64428	LPAKPEVSSDEDIQYR	1.235352232	3	3.84805
Q64428	MGLVDQLVDPLGPGIK	0.996337755	2	4.82547
Q64428	MGLVDQLVDPLGPGIK+Oxidation(1)	1.017454258	2	2.45139
Q64428	MQLLEIITTDK	0.994929817	2	4.02075
Q64428	MVGVPAAFDMMLTGR	0.990750518	2	3.236
Q64428	NLNSEIDNILVNLR	1.187256475	2	4.78831
Q64428	TGLEQGNDAGYLAESEK	0.912283122	2	5.13667
Q64428	TIEYLEEVAVNFAK	1.108561506	3	4.14897
Q64428	TVLGVPEVLLGILPGAGGTQR	0.972426233	3	5.0028
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.834038559	3	5.99101
Q64428	YESAYGTQFTPCQLLR	0.774153769	2	4.41325
Q64458	**CP2CT Cytochrome P450 2C29**	**0.985165236**	**9.33E-13**	**5**
Q64458	IKEHKESLDVTNPR	0.69871013	2	5.02222
Q64458	LPPGPTPLPIIGNFLQIDVK	1.472961902	3	4.37134
Q64458	VQEEAQCLVEELR	1.72506598	2	4.27546
Q64458	VQEEAQCLVEELRK	3.423111916	2	3.72657
Q64458	VQEEIDR	1.136308954	2	2.49553
Q64481	**CP3AG Cytochrome P450 3A16**	**1.03440943**	**0.965128**	**2**
Q64481	GSIDPYVYLPFGNGPR	0.930016695	2	3.94389
Q64481	VLQNFSFQPCK	1.302115136	2	2.60907
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**0.610950369**	**1.72E-11**	**4**
Q64550	GHEVVVIAPEASIHIK	0.592107707	2	4.66451
Q64550	NMIIALTENFLCR	0.924001199	2	4.65969
Q64550	SVFDQDPFLLR	0.8533145	2	3.4108
Q64550	VVYSPYGSLATEILQK	0.759736922	2	4.55075
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.362732654**	**0.066256**	**16**
Q64563	AAVDCTVVGWGSCTVVGAK	1.006340928	2	4.1815
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.038928869	3	5.84071
Q64563	ALGATDCLNPR	1.18229378	2	3.00825
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	1.113352785	3	5.56097
Q64563	FDLDLLVTHALPFDK	1.289063435	3	3.32062
Q64563	IIAIDINSEKFPK	1.022543602	2	2.65022
Q64563	INDAIDLMNQGK	1.279679467	2	4.34909
Q64563	KFDLDLLVTHALPFDK	1.350550509	3	5.69193
Q64563	KFDLDLLVTHALPFDKINDAIDLMNQGK	0.999380427	3	4.68295
Q64563	LCLSPLTNLCGK	1.759506322	2	2.31932
Q64563	SVDSVPNLVTDYK	1.236893111	2	3.2592
Q64563	TDSPLCIEEIEVSPPK	1.132891258	2	4.23241
Q64563	VCLIGCGFTSGYGAAINTAK	1.452003729	2	5.57483
Q64563	VDDEANLER	2.523468509	2	2.67538
Q64563	VDEMNISTVDMILGR	1.270716506	2	3.38787
Q64563	VIATCVCPTDINATNPK	1.384880922	2	4.22202
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**1.077635836**	**0.002749**	**15**
Q64565	AYSNHTDIISFR	1.132080097	2	3.35456
Q64565	GGNFSQTFR	0.928915527	2	2.4122
Q64565	GGVCIADEVQTGFGR	0.841301156	2	4.31466
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.07697394	2	3.19656
Q64565	GLMVGIEMVQDK	1.107685239	2	3.76253
Q64565	HNMPPCDFSPEK	0.833375145	2	3.32051
Q64565	LRDEFDIVGDVR	1.044708567	2	2.63533
Q64565	LSALLPEPLK	1.593660465	2	2.58472

Q64565	NSQEVGTYMLLK	1.187006544	2	2.37536
Q64565	SALTQHMER	1.07767837	2	2.71466
Q64565	TEVNQIHEDCK	0.824567177	2	3.26911
Q64565	TEVNQIHEDCKDMGLLVGR	0.779135308	2	5.22338
Q64565	VIFLVNSGSEANDLAMVMAR	1.268931986	2	5.691
Q64565	YIEQFK	0.990308969	1	2.05094
Q64565	YLDFFSGIVTVGVGHCHPK	0.938695012	2	2.78255
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**1.079234761**	**0.749501**	**4**
Q64578	DIVPGDIVEVAVGDKVPADIR	2.134966868	2	3.32976
Q64578	IGIFSENEEVADR	1.121628728	2	2.8996
Q64578	VGEATETALTTLVEK	0.995794547	2	4.03255
Q64578	YGPNELPAEEGK	1.014386201	2	2.54283
Q64581	**CP3AI Cytochrome P450 3A18**	**0.720758905**	**0.000275**	**3**
Q64581	KLQNEIDR	0.629683142	2	2.35801
Q64581	LAVIGVLQNFNIQPCEK	1.084222949	2	4.04989
Q64581	NPEYWLEPEEFNPER	0.548440335	2	4.24809
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.79668725**	**0.002109**	**9**
Q64591	ATAEEITSK	1.094223799	2	2.93847
Q64591	CDVRDPDMVHNTVLELIK	0.867228566	4	4.55172
Q64591	DPDMVHNTVLELIK	0.594781007	3	4.29253
Q64591	EEWDVIEGLIR	0.690556976	2	3.72404
Q64591	FFPPILKPMLPPNAFQGK	1.014446826	2	3.90599
Q64591	FNIIQPGPIK	0.7863246	2	3.11513
Q64591	NIDVLK	0.677844256	1	2.05703
Q64591	VAFITGGGTGLGK	1.009804829	2	2.91139
Q64591	VTKEEWDVIEGLIR	0.711441048	3	5.01698
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.036648211**	**0.992218**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.065942959	2	5.28833
Q64602	DIISLAPGSPNPK	1.035930742	2	3.07953
Q64602	EILLVPGNSFFVDNSAPSSFFR	0.90385007	2	2.32145
Q64602	FLYTIPNGNNPTGNSLTGDR	1.095855194	2	4.14295
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.142938216	3	6.37397
Q64602	SAVFTVENGSTIR	0.958923209	2	3.86083
Q64602	VLSQWKPEDSKDPTKR	3.071538956	3	3.946
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.073882064**	**0.786997**	**11**
Q64611	AQGGQGLEWR	1.19798501	2	3.03095
Q64611	CHGSQASYLFQQDK	1.419959336	2	5.26131
Q64611	FFNQLFSGLDPHALAGR	1.097079945	2	4.70159
Q64611	FYNVALDTGDK	1.145863924	2	3.08874
Q64611	GAAFLGLGTDSVR	1.159685522	2	3.44897
Q64611	IDQAFALTR	1.064361155	2	3.1894
Q64611	LLAAGLQCSALLLR	2.433187772	2	3.30395
Q64611	QLLDLELQSQGESR	0.92685328	2	4.09417
Q64611	TLDGDPVAVEALLR	1.036631042	2	5.03921
Q64611	VCEWKEPEELK	1.035547859	3	3.80184
Q64611	YLVEEIK	1.007480971	1	2.29702
Q64633	**UD17 UDP_glucuronosyltransferase 1_7**	**0.645455775**	**0.18862**	**2**
Q64633	QSSFDAVFLDPFDVCGLTVAK	0.897182666	2	2.38349
Q64633	TYSVSHTQEDLNR	0.613042904	2	3.27238
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**2.262849008**	**0.222239**	**2**
Q64638	TFLETSEILK	2.350808308	2	2.40635
Q64638	VVFETGNYVK	0.787846246	1	1.9622
Q64640	**ADK Adenosine kinase**	**0.896233019**	**0.000193**	**11**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.305958338	3	7.14884
Q64640	AATFFGCIGIDK	0.802933127	2	3.08279

Q64640	AGHYAASVIIR	1.104588892	3	3.32216
Q64640	FGEILK	1.09759978	2	2.38353
Q64640	FKVEYHAGGSTQNSMK	1.071676099	3	3.44435
Q64640	HKELFDELVK	0.90021917	2	2.75071
Q64640	HLDLENNWMLVEK	1.362832128	2	3.59592
Q64640	SLVANLAAANCYK	1.14464245	2	4.35412
Q64640	VEYHAGGSTQNSMK	0.909806597	2	3.81909
Q64640	VEYHAGGSTQNSMK+Oxidation(13)	0.925110288	2	3.61826
Q64640	YSLKPNDQILAEDK	1.205336917	3	4.23429
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.935209795**	**0.999625**	**8**
Q64654	EPAEDILQTLLDSTYK	1.085359702	2	3.46768
Q64654	GVAYDVPNAVFLEQK	1.094435019	2	4.03403
Q64654	NEDLNAEEVYGR	0.927804004	2	3.82225
Q64654	SGLNIAHFK	0.709081428	2	2.8667
Q64654	TFTYLLGSDAAALLFNSK	0.956902609	2	2.9327
Q64654	TVCGEDLPPLTYEQLK	0.769528856	2	4.12636
Q64654	YGPVFSFTMVGK	0.818658055	2	2.72998
Q64654	YLQDNPASGEK	0.829129042	2	2.84735
Q64737	**PUR2 Trifunctional purine biosynthetic protein adenosine_3**	**1.267761086**	**0.115635**	**2**
Q64737	DSGVDIAAGNMLVKK+Oxidation(11)	1.461736457	2	2.30757
Q64737	FGDPECQVILPLLK	1.219311704	2	2.45315
Q65CL1	**CTNA3 Catenin alpha_3**	**1.224558309**	**0.173473**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(1)	1.667262441	2	2.60014
Q65CL1	NLMNAVVQTVK	1.184267221	2	3.15576
Q65Z40	**WAPL Wings apart_like protein homolog**	**1.168816964**	**0.034009**	**3**
Q65Z40	EKSISRIPEDNANK	1.106677321	2	2.67828
Q65Z40	LGQKRPNFKPDIQEIPK	1.346747621	2	2.9131
Q65Z40	TESPSESCPVKGSVR	1.029185007	2	2.52443
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.156681893**	**0.454305**	**3**
Q66H12	CNINCEEDPK	0.58342634	2	2.40185
Q66H12	INQDPLGIQGR	1.082088734	2	2.45129
Q66H12	TISPQNIDILQNPLLIK	1.171887469	2	3.88138
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**1.097575326**	**0.872223**	**2**
Q66H15	AIPGEAGDAAMLSSLPQEGQEK	1.15148846	2	4.19845
Q66H15	AYSDMTELTEEESEKK	1.097135379	2	2.53358
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**1.063839969**	**0.806661**	**2**
Q66H45	LQGDVAGALEDLER	1.033255334	2	3.65898
Q66H45	RDFEQAAR	0.901114394	2	2.30456
Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**1.209868167**	**0.022722**	**2**
Q66H71	LTEQAVEAINK	1.20986793	2	3.69101
Q66H71	SIDEDDDYFNLTK	1.467157536	2	2.83518
Q66H80	**COPD Coatomer subunit delta**	**1.143351464**	**0.00013**	**5**
Q66H80	GVQLQTHPNVDKK	1.143391504	2	3.16658
Q66H80	LFTAESLIGLK	1.440021772	2	2.90407
Q66H80	NSNILEDLETLR	1.283754045	2	2.90668
Q66H80	NTLEWCLPVIDAK	1.066421836	2	3.29903
Q66H80	VAPAPARPSGPSK	1.121344051	2	2.49859
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.059915783**	**0.986254**	**5**
Q66HA8	AGGIETIANEFSDR	1.022200328	2	2.84213
Q66HA8	FVVQNVSAQK	1.024029977	2	2.68389
Q66HA8	LKETAENNLK	1.197125624	2	2.39828
Q66HA8	NQQITHANNTVSSFK	1.078416682	2	4.48275
Q66HA8	SVLDAAQIVGLNCLR	1.077500933	2	2.71907
Q66HD0	**ENPL Endoplasmin**	**1.135074184**	**9.9E-20**	**32**

Q66HD0	DISTNYYASQK	2.228775759	2	3.0676
Q66HD0	EATEKEFEPLLNWMK	1.140824117	2	3.13851
Q66HD0	EEASDYLELDTIK	1.169813257	2	4.28092
Q66HD0	EEEAIQLDGLNASQIR	1.344150011	2	4.54701
Q66HD0	EFEPLLNWMK	1.312385516	2	2.31512
Q66HD0	EVEEDEYK	1.053260923	1	2.38898
Q66HD0	FQSSHHSTDITSLDQYVER	1.197422081	3	6.20579
Q66HD0	GLFDEYGSK	1.105533449	2	2.3448
Q66HD0	GVVDSDDLPLNVSR	1.067018809	2	4.81291
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGK	1.707635422	2	3.72106
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	2.416418822	3	4.02401
Q66HD0	KEAESSPFVER	1.104567503	2	3.60572
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	2.459263275	3	4.41953
Q66HD0	LGVIEDHSNR	1.273955905	2	3.33103
Q66HD0	LIINSLYK	1.562988864	2	2.42603
Q66HD0	LISLTDENALAGNEELTVK	1.452517783	2	5.85154
Q66HD0	LTESPCALVASQYGWSGNMER	1.079837336	2	5.56655
Q66HD0	MKEKQDK	0.963227493	2	2.3302
Q66HD0	NLLHVTDTGVGMTR	1.197556245	3	4.03424
Q66HD0	NLLHVTDTGVGMTR+Oxidation(12)	1.28151323	2	2.98762
Q66HD0	RVFITDDFHDMMPK	1.195833705	3	3.33555
Q66HD0	SGTSEFLNK	1.175950457	2	3.10226
Q66HD0	SGYLLPDTK	1.08955093	2	3.16932
Q66HD0	SILFVPTSAPR	1.080824571	2	3.47421
Q66HD0	TDDEVVQR	1.016042051	2	2.94708
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	1.112143118	3	5.35128
Q66HD0	TETVEEPLEEDETAQEEK	0.715523872	2	5.18552
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	0.459653995	5	6.45001
Q66HD0	TFEINPR	1.106583886	2	2.72526
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.296404283	3	4.0271
Q66HD0	VFITDDFHDMMPK	1.019659472	2	4.02559
Q66HD0	YNDTFWK	1.11509685	1	2.19324
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.198276039**	**4.13E-05**	**12**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.353873308	2	3.97914
Q66HF1	DCFIVYQGHHGDVGAPIADVILPGAAYTEK	1.283979189	3	4.19905
Q66HF1	DDGAAILAAVSSIAQK	1.192855156	2	4.33777
Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	1.207265438	3	4.51977
Q66HF1	FASEIAGVDDLGTTGR	1.418831564	2	3.47735
Q66HF1	GLLTYTSWEDALSR	1.155125262	2	3.38385
Q66HF1	GWNILTNSEK	1.281430136	1	2.14628
Q66HF1	ILQDIASGNHEFSK	1.253221091	2	4.15575
Q66HF1	LGEVSPNLVR	1.218368549	2	3.16047
Q66HF1	LVDQEFLADPLVPPQLTIK	1.160475925	2	3.28564
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.878316845	2	4.63769
Q66HF1	YDHLGDSPK	1.122354026	2	2.55566
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.182951471**	**9.9E-20**	**11**
Q66HF8	ADVDLAVR	0.911252761	2	2.35765
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	1.37616016	3	3.854
Q66HF8	EEIFGPVQPLFK	0.957442688	2	3.21924
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.521974934	3	4.50441
Q66HF8	LAPALATGNTVVMK	1.543909633	2	3.2874
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.284418695	2	4.63639
Q66HF8	TFVEESIYHEFLER	1.187908744	2	3.81673
Q66HF8	VAEQTPLSALYLASLIK	1.898317047	2	3.17824
Q66HF8	VGNPFELDTQQGPQVDK	1.163619859	2	3.04173
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.495456102	2	4.47183

Q66HF8	YGLAAAVFTR	1.118047822	2	3.8565
Q66HG4	**GALM Aldose 1_epimerase**	**0.89787147**	**0.000597**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	1.002028075	2	4.70677
Q66HG4	TVFGELPSGGGAVEK	0.898317446	2	3.66841
Q66HG4	VSPDGEEGYPGELK	0.865519246	2	3.78502
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.032161827**	**0.001224**	**21**
Q66X93	ADDADEFGYSR	1.346105417	2	2.78396
Q66X93	ALLLPDHYLVTVMLSGIK	0.911131673	2	3.32896
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.473043588	3	5.5625
Q66X93	DTNGENIAESLVAEGLASR	0.989155269	2	5.02366
Q66X93	ETDGSETPEPFAAEAK	1.298999391	2	3.69383
Q66X93	FVDGEWYR	1.137539664	2	2.3191
Q66X93	GDVGLGLVK	1.110414549	2	2.70777
Q66X93	HFVDSHHQKPVNAIIEHVR	1.093815757	3	4.8688
Q66X93	LEGDNIQDK	1.136390142	2	2.70892
Q66X93	LSECEEQAK	2.117961589	2	2.60734
Q66X93	MVLSGCAIIVR	1.047381403	2	2.37148
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.154917572	2	5.4278
Q66X93	SAYYKPLLSAEEAAK	1.197840027	2	2.52288
Q66X93	SDISSHPPVEGAYAPR	1.011235327	3	4.61381
Q66X93	SSHYDELLAAEAR	1.19725499	2	3.74548
Q66X93	TCATVTIGGINIAEALVSK	1.17031249	2	3.9263
Q66X93	TDAVDSVVR	1.098297439	2	2.6558
Q66X93	VITEYLNAQESAK	1.51764491	2	3.78605
Q66X93	VMQVLNADAIVVK	1.387131948	2	3.98234
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.092251128	3	5.06376
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.903403877	3	4.57779
Q67FY2	**BCL9L B_cell CLL/lymphoma 9_like protein**	**0.743075126**	**0.027143**	**2**
Q67FY2	EAGTPSLDSEAKEVAPR	1.835169663	2	2.45155
Q67FY2	NLVGSEGLSKEQLEHRER	0.64557721	2	2.35388
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**1.128212762**	**1.12E-10**	**8**
Q68FP2	HNNWDLTPVK	0.986071989	2	3.30807
Q68FP2	IFLMDLNEPYPK	1.210692983	2	3.0599
Q68FP2	IQDPLSDNPR	1.03906167	2	2.87889
Q68FP2	LLIYNPEDPPGSEVLR	1.446858621	2	4.30688
Q68FP2	LVALTVLGASLALLGER	1.050469674	3	4.01535
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.238067055	2	4.95435
Q68FP2	VVAQGFSSANGITVSLDQK	0.975865022	2	4.17667
Q68FP2	YVYVADVTAK	1.106458008	1	2.89207
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.133686644**	**4.28E-06**	**5**
Q68FQ0	ETGANLAICQWGFDDEANHLLLQNGLPAVR	0.953654687	3	3.70901
Q68FQ0	GSNDMQYQHVIETLIGK	0.838159793	2	3.55981
Q68FQ0	HKLDVTSVEDYK	1.042763637	2	3.15753
Q68FQ0	SLHDALCVIR	1.334826046	2	2.99006
Q68FQ0	WVGGPEIELIAIATGGR	1.645975957	2	3.88525
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.142857387**	**1.25E-06**	**8**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.081146901	2	5.33845
Q68FR6	ALIAAQYSGAQIR	1.089630416	2	4.23001
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	2.193656763	2	3.76303
Q68FR6	ILGLLDTHLK	1.626379202	2	2.64118
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.161888143	2	4.26509
Q68FR6	KLDPGSEETQTLVR	1.173743435	2	3.91244
Q68FR6	LDPGSEETQTLVR	0.962619772	2	2.93884
Q68FR6	STFVLDEFKR	1.047663043	2	2.712
Q68FR9	**EF1D Elongation factor 1_delta**	**1.12703827**	**1.98E-06**	**6**
Q68FR9	ATAPQTQHVSPMR	1.056244719	2	3.05547

Q68FR9	FYEQMNGPVTAGSR	1.017513483	2	4.21964
Q68FR9	GVVQDLQQAISK	1.17167155	2	3.42603
Q68FR9	SIQLDGLVWGASK	1.028004158	2	2.7883
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.219862542	2	5.31664
Q68FR9	SSILLDVKPWDDETDMAQLETCVR	1.32155892	3	3.34009
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.060303318**	**1.45E-13**	**18**
Q68FS4	ADMGGAATICSAIVSAAK	1.068336417	2	5.38822
Q68FS4	DKDDDVPQFTSAGENFNK	0.993270715	2	5.0991
Q68FS4	GITFDSGGISIK	1.075927704	2	3.24256
Q68FS4	GLVLGIYSK	1.01428413	1	2.03481
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.981814412	3	5.98961
Q68FS4	GVLFASGQNLAR	1.339802043	2	3.61575
Q68FS4	LFEASVETGDR	1.116278256	2	3.50531
Q68FS4	LHGSGDLEAWEK	1.347078225	2	3.57463
Q68FS4	LNLPINIIGLAPLCENMPSGK	2.357138971	2	4.82862
Q68FS4	QLMESPANEMTPTR	0.980911849	2	3.38778
Q68FS4	QVIDCQLADVNNLGK	1.100637996	2	4.93342
Q68FS4	SAGACTAAAFLR	1.401405904	2	3.69069
Q68FS4	SAGVDDQENWHEGK	1.036766913	2	3.92773
Q68FS4	SWIEEQEMGSFLSVAK	1.327727153	2	5.50891
Q68FS4	TFYGLHQDFPSVVVVGLGK	0.985564158	2	4.90294
Q68FS4	TIQVDNTDAEGR	1.007545091	2	4.19492
Q68FS4	TLIEFLLR	1.139358251	2	2.69652
Q68FS4	WAHLDIAGVMTNKDEIPYLR	1.200348783	3	3.45658
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.147018345**	**0.001555**	**3**
Q68FT1	INDAMNMGHTAK+Oxidation(5)Oxidation(7)	1.354389235	2	2.79564
Q68FT1	LNHVLEEEQK	1.147585661	3	3.33539
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.936095244	3	4.67617
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**1.064516053**	**0.994661**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	1.036649721	2	3.65136
Q68FT3	ISQLDTQSPVTK	1.126826039	2	3.54838
Q68FT3	SLLLGTDVAENQK	0.963499439	2	2.88343
Q68FT3	TLGAQLPQYYEVLTAPISK	1.349448259	2	4.77135
Q68FT3	VFDCIEAYAPGFK	0.864178017	2	2.33233
Q68FT3	VLDQWFESEPLK	1.05883049	2	3.20256
Q68FT3	VQGVVLQGGEEVR	1.03314845	2	3.37083
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.215588794**	**7.11E-11**	**11**
Q68FT5	AGADVLQTFTFSAAEDR	2.125432931	2	3.84324
Q68FT5	AGANIIGVNCR	1.257029176	2	3.22084
Q68FT5	AGLWTPEAVVEYPSAVR	1.131083413	3	3.75279
Q68FT5	AIAEELAPER	1.224186994	2	3.81642
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.107755787	3	4.68161
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.29335714	2	3.89958
Q68FT5	FGPWTSLQTMK	0.951941299	2	3.08842
Q68FT5	GGFVDLPEYPFGLEPR	1.215882309	2	4.0726
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.227838133	2	5.36092
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	2.202037531	3	3.47218
Q68FT5	YIGGCCGFEPYHIR	2.601755052	2	4.62477
Q68FT9	**SCLY Selenocysteine lyase**	**0.995641362**	**5.6E-05**	**5**
Q68FT9	AEVDLIVQDLK	1.001490579	2	3.72334
Q68FT9	CFHEQQTLQGR	1.130775087	2	2.7595
Q68FT9	RVDVEDLGVDFLTIVGHK	1.933709823	3	5.92553
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	1.15099637	3	3.61384
Q68FT9	VLVHTDAAQALGK	0.967730015	2	3.03696

Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.990572692**	**0.666626**	**12**
Q68FU3	AGDLGVDLTSK	0.961530504	2	3.72701
Q68FU3	EIIAVSCGPPQCQETIR	0.993958743	2	4.86182
Q68FU3	GIHVEVPGAEAENLGPLQVAR	0.612697713	2	5.73982
Q68FU3	HSMNPFCEIAVEEAVR	1.055047167	2	5.69442
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(3)	1.255211844	2	4.28979
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	1.045985992	3	6.30781
Q68FU3	RVIDFAVK	1.098896879	2	2.38276
Q68FU3	SGVVTDGVK	0.914742882	2	2.88864
Q68FU3	VDLLFLGK	1.177745383	2	2.98201
Q68FU3	VETTEDLVAK	0.901694582	2	3.33574
Q68FU3	VIDFAVK	0.962287666	2	2.35314
Q68FU3	VSVISVEEPPQR	0.968081519	3	3.41222
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.15353752**	**0.999691**	**9**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.042081298	3	5.88093
Q68FY0	IEEVDAQMVR	0.959821525	2	3.68747
Q68FY0	LCTSATESEVTR	1.126610529	2	3.17305
Q68FY0	NALISHLDGTTPVCEDIGR	1.093047149	2	4.70271
Q68FY0	NNGAGYFLEHLAFK	1.138837404	2	3.42525
Q68FY0	RIPLAEWESR	1.094128519	2	2.78093
Q68FY0	TDLTDYLSR	1.107767366	2	2.6651
Q68FY0	VVELLADIVQNISLEDSQIEK	1.075461094	3	5.73479
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.181194769	2	5.11664
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**1.324782939**	**0.22661**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.946901056	2	4.6822
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	0.822849462	3	3.69798
Q68G31	GESGGQTTPYDFYSR	1.255507873	2	4.27822
Q68G31	LQPTDSFSQSSCFGLR	0.962240077	2	3.48853
Q68G31	NVNSTLTFVTLSGELK	1.060629042	2	3.7908
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.109194655	3	5.73998
Q68G31	VNTEPLPGIEK	0.908129321	2	3.03141
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.685513138**	**0.031803**	**2**
Q69Z23	GDPTRAEDQVLMRALR	1.688146377	2	2.33209
Q69Z23	YFIDLLMEK	1.390867616	1	2.15303
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.082047342**	**0.05887**	**2**
Q6A0A9	SQGGVQPIPSQGGK	1.19265329	2	3.14161
Q6A0A9	VEGSSTASSGSQLAEGK	1.07359686	2	4.29981
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.212252038**	**0.810262**	**4**
Q6AXM8	FQEEENSLLHLK	1.120312321	2	3.43416
Q6AXM8	LFVYDPNHPPSSEVLR	1.187187451	2	2.50171
Q6AXM8	LVAEGFDSANGINISPDKK	0.98757699	2	3.6571
Q6AXM8	VLQLGTLVDNLSIDPSSGDIWVGCHPNGQK	1.348461596	3	4.42927
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.990200403**	**0.816599**	**3**
Q6AXS5	EETQPPVALKK	0.975360648	2	2.74207
Q6AXS5	FDQLFDDESDPFEVLK	1.207121146	2	5.20506
Q6AXS5	SAAQAAAQTNSNAAGK	0.953943038	2	5.09851
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.984600653**	**0.746686**	**2**
Q6AXY0	FLQPGSQR	0.876159064	2	2.51271
Q6AXY0	YFPAFEK	1.070245365	1	1.91107
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**0.943297937**	**0.351562**	**5**
Q6AY09	ATENDIYNFFSPLNPMR	1.324499871	2	4.01809
Q6AY09	GLPWSCSAEEVMR	1.036506304	2	3.10273

Q6AY09	HTGPNSPDTANDGFVR	0.927249979	2	4.19408
Q6AY09	STGEAFVQFASQEIAEK	1.818049715	2	4.29085
Q6AY09	STGEAFVQFASQEIAEKALKK	0.917193968	2	2.54601
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**0.90971946**	**0.884165**	**2**
Q6AY20	HTLAGNFNPVSEER	0.904461151	2	4.30022
Q6AY20	SCDLVGEKDKESK	1.055095644	2	3.72064
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.049073125**	**0.33886**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.374974458	3	5.31295
Q6AY30	ATLVLNCVGPYR	1.041928803	2	2.56127
Q6AY30	GGGVFTPGAAFSR	0.877711634	2	2.36426
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.119280424	2	3.25374
Q6AY30	LQQVLEK	1.181637585	1	2.06796
Q6AY30	SVSNLKPVPVIGSK	0.934164161	2	3.61388
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.137287934**	**9.9E-20**	**9**
Q6AY56	AFVHWYVGEGMEEGEFSEAR	1.595366195	2	4.60202
Q6AY56	AVCMLSNTTAIAEAWAR	1.150271639	2	4.62518
Q6AY56	EDAANNYAR	0.997011704	1	2.07345
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.155588068	2	5.41057
Q6AY56	LISQIVSSITASLR	1.699078584	2	3.66662
Q6AY56	NLDIERPTYTNLNR	1.228738573	2	3.58131
Q6AY56	QLFHPEQLITGK	1.288764761	2	2.85151
Q6AY56	TIQFVDWCPTGFK	1.30126118	2	3.88179
Q6AY56	VGINYQPPTVVPGGDLAK	1.135028322	2	4.84352
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**1.124339045**	**0.387277**	**2**
Q6AY80	NDVTGALSNPEVFK	1.10387346	2	3.41516
Q6AY80	VLAPQISFGPEVSSEEQR	0.924182996	2	3.37897
Q6AYH5	**DCTN2 Dynactin subunit 2**	**1.471793156**	**0.038289**	**3**
Q6AYH5	ASVEDADTQNK	1.521265332	2	3.22234
Q6AYH5	LLGPDAAINLADPDGALAK	1.816692162	2	2.92557
Q6AYH5	WSPVASTLPELVQR	1.232754664	2	2.57043
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.908281496**	**0.997567**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	0.907204982	2	4.39808
Q6AYQ8	NLHHEVELGVLLGR	0.91890911	3	4.43868
Q6AYQ8	SFTSSCPVSAFVPK	0.942997944	2	4.08594
Q6AYR8	**SCRN2 Secernin_2**	**1.134836232**	**0.567716**	**3**
Q6AYR8	GHQAALGLMDEQEQAQLR	1.1083716	2	3.87286
Q6AYR8	QEQQSLEQEGLEALR	1.244350201	2	4.02417
Q6AYR8	TTASMVSVLPQDPTKPCVHFLTATPDPSR	1.488232984	3	3.57176
Q6AYS7	**ACY1A Aminoacylase_1A**	**2.079495186**	**0.000326**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	1.125278033	2	3.45931
Q6AYS7	ICTVQPNPDYGSAVTFLEER	2.256309428	2	4.42598
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.983311722**	**0.916643**	**3**
Q6AYS8	ALTDELAALGCTGVR	0.789401246	2	2.36128
Q6AYS8	NPSTNLGPTLEPEEVVEHLMHGILTNQK	1.069246207	3	3.66436
Q6AYS8	SVAGEIVLITGAGHGIGR	0.95827391	2	4.27673
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**1.038013804**	**0.999987**	**3**
Q6AYT9	AFIVLSPAYVSHDPEALTR	1.103947491	2	4.69183
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.965816656	2	3.37848
Q6AYT9	NDDVINSSSYR	1.001350894	2	3.3059
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.387095251**	**9.9E-20**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	0.881793072	2	5.30174
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	1.056608282	3	4.25554
Q6AYZ1	DVNAAIATIK	1.104848809	2	3.29598
Q6AYZ1	IHFPLATYAPVISAEK	1.425793797	2	3.90109

Q6AYZ1	TIGGGDDSFNTFFSETGAGK	2.451827541	2	5.56145
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.166168732	2	4.752
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**0.962941296**	**0.95583**	**7**
Q6DGG1	AVAIDLPGLGR	1.002768917	2	3.47876
Q6DGG1	FSSETWQNLGTLHR	1.184630728	2	3.57171
Q6DGG1	FSVLLLHGIR	1.064462707	2	3.01433
Q6DGG1	GYVPVAPICTDK	0.959279098	2	2.54214
Q6DGG1	INAADYAR	1.059004439	2	2.4013
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.008876741	2	4.96604
Q6DGG1	VLVMEGAGHPCYLDKPDEWHTGLLDFLQELA	1.383854785	3	3.89168
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.998416365**	**0.806131**	**2**
Q6EDY6	ELMESIK+Oxidation(3)	0.99770099	1	2.19212
Q6EDY6	IENYLLR	1.15866191	2	2.50396
Q6GQT9	**NOMO1 Nodal modulator 1**	**1.17421398**	**0.61297**	**2**
Q6GQT9	SSIDSEPALVLGPLK	1.140647501	2	2.69781
Q6GQT9	VQVVVPEAETR	1.127477368	2	2.84382
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**0.966246854**	**0.014739**	**2**
Q6I7R3	GLGSTVQEIDLTGVK	0.940201559	2	3.85579
Q6I7R3	ILGIPVIITEQYPK	1.449758082	2	3.27251
Q6IE52	**MUG2 Murinoglobulin_2**	**1.122792256**	**0.708017**	**13**
Q6IE52	AHFSVMGDILSSAIK	1.006579205	2	3.64351
Q6IE52	HGIPFFVK	1.710416761	2	2.81411
Q6IE52	HTSSWLVTPK	1.01101333	2	2.62551
Q6IE52	LPSSEEEESLDINIEGAK	1.151605201	2	5.40219
Q6IE52	MLIYTILPDGEVIADSVK	1.142873671	2	4.31631
Q6IE52	MLSGFIPLKPTVK	0.984731877	2	2.85549
Q6IE52	NLYPLKELVQDPK	1.032487309	1	2.14943
Q6IE52	QLSFSLSAEPIQGPYK	1.043862409	2	4.32059
Q6IE52	VHLSFSPSQSLPASQTHMR	1.021276366	3	3.55956
Q6IE52	VKTVPLTCNNPK	1.036803523	2	2.77076
Q6IE52	VLIVEPEGIKK	1.068088278	2	2.37251
Q6IE52	VTASPQSLCGLR	1.237187349	2	2.59525
Q6IE52	YMVLVPSQLYTETPEK	0.989073984	2	4.06017
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.062406693**	**0.039886**	**2**
Q6IFX1	**K1C24 Keratin_ type I cytoskeletal 24**	**1.103799004**	**0.301175**	**2**
Q6IFX1	LLNDMR	0.822415995	1	1.9204
Q6IFX1	QEAEKQFNER	1.104567503	2	2.56289
Q6IG00	**K2C4 Keratin_ type II cytoskeletal 4**	**1.116941548**	**0.762148**	**3**
Q6IG00	LMQDSVEDFK+Oxidation(2)	1.122193678	1	2.07506
Q6IG00	NLDLDGIIAEVR	1.00E+00	2	3.26766
Q6IG00	WNLLQQQTTTTSPR	2.895853372	2	4.36292
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**0.922188944**	**1**	**4**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.839888055	3	5.61614
Q6IRK9	IVVYNQPYTDYGK	1.010016639	2	2.40676
Q6IRK9	TYPDTDSFNTVAEITGSK	0.929066603	2	4.46419
Q6IRK9	VGAVASLIR	0.978097803	2	2.45549
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.960732153**	**0.997466**	**4**
Q6MGB5	AGVIGLTQTAAR	0.948157996	2	3.02583
Q6MGB5	GSIINISSIVGK	1.314795611	2	2.79226
Q6MGB5	LAAEGAAVAACDLDGAAAQDTVR	0.978945164	2	3.85238
Q6MGB5	VGNIGQTNYASSK	1.120258842	2	2.85543
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.025730791**	**0.438726**	**2**
Q6NSR8	HNSPSAAHFITR	1.071121	3	4.13622
Q6NSR8	TVEINNTDAEGR	0.997316589	2	3.02421

Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.269876936**	**0.165437**	**4**
Q6NYB7	EFADSLGIPFLETSAK	1.312179069	2	3.03324
Q6NYB7	MGPGATAGGAEK	1.017340687	2	3.54527
Q6NYB7	MGPGATAGGAEK+Oxidation(1)	1.261769849	2	2.44288
Q6NYB7	NATNVEQSFMTMAAEIK	1.298100202	2	4.54432
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.061965632**	**0.711851**	**6**
Q6NZJ6	GLPLVDDGGWNTVPISK	1.034784361	2	3.38518
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.048240381	3	3.35686
Q6NZJ6	IHNAENIQPGEQK	1.027137945	2	4.04524
Q6NZJ6	KVEYTLGEESEAPGQR	0.944411241	2	4.60225
Q6NZJ6	LKEELEEAR	1.086734614	2	2.67297
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	1.057112449	3	5.34378
Q6P0K8	**PLAK Junction plakoglobin**	**1.0779692**	**0.872187**	**4**
Q6P0K8	LLNDEDPVVVTK	0.969712949	2	2.74524
Q6P0K8	MEEIVEGCTGALHILAR	1.346102155	3	3.30865
Q6P0K8	NLALCPANHAPLQEAAVIPR	0.966632817	3	3.95562
Q6P0K8	TMQNTSDLDTAR	1.121913457	2	2.95566
Q6P2K6	**P4R3A Serine/threonine_protein phosphatase 4 regulatory subunit 3A**	**0.886098149**	**0.61574**	**3**
Q6P2K6	ESEEKEVLLK	0.708836151	1	2.02612
Q6P2K6	FKEVIPISDPELK	1.134021275	1	2.01321
Q6P2K6	LDSMRSILR	0.837504349	1	2.025
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.199211032**	**2.15E-08**	**12**
Q6P502	AMTGVEQWPYR	1.184063402	2	2.57014
Q6P502	AVAQALEVIPR	1.162858016	2	2.85293
Q6P502	DMMLNIINSSITTK	0.819523672	2	2.34828
Q6P502	EIQVQHPAAK	0.978490797	2	3.12741
Q6P502	IVLLDSSLEYK	1.490069502	2	2.46059
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.623834502	3	4.28636
Q6P502	KGESQTDIEITR	1.199169242	2	2.90251
Q6P502	NLQDAMQVCR	1.198678323	2	3.17285
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	1.481026854	2	4.08847
Q6P502	TAVETAVLLLR	1.352366234	2	2.80806
Q6P502	TLIQNCGASTIR	1.245315117	2	3.09467
Q6P502	WSSLACNIALDAVK	1.260487916	2	3.63207
Q6P6M7	**SPCS O_phosphoseryl_tRNA(Sec) selenium transferase**	**1.203919807**	**0.059756**	**4**
Q6P6M7	EMFVYLSTQLKK+Oxidation(2)	0.732634288	2	2.95783
Q6P6M7	KEMFVYLSTQLKK	1.105832724	2	2.54667
Q6P6M7	SGDISAVQPK	1.293702726	2	2.59318
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	0.847070099	2	3.66175
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**1.106637045**	**5.46E-05**	**10**
Q6P6R2	ALTGGIAHLFK	1.167955758	2	2.35699
Q6P6R2	IDVSVEAASGGK	1.008624844	2	3.2161
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.416369971	3	4.43588
Q6P6R2	NETLGGTCLNVGCIPSK	1.052886014	2	5.2592
Q6P6R2	NQVTATTADGSTQVIGTK	0.992286236	2	5.37436
Q6P6R2	RPFTQNLGLEELGIELDPK	1.170010103	3	3.74095
Q6P6R2	SEEQLKEEGVEFK	0.893576505	3	3.89455
Q6P6R2	TNADTDGMVK	0.978556998	2	2.87228
Q6P6R2	TNADTDGMVK+Oxidation(8)	1.355221425	2	2.68824
Q6P6R2	VCHAHPTLSEAFR	1.151792139	3	3.78727
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**1.162394034**	**0.935635**	**4**
Q6P6S9	AQTLLLEVEEIFK	1.182582599	2	2.98593

Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	1.148447486	2	4.11729
Q6P6S9	QGAETVQELLEVAK	1.157094366	2	3.08266
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	1.155553154	3	4.70138
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.359056317**	**4.31E-11**	**9**
Q6P6V0	AITDIINIGIGGSDLGPLMVTEALKPYSK	1.054495473	3	3.80874
Q6P6V0	DVMPEVNKVLDK+Oxidation(3)	0.869877075	2	2.36973
Q6P6V0	HFVALSTNTDK	1.388472532	2	3.16772
Q6P6V0	ILLANFLAQTEALMK	1.177220343	2	3.13455
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.086960627	3	4.83518
Q6P6V0	TFTTQETITNAETAK	1.236007995	2	5.13306
Q6P6V0	TLANLNPESSLFIIASK	1.519647316	3	5.02116
Q6P6V0	VFEGNRPTNSIVFTK	1.390288221	2	3.25581
Q6P6V0	VWFVSNIDGTHIAK	0.233304622	2	3.58876
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.114980165**	**0.551049**	**5**
Q6P7Q4	DFLLQQTMLR	1.040926827	2	3.25858
Q6P7Q4	FEELGVK	1.114183732	1	1.94432
Q6P7Q4	GFGHIGIAVPDVYEACK	1.20877647	2	3.71538
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.260338691	2	5.80451
Q6P7Q4	VLGLTLLQK	1.286783265	2	2.72294
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.184905347**	**0.07136**	**3**
Q6P7R8	LGEWAVVTGGTDGIGK	1.166431534	2	4.12365
Q6P7R8	LININVLSICK	2.955655987	2	2.6447
Q6P7R8	TIAVDFSLDDIYDK	1.314077791	2	2.96944
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.146415967**	**3.41E-14**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	1.007304362	2	4.73195
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(11)	1.110202196	2	2.51861
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.120906607	3	5.55761
Q6P9T8	EIVHLQAGQCGNQIGAK	0.933240136	2	5.10746
Q6P9T8	EVDEQMLNVQNK	1.209734854	2	4.19869
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	1.00204308	3	5.46878
Q6P9T8	INVYYNEATGGK	1.140703865	2	3.65263
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.286750313	3	5.75968
Q6P9T8	LHFFMPGFAPLTSR	2.825336839	2	2.98835
Q6P9T8	MSATFIGNSTAIQELFK	1.740835256	2	4.36637
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	0.830347987	3	3.94202
Q6P9T8	TAVCDIPPR	0.457076319	2	2.38873
Q6P9T8	YLTVAAVFR	1.073729747	2	2.71098
Q6PA06	**ATLA2 Atlastin_2**	**1.082171246**	**0.351992**	**4**
Q6PA06	AGLTDQVSHHAR	1.278390079	2	3.08449
Q6PA06	NLVPLLLAPENLVEK	1.138583218	2	2.82035
Q6PA06	QNQHEELQNVR	0.947676918	2	2.86737
Q6PA06	SMLQATAEANNLAAVAGAR	1.294191357	2	3.21715
Q6PCM2	**INT6 Integrator complex subunit 6**	**1.217243809**	**0.002908**	**2**
Q6PCM2	MLIEQLENFLDEIHRR+Oxidation(1)	0.510272645	2	2.50845
Q6PCM2	NPFFLEPAIIITITDGSK	1.348800885	2	2.34954
Q6PDV7	**RL10 60S ribosomal protein L10**	**1.38624645**	**0.335177**	**2**
Q6PDV7	FNADEFEDMVAEK	1.365712327	2	3.73322
Q6PDV7	FNADEFEDMVAEKR	0.874074394	2	2.65021
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.074020676**	**0.436104**	**4**
Q6PEC1	AEDGENYAIKK	1.196765867	2	2.57396
Q6PEC1	LEAAYTDLR	1.025577137	2	2.84698
Q6PEC1	QILESEKDLEEAEEYKEAR	1.120208698	3	4.09831
Q6PEC1	RLEAAYTDLR	1.147014148	2	2.47207
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.195958811**	**0.461655**	**3**
Q6PEC4	NDFTEEEEAQVR	0.979631458	2	3.18561
Q6PEC4	RTDDIPVWDQEFLK	1.173730801	2	3.10357
Q6PEC4	TDDIPVWDQEFLK	1.316794906	2	2.70944

Q6PGB8	**SMCA1 Probable global transcription activator SNF2L1**	**1.011000496**	**0.99494**	**2**
Q6PGB8	EMDPEYEEKMVNMPLK+Oxidation(13)	0.993862677	2	2.41012
Q6PGB8	IKTDVEKSLPPK	1.027655532	2	2.32029
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.015271219**	**0.00242**	**6**
Q6Q0N1	AVFQYIDENQDR	1.804731538	2	3.25158
Q6Q0N1	EGGSIPVTLTFQEATGK	1.06993685	2	2.75371
Q6Q0N1	LGGSVELVDIGK	1.430317184	2	2.38908
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	0.304759499	2	3.42259
Q6Q0N1	MTEAAAADVQR	1.14280874	2	2.58719
Q6Q0N1	TGQEIPVNLR	1.174668422	2	2.49549
Q6RT24	**CENPE Centromere_associated protein E**	**1.102587737**	**0.649249**	**2**
Q6RT24	DLLQKVQDEK	1.036015362	2	2.38172
Q6RT24	MELENVNMKLQEK	1.133161829	2	2.40345
Q6RUV5	**RAC1 Ras_related C3 botulinum toxin substrate 1**	**1.11457505**	**0.909999**	**2**
Q6RUV5	HHCPNTPIILVGTK	1.113533011	2	3.11598
Q6RUV5	LTPITYPQGLAMAK	1.132419676	2	2.98528
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.632371639**	**0.008947**	**2**
Q6SKG1	FDSTSILQTLSK	0.632394793	2	3.14342
Q6SKG1	TGTVLIPGTTQLTQK	0.609096185	2	2.52363
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.260703397**	**2.22E-16**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.227307836	2	4.73987
Q6TUG0	FQMTQEVVCDECPNVK	1.258081373	2	5.05019
Q6TUG0	KGEGLPNFDNNNIK	1.283188644	2	3.31929
Q6TUG0	TLEVEIEPGVR	1.237088562	2	3.03392
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.058517272**	**0.999994**	**17**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.075271577	2	4.5006
Q6UPE1	ALNEGGLQSIPK	0.952177294	2	3.48033
Q6UPE1	ASCDAQTYGIGLK	0.77366349	2	3.82602
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	0.900803652	2	4.65717
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.010312783	2	4.88455
Q6UPE1	GAPLNTPVTEDR	0.961253453	2	3.47627
Q6UPE1	GIATNDVGIQK	0.877400345	2	3.56135
Q6UPE1	HHPSIRPTLEGGK	0.751661433	2	2.31777
Q6UPE1	LQINAQNCVHCK	1.090628483	2	3.50742
Q6UPE1	LTFPGGLLIGCSPGFMNVPK	1.17063028	2	3.4681
Q6UPE1	NLSIYDGPEQR	0.944285259	2	2.62894
Q6UPE1	QLTSENLQSK	0.896986757	2	2.32219
Q6UPE1	SGSLAAEAIFK	0.938633285	2	3.29109
Q6UPE1	TAGLHVTEYEDNLK	0.85312694	2	3.69487
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	1.109424083	2	4.52092
Q6UPE1	VDHTVGWPLDR	0.89146099	2	2.49189
Q6UPE1	VTIFAEGCHGHLAK	1.00801814	2	3.79271
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**0.941693671**	**1.27E-10**	**7**
Q6URK4	EDSVKPGAHLTVK	1.068603035	2	3.69733
Q6URK4	GFAFVTFDDHDTVDK	1.090547348	2	3.84779
Q6URK4	IETIEVMEDR	1.028580688	2	3.36211
Q6URK4	IFVGGIKEDTEEYNLR	1.747646865	2	4.26382
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	0.823646213	2	4.6206
Q6URK4	WGTLTDCVVMR	1.021716863	2	3.02056
Q6URK4	YHTINGHNCEVK	1.304993142	2	3.57486
Q6URW6	**MYH14 Myosin_14**	**1.276351004**	**9.19E-10**	**4**
Q6URW6	EDQSILCTGESGAGK	1.358852902	2	4.61132
Q6URW6	FDQLLAEEK	1.067216772	1	2.01955

Q6URW6	KFDQLLAEEK	1.208048453	2	3.16765
Q6URW6	QLLQANPILEAFGNAK	1.424907459	2	4.59195
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**1.086408226**	**0.797447**	**4**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.700547011	2	3.83103
Q6XQN1	LDSGDLLQQAK	1.211526552	2	3.6439
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.281609347	2	5.46786
Q6XQN1	QLQNPAVYQVALSEK	1.11971347	2	3.15361
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**0.81405919**	**0.001017**	**2**
Q6ZPJ3	FRTTDIVIR	0.804684344	2	2.52438
Q6ZPJ3	NCAQGEGSMAKKVK	0.987669669	2	2.90382
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.190836182**	**0.608597**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	1.191825638	2	2.73531
Q70FJ1	HEAEITNYKIKLEMLEK+Oxidation(14)	1.152297619	2	2.51713
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.128620014**	**0.14711**	**4**
Q711G3	DCGTDVLDLWTLMQK	1.245162339	2	4.2189
Q711G3	DVEETKPELSLLGDGDH	1.012304998	2	3.64127
Q711G3	LNVAVGEYAK	1.142707335	2	2.55703
Q711G3	VILITPPPLCEAAWEK	1.283981137	2	2.83088
Q71LX4	**TLN2 Talin_2**	**1.113697023**	**0.700605**	**4**
Q71LX4	NCGEMSEIEAK	0.921185063	2	2.42786
Q71LX4	QEDVIATANLSR	0.90322424	2	3.11656
Q71LX4	QELTVFQSKDIPEK	1.427577589	2	2.32515
Q71LX4	QVAASTAQLLVACK	1.165355021	2	3.26186
Q71TY3	**RS27 40S ribosomal protein S27**	**1.196536382**	**0.279449**	**3**
Q71TY3	DLLHPSPEEEK	1.05045594	2	2.799
Q71TY3	LTEGCSFR	1.301341076	2	2.31795
Q71TY3	LVQSPNSYFMDVK	1.193267236	2	2.88016
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.108570741**	**0.446057**	**6**
Q75Q39	GLELISKAIEIDNK	1.299138256	2	2.33277
Q75Q39	NADLSTFYQNR	1.261386413	2	2.89764
Q75Q39	NREPLMPSPQFIK	0.940251516	2	2.32094
Q75Q39	SDEDKDKEGEALEVK	1.153194543	2	3.90736
Q75Q39	SYFSSFTDDIISQPMLK	1.010389684	2	2.9393
Q75Q39	YEQAIQCYTEAISLCPTEK	0.989283946	2	3.67149
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.245863683**	**1.18E-10**	**7**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.211611174	3	5.72103
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	1.102727779	3	5.08079
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.009177022	2	4.67477
Q76MZ3	LNIISNLDCVNEVIGIR	1.018675516	2	3.94119
Q76MZ3	LTQDQDVDVK	1.217236088	2	3.17939
Q76MZ3	NLCSDDTPMVR	1.178557138	2	2.44692
Q76MZ3	QLSQSLLPAIVELAEDAK	1.345767875	3	4.24492
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**1.017738942**	**0.81985**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	0.776505096	2	5.52695
Q78P75	NFGSYVTHETK	0.98189507	2	2.4998
Q78P75	YNPTWHCIVGR	1.167820499	2	2.94418
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**1.499317404**	**8.36E-12**	**5**
Q791V5	EEGIVGFFAGLIPR	1.486758188	2	3.32573
Q791V5	GLFTGLTPR	1.072315795	2	2.57159
Q791V5	LCSGVLGTVVHGK	1.605060484	2	3.09438
Q791V5	VLIQVGYEPLPPTIGR	1.128372294	2	4.3327
Q791V5	YCGLCDSIVTIYR	1.321734003	2	2.84627
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.545861324**	**0.012192**	**3**

Q794E4	ATENDIYNFFSPLNPVR	1.442453179	2	4.22032
Q794E4	HSGPNSADSANDGFVR	1.031805275	2	3.75325
Q794E4	VHIEIGPDGR	1.073915723	2	2.95532
Q7M0E3	**DEST Destrin**	**1.181682102**	**0.125886**	**3**
Q7M0E3	HEYQANGPEDLNR	1.203024829	2	4.63478
Q7M0E3	HFVGMLPEK	1.078680462	2	2.40532
Q7M0E3	HFVGMLPEKDCR	1.130649116	2	2.64655
Q7TMA5	**APOB Apolipoprotein B_100**	**0.984464853**	**0.718866**	**8**
Q7TMA5	GFEPTLEALFGK	1.120775677	2	2.36318
Q7TMA5	GIISLLEAMK	0.866707595	2	2.43707
Q7TMA5	IEGNLVFDPSSYLPK	1.194973735	2	3.41922
Q7TMA5	IEIDIPLPLGGK	0.904453723	2	2.82363
Q7TMA5	ITDNDVLIALDSAK	0.885280762	2	2.79383
Q7TMA5	LSISEQNAQR	1.169790009	2	2.40176
Q7TMA5	NFVASHIANILNSEELYVQDLK	1.026071839	3	3.41706
Q7TMA5	TILFDTFVNDVAPVEK	1.053354809	2	2.72205
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**0.9459624**	**0.999897**	**4**
Q7TNG8	AVVGSPHVSTASAVR	0.901086138	2	3.14608
Q7TNG8	AYSTDVCVPISR	0.956807393	2	3.79115
Q7TNG8	GSQGGLSQDFVEALK	0.994192945	2	3.0836
Q7TNG8	QLLQEEVGPVGVETMR	0.934536515	2	3.4754
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.213211089**	**0.140267**	**3**
Q7TP47	AGPIWDLR	1.251744179	2	2.40813
Q7TP47	DLFEDELVPLFEK	1.639094701	2	2.78842
Q7TP47	NLANTVTEEILEK	0.940337758	2	2.81012
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.26516941**	**1.33E-07**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	1.572077869	2	3.27708
Q7TP48	LENGEIETIAR	1.167093887	2	3.23254
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	1.208234399	3	4.21407
Q7TP48	LLLSSETPIEGK	1.659159633	2	3.0569
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.167174154**	**4.97E-05**	**7**
Q7TP52	AGVSVYGIIR	1.429269974	2	2.79577
Q7TP52	EDCSPADKPYIEEAR	1.06351238	2	3.50807
Q7TP52	KREDCSPADKPYIEEAR	1.066342009	3	3.78095
Q7TP52	LDYGGMGQEVQVEHIK	1.170647427	2	4.5555
Q7TP52	LKEHCIVNYQVK	1.329885712	2	4.14853
Q7TP52	NLIEWLNK	1.146200412	1	2.29394
Q7TP52	TFSGQTHGFVHR	1.187077555	2	3.41243
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.141020077**	**3.23E-05**	**7**
Q7TPB1	ALIAGGGAPEIELALR	1.244999346	2	3.73124
Q7TPB1	AQDIEAGDGTTSVVIIAGSLLDSCTK	0.714086298	2	4.78887
Q7TPB1	GDVTITNDGATILK	0.99687744	2	2.89459
Q7TPB1	GLEILTDMSRPVQLSDR	1.018321512	2	2.50612
Q7TPB1	LVIEEAER	1.342029641	2	2.35699
Q7TPB1	SIHDALCVIR	1.334826046	2	2.99006
Q7TPB1	VIDPATATSVDLR	1.154223448	2	4.01699
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.247767376**	**0.003546**	**2**
Q7TPJ0	GEDFPANNIVK	1.148895155	2	2.93958
Q7TPJ0	GTEDFIVESLDASFR	1.277187912	2	4.09007
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**0.792097154**	**0.241866**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(1)	0.792097154	2	2.50376
Q7TQ20	MMEEVEKLCDR+Oxidation(2)	0.792097154	2	2.40629
Q7TQ94	**NIT1 Nitrilase homolog 1**	**1.063426232**	**0.475495**	**2**
Q7TQ94	GQDWEQTQK	1.011884597	2	2.38114

Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.269094996	3	3.54657
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.115436135**	**0.818595**	**3**
Q7TQM4	AIWEAVQAYPK	0.923145881	2	2.96329
Q7TQM4	QDRPLPSTASDSTR	1.197164662	2	3.42218
Q7TQM4	TQCLEQAQR	1.091083704	2	2.95239
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.48011493**	**0.526904**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(2)	0.352261693	3	3.61374
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(6)	0.286159436	3	3.52766
Q7TSQ1	**CL18A C_type lectin domain family 18 member A**	**1.18455367**	**0.349032**	**2**
Q7TSQ1	MKCQGKGGVLAQIESQK	1.320231987	2	2.32263
Q7TSQ1	QANDSAGALPVAGKPEPMAR+Oxidation(18)	1.182990228	2	2.77812
Q80SY4	**MIB1 E3 ubiquitin_protein ligase MIB1**	**1.194738645**	**0.663004**	**2**
Q80SY4	LDIQDKDGDTPLHEALR	1.041384296	2	2.40636
Q80SY4	NTLIMGLGTQGAEKK	1.229646833	2	2.5059
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.249739871**	**9.9E-20**	**13**
Q80W21	CLDAFPNLK	1.159901771	2	3.11254
Q80W21	CLDAFPNLKDFIAR	1.066248388	2	3.24973
Q80W21	FKLGLDFPNLPYLIDGSHK	1.107395931	3	4.90866
Q80W21	HNLCGETEEER	0.938306102	2	3.94603
Q80W21	IRVDILENQLMDNR	0.999700029	2	2.93852
Q80W21	ITQSNAILR	1.253629882	2	3.07773
Q80W21	KHNLCGETEEER	1.119517705	3	4.11671
Q80W21	KISDYMK	0.97619847	1	1.95468
Q80W21	LFLEYTDSSYEEK	1.164431826	2	3.99566
Q80W21	LGLDFPNLPYLIDGSHK	1.269616573	3	4.79142
Q80W21	LKPGYLEQLPGMMR	0.929610493	2	3.29407
Q80W21	LYSEFLGK	1.145743459	2	2.4607
Q80W21	VDILENQLMDNR	0.730551787	2	3.50565
Q80WE4	**KI20B Kinesin_like protein KIF20B**	**1.599902187**	**0.794221**	**2**
Q80WE4	IKDLEVIVETQKDECK	1.024603647	2	2.39936
Q80WE4	KEEDCAELKEK	1.714694809	2	2.34652
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**0.926286834**	**0.943396**	**2**
Q80WS3	DHAVVVGVYRPPPK	0.954461917	3	3.40789
Q80WS3	TNIIPVLEDAR	0.920057695	2	2.42308
Q80X90	**FLNB Filamin_B**	**1.080814436**	**0.411324**	**6**
Q80X90	GAGIGGLGITVEGPSESK	1.12063774	2	3.62259
Q80X90	IEYDDQNDGSCDVK	0.836103289	2	4.03061
Q80X90	IGNLQTDLSDGLR	1.282343709	2	2.66318
Q80X90	VDIQTEDLEDGTCK	1.022119443	2	3.97526
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	0.825531272	2	4.93366
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.276754598	2	3.09653
Q80XB4	**NRAP Nebulin_related_anchoring protein**	**1.27572209**	**0.081122**	**2**
Q80XB4	EAFERMKGQMLGSR+Oxidation(10)	1.221443055	2	2.37604
Q80XB4	GRSQFHSRADQPGFLQAK	1.452517783	2	2.64978
Q80XC3	**US6NL USP6 N_terminal_like protein**	**1.090305904**	**0.746494**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	1.191273348	2	2.54277
Q80XC3	SVDEGSKNLK	0.948296951	2	2.38083
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**1.334508834**	**0.04469**	**2**
Q80XI3	EFEKDKADDDVFEK	1.922516573	2	2.60051
Q80XI3	NHDEESLECLCR	1.292838117	2	3.17286
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**0.909827125**	**0.861282**	**2**
Q80Y84	CDIGLLGLK	1.126537439	2	2.30576
Q80Y84	ETAAAMATLGEARLR	0.790516178	2	2.41049
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.00E+00**	**0.902384**	**3**

Q80Z25	ELEQEAERLEK	1.143267648	2	2.55917
Q80Z25	MIEESLK+Oxidation(1)	0.999136417	1	1.95163
Q80Z25	RMIEESLK+Oxidation(2)	1.082413803	2	2.3862
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**0.961025295**	**3.37E-05**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.1984158	2	3.87711
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.798979676	5	4.65457
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.329058255	2	4.48782
Q80Z29	YLLETSGNLDGLEYK	1.007989286	2	4.0702
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.068454132**	**0.25076**	**3**
Q811D2	AQEDFDK	1.067400244	1	1.94187
Q811D2	RSADQLSEKTMEQLR+Oxidation(11)	1.261773988	2	2.31818
Q811D2	SNLEEEARDLK	1.738682809	1	1.92413
Q811L6	**MAST4 Microtubule_associated serine/threonine_protein kinase 4**	**0.945047791**	**0.605461**	**2**
Q811L6	FPKATAQMEERLK+Oxidation(8)	0.893953926	2	2.33865
Q811L6	SGHFENTSAELPSVGSLLK	3.106715908	2	2.39822
Q811Q2	**CLIC6 Chloride intracellular channel protein 6**	**1.171470584**	**0.693371**	**2**
Q811Q2	AGSDGESIGNCPFSQR	1.183208846	2	3.72863
Q811Q2	FLDGDELTLADCNLLPK	0.888847093	2	2.31015
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.079954407**	**0.858706**	**5**
Q811X6	EMKSLEQSGSLK+Oxidation(2)	0.95643703	1	1.96783
Q811X6	IVDDQVILSSSSSCLLPSK	1.088445435	2	4.5418
Q811X6	LVEEGIVSPNDLDLVMSDGLGMR	0.812835047	2	3.44668
Q811X6	LYDIEQQQITNALESIR	1.251835008	2	4.84075
Q811X6	TFGPVPEFSGDTVEK	2.688614906	2	3.02316
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.01133388**	**6.55E-15**	**10**
Q8BFZ3	CDVDIRK	1.137014841	2	2.49921
Q8BFZ3	DLTDYLMK	1.250446142	1	2.30002
Q8BFZ3	HQGVMVGMGQK	1.100628017	3	3.94666
Q8BFZ3	HQGVMVGMGQK+Oxidation(5)	1.089506891	3	3.87484
Q8BFZ3	HQGVMVGMGQK+Oxidation(5)Oxidation(8)	1.228213723	3	3.58551
Q8BFZ3	HQGVMVGMGQK+Oxidation(8)	1.081017411	2	2.82784
Q8BFZ3	SYELPDGQVITIGNER	1.101904987	2	5.14862
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.012337857	3	6.91821
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(6)	0.926674899	3	5.71843
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.246957636	3	3.99302
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**1.132261536**	**0.990984**	**3**
Q8BG32	LYDNLLEQNLIR	1.117249124	2	2.85247
Q8BG32	TTANAIYCPPK	1.145316061	2	3.14203
Q8BG32	VQIEHISSLIK	1.13854376	2	2.85161
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**1.241427835**	**0.122786**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.715010529	2	3.16391
Q8BGT5	VLCIINPGNPTGQVQSR	1.243556823	2	4.74887
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.14586494**	**1.24E-09**	**4**
Q8BGY2	EDLKLPEGELGK	1.099679554	2	2.42868
Q8BGY2	KYEDICPSTHNMDVPNIK	1.097495882	3	4.73108
Q8BGY2	VHLVGIDIFTGK	1.313771311	3	3.65827
Q8BGY2	YEDICPSTHNMDVPNIK	1.041640421	2	4.09466
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.019022173**	**9.07E-06**	**9**
Q8BH00	ELLMLENFIGGK	1.224496141	2	3.91383
Q8BH00	ELNLPFGGMK	1.123092695	1	2.37774
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.009708581	3	5.11245
Q8BH00	ILCGEGVDQLSLPLR	1.090902428	2	4.68505
Q8BH00	ITQLSAPHCK	1.496361468	2	3.11784

Q8BH00	KLSLELGGK	1.250031627	2	2.40492
Q8BH00	LSLELGGK	0.939239657	1	1.91146
Q8BH00	NPAIIFEDANLEECIPATVR	1.196414833	2	4.44977
Q8BH00	SSFANQGEICLCTSR	1.178382713	2	4.16226
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.066829191**	**0.980827**	**7**
Q8BHN3	AEKDEPGAWEETFK	1.11586451	2	4.24326
Q8BHN3	MLDYLQGSGETPQTDIR	1.142331543	2	5.49508
Q8BHN3	REPWLLASQYQDAIR	1.065494316	2	2.88296
Q8BHN3	SGGIERPFVLSR	1.096945582	2	2.58723
Q8BHN3	THSDSKPYGPTSVGLDFSLPGMEHVYGIPEHADSLR	1.055887526	4	5.02082
Q8BHN3	VTEGGEPYR	0.704020186	2	2.3704
Q8BHN3	VVIMGAGKPAAVVLQTK	1.101070083	3	3.32274
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**0.824055459**	**0.480111**	**2**
Q8BIJ6	DTVLLPQTSFPMK	0.936512583	1	2.15259
Q8BIJ6	SCQTALAEILDVLVR	0.853089319	3	3.82016
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**0.839921702**	**0.630066**	**9**
Q8BJ64	ADSAYHPSCTCK	0.999001921	2	3.80893
Q8BJ64	AEVQTLVSR	1.105887527	2	2.75608
Q8BJ64	ELQPGSHVQSDK	0.785973477	2	3.15401
Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.946431685	2	3.96966
Q8BJ64	GGDGPLHVSR	0.862299715	2	2.45329
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.334871197	5	5.50551
Q8BJ64	TNHPLHQAFLQAAR	0.818795052	3	4.56059
Q8BJ64	VIGVENLR	0.976844182	2	2.72603
Q8BJ64	VLLLEAGPK	1.013524188	2	2.66874
Q8BL66	**EEA1 Early endosome antigen 1**	**1.067410941**	**0.346841**	**2**
Q8BL66	AAVLDLEK	1.113579377	1	1.98371
Q8BL66	IQAGEGETAVLNQLQEK	0.843026893	2	3.32089
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**1.091887388**	**0.95868**	**3**
Q8BP47	KEDGTFYEFGDDIPEAPER	1.082221089	2	3.95499
Q8BP47	LMTDTINEPILLCR	1.140957355	2	3.18834
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.066163549	2	2.6979
Q8BTM8	**FLNA Filamin_A**	**0.960102775**	**0.96651**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	1.159236139	2	3.07458
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	0.93453121	3	4.89505
Q8BTM8	ANLPQSFQVDTSK	1.08017026	2	2.57392
Q8BTM8	GAGTGGLGLAVEGPSEAK	1.303036765	2	3.53013
Q8BTM8	GLVEPVDVVDNADGTQTVNYVPSR	1.144814328	2	5.51661
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.106826711**	**0.039652**	**2**
Q8BTZ7	HHGQEGSILVTK	1.176583187	3	3.57086
Q8BTZ7	IGQNCSIGPNVSLGPGVVVEDGVCIR	0.82687618	2	2.74102
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.10669346**	**0.286157**	**4**
Q8BU33	AAVETLGVPCFLGGMSR	0.675726733	2	3.28772
Q8BU33	LPNSLMGR+Oxidation(6)	0.97604353	2	2.34866
Q8BU33	LTGTVGVAAVTAGPGLTNTVTAVK	1.126678579	2	3.15855
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.900865801	2	4.93042
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.084113513**	**0.958135**	**2**
Q8BWQ1	ADIWLIR	1.071627598	1	1.95712
Q8BWQ1	IHHDQPVKPLDR	1.09342255	3	3.75865
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**0.979422702**	**0.906983**	**2**
Q8BX70	ENALSELDVPFKVK	0.979673213	2	3.04153
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(20)	1.000213979	2	2.4807
Q8BZ81	**LRRT3 Leucine_rich repeat transmembrane neuronal protein 3**	**0.943211689**	**0.142094**	**2**
Q8BZ81	GLRENTIICASPK	0.649900936	1	1.94364

Q8BZ81	YPASMKQLQQR+Oxidation(5)	1.012950043	2	2.5831
Q8BZN6	**DOC10 Dedicator of cytokinesis protein 10**	**1.056212928**	**0.650416**	**2**
Q8BZN6	IIQDSNKVNPK	1.050391325	2	2.58512
Q8BZN6	LTQMEASALLYFFMRK+Oxidation(14)	1.145919278	2	2.38238
Q8C547	**HTR5B HEAT repeat_containing protein 5B**	**1.148212687**	**0.174875**	**2**
Q8C547	MVVSIAEDLLR+Oxidation(1)	1.504822425	2	2.30935
Q8C547	SAESQGRSEILMSLQK	1.08744894	2	2.33024
Q8C7R4	**UBA6 Ubiquitin_like modifier_activating enzyme 6**	**1.094705057**	**0.910349**	**2**
Q8C7R4	GMVTVTDPDLIEK+Oxidation(2)	1.143770279	1	1.99184
Q8C7R4	NFALLGVGTGREK	1.089856325	2	2.41899
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.523688234**	**0.008073**	**2**
Q8C7X2	FNVEDGEIVQQVR	1.269586601	2	4.06656
Q8C7X2	VMGDRSVLYK+Oxidation(2)	1.595896173	2	2.53927
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.053338305**	**0.964763**	**4**
Q8CC88	FLPSLAQSALEK	0.923263094	2	2.51206
Q8CC88	HQATGELDDAK	1.06118187	2	3.08075
Q8CC88	LQLTDEQLQNR	1.140279865	2	2.38746
Q8CC88	VSSDQLSSENLTSAVGQK	1.057116313	2	3.70536
Q8CCF0	**PRP31 U4/U6 small nuclear ribonucleoprotein Prp31**	**1.003239246**	**0.989135**	**2**
Q8CCF0	ERLGLTEIR	1.022676688	2	2.47975
Q8CCF0	YFSSMAEFLKVK	0.947553111	1	2.05222
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**0.989024968**	**0.001411**	**2**
Q8CDI6	EKVANMEVALDK+Oxidation(6)	0.999891602	2	2.61887
Q8CDI6	ELDDRNMEVQRLEALLK	0.510272645	2	2.35915
Q8CDI7	**CC150 Coiled_coil domain_containing protein 150**	**1.151605908**	**0.904723**	**2**
Q8CDI7	EDNRKLAMSLEQALQTNGHLQSK	99999.89988	2	2.34775
Q8CDI7	MNIFHLQTEKESNPQK+Oxidation(1)	1.151605201	2	2.58958
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**1.141593223**	**0.881961**	**2**
Q8CDM4	MEEESIDLIIK	1.145504612	2	2.30983
Q8CDM4	VTCQHKMEEESIDLIIK	1.10944955	2	2.51266
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.01416479**	**0.632454**	**3**
Q8CFN2	DDPSTIEK	1.198700897	1	2.09002
Q8CFN2	NVFDEAILAALEPPEPK	1.172139201	3	4.85586
Q8CFN2	YVECSALTQK	1.111583469	2	3.1282
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.109117464**	**0.001392**	**9**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	0.901854987	3	3.4997
Q8CG45	EHHFEAIALVEK	0.936305941	2	2.93758
Q8CG45	FFGNSWSETYR	1.159377255	2	2.6263
Q8CG45	FYAYNPLAGGLLTGK	1.657838478	2	4.11308
Q8CG45	MDASASAATVR	1.010952824	2	3.43906
Q8CG45	RMDASASAATVR	1.117633779	2	2.90672
Q8CG45	TTYGTSAPSMTSAALR	1.160644218	2	3.98997
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.812787114	3	5.48296
Q8CG45	WMYHHSQLQGTR	1.001802955	2	3.1312
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.031723226**	**0.655053**	**2**
Q8CG48	EEKLLEK	1.026942367	1	1.98204
Q8CG48	KIKALNCEIEELER	1.233451168	2	2.40289
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.083419461**	**0.018883**	**8**
Q8CGC7	AIQGATSHHLGQNFSK	1.026258215	2	4.54087
Q8CGC7	DQDVEPGAPSMGAK	0.790481631	2	2.98626
Q8CGC7	GDVSISVEEGKENLLR	1.148386422	2	3.49164
Q8CGC7	GSQFGQSCCLR	1.206836682	2	2.79695
Q8CGC7	KEENLAEWYSQVITK	0.97824799	2	3.83882
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.241631832	2	4.33003

Q8CGC7	SQGSGLSSGGAGEGQGPK	1.073388803	2	4.68017
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.818626209	2	3.19316
Q8CGN4	**BCOR BCL_6 corepressor**	**1.186920335**	**0.498261**	**2**
Q8CGN4	FLTDYLNDLQGR	1.210039173	1	2.1677
Q8CGN4	KQTQPSCTPASRLPAK	1.130443532	2	2.32961
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.398138069**	**0.106518**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(11)	1.166244311	2	2.62178
Q8CHB8	ISSATTGGQKPNTLPQK	1.402420256	2	2.32895
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.188746917**	**0.103211**	**7**
Q8CHM7	DTSKPCLINIMIEPQSTR	0.267451206	2	3.2152
Q8CHM7	GVVPDNHPNCVGAAR	1.078494539	2	3.4418
Q8CHM7	GYFVQTPEELQDSLR	1.150611643	2	3.48138
Q8CHM7	LVELCNLPFLPTPMGK	1.425731283	2	4.40297
Q8CHM7	NCFIVSEGANTMDIGR	1.383539922	2	4.69925
Q8CHM7	NQEAMGAFQEFPQVEACR	1.056527888	2	6.0686
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	0.803800859	3	4.66683
Q8CIB5	**FERM2 Fermitin family homolog 2**	**1.031895867**	**0.483489**	**2**
Q8CIB5	GCEVTPDVNISGQK	1.031885541	2	2.92657
Q8CIB5	TSTILGDITSIPELADYIK	1.083830175	2	3.63723
Q8CIE6	**COPA Coatomer subunit alpha**	**1.124192971**	**0.554462**	**11**
Q8CIE6	ASNLENSTYDLYTIPK	1.444333425	2	3.15713
Q8CIE6	DADSQNPDAPEGK	0.953339364	2	3.84997
Q8CIE6	GITGVDLFGTTDAVVK	1.151469418	2	3.81543
Q8CIE6	GTSPTQIWCNNSQLPVDHILAGSFETAMR	1.312306928	3	3.89174
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.183025565	3	3.65358
Q8CIE6	KKNLSPGAVESDVR	1.186693216	2	2.34388
Q8CIE6	LLELGPKPEVAQQTR	1.188140046	2	2.57984
Q8CIE6	QQPLFVSGGDDYK	1.191391085	2	2.39633
Q8CIE6	SILLSVPLLVVDNK	1.321510275	2	3.04838
Q8CIE6	SSGLTAVWVAR	1.038200448	2	2.66434
Q8CIE6	TLDLPIYVTR	1.066507617	2	2.40063
Q8CJF7	**ELYS Protein ELYS**	**1.120213933**	**0.399109**	**2**
Q8CJF7	QNSNRVNIEELLK	0.940251516	2	2.66119
Q8CJF7	SVENGQSTEILDDLK	1.210174266	2	2.63588
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.105486175**	**0.731046**	**3**
Q8JZN5	GIILVGNEEQK	1.058114844	2	2.71718
Q8JZN5	GSNTCEVHFENTR	1.152384685	2	4.03122
Q8JZN5	SGNVTTVMETIGR	1.13266549	2	3.40542
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.132033786**	**0.999994**	**16**
Q8K009	AGFSVFWADDGLDTGPILLQR	0.973627499	2	4.64112
Q8K009	AMVEAVQLIADGK	1.13799661	2	3.95633
Q8K009	ANNTEYGLASGVFTR	0.994130817	2	4.43284
Q8K009	DLGEEALNEYLK	1.262963841	2	3.65147
Q8K009	EESFGPIMVISK	1.055407727	2	2.831
Q8K009	FLFPEGIK	0.93238531	2	2.31671
Q8K009	FQNGDIDGVLQR	0.986126416	2	2.85882
Q8K009	GVINIIPGSGGVAGQR	1.052678616	2	3.81227
Q8K009	HGSIIYHPSLLPR	1.009913208	2	4.39677
Q8K009	KLGFTGSTSVGK	0.794417281	2	2.43473
Q8K009	KVSLELGGK	1.193310087	1	2.13021
Q8K009	NLQFEDGK	1.077773994	1	2.04405
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.104619711	2	4.03637
Q8K009	SCDVKPNDTVDSLYNR	1.120850724	2	3.91773
Q8K009	VVGVFTVPDKDGK	1.114791031	2	3.32507
Q8K009	YFAGWCDK	1.163649367	1	2.0913

Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.094987431**	**0.950534**	**5**
Q8K442	GQITAILGHSGAGK	1.146682955	2	3.44241
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	1.11128311	3	4.26047
Q8K442	LTGVCPQCNVQFDFLTVR	1.032118564	2	3.27415
Q8K442	NTQNILVQNLSGGQK	1.105832724	2	2.94326
Q8K442	STLLNVLSGLCVPTK	1.142336964	2	3.23935
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.939278013**	**9.9E-20**	**10**
Q8K4C0	CCLEEGLEPVCFER	1.067044329	2	4.23112
Q8K4C0	EYKNPVEFTGK	0.718189883	2	2.37341
Q8K4C0	FDHEMFGLKPK	0.715660624	2	3.18568
Q8K4C0	GYPIDILLSSR	0.93377032	2	3.05808
Q8K4C0	HSALGQHPTINDDLPNR	0.772962398	2	4.50408
Q8K4C0	IAVIGSGASGLTCIK	1.301315035	2	3.71171
Q8K4C0	KLPSQSEMMAEINK	0.788201746	2	4.17043
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.858856085	3	4.59094
Q8K4C0	KTILTTEDR	0.740008997	2	2.7001
Q8K4C0	SDDIGGLWR	0.817478989	2	2.92857
Q8K4G6	**MACD1 MACRO domain_containing protein 1 (Fragment)**	**1.043203832**	**0.971937**	**3**
Q8K4G6	AAGSLLTDECR	0.927236008	2	3.06968
Q8K4G6	HVIHTVGPIAVGQPTASQAAELR	0.889286189	3	5.09617
Q8K4G6	SCYLSSLDLLLEHR	1.022213553	2	3.06497
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.229842035**	**0.118905**	**3**
Q8K4T4	EVLNLTK	1.223197088	1	2.05644
Q8K4T4	IEELEETNKSLQK	1.229646833	2	2.40912
Q8K4T4	SSIISSDGGKGPSEDAKK	1.307338806	2	2.4481
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.05879213**	**0.596392**	**3**
Q8K4Z3	GNPSGIQPDLLISLTAPK	1.103139665	2	3.73116
Q8K4Z3	LFGYQPTIYYPK	1.368646765	2	2.39133
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.056920163	2	5.52377
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.326323554**	**0.008961**	**4**
Q8K586	FNVWDTAGQEK	1.216946934	2	3.26701
Q8K586	LVLVGDGGTGK	1.295253398	2	2.37527
Q8K586	NLQYYDISAK	1.303469226	2	2.77255
Q8K586	VCENIPIVLCGNK	1.30942242	2	4.06486
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.909563689**	**0.58448**	**2**
Q8QZY1	VFSDEVQQQAQLSTIR	0.969990992	2	4.13691
Q8QZY1	VYEIQDIYENSWTK	0.882283011	2	3.81218
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.23912714**	**0.968995**	**4**
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	0.965590967	3	4.67325
Q8R081	SDALETLGFLNHYQMK	1.239136864	2	3.64547
Q8R081	SSSGLLEWDSK	0.951547115	2	2.73648
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.815154546	3	7.07663
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.057228989**	**0.96698**	**5**
Q8R0F9	FDNTYSLLHTK	1.073003399	2	3.20181
Q8R0F9	GSSHQVENEILFPGCVLR	0.988935513	2	5.20031
Q8R0F9	VCEMLLHECELQSQK	1.165112646	2	4.9357
Q8R0F9	VGYTAEVLLPDK	0.813853529	2	2.59644
Q8R0F9	VGYTAEVLLPDKACEEK	1.228205158	2	2.41134
Q8R164	**BPHL Valacyclovir hydrolase**	**1.30876278**	**0.984863**	**3**
Q8R164	FTLVAWDPR	1.135546891	2	2.51417
Q8R164	QVSLLGWSDGGITALIAAAK	1.091638494	2	3.9416

Q8R164	TDFAPQLQSLNK	0.891028844	2	3.80318
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**1.286428794**	**0.924815**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	1.189947464	2	3.58074
Q8R1V4	QLLDQVEQIQK	1.040735269	2	3.4058
Q8R2H4	**KLH12 Kelch_like protein 12**	**0.381762101**	**0.020069**	**2**
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(15)	0.381762101	2	2.39592
Q8R2H4	DIMTNTHAKSILNSMNSLR+Oxidation(3)	0.381762101	2	2.65506
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**0.869432826**	**0.110656**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	0.938205296	2	3.69291
Q8R3Q6	NCIAQTSAVVK	0.862246717	2	3.00387
Q8R491	**EHD3 EH domain_containing protein 3**	**1.246003779**	**0.207381**	**3**
Q8R491	ADQIETQQLMR	1.261342529	2	3.08198
Q8R491	LFEAEEQDLFK	0.969576593	2	3.37225
Q8R491	MQDQLQAQDFSK	1.247621729	2	3.64173
Q8R508	**FAT3 Protocadherin Fat 3**	**0.728687534**	**0.000242**	**2**
Q8R508	FFIDPK	0.999802349	2	2.33149
Q8R508	QVSYHITGGNPR	0.708670828	2	2.58299
Q8R5M4	**OPTN Optineurin**	**0.832818373**	**0.522305**	**2**
Q8R5M4	LELQVESMRSEIK+Oxidation(8)	1.14247934	2	2.41691
Q8R5M4	NSATPSELNEK	0.739359459	1	2.18711
Q8VBU2	**NDRG2 Protein NDRG2**	**1.280400607**	**0.020076**	**3**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	1.220243137	2	5.83564
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.683917539	2	4.72307
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.385233929	2	4.63743
Q8VC12	**HUTU Urocanate hydratase**	**1.29185474**	**3.35E-14**	**6**
Q8VC12	HQLVVGSQAR	1.089866539	2	2.91621
Q8VC12	LLALEFAQELR	1.709196834	2	4.30324
Q8VC12	LVITNGMVIPNYSSR	1.199284826	2	3.59922
Q8VC12	MMLSWDVSNGVAR	1.101433794	2	2.46804
Q8VC12	VAIAVAINQAIASGK	1.172627697	2	2.6671
Q8VC12	VFVTSGLGGMSGAQAK	1.093259542	2	4.46392
Q8VC28	**AK1CD Aldo_keto reductase family 1 member C13**	**0.960524547**	**0.03477**	**2**
Q8VC28	ILNKPGLK	2.350424184	1	2.03048
Q8VC28	YKEWVDQNSPVLLNDPVLCDVAK	0.829637269	3	4.41749
Q8VCD5	**MED17 Mediator of RNA polymerase II transcription subunit 17**	**0.806473577**	**0.081277**	**2**
Q8VCD5	EIFAQLSREAVQIK	0.866122213	1	2.09659
Q8VCD5	MELLMSALSPCLL+Oxidation(1)Oxidation(5)	0.785281416	2	2.55652
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**0.982539556**	**0.661397**	**3**
Q8VDC1	GLELQVMQLQQEK	0.973598194	2	2.39601
Q8VDC1	MEEALASLAQELQDSK	1.307338806	2	2.40751
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(1)	1.045683539	2	2.35048
Q8VDD9	**PHIP PH_interacting protein**	**0.5598275**	**0.222914**	**2**
Q8VDD9	EDLLQK	0.585204301	1	1.96389
Q8VDD9	MELREQELMKIVGIK	0.525021322	2	2.44431
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**1.057991604**	**0.926424**	**2**
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.834310915**	**0.026704**	**3**
Q8VED5	NKYEDEINK	0.83234323	2	2.38147
Q8VED5	NKYEDEINKR	0.813776402	3	3.44299
Q8VED5	YEDEINK	1.160687538	1	2.17815
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.38750459**	**0.001079**	**10**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.370105444	3	4.94857
Q8VEK3	GGYSNRGNYNRGGMPNR	1.11689595	2	2.35311
Q8VEK3	LLEQYKEESK	0.83593905	2	3.07445

Q8VEK3	LLEQYKEESKK	1.081902353	2	3.73612
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.116998507	3	5.04553
Q8VEK3	NFILDQTNVSAAAQR	1.210174266	2	5.0719
Q8VEK3	TCNCETEDYGEK	1.217646849	2	3.35139
Q8VEK3	VSELKEELK	1.307922667	2	2.65716
Q8VEK3	VSELKEELKK	1.229382567	2	2.54108
Q8VEK3	YNILGTNTIMDK	1.130017045	2	3.31433
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.982425624**	**0.884543**	**9**
Q8VHE9	ATVQSVLLDSAGR	1.035184301	2	3.01075
Q8VHE9	FLPLPLTQLLNK	1.393667744	2	2.66105
Q8VHE9	GATYGADHDLAR	0.982292411	2	3.11181
Q8VHE9	NLYSDLQALGSK	1.037953974	2	3.70148
Q8VHE9	RPPEPLVTDK	0.963606444	2	3.01343
Q8VHE9	RPPEPLVTDKEAR	0.921386165	3	3.89332
Q8VHE9	VESVTGGSPLTNQYYLAAHR	1.546675978	2	4.07711
Q8VHE9	VLVLEQHTK	0.995772934	2	2.30949
Q8VHE9	VVAHGVSHAILLK	1.096056382	2	2.82372
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**1.181068013**	**0.870809**	**4**
Q8VHF5	ALGVLAQLIWSR	0.99316745	2	2.74879
Q8VHF5	GLVYETSVLDPDEGIR	1.191825638	2	3.50769
Q8VHF5	GYSIPECQK	1.147831065	2	2.50748
Q8VHF5	IVPNILLEQGK	1.157384587	2	2.56162
Q8VHN7	**GPR98 G_protein coupled receptor 98**	**1.019361359**	**0.970235**	**2**
Q8VHN7	FIVEEPEFNSVR	1.04679432	2	2.3042
Q8VHN7	ITMVASDAPYGR	1.016970947	2	2.64076
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.397446042**	**4.8E-05**	**2**
Q8VHT6	SLQNVHEEVISR	1.37439924	2	3.29829
Q8VHT6	TSADLQTNACVTPAK	1.407778191	2	3.97772
Q8VHX6	**FLNC Filamin_C**	**1.179816252**	**0.348553**	**2**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.180036397	2	3.8768
Q8VHX6	IECDDKGDGSCDVR	0.925081513	2	3.60212
Q8VI04	**ASGL1 L_asparaginase**	**1.094986155**	**0.704232**	**3**
Q8VI04	GLGGLILINK	1.133866011	2	2.43291
Q8VI04	GNLAYATSTGGIVNK	0.976031039	2	4.06886
Q8VI04	TVDEAATLALDYMK	1.223076239	2	2.60955
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.020439192**	**0.99624**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.047529586	2	4.57314
Q8VID1	LAEDGAHVVISSR	1.103350518	2	3.7078
Q8VID1	NFAAELAPK	0.96884886	2	2.32608
Q8VID1	VNCLAPGLIK	1.448152929	2	2.48954
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.753098139**	**0.002802**	**10**
Q8VIF7	CGPGYATPLEAMK	0.746290247	2	3.12463
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	0.782810759	2	4.82655
Q8VIF7	GGFVLLDGETFEVK	0.896048539	2	4.27773
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.881649902	2	3.90073
Q8VIF7	HEIIQTLQMK	0.791301955	2	2.71416
Q8VIF7	HNIMVSTEWAAPNVFK	0.682024488	2	4.73441
Q8VIF7	LTGQIFLGGSIVK	1.047738222	2	3.47141
Q8VIF7	NEGGTWSVEK	0.725997421	2	2.53446
Q8VIF7	NTGIEAPDYLATVDVDPK	0.757657506	2	4.62925
Q8VIF7	QYDISNPK	0.748600595	1	1.9925
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**0.975632896**	**0.924106**	**2**
Q8VIJ6	FGQGGAGPVGGQGPR	0.972168957	2	3.31355
Q8VIJ6	YGEPGEVFINK	1.09704397	2	2.32841
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**1.185939601**	**0.099353**	**5**

Q91VA0	AFIVLNPEFLSHDQEQLIK	1.296776425	2	5.45789
Q91VA0	AILPFDLQIIDEK	1.164478279	2	4.20049
Q91VA0	GNILPPNTEGYIGIR	1.12761814	2	3.1621
Q91VA0	HNQGLAFR	1.071634315	2	2.53382
Q91VA0	KVEFVSELPK	1.173632611	3	3.40725
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.86430122**	**0.966944**	**2**
Q91VM9	IIAINVNDPEAEK	0.896025691	2	2.9748
Q91VM9	MEIATEEPLNPIK	0.853692134	2	4.08789
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.892991098**	**0.736015**	**3**
Q91W43	EMLQALGLASIDELIEK	0.762339844	2	2.48427
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	1.03615494	2	4.24452
Q91W43	VSFQPNSGAQGEYAGLATIR	0.880525629	2	5.06191
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.021838093**	**0.994474**	**2**
Q91W90	SFEDTIAQGITFVK	1.053051664	2	2.66716
Q91W90	VDCTQHYAVCSEHQVR	0.999351564	3	4.73594
Q91X77	**CY250 Cytochrome P450 2C50**	**1.020080194**	**0.596948**	**4**
Q91X77	EHEESLDVTIPR	0.71710032	2	2.46047
Q91X77	IKEHEESLDVTIPR	0.999862284	2	3.75103
Q91X77	NFLLEK	0.928652326	1	2.08655
Q91X77	YALLLLLK	0.841795089	2	2.68429
Q91X78	**ERLN1 Erlin_1**	**1.056062427**	**0.698986**	**2**
Q91X78	ISEIEDAAFLAR	1.024161876	2	2.7968
Q91X78	SVQTTLQTDEVK	1.273252068	2	2.93127
Q91Y81	**SEPT2 Septin_2**	**1.053593241**	**0.426722**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	0.804032751	2	3.16139
Q91Y81	ILDEIEEHSIK	0.682355601	2	2.89625
Q91Y81	LTVVDTPGYGDAINSR	1.18464785	2	3.92305
Q91Y81	STLINSLFLTDLYPER	0.975737005	2	2.75811
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.159812903**	**0.002493**	**8**
Q91YT0	GAGAYICGEETALIESIEGK	1.355171874	2	4.39689
Q91YT0	GDARPAEIDSLWEISK	1.012423777	3	3.70816
Q91YT0	GEFYNEASNLQVAIR	1.156522401	2	3.40461
Q91YT0	GGAGFPTGLK	1.19530992	2	2.3387
Q91YT0	KTSFGSLKDEDR	1.400552111	2	2.84831
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.404814246	3	4.73246
Q91YT0	LVEGCLVGGR	1.122693976	2	2.79641
Q91YT0	YLVVNADEGEPGTCK	1.188589834	2	5.21125
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.117803992**	**0.488991**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.083638055	3	6.91365
Q91Z53	LLDAAGANLR	1.141410386	2	2.51596
Q91Z53	NCVILPHIGSATYK	1.130086946	2	3.58343
Q91Z53	NTMSLLAANNLLAGLR	0.963567665	2	4.77229
Q91Z53	RLPEAIEEVK	1.013511773	2	2.78499
Q91Z53	VISTLSVGVDHLALDEIK	1.27001151	2	4.13073
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**0.990917266**	**0.999999**	**16**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	0.937693876	3	4.97656
Q91ZJ5	EFPTVPLVK	0.925175748	1	2.04294
Q91ZJ5	FVQDLSK	0.972067159	1	1.9363
Q91ZJ5	GGTLTQYEGK	0.96493448	2	2.67015
Q91ZJ5	GLPDNISSVLNK	0.923171605	2	3.30691
Q91ZJ5	GTVIIIANHGDR	0.860168386	2	3.09703
Q91ZJ5	IDIPPGAVLENK	0.967671543	2	3.02958

Q91ZJ5	IQRPPEDSIQPYEK	0.967867574	3	4.58762
Q91ZJ5	LNGGLGTSMGCK	1.015767873	2	3.25159
Q91ZJ5	LQEQNAIDMEIIVNPK	0.904775638	2	4.19279
Q91ZJ5	LVEIAQVPK	1.06144251	2	2.46132
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.140347454	2	5.08602
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	0.96150978	3	4.56663
Q91ZJ5	SFENSLGINVPR	1.028463219	2	3.45933
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	0.895095842	2	5.4115
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.017960114	2	4.53734
Q91ZU6	**DYST Dystonin**	**1.141450873**	**0.464328**	**4**
Q91ZU6	LQVEQNK	1.225948415	1	1.92515
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(1)	1.198624525	2	2.51303
Q91ZU6	MMLATEETSPDLIGVKR+Oxidation(2)	1.198624525	2	2.5131
Q91ZU6	SAETNIDQDITNLK	1.080160207	2	2.43294
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**1.141314384**	**0.497616**	**2**
Q91ZV0	CGDLECETLISRVLALR	1.047397182	2	2.46943
Q91ZV0	KMLDQDDIVENDK+Oxidation(2)	1.3240339	2	2.41912
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.115613916**	**0.544026**	**3**
Q91ZX7	GCHVNECLSR	0.854851363	2	2.67998
Q91ZX7	MYDAQQQQVGTNK	1.180681794	2	4.09434
Q91ZX7	VFFTDYGQIPK	1.110660351	2	2.67292
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.156320124**	**0.748574**	**2**
Q920A6	DLDTVASDMMVLLK	1.183646856	2	2.38946
Q920A6	GLAEVSDIAEQVLNAVNK	1.051850619	3	5.8611
Q920B9	**SP16H FACT complex subunit SPT16**	**1.100777708**	**0.406636**	**2**
Q920B9	EMKIYIDK+Oxidation(2)	1.080794782	1	1.91105
Q920B9	ICDVYNSVMDVVKK	1.237130633	2	2.32906
Q920D2	**DYR Dihydrofolate reductase**	**1.241945995**	**3.02E-07**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	1.562007959	2	5.0294
Q920D2	LIEQPELASK	1.113310475	1	2.02803
Q920D2	LLPEYPGVLSEIQEEK	1.417218417	2	3.77679
Q920D2	NGDLPWPLLR	1.241941084	2	2.82504
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.904170456**	**0.000861**	**3**
Q920F5	EIAEVTGDPVHESLK	1.201328578	2	2.98233
Q920F5	ISECEAVHPVK	0.567474277	2	3.23478
Q920F5	WLLGLLNVQGK	1.756391006	2	2.3666
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.102063025**	**0.485727**	**2**
Q920J4	AGCECLNESDEHGFDNCLR	1.2266848	3	3.79469
Q920J4	IDQYQGADAVGLEEK	0.929552152	2	4.54866
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.100626617**	**0.413628**	**20**
Q920L2	ACALSIAESCRPGDK	0.768158285	2	2.35442
Q920L2	ACALSIAESCRPGDKVPPIK	1.11219817	3	3.34425
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.180252369	3	4.66975
Q920L2	ANAGEESVMNLDK	1.03825223	2	3.65202
Q920L2	GEGGILINSQGER	1.037661927	2	3.50224
Q920L2	GVIALCIEDGSIHR	0.77567276	2	4.02464
Q920L2	HTLSYVDTK	1.163683708	2	2.74252
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.113135848	3	6.50988
Q920L2	IDEYDYSKPIEGQQK	0.947213249	2	4.46356
Q920L2	KHTLSYVDTK	1.38182649	2	2.32885
Q920L2	LGANSLLDLVVFGR	1.398234623	2	2.36158
Q920L2	NTIIATGGYGR	0.997846477	2	2.43823
Q920L2	SMQSHAAVFR	1.033280903	2	2.30207
Q920L2	TGHSLLHTLYGR	1.248698222	2	3.0068
Q920L2	TLNEADCATVPPAIR	1.027056732	2	3.93699

Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.289162964	2	5.82082
Q920L2	VGSVLQEGCEK	1.008386422	2	3.67884
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.966264061	3	4.42785
Q920L2	VSQLYGDLQHLK	1.144235501	2	3.48149
Q920L2	VTLDYRPVIDK	0.950586854	2	3.13311
Q920P0	**DCXR L_xylulose reductase**	**1.008101897**	**0.980808**	**7**
Q920P0	ALTNHTVYCSTK	1.877698002	2	3.54928
Q920P0	AVVQVSQIVAR	1.022896821	1	2.4604
Q920P0	GVPGAIVNVSSQASQR	1.003763049	2	5.61999
Q920P0	SSMTTGSALPVDGGFLAT	0.954447633	1	2.55567
Q920P0	STVLALQAAGAQVVAVSR	0.764013793	2	3.79053
Q920P0	TREDLDSLVR	1.014423903	2	2.93862
Q920P0	VNAVNPTVVMTPMGR	0.704748722	2	3.28802
Q920P6	**ADA Adenosine deaminase**	**2.810402718**	**0.310368**	**2**
Q920P6	FKDDQANYSLNSDDPLIFK	1.29063584	2	2.66037
Q920P6	TVHAGEVGSAEVVR	7.389252167	2	3.45677
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.117032606**	**0.562107**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	1.122058973	2	4.17893
Q921F2	GISVHISNAEPK	1.087351173	2	2.5219
Q921F2	KDLKTGHSK	0.905511754	2	2.47245
Q921F2	TSDLIVLGLPWK	0.977848798	2	2.81391
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.066690694**	**2.44E-15**	**7**
Q922F4	ALTVPELTQQMFDAK	1.419420597	2	4.04999
Q922F4	GHYTEGAELVDSVLDVVR	1.115634973	2	6.77488
Q922F4	IREEYPDR	0.866225132	2	2.85394
Q922F4	MASTFIGNSTAIQELFK	1.740835256	2	4.43886
Q922F4	NMMAACDPR	1.084267588	2	2.51437
Q922F4	NSSYFVEWIPNNVK	1.103098	2	4.7016
Q922F4	YLTVATVFRGPMSMK+Oxidation(14)	0.722264282	2	2.31305
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.12425689**	**0.195452**	**2**
Q922J3	EMETMQAKLMK+Oxidation(5)	1.132581606	2	2.63983
Q922J3	HEEILQNLQKMLADTEDK	0.946431685	2	2.41927
Q923D2	**BLVRB Flavin reductase (NADPH)**	**1.062802195**	**0.998171**	**3**
Q923D2	LQDVTDDHIR	1.067235543	2	3.30509
Q923D2	TGLTTLAQAVQAGYEVTVLVR	0.970836386	3	4.01171
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.997344878	3	4.08565
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**1.082304934**	**0.835202**	**2**
Q923J6	LEFLTNLDIK	1.060617778	1	2.01331
Q923J6	MSDPNKTAITAEKEALNLK	1.093301038	2	2.466
Q923K9	**A1CF APOBEC1 complementation factor**	**1.406247197**	**0.007988**	**2**
Q923K9	LAPQILEEICQK	1.457625316	2	2.42998
Q923K9	TGYSLVQENGQR	1.244792162	2	2.77172
Q923V8	**SEP15 15 kDa selenoprotein**	**1.003943066**	**0.233121**	**2**
Q923V8	GCCQEEAQFETK	0.935193791	2	4.15206
Q923V8	LLDDNGNIAEELSILK	1.336157335	2	3.65501
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**1.107887122**	**0.897508**	**4**
Q924C3	AEYLHTWGGLLPVISK	1.057629836	3	3.6935
Q924C3	ELESPAAASLLAPMDLGEEPLEK	1.073029668	2	3.41619
Q924C3	SGTYFWPGSDVEIDGILPDIYK	0.947757332	2	3.6986
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	1.298302427	2	3.25038
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.036742638**	**0.999978**	**7**
Q924S5	AQSVLEEDHYGMEDVK	0.959517098	2	3.97115
Q924S5	FSVGGMTDVAEIK	1.092012884	2	2.87572
Q924S5	HVMDVVDEELSK	1.012950241	2	3.82484
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.04306185	3	6.39342

Q924S5	MEMINVSGYVAQEK	1.191885331	2	3.77971
Q924S5	QLEVEPEGLEPEAENK	1.065090352	2	4.16326
Q924S5	TENPLVLIDEVDK	1.124021765	2	2.4758
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**1.140460783**	**0.272832**	**3**
Q924W5	ELDMKEKELQEK	1.145146983	2	2.60381
Q924W5	MEEQQVRLNDAEKK	0.961177339	2	2.38744
Q924W5	TKEQINQGEERLTELK	1.206891259	2	2.56168
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.389756104**	**9.9E-20**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	1.34752267	2	4.11878
Q99020	FGEVVDCTIK	1.106891079	2	2.50071
Q99020	IFVGGLNPEATEEK	1.798696235	2	3.75335
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.157806341**	**0.002152**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.621723855	2	3.0218
Q99JI4	RLDEELEDAEK	1.210587488	2	2.91875
Q99JI4	VNEIVETNRPDSK	1.114468126	2	3.3329
Q99JW2	**ACY1 Aminoacylase_1**	**1.341270654**	**0.518126**	**2**
Q99JW2	FIEDTAAEK	1.101861816	2	2.63079
Q99JW2	SVSIQYLEAVR	1.272492202	2	2.39546
Q99K43	**PRC1 Protein regulator of cytokinesis 1**	**1.56665385**	**0.042074**	**2**
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(1)	1.56665385	2	2.36815
Q99K43	MNTTTMSSATPNSSIRPVFGGSVYR+Oxidation(6)	1.56665385	2	2.36833
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**1.231539412**	**0.033161**	**2**
Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(14)	1.227229049	2	2.51741
Q99KK9	YDLTVPFARYLAMNKLK+Oxidation(13)	1.232580329	2	2.59656
Q99KW3	**TARA TRIO and F_actin_binding protein**	**0.907232127**	**0.75284**	**2**
Q99KW3	AYQEELSRELSK	0.907160621	1	2.03069
Q99KW3	SEREIEQLK	1.064803125	1	1.9717
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.85151738**	**0.938253**	**2**
Q99L04	ATAQEAQSLGGR	0.886083263	2	3.34086
Q99L04	CVPVVCDSSQESEVK	0.747583965	2	4.44641
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.107608186**	**0.886768**	**4**
Q99LF4	GLGHQVATDALVAMEK	0.945728089	2	2.30945
Q99LF4	NLDFQDVLDK	0.882308202	2	2.88339
Q99LF4	NVTDVVNTCHDAGISK	1.114514755	2	4.27631
Q99LF4	TNLDESDVQPVK	1.108133961	2	3.692
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.037043011**	**0.939337**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(12)	1.037043011	2	2.33004
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(6)	1.037043011	2	2.3173
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**1.074851641**	**0.805208**	**2**
Q99M87	AQGLYETINVTIPAGIQTDQK	1.081129814	2	2.41028
Q99M87	GSIITNPCVVCR	1.070234314	2	2.59823
Q99ML9	**RN111 E3 ubiquitin_protein ligase Arkadia**	**1.21886127**	**0.361014**	**2**
Q99ML9	DMTGNQQEQEKSGVVRK	1.232598318	3	3.62336
Q99ML9	LHPHEVMQRMEVQR+Oxidation(7)	1.200633529	2	2.41263
Q99MN1	**SYK Lysyl_tRNA synthetase**	**1.078947966**	**0.017455**	**4**
Q99MN1	MATLQESEVKVDGEQKLSK+Oxidation(1)	0.773900478	2	2.33832
Q99MN1	RGDIIGVEGNPGK	1.249387475	2	3.32669
Q99MN1	SEEEFVHINNK	0.946039795	2	3.51425
Q99MN1	YLDLILNDFVR	1.481529604	2	2.69184
Q99MQ1	**BICC1 Protein bicaudal C homolog 1**	**1.182844983**	**0.610559**	**2**
Q99MQ1	EAKEMIMSVLDTK	1.055095644	2	2.39835

Q99MQ1	QYLMGCLPLVLMFDMK+Oxidation(15)	1.230136765	2	2.30176
Q99MS0	**S14L2 SEC14_like protein 2**	**1.087787776**	**0.331548**	**4**
Q99MS0	AGEMTEVLPNQR	1.043114649	2	3.82698
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	1.804657268	2	3.86068
Q99MS0	DQVKQQYEHSVQISR	1.091051022	2	2.38432
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.239975593	2	4.78036
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**1.000575364**	**0.503684**	**5**
Q99MZ8	GFSVVADTPELQR	0.970524696	2	3.58895
Q99MZ8	QQSELQSQVR	0.987049209	2	2.52025
Q99MZ8	QSFTMVADTPENLR	0.99535769	2	3.17551
Q99MZ8	TGDTGMLPANYVEAI	2.02203028	1	2.43065
Q99MZ8	TQDQISNIK	0.965051016	2	2.86952
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**1.149074393**	**0.004958**	**5**
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	1.024021004	2	6.94237
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.197756056	2	4.84822
Q99PF5	IGQQPQQPGAPPQQDYTK	0.862039199	2	4.05436
Q99PF5	IINDLLQSLR	1.349026413	2	2.57295
Q99PF5	SVSLTGAPESVQK	1.131293501	2	2.55032
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.199738797**	**0.000597**	**18**
Q99PL5	AENSQLTER	1.04432472	2	2.38333
Q99PL5	DALNQATSQVESK	0.959803618	2	3.31479
Q99PL5	EAEETQNSLQAECDQYR	1.056766026	2	5.64166
Q99PL5	EHTSHLEAELEK	1.086665567	2	3.35902
Q99PL5	GELESSDQVR	1.072142117	2	3.19865
Q99PL5	HMAAASAECQNYAK	1.052178288	2	4.30908
Q99PL5	HMAAASAECQNYAK+Oxidation(2)	1.284645512	2	3.95844
Q99PL5	IQEELEK	1.026942367	1	2.31276
Q99PL5	LKELESQVSCLEK	1.23455631	2	4.08
Q99PL5	LLATEQEDAAVAK	1.402176983	2	3.99225
Q99PL5	LQQENSILR	0.921224779	2	2.61145
Q99PL5	QLHLAEAQTK	1.037652815	2	2.35193
Q99PL5	RLEEVTR	1.024637078	2	2.44303
Q99PL5	TGVIQDTWHK	1.021395062	2	2.31916
Q99PL5	TILAETEGMLK	1.115767669	2	3.16586
Q99PL5	TLQEQLENGPNTQLAR	1.164702979	2	5.04458
Q99PL5	TLVSTVGSMVFSEGEAQR	1.217191069	2	4.28399
Q99PL5	VEPAVSSIVNSIQVLASK	1.285201717	2	4.01119
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**1.170647427**	**0.27073**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(10)	1.170647427	2	2.69381
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(4)Oxidation(11)	1.170647427	2	2.6509
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.056531929**	**0.997035**	**2**
Q9CPQ1	FGVAEPR	1.107011778	2	2.4323
Q9CPQ1	NYDSMKDFEEMR	1.047681815	2	3.79654
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**0.886675299**	**0.28416**	**2**
Q9CRB9	VAEELALEQAK	0.886525475	2	3.43956
Q9CRB9	YEYHPVCADLQTK	1.054831165	2	3.67846
Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**1.21978938**	**0.001019**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.197505916	2	2.66744
Q9CTN4	LKDSGDVSDIIEK	1.671921296	2	2.47877
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.962661482**	**0.999634**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	1.059437403	2	4.37884
Q9CW42	GLSVSEAECTAMGLR	1.027456998	2	3.17982
Q9CW42	LQQVGTVAQLWIYPIK	0.883749242	2	3.33923
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.597931233**	**0.011063**	**3**

Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.408254138	2	4.26136
Q9CWH6	ALLEVVQSGGK	1.456034486	2	2.94526
Q9CWH6	LTVEDPVTVEYITR	1.391380285	2	4.00701
Q9CWK8	**SNX2 Sorting nexin_2**	**0.901910374**	**0.998921**	**3**
Q9CWK8	ALSQLAEVEEK	0.97933912	2	2.37241
Q9CWK8	AVNTQALSGAGILR	1.070812837	2	3.51749
Q9CWK8	QQQFENLDQQLR	0.901515793	2	2.51388
Q9CXD6	**CC90A Coiled_coil domain_containing protein 90A_ mitochondrial**	**1.391253363**	**0.189025**	**2**
Q9CXD6	MLELRTEIVSLHAQQDR	1.427178659	2	2.68345
Q9CXD6	VRTDTKLNFNLEK	1.14247934	2	2.48492
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.894013177**	**0.411168**	**2**
Q9CYW4	LEDILTGLGLR	0.89256629	2	3.74447
Q9CYW4	RLEDILTGLGLR	1.030546137	2	3.28896
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.152871741**	**0.00191**	**2**
Q9CZY3	LLEELEEGQK	1.066979188	2	2.8116
Q9CZY3	VNMSGVSSSNGVVDPR	1.394295874	2	3.01999
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**1.127527143**	**0.004853**	**3**
Q9D024	ERIMNEEDPEKQR	1.723769322	2	2.58587
Q9D024	IMQEEGQPLKLPDTK	0.899090866	2	2.89921
Q9D024	RLEEAALR	1.215189571	2	2.61883
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.576274003**	**2.91E-13**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	1.079755721	3	4.27414
Q9D0M3	GLLSSLDHTSIR	1.135117606	2	2.77649
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.683155671	2	5.2655
Q9D0M3	HLVGVCYTEEEAK	1.276018515	2	3.93588
Q9D0M3	LSDYFPKPYPNPEAAR	1.217770342	3	3.41362
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**0.994340545**	**0.033157**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.948060907	2	2.94449
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.254733734	2	5.23579
Q9D0S9	SLPADILYEDQQCLVFR	1.270476997	2	4.47977
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**0.980836583**	**0.843108**	**5**
Q9D172	GVEVTVGHEQEEGGK	0.944464997	2	3.79367
Q9D172	GVTEAHVDQK	0.60128217	2	2.82717
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.17865089	2	4.33208
Q9D172	NLSTFAVDGK	0.933242648	1	2.92095
Q9D172	NVLAESAR	1.463110105	1	2.00769
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.052571787**	**0.899757**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(1)	1.001384735	2	2.36971
Q9D1Q6	NIIGYFEQK	1.071116115	1	2.47428
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.136211833	2	5.43729
Q9D1Q6	VDCDQHSDIAQR	1.050450238	2	3.5449
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.23529587**	**9.9E-20**	**5**
Q9D2U9	AMGIMNSFVNDIFER	1.307656985	2	5.17726
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)	1.424942513	2	4.3576
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(2)Oxidation(5)	1.147561064	2	3.08808
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(5)	1.430524942	2	3.88732
Q9D2U9	LLLPGELAK	1.275075985	2	2.41735
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.062160803**	**0.999349**	**2**
Q9D6M3	GAAVNLTLVTPEK	1.068446233	2	2.77061
Q9D6M3	GVNEDTYSGFLDCAR	0.973213089	2	4.65099
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.272489462**	**9.22E-06**	**10**
Q9D6Y9	CVAYAESHDQALVGDK	1.329753577	2	4.95768
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	1.727805867	3	3.91194
Q9D6Y9	GTHDLWDSR	1.351109859	2	2.364

Q9D6Y9	HFTSNVLPR	1.282805517	2	2.45332
Q9D6Y9	IVLDSDAAEYGGHQR	1.375065712	2	4.49128
Q9D6Y9	IYESHVGISSHEGK	1.21617286	2	4.53139
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	2.478133876	2	3.80441
Q9D6Y9	QFNLTDDDLLR	1.218132141	2	2.75404
Q9D6Y9	RQFNLTDDDLLR	1.140608262	2	2.86486
Q9D6Y9	WELYIPPK	1.368519198	2	2.38575
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.126956319**	**0.971574**	**2**
Q9D6Z1	ELNEEKLEK	0.945050276	2	2.46431
Q9D6Z1	IDCFSEVPTSVFGEK	1.130297756	2	2.75281
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.288178037**	**0.456676**	**4**
Q9D7B6	AVIFEDCAVPVANR	0.908930153	2	3.36135
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	2.241874378	2	4.92601
Q9D7B6	IGTEGQGFLIAMK	1.064603134	2	2.98046
Q9D7B6	VHQILEGSNEVMR	1.332155419	2	2.91191
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**1.158098457**	**0.320956**	**2**
Q9D7X8	ISDEMEDIIK	1.100666682	2	2.735
Q9D7X8	SNISSLDEQEGVK	1.167490072	2	3.74323
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.370201079**	**1.77E-10**	**5**
Q9D819	GISCMNTTVSESPFK	1.067841851	2	4.74466
Q9D819	GQYISPFHDVPIYADK	1.45291359	2	3.94182
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.311617816	3	4.98183
Q9D819	VLGILAMIDEGETDWK	1.761023502	2	4.29686
Q9D819	YVANLFPYK	1.196337237	1	2.13105
Q9D855	**QCR7 Cytochrome b_c1 complex subunit 7**	**1.117479426**	**0.991845**	**2**
Q9D855	RLPEDLYNDR	1.014460695	2	2.54444
Q9D855	YEEDKFYLEPYLK	1.092965601	2	4.62457
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.127357913**	**0.998539**	**3**
Q9D880	TIALNQVEDVR	0.960979891	2	3.12731
Q9D880	TVLEHYALEDDPLEAFK	1.139746175	2	4.92595
Q9D880	VLLDLSAFLK	0.9658427	2	2.55341
Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**1.274430999**	**0.425394**	**2**
Q9D8W5	MVQQCCTYVEEITDLPVK	1.394035388	2	4.88962
Q9D8W5	WSTLVEDYGVELR	1.097754141	2	3.08287
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**1.130032234**	**0.963378**	**2**
Q9DB15	NYVQGINLVQAK	1.130669377	2	2.78114
Q9DB15	SEALAGAPLDNAPK	0.976882634	2	3.1921
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.211549351**	**0.297546**	**2**
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	1.338646988	3	3.84182
Q9DBH5	WSELAGCTADFR	1.105002724	2	3.2839
Q9DCJ5	**NDUA8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8**	**1.039390139**	**0.899061**	**2**
Q9DCJ5	ARPEPNPVIEGDLKPAK	1.035574919	3	4.66534
Q9DCJ5	TDRPLPENPYHSR	0.992184073	3	3.89404
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**0.857514677**	**0.990777**	**3**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.120199483	3	4.18709
Q9DCM0	SLLPGCQSVISR	0.887029202	2	3.07383
Q9DCM0	TDFQQGCAK	0.855291699	2	2.91068
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.291652176**	**0.000427**	**3**
Q9DCS9	AYDLVVDWPVTLVR	1.286801957	2	4.4035
Q9DCS9	RVPDITECK	1.28764091	2	2.32679
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.997028297	2	2.97317

Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.209952266**	**0.000949**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.453768671	2	2.83333
Q9DCT2	ILTDYGFEGHPFR	0.790008244	2	2.89228
Q9DCT2	KFDLNSPWEAFPAYR	1.220230915	2	3.6585
Q9DCT2	SLADLTAVDVPTR	1.250938327	2	2.73654
Q9DCT2	VVAEPVELAQEFR	1.118611215	2	3.64921
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.063683374**	**0.999993**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.058731133	2	5.44603
Q9DCU9	LIEPNTAVTR	1.046172928	2	3.19021
Q9DCU9	TMDWFGYYGGPCR	1.197346864	2	3.53649
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.11692618**	**0.971663**	**9**
Q9EP89	EVWSEGLGYADVENR	0.85959861	2	3.02035
Q9EP89	FENSIESLR	0.7944652	2	2.97218
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	1.136248026	2	5.52239
Q9EP89	IKDEVGAPGIVVGVSVDGK	0.836464386	2	4.16343
Q9EP89	KNDFEQGELYLK	0.876027387	2	4.19493
Q9EP89	LDLDLPVQHYVPEFPEK	1.093147542	3	3.68893
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.120088096	3	3.80164
Q9EP89	LVNTPYVDNSYK	1.075351137	2	2.57741
Q9EP89	WAGGGFLSTVGDLLK	0.940281796	2	4.63273
Q9EPH2	**MRP MARCKS_related protein**	**1.040470228**	**0.257552**	**2**
Q9EPH2	AAATPESQEPQAK	1.074441415	2	2.66748
Q9EPH2	GDVTAEEAAGASPAK	0.881678885	2	3.05032
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.203618679**	**0.00299**	**7**
Q9EPH8	ALDTMNFDVIK	1.218838862	2	3.10565
Q9EPH8	GFGFVCFSSPEEATK	1.121477269	2	2.65519
Q9EPH8	GFGFVSFER	1.269578262	2	2.50765
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	1.052877037	3	4.73361
Q9EPH8	KEFSPFGTITSAK	0.959507294	2	3.18879
Q9EPH8	SKVDEAVAVLQAHQAK	1.175304262	3	4.31496
Q9EPH8	SLGYAYVNFQQPADAER	1.50998896	2	3.3638
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.124614596**	**9.9E-20**	**13**
Q9EQ76	ASIYQSVFTNSSK	1.234300149	2	2.78421
Q9EQ76	GTCILPSVNDMMDDIDEK	1.603440567	2	3.92551
Q9EQ76	ILCGTVSIKPNVK	1.122881177	2	2.91494
Q9EQ76	KEPVFNDELPAR	0.990833334	2	3.04971
Q9EQ76	LQEYITSFATEK	1.773811172	2	3.32958
Q9EQ76	NNEVTLYK	1.59306687	1	2.00318
Q9EQ76	NNLPTAISDWWYMK	1.504690343	2	3.01581
Q9EQ76	SCLEEGLEPTCFER	0.987380574	2	4.38774
Q9EQ76	SDDVGGLWK	1.440649933	2	2.83504
Q9EQ76	VAVIGAGVSGLAAIR	0.697170296	2	3.93654
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	1.461532528	3	4.00112
Q9EQ76	VWNDGYPWDMVVITR	1.514425088	2	3.86116
Q9EQ76	YIQFETLVTR	2.051096198	2	2.85477
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.234354877**	**1.17E-06**	**3**
Q9EQH3	IREDLPNLESSEETEQINK	1.239525928	2	5.09948
Q9EQH3	LNLEHIATSSAVSK	1.354349708	2	4.03579
Q9EQH3	VLETTVEIFNK	1.143609168	2	2.95944
Q9EQS0	**TALDO Transaldolase**	**1.103906713**	**2.6E-09**	**7**
Q9EQS0	ALAGCDFLTISPK	1.413862315	2	2.93502
Q9EQS0	ILDWHVANTDKK	1.268872772	2	3.25017

Q9EQS0	LGGPQEEQIK	1.350552703	2	2.67903
Q9EQS0	LSSTWEGIQAGK	1.042707691	2	2.71459
Q9EQS0	SYEPQEDPGVK	1.053033895	2	2.9091
Q9EQS0	VSTEVDAR	1.062604217	1	1.98173
Q9EQS0	WLHNEDQMAVEK	1.067058372	2	3.69067
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**0.86963369**	**0.510061**	**2**
Q9EQW7	DETIAVPLEENSALPK	0.841130121	2	2.66329
Q9EQW7	VTQWAEER	1.194156021	2	2.45283
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.211730271**	**1.88E-07**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.080904617	2	3.85704
Q9EQX9	SNEAQAIETAR	1.242027977	2	3.27673
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.011387765	3	3.99659
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**0.950209507**	**0.00047**	**17**
Q9ER34	ADIANLAEEFK	0.964459462	2	2.43871
Q9ER34	CTTDHISAAGPWLK	1.057444683	2	3.90674
Q9ER34	DINQEVYNFLATAGAK	0.920686507	2	4.1542
Q9ER34	FKLEAPDADELPR	1.128678484	2	3.69694
Q9ER34	FNPETDFLTGK	1.002557765	1	2.28887
Q9ER34	GHLDNISNNLLIGAINIENGK	0.978061996	2	5.61296
Q9ER34	IVYGHLDDPANQEIER	1.283361004	2	4.73193
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	1.189122414	3	4.09753
Q9ER34	LTGTLSGWTSPK	1.242921439	2	3.11681
Q9ER34	NAVTQEFGPVPDTAR	0.853106029	2	4.1567
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	1.133139442	3	4.21467
Q9ER34	QGLLPLTFADPSDYNK	0.980885325	2	3.57098
Q9ER34	SDFDPGQDTYQHPPK	0.913847608	2	2.91355
Q9ER34	SQFTITPGSEQIR	0.954944042	2	3.56567
Q9ER34	VDVSPTSQR	1.027292493	2	2.52144
Q9ER34	VGLIGSCTNSSYEDMGR	1.077944989	2	4.2311
Q9ER34	WVVIGDENYGEGSSR	1.036281827	2	4.2024
Q9ER72	**SYCC Cysteinyl_tRNA synthetase_ cytoplasmic**	**0.934148842**	**0.651247**	**2**
Q9ER72	LSETTDPDKR	0.911281791	2	2.43009
Q9ER72	QMLERIQNSVK+Oxidation(2)	1.115261473	2	2.46966
Q9ERK4	**XPO2 Exportin_2**	**1.361823392**	**0.12242**	**3**
Q9ERK4	IIIPEIQK	1.275075985	2	2.39852
Q9ERK4	LLQTDDEEEAGLLELLK	1.042888783	2	2.38439
Q9ERK4	SNNVNEFPVLK	1.379636716	2	2.49929
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.871946832**	**0.165972**	**3**
Q9ES21	HFDSQVIIYGK	0.864616488	2	2.45565
Q9ES21	LSNTSPEFQEMSLLER	1.790550529	2	3.60019
Q9ES21	TQLGLVMDGFNSLLR	0.866675559	2	3.98379
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.079957744**	**0.935809**	**12**
Q9ES38	ACQAAWALK	1.104542306	2	2.73196
Q9ES38	ADVWENFQQR	1.119973319	2	3.06449
Q9ES38	EGFDVGVIADPLYILDNK	1.15133673	2	4.91263
Q9ES38	GATAILVLPSK	1.151139496	2	2.92919
Q9ES38	IQDSLEITNTYK	1.189054233	2	3.65027
Q9ES38	LKEATIQEDK	1.299219231	2	2.80611
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.024181279	2	4.22972
Q9ES38	QGFCIPVETGKPGLLLTK	0.95067952	3	3.66282
Q9ES38	SISALSVFLGLAK	1.353484356	2	3.1983
Q9ES38	SLMPDVYQAVCEGTWK	1.378255948	2	3.91605
Q9ES38	YLCNVPGQPEDK	1.029479304	2	3.48668
Q9ES38	YLCNVPGQPEDKK	1.184929135	2	3.75664
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.973107838**	**0.879175**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.972998423	2	3.79005

Q9EST6	SLDLFGCEVTNR	1.137005472	2	2.74477
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.151647289**	**0.956564**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.127187055	3	5.728
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.120606265	3	5.98673
Q9ESW0	QGQGQLVTCSGAFK	1.062305642	2	2.35976
Q9HB97	**PARVA Alpha_parvin**	**1.21083487**	**0.054457**	**4**
Q9HB97	DLAEDLYDGQVLQK	1.660273574	2	2.35984
Q9HB97	LNVAEVTQSEIAQK	1.092054747	2	3.14655
Q9HB97	QIQEEITGNTEALSGR	1.230768673	2	3.16743
Q9HB97	VLIDWINDVLVGER	1.245931195	2	3.23792
Q9JHL4	**DBNL Drebrin_like protein**	**1.097792272**	**0.51209**	**2**
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**1.610589317**	**0.079732**	**2**
Q9JHZ9	AYEQLGYR	1.495714202	2	2.55003
Q9JHZ9	HLEGLLPVGMPTADTQR	1.626222609	2	3.79439
Q9JI57	**GT2D1 General transcription factor II_I repeat domain_containing protein 1**	**1.163071274**	**0.561226**	**2**
Q9JI57	EMEDINTLRECVQILFNSR	1.124098209	2	2.32258
Q9JI57	GTQPTTEGQAHPLVLPTR	1.330399803	2	2.37982
Q9JI85	**NUCB2 Nucleobindin_2**	**1.074918512**	**0.943288**	**5**
Q9JI85	FQQGIAPSGPAGELK	1.256256543	2	2.66386
Q9JI85	LSQELDLVSHK	1.052138068	2	2.75849
Q9JI85	QEYQQAVQQLEQK	1.089066765	2	4.3007
Q9JI85	TRLDELK	0.791869565	1	2.02823
Q9JI85	VHNVEPVESAR	1.093550206	2	2.89633
Q9JI91	**ACTN2 Alpha_actinin_2**	**1.107017682**	**0.020506**	**8**
Q9JI91	ACLISMGYDLGEAEFAR	1.195181647	2	4.42063
Q9JI91	GYEEWLLNEIR	1.924795817	2	2.85053
Q9JI91	HRPDLIDYSK	1.51647003	2	2.41712
Q9JI91	HTNYTMEHIR	1.077747733	2	2.80665
Q9JI91	KHEAFESDLAAHQDR	1.096219798	2	5.29776
Q9JI91	MLDAEDIVNTPKPDER	0.964654173	2	3.08899
Q9JI91	QSILAIQNEVEK	1.840385637	2	2.843
Q9JI91	TINEVETQILTR	1.776661086	2	3.16435
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.188269485**	**1.02E-08**	**9**
Q9JJ19	AVDPDSPAEASGLR	1.130666941	2	3.24841
Q9JJ19	IVEVNGVCMEGK	1.210227178	2	3.67466
Q9JJ19	LLVVDPETDEQLK	1.202690429	2	2.68992
Q9JJ19	LLVVDPETDEQLKK	1.580924402	2	2.86783
Q9JJ19	LVEPGSPAEK	1.135240189	2	2.56204
Q9JJ19	LVEVNGENVEK	1.21672718	2	2.88286
Q9JJ19	SEHTEPPAAADTK	0.800670067	2	3.20641
Q9JJ19	SEHTEPPAAADTKK	1.130555961	3	4.61147
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	1.245808393	3	3.91459
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.328480185**	**3.41E-12**	**3**
Q9JJ54	FGDVVDCTLK	1.051059407	2	2.72291
Q9JJ54	IDASKNEEDEGHSNSSPR	1.335889744	3	3.89747
Q9JJ54	IFVGGLSPDTPEEK	1.344856229	2	3.914
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**0.877835992**	**0.56181**	**3**
Q9JJ79	ASDLKDLNSR	1.117493337	2	2.35293
Q9JJ79	DQIEVMKGNVKSR	0.790134226	2	2.36657
Q9JJ79	NCLEEWTKAAGLEK	0.868682791	2	2.37231
Q9JJM9	**SEPT5 Septin_5**	**1.681458263**	**0.03561**	**2**
Q9JJM9	LIRMKDEELR	1.709196834	2	2.48162
Q9JJM9	MQEMLQKMK+Oxidation(4)	1.249072991	2	2.41791

Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.295040654**	**0.097869**	**2**
Q9JJU8	GDYDAFFEAR	1.368742874	2	2.54491
Q9JJU8	QQDVLCFLEANK	1.273573541	2	2.88103
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.222992376**	**5.48E-06**	**4**
Q9JK38	GRVEDVVVSDECR	1.214534339	2	3.45982
Q9JK38	ITLECLPQNVGFYK	1.434890506	2	3.74769
Q9JK38	VEDVVVSDECR	1.131334734	2	3.7012
Q9JK38	VLGQLTETGVVSPEQFMK	1.351211735	2	4.53933
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.144605803**	**0.808881**	**8**
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	0.739896353	3	3.9182
Q9JLA3	EGETYYDVVAVVDPVTR	0.871868249	2	2.60989
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.167317587	3	6.13379
Q9JLA3	IVPEWQDYDQEIK	1.160189703	2	3.56258
Q9JLA3	LGIEGLSLHNILK	1.682328746	3	3.88656
Q9JLA3	LNIQPSETDYAVDIR	1.21696611	2	4.13305
Q9JLA3	VEEDVASDLVMK	1.063505796	2	3.25843
Q9JLA3	YVLEPEISFTADNSFAK	1.121705587	2	3.72228
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.154045423**	**0.002028**	**17**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.148560176	2	4.44175
Q9JLJ3	ANDTTFGLAAGVFTR	0.974711046	2	4.90164
Q9JLJ3	CQVLLEAAR	1.260333549	2	3.03792
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.17586735	2	4.69072
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.133181358	2	4.65404
Q9JLJ3	EVNLAVENAK	1.160512012	2	2.97666
Q9JLJ3	GALLANFLTQGQVCCNGTR	0.920089569	2	5.34989
Q9JLJ3	GIKPITLELGGK	1.018472494	3	3.9211
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.197854832	2	4.58321
Q9JLJ3	IGDPLLEDTR	1.175186238	2	3.92716
Q9JLJ3	MGPLINAPHLER	1.16606593	2	3.49509
Q9JLJ3	MGPLINAPHLER+Oxidation(1)	1.208283253	2	3.01605
Q9JLJ3	RDEIAIMETINNGK	1.123720915	2	5.45677
Q9JLJ3	VEPVDASGTEK	1.152246341	2	2.32398
Q9JLJ3	VSFTGSVPTGMK	1.180242959	2	3.36805
Q9JLJ3	VSFTGSVPTGMK+Oxidation(11)	1.432832814	2	2.81419
Q9JLJ3	VTIEYYSQLK	1.848021047	2	3.19293
Q9JLT0	**MYH10 Myosin_10**	**1.305167321**	**5.91E-12**	**3**
Q9JLT0	AGVLAHLEEER	1.306023419	2	3.5163
Q9JLT0	DAAGLESQLQDTQELLQEETR	0.749422347	2	3.74688
Q9JLT0	DEELLKVKEK	1.062226968	1	2.1485
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.981775661**	**0.999999**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	0.991177034	2	5.8055
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.922143967	3	4.58183
Q9JLZ3	SEVPGIFCAGADLK	0.934114564	2	3.2591
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**0.823422132**	**0.947252**	**13**
Q9JM53	DGEQHEDLNEVAK	0.994819727	2	3.92656
Q9JM53	ILPEYLSNWTMEK	1.149202748	2	2.61018
Q9JM53	KSQASGIEVIQLFPEK	1.213392004	2	3.6479
Q9JM53	KVETDHIVTAVGLEPNVELAK	1.119080407	2	6.32523
Q9JM53	LNDGSQITFEK	1.148851107	2	3.57878
Q9JM53	SATEQSGTGIR	0.811742519	2	3.85415
Q9JM53	SITVIGGGFLGSELACALGR	0.894468239	2	3.41395
Q9JM53	SQASGIEVIQLFPEK	0.916960094	2	4.25662

Q9JM53	TGGLEIDSDFGGFR	1.062949616	2	3.81632
Q9JM53	VETDHIVTAVGLEPNVELAK	0.943908443	2	6.01878
Q9JM53	VLIVSEDPELPYMRPPLSK	1.074214444	3	3.70633
Q9JM53	VMPNAIVQSVGVSGGK	1.167500639	2	4.52316
Q9JM53	VNAELQAR	0.957720548	2	2.37445
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**1.208822892**	**0.886909**	**2**
Q9JMA1	CTESEEEEVTK	1.209676409	2	3.64424
Q9JMA1	EKESVNAKVLK	1.112275191	2	2.55952
Q9JMB7	**PIWL1 Piwi_like protein 1**	**1.230019418**	**0.417732**	**2**
Q9JMB7	ELIGLIVLTKYNNK	1.333312773	2	2.42495
Q9JMB7	SQELQISAGFQELSLAERGGRR	1.028925024	2	2.34077
Q9JMD3	**PCTL PCTP_like protein**	**1.365124442**	**6.26E-11**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.19348891	2	4.54436
Q9JMD3	ESVQVPDDQDFR	1.141758363	2	2.67156
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.48803895	3	4.43348
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(1)	1.33631202	3	3.57085
Q9JMD3	SSQFLAPK	1.184313766	2	2.3466
Q9JMD3	WDSNVIETFDIAR	1.458810138	2	4.12259
Q9JMK8	**VPS54 Vacuolar protein sorting_associated protein 54**	**0.890993484**	**0.839355**	**2**
Q9JMK8	DKIAQIDK	1.02844094	1	1.9337
Q9JMK8	STSLLGALQSQANK	0.875464496	2	2.35325
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.160572289**	**0.003009**	**5**
Q9QVC8	ALELDSNNEK	1.073573207	2	2.41537
Q9QVC8	GEPNNVAGNQAQVK	1.127028989	2	3.89297
Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.160780029	2	3.30028
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	1.119112863	3	6.1951
Q9QVC8	VLQLYPSNK	1.251496172	2	2.5176
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**0.90900344**	**0.020586**	**2**
Q9QWN8	IIGTQEQLNQR	1.549741948	2	2.45961
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	0.871110616	3	3.96011
Q9QX79	**FETUB Fetuin_B**	**0.987984222**	**0.76307**	**3**
Q9QX79	GSIQHLPEQEEPEDSKGK	1.116980911	3	3.92163
Q9QX79	IFYETVHGQCK	1.254067521	2	2.88449
Q9QX79	NTAPTSSPSITAPR	1.081745805	2	3.30721
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**1.19954136**	**0.282089**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	1.013528723	2	3.75332
Q9QXG4	IGPIATPDYIQNAPGLPK	1.292028672	2	2.87866
Q9QXK2	**RAD18 E3 ubiquitin_protein ligase RAD18**	**1.022624919**	**0.405384**	**2**
Q9QXK2	SAAEIVQEIESMEK	1.058122015	1	2.09077
Q9QXK2	TVYNLLSDR	0.414593785	2	2.34184
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**1.039968382**	**0.743432**	**2**
Q9QXK3	SIATLAITTLLK	1.210126832	2	3.02534
Q9QXK3	SSEPVQLTEAETEYFVR	0.967552855	2	3.84455
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.267559565**	**9.9E-20**	**28**
Q9QXQ0	ACLISLGYDVENDR	1.383858206	2	3.96035
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.178523205	3	3.31328
Q9QXQ0	AGTQIENIDEDFR	1.000613546	2	2.83635
Q9QXQ0	AGTQIENIDEDFRDGLK	1.142321695	2	4.47269
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.243539652	3	3.70906
Q9QXQ0	DDPVTNLNNAFEVAEK	2.009692818	2	3.63947
Q9QXQ0	ETTDTDTADQVIASFK	1.189401534	2	4.88499
Q9QXQ0	HRDYETATLSDIK	1.424852281	2	4.04131
Q9QXQ0	HRPELIEYDK	1.065045707	3	4.72497
Q9QXQ0	HTNYTMEHLR	1.077747733	2	2.80665
Q9QXQ0	ICDQWDNLGSLTHSR	1.295119804	2	4.03313
Q9QXQ0	ISIEMNGTLEDQLSHLK	0.9790242	2	2.83471

Q9QXQ0	KDDPVTNLNNAFEVAEK	1.071527441	3	4.9324
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.765425553	2	4.47107
Q9QXQ0	LVSIGAEEIVDGNAK	1.546451702	2	3.68215
Q9QXQ0	MAPYQGPDAAPGALDYK	1.296722509	2	4.32053
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(1)	1.314656887	2	3.09388
Q9QXQ0	MLDAEDIVNTARPDEK	1.268845102	2	4.05036
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(1)	0.973204561	2	2.64012
Q9QXQ0	NFITAEELR	1.136623228	1	2.14241
Q9QXQ0	QLETIDQLHLEYAK	1.338426336	2	3.10192
Q9QXQ0	RDHALLEEQSK	1.088322074	3	4.18005
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.459888754	3	3.6489
Q9QXQ0	TINEVENQILTR	1.156402553	2	3.3661
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	1.906545312	2	5.00096
Q9QXQ0	VGWEQLLTTIAR	1.388101799	2	4.24064
Q9QXQ0	VLAGDKNFITAEELR	0.984612678	2	3.77479
Q9QXQ0	VLAVNQENEHLMEDYER	1.177871689	2	5.55292
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.135049735**	**0.002037**	**4**
Q9QXT0	ALVDELEWEIAR	0.913926983	2	3.77627
Q9QXT0	INPDGSQSVVEVPYAR	1.502807735	2	3.7483
Q9QXT0	RTDLCDHALHR	1.07180691	3	3.35456
Q9QXT0	TDLCDHALHR	1.1171241	2	3.06739
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.087891219**	**1.72E-05**	**18**
Q9QXX4	ASGDAARPFLLQLAESAYR	0.853721314	3	3.32019
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.000436619	3	6.07012
Q9QXX4	DVEVTKEEFALAAQK	1.095364341	2	4.08506
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	0.968974395	2	6.55393
Q9QXX4	FGLYLPLFKPSASTSK	0.964922328	2	2.60592
Q9QXX4	GLLPQLLGVAPEK	1.197255398	2	3.18195
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.416366104	2	5.39013
Q9QXX4	ILREEGPK	1.060384126	2	2.40582
Q9QXX4	ITLPAPNPDHVGGYK	1.248074219	2	2.41677
Q9QXX4	KDVEVTKEEFALAAQK	0.934300456	2	5.51586
Q9QXX4	LQVAGEITTGPR	1.075470828	2	3.70581
Q9QXX4	LTVNDFVR	1.3035718	2	2.56114
Q9QXX4	NGEFFMSPHDFVTR	1.134629626	2	4.00643
Q9QXX4	SSPQFGVTLLTYELLQR	1.583730397	2	4.5386
Q9QXX4	STGSFVGELMYK	1.072265468	2	3.0857
Q9QXX4	TVELLSGVVDQTK	1.291439447	2	3.96633
Q9QXX4	YEGFFGLYR	1.039299368	2	2.71993
Q9QXX4	YLNIFGESQPNPK	1.016458496	2	4.32992
Q9QXY2	**SRCN1 SRC kinase signaling inhibitor 1**	**1.320897559**	**0.217513**	**2**
Q9QXY2	DINRLLEETQAELLK	1.777579425	2	2.41382
Q9QXY2	IIAELESGGGSVPPMK	0.981542842	2	2.4363
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.831444892**	**0.5117**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	1.146927846	2	4.05964
Q9QYU4	RAPAFLSADEVQDHLR	1.064107109	3	5.0788
Q9QYU4	SLGMAVEDLVAAK	0.869794935	2	3.62316
Q9QYU4	SSSLLIPPLEAALANFSK	0.751861135	2	3.13794
Q9QZ76	**MYG Myoglobin**	**1.157594571**	**0.984147**	**7**
Q9QZ76	GQHAAEIQPLAQSHATK	1.121253498	2	4.56899
Q9QZ76	HGCTVLTALGTILK	1.154817171	2	3.51214
Q9QZ76	HGCTVLTALGTILKK	1.532862211	3	3.70129
Q9QZ76	KGQHAAEIQPLAQSHATK	0.992257316	3	4.78344
Q9QZ76	KKGQHAAEIQPLAQSHATK	1.615037259	3	4.59734
Q9QZ76	VEGDLAGHGQEVLISLFK	2.020697425	3	4.34595

Q9QZ76	YSGDFGADAQGAMSK	1.763666719	2	4.03224
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.075256143**	**0.225109**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	0.8893907	2	3.46915
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.196169826	2	2.5066
Q9QZA2	FYNELTEILVR	1.044531653	2	2.70603
Q9QZA2	LLDEEEATDNDLR	1.029139577	2	3.67423
Q9QZA2	NIQVSHQEFSK	1.215137396	2	3.37834
Q9QZA2	NLATAYDNFVELVANLK	1.030495542	2	4.43371
Q9QZA2	STAVVEQGGIQTVDQLIK	1.007951397	2	4.4462
Q9QZA2	TMQGSEVVNVLK	0.856462267	2	3.34316
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.030422696**	**0.99997**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	1.018425435	2	4.95224
Q9QZD8	LFSGATMASSR	0.513703198	2	2.63167
Q9QZD8	MTGMALQVVR	1.028289368	2	2.66777
Q9QZD8	NYSHALDGLYR	1.051169775	2	2.92306
Q9QZD8	VHLQTQQEVK	1.030459271	2	2.85231
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.033367917	2	5.69168
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	1.061721638	3	3.80411
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.211730781**	**0.608996**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.148167228	2	4.18367
Q9QZH8	WFLQEDILEK	1.3346763	2	3.32079
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.438864893**	**5.22E-11**	**5**
Q9QZU7	IDANNVAYTTGK	1.484619149	2	3.30852
Q9QZU7	IIELDDKGQVVR	1.155982023	2	2.536
Q9QZU7	LLLEALDVNIR	1.862884916	2	2.83693
Q9QZU7	MNPGDVITFDNWR	1.46933693	2	2.72872
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.263118957	2	4.476
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.962982915**	**0.398996**	**10**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	1.442493487	3	4.35747
Q9R063	ETDLLLDDSLVSLFGNR	1.19755018	2	4.48853
Q9R063	GVLFGVPGAFTPGCSK	0.880029713	2	4.53883
Q9R063	KGVLFGVPGAFTPGCSK	0.877167832	2	3.5012
Q9R063	KVNLAELFK	0.865558873	2	2.3048
Q9R063	THLPGFVEQAGALK	0.970817459	3	4.34332
Q9R063	VGDTIPSVEVFEGEPGK	0.937709068	2	4.47727
Q9R063	VGDTIPSVEVFEGEPGKK	0.991388446	2	3.90015
Q9R063	VNLAELFK	0.851842162	2	2.72246
Q9R063	VQLLADPTGAFGK	1.069495641	2	3.71058
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**1.118923323**	**0.918424**	**2**
Q9R064	ADTSSLTVDVMSPASK	1.013426913	2	3.47929
Q9R064	LYVYNTDTDNCR	1.536037109	2	2.79704
Q9R0N0	**GALK1 Galactokinase**	**1.122436738**	**0.760739**	**4**
Q9R0N0	RQCEEVAQALGK	1.052875374	2	2.85715
Q9R0N0	SLETSLVPLSDPK	1.132589583	2	3.35619
Q9R0N0	TDGLVSLLTTSK	1.305296399	2	3.43189
Q9R0N0	VEELLAEAR	1.082342884	2	3.04239
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.085997398**	**0.092493**	**6**
Q9R0T3	AEPSVAEYTVR	1.016907029	2	2.82909
Q9R0T3	ICSEVLQLEPDNVNALK	1.359448215	2	5.56284
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	0.915109963	3	5.40821
Q9R0T3	LIGSAEELIR	1.349942174	2	2.86087
Q9R0T3	LKNDNTEAFYK	1.386536814	2	2.81941
Q9R0T3	SNPSENEEKEAQSQLVK	1.004857916	2	5.09155
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**0.934521964**	**0.973439**	**3**
Q9R112	EGNALFTFPNTPVK	0.935004492	2	3.04641

Q9R112	STLSVIPSGVQWIQDR	0.905492618	2	2.79513
Q9R112	VGAENVAIVEPSER	0.918742622	2	2.84465
Q9R1M5	**NALP5 NACHT_ LRR and PYD domains_containing protein 5**	**1.089300444**	**0.617603**	**2**
Q9R1M5	KMTSPENDSKSIQK	1.179426439	2	2.39211
Q9R1M5	SLDLGNNALGDK	1.08107345	1	1.91907
Q9R1T3	**CATZ Cathepsin Z**	**1.064603554**	**0.997049**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.065799963	2	4.19178
Q9R1T3	VGDYGSLSGR	0.990905712	2	2.4542
Q9R1T4	**SEPT6 Septin_6**	**0.851423637**	**0.402716**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(2)	1.053536159	1	1.99794
Q9R1T4	STLMDTLFNTK	0.798903786	2	2.44218
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**0.88009035**	**0.012247**	**4**
Q9R1Z0	LCQNNFALGYK	0.867602187	2	2.83575
Q9R1Z0	LTVDTIFVPNTGK	1.085755593	2	2.58844
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.74317061	2	4.1521
Q9R1Z0	WNTDNTLGTEISWENK	0.925444275	2	3.08431
Q9R257	**HEBP1 Heme_binding protein 1**	**1.47978291**	**0.044458**	**2**
Q9R257	EAMPKIMKYVGGTNDK+Oxidation(3)	1.064862767	2	2.32317
Q9R257	NSLFGSVETWPWQVLSTGGK	1.997397847	2	2.47443
Q9WTT6	**GUAD Guanine deaminase**	**0.917560761**	**5.96E-12**	**9**
Q9WTT6	AVMVSNVLLINK	1.143521886	2	2.85306
Q9WTT6	EIGNFEVGKDFDALLINPR	1.351498863	2	4.54572
Q9WTT6	ETTEESVKETER	0.885228421	2	3.41488
Q9WTT6	FQSTDVAEEVYTR	0.872081385	2	3.48267
Q9WTT6	FSLSCTETLMSELGNIAK	1.411604419	2	4.78656
Q9WTT6	IVFLEESSQQEK	1.169171442	2	4.16365
Q9WTT6	NYTDVYDKNNLLTNK	1.119489942	2	4.50372
Q9WTT6	THDLYIQSHISENREEIEAVK	1.391395569	3	4.0667
Q9WTT6	VCMDLNNTVPEYK	0.983761298	2	3.1372
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**1.158155762**	**0.259267**	**9**
Q9WU19	AIFVTVDTPYLGNR	1.254047726	2	3.74136
Q9WU19	AVFVGRPIIWGLAFQGEK	1.139930468	3	4.126
Q9WU19	GVQDVLEILK	1.05692797	2	3.60973
Q9WU19	GVQDVLEILKEEFR	1.233322083	2	4.38095
Q9WU19	HGVDGILVSNHGAR	1.063700885	3	4.84014
Q9WU19	MKNFETNDLAFSPK+Oxidation(1)	1.067841851	2	2.67536
Q9WU19	NFETNDLAFSPK	1.147553664	2	3.40445
Q9WU19	NVADIDLSTSVLGQR	1.008545283	2	5.09121
Q9WU19	VEVFLDGGVR	0.988008638	2	2.64355
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**1.316010021**	**2.59E-05**	**2**
Q9WU49	HETWSGHVISS	1.425311769	2	2.95887
Q9WU49	LQAVEVVITHLAPGTK	1.302399794	2	4.45315
Q9WU65	**GLPK2 Glycerol kinase 2**	**1.117942922**	**0.483317**	**2**
Q9WU65	GIICGLTQFTNK	1.112363136	2	3.5649
Q9WU65	LAEVNIDISNIK	1.490290764	2	2.33875
Q9WU82	**CTNB1 Catenin beta_1**	**1.135092927**	**5.27E-05**	**3**
Q9WU82	HQEAEMAQNAVR	1.210847841	2	3.34762
Q9WU82	LLNDEDQVVVNK	0.562301745	2	3.11464
Q9WU82	TMQNTNDVETAR	1.163222214	2	3.57758
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.075729569**	**0.987526**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.074788346	2	3.78846
Q9WUC4	VCIESEHSSDILLATLNK	1.100110365	2	5.88067
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**3.03716079**	**0.376539**	**2**
Q9WUH4	AIVAGDQNVEYK	2.370015427	2	2.39277
Q9WUH4	FCANTCVECR	3.754266212	2	2.78071

Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.218445674**	**0.430222**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7)	1.218445674	2	2.30964
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(8)	1.218445674	2	2.36096
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.884227164**	**0.168735**	**4**
Q9WUS0	GVLHQFSGTETNR	0.82419052	2	3.45654
Q9WUS0	TLVQAEALDR	0.863423983	2	2.63613
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.415596361	3	5.46836
Q9WUS0	YKDAAKPVIELYK	0.914193546	2	3.92473
Q9WVA1	**TIM8A Mitochondrial import inner membrane translocase subunit Tim8 A**	**1.252118227**	**0.187808**	**2**
Q9WVA1	AEACFVNCVER	1.022829813	2	2.46091
Q9WVA1	SKPVFSESLSD	1.252204107	2	2.91137
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.716771364**	**0.284294**	**2**
Q9WVF7	AANMPDSELFELISENR	0.683280398	2	2.43255
Q9WVF7	MAWQWRGEFMPASR+Oxidation(1)Oxidation(10)	1.609933845	2	2.37328
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.956618448**	**0.015864**	**13**
Q9WVK3	AGVYNLTK	0.962958175	2	2.72289
Q9WVK3	ASQPPSSSTQVTAIQCNIR	1.057358341	2	5.52789
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.04558809	3	7.0826
Q9WVK3	ELLHLGCNVVIASR	1.023156541	2	4.05062
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.453015915	2	5.45964
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(13)	1.327109322	2	3.55702
Q9WVK3	KEEEVNNLVK	0.990912739	3	3.92621
Q9WVK3	LTAAVDELR	1.27606982	2	2.78931
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.828882395	2	5.07459
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	0.893359677	3	4.06704
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.99692787	2	5.95371
Q9WVK3	TMALTWASSGVR	1.024333904	2	3.74431
Q9WVK3	TMALTWASSGVR+Oxidation(2)	0.974982528	2	2.30108
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.321270782**	**0.41349**	**14**
Q9WVK7	AADEFVEK	1.044023637	2	3.02559
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.086171573	2	5.71637
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	0.974543069	3	5.60531
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(22)	0.939529971	3	3.71528
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(9)	0.939529971	3	3.98668
Q9WVK7	GDASKEDIDTAMK	0.9951074	2	3.92682
Q9WVK7	GDASKEDIDTAMK+Oxidation(12)	1.109774973	2	3.18833
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.886210466	3	7.79915
Q9WVK7	KGIEESLK	1.010565072	2	2.54448
Q9WVK7	LKNELFQR	1.271977027	2	2.54428
Q9WVK7	LLVPYLIEAIR	1.675530972	2	2.67133
Q9WVK7	LVEVIK	0.990257028	1	2.01763
Q9WVK7	TFESLVDFCK	1.045594654	2	3.58949
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	1.09100473	3	6.46444
Q9WVL6	**EXTL3 Exostosin_like 3**	**1.135948297**	**0.844638**	**2**
Q9WVL6	QDLLQLK	0.977671409	1	2.15504
Q9WVL6	QELNSEIAKLNLK	1.151344088	2	2.57189
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.048527973**	**0.012549**	**2**
Q9Z0N2	IVLTNPVCTEVGEK	1.41003751	2	2.45389
Q9Z0N2	VGQEIEVRPGIVSK	1.046417918	2	3.56281
Q9Z0U5	**ADO Aldehyde oxidase**	**1.347555159**	**0.085391**	**16**
Q9Z0U5	DLEPLILTIEEAIQHK	1.093586907	2	3.00563

Q9Z0U5	EFQPLDPTQELIFPPELMR	1.422636959	2	3.0715
Q9Z0U5	ELSILYGGVGPTTIGAK	1.302738956	2	3.81327
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	1.402671515	2	4.80896
Q9Z0U5	GYESNINWEK	1.19387159	2	2.96313
Q9Z0U5	HIQDIVAATLK	1.356064168	2	2.60526
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	1.218452747	3	5.11972
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	1.265926139	3	3.98226
Q9Z0U5	KLECGNVDEAFK	1.129622242	2	3.60063
Q9Z0U5	LVLDEVTLAGSAPGGK	1.40428512	2	4.28152
Q9Z0U5	MTWISPVTLEELVEAK	1.450974766	2	3.71056
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	0.945729102	2	4.05961
Q9Z0U5	NMASLGGHIVSR	1.01646172	2	3.28819
Q9Z0U5	QQNALAIVNSGMR	1.436040721	2	2.58247
Q9Z0U5	RLEPIISK	1.155952055	2	2.35957
Q9Z0U5	VVENNVDPEMMLLPYLR	1.907145827	2	3.46685
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**1.039964171**	**0.499073**	**5**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	1.706736464	3	4.24427
Q9Z0V5	GLFIIDDK	1.071247128	2	3.05216
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	0.899754809	3	3.82161
Q9Z0V5	QITLNDLPVGR	1.157600433	2	3.33904
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	1.222860211	3	6.41208
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**1.061182246**	**0.999985**	**5**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	1.040689264	3	6.42745
Q9Z0V6	ANEFHDVNCEVVAVSVDSHFSHLAWINTPR	0.963929791	4	4.53227
Q9Z0V6	GLFIIDPNGVIK	1.072717741	2	3.40608
Q9Z0V6	GTAVVNGEFK	1.065199729	2	2.61022
Q9Z0V6	NGGLGHMNITLLSDLTK	0.906445664	2	2.59387
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.094468669**	**0.092712**	**2**
Q9Z0W7	FLDGDEMTLADCNLLPK	0.955265946	2	4.16415
Q9Z0W7	NSRPEANEALER	1.134669999	3	3.48992
Q9Z122	**FADS2 Fatty acid desaturase 2**	**0.865382061**	**0.544801**	**2**
Q9Z122	AFHLDLDFVGK	0.869671851	3	3.76755
Q9Z122	HGIEYQEKPLLR	0.635483936	2	3.53407
Q9Z1A6	**VIGLN Vigilin**	**1.077719523**	**0.094338**	**21**
Q9Z1A6	ANSFTVSSVSAPSWLHR	1.058961487	2	3.25595
Q9Z1A6	ASVITQVFHVPLEER	0.928517851	2	3.42711
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.242954649	2	3.32147
Q9Z1A6	ELQAEQEDR	0.813072104	2	2.37505
Q9Z1A6	GNSLQEILER	1.161335269	2	2.65138
Q9Z1A6	HEVLLISAEQDKR	1.305306417	3	4.39568
Q9Z1A6	IDLPAENSNSETIVITGK	1.090137517	2	5.22981
Q9Z1A6	IEGDPQGVQQAK	1.139505609	2	3.70458
Q9Z1A6	IIFPAAEDKDQDLITIIGK	1.024911825	2	2.98157
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.065502185	2	4.56491
Q9Z1A6	LGQALTEVYAK	1.200878495	2	3.36128
Q9Z1A6	LQDLELK	1.225948415	1	2.45152
Q9Z1A6	LQTQASATVPIPK	0.926891144	2	3.6283
Q9Z1A6	LVGEIMQETGTR	1.301712195	2	3.69458
Q9Z1A6	MDYVEINIDHK	1.060643341	2	2.91016
Q9Z1A6	MVADLVENSYSISVPIFK	0.97913848	2	3.7739
Q9Z1A6	RCDIIVISGR	1.073294363	2	3.22153
Q9Z1A6	TEIVFTGEKEQLAQAVAR	1.443430155	2	4.40461
Q9Z1A6	TGAHLELSLAK	1.150733056	3	3.39367
Q9Z1A6	TKDLIIEQR	0.934423723	2	2.7909
Q9Z1A6	VKELQAEQEDR	1.163681135	3	4.04412
Q9Z1J8	**S14L3 SEC14_like protein 3**	**1.150911182**	**0.631998**	**3**

Q9Z1J8	ENVQDVLPALPNPDDYFLLR	1.213579976	2	2.84877
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.34228502	2	4.34956
Q9Z1J8	GSSHQVEYEILFPGCVLR	1.040585229	2	4.86018
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.191771313**	**0.517362**	**5**
Q9Z1P2	DYETATLSEIK	1.105323153	1	2.01517
Q9Z1P2	GISQEQMNEFR	1.192768486	2	2.58896
Q9Z1P2	ICDQWDNLGALTQK	1.024993435	2	3.45856
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	1.061060018	2	4.60047
Q9Z1P2	MVSDINNAWGCLEQAEK	0.386827356	2	4.02755
Q9Z1W6	**LYRIC Protein LYRIC**	**0.968688255**	**0.999975**	**4**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	0.993668656	3	3.90182
Q9Z1W6	SWQDELAQQAEEGSAR	0.986634568	2	5.55355
Q9Z1W6	TELGLDLGLEPK	1.074454971	2	3.32661
Q9Z1W6	TLPPAISAEPSVTLSK	0.959579942	2	3.16591
Q9Z1Y3	**CADH2 Cadherin_2**	**1.156163267**	**0.425245**	**5**
Q9Z1Y3	FAILTDPNSNDGLVTVVKPIDFETNR	1.168276914	3	4.27371
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	1.380325394	2	3.72393
Q9Z1Y3	IDPVNGQITTIAVLDR	0.98575457	2	3.49788
Q9Z1Y3	YDEEGGGEEDQDYDLSQLQQPDTVEPDAIKPVGIR	0.965669983	3	5.94742
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	1.073127926	3	3.82607
Q9Z221	**PMFBP Polyamine_modulated factor 1_binding protein 1**	**0.920322825**	**0.674136**	**2**
Q9Z221	DHLHNVMAHLQQENK+Oxidation(7)	0.9114212	2	2.53716
Q9Z221	ELTNSLSKLQDELAETK	1.024129336	2	2.31656
Q9Z269	**VAPB Vesicle_associated membrane protein_associated protein B**	**1.081809837**	**0.826174**	**2**
Q9Z269	TEAPVAAKPLTSPLDDAEVKK	1.021218229	3	3.40028
Q9Z269	VEQVLSLEPQHELK	1.099484268	2	3.81399
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**0.977903029**	**0.982723**	**3**
Q9Z270	FKGPFTDVVTTNLK	0.961949846	2	2.99242
Q9Z270	HEQILVLDPPSDLK	1.05497212	2	3.92357
Q9Z270	QDGPLPKPHSVSLNDTETR	1.070168425	3	3.79417
Q9Z277	**BAZ1B Tyrosine_protein kinase BAZ1B**	**1.076871686**	**0.852553**	**2**
Q9Z277	IHPLEKVDEEAVEK	0.92206192	2	2.45424
Q9Z277	IHPLEKVDEEAVEKK	1.08744894	2	2.46699
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.970274221**	**0.583492**	**9**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.999445421	3	4.33226
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.372403337	2	4.81045
Q9Z2I8	INFDDNAEFR	0.987587064	2	3.2198
Q9Z2I8	LEGTNVQEAQNILK	0.940251516	2	4.87169
Q9Z2I8	SENEPIENEAAR	0.738227967	2	4.08061
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.976395216	2	6.24589
Q9Z2I8	SSGLPITSAVDLEDAAK	0.922805304	2	4.83936
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.902060915	2	3.12094
Q9Z2I8	VMVAEALDISR	0.966243668	2	3.22079
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.111133598**	**2.69E-05**	**7**
Q9Z2I9	AVSSQMIGQK	1.028966873	2	2.49486
Q9Z2I9	ICNQVLVCER	1.460576518	2	2.88812
Q9Z2I9	ILACDDLDEAAK	0.983237152	2	2.95316
Q9Z2I9	INFDSNSAYR	1.223536149	2	3.09646
Q9Z2I9	MGFPSNIVDSAAENMIK	1.056607046	2	3.88361
Q9Z2I9	SSDEAYAIAK	1.100008801	2	3.45449
Q9Z2I9	VQAILVNIFGGIMR	1.106029421	2	4.22782

Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.016688527**	**0.003159**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	1.117355891	2	4.25033
Q9Z2L0	KLETAVNLAWTAGNSNTR	0.947724292	2	5.8982
Q9Z2L0	LETAVNLAWTAGNSNTR	0.783786387	2	2.65625
Q9Z2L0	LTFDSSFSPNTGK	1.127295564	2	3.89905
Q9Z2L0	LTFDSSFSPNTGKK	1.119460285	2	3.21654
Q9Z2L0	LTLSALLDGK	1.732206998	2	2.35034
Q9Z2L0	SENGLEFTSSGSANTETTK	1.02654729	2	4.55913
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	1.070831353	2	5.31369
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	0.680717809	2	4.37721
Q9Z2L0	VTQSNFAVGYK	1.130885442	2	3.17937
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.019526096	2	4.84815
Q9Z2L0	WTEYGLTFTEK	1.045306706	2	2.68121
Q9Z2L0	YQVDPDACFSAK	1.09483036	2	3.31243
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.883174128**	**0.722271**	**4**
Q9Z2M4	GQVLQLHAGAAK	1.0247534	2	3.42596
Q9Z2M4	HLAVEWGPQNIR	0.912502338	2	3.11425
Q9Z2M4	TVVDIDTLGTFNVSR	0.834130128	2	2.83939
Q9Z2M4	VNSLAPGAISGTEGLR	0.891274069	2	2.94762
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.140562672**	**2.47E-05**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	0.822501163	2	3.56581
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.129417944	2	5.50129
Q9Z2Q1	CLSSATDPQTK	1.232227886	2	2.88988
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.198267866	2	3.75317
Q9Z2Q1	IIAGDKEVVIAQK	1.260859755	2	2.46917
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.481566136	2	5.13376
Q9Z2Q1	QVQHILASASPSGR	1.17410317	2	2.4283
Q9Z2Q1	RQPVFISQVVTEK	1.334767073	2	2.539
Q9Z2Q1	RQPVFISQVVTEKDFLSR	0.854802599	3	3.53821
Q9Z2Q1	SSYEGQPLPK	1.078663126	2	2.35385
Q9Z2Q1	TQPPEDISCIAWNR	1.136602308	2	3.58542
Q9Z2Q1	TTFEDLIQR	1.082796001	2	2.6834
Q9Z2Q1	VNFEEDSR	1.205522065	2	2.56008
Q9Z2Q1	VYSIMGGSIDGLR	1.041764734	2	2.37226
Q9Z2U2	**ZN292 Zinc finger protein 292**	**1.199323973**	**0.769201**	**3**
Q9Z2U2	KGQKSNNLNTPNHGK	1.012614028	2	2.57928
Q9Z2U2	KLEVLSNNPDRTVLK	0.986343972	2	2.40011
Q9Z2U2	LINEDSTNAENQGNTTLK	1.209038597	2	2.96563
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.085197374**	**0.999987**	**2**
Q9Z2Z8	AIECSYTSADGLK	1.091638342	2	3.62828
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.042008446	2	5.31211
Q9Z311	**MECR Trans_2_enoyl_CoA reductase_ mitochondrial**	**0.999004486**	**0.043613**	**2**
Q9Z311	DIPLQSAATLGVNPCTAYR	1.392861865	2	2.4319
Q9Z311	LKDLGADYVLTEEELR	0.577477637	2	2.61178
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.072436423**	**0.369076**	**5**
Q9Z339	GSAPPGPVPEGQIR	1.078350551	2	3.62903
Q9Z339	LEALELNECIDHTPK	1.060472149	2	4.22667
Q9Z339	LEEAMANKR	1.07237628	2	2.61762
Q9Z339	LEEAMANKR+Oxidation(5)	1.421769067	2	2.53372
Q9Z339	NPFGLVPVLENTQGHLITESVITCEYLDEAYPEKK	1.176080084	3	4.78282

Time point 4.0 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (4 h)**	**P-value (4 h)**	**Peptide number (4 h)**
Accession number	Peptide sequence	Peptide Ratio (4 h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**2.229060353**	**0.90061**	**2**
A0JPJ7	IGIVGLPNVGK	1.293125652	2	2.54238
A0JPJ7	YLEANMTQSALPK	1.105286331	2	2.67676
A1L108	**ARP5L Actin_related protein 2/3 complex subunit 5_like protein**	**2.207777029**	**0.93169**	**2**
A1L108	ALAVGGLGSIIR	1.283539466	2	2.75621
A1L108	SSEIEQAVQSLDR	1.140555463	2	2.73853
A1L1L2	**TM214 Transmembrane protein 214**	**2.058503376**	**0.64793**	**2**
A1L1L2	KGSGSNEHVVTCDTACK	0.879831794	3	3.52669
A1L1L2	YDLSSPIQPTSTLYER	1.124520587	2	3.33895
A2A6A1	**GPTC8 G patch domain_containing protein 8**	**1.919914225**	**0.26561**	**2**
A2A6A1	RVLEVEKEDTEELR	0.941123193	2	2.54085
A2A6A1	YKDYVDKEK	0.766404498	1	1.93375
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**2.021293781**	**0.62408**	**3**
A2AAE1	FQTNYASTTHLMTGK+Oxidation(11	1.102222383		
A2AAE1	LHYNSKTLKTESPNASR	0.797467882	2	2.55056
A2AAE1	QGTSSSQPGELRGRK	1.066751049	2	2.52225
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**2.327441866**	**0.77602**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	1.74383325	2	2.65825
A2ADY9	NPPLAEALLSGDLEK	1.229717106	2	2.84212
A2ADY9	VLVEQQQDR	1.013677922	2	2.88109
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**2.052397712**	**0.848**	**3**
A2AF47	LCSSVDVDMIQLQLK	1.343034013	2	2.50386
A2AF47	LTGLSEISLR	1.01938375	2	2.35212
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(0	1.178299797		
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**1.75856765**	**0.93266**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13	0.618168055		
A2AGT5	GESVQEELLK	1.075194617	1	1.93865
A2APB8	**TPX2 Targeting protein for Xklp2**	**1.979039371**	**0.8003**	**2**
A2APB8	GIGEPFQGKNSLRK	1.203975586	2	2.3504
A2APB8	NKKDESLLPSK	0.984306542	2	2.48351
A2AQP0	**MYH7B Myosin_7B**	**2.116763646**	**0.99445**	**7**
A2AQP0	AITDAAMMAEELKK	1.374673533	2	3.33736
A2AQP0	DIDDLELTLAK	1.007040066	2	3.61918
A2AQP0	EQDTSAHLER	1.21684194	2	2.84886
A2AQP0	HDCDLLR	1.414630253	1	2.05437
A2AQP0	KAITDAAMMAEELKK	1.85760228	3	3.62427
A2AQP0	VEDEQLVGVQLQK	1.817419259	2	2.41987
A2AQP0	VGNEYVTK	0.739264571	2	2.41493
A2ASS6	**TITIN Titin**	**2.076191224**	**0.99425**	**13**
A2ASS6	AENRFGIGPPAETIQRTTAR	1.447423417	2	2.51301
A2ASS6	ATNEVGSDTCACTVK	2.748871799	2	3.82115
A2ASS6	ETAMLSWDVPENDGGAPVK+Oxidation(3	1.198599078		
A2ASS6	KDLNMVVSAARISCGGAIR	1.001804703	2	2.36533
A2ASS6	RRTEEGYYEAITAVELK	1.05338869	2	2.57674
A2ASS6	TCEIEIGQLK	0.730229295	2	2.31167
A2ASS6	TDSGAYILTATNPGGFAK	1.103660325	2	2.39487
A2ASS6	TFLQDQLVSLQVLK	1.296532545	1	1.9207
A2ASS6	VGDDAWIKDTTGTALR	1.105788448	2	2.37483
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	1.718033364	3	4.42801

A2ASS6	VLDTPGPPQNLAVK	1.693731399	2	2.31419
A2ASS6	YDGGHKLTGYIVEK	1.241177677	2	2.30845
A2ASS6	YGIGEPLDSEPETAR	1.003125435	2	2.99747
A2AU72	**ARMC3 Armadillo repeat_containing protein 3**	**1.898308325**	**0.31148**	**2**
A2AU72	HASWAVMVCAGDEPMAVELCR+Oxidation(14	1.861646015		
A2AU72	TLGVITCDKEARTMLK+Oxidation(13	0.843904758		
A2AWL7	**MGAP MAX gene_associated protein**	**2.001023726**	**0.69848**	**2**
A2AWL7	ADVSLTTLLTAQASLK	0.98574184	2	2.46015
A2AWL7	TDQGILVTNRDARALLSR	1.942045056	3	3.32281
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**2.232342023**	**0.99095**	**11**
A2VCW9	AEGIVFNTQSTIK	0.99727303	2	2.48735
A2VCW9	AQEANMSLLDEVLK	1.327490933	2	3.46036
A2VCW9	GAQEVFNELPCEYVEPHELK	1.46893699	2	4.46829
A2VCW9	KTDGVYDPVEYEKYPER	1.098107081	3	3.61581
A2VCW9	KYDINTVNVTVGK	1.286975636	2	3.95365
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	0.985723322	3	4.1841
A2VCW9	QDAQSLLVPVK	0.942094216	2	2.55596
A2VCW9	REDVNAWER	1.419187083	2	2.975
A2VCW9	SSVVPVEGCPELPHK	0.772998621	2	2.7061
A2VCW9	VNMVTASYITPAMK	1.19349964	2	2.50333
A2VCW9	YDINTVNVTVGK	1.107161793	2	2.34604
A4Q9F4	**TTL11 Tubulin polyglutamylase TTLL11**	**2.077991822**	**0.80379**	**2**
A4Q9F4	ALRIMQNLFPEEYNFYPR+Oxidation(4	1.073166186		
A4Q9F4	NLKPMLLEVNANPSMR	0.962814943	2	2.4453
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**4107.471849**	**1**	**12**
A7VJC2	EESGKPGAHVTVK	0.804819861	2	3.13958
A7VJC2	GFGFVTFDDHDPVDK	1.164585879	2	4.34796
A7VJC2	GGGGNFGPGPGSNFR	0.928419848	2	3.18919
A7VJC2	GGNFGFGDSR	1.110176589	2	2.90223
A7VJC2	IDTIEIITDR	1.047275097	2	3.98512
A7VJC2	LFIGGLSFETTEESLR	2.501562479	2	3.64109
A7VJC2	LTDCVVMR	1.146842095	2	2.61326
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	12.00403497	2	6.06358
A7VJC2	NYYEQWGK	1.085719662	2	2.40653
A7VJC2	QEMQEVQSSR	0.827789812	2	3.02865
A7VJC2	QEMQEVQSSR+Oxidation(2	1.173458134		
A7VJC2	YHTINGHNAEVR	0.981685332	2	3.37763
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**2.176012126**	**0.67528**	**3**
B0BN93	GSIDEVDKR	1.038748248	2	2.47745
B0BN93	LNIGDLQATK	0.642888828	2	2.31404
B0BN93	SAWGQQPDLAANEAQLLR	1.840888698	2	2.81676
B0BNA7	**EIF3I Eukaryotic translation initiation factor 3 subunit I**	**2.085318416**	**0.96161**	**2**
B0BNA7	HVLTGSADNSCR	1.059463058	2	3.48495
B0BNA7	LFDSTSLEHQK	1.210134318	2	2.37482
B0BNE5	**ESTD S_formylglutathione hydrolase**	**2.020369168**	**0.897**	**7**
B0BNE5	AFNGYLGPDQSK	1.108510588	2	3.17033
B0BNE5	FAIYLPPQAESAK	1.324540086	2	2.67297
B0BNE5	MYSYVTEELPQLINANFPVDPQR	0.902819062	3	5.57758
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.0198507	2	5.77284
B0BNE5	SVSAFAPICNPVLCPWGK	1.189215816	3	4.20303
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.023563159	3	4.88916
B0BNE5	VFEHSSVELK	1.046519008	2	2.81127
B0BNN3	**CAH1 Carbonic anhydrase 1**	**1.558806947**	**0.0189**	**2**

B0BNN3	ADGLAIIGVLMK	0.783975424	2	3.30061
B0BNN3	HDSSLKPVSVSYNPATAK	0.633912531	3	5.06419
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.861154876**	**0.07181**	**3**
B0K020	AMVNLQIQK	0.847558258	2	2.62225
B0K020	HNEETGDNVGPLIIK	0.76499113	2	5.15707
B0K020	VVHAFDMEDLGDK	0.971005386	3	3.93878
B1H267	**SNX5 Sorting nexin_5**	**2.159613103**	**0.75998**	**2**
B1H267	NNVSLLQSCIDLFK	1.144108775	2	3.13254
B1H267	TTLPTFQSPEFSVTR	1.094931965	2	3.59221
B2GUV7	**IF2P Eukaryotic translation initiation factor 5B**	**2.259128892**	**0.73008**	**2**
B2GUV7	HLQAQGVEVPSK	1.015593801	2	2.76141
B2GUV7	LKEGDTIIVPGVEGPIVTQIR	1.20666641	3	3.36647
B2GUZ5	**CAZA1 F_actin_capping protein subunit alpha_1**	**2.216279196**	**0.64962**	**3**
B2GUZ5	EASDPQPEDVDGGLK	0.581121221	2	2.51639
B2GUZ5	FITHAPPGEFNEVFNDVR	1.148071586	3	3.70062
B2GUZ5	FTITPPTAQVVGVLK	1.195653185	2	2.94658
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**2.286456951**	**0.34373**	**3**
B2GV24	NNPVHLITEEDLK	1.084994538	2	2.54554
B2GV24	TYDLPGDFLTQALTQR	1.260999511	2	3.2333
B2GV24	VNIVDLQQVINVDLTHIENR	1.440945772	3	3.62073
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**2.087106102**	**0.99998**	**6**
B2RYW9	ALAAQLPLIPR	0.8892743	2	2.85767
B2RYW9	GETALSVAR	0.913572211	2	3.07367
B2RYW9	KGDEVQCEIEELGVIINK	1.124279733	2	4.81224
B2RYW9	TFDTFCPLGPALVTK	1.063615074	2	4.97568
B2RYW9	VICVGLNYADHCQEQNVR	1.089916663	2	2.97759
B2RYW9	VNGEIVQSSNTNQMVFK	0.991353828	2	4.78679
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**2.081940616**	**0.80685**	**2**
B2RZ78	GDFDESLNYPEQK	1.046743553	2	3.63955
B2RZ78	IQHILCTGNLCTK	1.16002291	2	3.03615
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**2.075987225**	**0.95853**	**6**
B3DMA2	AVLTVTQYR	0.969067769	2	2.48295
B3DMA2	GSHIQENTGIPLMEELISIYCR	0.534580171	2	2.32737
B3DMA2	LYEHEVVAHWIAK	0.909882804	3	3.70689
B3DMA2	MELQDQAR	1.072542164	2	2.47929
B3DMA2	NLPDSDNEECLVHGDFK	0.911710692	2	3.46237
B3DMA2	SGQSNPTFFLQK	0.998932416	2	2.58689
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**2.346990994**	**0.82899**	**4**
B5DFC8	FEELTNLIR	1.468927279	2	2.43461
B5DFC8	GTEITHAVVIK	1.181831647	2	2.89775
B5DFC8	LGSLVENNER	1.13508505	2	2.66618
B5DFC8	TEPTAQQNLALQLAEK	1.180030708	2	4.84914
B7ZNG0	**KIF7 Kinesin_like protein KIF7**	**1.90506092**	**0.01211**	**2**
B7ZNG0	ELGRHMWINQELK+Oxidation(5	0.683527529		
B7ZNG0	KEALMQEK	1.254178653	2	2.72165
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**2.220159037**	**0.9973**	**2**
D3ZTX0	QCFYEDITQGTK	0.972135667	2	2.74209
D3ZTX0	SVIDYQTHFR	1.198502527	2	2.83794
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**2.399345893**	**0.70458**	**5**
D3ZW55	DFGWDPCFQPDGYEQTYAEMPK	0.417715052	2	3.30029
D3ZW55	IDLPEYQGEPDEISIQK	1.143899311	2	4.34766

D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.25806754	3	4.41666
D3ZW55	LKPEGLYQLLAGFEDK	1.975312753	3	3.58711
D3ZW55	LQEYFGVTDGAGDH	1.298005211	2	3.41133
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**2.008880562**	**0.99722**	**2**
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(12	1.006391791		
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(9	1.006391791		
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**2.24326346**	**0.86221**	**4**
D4A4T9	FDPEANADDACTYHPGVPVFHDALK	1.159239941	3	3.53312
D4A4T9	HNSEKPPEPVKPEVK	0.949861085	3	3.65847
D4A4T9	KEEDSDEIKIGTSCK	1.10384439	2	2.53985
D4A4T9	LSSGNEEDKKEEDSDEIK	1.32661095	3	4.2974
D4A666	**UBN2 Ubinuclein_2**	**2.537061967**	**0.65252**	**2**
D4A666	GWMQARMLFK+Oxidation(2)Oxidation(6	1.626525763		
D4A666	KEEGEKEK	1.263311278	1	1.9093
E9Q557	**DESP Desmoplakin**	**1.864549662**	**0.80946**	**2**
E9Q557	KQVQTSQKNTLR	1.039024246	2	2.31847
E9Q557	SQCTQVVQER	0.845556661	2	2.45344
F6YLP3	EMFVYLSTQLKK+Oxidation(1	2.986815336		
F6YLP3	KEMFVYLSTQLKK	0.998668312	2	2.53663
F6YLP3	SGDISAVQPK	0.854966055	2	3.07669
F6YLP3	SMVTAGFEPVVIENVLEGDELR	0.888264922	2	3.59956
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**2.601528896**	**0.11334**	**2**
O08550	HAAVALGQARAMVPEDVPR	1.368879383	2	2.34271
O08550	MVQALTELLR+Oxidation(0	1.589926776		
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**2.308263985**	**0.02657**	**11**
O08557	DENATLDGGDVLFTGR	1.190259574	2	2.4135
O08557	DHLLIPVSNSEMEK	1.469602832	2	2.49321
O08557	DYAVSTVPVADSLHLK	1.23991509	2	3.67323
O08557	GAEILADTFK	0.985915013	1	2.09651
O08557	KEVDMMK	1.107220535	2	2.32322
O08557	LKDHLLIPVSNSEMEK	1.119127741	2	3.81113
O08557	LTVPDDMAANCIYLNIPSK	1.261574443	2	3.26704
O08557	SFCSMAGPNLIAIGSSESAQK	1.245090868	2	4.77321
O08557	SQGEEVDFAR	1.002213132	2	2.82443
O08557	TPEEYPESAK	1.623805616	2	2.36629
O08557	VDGLLTCCSVFINK	1.293290769	2	3.51176
O08583	**THOC4 THO complex subunit 4**	**1.978920549**	**0.95759**	**3**
O08583	MDMSLDDIIK	1.753084506	2	2.66865
O08583	QQLSAEELDAQLDAYNAR	0.926305889	2	3.40117
O08583	SLGTADVHFER	1.401814514	2	2.74813
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**2.180450755**	**0.28737**	**15**
O08601	EDTTMYLLALK	0.996751129	2	2.53186
O08601	EFYSYENEPVGIENLK	1.378121022	2	4.23238
O08601	GCPSLAEHWKSIR	1.029143475	2	3.84246
O08601	GHTTGLSLNNER	0.873764986	2	2.54587
O08601	GSFASNDIR	1.289064584	2	2.71859
O08601	LILGGLEKPEK	1.152368344	2	2.44707
O08601	MLSASGDPVSVVK	1.073588516	2	3.57881
O08601	NALLPEGIPLLLK	1.402239154	3	3.58331
O08601	NILLSIGELPK	1.51980217	2	3.74861
O08601	REEILQILK	2.238350966	3	3.47206
O08601	SDSSIILQER	1.172029989	2	3.10638
O08601	SGSSSAYTGYVER	0.881102003	2	3.67906

O08601	SNLNIFQYIGK	1.374898715	2	3.18284
O08601	TTAAAVILK	0.807051529	2	2.31374
O08601	VKEFYSYENEPVGIENLK	1.058200069	2	3.58374
O08629	**TIF1B Transcription intermediary factor 1_beta**	**1.986006374**	**0.99996**	**2**
O08629	IVAERPGTNSTGPGPMAPPR	1.045638134	3	3.91025
O08629	LDLDLTSDSQPPVFK	0.989799521	2	4.25639
O08795	**GLU2B Glucosidase 2 subunit beta**	**2.293993213**	**0.99995**	**6**
O08795	ETVVTSTTEPSR	1.188164645	2	3.10225
O08795	KLWEEQQAAAK	1.20121765	2	3.41721
O08795	LWEEQQAAAK	1.097539508	2	2.98051
O08795	MPPYDEETQAIIDAAQEAR	1.149710102	2	5.1853
O08795	SLEDQVETLR	0.810997134	2	3.15339
O08795	YEQGTGCWQGPNR	1.302775132	2	3.77679
O09158	**CP3AP Cytochrome P450 3A25**	**1.504861501**	**0.48368**	**2**
O09158	DVEINGVFIPK	0.444422728	2	3.14244
O09158	VDFLQLMMNTQNSK	0.718880498	2	3.1092
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.977243754**	**9.9E-20**	**14**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.347881837	2	6.13019
O09171	AGPWTPEAAVEHPEAVR	1.123334581	2	5.0058
O09171	GAAELMQQK	1.153128373	2	3.64947
O09171	GAAELMQQK+Oxidation(5	1.253217073		
O09171	HGSWGSGLDMHTKPWIR	2.027465118	3	4.70597
O09171	IFHQQLEVFMK	0.983459493	2	3.5635
O09171	ISGQKVNEAACDIAR	1.021302608	2	4.44903
O09171	KEYWQNLR	1.359312933	3	3.44041
O09171	LNAGEVVIGDGGFVFALEK	0.946474974	3	5.9219
O09171	QGFIDLPEFPFGLEPR	1.369559401	2	5.0369
O09171	QVADEGDALVAGGVSQTPSYLSCK	3.03125431	2	6.10976
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.363549387	3	6.19249
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9	1.400295872		
O09171	VNEAACDIAR	1.15495872	2	4.03534
O09173	**HGD Homogentisate 1_2_dioxygenase**	**2.343931258**	**0.99999**	**9**
O09173	CFYNSDGDFLIVPQK	0.855483705	2	3.09427
O09173	FSVDVFEETR	1.256928077	2	3.60658
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.109774056	3	3.74208
O09173	NCMSEFMGLIK	1.364460569	2	3.20137
O09173	QDVSPFNVVAWHGNYTPYK	1.492712675	2	3.75095
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	0.917275548	3	3.88122
O09173	SLRPGVAIADFVIFPPR	1.157916091	2	3.71214
O09173	TFRPPYYHR	0.894844619	3	3.49392
O09173	YISGFGNECASEDPR	1.482453557	2	3.92119
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**2.036935436**	**0.99986**	**17**
O35077	ANTIGISLIK	1.312094894	2	3.07506
O35077	DPAQGQLLK	1.116470317	2	2.38969
O35077	ELHSILQHK	1.088076132	2	2.56608
O35077	FCETTIGCK	0.9928411	2	2.66385
O35077	FCETTIGCKDPAQGQLLK	0.934925486	2	5.33586
O35077	GIDEGPNGLK	0.890517707	2	2.92108
O35077	GLVDKFPLFTAVYK	1.336529437	3	3.72259
O35077	ICDQLKGHLK	0.946501761	3	3.7979
O35077	ITVVQEVDTVEICGALK	1.796278791	2	3.1124
O35077	IVGSNASQLAHFDPR	1.540551772	2	3.11567
O35077	KLTEIINTQHENVK	1.109178813	2	5.27307
O35077	LTEIINTQHENVK	1.05878422	2	4.41608
O35077	NIVAVGAGFCDGLGFGDNTK	1.502692931	2	5.57218

O35077	SIEQLEK	1.016545114	2	2.38229
O35077	VCIVGSGNWGSAIAK	1.212052754	2	4.35355
O35077	VCYEGQPVGEFICCLQNHPEHM	1.319582555	2	4.13189
O35077	VTMWVFEEDIGGR	1.199412519	2	3.39004
O35078	**OXDA D_amino_acid oxidase**	**1.852780339**	**0.99965**	**2**
O35078	GQIIQVEAPWIK	0.867041979	2	3.09514
O35078	SCCQLEPTLK	1.299893233	2	2.64774
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**2.058075118**	**0.70506**	**4**
O35094	AISQGVESVKK	0.654618253	2	2.37212
O35094	KLEESDALQEAR	1.017011362	2	3.59226
O35094	TEMSEVLTEILR	1.107710834	2	3.27418
O35094	VTDLLGGLFSK	1.047307635	2	2.58215
O35142	**COPB2 Coatomer subunit beta_**	**2.805922988**	**0.00089**	**5**
O35142	AAESLADPTEYENLFPGLK	1.86016312	2	3.88585
O35142	EEPAMSMDANGKIIWAK	1.266551987	2	2.53063
O35142	FELALQLGELK	1.488839973	2	3.05484
O35142	GSNNVALGYDEGSIIVK	1.129254016	2	3.55879
O35142	TFEVCDLPVR	1.186813304	2	2.9816
O35244	**PRDX6 Peroxiredoxin_6**	**2.207877128**	**0.99366**	**8**
O35244	DINAYNGAAPTEK	0.708595403	2	3.95067
O35244	DLAILLGMLDPAEKDEK	1.213818017	2	3.95115
O35244	GESVMVLPTLPEEEAK	1.666326794	2	3.25513
O35244	KGESVMVLPTLPEEEAK	0.967146703	2	5.33237
O35244	LSILYPATTGR	1.237467246	2	3.14751
O35244	NFDEILR	0.966237846	1	2.27184
O35244	VVDSLQLTASNPVATPVDWK	1.058771276	3	5.52461
O35244	VVFIFGPDKK	0.85027013	2	2.89644
O35286	**DHX15 Putative pre_mRNA_splicing factor ATP_dependent RNA helicase DHX15**	**2.04035978**	**0.23945**	**2**
O35286	TCTDIKPEWLVK	0.696201399	2	2.41357
O35286	TLATDILMGVLK	1.199864984	2	3.72182
O35331	**PDXK Pyridoxal kinase**	**1.946551018**	**0.63901**	**2**
O35331	AEAGEGQKPSPAQLELR	0.634462942	3	3.84535
O35331	MGPDTVVITSSDLPSPK	1.006104456	2	3.6926
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**1.800506122**	**0.99589**	**2**
O35469	DLGYEPLVSWEEAK	1.398198147	2	4.34285
O35469	TSEWIGTLVEQHR	0.808134831	2	3.40918
O35509	**RB11B Ras_related protein Rab_11B**	**2.02475229**	**0.99975**	**5**
O35509	AQIWDTAGQER	1.112409352	2	3.23688
O35509	GAVGALLVYDIAK	1.135851892	2	3.98611
O35509	HLTYENVER	1.252048758	2	2.46795
O35509	NEFNLESK	0.972526549	1	2.14578
O35509	VVLIGDSGVGK	1.017376614	2	2.47453
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**1.822108781**	**0.8699**	**2**
O35547	LERFEIPIK	1.039174719	2	2.53965
O35547	TAEDYSVDENGQR	0.794490729	2	3.23898
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.941349949**	**0.01813**	**7**
O35567	ALFEEVPELLTEAEK	1.677389978	2	3.50382
O35567	DGQVIGIGAGQQSR	1.677233959	2	3.89758
O35567	EVSDGIVAPGYEEEALK	0.750775923	2	3.80849
O35567	HVSPAGAAVGVPLSEDEAR	1.054818783	2	5.15093
O35567	SGVAYIVAPSGSTADK	1.119004359	2	2.86537
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.188001408	2	5.41396
O35567	YTQSNSVCYAK	1.047498418	2	3.13696

O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**2.115197511**	**0.91471**	**3**
O35593	AVAVVVDPIQSVK	1.03996036	2	3.078
O35593	AVEEEDKMTPEQLAIK	0.981225482	2	4.72041
O35593	EMLELAKNYNK+Oxidation(1	1.198783572		
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.945836829**	**0.97475**	**3**
O35660	RYAMGDAPDYDR	0.900864561	2	3.37863
O35660	YAMGDAPDYDR	1.592004406	2	2.43877
O35660	YAMGDAPDYDR+Oxidation(2	2.783650688		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**1.440541191**	**0.00178**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	0.824451241	2	4.21381
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	0.509117082	3	3.41562
O35760	NCHLNENIDK	0.27606925	3	3.33813
O35760	NVTLNPDPNEIK	0.427480492	2	3.14002
O35763	**MOES Moesin**	**1.843383261**	**0.94546**	**5**
O35763	ALTSELANAR	0.875009213	2	2.52082
O35763	AQMVQEDLEK	0.929972508	2	2.49221
O35763	AQQELEEQTR	1.011421236	2	2.81598
O35763	FYPEDVSEELIQDITQR	1.099249575	3	3.34265
O35763	TQEQLASEMAELTAR	1.342572338	2	4.01775
O35783	**CALU Calumenin**	**1.897666677**	**0.90612**	**2**
O35783	HLVYESDQDKDGK	0.776377065	2	3.9685
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.087004898	3	5.23784
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**2.12433481**	**0.70809**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	1.114471784	2	4.78567
O35796	AFVEFLTDEIK	1.354258333	2	3.25357
O35796	AFVEFLTDEIKEEK	0.78027014	2	3.79041
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.490521212	3	5.68488
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.975464336**	**0.49145**	**7**
O35814	ALDLDSSCK	1.103183707	1	2.44694
O35814	ALSAGNIDDALQCYSEAIK	1.186559602	2	5.76436
O35814	AMADPEVQQIMSDPAMR	1.613522457	2	3.9249
O35814	CQQAEKILK	0.794629793	1	2.02042
O35814	DCEECIQLEPTFIK	1.919838275	2	4.42249
O35814	ELIEQLQNKPSDLGTK	1.126134795	2	4.02601
O35814	TVDLKPDWGK	1.163823834	2	2.68325
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**2.079346027**	**0.94107**	**2**
O35824	NVLCSACSGQGGK	1.04494678	2	3.26328
O35824	VSLEDLYNGK	1.245342396	2	2.33159
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**2.374087675**	**0.71615**	**8**
O35826	DEAVGALHLIQAAK	1.249995664	2	3.50699
O35826	EVGAFGTPVINLGTR	1.145230186	2	3.20231
O35826	ILGVGISTGGR	1.423829019	2	2.84115
O35826	IYGDGNAVPR	1.123471534	2	2.46368
O35826	SIDLQEPLQK	1.06242741	2	2.41405
O35826	TLVLFPNIDAGSK	1.372712834	2	2.66769
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.289523199	3	5.11907
O35826	VNPQEGVVLHSTK	1.290233237	2	2.53932
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**1.715627922**	**0.95105**	**5**
O35913	EGLQENVDGTENAK	0.756913242	2	3.75747
O35913	GASFVPAFFILR	0.850694362	2	2.63569
O35913	SLSGTYMNSMLTQIER	0.780310719	2	4.57415
O35913	SQTLNPTQDPSECVK	0.749425912	2	4.14458
O35913	TFQFPGDIESSK	0.754533332	2	2.40918

O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.950507266**	**0.99773**	**7**
O35952	ALLEVLGR	1.027724363	2	2.98591
O35952	FYEGTADEMYK	1.086584381	2	3.10067
O35952	HVEPGNTAVQEK	0.671541436	2	4.01675
O35952	LTTVLTTHHHWDHAGGNEK	1.252267878	3	3.5804
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.261343592	3	4.34602
O35952	TVQQHAGETDPVTTMR	0.988608075	2	4.74553
O35952	TVQQHAGETDPVTTMR+Oxidation(14	1.030225666		
O35987	**NSF1C NSFL1 cofactor p47**	**2.228028702**	**0.98997**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.065225994	2	4.47322
O35987	EANLLNAVIVQR	1.350872443	2	3.06276
O35987	LGAAPEEESAYVAGER	0.911423633	2	4.29335
O35987	SYQDPSNAQFLESIR	1.177419592	2	4.18961
O35987	TGFSLDNGDLR	0.782770418	2	2.91945
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**2.434189998**	**0.4203**	**3**
O54753	IVNVSSVLGR	1.545257993	2	2.57722
O54753	TWEATPEHIR	1.170181329	2	2.4014
O54753	YGVEAFSDVLR	1.609751537	2	3.29152
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**2.35767021**	**0.03006**	**3**
O54975	GSLTFEPLTLVPIQTK	1.252713414	2	4.09856
O54975	IENVVLVVPAK	1.040384504	2	2.6684
O54975	QQADFVDLSFPTISSTGPNGAIIHYAPIPETNR	1.408706967	3	3.71705
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.982852164**	**0.7792**	**4**
O55012	ATTLSNAVSSLASTGLSLTK	1.767030373	2	4.23092
O55012	ITAAQHSVTGSAVSK	1.11085011	2	4.63342
O55012	SGLQGYDMSTFIR	1.340498213	2	3.74714
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	0.901208883	3	5.7464
O55096	**DPP3 Dipeptidyl peptidase 3**	**2.299321252**	**0.11801**	**7**
O55096	AGLLALEFYTPETANWR	1.547706386	2	3.61981
O55096	GEFEGFVAMVNK	1.083703503	2	2.68955
O55096	LASVLNTEPALDSELTSK	1.450825076	2	2.9879
O55096	LEGSEVQLVEYEASAAGLIR	1.741740589	2	3.91228
O55096	NVSLGNVLAVAYATK	1.062502798	2	2.68389
O55096	SYEFQGNHFQVTR	1.007009727	2	4.03311
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.233923754	3	3.94689
O55125	**NIPS1 Protein NipSnap homolog 1**	**2.144034879**	**0.0002**	**4**
O55125	AGPNIYELR	0.936665357	2	2.99004
O55125	FSGGYPALMDCMNK	1.317733431	2	2.99941
O55125	GWDENVYYTVPLVR	0.75771287	2	3.60117
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.424457694	3	5.09872
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**2.207693869**	**1**	**6**
O55171	ADAGGELDLAR	0.905885541	2	2.80929
O55171	DGLLDVVEALQSPLVDKK	0.906460069	2	4.92443
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.125131038	3	4.40854
O55171	GGELGLAMASFLK	1.262111749	2	4.03292
O55171	IEYFEEAVNYLR	1.157153165	2	4.04899
O55171	SCWDEPLSITVR	1.026939982	2	3.99257
O70127	**ABCBB Bile salt export pump**	**2.351425921**	**0.77425**	**7**
O70127	AGQITSEALSNIR	1.000151189	2	3.17384
O70127	AGSIADEVLSSIR	1.389946965	2	2.9629
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.359427594	3	4.35131
O70127	ILLLDEATSALDTESEK	1.400242687	2	4.27576
O70127	ILLLDMATSALDNESEAR	4.607190327	2	2.31426

O70127	KFGEENHAFESDGSHNNDKK	0.977532136	3	4.49019
O70127	STALQLIQR	1.278729577	2	2.70162
O70133	**DHX9 ATP_dependent RNA helicase A**	**2.137469119**	**0.96945**	**3**
O70133	ELDALDANDELTPLGR	0.911103893	2	2.50678
O70133	KMTPAYEIRAVGNK	1.245051317	2	2.44311
O70133	YPSPFFVFGEKIR	0.924270176	2	2.38157
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**1.894448702**	**0.84525**	**2**
O70173	LLGDIGEKVK	1.116932295	2	2.31537
O70173	WTFSHPLEALGLLTSR	0.877317124	2	2.4256
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**2.389639769**	**3E-05**	**14**
O70199	EADLVFISVNTPTK	1.022126514	2	2.35235
O70199	EQIVVDLSHPGVSADDQVSR	1.503552053	2	5.61749
O70199	FSLQDPPNKKPK	1.743382235	2	2.38953
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.37716425	3	6.6251
O70199	IIDSLFNTVTDK	1.008292386	2	2.38015
O70199	IIDSLFNTVTDKK	0.986560558	2	3.73759
O70199	ILTTNTWSSELSK	1.085542182	2	3.84071
O70199	INAWNSPTLPIYEPGLK	1.263297945	2	4.20048
O70199	MLKPAFIFDGR	1.577454885	2	2.44935
O70199	NLFFSTNIDDAIR	1.08257483	2	3.42067
O70199	VLDGLHNELQTIGFQIETIGK	1.246190024	2	5.42973
O70199	VLIGGDETPEGQR	1.115088799	2	3.52231
O70199	VTVVDVNEAR	0.953780498	2	3.17918
O70199	YWQQVIDMNDYQR	1.637580095	2	4.28493
O70251	**EF1B Elongation factor 1_beta**	**2.784182592**	**0.9989**	**4**
O70251	SIQADGLVWGSSK	1.045609209	2	3.31493
O70251	SSILLDVKPWDDETDMTK	1.188416704	2	4.27211
O70251	SSILLDVKPWDDETDMTKLEECVR	1.494449037	3	5.22435
O70251	TPAGLQVLNDYLADK	1.111164956	2	3.97247
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.989446886**	**0.00166**	**17**
O70351	EVQAALTLAK	1.032527787	2	2.62171
O70351	GGIVGMTLPIAR	0.972488587	2	3.74667
O70351	GLVAVITGGASGLGLSTAK	0.965285771	2	4.84912
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.035365507	3	4.83826
O70351	IDVAVNCAGIAVAIK	1.275439918	2	4.43783
O70351	KLGGNCIFAPANVTSEK	0.907975719	2	4.85623
O70351	KNQVHTLEDFQR	0.813066032	2	3.95542
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	0.998400004	3	5.28533
O70351	LGGNCIFAPANVTSEK	1.11784569	2	3.42071
O70351	LVAGVMGQNEPDQGGQR	1.238237564	2	5.6786
O70351	LVGQGATAVLLDVPNSEGETEAK	1.51428719	2	5.41745
O70351	LVGQGATAVLLDVPNSEGETEAKK	0.817293498	3	4.28588
O70351	NFLASQVPFPSR	0.978039535	2	4.62477
O70351	NQVHTLEDFQR	1.061563889	2	3.33301
O70351	RLVGQGATAVLLDVPNSEGETEAK	0.905844361	2	5.55966
O70351	VINVNLIGTFNVIR	1.226304969	2	4.60512
O70351	VVTIAPGLFATPLLTTLPDK	0.952325472	2	5.04859
O70456	**1433S 14_3_3 protein sigma**	**1.831385026**	**9.6E-10**	**3**
O70456	DSTLIMQLLR	1.581626166	2	3.74881
O70456	NLLSVAYK	0.843148364	2	2.4321
O70456	VLSSIEQK	0.842274801	2	2.60992
O88202	**LPP60 60 kDa lysophospholipase**	**2.479531863**	**0.4869**	**4**
O88202	AAGAHLSPQELEDVGTELCR	1.204417646	3	3.89796
O88202	GEMTLPTTDDLLGDDMLGCR	3.157239721	2	3.82205
O88202	GVDVDACNEDGQSPLLLAVR	1.310068719	2	5.09815
O88202	SEGGVLVPGR	1.510070868	2	2.54307

O88379	**BAZ1A Bromodomain adjacent to zinc finger domain protein 1A**	**2.791510833**	**0.00076**	**2**
O88379	ERDKLLK	1.033796878	2	2.34406
O88379	NTAKSASKNLR	1.60273559	2	2.79429
O88397	**SO1A5 Solute carrier organic anion transporter family member 1A5**	**1.742771178**	**0.85836**	**2**
O88397	TCLHWGTLK	0.837890492	2	2.32256
O88397	YLEQQYGK	0.799256044	2	2.76794
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**2.17538225**	**0.14848**	**6**
O88428	GCTVWLTGLSGAGK	1.669511878	2	3.26724
O88428	GFTGIDSDYEKPETPECVLK	1.098859659	2	4.96753
O88428	GIHELFVPENK	1.297588023	2	2.75745
O88428	NLGFSAGDREENIR	0.990517451	2	3.30825
O88428	STNVVYQAHHVSR	0.724590567	2	4.25577
O88428	VLSMAPGLTSVEIIPFR	1.141247067	2	3.63824
O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**2.24433259**	**0.86832**	**3**
O88491	ENSEGAFGVLLPADAVQKAR	0.958114371	2	2.36579
O88491	ETGIPSLMPQTK	1.11927511	2	2.32075
O88491	SGKGEGLKLLNNMHEK	1.180030708	2	2.75928
O88600	**HSP74 Heat shock 70 kDa protein 4**	**2.202536665**	**0.99126**	**18**
O88600	AESEEMETSQAGSK	1.096284404	2	4.662
O88600	AFSDPFVEAEK	1.075716665	2	3.02864
O88600	AGGIETIANEYSDR	1.139182948	2	3.41349
O88600	FLEMCDDLLAR	0.942563021	2	2.50302
O88600	FQESEERPK	0.885531416	2	2.76374
O88600	FVSEDDRNNFTLK	1.46568883	2	2.78235
O88600	GCALQCAILSPAFK	1.067253617	2	3.80004
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	0.7361185	3	5.11052
O88600	LKETAESVLK	1.357779704	2	2.53628
O88600	MIMQDKLEK+Oxidation(0	1.000054114		
O88600	MQVDQEEPHTEEQQPQTPAENK	1.288948582	3	5.32193
O88600	NFTTEQVTAMLLSK	1.255368606	2	4.11704
O88600	NKEDQYEHLDAADMTK	1.100934781	3	3.74273
O88600	SNLAYDIVQLPTGLTGIK	1.35943495	2	4.08276
O88600	SVMDATQIAGLNCLR	1.652282547	2	3.59303
O88600	TSTVDLPIESQLLWQLDR	1.01650146	2	3.70737
O88600	VLATAFDTTLGGR	1.413345789	2	3.79454
O88600	WNSPAEEGSSDCEVFPK	1.14338479	2	3.82314
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**2.259729906**	**0.00046**	**21**
O88618	AFAACLGAIK	1.077937739	2	3.13147
O88618	AGEYEALPEK	1.175177663	2	2.79113
O88618	ALLDAAAFYCDK	1.626569831	2	3.5
O88618	ALLDAAAFYCDKEK	1.434908011	2	3.41544
O88618	EAQELNLPVVGSQLVGLVPLK	1.184182068	3	4.27521
O88618	GVSMDECVLCAK	1.348461539	2	3.70068
O88618	IIEYLVPDSGPEQSLLDASLR	0.894966991	2	4.86891
O88618	ISSLLQEAK	1.636547878	2	2.38561
O88618	KVQGIGWYLEEK	0.989406206	2	3.27075
O88618	LAEELNVPVYLYGEAAQMPSR	1.523964996	2	4.91619
O88618	LFVLEEEHR	1.203382576	2	2.84273
O88618	LGLDSLAPFDPK	2.023538941	2	3.84132
O88618	MGALDVCPFIPVR	1.440172535	2	3.93709
O88618	MGALDVCPFIPVR+Oxidation(0	0.620476599		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.71064453	3	4.10469
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.328751042	2	3.93634

O88618	TASQLIDMR	1.248425445	2	2.36918
O88618	TCALQEGLR	1.361759256	2	2.81015
O88618	TQAALVLGSLEAR	1.725236755	2	5.09415
O88618	TVYTFVGQPECVVEGALSAAR	1.157717217	2	4.75826
O88618	VQGIGWYLEEK	1.499680487	2	3.07695
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**2.094275065**	**0.99373**	**9**
O88637	AHHSSQEMSSEYR	1.104058568	3	3.78689
O88637	GPPVFTQEER	1.066141633	2	2.70262
O88637	HKGPPVFTQEER	1.052553611	2	3.10687
O88637	HNCDFCVHGNDITLTVDGR	1.061541148	3	3.88288
O88637	NRLEYEAR	1.171422683	2	2.40918
O88637	TEIVPDRDGSDPYEEPK	0.558574288	2	2.86998
O88637	TQGVSTTDLVGR	1.299458062	2	3.16976
O88637	WVDEVVPAAPYVTTLETLDK	1.541683582	2	2.62211
O88637	YVSEVVIGAPYSVTAELLNHFK	1.387130854	3	3.76594
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**1.981416424**	**0.99916**	**2**
O88656	ASSEGGAATGAGLDSLHK	0.918677174	2	4.29018
O88656	NSVSQISVLSGGK	0.992080668	2	2.53192
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**2.171758788**	**0.74618**	**2**
O88696	GQATDIAIQAEEIMK	1.66303088	2	4.27359
O88696	VLVHPPQDGEDEPELVQK	1.00965736	3	3.95258
O88735	**MAP7 Ensconsin**	**1.77206325**	**0.00204**	**2**
O88735	KTTEQRNGDIAK	0.824194789	2	2.57664
O88735	TSAGTTDPEEATR	1.17983048	2	2.6675
O88746	**TOM1 Target of Myb protein 1**	**1.78484308**	**0.93597**	**3**
O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	1.080654315	3	5.52596
O88746	QQSTGAIPATQAR	0.795613067	2	2.70142
O88746	YEAPQTTDGLAGALDAR	1.059949058	2	3.89056
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**2.199981638**	**0.86671**	**3**
O88761	DTSEDIEELVEPVAAHGPK	1.306651562	2	4.1809
O88761	QGALIASALIMIQQTEITCPK	1.584432973	2	2.41419
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.078048477	2	3.69429
O88767	**PARK7 Protein DJ_1**	**2.699830654**	**0.97809**	**8**
O88767	ALVILAK	1.246715698	2	2.37563
O88767	DVVICPDTSLEEAK	1.049749393	2	3.41998
O88767	GAEEMETVIPVDIMR	1.186599234	2	4.19968
O88767	GAEEMETVIPVDIMR+Oxidation(4	1.492554863		
O88767	GLIAAICAGPTALLAHEVGFGCK	1.484833635	2	4.45687
O88767	KGLIAAICAGPTALLAHEVGFGCK	1.392631764	3	3.99545
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	1.13170596	3	4.69795
O88767	VTVAGLAGKDPVQCSR	0.956976256	2	4.25168
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**2.094600251**	**0.99305**	**3**
O88794	FFTNYESR	1.043445214	2	2.32863
O88794	KKNEELGQLYR	0.917876377	2	2.98328
O88794	SSQIGAVVSR	1.568134414	2	2.81686
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.778393414**	**0.14057**	**14**
O88813	AEYLGSCLLHK	0.867397141	2	2.72412
O88813	AILEDLQK	0.79057226	1	2.23086
O88813	ATMLIENVEK	1.103176807	2	2.34114
O88813	FFQTQIK	0.90736412	1	2.02618
O88813	GAMLTHQNIVSNMAAFLK	1.225821874	3	3.59441
O88813	GLAVSDNGPCLGYR	0.88228811	2	3.43258
O88813	GSFEELCQNQCVK	0.789392114	2	4.42662

O88813	GYLKDPEK	0.689766836	2	2.3939
O88813	IGFFQGDIR	1.21895117	2	3.22653
O88813	SFLIGVVVPDPESLPSFAAK	0.852045841	2	4.35065
O88813	SIFVHPEPFSIENGLLTPTLK	1.338255997	2	3.63588
O88813	SRPILQVFVHGESLR	1.059467768	3	3.76821
O88813	TQEVLDKDGWLHTGDIGR	0.810037561	3	3.7425
O88813	TVILMDPFDDDLMK	0.751333812	2	3.51655
O88867	**KMO Kynurenine 3_monooxygenase**	**2.128543228**	**0.00034**	**7**
O88867	AVGLEDQIVSK	0.922935	2	2.49406
O88867	DFFLLPAQPMISVK	0.915355441	2	2.7583
O88867	DLLTAVESYPNAK	0.966103156	2	2.39351
O88867	FNNDLSVCLPEFSR	1.190601588	2	4.06053
O88867	NFPDAIPLMGEQALMR	1.155058165	2	3.27576
O88867	SINLALSYR	1.274707343	2	2.38707
O88867	SQYILSISR	0.834408506	2	2.41832
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**2.04587407**	**0.94882**	**3**
O88941	ALESHAAAFK	0.865443431	2	2.46837
O88941	DLALPTLLNPK	1.064538423	2	2.77078
O88941	MDPSLFPPVPLFSGVPSR	0.963180082	2	2.74233
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**2.01921755**	**0.96941**	**3**
O88986	GTDELLGVMDQVTIINSTLGK	1.011918634	2	3.99463
O88986	HLDMADLEAK	0.963990873	2	2.44538
O88986	VQISAVHSEEDIDR	1.116060585	2	3.96126
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**2.187511065**	**0.92647**	**9**
O88989	DLDVAVLVGSMPR	1.265436581	3	4.18611
O88989	EKMDLTAKELTEEK+Oxidation(2	1.350779509		
O88989	ELTEEKETAFEFLSSA	3.448559256	2	3.47368
O88989	EVGVYEALKDDSWLK	2.323127476	2	4.40612
O88989	FVEGLPINDFSR	1.65815639	2	3.41743
O88989	GEFITTVQQR	1.085953448	2	3.98075
O88989	LGVTADDVK	1.209678368	2	2.92232
O88989	NVIIWGNHSSTQYPDVNHAK	0.922820486	2	5.81141
O88989	VIVVGNPANTNCLTASK	1.139568052	2	5.24321
O88990	**ACTN3 Alpha_actinin_3**	**1.865524664**	**0.99999**	**10**
O88990	AGTQIENIEEDFR	0.933770123	2	3.56462
O88990	ALDFIASK	1.110112762	2	2.67111
O88990	CQLEINFNTLQTK	1.099234267	2	3.84887
O88990	FAIQDISVEETSAK	0.86557412	2	4.344
O88990	GAILGIQGEIQK	2.176749084	2	3.07425
O88990	GLSQEQLNEFR	1.234843642	2	2.71471
O88990	HEAFESDLAAHQDR	1.190236569	3	4.45058
O88990	TINEVENQVLTR	1.162451427	2	3.21732
O88990	VGWEQLLTSIAR	1.042063262	2	2.71509
O88990	VLAVNQENEK	1.392091552	2	2.32277
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**2.078392732**	**2.2E-06**	**4**
O88994	CVLTTVDPDTGIIDR	1.057461114	2	4.32217
O88994	GVSVCETECTDMGLR	1.131814649	2	3.36238
O88994	QLQQVGTVSK	0.724849305	1	2.1798
O88994	RQLQQVGTVSK	0.655024138	2	3.08204
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.994044868**	**0.96662**	**4**
O89000	GMGLACGQDPELVR	0.967802622	2	3.48695
O89000	LENNFDDIK	1.201096015	2	2.46471
O89000	QEYVGGLSTSEIPQFR	0.926964912	2	3.3358
O89000	TEQDETGNWVEDEEQIVR	2.870783463	2	4.66486
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**2.155819942**	**0.97429**	**2**

O89032	DDSDINTSKTGEVSKR	1.109043178	2	2.59507
O89032	FPIEGGQKDPK	1.103539561	2	2.37496
O89046	**COR1B Coronin_1B**	**1.97643163**	**0.30025**	**3**
O89046	NDQCYEDIR	1.18908132	2	3.17609
O89046	NVLSDSKPAGYSR	1.022015872	2	3.25174
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.726695109	2	3.86418
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.976545212**	**0.99709**	**5**
O89049	GFDQDMANK	0.66825452	2	2.45263
O89049	IEQIEAGTPGR	1.122139883	2	3.34847
O89049	IEQIEAGTPGRLK	1.368324233	2	2.63139
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.979547449	3	4.42204
O89049	WGLGGTCVNVGCIPK	0.83607682	2	3.63223
O89079	**COPE Coatomer subunit epsilon**	**2.314964026**	**0.90648**	**2**
O89079	NAFYIGSYQQCINEAQR	1.046476279	2	2.78795
O89079	YGVVLDEIKPSSAPELQAVR	1.21290728	3	4.07226
P00173	**CYB5 Cytochrome b5**	**1.737714735**	**6.7E-16**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	84.46146563	2	5.41112
P00173	FLEEHPGGEEVLR	0.842697368	2	4.13475
P00173	STWVILHHK	1.017785016	2	2.94549
P00173	TYIIGELHPDDR	0.843931877	2	4.08594
P00173	VYDLTK	0.847709192	1	2.04902
P00173	YYTLEEIQK	0.812209548	2	2.96554
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.904716097**	**0.99994**	**10**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.22189358	3	4.78158
P00388	GMSADPEEYDLADLSSLPEIDK	1.938118543	2	4.98285
P00388	HILAILQDYPSLRPPIDHLCELLPR	1.105179659	4	4.96519
P00388	KKEEIPEFSK	0.682836696	2	2.73618
P00388	LEQLGAQR	0.897110315	2	2.53135
P00388	LIHEGGAHIYVCGDAR	1.260047652	3	3.63829
P00388	RSDEDYLYR	0.928004895	2	2.80988
P00388	SYENQKPPFDAK	1.133771487	2	3.32394
P00388	TYEHFNAMGK	1.268371869	2	2.61355
P00388	VHPNSVHICAVAVEYEAK	0.970039967	2	4.69648
P00406	**COX2 Cytochrome c oxidase subunit 2**	**2.526231735**	**0.91115**	**4**
P00406	ILYMMDEINNPVLTVK	1.110666524	2	4.45263
P00406	LLEVDNR	1.310715011	2	2.40901
P00406	VVLPMELPIR	1.395220034	2	2.44059
P00406	VVLPMELPIR+Oxidation(4	1.296346235		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**2.158326517**	**0.00058**	**18**
P00481	EATIPIVNGLSDLYHPIQILADYLTLQEHYGSLK	1.122923853	3	5.48309
P00481	FGMHLQAATPK	1.153241944	3	3.94349
P00481	GEYLPLLQGK	1.173200874	2	3.09492
P00481	GGNVLITDTWISMGQEDEK	1.334617587	2	5.21338
P00481	GGNVLITDTWISMGQEDEKK	1.210933417	2	4.61875
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.030760654	2	4.17853
P00481	GYEPDPNIVK	0.93233524	2	2.61914
P00481	LQAFQGYQVTMK	1.352094474	2	4.04133
P00481	LSMTNDPLEAAR	1.097302884	2	2.92172
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.780580585	3	6.03413
P00481	QKGEYLPLLQGK	0.807105195	2	3.43646
P00481	QSDLDILAK	0.98752258	1	2.06386
P00481	SLGMIFEK	1.08318725	2	2.81479
P00481	SLVFPEAENR	1.055729956	2	2.67016
P00481	SLVFPEAENRK	0.948922992	2	2.93898
P00481	VLSSMTDAVLAR	1.109580013	2	3.93124
P00481	VLSSMTDAVLAR+Oxidation(4	1.329652009		

P00481	YGKPVQSQVQLK	0.507927755	2	3.06799
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**1.586579125**	**1.2E-06**	**2**
P00502	FIQSPEDLEK	0.322387153	2	2.77343
P00502	WLLAAAGVEFDEK	0.676559249	2	4.37535
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**2.24460983**	**1**	**19**
P00507	ASAELALGENSEVLK	0.946964685	2	4.71201
P00507	DAGMQLQGYR	1.260905601	2	2.72527
P00507	DDNGKPYVLPSVR	1.167402372	2	3.55012
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.228744836	3	5.22551
P00507	EYLPIGGLADFCK	1.281860595	2	2.88965
P00507	FVTVQTISGTGALR	1.025244855	2	5.16658
P00507	HFIEQGINVCLCQSYAK	1.078710357	2	4.88872
P00507	IAATILTSPDLR	1.731622536	2	3.05655
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.082627343	3	4.7361
P00507	ISVAGVTSGNVGYLAHAIHQVTK	1.395648256	2	4.42345
P00507	KMNLGVGAYR	0.937313436	2	2.65839
P00507	KQWLQEVK	0.698739427	1	2.16169
P00507	MNLGVGAYR	1.008999544	2	2.93945
P00507	NLDKEYLPIGGLADFCK	1.087257128	2	5.54931
P00507	NMGLYGER	1.022314627	2	2.66784
P00507	TCGFDFSGALEDISK	3.738197279	2	5.01904
P00507	TQLVSNLK	0.928305945	2	2.91855
P00507	VGAFTVVCK	1.090221947	2	3.23156
P00507	VGASFLQR	1.474534688	2	3.11008
P00564	**KCRM Creatine kinase M_type**	**7.684387075**	**0.99857**	**9**
P00564	DLFDPIIQDR	4.162904766	2	2.78149
P00564	FEEILTR	1.959158142	2	2.49143
P00564	GGDDLDPNYVLSSR	1.152529582	2	4.60846
P00564	GQSIDDMIPAQK	4.875989157	2	3.6771
P00564	GTGGVDTAAVGAVFDISNADR	4.886971108	2	5.34519
P00564	LGSSEVEQVQLVVDGVK	3.959086938	2	5.08929
P00564	LSVEALNSLTGEFK	1.631737025	2	4.29879
P00564	RGTGGVDTAAVGAVFDISNADR	5.507576186	2	4.14748
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	2.071404886	3	5.79625
P00787	**CATB Cathepsin B**	**2.108762816**	**0.98219**	**5**
P00787	EQWSNCPTIAQIR	1.346812551	2	2.63425
P00787	GENHCGIESEIVAGIPR	1.128827357	2	4.91291
P00787	HEAGDVMGGHAIR	1.071888213	3	3.86374
P00787	HEAGDVMGGHAIR+Oxidation(6	0.927556976		
P00787	MCEAGYSTSYKEDK	1.135667307	2	4.40045
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**2.086479994**	**0.99969**	**21**
P00884	ALQASALAAWGGK	1.248378689	2	4.98375
P00884	ATQEAFMK	1.170919766	2	2.75294
P00884	ATQEAFMK+Oxidation(6	0.991889346		
P00884	ELSEIAQR	1.98315971	1	2.19026
P00884	ETTIQGLDGLSER	1.199196812	2	3.87477
P00884	FPALTSEQK	1.196481324	2	2.35079
P00884	GILAADESVGTMGNR	1.12703401	2	5.41142
P00884	GILAADESVGTMGNR+Oxidation(11	2.595077598		
P00884	GIVVGIKLDQGGAPLAGTNK	1.92908536	2	4.37209
P00884	GIVVGIKLDQGGAPLAGTNKETTIQGLDGLSER	0.270391759	3	5.41877
P00884	IKVENTEENR	1.035490151	2	3.1908
P00884	IKVENTEENRR	0.829728025	2	3.15911
P00884	ISDQCPSSLAIQENANALAR	1.062579485	2	6.10385
P00884	KELSEIAQR	1.19981728	3	3.36062
P00884	KYTPEQVAMATVTALHR	1.045801223	3	6.03221
P00884	KYTPEQVAMATVTALHR+Oxidation(8	1.82898746		

P00884	LDQGGAPLAGTNK	1.171584904	2	4.65249
P00884	LDQGGAPLAGTNKETTIQGLDGLSER	0.242446997	3	4.3063
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.376709732	3	4.75731
P00884	YTPEQVAMATVTALHR	1.394003419	2	4.63929
P00884	YTPEQVAMATVTALHR+Oxidation(7	1.202874791		
P01015	**ANGT Angiotensinogen**	**4.129814911**	**9.9E-09**	**3**
P01015	GSYNLQDLLAQAK	2.266154826	2	3.1402
P01015	SLDLSTDPVLAAQK	2.044688079	2	3.32871
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	2.432730536	2	3.90488
P01026	**CO3 Complement C3**	**2.041845571**	**0.94565**	**21**
P01026	ACEPGVDYVYK	1.2827815	2	2.48401
P01026	ADIGCTPGSGK	1.045655462	2	3.02188
P01026	AFYEHAPK	0.962554134	2	2.44777
P01026	DSCVGTLVVKGDPR	1.073112651	2	2.58669
P01026	EYVLPSFEVLVEPTEK	1.023174619	2	3.70341
P01026	IFTVDNNLLPVGK	1.532376517	2	3.58548
P01026	IGLQEVEVK	1.007254986	2	2.6463
P01026	LPYSVVRNEQVEIR	1.43214375	2	2.3282
P01026	QNEGFSLTAK	0.905975239	2	2.45793
P01026	RVPVVTQGSDAQALTQDDGVAK	1.078847037	3	5.65816
P01026	SDVDEDIIPEEDIISR	1.303478886	2	4.50376
P01026	SGIPIVTSPYQIHFTK	1.021651435	2	2.94932
P01026	SGSDEVQAGQER	1.11816859	2	3.87248
P01026	SSVAVPYVIVPLK	1.472084929	2	2.97736
P01026	TNQGLQTDQREDPECAKPAAR	1.21641325	3	3.66002
P01026	TVLTGATGHLNR	1.342261254	2	2.84118
P01026	TVVIVIETPDGVPIKR	1.531109181	2	2.73759
P01026	VELKPGDNLNVNFHLR	1.368447154	3	3.91398
P01026	VHQFFNVGLIQPGSVK	1.179596525	3	4.15348
P01026	VLIEDGSGEAVLSR	1.309767872	2	3.98511
P01026	VPVVTQGSDAQALTQDDGVAK	0.83008758	2	5.56998
P01048	**KNT1 T_kininogen 1**	**2.045413471**	**0.92182**	**3**
P01048	FSVATQICNITPGK	0.830538701	2	3.33431
P01048	KTEEDLCVGCFQPIPMDSSDLKPVLK	1.03516003	4	4.65972
P01048	TELTADCETK	0.824693541	2	2.34715
P01946	**HBA Hemoglobin subunit alpha_1/2**	**1.68656922**	**1**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.978324021	3	7.45363
P01946	FLASVSTVLTSK	1.028534822	2	4.01308
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.842598	4	5.44757
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.781426593	5	6.35712
P01946	IGGHGGEYGEEALQR	0.747221175	3	5.093
P01946	LRVDPVNFK	0.820353056	2	2.572
P01946	MFAAFPTTK	0.621390437	2	2.76803
P01946	MFAAFPTTK+Oxidation(0	0.62903522		
P01946	TYFSHIDVSPGSAQVK	0.667055396	2	5.03779
P02089	**HBB2 Hemoglobin subunit beta_2**	**2.209905629**	**1**	**4**
P02089	GTFASLSELHCDK	0.605215831	2	3.76467
P02089	LHVDPENFR	0.714438538	2	2.51555
P02089	YFDSFGDLSSASAIMGNPK	0.890892959	2	6.51648
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14	1.145699641		
P02091	**HBB1 Hemoglobin subunit beta_1**	**1.635397241**	**1**	**10**
P02091	AAVNGLWGK	1.014781544	2	2.7712
P02091	AAVNGLWGKVNPDDVGGEALGR	0.893884139	3	3.61442
P02091	EFTPCAQAAFQK	0.771130926	2	3.17506
P02091	GTFAHLSELHCDK	0.714771983	2	4.40014
P02091	GTFAHLSELHCDKLHVDPENFR	0.558372573	3	3.95259
P02091	KVINAFNDGLK	0.593521523	2	3.60008

P02091	LLGNMIVIVLGHHLGK	0.888626298	4	4.61855
P02091	VINAFNDGLK	0.607812725	2	2.98589
P02091	VNPDDVGGEALGR	0.463675517	2	4.03006
P02091	VVAGVASALAHK	0.780503003	2	3.74172
P02401	**RLA2 60S acidic ribosomal protein P2**	**2.298360675**	**0.99485**	**6**
P02401	ILDSVGIEADDER	1.227721045	2	4.85031
P02401	KILDSVGIEADDER	0.603687478	2	4.00956
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.193163187	3	5.90573
P02401	NIEDVIAQGVGK	1.185277775	2	4.72825
P02401	VISELNGK	1.067472938	1	2.08877
P02401	YVASYLLAALGGNSNPSAK	1.184181912	2	5.22184
P02564	**MYH7 Myosin_7**	**2.061300309**	**0.99998**	**38**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	1.009216856	3	5.81066
P02564	ANDDLKENIAIVER	1.520810948	3	3.49
P02564	DLEEATLQHEATAAALR	1.059178306	2	4.96562
P02564	DVFVPDDKEEFVK	1.80735479	2	2.44454
P02564	EDQVMQQNPPK	1.284722711	2	3.04702
P02564	EEQAEPDGTEEADK	2.003549519	2	3.06285
P02564	ELENELEAEQK	0.898368432	2	2.37769
P02564	GQNVQQVAYAIGALAK	2.027185767	2	4.06569
P02564	GTLEDQIIQANPALEAFGNAK	0.767370109	3	5.69473
P02564	IEDEQALGSQLQK	1.890316945	2	5.09519
P02564	IEELEEELEAER	2.106753183	2	4.34576
P02564	IKELTYQTEEDRK	1.740836833	2	2.62685
P02564	ILNPAAIPEGQFIDSR	2.715933758	2	2.76913
P02564	KLAEKDEEMEQAK	1.339988824	3	3.65182
P02564	KLAEQELIETSER	0.9479432	2	3.50072
P02564	KLEDECSELKR	1.264183362	3	3.81971
P02564	KVQHELDEAEER	0.961768691	2	3.72532
P02564	LAEQELIETSER	1.015224201	2	3.39427
P02564	LDEAEQIALK	0.80316436	2	3.23504
P02564	LELDDVTSNMEQIIK	1.198290747	2	4.47015
P02564	LQDAEEAVEAVNAK	1.669268754	2	4.68299
P02564	LQNEIEDLMVDVER	1.391945416	2	3.89151
P02564	LTQESIMDLENDKQQLDER	2.187407097	3	3.82173
P02564	MDADLSQLQTEVEEAVQECR	1.653844086	2	4.98524
P02564	NALAHALQSAR	1.041467042	2	2.36926
P02564	NAYEESLEHLETFK	1.264260147	2	3.41042
P02564	NLQEEISDLTEQLGSTGK	1.741148435	2	5.07216
P02564	NLTEEMAGLDEIIVK	1.439204591	2	3.65398
P02564	NNLLQAELEELR	1.776229859	2	3.59633
P02564	QAEEAEEQANTNLSK	2.15485117	2	5.2352
P02564	QKYEESQSELESSQK	1.136515403	2	3.78316
P02564	QLEAEKLELQSALEEAEASLEHEEGK	2.196319512	3	3.60724
P02564	QREEQAEPDGTEEADK	1.387854604	2	3.76492
P02564	TLEDQMNEHR	1.333229231	2	2.53192
P02564	VQHELDEAEER	0.583805957	2	3.46862
P02564	VQLLHSQNTSLINQK	1.826031652	2	4.09822
P02564	VVDSLQTSLDAETR	1.035256417	2	4.1174
P02564	YEESQSELESSQK	2.669801614	2	4.32505
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**2.311003443**	**0.9988**	**12**
P02600	ALGTNPTNAEVK	1.474216736	2	3.33677
P02600	ALGTNPTNAEVKK	2.489988183	2	2.94539
P02600	DQGGYEDFVEGLR	1.434768048	2	3.81599
P02600	IEFEQFLPMMQAISNNK	1.261041866	3	3.91506
P02600	ITLSQVGDVLR	3.237315032	2	3.5886

P02600	KIEFEQFLPMMQAISNNK	0.672061692	2	4.90061
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	1.624259573	3	5.51342
P02600	KPAAAAPAPAPAPAPAPAKPK	2.280393976	3	3.70325
P02600	KPAAAAPAPAPAPAPAPAKPKEEK	2.77454483	3	5.2377
P02600	KVLGNPSNEEMNAK	2.620890816	2	3.65182
P02600	VLGNPSNEEMNAK	3.112670719	2	3.91882
P02600	VLGNPSNEEMNAK+Oxidation(9	1.314023753		
P02625	**PRVA Parvalbumin alpha**	**2.122717728**	**0.99944**	**5**
P02625	AIGAFTAADSFDHK	1.55083042	2	2.4556
P02625	AIGAFTAADSFDHKK	1.794490768	2	3.85334
P02625	SGFIEEDELGSILK	1.19865887	2	4.03336
P02625	TLMAAGDKDGDGK	0.921595392	2	3.38868
P02625	TLMAAGDKDGDGK+Oxidation(2	0.463398816		
P02650	**APOE Apolipoprotein E**	**1.848433717**	**0.95919**	**12**
P02650	ELEEQLGPVAEETR	1.598112922	2	4.21141
P02650	GRLEEVGNQAR	0.773814337	2	3.39432
P02650	GWFEPLVEDMQR	1.064122488	2	3.04135
P02650	LEEVGNQAR	0.778665059	2	2.44534
P02650	LGADMEDLR	0.975325714	2	3.16475
P02650	LGPLVEQGR	0.882826832	2	2.99943
P02650	LQAEIFQAR	0.930971605	2	2.53109
P02650	MEEQTQQIR	0.975059557	2	3.37692
P02650	NEVNTMLGQSTEELR	0.796176997	2	4.64819
P02650	SKMEEQTQQIR	0.801676962	2	3.338
P02650	SKMEEQTQQIR+Oxidation(2	0.889012495		
P02650	TANLGAGAAQPLR	0.863725044	2	4.00139
P02680	**FIBG Fibrinogen gamma chain**	**2.002211841**	**1**	**4**
P02680	LSIGDGQQHHMGGSK	1.17191596	2	3.40696
P02680	VGPESDKYR	0.935805994	2	2.7223
P02680	YEALLLTHESSIR	1.308956144	2	3.72808
P02680	YLQDIYTSNK	1.001219594	2	2.86956
P02692	**FABPL Fatty acid_binding protein_ liver**	**2.261343459**	**4.1E-10**	**14**
P02692	AMGLPEDLIQK	1.143733793	2	3.48702
P02692	AMGLPEDLIQK+Oxidation(1	0.980893667		
P02692	GVSEIVHEGK	1.00645933	2	3.45281
P02692	GVSEIVHEGKK	0.723904619	2	3.29625
P02692	MEGDNKMVTTFKGIK+Oxidation(6	0.888327962		
P02692	SVTEFNGDTITNTMTLGDIVYK	1.162314969	3	5.76839
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13	1.356546991		
P02692	SVTEFNGDTITNTMTLGDIVYKR	0.908259377	2	3.72356
P02692	VIHNEFTLGEECELETMTGEK	1.17741513	3	6.02258
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16	1.231466283		
P02692	VIHNEFTLGEECELETMTGEKVK	1.175939024	3	4.9054
P02692	VKLTITYGSK	1.174040995	1	2.02662
P02692	YQVQSQENFEPFMK	1.021831656	2	5.78362
P02692	YQVQSQENFEPFMK+Oxidation(12	0.937969601		
P02696	**RET1 Retinol_binding protein 1**	**2.246930517**	**0.99325**	**6**
P02696	ALDVNVALR	1.463778831	2	2.97428
P02696	CMTTVSWDGDKLQCVQK	0.881481212	2	4.23034
P02696	EFEEDLTGIDDR	1.087152988	2	3.24756
P02696	EFEEDLTGIDDRK	1.160790871	2	3.49205
P02696	MLSNENFEEYLR	1.144841255	2	3.86972
P02696	MLSNENFEEYLR+Oxidation(0	1.463184295		
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.963913255**	**1**	**5**
P02706	DYQDFQHLDNENDHHQLQR	0.944295575	3	4.12294
P02706	LVESQLEK	0.953771489	2	2.77993
P02706	SLSCQMAALR	0.939005542	2	2.80293

P02706	WVCETELGK	0.95577782	2	2.46677
P02706	WVDGTDYETGFK	1.044017446	2	3.1856
P02770	**ALBU Serum albumin**	**2.424517009**	**1**	**25**
P02770	AADKDNCFATEGPNLVAR	1.375822552	2	4.44865
P02770	AETFTFHSDICTLPDKEK	1.359659873	3	3.36995
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.265456641	2	5.04219
P02770	CCSGSLVER	1.014320302	2	2.88549
P02770	CCTLPEAQR	1.003808216	2	3.06953
P02770	DLGEQHFK	0.911105727	1	2.1346
P02770	ECCHGDLLECADDR	0.99443002	2	3.68599
P02770	ECCHGDLLECADDRAELAK	0.976181958	2	5.55439
P02770	FKDLGEQHFK	0.943926426	3	4.18445
P02770	GLVLIAFSQYLQK	0.77272413	2	4.12847
P02770	INKECCHGDLLECADDRAELAK	0.880262473	3	4.81183
P02770	KQTALAELVK	2.817663916	3	4.04055
P02770	KYEATLEK	0.805179118	1	2.61506
P02770	LGEYGFQNAVLVR	1.190471639	2	3.77918
P02770	LQACCDKPVLQK	1.135990697	2	4.0486
P02770	LVQEVTDFAK	1.200800691	2	3.51271
P02770	RHPDYSVSLLLR	2.391576436	3	5.36587
P02770	SIHTLFGDK	1.216752062	1	2.59696
P02770	TCVADENAENCDK	1.008945	2	4.58551
P02770	TNCELYEK	1.07898825	2	2.86214
P02770	TVMGDFAQFVDK	1.365562278	2	3.88801
P02770	YEATLEK	1.362758486	1	1.96369
P02770	YMCENQATISSK	1.097553157	2	4.14408
P02770	YMCENQATISSK+Oxidation(1	1.298382908		
P02770	YNEVLTQCCTESDK	1.169832588	2	5.52498
P02803	**MT1 Metallothionein_1**	**486.1581332**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	10.681939	3	6.52961
P02803	SCCSCCPVGCSK	4.199462124	2	4.11442
P04041	**GPX1 Glutathione peroxidase 1**	**2.541628458**	**0.73**	**11**
P04041	DYTEMNDLQK	37.00103438	2	2.41201
P04041	FLVGPDGVPVR	1.071008828	2	3.21799
P04041	GLVVLGFPCNQFGHQENGK	2.102102311	2	4.06915
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.964955892	3	4.20041
P04041	NALPAPSDDPTALMTDPK	2.959553718	2	3.17598
P04041	NALPAPSDDPTALMTDPK+Oxidation(13	0.75697058		
P04041	NDISWNFEK	1.104466761	2	3.02235
P04041	NEEILNSLK	1.169338305	2	2.48231
P04041	TIDIEPDIEALLSK	1.430817021	3	5.43006
P04041	YIIWSPVCR	1.250047793	2	2.80239
P04041	YVRPGGGFEPNFTLFEK	1.043662735	3	4.70879
P04167	**CP2B2 Cytochrome P450 2B2**	**1.785009588**	**0.44751**	**2**
P04167	GTIAVIEPIFK	0.863482167	2	2.91433
P04167	NLQEILDYIGHIVEK	0.7551573	2	4.33955
P04176	**PH4H Phenylalanine_4_hydroxylase**	**2.177665801**	**0.63047**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.367493152	3	3.50529
P04176	EDNIPQLEDVSQFLQTCTGFR	1.085872848	3	5.16658
P04176	FANQILSYGAELDADHPGFKDPVYR	1.26812339	3	3.98974
P04176	HGSKPMYTPEPDICHELLGHVPLFSDR	1.219177303	3	3.93199
P04176	ILADSINSEVGILCNALQK	1.271816432	3	6.47502
P04176	LNKDEYEFFTYLDK	3.339140209	2	3.57632
P04176	LNKDEYEFFTYLDKR	1.797700055	3	3.53333
P04176	LRPVAGLLSSR	1.479623174	2	2.69481
P04176	NDIGATVHELSR	1.184122363	2	3.75022
P04176	QFADIAYNYR	0.832258551	2	2.41491

P04176	SFAQFSQEIGLASLGAPDEYIEK	1.407775525	2	4.93304
P04176	THACYEHNHIFPLLEK	1.398096826	4	4.98313
P04176	VEVLDNTQQLK	1.070777523	2	3.83769
P04176	VEYTEEEK	1.045092112	2	2.74199
P04176	VEYTEEEKQTWGTVFR	1.00946981	2	3.89734
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.120627102	3	5.12928
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**2.308027211**	**0.54493**	**8**
P04182	AFYNNVLGEYEEYITK	1.318824162	2	4.60059
P04182	GIYMWDVEGR	0.974168624	2	3.12071
P04182	GLLNAIVIR	1.917277639	2	3.26114
P04182	KTEQGPPSSEYIFER	1.958272944	2	4.15833
P04182	TEQGPPSSEYIFER	1.181857797	2	3.9498
P04182	VLPMNTGVEAGETACK	1.408502477	2	4.1541
P04182	WLAVDHENVRPDIVLLGK	1.945278167	2	5.27923
P04182	YGAHNYHPLPVALER	1.668863848	2	4.21891
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**2.17263465**	**0.40767**	**4**
P04256	EDSQRPGAHLTVK	1.124880659	2	3.1967
P04256	IEVIEIMTDR	1.374226437	2	3.42468
P04256	NQGGYGGSSSSSSYGSGR	0.809427509	2	5.16704
P04256	YHTVNGHNCEVR	0.962443518	2	3.38097
P04276	**VTDB Vitamin D_binding protein**	**2.514453067**	**0.377**	**3**
P04276	CCSINSPPR	0.579425144	2	2.52545
P04276	SCESDAPFPVHPGTSECCTK	1.572187598	2	4.6312
P04276	YCSSQIDAEMR	1.709047485	2	3.21518
P04355	**MT2 Metallothionein_2**	**18030.30858**	**9.9E-20**	**2**
P04355	MDPNCSCATDGSCSCAGSCK	33.72861861	2	6.24475
P04355	SCCSCCPVGCAK	4.961920984	2	4.25339
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**5.098200435**	**0.99622**	**8**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.233098574	3	5.25676
P04466	GADPEDVITGAFK	1.657526014	2	4.19398
P04466	LKGADPEDVITGAFK	1.971576247	3	3.47748
P04466	NEELDAMMK	3.276992844	1	2.2033
P04466	NICYVITHGDAK	4.150837938	2	2.84465
P04466	NICYVITHGDAKDQE	2.259897944	2	4.43959
P04466	NMWAAFPPDVGGNVDYK	2.221927659	2	3.07871
P04466	QFLEELLTTQCDR	2.178144497	2	3.99813
P04550	**PTMS Parathymosin**	**1.95276871**	**0.98219**	**4**
P04550	RTAEEEDEADPKR	0.746436461	3	4.10261
P04550	SVEAAAELSAK	0.884512469	2	3.86464
P04550	TAEEEDEADPK	1.701255028	2	3.33814
P04550	TAEEEDEADPKR	1.094016872	2	3.77786
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.936779316**	**0.14634**	**19**
P04636	AGAGSATLSMAYAGAR	0.908935575	2	4.54798
P04636	AGAGSATLSMAYAGAR+Oxidation(9	1.106268447		
P04636	ANTFVAELK	0.913693088	2	3.36116
P04636	EGVIECSFVQSK	1.132761445	2	3.18595
P04636	ETECTYFSTPLLLGK	0.948953292	2	3.74073
P04636	FVFSLVDAMNGK	1.160561223	2	4.46147
P04636	GCDVVVIPAGVPR	0.918492485	2	4.35481
P04636	GYLGPEQLPDCLK	1.00970757	2	4.25715
P04636	IFGVTTLDIVR	0.957173116	2	3.35587
P04636	IQEAGTEVVK	0.865755566	2	2.76192
P04636	IQEAGTEVVKAK	0.410801717	2	2.8792
P04636	ITPFEEK	1.031866759	1	1.94166
P04636	LTLYDIAHTPGVAADLSHIETR	1.127050139	3	6.8526

P04636	MIAEAIPELK	0.839115299	2	3.46179
P04636	MIAEAIPELK+Oxidation(0	0.986087346		
P04636	TIIPLISQCTPK	0.88198723	2	3.55599
P04636	VAVLGASGGIGQPLSLLLK	0.799050504	2	6.29371
P04636	VDFPQDQLATLTGR	1.403776155	2	4.72404
P04636	VNVPVIGGHAGK	0.953943524	2	3.77754
P04638	**APOA2 Apolipoprotein A_II**	**1.706043068**	**0.42898**	**2**
P04638	AQPSEIQNQAK	0.787032308	2	2.74153
P04638	TGTNLMDFLSR	0.762983183	2	2.72502
P04639	**APOA1 Apolipoprotein A_I**	**1.817216312**	**0.9367**	**5**
P04639	LQEQLGPVTQEFWANLEK	1.172692018	2	3.51349
P04639	NEMNKDLENVK	0.74941289	2	3.59204
P04639	NHPTLIEYHTK	1.007954341	3	3.83728
P04639	QLNLNLLDNWDTLGSTVGR	1.12923655	2	4.19133
P04639	WNEEVEAYR	0.968352441	2	2.8765
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.849733173**	**0.54773**	**21**
P04642	DLADELALVDVIEDK	0.637170139	2	5.3144
P04642	DLADELALVDVIEDKLK	1.019650629	2	3.94485
P04642	DQLIVNLLK	1.302359198	2	3.0364
P04642	DQLIVNLLKEEQVPQNK	1.162861155	2	4.34529
P04642	EDVFLSVPCILGQNGISDVVK	1.161523311	2	4.86267
P04642	GEMMDLQHGSLFLK	1.487340727	2	4.11821
P04642	GEMMDLQHGSLFLK+Oxidation(2	1.097956275		
P04642	GEMMDLQHGSLFLK+Oxidation(3	1.34554317		
P04642	GYTSWAIGLSVADLAESIMK	0.841035264	2	4.88495
P04642	IVSSKDYSVTANSK	0.161438078	2	3.63953
P04642	KSADTLWGIQK	1.219351822	2	3.15057
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.129335857	3	5.72876
P04642	LKGEMMDLQHGSLFLK	1.398502705	2	3.99007
P04642	NVNIFK	1.34726852	1	2.07206
P04642	QVVDSAYEVIK	1.036671699	2	3.25565
P04642	RVHPISTMIK	0.909434654	2	2.55841
P04642	SADTLWGIQK	1.017759778	2	3.92659
P04642	SLNPQLGTDADK	1.060699635	2	2.77051
P04642	SLNPQLGTDADKEQWK	1.094143913	2	4.74541
P04642	SLNPQLGTDADKEQWKDVHK	1.097811047	3	3.43593
P04642	VTLTPDEEAR	1.104572223	2	3.01289
P04644	**RS17 40S ribosomal protein S17**	**2.083049763**	**0.92611**	**3**
P04644	DNYVPEVSALDQEIIEVDPDTK	5.290639476	2	4.27681
P04644	LLDFGSLSNLQVTQPTVGMNFK	1.156379602	2	4.72342
P04644	VCEEIAIIPSK	0.979773903	2	3.09423
P04692	**TPM1 Tropomyosin alpha_1 chain**	**2.152976545**	**0.96702**	**10**
P04692	AISEELDHALNDMTSI	1.201084514	2	2.56342
P04692	GTEDELDKYSEALK	1.330805083	2	3.24046
P04692	KLVIIESDLER	1.336300532	2	3.30136
P04692	LDKENALDR	0.959619784	2	3.08951
P04692	LKGTEDELDK	0.436407836	2	2.49803
P04692	LVIIESDLER	0.950813494	2	3.13081
P04692	MEIQEIQLK	1.016179377	2	3.1234
P04692	QLEDELVSLQK	2.177924179	2	2.40528
P04692	SIDDLEDELYAQK	4.807074888	2	4.38194
P04692	SKQLEDELVSLQK	0.677417471	2	3.05108
P04694	**ATTY Tyrosine aminotransferase**	**5.253431749**	**9.9E-20**	**6**
P04694	ILGPCTIVQGALK	2.698146233	2	2.93723
P04694	IQEFCEQHYHCAEGSQEECDK	#NUM!	3	4.92323
P04694	LIAEQAVHCLPATCFEYPNFFR	1.617477184	3	3.98137
P04694	TACLVVNNPSNPCGSVFSK	4.752233702	2	4.96927

P04694	TVISLSIGDPTVFGNLPTDPEVTQAMK	2.753757492	2	3.11028
P04694	YEPLANLSTNVPILSCGGLAK	6.352278643	2	3.60447
P04762	**CATA Catalase**	**1.905414167**	**3.6E-09**	**32**
P04762	APQKPDVLTTGGGNPIGDK	2.430161588	2	4.3417
P04762	DAMLFPSFIHSQK+Oxidation(2	1.018840348		
P04762	DAQLFIQR	0.990082067	2	2.96241
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	1.072148718	4	4.76379
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVKR	1.005304092	4	5.30929
P04762	DPASDQMK	1.000201014	1	2.55677
P04762	DPASDQMK+Oxidation(6	1.316168108		
P04762	DYPLIPVGK	1.308442104	1	2.26444
P04762	EAETFPFNPFDLTK	1.196070977	2	3.96457
P04762	FNSANEDNVTQVR	0.83428701	2	4.57475
P04762	FSTVAGESGSADTVR	0.962948745	2	5.07742
P04762	FSTVAGESGSADTVRDPR	0.841019181	2	2.65521
P04762	FYTEDGNWDLVGNNTPIFFIR	0.985250643	3	6.13444
P04762	GAGAFGYFEVTHDITR	0.86032136	2	4.89049
P04762	GPLLVQDVVFTDEMAHFDR	1.296894669	2	5.50944
P04762	HMNGYGSHTFK	0.920024033	3	4.30958
P04762	HMNGYGSHTFK+Oxidation(1	0.795908829		
P04762	LAQEDPDYGLR	1.413644019	2	2.92098
P04762	LCENIANHLK	0.949598739	3	4.04224
P04762	LFAYPDTHR	1.069308988	2	2.97332
P04762	LGPNYLQIPVNCPYR	1.286073545	2	4.02765
P04762	LNIMTAGPR	1.099934436	2	3.14891
P04762	LVNANGEAVYCK	1.340354463	2	3.90932
P04762	NAIHTYVQAGSHIAAK	2.042523731	3	5.6258
P04762	NFTDVHPDYGAR	1.155874502	2	4.02292
P04762	NLPVEEAGR	0.882031422	2	2.34334
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	0.920461992	3	5.57231
P04762	RFNSANEDNVTQVR	0.68747634	2	5.28592
P04762	VFEHIGK	0.934914593	2	2.44287
P04762	VFEHIGKR	0.597764067	2	2.71282
P04762	VQALLDQYNSQKPK	0.882281739	2	4.86796
P04762	VWPHKDYPLIPVGK	1.117259629	2	3.96364
P04764	**ENOA Alpha_enolase**	**1.81101491**	**0.97339**	**16**
P04764	AGYTDQVVIGMDVAASEFYR	2.148733972	2	4.85387
P04764	DATNVGDEGGFAPNILENK	1.644550082	2	5.63743
P04764	DYPVVSIEDPFDQDDWDAWQK	0.76431216	2	4.30796
P04764	FTATAGIQVVGDDLTVTNPK	1.388950878	2	4.72111
P04764	GNPTVEVDLYTAK	1.250887717	2	4.07359
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.327335597	3	6.15986
P04764	IDQLMIEMDGTENK	0.939106685	2	4.87195
P04764	IEEELGSK	0.996482737	2	2.54216
P04764	IGAEVYHNLK	1.11950454	2	3.30834
P04764	KLNVVEQEK	0.460398062	2	2.54152
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.238541012	3	5.9754
P04764	LNVVEQEK	1.069473551	2	3.0934
P04764	LNVVEQEKIDQLMIEMDGTENK	1.080137987	3	5.2948
P04764	SCNCLLLK	1.062128629	2	2.79394
P04764	VNQIGSVTESLQACK	1.048952023	2	4.95931
P04764	YITPDQLADLYK	2.053805738	2	3.61877
P04785	**PDIA1 Protein disulfide_isomerase**	**1.868235585**	**0.00333**	**25**
P04785	DHENIVIAK	0.858919189	2	2.74915
P04785	EADDIVNWLK	1.324723048	2	2.51986

P04785	HNQLPLVIEFTEQTAPK	1.01890819	3	5.45981
P04785	IFGGEIK	1.154138165	1	1.96317
P04785	IKPHLMSQELPEDWDKQPVK	0.887340881	3	4.95468
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5	1.195834717		
P04785	ILEFFGLK	1.349914606	2	2.95026
P04785	ILFIFIDSDHTDNQR	0.978200148	2	2.63651
P04785	LGETYKDHENIVIAK	1.076511708	3	5.50444
P04785	LITLEEEMTK	1.018513759	2	3.5772
P04785	LITLEEEMTK+Oxidation(7	1.118069562		
P04785	LKAEGSEIR	0.398612792	2	2.44262
P04785	LLDFIK	1.180378453	2	2.43801
P04785	MDSTANEVEAVK	0.892276166	2	4.26409
P04785	MDSTANEVEAVK+Oxidation(0	0.870034968		
P04785	NFEEVAFDEK	1.033313172	1	3.19827
P04785	NFEEVAFDEKK	1.009779108	2	3.97768
P04785	NNFEGEITK	0.964284539	2	2.59229
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	0.905702765	3	6.30544
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.042833348	3	6.16215
P04785	THILLFLPK	5.87942304	2	3.09429
P04785	TVIDYNGER	0.923140968	2	2.97578
P04785	VDATEESDLAQQYGVR	2.31673503	2	5.46142
P04785	YKPESDELTAEK	0.986085783	3	4.50905
P04785	YQLDKDGVVLFK	0.899359504	2	3.79384
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**2.439628388**	**2.3E-15**	**16**
P04797	GAAQNIIPASTGAAK	1.214908087	2	4.14523
P04797	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	2.200178511	3	4.71846
P04797	IVSNASCTTNCLAPLAK	1.326046213	2	4.96471
P04797	LISWYDNEYGYSNR	2.199079359	2	4.3046
P04797	LVINGKPITIFQER	1.693753253	3	4.37649
P04797	RVIISAPSADAPMFVMGVNHEK	1.958995707	3	5.95905
P04797	VGVNGFGR	1.61349548	2	2.34018
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.501569215	3	7.57061
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12	1.520456539		
P04797	VIISAPSADAPMFVMGVNHEK	1.447836476	2	4.62497
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11	1.569054009		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14	1.567854066		
P04797	VPTPNVSVVDLTCR	2.600892288	2	3.18092
P04797	VVDLMAYMASK	1.295014733	2	3.8111
P04797	VVDLMAYMASKE	0.948642281	2	2.41447
P04797	WGDAGAEYVVESTGVFTTMEK	1.630475162	2	5.5687
P04799	**CP1A2 Cytochrome P450 1A2**	**2.257357501**	**4.4E-07**	**8**
P04799	FLTNDNTAIDK	1.075152766	2	2.62703
P04799	IGSTPVVVLSGLNTIK	1.400739654	2	3.36481
P04799	IHEELDTVIGR	1.168122453	2	2.92841
P04799	KSEEMLNLVK	1.011509468	2	2.50428
P04799	NSIQDITGALFK	1.246253451	2	3.77559
P04799	SMTFNPDSGPVWAAR	1.220979941	2	3.42265
P04799	TCEHVQAWPR	1.33488131	2	2.5527
P04799	TVQEHYQDFNK	1.219839459	2	3.72857
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**1.910487066**	**8.2E-06**	**10**
P04903	DGNLMFDQVPMVEIDGMK	0.764500998	2	5.28943
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10	0.744681708		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16	0.719897605		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4	0.75032215		
P04903	KDGNLMFDQVPMVEIDGMK	0.962008682	2	5.05617
P04903	LIQSPEDLEK	1.022966475	2	3.17113
P04903	LKKDGNLMFDQVPMVEIDGMK	1.588801223	3	3.43062

P04903	WLLAAAGVEFEEK	1.24157261	2	3.68958
P04903	YDLYGK	0.701221981	1	1.97605
P04903	YLPAFEK	0.657461365	1	2.04342
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**2.223846807**	**9.9E-20**	**10**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	1.751011807	3	5.41861
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	0.99578384	4	7.75469
P04904	KPLEDEKCVESAVK	0.635132684	2	3.67708
P04904	LRNDGSLMFQQVPMVEIDGMK	1.336257942	2	4.82442
P04904	NDGSLMFQQVPMVEIDGMK	1.226631295	2	4.92645
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11	1.135754687		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17	1.114947282		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5	1.126763099		
P04904	SHGQDYLVGNR	0.960566293	2	3.93402
P04904	WLLAAAGVEFEEQFLK	0.942912075	2	5.70406
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.988647111**	**2.2E-16**	**14**
P04905	ADIVENQVMDNR	0.872385298	2	4.1382
P04905	ADIVENQVMDNR+Oxidation(8	0.952013981		
P04905	CLDAFPNLKDFLAR	1.11729632	2	3.11884
P04905	FKLGLDFPNLPYLIDGSR	1.203963126	3	5.37654
P04905	HHLCGETEEER	0.805879196	3	3.85558
P04905	IRADIVENQVMDNR	0.913324584	2	4.05557
P04905	ITQSNAIMR	1.061937635	2	3.10246
P04905	ITQSNAIMR+Oxidation(7	0.92979183		
P04905	KHHLCGETEEER	0.600531423	3	4.08363
P04905	KITQSNAIMR	0.750449222	3	4.16256
P04905	KITQSNAIMR+Oxidation(8	0.651262182		
P04905	LGLDFPNLPYLIDGSR	1.086654992	2	4.71755
P04905	MQLIMLCYNPDFEK	1.392974774	2	4.30947
P04905	YLSTPIFSK	0.93803571	2	2.79507
P04906	**GSTP1 Glutathione S_transferase P**	**2.082961346**	**0.9829**	**2**
P04906	EAALVDMVNDGVEDLR	1.059534796	2	5.01928
P04906	STCLYGQLPK	1.04391608	2	2.57489
P04937	**FINC Fibronectin**	**1.957427437**	**0.42808**	**7**
P04937	ATGVFTTLQPLR	1.283274735	2	2.39039
P04937	FTQVSPTTLTAQWTAPSVK	1.360569316	2	4.39166
P04937	HYQINQQWER	1.466539099	2	2.55867
P04937	ITYGETGGNSPVQEFTVPGSK	1.111060248	2	2.39202
P04937	SSPVVIDASTAIDAPSNLR	0.827708248	2	3.26054
P04937	SYTITGLQPGTDYK	0.778786976	2	3.01772
P04937	YIVNVYQISEEGK	1.059012183	2	2.84667
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**2.726298719**	**1**	**8**
P05065	ADDGRPFPQVIK	1.798948058	2	2.33158
P05065	ALANSLACQGK	1.093542852	2	2.87116
P05065	ALSDHHVYLEGTLLKPNMVTPGHACTQK	1	3	5.00818
P05065	FSNEEIAMATVTALR	1.558243874	2	4.15722
P05065	GILAADESTGSIAK	1.348726842	2	3.85415
P05065	GVVPLAGTNGETTTQGLDGLSER	1.263697607	2	5.19452
P05065	IGEHTPSSLAIMENANVLAR	1.022773743	2	4.4112
P05065	LQSIGTENTEENR	3.740250002	2	4.02651
P05065	RLQSIGTENTEENR	1.720646297	2	3.64054
P05178	**CP2C6 Cytochrome P450 2C6**	**1.530047939**	**4.8E-11**	**8**
P05178	DLGIVFSHGNR	0.743269894	2	2.38239
P05178	EALIDHGEEFAER	0.628349163	2	3.45801
P05178	EFPDPEIFDPGHFLDGNGK	0.994493989	2	2.91887
P05178	FDYKDQDFLNLMEK	0.60913491	3	4.91352
P05178	FIDLIPTNLPHAVTCDIK	0.702093207	2	3.5973
P05178	GTTIITSLSSVLHDSK	0.963847916	2	3.68069

P05178	MCAGEGLAR	0.664323562	2	2.73944
P05178	NITQSLTSFSK	0.571422259	2	2.68473
P05179	**CP2C7 Cytochrome P450 2C7**	**2.743336914**	**0.65164**	**7**
P05179	ACVGEGLAR	1.365854089	2	3.08125
P05179	FINFVPTNLPHAVTCDIK	2.398982489	3	3.34391
P05179	HMPYTDAMIHEVQR	1.60772687	3	3.96349
P05179	IEEHQESLDVTNPR	2.516104261	2	4.79203
P05179	KIEEHQESLDVTNPR	1.60928842	2	4.875
P05179	KLPPGPTPLPIIGNFLQIDVK	1.18998941	3	5.74599
P05179	VLTSLTSVLHDSK	2.26579046	2	2.86089
P05182	**CP2E1 Cytochrome P450 2E1**	**1.79865709**	**0.9996**	**16**
P05182	AKEHLQSLDINCAR	0.930440155	3	4.68477
P05182	DIDLSPVTVGFGSIPPQFK	0.812121287	2	2.75925
P05182	DRLDMPYMDAVVHEIQR	0.829759832	3	3.35647
P05182	DTVFQGYVIPK	0.69361358	2	2.62918
P05182	DVTDCLLIEMEK	0.85561368	2	2.65073
P05182	DVTDCLLIEMEKEK	1.483090945	2	3.09422
P05182	DVTDCLLIEMEKEK+Oxidation(9	0.797676045		
P05182	EHLQSLDINCAR	0.913981269	2	3.47016
P05182	FINLVPSNLPHEATR	0.843411276	2	3.66087
P05182	FKPEHFLNENGK	0.972108192	2	3.36973
P05182	GDIPVFQEYK	0.886009356	2	2.59419
P05182	GIIFNNGPTWK	0.76326664	2	2.75793
P05182	GTVVIPTLDSLLYDSHEFPDPEK	1.077077059	2	5.07511
P05182	LDMPYMDAVVHEIQR	0.959158465	2	3.11696
P05182	RVCVGEGLAR	0.985407958	2	2.35621
P05182	YGLLILMK	0.892342124	2	3.00967
P05183	**CP3A2 Cytochrome P450 3A2**	**2.115987744**	**0.99943**	**12**
P05183	DFGPVGIMGK	2.433236994	2	2.86713
P05183	DIELDGLFIPK	2.019040228	2	3.585
P05183	EMFPIIEQYGDILVK	1.363741823	2	3.93193
P05183	KDIELDGLFIPK	1.557913316	2	2.87139
P05183	KLQEEIDGALPSK	1.204320674	2	4.02133
P05183	LQEEIDGALPSK	0.977026377	2	4.09189
P05183	QAILEPEKPIVLK	1.008548734	2	3.41415
P05183	QEAETGKPVTMK	0.787726526	2	3.44976
P05183	QEAETGKPVTMK+Oxidation(10	1.131053906		
P05183	RDFGPVGIMGK	1.088063452	2	2.39059
P05183	VDFLQLMLNAHNNSK	0.855654868	2	3.371
P05183	YLKQEAETGKPVTMK	1.091280223	3	3.31601
P05197	**EF2 Elongation factor 2**	**2.040621696**	**0.09172**	**30**
P05197	ALLELQLEPEELYQTFQR	1.43206491	3	5.23297
P05197	ARPFPDGLAEDIDKGEVSAR	1.004221813	3	6.45462
P05197	AYLPVNESFGFTADLR	1.20608472	2	3.78199
P05197	CELLYEGPPDDEAAMGIK	1.0797102	2	3.65729
P05197	DLEEDHACIPIK	0.957859369	2	3.77374
P05197	DLEEDHACIPIKK	1.178462342	2	3.71966
P05197	EGIPALDNFLDK	0.577468498	2	2.67665
P05197	EGIPALDNFLDKL	1.725864581	2	3.4492
P05197	ETVSEESNVLCLSK	1.178300556	2	4.45299
P05197	GEGQLGAAER	1.354233298	2	3.04751
P05197	GHVFEESQVAGTPMFVVK	1.245521741	2	5.90146
P05197	IWCFGPDGTGPNILTDITK	1.506589954	2	5.20761
P05197	KEDLYLKPIQR	0.818361179	2	3.37276
P05197	KIWCFGPDGTGPNILTDITK	1.267231346	2	5.02003
P05197	KVEDMMK	0.870248572	2	2.574
P05197	KVEDMMK+Oxidation(4	1.058385041		

P05197	KVEDMMK+Oxidation(5	1.058385041		
P05197	LDSEDKDKEGKPLLK	0.907987788	2	4.06098
P05197	NMSVIAHVDHGK	0.513453749	2	3.65338
P05197	NMSVIAHVDHGK+Oxidation(1	1.032999867		
P05197	SDPVVSYR	1.096600744	2	2.30352
P05197	STLTDSLVCK	1.453624882	2	3.18135
P05197	TFCQLILDPIFK	1.319531279	2	4.19923
P05197	TGTITTFEHAHNMR	1.113003091	2	4.00219
P05197	VFDAIMNFR	1.793674642	2	3.31539
P05197	VFSGVVSTGLK	1.137919728	2	3.09305
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.431000126	3	3.5946
P05197	YEWDVAEAR	1.153574175	2	3.14639
P05197	YFDPANGK	1.066078718	1	2.21181
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.265051811	3	5.96445
P05369	**FPPS Farnesyl pyrophosphate synthase**	**2.814975694**	**0.03631**	**11**
P05369	ALYEELDLR	1.596410005	2	3.19343
P05369	EVLEYNTVGGK	0.627254688	2	3.00185
P05369	GLTVVQTFQELVEPR	0.624416534	3	4.21982
P05369	IKEVLEYNTVGGK	0.572860043	3	4.2431
P05369	QILEENYGQK	0.698033345	2	2.61646
P05369	QILEENYGQKDPEK	0.461227754	2	3.60068
P05369	SLIEQCSAPLPPSIFLELANK	0.586071827	2	4.8517
P05369	VGTDIQDNK	0.697128406	2	3.79731
P05369	VLTEDELGHPEK	0.780918903	2	2.77619
P05369	VLTEDELGHPEKGDAITR	0.524849778	2	4.68737
P05369	YEEDSYNR	1.250797181	2	2.4574
P05426	**RL7 60S ribosomal protein L7**	**2.565031432**	**0.94449**	**7**
P05426	AGNFYVPAEPK	1.011278543	2	3.06486
P05426	FGIICMEDLIHEIYTVGK	1.404303314	3	4.80491
P05426	KKVPAVPETLK	0.825579778	2	2.70811
P05426	NFAELK	1.017251823	1	1.90921
P05426	SVNELIYK	1.00215407	2	2.32386
P05426	TTHFVEGGDAGNR	1.227475632	3	3.75081
P05426	TTHFVEGGDAGNREDQINR	0.993995049	2	4.54414
P05544	**SPA3L Serine protease inhibitor A3L**	**3.329045764**	**0.0305**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	4.82147592	2	4.37677
P05544	DSTMEEILEGLK	2.008965571	2	3.11908
P05544	IAELFSDLEER	1.877213936	2	2.95923
P05544	MQQVESSLQPETLK	1.44089127	2	4.1842
P05544	MQQVESSLQPETLKK	1.852116423	2	3.91799
P05544	VFSQQADLSR	1.712140402	2	3.04575
P05545	**SPA3K Serine protease inhibitor A3K**	**3.077695196**	**0.00237**	**6**
P05545	AVLDVDETGTEGAAATAVTAALK	1.597441786	2	5.86145
P05545	IAELFSELDER	1.877549887	2	2.82554
P05545	IFSQQADLSR	1.394456715	2	2.55678
P05545	KIFSQQADLSR	1.563075444	2	2.39508
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	1.648917488	3	3.69476
P05545	NLHVSQVVHK	1.033409674	2	2.47458
P05712	**RAB2A Ras_related protein Rab_2A**	**2.060164382**	**0.99995**	**2**
P05712	IQEGVFDINNEANGIK	1.045517849	2	4.56114
P05712	TASNVEEAFINTAK	0.968988464	2	2.97454
P05765	**RS21 40S ribosomal protein S21**	**2.437623377**	**0.99994**	**3**
P05765	DHASIQMNVAEVDR	1.289438336	2	3.93561
P05765	MGESDDSILR	1.028607777	2	3.27114
P05765	TYGICGAIR	1.015554843	2	3.31347
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**1.814431127**	**0.14954**	**9**
P06214	AGADIIITYFAPQLLK	0.782277874	2	3.66608

P06214	AGAFDLR	0.857253005	2	2.50458
P06214	AGCQVVAPSDMMDGR	1.020084635	2	3.6028
P06214	CVLIFGVPSR	1.102954336	2	2.85991
P06214	DEQGSAADSEDSPTIEAVR	0.703345679	2	5.82811
P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.863227749	3	4.63134
P06214	TAVLESMTAFR	1.077642048	2	3.53858
P06214	VPKDEQGSAADSEDSPTIEAVR	0.832647697	3	5.806
P06214	YGVNQLEEMLRPLVEAGLR	0.859525277	3	4.66805
P06302	**PTMA Prothymosin alpha**	**1.649912167**	**0.00016**	**3**
P06302	RVAEDDEDDDVETKK	0.662878351	3	5.75299
P06302	VAEDDEDDDVETK	1.93442655	2	4.37964
P06302	VAEDDEDDDVETKK	0.902755021	2	4.80353
P06399	**FIBA Fibrinogen alpha chain**	**2.230074624**	**0.99498**	**9**
P06399	AQQIQVLQK	0.907654868	2	2.56098
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	1.658183239	3	3.61527
P06399	GDFANANNFDNTFGQVSEDLR	1.581845162	2	5.32089
P06399	GDFANANNFDNTFGQVSEDLRR	1.098097888	3	3.34685
P06399	GDKELLIGNEK	1.059165449	2	2.56571
P06399	GLIDEANQDFTNR	1.117374208	2	3.4943
P06399	MADEAASEAHQEGDTR	0.92323508	2	4.44889
P06399	SQLQEGPPEWK	1.196401031	2	2.88732
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	2.923525791	3	3.86129
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**2.026377591**	**0.97579**	**7**
P06685	AVAGDASESALLK	1.056773009	2	3.52351
P06685	AVFQANQENLPILK	1.023252727	2	3.18331
P06685	DKYEPAAVSEHGDKK	0.952610011	3	3.74223
P06685	DMTSEELDDILR	0.825324024	2	2.97013
P06685	LNIPVNQVNPR	1.071433356	2	3.00185
P06685	MSINAEDVVVGDLVEVK	2.115485581	2	2.95446
P06685	YEPAAVSEHGDKK	0.994697433	2	3.29365
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**2.01666998**	**0.98514**	**3**
P06687	DGPNALTPPPTTPEWVK	1.013091207	2	3.36608
P06687	GVGIISEGNETVEDIAAR	1.231582203	2	4.6752
P06687	QGAIVAVTGDGVNDSPALK	0.884685677	2	4.62584
P06757	**ADH1 Alcohol dehydrogenase 1**	**2.362734195**	**0.78681**	**16**
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.236804955	3	5.76734
P06757	FPLEPLITHVLPFEK	1.60761924	3	4.69981
P06757	GAIFGGFK	0.940948461	2	2.75724
P06757	GALLDGTSR	1.088824016	2	2.9695
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.689148427	3	5.34264
P06757	HPESNLCCQTK	1.15875709	2	3.24545
P06757	ICKHPESNLCCQTK	0.195543155	3	4.1981
P06757	IDAAAPLDK	7.699575955	2	2.91263
P06757	IIAVDINKDK	1.157567354	2	2.95461
P06757	INEAFDLLR	1.231256136	2	3.63854
P06757	KFPLEPLITHVLPFEK	1.748595852	3	4.64681
P06757	MVATGVCR	0.709800722	2	2.49079
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.256066295	4	7.54586
P06757	VCLIGCGFSTGYGSAVQVAK	1.098617832	2	6.31846
P06757	VIPLFSPQCGK	0.952666271	2	3.03683
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.244185755	2	5.06988
P06761	**GRP78 78 kDa glucose_regulated protein**	**2.14175353**	**1**	**31**
P06761	AKFEELNMDLFR	0.930347633	3	4.66838
P06761	DAGTIAGLNVMR	1.413744154	2	3.652

P06761	DNHLLGTFDLTGIPPAPR	1.214183389	2	4.32849
P06761	ELEEIVQPIISK	1.379282535	2	4.3178
P06761	ETAEAYLGK	1.093040854	1	2.07649
P06761	FEELNMDLFR	1.13487065	2	3.67616
P06761	IEIESFFEGEDFSETLTR	1.552261581	2	4.74762
P06761	IEWLESHQDADIEDFK	1.078116493	2	5.65328
P06761	IEWLESHQDADIEDFKAK	0.910783427	3	4.34794
P06761	IINEPTAAAIAYGLDKR	1.032294649	2	4.56116
P06761	ITITNDQNR	1.089143065	2	2.7296
P06761	ITPSYVAFTPEGER	1.079415823	2	4.08301
P06761	KKELEEIVQPIISK	0.928905144	2	5.24619
P06761	KSDIDEIVLVGGSTR	1.07774951	2	5.01469
P06761	KSQIFSTASDNQPTVTIK	0.983241479	2	5.27532
P06761	LYGSGGPPPTGEEDTSEKDEL	2.19593456	2	5.34628
P06761	MKETAEAYLGK	1.200728121	2	3.44756
P06761	MKETAEAYLGK+Oxidation(0	0.90476958		
P06761	MKETAEAYLGKK	0.775041107	2	2.85694
P06761	NELESYAYSLK	1.14897602	2	3.37148
P06761	NQLTSNPENTVFDAK	0.971121191	2	4.76765
P06761	SDIDEIVLVGGSTR	1.29299045	2	3.80536
P06761	SQIFSTASDNQPTVTIK	1.021502567	2	5.36966
P06761	TFAPEEISAMVLTK	1.124820604	3	4.75106
P06761	TFAPEEISAMVLTK+Oxidation(9	1.305234862		
P06761	TKPYIQVDIGGGQTK	1.097262314	3	4.71136
P06761	TWNDPSVQQDIK	1.049259982	2	3.9831
P06761	VLEDSDLK	1.172103353	2	2.47726
P06761	VLEDSDLKK	1.085577652	2	2.51852
P06761	VTHAVVTVPAYFNDAQR	1.02204777	2	5.06552
P06761	VYEGERPLTK	1.068300119	2	2.94021
P06866	**HPT Haptoglobin**	**5.25639317**	**2.2E-12**	**8**
P06866	ATDLKDWVQETMAK	1.649875055	2	3.63808
P06866	GAVSPVGVQPILNK	2.092683235	2	4.45439
P06866	HTFCAGLTK	2.47921369	1	2.4074
P06866	LQTEGDGIYTLNSEK	2.217332245	2	4.43493
P06866	NQLVEIEK	1.723225561	1	2.33215
P06866	SCAVAEYGVYVR	2.214516319	2	3.45217
P06866	SVVDIGLIK	2.379321063	1	2.0186
P06866	YVMLPVADQEK	2.054751249	2	2.5149
P07150	**ANXA1 Annexin A1**	**2.178614428**	**0.87341**	**2**
P07150	GLGTDEDTLIEILTTR	1.135055256	2	3.79267
P07150	GVDEATIIDILTK	1.115165442	3	4.0629
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**2.161846344**	**0.93126**	**16**
P07153	ASSFVLALEPELESR	1.318190302	2	4.2464
P07153	AVTSEIAVLQSR	1.247337599	2	3.89807
P07153	FVDHVFDEQVIDSLTVK	0.983967702	2	4.64806
P07153	GEDEEDNNLEVR	1.046750309	2	3.85473
P07153	HFDETVNR	0.933682572	1	2.71197
P07153	IDHILDAL	1.549915311	2	2.40005
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.331871629	3	4.91024
P07153	LKTEGSDLCDR	1.027740264	3	3.43198
P07153	NIQVDSPYDISR	0.890767174	2	3.50743
P07153	NLVEQHIQDIVVHYTFNK	1.541773948	3	4.90029
P07153	SEDILDYGPFK	1.148512705	2	3.48043
P07153	TEGSDLCDR	1.429097851	2	2.69471
P07153	TILPAAAQDVYYR	1.144833169	2	2.88432

P07153	TVDLSSHLAK	1.168353512	2	2.58741
P07153	VHYENNSPFLTITSMTR	1.470576389	2	4.03744
P07153	VTAEVVLAHPGGGSTAR	1.12968017	2	4.87007
P07323	**ENOG Gamma_enolase**	**2.473157684**	**0.97719**	**3**
P07323	AAVPSGASTGIYEALELR	1.309130805	2	5.28674
P07323	GNPTVEVDLHTAK	2.076532656	2	3.17231
P07323	SGETEDTFIADLVVGLCTGQIK	0.884732604	3	4.94792
P07335	**KCRB Creatine kinase B_type**	**2.279688977**	**0.96712**	**3**
P07335	FCTGLTQIETLFK	1.237583878	2	2.80903
P07335	LEQGQPIDDLMPAQK	0.989832596	2	2.72387
P07335	TDLNPDNLQGGDDLDPNYVLSSR	0.993786583	2	3.57291
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.812070005**	**0.58733**	**3**
P07340	AYGENIGYSEK	1.170143523	2	2.72504
P07340	VAPPGLTQIPQIQK	0.836177455	2	2.58273
P07340	YNPNVLPVQCTGK	0.946778745	2	2.61205
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**4.802477771**	**9.9E-20**	**18**
P07379	AINPENGFFGVAPGTSVK	2.137642555	2	4.44334
P07379	EEGWLAEHMLILGITNPEGK	2.427759536	2	5.14535
P07379	EIISFGSGYGGNSLLGK	2.43055177	2	2.55412
P07379	EVEEIDKYLEDQVNADLPYEIER	1.858607344	2	4.87224
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	1.764992924	3	5.19227
P07379	GLGDVNVEELFGISK	2.158081302	2	3.77223
P07379	IGIELTDSPYVVASMR	2.046923286	2	4.24743
P07379	MGTSVLEALGDGEFIK	2.236465809	2	4.75779
P07379	MGTSVLEALGDGEFIK+Oxidation(0	1.818106575		
P07379	TNLAMMNPTLPGWK	1.949388245	2	3.13418
P07379	TVIITQEQR	1.95187694	2	2.46263
P07379	VECVGDDIAWMK	2.363103868	2	3.83109
P07379	VIQGSLDSLPQEVR	2.47965013	2	3.90576
P07379	VLEWMFGR	2.418475027	2	2.53086
P07379	WMSEEDFEK	1.774853165	2	2.37451
P07379	YDNCWLALTDPR	2.110166414	2	2.51999
P07379	YLAAAFPSACGK	1.295877745	2	2.72062
P07379	YLEDQVNADLPYEIER	1.831989576	2	5.05747
P07483	**FABPH Fatty acid_binding protein_ heart**	**2.686600126**	**0.94103**	**2**
P07483	QVASMTKPTTIIEK	1.136862426	2	3.26915
P07483	WDGQETTLTR	1.433459422	2	2.53159
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**2.017979189**	**0.99998**	**4**
P07632	DGVANVSIEDR	1.962844832	2	2.73234
P07632	GDGPVQGVIHFEQK	1.134775581	2	3.79552
P07632	HVGDLGNVAAGK	1.031780048	2	4.04199
P07632	VISLSGEHSIIGR	1.043849803	2	3.02934
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**1.98168426**	**0.99983**	**10**
P07633	AFDNDVDALCNLR	1.141735193	2	4.07653
P07633	AYNMLDIIHAVIDER	0.971892245	2	3.88651
P07633	GFVDDIIQPSSTR	1.130745745	2	3.23984
P07633	HLLGDTNYAWPTAEIAVMGAK	1.219270957	2	5.75789
P07633	ICCDLEVLASK	0.952182277	2	3.49778
P07633	IMDQAITVGAPVIGLNDSGGAR	0.988487493	3	5.02559
P07633	LVPELDTVVPLESSK	1.236201056	2	3.70332
P07633	NKFPGDSVVTGR	0.957225556	2	2.40977
P07633	SVTNEDVTQEQLGGAK	0.652968527	2	5.2441
P07633	TVGIVGNQPNVASGCLDINSSVK	1.757093446	2	4.91488
P07687	**HYEP Epoxide hydrolase 1**	**1.927171582**	**0.99822**	**26**

P07687	DIELLYPYK	0.898226995	1	2.30278
P07687	DKEETLPLGDGWWGPGSKPSAK	1.252076367	3	5.65544
P07687	EDESIRPFK	0.915286942	2	2.95196
P07687	EDESIRPFKVETSDEEIKDLHQR	0.722207256	3	5.9852
P07687	ELEDGGLER	1.070190326	2	2.34874
P07687	ENLGQGIMVHK	0.939492083	2	3.20023
P07687	ENLGQGIMVHK+Oxidation(7	1.475995082		
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.185843892	3	5.66983
P07687	FHYGFNSNYMK	1.022346417	2	2.62501
P07687	FLGYTEKDIELLYPYK	0.962693815	3	4.74074
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.009931285	3	3.3837
P07687	GGHFAAFEEPK	0.992830732	2	3.46158
P07687	GLHLNMAFISR	1.266841412	2	2.79208
P07687	IEGLDIHFIHVKPPQLPSGR	0.877814914	3	4.26091
P07687	IIPLLTDPK	1.098426914	1	1.9007
P07687	KFVSLAELQ	0.914606666	2	2.80163
P07687	KQVEILNQYPHFK	0.751977426	3	5.21234
P07687	LLAQDIR	0.92792704	2	2.50907
P07687	QVEILNQYPHFK	0.733810677	2	3.5948
P07687	SEYRELEDGGLER	0.911243673	3	3.66431
P07687	SFYTMTPLLGQR	1.16172092	2	3.78076
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	0.991842266	3	6.59517
P07687	TKIEGLDIHFIHVKPPQLPSGR	0.689300165	3	4.03182
P07687	VETSDEEIK	0.911693251	2	2.62877
P07687	VETSDEEIKDLHQR	0.792377132	2	4.72047
P07687	VFVPTGFSAFPSELLHAPEK	1.134499424	2	4.54154
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**2.051685945**	**9.9E-20**	**99**
P07756	AADTIGYPVMIR	1.460917039	2	3.87525
P07756	AADTIGYPVMIR+Oxidation(9	1.590441099		
P07756	AERPDGLILGMGGQTALNCGVELFK	1.22957067	3	6.91184
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10	1.312073811		
P07756	AFAISGPFNVQFLVK	0.842740673	2	4.95617
P07756	AFAMTNQILVER	1.224571907	2	4.58938
P07756	AFAMTNQILVER+Oxidation(3	0.850648854		
P07756	ALENNMSLDEIVK	0.988616501	2	4.81389
P07756	ALENNMSLDEIVK+Oxidation(5	0.876210027		
P07756	AMLSTGFK	1.064111713	2	2.49318
P07756	AQTAHIVLEDGTK	0.982439703	2	4.47708
P07756	ATGYPLAFIAAK	1.065977327	2	3.18313
P07756	CEMASTGEVACFGEGIHTAFLK	1.082618482	3	5.4082
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2	1.152245647		
P07756	CLGLTEAQTR	0.9160607	2	3.61715
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	2.478637366	3	5.16436
P07756	DELGLNK	0.701149308	1	2.34751
P07756	DGSIDLVINLPNNNTK	0.801587217	2	5.31511
P07756	DILNMDK	1.722462738	1	2.03257
P07756	EIEYEVVR	1.041036393	1	2.09313
P07756	EIGFSDKQISK	0.929942782	2	3.1471
P07756	EPLFGISTGNIITGLAAGAK	1.053050282	3	5.65663
P07756	ETLMDLGTK	1.289216725	1	2.33659
P07756	EVEMDAVGK	1.419828529	1	2.1106
P07756	FIEGAREVEMDAVGKEGR	0.508893819	3	3.6484
P07756	FLEEATR	1.397173942	2	2.46326
P07756	FLGVAEQLHNEGFK	1.068501264	2	4.80351
P07756	FVHDNYVIR	1.178942654	3	3.35219

P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.302844147	3	6.06903
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15	1.653122366		
P07756	GILIGIQQSFRPR	1.101300627	2	2.46131
P07756	GLNSESVTEETLR	0.942983288	2	4.84807
P07756	GNDVLVIECNLR	0.932562235	2	4.45974
P07756	GQILTMANPIIGNGGAPDTTAR	0.896016675	2	6.00427
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5	1.098700727		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.876890836	3	4.91201
P07756	GQNQPVLNITNR	0.978585373	2	4.38972
P07756	GTTITSVLPKPALVASR	1.142615857	2	3.35451
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.061515022	3	5.98097
P07756	HLPTLEQPIIPSDYVAIK	1.016613845	2	5.58522
P07756	IALGIPLPEIK	1.401315328	2	2.82732
P07756	IAPSFAVESMEDALK	1.409667774	2	5.25688
P07756	IAPSFAVESMEDALK+Oxidation(9	1.18239329		
P07756	IAPSFAVESMEDALKAADTIGYPVMIR	0.923611883	3	4.13075
P07756	IEFEGQSVDFVDPNK	0.985252171	2	5.29866
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	0.980456276	3	5.55141
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.395988068	3	5.62339
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	0.884848031	3	4.69763
P07756	IMGTSPLQIDR	1.352177068	2	3.26957
P07756	IMGTSPLQIDR+Oxidation(1	1.724128068		
P07756	IMGTSPLQIDRAEDR	0.609485449	2	2.517
P07756	KEPLFGISTGNIITGLAAGAK	1.161991385	2	5.10797
P07756	KTVVVNCNPETVSTDFDECDK	1.077656539	2	4.98109
P07756	LFAEAVQK	0.998453635	2	3.44823
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.162729518	4	4.71588
P07756	LRDADPILR	1.044408398	2	3.21114
P07756	LTSIDKWFLYK	0.667647853	2	2.76499
P07756	LYFEELSLER	1.353015351	2	3.67267
P07756	MCHPSVDGFTPR	1.35496864	3	4.89757
P07756	MCHPSVDGFTPR+Oxidation(0	0.922782651		
P07756	MRDILNMDK	1.064284974	2	3.14774
P07756	MRDILNMDK+Oxidation(0	1.090806804		
P07756	QADAVYFLPITPQFVTEVIK	0.80481445	3	4.19449
P07756	QLFSDKLNEINEK	1.012798697	2	3.82525
P07756	QNLIAEVSTK	0.959002653	1	2.63927
P07756	RFLEEATR	0.957187164	2	2.68996
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.482589849	4	4.62964
P07756	RTAVDSGIALLTNFQVTK	1.013326318	2	5.16508
P07756	RTSINVVR	0.675935438	2	2.33993
P07756	SAYALGGLGSGICPNK	1.111180135	2	4.94947
P07756	SAYALGGLGSGICPNKETLMDLGTK	0.984265375	3	4.69494
P07756	SIFSAVLDELK	0.998687568	2	3.83489
P07756	SIFSAVLDELKVAQAPWK	0.694642119	3	4.29703
P07756	SLGQWLQEEK	1.01078093	2	4.06453
P07756	SLGQWLQEEKVPAIYGVDTR	1.443657581	2	3.7954
P07756	SVGEVMAIGR	0.931274444	2	3.51829
P07756	SVGEVMAIGR+Oxidation(5	0.856915334		
P07756	TAVDSGIALLTNFQVTK	1.05176325	3	6.50634
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	1.019231747	3	5.41638
P07756	TFEESFQK	1.020940417	2	2.50366
P07756	TLGVDFIDVATK	1.02615311	2	4.28344
P07756	TSACFEPSLDYMVTK	0.833126312	2	4.55608

P07756	TSACFEPSLDYMVTK+Oxidation(11	0.6866705		
P07756	TVLMNPNIASVQTNEVGLK	1.015030517	2	6.11632
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3	1.078241886		
P07756	TVVVNCNPETVSTDFDECDK	0.649627852	2	5.61548
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	1.15392564	3	5.56397
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	0.845772235	3	7.42585
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22	1.111410938		
P07756	VLGTSVESIMATEDR	1.235949594	2	4.70256
P07756	VLGTSVESIMATEDR+Oxidation(9	1.055296642		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.457895514	2	5.82353
P07756	VMIGESVDEK	0.984425356	2	3.68868
P07756	VMIGESVDEK+Oxidation(1	0.920692131		
P07756	VSQEHPVVLTK	0.915586925	2	3.84969
P07756	VVAVDCGIK	0.992081781	2	2.52538
P07756	VVAVDCGIKNNVIR	0.275330816	2	3.80094
P07756	YMESDGIK	0.862674923	2	2.61315
P07756	YMESDGIK+Oxidation(1	1.122046555		
P07824	**ARGI1 Arginase_1**	**2.550511089**	**0.38824**	**16**
P07824	ANEQLAAVVAETQK	1.217159596	2	5.20274
P07824	DHGDLAFVDVPNDSPFQIVK	1.863477836	2	6.21711
P07824	DIVYIGLR	1.066416971	2	2.3264
P07824	DVDPGEHYIIK	4.119667749	2	3.41139
P07824	EGNHKPETDYLKPPK	1.506957577	2	2.76863
P07824	GKFPDVPGFSWVTPCISAK	1.278799119	3	4.96103
P07824	LKETEYNVR	1.306325454	3	3.33979
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.332185953	3	4.34269
P07824	RPIHLSFDVDGLDPVFTPATGTPVVGGLSYR	2.285025207	3	5.75482
P07824	TGLLSGLDIMEVNPTLGK	1.764667679	2	5.64583
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9	1.187973694		
P07824	TVNTAVALTLSCFGTK	1.321175461	2	5.03746
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.741234244	4	5.50347
P07824	VMEETFSYLLGR	1.752820953	2	3.70997
P07824	YFSMTEVDK	1.333415016	1	2.3222
P07824	YFSMTEVDKLGIGK+Oxidation(3	1.04758221		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**1.706645095**	**2.2E-16**	**17**
P07871	AEELGLPILGVLR	0.843902199	2	4.30189
P07871	AEIVPVTTTVLDDK	0.859236974	2	4.7357
P07871	AEIVPVTTTVLDDKGDR	0.951768664	2	3.68683
P07871	AEIVPVTTTVLDDKGDRK	0.844030007	2	4.36588
P07871	DCLIPMGITSENVAER	0.641702907	2	3.91008
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	2.770280921	2	6.3436
P07871	IAQFLSGIPETVPLSAVNR	1.332338128	2	3.21586
P07871	KTITVSQDEGVRPSTTMEGLAK	0.793528715	3	3.7047
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.59821009	3	5.14145
P07871	QCSSGLQAVANIAGGIR	0.720960407	2	4.69981
P07871	QDAFALASQQK	0.925390616	2	3.75977
P07871	QKQDAFALASQQK	0.771089226	2	4.15368
P07871	QVVTLLNELK	2.135415497	2	2.38165
P07871	SKAEELGLPILGVLR	1.320832341	3	4.83084
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.920708307	3	4.74667
P07871	TITVSQDEGVRPSTTMEGLAK	0.727808005	2	4.3676
P07871	VNPLGGAIALGHPLGCTGAR	0.841077094	2	4.99562
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**1.819381963**	**0.72525**	**21**
P07872	AFTTWTANAGIEECR	1.77293218	2	3.81496
P07872	ASATFNPELITHILDGSPENTR	0.882277163	2	4.77986
P07872	ASEAHCHYVVVK	0.825449741	3	4.14354

P07872	EIENLILNDPDFQHEDYNFLTR	2.547453323	2	4.54409
P07872	EIGTHKPLPGITVGDIGPK	0.820636432	3	4.12068
P07872	EVAWNLTSVDLVR	1.098100825	2	3.14678
P07872	EYGISDPEEIMWFK	0.851557472	2	3.43568
P07872	FGYEEMDNGYLK	0.831208486	2	3.87587
P07872	GGDFLEGSIITGAQLSQVNAR	1.010823585	2	5.24332
P07872	GLETTATYDPK	0.787308352	2	3.67608
P07872	INESIGQGDLSELPELHALTAGLK	0.961330998	3	5.51523
P07872	LVEIAAK	0.869456711	1	2.20189
P07872	LVGGMVSYLNDLPSQR	1.689077721	2	3.23561
P07872	NLCLLYSLYGISQK	1.317238666	2	3.26243
P07872	QSEPEPQILDFQTQQYK	1.010551866	2	4.78958
P07872	SFLVGNAAQSLSK	0.847614713	2	4.29144
P07872	SKEVAWNLTSVDLVR	0.982212144	3	3.82654
P07872	TQEFILNSPTVTSIK	0.830548023	2	4.57435
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	1.102040075	4	4.92351
P07872	YAQVKPDGTYVKPLSNK	1.353117214	3	3.749
P07872	YDGNVYENLFEWAK	1.120135287	2	4.82144
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**1.799743771**	**0.99859**	**5**
P07895	AIWNVINWENVSQR	0.935996292	2	3.87497
P07895	GDVTTQVALQPALK	0.846705735	2	3.98569
P07895	GELLEAIKR	0.916101105	2	2.33723
P07895	HHATYVNNLNVTEEK	0.883984634	2	4.82983
P07895	NVRPDYLK	0.870909014	2	2.30242
P07896	**ECHP Peroxisomal bifunctional enzyme**	**1.589294943**	**9.9E-20**	**24**
P07896	EWQSLAGPHGSK	0.406465505	2	2.48304
P07896	GGPMFYAASVGLPTVLEK	1.342889167	2	3.88934
P07896	GQGLTGPSLPPGTPVR	0.762669576	2	3.92712
P07896	GWYQYDKPLGR	0.674663088	2	2.90122
P07896	IFNKPVPSLPNMDSVFAEAIAK	1.379297171	3	4.74482
P07896	IGVVVGNCYGFVGNR	1.652103371	2	3.44347
P07896	IIDKPIEPR	0.849892821	2	2.4274
P07896	KGQGLTGPSLPPGTPVR	0.661808644	2	4.26845
P07896	KQYPGVLAPETCVR	0.715628517	2	4.34685
P07896	LCNPPVNAVSPTVIR	0.891644119	2	4.2708
P07896	LGILDAVVK	0.938537674	2	2.81922
P07896	LLEVIPSR	0.796061142	2	2.82499
P07896	LVAQGSPPLK	0.846820135	2	2.54035
P07896	QNPDIPQLEPSDYLR	1.004017576	2	3.95562
P07896	QYPGVLAPETCVR	0.623768739	2	3.07371
P07896	RLVAQGSPPLK	0.56799686	2	2.33736
P07896	TASAQPVSSVGVLGLGTMGR	0.918717767	2	5.88839
P07896	TISKEEILER	0.765943183	2	2.65437
P07896	VGISVVAVESDPK	0.846981151	2	3.90225
P07896	VGLPEVTLGILPGAR	0.997964904	2	3.62223
P07896	VSDLAGLDVGWK	0.821531225	2	4.27189
P07896	YLSADEALR	1.127760135	2	2.97647
P07896	YSPLGDMLCEAGR	0.786805245	2	4.33706
P07896	YSSPTTIATVMSLSK	1.078377044	2	3.49345
P07943	**ALDR Aldose reductase**	**1.876499926**	**0.67361**	**2**
P07943	AIGVSNFNPLQIER	1.332338159	2	3.06443
P07943	HIDCAQVYQNEK	0.83570275	2	4.45897
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**2.478303068**	**0.05109**	**5**
P07953	HGESELNLR	1.09223569	2	2.59769
P07953	IGGDSGLSAR	0.653948678	2	2.77474

P07953	NYEFFRPDNTEAQLIR	3.358832667	2	3.39267
P07953	TIQTAEALGVPYEQWK	2.670337307	2	3.06574
P07953	YLNWIGTPTK	1.497803488	2	2.95927
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**2.094817561**	**0.87466**	**6**
P08009	LCYNPDFEK	1.379792708	2	3.04941
P08009	LLLEYTDSSYEEK	1.069184879	2	4.83114
P08009	LLLEYTDSSYEEKR	0.945890746	2	4.00991
P08009	NQVFEATCLDAFPNLK	0.89066946	2	4.56452
P08009	SQWLNEK	0.905139419	2	2.70843
P08009	YTMGDAPDFDR	1.235033478	2	2.81479
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.839699325**	**0.00773**	**15**
P08010	FLSKPIFAK	1.21143718	2	2.33711
P08010	IRVDVLENQAMDTR	1.174631425	3	4.2239
P08010	ITYVDFLVYDVLDQHR	0.961761992	2	5.01125
P08010	KKPEYLEGLPEK	0.975220398	3	4.16745
P08010	KPEYLEGLPEK	1.336054084	2	3.42906
P08010	KYSMGDAPDYDR	1.410438426	2	3.8264
P08010	LFLEYTDTSYEDK	0.975601381	2	5.54148
P08010	LFLEYTDTSYEDKK	0.965203725	2	4.36844
P08010	LQLAMVCYSPDFER	1.396372658	2	4.32852
P08010	LQLAMVCYSPDFER+Oxidation(4	1.780988811		
P08010	SQWLSEK	1.075780294	2	2.46407
P08010	VDVLENQAMDTR	1.11977028	2	4.69443
P08010	VDVLENQAMDTR+Oxidation(8	0.879364688		
P08010	YSMGDAPDYDR	2.610047645	2	3.3708
P08010	YSMGDAPDYDR+Oxidation(2	1.344057347		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**1.981364286**	**0.90841**	**6**
P08011	IYHTIAYLTPLPQPNR	0.602365143	2	5.3202
P08011	MMFLSSATAFQR	1.215321604	2	3.60354
P08011	MMFLSSATAFQR+Oxidation(0	1.312847065		
P08011	MMFLSSATAFQR+Oxidation(1	1.312847065		
P08011	VFANPEDCAGFGK	0.929937377	2	4.67898
P08011	VFANPEDCAGFGKGENAK	0.908156152	2	4.62132
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**2.096569162**	**0.79493**	**4**
P08032	ADVVESWIGEK	0.964369615	2	2.63621
P08032	DLVAAKNLLNR	1.344459652	2	2.43823
P08032	DQARDLTSAGNLLK	0.960267769	2	2.43349
P08032	QELNTRWNSLK	1.41263065	2	2.30182
P08081	**CLCA Clathrin light chain A**	**2.000821939**	**0.99048**	**2**
P08081	LEALDANSR	1.303999851	2	2.74592
P08081	WREEQTER	0.895039288	2	2.47819
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**2.294469935**	**0.97439**	**3**
P08290	DFQDIQQLDSEENDHQLIGDEEQGSHVQNLR	2.014271932	3	6.50026
P08290	EEQEFVVK	1.009087088	1	2.06398
P08290	WVDGTEYR	1.533366082	2	2.32283
P08430	**UD16 UDP_glucuronosyltransferase 1_6**	**2.128168044**	**0.81163**	**2**
P08430	GHDIVVLVPEVNLLLGESK	1.080997801	3	3.81951
P08430	YEILASDLLK	1.22749281	2	2.47489
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**2.702165039**	**0.92477**	**5**
P08461	AAPAAAAAAPPGPR	0.840987255	2	2.32012
P08461	DVPLGTPLCIIVEK	1.425567036	2	3.42531
P08461	DVPVGSIICITVEKPQDIEAFK	1.89734158	2	3.90108
P08461	GLETIASDVVSLASK	1.471058247	2	4.49826
P08461	VAPTPAGVFIDIPISNIR	2.045918378	2	4.57957

P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**2.141661902**	**1**	**9**
P08503	AFAGDIANQLATDAVQIFGGYGFNTEYPVEK	1.216585054	3	5.1906
P08503	AFTGFIVEADTPGIHIGK	1.052984252	2	4.44266
P08503	EEIIPVAPDYDK	1.044634673	2	3.57535
P08503	GITFEDVR	1.0144978	2	2.42656
P08503	IYQIYEGTAQIQR	1.072180366	2	4.73162
P08503	KGDEYVINGQK	0.978393346	2	4.12428
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	0.858536332	2	4.4693
P08503	SGEYPFPLIK	1.07195122	2	2.79131
P08503	TRPTVAAGAVGLAQR	0.989032801	2	4.41669
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**2.664756475**	**0.00033**	**11**
P08541	DELQNHFIK	1.583886595	2	2.59063
P08541	FEIFSTSISKDELQNHFIK	1.424982446	3	4.89458
P08541	FILPPSYVPVILSGLAGK	3.368630779	3	6.12973
P08541	GAAVSLNIR	1.446797352	2	2.919
P08541	GHEVTVLKPSAYFFLDPK	1.404629714	2	4.34859
P08541	HKEWDTFYSEILGRPTTVDETMSK	0.917503702	3	4.43988
P08541	LLDVWTYELPR	2.066624525	2	4.05144
P08541	NVMLLSTIHHDQPMKPLDR	1.06987725	3	3.78731
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(2	2.25459351		
P08541	VEIWLIR	1.532033586	2	3.025
P08541	VLVWPMDFSHWMNIK	1.20354079	2	2.48399
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**2.237450259**	**0.00399**	**6**
P08542	EIINNPFYK	1.062420113	1	2.07174
P08542	FETFPTSVSKDELENYFIK	1.138924232	2	4.18042
P08542	KWDPFYSEILGRPTTLAETMGK	2.027539018	2	4.06018
P08542	LVDVWTYELQR	1.336118663	2	3.5694
P08542	NAVWLSTIHHDQPMKPLDK	0.968076258	3	4.16042
P08542	WDPFYSEILGRPTTLAETMGK	1.411679001	2	3.7438
P08649	**CO4 Complement C4**	**2.29449925**	**0.64141**	**2**
P08649	SLEIPGSSDPNVIPDGDFSSFVR	1.115692617	2	2.86038
P08649	VTASEPLETLGSEGALSPGGVASLLR	1.561673224	2	2.87177
P08661	**MBL2 Mannose_binding protein C**	**1.85270413**	**0.09152**	**2**
P08661	ALCSELQGTVATPR	0.609017469	2	3.34046
P08661	TENVFEDLTGNR	1.03629126	2	2.85044
P08683	**CP2CB Cytochrome P450 2C11**	**2.453498007**	**0.99583**	**18**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	1.18392871	3	4.89658
P08683	EALVDLGEEFSGR	1.29385323	2	3.91402
P08683	EHQESLDKDNPR	0.898906117	2	3.97237
P08683	FDPGHFLDER	1.176857582	2	2.63743
P08683	FDYKDPTFLNLMHR	1.424185375	3	4.84963
P08683	FNENFR	1.119728363	1	2.09618
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	0.828389504	3	6.02482
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.737963884	2	4.99096
P08683	HNPQSEFTLESLVATVTDMFGAGTETTSTTLR	0.773795711		
P08683	ICAGEALAR	1.146916042	2	3.02145
P08683	LPPGPTPLPIIGNTLQIYMK	0.843633819	3	3.97036
P08683	NFFYIK	1.487895236	1	1.91941
P08683	NYVLEK	0.773549955	1	2.03016
P08683	SQMPYTDAVVHEIQR	1.187129951	2	4.43892
P08683	VKEHQESLDKDNPR	1.170520788	3	5.26034
P08683	VQEEIER	0.969363192	2	2.46213
P08683	YGLLLLLK	1.362681683	2	3.19947
P08683	YIDLVPTNLPHLVTR	0.833637988	2	4.23395
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**2.445762004**	**0.53786**	**3**

P08733	GADPEETILNAFK	1.211668327	2	2.32703
P08733	NEEIDEMIK	1.336317658	1	2.63221
P08733	NLVHIITHGEEKD	2.018249285	2	2.91725
P09006	**SPA3N Serine protease inhibitor A3N**	**16.61345481**	**0.04042**	**2**
P09006	AVLDVAETGTEAAAATGVK	2.322178546	2	4.87133
P09006	GNSMEEILEGLK	4.054283221	2	3.14438
P09034	**ASSY Argininosuccinate synthase**	**2.261999761**	**0.00823**	**17**
P09034	APNTPDVLEIEFK	1.664517165	2	3.66081
P09034	DGTTHSTSLDLFMYLNEVAGK	1.785958802	2	4.82449
P09034	EFVEEFIWPAVQSSALYEDR	1.779076297	3	5.72916
P09034	EQGYDVIAYLANIGQK	2.188101548	2	4.70463
P09034	FAELVYTGFWHSPECEFVR	1.288076604	2	4.59087
P09034	FELTCYSLAPQIK	1.420428948	2	4.46314
P09034	GRNDLMEYAK	1.495587387	2	3.33498
P09034	IDIVENR	1.208868191	2	2.37392
P09034	KVFIEDVSK	1.146291848	3	3.62154
P09034	NDLMEYAK	3.417604331	2	2.63173
P09034	NDLMEYAK+Oxidation(3	1.239897621		
P09034	NQAPPGLYTK	1.113393192	2	2.3122
P09034	SPWSMDENLMHISYEAGILENPK	1.849127857	3	5.63126
P09034	TQDPAKAPNTPDVLEIEFK	0.997167548	2	5.06488
P09034	TQDPAKAPNTPDVLEIEFKK	0.77069349	3	5.39563
P09034	VFIEDVSK	1.351469377	2	2.35657
P09034	VQVSVFK	1.10817925	2	2.4449
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.809505759**	**0.07806**	**5**
P09041	FHVEEEGK	0.826266596	2	2.6503
P09041	FHVEEEGKGK	0.696647139	2	2.52993
P09041	LGDVYVNDAFGTAHR	0.999534017	3	4.21655
P09041	VDFNVPMK	0.996880796	2	2.33805
P09041	VSHVSTGGGASLELLEGK	0.916128433	2	5.82734
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**2.312548534**	**0.64358**	**3**
P09117	VLAAVYK	1.202762632	2	2.68449
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	3.223216631	3	3.59953
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.365037186	3	5.11891
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.995360795**	**0.31108**	**3**
P09139	IGLLGYNATTENADR	0.996055792	2	3.11332
P09139	LLLGPGPSNLAPR	0.983976418	2	2.51964
P09139	VLNAPPGISLISFNDK	1.599071124	2	2.39283
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**8.077086357**	**6.4E-06**	**4**
P09367	ALGVNTVGAQTLK	3.244486916	2	3.54529
P09367	AQLGLNELLK	1.734683263	1	2.19022
P09367	LGLPATIVVPSTTPALTIER	4.635130123	2	2.70583
P09367	LKNEGATVEVVGEMLDEAIQLAK	2.261565613	3	3.97793
P09495	**TPM4 Tropomyosin alpha_4 chain**	**2.005680775**	**0.99995**	**12**
P09495	AEGDAAALNR	1.115300714	2	2.55131
P09495	EDKYEEEIK	1.43862109	1	2.69296
P09495	EENVGLHQTLDQTLNELNCI	1.99013129	2	5.23139
P09495	IQALQQQADDAEDR	1.584419588	2	4.46353
P09495	IQLVEEELDR	1.014542729	2	3.48684
P09495	IQLVEEELDRAQER	0.846908315	2	3.01552
P09495	KLVILEGELER	1.905860879	3	4.05098
P09495	LEEAEKAADESER	0.899345348	2	4.1334
P09495	LVILEGELER	1.899211405	2	3.14805
P09495	MEIQEMQLK	1.162224026	2	2.98138
P09495	RIQLVEEELDR	1.014409235	2	2.79499

P09495	YSEKEDKYEEEIK	0.992640953	2	4.535
P09527	**RAB7A Ras_related protein Rab_7a**	**2.054327542**	**0.81218**	**6**
P09527	ATIGADFLTK	0.853900554	2	2.61116
P09527	DPENFPFVVLGNK	1.709945055	2	3.79691
P09527	GADCCVLVFDVTAPNTFK	1.171019068	2	3.39603
P09527	TLDSWRDEFLIQASPR	1.126694829	3	3.50582
P09527	TSLMNQYVNK	0.921310787	2	2.83383
P09527	VIILGDSGVGK	1.035769005	2	2.42567
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**9.634761823**	**0.76563**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	2.64475024	2	3.8282
P09605	LSEMTEQDQQR	3.440345722	2	3.36361
P09606	**GLNA Glutamine synthetase**	**2.946014853**	**0.00232**	**8**
P09606	CIEEAIDK	1.677879963	2	2.34831
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.565155582	3	5.46739
P09606	LTGFHETSNINDFSAGVANR	1.270281325	2	6.01703
P09606	MGDHLWVAR	0.891275568	2	3.03217
P09606	QMYMNLPQGEK	1.132263104	2	2.38968
P09606	RLTGFHETSNINDFSAGVANR	1.12996352	3	5.51941
P09606	TCLLNETGDEPFQYK	1.738762606	2	5.30161
P09606	TCLLNETGDEPFQYKN	1.601531253	2	5.46664
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**2.06621406**	**0.97755**	**2**
P09626	VDNSSLTGESEPQTR	0.834124783	2	4.20254
P09626	VIMVTGDHPITAK	1.171964985	2	3.28713
P09811	**PYGL Glycogen phosphorylase_ liver form**	**2.257548842**	**1**	**27**
P09811	AWNTMVLR	1.377309652	2	2.39321
P09811	DFSELEPDKFQNK	1.036622341	2	3.48768
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.15434403	4	5.47697
P09811	DLSQLTK	1.165657331	1	2.1468
P09811	EGWQVEEADDWLR	0.992940115	2	3.71017
P09811	FSQFLEK	1.239521834	1	2.0447
P09811	GIVGVENVAELK	1.120819435	2	3.01163
P09811	GIVGVENVAELKK	1.013246499	2	3.33362
P09811	HLQIIYEINQK	1.002927868	2	3.79598
P09811	IFVDIEK	1.231631721	1	2.05413
P09811	INMAHLCIVGCHAVNGVAK	1.024629184	3	5.01629
P09811	INPSSMFDVHVK	1.209016807	2	3.1747
P09811	LVIDQIDNGFFSPNQPDLFK	1.695791944	2	5.27898
P09811	LVTSVAEVVNNDPMVGSK	1.512973749	2	4.67995
P09811	MSLIEEEGGK	1.055572039	2	2.42289
P09811	MSLIEEEGGKR	0.973306272	2	2.72165
P09811	RWLLLCNPGLADLIAEK	1.388894375	3	5.04234
P09811	TFAYTNHTVLPEALER	0.972680857	2	4.9232
P09811	VDDVAALDK	1.38979345	2	2.70679
P09811	VDDVAALDKK	1.053590562	3	3.77455
P09811	VFADYEAYVK	0.921423849	2	2.64659
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.342875966	2	5.96223
P09811	VLYPNDNFFEGK	1.222023809	2	2.64317
P09811	VSQLYMNQK	1.542676737	2	3.03173
P09811	WLLLCNPGLADLIAEK	0.980305063	2	4.83604
P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	1.112962363	3	4.28154
P09811	YEYGIFNQK	1.03730374	2	2.63368
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**2.317113639**	**0.82859**	**9**
P09812	GYNAQEYYDR	1.113160716	2	2.3255
P09812	HLQIIYEINQR	1.31714279	2	2.33396
P09812	LITAIGDVVNHDPAVGDR	1.461413846	2	3.2642
P09812	NLAENISR	1.066882336	2	2.72201

P09812	QIIEQLSSGFFSPK	1.844335364	2	3.66077
P09812	VIFLENYR	1.05945807	2	2.5118
P09812	VIPAADLSEQISTAGTEASGTGNMK	7.73780294	2	4.78652
P09812	WLVLCNPGLAEVIAER	1.566747128	2	3.8157
P09812	YEFGIFNQK	1.720823757	2	2.44447
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.632593667**	**0.00199**	**6**
P09875	ANVVASALAQIPQK	0.809228682	3	3.61551
P09875	FSGGLPLPPSYVPVVLSELSDR	0.887911018	3	3.61704
P09875	IILNELAQR	0.789544255	2	3.00327
P09875	SDLEYSFAK	0.571595012	2	2.35784
P09875	VDFSILSTTGLLTALK	0.786235313	2	4.55381
P09875	WIDEWTR	0.490534102	2	2.60036
P09895	**RL5 60S ribosomal protein L5**	**2.163562458**	**1**	**5**
P09895	GAVDGGLSIPHSTK	1.160871468	2	4.37423
P09895	HIMGQNVADYMR	0.970637764	2	3.54644
P09895	NNVTPDMMEEMYK	1.200738714	2	3.39451
P09895	RFPGYDSESK	1.009540488	2	2.84887
P09895	YLMEEDEDAYKK	1.09205018	2	3.54788
P0C0S7	**H2AZ Histone H2A.Z**	**1.82717042**	**1**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.860001792	2	3.51307
P0C0S7	GDEELDSLIK	0.90723595	2	3.40999
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**2.003983974**	**0.80429**	**20**
P0C2X9	AIEAAVLAR	1.033039896	2	2.90877
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	1.152668871	2	5.13168
P0C2X9	AQIFLK	1.016493409	2	2.31133
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	0.905841735	3	3.58991
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	33.38982202	2	5.29363
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	1.160231378	3	3.6695
P0C2X9	EEIFGPVLTVYVYPDEK	1.226483117	2	3.83408
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	1.818232664	2	5.51257
P0C2X9	KEWDLKPVADR	0.951815883	2	3.5834
P0C2X9	LYVPQSLWPQIK	1.393444345	2	3.20898
P0C2X9	NAAGNFYINDK	1.246542734	2	3.60515
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.11343778	2	5.73886
P0C2X9	SAFEYGGQK	0.846703398	1	2.43333
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	1.183572283	3	5.74857
P0C2X9	STGSVVGQQPFGGAR	2.526715159	2	4.39369
P0C2X9	TIVQEATR	0.875849891	2	2.92718
P0C2X9	VANEPILAFTQGSPER	1.149339423	2	5.214
P0C2X9	WKHASSLKVANEPILAFTQGSPER	2.396968111	2	2.50873
P0C2X9	YQLSPFNHGHK	0.716815062	2	2.98252
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	1.409829586	3	4.0534
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**2.192545107**	**0.96611**	**5**
P0C5H9	DRDVTFSPATIEEELIK	1.055419065	2	4.92631
P0C5H9	DVTFSPATIEEELIK	1.139370691	2	3.21595
P0C5H9	IINEVSKPLAHHIPVEK	1.14296673	3	4.04905
P0C5H9	ILDDWGEMCK	1.199907439	2	3.03043
P0C5H9	INELMPK	0.789941897	2	2.48919
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.70937344**	**0.4357**	**2**
P0C6F1	AMLPGEWENACNEMQRMLIVR+Oxidation(16	1.272074138		
P0C6F1	EKVEVMSLELEDAK+Oxidation(5	0.761325233		
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**2.141522816**	**0.9864**	**11**
P10111	EGMSIVEAMER	1.217363924	1	2.80427
P10111	FEDENFILK	0.947513541	2	3.42604

P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.161859265	3	6.09178
P10111	IIPGFMCQGGDFTR	1.157253224	2	3.41568
P10111	IIPGFMCQGGDFTR+Oxidation(5	1.312562141		
P10111	KITISDCGQL	1.530955964	2	3.51117
P10111	SIYGEKFEDENFILK	0.883480547	2	4.54036
P10111	TEWLDGK	1.155778493	2	2.30247
P10111	VCFELFADK	1.14623283	2	3.24606
P10111	VCFELFADKVPK	0.892092287	2	3.89845
P10111	VKEGMSIVEAMER	1.039701634	3	3.6379
P10536	**RAB1B Ras_related protein Rab_1B**	**2.274452798**	**0.99979**	**3**
P10536	MGPGAASGGERPNLK	0.939137483	2	4.09043
P10536	NATNVEQAFMTMAAEIK+Oxidation(11	1.214270416		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9	1.215031048		
P10633	**CP2D1 Cytochrome P450 2D1**	**1.936770041**	**5.3E-11**	**3**
P10633	SQGVILASYGPEWR	0.953654175	2	4.08668
P10633	TFMALLDNLLAENR	0.821951575	2	3.71049
P10633	YGDVFSLQK	0.706847719	2	2.71123
P10634	**CP2DQ Cytochrome P450 2D26**	**2.293334343**	**0.02547**	**21**
P10634	ACLGEPLAR	0.885673853	2	2.74757
P10634	AKGNPESSFNDENLR	0.965964841	2	3.44884
P10634	AVSNVIASLVYAR	1.203149757	2	4.24841
P10634	DETVWEKPLR	1.003350962	2	2.34993
P10634	DMTDAFLAEMQK	1.144525928	2	3.51868
P10634	EAEHPFNPSILLSK	1.199772432	2	2.66698
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.083009797	3	5.71514
P10634	FADIVPTNIPHMTSR	1.54191127	3	3.68723
P10634	FEYEDPFFNR	1.215847395	2	2.82611
P10634	FHPEHFLDAQGNFVK	1.070698518	3	4.70054
P10634	FQGFLIPK	0.746735293	2	2.32181
P10634	GNPESSFNDENLR	1.21027054	2	4.42134
P10634	GTTLIPNLSSVLK	0.947310097	2	2.40056
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.436301669	2	4.72424
P10634	GVVLAPYGPEWR	0.943966709	2	3.20211
P10634	LNSFIALVDK	1.441457383	2	3.26995
P10634	RFEYEDPFFNR	0.956318416	2	4.02844
P10634	RVHEEIDEVIGQVR	0.983925088	2	4.26971
P10634	SLEQWVTEEAGHLCDTFAK	1.115774654	2	4.79247
P10634	SWDPAQPPR	0.984563638	2	2.85481
P10634	VHEEIDEVIGQVR	0.978038256	2	4.8402
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**2.323622315**	**0.99982**	**32**
P10719	AHGGYSVFAGVGER	0.982018368	2	4.25433
P10719	AIAELGIYPAVDPLDSTSR	1.189443826	2	5.5855
P10719	EGNDLYHEMIESGVINLK	1.474436564	2	5.20792
P10719	EGNDLYHEMIESGVINLK+Oxidation(8	1.316255914		
P10719	FLSQPFQVAEVFTGHMGK	0.963474496	2	4.46316
P10719	FTQAGSEVSALLGR	1.073597858	2	4.85767
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	1.201581459	4	4.5936
P10719	IGLFGGAGVGK	1.14153567	2	3.29063
P10719	IGLFGGAGVGKTVLIMELINNVAK	0.717211245	3	3.51369
P10719	ILQDYK	1.004776441	1	2.03284
P10719	IMDPNIVGSEHYDVAR	1.019979662	2	4.96367
P10719	IMDPNIVGSEHYDVAR+Oxidation(1	1.040229777		
P10719	IMNVIGEPIDER	1.248308695	2	4.07792
P10719	IMNVIGEPIDER+Oxidation(1	1.228163558		
P10719	IPSAVGYQPTLATDMGTMQER	1.689850277	2	4.77871
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14	2.020928384		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17	2.020928384		

P10719	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	2.630331741	3	6.44076
P10719	LVLEVAQHLGESTVR	1.125270139	2	4.80138
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	0.793158665	3	4.91654
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.346288362	3	4.90977
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10	1.291579398		
P10719	TIAMDGTEGLVR	0.920397389	2	3.80455
P10719	TIAMDGTEGLVR+Oxidation(3	0.896463851		
P10719	TREGNDLYHEMIESGVINLK	0.85870376	2	6.03984
P10719	TVLIMELINNVAK	0.809535095	2	5.11593
P10719	TVLIMELINNVAK+Oxidation(4	0.990271867		
P10719	VALTGLTVAEYFR	1.671302615	2	4.06678
P10719	VALVYGQMNEPPGAR	1.336655086	2	4.02356
P10719	VLDSGAPIK	1.684783424	2	3.37277
P10719	VLDSGAPIKIPVGPETLGR	0.93947851	3	5.00241
P10719	VVDLLAPYAK	1.113769471	2	3.23735
P10760	**SAHH Adenosylhomocysteinase**	**2.143062676**	**3.6E-05**	**20**
P10760	AGIPVFAWK	1.327725657	2	2.84386
P10760	ALDIAENEMPGLMR	1.241130413	2	3.77382
P10760	ALDIAENEMPGLMR+Oxidation(12	2.168129416		
P10760	ATDVMIAGK	1.050176651	2	2.9032
P10760	DGPLNMILDDGGDLTNLIHTK	1.393984988	2	5.57914
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5	1.212519596		
P10760	EMYSASKPLK	1.3017793	2	2.36064
P10760	FDNLYGCR	0.889662495	2	2.8435
P10760	GETDEEYLWCIEQTLHFK	1.592867569	2	4.46233
P10760	GISEETTTGVHNLYK	1.10748455	2	4.23768
P10760	IILLAEGR	1.387432545	2	2.92536
P10760	KLDEAVAEAHLGK	1.116141755	3	5.05049
P10760	LDEAVAEAHLGK	1.218800273	2	3.67498
P10760	RATDVMIAGK	1.013796536	2	2.52628
P10760	SKFDNLYGCR	1.217595699	2	3.10014
P10760	VAVVAGYGDVGK	1.099143345	2	4.14517
P10760	VIITEIDPINALQAAMEGYEVTTMDEACK	0.947255069	3	6.54741
P10760	VNIKPQVDR	1.086297357	2	2.7501
P10760	WLNENAVEK	1.058800721	2	2.81673
P10760	WSSCNIFSTQDHAAAAIAK	0.869268175	2	5.17942
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**1.861765551**	**0.9993**	**2**
P10818	HEEHERPEFVAYPHLR	0.895884815	3	3.67167
P10818	SRHEEHERPEFVAYPHLR	0.91868651	3	4.10219
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**2.011080005**	**1**	**29**
P10860	ALASLMTYK	1.009935149	2	3.62211
P10860	CAVVDVPFGGAK	0.66427994	2	3.07172
P10860	CVGVGESDGSIWNPDGIDPK	1.653658856	2	5.09498
P10860	DDGSWEVIEGYR	0.934924229	2	3.97291
P10860	DIVHSGLAYTMER	1.054453422	2	3.36619
P10860	DIVHSGLAYTMER+Oxidation(10	1.217644333		
P10860	DSNYHLLMSVQESLER	1.128717767	2	4.23282
P10860	EDDPNFFK	0.93548835	1	2.15232
P10860	FTMELAK	1.159668054	2	2.39471
P10860	GASIVEDKLVEDLK	0.92647761	2	3.58532
P10860	GFIGPGIDVPAPDMSTGER	1.087725219	2	4.99593
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13	1.395774356		
P10860	HGGTIPVVPTAEFQDR	0.975619627	2	4.72888
P10860	IIAEGANGPTTPEADK	1.041707682	2	5.38195
P10860	IIAEGANGPTTPEADKIFLER	0.952917927	2	4.84898
P10860	ISGASEKDIVHSGLAYTMER	0.636226032	3	3.59329

P10860	KGFIGPGIDVPAPDMSTGER	0.923439667	2	5.13157
P10860	LQHGSILGFPK	0.961634688	1	3.08417
P10860	MVEGFFDR	1.000466778	2	2.89927
P10860	MVEGFFDR+Oxidation(0	1.106889272		
P10860	NLNHVSYGR	0.722881974	1	2.86818
P10860	NYTDNELEK	0.851182291	2	2.48609
P10860	RDDGSWEVIEGYR	0.938608598	2	4.43619
P10860	RFTMELAK	0.911723586	2	2.49237
P10860	TAAYVNAIEK	1.020300926	2	3.6314
P10860	TFVVQGFGNVGLHSMR	1.199036565	2	4.53745
P10860	VYEGSILEADCDILIPAASEK	0.979236531	3	6.00546
P10860	YNLGLDLR	1.007538093	2	3.16748
P10860	YSTDVSVDEVK	0.882143052	2	3.39863
P10867	**GGLO L_gulonolactone oxidase**	**2.277550637**	**1**	**7**
P10867	EKLDPTGMFLNSYLEK	1.391124391	3	3.53458
P10867	GDDILLSPCFQR	1.153646251	2	3.22715
P10867	LDPTGMFLNSYLEK	1.505389568	2	4.12281
P10867	LDYWLAYETIMK	1.064442757	2	4.0198
P10867	NADVFQAAR	1.187512333	2	2.86951
P10867	TYGCSPEVYYQPTSVEEVR	1.003469405	2	4.8395
P10867	VVAHYPVEVR	1.085513873	2	2.75673
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**2.41167307**	**0.03579**	**3**
P10868	EHWIIECNDGVFQR	1.167451066	3	3.80169
P10868	YTDITAMFEETQVPALLEAGFQR	1.01301348	3	4.58187
P10868	YYAFPQMITPLVTK	1.48196838	2	3.78
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**2.026171113**	**0.99845**	**7**
P10888	ADWSSLSR	1.313332316	2	2.34799
P10888	DYPLPDVAHVK	1.484456811	2	2.7672
P10888	IQFNESFAEMNK	1.060076485	2	4.04551
P10888	RDYPLPDVAHVK	0.775865512	2	2.30233
P10888	SEDYALPSYVDR	1.018349788	2	3.86736
P10888	VNPIQGFSAK	1.003980392	1	2.13487
P10888	WDYNKNEWK	0.950528181	2	2.39344
P10959	**EST2 Liver carboxylesterase 1**	**1.724220422**	**0.0661**	**3**
P10959	AISESGVVLTTNLDKK	0.560476455	2	3.41963
P10959	EGASEEETNLSKLVMK	1.064638401	2	2.66072
P10959	GNWAHLDQLAALR	1.212494338	2	3.01174
P11030	**ACBP Acyl_CoA_binding protein**	**1.962510874**	**0.99792**	**5**
P11030	AKWDSWNK	0.825021342	2	2.40659
P11030	QATVGDVNTDRPGLLDLK	1.205654877	2	3.65335
P11030	TQPTDEEMLFIYSHFK	1.111836308	2	3.91036
P11030	TYVEKVEELK	0.833099933	2	2.34317
P11030	WDSWNK	0.951132919	1	2.08017
P11232	**THIO Thioredoxin**	**1.982486509**	**0.99993**	**2**
P11232	EAFQEALAAAGDK	0.993181424	2	4.51578
P11232	VGEFSGANK	0.684933433	2	2.7038
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**2.200265735**	**0.1843**	**6**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.863800179	3	5.93058
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.632662295	3	6.98547
P11240	GMNTLVGYDLVPEPK	1.46500034	2	4.01758
P11240	IIDAALR	1.150829043	1	2.1019
P11240	LNDFASAVR	1.022524747	2	3.27435
P11240	RLNDFASAVR	1.055677817	2	2.48269
P11348	**DHPR Dihydropteridine reductase**	**2.608815348**	**0.92892**	**12**
P11348	AALDGTPGMIGYGMAK	1.317780654	2	3.86588

P11348	EGGLLTLAGAK	0.953578544	2	2.92322
P11348	GAVHQLCQSLAGK	1.197307306	3	4.29872
P11348	MTDSFTEQADQVTAEVGK	1.043601663	2	5.82575
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0	0.873090663		
P11348	NCDLMWK	0.990013671	2	2.35414
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.186096984	2	5.39483
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3	1.565346978		
P11348	QSIWTSTISSHLATK	1.072521463	2	3.81882
P11348	RPNSGSLIQVVTTDGK	1.01001563	2	3.71702
P11348	TELTPAYF	2.490972803	1	2.01746
P11348	VDAILCVAGGWAGGNAK	1.952108326	2	3.92479
P11442	**CLH Clathrin heavy chain 1**	**2.19003625**	**2.7E-06**	**39**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	1.742843839	3	4.05348
P11442	AFMTADLPNELIELLEK	0.892577833	3	4.69238
P11442	AHIAQLCEK	0.848505849	2	2.3787
P11442	AHTMTDDVTFWK	1.247923175	2	2.52308
P11442	ALEHFTDLYDIK	1.266468015	3	3.96542
P11442	CNEPAVWSQLAK	0.983137773	2	3.43146
P11442	FDVNTSAVQVLIEHIGNLDR	1.350861804	3	4.17424
P11442	FNALFAQGNYSEAAK	1.039294586	2	5.04448
P11442	GQCDLELINVCNENSLFK	1.18431895	2	5.56819
P11442	GQFSTDELVAEVEK	1.121708334	2	4.04968
P11442	GQFSTDELVAEVEKR	1.053149719	2	3.67921
P11442	HELIEFR	0.963868429	2	2.50616
P11442	HSSLAGCQIINYR	1.454735991	2	3.78654
P11442	IHEGCEEPATHNALAK	1.040477071	2	5.39535
P11442	ISGETIFVTAPHEATAGIIGVNR	1.287986999	2	5.21436
P11442	IVLDNSVFSEHR	1.103996007	2	2.94672
P11442	IYIDSNNNPER	2.435859552	2	3.02607
P11442	KDPELWGSVLLESNPYR	1.202754445	3	3.63699
P11442	KFDVNTSAVQVLIEHIGNLDR	1.172066415	3	6.13883
P11442	KFNALFAQGNYSEAAK	0.823500448	2	4.89737
P11442	LAELEEFINGPNNAHIQQVGDR	1.091302986	2	5.41117
P11442	LECSEELGDLVK	1.116504573	2	2.9125
P11442	LHIIEVGTPPTGNQPFPK	0.946790018	2	4.42141
P11442	LPVVIGGLLDVDCSEDVIK	1.342371881	2	4.81917
P11442	LTDQLPLIIVCDR	1.306179333	2	3.31382
P11442	NLQNLLILTAIK	1.172624629	3	4.23416
P11442	NNLAGAEELFAR	1.055342139	2	3.79278
P11442	NNRPSEGPLQTR	0.986040706	3	4.13976
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.208856422	3	6.30522
P11442	SVDPTLALSVYLR	1.149603112	2	2.60965
P11442	SVNESLNNLFITEEDYQALR	1.062167208	2	5.16167
P11442	TLQIFNIEMK	0.958133752	2	3.02098
P11442	TSIDAYDNFDNISLAQR	1.113858552	2	3.62563
P11442	VGEQAQVVIIDMNDPSNPIR	1.801094805	2	5.05414
P11442	VIQCFAETGQVQK	1.01871012	2	4.79582
P11442	VSQPIEGHAASFAQFK	0.850559487	2	4.38184
P11442	WLLLTGISAQQNR	1.094074954	2	3.64063
P11442	YESLELCRPVLQQGR	0.990582396	2	2.80687
P11442	YIEIYVQK	1.058131954	1	1.95379
P11497	**ACACA Acetyl_CoA carboxylase 1**	**2.22648386**	**0.12869**	**8**
P11497	DEPIHILNVAIK	1.387623419	2	2.56064
P11497	GGSWVVIDPTINPR	1.987989719	2	2.9903
P11497	LLETESFQLNR	0.72280333	2	2.42497
P11497	LLLEDLVK	1.787215368	2	2.37114
P11497	LPELLLK	3.519044863	2	2.37799

P11497	TLRDPSLPLLELQDIMTSVSGR	1.03098455	3	3.48147
P11497	TVELSVPADPANLDSEAK	0.913591357	2	2.53261
P11497	VQQAELHTGSLPQIQSTALR	0.528153285	3	3.53639
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**2.16472199**	**0.99969**	**8**
P11507	DIVPGDIVEIAVGDKVPADIR	1.437477309	2	2.86545
P11507	IGIFGQDEDVTSK	0.855143101	2	3.55969
P11507	IRDEMVATEQER	0.993844963	2	3.35055
P11507	KSEIGIAMGSGTAVAK	0.942989684	2	3.87256
P11507	LDEFGEQLSK	1.392493443	2	2.77234
P11507	NAENAIEALKEYEPEMGK	1.149732788	2	3.46581
P11507	SEIGIAMGSGTAVAK	0.998384951	2	3.37901
P11507	VDQSILTGESVSVIK	3.917948997	2	4.44379
P11598	**PDIA3 Protein disulfide_isomerase A3**	**2.050975523**	**1.4E-06**	**28**
P11598	DASVVGFFR	1.084746545	2	2.51231
P11598	DGEEAGAYDGPR	3.463120612	2	3.42295
P11598	DLFSDGHSEFLK	1.545965403	2	3.08118
P11598	DLLTAYYDVDYEK	1.622973283	2	3.58615
P11598	DPNIVIAK	1.082158513	2	2.45673
P11598	EATNPPIIQEEKPK	1.259153809	2	3.56968
P11598	ELNDFISYLQR	1.225120433	2	3.11032
P11598	EYDDNGEGITIFRPLHLANK	1.479291973	2	4.18492
P11598	FAHTNVESLVK	1.650616402	3	3.38123
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.182935484	3	4.99491
P11598	FISDKDASVVGFFR	1.075827732	2	4.36724
P11598	FLQEYFDGNLK	1.040304059	2	3.72212
P11598	FLQEYFDGNLKR	0.855551789	2	3.53128
P11598	FVMQEEFSR	1.103849306	2	2.92936
P11598	IFRDGEEAGAYDGPR	0.988171797	2	3.95445
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.391216403	3	4.38281
P11598	LAPEYEAAATR	1.052630194	2	2.89025
P11598	LNFAVASR	1.38793163	2	2.53544
P11598	LSKDPNIVIAK	1.103808532	3	4.0293
P11598	MDATANDVPSPYEVK	1.025470092	2	4.37502
P11598	MDATANDVPSPYEVK+Oxidation(0	1.006908963		
P11598	RLAPEYEAAATR	0.906163326	2	3.66656
P11598	SEPIPETNEGPVK	1.010858409	2	2.88446
P11598	TADGIVSHLK	1.653277841	2	2.7983
P11598	TFLDAGHK	0.755842967	1	1.90221
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.393133116	2	6.03875
P11598	VDCTANTNTCNK	0.842737478	2	3.88552
P11598	YGVSGYPTLK	0.903180177	2	3.21822
P11711	**CP2A1 Cytochrome P450 2A1**	**2.293012616**	**0.31606**	**6**
P11711	GEQATYNTLFK	0.922963495	2	2.56123
P11711	GTDVFPILGSLMTDPK	1.067888201	2	3.46086
P11711	ILEEAGYLIK	1.167198346	2	3.40363
P11711	LEDINESPKPLGFTR	0.748673583	2	3.42735
P11711	TVSNVISSIVFGER	1.337448899	2	3.6523
P11711	VHEEIEQVIGR	1.207051644	2	3.06757
P11714	**CP2D9 Cytochrome P450 2D9**	**2.02443333**	**0.66115**	**2**
P11714	GNPESSFNDENLLMVVR	1.096872558	2	2.44001
P11714	VQQEIDEVIGQVR	1.008882564	2	4.70771
P11862	**GAS2 Growth arrest_specific protein 2**	**2.509694014**	**0.71268**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.235659243	2	4.11684
P11862	LDNGALLCQLAATVQEK	1.327532034	2	3.8059
P11862	YGVEPPGLIK	1.045195982	2	2.32449
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**2.347821088**	**0.9844**	**27**

P11884	AAQAAFQLGSPWR	1.367218928	2	2.91178
P11884	DGMTIAKEEIFGPVMQILK	1.985308026	3	4.01103
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.456284168	3	4.45642
P11884	EEIFGPVMQILK	1.244560579	2	4.06304
P11884	EEIFGPVMQILK+Oxidation(7	0.989101479		
P11884	ELGEYGLQAYTEVK	1.516609743	2	4.38967
P11884	GYFIQPTVFGDVK	1.070878711	2	4.28528
P11884	HEPVGVCGQIIPWNFPLLMQAWK	0.997807757	3	4.24194
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.844452607	3	6.48146
P11884	LGPALATGNVVVMK	1.081534542	2	3.81526
P11884	LGPALATGNVVVMK+Oxidation(12	1.270149215		
P11884	LLCGGGAAADR	1.212754024	2	3.38588
P11884	RVTLELGGK	0.989023717	2	2.92244
P11884	TEQGPQVDETQFK	0.879773161	2	4.56965
P11884	TEQGPQVDETQFKK	0.989104946	2	3.56918
P11884	TFPTVNPSTGEVICQVAEGNK	1.029970167	2	5.29401
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	1.048080491	2	4.30225
P11884	TFVQEDVYDEFVER	1.356139281	2	5.11162
P11884	TIEEVVGR	0.886426122	2	2.98471
P11884	TIPIDGDFFSYTR	1.200769583	2	2.81701
P11884	VAEQTPLTALYVANLIK	0.95727922	2	5.49268
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.432819763	2	6.53716
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.537103911	3	3.99173
P11884	VTLELGGK	0.922923189	1	2.05357
P11884	VVGNPFDSR	1.042888247	2	2.95273
P11884	YGLAAAVFTK	0.963541404	2	4.04562
P11884	YYAGWADK	0.943413803	2	2.54063
P11915	**NLTP Non_specific lipid_transfer protein**	**1.965497845**	**0.96726**	**21**
P11915	ADCTITMADSDLLALMTGK	1.522320481	2	5.40223
P11915	ANLIFK	1.209005714	2	2.32691
P11915	AVEIVAQEMVTDMPSTFEEK	1.725458383	2	5.30567
P11915	GHPLGATGLAQCAELCWQLR	1.229935413	3	3.58373
P11915	GSVLPDSDK	0.763914951	1	2.08974
P11915	GSVLPDSDKK	0.61093527	2	2.60047
P11915	HIDVLINK	0.895310179	2	2.9382
P11915	HSVNNPYSQFQDEYSLDEIMK	0.974959274	3	6.17153
P11915	KADCTITMADSDLLALMTGK	1.388109022	3	3.48586
P11915	KLEEEGEEFVK	0.934196211	3	4.24514
P11915	KLEEEGEEFVKK	0.922210407	3	4.85396
P11915	LEEEGEEFVK	0.747255492	2	2.81904
P11915	LEEEGEEFVKK	0.963416	2	3.58774
P11915	LQSLQLQPDK	1.15341954	2	3.16929
P11915	MGFPEAASSFR	0.96187785	2	2.61485
P11915	MNPQSAFFQGK	0.877560297	2	3.22935
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.035539797	3	4.37054
P11915	THQISAAPTSSAGDGFK	0.939208168	2	4.64028
P11915	VFVVGVGMTK	0.853900554	2	2.67829
P11915	WVINPSGGLISK	1.263832977	2	3.11443
P11915	YGMSACPFAPQLFGSAGK	1.076116951	2	4.0614
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**2.140057521**	**0.93842**	**4**
P11980	GADYLVTEVENGGSLGSK	1.909695243	2	4.76206
P11980	GVNLPGAAVDLPAVSEK	1.361119138	2	4.06188
P11980	IYVDDGLISLQVK	1.508891921	2	2.44236
P11980	NTGIICTIGPASR	1.004670034	2	3.29981
P12001	**RL18 60S ribosomal protein L18**	**2.175987499**	**1.5E-05**	**5**
P12001	GTVLLSGPR	0.934334055	2	3.1428
P12001	ILTFDQLALESPK	1.262974178	2	4.85503

P12001	TAVVVGTITDDVR	1.124341954	2	4.33315
P12001	TNRPPLSLSR	1.033199658	3	3.66187
P12001	TNSTFNQVVLK	0.841081515	2	2.99677
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.923101679**	**0.97342**	**9**
P12007	AQEIDQSNDFK	2.15101854	2	3.43611
P12007	FVQENLAPK	0.93144915	2	2.94552
P12007	FWITNGPDADVLVVYAK	1.46083674	2	3.58472
P12007	GSNTCELVFEDCK	1.09449304	2	4.55817
P12007	GSNTCELVFEDCKVPAANILSQESK	1.191717443	3	5.22953
P12007	GVYVLMSGLDLER	1.109360062	2	2.95199
P12007	IGQFQLMQGK	1.256765758	2	2.76344
P12007	LYEIGGGTSEVR	1.080414746	2	2.8232
P12007	TDLTAVPASR	1.111065781	2	3.09366
P12075	**COX5B Cytochrome c oxidase subunit 5B_ mitochondrial**	**1.853897414**	**0.86905**	**2**
P12075	EDPNLVPSVSNK	0.890436316	2	3.22824
P12075	GLDPYNMLPPK	1.201207332	2	2.31776
P12336	**GTR2 Solute carrier family 2_ facilitated glucose transporter member 2**	**2.16548227**	**0.87482**	**3**
P12336	HVLGVPLDDR	1.506497697	2	2.33126
P12336	HVLGVPLDDRR	0.9277263	3	3.3095
P12336	SFDEIAAEFR	1.368411006	2	3.34138
P12346	**TRFE Serotransferrin**	**1.877735063**	**0.77823**	**23**
P12346	ADRDQYELLCLDNTR	0.774009281	2	4.31865
P12346	ASDSSINWNNLK	0.850619876	2	3.07084
P12346	DFQLFGSPLGK	2.068675318	2	3.59528
P12346	DGGGDVAFVK	0.948579336	2	2.46836
P12346	DLKQEDFQLLCPDGTK	0.692615704	2	4.57533
P12346	EGVCPEGSIDSAPVK	0.736568369	2	3.47231
P12346	EGYNGYTGAFQCLVEK	0.868933295	2	3.25762
P12346	FDEFFSQGCAPGYK	0.766522558	2	4.06314
P12346	GDKDCTGNFCLFR	0.82716252	2	3.58545
P12346	GTDFQLNQLQGK	0.827203294	2	3.51885
P12346	GYYAVAVVK	0.928959611	2	2.95011
P12346	HQTVLENTNGK	6.561540628	2	2.47251
P12346	HTTIFEVLPQK	0.676300131	3	4.01045
P12346	KGTDFQLNQLQGK	0.787636308	2	4.58998
P12346	KTSYQDCIK	0.753553945	2	2.64941
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.52994414	2	4.58329
P12346	NGDGKEDLIWEILK	1.068280901	2	3.69213
P12346	QEDFQLLCPDGTK	0.459583605	2	3.22916
P12346	SKDFQLFGSPLGK	0.731524915	2	3.14005
P12346	TSYQDCIK	0.760684926	2	2.46459
P12346	VSTVLTAQK	0.694531007	2	2.72709
P12346	WCALSHQER	0.665514704	2	3.18049
P12346	WCAVSEHENTK	0.784584219	2	3.61857
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.84792771**	**0.69231**	**3**
P12368	MFESFIESVPLFK	0.842614102	2	3.44172
P12368	NISHYEEQLVK	0.902932315	2	2.53913
P12368	NLDQEQLSQVLDAMFEK	0.931543319	3	3.89886
P12711	**ADHX Alcohol dehydrogenase class_3**	**2.236624782**	**2.4E-06**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.128259137	3	6.70961
P12711	AFDLMHSGNSIR	0.792283499	2	3.28735
P12711	AGDTVIPLYIPQCGECK	1.144362884	2	3.7181
P12711	AKEFGATECINPQDFSK	0.838642554	2	4.76371
P12711	EFGATECINPQDFSK	1.080807505	2	4.35277

P12711	IDPSAPLDK	1.385811655	1	2.17802
P12711	IIGIDINK	1.181023583	1	2.03836
P12711	IIGIDINKDK	1.159877363	2	2.43535
P12711	VCLLGCGISTGYGAAVNTAK	1.443797597	2	6.07831
P12711	VDEFVTGNLSFDQINK	1.038256084	2	4.99031
P12749	**RL26 60S ribosomal protein L26**	**2.101397838**	**0.99997**	**5**
P12749	DDEVQVVR	1.240998335	2	2.94547
P12749	FNPFVTSDR	0.983977974	2	2.75645
P12749	HFNAPSHIR	1.029493371	3	3.88091
P12749	KDDEVQVVR	1.071504206	2	3.26208
P12749	YVIYIER	0.961952337	1	1.97401
P12785	**FAS Fatty acid synthase**	**1.7215555**	**0.99057**	**45**
P12785	ACIDTALENLSTLK	1.439647573	2	4.47468
P12785	AEAVVAVLLTK	1.4824218	2	3.83213
P12785	AGSDTELAAPK	0.970927903	2	3.4142
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.593493766	3	5.52807
P12785	DAMLENQTPELFQDVNKPK	1.249800518	2	4.17341
P12785	DANLPAGSMAAVGLSWEECK	0.765230269	2	3.08915
P12785	DGGFLLMHTVLK	1.059030468	2	3.33915
P12785	DPETLLGYSMVGCQR	1.258318784	2	3.93981
P12785	DTSFEQHVLLHTGGK	1.416318688	2	2.99097
P12785	EEEPEAMLPGAQPTLISAISK	1.590879829	2	3.94726
P12785	EQGVTFPSGEAQEQLIR	0.842408159	2	4.29349
P12785	FDASFFGVHPK	1.157544909	2	3.4069
P12785	FDLSNNHPLGMAIFLK	1.575358859	2	3.43606
P12785	FVFTPHVEPECLSESAILQK	1.432664238	3	5.07461
P12785	GLESIINIIHSSLAEPR	1.380139725	2	4.416
P12785	GNAGQSNYGFANSTMER	1.573016286	2	4.70319
P12785	GVDLVLNSLAEEK	1.2136563	2	3.48034
P12785	HFQLEQDKPEEQTAHAFVNVLTR	1.296705346	3	3.40921
P12785	LFDHPEVPIPAESESVSR	0.734067738	2	4.26387
P12785	LLLPEDPLISGLLNSQALK	1.126418643	3	4.7815
P12785	LTPGCEAEAEAEAICFFIK	2.516207803	2	3.76223
P12785	MTVPGLEDLPQHGLPR	1.300625537	2	3.59142
P12785	QAQLNLSILLVNPEGPTLTR	1.292106689	2	3.08443
P12785	RQQEQLVPTLEK	0.658027906	2	3.12097
P12785	SDEALKPLGVK	1.01292474	2	2.97413
P12785	SFDDSGNGYCR	1.795260376	2	3.05912
P12785	SGECPAAIVGGINLLLKPNTSVQFMK	0.635926476	3	3.96689
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.449279692	2	5.23347
P12785	SNMGHPEPASGLAALTK	1.222507421	3	4.17648
P12785	SNMGHPEPASGLAALTK+Oxidation(2	0.741260721		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.203943123	2	5.04823
P12785	TGTVPLEVR	0.956122127	2	2.46229
P12785	TMEAVQGLLEQGR	1.305675315	2	3.88832
P12785	VFTTVGSAEK	1.189210745	2	2.3602
P12785	VGDPQELNGITR	0.71991192	2	3.15346
P12785	VHLTGIDINPNALFPPVEFPVPR	1.145110152	2	4.90093
P12785	VLEALLPLK	1.372285819	2	3.3012
P12785	VLESDLVMNVYR	1.289282564	2	3.40659
P12785	VSVHIIEGDHR	1.675417183	2	2.81774
P12785	VTAIYIDPATHLQK	1.319371101	2	3.80096
P12785	VYATILNAGTNTDGCK	1.209832505	2	4.98002
P12785	VYMLEGDTQVADVTTSR	1.842476262	2	3.58574
P12785	VYQWEDPDSK	0.909300615	2	3.2511
P12785	WLSTSIPEAQWQSSLAR	0.736311105	2	2.67496
P12785	YNGTLNLDR	1.169319135	1	2.10228

P12791	**CP2BA Cytochrome P450 2B10**	**2.181662167**	**0.99998**	**2**
P12791	IQEEAQCLVEELR	1.137358074	2	4.58548
P12791	IQEEAQCLVEELRK	1.112050098	2	3.76327
P12847	**MYH3 Myosin_3**	**2.203467043**	**0.91945**	**5**
P12847	GTLEDQIISANPLLEAFGNAK	0.574879494	2	3.11892
P12847	IEAQNQPFDAK	0.661909115	2	3.03745
P12847	KELEEKLVTLVQEK	0.828579852	2	2.76737
P12847	MKGTLEDQIISANPLLEAFGNAK	1.331275612	3	6.70384
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0	1.318618613		
P12928	**KPYR Pyruvate kinase isozymes R/L**	**2.632892409**	**0.0452**	**20**
P12928	AAVIAVTR	1.384018748	2	2.62289
P12928	AETSDVANAVLDGADCIMLSGETAK	1.453317648	2	5.97997
P12928	CCAAAIIVLTK	1.260592077	2	3.08597
P12928	CNLAGKPVVCATQMLESMITK	1.404479533	3	4.86376
P12928	EATESFATSPLSYRPVAIALDTK	2.026247034	2	4.02342
P12928	EPPEAIWADDVDR	3.156592423	2	2.64996
P12928	GDLGIEIPAEK	1.174139306	2	3.147
P12928	GSFPVEAVMMQHAIAR	1.21946981	2	3.91374
P12928	GSQVLVTVDPK	1.613683412	2	2.93878
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.830840857	2	4.90819
P12928	IGPEGLVTEVEHGGILGSR	1.938394246	2	5.04771
P12928	IYIDDGLISLVVQK	2.648991421	2	4.41485
P12928	KFDEILEVSDGIMVAR	1.580758349	2	4.93118
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	2.392729747	3	4.66172
P12928	LNFSHGSHEYHAESIANIR	2.581583083	2	5.72094
P12928	RVQFGIESGK	1.104741113	2	2.55405
P12928	STSIIATIGPASR	1.246786912	2	3.39026
P12928	TGVLQGGPESEVEIVK	1.522046864	2	5.06898
P12928	TVWVDYHNITR	1.537436212	2	2.68411
P12928	VQFGIESGK	1.740467672	2	2.46101
P12938	**CP2D3 Cytochrome P450 2D3**	**1.809945132**	**0.91698**	**7**
P12938	DLTDAFLAEIEK	0.847976262	2	4.42482
P12938	FDYGDPDFIK	1.444104135	2	2.76539
P12938	GNPESSFNDANLR	0.874391998	2	4.00462
P12938	RFDYGDPDFIK	0.740893774	2	3.0478
P12938	TFLTMVDNLVTEHK	1.518641569	2	3.33964
P12938	TWDPDQPPR	0.796774473	2	2.45075
P12938	TWDPDQPPRDLTDAFLAEIEK	0.831431221	3	3.67225
P12939	**CP2DA Cytochrome P450 2D10**	**3.657456454**	**0.26342**	**8**
P12939	ALCNVIASLIFAR	1.311185254	2	3.50722
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.516713184	3	5.59872
P12939	FEYEDPYLIR	1.742265342	2	2.45893
P12939	FGDIAPLNLPR	1.40911648	2	3.1325
P12939	ITSCDIEVQDFVIPK	2.447642612	2	4.36936
P12939	NLTDAFLAEVEK	1.890219115	2	4.16064
P12939	RFEYEDPYLIR	1.385062676	3	3.46783
P12939	TTWDPAQPPR	2.422858795	2	2.59151
P13084	**NPM Nucleophosmin**	**2.638356604**	**0.99746**	**2**
P13084	MTDQEAIQDLWQWR	1.091776322	2	3.27561
P13084	VDNDENEHQLSLR	1.445425746	2	4.12753
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**2.037261162**	**1**	**5**
P13086	HLGLPVFNTVK	1.09953044	2	2.33359
P13086	LIGPNCPGIINPGECK	1.146427423	2	4.43545
P13086	MGHAGAIIAGGK	0.998220233	3	3.46659
P13086	NIYIDK	0.92435848	1	2.1293
P13086	QGTFHSQQALEYGTK	1.034966182	2	2.72825

P13107	**CP2B3 Cytochrome P450 2B3**	**2.2510323**	**0.99981**	**8**
P13107	ATLDPNAPR	1.040603214	2	2.63511
P13107	EIDQVIGSQR	0.852062196	2	2.66546
P13107	EVLDYIDHSVENHR	1.095520039	2	4.08286
P13107	FSDVSPMGLPCR	1.149428812	2	3.44387
P13107	GIIAVLQPIMQEYGVSFVNEER	1.483498351	3	5.76416
P13107	MCLGEGIAR	1.204625608	2	2.69242
P13107	QSVEDQIKEEAK	1.184175406	2	2.91521
P13107	SFIQLQEK	0.854156207	2	2.43396
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**2.402419946**	**0.00291**	**7**
P13221	IGADFLGR	1.706526026	2	2.38995
P13221	ITWSNPPAQGAR	1.250520085	2	3.00608
P13221	IVATTLSNPELFK	1.585361331	2	3.78562
P13221	NLDYVATSINEAVTK	1.541585894	2	5.09798
P13221	SCASQLVLGDNSPALR	1.033197503	2	5.11447
P13221	TDDSQPWVLPVVR	1.041453405	2	3.26695
P13221	VGGVQSLGGTGALR	1.079878062	2	3.00787
P13255	**GNMT Glycine N_methyltransferase**	**1.923274458**	**0.99999**	**8**
P13255	AHMVTLDYTVQVPGAGR	0.932424965	2	5.07364
P13255	AWLLGLLR	1.09743395	2	2.57165
P13255	DITTSVLTVNNK	0.982760782	2	3.82661
P13255	LSYYPHCLASFTELVQEAFGGR	0.927370236	3	3.64388
P13255	NIASMVRPGGLLVIDHR	1.555064713	3	3.74856
P13255	NYDYILSTGCAPPGK	1.102492499	2	4.65123
P13255	SDLTKDITTSVLTVNNK	1.099888716	2	2.89718
P13255	SLGVAAEGIPDQYADGEAAR	0.916266528	2	5.25813
P13383	**NUCL Nucleolin**	**1.811411015**	**0.98956**	**8**
P13383	EAMEDGEIDGNK	1.576522956	2	2.93201
P13383	GFGFVDFNSEEDAK	1.277410603	2	2.87702
P13383	GLSEDTTEETLK	0.89221919	2	3.24166
P13383	GSPNARSQPSKTLFVK	1.191989829	2	2.33221
P13383	IEGSEPTTPFNLFIGNLNPNK	0.753517613	2	3.75733
P13383	NDLAAVDVR	0.989042938	2	2.56311
P13383	NLSFNITEDELK	1.086649257	2	2.6226
P13383	SEADAEKNLEEK	0.829213901	2	2.9488
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**1.98175926**	**0.99974**	**21**
P13437	AANEAGYFNEEMAPIEVK	1.171095922	2	5.1397
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11	1.552025103		
P13437	DAEVVLCGGTESMSQSPYSVR	1.145869109	3	5.0537
P13437	DFTATDLTEFAAR	0.84221934	2	4.0434
P13437	DMDLIDVNEAFAPQFLAVQK	1.867791061	3	6.51918
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1	1.654593236		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	2.73042678	3	5.77951
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	1.128347032	3	4.88921
P13437	GVFIVAAK	1.044798329	2	2.47247
P13437	HNFTPLAR	1.04880178	2	2.36927
P13437	ITAHLVHELR	1.062971791	2	3.51449
P13437	LCGSGFQSIVSGCQEICSK	1.434919934	2	5.64092
P13437	LEDTLWAGLTDQHVK	0.979860041	2	5.06277
P13437	RTPFGAYGGLLK	0.558009571	3	3.38314
P13437	SLDLDPSK	0.825419257	2	2.72636
P13437	TNVSGGAIALGHPLGGSGSR	0.912615779	2	5.99104
P13437	VGVPTETGALTLNR	0.932088289	2	3.63579
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	1.063731189	2	5.91279
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14	1.373823392		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.00035228	3	5.02973
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	0.84023202	3	4.51412

P13439	**UMPS Uridine 5__monophosphate synthase**	**2.25928978**	**0.38092**	**2**
P13439	SGLSSPVYIDLR	1.418621002	2	2.42861
P13439	VTDAIVLLDR	1.13947905	2	2.36203
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**2.328517047**	**6.2E-15**	**9**
P13444	FVIGGPQGDAGVTGR	1.034512236	2	4.51991
P13444	HIGYDDSAK	0.86099746	2	2.74085
P13444	ICDQISDAVLDAHLK	0.988049226	3	5.26489
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	2.115180309	3	6.92725
P13444	SEFPWEVPK	1.227558763	2	2.37817
P13444	SGVLPWLRPDSK	0.981323061	2	2.94306
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.679312495	3	5.99758
P13444	TQVTVQYVQDNGAVIPVR	1.278221291	2	5.43374
P13444	VHTIVISVQHNEDITLEAMR	1.298264783	3	4.07736
P13471	**RS14 40S ribosomal protein S14**	**2.039506532**	**0.95734**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	1.045061067	2	5.42994
P13471	ELGITALHIK	1.446870204	2	2.49773
P13471	IEDVTPIPSDSTR	0.807531822	2	3.9123
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**1.584619142**	**0.00139**	**20**
P13601	ANNTPYGLAAGVFTK	0.394431466	2	4.37942
P13601	EEIFGPVQQIMK	0.685174136	2	3.60608
P13601	EMGEQGVYEYTELK	0.660227711	2	3.53665
P13601	FPVINPATEEVICHVEEGDK	1.161021829	3	3.82828
P13601	FPVINPATEEVICHVEEGDKADVDK	0.948315664	4	5.05052
P13601	GFFVQPTVFSNVTDEMR	1.110789979	2	2.45955
P13601	IAKEEIFGPVQQIMK	0.872005187	2	3.72034
P13601	IFINNEWHNSLNGK	0.931784773	2	3.90821
P13601	IHGQTIPSDGDVFTYTR	0.833514732	3	3.89745
P13601	ILDLIESGK	0.984829278	2	3.19051
P13601	ILDLIESGKK	0.646708445	2	2.85552
P13601	KFPVINPATEEVICHVEEGDK	0.916448336	3	3.56804
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.953781397	4	4.87731
P13601	LFVEESIYDEFVR	0.602356465	2	3.60477
P13601	SIDEVIK	0.636110816	2	2.49596
P13601	VLLATMESMNAGK	0.66456969	2	4.44039
P13601	VSFTGSTEVGK	0.549800459	2	2.74865
P13601	YFAGWADK	0.637965152	2	2.31775
P13601	YVLGNPLDSGISQGPQIDK	0.757576035	2	4.75492
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.458991194	2	4.21713
P13697	**MAOX NADP_dependent malic enzyme**	**1.875954205**	**0.72278**	**6**
P13697	AECSAEECYK	0.974589793	2	3.12663
P13697	AIFASGSPFDPVTLPDGR	2.714553278	2	4.49689
P13697	GHIASVLNAWPEDVVK	2.640019564	2	3.59331
P13697	HINDSVFLTTAEVISQQVSDK	1.100765707	3	4.59759
P13697	ILGLGDLGCNGMGIPVGK	1.760161516	2	2.8062
P13697	NLEAIVQK	0.876750014	1	2.40288
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.86632326**	**0.15121**	**15**
P13803	AAVDAGFVPNDMQVGQTGK	3.430531	2	4.94719
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11	1.067497982		
P13803	DPEAPIFQVADYGIVADLFK	1.053403407	2	4.98397
P13803	GLLPEELTPLILETQK	1.063264306	2	4.48045
P13803	GTSFEAAAASGGSASSEK	1.012365516	2	5.1968
P13803	LGGEVSCLVAGTK	0.914008295	2	4.59815
P13803	LLYDLADQLHAAVGASR	1.223959312	2	5.04928
P13803	LNVAPVSDIIEIK	1.772069003	3	4.03899
P13803	QFSYTHICAGASAFGK	0.798907736	2	3.23217

P13803	SDRPELTGAK	0.804669633	3	3.54489
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.87705406	3	6.62075
P13803	TIYAGNALCTVK	0.790323884	2	3.70433
P13803	VLVAQHDAYK	0.859431339	2	3.56115
P13803	VVPEMTEILK	0.98079001	1	1.92887
P13803	VVQDLCK	0.853593529	2	2.63306
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**2.521893491**	**0.16249**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.338053884	2	5.08349
P13832	FTDEEVDELYR	0.789201364	2	3.78271
P13832	GNFNYIEFTR	1.057577515	2	3.193
P14046	**A1I3 Alpha_1_inhibitor 3**	**2.262297849**	**0.99334**	**5**
P14046	ETGLMAFTNLK	1.317549189	2	2.62673
P14046	GDPIPNEQVLIK	1.077589171	2	2.88023
P14046	GMYESLPVVAVK	1.073215298	2	3.34773
P14046	QQNSYGGFSSTQDTVVALDALSK	1.181685867	2	3.49092
P14046	QSPGPCGSEVATVPETGR	0.975327045	2	3.43119
P14141	**CAH3 Carbonic anhydrase 3**	**1.790151761**	**1**	**20**
P14141	DIRHDPSLQPWSVSYDPGSAK	0.246187423	3	3.86232
P14141	EAPFNHFDPSCLFPACR	1.148336045	2	4.23334
P14141	EKGEFQILLDALDK	1.215352992	2	4.67005
P14141	EKGEFQILLDALDKIK	0.787903947	2	3.70368
P14141	EPMTVSSDQMAK	1.731731518	1	3.24039
P14141	EWGYASHNGPEHWHELYPIAK	1.004364054	3	4.82179
P14141	GDNQSPIELHTK	1.065130697	2	3.23947
P14141	GEFQILLDALDK	1.067554791	2	4.56922
P14141	GEFQILLDALDKIK	1.176836755	2	3.59343
P14141	GGPLSGPYR	0.998529028	2	2.75937
P14141	GKEAPFNHFDPSCLFPACR	0.88057891	2	4.19625
P14141	HDPSLQPWSVSYDPGSAK	0.937580159	3	5.58667
P14141	QFHLHWGSSDDHGSEHTVDGVK	0.992418183	2	4.77049
P14141	QPDGIAVVGIFLK	1.494384065	3	3.54867
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.965142307	3	5.703
P14141	SLFASAENEPPVPLVGNWRPPQPIKGR	0.619294267	3	4.37209
P14141	VVFDDTFDR	0.850590196	2	3.3251
P14141	YAAELHLVHWNPK	1.048560145	2	4.23882
P14141	YNTFGEALK	1.124725836	2	2.55988
P14141	YNTFGEALKQPDGIAVVGIFLK	1.084600306	3	6.11241
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**2.25942905**	**4.4E-16**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	2.217143606	2	3.26032
P14173	ALIPTTAPQEPETYEDIIR	1.300133995	2	3.85561
P14173	GSNQLNETLLQR	1.294681815	2	2.98679
P14173	HSHQDSGLITDYR	1.077057594	3	3.77432
P14173	MLELPEAFLAGR	1.64772969	2	3.45539
P14173	QLQAASPELTQAALMEK	1.205411035	2	4.098
P14173	TDLTEAFNMDPVYLR	0.922317523	2	3.84325
P14173	TVESAHVQLAWEHIR	1.210229616	3	3.64039
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**2.102462137**	**0.97623**	**15**
P14408	AAAEVNQEYGLDPK	1.04267216	2	4.36643
P14408	AIEMLGGELGSK	0.940238175	2	3.95858
P14408	EFAQVIK	0.949862098	1	1.92098
P14408	IEYDTFGELK	0.893677629	2	3.25935
P14408	IEYDTFGELKVPTDK	0.916520666	2	3.73064
P14408	IYELAAGGTAVGTGLNTR	1.064187159	2	5.36743
P14408	LMNESLMLVTALNPHIGYDK	1.207920939	3	5.51642
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	1.09962424	3	6.87714
P14408	SGLGELILPENEPGSSIMPGK	0.938534627	2	4.63581
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17	1.348560256		

P14408	SKEFAQVIK	0.871799082	2	2.66651
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.312491388	3	4.78378
P14408	TAIELGYLTAEQFDEWVKPK	1.169845916	2	4.87841
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	0.921878088	3	5.89325
P14408	YYGAQTVR	0.881700343	2	2.4916
P14480	**FIBB Fibrinogen beta chain**	**1.821463553**	**0.85486**	**8**
P14480	AHYGGFTVQTEANK	1.263075435	2	3.46356
P14480	DNENVINEYSSILEDQK	1.098753764	2	3.93521
P14480	GFGNIATNEDTK	1.353726931	2	3.08932
P14480	GFGNIATNEDTKK	1.161892263	2	3.58305
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.195682886	3	4.97951
P14480	LYIDETVNDNIPLNLR	1.960356467	2	2.93289
P14480	TENGGWTVIQNR	0.783031665	2	3.20598
P14480	YCGLPGEYWLGNDK	1.241157219	2	3.15456
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**1.758432869**	**1**	**10**
P14604	AFAAGADIK	0.855672836	2	3.08522
P14604	AQFGQPEILLGTIPGAGGTQR	0.96458753	2	5.68471
P14604	ESVNAAFEMTLTEGNKLEK	1.348848321	2	2.68186
P14604	FLSHWDHITR	0.963099862	2	3.46626
P14604	IFPVETLVEEAIQCAEK	0.802423559	3	5.88413
P14604	NSSVGLIQLNRPK	0.992382983	2	3.57694
P14604	SLAMEMVLTGDR	1.08760125	2	3.80519
P14604	SLAMEMVLTGDR+Oxidation(3	1.046653643		
P14604	SLAMEMVLTGDR+Oxidation(5	1.046653643		
P14604	TFQDCYSGK	0.926485424	2	2.89127
P14668	**ANXA5 Annexin A5**	**1.843811641**	**0.99757**	**5**
P14668	EFRKNFATSLYSMIK	0.856631698	2	2.33736
P14668	ETSGNLENLLLAVVK	1.073623051	2	3.24921
P14668	GAGTDDHTLIR	0.913828328	2	2.75949
P14668	GLGTDEDSILNLLTAR	1.154298567	2	5.11611
P14668	GTVTDFSGFDGR	1.186940081	2	3.00392
P14669	**ANXA3 Annexin A3**	**2.099199263**	**0.99711**	**9**
P14669	GAGTDEFTLNR	0.961662842	2	2.66357
P14669	GMGTDEDTLIEILTTR	1.14153722	2	4.38738
P14669	GTINNYPGFNPSVDAEAIR	1.034128212	2	4.96496
P14669	KDAQTLYDAGEK	0.984772573	2	3.26496
P14669	KDAQTLYDAGEKK	1.021673894	3	3.88508
P14669	QYQEAYEQALK	0.848464854	2	2.9069
P14669	SEIDLLDIR	1.707699323	2	2.54409
P14669	TLINILTER	1.103346625	2	2.73803
P14669	WGTDEDKFTEILCLR	1.434961596	3	3.38065
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**2.031954873**	**0.87055**	**4**
P14685	AIQLEYSEAR	1.162685053	2	3.01918
P14685	HDADGQATLLNLLLR	1.39832564	2	3.79246
P14685	LQLDSPEDAEFIVAK	1.201319429	2	3.86703
P14685	SVFPEQANNNEWAR	1.011029429	2	3.28049
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.807538468**	**0.96122**	**5**
P14740	FRPAEPHFTSDGSSFYK	0.919779159	2	3.47716
P14740	HSYTASYSIYDLNKR	1.16922897	3	3.78152
P14740	LGTLEVEDQIEAAR	1.187005694	2	4.08775
P14740	VLEDNSALDK	0.817859628	2	2.61836
P14740	WEYYDSVYTER	0.744334622	2	2.5283
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.864927164**	**0.99185**	**15**
P14882	FLSDVYPDGFK	1.232381204	2	2.80381
P14882	FSSQEAASSFGDDR	1.220147544	2	3.92838

P14882	GVTHNIPLLR	1.113619135	2	2.39832
P14882	HGNALWLNER	1.115731239	2	3.31556
P14882	HIEIQVLGDK	1.105459815	2	2.41751
P14882	HKQEDIPISGWAVECR	0.945101455	2	2.44155
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	0.892062636	3	6.74303
P14882	LQVEHPVTECITGLDLVQEMILVAK	0.725113625	3	3.8112
P14882	MADEAVCVGPAPTSK	0.845903293	2	4.25564
P14882	MEDALDSYVIR	1.027538737	2	3.50691
P14882	SYLNMDAIMEAIK	1.344739526	2	3.28723
P14882	SYLNMDAIMEAIKK	1.571574608	2	3.13295
P14882	TGAQAVHPGYGFLSENK	0.984217608	2	4.01556
P14882	TVAIHSDVDASSVHVK	1.055094141	3	4.04437
P14882	VVEEAPSIFLDPETR	1.03060366	2	3.99447
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**2.198371822**	**0.84973**	**3**
P14942	DGCLLFGQVPLVEIDGMLLTQTR	1.955092445	3	4.15424
P14942	KPPPDGHYVDVVR	1.014956153	2	3.27493
P14942	YFPVFEK	0.848502061	1	1.99856
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.896145562**	**0.9999**	**4**
P15083	EIQNAGDQAQENR	0.738739613	2	4.02449
P15083	FSVLITGLR	1.217840048	2	2.79705
P15083	GSPHINPTDANAR	1.001112649	2	2.34721
P15083	GVTGGSVAIVCPYNPK	0.981724609	2	4.03122
P15149	**CP2A2 Cytochrome P450 2A2**	**2.453906882**	**0.98863**	**13**
P15149	DVQECILEEAGYLIK	0.858393681	3	3.94304
P15149	DVYSSITQLSER	2.244424637	2	3.11845
P15149	FKFPMNLEDINEYPSPIGFTR	0.982386094	3	3.74839
P15149	FSNLAPLGIPR	1.146568628	2	3.32725
P15149	GELPTFNILFK	0.705274188	2	2.69453
P15149	GTDVFPIIGSLMTEPK	0.841599598	2	4.13446
P15149	GYGFSLSNVEQAK	0.93859611	2	3.43163
P15149	IVVLYGYDAVK	1.658928465	2	2.60158
P15149	LEDFMIEK	0.971735152	1	1.9668
P15149	NFIDSFLIR	0.879486162	2	2.42815
P15149	QNHSTLDPNSPR	0.801082437	2	2.66313
P15149	TLQGTCGAPIDPSIYLSK	0.694992034	2	4.60939
P15149	TVSNVINSIVFGNR	1.420979832	2	3.2365
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**2.237173625**	**0.67851**	**3**
P15178	ALHHGIDLEK	1.120109071	3	3.30517
P15178	LEYCEALAMLR	1.684023601	2	2.95031
P15178	QMVKFAANINK+Oxidation(1	1.102517366		
P15429	**ENOB Beta_enolase**	**2.276570773**	**0.99853**	**6**
P15429	DATNVGDEGGFAPNILENNEALELLK	0.929514514	2	5.12995
P15429	FMIELDGTENK	1.762431787	2	3.28281
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	1.983412317	3	5.6371
P15429	IEEALGDK	3.887415404	1	2.41668
P15429	TAIQAAGYPDK	2.776644152	2	2.97379
P15429	VNQIGSVTESIQACK	1.048952023	2	4.95931
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**2.09765178**	**1**	**20**
P15650	AFVDSCLQLHETK	1.049578332	2	4.01376
P15650	AQDTAELFFEDVR	1.202211745	2	4.80286
P15650	AQDTAELFFEDVRLPASALLGEENK	1.212210851	3	5.32631
P15650	CIGAIAMTEPGAGSDLQGVR	1.252353157	2	6.35955
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6	1.070152764		
P15650	EQIEQFIPQMTAGK	1.81358136	2	4.98789
P15650	FFQEEVIPYHEEWEK	1.508297224	2	5.21064
P15650	GFYYLMQELPQER	1.005191861	2	4.14586

P15650	IFSSEHDIFR	1.119987233	2	3.04391
P15650	KFFQEEVIPYHEEWEK	1.14742715	2	5.14368
P15650	LDSASASMAK	0.787149778	2	2.50517
P15650	LDSASASMAK+Oxidation(7	1.038391296		
P15650	QGLLGINIAEK	1.106775024	2	3.28884
P15650	RLDSASASMAK	0.893649612	2	3.38134
P15650	RLDSASASMAK+Oxidation(8	0.925291826		
P15650	SGSDWILNGSK	1.057088089	2	2.69857
P15650	TNICVTR	0.972160778	2	2.35139
P15650	TVAHIQTVQHK	0.76502216	2	2.91804
P15650	VQPIYGGTNEIMK	0.962892503	2	3.20376
P15650	VQPIYGGTNEIMK+Oxidation(11	1.240412193		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**2.442415691**	**0.96331**	**9**
P15651	ASSTANLIFEDCR	0.983620227	2	3.35461
P15651	EEGDSWVLNGTK	1.167699679	2	2.76697
P15651	ELVPIAAQLDK	1.098078356	2	2.9567
P15651	ELVPIAAQLDKEHLFPTSQVK	1.209145259	2	4.48841
P15651	GISAFLVPMPTPGLTLGK	0.800727119	2	3.62999
P15651	IGCFALSEPGNGSDAGAASTTAR	1.10115648	2	6.30175
P15651	IGIASQALGIAQASLDCAVK	1.646430457	3	4.96987
P15651	ITEIYEGTSEIQR	1.038894048	2	4.42685
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.182924629	4	4.96333
P15684	**AMPN Aminopeptidase N**	**1.925316559**	**0.47678**	**5**
P15684	ALGDTPAPNIDTTELVER	1.080837431	2	4.32479
P15684	AQIIHDSFNLASAGK	0.944400922	2	3.7072
P15684	LRSALACSNEVWILNR	1.648151861	2	2.30839
P15684	VVATTQMQAADAR	0.935215959	2	3.71342
P15684	YVEAVSPNR	0.720379851	2	2.46438
P15709	**ST2A1 Bile salt sulfotransferase**	**2.397764094**	**0.63791**	**2**
P15709	GNVLYGSWFEHIR	1.194809962	2	2.60428
P15709	NHFTVSQAEAFDK	1.319987626	1	3.75484
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**2.62864233**	**0.13783**	**3**
P15978	GYEQHAYDGR	1.48323068	2	2.4385
P15978	VEHEGLPEPLSQR	0.862277001	2	3.09697
P15978	YDSDAENPR	2.266390651	2	2.83425
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.987220381**	**0.7097**	**26**
P15999	AVDSLVPIGR	0.995245279	2	3.57164
P15999	EIVTNFLAGFEP	1.355447029	2	2.43216
P15999	EVAAFAQFGSDLDAATQQLLSR	1.226930283	2	6.61768
P15999	FESAFLSHVVSQHQSLLGNIR	1.25700867	2	6.0138
P15999	GIRPAINVGLSVSR	0.928049505	3	3.93396
P15999	GMSLNLEPDNVGVVVFGNDK	1.126605731	2	5.63109
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1	1.24134837		
P15999	GYLDKLEPSK	1.256972152	1	2.82773
P15999	HALIIYDDLSK	1.947953026	2	2.7812
P15999	ILGADTSVDLEETGR	1.121788395	2	4.89381
P15999	LELAQYR	0.971723552	2	2.48399
P15999	LKEIVTNFLAGFEP	1.85961891	2	3.03922
P15999	LTDADAMK	0.905488089	2	2.66313
P15999	NVQAEEMVEFSSGLK	0.994555096	2	4.34027
P15999	QGQYSPMAIEEQVAVIYAGVR	1.018211419	3	5.25586
P15999	RLTDADAMK	0.895240041	2	2.92997
P15999	RSTVAQLVK	0.259382426	2	2.43216
P15999	RTGAIVDVPVGDELLGR	0.892162023	2	3.09896
P15999	STVAQLVK	0.852644504	2	2.52357

P15999	TGAIVDVPVGDELLGR	0.969960599	2	4.82722
P15999	TGTAEMSSILEER	0.814780117	2	4.37411
P15999	TGTAEMSSILEER+Oxidation(5	0.939595977		
P15999	TSIAIDTIINQK	1.093366955	2	4.61757
P15999	VLSIGDGIAR	0.840668518	2	2.91216
P15999	VVDALGNAIDGK	0.948997466	2	4.42404
P15999	VVDALGNAIDGKGPVGSK	0.962508935	2	3.72534
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**2.050606733**	**0.99854**	**9**
P16036	ALYSNILGEENTYLWR	0.899337024	2	3.14802
P16036	EEGLNAFYK	0.906175889	1	2.61662
P16036	EKGSTASQVLQR	0.951860823	2	3.08548
P16036	FGFYEVFK	1.506858533	2	2.32737
P16036	GIFNGFSITLK	1.288239452	2	3.04245
P16036	GSTASQVLQR	0.973866728	2	3.07759
P16036	GWAPTLIGYSMQGLCK	0.955174736	2	2.79063
P16036	IQTQPGYANTLR	1.005218426	2	3.7901
P16036	MYKEEGLNAFYK	0.928855953	3	3.67296
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.955135923**	**1**	**36**
P16086	ALINADELANDVAGAEALLDR	1.262400088	2	5.44427
P16086	ALSSEGKPYVTK	1.016083897	2	3.45721
P16086	DLASVQALLR	1.454749172	2	2.36186
P16086	DLSSVQTLLTK	0.967710881	2	3.14961
P16086	GNAMVEEGHFAAEDVK	1.202573741	2	4.10589
P16086	GVIDMGNSLIER	1.258833725	2	3.07557
P16086	HQAFEAELHANADR	1.23426672	2	2.91677
P16086	HQAFEAELSANQSR	0.702715014	2	4.25052
P16086	HQALQAEIAGHEPR	0.899782546	3	4.75946
P16086	HQEHKGEIDAHEDSFK	0.873277532	3	4.37673
P16086	HQLLEADISAHEDR	0.967931174	3	3.67163
P16086	KFEEFQTDLAAHEER	1.203899552	3	4.31921
P16086	LGDSHDLQR	1.07267336	2	3.20129
P16086	LGESQTLQQFSR	0.750021963	2	3.10756
P16086	LIQEQHPEEELIK	0.93733804	2	4.08782
P16086	LQQSHPLSANQIQVK	0.986227294	2	4.40617
P16086	LQTASDESYKDPTNIQSK	1.333196288	2	5.09226
P16086	LQVASDENYKDPTNLQGK	0.959060858	2	5.1868
P16086	LSDDNTIGQEEIQQR	0.953736404	2	4.07653
P16086	MQHNLEQQIQAR	1.355382543	2	3.36507
P16086	MQHNLEQQIQAR+Oxidation(0	0.771910019		
P16086	MTLVASEDYGDTLAAIQGLLK	1.071927266	2	3.79658
P16086	NQALNTDNYGHDLASVQALQR	0.883872764	2	6.16928
P16086	QFQDAGHFDAENIKK	1.086791819	2	2.84578
P16086	REELITNWEQIR	0.885259587	2	4.38016
P16086	SADESGQALLAAGHYASDEVR	1.287878701	2	4.57911
P16086	SLQQLAEER	0.960464859	2	2.86877
P16086	SQLLGSAHEVQR	0.581962966	2	3.29539
P16086	SSEEIESAFR	1.257407188	2	2.59749
P16086	SSLSSAQADFNQLAELDR	1.232855762	2	4.74207
P16086	TATDEAYKDPSNLQGK	1.131535607	2	4.35716
P16086	TKQEEVNAAWQR	1.611657701	2	3.4483
P16086	VLETAEDIQER	0.855944119	2	3.77127
P16086	VNDVCTNGQDLIK	1.09521896	2	3.16657
P16086	VNEVNQFAAK	0.932568581	2	2.56828
P16086	VNSLGETAQR	0.974307881	2	3.17674
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.782752319**	**0.94501**	**9**
P16232	EECALEIIK	0.802673576	1	2.06642

P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8	1.725741617		
P16232	ETSGIILSQAAPK	0.889177952	2	3.13336
P16232	FALDGFFSTIR	1.182645404	2	2.99853
P16232	FVVEAGK	0.791853209	1	1.92354
P16232	KDEVYYDK	0.92680514	2	2.32476
P16232	MGAHVVLTAR	1.853522382	1	1.94936
P16232	MTQPLIASYSASK	0.913059858	2	3.41385
P16232	SSWTPLLLGNPGR	0.896650864	2	3.74862
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.730644564**	**0.79629**	**9**
P16290	ALPFWNEEIAPK	1.734468893	2	2.85574
P16290	AMEAVAAQGK	0.776250995	2	2.58411
P16290	AMEAVAAQGK+Oxidation(1	0.940594154		
P16290	HGESSWNQENR	1.707674704	2	3.95107
P16290	HNYYASISK	1.952773599	2	2.52029
P16290	HYGGLTGLNK	0.754347496	1	3.19366
P16290	SFDTPPPPMDEK	2.005753256	2	2.60675
P16290	TLWTILDVTDQMWVPVVR+Oxidation(11	1.929849665		
P16290	VLIAAHGNSLR	0.872303764	2	2.94739
P16303	**CES3 Carboxylesterase 3**	**1.943356252**	**0.89159**	**16**
P16303	AKEAAEEPSHWK	0.83398572	2	4.06837
P16303	DGASEEETNLSK	1.074961918	2	4.18626
P16303	EAAEEPSHWK	1.026903421	2	2.86087
P16303	ESYPFLPTVIDGVVLPK	0.876949857	2	4.15355
P16303	FAPPQPAEPWNFVK	1.161399996	1	2.33905
P16303	IGASTQAAQR	0.814453382	2	2.80827
P16303	LDLLGNPK	0.955067714	2	2.56699
P16303	MIPVVAEK	1.026728899	1	1.98532
P16303	QEFGWIIPTLMGYPLSEGK	0.938511917	2	2.57027
P16303	QKTEDELLETSLK	0.939424334	2	3.51366
P16303	SFNTVPYIVGINK	0.795184041	2	3.32145
P16303	TEDELLETSLK	0.923257224	2	3.86506
P16303	TPEEILAEK	1.175666988	2	2.64664
P16303	TTTSAVMVHCLR	1.06756891	2	3.07174
P16303	TVIGDHGDELFSVFGSPFLK	1.068969964	2	5.47958
P16303	YFGGTDDPAK	0.951279084	2	2.87755
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.852456187**	**0.98797**	**4**
P16332	GDVGMAGVAIDTVEDTK	1.342572338	2	4.29565
P16332	IDSGSEVIVGVNK	0.914827225	2	3.77944
P16332	NTQIIIQEESGIPK	0.888964413	2	3.59562
P16332	TGLQAGLTIDEFAPR	1.31885878	2	3.40072
P16409	**MYL3 Myosin light chain 3**	**2.019015814**	**0.99962**	**8**
P16409	AAPAPAAAPAAAPEPERPK	3.073033983	2	4.46803
P16409	ALGQNPTQAEVLR	1.830489984	2	3.74313
P16409	EGNGTVMGAELR	1.221218621	2	2.73079
P16409	IEFTPEQIEEFK	1.619982754	2	3.01994
P16409	LTEDEVEK	1.354557373	1	2.14643
P16409	MMDFETFLPMLQHISK	0.903308115	3	3.83165
P16409	NKDTGTYEDFVEGLR	1.124633827	2	3.451
P16409	VFDKEGNGTVMGAELR	1.009596676	2	4.11548
P16617	**PGK1 Phosphoglycerate kinase 1**	**2.186081183**	**1.6E-12**	**18**
P16617	AHSSMVGVNLPQK	0.992218156	3	4.06088
P16617	AHSSMVGVNLPQK+Oxidation(4	1.010936033		
P16617	ALESPERPFLAILGGAK	1.098970845	3	4.75942
P16617	DCVGSEVENACANPAAGTVILLENLR	1.283399215	3	6.49956
P16617	FCLDNGAK	0.97881587	1	1.96106
P16617	GCITIIGGGDTATCCAK	0.985528093	2	5.55183
P16617	IQLINNMLDK	1.315481804	2	3.03563

P16617	IQLINNMLDK+Oxidation(6	1.718627662		
P16617	ITLPVDFVTADK	1.531450029	2	2.74657
P16617	ITLPVDFVTADKFDENAK	1.592098648	2	4.78655
P16617	SVVLMSHLGRPDGVPMPDK	1.087617556	3	3.74741
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.194854735	4	4.76504
P16617	TGQATVASGIPAGWMGLDCGTESSK	1.22057902	2	5.03905
P16617	TGQATVASGIPAGWMGLDCGTESSKK	0.941768102	3	4.07681
P16617	VLNNMEIGTSLYDEEGAK	1.765070443	2	5.24542
P16617	VLPGVDALSNV	1.850870471	2	3.28639
P16617	WNTEDKVSHVSTGGGASLELLEGK	0.797220376	3	4.835
P16617	YSLEPVAAELK	1.068057758	2	3.49632
P16638	**ACLY ATP_citrate synthase**	**2.419887418**	**0.09812**	**25**
P16638	AFDSGIIPMEFVNK	1.418809142	2	3.65403
P16638	AKPAMPQDSVPSPR	1.394347309	2	2.7421
P16638	DEPSVAAMVYPFTGDHK	0.963105874	2	2.95481
P16638	DLVSSLTSGLLTIGDR	0.809098507	2	3.70077
P16638	EAYPEEAYIADLDAK	1.277972949	2	3.62656
P16638	FGGALDAAAK	1.127355308	2	3.02035
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.328371616	2	4.09636
P16638	GGPNYQEGLR	1.575377498	2	2.95829
P16638	GVTIIGPATVGGIKPGCFK	1.771198493	2	3.70465
P16638	HLLVHAPEDK	0.878156892	2	2.68079
P16638	HLLVHAPEDKK	1.29375438	2	3.46117
P16638	IGNTGGMLDNILASK	1.504853541	2	4.10394
P16638	LGLVGVNLSLDGVK	2.395940411	2	2.49956
P16638	LNAEDIK	1.116690265	1	1.94409
P16638	QHFPATPLLDYALEVEK	1.160301405	3	3.84036
P16638	RGGPNYQEGLR	1.227352355	2	3.3
P16638	SAYDSTMETMNYAQIR	1.461415806	2	2.93082
P16638	SGGMSNELNNIISR	0.928754294	2	3.65613
P16638	SMGFIGHYLDQK	1.092025591	2	2.91414
P16638	TIAIIAEGIPEALTR	1.265799757	2	4.98087
P16638	TTDGVYEGVAIGGDR	1.010094059	2	3.3363
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	1.446929851	3	3.45261
P16638	VDATADYICK	1.114244995	2	2.63092
P16638	WGDIEFPPPFGR	1.162728365	2	3.90479
P16638	YICTTSAIQNR	1.25466303	2	3.1424
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**1.778338241**	**0.94556**	**10**
P16970	DQVIYPDGKEDQK	0.982856843	2	2.82678
P16970	EGGWDSVQDWMDVLSGGEK	1.077697456	2	2.89161
P16970	FDHVPLATPNGDILIQDLSFEVR	1.088281568	3	4.14856
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.822734887	3	5.36746
P16970	GISDQVLK	1.462282304	1	1.94651
P16970	GYLDNVQLGHILER	1.214585498	2	3.56445
P16970	HLHSTHSELLEDYYQSGR	0.899861292	3	5.85202
P16970	ITELMQVLK	1.641483087	2	2.83461
P16970	KGISDQVLK	0.781641101	2	2.51888
P16970	SGANVLICGPNGCGK	0.9412867	2	3.2054
P17074	**RS19 40S ribosomal protein S19**	**1.956814993**	**0.98973**	**5**
P17074	ELAPYDENWFYTR	1.135855309	2	2.95906
P17074	HKELAPYDENWFYTR	0.958111617	3	4.61017
P17074	LKVPEWVDTVK	1.299977318	3	3.3472
P17074	RVLQALEGLK	1.656033702	3	3.81539
P17074	VLQALEGLK	1.140315897	2	2.70721
P17077	**RL9 60S ribosomal protein L9**	**2.05370521**	**0.50811**	**8**
P17077	DFNHINVELSLLGK	1.372757364	2	3.0464

P17077	FLDGIYVSEK	1.214710255	2	3.12915
P17077	GTVQQPDE	17.80671636	1	2.03732
P17077	KFLDGIYVSEK	0.916889857	2	2.94164
P17077	SVYAHFPINVVIQENGSLVEIR	1.504038121	3	3.82579
P17077	TGVACSVSQAQK	1.026456145	2	3.50443
P17077	TICSHVQNMIK	1.145093701	2	3.17312
P17077	TILSNQTVDIPENVDITLK	1.353164109	2	4.8665
P17078	**RL35 60S ribosomal protein L35**	**2.001088569**	**0.99331**	**2**
P17078	QLDDLKVELSQLR	1.151119712	2	2.97702
P17078	VLTVINQTQK	1.000119526	2	2.92333
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**2.230931099**	**0.96619**	**5**
P17178	DHESTEGPGTGQDRPR	0.92483995	2	3.35757
P17178	SLAELPGPGTLR	1.227970763	2	2.61094
P17178	TNVNLASAPLLEQVMR	1.114752069	2	3.65578
P17178	VGCLEPSIPEDTATFIR	1.253840014	2	3.21551
P17178	YEVVLSPGMGEVK	1.118253867	2	3.42202
P17209	**MYL4 Myosin light chain 4**	**2.117170667**	**0.98177**	**2**
P17209	HVLATLGEK	1.790134421	1	2.64427
P17209	ITYGQCGDVLR	1.079627136	2	2.3725
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**1.90389968**	**0.00109**	**10**
P17425	ASAELFNQK	0.419197586	2	3.51042
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	0.378653102	3	5.27687
P17425	ITASLCDLK	0.512472022	2	2.53664
P17425	LEDTYFDRDVEK	0.580571098	2	2.96751
P17425	MFLNDFLNDQNR	0.801786613	2	3.48395
P17425	NSIYSGLEAFGDVK	0.858463788	2	3.22585
P17425	NSLSYDCIGR	0.187908382	1	2.08573
P17425	TCVAPDVFAENMK	0.464205438	2	3.25146
P17425	VTQDATPGSALDK	1.04301072	2	3.6139
P17425	YTIGLGQAR	0.488242588	2	2.76626
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**2.143545591**	**0.99966**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(6	1.149740117		
P17426	NADVELQQR	1.084578564	2	2.64205
P17426	VGGYILGEFGNLIAGDPR	1.106118962	2	3.94523
P17475	**A1AT Alpha_1_antiproteinase**	**3.377760174**	**0.06395**	**9**
P17475	AFHHLLQTLNRPDSELQLNTGNGLFVNK	0.747177563	3	4.54079
P17475	GTEAAGATVVEAVPMSLPPQVK	1.064299481	2	2.61991
P17475	MQHLEQTLTK	1.956270524	1	3.1274
P17475	MQHLEQTLTK+Oxidation(0	1.67367113		
P17475	NNYHSEAFSVNFADSEEAKK	1.543504056	3	5.07493
P17475	SAILYFPK	1.962004422	2	2.39516
P17475	TLLSSLGITR	2.056406533	2	2.98003
P17475	VFNNDADLSGITEDAPLK	2.331958435	2	5.83886
P17475	VINDYVEK	1.715113104	2	2.65176
P17702	**RL28 60S ribosomal protein L28**	**2.258025683**	**0.80142**	**2**
P17702	NCSSFLIK	1.508764932	2	2.42029
P17702	QTYSTEPNNLK	1.127527603	2	2.77923
P17712	**HXK4 Glucokinase**	**2.156337762**	**0.164**	**2**
P17712	ASGAEGNNIVGLLR	0.902264061	2	2.30268
P17712	STPEGSEVGDFLSLDLGGTNFR	1.956825435	2	3.17647
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**2.082831478**	**0.91948**	**15**
P17764	EEQDKYAIGSYTR	1.204051238	2	3.48772
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.296401311	3	3.96508
P17764	EVYMGNVIQGGEGQAPTR	0.855771179	2	5.06654
P17764	FANEITPITISVK	1.303869463	2	4.12178
P17764	GKPDVVVKEDEEYK	1.078687144	2	3.72773

P17764	GKPDVVVKEDEEYKR	0.93616044	2	5.17298
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.550694784	2	4.96492
P17764	IHMGNCAENTAK	1.165373559	3	3.55753
P17764	IHMGNCAENTAK+Oxidation(2	1.163885101		
P17764	LEDLIVK	0.98435829	2	2.40383
P17764	LGTIAIQGAIEK	1.331115757	2	3.37283
P17764	QATLGAGLPIATPCTTVNK	1.029457797	2	4.63856
P17764	QGEFGLASICNGGGGASAVLIEK	1.131605347	2	5.11913
P17764	TPIGSFLGSLASQPATK	1.67834301	2	4.31948
P17764	VNVHGGAVSLGHPIGMSGAR	0.945090011	2	5.8808
P17879	**HS71B Heat shock 70 kDa protein 1B**	**2.284362857**	**0.0239**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.137997252	3	5.54856
P17879	TTPSYVAFTDTER	0.987259635	2	3.62278
P17879	VEIIANDQGNR	4.461596363	2	3.76421
P17988	**ST1A1 Sulfotransferase 1A1**	**2.743200927**	**0.07122**	**4**
P17988	CPGVPSGLETLEETPAPR	1.402396963	2	4.23585
P17988	NTFTVAQNER	1.089785964	2	3.56406
P17988	SLPEETVDSIVHHTSFK	1.423437546	2	4.40445
P17988	THLPLSLLPQSLLDQK	1.683046047	2	4.71143
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**2.048427509**	**1**	**29**
P18163	AELSVIFADKPEK	0.918001127	2	3.35532
P18163	ALEDLGR	0.723973128	2	2.33962
P18163	ALKPPCDLSMQSVEVTGTTEGVR	0.928382418	2	4.30022
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9	1.154242786		
P18163	CGVEIIGLK	0.907984774	2	2.87604
P18163	DGWLHTGDIGK	1.011086147	2	2.7965
P18163	GAMVTHQNIMNDCSGFIK	1.183115692	2	5.14771
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2	0.887397957		
P18163	GFQGSFEELCR	1.005114117	2	3.64198
P18163	GIAVHPELFSIDNGLLTPTLK	1.30860479	2	5.30351
P18163	GIQVSNDGPCLGSR	0.906255681	2	4.54336
P18163	IENIYLR	1.043882263	2	2.80915
P18163	IFGQANTSVK	0.899890704	2	2.8254
P18163	IIVIMDSYDNDLVER	1.229122799	2	5.06847
P18163	LLLEGVENK	1.004602338	2	3.34425
P18163	LLMDDLK	0.968226992	2	2.50697
P18163	LMITGAAPVSATVLTFLR	0.723638768	3	4.11402
P18163	LVDVEDMNYQAAK	0.927702897	2	4.64933
P18163	NAGLKPFEQVK	0.922288355	2	3.77725
P18163	NNSLWDK	0.85366675	2	2.49225
P18163	QVAEMAECIGSALIQK	1.000150847	2	5.53411
P18163	SAVLEDDKLLLYYYDDVR	1.151298783	3	3.61841
P18163	SQIDELYSTIK	0.785156782	2	3.61558
P18163	SQIDELYSTIKI	1.151830118	2	3.94699
P18163	TAEALDKDGWLHTGDIGK	1.106509704	2	5.25147
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	0.772858284	3	5.15537
P18163	TMYDGFQR	1.581021925	1	1.94556
P18163	VLQPTIFPVVPR	1.47172545	2	3.59794
P18163	WLLDFASK	0.987827645	2	2.56555
P18297	**SPRE Sepiapterin reductase**	**2.50590386**	**0.54756**	**5**
P18297	LGCAVCVLTGASR	0.986549511	2	3.03202
P18297	LLLINNAGTLGDVSK	1.737399236	2	3.89844
P18297	LNSEGELVDCGTSAQK	1.055422232	2	4.89868
P18297	TVVNISSLCALQPFK	1.2137963	2	3.27479
P18297	VLSYAPGPLDTNMQQLAR	1.090161697	2	3.44383
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**2.076719812**	**0.99998**	**3**

P18298	IIVDTYGGWGAHGGGAFSGK	1.076806622	2	5.49793
P18298	KIIVDTYGGWGAHGGGAFSGK	1.085129818	3	4.14974
P18298	YLDEDTIYHLQPSGR	0.965591332	2	4.7805
P18418	**CALR Calreticulin**	**2.074326911**	**1**	**20**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	0.944534801	3	5.83845
P18418	CKDDEFTHLYTLIVRPDNTYEVK	0.99661853	3	4.92148
P18418	DMHGDSEYNIMFGPDICGPGTK	1.12736047	2	6.22996
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1	1.076920809		
P18418	EQFLDGDAWTNR	1.819706243	2	3.17007
P18418	FYALSAR	1.264733228	2	2.38506
P18418	FYGDQEK	1.091022382	1	2.11905
P18418	FYGDQEKDK	0.96199355	1	2.92285
P18418	GQTLVVQFTVK	1.069825874	2	2.93733
P18418	HEQNIDCGGGYVK	1.029163593	2	4.4037
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.824603904	3	4.30204
P18418	IDNSQVESGSLEDDWDFLPPK	1.126138925	2	5.36384
P18418	IDNSQVESGSLEDDWDFLPPKK	1.388762922	3	4.88656
P18418	IKDPDAAKPEDWDER	1.339144737	2	4.368
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.192917213	3	5.51373
P18418	KVHVIFNYK	1.072343976	2	2.33979
P18418	LFPGGLDQK	1.019041335	2	2.37105
P18418	QIDNPDYK	0.978090108	1	2.09044
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	0.861335578	3	4.7888
P18418	VHVIFNYK	1.093100195	1	2.55527
P18420	**PSA1 Proteasome subunit alpha type_1**	**2.273265915**	**0.98935**	**3**
P18420	AQPSQAADEPAEK	1.162526293	2	3.8529
P18420	IHQIEYAMEAVK	1.510987413	2	2.82726
P18420	NQYDNDVTVWSPQGR	1.407622376	2	2.99556
P18421	**PSB1 Proteasome subunit beta type_1**	**1.951594554**	**0.46474**	**4**
P18421	AGGSASAMLQPLLDNQVGFK	0.964244253	2	4.99356
P18421	AGGSASAMLQPLLDNQVGFK+Oxidation(7	3.979757702		
P18421	GAVYSFDPVGSYQR	1.112837971	2	3.00408
P18421	NMQNVEHVPLTLDR	1.141350623	2	3.64801
P18422	**PSA3 Proteasome subunit alpha type_3**	**2.249715833**	**0.33656**	**2**
P18422	AVENSSTAIGIR	1.169690564	2	3.23243
P18422	TEIEKLQMKEMTCR+Oxidation(10	1.571377703		
P18445	**RL27A 60S ribosomal protein L27a**	**1.996207526**	**0.99662**	**4**
P18445	LWTLVSEQTR	0.966500013	1	1.91416
P18445	NGVAPIIDVVR	1.099194196	1	2.15358
P18445	NQSFCPTVNLDK	0.995683029	2	3.29904
P18445	RNQSFCPTVNLDK	0.867253078	2	2.94568
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**2.548226286**	**0.41291**	**6**
P18484	FFQPTEMASQDFFQR	1.150123699	2	4.02479
P18484	FVNLFPEVK	1.44299264	2	2.83444
P18484	ILVAGDTMDSVK	1.059761161	2	2.74705
P18484	LTECLETILNK	1.315433576	2	2.42357
P18484	NNGVLFENQLLQIGLK	1.840726439	2	3.37997
P18484	THIETVINALK	0.763872162	2	2.8117
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**2.813916006**	**0.99176**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	4.081699191	2	3.38495
P18596	SLPSVETLGCTSVICSDK	2.036715102	2	4.61028
P18596	TGTLTTNQMSVCR	1.045915354	2	3.22655
P18596	VGEATETALTCLVEK	1.903138329	2	4.62514
P18757	**CGL Cystathionine gamma_lyase**	**2.025200396**	**0.00788**	**15**
P18757	AGDEVICMDEVYGGTNR	0.896215471	2	5.60928
P18757	ATLGISDTLIR	1.108629702	2	3.74076

P18757	AVVLPISLATTFK	1.339953887	3	4.28377
P18757	DLLEDLGQALK	1.189031472	2	3.35707
P18757	FLQNSLGAVPSPFDCYLCCR	1.489063512	2	3.91112
P18757	GTLQHAQVFLK	0.929407726	2	3.35526
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.44206739	3	4.42194
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	1.524534101	4	5.6156
P18757	LLEAAITPQTK	1.009135251	2	4.01647
P18757	LSVGLEDEKDLLEDLGQALK	1.291587557	3	6.35427
P18757	LVWIETPTNPTLK	1.187058109	2	3.88094
P18757	QCTGCPGMVSFYIK	1.116299498	2	3.72762
P18757	QDSPGQSSGFVYSR	1.084544754	2	3.85368
P18757	RVASEFGLK	1.017630899	2	2.49904
P18757	VIYPGLPSHPQHELAK	1.099396297	2	4.2341
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**2.337164507**	**0.99996**	**12**
P18886	ATNLTVSAVR	1.005785965	2	3.49467
P18886	ELHAHLLAQDK	1.271504981	2	3.65249
P18886	HSVGELQHMMAECSK	0.78918275	2	3.89476
P18886	LIFDGNEETLK	0.952599903	2	3.08487
P18886	QKLIFDGNEETLKK	1.226678105	2	2.33468
P18886	QYGQTVATYESCSTAAFK	1.136986029	2	3.69833
P18886	SEYNDQLTR	1.074603457	2	3.07104
P18886	TETIRPASIFTK	0.979533727	2	2.60541
P18886	TLQAGLLEPEVFHLNPSK	3.622616055	2	3.44897
P18886	TLSIDSIQFQR	1.118045536	2	3.0746
P18886	YILSDSSPVPEFPVAYLTSENR	1.229030164	2	5.31136
P18886	YLNAQKPLLDDSQFR	0.924898954	2	4.65914
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**2.372369317**	**0.0089**	**19**
P19112	AGGLATTGNEDILDIVPTEIHQK	1.101268102	3	6.45402
P19112	AGGTGEMTQLLNSLCTAIK	1.024738	3	5.55676
P19112	APVIMGSTEDVQEFLEIYNK	1.614547864	2	4.97642
P19112	APVIMGSTEDVQEFLEIYNKDK	1.34438614	3	3.55884
P19112	DFDPAINEYIQR	1.428105142	2	4.02159
P19112	ESPVHSICDELF	1.732444804	2	2.35021
P19112	FPPDNSAPYGAR	1.136485664	2	2.77043
P19112	GNIYSINEGYAK	1.050529805	2	3.99729
P19112	KGNIYSINEGYAK	0.699093339	2	4.48673
P19112	KLDILSNDLVINMLK	1.54247508	2	4.76317
P19112	KTSANEPSEKDALQPGR	1.093811225	3	4.17629
P19112	LDILSNDLVINMLK	1.173808911	2	5.10375
P19112	LLYECNPIAYVMEK	1.364872534	2	4.45432
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.245378701	3	5.78643
P19112	SRPSLPLPQSR	0.988500833	2	3.35377
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.269697078	3	5.16979
P19112	TLVYGGIFLYPANK	0.788843824	2	3.8419
P19112	TLVYGGIFLYPANKK	0.713737718	2	2.9054
P19112	TSANEPSEKDALQPGR	0.954460223	2	4.4773
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**2.126803689**	**0.69895**	**3**
P19123	AAVEQLTEEQKNEFK	2.162802708	2	2.55913
P19123	GKSEEELSDLFR	1.055273175	2	2.58643
P19123	SEEELSDLFR	3.754369679	2	2.8364
P19132	**FRIH Ferritin heavy chain**	**2.126883566**	**0.70573**	**2**
P19132	QNYHQDSEAAINR	1.577375589	2	2.88734
P19132	YFLHQSHEER	1.085414524	2	2.55777
P19225	**CP270 Cytochrome P450 2C70**	**2.170117872**	**0.99479**	**15**
P19225	ACIGEGLAR	0.991000997	2	2.64995

P19225	ASLNLSNPQDFIDYFLIK	1.069898335	2	3.1344
P19225	EALIDRGEEFSDK	1.33847834	2	3.25692
P19225	FDPGHFLDEK	1.305680135	2	2.46362
P19225	FILMEINR	1.226572158	2	2.63737
P19225	GTSVMACLTSALHDDKEFPNPEK	1.134201228	3	3.57707
P19225	IQEEITR	0.952292923	2	2.31765
P19225	IQEEVVYLLEALR	0.586753592	2	3.9269
P19225	KLPPGPTPLPIFGNILQVGVK	0.833045221	3	4.03319
P19225	KTTQDVEFR	0.748630594	2	2.30194
P19225	LPPGPTPLPIFGNILQVGVK	0.953384028	2	4.41558
P19225	NHMPYTDAVLHEIQR	1.004084648	3	3.82308
P19225	SDYFMAFSAGRR+Oxidation(4	0.734799552		
P19225	TTQDVEFR	0.813167263	2	2.43859
P19225	YIDFVPIPLPR	0.955607435	2	3.12531
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**2.15965838**	**0.99384**	**3**
P19234	DIEEIIDELR	1.868195347	2	3.61188
P19234	DTPENNPDTPFDFTPENYER	0.891257029	2	4.62126
P19234	FCCEPAGGLTSLTEPPK	1.143942696	2	3.13799
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**2.162630249**	**0.64937**	**9**
P19468	ASGELMTVAR	0.975395662	2	2.94006
P19468	CNQIANELCECPELLGSGFR	1.09736361	2	5.33809
P19468	IHLDDANESDHFENIQSTNWQTMR	0.970990909	3	5.0486
P19468	NTPSPFVETFPEDEEASK	1.253734824	2	4.59331
P19468	SLFFPDEAINK	1.251949282	2	2.60786
P19468	SRYDSIDSYLSK	1.095180724	2	2.70342
P19468	VQLLLNGGDVLETLQEK	1.312976476	2	4.6747
P19468	VVINVPIFK	1.558201978	2	2.69334
P19468	WGVISASVDDR	1.469991887	2	3.13825
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**2.301227885**	**0.86152**	**9**
P19488	AEMWLIR	1.397034366	2	2.89249
P19488	ANAIAWALAQIPQK	1.227196206	3	6.45927
P19488	FETFPTSVSK	1.048363052	1	1.90668
P19488	FETFPTSVSKDELEK	0.940117885	2	4.31848
P19488	GAAVTLNIR	1.201997819	2	2.56193
P19488	GHEVTVLKPSAYYVLDPK	0.891609145	2	4.53022
P19488	NWDPFYTEILGRPTTLAETMGK	2.027539018	2	4.86697
P19488	SDLFNALK	0.949186885	2	2.55647
P19488	TILDELVQR	1.065185554	2	3.39544
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.887536793**	**0.0205**	**10**
P19511	EGEHMINWVEK	1.122934926	2	2.32933
P19511	HVIQSISAQQEK	0.917216646	2	3.97659
P19511	HVIQSISAQQEKETIAK	0.679704853	3	4.75691
P19511	HYLFDVQR	0.9268356	2	2.68848
P19511	KEGEHMINWVEK	1.149223446	2	2.30447
P19511	LDYHISVQDMMR	1.534866269	3	4.55136
P19511	LNEEKIAQLEEIK	0.928408267	2	2.53071
P19511	NNIALALEVTYR	1.422770848	2	2.62271
P19511	YGASIGEFIDK	1.166019679	2	2.8361
P19511	YGASIGEFIDKLNEEK	1.451226111	2	3.47583
P19643	**AOFB Amine oxidase [flavin_containing] B**	**2.207606895**	**0.98344**	**13**
P19643	FIGGSGQVSER	1.277429581	2	3.31743
P19643	IISTTNGGQER	0.78449429	2	2.73166
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.499119789	3	4.63586
P19643	KFIGGSGQVSER	0.649368524	2	3.04442
P19643	KLCELYAK	0.849319837	2	2.52401
P19643	LERPVIHIDQTGENVVVK	1.00694245	2	5.29637

P19643	LLHDCGLSVVVLEAR	1.745262935	2	3.56399
P19643	TLNHEIYEAK	1.051014998	2	3.05249
P19643	TMDEMGQEIPSDAPWK	1.50669492	2	4.41484
P19643	VKLERPVIHIDQTGENVVVK	1.484774155	3	4.44664
P19643	VLNSQEALQPVHYEEK	1.149435582	2	4.6807
P19643	YVDLGGSYVGPTQNR	0.9836876	2	5.30995
P19643	YVISAIPPVLGMK	1.290188696	2	3.2598
P19804	**NDKB Nucleoside diphosphate kinase B**	**2.053479087**	**0.99962**	**9**
P19804	DRPFFPGLVK	1.217871239	2	2.51363
P19804	EIGLWFKPEELIDYK	1.144368929	2	3.83056
P19804	GDFCIQVGR	0.985828104	2	3.31658
P19804	NIIHGSDSVESAEK	1.090450369	3	4.01611
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.14901313	4	4.8357
P19804	TFIAIKPDGVQR	1.125060163	2	2.94786
P19804	VMLGETNPADSKPGTIR	1.322253631	2	4.49908
P19804	VMLGETNPADSKPGTIR+Oxidation(1	1.146315825		
P19804	YMNSGPVVAMVWEGLNVVK	1.061585363	2	5.32369
P19814	**TGON3 Trans_Golgi network integral membrane protein TGN38**	**6.621491021**	**0.0001**	**2**
P19814	DSGSPTGGDSDNTTGGDSNK	2.3243501	2	4.74314
P19814	TSGGDSNKPTGSDNDKPTGGDSNKPTSK	2.736222478	4	4.65954
P19944	**RLA1 60S acidic ribosomal protein P1**	**2.209873709**	**0.03279**	**2**
P19944	AAGVNVEPFWPGLFAK	1.31721954	2	2.94979
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.105413961	4	6.26471
P19945	**RLA0 60S acidic ribosomal protein P0**	**2.596970415**	**9.9E-20**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.106057772	2	6.14348
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.525988211	3	4.84083
P19945	CFIVGADNVGSK	1.067593993	2	3.4121
P19945	GHLENNPALEK	0.975684271	2	3.68968
P19945	GNVGFVFTK	1.004152187	2	2.77154
P19945	GTIEILSDVQLIK	1.318373315	2	3.62435
P19945	IIQLLDDYPK	1.722887514	2	3.74527
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.213638301	3	4.19996
P19945	TSFFQALGITTK	1.622569443	2	4.16189
P19945	VLALSVETDYTFPLAEK	1.414236252	2	3.38682
P20059	**HEMO Hemopexin**	**2.234596898**	**0.1168**	**5**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.18260895	2	5.17846
P20059	FNPVTGEVPPR	1.034471172	2	2.65569
P20059	LFQEEFPGIPYPPDAAVECHR	1.434443159	3	4.34402
P20059	SGAQATWAELSWPHEK	0.941645105	2	3.12737
P20059	VDGALCLEK	0.893367693	2	2.54823
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.924760825**	**1**	**6**
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	1.071446438	3	5.06436
P20070	LIDKEIISHDTR	0.926397572	3	4.14048
P20070	MSQYLENMNIGDTIEFR	0.785531883	2	4.42285
P20070	SSPAITLENPDIK	0.905792213	2	3.99659
P20070	SSPAITLENPDIKYPLR	0.9762439	2	3.88838
P20070	SVGMIAGGTGITPMLQVIR	1.025973198	2	4.46415
P20280	**RL21 60S ribosomal protein L21**	**2.025793625**	**0.99991**	**4**
P20280	HGVVPLATYMR	1.120261748	2	2.56905
P20280	KGDIVDIK	1.029402482	1	2.25277
P20280	TNGKEPELLEPIPYEFMA	0.974678862	2	3.6158
P20280	VYNVTQHAVGIIVNK	1.010786912	2	4.42374
P20673	**ARLY Argininosuccinate lyase**	**1.955401946**	**0.15174**	**16**
P20673	AEAECEVLFPGYTHLQR	0.892645663	2	4.92073
P20673	AEMQQILQGLDK	1.090162333	2	4.53292

P20673	AVVVAEMK	1.11002252	1	1.94993
P20673	EFNFVQLSDAYSTGSSLMPQK	1.246058482	2	5.80344
P20673	FNSSIAYDR	0.827028869	2	2.54475
P20673	HLWNVDLQGSK	1.002847821	1	3.30696
P20673	INVLPLGSGAIAGNPLGVDR	1.511633739	2	5.48454
P20673	KNPDSLELIR	0.962948084	2	2.61251
P20673	LKELIGEAAGK	0.954028346	2	3.19458
P20673	LYPNDEDIHTANER	1.365264733	2	3.91401
P20673	MAEDLILYGTK	0.782407059	2	3.70237
P20673	MAEDLILYGTK+Oxidation(0	0.917362462		
P20673	NDQVVTDLR	1.059450784	2	3.21711
P20673	SRNDQVVTDLR	1.051780439	2	2.88317
P20673	VAEEWAQGIFK	1.42964841	2	3.5697
P20673	VLIEAMVDR	1.183730629	2	2.75694
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.872529097**	**0.81985**	**6**
P20788	EIDQEAAVEVSQLR	0.731561682	2	4.2458
P20788	EIDQEAAVEVSQLRDPQHDLER	0.560434899	3	3.37509
P20788	ESLSGQAATRPLVATVGLNVPASVR	1.316050075	2	2.50068
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	0.895191113	3	4.80667
P20788	LSDIPEGK	0.965061166	1	2.02734
P20788	SGPFAPVLSATSR	0.945637312	2	2.8626
P20801	**TNNC2 Troponin C_ skeletal muscle**	**2.223818288**	**0.92173**	**4**
P20801	GKSEEELAECFR	2.3401461	2	3.24512
P20801	NADGYIDAEELAEIFR	1.105566324	2	4.82179
P20801	SEEELAECFR	1.940561819	2	3.2848
P20801	SYLSEEMIAEFK	2.433478306	2	2.67499
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**4.138460644**	**3.7E-11**	**3**
P20814	FDYEDKDFLNLIEK	1.92622561	3	3.99428
P20814	GTAVLTSLTSVLHDSK	2.143657215	2	3.73484
P20814	IKEHEESLDVSNPR	1.624955161	2	4.69764
P20817	**CP4AE Cytochrome P450 4A14**	**1.604100254**	**0.0003**	**6**
P20817	ACQIAHEHTDGVIK	0.641585619	2	4.26931
P20817	AQLQNEEELQK	0.654358907	2	3.20137
P20817	AVEDLNNLTFFR	0.808281517	2	3.3195
P20817	HLDFLDILLFAK	0.66787219	2	3.81993
P20817	MRKAQLQNEEELQK+Oxidation(0	0.979821406		
P20817	VLLYDPDYVK	0.452201511	2	2.71002
P20852	**CP2A5 Cytochrome P450 2A5**	**2.400029085**	**0.99747**	**3**
P20852	DFIDSFLIR	1.12391155	2	2.31995
P20852	DPKFFSNPKDFNPK	1.359803004	2	2.538
P20852	EALVDQAEEFSGR	0.802721463	2	3.36968
P21213	**HUTH Histidine ammonia_lyase**	**2.359352082**	**0.63198**	**12**
P21213	ALDYLAIGVHELAAISER	1.790157377	3	4.06758
P21213	DIITTELNSATDNPMVFASR	1.74841109	2	4.21956
P21213	GETISGGNFHGEYPAK	1.141451799	2	4.13415
P21213	GEWLAVPCQDGK	1.125453928	2	2.46894
P21213	GYSGISLETLK	1.258709188	2	2.74128
P21213	LQELQVNLVR	1.348936224	2	3.17782
P21213	NKPDNGGFTSVDEVR	1.219593945	2	3.9932
P21213	SHSSGVGKPLSPER	1.151061475	2	4.37341
P21213	SLLDSDHHPSEIAESHR	1.4312172	3	4.82797
P21213	TVVYGITTGFGK	1.259289701	2	3.29553
P21213	VWEVAAPYIEK	1.413374845	2	2.41887
P21213	YIALDGDSLSTEDLVNLGK	1.172778615	2	5.15879
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.862599268**	**0.90897**	**9**
P21396	DVPAIEITHTFLER	1.237319143	2	3.37243

P21396	FVGGSGQVSEQIMGLLGDK	1.022229973	2	3.14002
P21396	IFSVTNGGQER	0.732307418	2	2.6415
P21396	INVLVLEAR	1.135168176	2	3.18034
P21396	KDIWVEEPESK	0.902932315	2	3.30015
P21396	KICELYAK	0.849319837	2	2.52401
P21396	VLGSQEALYPVHYEEK	1.022510834	2	4.45402
P21396	WVDVGGAYVGPTQNR	0.812706989	2	4.50637
P21396	YVISAIPPILTAK	1.158262624	2	2.94856
P21531	**RL3 60S ribosomal protein L3**	**2.378512027**	**0.99691**	**7**
P21531	AHLMEIQVNGGTVAEK	0.914164869	2	5.38146
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	1.249984757	3	5.28547
P21531	HGSLGFLPR	1.009279075	2	2.92632
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.335725664	2	5.13959
P21531	NNASTDYDLSDK	1.055259879	2	3.70017
P21531	SINPLGGFVHYGEVTNDFIMLK	1.507362039	2	3.63843
P21531	TVFAEHISDECK	1.144074842	2	3.99984
P21533	**RL6 60S ribosomal protein L6**	**2.170412399**	**0.29246**	**10**
P21533	AVDSQILPK	0.999563093	2	2.78786
P21533	FVIATSTK	1.044574849	1	2.22856
P21533	HLTDAYFK	1.152558772	2	2.56802
P21533	HQEGEIFDTEK	1.087683477	2	3.36501
P21533	HQEGEIFDTEKEK	0.946150424	2	4.19414
P21533	HQEGEIFDTEKEKYEITEQR	0.857329379	3	4.55576
P21533	QLGSGLLLVTGPLALNR	1.127806489	2	5.19689
P21533	SQFSLTNGMYPHK	0.900606767	2	3.3313
P21533	SSITPGTVLIILTGR	0.992074454	2	4.13516
P21533	YYPTEDVPR	1.821082492	1	1.99562
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.981757265**	**0.73061**	**6**
P21571	FEVLDKPQS	0.920177787	2	2.89692
P21571	FPTFNFEDPKFEVLDKPQS	1.18314247	3	3.32777
P21571	GEMDKFPTFNFEDPK	0.965923331	3	3.96244
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.161996459	3	3.83114
P21571	LASGGPVDTGPEYQQEVDR	2.125300686	2	5.31505
P21571	LASGGPVDTGPEYQQEVDRELFK	2.156964026	2	2.94897
P21643	**T23O Tryptophan 2_3_dioxygenase**	**7.506576616**	**9.9E-20**	**9**
P21643	AGTGGSSGYYYLR	2.713488895	2	2.93286
P21643	DNFEGDYNELLLK	1.256125245	2	3.59625
P21643	GGLIYGDYLQLEK	5.378081207	2	3.62728
P21643	GLEEEFLK	2.557293825	1	2.24592
P21643	ILNAQELQSEIK	3.166716771	2	3.83426
P21643	KDSEEKEEQMAEFR	7.366499601	2	3.85829
P21643	NLSMEDNEEDGAQTGVNR	11.4514673	2	6.06042
P21643	YNHVCMVHRMLGSK+Oxidation(5	1.104754516		
P21643	YNHVCMVHRMLGSK+Oxidation(9	1.075453932		
P21670	**PSA4 Proteasome subunit alpha type_4**	**2.274178197**	**0.75664**	**2**
P21670	ATCIGNNSAAAVSMLK	0.949719654	2	3.41535
P21670	LLDEVFFSEK	1.544402885	2	3.375
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.885311003**	**0.07798**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	0.907292209	2	5.0123
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22	1.266089441		
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**2.326050349**	**0.21709**	**7**
P21913	CGPMVLDALIK	1.21863533	2	3.13622
P21913	CGPMVLDALIKIK	0.65078992	2	2.61755
P21913	CHTIMNCTQTCPK	0.94142518	2	4.48155
P21913	IDTDLGK	1.039342361	1	1.91315

P21913	IKNEIDSTLTFR	1.197063973	2	2.89163
P21913	LQDPFSLYR	1.376778133	2	2.76369
P21913	RIDTDLGK	1.001887172	2	2.58595
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**2.050515564**	**0.85557**	**6**
P21981	CDLEIQANGR	1.054279073	2	2.85641
P21981	DHHTADLCQEK	1.66521924	2	2.70764
P21981	KLVAEVSLK	1.023387651	2	2.45455
P21981	SEGTYCCGPVSVR	1.030962389	2	3.69216
P21981	VDLFPTDIGLHK	0.642185398	2	2.65927
P21981	YSGCLTESNLIK	1.064183258	2	3.55971
P22734	**COMT Catechol O_methyltransferase**	**2.105708454**	**0.99955**	**12**
P22734	AIYQGPSSPDKS	0.75303839	2	3.34702
P22734	EWAMNVGDAK	0.847318971	1	2.88443
P22734	GQIMDAVIR	0.880813748	2	2.9894
P22734	GQIMDAVIR+Oxidation(3	0.920112031		
P22734	GSSSFECTHYSSYLEYMK	0.652917909	2	4.43602
P22734	GTVLLADNVIVPGTPDFLAYVR	1.574256286	3	5.04401
P22734	KGTVLLADNVIVPGTPDFLAYVR	1.698164898	3	5.19426
P22734	KYDVDTLDMVFLDHWK	1.044353515	3	5.28126
P22734	VTILNGASQDLIPQLK	1.056054945	2	4.47632
P22734	YDVDTLDMVFLDHWK	1.182106444	2	4.49006
P22734	YLPDTLLLEK	1.052464361	2	3.00144
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.073470612	3	6.4661
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.906969518**	**0.99006**	**6**
P22789	EEDLILLTYPK	1.253267993	2	2.99747
P22789	ETLQNVCNK	1.665813747	2	2.35427
P22789	FVVKEEDLILLTYPK	1.430082668	3	3.4317
P22789	KLEPDELDLVLK	1.378276887	2	3.76198
P22789	LEPDELDLVLK	1.562444827	2	2.3574
P22789	NHFTVAQAEAFDK	0.918431401	2	3.44297
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.995051821**	**0.93719**	**23**
P22791	ASLDMFNK	0.98676173	2	2.79578
P22791	ASLDMFNKK	0.949697046	2	2.83551
P22791	DVGILALEVYFPAQYVDQTDLEK	1.037569808	3	5.66205
P22791	GLKLEETYTNK	1.416858766	2	2.84651
P22791	GLKLEETYTNKDVDK	0.863266128	3	3.37082
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.07176026	3	6.96637
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3	1.119210236		
P22791	IGAFSYGSGLAASFFSFR	1.221335182	2	3.2888
P22791	LEETYTNK	0.928920311	2	3.15436
P22791	LEETYTNKDVDK	0.794441275	2	4.12729
P22791	LEVGTETIIDK	0.69801173	2	3.78082
P22791	LMFNDFLSSSSDK	1.529454397	2	4.32502
P22791	LMFNDFLSSSSDK+Oxidation(1	1.567076241		
P22791	LMFNDFLSSSSDKQNNLYK	1.420564874	2	4.78452
P22791	LSIQCYLR	1.313798884	2	2.44313
P22791	LVSSVSDLPK	1.124229756	2	3.45192
P22791	MGFCSVQEDINSLCLTVVQR	1.295008682	2	4.1632
P22791	MSPEEFTEIMNQR	1.368898729	2	4.89085
P22791	MSPEEFTEIMNQR+Oxidation(0	0.938916849		
P22791	MSPEEFTEIMNQR+Oxidation(9	1.484566122		
P22791	TKLPWDAVGR	0.988845544	3	4.01192
P22791	VNFSPPGDTSNLFPGTWYLER	1.191770901	2	4.45927
P22791	YTVGLGQTR	0.997122357	2	3.44634
P22985	**XDH Xanthine dehydrogenase/oxidase**	**2.267283012**	**0.55346**	**10**

P22985	DEVTCVGHIIGAVVADTPEHAQR	1.084520685	3	3.8216
P22985	DGGCCGGSGNNPNCCMNQTK	1.034968653	2	5.7519
P22985	DPPANVQLFQEVPK	1.319299061	2	2.88138
P22985	LDPTFASATLLFQK	1.176867598	2	3.80933
P22985	NQPEPTVEEIENAFQGNLCR	1.485039202	2	5.0843
P22985	QLFQLDSPATPEK	1.18303025	2	3.4268
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.114420241	3	5.2065
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.441830002	3	5.30885
P22985	TLLRPEEILLSIEIPYSK	0.879749669	3	4.46445
P22985	TNLPSNTAFR	0.917110279	1	2.046
P23358	**RL12 60S ribosomal protein L12**	**2.309885543**	**1**	**5**
P23358	CTGGEVGATSALAPK	0.952405689	2	4.13048
P23358	EILGTAQSVGCNVDGR	1.365785971	2	4.50077
P23358	HNGNITFDEIVNIAR	1.257398732	2	3.85397
P23358	HPHDIIDDINSGAVECPAS	5.463528591	2	4.55591
P23358	QAQIEVVPSASALIIK	1.321444631	2	3.84584
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**2.557057169**	**0.7049**	**10**
P23457	ALDGLNR	0.996566439	2	2.39259
P23457	ELTQVFEFQLASEDMK	1.083844128	2	4.13405
P23457	HFDSAYLYEVEEEVGQAIR	1.46915856	2	5.99956
P23457	MLDYCK	1.173933294	1	2.14713
P23457	SIGVSNFNCR	1.109939044	2	3.40528
P23457	SKDIILVSYCTLGSSR	0.975298174	2	4.44201
P23457	SPVLLDDPVLCAIAK	1.342612065	2	4.21325
P23457	VALNDGNFIPVLGFGTTVPEK	1.99200044	2	4.86066
P23457	YFDDHPNHPFTDE	1.224235821	2	4.19011
P23457	YKPVCNQVECHLYLNQSK	0.955357607	2	4.63768
P23514	**COPB Coatomer subunit beta**	**2.041649245**	**0.6114**	**8**
P23514	EAGELKPEEEITVGPVQK	0.900695632	2	4.08284
P23514	LVEKPSPLTLAPHDFANIK	1.161376262	3	3.72948
P23514	NFENLIPDAPELIHDFLVNEK	1.216017268	3	4.80343
P23514	TLQLALDLVSSR	1.15739111	2	3.4115
P23514	TNNVSEHEDTDKYR	1.119083445	2	3.81448
P23514	VLQDLVMDILR	1.027824645	2	3.52052
P23514	VLSECSPLMNDIFNK	1.205750122	2	2.86366
P23514	YEAAGTLVTLSSAPTAIK	1.158593212	2	5.29004
P23739	**SUIS Sucrase_isomaltase_ intestinal**	**1.951855997**	**0.98686**	**2**
P23739	LPGFGFNDQFIQISTR	0.964833751	2	2.4404
P23739	RMMTLNYPPVFSPELR+Oxidation(1	1.013654417		
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**2.200119289**	**1**	**10**
P23965	ALQLGTLFPPAEALK	1.358658355	2	5.296
P23965	ATADNLIK	1.00615779	2	2.76712
P23965	AVQELWLR	1.552876346	2	2.72062
P23965	DNYVNTIGHR	1.34417159	2	2.67969
P23965	EGEAGIAVMK	0.957553949	1	2.00261
P23965	GVILTSERPGIFSAGLDLMEMYGR	1.096642742	3	5.49936
P23965	QREADIQNFTSFISR	1.022699518	2	3.04774
P23965	SLHVYLEK	0.836738843	1	2.1486
P23965	VGLVDEVVPEDQVHSK	0.979395714	2	4.8673
P23965	WFTIPDHSR	0.943725166	1	1.9616
P24049	**RL17 60S ribosomal protein L17**	**2.370944433**	**0.33284**	**4**
P24049	EQIVPKPEEEVAQK	1.029139851	2	3.8174
P24049	GLDVDSLVIEHIQVNK	1.293805604	2	4.39192
P24049	SAEFLLHMLK	2.62924295	2	2.84709
P24049	YSLDPENPTK	0.819316705	2	2.60598
P24050	**RS5 40S ribosomal protein S5**	**2.531559541**	**0.00971**	**5**
P24050	AQCPIVER	1.105157682	2	2.31387

P24050	QAVDVSPLR	2.459788181	2	2.31656
P24050	RQAVDVSPLR	1.139518962	2	2.33084
P24050	VNQAIWLLCTGAR	1.518695188	2	4.2079
P24050	WSTDDVQINDISLQDYIAVK	1.904243781	2	4.82144
P24090	**FETUA Alpha_2_HS_glycoprotein**	**2.103570175**	**0.89084**	**6**
P24090	ELACDDPETEHVALIAVDYLNK	1.185294918	2	4.2808
P24090	HAFSPVASVESASGEVLHSPK	1.114436812	3	6.05787
P24090	LGGEEVSVACK	1.478139552	2	3.71209
P24090	VGQPGDAGAAGPVAPLCPGR	0.909032844	2	5.20985
P24090	VLHAQCHSTPDSAEDVR	1.137567735	3	3.42023
P24090	VLHAQCHSTPDSAEDVRK	1.303210119	3	4.01869
P24268	**CATD Cathepsin D**	**2.861234336**	**0.04196**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.131917588	2	3.31334
P24268	DPTGQPGGELMLGGTDSR	1.662506319	2	4.73885
P24268	GGCEAIVDTGTSLLVGPVDEVK	0.971423986	3	3.50207
P24268	LGGQNYELHPEK	1.647128634	2	3.24573
P24329	**THTR Thiosulfate sulfurtransferase**	**1.928062419**	**0.99999**	**12**
P24329	EGHPVTSEPSRPEPAVFK	0.976976779	2	4.57323
P24329	FQLVDSR	0.868217764	2	2.38934
P24329	GSVNVPFMNFLTEDGFEK	1.122598441	2	3.25753
P24329	HVPGASFFDIEECR	1.307076806	2	4.10465
P24329	KVDLSQPLIATCR	0.937973328	2	4.65795
P24329	RFQLVDSR	0.777156376	2	2.49611
P24329	TVSVLNGGFR	1.098349965	2	2.91548
P24329	TYEQVLENLQSK	0.929150874	2	5.07622
P24329	VDLSQPLIATCR	1.082613431	2	3.73126
P24329	VLDASWYSPGTR	1.780195605	2	3.63676
P24329	WLAESIR	1.010714617	2	2.37692
P24329	YLGTQPEPDAVGLDSGHIR	0.963774114	3	4.79824
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**2.094067756**	**0.57367**	**9**
P24368	DKPLKDVIIVDCGK	1.071867256	3	3.82458
P24368	DTNGSQFFITTVK	1.076389145	2	3.83181
P24368	DVIIVDCGK	0.852698113	1	1.98992
P24368	HYGPGWVSMANAGK	0.994964054	2	4.00704
P24368	IEVEKPFAIAK	1.058923987	2	3.09217
P24368	IEVEKPFAIAKE	1.004852851	2	3.61651
P24368	TVDNFVALATGEK	1.198583095	2	4.10025
P24368	VLEGMDVVR	1.159999163	2	3.04046
P24368	VYFDFQIGDEPVGR	1.366107339	2	4.10535
P24457	**CP2DB Cytochrome P450 2D11**	**2.027338351**	**0.90472**	**2**
P24457	RFSVSTLR	0.80401156	2	2.564
P24457	SLEEWVTK	1.159374548	2	2.46066
P24470	**CP2CN Cytochrome P450 2C23**	**1.74983934**	**0.99687**	**12**
P24470	ACVGESLAR	0.967209645	2	2.75607
P24470	DLDIKPITTGIINLPPPYK	1.264296165	2	3.869
P24470	EALLQQGDEFLGR	0.727951016	2	2.69954
P24470	FGLLLLMK	0.984061907	2	3.08701
P24470	GTTVLPMLSSVMLDQK	1.280669072	2	3.98112
P24470	GYGLIFSNGER	0.86645909	2	3.7939
P24470	IEEEKDNLK	0.794923117	2	3.01472
P24470	LPPGPTPLPIIGNLLQLNLK	1.193011465	3	5.05692
P24470	RSLEERVQEEAR	0.977704406	2	2.49198
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	1.150235943	3	3.78411
P24470	TFLNLMDLLNK	1.082024766	2	3.9953
P24470	YITLLPSSLPHAVVQDTK	0.980084863	2	4.58589
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**1.981994798**	**0.98803**	**8**
P24473	AGMATAQAQHLLNK	1.009155509	2	4.19168

P24473	DEDITESQNILSAAEK	1.152419804	2	5.84502
P24473	DSGNQPPAMVPHK	1.132597558	2	2.75497
P24473	FLTAVSMEQPEMLEK	0.963638845	2	4.87768
P24473	IWSRDEDITESQNILSAAEK	1.478085166	3	3.67963
P24473	MELLAYLLGEK	1.270121102	2	3.85944
P24473	QLFQVPMSVPK	0.787331616	2	2.55549
P24473	YGAFGLPTTVAHVDGK	0.761303847	2	4.04841
P25093	**FAAA Fumarylacetoacetase**	**2.349047865**	**0.99807**	**16**
P25093	AIDVGQGQTR	0.962351622	2	3.46433
P25093	AQEHIFGMVLMNDWSAR	1.372642979	2	3.85305
P25093	ASLQNLLSASQAQLR	1.273603666	2	4.88459
P25093	ASLQNLLSASQAQLRDDK	1.268316733	2	3.58822
P25093	ASSVVVSGTPIR	1.167594563	2	3.83348
P25093	DIQQWEYVPLGPFLGK	0.996328481	2	4.99227
P25093	FGEPIPISK	1.022065496	2	2.89393
P25093	GEGMSQAATICR	1.103392232	2	3.74885
P25093	GEGMSQAATICR+Oxidation(3	0.962456433		
P25093	GKENALLPNWLHLPVGYHGR	0.921236235	4	4.53415
P25093	HLFTGPVLSK	1.135459756	1	2.73185
P25093	HQHVFDETTLNSFMGLGQAAWK	1.230439143	2	5.42357
P25093	IGVAIGDQILDLSVIK	1.322955561	2	5.40393
P25093	SFGTTISPWVVPMDALMPFVVPNPK	1.142443788		
P25093	TFLLDGDEVIITGHCQGDGYR	1.366204929	2	5.0738
P25093	VGFGQCAGK	0.664257621	2	2.35363
P25113	**PGAM1 Phosphoglycerate mutase 1**	**2.051391287**	**0.99151**	**7**
P25113	ALPFWNEEIVPQIK	1.205830502	2	3.509
P25113	FSGWYDADLSPAGHEEAK	1.076510014	2	5.07037
P25113	FSGWYDADLSPAGHEEAKR	1.160189215	2	4.2297
P25113	HGESAWNLENR	0.957103394	2	3.78706
P25113	SYDVPPPPMEPDHPFYSNISK	1.483647371	2	3.80281
P25113	YADLTEDQLPSCESLK	0.849308586	2	5.3641
P25113	YADLTEDQLPSCESLKDTIAR	1.405021427	2	5.06723
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**2.511857728**	**1.1E-08**	**15**
P25235	EDQVIQLMNTIFSK	0.921145579	2	3.88383
P25235	EETVLATVQALHTASHLSQQADLR	1.451615769	3	5.07798
P25235	FELDTSER	0.851118622	1	2.39473
P25235	FPEEEAPSTVLSQNLFTPK	1.088192475	2	3.8375
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.208878375	2	4.68701
P25235	KNFESLSEAFSVASAAAALSQNR	1.544182001	2	5.44087
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.314586709	3	5.14101
P25235	LQVSSVLSQPLAQAAVK	1.339272938	2	5.8478
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.965057665	3	5.56416
P25235	NFESLSEAFSVASAAAALSQNR	1.345317604	3	4.90533
P25235	NIVEEIEDLVAR	1.002267362	3	4.6323
P25235	NPILWNVADVVIK	1.226249546	2	3.25738
P25235	TGQEVVFVAEPDNK	0.981312177	2	4.32545
P25235	YHVPVVVVPEGSASDTQEQAILR	1.12269797	3	6.39832
P25235	YIANTVELR	1.212066124	2	2.82702
P25318	**chain**	**2.150014889**	**0.95635**	**3**
P25318	GEKGFGMPGLPGLK+Oxidation(6	1.09185945		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(12	1.105279288		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(9	1.105279288		
P25409	**ALAT1 Alanine aminotransferase 1**	**2.111086171**	**0.9253**	**3**

P25409	LTEQVFNEAPGIR	1.216172732	2	2.91472
P25409	VLCVINPGNPTGQVQTR	0.851020751	2	4.50118
P25409	VLTLDTMNPCVR	0.828170724	2	2.50242
P26039	**TLN1 Talin_1**	**2.020574757**	**0.59601**	**24**
P26039	ADAEGESDLENSR	1.296924551	2	3.62632
P26039	ADAEGESDLENSRK	1.226663015	2	3.20415
P26039	AGALQCSPSDVYTK	1.080300995	2	2.68833
P26039	ALEATTEHIR	1.028712907	2	2.36505
P26039	AQEACGPLEMDSALSVVQNLEK	1.221643403	2	4.49146
P26039	ASAGPQPLLVQSCK	1.10582598	2	2.87108
P26039	ASVPTIQDQASAMQLSQCAK	0.81416234	2	3.36574
P26039	AVAEQIPLLVQGVR	1.428967391	2	3.06253
P26039	EAAEGLRMATNAAAQNAIKK	1.134297232	2	2.65497
P26039	ILAQATSDLVNAIK	1.709452202	2	3.29756
P26039	LGAASLGAEDPETQVVLINAVK	1.238532539	2	4.27235
P26039	LLGEIAQGNENYAGIAAR	1.02012497	2	4.21337
P26039	LNEAAAGLNQAATELVQASR	1.234607194	2	5.11374
P26039	MATNAAAQNAIK	0.956025361	2	2.71029
P26039	NCGQMSEIEAK	1.216070756	2	2.94028
P26039	QFVQSAKEVANSTANLVK	1.000220385	2	2.39528
P26039	SNTSPEELGPLANQLTSDYGR	1.229615928	2	4.05546
P26039	TLAESALQLLYTAK	1.371521843	2	2.70907
P26039	TMLESAGGLIQTAR	1.230367029	2	2.61826
P26039	VGAIPANALDDGQWSQGLISAAR	1.400836094	2	5.05663
P26039	VGDDPAVWQLK	1.004173905	2	3.2794
P26039	VLGEAMTGISQNAK	0.923551994	2	3.32931
P26039	VLVQNAAGSQEK	0.991475722	2	3.15086
P26039	VVAPTISSPVCQEQLVEAGR	0.917537482	2	4.60903
P26043	**RADI Radixin**	**1.958495523**	**0.72745**	**11**
P26043	AFAAQEDLEK	0.895195458	2	3.02097
P26043	ALELEQER	0.945513143	2	2.47008
P26043	EIHKPGYLANDR	1.245637004	2	2.40559
P26043	FFPEDVSEELIQEITQR	1.034256544	3	4.0962
P26043	IQNWHEEHR	0.783188111	2	2.48059
P26043	KKEEEATEWQHK	0.447623938	3	4.19243
P26043	KTQNDVLHAENVK	0.951596969	2	5.06086
P26043	NQEQLAAELAEFTAK	1.434215457	2	5.10067
P26043	QLQALSSELAQAR	0.866291313	2	4.04214
P26043	RKPDTIEVQQMK	0.950683315	2	3.74671
P26043	TQNDVLHAENVK	1.066351551	2	4.11405
P26231	**CTNA1 Catenin alpha_1**	**2.567558023**	**0.36944**	**8**
P26231	LIEVANLACSISNNEEGVK	1.393145432	2	5.26296
P26231	LLEPLVTQVTTLVNTNSK	1.297935536	2	4.12106
P26231	NTSDVISAAK	0.957812345	2	2.39305
P26231	QIIVDPLSFSEER	1.450469253	2	2.88287
P26231	SAAGEFADDPCSSVK	1.085002061	2	4.39154
P26231	SDALNSAIDK	0.963117052	2	2.87703
P26231	TIADHCPDSACK	0.600527003	2	3.51977
P26231	VIHVVTSEMDNYEPGVYTEK	1.142737835	3	4.17196
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.803519465**	**0.25154**	**10**
P26284	AILAELTGR	1.029377148	2	2.6912
P26284	EEIQEVRSK	0.794629793	1	1.93804
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	1.142642136	3	6.51304
P26284	LEEGPPVTTVLTR	0.996309785	2	3.51335
P26284	MVNSNLASVEELK	1.006851087	2	2.91926
P26284	MVNSNLASVEELKEIDVEVR	1.304495222	2	4.36405

P26284	NFYGGNGIVGAQVPLGAGIALACK	1.652338786	2	4.20054
P26284	RGDFIPGLR	0.941577264	2	2.35812
P26284	TREEIQEVR	0.84228098	3	3.55589
P26284	VDGMDILCVR	1.099710986	2	3.43546
P26376	**IFM3 Interferon_induced transmembrane protein 3**	**1.851116542**	**0.90852**	**2**
P26376	IKEEYEVSELGAPHGSASVR	0.883549039	3	4.08259
P26376	KMVGDMTGAQAYASTAK+Oxidation(5	1.0458113		
P26453	**BASI Basigin**	**2.043137719**	**0.97887**	**7**
P26453	GNINVEGPPR	1.018650837	2	3.4814
P26453	KSEHASEGEFVK	0.826311789	3	3.40795
P26453	RKPDQTLDEDDPGAAPLK	1.120831427	3	4.00201
P26453	SEASHPPVDEWVWFK	1.229336769	2	3.28807
P26453	SEHASEGEFVK	1.096642841	3	3.74149
P26453	SGEYSCIFLPEPVGR	1.266914534	2	3.61876
P26453	VLQEDTLPDLQMK	1.146919019	2	4.11576
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**2.304681337**	**0.95829**	**2**
P26516	SVVALHNLINNK	1.213746594	2	2.76135
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	1.199045991	3	4.49596
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**1.942364246**	**0.99942**	**7**
P26772	GGEIQPVSVK	0.94637738	2	3.46954
P26772	GGIMLPEK	1.00605317	2	2.66682
P26772	GGIMLPEK+Oxidation(3	0.9000442		
P26772	GKGGEIQPVSVK	0.767619761	2	3.41747
P26772	VLLPEYGGTK	0.928213662	2	2.37234
P26772	VLQATVVAVGSGGK	0.931550121	2	5.39118
P26772	VVLDDKDYFLFR	1.178288064	3	3.69212
P27139	**CAH2 Carbonic anhydrase 2**	**1.921869739**	**0.97898**	**4**
P27139	AVQHPDGLAVLGIFLK	1.710615623	2	3.98462
P27139	IGPASQGLQK	0.874999263	2	3.5178
P27139	ITEALHSIK	1.097038477	2	2.45669
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	2.341851822	3	3.40572
P27321	**ICAL Calpastatin**	**1.970240587**	**0.62143**	**5**
P27321	GSDEVTASSAATGTSPR	1.395743521	2	4.2688
P27321	KGSDEVTASSAATGTSPR	1.117634216	2	5.21008
P27321	KVEEEVMNDQALQALSDSLGTR	1.663700295	3	3.67625
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	0.910859625	3	4.64595
P27321	SQSSEPPVIHEK	0.863337359	2	3.50463
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**1.930074214**	**0.96067**	**6**
P27364	AVLAANGSILK	0.912043437	2	2.99302
P27364	ETILNDREEEHR	0.926372817	2	2.92913
P27364	GDIVDAQFLR	0.859197922	2	3.05994
P27364	IVQMLVQEK	1.235427211	2	2.61716
P27364	NGGTFHTCALR	0.574894542	2	2.6045
P27364	QTILDVNVK	0.991333747	2	2.38779
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.83168265**	**0.99183**	**6**
P27605	DLNHVCVISESGK	0.962473031	2	3.43581
P27605	FFADLLDYIK	1.352151179	2	3.54966
P27605	NVLIVEDIIDTGK	0.803849318	2	3.86119
P27605	SVGYRPDFVGFEIPDK	1.155197921	3	4.03102
P27605	SYCNDQSTGDIK	1.144994232	2	4.00832
P27605	VIGGDDLSTLTGK	0.800689982	2	4.36202
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**2.008659894**	**0.99047**	**17**
P27653	ASQAPSSFQLLYDLK	1.030910121	2	3.97226

P27653	AYTEEDLDLVEK	0.794349757	2	3.19383
P27653	GDILVVATGQPEMVK	2.600892288	2	2.5026
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	0.883804206	3	4.79251
P27653	IFHELTQTDK	1.024070789	3	3.47881
P27653	ITIGQAPTEK	1.040083141	2	2.43887
P27653	IYGADDIELLPEAQNK	0.840967533	2	4.99348
P27653	KITIGQAPTEK	0.720017516	2	2.86934
P27653	KVVGDVAYDEAK	0.878554945	2	3.70243
P27653	LDIDPETITWQR	1.011782658	2	3.82933
P27653	MHGGGPTVTAGLPLPK	0.6469252	2	3.81227
P27653	QGFGNLPICMAK	1.115150853	2	2.78848
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.259050495	3	5.59788
P27653	TDPAALTDDEINR	1.050592542	2	4.09686
P27653	THLSLSHNPEQK	0.869945297	2	3.85035
P27653	VVGDVAYDEAK	1.169550235	2	3.40638
P27653	YVVVTGITPTPLGEGK	1.012871718	2	4.82229
P27657	**LIPP Pancreatic triacylglycerol lipase**	**2.013182856**	**0.93128**	**2**
P27657	ATYTQATQNVR	0.984614633	2	2.96299
P27657	NILSQIVDIDGIWEGTR	1.075877017	2	2.93919
P27661	**H2AX Histone H2A.x**	**2.224800258**	**0.27013**	**3**
P27661	AGLQFPVGR	0.922089044	2	3.22539
P27661	HLQLAIR	1.032653612	2	2.71001
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.184639816	2	4.39413
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**3.904685008**	**0.8286**	**4**
P27768	ELEDMNQK	2.108947646	2	2.30775
P27768	IDAAEEEKYDMEVK	2.180026196	2	3.25216
P27768	SVMLQIAATELEK	1.52715622	2	2.92447
P27768	SVMLQIAATELEKEESR	1.736840576	2	3.68925
P27867	**DHSO Sorbitol dehydrogenase**	**2.116566405**	**0.94869**	**14**
P27867	AMGASQVVVIDLSASR	1.411782126	2	4.07644
P27867	AVEAFETAK	1.090335975	1	1.94922
P27867	EVGADFTIQVAK	1.302896324	2	3.15665
P27867	GENLSLVVHGPGDIR	1.0728036	2	3.81485
P27867	HSADFCYK	1.058434646	2	2.90614
P27867	IGDFVVK	1.144533847	2	2.47232
P27867	LENYPIPELGPNDVLLK	1.013684503	2	4.88393
P27867	LPDSVTFEEGALIEPLSVGIYACR	0.976528651	3	4.1149
P27867	MHSVGICGSDVHYWEHGR	1.30165053	2	6.04524
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0	1.167216426		
P27867	TLNVKPLVTHR	1.251959729	2	3.23657
P27867	VAIEPGVPR	1.474722076	1	2.18025
P27867	VLVCGAGPIGIVTLLVAK	1.228666183	3	5.74355
P27867	YCNTWPMAVSMLASK	0.678852045	2	3.3753
P27952	**RS2 40S ribosomal protein S2**	**2.10652943**	**0.17608**	**6**
P27952	AEDKEWIPVTK	1.482990814	2	3.39259
P27952	AFVAIGDYNGHVGLGVK	1.417516873	2	3.3435
P27952	GCTATLGNFAK	1.069453216	2	3.20058
P27952	GTGIVSAPVPK	1.042124109	2	2.4959
P27952	SLEEIYLFSLPIK	0.477314367	2	3.49273
P27952	TYSYLTPDLWK	1.155362631	2	3.26723
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.895582998**	**0.27789**	**26**
P28037	ADPLGLEAEK	1.039096482	2	2.42663
P28037	ANATEFGLASGVFTR	0.966222292	2	4.85761
P28037	AVQMGMSSVFFNK	1.137029609	2	3.35546
P28037	DLGEAALNEYLR	0.881485949	2	3.47982
P28037	ECEVLPDDTVSTLYNR	1.314935331	2	4.36165

P28037	EESFGPIMIISR	1.068322353	2	3.07562
P28037	EGHEVVGVFTIPDKDGK	0.899128978	2	4.56391
P28037	GNDKVPGAWTEACGQK	0.824255127	2	3.83084
P28037	GQALPEVVAK	1.042675087	2	2.96649
P28037	GSASSDLELTEAELATAEAVR	0.903861042	2	6.31158
P28037	GVVNILPGSGSLVGQR	0.934517373	2	4.82736
P28037	IGFTGSTEVGK	0.938431071	2	2.78719
P28037	ILPNVPEVEDSTDFFK	1.387223445	2	3.59059
P28037	INWDQPAEAIHNWIR	1.036200986	2	4.25018
P28037	IQGATIPINQARPNR	0.927604553	2	2.34545
P28037	KEGHEVVGVFTIPDKDGK	0.938490035	3	4.18843
P28037	KIGFTGSTEVGK	0.974256313	2	3.13217
P28037	KLVEYCQR	0.88233474	2	2.41092
P28037	LFVEESIHNQFVQK	0.936434159	2	4.45707
P28037	LIAEGTAPR	0.852940745	2	3.52205
P28037	LSDHPDVR	0.701358168	1	2.10967
P28037	NIQLEDGK	0.857884445	1	2.3031
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.098015669	3	4.4148
P28037	TDVAAPFGGFK	0.926630968	2	3.11586
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	2.061793077	3	5.27368
P28037	VVEEVEK	1.408378675	1	2.07731
P28064	**PSB8 Proteasome subunit beta type_8**	**2.041824898**	**0.99558**	**3**
P28064	ASAGSYIATIR	1.31324355	2	2.77245
P28064	KGPGLYYVDDNGTR	0.904315802	2	2.84732
P28064	QDLSPEEAYDLAR	1.05859517	2	3.1804
P28480	**TCPA T_complex protein 1 subunit alpha**	**2.122256922**	**0.61887**	**10**
P28480	AFHNEAQVNPER	1.122298705	2	3.61945
P28480	FATEAAITILR	1.287170858	2	3.22714
P28480	HGGYENAVHSGALDD	1.035116457	2	3.34447
P28480	ICDDELILIK	1.167766595	2	3.19386
P28480	LLEVEHPAAK	1.410389064	2	2.77535
P28480	MLVDDIGDVTITNDGATILK	1.127181831	2	2.34524
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.027570693	2	4.93783
P28480	SQNVMAAASIANIVK	1.340367465	2	4.6017
P28480	SSLGPVGLDK	1.255056836	2	2.41221
P28480	YINENLIINTDELGR	2.035999684	2	4.56631
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**2.015977585**	**0.99397**	**5**
P28492	ATGLQTSDPR	1.008021047	2	2.7969
P28492	GTPHSHQPQHSDHDASNSGMLPR	1.102730712	3	3.73105
P28492	MVQESSSGGLLDR	0.958787856	2	3.62209
P28492	SNPDLWGVSLCTVDGQR	1.186276223	2	4.07981
P28492	TALHVAAAEGHIDVVK	0.993429502	3	3.58745
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**2.071039166**	**0.80934**	**2**
P28650	LDILDVLSEIK	0.750168752	2	3.20016
P28650	VVDLLATDADIVSR	1.057024648	2	2.47061
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.961252223**	**0.99821**	**19**
P29147	AVLVTGCDSGFGFSLAK	1.014783673	2	5.64348
P29147	EVAEVNLWGTVR	1.311762596	2	2.42346
P29147	FGVEAFSDCLR	1.033675779	2	3.66929
P29147	GFLVFAGCLLK	0.747200639	2	3.7283
P29147	KMWDELPEVVR	0.970053299	2	3.34313
P29147	KMWDELPEVVR+Oxidation(1	1.183773551		
P29147	MANPARSPYCITK+Oxidation(0	1.393019137		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.433745585	3	5.65484
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0	1.557035542		

P29147	MQVMTHFPGAISDK	0.858698005	2	4.82906
P29147	MQVMTHFPGAISDK+Oxidation(0	1.0682468		
P29147	MQVMTHFPGAISDK+Oxidation(3	1.0682468		
P29147	MWDELPEVVR	0.96621926	2	3.41854
P29147	MWDELPEVVR+Oxidation(0	1.014276071		
P29147	TIQLNVCNSEEVEK	0.80938423	2	4.33444
P29147	VSVVEPGNFIAATSLYSPER	0.944070433	2	5.99969
P29147	VVNISSMLGR	0.92970133	2	3.92976
P29147	YEMHPLGVK	0.955206429	1	2.55044
P29147	YEMHPLGVK+Oxidation(2	1.063395503		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**1.843119463**	**0.99999**	**9**
P29266	DLGLAQDSATSTK	0.801348056	2	3.74448
P29266	EAGEQVASSPADVAEK	0.819063628	2	4.98183
P29266	GSLLIDSSTIDPSVSK	1.371624318	2	5.07553
P29266	HGYPLILYDVFPDVCK	1.099010842	2	5.13612
P29266	KGSLLIDSSTIDPSVSK	0.85313753	2	4.08563
P29266	MGAVFMDAPVSGGVGAAR	1.050214028	2	5.32116
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0	0.939337783		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5	0.939337783		
P29266	TPILLGSVAHQIYR	1.093390981	3	3.84981
P29314	**RS9 40S ribosomal protein S9**	**2.08617862**	**0.93372**	**9**
P29314	IEDFLER	1.013997126	2	2.65748
P29314	IGVLDEGK	0.705311655	2	2.62025
P29314	KGQGGAGAGDDEEED	0.771224526	2	3.23612
P29314	KQVVNIPSFIVR	0.879066257	2	2.53673
P29314	LDYILGLK	1.233991633	2	3.04203
P29314	LFEGNALLR	1.137101759	2	3.00147
P29314	LIGEYGLR	1.224109395	2	2.56291
P29314	QVVNIPSFIVR	1.11711352	2	2.66039
P29314	SRLDQELK	1.015088218	3	3.49595
P29315	**RINI Ribonuclease inhibitor**	**2.167988824**	**0.99585**	**7**
P29315	ASLQELDLGSNK	0.874195191	2	2.43099
P29315	ELVLSNNDFHEAGIHTLCQGLK	1.175222413	3	3.50612
P29315	LDDCGLTEVR	1.113869836	2	3.14918
P29315	LENCGITSANCK	0.907011189	2	3.61645
P29315	LSLQNCSLTEAGCGVLPDVLR	1.091020495	2	3.14955
P29315	SAIQANPALTELSLR	1.182733372	2	4.43585
P29315	TNELGDAGVGLVLQGLQNPTCK	1.305659296	2	5.34337
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.887082804**	**1**	**11**
P29410	AMVASGSELGK	0.967726007	2	3.11276
P29410	AMVASGSELGK+Oxidation(1	0.955378139		
P29410	AMVASGSELGKK	1.223243234	2	2.89378
P29410	AVLLGPPGAGK	0.89196511	2	2.60096
P29410	EAMKDDITGEPLIR	1.326895203	2	3.13877
P29410	LEAYHTQTTPLVEYYR	1.025457804	2	5.00483
P29410	LVSDEMVVELIEK	1.124597508	2	4.1976
P29410	NGFLLDGFPR	0.980733698	2	2.87766
P29410	NLETPSCK	0.842172747	2	2.33067
P29410	SYHEEFNPPK	0.901720438	3	3.44782
P29410	TRLEAYHTQTTPLVEYYR	1.002670087	3	3.52619
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**2.020410861**	**0.92499**	**6**
P29411	AYEAQTEPVLQYYQK	1.007996104	2	4.58133
P29411	GVLETFSGTETNK	1.068461621	2	2.87436
P29411	NLTQCSWLLDGFPR	1.319202379	2	3.82705
P29411	TVGIDDLTGEPLIQR	1.064330064	2	3.71508

P29411	VYNIEFNPPK	0.922880169	2	2.6067
P29411	VYQIDTVINLNVPFEVIK	0.73341542	2	3.29517
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**2.525364574**	**0.25009**	**2**
P29419	ELAEAEDVSIFK	1.341401968	2	3.43257
P29419	YSALILGMAYGAK	1.325984587	2	4.09777
P29457	**SERPH Serpin H1**	**1.920824088**	**0.67499**	**2**
P29457	GVVEVTHDLQK	0.935853861	2	3.15294
P29457	SALQSINEWASQTTDGK	1.845605988	2	2.5135
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.740722852**	**0.98323**	**4**
P30009	AEDGAAPSPSSETPK	0.991053221	2	3.65815
P30009	EAEAAEPEQPEQPEQPAAEEPR	0.579422134	2	3.92005
P30009	EAGEGAEAEGATADGAK	1.050366302	2	4.31611
P30009	GEAAAERPGEAAVASSPSK	0.787819348	2	4.56594
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.697802368**	**0.81009**	**3**
P30349	GSPMEISLPIALSK	0.984674988	2	3.05245
P30349	SLSNVIAHEISHSWTGNLVTNK	0.376561105	3	3.86572
P30349	SSALQWLTPEQTSGK	1.231154028	2	3.83139
P30427	**PLEC Plectin**	**2.054761791**	**0.81645**	**5**
P30427	LLEAAAQSSK	0.867073471	2	2.43488
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0	1.114345473		
P30427	SDQLTGLSLLPLSEK	1.581528248	2	2.51199
P30427	SKELAEQEAAR	1.037876995	2	2.92077
P30427	VLALPEPSPAAPTLR	1.121757786	2	2.9817
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.926721471**	**0.99376**	**7**
P30713	AQVHEYLGWHADNIR	0.944858949	2	4.9227
P30713	GQHLSEQFSQVNCLK	0.871103176	2	5.01445
P30713	NSMVLALQR	0.875529178	2	3.29761
P30713	TLPVPPPEAHASMMLR	1.002700515	2	2.59385
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	1.093087697	3	4.0839
P30713	VLGPLIGVQVPEEK	1.103645027	2	4.0583
P30713	YQVADHWYPADLQAR	0.969913078	2	4.66661
P30835	**K6PL 6_phosphofructokinase_ liver type**	**2.280829824**	**0.07477**	**2**
P30835	NEWGSLLEELVK	1.403538645	2	2.83908
P30835	VFANAPDSACVIGLR	0.425081647	2	2.56271
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**2.122148571**	**0.49499**	**9**
P30839	DILAAIAADLSK	1.135026527	2	3.05435
P30839	EKDILAAIAADLSK	1.593890621	2	4.26661
P30839	FDHILYTGNTAVGK	0.864708201	2	4.05788
P30839	HLTPVTLELGGK	1.420381126	3	3.42677
P30839	LQQLEALR	1.152238519	1	2.07449
P30839	NVEEAINFINDR	1.104645972	2	4.2853
P30839	VMQEEIFGPILPIVSVK	1.003874033	2	4.88933
P30839	VMQEEIFGPILPIVSVK+Oxidation(1	1.228796877		
P30839	YIAPTILTDVDPNSK	1.105993781	2	4.07383
P30904	**MIF Macrophage migration inhibitory factor**	**2.539199149**	**4.2E-15**	**2**
P30904	LHISPDR	0.968891273	1	2.0557
P30904	LLCGLLSDR	1.718034005	2	2.92955
P30999	**CTND1 Catenin delta_1**	**2.203221296**	**0.9858**	**3**
P30999	GYELLFQPEVVR	0.966361949	2	2.5908
P30999	HIEWESVLTNTAGCLR	1.141544863	2	2.80348
P30999	SLDNNYSTLNER	1.089868249	2	2.46552
P31000	**VIME Vimentin**	**2.425244355**	**0.00059**	**17**
P31000	DGQVINETSQHHDDLE	1.485566616	2	3.04076
P31000	ETNLESLPLVDTHSK	0.879988892	2	2.37687
P31000	FADLSEAANR	0.92266946	2	2.89052
P31000	ILLAELEQLK	1.254465396	2	2.8724

P31000	KLLEGEESR	0.881008146	2	3.06194
P31000	KVESLQEEIAFLK	1.395538917	2	3.96662
P31000	KVESLQEEIAFLKK	0.72298344	2	2.33484
P31000	LGDLYEEEMR	0.897318319	2	2.78672
P31000	LLEGEESR	1.232812367	2	2.80147
P31000	LQDEIQNMKEEMAR	0.836993704	2	3.66286
P31000	NLQEAEEWYK	1.001539167	2	2.88632
P31000	QDVDNASLAR	0.790591865	2	2.96533
P31000	QVQSLTCEVDALK	0.878940309	2	3.30043
P31000	RQVDQLTNDK	0.717736062	2	3.02392
P31000	SLYSSSPGGAYVTR	0.973609045	2	2.86248
P31000	TNEKVELQELNDR	0.730525812	2	3.34615
P31000	VELQELNDR	0.843025595	2	2.99457
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**2.240997217**	**1**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	0.980138881	2	5.95288
P31044	LYTLVLTDPDAPSR	1.188429305	2	4.93028
P31044	VDYGGVTVDELGK	1.577052348	2	4.82221
P31044	VLTPTQVMNRPSSISWDGLDPGK	1.036845203	3	4.78184
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.155724123	2	5.12574
P31044	YVWLVYEQEQPLNCDEPILSNK	1.212201341	2	5.61372
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.890221039**	**1**	**18**
P31210	DELLTSLGK	1.183856947	2	2.79549
P31210	DIEALNK	0.744643124	1	2.55823
P31210	EEMKDIEALNK	0.734111886	2	3.31761
P31210	ENFQIFDFSLTK	1.045632428	2	3.34563
P31210	HIDGAYVYR	0.898352299	2	2.71516
P31210	IKENFQIFDFSLTK	1.009823092	2	4.35307
P31210	LWSTDHDPEMVRPALER	1.007269482	2	2.4929
P31210	NEHEVGEAIR	0.849229235	1	2.908
P31210	NPLWVNVSSPPLLK	1.108833579	2	4.37356
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.176829303	3	4.9156
P31210	QLEVILNKPGLK	0.722677714	2	3.41556
P31210	REEIFYCGK	0.673604811	2	3.14858
P31210	RQLEVILNKPGLK	0.763440875	3	4.26637
P31210	SNLCATWEALEACK	0.944182018	2	4.40664
P31210	SNLCATWEALEACKDAGLVK	0.732155992	2	5.079
P31210	TAIDEGYR	0.826936645	2	2.57374
P31210	TQAQIVLR	0.840881308	2	3.02636
P31210	YKPVTNQVECHPYFTQTK	0.96283762	2	5.72203
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**2.170384995**	**0.07812**	**2**
P31230	GAEADQIIEYLK	1.742603769	2	2.98636
P31230	TVVSGLVNHVPLEQMQNR	1.050525724	3	3.53475
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.99931411**	**0.99889**	**6**
P31399	ANVDKPGLVDDFK	1.043451425	2	3.80185
P31399	IPVPEDKYTALVDAEEKEDVK	0.856739407	3	3.32943
P31399	NCAQFVTGSQAR	1.056891	2	4.26891
P31399	NMIPFDQMTIDDLNEVFPETK	0.938047213	2	5.45486
P31399	SWNETFHTR	1.135952057	2	2.75927
P31399	YTALVDAEEKEDVK	0.962488974	2	3.77698
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.923913628**	**0.99756**	**5**
P32089	FIHDQTSSNPK	0.80989458	1	3.4529
P32089	GLSSLLYGSIPK	1.010302563	2	3.39515
P32089	NTLDCGVQILK	0.943224142	2	2.39629
P32089	SHGVLGLYR	1.051168705	1	2.02628

P32089	TQLQLDER	0.974909163	2	2.47254
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.985284696**	**0.99603**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	0.962602729	3	4.55885
P32198	GDTNPNIPKPTR	1.041735958	2	2.40292
P32198	MTALAQDFAVNLGPK	1.151684248	2	4.18235
P32198	SCTMESCNFVQAMMDPK	1.425233459	2	2.77267
P32198	TSPDAFIQLALQLAHYK	1.057577823	2	3.49923
P32198	YLESVRPLMK	1.063271481	2	2.32333
P32232	**CBS Cystathionine beta_synthase**	**2.303573497**	**0.0003**	**9**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.191871563	3	5.95485
P32232	ALGAEIVR	1.115586699	1	2.04501
P32232	CIIVMPEK	1.255847206	2	2.51768
P32232	FDSPESHVGVAWR	1.036596775	2	3.50131
P32232	NASNPLAHYDDTAEEILQQCDGK	1.376619348	2	5.66158
P32232	SNDDDSFAFAR	1.033860825	2	3.30077
P32232	VDMLVASAGTGGTITGIAR	1.56550235	2	4.62982
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.484694768	3	4.23577
P32232	VRPSDEVCK	0.762410088	3	3.75438
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**2.008825773**	**0.42523**	**11**
P32551	AVAFQNPQTR	0.737093433	2	3.35116
P32551	AVAQGNLSSADVQAAK	2.622816131	2	5.3487
P32551	GNNTTSLLSQSVAK	0.961966985	2	4.15908
P32551	IIENLHDVAYK	1.062216891	2	3.83772
P32551	ITSEELHYFVQNHFTSAR	1.029509496	3	4.04292
P32551	NALANPLYCPDYR	1.351730265	2	3.74444
P32551	RGNNTTSLLSQSVAK	0.686163326	2	3.30487
P32551	RWEVAALR	0.91707565	2	2.73014
P32551	SMTASGNLGHTPFLDEL	1.016609611	2	3.38016
P32551	TSAPGGVPLQPQELEFTK	0.987532234	2	4.04214
P32551	YENYNYLGTSHLLR	1.174803913	2	4.42947
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**2.040281738**	**3.8E-11**	**20**
P32755	AFEEEQALR	1.247678805	2	3.34721
P32755	DIAFEVEDCEHIVQK	1.27068667	2	4.08188
P32755	ENMDVLEELK	1.017494795	2	3.05278
P32755	EVVSHVIK	1.062492885	2	2.32575
P32755	FAVLQTYGDTTHTLVEK	1.358228183	2	5.25672
P32755	FLHFHSVTFWVGNAK	1.130631423	3	3.73515
P32755	FLPGFEAPTYK	1.224677125	2	2.7075
P32755	FWSVDDTQVHTEYSSLR	0.902597832	2	5.84082
P32755	GMEFLAVPSSYYR	1.562065007	2	3.28155
P32755	GNLTDLETNGVR	1.021503445	2	3.83297
P32755	HNHQGFGAGNFNSLFK	0.981836998	3	4.91846
P32755	ILVDYDEK	1.484148948	2	2.32865
P32755	IVFVLCSALNPWNK	1.26460403	2	2.96899
P32755	IVREPWVEEDKFGK	1.343982195	3	4.96986
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.294918124	3	7.34228
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK+Oxidation(20	1.672114928		
P32755	MGFEPLAYK	1.681772136	2	2.64896
P32755	SIVVANYEESIK	1.056278133	2	4.23279
P32755	SQIQEYVDYNGGAGVQHIALR	1.367214613	2	5.81498
P32755	TEDIITTIR	1.13578288	2	3.30782
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.924300722**	**1**	**2**
P33124	ALRPTIFPVVPR	1.471716117	2	3.02346
P33124	IENIYIR	1.043882263	2	2.80915

P33273	**CP255 Cytochrome P450 2C55**	**1.921410351**	**0.97087**	**2**
P33273	FDYKDENFLNLMEK	0.609518878	3	4.88464
P33273	NFAEIK	1.017251823	1	1.90921
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.994707173**	**1**	**26**
P34058	ADLINNLGTIAK	1.017830718	2	4.08765
P34058	EDQTEYLEER	1.818204503	2	3.55983
P34058	EGLELPEDEEEK	0.874330352	2	2.51252
P34058	EGLELPEDEEEKK	1.314773056	2	2.56271
P34058	EGLELPEDEEEKKK	1.011836505	2	3.1537
P34058	ELISNASDALDK	1.054328653	2	3.6059
P34058	FYEAFSK	0.912809443	1	1.95922
P34058	GVVDSEDLPLNISR	1.09153469	2	4.80619
P34058	HFSVEGQLEFR	1.017171317	2	2.66939
P34058	HLEINPDHPIVETLR	1.05223597	2	4.58497
P34058	HSQFIGYPITLYLEK	1.840772268	2	3.66626
P34058	IDIIPNPQER	0.901382973	2	3.05708
P34058	KHLEINPDHPIVETLR	1.12710057	2	4.83644
P34058	LGIHEDSTNR	0.976685664	2	2.90844
P34058	NPDDITQEEYGEFYK	0.799469154	2	4.96354
P34058	RAPFDLFENK	1.055384016	2	3.04066
P34058	RAPFDLFENKK	0.347111152	2	2.52583
P34058	SIYYITGESK	0.97209393	2	3.19449
P34058	SLTNDWEDHLAVK	1.120382684	2	4.32713
P34058	TLTLVDTGIGMTK	1.171868971	2	4.27911
P34058	TLTLVDTGIGMTK+Oxidation(10	1.578458894		
P34058	VILHLKEDQTEYLEER	1.034816498	3	4.04589
P34058	YESLTDPSK	0.996438629	1	2.70948
P34058	YESLTDPSKLDSGK	0.944583389	2	3.88405
P34058	YHTSQSGDEMTSLSEYVSR	1.145528258	2	5.48955
P34058	YIDQEELNK	1.167008135	2	3.48696
P34064	**PSA5 Proteasome subunit alpha type_5**	**2.327220372**	**0.53528**	**7**
P34064	AIGSASEGAQSSLQEVYHK	1.102717065	2	4.51446
P34064	EELEEVIKDI	1.218630176	2	2.5477
P34064	GVNTFSPEGR	1.196000741	2	3.08947
P34064	ITSPLMEPSSIEK	0.91177178	2	2.61133
P34064	LNATNIELATVQPGQNFHMFTK	1.477672284	3	3.44823
P34064	SSLIILK	1.70833272	2	2.39765
P34064	STTLKEAIKSSLIILK	0.860552549	2	2.3154
P34067	**PSB4 Proteasome subunit beta type_4**	**2.031161546**	**0.96621**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	0.973980775	2	3.13328
P34067	TQNPMVTGTSVLGVK	1.010980923	2	3.35656
P34067	VNDSTMLGASGDYADFQYLK	1.189089949	2	4.49448
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**2.028992596**	**1**	**2**
P35171	GGTSDALLYR	1.065012216	2	3.41543
P35171	LFQEDNGMPVHLK	1.020040938	2	4.38558
P35213	**1433B 14_3_3 protein beta/alpha**	**1.750609873**	**0.27994**	**7**
P35213	AVTEQGHELSNEER	0.793264636	2	4.48909
P35213	EKIEAELQDICSDVLELLDK	1.373015105	3	4.98565
P35213	QTTVSNSQQAYQEAFEISK	0.818506329	2	5.46302
P35213	TAFDEAIAELDTLNEESYK	1.193236924	2	4.81657
P35213	YDDMAAAMK	1.840471959	2	3.09257
P35213	YLILNATHAESK	1.362197122	2	3.58558
P35213	YLSEVASGDNK	1.003214532	2	3.04129
P35278	**RAB5C Ras_related protein Rab_5C**	**1.678517535**	**0.60305**	**4**
P35278	FEIWDTAGQER	0.733459702	2	3.16344
P35278	GVDLQESNPASR	1.008608643	2	2.70709

P35278	LVLLGESAVGK	1.120175233	2	2.75
P35278	NEPQNAAGAPGR	0.731007498	2	2.99653
P35427	**RL13A 60S ribosomal protein L13a**	**2.154963809**	**0.99551**	**2**
P35427	CEGINISGNFYR	1.094956668	2	3.14189
P35427	YQAVTATLEEK	1.189865035	2	3.1429
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**2.01507503**	**0.99197**	**2**
P35434	AQSELSGAADEAAR	1.010945389	2	4.66613
P35434	IEANEALVK	0.899418682	2	2.84138
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.943855195**	**1**	**7**
P35435	GLCGAIHSSVAK	0.842498525	2	3.69161
P35435	HLIIGVSSDR	0.960651575	2	3.0661
P35435	NASDMIDK	1.095318033	2	2.35038
P35435	NDMAALTAAGK	1.024180425	2	3.94464
P35435	NDMAALTAAGK+Oxidation(2	1.228037878		
P35435	THSDQFLVSFK	0.937624734	1	3.03538
P35435	VYGTGSLALYEK	1.160240444	2	3.10062
P35559	**IDE Insulin_degrading enzyme**	**2.037173415**	**0.52789**	**4**
P35559	AIEDMTEEAFQK	0.941406532	2	3.13722
P35559	DREVNAVDSEHEK	1.029262971	3	3.57133
P35559	SNPGHYLGHLIGHEGPGSLLSELK	0.791208681	3	3.30114
P35559	YTLETRPNQEGIDVR	1.390433905	2	2.53031
P35565	**CALX Calnexin**	**1.923667327**	**0.99973**	**11**
P35565	AEEDEILNR	1.104066953	2	2.69464
P35565	EIEDPEDRKPEDWDERPK	1.18139667	3	3.33168
P35565	GSLSGWILSK	1.666885109	2	2.50193
P35565	KIPNPDFFEDLEPFR	0.972365663	3	4.29534
P35565	NKGDEEEEEEKLEEK	0.961736486	3	5.05456
P35565	TDAPQPDVK	1.167633764	2	2.38776
P35565	TDAPQPDVKDEEGKEEEK	0.762658292	3	4.36467
P35565	TSELNLDQFHDK	1.144303025	2	3.6907
P35565	VVDDWANDGWGLK	0.864850781	2	4.23063
P35565	VVDDWANDGWGLKK	0.646225661	2	2.80435
P35565	WEVDEMKETK	0.968253686	2	2.8193
P35571	**GPDM Glycerol_3_phosphate dehydrogenase_ mitochondrial**	**1.860334886**	**0.84517**	**2**
P35571	AITNLDVEQYR	0.761490016	2	2.71551
P35571	KQEELETATR	0.901247013	2	2.33559
P35704	**PRDX2 Peroxiredoxin_2**	**2.004292785**	**1**	**5**
P35704	EGGLGPLNIPLLADVTK	1.067791972	2	3.47604
P35704	KEGGLGPLNIPLLADVTK	1.030381589	2	4.86094
P35704	NDEGIAYR	0.982932572	1	1.95971
P35704	QITVNDLPVGR	0.927601331	2	3.03412
P35704	SLSQNYGVLK	0.964024917	2	2.47037
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**2.026434196**	**0.73593**	**5**
P35738	AAVEQVPVEPYK	0.795626381	2	2.42939
P35738	GLLLSCIEDKNPCIFFEPK	1.537790248	2	3.66665
P35738	MNLFQSITSALDNSLAK	1.332384782	2	3.59215
P35738	SGDLFNCGSLTIR	1.133966391	2	3.01778
P35738	VCGYDTPFPHIFEPFYIPDK	1.187400996	3	3.49018
P35815	**PPM1B Protein phosphatase 1B**	**2.070265315**	**0.99995**	**2**
P35815	IQNAGGSVMIQR	1.052177002	2	2.82335
P35815	SGFALEPSVENVK	1.041303345	2	3.62746
P36201	**CRIP2 Cysteine_rich protein 2**	**1.864509457**	**0.85526**	**3**
P36201	ASSVTTFTGEPNMCPR	0.664047574	2	3.68081
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.01404436	3	6.47508
P36201	GVNTGAVGSYIYDKDPEGTVQP	0.872176414	2	4.31891

P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**1.875811615**	**0.98256**	**11**
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.228965722	3	3.61061
P36365	ASLYNSVVSNSSK	0.949989548	2	2.92251
P36365	CCLEEGLEPTCFER	0.734536736	2	4.28105
P36365	FTEHVEEGR	0.934623994	2	3.02412
P36365	HSGFGLCYCK	1.123285107	2	3.24699
P36365	NLLPTPVVSWLISK	1.313731885	2	2.49186
P36365	SCDLGGLWR	1.166360378	2	2.76923
P36365	TQLREPVLNDELPGR	0.805978809	3	4.57949
P36365	VAIVGAGVSGLASIK	2.147715296	2	2.82332
P36365	VEDGQASLYK	0.905645212	2	3.46588
P36365	VLVVGMGNSGTDIAVEASHLAK	1.0161328	2	4.55916
P36506	**MP2K2 Dual specificity mitogen_activated protein kinase kinase 2**	**1.994565821**	**0.64203**	**2**
P36506	ISELGAGNGGVVTK	1.492049372	2	2.36098
P36506	KLEELDLDEQQR	0.94946143	2	3.03969
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.904410301**	**0.99643**	**8**
P36511	ANIIAWALAQIPQK	0.87538753	3	5.48749
P36511	FVNVWTYELPR	1.202113976	2	3.6615
P36511	FVTFPTSFSSHDLENFFTR	1.178228222	2	4.44904
P36511	GHEVTVLRPSAFVFLDPK	1.263346364	3	3.96885
P36511	IILEELVQK	1.057153427	2	3.53459
P36511	NAMWLSTIHHDQPTKPLDR	1.056784319	3	3.41859
P36511	SDLLNALEEVIDNPFYK	0.113747312	3	5.33736
P36511	TLGRPTTLAEIMGK	1.100886225	2	3.1035
P36536	**SAR1A GTP_binding protein SAR1a**	**1.961183815**	**0.97372**	**2**
P36536	IDRTDAISEEK	0.892671991	2	2.4917
P36536	VELNALMTDETISNVPILILGNK	0.978615457	3	5.66942
P36953	**AFAM Afamin**	**1.937971668**	**0.91978**	**2**
P36953	FTDSENVCQER	0.948111553	2	2.99725
P36953	SLAMVQQECK	1.200842674	2	2.75056
P36972	**APT Adenine phosphoribosyltransferase**	**1.960350036**	**1**	**2**
P36972	IDYIAGLDSR	0.867388611	2	3.04337
P36972	SFPDFPIPGVLFR	1.042614933	2	3.25029
P37397	**CNN3 Calponin_3**	**1.931934446**	**0.53349**	**5**
P37397	AGQSVIGLQMGTNK	0.939862059	2	3.37461
P37397	LTLQPVDNSTISLQMGTNK	1.26081746	2	2.95356
P37397	MQTDKPFDQTTISLQMGTNK	1.074141911	3	3.55222
P37397	VNESSLNWPQLENIGNFIK	1.021619954	2	3.15147
P37397	YDQQAEEDLR	1.208969309	2	3.15414
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.888137087**	**0.29354**	**8**
P38650	DFPLNDLLSATELDKIR	1.147407247	2	2.38742
P38650	ILDDDTIITTLENLK	1.205261845	2	2.50648
P38650	QLQNISQAAAAGGAK	0.948869322	2	3.37664
P38650	VLLTTQGVDMISK	1.658008143	2	2.663
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	0.761970545	3	5.4378
P38650	VQGLTVEQAEAVAR	0.944262427	2	3.27985
P38650	VQVALEELQDLK	1.029848923	2	3.02736
P38650	VTDFGDKVEDPTFLNQLQSGVNR	1.145011183	3	4.16205
P38652	**PGM1 Phosphoglucomutase_1**	**1.991225876**	**0.0202**	**17**
P38652	ADNFEYSDPVDGSISK	1.045359503	2	4.82459
P38652	AIGGIILTASHNPGGPNGDFGIK	1.077933774	2	5.7588
P38652	FFGNLMDASK	1.178678433	2	2.51639
P38652	FNISNGGPAPEAITDK	1.181026774	2	4.30233
P38652	INQDPQVMLAPLISIALK	1.142190501	3	4.60659
P38652	KQRVEDILK	1.160151147	1	2.02672

P38652	LSGTGSAGATIR	1.462339733	2	3.48021
P38652	LVIGQNGILSTPAVSCIIR	1.439841848	2	4.08125
P38652	NIFDFNALK	1.215898071	2	2.92314
P38652	QEATLVVGGDGR	1.061278237	2	3.20018
P38652	QQFDLENK	0.75840935	1	2.12824
P38652	SGEHDFGAAFDGDGDR	0.873234868	2	4.4598
P38652	SGEHDFGAAFDGDGDRNMILGK	0.972304016	3	3.7608
P38652	TIEEYAICPDLK	0.89525074	2	4.43188
P38652	TQAYPDQKPGTSGLR	1.075276592	2	3.4881
P38652	VFQGNANYAENFIQSIVSTVEPALR	1.449611343		
P38652	YDYEEVEAEGANK	4.582605311	2	5.18105
P38656	**LA Lupus La protein homolog**	**2.471605457**	**0.71177**	**2**
P38656	ITDDQQESLNK	1.30584694	2	4.19315
P38656	LDEGWVPLETMIK	1.203975586	2	2.99039
P38659	**PDIA4 Protein disulfide_isomerase A4**	**2.283577144**	**0.98845**	**22**
P38659	DLGLSESGEDVNAAILDESGKK	2.649793393	2	5.15013
P38659	DNDPPIAVAK	0.879415534	2	2.40049
P38659	EVSQPDWTPPPEVTLTLTK	0.780411901	2	3.55213
P38659	FDVSGYPTIK	1.27296548	2	3.49007
P38659	FDVSGYPTLK	1.27296548	2	3.49007
P38659	FHHTFSTEIAK	1.127814394	3	3.50149
P38659	FIDEHATK	0.785513364	2	2.46554
P38659	FIDEHATKR	0.558052006	2	2.55172
P38659	GQAVDYDGSR	0.774157849	2	2.66653
P38659	GRPFDYNGPR	1.079134661	2	2.87645
P38659	IDATSASMLASK	0.943118028	2	3.97559
P38659	IDATSASMLASK+Oxidation(7	0.835302015		
P38659	KGQAVDYDGSR	2.093188761	2	2.93026
P38659	MDATANDITNDR	0.702839097	2	3.95544
P38659	MHVMDVQGSTEASAIK	1.168537616	2	4.62288
P38659	MHVMDVQGSTEASAIKDYVVK	0.811462944	3	4.59957
P38659	RFDVSGYPTLK	0.972281538	2	3.28803
P38659	RSPPIPLAK	1.071995227	2	2.40611
P38659	TFDAIVMDPK	0.914338637	2	3.53451
P38659	VDATEQTDLAK	1.114541265	2	4.12692
P38659	VEGFPTIYFAPSGDK	1.609255023	2	3.44627
P38659	YGIVDYMVEQSGPPSK	0.839305575	2	5.10871
P38718	**BR44 Brain protein 44**	**2.040973299**	**0.99691**	**2**
P38718	LRPLYNHPAGPR	1.031401876	2	2.82985
P38718	VELLLPK	0.906193582	1	2.22143
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**1.922718903**	**0.99991**	**5**
P38918	EEHFNGIALVEK	1.043919849	2	2.53456
P38918	FYAFNPLAGGLLTGR	1.154086243	2	4.63171
P38918	MDVTSSSASVR	0.801067095	2	3.58634
P38918	RMDVTSSSASVR	0.776866416	2	3.85364
P38918	TTYGPTAPSMISAAVR	0.946322507	2	3.96068
P38983	**RSSA 40S ribosomal protein SA**	**2.157482477**	**0.00752**	**8**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.262021724	3	5.86294
P38983	AIVAIENPADVSVISSR	1.115505386	2	4.80864
P38983	FAAATGATPIAGR	0.643020045	2	3.16064
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.409500362	3	3.62384
P38983	FTPGTFTNQIQAAFR	0.95863579	2	4.63599
P38983	KSDGIYIINLK	2.556995177	2	3.52242
P38983	SDGIYIINLK	1.150229705	2	3.02165
P38983	YVDIAIPCNNK	1.085229377	2	3.55075
P39032	**RL36 60S ribosomal protein L36**	**2.325916115**	**0.97466**	**2**
P39032	EELSNVLAAMR	1.132160166	2	2.40552

P39032	KREELSNVLAAMR	1.218228344	3	3.50914
P39052	**DYN2 Dynamin_2**	**2.198232124**	**0.79393**	**2**
P39052	ESSLILAVTPANMDLANSDALK	1.24193904	2	2.36734
P39052	NLVDSYVAIINK	1.118094129	2	3.11987
P40112	**PSB3 Proteasome subunit beta type_3**	**2.416839753**	**0.00798**	**2**
P40112	FGIQAQMVTTDFQK	1.759378369	2	3.43311
P40112	FGPYYTEPVIAGLDPK	1.251445486	2	3.09585
P40307	**PSB2 Proteasome subunit beta type_2**	**2.173846398**	**0.53674**	**3**
P40307	FILNLPTFSVR	1.72124111	2	3.28235
P40307	NGYELSPTAAANFTR	1.031806002	2	4.02458
P40307	VIDKDGIHNLENITFTK	1.027788814	2	4.03379
P41034	**TTPA Alpha_tocopherol transfer protein**	**2.440403066**	**0.68378**	**4**
P41034	AECPELSADLHPR	1.57529684	2	2.98702
P41034	AQEEGVPETPQPLTDAFLLR	1.370253507	2	3.71279
P41034	QLNEQPDHSPLVQPGLAELR	1.169502203	3	4.05484
P41034	VSLITSELIVQEVETQR	1.363549893	2	2.9696
P41123	**RL13 60S ribosomal protein L13**	**2.009512953**	**0.68711**	**3**
P41123	LATQLTGPVMPIR	1.946181436	2	3.12273
P41123	STESLQANVQR	0.962094177	2	3.88965
P41123	VDTWFNQPAR	1.010304868	2	3.46971
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**2.279977417**	**0.97404**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.257318831	2	4.24839
P41498	IELLGSYDPQK	1.045630253	2	3.22101
P41498	LVTDENVSDNWR	0.761226413	2	3.76149
P41542	**USO1 General vesicular transport factor p115**	**1.95748113**	**0.74206**	**14**
P41542	AWFEVGDENPGWSAQK	1.96337591	2	4.66609
P41542	CQNEQLQTAVTQQASQIQQHK	0.83893862	3	5.30596
P41542	EQDDLLVLLADQDQK	1.364651161	2	2.53703
P41542	GVMGGQSAGPQHTEAETIQK	1.01823574	2	4.35896
P41542	IVAFENAFER	0.996958716	2	3.05438
P41542	LQTENSELQQR	1.005284044	2	3.13897
P41542	LREEIEELR	0.915928569	2	2.72273
P41542	NNNSNQNFFK	0.847444691	2	2.71611
P41542	QLGPPVQQIILVSPMGVSK	1.556395203	2	4.0115
P41542	SHQVLLQSQLAEK	0.673797305	2	2.95188
P41542	SQLCSQSLEITR	1.132449975	2	3.36524
P41542	SVPVEGESELVTAAK	0.906920867	2	4.15425
P41542	TLEQHDNIVTHYK	0.758148755	2	3.904
P41542	VLVSPTNPPGATSSCQK	0.957204509	2	3.92053
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**2.219118913**	**0.99899**	**20**
P41562	ATDFVVPGPGK	1.006450532	2	3.63243
P41562	CATITPDEK	1.11073172	2	2.72004
P41562	DIFQEIYDK	0.94560455	1	2.39727
P41562	DLAACIK	0.625043637	1	1.90825
P41562	FKDIFQEIYDK	0.960187323	3	4.39488
P41562	GQETSTNPIASIFAWSR	1.041284586	2	4.79303
P41562	IHGGSVVEMQGDEMTR	1.293921954	2	5.30362
P41562	KIHGGSVVEMQGDEMTR	1.070605266	2	3.69044
P41562	LIDDMVAQAMK	1.323281985	2	4.45949
P41562	LIDDMVAQAMK+Oxidation(4	1.274103306		
P41562	LIDDMVAQAMK+Oxidation(9	0.863510186		
P41562	LILPYVELDLHSYDLGIENR	1.935974447	2	4.86949
P41562	LVTGWVKPIIIGR	1.218478436	2	3.24898
P41562	SDYLNTFEFMDK	1.531893144	2	4.46038
P41562	SDYLNTFEFMDK+Oxidation(9	2.754497174		

P41562	SEGGFIWACK	0.928274325	2	3.30598
P41562	SIEDFAHSSFQMALSK	1.170217696	2	5.08409
P41562	TVEAEAAHGTVTR	1.145599916	2	3.81893
P41562	VEITYTPK	0.971718048	2	2.45448
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.469550715	3	3.82442
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.97739108**	**0.99999**	**4**
P42123	DYSVTANSK	3.359474894	2	2.54543
P42123	IVADKDYSVTANSK	1.275720146	2	3.62665
P42123	SLADELALVDVLEDK	0.841204652	2	3.6337
P42123	VIGSGCNLDSAR	1.176655718	2	3.80732
P42228	**STAT4 Signal transducer and activator of transcription 4**	**2.035595732**	**0.65814**	**2**
P42228	FHSVEPYNK	1.336317658	1	1.91816
P42228	GDKGYVPSVFIPISTIR	0.918146027	2	2.73883
P42667	**SC11A Signal peptidase complex catalytic subunit SEC11A**	**2.151715972**	**0.91492**	**3**
P42667	GDLLFLTNR	1.12892939	2	2.43788
P42667	MLSLDFLDDVR	1.037201965	2	3.34428
P42667	VGEIVVFR	1.104747892	2	3.27065
P42676	**NEUL Neurolysin_ mitochondrial**	**1.930824423**	**0.5276**	**3**
P42676	AELGALPDDFIDSLEK	1.288366642	2	3.32762
P42676	NLILKPGGSLDGMDMLQNFLQR	1.309099788	3	4.1433
P42676	NLNEDDTSLVFSK	0.921608858	2	3.38772
P42930	**HSPB1 Heat shock protein beta_1**	**2.674402841**	**0.77938**	**2**
P42930	AQIGGPESEQSGAK	1.296397769	2	3.39337
P42930	VSLDVNHFAPEELTVK	2.441228306	2	2.58121
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.938804403**	**0.62342**	**10**
P42932	AIAGTGANVIVTGGK	1.196124178	2	2.75237
P42932	AVDDGVNTFK	1.218734962	2	2.51088
P42932	ELEVQHPAAK	1.341373028	2	2.85769
P42932	GEENLMDAQVK	0.957311924	2	3.58777
P42932	GSTDNLMDDIER	1.316549207	2	2.76197
P42932	HEKEDGAISTIVLR	2.301559748	2	2.92369
P42932	HFSGLEEAVYR	1.218901036	2	2.65739
P42932	NVGLDIEAEVPAVK	1.288860621	2	4.01113
P42932	QITSYGETCPGLEQYAIK	0.871454805	2	4.87195
P42932	TAEELMNFSK	1.048492883	2	2.58773
P43244	**MATR3 Matrin_3**	**2.373032728**	**0.99158**	**5**
P43244	ITPENLPQILLQLK	1.255816849	2	3.42861
P43244	NTHCSSLPHYQK	1.079918295	2	2.31662
P43244	TEEGPTLSYGR	1.077426264	2	2.55898
P43244	TENPAEGKEQEEK	0.83422403	2	3.38239
P43244	YQLLQLVEPFGVISNHLILNK	1.506596799	3	3.76019
P43274	**H14 Histone H1.4**	**1.866374518**	**0.97133**	**4**
P43274	ALAAAGYDVEK	0.987606748	2	3.86132
P43274	ALAAAGYDVEKNNSR	0.184918916	2	3.29513
P43274	SGVSLAALK	0.806259883	2	2.99182
P43274	SGVSLAALKK	0.638005769	2	2.68434
P43278	**H10 Histone H1.0**	**2.181589432**	**0.9971**	**2**
P43278	VGENADSQIK	0.839416632	2	3.4397
P43278	YSDMIVAAIQAEK	1.125713812	2	4.47286
P43883	**PLIN2 Perilipin_2**	**2.650935718**	**0.49572**	**2**
P43883	DSVASTVSGVVDK	1.35829778	2	2.35521
P43883	LEPQIAVANTYACK	1.796530246	2	3.94471
P45591	**COF2 Cofilin_2**	**3.101857652**	**0.99822**	**2**
P45591	HEWQVNGLDDIKDR	1.254766773	3	4.85484
P45591	QILVGDIGDTVEDPYTSFVK	1.724993643	2	3.86046

P45592	**COF1 Cofilin_1**	**2.227887464**	**0.99256**	**5**
P45592	EILVGDVGQTVDDPYTTFVK	1.165150831	2	5.11072
P45592	HELQANCYEEVK	0.980045065	2	3.83019
P45592	HELQANCYEEVKDR	1.070725984	3	5.62793
P45592	MLPDKDCR	1.029276909	2	2.33667
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.315587668	3	4.80309
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.79384965**	**0.45039**	**4**
P45878	GWDQGLLGMCEGEK	1.279108059	2	4.3016
P45878	KGDVLHMHYTGK	0.710558771	2	3.8757
P45878	KLVIPSELGYGER	1.216154915	2	2.74943
P45878	LVIPSELGYGER	1.254679901	2	2.79427
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**2.138136053**	**1**	**17**
P45953	AMVENGGLVTSNPLR	0.909988569	2	4.05193
P45953	AMVENGGLVTSNPLRV	1.13925577	2	4.19659
P45953	ASNTSEVYFDGVK	1.004692504	2	3.60534
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.393458293	3	5.12188
P45953	ENMASLQSNPQQQELFR	1.089486481	2	4.24987
P45953	FFEEVNDPAK	0.876684608	2	3.02512
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.071945017	3	5.58398
P45953	GIVNEQFLLQR	1.091879575	2	3.14125
P45953	IFEGTNDILR	1.57008727	2	3.14642
P45953	NDSLEKVEEDTLQGLK	1.160966854	2	3.64011
P45953	NPLGNVGLLIGEASK	1.381726592	2	3.70709
P45953	SFGGVTHGLPEK	1.070187694	2	2.60605
P45953	SFGGVTHGLPEKK	1.080748431	2	2.95757
P45953	SGELAVQALEQFATVVEAK	0.926618212	3	4.12116
P45953	SLSEGYPTAQHEK	1.015019809	2	3.42979
P45953	TGIGSGLSLSGIVHPELSR	1.179120715	3	4.60682
P45953	VEEDTLQGLK	1.011828701	2	2.76958
P46061	**RAGP1 Ran GTPase_activating protein 1**	**3.462360972**	**0.03954**	**2**
P46061	TAVLDAIDALMK	1.792719961	2	3.1766
P46061	VINLNDNTFTEK	1.188754466	2	2.51227
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.902499701**	**0.02017**	**4**
P46418	AILNYIATK	0.466079285	2	3.29148
P46418	SDGSLMFEQVPMVEIDGMK	0.814507443	2	4.38341
P46418	SHGQDYLVGNK	0.40407002	2	3.63771
P46418	VSNLPTVK	0.931605704	2	2.76883
P46425	**GSTP2 Glutathione S_transferase P 2**	**1.963574659**	**0.55245**	**3**
P46425	ALPGHLKPFETLLSQNQGGK	0.673303923	2	4.16265
P46425	FEDGDLTLYQSNAILR	0.686396842	2	4.53322
P46425	MLLADQGQSWK	1.128491091	2	2.50915
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.883461665**	**0.49124**	**24**
P46462	AIANECQANFISIK	1.183652544	2	3.70608
P46462	EDEEESLNEVGYDDIGGCR	5.136175153	2	5.30883
P46462	ELQELVQYPVEHPDK	1.004380929	2	4.56693
P46462	ETVVEVPQVTWEDIGGLEDVK	1.062705231	2	4.47217
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.583789366	2	4.11236
P46462	EVDIGIPDATGR	0.870655317	2	2.73949
P46462	GDDLSTAILK	1.250349165	2	3.06045
P46462	GGNIGDGGGAADR	2.092964966	2	3.05514
P46462	GILLYGPPGTGK	0.879195768	2	2.85287
P46462	IVSQLLTLMDGLK	1.473445333	2	3.5126
P46462	KYEMFAQTLQQSR	0.921982107	2	4.05685
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.600895414	3	6.14338
P46462	LAGESESNLRKAFEEAEK	0.901863356	2	2.57452
P46462	LDQLIYIPLPDEK	1.1634543	2	4.50735

P46462	LEILQIHTK	1.121254625	2	2.82824
P46462	LGDVISIQPCPDVK	0.945819773	2	3.96911
P46462	LIVDEAINEDNSVVSLSQPK	1.216883063	2	5.45228
P46462	MDELQLFR	1.289132162	2	3.19064
P46462	MTNGFSGADLTEICQR	0.797919503	2	4.46241
P46462	NAPAIIFIDELDAIAPK	0.735422994	2	4.93198
P46462	QTNPSAMEVEEDDPVPEIR	0.840633959	2	4.39636
P46462	RSVSDNDIR	0.790762206	2	2.60967
P46462	VINQILTEMDGMSTK	2.455609784	2	4.59131
P46462	WALSQSNPSALR	1.478237184	2	3.45111
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**2.272156194**	**0.41646**	**5**
P46664	FIEDELQIPVK	0.980454856	2	3.15279
P46664	LDILDMFTEIK	0.985161395	2	3.26603
P46664	MCDLVSDFDGFSER	1.951685661	2	3.66236
P46664	VGIGAFPTEQDNEIGELLQTR	1.646454265	2	4.38233
P46664	VVDLLAQDADIVCR	2.071132931	2	3.51888
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.844639827**	**0.06391**	**4**
P46720	ESEHTDVHGSPQVENDGELK	0.951752509	3	3.74553
P46720	GIGETPIVPLGISYIEDFAK	1.02811801	2	3.80164
P46720	GVQHQLHVESK	0.764610136	2	3.02143
P46720	SENSPLYIGILEMGK	1.267250495	2	3.43931
P46844	**BIEA Biliverdin reductase A**	**1.894491455**	**0.94715**	**4**
P46844	FGVVVVGVGR	0.974602933	2	2.83465
P46844	GLLSWIEEK	1.477192048	2	2.5176
P46844	LLDQVSAEDLAAEK	0.987900144	2	4.65823
P46844	MTVQLETQNK	0.921760614	2	2.49603
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**2.199023451**	**0.55313**	**10**
P46953	AQGSVALSVTQDPACK	0.926625204	2	4.52156
P46953	ASFQPPVCNK	1.123558644	2	2.55939
P46953	DLGTQLAPIIQEFFHSEQYR	1.063382561	2	3.54777
P46953	FANTMGLVIER	1.120921596	2	3.56083
P46953	METELDGLR	1.061097469	2	2.74081
P46953	QDVDVWLWQLEGSSK	1.374317167	2	2.34734
P46953	QGEIFLLPAR	0.660826691	2	2.76677
P46953	RMETELDGLR	1.203536807	2	2.48808
P46953	TGKPNPDQLLK	1.061436973	3	3.58246
P46953	YYVGDTEDVLFEK	1.281620238	2	3.54466
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.959790417**	**0.31871**	**7**
P46978	FESVIHEFDPYFNYR	1.266661412	2	2.34324
P46978	FGQVYTEAK	1.226416998	2	2.72455
P46978	FHNWFDDR	1.070536935	2	2.54638
P46978	FYSLLDPSYAK	1.394975137	2	2.89661
P46978	NLDISRPDKK	1.151805233	2	2.41254
P46978	VGQAMASTEEK	0.917182684	2	3.17066
P46978	VGQAMASTEEK+Oxidation(4	1.016188904		
P47198	**RL22 60S ribosomal protein L22**	**2.167662114**	**0.98635**	**2**
P47198	AGNLGGGVVTIER	1.013788251	2	3.06414
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.421177902	3	5.5319
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**2.079356138**	**0.69795**	**4**
P47875	GFGFGQGAGALVHSE	1.276225829	2	3.15801
P47875	GLESTTLADKDGEIYCK	1.292497406	2	5.25659
P47875	HEEAPGHRPTTNPNASK	0.816499857	2	3.63392
P47875	NLDSTTVAVHGEEIYCK	1.025996626	2	4.72147
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.981364404**	**0.99674**	**3**

P47942	FQMPDQGMTSADDFFQGTK	0.991741081	2	4.07667
P47942	GLYDGPVCEVSVTPK	0.975762129	2	3.56534
P47942	SITIANQTNCPLYVTK	0.915247753	2	3.4281
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.829438796**	**0.99998**	**2**
P48004	NYTDDAIETDDLTIK	0.841534806	2	4.54366
P48004	YVAEIEKEKEENEK	1.001433003	2	5.43228
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**2.36128198**	**0.84727**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.295045659	3	5.67617
P48024	TLTTVQGIADDYDK	1.161768639	2	3.66818
P48037	**ANXA6 Annexin A6**	**2.015495054**	**0.72637**	**20**
P48037	AANDFNPDADAK	0.822956055	2	3.55206
P48037	AINEAYKEDYHK	1.072650777	2	3.39675
P48037	ALIEILATR	1.143287468	2	3.21706
P48037	ALLALCGGED	1.28679005	1	2.15071
P48037	CLIEILASR	0.689243618	2	2.65755
P48037	DAFVAIVQSVK	2.532499918	2	3.82655
P48037	DLESDIIGDTSGHFQK	1.582224787	2	4.43676
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.593013684	2	5.15064
P48037	GELSGDFEK	1.033076359	1	2.18069
P48037	GFGSDKESILELITSR	0.996717624	2	4.27583
P48037	GIGTDEATIIDIITQR	1.095291967	2	4.26473
P48037	GSVHDFADFDANQDAEALYTAMK	1.003609363	3	4.13674
P48037	QRQEICQSYK	0.754704779	2	3.19726
P48037	SEIDLLNIR	1.46944127	2	3.07096
P48037	SEISGDLAR	1.018080035	2	2.34455
P48037	SELDMLDIR	0.954499708	2	2.96092
P48037	SLEDALSSDTSGHFK	1.105218444	2	3.67535
P48037	TNEQIHQLVAAYK	0.884435136	2	4.02279
P48037	TNYDIEHVIK	0.959965154	2	3.0886
P48037	TTGKPIEASIR	1.172057098	2	2.53742
P48500	**TPIS Triosephosphate isomerase**	**2.111194207**	**0.99966**	**15**
P48500	CLGELICTLNAAK	1.524861048	2	3.56666
P48500	CNVSEGVAQCTR	0.964605948	2	3.95579
P48500	DLGATWVVLGHSER	1.575369291	2	4.1648
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.178715319	4	5.94006
P48500	HIFGESDELIGQK	0.985425366	2	4.68053
P48500	IAVAAQNCYK	1.293315427	2	2.7012
P48500	IIYGGSVTGATCK	1.242627294	2	4.33989
P48500	LPADTEVVCAPPTAYIDFAR	2.102584955	2	4.41963
P48500	RHIFGESDELIGQK	1.063172348	2	4.41649
P48500	TATPQQAQEVHEK	0.95887848	2	3.63929
P48500	TATPQQAQEVHEKLR	0.739405492	2	2.39976
P48500	VNHALSEGLGVIACIGEK	1.348030539	2	5.67491
P48500	VTNGAFTGEISPGMIK	1.154699517	2	4.8655
P48500	VVFEQTK	0.939916768	1	1.93335
P48500	VVLAYEPVWAIGTGK	1.1058765	2	4.53242
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**1.659731584**	**1E-15**	**4**
P48508	ASTLHLQTGNLLNWGR	1.196758421	3	4.01161
P48508	EFPDVLECTMSHAVEK	0.959804865	2	3.59297
P48508	INPDEREEMK	0.835651671	2	2.64371
P48508	TLNEWSSQISPDLVR	0.623068069	2	4.68486
P48675	**DESM Desmin**	**2.714491982**	**0.99003**	**3**
P48675	NISEAEEWYKSK	1.145420689	2	2.32562
P48675	TSGGAGGLGSLR	1.146254896	2	2.70108
P48675	VSDLTQAANK	1.655522531	2	2.983
P48679	**LMNA Prelamin_A/C**	**1.796651211**	**0.41429**	**19**

P48679	AAYEAELGDAR	1.290187356	2	2.36502
P48679	AQHEDQVEQYK	0.87531877	2	3.04657
P48679	AQHEDQVEQYKK	0.998565241	2	4.33551
P48679	GSHCSSSGDPAEYNLR	0.892050111	2	3.95042
P48679	IDSLSAQLSQLQK	1.036532148	2	3.16959
P48679	ITESEEVVSR	0.849790917	2	3.1554
P48679	LEAALGEAK	0.889433764	2	2.31631
P48679	LKDLEALLNSK	0.918614204	2	2.86412
P48679	LQEKEDLQELNDR	1.00880205	2	4.2282
P48679	MQQQLDEYQELLDIK	1.107592846	2	4.55441
P48679	NIYSEELR	0.975154429	1	2.05941
P48679	NSNLVGAAHEELQQSR	0.897804974	2	4.71077
P48679	SGAQASSTPLSPTR	0.816078134	2	3.79115
P48679	SLETENAGLR	0.934062512	2	2.86808
P48679	SVGGSGGGSFGDNLVTR	0.92872988	2	3.58402
P48679	TALINATGEEVAMR	0.989192099	2	3.57683
P48679	TLEGELHDLR	1.360904122	2	2.4925
P48679	TVLCGTCGQPADK	0.86939906	2	3.44474
P48679	VAVEEVDEEGK	0.990612272	2	3.1088
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**2.110508041**	**1**	**30**
P48721	AQFEGIVTDLIK	1.097844791	2	3.72062
P48721	ASNGDAWVEAHGK	1.082285185	2	3.81592
P48721	DAGQISGLNVLR	1.909012404	2	2.75738
P48721	DDIENMVK	1.282333945	1	2.02243
P48721	EQQIVIQSSGGLSK	1.163103639	2	3.86301
P48721	EQQIVIQSSGGLSKDDIENMVK	1.214370508	2	4.52976
P48721	ERVEAVNMAEGIIHDTETK	0.885857105	3	5.56512
P48721	ETAENYLGHTAK	1.057134407	2	3.1378
P48721	GAVVGIDLGTTNSCVAVMEGK	1.424107488	2	5.38531
P48721	LFEMAYK	0.888089717	2	2.30513
P48721	LLGQFTLIGIPPAPR	1.252894903	2	3.73202
P48721	MEEFKDQLPADECNK	10.87167784	2	4.60724
P48721	MEEFKDQLPADECNK+Oxidation(0	1.229187029		
P48721	MKETAENYLGHTAK	0.917340048	2	4.30801
P48721	MKETAENYLGHTAK+Oxidation(0	0.89792347		
P48721	NAVITVPAYFNDSQR	1.011909291	2	3.46472
P48721	QAVTNPNNTFYATK	1.003254006	2	3.80291
P48721	RETGVDLTK	0.730365404	2	2.32814
P48721	RYDDPEVQK	0.982247865	2	3.23068
P48721	RYDDPEVQKDTK	0.729276973	2	3.78626
P48721	SDIGEVILVGGMTR	1.085581849	2	3.98357
P48721	SQVFSTAADGQTQVEIK	0.713004591	2	4.60531
P48721	STNGDTFLGGEDFDQALLR	0.97484974	2	6.07848
P48721	TTPSVVAFTPDGER	0.809546607	2	3.39462
P48721	VEAVNMAEGIIHDTETK	1.223073815	2	4.57309
P48721	VINEPTAAALAYGLDK	1.536960506	2	3.88297
P48721	VLENAEGAR	0.876708098	2	3.09374
P48721	VQQTVQDLFGR	0.941199397	2	3.72915
P48721	YDDPEVQK	0.998655265	2	2.35081
P48721	YDDPEVQKDTK	0.741029602	2	2.74901
P48998	**INVO Involucrin**	**1.834642584**	**0.37509**	**2**
P48998	ELLDQRLDQELVNK	0.92461003	2	2.32528
P48998	HKLENLTQKEK	0.800395405	1	1.93864
P49025	**CTRO Citron Rho_interacting kinase**	**1.987593666**	**0.7586**	**2**
P49025	LEEQLEK	0.914217935	1	2.01041
P49025	LMMNQLEEDLVSARR+Oxidation(1	1.117389967		
P49134	**ITB1 Integrin beta_1**	**1.783461778**	**0.96137**	**3**

P49134	CNCQSHGIPASPK	0.833031072	2	3.34812
P49134	FCECDNFNCDR	0.783868409	2	3.36757
P49134	GEFFNELVGQQR	0.8656778	2	2.88348
P49186	**MK09 Mitogen_activated protein kinase 9**	**2.00185753**	**0.87378**	**2**
P49186	DLLSKMLVIDPDK	0.719659369	1	1.97777
P49186	VIEQLGTPSAEFMK	1.004942396	2	2.60854
P49242	**RS3A 40S ribosomal protein S3a**	**2.073647044**	**1**	**9**
P49242	ACQSIYPLHDVFVR	1.178036674	2	4.31543
P49242	ADGYEPPVQESV	0.851420825	1	2.08067
P49242	LIPDSIGKDIEK	1.063942504	2	2.51284
P49242	LITEDVQGK	0.950942322	2	2.56336
P49242	LMELHGEGGSSGK	1.065408322	2	3.5162
P49242	LMELHGEGGSSGK+Oxidation(1	0.967639254		
P49242	NCLTNFHGMDLTR	1.122493682	2	3.9812
P49242	TTDGYLLR	0.763913255	2	2.71638
P49242	VFEVSLADLQNDEVAFR	1.194382561	2	4.54017
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**2.364575796**	**0.99669**	**7**
P49432	EAINQGMDEELERDEK	1.80158714	2	3.71386
P49432	ILEDNSIPQVK	0.937282463	2	3.38225
P49432	IMEGPAFNFLDAPAVR	1.199249401	2	4.53161
P49432	IMEGPAFNFLDAPAVR+Oxidation(1	1.086249386		
P49432	TIRPMDIEAIEASVMK	1.491162461	3	4.4636
P49432	VFLLGEEVAQYDGAYK	1.105901049	2	4.2258
P49432	VTGADVPMPYAK	0.933681426	2	2.55439
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**2.002259115**	**0.99423**	**12**
P49889	CKEDALFNR	1.101086878	2	2.50345
P49889	FEEHYQQQMK	1.082120529	2	2.98775
P49889	FEEHYQQQMK+Oxidation(8	0.954266375		
P49889	FMEGQVPYGSWYDHVK	1.03717345	2	4.12992
P49889	IIQHTSFQEMK	0.773796668	2	2.88298
P49889	LIEFLER	1.099359055	2	2.47141
P49889	LIEFLERDPSAELVDR	1.660486681	3	5.17127
P49889	NEDLINGIK	0.963748278	2	3.08119
P49889	NNPCTNYSMLPETMIDLK	0.915140352	2	5.26169
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13	1.21455247		
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8	1.21455247		
P49889	SGSTWISEIVDMIYK	0.812062333	2	4.06547
P50137	**TKT Transketolase**	**1.969360722**	**0.02864**	**24**
P50137	AVELAANTK	0.792941375	1	2.09332
P50137	GITGIEDK	0.929232714	1	2.56275
P50137	GITGIEDKEAWHGKPLPK	0.967920201	3	3.60674
P50137	HQPTAIIAK	0.476956091	2	2.33053
P50137	IIALDGDTK	1.842629459	2	2.67016
P50137	ILATPPQEDAPSVDIANIR	1.305798207	2	4.80141
P50137	ISSDLDGHPVPK	1.088981225	2	3.37287
P50137	KISSDLDGHPVPK	1.011624621	2	3.84016
P50137	LAVSQVPR	1.234563179	2	2.36242
P50137	LAVSQVPRSGKPAELLK	0.787058141	2	2.58743
P50137	LDNLVAIFDINR	0.971516095	2	4.52468
P50137	LGQSDPAPLQHQVDVYQK	1.302375252	2	3.86
P50137	MFGIDKDAIVQAVK	1.19592359	2	4.85396
P50137	MFGIDKDAIVQAVK+Oxidation(0	1.049423164		
P50137	NMAEQIIQEIYSQVQSK	0.993378594	3	6.02296
P50137	NSTFSELFK	1.279401586	2	2.41564
P50137	QAFTDVATGSLGQGLGAACGMAYTGK	1.814281267	3	4.37783
P50137	SGKPAELLK	0.478288612	3	3.30089

P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	1.46788487	3	4.59071
P50137	SVPMSTVFYPSDGVATEK	1.149023571	2	4.50025
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3	1.336395931		
P50137	TSRPENAIIYSNNEDFQVGQAK	0.977285848	3	5.89408
P50137	VLDPFTIKPLDK	1.293891142	2	3.24046
P50137	VLDPFTIKPLDKK	1.107734143	2	2.53447
P50169	**RDH3 Retinol dehydrogenase 3**	**1.973626317**	**0.97191**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.085677581	3	5.03017
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1	1.105591807		
P50169	FQDSYMK	0.987369987	1	1.98619
P50169	GLWGLVNNAGISVPVGPNEWMR	1.047911484	3	3.36717
P50169	KLWDQTTEEVK	1.063310679	2	3.05005
P50169	KLWDQTTEEVKEIYGEK	0.838879183	3	4.97876
P50169	LWDQTTEEVK	0.876233065	2	3.17013
P50169	LWDQTTEEVKEIYGEK	0.717253265	2	4.8106
P50169	MSLVGGGYCISK	1.010407316	2	4.05312
P50237	**ST1C1 Sulfotransferase 1C1**	**1.881639221**	**0.94639**	**12**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.888726238	3	5.27929
P50237	DISEEVLNK	0.571923157	1	2.4687
P50237	DLHLGEQDLQPETR	1.041696983	2	4.62826
P50237	EVNGILMSK	0.801236161	1	1.91602
P50237	FLEKDISEEVLNK	0.722393165	2	2.88934
P50237	HPFIEWTLPSPLNSGLDLANK	1.541412512	3	4.03658
P50237	IWNFQAKPDDLLIATYAK	1.398030883	3	3.67837
P50237	MKDLHLGEQDLQPETR	0.912564462	2	5.18946
P50237	MLPDPGTLGEYIEQFK	0.940094477	3	4.94631
P50237	MLPDPGTLGEYIEQFK+Oxidation(0	1.110195929		
P50237	THLPVHMLPPSFWK	1.771775419	3	3.71863
P50237	VLWGSWYDHVK	0.99702346	2	2.97803
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**2.022285866**	**0.65025**	**7**
P50398	FDLGQDVIDFTGHALALYR	1.341061025	3	4.61777
P50398	FQLLEGPPESMGR	1.171546585	2	3.95243
P50398	KQNDVFGEADQ	1.08071009	2	3.28881
P50398	NPYYGGESSSITPLEELYK	1.307726007	2	5.90962
P50398	QLICDPSYIPDR	0.775771086	2	3.01483
P50398	TDDYLDQPCLETINR	0.757723362	2	4.96161
P50398	TFEGVDPQTTSMR	1.027314137	2	3.38432
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**2.090244435**	**1.1E-05**	**15**
P50399	AYDATTHFETTCDDIK	0.96915387	2	4.12015
P50399	AYDATTHFETTCDDIKDIYK	1.327997415	3	6.22026
P50399	EIRPALELLEPIEQK	1.2617012	3	3.8109
P50399	EPEKEIRPALELLEPIEQK	1.155064633	3	3.42173
P50399	FDLGQDVIDFTGHSLALYR	0.963148087	3	4.04024
P50399	FKLPGQPPASMGR	1.173198533	2	2.6021
P50399	FVSISDLFVPK	1.266544745	2	3.26845
P50399	LSAIYGGTYMLNKPIEEIIVQNGK	1.960497814	3	4.58014
P50399	MLLFTEVTR	1.065257532	2	2.35783
P50399	MTGSEFDFEEMKR	1.04814712	2	3.63453
P50399	NTNDANSCQIIIPQNQVNR	0.971920001	2	4.37439
P50399	TDDYLDQPCCETINR	2.153949082	2	4.85099
P50399	TFEGVDPK	2.084198838	2	2.40487
P50399	VIEGSFVYK	0.951266155	2	2.33051
P50399	VLHMDQNPYYGGESASITPLEDLYK	1.194816603	2	5.5172
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**2.030121011**	**0.99999**	**7**
P50431	ALSDALTELGYK	1.682803781	2	4.08037
P50431	AVLEALGSCLNNK	1.063109567	2	4.27225

P50431	GLLEEDFQK	1.168406145	1	2.09667
P50431	IMGLDLPDGGHLTHGFMTDK	1.067238561	2	2.80099
P50431	IYQLQVLANCR	0.97766184	2	2.82082
P50431	VLEACSIACNK	1.021585883	2	4.01854
P50431	YSEGYPGQR	1.072678178	2	2.81589
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**2.109805591**	**1**	**16**
P50475	ASEWVQQVSGLMDGK	1.062196648	2	4.47846
P50475	AVFDETYPDPVR	0.994766672	2	3.273
P50475	DIINEEEVQFLK	1.171326838	2	2.7119
P50475	ESDGVLKPLPK	1.092209879	2	2.379
P50475	GLEATDDSPK	1.085682658	2	2.70135
P50475	HNDLDDVGK	1.064152366	2	2.55703
P50475	ITCLCQVPQNAANR	0.997808721	2	3.826
P50475	IVAVTGAEAQK	1.077201725	2	2.57376
P50475	NVGCLQEALQLATSFAQLR	0.997902777	3	3.9414
P50475	QIWQNLGLDEAK	1.209170485	2	3.04844
P50475	RIVAVTGAEAQK	1.082386631	2	2.77359
P50475	SVLGDADQK	0.919873494	1	2.2071
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	1.30135703	3	3.67529
P50475	TITVALADGGRPDNTGR	1.03744033	2	3.03316
P50475	VDDSSEDKTEFTVK	0.891469139	2	4.06605
P50475	VGAEDTDGIDMAYR	0.906669834	2	3.87138
P50503	**F10A1 Hsc70_interacting protein**	**2.4834456**	**0.00294**	**6**
P50503	AIDLFTDAIK	1.634825806	2	2.74328
P50503	AIEINPDSAQPYK	1.387782795	2	3.53018
P50503	GAAIDALNDGELQK	1.153123484	2	3.71006
P50503	KGAAIDALNDGELQK	1.294451165	2	4.68558
P50503	LDYDEDASAMLR	1.192813004	2	3.3433
P50503	QDPSVLHTEEMR	1.073397617	2	2.31945
P50516	**VATA V_type proton ATPase catalytic subunit A**	**2.141533605**	**0.47445**	**2**
P50516	TALVANTSNMPVAAR	0.881558219	2	3.19536
P50516	VLDALFPCVQGGTTAIPGAFGCGK	1.525493642	2	3.31272
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**2.076679161**	**0.89108**	**14**
P50554	GMCQLITMACGSCSNENAFK	1.198555774	2	4.55672
P50554	GNYLVDVDGNR	0.739674791	2	2.64162
P50554	GTFCSFDTPDEAIR	3.236171673	2	3.22422
P50554	HGCAFLVDEVQTGGGCTGK	0.909194811	2	6.11325
P50554	IDIPSFDWPIAPFPR	2.586369197	2	3.80431
P50554	IFNTWLGDPSK	1.417453941	2	3.00985
P50554	KHGCAFLVDEVQTGGGCTGK	0.928349179	2	5.03661
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.194492611	3	3.30369
P50554	MLDLYSQISSVPIGYNHPALAK	1.035037393	3	3.40676
P50554	NLLLAEVINIIK	1.061004535	3	5.32395
P50554	REDLLNNVAHAGK	1.062783567	3	3.6202
P50554	TLLTGLLDLQAQYPQFVSR	1.153774438	2	3.16171
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.529006423	2	4.021
P50554	VDFEFDYDGPLMK	1.307180216	2	4.04879
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.935635419**	**0.92135**	**2**
P50580	GDAMIMEETGK	0.915500841	2	2.66411
P50580	TIIQNPTDQQK	1.044705071	2	3.15499
P50878	**RL4 60S ribosomal protein L4**	**2.293198105**	**0.78797**	**11**
P50878	FCIWTESAFR	1.276688	2	2.56805
P50878	KLDELYGTWR	1.044257143	2	2.97075
P50878	KLEAAAAALAAK	1.037160995	3	4.94121
P50878	LDELYGTWR	0.983446789	2	2.57116
P50878	LEAAAAALAAK	1.619972509	2	3.61069

P50878	NIPGITLLNVSK	1.260170318	1	2.69627
P50878	NVTLPAVFK	1.177458148	1	2.24195
P50878	RGPCIIYNEDNGIIK	0.71394291	2	2.99068
P50878	SGQGAFGNMCR	1.250685282	2	2.83619
P50878	SNYNLPMHK	1.047482522	2	2.63791
P50878	YAICSALAASALPALVMSK	1.33764739	2	2.54864
P51583	**PUR6 Multifunctional protein ADE2**	**1.879819329**	**0.78366**	**3**
P51583	ACGNFGIPCELR	0.857507145	2	2.60087
P51583	SWLPQNCTLVDMK	0.842054118	2	2.7441
P51583	VVVLMGSTSDLGHCEK	1.297057716	2	3.03931
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.940461215**	**0.99985**	**7**
P51635	ALEALVAK	1.160731662	2	2.82697
P51635	GLEVTAYSPLGSSDR	1.066689931	2	4.1147
P51635	HHPEDVEPAVR	0.914964091	3	3.58958
P51635	HIDCASVYGNETEIGEALK	1.00721499	2	6.04121
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.955209397	3	6.26134
P51635	HPDEPVLLEEPVVLALAEK	1.445848895	3	6.06106
P51635	YIVPMITVDGK	1.246907717	2	2.32848
P51647	**AL1A1 Retinal dehydrogenase 1**	**1.723343258**	**1.3E-10**	**17**
P51647	ANNTTYGLAAGVFTK	0.594632385	2	4.60145
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	1.031983109	3	3.66767
P51647	FPVLNPATEEVICHVEEGDK	1.161021829	3	3.82828
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.948315664	4	5.05052
P51647	IFINNEWHDSVSGK	1.062924671	2	4.28061
P51647	IFVEESVYDEFVR	0.719593569	2	4.22951
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	1.037942372	3	5.61166
P51647	IHGQTIPSDGDIFTFTR	0.967543875	3	4.28068
P51647	KFPVLNPATEEVICHVEEGDK	0.916448336	3	3.56804
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.953781397	4	4.87731
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	0.782535136	3	5.52338
P51647	LLLATIEAINGGK	3.510487334	2	4.19882
P51647	VAFTGSTQVGK	1.32330905	2	2.51871
P51647	VFANAYLSDLGGSIK	1.209071615	2	4.44487
P51647	YCAGWADK	0.90045276	2	2.48925
P51647	YVLGNPLTQGINQGPQIDK	0.879833997	2	5.22237
P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.836579279	2	3.88679
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**2.202839101**	**0.99986**	**9**
P51650	EVGEVLCTDPLVSK	1.534279926	2	3.77634
P51650	GIHDSFVTK	0.852781119	2	2.40437
P51650	HQSGGNFFEPTLLSNVTR	1.038528803	2	3.784
P51650	IITAESGKPLK	1.049060755	2	2.82229
P51650	ILLHHAANSVK	1.212447411	2	2.61054
P51650	LGTVADCGVPEAR	0.754816619	2	3.66227
P51650	VGNGFEEGTTQGPLINEK	0.88046241	2	4.61066
P51650	WLPTPATFPVYDPASGAK	1.101746477	2	3.54446
P51650	YGIDEYLEVK	1.290310562	2	2.90843
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**2.184166056**	**0.91159**	**2**
P51863	ADDYEQVK	1.173533204	2	2.48969
P51863	LLFEGAGSNPGDK	1.093314931	2	3.05388
P51869	**CP4F4 Cytochrome P450 4F4**	**2.087847113**	**0.99758**	**4**
P51869	ALPSQHEDDILK	1.240066054	2	2.59484
P51869	NISLMTLDSLQK	1.184671976	2	3.52323
P51869	TLDFIDVLLLTK	1.173510885	2	3.61385
P51869	WQDLASGGSAR	1.02441401	2	3.17791
P51886	**LUM Lumican**	**2.113426429**	**0.4151**	**2**
P51886	NNQIDHIDEK	0.760125454	2	3.20646

P51886	SLQDLQLANNK	1.230202733	2	2.49798
P52296	**IMB1 Importin subunit beta_1**	**2.472035262**	**0.66139**	**7**
P52296	AAVENLPTFLVELSR	1.287234893	2	3.67735
P52296	GALQYLVPILTQTLTK	1.018123256	2	3.30453
P52296	GDQENVHPDVMLVQPR	1.070424621	2	2.9799
P52296	SNEILTAIIQGMR	1.58051566	2	2.9366
P52296	TVSPDRLELEAAQK	0.962480787	2	3.15176
P52296	VLANPGNSQVAR	0.990746579	2	3.05508
P52296	VQHQDALQISDVVMASLLR	1.820366481	2	2.88516
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.885790859**	**0.29419**	**5**
P52303	KPTETQELVQQVLSLATQDSDNPDLR	1.655678046	3	3.34658
P52303	MEPLNNLQVAVK	1.210413164	2	2.53966
P52303	NINLIVQK	0.795856603	1	2.40891
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.326270455	3	3.69346
P52303	SQPDMAIMAVNTFVK	1.151812145	2	3.3392
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**2.076238267**	**1**	**2**
P52504	IIACDGGGGALGHPK	1.100456705	2	4.12379
P52504	VYINLDKETK	1.011783882	2	2.61759
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**2.162938249**	**0.96002**	**3**
P52555	FDTQYPYGEK	1.346942312	2	2.6502
P52555	ILDQGEDFPASELAR	1.068991718	2	5.05383
P52555	SLNILTAFR	1.637028918	2	2.34129
P52631	**STAT3 Signal transducer and activator of transcription 3**	**3.016881847**	**0.00216**	**3**
P52631	GLSIEQLTTLAEK	1.528283705	2	2.39859
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	1.642902846	3	4.60514
P52631	MQQLEQMLTALDQMR	1.073973841	2	2.44068
P52759	**UK114 Ribonuclease UK114**	**2.506909744**	**6.4E-06**	**7**
P52759	AAGCDFTNVVK	1.528464457	2	3.06297
P52759	AAYQVAALPK	1.089086591	2	2.67974
P52759	IEIEAIAVQGPFTTAGL	1.34755947	2	3.24048
P52759	NLGEILK	1.293288571	1	2.28774
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.379895429	2	4.52571
P52759	TTVLLADINDFGTVNEIYK	1.738122151	2	5.66671
P52759	TYFQGNLPAR	1.166843451	2	2.5079
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**2.38248127**	**0.88809**	**2**
P52845	CKEDAIFNR	1.101086878	2	2.50345
P52845	SGSTWIGEIVDMIYK	1.312855503	2	3.36445
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**2.218161693**	**0.94018**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	1.41420305	2	4.46841
P52847	FLAGNVAYGSWFDHVK	0.882085613	2	3.85498
P52847	IEEFQSRPCDIVIPTYPK	1.057135277	3	5.26857
P52847	IVHHTSFEVMK	1.198366257	2	3.05329
P52847	NYFTMTQSEK	0.92395796	2	2.92485
P52847	SGVELLK	1.084493104	2	2.33994
P52847	THLPIDLLPK	1.293735581	3	3.55572
P52847	TLDEHTLER	1.055717115	2	3.09245
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**2.318240142**	**0.41454**	**39**
P52873	ADEAYLIGR	0.839103255	2	2.80685
P52873	ADFAQACQDAGVR	0.863532799	2	4.47163
P52873	AEAEAQAEELSFPR	0.964008758	2	4.704
P52873	AGTHILCIK	1.358213829	2	2.71725
P52873	ALAVSDLNR	0.98167514	2	2.58356
P52873	AYSEALAAFGNGALFVEK	1.633198665	2	3.68999
P52873	AYVEANQMLGDLIK	1.354510744	2	4.70824

P52873	DAHQSLLATR	1.160567064	1	3.17389
P52873	DFTATFGPLDSLNTR	1.253580032	2	3.75664
P52873	DMAGLLKPAACTMLVSSLR	1.373210441	3	3.38815
P52873	ELIPNIPFQMLLR	0.78366989	2	2.84916
P52873	ENGVDAVHPGYGFLSER	0.953920476	2	2.96989
P52873	FIGPSPEVVR	1.059577684	2	2.43668
P52873	FLYECPWR	0.920009882	2	2.60596
P52873	GANAVGYTNYPDNVVFK	1.212329537	2	4.57553
P52873	GLAPVQAYLHIPDIIK	1.592762482	2	2.98051
P52873	GQIGAPMPGK	1.006227097	2	2.42727
P52873	GTPLDTEVPLER	0.819188056	2	3.65032
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.644319024	3	5.41622
P52873	HIEVQILGDQYGNILHLYER	1.471744258	3	7.00833
P52873	HYFIEVNSR	0.926631865	2	2.33898
P52873	IAEEFEVELER	1.253307826	2	3.24429
P52873	IEGRPGASLPPLNLK	0.784954681	2	3.4374
P52873	INGCAIQCR	1.138954747	2	3.25095
P52873	IVGDLAQFMVQNGLSR	1.378638709	2	4.84208
P52873	LDNASAFQGAVISPHYDSLLVK	0.978115917	3	5.77047
P52873	LLHYLGHVMVNGPTTPIPVK	1.012822097	3	3.67751
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.278076993	4	6.50313
P52873	NHQGLLLMDTTFR	1.355553087	3	3.32054
P52873	QKADEAYLIGR	1.020300743	2	2.49514
P52873	QVGYENAGTVEFLVDK	1.312282603	2	3.77663
P52873	SSTAPVASPNVR	0.838041737	2	2.346
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.172336422	2	4.80542
P52873	TVAVYSEQDTGQMHR	1.285969126	2	4.56916
P52873	VFDYSEYWEGAR	1.117495409	2	4.53713
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.22208948	2	4.12303
P52873	VVEIAPATHLDPQLR	1.255194584	2	4.23659
P52873	VVHSYEELEENYTR	1.140042435	2	5.23838
P52873	YSLEYYMGLAEELVR	1.161930856	3	4.51031
P52925	**HMGB2 High mobility group protein B2**	**2.063034234**	**0.99978**	**2**
P52925	KHPDSSVNFAEFSK	1.04727526	2	2.74042
P52925	SEHPGLSIGDTAK	1.044767714	2	2.84615
P52944	**PDLI1 PDZ and LIM domain protein 1**	**2.189152307**	**0.05607**	**5**
P52944	CGTGIVGVFVK	1.077127785	2	2.43476
P52944	GHFFVGDQIYCEK	1.378534383	2	3.78768
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	0.88235236	3	4.49917
P52944	TSASGEEANSRPSAQPHPSGGLIIDKESEVYK	0.737071439	3	5.01539
P52944	VTPPEGYDVVTVFPK	1.116668126	2	2.71025
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**2.112245644**	**0.99217**	**4**
P53395	LREELKPVALAR	1.193707127	2	2.6741
P53395	LSDIGEGIR	1.070323256	2	3.02368
P53395	RLAMENNIK	1.456175372	2	2.37853
P53395	SYLENPAFMLLDLK	1.279432534	2	4.60672
P53987	**MOT1 Monocarboxylate transporter 1**	**1.965538249**	**1**	**5**
P53987	DGKEDETSTDVDEKPK	0.9884129	3	5.4891
P53987	DGKEDETSTDVDEKPKK	0.943688686	3	4.0479
P53987	EDETSTDVDEKPK	1.045310024	2	3.97638
P53987	ETQSPAPLQNSSGDPAEEESPV	0.705396385	2	5.04942
P53987	SDANTDLIGGSPK	1.13463653	2	4.13569
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**2.193962185**	**0.81272**	**2**
P54313	ACGDSTLTQITAGLDPVGR	1.231641871	2	3.99717

P54313	TFVSGACDASIK	0.902441754	2	2.7241
P54319	**PLAP Phospholipase A_2_activating protein**	**2.007541129**	**0.99962**	**3**
P54319	IGDVVGSSGANQQTSGK	0.979019848	2	4.65864
P54319	TGDLGDINAEQLPGR	1.021206692	2	4.13088
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.877300235	2	3.39071
P54822	**PUR8 Adenylosuccinate lyase**	**2.075074759**	**0.95295**	**2**
P54822	KVDIEVLSVLASLGASVHK	1.541831733	3	4.41643
P54822	VLSQQAAAVVK	0.984213046	2	2.85438
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.664591039**	**0.86592**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	0.70511649	3	4.89156
P54921	AIDIYEQVGTSAMDSPLLK	1.317594047	2	3.79316
P54921	IEEACEIYAR	0.719790426	2	2.75739
P54921	NSQSFFSGLFGGSSK	0.913373861	2	3.79222
P54921	YEELFPAFSDSR	1.392317685	2	2.62031
P55006	**RDH7 Retinol dehydrogenase 7**	**2.00122389**	**0.96787**	**11**
P55006	LETVILDVTK	1.154843293	2	3.51737
P55006	TESIVAATQWVK	1.049613549	2	4.08185
P55006	TNVTNMER	0.704912259	2	2.74532
P55006	TNVTNMER+Oxidation(5	0.868975992		
P55006	TSDRLETVILDVTK	1.370453506	3	4.58467
P55006	VAIIEPGGFK	0.949401566	2	2.38588
P55006	VLAACLTEK	1.053828326	2	3.07459
P55006	VVNIASTMGR	0.995755768	2	3.78917
P55006	VVNIASTMGR+Oxidation(7	0.989718722		
P55006	YGVEAFSDSLR	1.184505417	2	3.86489
P55006	YVFITGCDSGFGNLLAR	1.323749375	2	3.6655
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.608999954**	**0.00346**	**4**
P55051	ALGVGFATR	0.839609957	2	2.64514
P55051	LTDSQNFDEYMK	0.939915651	2	4.04984
P55051	QVGNVTKPTVIISQEGGK	0.652305888	3	4.12915
P55051	WDGKETNCVR	0.954269547	2	2.88639
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.848107436**	**0.9999**	**6**
P55053	FDETTADGR	1.067895776	2	3.20589
P55053	KTETVCTFTDGALVQHQK	0.807274499	3	5.30947
P55053	LVESHGFEDYMK	0.870499406	2	3.42733
P55053	MGAMAKPDCIITLDGNNLTVK	1.122619304	2	4.1249
P55053	MVVECVMNNAICTR	1.096096997	2	3.84754
P55053	TETVCTFTDGALVQHQK	0.9264584	2	4.68317
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.880646383**	**0.9952**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.349784383	3	5.8671
P55159	IFFYDSENPPGSEVLR	0.875860987	2	6.21527
P55159	IQSILSEDPK	0.99990261	2	3.25976
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	0.897548865	3	4.07499
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	0.840849638	3	5.40814
P55159	VVADGFDFANGIGISLDGK	0.901145811	2	4.4463
P55159	YVYIAELLAHK	1.237036065	2	2.67735
P55260	**ANXA4 Annexin A4**	**2.25229569**	**0.80751**	**4**
P55260	AEIDMLDIPANFK	1.185019692	1	2.17768
P55260	GAGTDEGCLIEILASR	1.141744462	2	3.78345
P55260	GLGTDEDAIIGVLACR	1.121530292	2	3.90833
P55260	INQTYQQQYGR	0.566081075	2	3.61678
P55770	**NH2L1 NHP2_like protein 1**	**2.074532678**	**0.99998**	**2**
P55770	LLDLVQQSCNYK	1.142988326	2	3.89196
P55770	QQIQSIQQSIER	1.037814119	2	2.92991
P55937	**GOGA3 Golgin subfamily A member 3**	**2.245570249**	**0.64192**	**2**
P55937	LDSEMKELRQELIK+Oxidation(4	1.293390396		
P55937	QWYQQQLTLAQEAR	1.14018981	2	2.44317

P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**2.257063915**	**0.98799**	**5**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.335975667	2	4.52467
P56399	IFQNAPTDPTQDFSTQVAK	1.177036502	2	4.19167
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.053002889	3	3.85841
P56399	KQEVQAWDGEVR	0.776081576	2	3.35561
P56399	SSENPNEVFR	1.165425474	2	2.45697
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.981398248**	**0.99128**	**4**
P56522	AGLLPSGPRPGYTAIQALLSDR	1.469695908	3	3.46841
P56522	LEGVGESTR	1.170420324	2	2.30893
P56522	TATEKPGVEEAAR	0.925969737	2	3.25808
P56522	TDITEVALGVLR	1.011741215	2	3.92462
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**2.249255102**	**0.99916**	**17**
P56574	ATDFVVDR	1.151279758	2	2.46367
P56574	CATITPDEAR	1.294153849	2	2.30452
P56574	DLAGCIHGLSNVK	1.109017434	2	2.50456
P56574	DQTNDQVTIDSALATQK	0.907248398	2	5.42566
P56574	FKDIFQEIFDK	1.240885601	2	3.43291
P56574	GKLDGNQDLIR	1.108881191	2	2.96892
P56574	IKVEKPVVEMDGDEMTR	1.257362493	3	3.47514
P56574	LDGNQDLIR	1.370254971	2	2.44979
P56574	LIDDMVAQVLK	2.051528493	2	4.05706
P56574	LNEHFLNTTDFLDTIK	1.121122905	2	4.56007
P56574	NILGGTVFR	1.009149961	2	2.78008
P56574	NILGGTVFREPIICK	3.458026153	2	3.00083
P56574	SSGGFVWACK	0.824056428	2	2.44972
P56574	TIEAEAAHGTVTR	1.117275675	2	3.92742
P56574	VCVQTVESGAMTK	1.022737644	2	3.86064
P56574	VEKPVVEMDGDEMTR	1.103883411	3	4.01855
P56574	YFDLGLPNR	1.279189006	2	2.52253
P56593	**CP2AC Cytochrome P450 2A12**	**2.043451458**	**0.58464**	**3**
P56593	MLQGTCGAPIDPTIYLSK	1.13575544	2	4.70444
P56593	NRQPQYEDHMK	0.83388802	3	4.13185
P56593	NRQPQYEDHMK+Oxidation(9	0.605193822		
P56656	**CP239 Cytochrome P450 2C39**	**1.820664943**	**0.00585**	**4**
P56656	EHQESLDVTNPR	0.73436731	2	3.68047
P56656	IKEHQESLDVTNPR	0.853419633	3	4.87248
P56656	NYLIPK	1.426222677	1	2.1687
P56656	VQEEIDHVIGR	1.32167443	2	3.6951
P56812	**PDCD5 Programmed cell death protein 5**	**1.667053539**	**0.97537**	**3**
P56812	HGDPGDAAQQEAK	0.6725385	2	4.39695
P56812	NSILAQVLDQSAR	1.167135099	2	3.84585
P56812	VSEQGLIEILEK	0.776272893	2	3.3304
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**1.926911781**	**0.86501**	**8**
P57093	AISCHYGSSDCK	0.716719292	2	3.22801
P57093	IQDFQQNEELFR	1.048899906	2	3.57945
P57093	KFYEENGFLVIK	1.033563812	2	2.67677
P57093	MDYTRAGAR	0.610555363	2	2.5605
P57093	MYHGIQDYDPDSPR	1.199614184	2	2.98107
P57093	NLVSDDDIQR	0.84055025	2	2.42821
P57093	NNGCLVVLPGTHK	1.326031628	2	2.92034
P57093	YCALPQIVK	0.868078656	1	2.07252
P57113	**MAAI Maleylacetoacetate isomerase**	**2.185340327**	**0.11403**	**11**
P57113	AITSGFNALEK	0.997991117	2	3.41554
P57113	ALLALEAFQVSHPCR	1.159936894	2	4.12713
P57113	DGGQQFSEEFQTLNPMK	1.101475549	2	4.92675

P57113	FKVDLSPYPTISHINK	0.993095881	2	4.90249
P57113	GIDYEIVPINLIK	1.205087611	2	4.40449
P57113	IDGITIGQSLAILEYLEETRPIPR	1.22734025	3	4.18634
P57113	MISDLIASGIQPLQNLSVLK	1.136328605	2	5.43574
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0	1.054280741		
P57113	QVGQENQMPWAQK	0.94337297	2	3.8213
P57113	VDLSPYPTISHINK	1.145170744	2	3.78273
P57113	YCVGDEVSMADVCLAPQVANAER	1.311676815	3	6.55903
P57722	**PCBP3 Poly(rC)_binding protein 3**	**2.305305306**	**0.9983**	**3**
P57722	ESTGAQVQVAGDMLPNSTER	1.280846705	2	5.28909
P57722	INISEGNCPER	1.069793202	2	3.5385
P57722	LVVPASQCGSLIGK	1.151343078	2	2.59727
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**2.193144271**	**0.9966**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	1.109178171	3	4.67889
P58321	WLPLEANPEVTNQFLK	1.135442952	2	3.01776
P58389	**PTPA Serine/threonine_protein phosphatase 2A activator**	**1.883817171**	**0.77163**	**3**
P58389	FGSLLPIHPVTSG	1.195068262	2	2.40448
P58389	KEIHTVPDMGK	0.889415268	2	2.42018
P58389	WIDETPPVDQPSR	0.881541558	2	3.47848
P58751	**RELN Reelin**	**1.626505906**	**0.35048**	**2**
P58751	CGILSSGNNLFFNEDGLR	0.690347115	2	2.32494
P58751	QNYMMNFSRQHGLR	0.791318088	2	2.42773
P58775	**TPM2 Tropomyosin beta chain**	**2.234936979**	**0.72266**	**11**
P58775	AISEELDNALNDITSL	0.756088061	2	4.39084
P58775	ATDAEADVASLNR	2.866391631	2	4.23221
P58775	DAQEKLEQAEK	0.986255809	2	2.9043
P58775	KATDAEADVASLNR	1.416888502	2	4.0868
P58775	LDKENAIDR	0.959619784	2	3.08951
P58775	LKGTEDEVEK	0.436407836	2	2.85641
P58775	MELQEMQLK	1.162224026	2	2.98138
P58775	QLEEEQQALQK	2.530110046	2	3.55414
P58775	SLEAQADKYSTK	1.0688813	2	3.75664
P58775	TIDDLEDEVYAQK	3.312027158	2	3.9504
P58775	YSESVKDAQEK	0.38844056	2	3.09924
P59242	**CING Cingulin**	**2.201882381**	**0.92531**	**2**
P59242	LGQEQQALNR	1.281021328	2	2.79354
P59242	LQGLEQEAENK	1.087834986	2	2.96285
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**2.430776929**	**0.33588**	**2**
P59999	ELLLQPVTISR	1.218555238	2	3.02599
P59999	FMRFMMMR+Oxidation(4)Oxidation(5	2.180002786		
P60335	**PCBP1 Poly(rC)_binding protein 1**	**2.351791522**	**0.49743**	**4**
P60335	AITIAGVPQSVTECVK	1.106186308	2	3.52901
P60335	IITLTGPTNAIFK	1.193534964	2	2.90487
P60335	LVVPATQCGSLIGK	1.256040883	2	2.98914
P60335	VMTIPYQPMPASSPVICAGGQDR	1.56500536	3	4.4385
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**2.278393495**	**0.64092**	**6**
P60843	ATQALVLAPTR	0.946430919	1	1.95849
P60843	GFKDQIYDIFQK	1.17086119	3	3.88621
P60843	GVAINMVTEEDKR	1.102624183	2	3.22981
P60843	KEELTLEGIR	1.363603151	2	2.35313
P60843	KGVAINMVTEEDKR	1.16505438	3	4.67023
P60843	LQMEAPHIIVGTPGR	1.259858897	3	3.87773
P60868	**RS20 40S ribosomal protein S20**	**2.114362751**	**0.89223**	**3**
P60868	DTGKTPVEPEVAIHR	1.039939762	3	4.41989

P60868	LIDLHSPSEIVK	1.11467137	2	3.13459
P60868	TPVEPEVAIHR	1.478668047	2	2.45865
P60901	**PSA6 Proteasome subunit alpha type_6**	**2.263826063**	**0.06672**	**2**
P60901	AINQGGLTSVAVR	1.178155943	2	3.41184
P60901	LLDSSTVTHLFK	1.480539905	2	3.00812
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.919394674**	**0.97739**	**2**
P61087	GEIAGPPDTPYEGGR	1.445038732	2	3.20526
P61087	VDLVDENFTELR	0.897825162	2	3.50466
P61107	**RAB14 Ras_related protein Rab_14**	**2.287281941**	**0.97077**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	1.090174693	3	3.72783
P61107	NLTNPNTVIILIGNK	0.906228137	2	3.98962
P61107	SCLLHQFTEK	1.116603574	2	3.08708
P61107	STYNHLSSWLTDAR	1.032355329	2	3.31572
P61107	TGENVEDAFLEAAK	1.210845298	2	3.69374
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**2.208366707**	**0.6456**	**3**
P61222	GSELQNYFTK	1.680363161	2	2.34013
P61222	NTVANSPQTLLAGMNK	1.147306668	2	4.09023
P61222	VAETANEEEVKK	0.83764061	2	2.96918
P61314	**RL15 60S ribosomal protein L15**	**1.992032412**	**1**	**5**
P61314	FFEVILIDPFHK	1.1470394	3	3.42168
P61314	GATYGKPVHHGVNQLK	0.894444149	2	4.38604
P61314	SLQSVAEER	0.982688382	2	2.79345
P61314	VLNSYWVGEDSTYK	1.200248868	2	4.08355
P61314	YIQELWR	1.172898685	2	2.61205
P61354	**RL27 60S ribosomal protein L27**	**1.874974058**	**0.97771**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	0.902334407	3	4.93704
P61354	VYNYNHLMPTR	1.089965163	2	3.01933
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**2.060539017**	**0.99991**	**3**
P61459	AVGWNELEGR	1.027757403	2	3.19697
P61459	LDHHPEWFNVYNK	1.118547821	3	4.97846
P61459	LSAEERDQLLPNLR	1.18883892	3	4.32026
P61589	**RHOA Transforming protein RhoA**	**1.823876483**	**0.95982**	**4**
P61589	HFCPNVPIILVGNK	1.857336056	2	3.29609
P61589	HFCPNVPIILVGNKK	0.963770155	3	4.5125
P61589	MKQEPVKPEEGR	0.8779464	3	4.12111
P61589	MKQEPVKPEEGR+Oxidation(0	0.780893522		
P61751	**ARF4 ADP_ribosylation factor 4**	**2.424603791**	**0.02467**	**6**
P61751	ILMVGLDAAGK	1.640764084	2	2.89038
P61751	IQEGAAVLQK	0.878487563	2	2.94305
P61751	KQMRILMVGLDAAGK	1.366902547	2	2.37147
P61751	LGEIVTTIPTIGFNVETVEYK	1.01412004	3	4.25597
P61751	NICFTVWDVGGQDK	1.242231201	2	4.21744
P61751	QDLPNAMAISEMTDK	1.570450916	2	3.60782
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.957047624**	**0.99999**	**2**
P61805	ADFQGISPER	1.019763046	2	3.11042
P61805	FLEEYLSSTPQR	0.937868508	2	3.78181
P61924	**COPZ1 Coatomer subunit zeta_1**	**2.512685403**	**0.00195**	**2**
P61924	GEDVPLTEQTVSQVLQSAK	1.351975029	2	4.62344
P61924	YYDDTYPSVK	1.047125442	2	2.4936
P61972	**NTF2 Nuclear transport factor 2**	**3.711833681**	**0.95368**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	1.893438278	3	4.2965
P61972	NINDAWVCTNDMFR	1.182072313	2	3.77299
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**2.098561666**	**0.06521**	**9**

P61980	GSDFDCELR	1.056998792	2	2.76896
P61980	GSYGDLGGPIITTQVTIPK	0.977538117	2	5.16481
P61980	IDEPLEGSEDR	1.831630157	2	3.67701
P61980	IILDLISESPIK	1.084137331	2	4.09562
P61980	IITITGTQDQIQNAQYLLQNSVK	1.178410192	3	7.09349
P61980	LFQECCPHSTDR	1.078326329	2	3.90689
P61980	NTDEMVELR	1.588722969	2	2.66511
P61980	RSRNTDEMVELR	1.00515016	2	2.50928
P61980	TDYNASVSVPDSSGPER	1.029913908	2	4.56336
P61983	**1433G 14_3_3 protein gamma**	**2.086843171**	**0.62559**	**4**
P61983	AYSEAHEISK	0.759664036	2	3.53049
P61983	NVTELNEPLSNEER	1.094772581	2	4.65729
P61983	TAFDDAIAELDTLNEDSYK	1.715364922	2	4.77342
P61983	YLAEVATGEK	0.955732464	2	3.08096
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**1.880184355**	**0.68076**	**5**
P62076	CIGKPGGSLDNSEQK	0.766100379	2	4.0928
P62076	KCIGKPGGSLDNSEQK	0.82286267	3	3.97799
P62076	LDPGAIMEQVK	0.846466408	2	2.94983
P62076	VQIAVANAQELLQR	1.093899565	2	5.01919
P62076	YMDAWNTVSR	0.91649778	2	3.08328
P62083	**RS7 40S ribosomal protein S7**	**2.565154656**	**0.89403**	**5**
P62083	AIIIFVPVPQLK	1.344175614	2	3.75935
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.361396013	3	5.18262
P62083	KAIIIFVPVPQLK	1.639642492	2	3.6696
P62083	TLTAVHDAILEDLVFPSEIVGK	1.052078252	2	5.1634
P62083	VETFSGVYK	0.692315066	2	2.32131
P62161	**CALM Calmodulin**	**2.187110532**	**1**	**4**
P62161	DGNGYISAAELR	0.991694277	2	2.97082
P62161	EADIDGDGQVNYEEFVQMMTAK	1.427667189	2	5.22869
P62161	EAFSLFDKDGDGTITTK	0.977689478	2	4.71599
P62161	VFDKDGNGYISAAELR	0.981311446	2	4.96889
P62193	**PRS4 26S protease regulatory subunit 4**	**1.92684323**	**0.97598**	**4**
P62193	AICTEAGLMALRERR+Oxidation(8	3.035976084		
P62193	AVANQTSATFLR	1.063977594	2	3.0933
P62193	NQEQMKPLEEK	0.945299838	2	3.54506
P62193	TMLELLNQLDGFDSR	1.039393408	2	4.13625
P62198	**PRS8 26S protease regulatory subunit 8**	**2.003142064**	**0.98878**	**6**
P62198	EVIELPVKHPELFEALGIAQPK	0.983418488	3	4.38787
P62198	IAELMPGASGAEVK	0.935542755	2	3.16113
P62198	LEGGSGGDSEVQR	1.167810088	2	3.70943
P62198	LLREELQLLQEQGSYVGEVVR	1.35036557	3	3.99668
P62198	TMLELLNQLDGFEATK	1.161854533	2	3.71609
P62198	VHVTQEDFEMAVAK	0.923286904	2	3.13595
P62243	**RS8 40S ribosomal protein S8**	**2.081449055**	**0.91989**	**9**
P62243	ADGYVLEGK	1.403027157	2	3.16979
P62243	IIDVVYNASNNELVR	1.354086001	2	4.22857
P62243	ISSLLEEQFQQGK	1.34458109	2	4.23977
P62243	KYELGRPAANTK	0.902864469	2	3.58783
P62243	LDVGNFSWGSECCTR	1.36664832	2	3.96338
P62243	LTPEEEEILNK	1.044421506	2	3.0717
P62243	NCIVLIDSTPYR	1.165781233	2	3.47589
P62243	QWYESHYALPLGR	0.968721308	2	2.92363
P62243	YELGRPAANTK	0.79624056	2	2.9545
P62246	**RS15A 40S ribosomal protein S15a**	**2.19458628**	**0.75066**	**4**
P62246	HGYIGEFEIIDDHR	1.134371535	3	4.92148
P62246	IVVNLTGR	1.449311801	2	2.32918

P62246	MNVLADALK	1.132764954	2	2.73914
P62246	WQNNLLPSR	1.055210771	2	3.11739
P62250	**RS16 40S ribosomal protein S16**	**2.210332568**	**0.97856**	**6**
P62250	ALVAYYQK	2.37003802	1	2.23972
P62250	EIKDILIQYDR	1.029399629	2	2.61425
P62250	GGGHVAQIYAIR	0.946710672	2	3.07535
P62250	LLEPVLLLGK	1.451125281	2	2.80302
P62250	TLLVADPR	1.077941327	2	2.6086
P62250	VNGRPLEMIEPR	1.151016168	2	2.69585
P62260	**1433E 14_3_3 protein epsilon**	**2.081838402**	**1.8E-05**	**9**
P62260	AAFDDAIAELDTLSEESYK	1.389908037	2	6.03811
P62260	EENKGGEDKLK	1.310982521	2	2.70242
P62260	HLIPAANTGESK	1.040385596	2	3.1987
P62260	IISSIEQK	1.089404738	2	2.60819
P62260	LICCDILDVLDK	2.055795812	2	4.0564
P62260	YDEMVESMK	1.299608281	2	2.71077
P62260	YDEMVESMKK	1.324707462	2	2.67483
P62260	YLAEFATGNDR	0.852703414	2	2.94223
P62260	YLAEFATGNDRK	1.125644341	2	2.73987
P62268	**RS23 40S ribosomal protein S23**	**2.155034727**	**0.9557**	**2**
P62268	GHAVGDIPGVR	1.109058447	2	2.74766
P62268	KGHAVGDIPGVR	1.034606428	2	2.82558
P62271	**RS18 40S ribosomal protein S18**	**2.318773467**	**0.9994**	**6**
P62271	AGELTEDEVER	1.089429319	2	3.69618
P62271	LREDLER	1.001323514	1	2.21055
P62271	RAGELTEDEVER	1.977734436	2	3.10514
P62271	VITIMQNPR	1.011799345	2	2.83899
P62271	VLNTNIDGR	1.492955352	2	3.12737
P62271	YSQVLANGLDNK	1.211363898	2	4.04299
P62278	**RS13 40S ribosomal protein S13**	**2.705238937**	**0.09157**	**5**
P62278	GLAPDLPEDLYHLIK	1.220378846	2	3.09192
P62278	GLSQSALPYR	0.934565539	2	2.47847
P62278	GLTPSQIGVILR	1.478106615	2	2.98124
P62278	KGLTPSQIGVILR	1.526466138	3	3.89147
P62278	LILIESR	1.320279555	1	2.0731
P62329	**TYB4 Thymosin beta_4**	**1.896276794**	**0.99949**	**3**
P62329	ETIEQEKQAGES	0.948695482	2	2.44625
P62329	NPLPSKETIEQEK	0.90301894	2	2.73218
P62329	TETQEKNPLPSK	0.944306183	2	3.73931
P62332	**ARF6 ADP_ribosylation factor 6**	**2.173325355**	**0.97455**	**2**
P62332	FNVWDVGGQDK	1.109718204	2	3.02465
P62332	LGQSVTTIPTVGFNVETVTYK	1.180392547	2	2.67368
P62334	**PRS10 26S protease regulatory subunit 10B**	**2.060785118**	**0.02822**	**5**
P62334	ADHDFVVQEDFMK	0.982510201	2	2.32383
P62334	ALQSVGQIVGEVLK	1.19827287	2	3.615
P62334	EVIELPLTNPELFQR	1.224500916	2	3.03575
P62334	HGEIDYEAIVK	0.558292527	2	3.53083
P62334	NVCTEAGMFAIR	0.940073118	2	2.76719
P62425	**RL7A 60S ribosomal protein L7a**	**2.068550345**	**0.88239**	**11**
P62425	AGVNTVTTLVENK	1.117555617	2	4.02915
P62425	AGVNTVTTLVENKK	1.470512485	2	3.33457
P62425	HWGGNVLGPK	1.009418689	1	2.91587
P62425	KVVNPLFEK	0.939180799	2	2.36608
P62425	LKVPPAINQFTQALDR	1.556838357	3	4.29622
P62425	NFGIGQDIQPK	0.962539927	2	3.36864
P62425	TCTTVAFTQVNSEDK	0.955435691	2	3.35062
P62425	TCTTVAFTQVNSEDKGALAK	1.075749239	2	4.68271

P62425	TNYNDRYDEIR	1.124575021	2	2.35689
P62425	VAPAPAVVK	0.979073998	1	2.15337
P62425	VPPAINQFTQALDR	1.155655062	2	3.69734
P62630	**EF1A1 Elongation factor 1_alpha 1**	**2.455128075**	**1.2E-14**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.270256492	3	4.9869
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.598868052	4	5.25064
P62630	MDSTEPPYSQK	1.184636987	2	3.74136
P62630	MDSTEPPYSQK+Oxidation(0	1.446732889		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.242638523	5	5.93441
P62630	RYEEIVK	1.023857319	2	2.7394
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.237933996	3	5.20747
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14	1.202936843		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8	1.450166314		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.393400154	3	5.63393
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9	1.25335048		
P62630	YEEIVK	1.085430005	2	2.34163
P62630	YYVTIIDAPGHR	1.013095189	3	4.104
P62632	**EF1A2 Elongation factor 1_alpha 2**	**2.156358015**	**0.01249**	**7**
P62632	EHALLAYTLGVK	1.120542395	3	3.70318
P62632	IGGIGTVPVGR	1.285827334	2	3.54856
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.231252116	3	4.56564
P62632	QLIVGVNK	1.078227781	1	2.43109
P62632	STTTGHLIYK	1.343594107	2	3.06981
P62632	THINIVVIGHVDSGK	1.000586413	2	5.39768
P62632	VETGILRPGMVVTFAPVNITTEVK	1.73774648	3	3.94433
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.93322098**	**0.99993**	**2**
P62634	CGETGHVAINCSK	0.890445457	2	4.45352
P62634	CYSCGEFGHIQK	1.037428695	2	3.37999
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**2.290182648**	**0.94226**	**5**
P62703	FDTGNLCMVTGGANLGR	1.219807356	2	4.77984
P62703	GIPHLVTHDAR	1.21149281	2	2.74673
P62703	LSNIFVIGK	1.483605019	2	3.12328
P62703	TDITYPAGFMDVISIDK	1.009678862	2	4.94691
P62703	VNDTIQIDLETGK	1.371479559	2	4.548
P62718	**RL18A 60S ribosomal protein L18a**	**2.152928023**	**0.9838**	**2**
P62718	DLTTAGAVTQCYR	0.790673895	2	3.16364
P62718	SSGEIVYCGQVFEKSPLR	1.639506596	2	2.50862
P62752	**RL23A 60S ribosomal protein L23a**	**2.072967484**	**1**	**7**
P62752	KLYDIDVAK	1.026027817	2	2.39104
P62752	LAPDYDALDVANK	1.120517627	2	3.71814
P62752	LDHYAIIK	1.110563361	2	2.52263
P62752	LYDIDVAK	1.025039926	1	1.98575
P62752	NKLDHYAIIK	1.036502536	3	3.39016
P62752	VNTLIRPDGEK	1.052579036	2	3.34056
P62752	VNTLIRPDGEKK	1.05111189	2	2.93046
P62755	**RS6 40S ribosomal protein S6**	**2.407133302**	**0.29877**	**4**
P62755	LIEVDDER	1.225507439	2	3.07724
P62755	LNISFPATGCQK	1.288707907	2	2.85092
P62755	MATEVAADALGEEWK	1.365399766	2	4.78582
P62755	MATEVAADALGEEWK+Oxidation(0	0.968172631		
P62775	**MTPN Myotrophin**	**1.817916711**	**0.94979**	**3**
P62775	GPDGLTALEATDNQAIK	1.478539371	2	3.90549
P62775	HHITPLLSAVYEGHVSCVK	1.09822199	3	3.94215
P62775	NGDLDEVKDYVAK	0.860990036	2	3.19191
P62804	**H4 Histone H4**	**2.109193245**	**1.1E-08**	**9**

P62804	DAVTYTEHAK	1.029669218	2	3.01126
P62804	DNIQGITKPAIR	0.97542667	2	3.14164
P62804	ISGLIYEETR	1.62932014	2	3.97264
P62804	KTVTAMDVVYALK	0.861933474	3	4.77401
P62804	RISGLIYEETR	1.133873243	2	2.40331
P62804	TVTAMDVVYALK	1.137985489	2	3.90066
P62804	TVTAMDVVYALK+Oxidation(4	1.130958917		
P62804	VFLENVIR	1.076112319	2	3.26437
P62804	VFLENVIRDAVTYTEHAK	1.208600974	3	3.87555
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**1.97136495**	**0.54842**	**3**
P62815	AVVQVFEGTSGIDAK	0.752903842	2	3.64331
P62815	IYPEEMIQTGISAIDGMNSIAR	1.240243586	3	3.44089
P62815	SGQVLEVSGSK	1.009273969	2	2.81217
P62845	**RS15 40S ribosomal protein S15**	**1.971399434**	**0.89562**	**2**
P62845	DMIILPEMVGSMVGVYNGK	1.102273393	2	3.15847
P62845	KEAPPMEKPEVVK	0.94330569	3	4.03212
P62850	**RS24 40S ribosomal protein S24**	**2.189556447**	**0.99172**	**2**
P62850	KQMVIDVLHPGK	1.192456281	3	3.67591
P62850	TTGFGMIYDSLDYAK	1.127981314	2	4.00406
P62856	**RS26 40S ribosomal protein S26**	**2.063002885**	**0.99997**	**4**
P62856	DISEASVFDAYVLPK	1.276810958	2	3.11
P62856	FRPAGAAPRPPPKPM	0.970440347	2	2.73655
P62856	LHYCVSCAIHSK	0.995693104	3	3.33788
P62856	NIVEAAAVR	1.043490631	2	3.01359
P62859	**RS28 40S ribosomal protein S28**	**2.513223659**	**0.93216**	**2**
P62859	EGDVLTLLESER	1.400431588	2	3.53634
P62859	VEFMDDTSR	1.213511857	2	2.70491
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**2.223596347**	**0.67885**	**3**
P62870	ADDTFEALR	1.059494482	2	2.5475
P62870	LYKDDQLLDDGK	1.074520334	2	2.9807
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.416390438	3	4.52014
P62890	**RL30 60S ribosomal protein L30**	**2.214316152**	**2.1E-05**	**3**
P62890	LVILANNCPALR	1.100915459	2	3.06541
P62890	TGVHHYSGNNIELGTACGK	1.13340943	2	5.68993
P62890	VCTLAIIDPGDSDIIR	2.46128668	2	4.24025
P62898	**CYC Cytochrome c_ somatic**	**2.036859995**	**0.99991**	**7**
P62898	ADLIAYLK	1.026326464	2	3.12513
P62898	ADLIAYLKKATNE	0.747027649	2	2.46253
P62898	GITWGEDTLMEYLENPK	1.200851442	2	4.98805
P62898	GITWGEDTLMEYLENPKK	1.044305649	2	4.31643
P62898	KTGQAAGFSYTDANK	0.781368817	2	5.1925
P62898	TGPNLHGLFGR	0.828097482	2	3.37204
P62898	TGQAAGFSYTDANK	1.018656278	2	4.18944
P62902	**RL31 60S ribosomal protein L31**	**2.703915121**	**0.95806**	**2**
P62902	NLQTVNVDEN	1.903428262	1	2.41981
P62902	SAINEVVTR	1.371777692	2	3.05434
P62907	**RL10A 60S ribosomal protein L10a**	**2.265049168**	**0.01137**	**6**
P62907	AVDIPHMDIEALK	1.232232492	2	3.03815
P62907	AVDIPHMDIEALKK	0.980474997	2	3.07241
P62907	FSVCVLGDQQHCDEAK	1.205111302	2	4.12317
P62907	KYDAFLASESLIK	1.026995126	2	3.84331
P62907	VLCLAVAVGHVK	0.940018639	2	3.23442
P62907	YDAFLASESLIK	1.209711395	2	3.306
P62909	**RS3 40S ribosomal protein S3**	**2.165917588**	**0.0101**	**10**
P62909	AELNEFLTR	1.088197694	2	3.19437

P62909	DEILPTTPISEQK	1.175419354	2	3.3224
P62909	ELAEDGYSGVEVR	1.022646755	2	3.83229
P62909	ELTAVVQK	1.139681856	1	2.05135
P62909	FGFPEGSVELYAEK	2.376280254	2	3.56604
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.396793749	3	4.76127
P62909	GCEVVVSGK	0.912736481	2	2.41689
P62909	GGKPEPPAMPQPVPTA	1.259957617	2	4.07126
P62909	GLCAIAQAESLR	0.933901297	2	3.36026
P62909	TEIIILATR	1.248626113	2	3.28158
P62912	**RL32 60S ribosomal protein L32**	**2.053072305**	**0.54668**	**3**
P62912	ELEVLLMCNK	0.921533489	2	3.29667
P62912	GQILMPNIGYGSNK	1.037717907	2	3.15751
P62912	SYCAEIAHNVSSK	1.200523908	2	4.41383
P62914	**RL11 60S ribosomal protein L11**	**2.124381381**	**0.96621**	**2**
P62914	VLEQLTGQTPVFSK	1.164848785	2	4.42675
P62914	YDGIILPGK	1.061956393	2	3.05924
P62919	**RL8 60S ribosomal protein L8**	**2.096781376**	**0.75958**	**4**
P62919	ASGNYATVISHNPETK	1.065127805	2	4.43514
P62919	AVDFAER	1.233475587	1	1.97741
P62919	AVVGVVAGGGR	1.068240596	2	3.61877
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.422405743	3	5.37276
P62944	**AP2B1 AP_2 complex subunit beta**	**2.024732682**	**0.58764**	**3**
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.637927561	3	3.30468
P62944	LQNNNVYTIAK	1.014934802	2	2.40778
P62944	SQPDMAIMAVNSFVK	0.966038105	2	2.97341
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**1.92424488**	**0.99943**	**7**
P62959	AQVAQPGGDTIFGK	0.939688555	2	4.75212
P62959	CAADLGLK	1.09496691	2	2.52929
P62959	CLAFHDISPQAPTHFLVIPK	1.313182261	3	4.29055
P62959	HISQISVADDDDESLLGHLMIVGK	1.147154836	3	6.72587
P62959	IIFEDDR	1.610012144	2	2.59956
P62959	KHISQISVADDDDESLLGHLMIVGK	1.143875169	3	5.49068
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.749697491	3	4.37994
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.646339079**	**0.53273**	**6**
P62961	EDGNEEDKENQGDETQGQQPPQR	0.799735726	3	5.12613
P62961	GAEAANVTGPGGVPVQGSK	0.784240453	2	4.97392
P62961	NEGSESAPEGQAQQR	0.656587146	2	5.21107
P62961	NYQQNYQNSESGEK	1.199976424	2	4.82381
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	0.790664997	3	5.12922
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.088459095	3	5.12013
P62963	**PROF1 Profilin_1**	**2.20474096**	**0.43267**	**6**
P62963	CYEMASHLR	1.36069087	2	2.39401
P62963	DSLLQDGEFTMDLR	1.274456773	2	3.40966
P62963	DSPSVWAAVPGK	0.760496715	2	2.74058
P62963	SSFFVNGLTLGGQK	1.153275728	2	4.35779
P62963	STGGAPTFNVTVTMTAK	1.291974658	2	3.43468
P62963	TFVSITPAEVGVLVGK	1.124387436	2	4.63715
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**2.194061074**	**5E-07**	**25**
P63018	ARFEELNADLFR	1.029696483	3	3.73955
P63018	CNEIISWLDK	1.001575458	2	3.17904
P63018	DAGTIAGLNVLR	1.830510331	2	3.69132
P63018	FDDAVVQSDMK	1.162349111	2	3.871
P63018	FEELNADLFR	1.114359551	2	3.28983
P63018	FELTGIPPAPR	1.078337459	2	3.13579
P63018	HWPFMVVNDAGRPK	2.153661393	3	3.51047
P63018	IINEPTAAAIAYGLDK	1.198045218	2	5.42855

P63018	IINEPTAAAIAYGLDKK	1.078290835	2	4.27956
P63018	LLQDFFNGK	1.560304334	2	2.69215
P63018	MKEIAEAYLGK	1.022769677	2	3.4522
P63018	MVNHFIAEFK	0.903214042	2	2.86187
P63018	NQTAEKEEFEHQQK	0.928603285	2	5.26832
P63018	NQVAMNPTNTVFDAK	0.953888819	2	4.97062
P63018	NQVAMNPTNTVFDAK+Oxidation(4	1.01361321		
P63018	NSLESYAFNMK	1.059216981	2	3.50634
P63018	RFDDAVVQSDMK	1.060831215	2	3.62859
P63018	SFYPEEVSSMVLTK	1.179666355	2	4.95721
P63018	SFYPEEVSSMVLTK+Oxidation(9	1.320149462		
P63018	SINPDEAVAYGAAVQAAILSGDK	1.366280917	2	5.93176
P63018	SQIHDIVLVGGSTR	1.03183522	2	4.46678
P63018	STAGDTHLGGEDFDNR	0.945656017	2	4.72993
P63018	TVTNAVVTVPAYFNDSQR	1.226794095	3	4.90088
P63018	VCNPIITK	1.131756887	2	2.53822
P63018	VQVEYKGETK	0.737087617	2	2.54376
P63029	**TCTP Translationally_controlled tumor protein**	**2.597147313**	**0.96677**	**3**
P63029	DLISHDELFSDIYK	1.405158256	2	3.90017
P63029	EIADGLCLEVEGK	1.025145904	2	3.26732
P63029	VKPFMTGAAEQIK	1.220658722	3	3.34117
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.889343166**	**1**	**7**
P63036	ETTYYDVLGVKPNATQEELKK	0.904418259	3	3.56827
P63036	HYNGEAYEDDEHHPR	0.845629697	3	4.9599
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.246877229	3	4.00024
P63036	NVVHQLSVTLEDLYNGATR	1.106660211	2	4.05001
P63036	QISQAYEVLADSK	0.939712054	2	3.17226
P63036	TIVITSHPGQIVK	0.918627729	2	3.62617
P63036	VNFPENGFLSPDK	0.893884139	2	3.42163
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.987759806**	**1**	**36**
P63039	AAVEEGIVLGGGCALLR	1.108006837	2	5.38005
P63039	ALMLQGVDLLADAVAVTMGPK	1.166292263	3	6.58248
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(17	1.030449265		
P63039	CEFQDAYVLLSEK	1.292650224	2	4.4081
P63039	CIPALDSLKPANEDQK	0.920243919	2	3.53513
P63039	DDAMLLK	1.327159794	1	1.99997
P63039	DIGNIISDAMK	2.196546618	2	3.37775
P63039	GIIDPTK	1.216855392	1	1.93064
P63039	GVMLAVDAVIAELK	1.086317494	2	4.53891
P63039	GVMLAVDAVIAELKK	1.467265855	2	4.63125
P63039	GYISPYFINTSK	0.963583554	2	3.09148
P63039	IGIEIIK	0.920779047	2	2.67976
P63039	IGIEIIKR	1.421767867	2	2.41996
P63039	ILQSSSEVGYDAMLGDFVNMVEK	1.199562927	3	5.09175
P63039	IQEITEQLDITTSEYEK	1.172619233	2	5.62386
P63039	IQEITEQLDITTSEYEKEK	0.97271233	2	5.26961
P63039	ISSVQSIVPALEIANAHR	1.285896277	2	4.32679
P63039	KISSVQSIVPALEIANAHR	1.148136358	3	4.38552
P63039	KPLVIIAEDVDGEALSTLVLNR	1.3224901	2	6.01495
P63039	LSDGVAVLK	1.086483422	2	2.96864
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.482867411	2	6.51714
P63039	NAGVEGSLIVEK	1.059425004	2	3.4122
P63039	QSKPVTTPEEIAQVATISANGDK	1.039865471	2	3.41524
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	0.909892825	3	4.84935
P63039	RGVMLAVDAVIAELKK	0.919084659	3	5.93169
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	2.125279028	3	5.14673
P63039	TLNDELEIIEGMK	1.128688556	2	4.79828

P63039	TLNDELEIIEGMK+Oxidation(11	1.969601291		
P63039	TVIIEQSWGSPK	0.913988551	2	4.42764
P63039	VGEVIVTK	0.983285552	2	3.24175
P63039	VGEVIVTKDDAMLLK	0.636469821	2	3.60917
P63039	VGGTSDVEVNEK	2.205573154	2	3.80371
P63039	VGGTSDVEVNEKK	0.936265432	2	3.73601
P63039	VGGTSDVEVNEKKDR	0.322039305	2	3.41717
P63039	VGLQVVAVK	0.973939225	2	3.09865
P63039	VTDALNATR	0.947962918	2	3.44299
P63092	**subunit alpha isoforms short**	**2.632397751**	**1.5E-05**	**2**
P63092	AFEPFYDEIKSKGALVK	1.435398962		
P63092	YTTPEDATPEPGEDPR	0.92692358		
P63102	**1433Z 14_3_3 protein zeta/delta**	**2.336009888**	**0.99979**	**10**
P63102	DICNDVLSLLEK	1.29478561	3	3.8173
P63102	EMQPTHPIR	1.375126618	2	2.32383
P63102	FLIPNASQPESK	1.024312921	2	2.90948
P63102	GIVDQSQQAYQEAFEISK	1.021321459	2	5.67016
P63102	KGIVDQSQQAYQEAFEISK	0.902027623	2	5.2667
P63102	SVTEQGAELSNEER	0.701846165	2	5.17422
P63102	TAFDEAIAELDTLSEESYK	1.224198767	3	4.63565
P63102	YDDMAACMK	1.877684718	2	2.52387
P63102	YLAEVAAGDDK	1.006086503	2	2.36058
P63102	YLAEVAAGDDKK	1.092097937	2	3.5155
P63159	**HMGB1 High mobility group protein B1**	**2.085267484**	**0.99893**	**6**
P63159	GEHPGLSIGDVAK	1.093255708	2	2.97856
P63159	GKFEDMAK	0.812749071	1	2.01504
P63159	IKGEHPGLSIGDVAK	1.284163634	2	4.02613
P63159	KHPDASVNFSEFSK	1.032758467	3	4.19383
P63159	KLGEMWNNTAADDKQPYEK	0.912104866	3	4.61693
P63159	LGEMWNNTAADDKQPYEK	1.059553778	2	4.93213
P63174	**RL38 60S ribosomal protein L38**	**2.353267968**	**0.1422**	**2**
P63174	IEEIKDFLLTAR	1.297742225	2	3.03256
P63174	KIEEIKDFLLTAR	1.234474497	2	4.6024
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**2.354125223**	**0.95802**	**13**
P63245	DETNYGIPQR	1.113028313	2	2.52143
P63245	DGQAMLWDLNEGK	1.15764962	2	3.3529
P63245	FSPNSSNPIIVSCGWDK	1.206295485	2	4.22051
P63245	GHNGWVTQIATTPQFPDMILSASR	1.047041948	3	4.1962
P63245	HLYTLDGGDIINALCFSPNR	1.269134525	2	6.13431
P63245	IIVDELK	1.264752931	2	2.49785
P63245	IIVDELKQEVISTSSK	1.241822345	3	4.08416
P63245	IWDLEGK	1.098798319	2	2.36423
P63245	LWDLTTGTTTR	0.8563463	1	1.95773
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.012129466	3	5.39473
P63245	VWNLANCK	0.999928234	2	2.58687
P63245	VWQVTIGTR	1.120538484	2	2.86244
P63245	YWLCAATGPSIK	0.875728839	2	3.53412
P63259	**ACTG Actin_ cytoplasmic 2**	**2.020414376**	**0.47319**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.665817444	3	5.68872
P63259	DLYANTVLSGGTTMYPGIADR	1.000574072	2	6.0936
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13	1.361802548		
P63259	GYSFTTTAER	0.94698717	2	3.51666
P63259	KDLYANTVLSGGTTMYPGIADR	1.116368148	2	6.30012
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14	1.101549978		
P63259	QEYDESGPSIVHR	2.995332991	3	3.50643
P63259	VAPEEHPVLLTEAPLNPK	1.104558104	2	4.68066

P63324	**RS12 40S ribosomal protein S12**	**2.134789053**	**0.98762**	**4**
P63324	KVVGCSCVVVK	0.868846351	2	3.27817
P63324	LGEWVGLCK	1.236379221	2	3.16608
P63324	QAHLCVLASNCDEPMYVK	1.144278997	3	3.98918
P63324	VVGCSCVVVK	1.107759555	2	3.23924
P67779	**PHB Prohibitin**	**1.761571931**	**0.97672**	**11**
P67779	AAELIANSLATAGDGLIELR	1.060840926	3	5.0684
P67779	AAIISAEGDSK	1.028678691	2	2.57841
P67779	DLQNVNITLR	0.745066787	2	3.24295
P67779	FDAGELITQR	0.907407873	2	3.72557
P67779	FGLALAVAGGVVNSALYNVDAGHR	1.252766051	3	3.37601
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	0.945090614	3	4.43454
P67779	IYTSIGEDYDER	1.193269248	2	3.50215
P67779	KLEAAEDIAYQLSR	0.814446835	2	4.64327
P67779	NVPVITGSK	0.817004973	1	2.28696
P67779	QVSDDLTER	0.636526049	2	2.45334
P67779	VLPSITTEILK	1.391047697	2	2.4025
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**2.132330815**	**0.74242**	**4**
P68037	ADLAEEYSK	2.430420051	2	2.38827
P68037	GQVCLPVISAENWKPATK	0.856074347	2	4.40799
P68037	IEINFPAEYPFKPPK	1.155367245	2	3.33293
P68037	TDQVIQSLIALVNDPQPEHPLR	1.31500757	2	5.28861
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.951152901**	**0.54423**	**5**
P68101	AGLNCSTETMPIK	1.222616174	2	3.12973
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.890352793	3	4.07829
P68101	HVAEVLEYTKDEQLESLFQR	0.904532273	3	4.00685
P68101	TEGLSVLNQAMAVIK	1.425572269	2	4.13596
P68101	VVTDTDETELAR	1.026169425	2	3.77996
P68136	**ACTS Actin_ alpha skeletal muscle**	**1.982641946**	**0.98528**	**18**
P68136	AGFAGDDAPR	1.281845333	2	3.46492
P68136	AVFPSIVGRPR	0.907298303	2	2.42247
P68136	DLYANNVMSGGTTMYPGIADR	1.091358203	2	4.72348
P68136	DSYVGDEAQSK	0.962795837	2	3.46228
P68136	DSYVGDEAQSKR	0.491525028	2	2.57108
P68136	EITALAPSTMK	1.270185702	2	2.98434
P68136	EITALAPSTMK+Oxidation(9	0.964077467		
P68136	GYSFVTTAER	1.235425393	2	3.72485
P68136	IWHHTFYNELR	1.936753501	2	2.96148
P68136	KDLYANNVMSGGTTMYPGIADR	3.632425841	2	5.14151
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14	1.230719014		
P68136	MQKEITALAPSTMK	1.004361659	2	3.51916
P68136	QEYDEAGPSIVHR	2.557387953	3	3.30013
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	1.449532849	3	6.09084
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28	2.120780207		
P68136	VAPEEHPTLLTEAPLNPK	1.285041636	2	4.24267
P68136	YPIEHGIITNWDDMEK	1.403128176	2	4.75753
P68136	YPIEHGIITNWDDMEK+Oxidation(13	1.529722354		
P68255	**1433T 14_3_3 protein theta**	**1.787562998**	**0.9897**	**7**
P68255	AVTEQGAELSNEER	0.710596124	2	4.6872
P68255	SICTTVLELLDK	1.139590803	2	3.22655
P68255	TAFDEAIAELDTLNEDSYK	1.155598745	2	3.28603
P68255	VISSIEQK	0.842274801	2	2.60992
P68255	YLAEVACGDDR	0.83824036	2	2.35311
P68255	YLAEVACGDDRK	0.90166136	2	3.1614
P68255	YLIANATNPESK	0.968230682	2	3.17227

P68511	**1433F 14_3_3 protein eta**	**2.255270635**	**0.97888**	**5**
P68511	AVTELNEPLSNEDR	1.135815864	2	4.9965
P68511	ELETVCNDVLALLDK	1.245363974	2	3.5725
P68511	NCNDFQYESK	1.214102644	2	2.61677
P68511	NSVVEASEAAYK	1.081608149	2	2.8063
P68511	YLAEVASGEK	1.340038954	2	2.54534
P69897	**TBB5 Tubulin beta_5 chain**	**2.404742756**	**3E-08**	**4**
P69897	ALTVPELTQQVFDAK	1.162995015	2	3.27548
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	1.506132019	3	4.5293
P69897	ISVYYNEATGGK	1.831925028	2	2.87951
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.987568133	2	5.17076
P70191	**TRAF5 TNF receptor_associated factor 5**	**1.895587951**	**0.86279**	**2**
P70191	SLRELNSVPICPVDK	0.746462548	2	2.34286
P70191	VTLMLLDQSGK	0.945199941	2	2.45972
P70372	**ELAV1 ELAV_like protein 1**	**2.432003388**	**0.34307**	**3**
P70372	SLFSSIGEVESAK	1.283230643	2	3.22271
P70372	TNLIVNYLPQNMTQEELR	1.077291348	2	3.54844
P70372	VLVDQTTGLSR	2.600338124	2	2.79901
P70470	**LYPA1 Acyl_protein thioesterase 1**	**2.395814145**	**0.89141**	**4**
P70470	ASFSQGPINSANR	1.465289911	2	3.09308
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.205444928	3	3.70286
P70470	GLVNPANVTFK	1.355110066	2	2.45555
P70470	VYEGMMHSSCQQEMMDVK	1.055142949	3	3.35158
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**1.7238892**	**9.8E-15**	**11**
P70473	ADVLLEPFR	0.870836337	2	3.33956
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	1.109326468	4	4.72753
P70473	DYGFSQEEIHQLHSDR	0.943708099	2	4.80469
P70473	GLGLESEELPSQMSIEDWPEMK	1.219773761	3	4.50279
P70473	GQNLLDGGAPFYTTYK	0.623816655	2	4.8595
P70473	GSFITDEEQHACPRPAPQLSR	0.530046989	3	4.29839
P70473	LGSVNHPSHLAR	0.824594675	2	3.31241
P70473	LQLGPETLR	0.777558565	2	2.40522
P70473	RDPSVGEHTVEVLK	0.80802851	3	4.24251
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.551459321	4	5.42512
P70473	TQAMGLWAQPR	0.899515893	2	3.47042
P70550	**RAB8B Ras_related protein Rab_8B**	**2.621896758**	**0.00629**	**2**
P70550	LLLIGDSGVGK	1.391992649	2	2.91201
P70550	NIEEHASSDVER	1.203963945	2	2.98077
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**2.04427831**	**0.99995**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	1.348926536	3	5.17034
P70552	VLGNNFYEYYVNDPPR	0.829589496	2	4.28155
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**1.875243782**	**0.98763**	**9**
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	1.568416242	3	5.38445
P70580	EGEEPTVYSDDEEPKDEAAR	0.651629447	2	4.59574
P70580	FYGPEGPYGVFAGR	0.950167166	2	4.53776
P70580	GDQPGASGDNDDDEPPPLPR	70.20216428	2	4.99778
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.139053651	3	5.5517
P70580	KFYGPEGPYGVFAGR	0.640299126	2	3.9042
P70580	LLKEGEEPTVYSDDEEPKDEAAR	1.088244336	3	4.28539
P70580	RYDGVQDPR	0.965418749	1	2.08088
P70580	YDGVQDPR	0.844461085	2	2.87635
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.867980874**	**0.18894**	**9**
P70584	ASSTCQLTFENVK	0.790305122	2	2.89981
P70584	FAQEQIAPLVSTMDENSK	0.901863356	2	4.61998

P70584	IFDFQGLQHQVAHVATQLEAAR	1.223647966	3	6.06027
P70584	IGTIYEGTSNIQLNTIAK	0.92766796	2	4.50766
P70584	KFAQEQIAPLVSTMDENSK	0.751435563	2	6.00841
P70584	SGNYYVINGSK	1.054996439	2	3.36215
P70584	SVIQGLFQQGMMGIEVEAK	1.227804586	2	4.49709
P70584	VDASVALLCDIQNTVINK	1.131859708	2	4.87087
P70584	YYASEVAGLTTSK	0.988143685	2	4.22422
P70615	**LMNB1 Lamin_B1**	**1.865089622**	**0.59397**	**5**
P70615	ALYETELADAR	1.399434366	2	3.11991
P70615	KESDLSGAQIK	0.938110956	2	2.45197
P70615	LSSEMNTSTVNSAR	1.167229542	2	3.93546
P70615	NQNSWGTGEDVK	0.856958501	2	3.36962
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.558734758	3	3.62123
P70712	**KYNU Kynureninase**	**2.027590433**	**0.51087**	**11**
P70712	FKDCFYIPK	1.192826984	2	2.65154
P70712	IATELNCDPTDER	1.481891029	2	3.81566
P70712	IGAYGHEVGK	2.027567461	2	2.83386
P70712	LDEEDKLK	0.581437024	2	2.33185
P70712	LDEEDKLKR	1.30806982	2	2.68761
P70712	LLTAILDSTERN	1.501937285	2	3.30672
P70712	MEDILEVIEK	1.830426337	2	3.05429
P70712	TYLEEELDK	1.60308893	1	2.10386
P70712	TYLEEELDKWAK	0.747064751	2	2.73616
P70712	VAPVPLYNSFHDVYK	1.447772558	2	3.42916
P70712	YLNSGAGGLAGAFIHEK	1.727323226	2	4.45625
P80067	**CATC Dipeptidyl peptidase 1**	**2.274160126**	**0.00859**	**5**
P80067	GINFVSPVR	1.007887587	2	3.00439
P80067	GTDECAIESIAMAAIPIPK	1.202462217	2	5.13728
P80067	NSWGSQWGESGYFR	1.377440762	2	3.41384
P80067	RGTDECAIESIAMAAIPIPK	1.362950834	2	4.1065
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.215531588	3	5.78283
P80254	**DOPD D_dopachrome decarboxylase**	**1.907111178**	**0.95448**	**4**
P80254	FFPLEPWQIGK	0.809946907	2	2.78907
P80254	FLTEELSLDQDR	1.045481625	2	3.73394
P80254	LCAATATILDKPEDR	1.253002778	2	4.48946
P80254	STEPCAHLLISSIGVVGTAEQNR	0.646273599	2	5.49589
P80299	**HYES Epoxide hydrolase 2**	**1.916846174**	**0.99834**	**4**
P80299	ATEMGGILVGTPEDPK	1.382671523	2	3.47082
P80299	GHIEDCGHWTQIEKPAEVNQILIK	0.904866163	3	4.25433
P80299	TEIQNPSVTSK	0.956025361	2	2.65669
P80299	TSDDMGLLTVNK	0.913375645	2	3.20538
P80313	**TCPH T_complex protein 1 subunit eta**	**2.365505989**	**0.63268**	**6**
P80313	ATISNDGATILK	1.2076955	2	2.63486
P80313	EGTDSSQGIPQLVSNISACQVIAEAVR	3.366113372	3	4.1569
P80313	GGAEQFMEETER	1.066389972	2	3.14914
P80313	LLDVVHPAAK	1.2122837	2	2.54936
P80313	QLCDNAGFDATNILNK	1.302154375	2	3.84561
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.339565276	2	3.45923
P80317	**TCPZ T_complex protein 1 subunit zeta**	**2.21822158**	**0.77837**	**10**
P80317	ALQFLEQVK	1.33513531	2	2.70419
P80317	DGNVLLHEMQIQHPTASLIAK	1.176759067	3	4.66417
P80317	GIDPFSLDALAK	1.818478846	2	2.82951
P80317	HKSETDTSLIR	1.096946457	2	3.14319
P80317	IITEGFEAAK	1.212066124	2	2.53183
P80317	MLVSGAGDIK	1.295214672	2	2.34865
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.049636452	3	3.73285
P80317	TEVNSGFFYK	1.090615149	2	2.66682

P80317	VATAQDDITGDGTTSNVLIIGELLK	1.145082616	2	4.71373
P80317	VLAQNSGFDLQETLVK	1.124987516	2	3.73282
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**1.690406961**	**0.83893**	**4**
P81155	LTFDTTFSPNTGK	1.194977665	2	3.5944
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.105696271	3	3.98552
P81155	VNNSSLIGVGYTQTLRPGVK	0.47170818	2	3.58643
P81155	YQLDPTASISAK	0.90660844	2	2.94988
P82198	**BGH3 Transforming growth factor_beta_induced protein ig_h3**	**2.032104137**	**0.56748**	**2**
P82198	MLTPPMGTVMDVLK+Oxidation(0)Oxidation(5	1.488294146		
P82198	SLQGDKLEVSSK	0.999092917	2	3.09666
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.99982331**	**0.52023**	**14**
P82995	DQVANSAFVER	0.939946714	2	2.6804
P82995	ELHINLIPNKQDR	0.751685253	2	2.8195
P82995	ELISNSSDALDK	1.160347827	2	2.92874
P82995	FYEQFSK	0.99822882	1	2.10674
P82995	HIYFITGETK	1.104534177	2	3.13323
P82995	HLEINPDHSIIETLR	1.034215961	2	4.68653
P82995	HSQFIGYPITLFVEK	1.598642281	3	3.72292
P82995	KHGLEVIYMIEPIDEYCVQQLK	1.301645216	3	3.33036
P82995	LGIHEDSQNR	0.888556526	1	3.11124
P82995	NPDDITNEEYGEFYK	0.843183798	2	5.08747
P82995	SLTNDWEEHLAVK	1.120329938	2	4.05766
P82995	TLTIVDTGIGMTK	1.171868971	2	4.27911
P82995	TLTIVDTGIGMTK+Oxidation(10	1.578458894		
P82995	YYTSASGDEMVSLK	1.263802327	2	3.13773
P83732	**RL24 60S ribosomal protein L24**	**2.263492235**	**0.99264**	**5**
P83732	AITGASLADIMAK	1.178337639	2	4.61999
P83732	CESAFLSK	1.156471848	2	2.36607
P83732	QINWTVLYR	1.207067495	2	2.59706
P83732	VELCSFSGYK	1.009451734	2	2.34048
P83732	VFQFLNAK	1.484895701	2	2.34652
P83868	**TEBP Prostaglandin E synthase 3**	**3.442527972**	**0.00113**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.785484074	3	4.05379
P83868	LTFSCLGGSDNFK	1.729298861	2	2.75563
P83883	**RL36A 60S ribosomal protein L36a**	**1.933974308**	**0.94488**	**2**
P83883	HFELGGDK	0.921954942	1	2.37839
P83883	LECVEPNCR	1.012594041	2	2.52478
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**2.260775514**	**0.91184**	**3**
P83941	AMLSGPGQFAENETNEVNFR	1.239476509	2	4.9483
P83941	LISSDGHEFIVK	1.074258889	2	2.40548
P83941	TYGGCEGPDAMYVK	1.167612138	2	3.82124
P84082	**ARF2 ADP_ribosylation factor 2**	**2.377076705**	**0.98076**	**4**
P84082	EELTRMLAEDELR+Oxidation(5	1.260223616		
P84082	MLAEDELR	0.904692647	2	2.60286
P84082	NISFTVWDVGGQDK	1.330993745	2	4.32412
P84082	QDLPNAMNAAEITDK	0.732320211	2	4.20599
P84083	**ARF5 ADP_ribosylation factor 5**	**2.099992209**	**0.87191**	**4**
P84083	DAVLLVFANK	1.253240071	2	4.12166
P84083	MLQEDELR	1.320996585	2	2.47275
P84083	QDMPNAMPVSELTDK	0.958255199	2	3.3521
P84083	VQESADELQK	0.979266306	2	3.07039
P84089	**ERH Enhancer of rudimentary homolog**	**2.090813942**	**0.99982**	**2**
P84089	ADTQTYQPYNK	0.99286975	2	2.60988
P84089	TYADYESVNECMEGVCK	1.098464308	2	4.88009

P84092	**AP2M1 AP_2 complex subunit mu**	**2.149178395**	**0.81281**	**3**
P84092	ISEENIK	0.871361055	1	1.94984
P84092	SNFKPSLLAQK	1.307945643	2	2.61487
P84092	VFEPKLNYSDHDVIK	0.974728429	2	2.74565
P84100	**RL19 60S ribosomal protein L19**	**2.045997001**	**0.98041**	**3**
P84100	ILMEHIHK	1.256186855	2	2.32009
P84100	LLADQAEAR	1.105614882	2	3.31571
P84100	VWLDPNETNEIANANSR	1.002419736	2	5.6317
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**2.151655**	**0.94291**	**2**
P84104	NPPGFAFVEFEDPRDAADAVR	1.123775402	2	2.57823
P84104	VYVGNLGNNGNK	0.96400364	2	2.43126
P84245	**H33 Histone H3.3**	**1.969475954**	**0.99717**	**6**
P84245	DIQLAR	174.0398298	1	2.10984
P84245	EIAQDFK	1.01918362	1	2.04089
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.05083441	4	4.91517
P84245	RVTIMPKDIQLAR+Oxidation(4	1.026797065		
P84245	STELLIR	0.975530146	2	2.60949
P84245	YRPGTVALR	0.943791712	2	2.38365
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.955232156**	**0.99939**	**4**
P84817	FQSEQAAGSVSK	0.954961982	2	3.05102
P84817	GIVLLEELLPK	1.137224768	2	2.95042
P84817	GLLQTEPQNNQAK	1.04031874	2	3.69501
P84817	KFQSEQAAGSVSK	0.873745567	2	4.47906
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**1.829701287**	**0.9851**	**16**
P85834	AEAGDNLGALVR	0.978408792	2	3.70053
P85834	DKPHVNVGTIGHVDHGK	1.187316234	2	3.84595
P85834	DLEKPFLLPVESVYSIPGR	1.190859458	2	4.22639
P85834	GDECELLGHNK	0.86106045	2	2.87543
P85834	GEETPVIVGSALCALEQR	1.284179818	2	4.40429
P85834	GITINAAHVEYSTAAR	0.847465346	2	2.84616
P85834	GTVVTGTLER	0.895035186	2	2.84794
P85834	HYAHTDCPGHADYVK	0.902494118	3	5.00971
P85834	KGDECELLGHNK	0.829947523	3	4.43353
P85834	KYEEIDNAPEER	0.848874667	2	3.79296
P85834	LLDAVDTYIPVPTR	1.299413085	2	3.68734
P85834	QIGVEHVVVYVNK	0.957700911	2	2.96328
P85834	TIGTGLVTDVPAMTEEDK	1.11827909	2	4.34158
P85834	TIGTGLVTDVPAMTEEDKNIK	1.064954523	2	4.45657
P85834	TVVTGIEMFHK	0.714039953	2	2.34417
P85834	YEEIDNAPEER	0.757678913	2	3.34903
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**2.304862434**	**0.99131**	**11**
P85968	AGQAVDDFIEK	1.035020057	2	3.25126
P85968	CLSSLKEER	0.989259751	2	2.59507
P85968	FQDTDGKELLPK	0.946275679	2	3.43098
P85968	GILFVGSGVSGGEEGAR	1.008968291	2	4.65492
P85968	HEMLPANLIQAQR	1.126426992	2	3.19334
P85968	LVPLLDTGDIIIDGGNSEYR	1.731089278	2	5.25314
P85968	NPELQNLLLDDFFK	1.255166576	2	4.43964
P85968	SAVDDCQDSWR	1.089984557	2	2.88359
P85968	TIFQAIAAK	0.737748865	2	2.69486
P85968	VGTGEPCCDWVGDEGAGHFVK	1.038311665	2	4.34917
P85968	YGPSLMPGGNK	1.048155019	2	2.48159
P85971	**6PGL 6_phosphogluconolactonase**	**2.052506383**	**0.88272**	**5**
P85971	DLPAATAPAGPASFAR	2.617731314	2	2.44906
P85971	ILEDQESALPAAMVQPR	0.825753593	2	4.80588
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.31137877	2	4.51289

P85971	TGALCWFLDEAAAR	0.471331959	2	3.57978
P85971	WTLGFCDER	1.175811817	2	2.58393
P85972	**VINC Vinculin**	**2.051459498**	**0.01732**	**15**
P85972	ALASQLQDSLK	1.050079171	2	2.60335
P85972	AQQVSQGLDVLTAK	1.007044988	2	4.30009
P85972	AVAGNISDPGLQK	0.864483468	2	3.35269
P85972	DPNASPGDAGEQAIR	1.02543246	2	2.36029
P85972	GNDIIAAAK	1.074205769	2	2.43386
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.68694846	3	5.11621
P85972	MLGQMTDQVADLR	1.013107616	2	3.52398
P85972	MSAEINEIIR	1.048281228	2	2.43627
P85972	MTGLVDEAIDTK	0.793759838	2	2.84285
P85972	QVATALQNLQTK	1.074983849	2	3.38661
P85972	SLLDASEEAIKK	1.156578354	2	2.73273
P85972	STVEGIQASVK	0.95853471	2	2.6099
P85972	VDQLAAQLADLAAR	1.333030107	2	3.26841
P85972	VLQLTSWDEDAWASK	1.292116798	2	3.26238
P85972	WIDNPTVDDR	1.655638119	2	2.97304
P85973	**PNPH Purine nucleoside phosphorylase**	**2.181235971**	**3E-06**	**13**
P85973	ASHQEVLEAGK	0.821042593	2	3.59789
P85973	DHINLPGFCGQNPLR	1.086712069	3	4.05178
P85973	ELQEGTYIMSAGPTFETVAESCLLR	1.114271641	2	5.21222
P85973	FEVGDIMLIR	1.183578614	2	3.79963
P85973	FHMYEGYSLSK	1.304362712	2	2.33016
P85973	HRPQVAVICGSGLGGLTAK	0.995519171	3	6.00344
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.565542486	3	3.77808
P85973	MLGADAVGMSTVPEVIVAR	1.205131438	2	5.9071
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0	1.590248056		
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(8	1.722157622		
P85973	VFGFSLITNK	1.139555229	2	3.13525
P85973	VFHLLGVDTLVVTNAAGGLNPK	1.613764058	2	5.39375
P85973	VVMDYNNLEK	1.142946838	2	2.4631
P86048	**RL10L 60S ribosomal protein L10_like**	**2.128881673**	**0.9745**	**6**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.328718326	3	6.04248
P86048	GAFGKPQGTVAR	1.006528249	2	2.82714
P86048	MLSCAGADR	0.95843807	2	2.36663
P86048	RLIPDGCGVK	0.756693855	2	2.31498
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.148233573	3	5.43705
P86048	VHIGQVIMSIR	2.03969836	2	3.01557
P86252		**1.967255278**	**0.9735**	**7**
P86252	ALELDPNLYR	1.024327761		
P86252	ANGFAELIPNAQLLQK	0.793750826		
P86252	CTSLGVNQGIYEEPK	0.913266571		
P86252	LGFQGAQDLANMFRFYALKPDR	1.664063887		
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	1.519512863	2	4.02937
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	2.884229341	3	4.51811
P86252	VASDAQLELDKLDGELKK	1.088526115		
P97313	**PRKDC DNA_dependent protein kinase catalytic subunit**	**2.346977218**	**0.51349**	**3**
P97313	FHGVMKTLCLEVVLCR+Oxidation(4	0.889348072		
P97313	LCHDAFTENMVGESQLLEK	3.045631857	2	2.53486
P97313	QLFSSLFSGILKEMNK+Oxidation(13	1.541877031		
P97384	**ANX11 Annexin A11**	**2.658838805**	**0.65767**	**2**
P97384	GFGTDEQAIIDCLGSR	1.226083555	2	3.95441
P97384	SELDLLDIR	1.707699323	2	2.54409
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**2.333942035**	**0.09686**	**8**

P97519	FDGVMQAAR	1.202115331	2	2.83092
P97519	GFEEAVAAGAK	1.060645555	2	3.3043
P97519	GYVSCALGCPYEGK	0.892910414	2	3.86554
P97519	KNVNCSIEESFQR	1.061949862	2	3.74566
P97519	LIDMLSEAGLPVIEATSFVSPK	1.194951221	2	3.10489
P97519	LLEAGDFICQALNR	1.258085062	2	4.5365
P97519	NVNCSIEESFQR	0.800035622	2	3.39504
P97519	WVPQMADHSDVLK	0.935118166	2	2.95169
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**2.152464799**	**7.5E-06**	**7**
P97521	CLLQIQASSGK	0.892793841	2	2.60499
P97521	EEGVTSLYK	0.851937036	1	2.03939
P97521	KLYQEFGIR	1.067233215	2	2.32925
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.244787433	2	3.84684
P97521	LYQEFGIR	1.171642353	2	2.76219
P97521	SVHDLSVPR	0.937282339	3	3.55046
P97521	YSGTLDCAK	1.008091505	2	2.35282
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**2.067463663**	**0.79582**	**13**
P97524	ALHDHLGLR	0.641668602	2	2.33459
P97524	GEVGLLICK	1.047144638	2	2.33828
P97524	MKENYEFNGK	0.967238967	2	2.80226
P97524	SLLHCFQCCGAK	0.931396967	2	2.95297
P97524	TILHVFLEQAR	0.846384672	2	3.18124
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	1.034554106	3	5.69118
P97524	TYVPMTEDIYNAIIDK	1.019525548	3	4.79446
P97524	VDGVSADPIPESWR	1.109629344	2	2.8722
P97524	VLLASPELHEAVEEVLPTLK	1.242540432	3	4.92837
P97524	VTLMEEGFNPSVIK	1.637186649	2	4.18738
P97524	YDVEKDEPVR	1.017091037	2	2.89871
P97524	YLCNTPQKPNDR	1.239331722	2	3.21542
P97524	YNATVIQYIGELLR	1.07522171	2	3.48417
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**2.225485321**	**9.9E-20**	**10**
P97532	AFGHHSVSLLDGGFR	0.966803438	3	3.68447
P97532	ALVSAQWVAEALK	1.180765409	2	3.89037
P97532	AQPEHVISQGR	0.662084619	2	3.20836
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.052564995	3	6.45815
P97532	FQGTQPEPR	0.897545765	2	3.61153
P97532	HIPGAAFFDIDR	1.22633043	2	2.55749
P97532	LLDASWYLPK	1.375950902	2	3.73522
P97532	SPSEPAEFCAQLDPSFIK	0.870199035	2	2.95029
P97532	THEDILENLDAR	0.995345157	2	3.8751
P97532	YWLSQNLPISSGK	1.154731281	2	3.95519
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**2.441957958**	**0.00017**	**7**
P97536	AADIDQEVK	0.822288472	2	2.4843
P97536	EGPAVVGQFIQDVK	1.761984258	2	2.72115
P97536	FTISDHPQPIDPLLK	1.279323076	2	2.59571
P97536	ITSEALLVTQQLVK	1.466123319	2	3.15254
P97536	LGTLSALDILIK	1.96891405	2	2.45544
P97536	SVILEAFSSPSEEVK	1.065519117	2	2.88589
P97536	TYIQCIAAISR	1.14169368	2	3.45873
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.970645228**	**0.98678**	**16**
P97562	ATFADFCAQGAEICR	0.923173961	2	4.74954
P97562	CSAQTAADFR	0.908432842	2	2.93616
P97562	DFSLLPELHALSTGMK	0.813149515	2	2.82399
P97562	EAFLDLLPLIR	0.673916333	2	2.86014
P97562	ILEYQTQQQK	0.896043379	2	3.73719

P97562	KVESIIQSDPVFNLK	1.199450668	2	5.03614
P97562	LDKEPEIQR	0.93415706	3	3.40215
P97562	LFEWAQK	0.971932407	2	2.52092
P97562	LGTPQSNYLGMLVTR	1.374576489	2	3.37665
P97562	LSGLPTLVAR	1.136643254	2	2.52578
P97562	LTNILDGGLPNTVLR	1.125744712	2	4.49674
P97562	SGVDQHDAWNQTTVIHLQAAK	1.074520491	3	6.02312
P97562	SLEDHTPLPGITVGDIGPK	1.12584411	3	4.34066
P97562	SLGSDEQIAK	0.932266007	2	3.00689
P97562	VESIIQSDPVFNLK	0.96898714	2	4.26298
P97562	VLDGNVNLSLHGVAMNAIR	0.873875829	2	4.33949
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.973527353**	**0.98602**	**4**
P97576	ALADTENLR	1.292120389	2	2.58873
P97576	DLLEVADILEK	0.951893963	2	3.68469
P97576	EEVSNNNPHLK	0.997549433	2	3.04738
P97576	TLRPALVGVVK	0.647008203	3	3.54107
P97584	**PTGR1 Prostaglandin reductase 1**	**2.052491992**	**0.97944**	**6**
P97584	ALTDLMNWVSEGK	1.308971598	2	4.18498
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.158268894	2	4.19693
P97584	HFEGFPTDSNFELR	1.025492223	2	3.78283
P97584	LKEGDSMMGEQVAR	0.685483906	2	3.77997
P97584	TGPCPPGPSPEVIIYQQLR	1.238850196	2	4.12981
P97584	YHEYITEGFEK	1.054010052	2	2.9319
P97608	**OPLA 5_oxoprolinase**	**1.988897157**	**0.99978**	**8**
P97608	AGDFGAAFVER	0.949668967	2	2.93049
P97608	GHTACADAYLTPTIQR	0.968794983	2	4.58662
P97608	GSILDPSPEAAVVGGNVLTSQR	1.27877125	2	4.96314
P97608	ISVGAEGPSMADTR+Oxidation(9	0.855655347		
P97608	ITDPEILESR	1.220196436	2	2.37036
P97608	LLSEDPANYADAPTEGIR	1.195519695	2	4.94868
P97608	SGLQLEDTPK	0.996679264	2	2.62954
P97608	TGDLLEIQQPVDLEALR	1.22867996	2	4.63633
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**2.127031065**	**0.69956**	**7**
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.487729475	3	3.97085
P97612	GTNCVTSYLTDCETQLSQAPR	1.181734858	2	4.94526
P97612	GYFGDIWDIILK	1.253238537	2	3.8686
P97612	NSVGLPVAVQCVALPWQEELCLR	1.6287528	3	3.81573
P97612	QGLLYGVPVSLK	1.010854884	2	2.85252
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	2.215490206	2	4.75659
P97612	VGYYETDNYTMPSPAMR	0.926715821	2	4.02943
P97690	**SMC3 Structural maintenance of chromosomes protein 3**	**2.174212757**	**0.87746**	**2**
P97690	KMVTKNDVMNLLESAGFSR+Oxidation(1	1.123017518		
P97690	NLEQYNKLDQDLNEVK	0.975321821	2	2.59066
P97697	**IMPA1 Inositol monophosphatase 1**	**1.958603469**	**0.99941**	**2**
P97697	SSPADLVTVTDQK	1.068399147	2	2.85215
P97697	VSQQEDITK	0.96937489	2	2.80689
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**2.264891703**	**0.12344**	**3**
P97700	AVVVNAAQLASYSQSK	0.977351224	2	4.98374
P97700	GIYTGLSAGLLR	1.618401808	2	2.9893
P97700	LTGADGTPPGFLLK	1.370744176	2	3.86219
P97834	**CSN1 COP9 signalosome complex subunit 1**	**2.18448912**	**0.95654**	**3**
P97834	EGSQGELTPANSQSR	1.12861742	2	2.88486
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(0	0.767831869		
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(4	0.767831869		
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**1.870624982**	**1.4E-09**	**25**

P97852	AAVAVPSRPPDAVLR	0.895442022	2	2.30481
P97852	AVANYDSVEAGEK	1.43912665	2	3.81081
P97852	AYALAFAER	1.051826193	2	3.41125
P97852	CEAVIADILDK	1.094947093	2	2.56768
P97852	DTTSLNQAALYR	0.674664239	2	2.89049
P97852	FVYEGSADFSCLPTFGVIVAQK	0.932172068	2	3.68289
P97852	GALVVVNDLGGDFK	1.355353198	2	3.86066
P97852	GSSAADKVVEEIR	0.768947389	2	3.45239
P97852	HVLQQFADNDVSR	0.847627448	2	4.7001
P97852	ICDFSNASKPK	1.150443874	3	3.90532
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	0.935107533	3	5.6722
P97852	IDVVVNNAGILR	0.93133921	2	4.07432
P97852	ISDEDWDIIQR	2.67733802	2	3.69188
P97852	KNNIHCNTIAPNAGSR	0.74288232	2	5.0497
P97852	LGLLGLANTLVIEGR	1.232281996	2	3.62375
P97852	LNPQNAFFSGR	0.862019385	2	2.83874
P97852	NGSGEVYQGPAK	0.745426752	2	3.49526
P97852	NNIHCNTIAPNAGSR	0.830136594	2	4.6499
P97852	NQPMTPEAVR	0.875793932	2	2.35201
P97852	SIQESTGGIIEVLHK	0.897780448	2	4.16707
P97852	SLMSGGLAEVPGLSINFAK	1.045613153	2	4.57451
P97852	TALDTFGR	1.184900216	2	2.33081
P97852	VLHGEQYLELYKPLPR	1.037308093	2	5.01675
P97852	VNAVFEWHITK	1.040158165	2	3.16815
P97852	VVLVTGAGGGLGR	0.927519725	2	4.37584
P97874	**GAK Cyclin_G_associated kinase**	**1.967755513**	**0.78474**	**2**
P97874	AMVEEEITRNTTPMYR+Oxidation(13	2.289681314		
P97874	QELARDTDPFKLK	0.941427128	2	2.40881
Q00238	**ICAM1 Intercellular adhesion molecule 1**	**2.324424403**	**0.72082**	**2**
Q00238	LDTPDLLEVGTQQK	1.216682075	2	3.51144
Q00238	VELDPLPAWQQVGK	1.225488974	2	2.48009
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**2.130202105**	**0.99032**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	1.305902047	2	4.6329
Q00438	IIVENLFYPVTLDVLHQIFSK	0.940806179	3	4.3289
Q00438	KLPSDVTEGEVISLGLPFGK	1.154751524	2	4.36934
Q00438	NNQFQALLQYADPVSAQHAK	1.090096589	2	5.46689
Q00981	**UCHL1 Ubiquitin carboxyl_terminal hydrolase isozyme L1**	**1.889067458**	**0.77082**	**2**
Q00981	KQIEELK	0.929339691	2	2.35295
Q00981	MQLKPMEINPEMLNK+Oxidation(0	0.883480547		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**2.528459182**	**0.54371**	**3**
Q00PI9	AVEEQGDDQDSEK	1.739745736	2	3.98971
Q00PI9	EEAQPIVTKYK	1.365747113	1	1.97118
Q00PI9	SGDETPGSEAPGDK	0.962888929	2	3.24144
Q01177	**PLMN Plasminogen**	**1.922685278**	**0.99749**	**3**
Q01177	ILGSDVQQIAVTK	0.933672251	2	3.79419
Q01177	LVLEPNDADIALLK	0.985442469	2	2.81975
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	0.943582209	3	4.06154
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.938321767**	**1**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.009243237	2	6.16508
Q01205	NDVITVQTPAFAESVTEGDVR	0.914483652	2	5.40729
Q01205	NVETMNYADIER	1.019618184	2	3.76866
Q01205	VEGGTPLFTLR	0.872819299	2	3.43586
Q01279	**EGFR Epidermal growth factor receptor**	**2.663930419**	**0.36013**	**2**

Q01279	NLQEILIGAVR	1.742111234	2	3.96008
Q01279	NYVVTDHGSCVR	0.834337869	2	2.69813
Q01405	**SC23A Protein transport protein Sec23A**	**2.2802157**	**0.18318**	**8**
Q01405	AETEEGPDVLR	1.198416697	2	3.22714
Q01405	AVLNPLCQVDYR	1.478795218	2	2.71889
Q01405	HFEALANR	0.86877013	1	2.021
Q01405	HLLQAPVDDAQEILHSR	0.990381841	3	5.49159
Q01405	MVVPVAALFTPLK	1.44676279	2	2.62188
Q01405	SGYQDMPEYENFR	0.387362879	2	3.09491
Q01405	SWHDIEKDNAK	1.137772857	2	3.13193
Q01405	YIDTEHGGSQAR	0.964244602	2	3.4385
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**2.216832064**	**0.99999**	**33**
Q02253	AEMEAAVAACK	1.054881198	2	4.01936
Q02253	AEMEAAVAACK+Oxidation(2	0.970004677		
Q02253	AEMEAAVAACKR	0.539172128	2	3.11029
Q02253	AFPAWADTSILSR	1.122165271	2	4.13204
Q02253	AISFVGSNQAGEYIFER	0.872365967	2	5.27586
Q02253	CMALSTAVLVGEAK	0.91031148	2	4.49299
Q02253	CMALSTAVLVGEAK+Oxidation(1	0.85561786		
Q02253	EEDATLSSPAVVMPTMGR	1.689299331	2	4.73156
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12	5.574012622		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15	5.574012622		
Q02253	EEIFGPVLVVLETETLDEAIK	0.773691379	2	3.30997
Q02253	ENTLNQLVGAAFGAAGQR	1.053908969	2	5.14734
Q02253	GDTNFYGK	0.963742128	2	2.61748
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.410166567	2	5.64712
Q02253	GYENGNFVGPTIISNVKPSMTCYK	1.020490925	3	3.85656
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.137658015	2	5.39841
Q02253	KWLPELVER	1.451014543	3	3.3318
Q02253	LFIDGK	1.295730328	1	2.01425
Q02253	LITLEQGK	1.114348891	2	2.82319
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.380772108	3	4.35551
Q02253	NHGVVMPDANK	0.985808276	2	3.56681
Q02253	NHGVVMPDANK+Oxidation(5	1.092864948		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	1.282124627	3	6.13728
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5	1.24720877		
Q02253	QGIQFYTQLK	0.779655202	2	2.79436
Q02253	SDKWIDIHNPATNEVVGR	0.900373218	2	5.26877
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	1.0234193	2	5.47582
Q02253	TLADAEGDVFR	0.899694497	2	3.67223
Q02253	VCNLIDSGAK	0.944048205	2	3.39308
Q02253	VNAGDQPGADLGPLITPQAK	1.166693535	2	5.87971
Q02253	WIDIHNPATNEVVGR	1.047070081	2	4.89131
Q02253	WLPELVER	0.913276214	2	2.40156
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.269719539	3	3.527
Q02769	**FDFT Squalene synthase**	**1.825566203**	**0.06734**	**4**
Q02769	KLEDFVKPENVDVAVK	0.510925964	2	4.03598
Q02769	SFAAVIQALDGDIR	0.857054478	2	3.66306
Q02769	TQSLPNCQLISR	0.426124017	2	2.91068
Q02769	VVLEDFPTISLEFR	0.932908331	2	3.28107
Q02874	**H2AY Core histone macro_H2A.1**	**2.441860245**	**0.75981**	**4**
Q02874	AASADSTTEGAPTDGFTVLSTK	1.140768312	2	4.1946
Q02874	GVTIASGGVLPNIHPELLAK	1.373371766	2	4.20125
Q02874	NCLALADDR	1.051412388	2	2.47509
Q02874	NGPLEVAGAAVSAGHGLPAK	0.848299619	2	2.81014

Q02974	**KHK Ketohexokinase**	**2.320086636**	**0.99654**	**8**
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.526535763	3	5.58082
Q02974	GGNASNSCTVLSLLGAR	0.916279613	2	4.72008
Q02974	GNSMQEALR	1.043841635	2	3.00488
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.867166577	3	5.85364
Q02974	IEQYNATQPLQQK	0.996967655	2	4.81642
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.833124024	3	6.50053
Q02974	TIILYDTNLPDVSAK	1.036983687	2	5.15103
Q02974	VSVEIEKPR	1.227518514	2	2.51895
Q03248	**BUP1 Beta_ureidopropionase**	**2.231595445**	**0.79649**	**15**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.153683569	2	6.14191
Q03248	EDLVLAPSSG	0.661659562	1	2.23347
Q03248	EKLPWTEFAESAEDGLTTR	0.854752041	2	4.72128
Q03248	ELAEAVKPNYSPNIVK	1.032602019	2	4.65263
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	2.45268141	3	3.49001
Q03248	HLPPDDLSQVK	0.947495246	2	2.52937
Q03248	HNMVVISPILER	1.194326783	2	3.08294
Q03248	HNMVVISPILER+Oxidation(2	1.167905718		
Q03248	IPLPTSAPVAEQVSALHK	1.520627168	3	4.87513
Q03248	KHNMVVISPILER	2.26354197	3	3.55404
Q03248	KHNMVVISPILER+Oxidation(3	0.791628541		
Q03248	NAAIANHCFTCALNR	1.245514814	2	4.68958
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.240327566	3	5.1116
Q03248	VGQEHYPNEFTSGDGK	1.224312663	2	4.35579
Q03248	VGQEHYPNEFTSGDGKK	1.085867768	3	4.79651
Q03336	**RGN Regucalcin**	**1.967235482**	**1**	**16**
Q03336	CGESPVWEEASK	1.025016493	2	4.66944
Q03336	CLLFVDIPSK	1.007522414	2	3.42409
Q03336	DEQIPDGMCIDVEGK	1.14425682	2	4.44365
Q03336	DYSEMYVTCAR	0.780152607	2	3.2685
Q03336	FNDGKVDPAGR	0.584940906	2	3.0518
Q03336	HQGSLYSLFPDHSVK	0.995578114	3	4.89784
Q03336	KYFDQVDISNGLDWSLDHK	1.09889657	3	4.96737
Q03336	LWVACYNGGR	1.344225598	2	2.76679
Q03336	MEKDEQIPDGMCIDVEGK	1.035585048	2	5.0652
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0	0.895600156		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10	1.150183055		
Q03336	QSGGYVATIGTK	0.997169766	2	2.78621
Q03336	VGVDAPVSSVALR	0.923463045	2	3.56801
Q03336	YFAGTMAEETAPAVLER	1.093839637	2	5.67048
Q03336	YFAGTMAEETAPAVLER+Oxidation(5	3.049891263		
Q03336	YFDQVDISNGLDWSLDHK	1.223689627	2	4.6959
Q03410	**SYCP1 Synaptonemal complex protein 1**	**2.013704647**	**0.70792**	**2**
Q03410	ATVDEAVKLQKEIDLR	0.877317124	2	2.46675
Q03410	LKMEQENTAILTDK	1.11128584	2	2.36828
Q03626	**MUG1 Murinoglobulin_1**	**2.293654256**	**0.02026**	**7**
Q03626	EDNSIHWERPQKPTK	1.002380808	2	2.6232
Q03626	EESSCIHSSCTAER	1.116859271	2	4.23187
Q03626	GGEFEMMPLGVNK	0.934335134	2	3.47751
Q03626	LTAQPAPSPEDLALSMGTIK	1.653315194	3	4.12259
Q03626	NLHPLNELFPLAYIEDPK	1.777866786	3	4.11805
Q03626	VQTVPLTCNNPK	1.096566812	2	2.96447
Q03626	VYHKEESSCIHSSCTAER	1.191877105	2	5.81911
Q04462	**SYVC Valyl_tRNA synthetase**	**1.887453871**	**0.88533**	**4**
Q04462	ALNPLEEWLR	0.927752715	2	2.33317
Q04462	ITPAHDQNDYEVGQR	1.0074488	2	3.68737
Q04462	LQQTEAELR	0.815780906	2	2.34132

Q04462	SVTQQPGSEITAPQK	0.910866614	2	3.54637
Q05982	**NDKA Nucleoside diphosphate kinase A**	**2.208193607**	**0.64885**	**2**
Q05982	EISLWFQPEELVDYK	1.235632932	2	2.85258
Q05982	FIQASEDLLK	1.142814308	2	2.36531
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**2.283799355**	**0.96123**	**8**
Q06647	FSPLTANLMNLLAENGR	1.308840812	2	4.31037
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.100269174	3	6.04703
Q06647	GQILNLEVK	0.834218679	2	2.73665
Q06647	LGNTQGVISAFSTIMSVHR	1.165450913	3	3.64138
Q06647	TDPSIMGGMIVR	1.084050284	2	3.32039
Q06647	TVLNSFLSK	0.950109804	2	2.72552
Q06647	VGQLLKDPK	0.803846562	1	2.1613
Q06647	VSLAVLNPYIK	1.314237736	2	3.58112
Q07071	**GCKR Glucokinase regulatory protein**	**2.691402974**	**0.00417**	**13**
Q07071	AAPISCHVQVAHEK	1.064497923	2	4.90169
Q07071	CIESLLQAIHFPQPLSDDVR	1.470486024	3	4.44121
Q07071	CLLEILR	1.576650555	2	2.52696
Q07071	GFLIGDHSDMFNQK	1.250110364	2	3.83192
Q07071	LLGQCDAEIFQEEGQIVPTYQR	2.720252806	2	5.03187
Q07071	LSAASSVCEVVR	1.074417588	2	2.792
Q07071	LYSESVLTTMLQVAGK	1.424304014	2	3.83555
Q07071	QEAFVLNPAIGPEGLSGSSR	1.34527982	2	4.86258
Q07071	TVDQGVVSSQR	1.340534783	2	3.56929
Q07071	VIPTALLSLLLR	0.842285816	2	2.96802
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.256085916	2	5.05545
Q07071	WVLNTVSTGAHVLLGK	2.005772885	2	3.4445
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.560512225	3	6.07007
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**1.992433434**	**0.98541**	**9**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.851753586	2	4.61876
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	1.837024547	3	3.93677
Q07116	FVDLHPGGQSK	1.216861808	2	2.67693
Q07116	IGELNPEDR	2.373852262	2	2.4432
Q07116	LCDVLAQAGHR	0.770850596	2	3.24045
Q07116	LHVVGAPGGQSLSLSLDDLHK	1.480034734	3	3.70607
Q07116	MSPPLEASDPYSNDPMR	2.231617531	2	3.82777
Q07116	NHLPVPNLDPDTYR	1.006326631	2	2.66884
Q07116	VSVESEESYSHWQR	0.797491636	2	4.12602
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.998975771**	**0.97566**	**3**
Q07205	AMGPLVLTEVLFDEK	0.851964006	2	3.67745
Q07205	LQDMLDGFIK	1.126308429	2	2.31177
Q07205	TVIVNMVDVAK	1.022900184	2	2.85976
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**1.74660106**	**0.99383**	**12**
Q07523	ALKEEKPTQSVPVSFPK	0.825505308	2	4.81859
Q07523	ALVITIDTPVLGNR	0.859008185	2	3.96141
Q07523	ASFCWNDLSLLQSITR	0.984649204	2	4.07296
Q07523	EDAELAMK	1.366628506	1	2.01864
Q07523	EEKPTQSVPVSFPK	0.985464063	2	3.76491
Q07523	EVLDILTAELHR	1.058750383	2	3.27532
Q07523	GEDGVKEVLDILTAELHR	0.934796122	3	5.12781
Q07523	HNVQGIVVSNHGGR	0.782392003	3	6.36064
Q07523	NQLNLEANILLK	1.058687255	2	3.88023
Q07523	QLDEVSASIDALR	1.065514521	2	3.11643
Q07523	TSWDFIEGEADDGITYSENIAAFK	0.887042384	3	3.30194
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	0.976800369	3	4.73957
Q07803	**EFGM Elongation factor G_ mitochondrial**	**2.31710555**	**0.64235**	**4**
Q07803	GIIDLIEER	1.368282475	2	2.86931
Q07803	LEFSDETFGANVPK	1.327076557	2	2.85278

Q07803	NYQGELKK	0.74403744	1	2.08622
Q07803	YQPCSPSTQEELVNK	1.756354408	2	3.09254
Q07936	**ANXA2 Annexin A2**	**2.037153516**	**0.99919**	**3**
Q07936	GLGTDEDSLIEIICSR	1.160568884	2	3.37049
Q07936	GVDEVTIVNILTNR	1.042573381	2	3.10122
Q07936	TNQELQEINR	0.959383942	2	2.95204
Q07984	**SSRD Translocon_associated protein subunit delta**	**2.429212607**	**0.00665**	**3**
Q07984	FFDEESYSLLR	1.316710104	2	3.67008
Q07984	NNEDVSIIPPLFTVSVDHR	1.280482425	2	4.33862
Q07984	VQNMALYADVSGK	1.008312517	2	3.69997
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**2.548541854**	**0.9938**	**7**
Q08163	ALLVTASQCQQPAGNK	0.890803445	2	4.09057
Q08163	KEPALLELEGK	1.177171095	2	2.34322
Q08163	LEAVSHTSDMHCGYGDSPSK	1.064124383	3	5.07489
Q08163	NSLDCEIVSAK	1.123662445	2	3.07278
Q08163	SALFAQINQGESITHALK	1.340931071	2	4.18021
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.767975338	2	4.26463
Q08163	VENQENVSNLVIDDTELK	1.404249817	2	5.36006
Q08201	**MDR2 Multidrug resistance protein 2**	**2.131870995**	**0.73589**	**2**
Q08201	AKLSAAYLFSLFERQPLIDSYSR	1.067236778	2	2.5521
Q08201	FDTLVGDRGAQLSGGQK	1.343034013	2	2.53732
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**3.13038061**	**0.50464**	**6**
Q08415	ATLQAMDER	0.933543861	2	2.43284
Q08415	EQQHFGQPSSYFLQLPQAMELNR	1.006127022	3	5.71025
Q08415	ILVLNTPNNPLGK	1.645555292	2	3.26915
Q08415	LGASNDWQLDPAELASK	2.256135772	2	4.25427
Q08415	RLDGIDQNLWVEFGK	0.827789213	2	2.36245
Q08415	VGWVMGPDNIMK	1.121186723	2	2.45041
Q09073	**ADT2 ADP/ATP translocase 2**	**1.861812939**	**0.99953**	**7**
Q09073	AAYFGIYDTAK	1.095496982	2	2.42624
Q09073	DFLAGGVAAAISK	4.602802468	2	4.93099
Q09073	GLGDCLVK	0.977017702	2	2.80029
Q09073	GTDIMYTGTLDCWR	1.173013268	2	3.61974
Q09073	KGTDIMYTGTLDCWR	0.799677703	3	3.78966
Q09073	LLLQVQHASK	0.933145388	2	2.77317
Q09073	QIFLGGVDKR	0.849168637	2	2.39185
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**2.12831709**	**0.90576**	**9**
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.174848495	3	4.13204
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	1.176155644	2	3.57721
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	0.819785745	3	3.53353
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	1.038994569	3	4.45837
Q0D2L3	SVDEGLLDSK	0.853401851	2	2.74482
Q0D2L3	SVDEGLLDSKR	0.746283599	2	3.14827
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.385388871	2	5.29579
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	1.637000319	3	5.56457
Q0D2L3	VVLAEDCWMK	1.042012015	2	2.52312
Q0VAV2	**EXPH5 Exophilin_5**	**1.956768656**	**0.93779**	**4**
Q0VAV2	DMDVSVSKDEQLNK	0.964185974	2	2.32847
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1	0.969580416		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)Oxidation(7	0.679926025		
Q0VAV2	SLSDQDPGQEQREEK	0.925042863	2	2.48273
Q0VGK3	**GLCTK Glycerate kinase**	**2.012706234**	**0.29951**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	1.033401039	2	5.17847
Q0VGK3	GATIQELNTIR	0.988148825	2	2.80106
Q0VGK3	QLFDSAVGAVQPGPMLQR	0.935853889	2	3.58777
Q0ZHH6	**ATLA3 Atlastin_3**	**2.619283348**	**0.86306**	**7**

Q0ZHH6	ALASVLLQDHIR	1.231563617	2	2.61704
Q0ZHH6	EHQHEEIQNVR	1.292277303	2	3.39878
Q0ZHH6	EQLQTLIPYVLNPSK	1.093997279	2	2.76003
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	0.835624673	2	4.5233
Q0ZHH6	IYQGEDLPHPK	1.049704594	2	2.52423
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2	1.434962353		
Q0ZHH6	YQQELEEEITELYENFCK	1.117461868	2	5.27601
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**1.831576769**	**0.72397**	**2**
Q10728	EQENEEKDKEEK	1.039844375	2	2.32477
Q10728	SLLEMEKRER+Oxidation(4	0.864258133		
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**2.014022828**	**0.0005**	**27**
Q10758	AEAETMYQIK	0.996105582	2	3.32209
Q10758	AQYEEIANR	0.928542566	2	3.13165
Q10758	ATLEAAIADAEQR	0.945139052	2	4.70628
Q10758	DVDEAYMNKVELESR	1.050456618	2	3.44792
Q10758	ELQSQISDTSVVLSMDNSR	4.311153608	2	6.24015
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	1.020528076	2	4.99104
Q10758	KDVDEAYMNK	1.047308721	2	3.31882
Q10758	LEGLTDEINFLR	1.160235486	2	4.39292
Q10758	LESGMQNMSIHTK	1.117331541	2	3.87926
Q10758	LEVDPNIQAVR	0.97669807	2	3.69396
Q10758	LEVELGNMQGLVEDFK	1.375747443	2	5.05751
Q10758	LKLEVELGNMQGLVEDFK	1.396235443	3	3.52064
Q10758	LQAEIDALK	0.960876998	2	2.97322
Q10758	LVSESSDIMSK	1.006907201	2	3.49612
Q10758	QIHEEEIR	0.831076245	1	2.19595
Q10758	QLEALGQEK	0.892315206	1	2.16785
Q10758	RQLEALGQEK	0.836510103	2	2.57175
Q10758	SKTEISEMNR	0.809521022	3	3.76008
Q10758	SKTEISEMNR+Oxidation(7	0.942088368		
Q10758	SLDMDSIIAEVR	0.994438023	2	4.67944
Q10758	SNMDNMFESYINNLR	1.350740174	2	4.2057
Q10758	SRAEAETMYQIK	0.976504481	2	3.67364
Q10758	TEISEMNR	1.276308413	2	2.32093
Q10758	TEMENEFVLIK	0.883368435	2	3.60466
Q10758	TEMENEFVLIK+Oxidation(2	0.924483133		
Q10758	WSLLQQQK	0.856889089	2	3.00572
Q10758	YEELQTLAGK	0.986508551	2	3.60237
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**1.846122789**	**0.99228**	**2**
Q148W0	LGQSHFINWDLQMYYAEK+Oxidation(12	0.984622958		
Q148W0	TCEVIKDGRFK	0.868338955	1	2.296
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**1.885971326**	**0.99999**	**7**
Q14DH7	CVPGYNVMILDDNMQK	1.375854814	2	2.97358
Q14DH7	IAIIYDSPVTDTK	0.969452908	2	2.93041
Q14DH7	STLSALVNGKPYK	0.721599164	2	2.78172
Q14DH7	THFAASVADPER	0.989000004	2	3.66633
Q14DH7	VDDVINVAGHR	0.907844307	2	3.61651
Q14DH7	VLAEHGVAALFTAPTAIR	0.960864203	2	4.42953
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.052751108	2	3.42567
Q1H5H1	**SELT Selenoprotein T**	**1.965414132**	**0.85192**	**2**
Q1H5H1	IEGENYLPQPIYR	1.342133396	2	2.83603
Q1H5H1	LESGHLPSMQQLVQILDNEMK	0.973394009	3	3.98488
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**1.986022235**	**0.99997**	**11**
Q1HCL7	GSSYSGLLER	0.973725137	2	2.43481

Q1HCL7	LKPVIGVNTDPER	1.168596667	3	3.4647
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.195669734	3	5.23048
Q1HCL7	NVEHIIDSLRDEGIEVR	1.026305648	2	3.5436
Q1HCL7	QGNLTLPLNK	1.127104866	2	2.48926
Q1HCL7	SEASGPQLLPVR	1.025759033	2	3.10753
Q1HCL7	SEGHLCLPVR	0.931733577	2	2.77451
Q1HCL7	SSGLNLCTGTGSK	0.933204286	2	3.61795
Q1HCL7	VTNEYNESLLYSPEEPK	1.137631654	2	4.72269
Q1HCL7	YAELSEEDLK	1.149802042	2	2.77213
Q1HCL7	YTHSFPEALQK	1.081994068	2	2.49373
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**2.299508614**	**0.94976**	**7**
Q1JU68	AVEDIHGLFSLSK	2.228317049	2	3.19418
Q1JU68	EEEEQRRAEEQMLK	1.12208579	2	2.4563
Q1JU68	FNVLQYVVPEVK	1.201881848	2	3.40989
Q1JU68	ILQEHEQIK	0.996209359	2	2.3826
Q1JU68	KGPEADSEWR	0.778527962	2	2.61071
Q1JU68	LLDMDGIIVEK	0.985912306	2	3.01552
Q1JU68	NQLTAMSSVLAK	0.873349168	2	2.77784
Q29RW1	**MYH4 Myosin_4**	**2.467396368**	**0.96734**	**13**
Q29RW1	ANLMQAEIEELR	2.798841858	2	2.94908
Q29RW1	ELENEVENEQKR	1.427805218	2	3.10978
Q29RW1	GQDDLKEQLAMVER	1.335246368	2	2.87192
Q29RW1	LQDAEEHVEAVNSK	0.972714893	2	4.84159
Q29RW1	LQDLVDKLQTK	1.426563204	1	1.94186
Q29RW1	MEGDLNEMEIQLNHANR	1.185114996	2	4.04416
Q29RW1	MEIDDLASNMETVSK	4.443828263	2	4.33588
Q29RW1	NAYEESLDQLETLKR	1.919251566	2	4.01644
Q29RW1	SAETEKEMATMK	1.282492564	2	2.77454
Q29RW1	SELQASLEEAEASLEHEEGK	1.227672932	2	4.85812
Q29RW1	TEGGATVTVK	1.354855291	2	2.91739
Q29RW1	TKLEQQVDDLEGSLEQEK	2.084453975	2	4.93899
Q29RW1	TKLEQQVDDLEGSLEQEKK	0.904096089	3	4.62526
Q2PQA9	**KINH Kinesin_1 heavy chain**	**2.359718341**	**0.98966**	**4**
Q2PQA9	HVAVTNMNEHSSR	1.960271794	3	4.04124
Q2PQA9	MEENEKELAACQLR	1.130874123	2	2.35641
Q2PQA9	SAEVDSDDTGGSAAQK	1.091667769	2	5.21531
Q2PQA9	TGAEGAVLDEAK	0.998302328	2	2.42435
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**1.844083377**	**0.46368**	**6**
Q2TA68	AKNEILDEVISLSQVTPK	1.700444404	2	3.96823
Q2TA68	AVEVAWETLQDEFSR	1.297885297	2	2.3639
Q2TA68	GKEHDDIFDK	0.998259838	2	2.40361
Q2TA68	IDQLQEELLHTQLK	0.843287163	2	2.64901
Q2TA68	TSVLEMIAQAR	1.296438447	2	3.29925
Q2TA68	VVVVGDQSAGK	0.912257408	2	2.54199
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.872480904**	**0.66557**	**7**
Q2V057	ASIYGQFVAGETAEEVR	1.737496701	2	3.18024
Q2V057	EDCTQPDYEATSR	0.967456666	2	3.92341
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.102473529	3	3.60321
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.090875398	2	5.4459
Q2V057	SIPYGCLEEVIPYLIR	1.675001638	2	2.53174
Q2V057	SVTQLHGKEDCTQPDYEATSR	0.837781896	3	5.44921
Q2V057	TSEAWYEGNLSAMLHCVDLSR	1.240516497	2	3.45397
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**2.29670865**	**0.98943**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	1.041472619	3	4.74095

Q3B7D0	FGLFTPGSR	1.059771712	2	2.33909
Q3B7D0	HCDDSYTPQDK	1.232424239	2	3.78569
Q3B7D0	LEEDGDELAR	1.614418583	2	2.82395
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**2.645762002**	**0.99963**	**4**
Q3B7U9	SCSQVLEHQPDNIK	1.076985863	2	4.13734
Q3B7U9	TAEDGPDLEMLSGQER	0.957204118	2	4.21666
Q3B7U9	VDMTCEEEEELLQLK	1.454716042	2	4.14715
Q3B7U9	VLAQQGEYSEAIPILR	1.086563222	2	3.4743
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**1.959432298**	**0.66727**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	0.971363296	2	4.58426
Q3B8Q2	GRDVIAQSQSGTGK	0.870015002	2	3.88809
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**2.192412273**	**0.95868**	**3**
Q3KRD8	ASFENNCEVGCFAK	1.111930621	2	2.43011
Q3KRD8	HGLLVPNNTTDQELQHIR	1.157060352	3	4.83218
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.165455117	3	3.90298
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**2.017201628**	**0.97218**	**3**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.0225967	2	3.66028
Q3KRE0	ISVLEALR	1.813843765	2	2.41864
Q3KRE0	QQQLLNEENLR	0.960687288	2	2.36425
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**2.151491617**	**0.382**	**2**
Q3KRE8	ALTVPELTQQMFDSK	1.104935258	2	3.22134
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.132364161	3	5.05137
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**2.024912813**	**0.96225**	**2**
Q3MIB4	MEIIQVPGYTQEEK	1.019895436	2	3.72723
Q3MIB4	TVGVNNPVFLLDEVDK	0.911383723	2	2.44436
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**2.010955722**	**0.79996**	**6**
Q3MIE0	DGQEGIEAFIQK	1.130206758	2	2.76709
Q3MIE0	SDILHEAESEDLK	1.019564867	3	3.66626
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.359277729	2	4.73243
Q3MIE0	VALEMLFTGEPISAQEALR	0.990721869	2	3.66328
Q3MIE0	VIIISAEGPVFSSGHDLK	0.901845432	2	4.47785
Q3MIE0	VVPEEQLEEEATR	0.848469202	2	3.97194
Q3MIF4	**XYLB Xylulose kinase**	**2.224184027**	**0.63166**	**8**
Q3MIF4	CCLGWDFSTQQVK	1.550680898	2	3.20523
Q3MIF4	DLPEFGTQGGVHVHK	0.957490269	2	2.75126
Q3MIF4	FNADNMEVSAFPGDVEIR	1.399997676	2	4.45379
Q3MIF4	IHAEGLGYR	1.168213725	2	2.34742
Q3MIF4	IRDESASCSWNK	1.129962731	2	4.17306
Q3MIF4	VVAFTGDNPASLAGMR	1.216261178	2	3.87135
Q3MIF4	VWSQACLDACAPHLK	1.41035353	2	3.81145
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	1.927097101	2	5.27579
Q3SWS9	**JKIP1 Janus kinase and microtubule_interacting protein 1**	**2.186429912**	**0.75809**	**2**
Q3SWS9	LEMEENQLK+Oxidation(2	0.749535615		
Q3SWS9	VKTALLADAREEAR	1.146475491	2	2.38817
Q3T1I4	**PRRC1 Protein PRRC1**	**2.328466942**	**0.67488**	**2**
Q3T1I4	GQDDAPAGGIWGFIK	1.209586568	2	3.68292
Q3T1I4	WSGLLVTVGEVLEK	1.288671136	2	2.7461
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**2.082152831**	**0.99029**	**4**
Q3T1J1	EDLRLPEGDLGK	0.983278397	2	2.96803
Q3T1J1	EDLRLPEGDLGKEIEQK	1.200271569	2	4.25702
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.177342586	2	5.07142
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.55230011	3	4.24045
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**2.325909231**	**0.99978**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.047704394	3	4.02543

Q3T1K5	FTVTPSTTQVVGILK	1.238163779	2	4.08574
Q3T1K5	KVDGQQTIIACIESHQFQAK	1.002663324	3	3.77062
Q3TDQ1	**STT3B Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3B**	**2.203381464**	**0.5822**	**2**
Q3TDQ1	FGEMQLDFR	1.358518719	2	2.33488
Q3TDQ1	HLEEAFTSEHWLVR	1.130963332	3	4.07701
Q3U0D9	**HACE1 E3 ubiquitin_protein ligase HACE1**	**1.888437568**	**0.67168**	**2**
Q3U0D9	DSIFRSSCEIVSKANCAK	0.834756987	2	2.3169
Q3U0D9	MERAMEQLNRLTR	1.416606342	2	2.32771
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**2.151532863**	**0.98649**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	1.042066029	2	2.52619
Q3U0J8	QIELDLLRTLPNNK	1.116334701	2	2.5996
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.993993988**	**0.94167**	**2**
Q3UHR0	MQILQRKDTWAPK+Oxidation(0	1.275354295		
Q3UHR0	NLEEPGLLSR	0.968981217	2	2.36867
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**2.258650907**	**0.42891**	**3**
Q3ULJ0	GIDEGPDGLK	0.978659807	2	2.82018
Q3ULJ0	LGLMEMIAFAK	1.403851473	2	3.81507
Q3ULJ0	LTDIINNDHENVKYLPGHK	1.873847235	2	2.40201
Q3UMF0	**COBL1 Cordon_bleu protein_like 1**	**1.696986715**	**0.20181**	**2**
Q3UMF0	RAPLPPMPTSQGAAQGQERR+Oxidation(6	1.257885835		
Q3UMF0	SQGTSTYVQDR	0.759288889	2	2.39346
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**2.313154929**	**0.01858**	**18**
Q3UQ44	ALVGSENPPLTVIR	1.158121123	2	3.85569
Q3UQ44	AWVNQLETQTGEASK	1.008391182	2	5.20005
Q3UQ44	GVLLGIDDLQTNQFK	1.231525352	2	4.29391
Q3UQ44	HTDNTVQWLR	1.067416639	2	3.00362
Q3UQ44	KKGGEIEILNNTDNK	1.027822165	2	2.37617
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.925231716	3	4.71034
Q3UQ44	LGIAPQIQDLLGK	1.850874585	2	2.9931
Q3UQ44	LPYDVTTEQALTYPEVK	1.495292609	2	4.10466
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.370278987	2	2.37227
Q3UQ44	LSAEEMDER	1.233329034	2	3.09178
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.194441655	2	5.23168
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.012066316	2	4.99026
Q3UQ44	TALEEEIK	1.071817702	2	2.40717
Q3UQ44	TLDTLLLPTANIR	1.02086671	2	3.57865
Q3UQ44	VDFTEEEISNMR	1.241127132	2	3.95305
Q3UQ44	VDQVQDIVTGNPTVIK	1.001159676	2	5.09797
Q3UQ44	YGSIVDDER	0.656848384	2	2.45914
Q3UQ44	YQDILNEIAK	1.13060558	2	3.06104
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**2.374208819**	**0.97065**	**2**
Q3UV17	AQYEDIAQK	0.794032269	1	2.12442
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5	1.254187375		
Q3V0K9	**PLSI Plastin_1**	**1.873670897**	**0.32073**	**3**
Q3V0K9	AYFHLLNQIAPK	0.886933723	2	3.05478
Q3V0K9	KIENCNYAVELGK	0.797978314	2	3.73083
Q3V0K9	QFVTPADVVSGNPK	1.038114434	2	3.30249
Q3V132	**ADT4 ADP/ATP translocase 4**	**2.180571234**	**0.99997**	**2**
Q3V132	GNLANVIR	1.107806721	2	2.75501
Q3V132	YFPTQALNFAFK	1.167265371	2	3.40525
Q3ZAV8	**EDC4 Enhancer of mRNA_decapping protein 4**	**1.816982413**	**0.83394**	**2**
Q3ZAV8	SSHSTWPVDVSQIK	1.305042983	2	2.33053
Q3ZAV8	VISVSTSERTLLK	0.85400341	2	2.57487

Q497B0	**NIT2 Omega_amidase NIT2**	**2.041079936**	**0.98823**	**15**
Q497B0	ADLYSVESK	1.085245427	2	3.06079
Q497B0	AGTEETILYSDIDLK	1.228527524	2	3.73211
Q497B0	ASYVAWGHSTVVDPWGQVLTK	1.221880942	3	5.85666
Q497B0	AVDNQVYVATASPAR	0.917227042	2	4.68021
Q497B0	AVDNQVYVATASPARDEK	0.931587848	2	3.58641
Q497B0	ENSIYLIGGSIPEEDDGK	0.827053953	2	3.46068
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.073185617	3	4.96519
Q497B0	FAELAQIYAR	1.471182707	2	3.92586
Q497B0	IHLFDIDVPGK	1.208631869	3	3.4871
Q497B0	KIHLFDIDVPGK	1.134185917	3	4.73521
Q497B0	LALIQLQVSSIK	2.057330412	2	3.06932
Q497B0	LYNTCAVFGPDGNLLVK	1.061992351	2	4.1224
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.005943079	3	4.97485
Q497B0	TLSPGDSFSTFDTPYCR	1.082990164	2	4.7758
Q497B0	VGLGICYDMR	1.407729958	2	2.86102
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**1.825644228**	**0.99696**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.855089312	2	4.56128
Q498D5	FCNLALLLPIVTK	1.088389045	2	3.2297
Q498D5	GQLQILEK	1.127806872	1	2.059
Q498D5	LNELLTNVEELKEEIK	1.040124115	2	2.87154
Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**1.863959312**	**0.84697**	**2**
Q498U4	EEEPPEKVVDMASEK	0.833507726	2	2.3657
Q498U4	FGIVTSSAGTGTTEDTEAK	0.898370511	2	3.34286
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**2.035522832**	**1**	**7**
Q499N5	GATLSHHNIVNNSNLIGQR	0.891302787	2	5.32955
Q499N5	GGENIYPAELEDFFHK	0.85625719	2	2.9767
Q499N5	SGETTTEEEIK	0.991633794	2	3.16073
Q499N5	TFETVGQDR	1.036117993	2	2.67236
Q499N5	TGDIASMDEQGFCR	1.051764305	2	3.72499
Q499N5	TVGECLDATAQR	1.06127718	2	2.90951
Q499N5	YIVFVEGYPLTVSGK	1.021510092	2	4.37984
Q4AEF8	**COPG Coatomer subunit gamma**	**1.979001387**	**0.93211**	**6**
Q4AEF8	FGAQNEEMLPSILVLLK	1.004529573	2	3.50185
Q4AEF8	SLPYNQPGTCYTLVALPK	1.137645733	2	2.44093
Q4AEF8	SSPEPVALTESETEYVIR	0.961533252	2	3.61256
Q4AEF8	TLEEAVGNIVK	0.928769796	2	2.64028
Q4AEF8	VVLEHEEVR	1.036915447	2	2.4354
Q4AEF8	VVVVQAISALCQK	2.053050953	2	2.46967
Q4FZT0	**STML2 Stomatin_like protein 2**	**2.418547351**	**0.4151**	**5**
Q4FZT0	AEQINQAAGEASAVLAK	0.944920089	2	4.7049
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.340021624	2	5.54852
Q4FZT0	ATVLESEGTR	0.8747872	2	2.80368
Q4FZT0	DVQTTDTSIEELGR	1.260989193	2	2.9225
Q4FZT0	ILEPGLNVLIPVLDR	0.988397152	2	3.01991
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.857389115**	**1**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.801972312	3	4.8805
Q4FZT9	FGGSGSQVDSAR	1.073000133	2	3.39619
Q4FZT9	SETELKDTYAR	1.016825686	2	3.04089
Q4FZT9	SGALLACGIVNSGVR	1.003290729	2	3.36753
Q4FZT9	SSTTSMTSVPKPLK	0.78526119	2	3.49787
Q4FZT9	TITGFQTHTTPVLLAHGER	0.887854702	3	3.92593
Q4FZT9	TPVQSQQPSATAPSGADEK	0.974194999	2	4.87975
Q4FZT9	VGQAVDVVGQAGKPK	0.887815735	2	3.46212

Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**3.916006191**	**0.17416**	**4**
Q4FZX7	GDAGSADVQDLEK	1.538589392	2	3.4692
Q4FZX7	GNSLTLIDLPGHESLR	1.262227562	2	2.80888
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.978085455	2	4.84289
Q4FZX7	VGDGAGGAFQPYLDSLR	1.299265865	2	3.1283
Q4FZY0	**EFHD2 EF_hand domain_containing protein D2**	**2.874766687**	**0.66023**	**2**
Q4FZY0	KQAEEVK	1.408378675	1	1.94405
Q4FZY0	LSEIDVSTEGVK	1.533336923	2	2.59805
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**2.415483983**	**0.98444**	**6**
Q4G061	AEEEGGSDGSAAEAEPR	0.740525284	2	4.95918
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	4.177650666	3	5.01134
Q4G061	DRPQEADGIDSVIVVDNVPQVGPDR	1.817989987	3	3.5612
Q4G061	GTQGVVTNFEIFR	1.022307486	2	3.00808
Q4G061	IINDYYPEEDGK	1.883945084	2	2.86532
Q4G061	TEDAEEDAEARPEPEVR	0.766646149	3	3.61913
Q4G063	**CREL2 Cysteine_rich with EGF_like domain protein 2**	**2.384163852**	**0.75172**	**2**
Q4G063	ACCLPGTYGPDCK	1.201643486	2	3.03808
Q4G063	FNQGMANTAR	1.840561727	2	2.4181
Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**1.846030526**	**0.96381**	**2**
Q4KLF8	ALAAGGVGSIVR	0.819335311	2	2.84465
Q4KLF8	QGNMTAALQAALK	1.048548511	2	2.3489
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**2.574498837**	**0.00232**	**16**
Q4KLP0	ARPSVDHGLAR	0.733882314	2	3.06238
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.319412404	3	5.71346
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.231946223	3	4.68575
Q4KLP0	LEELCPFPLDSLQQEMGK	1.364296654	3	5.42125
Q4KLP0	LLLESQEFDHFLATK	1.506767885	2	3.95675
Q4KLP0	LSAYGGITDIIIGMPHR	1.338984	3	4.44434
Q4KLP0	LVTVYCEHGHK	1.58331486	2	2.36789
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	1.49363949	2	2.63099
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.156080041	3	3.99712
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.088552256	3	5.02157
Q4KLP0	SSLYSSDIGK	0.938855046	2	2.83784
Q4KLP0	SVEVPEELQLHSHLLK	1.118393597	2	3.31004
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.36101638	3	3.36754
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.112748852	2	4.9568
Q4KLP0	YGGEGAESMMGFFHELLK	1.257584977	2	4.43611
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.27091477	3	4.56909
Q4KLZ6		**2.052826437**	**0.97496**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.392208416	2	4.91548
Q4KLZ6	AILEVLQTK	1.024038107	2	2.89094
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.436342966	2	3.61269
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	1.097961552	2	4.96248
Q4KLZ6	AVAQAGTAGTLLIVK	1.433823131	2	4.36264
Q4KLZ6	EGPTPASPAQVLSK	1.219270544	2	3.38581
Q4KLZ6	GLCGTILIHK	1.588625957	2	2.40148
Q4KLZ6	GVSLTLMLVDEPLLK	1.317356329	2	3.0735
Q4KLZ6	ISTTLIGLEEHLNALDR	2.482957453	2	3.60906
Q4KLZ6	LIDAETNAK	1.873557248	2	2.37296
Q4KLZ6	LNFGLAMEQAK	1.08299501	2	2.40456
Q4KLZ6	LSVLLLEK	1.989032837	2	2.60548
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	1.196950697	2	3.56324

Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.377727604	3	5.90822
Q4KLZ6	VAGALAEEGMGLEEITK	1.866194984	2	4.53581
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	1.20891877	2	5.35237
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.843792088**	**0.91924**	**5**
Q4KM49	AFCEPGNVENNGVLSFVK	0.776150667	2	2.47295
Q4KM49	IDVGEAEPR	0.801885941	2	2.35082
Q4KM49	QVEPLDPPAGSAPGER	0.875011296	2	2.59556
Q4KM49	TVVSGLVQFVPK	1.163225082	2	3.06702
Q4KM49	VDAQFGGIDQR	0.706836593	2	3.12845
Q4KM73	**KCY UMP_CMP kinase**	**2.2769724**	**0.82619**	**7**
Q4KM73	EMDQTMAANAQK	1.236250547	2	3.18346
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.280939013	3	4.59218
Q4KM73	IVPVEITISLLK	1.313691995	2	2.4975
Q4KM73	KNPDSQYGELIEK	1.017344749	2	3.80017
Q4KM73	NQDNLQGWNK	1.293867024	2	2.84177
Q4KM73	SVDEVFGDVMK	1.319078557	2	3.45938
Q4KM73	YGYTHLSAGELLR	0.891531793	3	4.27906
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.900331391**	**0.8999**	**5**
Q4KM74	DLQQYQSQAK	1.121166793	2	3.55237
Q4KM74	GEALSALDSK	1.196068456	2	2.85129
Q4KM74	IMVANIEEVLQR	1.194261698	2	2.78913
Q4KM74	NLGSINTELQDVQR	0.922156304	2	4.38384
Q4KM74	VADGLPLAASMQEDEQSGR	1.020162691	2	4.36481
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.901617948**	**0.99716**	**3**
Q4KMA2	IDIDPEETVK	0.949923738	2	2.75957
Q4KMA2	NFVVVMVTKPK	0.743071713	2	2.97463
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.118164855	2	4.24825
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**2.191803843**	**0.48817**	**6**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	1.513743877	3	3.56918
Q4QQW3	FLFDLNVDDGLAALGYSK	1.16242107	2	2.43737
Q4QQW3	HLETAEILGANIR	1.14694327	2	3.45891
Q4QQW3	IQDAGPVLADALR	0.606369518	2	2.9916
Q4QQW3	NLSQLPPVQIVMDSLSK	1.11942102	2	2.96438
Q4QQW3	TTDYAFEMAVSNIR	0.59379107	2	3.70436
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**2.690815158**	**0.00341**	**5**
Q4QRB4	AILVDLEPGTMDSVR	1.293511711	2	4.56213
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10	1.380586076		
Q4QRB4	EIVHIQAGQCGNQIGAK	2.05452639	2	4.93126
Q4QRB4	IMNTFSVVPSPK	1.177908158	2	4.1015
Q4QRB4	ISEQFTAMFR	1.317440619	2	3.37924
Q4V7C7	**ARP3 Actin_related protein 3**	**2.150296681**	**0.48857**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	1.861014138	2	4.38781
Q4V7C7	KDYEEIGPSICR	0.961963835	2	3.66302
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.549951198	2	3.34781
Q4V7C7	LSEELSGGR	1.089142032	2	2.56612
Q4V7C7	NIVLSGGSTMFR	1.082325297	2	3.0931
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1.042195939	3	5.24268
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**2.178498233**	**0.00238**	**6**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	1.082884542	3	3.73339
Q4V8K1	QVFVCGNDSK	0.880747361	2	2.38265
Q4V8K1	SDVIVLAVHR	1.108483016	2	2.82238
Q4V8K1	TCADEFPLTVDSSEK	1.142945508	2	4.48802
Q4V8K1	TLGLTPLDQGSLVAAK	1.210080034	2	3.81118
Q4V8K1	VLIDVSNNQK	0.908005862	2	2.53512

Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**2.304681071**	**0.87622**	**2**
Q501J6	ELAQQVQQVADDYGK	0.788885895	2	3.12204
Q501J6	VLEEANQAINPK	1.266429387	2	2.62331
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**1.911362141**	**0.51945**	**4**
Q505J8	LQQVQAGQAEK	0.742944826	2	2.6754
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	1.454253382	3	4.59039
Q505J8	SLQALGEVIEAELR	1.619192695	2	3.7452
Q505J8	VVDSIEDEVQR	1.353749362	2	2.93538
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**2.042654002**	**0.41747**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	0.588761418	2	4.09343
Q561R9	ILIDTGEPSVPEYISCLK	1.061088864	2	3.79122
Q561R9	NISNDATYCIK	0.901488239	2	2.95141
Q561R9	NNREEQIITVFR	0.707585815	2	2.69148
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**2.163922845**	**0.22356**	**6**
Q561S0	LLQYSDALEHLLSTGQGVVLER	1.70461181	3	3.76304
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	1.994018239	3	4.18579
Q561S0	VITVDGNICSGK	0.813062611	2	2.45809
Q561S0	VVEDIEYLNYNK	0.900479758	2	3.90041
Q561S0	YAPGYNADVGDK	0.776297476	2	2.66096
Q561S0	YGLLASILGDK	1.667178367	2	3.14905
Q562C4	**MET7B Methyltransferase_like protein 7B**	**2.029725267**	**1**	**5**
Q562C4	AQFSEVQLEWQPPPFK	1.037653791	2	4.51697
Q562C4	FIVAYGENMK	0.967209858	1	2.53391
Q562C4	HIGDGCHLTR	0.976167999	3	3.31753
Q562C4	VLQEVQR	0.855217044	2	2.54877
Q562C4	VTCVDPNPNFEK	0.743435823	2	3.60413
Q562C9	**MTND 1_2_dihydroxy_3_keto_5_methylthiopentene dioxygenase**	**2.324116333**	**0.92628**	**3**
Q562C9	GDMITLPAGIYHR	1.095127086	2	2.31988
Q562C9	LDADKYENDPELEQIR	1.239912866	2	4.20084
Q562C9	MFFEEHLHLDEEIR	2.880291371	2	2.4286
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**2.259662936**	**0.96602**	**11**
Q58FK9	AIILNTPHNPIGK	0.817504003	2	3.38963
Q58FK9	DSTLDAAEEIFR	1.197191132	2	3.19889
Q58FK9	DSTLDAAEEIFRTWNSR	1.439515121	2	2.3612
Q58FK9	IEGLDQNVWVEFTK	1.18629078	2	4.5557
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.252513174	3	4.48794
Q58FK9	MAGAVPVFIPLR	2.384303116	2	2.49665
Q58FK9	MDDPECYFNSLPK	1.307967105	2	4.18505
Q58FK9	RIEGLDQNVWVEFTK	1.171515313	2	3.72454
Q58FK9	RMDDPECYFNSLPK	1.099355181	2	2.76982
Q58FK9	SDEPYDYK	2.333006018	2	2.44851
Q58FK9	WTSSDWTFNPQELESK	1.206366327	2	5.06261
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**2.148896735**	**0.97969**	**3**
Q5BJQ0	AVLDSSPFLSEANAER	1.091426772	2	4.61341
Q5BJQ0	KMGGSFLICSKLK+Oxidation(1	1.232062967		
Q5BJQ0	TLNNDLGPHWR	1.133452978	2	2.5618
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**1.869444239**	**0.99599**	**25**
Q5BJY9	AQIFANSVDNAR	0.867464444	2	3.95999
Q5BJY9	AQYEQLAQK	0.890433373	2	3.47068
Q5BJY9	DAETTLLELR	2.688966882	2	2.94159
Q5BJY9	IREYLEK	0.901799297	2	2.40246
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	1.207443752	3	4.90783

Q5BJY9	KVVDDTNITR	0.820121328	2	3.07228
Q5BJY9	LEAEIATYR	1.009976336	2	3.28052
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	1.059729421	3	5.54595
Q5BJY9	LQLETEIEALKEELLFMK	1.419830309	2	5.04445
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	1.185378626	2	6.30482
Q5BJY9	NQNINLENNLGEVEAR	0.982061657	2	5.56496
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	0.989946455	3	5.18546
Q5BJY9	QSVESDIHGLR	0.941287315	2	2.85054
Q5BJY9	QSVESDIHGLRK	1.395294835	2	2.67645
Q5BJY9	QTQEYEALLNIK	1.057006425	2	3.52249
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	1.03389433	2	5.8958
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	0.847308892	3	4.34872
Q5BJY9	TLQTLEIDLDSMK	1.007468022	2	4.52038
Q5BJY9	VKLEAEIATYR	1.040696236	2	3.28103
Q5BJY9	VKYETELAMR	0.915831316	3	3.42398
Q5BJY9	VQMEQLNGVLLHLESELAQTR	0.881821084	2	5.27106
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.545981171	2	5.0705
Q5BJY9	VVDDTNITR	0.891065601	2	3.44837
Q5BJY9	YETELAMR	1.108842256	2	2.6174
Q5BJY9	YWSQQIEESTTVVTTK	0.973562891	2	3.89621
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**2.426539444**	**0.1817**	**4**
Q5BK63	AVQHSNVVINLIGR	0.839166484	2	3.65763
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.28164036	3	6.06694
Q5BK63	NFDFEDVFVNIPR	1.644496941	2	3.85634
Q5BK63	WLSSEIEETKPAK	1.278716584	2	3.29303
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**2.006023804**	**0.94954**	**3**
Q5BK81	DVPYPPPLPPAVEAIQK	2.126398014	2	2.66155
Q5BK81	TGNVAEQLR	1.456190199	2	2.93323
Q5BK81	VEEVSLPDTINEGQVR	0.921016678	2	4.07436
Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**2.103493815**	**0.85421**	**3**
Q5BQE6	LYEQHHVVQDMLVPMK	0.844661189	3	3.58048
Q5BQE6	QLGCQDAFPEVYDK	1.072021434	2	4.21588
Q5BQE6	YLFGWMVPPK	1.983689634	2	2.69534
Q5DTN8	**JKIP3 Janus kinase and microtubule_interacting protein 3**	**1.876091256**	**0.97205**	**2**
Q5DTN8	MKELQAVREALLR	1.347720596	2	2.32857
Q5DTN8	TREQLQAEIQRAQTR	0.877317124	2	2.98134
Q5DU56	**NLRC3 Protein NLRC3**	**2.029806467**	**0.59811**	**2**
Q5DU56	LTGLALGHLYR	1.258572182	2	2.36599
Q5DU56	TLEILDLR	1.019962587	2	2.50515
Q5EB77	**RAB18 Ras_related protein Rab_18**	**2.772033334**	**0.02453**	**2**
Q5EB77	NDIVNMLVGNK	1.573752019	2	3.46229
Q5EB77	TCDGVQCAFEELVEK	1.225902108	2	3.86545
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**2.190618152**	**0.71727**	**2**
Q5FVM4	MEELHNQEVQK	1.275221647	2	3.90704
Q5FVM4	RMEELHNQEVQK	1.005215572	3	4.28857
Q5FVQ4	**MLEC Malectin**	**1.910841043**	**0.99992**	**3**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	1.031706933	3	5.58868
Q5FVQ4	LSVQGEVSTFTGK	0.933794407	2	3.36708
Q5FVQ4	STPEDQILYQTER	0.931803222	2	4.69178
Q5FVR2	**TYPH Thymidine phosphorylase**	**2.482260193**	**0.91633**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10	1.3440327		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8	0.954658186		
Q5FVR2	FGGAAVFPDQEK	1.125816116	2	2.59456
Q5FVR2	KQEELLSPADGIVECVR	1.013384232	2	4.07112

Q5FVR2	VSLVLAPALAACGCK	1.326460481	2	3.05512
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**2.613578796**	**0.00835**	**3**
Q5FVR5	DEKENLFQSK	0.9644733	2	2.46325
Q5FVR5	ILFIVGENDQCLASK	1.382314843	2	3.73669
Q5FVR5	IQQPGIGVISVSK	1.472478916	2	3.3566
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**2.087108137**	**0.96895**	**3**
Q5FW57	AIDQEMFK	0.984569083	2	2.71364
Q5FW57	SSQMLQMLESSLR	1.154907011	2	4.10177
Q5FW57	VYGTVFHMNQGNPFK	0.421549263	2	3.73513
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**2.233908131**	**0.97637**	**8**
Q5I0C3	AGDALMVMIAMK	0.702678223	1	1.95855
Q5I0C3	HAPLVEFEEEEV	1.109486025	2	2.96482
Q5I0C3	IIEEAPAPGIDPEVR	0.854332941	2	3.86378
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	1.369053773	3	4.65818
Q5I0C3	QEGIIFIGPPSTAIR	0.78278797	2	2.49792
Q5I0C3	SEKEFQEQLESAR	0.860034763	2	3.47032
Q5I0C3	VFFSEGAQANR	1.158765587	2	2.44464
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	1.146866118	2	5.14113
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**2.174827991**	**0.47261**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	1.135897243	2	3.70615
Q5I0D1	HEEFEEGCK	0.778199008	2	2.87806
Q5I0D1	VTLAVSDLQK	0.929595842	2	2.49429
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**2.169374445**	**0.89276**	**2**
Q5I0D5	FRPGDEHHPEVR	1.116208402	3	3.65802
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.218396721	2	4.36325
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**2.4257531**	**0.80143**	**2**
Q5I0D7	GVNTDSGNVCR	1.275851422	2	3.1664
Q5I0D7	YAVDDVQYADEIASVLTSR	1.383386356	2	2.73932
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.951738161**	**0.94183**	**2**
Q5I0E7	QLVEQVEQIQK	0.96419575	2	3.5686
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.213652716	3	3.39444
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**2.374377708**	**0.98962**	**9**
Q5I0H9	DKNQDLCQQESVK	1.031252948	2	4.28053
Q5I0H9	FIEWMQNPEAPPPPEPTWEEQQTSVLHLVGDNFR	1.826425423	3	4.1226
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	1.078148445	3	3.64914
Q5I0H9	GPPLWEEDPGAK	1.081694617	2	3.37593
Q5I0H9	GQGTICWVDCGDAESR	1.492938102	2	4.1044
Q5I0H9	NGEQQAVPALR	0.992368454	2	2.55593
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.885575698	3	4.12575
Q5I0H9	NQDLCQQESVK	0.946739866	2	3.42543
Q5I0H9	TELGFTSFIR	1.090272943	2	2.44762
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**2.16772864**	**0.22858**	**7**
Q5I0J9	HANLLVGSPSALADQTTER	1.0680345	2	5.78434
Q5I0J9	LDAAGGLQSLR	1.101344352	2	3.99282
Q5I0J9	LEGPLAAAHSSGPR	1.018965399	2	3.75329
Q5I0J9	LGQSLVSR	1.142737975	2	2.31063
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.404466134	2	3.38819
Q5I0J9	NSNTMAAAALAAPSLGFDR	1.258637581	2	4.63596
Q5I0J9	TVLYEGPVR	1.029347834	2	2.62407
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**2.624766119**	**0.01917**	**6**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	1.750668218	3	3.37932
Q5I0M2	DNHVVAAGSMEK	1.119021461	2	2.65586

Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.771290831	3	4.80135
Q5I0M2	LYAEGDIPVPHAR	1.123765989	2	3.55439
Q5I0M2	VEVECSSLK	1.450728741	2	2.50724
Q5I0M2	YDLGGLVMVK	1.699886621	2	2.52426
Q5M7T9	**THNS2 Threonine synthase_like 2**	**2.410112592**	**0.08813**	**2**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	1.273403578	3	5.58988
Q5M7T9	LSEAVTSESVSDEAITQTMGR	0.636269867	2	4.48084
Q5M7U6	**ARP2 Actin_related protein 2**	**1.933985843**	**0.95261**	**5**
Q5M7U6	GYAFNHSADFETVR	0.917862978	2	4.00171
Q5M7U6	HLWDYTFGPEK	0.941268172	2	3.19684
Q5M7U6	ILLTEPPMNPTK	0.702661031	2	2.85151
Q5M7U6	SMLEVNYPMENGIVR	1.367183404	2	4.09419
Q5M7U6	VVVCDNGTGFVK	0.985551711	2	2.70943
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**1.923813517**	**1**	**10**
Q5M7W5	AAVGLTGNDIATPPNK	0.88955551	2	3.48093
Q5M7W5	ATSPSTLVSTGSSSR	0.940807016	2	3.8683
Q5M7W5	EAETALPIEMDLAPPEDVALPK	0.990542815	2	3.08068
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	1.39768007	2	4.18592
Q5M7W5	ETSGSQPPELCSGVSR	1.280886361	2	3.34701
Q5M7W5	NTAPPTEEETVPGK	1.104494714	2	2.58157
Q5M7W5	NTTPTGATPPAGMASTR	1.07013306	2	3.568
Q5M7W5	STLPVDEGSPLEK	1.045831204	2	2.47697
Q5M7W5	VGSLDNVGHLPAGGTVK	0.949608747	2	3.71376
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.044617287	2	3.14494
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**2.710812704**	**0.52635**	**7**
Q5M875	ALTAELDTLGK	1.325914102	2	3.07804
Q5M875	IQNIQFEAIVGHR	1.228497589	3	4.2412
Q5M875	LWPVLEPDEVAR	1.319190389	2	2.49488
Q5M875	NSGHIVTVASVCGHR	1.395131088	2	4.50165
Q5M875	SLIDGILTNK	1.43909606	2	3.31113
Q5M875	SVAGQTVLITGAGHGIGR	1.26990395	2	4.09628
Q5M875	TSCLCPVFVNTGFTK	1.289884238	2	3.94863
Q5M9G3	**CAPR1 Caprin_1**	**1.918331395**	**0.99989**	**2**
Q5M9G3	LNQDQLDAVSK	1.121621017	2	3.17975
Q5M9G3	YQEVTNNLEFAK	0.934368897	2	3.03739
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**2.572564988**	**0.83313**	**2**
Q5M9I5	EEEEEELVDPLTTVR	1.404361253	2	4.23759
Q5M9I5	SQTEEDCTEELFDFLHAR	1.321228989	2	4.83109
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.921273346**	**0.90225**	**10**
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	0.855779962	2	4.99629
Q5PPL3	DPQLVPVLIDAAR	1.067709206	2	2.42473
Q5PPL3	GQVTGTDLINEVSK	0.658652689	2	4.0784
Q5PPL3	GVSTVFHCASPPSNSNNK	0.691979822	2	4.30668
Q5PPL3	GYAVNVFDVR	1.084516524	2	3.56783
Q5PPL3	ILTGLNYEAPK	0.871110344	2	3.58762
Q5PPL3	KGQVTGTDLINEVSK	0.977538872	2	4.41052
Q5PPL3	NGTEDLPYAMKPIDYYTETK	0.799036965	2	3.93677
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.160936573	3	3.52041
Q5PPL3	VQFFIGDLCNQQDLYPALK	0.896988089	2	5.41096
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**2.488537729**	**0.98967**	**7**
Q5PQT3	AINQEMFK	0.891258821	1	1.9529
Q5PQT3	AIQNLASIHSLQVK	1.003265266	2	4.04558
Q5PQT3	DPENCQEFLGSSEVINWK	1.215153942	2	5.29151
Q5PQT3	KLFPSLLDTK	1.343434543	2	2.71433
Q5PQT3	LSSLDVTHAALVNK	1.2121176	2	3.61602

Q5PQT3	MGGTVPQYR	0.997798603	2	2.56175
Q5PQT3	QHLQIQSSQSHLNK	1.227630084	2	3.39338
Q5PQX1	**TOIP1 Torsin_1A_interacting protein 1**	**2.008622925**	**1**	**2**
Q5PQX1	LEQHSQQAQQQLSPATSGR	1.007017423	3	4.66536
Q5PQX1	SDFGNQSPSTSR	1.006205712	2	2.62768
Q5RJR2	**TWF1 Twinfilin_1**	**2.165164522**	**0.15912**	**2**
Q5RJR2	HQTLQGVAFPISR	0.994744892	2	3.02011
Q5RJR2	YLLSQSSPAPLTAAEEELR	1.748571588	2	4.32294
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.942916741**	**0.99946**	**5**
Q5RJR8	ATVLDLSCNK	0.928342478	2	2.81952
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	1.810323993	2	6.21131
Q5RJR8	LDGNELDLSLSDLNEVPVK	0.935660161	2	4.05641
Q5RJR8	LQQLPADFGR	1.182280134	1	1.92139
Q5RJR8	WLDLKDNPLDPVLAK	1.004758265	2	2.67182
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**2.323950125**	**0.52036**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.22344804	3	4.753
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	1.052281774	3	4.76568
Q5RKI0	YAPSGFYIASGDISGK	1.237682425	2	4.53409
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**2.306272935**	**0.06027**	**5**
Q5RKI1	ELAQQIQK	1.100530108	1	2.28296
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.597598579	2	3.61907
Q5RKI1	GYDVIAQAQSGTGK	1.920877571	2	5.13797
Q5RKI1	MFVLDEADEMLSR	1.439861919	2	4.4924
Q5RKI1	VLITTDLLAR	1.326732392	2	3.06854
Q5S6T3	**ISPD 2_C_methyl_D_erythritol 4_phosphate cytidylyltransferase_like protein**	**2.425745855**	**0.47832**	**2**
Q5S6T3	ISLAEAGATR	3.284652112	2	2.34198
Q5S6T3	MENLVWIRELAK	0.960267769	2	2.34806
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**2.168075534**	**0.86623**	**15**
Q5SGE0	AALDLEQVPSELAVTR	1.419385191	2	4.10799
Q5SGE0	CIANNQVETLEK	0.880891935	2	3.01274
Q5SGE0	GLDAIELSR	0.705198066	2	2.52148
Q5SGE0	HCVTMDTPAEK	0.811240916	2	2.96809
Q5SGE0	HDNAEDALNLK	1.343594157	2	3.64453
Q5SGE0	LIDYCK	1.530336669	1	1.93197
Q5SGE0	MEGANIQPNR	0.954161975	2	2.97081
Q5SGE0	SCGSLLPELSLAER	1.077333003	2	2.77297
Q5SGE0	SGSPGSNQALLLLR	1.021265419	2	2.88408
Q5SGE0	SGSQFDWALMR	1.341970328	2	2.39482
Q5SGE0	SSLSSSSPSAGDTVTEK	1.186593569	2	3.88544
Q5SGE0	SYVADKDVASAK	0.837679339	2	3.16469
Q5SGE0	TLLELIPELR	0.858836898	2	3.10069
Q5SGE0	TSQFTSSDLESTLEK	1.02041316	2	4.18987
Q5SGE0	VIEEQMEPALEK	1.050409213	2	3.11152
Q5SW19	**K0664 Protein KIAA0664**	**2.032155277**	**0.83935**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	0.908798278	2	3.38476
Q5SW19	IGIGELITR	1.52243114	2	2.40003
Q5SW19	SVEGLQEGSVLR	0.998278734	2	2.73793
Q5SX40	**MYH1 Myosin_1**	**2.928381671**	**1**	**86**
Q5SX40	AAYLQNLNSADLLK	2.510523193	2	3.44502
Q5SX40	ADIAESQVNK	3.482994561	2	3.70484
Q5SX40	AEDEEEINAELTAK	2.72708403	2	4.21949
Q5SX40	AGLLGLLEEMR	2.906276232	2	4.26557
Q5SX40	AGLLGLLEEMRDDK	1.93721157	2	3.38575
Q5SX40	ALQEAHQQTLDDLQAEEDK	2.496791073	3	4.51196
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	3.033895456	3	6.77841

Q5SX40	ANLLQAEIEELR	4.757268944	2	3.71783
Q5SX40	ANSEVAQWR	0.867362033	2	2.87563
Q5SX40	DDKLAQLITR	2.148314109	2	2.35281
Q5SX40	DLEEATLQHEATAATLR	1.815563564	2	5.08514
Q5SX40	DTQLHLDDALR	0.595905573	2	2.8452
Q5SX40	EEQAEPDGTEVADK	0.348673098	2	3.38988
Q5SX40	EFEMSNLQSK	2.0936304	1	2.63379
Q5SX40	ELEGEVENEQK	0.686943452	2	2.88145
Q5SX40	ELEGEVENEQKR	2.186985072	2	3.02863
Q5SX40	ELTYQTEEDRK	1.707382178	2	3.1274
Q5SX40	EMANMKEEFEK	1.622219496	2	2.82398
Q5SX40	ENQSILITGESGAGK	4.234506766	2	4.10837
Q5SX40	EQYEEEQEAK	1.399382132	1	3.21304
Q5SX40	GQEDLKEQLAMVER	1.3181802	2	4.41943
Q5SX40	GSSFQTVSALFR	1.016291941	2	3.06736
Q5SX40	HADSVAELGEQIDNLQR	1.433734159	2	6.01742
Q5SX40	IAEQELLDASER	2.339958791	2	3.23326
Q5SX40	IEAQNKPFDAK	1.058665639	2	3.03745
Q5SX40	IEDEQALGMQLQK	2.986666965	2	4.60505
Q5SX40	IEDEQALGMQLQK+Oxidation(8	2.528310654		
Q5SX40	IEDMAMMTHLHEPAVLYNLK	1.6097168	3	4.30286
Q5SX40	IEELEEEIEAER	2.106753183	2	4.34576
Q5SX40	IKLEQQVDDLEGSLEQEK	2.273490212	2	5.11645
Q5SX40	IKLEQQVDDLEGSLEQEKK	1.13462376	3	4.10119
Q5SX40	IQHELEEAEER	1.471771077	2	3.69329
Q5SX40	IQHELEEAEERADIAESQVNK	1.605468171	3	3.88024
Q5SX40	IQLELNQVK	1.103325901	2	2.70493
Q5SX40	KIAEQELLDASER	1.839690359	2	3.82823
Q5SX40	KIQHELEEAEER	1.350743079	3	4.11516
Q5SX40	KKEFEMSNLQSK	1.633034174	2	3.86205
Q5SX40	KKLETDISQIQGEMEDIVQEAR	1.578930178	3	6.08285
Q5SX40	KLEDECSELK	1.408530209	2	2.91871
Q5SX40	KLEDECSELKK	0.782929873	2	4.02704
Q5SX40	KLETDISQIQGEMEDIVQEAR	2.020218421	2	5.64785
Q5SX40	KMEGDLNEMEIQLNHSNR	1.140695049	3	4.61326
Q5SX40	LAQESTMDVENDKQQLDEK	3.043493087	2	4.86328
Q5SX40	LDEAEQLALK	0.80316436	2	3.23504
Q5SX40	LEDECSELKK	1.684811658	2	3.32472
Q5SX40	LEEAGGATSAQIEMNK	2.479744194	2	5.15375
Q5SX40	LEQQVDDLEGSLEQEK	1.422193909	2	5.46536
Q5SX40	LEQQVDDLEGSLEQEKK	0.980549179	2	4.1631
Q5SX40	LETDISQIQGEMEDIVQEAR	1.00198165	2	5.19096
Q5SX40	LINELTAQR	1.25917252	2	3.14717
Q5SX40	LQDAEEHVEAVNAK	1.737891887	2	4.81502
Q5SX40	LQDLVDK	2.179805106	2	2.44684
Q5SX40	LQDLVDKLQSK	1.425887982	2	2.55319
Q5SX40	LQNEVEDLMIDVER	1.650226117	2	4.46346
Q5SX40	LQTESGEYSR	1.162530002	2	2.51991
Q5SX40	LTGAVMHYGNMK	1.249169715	2	2.67692
Q5SX40	MEGDLNEMEIQLNHSNR	1.263620482	2	4.73322
Q5SX40	MEGDLNEMEIQLNHSNRMAAEALR+Oxidation(0)Oxidation(17	1.048428932		
Q5SX40	MEIDDLASNMEVISK	3.11778733	2	4.95757
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	1.314302307	3	6.37659
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0	1.318618613		
Q5SX40	NDLQLQVQSEADSLADAEER	8.191257777	2	6.30669
Q5SX40	NKDPLNETVVGLYQK	2.362430494	2	4.69152

Q5SX40	NLQQEISDLTEQIAEGGK	1.838206234	2	6.02876
Q5SX40	NLQQEISDLTEQIAEGGKR	1.870236532	2	4.27337
Q5SX40	NLTEEMAGLDETIAK	2.658329106	2	4.78848
Q5SX40	QAEEAEEQSNVNLAK	3.464182049	2	4.41122
Q5SX40	QKYEETHAELEASQK	1.546336714	2	3.91191
Q5SX40	QLDEKDSLVSQLSR	1.840468602	2	3.19078
Q5SX40	QLEEEIK	0.914217935	1	2.20342
Q5SX40	QREEQAEPDGTEVADK	2.266503107	2	4.12469
Q5SX40	RDLEEATLQHEATAATLR	1.142363536	3	3.62924
Q5SX40	SAETEKEMANMKEEFEK	0.749886146	3	4.01588
Q5SX40	SELQAALEEAEASLEHEEGK	1.717721789	2	5.74997
Q5SX40	SSVFVVDAK	2.015268005	2	2.52796
Q5SX40	TKYETDAIQR	1.142220324	3	3.45201
Q5SX40	TLEDQVSELK	2.167941329	2	2.94919
Q5SX40	TNAACAALDK	1.30195907	1	1.98446
Q5SX40	TNAACAALDKK	0.369007212	2	2.98051
Q5SX40	VLNASAIPEGQFIDSK	1.942310396	2	4.29797
Q5SX40	VQLLHTQNTSLINTK	0.498767895	2	4.71032
Q5SX40	VRELEGEVENEQK	0.522960736	2	3.85636
Q5SX40	VRELEGEVENEQKR	0.850319927	3	4.14079
Q5SX40	VVESMQSTLDAEIR	1.033389161	2	3.74154
Q5SX40	YEETHAELEASQK	1.793714168	2	4.73862
Q5SX40	YETDAIQR	1.479666738	2	2.62035
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.97869718**	**0.99987**	**5**
Q5U206	DTDSEEEIR	1.246571515	2	2.83205
Q5U206	KMKDTDSEEEIR	0.956971343	3	3.41088
Q5U206	KMKDTDSEEEIR+Oxidation(1	1.27227203		
Q5U206	MKDTDSEEEIR	0.935115057	3	4.32711
Q5U206	MKDTDSEEEIR+Oxidation(0	0.978519079		
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**2.309193563**	**0.56613**	**4**
Q5U2Q7	GFGGIGGILR	1.23004351	2	2.75822
Q5U2Q7	LSVLGAITSVQQR	1.251542595	2	2.93988
Q5U2Q7	YFDEISQDTGK	1.747202272	2	2.53487
Q5U2Q7	YVLHCQGTEEEK	1.140654234	2	3.68392
Q5U2S3	**ZUFSP Zinc finger with UFM1_specific peptidase domain protein**	**2.349747579**	**0.03503**	**2**
Q5U2S3	QYGLDNSGGYKQQQLR	1.229571913	2	2.67702
Q5U2S3	TLCLLIFDPGCPSREMQKLLK+Oxidation(15	7.399265822		
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**1.739814432**	**0.33904**	**5**
Q5U2U0	LLEGTIVNVPEK	1.638523124	2	2.62449
Q5U2U0	QQAEVEK	1.408378675	1	1.91779
Q5U2U0	SGESNTHQDIEEK	1.581099418	2	3.60002
Q5U2U0	SGESNTHQDIEEKDR	0.705355144	3	4.32588
Q5U2U0	SNILLLGPTGSGK	1.361469599	2	2.37762
Q5U2V4	**PLBL1 Phospholipase B_like 1**	**2.456186516**	**0.3845**	**2**
Q5U2V4	IWEMGHCSALIK+Oxidation(3	9.186260725		
Q5U2V4	LGLDYSYDLAPR	1.29636342	2	2.51104
Q5U2Z7	**RHG24 Rho GTPase_activating protein 24**	**2.206781662**	**0.83457**	**2**
Q5U2Z7	EEEAGVKELTKQVK	1.018947424	2	2.3874
Q5U2Z7	FTMIEIKMRNAER+Oxidation(7	1.605673084		
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**2.580241263**	**0.12765**	**14**
Q5U300	AAVASLLQSVQVPEFTPK	1.219573889	3	3.67161
Q5U300	AENYDISPADR	1.05340128	2	3.19107
Q5U300	DNPGVVTCLDEAR	0.948295855	2	3.39997
Q5U300	FEVQGLQPNGEEMTLK	1.335138829	2	4.01965

Q5U300	IHVSDQELQSANASVDDSR	1.748759887	3	3.48724
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.888081606	2	4.71172
Q5U300	LDQPMTEIVSR	1.382448507	2	3.39489
Q5U300	LKSDTAAAAVR	1.003649379	2	2.82246
Q5U300	NEEDATELVTLAQAVNAR	2.152713355	3	4.68795
Q5U300	NFPNAIEHTLQWAR	1.048996787	2	3.40726
Q5U300	SLPASLAEPDFVMTDFAK	0.83541819	2	4.05759
Q5U300	SPPAVQQDNVDEDLIR	1.037565699	2	4.76979
Q5U300	SPPAVQQDNVDEDLIRK	1.039510607	3	3.32207
Q5U300	VVQGHQQLDSYK	1.222223607	2	3.42621
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**1.878151707**	**0.76783**	**3**
Q5U4E6	EFNTQLAQK	0.895749024	2	2.34942
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(16	0.943979129		
Q5U4E6	VQQCAKDTESQLSELR	4.762932562	2	2.31087
Q5XFW8	**SEC13 Protein SEC13 homolog**	**1.947564284**	**0.99983**	**4**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	0.904167686	2	3.45853
Q5XFW8	EEEDGQWKEEQK	1.039844375	2	2.75701
Q5XFW8	LEAHSDWVR	0.974579273	2	2.36868
Q5XFW8	NGGQILIADLR	1.113132361	2	2.48169
Q5XFX0	**TAGL2 Transgelin_2**	**1.826237646**	**0.8733**	**6**
Q5XFX0	DDGLFSGDPNWFPK	2.278732494	2	3.66492
Q5XFX0	NFSDNQLQEGK	1.173029321	2	3.15758
Q5XFX0	NVIGLQMGTNR	0.827126067	2	3.02612
Q5XFX0	QMEQISQFLQAAER	1.076766717	2	2.80307
Q5XFX0	TLMNLGGLAVAR	1.091536567	2	3.3582
Q5XFX0	YGINTTDIFQTVDLWEGK	0.890422788	2	4.73927
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**2.084276831**	**0.97532**	**11**
Q5XHY5	AEHDSILAEK	0.97593258	2	2.83885
Q5XHY5	FLGDIEIWNQAEK	1.348023702	2	3.76226
Q5XHY5	FMVDIDLDPGCTLNK	1.115944251	2	3.7564
Q5XHY5	GFQEVVTPNIFNSR	1.920404518	2	3.90931
Q5XHY5	LKAEHDSILAEK	0.821545117	2	3.34697
Q5XHY5	NELSGALTGLTR	1.059981047	2	3.20448
Q5XHY5	QLENSLNEFGEK	1.158489321	2	3.15633
Q5XHY5	QVMVVPVGPTCDEYAQK	1.078257124	2	3.66822
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.090318462	2	4.1517
Q5XHY5	VVWDLDRPLETDCTLELLK	2.417558009	2	3.88131
Q5XHY5	WELNPGDGAFYGPK	1.333602233	2	3.96393
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**2.257963723**	**0.31114**	**14**
Q5XHZ0	AFLEALQHQAETSSR	1.240188456	2	4.68455
Q5XHZ0	AQLLQPTLEINPR	0.990460549	2	3.72326
Q5XHZ0	EGIVTTAEQDIKEDIAK	0.789628365	2	2.32675
Q5XHZ0	ELISNASDALEK	0.802792008	2	2.70663
Q5XHZ0	FEDTSPAGER	0.981756184	2	2.49638
Q5XHZ0	GTITIQDTGIGMTK	1.030508409	2	3.56485
Q5XHZ0	GVVDSEDIPLNLSR	1.09153469	2	4.80619
Q5XHZ0	HLAEHSPYYEAMK	1.043725047	2	3.72621
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.120893426	3	4.05658
Q5XHZ0	NIYYLCAPNR	1.034521664	2	2.41473
Q5XHZ0	SDCKDFANESR	1.007504911	2	2.70157
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	1.228661367	3	3.64968
Q5XHZ0	YESSALPAGQLTSLSDYASR	2.154632249	2	5.63993
Q5XHZ0	YIAQAYDKPR	1.256119189	2	2.66106
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.84138826**	**0.15432**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	0.843519756	2	4.99351
Q5XI22	ELGLSPEK	0.679806938	1	1.95042
Q5XI22	HGSNLEAMSK	1.835714025	2	2.68347

Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	0.916286434	3	5.21921
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	0.984645821	3	4.07326
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	0.927783537	3	4.53659
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	0.959871692	2	5.42234
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	0.751396853	2	5.18503
Q5XI22	VNIDGGAIALGHPLGASGCR	0.638083739	2	5.44328
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**2.020396325**	**0.89226**	**2**
Q5XI29	QNLSQFEAQAR	1.184678608	2	2.41633
Q5XI29	SIGVYDVVELK	1.014498244	2	2.36714
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**2.070334641**	**0.97807**	**8**
Q5XI32	GCWDSIHVVEVQEK	0.994939483	2	3.74296
Q5XI32	KLEVEANNAFDQYR	0.997952432	2	4.13815
Q5XI32	LEVEANNAFDQYR	1.318831972	2	3.75904
Q5XI32	LVEDMENK	1.311342328	2	2.66874
Q5XI32	NDLVEALK	1.128892588	2	2.40444
Q5XI32	SGSGTMNLGGSLTR	1.215383289	2	3.30343
Q5XI32	STLNEIYFGK	0.829769325	1	2.05758
Q5XI32	YDPPLEDGAMPSAR	0.911170448	2	3.58329
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.786312613**	**0.78719**	**3**
Q5XI60	ALDIAAGITR	0.647539424	2	3.26724
Q5XI60	HHVALDSAASQLSGR	0.927872944	2	4.60082
Q5XI60	NVATDALGALEAR	0.790772014	2	3.98321
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.845423168**	**0.99996**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.169040588	2	4.40899
Q5XI73	IDKTDYMVGSYGPR	1.076369454	2	3.98928
Q5XI73	SIQEIQELDKDDESLR	0.732877792	2	5.28958
Q5XI73	SIQEIQELDKDDESLRK	0.883883087	2	4.65383
Q5XI73	TDYMVGSYGPR	1.053258803	2	2.41423
Q5XI73	VAVSADPNVPNVIVTR	0.940966186	2	3.97865
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**2.167148275**	**0.98656**	**18**
Q5XI78	FGLEGCEVLIPALK	1.181851352	2	3.587
Q5XI78	FLDTAFDLDAFK	1.70178026	2	2.66043
Q5XI78	FLDTAFDLDAFKK	1.115723391	2	2.93743
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.230483817	3	5.9103
Q5XI78	ICEEAFTR	0.981201141	2	2.34013
Q5XI78	IEQLSPFPFDLLLK	0.80164646	2	3.32549
Q5XI78	LEAADEGSGDMK	0.881182868	2	3.51647
Q5XI78	LNVLANVIR	1.361159888	2	2.32154
Q5XI78	LVEDHLAVQSLIR	1.186921887	2	2.90109
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.517775562	2	5.5507
Q5XI78	NQGYYDYVKPR	1.009710246	2	2.37889
Q5XI78	NTNAGAPPGTAYQSPLSLSR	0.223482704	2	2.85357
Q5XI78	SSLATMAHAQSLVEAQPNVDK	1.071320922	3	4.4054
Q5XI78	TSFDEMLPGTHFQR	1.031060805	2	2.30849
Q5XI78	VIPEDGPAAQNPDK	1.206237489	2	2.94482
Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	1.398311959	3	4.24681
Q5XI78	YAELLVSQGVVNQPEYEEEISK	1.019197668	2	4.07064
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	1.988663064	3	3.93237
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**2.23671589**	**0.99602**	**6**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.793067625	2	3.94193
Q5XI95	FNIDPLITHTLTLSEANEAVQLMK	1.14192365	3	4.98578
Q5XI95	IIAVDINK	1.174302744	2	2.73793
Q5XI95	MVATGVCGTDIK	0.74452002	2	3.02144
Q5XI95	NNICTEIR	0.805824979	2	2.47322
Q5XI95	TVGATDCVDPR	0.790975867	2	2.82778

Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**2.02957519**	**0.99724**	**6**
Q5XIC0	AAEMLLFGK	1.837098967	2	2.45247
Q5XIC0	ATQQDFENAMNQVK	0.899224155	2	4.27289
Q5XIC0	GILVTSEGGITK	0.938987155	2	3.45074
Q5XIC0	LHAVNEEECTTLR	1.09311156	2	3.85118
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.889935918	2	5.40824
Q5XIC0	WDAWNALGSLPK	1.046603914	2	3.69137
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.925122082**	**0.86915**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	0.807947781	2	2.62822
Q5XIC1	VEGTPNDPNPNDPR	1.296843332	2	3.18967
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**2.228197585**	**0.99958**	**7**
Q5XIE6	AGIATHFVDSEK	0.933017103	2	3.11277
Q5XIE6	AVLIDKDQTPK	0.908892413	2	2.83667
Q5XIE6	GCAGVITLNRPK	1.014752173	2	2.91632
Q5XIE6	HTETAEVLLER	1.206862681	2	2.87884
Q5XIE6	INSCFSANTVEQILENLR	1.007213642	2	3.16181
Q5XIE6	LHVLEEELLALK	1.157149002	3	4.10167
Q5XIE6	WKPADLKDVTDEDLNSYFK	1.391028386	2	2.31577
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.808715804**	**0.31307**	**3**
Q5XIF3	DTQLITVDEK	0.69909342	2	2.48431
Q5XIF3	HGWSYDVEGR	0.986551154	2	2.88439
Q5XIF3	LDVTPLTGVPEEHIK	0.82130834	3	3.66129
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**2.313270975**	**0.21953**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	0.953398941	2	3.8446
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.210387649	2	5.22033
Q5XIF6	DVNAAIAAIK	1.359213867	2	3.10819
Q5XIF6	SIQFVDWCPTGFK	0.949942066	2	4.13838
Q5XIF6	TIGGGDDSFTTFFCETGAGK	1.373843163	2	2.78316
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**2.455960034**	**0.99955**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	1.313704788	2	4.39852
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.06075673	2	5.66521
Q5XIH7	**PHB2 Prohibitin_2**	**2.382305847**	**0.99946**	**10**
Q5XIH7	DLQMVNISLR	2.198085056	2	2.73049
Q5XIH7	FNASQLITQR	0.860399832	2	3.78161
Q5XIH7	IGGVQQDTILAEGLHFR	0.8085842	3	4.92463
Q5XIH7	IPWFQYPIIYDIR	1.162409815	2	2.4702
Q5XIH7	IVQAEGEAEAAK	0.918084504	2	4.05741
Q5XIH7	IYLTADNLVLNLQDESFTR	1.425048672	2	4.04246
Q5XIH7	LGLDYEER	0.847074819	2	2.46778
Q5XIH7	LLLGAGAVAYGVR	2.06621386	2	3.78403
Q5XIH7	VLPSIVNEVLK	0.607829167	1	2.29777
Q5XIH7	VLSRPNAQELPSMYQR	1.067686661	2	4.76181
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.889101786**	**0.03204**	**12**
Q5XIM9	DASLMVTNDGATILK	4.3149731	2	2.99152
Q5XIM9	EALLSSAVDHGSDEVK	1.411689196	2	4.25345
Q5XIM9	FWQDLMNIAGTTLSSK	1.526500596	2	3.4773
Q5XIM9	GATQQILDEAER	1.371725325	2	3.87399
Q5XIM9	GSGNLEAIHVIK	1.27385507	2	2.56925
Q5XIM9	HGINCFINR	0.783666295	2	2.65158
Q5XIM9	LIEEVMIGEDK	1.423316962	2	3.15561
Q5XIM9	MLPTIIADNAGYDSADLVAQLR	1.640703874	3	3.31328
Q5XIM9	NIGVDNPAAK	0.8892733	1	1.95384
Q5XIM9	SLHDALCVLAQTVK	1.209071615	2	3.89941
Q5XIM9	VAEIEHAEKEK	1.052140635	2	2.7948

Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.511076347	2	4.35294
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**2.181426012**	**0.38318**	**10**
Q5XIN6	AAEVEGEQVDNK	1.068061034	2	3.87772
Q5XIN6	AMYLPDTLSPADQLK	0.864295907	2	2.46615
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.800310803	2	4.54462
Q5XIN6	FLQDTIEEMALK	0.958140735	2	3.03683
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.001003534	2	3.72942
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	1.271127878	2	5.30412
Q5XIN6	LEEGGPVYSPPAQVVVK	1.002668746	2	3.39234
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.456547109	3	3.98203
Q5XIN6	LLELQSIGTNNFLR	1.313197774	2	3.46601
Q5XIN6	STLQTLPEIVAK	1.205736537	2	2.57672
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**2.035127631**	**1**	**9**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.937260934	2	5.22438
Q5XIT9	ALVNQLHER	1.169435154	2	2.68444
Q5XIT9	ALYGDTLVTGFAR	1.085612205	2	3.5122
Q5XIT9	AQEIALQNR	0.938205984	2	2.57048
Q5XIT9	LGTQPDSGSSTYQENYEQMK	0.92373189	2	5.25139
Q5XIT9	LWDDGIIDPVDTR	1.027445884	2	3.53647
Q5XIT9	LYGEEEVPAGGIITGIGR	1.35849434	2	4.76527
Q5XIT9	RFEEEGNPYYSSAR	0.783967197	2	4.25401
Q5XIT9	VSGVECMIVANDATVK	1.090791411	2	3.39354
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**1.80790496**	**0.59886**	**2**
Q5XIU5	ALIDPSSGLPNR	0.898250353	2	2.7933
Q5XIU5	SGIITPIHEQWEK	0.795255544	2	3.03607
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.876139848**	**0.99999**	**3**
Q5XIU9	GLATFCLDK	0.922614303	2	2.80292
Q5XIU9	GLCSGPGAGEESPAATLPR	0.903847445	2	4.83923
Q5XIU9	VFDVTK	1.02453028	1	1.98739
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**2.199445719**	**0.96529**	**9**
Q60587	ALAMGYKPK	0.686283974	2	2.40505
Q60587	AMDSDWFAQNYMGR	1.103988429	2	3.15826
Q60587	AQDEGHLSDIVPFK	0.819839843	2	2.48664
Q60587	DFIYVSQDPK	1.164428896	2	2.79556
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	1.492217415	3	4.6773
Q60587	DNGIRPSSLEQMAK	0.821986423	2	3.64398
Q60587	DQLLLGPTYATPK	1.265593173	2	3.75995
Q60587	MMLDLNK	0.888388502	1	2.12756
Q60587	NIVVVEGVR	0.971080903	2	3.06333
Q60598	**SRC8 Src substrate cortactin**	**1.727165256**	**0.69428**	**3**
Q60598	NASTFEEVVQVPSAYQK	1.06264318	2	3.54738
Q60598	TVQGSGHQEHINIHK	0.713368119	2	3.47368
Q60598	VDQSAVGFEYQGK	1.033682054	2	3.34599
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**2.222613566**	**0.60734**	**4**
Q60759	DILGGNGISDEYHVIR	1.348022653	2	3.86019
Q60759	DIVYEMGELGVLGPTIK	1.399568289	2	3.89685
Q60759	GYGCAGVSSVAYGLLTR	1.12951991	2	3.32187
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.395873361	3	5.09824
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.968835207**	**0.98081**	**3**
Q60817	DIELVMSQANVSR	1.568527663	2	3.41899
Q60817	IEDLSQQAQLAAAEK	0.952905341	2	4.676

Q60817	NILFVITKPDVYK	0.695568619	2	3.66666
Q60952	**CP250 Centrosome_associated protein CEP250**	**1.721853214**	**0.10047**	**2**
Q60952	GQIQDLKK	0.79057226	1	1.9552
Q60952	QQIDELQK	0.299575032	1	2.03522
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**2.042387545**	**0.519**	**2**
Q61029	SELVANNVTLPAGEQR	1.104362988	2	4.56692
Q61029	YGVNPGPIVGTTR	0.862674448	2	2.71646
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**2.427252939**	**0.86231**	**2**
Q61035	ASAEQIEEEVTK	1.3104346	2	2.77658
Q61035	REDLVEEIR	1.191641788	2	2.46645
Q61043	**NIN Ninein**	**1.909714234**	**0.97824**	**3**
Q61043	NEITTLNEEDSISNLK	0.770029676	2	2.47405
Q61043	RQLQMAFDEEKAQLQEELR+Oxidation(4	0.983131719		
Q61043	SLENVLAEK	0.98935418	1	2.02442
Q61301	**CTNA2 Catenin alpha_2**	**2.147168316**	**0.9846**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	1.284921638	2	3.82697
Q61301	TSVQTEDDQLIAGQSAR	1.020942635	2	5.00155
Q61301	WDDSGNDIIVLAK	1.238403244	2	3.0363
Q61335	**BAP31 B_cell receptor_associated protein 31**	**1.99434983**	**0.99958**	**5**
Q61335	AENEALAMQK	0.840820584	2	3.41615
Q61335	KYMEENDQLK	1.223085865	2	2.63751
Q61335	KYMEENDQLKK	0.859153041	3	3.96824
Q61335	YMEENDQLK	1.077312321	2	2.74282
Q61335	YMEENDQLKK	0.859250794	2	2.90167
Q61545	**EWS RNA_binding protein EWS**	**2.113130379**	**0.99961**	**2**
Q61545	GDATVSYEDPPTAK	1.055464221	2	3.41173
Q61545	GGPGGPGGPGGPMGR	1.187823969	2	2.86395
Q61595	**KTN1 Kinectin**	**1.826703035**	**0.96881**	**2**
Q61595	TAEHEAAQQDLQSK	0.900455316	2	4.37952
Q61595	VEPVLVTK	0.705774327	2	2.35715
Q61655	**DD19A ATP_dependent RNA helicase DDX19A**	**2.044718379**	**0.99999**	**2**
Q61655	SNLVDNTNQVEVLQR	0.874810605	2	4.18284
Q61655	TSTTAEKTEEEEKEDR	1.177233951	3	3.98546
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**2.408380864**	**5.4E-06**	**6**
Q61656	ELAQQVQQVAAEYCR	0.824016906	2	2.8823
Q61656	GDGPICLVLAPTR	1.358272794	2	2.95587
Q61656	MLDMGFEPQIR	1.381004069	2	3.34645
Q61656	NFYQEHPDLAR	1.477776131	2	3.30726
Q61656	STCIYGGAPK	0.964453547	2	2.47578
Q61656	TAQEVDTYR	1.04696994	2	2.31755
Q61830	**MRC1 Macrophage mannose receptor 1**	**2.082555144**	**0.81231**	**3**
Q61830	LKLPWHEAETYCK	0.928923041	2	2.35084
Q61830	WTVDEQVQFTHWNADMPGR+Oxidation(15	1.623462835		
Q61830	YLNWLPGSPSSEPGK	1.310565582	2	2.62816
Q61941	**transhydrogenase_ mitochondrial**	**2.192280237**	**0.0001**	**13**
Q61941	AQYPIADLVK	1.123654957	2	2.47929
Q61941	DDFDFGTMSHVIR	1.358189585	2	2.52687
Q61941	EANSIVITPGYGLCAAK	1.172698092	2	3.83934
Q61941	FFTGQITAAGK	1.163990793	2	2.74212
Q61941	GITHIGYTDLPSR	0.811236884	2	3.74714
Q61941	ILIVGGGVAGLASAGAAK	1.948684206	2	3.90539
Q61941	KTTVLAMDQVPR	0.990193408	2	3.28874
Q61941	MATQASTLYSNNITK	0.869290276	2	4.72669
Q61941	QGFNVVVESGAGEASK	1.129767537	2	4.14883
Q61941	SLGAEPLEVDLK	1.206129868	2	3.51381

Q61941	TTVLAMDQVPR	0.999007456	2	2.57553
Q61941	TVAELEAEK	0.941299149	2	2.98057
Q61941	VTIAQGYDALSSMANISGYK	1.350663552	2	5.33168
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**3.231814221**	**0.43595**	**2**
Q61990	AITIAGIPQSIIECVK	1.616744619	2	2.33291
Q61990	IITLAGPTNAIFK	1.79838002	2	2.54473
Q62009	**POSTN Periostin**	**2.451438447**	**0.59209**	**2**
Q62009	ISTGGGETGETLQKFLQK	1.091140996	2	2.52124
Q62009	TEGPAMTKIQIEGDPDFR	1.665719833	2	2.30993
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**2.702389325**	**0.19503**	**4**
Q62095	HVINFDLPSDIEEYVHR	1.435546349	3	4.44574
Q62095	SFLLDLLNATGK	1.301767081	2	4.17301
Q62095	VGNLGLATSFFNER	1.407762851	2	3.11215
Q62095	VGSTSENITQK	0.799682483	2	2.86075
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**2.037336584**	**0.8391**	**20**
Q62261	AKDEQSAVSMLK	0.983360669	2	2.47299
Q62261	ALVADSHPESER	1.18762505	2	3.19084
Q62261	DQNTVETLQR	0.942739928	2	2.99977
Q62261	EAEKLESEHPDQAQAILSR	2.471676258	3	3.84367
Q62261	EGMQLISEKPETEAVVKEK	1.380105175	2	2.34095
Q62261	EIEELQSQAQALSQEGK	0.845174027	2	3.78378
Q62261	FESLEPEMNNQASR	0.956032518	2	3.90479
Q62261	HLLGVEDLLQK	1.149382479	2	3.40903
Q62261	HQILEQAVEDYAETVHQLSK	1.21230831	3	5.53489
Q62261	ITDLYTDLR	0.993035375	2	2.43914
Q62261	LTTLELLEVR	1.634455455	2	2.91883
Q62261	LVSDGNINSDR	1.045564514	2	3.32429
Q62261	LVSQDNFGFDLPAVEAATK	1.729532727	2	3.17874
Q62261	SNAHYNLQNAFNLAEQHLGLTK	0.732929365	3	3.89783
Q62261	SQNIITDSSSLNAEAIR	0.844357128	2	5.24351
Q62261	TLETPAAQMEGFLNR	1.539236376	2	3.22523
Q62261	TQILAASYELHK	1.746165169	2	2.57199
Q62261	TQTAIASEDMPNTLTEAEK	1.035471953	2	5.21925
Q62261	VIESTQDLGNDLAGVMALQR	0.290198843	2	4.45921
Q62261	VLDNAIETEK	0.87752716	2	2.47117
Q62376	**RU17 U1 small nuclear ribonucleoprotein 70 kDa**	**1.8143047**	**0.87975**	**2**
Q62376	IERRQQEVETELK	0.858564838	2	2.30479
Q62376	RQQEVETELK	0.859458897	2	2.4842
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**2.003773832**	**0.31381**	**3**
Q62425	FYSVNVDYSK	1.009433768	2	2.84338
Q62425	KNNPEPWNK	0.509842603	2	2.54775
Q62425	LGPNEQYK	0.80304154	1	2.02545
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**2.277516142**	**0.85647**	**2**
Q62446	GWDEALLTMSK	1.289243876	2	2.47995
Q62446	SEETLDEGPPK	1.184437876	2	3.0409
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.618310859**	**9.9E-20**	**4**
Q62452	AMEIAEALGR	0.686913356	2	4.1044
Q62452	GAGVTLNVLEMTADDLENALK	0.853070699	2	5.39017
Q62452	WLPQNDLLGHPK	0.934496824	2	3.29481
Q62452	YTGTRPSNLAK	0.395560471	2	2.72087
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**2.043618348**	**0.99214**	**8**
Q62465	ACGLNFADLMGR	0.920633349	2	2.90657
Q62465	CLVLTGFGGYDK	1.701237443	2	2.92495
Q62465	ENGVTHPIDYHTTDYVDEIKK	1.069851635	3	3.54473
Q62465	GVDIVMDPLGGSDTAK	0.831837145	2	4.37029

Q62465	IDSVWPFEK	0.927178431	2	2.77437
Q62465	TVENVTVFGTASASK	0.893757118	2	3.5227
Q62465	VLLVPGPEKET	0.880512176	2	2.79258
Q62465	VVTYGMANLLTGPK	1.406950433	2	3.48565
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.884467831**	**0.959**	**4**
Q62636	INVNEIFYDLVR	1.407036673	2	4.0262
Q62636	LVVLGSGGVGK	1.071696406	2	2.63694
Q62636	QWSNCAFLESSAK	0.922398781	2	2.54085
Q62636	VKDTDDVPMILVGNK	0.912307854	2	2.78135
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**1.875447284**	**0.94349**	**4**
Q62651	HVLHVQLNRPEK	0.849116844	2	3.79476
Q62651	MMADEALDSGLVSR	0.96396126	2	4.37672
Q62651	RIPEEVSDHNYESIQVTSAQK	0.710687731	3	5.60781
Q62651	SLVNELTFTAR	0.912675943	2	3.1926
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**3.067693589**	**0.00637**	**7**
Q62730	AVLVTGADSGFGHALAK	1.592851381	2	4.34994
Q62730	DIQHAICAK	1.630642422	2	2.39238
Q62730	EIQENYGQEYVHTQK	1.505317743	2	4.50491
Q62730	EMSNPDITPVLR	1.929520449	2	2.66544
Q62730	LSVLQMDVTKPEQIK	2.662815572	2	3.69452
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.848299619	3	4.60785
Q62730	VVTIHPGGFQTNIVGSQDSWDK	2.253530397	2	5.81526
Q62736	**CALD1 Non_muscle caldesmon**	**1.880482459**	**0.99965**	**14**
Q62736	ASGDKEAEGAPQVEAGK	1.005235329	2	4.85141
Q62736	ASGDKEAEGAPQVEAGKR	1.039834176	3	3.97246
Q62736	EEIERR	1.12384808	1	1.90469
Q62736	EFDPTITDGSLSVPSR	0.947294736	2	3.67397
Q62736	GGNLGENQIKDEK	0.985113947	2	3.47579
Q62736	GSVFSSPSASGTPNK	0.910587355	2	2.30513
Q62736	KVLEEEEQR	0.802032132	2	2.74377
Q62736	LEQYTNAIEGTK	1.08254647	2	3.37348
Q62736	MQNNSAENETAEGEEK	0.86798966	2	4.88519
Q62736	MQNNSAENETAEGEEKGESR	0.698046522	3	4.62822
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0	0.744400284		
Q62736	RGETESEEFEK	1.067033558	2	3.31606
Q62736	RRGETESEEFEK	1.173274678	2	2.89916
Q62736	VLEEEEQR	0.97808711	2	2.59837
Q62745	**CD81 CD81 antigen**	**2.960115346**	**0.99307**	**2**
Q62745	NSLCPSSSNSFTQLLK	2.265794189	2	3.17297
Q62745	QFYDQALQQAVMDDDANNAK	1.515208665	2	5.03561
Q62769	**UN13B Protein unc_13 homolog B**	**1.913563885**	**0.6304**	**3**
Q62769	DHMVREETRNLTPK	0.967827203	2	2.58778
Q62769	ILSQRSNDEVAR	2.435358166	2	2.35181
Q62769	SNDEVAREFVK	0.737589231	1	1.93655
Q62770	**UN13C Protein unc_13 homolog C**	**2.19002236**	**0.85094**	**2**
Q62770	ENFPASNSERLQDLK	1.038416748	2	2.37452
Q62770	NLSMDETGLTILR	5.255989308	2	2.3763
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**2.577452436**	**0.8698**	**6**
Q62785	ANEEDEQEEGGDGASGDPK	1.622738806	2	5.57385
Q62785	ANEEDEQEEGGDGASGDPKK	0.873612046	3	3.51232
Q62785	GVEGLIDIENPNR	1.378886574	2	2.92045
Q62785	QKANEEDEQEEGGDGASGDPK	0.770050332	3	4.35504
Q62785	QKANEEDEQEEGGDGASGDPKK	0.736490674	3	3.43019
Q62785	YMKMHLAGKTEQAK	0.761325233	2	2.30757
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**2.16565629**	**0.9976**	**2**

Q62789	IILDELVQR	1.276729119	2	3.54343
Q62789	WIPQNDLLGHPK	0.934496824	2	3.29481
Q62812	**MYH9 Myosin_9**	**1.994873711**	**1**	**68**
Q62812	ALEEAMEQK	0.989193116	2	3.29544
Q62812	ALELDSNLYR	0.988002441	2	3.28462
Q62812	ALEQQVEEMK	1.282773762	2	3.3023
Q62812	ALEQQVEEMKTQLEELEDELQATEDAK	0.912483908	3	3.39235
Q62812	ANLQIDQINTDLNLER	2.8392583	2	5.43453
Q62812	ASIAALEAK	0.947596252	2	2.68672
Q62812	ASREEILAQAK	1.581475288	2	2.98513
Q62812	CQYLQAEK	0.807723957	1	2.33016
Q62812	DFSALESQLQDTQELLQEENR	5.731819498	3	6.72677
Q62812	DLEAHIDTANK	0.827314007	2	3.46763
Q62812	DLGEELEALKTELEDTLDSTAAQQELR	0.762772587	3	4.49373
Q62812	DLQGRDEQSEEK	0.77269226	2	2.92571
Q62812	EEILAQAK	0.913502321	1	2.37493
Q62812	EEILAQAKENEK	0.985113947	2	2.34371
Q62812	ELEDATETADAMNR	0.85183878	2	4.42332
Q62812	ELETQISELQEDLESER	1.199786267	2	4.86494
Q62812	EMEAELEDERK	0.743144998	2	3.32527
Q62812	HEAMITDLEER	0.770227912	2	3.27159
Q62812	HEDELLAK	0.96739347	2	3.04689
Q62812	HSQAVEELAEQLEQTK	0.917868263	2	5.02092
Q62812	HSQAVEELAEQLEQTKR	1.191979704	3	5.65885
Q62812	IIGLDQVAGMSETALPGAFK	1.754958971	2	5.39499
Q62812	IMGIPEDEQMGLLR	1.085134879	2	2.61722
Q62812	IRELETQISELQEDLESER	1.221215265	2	5.4351
Q62812	KEEELQAALAR	1.020120829	3	3.3629
Q62812	KKVEAQLQELQVK	0.773909096	2	4.62047
Q62812	KLEEDQIIMEDQNCK	1.059497971	2	6.00955
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.078900272	2	5.57834
Q62812	KQELEEICHDLEAR	0.981950249	2	4.73266
Q62812	KVEAQLQELQVK	1.099964693	2	4.55015
Q62812	LDPHLVLDQLR	1.126280217	3	3.42147
Q62812	LEEDQIIMEDQNCK	0.968003321	2	4.99045
Q62812	LEGDSTDLSDQIAELQAQIAELK	1.139521233	3	5.22578
Q62812	LEVNLQAMK	0.887340554	2	2.63661
Q62812	LQEMESAVK	1.021655137	2	2.75338
Q62812	LQQELDDLLVDLDHQR	0.989984035	2	4.81848
Q62812	LQVELDSVTGLLNQSDSK	1.190839539	2	5.48712
Q62812	LTEMETMQSQLMAEK	1.267088577	2	4.97254
Q62812	MEDGVGCLETAEEAK	0.993915268	2	4.37249
Q62812	MQQNIQELEEQLEEEESAR	1.061920743	2	6.32211
Q62812	NAEQFKDQADK	1.050127876	2	3.45815
Q62812	NKHEAMITDLEER	1.034741567	3	4.10279
Q62812	NLPIYSEEIVDMYK	1.231791091	2	3.79672
Q62812	NMDPLNDNIATLLHQSSDK	1.330181768	2	4.94688
Q62812	NTDQASMPDNTAAQK	4.566497037	2	5.31293
Q62812	NTDQASMPDNTAAQK+Oxidation(6	1.238752571		
Q62812	QAQQERDELADEIANSSGK	0.977738302	3	4.19502
Q62812	QIATLHAQVTDMK	0.587916358	2	2.38453
Q62812	QLEEAEEEAQR	1.000527556	2	3.8772
Q62812	QSVSNLEK	0.924305753	2	2.47082
Q62812	QTLENERGELANEVK	0.977381671	2	3.38568
Q62812	RGDMPFVVTR	0.964542803	2	2.96735
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.0110923	3	5.75843
Q62812	RQLEEAEEEAQR	0.811600234	2	4.60045

Q62812	SMEAEMIQLQEELAAAER	1.060594444	3	4.33539
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1	1.461435341		
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)Oxidation(5	1.087249242		
Q62812	TDLLLEPYNK	1.175258398	2	3.41927
Q62812	TELEDTLDSTAAQQELR	1.007197758	2	5.33869
Q62812	TEMEDLMSSK	1.187421297	2	2.58969
Q62812	THEAQIQEMR	0.985723044	3	3.43686
Q62812	TQLEELEDELQATEDAK	1.068359843	2	6.59084
Q62812	VAEFTTDLMEEEEK	1.182722775	2	4.48055
Q62812	VEAQLQELQVK	0.910721456	2	3.48367
Q62812	VEDMAELTCLNEASVLHNLK	1.183293416	2	4.49972
Q62812	VISGVLQLGNIVFK	1.414078416	2	3.75795
Q62812	VSHLLGINVTDFTR	1.521942866	2	3.8123
Q62812	YEILTPNSIPK	0.873363609	2	3.13421
Q62824	**EXOC4 Exocyst complex component 4**	**1.764829338**	**0.44752**	**2**
Q62824	EDLDCDPEENSTLFMGILIQGLAR	1.257125426	2	2.31916
Q62824	SQTGVGDQTTQNTR	0.773059286	2	3.11758
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**2.088616119**	**0.11595**	**7**
Q62826	ADILEDKDGK	1.09752484	2	2.79058
Q62826	AFITNIPFDVK	1.245961453	2	3.24089
Q62826	GIGMGNLGPAGMGMEGIGFGINK	1.95892273	2	3.91876
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.120550374	2	5.02905
Q62826	INEILSNALK	1.412722369	2	2.61269
Q62826	MGPAMGPALGAGIER	1.009852263	2	2.75543
Q62826	MGPVMDRMATGLER+Oxidation(0)Oxidation(4)Oxidation(7	1.648351881		
Q62868	**ROCK2 Rho_associated protein kinase 2**	**1.912592905**	**0.60287**	**2**
Q62868	DEEISAAAIK	2.561736724	1	1.90037
Q62868	QENNHLMEMKMNLEK+Oxidation(6	0.896899839		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**2.160540222**	**0.48642**	**2**
Q62871	ADAEEEAATR	1.404627666	2	3.17089
Q62871	SVSTPSEAGSQDSGDGAVGSR	0.671966099	2	5.21896
Q62902	**LMAN1 Protein ERGIC_53**	**2.153325302**	**1**	**7**
Q62902	GAGTPGQPGQVSQQELDTVVR	0.977337285	2	4.15028
Q62902	GHPDLQGQPADDIFESIGDR	1.121558726	2	5.01564
Q62902	LVSGVQHPGSAGVYETTQHFMDIK	1.119285221	3	3.42386
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.677012865	3	6.36976
Q62902	RGAGTPGQPGQVSQQELDTVVR	0.951364962	3	4.45438
Q62902	YQEEFEHFQQELDK	1.102088763	2	5.31401
Q62902	YVSSLTEEISR	1.037189593	2	3.04648
Q62904	**DHB7 3_keto_steroid reductase**	**2.053374634**	**0.9843**	**3**
Q62904	MDVDEDTAEK	1.935753572	2	2.38957
Q62904	YATDLLNVALNR	0.983949831	2	2.57317
Q62904	YLSGTTGLGTNYVK	1.012864262	2	2.98828
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**1.867929935**	**0.59295**	**2**
Q62967	GLQVAPVLLSDELK	0.94135554	2	3.74149
Q62967	VYGVEGDLSEVAR	0.694944735	2	3.42081
Q62991	**SCFD1 Sec1 family domain_containing protein 1**	**2.76044977**	**0.09945**	**3**
Q62991	ALTDAGCNLSPLQYIK	2.568882017	2	2.90419
Q62991	FGQDIISPLLSVK	1.4816759	2	2.36116
Q62991	SLLDVISDPDAGTPEDK	1.378847654	2	2.86206
Q63041	**A1M Alpha_1_macroglobulin**	**2.40015939**	**0.99964**	**12**
Q63041	AEDITHNGIVYTPK	0.979912588	2	3.66851
Q63041	AEQGAYLGPLPYK	0.834197494	2	3.23818
Q63041	AESPVFVQTDKPIYKPGQTVK	0.929469767	3	4.01247

Q63041	DTVVKPVIVEPEGIEK	1.005208923	2	3.75448
Q63041	GSIFNSGSHVLPLEQGK	0.894015108	2	4.07549
Q63041	KLQDQSNIQR	0.911716734	2	2.57123
Q63041	LIVYTILPNEELIADVQK	1.298831988	2	2.99863
Q63041	LQDQSNIQR	0.883704273	2	2.9837
Q63041	QDLNDNDAYSVFQSIGLK	1.479655311	2	2.6273
Q63041	VNTLPLNFDK	0.923838994	2	2.74901
Q63041	YNILPEAEGEAPFTLK	1.125733537	2	4.90899
Q63041	YVVLVPSELYAGVPEK	1.156371963	2	3.00918
Q63060	**GLPK Glycerol kinase**	**2.857250147**	**3.7E-08**	**12**
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.547635139	3	4.5678
Q63060	AVLGPLVGAVDQGTSSTR	1.516277974	2	5.19401
Q63060	CVFSEHGLLTTVAYK	1.010448524	2	4.28195
Q63060	DCGIPLSHLQVDGGMTSNK	1.214675689	2	4.43673
Q63060	EILQSVYECIEK	1.094233711	2	3.41925
Q63060	FEPQINAEESEIR	1.213658527	2	3.64244
Q63060	KVQEAVEENR	1.001745986	2	3.35223
Q63060	LGQLNIDISNIK	1.923197141	2	3.23066
Q63060	NTYGTGCFLLCNTGHK	0.9631205	2	3.81262
Q63060	SSSEIYGLMK	1.381369423	2	2.51534
Q63060	TAELLSHHQVEIK	1.468547941	2	3.45738
Q63060	VQEAVEENR	1.687592409	2	3.24487
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**2.268764598**	**1**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.113831323	3	5.12988
Q63081	GESPVDYDGGR	2.169532188	2	2.85702
Q63081	GSFSEQGINEFLR	0.916245659	2	4.19658
Q63081	GSTAPVGGGSFPNITPR	0.979659608	2	4.87822
Q63081	HQSLGGQYGVQGFPTIK	1.291268352	2	5.07805
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.992541569	3	5.23477
Q63081	NLEPEWAAAATEVK	1.076174544	2	4.02494
Q63081	NSYLEVLLK	1.233320588	2	2.97378
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.006889871	3	5.02229
Q63081	TGEAIVDAALSALR	1.08656067	3	4.87508
Q63081	VGAVNADKHQSLGGQYGVQGFPTIK	0.762758045	3	4.60694
Q63083	**NUCB1 Nucleobindin_1**	**2.023387524**	**0.82712**	**3**
Q63083	LSQETEALGR	1.082452234	2	2.81855
Q63083	VNVPGSQAQLK	0.920734748	2	2.44025
Q63083	YLQEVINVLETDGHFR	1.109248858	3	4.11414
Q63108	**EST3 Liver carboxylesterase 3**	**1.985654492**	**0.77409**	**4**
Q63108	GGTSKEEINLSK	0.65335184	2	3.42736
Q63108	LDPMTATSLLK	1.099866339	2	2.50753
Q63108	QKTEEELLETTLK	0.959231264	2	3.50025
Q63108	SSFLLNLPEEAIPVAVEK	1.236193253	2	4.83555
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**2.142372553**	**0.3711**	**7**
Q63120	ACALLPDLEILPGGDMAEIGEK	1.67805807	2	4.82756
Q63120	HGEIQFNNYQVR	1.407499725	2	2.72902
Q63120	IVEYGSPEELLSNR	1.541317943	2	3.31796
Q63120	QSQSQDVLVLEEAK	1.276114324	2	2.56377
Q63120	YFAWEPSFQEQVQGIR	1.412294536	2	3.93459
Q63120	YLGGDDLDTSAIR	0.333032868	2	2.36148
Q63120	YRPELDLVLK	1.248383069	3	3.66308
Q63150	**DPYS Dihydropyrimidinase**	**2.067841988**	**0.9835**	**10**
Q63150	ALGKDDFTK	0.972508326	2	2.55283
Q63150	DQTCTPIPVKR	1.545377451	2	2.49283
Q63150	EIGAIAQVHAENGDLIAEGAK	1.357285824	2	4.999
Q63150	FVAVTSTNAAK	1.0205137	2	3.17668

Q63150	GSSLIEAFETWR	1.143238801	2	3.5411
Q63150	IAVGSDADIVIWDPEATR	1.684892336	2	3.26214
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	1.164430759	3	3.74974
Q63150	VVNDDFSQVADVLVEDGVVR	1.049433896	2	5.95564
Q63150	VVYEAGVFDVTAGHGK	1.192754549	2	4.20199
Q63150	VVYGEPIAAGLGTDGTQYWNK	1.042261866	2	5.8231
Q63228	**GMFB Glia maturation factor beta**	**3.134895284**	**0.37209**	**2**
Q63228	LVVLDEELEGVSPDELKDELPER	1.649165044	3	3.70804
Q63228	NTEDLTEEWLR	1.588419151	2	2.59946
Q63269	**ITPR3 Inositol 1_4_5_trisphosphate receptor type 3**	**1.727629457**	**5.5E-05**	**2**
Q63269	LLDGGNTEIQK	0.766404498	1	2.45957
Q63269	QKLMRDENILK+Oxidation(3	1.09185945		
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**2.184991269**	**0.79162**	**19**
Q63270	AVEAGLNVKPYVK	1.044087098	2	2.96859
Q63270	AVLAESYER	0.894544737	2	2.6416
Q63270	DFSDSSQDPDFTQVVELDLK	1.596364282	2	3.66532
Q63270	FVEFFGPGVAQLSIADR	1.442125438	2	5.29679
Q63270	GFQVAPDHHNDHK	0.721915343	2	3.41537
Q63270	IDFEKEPLGVNAQGQQVFLK	1.122178626	3	6.12805
Q63270	IIPPGSGIIHQVNLEYLAR	1.221034535	2	2.52067
Q63270	KNDIENILNWSIMQHK	1.149186879	3	4.5379
Q63270	NCDEFLVK	1.033148118	2	2.32397
Q63270	NDIENILNWSIMQHK	1.169607598	2	2.51395
Q63270	NQDLEFER	0.885481301	1	2.69866
Q63270	QAPQTVHLPSGETLDVFDAAER	0.985761118	3	3.62427
Q63270	SIEVPFKPAR	1.032470637	2	2.54092
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.431711792	3	4.67185
Q63270	SPPFFESLTLDLQPPK	1.181863882	3	4.47541
Q63270	SWNALAAPSEK	0.990276178	2	2.60667
Q63270	TSLSPGSGVVTYYLR	1.478823756	2	3.54827
Q63270	VILQDFTGVPAVVDFAAMR	0.935414851	2	4.77858
Q63270	YQQAGLPLIVLAGK	1.099290303	2	3.55306
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.888916281**	**0.06159**	**18**
Q63276	AHGHFLFVVGEDDKNLNSK	1.287830918	2	6.07864
Q63276	ASEVGEVDLER	0.993709788	2	4.03287
Q63276	DDKGNLFNSQAFYR	0.905164232	2	3.3099
Q63276	GNLFNSQAFYR	0.889119072	2	2.67858
Q63276	LCHPYFPVEGK	1.176082798	3	3.5189
Q63276	LTAVPLSALVDEPVHIR	1.064203352	2	3.94814
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	1.150839416	4	4.63693
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.35538607	3	4.23705
Q63276	QHLNPGFNSQL	0.968958416	2	3.50833
Q63276	QITATVLINGPNFVSSNPHVYR	1.342583944	3	4.77909
Q63276	TFEETADK	1.380879552	1	1.92101
Q63276	TFEETADKDSK	0.832712347	2	3.79436
Q63276	VDLEYFEEGVEFLLR	0.866373668	2	4.3345
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.212840947	3	5.15794
Q63276	VISSSLDSLILER	0.638362309	2	4.49398
Q63276	VTGLTPFQVVCLQASLK	1.113791869	3	5.2183
Q63276	WYVAPGVTR	0.953921223	1	2.12347
Q63276	YCFPIEK	1.034139153	2	2.57902
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**2.294041079**	**9.9E-20**	**26**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.264348375	3	6.02255
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.176767435	2	4.73007
Q63342	DGLLFGPYESQEK	1.169244636	2	2.71546

Q63342	EGQESPPSPPEWK	1.457708629	2	2.68183
Q63342	GGYDVEIR	1.13834398	2	2.63564
Q63342	GQDSTQLLDHLCANVIPK	1.269877768	2	4.10056
Q63342	IHELFPLLNMDK	1.316473875	2	2.75267
Q63342	IHYDSIK	1.058375529	1	2.36116
Q63342	IMNAGQEEGIDNFGTYALNALR	0.682561131	2	4.48295
Q63342	ISDIPVTAIR	1.148630268	2	3.336
Q63342	ITEHVEAAMEMVPVLK	1.382941657	2	4.64274
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.314796469	3	5.93332
Q63342	LEEETGQVVGFHQPGSIR	1.087183623	2	4.83796
Q63342	LNKPADFTGK	1.382520307	2	3.01995
Q63342	LTSEDLSDDVFK	1.321848851	2	4.03729
Q63342	NITDELGVLGVAGPYAR	1.402620492	2	4.77046
Q63342	NYPATIIQEPLVLTEPTR	1.378842974	2	4.47272
Q63342	REDSAALYER	0.170099614	2	2.65566
Q63342	TNWHATEQYIIEPEK	0.98007806	2	3.71256
Q63342	VGFTNISHMLTPR	1.066938636	2	3.11369
Q63342	VGVIDLSPFGK	1.182603622	2	3.52946
Q63342	VIGNTTSGSYSYSIQK	1.197946515	2	4.33565
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.72406648	3	4.30877
Q63342	WIEEAAVR	1.46642413	2	2.8172
Q63342	WTTTQYTEAK	1.097134636	2	2.72726
Q63342	YLSDWILHGEPPFDLIELDPNR	1.10599143	2	4.49836
Q63347	**PRS7 26S protease regulatory subunit 7**	**2.424593116**	**0.37966**	**7**
Q63347	ALDEGDIALLK	1.358652689	2	2.819
Q63347	FDDGAGGDNEVQR	1.102579304	2	4.28376
Q63347	FVVDLSDQVAPTDIEEGMR	1.099272255	2	3.72301
Q63347	IINADSEDPK	0.885593354	2	3.20563
Q63347	QTLQSEQPLQVAR	1.314560965	2	3.67158
Q63347	QVEDDIQQLLK	1.317008673	2	2.98864
Q63347	TMLELINQLDGFDPR	1.123029671	2	3.01654
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**2.000948407**	**0.99964**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.121007499	2	5.70241
Q63362	KYTEQITSEK	0.94686162	2	2.72064
Q63362	TTGLVGLAVCDTPHER	1.005228036	2	4.25738
Q63362	YTEQITSEK	0.830475674	1	2.32351
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**2.437055129**	**0.54636**	**2**
Q63413	CIALAQLLVEQNFPAIAIHR	1.426728723	3	3.39219
Q63413	NCPHIVVGTPGR	1.206066885	2	2.98147
Q63429	**UBC Polyubiquitin_C**	**2.053307173**	**0.99646**	**3**
Q63429	ESTLHLVLR	0.919688195	2	2.50406
Q63429	TITLEVEPSDTIENVK	1.039521865	2	4.85392
Q63429	TLSDYNIQK	0.904528467	2	2.68568
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**2.178977941**	**0.36583**	**10**
Q63448	ADWLDSEAPLAAYR	1.625841358	2	4.32425
Q63448	EIHALASAGKPLASWTAQR	0.990243869	2	4.57415
Q63448	GGYISGEQTGK	0.837845291	2	3.01199
Q63448	LGASLGSLSSGR	1.014798029	2	2.7108
Q63448	NLWAAVLQQSGVLER	1.08151395	2	4.51784
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.975103342	3	4.51586
Q63448	TIFLDLIELQR	1.165922303	2	2.51954
Q63448	TIFSTLENDPLFARPFGADLPLEK	0.927124164	3	4.50697
Q63448	TTAHYDPATQEFILHSPDFEAAK	0.840228188	3	4.46822
Q63448	TVNFLEAYPGILGQK	1.164498541	2	5.11667
Q63507	**RL14 60S ribosomal protein L14**	**2.129411753**	**0.00094**	**3**
Q63507	CMQLTDFILK	0.800727679	2	2.75616

Q63507	LVAIVDVIDQNR	1.533289871	2	4.12323
Q63507	RFVEVGR	0.965553681	2	2.35885
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.941178988**	**0.99735**	**4**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	0.912441204	3	4.56427
Q63524	HEQEYMEVR	1.23432433	2	3.43714
Q63524	HEQEYMEVR+Oxidation(5	1.043695214		
Q63524	LEEMINELAVAMTAVK	0.942743418	2	3.54257
Q63525	**NUDC Nuclear migration protein nudC**	**2.087871966**	**0.61046**	**4**
Q63525	GQAPVIDGELYNEVK	0.958191918	2	3.61122
Q63525	LVTSDPEINTK	1.066501884	2	2.43712
Q63525	VEESSWLIEDGK	1.282107543	2	2.41713
Q63525	WTQTLSELDLAVPFR	1.296684256	2	2.8311
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**2.015476502**	**0.98018**	**6**
Q63569	AMEVDERPTEQYSDIGGLDK	1.045921641	3	5.32753
Q63569	CTDDFNGAQCK	1.189765396	2	3.26109
Q63569	MNVSPDVNYEELAR	1.046377863	2	3.57539
Q63569	QTYFLPVIGLVDAEK	1.13263591	2	2.46088
Q63569	TMLELLNQLDGFQPNTQVK	0.844463591	2	3.92939
Q63569	VDILDPALLR	1.19959476	2	2.91082
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.80379254**	**0.81521**	**4**
Q63570	FDAQTGADR	0.929926406	2	2.73814
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	0.965465237	3	5.80839
Q63570	KDEQEHEFYK	1.179455149	2	3.42068
Q63570	RFDAQTGADR	0.783923056	2	3.01869
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.964659799**	**0.89222**	**4**
Q63584	ITDSAGHILYAK	1.250637533	2	3.73348
Q63584	LEDLSESIVNDFAYMK	1.225859345	2	3.58185
Q63584	NYEEIAK	0.971646157	1	2.40973
Q63584	RLEDLSESIVNDFAYMK	1.065733433	2	3.66917
Q63598	**PLST Plastin_3**	**1.890785655**	**0.9905**	**13**
Q63598	AESMLQQADK	1.053961484	2	3.42438
Q63598	ATDDIIVNWVNGTLSEAGK	0.973709932	2	5.11268
Q63598	AVGDGIVLCK	1.550252208	2	2.44519
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	0.930456723	3	3.47384
Q63598	HVIPMNPNTDDLFK	0.911445702	2	3.03868
Q63598	IDINMSGFNETDDLKR	0.838104395	2	4.46001
Q63598	INNFSADIK	1.196481324	2	2.39374
Q63598	KLENCNYAVELGK	0.797978314	2	3.73083
Q63598	NEALAALLR	1.271829875	2	2.61155
Q63598	TISSSLAVVDLIDAIQPGCINYDLVK	0.854465786	3	3.56522
Q63598	VYALPEDLVEVKPK	1.060417719	2	3.09043
Q63598	YPALTKPENQDIDWTLLEGETR	1.083956644	3	5.3709
Q63598	YTLNVMEDLGEGQK	1.055751791	2	3.6831
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.924973522**	**1**	**8**
Q63610	IQVLQQQADDAEER	0.976962227	2	5.12508
Q63610	KIQVLQQQADDAEER	0.944833203	2	5.43538
Q63610	KLVIIEGDLER	1.010294163	2	3.22849
Q63610	LEKTIDDLEDKLK	2.700794785	2	2.71825
Q63610	LVIIEGDLER	1.128821291	2	2.94764
Q63610	MELQEIQLK	1.016179377	2	3.1234
Q63610	TIDDLEDKLK	0.944939887	2	2.6964
Q63610	YSQKEDKYEEEIK	0.928405693	2	4.94989
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**2.130744038**	**0.99949**	**15**
Q63617	AANSLEAFIFETQDK	1.454181154	2	2.56057
Q63617	DAVITVPAFFNQAER	0.8734798	2	2.80569

Q63617	EGETPDEKESGDKSEAQKPNEK	0.826976703	3	3.99105
Q63617	FLGDSAAGMAIK	1.135098069	2	2.52277
Q63617	GQAGPEGVPPAPEEEKK	1.014176592	2	3.41887
Q63617	LIPEMDQIFTDVEMTTLEK	0.954895951	2	3.35289
Q63617	LYQPEYQEVSTEEQR	1.034320786	2	5.26585
Q63617	NINADEAAAMGAVYQAAALSK	1.199334871	2	5.32702
Q63617	SLAEDFAEQPIK	0.859807065	2	2.98217
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.454889147	3	3.43942
Q63617	TLGGLEMELR	1.201491571	2	2.9743
Q63617	TVLSANADHMAQIEGLMDDVDFK	1.249519767	3	3.88961
Q63617	VEFEELCADLFDR	1.324829248	2	3.42113
Q63617	VESVFETLVEDSPEEESTLTK	0.98815533	2	4.01553
Q63617	VLQLINDNTATALSYGVFR	1.187075904	2	4.68982
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**2.28795011**	**0.33288**	**2**
Q63692	EGEEAGPGDPLLEAVPK	1.187057452	2	3.32555
Q63692	LGPGGLDPVEVYESLPEELQK	1.388680275	2	3.00766
Q63716	**PRDX1 Peroxiredoxin_1**	**2.094391253**	**0.2725**	**15**
Q63716	ADEGISFR	0.910491813	2	3.07918
Q63716	ATAVMPDGQFK	1.055812041	2	2.87378
Q63716	GLFIIDDKGILR	1.164359011	2	2.86201
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.004990345	4	5.82243
Q63716	IGHPAPSFK	1.495097415	1	1.91633
Q63716	KQGGLGPMNIPLVSDPK	0.850493571	2	4.07012
Q63716	KQGGLGPMNIPLVSDPKR	0.689716469	3	3.81001
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.528350737	3	3.39142
Q63716	LVQAFQFTDK	1.653346563	2	3.29712
Q63716	QGGLGPMNIPLVSDPK	1.067482379	2	3.13924
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6	1.232833897		
Q63716	QITINDLPVGR	1.053916138	2	3.15417
Q63716	RTIAQDYGVLK	1.21796732	2	2.48117
Q63716	SVDEILR	1.087291403	2	2.48281
Q63716	TIAQDYGVLK	1.088015803	2	3.21053
Q63797	**PSME1 Proteasome activator complex subunit 1**	**2.020807103**	**0.99715**	**10**
Q63797	ISELDAFLK	1.225618582	2	2.36917
Q63797	ISELDAFLKEPALNEANLSNLK	1.167386309	2	5.35168
Q63797	KGDEDDKGPPCGPVNCNEK	1.200223418	3	4.81628
Q63797	KISELDAFLKEPALNEANLSNLK	1.090354631	3	5.88134
Q63797	LEGFQTQISK	1.004137915	2	2.71279
Q63797	NAYAVLYDIILK	1.247324741	2	3.55742
Q63797	QLVHELDEAEYQEIR	0.994569574	2	4.18508
Q63797	TENLLGSYFPK	1.014847975	2	3.49483
Q63797	VDVFREDLCSK	0.879562093	2	2.5216
Q63797	VFELMTSLHTK	1.009969438	2	3.04794
Q63798	**PSME2 Proteasome activator complex subunit 2**	**2.078279975**	**0.97678**	**4**
Q63798	AFYAELHHIISSNLEK	1.028314737	2	3.91519
Q63798	IEDGNDFGVAIQEK	1.24250109	2	4.04959
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.121911891	3	3.63328
Q63798	TKVEAFQTAISK	0.797483267	2	3.56125
Q63836	**SBP2 Selenium_binding protein 2**	**2.200436601**	**0.38163**	**3**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.420041653	2	5.34098
Q63836	IYVVDVGSEPR	0.968391886	2	3.82812
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.202952804	3	3.84383
Q63945	**SET Protein SET**	**1.882409601**	**0.9886**	**2**
Q63945	IDFYFDENPYFENK	1.286883282	2	4.27991
Q63945	LNEQASEEILK	0.91256039	2	3.16709
Q63965	**SFXN1 Sideroflexin_1**	**2.295010924**	**0.71789**	**5**
Q63965	NILLTNEQLENAR	1.099922801	2	4.38984

Q63965	QAITQVVISR	1.327214964	2	2.33622
Q63965	QGIVPAGLTENELWR	1.283377964	2	3.17632
Q63965	WDQSTFIGR	0.993769508	2	2.79195
Q63965	YAYDSAFHPDTGEK	6.171564952	2	4.28447
Q64012	**RALY RNA_binding protein Raly**	**2.212377372**	**0.89747**	**2**
Q64012	LEQIAEEQK	1.115806259	2	2.5215
Q64012	SNIDALLGR	1.151472037	2	2.35616
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**2.429487815**	**0.01481**	**19**
Q64057	AWNIWADIPAPK	1.379570004	2	3.80585
Q64057	DYEETIGK	1.881365666	1	1.92867
Q64057	EDNEGVFNGSWGGR	1.292892128	2	3.68846
Q64057	FKNEEEVFEWNNEVK	0.958510603	2	5.75616
Q64057	GAPTTSLVSIAVTK	0.912213552	2	5.00509
Q64057	GEVITTYCPANNEPIAR	1.017753276	2	5.00784
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	4.06248898	2	5.6004
Q64057	LFLHESIHDEVVDR	1.274770957	2	4.37684
Q64057	LVSLEMGK	1.270263529	2	2.44717
Q64057	NEEEVFEWNNEVK	1.042078278	2	4.5694
Q64057	QAVSMFVQAVEEAK	1.523044846	2	3.39187
Q64057	QAVSMFVQAVEEAKK	1.123692852	2	2.83807
Q64057	QGLSSSIFTK	1.357153713	2	2.75333
Q64057	QVALMVQER	0.985519527	2	2.51664
Q64057	STCTINYSTALPLAQGIK	1.010793528	2	4.87192
Q64057	VGNPWDPNILYGPLHTK	1.503054636	3	4.39954
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.304011413	3	6.07284
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1	1.391085726		
Q64057	VNLLSFTGSTQVGK	1.516742974	2	4.68843
Q64112	**IFIT2 Interferon_induced protein with tetratricopeptide repeats 2**	**2.14316152**	**0.9614**	**2**
Q64112	DPSAIDTLLR	1.098514128	2	2.55843
Q64112	NQAMALVEEALK	1.311988272	2	2.31053
Q64119	**MYL6 Myosin light polypeptide 6**	**1.973917793**	**1**	**7**
Q64119	DQGTYEDYVEGLR	0.81935114	2	3.3784
Q64119	EGNGTVMGAEIR	1.221218621	2	2.73079
Q64119	HVLVTLGEK	0.948543329	2	2.57018
Q64119	ILYSQCGDVMR	1.120090606	2	2.91864
Q64119	NKDQGTYEDYVEGLR	0.994340908	2	4.14723
Q64119	VFDKEGNGTVMGAEIR	1.009596676	2	4.11548
Q64119	VLDFEHFLPMLQTVAK	1.014987111	2	4.78163
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**2.295702543**	**0.93984**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.281346673	2	5.23074
Q64122	LNGTDPEDVIR	1.032724229	2	2.60885
Q64176	**EST22 Liver carboxylesterase 22**	**1.942925423**	**0.0015**	**3**
Q64176	AISESGVALTAGLVK	0.982371146	2	4.58866
Q64176	EGYLQIGATTQQAQK	0.761325233	2	4.66931
Q64176	NFNTVPYIVGINK	0.627637076	2	3.46973
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**2.278651339**	**0.07069**	**7**
Q641Y0	ELGSECGIEFDEEK	1.131851027	2	4.04094
Q641Y0	NTLLIAGLQAR	1.598610638	2	3.42616
Q641Y0	SSLNPILFR	2.256416174	2	2.46711
Q641Y0	TADDPSLSLIK	1.004472866	2	2.57711
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.3283922	3	6.69727
Q641Y0	TLVLLDNLNVR	1.241017218	2	4.12485
Q641Y0	WVPFDGDDIQLEFVR	1.230893601	2	3.07863

Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.924317806**	**0.89595**	**4**
Q641Y2	GSGIQWDLR	0.976519315	2	2.52462
Q641Y2	IDEVEEMLTNNR	0.88322446	2	3.86051
Q641Y2	IIEQCLNK	0.850866952	2	2.74819
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.35657405	2	4.36947
Q641Z6	**EHD1 EH domain_containing protein 1**	**2.352084665**	**0.78677**	**2**
Q641Z6	LLDTVDDMLANDIAR	1.231614104	2	3.93503
Q641Z6	MQELLQTQDFSK	1.365043492	2	2.6241
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.993617218**	**0.9885**	**3**
Q64232	HYEVEIR	0.808233169	2	2.49738
Q64232	LCFLDKVEPQATISEIK	1.102060684	2	3.60549
Q64232	SLKDEDVLQK	0.99067873	2	3.56263
Q64240	**AMBP Protein AMBP**	**1.751823916**	**3.5E-05**	**2**
Q64240	AVLPQENEGSGSEPLITGTLK	0.84326109	2	4.17435
Q64240	TIAACNLPIVQGPCR	0.683527529	2	3.83851
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**2.163639885**	**0.969**	**2**
Q642G4	GGDGQINEQVEK	1.124640387	2	2.88597
Q642G4	LLGPQEEGEGVVDVK	0.955697263	2	2.78095
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.877494457**	**0.99521**	**20**
Q64380	AIDSLSIEK	0.96129589	2	3.00798
Q64380	AYGIESHVLSPAETK	1.053496007	2	4.94827
Q64380	DGTMDPAGTCTTLTR	1.244058775	2	3.8829
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	1.258813959	3	5.3948
Q64380	DLYPLMNVDDLYGTLYVPR	0.827491609	2	3.87208
Q64380	FHHSLTDHPR	0.91623432	2	2.64953
Q64380	FYLLGADAR	1.003580731	2	2.64328
Q64380	GAQVIENCAVTGIR	1.04259961	2	3.78505
Q64380	HGLVNAGYR	0.657958	2	2.68138
Q64380	IEGIQNMPNVR	0.89318546	2	3.19354
Q64380	LGVGGVVLLER	1.763897126	2	3.27762
Q64380	LQGDALSVGGYEANPIFWDEVSDK	2.867139223	2	4.20257
Q64380	NGDYALER	0.932741527	2	2.43571
Q64380	NYSVVFPHDEPLAGR	0.831458533	2	4.20826
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	1.257878103	3	4.07024
Q64380	RDPLHEELLGQGCVFQER	1.208209289	3	5.80591
Q64380	SDDSPLEAGLAFTCK	1.206794826	2	4.5192
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.914363713	3	4.86359
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16	1.028140053		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	1.039199944	3	5.76771
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**2.001207277**	**0.99597**	**29**
Q64428	ADMVIEAVFEDLAVK	0.786491614	3	4.11034
Q64428	ALMGLYNGQVLCK	1.209587442	2	3.45997
Q64428	CLAPMMSEVIR	1.838428161	2	2.49765
Q64428	DGPGFYTTR	2.321323384	2	2.31759
Q64428	DSIFSNLIGQLDYK	1.244500152	2	3.05077
Q64428	DTTASAVAVGLK	2.317230409	2	3.7994
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.811923698	3	6.31415
Q64428	EVQSEFVEVMNEIWANDQIR	0.851295647	3	4.20686
Q64428	FGELALTK	0.964143471	2	3.02917
Q64428	FGGGSVELLK	0.904131336	2	3.18877
Q64428	FVDLYGAQK	0.860270597	2	3.02356
Q64428	GFYIYQSGSK	0.83573576	2	3.05216
Q64428	ILQEGVDPK	1.165639017	2	3.18369
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	0.920270782	4	5.43653
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.052724413	3	4.15068

Q64428	KYESAYGTQFTPCQLLR	1.039333556	2	4.70469
Q64428	LPAKPEVSSDEDIQYR	1.287556118	3	4.46949
Q64428	MGLVDQLVDPLGPGIK	0.976545991	2	5.08455
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0	0.996701707		
Q64428	MQLLEIITTDK	1.013741243	2	3.82033
Q64428	MQLLEIITTDK+Oxidation(0	1.141554018		
Q64428	MVGVPAAFDMMLTGR	1.024112115	2	3.3376
Q64428	NLNSEIDNILVNLR	0.880468017	2	4.41511
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	1.169348662	3	3.88604
Q64428	TGLEQGNDAGYLAESEK	0.960431643	2	5.10275
Q64428	TIEYLEEVAVNFAK	1.03588912	2	3.80416
Q64428	TVLGVPEVLLGILPGAGGTQR	0.829477545	3	4.7512
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	1.003641035	3	6.03005
Q64428	YESAYGTQFTPCQLLR	1.201091767	2	4.00735
Q64458	**CP2CT Cytochrome P450 2C29**	**1.970350744**	**3.4E-05**	**6**
Q64458	EHKESLDVTNPR	0.73436731	2	3.40956
Q64458	IKEHKESLDVTNPR	0.822293186	3	5.20486
Q64458	LPPGPTPLPIIGNFLQIDVK	1.453168156	3	4.98668
Q64458	VQEEAQCLVEELR	2.137972853	2	4.2021
Q64458	VQEEAQCLVEELRK	1.420056325	2	3.80194
Q64458	VQEEIDR	1.020715092	2	2.53091
Q64464	**CP3AD Cytochrome P450 3A13**	**1.998388729**	**0.34345**	**2**
Q64464	ALLSPTFTSGR	1.003307558	2	2.89316
Q64464	LQDEIDAALPNK	0.644199391	2	2.41455
Q64481	**CP3AG Cytochrome P450 3A16**	**2.376182908**	**0.45954**	**3**
Q64481	EMFPVIEQYGDILVK	1.471280595	2	2.40379
Q64481	GSIDPYVYLPFGNGPR	0.996616905	2	4.04317
Q64481	VLQNFSFQPCK	1.39465618	2	2.78413
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.754553513**	**0.70655**	**4**
Q64550	GHEVVVIAPEASIHIK	0.614336307	2	4.61325
Q64550	NMIIALTENFLCR	0.749218554	2	4.50404
Q64550	SVFDQDPFLLR	1.04237333	2	3.46737
Q64550	VVYSPYGSLATEILQK	0.895185758	2	4.9668
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**1.947538247**	**0.9989**	**3**
Q64560	ACVDSNENGDLGK	0.850268368	2	3.48793
Q64560	GTLIEAFPVLGGK	0.903953243	2	3.17228
Q64560	HEQISDLDR	1.272115429	2	2.59638
Q64563	**ADH4 Alcohol dehydrogenase 4**	**2.291889728**	**0.99999**	**15**
Q64563	AAVDCTVVGWGSCTVVGAK	1.726144982	2	2.595
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.340615743	3	5.72197
Q64563	ALGATDCLNPR	1.770464701	2	3.23274
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	1.327222542	3	6.05482
Q64563	FDLDLLVTHALPFDK	1.118112411	3	4.3007
Q64563	IIAIDINSEKFPK	1.034809775	2	3.06966
Q64563	INDAIDLMNQGK	1.198445657	2	4.1661
Q64563	KFDLDLLVTHALPFDK	1.015330673	3	5.28022
Q64563	LCLSPLTNLCGK	1.091044402	2	2.46615
Q64563	SVDSVPNLVTDYK	1.151835509	2	3.49291
Q64563	TDSPLCIEEIEVSPPK	1.265485036	2	4.11312
Q64563	VCLIGCGFTSGYGAAINTAK	1.150221261	2	4.88096
Q64563	VDDEANLER	1.094166978	2	3.09107
Q64563	VDEMNISTVDMILGR	0.927287585	2	4.06999
Q64563	VIATCVCPTDINATNPK	1.594778993	2	4.70127
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**2.360701478**	**0.92014**	**15**
Q64565	AYSNHTDIISFR	1.02937445	2	3.48409
Q64565	GGNFSQTFR	0.941121873	2	2.59794

Q64565	GGVCIADEVQTGFGR	0.869065634	2	4.04195
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.276827513	2	4.32601
Q64565	GLMVGIEMVQDK	1.390307914	2	3.37818
Q64565	HNMPPCDFSPEK	1.117399265	2	3.2347
Q64565	LSALLPEPLK	2.244602249	2	2.75202
Q64565	NSQEVGTYMLLK	0.882874259	2	3.31882
Q64565	SALTQHMER	1.205756008	2	2.52906
Q64565	SALTQHMER+Oxidation(6	1.208473613		
Q64565	TEVNQIHEDCK	1.065886317	2	3.29699
Q64565	TEVNQIHEDCKDMGLLVGR	1.083441914	2	5.24897
Q64565	VIFLVNSGSEANDLAMVMAR	1.647572313	2	3.16691
Q64565	YIEQFK	1.07997107	1	2.2579
Q64565	YQSLAYNHVLEIHK	0.631769205	2	3.95398
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**4.248029897**	**0.99858**	**9**
Q64578	AVGIVATTGVSTEIGK	3.686307879	2	3.42593
Q64578	DIVPGDIVEVAVGDKVPADIR	4.081699191	2	3.38495
Q64578	IGIFSENEEVADR	1.537764027	2	3.40337
Q64578	IRDQMAATEQDKTPLQQK	1.6453676	3	4.39291
Q64578	MNVFNTEVR	1.435011913	2	2.78718
Q64578	REEMVLDDSAK	1.617013821	2	2.76877
Q64578	TGTLTTNQMSVCK	2.161343166	2	3.44584
Q64578	VGEATETALTTLVEK	2.68171235	2	4.49547
Q64578	YGPNELPAEEGK	1.734513938	2	3.01092
Q64581	**CP3AI Cytochrome P450 3A18**	**1.583543135**	**7.3E-06**	**3**
Q64581	AITMSEDEEWKR	0.494010925	2	2.31719
Q64581	LAVIGVLQNFNIQPCEK	0.784510923	2	3.20531
Q64581	NPEYWLEPEEFNPER	0.668588067	2	3.86108
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**1.764251965**	**0.88934**	**10**
Q64591	ATAEEITSK	0.938349074	2	3.01701
Q64591	CDVRDPDMVHNTVLELIK	0.783789296	4	5.05214
Q64591	DPDMVHNTVLELIK	1.016180815	3	4.14183
Q64591	EEWDVIEGLIR	1.011628611	2	3.54377
Q64591	FFPPILKPMLPPNAFQGK	0.880523105	2	3.25908
Q64591	FNIIQPGPIK	0.729377599	2	2.89204
Q64591	NIDVLK	0.76737823	1	2.28936
Q64591	SLAAEWGR	0.872399952	2	2.37682
Q64591	VAFITGGGTGLGK	1.104724966	2	2.69071
Q64591	VTKEEWDVIEGLIR	0.662053963	3	4.9013
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.90285502**	**0.99298**	**7**
Q64602	ASFSQVTPAQMDLVFQR	0.916720315	2	4.48882
Q64602	DIISLAPGSPNPK	0.695778816	2	3.218
Q64602	EILLVPGNSFFVDNSAPSSFFR	0.970854345	2	3.48101
Q64602	FLYTIPNGNNPTGNSLTGDR	0.989337165	2	3.98845
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.915404529	3	6.46759
Q64602	SAVFTVENGSTIR	0.880508874	2	4.10521
Q64602	VLSQWKPEDSKDPTKR	1.059975576	3	4.14068
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**2.07380742**	**0.99729**	**14**
Q64611	AQGGQGLEWR	1.116866393	2	2.93961
Q64611	CHGSQASYLFQQDK	0.99029518	2	4.96056
Q64611	DVFGIVVDEAIR	1.258839568	2	3.07635
Q64611	FFNQLFSGLDPHALAGR	1.558943284	3	3.85355
Q64611	FYNVALDTGDK	1.034452476	2	3.10677
Q64611	GAAFLGLGTDSVR	1.367678703	2	3.24536
Q64611	GTMMIGYQPHGTR	1.202181995	2	2.87285
Q64611	IDQAFALTR	0.914235636	2	3.46272

Q64611	KGTMMIGYQPHGTR	1.231995897	3	3.97922
Q64611	LSQVAPVLK	1.103739609	2	2.30197
Q64611	QLLDLELQSQGESR	1.069447585	2	4.51638
Q64611	TLDGDPVAVEALLR	0.506343053	2	4.6021
Q64611	VCEWKEPEELK	1.070866697	3	3.7241
Q64611	YLVEEIK	1.066192398	1	2.40722
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**2.081089122**	**0.65488**	**2**
Q64638	VVFETGNYVK	0.752950519	1	2.05845
Q64638	YESLASELLQR	1.062759972	2	3.03348
Q64640	**ADK Adenosine kinase**	**2.178730682**	**0.99999**	**11**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.308552022	3	7.1419
Q64640	AATFFGCIGIDK	1.272876423	2	3.33019
Q64640	AGHYAASVIIR	1.099637068	3	3.63438
Q64640	FGEILK	0.928293911	2	2.3522
Q64640	FKVEYHAGGSTQNSMK	1.004075011	2	4.10609
Q64640	HKELFDELVK	1.187493576	3	4.05358
Q64640	SLVANLAAANCYK	1.097918162	2	4.33123
Q64640	TGCTFPEKPDFH	1.34865543	2	2.74294
Q64640	VEYHAGGSTQNSMK	1.299260239	2	4.06014
Q64640	VEYHAGGSTQNSMK+Oxidation(12	1.127876875		
Q64640	YSLKPNDQILAEDK	1.039114214	3	4.25991
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**1.724114524**	**0.00119**	**8**
Q64654	EPAEDILQTLLDSTYK	0.971160691	2	3.82401
Q64654	GVAYDVPNAVFLEQK	0.742005872	2	4.32519
Q64654	NEDLNAEEVYGR	0.54160538	2	3.72399
Q64654	SGLNIAHFK	1.107525301	2	2.99592
Q64654	TFTYLLGSDAAALLFNSK	0.618001881	3	3.90519
Q64654	TVCGEDLPPLTYEQLK	0.491566295	2	4.42687
Q64654	YGPVFSFTMVGK	0.775479642	2	2.8097
Q64654	YLQDNPASGEK	0.498626798	2	2.79391
Q65Z40	**WAPL Wings apart_like protein homolog**	**2.179405645**	**0.38171**	**2**
Q65Z40	EKSISRIPEDNANK	1.090064553	2	2.58514
Q65Z40	LGQKRPNFKPDIQEIPK	1.15156591	2	2.39477
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**2.264009449**	**0.39441**	**5**
Q66H12	CNINCEEDPK	1.158630225	2	2.34034
Q66H12	INQDPLGIQGR	1.019566412	2	2.87806
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(0	1.444707383		
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(3	1.444707383		
Q66H12	TISPQNIDILQNPLLIK	1.32503784	2	3.43576
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**1.875350536**	**0.4152**	**2**
Q66H15	SLQGLAGEIVGEVR	0.908238322	2	3.3903
Q66H15	SQSLPNSLDYAQTSER	0.771689853	2	3.0147
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**2.062407123**	**0.53249**	**2**
Q66H45	ALELQGVR	0.579620506	2	2.47311
Q66H45	LQGDVAGALEDLER	1.050458284	2	3.75276
Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**2.077032656**	**0.9704**	**2**
Q66H71	LTEQAVEAINK	1.113153669	2	3.51174
Q66H71	SIDEDDDYFNLTK	0.921298596	2	2.98046
Q66H80	**COPD Coatomer subunit delta**	**2.098078565**	**0.99993**	**8**
Q66H80	GVQLQTHPNVDKK	0.908644614	2	3.51672
Q66H80	LFTAESLIGLK	1.058150274	2	3.02111
Q66H80	NSNILEDLETLR	1.075257964	2	3.51258
Q66H80	NTLEWCLPVIDAK	1.068532496	2	2.72746
Q66H80	SEGETIMSSNMGK	1.990759149	2	2.76797
Q66H80	TFTEMDSHEEK	0.762445632	2	2.65535

Q66H80	VAPAPARPSGPSK	1.079014917	2	2.54033
Q66H80	VTQVDGNSPVR	1.1912537	2	3.01899
Q66HA8	**HS105 Heat shock protein 105 kDa**	**2.197817291**	**0.66868**	**10**
Q66HA8	AGGIETIANEFSDR	1.225538438	2	2.94507
Q66HA8	FQEAEERPR	0.845439	2	2.45946
Q66HA8	FVVQNVSAQK	0.971537463	2	2.68755
Q66HA8	LKETAENNLK	0.922173169	2	2.58799
Q66HA8	NQQITHANNTVSSFK	1.05451811	2	4.7172
Q66HA8	RGPFELEAFYSDPQAVPYPEAK	1.38932283	3	3.78733
Q66HA8	SQFEELCAELLQK	1.126612589	2	2.60517
Q66HA8	SVLDAAQIVGLNCLR	1.499580406	2	3.70739
Q66HA8	VLGTAFDPFLGGK	1.153711074	2	2.98288
Q66HA8	YNHIDESEMK	1.931163396	2	2.50624
Q66HD0	**ENPL Endoplasmin**	**2.009882284**	**1**	**27**
Q66HD0	DISTNYYASQK	2.664425595	2	3.16239
Q66HD0	EATEKEFEPLLNWMK	1.257249362	2	3.5056
Q66HD0	EEASDYLELDTIK	0.838811276	2	4.25037
Q66HD0	EEEAIQLDGLNASQIR	1.218272962	2	4.60118
Q66HD0	EFEPLLNWMK	1.254131254	2	2.90662
Q66HD0	EVEEDEYK	0.98057786	1	2.44448
Q66HD0	FQSSHHSTDITSLDQYVER	1.052819965	3	6.63283
Q66HD0	GLFDEYGSK	1.353579547	2	2.44932
Q66HD0	GVVDSDDLPLNVSR	1.086486887	2	5.15077
Q66HD0	KEAESSPFVER	0.991369749	2	3.50719
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	0.820847204	3	3.59155
Q66HD0	LGVIEDHSNR	0.995438486	2	3.11669
Q66HD0	LISLTDENALAGNEELTVK	1.727189983	2	5.42867
Q66HD0	LTESPCALVASQYGWSGNMER	1.768108646	2	5.48347
Q66HD0	MKEKQDK	0.674216266	1	1.92505
Q66HD0	NLLHVTDTGVGMTR	1.01616953	3	4.14452
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11	1.120937224		
Q66HD0	RVFITDDFHDMMPK	1.103606272	3	3.72948
Q66HD0	SGTSEFLNK	1.05483623	2	3.05282
Q66HD0	SGYLLPDTK	0.988620587	2	3.44509
Q66HD0	SILFVPTSAPR	1.360980048	2	3.5311
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	4.844415632	3	5.15407
Q66HD0	TETVEEPLEEDETAQEEK	0.973436158	2	5.27976
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	1.058762111	5	6.24007
Q66HD0	TFEINPR	1.036367938	2	2.73857
Q66HD0	VFITDDFHDMMPK	1.339015997	2	4.01099
Q66HD0	YNDTFWK	1.048404153	2	2.38363
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**2.08767232**	**0.99929**	**15**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.307363094	3	3.93748
Q66HF1	AVTEGAQAVEEPSIC	0.916413693	2	2.80403
Q66HF1	DDGAAILAAVSSIAQK	0.948610856	2	4.35422
Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	2.307019414	3	4.26097
Q66HF1	FASEIAGVDDLGTTGR	1.217172736	2	4.58834
Q66HF1	GLLTYTSWEDALSR	1.076886921	2	3.6706
Q66HF1	GNDMQVGTYIEK	0.778941767	2	2.81418
Q66HF1	GWNILTNSEK	0.71582843	1	2.26339
Q66HF1	ILQDIASGNHEFSK	1.192171968	2	4.17614
Q66HF1	LGEVSPNLVR	0.866416942	2	3.00797
Q66HF1	LVDQEFLADPLVPPQLTIK	1.167719185	2	3.96118
Q66HF1	SATYVNTEGR	0.934862788	2	2.31744
Q66HF1	VAVTPPGLAR	0.802950394	2	2.53812
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	1.13202007	2	4.7317

Q66HF1	YDHLGDSPK	1.383929538	2	2.4766
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**2.455241177**	**0.01838**	**13**
Q66HF8	ADVDLAVR	1.131853802	2	2.36548
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	1.812725384	3	4.19254
Q66HF8	EEIFGPVQPLFK	1.247418021	2	3.2598
Q66HF8	IEEVIQR	2.364148172	2	2.30519
Q66HF8	KTFPTVNPTTGEVIGHVAEGDR	1.154936064	3	3.91188
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.148124283	3	4.16142
Q66HF8	LAPALATGNTVVMK	1.201666205	2	3.39251
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.482659624	2	4.88567
Q66HF8	TFVEESIYHEFLER	1.133599542	2	4.46208
Q66HF8	VAEQTPLSALYLASLIK	1.028914676	2	3.00276
Q66HF8	VGNPFELDTQQGPQVDK	1.013429194	2	4.40022
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.322595866	2	4.49705
Q66HF8	YGLAAAVFTR	1.133895598	2	3.29539
Q66HG4	**GALM Aldose 1_epimerase**	**1.970737036**	**0.34147**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	1.36257156	2	4.50189
Q66HG4	TVFGELPSGGGAVEK	0.850926802	2	3.84872
Q66HG4	VSPDGEEGYPGELK	0.878096494	2	4.07073
Q66HG9	**MAVS Mitochondrial antiviral_signaling protein**	**2.253138754**	**0.98159**	**3**
Q66HG9	ICELPGLAEQVTR	1.262413243	2	2.76479
Q66HG9	STAATPSTVPTNIAPSK	1.128504807	2	3.17831
Q66HG9	TTLSSSSTGSAFAK	0.883933816	2	2.34491
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**2.167614998**	**1**	**19**
Q66X93	ADDADEFGYSR	1.856570511	2	2.61315
Q66X93	ALLLPDHYLVTVMLSGIK	1.489420089	3	4.25504
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.244532779	3	6.06477
Q66X93	DTNGENIAESLVAEGLASR	1.006298544	2	4.34433
Q66X93	ETDGSETPEPFAAEAK	0.956442957	2	3.78974
Q66X93	FVDGEWYR	1.282471209	2	2.7819
Q66X93	GDVGLGLVK	1.000274308	2	2.57965
Q66X93	HFVDSHHQKPVNAIIEHVR	1.099406059	3	5.015
Q66X93	LEGDNIQDK	1.044233109	2	2.99266
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.130457677	2	5.73209
Q66X93	SAYYKPLLSAEEAAK	1.032636133	2	3.11338
Q66X93	SDISSHPPVEGAYAPR	1.009533135	3	4.41655
Q66X93	SSHYDELLAAEAR	1.095062363	2	4.0311
Q66X93	TCATVTIGGINIAEALVSK	1.048624166	2	3.49455
Q66X93	TDAVDSVVR	1.85004849	2	2.71306
Q66X93	VITEYLNAQESAK	1.126994234	2	3.92646
Q66X93	VMQVLNADAIVVK	1.48516124	2	4.10818
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.147786959	3	5.14646
Q66X93	VWAHYEEQPVEEVMPVLEEK	1.197153014	3	4.53355
Q68FL6	**SYMC Methionyl_tRNA synthetase_ cytoplasmic**	**2.044965634**	**0.98984**	**3**
Q68FL6	ADKNQVAAEVAK	1.092119926	2	3.05545
Q68FL6	LENDQIENLR	1.028223212	2	2.6913
Q68FL6	NNSELLNNLGNFINR	0.985472086	2	2.81915
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**2.208287213**	**0.65184**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.242538621	3	3.90271
Q68FP2	HNNWDLTPVK	1.06691168	2	3.2078
Q68FP2	IFLMDLNEPYPK	1.165983343	2	4.05185
Q68FP2	IQDPLSDNPR	1.020848316	2	3.0143
Q68FP2	KHNNWDLTPVK	0.603321507	2	2.49789
Q68FP2	LLIYNPEDPPGSEVLR	1.3275942	2	4.3891
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.081850281	3	4.59446
Q68FP2	YVYVADVTAK	1.037089786	1	2.99083

Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**2.100028145**	**0.99907**	**7**
Q68FQ0	GSNDMQYQHVIETLIGK	0.999385169	2	2.82305
Q68FQ0	GVIVDKDFSHPQMPK	1.164248653	2	2.80795
Q68FQ0	HKLDVTSVEDYK	1.18449228	2	3.63161
Q68FQ0	ISDNVLVDINNPEPLIQTAK	1.293160854	2	5.01982
Q68FQ0	LDVTSVEDYK	0.939138599	2	2.94363
Q68FQ0	SLHDALCVIR	1.154440145	2	2.69392
Q68FQ0	WVGGPEIELIAIATGGR	0.86292864	2	3.82036
Q68FR6	**EF1G Elongation factor 1_gamma**	**2.075024934**	**0.99982**	**8**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.005587027	2	4.98693
Q68FR6	ALIAAQYSGAQIR	1.043028316	2	4.33745
Q68FR6	ILGLLDTHLK	1.415925954	2	2.51264
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.060079612	2	4.21749
Q68FR6	KLDPGSEETQTLVR	0.981686316	2	4.10036
Q68FR6	LDPGSEETQTLVR	1.124888861	2	3.54414
Q68FR6	STFVLDEFKR	1.040820775	2	2.52096
Q68FR6	WFLTCINQPQFR	1.032880656	2	3.35302
Q68FR9	**EF1D Elongation factor 1_delta**	**2.282516655**	**0.10976**	**6**
Q68FR9	ATAPQTQHVSPMR	1.066308847	2	3.30142
Q68FR9	ATAPQTQHVSPMR+Oxidation(11	0.869284914		
Q68FR9	FYEQMNGPVTAGSR	1.263804556	2	4.52624
Q68FR9	GVVQDLQQAISK	1.211405688	2	3.43811
Q68FR9	SIQLDGLVWGASK	1.293727314	2	3.25988
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.115410737	2	5.38088
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**2.730294542**	**0.44978**	**3**
Q68FS2	ATTADGSSILDR	1.433459422	2	2.32801
Q68FS2	NAAQVLVGIPLETGQK	1.346234132	2	2.98284
Q68FS2	QIQSLCFQVNNLLEK	2.042048739	2	2.40834
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.925611337**	**7.4E-09**	**17**
Q68FS4	ADMGGAATICSAIVSAAK	1.229183961	2	5.1015
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2	1.264260147		
Q68FS4	DKDDDVPQFTSAGENFNK	1.078524564	2	5.38146
Q68FS4	GITFDSGGISIK	0.992563951	2	3.18221
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.399979948	3	6.16995
Q68FS4	GVLFASGQNLAR	0.770451413	2	3.43383
Q68FS4	LFEASVETGDR	1.001255354	2	3.58747
Q68FS4	LHGSGDLEAWEK	1.264799897	2	2.95171
Q68FS4	LNLPINIIGLAPLCENMPSGK	1.687769245	2	5.04497
Q68FS4	QLMESPANEMTPTR	0.928206037	2	3.65393
Q68FS4	QVIDCQLADVNNLGK	1.287546931	2	4.72913
Q68FS4	SAGACTAAAFLR	1.331225134	2	3.88623
Q68FS4	SAGVDDQENWHEGK	0.920294415	2	3.97118
Q68FS4	SWIEEQEMGSFLSVAK	1.192042346	2	5.14901
Q68FS4	TFYGLHQDFPSVVVVGLGK	1.277625161	2	4.70411
Q68FS4	TIQVDNTDAEGR	0.935819522	2	4.1452
Q68FS4	TLIEFLLR	1.068631959	2	2.78993
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**2.2388577**	**0.99821**	**4**
Q68FT1	INDAMNMGHTAK	0.923505654	2	3.10169
Q68FT1	LNHVLEEEQK	1.163591258	2	3.40032
Q68FT1	STGEALVQGLMGAAVTLK	1.145568445	2	3.76337
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.846496295	3	4.68254
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**2.189140917**	**1**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	1.089421418	2	3.80329
Q68FT3	ISQLDTQSPVTK	1.360506667	2	3.50086
Q68FT3	SLLLGTDVAENQK	0.96030336	2	3.4011

Q68FT3	TLGAQLPQYYEVLTAPISK	1.078167333	2	4.06975
Q68FT3	VFDCIEAYAPGFK	1.011621686	2	2.82351
Q68FT3	VLDQWFESEPLK	1.611824606	2	3.59083
Q68FT3	VQGVVLQGGEEVR	0.931181803	2	3.26104
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**2.189476439**	**9.9E-20**	**10**
Q68FT5	AGANIIGVNCR	1.187700003	2	3.62363
Q68FT5	AGLWTPEAVVEYPSAVR	1.058954308	3	4.09577
Q68FT5	AIAEELAPER	1.282899403	2	3.79623
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.449253235	3	4.69201
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.899235374	3	4.66815
Q68FT5	FGPWTSLQTMK	1.018182111	2	2.51008
Q68FT5	GGFVDLPEYPFGLEPR	1.243889716	2	4.21859
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.479310031	2	2.67014
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	1.367979962	3	3.66162
Q68FT5	YIGGCCGFEPYHIR	1.913798851	2	4.65506
Q68FT9	**SCLY Selenocysteine lyase**	**2.038007033**	**0.84957**	**6**
Q68FT9	AEVDLIVQDLK	1.161321049	2	3.90052
Q68FT9	CFHEQQTLQGR	1.048146092	2	2.76003
Q68FT9	NFRPGTENTPMIAGLGK	0.976605886	2	4.30324
Q68FT9	RVDVEDLGVDFLTIVGHK	1.222084453	3	5.33191
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	0.87358025	3	4.65663
Q68FT9	VLVHTDAAQALGK	0.845582193	3	3.31445
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**1.807176592**	**0.99995**	**13**
Q68FU3	AGDLGVDLTSK	0.809206645	2	3.49051
Q68FU3	EIDGGLETIR	1.332113099	2	2.33737
Q68FU3	EIIAVSCGPPQCQETIR	1.074169945	2	5.31334
Q68FU3	GIHVEVPGAEAENLGPLQVAR	1.226989324	2	5.84644
Q68FU3	HSMNPFCEIAVEEAVR	1.147573036	2	5.59787
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2	0.989103813		
Q68FU3	LKLPAVVTADLR	1.829335664	2	2.36035
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	2.574474205	3	5.73208
Q68FU3	RVIDFAVK	0.930528681	2	2.63964
Q68FU3	VDLLFLGK	0.946578286	2	2.73127
Q68FU3	VETTEDLVAK	0.848230797	2	3.56437
Q68FU3	VIDFAVK	0.776168471	2	2.42857
Q68FU3	VSVISVEEPPQR	0.91328214	2	3.56365
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.804183679**	**1**	**10**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.344644219	3	6.01256
Q68FY0	IEEVDAQMVR	0.980984952	2	3.84492
Q68FY0	LCTSATESEVTR	1.152633794	2	2.85525
Q68FY0	NALISHLDGTTPVCEDIGR	0.845361189	2	4.56618
Q68FY0	NNGAGYFLEHLAFK	1.111062964	2	3.52426
Q68FY0	RIPLAEWESR	0.763569956	2	2.67835
Q68FY0	SGMFWLR	1.017562395	2	2.39729
Q68FY0	TDLTDYLSR	0.821100249	2	2.9454
Q68FY0	VVELLADIVQNISLEDSQIEK	1.058721361	3	5.36858
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	2.157285204	3	5.23737
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**2.662806191**	**0.97688**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	1.66587922	2	4.72678
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	1.324061624	3	4.0088
Q68G31	GESGGQTTPYDFYSR	1.03553819	2	3.96294
Q68G31	LQPTDSFSQSSCFGLR	1.417800105	2	3.55103
Q68G31	NVNSTLTFVTLSGELK	0.986512473	2	4.2573
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.17691397	3	5.774

Q68G31	VNTEPLPGIEK	0.88013789	2	2.64245
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.893561526**	**0.76781**	**2**
Q69Z23	GDPTRAEDQVLMRALR	0.877317124	2	2.41662
Q69Z23	YFIDLLMEK	5.348430882	1	2.0173
Q6A028	**SWP70 Switch_associated protein 70**	**4.305293488**	**0.06594**	**2**
Q6A028	FILEKVQDNFDK	2.107552838	1	1.91264
Q6A028	KGDILLDENCCVESLPDKDGK	1.861646015	2	2.3398
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.835766712**	**0.97219**	**3**
Q6A0A9	LYEPDQLQELK	1.092974322	2	2.3939
Q6A0A9	SQGGVQPIPSQGGK	0.870792948	2	3.34622
Q6A0A9	VEGSSTASSGSQLAEGK	1.171081927	2	4.23287
Q6AW69	**CGNL1 Cingulin_like protein 1**	**2.302229293**	**0.98756**	**2**
Q6AW69	NRRELAEMQTQLK+Oxidation(7	1.041657398		
Q6AW69	QDSAGPILDGAR	1.28820032	2	2.50615
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.859903205**	**0.5044**	**3**
Q6AXM8	FQEEENSLLHLK	0.895451458	2	3.70879
Q6AXM8	LFVYDPNHPPSSEVLR	0.875569402	2	2.46719
Q6AXM8	LVAEGFDSANGINISPDKK	1.429135002	2	3.53868
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**1.627597015**	**0.42976**	**4**
Q6AXS5	EETQPPVALKK	0.444456257	2	2.42261
Q6AXS5	FDQLFDDESDPFEVLK	0.825691669	2	5.29557
Q6AXS5	RFEKPLEEK	1.060957391	2	2.42124
Q6AXS5	SAAQAAAQTNSNAAGK	0.442105322	2	4.54963
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**1.836272284**	**0.12175**	**2**
Q6AXY0	FLQPGSQR	0.737172685	2	2.5621
Q6AXY0	YFPAFEK	0.89637505	1	2.00928
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.994265078**	**0.97429**	**4**
Q6AY09	ATENDIYNFFSPLNPMR	1.407078345	2	2.784
Q6AY09	GLPWSCSAEEVMR	1.508370797	2	2.94583
Q6AY09	HTGPNSPDTANDGFVR	0.994491136	2	4.17416
Q6AY09	STGEAFVQFASQEIAEK	0.967105425	2	3.92796
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**2.032878458**	**0.99989**	**2**
Q6AY20	HTLAGNFNPVSEER	1.047685949	2	4.17523
Q6AY20	SCDLVGEKDKESK	0.877896026	2	3.68552
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.918379936**	**0.95705**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.54329451	3	4.01057
Q6AY30	ATLVLNCVGPYR	1.031938805	2	2.82379
Q6AY30	GGGVFTPGAAFSR	1.10605729	2	2.36506
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.185090878	2	2.92966
Q6AY30	LQQVLEK	0.903452153	1	2.32071
Q6AY30	SVSNLKPVPVIGSK	0.939124691	2	3.79931
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**2.247196332**	**0.64932**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	1.250401434	2	4.55811
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.105433229	2	5.10541
Q6AY56	LISQIVSSITASLR	1.725356125	2	3.7551
Q6AY56	NLDIERPTYTNLNR	1.112344855	2	3.3133
Q6AY56	QLFHPEQLITGK	1.061854869	2	3.09159
Q6AY56	TIQFVDWCPTGFK	1.11096468	2	3.70063
Q6AY56	VGINYQPPTVVPGGDLAK	1.064901142	2	4.39579
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**2.609300207**	**0.99763**	**5**
Q6AY80	ALTSDILEEQR	1.127907399	2	3.24238
Q6AY80	EEPIHCTPSWYFQG	1.385808331	2	2.69827

Q6AY80	NDVTGALSNPEVFK	1.856684325	2	3.93004
Q6AY80	VLAPQISFGPEVSSEEQR	1.246426663	2	4.34197
Q6AY80	VLCQGFAFDVPGFYDSGFLK	1.061538903	2	2.80055
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**1.934439971**	**0.72857**	**3**
Q6AYG5	DVLETLWGGPANLEAIAK	0.955637043	2	4.05122
Q6AYG5	ILEQFPGGSIDLQK	0.821313946	2	3.41098
Q6AYG5	NTFCSGSDLNAVK	0.790433095	2	2.48237
Q6AYH5	**DCTN2 Dynactin subunit 2**	**2.093739009**	**0.89038**	**3**
Q6AYH5	ASVEDADTQNK	0.788863532	2	2.80982
Q6AYH5	VNALDLAVLDQVEAR	1.173339608	2	3.41295
Q6AYH5	WSPVASTLPELVQR	1.082260739	2	2.90362
Q6AYK6	**CYBP Calcyclin_binding protein**	**2.779762061**	**0.60744**	**2**
Q6AYK6	IYEDGDDDMKR	1.616827885	2	2.40685
Q6AYK6	WDYLTQVEK	2.533590978	2	2.60189
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**2.09967027**	**1**	**4**
Q6AYQ8	IITLEEGDLILTGTPK	1.311112345	2	5.17019
Q6AYQ8	NLHHEVELGVLLGR	0.754491343	3	4.70732
Q6AYQ8	SFTSSCPVSAFVPK	1.031648558	2	3.98761
Q6AYQ8	STVLSEPVLFLKPSTAYAPEGSPVLMPAYCR	1.019868204	3	3.72354
Q6AYR8	**SCRN2 Secernin_2**	**2.144989702**	**0.94188**	**2**
Q6AYR8	GHQAALGLMDEQEQAQLR	0.981272401	3	4.30184
Q6AYR8	QEQQSLEQEGLEALR	1.151939891	2	3.88558
Q6AYS7	**ACY1A Aminoacylase_1A**	**2.147384458**	**0.02723**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	1.069620725	2	3.81153
Q6AYS7	ICTVQPNPDYGSAVTFLEER	3.021378636	2	4.57627
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**2.145839804**	**0.88801**	**3**
Q6AYS8	ALTDELAALGCTGVR	0.845753149	2	4.05791
Q6AYS8	FDAVVGYK	1.54381551	1	2.2866
Q6AYS8	SVAGEIVLITGAGHGIGR	0.900147753	2	4.02995
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**2.072081347**	**0.90964**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	1.185424969	2	3.43435
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	1.064002637	2	3.20889
Q6AYT9	NDDVINSSSYR	2.224682875	2	3.34475
Q6AYT9	TGVVMIPGISQLTQK	1.296814225	2	3.14431
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**2.061462703**	**0.72533**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	1.004500805	2	5.40966
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	1.169054431	3	4.14551
Q6AYZ1	DVNAAIATIK	1.055984342	2	3.17294
Q6AYZ1	IHFPLATYAPVISAEK	1.396444758	2	3.79999
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.566403268	2	5.46006
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.262010385	2	4.70229
Q6DGG0	**PPID Peptidyl_prolyl cis_trans isomerase D**	**2.189487329**	**0.79857**	**4**
Q6DGG0	GTGPTTGKPLHFK	0.794422098	2	2.35666
Q6DGG0	IVLELFADIVPK	1.810262789	2	2.31037
Q6DGG0	MLENVEVNGEKPAK	1.007466768	2	3.70808
Q6DGG0	VFFDVDIGGER	1.258934917	2	2.83679
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.939007615**	**1.8E-06**	**6**
Q6DGG1	AVAIDLPGLGR	1.003331792	2	3.56435
Q6DGG1	FSSETWQNLGTLHR	1.219473962	2	3.63614
Q6DGG1	FSVLLLHGIR	0.92387346	2	3.08848
Q6DGG1	GYVPVAPICTDK	0.904388087	1	2.65398
Q6DGG1	INAADYAR	0.979450916	2	2.46774
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.433546104	2	5.38226

Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**2.104625134**	**0.96586**	**2**
Q6EDY6	ELMESIK+Oxidation(2	1.260025131		
Q6EDY6	IENYLLR	1.066030741	2	2.45561
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**1.802396034**	**0.33633**	**2**
Q6GQP4	CDLSDIREVPLK	0.875987766	2	2.5344
Q6GQP4	CDLSDIREVPLKDAK	0.798995169	2	2.91608
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**2.677985344**	**0.4913**	**3**
Q6GQT1	ASVTVLGDILGSAMQNTQDLLK	0.994690163	2	2.35133
Q6GQT1	IQEEGTGVEETGK	5.318852562	2	3.72267
Q6GQT1	SSGSLLNNAMK	1.085811673	2	3.09788
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**2.49333929**	**0.34737**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	1.132363047	2	3.87937
Q6I7R3	ILGIPVIITEQYPK	1.70191464	2	3.00799
Q6I7R3	YFGDIISVGQR	1.338736821	2	2.57839
Q6IE52	**MUG2 Murinoglobulin_2**	**2.185272876**	**0.04816**	**14**
Q6IE52	AHFSVMGDILSSAIK	1.192206798	2	3.67194
Q6IE52	HGIPFFVK	1.190197778	2	2.74722
Q6IE52	HTSSWLVTPK	1.125207409	2	2.80894
Q6IE52	LPSSEEEESLDINIEGAK	1.588842536	2	2.88293
Q6IE52	MLIYTILPDGEVIADSVK	1.260634926	2	3.83604
Q6IE52	MLSGFIPLKPTVK	4.441628766	2	3.15561
Q6IE52	MLSGFIPLKPTVK+Oxidation(0	0.867859087		
Q6IE52	NLYPLKELVQDPK	1.240955726	1	2.04411
Q6IE52	QLSFSLSAEPIQGPYK	1.406788815	2	4.2773
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	1.180760239	3	3.65907
Q6IE52	VHLSFSPSQSLPASQTHMR	0.826953307	3	3.93723
Q6IE52	VKTVPLTCNNPK	1.102777139	2	2.96447
Q6IE52	VTASPQSLCGLR	1.638455246	2	2.50736
Q6IE52	YMVLVPSQLYTETPEK	1.187384171	2	3.72556
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.801225248**	**0.91956**	**2**
Q6IFW6	LENEIQTYR	0.849940413	2	2.34899
Q6IFW6	QSLEASLAETEGR	0.80892472	2	3.44501
Q6IFZ9	**K2C74 Keratin_ type II cytoskeletal 74**	**1.702833521**	**0.37247**	**2**
Q6IFZ9	FLEQQNQVLQTK	0.299535596	2	4.16948
Q6IFZ9	GDSALKDAWAKLDELEGALQQAK	2.261565613	3	3.60364
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**1.9788259**	**0.55942**	**4**
Q6IMF3	TNAENEFVTIK	0.491208242	2	2.75133
Q6IMF3	TNAENEFVTIKK	0.17497166	2	2.93977
Q6IMF3	WELLQQVDTSTR	0.766360267	2	3.61795
Q6IMF3	YEELQITAGK	0.986512696	2	3.46776
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**2.226247713**	**0.29171**	**7**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	1.113318595	3	5.46347
Q6IRK9	GEESAVMVVPR	1.050710096	2	2.82703
Q6IRK9	IVVYNQPYTDYGK	0.85834979	2	2.91765
Q6IRK9	LGLLVDTVGPR	1.482312952	2	2.98361
Q6IRK9	SVASFSIYSPHTGHQGYQDGVPK	1.200277083	3	3.45847
Q6IRK9	TYPDTDSFNTVAEITGSK	1.370511981	2	3.73194
Q6IRK9	VGAVASLIR	1.568660768	2	2.52945
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**2.184779462**	**0.99533**	**4**
Q6MGB5	AGVIGLTQTAAR	1.128133182	2	3.19555
Q6MGB5	CNSVLPGFIATPMTQK	1.373394241	2	2.34861
Q6MGB5	GSIINISSIVGK	1.743631505	2	2.7751
Q6MGB5	VGNIGQTNYASSK	0.993804163	2	2.76001
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**2.020403288**	**0.99997**	**3**
Q6NSR8	GIVYDTGGLSIK	1.015195587	2	2.36454

Q6NSR8	HNSPSAAHFITR	0.98316476	3	3.95459
Q6NSR8	TVEINNTDAEGR	0.892684353	2	2.9926
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**2.261820975**	**0.9922**	**3**
Q6NYB7	EFADSLGIPFLETSAK	0.944659543	2	3.79188
Q6NYB7	NATNVEQSFMTMAAEIK	1.188828667	2	5.09252
Q6NYB7	TITSSYYR	0.969142608	1	1.97861
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**2.354727356**	**0.89355**	**9**
Q6NZJ6	FMLQDVLDLR	1.371813546	2	2.79625
Q6NZJ6	GLPLVDDGGWNTVPISK	1.075868922	2	2.87266
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	0.974503233	3	3.35313
Q6NZJ6	IHNAENIQPGEQK	1.123065277	2	3.95514
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.152159026	3	3.56169
Q6NZJ6	KVEYTLGEESEAPGQR	0.932260669	2	4.75058
Q6NZJ6	LGIESTLER	1.168343199	2	2.4185
Q6NZJ6	LKEELEEAR	1.069288785	2	2.70229
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.810730943	3	4.99129
Q6P0K8	**PLAK Junction plakoglobin**	**2.121881707**	**0.98829**	**3**
Q6P0K8	LLNDEDPVVVTK	0.854064759	2	3.22565
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.109080491	3	3.62823
Q6P0K8	TMQNTSDLDTAR	1.023515587	2	3.25989
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**2.670871465**	**0.00282**	**14**
Q6P502	AMTGVEQWPYR	1.095098808	2	2.70722
Q6P502	AVAQALEVIPR	1.218581386	2	2.4506
Q6P502	DMMLNIINSSITTK	0.927991812	2	3.97657
Q6P502	EIQVQHPAAK	1.029808397	2	3.30226
Q6P502	GISDLAQHYLMR	1.506684159	2	3.04806
Q6P502	IVLLDSSLEYK	1.613729771	2	2.55909
Q6P502	IVSRPEELREDDVGTGAGLLEIK	2.064360358	3	4.09411
Q6P502	KGESQTDIEITR	1.073806436	2	3.27758
Q6P502	MLLDPMGGIVMTNDGNAILR	1.765974039	2	3.88515
Q6P502	NLQDAMQVCR	1.098008969	2	3.31944
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	2.164888833	2	3.87082
Q6P502	TAVETAVLLLR	1.378199912	2	3.73921
Q6P502	TLIQNCGASTIR	1.065680526	2	3.34592
Q6P502	WSSLACNIALDAVK	1.341776597	2	3.7964
Q6P6M7	**selenium transferase**	**1.845340407**	**0.90545**	**4**
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**1.878210434**	**0.99925**	**14**
Q6P6R2	ALLNNSHYYHLAHGK	0.774878933	2	3.3111
Q6P6R2	ALTGGIAHLFK	1.022937269	2	2.63245
Q6P6R2	EANLAASFGKPINF	1.18460319	1	1.92902
Q6P6R2	IDVSVEAASGGK	0.889570674	2	3.03946
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.071184924	3	3.99356
Q6P6R2	IPNIFAIGDVVAGPMLAHK	1.436560461	3	3.50005
Q6P6R2	NETLGGTCLNVGCIPSK	0.881470556	2	5.16718
Q6P6R2	NQVTATTADGSTQVIGTK	0.856160451	2	5.63074
Q6P6R2	RPFTQNLGLEELGIELDPK	1.066034947	3	4.60339
Q6P6R2	SEEQLKEEGVEFK	0.804818794	2	3.53124
Q6P6R2	TNADTDGMVK	0.787769384	2	2.82534
Q6P6R2	TNADTDGMVK+Oxidation(7	1.237439449		
Q6P6R2	VCHAHPTLSEAFR	1.109275285	3	3.78274
Q6P6R2	VVHVNGFGK	1.033375763	3	3.45103
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**1.796105599**	**0.65456**	**6**
Q6P6S9	AAETHLIDYEK	0.901288659	2	2.66759
Q6P6S9	AQTLLLEVEEIFK	0.947885585	2	3.27033

Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.936243497	2	4.39739
Q6P6S9	QGAETVQELLEVAK	0.806250694	2	3.14373
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	0.847427304	3	3.62794
Q6P6S9	WLEAEWIFGGVK	1.422180098	2	2.77027
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**2.248127696**	**0.7622**	**9**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2	1.066770608		
Q6P6V0	HFVALSTNTDK	1.203542567	1	3.25527
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.306231053	3	6.00124
Q6P6V0	MIPCDFLIPVQTQHPIR	2.35895579	2	2.42619
Q6P6V0	TFTTQETITNAETAK	1.400782205	2	4.75683
Q6P6V0	TLANLNPESSLFIIASK	0.974083616	3	5.20596
Q6P6V0	VDYQTGPIVWGEPGTNGQHAFYQLIHQGTK	1.276203838	3	4.02225
Q6P6V0	VFEGNRPTNSIVFTK	1.153755524	2	3.38279
Q6P6V0	VWFVSNIDGTHIAK	0.940928115	2	3.63236
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**2.376761901**	**0.71717**	**6**
Q6P7Q4	DFLLQQTMLR	1.298221124	2	3.38238
Q6P7Q4	FEELGVK	1.079920818	1	1.93778
Q6P7Q4	GFGHIGIAVPDVYEACK	1.442901567	2	4.0001
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.248570997	2	5.7382
Q6P7Q4	RFEELGVK	0.973801025	2	2.32368
Q6P7Q4	VLGLTLLQK	1.712470628	2	2.48099
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**2.287247234**	**0.90978**	**2**
Q6P7R8	GIFVQSVLPFFVATK	0.986845428	2	3.46805
Q6P7R8	LGEWAVVTGGTDGIGK	1.22637863	2	4.23867
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.974782542**	**0.76166**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	1.082022198	2	4.50998
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10	0.972950916		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	2.056931867	3	5.65801
Q6P9T8	EIVHLQAGQCGNQIGAK	2.05452639	2	4.93126
Q6P9T8	EVDEQMLNVQNK	0.919422629	2	4.47394
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	2.409177925	3	4.85032
Q6P9T8	INVYYNEATGGK	1.160105747	2	3.07603
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.327136971	3	6.60577
Q6P9T8	LHFFMPGFAPLTSR	1.266207873	2	3.26907
Q6P9T8	MSATFIGNSTAIQELFK	1.413119484	2	4.3316
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	1.314511039	3	5.80361
Q6P9T8	TAVCDIPPR	1.149230779	2	2.5009
Q6P9T8	YLTVAAVFR	1.77513541	2	2.68381
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.933486213**	**0.99706**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	0.979991558	3	3.73125
Q6P9U8	EGTGSTATSSSSTGGAVGK	0.935473213	2	4.27067
Q6PA06	**ATLA2 Atlastin_2**	**1.971585614**	**0.34827**	**5**
Q6PA06	AGLTDQVSHHAR	0.942499441	2	3.18057
Q6PA06	NLVPLLLAPENLVEK	1.207252133	2	3.02297
Q6PA06	QNQHEELQNVR	0.972446015	2	2.92974
Q6PA06	SMEQVCGGDKPYIAPSDLER	1.305729088	3	3.80321
Q6PA06	SMLQATAEANNLAAVAGAR	1.558049797	2	4.50093
Q6PCL9	**polymerase gamma**	**2.268841897**	**0.64703**	**2**
Q6PCL9	LTEILK	0.987632803		
Q6PCL9	QANNINMLKDGMK	1.18460319		
Q6PCU2	**VATE1 V_type proton ATPase subunit E 1**	**2.485599539**	**0.21702**	**2**
Q6PCU2	ARDDLITDLLNEAK	1.357831026	2	2.97243
Q6PCU2	LDLIAQQMMPEVR	1.243835613	2	2.56513
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.968853464**	**0.99977**	**2**
Q6PDM2	SHEGETAYIR	0.975059557	2	2.40953
Q6PDM2	TKDIEDVFYK	0.99427984	2	2.75332

Q6PDV7	**RL10 60S ribosomal protein L10**	**2.542427121**	**0.34217**	**2**
Q6PDV7	FNADEFEDMVAEK	1.262161294	2	3.81246
Q6PDV7	FNADEFEDMVAEKR	1.376498914	2	3.30423
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**2.048456939**	**0.94846**	**6**
Q6PEC1	AEDGENYAIK	1.028803355	2	2.6904
Q6PEC1	AEDGENYAIKK	0.965181948	2	2.47524
Q6PEC1	LEAAYTDLR	1.18329366	2	2.81162
Q6PEC1	MKAEDGENYAIK	0.226014161	2	2.79379
Q6PEC1	QAEILQESR	0.880940467	2	2.58364
Q6PEC1	QILESEKDLEEAEEYKEAR	1.105550482	3	4.09466
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**2.497963765**	**0.27764**	**3**
Q6PEC4	NDFTEEEEAQVR	1.515583436	2	3.45187
Q6PEC4	RTDDIPVWDQEFLK	0.88621266	2	3.02802
Q6PEC4	TDDIPVWDQEFLK	1.320311504	2	3.18925
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**2.366532821**	**0.9205**	**6**
Q6Q0N1	AVFQYIDENQDR	0.837198499	2	3.02616
Q6Q0N1	EGGSIPVTLTFQEATGK	1.252606136	2	2.76204
Q6Q0N1	LGGSVELVDIGK	1.017705065	2	3.58265
Q6Q0N1	MTEAAAADVQR	1.208026753	2	3.14374
Q6Q0N1	TGQEIPVNLR	1.25320623	2	2.57481
Q6Q0N1	TVFGVEPDLTR	1.305376058	2	2.39771
Q6RT24	**CENPE Centromere_associated protein E**	**1.937575392**	**0.93941**	**3**
Q6RT24	ENEDLKLK	1.012519186	2	2.32973
Q6RT24	MELENVNMKLQEK	0.848857709	2	2.55944
Q6RT24	NLQEYIDAQKSEKMK	0.888862211	2	2.40604
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**1.843311094**	**0.12837**	**2**
Q6SKG1	FDSTSILQTLSK	1.45434998	2	3.75613
Q6SKG1	TGTVLIPGTTQLTQK	0.797726602	2	2.85918
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**2.24754111**	**0.99576**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.368184479	2	4.64675
Q6TUG0	FQMTQEVVCDECPNVK	1.12218904	2	5.57842
Q6TUG0	KGEGLPNFDNNNIK	1.150335567	2	3.64917
Q6TUG0	TLEVEIEPGVR	1.355129762	2	3.1555
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.748319677**	**0.99264**	**19**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	0.949523808	2	5.09539
Q6UPE1	ALNEGGLQSIPK	0.852086469	2	3.36423
Q6UPE1	ASCDAQTYGIGLK	0.731380515	2	4.05393
Q6UPE1	DCTPIEYPKPDGQISFDLLSSVALSGTNHEHDQPAHLTLK	0.941596491	4	4.62569
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	1.573361081	2	3.08612
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.106936977	2	4.5225
Q6UPE1	GAPLNTPVTEDR	0.916862001	2	3.48264
Q6UPE1	GIATNDVGIQK	0.939156942	2	3.78917
Q6UPE1	HHPSIRPTLEGGK	0.734752842	2	2.4202
Q6UPE1	HHPSIRPTLEGGKR	0.993708457	2	2.82038
Q6UPE1	LQINAQNCVHCK	1.151179335	2	3.72339
Q6UPE1	NLSIYDGPEQR	1.16481114	2	3.14372
Q6UPE1	QLAAEQEKDIR	0.753028401	2	2.70154
Q6UPE1	QLTSENLQSK	0.756958783	2	2.46372
Q6UPE1	SGSLAAEAIFK	0.923555932	2	3.14082
Q6UPE1	TAGLHVTEYEDNLK	1.230529225	2	3.97349
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	1.62331693	2	4.39
Q6UPE1	VDHTVGWPLDR	0.892483682	2	2.47605
Q6UPE1	VTIFAEGCHGHLAK	1.016151614	2	3.67792
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**2.173693572**	**0.99225**	**8**

Q6URK4	EDSVKPGAHLTVK	1.061372205	2	3.48456
Q6URK4	EDTEEYNLR	0.989390621	2	2.45323
Q6URK4	GFAFVTFDDHDTVDK	1.12016866	2	4.09519
Q6URK4	IETIEVMEDR	1.077213953	2	3.4034
Q6URK4	IFVGGIKEDTEEYNLR	1.442253495	2	4.2578
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	0.78950854	2	5.22703
Q6URK4	WGTLTDCVVMR	1.168532261	2	3.2414
Q6URK4	YHTINGHNCEVK	0.994120878	2	3.50797
Q6URW6	**MYH14 Myosin_14**	**2.114347322**	**1**	**4**
Q6URW6	EDQSILCTGESGAGK	0.889819561	2	4.39641
Q6URW6	FDQLLAEEK	1.013477295	1	2.04082
Q6URW6	KFDQLLAEEK	0.96582528	2	2.83733
Q6URW6	QLLQANPILEAFGNAK	1.206595313	2	4.49156
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**1.649451756**	**0.50764**	**5**
Q6XQN1	AFAQQSLSR	1.108618117	2	2.49352
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.709814315	2	4.22268
Q6XQN1	LDSGDLLQQAK	0.78573567	2	3.06168
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.235134789	2	5.03625
Q6XQN1	QLQNPAVYQVALSEK	0.991110601	2	3.83193
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.997209796**	**0.99998**	**2**
Q6ZPJ3	FRTTDIVIR	0.996867679	2	2.60035
Q6ZPJ3	NCAQGEGSMAKKVK	1.028361339	2	2.8212
Q6ZPV2	**INO80 DNA helicase INO80**	**2.119191889**	**0.60985**	**2**
Q6ZPV2	FIDVSPAEMANLMLQGLLAR+Oxidation(12	0.690974776		
Q6ZPV2	KLDEEMREAK+Oxidation(5	1.083721668		
Q6ZWR6	**SYNE1 Nesprin_1**	**2.02200858**	**0.99852**	**4**
Q6ZWR6	FGSITNQLLK	0.999104369	2	2.39879
Q6ZWR6	KDEIEGWSNSSLPK	0.832254998	2	2.52539
Q6ZWR6	LETILK	0.987632803	1	1.90074
Q6ZWR6	LKAKTDDLVHAK	1.03834865	2	2.31459
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.752097959**	**0.11488**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	0.799067904	2	2.74204
Q70FJ1	MDQITQSLCNLNK+Oxidation(0	1.993114391		
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**2.177621219**	**0.27248**	**5**
Q711G3	DCGTDVLDLWTLMQK	0.578109941	2	4.40866
Q711G3	DVEETKPELSLLGDGDH	2.089735425	2	4.13121
Q711G3	LNVAVGEYAK	0.914237757	2	2.76331
Q711G3	QHVPLDEYSANLR	1.762562694	2	2.63208
Q711G3	VILITPPPLCEAAWEK	1.43486888	2	2.73393
Q71LX4	**TLN2 Talin_2**	**2.236499186**	**0.96816**	**3**
Q71LX4	QEDVIATANLSR	1.023712383	1	1.97032
Q71LX4	QVAASTAQLLVACK	1.164908571	2	3.18949
Q71LX4	VMVTNVTSLLK	1.018209128	2	2.37738
Q71TY3	**RS27 40S ribosomal protein S27**	**2.193234005**	**0.93061**	**3**
Q71TY3	DLLHPSPEEEK	1.43891478	2	2.91667
Q71TY3	LTEGCSFR	1.135457404	2	2.38761
Q71TY3	LVQSPNSYFMDVK	1.132616852	2	2.80042
Q75N33	**SC16B Protein transport protein Sec16B**	**2.864706356**	**0.36001**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	1.301538364	2	3.67124
Q75N33	VLEPDWLVQLR	1.520374931	2	2.80606
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**2.143129731**	**0.97737**	**6**
Q75Q39	NADLSTFYQNR	1.093984118	2	2.95816
Q75Q39	NREPLMPSPQFIK	0.928408267	2	2.82192
Q75Q39	QYMEEENYDK	#NUM!	1	1.94862
Q75Q39	SDEDKDKEGEALEVK	1.076847619	2	4.22832

Q75Q39	WKEVAQDCTK	0.954269547	2	2.33949
Q75Q39	YEQAIQCYTEAISLCPTEK	1.296171808	2	2.49781
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**2.154636085**	**0.98343**	**8**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.215463888	3	5.1377
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.265173602	2	4.99636
Q76MZ3	LSTIALALGVER	1.131417785	2	2.36096
Q76MZ3	LTQDQDVDVK	1.229564285	2	2.97982
Q76MZ3	QLSQSLLPAIVELAEDAK	0.844671785	3	4.13773
Q76MZ3	SALASVIMGLSPILGK	1.167543763	2	2.89103
Q76MZ3	SEIIPMFSNLASDEQDSVR	1.103943812	2	3.96919
Q76MZ3	VLELDNVK	1.107680891	2	2.5149
Q78IK4	**APOOL Apolipoprotein O_like**	**2.262365821**	**0.79585**	**2**
Q78IK4	EEEPKK	3.703498615	1	1.96138
Q78IK4	SESTSGTTQFIPDPK	1.044585641	2	2.42113
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**2.181560694**	**0.98734**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	3.257745141	3	5.66937
Q78P75	NFGSYVTHETK	1.377687914	2	2.92278
Q78P75	YNPTWHCIVGR	0.800292538	2	2.86639
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**2.23784742**	**0.07331**	**6**
Q791V5	EEGIVGFFAGLIPR	1.240462279	2	3.42882
Q791V5	GLFTGLTPR	1.043665649	2	2.58243
Q791V5	LCSGVLGTVVHGK	1.250895407	2	2.99564
Q791V5	SAATLITHPFHVITLR	1.009186382	3	3.56618
Q791V5	VLIQVGYEPLPPTIGR	1.093224146	2	4.18477
Q791V5	YCGLCDSIVTIYR	1.402748272	2	2.91509
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**2.143400895**	**0.98032**	**4**
Q794E4	ATENDIYNFFSPLNPVR	1.02909255	3	4.09186
Q794E4	HSGPNSADSANDGFVR	1.112745353	2	3.9465
Q794E4	ITGEAFVQFASQELAEK	1.198281246	2	2.71371
Q794E4	VHIEIGPDGR	1.152611022	2	2.7901
Q7M0E3	**DEST Destrin**	**2.40486061**	**0.8357**	**2**
Q7M0E3	HEYQANGPEDLNR	1.265541034	2	4.76629
Q7M0E3	HFVGMLPEKDCR	1.299334571	2	3.48551
Q7TMA5	**APOB Apolipoprotein B_100**	**1.871171418**	**0.39408**	**12**
Q7TMA5	ALEGKSDTVARLHTEK	1.180030708	2	2.41776
Q7TMA5	GFEPTLEALFGK	0.746420946	2	2.91823
Q7TMA5	IEGNLVFDPSSYLPK	1.051617287	2	2.99779
Q7TMA5	IEIDIPLPLGGK	0.470284855	2	2.77812
Q7TMA5	ITDNDVLIALDSAK	1.041677848	2	3.32554
Q7TMA5	KGTVATEMSTER	0.817848676	2	2.84147
Q7TMA5	LSISEQNAQR	0.567736272	2	2.74273
Q7TMA5	LSTSPFALNLTMLPK	1.098560118	1	1.90173
Q7TMA5	NFVASHIANILNSEELYVQDLK	0.804186975	3	3.84929
Q7TMA5	NLQHCDGFQPISTSVSPLALIK	0.611767694	3	3.79325
Q7TMA5	TILFDTFVNDVAPVEK	0.990087089	2	3.13251
Q7TMA5	VRSFTIDLLEIKAK	1.098560118	1	1.99944
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.92964143**	**1**	**4**
Q7TNG8	AVVGSPHVSTASAVR	0.849141836	2	2.93918
Q7TNG8	AYSTDVCVPISR	0.950106494	2	3.38022
Q7TNG8	GSQGGLSQDFVEALK	1.14433993	2	3.6321
Q7TNG8	QLLQEEVGPVGVETMR	1.157429157	2	3.22962
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**2.047566603**	**0.98345**	**2**
Q7TP47	DLFEDELVPLFEK	1.009669312	2	3.27966

Q7TP47	NLANTVTEEILEK	1.062857075	2	3.68663
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**2.182286383**	**0.19048**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	1.564363705	2	3.00243
Q7TP48	LENGEIETIAR	1.149220254	2	3.52103
Q7TP48	LLEYDTVTK	1.091515778	2	2.49107
Q7TP48	LLLSSETPIEGK	1.635976459	2	2.91197
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**2.065734562**	**0.99995**	**8**
Q7TP52	AGVSVYGIIR	0.915636858	2	2.74656
Q7TP52	EDCSPADKPYIEEAR	1.133364699	2	3.71484
Q7TP52	KREDCSPADKPYIEEAR	1.089971835	3	4.21316
Q7TP52	LDYGGMGQEVQVEHIK	1.293846496	2	4.61124
Q7TP52	LKEHCIVNYQVK	0.980676297	2	4.07233
Q7TP52	NLIEWLNK	1.297736988	2	2.3561
Q7TP52	REDCSPADKPYIEEAR	1.123074706	3	3.69844
Q7TP52	TFSGQTHGFVHR	1.080512739	2	3.66039
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**2.099600781**	**1**	**6**
Q7TPB1	ALIAGGGAPEIELALR	1.163007636	2	3.88185
Q7TPB1	ETLLNSATTSLNSK	1.131134261	2	3.31296
Q7TPB1	GDVTITNDGATILK	1.10030066	2	3.51737
Q7TPB1	SIHDALCVIR	1.154440145	2	2.69392
Q7TPB1	TGCNVLLIQK	0.928057374	2	2.60797
Q7TPB1	VIDPATATSVDLR	1.022277916	2	3.84164
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**2.125733299**	**0.99937**	**3**
Q7TPJ0	FLVGFTNK	1.435305973	2	2.48813
Q7TPJ0	GEDFPANNIVK	1.104449925	2	3.20333
Q7TPJ0	GTEDFIVESLDASFR	1.084663234	2	4.3717
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**2.0923617**	**0.99195**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(0	1.130631929		
Q7TQ20	QIEEVNELMRK+Oxidation(8	1.032112727		
Q7TQ94	**NIT1 Nitrilase homolog 1**	**2.53037884**	**0.4902**	**2**
Q7TQ94	GQDWEQTQK	1.340651543	2	2.46455
Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.317975483	3	4.21868
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.76406376**	**0.09171**	**3**
Q7TQM4	AIWEAVQAYPK	0.831461177	2	2.56319
Q7TQM4	QDRPLPSTASDSTR	0.759094116	2	2.84504
Q7TQM4	TQCLEQAQR	0.920808966	2	2.88386
Q7TSI0	**ZNF12 Zinc finger protein 12**	**1.871068749**	**0.99905**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(1	2.989184769		
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(5	0.898506784		
Q80V31	**CE104 Centrosomal protein of 104 kDa**	**2.053665074**	**0.96431**	**2**
Q80V31	IDGSVLPTEAEVRAQK	0.943683598	2	2.55886
Q80V31	KLMEMPVGTQK+Oxidation(2)Oxidation(4	1.039516348		
Q80VM7	**ANR24 Ankyrin repeat domain_containing protein 24**	**1.666502765**	**0.5174**	**2**
Q80VM7	ADEVDVLAQAGLTGTVIR	0.877317124	2	2.68819
Q80VM7	QNQELLEK	0.299575032	1	2.01925
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.848185752**	**1.7E-05**	**13**
Q80W21	CLDAFPNLK	0.938544488	2	3.2003
Q80W21	CLDAFPNLKDFIAR	1.11729632	2	3.11884
Q80W21	FKLGLDFPNLPYLIDGSHK	0.85012551	3	5.07351
Q80W21	HNLCGETEEER	0.879030078	2	3.89162
Q80W21	IRVDILENQLMDNR	1.16529926	2	3.04944
Q80W21	ITQSNAILR	1.139771023	2	3.07713
Q80W21	KHNLCGETEEER	0.888331121	2	3.9986
Q80W21	KISDYMK	0.831375311	1	2.00136
Q80W21	LFLEYTDSSYEEK	0.971695086	2	4.04387

Q80W21	LGLDFPNLPYLIDGSHK	1.377071423	3	4.67577
Q80W21	LKPGYLEQLPGMMR	1.168679862	2	3.18071
Q80W21	LYSEFLGK	1.068416044	2	2.35592
Q80W21	VDILENQLMDNR	1.304925437	2	3.71466
Q80W93	**HYDIN Hydrocephalus_inducing protein**	**2.712721503**	**0.54635**	**3**
Q80W93	ELERLAKEMQEK+Oxidation(8	1.949297095		
Q80W93	LAKEMQEK	1.263311278	1	1.93259
Q80W93	LQTLDEDEYDALTAEEK	1.481691958	2	2.30161
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**1.648985344**	**0.26768**	**3**
Q80WS3	DHAVVVGVYRPPPK	0.603871755	3	3.74093
Q80WS3	MKPAGGRGGWGWGGGK+Oxidation(0	1.191414649		
Q80WS3	TNIIPVLEDAR	1.097753654	2	2.40161
Q80X50	**UBP2L Ubiquitin_associated protein 2_like**	**2.046012672**	**0.8574**	**2**
Q80X50	IDLAVLLGK	1.00792636	2	3.14239
Q80X50	QRPQATAEQIR	1.176363273	2	2.51887
Q80X90	**FLNB Filamin_B**	**2.038672574**	**0.54482**	**11**
Q80X90	ADIEMPFDPSK	1.378057288	2	2.37343
Q80X90	FNDEHIPDSPYLVPVIAPSDDAR	1.583646717	3	3.64952
Q80X90	GAGIGGLGITVEGPSESK	1.312150843	2	3.8366
Q80X90	GEAGIPAEFSIWTR	1.139942026	2	2.31444
Q80X90	IGNLQTDLSDGLR	1.123320014	2	2.45996
Q80X90	ILAQDGEGQPIDIQMK	0.900625107	2	3.3675
Q80X90	TFEMSDFIVDTR	1.271637664	2	2.3016
Q80X90	VDIQTEDLEDGTCK	1.914613282	2	3.796
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	2.113934692	3	4.11054
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	0.993252114	3	3.47551
Q80X90	VVASGPGLEHGK	1.045107462	2	2.37975
Q80XC3	**US6NL USP6 N_terminal_like protein**	**2.066888471**	**0.96945**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	2.023500423	2	2.37964
Q80XC3	SVDEGSKNLK	1.013269132	2	2.41046
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**2.510852358**	**0.27633**	**3**
Q80XI3	FLKITKPTIDEK	0.85400341	2	2.60857
Q80XI3	FMLQDVIDLR	1.371813546	2	2.79625
Q80XI3	NHDEESLECLCR	1.258972351	2	3.36872
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**1.883930357**	**0.86313**	**2**
Q80Y84	CDIGLLGLK	0.914835179	1	2.0753
Q80Y84	SSSEKNDCLRGK	0.847678254	1	1.93582
Q80YR7	**CLSPN Claspin**	**2.02128273**	**0.99109**	**2**
Q80YR7	GASFLPTAGFRSPSPGLFR	1.011362559	2	2.41257
Q80YR7	LEGASHAKPGEKLQMLK+Oxidation(14	1.024590467		
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.925712747**	**0.99998**	**2**
Q80Z25	ELEQEAERLEK	0.945299838	2	2.93997
Q80Z25	MIEESLK+Oxidation(0	1.137296526		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**2.51816591**	**0.39553**	**4**
Q80Z29	NAQLNMEQDVAPH	0.792450584	2	2.53487
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.257325509	2	3.78835
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.248865871	2	5.37929
Q80Z29	YLLETSGNLDGLEYK	1.35103065	2	4.55266
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**2.030351329**	**0.26832**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	1.721366524	2	2.62699
Q80Z36	YPEEQLK	0.674216266	1	2.09197
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**2.063409013**	**0.65856**	**5**
Q811D2	AQEDFDK	0.674042407	1	1.91143

Q811D2	LSGSEDSQQKVEEK	1.615189836	2	2.3696
Q811D2	NKDDLTPMLLAVK	1.189127279	2	2.4119
Q811D2	SADQLSEK	1.075780294	2	2.3079
Q811D2	SNLEEEARDLK	1.04563849	1	1.99484
Q811X6	**CRYL1 Lambda_crystallin homolog**	**2.17990179**	**0.99589**	**4**
Q811X6	EMKSLEQSGSLK+Oxidation(1	0.868338955		
Q811X6	IVDDQVILSSSSSCLLPSK	1.124278348	2	3.9303
Q811X6	LYDIEQQQITNALESIR	1.053508867	2	4.27153
Q811X6	TFGPVPEFSGDTVEK	1.273350586	2	2.8986
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.833716091**	**1.2E-05**	**10**
Q8BFZ3	CDVDIR	1.566630551	2	2.32686
Q8BFZ3	DLTDYLMK	1.0706717	1	2.21593
Q8BFZ3	HQGVMVGMGQK	1.057583961	3	3.63664
Q8BFZ3	HQGVMVGMGQK+Oxidation(4	0.814391722		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)Oxidation(7	0.79769413		
Q8BFZ3	HQGVMVGMGQK+Oxidation(7	0.86784045		
Q8BFZ3	SYELPDGQVITIGNER	4.193885167	3	5.23031
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	0.951406077	3	6.64004
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5	1.035074052		
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.104573582	3	4.32967
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**2.236916602**	**0.67877**	**6**
Q8BG32	LYDNLLEQNLIR	1.256112563	2	3.3939
Q8BG32	TGQAAELGGLLK	1.131998951	2	3.1513
Q8BG32	TTANAIYCPPK	3.550358491	2	2.64396
Q8BG32	TYEAALETIQNMSK	1.157265878	2	2.37357
Q8BG32	VQIEHISSLIK	1.614679579	2	2.70242
Q8BG32	YQEALHLGSQLLR	1.115558946	2	2.50007
Q8BGD9	**IF4B Eukaryotic translation initiation factor 4B**	**1.710496818**	**0.97065**	**2**
Q8BGD9	SQSSDTEQPSPTSGGGK	0.774414307	2	5.37759
Q8BGD9	VDVADQAQDKDRDDR	1.274019092	2	2.37885
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**2.188468979**	**0.63067**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.665192367	2	3.8384
Q8BGT5	VLCIINPGNPTGQVQSR	1.178116996	2	5.07928
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**2.167776996**	**0.99894**	**3**
Q8BGY2	KYEDICPSTHNMDVPNIK	1.001619772	3	4.79291
Q8BGY2	VHLVGIDIFTGK	1.129524241	3	3.74122
Q8BGY2	YEDICPSTHNMDVPNIK	1.067569005	2	3.88257
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**2.560897242**	**2E-12**	**8**
Q8BH00	ELLMLENFIGGK	1.186150314	2	3.59371
Q8BH00	ELNLPFGGMK	1.348303207	1	2.49095
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	2.621613661	3	5.3076
Q8BH00	ILCGEGVDQLSLPLR	1.241132207	3	4.95457
Q8BH00	ITQLSAPHCK	1.15693356	2	3.12905
Q8BH00	KLSLELGGK	1.046432307	1	2.25505
Q8BH00	NPAIIFEDANLEECIPATVR	1.074699962	2	5.0365
Q8BH00	SSFANQGEICLCTSR	1.174788138	2	3.90093
Q8BH18	**TM117 Transmembrane protein 117**	**3.276496852**	**0.4331**	**2**
Q8BH18	FLKNEQGMENQDK	1.993114391	2	2.34406
Q8BH18	FLKNEQGMENQDK+Oxidation(7	1.687737088		
Q8BH59	**CMC1 Calcium_binding mitochondrial carrier protein Aralar1**	**2.120544756**	**0.70844**	**3**
Q8BH59	GLIPQLIGVAPEK	1.14777837	1	3.07248
Q8BH59	IAPLAEGALPYNLAELQR	1.482706032	2	2.85188
Q8BH59	YLGLYNDPNSNPK	0.941305253	2	3.11152
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**2.293157326**	**0.99415**	**11**

Q8BHN3	AEKDEPGAWEETFK	0.837077546	2	3.06362
Q8BHN3	DDNSVELTVAEGPYK	0.968172631	2	3.41011
Q8BHN3	LVAIVDPHIK	1.891416425	2	2.34349
Q8BHN3	MLDYLQGSGETPQTDIR	0.783634027	2	5.34461
Q8BHN3	REPWLLASQYQDAIR	1.200324909	3	4.33095
Q8BHN3	SGGIERPFVLSR	1.031630183	2	2.4538
Q8BHN3	SIRPGLSPYR	0.885033994	2	2.3565
Q8BHN3	SLLLSVNAR	0.923102606	2	2.48766
Q8BHN3	VDSGYRVHEELRNHGLYVK	0.766532318	2	2.33052
Q8BHN3	VTEGGEPYR	1.035939051	2	2.40752
Q8BHN3	VVIMGAGKPAAVVLQTK	1.661977357	3	3.8582
Q8BI84	**MIA3 Melanoma inhibitory activity protein 3**	**2.064281394**	**0.98593**	**2**
Q8BI84	DDNISALTNCITQLNR	1.043772317	2	2.32124
Q8BI84	TQTAVSIVEEDLK	1.04621925	2	2.43565
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**2.271805806**	**0.65956**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.18460319	1	2.19315
Q8BIJ6	SCQTALAEILDVLVR	0.995494754	2	3.51358
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.950622367**	**0.99987**	**10**
Q8BJ64	ADSAYHPSCTCK	0.573252659	2	3.18561
Q8BJ64	AEVQTLVSR	1.195356249	2	2.88709
Q8BJ64	ELQPGSHVQSDK	1.022812315	2	3.07472
Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.961841644	2	4.24555
Q8BJ64	GGDGPLHVSR	0.854682586	2	2.34865
Q8BJ64	HELGANMYR	0.850396288	2	2.34865
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.886617691	5	5.01656
Q8BJ64	TNHPLHQAFLQAAR	0.784178996	3	4.00004
Q8BJ64	VIGVENLR	0.986017278	2	2.74613
Q8BJ64	VLLLEAGPK	1.191672442	2	2.62868
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**2.23504915**	**0.01196**	**2**
Q8BJY1	GLTHPDDSVK	0.832015918	2	2.45672
Q8BJY1	TVAEIFGNSNYLR	1.915118346	2	2.48391
Q8BKC5	**IPO5 Importin_5**	**2.124365295**	**0.32099**	**2**
Q8BKC5	IFSIIAEGEMHEAIK	1.253783848	2	2.3325
Q8BKC5	VAAAESMPLLLECARVR+Oxidation(6	0.738829001		
Q8BKZ9	**ODPX Pyruvate dehydrogenase protein X component_ mitochondrial**	**1.927850726**	**0.93536**	**2**
Q8BKZ9	HSLDASQGTATGPR	0.945599412	2	3.94335
Q8BKZ9	VSVNDFIIR	1.540061287	2	3.05482
Q8BL66	**EEA1 Early endosome antigen 1**	**1.811650975**	**0.96442**	**2**
Q8BL66	MQAAVTELTAVKAQK	0.844571647	2	2.44298
Q8BL66	QESIKEITNLKDAK	1.089161248	2	2.30593
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**2.258846341**	**0.99747**	**2**
Q8BL97	NPPGFAFVEFEDPR	1.195991958	2	2.81618
Q8BL97	VYVGNLGTGAGK	1.021255152	2	2.56947
Q8BMA5	**NPAT Protein NPAT**	**1.88687369**	**0.99891**	**2**
Q8BMA5	AKETSNDVPTIMSSLWKK+Oxidation(11	0.895618707		
Q8BMA5	KKLPSSFPAGMDVDK+Oxidation(10	0.975637115		
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**2.308290509**	**0.66478**	**5**
Q8BP47	KEDGTFYEFGDDIPEAPER	0.684644818	2	4.40305
Q8BP47	LEDLVCDVVDR	0.905585406	2	2.81699
Q8BP47	LMTDTINEPILLCR	2.799640975	2	3.34017
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.25819378	2	2.9164
Q8BP47	YGTCPHGGYGLGLER	1.190720209	2	3.16098
Q8BTM8	**FLNA Filamin_A**	**2.140185155**	**0.99683**	**6**
Q8BTM8	AFGPGLQGGNAGSPAR	1.037895887	2	3.56198
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	1.246346893	3	3.62483

Q8BTM8	ANLPQSFQVDTSK	1.022894091	2	2.44741
Q8BTM8	GAGTGGLGLAVEGPSEAK	1.076776158	2	3.72377
Q8BTM8	IVSPSGAAVPCK	0.966367276	2	2.41114
Q8BTM8	VEPGLGADNSVVR	1.151504478	2	2.86012
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.995362092**	**0.99974**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	1.020386958	2	3.13355
Q8BU33	LPNSLMGR+Oxidation(5	0.997894215		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.93770838	3	3.95851
Q8BWM0	**PGES2 Prostaglandin E synthase 2**	**2.15965788**	**0.63401**	**2**
Q8BWM0	AFLDFHSLPYQVVEVNPVR	1.411992817	3	3.52985
Q8BWM0	KVPILVAQEGDSLQQLNDSSVIISALK	1.066455892	3	4.62097
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.878356301**	**0.01702**	**2**
Q8BWQ1	ADIWLIR	0.917735975	2	2.4481
Q8BWQ1	IHHDQPVKPLDR	0.784921501	3	3.51418
Q8BWR8	**RHPN2 Rhophilin_2**	**2.406520689**	**0.68334**	**2**
Q8BWR8	ETKEVDFSIVFK	1.056505526	2	2.53472
Q8BWR8	TGAENLLKVATNQK	1.32482534	2	2.48585
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**2.028339361**	**0.99971**	**2**
Q8BX70	ENALSELDVPFKVK	0.96898714	2	2.62614
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19	1.058392397		
Q8BY87	**UBP47 Ubiquitin carboxyl_terminal hydrolase 47**	**1.942203742**	**1**	**2**
Q8BY87	AGGDSGNVDDDCER	0.951590402	2	3.49961
Q8BY87	QNIFDEMKK	0.957863102	2	2.43066
Q8BZI0	**AF1L1 Actin filament_associated protein 1_like 1**	**1.850831664**	**0.81387**	**2**
Q8BZI0	IYDEVPYEK	0.87587369	1	2.0261
Q8BZI0	LSQEKQNSDSDSLGMNDSGSTLGRR	0.892971156	3	3.59391
Q8BZQ7	**ANC2 Anaphase_promoting complex subunit 2**	**2.323899369**	**0.70685**	**2**
Q8BZQ7	EIRNVELLK	1.245847251	2	2.41527
Q8BZQ7	QALEQFNQLSQVLHR	0.866513395	2	2.75226
Q8C6K9	**chain**	**2.145913924**	**0.99535**	**3**
Q8C6K9	NEHSFQVVGIQVR	1.150368973		
Q8C6K9	TMNPAFMGLDRATR+Oxidation(1)Oxidation(6	1.007009727		
Q8C6K9	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1.103400941		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**2.297231059**	**0.76792**	**2**
Q8C7X2	FNVEDGEIVQQVR	0.948573926	2	3.98422
Q8C7X2	VMGDRSVLYK+Oxidation(1	1.291836181		
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**2.156163762**	**0.23919**	**3**
Q8CC88	FLPSLAQSALEK	1.283274735	2	2.44075
Q8CC88	HQATGELDDAK	0.759749961	2	3.4104
Q8CC88	VSSDQLSSENLTSAVGQK	1.39297175	2	3.20769
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**2.01429079**	**0.86252**	**3**
Q8CDI6	EKELSLEKEQNK	1.292986131	2	2.35146
Q8CDI6	EKVANMEVALDK+Oxidation(5	0.992653776		
Q8CDI6	ELDDRNMEVQRLEALLK	0.911074378	2	2.32278
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.916917513**	**0.79501**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	1.038988925	3	4.68694
Q8CFN2	WVPEITHHCPK	0.398816979	2	2.50773
Q8CFN2	YVECSALTQK	1.042093939	1	2.70188
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**2.257183843**	**0.03179**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	1.120436865	3	3.74259
Q8CG45	EHHFEAIALVEK	1.144609276	2	2.98795
Q8CG45	FFGNSWSETYR	0.883815122	2	3.00953
Q8CG45	FYAYNPLAGGLLTGK	1.252079578	2	4.36607
Q8CG45	MDASASAATVR	1.079434291	2	3.83804
Q8CG45	QVETELLPCLR	1.395946245	2	3.03559

Q8CG45	RMDASASAATVR	1.026456145	2	3.31487
Q8CG45	TTYGTSAPSMTSAALR	1.065856084	2	4.45599
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.233808898	3	5.4736
Q8CG45	WMYHHSQLQGTR	1.144680132	3	3.74459
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.921418834**	**0.96989**	**3**
Q8CG48	EEKLLEK	0.914217935	1	1.92741
Q8CG48	IKALNCEIEELER	1.137358074	2	2.43912
Q8CG48	KIKALNCEIEELER	0.941461084	2	2.64722
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**2.140679711**	**0.72563**	**11**
Q8CGC7	AIQGATSHHLGQNFSK	1.069961115	2	4.59959
Q8CGC7	DQDVEPGAPSMGAK	0.822355302	2	3.35812
Q8CGC7	DQVDSAVQELLQLK	1.28151198	2	4.15179
Q8CGC7	FVELPGAEMGK	1.703436085	2	2.5284
Q8CGC7	GDVSISVEEGKENLLR	1.074950137	2	4.00271
Q8CGC7	GSQFGQSCCLR	1.131042813	2	2.86139
Q8CGC7	KEENLAEWYSQVITK	0.988344379	2	4.46688
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.5223868	2	4.36456
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.100012121	2	4.86416
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	1.058460914	3	3.47052
Q8CGC7	VYEELLAIPVVR	1.168552844	2	3.42992
Q8CGN4	**BCOR BCL_6 corepressor**	**1.991784551**	**0.53783**	**3**
Q8CGN4	FLTDYLNDLQGR	0.885531859	1	1.94041
Q8CGN4	NWLLLSDVLK	3.054794509	2	2.52787
Q8CGN4	VCIELTGLHPKK	1.055143786	2	2.34277
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**2.040778032**	**0.99934**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(10	1.010897496		
Q8CHB8	DSGGQTLSPSWAAK	1.231861592	1	2.13864
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**2.590955602**	**0.24124**	**8**
Q8CHM7	DTSKPCLINIMIEPQSTR	1.336884172	3	4.75379
Q8CHM7	GAAYSHAEDSIR	1.79489671	2	3.37647
Q8CHM7	GVVPDNHPNCVGAAR	1.175236888	2	3.24663
Q8CHM7	GYFVQTPEELQDSLR	1.905401526	2	3.83254
Q8CHM7	LVELCNLPFLPTPMGK	1.222773906	2	4.48063
Q8CHM7	NCFIVSEGANTMDIGR	1.050032921	2	4.69397
Q8CHM7	NQEAMGAFQEFPQVEACR	1.356491472	2	6.43392
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	1.351494079	3	4.01666
Q8CIB5	**FERM2 Fermitin family homolog 2**	**1.931131193**	**0.9616**	**2**
Q8CIB5	GCEVTPDVNISGQK	0.924489525	2	3.51374
Q8CIB5	TSTILGDITSIPELADYIK	1.06083052	2	2.72138
Q8CIE6	**COPA Coatomer subunit alpha**	**2.256390881**	**0.36188**	**10**
Q8CIE6	ASNLENSTYDLYTIPK	1.104909415	2	4.13394
Q8CIE6	DADSQNPDAPEGK	1.217394445	2	4.01827
Q8CIE6	GITGVDLFGTTDAVVK	1.599107284	2	3.716
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.361232234	3	3.78069
Q8CIE6	LLELGPKPEVAQQTR	1.053851292	2	3.15225
Q8CIE6	QELILSNSEDK	1.247152264	2	2.62028
Q8CIE6	QQPLFVSGGDDYK	1.032946111	2	2.7117
Q8CIE6	SILLSVPLLVVDNK	1.1034266	2	4.00956
Q8CIE6	SSGLTAVWVAR	0.88019886	2	2.44891
Q8CIE6	TLDLPIYVTR	1.135772523	2	2.82687
Q8CJ27	**ASPM Abnormal spindle_like microcephaly_associated protein homolog**	**1.634978914**	**0.43092**	**2**
Q8CJ27	ALHHLLTYKHLSAILDALK	0.877190054	2	2.36556
Q8CJ27	FLSLRKTAIWIQR	0.709213596	2	2.63605
Q8CJ40	**CROCC Rootletin**	**2.445860451**	**0.50525**	**4**
Q8CJ40	DLLQLGGELVRTSR	1.026797065	2	2.42963

Q8CJ40	ELEERTGNLGRQR	1.146447788	2	2.40207
Q8CJ40	LRDQTAASAQAQEDAQR	1.558049797	2	2.3698
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9	1.44635256		
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.816885028**	**0.93747**	**4**
Q8JZN5	GIILVGNEEQK	0.91519183	2	2.41553
Q8JZN5	GSNTCEVHFENTR	0.910636085	2	4.52701
Q8JZN5	NLSEFGLIQEK	1.213911679	2	2.4622
Q8JZN5	SGNVTTVMETIGR	0.756076393	2	2.96583
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.912214553**	**1**	**19**
Q8K009	AMVEAVQLIADGK	1.120923231	2	4.19427
Q8K009	ANNTEYGLASGVFTR	0.945932013	2	4.62549
Q8K009	DLGEEALNEYLK	1.171391385	2	3.77958
Q8K009	EESFGPIMVISK	1.411680007	2	3.05086
Q8K009	FLFPEGIK	0.882400124	2	2.45559
Q8K009	FQNGDIDGVLQR	0.832169438	2	3.21425
Q8K009	GVINIIPGSGGVAGQR	0.993516184	2	3.87897
Q8K009	HGSIIYHPSLLPR	0.815457105	2	4.36967
Q8K009	KLGFTGSTSVGK	0.851676777	2	2.49719
Q8K009	KVSLELGGK	0.489001741	1	2.03903
Q8K009	NGLVLFGNDGK	1.021024014	2	2.42723
Q8K009	NLQFEDGK	0.93937579	1	2.18625
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.062340077	3	4.02749
Q8K009	SCDVKPNDTVDSLYNR	1.226294823	2	4.48119
Q8K009	TDVAAPFGGMK+Oxidation(9	1.209489314		
Q8K009	TPQPEEGATYEGIQK	1.33105209	2	2.58287
Q8K009	VSYASLADVDR	1.007751263	2	2.91656
Q8K009	VVGVFTVPDKDGK	1.115015752	2	3.26216
Q8K009	YFAGWCDK	0.896164439	1	2.1003
Q8K1N2	**PHLB2 Pleckstrin homology_like domain family B member 2**	**1.613903559**	**0.72556**	**2**
Q8K1N2	EKENLCNLEKK	0.597754114	2	2.41911
Q8K1N2	LQEETSQRQKLIEK	1.060831072	2	2.38009
Q8K1Q0	**NMT1 Glycylpeptide N_tetradecanoyltransferase 1**	**2.050884307**	**0.73217**	**2**
Q8K1Q0	GNDMDSTQDQPVK	1.203887291	2	2.53111
Q8K1Q0	LGEVVNTHGPVEPDKDNIR	0.764855384	3	3.44455
Q8K1S6	**SPIR2 Protein spire homolog 2**	**2.799342075**	**0.02111**	**3**
Q8K1S6	ALFVETLELR	1.649358477	2	2.50528
Q8K1S6	DTADILLRR	1.46944127	2	2.31496
Q8K1S6	RDAFQSLQGPKWR	1.285889797	2	2.30447
Q8K2H2	**OTU6B OTU domain_containing protein 6B**	**1.946916294**	**0.96741**	**2**
Q8K2H2	EELEQLK	0.914217935	1	2.08084
Q8K2H2	EERIAEAEIENLSGAR	1.059186104	2	2.46803
Q8K2Z4	**CND1 Condensin complex subunit 1**	**2.125354979**	**0.47087**	**2**
Q8K2Z4	AIIDEFEQKLR	1.043028316	2	2.36961
Q8K2Z4	LLESFENMTSQTSLIDLDIGGK	1.472903406	2	2.44545
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**2.293977914**	**0.10131**	**2**
Q8K3J1	ILMWTELIR+Oxidation(2	1.649358477		
Q8K3J1	LCEAICPAQAITIEAEPR	1.193049653	3	4.90856
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**2.356928023**	**0.43139**	**6**
Q8K442	EDVQPLSQAFFK	1.397274148	2	2.89183
Q8K442	GQITAILGHSGAGK	1.11410552	2	3.74836
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	1.04680654	3	4.09428
Q8K442	LTGVCPQCNVQFDFLTVR	1.268340706	2	2.83254

Q8K442	NTQNILVQNLSGGQK	1.215133318	2	2.96951
Q8K442	STLLNVLSGLCVPTK	1.237061134	2	3.79413
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**1.946650912**	**3.3E-13**	**12**
Q8K4C0	CCLEEGLEPVCFER	0.831617282	2	4.39759
Q8K4C0	FDHEMFGLKPK	0.765222691	2	3.32328
Q8K4C0	GYPIDILLSSR	0.91098796	2	3.27162
Q8K4C0	HSALGQHPTINDDLPNR	0.73234559	2	4.99735
Q8K4C0	IAVIGSGASGLTCIK	0.968511662	2	4.19835
Q8K4C0	KLPSQSEMMAEINK	0.825451221	2	3.8894
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.714127124	3	4.74939
Q8K4C0	KTILTTEDR	0.562500434	2	2.80174
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	1.153157668	3	3.77859
Q8K4C0	SDDIGGLWR	0.758233302	2	3.02784
Q8K4C0	VFPPNLEKPTLAIIGLIQPLGAIMPISELQGR	0.917731778	4	5.0199
Q8K4C0	WATQVFK	0.813195081	1	1.9542
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**2.232712568**	**0.99708**	**3**
Q8K4T4	EVLNLTK	1.179393902	1	2.1182
Q8K4T4	IEELEETNKSLQK	1.372540445	2	2.558
Q8K4T4	IHELMNK	1.007335878	1	2.09297
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.997848177**	**0.86509**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	0.996572243	2	3.83324
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.165460419	2	5.80955
Q8K4Z5	**SF3A1 Splicing factor 3A subunit 1**	**2.393298747**	**0.73962**	**2**
Q8K4Z5	HKVSEFKEGK	1.093108645	2	2.30061
Q8K4Z5	IGEEEIQKPEEK	1.259178451	2	2.60164
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**2.072466986**	**0.98227**	**5**
Q8K586	FNVWDTAGQEK	1.106884981	2	3.31169
Q8K586	HLTGEFEK	0.949767411	1	2.04382
Q8K586	LVLVGDGGTGK	0.829091641	2	2.37278
Q8K586	NLQYYDISAK	1.05161221	1	2.13557
Q8K586	VCENIPIVLCGNK	0.899124351	2	3.72718
Q8K5B3	**MCFD2 Multiple coagulation factor deficiency protein 2 homolog**	**1.714721261**	**0.60535**	**2**
Q8K5B3	DDDKNNDGYIDYAEFAK	0.775127219	2	4.35357
Q8K5B3	STVHDQEHIMEHLEGVINQPEAEMSPQELQLHYFK	1.514385055	4	5.87028
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**2.321088556**	**0.86739**	**3**
Q8QZY1	VFSDEVQQQAQLSTIR	0.878447969	2	3.85333
Q8QZY1	VSGGPSLEQR	1.106878202	2	2.62712
Q8QZY1	VYEIQDIYENSWTK	1.336603629	2	3.92647
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.686199971**	**0.75357**	**6**
Q8R081	ASLNGADIYSGCCTLK	1.519289569	2	2.95599
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	1.01785961	3	5.0295
Q8R081	SDALETLGFLNHYQMK	1.191366785	2	3.68698
Q8R081	SKPGAAMVEMADGYAVDR	0.624699152	2	3.89393
Q8R081	SSSGLLEWDSK	0.866370727	2	2.32781
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.795737651	3	7.14297
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.758492179**	**0.67177**	**5**
Q8R0F9	FDNTYSLLHTK	0.854233654	2	3.13002
Q8R0F9	GSSHQVENEILFPGCVLR	0.749343744	2	4.7551
Q8R0F9	VCEMLLHECELQSQK	0.885272009	2	4.97628
Q8R0F9	VGYTAEVLLPDK	0.789582575	2	2.95609
Q8R0F9	VGYTAEVLLPDKACEEK	0.862515076	2	2.44847
Q8R0K2	**TRI31 E3 ubiquitin_protein ligase TRIM31**	**2.118164139**	**0.63618**	**2**

Q8R0K2	LQSSSMELLKDIKDALSR	1.053508867	2	2.552
Q8R0K2	QRLDEEESFLLSR	1.907414241	2	2.43184
Q8R164	**BPHL Valacyclovir hydrolase**	**2.109038693**	**0.97306**	**3**
Q8R164	FADEFNR	1.025610978	2	2.36687
Q8R164	FTLVAWDPR	1.110954118	2	2.98209
Q8R164	TDFAPQLQSLNK	1.04545287	2	3.728
Q8R1F5	**HYI Putative hydroxypyruvate isomerase**	**2.184727653**	**0.86175**	**2**
Q8R1F5	GDTVEGLSWLR	1.12716687	2	3.14266
Q8R1F5	GEMGLGAVPGR	1.571375188	2	2.53749
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**2.383886283**	**0.95449**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	2.055071827	2	4.48738
Q8R1V4	QLLDQVEQIQK	0.96419575	2	2.89605
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**1.883037716**	**0.92363**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	0.790327747	2	3.94613
Q8R3Q6	NCIAQTSAVVK	0.929726703	2	2.79186
Q8R491	**EHD3 EH domain_containing protein 3**	**2.391137186**	**0.95948**	**6**
Q8R491	ADQIETQQLMR	1.244132322	2	2.61221
Q8R491	GGAFEGTLQGPFGHGYGEGAGEGIDDAEWVVAR	21.69746844	3	4.333
Q8R491	LDISDEFSEVIK	1.195050261	2	3.63764
Q8R491	LFEAEEQDLFK	1.33546405	2	3.49502
Q8R491	MQDQLQAQDFSK	1.039959641	2	3.83833
Q8R491	QEETQRPVQMVK	1.031418588	2	2.7539
Q8VBU2	**NDRG2 Protein NDRG2**	**1.89457342**	**0.12451**	**6**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.865536773	3	5.11384
Q8VBU2	LDPTQTSFLK	0.933720492	1	2.08861
Q8VBU2	MADSGGQPQLTQPGK	1.204023636	2	3.1336
Q8VBU2	SLITHAPNLENIELYWNSYNNR	1.160872658	3	4.667
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.459486712	2	4.517
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.306273602	2	4.74081
Q8VC12	**HUTU Urocanate hydratase**	**1.878674478**	**0.00048**	**9**
Q8VC12	DHHDVSGTDSPFR	1.62619754	2	2.68359
Q8VC12	HQLVVGSQAR	0.88602683	2	2.91315
Q8VC12	LLALEFAQELR	2.121059373	2	3.96146
Q8VC12	LQYMDNIR	1.571427567	2	2.42834
Q8VC12	LVITNGMVIPNYSSR	1.363563394	2	3.82513
Q8VC12	MMLSWDVSNGVAR	1.337603463	2	3.17367
Q8VC12	VAIAVAINQAIASGK	2.775964139	2	4.00164
Q8VC12	VFVTSGLGGMSGAQAK	1.313532418	2	4.54127
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9	0.875883643		
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**2.022489318**	**0.65419**	**2**
Q8VDC1	GLELQVMQLQQEK	1.016947325	2	2.39016
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(0	0.799875388		
Q8VDG5	**PPCS Phosphopantothenate__cysteine ligase**	**2.035198257**	**0.81822**	**2**
Q8VDG5	FLDNFSSGR	1.234170331	2	2.45637
Q8VDG5	LETDPDIIISR	1.021769745	2	2.58724
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**1.370240786**	**0.02607**	**2**
Q8VE11	TMKGFMVLIEK+Oxidation(1	0.454429434		
Q8VE11	TMKGFMVLIEK+Oxidation(5	0.454429434		
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**1.831922955**	**0.25184**	**5**
Q8VED5	FLEQQNKVLETK	0.200390318	2	3.66851
Q8VED5	NKYEDEINK	0.957863102	2	2.95454
Q8VED5	NKYEDEINKR	0.836993633	3	3.33708
Q8VED5	NLDLDSIIAEVK	0.689825097	2	3.541
Q8VED5	YEDEINK	1.323075862	1	2.34168

Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**2.244136379**	**0.99993**	**12**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.287840832	3	4.77499
Q8VEK3	FIEIAAR	1.335169347	1	1.90702
Q8VEK3	GYFEYIEENK	0.833432783	2	3.37234
Q8VEK3	LLEQYKEESK	1.158761474	2	3.26815
Q8VEK3	LLEQYKEESKK	1.055143786	2	3.66877
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	0.984655162	3	4.75506
Q8VEK3	NFILDQTNVSAAAQR	1.115860294	2	4.89524
Q8VEK3	NGQDLGVAFK	1.027039295	2	2.40092
Q8VEK3	TCNCETEDYGEK	1.27909427	2	3.57562
Q8VEK3	VSELKEELK	1.22421583	2	2.89193
Q8VEK3	VSELKEELKK	1.07186603	2	2.68919
Q8VEK3	YNILGTNTIMDK	1.138231382	2	3.656
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**1.958984923**	**0.99996**	**8**
Q8VHE9	ATVQSVLLDSAGR	0.97989863	2	3.86813
Q8VHE9	FLPLPLTQLLNK	0.946378424	2	3.22782
Q8VHE9	GATYGADHDLAR	0.945055986	2	3.26791
Q8VHE9	NLYSDLQALGSK	1.007355348	2	3.6197
Q8VHE9	RPPEPLVTDK	0.902793707	2	2.95453
Q8VHE9	RPPEPLVTDKEAR	0.777937289	3	4.20689
Q8VHE9	VESVTGGSPLTNQYYLAAHR	1.053741096	2	3.9792
Q8VHE9	VVAHGVSHAILLK	1.21532669	2	2.87402
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**2.13306499**	**0.78842**	**4**
Q8VHF5	AYAEGINR	0.916508554	2	2.51807
Q8VHF5	EGSSIGAIDSK	1.034564731	2	2.35077
Q8VHF5	GLVYETSVLDPDEGIR	1.045069017	2	4.34381
Q8VHF5	GYSIPECQK	1.103509296	2	2.80161
Q8VHK7	**HDGF Hepatoma_derived growth factor**	**1.898556647**	**0.99413**	**3**
Q8VHK7	GFSEGLWEIENNPTVK	0.793524162	2	3.70253
Q8VHK7	NSTPSEPDSGQGPPPEEEEGEEEAAKEEAEAQGVR	0.694535549	3	6.10673
Q8VHK7	SCAEEPEVEPEAHEGDGDKK	1.036218732	3	3.9406
Q8VHT6	**AS3MT Arsenite methyltransferase**	**2.437864614**	**0.73562**	**4**
Q8VHT6	FAHDFLFTPVEASLLAPQTK	2.603408166	2	4.36773
Q8VHT6	ILDLGSGSGR	0.998525256	2	2.90833
Q8VHT6	SLQNVHEEVISR	1.682933523	2	3.20885
Q8VHT6	TSADLQTNACVTPAK	1.386593692	2	3.87555
Q8VHX6	**FLNC Filamin_C**	**2.213999264**	**0.98842**	**3**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.048600558	2	3.97345
Q8VHX6	IECDDKGDGSCDVR	1.083946184	2	3.44393
Q8VHX6	LIALLEVLSQK	1.648610748	2	2.62857
Q8VI04	**ASGL1 L_asparaginase**	**1.979638342**	**0.99961**	**5**
Q8VI04	DLSAGAVSAVRCIANPVK	0.877317124	2	2.35339
Q8VI04	FAADMGIPQTPAEK	0.986347431	2	3.44424
Q8VI04	GNLAYATSTGGIVNK	0.876237491	2	4.35895
Q8VI04	NSGTVGAVALDCK	0.940830172	2	3.29069
Q8VI04	TVDEAATLALDYMK	1.073157886	2	3.57368
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.954812496**	**0.9998**	**5**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.271453831	2	4.01386
Q8VID1	LAEDGAHVVISSR	2.059847917	2	3.70507
Q8VID1	NFAAELAPK	0.838853821	2	2.45876
Q8VID1	TALLGLTK	1.056301413	2	2.41564
Q8VID1	VNCLAPGLIK	1.104826657	2	2.51608
Q8VIF7	**SBP1 Selenium_binding protein 1**	**1.894530454**	**0.99982**	**11**
Q8VIF7	CGPGYATPLEAMK	0.614239249	2	3.10767
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.077586612	2	5.42326

Q8VIF7	GGFVLLDGETFEVK	1.442855314	2	3.90905
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.934564096	2	3.77977
Q8VIF7	HEIIQTLQMK	0.957547208	2	2.84595
Q8VIF7	HNIMVSTEWAAPNVFK	1.130980223	2	4.60945
Q8VIF7	LTGQIFLGGSIVK	0.860624376	2	3.01877
Q8VIF7	NEGGTWSVEK	0.837487299	2	3.16176
Q8VIF7	NTGIEAPDYLATVDVDPK	1.006638839	2	4.16405
Q8VIF7	QYDISNPK	0.77467208	1	2.11613
Q8VIF7	VIEPNEIHAK	1.056433467	2	2.96786
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.805044319**	**0.81196**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	0.852173341	2	3.2066
Q8VIJ6	MEELHSQEMQK	0.855329577	2	3.7953
Q8VIJ6	RMEELHSQEMQK	0.689444297	2	3.90017
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**2.158702082**	**0.06944**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	1.419834097	2	5.40929
Q91VA0	AILPFDLQIIDEK	1.110347201	2	3.85738
Q91VA0	GNILPPNTEGYIGIR	1.040819175	2	2.90914
Q91VA0	KVEFVSELPK	0.964432635	2	2.90151
Q91VA0	NKEFGQL	1.086406822	1	2.1487
Q91VA6	**PDIP2 Polymerase delta_interacting protein 2**	**2.870112171**	**0.07357**	**2**
Q91VA6	VLETVGVFEVPK	1.600436933	2	3.40001
Q91VA6	VTVIPFYMGMR+Oxidation(9	1.148716329		
Q91VM5	**RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1**	**1.879886554**	**0.99997**	**2**
Q91VM5	LFIGGLNTETNEK	0.936781439	2	2.79149
Q91VM5	VEQATKPSFESGR	0.900704918	2	3.93891
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**2.034027694**	**1**	**2**
Q91VM9	IIAINVNDPEAEK	0.904263428	2	3.21823
Q91VM9	MEIATEEPLNPIK	1.024789233	2	4.43456
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**1.977543156**	**0.47224**	**6**
Q91W43	AGHQLQHDLFFDTLK	1.257683226	2	3.02957
Q91W43	DISLVHSMIPLGSCTMK	1.018187701	2	2.72649
Q91W43	EMLQALGLASIDELIEK	0.970963922	2	2.54451
Q91W43	IDDIYGDQHLVCTCPPMEVYESPFSEQK	1.344657833	3	4.43025
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	1.876245952	3	4.64839
Q91W43	VSFQPNSGAQGEYAGLATIR	1.448201992	2	5.20353
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**2.086797466**	**0.9866**	**3**
Q91W90	GTVLALTEK	1.152408943	2	2.39144
Q91W90	SFEDTIAQGITFVK	1.06225087	2	4.02806
Q91W90	VDCTQHYAVCSEHQVR	1.03176748	3	4.48855
Q91WL5	**CP4CA Cytochrome P450 4A12A**	**1.925633831**	**0.98785**	**2**
Q91WL5	FELLPDPTR	1.077707421	2	2.66626
Q91WL5	IQLQDEEELEK	0.945299838	2	2.48758
Q91X77	**CY250 Cytochrome P450 2C50**	**1.90934966**	**0.57504**	**5**
Q91X77	EHEESLDVTIPR	0.73436731	2	2.30784
Q91X77	IKEHEESLDVTIPR	0.875796746	3	3.66349
Q91X77	NFLLEK	0.947047027	1	2.10253
Q91X77	NYFIPK	0.873072084	1	1.92056
Q91X77	YALLLLLK	0.71815008	2	2.92146
Q91X78	**ERLN1 Erlin_1**	**1.925497734**	**0.4194**	**4**
Q91X78	DLNTMAPGLTIQAVR	0.622078963	2	3.44246
Q91X78	ISEIEDAAFLAR	1.132855984	2	2.9784
Q91X78	RISEIEDAAFLAREK	1.183888547	2	2.30733
Q91X78	SVQTTLQTDEVK	0.845516555	2	3.09624

Q91Y78	**UCHL3 Ubiquitin carboxyl_terminal hydrolase isozyme L3**	**1.854737376**	**0.86869**	**2**
Q91Y78	FLEESVAMSPEER	1.015120091	2	3.26073
Q91Y78	HLENYDAIR	0.859249338	2	2.58245
Q91Y81	**SEPT2 Septin_2**	**2.055458259**	**0.8622**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	1.094967275	2	2.66018
Q91Y81	ILDEIEEHSIK	0.978766945	2	2.65335
Q91Y81	KVENEDMNKDQILLEK	0.945108821	3	3.69238
Q91Y81	LTVVDTPGYGDAINSR	0.882667718	2	4.37815
Q91YP0	**L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial**	**1.831777899**	**0.99851**	**3**
Q91YP0	LIQQEDIK	0.99777923	2	2.40078
Q91YP0	LIVAVEQEEIPR	0.873664922	2	2.80304
Q91YP0	NAPSPAATSSLAISR	0.835158225	2	3.29706
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**2.058374695**	**0.70978**	**10**
Q91YT0	GAGAYICGEETALIESIEGK	1.421434934	2	2.57513
Q91YT0	GDARPAEIDSLWEISK	1.244161491	2	2.87714
Q91YT0	GEFYNEASNLQVAIR	1.195654129	2	3.55235
Q91YT0	GGAGFPTGLK	0.970640013	2	2.37067
Q91YT0	HFRPELEDR	1.147476526	2	2.33197
Q91YT0	KTSFGSLKDEDR	0.895791671	2	3.48027
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.543241272	3	4.19768
Q91YT0	LVEGCLVGGR	1.125777019	2	2.7434
Q91YT0	TSFGSLKDEDR	1.010834882	2	2.49589
Q91YT0	YLVVNADEGEPGTCK	1.036647609	2	4.94173
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.884071251**	**1.1E-12**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.18308848	3	6.77683
Q91Z53	LLDAAGANLR	1.033693021	2	3.26251
Q91Z53	NCVILPHIGSATYK	0.910788202	2	3.70573
Q91Z53	NTMSLLAANNLLAGLR	1.760654156	2	4.73976
Q91Z53	RLPEAIEEVK	0.81083095	3	3.30049
Q91Z53	VISTLSVGVDHLALDEIK	1.487747014	2	4.75026
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**2.189321145**	**0.99937**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	1.107560209	2	4.69947
Q91ZJ5	GGTLTQYEGK	0.985101852	2	2.37103
Q91ZJ5	GLPDNISSVLNK	1.309570053	2	3.37689
Q91ZJ5	GTVIIIANHGDR	1.115887061	2	3.00819
Q91ZJ5	IDIPPGAVLENK	1.219258082	2	2.87701
Q91ZJ5	IQRPPEDSIQPYEK	1.072222347	3	5.17817
Q91ZJ5	LNGGLGTSMGCK	1.385151222	2	2.96923
Q91ZJ5	LVEIAQVPK	1.132441055	2	3.45131
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.116524389	2	5.0521
Q91ZJ5	RCEFVMEVTNK	0.790433095	2	2.37589
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	1.575734482	3	3.33507
Q91ZJ5	SFENSLGINVPR	1.114820997	2	3.44256
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	0.911157379	2	5.31327
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	0.950998656	2	4.49399
Q91ZU6	**DYST Dystonin**	**1.827731333**	**0.71416**	**2**
Q91ZU6	LDMLQQIATR+Oxidation(2	1.240910348		
Q91ZU6	SAETNIDQDITNLK	0.85438917	2	2.37363
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**2.82512393**	**0.7103**	**2**
Q91ZV0	CGDLECETLISRVLALR	2.120710582	2	2.41905
Q91ZV0	KMLDQDDIVENDK+Oxidation(1	1.19489481		

Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.77331028**	**0.00241**	**6**
Q91ZX7	CLQGACVVNK	1.177157852	2	2.43256
Q91ZX7	GCHVNECLSR	0.814219528	2	2.70352
Q91ZX7	ILQEDFTCR	0.904822597	2	2.4945
Q91ZX7	MYDAQQQQVGTNK	1.019043836	2	4.43759
Q91ZX7	TVLWPNGLSLDIPAGR	0.634765957	2	2.49056
Q91ZX7	VFFTDYGQIPK	0.997486177	2	3.27737
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**2.155180734**	**0.88204**	**2**
Q920A6	GLAEVSDIAEQVLNAVNK	1.077439804	3	5.64574
Q920A6	NTDGVNFYNILTK	1.143698571	2	2.91284
Q920D2	**DYR Dihydrofolate reductase**	**2.397440796**	**6.4E-11**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	1.283077095	2	4.6773
Q920D2	LIEQPELASK	0.904145115	2	3.00358
Q920D2	LLPEYPGVLSEIQEEK	1.320335813	2	3.70405
Q920D2	NGDLPWPLLR	1.259760484	2	3.2312
Q920F3	**KHDR2 KH domain_containing_ RNA_binding_ signal transduction_associated protein 2**	**1.973713532**	**0.8809**	**2**
Q920F3	LQEETGAKMSILGKGSMR+Oxidation(8	1.192632374		
Q920F3	MSHALEEIKK	0.980857318	1	2.2597
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**1.845024281**	**0.98393**	**5**
Q920F5	ADLLEAQALK	0.911310925	2	2.33896
Q920F5	EIAEVTGDPVHESLK	0.879680903	2	3.43761
Q920F5	ISECEAVHPVK	0.870095159	2	3.35816
Q920F5	LCSGLTASAMDELLR	0.956119846	2	2.30838
Q920F5	WLLGLLNVQGK	1.015387547	2	3.38123
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.960328479**	**0.85772**	**4**
Q920J4	AGCECLNESDEHGFDNCLR	1.115572013	3	4.03823
Q920J4	IDQYQGADAVGLEEK	0.939053178	2	4.82367
Q920J4	QHLENDPGSNEDTDIPK	1.432037057	2	2.38512
Q920J4	SEPTQALELTEDDIKEDGIVPLR	1.866237104	2	3.40548
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**2.194763142**	**0.8206**	**18**
Q920L2	ACALSIAESCRPGDK	0.599482215	2	2.87019
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.119230998	3	4.5069
Q920L2	ANAGEESVMNLDK	1.148837732	2	3.64589
Q920L2	GEGGILINSQGER	0.817390175	2	4.06212
Q920L2	GVIALCIEDGSIHR	0.961724053	2	3.35516
Q920L2	HTLSYVDTK	1.139321747	2	2.4893
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.027415179	3	6.76002
Q920L2	IDEYDYSKPIEGQQK	5.220100643	2	4.47603
Q920L2	KHTLSYVDTK	0.77768731	2	2.76582
Q920L2	NTIIATGGYGR	1.010273039	2	2.78549
Q920L2	SMQSHAAVFR	1.088875461	2	2.69007
Q920L2	TGHSLLHTLYGR	0.546399645	2	2.95551
Q920L2	TLNEADCATVPPAIR	0.941068965	2	3.69084
Q920L2	TYFSCTSAHTSTGDGTAMVTR	0.93448824	2	5.69867
Q920L2	VGSVLQEGCEK	0.985087869	2	3.54096
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	1.056453817	3	4.92184
Q920L2	VSQLYGDLQHLK	1.079716196	2	3.49626
Q920L2	VTLDYRPVIDK	0.877720068	2	2.97589
Q920P0	**DCXR L_xylulose reductase**	**2.106724768**	**0.73817**	**7**
Q920P0	ALTNHTVYCSTK	1.157000522	2	3.15117
Q920P0	AVVQVSQIVAR	1.105834976	2	3.16954
Q920P0	GVPGAIVNVSSQASQR	1.009813178	2	5.78407
Q920P0	SSMTTGSALPVDGGFLAT	1.199896025	2	2.85738
Q920P0	STVLALQAAGAQVVAVSR	1.130964839	2	3.9189

Q920P0	TREDLDSLVR	0.929280289	2	2.96284
Q920P0	VNAVNPTVVMTPMGR	1.389103759	2	3.44197
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.934527309**	**0.59295**	**5**
Q921F2	FGGNPGGFGNQGGFGNSR	0.97899336	2	4.41305
Q921F2	FTEYETQVK	1.120014109	2	2.63626
Q921F2	GISVHISNAEPK	0.777740771	2	2.52892
Q921F2	KDLKTGHSK	0.94637738	2	2.4425
Q921F2	TSDLIVLGLPWK	1.166352112	2	3.27269
Q921M3	**SF3B3 Splicing factor 3B subunit 3**	**1.964025418**	**0.5724**	**3**
Q921M3	FLAVGLVDNTVR	1.331123069	2	2.83468
Q921M3	LPPNTNDEVDEDPTGNK	0.721226976	2	2.6862
Q921M3	TVLDPVTGDLSDTR	1.116584313	2	2.66564
Q922F4	**TBB6 Tubulin beta_6 chain**	**2.206101613**	**0.00446**	**7**
Q922F4	ALTVPELTQQMFDAK	1.220573873	2	3.98424
Q922F4	ALTVPELTQQMFDAK+Oxidation(10	1.104458109		
Q922F4	GHYTEGAELVDSVLDVVR	1.209190885	2	6.63607
Q922F4	IREEYPDR	1.054968123	2	2.97651
Q922F4	MASTFIGNSTAIQELFK	1.413119484	2	4.34616
Q922F4	NMMAACDPR	1.141170884	2	2.75148
Q922F4	NSSYFVEWIPNNVK	1.200855616	2	4.74812
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**2.005310409**	**0.99945**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4	1.009543158		
Q922J3	HEEILQNLQKMLADTEDK	0.965533486	2	2.33487
Q923D2		**2.159651233**	**0.99961**	**4**
Q923D2	HDLGHFMLR	1.039486221	3	3.3618
Q923D2	LQDVTDDHIR	1.116442591	2	3.16677
Q923D2	TGLTTLAQAVQAGYEVTVLVR	1.029439801	3	4.15661
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	1.070200401	3	4.19365
Q923K9	**A1CF APOBEC1 complementation factor**	**2.466575063**	**0.05776**	**3**
Q923K9	LAPQILEEICQK	1.713349904	2	2.90155
Q923K9	TGYSLVQENGQR	0.899075142	2	2.51915
Q923K9	VTEGVVDVIVYPSAADK	1.124987516	2	3.78576
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**2.19721649**	**0.607**	**2**
Q923M1	SAVYPTSAVQMEAALK	1.487182017	2	4.21521
Q923M1	VISAEEALPGR	0.980526204	2	2.91798
Q923V8	**SEP15 15 kDa selenoprotein**	**2.311170702**	**0.88568**	**3**
Q923V8	GCCQEEAQFETK	0.999312378	2	4.15683
Q923V8	LLDDNGNIAEELSILK	1.31802887	2	4.0781
Q923V8	WNTDSVEEFLSEK	1.410470172	2	2.76854
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**3.367971597**	**0.69757**	**5**
Q924C3	AEYLHTWGGLLPVISK	1.335555628	3	3.91723
Q924C3	ELESPAAASLLAPMDLGEEPLEK	2.044514562	2	4.40713
Q924C3	GQPIWVTANHQEVR	0.857962266	2	3.3361
Q924C3	SGTYFWPGSDVEIDGILPDIYK	1.192359055	2	2.51833
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	1.569167471	2	3.87963
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.964443652**	**0.98806**	**14**
Q924S5	AGVTCIILPAENR	0.865936233	2	2.31455
Q924S5	AQLSATVLTLLIK	0.68046262	2	3.45383
Q924S5	AQSVLEEDHYGMEDVK	0.874594179	2	4.26816
Q924S5	EHQEALAVER	0.989444175	2	2.51945
Q924S5	ELGLEKDDKDAIEEK	0.849035933	2	3.74027
Q924S5	FSVGGMTDVAEIK	1.064426296	2	3.07037
Q924S5	GYQGDPSSALLELLDPEQNANFLDHYLDVPVDLSK	1.219521041	3	5.09929
Q924S5	HVMDVVDEELSK	0.779795379	2	3.62586

Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.185920117	3	5.92571
Q924S5	MEMINVSGYVAQEK	3.345947945	2	2.66099
Q924S5	QLEVEPEGLEPEAENK	0.964926757	2	4.35001
Q924S5	QSDENLDLAR	1.004985646	2	2.46775
Q924S5	TENPLVLIDEVDK	1.209781391	2	2.99689
Q924S5	VLEFIAVSQLR	1.264958154	2	2.77648
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**2.18178765**	**0.81996**	**2**
Q924W5	ELDMKEKELQEK	1.949297095	2	2.373
Q924W5	TKEQINQGEERLTELK	1.055981233	2	2.55773
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**2.398209795**	**0.01399**	**4**
Q99020	EYFGQFGEIEAIELPIDPK	1.409269299	2	3.56033
Q99020	FGEVVDCTIK	0.50079546	2	3.20895
Q99020	IFVGGLNPEATEEK	1.370627222	2	4.17422
Q99020	MFVGGLSWDTSK	1.505849967	2	2.55725
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**1.868753322**	**0.98437**	**2**
Q99068	EELKHFEAKIEK	0.89106006	2	2.43955
Q99068	HVESIGDPEHISR	0.903539649	3	4.12023
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**2.499997352**	**0.70662**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.731186247	2	2.98469
Q99JI4	RLDEELEDAEK	1.23919305	2	3.18615
Q99JI4	VNEIVETNRPDSK	1.321589295	2	3.70418
Q99JW2	**ACY1 Aminoacylase_1**	**2.009088286**	**0.92066**	**3**
Q99JW2	FIEDTAAEK	1.014903284	2	2.69077
Q99JW2	SVSIQYLEAVR	1.538802516	2	2.56252
Q99JW2	TIHMTFVPDEEVGGHK	0.95748372	3	3.91934
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**2.015366327**	**0.55589**	**2**
Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(13	0.992052401		
Q99KK9	YDLTVPFAR	1.249749834	2	2.36435
Q99KN9	**EPN4 Clathrin interactor 1**	**1.894675232**	**0.98708**	**3**
Q99KN9	GEFKDEEETVTTK	0.993513813	2	3.58409
Q99KN9	HIHITQATETTTTR	0.853094485	2	3.35389
Q99KN9	IGSTIDDTISK	1.029543092	2	2.55054
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**1.737789049**	**0.99038**	**3**
Q99L04	ATAQEAQSLGGR	0.77417407	2	3.32304
Q99L04	CVPVVCDSSQESEVK	0.796887125	2	4.30699
Q99L04	GQVCVVTGASR	1.025440705	2	2.812
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**2.055804846**	**0.97542**	**5**
Q99LF4	GLGHQVATDALVAMEK	1.001391846	2	3.69262
Q99LF4	NLDFQDVLDK	1.319113761	2	3.08327
Q99LF4	NVTDVVNTCHDAGISK	1.009654205	2	4.33442
Q99LF4	NYNDELQFLDK	1.777773225	2	3.18358
Q99LF4	TNLDESDVQPVK	1.495709781	2	3.46662
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**2.046357765**	**0.98865**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11	1.033058394		
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5	1.033058394		
Q99M73	**KRT84 Keratin_ type II cuticular Hb4**	**1.854633709**	**0.99787**	**2**
Q99M73	CKLADLEGALQQAKQDMAR	1.111092117	2	2.67274
Q99M73	EYQELMNVK	0.889372308	1	2.09333
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**1.92926274**	**0.69217**	**2**
Q99M87	GGPSVDPEELFR	1.119223094	2	2.3512

Q99M87	GSIITNPCVVCR	0.946495102	2	2.97703
Q99ML5	**PCYOX Prenylcysteine oxidase**	**1.984976353**	**0.46042**	**2**
Q99ML5	ELGLSSVPASGGLVGVYNGK	1.709338006	2	2.97188
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	0.926300092	3	4.82437
Q99MS0	**S14L2 SEC14_like protein 2**	**2.124515485**	**0.68641**	**6**
Q99MS0	AGEMTEVLPNQR	1.087206178	2	3.56896
Q99MS0	AGEMTEVLPNQR+Oxidation(3	0.908907874		
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	0.966749147	3	4.96753
Q99MS0	INYGGDIPK	0.879549613	2	2.41994
Q99MS0	QQYEHSVQISR	0.911452153	2	2.39323
Q99MS0	YNSHMVPEDGTLTCSEPGIYVLR	1.370897464	3	3.57075
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**2.398294741**	**0.90603**	**8**
Q99MZ8	GFSVVADTPELQR	0.875525474	2	3.64757
Q99MZ8	MGPSGGEGIEPER	0.909917248	2	3.35693
Q99MZ8	MGPSGGEGIEPERR	0.886333079	2	2.42232
Q99MZ8	QQSELQSQVR	0.868234792	2	2.98442
Q99MZ8	QSFTMVADTPENLR	0.854990253	2	3.56272
Q99MZ8	TGDTGMLPANYVEAI	1.631994422	1	2.20438
Q99MZ8	TQDQISNIK	0.850148419	2	2.70913
Q99MZ8	YHEEFEK	0.765314572	2	2.41015
Q99N27	**SNX1 Sorting nexin_1**	**1.886084773**	**0.55824**	**2**
Q99N27	LQEVECEEQR	0.867873721	2	2.49566
Q99N27	SLAMLGSSEDNTALSR	1.292889986	2	3.11309
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**2.412416441**	**0.85288**	**4**
Q99NA5	ENTEGEYSGIEHVIVDGVVQSIK	1.14511104	3	3.34318
Q99NA5	HMGLFDHAAK	1.271392665	3	3.41
Q99NA5	IEAACFATIK	1.54858222	2	2.61438
Q99NA5	NVTAIQGPGGK	1.038947262	2	2.54209
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**1.821899921**	**0.82175**	**2**
Q99NB7	GSISNTNVEALK	0.953641314	2	2.56565
Q99NB7	KGSISNTNVEALK	0.763783783	2	3.25764
Q99NB9	**SF3B1 Splicing factor 3B subunit 1**	**2.101604723**	**0.75491**	**3**
Q99NB9	EWMRICFELLELLK+Oxidation(2	1.072037216		
Q99NB9	GDTPGHATPGHGGATSSAR	0.681815566	3	3.77355
Q99NB9	WDQTADQTPGATPK	0.551724683	2	2.515
Q99P39	**NFS1 Cysteine desulfurase_ mitochondrial**	**1.933276166**	**0.24527**	**2**
Q99P39	AIGTDEDLAHSSIR	0.541303923	2	2.71838
Q99P39	VEALQSGGGQER	0.995110245	2	2.99854
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**2.277594165**	**0.36441**	**9**
Q99PF5	AINQQTGAFVEISR	1.157745228	2	3.49093
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	1.132692676	2	6.94084
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.269397395	2	4.96503
Q99PF5	IGQQPQQPGAPPQQDYTK	1.187511302	2	4.04874
Q99PF5	IINDLLQSLR	1.49690986	2	3.1882
Q99PF5	SVSLTGAPESVQK	0.84901691	2	2.56959
Q99PF5	VGGGIDVPVPR	0.848628728	2	3.21116
Q99PF5	VQISPDSGGLPER	0.798733561	2	2.48671
Q99PF5	VQQACEMVMDILR	1.006325395	2	2.34838
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**2.178078001**	**0.81816**	**20**
Q99PL5	AMEALALAER	1.156122136	2	2.93254
Q99PL5	DALNQATSQVESK	0.945220471	2	3.6129
Q99PL5	EAEETQNSLQAECDQYR	0.978272911	2	5.36002
Q99PL5	EHTSHLEAELEK	0.993737017	2	3.49551
Q99PL5	EQEIAAVQAR	1.602355736	2	2.48333
Q99PL5	GELESSDQVR	1.11918286	2	3.13698
Q99PL5	HLEDIVEK	1.236141824	2	2.38287

Q99PL5	HMAAASAECQNYAK	1.055037822	2	4.47872
Q99PL5	HMAAASAECQNYAK+Oxidation(1	1.149230375		
Q99PL5	IQEELEK	0.914217935	1	2.33836
Q99PL5	LIEILSEK	1.314921918	1	2.15009
Q99PL5	LKELESQVSCLEK	1.023250959	2	4.27782
Q99PL5	LLATEQEDAAVAK	1.032342852	2	3.70648
Q99PL5	LQQENSILR	0.78510728	2	2.67997
Q99PL5	LQSSEVEVK	1.197661269	2	2.73472
Q99PL5	QLLLESQSQLDEAK	0.850778174	2	2.3343
Q99PL5	TILAETEGMLK	1.898563361	2	2.78465
Q99PL5	TLQEQLENGPNTQLAR	1.025752933	2	5.0442
Q99PL5	TLVSTVGSMVFSEGEAQR	1.615554571	3	4.52774
Q99PL5	VEPAVSSIVNSIQVLASK	1.233595912	2	4.42531
Q99PP2		**1.882427473**	**1**	**69**
Q99PP2	AAGSLLTDECR	0.90607651	2	2.99542
Q99PP2	ADSAEYSVMTTGGQSSAK	1.732306741		
Q99PP2	AEVSELPSVVR	0.965862456	2	3.11991
Q99PP2	ALLTPVAIAAGR	1.534453079		
Q99PP2	ASMMGQRASLLTAR+Oxidation(2)Oxidation(3	0.959166528		
Q99PP2	AVAENQPFLIEAMTYR	0.858059879	2	3.5909
Q99PP2	AVDEAADALLK	1.19812902	2	2.59679
Q99PP2	DQMVKNNHFTLK+Oxidation(2	1.010687098		
Q99PP2	EEKIEKK	0.842680964		
Q99PP2	EELEKMK	0.674216266	1	1.93655
Q99PP2	EIAGATPYITAAEEK	1.583130621	2	3.12933
Q99PP2	EKMNKPELFNGGEKK	1.343034013		
Q99PP2	ELDSITPDITPGWK	1.237262606	2	2.938
Q99PP2	EQVIESRRQMQAVK	1.911151226		
Q99PP2	FEFEQDLSEK	1.020674388	2	2.6752
Q99PP2	FFRPHFLQAPGDLTVQEGK	1.113479642		
Q99PP2	FKLINSTNIR	1.486749505		
Q99PP2	GIEQAVQSHAVAEEEAR	1.155115636	2	4.97611
Q99PP2	GNIYSLNEGYAK	1.050529805	2	3.99729
Q99PP2	GSAAAAATTSTREAEGAERR	0.975321821		
Q99PP2	GVYSEETLR	0.928875611	2	2.46495
Q99PP2	HFVTISSPLATQIPQAVGAAYAAK	1.152202489	2	4.91951
Q99PP2	HLQTYGEHYPLDHFDK	0.886011177	3	3.69136
Q99PP2	HVIHTVGPIAVGQPTASQAAELR	0.919366863	3	5.34375
Q99PP2	IENWPFSIKPTLR	1.621520901		
Q99PP2	IGHHSTSDDSSAYR	1.31071369	3	4.53531
Q99PP2	INLSNNK	1.116690265		
Q99PP2	KAMQEINYGPSPDNSIKLVR	1.228111187		
Q99PP2	KGNIYSLNEGYAK	0.699093339	2	4.48673
Q99PP2	KLQHELEEAEER	1.350743079	3	4.11516
Q99PP2	LEFIQPNVISGIPIYR	1.040860393	2	2.43712
Q99PP2	LFDDRLESIIQK	0.200390318		
Q99PP2	LGDAVEQGVINNSVLGYFIGR	0.900092977	2	3.79255
Q99PP2	LIEVEGPNSLGK	1.107557079		
Q99PP2	LKLVMNNFIYQTK	1.060687079		
Q99PP2	LMQVNDTLTSEDAGLR	0.799067904		
Q99PP2	LQHELEEAEER	1.471771077	2	3.69329
Q99PP2	LQHELEEAEERADIAESQVNK	1.605468171	3	3.88024
Q99PP2	MKKNMEQTVK+Oxidation(4	1.024922046		
Q99PP2	MNLQDELDELK	0.936910973	2	2.3215
Q99PP2	MNLQDELDELK+Oxidation(0	0.896004363		
Q99PP2	MQQVEASLQPETLK+Oxidation(0	1.44089127		
Q99PP2	MQQVEASLQPETLKK+Oxidation(0	1.852116423		

Q99PP2	NESGLDSGRSQR	1.083716226		
Q99PP2	NNGYAISTPTSEQYR	0.873481212	2	3.81349
Q99PP2	QGQIINPSEDPHLPQEEVLK	0.617565919	2	2.64279
Q99PP2	QRAEQETKLK	1.152180771		
Q99PP2	QTCLKTVVLLTDNK	1.098560118		
Q99PP2	QTITAQNAAVQAVK	1.06432632	2	3.96323
Q99PP2	QYLLNQGWWDEEQEK	1.091270248	2	3.43724
Q99PP2	RAALQAEIEELR	4.757268944	2	3.75052
Q99PP2	RFSTEVGSDCVSDNDR	2.001121619		
Q99PP2	SCYDLSCHAR	1.007228885	2	2.33992
Q99PP2	SCYLSSLDLLLEHR	1.307216265	2	2.63077
Q99PP2	SLEDALNQTATVTR	1.064917138	2	4.42391
Q99PP2	SMTLLNTMDR	1.119721931	2	2.75019
Q99PP2	SVDEVNYWDK	1.061279138	2	2.56256
Q99PP2	TAMDNSEIAGEK	0.995312723	2	2.41014
Q99PP2	TAMDNSEIAGEKK	1.12074282	2	2.50219
Q99PP2	TLHVEEVVPSVIEPSFGLGR	1.069046131	3	3.68518
Q99PP2	TSSAEMPTIPLGSAVEAIR	0.895563236	2	3.88487
Q99PP2	TWTAADMAAQITR+Oxidation(6	1.233732556		
Q99PP2	VDDSSGSIGR	0.912661008	2	2.86711
Q99PP2	VDGNDVFAVYNATK	0.716467695	2	2.85901
Q99PP2	VMEAFEQAER	0.851462141	2	3.28826
Q99PP2	VTMQNKISEATQEEDRL+Oxidation(2	0.901863356		
Q99PP2	VVSQYHELVVQAR	1.768434694	2	3.52323
Q99PP2	YNENHQHGK	0.631615992		
Q99PP2	YSTSSSSGVTAGK	0.788994072	2	2.89248
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**2.454808313**	**0.99502**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(10	1.295610374		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(9	1.295610374		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**2.010622568**	**1**	**2**
Q9CPQ1	FGVAEPR	1.0465407	2	2.45255
Q9CPQ1	NYDSMKDFEEMR	0.955211772	2	3.76256
Q9CQ75	**NDUA2 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2**	**2.128954452**	**0.95252**	**2**
Q9CQ75	EIRVHLCQRSPGSQGVR	1.11980199	2	2.33404
Q9CQ75	TVSLNNLSADEVTR	1.036802424	2	2.41194
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**2.026808375**	**0.99988**	**2**
Q9CQS8	FYTEDSPGLK	1.024040899	2	2.43288
Q9CQS8	TTSAGTGGMWR	0.998485385	2	2.34406
Q9CQZ5	**NDUA6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6**	**2.489265231**	**0.94279**	**3**
Q9CQZ5	EVPNTVHLMQLDITVK	1.111140493	2	2.49098
Q9CQZ5	FFHETETPRPK	1.108814904	2	2.90883
Q9CQZ5	VVDLLVIK	1.345469339	2	2.93884
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.898062359**	**0.99527**	**2**
Q9CRB9	VAEELALEQAK	0.923596432	2	3.64654
Q9CRB9	YEYHPVCADLQTK	0.930924747	2	3.78162
Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**2.322159364**	**0.84564**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.475759639	2	2.5715
Q9CTN4	LKDSGDVSDIIEK	0.878888569	2	2.46851
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**1.987247319**	**0.83473**	**2**
Q9CW42	DLLLPITPPATNPLLQCR	0.775365614	3	3.51864
Q9CW42	GLSVSEAECTAMGLR	1.002596495	2	3.90406

Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**2.26970248**	**0.00563**	**4**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	0.987553606	2	4.46849
Q9CWH6	ALLEVVQSGGK	1.018631949	2	3.03472
Q9CWH6	LTVEDPVTVEYITR	1.20328278	2	4.0456
Q9CWH6	LYQTDPSGTYHAWK	1.101270044	2	2.89263
Q9CWK8	**SNX2 Sorting nexin_2**	**2.15035902**	**0.67923**	**4**
Q9CWK8	AVNTQALSGAGILR	1.058836086	2	3.21274
Q9CWK8	QQQFENLDQQLR	1.041661681	2	2.51612
Q9CWK8	WEDAQITLLK	1.115762849	2	2.47912
Q9CWK8	YLESLVQTQQQLIK	1.231529669	2	4.00882
Q9CWL2	**CASZ1 Zinc finger protein castor homolog 1**	**2.273008674**	**0.32845**	**2**
Q9CWL2	ISASKGLISPMMAR+Oxidation(10	1.18460319		
Q9CWL2	ISASKGLISPMMAR+Oxidation(11	1.18460319		
Q9CXS4	**CENPV Centromere protein V**	**2.534751761**	**0.92025**	**2**
Q9CXS4	LLLDTFEYQGLVK	1.35395709	2	3.90584
Q9CXS4	SNPGGFGIAPHCLDEGTVR	1.078012581	2	2.56592
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**2.074794624**	**0.24771**	**2**
Q9CYN2	LHDSLATER	0.660080535	2	2.6823
Q9CYN2	YVENFGLIDGR	1.474370196	2	2.8862
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**2.551798048**	**0.98722**	**2**
Q9CYW4	LEDILTGLGLR	1.140203268	2	4.38331
Q9CYW4	RLEDILTGLGLR	1.351748426	3	3.53366
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**2.225569927**	**0.94235**	**3**
Q9CZY3	LLEELEEGQK	0.785758081	1	2.98371
Q9CZY3	VNMSGVSSSNGVVDPR	1.187576443	2	3.10704
Q9CZY3	WTGMIIGPPR	1.021463509	2	2.86174
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**1.739182317**	**0.99977**	**3**
Q9D024	ERIMNEEDPEKQR	0.96065774	2	2.45902
Q9D024	IMQEEGQPLKLPDTK	0.794490902	2	3.19694
Q9D024	RLEEAALR	1.186581183	2	2.60542
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**2.097422715**	**0.98967**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	1.535781838	3	4.23743
Q9D0M3	GLLSSLDHTSIR	3.571821349	2	3.02922
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.200785516	3	5.55728
Q9D0M3	HLVGVCYTEEEAK	1.070310402	2	3.83048
Q9D0M3	LSDYFPKPYPNPEAAR	0.975913926	3	3.89529
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**2.226674194**	**0.00237**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.922782977	2	2.94313
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.504192069	2	4.73959
Q9D0S9	SLPADILYEDQQCLVFR	1.294390886	2	3.54147
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**2.19455889**	**0.00026**	**3**
Q9D172	GVEVTVGHEQEEGGK	0.968805456	2	4.07892
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.393031769	3	4.59366
Q9D172	NLSTFAVDGK	0.970950462	1	2.44705
Q9D180	**WDR65 WD repeat_containing protein 65**	**1.860628963**	**0.66583**	**2**
Q9D180	ERDLEALVR	0.87615363	2	2.56195
Q9D180	KNQELEK	0.914217935	1	2.17912
Q9D1M7	**FKB11 Peptidyl_prolyl cis_trans isomerase FKBP11**	**2.231805811**	**0.83424**	**2**
Q9D1M7	IIDTSLTRDPLVIELGQK	0.981679156	3	3.42869
Q9D1M7	QVIPGLEQSLLDMCVGEK	1.170082036	2	3.19027
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.905306982**	**0.83485**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0	1.350790002		
Q9D1Q6	NIIGYFEQK	1.049636958	1	2.37718
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.142725667	2	5.56591
Q9D1Q6	VDCDQHSDIAQR	0.924470707	2	3.62531

Q9D2U9	**H2B3A Histone H2B type 3_A**	**2.237433521**	**0.99999**	**5**
Q9D2U9	AMGIMNSFVNDIFER	1.088660375	2	5.12262
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1	1.219696127		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)Oxidation(4	0.876539625		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4	1.127707393		
Q9D2U9	LLLPGELAK	1.149133889	2	2.5265
Q9D417	**FBX24 F_box only protein 24**	**2.053924536**	**0.82643**	**2**
Q9D417	MKEIVGWMPLMAAQK+Oxidation(7	1.343034013		
Q9D417	RSCPSCGLEAGSEKK	1.031060805	2	2.4098
Q9D662	**SC23B Protein transport protein Sec23B**	**2.687407105**	**0.33732**	**2**
Q9D662	HLLQAPLDDAQEILQAR	1.441616818	3	3.98888
Q9D662	IDMNLTDLLGELQR	1.425208545	2	4.12283
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**2.185685716**	**0.96733**	**3**
Q9D6M3	GAAVNLTLVTPEK	1.242274955	2	3.3446
Q9D6M3	GVNEDTYSGFLDCAR	1.048430792	2	4.71079
Q9D6M3	NHGIAGLYK	0.982430606	1	2.21762
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**2.017959693**	**0.92295**	**11**
Q9D6Y9	CVAYAESHDQALVGDK	1.50759783	2	5.01181
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	0.952148377	3	3.30356
Q9D6Y9	FLNNFDR	1.321413913	2	2.40365
Q9D6Y9	GTHDLWDSR	1.389500851	2	2.74207
Q9D6Y9	GYESFGIHR	1.310370602	2	2.37497
Q9D6Y9	IVLDSDAAEYGGHQR	0.934826233	2	4.55543
Q9D6Y9	IYESHVGISSHEGK	1.306456303	2	4.5919
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.366638778	3	3.46496
Q9D6Y9	QFNLTDDDLLR	1.540725009	2	2.73187
Q9D6Y9	RQFNLTDDDLLR	1.00515016	2	3.20689
Q9D6Y9	WELYIPPK	1.560495924	2	2.5054
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.699880051**	**0.17767**	**2**
Q9D6Z1	ELNEEKLEK	0.737093433	2	2.44064
Q9D6Z1	IDCFSEVPTSVFGEK	1.551826079	2	2.53695
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.903119185**	**0.9532**	**6**
Q9D7B6	AVIFEDCAVPVANR	0.931332612	2	3.80757
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	1.490484657	2	4.50287
Q9D7B6	IGTEGQGFLIAMK	0.912881015	2	3.01147
Q9D7B6	TAAVALQEER	0.889564164	2	3.19025
Q9D7B6	TDVGGSGLSR	0.872116798	2	2.50662
Q9D7B6	VHQILEGSNEVMR	1.458647406	2	3.39504
Q9D7P6	**ISCU Iron_sulfur cluster assembly enzyme ISCU_ mitochondrial**	**1.854549703**	**0.79417**	**2**
Q9D7P6	NVGTGLVGAPACGDVMK	0.892019605	2	3.61298
Q9D7P6	VVDHYENPR	0.763453806	2	2.51709
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**2.060946711**	**0.97807**	**2**
Q9D7X8	ISDEMEDIIK	1.274858958	2	2.74569
Q9D7X8	SNISSLDEQEGVK	1.040109035	2	3.43341
Q9D819	**IPYR Inorganic pyrophosphatase**	**2.159662357**	**0.86664**	**5**
Q9D819	GISCMNTTVSESPFK	1.137339776	2	5.1814
Q9D819	GQYISPFHDVPIYADK	1.477634382	2	3.20145
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.124857462	3	5.18851
Q9D819	VLGILAMIDEGETDWK	1.020391196	2	4.11798
Q9D819	YVANLFPYK	1.022033232	1	2.05646
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**2.279904149**	**0.70456**	**3**
Q9D880	TIALNQVEDVR	0.890823809	2	2.95796
Q9D880	TVLEHYALEDDPLEAFK	1.168730671	2	4.70519
Q9D880	VLLDLSAFLK	1.277099018	2	2.34876

Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**2.506617051**	**0.87449**	**3**
Q9D8W5	LQEVIETLLSLEK	1.082077331	2	3.79144
Q9D8W5	TASDMVSTSR	1.325582741	2	2.34834
Q9D8W5	WSTLVEDYGVELR	2.61125504	2	3.12653
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**1.82480316**	**0.58538**	**3**
Q9DB15	KLVESLPQEIK	0.867295643	2	3.00219
Q9DB15	NYVQGINLVQAK	1.14178388	2	2.49881
Q9DB15	SEALAGAPLDNAPK	0.667509892	2	2.3292
Q9DBC0	**SELO Selenoprotein O**	**1.917270297**	**0.79022**	**2**
Q9DBC0	LGLIRVEK	0.938537674	2	2.30264
Q9DBC0	LLESPYHSEEEATGPEAVAR	1.076991136	3	3.36063
Q9DBG7	**SRPR Signal recognition particle receptor subunit alpha**	**2.12832805**	**0.7792**	**2**
Q9DBG7	GLVGSKSLSREDMESVLDK+Oxidation(12	1.083778611		
Q9DBG7	NQGFDVVLVDTAGR	1.127004027	2	2.91026
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**2.079621361**	**0.93534**	**2**
Q9DBH5	TPEEESIDWTK	1.60540957	2	2.47024
Q9DBH5	WSELAGCTADFR	1.056276276	2	3.36558
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**2.4308883**	**0.43786**	**4**
Q9DC70	LDDLINWAR	1.227316477	2	3.04387
Q9DC70	MAPALRKVYDQMPEPR+Oxidation(0)Oxidation(11	1.143775741		
Q9DC70	QADVMIVAGTLTNK	1.425997394	2	3.52124
Q9DC70	VYDQMPEPR	1.922250622	2	2.45812
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**2.036476199**	**0.41653**	**2**
Q9DCH4	FLMSLVNQVPK	1.445451138	2	2.76412
Q9DCH4	VIGLSSDLQQVGGASAR	1.008723754	2	4.69164
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.826615962**	**0.01559**	**2**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.758108989	3	4.31114
Q9DCM0	SLLPGCQSVISR	0.802385827	2	2.98589
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**2.161550587**	**0.66607**	**2**
Q9DCS9	AYDLVVDWPVTLVR	1.101789616	2	4.657
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.328355436	2	3.44819
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**2.751420752**	**0.85819**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.594459142	2	3.22539
Q9DCT2	ILTDYGFEGHPFR	1.150267186	2	2.80008
Q9DCT2	KFDLNSPWEAFPAYR	1.417676549	2	3.55867
Q9DCT2	SLADLTAVDVPTR	1.271377256	2	3.4189
Q9DCT2	VVAEPVELAQEFR	0.961540955	2	3.78415
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**2.022658349**	**0.76129**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.097380435	2	5.34437
Q9DCU9	LIEPNTAVTR	1.011316237	2	3.35929
Q9DCU9	TMDWFGYYGGPCR	1.173803951	2	3.6921
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**2.807371314**	**0.07754**	**2**
Q9EP75	DEDGKELSDEDIR	2.017688855	2	3.02796
Q9EP75	IFNDSTNIMHAK	1.46392297	2	3.67793
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**2.055175638**	**0.00236**	**10**
Q9EP89	EVWSEGLGYADVENR	1.033886565	2	3.83023
Q9EP89	FENSIESLR	0.856942493	2	2.75824
Q9EP89	GIIVSIICNMQSVGLNSTALK	1.017117919	3	3.96068

Q9EP89	IFHDLDMLTTVQEENEPVIYNR	2.087665645	2	5.67587
Q9EP89	IKDEVGAPGIVVGVSVDGK	1.067502415	2	4.54509
Q9EP89	KNDFEQGELYLK	0.641782605	2	3.99431
Q9EP89	LDLDLPVQHYVPEFPEK	1.622522007	3	3.7387
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.386334862	3	3.98909
Q9EP89	LVNTPYVDNSYK	0.882961367	2	3.16289
Q9EP89	WAGGGFLSTVGDLLK	1.433511783	2	4.43359
Q9EPH2	**MRP MARCKS_related protein**	**1.895354249**	**0.99865**	**2**
Q9EPH2	AAATPESQEPQAK	1.032351997	2	2.44346
Q9EPH2	GDVTAEEAAGASPAK	0.88368669	2	3.30681
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**2.357222569**	**0.79229**	**10**
Q9EPH8	ALDTMNFDVIK	1.111019141	2	3.28561
Q9EPH8	GFGFVSFER	1.588296638	2	2.73177
Q9EPH8	GYGFVHFETQEAAER	1.08002424	2	3.29591
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	1.681891006	3	3.81052
Q9EPH8	KEFSPFGTITSAK	1.165500108	2	3.36882
Q9EPH8	NFGEDMDDER	10.11003413	2	2.56251
Q9EPH8	NLDDGIDDER	0.997470399	2	2.36495
Q9EPH8	SGVGNIFIK	1.084125338	2	2.76801
Q9EPH8	SKVDEAVAVLQAHQAK	1.141553924	2	5.10185
Q9EPH8	VDEAVAVLQAHQAK	1.499773081	2	2.85554
Q9EPJ0	**NUCKS Nuclear ubiquitous casein and cyclin_dependent kinases substrate**	**1.652286323**	**0.61695**	**2**
Q9EPJ0	NSQEDSEDSEEKDVK	0.719524659	2	3.54184
Q9EPJ0	TPSPKEEDEEAESPPEK	1.595678677	2	2.31661
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**3.714049274**	**9.9E-20**	**13**
Q9EQ76	ASIYQSVFTNSSK	1.656929132	2	3.1403
Q9EQ76	GTCILPSVNDMMDDIDEK	3.199947162	2	3.93977
Q9EQ76	ILCGTVSIKPNVK	1.074409706	2	3.00218
Q9EQ76	KEPVFNDELPAR	2.708798103	3	3.60438
Q9EQ76	LQEYITSFATEK	3.153143634	2	3.54957
Q9EQ76	NNEVTLYK	2.939844473	2	2.49475
Q9EQ76	NNLPTAISDWWYMK	2.240727606	2	2.50337
Q9EQ76	SCLEEGLEPTCFER	1.626487287	2	4.31256
Q9EQ76	SDDVGGLWK	2.927984759	2	2.92234
Q9EQ76	VAVIGAGVSGLAAIR	6.77279499	2	4.19912
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	1.611591556	3	3.69841
Q9EQ76	VWNDGYPWDMVVITR	2.08415939	2	3.88801
Q9EQ76	YIQFETLVTR	3.905728603	2	3.18684
Q9EQG6	**KDIS Kinase D_interacting substrate of 220 kDa**	**2.686220255**	**0.40444**	**2**
Q9EQG6	HLLAMGADVDQEGANSMTALIVAVK+Oxidation(4	1.661766194		
Q9EQG6	SSERPSLFQTDLKLK	1.251488521	2	2.32997
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**2.245234485**	**0.9776**	**8**
Q9EQH3	HFHNTLEHLR	1.435975879	3	3.43914
Q9EQH3	IREDLPNLESSEETEQINK	1.115977446	2	5.51478
Q9EQH3	LFDIFSQQVATVIQSR	1.659086127	3	3.32909
Q9EQH3	LLDEAIQAVK	0.89126097	2	2.5808
Q9EQH3	LNLEHIATSSAVSK	1.249596333	2	4.2774
Q9EQH3	LSQLEGVNVER	1.145285411	2	3.01868
Q9EQH3	NIIIALIDR	1.501957305	2	2.41171
Q9EQH3	VLETTVEIFNK	1.164165546	2	2.87067
Q9EQS0	**TALDO Transaldolase**	**1.989785812**	**0.97785**	**6**
Q9EQS0	ALAGCDFLTISPK	1.08188567	2	3.30839
Q9EQS0	ILDWHVANTDKK	1.121669358	2	3.47564
Q9EQS0	LGGPQEEQIK	1.199113409	2	3.3097

Q9EQS0	LSSTWEGIQAGK	1.524504354	2	2.71191
Q9EQS0	SYEPQEDPGVK	0.899356055	2	2.82443
Q9EQS0	WLHNEDQMAVEK	0.988811159	2	3.75689
Q9EQS3	**MYCBP C_Myc_binding protein**	**2.150676433**	**0.60967**	**2**
Q9EQS3	LVQYEPPQEEK	1.06431865	2	2.47627
Q9EQS3	VLVALYEEPEKPTSALDFLK	1.155672773	3	3.44915
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**2.015953284**	**0.97435**	**3**
Q9EQW7	ADLTDSRALEKAVSR	1.058755794	3	3.3419
Q9EQW7	DETIAVPLEENSALPK	0.967827203	2	2.59086
Q9EQW7	VTQWAEER	1.013084893	2	2.43305
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**2.373932875**	**0.98407**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.107320199	2	4.34295
Q9EQX9	SNEAQAIETAR	1.011856824	2	3.37589
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.263049705	3	4.48138
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.920504474**	**1**	**19**
Q9ER34	ADIANLAEEFK	1.279964029	2	3.56502
Q9ER34	CTTDHISAAGPWLK	1.114097737	2	4.01984
Q9ER34	DINQEVYNFLATAGAK	1.20411634	2	3.3442
Q9ER34	DLEDLQILIK	1.671485966	2	2.47384
Q9ER34	FKLEAPDADELPR	1.018336337	3	4.16928
Q9ER34	FNPETDFLTGK	1.494436164	1	2.48704
Q9ER34	GHLDNISNNLLIGAINIENGK	1.175184166	2	5.80545
Q9ER34	IVYGHLDDPANQEIER	1.150351668	2	4.60139
Q9ER34	LNRPLTLSEK	1.789716616	2	2.4509
Q9ER34	LTGTLSGWTSPK	0.940451964	2	2.99456
Q9ER34	NAVTQEFGPVPDTAR	0.932937082	2	4.43713
Q9ER34	NTIVTSYNR	0.983451685	1	1.94905
Q9ER34	QGLLPLTFADPSDYNK	1.015256542	2	3.35535
Q9ER34	SDFDPGQDTYQHPPK	1.225512101	2	2.87933
Q9ER34	SQFTITPGSEQIR	0.941389479	2	3.91078
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	1.365359022	2	4.78304
Q9ER34	VDVSPTSQR	0.881095987	2	2.44661
Q9ER34	VGLIGSCTNSSYEDMGR	1.000440862	2	4.20039
Q9ER34	WVVIGDENYGEGSSR	0.988282288	2	4.41423
Q9ERU9	**RBP2 E3 SUMO_protein ligase RanBP2**	**2.039298103**	**0.96187**	**2**
Q9ERU9	EINSLRGQEK	1.149395643	2	2.61337
Q9ERU9	NLFRFGESTTGFNFSFK	1.020751439	2	2.32362
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**1.873812102**	**0.98955**	**5**
Q9ES21	HFDSQVIIYGK	0.857562461	2	2.79587
Q9ES21	LEEQDEFEK	2.298585267	2	2.75949
Q9ES21	TNVIQSLLAR	2.681032935	2	2.3946
Q9ES21	TQLGLVMDGFNSLLR	1.042951422	2	3.947
Q9ES21	VVTNQEGVFR	0.904332343	2	2.81056
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**2.01247195**	**1**	**14**
Q9ES38	ACQAAWALK	1.11554672	2	2.57269
Q9ES38	ADVWENFQQR	0.893668999	2	2.95416
Q9ES38	EGFDVGVIADPLYILDNK	0.8998875	2	5.37182
Q9ES38	GATAILVLPSK	1.032186695	2	3.20712
Q9ES38	HPPELFVDALEQQAQARPDQVALVCTGSEGCSITNR	1.045271361	4	4.54622
Q9ES38	IQDSLEITNTYK	1.233441371	2	3.81516
Q9ES38	LKEATIQEDK	0.94821185	2	2.83381
Q9ES38	LLAENIR	0.92792704	2	2.46671
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.219353064	2	4.20163
Q9ES38	QGFCIPVETGKPGLLLTK	1.040313772	3	3.88201
Q9ES38	SISALSVFLGLAK	1.541801308	2	3.32014
Q9ES38	SLMPDVYQAVCEGTWK	0.966231157	2	3.90565
Q9ES38	YLCNVPGQPEDK	0.963796707	2	3.37767

Q9ES38	YLCNVPGQPEDKK	1.099582252	2	3.76698
Q9ESP1	**SDF2L Stromal cell_derived factor 2_like protein 1**	**2.164153125**	**0.99442**	**2**
Q9ESP1	ASAGLVTCGSVLK	1.156528658	2	3.59286
Q9ESP1	GQHEVHGMPSANAHNTWK	0.947774646	3	3.81913
Q9ESR9	**ABCA2 ATP_binding cassette sub_family A member 2**	**2.247918226**	**0.00468**	**2**
Q9ESR9	KEMDKMIEDLELSNK+Oxidation(2)Oxidation(5	1.234353356		
Q9ESR9	RHSLVQTLSGGMKR	1.009813178	2	2.36262
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**1.709275731**	**0.14024**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.57729661	2	4.14051
Q9EST6	SLDLFGCEVTNR	1.174074177	2	2.97743
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**2.424191617**	**0.49798**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.331080465	3	5.82827
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.294755163	3	4.50159
Q9ESW0	QGQGQLVTCSGAFK	1.074442035	2	2.36767
Q9HB97	**PARVA Alpha_parvin**	**2.528042425**	**0.78468**	**3**
Q9HB97	LNVAEVTQSEIAQK	0.964591815	2	4.31417
Q9HB97	QIQEEITGNTEALSGR	1.10589212	2	3.70708
Q9HB97	VLIDWINDVLVGER	1.442109749	2	2.3004
Q9JHL4	**DBNL Drebrin_like protein**	**1.753347185**	**0.33424**	**3**
Q9JHL4	AMSTTSVSSSQPGK	0.828562263	2	2.55232
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3	0.460421113		
Q9JHL4	TGELEQEVVSR	0.783085977	2	3.26564
Q9JHW0	**PSB7 Proteasome subunit beta type_7**	**2.114571378**	**0.99826**	**2**
Q9JHW0	ATEGMVVADK	0.978752538	2	2.57047
Q9JHW0	FRPDMEEEEAKK	1.089235957	3	3.81746
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**3.530538195**	**6.8E-06**	**3**
Q9JHZ9	AYEQLGYR	1.441463108	2	2.39203
Q9JHZ9	HLEGLLPVGMPTADTQR	1.87240985	2	3.9868
Q9JHZ9	MEIPRQTEMVELVPNGK+Oxidation(0)Oxidation(8	1.224682209		
Q9JI85	**NUCB2 Nucleobindin_2**	**1.925093946**	**0.99773**	**8**
Q9JI85	FQQGIAPSGPAGELK	0.941769235	2	3.1531
Q9JI85	HEEFKKYEMMK+Oxidation(8	0.784493282		
Q9JI85	HEEFKKYEMMK+Oxidation(9	0.784493282		
Q9JI85	LSQELDLVSHK	1.168754861	2	2.62893
Q9JI85	QEYQQAVQQLEQK	0.914539285	2	4.59552
Q9JI85	TRLDELK	1.13242612	1	2.01113
Q9JI85	VHNVEPVESAR	0.938311968	2	3.08007
Q9JI85	VYNPQNAEDDMIEMEEER	1.204291289	2	3.972
Q9JI91	**ACTN2 Alpha_actinin_2**	**2.589029197**	**0.92219**	**8**
Q9JI91	ETADTDTAEQVIASFR	1.527658217	2	3.06421
Q9JI91	GYEEWLLNEIR	1.389998986	2	3.4865
Q9JI91	HTNYTMEHIR	1.021036684	3	3.5452
Q9JI91	KHEAFESDLAAHQDR	1.262720369	2	5.36311
Q9JI91	MLDAEDIVNTPKPDER	0.98497486	2	3.2126
Q9JI91	QSILAIQNEVEK	1.612628963	2	2.72277
Q9JI91	SSIQITGALEDQMNQLK	1.441028085	2	3.08532
Q9JI91	TINEVETQILTR	1.368111447	2	3.14469
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.994615933**	**0.91113**	**7**
Q9JJ19	AVDPDSPAEASGLR	0.837210251	2	3.45978
Q9JJ19	IVEVNGVCMEGK	0.982380957	2	3.72394
Q9JJ19	LLVVDPETDEQLKK	1.028293516	2	2.85416
Q9JJ19	LVEPGSPAEK	0.780599981	2	2.7024
Q9JJ19	LVEVNGENVEK	1.091746233	2	3.04663

Q9JJ19	SEHTEPPAAADTK	0.988245859	2	3.32679
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	1.270056566	3	3.55325
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**2.138021907**	**0.78008**	**5**
Q9JJ40	AGVLADDHLIEVNGENVENASHEEVVEK	1.763261773	3	5.38256
Q9JJ40	GVFLTDITPQGVAMK	1.078636591	2	3.37839
Q9JJ40	IEKDTDGHLVR	0.940250876	2	3.19373
Q9JJ40	SGNSVTLLVLDGDSYEK	1.942268009	2	3.79667
Q9JJ40	VIEEGSPAEK	0.953532744	2	2.41843
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.783854606**	**0.36731**	**2**
Q9JJ46	HLTNAQSMLDNK	0.897604263	2	3.75976
Q9JJ46	VSVVPLGTGR	0.720595904	2	2.45105
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.904098971**	**0.57293**	**4**
Q9JJ54	FGDVVDCTLK	0.904842015	2	2.80834
Q9JJ54	IDASKNEEDEGHSNSSPR	1.21193401	3	4.66094
Q9JJ54	IFVGGLSPDTPEEK	1.356772254	2	4.03937
Q9JJ54	IFVGGLSPDTPEEKIR	2.46128668	2	2.40501
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**2.253094172**	**0.07498**	**4**
Q9JJ79	NCLEEWTKAAGLEK	0.860872179	2	2.65048
Q9JJ79	RASTAAAPLAAWVK	1.09133173	2	2.53825
Q9JJ79	TVLRGSGNLLR	1.430679285	2	2.46618
Q9JJ79	YVVQIGDK	1.239525392	1	2.30272
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**2.082069855**	**0.54791**	**2**
Q9JJU8	GDYDAFFEAR	1.055885635	2	3.18598
Q9JJU8	QQDVLCFLEANK	1.220122982	2	3.21735
Q9JJW3	**USMG5 Up_regulated during skeletal muscle growth protein 5**	**2.018718207**	**0.83854**	**2**
Q9JJW3	MAGPESDGQFQFTGIKK+Oxidation(0	2.253299495		
Q9JJW3	YFNSYTLTGR	1.013237506	2	2.80612
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**2.680840481**	**1.3E-09**	**4**
Q9JK38	GRVEDVVVSDECR	1.282232905	2	2.51818
Q9JK38	ITLECLPQNVGFYK	1.566378659	2	3.47628
Q9JK38	VEDVVVSDECR	2.426957532	2	3.36651
Q9JK38	VLGQLTETGVVSPEQFMK	1.33926397	2	4.63243
Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**2.080738339**	**0.91627**	**2**
Q9JK72	GDLGNVHAEASGR	1.172459506	2	3.22151
Q9JK72	SLVVDEGEDDLGR	1.021988092	2	3.02231
Q9JKJ9	**CP39A 24_hydroxycholesterol 7_alpha_hydroxylase**	**2.553083713**	**0.14252**	**2**
Q9JKJ9	TVLESISSVFGTAGK	1.19334401	2	3.33597
Q9JKJ9	TYDEGFEYGSQLPEWLLR	1.550944391	2	3.20149
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**2.084337488**	**0.95604**	**4**
Q9JKS4	DFNMPLTISR	1.158999777	2	2.34284
Q9JKS4	DLAVDSASPVYQAVIK	1.014019803	2	3.59309
Q9JKS4	GAPAYNPTGPQVTPLAR	1.303460753	2	3.12809
Q9JKS4	TQSKPEDEADEWAR	2.105567574	2	3.81607
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**2.960608308**	**0.86431**	**11**
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	1.397807067	3	3.31771
Q9JLA3	FLFVDADQIVR	1.634037751	2	2.62032
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.140771955	3	6.0139
Q9JLA3	IEYQFFEDK	1.12011231	2	2.34456

Q9JLA3	ILETTTFFQR	1.396010633	2	2.8417
Q9JLA3	IVPEWQDYDQEIK	1.063911697	2	3.31969
Q9JLA3	LNIQPSETDYAVDIR	1.74870995	2	4.11147
Q9JLA3	TAAIANSMNYLTK	1.250143596	2	2.5771
Q9JLA3	VDALLSAQPK	1.224521011	2	2.7415
Q9JLA3	VEEDVASDLVMK	1.654534783	2	3.82461
Q9JLA3	VWQLQDLSFQTAAR	1.156779078	2	4.65391
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**1.799344665**	**0.96474**	**2**
Q9JLH7	GSDALTLLEYPETR	0.975437381	2	2.90587
Q9JLH7	KEEEGQAGAAEMR	0.846748841	2	3.70517
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**2.073501939**	**0.99843**	**18**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.661567116	2	4.75727
Q9JLJ3	ANDTTFGLAAGVFTR	1.095372167	2	4.92879
Q9JLJ3	CQVLLEAAR	1.068619591	2	3.30374
Q9JLJ3	EQGATVLCGGEPYAPEDPK	0.988739458	2	4.95438
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	0.948998505	3	3.39479
Q9JLJ3	EVNLAVENAK	1.112055125	2	3.15041
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.128864111	2	5.57225
Q9JLJ3	GIKPITLELGGK	0.905092474	3	3.96727
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.230353366	3	4.23865
Q9JLJ3	IGDPLLEDTR	1.135262608	2	3.7055
Q9JLJ3	MGPLINAPHLER	0.993572378	2	3.26442
Q9JLJ3	MGPLINAPHLER+Oxidation(0	0.942413097		
Q9JLJ3	RDEIAIMETINNGK	1.063211289	2	5.29883
Q9JLJ3	SPLIIFSDCNMK	1.511407739	2	2.60824
Q9JLJ3	VEPVDASGTEK	1.008105462	2	2.41424
Q9JLJ3	VSFTGSVPTGMK	1.056803096	2	3.10514
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10	1.184858501		
Q9JLJ3	VTIEYYSQLK	1.214009878	2	3.08449
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**2.134403728**	**0.38529**	**2**
Q9JLR1	IIEVGDTPK	1.055618745	2	2.66552
Q9JLR1	TWIEVSGSSAK	1.284449549	2	2.7547
Q9JLT0	**MYH10 Myosin_10**	**2.455809007**	**0.75751**	**2**
Q9JLT0	AGVLAHLEEER	1.195279347	2	3.4286
Q9JLT0	DAAGLESQLQDTQELLQEETR	1.392469837	2	3.18175
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**2.378251465**	**0.3446**	**2**
Q9JLZ1	LEAEAVPEVSEK	0.615105782	2	2.31979
Q9JLZ1	YEISSVPTFLFFK	1.901370202	2	2.58476
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**2.085250366**	**0.34625**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	1.271963105	2	5.61671
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.631607409	3	4.47002
Q9JLZ3	SEVPGIFCAGADLK	0.949548432	2	2.95344
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**2.097631466**	**0.99999**	**15**
Q9JM53	AIASAAEGGSVPPIR	0.970080332	2	2.76764
Q9JM53	CLIATGGTPR	0.964780241	2	2.4216
Q9JM53	DGEQHEDLNEVAK	0.831194213	2	3.82964
Q9JM53	ILPEYLSNWTMEK	1.169359976	2	3.49459
Q9JM53	IMGLGLSPEEK	1.14512706	2	2.80551
Q9JM53	KSQASGIEVIQLFPEK	1.27928527	2	3.70989
Q9JM53	KVETDHIVTAVGLEPNVELAK	0.980038424	2	6.17864
Q9JM53	LNDGSQITFEK	1.031860183	2	3.50826
Q9JM53	SITVIGGGFLGSELACALGR	0.780158168	2	2.65708
Q9JM53	SQASGIEVIQLFPEK	1.328613541	2	4.13179

Q9JM53	TGGLEIDSDFGGFR	0.986806419	2	4.18675
Q9JM53	VETDHIVTAVGLEPNVELAK	1.20333813	2	5.18247
Q9JM53	VLIVSEDPELPYMRPPLSK	0.794346265	3	3.93852
Q9JM53	VMPNAIVQSVGVSGGK	1.090405991	2	4.28328
Q9JM53	VNAELQAR	0.889594733	2	2.60174
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**2.881822704**	**0.73254**	**2**
Q9JMA1	CTESEEEEVTK	1.305652081	2	3.69407
Q9JMA1	EKESVNAKVLK	2.147032032	2	2.37533
Q9JMD3	**PCTL PCTP_like protein**	**2.340354919**	**3.3E-10**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.226678105	2	4.66817
Q9JMD3	ESVQVPDDQDFR	1.536038193	2	2.83565
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.592559159	3	4.40511
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0	1.255469202		
Q9JMD3	SSQFLAPK	0.730375273	2	2.35623
Q9JMD3	WDSNVIETFDIAR	1.109880182	2	4.53405
Q9JME5	**AP3B2 AP_3 complex subunit beta_2**	**2.11770654**	**0.65561**	**2**
Q9JME5	DELVVAESVVVIK	1.575110428	2	2.51605
Q9JME5	LLQMQPAQHGEIIK	0.948210021	2	2.55969
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.966066699**	**0.99996**	**7**
Q9QVC8	ALELDSNNEK	1.007875724	2	2.63056
Q9QVC8	GEPNNVAGNQAQVK	0.984532697	2	3.85957
Q9QVC8	TEVAAGDHPTDAEMK	1.129667155	2	3.66787
Q9QVC8	TQLAVCQQR	0.874439004	2	2.72842
Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.033301296	2	3.92937
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	0.945168554	3	5.9155
Q9QVC8	VLQLYPSNK	0.939560155	2	2.33325
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.994288091**	**0.1999**	**3**
Q9QWN8	ALAQEDQSAGEVER	0.814195459	2	3.77066
Q9QWN8	FETLEPEMNALAAR	1.569519504	2	2.72911
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	0.906031603	3	4.22452
Q9QX79	**FETUB Fetuin_B**	**1.864221225**	**0.99024**	**3**
Q9QX79	GSIQHLPEQEEPEDSKGK	0.845928113	3	3.83006
Q9QX79	IFYETVHGQCK	0.967032549	2	2.38993
Q9QX79	NTAPTSSPSITAPR	1.385625903	2	3.15038
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**2.21956419**	**0.94802**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	0.722504978	2	3.67931
Q9QXG4	IGPIATPDYIQNAPGLPK	1.243212337	2	3.2977
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.935384792**	**0.99559**	**32**
Q9QXQ0	ACLISLGYDVENDR	1.303028624	2	4.02405
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.308343839	3	3.85267
Q9QXQ0	AGTQIENIDEDFR	1.142566948	2	3.56221
Q9QXQ0	AGTQIENIDEDFRDGLK	1.122133272	2	4.2579
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.261862842	3	3.36847
Q9QXQ0	ASIHEAWTDGK	0.600922637	2	2.45294
Q9QXQ0	DDPVTNLNNAFEVAEK	1.079378662	2	3.60693
Q9QXQ0	ETTDTDTADQVIASFK	0.835871538	2	4.71037
Q9QXQ0	HRDYETATLSDIK	1.197627085	2	3.88742
Q9QXQ0	HRPELIEYDK	0.956756761	3	4.40283
Q9QXQ0	HTNYTMEHLR	1.021036684	3	3.5452
Q9QXQ0	ICDQWDNLGSLTHSR	1.000973399	2	4.59372
Q9QXQ0	INNVNKALDFIASK	0.993168629	2	2.30311
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.964394712	2	4.73469
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.224300483	2	4.42651
Q9QXQ0	LVSIGAEEIVDGNAK	1.359410931	2	3.15663
Q9QXQ0	MAPYQGPDAAPGALDYK	1.008198357	2	4.98175
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0	0.889723395		
Q9QXQ0	MLDAEDIVNTARPDEK	0.958960111	2	3.8771

Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(0	0.877347644		
Q9QXQ0	MVSDINNGWQHLEQAEK	1.076213313	2	4.71801
Q9QXQ0	NFITAEELR	1.110664128	1	2.125
Q9QXQ0	NVNVQNFHISWK	0.419558845	2	2.34403
Q9QXQ0	QFASQANMVGPWIQTK	0.970809236	2	3.63946
Q9QXQ0	QLETIDQLHLEYAK	0.954902562	2	3.28057
Q9QXQ0	RDHALLEEQSK	0.921585794	3	3.88131
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.817858955	3	4.69341
Q9QXQ0	TINEVENQILTR	0.955797932	2	3.67342
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	1.478437181	3	5.40346
Q9QXQ0	VGWEQLLTTIAR	1.240210855	2	4.10189
Q9QXQ0	VLAGDKNFITAEELR	0.798206536	2	3.23279
Q9QXQ0	VLAVNQENEHLMEDYER	1.071497451	2	5.72971
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.87224045**	**1**	**5**
Q9QXT0	ALVDELEWEIAR	0.990456705	2	3.58611
Q9QXT0	IDSDISGTLK	1.085159104	2	2.62545
Q9QXT0	INPDGSQSVVEVPYAR	1.076208557	2	3.66256
Q9QXT0	RTDLCDHALHR	0.800161057	3	3.92513
Q9QXT0	TDLCDHALHR	0.978317921	2	3.20789
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**2.301481022**	**0.0041**	**18**
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.287823328	3	5.82647
Q9QXX4	DVEVTKEEFALAAQK	0.922454163	2	4.47879
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.072762344	2	5.96835
Q9QXX4	FGLYLPLFKPSASTSK	1.541021713	2	2.75989
Q9QXX4	GLLPQLLGVAPEK	1.14777837	1	3.07248
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.31061119	2	5.23561
Q9QXX4	ITLPAPNPDHVGGYK	1.226326145	2	3.00412
Q9QXX4	KDVEVTKEEFALAAQK	0.929729643	2	5.62031
Q9QXX4	LQVAGEITTGPR	1.167170531	2	3.7317
Q9QXX4	LTVNDFVR	1.28508065	2	2.31738
Q9QXX4	NGEFFMSPHDFVTR	0.980279818	2	4.20744
Q9QXX4	NSFDCFK	1.122905572	1	1.9736
Q9QXX4	SSPQFGVTLLTYELLQR	1.537177422	2	3.8108
Q9QXX4	STGSFVGELMYK	1.461200877	2	3.43736
Q9QXX4	TVELLSGVVDQTK	1.261687256	2	4.51176
Q9QXX4	VSALSVVR	1.345465542	2	2.3056
Q9QXX4	YEGFFGLYR	1.19973757	2	2.74486
Q9QXX4	YLNIFGESQPNPK	0.928138495	2	4.43402
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**1.972636021**	**0.99936**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	0.980208099	2	4.57612
Q9QYU4	RAPAFLSADEVQDHLR	1.151928154	3	3.84162
Q9QYU4	SLGMAVEDLVAAK	0.927132122	2	3.76128
Q9QYU4	SSSLLIPPLEAALANFSK	0.971533566	2	2.89721
Q9QZ76	**MYG Myoglobin**	**2.590312497**	**0.99512**	**6**
Q9QZ76	GQHAAEIQPLAQSHATK	0.780759538	2	4.91335
Q9QZ76	HGCTVLTALGTILK	1.363710305	2	3.66195
Q9QZ76	KGQHAAEIQPLAQSHATK	3.563263603	3	5.45922
Q9QZ76	KKGQHAAEIQPLAQSHATK	1.519887049	3	4.50123
Q9QZ76	VEGDLAGHGQEVLISLFK	0.263157912	3	4.11227
Q9QZ76	YSGDFGADAQGAMSK	6.060934741	2	3.92959
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**2.064120863**	**0.91069**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	0.909277216	2	3.26783
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.23639601	2	3.39303
Q9QZA2	HEGALETLLR	0.952608692	2	2.32565

Q9QZA2	LLDEEEATDNDLR	0.999328101	2	4.05015
Q9QZA2	MVPVSVQQSLAVFSQR	1.205093282	2	3.13145
Q9QZA2	NIQVSHQEFSK	1.013981997	2	3.35185
Q9QZA2	STAVVEQGGIQTVDQLIK	1.225634829	2	4.29954
Q9QZA2	TMQGSEVVNVLK	0.848992282	2	3.2771
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.958297598**	**0.99953**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	0.964983538	2	5.08236
Q9QZD8	LFSGATMASSR	0.74709972	2	2.51429
Q9QZD8	MTGMALQVVR	1.101512281	2	2.78806
Q9QZD8	NYSHALDGLYR	1.005135755	2	2.83243
Q9QZD8	VHLQTQQEVK	1.07734799	2	3.04864
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.110568688	2	5.68047
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	1.155618418	3	3.5388
Q9QZH8	**AAAD Arylacetamide deacetylase**	**2.729130206**	**0.9901**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.58517315	2	4.11496
Q9QZH8	WFLQEDILEK	1.1722733	2	2.94973
Q9QZR9	**chain**	**2.006730489**	**0.74034**	**2**
Q9QZR9	EGPSGPFGALGQDGKDGPR	16.88433779		
Q9QZR9	GASGLLEMGPPGPMGMPGQK	0.981266293		
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**2.504144155**	**0.5204**	**5**
Q9QZU7	IDANNVAYTTGK	1.667509827	2	3.07129
Q9QZU7	MDDLTFDQK	2.518101613	2	2.55431
Q9QZU7	MNPGDVITFDNWR	1.330927999	2	2.80838
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.046500531	2	4.7948
Q9QZU7	SYEAGTEISR	1.235213589	2	2.75401
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**2.405994596**	**0.30769**	**2**
Q9QZX8	GIGETPIVPLGISYLDDFAK	1.322541398	2	3.48901
Q9QZX8	QFTDEGNPDSVNK	1.043644899	2	3.58281
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**1.933073078**	**0.99946**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	0.893283196	3	4.80459
Q9R063	ETDLLLDDSLVSLFGNR	0.901121406	2	4.02467
Q9R063	GVLFGVPGAFTPGCSK	1.006464659	2	4.19188
Q9R063	THLPGFVEQAGALK	0.902863055	3	4.48427
Q9R063	VGDTIPSVEVFEGEPGK	0.98315245	2	4.23487
Q9R063	VGDTIPSVEVFEGEPGKK	0.852146775	2	4.17005
Q9R063	VNLAELFK	0.96575364	2	2.56489
Q9R063	VQLLADPTGAFGK	1.022828364	2	3.55715
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**2.775696158**	**0.61958**	**2**
Q9R064	ADTSSLTVDVMSPASK	1.391276832	2	4.27413
Q9R064	LYVYNTDTDNCR	1.488176374	2	2.53103
Q9R099	**TBL2 Transducin beta_like protein 2**	**2.184826708**	**0.98701**	**4**
Q9R099	ANVELDHATLVR	1.206423597	2	2.42379
Q9R099	FEEASTMPCR	0.952669805	2	2.66621
Q9R099	FLASCGDR	0.916546031	2	2.33993
Q9R099	LQQQLTQAQEALK	1.224727308	2	4.10972
Q9R0N0	**GALK1 Galactokinase**	**2.233794217**	**0.93055**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	0.961779063	3	4.46415
Q9R0N0	MEELEAGR	0.966398404	2	2.45974
Q9R0N0	RQCEEVAQALGK	0.935389584	2	3.20385
Q9R0N0	SLETSLVPLSDPK	1.336540292	2	3.28885
Q9R0N0	TDGLVSLLTTSK	1.183735167	2	3.80247
Q9R0N0	VEELLAEAR	0.997163592	2	3.11637
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**2.000090616**	**2.8E-07**	**6**
Q9R0T3	AEPSVAEYTVR	0.976410785	2	2.4658
Q9R0T3	ICSEVLQLEPDNVNALK	1.435398962	2	4.75959
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	0.95493041	3	5.65813

Q9R0T3	LIGSAEELIR	1.155201953	2	2.61684
Q9R0T3	LKNDNTEAFYK	1.347553543	2	2.6493
Q9R0T3	SNPSENEEKEAQSQLVK	0.93297309	2	5.15766
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**2.003909416**	**0.89551**	**4**
Q9R112	EGNALFTFPNTPVK	1.580320644	2	3.0399
Q9R112	STLSVIPSGVQWIQDR	1.475777661	2	2.79017
Q9R112	TAAAVAAQSGILDR	0.925753546	2	3.32618
Q9R112	VGAENVAIVEPSER	0.900170236	2	2.86908
Q9R172	**NOTC3 Neurogenic locus notch homolog protein 3**	**2.114019923**	**0.9706**	**2**
Q9R172	CTHQQPSREAACLCLPGWVGER	1.243587755	3	3.39699
Q9R172	YGGKCLDLVDK	1.029803486	1	1.98789
Q9R1T3	**CATZ Cathepsin Z**	**2.065182318**	**1**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.100595773	2	3.86547
Q9R1T3	VGDYGSLSGR	1.045519206	2	2.82876
Q9R1T4	**SEPT6 Septin_6**	**2.338744402**	**0.38266**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(1	0.625705463		
Q9R1T4	STLMDTLFNTK	1.456607574	2	2.87976
Q9R1T5	**ACY2 Aspartoacylase**	**2.715532775**	**0.49908**	**2**
Q9R1T5	EAFAKTTKLTLNAK	23.52166577	2	2.52017
Q9R1T5	VIPLGGDCTVYPVFVNEAAYYEK	1.4318785	3	3.58684
Q9R1T9	**KCNH4 Potassium voltage_gated channel subfamily H member 4**	**1.795535831**	**0.61513**	**2**
Q9R1T9	DGSAFWCLLDMMPIK+Oxidation(10	1.410610206		
Q9R1T9	KDGSAFWCLLDMMPIK+Oxidation(11)Oxidation(12	0.8188369		
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**2.156063887**	**0.00038**	**4**
Q9R1Z0	LCQNNFALGYK	1.231521813	2	2.40341
Q9R1Z0	LTLSALVDGK	1.725089086	2	2.30016
Q9R1Z0	LTVDTIFVPNTGK	1.236958324	2	2.96183
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.854095583	2	4.29561
Q9WTR8	**PHLP1 PH domain leucine_rich repeat protein phosphatase 1**	**2.00441328**	**0.98865**	**2**
Q9WTR8	LEELEEIDISGNK	1.273089019	2	2.72164
Q9WTR8	LEELEEIDISGNKLK	0.997147677	2	2.39603
Q9WTT6	**GUAD Guanine deaminase**	**1.886639348**	**0.99523**	**10**
Q9WTT6	EIGNFEVGKDFDALLINPR	1.363814612	2	4.08246
Q9WTT6	ETTEESVKETER	0.859346647	2	3.16279
Q9WTT6	FQSTDVAEEVYTR	1.034049497	2	3.7186
Q9WTT6	FSLSCTETLMSELGNIAK	1.382046154	2	3.6433
Q9WTT6	GTFVHSTWTCPMEVLR	1.147338962	2	3.15965
Q9WTT6	IVFLEESSQQEK	1.022725196	2	4.25337
Q9WTT6	NIEEVYVGGK	0.875282987	1	2.69527
Q9WTT6	NYTDVYDKNNLLTNK	0.693385296	2	4.41706
Q9WTT6	THDLYIQSHISENREEIEAVK	1.239584276	3	4.47567
Q9WTT6	VCMDLNNTVPEYK	1.214661039	2	3.61848
Q9WTT7	**BZW2 Basic leucine zipper and W2 domain_containing protein 2**	**2.052329154**	**0.63951**	**2**
Q9WTT7	AWMAEKDANSVTSSLR+Oxidation(2	1.494118791		
Q9WTT7	ELQERLSQECPIK	0.97045738	2	2.55037
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**2.267520641**	**1**	**9**
Q9WU19	AIFVTVDTPYLGNR	0.862163967	2	4.25409
Q9WU19	AVFVGRPIIWGLAFQGEK	0.965417175	3	4.01176
Q9WU19	GVQDVLEILK	1.210249414	2	3.62784
Q9WU19	GVQDVLEILKEEFR	0.955982388	2	4.30141
Q9WU19	HGVDGILVSNHGAR	0.987794951	3	4.53181
Q9WU19	MKNFETNDLAFSPK+Oxidation(0	1.137339776		

Q9WU19	NFETNDLAFSPK	0.958123771	2	3.57137
Q9WU19	NVADIDLSTSVLGQR	1.093530066	2	4.94347
Q9WU19	VEVFLDGGVR	1.031304432	2	2.6852
Q9WU79	**PROD Proline dehydrogenase 1_ mitochondrial**	**2.107887975**	**0.95316**	**2**
Q9WU79	FTEEEEQQMK	1.077077811	2	3.11878
Q9WU79	HLVVPNVQTGQLEPLLSR	1.070238592	2	2.33994
Q9WU82	**CTNB1 Catenin beta_1**	**1.922238891**	**0.17703**	**5**
Q9WU82	HQEAEMAQNAVR	1.185191618	2	3.40978
Q9WU82	LLNDEDQVVVNK	1.074096619	2	3.30851
Q9WU82	TMQNTNDVETAR	0.826069762	2	3.58624
Q9WU82	TMQNTNDVETAR+Oxidation(1	1.087154588		
Q9WU82	TSMGGTQQQFVEGVR	1.233395836	2	3.52761
Q9WUA2	**SYFB Phenylalanyl_tRNA synthetase beta chain**	**2.057353611**	**0.87192**	**3**
Q9WUA2	EMVRADLINKK	1.112322819	2	2.38823
Q9WUA2	KEMVRADLINK	1.112322819	2	2.36095
Q9WUA2	TYTIANQFPLNK	0.951250768	2	2.44837
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**2.332247136**	**0.96328**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.052031491	2	3.62919
Q9WUC4	VCIESEHSSDILLATLNK	1.225236767	2	5.74279
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**4.573856495**	**0.80138**	**3**
Q9WUH4	AIVAGDQNVEYK	1.823739157	2	2.67463
Q9WUH4	FCANTCVECR	1.712338079	2	2.71892
Q9WUH4	FVFHNEQVYCPDCAK	2.419049182	2	4.21178
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**2.110881467**	**0.76987**	**2**
Q9WUI1	ILDFGLAR	1.058453058	2	2.73213
Q9WUI1	QELNKTVWEVPQR	1.137919241	2	2.43044
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.897574015**	**1**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(6	0.923174168		
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7	0.92468407		
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**1.961561168**	**0.60746**	**5**
Q9WUS0	AVILGPPGSGK	0.807354777	2	2.45807
Q9WUS0	GVLHQFSGTETNR	0.994272172	2	3.55004
Q9WUS0	TLVQAEALDR	0.806098298	2	2.82175
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.43387494	3	5.10579
Q9WUS0	YKDAAKPVIELYK	0.86474178	2	3.55925
Q9WUU8	**TNIP1 TNFAIP3_interacting protein 1**	**2.182524987**	**0.68172**	**2**
Q9WUU8	IFEEDFQRER	1.198783572	2	2.3264
Q9WUU8	QENEALK	1.12384808	1	2.29213
Q9WV85	**NDK3 Nucleoside diphosphate kinase 3**	**1.868726031**	**0.48407**	**3**
Q9WV85	LVKYMSSGPVVAMVWQGLDVVHASR+Oxidation(4)Oxidation(12	0.90574283		
Q9WV85	LVQASEELLR	1.139416847	2	2.70901
Q9WV85	TFLAVKPDGVQR	0.757060059	2	2.67797
Q9WVC0	**SEPT7 Septin_7**	**2.647175903**	**0.91555**	**3**
Q9WVC0	ADTLTPEECQQFK	0.749116602	2	2.85777
Q9WVC0	FEDYLNAESR	1.184755538	2	2.76163
Q9WVC0	NLEGYVGFANLPNQVYR	1.434680055	2	3.62276
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**3.12578256**	**0.00782**	**3**
Q9WVD5	DGPLGFYHGLSSTLLR	1.743109145	2	2.92424
Q9WVD5	LQTMYEMETSGK	1.674270393	2	3.12805
Q9WVD5	NEGITALYSGLKPTMIR	1.140167972	2	3.34505
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**2.809825248**	**0.61566**	**2**
Q9WVF7	AANMPDSELFELISENR	1.355490687	2	2.4759
Q9WVF7	MAWQWRGEFMPASR+Oxidation(0)Oxidation(9	3.839182159		
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**1.900964967**	**0.09809**	**13**
Q9WVK3	AGVYNLTK	0.962049401	2	2.52272

Q9WVK3	ASQPPSSSTQVTAIQCNIR	0.876195903	2	5.53707
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	0.879776715	3	6.29974
Q9WVK3	ELLHLGCNVVIASR	1.05827583	2	4.24377
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.109741513	2	5.48502
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12	2.152482921		
Q9WVK3	KEEEVNNLVK	0.905286154	3	4.01885
Q9WVK3	LTAAVDELR	1.066874929	2	3.18741
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.96912264	2	5.02034
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	0.880202116	3	3.75714
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	1.024121036	2	6.21111
Q9WVK3	TMALTWASSGVR	0.853009537	2	3.80029
Q9WVK3	TMALTWASSGVR+Oxidation(1	1.08303871		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**2.178476444**	**0.99996**	**17**
Q9WVK7	AADEFVEK	0.925700454	2	3.35121
Q9WVK7	DTPGFIVNR	1.104058288	2	2.70301
Q9WVK7	EDIDTAMK	0.740836711	1	2.15194
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.212357254	3	4.76593
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	1.138819982	3	5.48344
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(21	1.410185245		
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(8	1.41386392		
Q9WVK7	GDASKEDIDTAMK	0.842528627	2	3.89158
Q9WVK7	GDASKEDIDTAMK+Oxidation(11	1.049636704		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	1.049126037	4	5.89555
Q9WVK7	KGIEESLK	1.014885845	2	2.4333
Q9WVK7	KGIEESLKR	0.990027197	2	2.42959
Q9WVK7	LKNELFQR	1.149236893	2	2.64532
Q9WVK7	LLVPYLIEAIR	0.743300867	2	2.75832
Q9WVK7	LVEVIK	1.035626722	2	2.41188
Q9WVK7	TFESLVDFCK	1.09690717	2	3.44328
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	1.020661057	3	6.05685
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.980427193**	**0.99836**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	0.929263138	2	2.91434
Q9Z0N2	SFDVNKPGCEVDDLK	1.401318487	2	3.33122
Q9Z0N2	VGQEIEVRPGIVSK	1.000494978	2	3.25902
Q9Z0U5	**ADO Aldehyde oxidase**	**2.071920034**	**0.99999**	**17**
Q9Z0U5	EFQPLDPTQELIFPPELMR	0.952881294	2	2.62625
Q9Z0U5	ELSILYGGVGPTTIGAK	0.764081468	2	3.54661
Q9Z0U5	GEDMLITGGR	1.141768079	2	2.6167
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	0.9198777	2	4.60753
Q9Z0U5	GYESNINWEK	0.978283757	2	2.6265
Q9Z0U5	HATGEAIYCDDMPAVDR	1.355200049	2	2.70454
Q9Z0U5	HIQDIVAATLK	0.886659994	2	2.72739
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	0.970712128	3	3.68698
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	0.611818692	3	3.49852
Q9Z0U5	KLECGNVDEAFK	0.792845787	2	3.65669
Q9Z0U5	LVLDEVTLAGSAPGGK	0.938750071	2	3.72604
Q9Z0U5	MTWISPVTLEELVEAK	0.876305904	2	3.41583
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	0.971446966	2	3.09925
Q9Z0U5	NMASLGGHIVSR	0.930351984	2	3.17092
Q9Z0U5	QQNALAIVNSGMR	1.098121165	2	2.47314
Q9Z0U5	RLEPIISK	0.636002286	2	2.32455
Q9Z0U5	VVENNVDPEMMLLPYLR	1.365127143	2	2.83989
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**2.184209984**	**1**	**5**

Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.904110887	3	5.18964
Q9Z0V5	GLFIIDDK	1.19896251	2	3.0266
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	1.085012134	3	3.55903
Q9Z0V5	QITLNDLPVGR	1.053916138	2	3.15417
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	0.934185598	3	5.6153
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**2.009451426**	**0.99988**	**5**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	0.937111852	3	5.43629
Q9Z0V6	GLFIIDPNGVIK	1.096522977	2	3.06107
Q9Z0V6	GTAVVNGEFK	0.978399388	2	2.72945
Q9Z0V6	HLSVNDLPVGR	0.985039787	2	2.58903
Q9Z0V6	NGGLGHMNITLLSDLTK	0.919161863	3	3.48105
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.962938149**	**0.84719**	**3**
Q9Z0W7	DEFTNTCPSDKEVEIAYSDVAK	0.718033136	3	3.64276
Q9Z0W7	FLDGDEMTLADCNLLPK	1.228233072	2	4.24368
Q9Z0W7	NSRPEANEALER	0.973746803	3	4.29236
Q9Z142	**TMM33 Transmembrane protein 33**	**2.767609286**	**0.44476**	**2**
Q9Z142	ALLANALTSALR	1.550033295	2	3.75411
Q9Z142	LSTNQQNILK	1.235554658	2	2.43705
Q9Z1A6	**VIGLN Vigilin**	**2.021433213**	**0.96194**	**22**
Q9Z1A6	ASVITQVFHVPLEER	1.265384683	2	3.28023
Q9Z1A6	DLANIAEVEVSIPAK	3.655316013	2	2.54246
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.012427742	3	3.45362
Q9Z1A6	ELQAEQEDR	1.159120656	2	2.41051
Q9Z1A6	HEVLLISAEQDKR	1.045647823	3	4.51871
Q9Z1A6	ICLEIMQR	1.047202596	2	2.52203
Q9Z1A6	IDLPAENSNSETIVITGK	0.806151732	2	4.22862
Q9Z1A6	IEGDPQGVQQAK	1.002450222	2	3.46137
Q9Z1A6	IIFPAAEDKDQDLITIIGK	1.29137226	2	4.47798
Q9Z1A6	IQIPRPDDPSNQIK	1.157650173	2	2.50082
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.685546996	2	3.47024
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.259865873	2	4.77892
Q9Z1A6	LGQALTEVYAK	1.251241495	2	3.45592
Q9Z1A6	LQDLELK	1.337948756	1	2.39277
Q9Z1A6	LQTQASATVPIPK	0.9808635	2	3.64996
Q9Z1A6	LVGEIMQETGTR	1.167533001	2	3.51438
Q9Z1A6	MDYVEINIDHK	1.008799117	2	2.80396
Q9Z1A6	MVADLVENSYSISVPIFK	1.044943685	3	3.4058
Q9Z1A6	RCDIIVISGR	1.046991398	2	2.95816
Q9Z1A6	TGAHLELSLAK	1.080532139	3	3.80012
Q9Z1A6	TKDLIIEQR	1.048095977	2	2.67492
Q9Z1A6	VKELQAEQEDR	1.036783102	3	3.74886
Q9Z1J8	**S14L3 SEC14_like protein 3**	**2.053175182**	**0.83971**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.726924226	2	2.63266
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.043361575	3	4.35021
Q9Z1J8	GSSHQVEYEILFPGCVLR	1.490187552	2	4.8928
Q9Z1L0	**PK3CB Phosphatidylinositol_4_5_bisphosphate 3_kinase catalytic subunit beta isoform**	**2.328231841**	**0.40092**	**2**
Q9Z1L0	MARLCFAVYAVLDK+Oxidation(0	1.127146504		
Q9Z1L0	QPYYYPPFDK	1.220752388	1	1.94183
Q9Z1M9	**SMC1A Structural maintenance of chromosomes protein 1A**	**2.412074604**	**0.85059**	**3**
Q9Z1M9	EIKEKDSELNQK	1.169165566	2	2.56367
Q9Z1M9	IIDETMAQLQDLK	1.402577765	2	2.42764
Q9Z1M9	SGVISGGASDLKAKAR	1.270975711	2	2.33799
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**2.183815784**	**0.88524**	**2**
Q9Z1N1	YVGSMVADVHR	1.120529835	2	2.69828

Q9Z1N1	YVGSMVADVHR+Oxidation(4	1.1272703		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.935017509**	**0.413**	**5**
Q9Z1P2	DYETATLSEIK	1.231196428	1	1.97016
Q9Z1P2	GISQEQMNEFR	0.943675674	2	2.8984
Q9Z1P2	ICDQWDNLGALTQK	0.883836942	2	4.1241
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	1.264224051	3	3.91686
Q9Z1P2	MVSDINNAWGCLEQAEK	0.634153299	2	2.7107
Q9Z1W6	**LYRIC Protein LYRIC**	**2.00468764**	**0.99768**	**5**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	0.914406907	3	4.56793
Q9Z1W6	SSSQVPPMLQDTDKPK	0.997994562	2	3.41163
Q9Z1W6	SWQDELAQQAEEGSAR	1.186493731	2	5.682
Q9Z1W6	TELGLDLGLEPK	1.697540533	2	3.37922
Q9Z1W6	TLPPAISAEPSVTLSK	1.113729808	2	2.93514
Q9Z1Y3	**CADH2 Cadherin_2**	**2.47985252**	**0.96625**	**4**
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	1.366534031	2	3.95178
Q9Z1Y3	IDPVNGQITTIAVLDR	1.045476804	2	3.92623
Q9Z1Y3	VCQCDSNGDCTDVDR	1.311585386	2	5.10662
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	1.236466785	3	3.59729
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.896542438**	**0.99502**	**3**
Q9Z270	FKGPFTDVVTTNLK	0.914547791	2	3.04318
Q9Z270	HEQILVLDPPSDLK	0.923393461	2	3.7484
Q9Z270	QDGPLPKPHSVSLNDTETR	1.283981012	3	3.40779
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**1.901073995**	**0.61088**	**2**
Q9Z2C8	SVGDGETVEFDVVEGEK	1.276394446	2	3.4501
Q9Z2C8	WFNVRNGYGFINRNDTK	0.792847216	2	2.30786
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**1.949302183**	**0.99995**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.578999731	2	5.00327
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.06018008	3	4.67838
Q9Z2I8	INFDDNAEFR	0.884822298	2	3.1599
Q9Z2I8	LEGTNVQEAQNILK	0.928408267	2	5.20132
Q9Z2I8	SENEPIENEAAR	0.99714586	2	4.19703
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.940217643	2	6.15073
Q9Z2I8	SSGLPITSAVDLEDAAK	1.082255194	2	4.96308
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.786600599	2	2.70027
Q9Z2I8	VMVAEALDISR	1.108375618	2	3.19775
Q9Z2I8	VVGELAQQMIGYNLATK	1.24750015	3	3.3922
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**2.040991032**	**0.97514**	**9**
Q9Z2I9	ALIADSGLK	1.11299471	1	2.15611
Q9Z2I9	AVSSQMIGQK	0.993874411	2	2.92479
Q9Z2I9	ICNQVLVCER	1.480461575	2	2.9847
Q9Z2I9	ILACDDLDEAAK	1.085236262	2	3.31227
Q9Z2I9	INFDSNSAYR	0.988774228	2	3.01595
Q9Z2I9	LSEIVTLAK	1.068963152	2	2.39499
Q9Z2I9	MGFPSNIVDSAAENMIK	1.126437313	2	4.20081
Q9Z2I9	SSDEAYAIAK	1.08526489	2	3.35545
Q9Z2I9	VQAILVNIFGGIMR	1.179881462	2	3.83501
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**2.296654871**	**0.99313**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	2.10950926	2	3.12806
Q9Z2L0	KLETAVNLAWTAGNSNTR	1.077596895	2	5.44818
Q9Z2L0	LTFDSSFSPNTGK	0.987061234	2	3.72068
Q9Z2L0	LTFDSSFSPNTGKK	1.152672797	2	2.79907
Q9Z2L0	LTLSALLDGK	1.949796936	2	2.6867
Q9Z2L0	SENGLEFTSSGSANTETTK	1.029433756	2	3.76303

Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	1.285286283	2	4.98805
Q9Z2L0	TKSENGLEFTSSGSANTETTK	0.854175676	3	3.5979
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	0.697030843	2	4.7374
Q9Z2L0	VTQSNFAVGYK	1.072862012	2	3.43257
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.100042499	2	4.91543
Q9Z2L0	WTEYGLTFTEK	1.203691468	1	2.90325
Q9Z2L0	YQVDPDACFSAK	0.984789412	2	3.3941
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**1.725112026**	**3.1E-15**	**6**
Q9Z2M4	AAVDAMTR	0.851982951	2	2.32431
Q9Z2M4	GQVLQLHAGAAK	1.060308585	2	3.42674
Q9Z2M4	HLAVEWGPQNIR	1.072134115	2	3.49879
Q9Z2M4	LLEFESSSAK	0.791896461	2	2.30242
Q9Z2M4	VNSLAPGAISGTEGLR	0.739068374	2	3.83141
Q9Z2M4	VPPAVMAAVDQALK	1.788577323	2	3.34092
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.658793672**	**0.67537**	**3**
Q9Z2M7	IGVVGGSDFEK	1.333907928	2	2.35358
Q9Z2M7	LQEQLGNDVVEK	0.614048065	2	3.86212
Q9Z2M7	TVGYTVTAPEDTR	0.874790685	2	2.659
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**2.010139641**	**0.0048**	**17**
Q9Z2Q1	AQDGSNPLSLQDLIEK	0.833855326	2	3.42091
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.243973325	2	4.63233
Q9Z2Q1	CLSSATDPQTK	1.208607157	2	2.85184
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.443445709	2	3.4088
Q9Z2Q1	GGPGPLAGHPQVSR	0.594770731	2	3.11751
Q9Z2Q1	IDASQTDFEK	0.933846767	2	2.33075
Q9Z2Q1	IIAGDKEVVIAQK	0.958741521	2	3.03742
Q9Z2Q1	KIDASQTDFEK	0.971004649	2	2.51688
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.569552436	2	3.07342
Q9Z2Q1	QVQHILASASPSGR	1.175099468	2	3.27865
Q9Z2Q1	RQPVFISQVVTEK	0.506051721	2	3.7406
Q9Z2Q1	RQPVFISQVVTEKDFLSR	0.885856118	3	3.53808
Q9Z2Q1	TQPPEDISCIAWNR	1.039512168	2	2.96668
Q9Z2Q1	TTFEDLIQR	0.788512103	2	2.40678
Q9Z2Q1	VNFEEDSR	1.028772977	2	2.39294
Q9Z2Q1	VYSIMGGSIDGLR	1.201961742	2	2.80104
Q9Z2Q1	YLELLGYR	0.955636868	2	2.3738
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.898375621**	**0.99691**	**4**
Q9Z2Z8	AIECSYTSADGLK	0.869754151	2	3.40947
Q9Z2Z8	ASLADIWAK	1.005220753	2	2.35279
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	0.927447716	2	5.56653
Q9Z2Z8	GYLFPTSAEDCK	0.90467565	2	2.7939
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.940233804**	**0.99954**	**2**
Q9Z339	GSAPPGPVPEGQIR	0.956231282	2	3.15614
Q9Z339	LEALELNECIDHTPK	0.791318088	2	3.68915

Time point 5.5 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (5.5 h)**	**P-value (5.5 h)**	**Peptide number (5.5 h)**
Accession number	Peptide sequence	Peptide Ratio (5.5 h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**1.324430315**	**0.781807**	**2**
A0JPJ7	IGIVGLPNVGK	1.12064107	2	2.542382
A0JPJ7	YLEANMTQSALPK	1.350837315	2	2.676756
A1L108	**ARP5L Actin_related protein 2/3 complex subunit 5_like protein**	**1.421934404**	**0.230157**	**2**
A1L108	ALAVGGLGSIIR	1.145335799	2	2.756212
A1L108	SSEIEQAVQSLDR	1.452325664	2	2.738532
A1L1L2	**TM214 Transmembrane protein 214**	**1.057303383**	**0.613881**	**2**
A1L1L2	KGSGSNEHVVTCDTACK	2.126032127	3	3.526686
A1L1L2	YDLSSPIQPTSTLYER	0.952614893	2	3.338955
A2A6A1	**GPTC8 G patch domain_containing protein 8**	**0.966286871**	**0.992867**	**2**
A2A6A1	RVLEVEKEDTEELR	0.96518967	2	2.540848
A2A6A1	YKDYVDKEK	0.972453043	1	1.933748
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**1.140764299**	**0.613307**	**3**
A2AAE1	FQTNYASTTHLMTGK+Oxidation(11	1.141038937		
A2AAE1	LHYNSKTLKTESPNASR	1.506106979	2	2.550557
A2AAE1	QGTSSSQPGELRGRK	1.049318578	2	2.52225
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.077485122**	**0.678762**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	2.336188907	2	2.658247
A2ADY9	NPPLAEALLSGDLEK	1.198842683	2	2.842125
A2ADY9	VLVEQQQDR	1.077457589	2	2.881089
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**0.935704146**	**0.641989**	**3**
A2AF47	LCSSVDVDMIQLQLK	1.88899599	2	2.503863
A2AF47	LTGLSEISLR	0.882450159	2	2.352121
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(0	0.928071539		
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.626614608**	**0.143882**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13	0.301349599		
A2AGT5	GESVQEELLK	1.197906482	1	1.938651
A2APB8	**TPX2 Targeting protein for Xklp2**	**1.052188233**	**0.351731**	**2**
A2APB8	GIGEPFQGKNSLRK	1.680609349	2	2.350399
A2APB8	NKKDESLLPSK	1.043172803	2	2.483507
A2AQP0	**MYH7B Myosin_7B**	**1.487742761**	**0.88586**	**7**
A2AQP0	AITDAAMMAEELKK	1.847711232	2	3.337356
A2AQP0	DIDDLELTLAK	4.197592256	2	3.619182
A2AQP0	EQDTSAHLER	1.461140848	2	2.848862
A2AQP0	HDCDLLR	1.993907772	1	2.054365
A2AQP0	KAITDAAMMAEELKK	1.859482211	3	3.624275
A2AQP0	VEDEQLVGVQLQK	2.802171883	2	2.41987
A2AQP0	VGNEYVTK	1.15235883	2	2.414934
A2ASS6	**TITIN Titin**	**1.148537641**	**0.533354**	**13**
A2ASS6	AENRFGIGPPAETIQRTTAR	1.993462014	2	2.513006
A2ASS6	ATNEVGSDTCACTVK	2.945630596	2	3.821153
A2ASS6	ETAMLSWDVPENDGGAPVK+Oxidation(3	1.115683744		
A2ASS6	KDLNMVVSAARISCGGAIR	0.966772736	2	2.365329
A2ASS6	RRTEEGYYEAITAVELK	1.654525272	2	2.57674
A2ASS6	TCEIEIGQLK	1.851542992	2	2.311668
A2ASS6	TDSGAYILTATNPGGFAK	1.645444962	2	2.394869
A2ASS6	TFLQDQLVSLQVLK	1.388802796	1	1.920698
A2ASS6	VGDDAWIKDTTGTALR	1.276746459	2	2.374833
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	1.674495659	3	4.428012

A2ASS6	VLDTPGPPQNLAVK	1.893828831	2	2.314192
A2ASS6	YDGGHKLTGYIVEK	1.658502664	2	2.308454
A2ASS6	YGIGEPLDSEPETAR	1.447119665	2	2.997469
A2AU72	**ARMC3 Armadillo repeat_containing protein 3**	**1.525981119**	**0.000796**	**2**
A2AU72	HASWAVMVCAGDEPMAVELCR+Oxidation(14	1.960211218		
A2AU72	TLGVITCDKEARTMLK+Oxidation(13	1.521512231		
A2AWL7	**MGAP MAX gene_associated protein**	**1.463051856**	**0.015135**	**2**
A2AWL7	ADVSLTTLLTAQASLK	1.382455136	2	2.460145
A2AWL7	TDQGILVTNRDARALLSR	2.797594712	3	3.322809
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.805822617**	**9.9E-20**	**11**
A2VCW9	AEGIVFNTQSTIK	1.868072166	2	2.487345
A2VCW9	AQEANMSLLDEVLK	1.525073192	2	3.460364
A2VCW9	GAQEVFNELPCEYVEPHELK	1.885207474	2	4.468286
A2VCW9	KTDGVYDPVEYEKYPER	1.473652558	3	3.615807
A2VCW9	KYDINTVNVTVGK	1.889082648	2	3.953647
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	1.280022688	3	4.184101
A2VCW9	QDAQSLLVPVK	1.404536439	2	2.555958
A2VCW9	REDVNAWER	1.861204269	2	2.974995
A2VCW9	SSVVPVEGCPELPHK	0.946818303	2	2.706103
A2VCW9	VNMVTASYITPAMK	1.48456518	2	2.503334
A2VCW9	YDINTVNVTVGK	1.041330453	2	2.346035
A4Q9F4	**TTL11 Tubulin polyglutamylase TTLL11**	**1.285271757**	**0.023418**	**2**
A4Q9F4	ALRIMQNLFPEEYNFYPR+Oxidation(4	1.287334545		
A4Q9F4	NLKPMLLEVNANPSMR	1.171384531	2	2.445297
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.268938975**	**0.010257**	**12**
A7VJC2	EESGKPGAHVTVK	1.403353724	2	3.13958
A7VJC2	GFGFVTFDDHDPVDK	1.254683473	2	4.347961
A7VJC2	GGGGNFGPGPGSNFR	1.271044642	2	3.189192
A7VJC2	GGNFGFGDSR	1.524768466	2	2.902228
A7VJC2	IDTIEIITDR	1.121553378	2	3.985121
A7VJC2	LFIGGLSFETTEESLR	2.606891745	2	3.641094
A7VJC2	LTDCVVMR	1.556819015	2	2.613261
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	1.639499471	2	6.063583
A7VJC2	NYYEQWGK	1.308289238	2	2.406525
A7VJC2	QEMQEVQSSR	0.875366526	2	3.028653
A7VJC2	QEMQEVQSSR+Oxidation(2	1.124895308		
A7VJC2	YHTINGHNAEVR	1.229193833	2	3.37763
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.720019135**	**0.192628**	**3**
B0BN93	GSIDEVDKR	1.464406589	2	2.47745
B0BN93	LNIGDLQATK	0.517221376	2	2.314041
B0BN93	SAWGQQPDLAANEAQLLR	2.288096992	2	2.816758
B0BNA7	**EIF3I Eukaryotic translation initiation factor 3 subunit I**	**1.280418535**	**0.529934**	**2**
B0BNA7	HVLTGSADNSCR	1.280418477	2	3.484948
B0BNA7	LFDSTSLEHQK	1.294805253	2	2.374824
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.099754257**	**0.19904**	**7**
B0BNE5	AFNGYLGPDQSK	0.970456574	2	3.17033
B0BNE5	FAIYLPPQAESAK	1.368897171	2	2.672967
B0BNE5	MYSYVTEELPQLINANFPVDPQR	1.111386162	3	5.577575
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.036778542	2	5.772836
B0BNE5	SVSAFAPICNPVLCPWGK	1.18177701	3	4.203033
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.088898679	3	4.889162
B0BNE5	VFEHSSVELK	1.180471545	2	2.811266
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.708356017**	**0.24013**	**2**

B0BNN3	ADGLAIIGVLMK	0.669910458	2	3.300611
B0BNN3	HDSSLKPVSVSYNPATAK	1.49624197	3	5.064192
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.007132261**	**0.936945**	**3**
B0K020	AMVNLQIQK	0.927481835	2	2.622246
B0K020	HNEETGDNVGPLIIK	0.928059633	2	5.157075
B0K020	VVHAFDMEDLGDK	1.191587793	3	3.938781
B1H267	**SNX5 Sorting nexin_5**	**1.340945808**	**0.065132**	**2**
B1H267	NNVSLLQSCIDLFK	1.314732725	2	3.132536
B1H267	TTLPTFQSPEFSVTR	1.36735318	2	3.592205
B2GUV7	**IF2P Eukaryotic translation initiation factor 5B**	**1.581354707**	**0.075027**	**2**
B2GUV7	HLQAQGVEVPSK	1.2562521	2	2.761408
B2GUV7	LKEGDTIIVPGVEGPIVTQIR	1.582196462	3	3.36647
B2GUZ5	**CAZA1 F_actin_capping protein subunit alpha_1**	**1.044613187**	**0.352361**	**3**
B2GUZ5	EASDPQPEDVDGGLK	0.687551106	2	2.516387
B2GUZ5	FITHAPPGEFNEVFNDVR	1.776338146	3	3.700615
B2GUZ5	FTITPPTAQVVGVLK	0.812357229	2	2.946579
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.439985279**	**1.61E-05**	**3**
B2GV24	NNPVHLITEEDLK	1.267633925	2	2.545538
B2GV24	TYDLPGDFLTQALTQR	2.466970491	2	3.2333
B2GV24	VNIVDLQQVINVDLTHIENR	1.483555249	3	3.620727
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**1.312772077**	**0.004643**	**6**
B2RYW9	ALAAQLPLIPR	0.777077162	2	2.857671
B2RYW9	GETALSVAR	1.304441352	2	3.073675
B2RYW9	KGDEVQCEIEELGVIINK	1.736948587	2	4.812235
B2RYW9	TFDTFCPLGPALVTK	1.353753001	2	4.975682
B2RYW9	VICVGLNYADHCQEQNVR	1.281428975	2	2.97759
B2RYW9	VNGEIVQSSNTNQMVFK	1.17043199	2	4.786794
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**1.133295636**	**0.692454**	**2**
B2RZ78	GDFDESLNYPEQK	1.133278107	2	3.639549
B2RZ78	IQHILCTGNLCTK	1.498421959	2	3.036149
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.030261277**	**0.968105**	**6**
B3DMA2	AVLTVTQYR	1.020494516	2	2.482949
B3DMA2	GSHIQENTGIPLMEELISIYCR	1.274621132	2	2.327374
B3DMA2	LYEHEVVAHWIAK	1.038881318	3	3.706887
B3DMA2	MELQDQAR	1.480965906	2	2.479287
B3DMA2	NLPDSDNEECLVHGDFK	0.89382149	2	3.462373
B3DMA2	SGQSNPTFFLQK	0.947261031	2	2.586889
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.647869874**	**2.22E-07**	**4**
B5DFC8	FEELTNLIR	1.784466046	2	2.434606
B5DFC8	GTEITHAVVIK	1.807878221	2	2.897748
B5DFC8	LGSLVENNER	1.626731098	2	2.666179
B5DFC8	TEPTAQQNLALQLAEK	1.585918864	2	4.849144
B7ZNG0	**KIF7 Kinesin_like protein KIF7**	**0.961037475**	**0.076641**	**2**
B7ZNG0	ELGRHMWINQELK+Oxidation(5	0.675824725		
B7ZNG0	KEALMQEK	1.390763173	2	2.721646
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.423793881**	**0.36674**	**2**
D3ZTX0	QCFYEDITQGTK	1.586009086	2	2.74209
D3ZTX0	SVIDYQTHFR	1.421238921	2	2.837945
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.425679397**	**0.035724**	**5**
D3ZW55	DFGWDPCFQPDGYEQTYAEMPK	0.894172066	2	3.30029
D3ZW55	IDLPEYQGEPDEISIQK	3.138434212	2	4.347663

D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.477955378	3	4.416661
D3ZW55	LKPEGLYQLLAGFEDK	2.410324717	3	3.58711
D3ZW55	LQEYFGVTDGAGDH	1.634658916	2	3.41133
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.298128957**	**0.019299**	**2**
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(12	1.298128957		
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(9	1.298128957		
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.585102391**	**0.121716**	**4**
D4A4T9	FDPEANADDACTYHPGVPVFHDALK	1.567467858	3	3.533117
D4A4T9	HNSEKPPEPVKPEVK	1.534029391	3	3.658474
D4A4T9	KEEDSDEIKIGTSCK	0.977405565	2	2.53985
D4A4T9	LSSGNEEDKKEEDSDEIK	1.589778646	3	4.297395
D4A666	**UBN2 Ubinuclein_2**	**1.573669575**	**0.161782**	**2**
D4A666	GWMQARMLFK+Oxidation(2)Oxidation(6	2.358076337		
D4A666	KEEGEKEK	1.417053259	1	1.909301
E9Q557	**DESP Desmoplakin**	**0.896230608**	**0.010116**	**2**
E9Q557	KQVQTSQKNTLR	0.889690279	2	2.318473
E9Q557	SQCTQVVQER	1.221518908	2	2.45344
F6YLP3	EMFVYLSTQLKK+Oxidation(1	5.454758561		
F6YLP3	KEMFVYLSTQLKK	1.046220669	2	2.536631
F6YLP3	SGDISAVQPK	0.902427692	2	3.076685
F6YLP3	SMVTAGFEPVVIENVLEGDELR	2.001635645	2	3.599561
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**1.940119167**	**0.00571**	**2**
O08550	HAAVALGQARAMVPEDVPR	1.711420419	2	2.342709
O08550	MVQALTELLR+Oxidation(0	2.067490643		
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.131941183**	**0.064806**	**11**
O08557	DENATLDGGDVLFTGR	1.031837845	2	2.413503
O08557	DHLLIPVSNSEMEK	1.177800785	2	2.493207
O08557	DYAVSTVPVADSLHLK	1.383461245	2	3.67323
O08557	GAEILADTFK	1.06221567	1	2.096512
O08557	KEVDMMK	1.884871849	2	2.323218
O08557	LKDHLLIPVSNSEMEK	1.76358857	2	3.811135
O08557	LTVPDDMAANCIYLNIPSK	1.251961404	2	3.267039
O08557	SFCSMAGPNLIAIGSSESAQK	1.495472121	2	4.773208
O08557	SQGEEVDFAR	4.467610317	2	2.824431
O08557	TPEEYPESAK	1.397769809	2	2.366291
O08557	VDGLLTCCSVFINK	1.135619187	2	3.511756
O08583	**THOC4 THO complex subunit 4**	**1.281675041**	**0.105259**	**3**
O08583	MDMSLDDIIK	2.196702982	2	2.668649
O08583	QQLSAEELDAQLDAYNAR	1.205498193	2	3.401165
O08583	SLGTADVHFER	1.571584558	2	2.748129
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.256783687**	**0.022994**	**15**
O08601	EDTTMYLLALK	1.42998987	2	2.531857
O08601	EFYSYENEPVGIENLK	1.395715928	2	4.23238
O08601	GCPSLAEHWKSIR	1.112698058	2	3.842463
O08601	GHTTGLSLNNER	1.119422503	2	2.545867
O08601	GSFASNDIR	1.541325375	2	2.718593
O08601	LILGGLEKPEK	0.987319562	2	2.447072
O08601	MLSASGDPVSVVK	1.241878992	2	3.578808
O08601	NALLPEGIPLLLK	2.325414423	3	3.583309
O08601	NILLSIGELPK	1.205936517	2	3.748615
O08601	REEILQILK	2.033685584	3	3.47206
O08601	SDSSIILQER	1.406135828	2	3.106385
O08601	SGSSSAYTGYVER	1.02853475	2	3.67906

O08601	SNLNIFQYIGK	0.854880801	2	3.182842
O08601	TTAAAVILK	1.090888457	2	2.313745
O08601	VKEFYSYENEPVGIENLK	1.009725652	2	3.583745
O08629	**TIF1B Transcription intermediary factor 1_beta**	**2.108257605**	**0.061196**	**2**
O08629	IVAERPGTNSTGPGPMAPPR	1.564865985	3	3.910246
O08629	LDLDLTSDSQPPVFK	2.109155809	2	4.256386
O08795	**GLU2B Glucosidase 2 subunit beta**	**1.61626179**	**0.23029**	**6**
O08795	ETVVTSTTEPSR	1.496704158	2	3.102255
O08795	KLWEEQQAAAK	1.281418629	2	3.417211
O08795	LWEEQQAAAK	1.463373494	2	2.980506
O08795	MPPYDEETQAIIDAAQEAR	2.657673584	2	5.185298
O08795	SLEDQVETLR	0.959949292	2	3.153387
O08795	YEQGTGCWQGPNR	1.332651249	2	3.776794
O09158	**CP3AP Cytochrome P450 3A25**	**2.625329574**	**0.343126**	**2**
O09158	DVEINGVFIPK	2.703825477	2	3.142442
O09158	VDFLQLMMNTQNSK	1.194705631	2	3.109197
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.580624232**	**9.9E-20**	**14**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.419502983	2	6.130187
O09171	AGPWTPEAAVEHPEAVR	1.167589735	2	5.005803
O09171	GAAELMQQK	1.294754905	2	3.649472
O09171	GAAELMQQK+Oxidation(5	1.366699737		
O09171	HGSWGSGLDMHTKPWIR	1.107672113	3	4.705975
O09171	IFHQQLEVFMK	1.057228369	2	3.563496
O09171	ISGQKVNEAACDIAR	1.440724657	2	4.449034
O09171	KEYWQNLR	1.073000251	3	3.440414
O09171	LNAGEVVIGDGGFVFALEK	1.819302191	3	5.921896
O09171	QGFIDLPEFPFGLEPR	2.034446769	2	5.036897
O09171	QVADEGDALVAGGVSQTPSYLSCK	63.33225931	2	6.109756
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.431180178	3	6.19249
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9	1.825515298		
O09171	VNEAACDIAR	1.189606721	2	4.035338
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.112**	**0.00296**	**9**
O09173	CFYNSDGDFLIVPQK	1.483680308	2	3.094269
O09173	FSVDVFEETR	1.484381227	2	3.606579
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.451371215	3	3.742076
O09173	NCMSEFMGLIK	1.157577191	2	3.201366
O09173	QDVSPFNVVAWHGNYTPYK	1.413793797	2	3.750953
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.156770019	3	3.881219
O09173	SLRPGVAIADFVIFPPR	1.54289624	2	3.712141
O09173	TFRPPYYHR	0.757887576	3	3.493924
O09173	YISGFGNECASEDPR	1.642565297	2	3.92119
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.160825793**	**0.000975**	**17**
O35077	ANTIGISLIK	1.133186618	2	3.07506
O35077	DPAQGQLLK	1.520761423	2	2.389694
O35077	ELHSILQHK	1.16417866	2	2.566083
O35077	FCETTIGCK	1.114067583	2	2.663847
O35077	FCETTIGCKDPAQGQLLK	1.094849289	2	5.335864
O35077	GIDEGPNGLK	1.136780213	2	2.921076
O35077	GLVDKFPLFTAVYK	1.044012095	3	3.722587
O35077	ICDQLKGHLK	1.080730837	3	3.797898
O35077	ITVVQEVDTVEICGALK	2.680793306	2	3.1124
O35077	IVGSNASQLAHFDPR	1.697080121	2	3.115673
O35077	KLTEIINTQHENVK	1.182156966	2	5.273067
O35077	LTEIINTQHENVK	1.150890591	2	4.416082
O35077	NIVAVGAGFCDGLGFGDNTK	1.417704671	2	5.572182

O35077	SIEQLEK	1.107411293	2	2.382285
O35077	VCIVGSGNWGSAIAK	1.382248332	2	4.353549
O35077	VCYEGQPVGEFICCLQNHPEHM	1.445381929	2	4.131886
O35077	VTMWVFEEDIGGR	1.425881711	2	3.390036
O35078	**OXDA D_amino_acid oxidase**	**1.562609836**	**0.310687**	**2**
O35078	GQIIQVEAPWIK	1.320017746	2	3.09514
O35078	SCCQLEPTLK	4.228099679	2	2.647738
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**1.1767615**	**0.382269**	**4**
O35094	AISQGVESVKK	0.937589915	2	2.372121
O35094	KLEESDALQEAR	1.228389314	2	3.592262
O35094	TEMSEVLTEILR	1.394024202	2	3.274178
O35094	VTDLLGGLFSK	1.144637666	2	2.582153
O35142	**COPB2 Coatomer subunit beta_**	**1.432302663**	**0.125739**	**5**
O35142	AAESLADPTEYENLFPGLK	2.281527695	2	3.885855
O35142	EEPAMSMDANGKIIWAK	1.609553778	2	2.530629
O35142	FELALQLGELK	1.46413584	2	3.054841
O35142	GSNNVALGYDEGSIIVK	1.069204587	2	3.558794
O35142	TFEVCDLPVR	1.255048429	2	2.9816
O35244	**PRDX6 Peroxiredoxin_6**	**1.223641773**	**5.27E-08**	**8**
O35244	DINAYNGAAPTEK	1.388483156	2	3.95067
O35244	DLAILLGMLDPAEKDEK	1.223251401	2	3.951146
O35244	GESVMVLPTLPEEEAK	1.950874585	2	3.255132
O35244	KGESVMVLPTLPEEEAK	1.404939885	2	5.332367
O35244	LSILYPATTGR	1.569409997	2	3.147505
O35244	NFDEILR	1.148022448	1	2.271842
O35244	VVDSLQLTASNPVATPVDWK	1.269545356	3	5.524613
O35244	VVFIFGPDKK	0.751761409	2	2.896443
O35286	**DHX15 Putative pre_mRNA_splicing factor ATP_dependent RNA helicase DHX15**	**1.553983801**	**0.020963**	**2**
O35286	TCTDIKPEWLVK	1.583166253	2	2.413568
O35286	TLATDILMGVLK	1.552858496	2	3.721823
O35331	**PDXK Pyridoxal kinase**	**0.935086381**	**0.624261**	**2**
O35331	AEAGEGQKPSPAQLELR	0.673082229	3	3.845347
O35331	MGPDTVVITSSDLPSPK	0.9403327	2	3.6926
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**1.029195718**	**0.905311**	**2**
O35469	DLGYEPLVSWEEAK	0.906574344	2	4.342849
O35469	TSEWIGTLVEQHR	1.069393243	2	3.409183
O35509	**RB11B Ras_related protein Rab_11B**	**1.268011204**	**0.266671**	**5**
O35509	AQIWDTAGQER	1.126203807	2	3.236881
O35509	GAVGALLVYDIAK	1.195342678	2	3.986113
O35509	HLTYENVER	1.621688672	2	2.467955
O35509	NEFNLESK	1.253280288	1	2.145783
O35509	VVLIGDSGVGK	1.251786557	2	2.474531
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**0.926839009**	**0.663114**	**2**
O35547	LERFEIPIK	1.219249071	2	2.539652
O35547	TAEDYSVDENGQR	0.878559442	2	3.238975
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.169075591**	**0.000108**	**7**
O35567	ALFEEVPELLTEAEK	1.771260582	2	3.503824
O35567	DGQVIGIGAGQQSR	2.941355174	2	3.897578
O35567	EVSDGIVAPGYEEEALK	1.016775051	2	3.80849
O35567	HVSPAGAAVGVPLSEDEAR	1.071109867	2	5.150934
O35567	SGVAYIVAPSGSTADK	1.101828057	2	2.86537
O35567	VTVVCEPEDYGAVAAEMQGSGNK	0.686301414	2	5.41396
O35567	YTQSNSVCYAK	0.977976481	2	3.136958

O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**1.252935731**	**0.096468**	**3**
O35593	AVAVVVDPIQSVK	1.222926713	2	3.077998
O35593	AVEEEDKMTPEQLAIK	1.24922441	2	4.720413
O35593	EMLELAKNYNK+Oxidation(1	1.30951591		
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.146574747**	**0.959662**	**3**
O35660	RYAMGDAPDYDR	1.187775192	2	3.378629
O35660	YAMGDAPDYDR	1.481827871	2	2.438771
O35660	YAMGDAPDYDR+Oxidation(2	1.064635677		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**2.257223451**	**0.778355**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	7.613905506	2	4.213808
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	1.93174683	3	3.415622
O35760	NCHLNENIDK	1.016952501	3	3.338125
O35760	NVTLNPDPNEIK	1.295714295	2	3.140018
O35763	**MOES Moesin**	**1.139555277**	**0.17914**	**5**
O35763	ALTSELANAR	1.195293711	2	2.520818
O35763	AQMVQEDLEK	0.999154852	2	2.492213
O35763	AQQELEEQTR	1.307591366	2	2.815982
O35763	FYPEDVSEELIQDITQR	1.019472203	3	3.342651
O35763	TQEQLASEMAELTAR	1.747794059	2	4.017751
O35783	**CALU Calumenin**	**0.903571666**	**0.998694**	**2**
O35783	HLVYESDQDKDGK	0.902607666	2	3.968505
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.031164946	3	5.237835
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.122088656**	**0.186145**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	1.205075581	2	4.785666
O35796	AFVEFLTDEIK	1.680977462	2	3.253572
O35796	AFVEFLTDEIKEEK	0.858141177	2	3.790412
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.88452679	3	5.684881
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**0.888982125**	**0.032896**	**7**
O35814	ALDLDSSCK	1.275324308	1	2.446944
O35814	ALSAGNIDDALQCYSEAIK	1.252260651	2	5.764358
O35814	AMADPEVQQIMSDPAMR	5.676441728	2	3.9249
O35814	CQQAEKILK	0.954927935	1	2.020421
O35814	DCEECIQLEPTFIK	1.205269949	2	4.422485
O35814	ELIEQLQNKPSDLGTK	0.870336783	2	4.026013
O35814	TVDLKPDWGK	1.513884912	2	2.683254
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**1.218163983**	**0.390709**	**2**
O35824	NVLCSACSGQGGK	1.197704531	2	3.263285
O35824	VSLEDLYNGK	1.626340907	2	2.331587
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.19811802**	**0.659284**	**8**
O35826	DEAVGALHLIQAAK	1.434595671	2	3.506987
O35826	EVGAFGTPVINLGTR	1.221659196	2	3.202315
O35826	ILGVGISTGGR	1.937308209	2	2.84115
O35826	IYGDGNAVPR	1.139233383	2	2.463682
O35826	SIDLQEPLQK	1.0298635	2	2.414048
O35826	TLVLFPNIDAGSK	1.077368848	2	2.667685
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.244632302	3	5.11907
O35826	VNPQEGVVLHSTK	1.420959933	2	2.539319
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**1.029850825**	**0.554493**	**5**
O35913	EGLQENVDGTENAK	1.139986031	2	3.757473
O35913	GASFVPAFFILR	1.597891707	2	2.635695
O35913	SLSGTYMNSMLTQIER	0.971888581	2	4.574149
O35913	SQTLNPTQDPSECVK	0.853922984	2	4.144578
O35913	TFQFPGDIESSK	1.243253264	2	2.409178

O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.342688651**	**0.127778**	**7**
O35952	ALLEVLGR	1.130660691	2	2.985906
O35952	FYEGTADEMYK	1.365347695	2	3.100673
O35952	HVEPGNTAVQEK	1.005823645	2	4.01675
O35952	LTTVLTTHHHWDHAGGNEK	1.27233716	3	3.580404
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.52492333	3	4.346018
O35952	TVQQHAGETDPVTTMR	1.636241561	2	4.745533
O35952	TVQQHAGETDPVTTMR+Oxidation(14	1.191778721		
O35987	**NSF1C NSFL1 cofactor p47**	**0.825774743**	**0.004274**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.341592715	2	4.473217
O35987	EANLLNAVIVQR	1.45907816	2	3.062762
O35987	LGAAPEEESAYVAGER	0.823112107	2	4.293351
O35987	SYQDPSNAQFLESIR	1.486193919	2	4.189614
O35987	TGFSLDNGDLR	0.704817848	2	2.919451
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.802417354**	**0.2235**	**3**
O54753	IVNVSSVLGR	1.541481658	2	2.577216
O54753	TWEATPEHIR	1.87233229	2	2.401402
O54753	YGVEAFSDVLR	1.55776207	2	3.291524
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.285699243**	**0.053447**	**3**
O54975	GSLTFEPLTLVPIQTK	1.295771839	2	4.098561
O54975	IENVVLVVPAK	1.187419705	2	2.668395
O54975	QQADFVDLSFPTISSTGPNGAIIHYAPIPETNR	1.51935825	3	3.717046
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.368466683**	**0.001849**	**4**
O55012	ATTLSNAVSSLASTGLSLTK	1.457650892	2	4.230917
O55012	ITAAQHSVTGSAVSK	1.379286576	2	4.633418
O55012	SGLQGYDMSTFIR	1.419652062	2	3.747138
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	1.171730059	3	5.746399
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.159546317**	**2.11E-05**	**7**
O55096	AGLLALEFYTPETANWR	2.058237019	2	3.619805
O55096	GEFEGFVAMVNK	1.028422646	2	2.689551
O55096	LASVLNTEPALDSELTSK	1.444320959	2	2.987895
O55096	LEGSEVQLVEYEASAAGLIR	1.977412043	2	3.912282
O55096	NVSLGNVLAVAYATK	0.94613353	2	2.683892
O55096	SYEFQGNHFQVTR	1.22669099	2	4.033111
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.121053268	3	3.946887
O55125	**NIPS1 Protein NipSnap homolog 1**	**1.336495521**	**0.013629**	**4**
O55125	AGPNIYELR	1.164627683	2	2.990045
O55125	FSGGYPALMDCMNK	1.333423914	2	2.999415
O55125	GWDENVYYTVPLVR	0.923732869	2	3.601168
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.664393644	3	5.098723
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.157611397**	**0.001692**	**6**
O55171	ADAGGELDLAR	0.992750723	2	2.809288
O55171	DGLLDVVEALQSPLVDKK	0.958512374	2	4.924433
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.66575859	3	4.408544
O55171	GGELGLAMASFLK	1.874759971	2	4.03292
O55171	IEYFEEAVNYLR	1.50750298	2	4.048993
O55171	SCWDEPLSITVR	1.333953657	2	3.99257
O70127	**ABCBB Bile salt export pump**	**1.319177166**	**1.61E-05**	**7**
O70127	AGQITSEALSNIR	1.250445308	2	3.173836
O70127	AGSIADEVLSSIR	1.844782851	2	2.9629
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.991430797	3	4.351305
O70127	ILLLDEATSALDTESEK	1.640422601	2	4.275761
O70127	ILLLDMATSALDNESEAR	7.138849292	2	2.314258

O70127	KFGEENHAFESDGSHNNDKK	2.182432647	3	4.490193
O70127	STALQLIQR	0.979242522	2	2.701622
O70133	**DHX9 ATP_dependent RNA helicase A**	**1.318716911**	**0.394737**	**3**
O70133	ELDALDANDELTPLGR	1.165516043	2	2.50678
O70133	KMTPAYEIRAVGNK	1.890758805	2	2.443112
O70133	YPSPFFVFGEKIR	0.857861833	2	2.38157
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**1.310037179**	**0.255747**	**2**
O70173	LLGDIGEKVK	1.313997603	2	2.31537
O70173	WTFSHPLEALGLLTSR	1.279204484	2	2.425597
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.75343849**	**9.9E-20**	**14**
O70199	EADLVFISVNTPTK	1.422915103	2	2.352349
O70199	EQIVVDLSHPGVSADDQVSR	1.317088886	2	5.617486
O70199	FSLQDPPNKKPK	2.014697551	2	2.389528
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.906637651	3	6.625101
O70199	IIDSLFNTVTDK	1.928405618	2	2.38015
O70199	IIDSLFNTVTDKK	1.219966435	2	3.73759
O70199	ILTTNTWSSELSK	1.229141326	2	3.840705
O70199	INAWNSPTLPIYEPGLK	1.678804106	2	4.200477
O70199	MLKPAFIFDGR	2.157126764	2	2.449353
O70199	NLFFSTNIDDAIR	1.352637321	2	3.420667
O70199	VLDGLHNELQTIGFQIETIGK	1.726151646	2	5.429731
O70199	VLIGGDETPEGQR	1.276407794	2	3.52231
O70199	VTVVDVNEAR	1.464030016	2	3.179179
O70199	YWQQVIDMNDYQR	2.782247925	2	4.284932
O70251	**EF1B Elongation factor 1_beta**	**1.607743816**	**0.000212**	**4**
O70251	SIQADGLVWGSSK	1.189367853	2	3.314929
O70251	SSILLDVKPWDDETDMTK	2.010988048	2	4.272106
O70251	SSILLDVKPWDDETDMTKLEECVR	2.223709005	3	5.224351
O70251	TPAGLQVLNDYLADK	1.242280937	2	3.97247
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.401591851**	**9.9E-20**	**17**
O70351	EVQAALTLAK	1.307367689	2	2.621706
O70351	GGIVGMTLPIAR	1.426616509	2	3.746668
O70351	GLVAVITGGASGLGLSTAK	1.350229678	2	4.849121
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.38102437	3	4.83826
O70351	IDVAVNCAGIAVAIK	1.669322342	2	4.437831
O70351	KLGGNCIFAPANVTSEK	1.240622138	2	4.856229
O70351	KNQVHTLEDFQR	1.073618584	2	3.955417
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.385759977	3	5.285328
O70351	LGGNCIFAPANVTSEK	1.302276384	2	3.420713
O70351	LVAGVMGQNEPDQGGQR	4.82499947	2	5.6786
O70351	LVGQGATAVLLDVPNSEGETEAK	2.086197138	2	5.417454
O70351	LVGQGATAVLLDVPNSEGETEAKK	1.047139324	3	4.285881
O70351	NFLASQVPFPSR	1.212901944	2	4.624768
O70351	NQVHTLEDFQR	1.296181766	2	3.333013
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.240653277	2	5.55966
O70351	VINVNLIGTFNVIR	1.496979054	2	4.605125
O70351	VVTIAPGLFATPLLTTLPDK	1.247544733	2	5.048592
O70456	**1433S 14_3_3 protein sigma**	**0.946223428**	**9.9E-20**	**3**
O70456	DSTLIMQLLR	2.095973533	2	3.748806
O70456	NLLSVAYK	0.791190162	2	2.432096
O70456	VLSSIEQK	0.945421048	2	2.609917
O88202	**LPP60 60 kDa lysophospholipase**	**1.777908584**	**0.031884**	**4**
O88202	AAGAHLSPQELEDVGTELCR	1.498775919	3	3.897959
O88202	GEMTLPTTDDLLGDDMLGCR	4.034655227	2	3.822053
O88202	GVDVDACNEDGQSPLLLAVR	1.792903693	2	5.098151
O88202	SEGGVLVPGR	1.467892535	2	2.543075

O88379	**BAZ1A Bromodomain adjacent to zinc finger domain protein 1A**	**2.101427818**	**9.99E-10**	**2**
O88379	ERDKLLK	2.044006999	2	2.344065
O88379	NTAKSASKNLR	2.103564652	2	2.794291
O88397	**SO1A5 Solute carrier organic anion transporter family member 1A5**	**0.831717765**	**0.036827**	**2**
O88397	TCLHWGTLK	0.829239457	2	2.322559
O88397	YLEQQYGK	1.432472873	2	2.767943
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.297890019**	**2.01E-14**	**6**
O88428	GCTVWLTGLSGAGK	1.892448166	2	3.267237
O88428	GFTGIDSDYEKPETPECVLK	1.311690943	2	4.967531
O88428	GIHELFVPENK	1.70272642	2	2.757452
O88428	NLGFSAGDREENIR	1.077322168	2	3.308253
O88428	STNVVYQAHHVSR	0.787049214	2	4.255774
O88428	VLSMAPGLTSVEIIPFR	1.459194764	2	3.638241
O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**0.864318826**	**0.026267**	**3**
O88491	ENSEGAFGVLLPADAVQKAR	0.817796032	2	2.365793
O88491	ETGIPSLMPQTK	1.600185208	2	2.320754
O88491	SGKGEGLKLLNNMHEK	1.585918864	2	2.759278
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.131277061**	**2.24E-06**	**18**
O88600	AESEEMETSQAGSK	1.486124868	2	4.662004
O88600	AFSDPFVEAEK	1.077576392	2	3.02864
O88600	AGGIETIANEYSDR	1.416873247	2	3.413489
O88600	FLEMCDDLLAR	0.849487474	2	2.503016
O88600	FQESEERPK	1.067721269	2	2.763741
O88600	FVSEDDRNNFTLK	1.456621572	2	2.782351
O88600	GCALQCAILSPAFK	1.043902494	2	3.800041
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	0.755822278	3	5.110522
O88600	LKETAESVLK	2.884615961	2	2.53628
O88600	MIMQDKLEK+Oxidation(0	1.205458895		
O88600	MQVDQEEPHTEEQQPQTPAENK	1.209196213	3	5.32193
O88600	NFTTEQVTAMLLSK	1.57975339	2	4.117039
O88600	NKEDQYEHLDAADMTK	1.77617128	3	3.74273
O88600	SNLAYDIVQLPTGLTGIK	1.150508463	2	4.082756
O88600	SVMDATQIAGLNCLR	2.2329974	2	3.593034
O88600	TSTVDLPIESQLLWQLDR	1.365052283	2	3.707368
O88600	VLATAFDTTLGGR	1.408411117	2	3.794535
O88600	WNSPAEEGSSDCEVFPK	1.291490099	2	3.823145
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.31518901**	**9.9E-20**	**21**
O88618	AFAACLGAIK	1.172590318	2	3.131469
O88618	AGEYEALPEK	0.965654819	2	2.791129
O88618	ALLDAAAFYCDK	2.174343881	2	3.499999
O88618	ALLDAAAFYCDKEK	1.846303138	2	3.415438
O88618	EAQELNLPVVGSQLVGLVPLK	1.350700957	3	4.275215
O88618	GVSMDECVLCAK	1.339453602	2	3.700679
O88618	IIEYLVPDSGPEQSLLDASLR	1.176826031	2	4.868913
O88618	ISSLLQEAK	1.603932274	2	2.385606
O88618	KVQGIGWYLEEK	1.126805109	2	3.27075
O88618	LAEELNVPVYLYGEAAQMPSR	1.48545279	2	4.916192
O88618	LFVLEEEHR	1.028682013	2	2.84273
O88618	LGLDSLAPFDPK	1.946952329	2	3.841317
O88618	MGALDVCPFIPVR	1.326041056	2	3.937094
O88618	MGALDVCPFIPVR+Oxidation(0	0.403679326		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	2.321956985	3	4.104687
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.674941144	2	3.936341

O88618	TASQLIDMR	1.251623837	2	2.369181
O88618	TCALQEGLR	1.601259835	2	2.810153
O88618	TQAALVLGSLEAR	1.42820531	2	5.094145
O88618	TVYTFVGQPECVVEGALSAAR	0.925315805	2	4.758255
O88618	VQGIGWYLEEK	1.235553629	2	3.076946
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.231663542**	**0.113582**	**9**
O88637	AHHSSQEMSSEYR	1.625142128	3	3.786894
O88637	GPPVFTQEER	1.345262699	2	2.70262
O88637	HKGPPVFTQEER	1.314278971	2	3.10687
O88637	HNCDFCVHGNDITLTVDGR	1.419310075	3	3.882883
O88637	NRLEYEAR	1.571181135	2	2.409177
O88637	TEIVPDRDGSDPYEEPK	0.93134031	2	2.869979
O88637	TQGVSTTDLVGR	1.219905078	2	3.16976
O88637	WVDEVVPAAPYVTTLETLDK	1.740378021	2	2.622114
O88637	YVSEVVIGAPYSVTAELLNHFK	1.402755712	3	3.765941
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**0.990851827**	**0.616942**	**2**
O88656	ASSEGGAATGAGLDSLHK	0.969652443	2	4.290176
O88656	NSVSQISVLSGGK	1.28337318	2	2.531919
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**1.402680062**	**0.475913**	**2**
O88696	GQATDIAIQAEEIMK	3.626477071	2	4.273593
O88696	VLVHPPQDGEDEPELVQK	1.277246457	3	3.952577
O88735	**MAP7 Ensconsin**	**0.92588366**	**0.382658**	**2**
O88735	KTTEQRNGDIAK	0.821858352	2	2.57664
O88735	TSAGTTDPEEATR	1.190405468	2	2.667503
O88746	**TOM1 Target of Myb protein 1**	**1.28588185**	**0.417966**	**3**
O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	1.380223523	3	5.525964
O88746	QQSTGAIPATQAR	1.266225555	2	2.701421
O88746	YEAPQTTDGLAGALDAR	1.41434868	2	3.890565
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.198468164**	**0.784827**	**3**
O88761	DTSEDIEELVEPVAAHGPK	1.156163407	2	4.180901
O88761	QGALIASALIMIQQTEITCPK	1.381032297	2	2.414191
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.205870084	2	3.694288
O88767	**PARK7 Protein DJ_1**	**1.274626408**	**7.08E-07**	**8**
O88767	ALVILAK	2.050276846	2	2.375635
O88767	DVVICPDTSLEEAK	0.839542931	2	3.41998
O88767	GAEEMETVIPVDIMR	0.941742078	2	4.199682
O88767	GAEEMETVIPVDIMR+Oxidation(4	1.439442181		
O88767	GLIAAICAGPTALLAHEVGFGCK	1.41547335	2	4.456868
O88767	KGLIAAICAGPTALLAHEVGFGCK	0.505347947	3	3.99545
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	1.263985386	3	4.697952
O88767	VTVAGLAGKDPVQCSR	1.29630473	2	4.251676
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**1.560324222**	**0.639302**	**3**
O88794	FFTNYESR	1.699466171	2	2.328628
O88794	KKNEELGQLYR	1.385272766	2	2.983276
O88794	SSQIGAVVSR	2.241122602	2	2.816856
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.337584117**	**0.004411**	**14**
O88813	AEYLGSCLLHK	0.689582293	2	2.72412
O88813	AILEDLQK	1.239418489	1	2.230862
O88813	ATMLIENVEK	1.386837723	2	2.341135
O88813	FFQTQIK	1.466152213	1	2.026177
O88813	GAMLTHQNIVSNMAAFLK	1.240126805	3	3.594405
O88813	GLAVSDNGPCLGYR	1.611581679	2	3.432582
O88813	GSFEELCQNQCVK	1.312315407	2	4.42662

O88813	GYLKDPEK	1.101751464	2	2.393895
O88813	IGFFQGDIR	1.379383067	2	3.226534
O88813	SFLIGVVVPDPESLPSFAAK	1.212210916	2	4.350648
O88813	SIFVHPEPFSIENGLLTPTLK	1.648812997	2	3.635881
O88813	SRPILQVFVHGESLR	0.723251445	3	3.768208
O88813	TQEVLDKDGWLHTGDIGR	1.364535091	3	3.742496
O88813	TVILMDPFDDDLMK	2.155714858	2	3.516551
O88867	**KMO Kynurenine 3_monooxygenase**	**1.202153566**	**0.132378**	**7**
O88867	AVGLEDQIVSK	1.201335496	2	2.494055
O88867	DFFLLPAQPMISVK	1.372694779	2	2.758301
O88867	DLLTAVESYPNAK	0.95817993	2	2.393507
O88867	FNNDLSVCLPEFSR	1.204305748	2	4.060529
O88867	NFPDAIPLMGEQALMR	1.508258229	2	3.275759
O88867	SINLALSYR	1.447274472	2	2.387067
O88867	SQYILSISR	0.993983582	2	2.418317
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.15001843**	**0.689736**	**3**
O88941	ALESHAAAFK	0.768179199	2	2.468373
O88941	DLALPTLLNPK	1.163920651	2	2.770781
O88941	MDPSLFPPVPLFSGVPSR	1.235001415	2	2.742331
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.618511977**	**0.242284**	**3**
O88986	GTDELLGVMDQVTIINSTLGK	1.620264879	2	3.994629
O88986	HLDMADLEAK	1.272479989	2	2.445382
O88986	VQISAVHSEEDIDR	1.332197691	2	3.961258
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.193157756**	**5.78E-12**	**9**
O88989	DLDVAVLVGSMPR	2.970839246	3	4.186115
O88989	EKMDLTAKELTEEK+Oxidation(2	1.692698886		
O88989	ELTEEKETAFEFLSSA	5.377448833	2	3.473678
O88989	EVGVYEALKDDSWLK	2.531524511	2	4.40612
O88989	FVEGLPINDFSR	1.17498146	2	3.417434
O88989	GEFITTVQQR	1.238375319	2	3.980754
O88989	LGVTADDVK	1.120469941	2	2.922318
O88989	NVIIWGNHSSTQYPDVNHAK	1.231381412	2	5.81141
O88989	VIVVGNPANTNCLTASK	1.193031278	2	5.243211
O88990	**ACTN3 Alpha_actinin_3**	**1.35574942**	**0.708596**	**10**
O88990	AGTQIENIEEDFR	1.260993867	2	3.564615
O88990	ALDFIASK	1.455250916	2	2.671113
O88990	CQLEINFNTLQTK	1.253264295	2	3.848874
O88990	FAIQDISVEETSAK	1.397411008	2	4.343997
O88990	GAILGIQGEIQK	1.724600419	2	3.074251
O88990	GLSQEQLNEFR	1.283936582	2	2.714711
O88990	HEAFESDLAAHQDR	1.332086884	3	4.450583
O88990	TINEVENQVLTR	1.204431959	2	3.217324
O88990	VGWEQLLTSIAR	1.218527627	2	2.715092
O88990	VLAVNQENEK	2.150636974	2	2.322774
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.832032733**	**2.96E-13**	**4**
O88994	CVLTTVDPDTGIIDR	1.0386196	2	4.322171
O88994	GVSVCETECTDMGLR	1.36799007	2	3.362385
O88994	QLQQVGTVSK	0.850582693	1	2.179801
O88994	RQLQQVGTVSK	0.517779568	2	3.082038
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**0.981514503**	**0.460665**	**4**
O89000	GMGLACGQDPELVR	1.16207689	2	3.486953
O89000	LENNFDDIK	1.663841832	2	2.46471
O89000	QEYVGGLSTSEIPQFR	0.948915823	2	3.335798
O89000	TEQDETGNWVEDEEQIVR	3.333649868	2	4.664864
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**0.986584593**	**0.900729**	**2**

O89032	DDSDINTSKTGEVSKR	0.954769998	2	2.595072
O89032	FPIEGGQKDPK	1.172098617	2	2.374957
O89046	**COR1B Coronin_1B**	**1.269251681**	**6.61E-06**	**3**
O89046	NDQCYEDIR	1.582514475	2	3.176092
O89046	NVLSDSKPAGYSR	1.271383157	2	3.251743
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.50953341	2	3.864176
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.044337649**	**0.629606**	**5**
O89049	GFDQDMANK	1.454802009	2	2.452626
O89049	IEQIEAGTPGR	0.76566776	2	3.34847
O89049	IEQIEAGTPGRLK	1.602260345	2	2.63139
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.941770479	3	4.422039
O89049	WGLGGTCVNVGCIPK	1.080311955	2	3.632229
O89079	**COPE Coatomer subunit epsilon**	**1.239314642**	**0.45929**	**2**
O89079	NAFYIGSYQQCINEAQR	1.84456159	2	2.78795
O89079	YGVVLDEIKPSSAPELQAVR	1.236856105	3	4.072258
P00173	**CYB5 Cytochrome b5**	**0.986262509**	**0.999967**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	0.947475649	2	5.411125
P00173	FLEEHPGGEEVLR	1.0329817	2	4.134752
P00173	STWVILHHK	1.069222571	2	2.945485
P00173	TYIIGELHPDDR	0.978193095	2	4.085944
P00173	VYDLTK	1.098741739	1	2.04902
P00173	YYTLEEIQK	0.960067697	2	2.965537
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.269960332**	**8.16E-05**	**10**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	2.206396444	3	4.781581
P00388	GMSADPEEYDLADLSSLPEIDK	1.152665163	2	4.982845
P00388	HILAILQDYPSLRPPIDHLCELLPR	1.567721295	4	4.965195
P00388	KKEEIPEFSK	0.970092856	2	2.736175
P00388	LEQLGAQR	1.431986861	2	2.531348
P00388	LIHEGGAHIYVCGDAR	1.85107119	3	3.638287
P00388	RSDEDYLYR	1.249346565	2	2.809881
P00388	SYENQKPPFDAK	1.828832832	2	3.323937
P00388	TYEHFNAMGK	1.374130491	2	2.613553
P00388	VHPNSVHICAVAVEYEAK	2.572794144	2	4.696477
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.695407816**	**0.000348**	**4**
P00406	ILYMMDEINNPVLTVK	1.481788165	2	4.452632
P00406	LLEVDNR	1.674955923	2	2.409011
P00406	VVLPMELPIR	1.293270023	2	2.440593
P00406	VVLPMELPIR+Oxidation(4	1.838468739		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.09580571**	**1.15E-09**	**18**
P00481	EATIPIVNGLSDLYHPIQILADYLTLQEHYGSLK	1.333097622	3	5.483086
P00481	FGMHLQAATPK	1.191076743	3	3.94349
P00481	GEYLPLLQGK	1.284136667	2	3.094919
P00481	GGNVLITDTWISMGQEDEK	0.886137708	2	5.213381
P00481	GGNVLITDTWISMGQEDEKK	0.967053749	2	4.618746
P00481	GLTLSWIGDGNNILHSIMMSAAK	2.050524738	2	4.178525
P00481	GYEPDPNIVK	0.90943518	2	2.61914
P00481	LQAFQGYQVTMK	1.43828067	2	4.041335
P00481	LSMTNDPLEAAR	1.29348337	2	2.92172
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.76786702	3	6.03413
P00481	QKGEYLPLLQGK	0.958910982	2	3.436462
P00481	QSDLDILAK	1.121707961	1	2.063864
P00481	SLGMIFEK	1.170880614	2	2.814793
P00481	SLVFPEAENR	1.007871142	2	2.670156
P00481	SLVFPEAENRK	1.084576372	2	2.938981
P00481	VLSSMTDAVLAR	1.477924001	2	3.931244
P00481	VLSSMTDAVLAR+Oxidation(4	1.825938664		

P00481	YGKPVQSQVQLK	1.057715211	2	3.067989
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.858498391**	**1**	**2**
P00502	FIQSPEDLEK	1.070525867	2	2.773433
P00502	WLLAAAGVEFDEK	0.800846337	2	4.375349
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.243263031**	**0.003731**	**19**
P00507	ASAELALGENSEVLK	1.136780843	2	4.712006
P00507	DAGMQLQGYR	1.261379248	2	2.725268
P00507	DDNGKPYVLPSVR	1.031219168	2	3.550121
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.357264657	3	5.225506
P00507	EYLPIGGLADFCK	1.514661542	2	2.889647
P00507	FVTVQTISGTGALR	1.23881748	2	5.166576
P00507	HFIEQGINVCLCQSYAK	1.577608217	2	4.888722
P00507	IAATILTSPDLR	1.45927343	2	3.056549
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.341169487	3	4.736098
P00507	ISVAGVTSGNVGYLAHAIHQVTK	0.99672822	2	4.423451
P00507	KMNLGVGAYR	1.827048852	2	2.658391
P00507	KQWLQEVK	0.924184828	1	2.16169
P00507	MNLGVGAYR	1.172705347	2	2.93945
P00507	NLDKEYLPIGGLADFCK	1.204636774	2	5.549309
P00507	NMGLYGER	1.417560928	2	2.667841
P00507	TCGFDFSGALEDISK	1.352582844	2	5.019045
P00507	TQLVSNLK	1.141926501	2	2.918554
P00507	VGAFTVVCK	1.233498004	2	3.231564
P00507	VGASFLQR	2.276489805	2	3.110078
P00564	**KCRM Creatine kinase M_type**	**3.090926809**	**0.990573**	**9**
P00564	DLFDPIIQDR	2.878492391	2	2.781486
P00564	FEEILTR	2.153419516	2	2.491427
P00564	GGDDLDPNYVLSSR	1.341757266	2	4.60846
P00564	GQSIDDMIPAQK	6.326523719	2	3.677099
P00564	GTGGVDTAAVGAVFDISNADR	5.995813211	2	5.345188
P00564	LGSSEVEQVQLVVDGVK	4.123561904	2	5.089286
P00564	LSVEALNSLTGEFK	0.9851621	2	4.298793
P00564	RGTGGVDTAAVGAVFDISNADR	6.111377067	2	4.147481
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	3.287746138	3	5.796252
P00787	**CATB Cathepsin B**	**1.283032814**	**0.000333**	**5**
P00787	EQWSNCPTIAQIR	1.594548608	2	2.634252
P00787	GENHCGIESEIVAGIPR	1.188093803	2	4.912913
P00787	HEAGDVMGGHAIR	1.316983247	3	3.86374
P00787	HEAGDVMGGHAIR+Oxidation(6	1.505955461		
P00787	MCEAGYSTSYKEDK	1.682584419	2	4.400453
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.111920169**	**4.01E-08**	**21**
P00884	ALQASALAAWGGK	1.510748995	2	4.983746
P00884	ATQEAFMK	1.387985014	2	2.752935
P00884	ATQEAFMK+Oxidation(6	1.314914784		
P00884	ELSEIAQR	1.389888611	1	2.190262
P00884	ETTIQGLDGLSER	1.20046862	2	3.874769
P00884	FPALTSEQK	1.477151766	2	2.350795
P00884	GILAADESVGTMGNR	0.962704354	2	5.411417
P00884	GILAADESVGTMGNR+Oxidation(11	0.968491126		
P00884	GIVVGIKLDQGGAPLAGTNK	1.704775609	2	4.372091
P00884	GIVVGIKLDQGGAPLAGTNKETTIQGLDGLSER	1.229893413	3	5.418768
P00884	IKVENTEENR	0.996841886	2	3.190797
P00884	IKVENTEENRR	0.487748715	2	3.159109
P00884	ISDQCPSSLAIQENANALAR	1.060216297	2	6.103848
P00884	KELSEIAQR	1.288113721	3	3.360617
P00884	KYTPEQVAMATVTALHR	2.226828809	3	6.032208
P00884	KYTPEQVAMATVTALHR+Oxidation(8	1.62446754		

P00884	LDQGGAPLAGTNK	1.098319378	2	4.652489
P00884	LDQGGAPLAGTNKETTIQGLDGLSER	0.768491863	3	4.306296
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.093324844	3	4.757306
P00884	YTPEQVAMATVTALHR	1.32522282	2	4.639291
P00884	YTPEQVAMATVTALHR+Oxidation(7	1.765303969		
P01015	**ANGT Angiotensinogen**	**2.54017702**	**9.9E-20**	**3**
P01015	GSYNLQDLLAQAK	2.871784984	2	3.140197
P01015	SLDLSTDPVLAAQK	2.442448093	2	3.328705
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	2.767729509	2	3.904883
P01026	**CO3 Complement C3**	**1.360269594**	**0.003746**	**21**
P01026	ACEPGVDYVYK	1.319157405	2	2.484009
P01026	ADIGCTPGSGK	1.083886215	2	3.021878
P01026	AFYEHAPK	1.099697201	2	2.447774
P01026	DSCVGTLVVKGDPR	0.998040767	2	2.586686
P01026	EYVLPSFEVLVEPTEK	1.20710663	2	3.703407
P01026	IFTVDNNLLPVGK	1.592963301	2	3.585476
P01026	IGLQEVEVK	1.073125434	2	2.646303
P01026	LPYSVVRNEQVEIR	2.166636625	2	2.328201
P01026	QNEGFSLTAK	1.081088943	2	2.457929
P01026	RVPVVTQGSDAQALTQDDGVAK	1.360160107	3	5.65816
P01026	SDVDEDIIPEEDIISR	1.408673075	2	4.503762
P01026	SGIPIVTSPYQIHFTK	1.577368601	2	2.949319
P01026	SGSDEVQAGQER	1.526072899	2	3.872476
P01026	SSVAVPYVIVPLK	1.145891608	2	2.97736
P01026	TNQGLQTDQREDPECAKPAAR	1.573749993	3	3.660022
P01026	TVLTGATGHLNR	1.882609481	2	2.841178
P01026	TVVIVIETPDGVPIKR	1.683074105	2	2.737586
P01026	VELKPGDNLNVNFHLR	1.443433368	3	3.913981
P01026	VHQFFNVGLIQPGSVK	1.212088183	3	4.15348
P01026	VLIEDGSGEAVLSR	1.296573212	2	3.985111
P01026	VPVVTQGSDAQALTQDDGVAK	0.762142567	2	5.569983
P01048	**KNT1 T_kininogen 1**	**0.99594863**	**0.943175**	**3**
P01048	FSVATQICNITPGK	0.980681826	2	3.334308
P01048	KTEEDLCVGCFQPIPMDSSDLKPVLK	1.228548716	4	4.659724
P01048	TELTADCETK	0.951048807	2	2.347149
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.783535897**	**0.999837**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.679772608	3	7.45363
P01946	FLASVSTVLTSK	0.773696345	2	4.013084
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	1.118030296	4	5.447568
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.98149929	5	6.357115
P01946	IGGHGGEYGEEALQR	0.586792246	3	5.092999
P01946	LRVDPVNFK	1.386040984	2	2.572003
P01946	MFAAFPTTK	0.722079957	2	2.768029
P01946	MFAAFPTTK+Oxidation(0	0.775377027		
P01946	TYFSHIDVSPGSAQVK	0.615123083	2	5.037786
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.7075072**	**0.312903**	**4**
P02089	GTFASLSELHCDK	0.933027006	2	3.764668
P02089	LHVDPENFR	0.748314416	2	2.515554
P02089	YFDSFGDLSSASAIMGNPK	0.718135741	2	6.516482
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14	0.656583846		
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.787660792**	**0.999595**	**10**
P02091	AAVNGLWGK	0.80102012	2	2.771197
P02091	AAVNGLWGKVNPDDVGGEALGR	1.109849326	3	3.614424
P02091	EFTPCAQAAFQK	0.805023866	2	3.175062
P02091	GTFAHLSELHCDK	1.043609471	2	4.400136
P02091	GTFAHLSELHCDKLHVDPENFR	0.655697673	3	3.95259
P02091	KVINAFNDGLK	0.973995569	2	3.600078

P02091	LLGNMIVIVLGHHLGK	1.159738805	4	4.618551
P02091	VINAFNDGLK	0.628319027	2	2.985891
P02091	VNPDDVGGEALGR	0.936480079	2	4.030057
P02091	VVAGVASALAHK	0.282382966	2	3.741721
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.357581249**	**9.9E-20**	**6**
P02401	ILDSVGIEADDER	1.157377821	2	4.850311
P02401	KILDSVGIEADDER	0.601921972	2	4.009557
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.32255225	3	5.905732
P02401	NIEDVIAQGVGK	1.087080715	2	4.728252
P02401	VISELNGK	1.342992086	1	2.088771
P02401	YVASYLLAALGGNSNPSAK	1.384548978	2	5.22184
P02564	**MYH7 Myosin_7**	**0.965163305**	**0.985873**	**38**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.967350157	3	5.810663
P02564	ANDDLKENIAIVER	1.937599728	3	3.490001
P02564	DLEEATLQHEATAAALR	1.424418977	2	4.965621
P02564	DVFVPDDKEEFVK	2.304340518	2	2.444539
P02564	EDQVMQQNPPK	1.48989066	2	3.047023
P02564	EEQAEPDGTEEADK	2.885334337	2	3.062848
P02564	ELENELEAEQK	0.983508716	2	2.377688
P02564	GQNVQQVAYAIGALAK	3.046350016	2	4.065691
P02564	GTLEDQIIQANPALEAFGNAK	1.12027908	3	5.694728
P02564	IEDEQALGSQLQK	3.39953928	2	5.095191
P02564	IEELEEELEAER	2.77386642	2	4.345762
P02564	IKELTYQTEEDRK	2.39683867	2	2.626855
P02564	ILNPAAIPEGQFIDSR	4.623136485	2	2.769127
P02564	KLAEKDEEMEQAK	3.019376308	3	3.651816
P02564	KLAEQELIETSER	1.368783013	2	3.500719
P02564	KLEDECSELKR	1.236321909	3	3.819714
P02564	KVQHELDEAEER	1.390188746	2	3.725316
P02564	LAEQELIETSER	0.85218792	2	3.394273
P02564	LDEAEQIALK	3.263276505	2	3.235038
P02564	LELDDVTSNMEQIIK	1.424018352	2	4.470151
P02564	LQDAEEAVEAVNAK	3.270620391	2	4.68299
P02564	LQNEIEDLMVDVER	2.480710518	2	3.891513
P02564	LTQESIMDLENDKQQLDER	4.801919723	3	3.821725
P02564	MDADLSQLQTEVEEAVQECR	1.387967612	2	4.985244
P02564	NALAHALQSAR	1.60842581	2	2.369261
P02564	NAYEESLEHLETFK	1.295587226	2	3.410417
P02564	NLQEEISDLTEQLGSTGK	2.530584529	2	5.072156
P02564	NLTEEMAGLDEIIVK	1.773530832	2	3.653981
P02564	NNLLQAELEELR	1.968238902	2	3.596327
P02564	QAEEAEEQANTNLSK	4.895013951	2	5.235196
P02564	QKYEESQSELESSQK	1.51238015	2	3.783156
P02564	QLEAEKLELQSALEEAEASLEHEEGK	2.987316175	3	3.607239
P02564	QREEQAEPDGTEEADK	2.237762742	2	3.764917
P02564	TLEDQMNEHR	2.11701936	2	2.531919
P02564	VQHELDEAEER	0.813912296	2	3.46862
P02564	VQLLHSQNTSLINQK	1.529627108	2	4.098217
P02564	VVDSLQTSLDAETR	0.783581629	2	4.117401
P02564	YEESQSELESSQK	3.88520569	2	4.325049
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**1.721342112**	**0.981689**	**12**
P02600	ALGTNPTNAEVK	1.648011377	2	3.336773
P02600	ALGTNPTNAEVKK	2.657706313	2	2.945386
P02600	DQGGYEDFVEGLR	0.75563601	2	3.815994
P02600	IEFEQFLPMMQAISNNK	1.278831883	3	3.915058
P02600	ITLSQVGDVLR	3.843480863	2	3.588605

P02600	KIEFEQFLPMMQAISNNK	1.480198597	2	4.90061
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	3.146147215	3	5.513417
P02600	KPAAAAPAPAPAPAPAPAKPK	1.023549747	3	3.703246
P02600	KPAAAPAPAPAPAPAPAKPKEEK	1.716978305	3	5.237701
P02600	KVLGNPSNEEMNAK	2.604845575	2	3.651822
P02600	VLGNPSNEEMNAK	2.612561359	2	3.918817
P02600	VLGNPSNEEMNAK+Oxidation(9	1.800386273		
P02625	**PRVA Parvalbumin alpha**	**1.645005904**	**0.061193**	**5**
P02625	AIGAFTAADSFDHK	1.803121633	2	2.455598
P02625	AIGAFTAADSFDHKK	1.93554752	2	3.85334
P02625	SGFIEEDELGSILK	1.733656974	2	4.033356
P02625	TLMAAGDKDGDGK	1.338216262	2	3.388679
P02625	TLMAAGDKDGDGK+Oxidation(2	1.578039662		
P02650	**APOE Apolipoprotein E**	**1.198481565**	**0.993514**	**12**
P02650	ELEEQLGPVAEETR	0.742811785	2	4.211415
P02650	GRLEEVGNQAR	1.03824287	2	3.39432
P02650	GWFEPLVEDMQR	1.304390526	2	3.041346
P02650	LEEVGNQAR	0.995572267	2	2.445335
P02650	LGADMEDLR	1.126213742	2	3.164751
P02650	LGPLVEQGR	1.196155038	2	2.999426
P02650	LQAEIFQAR	1.138479545	2	2.531088
P02650	MEEQTQQIR	1.31100481	2	3.376917
P02650	NEVNTMLGQSTEELR	1.012474802	2	4.648191
P02650	SKMEEQTQQIR	1.287326369	2	3.337996
P02650	SKMEEQTQQIR+Oxidation(2	0.808155293		
P02650	TANLGAGAAQPLR	1.039753351	2	4.001391
P02680	**FIBG Fibrinogen gamma chain**	**1.200234556**	**0.81336**	**4**
P02680	LSIGDGQQHHMGGSK	1.521356611	2	3.406957
P02680	VGPESDKYR	1.052544423	2	2.722304
P02680	YEALLLTHESSIR	0.758112285	2	3.728083
P02680	YLQDIYTSNK	1.316623294	2	2.869562
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.217442407**	**9.9E-20**	**14**
P02692	AMGLPEDLIQK	1.313742178	2	3.487025
P02692	AMGLPEDLIQK+Oxidation(1	1.027086836		
P02692	GVSEIVHEGK	1.302523419	2	3.45281
P02692	GVSEIVHEGKK	1.105770585	2	3.296251
P02692	MEGDNKMVTTFKGIK+Oxidation(6	1.055644465		
P02692	SVTEFNGDTITNTMTLGDIVYK	1.262404657	3	5.768391
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13	0.893703167		
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.311816315	2	3.72356
P02692	VIHNEFTLGEECELETMTGEK	1.405466221	3	6.022576
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16	1.234889283		
P02692	VIHNEFTLGEECELETMTGEKVK	1.487470552	3	4.905397
P02692	VKLTITYGSK	1.053961842	1	2.026615
P02692	YQVQSQENFEPFMK	1.15627468	2	5.783623
P02692	YQVQSQENFEPFMK+Oxidation(12	0.858383118		
P02696	**RET1 Retinol_binding protein 1**	**1.202414368**	**0.843886**	**6**
P02696	ALDVNVALR	1.503581363	2	2.974282
P02696	CMTTVSWDGDKLQCVQK	0.893192911	2	4.230336
P02696	EFEEDLTGIDDR	1.328206579	2	3.247561
P02696	EFEEDLTGIDDRK	1.224643605	2	3.492052
P02696	MLSNENFEEYLR	1.153589618	2	3.869723
P02696	MLSNENFEEYLR+Oxidation(0	1.797741044		
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.260262431**	**0.636459**	**5**
P02706	DYQDFQHLDNENDHHQLQR	1.044297782	3	4.122937
P02706	LVESQLEK	1.261835514	2	2.77993
P02706	SLSCQMAALR	1.336671007	2	2.802929

P02706	WVCETELGK	1.013692956	2	2.466769
P02706	WVDGTDYETGFK	1.053778357	2	3.185601
P02770	**ALBU Serum albumin**	**1.289493568**	**0.004878**	**25**
P02770	AADKDNCFATEGPNLVAR	1.343278229	2	4.448647
P02770	AETFTFHSDICTLPDKEK	1.225664372	3	3.369953
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	2.822753195	2	5.042186
P02770	CCSGSLVER	1.404161344	2	2.885491
P02770	CCTLPEAQR	1.335514088	2	3.069529
P02770	DLGEQHFK	1.573665167	1	2.134603
P02770	ECCHGDLLECADDR	1.312230378	2	3.685987
P02770	ECCHGDLLECADDRAELAK	1.507967496	2	5.554394
P02770	FKDLGEQHFK	1.1171892	3	4.184448
P02770	GLVLIAFSQYLQK	1.779300383	2	4.128474
P02770	INKECCHGDLLECADDRAELAK	1.470163147	3	4.811833
P02770	KQTALAELVK	1.038725531	3	4.040548
P02770	KYEATLEK	0.370276955	1	2.615062
P02770	LGEYGFQNAVLVR	58.11781446	2	3.779178
P02770	LQACCDKPVLQK	1.401885002	2	4.048597
P02770	LVQEVTDFAK	1.008127475	2	3.512712
P02770	RHPDYSVSLLLR	1.048995699	3	5.365872
P02770	SIHTLFGDK	1.465074115	1	2.59696
P02770	TCVADENAENCDK	1.051128003	2	4.585509
P02770	TNCELYEK	1.272554985	2	2.86214
P02770	TVMGDFAQFVDK	1.292350465	2	3.88801
P02770	YEATLEK	2.040463362	1	1.963686
P02770	YMCENQATISSK	1.313113686	2	4.144084
P02770	YMCENQATISSK+Oxidation(1	1.82144217		
P02770	YNEVLTQCCTESDK	1.267980409	2	5.524978
P02803	**MT1 Metallothionein_1**	**13.76330663**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	23.92837693	3	6.52961
P02803	SCCSCCPVGCSK	8.569997423	2	4.114416
P04041	**GPX1 Glutathione peroxidase 1**	**1.153325294**	**6.75E-11**	**11**
P04041	DYTEMNDLQK	32.24002413	2	2.412008
P04041	FLVGPDGVPVR	1.124078371	2	3.217993
P04041	GLVVLGFPCNQFGHQENGK	1.835933058	2	4.069147
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	1.284024652	3	4.200408
P04041	NALPAPSDDPTALMTDPK	1.12649402	2	3.175985
P04041	NALPAPSDDPTALMTDPK+Oxidation(13	0.720173596		
P04041	NDISWNFEK	1.163465181	2	3.022348
P04041	NEEILNSLK	1.316387945	2	2.482306
P04041	TIDIEPDIEALLSK	1.307123949	3	5.43006
P04041	YIIWSPVCR	1.247149823	2	2.802387
P04041	YVRPGGGFEPNFTLFEK	1.376235198	3	4.708787
P04167	**CP2B2 Cytochrome P450 2B2**	**1.26515815**	**0.577462**	**2**
P04167	GTIAVIEPIFK	2.36853615	2	2.914334
P04167	NLQEILDYIGHIVEK	1.190366665	2	4.339555
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.209171133**	**0.000129**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.421590132	3	3.505288
P04176	EDNIPQLEDVSQFLQTCTGFR	0.992662994	3	5.16658
P04176	FANQILSYGAELDADHPGFKDPVYR	1.539958223	3	3.989741
P04176	HGSKPMYTPEPDICHELLGHVPLFSDR	1.325757385	3	3.931993
P04176	ILADSINSEVGILCNALQK	1.176728149	3	6.475022
P04176	LNKDEYEFFTYLDK	4.056171088	2	3.576324
P04176	LNKDEYEFFTYLDKR	1.65551368	3	3.533329
P04176	LRPVAGLLSSR	1.566076957	2	2.694805
P04176	NDIGATVHELSR	1.416192676	2	3.75022
P04176	QFADIAYNYR	0.829017785	2	2.414913

P04176	SFAQFSQEIGLASLGAPDEYIEK	1.264181242	2	4.93304
P04176	THACYEHNHIFPLLEK	1.24443939	4	4.983132
P04176	VEVLDNTQQLK	1.14948189	2	3.837695
P04176	VEYTEEEK	1.092029351	2	2.741987
P04176	VEYTEEEKQTWGTVFR	1.460642624	2	3.897341
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	0.98025975	3	5.129281
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.882364693**	**0.754475**	**8**
P04182	AFYNNVLGEYEEYITK	1.275930945	2	4.600586
P04182	GIYMWDVEGR	0.845999925	2	3.120709
P04182	GLLNAIVIR	0.837774644	2	3.261144
P04182	KTEQGPPSSEYIFER	1.748109773	2	4.158332
P04182	TEQGPPSSEYIFER	0.66195481	2	3.949803
P04182	VLPMNTGVEAGETACK	1.272624208	2	4.154099
P04182	WLAVDHENVRPDIVLLGK	1.429757333	2	5.279231
P04182	YGAHNYHPLPVALER	0.967119774	2	4.218908
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.526628471**	**8.77E-15**	**4**
P04256	EDSQRPGAHLTVK	1.600817562	2	3.196701
P04256	IEVIEIMTDR	1.466008864	2	3.424683
P04256	NQGGYGGSSSSSSYGSGR	1.001545486	2	5.167044
P04256	YHTVNGHNCEVR	0.670479417	2	3.380974
P04276	**VTDB Vitamin D_binding protein**	**1.343244784**	**0.050511**	**3**
P04276	CCSINSPPR	0.807529305	2	2.525448
P04276	SCESDAPFPVHPGTSECCTK	1.892683782	2	4.631196
P04276	YCSSQIDAEMR	1.853349353	2	3.215176
P04355	**MT2 Metallothionein_2**	**28.1664641**	**9.9E-20**	**2**
P04355	MDPNCSCATDGSCSCAGSCK	49.52415953	2	6.244748
P04355	SCCSCCPVGCAK	13.66557383	2	4.253392
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**2.850042163**	**0.910385**	**8**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.031089929	3	5.256758
P04466	GADPEDVITGAFK	0.611077583	2	4.193979
P04466	LKGADPEDVITGAFK	2.143853621	3	3.477483
P04466	NEELDAMMK	3.487693079	1	2.203295
P04466	NICYVITHGDAK	6.311019189	2	2.844647
P04466	NICYVITHGDAKDQE	3.48985601	2	4.439586
P04466	NMWAAFPPDVGGNVDYK	2.53191097	2	3.078714
P04466	QFLEELLTTQCDR	2.978034602	2	3.998131
P04550	**PTMS Parathymosin**	**1.025461333**	**0.098117**	**4**
P04550	RTAEEEDEADPKR	0.863617628	3	4.10261
P04550	SVEAAAELSAK	0.92210909	2	3.864644
P04550	TAEEEDEADPK	2.074737039	2	3.33814
P04550	TAEEEDEADPKR	1.119255427	2	3.777864
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.209794009**	**9.9E-20**	**19**
P04636	AGAGSATLSMAYAGAR	1.116782996	2	4.547983
P04636	AGAGSATLSMAYAGAR+Oxidation(9	1.569490289		
P04636	ANTFVAELK	0.90674501	2	3.36116
P04636	EGVIECSFVQSK	1.428128792	2	3.185955
P04636	ETECTYFSTPLLLGK	1.387924485	2	3.740728
P04636	FVFSLVDAMNGK	1.487078663	2	4.46147
P04636	GCDVVVIPAGVPR	1.072728153	2	4.354813
P04636	GYLGPEQLPDCLK	1.199912468	2	4.257149
P04636	IFGVTTLDIVR	1.717400026	2	3.355865
P04636	IQEAGTEVVK	1.068703431	2	2.761916
P04636	IQEAGTEVVKAK	1.058492083	2	2.879199
P04636	ITPFEEK	1.296135002	1	1.941665
P04636	LTLYDIAHTPGVAADLSHIETR	1.472691942	3	6.852603

P04636	MIAEAIPELK	1.059041586	2	3.461792
P04636	MIAEAIPELK+Oxidation(0	1.405847839		
P04636	TIIPLISQCTPK	0.891033558	2	3.555985
P04636	VAVLGASGGIGQPLSLLLK	1.249785116	2	6.293713
P04636	VDFPQDQLATLTGR	1.020906386	2	4.724039
P04636	VNVPVIGGHAGK	1.255893726	2	3.777545
P04638	**APOA2 Apolipoprotein A_II**	**1.09551142**	**0.99938**	**2**
P04638	AQPSEIQNQAK	1.039480695	2	2.741534
P04638	TGTNLMDFLSR	1.108888134	2	2.725024
P04639	**APOA1 Apolipoprotein A_I**	**1.286691333**	**0.528212**	**5**
P04639	LQEQLGPVTQEFWANLEK	1.594587631	2	3.513486
P04639	NEMNKDLENVK	1.091050191	2	3.592044
P04639	NHPTLIEYHTK	0.918220705	3	3.837276
P04639	QLNLNLLDNWDTLGSTVGR	1.317348803	2	4.191335
P04639	WNEEVEAYR	1.309991454	2	2.876504
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.118275145**	**2.22E-16**	**21**
P04642	DLADELALVDVIEDK	1.356079265	2	5.314399
P04642	DLADELALVDVIEDKLK	1.200077056	2	3.944847
P04642	DQLIVNLLK	1.426683728	2	3.036397
P04642	DQLIVNLLKEEQVPQNK	1.295506611	2	4.345291
P04642	EDVFLSVPCILGQNGISDVVK	1.30888881	2	4.862667
P04642	GEMMDLQHGSLFLK	1.480512272	2	4.118213
P04642	GEMMDLQHGSLFLK+Oxidation(2	1.537900459		
P04642	GEMMDLQHGSLFLK+Oxidation(3	1.68960919		
P04642	GYTSWAIGLSVADLAESIMK	0.813939207	2	4.884945
P04642	IVSSKDYSVTANSK	1.009994645	2	3.639529
P04642	KSADTLWGIQK	1.378414705	2	3.15057
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.042722835	3	5.728759
P04642	LKGEMMDLQHGSLFLK	1.592841302	2	3.990065
P04642	NVNIFK	1.381498798	1	2.072055
P04642	QVVDSAYEVIK	1.199190667	2	3.255652
P04642	RVHPISTMIK	1.137584042	2	2.558411
P04642	SADTLWGIQK	1.090251038	2	3.926585
P04642	SLNPQLGTDADK	0.79023373	2	2.77051
P04642	SLNPQLGTDADKEQWK	1.274066871	2	4.745414
P04642	SLNPQLGTDADKEQWKDVHK	1.652533497	3	3.435927
P04642	VTLTPDEEAR	0.960818622	2	3.012887
P04644	**RS17 40S ribosomal protein S17**	**1.698291145**	**0.000445**	**3**
P04644	DNYVPEVSALDQEIIEVDPDTK	5.561457182	2	4.276811
P04644	LLDFGSLSNLQVTQPTVGMNFK	2.587893833	2	4.723415
P04644	VCEEIAIIPSK	1.064182231	2	3.094233
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.363725663**	**0.844315**	**10**
P04692	AISEELDHALNDMTSI	2.581030704	2	2.563417
P04692	GTEDELDKYSEALK	1.744105591	2	3.240455
P04692	KLVIIESDLER	1.536086592	2	3.301363
P04692	LDKENALDR	1.810926825	2	3.089513
P04692	LKGTEDELDK	0.452492494	2	2.498027
P04692	LVIIESDLER	1.139755055	2	3.130812
P04692	MEIQEIQLK	1.175448826	2	3.123402
P04692	QLEDELVSLQK	3.032265647	2	2.405284
P04692	SIDDLEDELYAQK	8.422939369	2	4.381942
P04692	SKQLEDELVSLQK	0.628465677	2	3.051079
P04694	**ATTY Tyrosine aminotransferase**	**4.939624475**	**9.9E-20**	**6**
P04694	ILGPCTIVQGALK	4.856886189	2	2.937231
P04694	IQEFCEQHYHCAEGSQEECDK	#NUM!	3	4.923231
P04694	LIAEQAVHCLPATCFEYPNFFR	3.160333525	3	3.981366
P04694	TACLVVNNPSNPCGSVFSK	10.06198453	2	4.969268

P04694	TVISLSIGDPTVFGNLPTDPEVTQAMK	4.241275132	2	3.110275
P04694	YEPLANLSTNVPILSCGGLAK	17.11084775	2	3.604469
P04762	**CATA Catalase**	**0.84601082**	**9.91E-06**	**32**
P04762	APQKPDVLTTGGGNPIGDK	1.05895024	2	4.341702
P04762	DAMLFPSFIHSQK+Oxidation(2	1.192846631		
P04762	DAQLFIQR	1.043151587	2	2.962406
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	0.899310084	4	4.763788
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVKR	1.04003926	4	5.309287
P04762	DPASDQMK	1.291356568	1	2.556772
P04762	DPASDQMK+Oxidation(6	1.09600663		
P04762	DYPLIPVGK	3.194275441	1	2.264439
P04762	EAETFPFNPFDLTK	1.330696327	2	3.964568
P04762	FNSANEDNVTQVR	1.821542432	2	4.574751
P04762	FSTVAGESGSADTVR	0.782977467	2	5.077415
P04762	FSTVAGESGSADTVRDPR	0.962565898	2	2.655206
P04762	FYTEDGNWDLVGNNTPIFFIR	1.31044547	3	6.134441
P04762	GAGAFGYFEVTHDITR	1.099173995	2	4.890486
P04762	GPLLVQDVVFTDEMAHFDR	1.24291938	2	5.509444
P04762	HMNGYGSHTFK	1.22770775	3	4.309582
P04762	HMNGYGSHTFK+Oxidation(1	0.73806574		
P04762	LAQEDPDYGLR	1.031119334	2	2.920977
P04762	LCENIANHLK	1.085064352	3	4.042245
P04762	LFAYPDTHR	1.236161646	2	2.973321
P04762	LGPNYLQIPVNCPYR	1.296735996	2	4.027653
P04762	LNIMTAGPR	1.451270397	2	3.148905
P04762	LVNANGEAVYCK	1.057128238	2	3.909321
P04762	NAIHTYVQAGSHIAAK	1.668221766	3	5.625795
P04762	NFTDVHPDYGAR	0.847266333	2	4.022915
P04762	NLPVEEAGR	0.893323298	2	2.343341
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	2.033487956	3	5.572305
P04762	RFNSANEDNVTQVR	0.921306615	2	5.285923
P04762	VFEHIGK	1.081246238	2	2.442874
P04762	VFEHIGKR	0.532726506	2	2.712823
P04762	VQALLDQYNSQKPK	0.94834156	2	4.867963
P04762	VWPHKDYPLIPVGK	1.14339654	2	3.963643
P04764	**ENOA Alpha_enolase**	**1.205809141**	**4.86E-07**	**16**
P04764	AGYTDQVVIGMDVAASEFYR	2.230330682	2	4.853869
P04764	DATNVGDEGGFAPNILENK	1.17712516	2	5.637426
P04764	DYPVVSIEDPFDQDDWDAWQK	1.362540902	2	4.307965
P04764	FTATAGIQVVGDDLTVTNPK	1.39910473	2	4.721107
P04764	GNPTVEVDLYTAK	1.459585843	2	4.073594
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.341082391	3	6.159861
P04764	IDQLMIEMDGTENK	0.992827712	2	4.87195
P04764	IEEELGSK	1.159453003	2	2.542156
P04764	IGAEVYHNLK	1.111028496	2	3.308343
P04764	KLNVVEQEK	0.241890614	2	2.541519
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.222677543	3	5.975399
P04764	LNVVEQEK	1.159830043	2	3.093401
P04764	LNVVEQEKIDQLMIEMDGTENK	2.848578294	3	5.294797
P04764	SCNCLLLK	1.2459879	2	2.793944
P04764	VNQIGSVTESLQACK	1.105479116	2	4.959307
P04764	YITPDQLADLYK	1.483077325	2	3.618766
P04785	**PDIA1 Protein disulfide_isomerase**	**1.169093991**	**9.9E-20**	**25**
P04785	DHENIVIAK	1.144426432	2	2.749153
P04785	EADDIVNWLK	1.132130803	2	2.519857

P04785	HNQLPLVIEFTEQTAPK	1.222008428	3	5.459813
P04785	IFGGEIK	1.491064969	1	1.963166
P04785	IKPHLMSQELPEDWDKQPVK	1.222477373	3	4.954683
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5	2.059775619		
P04785	ILEFFGLK	1.666516454	2	2.950265
P04785	ILFIFIDSDHTDNQR	1.093004928	2	2.636509
P04785	LGETYKDHENIVIAK	1.189425478	3	5.504439
P04785	LITLEEEMTK	1.256077153	2	3.577197
P04785	LITLEEEMTK+Oxidation(7	1.744337845		
P04785	LKAEGSEIR	0.153068453	2	2.44262
P04785	LLDFIK	1.397280442	2	2.438009
P04785	MDSTANEVEAVK	2.761589716	2	4.264087
P04785	MDSTANEVEAVK+Oxidation(0	0.986674738		
P04785	NFEEVAFDEK	1.093354633	1	3.19827
P04785	NFEEVAFDEKK	1.318461068	2	3.977684
P04785	NNFEGEITK	1.252557444	2	2.592288
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.335912191	3	6.305442
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.388418704	3	6.16215
P04785	THILLFLPK	1.513475328	2	3.094292
P04785	TVIDYNGER	1.003766035	2	2.975783
P04785	VDATEESDLAQQYGVR	0.971469623	2	5.461422
P04785	YKPESDELTAEK	1.128738338	3	4.509046
P04785	YQLDKDGVVLFK	1.349174999	2	3.793841
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.495740086**	**9.9E-20**	**16**
P04797	GAAQNIIPASTGAAK	1.584544365	2	4.145235
P04797	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	2.676532052	3	4.718456
P04797	IVSNASCTTNCLAPLAK	1.3132259	2	4.96471
P04797	LISWYDNEYGYSNR	2.424567633	2	4.304602
P04797	LVINGKPITIFQER	1.329977084	3	4.376493
P04797	RVIISAPSADAPMFVMGVNHEK	1.308087443	3	5.959051
P04797	VGVNGFGR	2.564436014	2	2.34018
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.495139753	3	7.570611
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12	1.683329006		
P04797	VIISAPSADAPMFVMGVNHEK	1.486344044	2	4.624974
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11	1.628805837		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14	1.62453679		
P04797	VPTPNVSVVDLTCR	1.588412231	2	3.180923
P04797	VVDLMAYMASK	1.34944365	2	3.8111
P04797	VVDLMAYMASKE	0.967652678	2	2.414471
P04797	WGDAGAEYVVESTGVFTTMEK	1.435635203	2	5.568699
P04799	**CP1A2 Cytochrome P450 1A2**	**1.916559844**	**1.11E-12**	**8**
P04799	FLTNDNTAIDK	1.463789746	2	2.627031
P04799	IGSTPVVVLSGLNTIK	1.516741831	2	3.364811
P04799	IHEELDTVIGR	1.588025119	2	2.928411
P04799	KSEEMLNLVK	0.887686724	2	2.504278
P04799	NSIQDITGALFK	2.193250863	2	3.775587
P04799	SMTFNPDSGPVWAAR	0.982858074	2	3.422653
P04799	TCEHVQAWPR	2.348907061	2	2.552703
P04799	TVQEHYQDFNK	1.779985965	2	3.728571
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**1.181825124**	**0.987208**	**10**
P04903	DGNLMFDQVPMVEIDGMK	1.741631521	2	5.289428
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10	1.119984567		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16	1.045976521		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4	1.159709869		
P04903	KDGNLMFDQVPMVEIDGMK	1.414953923	2	5.05617
P04903	LIQSPEDLEK	7.560786257	2	3.171128

P04903	LKKDGNLMFDQVPMVEIDGMK	1.231112257	3	3.430617
P04903	WLLAAAGVEFEEK	1.300384811	2	3.689583
P04903	YDLYGK	1.101034155	1	1.976047
P04903	YLPAFEK	1.097561276	1	2.043417
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**1.274682334**	**9.9E-20**	**10**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	1.528020109	3	5.418612
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	1.587672389	4	7.754688
P04904	KPLEDEKCVESAVK	0.837384049	2	3.677078
P04904	LRNDGSLMFQQVPMVEIDGMK	1.248541594	2	4.824424
P04904	NDGSLMFQQVPMVEIDGMK	1.324546195	2	4.926454
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11	1.104010166		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17	1.104643963		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5	1.096483673		
P04904	SHGQDYLVGNR	1.130991988	2	3.934017
P04904	WLLAAAGVEFEEQFLK	1.505525959	2	5.704055
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.055897756**	**9.9E-20**	**14**
P04905	ADIVENQVMDNR	1.039295931	2	4.138205
P04905	ADIVENQVMDNR+Oxidation(8	1.132214208		
P04905	CLDAFPNLKDFLAR	1.250663046	2	3.118843
P04905	FKLGLDFPNLPYLIDGSR	1.425410657	3	5.376539
P04905	HHLCGETEEER	0.906597139	3	3.855581
P04905	IRADIVENQVMDNR	1.778638969	2	4.055571
P04905	ITQSNAIMR	1.550510747	2	3.102464
P04905	ITQSNAIMR+Oxidation(7	1.155991495		
P04905	KHHLCGETEEER	1.120740526	3	4.083635
P04905	KITQSNAIMR	0.68157709	3	4.162561
P04905	KITQSNAIMR+Oxidation(8	0.487626162		
P04905	LGLDFPNLPYLIDGSR	1.494051057	2	4.717553
P04905	MQLIMLCYNPDFEK	3.724823813	2	4.30947
P04905	YLSTPIFSK	0.87638078	2	2.79507
P04906	**GSTP1 Glutathione S_transferase P**	**1.046724887**	**0.796665**	**2**
P04906	EAALVDMVNDGVEDLR	1.012063182	2	5.019281
P04906	STCLYGQLPK	1.468765107	2	2.574893
P04937	**FINC Fibronectin**	**0.978442003**	**0.033916**	**7**
P04937	ATGVFTTLQPLR	1.283429889	2	2.390386
P04937	FTQVSPTTLTAQWTAPSVK	1.529034595	2	4.391664
P04937	HYQINQQWER	3.156426787	2	2.558666
P04937	ITYGETGGNSPVQEFTVPGSK	1.352897407	2	2.392025
P04937	SSPVVIDASTAIDAPSNLR	0.892167716	2	3.260541
P04937	SYTITGLQPGTDYK	0.902587529	2	3.01772
P04937	YIVNVYQISEEGK	0.732314666	2	2.846673
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.547556036**	**0.9999**	**9**
P05065	ADDGRPFPQVIK	1.920184269	2	2.331577
P05065	ALANSLACQGK	1.539302828	2	2.871161
P05065	ALSDHHVYLEGTLLKPNMVTPGHACTQK	3.967856576	3	5.008176
P05065	FSNEEIAMATVTALR	1.910770858	2	4.15722
P05065	GILAADESTGSIAK	1.777405651	2	3.854153
P05065	GVVPLAGTNGETTTQGLDGLSER	1.466826487	2	5.194525
P05065	IGEHTPSSLAIMENANVLAR	1.262063166	2	4.411204
P05065	LQSIGTENTEENR	4.437548516	2	4.026505
P05065	RLQSIGTENTEENR	2.077503136	2	3.640539
P05178	**CP2C6 Cytochrome P450 2C6**	**0.916178746**	**0.474415**	**8**
P05178	DLGIVFSHGNR	1.261851058	2	2.38239
P05178	EALIDHGEEFAER	0.960999738	2	3.45801
P05178	EFPDPEIFDPGHFLDGNGK	0.953278321	2	2.918871
P05178	FDYKDQDFLNLMEK	1.557166823	3	4.913518
P05178	FIDLIPTNLPHAVTCDIK	1.007063042	2	3.597299

P05178	GTTIITSLSSVLHDSK	1.167511975	2	3.680686
P05178	MCAGEGLAR	1.032180182	2	2.739445
P05178	NITQSLTSFSK	0.621491834	2	2.684732
P05179	**CP2C7 Cytochrome P450 2C7**	**1.449434243**	**0.009221**	**7**
P05179	ACVGEGLAR	1.331777772	2	3.081254
P05179	FINFVPTNLPHAVTCDIK	1.893495328	3	3.343906
P05179	HMPYTDAMIHEVQR	1.392138755	3	3.963491
P05179	IEEHQESLDVTNPR	3.204626667	2	4.79203
P05179	KIEEHQESLDVTNPR	1.728263903	2	4.875001
P05179	KLPPGPTPLPIIGNFLQIDVK	1.731650828	3	5.745987
P05179	VLTSLTSVLHDSK	1.333479832	2	2.860887
P05182	**CP2E1 Cytochrome P450 2E1**	**0.945595787**	**0.170373**	**16**
P05182	AKEHLQSLDINCAR	1.562358342	3	4.68477
P05182	DIDLSPVTVGFGSIPPQFK	1.869749451	2	2.759254
P05182	DRLDMPYMDAVVHEIQR	1.224195069	3	3.35647
P05182	DTVFQGYVIPK	0.762862809	2	2.629179
P05182	DVTDCLLIEMEK	1.519343367	2	2.650728
P05182	DVTDCLLIEMEKEK	1.191376532	2	3.094224
P05182	DVTDCLLIEMEKEK+Oxidation(9	1.21654358		
P05182	EHLQSLDINCAR	1.42209565	2	3.470162
P05182	FINLVPSNLPHEATR	0.945559773	2	3.660868
P05182	FKPEHFLNENGK	0.958792938	2	3.369728
P05182	GDIPVFQEYK	0.949901185	2	2.594187
P05182	GIIFNNGPTWK	0.874642095	2	2.757926
P05182	GTVVIPTLDSLLYDSHEFPDPEK	2.321842035	2	5.07511
P05182	LDMPYMDAVVHEIQR	1.338833205	2	3.116959
P05182	RVCVGEGLAR	1.666082659	2	2.356209
P05182	YGLLILMK	0.977369439	2	3.009668
P05183	**CP3A2 Cytochrome P450 3A2**	**1.037092215**	**0.021741**	**12**
P05183	DFGPVGIMGK	4.126964026	2	2.867133
P05183	DIELDGLFIPK	2.626982303	2	3.584995
P05183	EMFPIIEQYGDILVK	2.462624626	2	3.931931
P05183	KDIELDGLFIPK	1.775799335	2	2.871392
P05183	KLQEEIDGALPSK	1.540543221	2	4.021334
P05183	LQEEIDGALPSK	0.887377223	2	4.091887
P05183	QAILEPEKPIVLK	1.020810108	2	3.414145
P05183	QEAETGKPVTMK	0.943317727	2	3.44976
P05183	QEAETGKPVTMK+Oxidation(10	0.867028531		
P05183	RDFGPVGIMGK	1.247759791	2	2.390586
P05183	VDFLQLMLNAHNNSK	1.100075966	2	3.371002
P05183	YLKQEAETGKPVTMK	1.352615687	3	3.316013
P05197	**EF2 Elongation factor 2**	**1.189822017**	**9.9E-20**	**30**
P05197	ALLELQLEPEELYQTFQR	2.124603475	3	5.232966
P05197	ARPFPDGLAEDIDKGEVSAR	1.22681653	3	6.454622
P05197	AYLPVNESFGFTADLR	1.346724924	2	3.781986
P05197	CELLYEGPPDDEAAMGIK	1.263142045	2	3.657288
P05197	DLEEDHACIPIK	1.367422478	2	3.773742
P05197	DLEEDHACIPIKK	1.647062784	2	3.719656
P05197	EGIPALDNFLDK	0.799559196	2	2.676648
P05197	EGIPALDNFLDKL	2.899205895	2	3.449203
P05197	ETVSEESNVLCLSK	0.893066028	2	4.452994
P05197	GEGQLGAAER	0.966826395	2	3.04751
P05197	GHVFEESQVAGTPMFVVK	1.684419428	2	5.90146
P05197	IWCFGPDGTGPNILTDITK	1.673448524	2	5.207613
P05197	KEDLYLKPIQR	1.424568099	2	3.372756
P05197	KIWCFGPDGTGPNILTDITK	1.671443903	2	5.020032
P05197	KVEDMMK	1.876063084	2	2.574003

P05197	KVEDMMK+Oxidation(4	1.671215275		
P05197	KVEDMMK+Oxidation(5	1.671215275		
P05197	LDSEDKDKEGKPLLK	1.760746676	2	4.060977
P05197	NMSVIAHVDHGK	0.622968544	2	3.653381
P05197	NMSVIAHVDHGK+Oxidation(1	1.436950326		
P05197	SDPVVSYR	1.366263173	2	2.303515
P05197	STLTDSLVCK	1.886167681	2	3.181352
P05197	TFCQLILDPIFK	1.631963864	2	4.19923
P05197	TGTITTFEHAHNMR	1.383637413	2	4.00219
P05197	VFDAIMNFR	2.381462988	2	3.315394
P05197	VFSGVVSTGLK	1.557752076	2	3.093052
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.24082258	3	3.594603
P05197	YEWDVAEAR	1.238833483	2	3.146391
P05197	YFDPANGK	1.457547201	1	2.211807
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	2.109049996	3	5.964453
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.820415509**	**0.123118**	**11**
P05369	ALYEELDLR	1.58565784	2	3.193428
P05369	EVLEYNTVGGK	2.869884181	2	3.001854
P05369	GLTVVQTFQELVEPR	1.442692227	3	4.219821
P05369	IKEVLEYNTVGGK	2.096686893	3	4.243099
P05369	QILEENYGQK	1.919452939	2	2.616464
P05369	QILEENYGQKDPEK	3.155848161	2	3.600684
P05369	SLIEQCSAPLPPSIFLELANK	1.577634836	2	4.851699
P05369	VGTDIQDNK	1.107490869	2	3.797306
P05369	VLTEDELGHPEK	1.41842529	2	2.776193
P05369	VLTEDELGHPEKGDAITR	1.80260279	2	4.68737
P05369	YEEDSYNR	3.747013354	2	2.457397
P05426	**RL7 60S ribosomal protein L7**	**1.287145839**	**2.22E-16**	**7**
P05426	AGNFYVPAEPK	1.417374434	2	3.064858
P05426	FGIICMEDLIHEIYTVGK	1.577630894	3	4.804914
P05426	KKVPAVPETLK	1.048969855	2	2.708109
P05426	NFAELK	1.494497374	1	1.909209
P05426	SVNELIYK	1.281073784	2	2.323863
P05426	TTHFVEGGDAGNR	1.227754936	3	3.750811
P05426	TTHFVEGGDAGNREDQINR	1.200264048	2	4.544138
P05544	**SPA3L Serine protease inhibitor A3L**	**2.023862473**	**1.04E-08**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	6.051883625	2	4.376772
P05544	DSTMEEILEGLK	1.680154061	2	3.119078
P05544	IAELFSDLEER	2.13989794	2	2.959225
P05544	MQQVESSLQPETLK	1.493778794	2	4.184197
P05544	MQQVESSLQPETLKK	2.238396823	2	3.917989
P05544	VFSQQADLSR	2.647129576	2	3.045752
P05545	**SPA3K Serine protease inhibitor A3K**	**1.622229763**	**2.39E-08**	**6**
P05545	AVLDVDETGTEGAAATAVTAALK	1.573902658	2	5.861452
P05545	IAELFSELDER	2.146811422	2	2.825539
P05545	IFSQQADLSR	1.787851516	2	2.556782
P05545	KIFSQQADLSR	2.077765332	2	2.395085
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	1.533159602	3	3.694756
P05545	NLHVSQVVHK	1.09179822	2	2.474578
P05712	**RAB2A Ras_related protein Rab_2A**	**1.244685716**	**0.717861**	**2**
P05712	IQEGVFDINNEANGIK	1.310989446	2	4.561138
P05712	TASNVEEAFINTAK	0.937588965	2	2.974536
P05765	**RS21 40S ribosomal protein S21**	**1.3507678**	**0.039526**	**3**
P05765	DHASIQMNVAEVDR	2.003326422	2	3.935605
P05765	MGESDDSILR	4.484693407	2	3.271136
P05765	TYGICGAIR	1.284477217	2	3.313471
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.756730626**	**0.116265**	**9**

P06214	AGADIIITYFAPQLLK	1.345750417	2	3.666084
P06214	AGAFDLR	1.374671193	2	2.504581
P06214	AGCQVVAPSDMMDGR	1.097770954	2	3.602797
P06214	CVLIFGVPSR	1.095038847	2	2.85991
P06214	DEQGSAADSEDSPTIEAVR	0.673222272	2	5.828111
P06214	DIQEGADILMVKPGLPYLDMVQEVK	1.439497384	3	4.631339
P06214	TAVLESMTAFR	0.920643151	2	3.538585
P06214	VPKDEQGSAADSEDSPTIEAVR	0.81696336	3	5.806003
P06214	YGVNQLEEMLRPLVEAGLR	1.394027316	3	4.668053
P06302	**PTMA Prothymosin alpha**	**0.93754315**	**0.987215**	**3**
P06302	RVAEDDEDDDVETKK	0.944077646	3	5.752995
P06302	VAEDDEDDDVETK	0.873308436	2	4.379636
P06302	VAEDDEDDDVETKK	0.916002384	2	4.803526
P06399	**FIBA Fibrinogen alpha chain**	**1.354817145**	**0.792294**	**9**
P06399	AQQIQVLQK	1.10119988	2	2.560978
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	4.708863886	3	3.615273
P06399	GDFANANNFDNTFGQVSEDLR	1.680057256	2	5.320885
P06399	GDFANANNFDNTFGQVSEDLRR	1.19980289	3	3.346849
P06399	GDKELLIGNEK	1.175355375	2	2.565715
P06399	GLIDEANQDFTNR	1.089643966	2	3.494299
P06399	MADEAASEAHQEGDTR	0.872313049	2	4.448887
P06399	SQLQEGPPEWK	1.473533921	2	2.887321
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	4.926437433	3	3.861285
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.277285178**	**0.033164**	**7**
P06685	AVAGDASESALLK	1.416038992	2	3.523507
P06685	AVFQANQENLPILK	1.527077531	2	3.183305
P06685	DKYEPAAVSEHGDKK	1.711021726	3	3.742233
P06685	DMTSEELDDILR	0.60518275	2	2.970131
P06685	LNIPVNQVNPR	1.160948304	2	3.001853
P06685	MSINAEDVVVGDLVEVK	3.119732564	2	2.954459
P06685	YEPAAVSEHGDKK	1.247360604	2	3.293648
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.467936728**	**0.131024**	**3**
P06687	DGPNALTPPPTTPEWVK	1.359218514	2	3.36608
P06687	GVGIISEGNETVEDIAAR	1.664602841	2	4.675199
P06687	QGAIVAVTGDGVNDSPALK	1.500852154	2	4.625836
P06757	**ADH1 Alcohol dehydrogenase 1**	**1.101200798**	**9.68E-06**	**16**
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.475178648	3	5.767336
P06757	FPLEPLITHVLPFEK	1.382981968	3	4.699811
P06757	GAIFGGFK	0.980019871	2	2.757236
P06757	GALLDGTSR	1.192672281	2	2.969497
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.901240762	3	5.342637
P06757	HPESNLCCQTK	0.964349108	2	3.245449
P06757	ICKHPESNLCCQTK	0.591235234	3	4.198095
P06757	IDAAAPLDK	1.208630012	2	2.912627
P06757	IIAVDINKDK	1.437288528	2	2.954609
P06757	INEAFDLLR	1.226320457	2	3.638535
P06757	KFPLEPLITHVLPFEK	0.736979115	3	4.646807
P06757	MVATGVCR	0.607265458	2	2.490789
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.325084215	4	7.545864
P06757	VCLIGCGFSTGYGSAVQVAK	1.369773914	2	6.318457
P06757	VIPLFSPQCGK	1.223642486	2	3.036831
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.385493675	2	5.069885
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.176377608**	**9.9E-20**	**31**
P06761	AKFEELNMDLFR	1.460923331	3	4.668384

P06761	DAGTIAGLNVMR	1.363363292	2	3.651995
P06761	DNHLLGTFDLTGIPPAPR	3.518926037	2	4.328493
P06761	ELEEIVQPIISK	1.612227434	2	4.317802
P06761	ETAEAYLGK	2.571891981	1	2.076486
P06761	FEELNMDLFR	1.315918549	2	3.676165
P06761	IEIESFFEGEDFSETLTR	1.685026988	2	4.74762
P06761	IEWLESHQDADIEDFK	1.140411831	2	5.653275
P06761	IEWLESHQDADIEDFKAK	1.292517455	3	4.347935
P06761	IINEPTAAAIAYGLDKR	1.208059009	2	4.561165
P06761	ITITNDQNR	1.304246455	2	2.729604
P06761	ITPSYVAFTPEGER	1.203267925	2	4.083008
P06761	KKELEEIVQPIISK	0.940037502	2	5.246193
P06761	KSDIDEIVLVGGSTR	1.172727727	2	5.014695
P06761	KSQIFSTASDNQPTVTIK	0.909766003	2	5.275321
P06761	LYGSGGPPPTGEEDTSEKDEL	0.64614019	2	5.346279
P06761	MKETAEAYLGK	1.711186229	2	3.44756
P06761	MKETAEAYLGK+Oxidation(0	1.483145375		
P06761	MKETAEAYLGKK	1.341706578	2	2.85694
P06761	NELESYAYSLK	1.16286533	2	3.371479
P06761	NQLTSNPENTVFDAK	1.140139539	2	4.767647
P06761	SDIDEIVLVGGSTR	1.104933162	2	3.805362
P06761	SQIFSTASDNQPTVTIK	0.954683265	2	5.369656
P06761	TFAPEEISAMVLTK	1.703909248	3	4.75106
P06761	TFAPEEISAMVLTK+Oxidation(9	1.760503471		
P06761	TKPYIQVDIGGGQTK	1.309698933	3	4.711359
P06761	TWNDPSVQQDIK	1.091205218	2	3.983099
P06761	VLEDSDLK	1.449853139	2	2.477257
P06761	VLEDSDLKK	1.255681694	2	2.518519
P06761	VTHAVVTVPAYFNDAQR	1.233475539	2	5.065519
P06761	VYEGERPLTK	1.215940068	2	2.940212
P06866	**HPT Haptoglobin**	**1.701034165**	**9.9E-20**	**8**
P06866	ATDLKDWVQETMAK	1.495551037	2	3.638083
P06866	GAVSPVGVQPILNK	1.821889189	2	4.454386
P06866	HTFCAGLTK	3.519790333	1	2.4074
P06866	LQTEGDGIYTLNSEK	2.232666392	2	4.434931
P06866	NQLVEIEK	1.769605499	1	2.332147
P06866	SCAVAEYGVYVR	2.297889867	2	3.452167
P06866	SVVDIGLIK	2.241075561	1	2.018603
P06866	YVMLPVADQEK	1.620955772	2	2.514901
P07150	**ANXA1 Annexin A1**	**1.759032047**	**0.008373**	**2**
P07150	GLGTDEDTLIEILTTR	1.847891266	2	3.792672
P07150	GVDEATIIDILTK	1.500180415	3	4.062901
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.251110304**	**9.9E-20**	**16**
P07153	ASSFVLALEPELESR	1.614504006	2	4.246402
P07153	AVTSEIAVLQSR	0.983710773	2	3.898068
P07153	FVDHVFDEQVIDSLTVK	1.236537936	2	4.648064
P07153	GEDEEDNNLEVR	1.610049102	2	3.854733
P07153	HFDETVNR	1.233623911	1	2.711969
P07153	IDHILDAL	3.086249731	2	2.40005
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.018519423	3	4.910236
P07153	LKTEGSDLCDR	1.637170754	3	3.43198
P07153	NIQVDSPYDISR	0.873899474	2	3.507428
P07153	NLVEQHIQDIVVHYTFNK	1.201143275	3	4.90029
P07153	SEDILDYGPFK	2.553003906	2	3.48043
P07153	TEGSDLCDR	2.882860503	2	2.694712

P07153	TILPAAAQDVYYR	1.47725789	2	2.884317
P07153	TVDLSSHLAK	1.519192696	2	2.587414
P07153	VHYENNSPFLTITSMTR	2.770507837	2	4.037441
P07153	VTAEVVLAHPGGGSTAR	1.316822093	2	4.87007
P07323	**ENOG Gamma_enolase**	**1.20061526**	**5.59E-05**	**3**
P07323	AAVPSGASTGIYEALELR	1.198871349	2	5.286743
P07323	GNPTVEVDLHTAK	2.48297022	2	3.172306
P07323	SGETEDTFIADLVVGLCTGQIK	1.358876996	3	4.947917
P07335	**KCRB Creatine kinase B_type**	**1.170932452**	**0.116014**	**3**
P07335	FCTGLTQIETLFK	1.501517803	2	2.809034
P07335	LEQGQPIDDLMPAQK	0.760372128	2	2.723867
P07335	TDLNPDNLQGGDDLDPNYVLSSR	0.867031402	2	3.57291
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.120903862**	**0.906223**	**3**
P07340	AYGENIGYSEK	1.168424622	2	2.725038
P07340	VAPPGLTQIPQIQK	1.17145097	2	2.582728
P07340	YNPNVLPVQCTGK	1.071620054	2	2.612048
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**3.165711974**	**9.9E-20**	**18**
P07379	AINPENGFFGVAPGTSVK	3.338916923	2	4.443338
P07379	EEGWLAEHMLILGITNPEGK	3.836574611	2	5.145349
P07379	EIISFGSGYGGNSLLGK	3.902846301	2	2.554124
P07379	EVEEIDKYLEDQVNADLPYEIER	1.689524321	2	4.872244
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	2.959714443	3	5.192271
P07379	GLGDVNVEELFGISK	10.57274824	2	3.772233
P07379	IGIELTDSPYVVASMR	2.872635149	2	4.247428
P07379	MGTSVLEALGDGEFIK	3.024849917	2	4.757786
P07379	MGTSVLEALGDGEFIK+Oxidation(0	3.130995958		
P07379	TNLAMMNPTLPGWK	2.178557326	2	3.134183
P07379	TVIITQEQR	2.911615188	2	2.462635
P07379	VECVGDDIAWMK	3.242601604	2	3.831092
P07379	VIQGSLDSLPQEVR	2.476831779	2	3.90576
P07379	VLEWMFGR	3.880965946	2	2.530855
P07379	WMSEEDFEK	2.813464716	2	2.374507
P07379	YDNCWLALTDPR	2.814349484	2	2.519993
P07379	YLAAAFPSACGK	1.844232637	2	2.720623
P07379	YLEDQVNADLPYEIER	1.856843571	2	5.057472
P07483	**FABPH Fatty acid_binding protein_ heart**	**2.109694371**	**0.625237**	**2**
P07483	QVASMTKPTTIIEK	1.529417142	2	3.269153
P07483	WDGQETTLTR	2.272749317	2	2.531591
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.227192434**	**0.863009**	**4**
P07632	DGVANVSIEDR	1.022977153	2	2.732336
P07632	GDGPVQGVIHFEQK	1.21677781	2	3.795519
P07632	HVGDLGNVAAGK	1.258763541	2	4.041987
P07632	VISLSGEHSIIGR	1.288422297	2	3.029337
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**1.056435611**	**0.160557**	**10**
P07633	AFDNDVDALCNLR	1.108523191	2	4.076532
P07633	AYNMLDIIHAVIDER	1.285240163	2	3.886509
P07633	GFVDDIIQPSSTR	1.645753276	2	3.239844
P07633	HLLGDTNYAWPTAEIAVMGAK	1.353510087	2	5.757886
P07633	ICCDLEVLASK	1.206250397	2	3.497784
P07633	IMDQAITVGAPVIGLNDSGGAR	1.107450324	3	5.025589
P07633	LVPELDTVVPLESSK	1.590362571	2	3.703315
P07633	NKFPGDSVVTGR	0.629919888	2	2.409773
P07633	SVTNEDVTQEQLGGAK	0.824389535	2	5.244103
P07633	TVGIVGNQPNVASGCLDINSSVK	2.02706746	2	4.914876

P07687	**HYEP Epoxide hydrolase 1**	**1.462802439**	**9.9E-20**	**26**
P07687	DIELLYPYK	0.997355362	1	2.302778
P07687	DKEETLPLGDGWWGPGSKPSAK	1.779797694	3	5.655436
P07687	EDESIRPFK	1.1393808	2	2.951956
P07687	EDESIRPFKVETSDEEIKDLHQR	1.43624103	3	5.9852
P07687	ELEDGGLER	2.634708535	2	2.348743
P07687	ENLGQGIMVHK	2.269607663	2	3.200235
P07687	ENLGQGIMVHK+Oxidation(7	1.177337096		
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.702586176	3	5.669833
P07687	FHYGFNSNYMK	1.095742693	2	2.625009
P07687	FLGYTEKDIELLYPYK	1.606271893	3	4.740737
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.494227605	3	3.383703
P07687	GGHFAAFEEPK	1.531574913	2	3.461584
P07687	GLHLNMAFISR	1.967737819	2	2.792075
P07687	IEGLDIHFIHVKPPQLPSGR	1.05352536	3	4.260906
P07687	IIPLLTDPK	2.156482793	1	1.900701
P07687	KFVSLAELQ	1.514424765	2	2.801633
P07687	KQVEILNQYPHFK	1.51171646	3	5.212343
P07687	LLAQDIR	1.436324566	2	2.509065
P07687	QVEILNQYPHFK	1.12395996	2	3.594804
P07687	SEYRELEDGGLER	1.156100219	3	3.664314
P07687	SFYTMTPLLGQR	1.674150812	2	3.780762
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.883350155	3	6.595165
P07687	TKIEGLDIHFIHVKPPQLPSGR	1.200754556	3	4.031816
P07687	VETSDEEIK	1.049283924	2	2.628767
P07687	VETSDEEIKDLHQR	1.414642787	2	4.720473
P07687	VFVPTGFSAFPSELLHAPEK	1.644047389	2	4.541538
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.204391559**	**9.9E-20**	**99**
P07756	AADTIGYPVMIR	1.362680119	2	3.875254
P07756	AADTIGYPVMIR+Oxidation(9	1.4707704		
P07756	AERPDGLILGMGGQTALNCGVELFK	1.540776039	3	6.911839
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10	1.449367277		
P07756	AFAISGPFNVQFLVK	1.430018388	2	4.956167
P07756	AFAMTNQILVER	1.394853653	2	4.58938
P07756	AFAMTNQILVER+Oxidation(3	1.493390548		
P07756	ALENNMSLDEIVK	1.20159126	2	4.813889
P07756	ALENNMSLDEIVK+Oxidation(5	1.333070767		
P07756	AMLSTGFK	1.261182033	2	2.49318
P07756	AQTAHIVLEDGTK	1.058275041	2	4.477083
P07756	ATGYPLAFIAAK	0.821921222	2	3.183129
P07756	CEMASTGEVACFGEGIHTAFLK	1.163949631	3	5.408203
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2	1.380899182		
P07756	CLGLTEAQTR	1.109128873	2	3.61715
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	3.827529453	3	5.164364
P07756	DELGLNK	1.298965767	1	2.347505
P07756	DGSIDLVINLPNNNTK	0.88890865	2	5.315105
P07756	DILNMDK	1.293051745	1	2.032569
P07756	EIEYEVVR	2.689141209	1	2.093131
P07756	EIGFSDKQISK	1.491085931	2	3.147104
P07756	EPLFGISTGNIITGLAAGAK	1.168951348	3	5.656631
P07756	ETLMDLGTK	1.71406816	1	2.33659
P07756	EVEMDAVGK	2.339963785	1	2.110601
P07756	FIEGAREVEMDAVGKEGR	1.11589578	3	3.648398
P07756	FLEEATR	249.6600141	2	2.46326
P07756	FLGVAEQLHNEGFK	1.063857905	2	4.80351

P07756	FVHDNYVIR	1.026871561	3	3.352191
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.6363095	3	6.069028
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15	1.588320029		
P07756	GILIGIQQSFRPR	1.560848789	2	2.461312
P07756	GLNSESVTEETLR	1.141494381	2	4.848074
P07756	GNDVLVIECNLR	1.102009094	2	4.459745
P07756	GQILTMANPIIGNGGAPDTTAR	0.954819742	2	6.004269
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5	1.416247985		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	1.030417008	3	4.912012
P07756	GQNQPVLNITNR	1.060736671	2	4.38972
P07756	GTTITSVLPKPALVASR	1.485563234	2	3.354508
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.296666613	3	5.980975
P07756	HLPTLEQPIIPSDYVAIK	1.27098293	2	5.585216
P07756	IALGIPLPEIK	1.42052455	2	2.827316
P07756	IAPSFAVESMEDALK	1.925085562	2	5.256878
P07756	IAPSFAVESMEDALK+Oxidation(9	1.400248592		
P07756	IAPSFAVESMEDALKAADTIGYPVMIR	1.639343725	3	4.130747
P07756	IEFEGQSVDFVDPNK	1.429143453	2	5.298659
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	0.930172006	3	5.551414
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.628827804	3	5.62339
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	1.292223019	3	4.697627
P07756	IMGTSPLQIDR	1.678527472	2	3.269569
P07756	IMGTSPLQIDR+Oxidation(1	2.914839586		
P07756	IMGTSPLQIDRAEDR	1.0448469	2	2.517004
P07756	KEPLFGISTGNIITGLAAGAK	1.313767401	2	5.107969
P07756	KTVVVNCNPETVSTDFDECDK	0.34024483	2	4.981089
P07756	LFAEAVQK	1.223581332	2	3.44823
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.502707992	4	4.715882
P07756	LRDADPILR	1.332214844	2	3.211143
P07756	LTSIDKWFLYK	0.861503281	2	2.764988
P07756	LYFEELSLER	2.783683997	2	3.672669
P07756	MCHPSVDGFTPR	1.62957446	3	4.897567
P07756	MCHPSVDGFTPR+Oxidation(0	1.33975969		
P07756	MRDILNMDK	1.404411704	2	3.147745
P07756	MRDILNMDK+Oxidation(0	1.586056572		
P07756	QADAVYFLPITPQFVTEVIK	1.417012777	3	4.194491
P07756	QLFSDKLNEINEK	1.207667913	2	3.825253
P07756	QNLIAEVSTK	1.041919132	1	2.639273
P07756	RFLEEATR	1.293479338	2	2.689963
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.824804009	4	4.629644
P07756	RTAVDSGIALLTNFQVTK	1.189396673	2	5.165077
P07756	RTSINVVR	0.840383742	2	2.339925
P07756	SAYALGGLGSGICPNK	1.090737213	2	4.949467
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.236020637	3	4.694944
P07756	SIFSAVLDELK	1.08145144	2	3.834886
P07756	SIFSAVLDELKVAQAPWK	1.262271901	3	4.29703
P07756	SLGQWLQEEK	1.124373705	2	4.064531
P07756	SLGQWLQEEKVPAIYGVDTR	1.369626065	2	3.795402
P07756	SVGEVMAIGR	1.136216573	2	3.518286
P07756	SVGEVMAIGR+Oxidation(5	0.845216682		
P07756	TAVDSGIALLTNFQVTK	1.370039852	3	6.506335
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	1.567858885	3	5.416379
P07756	TFEESFQK	1.121934336	2	2.50366
P07756	TLGVDFIDVATK	1.003628126	2	4.283441

P07756	TSACFEPSLDYMVTK	1.132763365	2	4.556084
P07756	TSACFEPSLDYMVTK+Oxidation(11	0.798624598		
P07756	TVLMNPNIASVQTNEVGLK	1.101426289	2	6.116317
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3	1.41914138		
P07756	TVVVNCNPETVSTDFDECDK	0.568097758	2	5.61548
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	2.671618651	3	5.563974
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	1.26446367	3	7.425854
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22	1.498655804		
P07756	VLGTSVESIMATEDR	1.183247211	2	4.702561
P07756	VLGTSVESIMATEDR+Oxidation(9	1.032500186		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.435490597	2	5.823526
P07756	VMIGESVDEK	1.141673771	2	3.688676
P07756	VMIGESVDEK+Oxidation(1	0.970865731		
P07756	VSQEHPVVLTK	1.37248489	2	3.84969
P07756	VVAVDCGIK	1.525074745	2	2.525378
P07756	VVAVDCGIKNNVIR	1.000113056	2	3.800945
P07756	YMESDGIK	1.073039347	2	2.613149
P07756	YMESDGIK+Oxidation(1	1.288197034		
P07824	**ARGI1 Arginase_1**	**1.281229735**	**4.72E-11**	**16**
P07824	ANEQLAAVVAETQK	1.041108793	2	5.202744
P07824	DHGDLAFVDVPNDSPFQIVK	1.198559552	2	6.217107
P07824	DIVYIGLR	1.027814167	2	2.326401
P07824	DVDPGEHYIIK	2.503452174	2	3.411388
P07824	EGNHKPETDYLKPPK	1.702084737	2	2.768633
P07824	GKFPDVPGFSWVTPCISAK	1.037214957	3	4.961032
P07824	LKETEYNVR	1.095471238	3	3.339787
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.327247138	3	4.342688
P07824	RPIHLSFDVDGLDPVFTPATGTPVVGGLSYR	2.218188914	3	5.754816
P07824	TGLLSGLDIMEVNPTLGK	1.251639457	2	5.645827
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9	1.154748078		
P07824	TVNTAVALTLSCFGTK	1.282212292	2	5.037458
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.981031184	4	5.503472
P07824	VMEETFSYLLGR	1.251083159	2	3.709967
P07824	YFSMTEVDK	1.209386817	1	2.322202
P07824	YFSMTEVDKLGIGK+Oxidation(3	1.182060069		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.95643673**	**0.973638**	**17**
P07871	AEELGLPILGVLR	0.891502664	2	4.301894
P07871	AEIVPVTTTVLDDK	0.959095821	2	4.735701
P07871	AEIVPVTTTVLDDKGDR	1.112801194	2	3.686832
P07871	AEIVPVTTTVLDDKGDRK	1.018436674	2	4.365884
P07871	DCLIPMGITSENVAER	2.317715071	2	3.910081
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	1.268173496	2	6.343596
P07871	IAQFLSGIPETVPLSAVNR	1.330644366	2	3.215863
P07871	KTITVSQDEGVRPSTTMEGLAK	1.077336899	3	3.704695
P07871	LKPECLGDISVGNVLQPGAGAAMAR	1.00415076	3	5.14145
P07871	QCSSGLQAVANIAGGIR	1.051627582	2	4.699809
P07871	QDAFALASQQK	1.129251646	2	3.759766
P07871	QKQDAFALASQQK	1.035689015	2	4.153682
P07871	QVVTLLNELK	1.076887908	2	2.38165
P07871	SKAEELGLPILGVLR	0.804392622	3	4.830839
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.973329713	3	4.746675
P07871	TITVSQDEGVRPSTTMEGLAK	0.815113654	2	4.367602
P07871	VNPLGGAIALGHPLGCTGAR	0.935571634	2	4.995617
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**1.259039353**	**9.9E-20**	**21**
P07872	AFTTWTANAGIEECR	2.384821615	2	3.814965
P07872	ASATFNPELITHILDGSPENTR	1.131045318	2	4.779863

P07872	ASEAHCHYVVVK	1.260938856	3	4.143539
P07872	EIENLILNDPDFQHEDYNFLTR	3.059753674	2	4.544086
P07872	EIGTHKPLPGITVGDIGPK	1.10628393	3	4.120678
P07872	EVAWNLTSVDLVR	1.444891213	2	3.14678
P07872	EYGISDPEEIMWFK	1.128905295	2	3.435677
P07872	FGYEEMDNGYLK	0.919731293	2	3.875867
P07872	GGDFLEGSIITGAQLSQVNAR	1.998850378	2	5.243323
P07872	GLETTATYDPK	1.183240014	2	3.676084
P07872	INESIGQGDLSELPELHALTAGLK	1.306627395	3	5.515228
P07872	LVEIAAK	1.376020943	1	2.20189
P07872	LVGGMVSYLNDLPSQR	1.834333427	2	3.235612
P07872	NLCLLYSLYGISQK	1.552096667	2	3.262428
P07872	QSEPEPQILDFQTQQYK	1.259764965	2	4.789578
P07872	SFLVGNAAQSLSK	1.030478845	2	4.291443
P07872	SKEVAWNLTSVDLVR	1.751674935	3	3.826543
P07872	TQEFILNSPTVTSIK	1.255135172	2	4.574351
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	1.246488192	4	4.923507
P07872	YAQVKPDGTYVKPLSNK	1.457759378	3	3.749005
P07872	YDGNVYENLFEWAK	2.15760853	2	4.821437
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.924360512**	**0.916436**	**5**
P07895	AIWNVINWENVSQR	1.128378015	2	3.874971
P07895	GDVTTQVALQPALK	0.923270786	2	3.985694
P07895	GELLEAIKR	1.157405653	2	2.337225
P07895	HHATYVNNLNVTEEK	0.854031176	2	4.829825
P07895	NVRPDYLK	1.242556424	2	2.302418
P07896	**ECHP Peroxisomal bifunctional enzyme**	**1.049886524**	**0.553269**	**24**
P07896	EWQSLAGPHGSK	1.265168988	2	2.483037
P07896	GGPMFYAASVGLPTVLEK	1.50576712	2	3.889342
P07896	GQGLTGPSLPPGTPVR	0.891533995	2	3.927125
P07896	GWYQYDKPLGR	1.223786837	2	2.901222
P07896	IFNKPVPSLPNMDSVFAEAIAK	2.304644207	3	4.744816
P07896	IGVVVGNCYGFVGNR	2.409781392	2	3.443466
P07896	IIDKPIEPR	1.288630314	2	2.427397
P07896	KGQGLTGPSLPPGTPVR	0.856859055	2	4.268447
P07896	KQYPGVLAPETCVR	1.126565058	2	4.346848
P07896	LCNPPVNAVSPTVIR	1.158461068	2	4.270799
P07896	LGILDAVVK	1.246666527	2	2.819221
P07896	LLEVIPSR	0.906938296	2	2.824992
P07896	LVAQGSPPLK	1.381430235	2	2.54035
P07896	QNPDIPQLEPSDYLR	0.952317304	2	3.955622
P07896	QYPGVLAPETCVR	0.899529268	2	3.073713
P07896	RLVAQGSPPLK	0.665078866	2	2.337364
P07896	TASAQPVSSVGVLGLGTMGR	1.199712996	2	5.888388
P07896	TISKEEILER	1.293136016	2	2.654372
P07896	VGISVVAVESDPK	1.395157297	2	3.902246
P07896	VGLPEVTLGILPGAR	1.340408766	2	3.622226
P07896	VSDLAGLDVGWK	1.129871239	2	4.271889
P07896	YLSADEALR	2.704555644	2	2.976469
P07896	YSPLGDMLCEAGR	1.111228325	2	4.337061
P07896	YSSPTTIATVMSLSK	1.243244353	2	3.493452
P07943	**ALDR Aldose reductase**	**1.17802701**	**0.269691**	**2**
P07943	AIGVSNFNPLQIER	1.672817651	2	3.064428
P07943	HIDCAQVYQNEK	1.136188242	2	4.458974
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**1.507684159**	**0.022387**	**5**

P07953	HGESELNLR	1.302332549	2	2.597691
P07953	IGGDSGLSAR	0.535829593	2	2.774735
P07953	NYEFFRPDNTEAQLIR	1.744967445	2	3.392666
P07953	TIQTAEALGVPYEQWK	2.323308813	2	3.065735
P07953	YLNWIGTPTK	1.086263718	2	2.959269
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.039764508**	**0.001572**	**6**
P08009	LCYNPDFEK	2.25335066	2	3.049408
P08009	LLLEYTDSSYEEK	0.715619248	2	4.831135
P08009	LLLEYTDSSYEEKR	1.112437905	2	4.009915
P08009	NQVFEATCLDAFPNLK	1.009980085	2	4.564517
P08009	SQWLNEK	1.232037005	2	2.708434
P08009	YTMGDAPDFDR	0.997937519	2	2.814792
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**0.823243645**	**9.9E-20**	**15**
P08010	FLSKPIFAK	1.847796973	2	2.337114
P08010	IRVDVLENQAMDTR	1.797117041	3	4.223902
P08010	ITYVDFLVYDVLDQHR	1.431518306	2	5.011247
P08010	KKPEYLEGLPEK	1.112711437	3	4.167448
P08010	KPEYLEGLPEK	1.303882889	2	3.429055
P08010	KYSMGDAPDYDR	1.639957955	2	3.826402
P08010	LFLEYTDTSYEDK	0.544422042	2	5.54148
P08010	LFLEYTDTSYEDKK	1.293394397	2	4.368438
P08010	LQLAMVCYSPDFER	1.979320605	2	4.328523
P08010	LQLAMVCYSPDFER+Oxidation(4	2.458859303		
P08010	SQWLSEK	1.366819755	2	2.464066
P08010	VDVLENQAMDTR	0.356150689	2	4.694429
P08010	VDVLENQAMDTR+Oxidation(8	1.478054769		
P08010	YSMGDAPDYDR	1.105791152	2	3.370795
P08010	YSMGDAPDYDR+Oxidation(2	1.311478859		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.866022679**	**0.002854**	**6**
P08011	IYHTIAYLTPLPQPNR	0.666126258	2	5.320198
P08011	MMFLSSATAFQR	0.848911099	2	3.603543
P08011	MMFLSSATAFQR+Oxidation(0	1.471430737		
P08011	MMFLSSATAFQR+Oxidation(1	1.471430737		
P08011	VFANPEDCAGFGK	0.847497116	2	4.678979
P08011	VFANPEDCAGFGKGENAK	1.535545371	2	4.621316
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**0.994790824**	**0.905328**	**4**
P08032	ADVVESWIGEK	0.989107438	2	2.636208
P08032	DLVAAKNLLNR	1.300399247	2	2.438226
P08032	DQARDLTSAGNLLK	1.028842691	2	2.433487
P08032	QELNTRWNSLK	2.05621624	2	2.301824
P08081	**CLCA Clathrin light chain A**	**1.050426841**	**0.54441**	**2**
P08081	LEALDANSR	2.012171242	2	2.745923
P08081	WREEQTER	0.986235481	2	2.478195
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**1.566076596**	**0.080395**	**3**
P08290	DFQDIQQLDSEENDHQLIGDEEQGSHVQNLR	1.493923038	3	6.50026
P08290	EEQEFVVK	1.684482879	1	2.063976
P08290	WVDGTEYR	2.697573333	2	2.322834
P08430	**UD16 UDP_glucuronosyltransferase 1_6**	**1.537763689**	**4.47E-05**	**2**
P08430	GHDIVVLVPEVNLLLGESK	1.490024735	3	3.819506
P08430	YEILASDLLK	1.790276754	2	2.47489
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.190289788**	**6.92E-05**	**5**
P08461	AAPAAAAAAPPGPR	1.029991484	2	2.320115
P08461	DVPLGTPLCIIVEK	1.045789584	2	3.425307
P08461	DVPVGSIICITVEKPQDIEAFK	1.530111327	2	3.90108
P08461	GLETIASDVVSLASK	1.852552319	2	4.498261

P08461	VAPTPAGVFIDIPISNIR	1.452822904	2	4.579574
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.125724128**	**0.016179**	**9**
P08503	AFAGDIANQLATDAVQIFGGYGFNTEYPVEK	1.25603889	3	5.190603
P08503	AFTGFIVEADTPGIHIGK	1.248771304	2	4.442656
P08503	EEIIPVAPDYDK	1.184184514	2	3.575352
P08503	GITFEDVR	1.117652568	2	2.426563
P08503	IYQIYEGTAQIQR	1.213197773	2	4.731617
P08503	KGDEYVINGQK	1.162299424	2	4.124278
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	1.644403074	2	4.469299
P08503	SGEYPFPLIK	1.243428544	2	2.79131
P08503	TRPTVAAGAVGLAQR	1.353852707	2	4.416687
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.553161607**	**5.94E-13**	**11**
P08541	DELQNHFIK	1.214920806	2	2.590626
P08541	FEIFSTSISKDELQNHFIK	1.822955011	3	4.89458
P08541	FILPPSYVPVILSGLAGK	1.645229595	3	6.129734
P08541	GAAVSLNIR	1.405720489	2	2.918998
P08541	GHEVTVLKPSAYFFLDPK	2.035732235	2	4.348586
P08541	HKEWDTFYSEILGRPTTVDETMSK	1.201800234	3	4.439881
P08541	LLDVWTYELPR	1.678172133	2	4.051437
P08541	NVMLLSTIHHDQPMKPLDR	0.766964978	3	3.78731
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(2	1.99487432		
P08541	VEIWLIR	1.714710872	2	3.025002
P08541	VLVWPMDFSHWMNIK	1.872491913	2	2.483992
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.586061471**	**9.9E-20**	**6**
P08542	EIINNPFYK	1.469072097	1	2.071739
P08542	FETFPTSVSKDELENYFIK	1.564168023	2	4.18042
P08542	KWDPFYSEILGRPTTLAETMGK	1.841080479	2	4.060183
P08542	LVDVWTYELQR	1.484001178	2	3.5694
P08542	NAVWLSTIHHDQPMKPLDK	0.724892693	3	4.160419
P08542	WDPFYSEILGRPTTLAETMGK	1.879249547	2	3.743805
P08649	**CO4 Complement C4**	**1.192303243**	**0.643746**	**2**
P08649	SLEIPGSSDPNVIPDGDFSSFVR	1.311355392	2	2.860376
P08649	VTASEPLETLGSEGALSPGGVASLLR	0.772768719	2	2.871773
P08661	**MBL2 Mannose_binding protein C**	**0.821255896**	**0.007074**	**2**
P08661	ALCSELQGTVATPR	0.495188488	2	3.340457
P08661	TENVFEDLTGNR	1.17877014	2	2.850439
P08683	**CP2CB Cytochrome P450 2C11**	**0.959330726**	**0.138305**	**18**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	1.119738883	3	4.896581
P08683	EALVDLGEEFSGR	1.304361335	2	3.914018
P08683	EHQESLDKDNPR	0.882303912	2	3.972373
P08683	FDPGHFLDER	1.123835833	2	2.637429
P08683	FDYKDPTFLNLMHR	1.435897466	3	4.849626
P08683	FNENFR	1.099136009	1	2.09618
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	0.956193205	3	6.024824
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.103914733	2	4.990959
P08683	HNPQSEFTLESLVATVTDMFGAGTETTSTTLR	0.746695707		
P08683	ICAGEALAR	1.263986116	2	3.021448
P08683	LPPGPTPLPIIGNTLQIYMK	1.186871105	3	3.970359
P08683	NFFYIK	1.26595338	1	1.91941
P08683	NYVLEK	0.562689168	1	2.030156
P08683	SQMPYTDAVVHEIQR	1.105256724	2	4.438921
P08683	VKEHQESLDKDNPR	1.01058626	3	5.260345
P08683	VQEEIER	0.994442891	2	2.462134
P08683	YGLLLLLK	1.543275156	2	3.199466
P08683	YIDLVPTNLPHLVTR	1.33094377	2	4.233949

P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**1.250914557**	**0.699455**	**3**
P08733	GADPEETILNAFK	1.128235853	2	2.327029
P08733	NEEIDEMIK	1.228767988	1	2.632213
P08733	NLVHIITHGEEKD	2.392199011	2	2.917254
P09006	**SPA3N Serine protease inhibitor A3N**	**4.027220531**	**0.000313**	**2**
P09006	AVLDVAETGTEAAAATGVK	2.594523637	2	4.871326
P09006	GNSMEEILEGLK	5.740535835	2	3.144378
P09034	**ASSY Argininosuccinate synthase**	**1.345956029**	**9.9E-20**	**17**
P09034	APNTPDVLEIEFK	1.469644189	2	3.660811
P09034	DGTTHSTSLDLFMYLNEVAGK	1.629773485	2	4.824489
P09034	EFVEEFIWPAVQSSALYEDR	2.551369567	3	5.729157
P09034	EQGYDVIAYLANIGQK	1.77792102	2	4.704628
P09034	FAELVYTGFWHSPECEFVR	1.519538077	2	4.590873
P09034	FELTCYSLAPQIK	1.497835673	2	4.463135
P09034	GRNDLMEYAK	1.810317329	2	3.334978
P09034	IDIVENR	1.123284163	2	2.373924
P09034	KVFIEDVSK	1.336056919	3	3.621536
P09034	NDLMEYAK	1.821153158	2	2.631735
P09034	NDLMEYAK+Oxidation(3	1.706931895		
P09034	NQAPPGLYTK	1.359371723	2	2.3122
P09034	SPWSMDENLMHISYEAGILENPK	1.664879427	3	5.631264
P09034	TQDPAKAPNTPDVLEIEFK	1.412704406	2	5.064881
P09034	TQDPAKAPNTPDVLEIEFKK	1.232106483	3	5.395626
P09034	VFIEDVSK	1.43481765	2	2.356571
P09034	VQVSVFK	1.19441599	2	2.444903
P09041	**PGK2 Phosphoglycerate kinase 2**	**0.85634855**	**0.966419**	**5**
P09041	FHVEEEGK	0.868107373	2	2.650303
P09041	FHVEEEGKGK	0.944186978	2	2.529925
P09041	LGDVYVNDAFGTAHR	1.1625532	3	4.216554
P09041	VDFNVPMK	1.177799408	2	2.338053
P09041	VSHVSTGGGASLELLEGK	0.817769528	2	5.827338
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.354281837**	**0.002977**	**3**
P09117	VLAAVYK	1.332103917	2	2.684492
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	4.436607344	3	3.599531
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.58818414	3	5.118912
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.091493349**	**0.073357**	**3**
P09139	IGLLGYNATTENADR	1.029342733	2	3.11332
P09139	LLLGPGPSNLAPR	1.205316255	2	2.51964
P09139	VLNAPPGISLISFNDK	2.029468242	2	2.392833
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**7.953534537**	**0.003381**	**4**
P09367	ALGVNTVGAQTLK	8.10928712	2	3.545291
P09367	AQLGLNELLK	2.623591559	1	2.190217
P09367	LGLPATIVVPSTTPALTIER	7.797084492	2	2.705829
P09367	LKNEGATVEVVGEMLDEAIQLAK	4.795232271	3	3.977926
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.424631066**	**0.547202**	**12**
P09495	AEGDAAALNR	0.972846894	2	2.551312
P09495	EDKYEEEIK	1.464631386	1	2.692958
P09495	EENVGLHQTLDQTLNELNCI	3.166004479	2	5.231386
P09495	IQALQQQADDAEDR	1.648019522	2	4.463531
P09495	IQLVEEELDR	1.177150017	2	3.486837
P09495	IQLVEEELDRAQER	1.128802633	2	3.015518
P09495	KLVILEGELER	2.264292375	3	4.050983
P09495	LEEAEKAADESER	1.749633128	2	4.133396
P09495	LVILEGELER	2.248495732	2	3.148052

P09495	MEIQEMQLK	1.090693878	2	2.981383
P09495	RIQLVEEELDR	1.265034722	2	2.794991
P09495	YSEKEDKYEEEIK	1.430774848	2	4.535002
P09527	**RAB7A Ras_related protein Rab_7a**	**1.454898808**	**0.009927**	**6**
P09527	ATIGADFLTK	1.079271642	2	2.611155
P09527	DPENFPFVVLGNK	1.955246827	2	3.796908
P09527	GADCCVLVFDVTAPNTFK	1.307539894	2	3.396025
P09527	TLDSWRDEFLIQASPR	1.504643432	3	3.505819
P09527	TSLMNQYVNK	1.45400079	2	2.833833
P09527	VIILGDSGVGK	1.225566101	2	2.425672
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**2.95232038**	**0.667979**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	3.135729729	2	3.828196
P09605	LSEMTEQDQQR	2.939557784	2	3.363609
P09606	**GLNA Glutamine synthetase**	**1.392003898**	**0.893855**	**8**
P09606	CIEEAIDK	2.101243887	2	2.348305
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.283001181	3	5.467392
P09606	LTGFHETSNINDFSAGVANR	1.296834977	2	6.017028
P09606	MGDHLWVAR	1.078227006	2	3.032172
P09606	QMYMNLPQGEK	1.264632715	2	2.389685
P09606	RLTGFHETSNINDFSAGVANR	1.214014855	3	5.519413
P09606	TCLLNETGDEPFQYK	0.848275693	2	5.301614
P09606	TCLLNETGDEPFQYKN	1.018692222	2	5.466637
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**1.495160828**	**0.495172**	**2**
P09626	VDNSSLTGESEPQTR	1.442636192	2	4.202542
P09626	VIMVTGDHPITAK	1.512805034	2	3.287132
P09811	**PYGL Glycogen phosphorylase_ liver form**	**0.908971346**	**0.723908**	**27**
P09811	AWNTMVLR	1.809574654	2	2.39321
P09811	DFSELEPDKFQNK	1.242795938	2	3.487676
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.88573843	4	5.476968
P09811	DLSQLTK	0.957829089	1	2.146802
P09811	EGWQVEEADDWLR	1.014950654	2	3.710165
P09811	FSQFLEK	1.258599112	1	2.0447
P09811	GIVGVENVAELK	1.14339414	2	3.011632
P09811	GIVGVENVAELKK	1.349904052	2	3.333617
P09811	HLQIIYEINQK	0.646327349	2	3.795975
P09811	IFVDIEK	1.081602099	1	2.05413
P09811	INMAHLCIVGCHAVNGVAK	0.660485284	3	5.016294
P09811	INPSSMFDVHVK	1.005369594	2	3.174701
P09811	LVIDQIDNGFFSPNQPDLFK	1.042577734	2	5.27898
P09811	LVTSVAEVVNNDPMVGSK	1.59325766	2	4.679949
P09811	MSLIEEEGGK	0.977569485	2	2.422891
P09811	MSLIEEEGGKR	0.295919677	2	2.721649
P09811	RWLLLCNPGLADLIAEK	1.396460865	3	5.042345
P09811	TFAYTNHTVLPEALER	1.051213029	2	4.923197
P09811	VDDVAALDK	1.004432766	2	2.70679
P09811	VDDVAALDKK	1.053836314	3	3.774551
P09811	VFADYEAYVK	1.175814207	2	2.646587
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.431232548	2	5.962235
P09811	VLYPNDNFFEGK	1.259873754	2	2.643168
P09811	VSQLYMNQK	0.77465877	2	3.031734
P09811	WLLLCNPGLADLIAEK	1.248680284	2	4.836044
P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	1.968262958	3	4.281541
P09811	YEYGIFNQK	0.897288003	2	2.633682
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**1.180038464**	**0.915992**	**9**
P09812	GYNAQEYYDR	0.973510756	2	2.325497
P09812	HLQIIYEINQR	1.164046885	2	2.333961

P09812	LITAIGDVVNHDPAVGDR	1.872109563	2	3.2642
P09812	NLAENISR	1.179536874	2	2.722011
P09812	QIIEQLSSGFFSPK	2.166102756	2	3.66077
P09812	VIFLENYR	1.147627205	2	2.511802
P09812	VIPAADLSEQISTAGTEASGTGNMK	7.144337373	2	4.78652
P09812	WLVLCNPGLAEVIAER	1.411524922	2	3.815702
P09812	YEFGIFNQK	1.564424888	2	2.444473
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.20288544**	**0.035473**	**6**
P09875	ANVVASALAQIPQK	1.07007937	3	3.615512
P09875	FSGGLPLPPSYVPVVLSELSDR	1.501927621	3	3.617036
P09875	IILNELAQR	1.359149719	2	3.003271
P09875	SDLEYSFAK	1.12221344	2	2.357844
P09875	VDFSILSTTGLLTALK	1.162438055	2	4.553809
P09875	WIDEWTR	0.658868018	2	2.600365
P09895	**RL5 60S ribosomal protein L5**	**1.295358049**	**6.56E-05**	**5**
P09895	GAVDGGLSIPHSTK	1.401160818	2	4.374233
P09895	HIMGQNVADYMR	1.48973154	2	3.546436
P09895	NNVTPDMMEEMYK	1.332537625	2	3.394506
P09895	RFPGYDSESK	1.287385998	2	2.848871
P09895	YLMEEDEDAYKK	0.933934439	2	3.547877
P0C0S7	**H2AZ Histone H2A.Z**	**0.81548685**	**0.980432**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.812823142	2	3.513066
P0C0S7	GDEELDSLIK	1.035727857	2	3.409993
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.979674009**	**0.368593**	**20**
P0C2X9	AIEAAVLAR	1.216134262	2	2.908767
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	1.297025872	2	5.131677
P0C2X9	AQIFLK	1.311290055	2	2.311332
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	0.689790164	3	3.58991
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	35.62558301	2	5.293629
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	1.302909009	3	3.669496
P0C2X9	EEIFGPVLTVYVYPDEK	0.967867942	2	3.834084
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	2.158966273	2	5.512571
P0C2X9	KEWDLKPVADR	1.178655424	2	3.583397
P0C2X9	LYVPQSLWPQIK	1.637973537	2	3.208982
P0C2X9	NAAGNFYINDK	1.269643504	2	3.60515
P0C2X9	NFHFVHSSADVDSVVSGTLR	0.946995024	2	5.738863
P0C2X9	SAFEYGGQK	1.092751089	1	2.433331
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.95785813	3	5.748569
P0C2X9	STGSVVGQQPFGGAR	1.046193318	2	4.393694
P0C2X9	TIVQEATR	1.085031004	2	2.927183
P0C2X9	VANEPILAFTQGSPER	0.993627639	2	5.214002
P0C2X9	WKHASSLKVANEPILAFTQGSPER	3.546836536	2	2.508734
P0C2X9	YQLSPFNHGHK	0.939804034	2	2.982525
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	1.590798433	3	4.053402
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.345520691**	**6.64E-06**	**5**
P0C5H9	DRDVTFSPATIEEELIK	1.438370178	2	4.926311
P0C5H9	DVTFSPATIEEELIK	1.138645593	2	3.215951
P0C5H9	IINEVSKPLAHHIPVEK	1.96879691	3	4.049046
P0C5H9	ILDDWGEMCK	6.546523827	2	3.030432
P0C5H9	INELMPK	1.08780192	2	2.489192
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**0.925326479**	**0.860623**	**2**
P0C6F1	AMLPGEWENACNEMQRMLIVR+Oxidation(16	0.764911798		
P0C6F1	EKVEVMSLELEDAK+Oxidation(5	0.927439442		
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.057203255**	**2.16E-10**	**11**

P10111	EGMSIVEAMER	1.431570141	1	2.804266
P10111	FEDENFILK	1.051274442	2	3.426039
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	0.948721402	3	6.091782
P10111	IIPGFMCQGGDFTR	1.6651069	2	3.415679
P10111	IIPGFMCQGGDFTR+Oxidation(5	1.767235306		
P10111	KITISDCGQL	1.236939799	2	3.511175
P10111	SIYGEKFEDENFILK	1.334345017	2	4.540363
P10111	TEWLDGK	1.761088991	2	2.302468
P10111	VCFELFADK	1.40053373	2	3.246058
P10111	VCFELFADKVPK	0.993862508	2	3.898452
P10111	VKEGMSIVEAMER	1.308059276	3	3.637903
P10536	**RAB1B Ras_related protein Rab_1B**	**1.553064177**	**0.477741**	**3**
P10536	MGPGAASGGERPNLK	1.233948489	2	4.090434
P10536	NATNVEQAFMTMAAEIK+Oxidation(11	1.678060171		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9	1.619827426		
P10633	**CP2D1 Cytochrome P450 2D1**	**1.063253881**	**1.47E-12**	**3**
P10633	SQGVILASYGPEWR	1.047130729	2	4.086678
P10633	TFMALLDNLLAENR	2.106202636	2	3.710493
P10633	YGDVFSLQK	1.251670132	2	2.711225
P10634	**CP2DQ Cytochrome P450 2D26**	**1.105455363**	**0.010723**	**21**
P10634	ACLGEPLAR	1.072760914	2	2.747574
P10634	AKGNPESSFNDENLR	1.957677254	2	3.448844
P10634	AVSNVIASLVYAR	0.969113532	2	4.248408
P10634	DETVWEKPLR	1.356618223	2	2.349931
P10634	DMTDAFLAEMQK	1.097196722	2	3.518677
P10634	EAEHPFNPSILLSK	1.152017719	2	2.66698
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.149106175	3	5.715136
P10634	FADIVPTNIPHMTSR	1.170477889	3	3.687232
P10634	FEYEDPFFNR	1.087055947	2	2.826111
P10634	FHPEHFLDAQGNFVK	1.215900969	3	4.700538
P10634	FQGFLIPK	0.621787414	2	2.32181
P10634	GNPESSFNDENLR	1.37856245	2	4.421339
P10634	GTTLIPNLSSVLK	0.834530324	2	2.400562
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.319856541	2	4.724244
P10634	GVVLAPYGPEWR	1.114010976	2	3.202109
P10634	LNSFIALVDK	1.793946048	2	3.269951
P10634	RFEYEDPFFNR	0.911094637	2	4.028438
P10634	RVHEEIDEVIGQVR	1.368293525	2	4.269707
P10634	SLEQWVTEEAGHLCDTFAK	1.11306002	2	4.792475
P10634	SWDPAQPPR	0.974501312	2	2.854806
P10634	VHEEIDEVIGQVR	0.923760371	2	4.840197
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.172603478**	**9.9E-20**	**32**
P10719	AHGGYSVFAGVGER	1.257519224	2	4.254332
P10719	AIAELGIYPAVDPLDSTSR	1.286385499	2	5.585495
P10719	EGNDLYHEMIESGVINLK	1.062848974	2	5.207921
P10719	EGNDLYHEMIESGVINLK+Oxidation(8	2.571392456		
P10719	FLSQPFQVAEVFTGHMGK	1.84194138	2	4.463165
P10719	FTQAGSEVSALLGR	1.281419439	2	4.857674
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	1.961422584	4	4.5936
P10719	IGLFGGAGVGK	1.123544702	2	3.290629
P10719	IGLFGGAGVGKTVLIMELINNVAK	1.224295872	3	3.513694
P10719	ILQDYK	1.323490895	1	2.032839
P10719	IMDPNIVGSEHYDVAR	1.267749847	2	4.963674
P10719	IMDPNIVGSEHYDVAR+Oxidation(1	1.589241225		
P10719	IMNVIGEPIDER	1.400032839	2	4.07792
P10719	IMNVIGEPIDER+Oxidation(1	1.597540066		
P10719	IPSAVGYQPTLATDMGTMQER	1.641367477	2	4.778714

P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14	1.587086538		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17	1.587086538		
P10719	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	2.20257431	3	6.440765
P10719	LVLEVAQHLGESTVR	1.507110984	2	4.801384
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	1.613093701	3	4.916537
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.328639159	3	4.909769
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10	1.677911977		
P10719	TIAMDGTEGLVR	1.118591937	2	3.804547
P10719	TIAMDGTEGLVR+Oxidation(3	1.188667923		
P10719	TREGNDLYHEMIESGVINLK	1.061817984	2	6.039838
P10719	TVLIMELINNVAK	1.828650414	2	5.115932
P10719	TVLIMELINNVAK+Oxidation(4	1.070419138		
P10719	VALTGLTVAEYFR	1.249684777	2	4.066783
P10719	VALVYGQMNEPPGAR	1.433354738	2	4.02356
P10719	VLDSGAPIK	0.966862091	2	3.372767
P10719	VLDSGAPIKIPVGPETLGR	1.216656182	3	5.002406
P10719	VVDLLAPYAK	1.301375948	2	3.237348
P10760	**SAHH Adenosylhomocysteinase**	**1.307329558**	**9.9E-20**	**20**
P10760	AGIPVFAWK	1.497992253	2	2.843862
P10760	ALDIAENEMPGLMR	1.112830317	2	3.773821
P10760	ALDIAENEMPGLMR+Oxidation(12	2.457197103		
P10760	ATDVMIAGK	1.558810762	2	2.903197
P10760	DGPLNMILDDGGDLTNLIHTK	1.556554398	2	5.579138
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5	1.308929988		
P10760	EMYSASKPLK	1.908753941	2	2.360639
P10760	FDNLYGCR	1.013942364	2	2.843503
P10760	GETDEEYLWCIEQTLHFK	2.318300015	2	4.462327
P10760	GISEETTTGVHNLYK	1.312893979	2	4.237678
P10760	IILLAEGR	1.699756525	2	2.925361
P10760	KLDEAVAEAHLGK	1.496979592	3	5.050492
P10760	LDEAVAEAHLGK	1.009652431	2	3.67498
P10760	RATDVMIAGK	1.324895005	2	2.526277
P10760	SKFDNLYGCR	1.42275382	2	3.100143
P10760	VAVVAGYGDVGK	1.320025507	2	4.145174
P10760	VIITEIDPINALQAAMEGYEVTTMDEACK	1.034769951	3	6.547412
P10760	VNIKPQVDR	1.331588121	2	2.750098
P10760	WLNENAVEK	1.333580818	2	2.816735
P10760	WSSCNIFSTQDHAAAAIAK	0.803723766	2	5.179422
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**1.355012679**	**0.228656**	**2**
P10818	HEEHERPEFVAYPHLR	1.257393996	3	3.671675
P10818	SRHEEHERPEFVAYPHLR	1.366850929	3	4.102187
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**1.210967709**	**7.45E-05**	**29**
P10860	ALASLMTYK	1.017931654	2	3.622105
P10860	CAVVDVPFGGAK	0.648649256	2	3.071723
P10860	CVGVGESDGSIWNPDGIDPK	1.243943516	2	5.094982
P10860	DDGSWEVIEGYR	0.915246565	2	3.972912
P10860	DIVHSGLAYTMER	1.428723076	2	3.366187
P10860	DIVHSGLAYTMER+Oxidation(10	1.464644758		
P10860	DSNYHLLMSVQESLER	1.291119498	2	4.232818
P10860	EDDPNFFK	0.900906486	1	2.152318
P10860	FTMELAK	1.779721294	2	2.394711
P10860	GASIVEDKLVEDLK	1.148825317	2	3.585323
P10860	GFIGPGIDVPAPDMSTGER	1.176631042	2	4.995929
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13	1.471661651		
P10860	HGGTIPVVPTAEFQDR	0.928719905	2	4.728883
P10860	IIAEGANGPTTPEADK	0.808474665	2	5.381951

P10860	IIAEGANGPTTPEADKIFLER	1.132700258	2	4.848978
P10860	ISGASEKDIVHSGLAYTMER	0.996534067	3	3.593291
P10860	KGFIGPGIDVPAPDMSTGER	1.100807244	2	5.131566
P10860	LQHGSILGFPK	0.863189471	1	3.084173
P10860	MVEGFFDR	1.06822967	2	2.899273
P10860	MVEGFFDR+Oxidation(0	1.484092917		
P10860	NLNHVSYGR	0.6125355	1	2.868178
P10860	NYTDNELEK	1.054256603	2	2.486093
P10860	RDDGSWEVIEGYR	0.937401515	2	4.436192
P10860	RFTMELAK	1.096590503	2	2.492365
P10860	TAAYVNAIEK	1.071242906	2	3.631395
P10860	TFVVQGFGNVGLHSMR	1.189439858	2	4.537451
P10860	VYEGSILEADCDILIPAASEK	0.895513182	3	6.005457
P10860	YNLGLDLR	1.155739822	2	3.167477
P10860	YSTDVSVDEVK	0.903940835	2	3.398627
P10867	**GGLO L_gulonolactone oxidase**	**1.113108599**	**0.089288**	**7**
P10867	EKLDPTGMFLNSYLEK	1.29399181	3	3.534583
P10867	GDDILLSPCFQR	1.136370149	2	3.227153
P10867	LDPTGMFLNSYLEK	1.230638762	2	4.122806
P10867	LDYWLAYETIMK	1.210083229	2	4.019799
P10867	NADVFQAAR	1.233627988	2	2.869512
P10867	TYGCSPEVYYQPTSVEEVR	0.753022002	2	4.839495
P10867	VVAHYPVEVR	1.163952238	2	2.756726
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.314830512**	**0.011719**	**3**
P10868	EHWIIECNDGVFQR	1.631994225	3	3.801689
P10868	YTDITAMFEETQVPALLEAGFQR	1.313731991	3	4.581868
P10868	YYAFPQMITPLVTK	1.492723291	2	3.78
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.138149926**	**0.039958**	**7**
P10888	ADWSSLSR	1.78869407	2	2.347992
P10888	DYPLPDVAHVK	1.804762112	2	2.767204
P10888	IQFNESFAEMNK	1.624750805	2	4.045511
P10888	RDYPLPDVAHVK	1.178151584	2	2.302327
P10888	SEDYALPSYVDR	1.058744717	2	3.867359
P10888	VNPIQGFSAK	1.230920412	1	2.134869
P10888	WDYNKNEWK	1.512578066	2	2.393436
P10959	**EST2 Liver carboxylesterase 1**	**1.434368845**	**0.189452**	**3**
P10959	AISESGVVLTTNLDKK	1.099413904	2	3.419629
P10959	EGASEEETNLSKLVMK	1.550485154	2	2.660723
P10959	GNWAHLDQLAALR	7.634282032	2	3.011742
P11030	**ACBP Acyl_CoA_binding protein**	**1.264923813**	**0.984428**	**5**
P11030	AKWDSWNK	1.060755757	2	2.406585
P11030	QATVGDVNTDRPGLLDLK	1.070750829	2	3.653354
P11030	TQPTDEEMLFIYSHFK	1.677254311	2	3.910361
P11030	TYVEKVEELK	1.256821852	2	2.343174
P11030	WDSWNK	1.231201353	1	2.080174
P11232	**THIO Thioredoxin**	**0.670134944**	**0.118543**	**2**
P11232	EAFQEALAAAGDK	1.134805207	2	4.515783
P11232	VGEFSGANK	0.346012073	2	2.7038
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**1.489999025**	**9.9E-20**	**6**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.562048938	3	5.930583
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	2.405335405	3	6.98547
P11240	GMNTLVGYDLVPEPK	1.466838565	2	4.01758
P11240	IIDAALR	1.580901508	1	2.101904
P11240	LNDFASAVR	1.218499702	2	3.27435
P11240	RLNDFASAVR	1.479743247	2	2.482695

P11348	**DHPR Dihydropteridine reductase**	**1.271670893**	**0.098895**	**12**
P11348	AALDGTPGMIGYGMAK	1.234251994	2	3.86588
P11348	EGGLLTLAGAK	1.047206435	2	2.92322
P11348	GAVHQLCQSLAGK	1.170278855	3	4.298717
P11348	MTDSFTEQADQVTAEVGK	1.272520045	2	5.825748
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0	1.025875134		
P11348	NCDLMWK	1.262576025	2	2.354143
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.202977136	2	5.394826
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3	1.669130449		
P11348	QSIWTSTISSHLATK	1.235474237	2	3.818817
P11348	RPNSGSLIQVVTTDGK	0.976376522	2	3.71702
P11348	TELTPAYF	2.707607396	1	2.017455
P11348	VDAILCVAGGWAGGNAK	2.090450766	2	3.924789
P11442	**CLH Clathrin heavy chain 1**	**1.317826266**	**9.9E-20**	**39**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	2.199164086	3	4.053478
P11442	AFMTADLPNELIELLEK	1.381585079	3	4.692377
P11442	AHIAQLCEK	1.312313752	2	2.378703
P11442	AHTMTDDVTFWK	1.754665696	2	2.523079
P11442	ALEHFTDLYDIK	1.712161457	3	3.965422
P11442	CNEPAVWSQLAK	1.138589153	2	3.431461
P11442	FDVNTSAVQVLIEHIGNLDR	1.474055213	3	4.174235
P11442	FNALFAQGNYSEAAK	1.17744651	2	5.044479
P11442	GQCDLELINVCNENSLFK	1.196393095	2	5.568188
P11442	GQFSTDELVAEVEK	1.423363785	2	4.049675
P11442	GQFSTDELVAEVEKR	1.390757391	2	3.679213
P11442	HELIEFR	1.266055656	2	2.506155
P11442	HSSLAGCQIINYR	1.739209658	2	3.786544
P11442	IHEGCEEPATHNALAK	1.509082878	2	5.39535
P11442	ISGETIFVTAPHEATAGIIGVNR	1.497962824	2	5.214356
P11442	IVLDNSVFSEHR	1.138616662	2	2.94672
P11442	IYIDSNNNPER	1.209589024	2	3.026072
P11442	KDPELWGSVLLESNPYR	1.613439389	3	3.636993
P11442	KFDVNTSAVQVLIEHIGNLDR	1.526586023	3	6.138827
P11442	KFNALFAQGNYSEAAK	0.94148172	2	4.897373
P11442	LAELEEFINGPNNAHIQQVGDR	1.491681937	2	5.411171
P11442	LECSEELGDLVK	1.219989898	2	2.9125
P11442	LHIIEVGTPPTGNQPFPK	1.204636664	2	4.421409
P11442	LPVVIGGLLDVDCSEDVIK	1.616601752	2	4.819174
P11442	LTDQLPLIIVCDR	1.115960605	2	3.313821
P11442	NLQNLLILTAIK	1.452340506	3	4.234161
P11442	NNLAGAEELFAR	1.516300587	2	3.792782
P11442	NNRPSEGPLQTR	1.313430942	3	4.13976
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.463206364	3	6.305215
P11442	SVDPTLALSVYLR	1.540194569	2	2.609646
P11442	SVNESLNNLFITEEDYQALR	1.319355963	2	5.161675
P11442	TLQIFNIEMK	1.73892809	2	3.020983
P11442	TSIDAYDNFDNISLAQR	0.906577946	2	3.625626
P11442	VGEQAQVVIIDMNDPSNPIR	1.438926557	2	5.054142
P11442	VIQCFAETGQVQK	2.551557159	2	4.795819
P11442	VSQPIEGHAASFAQFK	0.829455528	2	4.381845
P11442	WLLLTGISAQQNR	1.772176808	2	3.640633
P11442	YESLELCRPVLQQGR	1.158692325	2	2.80687
P11442	YIEIYVQK	1.391506702	1	1.953786
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.064144515**	**0.038916**	**8**
P11497	DEPIHILNVAIK	1.145524968	2	2.560642
P11497	GGSWVVIDPTINPR	2.367118891	2	2.9903
P11497	LLETESFQLNR	1.015388261	2	2.424971

P11497	LLLEDLVK	1.735649121	2	2.371135
P11497	LPELLLK	4.331247733	2	2.377985
P11497	TLRDPSLPLLELQDIMTSVSGR	1.867661807	3	3.481469
P11497	TVELSVPADPANLDSEAK	0.655458223	2	2.532607
P11497	VQQAELHTGSLPQIQSTALR	0.356865163	3	3.536391
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.97480487**	**0.89868**	**8**
P11507	DIVPGDIVEIAVGDKVPADIR	1.185739653	2	2.865445
P11507	IGIFGQDEDVTSK	0.859245825	2	3.55969
P11507	IRDEMVATEQER	1.331924268	2	3.350554
P11507	KSEIGIAMGSGTAVAK	1.135225422	2	3.872559
P11507	LDEFGEQLSK	1.893733065	2	2.772338
P11507	NAENAIEALKEYEPEMGK	1.34223746	2	3.465812
P11507	SEIGIAMGSGTAVAK	1.177685017	2	3.379007
P11507	VDQSILTGESVSVIK	4.019391451	2	4.443788
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.08464316**	**2.22E-16**	**28**
P11598	DASVVGFFR	1.580703393	2	2.512311
P11598	DGEEAGAYDGPR	1.597272823	2	3.422953
P11598	DLFSDGHSEFLK	2.238183081	2	3.08118
P11598	DLLTAYYDVDYEK	2.040847317	2	3.586147
P11598	DPNIVIAK	1.102152766	2	2.456733
P11598	EATNPPIIQEEKPK	1.267106914	2	3.569679
P11598	ELNDFISYLQR	1.445942243	2	3.110319
P11598	EYDDNGEGITIFRPLHLANK	1.485816522	2	4.184924
P11598	FAHTNVESLVK	1.397690119	3	3.381225
P11598	FIQESIFGLCPHMTEDNKDLIQGK	2.039123154	3	4.994908
P11598	FISDKDASVVGFFR	1.3532384	2	4.367239
P11598	FLQEYFDGNLK	1.002097883	2	3.722122
P11598	FLQEYFDGNLKR	1.16804705	2	3.531277
P11598	FVMQEEFSR	1.076816496	2	2.929364
P11598	IFRDGEEAGAYDGPR	0.94895255	2	3.954452
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.875147452	3	4.382811
P11598	LAPEYEAAATR	1.218811741	2	2.890248
P11598	LNFAVASR	1.753049128	2	2.53544
P11598	LSKDPNIVIAK	1.466320549	3	4.029299
P11598	MDATANDVPSPYEVK	1.218386998	2	4.375015
P11598	MDATANDVPSPYEVK+Oxidation(0	1.396017507		
P11598	RLAPEYEAAATR	1.128431773	2	3.666562
P11598	SEPIPETNEGPVK	1.085425615	2	2.884461
P11598	TADGIVSHLK	1.366611854	2	2.798299
P11598	TFLDAGHK	0.963749864	1	1.902213
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.182606892	2	6.038745
P11598	VDCTANTNTCNK	0.915138059	2	3.885523
P11598	YGVSGYPTLK	1.133680633	2	3.218223
P11711	**CP2A1 Cytochrome P450 2A1**	**1.327427635**	**0.127443**	**6**
P11711	GEQATYNTLFK	1.118714727	2	2.561234
P11711	GTDVFPILGSLMTDPK	1.200162931	2	3.460859
P11711	ILEEAGYLIK	1.128897328	2	3.403633
P11711	LEDINESPKPLGFTR	1.12267169	2	3.427345
P11711	TVSNVISSIVFGER	1.329454139	2	3.652304
P11711	VHEEIEQVIGR	1.79780606	2	3.067573
P11714	**CP2D9 Cytochrome P450 2D9**	**0.894224495**	**0.09299**	**2**
P11714	GNPESSFNDENLLMVVR	1.278635249	2	2.440007
P11714	VQQEIDEVIGQVR	0.890079782	2	4.707709
P11862	**GAS2 Growth arrest_specific protein 2**	**1.434943381**	**0.01315**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.216042572	2	4.116838
P11862	LDNGALLCQLAATVQEK	1.663896847	2	3.805905

P11862	YGVEPPGLIK	1.231163778	2	2.324488
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**1.012449743**	**9.9E-20**	**27**
P11884	AAQAAFQLGSPWR	1.481467338	2	2.911781
P11884	DGMTIAKEEIFGPVMQILK	2.73756822	3	4.011028
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	1.042511313	3	4.456418
P11884	EEIFGPVMQILK	1.463658364	2	4.063035
P11884	EEIFGPVMQILK+Oxidation(7	1.238434891		
P11884	ELGEYGLQAYTEVK	1.862203169	2	4.38967
P11884	GYFIQPTVFGDVK	0.862728678	2	4.285276
P11884	HEPVGVCGQIIPWNFPLLMQAWK	1.543093443	3	4.241936
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	1.041018682	3	6.481459
P11884	LGPALATGNVVVMK	1.465937442	2	3.815257
P11884	LGPALATGNVVVMK+Oxidation(12	1.361650981		
P11884	LLCGGGAAADR	1.791140083	2	3.385876
P11884	RVTLELGGK	1.372391836	2	2.922444
P11884	TEQGPQVDETQFK	0.953599042	2	4.56965
P11884	TEQGPQVDETQFKK	1.354365964	2	3.569177
P11884	TFPTVNPSTGEVICQVAEGNK	1.026187452	2	5.294014
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	1.121963656	2	4.302246
P11884	TFVQEDVYDEFVER	0.953248006	2	5.111619
P11884	TIEEVVGR	1.256630399	2	2.984706
P11884	TIPIDGDFFSYTR	1.260161306	2	2.817014
P11884	VAEQTPLTALYVANLIK	1.321322607	2	5.492676
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.062430467	2	6.537161
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.698833672	3	3.991735
P11884	VTLELGGK	1.022094562	1	2.053567
P11884	VVGNPFDSR	16.42043727	2	2.952728
P11884	YGLAAAVFTK	1.284480617	2	4.045621
P11884	YYAGWADK	0.942402539	2	2.540632
P11915	**NLTP Non_specific lipid_transfer protein**	**1.30630824**	**9.9E-20**	**21**
P11915	ADCTITMADSDLLALMTGK	1.361304471	2	5.40223
P11915	ANLIFK	1.980923413	2	2.326914
P11915	AVEIVAQEMVTDMPSTFEEK	2.089740647	2	5.305671
P11915	GHPLGATGLAQCAELCWQLR	1.139053172	3	3.583726
P11915	GSVLPDSDK	0.819268136	1	2.089741
P11915	GSVLPDSDKK	0.37827862	2	2.600466
P11915	HIDVLINK	1.245062853	2	2.938199
P11915	HSVNNPYSQFQDEYSLDEIMK	1.76189021	3	6.171529
P11915	KADCTITMADSDLLALMTGK	1.786052873	3	3.485859
P11915	KLEEEGEEFVK	1.097021994	3	4.245136
P11915	KLEEEGEEFVKK	1.185630207	3	4.853965
P11915	LEEEGEEFVK	0.3923907	2	2.819041
P11915	LEEEGEEFVKK	0.906287979	2	3.587742
P11915	LQSLQLQPDK	1.450713209	2	3.169294
P11915	MGFPEAASSFR	1.090897948	2	2.614854
P11915	MNPQSAFFQGK	0.814936905	2	3.229347
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.481814745	3	4.370543
P11915	THQISAAPTSSAGDGFK	1.62858273	2	4.640283
P11915	VFVVGVGMTK	1.079271642	2	2.678288
P11915	WVINPSGGLISK	1.493246653	2	3.114433
P11915	YGMSACPFAPQLFGSAGK	1.572887776	2	4.061396
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.504982292**	**0.683115**	**4**
P11980	GADYLVTEVENGGSLGSK	2.404192904	2	4.762059
P11980	GVNLPGAAVDLPAVSEK	1.486495363	2	4.061876
P11980	IYVDDGLISLQVK	2.019823824	2	2.442359
P11980	NTGIICTIGPASR	1.326045182	2	3.299815
P12001	**RL18 60S ribosomal protein L18**	**1.462869037**	**9.9E-20**	**5**

P12001	GTVLLSGPR	1.21858574	2	3.142797
P12001	ILTFDQLALESPK	1.663890559	2	4.85503
P12001	TAVVVGTITDDVR	1.299317504	2	4.333145
P12001	TNRPPLSLSR	1.120234314	3	3.661873
P12001	TNSTFNQVVLK	1.035925504	2	2.996768
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.138924458**	**0.03755**	**9**
P12007	AQEIDQSNDFK	1.396630527	2	3.436113
P12007	FVQENLAPK	1.108067019	2	2.945521
P12007	FWITNGPDADVLVVYAK	1.46526448	2	3.584719
P12007	GSNTCELVFEDCK	0.938505263	2	4.558173
P12007	GSNTCELVFEDCKVPAANILSQESK	1.005974937	3	5.229532
P12007	GVYVLMSGLDLER	1.455711667	2	2.951986
P12007	IGQFQLMQGK	1.136454307	2	2.763439
P12007	LYEIGGGTSEVR	1.126281871	2	2.823203
P12007	TDLTAVPASR	0.946007824	2	3.093655
P12075	**COX5B Cytochrome c oxidase subunit 5B_ mitochondrial**	**1.485886532**	**0.304462**	**2**
P12075	EDPNLVPSVSNK	1.485680073	2	3.228238
P12075	GLDPYNMLPPK	1.532079542	2	2.317757
P12336	**GTR2 Solute carrier family 2_ facilitated glucose transporter member 2**	**1.32686118**	**0.000402**	**3**
P12336	HVLGVPLDDR	2.162105078	2	2.331264
P12336	HVLGVPLDDRR	1.237119901	3	3.309498
P12336	SFDEIAAEFR	1.383838638	2	3.341381
P12346	**TRFE Serotransferrin**	**1.050298448**	**0.003355**	**23**
P12346	ADRDQYELLCLDNTR	1.226657691	2	4.318649
P12346	ASDSSINWNNLK	0.909464363	2	3.070838
P12346	DFQLFGSPLGK	3.406133858	2	3.595276
P12346	DGGGDVAFVK	1.898451444	2	2.468362
P12346	DLKQEDFQLLCPDGTK	1.217152205	2	4.575334
P12346	EGVCPEGSIDSAPVK	1.594177422	2	3.47231
P12346	EGYNGYTGAFQCLVEK	1.044000359	2	3.25762
P12346	FDEFFSQGCAPGYK	1.048494305	2	4.063144
P12346	GDKDCTGNFCLFR	0.835994617	2	3.585454
P12346	GTDFQLNQLQGK	0.896679055	2	3.518849
P12346	GYYAVAVVK	1.074843771	2	2.950112
P12346	HQTVLENTNGK	9.223189542	2	2.472506
P12346	HTTIFEVLPQK	0.430718893	3	4.010453
P12346	KGTDFQLNQLQGK	1.054013052	2	4.589984
P12346	KTSYQDCIK	1.116988207	2	2.649408
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.141993352	2	4.583292
P12346	NGDGKEDLIWEILK	1.07266897	2	3.692132
P12346	QEDFQLLCPDGTK	0.555116894	2	3.229157
P12346	SKDFQLFGSPLGK	1.007189935	2	3.140049
P12346	TSYQDCIK	0.94663166	2	2.464587
P12346	VSTVLTAQK	0.74114504	2	2.727088
P12346	WCALSHQER	1.299543158	2	3.180489
P12346	WCAVSEHENTK	0.890282059	2	3.618573
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.405955117**	**0.000449**	**3**
P12368	MFESFIESVPLFK	1.349461131	2	3.441716
P12368	NISHYEEQLVK	0.971155915	2	2.539134
P12368	NLDQEQLSQVLDAMFEK	1.795766495	3	3.898859
P12711	**ADHX Alcohol dehydrogenase class_3**	**1.165299595**	**9.9E-20**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.604614958	3	6.70961
P12711	AFDLMHSGNSIR	0.917081411	2	3.287355

P12711	AGDTVIPLYIPQCGECK	1.310105724	2	3.718103
P12711	AKEFGATECINPQDFSK	1.014328342	2	4.763711
P12711	EFGATECINPQDFSK	6.026188629	2	4.352767
P12711	IDPSAPLDK	1.671583402	1	2.17802
P12711	IIGIDINK	1.345920322	1	2.038364
P12711	IIGIDINKDK	1.441832479	2	2.435354
P12711	VCLLGCGISTGYGAAVNTAK	1.504785652	2	6.078312
P12711	VDEFVTGNLSFDQINK	1.057778778	2	4.990308
P12749	**RL26 60S ribosomal protein L26**	**1.274607161**	**4.23E-05**	**5**
P12749	DDEVQVVR	1.431949682	2	2.945473
P12749	FNPFVTSDR	1.151859349	2	2.756455
P12749	HFNAPSHIR	1.25010643	3	3.880914
P12749	KDDEVQVVR	1.312790577	2	3.262084
P12749	YVIYIER	0.904953358	1	1.974013
P12785	**FAS Fatty acid synthase**	**1.683088542**	**9.9E-20**	**45**
P12785	ACIDTALENLSTLK	2.179822499	2	4.474679
P12785	AEAVVAVLLTK	1.706906687	2	3.832134
P12785	AGSDTELAAPK	1.53511506	2	3.414196
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	2.13080018	3	5.52807
P12785	DAMLENQTPELFQDVNKPK	1.430305327	2	4.173407
P12785	DANLPAGSMAAVGLSWEECK	0.831759899	2	3.089152
P12785	DGGFLLMHTVLK	1.159953001	2	3.339146
P12785	DPETLLGYSMVGCQR	1.764895309	2	3.939814
P12785	DTSFEQHVLLHTGGK	2.927790655	2	2.990969
P12785	EEEPEAMLPGAQPTLISAISK	3.159375078	2	3.947263
P12785	EQGVTFPSGEAQEQLIR	1.164751396	2	4.293488
P12785	FDASFFGVHPK	1.656170454	2	3.406901
P12785	FDLSNNHPLGMAIFLK	2.320076201	2	3.436061
P12785	FVFTPHVEPECLSESAILQK	2.342156639	3	5.07461
P12785	GLESIINIIHSSLAEPR	1.749715587	2	4.415999
P12785	GNAGQSNYGFANSTMER	3.168732436	2	4.703185
P12785	GVDLVLNSLAEEK	2.393266081	2	3.48034
P12785	HFQLEQDKPEEQTAHAFVNVLTR	1.616096136	3	3.409205
P12785	LFDHPEVPIPAESESVSR	1.252310029	2	4.263873
P12785	LLLPEDPLISGLLNSQALK	1.842570054	3	4.781498
P12785	LTPGCEAEAEAEAICFFIK	2.899794355	2	3.762229
P12785	MTVPGLEDLPQHGLPR	1.671397722	2	3.591424
P12785	QAQLNLSILLVNPEGPTLTR	1.902217641	2	3.084434
P12785	RQQEQLVPTLEK	0.855216335	2	3.120968
P12785	SDEALKPLGVK	1.383574186	2	2.974132
P12785	SFDDSGNGYCR	1.339913386	2	3.059119
P12785	SGECPAAIVGGINLLLKPNTSVQFMK	0.636307221	3	3.966894
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.764677632	2	5.233467
P12785	SNMGHPEPASGLAALTK	1.666743874	3	4.176483
P12785	SNMGHPEPASGLAALTK+Oxidation(2	1.710994695		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.16703779	2	5.048231
P12785	TGTVPLEVR	1.231738664	2	2.462291
P12785	TMEAVQGLLEQGR	1.684745853	2	3.88832
P12785	VFTTVGSAEK	2.197817517	2	2.3602
P12785	VGDPQELNGITR	0.960039434	2	3.153459
P12785	VHLTGIDINPNALFPPVEFPVPR	2.133692145	2	4.900929
P12785	VLEALLPLK	1.849740577	2	3.301196
P12785	VLESDLVMNVYR	1.806728468	2	3.406588
P12785	VSVHIIEGDHR	3.002911555	2	2.817744
P12785	VTAIYIDPATHLQK	1.820238596	2	3.800963
P12785	VYATILNAGTNTDGCK	1.664002902	2	4.980019
P12785	VYMLEGDTQVADVTTSR	2.519505809	2	3.585744

P12785	VYQWEDPDSK	1.900912277	2	3.251095
P12785	WLSTSIPEAQWQSSLAR	0.746830661	2	2.674955
P12785	YNGTLNLDR	1.895296919	1	2.102278
P12791	**CP2BA Cytochrome P450 2B10**	**1.142255722**	**0.998104**	**2**
P12791	IQEEAQCLVEELR	1.156942533	2	4.585475
P12791	IQEEAQCLVEELRK	1.137651333	2	3.763267
P12847	**MYH3 Myosin_3**	**0.877575457**	**0.553749**	**5**
P12847	GTLEDQIISANPLLEAFGNAK	0.56925232	2	3.118917
P12847	IEAQNQPFDAK	0.561186862	2	3.037445
P12847	KELEEKLVTLVQEK	0.700881192	2	2.767368
P12847	MKGTLEDQIISANPLLEAFGNAK	3.223651381	3	6.703844
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0	2.317101801		
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.487963595**	**2.17E-08**	**20**
P12928	AAVIAVTR	1.110899844	2	2.622893
P12928	AETSDVANAVLDGADCIMLSGETAK	2.704385494	2	5.979966
P12928	CCAAAIIVLTK	1.224288719	2	3.085968
P12928	CNLAGKPVVCATQMLESMITK	1.453528153	3	4.863765
P12928	EATESFATSPLSYRPVAIALDTK	1.545628065	2	4.023415
P12928	EPPEAIWADDVDR	1.30027282	2	2.649955
P12928	GDLGIEIPAEK	0.839998324	2	3.147001
P12928	GSFPVEAVMMQHAIAR	1.235009053	2	3.913738
P12928	GSQVLVTVDPK	1.246595624	2	2.938781
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.541441856	2	4.908193
P12928	IGPEGLVTEVEHGGILGSR	1.447211851	2	5.047713
P12928	IYIDDGLISLVVQK	1.914850628	2	4.41485
P12928	KFDEILEVSDGIMVAR	1.43725151	2	4.931178
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.53351041	3	4.661717
P12928	LNFSHGSHEYHAESIANIR	2.139304489	2	5.720943
P12928	RVQFGIESGK	1.070672552	2	2.554047
P12928	STSIIATIGPASR	0.97941497	2	3.390264
P12928	TGVLQGGPESEVEIVK	1.068343239	2	5.068977
P12928	TVWVDYHNITR	1.252952077	2	2.684114
P12928	VQFGIESGK	1.388668803	2	2.461007
P12938	**CP2D3 Cytochrome P450 2D3**	**0.898553628**	**0.713584**	**7**
P12938	DLTDAFLAEIEK	0.975094819	2	4.424824
P12938	FDYGDPDFIK	2.269717246	2	2.765387
P12938	GNPESSFNDANLR	1.491271039	2	4.004616
P12938	RFDYGDPDFIK	0.908358076	2	3.047796
P12938	TFLTMVDNLVTEHK	1.564006891	2	3.339642
P12938	TWDPDQPPR	0.687883096	2	2.450746
P12938	TWDPDQPPRDLTDAFLAEIEK	1.201560046	3	3.672248
P12939	**CP2DA Cytochrome P450 2D10**	**2.933716174**	**9.27E-11**	**8**
P12939	ALCNVIASLIFAR	2.150538622	2	3.507223
P12939	AVQEVLVTHGEDTADRPPVPIFK	2.324457259	3	5.598721
P12939	FEYEDPYLIR	3.032715427	2	2.458931
P12939	FGDIAPLNLPR	2.099407381	2	3.132499
P12939	ITSCDIEVQDFVIPK	2.653806761	2	4.369359
P12939	NLTDAFLAEVEK	2.934571206	2	4.160637
P12939	RFEYEDPYLIR	2.334792369	3	3.467832
P12939	TTWDPAQPPR	4.286982066	2	2.591508
P13084	**NPM Nucleophosmin**	**1.797617451**	**6.66E-16**	**2**
P13084	MTDQEAIQDLWQWR	1.55643712	2	3.275612
P13084	VDNDENEHQLSLR	1.985115947	2	4.127531
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.28554308**	**0.347049**	**5**
P13086	HLGLPVFNTVK	1.852095391	2	2.333587
P13086	LIGPNCPGIINPGECK	1.04888536	2	4.435453

P13086	MGHAGAIIAGGK	1.355971738	3	3.466594
P13086	NIYIDK	1.125486176	1	2.129305
P13086	QGTFHSQQALEYGTK	1.449911258	2	2.728255
P13107	**CP2B3 Cytochrome P450 2B3**	**1.173586057**	**0.545786**	**8**
P13107	ATLDPNAPR	1.194254176	2	2.635109
P13107	EIDQVIGSQR	1.295141848	2	2.665457
P13107	EVLDYIDHSVENHR	1.104809692	2	4.08286
P13107	FSDVSPMGLPCR	1.275970422	2	3.443871
P13107	GIIAVLQPIMQEYGVSFVNEER	1.355000365	3	5.764159
P13107	MCLGEGIAR	1.359608	2	2.692423
P13107	QSVEDQIKEEAK	1.23315726	2	2.91521
P13107	SFIQLQEK	0.321714516	2	2.433958
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.456083545**	**2.6E-09**	**7**
P13221	IGADFLGR	2.281474244	2	2.389949
P13221	ITWSNPPAQGAR	1.935599708	2	3.006084
P13221	IVATTLSNPELFK	1.774717521	2	3.785616
P13221	NLDYVATSINEAVTK	1.905307114	2	5.097983
P13221	SCASQLVLGDNSPALR	1.137850324	2	5.11447
P13221	TDDSQPWVLPVVR	1.481361046	2	3.266952
P13221	VGGVQSLGGTGALR	0.51086471	2	3.007875
P13255	**GNMT Glycine N_methyltransferase**	**1.101375325**	**0.542956**	**8**
P13255	AHMVTLDYTVQVPGAGR	1.043038616	2	5.07364
P13255	AWLLGLLR	1.248018154	2	2.571646
P13255	DITTSVLTVNNK	1.40059809	2	3.826614
P13255	LSYYPHCLASFTELVQEAFGGR	1.769636116	3	3.643876
P13255	NIASMVRPGGLLVIDHR	1.655099596	3	3.748565
P13255	NYDYILSTGCAPPGK	1.277229955	2	4.651227
P13255	SDLTKDITTSVLTVNNK	1.201608746	2	2.897185
P13255	SLGVAAEGIPDQYADGEAAR	0.820108439	2	5.258135
P13383	**NUCL Nucleolin**	**1.217351331**	**0.11793**	**8**
P13383	EAMEDGEIDGNK	2.447183142	2	2.932014
P13383	GFGFVDFNSEEDAK	2.177430456	2	2.87702
P13383	GLSEDTTEETLK	0.872531799	2	3.241655
P13383	GSPNARSQPSKTLFVK	1.019506011	2	2.332206
P13383	IEGSEPTTPFNLFIGNLNPNK	0.626493045	2	3.757329
P13383	NDLAAVDVR	1.296746113	2	2.563109
P13383	NLSFNITEDELK	1.152322922	2	2.622602
P13383	SEADAEKNLEEK	1.157132391	2	2.948799
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.973516383**	**0.995719**	**21**
P13437	AANEAGYFNEEMAPIEVK	0.507453805	2	5.1397
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11	1.148942171		
P13437	DAEVVLCGGTESMSQSPYSVR	1.627539413	3	5.0537
P13437	DFTATDLTEFAAR	1.241162679	2	4.0434
P13437	DMDLIDVNEAFAPQFLAVQK	1.496129468	3	6.519181
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1	2.028209144		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.874960629	3	5.779508
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	1.009118623	3	4.889211
P13437	GVFIVAAK	1.428122275	2	2.472465
P13437	HNFTPLAR	1.192192031	2	2.369266
P13437	ITAHLVHELR	1.420189033	2	3.51449
P13437	LCGSGFQSIVSGCQEICSK	1.355691715	2	5.640916
P13437	LEDTLWAGLTDQHVK	0.96783129	2	5.062773
P13437	RTPFGAYGGLLK	0.59621568	3	3.38314
P13437	SLDLDPSK	0.73208704	2	2.726357
P13437	TNVSGGAIALGHPLGGSGSR	1.043835351	2	5.991042
P13437	VGVPTETGALTLNR	0.872586086	2	3.635789
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	0.985364355	2	5.912787

P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14	1.053545175		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.049218272	3	5.029734
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	1.022471331	3	4.514121
P13439	**UMPS Uridine 5__monophosphate synthase**	**1.589609827**	**0.057292**	**2**
P13439	SGLSSPVYIDLR	1.602406504	2	2.428607
P13439	VTDAIVLLDR	1.284802355	2	2.362031
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.934507035**	**9.9E-20**	**9**
P13444	FVIGGPQGDAGVTGR	1.33725278	2	4.519907
P13444	HIGYDDSAK	0.806822547	2	2.740845
P13444	ICDQISDAVLDAHLK	1.549924957	3	5.264887
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	5.58675748	3	6.927251
P13444	SEFPWEVPK	1.579937745	2	2.378173
P13444	SGVLPWLRPDSK	1.121724408	2	2.943056
P13444	TCNVLVALEQQSPDIAQCVHLDR	2.021876717	3	5.997582
P13444	TQVTVQYVQDNGAVIPVR	1.662026527	2	5.433738
P13444	VHTIVISVQHNEDITLEAMR	2.374456061	3	4.077361
P13471	**RS14 40S ribosomal protein S14**	**1.19758059**	**0.030074**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	1.41550782	2	5.429939
P13471	ELGITALHIK	1.777651937	2	2.49773
P13471	IEDVTPIPSDSTR	1.169632302	2	3.912302
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.737135937**	**0.000554**	**20**
P13601	ANNTPYGLAAGVFTK	0.851459754	2	4.379419
P13601	EEIFGPVQQIMK	0.874994137	2	3.60608
P13601	EMGEQGVYEYTELK	0.542066216	2	3.536651
P13601	FPVINPATEEVICHVEEGDK	1.467741612	3	3.828281
P13601	FPVINPATEEVICHVEEGDKADVDK	1.462864771	4	5.050517
P13601	GFFVQPTVFSNVTDEMR	1.582857386	2	2.459547
P13601	IAKEEIFGPVQQIMK	0.932520818	2	3.720336
P13601	IFINNEWHNSLNGK	0.709941807	2	3.908209
P13601	IHGQTIPSDGDVFTYTR	0.532920453	3	3.897451
P13601	ILDLIESGK	0.91143956	2	3.190511
P13601	ILDLIESGKK	0.888931979	2	2.855522
P13601	KFPVINPATEEVICHVEEGDK	0.916797142	3	3.568044
P13601	KFPVINPATEEVICHVEEGDKADVDK	1.384229137	4	4.877313
P13601	LFVEESIYDEFVR	0.521082782	2	3.60477
P13601	SIDEVIK	0.611048724	2	2.495962
P13601	VLLATMESMNAGK	0.753846271	2	4.440385
P13601	VSFTGSTEVGK	0.50253904	2	2.748649
P13601	YFAGWADK	0.723107363	2	2.317746
P13601	YVLGNPLDSGISQGPQIDK	1.116913165	2	4.75492
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.33560832	2	4.217129
P13697	**MAOX NADP_dependent malic enzyme**	**2.72537568**	**8.38E-05**	**6**
P13697	AECSAEECYK	1.807410329	2	3.126628
P13697	AIFASGSPFDPVTLPDGR	2.047865934	2	4.496891
P13697	GHIASVLNAWPEDVVK	4.789723097	2	3.593307
P13697	HINDSVFLTTAEVISQQVSDK	1.809675292	3	4.597589
P13697	ILGLGDLGCNGMGIPVGK	2.462657052	2	2.806196
P13697	NLEAIVQK	1.362614939	1	2.402876
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.161664107**	**9.9E-20**	**15**
P13803	AAVDAGFVPNDMQVGQTGK	0.854614449	2	4.947187
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11	1.566176991		
P13803	DPEAPIFQVADYGIVADLFK	0.766557393	2	4.983968
P13803	GLLPEELTPLILETQK	1.318232656	2	4.480448
P13803	GTSFEAAAASGGSASSEK	1.002753778	2	5.196799
P13803	LGGEVSCLVAGTK	1.09029232	2	4.598153

P13803	LLYDLADQLHAAVGASR	1.562014793	2	5.049285
P13803	LNVAPVSDIIEIK	1.476590442	3	4.03899
P13803	QFSYTHICAGASAFGK	0.712637497	2	3.232169
P13803	SDRPELTGAK	0.937623904	3	3.544892
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	1.112352503	3	6.620749
P13803	TIYAGNALCTVK	0.960649167	2	3.704326
P13803	VLVAQHDAYK	1.286868182	2	3.561146
P13803	VVPEMTEILK	1.457850738	1	1.928873
P13803	VVQDLCK	0.97485635	2	2.633058
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.307040392**	**1.52E-12**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.763380845	2	5.083485
P13832	FTDEEVDELYR	1.038596708	2	3.782711
P13832	GNFNYIEFTR	1.145140896	2	3.193
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.996683643**	**0.901663**	**5**
P14046	ETGLMAFTNLK	1.295686427	2	2.626735
P14046	GDPIPNEQVLIK	0.795044765	2	2.880228
P14046	GMYESLPVVAVK	0.99611894	2	3.34773
P14046	QQNSYGGFSSTQDTVVALDALSK	1.204342598	2	3.490916
P14046	QSPGPCGSEVATVPETGR	0.720760427	2	3.431194
P14141	**CAH3 Carbonic anhydrase 3**	**1.189296929**	**2E-09**	**20**
P14141	DIRHDPSLQPWSVSYDPGSAK	0.752208284	3	3.862322
P14141	EAPFNHFDPSCLFPACR	1.240521334	2	4.233335
P14141	EKGEFQILLDALDK	1.544218386	2	4.67005
P14141	EKGEFQILLDALDKIK	1.211158145	2	3.703685
P14141	EPMTVSSDQMAK	1.053494681	1	3.240386
P14141	EWGYASHNGPEHWHELYPIAK	1.073387747	3	4.821795
P14141	GDNQSPIELHTK	1.191034459	2	3.239465
P14141	GEFQILLDALDK	1.288957263	2	4.569219
P14141	GEFQILLDALDKIK	1.588800632	2	3.593432
P14141	GGPLSGPYR	1.11803747	2	2.759366
P14141	GKEAPFNHFDPSCLFPACR	1.251937551	2	4.196252
P14141	HDPSLQPWSVSYDPGSAK	0.724837158	3	5.586672
P14141	QFHLHWGSSDDHGSEHTVDGVK	1.227229765	2	4.770493
P14141	QPDGIAVVGIFLK	1.364430743	3	3.548666
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.972272411	3	5.703003
P14141	SLFASAENEPPVPLVGNWRPPQPIKGR	1.472216161	3	4.372089
P14141	VVFDDTFDR	0.825527308	2	3.3251
P14141	YAAELHLVHWNPK	1.044099306	2	4.238825
P14141	YNTFGEALK	1.084578162	2	2.559881
P14141	YNTFGEALKQPDGIAVVGIFLK	1.33319911	3	6.112409
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.649381995**	**1.36E-10**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	2.157764885	2	3.260318
P14173	ALIPTTAPQEPETYEDIIR	1.535317327	2	3.855607
P14173	GSNQLNETLLQR	1.542853181	2	2.986794
P14173	HSHQDSGLITDYR	1.072696321	3	3.77432
P14173	MLELPEAFLAGR	1.634662334	2	3.455392
P14173	QLQAASPELTQAALMEK	1.25516362	2	4.097996
P14173	TDLTEAFNMDPVYLR	1.654883507	2	3.843246
P14173	TVESAHVQLAWEHIR	1.291104052	3	3.640392
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.063572516**	**2.91E-12**	**15**
P14408	AAAEVNQEYGLDPK	1.161599091	2	4.366432
P14408	AIEMLGGELGSK	1.0916118	2	3.95858
P14408	EFAQVIK	1.472843941	1	1.92098
P14408	IEYDTFGELK	0.867281925	2	3.25935
P14408	IEYDTFGELKVPTDK	1.330349513	2	3.730645
P14408	IYELAAGGTAVGTGLNTR	1.068559928	2	5.367426
P14408	LMNESLMLVTALNPHIGYDK	1.907530677	3	5.516424

P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	1.335348033	3	6.87714
P14408	SGLGELILPENEPGSSIMPGK	1.422888423	2	4.63581
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17	2.071452537		
P14408	SKEFAQVIK	1.209173888	2	2.666512
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.498940366	3	4.783782
P14408	TAIELGYLTAEQFDEWVKPK	1.651893608	2	4.878406
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.64665858	3	5.893252
P14408	YYGAQTVR	1.118382417	2	2.491598
P14480	**FIBB Fibrinogen beta chain**	**1.309856477**	**3.42E-10**	**8**
P14480	AHYGGFTVQTEANK	2.032250747	2	3.463562
P14480	DNENVINEYSSILEDQK	1.09797664	2	3.935209
P14480	GFGNIATNEDTK	1.597546344	2	3.089324
P14480	GFGNIATNEDTKK	1.736216563	2	3.583051
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.588506228	3	4.979515
P14480	LYIDETVNDNIPLNLR	2.291169243	2	2.932892
P14480	TENGGWTVIQNR	1.112058031	2	3.205982
P14480	YCGLPGEYWLGNDK	1.459425998	2	3.154557
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**1.232785068**	**0.266231**	**10**
P14604	AFAAGADIK	1.286477339	2	3.085218
P14604	AQFGQPEILLGTIPGAGGTQR	1.025429564	2	5.684713
P14604	ESVNAAFEMTLTEGNKLEK	1.871030643	2	2.681858
P14604	FLSHWDHITR	1.403496905	2	3.466257
P14604	IFPVETLVEEAIQCAEK	1.14321562	3	5.884126
P14604	NSSVGLIQLNRPK	1.219031409	2	3.576939
P14604	SLAMEMVLTGDR	1.394106324	2	3.805194
P14604	SLAMEMVLTGDR+Oxidation(3	1.282466896		
P14604	SLAMEMVLTGDR+Oxidation(5	1.282466896		
P14604	TFQDCYSGK	1.290543055	2	2.89127
P14668	**ANXA5 Annexin A5**	**0.988145093**	**0.000169**	**5**
P14668	EFRKNFATSLYSMIK	0.949733309	2	2.337358
P14668	ETSGNLENLLLAVVK	1.523145385	2	3.249208
P14668	GAGTDDHTLIR	0.878859795	2	2.759493
P14668	GLGTDEDSILNLLTAR	1.769290653	2	5.116106
P14668	GTVTDFSGFDGR	1.035770501	2	3.003924
P14669	**ANXA3 Annexin A3**	**1.437822715**	**0.000158**	**9**
P14669	GAGTDEFTLNR	0.954918411	2	2.663575
P14669	GMGTDEDTLIEILTTR	1.522026121	2	4.38738
P14669	GTINNYPGFNPSVDAEAIR	1.422261144	2	4.964958
P14669	KDAQTLYDAGEK	1.416012286	2	3.264964
P14669	KDAQTLYDAGEKK	1.661220946	3	3.885076
P14669	QYQEAYEQALK	1.076071243	2	2.906896
P14669	SEIDLLDIR	2.324100761	2	2.544088
P14669	TLINILTER	2.036362772	2	2.73803
P14669	WGTDEDKFTEILCLR	2.163039895	3	3.380649
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.255511349**	**0.283829**	**4**
P14685	AIQLEYSEAR	1.40816328	2	3.019181
P14685	HDADGQATLLNLLLR	1.748259947	2	3.79246
P14685	LQLDSPEDAEFIVAK	1.203413511	2	3.867032
P14685	SVFPEQANNNEWAR	1.138568863	2	3.28049
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.535291181**	**0.002006**	**5**
P14740	FRPAEPHFTSDGSSFYK	1.561737597	2	3.47716
P14740	HSYTASYSIYDLNKR	1.474210552	3	3.781524
P14740	LGTLEVEDQIEAAR	1.895554633	2	4.087747
P14740	VLEDNSALDK	1.74711625	2	2.618365
P14740	WEYYDSVYTER	0.944984735	2	2.528301

P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.145949437**	**0.186528**	**15**
P14882	FLSDVYPDGFK	1.703373535	2	2.80381
P14882	FSSQEAASSFGDDR	0.77836757	2	3.928383
P14882	GVTHNIPLLR	1.907856926	2	2.398324
P14882	HGNALWLNER	1.916133318	2	3.315561
P14882	HIEIQVLGDK	1.837173823	2	2.41751
P14882	HKQEDIPISGWAVECR	0.936558312	2	2.441552
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	0.607971516	3	6.743031
P14882	LQVEHPVTECITGLDLVQEMILVAK	1.925775592	3	3.8112
P14882	MADEAVCVGPAPTSK	0.93727643	2	4.255637
P14882	MEDALDSYVIR	1.267162933	2	3.506907
P14882	SYLNMDAIMEAIK	1.397058581	2	3.287227
P14882	SYLNMDAIMEAIKK	2.161910437	2	3.132951
P14882	TGAQAVHPGYGFLSENK	1.260913947	2	4.015559
P14882	TVAIHSDVDASSVHVK	1.591916322	3	4.04437
P14882	VVEEAPSIFLDPETR	1.120511745	2	3.994475
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**1.135413698**	**0.148646**	**3**
P14942	DGCLLFGQVPLVEIDGMLLTQTR	3.894791483	3	4.154245
P14942	KPPPDGHYVDVVR	1.142461194	2	3.274932
P14942	YFPVFEK	1.095445423	1	1.998563
P15083	**PIGR Polymeric immunoglobulin receptor**	**0.957399614**	**0.961147**	**4**
P15083	EIQNAGDQAQENR	0.813052775	2	4.024494
P15083	FSVLITGLR	0.940012329	2	2.797048
P15083	GSPHINPTDANAR	0.918971418	2	2.34721
P15083	GVTGGSVAIVCPYNPK	1.001226052	2	4.031221
P15149	**CP2A2 Cytochrome P450 2A2**	**0.911977062**	**0.000252**	**13**
P15149	DVQECILEEAGYLIK	1.512930665	3	3.943042
P15149	DVYSSITQLSER	3.303300046	2	3.118455
P15149	FKFPMNLEDINEYPSPIGFTR	1.479067113	3	3.74839
P15149	FSNLAPLGIPR	1.21742892	2	3.327245
P15149	GELPTFNILFK	0.599345049	2	2.694533
P15149	GTDVFPIIGSLMTEPK	0.929940414	2	4.134461
P15149	GYGFSLSNVEQAK	0.92890326	2	3.431632
P15149	IVVLYGYDAVK	1.823161174	2	2.601579
P15149	LEDFMIEK	1.52986143	1	1.966799
P15149	NFIDSFLIR	1.323238019	2	2.428145
P15149	QNHSTLDPNSPR	0.866515155	2	2.663126
P15149	TLQGTCGAPIDPSIYLSK	0.668777555	2	4.60939
P15149	TVSNVINSIVFGNR	1.309928271	2	3.236496
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.964573672**	**0.021733**	**3**
P15178	ALHHGIDLEK	1.990711852	3	3.305166
P15178	LEYCEALAMLR	1.977769584	2	2.950308
P15178	QMVKFAANINK+Oxidation(1	1.410851703		
P15429	**ENOB Beta_enolase**	**1.54210328**	**0.995355**	**6**
P15429	DATNVGDEGGFAPNILENNEALELLK	1.424285222	2	5.129951
P15429	FMIELDGTENK	2.049591372	2	3.282815
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	2.308098156	3	5.6371
P15429	IEEALGDK	3.5101415	1	2.41668
P15429	TAIQAAGYPDK	3.372428139	2	2.973786
P15429	VNQIGSVTESIQACK	1.105479116	2	4.959307
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.584626094**	**9.9E-20**	**20**
P15650	AFVDSCLQLHETK	1.324620754	2	4.013764
P15650	AQDTAELFFEDVR	1.78405946	2	4.802862
P15650	AQDTAELFFEDVRLPASALLGEENK	1.388847506	3	5.326312
P15650	CIGAIAMTEPGAGSDLQGVR	2.085589815	2	6.359548

P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6	1.654033053		
P15650	EQIEQFIPQMTAGK	1.944690658	2	4.987886
P15650	FFQEEVIPYHEEWEK	2.696591847	2	5.210644
P15650	GFYYLMQELPQER	1.860660546	2	4.145862
P15650	IFSSEHDIFR	1.153472822	2	3.043908
P15650	KFFQEEVIPYHEEWEK	1.691665618	2	5.143679
P15650	LDSASASMAK	1.236129976	2	2.505171
P15650	LDSASASMAK+Oxidation(7	1.48281605		
P15650	QGLLGINIAEK	1.145269618	2	3.288843
P15650	RLDSASASMAK	1.244373362	2	3.381341
P15650	RLDSASASMAK+Oxidation(8	0.800714254		
P15650	SGSDWILNGSK	1.238791965	2	2.698575
P15650	TNICVTR	1.154694681	2	2.351386
P15650	TVAHIQTVQHK	0.801044384	2	2.918038
P15650	VQPIYGGTNEIMK	1.115907927	2	3.203755
P15650	VQPIYGGTNEIMK+Oxidation(11	1.599542128		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.22727084**	**6.17E-07**	**9**
P15651	ASSTANLIFEDCR	0.810240611	2	3.354609
P15651	EEGDSWVLNGTK	0.916834166	2	2.766969
P15651	ELVPIAAQLDK	1.086268513	2	2.9567
P15651	ELVPIAAQLDKEHLFPTSQVK	0.90354279	2	4.488413
P15651	GISAFLVPMPTPGLTLGK	1.221340057	2	3.629989
P15651	IGCFALSEPGNGSDAGAASTTAR	1.406258624	2	6.301752
P15651	IGIASQALGIAQASLDCAVK	1.74969458	3	4.969865
P15651	ITEIYEGTSEIQR	1.265438056	2	4.426855
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.461847987	4	4.96333
P15684	**AMPN Aminopeptidase N**	**1.200950356**	**0.008764**	**5**
P15684	ALGDTPAPNIDTTELVER	2.38056517	2	4.324793
P15684	AQIIHDSFNLASAGK	1.10802826	2	3.707201
P15684	LRSALACSNEVWILNR	1.947454933	2	2.308394
P15684	VVATTQMQAADAR	2.091878887	2	3.713423
P15684	YVEAVSPNR	0.910486634	2	2.464384
P15709	**ST2A1 Bile salt sulfotransferase**	**1.198214945**	**0.647248**	**2**
P15709	GNVLYGSWFEHIR	1.156705613	2	2.604277
P15709	NHFTVSQAEAFDK	1.586534405	1	3.754843
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.521183908**	**0.080446**	**3**
P15978	GYEQHAYDGR	5.585920348	2	2.438502
P15978	VEHEGLPEPLSQR	1.036105081	2	3.096969
P15978	YDSDAENPR	2.76441865	2	2.834245
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.089902286**	**9.9E-20**	**26**
P15999	AVDSLVPIGR	1.243259559	2	3.571636
P15999	EIVTNFLAGFEP	0.965285954	2	2.432156
P15999	EVAAFAQFGSDLDAATQQLLSR	1.444688249	2	6.617678
P15999	FESAFLSHVVSQHQSLLGNIR	1.785322141	2	6.013795
P15999	GIRPAINVGLSVSR	1.025758991	3	3.933965
P15999	GMSLNLEPDNVGVVVFGNDK	1.12130867	2	5.631094
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1	1.474926833		
P15999	GYLDKLEPSK	1.273472087	1	2.827728
P15999	HALIIYDDLSK	1.751826536	2	2.781202
P15999	ILGADTSVDLEETGR	3.346371202	2	4.893807
P15999	LELAQYR	1.200739909	2	2.483994
P15999	LKEIVTNFLAGFEP	2.546214149	2	3.039215
P15999	LTDADAMK	0.848720769	2	2.663126
P15999	NVQAEEMVEFSSGLK	1.249864721	2	4.340268
P15999	QGQYSPMAIEEQVAVIYAGVR	1.155590255	3	5.255859

P15999	RLTDADAMK	1.165893529	2	2.929972
P15999	RSTVAQLVK	0.054169785	2	2.432156
P15999	RTGAIVDVPVGDELLGR	1.288592879	2	3.098962
P15999	STVAQLVK	1.293944264	2	2.523568
P15999	TGAIVDVPVGDELLGR	1.325790278	2	4.82722
P15999	TGTAEMSSILEER	0.755721546	2	4.374113
P15999	TGTAEMSSILEER+Oxidation(5	1.128520043		
P15999	TSIAIDTIINQK	1.217384338	2	4.61757
P15999	VLSIGDGIAR	0.954586707	2	2.912164
P15999	VVDALGNAIDGK	1.141849504	2	4.424037
P15999	VVDALGNAIDGKGPVGSK	1.355508592	2	3.72534
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.141736508**	**0.001344**	**9**
P16036	ALYSNILGEENTYLWR	1.069174939	2	3.148023
P16036	EEGLNAFYK	1.120588332	1	2.616619
P16036	EKGSTASQVLQR	1.244777666	2	3.085478
P16036	FGFYEVFK	1.949979938	2	2.327374
P16036	GIFNGFSITLK	1.421898651	2	3.042446
P16036	GSTASQVLQR	1.174889556	2	3.077588
P16036	GWAPTLIGYSMQGLCK	1.056981007	2	2.790632
P16036	IQTQPGYANTLR	1.239795121	2	3.790099
P16036	MYKEEGLNAFYK	0.930028208	3	3.672956
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.137084329**	**0.000379**	**36**
P16086	ALINADELANDVAGAEALLDR	1.413359891	2	5.444268
P16086	ALSSEGKPYVTK	1.527099134	2	3.457214
P16086	DLASVQALLR	1.970110928	2	2.36186
P16086	DLSSVQTLLTK	1.449147652	2	3.149606
P16086	GNAMVEEGHFAAEDVK	1.659354682	2	4.105893
P16086	GVIDMGNSLIER	1.243251157	2	3.075566
P16086	HQAFEAELHANADR	1.673876264	2	2.916769
P16086	HQAFEAELSANQSR	0.672204109	2	4.250525
P16086	HQALQAEIAGHEPR	0.847735763	3	4.759455
P16086	HQEHKGEIDAHEDSFK	0.981051955	3	4.376729
P16086	HQLLEADISAHEDR	1.299354152	3	3.671631
P16086	KFEEFQTDLAAHEER	1.578977352	3	4.319211
P16086	LGDSHDLQR	1.61108769	2	3.201288
P16086	LGESQTLQQFSR	0.537541871	2	3.10756
P16086	LIQEQHPEEELIK	1.302274593	2	4.087823
P16086	LQQSHPLSANQIQVK	1.12548495	2	4.406167
P16086	LQTASDESYKDPTNIQSK	1.177320938	2	5.092257
P16086	LQVASDENYKDPTNLQGK	2.844285481	2	5.186798
P16086	LSDDNTIGQEEIQQR	1.889478194	2	4.076528
P16086	MQHNLEQQIQAR	2.408094396	2	3.365072
P16086	MQHNLEQQIQAR+Oxidation(0	1.261725932		
P16086	MTLVASEDYGDTLAAIQGLLK	1.281377146	2	3.796584
P16086	NQALNTDNYGHDLASVQALQR	1.14096794	2	6.16928
P16086	QFQDAGHFDAENIKK	1.306605689	2	2.845783
P16086	REELITNWEQIR	1.409780878	2	4.380161
P16086	SADESGQALLAAGHYASDEVR	1.678684751	2	4.579109
P16086	SLQQLAEER	1.018733043	2	2.86877
P16086	SQLLGSAHEVQR	0.620515694	2	3.29539
P16086	SSEEIESAFR	1.704203209	2	2.597491
P16086	SSLSSAQADFNQLAELDR	1.50962279	2	4.742074
P16086	TATDEAYKDPSNLQGK	1.197638443	2	4.357157
P16086	TKQEEVNAAWQR	1.444108715	2	3.448297
P16086	VLETAEDIQER	0.97493714	2	3.771271
P16086	VNDVCTNGQDLIK	1.186292732	2	3.166574
P16086	VNEVNQFAAK	1.200102384	2	2.568281

P16086	VNSLGETAQR	1.145159048	2	3.17674
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.247270703**	**0.044403**	**9**
P16232	EECALEIIK	1.232134416	1	2.06642
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8	2.214311198		
P16232	ETSGIILSQAAPK	1.092179918	2	3.133364
P16232	FALDGFFSTIR	1.466782074	2	2.998532
P16232	FVVEAGK	1.192786059	1	1.923535
P16232	KDEVYYDK	0.614113266	2	2.324755
P16232	MGAHVVLTAR	4.756385812	1	1.949364
P16232	MTQPLIASYSASK	1.003724587	2	3.413851
P16232	SSWTPLLLGNPGR	1.240622148	2	3.748619
P16290	**PGAM2 Phosphoglycerate mutase 2**	**0.892976614**	**0.811788**	**9**
P16290	ALPFWNEEIAPK	1.504561144	2	2.855736
P16290	AMEAVAAQGK	0.889816036	2	2.584114
P16290	AMEAVAAQGK+Oxidation(1	1.001667608		
P16290	HGESSWNQENR	2.707670756	2	3.951072
P16290	HNYYASISK	1.458786391	2	2.520293
P16290	HYGGLTGLNK	1.029744352	1	3.193656
P16290	SFDTPPPPMDEK	2.768607203	2	2.606753
P16290	TLWTILDVTDQMWVPVVR+Oxidation(11	1.859915218		
P16290	VLIAAHGNSLR	1.009562815	2	2.947394
P16303	**CES3 Carboxylesterase 3**	**1.121286633**	**4.8E-06**	**16**
P16303	AKEAAEEPSHWK	1.117942868	2	4.068367
P16303	DGASEEETNLSK	1.219862944	2	4.186258
P16303	EAAEEPSHWK	1.407388896	2	2.860868
P16303	ESYPFLPTVIDGVVLPK	1.140232617	2	4.153554
P16303	FAPPQPAEPWNFVK	0.864617833	1	2.33905
P16303	IGASTQAAQR	1.113947314	2	2.808269
P16303	LDLLGNPK	1.120267192	2	2.566988
P16303	MIPVVAEK	1.696185867	1	1.985317
P16303	QEFGWIIPTLMGYPLSEGK	1.605201346	2	2.570275
P16303	QKTEDELLETSLK	1.442173605	2	3.513659
P16303	SFNTVPYIVGINK	0.849999142	2	3.321455
P16303	TEDELLETSLK	1.282469148	2	3.865056
P16303	TPEEILAEK	1.09527473	2	2.646644
P16303	TTTSAVMVHCLR	2.048613697	2	3.071745
P16303	TVIGDHGDELFSVFGSPFLK	1.474501361	2	5.479584
P16303	YFGGTDDPAK	1.968762032	2	2.877553
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.191022686**	**0.140033**	**4**
P16332	GDVGMAGVAIDTVEDTK	1.747794059	2	4.295653
P16332	IDSGSEVIVGVNK	1.553947948	2	3.779443
P16332	NTQIIIQEESGIPK	1.048351405	2	3.595622
P16332	TGLQAGLTIDEFAPR	1.431465786	2	3.400716
P16409	**MYL3 Myosin light chain 3**	**1.481335399**	**0.617654**	**8**
P16409	AAPAPAAAPAAAPEPERPK	2.628655032	2	4.46803
P16409	ALGQNPTQAEVLR	2.551629967	2	3.743129
P16409	EGNGTVMGAELR	1.322425976	2	2.730787
P16409	IEFTPEQIEEFK	1.936320131	2	3.019943
P16409	LTEDEVEK	1.63291029	1	2.146427
P16409	MMDFETFLPMLQHISK	2.079257658	3	3.831653
P16409	NKDTGTYEDFVEGLR	1.546580132	2	3.451002
P16409	VFDKEGNGTVMGAELR	1.356200473	2	4.115485
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.233445641**	**9.9E-20**	**18**
P16617	AHSSMVGVNLPQK	1.213774522	3	4.060881
P16617	AHSSMVGVNLPQK+Oxidation(4	1.478983546		

P16617	ALESPERPFLAILGGAK	1.206240894	3	4.75942
P16617	DCVGSEVENACANPAAGTVILLENLR	1.509873626	3	6.499562
P16617	FCLDNGAK	1.230821145	1	1.961058
P16617	GCITIIGGGDTATCCAK	1.187040864	2	5.551831
P16617	IQLINNMLDK	1.325773992	2	3.035633
P16617	IQLINNMLDK+Oxidation(6	2.492317358		
P16617	ITLPVDFVTADK	1.536262851	2	2.746565
P16617	ITLPVDFVTADKFDENAK	2.092639548	2	4.786545
P16617	SVVLMSHLGRPDGVPMPDK	0.888007928	3	3.747412
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.641130518	4	4.765045
P16617	TGQATVASGIPAGWMGLDCGTESSK	1.256394596	2	5.039053
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.205142392	3	4.076807
P16617	VLNNMEIGTSLYDEEGAK	2.07235266	2	5.245418
P16617	VLPGVDALSNV	1.853589892	2	3.286389
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.237841216	3	4.834997
P16617	YSLEPVAAELK	1.215999785	2	3.49632
P16638	**ACLY ATP_citrate synthase**	**1.747861923**	**9.9E-20**	**25**
P16638	AFDSGIIPMEFVNK	2.182052251	2	3.654032
P16638	AKPAMPQDSVPSPR	2.008259175	2	2.742096
P16638	DEPSVAAMVYPFTGDHK	1.076331082	2	2.954812
P16638	DLVSSLTSGLLTIGDR	1.761836426	2	3.700773
P16638	EAYPEEAYIADLDAK	1.622729746	2	3.626558
P16638	FGGALDAAAK	1.745575861	2	3.020345
P16638	GAIVPAQEVPPPTVPMDYSWAR	2.090698513	2	4.096361
P16638	GGPNYQEGLR	2.236612505	2	2.958294
P16638	GVTIIGPATVGGIKPGCFK	2.267526219	2	3.704646
P16638	HLLVHAPEDK	1.157729119	2	2.680789
P16638	HLLVHAPEDKK	1.685659731	2	3.461171
P16638	IGNTGGMLDNILASK	2.006790404	2	4.103945
P16638	LGLVGVNLSLDGVK	3.12108385	2	2.499557
P16638	LNAEDIK	1.699433141	1	1.944088
P16638	QHFPATPLLDYALEVEK	1.470340091	3	3.840355
P16638	RGGPNYQEGLR	2.351812538	2	3.299999
P16638	SAYDSTMETMNYAQIR	2.957704617	2	2.930823
P16638	SGGMSNELNNIISR	0.990948592	2	3.656127
P16638	SMGFIGHYLDQK	1.137056996	2	2.914143
P16638	TIAIIAEGIPEALTR	1.702882727	2	4.98087
P16638	TTDGVYEGVAIGGDR	1.148481305	2	3.336302
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	2.39414382	3	3.452608
P16638	VDATADYICK	1.268728519	2	2.630916
P16638	WGDIEFPPPFGR	1.708783862	2	3.904791
P16638	YICTTSAIQNR	1.90480472	2	3.142399
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.93009123**	**0.375584**	**10**
P16970	DQVIYPDGKEDQK	1.304952354	2	2.826781
P16970	EGGWDSVQDWMDVLSGGEK	1.736015168	2	2.891609
P16970	FDHVPLATPNGDILIQDLSFEVR	0.899570033	3	4.148556
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.688359837	3	5.367455
P16970	GISDQVLK	1.743281995	1	1.946506
P16970	GYLDNVQLGHILER	1.302481116	2	3.564452
P16970	HLHSTHSELLEDYYQSGR	1.182845348	3	5.852018
P16970	ITELMQVLK	2.389622967	2	2.83461
P16970	KGISDQVLK	0.803819555	2	2.518878
P16970	SGANVLICGPNGCGK	0.839553862	2	3.205405
P17074	**RS19 40S ribosomal protein S19**	**1.571868347**	**3.8E-08**	**5**
P17074	ELAPYDENWFYTR	1.107727023	2	2.959055
P17074	HKELAPYDENWFYTR	1.574906599	3	4.61017

P17074	LKVPEWVDTVK	1.685365463	3	3.347196
P17074	RVLQALEGLK	3.081770604	3	3.815389
P17074	VLQALEGLK	1.500785928	2	2.707209
P17077	**RL9 60S ribosomal protein L9**	**1.445158978**	**0.015919**	**8**
P17077	DFNHINVELSLLGK	1.873628387	2	3.046404
P17077	FLDGIYVSEK	1.314793984	2	3.129148
P17077	GTVQQPDE	26.47601539	1	2.037316
P17077	KFLDGIYVSEK	1.082693772	2	2.941645
P17077	SVYAHFPINVVIQENGSLVEIR	1.760022803	3	3.825795
P17077	TGVACSVSQAQK	1.032347398	2	3.504431
P17077	TICSHVQNMIK	1.585042938	2	3.173116
P17077	TILSNQTVDIPENVDITLK	1.826933311	2	4.866496
P17078	**RL35 60S ribosomal protein L35**	**1.253794859**	**7.93E-08**	**2**
P17078	QLDDLKVELSQLR	1.618805269	2	2.977016
P17078	VLTVINQTQK	1.248847472	2	2.92333
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.516029637**	**1.29E-10**	**5**
P17178	DHESTEGPGTGQDRPR	1.637916211	2	3.357571
P17178	SLAELPGPGTLR	1.626747503	2	2.610941
P17178	TNVNLASAPLLEQVMR	1.606409067	2	3.655778
P17178	VGCLEPSIPEDTATFIR	1.198744791	2	3.215505
P17178	YEVVLSPGMGEVK	1.367927662	2	3.422017
P17209	**MYL4 Myosin light chain 4**	**1.176061556**	**0.974407**	**2**
P17209	HVLATLGEK	1.771656035	1	2.644267
P17209	ITYGQCGDVLR	1.157263396	2	2.372502
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**1.29589867**	**0.479244**	**10**
P17425	ASAELFNQK	1.660280534	2	3.51042
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	1.232929907	3	5.276865
P17425	ITASLCDLK	1.543840978	2	2.536643
P17425	LEDTYFDRDVEK	1.816347682	2	2.967508
P17425	MFLNDFLNDQNR	2.828345657	2	3.483951
P17425	NSIYSGLEAFGDVK	1.134697046	2	3.225848
P17425	NSLSYDCIGR	0.779830173	1	2.085731
P17425	TCVAPDVFAENMK	1.329833857	2	3.25146
P17425	VTQDATPGSALDK	0.570209226	2	3.613897
P17425	YTIGLGQAR	1.354405369	2	2.766264
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.354581023**	**0.000238**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(6	1.607766319		
P17426	NADVELQQR	1.341860674	2	2.642045
P17426	VGGYILGEFGNLIAGDPR	1.406354816	2	3.945225
P17475	**A1AT Alpha_1_antiproteinase**	**1.906117502**	**2.38E-14**	**9**
P17475	AFHHLLQTLNRPDSELQLNTGNGLFVNK	1.008819655	3	4.54079
P17475	GTEAAGATVVEAVPMSLPPQVK	1.387352855	2	2.619911
P17475	MQHLEQTLTK	2.896329802	1	3.127402
P17475	MQHLEQTLTK+Oxidation(0	2.562796397		
P17475	NNYHSEAFSVNFADSEEAKK	2.998351065	3	5.074931
P17475	SAILYFPK	3.218906771	2	2.395156
P17475	TLLSSLGITR	2.718073328	2	2.98003
P17475	VFNNDADLSGITEDAPLK	1.632604845	2	5.838858
P17475	VINDYVEK	1.888771813	2	2.65176
P17702	**RL28 60S ribosomal protein L28**	**1.684306204**	**7.79E-07**	**2**
P17702	NCSSFLIK	2.107077531	2	2.420293
P17702	QTYSTEPNNLK	1.678337865	2	2.77923
P17712	**HXK4 Glucokinase**	**1.094889833**	**0.21023**	**2**
P17712	ASGAEGNNIVGLLR	0.912221791	2	2.302684
P17712	STPEGSEVGDFLSLDLGGTNFR	1.766771053	2	3.176468
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.087667768**	**2.22E-16**	**15**

P17764	EEQDKYAIGSYTR	1.479864213	2	3.487716
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.69179389	3	3.965082
P17764	EVYMGNVIQGGEGQAPTR	0.633070161	2	5.066541
P17764	FANEITPITISVK	0.950217579	2	4.121784
P17764	GKPDVVVKEDEEYK	1.309483179	2	3.72773
P17764	GKPDVVVKEDEEYKR	1.123272102	2	5.172976
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.629076845	2	4.964918
P17764	IHMGNCAENTAK	1.323347128	3	3.55753
P17764	IHMGNCAENTAK+Oxidation(2	1.07404943		
P17764	LEDLIVK	1.139081447	2	2.403829
P17764	LGTIAIQGAIEK	1.438033824	2	3.372826
P17764	QATLGAGLPIATPCTTVNK	1.115216074	2	4.638556
P17764	QGEFGLASICNGGGGASAVLIEK	1.143379247	2	5.119126
P17764	TPIGSFLGSLASQPATK	1.147666828	2	4.31948
P17764	VNVHGGAVSLGHPIGMSGAR	1.262404615	2	5.880795
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.253138533**	**1.11E-16**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.256881993	3	5.548559
P17879	TTPSYVAFTDTER	1.017052606	2	3.622778
P17879	VEIIANDQGNR	1.928741581	2	3.764211
P17988	**ST1A1 Sulfotransferase 1A1**	**1.38524952**	**9.9E-20**	**4**
P17988	CPGVPSGLETLEETPAPR	1.373968891	2	4.23585
P17988	NTFTVAQNER	1.185342685	2	3.564058
P17988	SLPEETVDSIVHHTSFK	1.389299792	2	4.404452
P17988	THLPLSLLPQSLLDQK	1.430637233	2	4.711433
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.228373398**	**6.31E-07**	**29**
P18163	AELSVIFADKPEK	1.083854646	2	3.355317
P18163	ALEDLGR	0.802981086	2	2.339623
P18163	ALKPPCDLSMQSVEVTGTTEGVR	1.087349696	2	4.30022
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9	1.41086326		
P18163	CGVEIIGLK	1.018457919	2	2.876044
P18163	DGWLHTGDIGK	1.240394599	2	2.796502
P18163	GAMVTHQNIMNDCSGFIK	0.834809089	2	5.147714
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2	1.126117864		
P18163	GFQGSFEELCR	1.020201004	2	3.64198
P18163	GIAVHPELFSIDNGLLTPTLK	1.497939381	2	5.303509
P18163	GIQVSNDGPCLGSR	1.218015951	2	4.543355
P18163	IENIYLR	1.085141825	2	2.80915
P18163	IFGQANTSVK	1.121682745	2	2.825404
P18163	IIVIMDSYDNDLVER	1.363431486	2	5.068473
P18163	LLLEGVENK	1.121253763	2	3.344246
P18163	LLMDDLK	1.145262813	2	2.506974
P18163	LMITGAAPVSATVLTFLR	1.387852401	3	4.114018
P18163	LVDVEDMNYQAAK	0.91472041	2	4.649327
P18163	NAGLKPFEQVK	1.136558824	2	3.77725
P18163	NNSLWDK	1.061310344	2	2.492246
P18163	QVAEMAECIGSALIQK	1.253171161	2	5.534113
P18163	SAVLEDDKLLLYYYDDVR	2.409720597	3	3.618413
P18163	SQIDELYSTIK	0.786959672	2	3.615584
P18163	SQIDELYSTIKI	1.584589581	2	3.946987
P18163	TAEALDKDGWLHTGDIGK	1.301623659	2	5.251466
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	0.386498339	3	5.155368
P18163	TMYDGFQR	2.971380755	1	1.945556
P18163	VLQPTIFPVVPR	1.25717337	2	3.597943
P18163	WLLDFASK	1.233672504	2	2.565551
P18297	**SPRE Sepiapterin reductase**	**1.087059985**	**0.275996**	**5**
P18297	LGCAVCVLTGASR	1.272809935	2	3.032018
P18297	LLLINNAGTLGDVSK	1.740294532	2	3.89844

P18297	LNSEGELVDCGTSAQK	1.296369549	2	4.898677
P18297	TVVNISSLCALQPFK	1.205501239	2	3.274786
P18297	VLSYAPGPLDTNMQQLAR	0.822997638	2	3.443828
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.434486881**	**0.000948**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.638460893	2	5.497928
P18298	KIIVDTYGGWGAHGGGAFSGK	1.285464612	3	4.149744
P18298	YLDEDTIYHLQPSGR	1.419004063	2	4.7805
P18418	**CALR Calreticulin**	**1.132703188**	**5.55E-16**	**20**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	1.333590789	3	5.838455
P18418	CKDDEFTHLYTLIVRPDNTYEVK	1.060076488	3	4.921481
P18418	DMHGDSEYNIMFGPDICGPGTK	1.488142537	2	6.22996
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1	1.351172782		
P18418	EQFLDGDAWTNR	2.373967848	2	3.170068
P18418	FYALSAR	1.615434185	2	2.385056
P18418	FYGDQEK	1.091026141	1	2.119054
P18418	FYGDQEKDK	1.211799893	1	2.922854
P18418	GQTLVVQFTVK	0.851566063	2	2.937333
P18418	HEQNIDCGGGYVK	1.13115215	2	4.403697
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	0.887680865	3	4.302038
P18418	IDNSQVESGSLEDDWDFLPPK	2.004418847	2	5.363841
P18418	IDNSQVESGSLEDDWDFLPPKK	6.179247769	3	4.886557
P18418	IKDPDAAKPEDWDER	1.691610156	2	4.368005
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.107687827	3	5.513727
P18418	KVHVIFNYK	0.727643615	2	2.339793
P18418	LFPGGLDQK	1.406616667	2	2.37105
P18418	QIDNPDYK	1.099389426	1	2.090438
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.308946435	3	4.7888
P18418	VHVIFNYK	1.081496935	1	2.55527
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.283213559**	**0.241786**	**3**
P18420	AQPSQAADEPAEK	1.222725766	2	3.852897
P18420	IHQIEYAMEAVK	2.645254337	2	2.827256
P18420	NQYDNDVTVWSPQGR	1.680240001	2	2.995564
P18421	**PSB1 Proteasome subunit beta type_1**	**1.087985453**	**0.018208**	**4**
P18421	AGGSASAMLQPLLDNQVGFK	1.06472895	2	4.993559
P18421	AGGSASAMLQPLLDNQVGFK+Oxidation(7	5.72531586		
P18421	GAVYSFDPVGSYQR	1.195339181	2	3.00408
P18421	NMQNVEHVPLTLDR	1.19387844	2	3.648014
P18422	**PSA3 Proteasome subunit alpha type_3**	**1.350628135**	**0.000695**	**2**
P18422	AVENSSTAIGIR	1.350591692	2	3.232425
P18422	TEIEKLQMKEMTCR+Oxidation(10	2.562773123		
P18445	**RL27A 60S ribosomal protein L27a**	**1.123398048**	**0.499749**	**4**
P18445	LWTLVSEQTR	1.289279412	1	1.914163
P18445	NGVAPIIDVVR	1.566568014	1	2.153581
P18445	NQSFCPTVNLDK	1.146010518	2	3.299043
P18445	RNQSFCPTVNLDK	0.937405696	2	2.94568
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**2.003743677**	**3.19E-05**	**6**
P18484	FFQPTEMASQDFFQR	1.607371242	2	4.024792
P18484	FVNLFPEVK	1.83683408	2	2.834444
P18484	ILVAGDTMDSVK	1.386040436	2	2.747047
P18484	LTECLETILNK	1.575045011	2	2.42357
P18484	NNGVLFENQLLQIGLK	2.109839846	2	3.379971
P18484	THIETVINALK	0.616039034	2	2.811701
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.32613687**	**0.084339**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	3.829999621	2	3.384947
P18596	SLPSVETLGCTSVICSDK	2.713254403	2	4.610282

P18596	TGTLTTNQMSVCR	1.293021551	2	3.226547
P18596	VGEATETALTCLVEK	1.636918028	2	4.625138
P18757	**CGL Cystathionine gamma_lyase**	**0.993335518**	**9.9E-20**	**15**
P18757	AGDEVICMDEVYGGTNR	0.599981341	2	5.609281
P18757	ATLGISDTLIR	1.124197627	2	3.740761
P18757	AVVLPISLATTFK	0.905710618	3	4.283768
P18757	DLLEDLGQALK	1.288172767	2	3.357074
P18757	FLQNSLGAVPSPFDCYLCCR	2.188542242	2	3.911115
P18757	GTLQHAQVFLK	1.157980483	2	3.355264
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	2.122206478	3	4.421936
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	2.540119887	4	5.615601
P18757	LLEAAITPQTK	1.123777497	2	4.016467
P18757	LSVGLEDEKDLLEDLGQALK	1.364551786	3	6.354272
P18757	LVWIETPTNPTLK	1.264985994	2	3.88094
P18757	QCTGCPGMVSFYIK	1.627148516	2	3.727621
P18757	QDSPGQSSGFVYSR	1.033535298	2	3.853681
P18757	RVASEFGLK	1.548226559	2	2.499044
P18757	VIYPGLPSHPQHELAK	1.021763886	2	4.234103
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.041240166**	**0.000851**	**12**
P18886	ATNLTVSAVR	1.453743583	2	3.494674
P18886	ELHAHLLAQDK	2.170863238	2	3.652485
P18886	HSVGELQHMMAECSK	0.432174275	2	3.894764
P18886	LIFDGNEETLK	1.192468692	2	3.084874
P18886	QKLIFDGNEETLKK	1.353709701	2	2.33468
P18886	QYGQTVATYESCSTAAFK	1.130606859	2	3.698326
P18886	SEYNDQLTR	1.655864187	2	3.071038
P18886	TETIRPASIFTK	0.991990257	2	2.605407
P18886	TLQAGLLEPEVFHLNPSK	0.40290636	2	3.448968
P18886	TLSIDSIQFQR	1.602871044	2	3.074601
P18886	YILSDSSPVPEFPVAYLTSENR	1.132949325	2	5.311357
P18886	YLNAQKPLLDDSQFR	1.158329569	2	4.659139
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.21084617**	**9.9E-20**	**19**
P19112	AGGLATTGNEDILDIVPTEIHQK	1.24009757	3	6.45402
P19112	AGGTGEMTQLLNSLCTAIK	1.196789673	3	5.556763
P19112	APVIMGSTEDVQEFLEIYNK	2.254520823	2	4.97642
P19112	APVIMGSTEDVQEFLEIYNKDK	1.57489786	3	3.558839
P19112	DFDPAINEYIQR	1.29790535	2	4.021592
P19112	ESPVHSICDELF	1.377809487	2	2.350213
P19112	FPPDNSAPYGAR	0.944196044	2	2.770434
P19112	GNIYSINEGYAK	1.179019525	2	3.997293
P19112	KGNIYSINEGYAK	0.847694745	2	4.48673
P19112	KLDILSNDLVINMLK	1.458909978	2	4.763169
P19112	KTSANEPSEKDALQPGR	1.237419316	3	4.176288
P19112	LDILSNDLVINMLK	1.470384848	2	5.103749
P19112	LLYECNPIAYVMEK	1.435231251	2	4.454319
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.213758238	3	5.786427
P19112	SRPSLPLPQSR	0.447595629	2	3.353765
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.413665341	3	5.169792
P19112	TLVYGGIFLYPANK	0.805512597	2	3.841897
P19112	TLVYGGIFLYPANKK	0.745899127	2	2.9054
P19112	TSANEPSEKDALQPGR	1.141570112	2	4.477299
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**1.012689865**	**0.382897**	**3**
P19123	AAVEQLTEEQKNEFK	3.455896302	2	2.559125
P19123	GKSEEELSDLFR	0.985053876	2	2.586432
P19123	SEEELSDLFR	4.82143244	2	2.836403

P19132	**FRIH Ferritin heavy chain**	**1.386707887**	**0.057328**	**2**
P19132	QNYHQDSEAAINR	2.102741839	2	2.887335
P19132	YFLHQSHEER	1.386644346	2	2.557775
P19225	**CP270 Cytochrome P450 2C70**	**1.244124316**	**3.38E-06**	**15**
P19225	ACIGEGLAR	1.702373399	2	2.649945
P19225	ASLNLSNPQDFIDYFLIK	1.795498853	2	3.134395
P19225	EALIDRGEEFSDK	1.64219872	2	3.256918
P19225	FDPGHFLDEK	1.127967269	2	2.463623
P19225	FILMEINR	2.283496673	2	2.63737
P19225	GTSVMACLTSALHDDKEFPNPEK	2.080004541	3	3.577065
P19225	IQEEITR	1.439481799	2	2.317652
P19225	IQEEVVYLLEALR	2.651108112	2	3.926897
P19225	KLPPGPTPLPIFGNILQVGVK	0.926976315	3	4.033191
P19225	KTTQDVEFR	1.72499265	2	2.301944
P19225	LPPGPTPLPIFGNILQVGVK	1.330183375	2	4.41558
P19225	NHMPYTDAVLHEIQR	1.520454864	3	3.82308
P19225	SDYFMAFSAGRR+Oxidation(4	0.675064608		
P19225	TTQDVEFR	1.333779952	2	2.438585
P19225	YIDFVPIPLPR	1.224176036	2	3.125314
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.292893832**	**0.756779**	**3**
P19234	DIEEIIDELR	7.793886155	2	3.611884
P19234	DTPENNPDTPFDFTPENYER	0.624657852	2	4.621257
P19234	FCCEPAGGLTSLTEPPK	1.215071114	2	3.137991
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.195656468**	**4.24E-09**	**9**
P19468	ASGELMTVAR	1.18304717	2	2.940057
P19468	CNQIANELCECPELLGSGFR	1.236100474	2	5.338086
P19468	IHLDDANESDHFENIQSTNWQTMR	0.681428872	3	5.048603
P19468	NTPSPFVETFPEDEEASK	1.251665118	2	4.593307
P19468	SLFFPDEAINK	1.398181417	2	2.607862
P19468	SRYDSIDSYLSK	0.795281485	2	2.703424
P19468	VQLLLNGGDVLETLQEK	1.64327319	2	4.674703
P19468	VVINVPIFK	2.388361853	2	2.693337
P19468	WGVISASVDDR	1.783373893	2	3.138253
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.019823881**	**0.111132**	**9**
P19488	AEMWLIR	1.784155493	2	2.892491
P19488	ANAIAWALAQIPQK	1.482965394	3	6.459273
P19488	FETFPTSVSK	1.201479203	1	1.906678
P19488	FETFPTSVSKDELEK	0.806775431	2	4.318477
P19488	GAAVTLNIR	1.419526466	2	2.561926
P19488	GHEVTVLKPSAYYVLDPK	0.83773028	2	4.530221
P19488	NWDPFYTEILGRPTTLAETMGK	1.841080479	2	4.866966
P19488	SDLFNALK	1.06685648	2	2.556469
P19488	TILDELVQR	1.157477086	2	3.395438
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.182496224**	**0.112683**	**10**
P19511	EGEHMINWVEK	1.645498355	2	2.329333
P19511	HVIQSISAQQEK	1.164080114	2	3.976594
P19511	HVIQSISAQQEKETIAK	1.203109708	3	4.756908
P19511	HYLFDVQR	1.195144505	2	2.688479
P19511	KEGEHMINWVEK	1.481282681	2	2.304466
P19511	LDYHISVQDMMR	1.620345865	3	4.551365
P19511	LNEEKIAQLEEIK	1.018151276	2	2.530715
P19511	NNIALALEVTYR	2.083912735	2	2.622712
P19511	YGASIGEFIDK	1.29720992	2	2.836105
P19511	YGASIGEFIDKLNEEK	1.827126944	2	3.475832
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.099838337**	**1.73E-13**	**13**
P19643	FIGGSGQVSER	1.591128106	2	3.31743

P19643	IISTTNGGQER	0.335383829	2	2.731662
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.628520856	3	4.635859
P19643	KFIGGSGQVSER	0.742434012	2	3.044423
P19643	KLCELYAK	0.815832467	2	2.524009
P19643	LERPVIHIDQTGENVVVK	1.248892469	2	5.296371
P19643	LLHDCGLSVVVLEAR	2.5953114	2	3.563993
P19643	TLNHEIYEAK	1.408339717	2	3.052488
P19643	TMDEMGQEIPSDAPWK	1.763154653	2	4.414841
P19643	VKLERPVIHIDQTGENVVVK	0.523433295	3	4.446641
P19643	VLNSQEALQPVHYEEK	1.543903632	2	4.680696
P19643	YVDLGGSYVGPTQNR	0.973957846	2	5.309948
P19643	YVISAIPPVLGMK	1.757410647	2	3.259796
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.32119561**	**9.9E-20**	**9**
P19804	DRPFFPGLVK	1.676465806	2	2.513633
P19804	EIGLWFKPEELIDYK	1.705615417	2	3.830557
P19804	GDFCIQVGR	1.247106213	2	3.316579
P19804	NIIHGSDSVESAEK	1.313303622	3	4.016108
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.910781281	4	4.835697
P19804	TFIAIKPDGVQR	1.624503368	2	2.947857
P19804	VMLGETNPADSKPGTIR	3.148999817	2	4.499082
P19804	VMLGETNPADSKPGTIR+Oxidation(1	1.302420665		
P19804	YMNSGPVVAMVWEGLNVVK	1.68216536	2	5.323691
P19814	**TGON3 Trans_Golgi network integral membrane protein TGN38**	**3.63368442**	**1.16E-10**	**2**
P19814	DSGSPTGGDSDNTTGGDSNK	2.964404035	2	4.74314
P19814	TSGGDSNKPTGSDNDKPTGGDSNKPTSK	3.823057466	4	4.65954
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.333872179**	**0.001705**	**2**
P19944	AAGVNVEPFWPGLFAK	1.33497087	2	2.94979
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.237896805	4	6.264713
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.544159108**	**9.9E-20**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.191630066	2	6.143483
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.038594113	3	4.840834
P19945	CFIVGADNVGSK	1.343465487	2	3.412104
P19945	GHLENNPALEK	1.249468729	2	3.68968
P19945	GNVGFVFTK	0.917373508	2	2.771543
P19945	GTIEILSDVQLIK	1.549128072	2	3.624354
P19945	IIQLLDDYPK	2.306266007	2	3.745273
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.223222123	3	4.199956
P19945	TSFFQALGITTK	1.635370156	2	4.161887
P19945	VLALSVETDYTFPLAEK	1.882112698	2	3.386822
P20059	**HEMO Hemopexin**	**1.132881091**	**0.005345**	**5**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.155228137	2	5.178461
P20059	FNPVTGEVPPR	1.150294783	2	2.655689
P20059	LFQEEFPGIPYPPDAAVECHR	1.366082525	3	4.344021
P20059	SGAQATWAELSWPHEK	0.558665378	2	3.127366
P20059	VDGALCLEK	1.353335995	2	2.54823
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.559625029**	**0.055029**	**6**
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	2.004703295	3	5.064362
P20070	LIDKEIISHDTR	1.525306137	3	4.140484
P20070	MSQYLENMNIGDTIEFR	0.837307079	2	4.422855
P20070	SSPAITLENPDIK	1.116405634	2	3.996587
P20070	SSPAITLENPDIKYPLR	1.512531969	2	3.888384
P20070	SVGMIAGGTGITPMLQVIR	1.20195332	2	4.464146
P20280	**RL21 60S ribosomal protein L21**	**1.231791526**	**0.331215**	**4**
P20280	HGVVPLATYMR	1.244795856	2	2.569047
P20280	KGDIVDIK	1.243060877	1	2.252773

P20280	TNGKEPELLEPIPYEFMA	1.171810776	2	3.615796
P20280	VYNVTQHAVGIIVNK	1.066370926	2	4.423737
P20673	**ARLY Argininosuccinate lyase**	**1.3499809**	**9.9E-20**	**16**
P20673	AEAECEVLFPGYTHLQR	1.188596125	2	4.920734
P20673	AEMQQILQGLDK	1.285918567	2	4.53292
P20673	AVVVAEMK	1.675068259	1	1.949932
P20673	EFNFVQLSDAYSTGSSLMPQK	1.737212876	2	5.803443
P20673	FNSSIAYDR	1.113299772	2	2.544749
P20673	HLWNVDLQGSK	1.226640688	1	3.306964
P20673	INVLPLGSGAIAGNPLGVDR	1.768939904	2	5.484537
P20673	KNPDSLELIR	1.099957079	2	2.612514
P20673	LKELIGEAAGK	1.658715617	2	3.194577
P20673	LYPNDEDIHTANER	12.81732442	2	3.914005
P20673	MAEDLILYGTK	1.350759302	2	3.702366
P20673	MAEDLILYGTK+Oxidation(0	1.641985076		
P20673	NDQVVTDLR	1.300157513	2	3.217111
P20673	SRNDQVVTDLR	1.656047865	2	2.883168
P20673	VAEEWAQGIFK	1.75561259	2	3.569699
P20673	VLIEAMVDR	1.664351823	2	2.756938
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.153764193**	**0.69985**	**6**
P20788	EIDQEAAVEVSQLR	0.923099243	2	4.245802
P20788	EIDQEAAVEVSQLRDPQHDLER	0.820521909	3	3.375093
P20788	ESLSGQAATRPLVATVGLNVPASVR	2.012908853	2	2.500675
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.152235106	3	4.806671
P20788	LSDIPEGK	1.245155923	1	2.027337
P20788	SGPFAPVLSATSR	1.172884232	2	2.862601
P20801	**TNNC2 Troponin C_ skeletal muscle**	**1.41471906**	**0.770386**	**4**
P20801	GKSEEELAECFR	2.820957973	2	3.245115
P20801	NADGYIDAEELAEIFR	1.248413929	2	4.821789
P20801	SEEELAECFR	2.167539111	2	3.284803
P20801	SYLSEEMIAEFK	2.176797888	2	2.674991
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**2.132677227**	**8.88E-15**	**3**
P20814	FDYEDKDFLNLIEK	2.237311757	3	3.994282
P20814	GTAVLTSLTSVLHDSK	1.895929888	2	3.734842
P20814	IKEHEESLDVSNPR	2.176121885	2	4.697644
P20817	**CP4AE Cytochrome P450 4A14**	**1.053088166**	**0.801861**	**6**
P20817	ACQIAHEHTDGVIK	1.078674915	2	4.269307
P20817	AQLQNEEELQK	1.094047494	2	3.201374
P20817	AVEDLNNLTFFR	1.081276127	2	3.319497
P20817	HLDFLDILLFAK	1.548687756	2	3.819928
P20817	MRKAQLQNEEELQK+Oxidation(0	1.05699261		
P20817	VLLYDPDYVK	0.792491351	2	2.710024
P20852	**CP2A5 Cytochrome P450 2A5**	**1.17621285**	**0.431328**	**3**
P20852	DFIDSFLIR	1.414460889	2	2.319948
P20852	DPKFFSNPKDFNPK	1.772660931	2	2.538004
P20852	EALVDQAEEFSGR	0.876019109	2	3.369677
P21213	**HUTH Histidine ammonia_lyase**	**1.292406008**	**0.84121**	**12**
P21213	ALDYLAIGVHELAAISER	1.605978316	3	4.067576
P21213	DIITTELNSATDNPMVFASR	1.308129954	2	4.219561
P21213	GETISGGNFHGEYPAK	1.126127579	2	4.134145
P21213	GEWLAVPCQDGK	1.193855691	2	2.46894
P21213	GYSGISLETLK	1.184142227	2	2.741279
P21213	LQELQVNLVR	1.293041926	2	3.177824
P21213	NKPDNGGFTSVDEVR	1.192262945	2	3.9932
P21213	SHSSGVGKPLSPER	0.8812196	2	4.37341
P21213	SLLDSDHHPSEIAESHR	1.05397726	3	4.827968

P21213	TVVYGITTGFGK	1.032356038	2	3.295527
P21213	VWEVAAPYIEK	1.312334578	2	2.418866
P21213	YIALDGDSLSTEDLVNLGK	2.14298459	2	5.15879
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.146540613**	**0.717786**	**9**
P21396	DVPAIEITHTFLER	1.620549771	2	3.372434
P21396	FVGGSGQVSEQIMGLLGDK	1.380759691	2	3.140022
P21396	IFSVTNGGQER	1.000337442	2	2.641504
P21396	INVLVLEAR	1.721419316	2	3.180335
P21396	KDIWVEEPESK	0.971155915	2	3.300155
P21396	KICELYAK	0.815832467	2	2.524009
P21396	VLGSQEALYPVHYEEK	1.10563919	2	4.454023
P21396	WVDVGGAYVGPTQNR	0.984679762	2	4.506373
P21396	YVISAIPPILTAK	1.37993173	2	2.948556
P21531	**RL3 60S ribosomal protein L3**	**1.834829128**	**5.68E-14**	**7**
P21531	AHLMEIQVNGGTVAEK	1.318852242	2	5.381459
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	1.719702184	3	5.285472
P21531	HGSLGFLPR	0.969025845	2	2.926322
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.843369589	2	5.13959
P21531	NNASTDYDLSDK	1.062425341	2	3.700171
P21531	SINPLGGFVHYGEVTNDFIMLK	2.179548341	2	3.638427
P21531	TVFAEHISDECK	1.634274809	2	3.999843
P21533	**RL6 60S ribosomal protein L6**	**1.399976472**	**9.9E-20**	**10**
P21533	AVDSQILPK	1.059180698	2	2.787864
P21533	FVIATSTK	1.30022975	1	2.228564
P21533	HLTDAYFK	1.493768682	2	2.568016
P21533	HQEGEIFDTEK	1.467329415	2	3.365013
P21533	HQEGEIFDTEKEK	1.428605006	2	4.194141
P21533	HQEGEIFDTEKEKYEITEQR	1.436963381	3	4.555762
P21533	QLGSGLLLVTGPLALNR	1.448843592	2	5.196892
P21533	SQFSLTNGMYPHK	1.00446293	2	3.331298
P21533	SSITPGTVLIILTGR	2.289232273	2	4.135162
P21533	YYPTEDVPR	2.576952145	1	1.995616
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**0.928169908**	**4.92E-05**	**6**
P21571	FEVLDKPQS	0.764694661	2	2.896924
P21571	FPTFNFEDPKFEVLDKPQS	1.223813945	3	3.327766
P21571	GEMDKFPTFNFEDPK	0.922052658	3	3.962435
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.082129931	3	3.831141
P21571	LASGGPVDTGPEYQQEVDR	1.234167381	2	5.31505
P21571	LASGGPVDTGPEYQQEVDRELFK	2.759044444	2	2.948967
P21643	**T23O Tryptophan 2_3_dioxygenase**	**5.046979867**	**9.9E-20**	**9**
P21643	AGTGGSSGYYYLR	3.82219199	2	2.932857
P21643	DNFEGDYNELLLK	1.588882432	2	3.596245
P21643	GGLIYGDYLQLEK	14.5937292	2	3.62728
P21643	GLEEEFLK	1.630106107	1	2.245919
P21643	ILNAQELQSEIK	6.340529656	2	3.834261
P21643	KDSEEKEEQMAEFR	17.93794383	2	3.858294
P21643	NLSMEDNEEDGAQTGVNR	36.30795981	2	6.060421
P21643	YNHVCMVHRMLGSK+Oxidation(5	1.971990865		
P21643	YNHVCMVHRMLGSK+Oxidation(9	1.80589622		
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.9656356**	**0.001963**	**2**
P21670	ATCIGNNSAAAVSMLK	1.053933386	2	3.415352
P21670	LLDEVFFSEK	2.037984202	2	3.375
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.117690395**	**0.578345**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	1.086833337	2	5.012298
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22	1.357647491		

P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.346444874**	**6.09E-08**	**7**
P21913	CGPMVLDALIK	1.361280585	2	3.136224
P21913	CGPMVLDALIKIK	0.528015234	2	2.617555
P21913	CHTIMNCTQTCPK	1.507912935	2	4.481551
P21913	IDTDLGK	1.110508401	1	1.913149
P21913	IKNEIDSTLTFR	1.716427258	2	2.891634
P21913	LQDPFSLYR	2.00081159	2	2.763685
P21913	RIDTDLGK	1.258225778	2	2.585951
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.17298546**	**0.018914**	**6**
P21981	CDLEIQANGR	1.452710501	2	2.856411
P21981	DHHTADLCQEK	0.890717094	2	2.707641
P21981	KLVAEVSLK	2.087282077	2	2.454549
P21981	SEGTYCCGPVSVR	1.515464612	2	3.692155
P21981	VDLFPTDIGLHK	0.647613299	2	2.659267
P21981	YSGCLTESNLIK	1.172425907	2	3.559706
P22734	**COMT Catechol O_methyltransferase**	**1.09917022**	**9.9E-20**	**12**
P22734	AIYQGPSSPDKS	1.025994388	2	3.347022
P22734	EWAMNVGDAK	1.69625458	1	2.884434
P22734	GQIMDAVIR	1.228975217	2	2.989397
P22734	GQIMDAVIR+Oxidation(3	1.785356123		
P22734	GSSSFECTHYSSYLEYMK	0.924240643	2	4.43602
P22734	GTVLLADNVIVPGTPDFLAYVR	2.330509573	3	5.044014
P22734	KGTVLLADNVIVPGTPDFLAYVR	2.398272834	3	5.194256
P22734	KYDVDTLDMVFLDHWK	1.788219155	3	5.281262
P22734	VTILNGASQDLIPQLK	1.310629297	2	4.476315
P22734	YDVDTLDMVFLDHWK	1.55917039	2	4.490059
P22734	YLPDTLLLEK	1.495391811	2	3.001435
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.405526951	3	6.466105
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.676103234**	**0.111447**	**6**
P22789	EEDLILLTYPK	1.925798883	2	2.997475
P22789	ETLQNVCNK	2.375759248	2	2.354265
P22789	FVVKEEDLILLTYPK	2.25087217	3	3.431701
P22789	KLEPDELDLVLK	1.605771553	2	3.761976
P22789	LEPDELDLVLK	1.806463273	2	2.357396
P22789	NHFTVAQAEAFDK	1.528244516	2	3.442972
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.081610071**	**1.12E-11**	**23**
P22791	ASLDMFNK	1.071818202	2	2.795781
P22791	ASLDMFNKK	1.176792553	2	2.835513
P22791	DVGILALEVYFPAQYVDQTDLEK	1.053482765	3	5.662047
P22791	GLKLEETYTNK	3.538404403	2	2.846511
P22791	GLKLEETYTNKDVDK	1.182550252	3	3.370818
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.212040065	3	6.966366
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3	1.395147199		
P22791	IGAFSYGSGLAASFFSFR	1.73343827	2	3.2888
P22791	LEETYTNK	1.002048925	2	3.154362
P22791	LEETYTNKDVDK	1.004340212	2	4.127285
P22791	LEVGTETIIDK	0.905150672	2	3.780823
P22791	LMFNDFLSSSSDK	1.777962456	2	4.325021
P22791	LMFNDFLSSSSDK+Oxidation(1	1.433509547		
P22791	LMFNDFLSSSSDKQNNLYK	1.622654805	2	4.784518
P22791	LSIQCYLR	1.11479487	2	2.443127
P22791	LVSSVSDLPK	1.335133009	2	3.451921
P22791	MGFCSVQEDINSLCLTVVQR	1.607735521	2	4.1632
P22791	MSPEEFTEIMNQR	0.801013884	2	4.890848

P22791	MSPEEFTEIMNQR+Oxidation(0	1.016764417		
P22791	MSPEEFTEIMNQR+Oxidation(9	1.098199396		
P22791	TKLPWDAVGR	1.031087848	3	4.011916
P22791	VNFSPPGDTSNLFPGTWYLER	1.256081895	2	4.459269
P22791	YTVGLGQTR	1.131561783	2	3.446344
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.532744856**	**9.9E-20**	**10**
P22985	DEVTCVGHIIGAVVADTPEHAQR	1.283211287	3	3.821598
P22985	DGGCCGGSGNNPNCCMNQTK	1.714167025	2	5.751899
P22985	DPPANVQLFQEVPK	1.476119699	2	2.881377
P22985	LDPTFASATLLFQK	1.512733234	2	3.80933
P22985	NQPEPTVEEIENAFQGNLCR	1.514723247	2	5.084301
P22985	QLFQLDSPATPEK	1.00720612	2	3.426797
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.489951924	3	5.206497
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.607871365	3	5.30885
P22985	TLLRPEEILLSIEIPYSK	1.127351418	3	4.464454
P22985	TNLPSNTAFR	1.605596997	1	2.045998
P23358	**RL12 60S ribosomal protein L12**	**1.649361351**	**1.41E-08**	**5**
P23358	CTGGEVGATSALAPK	1.166324517	2	4.130478
P23358	EILGTAQSVGCNVDGR	1.656965252	2	4.500772
P23358	HNGNITFDEIVNIAR	1.668350968	2	3.853965
P23358	HPHDIIDDINSGAVECPAS	0.99866517	2	4.555913
P23358	QAQIEVVPSASALIIK	1.878153431	2	3.845843
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.133218071**	**9.9E-20**	**10**
P23457	ALDGLNR	1.15207457	2	2.392593
P23457	ELTQVFEFQLASEDMK	1.814548427	2	4.134054
P23457	HFDSAYLYEVEEEVGQAIR	1.487904915	2	5.999561
P23457	MLDYCK	1.473401461	1	2.147129
P23457	SIGVSNFNCR	1.190229672	2	3.405276
P23457	SKDIILVSYCTLGSSR	0.774607588	2	4.442013
P23457	SPVLLDDPVLCAIAK	1.092840451	2	4.213246
P23457	VALNDGNFIPVLGFGTTVPEK	1.579457643	2	4.860663
P23457	YFDDHPNHPFTDE	1.303962718	2	4.190112
P23457	YKPVCNQVECHLYLNQSK	0.529135845	2	4.63768
P23514	**COPB Coatomer subunit beta**	**1.385753071**	**6.94E-09**	**8**
P23514	EAGELKPEEEITVGPVQK	1.040273397	2	4.082841
P23514	LVEKPSPLTLAPHDFANIK	1.493014722	3	3.729482
P23514	NFENLIPDAPELIHDFLVNEK	1.442045395	3	4.803425
P23514	TLQLALDLVSSR	1.373945492	2	3.411503
P23514	TNNVSEHEDTDKYR	1.735847001	2	3.814476
P23514	VLQDLVMDILR	1.602830703	2	3.520522
P23514	VLSECSPLMNDIFNK	1.251940885	2	2.863657
P23514	YEAAGTLVTLSSAPTAIK	1.555922211	2	5.290037
P23739	**SUIS Sucrase_isomaltase_ intestinal**	**1.016075829**	**0.946391**	**2**
P23739	LPGFGFNDQFIQISTR	1.015961009	2	2.4404
P23739	RMMTLNYPPVFSPELR+Oxidation(1	1.177782368		
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**1.132501837**	**5.41E-13**	**10**
P23965	ALQLGTLFPPAEALK	1.372139702	2	5.296002
P23965	ATADNLIK	1.074339782	2	2.767118
P23965	AVQELWLR	1.883118614	2	2.72062
P23965	DNYVNTIGHR	1.469217239	2	2.679685
P23965	EGEAGIAVMK	1.234742661	1	2.002609
P23965	GVILTSERPGIFSAGLDLMEMYGR	2.015988345	3	5.499359
P23965	QREADIQNFTSFISR	1.085828841	2	3.047743
P23965	SLHVYLEK	0.81219311	1	2.1486
P23965	VGLVDEVVPEDQVHSK	1.144162843	2	4.867299
P23965	WFTIPDHSR	0.911918121	1	1.961597
P24049	**RL17 60S ribosomal protein L17**	**1.712927409**	**5.52E-06**	**4**

P24049	EQIVPKPEEEVAQK	1.235444183	2	3.817396
P24049	GLDVDSLVIEHIQVNK	1.759093974	2	4.39192
P24049	SAEFLLHMLK	2.573906121	2	2.847092
P24049	YSLDPENPTK	1.155352869	2	2.605978
P24050	**RS5 40S ribosomal protein S5**	**1.947803719**	**3.17E-05**	**5**
P24050	AQCPIVER	1.551952787	2	2.313868
P24050	QAVDVSPLR	3.609538604	2	2.316564
P24050	RQAVDVSPLR	1.74353461	2	2.330836
P24050	VNQAIWLLCTGAR	1.954340593	2	4.2079
P24050	WSTDDVQINDISLQDYIAVK	3.734058704	2	4.82144
P24090	**FETUA Alpha_2_HS_glycoprotein**	**0.808309012**	**0.164971**	**6**
P24090	ELACDDPETEHVALIAVDYLNK	0.771118206	2	4.280798
P24090	HAFSPVASVESASGEVLHSPK	1.103069977	3	6.057868
P24090	LGGEEVSVACK	0.976783414	2	3.712094
P24090	VGQPGDAGAAGPVAPLCPGR	0.948889754	2	5.209847
P24090	VLHAQCHSTPDSAEDVR	1.250100706	3	3.42023
P24090	VLHAQCHSTPDSAEDVRK	1.843324762	3	4.018685
P24268	**CATD Cathepsin D**	**1.570654972**	**1.46E-09**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.83632536	2	3.31334
P24268	DPTGQPGGELMLGGTDSR	0.776414174	2	4.738847
P24268	GGCEAIVDTGTSLLVGPVDEVK	1.055119348	3	3.502074
P24268	LGGQNYELHPEK	2.264175298	2	3.245731
P24329	**THTR Thiosulfate sulfurtransferase**	**1.026391124**	**0.975397**	**12**
P24329	EGHPVTSEPSRPEPAVFK	1.138177045	2	4.573226
P24329	FQLVDSR	0.774869697	2	2.389337
P24329	GSVNVPFMNFLTEDGFEK	1.45110911	2	3.257531
P24329	HVPGASFFDIEECR	1.295487763	2	4.104652
P24329	KVDLSQPLIATCR	0.866366735	2	4.65795
P24329	RFQLVDSR	0.813464658	2	2.496114
P24329	TVSVLNGGFR	1.106075342	2	2.915481
P24329	TYEQVLENLQSK	1.037515403	2	5.076224
P24329	VDLSQPLIATCR	1.160846279	2	3.731257
P24329	VLDASWYSPGTR	1.891113591	2	3.63676
P24329	WLAESIR	1.502083316	2	2.37692
P24329	YLGTQPEPDAVGLDSGHIR	1.033702466	3	4.798242
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.575131225**	**0.01354**	**9**
P24368	DKPLKDVIIVDCGK	1.243847114	3	3.824583
P24368	DTNGSQFFITTVK	1.24719744	2	3.831807
P24368	DVIIVDCGK	0.786486417	1	1.989922
P24368	HYGPGWVSMANAGK	9.574341006	2	4.007035
P24368	IEVEKPFAIAK	1.053068961	2	3.092169
P24368	IEVEKPFAIAKE	1.340951116	2	3.61651
P24368	TVDNFVALATGEK	1.191042378	2	4.100255
P24368	VLEGMDVVR	1.507042645	2	3.040464
P24368	VYFDFQIGDEPVGR	1.831642696	2	4.105346
P24457	**CP2DB Cytochrome P450 2D11**	**0.957760866**	**0.196245**	**2**
P24457	RFSVSTLR	0.800067155	2	2.564001
P24457	SLEEWVTK	1.792620691	2	2.460664
P24470	**CP2CN Cytochrome P450 2C23**	**1.150589919**	**1.8E-05**	**12**
P24470	ACVGESLAR	1.402654854	2	2.756069
P24470	DLDIKPITTGIINLPPPYK	1.112228456	2	3.869002
P24470	EALLQQGDEFLGR	0.767702895	2	2.69954
P24470	FGLLLLMK	1.608242385	2	3.087009
P24470	GTTVLPMLSSVMLDQK	1.442249067	2	3.981119
P24470	GYGLIFSNGER	1.208899398	2	3.793898
P24470	IEEEKDNLK	0.999742805	2	3.014717
P24470	LPPGPTPLPIIGNLLQLNLK	1.227344204	3	5.056924

P24470	RSLEERVQEEAR	1.113801038	2	2.491975
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	1.742923228	3	3.784114
P24470	TFLNLMDLLNK	1.801328901	2	3.995301
P24470	YITLLPSSLPHAVVQDTK	0.943406151	2	4.585886
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**1.163610824**	**4.05E-12**	**8**
P24473	AGMATAQAQHLLNK	1.187780999	2	4.191675
P24473	DEDITESQNILSAAEK	1.214423238	2	5.845017
P24473	DSGNQPPAMVPHK	1.56574645	2	2.754972
P24473	FLTAVSMEQPEMLEK	1.213896081	2	4.87768
P24473	IWSRDEDITESQNILSAAEK	2.034084948	3	3.679632
P24473	MELLAYLLGEK	1.638076714	2	3.859443
P24473	QLFQVPMSVPK	0.838881708	2	2.55549
P24473	YGAFGLPTTVAHVDGK	0.8547165	2	4.048415
P25093	**FAAA Fumarylacetoacetase**	**1.126723747**	**9.9E-20**	**16**
P25093	AIDVGQGQTR	1.096056921	2	3.464326
P25093	AQEHIFGMVLMNDWSAR	2.531659687	2	3.853046
P25093	ASLQNLLSASQAQLR	1.098579698	2	4.884591
P25093	ASLQNLLSASQAQLRDDK	1.614233031	2	3.58822
P25093	ASSVVVSGTPIR	1.10418075	2	3.83348
P25093	DIQQWEYVPLGPFLGK	1.363565748	2	4.992272
P25093	FGEPIPISK	1.126556088	2	2.893934
P25093	GEGMSQAATICR	1.358092694	2	3.748846
P25093	GEGMSQAATICR+Oxidation(3	1.216211462		
P25093	GKENALLPNWLHLPVGYHGR	1.410489301	4	4.534149
P25093	HLFTGPVLSK	1.51082833	1	2.731852
P25093	HQHVFDETTLNSFMGLGQAAWK	1.358159103	2	5.423573
P25093	IGVAIGDQILDLSVIK	1.934167256	2	5.403927
P25093	SFGTTISPWVVPMDALMPFVVPNPK	1.179521168		
P25093	TFLLDGDEVIITGHCQGDGYR	1.544919652	2	5.073804
P25093	VGFGQCAGK	0.392166262	2	2.35363
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.251828111**	**0.673189**	**7**
P25113	ALPFWNEEIVPQIK	1.175892032	2	3.509002
P25113	FSGWYDADLSPAGHEEAK	1.144809431	2	5.070369
P25113	FSGWYDADLSPAGHEEAKR	1.325956789	2	4.2297
P25113	HGESAWNLENR	1.252152946	2	3.787056
P25113	SYDVPPPPMEPDHPFYSNISK	1.224182906	2	3.802812
P25113	YADLTEDQLPSCESLK	0.99510253	2	5.364097
P25113	YADLTEDQLPSCESLKDTIAR	1.331980226	2	5.067235
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.140404463**	**9.9E-20**	**15**
P25235	EDQVIQLMNTIFSK	1.302458354	2	3.883828
P25235	EETVLATVQALHTASHLSQQADLR	1.729869242	3	5.077978
P25235	FELDTSER	1.090239564	1	2.394733
P25235	FPEEEAPSTVLSQNLFTPK	1.145711538	2	3.837504
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.37680073	2	4.687008
P25235	KNFESLSEAFSVASAAAALSQNR	1.670694964	2	5.440873
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.315936295	3	5.14101
P25235	LQVSSVLSQPLAQAAVK	1.791603981	2	5.847798
P25235	LSKEETVLATVQALHTASHLSQQADLR	2.044367621	3	5.564164
P25235	NFESLSEAFSVASAAAALSQNR	2.244605432	3	4.905325
P25235	NIVEEIEDLVAR	1.31065358	3	4.632297
P25235	NPILWNVADVVIK	0.972894759	2	3.257379
P25235	TGQEVVFVAEPDNK	0.943110087	2	4.325447
P25235	YHVPVVVVPEGSASDTQEQAILR	1.234492961	3	6.398319
P25235	YIANTVELR	1.501720114	2	2.827023
P25318	**chain**	**1.267835558**	**0.066486**	**3**

P25318	GEKGFGMPGLPGLK+Oxidation(6	1.248703226		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(12	1.270090024		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(9	1.270090024		
P25409	**ALAT1 Alanine aminotransferase 1**	**1.080039247**	**0.940345**	**3**
P25409	LTEQVFNEAPGIR	1.083950303	2	2.914719
P25409	VLCVINPGNPTGQVQTR	0.906041265	2	4.501179
P25409	VLTLDTMNPCVR	1.268059617	2	2.502423
P26039	**TLN1 Talin_1**	**1.276359912**	**2E-08**	**24**
P26039	ADAEGESDLENSR	1.56901909	2	3.626325
P26039	ADAEGESDLENSRK	1.420500898	2	3.20415
P26039	AGALQCSPSDVYTK	1.232641558	2	2.688327
P26039	ALEATTEHIR	1.254415681	2	2.365054
P26039	AQEACGPLEMDSALSVVQNLEK	1.442517526	2	4.491464
P26039	ASAGPQPLLVQSCK	1.229317696	2	2.871083
P26039	ASVPTIQDQASAMQLSQCAK	0.79353427	2	3.365744
P26039	AVAEQIPLLVQGVR	1.38509678	2	3.062533
P26039	EAAEGLRMATNAAAQNAIKK	1.150728798	2	2.654973
P26039	ILAQATSDLVNAIK	2.334773423	2	3.297559
P26039	LGAASLGAEDPETQVVLINAVK	1.713987716	2	4.272346
P26039	LLGEIAQGNENYAGIAAR	0.886522596	2	4.213369
P26039	LNEAAAGLNQAATELVQASR	1.334733344	2	5.113737
P26039	MATNAAAQNAIK	0.867634965	2	2.710288
P26039	NCGQMSEIEAK	1.389455906	2	2.940279
P26039	QFVQSAKEVANSTANLVK	1.181976335	2	2.395279
P26039	SNTSPEELGPLANQLTSDYGR	0.97128831	2	4.055459
P26039	TLAESALQLLYTAK	2.024672811	2	2.709065
P26039	TMLESAGGLIQTAR	0.978307882	2	2.618257
P26039	VGAIPANALDDGQWSQGLISAAR	1.325129045	2	5.05663
P26039	VGDDPAVWQLK	0.939839661	2	3.279398
P26039	VLGEAMTGISQNAK	1.071470276	2	3.329312
P26039	VLVQNAAGSQEK	1.377460518	2	3.150865
P26039	VVAPTISSPVCQEQLVEAGR	0.90612624	2	4.609031
P26043	**RADI Radixin**	**1.367866729**	**8.22E-15**	**11**
P26043	AFAAQEDLEK	1.118380077	2	3.020972
P26043	ALELEQER	1.137740232	2	2.470081
P26043	EIHKPGYLANDR	1.827377234	2	2.405591
P26043	FFPEDVSEELIQEITQR	1.658184245	3	4.096204
P26043	IQNWHEEHR	0.991245632	2	2.480586
P26043	KKEEEATEWQHK	0.408072874	3	4.192433
P26043	KTQNDVLHAENVK	1.409887252	2	5.060863
P26043	NQEQLAAELAEFTAK	1.67797344	2	5.100673
P26043	QLQALSSELAQAR	1.048349605	2	4.042141
P26043	RKPDTIEVQQMK	1.343822511	2	3.74671
P26043	TQNDVLHAENVK	1.216987294	2	4.114049
P26231	**CTNA1 Catenin alpha_1**	**1.345495093**	**2.91E-10**	**8**
P26231	LIEVANLACSISNNEEGVK	2.25320098	2	5.262959
P26231	LLEPLVTQVTTLVNTNSK	1.427095135	2	4.121065
P26231	NTSDVISAAK	1.354611384	2	2.393048
P26231	QIIVDPLSFSEER	1.611980135	2	2.882873
P26231	SAAGEFADDPCSSVK	0.991173699	2	4.39154
P26231	SDALNSAIDK	1.497005713	2	2.877034
P26231	TIADHCPDSACK	0.832289857	2	3.519769
P26231	VIHVVTSEMDNYEPGVYTEK	1.321922085	3	4.171963
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.165204058**	**0.435848**	**10**

P26284	AILAELTGR	1.312897158	2	2.691204
P26284	EEIQEVRSK	0.954927935	1	1.938042
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	1.251211498	3	6.513037
P26284	LEEGPPVTTVLTR	1.294038476	2	3.513348
P26284	MVNSNLASVEELK	1.076078172	2	2.919255
P26284	MVNSNLASVEELKEIDVEVR	1.463734745	2	4.364052
P26284	NFYGGNGIVGAQVPLGAGIALACK	1.362837492	2	4.200545
P26284	RGDFIPGLR	1.581524015	2	2.358117
P26284	TREEIQEVR	1.164447008	3	3.555892
P26284	VDGMDILCVR	1.649155329	2	3.435465
P26376	**IFM3 Interferon_induced transmembrane protein 3**	**0.82465668**	**0.48923**	**2**
P26376	IKEEYEVSELGAPHGSASVR	1.583942574	3	4.082586
P26376	KMVGDMTGAQAYASTAK+Oxidation(5	0.746527381		
P26453	**BASI Basigin**	**1.444059444**	**1.09E-05**	**7**
P26453	GNINVEGPPR	1.445068032	2	3.481402
P26453	KSEHASEGEFVK	0.698947504	3	3.40795
P26453	RKPDQTLDEDDPGAAPLK	1.347442658	3	4.00201
P26453	SEASHPPVDEWVWFK	1.62195425	2	3.288069
P26453	SEHASEGEFVK	1.398363035	3	3.741488
P26453	SGEYSCIFLPEPVGR	1.535815371	2	3.618756
P26453	VLQEDTLPDLQMK	1.500316634	2	4.115759
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**1.696383588**	**0.412515**	**2**
P26516	SVVALHNLINNK	2.213628362	2	2.76135
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	1.610696534	3	4.495963
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.871212795**	**0.936722**	**7**
P26772	GGEIQPVSVK	1.150931273	2	3.469545
P26772	GGIMLPEK	1.137278155	2	2.666815
P26772	GGIMLPEK+Oxidation(3	1.244910061		
P26772	GKGGEIQPVSVK	1.08671342	2	3.417467
P26772	VLLPEYGGTK	1.04995548	2	2.372341
P26772	VLQATVVAVGSGGK	1.139441081	2	5.391181
P26772	VVLDDKDYFLFR	0.772708238	3	3.692116
P27139	**CAH2 Carbonic anhydrase 2**	**1.295894899**	**0.528945**	**4**
P27139	AVQHPDGLAVLGIFLK	1.877261295	2	3.984617
P27139	IGPASQGLQK	1.106687547	2	3.517799
P27139	ITEALHSIK	1.546099889	2	2.456688
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	2.52967372	3	3.405724
P27321	**ICAL Calpastatin**	**1.104780332**	**0.242289**	**5**
P27321	GSDEVTASSAATGTSPR	2.857181774	2	4.268798
P27321	KGSDEVTASSAATGTSPR	1.334162643	2	5.210084
P27321	KVEEEVMNDQALQALSDSLGTR	2.05061319	3	3.67625
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	1.103947096	3	4.645947
P27321	SQSSEPPVIHEK	0.823881934	2	3.504628
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.983930723**	**0.459697**	**6**
P27364	AVLAANGSILK	1.168914478	2	2.993024
P27364	ETILNDREEEHR	1.161665872	2	2.929133
P27364	GDIVDAQFLR	1.10600353	2	3.059942
P27364	IVQMLVQEK	2.095210752	2	2.617155
P27364	NGGTFHTCALR	0.420187037	2	2.604505
P27364	QTILDVNVK	1.077092335	2	2.387791
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.229302373**	**5.79E-06**	**6**
P27605	DLNHVCVISESGK	0.979668931	2	3.435813
P27605	FFADLLDYIK	1.980193618	2	3.549659

P27605	NVLIVEDIIDTGK	0.987113105	2	3.861195
P27605	SVGYRPDFVGFEIPDK	1.159739745	3	4.031015
P27605	SYCNDQSTGDIK	1.244306389	2	4.008319
P27605	VIGGDDLSTLTGK	0.886694814	2	4.36202
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.042374119**	**0.006732**	**17**
P27653	ASQAPSSFQLLYDLK	1.56711234	2	3.97226
P27653	AYTEEDLDLVEK	0.464055947	2	3.193828
P27653	GDILVVATGQPEMVK	1.588412231	2	2.502603
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.01040294	3	4.792505
P27653	IFHELTQTDK	1.340529348	3	3.478808
P27653	ITIGQAPTEK	1.345945395	2	2.438868
P27653	IYGADDIELLPEAQNK	1.491416729	2	4.993477
P27653	KITIGQAPTEK	0.959299197	2	2.869341
P27653	KVVGDVAYDEAK	1.073173458	2	3.702427
P27653	LDIDPETITWQR	1.074630545	2	3.829334
P27653	MHGGGPTVTAGLPLPK	0.93903828	2	3.812268
P27653	QGFGNLPICMAK	1.222080428	2	2.788481
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.602314558	3	5.597878
P27653	TDPAALTDDEINR	1.03885615	2	4.096861
P27653	THLSLSHNPEQK	0.999393385	2	3.850346
P27653	VVGDVAYDEAK	1.332944795	2	3.40638
P27653	YVVVTGITPTPLGEGK	1.271745936	2	4.822294
P27657	**LIPP Pancreatic triacylglycerol lipase**	**1.225619604**	**0.38467**	**2**
P27657	ATYTQATQNVR	1.127740794	2	2.962993
P27657	NILSQIVDIDGIWEGTR	1.709330007	2	2.93919
P27661	**H2AX Histone H2A.x**	**1.269133072**	**0.008877**	**3**
P27661	AGLQFPVGR	0.967337455	2	3.225393
P27661	HLQLAIR	1.239887521	2	2.710006
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.558249877	2	4.394127
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**2.143333115**	**0.705367**	**4**
P27768	ELEDMNQK	2.793765508	2	2.307754
P27768	IDAAEEEKYDMEVK	2.456990651	2	3.252158
P27768	SVMLQIAATELEK	1.665067825	2	2.92447
P27768	SVMLQIAATELEKEESR	1.872350923	2	3.68925
P27867	**DHSO Sorbitol dehydrogenase**	**1.306841538**	**6.87E-09**	**14**
P27867	AMGASQVVVIDLSASR	1.469930767	2	4.07644
P27867	AVEAFETAK	1.345707657	1	1.949219
P27867	EVGADFTIQVAK	2.182807928	2	3.156653
P27867	GENLSLVVHGPGDIR	1.126008679	2	3.81485
P27867	HSADFCYK	1.222005377	2	2.906139
P27867	IGDFVVK	1.510951567	2	2.472324
P27867	LENYPIPELGPNDVLLK	0.953340496	2	4.88393
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.399877053	3	4.1149
P27867	MHSVGICGSDVHYWEHGR	1.547935286	2	6.045235
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0	1.346989525		
P27867	TLNVKPLVTHR	1.393307395	2	3.236574
P27867	VAIEPGVPR	1.870838509	1	2.180248
P27867	VLVCGAGPIGIVTLLVAK	1.723157361	3	5.74355
P27867	YCNTWPMAVSMLASK	0.871141239	2	3.375303
P27952	**RS2 40S ribosomal protein S2**	**1.309914514**	**9.9E-20**	**6**
P27952	AEDKEWIPVTK	2.016898052	2	3.392588
P27952	AFVAIGDYNGHVGLGVK	1.977590782	2	3.343497
P27952	GCTATLGNFAK	1.268299993	2	3.200577
P27952	GTGIVSAPVPK	1.326937253	2	2.4959
P27952	SLEEIYLFSLPIK	0.773450528	2	3.492726
P27952	TYSYLTPDLWK	1.432929619	2	3.267227

P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.220736413**	**1.11E-16**	**26**
P28037	ADPLGLEAEK	1.325795735	2	2.426627
P28037	ANATEFGLASGVFTR	1.348374167	2	4.857612
P28037	AVQMGMSSVFFNK	1.681034425	2	3.355463
P28037	DLGEAALNEYLR	0.885103557	2	3.479824
P28037	ECEVLPDDTVSTLYNR	2.911471065	2	4.36165
P28037	EESFGPIMIISR	1.390707033	2	3.075621
P28037	EGHEVVGVFTIPDKDGK	1.20470523	2	4.563906
P28037	GNDKVPGAWTEACGQK	1.312680114	2	3.830837
P28037	GQALPEVVAK	1.232298631	2	2.966491
P28037	GSASSDLELTEAELATAEAVR	1.050504972	2	6.311581
P28037	GVVNILPGSGSLVGQR	1.200081688	2	4.82736
P28037	IGFTGSTEVGK	1.162219548	2	2.787187
P28037	ILPNVPEVEDSTDFFK	2.003743691	2	3.590592
P28037	INWDQPAEAIHNWIR	1.462213089	2	4.250182
P28037	IQGATIPINQARPNR	1.293907504	2	2.345448
P28037	KEGHEVVGVFTIPDKDGK	1.406144513	3	4.188428
P28037	KIGFTGSTEVGK	0.928747413	2	3.132167
P28037	KLVEYCQR	1.022920734	2	2.410924
P28037	LFVEESIHNQFVQK	1.281679354	2	4.457075
P28037	LIAEGTAPR	1.171912932	2	3.522048
P28037	LSDHPDVR	0.780389078	1	2.109669
P28037	NIQLEDGK	1.155432685	1	2.303102
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.075683886	3	4.414799
P28037	TDVAAPFGGFK	1.155314329	2	3.115859
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	1.79405401	3	5.273676
P28037	VVEEVEK	1.02047862	1	2.077307
P28064	**PSB8 Proteasome subunit beta type_8**	**1.01608292**	**0.920387**	**3**
P28064	ASAGSYIATIR	1.775728199	2	2.77245
P28064	KGPGLYYVDDNGTR	0.979314282	2	2.847317
P28064	QDLSPEEAYDLAR	1.178169014	2	3.1804
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.374457391**	**1.27E-11**	**10**
P28480	AFHNEAQVNPER	1.588949864	2	3.619452
P28480	FATEAAITILR	1.360421807	2	3.227144
P28480	HGGYENAVHSGALDD	1.273814496	2	3.344471
P28480	ICDDELILIK	1.363112955	2	3.193856
P28480	LLEVEHPAAK	1.500010117	2	2.775349
P28480	MLVDDIGDVTITNDGATILK	1.112275986	2	2.345243
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.390076161	2	4.937828
P28480	SQNVMAAASIANIVK	1.798556498	2	4.601695
P28480	SSLGPVGLDK	1.619767171	2	2.412212
P28480	YINENLIINTDELGR	1.102387565	2	4.566308
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**1.078562302**	**0.98808**	**5**
P28492	ATGLQTSDPR	0.981183288	2	2.796903
P28492	GTPHSHQPQHSDHDASNSGMLPR	0.960764199	3	3.731055
P28492	MVQESSSGGLLDR	1.048797202	2	3.62209
P28492	SNPDLWGVSLCTVDGQR	1.020057124	2	4.07981
P28492	TALHVAAAEGHIDVVK	1.32104012	3	3.587453
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**1.244166954**	**0.722157**	**2**
P28650	LDILDVLSEIK	1.524737976	2	3.200155
P28650	VVDLLATDADIVSR	1.235017768	2	2.470608
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.179126619**	**2.34E-13**	**19**
P29147	AVLVTGCDSGFGFSLAK	1.050176644	2	5.64348
P29147	EVAEVNLWGTVR	1.918222574	2	2.423464
P29147	FGVEAFSDCLR	1.475832946	2	3.669291

P29147	GFLVFAGCLLK	0.99642361	2	3.728299
P29147	KMWDELPEVVR	1.069436022	2	3.343125
P29147	KMWDELPEVVR+Oxidation(1	1.329674868		
P29147	MANPARSPYCITK+Oxidation(0	1.018170945		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.067378482	3	5.654841
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0	1.126198753		
P29147	MQVMTHFPGAISDK	0.676674625	2	4.829058
P29147	MQVMTHFPGAISDK+Oxidation(0	1.118993846		
P29147	MQVMTHFPGAISDK+Oxidation(3	1.118993846		
P29147	MWDELPEVVR	0.989711978	2	3.418539
P29147	MWDELPEVVR+Oxidation(0	1.105636962		
P29147	TIQLNVCNSEEVEK	0.908808004	2	4.334439
P29147	VSVVEPGNFIAATSLYSPER	1.117428855	2	5.999694
P29147	VVNISSMLGR	1.217827185	2	3.929763
P29147	YEMHPLGVK	1.274112976	1	2.550442
P29147	YEMHPLGVK+Oxidation(2	1.682581546		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.858019441**	**0.668706**	**9**
P29266	DLGLAQDSATSTK	1.243806303	2	3.744483
P29266	EAGEQVASSPADVAEK	0.723653021	2	4.98183
P29266	GSLLIDSSTIDPSVSK	1.59517194	2	5.07553
P29266	HGYPLILYDVFPDVCK	1.375446443	2	5.136118
P29266	KGSLLIDSSTIDPSVSK	0.863748556	2	4.085631
P29266	MGAVFMDAPVSGGVGAAR	1.066808095	2	5.321157
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0	1.436538296		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5	1.436538296		
P29266	TPILLGSVAHQIYR	1.043992094	3	3.849808
P29314	**RS9 40S ribosomal protein S9**	**1.315181141**	**6.66E-08**	**9**
P29314	IEDFLER	1.124709282	2	2.657478
P29314	IGVLDEGK	0.678447406	2	2.620249
P29314	KGQGGAGAGDDEEED	1.874743304	2	3.236123
P29314	KQVVNIPSFIVR	0.910924815	2	2.536729
P29314	LDYILGLK	1.409920056	2	3.042031
P29314	LFEGNALLR	1.504093725	2	3.001467
P29314	LIGEYGLR	1.647079926	2	2.562906
P29314	QVVNIPSFIVR	1.563045212	2	2.660387
P29314	SRLDQELK	1.298459422	3	3.495952
P29315	**RINI Ribonuclease inhibitor**	**1.187977808**	**0.001207**	**7**
P29315	ASLQELDLGSNK	1.732993851	2	2.43099
P29315	ELVLSNNDFHEAGIHTLCQGLK	1.234545301	3	3.506119
P29315	LDDCGLTEVR	1.124568114	2	3.149182
P29315	LENCGITSANCK	1.03822689	2	3.616455
P29315	LSLQNCSLTEAGCGVLPDVLR	1.217354242	2	3.149546
P29315	SAIQANPALTELSLR	1.399067432	2	4.435854
P29315	TNELGDAGVGLVLQGLQNPTCK	1.735457783	2	5.343365
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.160930334**	**8.78E-14**	**11**
P29410	AMVASGSELGK	1.22528375	2	3.112761
P29410	AMVASGSELGK+Oxidation(1	1.172684077		
P29410	AMVASGSELGKK	1.454156595	2	2.893778
P29410	AVLLGPPGAGK	1.078282306	2	2.600957
P29410	EAMKDDITGEPLIR	1.556004116	2	3.138767
P29410	LEAYHTQTTPLVEYYR	1.3044995	2	5.004831
P29410	LVSDEMVVELIEK	1.674042928	2	4.197601
P29410	NGFLLDGFPR	1.084794226	2	2.877662
P29410	NLETPSCK	0.812456392	2	2.330671
P29410	SYHEEFNPPK	0.919186611	3	3.447819

P29410	TRLEAYHTQTTPLVEYYR	1.14999534	3	3.526194
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**1.199095965**	**0.015064**	**6**
P29411	AYEAQTEPVLQYYQK	1.120435051	2	4.581332
P29411	GVLETFSGTETNK	1.021123184	2	2.874358
P29411	NLTQCSWLLDGFPR	1.537780621	2	3.827046
P29411	TVGIDDLTGEPLIQR	1.265069579	2	3.715079
P29411	VYNIEFNPPK	0.757109937	2	2.606701
P29411	VYQIDTVINLNVPFEVIK	1.314448347	2	3.295174
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**0.750895614**	**0.012956**	**2**
P29419	ELAEAEDVSIFK	0.728525736	2	3.432571
P29419	YSALILGMAYGAK	1.560826153	2	4.097771
P29457	**SERPH Serpin H1**	**1.213556656**	**0.638971**	**2**
P29457	GVVEVTHDLQK	1.191052134	2	3.152941
P29457	SALQSINEWASQTTDGK	1.577738531	2	2.513504
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.040175283**	**0.956498**	**4**
P30009	AEDGAAPSPSSETPK	1.106975026	2	3.658145
P30009	EAEAAEPEQPEQPEQPAAEEPR	0.546977374	2	3.92005
P30009	EAGEGAEAEGATADGAK	1.37480306	2	4.31611
P30009	GEAAAERPGEAAVASSPSK	1.023635637	2	4.565935
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.419788347**	**0.021537**	**3**
P30349	GSPMEISLPIALSK	1.12342008	2	3.052447
P30349	SLSNVIAHEISHSWTGNLVTNK	0.283266192	3	3.865724
P30349	SSALQWLTPEQTSGK	1.548691198	2	3.831389
P30427	**PLEC Plectin**	**1.083153537**	**0.013306**	**5**
P30427	LLEAAAQSSK	1.114056771	2	2.434876
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0	1.339199088		
P30427	SDQLTGLSLLPLSEK	2.28267101	2	2.511992
P30427	SKELAEQEAAR	0.874994922	2	2.920767
P30427	VLALPEPSPAAPTLR	1.360345561	2	2.981697
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.086673048**	**0.049166**	**7**
P30713	AQVHEYLGWHADNIR	1.086641652	2	4.922705
P30713	GQHLSEQFSQVNCLK	1.096584437	2	5.014446
P30713	NSMVLALQR	1.198667703	2	3.297612
P30713	TLPVPPPEAHASMMLR	1.474410348	2	2.593854
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	1.295760084	3	4.0839
P30713	VLGPLIGVQVPEEK	1.296182383	2	4.058301
P30713	YQVADHWYPADLQAR	1.327229828	2	4.66661
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.079536064**	**0.018635**	**2**
P30835	NEWGSLLEELVK	1.671337961	2	2.839077
P30835	VFANAPDSACVIGLR	0.46288211	2	2.562708
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.163134184**	**8.22E-05**	**9**
P30839	DILAAIAADLSK	2.553794719	2	3.054347
P30839	EKDILAAIAADLSK	1.197196124	2	4.266608
P30839	FDHILYTGNTAVGK	1.0334983	2	4.057884
P30839	HLTPVTLELGGK	1.405745564	3	3.426769
P30839	LQQLEALR	1.410393678	1	2.074491
P30839	NVEEAINFINDR	1.129870901	2	4.285296
P30839	VMQEEIFGPILPIVSVK	1.171737031	2	4.889335
P30839	VMQEEIFGPILPIVSVK+Oxidation(1	1.362970157		
P30839	YIAPTILTDVDPNSK	1.214977373	2	4.073834
P30904	**MIF Macrophage migration inhibitory factor**	**1.745126077**	**9.9E-20**	**2**
P30904	LHISPDR	0.709928167	1	2.055697
P30904	LLCGLLSDR	1.845541823	2	2.929551
P30999	**CTND1 Catenin delta_1**	**1.519260632**	**0.019552**	**3**
P30999	GYELLFQPEVVR	1.370891987	2	2.590799

P30999	HIEWESVLTNTAGCLR	1.522617802	2	2.803481
P30999	SLDNNYSTLNER	2.05200996	2	2.465525
P31000	**VIME Vimentin**	**1.043780034**	**0.965711**	**17**
P31000	DGQVINETSQHHDDLE	0.909590013	2	3.040758
P31000	ETNLESLPLVDTHSK	1.009169386	2	2.376868
P31000	FADLSEAANR	1.215688626	2	2.89052
P31000	ILLAELEQLK	1.620492294	2	2.872403
P31000	KLLEGEESR	1.214951303	2	3.06194
P31000	KVESLQEEIAFLK	1.452385408	2	3.966615
P31000	KVESLQEEIAFLKK	1.02766168	2	2.334838
P31000	LGDLYEEEMR	0.590651606	2	2.786717
P31000	LLEGEESR	1.141796701	2	2.801466
P31000	LQDEIQNMKEEMAR	1.127149441	2	3.662861
P31000	NLQEAEEWYK	1.121663383	2	2.886325
P31000	QDVDNASLAR	1.097339241	2	2.965332
P31000	QVQSLTCEVDALK	1.062686287	2	3.300431
P31000	RQVDQLTNDK	0.832309998	2	3.023922
P31000	SLYSSSPGGAYVTR	1.118941791	2	2.862483
P31000	TNEKVELQELNDR	0.895811485	2	3.346155
P31000	VELQELNDR	0.829420792	2	2.994569
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**1.235637642**	**9.9E-20**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.22193761	2	5.95288
P31044	LYTLVLTDPDAPSR	1.554369947	2	4.930282
P31044	VDYGGVTVDELGK	1.264199159	2	4.822209
P31044	VLTPTQVMNRPSSISWDGLDPGK	1.540921748	3	4.781842
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.224673372	2	5.125744
P31044	YVWLVYEQEQPLNCDEPILSNK	1.541758745	2	5.613725
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.209475717**	**8.76E-05**	**18**
P31210	DELLTSLGK	1.123632176	2	2.795493
P31210	DIEALNK	1.558493442	1	2.558228
P31210	EEMKDIEALNK	2.219704013	2	3.317614
P31210	ENFQIFDFSLTK	1.441438406	2	3.345633
P31210	HIDGAYVYR	1.46561454	2	2.715158
P31210	IKENFQIFDFSLTK	1.707401365	2	4.353075
P31210	LWSTDHDPEMVRPALER	1.198654514	2	2.492904
P31210	NEHEVGEAIR	1.186815083	1	2.907996
P31210	NPLWVNVSSPPLLK	1.364897684	2	4.373562
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.737540271	3	4.9156
P31210	QLEVILNKPGLK	0.658820394	2	3.415557
P31210	REEIFYCGK	1.361106543	2	3.148578
P31210	RQLEVILNKPGLK	0.85587422	3	4.266369
P31210	SNLCATWEALEACK	1.567203711	2	4.406641
P31210	SNLCATWEALEACKDAGLVK	1.205493953	2	5.079002
P31210	TAIDEGYR	0.891630067	2	2.573744
P31210	TQAQIVLR	1.617621046	2	3.026363
P31210	YKPVTNQVECHPYFTQTK	1.208983691	2	5.722028
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.351820023**	**0.000114**	**2**
P31230	GAEADQIIEYLK	2.068847575	2	2.986363
P31230	TVVSGLVNHVPLEQMQNR	1.191986236	3	3.534745
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.192042152**	**0.158787**	**6**
P31399	ANVDKPGLVDDFK	1.188836105	2	3.801852
P31399	IPVPEDKYTALVDAEEKEDVK	1.071136565	3	3.32943
P31399	NCAQFVTGSQAR	1.19105261	2	4.268908
P31399	NMIPFDQMTIDDLNEVFPETK	1.793589072	2	5.454863
P31399	SWNETFHTR	1.30755061	2	2.759272

P31399	YTALVDAEEKEDVK	0.949748083	2	3.776985
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**0.943456382**	**0.657758**	**5**
P32089	FIHDQTSSNPK	1.083991063	1	3.452902
P32089	GLSSLLYGSIPK	1.538868952	2	3.395151
P32089	NTLDCGVQILK	0.933651346	2	2.396292
P32089	SHGVLGLYR	1.099074821	1	2.026277
P32089	TQLQLDER	1.340452512	2	2.47254
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.05037293**	**0.529111**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	1.162140173	3	4.558847
P32198	GDTNPNIPKPTR	1.443606058	2	2.402919
P32198	MTALAQDFAVNLGPK	1.049222045	2	4.182351
P32198	SCTMESCNFVQAMMDPK	1.342405262	2	2.772666
P32198	TSPDAFIQLALQLAHYK	1.241012142	2	3.49923
P32198	YLESVRPLMK	1.493874304	2	2.323328
P32232	**CBS Cystathionine beta_synthase**	**1.203294037**	**9.9E-20**	**9**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.668499247	3	5.954854
P32232	ALGAEIVR	1.141944919	1	2.04501
P32232	CIIVMPEK	1.487115219	2	2.517678
P32232	FDSPESHVGVAWR	0.962194805	2	3.501314
P32232	NASNPLAHYDDTAEEILQQCDGK	1.494373489	2	5.661582
P32232	SNDDDSFAFAR	1.15992905	2	3.300774
P32232	VDMLVASAGTGGTITGIAR	1.864158557	2	4.629823
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.807345801	3	4.235768
P32232	VRPSDEVCK	0.50937382	3	3.754385
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.044671371**	**0.168024**	**11**
P32551	AVAFQNPQTR	1.045957774	2	3.351161
P32551	AVAQGNLSSADVQAAK	1.199191129	2	5.3487
P32551	GNNTTSLLSQSVAK	1.217258892	2	4.159082
P32551	IIENLHDVAYK	1.579206522	2	3.837723
P32551	ITSEELHYFVQNHFTSAR	1.341239594	3	4.042922
P32551	NALANPLYCPDYR	2.416420269	2	3.744445
P32551	RGNNTTSLLSQSVAK	0.921798044	2	3.304866
P32551	RWEVAALR	1.1256529	2	2.730141
P32551	SMTASGNLGHTPFLDEL	1.103914199	2	3.380163
P32551	TSAPGGVPLQPQELEFTK	1.145688897	2	4.042141
P32551	YENYNYLGTSHLLR	1.085544268	2	4.429471
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.381411391**	**9.9E-20**	**20**
P32755	AFEEEQALR	1.319334306	2	3.347206
P32755	DIAFEVEDCEHIVQK	1.531749643	2	4.081878
P32755	ENMDVLEELK	1.798797205	2	3.052785
P32755	EVVSHVIK	1.095036491	2	2.325745
P32755	FAVLQTYGDTTHTLVEK	1.42239316	2	5.256718
P32755	FLHFHSVTFWVGNAK	1.1252421	3	3.735149
P32755	FLPGFEAPTYK	1.396218947	2	2.707504
P32755	FWSVDDTQVHTEYSSLR	0.901216286	2	5.840824
P32755	GMEFLAVPSSYYR	1.810941884	2	3.281549
P32755	GNLTDLETNGVR	1.32387174	2	3.832973
P32755	HNHQGFGAGNFNSLFK	1.066887643	3	4.918463
P32755	ILVDYDEK	1.353539106	2	2.328653
P32755	IVFVLCSALNPWNK	1.407520175	2	2.968987
P32755	IVREPWVEEDKFGK	1.852437553	3	4.969857
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.753578405	3	7.342283
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK+Oxidation(20	2.039960957		

P32755	MGFEPLAYK	1.205697033	2	2.648959
P32755	SIVVANYEESIK	1.051818113	2	4.232787
P32755	SQIQEYVDYNGGAGVQHIALR	1.161433267	2	5.814981
P32755	TEDIITTIR	1.144613786	2	3.30782
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.120437435**	**0.50773**	**2**
P33124	ALRPTIFPVVPR	1.276572572	2	3.023458
P33124	IENIYIR	1.085141825	2	2.80915
P33273	**CP255 Cytochrome P450 2C55**	**1.585609198**	**0.003547**	**2**
P33273	FDYKDENFLNLMEK	1.588897361	3	4.884644
P33273	NFAEIK	1.494497374	1	1.909209
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.12584016**	**3.77E-15**	**26**
P34058	ADLINNLGTIAK	1.018906285	2	4.087645
P34058	EDQTEYLEER	1.827270322	2	3.559829
P34058	EGLELPEDEEEK	0.996612439	2	2.512519
P34058	EGLELPEDEEEKK	1.387490986	2	2.562706
P34058	EGLELPEDEEEKKK	1.358455602	2	3.153703
P34058	ELISNASDALDK	1.174304016	2	3.605897
P34058	FYEAFSK	1.383003919	1	1.959222
P34058	GVVDSEDLPLNISR	1.356115972	2	4.806192
P34058	HFSVEGQLEFR	1.24374686	2	2.66939
P34058	HLEINPDHPIVETLR	1.076209556	2	4.584974
P34058	HSQFIGYPITLYLEK	1.956882749	2	3.666264
P34058	IDIIPNPQER	1.07019832	2	3.057075
P34058	KHLEINPDHPIVETLR	1.395035543	2	4.836435
P34058	LGIHEDSTNR	1.358586732	2	2.90844
P34058	NPDDITQEEYGEFYK	0.848393475	2	4.963541
P34058	RAPFDLFENK	1.318144309	2	3.040661
P34058	RAPFDLFENKK	0.827705786	2	2.525829
P34058	SIYYITGESK	0.899595379	2	3.194491
P34058	SLTNDWEDHLAVK	1.123988593	2	4.327127
P34058	TLTLVDTGIGMTK	1.321357909	2	4.279113
P34058	TLTLVDTGIGMTK+Oxidation(10	1.877561295		
P34058	VILHLKEDQTEYLEER	1.368615311	3	4.045892
P34058	YESLTDPSK	1.107236793	1	2.709481
P34058	YESLTDPSKLDSGK	1.212555238	2	3.88405
P34058	YHTSQSGDEMTSLSEYVSR	1.312369045	2	5.489552
P34058	YIDQEELNK	2.732173077	2	3.486965
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.145828346**	**0.309021**	**7**
P34064	AIGSASEGAQSSLQEVYHK	1.105475516	2	4.514455
P34064	EELEEVIKDI	1.370697711	2	2.547695
P34064	GVNTFSPEGR	1.208668875	2	3.089472
P34064	ITSPLMEPSSIEK	0.86661783	2	2.611329
P34064	LNATNIELATVQPGQNFHMFTK	1.628566151	3	3.448226
P34064	SSLIILK	2.333135745	2	2.397651
P34064	STTLKEAIKSSLIILK	0.997398265	2	2.315405
P34067	**PSB4 Proteasome subunit beta type_4**	**1.174056358**	**0.466021**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.590429071	2	3.133276
P34067	TQNPMVTGTSVLGVK	1.186771339	2	3.356557
P34067	VNDSTMLGASGDYADFQYLK	1.174049563	2	4.494485
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.184464334**	**0.719239**	**2**
P35171	GGTSDALLYR	1.041665469	2	3.415427
P35171	LFQEDNGMPVHLK	1.2132571	2	4.385578
P35213	**1433B 14_3_3 protein beta/alpha**	**1.33579555**	**2.48E-07**	**7**
P35213	AVTEQGHELSNEER	0.872443712	2	4.489092
P35213	EKIEAELQDICSDVLELLDK	1.905293822	3	4.985651
P35213	QTTVSNSQQAYQEAFEISK	1.115822597	2	5.463017

P35213	TAFDEAIAELDTLNEESYK	1.25941324	2	4.81657
P35213	YDDMAAAMK	3.902389276	2	3.092565
P35213	YLILNATHAESK	1.743422103	2	3.585578
P35213	YLSEVASGDNK	0.945573736	2	3.041293
P35278	**RAB5C Ras_related protein Rab_5C**	**0.938249798**	**0.878745**	**4**
P35278	FEIWDTAGQER	0.823677495	2	3.163441
P35278	GVDLQESNPASR	1.116240567	2	2.707087
P35278	LVLLGESAVGK	1.371144957	2	2.749998
P35278	NEPQNAAGAPGR	0.936275464	2	2.996528
P35427	**RL13A 60S ribosomal protein L13a**	**1.27149951**	**0.165237**	**2**
P35427	CEGINISGNFYR	1.326750564	2	3.141887
P35427	YQAVTATLEEK	1.239860479	2	3.142895
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**1.152465645**	**0.990307**	**2**
P35434	AQSELSGAADEAAR	1.193776714	2	4.666125
P35434	IEANEALVK	1.116092918	2	2.84138
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.267441325**	**7.42E-08**	**7**
P35435	GLCGAIHSSVAK	1.295304777	2	3.691612
P35435	HLIIGVSSDR	1.267435436	2	3.066098
P35435	NASDMIDK	1.272330651	2	2.350382
P35435	NDMAALTAAGK	1.449806713	2	3.944636
P35435	NDMAALTAAGK+Oxidation(2	1.960836429		
P35435	THSDQFLVSFK	0.818905583	1	3.035378
P35435	VYGTGSLALYEK	1.892039836	2	3.100615
P35559	**IDE Insulin_degrading enzyme**	**0.980499781**	**0.555663**	**4**
P35559	AIEDMTEEAFQK	1.211221579	2	3.137216
P35559	DREVNAVDSEHEK	1.500532479	3	3.571326
P35559	SNPGHYLGHLIGHEGPGSLLSELK	0.383963141	3	3.30114
P35559	YTLETRPNQEGIDVR	1.124513282	2	2.530306
P35565	**CALX Calnexin**	**1.323196844**	**4.86E-09**	**11**
P35565	AEEDEILNR	0.941922261	2	2.694638
P35565	EIEDPEDRKPEDWDERPK	2.146513474	3	3.331678
P35565	GSLSGWILSK	2.447484407	2	2.50193
P35565	KIPNPDFFEDLEPFR	1.298956879	3	4.295339
P35565	NKGDEEEEEEKLEEK	1.220166099	3	5.054557
P35565	TDAPQPDVK	1.402045736	2	2.387764
P35565	TDAPQPDVKDEEGKEEEK	0.814746582	3	4.364666
P35565	TSELNLDQFHDK	1.355072835	2	3.690699
P35565	VVDDWANDGWGLK	1.367771166	2	4.230627
P35565	VVDDWANDGWGLKK	0.974360993	2	2.804354
P35565	WEVDEMKETK	1.34973024	2	2.819301
P35571	**GPDM Glycerol_3_phosphate dehydrogenase_ mitochondrial**	**1.259529158**	**0.294591**	**2**
P35571	AITNLDVEQYR	0.464079425	2	2.715509
P35571	KQEELETATR	1.274085197	2	2.33559
P35704	**PRDX2 Peroxiredoxin_2**	**1.17466764**	**0.172065**	**5**
P35704	EGGLGPLNIPLLADVTK	1.200090832	2	3.476043
P35704	KEGGLGPLNIPLLADVTK	1.306301148	2	4.860938
P35704	NDEGIAYR	1.465295816	1	1.959707
P35704	QITVNDLPVGR	1.05507617	2	3.034123
P35704	SLSQNYGVLK	0.998960579	2	2.47037
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.994940244**	**0.782841**	**5**
P35738	AAVEQVPVEPYK	0.849577697	2	2.429388
P35738	GLLLSCIEDKNPCIFFEPK	1.824750914	2	3.666654
P35738	MNLFQSITSALDNSLAK	1.171504527	2	3.592146
P35738	SGDLFNCGSLTIR	0.970882917	2	3.017777

P35738	VCGYDTPFPHIFEPFYIPDK	1.156626696	3	3.49018
P35815	**PPM1B Protein phosphatase 1B**	**1.404184439**	**0.277679**	**2**
P35815	IQNAGGSVMIQR	1.41442597	2	2.823351
P35815	SGFALEPSVENVK	1.094853297	2	3.627459
P36201	**CRIP2 Cysteine_rich protein 2**	**0.943107315**	**0.74273**	**3**
P36201	ASSVTTFTGEPNMCPR	0.568144816	2	3.680811
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	0.943927386	3	6.475083
P36201	GVNTGAVGSYIYDKDPEGTVQP	0.885596486	2	4.318913
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**1.106879813**	**0.11369**	**11**
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.629833351	3	3.610614
P36365	ASLYNSVVSNSSK	0.824775088	2	2.922509
P36365	CCLEEGLEPTCFER	0.69946062	2	4.281052
P36365	FTEHVEEGR	1.201582417	2	3.024117
P36365	HSGFGLCYCK	0.798727045	2	3.246991
P36365	NLLPTPVVSWLISK	1.354382436	2	2.491857
P36365	SCDLGGLWR	1.09055306	2	2.769229
P36365	TQLREPVLNDELPGR	1.06573876	3	4.579488
P36365	VAIVGAGVSGLASIK	2.16689187	2	2.823316
P36365	VEDGQASLYK	1.072664436	2	3.465876
P36365	VLVVGMGNSGTDIAVEASHLAK	1.346937173	2	4.559155
P36506	**MP2K2 Dual specificity mitogen_activated protein kinase kinase 2**	**2.03011485**	**0.153072**	**2**
P36506	ISELGAGNGGVVTK	2.123959296	2	2.360976
P36506	KLEELDLDEQQR	1.939049916	2	3.039693
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**0.95224601**	**0.000487**	**8**
P36511	ANIIAWALAQIPQK	1.942116399	3	5.487491
P36511	FVNVWTYELPR	1.189936026	2	3.6615
P36511	FVTFPTSFSSHDLENFFTR	1.426419402	2	4.449045
P36511	GHEVTVLRPSAFVFLDPK	1.164903033	3	3.968846
P36511	IILEELVQK	1.432385096	2	3.534591
P36511	NAMWLSTIHHDQPTKPLDR	1.56293494	3	3.418586
P36511	SDLLNALEEVIDNPFYK	0.935797788	3	5.337359
P36511	TLGRPTTLAEIMGK	1.311039387	2	3.103503
P36536	**SAR1A GTP_binding protein SAR1a**	**1.72371663**	**0.179488**	**2**
P36536	IDRTDAISEEK	1.938100313	2	2.491702
P36536	VELNALMTDETISNVPILILGNK	1.639229821	3	5.669423
P36953	**AFAM Afamin**	**1.078432147**	**0.777425**	**2**
P36953	FTDSENVCQER	0.975309392	2	2.997247
P36953	SLAMVQQECK	1.435915275	2	2.750564
P36972	**APT Adenine phosphoribosyltransferase**	**1.266386408**	**0.000207**	**2**
P36972	IDYIAGLDSR	1.054817037	2	3.043373
P36972	SFPDFPIPGVLFR	1.267105371	2	3.250291
P37397	**CNN3 Calponin_3**	**1.160846995**	**0.685204**	**5**
P37397	AGQSVIGLQMGTNK	1.074648701	2	3.374611
P37397	LTLQPVDNSTISLQMGTNK	0.825752346	2	2.953562
P37397	MQTDKPFDQTTISLQMGTNK	1.278308196	3	3.552221
P37397	VNESSLNWPQLENIGNFIK	1.168991035	2	3.15147
P37397	YDQQAEEDLR	1.154593966	2	3.154138
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.27509694**	**0.403864**	**8**
P38650	DFPLNDLLSATELDKIR	1.520419712	2	2.387416
P38650	ILDDDTIITTLENLK	1.040134656	2	2.506484
P38650	QLQNISQAAAAGGAK	0.946199354	2	3.37664
P38650	VLLTTQGVDMISK	1.41007091	2	2.663003
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	1.315261671	3	5.437798
P38650	VQGLTVEQAEAVAR	1.20142059	2	3.279849
P38650	VQVALEELQDLK	1.316978967	2	3.027358

P38650	VTDFGDKVEDPTFLNQLQSGVNR	1.605844365	3	4.162052
P38652	**PGM1 Phosphoglucomutase_1**	**1.261502899**	**0.00188**	**17**
P38652	ADNFEYSDPVDGSISK	0.969144945	2	4.824588
P38652	AIGGIILTASHNPGGPNGDFGIK	1.214551593	2	5.758801
P38652	FFGNLMDASK	1.40169764	2	2.516388
P38652	FNISNGGPAPEAITDK	1.067752541	2	4.302326
P38652	INQDPQVMLAPLISIALK	1.22271221	3	4.606595
P38652	KQRVEDILK	1.442305303	1	2.026721
P38652	LSGTGSAGATIR	1.806662425	2	3.480213
P38652	LVIGQNGILSTPAVSCIIR	1.72307067	2	4.081246
P38652	NIFDFNALK	1.152666433	2	2.923143
P38652	QEATLVVGGDGR	1.286976573	2	3.200179
P38652	QQFDLENK	0.744880988	1	2.128239
P38652	SGEHDFGAAFDGDGDR	0.861732716	2	4.459804
P38652	SGEHDFGAAFDGDGDRNMILGK	1.480483684	3	3.760799
P38652	TIEEYAICPDLK	1.363412408	2	4.431875
P38652	TQAYPDQKPGTSGLR	0.751528623	2	3.488104
P38652	VFQGNANYAENFIQSIVSTVEPALR	1.146740605		
P38652	YDYEEVEAEGANK	0.850991135	2	5.181049
P38656	**LA Lupus La protein homolog**	**1.269390164**	**0.014824**	**2**
P38656	ITDDQQESLNK	1.369389895	2	4.193151
P38656	LDEGWVPLETMIK	1.680609349	2	2.990392
P38659	**PDIA4 Protein disulfide_isomerase A4**	**0.969046518**	**0.23206**	**22**
P38659	DLGLSESGEDVNAAILDESGKK	1.41553176	2	5.150129
P38659	DNDPPIAVAK	0.907823772	2	2.400485
P38659	EVSQPDWTPPPEVTLTLTK	0.863609238	2	3.552126
P38659	FDVSGYPTIK	0.988659521	2	3.490073
P38659	FDVSGYPTLK	0.988659521	2	3.490073
P38659	FHHTFSTEIAK	1.057427935	3	3.501489
P38659	FIDEHATK	0.886808269	2	2.465545
P38659	FIDEHATKR	0.400643859	2	2.551716
P38659	GQAVDYDGSR	0.788927231	2	2.66653
P38659	GRPFDYNGPR	1.282605484	2	2.876454
P38659	IDATSASMLASK	1.087009706	2	3.975591
P38659	IDATSASMLASK+Oxidation(7	1.103606524		
P38659	KGQAVDYDGSR	2.216664869	2	2.930255
P38659	MDATANDITNDR	0.940697487	2	3.955441
P38659	MHVMDVQGSTEASAIK	1.359146802	2	4.622877
P38659	MHVMDVQGSTEASAIKDYVVK	1.029180991	3	4.599572
P38659	RFDVSGYPTLK	1.065462954	2	3.288025
P38659	RSPPIPLAK	2.425462004	2	2.406114
P38659	TFDAIVMDPK	0.895225695	2	3.53451
P38659	VDATEQTDLAK	1.188430522	2	4.126925
P38659	VEGFPTIYFAPSGDK	1.427777243	2	3.446272
P38659	YGIVDYMVEQSGPPSK	0.843793365	2	5.10871
P38718	**BR44 Brain protein 44**	**1.180527475**	**0.662507**	**2**
P38718	LRPLYNHPAGPR	1.381238848	2	2.829848
P38718	VELLLPK	0.765122701	1	2.221431
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**1.252472066**	**0.006608**	**5**
P38918	EEHFNGIALVEK	1.440725152	2	2.534561
P38918	FYAFNPLAGGLLTGR	2.02768225	2	4.631714
P38918	MDVTSSSASVR	1.261874597	2	3.586335
P38918	RMDVTSSSASVR	1.555890356	2	3.853636
P38918	TTYGPTAPSMISAAVR	1.342536901	2	3.96068
P38983	**RSSA 40S ribosomal protein SA**	**1.39253794**	**1.62E-13**	**8**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.543974927	3	5.862941

P38983	AIVAIENPADVSVISSR	1.227219623	2	4.808642
P38983	FAAATGATPIAGR	0.328256301	2	3.160638
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.414445612	3	3.623837
P38983	FTPGTFTNQIQAAFR	1.550217127	2	4.635994
P38983	KSDGIYIINLK	2.063078046	2	3.522424
P38983	SDGIYIINLK	1.357761292	2	3.021649
P38983	YVDIAIPCNNK	1.039489222	2	3.550746
P39032	**RL36 60S ribosomal protein L36**	**1.97697289**	**0.50622**	**2**
P39032	EELSNVLAAMR	1.413095124	2	2.405522
P39032	KREELSNVLAAMR	1.993021371	3	3.509144
P39052	**DYN2 Dynamin_2**	**1.241485091**	**0.440646**	**2**
P39052	ESSLILAVTPANMDLANSDALK	1.571597804	2	2.367339
P39052	NLVDSYVAIINK	1.213322602	2	3.119872
P40112	**PSB3 Proteasome subunit beta type_3**	**1.423310778**	**2.6E-10**	**2**
P40112	FGIQAQMVTTDFQK	2.341851176	2	3.433114
P40112	FGPYYTEPVIAGLDPK	1.410406546	2	3.095845
P40307	**PSB2 Proteasome subunit beta type_2**	**1.033698106**	**0.002239**	**3**
P40307	FILNLPTFSVR	1.972301499	2	3.282346
P40307	NGYELSPTAAANFTR	1.267814787	2	4.02458
P40307	VIDKDGIHNLENITFTK	0.900348102	2	4.03379
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.689425145**	**9.9E-20**	**4**
P41034	AECPELSADLHPR	2.026163741	2	2.987019
P41034	AQEEGVPETPQPLTDAFLLR	2.056976363	2	3.712788
P41034	QLNEQPDHSPLVQPGLAELR	1.534998322	3	4.054836
P41034	VSLITSELIVQEVETQR	1.615849702	2	2.969604
P41123	**RL13 60S ribosomal protein L13**	**1.222470719**	**3.93E-06**	**3**
P41123	LATQLTGPVMPIR	2.411611952	2	3.122726
P41123	STESLQANVQR	1.221095121	2	3.889652
P41123	VDTWFNQPAR	1.209014522	2	3.46971
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.025967115**	**0.976349**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.933285134	2	4.248387
P41498	IELLGSYDPQK	1.030687463	2	3.221006
P41498	LVTDENVSDNWR	0.863655827	2	3.761487
P41542	**USO1 General vesicular transport factor p115**	**1.157571425**	**1.47E-05**	**14**
P41542	AWFEVGDENPGWSAQK	1.558298776	2	4.666094
P41542	CQNEQLQTAVTQQASQIQQHK	1.043908102	3	5.305961
P41542	EQDDLLVLLADQDQK	1.357215532	2	2.537033
P41542	GVMGGQSAGPQHTEAETIQK	1.305045188	2	4.358958
P41542	IVAFENAFER	1.221039616	2	3.054385
P41542	LQTENSELQQR	1.26719106	2	3.13897
P41542	LREEIEELR	1.214357449	2	2.72273
P41542	NNNSNQNFFK	0.773496176	2	2.716114
P41542	QLGPPVQQIILVSPMGVSK	2.109830473	2	4.011497
P41542	SHQVLLQSQLAEK	0.624868207	2	2.951881
P41542	SQLCSQSLEITR	1.307793193	2	3.365236
P41542	SVPVEGESELVTAAK	0.637631724	2	4.154253
P41542	TLEQHDNIVTHYK	1.074880107	2	3.904003
P41542	VLVSPTNPPGATSSCQK	1.331246463	2	3.920532
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**1.109956023**	**9.9E-20**	**20**
P41562	ATDFVVPGPGK	1.071131729	2	3.632432
P41562	CATITPDEK	1.125088086	2	2.720041
P41562	DIFQEIYDK	0.776710869	1	2.397274
P41562	DLAACIK	0.521939893	1	1.908251
P41562	FKDIFQEIYDK	1.281392272	3	4.394885
P41562	GQETSTNPIASIFAWSR	1.428264555	2	4.793027

P41562	IHGGSVVEMQGDEMTR	1.936854076	2	5.303621
P41562	KIHGGSVVEMQGDEMTR	1.204510807	2	3.690441
P41562	LIDDMVAQAMK	0.921275457	2	4.459492
P41562	LIDDMVAQAMK+Oxidation(4	1.563386437		
P41562	LIDDMVAQAMK+Oxidation(9	0.900300468		
P41562	LILPYVELDLHSYDLGIENR	2.297401005	2	4.869486
P41562	LVTGWVKPIIIGR	1.722882907	2	3.248983
P41562	SDYLNTFEFMDK	1.755531975	2	4.460377
P41562	SDYLNTFEFMDK+Oxidation(9	4.091257669		
P41562	SEGGFIWACK	1.080418297	2	3.305981
P41562	SIEDFAHSSFQMALSK	1.446460096	2	5.084091
P41562	TVEAEAAHGTVTR	1.228588708	2	3.818926
P41562	VEITYTPK	0.973324691	2	2.454478
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.700578971	3	3.824423
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.179932955**	**0.377529**	**4**
P42123	DYSVTANSK	1.317046663	2	2.545432
P42123	IVADKDYSVTANSK	2.458106782	2	3.626652
P42123	SLADELALVDVLEDK	0.919967216	2	3.633703
P42123	VIGSGCNLDSAR	1.16382198	2	3.807324
P42228	**STAT4 Signal transducer and activator of transcription 4**	**1.045434718**	**0.615585**	**2**
P42228	FHSVEPYNK	1.228767988	1	1.918164
P42228	GDKGYVPSVFIPISTIR	0.926833703	2	2.738825
P42667	**SC11A Signal peptidase complex catalytic subunit SEC11A**	**1.162906221**	**0.041032**	**3**
P42667	GDLLFLTNR	1.411291799	2	2.437879
P42667	MLSLDFLDDVR	0.959559227	2	3.344279
P42667	VGEIVVFR	1.253651156	2	3.270651
P42676	**NEUL Neurolysin_ mitochondrial**	**1.066341975**	**0.01296**	**3**
P42676	AELGALPDDFIDSLEK	1.036273567	2	3.32762
P42676	NLILKPGGSLDGMDMLQNFLQR	1.415435805	3	4.143296
P42676	NLNEDDTSLVFSK	1.06785004	2	3.387716
P42930	**HSPB1 Heat shock protein beta_1**	**1.366693451**	**0.705418**	**2**
P42930	AQIGGPESEQSGAK	1.275377512	2	3.393374
P42930	VSLDVNHFAPEELTVK	2.676923244	2	2.581209
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.192213908**	**0.002613**	**10**
P42932	AIAGTGANVIVTGGK	1.482631216	2	2.752374
P42932	AVDDGVNTFK	1.02303088	2	2.510876
P42932	ELEVQHPAAK	1.659905227	2	2.857693
P42932	GEENLMDAQVK	0.926229289	2	3.587769
P42932	GSTDNLMDDIER	1.600580053	2	2.76197
P42932	HEKEDGAISTIVLR	6.517346928	2	2.923689
P42932	HFSGLEEAVYR	1.332140818	2	2.657388
P42932	NVGLDIEAEVPAVK	1.455581137	2	4.01113
P42932	QITSYGETCPGLEQYAIK	1.160129221	2	4.871949
P42932	TAEELMNFSK	1.14784935	2	2.587728
P43244	**MATR3 Matrin_3**	**0.965055113**	**0.004155**	**5**
P43244	ITPENLPQILLQLK	1.630688191	2	3.428613
P43244	NTHCSSLPHYQK	1.232179839	2	2.316619
P43244	TEEGPTLSYGR	1.316971392	2	2.558978
P43244	TENPAEGKEQEEK	0.936725937	2	3.382387
P43244	YQLLQLVEPFGVISNHLILNK	1.289336766	3	3.760192
P43274	**H14 Histone H1.4**	**1.191190429**	**0.971828**	**4**
P43274	ALAAAGYDVEK	1.219559882	2	3.861321
P43274	ALAAAGYDVEKNNSR	0.736391101	2	3.29513
P43274	SGVSLAALK	0.947464223	2	2.991817
P43274	SGVSLAALKK	0.95249938	2	2.68434

P43278	**H10 Histone H1.0**	**1.057889912**	**0.000577**	**2**
P43278	VGENADSQIK	0.921378558	2	3.439698
P43278	YSDMIVAAIQAEK	1.365986629	2	4.472862
P43883	**PLIN2 Perilipin_2**	**1.260607519**	**0.324904**	**2**
P43883	DSVASTVSGVVDK	1.287091354	2	2.35521
P43883	LEPQIAVANTYACK	0.257516695	2	3.944712
P45591	**COF2 Cofilin_2**	**1.37480907**	**0.10027**	**2**
P45591	HEWQVNGLDDIKDR	1.626957244	3	4.854836
P45591	QILVGDIGDTVEDPYTSFVK	1.355620714	2	3.860456
P45592	**COF1 Cofilin_1**	**1.274951468**	**8.88E-06**	**5**
P45592	EILVGDVGQTVDDPYTTFVK	1.242829012	2	5.110716
P45592	HELQANCYEEVK	1.061421382	2	3.830191
P45592	HELQANCYEEVKDR	1.559909642	3	5.627933
P45592	MLPDKDCR	1.452580394	2	2.336674
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.413225909	3	4.803088
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.141232369**	**0.003903**	**4**
P45878	GWDQGLLGMCEGEK	0.958521793	2	4.301601
P45878	KGDVLHMHYTGK	0.577251154	2	3.875701
P45878	KLVIPSELGYGER	1.617460468	2	2.749429
P45878	LVIPSELGYGER	1.478817354	2	2.794266
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.151498077**	**2.73E-05**	**17**
P45953	AMVENGGLVTSNPLR	0.807909224	2	4.051934
P45953	AMVENGGLVTSNPLRV	1.588791507	2	4.196594
P45953	ASNTSEVYFDGVK	1.419194569	2	3.605339
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.875444012	3	5.121884
P45953	ENMASLQSNPQQQELFR	1.41259735	2	4.249867
P45953	FFEEVNDPAK	0.888272288	2	3.025122
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.357485658	3	5.583981
P45953	GIVNEQFLLQR	1.112518851	2	3.141248
P45953	IFEGTNDILR	1.860228864	2	3.146416
P45953	NDSLEKVEEDTLQGLK	1.325133302	2	3.640109
P45953	NPLGNVGLLIGEASK	1.149868591	2	3.707093
P45953	SFGGVTHGLPEK	1.412767641	2	2.606049
P45953	SFGGVTHGLPEKK	1.00307257	2	2.957566
P45953	SGELAVQALEQFATVVEAK	1.336770604	3	4.121156
P45953	SLSEGYPTAQHEK	1.332434375	2	3.429792
P45953	TGIGSGLSLSGIVHPELSR	1.214654604	3	4.606817
P45953	VEEDTLQGLK	0.698142467	2	2.769583
P46061	**RAGP1 Ran GTPase_activating protein 1**	**1.632632807**	**0.005179**	**2**
P46061	TAVLDAIDALMK	1.551727987	2	3.176596
P46061	VINLNDNTFTEK	1.665008237	2	2.512266
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.168845825**	**8.83E-05**	**4**
P46418	AILNYIATK	0.567546936	2	3.291475
P46418	SDGSLMFEQVPMVEIDGMK	1.355469133	2	4.38341
P46418	SHGQDYLVGNK	1.515734882	2	3.637712
P46418	VSNLPTVK	1.151555987	2	2.768827
P46425	**GSTP2 Glutathione S_transferase P 2**	**1.071575894**	**0.024477**	**3**
P46425	ALPGHLKPFETLLSQNQGGK	0.84371464	2	4.162653
P46425	FEDGDLTLYQSNAILR	1.083732342	2	4.533219
P46425	MLLADQGQSWK	1.384422506	2	2.509147
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**0.928636944**	**3E-15**	**24**
P46462	AIANECQANFISIK	0.989466611	2	3.706075
P46462	EDEEESLNEVGYDDIGGCR	18.05749624	2	5.308833
P46462	ELQELVQYPVEHPDK	1.188640555	2	4.566929
P46462	ETVVEVPQVTWEDIGGLEDVK	0.805254663	2	4.472165
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.450560332	2	4.112364

P46462	EVDIGIPDATGR	0.99312249	2	2.739487
P46462	GDDLSTAILK	1.23371034	2	3.060446
P46462	GGNIGDGGGAADR	1.311640022	2	3.055141
P46462	GILLYGPPGTGK	1.070541695	2	2.852868
P46462	IVSQLLTLMDGLK	1.991145141	2	3.512601
P46462	KYEMFAQTLQQSR	1.541428715	2	4.056845
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	2.147031743	3	6.143382
P46462	LAGESESNLRKAFEEAEK	1.274084361	2	2.574522
P46462	LDQLIYIPLPDEK	1.51749262	2	4.507355
P46462	LEILQIHTK	1.220220682	2	2.828236
P46462	LGDVISIQPCPDVK	1.015240739	2	3.969112
P46462	LIVDEAINEDNSVVSLSQPK	1.398665092	2	5.452277
P46462	MDELQLFR	1.362546623	2	3.190644
P46462	MTNGFSGADLTEICQR	0.5827602	2	4.462412
P46462	NAPAIIFIDELDAIAPK	0.774348967	2	4.931983
P46462	QTNPSAMEVEEDDPVPEIR	0.804277321	2	4.396362
P46462	RSVSDNDIR	0.791116291	2	2.609674
P46462	VINQILTEMDGMSTK	1.747539067	2	4.591311
P46462	WALSQSNPSALR	1.874595511	2	3.451112
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**1.737264448**	**0.000658**	**5**
P46664	FIEDELQIPVK	1.004771006	2	3.152793
P46664	LDILDMFTEIK	1.692807769	2	3.266029
P46664	MCDLVSDFDGFSER	3.104625564	2	3.662362
P46664	VGIGAFPTEQDNEIGELLQTR	1.919166124	2	4.382331
P46664	VVDLLAQDADIVCR	2.202514422	2	3.518876
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**0.819073897**	**0.133509**	**4**
P46720	ESEHTDVHGSPQVENDGELK	1.364751731	3	3.745527
P46720	GIGETPIVPLGISYIEDFAK	1.428606184	2	3.801636
P46720	GVQHQLHVESK	0.793567568	2	3.021428
P46720	SENSPLYIGILEMGK	1.553852278	2	3.439306
P46844	**BIEA Biliverdin reductase A**	**1.081425743**	**0.681209**	**4**
P46844	FGVVVVGVGR	1.524713708	2	2.834647
P46844	GLLSWIEEK	1.689100081	2	2.517597
P46844	LLDQVSAEDLAAEK	1.065012689	2	4.658231
P46844	MTVQLETQNK	1.009849315	2	2.496026
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.332255362**	**0.227119**	**10**
P46953	AQGSVALSVTQDPACK	2.334356523	2	4.521562
P46953	ASFQPPVCNK	1.315053166	2	2.55939
P46953	DLGTQLAPIIQEFFHSEQYR	1.316655256	2	3.547767
P46953	FANTMGLVIER	1.249138743	2	3.56083
P46953	METELDGLR	1.391096362	2	2.740808
P46953	QDVDVWLWQLEGSSK	1.436227169	2	2.347336
P46953	QGEIFLLPAR	1.060512613	2	2.766766
P46953	RMETELDGLR	1.004603198	2	2.488079
P46953	TGKPNPDQLLK	1.252579576	3	3.582463
P46953	YYVGDTEDVLFEK	1.340382164	2	3.544656
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.451017894**	**5.25E-06**	**7**
P46978	FESVIHEFDPYFNYR	1.8559928	2	2.343237
P46978	FGQVYTEAK	1.48540445	2	2.724549
P46978	FHNWFDDR	1.533227619	2	2.546376
P46978	FYSLLDPSYAK	1.543653739	2	2.896611
P46978	NLDISRPDKK	1.641163746	2	2.412539
P46978	VGQAMASTEEK	0.752134388	2	3.170659
P46978	VGQAMASTEEK+Oxidation(4	1.030202697		

P47198	**RL22 60S ribosomal protein L22**	**1.711771799**	**7.61E-05**	**2**
P47198	AGNLGGGVVTIER	1.208893469	2	3.064136
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.856418427	3	5.531898
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**0.991046991**	**0.000145**	**4**
P47875	GFGFGQGAGALVHSE	1.389077759	2	3.158011
P47875	GLESTTLADKDGEIYCK	1.680198265	2	5.256585
P47875	HEEAPGHRPTTNPNASK	0.629366604	2	3.633925
P47875	NLDSTTVAVHGEEIYCK	1.011287311	2	4.721465
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.08670353**	**0.959267**	**3**
P47942	FQMPDQGMTSADDFFQGTK	0.97213558	2	4.076668
P47942	GLYDGPVCEVSVTPK	1.429788723	2	3.565344
P47942	SITIANQTNCPLYVTK	1.085374329	2	3.428096
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.049784092**	**0.07551**	**2**
P48004	NYTDDAIETDDLTIK	0.867331385	2	4.543657
P48004	YVAEIEKEKEENEK	1.371580719	2	5.432276
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**1.510962779**	**0.01467**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.516915738	3	5.676169
P48024	TLTTVQGIADDYDK	1.340685898	2	3.668185
P48037	**ANXA6 Annexin A6**	**1.361877372**	**2.72E-13**	**20**
P48037	AANDFNPDADAK	0.873011532	2	3.552063
P48037	AINEAYKEDYHK	1.307678429	2	3.396749
P48037	ALIEILATR	1.418733078	2	3.217064
P48037	ALLALCGGED	1.754038905	1	2.150714
P48037	CLIEILASR	1.051615756	2	2.657546
P48037	DAFVAIVQSVK	1.16061831	2	3.826552
P48037	DLESDIIGDTSGHFQK	1.520450789	2	4.436759
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.154637154	2	5.15064
P48037	GELSGDFEK	0.996250875	1	2.180691
P48037	GFGSDKESILELITSR	0.922202856	2	4.275832
P48037	GIGTDEATIIDIITQR	1.50219173	2	4.264729
P48037	GSVHDFADFDANQDAEALYTAMK	1.283081776	3	4.136739
P48037	QRQEICQSYK	1.044586948	2	3.197263
P48037	SEIDLLNIR	1.856172821	2	3.070961
P48037	SEISGDLAR	1.450373206	2	2.344545
P48037	SELDMLDIR	1.252187705	2	2.960925
P48037	SLEDALSSDTSGHFK	1.400194738	2	3.675353
P48037	TNEQIHQLVAAYK	1.260832629	2	4.02279
P48037	TNYDIEHVIK	1.072493331	2	3.088604
P48037	TTGKPIEASIR	1.826294519	2	2.537423
P48500	**TPIS Triosephosphate isomerase**	**1.137393007**	**0.011509**	**15**
P48500	CLGELICTLNAAK	1.407876852	2	3.566662
P48500	CNVSEGVAQCTR	1.515147439	2	3.955785
P48500	DLGATWVVLGHSER	1.92382809	2	4.164804
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.211549479	4	5.940062
P48500	HIFGESDELIGQK	1.246854049	2	4.680532
P48500	IAVAAQNCYK	1.688171805	2	2.7012
P48500	IIYGGSVTGATCK	1.288210646	2	4.339893
P48500	LPADTEVVCAPPTAYIDFAR	1.337374437	2	4.41963
P48500	RHIFGESDELIGQK	1.325601918	2	4.416492
P48500	TATPQQAQEVHEK	1.165040062	2	3.639288
P48500	TATPQQAQEVHEKLR	0.925384438	2	2.399762
P48500	VNHALSEGLGVIACIGEK	1.633421792	2	5.674907
P48500	VTNGAFTGEISPGMIK	1.137045437	2	4.865503
P48500	VVFEQTK	1.157432879	1	1.933349
P48500	VVLAYEPVWAIGTGK	1.209603754	2	4.532421
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.90452813**	**0.087282**	**4**

P48508	ASTLHLQTGNLLNWGR	0.934551616	3	4.011608
P48508	EFPDVLECTMSHAVEK	1.075876838	2	3.592967
P48508	INPDEREEMK	1.445457993	2	2.643714
P48508	TLNEWSSQISPDLVR	0.887987632	2	4.684856
P48675	**DESM Desmin**	**1.757733272**	**0.59285**	**3**
P48675	NISEAEEWYKSK	1.687128068	2	2.325622
P48675	TSGGAGGLGSLR	1.85765017	2	2.701077
P48675	VSDLTQAANK	3.109176993	2	2.982995
P48679	**LMNA Prelamin_A/C**	**1.1918134**	**0.063984**	**19**
P48679	AAYEAELGDAR	1.43144658	2	2.365023
P48679	AQHEDQVEQYK	1.007764217	2	3.046567
P48679	AQHEDQVEQYKK	1.250143235	2	4.33551
P48679	GSHCSSSGDPAEYNLR	1.336189519	2	3.950425
P48679	IDSLSAQLSQLQK	1.30044057	2	3.169589
P48679	ITESEEVVSR	1.099492201	2	3.155397
P48679	LEAALGEAK	1.800871257	2	2.316311
P48679	LKDLEALLNSK	1.254444441	2	2.864124
P48679	LQEKEDLQELNDR	1.504779926	2	4.228195
P48679	MQQQLDEYQELLDIK	1.580365384	2	4.554407
P48679	NIYSEELR	1.390924222	1	2.059408
P48679	NSNLVGAAHEELQQSR	1.019211061	2	4.710769
P48679	SGAQASSTPLSPTR	1.071371014	2	3.791151
P48679	SLETENAGLR	1.289300236	2	2.868083
P48679	SVGGSGGGSFGDNLVTR	1.006755854	2	3.584023
P48679	TALINATGEEVAMR	1.211059205	2	3.576835
P48679	TLEGELHDLR	2.45899108	2	2.492499
P48679	TVLCGTCGQPADK	1.108379323	2	3.44474
P48679	VAVEEVDEEGK	1.286991821	2	3.108805
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.306579348**	**9.9E-20**	**30**
P48721	AQFEGIVTDLIK	1.364608166	2	3.720623
P48721	ASNGDAWVEAHGK	1.552509166	2	3.815917
P48721	DAGQISGLNVLR	2.525057378	2	2.757384
P48721	DDIENMVK	1.925511402	1	2.022432
P48721	EQQIVIQSSGGLSK	1.207659193	2	3.863011
P48721	EQQIVIQSSGGLSKDDIENMVK	1.732435749	2	4.529761
P48721	ERVEAVNMAEGIIHDTETK	1.128067991	3	5.565117
P48721	ETAENYLGHTAK	1.32494672	2	3.1378
P48721	GAVVGIDLGTTNSCVAVMEGK	1.31184849	2	5.385311
P48721	LFEMAYK	1.218897742	2	2.305128
P48721	LLGQFTLIGIPPAPR	2.128028954	2	3.732023
P48721	MEEFKDQLPADECNK	2.215066059	2	4.607238
P48721	MEEFKDQLPADECNK+Oxidation(0	2.323596367		
P48721	MKETAENYLGHTAK	1.113441904	2	4.308012
P48721	MKETAENYLGHTAK+Oxidation(0	1.261060462		
P48721	NAVITVPAYFNDSQR	1.348718912	2	3.464715
P48721	QAVTNPNNTFYATK	1.119435868	2	3.802908
P48721	RETGVDLTK	0.732215906	2	2.32814
P48721	RYDDPEVQK	1.289742152	2	3.230685
P48721	RYDDPEVQKDTK	1.276764323	2	3.78626
P48721	SDIGEVILVGGMTR	1.326177554	2	3.983572
P48721	SQVFSTAADGQTQVEIK	1.06350217	2	4.605309
P48721	STNGDTFLGGEDFDQALLR	1.243690133	2	6.078481
P48721	TTPSVVAFTPDGER	1.036435001	2	3.394622
P48721	VEAVNMAEGIIHDTETK	1.462427192	2	4.573091
P48721	VINEPTAAALAYGLDK	1.614681026	2	3.882973
P48721	VLENAEGAR	0.961763541	2	3.093744
P48721	VQQTVQDLFGR	1.071966545	2	3.729154

P48721	YDDPEVQK	1.387963131	2	2.350807
P48721	YDDPEVQKDTK	1.374507462	2	2.749007
P48998	**INVO Involucrin**	**1.179363741**	**0.275794**	**2**
P48998	ELLDQRLDQELVNK	1.209500979	2	2.325285
P48998	HKLENLTQKEK	1.177939853	1	1.938639
P49025	**CTRO Citron Rho_interacting kinase**	**1.45153271**	**0.160306**	**2**
P49025	LEEQLEK	1.452879988	1	2.010406
P49025	LMMNQLEEDLVSARR+Oxidation(1	1.07677102		
P49134	**ITB1 Integrin beta_1**	**1.109349872**	**0.645783**	**3**
P49134	CNCQSHGIPASPK	1.393175679	2	3.348118
P49134	FCECDNFNCDR	0.785128547	2	3.367566
P49134	GEFFNELVGQQR	0.989868246	2	2.883482
P49186	**MK09 Mitogen_activated protein kinase 9**	**1.061147337**	**0.287732**	**2**
P49186	DLLSKMLVIDPDK	0.934826694	1	1.977767
P49186	VIEQLGTPSAEFMK	1.365872011	2	2.60854
P49242	**RS3A 40S ribosomal protein S3a**	**0.947548664**	**1.39E-07**	**9**
P49242	ACQSIYPLHDVFVR	1.568751642	2	4.315433
P49242	ADGYEPPVQESV	0.824565864	1	2.080672
P49242	LIPDSIGKDIEK	1.414697422	2	2.512843
P49242	LITEDVQGK	7.189141511	2	2.563357
P49242	LMELHGEGGSSGK	1.574189226	2	3.516199
P49242	LMELHGEGGSSGK+Oxidation(1	0.963604678		
P49242	NCLTNFHGMDLTR	0.987420482	2	3.981197
P49242	TTDGYLLR	1.826481407	2	2.716384
P49242	VFEVSLADLQNDEVAFR	1.772611831	2	4.54017
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**1.09999621**	**0.218412**	**7**
P49432	EAINQGMDEELERDEK	2.469833317	2	3.713857
P49432	ILEDNSIPQVK	1.051653518	2	3.382252
P49432	IMEGPAFNFLDAPAVR	1.431991232	2	4.531613
P49432	IMEGPAFNFLDAPAVR+Oxidation(1	1.077503674		
P49432	TIRPMDIEAIEASVMK	1.089417569	3	4.463601
P49432	VFLLGEEVAQYDGAYK	1.436214901	2	4.225796
P49432	VTGADVPMPYAK	0.874387924	2	2.554392
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**1.023035238**	**0.993418**	**12**
P49889	CKEDALFNR	1.070689934	2	2.503449
P49889	FEEHYQQQMK	1.055181313	2	2.987748
P49889	FEEHYQQQMK+Oxidation(8	0.996102433		
P49889	FMEGQVPYGSWYDHVK	1.199542338	2	4.129925
P49889	IIQHTSFQEMK	0.712909888	2	2.882983
P49889	LIEFLER	1.057661724	2	2.471407
P49889	LIEFLERDPSAELVDR	2.931656713	3	5.171266
P49889	NEDLINGIK	0.920384872	2	3.081187
P49889	NNPCTNYSMLPETMIDLK	0.963177211	2	5.26169
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13	1.292597125		
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8	1.292597125		
P49889	SGSTWISEIVDMIYK	1.133922358	2	4.065467
P50137	**TKT Transketolase**	**1.051577575**	**9.88E-15**	**24**
P50137	AVELAANTK	0.715874748	1	2.093319
P50137	GITGIEDK	1.097209274	1	2.562754
P50137	GITGIEDKEAWHGKPLPK	1.104294955	3	3.606737
P50137	HQPTAIIAK	0.067048466	2	2.330532
P50137	IIALDGDTK	2.507614431	2	2.670165
P50137	ILATPPQEDAPSVDIANIR	1.310348469	2	4.801414
P50137	ISSDLDGHPVPK	1.156341464	2	3.372873
P50137	KISSDLDGHPVPK	1.030948782	2	3.840163
P50137	LAVSQVPR	1.171870016	2	2.36242

P50137	LAVSQVPRSGKPAELLK	1.25138548	2	2.587433
P50137	LDNLVAIFDINR	1.25489249	2	4.524677
P50137	LGQSDPAPLQHQVDVYQK	1.364070995	2	3.860001
P50137	MFGIDKDAIVQAVK	1.21549642	2	4.853958
P50137	MFGIDKDAIVQAVK+Oxidation(0	1.273727251		
P50137	NMAEQIIQEIYSQVQSK	1.051441183	3	6.022956
P50137	NSTFSELFK	1.22686989	2	2.415645
P50137	QAFTDVATGSLGQGLGAACGMAYTGK	2.223257191	3	4.37783
P50137	SGKPAELLK	0.14006102	3	3.300893
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	1.423588802	3	4.590706
P50137	SVPMSTVFYPSDGVATEK	1.131889716	2	4.500248
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3	1.493904838		
P50137	TSRPENAIIYSNNEDFQVGQAK	0.956973511	3	5.894084
P50137	VLDPFTIKPLDK	1.191303352	2	3.240458
P50137	VLDPFTIKPLDKK	0.847106988	2	2.534468
P50169	**RDH3 Retinol dehydrogenase 3**	**1.17487332**	**0.00466**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.289889358	3	5.030165
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1	1.315179833		
P50169	FQDSYMK	1.332188514	1	1.986191
P50169	GLWGLVNNAGISVPVGPNEWMR	1.664682379	3	3.367166
P50169	KLWDQTTEEVK	1.475142553	2	3.050054
P50169	KLWDQTTEEVKEIYGEK	1.178425688	3	4.978757
P50169	LWDQTTEEVK	1.063924663	2	3.170134
P50169	LWDQTTEEVKEIYGEK	1.247910544	2	4.810603
P50169	MSLVGGGYCISK	1.172745691	2	4.053123
P50237	**ST1C1 Sulfotransferase 1C1**	**1.348995239**	**0.00415**	**12**
P50237	AGTTWTQEIVDMIQNDGDVQK	1.394854012	3	5.279291
P50237	DISEEVLNK	0.988796791	1	2.468704
P50237	DLHLGEQDLQPETR	1.21586271	2	4.628257
P50237	EVNGILMSK	0.818270831	1	1.916024
P50237	FLEKDISEEVLNK	1.163836951	2	2.889341
P50237	HPFIEWTLPSPLNSGLDLANK	1.467651191	3	4.036582
P50237	IWNFQAKPDDLLIATYAK	1.816155087	3	3.678375
P50237	MKDLHLGEQDLQPETR	1.317406607	2	5.189457
P50237	MLPDPGTLGEYIEQFK	1.21287782	3	4.946307
P50237	MLPDPGTLGEYIEQFK+Oxidation(0	1.982092251		
P50237	THLPVHMLPPSFWK	3.403710324	3	3.71863
P50237	VLWGSWYDHVK	1.047721968	2	2.978031
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**1.287193391**	**1.11E-16**	**7**
P50398	FDLGQDVIDFTGHALALYR	1.495982101	3	4.617767
P50398	FQLLEGPPESMGR	1.388675649	2	3.952432
P50398	KQNDVFGEADQ	1.485946018	2	3.288814
P50398	NPYYGGESSSITPLEELYK	1.472360965	2	5.909615
P50398	QLICDPSYIPDR	0.686665151	2	3.014831
P50398	TDDYLDQPCLETINR	0.599309166	2	4.961609
P50398	TFEGVDPQTTSMR	1.364921538	2	3.384315
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.229278207**	**0.000376**	**15**
P50399	AYDATTHFETTCDDIK	0.881037423	2	4.120151
P50399	AYDATTHFETTCDDIKDIYK	1.493750319	3	6.220264
P50399	EIRPALELLEPIEQK	1.176163365	3	3.8109
P50399	EPEKEIRPALELLEPIEQK	1.371312385	3	3.421732
P50399	FDLGQDVIDFTGHSLALYR	1.356572837	3	4.040238
P50399	FKLPGQPPASMGR	1.69639905	2	2.602103
P50399	FVSISDLFVPK	1.202035149	2	3.268447
P50399	LSAIYGGTYMLNKPIEEIIVQNGK	2.851199521	3	4.580137
P50399	MLLFTEVTR	1.301607586	2	2.357827

P50399	MTGSEFDFEEMKR	1.283955528	2	3.634531
P50399	NTNDANSCQIIIPQNQVNR	0.784693591	2	4.37439
P50399	TDDYLDQPCCETINR	1.596412088	2	4.850991
P50399	TFEGVDPK	1.919010289	2	2.404865
P50399	VIEGSFVYK	1.366410341	2	2.330506
P50399	VLHMDQNPYYGGESASITPLEDLYK	1.423965253	2	5.517198
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.173072917**	**0.925323**	**7**
P50431	ALSDALTELGYK	1.157610923	2	4.080372
P50431	AVLEALGSCLNNK	1.08590256	2	4.272254
P50431	GLLEEDFQK	1.403076656	1	2.096672
P50431	IMGLDLPDGGHLTHGFMTDK	1.0636523	2	2.800994
P50431	IYQLQVLANCR	1.086219422	2	2.820818
P50431	VLEACSIACNK	1.173462337	2	4.01854
P50431	YSEGYPGQR	1.217713003	2	2.81589
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**1.117883405**	**0.126156**	**16**
P50475	ASEWVQQVSGLMDGK	1.167506338	2	4.478455
P50475	AVFDETYPDPVR	1.092587498	2	3.272998
P50475	DIINEEEVQFLK	1.427069964	2	2.711903
P50475	ESDGVLKPLPK	1.482882616	2	2.379001
P50475	GLEATDDSPK	1.277728113	2	2.701353
P50475	HNDLDDVGK	1.100141642	2	2.557026
P50475	ITCLCQVPQNAANR	1.108263745	2	3.826
P50475	IVAVTGAEAQK	1.39151341	2	2.573763
P50475	NVGCLQEALQLATSFAQLR	1.555883859	3	3.941396
P50475	QIWQNLGLDEAK	1.462137389	2	3.048444
P50475	RIVAVTGAEAQK	1.740081235	2	2.773591
P50475	SVLGDADQK	1.496572718	1	2.207099
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	1.735822994	3	3.675295
P50475	TITVALADGGRPDNTGR	1.101923753	2	3.033164
P50475	VDDSSEDKTEFTVK	1.223116572	2	4.066047
P50475	VGAEDTDGIDMAYR	1.386911951	2	3.871379
P50503	**F10A1 Hsc70_interacting protein**	**1.402174989**	**5.08E-13**	**6**
P50503	AIDLFTDAIK	1.737206673	2	2.743276
P50503	AIEINPDSAQPYK	1.402108567	2	3.530184
P50503	GAAIDALNDGELQK	1.140693274	2	3.710059
P50503	KGAAIDALNDGELQK	1.620963842	2	4.685584
P50503	LDYDEDASAMLR	1.198303116	2	3.343299
P50503	QDPSVLHTEEMR	1.526027168	2	2.319453
P50516	**VATA V_type proton ATPase catalytic subunit A**	**1.467185049**	**0.337516**	**2**
P50516	TALVANTSNMPVAAR	1.216070919	2	3.195357
P50516	VLDALFPCVQGGTTAIPGAFGCGK	1.471570345	2	3.312716
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**1.45035747**	**0.000389**	**14**
P50554	GMCQLITMACGSCSNENAFK	1.669408763	2	4.556716
P50554	GNYLVDVDGNR	2.056810575	2	2.64162
P50554	GTFCSFDTPDEAIR	5.597399775	2	3.224224
P50554	HGCAFLVDEVQTGGGCTGK	1.116355396	2	6.113246
P50554	IDIPSFDWPIAPFPR	1.229669041	2	3.804311
P50554	IFNTWLGDPSK	1.786877085	2	3.009854
P50554	KHGCAFLVDEVQTGGGCTGK	1.243772955	2	5.036607
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.278884827	3	3.303688
P50554	MLDLYSQISSVPIGYNHPALAK	1.303836757	3	3.406765
P50554	NLLLAEVINIIK	1.124032694	3	5.323947
P50554	REDLLNNVAHAGK	1.215233463	3	3.620203
P50554	TLLTGLLDLQAQYPQFVSR	2.467254056	2	3.161711
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.679833814	2	4.021005
P50554	VDFEFDYDGPLMK	1.615898859	2	4.048791

P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.098046528**	**0.999351**	**2**
P50580	GDAMIMEETGK	0.993747779	2	2.664113
P50580	TIIQNPTDQQK	1.098835063	2	3.154985
P50878	**RL4 60S ribosomal protein L4**	**1.227536852**	**9.9E-20**	**11**
P50878	FCIWTESAFR	1.625319201	2	2.56805
P50878	KLDELYGTWR	1.347286169	2	2.970752
P50878	KLEAAAAALAAK	1.315332926	3	4.941208
P50878	LDELYGTWR	1.49249486	2	2.571163
P50878	LEAAAAALAAK	2.187580976	2	3.610692
P50878	NIPGITLLNVSK	1.48596811	1	2.696272
P50878	NVTLPAVFK	1.409276741	1	2.241946
P50878	RGPCIIYNEDNGIIK	0.713972928	2	2.990682
P50878	SGQGAFGNMCR	1.596873942	2	2.836194
P50878	SNYNLPMHK	1.541209961	2	2.637905
P50878	YAICSALAASALPALVMSK	1.588764929	2	2.548637
P51583	**PUR6 Multifunctional protein ADE2**	**1.127802226**	**0.851224**	**3**
P51583	ACGNFGIPCELR	1.067827343	2	2.600871
P51583	SWLPQNCTLVDMK	1.312019249	2	2.744097
P51583	VVVLMGSTSDLGHCEK	1.653733044	2	3.039305
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.100730255**	**3.44E-15**	**7**
P51635	ALEALVAK	1.716620913	2	2.826975
P51635	GLEVTAYSPLGSSDR	0.780285388	2	4.114704
P51635	HHPEDVEPAVR	1.244947083	3	3.589575
P51635	HIDCASVYGNETEIGEALK	1.06782557	2	6.041212
P51635	HIDCASVYGNETEIGEALKESVGAGK	1.279558151	3	6.261342
P51635	HPDEPVLLEEPVVLALAEK	2.291359552	3	6.061058
P51635	YIVPMITVDGK	1.317818641	2	2.328477
P51647	**AL1A1 Retinal dehydrogenase 1**	**1.195043047**	**9.9E-20**	**17**
P51647	ANNTTYGLAAGVFTK	1.187587799	2	4.601446
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	1.570942823	3	3.667674
P51647	FPVLNPATEEVICHVEEGDK	1.467741612	3	3.828281
P51647	FPVLNPATEEVICHVEEGDKADVDK	1.462864771	4	5.050517
P51647	IFINNEWHDSVSGK	1.666623043	2	4.280609
P51647	IFVEESVYDEFVR	1.613109981	2	4.22951
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	2.032536669	3	5.611658
P51647	IHGQTIPSDGDIFTFTR	1.87033087	3	4.280681
P51647	KFPVLNPATEEVICHVEEGDK	0.916797142	3	3.568044
P51647	KFPVLNPATEEVICHVEEGDKADVDK	1.384229137	4	4.877313
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	1.248783329	3	5.523383
P51647	LLLATIEAINGGK	9.265571678	2	4.19882
P51647	VAFTGSTQVGK	2.361505055	2	2.518713
P51647	VFANAYLSDLGGSIK	2.075837235	2	4.444872
P51647	YCAGWADK	1.598894936	2	2.489247
P51647	YVLGNPLTQGINQGPQIDK	1.286458082	2	5.22237
P51647	YVLGNPLTQGINQGPQIDKEQHDK	1.225281905	2	3.886786
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**1.000170962**	**0.460372**	**9**
P51650	EVGEVLCTDPLVSK	2.671774456	2	3.776339
P51650	GIHDSFVTK	1.084208361	2	2.404372
P51650	HQSGGNFFEPTLLSNVTR	1.206263153	2	3.784001
P51650	IITAESGKPLK	1.672848997	2	2.822287
P51650	ILLHHAANSVK	1.472760394	2	2.61054
P51650	LGTVADCGVPEAR	0.841082623	2	3.662265
P51650	VGNGFEEGTTQGPLINEK	0.917043755	2	4.610662
P51650	WLPTPATFPVYDPASGAK	1.127275678	2	3.544464
P51650	YGIDEYLEVK	1.709397262	2	2.908433
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**1.068159579**	**0.767255**	**2**

P51863	ADDYEQVK	1.306689	2	2.489688
P51863	LLFEGAGSNPGDK	0.941328509	2	3.053885
P51869	**CP4F4 Cytochrome P450 4F4**	**1.625285622**	**2.43E-09**	**4**
P51869	ALPSQHEDDILK	1.515960368	2	2.594843
P51869	NISLMTLDSLQK	1.517803529	2	3.523234
P51869	TLDFIDVLLLTK	2.04412339	2	3.613848
P51869	WQDLASGGSAR	1.323866666	2	3.177908
P51886	**LUM Lumican**	**1.111313778**	**0.867984**	**2**
P51886	NNQIDHIDEK	1.10675397	2	3.206459
P51886	SLQDLQLANNK	1.176606723	2	2.497982
P52296	**IMB1 Importin subunit beta_1**	**1.50820792**	**0.489851**	**7**
P52296	AAVENLPTFLVELSR	1.289969012	2	3.67735
P52296	GALQYLVPILTQTLTK	1.710433829	2	3.304526
P52296	GDQENVHPDVMLVQPR	1.259068745	2	2.979903
P52296	SNEILTAIIQGMR	1.588099338	2	2.936603
P52296	TVSPDRLELEAAQK	1.04945754	2	3.151765
P52296	VLANPGNSQVAR	1.249848306	2	3.055084
P52296	VQHQDALQISDVVMASLLR	1.638650659	2	2.885161
P52303	**AP1B1 AP_1 complex subunit beta_1**	**0.850635884**	**0.040968**	**5**
P52303	KPTETQELVQQVLSLATQDSDNPDLR	1.759977315	3	3.346579
P52303	MEPLNNLQVAVK	1.572882955	2	2.539657
P52303	NINLIVQK	0.750919908	1	2.408912
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.341250009	3	3.693463
P52303	SQPDMAIMAVNTFVK	1.462994756	2	3.339198
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**1.430091874**	**0.000438**	**2**
P52504	IIACDGGGGALGHPK	1.477073515	2	4.123787
P52504	VYINLDKETK	1.328741043	2	2.617587
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.287631828**	**0.97865**	**3**
P52555	FDTQYPYGEK	1.763895722	2	2.650203
P52555	ILDQGEDFPASELAR	1.183295957	2	5.053833
P52555	SLNILTAFR	1.414641272	2	2.341288
P52631	**STAT3 Signal transducer and activator of transcription 3**	**3.317214313**	**2.01E-08**	**3**
P52631	GLSIEQLTTLAEK	2.111161451	2	2.39859
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	3.319907367	3	4.605139
P52631	MQQLEQMLTALDQMR	1.578204963	2	2.440681
P52759	**UK114 Ribonuclease UK114**	**1.141705882**	**0.040999**	**7**
P52759	AAGCDFTNVVK	2.008259939	2	3.062975
P52759	AAYQVAALPK	0.757487447	2	2.679744
P52759	IEIEAIAVQGPFTTAGL	1.192975955	2	3.240477
P52759	NLGEILK	0.990341449	1	2.287736
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.346389135	2	4.525706
P52759	TTVLLADINDFGTVNEIYK	1.7277155	2	5.666708
P52759	TYFQGNLPAR	1.152338649	2	2.507899
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.08446115**	**0.852974**	**2**
P52845	CKEDAIFNR	1.070689934	2	2.503449
P52845	SGSTWIGEIVDMIYK	1.962267913	2	3.364449
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.395642868**	**8.42E-08**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	2.477858758	2	4.468409
P52847	FLAGNVAYGSWFDHVK	0.890784519	2	3.854979
P52847	IEEFQSRPCDIVIPTYPK	1.519127666	3	5.26857
P52847	IVHHTSFEVMK	1.136408265	2	3.053289
P52847	NYFTMTQSEK	1.270481079	2	2.924855
P52847	SGVELLK	1.497405938	2	2.339941
P52847	THLPIDLLPK	1.725091088	3	3.555724

P52847	TLDEHTLER	1.39539044	2	3.092446
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**0.97774791**	**9.9E-20**	**39**
P52873	ADEAYLIGR	1.040028787	2	2.806849
P52873	ADFAQACQDAGVR	0.653052199	2	4.47163
P52873	AEAEAQAEELSFPR	1.134079162	2	4.704005
P52873	AGTHILCIK	2.390697787	2	2.71725
P52873	ALAVSDLNR	1.108452764	2	2.583564
P52873	AYSEALAAFGNGALFVEK	2.558480402	2	3.689992
P52873	AYVEANQMLGDLIK	1.56924885	2	4.70824
P52873	DAHQSLLATR	1.495842366	1	3.173891
P52873	DFTATFGPLDSLNTR	2.637863128	2	3.756638
P52873	DMAGLLKPAACTMLVSSLR	1.600627239	3	3.388147
P52873	ELIPNIPFQMLLR	1.381989827	2	2.849156
P52873	ENGVDAVHPGYGFLSER	1.484792147	2	2.969886
P52873	FIGPSPEVVR	1.014804846	2	2.436676
P52873	FLYECPWR	1.310849928	2	2.605958
P52873	GANAVGYTNYPDNVVFK	1.252059993	2	4.575528
P52873	GLAPVQAYLHIPDIIK	0.755209419	2	2.980513
P52873	GQIGAPMPGK	1.276570756	2	2.427273
P52873	GTPLDTEVPLER	0.854807098	2	3.65032
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	2.391392995	3	5.416217
P52873	HIEVQILGDQYGNILHLYER	1.789166875	3	7.008325
P52873	HYFIEVNSR	1.236275076	2	2.338978
P52873	IAEEFEVELER	1.394065729	2	3.24429
P52873	IEGRPGASLPPLNLK	0.971935711	2	3.437396
P52873	INGCAIQCR	1.387500142	2	3.250948
P52873	IVGDLAQFMVQNGLSR	1.74210896	2	4.842085
P52873	LDNASAFQGAVISPHYDSLLVK	1.26927529	3	5.770468
P52873	LLHYLGHVMVNGPTTPIPVK	1.686727908	3	3.677512
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.307987796	4	6.503133
P52873	NHQGLLLMDTTFR	1.005048579	3	3.320544
P52873	QKADEAYLIGR	1.35878274	2	2.495136
P52873	QVGYENAGTVEFLVDK	1.755455114	2	3.776635
P52873	SSTAPVASPNVR	0.992647851	2	2.345997
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.261014291	2	4.805422
P52873	TVAVYSEQDTGQMHR	1.447129695	2	4.569159
P52873	VFDYSEYWEGAR	1.481234388	2	4.537129
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.318075616	2	4.123032
P52873	VVEIAPATHLDPQLR	1.351034478	2	4.236594
P52873	VVHSYEELEENYTR	1.270732322	2	5.238379
P52873	YSLEYYMGLAEELVR	1.501781124	3	4.510306
P52925	**HMGB2 High mobility group protein B2**	**1.198583338**	**0.53246**	**2**
P52925	KHPDSSVNFAEFSK	1.222941532	2	2.740416
P52925	SEHPGLSIGDTAK	1.1972639	2	2.846153
P52944	**PDLI1 PDZ and LIM domain protein 1**	**1.305995941**	**0.000558**	**5**
P52944	CGTGIVGVFVK	1.302932395	2	2.434757
P52944	GHFFVGDQIYCEK	1.461754854	2	3.787676
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	1.304402912	3	4.499169
P52944	TSASGEEANSRPSAQPHPSGGLIIDKESEVYK	1.988863971	3	5.015387
P52944	VTPPEGYDVVTVFPK	1.320151183	2	2.710248
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.768598852**	**2.08E-14**	**4**
P53395	LREELKPVALAR	1.904324853	2	2.674104
P53395	LSDIGEGIR	1.66486702	2	3.023681
P53395	RLAMENNIK	1.279080933	2	2.378535
P53395	SYLENPAFMLLDLK	1.84403411	2	4.606715

P53987	**MOT1 Monocarboxylate transporter 1**	**1.259789576**	**0.000283**	**5**
P53987	DGKEDETSTDVDEKPK	1.677802551	3	5.489101
P53987	DGKEDETSTDVDEKPKK	1.057754913	3	4.047904
P53987	EDETSTDVDEKPK	1.232497698	2	3.976382
P53987	ETQSPAPLQNSSGDPAEEESPV	0.935631384	2	5.049421
P53987	SDANTDLIGGSPK	1.126966901	2	4.135689
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**1.529193839**	**0.168717**	**2**
P54313	ACGDSTLTQITAGLDPVGR	1.741795127	2	3.997175
P54313	TFVSGACDASIK	1.081767748	2	2.724099
P54319	**PLAP Phospholipase A_2_activating protein**	**1.007973541**	**0.916248**	**3**
P54319	IGDVVGSSGANQQTSGK	1.031861129	2	4.658643
P54319	TGDLGDINAEQLPGR	1.823951305	2	4.130882
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.781325998	2	3.390711
P54822	**PUR8 Adenylosuccinate lyase**	**1.366908333**	**0.164231**	**2**
P54822	KVDIEVLSVLASLGASVHK	1.811965979	3	4.416427
P54822	VLSQQAAAVVK	1.319898992	2	2.854376
P54921	**SNAA Alpha_soluble NSF attachment protein**	**0.770634128**	**0.515942**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	1.531727999	3	4.891563
P54921	AIDIYEQVGTSAMDSPLLK	2.074031015	2	3.793165
P54921	IEEACEIYAR	0.76734253	2	2.757394
P54921	NSQSFFSGLFGGSSK	1.097558957	2	3.792224
P54921	YEELFPAFSDSR	1.579847356	2	2.620309
P55006	**RDH7 Retinol dehydrogenase 7**	**1.127778746**	**3.67E-07**	**11**
P55006	LETVILDVTK	1.313042865	2	3.517367
P55006	TESIVAATQWVK	1.2211044	2	4.081845
P55006	TNVTNMER	0.558052961	2	2.74532
P55006	TNVTNMER+Oxidation(5	0.378136132		
P55006	TSDRLETVILDVTK	1.709541368	3	4.584667
P55006	VAIIEPGGFK	0.650341866	2	2.385883
P55006	VLAACLTEK	1.333504321	2	3.074588
P55006	VVNIASTMGR	1.197451971	2	3.78917
P55006	VVNIASTMGR+Oxidation(7	1.321755945		
P55006	YGVEAFSDSLR	1.3950914	2	3.864886
P55006	YVFITGCDSGFGNLLAR	1.539228599	2	3.665496
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.143452416**	**0.652887**	**4**
P55051	ALGVGFATR	1.599847392	2	2.645137
P55051	LTDSQNFDEYMK	1.745056645	2	4.049841
P55051	QVGNVTKPTVIISQEGGK	1.132300008	3	4.129147
P55051	WDGKETNCVR	1.044591459	2	2.886392
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.212443395**	**0.931097**	**6**
P55053	FDETTADGR	1.181290792	2	3.205886
P55053	KTETVCTFTDGALVQHQK	1.312946308	3	5.30947
P55053	LVESHGFEDYMK	1.492948552	2	3.427332
P55053	MGAMAKPDCIITLDGNNLTVK	1.158670218	2	4.124904
P55053	MVVECVMNNAICTR	1.594361663	2	3.847544
P55053	TETVCTFTDGALVQHQK	1.210799506	2	4.683166
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.296107251**	**3.9E-11**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	2.185925369	3	5.867096
P55159	IFFYDSENPPGSEVLR	1.101869801	2	6.215265
P55159	IQSILSEDPK	1.37179011	2	3.259762
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.627219412	3	4.074989
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	1.298338147	3	5.408141
P55159	VVADGFDFANGIGISLDGK	1.279523316	2	4.446301
P55159	YVYIAELLAHK	1.770786145	2	2.677353
P55260	**ANXA4 Annexin A4**	**1.387107178**	**0.280695**	**4**
P55260	AEIDMLDIPANFK	1.212328926	1	2.177678

P55260	GAGTDEGCLIEILASR	1.341511729	2	3.783448
P55260	GLGTDEDAIIGVLACR	1.412892603	2	3.908335
P55260	INQTYQQQYGR	1.281262294	2	3.616781
P55770	**NH2L1 NHP2_like protein 1**	**1.387492629**	**0.054318**	**2**
P55770	LLDLVQQSCNYK	1.49424454	2	3.891955
P55770	QQIQSIQQSIER	1.372526419	2	2.929913
P55937	**GOGA3 Golgin subfamily A member 3**	**1.396911388**	**0.482286**	**2**
P55937	LDSEMKELRQELIK+Oxidation(4	1.316066522		
P55937	QWYQQQLTLAQEAR	1.486929107	2	2.44317
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.192605191**	**0.350876**	**5**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.341422419	2	4.524675
P56399	IFQNAPTDPTQDFSTQVAK	0.854103737	2	4.191671
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.151582922	3	3.858413
P56399	KQEVQAWDGEVR	1.144384809	2	3.355608
P56399	SSENPNEVFR	1.556243782	2	2.456969
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.235878628**	**0.540911**	**4**
P56522	AGLLPSGPRPGYTAIQALLSDR	2.588731949	3	3.46841
P56522	LEGVGESTR	0.849165726	2	2.308931
P56522	TATEKPGVEEAAR	1.159299792	2	3.258079
P56522	TDITEVALGVLR	1.244750603	2	3.924618
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.011021216**	**0.005404**	**17**
P56574	ATDFVVDR	1.613120077	2	2.463671
P56574	CATITPDEAR	2.12583761	2	2.304518
P56574	DLAGCIHGLSNVK	1.520094541	2	2.50456
P56574	DQTNDQVTIDSALATQK	0.601705761	2	5.425661
P56574	FKDIFQEIFDK	1.259297651	2	3.432907
P56574	GKLDGNQDLIR	11.12353789	2	2.968915
P56574	IKVEKPVVEMDGDEMTR	1.927601489	3	3.475136
P56574	LDGNQDLIR	0.758458588	2	2.449787
P56574	LIDDMVAQVLK	2.62423814	2	4.057062
P56574	LNEHFLNTTDFLDTIK	1.741718622	2	4.560071
P56574	NILGGTVFR	1.29168595	2	2.780075
P56574	NILGGTVFREPIICK	5.46070947	2	3.000834
P56574	SSGGFVWACK	0.515899864	2	2.449724
P56574	TIEAEAAHGTVTR	1.308643196	2	3.927422
P56574	VCVQTVESGAMTK	1.20496812	2	3.860638
P56574	VEKPVVEMDGDEMTR	1.241234082	3	4.018549
P56574	YFDLGLPNR	1.05003669	2	2.522527
P56593	**CP2AC Cytochrome P450 2A12**	**1.107821955**	**0.968976**	**3**
P56593	MLQGTCGAPIDPTIYLSK	1.044090888	2	4.70444
P56593	NRQPQYEDHMK	1.271444627	3	4.131853
P56593	NRQPQYEDHMK+Oxidation(9	0.952236033		
P56656	**CP239 Cytochrome P450 2C39**	**1.102243208**	**0.683693**	**4**
P56656	EHQESLDVTNPR	1.21823895	2	3.680467
P56656	IKEHQESLDVTNPR	1.017648056	3	4.872485
P56656	NYLIPK	1.524705192	1	2.1687
P56656	VQEEIDHVIGR	2.181416972	2	3.695102
P56812	**PDCD5 Programmed cell death protein 5**	**0.859350705**	**0.999999**	**3**
P56812	HGDPGDAAQQEAK	0.782707473	2	4.396952
P56812	NSILAQVLDQSAR	0.972841665	2	3.845855
P56812	VSEQGLIEILEK	1.05150753	2	3.330403
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.712331813**	**5.77E-15**	**8**
P57093	AISCHYGSSDCK	0.352294948	2	3.228014
P57093	IQDFQQNEELFR	1.182697773	2	3.579447
P57093	KFYEENGFLVIK	1.312180116	2	2.676775

P57093	MDYTRAGAR	0.675900706	2	2.560495
P57093	MYHGIQDYDPDSPR	1.340650716	2	2.98107
P57093	NLVSDDDIQR	0.687657616	2	2.428208
P57093	NNGCLVVLPGTHK	0.94245894	2	2.920339
P57093	YCALPQIVK	0.671981767	1	2.07252
P57113	**MAAI Maleylacetoacetate isomerase**	**1.624247469**	**0.0433**	**11**
P57113	AITSGFNALEK	1.144503621	2	3.415542
P57113	ALLALEAFQVSHPCR	1.631039915	2	4.127131
P57113	DGGQQFSEEFQTLNPMK	1.303995033	2	4.926748
P57113	FKVDLSPYPTISHINK	1.192869281	2	4.902491
P57113	GIDYEIVPINLIK	1.090885639	2	4.404492
P57113	IDGITIGQSLAILEYLEETRPIPR	1.275697815	3	4.186342
P57113	MISDLIASGIQPLQNLSVLK	1.320570193	2	5.435742
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0	1.393143557		
P57113	QVGQENQMPWAQK	1.198537492	2	3.821304
P57113	VDLSPYPTISHINK	1.073565149	2	3.782733
P57113	YCVGDEVSMADVCLAPQVANAER	4.627258802	3	6.559028
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.504725783**	**3.49E-11**	**3**
P57722	ESTGAQVQVAGDMLPNSTER	1.487649872	2	5.28909
P57722	INISEGNCPER	1.506064911	2	3.538505
P57722	LVVPASQCGSLIGK	1.545594235	2	2.59727
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**1.494417648**	**0.016858**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	1.224507124	3	4.678893
P58321	WLPLEANPEVTNQFLK	1.668742975	2	3.017756
P58389	**PTPA Serine/threonine_protein phosphatase 2A activator**	**0.955858671**	**0.52856**	**3**
P58389	FGSLLPIHPVTSG	1.156620796	2	2.404476
P58389	KEIHTVPDMGK	1.533617718	2	2.420179
P58389	WIDETPPVDQPSR	0.955707549	2	3.478476
P58751	**RELN Reelin**	**0.656085382**	**0.391926**	**2**
P58751	CGILSSGNNLFFNEDGLR	0.670560496	2	2.32494
P58751	QNYMMNFSRQHGLR	0.638276947	2	2.427728
P58775	**TPM2 Tropomyosin beta chain**	**1.343614194**	**0.165562**	**11**
P58775	AISEELDNALNDITSL	2.002640954	2	4.390842
P58775	ATDAEADVASLNR	3.885977969	2	4.232215
P58775	DAQEKLEQAEK	1.28949819	2	2.904305
P58775	KATDAEADVASLNR	1.490746102	2	4.086799
P58775	LDKENAIDR	1.810926825	2	3.089513
P58775	LKGTEDEVEK	0.452492494	2	2.856405
P58775	MELQEMQLK	1.090693878	2	2.981383
P58775	QLEEEQQALQK	0.964568629	2	3.554138
P58775	SLEAQADKYSTK	2.141668765	2	3.756636
P58775	TIDDLEDEVYAQK	2.613108988	2	3.950403
P58775	YSESVKDAQEK	0.356972246	2	3.099243
P59242	**CING Cingulin**	**1.576130394**	**0.005616**	**2**
P59242	LGQEQQALNR	1.906148171	2	2.793544
P59242	LQGLEQEAENK	1.488227226	2	2.96285
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.640208285**	**0.004684**	**2**
P59999	ELLLQPVTISR	1.339012547	2	3.025986
P59999	FMRFMMMR+Oxidation(4)Oxidation(5	2.972953833		
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.577450109**	**2.85E-11**	**4**
P60335	AITIAGVPQSVTECVK	1.396852213	2	3.529007
P60335	IITLTGPTNAIFK	1.809286013	2	2.904875
P60335	LVVPATQCGSLIGK	1.586771523	2	2.989144
P60335	VMTIPYQPMPASSPVICAGGQDR	1.716438406	3	4.438498

P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.799863698**	**2.82E-06**	**6**
P60843	ATQALVLAPTR	1.001567289	1	1.958489
P60843	GFKDQIYDIFQK	1.822456895	3	3.886211
P60843	GVAINMVTEEDKR	1.496145751	2	3.229809
P60843	KEELTLEGIR	1.626486008	2	2.353129
P60843	KGVAINMVTEEDKR	1.872620409	3	4.670231
P60843	LQMEAPHIIVGTPGR	1.464520378	3	3.87773
P60868	**RS20 40S ribosomal protein S20**	**1.274408336**	**0.000636**	**3**
P60868	DTGKTPVEPEVAIHR	1.503047024	3	4.419885
P60868	LIDLHSPSEIVK	1.245962643	2	3.134587
P60868	TPVEPEVAIHR	2.161191685	2	2.458653
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.163662327**	**0.157982**	**2**
P60901	AINQGGLTSVAVR	1.131159078	2	3.411844
P60901	LLDSSTVTHLFK	1.642051113	2	3.008124
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**0.988093897**	**0.071146**	**2**
P61087	GEIAGPPDTPYEGGR	1.363403038	2	3.205256
P61087	VDLVDENFTELR	0.97386033	2	3.504663
P61107	**RAB14 Ras_related protein Rab_14**	**1.25577848**	**0.011623**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	1.147659547	3	3.727832
P61107	NLTNPNTVIILIGNK	1.07409059	2	3.989622
P61107	SCLLHQFTEK	1.682514762	2	3.087084
P61107	STYNHLSSWLTDAR	1.178093452	2	3.315717
P61107	TGENVEDAFLEAAK	1.255917053	2	3.693744
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.278276657**	**0.313452**	**3**
P61222	GSELQNYFTK	1.365256361	2	2.340125
P61222	NTVANSPQTLLAGMNK	1.291802764	2	4.090226
P61222	VAETANEEEVKK	1.033297971	2	2.96918
P61314	**RL15 60S ribosomal protein L15**	**1.032826556**	**9.9E-20**	**5**
P61314	FFEVILIDPFHK	1.7949457	3	3.421684
P61314	GATYGKPVHHGVNQLK	1.452270079	2	4.386039
P61314	SLQSVAEER	1.383124261	2	2.793447
P61314	VLNSYWVGEDSTYK	1.465059888	2	4.083551
P61314	YIQELWR	1.028539255	2	2.612045
P61354	**RL27 60S ribosomal protein L27**	**1.177094306**	**0.761203**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	1.177083306	3	4.937042
P61354	VYNYNHLMPTR	1.246503316	2	3.019335
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.120701612**	**0.999999**	**3**
P61459	AVGWNELEGR	1.122411529	2	3.196966
P61459	LDHHPEWFNVYNK	0.85479796	3	4.978459
P61459	LSAEERDQLLPNLR	1.14968915	3	4.320259
P61589	**RHOA Transforming protein RhoA**	**1.307724097**	**0.057474**	**4**
P61589	HFCPNVPIILVGNK	2.79744771	2	3.296093
P61589	HFCPNVPIILVGNKK	1.453059166	3	4.512496
P61589	MKQEPVKPEEGR	1.374706158	3	4.121106
P61589	MKQEPVKPEEGR+Oxidation(0	0.909432834		
P61751	**ARF4 ADP_ribosylation factor 4**	**1.572544718**	**5.35E-14**	**6**
P61751	ILMVGLDAAGK	2.002613289	2	2.890382
P61751	IQEGAAVLQK	1.240874217	2	2.943055
P61751	KQMRILMVGLDAAGK	1.426470997	2	2.371472
P61751	LGEIVTTIPTIGFNVETVEYK	1.454286511	3	4.255967
P61751	NICFTVWDVGGQDK	1.496516203	2	4.217439
P61751	QDLPNAMAISEMTDK	1.860801425	2	3.607818
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.318446286**	**0.976068**	**2**
P61805	ADFQGISPER	1.145554184	2	3.110425

P61805	FLEEYLSSTPQR	1.337656968	2	3.781814
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.346469025**	**0.015523**	**2**
P61924	GEDVPLTEQTVSQVLQSAK	1.347703165	2	4.62344
P61924	YYDDTYPSVK	1.131366874	2	2.493596
P61972	**NTF2 Nuclear transport factor 2**	**2.106983253**	**0.192583**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	3.357575951	3	4.296495
P61972	NINDAWVCTNDMFR	1.290274923	2	3.772995
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.320646784**	**9.9E-20**	**9**
P61980	GSDFDCELR	2.090272619	2	2.768961
P61980	GSYGDLGGPIITTQVTIPK	1.052808937	2	5.164811
P61980	IDEPLEGSEDR	2.193618454	2	3.677006
P61980	IILDLISESPIK	1.456100938	2	4.095618
P61980	IITITGTQDQIQNAQYLLQNSVK	1.371333172	3	7.09349
P61980	LFQECCPHSTDR	1.434175651	2	3.90689
P61980	NTDEMVELR	2.214357177	2	2.665109
P61980	RSRNTDEMVELR	1.155720418	2	2.50928
P61980	TDYNASVSVPDSSGPER	1.047836921	2	4.563363
P61983	**1433G 14_3_3 protein gamma**	**1.327014985**	**0.000727**	**4**
P61983	AYSEAHEISK	0.655936645	2	3.530486
P61983	NVTELNEPLSNEER	1.335613236	2	4.657289
P61983	TAFDDAIAELDTLNEDSYK	1.061633779	2	4.773418
P61983	YLAEVATGEK	1.194625452	2	3.080956
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**1.307744936**	**0.191014**	**5**
P62076	CIGKPGGSLDNSEQK	1.128970835	2	4.092801
P62076	KCIGKPGGSLDNSEQK	1.387441553	3	3.977994
P62076	LDPGAIMEQVK	0.948691735	2	2.949828
P62076	VQIAVANAQELLQR	1.297558891	2	5.01919
P62076	YMDAWNTVSR	1.121419863	2	3.083282
P62083	**RS7 40S ribosomal protein S7**	**1.611057306**	**9.9E-20**	**5**
P62083	AIIIFVPVPQLK	1.766891059	2	3.759352
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	2.13367978	3	5.182621
P62083	KAIIIFVPVPQLK	1.227699182	2	3.6696
P62083	TLTAVHDAILEDLVFPSEIVGK	1.613711413	2	5.163402
P62083	VETFSGVYK	0.92435962	2	2.321308
P62161	**CALM Calmodulin**	**1.276137337**	**0.869616**	**4**
P62161	DGNGYISAAELR	1.301840483	2	2.970815
P62161	EADIDGDGQVNYEEFVQMMTAK	2.448737165	2	5.228692
P62161	EAFSLFDKDGDGTITTK	1.100195089	2	4.715992
P62161	VFDKDGNGYISAAELR	1.071749657	2	4.968894
P62193	**PRS4 26S protease regulatory subunit 4**	**1.3063489**	**0.000388**	**4**
P62193	AICTEAGLMALRERR+Oxidation(8	4.073505431		
P62193	AVANQTSATFLR	1.392875952	2	3.093301
P62193	NQEQMKPLEEK	1.093829753	2	3.545059
P62193	TMLELLNQLDGFDSR	2.279860584	2	4.136252
P62198	**PRS8 26S protease regulatory subunit 8**	**1.572181983**	**1.91E-05**	**6**
P62198	EVIELPVKHPELFEALGIAQPK	1.182338788	3	4.387872
P62198	IAELMPGASGAEVK	1.102790788	2	3.161131
P62198	LEGGSGGDSEVQR	1.649085911	2	3.709428
P62198	LLREELQLLQEQGSYVGEVVR	1.670210827	3	3.996678
P62198	TMLELLNQLDGFEATK	2.240152932	2	3.716094
P62198	VHVTQEDFEMAVAK	1.091064069	2	3.13595
P62243	**RS8 40S ribosomal protein S8**	**1.329273198**	**9.9E-20**	**9**
P62243	ADGYVLEGK	2.496424535	2	3.169785
P62243	IIDVVYNASNNELVR	1.951689151	2	4.228573
P62243	ISSLLEEQFQQGK	1.619451351	2	4.239766

P62243	KYELGRPAANTK	1.338092231	2	3.587833
P62243	LDVGNFSWGSECCTR	1.356057325	2	3.963382
P62243	LTPEEEEILNK	1.207165831	2	3.071696
P62243	NCIVLIDSTPYR	1.384474169	2	3.475894
P62243	QWYESHYALPLGR	2.343509994	2	2.923625
P62243	YELGRPAANTK	1.456725791	2	2.954505
P62246	**RS15A 40S ribosomal protein S15a**	**1.390201034**	**2.21E-05**	**4**
P62246	HGYIGEFEIIDDHR	1.379154635	3	4.921476
P62246	IVVNLTGR	1.979987844	2	2.329178
P62246	MNVLADALK	1.435801124	2	2.739142
P62246	WQNNLLPSR	1.220187233	2	3.117388
P62250	**RS16 40S ribosomal protein S16**	**1.423412673**	**0.004431**	**6**
P62250	ALVAYYQK	3.285297469	1	2.239725
P62250	EIKDILIQYDR	1.493967682	2	2.614253
P62250	GGGHVAQIYAIR	2.000135148	2	3.075345
P62250	LLEPVLLLGK	1.386531878	2	2.803022
P62250	TLLVADPR	1.416437931	2	2.608602
P62250	VNGRPLEMIEPR	1.330421329	2	2.695855
P62260	**1433E 14_3_3 protein epsilon**	**1.744980851**	**9.9E-20**	**9**
P62260	AAFDDAIAELDTLSEESYK	1.298016611	2	6.038109
P62260	EENKGGEDKLK	1.774121461	2	2.702422
P62260	HLIPAANTGESK	1.337264061	2	3.198699
P62260	IISSIEQK	1.368598039	2	2.608193
P62260	LICCDILDVLDK	2.837537654	2	4.056403
P62260	YDEMVESMK	1.177472443	2	2.710773
P62260	YDEMVESMKK	1.930717724	2	2.674832
P62260	YLAEFATGNDR	0.915743539	2	2.942227
P62260	YLAEFATGNDRK	1.704141967	2	2.73987
P62268	**RS23 40S ribosomal protein S23**	**1.490773829**	**0.003904**	**2**
P62268	GHAVGDIPGVR	1.497148733	2	2.747655
P62268	KGHAVGDIPGVR	1.22790337	2	2.825577
P62271	**RS18 40S ribosomal protein S18**	**1.150799455**	**9.9E-20**	**6**
P62271	AGELTEDEVER	2.628266555	2	3.696181
P62271	LREDLER	1.374402617	1	2.21055
P62271	RAGELTEDEVER	0.486424343	2	3.105144
P62271	VITIMQNPR	1.171305427	2	2.838989
P62271	VLNTNIDGR	2.567045282	2	3.127369
P62271	YSQVLANGLDNK	1.594186112	2	4.042987
P62278	**RS13 40S ribosomal protein S13**	**1.468796142**	**1.67E-08**	**5**
P62278	GLAPDLPEDLYHLIK	1.473927876	2	3.091916
P62278	GLSQSALPYR	1.176171618	2	2.478468
P62278	GLTPSQIGVILR	1.450647303	2	2.981237
P62278	KGLTPSQIGVILR	1.11450151	3	3.891465
P62278	LILIESR	1.670639205	1	2.073099
P62329	**TYB4 Thymosin beta_4**	**1.143491557**	**0.992834**	**3**
P62329	ETIEQEKQAGES	1.194227368	2	2.446251
P62329	NPLPSKETIEQEK	1.038560191	2	2.73218
P62329	TETQEKNPLPSK	1.087457642	2	3.739312
P62332	**ARF6 ADP_ribosylation factor 6**	**1.394728451**	**0.021122**	**2**
P62332	FNVWDVGGQDK	1.326790041	2	3.024646
P62332	LGQSVTTIPTVGFNVETVTYK	1.513923946	2	2.673682
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.135315179**	**0.009127**	**5**
P62334	ADHDFVVQEDFMK	1.212015989	2	2.323827
P62334	ALQSVGQIVGEVLK	1.225928834	2	3.615002
P62334	EVIELPLTNPELFQR	1.516453358	2	3.035747
P62334	HGEIDYEAIVK	0.812624017	2	3.530829
P62334	NVCTEAGMFAIR	1.32377981	2	2.767191

P62425	**RL7A 60S ribosomal protein L7a**	**1.186414464**	**0.011324**	**11**
P62425	AGVNTVTTLVENK	1.265666655	2	4.029154
P62425	AGVNTVTTLVENKK	2.625007616	2	3.334574
P62425	HWGGNVLGPK	1.262019062	1	2.915874
P62425	KVVNPLFEK	0.984017039	2	2.366081
P62425	LKVPPAINQFTQALDR	1.8017354	3	4.296217
P62425	NFGIGQDIQPK	1.097084132	2	3.368641
P62425	TCTTVAFTQVNSEDK	1.466184071	2	3.350617
P62425	TCTTVAFTQVNSEDKGALAK	1.77681822	2	4.682706
P62425	TNYNDRYDEIR	1.324174544	2	2.356894
P62425	VAPAPAVVK	0.959288616	1	2.153366
P62425	VPPAINQFTQALDR	1.202195142	2	3.697337
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.374938425**	**9.9E-20**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.496107526	3	4.986901
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.591684653	4	5.250643
P62630	MDSTEPPYSQK	1.397891332	2	3.741361
P62630	MDSTEPPYSQK+Oxidation(0	1.545744569		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.484059668	5	5.934408
P62630	RYEEIVK	1.112996025	2	2.739399
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.300876156	3	5.207468
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14	1.612532059		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8	1.483903576		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.846109997	3	5.633935
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9	0.883725967		
P62630	YEEIVK	1.247139086	2	2.341627
P62630	YYVTIIDAPGHR	0.827074111	3	4.103999
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.858046601**	**9.9E-20**	**7**
P62632	EHALLAYTLGVK	1.645459731	3	3.703176
P62632	IGGIGTVPVGR	1.574507109	2	3.548563
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.367007625	3	4.565644
P62632	QLIVGVNK	1.237582204	1	2.43109
P62632	STTTGHLIYK	5.47519879	2	3.069805
P62632	THINIVVIGHVDSGK	1.987989594	2	5.397683
P62632	VETGILRPGMVVTFAPVNITTEVK	2.058859589	3	3.944329
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.352336272**	**2.25E-05**	**2**
P62634	CGETGHVAINCSK	1.339475674	2	4.453517
P62634	CYSCGEFGHIQK	1.380664267	2	3.379993
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.378961432**	**0.418106**	**5**
P62703	FDTGNLCMVTGGANLGR	1.360763731	2	4.779842
P62703	GIPHLVTHDAR	1.328711324	2	2.746728
P62703	LSNIFVIGK	1.471788869	2	3.123281
P62703	TDITYPAGFMDVISIDK	1.575735511	2	4.946909
P62703	VNDTIQIDLETGK	1.691019829	2	4.548001
P62718	**RL18A 60S ribosomal protein L18a**	**1.118609912**	**0.453208**	**2**
P62718	DLTTAGAVTQCYR	1.063960624	2	3.163642
P62718	SSGEIVYCGQVFEKSPLR	2.296444126	2	2.508621
P62752	**RL23A 60S ribosomal protein L23a**	**1.459303804**	**1.12E-08**	**7**
P62752	KLYDIDVAK	1.374954902	2	2.391035
P62752	LAPDYDALDVANK	1.356730231	2	3.71814
P62752	LDHYAIIK	1.378132138	2	2.522631
P62752	LYDIDVAK	1.444073893	1	1.985749
P62752	NKLDHYAIIK	1.191710535	3	3.39016
P62752	VNTLIRPDGEK	1.462777011	2	3.340559
P62752	VNTLIRPDGEKK	1.554383751	2	2.930458
P62755	**RS6 40S ribosomal protein S6**	**1.238498962**	**3.33E-16**	**4**

P62755	LIEVDDER	1.040651638	2	3.077241
P62755	LNISFPATGCQK	1.11007233	2	2.850919
P62755	MATEVAADALGEEWK	1.758637424	2	4.785816
P62755	MATEVAADALGEEWK+Oxidation(0	1.237797165		
P62775	**MTPN Myotrophin**	**1.039234478**	**0.970062**	**3**
P62775	GPDGLTALEATDNQAIK	1.375085301	2	3.90549
P62775	HHITPLLSAVYEGHVSCVK	0.989225657	3	3.942154
P62775	NGDLDEVKDYVAK	1.035095652	2	3.191914
P62804	**H4 Histone H4**	**1.059657534**	**9.9E-20**	**9**
P62804	DAVTYTEHAK	1.620315241	2	3.011259
P62804	DNIQGITKPAIR	1.415556714	2	3.141638
P62804	ISGLIYEETR	1.428674474	2	3.972643
P62804	KTVTAMDVVYALK	1.303928622	3	4.774006
P62804	RISGLIYEETR	1.37619173	2	2.403309
P62804	TVTAMDVVYALK	1.052567308	2	3.900661
P62804	TVTAMDVVYALK+Oxidation(4	1.614298065		
P62804	VFLENVIR	1.330762913	2	3.264373
P62804	VFLENVIRDAVTYTEHAK	1.232035946	3	3.87555
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**1.205481821**	**0.21529**	**3**
P62815	AVVQVFEGTSGIDAK	0.763286978	2	3.643313
P62815	IYPEEMIQTGISAIDGMNSIAR	2.167875142	3	3.440888
P62815	SGQVLEVSGSK	1.218735013	2	2.812166
P62845	**RS15 40S ribosomal protein S15**	**1.393499277**	**0.157987**	**2**
P62845	DMIILPEMVGSMVGVYNGK	1.416301997	2	3.158473
P62845	KEAPPMEKPEVVK	1.387389892	3	4.032125
P62850	**RS24 40S ribosomal protein S24**	**1.588042084**	**1.25E-09**	**2**
P62850	KQMVIDVLHPGK	2.04840906	3	3.67591
P62850	TTGFGMIYDSLDYAK	1.584960907	2	4.004062
P62856	**RS26 40S ribosomal protein S26**	**1.380773256**	**3.59E-07**	**4**
P62856	DISEASVFDAYVLPK	1.705271908	2	3.110003
P62856	FRPAGAAPRPPPKPM	1.066022252	2	2.73655
P62856	LHYCVSCAIHSK	1.193687655	3	3.337881
P62856	NIVEAAAVR	1.379817189	2	3.013587
P62859	**RS28 40S ribosomal protein S28**	**1.552878505**	**3.79E-05**	**2**
P62859	EGDVLTLLESER	1.566831609	2	3.536335
P62859	VEFMDDTSR	1.339545004	2	2.704906
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.270443679**	**0.325442**	**3**
P62870	ADDTFEALR	1.226464648	2	2.547496
P62870	LYKDDQLLDDGK	1.270282833	2	2.9807
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.383950547	3	4.520145
P62890	**RL30 60S ribosomal protein L30**	**0.925188169**	**2.54E-10**	**3**
P62890	LVILANNCPALR	1.389991781	2	3.065414
P62890	TGVHHYSGNNIELGTACGK	1.13458164	2	5.689928
P62890	VCTLAIIDPGDSDIIR	2.332337473	2	4.240249
P62898	**CYC Cytochrome c_ somatic**	**1.320200959**	**9.9E-20**	**7**
P62898	ADLIAYLK	1.156404025	2	3.125129
P62898	ADLIAYLKKATNE	1.294159208	2	2.462525
P62898	GITWGEDTLMEYLENPK	1.786699596	2	4.988049
P62898	GITWGEDTLMEYLENPKK	1.637274385	2	4.316432
P62898	KTGQAAGFSYTDANK	1.14032494	2	5.192502
P62898	TGPNLHGLFGR	0.919721103	2	3.372039
P62898	TGQAAGFSYTDANK	1.348162362	2	4.189436
P62902	**RL31 60S ribosomal protein L31**	**1.5435816**	**0.15882**	**2**
P62902	NLQTVNVDEN	1.484306247	1	2.419814
P62902	SAINEVVTR	1.863787529	2	3.054344

P62907	**RL10A 60S ribosomal protein L10a**	**1.380327117**	**5.23E-09**	**6**
P62907	AVDIPHMDIEALK	1.434039061	2	3.038153
P62907	AVDIPHMDIEALKK	1.179370966	2	3.072406
P62907	FSVCVLGDQQHCDEAK	1.393138236	2	4.123172
P62907	KYDAFLASESLIK	1.348078354	2	3.843312
P62907	VLCLAVAVGHVK	0.898546868	2	3.234421
P62907	YDAFLASESLIK	1.024898359	2	3.305998
P62909	**RS3 40S ribosomal protein S3**	**1.543495245**	**9.9E-20**	**10**
P62909	AELNEFLTR	1.328881768	2	3.194365
P62909	DEILPTTPISEQK	1.312305972	2	3.3224
P62909	ELAEDGYSGVEVR	1.546945388	2	3.832286
P62909	ELTAVVQK	1.40629574	1	2.051346
P62909	FGFPEGSVELYAEK	3.699060133	2	3.56604
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.546004516	3	4.761268
P62909	GCEVVVSGK	1.231278715	2	2.416892
P62909	GGKPEPPAMPQPVPTA	1.588476728	2	4.071256
P62909	GLCAIAQAESLR	1.0806369	2	3.360262
P62909	TEIIILATR	1.723969098	2	3.281584
P62912	**RL32 60S ribosomal protein L32**	**1.193757919**	**6.22E-05**	**3**
P62912	ELEVLLMCNK	1.330012674	2	3.296674
P62912	GQILMPNIGYGSNK	1.192659644	2	3.15751
P62912	SYCAEIAHNVSSK	1.2801797	2	4.413827
P62914	**RL11 60S ribosomal protein L11**	**1.074182408**	**0.017651**	**2**
P62914	VLEQLTGQTPVFSK	1.038920635	2	4.426752
P62914	YDGIILPGK	1.27362103	2	3.059244
P62919	**RL8 60S ribosomal protein L8**	**1.40277895**	**9.9E-20**	**4**
P62919	ASGNYATVISHNPETK	1.385647959	2	4.435143
P62919	AVDFAER	1.47502699	1	1.977413
P62919	AVVGVVAGGGR	1.402988217	2	3.618767
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.391883554	3	5.372764
P62944	**AP2B1 AP_2 complex subunit beta**	**1.645891622**	**0.080759**	**3**
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.964717494	3	3.304678
P62944	LQNNNVYTIAK	1.647488535	2	2.407783
P62944	SQPDMAIMAVNSFVK	1.172600668	2	2.973409
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**1.01216546**	**0.06832**	**7**
P62959	AQVAQPGGDTIFGK	1.059973199	2	4.752118
P62959	CAADLGLK	1.221885941	2	2.52929
P62959	CLAFHDISPQAPTHFLVIPK	1.322582227	3	4.290545
P62959	HISQISVADDDDESLLGHLMIVGK	1.555166418	3	6.725867
P62959	IIFEDDR	1.344967773	2	2.599562
P62959	KHISQISVADDDDESLLGHLMIVGK	1.476040105	3	5.490684
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.701857931	3	4.379941
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.351064558**	**0.873749**	**6**
P62961	EDGNEEDKENQGDETQGQQPPQR	1.251609846	3	5.126131
P62961	GAEAANVTGPGGVPVQGSK	0.926404331	2	4.973924
P62961	NEGSESAPEGQAQQR	1.407534163	2	5.211066
P62961	NYQQNYQNSESGEK	1.177158453	2	4.823812
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	0.907094419	3	5.129217
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.386984191	3	5.12013
P62963	**PROF1 Profilin_1**	**1.371950471**	**3.33E-16**	**6**
P62963	CYEMASHLR	1.815106173	2	2.394007
P62963	DSLLQDGEFTMDLR	1.807527784	2	3.409657
P62963	DSPSVWAAVPGK	1.314781859	2	2.740582
P62963	SSFFVNGLTLGGQK	1.370908333	2	4.35779
P62963	STGGAPTFNVTVTMTAK	1.375600917	2	3.434676

P62963	TFVSITPAEVGVLVGK	1.243676657	2	4.637149
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.32474456**	**9.9E-20**	**25**
P63018	ARFEELNADLFR	1.481290384	3	3.739548
P63018	CNEIISWLDK	1.777450554	2	3.179036
P63018	DAGTIAGLNVLR	2.084632008	2	3.69132
P63018	FDDAVVQSDMK	1.192492537	2	3.871005
P63018	FEELNADLFR	1.265826103	2	3.289832
P63018	FELTGIPPAPR	1.283951216	2	3.13579
P63018	HWPFMVVNDAGRPK	3.945572633	3	3.510468
P63018	IINEPTAAAIAYGLDK	1.459092411	2	5.428555
P63018	IINEPTAAAIAYGLDKK	1.320943348	2	4.279563
P63018	LLQDFFNGK	1.751683243	2	2.692153
P63018	MKEIAEAYLGK	1.219546556	2	3.452201
P63018	MVNHFIAEFK	0.8824493	2	2.861875
P63018	NQTAEKEEFEHQQK	1.139111927	2	5.268318
P63018	NQVAMNPTNTVFDAK	1.102424894	2	4.970622
P63018	NQVAMNPTNTVFDAK+Oxidation(4	1.471028004		
P63018	NSLESYAFNMK	1.079470143	2	3.506338
P63018	RFDDAVVQSDMK	1.259581337	2	3.628594
P63018	SFYPEEVSSMVLTK	1.353107654	2	4.957209
P63018	SFYPEEVSSMVLTK+Oxidation(9	1.665769192		
P63018	SINPDEAVAYGAAVQAAILSGDK	1.688094215	2	5.931759
P63018	SQIHDIVLVGGSTR	1.29022323	2	4.466779
P63018	STAGDTHLGGEDFDNR	1.22909594	2	4.729926
P63018	TVTNAVVTVPAYFNDSQR	1.310316312	3	4.900881
P63018	VCNPIITK	1.321984005	2	2.538222
P63018	VQVEYKGETK	1.402684334	2	2.543759
P63029	**TCTP Translationally_controlled tumor protein**	**1.360987437**	**0.347048**	**3**
P63029	DLISHDELFSDIYK	1.787080836	2	3.900172
P63029	EIADGLCLEVEGK	1.33630013	2	3.267323
P63029	VKPFMTGAAEQIK	1.389935329	3	3.341167
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.328258824**	**0.284268**	**7**
P63036	ETTYYDVLGVKPNATQEELKK	1.08191331	3	3.56827
P63036	HYNGEAYEDDEHHPR	1.33108795	3	4.959896
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.579041605	3	4.00024
P63036	NVVHQLSVTLEDLYNGATR	1.043724666	2	4.050008
P63036	QISQAYEVLADSK	1.115501242	2	3.17226
P63036	TIVITSHPGQIVK	1.637555881	2	3.626172
P63036	VNFPENGFLSPDK	1.109849326	2	3.421634
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.236456498**	**9.9E-20**	**36**
P63039	AAVEEGIVLGGGCALLR	1.484093365	2	5.380049
P63039	ALMLQGVDLLADAVAVTMGPK	1.541934043	3	6.582479
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(17	1.455670602		
P63039	CEFQDAYVLLSEK	2.853100567	2	4.408102
P63039	CIPALDSLKPANEDQK	1.061561605	2	3.53513
P63039	DDAMLLK	1.479996464	1	1.999974
P63039	DIGNIISDAMK	1.064530821	2	3.37775
P63039	GIIDPTK	1.267060712	1	1.930636
P63039	GVMLAVDAVIAELK	1.471459806	2	4.538907
P63039	GVMLAVDAVIAELKK	1.179457774	2	4.63125
P63039	GYISPYFINTSK	0.603962059	2	3.091484
P63039	IGIEIIK	0.962287263	2	2.679756
P63039	IGIEIIKR	2.808531809	2	2.419956
P63039	ILQSSSEVGYDAMLGDFVNMVEK	2.266908919	3	5.091751
P63039	IQEITEQLDITTSEYEK	1.529429173	2	5.623862
P63039	IQEITEQLDITTSEYEKEK	1.254762585	2	5.269607
P63039	ISSVQSIVPALEIANAHR	1.633554939	2	4.326787

P63039	KISSVQSIVPALEIANAHR	2.17499898	3	4.38552
P63039	KPLVIIAEDVDGEALSTLVLNR	1.787163008	2	6.014946
P63039	LSDGVAVLK	1.275222872	2	2.968635
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.356894809	2	6.517145
P63039	NAGVEGSLIVEK	1.266648076	2	3.412197
P63039	QSKPVTTPEEIAQVATISANGDK	1.206951584	2	3.415241
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.011555619	3	4.849346
P63039	RGVMLAVDAVIAELKK	0.145051452	3	5.931686
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	3.135487408	3	5.146729
P63039	TLNDELEIIEGMK	1.352671817	2	4.79828
P63039	TLNDELEIIEGMK+Oxidation(11	2.938070601		
P63039	TVIIEQSWGSPK	1.086883698	2	4.427644
P63039	VGEVIVTK	1.090346342	2	3.241752
P63039	VGEVIVTKDDAMLLK	1.125940046	2	3.609174
P63039	VGGTSDVEVNEK	0.420282059	2	3.803713
P63039	VGGTSDVEVNEKK	1.376505883	2	3.736011
P63039	VGGTSDVEVNEKKDR	0.831625221	2	3.417169
P63039	VGLQVVAVK	1.377302574	2	3.098645
P63039	VTDALNATR	1.167788386	2	3.442991
P63092	**subunit alpha isoforms short**	**1.350494623**	**0.001777**	**2**
P63092	AFEPFYDEIKSKGALVK	1.351439254		
P63092	YTTPEDATPEPGEDPR	0.75761715		
P63102	**1433Z 14_3_3 protein zeta/delta**	**1.115627325**	**0.131009**	**10**
P63102	DICNDVLSLLEK	1.703340708	3	3.817304
P63102	EMQPTHPIR	2.255925702	2	2.323834
P63102	FLIPNASQPESK	1.110915349	2	2.909475
P63102	GIVDQSQQAYQEAFEISK	1.304108632	2	5.67016
P63102	KGIVDQSQQAYQEAFEISK	0.979393391	2	5.266699
P63102	SVTEQGAELSNEER	0.759435619	2	5.174216
P63102	TAFDEAIAELDTLSEESYK	2.483904322	3	4.635648
P63102	YDDMAACMK	1.735806216	2	2.523872
P63102	YLAEVAAGDDK	1.575688785	2	2.360577
P63102	YLAEVAAGDDKK	1.371723646	2	3.515499
P63159	**HMGB1 High mobility group protein B1**	**1.241174938**	**0.010862**	**6**
P63159	GEHPGLSIGDVAK	1.097618821	2	2.978562
P63159	GKFEDMAK	1.227974142	1	2.015042
P63159	IKGEHPGLSIGDVAK	1.925819054	2	4.02613
P63159	KHPDASVNFSEFSK	1.162966965	3	4.193828
P63159	KLGEMWNNTAADDKQPYEK	1.268520417	3	4.61693
P63159	LGEMWNNTAADDKQPYEK	1.446228163	2	4.932132
P63174	**RL38 60S ribosomal protein L38**	**1.388112313**	**7.82E-07**	**2**
P63174	IEEIKDFLLTAR	1.566803489	2	3.032556
P63174	KIEEIKDFLLTAR	1.370084225	2	4.602397
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.336982775**	**7.26E-05**	**13**
P63245	DETNYGIPQR	1.037130767	2	2.521435
P63245	DGQAMLWDLNEGK	1.891036188	2	3.3529
P63245	FSPNSSNPIIVSCGWDK	1.22898696	2	4.22051
P63245	GHNGWVTQIATTPQFPDMILSASR	1.426645182	3	4.196202
P63245	HLYTLDGGDIINALCFSPNR	1.715164224	2	6.134309
P63245	IIVDELK	1.807093687	2	2.497849
P63245	IIVDELKQEVISTSSK	1.391292238	3	4.084158
P63245	IWDLEGK	1.33681765	2	2.364232
P63245	LWDLTTGTTTR	0.80297469	1	1.957726
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.103148216	3	5.394726
P63245	VWNLANCK	1.281483841	2	2.586869
P63245	VWQVTIGTR	1.627774198	2	2.862437

P63245	YWLCAATGPSIK	0.810807843	2	3.534124
P63259	**ACTG Actin_ cytoplasmic 2**	**1.11919066**	**4.04E-14**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.410779392	3	5.688723
P63259	DLYANTVLSGGTTMYPGIADR	0.773509301	2	6.093601
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13	0.990423459		
P63259	GYSFTTTAER	1.099556333	2	3.516659
P63259	KDLYANTVLSGGTTMYPGIADR	1.293340045	2	6.300117
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14	1.36332363		
P63259	QEYDESGPSIVHR	1.263221125	3	3.506428
P63259	VAPEEHPVLLTEAPLNPK	1.349796887	2	4.680664
P63324	**RS12 40S ribosomal protein S12**	**1.495008136**	**0.029727**	**4**
P63324	KVVGCSCVVVK	1.054969471	2	3.278168
P63324	LGEWVGLCK	1.541151202	2	3.16608
P63324	QAHLCVLASNCDEPMYVK	1.504650863	3	3.989175
P63324	VVGCSCVVVK	1.51279849	2	3.239241
P67779	**PHB Prohibitin**	**1.219471066**	**0.412215**	**11**
P67779	AAELIANSLATAGDGLIELR	1.183285511	3	5.068403
P67779	AAIISAEGDSK	1.423941983	2	2.578406
P67779	DLQNVNITLR	0.916023211	2	3.242949
P67779	FDAGELITQR	0.798385666	2	3.725565
P67779	FGLALAVAGGVVNSALYNVDAGHR	1.589078235	3	3.376012
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.497770588	3	4.434541
P67779	IYTSIGEDYDER	1.394169232	2	3.502151
P67779	KLEAAEDIAYQLSR	1.097723961	2	4.643274
P67779	NVPVITGSK	0.994509381	1	2.286965
P67779	QVSDDLTER	0.835781909	2	2.453339
P67779	VLPSITTEILK	1.852254675	2	2.402501
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.384598024**	**5.79E-12**	**4**
P68037	ADLAEEYSK	3.687347856	2	2.388268
P68037	GQVCLPVISAENWKPATK	0.926921744	2	4.407991
P68037	IEINFPAEYPFKPPK	0.861680797	2	3.332929
P68037	TDQVIQSLIALVNDPQPEHPLR	1.395851801	2	5.288611
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.083916215**	**0.243276**	**5**
P68101	AGLNCSTETMPIK	1.448950485	2	3.129727
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.945780153	3	4.078288
P68101	HVAEVLEYTKDEQLESLFQR	1.050223166	3	4.00685
P68101	TEGLSVLNQAMAVIK	1.455480713	2	4.135961
P68101	VVTDTDETELAR	0.872473635	2	3.779957
P68136	**ACTS Actin_ alpha skeletal muscle**	**0.9122363**	**0.366424**	**18**
P68136	AGFAGDDAPR	1.360175994	2	3.464919
P68136	AVFPSIVGRPR	0.976359361	2	2.422471
P68136	DLYANNVMSGGTTMYPGIADR	1.16574161	2	4.723485
P68136	DSYVGDEAQSK	162.4691371	2	3.462277
P68136	DSYVGDEAQSKR	0.885866539	2	2.571075
P68136	EITALAPSTMK	1.214340084	2	2.984336
P68136	EITALAPSTMK+Oxidation(9	1.12135878		
P68136	GYSFVTTAER	1.575256302	2	3.724853
P68136	IWHHTFYNELR	2.241059008	2	2.961479
P68136	KDLYANNVMSGGTTMYPGIADR	0.640887914	2	5.141508
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14	1.583525653		
P68136	MQKEITALAPSTMK	14.85240319	2	3.519155
P68136	QEYDEAGPSIVHR	3.948520469	3	3.300134
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	2.981544969	3	6.090837
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28	5.300009984		
P68136	VAPEEHPTLLTEAPLNPK	1.853344195	2	4.242673

P68136	YPIEHGIITNWDDMEK	1.419205469	2	4.757529
P68136	YPIEHGIITNWDDMEK+Oxidation(13	1.589134366		
P68255	**1433T 14_3_3 protein theta**	**0.947183444**	**0.543844**	**7**
P68255	AVTEQGAELSNEER	0.773281969	2	4.687196
P68255	SICTTVLELLDK	1.796885125	2	3.226551
P68255	TAFDEAIAELDTLNEDSYK	1.052985784	2	3.286028
P68255	VISSIEQK	0.945421048	2	2.609917
P68255	YLAEVACGDDR	0.742042868	2	2.353106
P68255	YLAEVACGDDRK	1.458087867	2	3.161403
P68255	YLIANATNPESK	1.651866412	2	3.172269
P68511	**1433F 14_3_3 protein eta**	**1.39132847**	**0.686712**	**5**
P68511	AVTELNEPLSNEDR	1.169167408	2	4.996502
P68511	ELETVCNDVLALLDK	0.943958579	2	3.572496
P68511	NCNDFQYESK	1.276398006	2	2.616769
P68511	NSVVEASEAAYK	1.430011727	2	2.806298
P68511	YLAEVASGEK	2.274243973	2	2.54534
P69897	**TBB5 Tubulin beta_5 chain**	**1.372107922**	**9.9E-20**	**4**
P69897	ALTVPELTQQVFDAK	1.402395984	2	3.275477
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	1.395650622	3	4.529301
P69897	ISVYYNEATGGK	1.779829583	2	2.879512
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.129457633	2	5.170762
P70191	**TRAF5 TNF receptor_associated factor 5**	**1.086611622**	**0.4836**	**2**
P70191	SLRELNSVPICPVDK	0.371378072	2	2.342856
P70191	VTLMLLDQSGK	1.090352695	2	2.459722
P70372	**ELAV1 ELAV_like protein 1**	**1.520919702**	**0.016731**	**3**
P70372	SLFSSIGEVESAK	1.589189885	2	3.222713
P70372	TNLIVNYLPQNMTQEELR	1.534161166	2	3.548444
P70372	VLVDQTTGLSR	1.005357511	2	2.79901
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.34323837**	**0.518485**	**4**
P70470	ASFSQGPINSANR	1.232174469	2	3.093076
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.387236461	3	3.702856
P70470	GLVNPANVTFK	1.298546458	2	2.455553
P70470	VYEGMMHSSCQQEMMDVK	1.34328024	3	3.351581
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**1.016641819**	**0.019587**	**11**
P70473	ADVLLEPFR	1.048525278	2	3.339565
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	1.563700183	4	4.72753
P70473	DYGFSQEEIHQLHSDR	1.259919775	2	4.804685
P70473	GLGLESEELPSQMSIEDWPEMK	1.542994555	3	4.502789
P70473	GQNLLDGGAPFYTTYK	0.889146234	2	4.859505
P70473	GSFITDEEQHACPRPAPQLSR	1.133137524	3	4.298388
P70473	LGSVNHPSHLAR	1.542861176	2	3.312409
P70473	LQLGPETLR	1.021129123	2	2.405218
P70473	RDPSVGEHTVEVLK	0.988925053	3	4.242515
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.879248602	4	5.425123
P70473	TQAMGLWAQPR	1.342345443	2	3.47042
P70550	**RAB8B Ras_related protein Rab_8B**	**1.672026887**	**2.82E-07**	**2**
P70550	LLLIGDSGVGK	1.672046722	2	2.912005
P70550	NIEEHASSDVER	1.527805878	2	2.980766
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**1.103399091**	**0.049514**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	1.068905351	3	5.170335
P70552	VLGNNFYEYYVNDPPR	1.226523697	2	4.281553
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.925623514**	**0.798795**	**9**
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	2.189366516	3	5.384453
P70580	EGEEPTVYSDDEEPKDEAAR	0.500035988	2	4.595736
P70580	FYGPEGPYGVFAGR	1.038979762	2	4.537755

P70580	GDQPGASGDNDDDEPPPLPR	66.63741586	2	4.997778
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.486758316	3	5.551701
P70580	KFYGPEGPYGVFAGR	0.733834937	2	3.904198
P70580	LLKEGEEPTVYSDDEEPKDEAAR	1.259107772	3	4.285386
P70580	RYDGVQDPR	1.542842431	1	2.080881
P70580	YDGVQDPR	0.84636858	2	2.876349
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.286654433**	**0.000132**	**9**
P70584	ASSTCQLTFENVK	1.718859957	2	2.89981
P70584	FAQEQIAPLVSTMDENSK	1.274084361	2	4.619984
P70584	IFDFQGLQHQVAHVATQLEAAR	1.665426294	3	6.060272
P70584	IGTIYEGTSNIQLNTIAK	1.434573137	2	4.507664
P70584	KFAQEQIAPLVSTMDENSK	1.016186681	2	6.008411
P70584	SGNYYVINGSK	1.457182112	2	3.362151
P70584	SVIQGLFQQGMMGIEVEAK	1.632913156	2	4.497092
P70584	VDASVALLCDIQNTVINK	2.348545482	2	4.870868
P70584	YYASEVAGLTTSK	1.119912659	2	4.224216
P70615	**LMNB1 Lamin_B1**	**1.687170805**	**0.015494**	**5**
P70615	ALYETELADAR	1.649012006	2	3.119909
P70615	KESDLSGAQIK	1.231807707	2	2.451973
P70615	LSSEMNTSTVNSAR	1.413662073	2	3.935456
P70615	NQNSWGTGEDVK	1.153775098	2	3.369616
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.756062164	3	3.621233
P70712	**KYNU Kynureninase**	**1.286979391**	**0.000317**	**11**
P70712	FKDCFYIPK	1.303251886	2	2.651535
P70712	IATELNCDPTDER	2.279173301	2	3.815662
P70712	IGAYGHEVGK	5.04303098	2	2.833856
P70712	LDEEDKLK	0.549380692	2	2.331851
P70712	LDEEDKLKR	1.405483851	2	2.687615
P70712	LLTAILDSTERN	1.568116366	2	3.306723
P70712	MEDILEVIEK	1.448112991	2	3.054292
P70712	TYLEEELDK	1.518314653	1	2.103857
P70712	TYLEEELDKWAK	0.855614425	2	2.736161
P70712	VAPVPLYNSFHDVYK	1.604369986	2	3.42916
P70712	YLNSGAGGLAGAFIHEK	1.503696105	2	4.456246
P80067	**CATC Dipeptidyl peptidase 1**	**1.467645518**	**9.9E-20**	**5**
P80067	GINFVSPVR	0.985021356	2	3.004387
P80067	GTDECAIESIAMAAIPIPK	1.380005347	2	5.137283
P80067	NSWGSQWGESGYFR	1.782527964	2	3.413845
P80067	RGTDECAIESIAMAAIPIPK	1.787984772	2	4.106503
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.397131474	3	5.782828
P80254	**DOPD D_dopachrome decarboxylase**	**1.013473706**	**2.31E-05**	**4**
P80254	FFPLEPWQIGK	0.81653634	2	2.789074
P80254	FLTEELSLDQDR	1.979796267	2	3.733937
P80254	LCAATATILDKPEDR	2.038058409	2	4.48946
P80254	STEPCAHLLISSIGVVGTAEQNR	1.004185032	2	5.495889
P80299	**HYES Epoxide hydrolase 2**	**1.072220949**	**0.842098**	**4**
P80299	ATEMGGILVGTPEDPK	1.583387609	2	3.470818
P80299	GHIEDCGHWTQIEKPAEVNQILIK	0.94008969	3	4.254334
P80299	TEIQNPSVTSK	0.867634965	2	2.656689
P80299	TSDDMGLLTVNK	1.134042437	2	3.205378
P80313	**TCPH T_complex protein 1 subunit eta**	**1.249929949**	**3.45E-05**	**6**
P80313	ATISNDGATILK	1.486537115	2	2.634861
P80313	EGTDSSQGIPQLVSNISACQVIAEAVR	3.990613848	3	4.156898
P80313	GGAEQFMEETER	1.248277722	2	3.149136
P80313	LLDVVHPAAK	1.525824358	2	2.549361
P80313	QLCDNAGFDATNILNK	1.169878783	2	3.845605

P80313	SQDAEVGDGTTSVTLLAAEFLK	1.5876455	2	3.459234
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.159759266**	**1.28E-05**	**10**
P80317	ALQFLEQVK	2.462639142	2	2.704194
P80317	DGNVLLHEMQIQHPTASLIAK	1.785514348	3	4.664173
P80317	GIDPFSLDALAK	2.448130493	2	2.829506
P80317	HKSETDTSLIR	1.321383238	2	3.143186
P80317	IITEGFEAAK	1.501720114	2	2.531834
P80317	MLVSGAGDIK	0.628498295	2	2.348649
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.201163495	3	3.732854
P80317	TEVNSGFFYK	1.18776241	2	2.666821
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.216665531	2	4.713727
P80317	VLAQNSGFDLQETLVK	1.151046403	2	3.732818
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.8110784**	**0.230722**	**4**
P81155	LTFDTTFSPNTGK	1.237960996	2	3.594403
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.639479737	3	3.985525
P81155	VNNSSLIGVGYTQTLRPGVK	0.783266055	2	3.586435
P81155	YQLDPTASISAK	0.801490061	2	2.949876
P82198	**BGH3 Transforming growth factor_beta_induced protein ig_h3**	**1.31975864**	**0.400792**	**2**
P82198	MLTPPMGTVMDVLK+Oxidation(0)Oxidation(5	1.685194013		
P82198	SLQGDKLEVSSK	1.315271624	2	3.096658
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.22229898**	**0.004281**	**14**
P82995	DQVANSAFVER	0.851527094	2	2.680401
P82995	ELHINLIPNKQDR	1.850335652	2	2.819498
P82995	ELISNSSDALDK	1.294336099	2	2.928744
P82995	FYEQFSK	1.186749161	1	2.106743
P82995	HIYFITGETK	1.056804164	2	3.133231
P82995	HLEINPDHSIIETLR	1.251776902	2	4.686529
P82995	HSQFIGYPITLFVEK	2.510589025	3	3.722916
P82995	KHGLEVIYMIEPIDEYCVQQLK	1.756441414	3	3.330358
P82995	LGIHEDSQNR	1.071419252	1	3.111243
P82995	NPDDITNEEYGEFYK	6.691570527	2	5.087471
P82995	SLTNDWEEHLAVK	1.141685735	2	4.057657
P82995	TLTIVDTGIGMTK	1.321357909	2	4.279113
P82995	TLTIVDTGIGMTK+Oxidation(10	1.877561295		
P82995	YYTSASGDEMVSLK	1.682288538	2	3.137735
P83732	**RL24 60S ribosomal protein L24**	**1.584334595**	**1.11E-16**	**5**
P83732	AITGASLADIMAK	1.585842867	2	4.619991
P83732	CESAFLSK	1.566707747	2	2.366067
P83732	QINWTVLYR	1.553115883	2	2.597057
P83732	VELCSFSGYK	1.091682906	2	2.340479
P83732	VFQFLNAK	1.916764749	2	2.346518
P83868	**TEBP Prostaglandin E synthase 3**	**1.554662489**	**3.67E-07**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.761733113	3	4.053787
P83868	LTFSCLGGSDNFK	1.554388029	2	2.755632
P83883	**RL36A 60S ribosomal protein L36a**	**1.221012513**	**1.55E-11**	**2**
P83883	HFELGGDK	1.133447785	1	2.378389
P83883	LECVEPNCR	1.391942053	2	2.524775
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.382572525**	**0.119329**	**3**
P83941	AMLSGPGQFAENETNEVNFR	1.463037581	2	4.948304
P83941	LISSDGHEFIVK	1.464816391	2	2.405482
P83941	TYGGCEGPDAMYVK	1.380260211	2	3.821238
P84082	**ARF2 ADP_ribosylation factor 2**	**1.247048742**	**0.940853**	**4**
P84082	EELTRMLAEDELR+Oxidation(5	1.583460624		
P84082	MLAEDELR	1.205568739	2	2.602858

P84082	NISFTVWDVGGQDK	1.287285081	2	4.324118
P84082	QDLPNAMNAAEITDK	0.878634664	2	4.205989
P84083	**ARF5 ADP_ribosylation factor 5**	**0.99476966**	**1.03E-05**	**4**
P84083	DAVLLVFANK	1.345317802	2	4.121659
P84083	MLQEDELR	1.27439357	2	2.472753
P84083	QDMPNAMPVSELTDK	0.795237896	2	3.352104
P84083	VQESADELQK	1.025412366	2	3.070387
P84089	**ERH Enhancer of rudimentary homolog**	**1.165300945**	**0.781423**	**2**
P84089	ADTQTYQPYNK	1.159977047	2	2.609885
P84089	TYADYESVNECMEGVCK	1.408028272	2	4.880086
P84092	**AP2M1 AP_2 complex subunit mu**	**1.203085287**	**0.168696**	**3**
P84092	ISEENIK	1.235776642	1	1.949835
P84092	SNFKPSLLAQK	1.536766662	2	2.61487
P84092	VFEPKLNYSDHDVIK	1.155453604	2	2.745652
P84100	**RL19 60S ribosomal protein L19**	**1.324524248**	**0.007482**	**3**
P84100	ILMEHIHK	2.049938256	2	2.320086
P84100	LLADQAEAR	1.312205991	2	3.31571
P84100	VWLDPNETNEIANANSR	1.427518846	2	5.631696
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**1.012080152**	**0.050156**	**2**
P84104	NPPGFAFVEFEDPRDAADAVR	1.912080943	2	2.578234
P84104	VYVGNLGNNGNK	0.286993936	2	2.431258
P84245	**H33 Histone H3.3**	**1.274697695**	**0.313158**	**6**
P84245	DIQLAR	248.5682253	1	2.109842
P84245	EIAQDFK	1.72792606	1	2.040887
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.711386511	4	4.915173
P84245	RVTIMPKDIQLAR+Oxidation(4	1.284512174		
P84245	STELLIR	1.205720939	2	2.609493
P84245	YRPGTVALR	1.024451311	2	2.383649
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.20518337**	**0.040325**	**4**
P84817	FQSEQAAGSVSK	1.28834866	2	3.051023
P84817	GIVLLEELLPK	1.644282198	2	2.950423
P84817	GLLQTEPQNNQAK	1.19509342	2	3.695009
P84817	KFQSEQAAGSVSK	0.946308422	2	4.479058
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**1.192331931**	**0.048397**	**16**
P85834	AEAGDNLGALVR	1.145182467	2	3.700528
P85834	DKPHVNVGTIGHVDHGK	1.480378833	2	3.845953
P85834	DLEKPFLLPVESVYSIPGR	1.549188823	2	4.226386
P85834	GDECELLGHNK	1.240067909	2	2.875432
P85834	GEETPVIVGSALCALEQR	1.323333872	2	4.404292
P85834	GITINAAHVEYSTAAR	1.892374139	2	2.84616
P85834	GTVVTGTLER	1.123341413	2	2.84794
P85834	HYAHTDCPGHADYVK	1.191006333	3	5.009711
P85834	KGDECELLGHNK	1.095194216	3	4.43353
P85834	KYEEIDNAPEER	1.123794726	2	3.792962
P85834	LLDAVDTYIPVPTR	1.382703287	2	3.687344
P85834	QIGVEHVVVYVNK	0.90079355	2	2.963275
P85834	TIGTGLVTDVPAMTEEDK	1.626428824	2	4.341583
P85834	TIGTGLVTDVPAMTEEDKNIK	1.333120814	2	4.456575
P85834	TVVTGIEMFHK	0.665085369	2	2.344173
P85834	YEEIDNAPEER	0.804841218	2	3.349031
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.383064434**	**4.91E-14**	**11**
P85968	AGQAVDDFIEK	1.391609199	2	3.251263
P85968	CLSSLKEER	1.665597273	2	2.595069
P85968	FQDTDGKELLPK	1.280719934	2	3.430985
P85968	GILFVGSGVSGGEEGAR	1.144588057	2	4.654916
P85968	HEMLPANLIQAQR	1.218196411	2	3.193345

P85968	LVPLLDTGDIIIDGGNSEYR	3.711596477	2	5.253135
P85968	NPELQNLLLDDFFK	1.962528495	2	4.439637
P85968	SAVDDCQDSWR	0.827864244	2	2.88359
P85968	TIFQAIAAK	0.632874495	2	2.694856
P85968	VGTGEPCCDWVGDEGAGHFVK	1.379321991	2	4.349175
P85968	YGPSLMPGGNK	1.609396026	2	2.481591
P85971	**6PGL 6_phosphogluconolactonase**	**2.202866587**	**0.000359**	**5**
P85971	DLPAATAPAGPASFAR	3.812461405	2	2.449059
P85971	ILEDQESALPAAMVQPR	0.867208184	2	4.805883
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	2.203163819	2	4.512886
P85971	TGALCWFLDEAAAR	1.833262309	2	3.579779
P85971	WTLGFCDER	1.291502397	2	2.583934
P85972	**VINC Vinculin**	**1.194342795**	**0.011601**	**15**
P85972	ALASQLQDSLK	1.373195324	2	2.603351
P85972	AQQVSQGLDVLTAK	1.191759042	2	4.300091
P85972	AVAGNISDPGLQK	0.915961039	2	3.352688
P85972	DPNASPGDAGEQAIR	0.977704061	2	2.360285
P85972	GNDIIAAAK	1.40896373	2	2.433863
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.791919529	3	5.116208
P85972	MLGQMTDQVADLR	1.250435016	2	3.52398
P85972	MSAEINEIIR	1.257357355	2	2.436271
P85972	MTGLVDEAIDTK	2.233687835	2	2.842847
P85972	QVATALQNLQTK	1.40964114	2	3.386614
P85972	SLLDASEEAIKK	1.355882329	2	2.73273
P85972	STVEGIQASVK	1.254320671	2	2.609895
P85972	VDQLAAQLADLAAR	1.427568867	2	3.268409
P85972	VLQLTSWDEDAWASK	1.317089431	2	3.26238
P85972	WIDNPTVDDR	2.138253267	2	2.97304
P85973	**PNPH Purine nucleoside phosphorylase**	**0.869821913**	**9.9E-20**	**13**
P85973	ASHQEVLEAGK	0.896968054	2	3.597887
P85973	DHINLPGFCGQNPLR	1.463234628	3	4.051781
P85973	ELQEGTYIMSAGPTFETVAESCLLR	1.550890645	2	5.212224
P85973	FEVGDIMLIR	1.510378226	2	3.799633
P85973	FHMYEGYSLSK	2.563859911	2	2.33016
P85973	HRPQVAVICGSGLGGLTAK	0.856813005	3	6.003437
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.980184765	3	3.778079
P85973	MLGADAVGMSTVPEVIVAR	1.343718857	2	5.907095
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0	2.640889851		
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(8	2.805233231		
P85973	VFGFSLITNK	1.764089025	2	3.135253
P85973	VFHLLGVDTLVVTNAAGGLNPK	2.017224318	2	5.393752
P85973	VVMDYNNLEK	1.656220407	2	2.4631
P86048	**RL10L 60S ribosomal protein L10_like**	**1.587661608**	**2.83E-07**	**6**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.724563336	3	6.042484
P86048	GAFGKPQGTVAR	1.520571335	2	2.827141
P86048	MLSCAGADR	1.288911997	2	2.366628
P86048	RLIPDGCGVK	1.0162155	2	2.314985
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.955568887	3	5.43705
P86048	VHIGQVIMSIR	1.350647596	2	3.015568
P86252		**1.126530767**	**0.474388**	**7**
P86252	ALELDPNLYR	1.411242237		
P86252	ANGFAELIPNAQLLQK	0.68583745		
P86252	CTSLGVNQGIYEEPK	0.940351501		
P86252	LGFQGAQDLANMFRFYALKPDR	1.997001406		
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	2.23189112	2	4.029375
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	2.911131645	3	4.518113
P86252	VASDAQLELDKLDGELKK	1.711482813		

P97313	**PRKDC DNA_dependent protein kinase catalytic subunit**	**2.6024843**	**0.092148**	**3**
P97313	FHGVMKTLCLEVVLCR+Oxidation(4	1.382133703		
P97313	LCHDAFTENMVGESQLLEK	2.998039548	2	2.534858
P97313	QLFSSLFSGILKEMNK+Oxidation(13	2.187664839		
P97384	**ANX11 Annexin A11**	**2.298795649**	**0.128948**	**2**
P97384	GFGTDEQAIIDCLGSR	1.507099016	2	3.95441
P97384	SELDLLDIR	2.324100761	2	2.544088
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.244328213**	**0.011604**	**8**
P97519	FDGVMQAAR	2.080173684	2	2.830923
P97519	GFEEAVAAGAK	3.960021519	2	3.3043
P97519	GYVSCALGCPYEGK	1.098809387	2	3.865539
P97519	KNVNCSIEESFQR	1.16933937	2	3.74566
P97519	LIDMLSEAGLPVIEATSFVSPK	1.583876764	2	3.104891
P97519	LLEAGDFICQALNR	2.041312725	2	4.536502
P97519	NVNCSIEESFQR	1.061900072	2	3.395039
P97519	WVPQMADHSDVLK	0.950747433	2	2.951693
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**1.32542201**	**6.15E-06**	**7**
P97521	CLLQIQASSGK	1.25295208	2	2.604986
P97521	EEGVTSLYK	0.835887245	1	2.03939
P97521	KLYQEFGIR	1.858722233	2	2.32925
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.538185905	2	3.846842
P97521	LYQEFGIR	1.51253673	2	2.762195
P97521	SVHDLSVPR	1.429990167	3	3.550459
P97521	YSGTLDCAK	1.272762166	2	2.352825
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.134946275**	**3.45E-08**	**13**
P97524	ALHDHLGLR	0.795114051	2	2.334589
P97524	GEVGLLICK	1.388208809	2	2.338283
P97524	MKENYEFNGK	1.431870798	2	2.802262
P97524	SLLHCFQCCGAK	0.760374827	2	2.95297
P97524	TILHVFLEQAR	1.006136362	2	3.181235
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	1.176113209	3	5.691184
P97524	TYVPMTEDIYNAIIDK	1.259078839	3	4.794456
P97524	VDGVSADPIPESWR	1.276143189	2	2.872199
P97524	VLLASPELHEAVEEVLPTLK	1.60548125	3	4.928368
P97524	VTLMEEGFNPSVIK	2.420309885	2	4.187378
P97524	YDVEKDEPVR	1.134072067	2	2.898706
P97524	YLCNTPQKPNDR	1.8138425	2	3.215416
P97524	YNATVIQYIGELLR	1.043187101	2	3.484168
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.089269686**	**8.88E-16**	**10**
P97532	AFGHHSVSLLDGGFR	1.369157007	3	3.68447
P97532	ALVSAQWVAEALK	1.430542396	2	3.89037
P97532	AQPEHVISQGR	1.090437458	2	3.208365
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.746869441	3	6.458148
P97532	FQGTQPEPR	1.087700324	2	3.611533
P97532	HIPGAAFFDIDR	1.450852306	2	2.557489
P97532	LLDASWYLPK	1.925220362	2	3.735216
P97532	SPSEPAEFCAQLDPSFIK	0.52377779	2	2.950286
P97532	THEDILENLDAR	1.181695695	2	3.875099
P97532	YWLSQNLPISSGK	1.223646943	2	3.955185
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.390956364**	**0.000848**	**7**
P97536	AADIDQEVK	1.259773047	2	2.484295
P97536	EGPAVVGQFIQDVK	2.54224676	2	2.721148
P97536	FTISDHPQPIDPLLK	1.013034023	2	2.595715

P97536	ITSEALLVTQQLVK	1.557632993	2	3.152541
P97536	LGTLSALDILIK	3.501570595	2	2.455437
P97536	SVILEAFSSPSEEVK	1.893671921	2	2.885886
P97536	TYIQCIAAISR	1.15591184	2	3.45873
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.136240954**	**0.005272**	**16**
P97562	ATFADFCAQGAEICR	0.878156828	2	4.749543
P97562	CSAQTAADFR	1.156210614	2	2.936164
P97562	DFSLLPELHALSTGMK	1.015581348	2	2.823986
P97562	EAFLDLLPLIR	0.973425093	2	2.860144
P97562	ILEYQTQQQK	1.0172394	2	3.737188
P97562	KVESIIQSDPVFNLK	1.055359072	2	5.036143
P97562	LDKEPEIQR	1.012115181	3	3.402149
P97562	LFEWAQK	0.99947035	2	2.520918
P97562	LGTPQSNYLGMLVTR	1.496265262	2	3.376647
P97562	LSGLPTLVAR	1.43751888	2	2.525777
P97562	LTNILDGGLPNTVLR	1.197526963	2	4.496737
P97562	SGVDQHDAWNQTTVIHLQAAK	0.965119866	3	6.023118
P97562	SLEDHTPLPGITVGDIGPK	0.979935941	3	4.34066
P97562	SLGSDEQIAK	2.616997292	2	3.006895
P97562	VESIIQSDPVFNLK	1.015943943	2	4.26298
P97562	VLDGNVNLSLHGVAMNAIR	1.207772127	2	4.339486
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.233936755**	**0.330753**	**4**
P97576	ALADTENLR	2.000781893	2	2.588734
P97576	DLLEVADILEK	1.021120216	2	3.684689
P97576	EEVSNNNPHLK	1.329115671	2	3.047381
P97576	TLRPALVGVVK	1.076684891	3	3.541067
P97584	**PTGR1 Prostaglandin reductase 1**	**1.213937236**	**0.137698**	**6**
P97584	ALTDLMNWVSEGK	1.227061631	2	4.184976
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.56687103	2	4.196931
P97584	HFEGFPTDSNFELR	1.206877671	2	3.782829
P97584	LKEGDSMMGEQVAR	1.217829441	2	3.779966
P97584	TGPCPPGPSPEVIIYQQLR	1.37524298	2	4.129807
P97584	YHEYITEGFEK	1.209933544	2	2.931904
P97608	**OPLA 5_oxoprolinase**	**1.276469533**	**0.05553**	**8**
P97608	AGDFGAAFVER	1.252974978	2	2.930494
P97608	GHTACADAYLTPTIQR	1.402203427	2	4.586618
P97608	GSILDPSPEAAVVGGNVLTSQR	2.040164735	2	4.963136
P97608	ISVGAEGPSMADTR+Oxidation(9	0.700987989		
P97608	ITDPEILESR	1.713516302	2	2.370362
P97608	LLSEDPANYADAPTEGIR	0.965295343	2	4.948683
P97608	SGLQLEDTPK	1.40903773	2	2.629538
P97608	TGDLLEIQQPVDLEALR	1.245067259	2	4.636333
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.098264191**	**4.04E-06**	**7**
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.464222953	3	3.970855
P97612	GTNCVTSYLTDCETQLSQAPR	1.147003831	2	4.945265
P97612	GYFGDIWDIILK	1.962668146	2	3.8686
P97612	NSVGLPVAVQCVALPWQEELCLR	2.112178061	3	3.815731
P97612	QGLLYGVPVSLK	0.902706782	2	2.852521
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	0.968073152	2	4.756588
P97612	VGYYETDNYTMPSPAMR	0.941558302	2	4.029428
P97690	**SMC3 Structural maintenance of chromosomes protein 3**	**1.505890006**	**0.059709**	**2**
P97690	KMVTKNDVMNLLESAGFSR+Oxidation(1	1.542297664		
P97690	NLEQYNKLDQDLNEVK	1.395010093	2	2.590656
P97697	**IMPA1 Inositol monophosphatase 1**	**1.256476118**	**0.602135**	**2**
P97697	SSPADLVTVTDQK	1.227666548	2	2.85215
P97697	VSQQEDITK	1.272231388	2	2.806889

P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.131335865**	**0.183471**	**3**
P97700	AVVVNAAQLASYSQSK	1.045211284	2	4.983741
P97700	GIYTGLSAGLLR	1.168565451	2	2.989297
P97700	LTGADGTPPGFLLK	1.393081578	2	3.86219
P97834	**CSN1 COP9 signalosome complex subunit 1**	**1.591434483**	**0.252407**	**3**
P97834	EGSQGELTPANSQSR	1.771439045	2	2.88486
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(0	1.533767108		
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(4	1.533767108		
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**1.09316267**	**9.69E-05**	**25**
P97852	AAVAVPSRPPDAVLR	0.954920071	2	2.304813
P97852	AVANYDSVEAGEK	1.005065018	2	3.810808
P97852	AYALAFAER	0.927235428	2	3.411252
P97852	CEAVIADILDK	1.034277885	2	2.567678
P97852	DTTSLNQAALYR	1.083924138	2	2.890492
P97852	FVYEGSADFSCLPTFGVIVAQK	0.698083991	2	3.682887
P97852	GALVVVNDLGGDFK	1.186068941	2	3.860662
P97852	GSSAADKVVEEIR	1.053196739	2	3.452387
P97852	HVLQQFADNDVSR	0.967778371	2	4.700099
P97852	ICDFSNASKPK	1.420094749	3	3.905319
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	1.061977922	3	5.672197
P97852	IDVVVNNAGILR	1.073842177	2	4.074324
P97852	ISDEDWDIIQR	1.791580408	2	3.691881
P97852	KNNIHCNTIAPNAGSR	0.815015053	2	5.049695
P97852	LGLLGLANTLVIEGR	1.689152154	2	3.623751
P97852	LNPQNAFFSGR	0.891464977	2	2.838742
P97852	NGSGEVYQGPAK	0.938772785	2	3.49526
P97852	NNIHCNTIAPNAGSR	1.007872577	2	4.649899
P97852	NQPMTPEAVR	0.983679323	2	2.352014
P97852	SIQESTGGIIEVLHK	1.082973701	2	4.167066
P97852	SLMSGGLAEVPGLSINFAK	1.141251889	2	4.574514
P97852	TALDTFGR	1.418784642	2	2.330812
P97852	VLHGEQYLELYKPLPR	0.926592281	2	5.016753
P97852	VNAVFEWHITK	0.789173298	2	3.16815
P97852	VVLVTGAGGGLGR	1.124611443	2	4.375841
P97874	**GAK Cyclin_G_associated kinase**	**1.210804807**	**0.374386**	**2**
P97874	AMVEEEITRNTTPMYR+Oxidation(13	3.51635784		
P97874	QELARDTDPFKLK	1.083885289	2	2.408808
Q00238	**ICAM1 Intercellular adhesion molecule 1**	**1.354798828**	**0.183631**	**2**
Q00238	LDTPDLLEVGTQQK	1.329356345	2	3.511435
Q00238	VELDPLPAWQQVGK	1.654567097	2	2.480091
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.674347835**	**3.93E-10**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	1.498602625	2	4.632898
Q00438	IIVENLFYPVTLDVLHQIFSK	1.490414845	3	4.328897
Q00438	KLPSDVTEGEVISLGLPFGK	1.67385118	2	4.369342
Q00438	NNQFQALLQYADPVSAQHAK	1.680202939	2	5.466889
Q00981	**UCHL1 Ubiquitin carboxyl_terminal hydrolase isozyme L1**	**1.280520511**	**0.390543**	**2**
Q00981	KQIEELK	1.110708926	2	2.352952
Q00981	MQLKPMEINPEMLNK+Oxidation(0	1.334345017		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.507977873**	**0.615487**	**3**
Q00PI9	AVEEQGDDQDSEK	1.524318092	2	3.989712
Q00PI9	EEAQPIVTKYK	1.448875848	1	1.971182
Q00PI9	SGDETPGSEAPGDK	1.400045955	2	3.241435
Q01177	**PLMN Plasminogen**	**0.908571711**	**0.194122**	**3**
Q01177	ILGSDVQQIAVTK	0.94833013	2	3.794187

Q01177	LVLEPNDADIALLK	0.830141568	2	2.819751
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	1.034912393	3	4.061543
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.194513844**	**0.001203**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.134154917	2	6.165077
Q01205	NDVITVQTPAFAESVTEGDVR	1.455697446	2	5.407289
Q01205	NVETMNYADIER	0.965695802	2	3.768661
Q01205	VEGGTPLFTLR	1.184758383	2	3.435865
Q01279	**EGFR Epidermal growth factor receptor**	**1.250760722**	**0.237469**	**2**
Q01279	NLQEILIGAVR	2.107005268	2	3.96008
Q01279	NYVVTDHGSCVR	1.200009278	2	2.698134
Q01405	**SC23A Protein transport protein Sec23A**	**1.121159757**	**7.44E-06**	**8**
Q01405	AETEEGPDVLR	1.17854683	2	3.227137
Q01405	AVLNPLCQVDYR	1.609513092	2	2.718889
Q01405	HFEALANR	1.084774586	1	2.021003
Q01405	HLLQAPVDDAQEILHSR	1.166187382	3	5.491585
Q01405	MVVPVAALFTPLK	1.255638814	2	2.621876
Q01405	SGYQDMPEYENFR	0.110097596	2	3.094906
Q01405	SWHDIEKDNAK	1.435142326	2	3.13193
Q01405	YIDTEHGGSQAR	1.152936488	2	3.438504
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**1.301240524**	**9.9E-20**	**33**
Q02253	AEMEAAVAACK	1.151048795	2	4.01936
Q02253	AEMEAAVAACK+Oxidation(2	1.258153153		
Q02253	AEMEAAVAACKR	0.980917827	2	3.11029
Q02253	AFPAWADTSILSR	1.398115614	2	4.132041
Q02253	AISFVGSNQAGEYIFER	1.381642312	2	5.275858
Q02253	CMALSTAVLVGEAK	1.985089442	2	4.492992
Q02253	CMALSTAVLVGEAK+Oxidation(1	1.195517588		
Q02253	EEDATLSSPAVVMPTMGR	1.577416996	2	4.731556
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12	9.594247886		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15	9.594247886		
Q02253	EEIFGPVLVVLETETLDEAIK	0.805501311	2	3.309968
Q02253	ENTLNQLVGAAFGAAGQR	1.066031779	2	5.147336
Q02253	GDTNFYGK	1.028526197	2	2.617481
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.565678029	2	5.647118
Q02253	GYENGNFVGPTIISNVKPSMTCYK	1.209286911	3	3.856564
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.133583865	2	5.398407
Q02253	KWLPELVER	1.971414371	3	3.331805
Q02253	LFIDGK	3.765486415	1	2.014251
Q02253	LITLEQGK	1.257700343	2	2.82319
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	0.975517425	3	4.355514
Q02253	NHGVVMPDANK	0.923840174	2	3.566811
Q02253	NHGVVMPDANK+Oxidation(5	1.212174078		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	1.749920621	3	6.137279
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5	1.765906002		
Q02253	QGIQFYTQLK	0.984827894	2	2.794362
Q02253	SDKWIDIHNPATNEVVGR	1.045647439	2	5.26877
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	1.250384655	2	5.475821
Q02253	TLADAEGDVFR	1.036958021	2	3.672229
Q02253	VCNLIDSGAK	0.87438932	2	3.393078
Q02253	VNAGDQPGADLGPLITPQAK	0.500058345	2	5.879705
Q02253	WIDIHNPATNEVVGR	0.972992661	2	4.891312
Q02253	WLPELVER	1.111697156	2	2.401557
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.802430809	3	3.527001

Q02769	**FDFT Squalene synthase**	**1.064810093**	**0.317322**	**4**
Q02769	KLEDFVKPENVDVAVK	1.355483917	2	4.035981
Q02769	SFAAVIQALDGDIR	1.049526358	2	3.663059
Q02769	TQSLPNCQLISR	1.275949262	2	2.91068
Q02769	VVLEDFPTISLEFR	1.580477049	2	3.281074
Q02874	**H2AY Core histone macro_H2A.1**	**1.174600278**	**0.025276**	**4**
Q02874	AASADSTTEGAPTDGFTVLSTK	0.901000652	2	4.194602
Q02874	GVTIASGGVLPNIHPELLAK	1.175260418	2	4.201245
Q02874	NCLALADDR	1.491469109	2	2.475091
Q02874	NGPLEVAGAAVSAGHGLPAK	1.097543919	2	2.810144
Q02974	**KHK Ketohexokinase**	**1.355712628**	**2.9E-05**	**8**
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.393154039	3	5.580824
Q02974	GGNASNSCTVLSLLGAR	1.255535489	2	4.720075
Q02974	GNSMQEALR	1.231512879	2	3.004877
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.095446803	3	5.853639
Q02974	IEQYNATQPLQQK	0.797533799	2	4.816424
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.440004688	3	6.500533
Q02974	TIILYDTNLPDVSAK	1.272074511	2	5.151032
Q02974	VSVEIEKPR	1.188167495	2	2.51895
Q03248	**BUP1 Beta_ureidopropionase**	**1.383428882**	**9.9E-20**	**15**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.322261921	2	6.141911
Q03248	EDLVLAPSSG	1.082216145	1	2.23347
Q03248	EKLPWTEFAESAEDGLTTR	1.277703032	2	4.721282
Q03248	ELAEAVKPNYSPNIVK	1.237500691	2	4.652629
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	4.370089627	3	3.490008
Q03248	HLPPDDLSQVK	1.052166418	2	2.529366
Q03248	HNMVVISPILER	1.529239006	2	3.082943
Q03248	HNMVVISPILER+Oxidation(2	1.493928681		
Q03248	IPLPTSAPVAEQVSALHK	1.515349431	3	4.875127
Q03248	KHNMVVISPILER	0.837707428	3	3.55404
Q03248	KHNMVVISPILER+Oxidation(3	1.521744332		
Q03248	NAAIANHCFTCALNR	1.355206279	2	4.689579
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.517897062	3	5.111598
Q03248	VGQEHYPNEFTSGDGK	1.793758787	2	4.355787
Q03248	VGQEHYPNEFTSGDGKK	1.430346293	3	4.796508
Q03336	**RGN Regucalcin**	**0.848526316**	**6.01E-10**	**16**
Q03336	CGESPVWEEASK	1.125846834	2	4.669443
Q03336	CLLFVDIPSK	1.216772627	2	3.424089
Q03336	DEQIPDGMCIDVEGK	0.851769327	2	4.443646
Q03336	DYSEMYVTCAR	1.163279502	2	3.268499
Q03336	FNDGKVDPAGR	1.082713338	2	3.051797
Q03336	HQGSLYSLFPDHSVK	0.871013247	3	4.897844
Q03336	KYFDQVDISNGLDWSLDHK	1.633622908	3	4.967375
Q03336	LWVACYNGGR	1.100098904	2	2.766793
Q03336	MEKDEQIPDGMCIDVEGK	1.114965981	2	5.065202
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0	1.175018807		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10	1.472874111		
Q03336	QSGGYVATIGTK	1.175310592	2	2.786207
Q03336	VGVDAPVSSVALR	1.064180775	2	3.568007
Q03336	YFAGTMAEETAPAVLER	1.289173519	2	5.670483
Q03336	YFAGTMAEETAPAVLER+Oxidation(5	0.950013073		
Q03336	YFDQVDISNGLDWSLDHK	0.693075708	2	4.695905
Q03410	**SYCP1 Synaptonemal complex protein 1**	**1.252653903**	**0.310758**	**2**
Q03410	ATVDEAVKLQKEIDLR	1.279204484	2	2.466755
Q03410	LKMEQENTAILTDK	1.250025302	2	2.368283
Q03626	**MUG1 Murinoglobulin_1**	**1.238008832**	**6.28E-06**	**7**
Q03626	EDNSIHWERPQKPTK	0.985584104	2	2.623197

Q03626	EESSCIHSSCTAER	1.09314182	2	4.231871
Q03626	GGEFEMMPLGVNK	1.069125823	2	3.477507
Q03626	LTAQPAPSPEDLALSMGTIK	1.402610093	3	4.122586
Q03626	NLHPLNELFPLAYIEDPK	1.662468184	3	4.118049
Q03626	VQTVPLTCNNPK	1.013602703	2	2.964466
Q03626	VYHKEESSCIHSSCTAER	1.277292605	2	5.819111
Q04462	**SYVC Valyl_tRNA synthetase**	**0.929583155**	**0.620526**	**4**
Q04462	ALNPLEEWLR	1.179733259	2	2.333169
Q04462	ITPAHDQNDYEVGQR	1.28771495	2	3.687371
Q04462	LQQTEAELR	1.212393521	2	2.341319
Q04462	SVTQQPGSEITAPQK	0.928831042	2	3.546373
Q05982	**NDKA Nucleoside diphosphate kinase A**	**1.609759115**	**0.301864**	**2**
Q05982	EISLWFQPEELVDYK	1.589653111	2	2.852583
Q05982	FIQASEDLLK	1.629606359	2	2.365308
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.380742574**	**9.9E-20**	**8**
Q06647	FSPLTANLMNLLAENGR	1.824062071	2	4.310371
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.330013753	3	6.047032
Q06647	GQILNLEVK	0.909504781	2	2.736655
Q06647	LGNTQGVISAFSTIMSVHR	1.79306337	3	3.641376
Q06647	TDPSIMGGMIVR	1.378716402	2	3.320391
Q06647	TVLNSFLSK	1.168550267	2	2.725518
Q06647	VGQLLKDPK	2.228255839	1	2.161299
Q06647	VSLAVLNPYIK	1.137581216	2	3.581119
Q07071	**GCKR Glucokinase regulatory protein**	**1.615397109**	**2.08E-07**	**13**
Q07071	AAPISCHVQVAHEK	1.303178479	2	4.901689
Q07071	CIESLLQAIHFPQPLSDDVR	1.664703275	3	4.441214
Q07071	CLLEILR	1.53469411	2	2.526961
Q07071	GFLIGDHSDMFNQK	1.48850977	2	3.831923
Q07071	LLGQCDAEIFQEEGQIVPTYQR	4.206109636	2	5.031868
Q07071	LSAASSVCEVVR	2.539675116	2	2.791999
Q07071	LYSESVLTTMLQVAGK	1.576926479	2	3.835548
Q07071	QEAFVLNPAIGPEGLSGSSR	1.615568918	2	4.862584
Q07071	TVDQGVVSSQR	1.098454745	2	3.56929
Q07071	VIPTALLSLLLR	1.832449564	2	2.968017
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.383891055	2	5.05545
Q07071	WVLNTVSTGAHVLLGK	2.366753594	2	3.444504
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.016900874	3	6.070068
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**1.0121167**	**0.379364**	**9**
Q07116	AVDDSYNVQPDTVAPIWNLR	1.550399096	2	4.618759
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	2.294680418	3	3.936766
Q07116	FVDLHPGGQSK	1.501954202	2	2.676932
Q07116	IGELNPEDR	1.128040844	2	2.443203
Q07116	LCDVLAQAGHR	0.778685457	2	3.240449
Q07116	LHVVGAPGGQSLSLSLDDLHK	1.640630889	3	3.706066
Q07116	MSPPLEASDPYSNDPMR	5.001763559	2	3.827767
Q07116	NHLPVPNLDPDTYR	1.082072972	2	2.668844
Q07116	VSVESEESYSHWQR	0.74322822	2	4.126024
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.096750055**	**0.262878**	**3**
Q07205	AMGPLVLTEVLFDEK	1.744390049	2	3.677452
Q07205	LQDMLDGFIK	1.206924098	2	2.311766
Q07205	TVIVNMVDVAK	1.096016503	2	2.859763
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.821111171**	**0.657183**	**12**
Q07523	ALKEEKPTQSVPVSFPK	0.735615885	2	4.818585
Q07523	ALVITIDTPVLGNR	0.801221927	2	3.961407
Q07523	ASFCWNDLSLLQSITR	1.113059544	2	4.07296
Q07523	EDAELAMK	1.58143216	1	2.018636
Q07523	EEKPTQSVPVSFPK	0.855703606	2	3.764906

Q07523	EVLDILTAELHR	1.099061847	2	3.275317
Q07523	GEDGVKEVLDILTAELHR	1.173759151	3	5.127806
Q07523	HNVQGIVVSNHGGR	0.765503196	3	6.360639
Q07523	NQLNLEANILLK	0.95435238	2	3.880228
Q07523	QLDEVSASIDALR	0.952749534	2	3.11643
Q07523	TSWDFIEGEADDGITYSENIAAFK	0.994558615	3	3.301944
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	0.861763674	3	4.73957
Q07803	**EFGM Elongation factor G_ mitochondrial**	**1.869067056**	**0.17457**	**4**
Q07803	GIIDLIEER	1.974913625	2	2.869314
Q07803	LEFSDETFGANVPK	1.355043306	2	2.852776
Q07803	NYQGELKK	0.520894464	1	2.086219
Q07803	YQPCSPSTQEELVNK	3.161743052	2	3.092536
Q07936	**ANXA2 Annexin A2**	**1.186988854**	**0.815507**	**3**
Q07936	GLGTDEDSLIEIICSR	1.28687049	2	3.370492
Q07936	GVDEVTIVNILTNR	1.120179657	2	3.101222
Q07936	TNQELQEINR	1.641671423	2	2.952035
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.564577833**	**1.3E-10**	**3**
Q07984	FFDEESYSLLR	2.083549618	2	3.67008
Q07984	NNEDVSIIPPLFTVSVDHR	1.438858992	2	4.338617
Q07984	VQNMALYADVSGK	1.266013097	2	3.699968
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**1.118172553**	**0.296572**	**7**
Q08163	ALLVTASQCQQPAGNK	1.074277795	2	4.090575
Q08163	KEPALLELEGK	1.534890993	2	2.343218
Q08163	LEAVSHTSDMHCGYGDSPSK	1.425854763	3	5.074891
Q08163	NSLDCEIVSAK	1.066562638	2	3.072783
Q08163	SALFAQINQGESITHALK	1.177971332	2	4.180212
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.172083201	2	4.264634
Q08163	VENQENVSNLVIDDTELK	1.696345466	2	5.36006
Q08201	**MDR2 Multidrug resistance protein 2**	**1.975039996**	**0.174304**	**2**
Q08201	AKLSAAYLFSLFERQPLIDSYSR	2.048784356	2	2.552104
Q08201	FDTLVGDRGAQLSGGQK	1.88899599	2	2.537317
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.501745603**	**7.07E-12**	**6**
Q08415	ATLQAMDER	1.402595072	2	2.432838
Q08415	EQQHFGQPSSYFLQLPQAMELNR	1.500097393	3	5.710249
Q08415	ILVLNTPNNPLGK	2.192924272	2	3.269145
Q08415	LGASNDWQLDPAELASK	2.945039155	2	4.254275
Q08415	RLDGIDQNLWVEFGK	1.387560994	2	2.362453
Q08415	VGWVMGPDNIMK	1.480287419	2	2.450415
Q09073	**ADT2 ADP/ATP translocase 2**	**1.13188043**	**0.959586**	**7**
Q09073	AAYFGIYDTAK	1.163745809	2	2.426242
Q09073	DFLAGGVAAAISK	0.901242914	2	4.93099
Q09073	GLGDCLVK	1.369463986	2	2.800288
Q09073	GTDIMYTGTLDCWR	1.549761138	2	3.619744
Q09073	KGTDIMYTGTLDCWR	1.128493077	3	3.789656
Q09073	LLLQVQHASK	1.403125175	2	2.773169
Q09073	QIFLGGVDKR	1.017990743	2	2.391847
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**1.370619186**	**0.00562**	**9**
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.562767499	3	4.13204
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	1.5113448	2	3.57721
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	1.12981051	3	3.533533
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	1.273853337	3	4.458374
Q0D2L3	SVDEGLLDSK	0.604800513	2	2.74482
Q0D2L3	SVDEGLLDSKR	1.294266222	2	3.14827
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.61465944	2	5.295788
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	2.598543603	3	5.564571
Q0D2L3	VVLAEDCWMK	1.34019607	2	2.523122

Q0VAV2	**EXPH5 Exophilin_5**	**0.673869263**	**0.32308**	**4**
Q0VAV2	DMDVSVSKDEQLNK	1.120902319	2	2.328467
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1	0.587209183		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)Oxidation(7	0.756916326		
Q0VAV2	SLSDQDPGQEQREEK	1.119148975	2	2.482729
Q0VGK3	**GLCTK Glycerate kinase**	**1.381055843**	**0.000406**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	1.587214288	2	5.178473
Q0VGK3	GATIQELNTIR	1.951094173	2	2.801062
Q0VGK3	QLFDSAVGAVQPGPMLQR	1.308788976	2	3.58777
Q0ZHH6	**ATLA3 Atlastin_3**	**1.373337988**	**0.000779**	**7**
Q0ZHH6	ALASVLLQDHIR	1.558190151	2	2.617037
Q0ZHH6	EHQHEEIQNVR	1.269120675	2	3.398778
Q0ZHH6	EQLQTLIPYVLNPSK	1.415983936	2	2.760027
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	1.227758242	2	4.523299
Q0ZHH6	IYQGEDLPHPK	1.370426136	2	2.524233
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2	1.380829938		
Q0ZHH6	YQQELEEEITELYENFCK	2.052206797	2	5.276007
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**1.192568354**	**0.769858**	**2**
Q10728	EQENEEKDKEEK	1.023419112	2	2.324766
Q10728	SLLEMEKRER+Oxidation(4	1.211166517		
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**1.212423053**	**9.9E-20**	**27**
Q10758	AEAETMYQIK	1.387912477	2	3.322094
Q10758	AQYEEIANR	1.252159212	2	3.131649
Q10758	ATLEAAIADAEQR	1.171842416	2	4.70628
Q10758	DVDEAYMNKVELESR	1.031565482	2	3.447923
Q10758	ELQSQISDTSVVLSMDNSR	2.037002981	2	6.240154
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	1.274646656	2	4.991036
Q10758	KDVDEAYMNK	1.814860598	2	3.318818
Q10758	LEGLTDEINFLR	1.510594495	2	4.392922
Q10758	LESGMQNMSIHTK	1.645512525	2	3.879261
Q10758	LEVDPNIQAVR	1.254240986	2	3.693965
Q10758	LEVELGNMQGLVEDFK	1.376617599	2	5.057513
Q10758	LKLEVELGNMQGLVEDFK	1.588306965	3	3.520644
Q10758	LQAEIDALK	1.334298956	2	2.973222
Q10758	LVSESSDIMSK	1.210168318	2	3.496125
Q10758	QIHEEEIR	1.216260635	1	2.195948
Q10758	QLEALGQEK	1.393931874	1	2.167854
Q10758	RQLEALGQEK	1.238789486	2	2.57175
Q10758	SKTEISEMNR	1.43339064	3	3.760076
Q10758	SKTEISEMNR+Oxidation(7	1.04025114		
Q10758	SLDMDSIIAEVR	1.197430661	2	4.67944
Q10758	SNMDNMFESYINNLR	1.074824146	2	4.205699
Q10758	SRAEAETMYQIK	1.602553363	2	3.673638
Q10758	TEISEMNR	1.858808489	2	2.320929
Q10758	TEMENEFVLIK	1.368100175	2	3.604664
Q10758	TEMENEFVLIK+Oxidation(2	1.443231032		
Q10758	WSLLQQQK	1.015360382	2	3.005718
Q10758	YEELQTLAGK	1.463748301	2	3.60237
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**1.044118265**	**0.001162**	**2**
Q148W0	LGQSHFINWDLQMYYAEK+Oxidation(12	1.058565335		
Q148W0	TCEVIKDGRFK	1.352360827	1	2.296004
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**1.544236295**	**0.586587**	**7**
Q14DH7	CVPGYNVMILDDNMQK	1.84107242	2	2.973577
Q14DH7	IAIIYDSPVTDTK	0.940102451	2	2.930412

Q14DH7	STLSALVNGKPYK	0.830218515	2	2.781722
Q14DH7	THFAASVADPER	1.494496552	2	3.666326
Q14DH7	VDDVINVAGHR	1.752016803	2	3.616512
Q14DH7	VLAEHGVAALFTAPTAIR	1.122795671	2	4.429534
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.195488958	2	3.425675
Q1H5H1	**SELT Selenoprotein T**	**1.64997385**	**0.038644**	**2**
Q1H5H1	IEGENYLPQPIYR	1.450951865	2	2.836025
Q1H5H1	LESGHLPSMQQLVQILDNEMK	1.725872714	3	3.984879
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**1.406162971**	**0.008262**	**11**
Q1HCL7	GSSYSGLLER	1.298717048	2	2.434811
Q1HCL7	LKPVIGVNTDPER	1.405618834	3	3.464705
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.414717553	3	5.230477
Q1HCL7	NVEHIIDSLRDEGIEVR	1.200793376	2	3.543599
Q1HCL7	QGNLTLPLNK	1.602366221	2	2.489264
Q1HCL7	SEASGPQLLPVR	1.330956302	2	3.107535
Q1HCL7	SEGHLCLPVR	0.92669633	2	2.774505
Q1HCL7	SSGLNLCTGTGSK	1.137710489	2	3.617954
Q1HCL7	VTNEYNESLLYSPEEPK	1.420742073	2	4.722686
Q1HCL7	YAELSEEDLK	1.310990001	2	2.772131
Q1HCL7	YTHSFPEALQK	1.561030448	2	2.493729
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.075509214**	**0.438743**	**7**
Q1JU68	AVEDIHGLFSLSK	2.580962848	2	3.19418
Q1JU68	EEEEQRRAEEQMLK	1.539126061	2	2.456296
Q1JU68	FNVLQYVVPEVK	1.920494315	2	3.409885
Q1JU68	ILQEHEQIK	1.142807507	2	2.3826
Q1JU68	KGPEADSEWR	0.880076155	2	2.610711
Q1JU68	LLDMDGIIVEK	0.759830397	2	3.015522
Q1JU68	NQLTAMSSVLAK	1.028754671	2	2.777844
Q29RW1	**MYH4 Myosin_4**	**2.291408182**	**0.936746**	**13**
Q29RW1	ANLMQAEIEELR	3.166208333	2	2.94908
Q29RW1	ELENEVENEQKR	3.955705456	2	3.109784
Q29RW1	GQDDLKEQLAMVER	1.348404454	2	2.87192
Q29RW1	LQDAEEHVEAVNSK	5.690837832	2	4.841591
Q29RW1	LQDLVDKLQTK	1.953713648	1	1.941858
Q29RW1	MEGDLNEMEIQLNHANR	1.435522126	2	4.044161
Q29RW1	MEIDDLASNMETVSK	13.25353553	2	4.335881
Q29RW1	NAYEESLDQLETLKR	2.578301929	2	4.016444
Q29RW1	SAETEKEMATMK	1.119215845	2	2.774539
Q29RW1	SELQASLEEAEASLEHEEGK	2.9683324	2	4.858123
Q29RW1	TEGGATVTVK	2.549151508	2	2.917394
Q29RW1	TKLEQQVDDLEGSLEQEK	1.988537482	2	4.93899
Q29RW1	TKLEQQVDDLEGSLEQEKK	0.3095138	3	4.625255
Q2PQA9	**KINH Kinesin_1 heavy chain**	**3.175890889**	**0.099359**	**4**
Q2PQA9	HVAVTNMNEHSSR	3.33275972	3	4.041239
Q2PQA9	MEENEKELAACQLR	1.468834184	2	2.356405
Q2PQA9	SAEVDSDDTGGSAAQK	1.232842531	2	5.215311
Q2PQA9	TGAEGAVLDEAK	1.484954238	2	2.424347
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**0.945938797**	**0.27717**	**6**
Q2TA68	AKNEILDEVISLSQVTPK	1.792782132	2	3.968228
Q2TA68	AVEVAWETLQDEFSR	1.350624437	2	2.363897
Q2TA68	GKEHDDIFDK	1.272302654	2	2.403606
Q2TA68	IDQLQEELLHTQLK	0.945559479	2	2.64901
Q2TA68	TSVLEMIAQAR	1.125343921	2	3.299251
Q2TA68	VVVVGDQSAGK	1.483133237	2	2.54199
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.596349915**	**0.042245**	**7**

Q2V057	ASIYGQFVAGETAEEVR	2.074644233	2	3.180244
Q2V057	EDCTQPDYEATSR	2.006232551	2	3.92341
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.357144586	3	3.603206
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.393971988	2	5.445899
Q2V057	SIPYGCLEEVIPYLIR	2.606420763	2	2.531735
Q2V057	SVTQLHGKEDCTQPDYEATSR	1.259754159	3	5.449209
Q2V057	TSEAWYEGNLSAMLHCVDLSR	1.59974052	2	3.453966
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.63096612**	**0.0092**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	1.269922502	3	4.740949
Q3B7D0	FGLFTPGSR	1.171737175	2	2.33909
Q3B7D0	HCDDSYTPQDK	1.751978578	2	3.785692
Q3B7D0	LEEDGDELAR	3.483305571	2	2.823946
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.245750425**	**0.644976**	**4**
Q3B7U9	SCSQVLEHQPDNIK	1.24357546	2	4.137336
Q3B7U9	TAEDGPDLEMLSGQER	1.27415677	2	4.216661
Q3B7U9	VDMTCEEEEELLQLK	1.543167357	2	4.147151
Q3B7U9	VLAQQGEYSEAIPILR	1.154589784	2	3.4743
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**0.91639012**	**0.076106**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	0.913642879	2	4.584264
Q3B8Q2	GRDVIAQSQSGTGK	1.372615303	2	3.888091
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.494767239**	**0.06251**	**3**
Q3KRD8	ASFENNCEVGCFAK	1.491106128	2	2.430109
Q3KRD8	HGLLVPNNTTDQELQHIR	1.470903211	3	4.832182
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.497495554	3	3.902983
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.114422985**	**0.385162**	**3**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	0.948288429	2	3.66028
Q3KRE0	ISVLEALR	3.15783393	2	2.418639
Q3KRE0	QQQLLNEENLR	1.197180066	2	2.364246
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**1.242002661**	**0.000154**	**2**
Q3KRE8	ALTVPELTQQMFDSK	1.24446708	2	3.22134
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.966550383	3	5.051366
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**1.111236733**	**0.877931**	**2**
Q3MIB4	MEIIQVPGYTQEEK	1.107661211	2	3.727233
Q3MIB4	TVGVNNPVFLLDEVDK	1.138986151	2	2.444358
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**1.164596617**	**0.747482**	**6**
Q3MIE0	DGQEGIEAFIQK	1.279196913	2	2.767094
Q3MIE0	SDILHEAESEDLK	0.989885221	3	3.666263
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.25100771	2	4.732429
Q3MIE0	VALEMLFTGEPISAQEALR	0.993802932	2	3.663281
Q3MIE0	VIIISAEGPVFSSGHDLK	0.943776679	2	4.477846
Q3MIE0	VVPEEQLEEEATR	1.131600171	2	3.971935
Q3MIF4	**XYLB Xylulose kinase**	**1.271479998**	**0.005583**	**8**
Q3MIF4	CCLGWDFSTQQVK	1.697100579	2	3.205227
Q3MIF4	DLPEFGTQGGVHVHK	1.196358063	2	2.751265
Q3MIF4	FNADNMEVSAFPGDVEIR	1.441448444	2	4.45379
Q3MIF4	IHAEGLGYR	1.458608827	2	2.347418
Q3MIF4	IRDESASCSWNK	1.510982391	2	4.173065
Q3MIF4	VVAFTGDNPASLAGMR	1.13699995	2	3.871351
Q3MIF4	VWSQACLDACAPHLK	2.153734599	2	3.811449
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	1.261598606	2	5.275795
Q3SWS9	**JKIP1 Janus kinase and microtubule_interacting protein 1**	**1.360458491**	**0.339564**	**2**
Q3SWS9	LEMEENQLK+Oxidation(2	0.826767231		
Q3SWS9	VKTALLADAREEAR	1.382555454	2	2.38817

Q3T1I4	**PRRC1 Protein PRRC1**	**1.061257677**	**6.94E-05**	**2**
Q3T1I4	GQDDAPAGGIWGFIK	1.305420386	2	3.682922
Q3T1I4	WSGLLVTVGEVLEK	0.793917268	2	2.746097
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.551974792**	**0.000663**	**4**
Q3T1J1	EDLRLPEGDLGK	1.301062704	2	2.968026
Q3T1J1	EDLRLPEGDLGKEIEQK	1.332777384	2	4.257016
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.943138464	2	5.071415
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	2.247762588	3	4.240447
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.091615739**	**0.000163**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.442501145	3	4.025432
Q3T1K5	FTVTPSTTQVVGILK	1.507028383	2	4.085737
Q3T1K5	KVDGQQTIIACIESHQFQAK	1.008255381	3	3.770624
Q3TDQ1	**STT3B Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3B**	**1.333978634**	**0.095779**	**2**
Q3TDQ1	FGEMQLDFR	1.535172342	2	2.334878
Q3TDQ1	HLEEAFTSEHWLVR	1.331577145	3	4.077015
Q3U0D9	**HACE1 E3 ubiquitin_protein ligase HACE1**	**1.178245727**	**0.370816**	**2**
Q3U0D9	DSIFRSSCEIVSKANCAK	1.064211667	2	2.3169
Q3U0D9	MERAMEQLNRLTR	2.037651304	2	2.32771
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**1.258466425**	**0.31345**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	1.220797173	2	2.526188
Q3U0J8	QIELDLLRTLPNNK	1.279109659	2	2.5996
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**0.982999817**	**0.758081**	**2**
Q3UHR0	MQILQRKDTWAPK+Oxidation(0	1.623596149		
Q3UHR0	NLEEPGLLSR	1.022008175	2	2.368669
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**0.810324071**	**9.9E-20**	**3**
Q3ULJ0	GIDEGPDGLK	0.63866536	2	2.820177
Q3ULJ0	LGLMEMIAFAK	1.911571817	2	3.815067
Q3ULJ0	LTDIINNDHENVKYLPGHK	1.76269061	2	2.40201
Q3UMF0	**COBL1 Cordon_bleu protein_like 1**	**1.252772163**	**0.476993**	**2**
Q3UMF0	RAPLPPMPTSQGAAQGQERR+Oxidation(6	1.354019372		
Q3UMF0	SQGTSTYVQDR	1.249967235	2	2.393463
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.450575835**	**1.11E-16**	**18**
Q3UQ44	ALVGSENPPLTVIR	1.112983575	2	3.855686
Q3UQ44	AWVNQLETQTGEASK	1.1972331	2	5.200054
Q3UQ44	GVLLGIDDLQTNQFK	1.355290758	2	4.293905
Q3UQ44	HTDNTVQWLR	1.355901964	2	3.003618
Q3UQ44	KKGGEIEILNNTDNK	1.129779546	2	2.37617
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	2.586259852	3	4.710339
Q3UQ44	LGIAPQIQDLLGK	2.091561108	2	2.993097
Q3UQ44	LPYDVTTEQALTYPEVK	1.78668387	2	4.104656
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.490427264	2	2.372267
Q3UQ44	LSAEEMDER	1.220284057	2	3.091775
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.396426864	2	5.231676
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.28755393	2	4.990259
Q3UQ44	TALEEEIK	1.460805748	2	2.407169
Q3UQ44	TLDTLLLPTANIR	1.123576494	2	3.578648
Q3UQ44	VDFTEEEISNMR	2.212389975	2	3.953048
Q3UQ44	VDQVQDIVTGNPTVIK	0.939670301	2	5.097965
Q3UQ44	YGSIVDDER	0.955204204	2	2.459141
Q3UQ44	YQDILNEIAK	1.374359453	2	3.061035
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**1.193870741**	**0.080858**	**2**
Q3UV17	AQYEDIAQK	1.057858286	1	2.124419
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5	1.217469564		

Q3V0K9	**PLSI Plastin_1**	**1.350645666**	**0.823915**	**3**
Q3V0K9	AYFHLLNQIAPK	1.008911713	2	3.054777
Q3V0K9	KIENCNYAVELGK	1.258443113	2	3.730831
Q3V0K9	QFVTPADVVSGNPK	1.363082571	2	3.302485
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.416672136**	**0.712225**	**2**
Q3V132	GNLANVIR	1.429242991	2	2.75501
Q3V132	YFPTQALNFAFK	1.399504848	2	3.405254
Q3ZAV8	**EDC4 Enhancer of mRNA_decapping protein 4**	**1.293305471**	**0.267575**	**2**
Q3ZAV8	SSHSTWPVDVSQIK	2.082275072	2	2.330533
Q3ZAV8	VISVSTSERTLLK	1.169734134	2	2.574868
Q497B0	**NIT2 Omega_amidase NIT2**	**1.178114882**	**9.9E-20**	**15**
Q497B0	ADLYSVESK	1.288015643	2	3.060788
Q497B0	AGTEETILYSDIDLK	1.596729985	2	3.732111
Q497B0	ASYVAWGHSTVVDPWGQVLTK	1.176694204	3	5.856664
Q497B0	AVDNQVYVATASPAR	1.177958632	2	4.680212
Q497B0	AVDNQVYVATASPARDEK	1.179884485	2	3.586406
Q497B0	ENSIYLIGGSIPEEDDGK	1.279828199	2	3.460678
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.175712366	3	4.96519
Q497B0	FAELAQIYAR	1.519232165	2	3.925858
Q497B0	IHLFDIDVPGK	1.391793123	3	3.4871
Q497B0	KIHLFDIDVPGK	1.605963466	3	4.735209
Q497B0	LALIQLQVSSIK	2.07733808	2	3.069322
Q497B0	LYNTCAVFGPDGNLLVK	1.345417255	2	4.122396
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.413213807	3	4.97485
Q497B0	TLSPGDSFSTFDTPYCR	1.482405879	2	4.775801
Q497B0	VGLGICYDMR	1.611678387	2	2.861018
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**1.300427034**	**0.721379**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.888146233	2	4.561281
Q498D5	FCNLALLLPIVTK	1.883911634	2	3.229704
Q498D5	GQLQILEK	1.281071219	1	2.059002
Q498D5	LNELLTNVEELKEEIK	1.300382478	2	2.871537
Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**0.756035823**	**0.11777**	**2**
Q498U4	EEEPPEKVVDMASEK	0.425716369	2	2.365702
Q498U4	FGIVTSSAGTGTTEDTEAK	1.304778514	2	3.342865
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.216918863**	**0.072208**	**7**
Q499N5	GATLSHHNIVNNSNLIGQR	1.76543428	2	5.329549
Q499N5	GGENIYPAELEDFFHK	1.140501295	2	2.976698
Q499N5	SGETTTEEEIK	1.229909228	2	3.160728
Q499N5	TFETVGQDR	2.140909297	2	2.672361
Q499N5	TGDIASMDEQGFCR	1.334691338	2	3.724995
Q499N5	TVGECLDATAQR	3.510654552	2	2.909511
Q499N5	YIVFVEGYPLTVSGK	1.47818703	2	4.379837
Q4AEF8	**COPG Coatomer subunit gamma**	**1.222570575**	**0.510987**	**6**
Q4AEF8	FGAQNEEMLPSILVLLK	1.43457921	2	3.501854
Q4AEF8	SLPYNQPGTCYTLVALPK	1.008019041	2	2.440931
Q4AEF8	SSPEPVALTESETEYVIR	1.267114819	2	3.612556
Q4AEF8	TLEEAVGNIVK	1.105487706	2	2.640277
Q4AEF8	VVLEHEEVR	1.892230589	2	2.4354
Q4AEF8	VVVVQAISALCQK	3.53956797	2	2.469675
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.600637348**	**0.000567**	**5**
Q4FZT0	AEQINQAAGEASAVLAK	1.159053909	2	4.704899
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.678504623	2	5.548516
Q4FZT0	ATVLESEGTR	1.152884245	2	2.803684
Q4FZT0	DVQTTDTSIEELGR	2.07180802	2	2.922502
Q4FZT0	ILEPGLNVLIPVLDR	1.307309715	2	3.019914

Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.091855638**	**0.5373**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	1.06770761	3	4.8805
Q4FZT9	FGGSGSQVDSAR	1.31978203	2	3.396187
Q4FZT9	SETELKDTYAR	1.344622931	2	3.040888
Q4FZT9	SGALLACGIVNSGVR	1.222074466	2	3.367528
Q4FZT9	SSTTSMTSVPKPLK	1.015659168	2	3.497869
Q4FZT9	TITGFQTHTTPVLLAHGER	0.83396701	3	3.925929
Q4FZT9	TPVQSQQPSATAPSGADEK	0.980444623	2	4.879749
Q4FZT9	VGQAVDVVGQAGKPK	1.215644207	2	3.462116
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.243280493**	**0.378621**	**4**
Q4FZX7	GDAGSADVQDLEK	2.861786077	2	3.469195
Q4FZX7	GNSLTLIDLPGHESLR	1.284181174	2	2.808884
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.34532226	2	4.842886
Q4FZX7	VGDGAGGAFQPYLDSLR	1.237819332	2	3.128299
Q4FZY0	**EFHD2 EF_hand domain_containing protein D2**	**1.305342232**	**0.552924**	**2**
Q4FZY0	KQAEEVK	1.02047862	1	1.944053
Q4FZY0	LSEIDVSTEGVK	2.388035322	2	2.598047
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.154486264**	**0.810324**	**6**
Q4G061	AEEEGGSDGSAAEAEPR	0.764796595	2	4.959178
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	7.552335197	3	5.011341
Q4G061	DRPQEADGIDSVIVVDNVPQVGPDR	2.518695145	3	3.561203
Q4G061	GTQGVVTNFEIFR	1.198205296	2	3.00808
Q4G061	IINDYYPEEDGK	2.55678853	2	2.865315
Q4G061	TEDAEEDAEARPEPEVR	0.728897929	3	3.619127
Q4G063	**CREL2 Cysteine_rich with EGF_like domain protein 2**	**1.775885078**	**0.28255**	**2**
Q4G063	ACCLPGTYGPDCK	1.654394799	2	3.03808
Q4G063	FNQGMANTAR	3.183407511	2	2.418098
Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**1.115087126**	**0.782479**	**2**
Q4KLF8	ALAAGGVGSIVR	0.924388895	2	2.844649
Q4KLF8	QGNMTAALQAALK	1.437986531	2	2.348902
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.39154201**	**1.85E-13**	**16**
Q4KLP0	ARPSVDHGLAR	0.703413886	2	3.062382
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.330281445	3	5.713457
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.528463903	3	4.68575
Q4KLP0	LEELCPFPLDSLQQEMGK	1.016944598	3	5.421255
Q4KLP0	LLLESQEFDHFLATK	1.733041844	2	3.956747
Q4KLP0	LSAYGGITDIIIGMPHR	1.91376521	3	4.444344
Q4KLP0	LVTVYCEHGHK	1.156642468	2	2.367888
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	2.17277684	2	2.630986
Q4KLP0	QWGHNELDEPFFTNPVMYK	0.95307155	3	3.997117
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.325510064	3	5.021566
Q4KLP0	SSLYSSDIGK	0.930145349	2	2.837844
Q4KLP0	SVEVPEELQLHSHLLK	1.358390425	2	3.310037
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.286710809	3	3.36754
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.52663346	2	4.956798
Q4KLP0	YGGEGAESMMGFFHELLK	1.380840454	2	4.436105
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.408559533	3	4.569089
Q4KLZ6		**1.178140237**	**4.18E-07**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.872231851	2	4.915477
Q4KLZ6	AILEVLQTK	0.804608133	2	2.89094
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.396283261	2	3.612692

Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	1.175212969	2	4.962479
Q4KLZ6	AVAQAGTAGTLLIVK	1.373925855	2	4.362641
Q4KLZ6	EGPTPASPAQVLSK	1.134503163	2	3.385814
Q4KLZ6	GLCGTILIHK	1.4675571	2	2.401484
Q4KLZ6	GVSLTLMLVDEPLLK	1.417744211	2	3.0735
Q4KLZ6	ISTTLIGLEEHLNALDR	2.876702702	2	3.609056
Q4KLZ6	LIDAETNAK	2.244498929	2	2.372961
Q4KLZ6	LNFGLAMEQAK	0.960801403	2	2.404557
Q4KLZ6	LSVLLLEK	1.603636816	2	2.605484
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	1.76603122	2	3.563245
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.27836967	3	5.908218
Q4KLZ6	VAGALAEEGMGLEEITK	1.625713655	2	4.535806
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	1.894603643	2	5.352368
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.31000023**	**0.163505**	**5**
Q4KM49	AFCEPGNVENNGVLSFVK	0.873201457	2	2.472954
Q4KM49	IDVGEAEPR	0.626205933	2	2.350825
Q4KM49	QVEPLDPPAGSAPGER	1.587481163	2	2.595564
Q4KM49	TVVSGLVQFVPK	0.905458326	2	3.067024
Q4KM49	VDAQFGGIDQR	0.429851941	2	3.128448
Q4KM73	**KCY UMP_CMP kinase**	**1.51919919**	**9.99E-15**	**7**
Q4KM73	EMDQTMAANAQK	1.529107182	2	3.183456
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.526547187	3	4.592179
Q4KM73	IVPVEITISLLK	1.477194699	2	2.497502
Q4KM73	KNPDSQYGELIEK	1.241756713	2	3.800174
Q4KM73	NQDNLQGWNK	1.619038215	2	2.841768
Q4KM73	SVDEVFGDVMK	1.384675814	2	3.45938
Q4KM73	YGYTHLSAGELLR	0.999003429	3	4.279063
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.220665283**	**1.53E-05**	**5**
Q4KM74	DLQQYQSQAK	1.593860602	2	3.552372
Q4KM74	GEALSALDSK	1.541652168	2	2.851285
Q4KM74	IMVANIEEVLQR	1.244842016	2	2.789131
Q4KM74	NLGSINTELQDVQR	1.090228175	2	4.383837
Q4KM74	VADGLPLAASMQEDEQSGR	0.860899906	2	4.364812
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.165644056**	**0.302655**	**3**
Q4KMA2	IDIDPEETVK	1.135522118	2	2.759573
Q4KMA2	NFVVVMVTKPK	1.052447993	2	2.97463
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.347651006	2	4.24825
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**1.271233086**	**0.370904**	**6**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	1.395533738	3	3.569177
Q4QQW3	FLFDLNVDDGLAALGYSK	1.695689796	2	2.437374
Q4QQW3	HLETAEILGANIR	1.285096572	2	3.458913
Q4QQW3	IQDAGPVLADALR	0.619603045	2	2.9916
Q4QQW3	NLSQLPPVQIVMDSLSK	1.39006775	2	2.964382
Q4QQW3	TTDYAFEMAVSNIR	0.425056466	2	3.704363
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.465756916**	**1.66E-05**	**5**
Q4QRB4	AILVDLEPGTMDSVR	1.683878537	2	4.562135
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10	1.905171439		
Q4QRB4	EIVHIQAGQCGNQIGAK	1.361507424	2	4.93126
Q4QRB4	IMNTFSVVPSPK	1.827690767	2	4.101501
Q4QRB4	ISEQFTAMFR	1.408706166	2	3.379239
Q4V7C7	**ARP3 Actin_related protein 3**	**1.247945458**	**0.042336**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	1.621335482	2	4.387814
Q4V7C7	KDYEEIGPSICR	1.198743098	2	3.663021
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.413805243	2	3.347808
Q4V7C7	LSEELSGGR	1.412747974	2	2.566124

Q4V7C7	NIVLSGGSTMFR	0.982445499	2	3.093104
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1.227246791	3	5.242676
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**1.308995667**	**0.003605**	**6**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	1.320339868	3	3.733385
Q4V8K1	QVFVCGNDSK	1.142202612	2	2.382655
Q4V8K1	SDVIVLAVHR	1.456071942	2	2.82238
Q4V8K1	TCADEFPLTVDSSEK	1.340845916	2	4.488022
Q4V8K1	TLGLTPLDQGSLVAAK	1.395699084	2	3.811183
Q4V8K1	VLIDVSNNQK	1.088382013	2	2.535116
Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**0.861403249**	**0.352503**	**2**
Q501J6	ELAQQVQQVADDYGK	0.562297021	2	3.122041
Q501J6	VLEEANQAINPK	0.865657549	2	2.623311
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.772427302**	**0.000199**	**4**
Q505J8	LQQVQAGQAEK	0.71400263	2	2.675399
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	2.091606208	3	4.590388
Q505J8	SLQALGEVIEAELR	1.173552352	2	3.745198
Q505J8	VVDSIEDEVQR	1.819994155	2	2.935382
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**1.210358539**	**0.17223**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	0.966343168	2	4.093429
Q561R9	ILIDTGEPSVPEYISCLK	1.232625527	2	3.791219
Q561R9	NISNDATYCIK	1.461282628	2	2.951407
Q561R9	NNREEQIITVFR	0.694062148	2	2.691479
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.153336044**	**0.026325**	**6**
Q561S0	LLQYSDALEHLLSTGQGVVLER	1.995247796	3	3.763039
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	1.571843654	3	4.185788
Q561S0	VITVDGNICSGK	0.9780776	2	2.458092
Q561S0	VVEDIEYLNYNK	0.932076738	2	3.900411
Q561S0	YAPGYNADVGDK	0.600402144	2	2.66096
Q561S0	YGLLASILGDK	2.030470162	2	3.149049
Q562C4	**MET7B Methyltransferase_like protein 7B**	**1.151166947**	**0.080379**	**5**
Q562C4	AQFSEVQLEWQPPPFK	1.542300119	2	4.516967
Q562C4	FIVAYGENMK	1.10195976	1	2.533913
Q562C4	HIGDGCHLTR	1.428465249	3	3.317531
Q562C4	VLQEVQR	1.144485549	2	2.548768
Q562C4	VTCVDPNPNFEK	1.110609628	2	3.604127
Q562C9	**MTND 1_2_dihydroxy_3_keto_5_methylthiopentene dioxygenase**	**1.21800902**	**0.733397**	**3**
Q562C9	GDMITLPAGIYHR	1.20539181	2	2.319875
Q562C9	LDADKYENDPELEQIR	1.353170393	2	4.200839
Q562C9	MFFEEHLHLDEEIR	3.124360551	2	2.428597
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.095127575**	**0.522193**	**11**
Q58FK9	AIILNTPHNPIGK	0.806503655	2	3.389632
Q58FK9	DSTLDAAEEIFR	13.57289485	2	3.198891
Q58FK9	DSTLDAAEEIFRTWNSR	1.448771423	2	2.361196
Q58FK9	IEGLDQNVWVEFTK	1.89928252	2	4.555703
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.195300103	3	4.487945
Q58FK9	MAGAVPVFIPLR	1.613485966	2	2.496653
Q58FK9	MDDPECYFNSLPK	0.950504128	2	4.185047
Q58FK9	RIEGLDQNVWVEFTK	1.331130131	2	3.72454
Q58FK9	RMDDPECYFNSLPK	1.015617278	2	2.769822
Q58FK9	SDEPYDYK	2.63672916	2	2.448512
Q58FK9	WTSSDWTFNPQELESK	0.956033096	2	5.062608
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.258696544**	**3.97E-07**	**3**

Q5BJQ0	AVLDSSPFLSEANAER	1.101135448	2	4.613414
Q5BJQ0	KMGGSFLICSKLK+Oxidation(1	1.684423872		
Q5BJQ0	TLNNDLGPHWR	1.679768993	2	2.561803
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**1.327087029**	**9.9E-20**	**25**
Q5BJY9	AQIFANSVDNAR	1.112325817	2	3.959989
Q5BJY9	AQYEQLAQK	1.196095236	2	3.47068
Q5BJY9	DAETTLLELR	1.499652206	2	2.941591
Q5BJY9	IREYLEK	1.476709994	2	2.402464
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	2.16706324	3	4.90783
Q5BJY9	KVVDDTNITR	1.165689317	2	3.072279
Q5BJY9	LEAEIATYR	1.126613327	2	3.280515
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	1.173011273	3	5.545954
Q5BJY9	LQLETEIEALKEELLFMK	2.587413634	2	5.044447
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	1.350197859	2	6.304823
Q5BJY9	NQNINLENNLGEVEAR	1.704766195	2	5.564956
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	1.172871741	3	5.18546
Q5BJY9	QSVESDIHGLR	1.339726256	2	2.85054
Q5BJY9	QSVESDIHGLRK	2.302588957	2	2.676454
Q5BJY9	QTQEYEALLNIK	1.497028116	2	3.522492
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	1.365253188	2	5.895795
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	1.437323097	3	4.348719
Q5BJY9	TLQTLEIDLDSMK	1.375842631	2	4.520379
Q5BJY9	VKLEAEIATYR	1.623361116	2	3.281035
Q5BJY9	VKYETELAMR	1.345404085	3	3.423982
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.817282165	2	5.271057
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.598265105	2	5.070503
Q5BJY9	VVDDTNITR	1.063722209	2	3.448374
Q5BJY9	YETELAMR	0.967232816	2	2.617405
Q5BJY9	YWSQQIEESTTVVTTK	1.182900024	2	3.896211
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.947886376**	**4.87E-08**	**4**
Q5BK63	AVQHSNVVINLIGR	0.966779759	2	3.657626
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.333902055	3	6.066943
Q5BK63	NFDFEDVFVNIPR	2.389068614	2	3.856344
Q5BK63	WLSSEIEETKPAK	1.49814881	2	3.293032
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**1.080022214**	**0.570351**	**3**
Q5BK81	DVPYPPPLPPAVEAIQK	10.6806585	2	2.661551
Q5BK81	TGNVAEQLR	2.216031608	2	2.933232
Q5BK81	VEEVSLPDTINEGQVR	0.944524103	2	4.074362
Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**1.295722913**	**0.877567**	**3**
Q5BQE6	LYEQHHVVQDMLVPMK	1.390150742	3	3.580483
Q5BQE6	QLGCQDAFPEVYDK	1.302252395	2	4.215884
Q5BQE6	YLFGWMVPPK	1.151910805	2	2.695338
Q5DTN8	**JKIP3 Janus kinase and microtubule_interacting protein 3**	**1.2906098**	**0.680129**	**2**
Q5DTN8	MKELQAVREALLR	1.40637611	2	2.32857
Q5DTN8	TREQLQAEIQRAQTR	1.279204484	2	2.981337
Q5DU56	**NLRC3 Protein NLRC3**	**1.136917683**	**0.404778**	**2**
Q5DU56	LTGLALGHLYR	1.366412082	2	2.365989
Q5DU56	TLEILDLR	1.043702643	2	2.505149
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.133435637**	**0.000122**	**2**
Q5EB77	NDIVNMLVGNK	1.073332517	2	3.462287
Q5EB77	TCDGVQCAFEELVEK	1.408993458	2	3.865454
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.644120423**	**0.001812**	**2**
Q5FVM4	MEELHNQEVQK	1.644661608	2	3.907037
Q5FVM4	RMEELHNQEVQK	1.549618792	3	4.288568

Q5FVQ4	**MLEC Malectin**	**1.328559629**	**0.575975**	**3**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	1.331088673	3	5.588675
Q5FVQ4	LSVQGEVSTFTGK	1.257938926	2	3.367083
Q5FVQ4	STPEDQILYQTER	1.179906647	2	4.691784
Q5FVR2	**TYPH Thymidine phosphorylase**	**1.342078006**	**0.714534**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10	1.513481379		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8	0.896533471		
Q5FVR2	FGGAAVFPDQEK	0.969798	2	2.594561
Q5FVR2	KQEELLSPADGIVECVR	1.295119821	2	4.071118
Q5FVR2	VSLVLAPALAACGCK	1.370802413	2	3.055124
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.446293151**	**0.22284**	**3**
Q5FVR5	DEKENLFQSK	0.989790385	2	2.463252
Q5FVR5	ILFIVGENDQCLASK	1.430304772	2	3.736695
Q5FVR5	IQQPGIGVISVSK	1.451790735	2	3.356598
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**1.291135502**	**0.791881**	**3**
Q5FW57	AIDQEMFK	1.285423883	2	2.713635
Q5FW57	SSQMLQMLESSLR	1.380631617	2	4.101768
Q5FW57	VYGTVFHMNQGNPFK	1.087922637	2	3.735129
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**1.308934692**	**0.38702**	**8**
Q5I0C3	AGDALMVMIAMK	0.916243768	1	1.958551
Q5I0C3	HAPLVEFEEEEV	1.320899359	2	2.964818
Q5I0C3	IIEEAPAPGIDPEVR	0.997231541	2	3.863775
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	1.608438545	3	4.658177
Q5I0C3	QEGIIFIGPPSTAIR	0.90112841	2	2.497921
Q5I0C3	SEKEFQEQLESAR	1.05559609	2	3.470319
Q5I0C3	VFFSEGAQANR	1.37724473	2	2.444635
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	1.406308826	2	5.141131
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**1.111651748**	**0.041216**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	2.013999152	2	3.70615
Q5I0D1	HEEFEEGCK	1.236305655	2	2.878057
Q5I0D1	VTLAVSDLQK	1.201727173	2	2.494292
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**1.291293604**	**0.004396**	**2**
Q5I0D5	FRPGDEHHPEVR	1.348776935	3	3.658023
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.173154209	2	4.363254
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.706815074**	**0.06573**	**2**
Q5I0D7	GVNTDSGNVCR	1.605320331	2	3.166402
Q5I0D7	YAVDDVQYADEIASVLTSR	1.993077582	2	2.73932
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.224591335**	**0.297938**	**2**
Q5I0E7	QLVEQVEQIQK	1.149476059	2	3.5686
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.502025008	3	3.394444
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**1.363165733**	**0.012914**	**9**
Q5I0H9	DKNQDLCQQESVK	1.804152387	2	4.280535
Q5I0H9	FIEWMQNPEAPPPPEPTWEEQQTSVLHLVGDNFR	1.698071273	3	4.122601
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	1.699242655	3	3.649138
Q5I0H9	GPPLWEEDPGAK	1.283620006	2	3.375934
Q5I0H9	GQGTICWVDCGDAESR	1.080708378	2	4.104399
Q5I0H9	NGEQQAVPALR	1.290818997	2	2.555932
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	2.772656819	3	4.125755
Q5I0H9	NQDLCQQESVK	2.210924526	2	3.425429
Q5I0H9	TELGFTSFIR	1.152135895	2	2.447618
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.290543357**	**0.00014**	**7**
Q5I0J9	HANLLVGSPSALADQTTER	1.160148485	2	5.784337
Q5I0J9	LDAAGGLQSLR	0.95278987	2	3.992821

Q5I0J9	LEGPLAAAHSSGPR	1.166351532	2	3.75329
Q5I0J9	LGQSLVSR	1.510083104	2	2.310632
Q5I0J9	MAGSVPPALQLEDLTTLEER	2.024065029	2	3.388189
Q5I0J9	NSNTMAAAALAAPSLGFDR	1.300497051	2	4.635964
Q5I0J9	TVLYEGPVR	1.221585238	2	2.624068
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.558320451**	**5.88E-08**	**6**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	2.107626769	3	3.379321
Q5I0M2	DNHVVAAGSMEK	1.58243531	2	2.655863
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.813753713	3	4.801347
Q5I0M2	LYAEGDIPVPHAR	1.470201208	2	3.554389
Q5I0M2	VEVECSSLK	1.605110265	2	2.507241
Q5I0M2	YDLGGLVMVK	1.869786883	2	2.524256
Q5M7T9	**THNS2 Threonine synthase_like 2**	**1.703888537**	**5.55E-15**	**2**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	1.705504585	3	5.589877
Q5M7T9	LSEAVTSESVSDEAITQTMGR	1.450582792	2	4.480843
Q5M7U6	**ARP2 Actin_related protein 2**	**1.254355475**	**0.663965**	**5**
Q5M7U6	GYAFNHSADFETVR	1.131155649	2	4.001706
Q5M7U6	HLWDYTFGPEK	1.137770307	2	3.196839
Q5M7U6	ILLTEPPMNPTK	1.009105937	2	2.851513
Q5M7U6	SMLEVNYPMENGIVR	1.415298823	2	4.094187
Q5M7U6	VVVCDNGTGFVK	1.294329738	2	2.709429
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**1.367018408**	**0.83808**	**10**
Q5M7W5	AAVGLTGNDIATPPNK	2.36708405	2	3.480933
Q5M7W5	ATSPSTLVSTGSSSR	1.465134829	2	3.868305
Q5M7W5	EAETALPIEMDLAPPEDVALPK	1.250443579	2	3.080683
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	0.68043427	2	4.185924
Q5M7W5	ETSGSQPPELCSGVSR	1.7623205	2	3.347014
Q5M7W5	NTAPPTEEETVPGK	1.519829813	2	2.581572
Q5M7W5	NTTPTGATPPAGMASTR	1.486704541	2	3.567999
Q5M7W5	STLPVDEGSPLEK	1.311620167	2	2.476973
Q5M7W5	VGSLDNVGHLPAGGTVK	1.055015033	2	3.713764
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.135105446	2	3.144942
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.400388564**	**0.13843**	**7**
Q5M875	ALTAELDTLGK	1.170437256	2	3.078044
Q5M875	IQNIQFEAIVGHR	1.461201067	3	4.241198
Q5M875	LWPVLEPDEVAR	1.189643836	2	2.494882
Q5M875	NSGHIVTVASVCGHR	2.013671962	2	4.501653
Q5M875	SLIDGILTNK	1.527080423	2	3.311132
Q5M875	SVAGQTVLITGAGHGIGR	1.260499667	2	4.096278
Q5M875	TSCLCPVFVNTGFTK	1.165988315	2	3.948629
Q5M9G3	**CAPR1 Caprin_1**	**1.005225531**	**0.296376**	**2**
Q5M9G3	LNQDQLDAVSK	1.490941448	2	3.179749
Q5M9G3	YQEVTNNLEFAK	0.992148593	2	3.037392
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.804765278**	**0.001892**	**2**
Q5M9I5	EEEEEELVDPLTTVR	1.690528689	2	4.23759
Q5M9I5	SQTEEDCTEELFDFLHAR	2.646223875	2	4.831091
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.490732276**	**0.000441**	**10**
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	0.857921922	2	4.996286
Q5PPL3	DPQLVPVLIDAAR	1.830792217	2	2.42473
Q5PPL3	GQVTGTDLINEVSK	1.359612578	2	4.078396
Q5PPL3	GVSTVFHCASPPSNSNNK	1.204810058	2	4.306683
Q5PPL3	GYAVNVFDVR	1.924473281	2	3.567833
Q5PPL3	ILTGLNYEAPK	1.579334771	2	3.587623

Q5PPL3	KGQVTGTDLINEVSK	1.988522615	2	4.41052
Q5PPL3	NGTEDLPYAMKPIDYYTETK	1.5204246	2	3.936774
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.541253396	3	3.520414
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.282740843	2	5.410961
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.161813432**	**0.187321**	**7**
Q5PQT3	AINQEMFK	1.436731576	1	1.952903
Q5PQT3	AIQNLASIHSLQVK	1.015258986	2	4.045582
Q5PQT3	DPENCQEFLGSSEVINWK	2.054142212	2	5.291511
Q5PQT3	KLFPSLLDTK	0.891339716	2	2.714327
Q5PQT3	LSSLDVTHAALVNK	1.369794886	2	3.616019
Q5PQT3	MGGTVPQYR	1.565858418	2	2.561755
Q5PQT3	QHLQIQSSQSHLNK	1.736268229	2	3.393383
Q5PQX1	**TOIP1 Torsin_1A_interacting protein 1**	**1.058440691**	**0.849598**	**2**
Q5PQX1	LEQHSQQAQQQLSPATSGR	1.353469946	3	4.665357
Q5PQX1	SDFGNQSPSTSR	1.052571692	2	2.627681
Q5RJR2	**TWF1 Twinfilin_1**	**1.316058057**	**0.013574**	**2**
Q5RJR2	HQTLQGVAFPISR	1.175910526	2	3.020106
Q5RJR2	YLLSQSSPAPLTAAEEELR	1.316060269	2	4.322939
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.055666417**	**0.410958**	**5**
Q5RJR8	ATVLDLSCNK	1.053817299	2	2.81952
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	1.618115109	2	6.211306
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.386318737	2	4.056415
Q5RJR8	LQQLPADFGR	1.594693296	1	1.92139
Q5RJR8	WLDLKDNPLDPVLAK	1.247862897	2	2.671821
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.619688047**	**4.4E-07**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.860882446	3	4.753004
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	1.232824324	3	4.765683
Q5RKI0	YAPSGFYIASGDISGK	1.57919081	2	4.534091
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.625884681**	**1.83E-13**	**5**
Q5RKI1	ELAQQIQK	1.527838276	1	2.28296
Q5RKI1	GIDVQQVSLVINYDLPTNR	2.214159999	2	3.619074
Q5RKI1	GYDVIAQAQSGTGK	1.28025789	2	5.137969
Q5RKI1	MFVLDEADEMLSR	2.23077203	2	4.492397
Q5RKI1	VLITTDLLAR	1.535002177	2	3.068539
Q5S6T3	**ISPD 2_C_methyl_D_erythritol 4_phosphate cytidylyltransferase_like protein**	**1.080997788**	**0.574399**	**2**
Q5S6T3	ISLAEAGATR	4.501355444	2	2.341984
Q5S6T3	MENLVWIRELAK	1.028842691	2	2.348057
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.252629717**	**2.94E-10**	**15**
Q5SGE0	AALDLEQVPSELAVTR	0.6996564	2	4.107992
Q5SGE0	CIANNQVETLEK	1.291994817	2	3.012738
Q5SGE0	GLDAIELSR	0.743652745	2	2.521475
Q5SGE0	HCVTMDTPAEK	1.520929452	2	2.968091
Q5SGE0	HDNAEDALNLK	1.824205084	2	3.644531
Q5SGE0	LIDYCK	2.374588135	1	1.93197
Q5SGE0	MEGANIQPNR	1.352138529	2	2.97081
Q5SGE0	SCGSLLPELSLAER	1.475756309	2	2.77297
Q5SGE0	SGSPGSNQALLLLR	1.672342233	2	2.884081
Q5SGE0	SGSQFDWALMR	1.515879273	2	2.394822
Q5SGE0	SSLSSSSPSAGDTVTEK	2.510708681	2	3.885435
Q5SGE0	SYVADKDVASAK	1.367109537	2	3.164685
Q5SGE0	TLLELIPELR	1.441540406	2	3.100693
Q5SGE0	TSQFTSSDLESTLEK	1.544174648	2	4.18987
Q5SGE0	VIEEQMEPALEK	1.38026497	2	3.111521
Q5SW19	**K0664 Protein KIAA0664**	**1.389006116**	**0.221598**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	1.004457657	2	3.384758

Q5SW19	IGIGELITR	1.703757846	2	2.400033
Q5SW19	SVEGLQEGSVLR	1.400108502	2	2.737927
Q5SX40	**MYH1 Myosin_1**	**1.682157062**	**1**	**86**
Q5SX40	AAYLQNLNSADLLK	1.346412282	2	3.44502
Q5SX40	ADIAESQVNK	2.959708003	2	3.704841
Q5SX40	AEDEEEINAELTAK	5.487019972	2	4.21949
Q5SX40	AGLLGLLEEMR	4.45708039	2	4.265569
Q5SX40	AGLLGLLEEMRDDK	2.262447134	2	3.385749
Q5SX40	ALQEAHQQTLDDLQAEEDK	4.528766914	3	4.511956
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	0.444375318	3	6.778407
Q5SX40	ANLLQAEIEELR	5.022936209	2	3.717834
Q5SX40	ANSEVAQWR	1.241203648	2	2.875629
Q5SX40	DDKLAQLITR	2.952572064	2	2.352811
Q5SX40	DLEEATLQHEATAATLR	2.140634801	2	5.085145
Q5SX40	DTQLHLDDALR	0.7521422	2	2.845197
Q5SX40	EEQAEPDGTEVADK	0.776967909	2	3.389882
Q5SX40	EFEMSNLQSK	3.166259537	1	2.63379
Q5SX40	ELEGEVENEQK	0.662157159	2	2.881448
Q5SX40	ELEGEVENEQKR	2.70145141	2	3.028635
Q5SX40	ELTYQTEEDRK	1.645001771	2	3.127402
Q5SX40	EMANMKEEFEK	2.750105975	2	2.823982
Q5SX40	ENQSILITGESGAGK	6.347289101	2	4.108367
Q5SX40	EQYEEEQEAK	2.5216553	1	3.213044
Q5SX40	GQEDLKEQLAMVER	1.893321107	2	4.419429
Q5SX40	GSSFQTVSALFR	0.82084765	2	3.067356
Q5SX40	HADSVAELGEQIDNLQR	3.439204368	2	6.017416
Q5SX40	IAEQELLDASER	2.770951311	2	3.233256
Q5SX40	IEAQNKPFDAK	0.993198015	2	3.037445
Q5SX40	IEDEQALGMQLQK	5.454679777	2	4.605048
Q5SX40	IEDEQALGMQLQK+Oxidation(8	4.058174026		
Q5SX40	IEDMAMMTHLHEPAVLYNLK	2.047843282	3	4.302855
Q5SX40	IEELEEEIEAER	2.77386642	2	4.345762
Q5SX40	IKLEQQVDDLEGSLEQEK	2.562264197	2	5.116448
Q5SX40	IKLEQQVDDLEGSLEQEKK	1.256005111	3	4.101195
Q5SX40	IQHELEEAEER	2.195389801	2	3.693294
Q5SX40	IQHELEEAEERADIAESQVNK	2.38001533	3	3.880238
Q5SX40	IQLELNQVK	1.814339637	2	2.704928
Q5SX40	KIAEQELLDASER	2.226737544	2	3.828229
Q5SX40	KIQHELEEAEER	2.28815399	3	4.115162
Q5SX40	KKEFEMSNLQSK	2.497534806	2	3.862054
Q5SX40	KKLETDISQIQGEMEDIVQEAR	2.063931141	3	6.08285
Q5SX40	KLEDECSELK	1.719861537	2	2.918715
Q5SX40	KLEDECSELKK	0.886386439	2	4.027037
Q5SX40	KLETDISQIQGEMEDIVQEAR	2.670558012	2	5.647849
Q5SX40	KMEGDLNEMEIQLNHSNR	1.679031687	3	4.613261
Q5SX40	LAQESTMDVENDKQQLDEK	2.995964167	2	4.863285
Q5SX40	LDEAEQLALK	3.263276505	2	3.235038
Q5SX40	LEDECSELKK	2.693548667	2	3.32472
Q5SX40	LEEAGGATSAQIEMNK	2.524733667	2	5.153748
Q5SX40	LEQQVDDLEGSLEQEK	0.873713229	2	5.465362
Q5SX40	LEQQVDDLEGSLEQEKK	1.406581304	2	4.163102
Q5SX40	LETDISQIQGEMEDIVQEAR	0.693351073	2	5.190956
Q5SX40	LINELTAQR	11.50769656	2	3.147175
Q5SX40	LQDAEEHVEAVNAK	2.279605828	2	4.815016
Q5SX40	LQDLVDK	0.38687325	2	2.446842
Q5SX40	LQDLVDKLQSK	2.062245681	2	2.553188
Q5SX40	LQNEVEDLMIDVER	3.220665195	2	4.46346

Q5SX40	LQTESGEYSR	1.379791619	2	2.519906
Q5SX40	LTGAVMHYGNMK	1.573822981	2	2.676922
Q5SX40	MEGDLNEMEIQLNHSNR	1.505056359	2	4.733225
Q5SX40	MEGDLNEMEIQLNHSNRMAAEALR+Oxidation(0)Oxidation(17	1.369088536		
Q5SX40	MEIDDLASNMEVISK	0.456640339	2	4.957572
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	3.090767526	3	6.376588
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0	2.317101801		
Q5SX40	NDLQLQVQSEADSLADAEER	13.52240409	2	6.306685
Q5SX40	NKDPLNETVVGLYQK	2.975684322	2	4.691516
Q5SX40	NLQQEISDLTEQIAEGGK	3.003001839	2	6.028763
Q5SX40	NLQQEISDLTEQIAEGGKR	1.906640403	2	4.273369
Q5SX40	NLTEEMAGLDETIAK	2.750986211	2	4.788482
Q5SX40	QAEEAEEQSNVNLAK	6.789264469	2	4.411219
Q5SX40	QKYEETHAELEASQK	1.74857052	2	3.911906
Q5SX40	QLDEKDSLVSQLSR	1.651137971	2	3.190784
Q5SX40	QLEEEIK	1.452879988	1	2.203425
Q5SX40	QREEQAEPDGTEVADK	3.463348193	2	4.124691
Q5SX40	RDLEEATLQHEATAATLR	1.499858601	3	3.629238
Q5SX40	SAETEKEMANMKEEFEK	0.573533167	3	4.015881
Q5SX40	SELQAALEEAEASLEHEEGK	0.71969135	2	5.749967
Q5SX40	SSVFVVDAK	2.722855354	2	2.527957
Q5SX40	TKYETDAIQR	1.746831387	3	3.452014
Q5SX40	TLEDQVSELK	4.33054779	2	2.949191
Q5SX40	TNAACAALDK	1.673083454	1	1.98446
Q5SX40	TNAACAALDKK	0.349618499	2	2.980511
Q5SX40	VLNASAIPEGQFIDSK	2.780279952	2	4.297973
Q5SX40	VQLLHTQNTSLINTK	1.863736383	2	4.710315
Q5SX40	VRELEGEVENEQK	0.562540648	2	3.856357
Q5SX40	VRELEGEVENEQKR	1.893410277	3	4.14079
Q5SX40	VVESMQSTLDAEIR	1.024666138	2	3.741544
Q5SX40	YEETHAELEASQK	2.225157036	2	4.738616
Q5SX40	YETDAIQR	2.657076783	2	2.620345
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.36131707**	**0.384846**	**5**
Q5U206	DTDSEEEIR	1.326789198	2	2.832051
Q5U206	KMKDTDSEEEIR	1.413790792	3	3.410882
Q5U206	KMKDTDSEEEIR+Oxidation(1	1.881262062		
Q5U206	MKDTDSEEEIR	1.18334788	3	4.327105
Q5U206	MKDTDSEEEIR+Oxidation(0	1.171323681		
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.46605492**	**1.48E-08**	**4**
Q5U2Q7	GFGGIGGILR	1.505528068	2	2.758224
Q5U2Q7	LSVLGAITSVQQR	1.679394233	2	2.939879
Q5U2Q7	YFDEISQDTGK	2.365610628	2	2.534869
Q5U2Q7	YVLHCQGTEEEK	1.452044887	2	3.683923
Q5U2S3	**ZUFSP Zinc finger with UFM1_specific peptidase domain protein**	**1.369662613**	**0.002215**	**2**
Q5U2S3	QYGLDNSGGYKQQQLR	1.367109625	2	2.677021
Q5U2S3	TLCLLIFDPGCPSREMQKLLK+Oxidation(15	5.219267025		
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**0.846211941**	**0.242751**	**5**
Q5U2U0	LLEGTIVNVPEK	1.872522954	2	2.624495
Q5U2U0	QQAEVEK	1.02047862	1	1.917793
Q5U2U0	SGESNTHQDIEEK	1.525608401	2	3.600021
Q5U2U0	SGESNTHQDIEEKDR	0.831136432	3	4.32588
Q5U2U0	SNILLLGPTGSGK	1.395717562	2	2.37762
Q5U2V4	**PLBL1 Phospholipase B_like 1**	**1.698093948**	**0.060074**	**2**

Q5U2V4	IWEMGHCSALIK+Oxidation(3	14.43555928		
Q5U2V4	LGLDYSYDLAPR	1.397158857	2	2.51104
Q5U2Z7	**RHG24 Rho GTPase_activating protein 24**	**1.302646379**	**0.36591**	**2**
Q5U2Z7	EEEAGVKELTKQVK	1.312432178	2	2.387398
Q5U2Z7	FTMIEIKMRNAER+Oxidation(7	1.279289312		
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.291910569**	**7.07E-05**	**14**
Q5U300	AAVASLLQSVQVPEFTPK	1.29579718	3	3.671613
Q5U300	AENYDISPADR	0.971623883	2	3.191067
Q5U300	DNPGVVTCLDEAR	1.357288585	2	3.399971
Q5U300	FEVQGLQPNGEEMTLK	1.540835879	2	4.019649
Q5U300	IHVSDQELQSANASVDDSR	1.999774994	3	3.487239
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.380510383	2	4.711717
Q5U300	LDQPMTEIVSR	1.126582998	2	3.394889
Q5U300	LKSDTAAAAVR	1.435322268	2	2.822456
Q5U300	NEEDATELVTLAQAVNAR	1.744202624	3	4.687948
Q5U300	NFPNAIEHTLQWAR	1.268251356	2	3.407256
Q5U300	SLPASLAEPDFVMTDFAK	1.165985625	2	4.057586
Q5U300	SPPAVQQDNVDEDLIR	1.147649251	2	4.76979
Q5U300	SPPAVQQDNVDEDLIRK	1.438382024	3	3.322069
Q5U300	VVQGHQQLDSYK	1.462055339	2	3.426212
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**1.196045095**	**0.193324**	**3**
Q5U4E6	EFNTQLAQK	1.19460047	2	2.349419
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(16	1.992643889		
Q5U4E6	VQQCAKDTESQLSELR	5.501797198	2	2.310873
Q5XFW8	**SEC13 Protein SEC13 homolog**	**0.906366328**	**0.926136**	**4**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	0.89722706	2	3.45853
Q5XFW8	EEEDGQWKEEQK	1.023419112	2	2.757006
Q5XFW8	LEAHSDWVR	1.125016821	2	2.368684
Q5XFW8	NGGQILIADLR	1.274145497	2	2.481695
Q5XFX0	**TAGL2 Transgelin_2**	**1.072511218**	**3.92E-05**	**6**
Q5XFX0	DDGLFSGDPNWFPK	3.908129087	2	3.66492
Q5XFX0	NFSDNQLQEGK	0.898680315	2	3.157585
Q5XFX0	NVIGLQMGTNR	0.767969207	2	3.026118
Q5XFX0	QMEQISQFLQAAER	1.196237419	2	2.803067
Q5XFX0	TLMNLGGLAVAR	1.534308233	2	3.358201
Q5XFX0	YGINTTDIFQTVDLWEGK	1.729776532	2	4.739267
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.415891072**	**2.38E-09**	**11**
Q5XHY5	AEHDSILAEK	1.58893844	2	2.838853
Q5XHY5	FLGDIEIWNQAEK	1.488921424	2	3.762261
Q5XHY5	FMVDIDLDPGCTLNK	1.240854508	2	3.756401
Q5XHY5	GFQEVVTPNIFNSR	2.723282272	2	3.90931
Q5XHY5	LKAEHDSILAEK	0.836930056	2	3.346968
Q5XHY5	NELSGALTGLTR	1.125393906	2	3.20448
Q5XHY5	QLENSLNEFGEK	1.002556066	2	3.156332
Q5XHY5	QVMVVPVGPTCDEYAQK	1.593319955	2	3.668219
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.385225187	2	4.151703
Q5XHY5	VVWDLDRPLETDCTLELLK	3.002198476	2	3.881314
Q5XHY5	WELNPGDGAFYGPK	1.636427292	2	3.963933
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.542284156**	**1.2E-08**	**14**
Q5XHZ0	AFLEALQHQAETSSR	1.33264362	2	4.684554
Q5XHZ0	AQLLQPTLEINPR	1.235951377	2	3.723259
Q5XHZ0	EGIVTTAEQDIKEDIAK	0.808144667	2	2.326745
Q5XHZ0	ELISNASDALEK	0.287161115	2	2.706632
Q5XHZ0	FEDTSPAGER	2.023619192	2	2.496381
Q5XHZ0	GTITIQDTGIGMTK	1.333257536	2	3.56485
Q5XHZ0	GVVDSEDIPLNLSR	1.356115972	2	4.806192

Q5XHZ0	HLAEHSPYYEAMK	1.856326403	2	3.726214
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.269740231	3	4.056579
Q5XHZ0	NIYYLCAPNR	1.066575124	2	2.414728
Q5XHZ0	SDCKDFANESR	1.5791712	2	2.701574
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	1.598774305	3	3.64968
Q5XHZ0	YESSALPAGQLTSLSDYASR	2.087433547	2	5.63993
Q5XHZ0	YIAQAYDKPR	1.755306023	2	2.661063
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**2.244130102**	**0.005778**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	2.471234883	2	4.993508
Q5XI22	ELGLSPEK	2.414883255	1	1.950416
Q5XI22	HGSNLEAMSK	1.619634832	2	2.683468
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	2.165849766	3	5.219206
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	1.863724481	3	4.073259
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	2.191675168	3	4.536588
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	2.850051021	2	5.422345
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	1.741305889	2	5.185032
Q5XI22	VNIDGGAIALGHPLGASGCR	1.693836721	2	5.443277
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**1.081445039**	**0.507712**	**2**
Q5XI29	QNLSQFEAQAR	1.352966019	2	2.416333
Q5XI29	SIGVYDVVELK	1.081434832	2	2.367136
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.190870106**	**0.000422**	**8**
Q5XI32	GCWDSIHVVEVQEK	1.156789777	2	3.742956
Q5XI32	KLEVEANNAFDQYR	1.447177341	2	4.138146
Q5XI32	LEVEANNAFDQYR	0.895760093	2	3.759038
Q5XI32	LVEDMENK	1.690644633	2	2.668736
Q5XI32	NDLVEALK	1.248876182	2	2.404436
Q5XI32	SGSGTMNLGGSLTR	1.621497769	2	3.303425
Q5XI32	STLNEIYFGK	1.10633424	1	2.057582
Q5XI32	YDPPLEDGAMPSAR	0.986272848	2	3.583294
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.393095393**	**0.968666**	**3**
Q5XI60	ALDIAAGITR	1.209046391	2	3.267238
Q5XI60	HHVALDSAASQLSGR	1.340020182	2	4.600824
Q5XI60	NVATDALGALEAR	1.489955954	2	3.983206
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.370985925**	**0.610823**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.662536436	2	4.40899
Q5XI73	IDKTDYMVGSYGPR	1.443437171	2	3.989285
Q5XI73	SIQEIQELDKDDESLR	0.622287921	2	5.289581
Q5XI73	SIQEIQELDKDDESLRK	1.013472089	2	4.653828
Q5XI73	TDYMVGSYGPR	1.425977299	2	2.414232
Q5XI73	VAVSADPNVPNVIVTR	0.814001217	2	3.97865
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**0.836859061**	**0.014853**	**18**
Q5XI78	FGLEGCEVLIPALK	1.419465864	2	3.587001
Q5XI78	FLDTAFDLDAFK	2.054391448	2	2.660427
Q5XI78	FLDTAFDLDAFKK	1.644976861	2	2.93743
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.330702553	3	5.910299
Q5XI78	ICEEAFTR	1.489800069	2	2.340133
Q5XI78	IEQLSPFPFDLLLK	1.033250458	2	3.325492
Q5XI78	LEAADEGSGDMK	0.939277294	2	3.516473
Q5XI78	LNVLANVIR	17.04169287	2	2.321543
Q5XI78	LVEDHLAVQSLIR	1.649364972	2	2.901086
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.301558995	2	5.550704
Q5XI78	NQGYYDYVKPR	1.245623396	2	2.378892
Q5XI78	NTNAGAPPGTAYQSPLSLSR	0.081739768	2	2.853565
Q5XI78	SSLATMAHAQSLVEAQPNVDK	0.834179462	3	4.405403
Q5XI78	TSFDEMLPGTHFQR	1.28144421	2	2.308486

Q5XI78	VIPEDGPAAQNPDK	1.521042484	2	2.944821
Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	1.714373082	3	4.246809
Q5XI78	YAELLVSQGVVNQPEYEEEISK	2.047498999	2	4.070637
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	3.475808796	3	3.932368
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**1.344123126**	**0.018432**	**6**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	1.466282233	2	3.941933
Q5XI95	FNIDPLITHTLTLSEANEAVQLMK	1.622827212	3	4.985782
Q5XI95	IIAVDINK	1.344001722	2	2.737931
Q5XI95	MVATGVCGTDIK	1.170245387	2	3.021445
Q5XI95	NNICTEIR	1.637827241	2	2.47322
Q5XI95	TVGATDCVDPR	2.6909777	2	2.827778
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.23595656**	**0.195329**	**6**
Q5XIC0	AAEMLLFGK	2.155472951	2	2.45247
Q5XIC0	ATQQDFENAMNQVK	1.084421194	2	4.272891
Q5XIC0	GILVTSEGGITK	1.217745925	2	3.450741
Q5XIC0	LHAVNEEECTTLR	1.235957928	2	3.851182
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.792568562	2	5.408242
Q5XIC0	WDAWNALGSLPK	1.105766584	2	3.691369
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.114209432**	**0.418803**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	0.695117519	2	2.628219
Q5XIC1	VEGTPNDPNPNDPR	2.600550663	2	3.189665
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.358191707**	**0.028678**	**7**
Q5XIE6	AGIATHFVDSEK	1.165193668	2	3.112767
Q5XIE6	AVLIDKDQTPK	1.409982053	2	2.836672
Q5XIE6	GCAGVITLNRPK	0.865919805	2	2.91632
Q5XIE6	HTETAEVLLER	1.947192071	2	2.878844
Q5XIE6	INSCFSANTVEQILENLR	1.675194684	2	3.161813
Q5XIE6	LHVLEEELLALK	2.56354498	3	4.101669
Q5XIE6	WKPADLKDVTDEDLNSYFK	2.03830453	2	2.315773
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.247755536**	**0.868794**	**3**
Q5XIF3	DTQLITVDEK	0.910843483	2	2.484307
Q5XIF3	HGWSYDVEGR	1.250764602	2	2.884388
Q5XIF3	LDVTPLTGVPEEHIK	1.20664954	3	3.661286
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.333662165**	**9.22E-12**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	1.211785324	2	3.844597
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.334157375	2	5.220331
Q5XIF6	DVNAAIAAIK	2.006480493	2	3.108192
Q5XIF6	SIQFVDWCPTGFK	1.093238333	2	4.138381
Q5XIF6	TIGGGDDSFTTFFCETGAGK	1.764991624	2	2.78316
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.198067725**	**0.587159**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	1.72902682	2	4.398521
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.186668941	2	5.665212
Q5XIH7	**PHB2 Prohibitin_2**	**1.130181677**	**1.06E-07**	**10**
Q5XIH7	DLQMVNISLR	4.71785153	2	2.730489
Q5XIH7	FNASQLITQR	0.886104862	2	3.781612
Q5XIH7	IGGVQQDTILAEGLHFR	1.449995638	3	4.924634
Q5XIH7	IPWFQYPIIYDIR	2.331284998	2	2.470196
Q5XIH7	IVQAEGEAEAAK	1.074954169	2	4.057411
Q5XIH7	IYLTADNLVLNLQDESFTR	1.942192361	2	4.042464
Q5XIH7	LGLDYEER	0.962468469	2	2.467785
Q5XIH7	LLLGAGAVAYGVR	3.328856386	2	3.784027
Q5XIH7	VLPSIVNEVLK	1.514243369	1	2.297766
Q5XIH7	VLSRPNAQELPSMYQR	1.816673617	2	4.761806
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**2.340130569**	**9.9E-20**	**12**

Q5XIM9	DASLMVTNDGATILK	5.668111812	2	2.991523
Q5XIM9	EALLSSAVDHGSDEVK	2.067277136	2	4.253445
Q5XIM9	FWQDLMNIAGTTLSSK	1.64184021	2	3.477302
Q5XIM9	GATQQILDEAER	1.516757891	2	3.873988
Q5XIM9	GSGNLEAIHVIK	1.219000949	2	2.569248
Q5XIM9	HGINCFINR	0.658322356	2	2.651577
Q5XIM9	LIEEVMIGEDK	1.144240272	2	3.155605
Q5XIM9	MLPTIIADNAGYDSADLVAQLR	1.258891186	3	3.31328
Q5XIM9	NIGVDNPAAK	1.236129549	1	1.953843
Q5XIM9	SLHDALCVLAQTVK	2.075837235	2	3.899406
Q5XIM9	VAEIEHAEKEK	1.400257636	2	2.794805
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	2.376671151	2	4.352936
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.267780735**	**0.009774**	**10**
Q5XIN6	AAEVEGEQVDNK	1.285956901	2	3.877725
Q5XIN6	AMYLPDTLSPADQLK	1.104622869	2	2.466151
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.749269734	2	4.544624
Q5XIN6	FLQDTIEEMALK	1.684388624	2	3.036834
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.430819779	2	3.729424
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	1.257890415	2	5.304123
Q5XIN6	LEEGGPVYSPPAQVVVK	0.812107417	2	3.392336
Q5XIN6	LFEDELTLDNLTRPQLVALCK	2.06906534	3	3.982033
Q5XIN6	LLELQSIGTNNFLR	1.294281214	2	3.466008
Q5XIN6	STLQTLPEIVAK	1.098192436	2	2.576723
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**1.236569876**	**0.578609**	**9**
Q5XIT9	AATGEEVSAEDLGGADLHCR	1.20572569	2	5.224376
Q5XIT9	ALVNQLHER	1.22701832	2	2.684438
Q5XIT9	ALYGDTLVTGFAR	1.005423593	2	3.512196
Q5XIT9	AQEIALQNR	1.238431425	2	2.570481
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.298665223	2	5.251388
Q5XIT9	LWDDGIIDPVDTR	1.20604512	2	3.53647
Q5XIT9	LYGEEEVPAGGIITGIGR	5.031394103	2	4.765272
Q5XIT9	RFEEEGNPYYSSAR	2.114998043	2	4.254006
Q5XIT9	VSGVECMIVANDATVK	1.439629916	2	3.39354
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**0.74800704**	**0.1477**	**2**
Q5XIU5	ALIDPSSGLPNR	0.766233568	2	2.7933
Q5XIU5	SGIITPIHEQWEK	0.660177194	2	3.036075
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.002358402**	**0.080893**	**3**
Q5XIU9	GLATFCLDK	1.354434456	2	2.80292
Q5XIU9	GLCSGPGAGEESPAATLPR	0.994941065	2	4.839227
Q5XIU9	VFDVTK	1.323258746	1	1.987391
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**1.307683989**	**0.002606**	**9**
Q60587	ALAMGYKPK	0.512411007	2	2.405054
Q60587	AMDSDWFAQNYMGR	1.959673093	2	3.158256
Q60587	AQDEGHLSDIVPFK	0.81914138	2	2.486638
Q60587	DFIYVSQDPK	0.589641096	2	2.795557
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	1.632852639	3	4.677299
Q60587	DNGIRPSSLEQMAK	1.222362193	2	3.64398
Q60587	DQLLLGPTYATPK	1.554810954	2	3.759946
Q60587	MMLDLNK	1.088708642	1	2.127558
Q60587	NIVVVEGVR	1.450905387	2	3.063334
Q60598	**SRC8 Src substrate cortactin**	**1.250060718**	**0.369875**	**3**
Q60598	NASTFEEVVQVPSAYQK	1.267614215	2	3.547376
Q60598	TVQGSGHQEHINIHK	0.800977289	2	3.473675

Q60598	VDQSAVGFEYQGK	1.207120499	2	3.345992
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.583467**	**0.00014**	**4**
Q60759	DILGGNGISDEYHVIR	1.675387111	2	3.860195
Q60759	DIVYEMGELGVLGPTIK	1.586905304	2	3.896854
Q60759	GYGCAGVSSVAYGLLTR	1.268021347	2	3.321871
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.585282891	3	5.098244
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.207390049**	**0.362832**	**3**
Q60817	DIELVMSQANVSR	1.380061243	2	3.418987
Q60817	IEDLSQQAQLAAAEK	1.178655144	2	4.676005
Q60817	NILFVITKPDVYK	0.841941385	2	3.66666
Q60952	**CP250 Centrosome_associated protein CEP250**	**1.254028217**	**0.491586**	**2**
Q60952	GQIQDLKK	1.239418489	1	1.955204
Q60952	QQIDELQK	2.653689461	1	2.035223
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**1.039060627**	**0.998882**	**2**
Q61029	SELVANNVTLPAGEQR	1.04476342	2	4.566918
Q61029	YGVNPGPIVGTTR	1.038660291	2	2.71646
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.367822652**	**0.235587**	**2**
Q61035	ASAEQIEEEVTK	1.958353098	2	2.776581
Q61035	REDLVEEIR	1.333993314	2	2.466448
Q61043	**NIN Ninein**	**1.006045848**	**0.854161**	**3**
Q61043	NEITTLNEEDSISNLK	0.754345454	2	2.474047
Q61043	RQLQMAFDEEKAQLQEELR+Oxidation(4	0.80672053		
Q61043	SLENVLAEK	1.14693076	1	2.024421
Q61301	**CTNA2 Catenin alpha_2**	**1.339428835**	**0.000161**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	1.417441976	2	3.826974
Q61301	TSVQTEDDQLIAGQSAR	1.532785037	2	5.001553
Q61301	WDDSGNDIIVLAK	1.300460976	2	3.036304
Q61335	**BAP31 B_cell receptor_associated protein 31**	**1.079371289**	**0.92929**	**5**
Q61335	AENEALAMQK	1.254346901	2	3.416152
Q61335	KYMEENDQLK	1.287733224	2	2.637512
Q61335	KYMEENDQLKK	0.943465795	3	3.968243
Q61335	YMEENDQLK	1.425183443	2	2.742815
Q61335	YMEENDQLKK	1.105374176	2	2.901673
Q61545	**EWS RNA_binding protein EWS**	**1.363705663**	**0.315585**	**2**
Q61545	GDATVSYEDPPTAK	1.887299725	2	3.41173
Q61545	GGPGGPGGPGGPMGR	1.645020106	2	2.863945
Q61595	**KTN1 Kinectin**	**1.055373376**	**0.241105**	**2**
Q61595	TAEHEAAQQDLQSK	1.378729564	2	4.379523
Q61595	VEPVLVTK	0.440805875	2	2.357152
Q61655	**DD19A ATP_dependent RNA helicase DDX19A**	**1.27171181**	**0.118856**	**2**
Q61655	SNLVDNTNQVEVLQR	1.158738687	2	4.182843
Q61655	TSTTAEKTEEEEKEDR	1.72842641	3	3.985461
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**1.269584371**	**1.36E-11**	**6**
Q61656	ELAQQVQQVAAEYCR	1.19607752	2	2.882295
Q61656	GDGPICLVLAPTR	1.949442819	2	2.955872
Q61656	MLDMGFEPQIR	1.879670988	2	3.346453
Q61656	NFYQEHPDLAR	2.09042305	2	3.307261
Q61656	STCIYGGAPK	1.53028282	2	2.475777
Q61656	TAQEVDTYR	1.487958217	2	2.31755
Q61830	**MRC1 Macrophage mannose receptor 1**	**1.463904177**	**0.32152**	**3**
Q61830	LKLPWHEAETYCK	1.182264003	2	2.350836
Q61830	WTVDEQVQFTHWNADMPGR+Oxidation(15	2.484118974		
Q61830	YLNWLPGSPSSEPGK	1.446813476	2	2.628163

Q61941	**transhydrogenase_ mitochondrial**	**1.207942129**	**0.000245**	**13**
Q61941	AQYPIADLVK	1.334273573	2	2.479295
Q61941	DDFDFGTMSHVIR	1.468114193	2	2.526869
Q61941	EANSIVITPGYGLCAAK	1.429580916	2	3.839342
Q61941	FFTGQITAAGK	1.164079006	2	2.742116
Q61941	GITHIGYTDLPSR	1.035275131	2	3.747139
Q61941	ILIVGGGVAGLASAGAAK	2.284312419	2	3.90539
Q61941	KTTVLAMDQVPR	1.088227054	2	3.288739
Q61941	MATQASTLYSNNITK	1.10772986	2	4.726693
Q61941	QGFNVVVESGAGEASK	1.249961961	2	4.148831
Q61941	SLGAEPLEVDLK	1.230289952	2	3.513805
Q61941	TTVLAMDQVPR	1.22135314	2	2.575528
Q61941	TVAELEAEK	1.1866038	2	2.980571
Q61941	VTIAQGYDALSSMANISGYK	1.402366351	2	5.331681
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**1.741044968**	**0.015548**	**2**
Q61990	AITIAGIPQSIIECVK	1.713725798	2	2.332909
Q61990	IITLAGPTNAIFK	2.575815668	2	2.544732
Q62009	**POSTN Periostin**	**1.618463639**	**0.230823**	**2**
Q62009	ISTGGGETGETLQKFLQK	1.291888728	2	2.521237
Q62009	TEGPAMTKIQIEGDPDFR	1.722105217	2	2.309934
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.77121853**	**9.9E-20**	**4**
Q62095	HVINFDLPSDIEEYVHR	2.23037059	3	4.445738
Q62095	SFLLDLLNATGK	1.943070929	2	4.173014
Q62095	VGNLGLATSFFNER	1.6560836	2	3.112155
Q62095	VGSTSENITQK	0.615536428	2	2.860748
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.280617957**	**1.39E-06**	**20**
Q62261	AKDEQSAVSMLK	1.34715254	2	2.472989
Q62261	ALVADSHPESER	1.477921595	2	3.190837
Q62261	DQNTVETLQR	1.258957737	2	2.999768
Q62261	EAEKLESEHPDQAQAILSR	2.099342288	3	3.843669
Q62261	EGMQLISEKPETEAVVKEK	1.638277009	2	2.340947
Q62261	EIEELQSQAQALSQEGK	0.957079587	2	3.783779
Q62261	FESLEPEMNNQASR	1.294362409	2	3.904787
Q62261	HLLGVEDLLQK	1.486811101	2	3.409025
Q62261	HQILEQAVEDYAETVHQLSK	1.27214468	3	5.534888
Q62261	ITDLYTDLR	1.222859158	2	2.439145
Q62261	LTTLELLEVR	2.400421278	2	2.91883
Q62261	LVSDGNINSDR	1.245657509	2	3.324292
Q62261	LVSQDNFGFDLPAVEAATK	2.018259894	2	3.178743
Q62261	SNAHYNLQNAFNLAEQHLGLTK	1.217322358	3	3.897827
Q62261	SQNIITDSSSLNAEAIR	1.022260847	2	5.243514
Q62261	TLETPAAQMEGFLNR	2.306975447	2	3.225232
Q62261	TQILAASYELHK	1.550778906	2	2.571994
Q62261	TQTAIASEDMPNTLTEAEK	1.468242869	2	5.219253
Q62261	VIESTQDLGNDLAGVMALQR	0.233207037	2	4.459213
Q62261	VLDNAIETEK	1.014774987	2	2.471166
Q62376	**RU17 U1 small nuclear ribonucleoprotein 70 kDa**	**1.065752234**	**0.57195**	**2**
Q62376	IERRQQEVETELK	0.584584809	2	2.304791
Q62376	RQQEVETELK	1.100889316	2	2.484204
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.062272111**	**0.320788**	**3**
Q62425	FYSVNVDYSK	1.072701236	2	2.843378
Q62425	KNNPEPWNK	0.507523455	2	2.547746
Q62425	LGPNEQYK	0.993774832	1	2.025448
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**1.614882623**	**0.018602**	**2**
Q62446	GWDEALLTMSK	1.691223926	2	2.479952
Q62446	SEETLDEGPPK	1.611918717	2	3.040901

Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**0.751168565**	**0.000115**	**4**
Q62452	AMEIAEALGR	1.032515447	2	4.104401
Q62452	GAGVTLNVLEMTADDLENALK	1.203858933	2	5.390175
Q62452	WLPQNDLLGHPK	1.116147905	2	3.294807
Q62452	YTGTRPSNLAK	0.396427513	2	2.720869
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.09038849**	**0.051396**	**8**
Q62465	ACGLNFADLMGR	1.322599573	2	2.906566
Q62465	CLVLTGFGGYDK	0.966092294	2	2.924945
Q62465	ENGVTHPIDYHTTDYVDEIKK	1.235207885	3	3.544729
Q62465	GVDIVMDPLGGSDTAK	0.968926643	2	4.370294
Q62465	IDSVWPFEK	1.065725032	2	2.774368
Q62465	TVENVTVFGTASASK	1.131913332	2	3.522699
Q62465	VLLVPGPEKET	1.150007611	2	2.792584
Q62465	VVTYGMANLLTGPK	1.348105375	2	3.48565
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.604654274**	**4.5E-11**	**4**
Q62636	INVNEIFYDLVR	1.80009354	2	4.026201
Q62636	LVVLGSGGVGK	1.672088878	2	2.636943
Q62636	QWSNCAFLESSAK	1.000866213	2	2.540851
Q62636	VKDTDDVPMILVGNK	1.034375888	2	2.781354
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**1.239730269**	**0.351322**	**4**
Q62651	HVLHVQLNRPEK	1.485537327	2	3.794765
Q62651	MMADEALDSGLVSR	1.229483714	2	4.376722
Q62651	RIPEEVSDHNYESIQVTSAQK	1.291790495	3	5.607813
Q62651	SLVNELTFTAR	1.22050891	2	3.1926
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**1.401803633**	**0.890601**	**7**
Q62730	AVLVTGADSGFGHALAK	1.083914221	2	4.349936
Q62730	DIQHAICAK	1.362330888	2	2.392377
Q62730	EIQENYGQEYVHTQK	1.417780417	2	4.504911
Q62730	EMSNPDITPVLR	1.147187615	2	2.665439
Q62730	LSVLQMDVTKPEQIK	1.748940073	2	3.694517
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	1.097543919	3	4.607848
Q62730	VVTIHPGGFQTNIVGSQDSWDK	1.465736375	2	5.815256
Q62736	**CALD1 Non_muscle caldesmon**	**1.252741327**	**0.000665**	**14**
Q62736	ASGDKEAEGAPQVEAGK	1.320947814	2	4.851412
Q62736	ASGDKEAEGAPQVEAGKR	1.504804869	3	3.97246
Q62736	EEIERR	1.679060897	1	1.904695
Q62736	EFDPTITDGSLSVPSR	1.443775918	2	3.67397
Q62736	GGNLGENQIKDEK	1.237778824	2	3.475792
Q62736	GSVFSSPSASGTPNK	1.250557076	2	2.305127
Q62736	KVLEEEEQR	0.866046394	2	2.743766
Q62736	LEQYTNAIEGTK	1.129675879	2	3.373482
Q62736	MQNNSAENETAEGEEK	1.039977633	2	4.885186
Q62736	MQNNSAENETAEGEEKGESR	0.893428469	3	4.628217
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0	0.823096867		
Q62736	RGETESEEFEK	1.295136195	2	3.316064
Q62736	RRGETESEEFEK	1.347798928	2	2.899158
Q62736	VLEEEEQR	1.321171333	2	2.598369
Q62745	**CD81 CD81 antigen**	**1.694436991**	**0.692528**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.796844012	2	3.172975
Q62745	QFYDQALQQAVMDDDANNAK	1.681835509	2	5.035611
Q62769	**UN13B Protein unc_13 homolog B**	**0.92700963**	**0.482266**	**3**
Q62769	DHMVREETRNLTPK	0.929931728	2	2.587775
Q62769	ILSQRSNDEVAR	3.098432238	2	2.351807
Q62769	SNDEVAREFVK	0.651841054	1	1.936553
Q62770	**UN13C Protein unc_13 homolog C**	**1.756792773**	**0.243238**	**2**

Q62770	ENFPASNSERLQDLK	1.199569342	2	2.374516
Q62770	NLSMDETGLTILR	10.66422215	2	2.376304
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.47121466**	**0.968564**	**6**
Q62785	ANEEDEQEEGGDGASGDPK	1.421656067	2	5.573848
Q62785	ANEEDEQEEGGDGASGDPKK	1.277208646	3	3.51232
Q62785	GVEGLIDIENPNR	1.734579593	2	2.92045
Q62785	QKANEEDEQEEGGDGASGDPK	1.295360199	3	4.35504
Q62785	QKANEEDEQEEGGDGASGDPKK	0.914019063	3	3.430189
Q62785	YMKMHLAGKTEQAK	0.927439442	2	2.307572
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.227226176**	**0.020665**	**2**
Q62789	IILDELVQR	1.246787067	2	3.543433
Q62789	WIPQNDLLGHPK	1.116147905	2	3.294807
Q62812	**MYH9 Myosin_9**	**1.154964667**	**9.9E-20**	**68**
Q62812	ALEEAMEQK	1.129013872	2	3.295444
Q62812	ALELDSNLYR	1.462218882	2	3.284624
Q62812	ALEQQVEEMK	2.055745	2	3.302304
Q62812	ALEQQVEEMKTQLEELEDELQATEDAK	1.627885459	3	3.392353
Q62812	ANLQIDQINTDLNLER	1.692036662	2	5.434532
Q62812	ASIAALEAK	1.322835731	2	2.686718
Q62812	ASREEILAQAK	2.076625634	2	2.985129
Q62812	CQYLQAEK	1.312629209	1	2.330164
Q62812	DFSALESQLQDTQELLQEENR	1.149742922	3	6.726772
Q62812	DLEAHIDTANK	1.426696742	2	3.467631
Q62812	DLGEELEALKTELEDTLDSTAAQQELR	1.078421542	3	4.493731
Q62812	DLQGRDEQSEEK	1.178692908	2	2.925707
Q62812	EEILAQAK	1.222775461	1	2.374926
Q62812	EEILAQAKENEK	1.237778824	2	2.343708
Q62812	ELEDATETADAMNR	1.342955162	2	4.423321
Q62812	ELETQISELQEDLESER	2.531398447	2	4.864941
Q62812	EMEAELEDERK	0.921372681	2	3.325268
Q62812	HEAMITDLEER	0.819114238	2	3.271591
Q62812	HEDELLAK	1.140343971	2	3.046887
Q62812	HSQAVEELAEQLEQTK	1.155464016	2	5.020916
Q62812	HSQAVEELAEQLEQTKR	1.108183965	3	5.658849
Q62812	IIGLDQVAGMSETALPGAFK	2.39698403	2	5.394994
Q62812	IMGIPEDEQMGLLR	1.361938014	2	2.617218
Q62812	IRELETQISELQEDLESER	1.497749701	2	5.435102
Q62812	KEEELQAALAR	1.314581728	3	3.362902
Q62812	KKVEAQLQELQVK	1.038390639	2	4.620467
Q62812	KLEEDQIIMEDQNCK	1.139486575	2	6.009548
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.913425895	2	5.578339
Q62812	KQELEEICHDLEAR	1.197272154	2	4.73266
Q62812	KVEAQLQELQVK	1.372829404	2	4.550151
Q62812	LDPHLVLDQLR	1.289353731	3	3.421467
Q62812	LEEDQIIMEDQNCK	0.898127478	2	4.990447
Q62812	LEGDSTDLSDQIAELQAQIAELK	1.483866478	3	5.225784
Q62812	LEVNLQAMK	0.885378788	2	2.636608
Q62812	LQEMESAVK	1.351214315	2	2.753379
Q62812	LQQELDDLLVDLDHQR	1.360599693	2	4.818476
Q62812	LQVELDSVTGLLNQSDSK	1.265457374	2	5.487123
Q62812	LTEMETMQSQLMAEK	1.563889094	2	4.972543
Q62812	MEDGVGCLETAEEAK	1.223626759	2	4.37249
Q62812	MQQNIQELEEQLEEEESAR	1.249495549	2	6.322113
Q62812	NAEQFKDQADK	1.377486896	2	3.458148
Q62812	NKHEAMITDLEER	1.607083446	3	4.102787
Q62812	NLPIYSEEIVDMYK	1.762625525	2	3.796722

Q62812	NMDPLNDNIATLLHQSSDK	1.629341012	2	4.946885
Q62812	NTDQASMPDNTAAQK	2.489611127	2	5.312929
Q62812	NTDQASMPDNTAAQK+Oxidation(6	2.4365469		
Q62812	QAQQERDELADEIANSSGK	1.02083541	3	4.195017
Q62812	QIATLHAQVTDMK	0.698034529	2	2.384528
Q62812	QLEEAEEEAQR	2.016552075	2	3.877197
Q62812	QSVSNLEK	1.23477235	2	2.470817
Q62812	QTLENERGELANEVK	0.622296655	2	3.385685
Q62812	RGDMPFVVTR	0.958491323	2	2.967351
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.225565112	3	5.758426
Q62812	RQLEEAEEEAQR	1.064017156	2	4.600445
Q62812	SMEAEMIQLQEELAAAER	1.422366458	3	4.335388
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1	2.367589465		
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)Oxidation(5	1.14654599		
Q62812	TDLLLEPYNK	1.032040105	2	3.419269
Q62812	TELEDTLDSTAAQQELR	0.801775671	2	5.338693
Q62812	TEMEDLMSSK	1.971452765	2	2.589689
Q62812	THEAQIQEMR	1.273594506	3	3.436859
Q62812	TQLEELEDELQATEDAK	1.022456309	2	6.590839
Q62812	VAEFTTDLMEEEK	1.775307645	2	4.480554
Q62812	VEAQLQELQVK	0.714128403	2	3.483668
Q62812	VEDMAELTCLNEASVLHNLK	1.330945364	2	4.499723
Q62812	VISGVLQLGNIVFK	1.445577332	2	3.757948
Q62812	VSHLLGINVTDFTR	1.673535748	2	3.812301
Q62812	YEILTPNSIPK	1.115655991	2	3.134212
Q62824	**EXOC4 Exocyst complex component 4**	**1.580159538**	**0.148369**	**2**
Q62824	EDLDCDPEENSTLFMGILIQGLAR	1.532693763	2	2.31916
Q62824	SQTGVGDQTTQNTR	1.581491916	2	3.117584
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.315366122**	**0.00615**	**7**
Q62826	ADILEDKDGK	1.565682349	2	2.790576
Q62826	AFITNIPFDVK	1.627099064	2	3.240886
Q62826	GIGMGNLGPAGMGMEGIGFGINK	2.274128784	2	3.918765
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	0.957950605	2	5.029048
Q62826	INEILSNALK	1.873636667	2	2.612685
Q62826	MGPAMGPALGAGIER	1.225096735	2	2.755434
Q62826	MGPVMDRMATGLER+Oxidation(0)Oxidation(4)Oxidation(7	1.189433693		
Q62868	**ROCK2 Rho_associated protein kinase 2**	**1.929157671**	**0.164507**	**2**
Q62868	DEEISAAAIK	4.896042077	1	1.900369
Q62868	QENNHLMEMKMNLEK+Oxidation(6	1.737580698		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**0.918411816**	**0.028043**	**2**
Q62871	ADAEEEAATR	2.589689938	2	3.170895
Q62871	SVSTPSEAGSQDSGDGAVGSR	0.717450357	2	5.218959
Q62902	**LMAN1 Protein ERGIC_53**	**1.26906092**	**5.87E-05**	**7**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.134272328	2	4.150277
Q62902	GHPDLQGQPADDIFESIGDR	1.526150399	2	5.01564
Q62902	LVSGVQHPGSAGVYETTQHFMDIK	1.181364666	3	3.42386
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.032484869	3	6.36976
Q62902	RGAGTPGQPGQVSQQELDTVVR	1.215040333	3	4.454383
Q62902	YQEEFEHFQQELDK	1.163329969	2	5.314008
Q62902	YVSSLTEEISR	1.287865256	2	3.046477
Q62904	**DHB7 3_keto_steroid reductase**	**1.167437757**	**0.632979**	**3**
Q62904	MDVDEDTAEK	6.83734228	2	2.389572
Q62904	YATDLLNVALNR	1.167440833	2	2.573166
Q62904	YLSGTTGLGTNYVK	0.952416225	2	2.988279

Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.943899563**	**0.162746**	**2**
Q62967	GLQVAPVLLSDELK	0.925413806	2	3.741494
Q62967	VYGVEGDLSEVAR	2.301867891	2	3.420812
Q62991	**SCFD1 Sec1 family domain_containing protein 1**	**1.416394696**	**0.01896**	**3**
Q62991	ALTDAGCNLSPLQYIK	3.764775255	2	2.904189
Q62991	FGQDIISPLLSVK	1.42823257	2	2.361158
Q62991	SLLDVISDPDAGTPEDK	1.317091402	2	2.862056
Q63041	**A1M Alpha_1_macroglobulin**	**0.871721691**	**0.927569**	**12**
Q63041	AEDITHNGIVYTPK	0.886284969	2	3.668512
Q63041	AEQGAYLGPLPYK	0.694012124	2	3.238184
Q63041	AESPVFVQTDKPIYKPGQTVK	0.78831905	3	4.012474
Q63041	DTVVKPVIVEPEGIEK	0.741858785	2	3.754483
Q63041	GSIFNSGSHVLPLEQGK	0.835030002	2	4.075487
Q63041	KLQDQSNIQR	0.832596224	2	2.571226
Q63041	LIVYTILPNEELIADVQK	1.592163163	2	2.998634
Q63041	LQDQSNIQR	0.644049074	2	2.9837
Q63041	QDLNDNDAYSVFQSIGLK	1.005698311	2	2.6273
Q63041	VNTLPLNFDK	0.783958296	2	2.749008
Q63041	YNILPEAEGEAPFTLK	1.106055283	2	4.908989
Q63041	YVVLVPSELYAGVPEK	1.15080711	2	3.009185
Q63060	**GLPK Glycerol kinase**	**1.30708537**	**2.86E-12**	**12**
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.8937098	3	4.567799
Q63060	AVLGPLVGAVDQGTSSTR	1.325998605	2	5.194014
Q63060	CVFSEHGLLTTVAYK	0.920065507	2	4.281955
Q63060	DCGIPLSHLQVDGGMTSNK	1.33740896	2	4.436728
Q63060	EILQSVYECIEK	1.197998392	2	3.419255
Q63060	FEPQINAEESEIR	1.582856259	2	3.642443
Q63060	KVQEAVEENR	0.661721334	2	3.352234
Q63060	LGQLNIDISNIK	1.825629653	2	3.230658
Q63060	NTYGTGCFLLCNTGHK	0.91428915	2	3.812618
Q63060	SSSEIYGLMK	1.832566003	2	2.515342
Q63060	TAELLSHHQVEIK	1.486787182	2	3.457383
Q63060	VQEAVEENR	1.617527432	2	3.244871
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**1.181020939**	**2.2E-13**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.273153718	3	5.129878
Q63081	GESPVDYDGGR	2.658027757	2	2.857019
Q63081	GSFSEQGINEFLR	1.349908707	2	4.196577
Q63081	GSTAPVGGGSFPNITPR	1.057461904	2	4.878219
Q63081	HQSLGGQYGVQGFPTIK	1.370709667	2	5.078053
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.918980535	3	5.234771
Q63081	NLEPEWAAAATEVK	1.102205961	2	4.024937
Q63081	NSYLEVLLK	1.471002432	2	2.973777
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.179299049	3	5.022287
Q63081	TGEAIVDAALSALR	1.184520625	3	4.875083
Q63081	VGAVNADKHQSLGGQYGVQGFPTIK	0.824817734	3	4.606942
Q63083	**NUCB1 Nucleobindin_1**	**1.450038708**	**0.023004**	**3**
Q63083	LSQETEALGR	2.168874663	2	2.818551
Q63083	VNVPGSQAQLK	1.244865017	2	2.440251
Q63083	YLQEVINVLETDGHFR	1.500559577	3	4.114141
Q63108	**EST3 Liver carboxylesterase 3**	**1.22808676**	**0.446722**	**4**
Q63108	GGTSKEEINLSK	0.900229441	2	3.427361
Q63108	LDPMTATSLLK	1.047457377	2	2.507528
Q63108	QKTEEELLETTLK	1.391814238	2	3.500254
Q63108	SSFLLNLPEEAIPVAVEK	1.228552856	2	4.83555
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.531888957**	**0.000135**	**7**
Q63120	ACALLPDLEILPGGDMAEIGEK	3.167243907	2	4.827564

Q63120	HGEIQFNNYQVR	2.019025575	2	2.729025
Q63120	IVEYGSPEELLSNR	2.076173091	2	3.317959
Q63120	QSQSQDVLVLEEAK	1.721356845	2	2.563772
Q63120	YFAWEPSFQEQVQGIR	1.930108456	2	3.934591
Q63120	YLGGDDLDTSAIR	0.370174253	2	2.361479
Q63120	YRPELDLVLK	0.956421649	3	3.663076
Q63150	**DPYS Dihydropyrimidinase**	**1.162318984**	**0.067961**	**10**
Q63150	ALGKDDFTK	1.288682441	2	2.55283
Q63150	DQTCTPIPVKR	2.042097126	2	2.492831
Q63150	EIGAIAQVHAENGDLIAEGAK	1.654234935	2	4.998999
Q63150	FVAVTSTNAAK	1.174203645	2	3.176676
Q63150	GSSLIEAFETWR	1.845944622	2	3.541104
Q63150	IAVGSDADIVIWDPEATR	1.846778108	2	3.262145
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	1.121428811	3	3.749743
Q63150	VVNDDFSQVADVLVEDGVVR	1.15818225	2	5.955635
Q63150	VVYEAGVFDVTAGHGK	1.276550728	2	4.201988
Q63150	VVYGEPIAAGLGTDGTQYWNK	3.234830345	2	5.823098
Q63228	**GMFB Glia maturation factor beta**	**1.944176656**	**0.190211**	**2**
Q63228	LVVLDEELEGVSPDELKDELPER	2.100022402	3	3.70804
Q63228	NTEDLTEEWLR	1.594112792	2	2.599456
Q63269	**ITPR3 Inositol 1_4_5_trisphosphate receptor type 3**	**1.005477315**	**0.4944**	**2**
Q63269	LLDGGNTEIQK	0.972453043	1	2.459567
Q63269	QKLMRDENILK+Oxidation(3	1.248703226		
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.34551554**	**9.9E-20**	**19**
Q63270	AVEAGLNVKPYVK	0.995731084	2	2.968586
Q63270	AVLAESYER	2.240173445	2	2.641603
Q63270	DFSDSSQDPDFTQVVELDLK	1.357890441	2	3.665324
Q63270	FVEFFGPGVAQLSIADR	2.045704089	2	5.296787
Q63270	GFQVAPDHHNDHK	0.217248607	2	3.415375
Q63270	IDFEKEPLGVNAQGQQVFLK	1.258714328	3	6.128051
Q63270	IIPPGSGIIHQVNLEYLAR	1.442140137	2	2.520668
Q63270	KNDIENILNWSIMQHK	1.612945094	3	4.5379
Q63270	NCDEFLVK	1.566636102	2	2.32397
Q63270	NDIENILNWSIMQHK	1.525871072	2	2.513948
Q63270	NQDLEFER	1.068953393	1	2.698658
Q63270	QAPQTVHLPSGETLDVFDAAER	0.944055012	3	3.624273
Q63270	SIEVPFKPAR	0.994103364	2	2.540916
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.954696457	3	4.671852
Q63270	SPPFFESLTLDLQPPK	1.295554669	3	4.475412
Q63270	SWNALAAPSEK	1.281903168	2	2.606666
Q63270	TSLSPGSGVVTYYLR	1.555876786	2	3.548267
Q63270	VILQDFTGVPAVVDFAAMR	1.474329638	2	4.778577
Q63270	YQQAGLPLIVLAGK	1.151290035	2	3.553062
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.124338795**	**8.23E-13**	**18**
Q63276	AHGHFLFVVGEDDKNLNSK	1.133647437	2	6.078642
Q63276	ASEVGEVDLER	1.975925339	2	4.032866
Q63276	DDKGNLFNSQAFYR	1.137345194	2	3.3099
Q63276	GNLFNSQAFYR	0.852122817	2	2.678582
Q63276	LCHPYFPVEGK	1.700891624	3	3.518904
Q63276	LTAVPLSALVDEPVHIR	1.426448069	2	3.948138
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	1.191159401	4	4.636931
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.720654302	3	4.237051
Q63276	QHLNPGFNSQL	1.113615889	2	3.50833
Q63276	QITATVLINGPNFVSSNPHVYR	1.294584217	3	4.779086
Q63276	TFEETADK	1.200630259	1	1.921011
Q63276	TFEETADKDSK	0.942226546	2	3.79436

Q63276	VDLEYFEEGVEFLLR	1.523692077	2	4.334498
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.920895524	3	5.157936
Q63276	VISSSLDSLILER	1.290933178	2	4.493979
Q63276	VTGLTPFQVVCLQASLK	0.880627765	3	5.2183
Q63276	WYVAPGVTR	0.954002998	1	2.123471
Q63276	YCFPIEK	1.237885063	2	2.579024
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**0.964750056**	**0.142197**	**26**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.354907976	3	6.022555
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.25784953	2	4.730072
Q63342	DGLLFGPYESQEK	1.438873567	2	2.71546
Q63342	EGQESPPSPPEWK	1.66252235	2	2.68183
Q63342	GGYDVEIR	1.187145919	2	2.635637
Q63342	GQDSTQLLDHLCANVIPK	1.136378234	2	4.100558
Q63342	IHELFPLLNMDK	0.944390372	2	2.75267
Q63342	IHYDSIK	0.97212034	1	2.36116
Q63342	IMNAGQEEGIDNFGTYALNALR	0.977341192	2	4.482948
Q63342	ISDIPVTAIR	1.125812101	2	3.336002
Q63342	ITEHVEAAMEMVPVLK	1.548213407	2	4.64274
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.319516839	3	5.933321
Q63342	LEEETGQVVGFHQPGSIR	1.013055811	2	4.837958
Q63342	LNKPADFTGK	1.807042646	2	3.019946
Q63342	LTSEDLSDDVFK	1.038733088	2	4.03729
Q63342	NITDELGVLGVAGPYAR	1.682521858	2	4.770461
Q63342	NYPATIIQEPLVLTEPTR	1.147530842	2	4.47272
Q63342	REDSAALYER	0.576733887	2	2.65566
Q63342	TNWHATEQYIIEPEK	0.784747881	2	3.712564
Q63342	VGFTNISHMLTPR	0.912974016	2	3.113694
Q63342	VGVIDLSPFGK	1.121169685	2	3.529462
Q63342	VIGNTTSGSYSYSIQK	1.179872261	2	4.335649
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	2.01922086	3	4.308772
Q63342	WIEEAAVR	1.375636555	2	2.817202
Q63342	WTTTQYTEAK	1.035007384	2	2.727261
Q63342	YLSDWILHGEPPFDLIELDPNR	1.239205245	2	4.498356
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.4477682**	**0.003745**	**7**
Q63347	ALDEGDIALLK	1.077511159	2	2.819002
Q63347	FDDGAGGDNEVQR	1.229033193	2	4.283764
Q63347	FVVDLSDQVAPTDIEEGMR	1.147817347	2	3.72301
Q63347	IINADSEDPK	1.305501367	2	3.205634
Q63347	QTLQSEQPLQVAR	1.490249388	2	3.671575
Q63347	QVEDDIQQLLK	1.38698462	2	2.988644
Q63347	TMLELINQLDGFDPR	1.478970023	2	3.016543
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.160410218**	**0.374127**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.221841525	2	5.702415
Q63362	KYTEQITSEK	1.205620999	2	2.72064
Q63362	TTGLVGLAVCDTPHER	0.914703166	2	4.25738
Q63362	YTEQITSEK	1.204473101	1	2.323508
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**1.914265479**	**0.054664**	**2**
Q63413	CIALAQLLVEQNFPAIAIHR	1.915732347	3	3.392187
Q63413	NCPHIVVGTPGR	1.47938345	2	2.981466
Q63429	**UBC Polyubiquitin_C**	**1.216336404**	**0.082153**	**3**
Q63429	ESTLHLVLR	1.010109042	2	2.504061
Q63429	TITLEVEPSDTIENVK	1.216358747	2	4.853921
Q63429	TLSDYNIQK	1.301412245	2	2.685681
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**0.932873661**	**2.58E-12**	**10**
Q63448	ADWLDSEAPLAAYR	0.967039978	2	4.324253

Q63448	EIHALASAGKPLASWTAQR	1.119956295	2	4.574153
Q63448	GGYISGEQTGK	0.816007385	2	3.011995
Q63448	LGASLGSLSSGR	0.751606139	2	2.710799
Q63448	NLWAAVLQQSGVLER	1.215360376	2	4.517843
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.920755484	3	4.515859
Q63448	TIFLDLIELQR	1.745992255	2	2.51954
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.254290748	3	4.506968
Q63448	TTAHYDPATQEFILHSPDFEAAK	0.931071933	3	4.468224
Q63448	TVNFLEAYPGILGQK	1.248847852	2	5.116671
Q63507	**RL14 60S ribosomal protein L14**	**1.502985457**	**1.69E-06**	**3**
Q63507	CMQLTDFILK	1.00715588	2	2.756161
Q63507	LVAIVDVIDQNR	1.776351193	2	4.12323
Q63507	RFVEVGR	1.194671632	2	2.35885
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.317281551**	**0.001687**	**4**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.241325295	3	4.564274
Q63524	HEQEYMEVR	1.629419825	2	3.437142
Q63524	HEQEYMEVR+Oxidation(5	1.372459103		
Q63524	LEEMINELAVAMTAVK	1.215448243	2	3.542566
Q63525	**NUDC Nuclear migration protein nudC**	**1.317905922**	**0.014991**	**4**
Q63525	GQAPVIDGELYNEVK	1.13416497	2	3.611216
Q63525	LVTSDPEINTK	1.441400313	2	2.437115
Q63525	VEESSWLIEDGK	1.249769001	2	2.417131
Q63525	WTQTLSELDLAVPFR	1.387748591	2	2.831102
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.277422115**	**0.001865**	**6**
Q63569	AMEVDERPTEQYSDIGGLDK	1.153311069	3	5.327534
Q63569	CTDDFNGAQCK	2.058883014	2	3.261086
Q63569	MNVSPDVNYEELAR	1.280198086	2	3.575395
Q63569	QTYFLPVIGLVDAEK	1.186642112	2	2.46088
Q63569	TMLELLNQLDGFQPNTQVK	0.7730739	2	3.929385
Q63569	VDILDPALLR	1.371222081	2	2.910823
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.118767083**	**0.403472**	**4**
Q63570	FDAQTGADR	1.420442194	2	2.738136
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.242049968	3	5.808391
Q63570	KDEQEHEFYK	1.387577853	2	3.420682
Q63570	RFDAQTGADR	0.875558453	2	3.018686
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.391601343**	**1.67E-14**	**4**
Q63584	ITDSAGHILYAK	1.446754912	2	3.733475
Q63584	LEDLSESIVNDFAYMK	1.942877344	2	3.581854
Q63584	NYEEIAK	1.423706558	1	2.409726
Q63584	RLEDLSESIVNDFAYMK	1.384415609	2	3.669169
Q63598	**PLST Plastin_3**	**1.183161561**	**0.102968**	**13**
Q63598	AESMLQQADK	1.468166406	2	3.424381
Q63598	ATDDIIVNWVNGTLSEAGK	0.95477258	2	5.112678
Q63598	AVGDGIVLCK	3.12923071	2	2.445187
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	0.98321249	3	3.473838
Q63598	HVIPMNPNTDDLFK	1.165954808	2	3.038685
Q63598	IDINMSGFNETDDLKR	1.195244099	2	4.460014
Q63598	INNFSADIK	1.477151766	2	2.393737
Q63598	KLENCNYAVELGK	1.258443113	2	3.730831
Q63598	NEALAALLR	1.074990404	2	2.611552
Q63598	TISSSLAVVDLIDAIQPGCINYDLVK	1.263024523	3	3.565217
Q63598	VYALPEDLVEVKPK	1.335079037	2	3.090429
Q63598	YPALTKPENQDIDWTLLEGETR	1.255465716	3	5.370895
Q63598	YTLNVMEDLGEGQK	1.085268208	2	3.683099
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.198381769**	**0.997082**	**8**

Q63610	IQVLQQQADDAEER	1.297626689	2	5.125083
Q63610	KIQVLQQQADDAEER	1.273066144	2	5.435381
Q63610	KLVIIEGDLER	1.292661925	2	3.228494
Q63610	LEKTIDDLEDKLK	3.055996836	2	2.718252
Q63610	LVIIEGDLER	1.17089355	2	2.947642
Q63610	MELQEIQLK	1.175448826	2	3.123402
Q63610	TIDDLEDKLK	1.2823218	2	2.696399
Q63610	YSQKEDKYEEEIK	1.182447896	2	4.949893
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.208400172**	**0.001898**	**15**
Q63617	AANSLEAFIFETQDK	1.638951787	2	2.560568
Q63617	DAVITVPAFFNQAER	1.01948578	2	2.80569
Q63617	EGETPDEKESGDKSEAQKPNEK	1.004999854	3	3.991046
Q63617	FLGDSAAGMAIK	1.027264936	2	2.522767
Q63617	GQAGPEGVPPAPEEEKK	1.28771306	2	3.41887
Q63617	LIPEMDQIFTDVEMTTLEK	1.534994164	2	3.352895
Q63617	LYQPEYQEVSTEEQR	1.159927332	2	5.265845
Q63617	NINADEAAAMGAVYQAAALSK	1.379137668	2	5.327019
Q63617	SLAEDFAEQPIK	1.196298757	2	2.982169
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.850523432	3	3.439419
Q63617	TLGGLEMELR	1.337502804	2	2.974303
Q63617	TVLSANADHMAQIEGLMDDVDFK	1.551156836	3	3.889606
Q63617	VEFEELCADLFDR	2.157563798	2	3.421132
Q63617	VESVFETLVEDSPEEESTLTK	1.527394027	2	4.015532
Q63617	VLQLINDNTATALSYGVFR	1.176941448	2	4.689823
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**1.583194236**	**0.024865**	**2**
Q63692	EGEEAGPGDPLLEAVPK	1.583221155	2	3.325545
Q63692	LGPGGLDPVEVYESLPEELQK	1.411171802	2	3.007656
Q63716	**PRDX1 Peroxiredoxin_1**	**1.207947959**	**0.060274**	**15**
Q63716	ADEGISFR	1.107925795	2	3.079179
Q63716	ATAVMPDGQFK	1.199077157	2	2.873782
Q63716	GLFIIDDKGILR	1.31348609	2	2.862012
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.247772418	4	5.822434
Q63716	IGHPAPSFK	3.105697639	1	1.91633
Q63716	KQGGLGPMNIPLVSDPK	1.149346948	2	4.070116
Q63716	KQGGLGPMNIPLVSDPKR	0.874466472	3	3.810011
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.631146107	3	3.391421
Q63716	LVQAFQFTDK	1.680162029	2	3.297121
Q63716	QGGLGPMNIPLVSDPK	1.08473873	2	3.139241
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6	1.319425625		
Q63716	QITINDLPVGR	1.135630509	2	3.154166
Q63716	RTIAQDYGVLK	1.354966651	2	2.481167
Q63716	SVDEILR	1.2589895	2	2.482807
Q63716	TIAQDYGVLK	1.154550874	2	3.210533
Q63797	**PSME1 Proteasome activator complex subunit 1**	**1.179727158**	**3.63E-07**	**10**
Q63797	ISELDAFLK	1.169137038	2	2.369173
Q63797	ISELDAFLKEPALNEANLSNLK	1.567313415	2	5.35168
Q63797	KGDEDDKGPPCGPVNCNEK	1.450819499	3	4.816278
Q63797	KISELDAFLKEPALNEANLSNLK	1.08393015	3	5.881336
Q63797	LEGFQTQISK	1.333334291	2	2.71279
Q63797	NAYAVLYDIILK	2.04949205	2	3.557421
Q63797	QLVHELDEAEYQEIR	1.184417614	2	4.185077
Q63797	TENLLGSYFPK	1.118646182	2	3.494833
Q63797	VDVFREDLCSK	1.241781655	2	2.521598
Q63797	VFELMTSLHTK	1.045800682	2	3.047935
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.141367391**	**0.185087**	**4**
Q63798	AFYAELHHIISSNLEK	1.047022884	2	3.915185
Q63798	IEDGNDFGVAIQEK	1.702430365	2	4.049587

Q63798	KIISLSQLLQEDSLNVADLSSLR	1.518618868	3	3.63328
Q63798	TKVEAFQTAISK	1.038793127	2	3.561247
Q63836	**SBP2 Selenium_binding protein 2**	**1.56740554**	**4.77E-05**	**3**
Q63836	GGSVQVLEDQELTCQPEPLVVK	2.477971339	2	5.340981
Q63836	IYVVDVGSEPR	1.279876385	2	3.828118
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.333259684	3	3.843831
Q63945	**SET Protein SET**	**1.464765206**	**0.008916**	**2**
Q63945	IDFYFDENPYFENK	2.013264244	2	4.279914
Q63945	LNEQASEEILK	1.349910928	2	3.167086
Q63965	**SFXN1 Sideroflexin_1**	**1.243508781**	**0.09474**	**5**
Q63965	NILLTNEQLENAR	1.169781008	2	4.389843
Q63965	QAITQVVISR	1.388356823	2	2.336221
Q63965	QGIVPAGLTENELWR	1.539454116	2	3.176319
Q63965	WDQSTFIGR	1.005016449	2	2.791946
Q63965	YAYDSAFHPDTGEK	1.360527479	2	4.284468
Q64012	**RALY RNA_binding protein Raly**	**1.265907245**	**0.364747**	**2**
Q64012	LEQIAEEQK	1.384705454	2	2.521497
Q64012	SNIDALLGR	1.253587995	2	2.356158
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**1.198189618**	**9.9E-20**	**19**
Q64057	AWNIWADIPAPK	1.470463929	2	3.805845
Q64057	DYEETIGK	2.166126113	1	1.928674
Q64057	EDNEGVFNGSWGGR	1.325183912	2	3.688457
Q64057	FKNEEEVFEWNNEVK	1.178584182	2	5.75616
Q64057	GAPTTSLVSIAVTK	1.122465233	2	5.005093
Q64057	GEVITTYCPANNEPIAR	1.113157346	2	5.007843
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.879741523	2	5.600403
Q64057	LFLHESIHDEVVDR	1.760839572	2	4.37684
Q64057	LVSLEMGK	1.920957694	2	2.44717
Q64057	NEEEVFEWNNEVK	1.290003756	2	4.569401
Q64057	QAVSMFVQAVEEAK	1.602287116	2	3.391872
Q64057	QAVSMFVQAVEEAKK	1.309856327	2	2.838072
Q64057	QGLSSSIFTK	1.886140184	2	2.753333
Q64057	QVALMVQER	1.308486111	2	2.516644
Q64057	STCTINYSTALPLAQGIK	0.882040281	2	4.87192
Q64057	VGNPWDPNILYGPLHTK	1.595549102	3	4.399542
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.631703041	3	6.072845
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1	1.854211072		
Q64057	VNLLSFTGSTQVGK	1.707604041	2	4.68843
Q64112	**IFIT2 Interferon_induced protein with tetratricopeptide repeats 2**	**0.984946611**	**0.207759**	**2**
Q64112	DPSAIDTLLR	0.941894053	2	2.558428
Q64112	NQAMALVEEALK	2.038285311	2	2.310532
Q64119	**MYL6 Myosin light polypeptide 6**	**1.197364011**	**9.9E-20**	**7**
Q64119	DQGTYEDYVEGLR	0.875638487	2	3.378403
Q64119	EGNGTVMGAEIR	1.322425976	2	2.730787
Q64119	HVLVTLGEK	1.264977066	2	2.570175
Q64119	ILYSQCGDVMR	1.367168283	2	2.918643
Q64119	NKDQGTYEDYVEGLR	1.194428253	2	4.147234
Q64119	VFDKEGNGTVMGAEIR	1.356200473	2	4.115485
Q64119	VLDFEHFLPMLQTVAK	1.351103213	2	4.781628
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**1.35511588**	**0.019639**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.365566108	2	5.230736
Q64122	LNGTDPEDVIR	1.163324272	2	2.608849
Q64176	**EST22 Liver carboxylesterase 22**	**1.150778203**	**0.968186**	**3**
Q64176	AISESGVALTAGLVK	1.15969218	2	4.588659
Q64176	EGYLQIGATTQQAQK	0.927439442	2	4.669311

Q64176	NFNTVPYIVGINK	0.91693973	2	3.469729
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.710855063**	**9.9E-20**	**7**
Q641Y0	ELGSECGIEFDEEK	1.191478248	2	4.040938
Q641Y0	NTLLIAGLQAR	2.079726688	2	3.426159
Q641Y0	SSLNPILFR	3.115589093	2	2.467113
Q641Y0	TADDPSLSLIK	1.188667494	2	2.577113
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.721857409	3	6.69727
Q641Y0	TLVLLDNLNVR	1.501201569	2	4.124851
Q641Y0	WVPFDGDDIQLEFVR	1.742555774	2	3.078633
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.146037546**	**0.86606**	**4**
Q641Y2	GSGIQWDLR	1.201322365	2	2.524621
Q641Y2	IDEVEEMLTNNR	1.288478531	2	3.860513
Q641Y2	IIEQCLNK	1.118247451	2	2.748193
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.255911418	2	4.369472
Q641Z6	**EHD1 EH domain_containing protein 1**	**1.515488318**	**0.13936**	**2**
Q641Z6	LLDTVDDMLANDIAR	1.514976079	2	3.935029
Q641Z6	MQELLQTQDFSK	1.526877193	2	2.624095
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.411921235**	**0.006413**	**3**
Q64232	HYEVEIR	1.359539926	2	2.497379
Q64232	LCFLDKVEPQATISEIK	1.947122283	2	3.605485
Q64232	SLKDEDVLQK	1.305119819	2	3.562632
Q64240	**AMBP Protein AMBP**	**0.678512887**	**0.000217**	**2**
Q64240	AVLPQENEGSGSEPLITGTLK	1.042097169	2	4.174345
Q64240	TIAACNLPIVQGPCR	0.675824725	2	3.838509
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**1.332959**	**0.536323**	**2**
Q642G4	GGDGQINEQVEK	1.335390618	2	2.885967
Q642G4	LLGPQEEGEGVVDVK	1.328977015	2	2.780948
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.343337201**	**0.345145**	**20**
Q64380	AIDSLSIEK	1.032182753	2	3.007977
Q64380	AYGIESHVLSPAETK	1.299791597	2	4.948268
Q64380	DGTMDPAGTCTTLTR	0.822414259	2	3.882903
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	2.607319692	3	5.3948
Q64380	DLYPLMNVDDLYGTLYVPR	1.127268685	2	3.872077
Q64380	FHHSLTDHPR	0.62721607	2	2.649528
Q64380	FYLLGADAR	1.029512989	2	2.643284
Q64380	GAQVIENCAVTGIR	0.92746349	2	3.785055
Q64380	HGLVNAGYR	0.795084942	2	2.681378
Q64380	IEGIQNMPNVR	0.906857109	2	3.193539
Q64380	LGVGGVVLLER	2.636977911	2	3.277625
Q64380	LQGDALSVGGYEANPIFWDEVSDK	3.111842769	2	4.202571
Q64380	NGDYALER	0.840821656	2	2.435715
Q64380	NYSVVFPHDEPLAGR	0.77321806	2	4.208261
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	1.04507059	3	4.07024
Q64380	RDPLHEELLGQGCVFQER	3.697104896	3	5.805913
Q64380	SDDSPLEAGLAFTCK	1.981744661	2	4.519202
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.897631321	3	4.863589
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16	1.370759094		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	1.048418556	3	5.767711
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.18104816**	**4.55E-13**	**29**
Q64428	ADMVIEAVFEDLAVK	1.437831146	3	4.110341
Q64428	ALMGLYNGQVLCK	1.558675988	2	3.459968
Q64428	CLAPMMSEVIR	2.923552914	2	2.497653
Q64428	DGPGFYTTR	5.86947697	2	2.31759

Q64428	DSIFSNLIGQLDYK	1.314277542	2	3.05077
Q64428	DTTASAVAVGLK	1.563630456	2	3.799399
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.958894524	3	6.314146
Q64428	EVQSEFVEVMNEIWANDQIR	1.634523781	3	4.206859
Q64428	FGELALTK	1.194063396	2	3.02917
Q64428	FGGGSVELLK	1.160327476	2	3.188765
Q64428	FVDLYGAQK	1.205430977	2	3.02356
Q64428	GFYIYQSGSK	0.997936927	2	3.05216
Q64428	ILQEGVDPK	1.616764482	2	3.18369
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.224100758	4	5.436531
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.510723189	3	4.150676
Q64428	KYESAYGTQFTPCQLLR	1.691675574	2	4.704691
Q64428	LPAKPEVSSDEDIQYR	1.128670842	3	4.469494
Q64428	MGLVDQLVDPLGPGIK	1.273170945	2	5.084553
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0	0.970700559		
Q64428	MQLLEIITTDK	1.24348143	2	3.820327
Q64428	MQLLEIITTDK+Oxidation(0	1.680899095		
Q64428	MVGVPAAFDMMLTGR	1.77525903	2	3.337604
Q64428	NLNSEIDNILVNLR	1.157277725	2	4.415108
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	1.360717637	3	3.886035
Q64428	TGLEQGNDAGYLAESEK	1.194763844	2	5.102751
Q64428	TIEYLEEVAVNFAK	1.365123312	2	3.804162
Q64428	TVLGVPEVLLGILPGAGGTQR	1.208682416	3	4.751201
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	1.324693089	3	6.030047
Q64428	YESAYGTQFTPCQLLR	1.382325084	2	4.007347
Q64458	**CP2CT Cytochrome P450 2C29**	**1.069589859**	**0.000126**	**6**
Q64458	EHKESLDVTNPR	1.21823895	2	3.409563
Q64458	IKEHKESLDVTNPR	1.003556432	3	5.204857
Q64458	LPPGPTPLPIIGNFLQIDVK	2.16952633	3	4.986677
Q64458	VQEEAQCLVEELR	1.683004827	2	4.202095
Q64458	VQEEAQCLVEELRK	1.178211243	2	3.801943
Q64458	VQEEIDR	1.134370959	2	2.530909
Q64464	**CP3AD Cytochrome P450 3A13**	**1.159077333**	**0.960042**	**2**
Q64464	ALLSPTFTSGR	1.159364398	2	2.893162
Q64464	LQDEIDAALPNK	1.102158536	2	2.414547
Q64481	**CP3AG Cytochrome P450 3A16**	**0.993127719**	**0.086862**	**3**
Q64481	EMFPVIEQYGDILVK	1.931751086	2	2.403791
Q64481	GSIDPYVYLPFGNGPR	1.161579858	2	4.043172
Q64481	VLQNFSFQPCK	0.981474691	2	2.78413
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**0.894942709**	**1.05E-10**	**4**
Q64550	GHEVVVIAPEASIHIK	1.318378827	2	4.61325
Q64550	NMIIALTENFLCR	1.184983411	2	4.504038
Q64550	SVFDQDPFLLR	3.393885971	2	3.46737
Q64550	VVYSPYGSLATEILQK	1.270265067	2	4.966804
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**0.974449826**	**0.696016**	**3**
Q64560	ACVDSNENGDLGK	0.972588573	2	3.487929
Q64560	GTLIEAFPVLGGK	1.115552946	2	3.172281
Q64560	HEQISDLDR	1.494856769	2	2.596377
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.080486573**	**0.646806**	**15**
Q64563	AAVDCTVVGWGSCTVVGAK	2.77334578	2	2.594997
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.585458291	3	5.721965
Q64563	ALGATDCLNPR	2.007193719	2	3.232743
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	1.964934578	3	6.054819
Q64563	FDLDLLVTHALPFDK	1.49373213	3	4.300697
Q64563	IIAIDINSEKFPK	0.920217369	2	3.069661
Q64563	INDAIDLMNQGK	1.647620023	2	4.166101
Q64563	KFDLDLLVTHALPFDK	1.028423487	3	5.280221

Q64563	LCLSPLTNLCGK	0.95186328	2	2.466152
Q64563	SVDSVPNLVTDYK	2.254471136	2	3.492907
Q64563	TDSPLCIEEIEVSPPK	1.367932365	2	4.113116
Q64563	VCLIGCGFTSGYGAAINTAK	0.346294984	2	4.880959
Q64563	VDDEANLER	1.48975909	2	3.091066
Q64563	VDEMNISTVDMILGR	1.575651238	2	4.069987
Q64563	VIATCVCPTDINATNPK	1.417642595	2	4.701272
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**1.009707273**	**0.12248**	**15**
Q64565	AYSNHTDIISFR	1.371443764	2	3.484087
Q64565	GGNFSQTFR	1.011148889	2	2.597938
Q64565	GGVCIADEVQTGFGR	0.76464025	2	4.041951
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.405128412	2	4.326011
Q64565	GLMVGIEMVQDK	1.846572369	2	3.37818
Q64565	HNMPPCDFSPEK	0.892620391	2	3.234702
Q64565	LSALLPEPLK	1.712911095	2	2.752019
Q64565	NSQEVGTYMLLK	0.788550096	2	3.318816
Q64565	SALTQHMER	1.66351155	2	2.529057
Q64565	SALTQHMER+Oxidation(6	1.521226493		
Q64565	TEVNQIHEDCK	1.064476164	2	3.296992
Q64565	TEVNQIHEDCKDMGLLVGR	1.123005344	2	5.248972
Q64565	VIFLVNSGSEANDLAMVMAR	2.131051548	2	3.166913
Q64565	YIEQFK	1.054067125	1	2.257898
Q64565	YQSLAYNHVLEIHK	1.727170777	2	3.953983
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**2.233482629**	**0.980983**	**9**
Q64578	AVGIVATTGVSTEIGK	3.981403865	2	3.425933
Q64578	DIVPGDIVEVAVGDKVPADIR	3.829999621	2	3.384947
Q64578	IGIFSENEEVADR	1.688160667	2	3.403374
Q64578	IRDQMAATEQDKTPLQQK	2.14434084	3	4.392905
Q64578	MNVFNTEVR	1.621011372	2	2.787178
Q64578	REEMVLDDSAK	2.245782223	2	2.768773
Q64578	TGTLTTNQMSVCK	2.61004409	2	3.445841
Q64578	VGEATETALTTLVEK	3.531420682	2	4.49547
Q64578	YGPNELPAEEGK	2.079388634	2	3.010919
Q64581	**CP3AI Cytochrome P450 3A18**	**0.825544941**	**0.732816**	**3**
Q64581	AITMSEDEEWKR	1.141309668	2	2.317189
Q64581	LAVIGVLQNFNIQPCEK	1.528443403	2	3.205315
Q64581	NPEYWLEPEEFNPER	1.100070574	2	3.861085
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**1.045965786**	**0.583106**	**10**
Q64591	ATAEEITSK	1.371153141	2	3.017014
Q64591	CDVRDPDMVHNTVLELIK	0.973525307	4	5.052145
Q64591	DPDMVHNTVLELIK	1.201628704	3	4.141829
Q64591	EEWDVIEGLIR	0.74573415	2	3.543766
Q64591	FFPPILKPMLPPNAFQGK	1.005324496	2	3.259077
Q64591	FNIIQPGPIK	0.6291568	2	2.892037
Q64591	NIDVLK	0.915040838	1	2.289355
Q64591	SLAAEWGR	0.947764227	2	2.376821
Q64591	VAFITGGGTGLGK	1.31477292	2	2.690706
Q64591	VTKEEWDVIEGLIR	0.960718703	3	4.901304
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.420324859**	**2.24E-05**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.29835865	2	4.488817
Q64602	DIISLAPGSPNPK	0.726620223	2	3.217999
Q64602	EILLVPGNSFFVDNSAPSSFFR	1.608977491	2	3.481009
Q64602	FLYTIPNGNNPTGNSLTGDR	1.19160931	2	3.988447
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	2.110876027	3	6.467585

Q64602	SAVFTVENGSTIR	1.150406262	2	4.105209
Q64602	VLSQWKPEDSKDPTKR	1.420333715	3	4.140683
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.214150449**	**0.683657**	**14**
Q64611	AQGGQGLEWR	1.254990701	2	2.939613
Q64611	CHGSQASYLFQQDK	0.880711534	2	4.960562
Q64611	DVFGIVVDEAIR	1.724357129	2	3.076346
Q64611	FFNQLFSGLDPHALAGR	1.22226713	3	3.853553
Q64611	FYNVALDTGDK	0.965734195	2	3.106771
Q64611	GAAFLGLGTDSVR	1.317698702	2	3.245358
Q64611	GTMMIGYQPHGTR	1.437155045	2	2.872854
Q64611	IDQAFALTR	1.127760457	2	3.462724
Q64611	KGTMMIGYQPHGTR	1.451212879	3	3.979218
Q64611	LSQVAPVLK	0.824929638	2	2.301967
Q64611	QLLDLELQSQGESR	1.160670997	2	4.516384
Q64611	TLDGDPVAVEALLR	1.160413758	2	4.602102
Q64611	VCEWKEPEELK	1.325812035	3	3.724098
Q64611	YLVEEIK	1.357973537	1	2.407216
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**1.282685042**	**0.039728**	**2**
Q64638	VVFETGNYVK	1.214852444	1	2.058449
Q64638	YESLASELLQR	1.292191869	2	3.033484
Q64640	**ADK Adenosine kinase**	**1.138777381**	**0.027331**	**11**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.344605118	3	7.141896
Q64640	AATFFGCIGIDK	1.134651274	2	3.330186
Q64640	AGHYAASVIIR	1.350300012	3	3.634379
Q64640	FGEILK	1.202468201	2	2.352203
Q64640	FKVEYHAGGSTQNSMK	1.174676901	2	4.106092
Q64640	HKELFDELVK	1.04020625	3	4.053576
Q64640	SLVANLAAANCYK	1.098442419	2	4.331227
Q64640	TGCTFPEKPDFH	1.663961713	2	2.742945
Q64640	VEYHAGGSTQNSMK	1.604017084	2	4.060144
Q64640	VEYHAGGSTQNSMK+Oxidation(12	1.131344939		
Q64640	YSLKPNDQILAEDK	1.238237333	3	4.259914
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**1.213462568**	**0.241415**	**8**
Q64654	EPAEDILQTLLDSTYK	1.023189421	2	3.824011
Q64654	GVAYDVPNAVFLEQK	1.013792163	2	4.325193
Q64654	NEDLNAEEVYGR	0.789933574	2	3.723989
Q64654	SGLNIAHFK	6.793293377	2	2.99592
Q64654	TFTYLLGSDAAALLFNSK	2.025779653	3	3.90519
Q64654	TVCGEDLPPLTYEQLK	1.214930458	2	4.42687
Q64654	YGPVFSFTMVGK	1.20088762	2	2.809703
Q64654	YLQDNPASGEK	1.725590242	2	2.793907
Q65Z40	**WAPL Wings apart_like protein homolog**	**1.325291005**	**0.022382**	**2**
Q65Z40	EKSISRIPEDNANK	1.168665267	2	2.585145
Q65Z40	LGQKRPNFKPDIQEIPK	1.330964735	2	2.394772
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.72882082**	**0.002409**	**5**
Q66H12	CNINCEEDPK	1.866015811	2	2.340341
Q66H12	INQDPLGIQGR	1.32577965	2	2.878064
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(0	1.464708226		
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(3	1.464708226		
Q66H12	TISPQNIDILQNPLLIK	1.820763077	2	3.435765
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**0.697515635**	**0.079765**	**2**
Q66H15	SLQGLAGEIVGEVR	1.147997732	2	3.390301
Q66H15	SQSLPNSLDYAQTSER	0.591600649	2	3.014697
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**1.135150034**	**0.210775**	**2**
Q66H45	ALELQGVR	0.601440225	2	2.473109
Q66H45	LQGDVAGALEDLER	1.139579751	2	3.752761

Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**1.030189142**	**0.005215**	**2**
Q66H71	LTEQAVEAINK	1.024746736	2	3.511743
Q66H71	SIDEDDDYFNLTK	1.859625064	2	2.980465
Q66H80	**COPD Coatomer subunit delta**	**1.671313291**	**5.15E-07**	**8**
Q66H80	GVQLQTHPNVDKK	1.396896331	2	3.516724
Q66H80	LFTAESLIGLK	1.751367864	2	3.021107
Q66H80	NSNILEDLETLR	2.090396657	2	3.512583
Q66H80	NTLEWCLPVIDAK	1.219151712	2	2.727463
Q66H80	SEGETIMSSNMGK	3.815051277	2	2.767968
Q66H80	TFTEMDSHEEK	0.835967668	2	2.655349
Q66H80	VAPAPARPSGPSK	1.426117606	2	2.54033
Q66H80	VTQVDGNSPVR	1.251250132	2	3.018992
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.256440283**	**0.003579**	**10**
Q66HA8	AGGIETIANEFSDR	1.27440334	2	2.94507
Q66HA8	FQEAEERPR	0.77335226	2	2.459458
Q66HA8	FVVQNVSAQK	1.32840348	2	2.68755
Q66HA8	LKETAENNLK	1.173222879	2	2.587992
Q66HA8	NQQITHANNTVSSFK	1.248990719	2	4.717197
Q66HA8	RGPFELEAFYSDPQAVPYPEAK	1.982478787	3	3.787335
Q66HA8	SQFEELCAELLQK	1.242340072	2	2.605168
Q66HA8	SVLDAAQIVGLNCLR	1.705644025	2	3.707395
Q66HA8	VLGTAFDPFLGGK	1.07966671	2	2.982876
Q66HA8	YNHIDESEMK	2.324150081	2	2.506241
Q66HD0	**ENPL Endoplasmin**	**1.063324609**	**9.9E-20**	**27**
Q66HD0	DISTNYYASQK	1.461212463	2	3.162388
Q66HD0	EATEKEFEPLLNWMK	1.725366037	2	3.505596
Q66HD0	EEASDYLELDTIK	1.515294727	2	4.250368
Q66HD0	EEEAIQLDGLNASQIR	1.894032541	2	4.601177
Q66HD0	EFEPLLNWMK	1.538569734	2	2.906619
Q66HD0	EVEEDEYK	1.248985418	1	2.44448
Q66HD0	FQSSHHSTDITSLDQYVER	1.221428046	3	6.632833
Q66HD0	GLFDEYGSK	1.847892724	2	2.449319
Q66HD0	GVVDSDDLPLNVSR	0.811342904	2	5.150775
Q66HD0	KEAESSPFVER	1.254773927	2	3.507187
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	1.079111886	3	3.591553
Q66HD0	LGVIEDHSNR	1.343973792	2	3.116692
Q66HD0	LISLTDENALAGNEELTVK	2.215245213	2	5.428667
Q66HD0	LTESPCALVASQYGWSGNMER	1.829641901	2	5.483465
Q66HD0	MKEKQDK	0.378067556	1	1.925055
Q66HD0	NLLHVTDTGVGMTR	1.168634408	3	4.144524
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11	1.518119137		
Q66HD0	RVFITDDFHDMMPK	1.44033906	3	3.72948
Q66HD0	SGTSEFLNK	1.286601293	2	3.052815
Q66HD0	SGYLLPDTK	1.07529617	2	3.445093
Q66HD0	SILFVPTSAPR	1.730483474	2	3.531105
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	1.875604209	3	5.154072
Q66HD0	TETVEEPLEEDETAQEEK	0.621326018	2	5.279763
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	0.80054658	5	6.240074
Q66HD0	TFEINPR	1.247473171	2	2.73857
Q66HD0	VFITDDFHDMMPK	1.44775266	2	4.010989
Q66HD0	YNDTFWK	1.028507217	2	2.383627
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.232470143**	**0.000193**	**15**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.548400142	3	3.937481
Q66HF1	AVTEGAQAVEEPSIC	1.25599655	2	2.804026
Q66HF1	DDGAAILAAVSSIAQK	1.037848436	2	4.354223

Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	2.694115845	3	4.260973
Q66HF1	FASEIAGVDDLGTTGR	1.625834014	2	4.588344
Q66HF1	GLLTYTSWEDALSR	1.2385919	2	3.670604
Q66HF1	GNDMQVGTYIEK	0.79918383	2	2.814176
Q66HF1	GWNILTNSEK	1.132845631	1	2.263394
Q66HF1	ILQDIASGNHEFSK	1.827701637	2	4.176137
Q66HF1	LGEVSPNLVR	1.334579926	2	3.007973
Q66HF1	LVDQEFLADPLVPPQLTIK	1.206125418	2	3.961185
Q66HF1	SATYVNTEGR	0.872089876	2	2.317441
Q66HF1	VAVTPPGLAR	0.73483841	2	2.538117
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.736200804	2	4.731698
Q66HF1	YDHLGDSPK	1.31692308	2	2.476601
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.180951576**	**9.9E-20**	**13**
Q66HF8	ADVDLAVR	0.729081441	2	2.365483
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	2.119635263	3	4.192543
Q66HF8	EEIFGPVQPLFK	1.46278281	2	3.259798
Q66HF8	IEEVIQR	5.040922612	2	2.30519
Q66HF8	KTFPTVNPTTGEVIGHVAEGDR	1.253409027	3	3.911878
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.371132252	3	4.161424
Q66HF8	LAPALATGNTVVMK	1.467181938	2	3.392511
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.753177906	2	4.885669
Q66HF8	TFVEESIYHEFLER	1.158325957	2	4.462079
Q66HF8	VAEQTPLSALYLASLIK	2.891220016	2	3.002755
Q66HF8	VGNPFELDTQQGPQVDK	1.239879403	2	4.400221
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.524172008	2	4.497054
Q66HF8	YGLAAAVFTR	1.684715018	2	3.295395
Q66HG4	**GALM Aldose 1_epimerase**	**1.280182564**	**0.215359**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	1.359868361	2	4.50189
Q66HG4	TVFGELPSGGGAVEK	0.939171471	2	3.848718
Q66HG4	VSPDGEEGYPGELK	1.417294448	2	4.070729
Q66HG9	**MAVS Mitochondrial antiviral_signaling protein**	**1.108390988**	**0.43706**	**3**
Q66HG9	ICELPGLAEQVTR	1.680169015	2	2.764787
Q66HG9	STAATPSTVPTNIAPSK	1.10672083	2	3.178306
Q66HG9	TTLSSSSTGSAFAK	1.291600479	2	2.344908
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.051864704**	**9.9E-20**	**19**
Q66X93	ADDADEFGYSR	0.886503027	2	2.613153
Q66X93	ALLLPDHYLVTVMLSGIK	1.689977525	3	4.255041
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.184877505	3	6.064765
Q66X93	DTNGENIAESLVAEGLASR	1.604313286	2	4.344325
Q66X93	ETDGSETPEPFAAEAK	1.441428395	2	3.789739
Q66X93	FVDGEWYR	1.949087681	2	2.7819
Q66X93	GDVGLGLVK	1.189755918	2	2.579649
Q66X93	HFVDSHHQKPVNAIIEHVR	1.643389847	3	5.015004
Q66X93	LEGDNIQDK	0.971797338	2	2.992664
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.769302102	2	5.73209
Q66X93	SAYYKPLLSAEEAAK	0.946481018	2	3.113378
Q66X93	SDISSHPPVEGAYAPR	1.143880566	3	4.416551
Q66X93	SSHYDELLAAEAR	1.402040574	2	4.031101
Q66X93	TCATVTIGGINIAEALVSK	1.317914145	2	3.494553
Q66X93	TDAVDSVVR	16.46425334	2	2.713062
Q66X93	VITEYLNAQESAK	1.152772232	2	3.926461
Q66X93	VMQVLNADAIVVK	2.183333911	2	4.10818
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.125880671	3	5.146455
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.963856189	3	4.533551
Q68FL6	**SYMC Methionyl_tRNA synthetase_ cytoplasmic**	**1.089540426**	**0.45511**	**3**
Q68FL6	ADKNQVAAEVAK	1.456518162	2	3.055454

Q68FL6	LENDQIENLR	0.884742526	2	2.691295
Q68FL6	NNSELLNNLGNFINR	1.503595687	2	2.819151
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**1.361230262**	**1.66E-11**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.599547191	3	3.902705
Q68FP2	HNNWDLTPVK	1.376813649	2	3.207797
Q68FP2	IFLMDLNEPYPK	1.778139743	2	4.051851
Q68FP2	IQDPLSDNPR	1.196903652	2	3.014298
Q68FP2	KHNNWDLTPVK	0.790152259	2	2.497894
Q68FP2	LLIYNPEDPPGSEVLR	0.989023663	2	4.389105
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.364320242	3	4.59446
Q68FP2	YVYVADVTAK	1.178170621	1	2.99083
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.525470284**	**3.51E-07**	**7**
Q68FQ0	GSNDMQYQHVIETLIGK	1.263932635	2	2.823049
Q68FQ0	GVIVDKDFSHPQMPK	1.784878406	2	2.807951
Q68FQ0	HKLDVTSVEDYK	1.80033817	2	3.631608
Q68FQ0	ISDNVLVDINNPEPLIQTAK	2.408357785	2	5.01982
Q68FQ0	LDVTSVEDYK	1.11987931	2	2.943625
Q68FQ0	SLHDALCVIR	1.736469509	2	2.693924
Q68FQ0	WVGGPEIELIAIATGGR	1.438267421	2	3.820365
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.209744371**	**7.94E-08**	**8**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.222259632	2	4.98693
Q68FR6	ALIAAQYSGAQIR	1.358065217	2	4.337448
Q68FR6	ILGLLDTHLK	1.87259302	2	2.512637
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.279006699	2	4.217491
Q68FR6	KLDPGSEETQTLVR	1.371035856	2	4.100359
Q68FR6	LDPGSEETQTLVR	2.631785449	2	3.544139
Q68FR6	STFVLDEFKR	1.242341027	2	2.520959
Q68FR6	WFLTCINQPQFR	1.197635588	2	3.353024
Q68FR9	**EF1D Elongation factor 1_delta**	**1.545751882**	**9.9E-20**	**6**
Q68FR9	ATAPQTQHVSPMR	1.520384868	2	3.301425
Q68FR9	ATAPQTQHVSPMR+Oxidation(11	1.160627557		
Q68FR9	FYEQMNGPVTAGSR	1.434634729	2	4.526236
Q68FR9	GVVQDLQQAISK	1.547042449	2	3.438109
Q68FR9	SIQLDGLVWGASK	1.546356049	2	3.25988
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.681661701	2	5.380884
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**1.649514682**	**0.173602**	**3**
Q68FS2	ATTADGSSILDR	2.272749317	2	2.328008
Q68FS2	NAAQVLVGIPLETGQK	1.624508144	2	2.982836
Q68FS2	QIQSLCFQVNNLLEK	1.677630365	2	2.408341
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.575169184**	**9.9E-20**	**17**
Q68FS4	ADMGGAATICSAIVSAAK	1.231752203	2	5.101499
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2	1.295587226		
Q68FS4	DKDDDVPQFTSAGENFNK	0.975458611	2	5.381462
Q68FS4	GITFDSGGISIK	1.222698245	2	3.182206
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.578553272	3	6.169946
Q68FS4	GVLFASGQNLAR	1.182368088	2	3.43383
Q68FS4	LFEASVETGDR	1.330783582	2	3.587468
Q68FS4	LHGSGDLEAWEK	1.758093272	2	2.95171
Q68FS4	LNLPINIIGLAPLCENMPSGK	2.091995277	2	5.044971
Q68FS4	QLMESPANEMTPTR	1.230603552	2	3.653934
Q68FS4	QVIDCQLADVNNLGK	49.54890313	2	4.729132
Q68FS4	SAGACTAAAFLR	1.105731708	2	3.886227
Q68FS4	SAGVDDQENWHEGK	1.01669484	2	3.971177
Q68FS4	SWIEEQEMGSFLSVAK	1.579774716	2	5.149011
Q68FS4	TFYGLHQDFPSVVVVGLGK	1.478102936	2	4.70411
Q68FS4	TIQVDNTDAEGR	0.985393517	2	4.145203
Q68FS4	TLIEFLLR	1.539654156	2	2.789928

Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.322320516**	**0.446601**	**4**
Q68FT1	INDAMNMGHTAK	1.580680225	2	3.10169
Q68FT1	LNHVLEEEQK	1.439472786	2	3.400321
Q68FT1	STGEALVQGLMGAAVTLK	1.305497275	2	3.763371
Q68FT1	YTDQSGEEEEDYESEEQIQHR	1.117117516	3	4.682537
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.800544017**	**0.999475**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	0.922352857	2	3.803288
Q68FT3	ISQLDTQSPVTK	1.680678396	2	3.500858
Q68FT3	SLLLGTDVAENQK	0.897408293	2	3.401096
Q68FT3	TLGAQLPQYYEVLTAPISK	1.003308426	2	4.069752
Q68FT3	VFDCIEAYAPGFK	0.631413815	2	2.823511
Q68FT3	VLDQWFESEPLK	1.604846998	2	3.590827
Q68FT3	VQGVVLQGGEEVR	0.852403478	2	3.261044
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.316815394**	**9.9E-20**	**10**
Q68FT5	AGANIIGVNCR	1.317022252	2	3.623626
Q68FT5	AGLWTPEAVVEYPSAVR	1.086119333	3	4.09577
Q68FT5	AIAEELAPER	1.446235821	2	3.796228
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.580025174	3	4.692014
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.702612045	3	4.668151
Q68FT5	FGPWTSLQTMK	1.481878885	2	2.510084
Q68FT5	GGFVDLPEYPFGLEPR	1.295087572	2	4.218585
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.557728763	2	2.670145
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	1.151995992	3	3.661617
Q68FT5	YIGGCCGFEPYHIR	2.459712564	2	4.655065
Q68FT9	**SCLY Selenocysteine lyase**	**1.246873935**	**6.23E-13**	**6**
Q68FT9	AEVDLIVQDLK	1.438349662	2	3.900523
Q68FT9	CFHEQQTLQGR	1.144081042	2	2.760026
Q68FT9	NFRPGTENTPMIAGLGK	0.614104222	2	4.303239
Q68FT9	RVDVEDLGVDFLTIVGHK	1.662827708	3	5.331914
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	1.205123668	3	4.656634
Q68FT9	VLVHTDAAQALGK	1.26989717	3	3.314451
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.998483581**	**0.773543**	**13**
Q68FU3	AGDLGVDLTSK	1.06214367	2	3.490509
Q68FU3	EIDGGLETIR	2.007418595	2	2.337366
Q68FU3	EIIAVSCGPPQCQETIR	1.01518143	2	5.313342
Q68FU3	GIHVEVPGAEAENLGPLQVAR	0.677190959	2	5.84644
Q68FU3	HSMNPFCEIAVEEAVR	1.734384131	2	5.597868
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2	1.333572654		
Q68FU3	LKLPAVVTADLR	2.713606266	2	2.360348
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	2.274440275	3	5.732076
Q68FU3	RVIDFAVK	1.286077916	2	2.639637
Q68FU3	VDLLFLGK	0.986095242	2	2.73127
Q68FU3	VETTEDLVAK	1.809288308	2	3.564368
Q68FU3	VIDFAVK	0.839564315	2	2.428571
Q68FU3	VSVISVEEPPQR	0.997045879	2	3.563654
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.05076592**	**0.259028**	**10**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.873883567	3	6.012558
Q68FY0	IEEVDAQMVR	1.165916165	2	3.844921
Q68FY0	LCTSATESEVTR	1.414671632	2	2.855254
Q68FY0	NALISHLDGTTPVCEDIGR	1.262937521	2	4.566181
Q68FY0	NNGAGYFLEHLAFK	1.029367757	2	3.524264
Q68FY0	RIPLAEWESR	0.866670665	2	2.678354
Q68FY0	SGMFWLR	1.066896408	2	2.397294

Q68FY0	TDLTDYLSR	1.070949065	2	2.945399
Q68FY0	VVELLADIVQNISLEDSQIEK	1.495019747	3	5.368584
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.043785396	3	5.237371
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**1.301148672**	**7.76E-05**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.892535846	2	4.72678
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	1.605510648	3	4.008799
Q68G31	GESGGQTTPYDFYSR	1.292336755	2	3.96294
Q68G31	LQPTDSFSQSSCFGLR	1.410757057	2	3.551032
Q68G31	NVNSTLTFVTLSGELK	0.890856646	2	4.257295
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.646691937	3	5.774004
Q68G31	VNTEPLPGIEK	1.007083991	2	2.642453
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.320186151**	**0.478231**	**2**
Q69Z23	GDPTRAEDQVLMRALR	1.279204484	2	2.416615
Q69Z23	YFIDLLMEK	8.603662246	1	2.017305
Q6A028	**SWP70 Switch_associated protein 70**	**3.005687266**	**0.02068**	**2**
Q6A028	FILEKVQDNFDK	3.006850535	1	1.912642
Q6A028	KGDILLDENCCVESLPDKDGK	1.960211218	2	2.339804
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.610630191**	**3.78E-07**	**3**
Q6A0A9	LYEPDQLQELK	1.113461531	2	2.393905
Q6A0A9	SQGGVQPIPSQGGK	1.622463257	2	3.346219
Q6A0A9	VEGSSTASSGSQLAEGK	1.30043653	2	4.232867
Q6AW69	**CGNL1 Cingulin_like protein 1**	**1.274199455**	**0.627918**	**2**
Q6AW69	NRRELAEMQTQLK+Oxidation(7	1.753712952		
Q6AW69	QDSAGPILDGAR	1.274199449	2	2.506153
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.060364544**	**0.308866**	**3**
Q6AXM8	FQEEENSLLHLK	1.059205518	2	3.708792
Q6AXM8	LFVYDPNHPPSSEVLR	1.308886411	2	2.46719
Q6AXM8	LVAEGFDSANGINISPDKK	1.500255415	2	3.538681
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.970195521**	**0.269928**	**4**
Q6AXS5	EETQPPVALKK	0.756669634	2	2.422615
Q6AXS5	FDQLFDDESDPFEVLK	0.980096643	2	5.295574
Q6AXS5	RFEKPLEEK	1.456620664	2	2.421241
Q6AXS5	SAAQAAAQTNSNAAGK	0.512703387	2	4.549628
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**1.040793669**	**0.99999**	**2**
Q6AXY0	FLQPGSQR	1.01502838	2	2.562101
Q6AXY0	YFPAFEK	1.051429415	1	2.009278
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.236180584**	**0.009382**	**4**
Q6AY09	ATENDIYNFFSPLNPMR	1.485344159	2	2.783998
Q6AY09	GLPWSCSAEEVMR	1.595344973	2	2.945832
Q6AY09	HTGPNSPDTANDGFVR	1.22625084	2	4.174157
Q6AY09	STGEAFVQFASQEIAEK	1.328805807	2	3.927957
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**1.318492461**	**0.00033**	**2**
Q6AY20	HTLAGNFNPVSEER	1.318408609	2	4.175228
Q6AY20	SCDLVGEKDKESK	1.50627721	2	3.685519
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.162999452**	**0.307865**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	2.101985212	3	4.010573
Q6AY30	ATLVLNCVGPYR	0.910918758	2	2.823792
Q6AY30	GGGVFTPGAAFSR	1.21478224	2	2.365057
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.355066428	2	2.929661
Q6AY30	LQQVLEK	1.107899833	1	2.320714
Q6AY30	SVSNLKPVPVIGSK	1.221742751	2	3.799309
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.263670257**	**9.9E-20**	**7**

Q6AY56	AVCMLSNTTAIAEAWAR	1.239357474	2	4.558115
Q6AY56	FDGALNVDLTEFQTNLVPYPR	0.791350559	2	5.105412
Q6AY56	LISQIVSSITASLR	2.450349101	2	3.755096
Q6AY56	NLDIERPTYTNLNR	1.297933903	2	3.313298
Q6AY56	QLFHPEQLITGK	0.952540993	2	3.091588
Q6AY56	TIQFVDWCPTGFK	1.358735622	2	3.70063
Q6AY56	VGINYQPPTVVPGGDLAK	1.254323042	2	4.395792
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**1.359930117**	**0.542912**	**5**
Q6AY80	ALTSDILEEQR	1.46130133	2	3.242375
Q6AY80	EEPIHCTPSWYFQG	1.593858856	2	2.698269
Q6AY80	NDVTGALSNPEVFK	1.043133899	2	3.930036
Q6AY80	VLAPQISFGPEVSSEEQR	1.225724974	2	4.341974
Q6AY80	VLCQGFAFDVPGFYDSGFLK	1.588111884	2	2.800551
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**1.029687797**	**0.662865**	**3**
Q6AYG5	DVLETLWGGPANLEAIAK	1.655606197	2	4.051223
Q6AYG5	ILEQFPGGSIDLQK	0.995187384	2	3.41098
Q6AYG5	NTFCSGSDLNAVK	1.218283395	2	2.48237
Q6AYH5	**DCTN2 Dynactin subunit 2**	**1.465281597**	**0.03363**	**3**
Q6AYH5	ASVEDADTQNK	1.320858546	2	2.809825
Q6AYH5	VNALDLAVLDQVEAR	1.718580561	2	3.412948
Q6AYH5	WSPVASTLPELVQR	1.26345758	2	2.903625
Q6AYK6	**CYBP Calcyclin_binding protein**	**1.406550015**	**0.547593**	**2**
Q6AYK6	IYEDGDDDMKR	0.921901222	2	2.406855
Q6AYK6	WDYLTQVEK	4.661245887	2	2.601891
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.903715871**	**0.905676**	**4**
Q6AYQ8	IITLEEGDLILTGTPK	1.450047822	2	5.170192
Q6AYQ8	NLHHEVELGVLLGR	0.903531546	3	4.707316
Q6AYQ8	SFTSSCPVSAFVPK	1.012608902	2	3.98761
Q6AYQ8	STVLSEPVLFLKPSTAYAPEGSPVLMPAYCR	1.114054113	3	3.723543
Q6AYR8	**SCRN2 Secernin_2**	**1.305596074**	**0.168289**	**2**
Q6AYR8	GHQAALGLMDEQEQAQLR	1.244100147	3	4.301841
Q6AYR8	QEQQSLEQEGLEALR	1.324723247	2	3.885577
Q6AYS7	**ACY1A Aminoacylase_1A**	**1.875521869**	**0.001487**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	1.480945549	2	3.811532
Q6AYS7	ICTVQPNPDYGSAVTFLEER	4.112027738	2	4.576272
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**1.248216356**	**0.74922**	**3**
Q6AYS8	ALTDELAALGCTGVR	1.116829446	2	4.057905
Q6AYS8	FDAVVGYK	1.482535704	1	2.286601
Q6AYS8	SVAGEIVLITGAGHGIGR	1.147478756	2	4.029947
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.733882386**	**0.959647**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	0.854425485	2	3.434348
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.615705122	2	3.208886
Q6AYT9	NDDVINSSSYR	3.527386279	2	3.34475
Q6AYT9	TGVVMIPGISQLTQK	0.654042304	2	3.144312
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.367211468**	**9.9E-20**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	1.261768672	2	5.409662
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	1.371353997	3	4.145511
Q6AYZ1	DVNAAIATIK	1.044588656	2	3.172939
Q6AYZ1	IHFPLATYAPVISAEK	2.093115062	2	3.799992
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.597629449	2	5.460062
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.404148071	2	4.702286
Q6DGG0	**PPID Peptidyl_prolyl cis_trans isomerase D**	**0.990201045**	**0.398367**	**4**
Q6DGG0	GTGPTTGKPLHFK	0.593115784	2	2.356661
Q6DGG0	IVLELFADIVPK	1.124275175	2	2.310369

Q6DGG0	MLENVEVNGEKPAK	1.603417552	2	3.708082
Q6DGG0	VFFDVDIGGER	0.95601272	2	2.836786
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.045736199**	**5.51E-05**	**6**
Q6DGG1	AVAIDLPGLGR	1.131035413	2	3.564353
Q6DGG1	FSSETWQNLGTLHR	1.260414008	2	3.636135
Q6DGG1	FSVLLLHGIR	1.872913752	2	3.088484
Q6DGG1	GYVPVAPICTDK	1.03086928	1	2.653982
Q6DGG1	INAADYAR	1.259905921	2	2.467744
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.37064767	2	5.382257
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**1.073956095**	**0.43451**	**2**
Q6EDY6	ELMESIK+Oxidation(2	1.701431195		
Q6EDY6	IENYLLR	1.072536887	2	2.455609
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.89066197**	**0.773475**	**2**
Q6GQP4	CDLSDIREVPLK	0.890640642	2	2.5344
Q6GQP4	CDLSDIREVPLKDAK	0.89848344	2	2.916077
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**2.409483891**	**0.093015**	**3**
Q6GQT1	ASVTVLGDILGSAMQNTQDLLK	1.070939607	2	2.351327
Q6GQT1	IQEEGTGVEETGK	15.40852594	2	3.722674
Q6GQT1	SSGSLLNNAMK	1.231568196	2	3.097877
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**1.520768164**	**0.000378**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	1.324206642	2	3.879374
Q6I7R3	ILGIPVIITEQYPK	1.529546516	2	3.007985
Q6I7R3	YFGDIISVGQR	1.73338597	2	2.578387
Q6IE52	**MUG2 Murinoglobulin_2**	**1.109447274**	**0.932004**	**14**
Q6IE52	AHFSVMGDILSSAIK	1.050212604	2	3.671941
Q6IE52	HGIPFFVK	1.042141802	2	2.747216
Q6IE52	HTSSWLVTPK	0.741008999	2	2.808944
Q6IE52	LPSSEEEESLDINIEGAK	1.43312948	2	2.88293
Q6IE52	MLIYTILPDGEVIADSVK	1.151850299	2	3.836036
Q6IE52	MLSGFIPLKPTVK	1.008795017	2	3.155607
Q6IE52	MLSGFIPLKPTVK+Oxidation(0	0.723062528		
Q6IE52	NLYPLKELVQDPK	1.524103577	1	2.044113
Q6IE52	QLSFSLSAEPIQGPYK	1.162282159	2	4.277303
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	1.209849028	3	3.659071
Q6IE52	VHLSFSPSQSLPASQTHMR	0.694820967	3	3.93723
Q6IE52	VKTVPLTCNNPK	1.020117374	2	2.964466
Q6IE52	VTASPQSLCGLR	2.414432069	2	2.507361
Q6IE52	YMVLVPSQLYTETPEK	1.013752901	2	3.725561
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**0.594444131**	**0.322034**	**2**
Q6IFW6	LENEIQTYR	0.974022775	2	2.348988
Q6IFW6	QSLEASLAETEGR	0.352565835	2	3.44501
Q6IFZ9	**K2C74 Keratin_ type II cytoskeletal 74**	**0.874568146**	**0.402137**	**2**
Q6IFZ9	FLEQQNQVLQTK	0.525871347	2	4.169481
Q6IFZ9	GDSALKDAWAKLDELEGALQQAK	4.795232271	3	3.603644
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**1.210635416**	**4.44E-16**	**4**
Q6IMF3	TNAENEFVTIK	1.074450056	2	2.751327
Q6IMF3	TNAENEFVTIKK	0.373200106	2	2.93977
Q6IMF3	WELLQQVDTSTR	0.799799807	2	3.617955
Q6IMF3	YEELQITAGK	1.463733029	2	3.467762
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**1.266638678**	**1.79E-09**	**7**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	1.219544023	3	5.463465
Q6IRK9	GEESAVMVVPR	1.602393364	2	2.827027
Q6IRK9	IVVYNQPYTDYGK	1.41543748	2	2.917647
Q6IRK9	LGLLVDTVGPR	1.848830869	2	2.983609

Q6IRK9	SVASFSIYSPHTGHQGYQDGVPK	1.391124729	3	3.458466
Q6IRK9	TYPDTDSFNTVAEITGSK	1.665871528	2	3.731941
Q6IRK9	VGAVASLIR	2.085223573	2	2.529449
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**1.243605562**	**0.405249**	**4**
Q6MGB5	AGVIGLTQTAAR	1.45516836	2	3.195551
Q6MGB5	CNSVLPGFIATPMTQK	2.052306863	2	2.348606
Q6MGB5	GSIINISSIVGK	2.246736477	2	2.775103
Q6MGB5	VGNIGQTNYASSK	0.929124045	2	2.760011
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.033244535**	**0.841425**	**3**
Q6NSR8	GIVYDTGGLSIK	1.068143635	2	2.364544
Q6NSR8	HNSPSAAHFITR	0.757060121	3	3.954587
Q6NSR8	TVEINNTDAEGR	1.051863938	2	2.9926
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**0.818516299**	**0.299724**	**3**
Q6NYB7	EFADSLGIPFLETSAK	0.798480789	2	3.791878
Q6NYB7	NATNVEQSFMTMAAEIK	1.591865063	2	5.092525
Q6NYB7	TITSSYYR	1.375871549	1	1.978612
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.324979932**	**2.03E-06**	**9**
Q6NZJ6	FMLQDVLDLR	1.73447212	2	2.796247
Q6NZJ6	GLPLVDDGGWNTVPISK	1.047629904	2	2.872664
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.357500531	3	3.353128
Q6NZJ6	IHNAENIQPGEQK	1.256484703	2	3.955145
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.476891822	3	3.561689
Q6NZJ6	KVEYTLGEESEAPGQR	1.322674031	2	4.750581
Q6NZJ6	LGIESTLER	1.419711116	2	2.4185
Q6NZJ6	LKEELEEAR	1.326656758	2	2.702291
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	1.290710347	3	4.991287
Q6P0K8	**PLAK Junction plakoglobin**	**1.326915442**	**0.09421**	**3**
Q6P0K8	LLNDEDPVVVTK	1.098058043	2	3.225651
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.326919616	3	3.628233
Q6P0K8	TMQNTSDLDTAR	1.368234476	2	3.259889
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.516681547**	**7.11E-10**	**14**
Q6P502	AMTGVEQWPYR	1.221361727	2	2.707216
Q6P502	AVAQALEVIPR	1.80096083	2	2.450603
Q6P502	DMMLNIINSSITTK	0.703799338	2	3.976569
Q6P502	EIQVQHPAAK	1.294006165	2	3.302261
Q6P502	GISDLAQHYLMR	1.546161116	2	3.048059
Q6P502	IVLLDSSLEYK	1.836208335	2	2.559093
Q6P502	IVSRPEELREDDVGTGAGLLEIK	2.213732238	3	4.094107
Q6P502	KGESQTDIEITR	1.139871068	2	3.277578
Q6P502	MLLDPMGGIVMTNDGNAILR	2.330622817	2	3.885154
Q6P502	NLQDAMQVCR	4.667575398	2	3.31944
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	2.311332463	2	3.870822
Q6P502	TAVETAVLLLR	1.89812389	2	3.73921
Q6P502	TLIQNCGASTIR	1.419551035	2	3.345924
Q6P502	WSSLACNIALDAVK	1.498046405	2	3.796398
Q6P6M7	**selenium transferase**	**1.031407061**	**0.912081**	**4**
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.99039799**	**1.09E-11**	**14**
Q6P6R2	ALLNNSHYYHLAHGK	0.663325581	2	3.3111
Q6P6R2	ALTGGIAHLFK	0.855241306	2	2.632448
Q6P6R2	EANLAASFGKPINF	1.180310752	1	1.929015
Q6P6R2	IDVSVEAASGGK	1.195508327	2	3.039462
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.178569608	3	3.993563
Q6P6R2	IPNIFAIGDVVAGPMLAHK	1.627122307	3	3.50005
Q6P6R2	NETLGGTCLNVGCIPSK	0.881054859	2	5.167176
Q6P6R2	NQVTATTADGSTQVIGTK	0.981303581	2	5.630736

Q6P6R2	RPFTQNLGLEELGIELDPK	1.530995885	3	4.603387
Q6P6R2	SEEQLKEEGVEFK	0.982830053	2	3.531238
Q6P6R2	TNADTDGMVK	1.189417853	2	2.825343
Q6P6R2	TNADTDGMVK+Oxidation(7	1.306488265		
Q6P6R2	VCHAHPTLSEAFR	1.193489387	3	3.782745
Q6P6R2	VVHVNGFGK	1.65807876	3	3.45103
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**1.283430338**	**0.031947**	**6**
Q6P6S9	AAETHLIDYEK	1.266932017	2	2.667594
Q6P6S9	AQTLLLEVEEIFK	1.193188206	2	3.270327
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	1.095363408	2	4.397387
Q6P6S9	QGAETVQELLEVAK	1.177656733	2	3.143733
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	1.322685363	3	3.627939
Q6P6S9	WLEAEWIFGGVK	1.500947782	2	2.770267
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.512733929**	**2.49E-07**	**9**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2	1.446724558		
Q6P6V0	HFVALSTNTDK	1.439251851	1	3.255269
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.422206047	3	6.001237
Q6P6V0	MIPCDFLIPVQTQHPIR	1.941512392	2	2.426195
Q6P6V0	TFTTQETITNAETAK	1.459403209	2	4.756831
Q6P6V0	TLANLNPESSLFIIASK	1.223929858	3	5.205965
Q6P6V0	VDYQTGPIVWGEPGTNGQHAFYQLIHQGTK	1.261920214	3	4.022248
Q6P6V0	VFEGNRPTNSIVFTK	1.354696153	2	3.38279
Q6P6V0	VWFVSNIDGTHIAK	0.355772563	2	3.63236
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.440655523**	**0.0068**	**6**
Q6P7Q4	DFLLQQTMLR	2.21725706	2	3.382379
Q6P7Q4	FEELGVK	1.135196872	1	1.937783
Q6P7Q4	GFGHIGIAVPDVYEACK	1.221126879	2	4.000095
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.443701742	2	5.738204
Q6P7Q4	RFEELGVK	1.215765073	2	2.323681
Q6P7Q4	VLGLTLLQK	1.762635195	2	2.480991
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.503240484**	**0.271043**	**2**
Q6P7R8	GIFVQSVLPFFVATK	1.369480416	2	3.46805
Q6P7R8	LGEWAVVTGGTDGIGK	1.504351754	2	4.23867
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.101241068**	**9.9E-20**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	1.488106903	2	4.509984
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10	1.120441697		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.490435206	3	5.658007
Q6P9T8	EIVHLQAGQCGNQIGAK	1.361507424	2	4.93126
Q6P9T8	EVDEQMLNVQNK	2.257634374	2	4.473939
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	1.345251686	3	4.850315
Q6P9T8	INVYYNEATGGK	1.244958186	2	3.076027
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.790864698	3	6.605772
Q6P9T8	LHFFMPGFAPLTSR	2.361073458	2	3.269073
Q6P9T8	MSATFIGNSTAIQELFK	1.703716857	2	4.331597
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	1.616975752	3	5.803611
Q6P9T8	TAVCDIPPR	1.571315933	2	2.500897
Q6P9T8	YLTVAAVFR	1.764940692	2	2.683813
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.499383105**	**0.000324**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	1.076357304	3	3.731251
Q6P9U8	EGTGSTATSSSSTGGAVGK	1.824336502	2	4.270665
Q6PA06	**ATLA2 Atlastin_2**	**1.233119337**	**0.000436**	**5**
Q6PA06	AGLTDQVSHHAR	1.456731686	2	3.18057
Q6PA06	NLVPLLLAPENLVEK	1.411350878	2	3.022973
Q6PA06	QNQHEELQNVR	1.149892055	2	2.929742
Q6PA06	SMEQVCGGDKPYIAPSDLER	1.210280506	3	3.803212

Q6PA06	SMLQATAEANNLAAVAGAR	1.596211088	2	4.500933
Q6PCL9	**polymerase gamma**	**1.316888619**	**0.381032**	**2**
Q6PCL9	LTEILK	1.38313251		
Q6PCL9	QANNINMLKDGMK	1.180310752		
Q6PCU2	**VATE1 V_type proton ATPase subunit E 1**	**1.727867307**	**0.010341**	**2**
Q6PCU2	ARDDLITDLLNEAK	1.794176239	2	2.972431
Q6PCU2	LDLIAQQMMPEVR	1.331034435	2	2.565131
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.285321729**	**0.569787**	**2**
Q6PDM2	SHEGETAYIR	1.31100481	2	2.40953
Q6PDM2	TKDIEDVFYK	1.273996142	2	2.753317
Q6PDV7	**RL10 60S ribosomal protein L10**	**1.638565084**	**5.39E-07**	**2**
Q6PDV7	FNADEFEDMVAEK	1.650057572	2	3.812463
Q6PDV7	FNADEFEDMVAEKR	1.523589192	2	3.304233
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.486173528**	**0.290479**	**6**
Q6PEC1	AEDGENYAIK	1.220022906	2	2.690401
Q6PEC1	AEDGENYAIKK	1.493670021	2	2.475244
Q6PEC1	LEAAYTDLR	1.763035169	2	2.811616
Q6PEC1	MKAEDGENYAIK	0.109108309	2	2.793792
Q6PEC1	QAEILQESR	0.861978794	2	2.583644
Q6PEC1	QILESEKDLEEAEEYKEAR	1.212209357	3	4.09466
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.063717304**	**0.445013**	**3**
Q6PEC4	NDFTEEEEAQVR	1.062665056	2	3.451865
Q6PEC4	RTDDIPVWDQEFLK	1.183601248	2	3.028023
Q6PEC4	TDDIPVWDQEFLK	1.313830783	2	3.189246
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.242599582**	**0.22268**	**6**
Q6Q0N1	AVFQYIDENQDR	0.551228791	2	3.026163
Q6Q0N1	EGGSIPVTLTFQEATGK	1.184496499	2	2.762043
Q6Q0N1	LGGSVELVDIGK	1.056723063	2	3.582653
Q6Q0N1	MTEAAAADVQR	1.490056823	2	3.143737
Q6Q0N1	TGQEIPVNLR	1.547816078	2	2.574807
Q6Q0N1	TVFGVEPDLTR	1.470746786	2	2.397709
Q6RT24	**CENPE Centromere_associated protein E**	**1.307534352**	**0.06683**	**3**
Q6RT24	ENEDLKLK	1.309487483	2	2.329729
Q6RT24	MELENVNMKLQEK	1.306659051	2	2.559444
Q6RT24	NLQEYIDAQKSEKMK	1.2770583	2	2.406041
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.925538081**	**0.633668**	**2**
Q6SKG1	FDSTSILQTLSK	1.29352498	2	3.756126
Q6SKG1	TGTVLIPGTTQLTQK	0.826646929	2	2.859184
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.280854413**	**0.788301**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.28489134	2	4.646751
Q6TUG0	FQMTQEVVCDECPNVK	1.257222388	2	5.578425
Q6TUG0	KGEGLPNFDNNNIK	1.095659048	2	3.649173
Q6TUG0	TLEVEIEPGVR	1.4191074	2	3.155499
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.158481672**	**5.38E-07**	**19**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.040294384	2	5.095387
Q6UPE1	ALNEGGLQSIPK	0.940184449	2	3.364232
Q6UPE1	ASCDAQTYGIGLK	1.096521118	2	4.053927
Q6UPE1	DCTPIEYPKPDGQISFDLLSSVALSGTNHEHDQPAHLTLK	0.768543816	4	4.625688
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	2.063918916	2	3.086116
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.640898964	2	4.522505
Q6UPE1	GAPLNTPVTEDR	0.854551837	2	3.482643
Q6UPE1	GIATNDVGIQK	1.280230022	2	3.789166
Q6UPE1	HHPSIRPTLEGGK	0.763273918	2	2.420196
Q6UPE1	HHPSIRPTLEGGKR	1.239709906	2	2.820377
Q6UPE1	LQINAQNCVHCK	1.927441401	2	3.723388

Q6UPE1	NLSIYDGPEQR	1.034691831	2	3.143724
Q6UPE1	QLAAEQEKDIR	1.293405505	2	2.701544
Q6UPE1	QLTSENLQSK	1.105430226	2	2.463722
Q6UPE1	SGSLAAEAIFK	0.935880537	2	3.140819
Q6UPE1	TAGLHVTEYEDNLK	1.370206051	2	3.973487
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	6.975930066	2	4.390004
Q6UPE1	VDHTVGWPLDR	0.967565582	2	2.476052
Q6UPE1	VTIFAEGCHGHLAK	0.871299194	2	3.677919
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**1.374371663**	**2.75E-14**	**8**
Q6URK4	EDSVKPGAHLTVK	1.378893867	2	3.48456
Q6URK4	EDTEEYNLR	1.361727572	2	2.453233
Q6URK4	GFAFVTFDDHDTVDK	5.15266146	2	4.095193
Q6URK4	IETIEVMEDR	1.461238077	2	3.4034
Q6URK4	IFVGGIKEDTEEYNLR	1.914797654	2	4.257796
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	1.176237619	2	5.227034
Q6URK4	WGTLTDCVVMR	1.542041932	2	3.241398
Q6URK4	YHTINGHNCEVK	1.082198839	2	3.507973
Q6URW6	**MYH14 Myosin_14**	**1.12181075**	**0.963624**	**4**
Q6URW6	EDQSILCTGESGAGK	1.187396642	2	4.396406
Q6URW6	FDQLLAEEK	1.266291779	1	2.04082
Q6URW6	KFDQLLAEEK	1.109159399	2	2.837328
Q6URW6	QLLQANPILEAFGNAK	1.045037934	2	4.491557
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.765352182**	**0.109785**	**5**
Q6XQN1	AFAQQSLSR	1.798350329	2	2.493515
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.704993385	2	4.222678
Q6XQN1	LDSGDLLQQAK	0.898960309	2	3.061677
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.488021134	2	5.036246
Q6XQN1	QLQNPAVYQVALSEK	1.656851791	2	3.831927
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.353429817**	**0.162159**	**2**
Q6ZPJ3	FRTTDIVIR	1.046562534	2	2.600351
Q6ZPJ3	NCAQGEGSMAKKVK	2.570338892	2	2.821203
Q6ZPV2	**INO80 DNA helicase INO80**	**1.094068856**	**0.672669**	**2**
Q6ZPV2	FIDVSPAEMANLMLQGLLAR+Oxidation(12	0.74996504		
Q6ZPV2	KLDEEMREAK+Oxidation(5	1.149908345		
Q6ZWR6	**SYNE1 Nesprin_1**	**1.216828979**	**0.486346**	**4**
Q6ZWR6	FGSITNQLLK	1.246067126	2	2.398786
Q6ZWR6	KDEIEGWSNSSLPK	0.705237457	2	2.525392
Q6ZWR6	LETILK	1.38313251	1	1.900741
Q6ZWR6	LKAKTDDLVHAK	1.0690319	2	2.314591
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.373462157**	**0.068969**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	0.779889356	2	2.742035
Q70FJ1	MDQITQSLCNLNK+Oxidation(0	2.186403868		
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.701508425**	**6.22E-05**	**5**
Q711G3	DCGTDVLDLWTLMQK	1.580999506	2	4.408664
Q711G3	DVEETKPELSLLGDGDH	2.944082802	2	4.131206
Q711G3	LNVAVGEYAK	1.269919159	2	2.763311
Q711G3	QHVPLDEYSANLR	2.520516785	2	2.632076
Q711G3	VILITPPPLCEAAWEK	1.833054279	2	2.733925
Q71LX4	**TLN2 Talin_2**	**1.117894753**	**0.483259**	**3**
Q71LX4	QEDVIATANLSR	1.300875931	1	1.970315
Q71LX4	QVAASTAQLLVACK	1.115587671	2	3.189486
Q71LX4	VMVTNVTSLLK	0.488778183	2	2.377382
Q71TY3	**RS27 40S ribosomal protein S27**	**1.617531246**	**0.026163**	**3**
Q71TY3	DLLHPSPEEEK	1.972062546	2	2.916672
Q71TY3	LTEGCSFR	1.421580466	2	2.387608

Q71TY3	LVQSPNSYFMDVK	1.359264114	2	2.800424
Q75N33	**SC16B Protein transport protein Sec16B**	**1.384734316**	**0.397103**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	0.700720233	2	3.67124
Q75N33	VLEPDWLVQLR	1.633056822	2	2.806057
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.048366691**	**0.675028**	**6**
Q75Q39	NADLSTFYQNR	1.559716112	2	2.958164
Q75Q39	NREPLMPSPQFIK	1.018151276	2	2.821916
Q75Q39	QYMEEENYDK	#NUM!	1	1.948622
Q75Q39	SDEDKDKEGEALEVK	1.577628956	2	4.228317
Q75Q39	WKEVAQDCTK	1.044591459	2	2.339485
Q75Q39	YEQAIQCYTEAISLCPTEK	1.007990481	2	2.497809
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.572632297**	**0.160696**	**8**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.161461893	3	5.137702
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.403526299	2	4.996356
Q76MZ3	LSTIALALGVER	1.487350977	2	2.360965
Q76MZ3	LTQDQDVDVK	1.618042576	2	2.979821
Q76MZ3	QLSQSLLPAIVELAEDAK	1.876463637	3	4.137728
Q76MZ3	SALASVIMGLSPILGK	1.115072313	2	2.891028
Q76MZ3	SEIIPMFSNLASDEQDSVR	1.281945811	2	3.969186
Q76MZ3	VLELDNVK	1.454334246	2	2.514905
Q78IK4	**APOOL Apolipoprotein O_like**	**1.188493503**	**0.655548**	**2**
Q78IK4	EEEPKK	5.253452119	1	1.961384
Q78IK4	SESTSGTTQFIPDPK	1.163903552	2	2.42113
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**0.865328237**	**0.13733**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	0.65236453	3	5.66937
Q78P75	NFGSYVTHETK	1.152380971	2	2.922776
Q78P75	YNPTWHCIVGR	0.83625566	2	2.86639
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**1.007731797**	**0.921581**	**6**
Q791V5	EEGIVGFFAGLIPR	0.808139625	2	3.428821
Q791V5	GLFTGLTPR	1.118752754	2	2.58243
Q791V5	LCSGVLGTVVHGK	0.924991534	2	2.995635
Q791V5	SAATLITHPFHVITLR	0.808364671	3	3.566185
Q791V5	VLIQVGYEPLPPTIGR	1.094673318	2	4.184767
Q791V5	YCGLCDSIVTIYR	1.465536883	2	2.915088
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.441941189**	**5.69E-06**	**4**
Q794E4	ATENDIYNFFSPLNPVR	1.220117667	3	4.091864
Q794E4	HSGPNSADSANDGFVR	1.375278133	2	3.946498
Q794E4	ITGEAFVQFASQELAEK	1.250265783	2	2.713714
Q794E4	VHIEIGPDGR	1.477341886	2	2.790099
Q7M0E3	**DEST Destrin**	**1.176491648**	**3.36E-09**	**2**
Q7M0E3	HEYQANGPEDLNR	1.175399842	2	4.766291
Q7M0E3	HFVGMLPEKDCR	1.90365344	2	3.485506
Q7TMA5	**APOB Apolipoprotein B_100**	**1.012622353**	**0.862569**	**12**
Q7TMA5	ALEGKSDTVARLHTEK	1.585918864	2	2.417762
Q7TMA5	GFEPTLEALFGK	1.098888071	2	2.918231
Q7TMA5	IEGNLVFDPSSYLPK	1.10279016	2	2.997787
Q7TMA5	IEIDIPLPLGGK	0.481099116	2	2.778122
Q7TMA5	ITDNDVLIALDSAK	1.066772622	2	3.325538
Q7TMA5	KGTVATEMSTER	1.065952109	2	2.841465
Q7TMA5	LSISEQNAQR	1.026645703	2	2.742728
Q7TMA5	LSTSPFALNLTMLPK	1.14196801	1	1.901728
Q7TMA5	NFVASHIANILNSEELYVQDLK	0.783429741	3	3.849286
Q7TMA5	NLQHCDGFQPISTSVSPLALIK	1.314196227	3	3.793248
Q7TMA5	TILFDTFVNDVAPVEK	1.004049439	2	3.132509

Q7TMA5	VRSFTIDLLEIKAK	1.14196801	1	1.999437
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.277211866**	**0.11428**	**4**
Q7TNG8	AVVGSPHVSTASAVR	1.069209257	2	2.939182
Q7TNG8	AYSTDVCVPISR	1.292596757	2	3.380218
Q7TNG8	GSQGGLSQDFVEALK	1.214044641	2	3.632104
Q7TNG8	QLLQEEVGPVGVETMR	0.662178526	2	3.229623
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.314552702**	**0.067994**	**2**
Q7TP47	DLFEDELVPLFEK	1.964862689	2	3.279659
Q7TP47	NLANTVTEEILEK	1.260083183	2	3.686627
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.163039335**	**0.007999**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	1.685120396	2	3.002428
Q7TP48	LENGEIETIAR	1.14338309	2	3.52103
Q7TP48	LLEYDTVTK	1.36635014	2	2.491065
Q7TP48	LLLSSETPIEGK	1.187794768	2	2.911974
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.244930343**	**0.079255**	**8**
Q7TP52	AGVSVYGIIR	1.529878555	2	2.746556
Q7TP52	EDCSPADKPYIEEAR	1.119128176	2	3.714843
Q7TP52	KREDCSPADKPYIEEAR	1.347508004	3	4.213161
Q7TP52	LDYGGMGQEVQVEHIK	1.345390367	2	4.611239
Q7TP52	LKEHCIVNYQVK	1.114308623	2	4.07233
Q7TP52	NLIEWLNK	1.667915064	2	2.356101
Q7TP52	REDCSPADKPYIEEAR	1.296005753	3	3.698438
Q7TP52	TFSGQTHGFVHR	1.196725382	2	3.660386
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**0.865476013**	**0.348995**	**6**
Q7TPB1	ALIAGGGAPEIELALR	1.608337927	2	3.881849
Q7TPB1	ETLLNSATTSLNSK	1.657052548	2	3.312957
Q7TPB1	GDVTITNDGATILK	1.412521545	2	3.517375
Q7TPB1	SIHDALCVIR	1.736469509	2	2.693924
Q7TPB1	TGCNVLLIQK	0.753339354	2	2.607968
Q7TPB1	VIDPATATSVDLR	0.976176732	2	3.841635
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.335188473**	**1.4E-09**	**3**
Q7TPJ0	FLVGFTNK	1.771772996	2	2.488126
Q7TPJ0	GEDFPANNIVK	1.28343427	2	3.203325
Q7TPJ0	GTEDFIVESLDASFR	1.416202915	2	4.371697
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**1.276635523**	**0.676263**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(0	1.288528674		
Q7TQ20	QIEEVNELMRK+Oxidation(8	1.258151029		
Q7TQ94	**NIT1 Nitrilase homolog 1**	**1.535504065**	**0.084378**	**2**
Q7TQ94	GQDWEQTQK	1.371484731	2	2.464553
Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.584930976	3	4.218682
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**0.910236433**	**0.213292**	**3**
Q7TQM4	AIWEAVQAYPK	0.923191151	2	2.563189
Q7TQM4	QDRPLPSTASDSTR	1.058200248	2	2.845041
Q7TQM4	TQCLEQAQR	0.805064263	2	2.883857
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.777036323**	**0.928268**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(1	0.829090916		
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(5	0.696230725		
Q80V31	**CE104 Centrosomal protein of 104 kDa**	**1.237006929**	**0.399433**	**2**
Q80V31	IDGSVLPTEAEVRAQK	1.223648734	2	2.558857
Q80V31	KLMEMPVGTQK+Oxidation(2)Oxidation(4	1.296332672		
Q80VM7	**ANR24 Ankyrin repeat domain_containing protein 24**	**1.328407841**	**0.501004**	**2**
Q80VM7	ADEVDVLAQAGLTGTVIR	1.279204484	2	2.688193
Q80VM7	QNQELLEK	2.653689461	1	2.019255

Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.166410888**	**9.9E-20**	**13**
Q80W21	CLDAFPNLK	1.117049405	2	3.2003
Q80W21	CLDAFPNLKDFIAR	1.250663046	2	3.118843
Q80W21	FKLGLDFPNLPYLIDGSHK	1.516879703	3	5.07351
Q80W21	HNLCGETEEER	0.887519608	2	3.891625
Q80W21	IRVDILENQLMDNR	1.286944794	2	3.049441
Q80W21	ITQSNAILR	1.456772945	2	3.077128
Q80W21	KHNLCGETEEER	1.165381377	2	3.998601
Q80W21	KISDYMK	1.16701232	1	2.001362
Q80W21	LFLEYTDSSYEEK	0.542105032	2	4.043871
Q80W21	LGLDFPNLPYLIDGSHK	0.92705641	3	4.67577
Q80W21	LKPGYLEQLPGMMR	1.285158443	2	3.180714
Q80W21	LYSEFLGK	1.201057298	2	2.355919
Q80W21	VDILENQLMDNR	1.33568917	2	3.714658
Q80W93	**HYDIN Hydrocephalus_inducing protein**	**2.039340934**	**0.088287**	**3**
Q80W93	ELERLAKEMQEK+Oxidation(8	3.641240331		
Q80W93	LAKEMQEK	1.417053259	1	1.932595
Q80W93	LQTLDEDEYDALTAEEK	2.053219857	2	2.301608
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**1.002396501**	**0.7074**	**3**
Q80WS3	DHAVVVGVYRPPPK	0.964669746	3	3.740932
Q80WS3	MKPAGGRGGWGWGGGK+Oxidation(0	1.274819619		
Q80WS3	TNIIPVLEDAR	1.305039547	2	2.401611
Q80X50	**UBP2L Ubiquitin_associated protein 2_like**	**1.270367605**	**0.124186**	**2**
Q80X50	IDLAVLLGK	1.249309767	2	3.142393
Q80X50	QRPQATAEQIR	1.403527462	2	2.518869
Q80X90	**FLNB Filamin_B**	**1.411792319**	**9.44E-05**	**11**
Q80X90	ADIEMPFDPSK	1.405231186	2	2.373427
Q80X90	FNDEHIPDSPYLVPVIAPSDDAR	1.685956473	3	3.64952
Q80X90	GAGIGGLGITVEGPSESK	1.41580321	2	3.836604
Q80X90	GEAGIPAEFSIWTR	1.333215916	2	2.314445
Q80X90	IGNLQTDLSDGLR	1.570773812	2	2.45996
Q80X90	ILAQDGEGQPIDIQMK	1.084630931	2	3.3675
Q80X90	TFEMSDFIVDTR	1.709469461	2	2.301604
Q80X90	VDIQTEDLEDGTCK	1.087342056	2	3.796
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	0.968347511	3	4.110542
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.361588938	3	3.475507
Q80X90	VVASGPGLEHGK	1.166104402	2	2.379746
Q80XC3	**US6NL USP6 N_terminal_like protein**	**1.128810906**	**0.616497**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	1.711314513	2	2.37964
Q80XC3	SVDEGSKNLK	1.122016291	2	2.410464
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**1.614816788**	**3.78E-07**	**3**
Q80XI3	FLKITKPTIDEK	1.169734134	2	2.608567
Q80XI3	FMLQDVIDLR	1.73447212	2	2.796247
Q80XI3	NHDEESLECLCR	1.649075959	2	3.368722
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**1.086286768**	**0.937177**	**2**
Q80Y84	CDIGLLGLK	1.010174154	1	2.075303
Q80Y84	SSSEKNDCLRGK	1.130029489	1	1.93582
Q80YR7	**CLSPN Claspin**	**1.315529998**	**0.007704**	**2**
Q80YR7	GASFLPTAGFRSPSPGLFR	1.300460406	2	2.412566
Q80YR7	LEGASHAKPGEKLQMLK+Oxidation(14	1.316587108		
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.09383641**	**0.98231**	**2**
Q80Z25	ELEQEAERLEK	1.093829753	2	2.939973
Q80Z25	MIEESLK+Oxidation(0	1.185854038		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.368864862**	**9.55E-15**	**4**

Q80Z29	NAQLNMEQDVAPH	1.007780506	2	2.534869
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.72912843	2	3.788352
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.323815428	2	5.379294
Q80Z29	YLLETSGNLDGLEYK	1.695998139	2	4.552656
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**1.221729391**	**0.001422**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	2.211505024	2	2.626986
Q80Z36	YPEEQLK	0.378067556	1	2.09197
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.353366626**	**0.099499**	**5**
Q811D2	AQEDFDK	0.485527432	1	1.911425
Q811D2	LSGSEDSQQKVEEK	1.992326397	2	2.369598
Q811D2	NKDDLTPMLLAVK	1.5138414	2	2.4119
Q811D2	SADQLSEK	1.366819755	2	2.307898
Q811D2	SNLEEEARDLK	1.181667071	1	1.994843
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.503295235**	**0.056046**	**4**
Q811X6	EMKSLEQSGSLK+Oxidation(1	1.352360827		
Q811X6	IVDDQVILSSSSSCLLPSK	1.130342862	2	3.930299
Q811X6	LYDIEQQQITNALESIR	1.324918655	2	4.27153
Q811X6	TFGPVPEFSGDTVEK	1.596795647	2	2.898605
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.057998591**	**9.9E-20**	**10**
Q8BFZ3	CDVDIR	2.715432221	2	2.32686
Q8BFZ3	DLTDYLMK	1.616518272	1	2.215929
Q8BFZ3	HQGVMVGMGQK	1.636327694	3	3.636645
Q8BFZ3	HQGVMVGMGQK+Oxidation(4	1.008876076		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)Oxidation(7	1.015031594		
Q8BFZ3	HQGVMVGMGQK+Oxidation(7	0.937849031		
Q8BFZ3	SYELPDGQVITIGNER	0.91297209	3	5.230312
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.374144695	3	6.640037
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5	1.677253923		
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.350072303	3	4.329675
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**1.509049679**	**0.178903**	**6**
Q8BG32	LYDNLLEQNLIR	1.814752437	2	3.393902
Q8BG32	TGQAAELGGLLK	0.967711893	2	3.151299
Q8BG32	TTANAIYCPPK	10.80824394	2	2.643955
Q8BG32	TYEAALETIQNMSK	1.35940888	2	2.373568
Q8BG32	VQIEHISSLIK	1.641855071	2	2.70242
Q8BG32	YQEALHLGSQLLR	1.509241747	2	2.500066
Q8BGD9	**IF4B Eukaryotic translation initiation factor 4B**	**1.365915316**	**0.029665**	**2**
Q8BGD9	SQSSDTEQPSPTSGGGK	1.348687493	2	5.377588
Q8BGD9	VDVADQAQDKDRDDR	2.128355657	2	2.378849
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**0.978023023**	**0.659458**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.403911771	2	3.838397
Q8BGT5	VLCIINPGNPTGQVQSR	1.025796714	2	5.079283
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.350821911**	**1.11E-16**	**3**
Q8BGY2	KYEDICPSTHNMDVPNIK	1.353293409	3	4.792913
Q8BGY2	VHLVGIDIFTGK	1.550900273	3	3.741223
Q8BGY2	YEDICPSTHNMDVPNIK	1.281537414	2	3.882569
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.438500483**	**9.9E-20**	**8**
Q8BH00	ELLMLENFIGGK	1.464074639	2	3.593711
Q8BH00	ELNLPFGGMK	1.690034839	1	2.49095
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.155942628	3	5.307595
Q8BH00	ILCGEGVDQLSLPLR	1.473924158	3	4.954574
Q8BH00	ITQLSAPHCK	1.513824623	2	3.129054
Q8BH00	KLSLELGGK	1.307252088	1	2.255054

Q8BH00	NPAIIFEDANLEECIPATVR	1.366018734	2	5.0365
Q8BH00	SSFANQGEICLCTSR	1.44501584	2	3.900934
Q8BH18	**TM117 Transmembrane protein 117**	**1.992045169**	**0.174351**	**2**
Q8BH18	FLKNEQGMENQDK	2.186403868	2	2.344062
Q8BH18	FLKNEQGMENQDK+Oxidation(7	1.52951167		
Q8BH59	**CMC1 Calcium_binding mitochondrial carrier protein Aralar1**	**1.425012866**	**5.22E-05**	**3**
Q8BH59	GLIPQLIGVAPEK	1.396850676	1	3.072476
Q8BH59	IAPLAEGALPYNLAELQR	1.7925514	2	2.851885
Q8BH59	YLGLYNDPNSNPK	1.524675019	2	3.111524
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.290880332**	**0.312977**	**11**
Q8BHN3	AEKDEPGAWEETFK	1.25320412	2	3.063616
Q8BHN3	DDNSVELTVAEGPYK	1.237797165	2	3.410111
Q8BHN3	LVAIVDPHIK	0.991376526	2	2.343493
Q8BHN3	MLDYLQGSGETPQTDIR	1.129720811	2	5.344609
Q8BHN3	REPWLLASQYQDAIR	1.468035532	3	4.330945
Q8BHN3	SGGIERPFVLSR	1.167369274	2	2.453803
Q8BHN3	SIRPGLSPYR	0.731934435	2	2.356498
Q8BHN3	SLLLSVNAR	1.12845361	2	2.487659
Q8BHN3	VDSGYRVHEELRNHGLYVK	0.743903242	2	2.330521
Q8BHN3	VTEGGEPYR	1.413196382	2	2.407525
Q8BHN3	VVIMGAGKPAAVVLQTK	2.40226734	3	3.858203
Q8BI84	**MIA3 Melanoma inhibitory activity protein 3**	**1.620085384**	**0.291859**	**2**
Q8BI84	DDNISALTNCITQLNR	1.817449231	2	2.321241
Q8BI84	TQTAVSIVEEDLK	1.606041408	2	2.435646
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**1.255552485**	**0.638891**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.180310752	1	2.193151
Q8BIJ6	SCQTALAEILDVLVR	1.313704276	2	3.513583
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.060289006**	**0.72125**	**10**
Q8BJ64	ADSAYHPSCTCK	0.201428657	2	3.185607
Q8BJ64	AEVQTLVSR	1.245839502	2	2.887091
Q8BJ64	ELQPGSHVQSDK	1.063431315	2	3.07472
Q8BJ64	ELQPGSHVQSDKEIDAFVR	1.153551891	2	4.245545
Q8BJ64	GGDGPLHVSR	1.03120408	2	2.348651
Q8BJ64	HELGANMYR	0.981415728	2	2.348654
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.309159203	5	5.016565
Q8BJ64	TNHPLHQAFLQAAR	1.518635685	3	4.000042
Q8BJ64	VIGVENLR	1.171595655	2	2.746133
Q8BJ64	VLLLEAGPK	1.718314935	2	2.62868
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**1.418139468**	**0.036141**	**2**
Q8BJY1	GLTHPDDSVK	1.114401485	2	2.456716
Q8BJY1	TVAEIFGNSNYLR	2.424138192	2	2.483907
Q8BKC5	**IPO5 Importin_5**	**1.219548058**	**0.284009**	**2**
Q8BKC5	IFSIIAEGEMHEAIK	1.331767507	2	2.3325
Q8BKC5	VAAAESMPLLLECARVR+Oxidation(6	0.599520041		
Q8BKZ9	**ODPX Pyruvate dehydrogenase protein X component_ mitochondrial**	**1.116322805**	**0.356262**	**2**
Q8BKZ9	HSLDASQGTATGPR	1.094521586	2	3.943347
Q8BKZ9	VSVNDFIIR	3.278770435	2	3.054825
Q8BL66	**EEA1 Early endosome antigen 1**	**0.963552043**	**0.349755**	**2**
Q8BL66	MQAAVTELTAVKAQK	0.508486887	2	2.442981
Q8BL66	QESIKEITNLKDAK	2.841928902	2	2.305933
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.327915302**	**0.12588**	**2**
Q8BL97	NPPGFAFVEFEDPR	1.357093983	2	2.816183
Q8BL97	VYVGNLGTGAGK	1.178530999	2	2.569474
Q8BMA5	**NPAT Protein NPAT**	**1.061739927**	**0.99151**	**2**

Q8BMA5	AKETSNDVPTIMSSLWKK+Oxidation(11	1.132862175		
Q8BMA5	KKLPSSFPAGMDVDK+Oxidation(10	1.04236927		
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**1.43899193**	**0.195253**	**5**
Q8BP47	KEDGTFYEFGDDIPEAPER	0.850894386	2	4.403046
Q8BP47	LEDLVCDVVDR	1.3227546	2	2.816987
Q8BP47	LMTDTINEPILLCR	3.776695777	2	3.340169
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.427431994	2	2.916399
Q8BP47	YGTCPHGGYGLGLER	1.605773859	2	3.160977
Q8BTM8	**FLNA Filamin_A**	**0.912181244**	**0.689698**	**6**
Q8BTM8	AFGPGLQGGNAGSPAR	1.435588326	2	3.561977
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	1.263662494	3	3.62483
Q8BTM8	ANLPQSFQVDTSK	0.977217227	2	2.44741
Q8BTM8	GAGTGGLGLAVEGPSEAK	0.885728305	2	3.723769
Q8BTM8	IVSPSGAAVPCK	1.176274402	2	2.411139
Q8BTM8	VEPGLGADNSVVR	1.39892811	2	2.860118
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.104610234**	**0.775**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	0.871174176	2	3.133554
Q8BU33	LPNSLMGR+Oxidation(5	1.117894948		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.765442183	3	3.958508
Q8BWM0	**PGES2 Prostaglandin E synthase 2**	**1.266761105**	**0.412825**	**2**
Q8BWM0	AFLDFHSLPYQVVEVNPVR	1.312761046	3	3.529848
Q8BWM0	KVPILVAQEGDSLQQLNDSSVIISALK	1.141847664	3	4.620969
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.252106723**	**0.272389**	**2**
Q8BWQ1	ADIWLIR	1.25826842	2	2.448104
Q8BWQ1	IHHDQPVKPLDR	1.246052421	3	3.514179
Q8BWR8	**RHPN2 Rhophilin_2**	**1.413277856**	**0.725675**	**2**
Q8BWR8	ETKEVDFSIVFK	1.235817932	2	2.53472
Q8BWR8	TGAENLLKVATNQK	1.615423109	2	2.485848
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**1.020313992**	**0.878473**	**2**
Q8BX70	ENALSELDVPFKVK	1.015943943	2	2.626139
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19	1.213851083		
Q8BY87	**UBP47 Ubiquitin carboxyl_terminal hydrolase 47**	**1.186887331**	**0.098735**	**2**
Q8BY87	AGGDSGNVDDDCER	1.737827495	2	3.499607
Q8BY87	QNIFDEMKK	1.184802213	2	2.430665
Q8BZI0	**AF1L1 Actin filament_associated protein 1_like 1**	**0.909363626**	**0.255499**	**2**
Q8BZI0	IYDEVPYEK	1.046338332	1	2.0261
Q8BZI0	LSQEKQNSDSDSLGMNDSGSTLGRR	0.523488832	3	3.59391
Q8BZQ7	**ANC2 Anaphase_promoting complex subunit 2**	**1.056366109**	**0.541211**	**2**
Q8BZQ7	EIRNVELLK	1.268629209	2	2.415272
Q8BZQ7	QALEQFNQLSQVLHR	0.808218814	2	2.752257
Q8C6K9	**chain**	**1.262707113**	**0.455402**	**3**
Q8C6K9	NEHSFQVVGIQVR	1.414181345		
Q8C6K9	TMNPAFMGLDRATR+Oxidation(1)Oxidation(6	1.22669099		
Q8C6K9	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1.336776684		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**0.996105663**	**0.803052**	**2**
Q8C7X2	FNVEDGEIVQQVR	1.007149614	2	3.984222
Q8C7X2	VMGDRSVLYK+Oxidation(1	0.946799448		
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.185439574**	**0.406505**	**3**
Q8CC88	FLPSLAQSALEK	1.283429889	2	2.440753
Q8CC88	HQATGELDDAK	1.18543603	2	3.410404
Q8CC88	VSSDQLSSENLTSAVGQK	1.535231209	2	3.207691
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**1.20895004**	**0.455586**	**3**
Q8CDI6	EKELSLEKEQNK	1.562466263	2	2.35146
Q8CDI6	EKVANMEVALDK+Oxidation(5	1.190840229		

Q8CDI6	ELDDRNMEVQRLEALLK	0.928308116	2	2.322781
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.256500111**	**0.464224**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	1.427967404	3	4.686936
Q8CFN2	WVPEITHHCPK	0.388750743	2	2.507734
Q8CFN2	YVECSALTQK	1.261003018	1	2.701882
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.26312945**	**5.19E-06**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	1.232696893	3	3.74259
Q8CG45	EHHFEAIALVEK	1.488275222	2	2.987954
Q8CG45	FFGNSWSETYR	1.240405517	2	3.009532
Q8CG45	FYAYNPLAGGLLTGK	1.358210984	2	4.366068
Q8CG45	MDASASAATVR	1.484436419	2	3.838039
Q8CG45	QVETELLPCLR	1.301902929	2	3.035589
Q8CG45	RMDASASAATVR	1.032347398	2	3.314865
Q8CG45	TTYGTSAPSMTSAALR	1.230556885	2	4.455987
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.230510792	3	5.473598
Q8CG45	WMYHHSQLQGTR	1.09566689	3	3.744586
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.320996752**	**0.316049**	**3**
Q8CG48	EEKLLEK	1.452879988	1	1.927409
Q8CG48	IKALNCEIEELER	1.156942533	2	2.439118
Q8CG48	KIKALNCEIEELER	1.056708735	2	2.647216
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.38685749**	**4.23E-05**	**11**
Q8CGC7	AIQGATSHHLGQNFSK	1.21489915	2	4.599587
Q8CGC7	DQDVEPGAPSMGAK	0.954659797	2	3.358124
Q8CGC7	DQVDSAVQELLQLK	1.357679184	2	4.151786
Q8CGC7	FVELPGAEMGK	2.179451928	2	2.528395
Q8CGC7	GDVSISVEEGKENLLR	1.396220211	2	4.002715
Q8CGC7	GSQFGQSCCLR	1.372817853	2	2.861389
Q8CGC7	KEENLAEWYSQVITK	1.392214055	2	4.466881
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.649713424	2	4.364565
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.344660507	2	4.864162
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	1.21126598	3	3.470516
Q8CGC7	VYEELLAIPVVR	1.676248449	2	3.429921
Q8CGN4	**BCOR BCL_6 corepressor**	**1.18122736**	**0.165253**	**3**
Q8CGN4	FLTDYLNDLQGR	0.999559139	1	1.940411
Q8CGN4	NWLLLSDVLK	4.178001839	2	2.527874
Q8CGN4	VCIELTGLHPKK	1.301232596	2	2.342775
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.077652973**	**0.99297**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(10	1.049281902		
Q8CHB8	DSGGQTLSPSWAAK	1.337925824	1	2.138637
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.661882323**	**0.035753**	**8**
Q8CHM7	DTSKPCLINIMIEPQSTR	1.315779774	3	4.753793
Q8CHM7	GAAYSHAEDSIR	1.065442246	2	3.376467
Q8CHM7	GVVPDNHPNCVGAAR	1.343775758	2	3.246629
Q8CHM7	GYFVQTPEELQDSLR	2.346454573	2	3.832544
Q8CHM7	LVELCNLPFLPTPMGK	1.321101498	2	4.480631
Q8CHM7	NCFIVSEGANTMDIGR	1.616105717	2	4.693971
Q8CHM7	NQEAMGAFQEFPQVEACR	1.42368511	2	6.433916
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	1.473235499	3	4.016663
Q8CIB5	**FERM2 Fermitin family homolog 2**	**1.031518887**	**0.552649**	**2**
Q8CIB5	GCEVTPDVNISGQK	1.030736754	2	3.513737
Q8CIB5	TSTILGDITSIPELADYIK	1.391172451	2	2.721384
Q8CIE6	**COPA Coatomer subunit alpha**	**1.435706878**	**7.88E-10**	**10**
Q8CIE6	ASNLENSTYDLYTIPK	1.60975183	2	4.133943
Q8CIE6	DADSQNPDAPEGK	1.612608757	2	4.018267
Q8CIE6	GITGVDLFGTTDAVVK	1.581493292	2	3.716005

Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.239219079	3	3.780686
Q8CIE6	LLELGPKPEVAQQTR	1.411318657	2	3.152246
Q8CIE6	QELILSNSEDK	1.747381401	2	2.620279
Q8CIE6	QQPLFVSGGDDYK	1.1535373	2	2.711696
Q8CIE6	SILLSVPLLVVDNK	1.246088601	2	4.009565
Q8CIE6	SSGLTAVWVAR	0.903532931	2	2.44891
Q8CIE6	TLDLPIYVTR	1.274515758	2	2.826869
Q8CJ27	**ASPM Abnormal spindle_like microcephaly_associated protein homolog**	**0.782781078**	**0.590299**	**2**
Q8CJ27	ALHHLLTYKHLSAILDALK	1.065358046	2	2.365558
Q8CJ27	FLSLRKTAIWIQR	0.744812001	2	2.636055
Q8CJ40	**CROCC Rootletin**	**1.464323296**	**0.033083**	**4**
Q8CJ40	DLLQLGGELVRTSR	1.284512174	2	2.429625
Q8CJ40	ELEERTGNLGRQR	1.617706225	2	2.402068
Q8CJ40	LRDQTAASAQAQEDAQR	1.596211088	2	2.369804
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9	1.279590451		
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.202302525**	**0.522678**	**4**
Q8JZN5	GIILVGNEEQK	1.220399119	2	2.41553
Q8JZN5	GSNTCEVHFENTR	1.20620776	2	4.527013
Q8JZN5	NLSEFGLIQEK	1.260393453	2	2.462198
Q8JZN5	SGNVTTVMETIGR	0.75490096	2	2.965831
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.267016703**	**0.960485**	**19**
Q8K009	AMVEAVQLIADGK	1.26586342	2	4.194268
Q8K009	ANNTEYGLASGVFTR	1.089371542	2	4.625493
Q8K009	DLGEEALNEYLK	0.970320845	2	3.779577
Q8K009	EESFGPIMVISK	1.282154149	2	3.050856
Q8K009	FLFPEGIK	0.809743032	2	2.455593
Q8K009	FQNGDIDGVLQR	0.915425633	2	3.21425
Q8K009	GVINIIPGSGGVAGQR	1.122429972	2	3.878968
Q8K009	HGSIIYHPSLLPR	1.14890215	2	4.369674
Q8K009	KLGFTGSTSVGK	1.339894526	2	2.497195
Q8K009	KVSLELGGK	0.261350713	1	2.039033
Q8K009	NGLVLFGNDGK	1.24349554	2	2.427232
Q8K009	NLQFEDGK	0.99219803	1	2.186249
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.181442029	3	4.027486
Q8K009	SCDVKPNDTVDSLYNR	4.953302264	2	4.481185
Q8K009	TDVAAPFGGMK+Oxidation(9	1.625444373		
Q8K009	TPQPEEGATYEGIQK	1.004820115	2	2.582869
Q8K009	VSYASLADVDR	1.203613065	2	2.916564
Q8K009	VVGVFTVPDKDGK	1.33944062	2	3.262164
Q8K009	YFAGWCDK	0.98401117	1	2.100296
Q8K1N2	**PHLB2 Pleckstrin homology_like domain family B member 2**	**0.850038035**	**0.949063**	**2**
Q8K1N2	EKENLCNLEKK	0.843928752	2	2.419114
Q8K1N2	LQEETSQRQKLIEK	0.886868185	2	2.380094
Q8K1Q0	**NMT1 Glycylpeptide N_tetradecanoyltransferase 1**	**1.318877868**	**0.652114**	**2**
Q8K1Q0	GNDMDSTQDQPVK	1.942613166	2	2.531109
Q8K1Q0	LGEVVNTHGPVEPDKDNIR	1.047172946	3	3.444547
Q8K1S6	**SPIR2 Protein spire homolog 2**	**1.955708528**	**0.000116**	**3**
Q8K1S6	ALFVETLELR	2.242290231	2	2.505284
Q8K1S6	DTADILLRR	1.856172821	2	2.314963
Q8K1S6	RDAFQSLQGPKWR	1.491644537	2	2.304473
Q8K2H2	**OTU6B OTU domain_containing protein 6B**	**1.451273641**	**0.006217**	**2**
Q8K2H2	EELEQLK	1.452879988	1	2.080839

Q8K2H2	EERIAEAEIENLSGAR	1.195536572	2	2.468031
Q8K2Z4	**CND1 Condensin complex subunit 1**	**1.710084939**	**0.005963**	**2**
Q8K2Z4	AIIDEFEQKLR	1.358065217	2	2.369612
Q8K2Z4	LLESFENMTSQTSLIDLDIGGK	2.088121904	2	2.445446
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**1.310558757**	**0.001901**	**2**
Q8K3J1	ILMWTELIR+Oxidation(2	2.242290231		
Q8K3J1	LCEAICPAQAITIEAEPR	1.293833476	3	4.908556
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.473611325**	**1.99E-06**	**6**
Q8K442	EDVQPLSQAFFK	1.659931937	2	2.891826
Q8K442	GQITAILGHSGAGK	1.470679166	2	3.748363
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	1.472298028	3	4.094284
Q8K442	LTGVCPQCNVQFDFLTVR	1.579410797	2	2.832537
Q8K442	NTQNILVQNLSGGQK	1.332701412	2	2.969511
Q8K442	STLLNVLSGLCVPTK	2.105190986	2	3.794128
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.91473197**	**0.642267**	**12**
Q8K4C0	CCLEEGLEPVCFER	1.235639423	2	4.397594
Q8K4C0	FDHEMFGLKPK	1.488312244	2	3.323276
Q8K4C0	GYPIDILLSSR	1.25550773	2	3.271616
Q8K4C0	HSALGQHPTINDDLPNR	1.14514168	2	4.997354
Q8K4C0	IAVIGSGASGLTCIK	1.455843381	2	4.198352
Q8K4C0	KLPSQSEMMAEINK	0.793331233	2	3.889401
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.945320208	3	4.749394
Q8K4C0	KTILTTEDR	0.87100957	2	2.801741
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	1.595775516	3	3.778594
Q8K4C0	SDDIGGLWR	1.042211377	2	3.027843
Q8K4C0	VFPPNLEKPTLAIIGLIQPLGAIMPISELQGR	0.989531257	4	5.019901
Q8K4C0	WATQVFK	1.485936406	1	1.954203
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.3872141**	**0.522219**	**3**
Q8K4T4	EVLNLTK	1.217581303	1	2.118205
Q8K4T4	IEELEETNKSLQK	1.699685929	2	2.558
Q8K4T4	IHELMNK	2.060433313	1	2.092971
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.28619676**	**0.002203**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	1.284693814	2	3.833237
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.369312338	2	5.809548
Q8K4Z5	**SF3A1 Splicing factor 3A subunit 1**	**1.734843837**	**0.015097**	**2**
Q8K4Z5	HKVSEFKEGK	1.621322788	2	2.300611
Q8K4Z5	IGEEEIQKPEEK	1.736659932	2	2.601644
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.273108946**	**0.004392**	**5**
Q8K586	FNVWDTAGQEK	1.072714879	2	3.311691
Q8K586	HLTGEFEK	1.332506502	1	2.043822
Q8K586	LVLVGDGGTGK	1.102933096	2	2.372777
Q8K586	NLQYYDISAK	1.249732288	1	2.135574
Q8K586	VCENIPIVLCGNK	1.164699734	2	3.72718
Q8K5B3	**MCFD2 Multiple coagulation factor deficiency protein 2 homolog**	**0.928518487**	**0.230328**	**2**
Q8K5B3	DDDKNNDGYIDYAEFAK	0.907218875	2	4.353566
Q8K5B3	STVHDQEHIMEHLEGVINQPEAEMSPQELQLHYFK	2.002764737	4	5.870281
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**1.033331347**	**0.079474**	**3**
Q8QZY1	VFSDEVQQQAQLSTIR	0.918061994	2	3.853329
Q8QZY1	VSGGPSLEQR	1.470017952	2	2.627123
Q8QZY1	VYEIQDIYENSWTK	1.623483606	2	3.926468

Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.35809404**	**0.000482**	**6**
Q8R081	ASLNGADIYSGCCTLK	3.831031276	2	2.955995
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	0.907000745	3	5.029496
Q8R081	SDALETLGFLNHYQMK	1.541436381	2	3.686985
Q8R081	SKPGAAMVEMADGYAVDR	0.64997152	2	3.893934
Q8R081	SSSGLLEWDSK	0.801007963	2	2.327813
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	1.273203788	3	7.14297
Q8R0F9	**S14L4 SEC14_like protein 4**	**0.949314165**	**0.094178**	**5**
Q8R0F9	FDNTYSLLHTK	1.764488736	2	3.130025
Q8R0F9	GSSHQVENEILFPGCVLR	0.947329694	2	4.755095
Q8R0F9	VCEMLLHECELQSQK	1.926591308	2	4.976276
Q8R0F9	VGYTAEVLLPDK	1.397695742	2	2.956088
Q8R0F9	VGYTAEVLLPDKACEEK	1.145856764	2	2.448467
Q8R0K2	**TRI31 E3 ubiquitin_protein ligase TRIM31**	**1.387490139**	**0.317592**	**2**
Q8R0K2	LQSSSMELLKDIKDALSR	1.324918655	2	2.552
Q8R0K2	QRLDEEESFLLSR	2.017149846	2	2.431845
Q8R164	**BPHL Valacyclovir hydrolase**	**1.05574167**	**0.456473**	**3**
Q8R164	FADEFNR	1.963279275	2	2.366869
Q8R164	FTLVAWDPR	1.269429642	2	2.982094
Q8R164	TDFAPQLQSLNK	0.971036586	2	3.728002
Q8R1F5	**HYI Putative hydroxypyruvate isomerase**	**1.359732976**	**0.275142**	**2**
Q8R1F5	GDTVEGLSWLR	1.330418397	2	3.142664
Q8R1F5	GEMGLGAVPGR	2.232445596	2	2.537495
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**1.252286433**	**0.254298**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	2.364889089	2	4.48738
Q8R1V4	QLLDQVEQIQK	1.149476059	2	2.896046
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**1.04316614**	**0.093749**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	1.087402281	2	3.946125
Q8R3Q6	NCIAQTSAVVK	1.358922355	2	2.791858
Q8R491	**EHD3 EH domain_containing protein 3**	**1.374657124**	**0.01467**	**6**
Q8R491	ADQIETQQLMR	1.659800688	2	2.612211
Q8R491	GGAFEGTLQGPFGHGYGEGAGEGIDDAEWVVAR	3.508404009	3	4.332998
Q8R491	LDISDEFSEVIK	1.189417633	2	3.637642
Q8R491	LFEAEEQDLFK	2.025960426	2	3.495023
Q8R491	MQDQLQAQDFSK	1.524332615	2	3.838326
Q8R491	QEETQRPVQMVK	1.545459607	2	2.753904
Q8VBU2	**NDRG2 Protein NDRG2**	**0.828535588**	**0.016675**	**6**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.698676012	3	5.113845
Q8VBU2	LDPTQTSFLK	1.261056262	1	2.088614
Q8VBU2	MADSGGQPQLTQPGK	1.046013329	2	3.133596
Q8VBU2	SLITHAPNLENIELYWNSYNNR	1.451951616	3	4.667002
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.811462815	2	4.516999
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.607895933	2	4.740813
Q8VC12	**HUTU Urocanate hydratase**	**0.986785186**	**9.9E-20**	**9**
Q8VC12	DHHDVSGTDSPFR	1.842127487	2	2.683586
Q8VC12	HQLVVGSQAR	0.595578273	2	2.913155
Q8VC12	LLALEFAQELR	2.503112476	2	3.961465
Q8VC12	LQYMDNIR	1.277143967	2	2.428343
Q8VC12	LVITNGMVIPNYSSR	1.34141728	2	3.825133
Q8VC12	MMLSWDVSNGVAR	1.243647526	2	3.173674
Q8VC12	VAIAVAINQAIASGK	2.173317325	2	4.001644
Q8VC12	VFVTSGLGGMSGAQAK	1.105599766	2	4.541272
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9	0.947471136		
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**1.221271107**	**0.07925**	**2**

Q8VDC1	GLELQVMQLQQEK	1.335949759	2	2.390159
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(0	0.715228892		
Q8VDG5	**PPCS Phosphopantothenate__cysteine ligase**	**1.251449883**	**0.459404**	**2**
Q8VDG5	FLDNFSSGR	1.78537298	2	2.456367
Q8VDG5	LETDPDIIISR	1.206558924	2	2.58724
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**0.247337323**	**0.001189**	**2**
Q8VE11	TMKGFMVLIEK+Oxidation(1	0.247337323		
Q8VE11	TMKGFMVLIEK+Oxidation(5	0.247337323		
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**1.114277178**	**0.765229**	**5**
Q8VED5	FLEQQNKVLETK	0.164275467	2	3.668514
Q8VED5	NKYEDEINK	1.184802213	2	2.954535
Q8VED5	NKYEDEINKR	1.067205171	3	3.337077
Q8VED5	NLDLDSIIAEVK	0.745458812	2	3.541003
Q8VED5	YEDEINK	0.983547465	1	2.341678
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.301156936**	**1.02E-14**	**12**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.31277918	3	4.774993
Q8VEK3	FIEIAAR	1.739705752	1	1.907015
Q8VEK3	GYFEYIEENK	0.930443199	2	3.372343
Q8VEK3	LLEQYKEESK	1.395002754	2	3.26815
Q8VEK3	LLEQYKEESKK	1.301232596	2	3.668766
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.078066432	3	4.755062
Q8VEK3	NFILDQTNVSAAAQR	1.162641607	2	4.89524
Q8VEK3	NGQDLGVAFK	1.312860725	2	2.400917
Q8VEK3	TCNCETEDYGEK	1.532775718	2	3.575615
Q8VEK3	VSELKEELK	2.827390556	2	2.891933
Q8VEK3	VSELKEELKK	1.502160502	2	2.689186
Q8VEK3	YNILGTNTIMDK	1.424023686	2	3.655999
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**1.689566116**	**0.063058**	**8**
Q8VHE9	ATVQSVLLDSAGR	1.494278601	2	3.868125
Q8VHE9	FLPLPLTQLLNK	2.297488856	2	3.22782
Q8VHE9	GATYGADHDLAR	1.71452058	2	3.267914
Q8VHE9	NLYSDLQALGSK	1.720401248	2	3.619696
Q8VHE9	RPPEPLVTDK	1.804522015	2	2.954525
Q8VHE9	RPPEPLVTDKEAR	2.046962204	3	4.206893
Q8VHE9	VESVTGGSPLTNQYYLAAHR	1.366241934	2	3.979195
Q8VHE9	VVAHGVSHAILLK	2.390062137	2	2.874022
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**1.444574739**	**0.483463**	**4**
Q8VHF5	AYAEGINR	1.172916113	2	2.518066
Q8VHF5	EGSSIGAIDSK	1.396867833	2	2.350767
Q8VHF5	GLVYETSVLDPDEGIR	2.44763318	2	4.343808
Q8VHF5	GYSIPECQK	1.038358228	2	2.80161
Q8VHK7	**HDGF Hepatoma_derived growth factor**	**0.891202407**	**0.947021**	**3**
Q8VHK7	GFSEGLWEIENNPTVK	0.769532449	2	3.702526
Q8VHK7	NSTPSEPDSGQGPPPEEEEGEEEAAKEEAEAQGVR	0.757119855	3	6.10673
Q8VHK7	SCAEEPEVEPEAHEGDGDKK	1.48963354	3	3.940601
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.435022826**	**0.577982**	**4**
Q8VHT6	FAHDFLFTPVEASLLAPQTK	2.182894185	2	4.367731
Q8VHT6	ILDLGSGSGR	1.103149052	2	2.908334
Q8VHT6	SLQNVHEEVISR	1.598432479	2	3.208845
Q8VHT6	TSADLQTNACVTPAK	1.196826939	2	3.875553
Q8VHX6	**FLNC Filamin_C**	**1.160930864**	**0.604651**	**3**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.160055719	2	3.973449
Q8VHX6	IECDDKGDGSCDVR	1.522103105	2	3.443933
Q8VHX6	LIALLEVLSQK	2.444446095	2	2.628568
Q8VI04	**ASGL1 L_asparaginase**	**1.048002913**	**0.812915**	**5**
Q8VI04	DLSAGAVSAVRCIANPVK	1.279204484	2	2.353392

Q8VI04	FAADMGIPQTPAEK	1.048042314	2	3.44424
Q8VI04	GNLAYATSTGGIVNK	1.031449016	2	4.358949
Q8VI04	NSGTVGAVALDCK	1.200083371	2	3.290692
Q8VI04	TVDEAATLALDYMK	1.322580812	2	3.573679
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**0.868412788**	**5.23E-05**	**5**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.640649341	2	4.013859
Q8VID1	LAEDGAHVVISSR	1.12521014	2	3.70507
Q8VID1	NFAAELAPK	0.754296253	2	2.458763
Q8VID1	TALLGLTK	1.388154953	2	2.415642
Q8VID1	VNCLAPGLIK	1.724764374	2	2.516085
Q8VIF7	**SBP1 Selenium_binding protein 1**	**1.290797035**	**6.48E-05**	**11**
Q8VIF7	CGPGYATPLEAMK	0.392583284	2	3.107667
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.71810063	2	5.423259
Q8VIF7	GGFVLLDGETFEVK	2.21555868	2	3.909051
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	1.778681603	2	3.779766
Q8VIF7	HEIIQTLQMK	1.560474749	2	2.84595
Q8VIF7	HNIMVSTEWAAPNVFK	1.586744543	2	4.609447
Q8VIF7	LTGQIFLGGSIVK	1.368385244	2	3.018772
Q8VIF7	NEGGTWSVEK	1.285473682	2	3.161759
Q8VIF7	NTGIEAPDYLATVDVDPK	1.217585063	2	4.164054
Q8VIF7	QYDISNPK	1.162478907	1	2.116134
Q8VIF7	VIEPNEIHAK	1.640179015	2	2.967858
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**0.970236662**	**0.99712**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	0.964324582	2	3.206601
Q8VIJ6	MEELHSQEMQK	1.089780572	2	3.795302
Q8VIJ6	RMEELHSQEMQK	1.091100004	2	3.900165
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**1.123836087**	**0.765551**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	1.471511489	2	5.409288
Q91VA0	AILPFDLQIIDEK	0.919721242	2	3.857377
Q91VA0	GNILPPNTEGYIGIR	0.888513212	2	2.909138
Q91VA0	KVEFVSELPK	0.885615559	2	2.901508
Q91VA0	NKEFGQL	1.398951647	1	2.148697
Q91VA6	**PDIP2 Polymerase delta_interacting protein 2**	**1.065342566**	**0.665998**	**2**
Q91VA6	VLETVGVFEVPK	1.03042095	2	3.40001
Q91VA6	VTVIPFYMGMR+Oxidation(9	1.755531787		
Q91VM5	**RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1**	**1.074431058**	**0.540667**	**2**
Q91VM5	LFIGGLNTETNEK	0.83763089	2	2.791485
Q91VM5	VEQATKPSFESGR	1.21811481	2	3.938913
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.943020959**	**0.99529**	**2**
Q91VM9	IIAINVNDPEAEK	0.857162958	2	3.218228
Q91VM9	MEIATEEPLNPIK	1.504924784	2	4.434556
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**1.144309069**	**0.488234**	**6**
Q91W43	AGHQLQHDLFFDTLK	0.961332999	2	3.029573
Q91W43	DISLVHSMIPLGSCTMK	1.049996994	2	2.726485
Q91W43	EMLQALGLASIDELIEK	1.386285594	2	2.544508
Q91W43	IDDIYGDQHLVCTCPPMEVYESPFSEQK	1.835361039	3	4.430251
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	2.701577171	3	4.648387
Q91W43	VSFQPNSGAQGEYAGLATIR	1.569847546	2	5.203534
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.471299395**	**0.278687**	**3**
Q91W90	GTVLALTEK	1.957663149	2	2.391437
Q91W90	SFEDTIAQGITFVK	1.487354276	2	4.028061
Q91W90	VDCTQHYAVCSEHQVR	1.241132033	3	4.488551

Q91WL5	**CP4CA Cytochrome P450 4A12A**	**1.093836016**	**0.836574**	**2**
Q91WL5	FELLPDPTR	1.465975274	2	2.666255
Q91WL5	IQLQDEEELEK	1.093829753	2	2.487579
Q91X77	**CY250 Cytochrome P450 2C50**	**1.06680354**	**0.964452**	**5**
Q91X77	EHEESLDVTIPR	1.21823895	2	2.307839
Q91X77	IKEHEESLDVTIPR	1.047044501	3	3.663489
Q91X77	NFLLEK	1.096145291	1	2.102529
Q91X77	NYFIPK	0.828539163	1	1.920561
Q91X77	YALLLLLK	1.263484261	2	2.921456
Q91X78	**ERLN1 Erlin_1**	**1.208168544**	**0.220945**	**4**
Q91X78	DLNTMAPGLTIQAVR	1.36639281	2	3.442455
Q91X78	ISEIEDAAFLAR	1.298926077	2	2.978405
Q91X78	RISEIEDAAFLAREK	1.441796188	2	2.307327
Q91X78	SVQTTLQTDEVK	0.90097666	2	3.096241
Q91Y78	**UCHL3 Ubiquitin carboxyl_terminal hydrolase isozyme L3**	**1.182284457**	**0.821777**	**2**
Q91Y78	FLEESVAMSPEER	1.353841995	2	3.260727
Q91Y78	HLENYDAIR	1.155266341	2	2.582448
Q91Y81	**SEPT2 Septin_2**	**1.232272635**	**0.340841**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	1.988926216	2	2.660184
Q91Y81	ILDEIEEHSIK	1.138697958	2	2.653354
Q91Y81	KVENEDMNKDQILLEK	1.089486709	3	3.692378
Q91Y81	LTVVDTPGYGDAINSR	0.998830381	2	4.378148
Q91YP0	**L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial**	**1.093673087**	**0.838033**	**3**
Q91YP0	LIQQEDIK	1.070313603	2	2.400776
Q91YP0	LIVAVEQEEIPR	1.451894188	2	2.803038
Q91YP0	NAPSPAATSSLAISR	1.009309825	2	3.297056
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.135719756**	**0.000292**	**10**
Q91YT0	GAGAYICGEETALIESIEGK	1.459284393	2	2.575128
Q91YT0	GDARPAEIDSLWEISK	1.668134297	2	2.877144
Q91YT0	GEFYNEASNLQVAIR	1.509827538	2	3.552352
Q91YT0	GGAGFPTGLK	1.24414442	2	2.37067
Q91YT0	HFRPELEDR	1.734403594	2	2.331968
Q91YT0	KTSFGSLKDEDR	1.311086197	2	3.480266
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.829627719	3	4.197679
Q91YT0	LVEGCLVGGR	1.024539995	2	2.743399
Q91YT0	TSFGSLKDEDR	1.417057923	2	2.49589
Q91YT0	YLVVNADEGEPGTCK	1.128317318	2	4.941728
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.122124034**	**5.27E-10**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.468949827	3	6.776829
Q91Z53	LLDAAGANLR	0.989878639	2	3.262514
Q91Z53	NCVILPHIGSATYK	0.864366605	2	3.70573
Q91Z53	NTMSLLAANNLLAGLR	1.586437259	2	4.739762
Q91Z53	RLPEAIEEVK	1.070539594	3	3.300493
Q91Z53	VISTLSVGVDHLALDEIK	1.884010705	2	4.75026
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**1.302394079**	**9.9E-20**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	2.141934479	2	4.699468
Q91ZJ5	GGTLTQYEGK	1.155686948	2	2.371033
Q91ZJ5	GLPDNISSVLNK	1.255792546	2	3.376895
Q91ZJ5	GTVIIIANHGDR	1.444105031	2	3.008195
Q91ZJ5	IDIPPGAVLENK	1.230965721	2	2.877012
Q91ZJ5	IQRPPEDSIQPYEK	1.422962349	3	5.178171

Q91ZJ5	LNGGLGTSMGCK	1.750345916	2	2.969231
Q91ZJ5	LVEIAQVPK	1.525722	2	3.451312
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.511789487	2	5.052098
Q91ZJ5	RCEFVMEVTNK	1.218283395	2	2.375895
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	1.844600592	3	3.335068
Q91ZJ5	SFENSLGINVPR	1.326976187	2	3.442564
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	1.217954111	2	5.313269
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.39940565	2	4.49399
Q91ZU6	**DYST Dystonin**	**0.992199258**	**0.154927**	**2**
Q91ZU6	LDMLQQIATR+Oxidation(2	1.525925368		
Q91ZU6	SAETNIDQDITNLK	0.67497334	2	2.373625
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**1.744785282**	**0.223708**	**2**
Q91ZV0	CGDLECETLISRVLALR	1.746766474	2	2.419046
Q91ZV0	KMLDQDDIVENDK+Oxidation(1	1.513431159		
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.208244777**	**0.376146**	**6**
Q91ZX7	CLQGACVVNK	1.408527195	2	2.432559
Q91ZX7	GCHVNECLSR	1.100664543	2	2.703519
Q91ZX7	ILQEDFTCR	1.084781512	2	2.494498
Q91ZX7	MYDAQQQQVGTNK	1.035602768	2	4.437589
Q91ZX7	TVLWPNGLSLDIPAGR	0.675991547	2	2.490558
Q91ZX7	VFFTDYGQIPK	1.311675162	2	3.277374
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.913884517**	**1E-12**	**2**
Q920A6	GLAEVSDIAEQVLNAVNK	1.915263435	3	5.645745
Q920A6	NTDGVNFYNILTK	1.386732743	2	2.912838
Q920D2	**DYR Dihydrofolate reductase**	**1.413026975**	**9.9E-20**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	1.314727719	2	4.677299
Q920D2	LIEQPELASK	1.041586671	2	3.003575
Q920D2	LLPEYPGVLSEIQEEK	1.439192977	2	3.704051
Q920D2	NGDLPWPLLR	1.335904608	2	3.231205
Q920F3	**KHDR2 KH domain_containing_ RNA_binding_ signal transduction_associated protein 2**	**1.025312387**	**0.316873**	**2**
Q920F3	LQEETGAKMSILGKGSMR+Oxidation(8	1.768961571		
Q920F3	MSHALEEIKK	1.023989847	1	2.259695
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**1.244557672**	**0.559398**	**5**
Q920F5	ADLLEAQALK	1.218574345	2	2.338957
Q920F5	EIAEVTGDPVHESLK	1.357389882	2	3.437613
Q920F5	ISECEAVHPVK	1.259685753	2	3.358164
Q920F5	LCSGLTASAMDELLR	0.812137808	2	2.30838
Q920F5	WLLGLLNVQGK	1.228513144	2	3.381225
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**0.999392048**	**0.430288**	**4**
Q920J4	AGCECLNESDEHGFDNCLR	1.172240306	3	4.038232
Q920J4	IDQYQGADAVGLEEK	0.87071789	2	4.823668
Q920J4	QHLENDPGSNEDTDIPK	1.88344931	2	2.385123
Q920J4	SEPTQALELTEDDIKEDGIVPLR	1.795543009	2	3.405476
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.304303059**	**0.000136**	**18**
Q920L2	ACALSIAESCRPGDK	0.753570801	2	2.870187
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.297917711	3	4.506897
Q920L2	ANAGEESVMNLDK	1.296064996	2	3.645887
Q920L2	GEGGILINSQGER	0.982010574	2	4.062121
Q920L2	GVIALCIEDGSIHR	1.256324158	2	3.355162
Q920L2	HTLSYVDTK	2.370016244	2	2.489301
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.224867055	3	6.760015
Q920L2	IDEYDYSKPIEGQQK	1.234231283	2	4.476025
Q920L2	KHTLSYVDTK	0.597810136	2	2.765818

Q920L2	NTIIATGGYGR	1.07197091	2	2.785492
Q920L2	SMQSHAAVFR	1.341141323	2	2.690073
Q920L2	TGHSLLHTLYGR	0.872772517	2	2.955507
Q920L2	TLNEADCATVPPAIR	1.133855566	2	3.690838
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.323088969	2	5.698668
Q920L2	VGSVLQEGCEK	1.212960762	2	3.540959
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	2.283120328	3	4.921842
Q920L2	VSQLYGDLQHLK	1.187679545	2	3.496259
Q920L2	VTLDYRPVIDK	1.105923498	2	2.975891
Q920P0	**DCXR L_xylulose reductase**	**1.203794241**	**0.761173**	**7**
Q920P0	ALTNHTVYCSTK	1.164881691	2	3.151167
Q920P0	AVVQVSQIVAR	1.316011134	2	3.169536
Q920P0	GVPGAIVNVSSQASQR	1.052213942	2	5.78407
Q920P0	SSMTTGSALPVDGGFLAT	1.293442341	2	2.857385
Q920P0	STVLALQAAGAQVVAVSR	1.206241893	2	3.918899
Q920P0	TREDLDSLVR	1.138025263	2	2.96284
Q920P0	VNAVNPTVVMTPMGR	1.628126282	2	3.441971
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.123666135**	**0.01051**	**5**
Q921F2	FGGNPGGFGNQGGFGNSR	1.11877145	2	4.413055
Q921F2	FTEYETQVK	1.348196926	2	2.636263
Q921F2	GISVHISNAEPK	1.096186677	2	2.528919
Q921F2	KDLKTGHSK	1.150931273	2	2.442498
Q921F2	TSDLIVLGLPWK	1.40912539	2	3.272691
Q921M3	**SF3B3 Splicing factor 3B subunit 3**	**0.911779616**	**0.664432**	**3**
Q921M3	FLAVGLVDNTVR	1.721776207	2	2.834676
Q921M3	LPPNTNDEVDEDPTGNK	0.772580561	2	2.686201
Q921M3	TVLDPVTGDLSDTR	0.924048816	2	2.665644
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.291536547**	**9.9E-20**	**7**
Q922F4	ALTVPELTQQMFDAK	1.486628187	2	3.984235
Q922F4	ALTVPELTQQMFDAK+Oxidation(10	1.244505732		
Q922F4	GHYTEGAELVDSVLDVVR	1.388137095	2	6.636072
Q922F4	IREEYPDR	1.291280032	2	2.97651
Q922F4	MASTFIGNSTAIQELFK	1.703716857	2	4.346158
Q922F4	NMMAACDPR	1.717159968	2	2.751477
Q922F4	NSSYFVEWIPNNVK	1.407808891	2	4.748125
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.274868084**	**0.041143**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4	1.316446931		
Q922J3	HEEILQNLQKMLADTEDK	1.159922889	2	2.334868
Q923D2		**1.638968265**	**0.027592**	**4**
Q923D2	HDLGHFMLR	1.291943423	3	3.361802
Q923D2	LQDVTDDHIR	1.541696414	2	3.166772
Q923D2	TGLTTLAQAVQAGYEVTVLVR	1.650066762	3	4.15661
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	1.373583954	3	4.193653
Q923K9	**A1CF APOBEC1 complementation factor**	**1.166850609**	**0.037188**	**3**
Q923K9	LAPQILEEICQK	2.584424759	2	2.901546
Q923K9	TGYSLVQENGQR	1.166138116	2	2.519145
Q923K9	VTEGVVDVIVYPSAADK	1.151046403	2	3.785762
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**1.387922178**	**0.167285**	**2**
Q923M1	SAVYPTSAVQMEAALK	1.561439573	2	4.215207
Q923M1	VISAEEALPGR	1.32271051	2	2.917979
Q923V8	**SEP15 15 kDa selenoprotein**	**1.187722864**	**9.8E-05**	**3**
Q923V8	GCCQEEAQFETK	1.184881225	2	4.156827
Q923V8	LLDDNGNIAEELSILK	1.942652045	2	4.078097
Q923V8	WNTDSVEEFLSEK	2.122645356	2	2.768538

Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**2.264676022**	**0.102141**	**5**
Q924C3	AEYLHTWGGLLPVISK	2.270953561	3	3.917227
Q924C3	ELESPAAASLLAPMDLGEEPLEK	2.151525008	2	4.407134
Q924C3	GQPIWVTANHQEVR	0.864165746	2	3.336105
Q924C3	SGTYFWPGSDVEIDGILPDIYK	1.899563804	2	2.518334
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	1.613114391	2	3.879627
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.114093232**	**0.815372**	**14**
Q924S5	AGVTCIILPAENR	0.969696021	2	2.314547
Q924S5	AQLSATVLTLLIK	0.97850511	2	3.453834
Q924S5	AQSVLEEDHYGMEDVK	1.223068602	2	4.268158
Q924S5	EHQEALAVER	1.36374692	2	2.519455
Q924S5	ELGLEKDDKDAIEEK	0.87276498	2	3.74027
Q924S5	FSVGGMTDVAEIK	1.076637594	2	3.070374
Q924S5	GYQGDPSSALLELLDPEQNANFLDHYLDVPVDLSK	1.331947712	3	5.099291
Q924S5	HVMDVVDEELSK	0.882349243	2	3.625859
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.57454207	3	5.925712
Q924S5	MEMINVSGYVAQEK	2.14392854	2	2.660993
Q924S5	QLEVEPEGLEPEAENK	1.083499189	2	4.350005
Q924S5	QSDENLDLAR	1.513435764	2	2.467745
Q924S5	TENPLVLIDEVDK	1.364083372	2	2.996889
Q924S5	VLEFIAVSQLR	0.950968461	2	2.776484
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**1.614290049**	**0.148456**	**2**
Q924W5	ELDMKEKELQEK	3.641240331	2	2.372996
Q924W5	TKEQINQGEERLTELK	1.572176131	2	2.557731
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.079650579**	**8.3E-13**	**4**
Q99020	EYFGQFGEIEAIELPIDPK	2.994441069	2	3.560331
Q99020	FGEVVDCTIK	0.608462407	2	3.208948
Q99020	IFVGGLNPEATEEK	1.678243597	2	4.174219
Q99020	MFVGGLSWDTSK	1.606025878	2	2.557251
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**1.132116642**	**0.957699**	**2**
Q99068	EELKHFEAKIEK	1.144196187	2	2.439551
Q99068	HVESIGDPEHISR	1.12645341	3	4.120231
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.439017911**	**0.124952**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.982575096	2	2.98469
Q99JI4	RLDEELEDAEK	1.625584108	2	3.186154
Q99JI4	VNEIVETNRPDSK	1.43380954	2	3.70418
Q99JW2	**ACY1 Aminoacylase_1**	**1.082713068**	**0.380723**	**3**
Q99JW2	FIEDTAAEK	1.07540783	2	2.690768
Q99JW2	SVSIQYLEAVR	1.750056364	2	2.56252
Q99JW2	TIHMTFVPDEEVGGHK	0.684144686	3	3.919342
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**1.332585149**	**0.122709**	**2**
Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(13	1.167826546		
Q99KK9	YDLTVPFAR	1.492904773	2	2.364349
Q99KN9	**EPN4 Clathrin interactor 1**	**1.222414748**	**0.618722**	**3**
Q99KN9	GEFKDEEETVTTK	1.175642351	2	3.58409
Q99KN9	HIHITQATETTTTR	1.259911256	2	3.353887
Q99KN9	IGSTIDDTISK	1.130406392	2	2.55054
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.973733041**	**0.999999**	**3**
Q99L04	ATAQEAQSLGGR	0.872261808	2	3.323043

Q99L04	CVPVVCDSSQESEVK	1.179887736	2	4.306995
Q99L04	GQVCVVTGASR	0.991130164	2	2.812001
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.279707025**	**0.080896**	**5**
Q99LF4	GLGHQVATDALVAMEK	1.039445612	2	3.692619
Q99LF4	NLDFQDVLDK	1.96311907	2	3.083274
Q99LF4	NVTDVVNTCHDAGISK	1.157658192	2	4.334417
Q99LF4	NYNDELQFLDK	1.591833406	2	3.183576
Q99LF4	TNLDESDVQPVK	1.157645669	2	3.466625
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.431660007**	**0.043076**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11	1.431660007		
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5	1.431660007		
Q99M73	**KRT84 Keratin_ type II cuticular Hb4**	**1.384608846**	**0.703912**	**2**
Q99M73	CKLADLEGALQQAKQDMAR	1.090947617	2	2.672738
Q99M73	EYQELMNVK	1.666338005	1	2.093333
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**0.93226741**	**0.615732**	**2**
Q99M87	GGPSVDPEELFR	1.26146589	2	2.351203
Q99M87	GSIITNPCVVCR	0.93171223	2	2.977026
Q99ML5	**PCYOX Prenylcysteine oxidase**	**1.451075961**	**0.067428**	**2**
Q99ML5	ELGLSSVPASGGLVGVYNGK	1.505981458	2	2.971882
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	1.449295053	3	4.824368
Q99MS0	**S14L2 SEC14_like protein 2**	**1.340467605**	**0.123255**	**6**
Q99MS0	AGEMTEVLPNQR	1.362453618	2	3.568959
Q99MS0	AGEMTEVLPNQR+Oxidation(3	1.557710108		
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	0.962817434	3	4.967525
Q99MS0	INYGGDIPK	1.188803182	2	2.419945
Q99MS0	QQYEHSVQISR	1.338803096	2	2.393233
Q99MS0	YNSHMVPEDGTLTCSEPGIYVLR	1.42801955	3	3.570745
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.938761278**	**0.505515**	**8**
Q99MZ8	GFSVVADTPELQR	1.231040649	2	3.647566
Q99MZ8	MGPSGGEGIEPER	1.109142055	2	3.356931
Q99MZ8	MGPSGGEGIEPERR	1.155249469	2	2.422318
Q99MZ8	QQSELQSQVR	1.258163033	2	2.984425
Q99MZ8	QSFTMVADTPENLR	0.899512973	2	3.562724
Q99MZ8	TGDTGMLPANYVEAI	1.44725085	1	2.204384
Q99MZ8	TQDQISNIK	1.163024401	2	2.709134
Q99MZ8	YHEEFEK	0.673766803	2	2.410148
Q99N27	**SNX1 Sorting nexin_1**	**1.226410195**	**0.095047**	**2**
Q99N27	LQEVECEEQR	1.125806501	2	2.495664
Q99N27	SLAMLGSSEDNTALSR	1.789041768	2	3.113087
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**1.397970857**	**0.530899**	**4**
Q99NA5	ENTEGEYSGIEHVIVDGVVQSIK	1.3090405	3	3.343175
Q99NA5	HMGLFDHAAK	2.364813339	3	3.410003
Q99NA5	IEAACFATIK	0.978216889	2	2.614379
Q99NA5	NVTAIQGPGGK	1.362373813	2	2.542091
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**1.148983208**	**0.909365**	**2**
Q99NB7	GSISNTNVEALK	1.186425956	2	2.565649
Q99NB7	KGSISNTNVEALK	0.851885138	2	3.257645
Q99NB9	**SF3B1 Splicing factor 3B subunit 1**	**0.907487276**	**0.589821**	**3**
Q99NB9	EWMRICFELLELLK+Oxidation(2	0.801445763		
Q99NB9	GDTPGHATPGHGGATSSAR	1.079939226	3	3.773548
Q99NB9	WDQTADQTPGATPK	0.418530401	2	2.514996
Q99P39	**NFS1 Cysteine desulfurase_ mitochondrial**	**1.172927792**	**0.984067**	**2**
Q99P39	AIGTDEDLAHSSIR	0.918415126	2	2.718382
Q99P39	VEALQSGGGQER	1.173141277	2	2.998538
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**0.983271534**	**5.74E-06**	**9**

Q99PF5	AINQQTGAFVEISR	1.309612709	2	3.490928
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	1.254157141	2	6.940836
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	2.078456671	2	4.965032
Q99PF5	IGQQPQQPGAPPQQDYTK	0.730857369	2	4.048737
Q99PF5	IINDLLQSLR	1.901725748	2	3.1882
Q99PF5	SVSLTGAPESVQK	0.974935574	2	2.56959
Q99PF5	VGGGIDVPVPR	1.010952132	2	3.211156
Q99PF5	VQISPDSGGLPER	0.586643572	2	2.486714
Q99PF5	VQQACEMVMDILR	1.33207556	2	2.348382
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.585627879**	**9.9E-20**	**20**
Q99PL5	AMEALALAER	0.744302235	2	2.932542
Q99PL5	DALNQATSQVESK	3.490996784	2	3.612901
Q99PL5	EAEETQNSLQAECDQYR	1.24452669	2	5.36002
Q99PL5	EHTSHLEAELEK	1.671384955	2	3.49551
Q99PL5	EQEIAAVQAR	2.537261715	2	2.483325
Q99PL5	GELESSDQVR	1.078312228	2	3.136981
Q99PL5	HLEDIVEK	1.473397906	2	2.382866
Q99PL5	HMAAASAECQNYAK	1.863910102	2	4.478719
Q99PL5	HMAAASAECQNYAK+Oxidation(1	1.444753187		
Q99PL5	IQEELEK	1.452879988	1	2.338361
Q99PL5	LIEILSEK	1.569497061	1	2.150092
Q99PL5	LKELESQVSCLEK	1.511495268	2	4.277822
Q99PL5	LLATEQEDAAVAK	1.33354324	2	3.70648
Q99PL5	LQQENSILR	0.977929921	2	2.679968
Q99PL5	LQSSEVEVK	1.563615047	2	2.734719
Q99PL5	QLLLESQSQLDEAK	0.89162686	2	2.334303
Q99PL5	TILAETEGMLK	2.067889913	2	2.784647
Q99PL5	TLQEQLENGPNTQLAR	1.095530127	2	5.0442
Q99PL5	TLVSTVGSMVFSEGEAQR	1.701115805	3	4.52774
Q99PL5	VEPAVSSIVNSIQVLASK	1.629339338	2	4.425313
Q99PP2		**1.347241955**	**0.002417**	**69**
Q99PP2	AAGSLLTDECR	1.05423224	2	2.995425
Q99PP2	ADSAEYSVMTTGGQSSAK	2.56632498		
Q99PP2	AEVSELPSVVR	1.138596023	2	3.119912
Q99PP2	ALLTPVAIAAGR	1.325427552		
Q99PP2	ASMMGQRASLLTAR+Oxidation(2)Oxidation(3	1.384191862		
Q99PP2	AVAENQPFLIEAMTYR	1.260503959	2	3.590897
Q99PP2	AVDEAADALLK	1.511051554	2	2.59679
Q99PP2	DQMVKNNHFTLK+Oxidation(2	1.032617092		
Q99PP2	EEKIEKK	0.941360101		
Q99PP2	EELEKMK	0.378067556	1	1.936553
Q99PP2	EIAGATPYITAAEEK	2.183943836	2	3.129329
Q99PP2	EKMNKPELFNGGEKK	1.88899599		
Q99PP2	ELDSITPDITPGWK	1.569293551	2	2.938004
Q99PP2	EQVIESRRQMQAVK	0.942815026		
Q99PP2	FEFEQDLSEK	1.158640979	2	2.675205
Q99PP2	FFRPHFLQAPGDLTVQEGK	1.333572272		
Q99PP2	FKLINSTNIR	2.197720045		
Q99PP2	GIEQAVQSHAVAEEEAR	1.516349735	2	4.976109
Q99PP2	GNIYSLNEGYAK	1.179019525	2	3.997293
Q99PP2	GSAAAAATTSTREAEGAERR	1.395010093		
Q99PP2	GVYSEETLR	1.224970464	2	2.464947
Q99PP2	HFVTISSPLATQIPQAVGAAYAAK	1.15070524	2	4.91951
Q99PP2	HLQTYGEHYPLDHFDK	1.122599298	3	3.691361
Q99PP2	HVIHTVGPIAVGQPTASQAAELR	1.273064517	3	5.343746
Q99PP2	IENWPFSIKPTLR	1.379066029		
Q99PP2	IGHHSTSDDSSAYR	0.770787996	3	4.53531

Q99PP2	INLSNNK	1.699433141		
Q99PP2	KAMQEINYGPSPDNSIKLVR	1.751929305		
Q99PP2	KGNIYSLNEGYAK	0.847694745	2	4.48673
Q99PP2	KLQHELEEAEER	2.28815399	3	4.115162
Q99PP2	LEFIQPNVISGIPIYR	0.891532939	2	2.43712
Q99PP2	LFDDRLESIIQK	0.164275467		
Q99PP2	LGDAVEQGVINNSVLGYFIGR	1.673249788	2	3.792546
Q99PP2	LIEVEGPNSLGK	1.31523021		
Q99PP2	LKLVMNNFIYQTK	1.079677105		
Q99PP2	LMQVNDTLTSEDAGLR	0.779889356		
Q99PP2	LQHELEEAEER	2.195389801	2	3.693294
Q99PP2	LQHELEEAEERADIAESQVNK	2.38001533	3	3.880238
Q99PP2	MKKNMEQTVK+Oxidation(4	1.218768815		
Q99PP2	MNLQDELDELK	1.12934149	2	2.321496
Q99PP2	MNLQDELDELK+Oxidation(0	0.766666991		
Q99PP2	MQQVEASLQPETLK+Oxidation(0	1.493778794		
Q99PP2	MQQVEASLQPETLKK+Oxidation(0	2.238396823		
Q99PP2	NESGLDSGRSQR	1.062733444		
Q99PP2	NNGYAISTPTSEQYR	0.860679502	2	3.813489
Q99PP2	QGQIINPSEDPHLPQEEVLK	0.720665931	2	2.642791
Q99PP2	QRAEQETKLK	1.776162877		
Q99PP2	QTCLKTVVLLTDNK	1.14196801		
Q99PP2	QTITAQNAAVQAVK	1.481682277	2	3.963229
Q99PP2	QYLLNQGWWDEEQEK	0.937615362	2	3.437244
Q99PP2	RAALQAEIEELR	5.022936209	2	3.750518
Q99PP2	RFSTEVGSDCVSDNDR	3.128860439		
Q99PP2	SCYDLSCHAR	1.313639226	2	2.33992
Q99PP2	SCYLSSLDLLLEHR	1.003325592	2	2.630773
Q99PP2	SLEDALNQTATVTR	0.781547875	2	4.423911
Q99PP2	SMTLLNTMDR	0.912636732	2	2.750193
Q99PP2	SVDEVNYWDK	1.000757303	2	2.562562
Q99PP2	TAMDNSEIAGEK	1.487260408	2	2.410137
Q99PP2	TAMDNSEIAGEKK	1.615240077	2	2.502185
Q99PP2	TLHVEEVVPSVIEPSFGLGR	1.122271491	3	3.685176
Q99PP2	TSSAEMPTIPLGSAVEAIR	1.371331082	2	3.884869
Q99PP2	TWTAADMAAQITR+Oxidation(6	1.140224066		
Q99PP2	VDDSSGSIGR	1.0531118	2	2.867106
Q99PP2	VDGNDVFAVYNATK	0.918616287	2	2.859012
Q99PP2	VMEAFEQAER	0.703264742	2	3.288264
Q99PP2	VTMQNKISEATQEEDRL+Oxidation(2	1.274084361		
Q99PP2	VVSQYHELVVQAR	2.417484633	2	3.523229
Q99PP2	YNENHQHGK	0.617324967		
Q99PP2	YSTSSSSGVTAGK	1.305676625	2	2.892481
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**1.513836188**	**0.671579**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(10	1.513836188		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(9	1.513836188		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.301172613**	**0.485925**	**2**
Q9CPQ1	FGVAEPR	1.319661501	2	2.452548
Q9CPQ1	NYDSMKDFEEMR	1.231161058	2	3.762555
Q9CQ75	**NDUA2 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2**	**1.52975459**	**0.262751**	**2**
Q9CQ75	EIRVHLCQRSPGSQGVR	1.529925052	2	2.334036
Q9CQ75	TVSLNNLSADEVTR	1.377721671	2	2.411937
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**1.280478887**	**0.633119**	**2**
Q9CQS8	FYTEDSPGLK	1.280048471	2	2.432882
Q9CQS8	TTSAGTGGMWR	1.329101732	2	2.344058

Q9CQZ5	**NDUA6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6**	**1.632588596**	**0.000162**	**3**
Q9CQZ5	EVPNTVHLMQLDITVK	1.645274985	2	2.490978
Q9CQZ5	FFHETETPRPK	1.695932045	2	2.908828
Q9CQZ5	VVDLLVIK	1.513717768	2	2.938837
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**0.870496369**	**0.937184**	**2**
Q9CRB9	VAEELALEQAK	0.910487211	2	3.646535
Q9CRB9	YEYHPVCADLQTK	0.825372584	2	3.78162
Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**1.740508506**	**0.49254**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.761693808	2	2.571501
Q9CTN4	LKDSGDVSDIIEK	1.147916997	2	2.468512
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**1.295516855**	**0.642224**	**2**
Q9CW42	DLLLPITPPATNPLLQCR	0.984310038	3	3.518643
Q9CW42	GLSVSEAECTAMGLR	1.29621527	2	3.904058
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.220891675**	**0.008872**	**4**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.128904777	2	4.468487
Q9CWH6	ALLEVVQSGGK	0.938409938	2	3.034716
Q9CWH6	LTVEDPVTVEYITR	1.221193361	2	4.0456
Q9CWH6	LYQTDPSGTYHAWK	1.014267287	2	2.892626
Q9CWK8	**SNX2 Sorting nexin_2**	**1.289336607**	**0.230663**	**4**
Q9CWK8	AVNTQALSGAGILR	1.377776124	2	3.212738
Q9CWK8	QQQFENLDQQLR	1.234916348	2	2.516118
Q9CWK8	WEDAQITLLK	1.248526326	2	2.479125
Q9CWK8	YLESLVQTQQQLIK	1.390187254	2	4.008821
Q9CWL2	**CASZ1 Zinc finger protein castor homolog 1**	**1.180310752**	**0.705998**	**2**
Q9CWL2	ISASKGLISPMMAR+Oxidation(10	1.180310752		
Q9CWL2	ISASKGLISPMMAR+Oxidation(11	1.180310752		
Q9CXS4	**CENPV Centromere protein V**	**2.246547837**	**3.01E-05**	**2**
Q9CXS4	LLLDTFEYQGLVK	2.248829486	2	3.905836
Q9CXS4	SNPGGFGIAPHCLDEGTVR	1.680586323	2	2.565918
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**0.92330486**	**0.11178**	**2**
Q9CYN2	LHDSLATER	0.67370458	2	2.682302
Q9CYN2	YVENFGLIDGR	1.618798574	2	2.886197
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.949424472**	**0.166505**	**2**
Q9CYW4	LEDILTGLGLR	1.413707763	2	4.383315
Q9CYW4	RLEDILTGLGLR	0.532686794	3	3.533661
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.076379964**	**0.971255**	**3**
Q9CZY3	LLEELEEGQK	0.92702853	1	2.98371
Q9CZY3	VNMSGVSSSNGVVDPR	1.091168706	2	3.107043
Q9CZY3	WTGMIIGPPR	1.176196971	2	2.861742
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**0.891637893**	**2.61E-06**	**3**
Q9D024	ERIMNEEDPEKQR	1.923199929	2	2.459018
Q9D024	IMQEEGQPLKLPDTK	0.635384641	2	3.19694
Q9D024	RLEEAALR	1.441840152	2	2.605419
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.40414709**	**1.52E-14**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	2.176941296	3	4.237427
Q9D0M3	GLLSSLDHTSIR	1.046141086	2	3.029222
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.483769675	3	5.557282
Q9D0M3	HLVGVCYTEEEAK	1.461167222	2	3.830478
Q9D0M3	LSDYFPKPYPNPEAAR	1.289632449	3	3.895288
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.761738143**	**9.9E-20**	**3**

Q9D0S9	DVAPQAPVHFLVIPR	1.283507667	2	2.94313
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.866298433	2	4.739595
Q9D0S9	SLPADILYEDQQCLVFR	1.89293063	2	3.541469
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.837923845**	**9.9E-20**	**3**
Q9D172	GVEVTVGHEQEEGGK	1.148276114	2	4.078919
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.885403872	3	4.593657
Q9D172	NLSTFAVDGK	1.288747609	1	2.447046
Q9D180	**WDR65 WD repeat_containing protein 65**	**1.049560726**	**0.002571**	**2**
Q9D180	ERDLEALVR	0.854666356	2	2.561948
Q9D180	KNQELEK	1.452879988	1	2.179122
Q9D1M7	**FKB11 Peptidyl_prolyl cis_trans isomerase FKBP11**	**1.428877969**	**0.191532**	**2**
Q9D1M7	IIDTSLTRDPLVIELGQK	1.32830593	3	3.428686
Q9D1M7	QVIPGLEQSLLDMCVGEK	1.544723076	2	3.190273
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.330976527**	**3.94E-11**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0	2.574522702		
Q9D1Q6	NIIGYFEQK	1.284730044	1	2.377177
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.33058351	2	5.565913
Q9D1Q6	VDCDQHSDIAQR	1.150693622	2	3.625312
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.388545079**	**9.9E-20**	**5**
Q9D2U9	AMGIMNSFVNDIFER	1.504982553	2	5.122623
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1	1.287258723		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)Oxidation(4	1.239917158		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4	1.46282543		
Q9D2U9	LLLPGELAK	1.555324312	2	2.526498
Q9D417	**FBX24 F_box only protein 24**	**1.316592345**	**0.53372**	**2**
Q9D417	MKEIVGWMPLMAAQK+Oxidation(7	1.88899599		
Q9D417	RSCPSCGLEAGSEKK	1.28144421	2	2.409802
Q9D662	**SC23B Protein transport protein Sec23B**	**1.868994913**	**0.020658**	**2**
Q9D662	HLLQAPLDDAQEILQAR	1.965665504	3	3.988877
Q9D662	IDMNLTDLLGELQR	1.862793295	2	4.122829
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.307740882**	**0.762928**	**3**
Q9D6M3	GAAVNLTLVTPEK	1.297161403	2	3.344604
Q9D6M3	GVNEDTYSGFLDCAR	1.416355592	2	4.710788
Q9D6M3	NHGIAGLYK	1.30597904	1	2.21762
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.115135178**	**0.851679**	**11**
Q9D6Y9	CVAYAESHDQALVGDK	1.428457812	2	5.011806
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	0.961609677	3	3.30356
Q9D6Y9	FLNNFDR	1.239295916	2	2.40365
Q9D6Y9	GTHDLWDSR	1.188871727	2	2.742074
Q9D6Y9	GYESFGIHR	1.240460166	2	2.37497
Q9D6Y9	IVLDSDAAEYGGHQR	0.89716623	2	4.555433
Q9D6Y9	IYESHVGISSHEGK	1.21283826	2	4.591901
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.273701923	3	3.464961
Q9D6Y9	QFNLTDDDLLR	1.311452851	2	2.731868
Q9D6Y9	RQFNLTDDDLLR	1.155720418	2	3.206887
Q9D6Y9	WELYIPPK	1.401576205	2	2.505399
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.187569225**	**0.626432**	**2**
Q9D6Z1	ELNEEKLEK	1.045957774	2	2.440639
Q9D6Z1	IDCFSEVPTSVFGEK	1.699159507	2	2.53695
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**0.9257621**	**0.846498**	**6**
Q9D7B6	AVIFEDCAVPVANR	0.891544478	2	3.80757
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	3.058110086	2	4.502868
Q9D7B6	IGTEGQGFLIAMK	1.222480765	2	3.01147
Q9D7B6	TAAVALQEER	1.357475793	2	3.190252
Q9D7B6	TDVGGSGLSR	1.138722051	2	2.506622
Q9D7B6	VHQILEGSNEVMR	1.04722929	2	3.39504

Q9D7P6	**ISCU Iron_sulfur cluster assembly enzyme ISCU_ mitochondrial**	**0.977322451**	**0.916853**	**2**
Q9D7P6	NVGTGLVGAPACGDVMK	0.975962139	2	3.612981
Q9D7P6	VVDHYENPR	1.158743666	2	2.517086
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**1.307160874**	**0.36095**	**2**
Q9D7X8	ISDEMEDIIK	1.525389627	2	2.74569
Q9D7X8	SNISSLDEQEGVK	1.306373016	2	3.433414
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.539797758**	**0.001681**	**5**
Q9D819	GISCMNTTVSESPFK	1.187970896	2	5.1814
Q9D819	GQYISPFHDVPIYADK	1.770364625	2	3.201455
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.304929881	3	5.188514
Q9D819	VLGILAMIDEGETDWK	1.918793421	2	4.117979
Q9D819	YVANLFPYK	0.92891506	1	2.056457
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.155984825**	**0.001095**	**3**
Q9D880	TIALNQVEDVR	1.079324784	2	2.957961
Q9D880	TVLEHYALEDDPLEAFK	1.42382097	2	4.70519
Q9D880	VLLDLSAFLK	2.072622459	2	2.348762
Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**1.671839249**	**0.001732**	**3**
Q9D8W5	LQEVIETLLSLEK	1.66357074	2	3.791436
Q9D8W5	TASDMVSTSR	1.980553709	2	2.348341
Q9D8W5	WSTLVEDYGVELR	2.935323898	2	3.126532
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**0.886871488**	**0.699324**	**3**
Q9DB15	KLVESLPQEIK	1.266946604	2	3.002186
Q9DB15	NYVQGINLVQAK	1.331070358	2	2.498806
Q9DB15	SEALAGAPLDNAPK	0.886819979	2	2.329203
Q9DBC0	**SELO Selenoprotein O**	**1.266016987**	**0.172024**	**2**
Q9DBC0	LGLIRVEK	1.246666527	2	2.302638
Q9DBC0	LLESPYHSEEEATGPEAVAR	1.473543629	3	3.360631
Q9DBG7	**SRPR Signal recognition particle receptor subunit alpha**	**1.396409423**	**0.088456**	**2**
Q9DBG7	GLVGSKSLSREDMESVLDK+Oxidation(12	1.058504249		
Q9DBG7	NQGFDVVLVDTAGR	1.495276972	2	2.910258
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.224098914**	**0.039197**	**2**
Q9DBH5	TPEEESIDWTK	0.543562254	2	2.470237
Q9DBH5	WSELAGCTADFR	1.22738243	2	3.365577
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**1.685372613**	**0.000488**	**4**
Q9DC70	LDDLINWAR	1.454200215	2	3.043871
Q9DC70	MAPALRKVYDQMPEPR+Oxidation(0)Oxidation(11	1.624975873		
Q9DC70	QADVMIVAGTLTNK	1.705144791	2	3.521243
Q9DC70	VYDQMPEPR	3.278951121	2	2.458122
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**1.271401947**	**0.128362**	**2**
Q9DCH4	FLMSLVNQVPK	1.554052862	2	2.764124
Q9DCH4	VIGLSSDLQQVGGASAR	1.054127934	2	4.691638
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.308265729**	**0.16009**	**2**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	2.451895771	3	4.311144
Q9DCM0	SLLPGCQSVISR	0.787929802	2	2.985887
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.561328464**	**1.94E-05**	**2**
Q9DCS9	AYDLVVDWPVTLVR	1.569342677	2	4.656997
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.094304303	2	3.448193
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.794026601**	**3.09E-09**	**5**

Q9DCT2	FDLNSPWEAFPAYR	1.586497254	2	3.225391
Q9DCT2	ILTDYGFEGHPFR	2.240536354	2	2.800082
Q9DCT2	KFDLNSPWEAFPAYR	1.856135743	2	3.558665
Q9DCT2	SLADLTAVDVPTR	1.221862035	2	3.4189
Q9DCT2	VVAEPVELAQEFR	0.896126187	2	3.784154
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.289504609**	**4.44E-13**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.277294425	2	5.344366
Q9DCU9	LIEPNTAVTR	1.380673001	2	3.35929
Q9DCU9	TMDWFGYYGGPCR	1.346116456	2	3.692101
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.669668952**	**0.020173**	**2**
Q9EP75	DEDGKELSDEDIR	13.9940468	2	3.027963
Q9EP75	IFNDSTNIMHAK	1.654052243	2	3.67793
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.080902082**	**2.55E-13**	**10**
Q9EP89	EVWSEGLGYADVENR	1.978731995	2	3.830234
Q9EP89	FENSIESLR	0.965913184	2	2.758235
Q9EP89	GIIVSIICNMQSVGLNSTALK	1.21344639	3	3.960681
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	2.920912453	2	5.675873
Q9EP89	IKDEVGAPGIVVGVSVDGK	1.858707012	2	4.545087
Q9EP89	KNDFEQGELYLK	0.672691481	2	3.994308
Q9EP89	LDLDLPVQHYVPEFPEK	2.341836962	3	3.738698
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.730365396	3	3.989088
Q9EP89	LVNTPYVDNSYK	1.495793714	2	3.16289
Q9EP89	WAGGGFLSTVGDLLK	1.744566842	2	4.43359
Q9EPH2	**MRP MARCKS_related protein**	**1.045195625**	**0.496983**	**2**
Q9EPH2	AAATPESQEPQAK	1.216619013	2	2.443464
Q9EPH2	GDVTAEEAAGASPAK	0.9585024	2	3.306813
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.793063106**	**1.05E-07**	**10**
Q9EPH8	ALDTMNFDVIK	1.694954919	2	3.285613
Q9EPH8	GFGFVSFER	1.799775002	2	2.731773
Q9EPH8	GYGFVHFETQEAAER	1.424670863	2	3.295907
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	2.901502738	3	3.810517
Q9EPH8	KEFSPFGTITSAK	1.598737975	2	3.368816
Q9EPH8	NFGEDMDDER	22.96041597	2	2.562508
Q9EPH8	NLDDGIDDER	0.795819222	2	2.364954
Q9EPH8	SGVGNIFIK	1.342362875	2	2.768008
Q9EPH8	SKVDEAVAVLQAHQAK	1.563305664	2	5.101853
Q9EPH8	VDEAVAVLQAHQAK	2.045572218	2	2.855544
Q9EPJ0	**NUCKS Nuclear ubiquitous casein and cyclin_dependent kinases substrate**	**0.94632696**	**0.719648**	**2**
Q9EPJ0	NSQEDSEDSEEKDVK	0.94170034	2	3.541842
Q9EPJ0	TPSPKEEDEEAESPPEK	2.529862079	2	2.316608
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**2.364323844**	**9.9E-20**	**13**
Q9EQ76	ASIYQSVFTNSSK	0.884326334	2	3.140303
Q9EQ76	GTCILPSVNDMMDDIDEK	2.599196228	2	3.939768
Q9EQ76	ILCGTVSIKPNVK	1.022584692	2	3.002185
Q9EQ76	KEPVFNDELPAR	1.63982349	3	3.604383
Q9EQ76	LQEYITSFATEK	2.621719691	2	3.549567
Q9EQ76	NNEVTLYK	2.739074431	2	2.494755
Q9EQ76	NNLPTAISDWWYMK	2.642794773	2	2.503373
Q9EQ76	SCLEEGLEPTCFER	1.593796086	2	4.312561
Q9EQ76	SDDVGGLWK	1.853309429	2	2.92234
Q9EQ76	VAVIGAGVSGLAAIR	3.515186438	2	4.199125
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.828796815	3	3.698405
Q9EQ76	VWNDGYPWDMVVITR	2.342056067	2	3.888012

Q9EQ76	YIQFETLVTR	3.707308756	2	3.186839
Q9EQG6	**KDIS Kinase D_interacting substrate of 220 kDa**	**1.292913163**	**0.597437**	**2**
Q9EQG6	HLLAMGADVDQEGANSMTALIVAVK+Oxidation(4	1.358364794		
Q9EQG6	SSERPSLFQTDLKLK	1.017222078	2	2.329966
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.288115301**	**0.015995**	**8**
Q9EQH3	HFHNTLEHLR	2.275533439	3	3.439142
Q9EQH3	IREDLPNLESSEETEQINK	1.467644898	2	5.514778
Q9EQH3	LFDIFSQQVATVIQSR	3.246684131	3	3.329094
Q9EQH3	LLDEAIQAVK	0.917474439	2	2.580805
Q9EQH3	LNLEHIATSSAVSK	1.724942592	2	4.277401
Q9EQH3	LSQLEGVNVER	1.152926102	2	3.018682
Q9EQH3	NIIIALIDR	1.670235554	2	2.411707
Q9EQH3	VLETTVEIFNK	1.420701902	2	2.870666
Q9EQS0	**TALDO Transaldolase**	**1.201862256**	**7.72E-06**	**6**
Q9EQS0	ALAGCDFLTISPK	1.225330705	2	3.308388
Q9EQS0	ILDWHVANTDKK	1.574186217	2	3.475639
Q9EQS0	LGGPQEEQIK	1.29702839	2	3.309699
Q9EQS0	LSSTWEGIQAGK	2.134686209	2	2.71191
Q9EQS0	SYEPQEDPGVK	0.881290951	2	2.824434
Q9EQS0	WLHNEDQMAVEK	1.361839934	2	3.75689
Q9EQS3	**MYCBP C_Myc_binding protein**	**1.442409199**	**0.19751**	**2**
Q9EQS3	LVQYEPPQEEK	1.442430744	2	2.476275
Q9EQS3	VLVALYEEPEKPTSALDFLK	1.398002923	3	3.449148
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**1.015362192**	**0.164158**	**3**
Q9EQW7	ADLTDSRALEKAVSR	1.062232268	3	3.341904
Q9EQW7	DETIAVPLEENSALPK	0.929931728	2	2.590858
Q9EQW7	VTQWAEER	1.3624579	2	2.43305
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.189321446**	**0.013312**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.206135176	2	4.342946
Q9EQX9	SNEAQAIETAR	1.067944585	2	3.375891
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.06522428	3	4.481384
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.533818255**	**0.000262**	**19**
Q9ER34	ADIANLAEEFK	1.346864445	2	3.565021
Q9ER34	CTTDHISAAGPWLK	1.371963945	2	4.019836
Q9ER34	DINQEVYNFLATAGAK	1.608302573	2	3.344197
Q9ER34	DLEDLQILIK	0.724754538	2	2.47384
Q9ER34	FKLEAPDADELPR	1.120477154	3	4.169275
Q9ER34	FNPETDFLTGK	1.641488905	1	2.487037
Q9ER34	GHLDNISNNLLIGAINIENGK	1.554651426	2	5.80545
Q9ER34	IVYGHLDDPANQEIER	1.372238785	2	4.601389
Q9ER34	LNRPLTLSEK	1.957547399	2	2.450898
Q9ER34	LTGTLSGWTSPK	0.973049807	2	2.994564
Q9ER34	NAVTQEFGPVPDTAR	1.099010581	2	4.437135
Q9ER34	NTIVTSYNR	1.345432384	1	1.949047
Q9ER34	QGLLPLTFADPSDYNK	1.343758353	2	3.35535
Q9ER34	SDFDPGQDTYQHPPK	1.607728322	2	2.879334
Q9ER34	SQFTITPGSEQIR	1.078084581	2	3.910782
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	1.741952981	2	4.78304
Q9ER34	VDVSPTSQR	1.276165643	2	2.446613
Q9ER34	VGLIGSCTNSSYEDMGR	1.284930162	2	4.200393
Q9ER34	WVVIGDENYGEGSSR	1.268003621	2	4.414227
Q9ERU9	**RBP2 E3 SUMO_protein ligase RanBP2**	**1.422399416**	**0.503851**	**2**
Q9ERU9	EINSLRGQEK	1.475181149	2	2.613367
Q9ERU9	NLFRFGESTTGFNFSFK	1.021946353	2	2.323624
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**1.365850088**	**0.025727**	**5**
Q9ES21	HFDSQVIIYGK	1.34684455	2	2.795872

Q9ES21	LEEQDEFEK	1.336878751	2	2.759493
Q9ES21	TNVIQSLLAR	4.270995955	2	2.394595
Q9ES21	TQLGLVMDGFNSLLR	1.507959879	2	3.946997
Q9ES21	VVTNQEGVFR	1.320080306	2	2.810562
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.218882731**	**7.45E-05**	**14**
Q9ES38	ACQAAWALK	1.655850204	2	2.572693
Q9ES38	ADVWENFQQR	1.154951163	2	2.954156
Q9ES38	EGFDVGVIADPLYILDNK	1.145696838	2	5.371817
Q9ES38	GATAILVLPSK	1.287628955	2	3.207123
Q9ES38	HPPELFVDALEQQAQARPDQVALVCTGSEGCSITNR	1.479934075	4	4.546221
Q9ES38	IQDSLEITNTYK	1.592455055	2	3.815158
Q9ES38	LKEATIQEDK	1.759245291	2	2.833807
Q9ES38	LLAENIR	1.436324566	2	2.466706
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.91211751	2	4.201634
Q9ES38	QGFCIPVETGKPGLLLTK	1.867377334	3	3.882008
Q9ES38	SISALSVFLGLAK	1.477990563	2	3.320139
Q9ES38	SLMPDVYQAVCEGTWK	1.067726131	2	3.905647
Q9ES38	YLCNVPGQPEDK	1.191299173	2	3.377668
Q9ES38	YLCNVPGQPEDKK	1.623639587	2	3.766982
Q9ESP1	**SDF2L Stromal cell_derived factor 2_like protein 1**	**0.933871367**	**0.757499**	**2**
Q9ESP1	ASAGLVTCGSVLK	0.933620691	2	3.592859
Q9ESP1	GQHEVHGMPSANAHNTWK	0.934694691	3	3.819128
Q9ESR9	**ABCA2 ATP_binding cassette sub_family A member 2**	**1.350168501**	**2.9E-05**	**2**
Q9ESR9	KEMDKMIEDLELSNK+Oxidation(2)Oxidation(5	1.371873141		
Q9ESR9	RHSLVQTLSGGMKR	1.052213942	2	2.362616
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.744092485**	**2.63E-06**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.53055478	2	4.140507
Q9EST6	SLDLFGCEVTNR	1.746626984	2	2.977428
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.300462899**	**0.017567**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.421210738	3	5.828272
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.270838985	3	4.501591
Q9ESW0	QGQGQLVTCSGAFK	1.282833581	2	2.367665
Q9HB97	**PARVA Alpha_parvin**	**1.109316131**	**0.287108**	**3**
Q9HB97	LNVAEVTQSEIAQK	0.866298971	2	4.314168
Q9HB97	QIQEEITGNTEALSGR	1.561393873	2	3.707076
Q9HB97	VLIDWINDVLVGER	2.604428511	2	2.300397
Q9JHL4	**DBNL Drebrin_like protein**	**0.627372552**	**0.42189**	**3**
Q9JHL4	AMSTTSVSSSQPGK	1.063450592	2	2.552316
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3	0.446312405		
Q9JHL4	TGELEQEVVSR	0.840236775	2	3.265641
Q9JHW0	**PSB7 Proteasome subunit beta type_7**	**1.09442051**	**0.989529**	**2**
Q9JHW0	ATEGMVVADK	1.072253757	2	2.57047
Q9JHW0	FRPDMEEEEAKK	1.159447539	3	3.817457
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**2.426199171**	**6.01E-08**	**3**
Q9JHZ9	AYEQLGYR	1.657299038	2	2.392027
Q9JHZ9	HLEGLLPVGMPTADTQR	2.56311883	2	3.986796
Q9JHZ9	MEIPRQTEMVELVPNGK+Oxidation(0)Oxidation(8	1.291764128		
Q9JI85	**NUCB2 Nucleobindin_2**	**1.225370716**	**0.70133**	**8**
Q9JI85	FQQGIAPSGPAGELK	1.222160288	2	3.153102
Q9JI85	HEEFKKYEMMK+Oxidation(8	0.69511367		
Q9JI85	HEEFKKYEMMK+Oxidation(9	0.69511367		
Q9JI85	LSQELDLVSHK	1.395133689	2	2.628928
Q9JI85	QEYQQAVQQLEQK	1.192545875	2	4.595516
Q9JI85	TRLDELK	1.267788821	1	2.011131

Q9JI85	VHNVEPVESAR	1.215038696	2	3.080074
Q9JI85	VYNPQNAEDDMIEMEEER	2.056858038	2	3.972005
Q9JI91	**ACTN2 Alpha_actinin_2**	**1.600537934**	**6.54E-09**	**8**
Q9JI91	ETADTDTAEQVIASFR	1.668111447	2	3.064212
Q9JI91	GYEEWLLNEIR	2.472267821	2	3.486504
Q9JI91	HTNYTMEHIR	1.176388346	3	3.545197
Q9JI91	KHEAFESDLAAHQDR	1.600954529	2	5.363108
Q9JI91	MLDAEDIVNTPKPDER	1.369657702	2	3.212601
Q9JI91	QSILAIQNEVEK	1.835224435	2	2.722774
Q9JI91	SSIQITGALEDQMNQLK	1.600679781	2	3.085317
Q9JI91	TINEVETQILTR	1.702860945	2	3.144686
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.10104766**	**0.35961**	**7**
Q9JJ19	AVDPDSPAEASGLR	1.111703314	2	3.459783
Q9JJ19	IVEVNGVCMEGK	1.126620638	2	3.723942
Q9JJ19	LLVVDPETDEQLKK	1.303702802	2	2.854161
Q9JJ19	LVEPGSPAEK	0.658587551	2	2.702399
Q9JJ19	LVEVNGENVEK	1.092777124	2	3.046629
Q9JJ19	SEHTEPPAAADTK	1.097658411	2	3.326792
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	1.1724758	3	3.553252
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**2.261213764**	**9.43E-05**	**5**
Q9JJ40	AGVLADDHLIEVNGENVENASHEEVVEK	2.873080368	3	5.382559
Q9JJ40	GVFLTDITPQGVAMK	1.308244874	2	3.378388
Q9JJ40	IEKDTDGHLVR	1.492245136	2	3.193734
Q9JJ40	SGNSVTLLVLDGDSYEK	2.325903184	2	3.796674
Q9JJ40	VIEEGSPAEK	1.628860863	2	2.418427
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.982538094**	**0.003298**	**2**
Q9JJ46	HLTNAQSMLDNK	1.99299934	2	3.759764
Q9JJ46	VSVVPLGTGR	1.586451682	2	2.451048
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.256215897**	**0.004227**	**4**
Q9JJ54	FGDVVDCTLK	0.689007529	2	2.808339
Q9JJ54	IDASKNEEDEGHSNSSPR	1.253343055	3	4.660944
Q9JJ54	IFVGGLSPDTPEEK	1.378606866	2	4.03937
Q9JJ54	IFVGGLSPDTPEEKIR	2.332337473	2	2.405009
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.267089472**	**0.074966**	**4**
Q9JJ79	NCLEEWTKAAGLEK	1.2121393	2	2.650479
Q9JJ79	RASTAAAPLAAWVK	1.372928153	2	2.538248
Q9JJ79	TVLRGSGNLLR	1.440217832	2	2.466182
Q9JJ79	YVVQIGDK	1.296751911	1	2.302719
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.418770954**	**0.361359**	**2**
Q9JJU8	GDYDAFFEAR	1.433945652	2	3.185981
Q9JJU8	QQDVLCFLEANK	1.417247488	2	3.217353
Q9JJW3	**USMG5 Up_regulated during skeletal muscle growth protein 5**	**1.059574627**	**0.674158**	**2**
Q9JJW3	MAGPESDGQFQFTGIKK+Oxidation(0	3.372262249		
Q9JJW3	YFNSYTLTGR	1.058375169	2	2.806125
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.326915128**	**3.77E-09**	**4**
Q9JK38	GRVEDVVVSDECR	1.679411423	2	2.518183
Q9JK38	ITLECLPQNVGFYK	1.196899482	2	3.476281
Q9JK38	VEDVVVSDECR	1.448443162	2	3.366512
Q9JK38	VLGQLTETGVVSPEQFMK	1.472918095	2	4.632431

Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**1.435259283**	**0.735208**	**2**
Q9JK72	GDLGNVHAEASGR	1.309112676	2	3.221515
Q9JK72	SLVVDEGEDDLGR	1.435592274	2	3.022307
Q9JKJ9	**CP39A 24_hydroxycholesterol 7_alpha_hydroxylase**	**1.372232888**	**0.000197**	**2**
Q9JKJ9	TVLESISSVFGTAGK	1.403005014	2	3.335968
Q9JKJ9	TYDEGFEYGSQLPEWLLR	1.359391182	2	3.201489
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**1.339631537**	**0.596123**	**4**
Q9JKS4	DFNMPLTISR	1.331273906	2	2.342838
Q9JKS4	DLAVDSASPVYQAVIK	1.004767363	2	3.593089
Q9JKS4	GAPAYNPTGPQVTPLAR	2.207753265	2	3.128092
Q9JKS4	TQSKPEDEADEWAR	2.904692581	2	3.816067
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.592975375**	**0.001178**	**11**
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	1.762797654	3	3.317707
Q9JLA3	FLFVDADQIVR	1.980899365	2	2.620317
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.628323441	3	6.0139
Q9JLA3	IEYQFFEDK	1.981602823	2	2.344564
Q9JLA3	ILETTTFFQR	2.302364319	2	2.8417
Q9JLA3	IVPEWQDYDQEIK	1.258434394	2	3.319689
Q9JLA3	LNIQPSETDYAVDIR	1.767837047	2	4.111472
Q9JLA3	TAAIANSMNYLTK	1.053737555	2	2.577098
Q9JLA3	VDALLSAQPK	1.778623582	2	2.741501
Q9JLA3	VEEDVASDLVMK	2.363887768	2	3.824609
Q9JLA3	VWQLQDLSFQTAAR	1.351622523	2	4.653905
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**1.038332136**	**0.971325**	**2**
Q9JLH7	GSDALTLLEYPETR	0.980978036	2	2.905873
Q9JLH7	KEEEGQAGAAEMR	1.196018953	2	3.705168
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.16234521**	**2.16E-05**	**18**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.338589801	2	4.757272
Q9JLJ3	ANDTTFGLAAGVFTR	1.285072981	2	4.928795
Q9JLJ3	CQVLLEAAR	1.214718643	2	3.303736
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.147316327	2	4.954382
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.227139241	3	3.39479
Q9JLJ3	EVNLAVENAK	1.267747745	2	3.150413
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.046555288	2	5.572246
Q9JLJ3	GIKPITLELGGK	0.816496031	3	3.96727
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.577788606	3	4.238648
Q9JLJ3	IGDPLLEDTR	1.156092234	2	3.705498
Q9JLJ3	MGPLINAPHLER	1.26636208	2	3.264421
Q9JLJ3	MGPLINAPHLER+Oxidation(0	1.271936246		
Q9JLJ3	RDEIAIMETINNGK	1.174383441	2	5.298826
Q9JLJ3	SPLIIFSDCNMK	0.998634184	2	2.60824
Q9JLJ3	VEPVDASGTEK	1.150731718	2	2.414235
Q9JLJ3	VSFTGSVPTGMK	1.165593801	2	3.105139
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10	1.129901139		
Q9JLJ3	VTIEYYSQLK	1.248414642	2	3.084486
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**1.174835495**	**0.000137**	**2**
Q9JLR1	IIEVGDTPK	1.073001707	2	2.665517
Q9JLR1	TWIEVSGSSAK	1.595552193	2	2.754697
Q9JLT0	**MYH10 Myosin_10**	**1.654383731**	**8.19E-06**	**2**
Q9JLT0	AGVLAHLEEER	1.637551152	2	3.428601
Q9JLT0	DAAGLESQLQDTQELLQEETR	3.080835514	2	3.181751
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**0.838473829**	**0.569605**	**2**

Q9JLZ1	LEAEAVPEVSEK	0.660226209	2	2.319788
Q9JLZ1	YEISSVPTFLFFK	1.977989198	2	2.584764
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.832571385**	**0.596663**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	1.107119303	2	5.616707
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.686106083	3	4.470016
Q9JLZ3	SEVPGIFCAGADLK	1.145036923	2	2.953438
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**1.077025315**	**0.005358**	**15**
Q9JM53	AIASAAEGGSVPPIR	1.160814456	2	2.767638
Q9JM53	CLIATGGTPR	0.982882208	2	2.421601
Q9JM53	DGEQHEDLNEVAK	0.885388276	2	3.829643
Q9JM53	ILPEYLSNWTMEK	1.457861897	2	3.494593
Q9JM53	IMGLGLSPEEK	1.387471725	2	2.805508
Q9JM53	KSQASGIEVIQLFPEK	1.429681604	2	3.709891
Q9JM53	KVETDHIVTAVGLEPNVELAK	1.028296646	2	6.178644
Q9JM53	LNDGSQITFEK	1.234259157	2	3.508256
Q9JM53	SITVIGGGFLGSELACALGR	1.135429767	2	2.657076
Q9JM53	SQASGIEVIQLFPEK	1.621774477	2	4.131787
Q9JM53	TGGLEIDSDFGGFR	1.081781065	2	4.186753
Q9JM53	VETDHIVTAVGLEPNVELAK	1.145533654	2	5.182467
Q9JM53	VLIVSEDPELPYMRPPLSK	1.189195471	3	3.938525
Q9JM53	VMPNAIVQSVGVSGGK	1.366734978	2	4.283277
Q9JM53	VNAELQAR	1.129314617	2	2.60174
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**2.119222907**	**0.027621**	**2**
Q9JMA1	CTESEEEEVTK	1.95021188	2	3.694068
Q9JMA1	EKESVNAKVLK	3.557942735	2	2.375329
Q9JMD3	**PCTL PCTP_like protein**	**0.946800256**	**9.9E-20**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.353709701	2	4.66817
Q9JMD3	ESVQVPDDQDFR	1.588254481	2	2.835652
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.722444008	3	4.405108
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0	1.540824785		
Q9JMD3	SSQFLAPK	0.681326279	2	2.35623
Q9JMD3	WDSNVIETFDIAR	1.440846089	2	4.534047
Q9JME5	**AP3B2 AP_3 complex subunit beta_2**	**1.308585744**	**0.003605**	**2**
Q9JME5	DELVVAESVVVIK	2.301367839	2	2.51605
Q9JME5	LLQMQPAQHGEIIK	1.30560294	2	2.55969
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.13076804**	**0.914418**	**7**
Q9QVC8	ALELDSNNEK	1.182154872	2	2.630562
Q9QVC8	GEPNNVAGNQAQVK	1.037360455	2	3.859574
Q9QVC8	TEVAAGDHPTDAEMK	0.93363608	2	3.667866
Q9QVC8	TQLAVCQQR	1.146248184	2	2.728419
Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.115787063	2	3.929371
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	0.969233559	3	5.915501
Q9QVC8	VLQLYPSNK	0.72009391	2	2.333246
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.353245263**	**0.046449**	**3**
Q9QWN8	ALAQEDQSAGEVER	1.337436479	2	3.770663
Q9QWN8	FETLEPEMNALAAR	2.001866725	2	2.72911
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	1.196059211	3	4.224523
Q9QX79	**FETUB Fetuin_B**	**1.159157713**	**0.384415**	**3**
Q9QX79	GSIQHLPEQEEPEDSKGK	1.458096185	3	3.830061
Q9QX79	IFYETVHGQCK	1.07639179	2	2.389929
Q9QX79	NTAPTSSPSITAPR	1.610592295	2	3.150381
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**1.904712222**	**0.055573**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	1.922387401	2	3.679306
Q9QXG4	IGPIATPDYIQNAPGLPK	1.874066587	2	3.297698

Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.093124061**	**9.9E-20**	**32**
Q9QXQ0	ACLISLGYDVENDR	1.5253599	2	4.024054
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.708095593	3	3.852667
Q9QXQ0	AGTQIENIDEDFR	1.086270569	2	3.562215
Q9QXQ0	AGTQIENIDEDFRDGLK	1.188527708	2	4.257896
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.336508616	3	3.368466
Q9QXQ0	ASIHEAWTDGK	0.963993383	2	2.45294
Q9QXQ0	DDPVTNLNNAFEVAEK	1.64732522	2	3.606934
Q9QXQ0	ETTDTDTADQVIASFK	2.396408511	2	4.710371
Q9QXQ0	HRDYETATLSDIK	2.066975224	2	3.887416
Q9QXQ0	HRPELIEYDK	1.094896264	3	4.402828
Q9QXQ0	HTNYTMEHLR	1.176388346	3	3.545197
Q9QXQ0	ICDQWDNLGSLTHSR	1.296543859	2	4.593717
Q9QXQ0	INNVNKALDFIASK	1.002602966	2	2.303109
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.8260547	2	4.734687
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.479858409	2	4.426512
Q9QXQ0	LVSIGAEEIVDGNAK	1.556510624	2	3.156628
Q9QXQ0	MAPYQGPDAAPGALDYK	1.275760871	2	4.98175
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0	1.103789117		
Q9QXQ0	MLDAEDIVNTARPDEK	0.819837294	2	3.877101
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(0	1.162526485		
Q9QXQ0	MVSDINNGWQHLEQAEK	1.472453804	2	4.718013
Q9QXQ0	NFITAEELR	1.280616203	1	2.125005
Q9QXQ0	NVNVQNFHISWK	0.47654011	2	2.344028
Q9QXQ0	QFASQANMVGPWIQTK	1.059012571	2	3.639458
Q9QXQ0	QLETIDQLHLEYAK	1.395045127	2	3.280569
Q9QXQ0	RDHALLEEQSK	1.086438235	3	3.881314
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	2.32226002	3	4.69341
Q9QXQ0	TINEVENQILTR	0.882642733	2	3.673417
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	2.362712668	3	5.403461
Q9QXQ0	VGWEQLLTTIAR	1.500990417	2	4.10189
Q9QXQ0	VLAGDKNFITAEELR	0.978035303	2	3.232787
Q9QXQ0	VLAVNQENEHLMEDYER	1.339620839	2	5.729714
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.341420459**	**0.011222**	**5**
Q9QXT0	ALVDELEWEIAR	1.544896983	2	3.58611
Q9QXT0	IDSDISGTLK	1.15819946	2	2.625451
Q9QXT0	INPDGSQSVVEVPYAR	1.254111851	2	3.662562
Q9QXT0	RTDLCDHALHR	1.530146373	3	3.925126
Q9QXT0	TDLCDHALHR	1.246659319	2	3.207888
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.552337381**	**9.9E-20**	**18**
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.652083384	3	5.826471
Q9QXX4	DVEVTKEEFALAAQK	1.268851265	2	4.478793
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.294725937	2	5.968352
Q9QXX4	FGLYLPLFKPSASTSK	1.230157647	2	2.759892
Q9QXX4	GLLPQLLGVAPEK	1.396850676	1	3.072476
Q9QXX4	IAPLEEGMLPFNLAEAQR	2.276381792	2	5.235605
Q9QXX4	ITLPAPNPDHVGGYK	0.733881158	2	3.004119
Q9QXX4	KDVEVTKEEFALAAQK	1.221037194	2	5.620311
Q9QXX4	LQVAGEITTGPR	1.392464872	2	3.731696
Q9QXX4	LTVNDFVR	1.894311501	2	2.31738
Q9QXX4	NGEFFMSPHDFVTR	1.241781082	2	4.20744
Q9QXX4	NSFDCFK	1.29025856	1	1.973604
Q9QXX4	SSPQFGVTLLTYELLQR	1.849109202	2	3.8108
Q9QXX4	STGSFVGELMYK	1.859572197	2	3.437364
Q9QXX4	TVELLSGVVDQTK	1.638109581	2	4.511763
Q9QXX4	VSALSVVR	1.466555026	2	2.305602

Q9QXX4	YEGFFGLYR	1.302734346	2	2.744856
Q9QXX4	YLNIFGESQPNPK	0.987257723	2	4.434021
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**1.307681018**	**0.984927**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	1.169207568	2	4.576121
Q9QYU4	RAPAFLSADEVQDHLR	1.147996052	3	3.84162
Q9QYU4	SLGMAVEDLVAAK	1.130635039	2	3.761277
Q9QYU4	SSSLLIPPLEAALANFSK	1.447702466	2	2.897213
Q9QZ76	**MYG Myoglobin**	**1.586870461**	**0.909053**	**6**
Q9QZ76	GQHAAEIQPLAQSHATK	0.580926979	2	4.913355
Q9QZ76	HGCTVLTALGTILK	0.636662642	2	3.66195
Q9QZ76	KGQHAAEIQPLAQSHATK	5.93681432	3	5.459224
Q9QZ76	KKGQHAAEIQPLAQSHATK	2.825671316	3	4.50123
Q9QZ76	VEGDLAGHGQEVLISLFK	1.373221956	3	4.112271
Q9QZ76	YSGDFGADAQGAMSK	8.180464141	2	3.929589
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.200930093**	**0.547067**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	1.368768024	2	3.267828
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.325083527	2	3.393026
Q9QZA2	HEGALETLLR	1.142062273	2	2.325645
Q9QZA2	LLDEEEATDNDLR	1.145577885	2	4.050151
Q9QZA2	MVPVSVQQSLAVFSQR	1.358521428	2	3.131446
Q9QZA2	NIQVSHQEFSK	1.357307127	2	3.351847
Q9QZA2	STAVVEQGGIQTVDQLIK	1.286270308	2	4.299539
Q9QZA2	TMQGSEVVNVLK	1.281845497	2	3.277102
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.165413985**	**0.000418**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	1.097292546	2	5.082359
Q9QZD8	LFSGATMASSR	0.871344864	2	2.514286
Q9QZD8	MTGMALQVVR	1.341753542	2	2.78806
Q9QZD8	NYSHALDGLYR	1.286999552	2	2.832427
Q9QZD8	VHLQTQQEVK	1.190342966	2	3.048643
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.166351848	2	5.680471
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	1.248935912	3	3.538801
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.52396757**	**0.000192**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.494809405	2	4.114955
Q9QZH8	WFLQEDILEK	1.530869938	2	2.949725
Q9QZR9	**chain**	**1.102265121**	**0.56282**	**2**
Q9QZR9	EGPSGPFGALGQDGKDGPR	20.19202609		
Q9QZR9	GASGLLEMGPPGPMGMPGQK	1.071531123		
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.487529971**	**5.97E-08**	**5**
Q9QZU7	IDANNVAYTTGK	0.963179476	2	3.07129
Q9QZU7	MDDLTFDQK	3.002824085	2	2.554308
Q9QZU7	MNPGDVITFDNWR	1.587681351	2	2.808377
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.22327077	2	4.794799
Q9QZU7	SYEAGTEISR	1.754486442	2	2.754013
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**1.948036938**	**0.000113**	**2**
Q9QZX8	GIGETPIVPLGISYLDDFAK	1.953926092	2	3.489009
Q9QZX8	QFTDEGNPDSVNK	1.082737648	2	3.582814
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**1.187501277**	**4.62E-07**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	2.616422324	3	4.804595
Q9R063	ETDLLLDDSLVSLFGNR	1.488658118	2	4.024667
Q9R063	GVLFGVPGAFTPGCSK	1.354819794	2	4.191882
Q9R063	THLPGFVEQAGALK	1.092897017	3	4.484272
Q9R063	VGDTIPSVEVFEGEPGK	1.208733756	2	4.234874
Q9R063	VGDTIPSVEVFEGEPGKK	1.073334916	2	4.170047
Q9R063	VNLAELFK	1.334292662	2	2.564893

Q9R063	VQLLADPTGAFGK	1.306562405	2	3.557152
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**0.954539535**	**0.173453**	**2**
Q9R064	ADTSSLTVDVMSPASK	0.91445344	2	4.274127
Q9R064	LYVYNTDTDNCR	2.32391518	2	2.531029
Q9R099	**TBL2 Transducin beta_like protein 2**	**1.509951889**	**9.79E-07**	**4**
Q9R099	ANVELDHATLVR	1.729017682	2	2.423787
Q9R099	FEEASTMPCR	1.133565469	2	2.666215
Q9R099	FLASCGDR	1.184137956	2	2.339933
Q9R099	LQQQLTQAQEALK	1.920770264	2	4.109718
Q9R0N0	**GALK1 Galactokinase**	**1.449309479**	**6.78E-08**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	1.271574181	3	4.464148
Q9R0N0	MEELEAGR	1.541487906	2	2.459736
Q9R0N0	RQCEEVAQALGK	1.004300469	2	3.20385
Q9R0N0	SLETSLVPLSDPK	1.449281248	2	3.288851
Q9R0N0	TDGLVSLLTTSK	1.414104411	2	3.802475
Q9R0N0	VEELLAEAR	1.483784519	2	3.116374
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.149370025**	**6.84E-05**	**6**
Q9R0T3	AEPSVAEYTVR	1.185374292	2	2.4658
Q9R0T3	ICSEVLQLEPDNVNALK	1.351439254	2	4.759593
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	0.977908161	3	5.658128
Q9R0T3	LIGSAEELIR	1.110316865	2	2.616841
Q9R0T3	LKNDNTEAFYK	1.53832142	2	2.649298
Q9R0T3	SNPSENEEKEAQSQLVK	1.249924349	2	5.157658
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.196503095**	**0.012203**	**4**
Q9R112	EGNALFTFPNTPVK	1.360500721	2	3.039901
Q9R112	STLSVIPSGVQWIQDR	1.578031615	2	2.790172
Q9R112	TAAAVAAQSGILDR	1.076607688	2	3.326176
Q9R112	VGAENVAIVEPSER	1.142053338	2	2.86908
Q9R172	**NOTC3 Neurogenic locus notch homolog protein 3**	**1.213822036**	**0.652043**	**2**
Q9R172	CTHQQPSREAACLCLPGWVGER	1.719405075	3	3.396993
Q9R172	YGGKCLDLVDK	1.162773909	1	1.987887
Q9R1T3	**CATZ Cathepsin Z**	**1.652050852**	**8.2E-09**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.655091139	2	3.865475
Q9R1T3	VGDYGSLSGR	1.389162719	2	2.828759
Q9R1T4	**SEPT6 Septin_6**	**1.456304266**	**0.300163**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(1	0.885772637		
Q9R1T4	STLMDTLFNTK	2.384076084	2	2.879758
Q9R1T5	**ACY2 Aspartoacylase**	**1.698446794**	**0.214048**	**2**
Q9R1T5	EAFAKTTKLTLNAK	28.14072247	2	2.520172
Q9R1T5	VIPLGGDCTVYPVFVNEAAYYEK	1.33375068	3	3.586843
Q9R1T9	**KCNH4 Potassium voltage_gated channel subfamily H member 4**	**1.772249425**	**0.174875**	**2**
Q9R1T9	DGSAFWCLLDMMPIK+Oxidation(10	1.8014346		
Q9R1T9	KDGSAFWCLLDMMPIK+Oxidation(11)Oxidation(12	1.117325348		
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**0.945356556**	**0.003325**	**4**
Q9R1Z0	LCQNNFALGYK	1.406916737	2	2.403408
Q9R1Z0	LTLSALVDGK	1.81617123	2	2.300163
Q9R1Z0	LTVDTIFVPNTGK	1.319665334	2	2.961826
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.915670316	2	4.295606
Q9WTR8	**PHLP1 PH domain leucine_rich repeat protein phosphatase 1**	**1.582118799**	**0.574171**	**2**
Q9WTR8	LEELEEIDISGNK	2.65395794	2	2.721641
Q9WTR8	LEELEEIDISGNKLK	1.300636768	2	2.396025
Q9WTT6	**GUAD Guanine deaminase**	**0.921363953**	**4.81E-08**	**10**

Q9WTT6	EIGNFEVGKDFDALLINPR	1.661638397	2	4.082459
Q9WTT6	ETTEESVKETER	1.412734653	2	3.162794
Q9WTT6	FQSTDVAEEVYTR	1.150583881	2	3.718604
Q9WTT6	FSLSCTETLMSELGNIAK	1.598288709	2	3.643303
Q9WTT6	GTFVHSTWTCPMEVLR	1.227239112	2	3.159654
Q9WTT6	IVFLEESSQQEK	1.26287847	2	4.253374
Q9WTT6	NIEEVYVGGK	0.770251944	1	2.695272
Q9WTT6	NYTDVYDKNNLLTNK	0.653635649	2	4.417058
Q9WTT6	THDLYIQSHISENREEIEAVK	1.742790863	3	4.475668
Q9WTT6	VCMDLNNTVPEYK	1.130015914	2	3.618476
Q9WTT7	**BZW2 Basic leucine zipper and W2 domain_containing protein 2**	**1.413454064**	**0.291203**	**2**
Q9WTT7	AWMAEKDANSVTSSLR+Oxidation(2	1.483995203		
Q9WTT7	ELQERLSQECPIK	1.400636908	2	2.550366
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**1.022663202**	**0.109998**	**9**
Q9WU19	AIFVTVDTPYLGNR	0.808275328	2	4.254089
Q9WU19	AVFVGRPIIWGLAFQGEK	0.823057542	3	4.011765
Q9WU19	GVQDVLEILK	1.19880855	2	3.62784
Q9WU19	GVQDVLEILKEEFR	1.202647961	2	4.301413
Q9WU19	HGVDGILVSNHGAR	1.101736149	3	4.531812
Q9WU19	MKNFETNDLAFSPK+Oxidation(0	1.187970896		
Q9WU19	NFETNDLAFSPK	0.762846363	2	3.57137
Q9WU19	NVADIDLSTSVLGQR	1.484891148	2	4.943469
Q9WU19	VEVFLDGGVR	1.588374279	2	2.685202
Q9WU79	**PROD Proline dehydrogenase 1_ mitochondrial**	**0.984147728**	**0.562816**	**2**
Q9WU79	FTEEEEQQMK	0.979053005	2	3.118779
Q9WU79	HLVVPNVQTGQLEPLLSR	1.476877101	2	2.339939
Q9WU82	**CTNB1 Catenin beta_1**	**1.292035571**	**5.3E-06**	**5**
Q9WU82	HQEAEMAQNAVR	1.62593715	2	3.409784
Q9WU82	LLNDEDQVVVNK	0.201578033	2	3.308506
Q9WU82	TMQNTNDVETAR	0.98740493	2	3.586241
Q9WU82	TMQNTNDVETAR+Oxidation(1	1.614984141		
Q9WU82	TSMGGTQQQFVEGVR	1.357390218	2	3.527608
Q9WUA2	**SYFB Phenylalanyl_tRNA synthetase beta chain**	**1.158420746**	**0.499298**	**3**
Q9WUA2	EMVRADLINKK	1.241548526	2	2.388232
Q9WUA2	KEMVRADLINK	1.241548526	2	2.360949
Q9WUA2	TYTIANQFPLNK	1.134490745	2	2.448366
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.467796978**	**1.41E-06**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.227810958	2	3.629192
Q9WUC4	VCIESEHSSDILLATLNK	1.495407692	2	5.742793
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**2.634288541**	**0.746082**	**3**
Q9WUH4	AIVAGDQNVEYK	2.919422016	2	2.674625
Q9WUH4	FCANTCVECR	1.936559719	2	2.718921
Q9WUH4	FVFHNEQVYCPDCAK	2.543734817	2	4.21178
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**1.461356905**	**0.116049**	**2**
Q9WUI1	ILDFGLAR	1.430380465	2	2.732132
Q9WUI1	QELNKTVWEVPQR	1.700089199	2	2.430439
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.142197368**	**0.969544**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(6	1.12202703		
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7	1.152979962		
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**1.067911799**	**0.87536**	**5**
Q9WUS0	AVILGPPGSGK	1.103523726	2	2.458071
Q9WUS0	GVLHQFSGTETNR	1.153334972	2	3.550042
Q9WUS0	TLVQAEALDR	1.03505339	2	2.821752
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.787392202	3	5.105786
Q9WUS0	YKDAAKPVIELYK	1.292500695	2	3.559247

Q9WUU8	**TNIP1 TNFAIP3_interacting protein 1**	**1.640425183**	**0.062748**	**2**
Q9WUU8	IFEEDFQRER	1.30951591	2	2.326398
Q9WUU8	QENEALK	1.679060897	1	2.292133
Q9WV85	**NDK3 Nucleoside diphosphate kinase 3**	**1.127566591**	**0.039927**	**3**
Q9WV85	LVKYMSSGPVVAMVWQGLDVVHASR+Oxidation(4)Oxidation(12	1.624579195		
Q9WV85	LVQASEELLR	1.484091092	2	2.709014
Q9WV85	TFLAVKPDGVQR	0.860482976	2	2.677974
Q9WVC0	**SEPT7 Septin_7**	**1.160369821**	**0.092747**	**3**
Q9WVC0	ADTLTPEECQQFK	0.990297737	2	2.857772
Q9WVC0	FEDYLNAESR	1.851000058	2	2.761629
Q9WVC0	NLEGYVGFANLPNQVYR	1.448255883	2	3.62276
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**2.988334864**	**1.14E-08**	**3**
Q9WVD5	DGPLGFYHGLSSTLLR	2.107277806	2	2.924236
Q9WVD5	LQTMYEMETSGK	2.989985649	2	3.128049
Q9WVD5	NEGITALYSGLKPTMIR	1.853353058	2	3.345052
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.973821223**	**0.352468**	**2**
Q9WVF7	AANMPDSELFELISENR	1.764072247	2	2.475903
Q9WVF7	MAWQWRGEFMPASR+Oxidation(0)Oxidation(9	0.591455904		
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**1.147819164**	**2.55E-07**	**13**
Q9WVK3	AGVYNLTK	1.190284774	2	2.52272
Q9WVK3	ASQPPSSSTQVTAIQCNIR	1.017477669	2	5.537068
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.087552783	3	6.299735
Q9WVK3	ELLHLGCNVVIASR	1.189997813	2	4.243767
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.327693891	2	5.485016
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12	3.22099089		
Q9WVK3	KEEEVNNLVK	1.160738881	3	4.018847
Q9WVK3	LTAAVDELR	1.379023086	2	3.187407
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	1.147769288	2	5.020341
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	1.311189494	3	3.757136
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	1.050091523	2	6.211107
Q9WVK3	TMALTWASSGVR	0.874851719	2	3.800287
Q9WVK3	TMALTWASSGVR+Oxidation(1	1.28366328		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.311705715**	**0.360711**	**17**
Q9WVK7	AADEFVEK	1.122492284	2	3.351208
Q9WVK7	DTPGFIVNR	1.551664688	2	2.703011
Q9WVK7	EDIDTAMK	0.811271323	1	2.151941
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.052915201	3	4.765929
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	1.246311777	3	5.483439
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(21	1.244332462		
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(8	1.277738787		
Q9WVK7	GDASKEDIDTAMK	0.950484903	2	3.891581
Q9WVK7	GDASKEDIDTAMK+Oxidation(11	1.008842846		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.968266644	4	5.895552
Q9WVK7	KGIEESLK	0.982246934	2	2.433297
Q9WVK7	KGIEESLKR	1.32102057	2	2.429588
Q9WVK7	LKNELFQR	1.492122064	2	2.645324
Q9WVK7	LLVPYLIEAIR	1.158583213	2	2.758321
Q9WVK7	LVEVIK	1.115661927	2	2.411884
Q9WVK7	TFESLVDFCK	1.335813701	2	3.443285
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	0.940444885	3	6.056847
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.270381318**	**0.002363**	**3**

Q9Z0N2	IVLTNPVCTEVGEK	1.010542155	2	2.914335
Q9Z0N2	SFDVNKPGCEVDDLK	1.638727407	2	3.331222
Q9Z0N2	VGQEIEVRPGIVSK	1.325727385	2	3.259018
Q9Z0U5	**ADO Aldehyde oxidase**	**2.589853471**	**1.06E-07**	**17**
Q9Z0U5	EFQPLDPTQELIFPPELMR	1.863740945	2	2.626255
Q9Z0U5	ELSILYGGVGPTTIGAK	1.779317875	2	3.546606
Q9Z0U5	GEDMLITGGR	2.543877973	2	2.6167
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	1.76371811	2	4.607535
Q9Z0U5	GYESNINWEK	2.605350787	2	2.626504
Q9Z0U5	HATGEAIYCDDMPAVDR	3.921427703	2	2.704537
Q9Z0U5	HIQDIVAATLK	1.82430604	2	2.727388
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	2.235409296	3	3.686975
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	1.579983612	3	3.498518
Q9Z0U5	KLECGNVDEAFK	1.743016146	2	3.656691
Q9Z0U5	LVLDEVTLAGSAPGGK	2.988737626	2	3.726038
Q9Z0U5	MTWISPVTLEELVEAK	1.483634028	2	3.41583
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	2.519621073	2	3.099247
Q9Z0U5	NMASLGGHIVSR	1.895580455	2	3.170923
Q9Z0U5	QQNALAIVNSGMR	1.137342413	2	2.473143
Q9Z0U5	RLEPIISK	3.779747974	2	2.324546
Q9Z0U5	VVENNVDPEMMLLPYLR	2.299909997	2	2.839889
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**1.151775947**	**0.248504**	**5**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.96990999	3	5.189641
Q9Z0V5	GLFIIDDK	1.21613791	2	3.026597
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	1.353351915	3	3.559027
Q9Z0V5	QITLNDLPVGR	1.135630509	2	3.154166
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	1.146411824	3	5.615305
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**1.256612965**	**0.001036**	**5**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	1.302660647	3	5.436292
Q9Z0V6	GLFIIDPNGVIK	1.336498136	2	3.061068
Q9Z0V6	GTAVVNGEFK	1.290375797	2	2.729446
Q9Z0V6	HLSVNDLPVGR	1.249086791	2	2.589033
Q9Z0V6	NGGLGHMNITLLSDLTK	0.953143901	3	3.481045
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.20473438**	**0.0014**	**3**
Q9Z0W7	DEFTNTCPSDKEVEIAYSDVAK	1.046201522	3	3.642764
Q9Z0W7	FLDGDEMTLADCNLLPK	1.156642252	2	4.24368
Q9Z0W7	NSRPEANEALER	1.215910575	3	4.292357
Q9Z142	**TMM33 Transmembrane protein 33**	**1.57622355**	**0.054875**	**2**
Q9Z142	ALLANALTSALR	1.558944845	2	3.754112
Q9Z142	LSTNQQNILK	1.879139284	2	2.437054
Q9Z1A6	**VIGLN Vigilin**	**1.551855604**	**9.9E-20**	**22**
Q9Z1A6	ASVITQVFHVPLEER	2.046043663	2	3.280233
Q9Z1A6	DLANIAEVEVSIPAK	5.674118556	2	2.542457
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.795342381	3	3.453621
Q9Z1A6	ELQAEQEDR	1.368572157	2	2.410506
Q9Z1A6	HEVLLISAEQDKR	1.149790014	3	4.518711
Q9Z1A6	ICLEIMQR	1.138620611	2	2.52203
Q9Z1A6	IDLPAENSNSETIVITGK	0.85461076	2	4.228618
Q9Z1A6	IEGDPQGVQQAK	1.017347117	2	3.461374
Q9Z1A6	IIFPAAEDKDQDLITIIGK	1.163866617	2	4.477977
Q9Z1A6	IQIPRPDDPSNQIK	1.508362249	2	2.500819
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.584085077	2	3.470239
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.544334609	2	4.778924
Q9Z1A6	LGQALTEVYAK	1.245724048	2	3.455918
Q9Z1A6	LQDLELK	1.381326732	1	2.392766
Q9Z1A6	LQTQASATVPIPK	0.90294585	2	3.649959

Q9Z1A6	LVGEIMQETGTR	1.566188089	2	3.514382
Q9Z1A6	MDYVEINIDHK	1.342181871	2	2.803955
Q9Z1A6	MVADLVENSYSISVPIFK	1.345630696	3	3.405799
Q9Z1A6	RCDIIVISGR	1.209498271	2	2.958162
Q9Z1A6	TGAHLELSLAK	1.451501933	3	3.800119
Q9Z1A6	TKDLIIEQR	1.61254724	2	2.67492
Q9Z1A6	VKELQAEQEDR	1.361991409	3	3.748861
Q9Z1J8	**S14L3 SEC14_like protein 3**	**1.380106557**	**6.02E-05**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.904021727	2	2.632661
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.815668263	3	4.350212
Q9Z1J8	GSSHQVEYEILFPGCVLR	2.256088179	2	4.892803
Q9Z1L0	**PK3CB Phosphatidylinositol_4_5_bisphosphate 3_kinase catalytic subunit beta isoform**	**1.148731277**	**0.346068**	**2**
Q9Z1L0	MARLCFAVYAVLDK+Oxidation(0	1.173487541		
Q9Z1L0	QPYYYPPFDK	1.148693153	1	1.941834
Q9Z1M9	**SMC1A Structural maintenance of chromosomes protein 1A**	**1.811973263**	**0.082242**	**3**
Q9Z1M9	EIKEKDSELNQK	1.401144131	2	2.563669
Q9Z1M9	IIDETMAQLQDLK	1.740715545	2	2.427644
Q9Z1M9	SGVISGGASDLKAKAR	1.81491328	2	2.337994
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**1.293935741**	**0.319881**	**2**
Q9Z1N1	YVGSMVADVHR	1.198691255	2	2.698278
Q9Z1N1	YVGSMVADVHR+Oxidation(4	1.604835775		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.033928274**	**0.000462**	**5**
Q9Z1P2	DYETATLSEIK	1.450398996	1	1.970158
Q9Z1P2	GISQEQMNEFR	1.279229761	2	2.898403
Q9Z1P2	ICDQWDNLGALTQK	1.439355443	2	4.124104
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	2.184190085	3	3.916862
Q9Z1P2	MVSDINNAWGCLEQAEK	0.953093098	2	2.710698
Q9Z1W6	**LYRIC Protein LYRIC**	**1.283907926**	**0.523304**	**5**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.282307016	3	4.567927
Q9Z1W6	SSSQVPPMLQDTDKPK	1.53861349	2	3.411627
Q9Z1W6	SWQDELAQQAEEGSAR	2.037656184	2	5.682002
Q9Z1W6	TELGLDLGLEPK	1.584747154	2	3.379224
Q9Z1W6	TLPPAISAEPSVTLSK	1.211211346	2	2.935138
Q9Z1Y3	**CADH2 Cadherin_2**	**1.862617062**	**0.051725**	**4**
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	2.04724031	2	3.951784
Q9Z1Y3	IDPVNGQITTIAVLDR	1.472305584	2	3.926228
Q9Z1Y3	VCQCDSNGDCTDVDR	2.163155961	2	5.106618
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	1.307281233	3	3.597292
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.138406028**	**0.843769**	**3**
Q9Z270	FKGPFTDVVTTNLK	1.077213168	2	3.043178
Q9Z270	HEQILVLDPPSDLK	1.159788188	2	3.748403
Q9Z270	QDGPLPKPHSVSLNDTETR	2.041958611	3	3.40779
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**1.588364871**	**0.284495**	**2**
Q9Z2C8	SVGDGETVEFDVVEGEK	1.636492966	2	3.4501
Q9Z2C8	WFNVRNGYGFINRNDTK	1.567406295	2	2.30786
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**1.182779329**	**0.515035**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	1.115823714	2	5.003272
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.216293534	3	4.678381
Q9Z2I8	INFDDNAEFR	0.787848229	2	3.159896
Q9Z2I8	LEGTNVQEAQNILK	1.018151276	2	5.201319
Q9Z2I8	SENEPIENEAAR	0.955074241	2	4.197033
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	1.375130777	2	6.150728
Q9Z2I8	SSGLPITSAVDLEDAAK	1.246109554	2	4.963078

Q9Z2I8	SSGLPITSAVDLEDAAKK	1.000200905	2	2.700267
Q9Z2I8	VMVAEALDISR	1.289048625	2	3.197753
Q9Z2I8	VVGELAQQMIGYNLATK	1.637471764	3	3.392198
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.465099294**	**6.45E-07**	**9**
Q9Z2I9	ALIADSGLK	1.548033387	1	2.156108
Q9Z2I9	AVSSQMIGQK	1.703060819	2	2.924787
Q9Z2I9	ICNQVLVCER	1.570941284	2	2.984698
Q9Z2I9	ILACDDLDEAAK	1.063179686	2	3.312271
Q9Z2I9	INFDSNSAYR	1.25461892	2	3.015954
Q9Z2I9	LSEIVTLAK	1.325450623	2	2.394992
Q9Z2I9	MGFPSNIVDSAAENMIK	1.321545676	2	4.200814
Q9Z2I9	SSDEAYAIAK	1.464990576	2	3.355447
Q9Z2I9	VQAILVNIFGGIMR	1.842290931	2	3.835011
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.069442386**	**1.05E-08**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	2.959987534	2	3.128056
Q9Z2L0	KLETAVNLAWTAGNSNTR	1.374689162	2	5.448183
Q9Z2L0	LTFDSSFSPNTGK	1.221664034	2	3.720677
Q9Z2L0	LTFDSSFSPNTGKK	1.696936714	2	2.799069
Q9Z2L0	LTLSALLDGK	2.838448004	2	2.686695
Q9Z2L0	SENGLEFTSSGSANTETTK	1.02800518	2	3.763026
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	1.422651276	2	4.988048
Q9Z2L0	TKSENGLEFTSSGSANTETTK	0.635775389	3	3.597896
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	0.859569347	2	4.7374
Q9Z2L0	VTQSNFAVGYK	1.349326955	2	3.432572
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.034241657	2	4.915426
Q9Z2L0	WTEYGLTFTEK	1.660092294	1	2.90325
Q9Z2L0	YQVDPDACFSAK	1.244022241	2	3.394097
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.896453561**	**1.32E-05**	**6**
Q9Z2M4	AAVDAMTR	0.933098276	2	2.32431
Q9Z2M4	GQVLQLHAGAAK	0.960966571	2	3.42674
Q9Z2M4	HLAVEWGPQNIR	1.159120524	2	3.498792
Q9Z2M4	LLEFESSSAK	1.00838315	2	2.302423
Q9Z2M4	VNSLAPGAISGTEGLR	0.799646921	2	3.831405
Q9Z2M4	VPPAVMAAVDQALK	2.403424448	2	3.340923
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.060152878**	**0.028744**	**3**
Q9Z2M7	IGVVGGSDFEK	1.953603259	2	2.353583
Q9Z2M7	LQEQLGNDVVEK	0.347944701	2	3.862124
Q9Z2M7	TVGYTVTAPEDTR	1.14035168	2	2.658996
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.292895927**	**0.000296**	**17**
Q9Z2Q1	AQDGSNPLSLQDLIEK	1.074972053	2	3.420906
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.572903739	2	4.632329
Q9Z2Q1	CLSSATDPQTK	0.6267439	2	2.851838
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.51370739	2	3.408799
Q9Z2Q1	GGPGPLAGHPQVSR	0.711650682	2	3.117505
Q9Z2Q1	IDASQTDFEK	1.009359716	2	2.330748
Q9Z2Q1	IIAGDKEVVIAQK	1.417168835	2	3.037421
Q9Z2Q1	KIDASQTDFEK	1.254454723	2	2.516876
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.119972257	2	3.073418
Q9Z2Q1	QVQHILASASPSGR	1.683566053	2	3.278647
Q9Z2Q1	RQPVFISQVVTEK	0.568364087	2	3.740601
Q9Z2Q1	RQPVFISQVVTEKDFLSR	0.979611439	3	3.538083
Q9Z2Q1	TQPPEDISCIAWNR	1.227759369	2	2.966684
Q9Z2Q1	TTFEDLIQR	0.839534545	2	2.40678
Q9Z2Q1	VNFEEDSR	1.354798243	2	2.39294
Q9Z2Q1	VYSIMGGSIDGLR	1.292534792	2	2.801044

Q9Z2Q1	YLELLGYR	1.182040245	2	2.373797
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.596517163**	**0.023191**	**4**
Q9Z2Z8	AIECSYTSADGLK	5.664229141	2	3.409475
Q9Z2Z8	ASLADIWAK	2.032338295	2	2.352791
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.94806071	2	5.566527
Q9Z2Z8	GYLFPTSAEDCK	1.28964794	2	2.793896
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.072424302**	**0.983968**	**2**
Q9Z339	GSAPPGPVPEGQIR	1.081541706	2	3.156141
Q9Z339	LEALELNECIDHTPK	0.638276947	2	3.689148

Time point 8.0 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (8h)**	**P-value (8 h)**	**Peptide number (8 h)**
Accession number	Peptide sequence	Peptide Ratio (8 h)	Charge state	Xcorr
A0JPJ7	**OLA1 Obg_like ATPase 1**	**1.40865398**	**0.6206**	**2**
A0JPJ7	IGIVGLPNVGK	1.13690632	2	2.54238
A0JPJ7	YLEANMTQSALPK	1.42298935	2	2.67676
A1L108	**ARP5L Actin_related protein 2/3 complex subunit 5_like protein**	**1.09979983**	**0.57828**	**2**
A1L108	ALAVGGLGSIIR	1.03329037	2	2.75621
A1L108	SSEIEQAVQSLDR	1.39335751	2	2.73853
A1L1L2	**TM214 Transmembrane protein 214**	**0.89594331**	**0.3291**	**2**
A1L1L2	KGSGSNEHVVTCDTACK	6.40797431	3	3.52669
A1L1L2	YDLSSPIQPTSTLYER	0.8522633	2	3.33895
A2A6A1	**GPTC8 G patch domain_containing protein 8**	**0.81923758**	**0.30154**	**2**
A2A6A1	RVLEVEKEDTEELR	0.85396447	2	2.54085
A2A6A1	YKDYVDKEK	0.7699839	1	1.93375
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**0.99292784**	**0.73818**	**3**
A2AAE1	FQTNYASTTHLMTGK+Oxidation(11	0.95850479		
A2AAE1	LHYNSKTLKTESPNASR	1.26072582	2	2.55056
A2AAE1	QGTSSSQPGELRGRK	0.81014243	2	2.52225
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.13267972**	**0.89008**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	2.4549296	2	2.65825
A2ADY9	NPPLAEALLSGDLEK	1.05896184	2	2.84212
A2ADY9	VLVEQQQDR	1.21461843	2	2.88109
A2AF47	**DOC11 Dedicator of cytokinesis protein 11**	**1.0118257**	**0.87655**	**3**
A2AF47	LCSSVDVDMIQLQLK	1.9301454	2	2.50386
A2AF47	LTGLSEISLR	0.92904471	2	2.35212
A2AF47	MPFAWAARPIFKDVQGSLDLDGR+Oxidation(0	1.01387062		
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.7866659**	**0.05365**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13	0.17451111		
A2AGT5	GESVQEELLK	1.05596138	1	1.93865
A2APB8	**TPX2 Targeting protein for Xklp2**	**1.11277552**	**0.47697**	**2**
A2APB8	GIGEPFQGKNSLRK	1.31194845	2	2.3504
A2APB8	NKKDESLLPSK	1.11182123	2	2.48351
A2AQP0	**MYH7B Myosin_7B**	**1.72793203**	**0.49598**	**7**
A2AQP0	AITDAAMMAEELKK	1.87893166	2	3.33736
A2AQP0	DIDDLELTLAK	1.01435925	2	3.61918
A2AQP0	EQDTSAHLER	3.13263251	2	2.84886
A2AQP0	HDCDLLR	3.10487384	1	2.05437
A2AQP0	KAITDAAMMAEELKK	2.70280187	3	3.62427
A2AQP0	VEDEQLVGVQLQK	2.8524123	2	2.41987
A2AQP0	VGNEYVTK	3.06719234	2	2.41493
A2ASS6	**TITIN Titin**	**1.14959002**	**0.76202**	**13**
A2ASS6	AENRFGIGPPAETIQRTTAR	1.79853662	2	2.51301
A2ASS6	ATNEVGSDTCACTVK	4.32245096	2	3.82115
A2ASS6	ETAMLSWDVPENDGGAPVK+Oxidation(3	0.85174069		
A2ASS6	KDLNMVVSAARISCGGAIR	1.0957311	2	2.36533
A2ASS6	RRTEEGYYEAITAVELK	1.35579733	2	2.57674
A2ASS6	TCEIEIGQLK	1.05608248	2	2.31167
A2ASS6	TDSGAYILTATNPGGFAK	1.6278045	2	2.39487
A2ASS6	TFLQDQLVSLQVLK	1.30712124	1	1.9207
A2ASS6	VGDDAWIKDTTGTALR	1.16624631	2	2.37483
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	1.99702806	3	4.42801

A2ASS6	VLDTPGPPQNLAVK	1.73728716	2	2.31419
A2ASS6	YDGGHKLTGYIVEK	2.10392686	2	2.30845
A2ASS6	YGIGEPLDSEPETAR	1.19155519	2	2.99747
A2AU72	**ARMC3 Armadillo repeat_containing protein 3**	**1.381323**	**0.09607**	**2**
A2AU72	HASWAVMVCAGDEPMAVELCR+Oxidation(14	2.84407337		
A2AU72	TLGVITCDKEARTMLK+Oxidation(13	1.29865695		
A2AWL7	**MGAP MAX gene_associated protein**	**1.55749245**	**0.20224**	**2**
A2AWL7	ADVSLTTLLTAQASLK	1.47820968	2	2.46015
A2AWL7	TDQGILVTNRDARALLSR	2.37203638	3	3.32281
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.38025486**	**4.2E-05**	**11**
A2VCW9	AEGIVFNTQSTIK	1.90087904	2	2.48735
A2VCW9	AQEANMSLLDEVLK	1.86119741	2	3.46036
A2VCW9	GAQEVFNELPCEYVEPHELK	2.09044719	2	4.46829
A2VCW9	KTDGVYDPVEYEKYPER	1.48777669	3	3.61581
A2VCW9	KYDINTVNVTVGK	1.99361673	2	3.95365
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	1.32993621	3	4.1841
A2VCW9	QDAQSLLVPVK	1.14420603	2	2.55596
A2VCW9	REDVNAWER	1.97438594	2	2.975
A2VCW9	SSVVPVEGCPELPHK	1.38025958	2	2.7061
A2VCW9	VNMVTASYITPAMK	1.7541349	2	2.50333
A2VCW9	YDINTVNVTVGK	0.87700482	2	2.34604
A4Q9F4	**TTL11 Tubulin polyglutamylase TTLL11**	**1.01660069**	**0.99769**	**2**
A4Q9F4	ALRIMQNLFPEEYNFYPR+Oxidation(4	1.02246689		
A4Q9F4	NLKPMLLEVNANPSMR	1.01330078	2	2.4453
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.36347439**	**0.57388**	**12**
A7VJC2	EESGKPGAHVTVK	2.28066054	2	3.13958
A7VJC2	GFGFVTFDDHDPVDK	0.95606034	2	4.34796
A7VJC2	GGGGNFGPGPGSNFR	1.16167345	2	3.18919
A7VJC2	GGNFGFGDSR	1.65304791	2	2.90223
A7VJC2	IDTIEIITDR	0.95943252	2	3.98512
A7VJC2	LFIGGLSFETTEESLR	2.59853363	2	3.64109
A7VJC2	LTDCVVMR	1.48564801	2	2.61326
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	1.5918798	2	6.06358
A7VJC2	NYYEQWGK	1.59521873	2	2.40653
A7VJC2	QEMQEVQSSR	1.02869062	2	3.02865
A7VJC2	QEMQEVQSSR+Oxidation(2	1.30332257		
A7VJC2	YHTINGHNAEVR	1.18833124	2	3.37763
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.51926309**	**0.31088**	**3**
B0BN93	GSIDEVDKR	1.51890933	2	2.47745
B0BN93	LNIGDLQATK	0.61070513	2	2.31404
B0BN93	SAWGQQPDLAANEAQLLR	2.07331734	2	2.81676
B0BNA7	**EIF3I Eukaryotic translation initiation factor 3 subunit I**	**1.63791506**	**0.00089**	**2**
B0BNA7	HVLTGSADNSCR	1.63768112	2	3.48495
B0BNA7	LFDSTSLEHQK	1.81524978	2	2.37482
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.24129995**	**0.01659**	**7**
B0BNE5	AFNGYLGPDQSK	0.93940844	2	3.17033
B0BNE5	FAIYLPPQAESAK	1.65162039	2	2.67297
B0BNE5	MYSYVTEELPQLINANFPVDPQR	1.24283185	3	5.57758
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.06218984	2	5.77284
B0BNE5	SVSAFAPICNPVLCPWGK	1.25661987	3	4.20303
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.34895726	3	4.88916
B0BNE5	VFEHSSVELK	1.20484218	2	2.81127
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.6298021**	**0.13345**	**2**

B0BNN3	ADGLAIIGVLMK	0.60703258	2	3.30061
B0BNN3	HDSSLKPVSVSYNPATAK	0.64021625	3	5.06419
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**0.96297256**	**0.0057**	**3**
B0K020	AMVNLQIQK	0.88615692	2	2.62225
B0K020	HNEETGDNVGPLIIK	0.75559022	2	5.15707
B0K020	VVHAFDMEDLGDK	1.28399294	3	3.93878
B1H267	**SNX5 Sorting nexin_5**	**1.07027687**	**0.99232**	**2**
B1H267	NNVSLLQSCIDLFK	1.08005968	2	3.13254
B1H267	TTLPTFQSPEFSVTR	1.06157292	2	3.59221
B2GUV7	**IF2P Eukaryotic translation initiation factor 5B**	**1.42141543**	**0.16066**	**2**
B2GUV7	HLQAQGVEVPSK	1.32187701	2	2.76141
B2GUV7	LKEGDTIIVPGVEGPIVTQIR	1.68805079	3	3.36647
B2GUZ5	**CAZA1 F_actin_capping protein subunit alpha_1**	**1.00416132**	**0.56452**	**3**
B2GUZ5	EASDPQPEDVDGGLK	0.49476323	2	2.51639
B2GUZ5	FITHAPPGEFNEVFNDVR	1.58485097	3	3.70062
B2GUZ5	FTITPPTAQVVGVLK	1.20322833	2	2.94658
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.69009141**	**0.01669**	**3**
B2GV24	NNPVHLITEEDLK	1.36539097	2	2.54554
B2GV24	TYDLPGDFLTQALTQR	1.71926139	2	3.2333
B2GV24	VNIVDLQQVINVDLTHIENR	1.33422075	3	3.62073
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**1.17615825**	**0.99286**	**6**
B2RYW9	ALAAQLPLIPR	0.82241576	2	2.85767
B2RYW9	GETALSVAR	1.21997775	2	3.07367
B2RYW9	KGDEVQCEIEELGVIINK	1.71454064	2	4.81224
B2RYW9	TFDTFCPLGPALVTK	1.09398729	2	4.97568
B2RYW9	VICVGLNYADHCQEQNVR	1.14100058	2	2.97759
B2RYW9	VNGEIVQSSNTNQMVFK	1.14551399	2	4.78679
B2RZ78	**VPS29 Vacuolar protein sorting_associated protein 29**	**0.87014268**	**0.50628**	**2**
B2RZ78	GDFDESLNYPEQK	0.86968031	2	3.63955
B2RZ78	IQHILCTGNLCTK	1.77658447	2	3.03615
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.05014867**	**0.99287**	**6**
B3DMA2	AVLTVTQYR	0.94835077	2	2.48295
B3DMA2	GSHIQENTGIPLMEELISIYCR	0.76797477	2	2.32737
B3DMA2	LYEHEVVAHWIAK	0.98131707	3	3.70689
B3DMA2	MELQDQAR	1.11052019	2	2.47929
B3DMA2	NLPDSDNEECLVHGDFK	0.81114564	2	3.46237
B3DMA2	SGQSNPTFFLQK	1.30026271	2	2.58689
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.75728066**	**0.00019**	**4**
B5DFC8	FEELTNLIR	1.757273	2	2.43461
B5DFC8	GTEITHAVVIK	1.8912631	2	2.89775
B5DFC8	LGSLVENNER	1.79914598	2	2.66618
B5DFC8	TEPTAQQNLALQLAEK	1.44767081	2	4.84914
B7ZNG0	**KIF7 Kinesin_like protein KIF7**	**1.06469971**	**2.1E-06**	**2**
B7ZNG0	ELGRHMWINQELK+Oxidation(5	0.75766377		
B7ZNG0	KEALMQEK	2.22489156	2	2.72165
D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.54579634**	**0.20442**	**2**
D3ZTX0	QCFYEDITQGTK	1.44408493	2	2.74209
D3ZTX0	SVIDYQTHFR	1.54589286	2	2.83794
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.94187714**	**0.0279**	**5**
D3ZW55	DFGWDPCFQPDGYEQTYAEMPK	2.46657909	2	3.30029
D3ZW55	IDLPEYQGEPDEISIQK	2.13299162	2	4.34766

D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.47109496	3	4.41666
D3ZW55	LKPEGLYQLLAGFEDK	2.77889656	3	3.58711
D3ZW55	LQEYFGVTDGAGDH	1.72828956	2	3.41133
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.12591459**	**0.76481**	**2**
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(12	1.12591459		
D3ZZL9	EKSQNDQNIMVQMK+Oxidation(9	1.12591459		
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.50621188**	**0.06192**	**4**
D4A4T9	FDPEANADDACTYHPGVPVFHDALK	1.4543904	3	3.53312
D4A4T9	HNSEKPPEPVKPEVK	1.40429233	3	3.65847
D4A4T9	KEEDSDEIKIGTSCK	1.10231009	2	2.53985
D4A4T9	LSSGNEEDKKEEDSDEIK	1.58604155	3	4.2974
D4A666	**UBN2 Ubinuclein_2**	**2.28929672**	**0.01356**	**2**
D4A666	GWMQARMLFK+Oxidation(2)Oxidation(6	2.23123871		
D4A666	KEEGEKEK	2.29585957	1	1.9093
E9Q557	**DESP Desmoplakin**	**0.91381949**	**0.91863**	**2**
E9Q557	KQVQTSQKNTLR	0.91154611	2	2.31847
E9Q557	SQCTQVVQER	1.12243702	2	2.45344
F6YLP3	EMFVYLSTQLKK+Oxidation(1	5.40002434		
F6YLP3	KEMFVYLSTQLKK	0.98442045	2	2.53663
F6YLP3	SGDISAVQPK	0.95881318	2	3.07669
F6YLP3	SMVTAGFEPVVIENVLEGDELR	1.76454178	2	3.59956
O08550	**MLL4 Histone_lysine N_methyltransferase MLL4**	**1.79828537**	**0.02559**	**2**
O08550	HAAVALGQARAMVPEDVPR	1.78647748	2	2.34271
O08550	MVQALTELLR+Oxidation(0	1.80288089		
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.24767761**	**0.49476**	**11**
O08557	DENATLDGGDVLFTGR	0.99825761	2	2.4135
O08557	DHLLIPVSNSEMEK	1.01290536	2	2.49321
O08557	DYAVSTVPVADSLHLK	1.16359751	2	3.67323
O08557	GAEILADTFK	0.97072793	1	2.09651
O08557	KEVDMMK	1.80431757	2	2.32322
O08557	LKDHLLIPVSNSEMEK	1.38024776	2	3.81113
O08557	LTVPDDMAANCIYLNIPSK	1.32931374	2	3.26704
O08557	SFCSMAGPNLIAIGSSESAQK	1.15216881	2	4.77321
O08557	SQGEEVDFAR	2.95371148	2	2.82443
O08557	TPEEYPESAK	2.0472271	2	2.36629
O08557	VDGLLTCCSVFINK	1.05758405	2	3.51176
O08583	**THOC4 THO complex subunit 4**	**0.94275643**	**0.54619**	**3**
O08583	MDMSLDDIIK	2.73321492	2	2.66865
O08583	QQLSAEELDAQLDAYNAR	0.87705578	2	3.40117
O08583	SLGTADVHFER	1.63960493	2	2.74813
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.18637803**	**0.10443**	**15**
O08601	EDTTMYLLALK	1.44249	2	2.53186
O08601	EFYSYENEPVGIENLK	1.68727966	2	4.23238
O08601	GCPSLAEHWKSIR	1.02217683	2	3.84246
O08601	GHTTGLSLNNER	1.54784362	2	2.54587
O08601	GSFASNDIR	1.31302457	2	2.71859
O08601	LILGGLEKPEK	0.94725772	2	2.44707
O08601	MLSASGDPVSVVK	1.21626056	2	3.57881
O08601	NALLPEGIPLLLK	2.05906839	3	3.58331
O08601	NILLSIGELPK	1.16004362	2	3.74861
O08601	REEILQILK	1.47581219	3	3.47206
O08601	SDSSIILQER	1.37201837	2	3.10638
O08601	SGSSSAYTGYVER	0.99114868	2	3.67906

O08601	SNLNIFQYIGK	1.17675945	2	3.18284
O08601	TTAAAVILK	1.0627737	2	2.31374
O08601	VKEFYSYENEPVGIENLK	1.29137664	2	3.58374
O08629	**TIF1B Transcription intermediary factor 1_beta**	**1.36518305**	**0.05272**	**2**
O08629	IVAERPGTNSTGPGPMAPPR	1.44093879	3	3.91025
O08629	LDLDLTSDSQPPVFK	1.27415839	2	4.25639
O08795	**GLU2B Glucosidase 2 subunit beta**	**1.98967605**	**0.2782**	**6**
O08795	ETVVTSTTEPSR	1.45790465	2	3.10225
O08795	KLWEEQQAAAK	1.10866076	2	3.41721
O08795	LWEEQQAAAK	1.32269711	2	2.98051
O08795	MPPYDEETQAIIDAAQEAR	3.26737086	2	5.1853
O08795	SLEDQVETLR	0.87143773	2	3.15339
O08795	YEQGTGCWQGPNR	1.23199517	2	3.77679
O09158	**CP3AP Cytochrome P450 3A25**	**0.37766123**	**0.76963**	**2**
O09158	DVEINGVFIPK	0.37766122	2	3.14244
O09158	VDFLQLMMNTQNSK	1.01639436	2	3.1092
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**2.00787248**	**9.9E-20**	**14**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.64124475	2	6.13019
O09171	AGPWTPEAAVEHPEAVR	2.00780554	2	5.0058
O09171	GAAELMQQK	2.02469526	2	3.64947
O09171	GAAELMQQK+Oxidation(5	2.71628326		
O09171	HGSWGSGLDMHTKPWIR	3.8276928	3	4.70597
O09171	IFHQQLEVFMK	1.28505605	2	3.5635
O09171	ISGQKVNEAACDIAR	1.50448183	2	4.44903
O09171	KEYWQNLR	2.31599925	3	3.44041
O09171	LNAGEVVIGDGGFVFALEK	3.10319129	3	5.9219
O09171	QGFIDLPEFPFGLEPR	2.54655316	2	5.0369
O09171	QVADEGDALVAGGVSQTPSYLSCK	86.9937927	2	6.10976
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	2.03762992	3	6.19249
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9	2.71146481		
O09171	VNEAACDIAR	1.81699618	2	4.03534
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.30059597**	**8.5E-09**	**9**
O09173	CFYNSDGDFLIVPQK	1.106306	2	3.09427
O09173	FSVDVFEETR	1.62636463	2	3.60658
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.61647938	3	3.74208
O09173	NCMSEFMGLIK	1.50534604	2	3.20137
O09173	QDVSPFNVVAWHGNYTPYK	1.81874896	2	3.75095
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.29829795	3	3.88122
O09173	SLRPGVAIADFVIFPPR	0.86444516	2	3.71214
O09173	TFRPPYYHR	0.91547103	3	3.49392
O09173	YISGFGNECASEDPR	1.34186867	2	3.92119
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.11493379**	**0.1853**	**17**
O35077	ANTIGISLIK	1.02657747	2	3.07506
O35077	DPAQGQLLK	1.52893977	2	2.38969
O35077	ELHSILQHK	1.05996599	2	2.56608
O35077	FCETTIGCK	1.17601039	2	2.66385
O35077	FCETTIGCKDPAQGQLLK	1.14709079	2	5.33586
O35077	GIDEGPNGLK	1.35891972	2	2.92108
O35077	GLVDKFPLFTAVYK	0.95688239	3	3.72259
O35077	ICDQLKGHLK	0.94747104	3	3.7979
O35077	ITVVQEVDTVEICGALK	2.45127279	2	3.1124
O35077	IVGSNASQLAHFDPR	1.83475113	2	3.11567
O35077	KLTEIINTQHENVK	1.12197783	2	5.27307
O35077	LTEIINTQHENVK	1.13464383	2	4.41608

O35077	NIVAVGAGFCDGLGFGDNTK	1.97821781	2	5.57218
O35077	SIEQLEK	1.08727877	2	2.38229
O35077	VCIVGSGNWGSAIAK	1.38192748	2	4.35355
O35077	VCYEGQPVGEFICCLQNHPEHM	1.65887507	2	4.13189
O35077	VTMWVFEEDIGGR	1.45961966	2	3.39004
O35078	**OXDA D_amino_acid oxidase**	**0.86698063**	**0.26415**	**2**
O35078	GQIIQVEAPWIK	0.83743558	2	3.09514
O35078	SCCQLEPTLK	6.0590146	2	2.64774
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**1.23956272**	**0.77895**	**4**
O35094	AISQGVESVKK	1.1699592	2	2.37212
O35094	KLEESDALQEAR	1.24595013	2	3.59226
O35094	TEMSEVLTEILR	1.36501143	2	3.27418
O35094	VTDLLGGLFSK	1.10372491	2	2.58215
O35142	**COPB2 Coatomer subunit beta_**	**1.34910551**	**3.4E-05**	**5**
O35142	AAESLADPTEYENLFPGLK	2.02057096	2	3.88585
O35142	EEPAMSMDANGKIIWAK	1.84132163	2	2.53063
O35142	FELALQLGELK	1.62079622	2	3.05484
O35142	GSNNVALGYDEGSIIVK	1.13729822	2	3.55879
O35142	TFEVCDLPVR	1.19512389	2	2.9816
O35244	**PRDX6 Peroxiredoxin_6**	**1.24464939**	**0.38518**	**8**
O35244	DINAYNGAAPTEK	1.34015048	2	3.95067
O35244	DLAILLGMLDPAEKDEK	1.36817813	2	3.95115
O35244	GESVMVLPTLPEEEAK	1.81462306	2	3.25513
O35244	KGESVMVLPTLPEEEAK	1.20626272	2	5.33237
O35244	LSILYPATTGR	1.50702705	2	3.14751
O35244	NFDEILR	1.09015887	1	2.27184
O35244	VVDSLQLTASNPVATPVDWK	1.48836852	3	5.52461
O35244	VVFIFGPDKK	1.1158099	2	2.89644
O35286	**DHX15 Putative pre_mRNA_splicing factor ATP_dependent RNA helicase DHX15**	**1.54341625**	**0.00272**	**2**
O35286	TCTDIKPEWLVK	0.90503705	2	2.41357
O35286	TLATDILMGVLK	1.60758529	2	3.72182
O35331	**PDXK Pyridoxal kinase**	**0.86918549**	**0.11205**	**2**
O35331	AEAGEGQKPSPAQLELR	0.40969742	3	3.84535
O35331	MGPDTVVITSSDLPSPK	0.86975848	2	3.6926
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.99681689**	**0.83037**	**2**
O35469	DLGYEPLVSWEEAK	1.08876386	2	4.34285
O35469	TSEWIGTLVEQHR	0.79350611	2	3.40918
O35509	**RB11B Ras_related protein Rab_11B**	**1.18338016**	**0.89746**	**5**
O35509	AQIWDTAGQER	1.05293517	2	3.23688
O35509	GAVGALLVYDIAK	1.13877865	2	3.98611
O35509	HLTYENVER	1.35860405	2	2.46795
O35509	NEFNLESK	1.19164476	1	2.14578
O35509	VVLIGDSGVGK	1.12369851	2	2.47453
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**0.95896561**	**0.98485**	**2**
O35547	LERFEIPIK	1.00084437	2	2.53965
O35547	TAEDYSVDENGQR	0.92823412	2	3.23898
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**0.96050958**	**0.78162**	**7**
O35567	ALFEEVPELLTEAEK	1.55217648	2	3.50382
O35567	DGQVIGIGAGQQSR	2.50585164	2	3.89758
O35567	EVSDGIVAPGYEEEALK	0.9299747	2	3.80849
O35567	HVSPAGAAVGVPLSEDEAR	1.08958134	2	5.15093
O35567	SGVAYIVAPSGSTADK	1.06510506	2	2.86537
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.04184085	2	5.41396

O35567	YTQSNSVCYAK	1.17893529	2	3.13696
O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**1.06560585**	**0.88182**	**3**
O35593	AVAVVVDPIQSVK	1.04736025	2	3.078
O35593	AVEEEDKMTPEQLAIK	1.172301	2	4.72041
O35593	EMLELAKNYNK+Oxidation(1	1.18938986		
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.2278658**	**0.94278**	**3**
O35660	RYAMGDAPDYDR	1.20778961	2	3.37863
O35660	YAMGDAPDYDR	1.58047087	2	2.43877
O35660	YAMGDAPDYDR+Oxidation(2	1.2278818		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**1.57654141**	**0.81219**	**4**
O35760	AELGIPLEEVDLNEMNYLTR	4.32888066	2	4.21381
O35760	ITFPGCFTNSCCSHPLNNPGELEENDAMGVK	0.69372056	3	3.41562
O35760	NCHLNENIDK	0.67360857	3	3.33813
O35760	NVTLNPDPNEIK	0.56706715	2	3.14002
O35763	**MOES Moesin**	**0.97549536**	**0.8533**	**5**
O35763	ALTSELANAR	0.9603814	2	2.52082
O35763	AQMVQEDLEK	1.01560326	2	2.49221
O35763	AQQELEEQTR	0.94823124	2	2.81598
O35763	FYPEDVSEELIQDITQR	1.76983894	3	3.34265
O35763	TQEQLASEMAELTAR	1.47723948	2	4.01775
O35783	**CALU Calumenin**	**0.88802488**	**0.98628**	**2**
O35783	HLVYESDQDKDGK	1.00081876	2	3.9685
O35783	VHNDAQNFDYDHDAFLGAEEAK	0.88791612	3	5.23784
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**0.88696067**	**0.00209**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	1.30407039	2	4.78567
O35796	AFVEFLTDEIK	1.56619553	2	3.25357
O35796	AFVEFLTDEIKEEK	0.64691248	2	3.79041
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	2.04513365	3	5.68488
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.03851788**	**0.87555**	**7**
O35814	ALDLDSSCK	1.32323375	1	2.44694
O35814	ALSAGNIDDALQCYSEAIK	1.24044208	2	5.76436
O35814	AMADPEVQQIMSDPAMR	2.76322539	2	3.9249
O35814	CQQAEKILK	0.80515065	1	2.02042
O35814	DCEECIQLEPTFIK	1.55342208	2	4.42249
O35814	ELIEQLQNKPSDLGTK	0.9799319	2	4.02601
O35814	TVDLKPDWGK	1.04958891	2	2.68325
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**1.27392902**	**0.18531**	**2**
O35824	NVLCSACSGQGGK	1.27367349	2	3.26328
O35824	VSLEDLYNGK	1.4200427	2	2.33159
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.16382246**	**0.08412**	**8**
O35826	DEAVGALHLIQAAK	1.4177701	2	3.50699
O35826	EVGAFGTPVINLGTR	1.17858434	2	3.20231
O35826	ILGVGISTGGR	1.94555707	2	2.84115
O35826	IYGDGNAVPR	1.31090643	2	2.46368
O35826	SIDLQEPLQK	1.16240922	2	2.41405
O35826	TLVLFPNIDAGSK	1.25361978	2	2.66769
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.18151852	3	5.11907
O35826	VNPQEGVVLHSTK	2.03148359	2	2.53932
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.83832346**	**0.96853**	**5**
O35913	EGLQENVDGTENAK	0.816419	2	3.75747
O35913	GASFVPAFFILR	1.06752338	2	2.63569
O35913	SLSGTYMNSMLTQIER	0.78517988	2	4.57415

O35913	SQTLNPTQDPSECVK	1.40603821	2	4.14458
O35913	TFQFPGDIESSK	0.85495137	2	2.40918
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.03071565**	**0.65343**	**7**
O35952	ALLEVLGR	1.06890505	2	2.98591
O35952	FYEGTADEMYK	1.16313807	2	3.10067
O35952	HVEPGNTAVQEK	0.94919241	2	4.01675
O35952	LTTVLTTHHHWDHAGGNEK	1.58113796	3	3.5804
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.37998735	3	4.34602
O35952	TVQQHAGETDPVTTMR	1.15656236	2	4.74553
O35952	TVQQHAGETDPVTTMR+Oxidation(14	1.18512541		
O35987	**NSF1C NSFL1 cofactor p47**	**1.29405731**	**0.38952**	**5**
O35987	ASSSILINEAEPTTNIQIR	1.18589978	2	4.47322
O35987	EANLLNAVIVQR	1.56839947	2	3.06276
O35987	LGAAPEEESAYVAGER	0.82588255	2	4.29335
O35987	SYQDPSNAQFLESIR	1.31546547	2	4.18961
O35987	TGFSLDNGDLR	0.59913925	2	2.91945
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.51891678**	**0.40517**	**3**
O54753	IVNVSSVLGR	1.514577	2	2.57722
O54753	TWEATPEHIR	1.7458125	2	2.4014
O54753	YGVEAFSDVLR	1.30279464	2	3.29152
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.25782998**	**0.00534**	**3**
O54975	GSLTFEPLTLVPIQTK	1.27429202	2	4.09856
O54975	IENVVLVVPAK	1.03928064	2	2.6684
O54975	QQADFVDLSFPTISSTGPNGAIIHYAPIPETNR	1.50613094	3	3.71705
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.13875712**	**0.27928**	**4**
O55012	ATTLSNAVSSLASTGLSLTK	2.92826001	2	4.23092
O55012	ITAAQHSVTGSAVSK	1.4539245	2	4.63342
O55012	SGLQGYDMSTFIR	1.52683028	2	3.74714
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	1.10935269	3	5.7464
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.17470723**	**0.0006**	**7**
O55096	AGLLALEFYTPETANWR	2.23676067	2	3.61981
O55096	GEFEGFVAMVNK	0.95043144	2	2.68955
O55096	LASVLNTEPALDSELTSK	1.43740419	2	2.9879
O55096	LEGSEVQLVEYEASAAGLIR	2.00073909	2	3.91228
O55096	NVSLGNVLAVAYATK	0.86644788	2	2.68389
O55096	SYEFQGNHFQVTR	0.94983422	2	4.03311
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.17884592	3	3.94689
O55125	**NIPS1 Protein NipSnap homolog 1**	**1.43290475**	**0.01394**	**4**
O55125	AGPNIYELR	1.11839333	2	2.99004
O55125	FSGGYPALMDCMNK	1.53982333	2	2.99941
O55125	GWDENVYYTVPLVR	1.07627073	2	3.60117
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.67012461	3	5.09872
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.38135751**	**0.99445**	**6**
O55171	ADAGGELDLAR	1.00167037	2	2.80929
O55171	DGLLDVVEALQSPLVDKK	1.40399848	2	4.92443
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.36659516	3	4.40854
O55171	GGELGLAMASFLK	1.79450372	2	4.03292
O55171	IEYFEEAVNYLR	1.22131889	2	4.04899
O55171	SCWDEPLSITVR	1.14469672	2	3.99257
O70127	**ABCBB Bile salt export pump**	**1.72313326**	**2.9E-07**	**7**
O70127	AGQITSEALSNIR	1.23869247	2	3.17384
O70127	AGSIADEVLSSIR	2.03626519	2	2.9629
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.83102769	3	4.35131

O70127	ILLLDEATSALDTESEK	1.89037799	2	4.27576
O70127	ILLLDMATSALDNESEAR	6.08281015	2	2.31426
O70127	KFGEENHAFESDGSHNNDKK	2.11662497	3	4.49019
O70127	STALQLIQR	1.15035401	2	2.70162
O70133	**DHX9 ATP_dependent RNA helicase A**	**0.98224661**	**0.96621**	**3**
O70133	ELDALDANDELTPLGR	0.81734627	2	2.50678
O70133	KMTPAYEIRAVGNK	1.14172031	2	2.44311
O70133	YPSPFFVFGEKIR	1.11173923	2	2.38157
O70173	**P3C2G Phosphatidylinositol_4_phosphate 3_kinase C2 domain_containing subunit gamma**	**0.98898843**	**0.9977**	**2**
O70173	LLGDIGEKVK	0.98751387	2	2.31537
O70173	WTFSHPLEALGLLTSR	0.98925174	2	2.4256
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.38557999**	**9.9E-20**	**14**
O70199	EADLVFISVNTPTK	1.29269311	2	2.35235
O70199	EQIVVDLSHPGVSADDQVSR	1.07126928	2	5.61749
O70199	FSLQDPPNKKPK	1.76557242	2	2.38953
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.68378436	3	6.6251
O70199	IIDSLFNTVTDK	1.66447269	2	2.38015
O70199	IIDSLFNTVTDKK	1.03346968	2	3.73759
O70199	ILTTNTWSSELSK	1.19349718	2	3.84071
O70199	INAWNSPTLPIYEPGLK	1.34136417	2	4.20048
O70199	MLKPAFIFDGR	1.889091	2	2.44935
O70199	NLFFSTNIDDAIR	1.29438212	2	3.42067
O70199	VLDGLHNELQTIGFQIETIGK	1.40550073	2	5.42973
O70199	VLIGGDETPEGQR	1.19475382	2	3.52231
O70199	VTVVDVNEAR	1.31216125	2	3.17918
O70199	YWQQVIDMNDYQR	2.07095633	2	4.28493
O70251	**EF1B Elongation factor 1_beta**	**1.56093571**	**0.28981**	**4**
O70251	SIQADGLVWGSSK	1.15273608	2	3.31493
O70251	SSILLDVKPWDDETDMTK	1.76847219	2	4.27211
O70251	SSILLDVKPWDDETDMTKLEECVR	2.00161823	3	5.22435
O70251	TPAGLQVLNDYLADK	1.58895976	2	3.97247
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.27098492**	**2.6E-10**	**17**
O70351	EVQAALTLAK	1.1502807	2	2.62171
O70351	GGIVGMTLPIAR	1.32050338	2	3.74667
O70351	GLVAVITGGASGLGLSTAK	1.2642467	2	4.84912
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.33177989	3	4.83826
O70351	IDVAVNCAGIAVAIK	2.26301345	2	4.43783
O70351	KLGGNCIFAPANVTSEK	1.19838152	2	4.85623
O70351	KNQVHTLEDFQR	1.40585849	2	3.95542
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.20108994	3	5.28533
O70351	LGGNCIFAPANVTSEK	1.32998876	2	3.42071
O70351	LVAGVMGQNEPDQGGQR	1.58888414	2	5.6786
O70351	LVGQGATAVLLDVPNSEGETEAK	1.96807254	2	5.41745
O70351	LVGQGATAVLLDVPNSEGETEAKK	1.04553023	3	4.28588
O70351	NFLASQVPFPSR	1.04828522	2	4.62477
O70351	NQVHTLEDFQR	1.2378566	2	3.33301
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.09638928	2	5.55966
O70351	VINVNLIGTFNVIR	1.4751742	2	4.60512
O70351	VVTIAPGLFATPLLTTLPDK	1.33191337	2	5.04859
O70456	**1433S 14_3_3 protein sigma**	**1.0367159**	**2.1E-12**	**3**
O70456	DSTLIMQLLR	1.84480285	2	3.74881
O70456	NLLSVAYK	0.89347451	2	2.4321
O70456	VLSSIEQK	1.07297529	2	2.60992
O88202	**LPP60 60 kDa lysophospholipase**	**1.94462381**	**0.03464**	**4**
O88202	AAGAHLSPQELEDVGTELCR	1.62742804	3	3.89796

O88202	GEMTLPTTDDLLGDDMLGCR	4.35111005	2	3.82205
O88202	GVDVDACNEDGQSPLLLAVR	1.97338525	2	5.09815
O88202	SEGGVLVPGR	1.82681004	2	2.54307
O88379	**BAZ1A Bromodomain adjacent to zinc finger domain protein 1A**	**1.83333042**	**6.8E-05**	**2**
O88379	ERDKLLK	2.07316173	2	2.34406
O88379	NTAKSASKNLR	1.82794324	2	2.79429
O88397	**SO1A5 Solute carrier organic anion transporter family member 1A5**	**1.04084109**	**0.51693**	**2**
O88397	TCLHWGTLK	0.71103936	2	2.32256
O88397	YLEQQYGK	1.11050969	2	2.76794
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.30561181**	**0.00062**	**6**
O88428	GCTVWLTGLSGAGK	2.84850617	2	3.26724
O88428	GFTGIDSDYEKPETPECVLK	1.30211866	2	4.96753
O88428	GIHELFVPENK	1.41374576	2	2.75745
O88428	NLGFSAGDREENIR	1.15311423	2	3.30825
O88428	STNVVYQAHHVSR	1.14192481	2	4.25577
O88428	VLSMAPGLTSVEIIPFR	1.47028073	2	3.63824
O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**1.16110319**	**0.08452**	**3**
O88491	ENSEGAFGVLLPADAVQKAR	0.85410552	2	2.36579
O88491	ETGIPSLMPQTK	1.61027457	2	2.32075
O88491	SGKGEGLKLLNNMHEK	1.44767081	2	2.75928
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.20636964**	**0.48232**	**18**
O88600	AESEEMETSQAGSK	1.25225677	2	4.662
O88600	AFSDPFVEAEK	1.06796175	2	3.02864
O88600	AGGIETIANEYSDR	1.31880696	2	3.41349
O88600	FLEMCDDLLAR	0.87139123	2	2.50302
O88600	FQESEERPK	1.19411336	2	2.76374
O88600	FVSEDDRNNFTLK	1.07593655	2	2.78235
O88600	GCALQCAILSPAFK	1.05583678	2	3.80004
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	1.08902184	3	5.11052
O88600	LKETAESVLK	2.30858962	2	2.53628
O88600	MIMQDKLEK+Oxidation(0	1.23698334		
O88600	MQVDQEEPHTEEQQPQTPAENK	1.09174666	3	5.32193
O88600	NFTTEQVTAMLLSK	1.60501971	2	4.11704
O88600	NKEDQYEHLDAADMTK	1.55215478	3	3.74273
O88600	SNLAYDIVQLPTGLTGIK	1.28393883	2	4.08276
O88600	SVMDATQIAGLNCLR	1.41762028	2	3.59303
O88600	TSTVDLPIESQLLWQLDR	1.34443629	2	3.70737
O88600	VLATAFDTTLGGR	1.39372388	2	3.79454
O88600	WNSPAEEGSSDCEVFPK	1.29711013	2	3.82314
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.84181296**	**9.9E-20**	**21**
O88618	AFAACLGAIK	1.47897488	2	3.13147
O88618	AGEYEALPEK	1.23330247	2	2.79113
O88618	ALLDAAAFYCDK	2.12022006	2	3.5
O88618	ALLDAAAFYCDKEK	1.58273475	2	3.41544
O88618	EAQELNLPVVGSQLVGLVPLK	1.84538172	3	4.27521
O88618	GVSMDECVLCAK	1.68190209	2	3.70068
O88618	IIEYLVPDSGPEQSLLDASLR	1.61256898	2	4.86891
O88618	ISSLLQEAK	1.8386137	2	2.38561
O88618	KVQGIGWYLEEK	1.17579881	2	3.27075
O88618	LAEELNVPVYLYGEAAQMPSR	2.28962048	2	4.91619
O88618	LFVLEEEHR	1.34606116	2	2.84273
O88618	LGLDSLAPFDPK	2.04889317	2	3.84132
O88618	MGALDVCPFIPVR	1.48552456	2	3.93709

O88618	MGALDVCPFIPVR+Oxidation(0	0.47044589		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	2.92936006	3	4.10469
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	2.39647616	2	3.93634
O88618	TASQLIDMR	1.5510969	2	2.36918
O88618	TCALQEGLR	1.79250172	2	2.81015
O88618	TQAALVLGSLEAR	1.41692011	2	5.09415
O88618	TVYTFVGQPECVVEGALSAAR	1.34702958	2	4.75826
O88618	VQGIGWYLEEK	1.63174266	2	3.07695
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.33879856**	**0.23533**	**9**
O88637	AHHSSQEMSSEYR	1.90560117	3	3.78689
O88637	GPPVFTQEER	1.22402804	2	2.70262
O88637	HKGPPVFTQEER	1.2005746	2	3.10687
O88637	HNCDFCVHGNDITLTVDGR	1.49175107	3	3.88288
O88637	NRLEYEAR	1.52022435	2	2.40918
O88637	TEIVPDRDGSDPYEEPK	1.36436023	2	2.86998
O88637	TQGVSTTDLVGR	1.7686705	2	3.16976
O88637	WVDEVVPAAPYVTTLETLDK	1.73946461	2	2.62211
O88637	YVSEVVIGAPYSVTAELLNHFK	1.50667196	3	3.76594
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**1.01325131**	**0.95547**	**2**
O88656	ASSEGGAATGAGLDSLHK	1.00749511	2	4.29018
O88656	NSVSQISVLSGGK	1.02271923	2	2.53192
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**1.26596389**	**0.51929**	**2**
O88696	GQATDIAIQAEEIMK	2.93657187	2	4.27359
O88696	VLVHPPQDGEDEPELVQK	1.18649952	3	3.95258
O88735	**MAP7 Ensconsin**	**1.30460494**	**0.75333**	**2**
O88735	KTTEQRNGDIAK	1.09532276	2	2.57664
O88735	TSAGTTDPEEATR	1.31753704	2	2.6675
O88746	**TOM1 Target of Myb protein 1**	**1.18700637**	**0.9688**	**3**
O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	1.11907589	3	5.52596
O88746	QQSTGAIPATQAR	1.02655153	2	2.70142
O88746	YEAPQTTDGLAGALDAR	1.20117859	2	3.89056
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.10745008**	**0.8859**	**3**
O88761	DTSEDIEELVEPVAAHGPK	0.90349433	2	4.1809
O88761	QGALIASALIMIQQTEITCPK	1.7002896	2	2.41419
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.107472	2	3.69429
O88767	**PARK7 Protein DJ_1**	**1.13702225**	**0.48769**	**8**
O88767	ALVILAK	1.96535925	2	2.37563
O88767	DVVICPDTSLEEAK	1.03484147	2	3.41998
O88767	GAEEMETVIPVDIMR	1.24263645	2	4.19968
O88767	GAEEMETVIPVDIMR+Oxidation(4	1.43550294		
O88767	GLIAAICAGPTALLAHEVGFGCK	1.42956215	2	4.45687
O88767	KGLIAAICAGPTALLAHEVGFGCK	0.92582015	3	3.99545
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	1.13764886	3	4.69795
O88767	VTVAGLAGKDPVQCSR	1.12756201	2	4.25168
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**1.42843982**	**0.71016**	**3**
O88794	FFTNYESR	1.72262823	2	2.32863
O88794	KKNEELGQLYR	1.18973901	2	2.98328
O88794	SSQIGAVVSR	2.18119798	2	2.81686
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.39555258**	**0.20108**	**14**
O88813	AEYLGSCLLHK	1.04373626	2	2.72412
O88813	AILEDLQK	0.88361013	1	2.23086
O88813	ATMLIENVEK	1.31269642	2	2.34114
O88813	FFQTQIK	1.20843173	1	2.02618

O88813	GAMLTHQNIVSNMAAFLK	0.86578452	3	3.59441
O88813	GLAVSDNGPCLGYR	1.14789917	2	3.43258
O88813	GSFEELCQNQCVK	0.91979978	2	4.42662
O88813	GYLKDPEK	1.08027857	2	2.3939
O88813	IGFFQGDIR	1.45683256	2	3.22653
O88813	SFLIGVVVPDPESLPSFAAK	1.05669263	2	4.35065
O88813	SIFVHPEPFSIENGLLTPTLK	1.62370146	2	3.63588
O88813	SRPILQVFVHGESLR	0.58539986	3	3.76821
O88813	TQEVLDKDGWLHTGDIGR	1.06371289	3	3.7425
O88813	TVILMDPFDDDLMK	2.15615616	2	3.51655
O88867	**KMO Kynurenine 3_monooxygenase**	**1.00073991**	**0.99191**	**7**
O88867	AVGLEDQIVSK	0.97617152	2	2.49406
O88867	DFFLLPAQPMISVK	1.5302737	2	2.7583
O88867	DLLTAVESYPNAK	0.81239103	2	2.39351
O88867	FNNDLSVCLPEFSR	1.11199804	2	4.06053
O88867	NFPDAIPLMGEQALMR	1.16162127	2	3.27576
O88867	SINLALSYR	1.35332412	2	2.38707
O88867	SQYILSISR	0.96686431	2	2.41832
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.08174877**	**0.74532**	**3**
O88941	ALESHAAAFK	0.8331269	2	2.46837
O88941	DLALPTLLNPK	1.09945991	2	2.77078
O88941	MDPSLFPPVPLFSGVPSR	1.18893271	2	2.74233
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.42708584**	**0.53749**	**3**
O88986	GTDELLGVMDQVTIINSTLGK	1.39589832	2	3.99463
O88986	HLDMADLEAK	1.52480045	2	2.44538
O88986	VQISAVHSEEDIDR	1.2627828	2	3.96126
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.43508121**	**3.2E-09**	**9**
O88989	DLDVAVLVGSMPR	1.97187185	3	4.18611
O88989	EKMDLTAKELTEEK+Oxidation(2	1.61357158		
O88989	ELTEEKETAFEFLSSA	4.66833041	2	3.47368
O88989	EVGVYEALKDDSWLK	2.69442883	2	4.40612
O88989	FVEGLPINDFSR	1.87471445	2	3.41743
O88989	GEFITTVQQR	1.28907499	2	3.98075
O88989	LGVTADDVK	1.45568858	2	2.92232
O88989	NVIIWGNHSSTQYPDVNHAK	1.28798694	2	5.81141
O88989	VIVVGNPANTNCLTASK	1.33664673	2	5.24321
O88990	**ACTN3 Alpha_actinin_3**	**1.2397554**	**0.58878**	**10**
O88990	AGTQIENIEEDFR	0.83125714	2	3.56462
O88990	ALDFIASK	1.30283299	2	2.67111
O88990	CQLEINFNTLQTK	1.25869078	2	3.84887
O88990	FAIQDISVEETSAK	1.46278406	2	4.344
O88990	GAILGIQGEIQK	2.24635455	2	3.07425
O88990	GLSQEQLNEFR	1.58453827	2	2.71471
O88990	HEAFESDLAAHQDR	1.50194211	3	4.45058
O88990	TINEVENQVLTR	1.26605811	2	3.21732
O88990	VGWEQLLTSIAR	1.35302343	2	2.71509
O88990	VLAVNQENEK	2.82949932	2	2.32277
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.97714946**	**0.00503**	**4**
O88994	CVLTTVDPDTGIIDR	1.01585171	2	4.32217
O88994	GVSVCETECTDMGLR	1.74130247	2	3.36238
O88994	QLQQVGTVSK	1.00173333	1	2.1798
O88994	RQLQQVGTVSK	0.79062181	2	3.08204
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.07648006**	**0.48896**	**4**
O89000	GMGLACGQDPELVR	1.07653445	2	3.48695

O89000	LENNFDDIK	1.49044795	2	2.46471
O89000	QEYVGGLSTSEIPQFR	0.8561579	2	3.3358
O89000	TEQDETGNWVEDEEQIVR	2.9081277	2	4.66486
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**0.91804164**	**0.99861**	**2**
O89032	DDSDINTSKTGEVSKR	0.89582959	2	2.59507
O89032	FPIEGGQKDPK	0.99477198	2	2.37496
O89046	**COR1B Coronin_1B**	**1.21328948**	**0.04205**	**3**
O89046	NDQCYEDIR	1.44764934	2	3.17609
O89046	NVLSDSKPAGYSR	1.21066132	2	3.25174
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.70128483	2	3.86418
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**0.976482**	**0.30607**	**5**
O89049	GFDQDMANK	0.45354325	2	2.45263
O89049	IEQIEAGTPGR	1.05676729	2	3.34847
O89049	IEQIEAGTPGRLK	1.57513707	2	2.63139
O89049	VVGFHVLGPNAGEVTQGFAAALK	1.04796615	3	4.42204
O89049	WGLGGTCVNVGCIPK	1.07726475	2	3.63223
O89079	**COPE Coatomer subunit epsilon**	**1.13148942**	**0.6967**	**2**
O89079	NAFYIGSYQQCINEAQR	1.94075955	2	2.78795
O89079	YGVVLDEIKPSSAPELQAVR	1.1194026	3	4.07226
P00173	**CYB5 Cytochrome b5**	**0.86573855**	**1.3E-15**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	0.80217288	2	5.41112
P00173	FLEEHPGGEEVLR	0.84716677	2	4.13475
P00173	STWVILHHK	0.77192287	2	2.94549
P00173	TYIIGELHPDDR	0.84034573	2	4.08594
P00173	VYDLTK	0.94652465	1	2.04902
P00173	YYTLEEIQK	0.86974474	2	2.96554
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.77388029**	**0.00035**	**10**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	2.08522338	3	4.78158
P00388	GMSADPEEYDLADLSSLPEIDK	2.73988073	2	4.98285
P00388	HILAILQDYPSLRPPIDHLCELLPR	1.76936714	4	4.96519
P00388	KKEEIPEFSK	1.09426062	2	2.73618
P00388	LEQLGAQR	1.5229697	2	2.53135
P00388	LIHEGGAHIYVCGDAR	2.25262042	3	3.63829
P00388	RSDEDYLYR	1.44503911	2	2.80988
P00388	SYENQKPPFDAK	1.90257601	2	3.32394
P00388	TYEHFNAMGK	1.51842306	2	2.61355
P00388	VHPNSVHICAVAVEYEAK	1.2621954	2	4.69648
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.51751752**	**0.30009**	**4**
P00406	ILYMMDEINNPVLTVK	1.15503938	2	4.45263
P00406	LLEVDNR	1.83225641	2	2.40901
P00406	VVLPMELPIR	1.4381773	2	2.44059
P00406	VVLPMELPIR+Oxidation(4	1.85367576		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.17621042**	**0.01028**	**18**
P00481	EATIPIVNGLSDLYHPIQILADYLTLQEHYGSLK	1.28480728	3	5.48309
P00481	FGMHLQAATPK	0.96354453	3	3.94349
P00481	GEYLPLLQGK	0.96529586	2	3.09492
P00481	GGNVLITDTWISMGQEDEK	1.20033069	2	5.21338
P00481	GGNVLITDTWISMGQEDEKK	0.89988873	2	4.61875
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.65863577	2	4.17853
P00481	GYEPDPNIVK	0.88425012	2	2.61914
P00481	LQAFQGYQVTMK	1.70016278	2	4.04133
P00481	LSMTNDPLEAAR	1.33781301	2	2.92172
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	2.17613004	3	6.03413
P00481	QKGEYLPLLQGK	0.91282143	2	3.43646
P00481	QSDLDILAK	1.09665517	1	2.06386

P00481	SLGMIFEK	1.19272719	2	2.81479
P00481	SLVFPEAENR	1.0168562	2	2.67016
P00481	SLVFPEAENRK	1.19621616	2	2.93898
P00481	VLSSMTDAVLAR	1.29919018	2	3.93124
P00481	VLSSMTDAVLAR+Oxidation(4	1.54830636		
P00481	YGKPVQSQVQLK	0.84967431	2	3.06799
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.76707356**	**6E-14**	**2**
P00502	FIQSPEDLEK	0.7676589	2	2.77343
P00502	WLLAAAGVEFDEK	0.62882315	2	4.37535
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.12544467**	**0.85136**	**19**
P00507	ASAELALGENSEVLK	0.99364577	2	4.71201
P00507	DAGMQLQGYR	1.62840744	2	2.72527
P00507	DDNGKPYVLPSVR	0.8807642	2	3.55012
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.03321732	3	5.22551
P00507	EYLPIGGLADFCK	1.27627506	2	2.88965
P00507	FVTVQTISGTGALR	1.14106586	2	5.16658
P00507	HFIEQGINVCLCQSYAK	1.66225114	2	4.88872
P00507	IAATILTSPDLR	2.06465448	2	3.05655
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.38311626	3	4.7361
P00507	ISVAGVTSGNVGYLAHAIHQVTK	1.26532493	2	4.42345
P00507	KMNLGVGAYR	1.74427874	2	2.65839
P00507	KQWLQEVK	0.77746952	1	2.16169
P00507	MNLGVGAYR	1.07681819	2	2.93945
P00507	NLDKEYLPIGGLADFCK	1.05286141	2	5.54931
P00507	NMGLYGER	1.26774242	2	2.66784
P00507	TCGFDFSGALEDISK	1.03098756	2	5.01904
P00507	TQLVSNLK	1.14224413	2	2.91855
P00507	VGAFTVVCK	1.12565628	2	3.23156
P00507	VGASFLQR	2.12880896	2	3.11008
P00564	**KCRM Creatine kinase M_type**	**5.17025317**	**0.39888**	**9**
P00564	DLFDPIIQDR	2.72151653	2	2.78149
P00564	FEEILTR	2.05135496	2	2.49143
P00564	GGDDLDPNYVLSSR	3.43778108	2	4.60846
P00564	GQSIDDMIPAQK	1.00822579	2	3.6771
P00564	GTGGVDTAAVGAVFDISNADR	6.03957764	2	5.34519
P00564	LGSSEVEQVQLVVDGVK	3.84030582	2	5.08929
P00564	LSVEALNSLTGEFK	2.3190502	2	4.29879
P00564	RGTGGVDTAAVGAVFDISNADR	5.42005041	2	4.14748
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	3.36899399	3	5.79625
P00787	**CATB Cathepsin B**	**1.25742108**	**0.16111**	**5**
P00787	EQWSNCPTIAQIR	1.66707968	2	2.63425
P00787	GENHCGIESEIVAGIPR	1.10417862	2	4.91291
P00787	HEAGDVMGGHAIR	1.35071609	3	3.86374
P00787	HEAGDVMGGHAIR+Oxidation(6	1.49554146		
P00787	MCEAGYSTSYKEDK	1.57613834	2	4.40045
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.18324772**	**5.7E-15**	**21**
P00884	ALQASALAAWGGK	1.80880345	2	4.98375
P00884	ATQEAFMK	1.51339804	2	2.75294
P00884	ATQEAFMK+Oxidation(6	1.64475155		
P00884	ELSEIAQR	1.67056606	1	2.19026
P00884	ETTIQGLDGLSER	1.29892059	2	3.87477
P00884	FPALTSEQK	1.46183415	2	2.35079
P00884	GILAADESVGTMGNR	1.08547519	2	5.41142
P00884	GILAADESVGTMGNR+Oxidation(11	0.73955575		
P00884	GIVVGIKLDQGGAPLAGTNK	1.65376094	2	4.37209
P00884	GIVVGIKLDQGGAPLAGTNKETTIQGLDGLSER	2.42902712	3	5.41877

P00884	IKVENTEENR	1.09108376	2	3.1908
P00884	IKVENTEENRR	1.19477076	2	3.15911
P00884	ISDQCPSSLAIQENANALAR	3.34459144	2	6.10385
P00884	KELSEIAQR	1.43752286	3	3.36062
P00884	KYTPEQVAMATVTALHR	1.99537158	3	6.03221
P00884	KYTPEQVAMATVTALHR+Oxidation(8	2.18850283		
P00884	LDQGGAPLAGTNK	1.35433188	2	4.65249
P00884	LDQGGAPLAGTNKETTIQGLDGLSER	1.36999516	3	4.3063
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.50805454	3	4.75731
P00884	YTPEQVAMATVTALHR	1.3873107	2	4.63929
P00884	YTPEQVAMATVTALHR+Oxidation(7	1.88930094		
P01015	**ANGT Angiotensinogen**	**2.71242382**	**1.6E-06**	**3**
P01015	GSYNLQDLLAQAK	2.86133906	2	3.1402
P01015	SLDLSTDPVLAAQK	2.50140172	2	3.32871
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	3.18784228	2	3.90488
P01026	**CO3 Complement C3**	**1.12786923**	**1.6E-06**	**21**
P01026	ACEPGVDYVYK	1.27119507	2	2.48401
P01026	ADIGCTPGSGK	1.69697881	2	3.02188
P01026	AFYEHAPK	0.98770295	2	2.44777
P01026	DSCVGTLVVKGDPR	0.86990133	2	2.58669
P01026	EYVLPSFEVLVEPTEK	1.48283361	2	3.70341
P01026	IFTVDNNLLPVGK	1.48232142	2	3.58548
P01026	IGLQEVEVK	1.11368774	2	2.6463
P01026	LPYSVVRNEQVEIR	2.25935773	2	2.3282
P01026	QNEGFSLTAK	1.12088722	2	2.45793
P01026	RVPVVTQGSDAQALTQDDGVAK	1.18923902	3	5.65816
P01026	SDVDEDIIPEEDIISR	1.79671835	2	4.50376
P01026	SGIPIVTSPYQIHFTK	2.20560885	2	2.94932
P01026	SGSDEVQAGQER	2.09588601	2	3.87248
P01026	SSVAVPYVIVPLK	1.96520438	2	2.97736
P01026	TNQGLQTDQREDPECAKPAAR	1.6133632	3	3.66002
P01026	TVLTGATGHLNR	1.59886378	2	2.84118
P01026	TVVIVIETPDGVPIKR	1.61957795	2	2.73759
P01026	VELKPGDNLNVNFHLR	1.56212291	3	3.91398
P01026	VHQFFNVGLIQPGSVK	1.292827	3	4.15348
P01026	VLIEDGSGEAVLSR	1.21918379	2	3.98511
P01026	VPVVTQGSDAQALTQDDGVAK	0.89333642	2	5.56998
P01048	**KNT1 T_kininogen 1**	**0.91353645**	**0.89856**	**3**
P01048	FSVATQICNITPGK	0.71635617	2	3.33431
P01048	KTEEDLCVGCFQPIPMDSSDLKPVLK	0.9154173	4	4.65972
P01048	TELTADCETK	0.90768732	2	2.34715
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.58855032**	**1**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.68166764	3	7.45363
P01946	FLASVSTVLTSK	0.58768471	2	4.01308
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.78330168	4	5.44757
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.88382356	5	6.35712
P01946	IGGHGGEYGEEALQR	0.56845425	3	5.093
P01946	LRVDPVNFK	0.80360012	2	2.572
P01946	MFAAFPTTK	0.56493126	2	2.76803
P01946	MFAAFPTTK+Oxidation(0	0.65062727		
P01946	TYFSHIDVSPGSAQVK	0.62631031	2	5.03779
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.66010021**	**0.81507**	**4**
P02089	GTFASLSELHCDK	0.68909774	2	3.76467
P02089	LHVDPENFR	0.723645	2	2.51555
P02089	YFDSFGDLSSASAIMGNPK	0.46490108	2	6.51648
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14	1.14850837		

P02091	**HBB1 Hemoglobin subunit beta_1**	**0.73216526**	**1**	**10**
P02091	AAVNGLWGK	1.13962793	2	2.7712
P02091	AAVNGLWGKVNPDDVGGEALGR	1.05857658	3	3.61442
P02091	EFTPCAQAAFQK	0.76119372	2	3.17506
P02091	GTFAHLSELHCDK	0.74293999	2	4.40014
P02091	GTFAHLSELHCDKLHVDPENFR	0.58218921	3	3.95259
P02091	KVINAFNDGLK	0.50014971	2	3.60008
P02091	LLGNMIVIVLGHHLGK	0.73125246	4	4.61855
P02091	VINAFNDGLK	0.57743964	2	2.98589
P02091	VNPDDVGGEALGR	0.59742104	2	4.03006
P02091	VVAGVASALAHK	0.88336114	2	3.74172
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.18635319**	**1.1E-16**	**6**
P02401	ILDSVGIEADDER	1.67523793	2	4.85031
P02401	KILDSVGIEADDER	1.07065355	2	4.00956
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.09293208	3	5.90573
P02401	NIEDVIAQGVGK	0.97976061	2	4.72825
P02401	VISELNGK	1.54346064	1	2.08877
P02401	YVASYLLAALGGNSNPSAK	1.42607858	2	5.22184
P02564	**MYH7 Myosin_7**	**1.17292152**	**0.67816**	**38**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	1.17596818	3	5.81066
P02564	ANDDLKENIAIVER	1.73079809	3	3.49
P02564	DLEEATLQHEATAAALR	1.31474613	2	4.96562
P02564	DVFVPDDKEEFVK	2.57342909	2	2.44454
P02564	EDQVMQQNPPK	2.10197142	2	3.04702
P02564	EEQAEPDGTEEADK	6.51845034	2	3.06285
P02564	ELENELEAEQK	1.11723916	2	2.37769
P02564	GQNVQQVAYAIGALAK	3.12505098	2	4.06569
P02564	GTLEDQIIQANPALEAFGNAK	6.12742452	3	5.69473
P02564	IEDEQALGSQLQK	5.09411863	2	5.09519
P02564	IEELEEELEAER	3.46859938	2	4.34576
P02564	IKELTYQTEEDRK	2.0421141	2	2.62685
P02564	ILNPAAIPEGQFIDSR	5.58216182	2	2.76913
P02564	KLAEKDEEMEQAK	5.42951607	3	3.65182
P02564	KLAEQELIETSER	1.8940881	2	3.50072
P02564	KLEDECSELKR	1.96127162	3	3.81971
P02564	KVQHELDEAEER	2.50206772	2	3.72532
P02564	LAEQELIETSER	0.77419458	2	3.39427
P02564	LDEAEQIALK	4.65759526	2	3.23504
P02564	LELDDVTSNMEQIIK	1.53614317	2	4.47015
P02564	LQDAEEAVEAVNAK	3.58009334	2	4.68299
P02564	LQNEIEDLMVDVER	2.97727851	2	3.89151
P02564	LTQESIMDLENDKQQLDER	5.35835784	3	3.82173
P02564	MDADLSQLQTEVEEAVQECR	2.94073304	2	4.98524
P02564	NALAHALQSAR	2.06266165	2	2.36926
P02564	NAYEESLEHLETFK	1.10785755	2	3.41042
P02564	NLQEEISDLTEQLGSTGK	2.72198042	2	5.07216
P02564	NLTEEMAGLDEIIVK	1.71334729	2	3.65398
P02564	NNLLQAELEELR	2.49078974	2	3.59633
P02564	QAEEAEEQANTNLSK	6.36847171	2	5.2352
P02564	QKYEESQSELESSQK	2.38325953	2	3.78316
P02564	QLEAEKLELQSALEEAEASLEHEEGK	4.92360114	3	3.60724
P02564	QREEQAEPDGTEEADK	4.426567	2	3.76492
P02564	TLEDQMNEHR	3.4808202	2	2.53192
P02564	VQHELDEAEER	1.42601892	2	3.46862
P02564	VQLLHSQNTSLINQK	0.91987077	2	4.09822
P02564	VVDSLQTSLDAETR	1.83492658	2	4.1174
P02564	YEESQSELESSQK	4.09841606	2	4.32505

P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**1.58100406**	**0.52975**	**12**
P02600	ALGTNPTNAEVK	2.23524485	2	3.33677
P02600	ALGTNPTNAEVKK	4.38100807	2	2.94539
P02600	DQGGYEDFVEGLR	6.9256245	2	3.81599
P02600	IEFEQFLPMMQAISNNK	1.66617337	3	3.91506
P02600	ITLSQVGDVLR	4.59534111	2	3.5886
P02600	KIEFEQFLPMMQAISNNK	2.00558501	2	4.90061
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	2.68308016	3	5.51342
P02600	KPAAAAPAPAPAPAPAPAKPK	3.45055701	3	3.70325
P02600	KPAAAAPAPAPAPAPAPAKPKEEK	3.13087078	3	5.2377
P02600	KVLGNPSNEEMNAK	4.17810536	2	3.65182
P02600	VLGNPSNEEMNAK	4.52530492	2	3.91882
P02600	VLGNPSNEEMNAK+Oxidation(9	2.19089998		
P02625	**PRVA Parvalbumin alpha**	**1.82393717**	**0.38141**	**5**
P02625	AIGAFTAADSFDHK	2.09902528	2	2.4556
P02625	AIGAFTAADSFDHKK	2.33993698	2	3.85334
P02625	SGFIEEDELGSILK	1.61545373	2	4.03336
P02625	TLMAAGDKDGDGK	1.15270992	2	3.38868
P02625	TLMAAGDKDGDGK+Oxidation(2	11.386101		
P02650	**APOE Apolipoprotein E**	**1.19251159**	**0.81028**	**12**
P02650	ELEEQLGPVAEETR	0.89594078	2	4.21141
P02650	GRLEEVGNQAR	1.10224036	2	3.39432
P02650	GWFEPLVEDMQR	1.2273028	2	3.04135
P02650	LEEVGNQAR	1.13175888	2	2.44534
P02650	LGADMEDLR	1.12521084	2	3.16475
P02650	LGPLVEQGR	1.11451575	2	2.99943
P02650	LQAEIFQAR	1.3360973	2	2.53109
P02650	MEEQTQQIR	1.25656646	2	3.37692
P02650	NEVNTMLGQSTEELR	1.02703902	2	4.64819
P02650	SKMEEQTQQIR	1.16031567	2	3.338
P02650	SKMEEQTQQIR+Oxidation(2	1.70307427		
P02650	TANLGAGAAQPLR	1.0031078	2	4.00139
P02680	**FIBG Fibrinogen gamma chain**	**1.11695383**	**0.73875**	**4**
P02680	LSIGDGQQHHMGGSK	1.5030794	2	3.40696
P02680	VGPESDKYR	1.22637447	2	2.7223
P02680	YEALLLTHESSIR	1.01034166	2	3.72808
P02680	YLQDIYTSNK	1.0559404	2	2.86956
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.12920627**	**1.8E-05**	**14**
P02692	AMGLPEDLIQK	0.87804539	2	3.48702
P02692	AMGLPEDLIQK+Oxidation(1	1.07640177		
P02692	GVSEIVHEGK	1.11097127	2	3.45281
P02692	GVSEIVHEGKK	1.17177392	2	3.29625
P02692	MEGDNKMVTTFKGIK+Oxidation(6	0.70726209		
P02692	SVTEFNGDTITNTMTLGDIVYK	1.40543615	3	5.76839
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13	1.58883212		
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.11550713	2	3.72356
P02692	VIHNEFTLGEECELETMTGEK	1.14736422	3	6.02258
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16	1.08900886		
P02692	VIHNEFTLGEECELETMTGEKVK	1.53418672	3	4.9054
P02692	VKLTITYGSK	0.99751521	1	2.02662
P02692	YQVQSQENFEPFMK	0.97686495	2	5.78362
P02692	YQVQSQENFEPFMK+Oxidation(12	0.88843355		
P02696	**RET1 Retinol_binding protein 1**	**1.72797574**	**1.2E-06**	**6**
P02696	ALDVNVALR	2.16316926	2	2.97428
P02696	CMTTVSWDGDKLQCVQK	1.15553324	2	4.23034
P02696	EFEEDLTGIDDR	1.72060392	2	3.24756

P02696	EFEEDLTGIDDRK	1.68175064	2	3.49205
P02696	MLSNENFEEYLR	1.6099511	2	3.86972
P02696	MLSNENFEEYLR+Oxidation(0	2.40142631		
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.07733533**	**0.88362**	**5**
P02706	DYQDFQHLDNENDHHQLQR	0.89864124	3	4.12294
P02706	LVESQLEK	1.24073903	2	2.77993
P02706	SLSCQMAALR	1.24738927	2	2.80293
P02706	WVCETELGK	0.99402342	2	2.46677
P02706	WVDGTDYETGFK	0.87747187	2	3.1856
P02770	**ALBU Serum albumin**	**1.02896431**	**1.1E-08**	**25**
P02770	AADKDNCFATEGPNLVAR	1.76168766	2	4.44865
P02770	AETFTFHSDICTLPDKEK	1.65960421	3	3.36995
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	3.1601892	2	5.04219
P02770	CCSGSLVER	1.62227652	2	2.88549
P02770	CCTLPEAQR	1.49685344	2	3.06953
P02770	DLGEQHFK	1.58932129	1	2.1346
P02770	ECCHGDLLECADDR	1.39545497	2	3.68599
P02770	ECCHGDLLECADDRAELAK	1.40670727	2	5.55439
P02770	FKDLGEQHFK	1.24635065	3	4.18445
P02770	GLVLIAFSQYLQK	2.31713381	2	4.12847
P02770	INKECCHGDLLECADDRAELAK	1.67652174	3	4.81183
P02770	KQTALAELVK	1.23942517	3	4.04055
P02770	KYEATLEK	0.74598237	1	2.61506
P02770	LGEYGFQNAVLVR	40.790676	2	3.77918
P02770	LQACCDKPVLQK	1.54599048	2	4.0486
P02770	LVQEVTDFAK	0.54650379	2	3.51271
P02770	RHPDYSVSLLLR	1.53840282	3	5.36587
P02770	SIHTLFGDK	1.47623754	1	2.59696
P02770	TCVADENAENCDK	1.2375622	2	4.58551
P02770	TNCELYEK	1.51124858	2	2.86214
P02770	TVMGDFAQFVDK	1.29530173	2	3.88801
P02770	YEATLEK	1.72071031	1	1.96369
P02770	YMCENQATISSK	1.09151269	2	4.14408
P02770	YMCENQATISSK+Oxidation(1	2.03712812		
P02770	YNEVLTQCCTESDK	1.41510461	2	5.52498
P02803	**MT1 Metallothionein_1**	**25.9105534**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	32.7174683	3	6.52961
P02803	SCCSCCPVGCSK	13.9910357	2	4.11442
P04041	**GPX1 Glutathione peroxidase 1**	**1.05254886**	**0.67585**	**11**
P04041	DYTEMNDLQK	26.589377	2	2.41201
P04041	FLVGPDGVPVR	1.04573087	2	3.21799
P04041	GLVVLGFPCNQFGHQENGK	2.01520494	2	4.06915
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	1.29964886	3	4.20041
P04041	NALPAPSDDPTALMTDPK	1.22446569	2	3.17598
P04041	NALPAPSDDPTALMTDPK+Oxidation(13	0.89404619		
P04041	NDISWNFEK	1.10835438	2	3.02235
P04041	NEEILNSLK	1.28649925	2	2.48231
P04041	TIDIEPDIEALLSK	1.42229508	3	5.43006
P04041	YIIWSPVCR	1.38138414	2	2.80239
P04041	YVRPGGGFEPNFTLFEK	1.34399455	3	4.70879
P04167	**CP2B2 Cytochrome P450 2B2**	**1.24416803**	**0.79102**	**2**
P04167	GTIAVIEPIFK	1.73181788	2	2.91433
P04167	NLQEILDYIGHIVEK	1.13679302	2	4.33955
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.42723463**	**3.6E-05**	**16**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.74589297	3	3.50529
P04176	EDNIPQLEDVSQFLQTCTGFR	1.33583172	3	5.16658
P04176	FANQILSYGAELDADHPGFKDPVYR	1.49612657	3	3.98974

P04176	HGSKPMYTPEPDICHELLGHVPLFSDR	1.55160668	3	3.93199
P04176	ILADSINSEVGILCNALQK	1.39437076	3	6.47502
P04176	LNKDEYEFFTYLDK	3.72512986	2	3.57632
P04176	LNKDEYEFFTYLDKR	1.58148347	3	3.53333
P04176	LRPVAGLLSSR	1.91799379	2	2.69481
P04176	NDIGATVHELSR	1.37139351	2	3.75022
P04176	QFADIAYNYR	1.18332358	2	2.41491
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.9707314	2	4.93304
P04176	THACYEHNHIFPLLEK	1.38657529	4	4.98313
P04176	VEVLDNTQQLK	1.21048003	2	3.83769
P04176	VEYTEEEK	1.44159934	2	2.74199
P04176	VEYTEEEKQTWGTVFR	1.39347864	2	3.89734
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.27593659	3	5.12928
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**1.04130176**	**0.97963**	**8**
P04182	AFYNNVLGEYEEYITK	1.37780052	2	4.60059
P04182	GIYMWDVEGR	0.95324287	2	3.12071
P04182	GLLNAIVIR	1.18092639	2	3.26114
P04182	KTEQGPPSSEYIFER	1.03395436	2	4.15833
P04182	TEQGPPSSEYIFER	0.81124451	2	3.9498
P04182	VLPMNTGVEAGETACK	1.23085658	2	4.1541
P04182	WLAVDHENVRPDIVLLGK	1.2143351	2	5.27923
P04182	YGAHNYHPLPVALER	1.26239787	2	4.21891
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.28199538**	**0.13542**	**4**
P04256	EDSQRPGAHLTVK	1.54821059	2	3.1967
P04256	IEVIEIMTDR	1.29783706	2	3.42468
P04256	NQGGYGGSSSSSSYGSGR	1.12382772	2	5.16704
P04256	YHTVNGHNCEVR	1.18601962	2	3.38097
P04276	**VTDB Vitamin D_binding protein**	**1.24403995**	**0.00461**	**3**
P04276	CCSINSPPR	1.08417959	2	2.52545
P04276	SCESDAPFPVHPGTSECCTK	1.66966286	2	4.6312
P04276	YCSSQIDAEMR	1.91652921	2	3.21518
P04355	**MT2 Metallothionein_2**	**92.6728192**	**9.9E-20**	**2**
P04355	MDPNCSCATDGSCSCAGSCK	229.595447	2	6.24475
P04355	SCCSCCPVGCAK	25.6360153	2	4.25339
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**3.75514752**	**0.41715**	**8**
P04466	AAAEGSSNVFSMFDQTQIQEFK	2.13063038	3	5.25676
P04466	GADPEDVITGAFK	1.9391371	2	4.19398
P04466	LKGADPEDVITGAFK	3.14830734	3	3.47748
P04466	NEELDAMMK	3.63472351	1	2.2033
P04466	NICYVITHGDAK	5.35422	2	2.84465
P04466	NICYVITHGDAKDQE	5.47818211	2	4.43959
P04466	NMWAAFPPDVGGNVDYK	2.76887155	2	3.07871
P04466	QFLEELLTTQCDR	2.80134658	2	3.99813
P04550	**PTMS Parathymosin**	**0.95746371**	**0.0655**	**4**
P04550	RTAEEEDEADPKR	1.22962287	3	4.10261
P04550	SVEAAAELSAK	0.83983963	2	3.86464
P04550	TAEEEDEADPK	2.3699157	2	3.33814
P04550	TAEEEDEADPKR	1.84542919	2	3.77786
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.10184466**	**7.8E-16**	**19**
P04636	AGAGSATLSMAYAGAR	1.16836233	2	4.54798
P04636	AGAGSATLSMAYAGAR+Oxidation(9	1.62149308		
P04636	ANTFVAELK	0.9592391	2	3.36116
P04636	EGVIECSFVQSK	1.31511349	2	3.18595
P04636	ETECTYFSTPLLLGK	1.52768748	2	3.74073
P04636	FVFSLVDAMNGK	1.18177661	2	4.46147

P04636	GCDVVVIPAGVPR	0.68701174	2	4.35481
P04636	GYLGPEQLPDCLK	1.09106155	2	4.25715
P04636	IFGVTTLDIVR	1.8130532	2	3.35587
P04636	IQEAGTEVVK	1.05183131	2	2.76192
P04636	IQEAGTEVVKAK	1.29865036	2	2.8792
P04636	ITPFEEK	1.19564224	1	1.94166
P04636	LTLYDIAHTPGVAADLSHIETR	1.30089055	3	6.8526
P04636	MIAEAIPELK	1.00123955	2	3.46179
P04636	MIAEAIPELK+Oxidation(0	1.29456393		
P04636	TIIPLISQCTPK	1.16136385	2	3.55599
P04636	VAVLGASGGIGQPLSLLLK	2.40740257	2	6.29371
P04636	VDFPQDQLATLTGR	0.75857059	2	4.72404
P04636	VNVPVIGGHAGK	1.08675805	2	3.77754
P04638	**APOA2 Apolipoprotein A_II**	**0.88595377**	**0.93224**	**2**
P04638	AQPSEIQNQAK	0.84822843	2	2.74153
P04638	TGTNLMDFLSR	0.99419896	2	2.72502
P04639	**APOA1 Apolipoprotein A_I**	**1.68483284**	**0.48764**	**5**
P04639	LQEQLGPVTQEFWANLEK	1.77744516	2	3.51349
P04639	NEMNKDLENVK	1.19611861	2	3.59204
P04639	NHPTLIEYHTK	0.92752532	3	3.83728
P04639	QLNLNLLDNWDTLGSTVGR	1.77194585	2	4.19133
P04639	WNEEVEAYR	1.24106741	2	2.8765
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.19866533**	**3.2E-07**	**21**
P04642	DLADELALVDVIEDK	1.31460741	2	5.3144
P04642	DLADELALVDVIEDKLK	1.10928586	2	3.94485
P04642	DQLIVNLLK	1.40602188	2	3.0364
P04642	DQLIVNLLKEEQVPQNK	1.75572755	2	4.34529
P04642	EDVFLSVPCILGQNGISDVVK	1.33108079	2	4.86267
P04642	GEMMDLQHGSLFLK	1.48012003	2	4.11821
P04642	GEMMDLQHGSLFLK+Oxidation(2	0.66727455		
P04642	GEMMDLQHGSLFLK+Oxidation(3	1.63225325		
P04642	GYTSWAIGLSVADLAESIMK	0.84641743	2	4.88495
P04642	IVSSKDYSVTANSK	0.90954846	2	3.63953
P04642	KSADTLWGIQK	1.54510554	2	3.15057
P04642	LGVHPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLK	1.94158776	3	5.72876
P04642	LKGEMMDLQHGSLFLK	1.76683592	2	3.99007
P04642	NVNIFK	2.56107407	1	2.07206
P04642	QVVDSAYEVIK	1.16838479	2	3.25565
P04642	RVHPISTMIK	1.14730627	2	2.55841
P04642	SADTLWGIQK	1.18133678	2	3.92659
P04642	SLNPQLGTDADK	0.87073682	2	2.77051
P04642	SLNPQLGTDADKEQWK	1.157472	2	4.74541
P04642	SLNPQLGTDADKEQWKDVHK	1.71729037	3	3.43593
P04642	VTLTPDEEAR	1.2212979	2	3.01289
P04644	**RS17 40S ribosomal protein S17**	**1.41038186**	**0.00216**	**3**
P04644	DNYVPEVSALDQEIIEVDPDTK	6.05428985	2	4.27681
P04644	LLDFGSLSNLQVTQPTVGMNFK	1.95934963	2	4.72342
P04644	VCEEIAIIPSK	1.12775101	2	3.09423
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.54**	**0.73088**	**10**
P04692	AISEELDHALNDMTSI	3.39566568	2	2.56342
P04692	GTEDELDKYSEALK	1.50779532	2	3.24046
P04692	KLVIIESDLER	1.61978174	2	3.30136
P04692	LDKENALDR	2.16502467	2	3.08951
P04692	LKGTEDELDK	3.79764805	2	2.49803
P04692	LVIIESDLER	0.95601111	2	3.13081
P04692	MEIQEIQLK	1.12386906	2	3.1234
P04692	QLEDELVSLQK	2.68087436	2	2.40528

P04692	SIDDLEDELYAQK	4.84560529	2	4.38194
P04692	SKQLEDELVSLQK	0.5372453	2	3.05108
P04694	**ATTY Tyrosine aminotransferase**	**6.54678374**	**9.9E-20**	**6**
P04694	ILGPCTIVQGALK	5.76189127	2	2.93723
P04694	IQEFCEQHYHCAEGSQEECDK	#NUM!	3	4.92323
P04694	LIAEQAVHCLPATCFEYPNFFR	3.14523317	3	3.98137
P04694	TACLVVNNPSNPCGSVFSK	9.03844365	2	4.96927
P04694	TVISLSIGDPTVFGNLPTDPEVTQAMK	5.13221905	2	3.11028
P04694	YEPLANLSTNVPILSCGGLAK	14.704292	2	3.60447
P04762	**CATA Catalase**	**1.06254621**	**2.4E-05**	**32**
P04762	APQKPDVLTTGGGNPIGDK	2.73883172	2	4.3417
P04762	DAMLFPSFIHSQK+Oxidation(2	1.27408355		
P04762	DAQLFIQR	0.99058025	2	2.96241
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	0.8933328	4	4.76379
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVKR	1.02709713	4	5.30929
P04762	DPASDQMK	1.38479045	1	2.55677
P04762	DPASDQMK+Oxidation(6	1.37868414		
P04762	DYPLIPVGK	0.77597163	1	2.26444
P04762	EAETFPFNPFDLTK	1.02010452	2	3.96457
P04762	FNSANEDNVTQVR	1.54874206	2	4.57475
P04762	FSTVAGESGSADTVR	0.79102342	2	5.07742
P04762	FSTVAGESGSADTVRDPR	0.87894667	2	2.65521
P04762	FYTEDGNWDLVGNNTPIFFIR	2.61586815	3	6.13444
P04762	GAGAFGYFEVTHDITR	0.94982796	2	4.89049
P04762	GPLLVQDVVFTDEMAHFDR	1.55569491	2	5.50944
P04762	HMNGYGSHTFK	1.00915303	3	4.30958
P04762	HMNGYGSHTFK+Oxidation(1	0.81043352		
P04762	LAQEDPDYGLR	3.50904374	2	2.92098
P04762	LCENIANHLK	1.00834027	3	4.04224
P04762	LFAYPDTHR	1.08641168	2	2.97332
P04762	LGPNYLQIPVNCPYR	1.23165846	2	4.02765
P04762	LNIMTAGPR	1.15791414	2	3.14891
P04762	LVNANGEAVYCK	0.94098786	2	3.90932
P04762	NAIHTYVQAGSHIAAK	0.94255548	3	5.6258
P04762	NFTDVHPDYGAR	0.80232886	2	4.02292
P04762	NLPVEEAGR	0.7827379	2	2.34334
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	2.12953975	3	5.57231
P04762	RFNSANEDNVTQVR	0.74938894	2	5.28592
P04762	VFEHIGK	0.92983503	2	2.44287
P04762	VFEHIGKR	0.6585704	2	2.71282
P04762	VQALLDQYNSQKPK	0.8571235	2	4.86796
P04762	VWPHKDYPLIPVGK	0.98451688	2	3.96364
P04764	**ENOA Alpha_enolase**	**1.17838739**	**9.9E-12**	**16**
P04764	AGYTDQVVIGMDVAASEFYR	2.32186618	2	4.85387
P04764	DATNVGDEGGFAPNILENK	0.84977509	2	5.63743
P04764	DYPVVSIEDPFDQDDWDAWQK	1.17853959	2	4.30796
P04764	FTATAGIQVVGDDLTVTNPK	1.45949661	2	4.72111
P04764	GNPTVEVDLYTAK	1.54747753	2	4.07359
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.43541831	3	6.15986
P04764	IDQLMIEMDGTENK	1.21471427	2	4.87195
P04764	IEEELGSK	1.18796187	2	2.54216
P04764	IGAEVYHNLK	1.31684178	2	3.30834
P04764	KLNVVEQEK	0.35146807	2	2.54152
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.48259135	3	5.9754
P04764	LNVVEQEK	1.19805807	2	3.0934

P04764	LNVVEQEKIDQLMIEMDGTENK	1.38670278	3	5.2948
P04764	SCNCLLLK	1.19418161	2	2.79394
P04764	VNQIGSVTESLQACK	1.16956192	2	4.95931
P04764	YITPDQLADLYK	1.38441581	2	3.61877
P04785	**PDIA1 Protein disulfide_isomerase**	**1.22220973**	**9.9E-20**	**25**
P04785	DHENIVIAK	1.16589866	2	2.74915
P04785	EADDIVNWLK	1.15948519	2	2.51986
P04785	HNQLPLVIEFTEQTAPK	1.19982029	3	5.45981
P04785	IFGGEIK	1.4324302	1	1.96317
P04785	IKPHLMSQELPEDWDKQPVK	1.22395655	3	4.95468
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5	1.89316895		
P04785	ILEFFGLK	1.73879497	2	2.95026
P04785	ILFIFIDSDHTDNQR	0.77299049	2	2.63651
P04785	LGETYKDHENIVIAK	1.26538579	3	5.50444
P04785	LITLEEEMTK	1.14618144	2	3.5772
P04785	LITLEEEMTK+Oxidation(7	1.54440142		
P04785	LKAEGSEIR	0.70996233	2	2.44262
P04785	LLDFIK	1.36492933	2	2.43801
P04785	MDSTANEVEAVK	1.63037537	2	4.26409
P04785	MDSTANEVEAVK+Oxidation(0	1.06894616		
P04785	NFEEVAFDEK	1.0951582	1	3.19827
P04785	NFEEVAFDEKK	1.08309794	2	3.97768
P04785	NNFEGEITK	1.2622311	2	2.59229
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.39702267	3	6.30544
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.30858802	3	6.16215
P04785	THILLFLPK	1.83018884	2	3.09429
P04785	TVIDYNGER	1.06825481	2	2.97578
P04785	VDATEESDLAQQYGVR	0.99103982	2	5.46142
P04785	YKPESDELTAEK	1.12855662	3	4.50905
P04785	YQLDKDGVVLFK	1.12810611	2	3.79384
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.87629516**	**9.9E-20**	**16**
P04797	GAAQNIIPASTGAAK	1.84367987	2	4.14523
P04797	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	2.94543019	3	4.71846
P04797	IVSNASCTTNCLAPLAK	1.53399813	2	4.96471
P04797	LISWYDNEYGYSNR	2.69838104	2	4.3046
P04797	LVINGKPITIFQER	1.42636451	3	4.37649
P04797	RVIISAPSADAPMFVMGVNHEK	1.66385286	3	5.95905
P04797	VGVNGFGR	2.48258751	2	2.34018
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.48834985	3	7.57061
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12	1.97061976		
P04797	VIISAPSADAPMFVMGVNHEK	1.40834386	2	4.62497
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11	1.7594826		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14	1.75546295		
P04797	VPTPNVSVVDLTCR	3.76343758	2	3.18092
P04797	VVDLMAYMASK	1.74634291	2	3.8111
P04797	VVDLMAYMASKE	1.19286771	2	2.41447
P04797	WGDAGAEYVVESTGVFTTMEK	1.83078258	2	5.5687
P04799	**CP1A2 Cytochrome P450 1A2**	**1.83732371**	**1.1E-16**	**8**
P04799	FLTNDNTAIDK	1.4567639	2	2.62703
P04799	IGSTPVVVLSGLNTIK	1.80544963	2	3.36481
P04799	IHEELDTVIGR	1.68866682	2	2.92841
P04799	KSEEMLNLVK	1.22885302	2	2.50428
P04799	NSIQDITGALFK	2.08285654	2	3.77559
P04799	SMTFNPDSGPVWAAR	1.66494993	2	3.42265
P04799	TCEHVQAWPR	1.80586542	2	2.5527
P04799	TVQEHYQDFNK	1.71752313	2	3.72857

P04903	**GSTA2 Glutathione S_transferase alpha_2**	**1.08015205**	**0.00793**	**10**
P04903	DGNLMFDQVPMVEIDGMK	0.86961018	2	5.28943
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10	0.77815504		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16	0.76957876		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4	1.08745338		
P04903	KDGNLMFDQVPMVEIDGMK	0.80266139	2	5.05617
P04903	LIQSPEDLEK	1.22805926	2	3.17113
P04903	LKKDGNLMFDQVPMVEIDGMK	1.78703262	3	3.43062
P04903	WLLAAAGVEFEEK	1.29018519	2	3.68958
P04903	YDLYGK	0.65649354	1	1.97605
P04903	YLPAFEK	0.6058101	1	2.04342
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**1.34606216**	**3.9E-15**	**10**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	2.00819588	3	5.41861
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	2.23587267	4	7.75469
P04904	KPLEDEKCVESAVK	0.98839451	2	3.67708
P04904	LRNDGSLMFQQVPMVEIDGMK	1.78577812	2	4.82442
P04904	NDGSLMFQQVPMVEIDGMK	1.4920091	2	4.92645
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11	1.38229184		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17	1.38105339		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5	1.38268398		
P04904	SHGQDYLVGNR	0.83357554	2	3.93402
P04904	WLLAAAGVEFEEQFLK	1.39737788	2	5.70406
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.19882776**	**9.9E-20**	**14**
P04905	ADIVENQVMDNR	0.86512336	2	4.1382
P04905	ADIVENQVMDNR+Oxidation(8	1.2420487		
P04905	CLDAFPNLKDFLAR	1.15731085	2	3.11884
P04905	FKLGLDFPNLPYLIDGSR	1.25628243	3	5.37654
P04905	HHLCGETEEER	1.10047536	3	3.85558
P04905	IRADIVENQVMDNR	1.39269198	2	4.05557
P04905	ITQSNAIMR	1.43809564	2	3.10246
P04905	ITQSNAIMR+Oxidation(7	1.27078692		
P04905	KHHLCGETEEER	0.98413832	3	4.08363
P04905	KITQSNAIMR	1.20254587	3	4.16256
P04905	KITQSNAIMR+Oxidation(8	0.66962254		
P04905	LGLDFPNLPYLIDGSR	1.92785409	2	4.71755
P04905	MQLIMLCYNPDFEK	1.78347818	2	4.30947
P04905	YLSTPIFSK	0.9553412	2	2.79507
P04906	**GSTP1 Glutathione S_transferase P**	**1.2374659**	**0.48137**	**2**
P04906	EAALVDMVNDGVEDLR	1.23750499	2	5.01928
P04906	STCLYGQLPK	1.23157992	2	2.57489
P04937	**FINC Fibronectin**	**1.13675349**	**0.16678**	**7**
P04937	ATGVFTTLQPLR	1.07431662	2	2.39039
P04937	FTQVSPTTLTAQWTAPSVK	1.20850928	2	4.39166
P04937	HYQINQQWER	2.88828533	2	2.55867
P04937	ITYGETGGNSPVQEFTVPGSK	1.4660085	2	2.39202
P04937	SSPVVIDASTAIDAPSNLR	0.6871187	2	3.26054
P04937	SYTITGLQPGTDYK	0.99380724	2	3.01772
P04937	YIVNVYQISEEGK	0.64742327	2	2.84667
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.6828596**	**0.85963**	**9**
P05065	ADDGRPFPQVIK	1.90512839	2	2.33158
P05065	ALANSLACQGK	1.84713225	2	2.87116
P05065	ALSDHHVYLEGTLLKPNMVTPGHACTQK	5.01653896	3	5.00818
P05065	FSNEEIAMATVTALR	2.17693419	2	4.15722
P05065	GILAADESTGSIAK	1.77182343	2	3.85415
P05065	GVVPLAGTNGETTTQGLDGLSER	1.54111947	2	5.19452
P05065	IGEHTPSSLAIMENANVLAR	1.38213603	2	4.4112
P05065	LQSIGTENTEENR	4.81869681	2	4.02651

P05065	RLQSIGTENTEENR	3.03605082	2	3.64054
P05178	**CP2C6 Cytochrome P450 2C6**	**0.86340001**	**0.00028**	**8**
P05178	DLGIVFSHGNR	1.23889034	2	2.38239
P05178	EALIDHGEEFAER	0.79744289	2	3.45801
P05178	EFPDPEIFDPGHFLDGNGK	0.72740427	2	2.91887
P05178	FDYKDQDFLNLMEK	0.91436394	3	4.91352
P05178	FIDLIPTNLPHAVTCDIK	0.72305175	2	3.5973
P05178	GTTIITSLSSVLHDSK	1.19698116	2	3.68069
P05178	MCAGEGLAR	0.8594116	2	2.73944
P05178	NITQSLTSFSK	0.61812152	2	2.68473
P05179	**CP2C7 Cytochrome P450 2C7**	**1.80096002**	**9.5E-15**	**7**
P05179	ACVGEGLAR	1.8219714	2	3.08125
P05179	FINFVPTNLPHAVTCDIK	2.88507596	3	3.34391
P05179	HMPYTDAMIHEVQR	1.98749979	3	3.96349
P05179	IEEHQESLDVTNPR	3.01470623	2	4.79203
P05179	KIEEHQESLDVTNPR	2.50243054	2	4.875
P05179	KLPPGPTPLPIIGNFLQIDVK	2.58761105	3	5.74599
P05179	VLTSLTSVLHDSK	1.29100854	2	2.86089
P05182	**CP2E1 Cytochrome P450 2E1**	**1.272382**	**0.99917**	**16**
P05182	AKEHLQSLDINCAR	1.14573395	3	4.68477
P05182	DIDLSPVTVGFGSIPPQFK	1.19533685	2	2.75925
P05182	DRLDMPYMDAVVHEIQR	0.94238164	3	3.35647
P05182	DTVFQGYVIPK	1.27990179	2	2.62918
P05182	DVTDCLLIEMEK	1.68700963	2	2.65073
P05182	DVTDCLLIEMEKEK	3.10848197	2	3.09422
P05182	DVTDCLLIEMEKEK+Oxidation(9	0.84981648		
P05182	EHLQSLDINCAR	1.16990119	2	3.47016
P05182	FINLVPSNLPHEATR	1.11536822	2	3.66087
P05182	FKPEHFLNENGK	0.88304711	2	3.36973
P05182	GDIPVFQEYK	0.91306757	2	2.59419
P05182	GIIFNNGPTWK	0.95668481	2	2.75793
P05182	GTVVIPTLDSLLYDSHEFPDPEK	1.47471562	2	5.07511
P05182	LDMPYMDAVVHEIQR	1.0051775	2	3.11696
P05182	RVCVGEGLAR	1.93053935	2	2.35621
P05182	YGLLILMK	1.37001906	2	3.00967
P05183	**CP3A2 Cytochrome P450 3A2**	**1.23075836**	**0.10398**	**12**
P05183	DFGPVGIMGK	3.57017136	2	2.86713
P05183	DIELDGLFIPK	2.81973643	2	3.585
P05183	EMFPIIEQYGDILVK	2.32281961	2	3.93193
P05183	KDIELDGLFIPK	1.19248842	2	2.87139
P05183	KLQEEIDGALPSK	1.55209323	2	4.02133
P05183	LQEEIDGALPSK	0.72684596	2	4.09189
P05183	QAILEPEKPIVLK	1.04321954	2	3.41415
P05183	QEAETGKPVTMK	0.98227016	2	3.44976
P05183	QEAETGKPVTMK+Oxidation(10	1.3770118		
P05183	RDFGPVGIMGK	1.33032341	2	2.39059
P05183	VDFLQLMLNAHNNSK	1.03577912	2	3.371
P05183	YLKQEAETGKPVTMK	1.43983858	3	3.31601
P05197	**EF2 Elongation factor 2**	**1.57546424**	**9.9E-20**	**30**
P05197	ALLELQLEPEELYQTFQR	2.25943579	3	5.23297
P05197	ARPFPDGLAEDIDKGEVSAR	1.27519533	3	6.45462
P05197	AYLPVNESFGFTADLR	1.59202275	2	3.78199
P05197	CELLYEGPPDDEAAMGIK	1.20415501	2	3.65729
P05197	DLEEDHACIPIK	1.19142096	2	3.77374
P05197	DLEEDHACIPIKK	1.53484037	2	3.71966
P05197	EGIPALDNFLDK	0.90950575	2	2.67665
P05197	EGIPALDNFLDKL	4.13403131	2	3.4492

P05197	ETVSEESNVLCLSK	1.88640345	2	4.45299
P05197	GEGQLGAAER	1.7405824	2	3.04751
P05197	GHVFEESQVAGTPMFVVK	1.73371083	2	5.90146
P05197	IWCFGPDGTGPNILTDITK	1.84120235	2	5.20761
P05197	KEDLYLKPIQR	1.70378094	2	3.37276
P05197	KIWCFGPDGTGPNILTDITK	1.40438574	2	5.02003
P05197	KVEDMMK	1.80366751	2	2.574
P05197	KVEDMMK+Oxidation(4	1.77199142		
P05197	KVEDMMK+Oxidation(5	1.77199142		
P05197	LDSEDKDKEGKPLLK	1.39248896	2	4.06098
P05197	NMSVIAHVDHGK	0.85913829	2	3.65338
P05197	NMSVIAHVDHGK+Oxidation(1	1.63344962		
P05197	SDPVVSYR	1.69686182	2	2.30352
P05197	STLTDSLVCK	1.62700191	2	3.18135
P05197	TFCQLILDPIFK	1.86492604	2	4.19923
P05197	TGTITTFEHAHNMR	1.45971826	2	4.00219
P05197	VFDAIMNFR	2.47032614	2	3.31539
P05197	VFSGVVSTGLK	1.62966026	2	3.09305
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.50258962	3	3.5946
P05197	YEWDVAEAR	1.26567578	2	3.14639
P05197	YFDPANGK	1.46440377	1	2.21181
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.89271317	3	5.96445
P05369	**FPPS Farnesyl pyrophosphate synthase**	**0.9550378**	**0.9925**	**11**
P05369	ALYEELDLR	1.12257678	2	3.19343
P05369	EVLEYNTVGGK	1.20942891	2	3.00185
P05369	GLTVVQTFQELVEPR	0.90318457	3	4.21982
P05369	IKEVLEYNTVGGK	1.004163	3	4.2431
P05369	QILEENYGQK	1.30496174	2	2.61646
P05369	QILEENYGQKDPEK	0.53815043	2	3.60068
P05369	SLIEQCSAPLPPSIFLELANK	1.22933994	2	4.8517
P05369	VGTDIQDNK	1.0507253	2	3.79731
P05369	VLTEDELGHPEK	0.67560729	2	2.77619
P05369	VLTEDELGHPEKGDAITR	1.00408753	2	4.68737
P05369	YEEDSYNR	2.22078788	2	2.4574
P05426	**RL7 60S ribosomal protein L7**	**1.21259684**	**1.4E-15**	**7**
P05426	AGNFYVPAEPK	1.24166014	2	3.06486
P05426	FGIICMEDLIHEIYTVGK	1.89829441	3	4.80491
P05426	KKVPAVPETLK	1.13515623	2	2.70811
P05426	NFAELK	1.45516058	1	1.90921
P05426	SVNELIYK	1.2301028	2	2.32386
P05426	TTHFVEGGDAGNR	1.08076496	3	3.75081
P05426	TTHFVEGGDAGNREDQINR	1.26842133	2	4.54414
P05544	**SPA3L Serine protease inhibitor A3L**	**2.2220884**	**1.2E-08**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	3.21357899	2	4.37677
P05544	DSTMEEILEGLK	1.8541345	2	3.11908
P05544	IAELFSDLEER	2.07935173	2	2.95923
P05544	MQQVESSLQPETLK	1.47871722	2	4.1842
P05544	MQQVESSLQPETLKK	2.31100767	2	3.91799
P05544	VFSQQADLSR	2.49077095	2	3.04575
P05545	**SPA3K Serine protease inhibitor A3K**	**1.54996774**	**0.00228**	**6**
P05545	AVLDVDETGTEGAAATAVTAALK	1.54979085	2	5.86145
P05545	IAELFSELDER	2.07946259	2	2.82554
P05545	IFSQQADLSR	1.60457586	2	2.55678
P05545	KIFSQQADLSR	1.92275177	2	2.39508
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	1.19067452	3	3.69476
P05545	NLHVSQVVHK	1.3953191	2	2.47458
P05712	**RAB2A Ras_related protein Rab_2A**	**1.1591831**	**0.96618**	**2**

P05712	IQEGVFDINNEANGIK	1.16105047	2	4.56114
P05712	TASNVEEAFINTAK	1.15587921	2	2.97454
P05765	**RS21 40S ribosomal protein S21**	**1.33279039**	**0.0175**	**3**
P05765	DHASIQMNVAEVDR	1.63192683	2	3.93561
P05765	MGESDDSILR	1.30797011	2	3.27114
P05765	TYGICGAIR	1.35037273	2	3.31347
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.85849824**	**0.02854**	**9**
P06214	AGADIIITYFAPQLLK	1.35208333	2	3.66608
P06214	AGAFDLR	1.10013842	2	2.50458
P06214	AGCQVVAPSDMMDGR	0.85864185	2	3.6028
P06214	CVLIFGVPSR	1.05273376	2	2.85991
P06214	DEQGSAADSEDSPTIEAVR	0.5717238	2	5.82811
P06214	DIQEGADILMVKPGLPYLDMVQEVK	1.05344762	3	4.63134
P06214	TAVLESMTAFR	1.21283398	2	3.53858
P06214	VPKDEQGSAADSEDSPTIEAVR	0.9487517	3	5.806
P06214	YGVNQLEEMLRPLVEAGLR	1.03349514	3	4.66805
P06302	**PTMA Prothymosin alpha**	**1.08626244**	**0.99996**	**3**
P06302	RVAEDDEDDDVETKK	1.02750253	3	5.75299
P06302	VAEDDEDDDVETK	1.16651616	2	4.37964
P06302	VAEDDEDDDVETKK	1.19408678	2	4.80353
P06399	**FIBA Fibrinogen alpha chain**	**1.14781515**	**0.80834**	**9**
P06399	AQQIQVLQK	0.88719364	2	2.56098
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	2.28874759	3	3.61527
P06399	GDFANANNFDNTFGQVSEDLR	1.78370103	2	5.32089
P06399	GDFANANNFDNTFGQVSEDLRR	1.33449189	3	3.34685
P06399	GDKELLIGNEK	1.33938968	2	2.56571
P06399	GLIDEANQDFTNR	0.91110867	2	3.4943
P06399	MADEAASEAHQEGDTR	1.12323429	2	4.44889
P06399	SQLQEGPPEWK	1.34476319	2	2.88732
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	3.73684403	3	3.86129
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.14788845**	**0.0063**	**7**
P06685	AVAGDASESALLK	1.24914029	2	3.52351
P06685	AVFQANQENLPILK	1.29681771	2	3.18331
P06685	DKYEPAAVSEHGDKK	1.37716953	3	3.74223
P06685	DMTSEELDDILR	0.57198655	2	2.97013
P06685	LNIPVNQVNPR	1.13258396	2	3.00185
P06685	MSINAEDVVVGDLVEVK	2.50015427	2	2.95446
P06685	YEPAAVSEHGDKK	1.30138241	2	3.29365
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.18435792**	**0.17841**	**3**
P06687	DGPNALTPPPTTPEWVK	1.0304086	2	3.36608
P06687	GVGIISEGNETVEDIAAR	1.34591782	2	4.6752
P06687	QGAIVAVTGDGVNDSPALK	1.11044327	2	4.62584
P06757	**ADH1 Alcohol dehydrogenase 1**	**1.17025798**	**1**	**16**
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.2335721	3	5.76734
P06757	FPLEPLITHVLPFEK	1.24738772	3	4.69981
P06757	GAIFGGFK	0.69853572	2	2.75724
P06757	GALLDGTSR	1.00439149	2	2.9695
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.87165292	3	5.34264
P06757	HPESNLCCQTK	1.03568755	2	3.24545
P06757	ICKHPESNLCCQTK	0.73799729	3	4.1981
P06757	IDAAAPLDK	1.19385639	2	2.91263
P06757	IIAVDINKDK	0.98274066	2	2.95461
P06757	INEAFDLLR	0.94384673	2	3.63854
P06757	KFPLEPLITHVLPFEK	0.93769498	3	4.64681
P06757	MVATGVCR	0.68664335	2	2.49079

P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.20557068	4	7.54586
P06757	VCLIGCGFSTGYGSAVQVAK	1.02074402	2	6.31846
P06757	VIPLFSPQCGK	0.84737327	2	3.03683
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.38005492	2	5.06988
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.25950205**	**3.8E-07**	**31**
P06761	AKFEELNMDLFR	1.37942962	3	4.66838
P06761	DAGTIAGLNVMR	1.3229946	2	3.652
P06761	DNHLLGTFDLTGIPPAPR	1.29500713	2	4.32849
P06761	ELEEIVQPIISK	1.25271609	2	4.3178
P06761	ETAEAYLGK	1.90597219	1	2.07649
P06761	FEELNMDLFR	1.1160365	2	3.67616
P06761	IEIESFFEGEDFSETLTR	1.88107876	2	4.74762
P06761	IEWLESHQDADIEDFK	1.29846612	2	5.65328
P06761	IEWLESHQDADIEDFKAK	1.12381384	3	4.34794
P06761	IINEPTAAAIAYGLDKR	1.39874982	2	4.56116
P06761	ITITNDQNR	1.32255119	2	2.7296
P06761	ITPSYVAFTPEGER	1.40945772	2	4.08301
P06761	KKELEEIVQPIISK	0.95812814	2	5.24619
P06761	KSDIDEIVLVGGSTR	1.16447684	2	5.01469
P06761	KSQIFSTASDNQPTVTIK	0.86906708	2	5.27532
P06761	LYGSGGPPPTGEEDTSEKDEL	2.1782596	2	5.34628
P06761	MKETAEAYLGK	1.64860192	2	3.44756
P06761	MKETAEAYLGK+Oxidation(0	1.46449768		
P06761	MKETAEAYLGKK	1.07705596	2	2.85694
P06761	NELESYAYSLK	1.08069173	2	3.37148
P06761	NQLTSNPENTVFDAK	1.07930015	2	4.76765
P06761	SDIDEIVLVGGSTR	1.09293837	2	3.80536
P06761	SQIFSTASDNQPTVTIK	0.94244632	2	5.36966
P06761	TFAPEEISAMVLTK	1.60348144	3	4.75106
P06761	TFAPEEISAMVLTK+Oxidation(9	1.77360899		
P06761	TKPYIQVDIGGGQTK	1.16269767	3	4.71136
P06761	TWNDPSVQQDIK	0.91216799	2	3.9831
P06761	VLEDSDLK	1.34171618	2	2.47726
P06761	VLEDSDLKK	1.24978718	2	2.51852
P06761	VTHAVVTVPAYFNDAQR	1.22741491	2	5.06552
P06761	VYEGERPLTK	1.14501272	2	2.94021
P06866	**HPT Haptoglobin**	**1.8446014**	**9.9E-20**	**8**
P06866	ATDLKDWVQETMAK	1.32688624	2	3.63808
P06866	GAVSPVGVQPILNK	1.9328832	2	4.45439
P06866	HTFCAGLTK	3.59635864	1	2.4074
P06866	LQTEGDGIYTLNSEK	1.95667746	2	4.43493
P06866	NQLVEIEK	1.68692798	1	2.33215
P06866	SCAVAEYGVYVR	3.26832397	2	3.45217
P06866	SVVDIGLIK	2.06521847	1	2.0186
P06866	YVMLPVADQEK	1.86537504	2	2.5149
P07150	**ANXA1 Annexin A1**	**1.20532831**	**0.69198**	**2**
P07150	GLGTDEDTLIEILTTR	1.3366121	2	3.79267
P07150	GVDEATIIDILTK	1.17232427	3	4.0629
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.44208424**	**3.4E-06**	**16**
P07153	ASSFVLALEPELESR	1.56531831	2	4.2464
P07153	AVTSEIAVLQSR	1.17365992	2	3.89807
P07153	FVDHVFDEQVIDSLTVK	1.51918047	2	4.64806
P07153	GEDEEDNNLEVR	1.96253994	2	3.85473
P07153	HFDETVNR	1.03060778	1	2.71197

P07153	IDHILDAL	2.54709382	2	2.40005
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.12212206	3	4.91024
P07153	LKTEGSDLCDR	1.34918045	3	3.43198
P07153	NIQVDSPYDISR	1.1983813	2	3.50743
P07153	NLVEQHIQDIVVHYTFNK	1.44395997	3	4.90029
P07153	SEDILDYGPFK	2.91595318	2	3.48043
P07153	TEGSDLCDR	2.47448011	2	2.69471
P07153	TILPAAAQDVYYR	1.51764558	2	2.88432
P07153	TVDLSSHLAK	1.37300276	2	2.58741
P07153	VHYENNSPFLTITSMTR	2.41718851	2	4.03744
P07153	VTAEVVLAHPGGGSTAR	1.30889891	2	4.87007
P07323	**ENOG Gamma_enolase**	**1.71281225**	**9.9E-06**	**3**
P07323	AAVPSGASTGIYEALELR	1.79888479	2	5.28674
P07323	GNPTVEVDLHTAK	3.5801936	2	3.17231
P07323	SGETEDTFIADLVVGLCTGQIK	1.37959657	3	4.94792
P07335	**KCRB Creatine kinase B_type**	**1.24716239**	**0.16723**	**3**
P07335	FCTGLTQIETLFK	1.31485263	2	2.80903
P07335	LEQGQPIDDLMPAQK	0.69317051	2	2.72387
P07335	TDLNPDNLQGGDDLDPNYVLSSR	0.87584289	2	3.57291
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.14681459**	**0.34725**	**3**
P07340	AYGENIGYSEK	1.44662388	2	2.72504
P07340	VAPPGLTQIPQIQK	1.29095389	2	2.58273
P07340	YNPNVLPVQCTGK	1.14258716	2	2.61205
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**2.27848745**	**9.9E-20**	**18**
P07379	AINPENGFFGVAPGTSVK	2.43939714	2	4.44334
P07379	EEGWLAEHMLILGITNPEGK	2.64091066	2	5.14535
P07379	EIISFGSGYGGNSLLGK	3.44177475	2	2.55412
P07379	EVEEIDKYLEDQVNADLPYEIER	1.97245175	2	4.87224
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	2.30180541	3	5.19227
P07379	GLGDVNVEELFGISK	5.92022654	2	3.77223
P07379	IGIELTDSPYVVASMR	2.49811279	2	4.24743
P07379	MGTSVLEALGDGEFIK	2.29830276	2	4.75779
P07379	MGTSVLEALGDGEFIK+Oxidation(0	2.63880278		
P07379	TNLAMMNPTLPGWK	1.9476123	2	3.13418
P07379	TVIITQEQR	2.4205682	2	2.46263
P07379	VECVGDDIAWMK	2.53987702	2	3.83109
P07379	VIQGSLDSLPQEVR	2.18733425	2	3.90576
P07379	VLEWMFGR	2.68203727	2	2.53086
P07379	WMSEEDFEK	2.11842718	2	2.37451
P07379	YDNCWLALTDPR	1.75505642	2	2.51999
P07379	YLAAAFPSACGK	1.54307981	2	2.72062
P07379	YLEDQVNADLPYEIER	1.34797193	2	5.05747
P07483	**FABPH Fatty acid_binding protein_ heart**	**2.78694446**	**0.55964**	**2**
P07483	QVASMTKPTTIIEK	1.97117254	2	3.26915
P07483	WDGQETTLTR	2.78705777	2	2.53159
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.0859406**	**0.99999**	**4**
P07632	DGVANVSIEDR	1.02398354	2	2.73234
P07632	GDGPVQGVIHFEQK	1.06531737	2	3.79552
P07632	HVGDLGNVAAGK	1.09516719	2	4.04199
P07632	VISLSGEHSIIGR	1.23983753	2	3.02934
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.99141169**	**0.65071**	**10**
P07633	AFDNDVDALCNLR	1.19447917	2	4.07653
P07633	AYNMLDIIHAVIDER	1.27294983	2	3.88651
P07633	GFVDDIIQPSSTR	1.11621663	2	3.23984

P07633	HLLGDTNYAWPTAEIAVMGAK	1.44583778	2	5.75789
P07633	ICCDLEVLASK	1.13458626	2	3.49778
P07633	IMDQAITVGAPVIGLNDSGGAR	0.79620848	3	5.02559
P07633	LVPELDTVVPLESSK	1.21425592	2	3.70332
P07633	NKFPGDSVVTGR	0.32304545	2	2.40977
P07633	SVTNEDVTQEQLGGAK	1.12967227	2	5.2441
P07633	TVGIVGNQPNVASGCLDINSSVK	1.25199213	2	4.91488
P07687	**HYEP Epoxide hydrolase 1**	**1.07769545**	**0.98116**	**26**
P07687	DIELLYPYK	0.45183032	1	2.30278
P07687	DKEETLPLGDGWWGPGSKPSAK	1.23841604	3	5.65544
P07687	EDESIRPFK	1.05787645	2	2.95196
P07687	EDESIRPFKVETSDEEIKDLHQR	1.02985727	3	5.9852
P07687	ELEDGGLER	2.11603287	2	2.34874
P07687	ENLGQGIMVHK	1.47563083	2	3.20023
P07687	ENLGQGIMVHK+Oxidation(7	1.32775108		
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.29070827	3	5.66983
P07687	FHYGFNSNYMK	0.78398993	2	2.62501
P07687	FLGYTEKDIELLYPYK	1.00170262	3	4.74074
P07687	FYIQGGDWGSLICTNMAQMVPNHVK	1.27649814	3	3.3837
P07687	GGHFAAFEEPK	1.16222055	2	3.46158
P07687	GLHLNMAFISR	0.78029104	2	2.79208
P07687	IEGLDIHFIHVKPPQLPSGR	0.87300212	3	4.26091
P07687	IIPLLTDPK	1.32152397	1	1.9007
P07687	KFVSLAELQ	1.36306607	2	2.80163
P07687	KQVEILNQYPHFK	0.86649356	3	5.21234
P07687	LLAQDIR	1.19922834	2	2.50907
P07687	QVEILNQYPHFK	0.81552493	2	3.5948
P07687	SEYRELEDGGLER	0.85574436	3	3.66431
P07687	SFYTMTPLLGQR	1.67215189	2	3.78076
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.22748457	3	6.59517
P07687	TKIEGLDIHFIHVKPPQLPSGR	1.3317682	3	4.03182
P07687	VETSDEEIK	0.90213581	2	2.62877
P07687	VETSDEEIKDLHQR	1.00484127	2	4.72047
P07687	VFVPTGFSAFPSELLHAPEK	1.09514358	2	4.54154
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.023641**	**9.9E-20**	**99**
P07756	AADTIGYPVMIR	1.69421344	2	3.87525
P07756	AADTIGYPVMIR+Oxidation(9	2.24184202		
P07756	AERPDGLILGMGGQTALNCGVELFK	1.71078274	3	6.91184
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10	1.54804296		
P07756	AFAISGPFNVQFLVK	2.05247329	2	4.95617
P07756	AFAMTNQILVER	1.41850434	2	4.58938
P07756	AFAMTNQILVER+Oxidation(3	1.43850104		
P07756	ALENNMSLDEIVK	0.85109376	2	4.81389
P07756	ALENNMSLDEIVK+Oxidation(5	1.30105994		
P07756	AMLSTGFK	1.36506611	2	2.49318
P07756	AQTAHIVLEDGTK	1.02293513	2	4.47708
P07756	ATGYPLAFIAAK	1.24287794	2	3.18313
P07756	CEMASTGEVACFGEGIHTAFLK	1.33031157	3	5.4082
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2	1.24233681		
P07756	CLGLTEAQTR	1.12328689	2	3.61715
P07756	DADDNCVTVCNMENVDAMGVHTGDSVVVAPAQTLSNAEFQMLR	3.21206798	3	5.16436
P07756	DELGLNK	1.26457267	1	2.34751
P07756	DGSIDLVINLPNNNTK	0.81943169	2	5.31511
P07756	DILNMDK	1.21466738	1	2.03257
P07756	EIEYEVVR	3.24715349	1	2.09313

P07756	EIGFSDKQISK	1.57826064	2	3.1471
P07756	EPLFGISTGNIITGLAAGAK	1.49772829	3	5.65663
P07756	ETLMDLGTK	1.77179049	1	2.33659
P07756	EVEMDAVGK	1.7422382	1	2.1106
P07756	FIEGAREVEMDAVGKEGR	1.14887786	3	3.6484
P07756	FLEEATR	2.40795448	2	2.46326
P07756	FLGVAEQLHNEGFK	1.14321715	2	4.80351
P07756	FVHDNYVIR	1.11519774	3	3.35219
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.60379718	3	6.06903
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15	2.07267774		
P07756	GILIGIQQSFRPR	1.87678461	2	2.46131
P07756	GLNSESVTEETLR	1.08643483	2	4.84807
P07756	GNDVLVIECNLR	1.05406848	2	4.45974
P07756	GQILTMANPIIGNGGAPDTTAR	1.16537729	2	6.00427
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5	1.29750746		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.95579277	3	4.91201
P07756	GQNQPVLNITNR	1.00542344	2	4.38972
P07756	GTTITSVLPKPALVASR	1.34645287	2	3.35451
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	2.61505682	3	5.98097
P07756	HLPTLEQPIIPSDYVAIK	1.25789187	2	5.58522
P07756	IALGIPLPEIK	2.42120839	2	2.82732
P07756	IAPSFAVESMEDALK	2.55727814	2	5.25688
P07756	IAPSFAVESMEDALK+Oxidation(9	1.28030009		
P07756	IAPSFAVESMEDALKAADTIGYPVMIR	1.7151316	3	4.13075
P07756	IEFEGQSVDFVDPNK	1.35080984	2	5.29866
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	1.22421439	3	5.55141
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.73284419	3	5.62339
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	1.42710007	3	4.69763
P07756	IMGTSPLQIDR	1.88484814	2	3.26957
P07756	IMGTSPLQIDR+Oxidation(1	3.06914938		
P07756	IMGTSPLQIDRAEDR	0.72835389	2	2.517
P07756	KEPLFGISTGNIITGLAAGAK	1.44000092	2	5.10797
P07756	KTVVVNCNPETVSTDFDECDK	0.40295078	2	4.98109
P07756	LFAEAVQK	1.27319929	2	3.44823
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.35126075	4	4.71588
P07756	LRDADPILR	1.4305999	2	3.21114
P07756	LTSIDKWFLYK	1.31189798	2	2.76499
P07756	LYFEELSLER	2.8619756	2	3.67267
P07756	MCHPSVDGFTPR	1.27675141	3	4.89757
P07756	MCHPSVDGFTPR+Oxidation(0	1.48271924		
P07756	MRDILNMDK	1.37501424	2	3.14774
P07756	MRDILNMDK+Oxidation(0	1.95166167		
P07756	QADAVYFLPITPQFVTEVIK	3.26515473	3	4.19449
P07756	QLFSDKLNEINEK	1.24740812	2	3.82525
P07756	QNLIAEVSTK	0.97432891	1	2.63927
P07756	RFLEEATR	1.28320141	2	2.68996
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	2.28120924	4	4.62964
P07756	RTAVDSGIALLTNFQVTK	1.23106277	2	5.16508
P07756	RTSINVVR	0.74661778	2	2.33993
P07756	SAYALGGLGSGICPNK	1.4030982	2	4.94947
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.39242226	3	4.69494
P07756	SIFSAVLDELK	1.29522062	2	3.83489
P07756	SIFSAVLDELKVAQAPWK	2.05871541	3	4.29703
P07756	SLGQWLQEEK	0.96417652	2	4.06453

P07756	SLGQWLQEEKVPAIYGVDTR	2.28807738	2	3.7954
P07756	SVGEVMAIGR	1.02859555	2	3.51829
P07756	SVGEVMAIGR+Oxidation(5	1.62865879		
P07756	TAVDSGIALLTNFQVTK	1.3662996	3	6.50634
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	1.28812085	3	5.41638
P07756	TFEESFQK	1.06118068	2	2.50366
P07756	TLGVDFIDVATK	1.01333275	2	4.28344
P07756	TSACFEPSLDYMVTK	1.22481588	2	4.55608
P07756	TSACFEPSLDYMVTK+Oxidation(11	1.20706248		
P07756	TVLMNPNIASVQTNEVGLK	1.19307691	2	6.11632
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3	0.98009141		
P07756	TVVVNCNPETVSTDFDECDK	0.85931473	2	5.61548
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	3.12543931	3	5.56397
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	1.44241862	3	7.42585
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22	1.52386182		
P07756	VLGTSVESIMATEDR	1.10884625	2	4.70256
P07756	VLGTSVESIMATEDR+Oxidation(9	1.19444863		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.83912604	2	5.82353
P07756	VMIGESVDEK	1.30277544	2	3.68868
P07756	VMIGESVDEK+Oxidation(1	1.67659962		
P07756	VSQEHPVVLTK	1.31316268	2	3.84969
P07756	VVAVDCGIK	1.52910399	2	2.52538
P07756	VVAVDCGIKNNVIR	1.26964546	2	3.80094
P07756	YMESDGIK	1.1816082	2	2.61315
P07756	YMESDGIK+Oxidation(1	1.49872146		
P07824	**ARGI1 Arginase_1**	**1.35902369**	**9.9E-20**	**16**
P07824	ANEQLAAVVAETQK	1.22728648	2	5.20274
P07824	DHGDLAFVDVPNDSPFQIVK	0.99228937	2	6.21711
P07824	DIVYIGLR	1.10786401	2	2.3264
P07824	DVDPGEHYIIK	2.52620829	2	3.41139
P07824	EGNHKPETDYLKPPK	1.98388659	2	2.76863
P07824	GKFPDVPGFSWVTPCISAK	1.80363599	3	4.96103
P07824	LKETEYNVR	1.46754449	3	3.33979
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.46865453	3	4.34269
P07824	RPIHLSFDVDGLDPVFTPATGTPVVGGLSYR	3.48768907	3	5.75482
P07824	TGLLSGLDIMEVNPTLGK	1.78751006	2	5.64583
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9	1.17778538		
P07824	TVNTAVALTLSCFGTK	1.91752566	2	5.03746
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	2.9934064	4	5.50347
P07824	VMEETFSYLLGR	2.39168338	2	3.70997
P07824	YFSMTEVDK	1.64185178	1	2.3222
P07824	YFSMTEVDKLGIGK+Oxidation(3	1.2153622		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.80860454**	**0.04663**	**17**
P07871	AEELGLPILGVLR	0.85595975	2	4.30189
P07871	AEIVPVTTTVLDDK	0.93430609	2	4.7357
P07871	AEIVPVTTTVLDDKGDR	1.09169593	2	3.68683
P07871	AEIVPVTTTVLDDKGDRK	0.85655516	2	4.36588
P07871	DCLIPMGITSENVAER	1.59970459	2	3.91008
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.88309191	2	6.3436
P07871	IAQFLSGIPETVPLSAVNR	1.59949917	2	3.21586
P07871	KTITVSQDEGVRPSTTMEGLAK	0.90414678	3	3.7047
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.75294915	3	5.14145
P07871	QCSSGLQAVANIAGGIR	0.81953977	2	4.69981
P07871	QDAFALASQQK	0.98328603	2	3.75977
P07871	QKQDAFALASQQK	0.96658966	2	4.15368
P07871	QVVTLLNELK	0.49607692	2	2.38165

P07871	SKAEELGLPILGVLR	0.70797297	3	4.83084
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.88032351	3	4.74667
P07871	TITVSQDEGVRPSTTMEGLAK	0.79788176	2	4.3676
P07871	VNPLGGAIALGHPLGCTGAR	0.90737692	2	4.99562
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**1.06821622**	**0.3203**	**21**
P07872	AFTTWTANAGIEECR	2.42611568	2	3.81496
P07872	ASATFNPELITHILDGSPENTR	0.81884288	2	4.77986
P07872	ASEAHCHYVVVK	0.89191997	3	4.14354
P07872	EIENLILNDPDFQHEDYNFLTR	2.06748565	2	4.54409
P07872	EIGTHKPLPGITVGDIGPK	0.83864614	3	4.12068
P07872	EVAWNLTSVDLVR	1.2545391	2	3.14678
P07872	EYGISDPEEIMWFK	0.96279283	2	3.43568
P07872	FGYEEMDNGYLK	0.60361322	2	3.87587
P07872	GGDFLEGSIITGAQLSQVNAR	2.04553378	2	5.24332
P07872	GLETTATYDPK	1.05964707	2	3.67608
P07872	INESIGQGDLSELPELHALTAGLK	0.92733733	3	5.51523
P07872	LVEIAAK	0.91527495	1	2.20189
P07872	LVGGMVSYLNDLPSQR	1.35171882	2	3.23561
P07872	NLCLLYSLYGISQK	1.71142797	2	3.26243
P07872	QSEPEPQILDFQTQQYK	0.82622241	2	4.78958
P07872	SFLVGNAAQSLSK	0.83220998	2	4.29144
P07872	SKEVAWNLTSVDLVR	1.54125806	3	3.82654
P07872	TQEFILNSPTVTSIK	0.836839	2	4.57435
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	1.06519505	4	4.92351
P07872	YAQVKPDGTYVKPLSNK	1.84318126	3	3.749
P07872	YDGNVYENLFEWAK	2.03395104	2	4.82144
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.97497726**	**0.99845**	**5**
P07895	AIWNVINWENVSQR	0.9749198	2	3.87497
P07895	GDVTTQVALQPALK	1.02895728	2	3.98569
P07895	GELLEAIKR	1.01638907	2	2.33723
P07895	HHATYVNNLNVTEEK	1.38027117	2	4.82983
P07895	NVRPDYLK	1.28059063	2	2.30242
P07896	**ECHP Peroxisomal bifunctional enzyme**	**1.05460803**	**2.4E-11**	**24**
P07896	EWQSLAGPHGSK	0.48161914	2	2.48304
P07896	GGPMFYAASVGLPTVLEK	1.30852779	2	3.88934
P07896	GQGLTGPSLPPGTPVR	1.05461641	2	3.92712
P07896	GWYQYDKPLGR	1.01802724	2	2.90122
P07896	IFNKPVPSLPNMDSVFAEAIAK	1.96422559	3	4.74482
P07896	IGVVVGNCYGFVGNR	2.06300017	2	3.44347
P07896	IIDKPIEPR	0.92671053	2	2.4274
P07896	KGQGLTGPSLPPGTPVR	0.8576032	2	4.26845
P07896	KQYPGVLAPETCVR	0.78668205	2	4.34685
P07896	LCNPPVNAVSPTVIR	0.92913603	2	4.2708
P07896	LGILDAVVK	0.95944797	2	2.81922
P07896	LLEVIPSR	0.68073448	2	2.82499
P07896	LVAQGSPPLK	1.04899323	2	2.54035
P07896	QNPDIPQLEPSDYLR	0.62147706	2	3.95562
P07896	QYPGVLAPETCVR	0.66013514	2	3.07371
P07896	RLVAQGSPPLK	0.67813325	2	2.33736
P07896	TASAQPVSSVGVLGLGTMGR	0.90255111	2	5.88839
P07896	TISKEEILER	0.88543227	2	2.65437
P07896	VGISVVAVESDPK	1.09541725	2	3.90225
P07896	VGLPEVTLGILPGAR	0.91591015	2	3.62223
P07896	VSDLAGLDVGWK	0.71021972	2	4.27189
P07896	YLSADEALR	1.3322235	2	2.97647
P07896	YSPLGDMLCEAGR	0.7619019	2	4.33706

P07896	YSSPTTIATVMSLSK	0.74665882	2	3.49345
P07943	**ALDR Aldose reductase**	**1.24000958**	**0.71903**	**2**
P07943	AIGVSNFNPLQIER	1.5051292	2	3.06443
P07943	HIDCAQVYQNEK	1.12052937	2	4.45897
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**1.76253494**	**0.01912**	**5**
P07953	HGESELNLR	1.15585012	2	2.59769
P07953	IGGDSGLSAR	0.61740342	2	2.77474
P07953	NYEFFRPDNTEAQLIR	3.90133985	2	3.39267
P07953	TIQTAEALGVPYEQWK	2.68672473	2	3.06574
P07953	YLNWIGTPTK	1.32325492	2	2.95927
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**0.81278215**	**0.60717**	**6**
P08009	LCYNPDFEK	1.54017304	2	3.04941
P08009	LLLEYTDSSYEEK	0.73752428	2	4.83114
P08009	LLLEYTDSSYEEKR	1.26976247	2	4.00991
P08009	NQVFEATCLDAFPNLK	0.8169695	2	4.56452
P08009	SQWLNEK	1.14533596	2	2.70843
P08009	YTMGDAPDFDR	0.8832064	2	2.81479
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.09428556**	**9E-06**	**15**
P08010	FLSKPIFAK	1.23209307	2	2.33711
P08010	IRVDVLENQAMDTR	1.25720705	3	4.2239
P08010	ITYVDFLVYDVLDQHR	1.3401228	2	5.01125
P08010	KKPEYLEGLPEK	0.88471459	3	4.16745
P08010	KPEYLEGLPEK	1.03960315	2	3.42906
P08010	KYSMGDAPDYDR	1.65092837	2	3.8264
P08010	LFLEYTDTSYEDK	0.27114906	2	5.54148
P08010	LFLEYTDTSYEDKK	0.9794887	2	4.36844
P08010	LQLAMVCYSPDFER	1.62872848	2	4.32852
P08010	LQLAMVCYSPDFER+Oxidation(4	1.77403467		
P08010	SQWLSEK	1.15989042	2	2.46407
P08010	VDVLENQAMDTR	0.76707027	2	4.69443
P08010	VDVLENQAMDTR+Oxidation(8	1.15525859		
P08010	YSMGDAPDYDR	1.22816014	2	3.3708
P08010	YSMGDAPDYDR+Oxidation(2	1.28036152		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.83517581**	**0.50346**	**6**
P08011	IYHTIAYLTPLPQPNR	0.76436166	2	5.3202
P08011	MMFLSSATAFQR	1.15299231	2	3.60354
P08011	MMFLSSATAFQR+Oxidation(0	1.45495502		
P08011	MMFLSSATAFQR+Oxidation(1	1.45495502		
P08011	VFANPEDCAGFGK	0.83112546	2	4.67898
P08011	VFANPEDCAGFGKGENAK	1.02406192	2	4.62132
P08032	**SPTA1 Spectrin alpha chain_ erythrocyte**	**0.88461498**	**0.70579**	**4**
P08032	ADVVESWIGEK	0.87333793	2	2.63621
P08032	DLVAAKNLLNR	1.22682182	2	2.43823
P08032	DQARDLTSAGNLLK	0.95836869	2	2.43349
P08032	QELNTRWNSLK	1.88850578	2	2.30182
P08081	**CLCA Clathrin light chain A**	**1.15445219**	**0.75669**	**2**
P08081	LEALDANSR	1.75536564	2	2.74592
P08081	WREEQTER	1.13998202	2	2.47819
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**1.6137643**	**0.14872**	**3**
P08290	DFQDIQQLDSEENDHQLIGDEEQGSHVQNLR	1.64582043	3	6.50026
P08290	EEQEFVVK	1.4916931	1	2.06398
P08290	WVDGTEYR	2.59041303	2	2.32283
P08430	**UD16 UDP_glucuronosyltransferase 1_6**	**1.19880138**	**0.77158**	**2**
P08430	GHDIVVLVPEVNLLLGESK	1.0094338	3	3.81951
P08430	YEILASDLLK	1.19915354	2	2.47489

P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.30171464**	**1.9E-05**	**5**
P08461	AAPAAAAAAPPGPR	1.15147628	2	2.32012
P08461	DVPLGTPLCIIVEK	1.23391298	2	3.42531
P08461	DVPVGSIICITVEKPQDIEAFK	2.79383658	2	3.90108
P08461	GLETIASDVVSLASK	1.2926063	2	4.49826
P08461	VAPTPAGVFIDIPISNIR	1.69276026	2	4.57957
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.22235574**	**0.72081**	**9**
P08503	AFAGDIANQLATDAVQIFGGYGFNTEYPVEK	1.43991276	3	5.1906
P08503	AFTGFIVEADTPGIHIGK	1.09057168	2	4.44266
P08503	EEIIPVAPDYDK	0.96400405	2	3.57535
P08503	GITFEDVR	1.02235877	2	2.42656
P08503	IYQIYEGTAQIQR	1.18629472	2	4.73162
P08503	KGDEYVINGQK	1.13252986	2	4.12428
P08503	MTEQPMMCAYCVTEPSAGSDVAGIK	1.21175294	2	4.4693
P08503	SGEYPFPLIK	1.29301419	2	2.79131
P08503	TRPTVAAGAVGLAQR	1.22391528	2	4.41669
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**0.8930337**	**0.00086**	**11**
P08541	DELQNHFIK	1.86714714	2	2.59063
P08541	FEIFSTSISKDELQNHFIK	1.63508057	3	4.89458
P08541	FILPPSYVPVILSGLAGK	0.37636803	3	6.12973
P08541	GAAVSLNIR	1.65447338	2	2.919
P08541	GHEVTVLKPSAYFFLDPK	1.65697375	2	4.34859
P08541	HKEWDTFYSEILGRPTTVDETMSK	1.00799774	3	4.43988
P08541	LLDVWTYELPR	1.8886967	2	4.05144
P08541	NVMLLSTIHHDQPMKPLDR	1.19461202	3	3.78731
P08541	NVMLLSTIHHDQPMKPLDR+Oxidation(2	2.57132828		
P08541	VEIWLIR	1.64767479	2	3.025
P08541	VLVWPMDFSHWMNIK	1.78388412	2	2.48399
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**0.97810598**	**0.94745**	**6**
P08542	EIINNPFYK	1.19380015	1	2.07174
P08542	FETFPTSVSKDELENYFIK	1.107028	2	4.18042
P08542	KWDPFYSEILGRPTTLAETMGK	1.55986779	2	4.06018
P08542	LVDVWTYELQR	1.2433478	2	3.5694
P08542	NAVWLSTIHHDQPMKPLDK	0.60880784	3	4.16042
P08542	WDPFYSEILGRPTTLAETMGK	1.51653349	2	3.7438
P08649	**CO4 Complement C4**	**1.81412538**	**0.33745**	**2**
P08649	SLEIPGSSDPNVIPDGDFSSFVR	1.39407997	2	2.86038
P08649	VTASEPLETLGSEGALSPGGVASLLR	1.84586413	2	2.87177
P08661	**MBL2 Mannose_binding protein C**	**0.71229547**	**0.00312**	**2**
P08661	ALCSELQGTVATPR	0.44991617	2	3.34046
P08661	TENVFEDLTGNR	0.83325154	2	2.85044
P08683	**CP2CB Cytochrome P450 2C11**	**0.90304567**	**1**	**18**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	1.05658948	3	4.89658
P08683	EALVDLGEEFSGR	0.95494539	2	3.91402
P08683	EHQESLDKDNPR	1.60281228	2	3.97237
P08683	FDPGHFLDER	1.02133781	2	2.63743
P08683	FDYKDPTFLNLMHR	1.15906907	3	4.84963
P08683	FNENFR	1.09865945	1	2.09618
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	0.92878527	3	6.02482
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.16302863	2	4.99096
P08683	HNPQSEFTLESLVATVTDMFGAGTETTSTTLR	0.81874437		
P08683	ICAGEALAR	1.19724244	2	3.02145
P08683	LPPGPTPLPIIGNTLQIYMK	1.53636426	3	3.97036
P08683	NFFYIK	1.46734651	1	1.91941

P08683	NYVLEK	0.80840748	1	2.03016
P08683	SQMPYTDAVVHEIQR	1.00405133	2	4.43892
P08683	VKEHQESLDKDNPR	1.62661064	3	5.26034
P08683	VQEEIER	0.88802478	2	2.46213
P08683	YGLLLLLK	1.24108652	2	3.19947
P08683	YIDLVPTNLPHLVTR	1.23871723	2	4.23395
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**1.4034674**	**0.40742**	**3**
P08733	GADPEETILNAFK	1.21249563	2	2.32703
P08733	NEEIDEMIK	1.87917012	1	2.63221
P08733	NLVHIITHGEEKD	4.49705767	2	2.91725
P09006	**SPA3N Serine protease inhibitor A3N**	**4.63125073**	**7E-05**	**2**
P09006	AVLDVAETGTEAAAATGVK	3.56731784	2	4.87133
P09006	GNSMEEILEGLK	6.4598253	2	3.14438
P09034	**ASSY Argininosuccinate synthase**	**2.12625545**	**9.9E-20**	**17**
P09034	APNTPDVLEIEFK	4.01139582	2	3.66081
P09034	DGTTHSTSLDLFMYLNEVAGK	2.75678671	2	4.82449
P09034	EFVEEFIWPAVQSSALYEDR	3.95319414	3	5.72916
P09034	EQGYDVIAYLANIGQK	2.49677974	2	4.70463
P09034	FAELVYTGFWHSPECEFVR	7.6680434	2	4.59087
P09034	FELTCYSLAPQIK	2.59272171	2	4.46314
P09034	GRNDLMEYAK	2.48000383	2	3.33498
P09034	IDIVENR	1.40591428	2	2.37392
P09034	KVFIEDVSK	1.80958493	3	3.62154
P09034	NDLMEYAK	2.06148532	2	2.63173
P09034	NDLMEYAK+Oxidation(3	2.38827183		
P09034	NQAPPGLYTK	1.73124762	2	2.3122
P09034	SPWSMDENLMHISYEAGILENPK	4.91542286	3	5.63126
P09034	TQDPAKAPNTPDVLEIEFK	2.05074182	2	5.06488
P09034	TQDPAKAPNTPDVLEIEFKK	1.91351169	3	5.39563
P09034	VFIEDVSK	1.76989806	2	2.35657
P09034	VQVSVFK	1.5431422	2	2.4449
P09041	**PGK2 Phosphoglycerate kinase 2**	**0.87183528**	**0.55726**	**5**
P09041	FHVEEEGK	1.10209621	2	2.6503
P09041	FHVEEEGKGK	1.17660004	2	2.52993
P09041	LGDVYVNDAFGTAHR	1.24037854	3	4.21655
P09041	VDFNVPMK	1.13277703	2	2.33805
P09041	VSHVSTGGGASLELLEGK	0.87165481	2	5.82734
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.60570934**	**1.6E-12**	**3**
P09117	VLAAVYK	1.57039034	2	2.68449
P09117	YASICQQNGIVPIVEPEILPDGDHDLK	4.40890441	3	3.59953
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.63323683	3	5.11891
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.58432015**	**0.12953**	**3**
P09139	IGLLGYNATTENADR	1.28322742	2	3.11332
P09139	LLLGPGPSNLAPR	2.25397544	2	2.51964
P09139	VLNAPPGISLISFNDK	2.04511751	2	2.39283
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**8.72954001**	**4.5E-08**	**4**
P09367	ALGVNTVGAQTLK	8.42149834	2	3.54529
P09367	AQLGLNELLK	1.95162481	1	2.19022
P09367	LGLPATIVVPSTTPALTIER	9.61856365	2	2.70583
P09367	LKNEGATVEVVGEMLDEAIQLAK	6.05379838	3	3.97793
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.2920723**	**0.76899**	**12**
P09495	AEGDAAALNR	1.11371545	2	2.55131
P09495	EDKYEEEIK	1.5928492	1	2.69296
P09495	EENVGLHQTLDQTLNELNCI	3.25792258	2	5.23139

P09495	IQALQQQADDAEDR	1.28544219	2	4.46353
P09495	IQLVEEELDR	1.11762124	2	3.48684
P09495	IQLVEEELDRAQER	1.2550012	2	3.01552
P09495	KLVILEGELER	0.5562473	3	4.05098
P09495	LEEAEKAADESER	2.05501606	2	4.1334
P09495	LVILEGELER	2.11363608	2	3.14805
P09495	MEIQEMQLK	0.98903137	2	2.98138
P09495	RIQLVEEELDR	1.19488775	2	2.79499
P09495	YSEKEDKYEEEIK	1.29993761	2	4.535
P09527	**RAB7A Ras_related protein Rab_7a**	**0.97048039**	**0.08053**	**6**
P09527	ATIGADFLTK	0.99949564	2	2.61116
P09527	DPENFPFVVLGNK	2.03978503	2	3.79691
P09527	GADCCVLVFDVTAPNTFK	1.35949287	2	3.39603
P09527	TLDSWRDEFLIQASPR	1.46704965	3	3.50582
P09527	TSLMNQYVNK	1.05752621	2	2.83383
P09527	VIILGDSGVGK	0.96811278	2	2.42567
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**4.90642427**	**0.16593**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	3.92840534	2	3.8282
P09605	LSEMTEQDQQR	5.12058071	2	3.36361
P09606	**GLNA Glutamine synthetase**	**1.41936084**	**4.5E-09**	**8**
P09606	CIEEAIDK	2.2244602	2	2.34831
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.66536415	3	5.46739
P09606	LTGFHETSNINDFSAGVANR	1.45629973	2	6.01703
P09606	MGDHLWVAR	1.50389828	2	3.03217
P09606	QMYMNLPQGEK	1.29458202	2	2.38968
P09606	RLTGFHETSNINDFSAGVANR	1.19892588	3	5.51941
P09606	TCLLNETGDEPFQYK	1.24810314	2	5.30161
P09606	TCLLNETGDEPFQYKN	1.50273811	2	5.46664
P09626	**ATP4A Potassium_transporting ATPase alpha chain 1**	**1.34056806**	**0.69323**	**2**
P09626	VDNSSLTGESEPQTR	1.26508924	2	4.20254
P09626	VIMVTGDHPITAK	1.36955977	2	3.28713
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.08781282**	**0.55794**	**27**
P09811	AWNTMVLR	1.90237494	2	2.39321
P09811	DFSELEPDKFQNK	1.37318204	2	3.48768
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.71963422	4	5.47697
P09811	DLSQLTK	1.15578772	1	2.1468
P09811	EGWQVEEADDWLR	1.48155307	2	3.71017
P09811	FSQFLEK	1.23522958	1	2.0447
P09811	GIVGVENVAELK	1.10586524	2	3.01163
P09811	GIVGVENVAELKK	0.95288408	2	3.33362
P09811	HLQIIYEINQK	0.86239821	2	3.79598
P09811	IFVDIEK	1.13747538	1	2.05413
P09811	INMAHLCIVGCHAVNGVAK	1.36411221	3	5.01629
P09811	INPSSMFDVHVK	1.32559029	2	3.1747
P09811	LVIDQIDNGFFSPNQPDLFK	1.29442905	2	5.27898
P09811	LVTSVAEVVNNDPMVGSK	1.71996933	2	4.67995
P09811	MSLIEEEGGK	1.28833854	2	2.42289
P09811	MSLIEEEGGKR	0.2922443	2	2.72165
P09811	RWLLLCNPGLADLIAEK	1.35887369	3	5.04234
P09811	TFAYTNHTVLPEALER	1.11512555	2	4.9232
P09811	VDDVAALDK	1.01113588	2	2.70679
P09811	VDDVAALDKK	1.1001403	3	3.77455
P09811	VFADYEAYVK	1.21945627	2	2.64659
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.29106538	2	5.96223
P09811	VLYPNDNFFEGK	1.28377241	2	2.64317
P09811	VSQLYMNQK	0.59924152	2	3.03173

P09811	WLLLCNPGLADLIAEK	2.8195983	2	4.83604
P09811	WVDTQVVLALPYDTPVPGYMNNTVNTMR	1.75048752	3	4.28154
P09811	YEYGIFNQK	1.09054531	2	2.63368
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**1.35975749**	**0.21674**	**9**
P09812	GYNAQEYYDR	2.36614233	2	2.3255
P09812	HLQIIYEINQR	1.18639356	2	2.33396
P09812	LITAIGDVVNHDPAVGDR	1.85921934	2	3.2642
P09812	NLAENISR	1.25198284	2	2.72201
P09812	QIIEQLSSGFFSPK	2.38499856	2	3.66077
P09812	VIFLENYR	1.34588515	2	2.5118
P09812	VIPAADLSEQISTAGTEASGTGNMK	5.00491054	2	4.78652
P09812	WLVLCNPGLAEVIAER	1.60785967	2	3.8157
P09812	YEFGIFNQK	1.68382817	2	2.44447
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.12392165**	**0.18895**	**6**
P09875	ANVVASALAQIPQK	0.79731608	3	3.61551
P09875	FSGGLPLPPSYVPVVLSELSDR	1.30697709	3	3.61704
P09875	IILNELAQR	1.16593247	2	3.00327
P09875	SDLEYSFAK	0.74083114	2	2.35784
P09875	VDFSILSTTGLLTALK	1.05736116	2	4.55381
P09875	WIDEWTR	0.50188798	2	2.60036
P09895	**RL5 60S ribosomal protein L5**	**1.38106823**	**0.00348**	**5**
P09895	GAVDGGLSIPHSTK	1.46138347	2	4.37423
P09895	HIMGQNVADYMR	1.37554024	2	3.54644
P09895	NNVTPDMMEEMYK	1.23092371	2	3.39451
P09895	RFPGYDSESK	1.31887423	2	2.84887
P09895	YLMEEDEDAYKK	1.31736052	2	3.54788
P0C0S7	**H2AZ Histone H2A.Z**	**1.05432024**	**0.97168**	**2**
P0C0S7	ATIAGGGVIPHIHK	1.05489725	2	3.51307
P0C0S7	GDEELDSLIK	0.90407172	2	3.40999
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.91859622**	**0.00623**	**20**
P0C2X9	AIEAAVLAR	1.10382218	2	2.90877
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	1.48790141	2	5.13168
P0C2X9	AQIFLK	1.30781403	2	2.31133
P0C2X9	DPQEPIMKEEIFGPVLTVYVYPDEK	0.61270181	3	3.58991
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	6.07629655	2	5.29363
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	1.55735508	3	3.6695
P0C2X9	EEIFGPVLTVYVYPDEK	0.49828917	2	3.83408
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	2.26059434	2	5.51257
P0C2X9	KEWDLKPVADR	1.08483172	2	3.5834
P0C2X9	LYVPQSLWPQIK	2.52505368	2	3.20898
P0C2X9	NAAGNFYINDK	1.67563237	2	3.60515
P0C2X9	NFHFVHSSADVDSVVSGTLR	0.95245005	2	5.73886
P0C2X9	SAFEYGGQK	1.04263562	1	2.43333
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	2.01829494	3	5.74857
P0C2X9	STGSVVGQQPFGGAR	0.90036163	2	4.39369
P0C2X9	TIVQEATR	0.99244333	2	2.92718
P0C2X9	VANEPILAFTQGSPER	1.0752331	2	5.214
P0C2X9	WKHASSLKVANEPILAFTQGSPER	2.21230001	2	2.50873
P0C2X9	YQLSPFNHGHK	0.648169	2	2.98252
P0C2X9	YRETLQLVDSTTSYGLTGAVFAQDK	2.02052047	3	4.0534
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.28751694**	**0.57275**	**5**
P0C5H9	DRDVTFSPATIEEELIK	1.08919544	2	4.92631
P0C5H9	DVTFSPATIEEELIK	1.25758304	2	3.21595
P0C5H9	IINEVSKPLAHHIPVEK	1.66651846	3	4.04905

P0C5H9	ILDDWGEMCK	0.59601944	2	3.03043
P0C5H9	INELMPK	1.11084866	2	2.48919
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**0.752982**	**0.34246**	**2**
P0C6F1	AMLPGEWENACNEMQRMLIVR+Oxidation(16	0.71795247		
P0C6F1	EKVEVMSLELEDAK+Oxidation(5	0.75392153		
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.16479351**	**1.4E-14**	**11**
P10111	EGMSIVEAMER	1.51728733	1	2.80427
P10111	FEDENFILK	1.03225937	2	3.42604
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.24025066	3	6.09178
P10111	IIPGFMCQGGDFTR	1.40079647	2	3.41568
P10111	IIPGFMCQGGDFTR+Oxidation(5	1.72242098		
P10111	KITISDCGQL	1.25616005	2	3.51117
P10111	SIYGEKFEDENFILK	1.20175907	2	4.54036
P10111	TEWLDGK	1.49815166	2	2.30247
P10111	VCFELFADK	1.66469817	2	3.24606
P10111	VCFELFADKVPK	0.88593959	2	3.89845
P10111	VKEGMSIVEAMER	1.00300599	3	3.6379
P10536	**RAB1B Ras_related protein Rab_1B**	**1.74323116**	**0.83709**	**3**
P10536	MGPGAASGGERPNLK	1.33036764	2	4.09043
P10536	NATNVEQAFMTMAAEIK+Oxidation(11	1.94085455		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9	1.91678616		
P10633	**CP2D1 Cytochrome P450 2D1**	**1.17977473**	**0.00018**	**3**
P10633	SQGVILASYGPEWR	0.76420368	2	4.08668
P10633	TFMALLDNLLAENR	1.40009755	2	3.71049
P10633	YGDVFSLQK	0.99746557	2	2.71123
P10634	**CP2DQ Cytochrome P450 2D26**	**1.20616211**	**0.99878**	**21**
P10634	ACLGEPLAR	0.99124692	2	2.74757
P10634	AKGNPESSFNDENLR	1.66540302	2	3.44884
P10634	AVSNVIASLVYAR	1.1461883	2	4.24841
P10634	DETVWEKPLR	1.07829169	2	2.34993
P10634	DMTDAFLAEMQK	1.54013704	2	3.51868
P10634	EAEHPFNPSILLSK	1.28545318	2	2.66698
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.18539619	3	5.71514
P10634	FADIVPTNIPHMTSR	1.71866347	3	3.68723
P10634	FEYEDPFFNR	1.08959914	2	2.82611
P10634	FHPEHFLDAQGNFVK	1.10996398	3	4.70054
P10634	FQGFLIPK	0.76964239	2	2.32181
P10634	GNPESSFNDENLR	1.41038442	2	4.42134
P10634	GTTLIPNLSSVLK	0.8745099	2	2.40056
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.09886257	2	4.72424
P10634	GVVLAPYGPEWR	1.07666242	2	3.20211
P10634	LNSFIALVDK	2.2314575	2	3.26995
P10634	RFEYEDPFFNR	1.02405176	2	4.02844
P10634	RVHEEIDEVIGQVR	1.23904979	2	4.26971
P10634	SLEQWVTEEAGHLCDTFAK	1.18452728	2	4.79247
P10634	SWDPAQPPR	1.07841595	2	2.85481
P10634	VHEEIDEVIGQVR	1.04573847	2	4.8402
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.45756337**	**9.9E-20**	**32**
P10719	AHGGYSVFAGVGER	0.96949418	2	4.25433
P10719	AIAELGIYPAVDPLDSTSR	1.31556892	2	5.5855
P10719	EGNDLYHEMIESGVINLK	1.31067456	2	5.20792
P10719	EGNDLYHEMIESGVINLK+Oxidation(8	2.06564097		
P10719	FLSQPFQVAEVFTGHMGK	2.77252213	2	4.46316
P10719	FTQAGSEVSALLGR	1.28605074	2	4.85767
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	2.22666458	4	4.5936
P10719	IGLFGGAGVGK	0.91020401	2	3.29063
P10719	IGLFGGAGVGKTVLIMELINNVAK	0.8669037	3	3.51369

P10719	ILQDYK	1.31058787	1	2.03284
P10719	IMDPNIVGSEHYDVAR	1.2837898	2	4.96367
P10719	IMDPNIVGSEHYDVAR+Oxidation(1	1.28684935		
P10719	IMNVIGEPIDER	1.49225262	2	4.07792
P10719	IMNVIGEPIDER+Oxidation(1	1.80210633		
P10719	IPSAVGYQPTLATDMGTMQER	2.5671665	2	4.77871
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14	2.50720162		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17	2.50720162		
P10719	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	1.76319662	3	6.44076
P10719	LVLEVAQHLGESTVR	1.4713261	2	4.80138
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	1.57796505	3	4.91654
P10719	SLQDIIAILGMDELSEEDKLTVSR	1.55655013	3	4.90977
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10	1.47171813		
P10719	TIAMDGTEGLVR	1.13382331	2	3.80455
P10719	TIAMDGTEGLVR+Oxidation(3	1.45752319		
P10719	TREGNDLYHEMIESGVINLK	0.65746711	2	6.03984
P10719	TVLIMELINNVAK	1.01032075	2	5.11593
P10719	TVLIMELINNVAK+Oxidation(4	1.32186875		
P10719	VALTGLTVAEYFR	2.67361844	2	4.06678
P10719	VALVYGQMNEPPGAR	1.75424623	2	4.02356
P10719	VLDSGAPIK	1.24446576	2	3.37277
P10719	VLDSGAPIKIPVGPETLGR	1.21212466	3	5.00241
P10719	VVDLLAPYAK	1.28881069	2	3.23735
P10760	**SAHH Adenosylhomocysteinase**	**1.42548051**	**9.9E-20**	**20**
P10760	AGIPVFAWK	1.73117662	2	2.84386
P10760	ALDIAENEMPGLMR	1.22697541	2	3.77382
P10760	ALDIAENEMPGLMR+Oxidation(12	2.21889588		
P10760	ATDVMIAGK	1.48767659	2	2.9032
P10760	DGPLNMILDDGGDLTNLIHTK	1.47307297	2	5.57914
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5	1.73012637		
P10760	EMYSASKPLK	2.06495768	2	2.36064
P10760	FDNLYGCR	1.42145537	2	2.8435
P10760	GETDEEYLWCIEQTLHFK	2.1693631	2	4.46233
P10760	GISEETTTGVHNLYK	1.13360999	2	4.23768
P10760	IILLAEGR	1.85424065	2	2.92536
P10760	KLDEAVAEAHLGK	1.46478547	3	5.05049
P10760	LDEAVAEAHLGK	1.15499157	2	3.67498
P10760	RATDVMIAGK	1.44646263	2	2.52628
P10760	SKFDNLYGCR	1.53895612	2	3.10014
P10760	VAVVAGYGDVGK	1.35936118	2	4.14517
P10760	VIITEIDPINALQAAMEGYEVTTMDEACK	1.05960357	3	6.54741
P10760	VNIKPQVDR	1.36077442	2	2.7501
P10760	WLNENAVEK	1.36281241	2	2.81673
P10760	WSSCNIFSTQDHAAAAIAK	1.07159978	2	5.17942
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**1.40597039**	**0.61622**	**2**
P10818	HEEHERPEFVAYPHLR	1.39246547	3	3.67167
P10818	SRHEEHERPEFVAYPHLR	1.41125375	3	4.10219
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**0.97448551**	**0.85585**	**29**
P10860	ALASLMTYK	1.09864925	2	3.62211
P10860	CAVVDVPFGGAK	0.77051247	2	3.07172
P10860	CVGVGESDGSIWNPDGIDPK	1.02968619	2	5.09498
P10860	DDGSWEVIEGYR	0.68397858	2	3.97291
P10860	DIVHSGLAYTMER	1.53410208	2	3.36619
P10860	DIVHSGLAYTMER+Oxidation(10	1.55295984		
P10860	DSNYHLLMSVQESLER	0.96989731	2	4.23282

P10860	EDDPNFFK	0.68696076	1	2.15232
P10860	FTMELAK	1.57341915	2	2.39471
P10860	GASIVEDKLVEDLK	1.22012004	2	3.58532
P10860	GFIGPGIDVPAPDMSTGER	1.36522357	2	4.99593
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13	1.12342341		
P10860	HGGTIPVVPTAEFQDR	1.05599118	2	4.72888
P10860	IIAEGANGPTTPEADK	1.22447149	2	5.38195
P10860	IIAEGANGPTTPEADKIFLER	1.09208133	2	4.84898
P10860	ISGASEKDIVHSGLAYTMER	1.19737858	3	3.59329
P10860	KGFIGPGIDVPAPDMSTGER	1.01919663	2	5.13157
P10860	LQHGSILGFPK	1.06722037	1	3.08417
P10860	MVEGFFDR	1.08477145	2	2.89927
P10860	MVEGFFDR+Oxidation(0	1.37246347		
P10860	NLNHVSYGR	0.81497265	1	2.86818
P10860	NYTDNELEK	1.10895133	2	2.48609
P10860	RDDGSWEVIEGYR	0.75549244	2	4.43619
P10860	RFTMELAK	1.08225703	2	2.49237
P10860	TAAYVNAIEK	1.25010346	2	3.6314
P10860	TFVVQGFGNVGLHSMR	1.24948144	2	4.53745
P10860	VYEGSILEADCDILIPAASEK	1.19281506	3	6.00546
P10860	YNLGLDLR	1.12255795	2	3.16748
P10860	YSTDVSVDEVK	0.70205421	2	3.39863
P10867	**GGLO L_gulonolactone oxidase**	**1.18680711**	**0.61974**	**7**
P10867	EKLDPTGMFLNSYLEK	1.24108342	3	3.53458
P10867	GDDILLSPCFQR	1.20847358	2	3.22715
P10867	LDPTGMFLNSYLEK	1.29127045	2	4.12281
P10867	LDYWLAYETIMK	1.23590727	2	4.0198
P10867	NADVFQAAR	1.20927206	2	2.86951
P10867	TYGCSPEVYYQPTSVEEVR	0.97755868	2	4.8395
P10867	VVAHYPVEVR	1.25377123	2	2.75673
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.65984513**	**0.02247**	**3**
P10868	EHWIIECNDGVFQR	1.28305562	3	3.80169
P10868	YTDITAMFEETQVPALLEAGFQR	1.38089591	3	4.58187
P10868	YYAFPQMITPLVTK	1.99313669	2	3.78
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.05643164**	**0.62536**	**7**
P10888	ADWSSLSR	1.34100496	2	2.34799
P10888	DYPLPDVAHVK	1.7636404	2	2.7672
P10888	IQFNESFAEMNK	1.51359598	2	4.04551
P10888	RDYPLPDVAHVK	1.05287997	2	2.30233
P10888	SEDYALPSYVDR	0.95146544	2	3.86736
P10888	VNPIQGFSAK	0.91578186	1	2.13487
P10888	WDYNKNEWK	1.48930245	2	2.39344
P10959	**EST2 Liver carboxylesterase 1**	**1.26678984**	**0.21779**	**3**
P10959	AISESGVVLTTNLDKK	0.67437505	2	3.41963
P10959	EGASEEETNLSKLVMK	1.26772637	2	2.66072
P10959	GNWAHLDQLAALR	0.83875303	2	3.01174
P11030	**ACBP Acyl_CoA_binding protein**	**1.23965758**	**0.92979**	**5**
P11030	AKWDSWNK	1.05416325	2	2.40659
P11030	QATVGDVNTDRPGLLDLK	1.37445327	2	3.65335
P11030	TQPTDEEMLFIYSHFK	1.62665003	2	3.91036
P11030	TYVEKVEELK	1.17303846	2	2.34317
P11030	WDSWNK	1.12364466	1	2.08017
P11232	**THIO Thioredoxin**	**0.99720134**	**0.84983**	**2**
P11232	EAFQEALAAAGDK	1.1664865	2	4.51578
P11232	VGEFSGANK	0.59538114	2	2.7038

P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**1.21144168**	**9.7E-06**	**6**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.54640484	3	5.93058
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	2.31608829	3	6.98547
P11240	GMNTLVGYDLVPEPK	1.26866014	2	4.01758
P11240	IIDAALR	1.54594683	1	2.1019
P11240	LNDFASAVR	1.18329188	2	3.27435
P11240	RLNDFASAVR	1.33952937	2	2.48269
P11348	**DHPR Dihydropteridine reductase**	**1.07367403**	**0.14794**	**12**
P11348	AALDGTPGMIGYGMAK	1.02404715	2	3.86588
P11348	EGGLLTLAGAK	1.07421518	2	2.92322
P11348	GAVHQLCQSLAGK	1.5003906	3	4.29872
P11348	MTDSFTEQADQVTAEVGK	1.31146011	2	5.82575
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0	0.87154267		
P11348	NCDLMWK	1.05679571	2	2.35414
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.24143732	2	5.39483
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3	2.09758556		
P11348	QSIWTSTISSHLATK	1.53305716	2	3.81882
P11348	RPNSGSLIQVVTTDGK	1.52682759	2	3.71702
P11348	TELTPAYF	2.9610965	1	2.01746
P11348	VDAILCVAGGWAGGNAK	1.51939022	2	3.92479
P11442	**CLH Clathrin heavy chain 1**	**1.21827833**	**7.3E-07**	**39**
P11442	ADDPSSYMEVVQAANTSGNWEELVK	1.91205079	3	4.05348
P11442	AFMTADLPNELIELLEK	1.14673406	3	4.69238
P11442	AHIAQLCEK	1.65538892	2	2.3787
P11442	AHTMTDDVTFWK	1.52247265	2	2.52308
P11442	ALEHFTDLYDIK	1.49071253	3	3.96542
P11442	CNEPAVWSQLAK	1.1235856	2	3.43146
P11442	FDVNTSAVQVLIEHIGNLDR	1.48718711	3	4.17424
P11442	FNALFAQGNYSEAAK	1.1993055	2	5.04448
P11442	GQCDLELINVCNENSLFK	1.51775979	2	5.56819
P11442	GQFSTDELVAEVEK	1.63826099	2	4.04968
P11442	GQFSTDELVAEVEKR	1.20548687	2	3.67921
P11442	HELIEFR	1.17251459	2	2.50616
P11442	HSSLAGCQIINYR	1.4564537	2	3.78654
P11442	IHEGCEEPATHNALAK	1.26238594	2	5.39535
P11442	ISGETIFVTAPHEATAGIIGVNR	1.18731024	2	5.21436
P11442	IVLDNSVFSEHR	1.09063614	2	2.94672
P11442	IYIDSNNNPER	1.82975174	2	3.02607
P11442	KDPELWGSVLLESNPYR	1.30048065	3	3.63699
P11442	KFDVNTSAVQVLIEHIGNLDR	1.20483668	3	6.13883
P11442	KFNALFAQGNYSEAAK	0.87514008	2	4.89737
P11442	LAELEEFINGPNNAHIQQVGDR	1.05378924	2	5.41117
P11442	LECSEELGDLVK	1.13603661	2	2.9125
P11442	LHIIEVGTPPTGNQPFPK	1.11406329	2	4.42141
P11442	LPVVIGGLLDVDCSEDVIK	2.03120822	2	4.81917
P11442	LTDQLPLIIVCDR	1.22986742	2	3.31382
P11442	NLQNLLILTAIK	1.44615273	3	4.23416
P11442	NNLAGAEELFAR	1.31273173	2	3.79278
P11442	NNRPSEGPLQTR	1.16373937	3	4.13976
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.33966019	3	6.30522
P11442	SVDPTLALSVYLR	1.33146219	2	2.60965
P11442	SVNESLNNLFITEEDYQALR	1.29523516	2	5.16167
P11442	TLQIFNIEMK	1.61197766	2	3.02098
P11442	TSIDAYDNFDNISLAQR	0.80508844	2	3.62563
P11442	VGEQAQVVIIDMNDPSNPIR	1.64010397	2	5.05414
P11442	VIQCFAETGQVQK	1.18414855	2	4.79582

P11442	VSQPIEGHAASFAQFK	0.96643492	2	4.38184
P11442	WLLLTGISAQQNR	1.38104942	2	3.64063
P11442	YESLELCRPVLQQGR	1.16879729	2	2.80687
P11442	YIEIYVQK	1.30535484	1	1.95379
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.25032557**	**0.05345**	**8**
P11497	DEPIHILNVAIK	0.94089158	2	2.56064
P11497	GGSWVVIDPTINPR	2.04714371	2	2.9903
P11497	LLETESFQLNR	1.23438267	2	2.42497
P11497	LLLEDLVK	2.40752478	2	2.37114
P11497	LPELLLK	3.78255111	2	2.37799
P11497	TLRDPSLPLLELQDIMTSVSGR	2.25399759	3	3.48147
P11497	TVELSVPADPANLDSEAK	0.75584807	2	2.53261
P11497	VQQAELHTGSLPQIQSTALR	0.70758012	3	3.53639
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**1.06333431**	**0.96035**	**8**
P11507	DIVPGDIVEIAVGDKVPADIR	2.37890455	2	2.86545
P11507	IGIFGQDEDVTSK	0.98965185	2	3.55969
P11507	IRDEMVATEQER	1.20777059	2	3.35055
P11507	KSEIGIAMGSGTAVAK	1.19751475	2	3.87256
P11507	LDEFGEQLSK	1.6899191	2	2.77234
P11507	NAENAIEALKEYEPEMGK	1.08996931	2	3.46581
P11507	SEIGIAMGSGTAVAK	1.05861988	2	3.37901
P11507	VDQSILTGESVSVIK	2.88404088	2	4.44379
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.05691537**	**0.00043**	**28**
P11598	DASVVGFFR	1.43276979	2	2.51231
P11598	DGEEAGAYDGPR	1.67549944	2	3.42295
P11598	DLFSDGHSEFLK	1.84995587	2	3.08118
P11598	DLLTAYYDVDYEK	1.86880325	2	3.58615
P11598	DPNIVIAK	1.33682862	2	2.45673
P11598	EATNPPIIQEEKPK	1.23313296	2	3.56968
P11598	ELNDFISYLQR	1.19211199	2	3.11032
P11598	EYDDNGEGITIFRPLHLANK	1.36647595	2	4.18492
P11598	FAHTNVESLVK	1.86704704	3	3.38123
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.94139165	3	4.99491
P11598	FISDKDASVVGFFR	0.99595786	2	4.36724
P11598	FLQEYFDGNLK	0.97148643	2	3.72212
P11598	FLQEYFDGNLKR	1.05539003	2	3.53128
P11598	FVMQEEFSR	1.05042481	2	2.92936
P11598	IFRDGEEAGAYDGPR	1.03090419	2	3.95445
P11598	KTFSHELSDFGLESTTGEIPVVAIR	1.40503635	3	4.38281
P11598	LAPEYEAAATR	1.1475946	2	2.89025
P11598	LNFAVASR	1.66423652	2	2.53544
P11598	LSKDPNIVIAK	1.46365482	3	4.0293
P11598	MDATANDVPSPYEVK	1.22904866	2	4.37502
P11598	MDATANDVPSPYEVK+Oxidation(0	2.01265825		
P11598	RLAPEYEAAATR	0.99672112	2	3.66656
P11598	SEPIPETNEGPVK	1.07315907	2	2.88446
P11598	TADGIVSHLK	2.18045392	2	2.7983
P11598	TFLDAGHK	0.62462762	1	1.90221
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.29623485	2	6.03875
P11598	VDCTANTNTCNK	1.03751764	2	3.88552
P11598	YGVSGYPTLK	0.85190025	2	3.21822
P11711	**CP2A1 Cytochrome P450 2A1**	**1.14328032**	**0.06147**	**6**
P11711	GEQATYNTLFK	1.31953736	2	2.56123
P11711	GTDVFPILGSLMTDPK	1.0907062	2	3.46086
P11711	ILEEAGYLIK	1.05419625	2	3.40363
P11711	LEDINESPKPLGFTR	1.17738066	2	3.42735

P11711	TVSNVISSIVFGER	1.4963796	2	3.6523
P11711	VHEEIEQVIGR	1.3695416	2	3.06757
P11714	**CP2D9 Cytochrome P450 2D9**	**0.97090096**	**0.92688**	**2**
P11714	GNPESSFNDENLLMVVR	0.87344051	2	2.44001
P11714	VQQEIDEVIGQVR	0.97090099	2	4.70771
P11862	**GAS2 Growth arrest_specific protein 2**	**1.45072524**	**0.31843**	**3**
P11862	EIEQEETLSAPSPSPSPSSK	1.10216425	2	4.11684
P11862	LDNGALLCQLAATVQEK	1.72391034	2	3.8059
P11862	YGVEPPGLIK	1.14064826	2	2.32449
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**1.10973457**	**2.9E-13**	**27**
P11884	AAQAAFQLGSPWR	1.53073276	2	2.91178
P11884	DGMTIAKEEIFGPVMQILK	2.66674708	3	4.01103
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.97714069	3	4.45642
P11884	EEIFGPVMQILK	1.25915184	2	4.06304
P11884	EEIFGPVMQILK+Oxidation(7	1.11772423		
P11884	ELGEYGLQAYTEVK	1.94126859	2	4.38967
P11884	GYFIQPTVFGDVK	1.15468638	2	4.28528
P11884	HEPVGVCGQIIPWNFPLLMQAWK	1.77506904	3	4.24194
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.97667675	3	6.48146
P11884	LGPALATGNVVVMK	1.3564339	2	3.81526
P11884	LGPALATGNVVVMK+Oxidation(12	1.29220751		
P11884	LLCGGGAAADR	1.55646016	2	3.38588
P11884	RVTLELGGK	1.32209519	2	2.92244
P11884	TEQGPQVDETQFK	0.95333157	2	4.56965
P11884	TEQGPQVDETQFKK	1.32100826	2	3.56918
P11884	TFPTVNPSTGEVICQVAEGNK	0.92758968	2	5.29401
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	1.14193502	2	4.30225
P11884	TFVQEDVYDEFVER	1.0992766	2	5.11162
P11884	TIEEVVGR	1.17930899	2	2.98471
P11884	TIPIDGDFFSYTR	1.55210015	2	2.81701
P11884	VAEQTPLTALYVANLIK	1.60921277	2	5.49268
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.24889691	2	6.53716
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	2.23075214	3	3.99173
P11884	VTLELGGK	1.06350325	1	2.05357
P11884	VVGNPFDSR	2.11803337	2	2.95273
P11884	YGLAAAVFTK	1.39088796	2	4.04562
P11884	YYAGWADK	1.09887827	2	2.54063
P11915	**NLTP Non_specific lipid_transfer protein**	**1.21647967**	**2E-05**	**21**
P11915	ADCTITMADSDLLALMTGK	1.45559299	2	5.40223
P11915	ANLIFK	1.64527875	2	2.32691
P11915	AVEIVAQEMVTDMPSTFEEK	1.42277057	2	5.30567
P11915	GHPLGATGLAQCAELCWQLR	1.6313585	3	3.58373
P11915	GSVLPDSDK	0.87325321	1	2.08974
P11915	GSVLPDSDKK	0.48964828	2	2.60047
P11915	HIDVLINK	1.18594804	2	2.9382
P11915	HSVNNPYSQFQDEYSLDEIMK	1.35672589	3	6.17153
P11915	KADCTITMADSDLLALMTGK	1.67352885	3	3.48586
P11915	KLEEEGEEFVK	1.03404352	3	4.24514
P11915	KLEEEGEEFVKK	1.12711381	3	4.85396
P11915	LEEEGEEFVK	0.42921792	2	2.81904
P11915	LEEEGEEFVKK	0.95882938	2	3.58774
P11915	LQSLQLQPDK	1.26835814	2	3.16929
P11915	MGFPEAASSFR	1.24346263	2	2.61485
P11915	MNPQSAFFQGK	0.80524628	2	3.22935
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.5405758	3	4.37054
P11915	THQISAAPTSSAGDGFK	1.25542823	2	4.64028

P11915	VFVVGVGMTK	0.99949564	2	2.67829
P11915	WVINPSGGLISK	1.27307516	2	3.11443
P11915	YGMSACPFAPQLFGSAGK	1.60614207	2	4.0614
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.4061498**	**0.40806**	**4**
P11980	GADYLVTEVENGGSLGSK	2.36258836	2	4.76206
P11980	GVNLPGAAVDLPAVSEK	1.50021325	2	4.06188
P11980	IYVDDGLISLQVK	2.03660253	2	2.44236
P11980	NTGIICTIGPASR	1.26009966	2	3.29981
P12001	**RL18 60S ribosomal protein L18**	**1.16722092**	**9.9E-20**	**5**
P12001	GTVLLSGPR	1.31157194	2	3.1428
P12001	ILTFDQLALESPK	1.55227428	2	4.85503
P12001	TAVVVGTITDDVR	1.23975857	2	4.33315
P12001	TNRPPLSLSR	1.32750578	3	3.66187
P12001	TNSTFNQVVLK	0.80093355	2	2.99677
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.13118118**	**0.35497**	**9**
P12007	AQEIDQSNDFK	0.73934627	2	3.43611
P12007	FVQENLAPK	1.13201068	2	2.94552
P12007	FWITNGPDADVLVVYAK	1.72045495	2	3.58472
P12007	GSNTCELVFEDCK	1.12054647	2	4.55817
P12007	GSNTCELVFEDCKVPAANILSQESK	1.16567856	3	5.22953
P12007	GVYVLMSGLDLER	1.33189778	2	2.95199
P12007	IGQFQLMQGK	1.29430985	2	2.76344
P12007	LYEIGGGTSEVR	1.15185442	2	2.8232
P12007	TDLTAVPASR	0.96184239	2	3.09366
P12075	**COX5B Cytochrome c oxidase subunit 5B_ mitochondrial**	**1.2695174**	**0.37619**	**2**
P12075	EDPNLVPSVSNK	1.26645858	2	3.22824
P12075	GLDPYNMLPPK	1.52132491	2	2.31776
P12336	**GTR2 Solute carrier family 2_ facilitated glucose transporter member 2**	**1.27928492**	**0.05748**	**3**
P12336	HVLGVPLDDR	1.73870732	2	2.33126
P12336	HVLGVPLDDRR	1.31207228	3	3.3095
P12336	SFDEIAAEFR	1.27923696	2	3.34138
P12346	**TRFE Serotransferrin**	**1.11956905**	**0.04417**	**23**
P12346	ADRDQYELLCLDNTR	1.31903216	2	4.31865
P12346	ASDSSINWNNLK	1.34064596	2	3.07084
P12346	DFQLFGSPLGK	2.64057564	2	3.59528
P12346	DGGGDVAFVK	1.71361058	2	2.46836
P12346	DLKQEDFQLLCPDGTK	1.41693305	2	4.57533
P12346	EGVCPEGSIDSAPVK	1.17220182	2	3.47231
P12346	EGYNGYTGAFQCLVEK	1.41574771	2	3.25762
P12346	FDEFFSQGCAPGYK	1.01749215	2	4.06314
P12346	GDKDCTGNFCLFR	1.24143832	2	3.58545
P12346	GTDFQLNQLQGK	1.12408936	2	3.51885
P12346	GYYAVAVVK	1.08860503	2	2.95011
P12346	HQTVLENTNGK	9.97004294	2	2.47251
P12346	HTTIFEVLPQK	0.87652682	3	4.01045
P12346	KGTDFQLNQLQGK	1.17562043	2	4.58998
P12346	KTSYQDCIK	1.38268817	2	2.64941
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.88618288	2	4.58329
P12346	NGDGKEDLIWEILK	1.12033155	2	3.69213
P12346	QEDFQLLCPDGTK	1.06357844	2	3.22916
P12346	SKDFQLFGSPLGK	1.25644135	2	3.14005
P12346	TSYQDCIK	1.15886246	2	2.46459
P12346	VSTVLTAQK	1.13322635	2	2.72709
P12346	WCALSHQER	1.45344919	2	3.18049

P12346	WCAVSEHENTK	1.22742353	2	3.61857
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.88735251**	**0.00223**	**3**
P12368	MFESFIESVPLFK	1.56508083	2	3.44172
P12368	NISHYEEQLVK	0.89573526	2	2.53913
P12368	NLDQEQLSQVLDAMFEK	1.91075806	3	3.89886
P12711	**ADHX Alcohol dehydrogenase class_3**	**1.07872026**	**0.02083**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	1.54797803	3	6.70961
P12711	AFDLMHSGNSIR	0.62943654	2	3.28735
P12711	AGDTVIPLYIPQCGECK	1.24851614	2	3.7181
P12711	AKEFGATECINPQDFSK	0.9443709	2	4.76371
P12711	EFGATECINPQDFSK	5.17505526	2	4.35277
P12711	IDPSAPLDK	1.0508139	1	2.17802
P12711	IIGIDINK	0.88528558	1	2.03836
P12711	IIGIDINKDK	0.98411783	2	2.43535
P12711	VCLLGCGISTGYGAAVNTAK	1.59549408	2	6.07831
P12711	VDEFVTGNLSFDQINK	1.0440214	2	4.99031
P12749	**RL26 60S ribosomal protein L26**	**1.34431975**	**0.41275**	**5**
P12749	DDEVQVVR	1.2668946	2	2.94547
P12749	FNPFVTSDR	1.08372732	2	2.75645
P12749	HFNAPSHIR	1.2818161	3	3.88091
P12749	KDDEVQVVR	1.57538048	2	3.26208
P12749	YVIYIER	0.97021223	1	1.97401
P12785	**FAS Fatty acid synthase**	**1.77477926**	**9.9E-20**	**45**
P12785	ACIDTALENLSTLK	2.52740502	2	4.47468
P12785	AEAVVAVLLTK	1.83903259	2	3.83213
P12785	AGSDTELAAPK	1.61957321	2	3.4142
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	2.24442401	3	5.52807
P12785	DAMLENQTPELFQDVNKPK	1.81180141	2	4.17341
P12785	DANLPAGSMAAVGLSWEECK	0.80178968	2	3.08915
P12785	DGGFLLMHTVLK	1.16140145	2	3.33915
P12785	DPETLLGYSMVGCQR	1.85560341	2	3.93981
P12785	DTSFEQHVLLHTGGK	2.26087687	2	2.99097
P12785	EEEPEAMLPGAQPTLISAISK	2.18694559	2	3.94726
P12785	EQGVTFPSGEAQEQLIR	0.97029669	2	4.29349
P12785	FDASFFGVHPK	1.53162248	2	3.4069
P12785	FDLSNNHPLGMAIFLK	2.76657426	2	3.43606
P12785	FVFTPHVEPECLSESAILQK	2.40265766	3	5.07461
P12785	GLESIINIIHSSLAEPR	1.850112	2	4.416
P12785	GNAGQSNYGFANSTMER	1.64031868	2	4.70319
P12785	GVDLVLNSLAEEK	1.77108139	2	3.48034
P12785	HFQLEQDKPEEQTAHAFVNVLTR	1.94176253	3	3.40921
P12785	LFDHPEVPIPAESESVSR	1.61464545	2	4.26387
P12785	LLLPEDPLISGLLNSQALK	1.89853065	3	4.7815
P12785	LTPGCEAEAEAEAICFFIK	4.1565744	2	3.76223
P12785	MTVPGLEDLPQHGLPR	1.56897128	2	3.59142
P12785	QAQLNLSILLVNPEGPTLTR	2.3190757	2	3.08443
P12785	RQQEQLVPTLEK	1.26437138	2	3.12097
P12785	SDEALKPLGVK	1.32779759	2	2.97413
P12785	SFDDSGNGYCR	1.20698294	2	3.05912
P12785	SGECPAAIVGGINLLLKPNTSVQFMK	0.8162356	3	3.96689
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.95399889	2	5.23347
P12785	SNMGHPEPASGLAALTK	1.53889704	3	4.17648
P12785	SNMGHPEPASGLAALTK+Oxidation(2	2.32131777		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.38800327	2	5.04823
P12785	TGTVPLEVR	1.30496064	2	2.46229
P12785	TMEAVQGLLEQGR	1.62030186	2	3.88832

P12785	VFTTVGSAEK	2.2743033	2	2.3602
P12785	VGDPQELNGITR	0.54274212	2	3.15346
P12785	VHLTGIDINPNALFPPVEFPVPR	2.25918257	2	4.90093
P12785	VLEALLPLK	1.97723445	2	3.3012
P12785	VLESDLVMNVYR	1.94646071	2	3.40659
P12785	VSVHIIEGDHR	2.14796524	2	2.81774
P12785	VTAIYIDPATHLQK	1.9190315	2	3.80096
P12785	VYATILNAGTNTDGCK	2.01765524	2	4.98002
P12785	VYMLEGDTQVADVTTSR	2.4583783	2	3.58574
P12785	VYQWEDPDSK	1.60209727	2	3.2511
P12785	WLSTSIPEAQWQSSLAR	0.70168075	2	2.67496
P12785	YNGTLNLDR	2.42431794	1	2.10228
P12791	**CP2BA Cytochrome P450 2B10**	**1.03911606**	**1**	**2**
P12791	IQEEAQCLVEELR	1.06034098	2	4.58548
P12791	IQEEAQCLVEELRK	1.03883726	2	3.76327
P12847	**MYH3 Myosin_3**	**1.06077458**	**0.18295**	**5**
P12847	GTLEDQIISANPLLEAFGNAK	0.58702895	2	3.11892
P12847	IEAQNQPFDAK	0.87070516	2	3.03745
P12847	KELEEKLVTLVQEK	0.67212874	2	2.76737
P12847	MKGTLEDQIISANPLLEAFGNAK	3.77365612	3	6.70384
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0	2.63358265		
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.52338602**	**6.7E-13**	**20**
P12928	AAVIAVTR	1.84571095	2	2.62289
P12928	AETSDVANAVLDGADCIMLSGETAK	2.77188601	2	5.97997
P12928	CCAAAIIVLTK	1.23330357	2	3.08597
P12928	CNLAGKPVVCATQMLESMITK	1.72225875	3	4.86376
P12928	EATESFATSPLSYRPVAIALDTK	2.20906828	2	4.02342
P12928	EPPEAIWADDVDR	1.95504405	2	2.64996
P12928	GDLGIEIPAEK	1.16817566	2	3.147
P12928	GSFPVEAVMMQHAIAR	1.98312283	2	3.91374
P12928	GSQVLVTVDPK	1.62111912	2	2.93878
P12928	GVNLPNTEVDLPGLSEQDLLDLR	2.97379909	2	4.90819
P12928	IGPEGLVTEVEHGGILGSR	1.47275283	2	5.04771
P12928	IYIDDGLISLVVQK	2.49225432	2	4.41485
P12928	KFDEILEVSDGIMVAR	1.32196137	2	4.93118
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	2.44391071	3	4.66172
P12928	LNFSHGSHEYHAESIANIR	2.83551733	2	5.72094
P12928	RVQFGIESGK	0.87400784	2	2.55405
P12928	STSIIATIGPASR	1.1742207	2	3.39026
P12928	TGVLQGGPESEVEIVK	1.38707333	2	5.06898
P12928	TVWVDYHNITR	1.7966444	2	2.68411
P12928	VQFGIESGK	1.72151837	2	2.46101
P12938	**CP2D3 Cytochrome P450 2D3**	**0.89424599**	**0.98806**	**7**
P12938	DLTDAFLAEIEK	0.88591905	2	4.42482
P12938	FDYGDPDFIK	1.76905204	2	2.76539
P12938	GNPESSFNDANLR	0.85865061	2	4.00462
P12938	RFDYGDPDFIK	0.79083129	2	3.0478
P12938	TFLTMVDNLVTEHK	1.3331383	2	3.33964
P12938	TWDPDQPPR	0.7189807	2	2.45075
P12938	TWDPDQPPRDLTDAFLAEIEK	1.11681562	3	3.67225
P12939	**CP2DA Cytochrome P450 2D10**	**1.32407393**	**0.04307**	**8**
P12939	ALCNVIASLIFAR	2.09363093	2	3.50722
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.30957758	3	5.59872
P12939	FEYEDPYLIR	1.35670096	2	2.45893
P12939	FGDIAPLNLPR	1.48217823	2	3.1325
P12939	ITSCDIEVQDFVIPK	2.32742386	2	4.36936
P12939	NLTDAFLAEVEK	1.63529922	2	4.16064

P12939	RFEYEDPYLIR	1.30566242	3	3.46783
P12939	TTWDPAQPPR	2.37814844	2	2.59151
P13084	**NPM Nucleophosmin**	**1.8209426**	**0.00029**	**2**
P13084	MTDQEAIQDLWQWR	1.43698789	2	3.27561
P13084	VDNDENEHQLSLR	2.32261387	2	4.12753
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.3595564**	**0.69203**	**5**
P13086	HLGLPVFNTVK	2.06098664	2	2.33359
P13086	LIGPNCPGIINPGECK	1.19453439	2	4.43545
P13086	MGHAGAIIAGGK	1.49365864	3	3.46659
P13086	NIYIDK	1.02525575	1	2.1293
P13086	QGTFHSQQALEYGTK	1.37162142	2	2.72825
P13107	**CP2B3 Cytochrome P450 2B3**	**1.20095516**	**0.83492**	**8**
P13107	ATLDPNAPR	1.20304905	2	2.63511
P13107	EIDQVIGSQR	0.66144557	2	2.66546
P13107	EVLDYIDHSVENHR	1.35326193	2	4.08286
P13107	FSDVSPMGLPCR	1.52037179	2	3.44387
P13107	GIIAVLQPIMQEYGVSFVNEER	1.44801745	3	5.76416
P13107	MCLGEGIAR	1.18685058	2	2.69242
P13107	QSVEDQIKEEAK	1.17566109	2	2.91521
P13107	SFIQLQEK	0.37176947	2	2.43396
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.53844788**	**4.7E-13**	**7**
P13221	IGADFLGR	4.10303752	2	2.38995
P13221	ITWSNPPAQGAR	2.60079331	2	3.00608
P13221	IVATTLSNPELFK	2.08483882	2	3.78562
P13221	NLDYVATSINEAVTK	2.45961583	2	5.09798
P13221	SCASQLVLGDNSPALR	1.53847332	2	5.11447
P13221	TDDSQPWVLPVVR	1.04571431	2	3.26695
P13221	VGGVQSLGGTGALR	0.67644075	2	3.00787
P13255	**GNMT Glycine N_methyltransferase**	**1.16964541**	**0.07964**	**8**
P13255	AHMVTLDYTVQVPGAGR	1.44947443	2	5.07364
P13255	AWLLGLLR	1.29625864	2	2.57165
P13255	DITTSVLTVNNK	1.61125048	2	3.82661
P13255	LSYYPHCLASFTELVQEAFGGR	2.0989385	3	3.64388
P13255	NIASMVRPGGLLVIDHR	2.35968563	3	3.74856
P13255	NYDYILSTGCAPPGK	1.37393987	2	4.65123
P13255	SDLTKDITTSVLTVNNK	1.71047019	2	2.89718
P13255	SLGVAAEGIPDQYADGEAAR	0.85643637	2	5.25813
P13383	**NUCL Nucleolin**	**1.35444869**	**0.0761**	**8**
P13383	EAMEDGEIDGNK	2.6113868	2	2.93201
P13383	GFGFVDFNSEEDAK	1.76855147	2	2.87702
P13383	GLSEDTTEETLK	1.03757967	2	3.24166
P13383	GSPNARSQPSKTLFVK	1.22775826	2	2.33221
P13383	IEGSEPTTPFNLFIGNLNPNK	0.73935617	2	3.75733
P13383	NDLAAVDVR	1.42032858	2	2.56311
P13383	NLSFNITEDELK	1.24300459	2	2.6226
P13383	SEADAEKNLEEK	1.35415494	2	2.9488
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**1.08355069**	**0.51966**	**21**
P13437	AANEAGYFNEEMAPIEVK	0.93498733	2	5.1397
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11	1.41527254		
P13437	DAEVVLCGGTESMSQSPYSVR	1.53410513	3	5.0537
P13437	DFTATDLTEFAAR	1.11671225	2	4.0434
P13437	DMDLIDVNEAFAPQFLAVQK	1.92661578	3	6.51918
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1	1.86968037		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.97172236	3	5.77951
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	1.15098114	3	4.88921
P13437	GVFIVAAK	1.50457515	2	2.47247

P13437	HNFTPLAR	1.31020944	2	2.36927
P13437	ITAHLVHELR	2.39554572	2	3.51449
P13437	LCGSGFQSIVSGCQEICSK	1.59875089	2	5.64092
P13437	LEDTLWAGLTDQHVK	0.9721156	2	5.06277
P13437	RTPFGAYGGLLK	0.64746256	3	3.38314
P13437	SLDLDPSK	0.58598299	2	2.72636
P13437	TNVSGGAIALGHPLGGSGSR	0.95201086	2	5.99104
P13437	VGVPTETGALTLNR	0.9950495	2	3.63579
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	1.06662721	2	5.91279
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14	1.53401466		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.46214711	3	5.02973
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	1.03123661	3	4.51412
P13439	**UMPS Uridine 5__monophosphate synthase**	**1.39982443**	**0.06901**	**2**
P13439	SGLSSPVYIDLR	1.40388784	2	2.42861
P13439	VTDAIVLLDR	1.39788349	2	2.36203
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.34871109**	**9.9E-20**	**9**
P13444	FVIGGPQGDAGVTGR	1.38559095	2	4.51991
P13444	HIGYDDSAK	1.2339936	2	2.74085
P13444	ICDQISDAVLDAHLK	1.42180751	3	5.26489
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.23614917	3	6.92725
P13444	SEFPWEVPK	1.53801019	2	2.37817
P13444	SGVLPWLRPDSK	1.16586277	2	2.94306
P13444	TCNVLVALEQQSPDIAQCVHLDR	2.21045632	3	5.99758
P13444	TQVTVQYVQDNGAVIPVR	1.9149268	2	5.43374
P13444	VHTIVISVQHNEDITLEAMR	2.27648142	3	4.07736
P13471	**RS14 40S ribosomal protein S14**	**1.30323642**	**0.15234**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	1.33532241	2	5.42994
P13471	ELGITALHIK	1.94373621	2	2.49773
P13471	IEDVTPIPSDSTR	0.84634902	2	3.9123
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.88911348**	**0.11641**	**20**
P13601	ANNTPYGLAAGVFTK	0.72411642	2	4.37942
P13601	EEIFGPVQQIMK	0.64559263	2	3.60608
P13601	EMGEQGVYEYTELK	0.6100144	2	3.53665
P13601	FPVINPATEEVICHVEEGDK	0.23714866	3	3.82828
P13601	FPVINPATEEVICHVEEGDKADVDK	0.96036448	4	5.05052
P13601	GFFVQPTVFSNVTDEMR	1.21266957	2	2.45955
P13601	IAKEEIFGPVQQIMK	0.9599949	2	3.72034
P13601	IFINNEWHNSLNGK	0.83890946	2	3.90821
P13601	IHGQTIPSDGDVFTYTR	0.77061699	3	3.89745
P13601	ILDLIESGK	0.91017213	2	3.19051
P13601	ILDLIESGKK	0.66483419	2	2.85552
P13601	KFPVINPATEEVICHVEEGDK	0.70564703	3	3.56804
P13601	KFPVINPATEEVICHVEEGDKADVDK	1.35845386	4	4.87731
P13601	LFVEESIYDEFVR	0.55331535	2	3.60477
P13601	SIDEVIK	0.70583018	2	2.49596
P13601	VLLATMESMNAGK	0.72067925	2	4.44039
P13601	VSFTGSTEVGK	0.57192194	2	2.74865
P13601	YFAGWADK	0.68414992	2	2.31775
P13601	YVLGNPLDSGISQGPQIDK	0.87093604	2	4.75492
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.39978617	2	4.21713
P13697	**MAOX NADP_dependent malic enzyme**	**1.26354235**	**0.00257**	**6**
P13697	AECSAEECYK	1.75455345	2	3.12663
P13697	AIFASGSPFDPVTLPDGR	1.49982393	2	4.49689
P13697	GHIASVLNAWPEDVVK	3.00776032	2	3.59331
P13697	HINDSVFLTTAEVISQQVSDK	1.50324847	3	4.59759
P13697	ILGLGDLGCNGMGIPVGK	1.91018015	2	2.8062

P13697	NLEAIVQK	1.26353849	1	2.40288
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**0.95532569**	**0.00231**	**15**
P13803	AAVDAGFVPNDMQVGQTGK	0.80224613	2	4.94719
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11	1.24124996		
P13803	DPEAPIFQVADYGIVADLFK	1.13403692	2	4.98397
P13803	GLLPEELTPLILETQK	1.2282617	2	4.48045
P13803	GTSFEAAAASGGSASSEK	0.99223728	2	5.1968
P13803	LGGEVSCLVAGTK	1.0670363	2	4.59815
P13803	LLYDLADQLHAAVGASR	1.96867011	2	5.04928
P13803	LNVAPVSDIIEIK	1.49974064	3	4.03899
P13803	QFSYTHICAGASAFGK	0.79470242	2	3.23217
P13803	SDRPELTGAK	1.10832142	3	3.54489
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	1.33404194	3	6.62075
P13803	TIYAGNALCTVK	0.90432377	2	3.70433
P13803	VLVAQHDAYK	1.15008706	2	3.56115
P13803	VVPEMTEILK	0.94995531	1	1.92887
P13803	VVQDLCK	1.18970649	2	2.63306
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.17295281**	**0.22662**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.43308469	2	5.08349
P13832	FTDEEVDELYR	0.8835519	2	3.78271
P13832	GNFNYIEFTR	1.14517932	2	3.193
P14046	**A1I3 Alpha_1_inhibitor 3**	**1.08469358**	**0.96731**	**5**
P14046	ETGLMAFTNLK	1.40408805	2	2.62673
P14046	GDPIPNEQVLIK	0.76617007	2	2.88023
P14046	GMYESLPVVAVK	1.03486627	2	3.34773
P14046	QQNSYGGFSSTQDTVVALDALSK	1.1498406	2	3.49092
P14046	QSPGPCGSEVATVPETGR	0.80028055	2	3.43119
P14141	**CAH3 Carbonic anhydrase 3**	**1.24775607**	**0.02473**	**20**
P14141	DIRHDPSLQPWSVSYDPGSAK	0.66940212	3	3.86232
P14141	EAPFNHFDPSCLFPACR	1.3356503	2	4.23334
P14141	EKGEFQILLDALDK	1.30726858	2	4.67005
P14141	EKGEFQILLDALDKIK	0.93462184	2	3.70368
P14141	EPMTVSSDQMAK	1.27830342	1	3.24039
P14141	EWGYASHNGPEHWHELYPIAK	0.97239247	3	4.82179
P14141	GDNQSPIELHTK	0.9579332	2	3.23947
P14141	GEFQILLDALDK	1.14211978	2	4.56922
P14141	GEFQILLDALDKIK	1.38434883	2	3.59343
P14141	GGPLSGPYR	1.045124	2	2.75937
P14141	GKEAPFNHFDPSCLFPACR	0.94116121	2	4.19625
P14141	HDPSLQPWSVSYDPGSAK	0.70228579	3	5.58667
P14141	QFHLHWGSSDDHGSEHTVDGVK	1.10730415	2	4.77049
P14141	QPDGIAVVGIFLK	0.97443402	3	3.54867
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.95898355	3	5.703
P14141	SLFASAENEPPVPLVGNWRPPQPIKGR	1.48742269	3	4.37209
P14141	VVFDDTFDR	1.24972229	2	3.3251
P14141	YAAELHLVHWNPK	1.13350192	2	4.23882
P14141	YNTFGEALK	0.92518655	2	2.55988
P14141	YNTFGEALKQPDGIAVVGIFLK	1.07746705	3	6.11241
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.34099626**	**7.7E-05**	**8**
P14173	AGEGGGVIQGSASEATLVALLAAR	2.05340569	2	3.26032
P14173	ALIPTTAPQEPETYEDIIR	1.24902738	2	3.85561
P14173	GSNQLNETLLQR	1.22818073	2	2.98679
P14173	HSHQDSGLITDYR	0.98073248	3	3.77432
P14173	MLELPEAFLAGR	1.41099567	2	3.45539
P14173	QLQAASPELTQAALMEK	1.33996184	2	4.098
P14173	TDLTEAFNMDPVYLR	2.83513592	2	3.84325

P14173	TVESAHVQLAWEHIR	1.40744867	3	3.64039
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.33433059**	**0.00207**	**15**
P14408	AAAEVNQEYGLDPK	1.55328201	2	4.36643
P14408	AIEMLGGELGSK	1.00536011	2	3.95858
P14408	EFAQVIK	1.37110133	1	1.92098
P14408	IEYDTFGELK	0.82770218	2	3.25935
P14408	IEYDTFGELKVPTDK	1.09392621	2	3.73064
P14408	IYELAAGGTAVGTGLNTR	1.18480772	2	5.36743
P14408	LMNESLMLVTALNPHIGYDK	2.18291547	3	5.51642
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	1.44868437	3	6.87714
P14408	SGLGELILPENEPGSSIMPGK	1.34523533	2	4.63581
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17	1.65650541		
P14408	SKEFAQVIK	1.41329605	2	2.66651
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	1.64344031	3	4.78378
P14408	TAIELGYLTAEQFDEWVKPK	1.46972982	2	4.87841
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.66694715	3	5.89325
P14408	YYGAQTVR	1.12464251	2	2.4916
P14480	**FIBB Fibrinogen beta chain**	**1.6672256**	**4.7E-15**	**8**
P14480	AHYGGFTVQTEANK	2.46259499	2	3.46356
P14480	DNENVINEYSSILEDQK	1.42845264	2	3.93521
P14480	GFGNIATNEDTK	1.80209272	2	3.08932
P14480	GFGNIATNEDTKK	2.05317989	2	3.58305
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	2.69822543	3	4.97951
P14480	LYIDETVNDNIPLNLR	2.17250168	2	2.93289
P14480	TENGGWTVIQNR	1.23955142	2	3.20598
P14480	YCGLPGEYWLGNDK	1.41037563	2	3.15456
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**1.28875944**	**0.48032**	**10**
P14604	AFAAGADIK	1.22591751	2	3.08522
P14604	AQFGQPEILLGTIPGAGGTQR	1.04674075	2	5.68471
P14604	ESVNAAFEMTLTEGNKLEK	2.09284899	2	2.68186
P14604	FLSHWDHITR	1.48963549	2	3.46626
P14604	IFPVETLVEEAIQCAEK	1.5077521	3	5.88413
P14604	NSSVGLIQLNRPK	1.0215823	2	3.57694
P14604	SLAMEMVLTGDR	1.2594559	2	3.80519
P14604	SLAMEMVLTGDR+Oxidation(3	1.36364405		
P14604	SLAMEMVLTGDR+Oxidation(5	1.36364405		
P14604	TFQDCYSGK	1.27542213	2	2.89127
P14668	**ANXA5 Annexin A5**	**1.19582525**	**1.6E-05**	**5**
P14668	EFRKNFATSLYSMIK	0.98173955	2	2.33736
P14668	ETSGNLENLLLAVVK	1.61615065	2	3.24921
P14668	GAGTDDHTLIR	0.89679755	2	2.75949
P14668	GLGTDEDSILNLLTAR	1.46890316	2	5.11611
P14668	GTVTDFSGFDGR	1.08777737	2	3.00392
P14669	**ANXA3 Annexin A3**	**0.9297613**	**0.43701**	**9**
P14669	GAGTDEFTLNR	0.68278323	2	2.66357
P14669	GMGTDEDTLIEILTTR	1.26777422	2	4.38738
P14669	GTINNYPGFNPSVDAEAIR	1.05587402	2	4.96496
P14669	KDAQTLYDAGEK	1.03526958	2	3.26496
P14669	KDAQTLYDAGEKK	0.88565024	3	3.88508
P14669	QYQEAYEQALK	0.78790852	2	2.9069
P14669	SEIDLLDIR	1.87433159	2	2.54409
P14669	TLINILTER	1.20373206	2	2.73803
P14669	WGTDEDKFTEILCLR	1.57314952	3	3.38065
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.34939341**	**0.53862**	**4**
P14685	AIQLEYSEAR	1.19276029	2	3.01918
P14685	HDADGQATLLNLLLR	1.82020074	2	3.79246

P14685	LQLDSPEDAEFIVAK	1.43477699	2	3.86703
P14685	SVFPEQANNNEWAR	1.36436112	2	3.28049
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.0460992**	**0.84554**	**5**
P14740	FRPAEPHFTSDGSSFYK	1.10074709	2	3.47716
P14740	HSYTASYSIYDLNKR	1.30570768	3	3.78152
P14740	LGTLEVEDQIEAAR	1.49941012	2	4.08775
P14740	VLEDNSALDK	1.00094482	2	2.61836
P14740	WEYYDSVYTER	0.8310823	2	2.5283
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.06584767**	**0.95092**	**15**
P14882	FLSDVYPDGFK	0.95755444	2	2.80381
P14882	FSSQEAASSFGDDR	1.20302467	2	3.92838
P14882	GVTHNIPLLR	1.56484225	2	2.39832
P14882	HGNALWLNER	1.67167674	2	3.31556
P14882	HIEIQVLGDK	1.4077874	2	2.41751
P14882	HKQEDIPISGWAVECR	0.92311477	2	2.44155
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	1.02987345	3	6.74303
P14882	LQVEHPVTECITGLDLVQEMILVAK	1.77141274	3	3.8112
P14882	MADEAVCVGPAPTSK	1.04078057	2	4.25564
P14882	MEDALDSYVIR	1.17074632	2	3.50691
P14882	SYLNMDAIMEAIK	1.42987638	2	3.28723
P14882	SYLNMDAIMEAIKK	1.75526137	2	3.13295
P14882	TGAQAVHPGYGFLSENK	1.08153737	2	4.01556
P14882	TVAIHSDVDASSVHVK	1.4004809	3	4.04437
P14882	VVEEAPSIFLDPETR	0.9816666	2	3.99447
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**1.07427644**	**0.3297**	**3**
P14942	DGCLLFGQVPLVEIDGMLLTQTR	3.09151853	3	4.15424
P14942	KPPPDGHYVDVVR	1.33126939	2	3.27493
P14942	YFPVFEK	0.95328285	1	1.99856
P15083	**PIGR Polymeric immunoglobulin receptor**	**0.81616279**	**0.76212**	**4**
P15083	EIQNAGDQAQENR	0.67764449	2	4.02449
P15083	FSVLITGLR	0.89062343	2	2.79705
P15083	GSPHINPTDANAR	1.11879464	2	2.34721
P15083	GVTGGSVAIVCPYNPK	0.82038074	2	4.03122
P15149	**CP2A2 Cytochrome P450 2A2**	**1.13746266**	**8.3E-14**	**13**
P15149	DVQECILEEAGYLIK	6.20661973	3	3.94304
P15149	DVYSSITQLSER	2.97438116	2	3.11845
P15149	FKFPMNLEDINEYPSPIGFTR	1.32335015	3	3.74839
P15149	FSNLAPLGIPR	0.9995273	2	3.32725
P15149	GELPTFNILFK	0.37589282	2	2.69453
P15149	GTDVFPIIGSLMTEPK	0.66848246	2	4.13446
P15149	GYGFSLSNVEQAK	0.87099182	2	3.43163
P15149	IVVLYGYDAVK	2.47466151	2	2.60158
P15149	LEDFMIEK	1.30087128	1	1.9668
P15149	NFIDSFLIR	1.14063112	2	2.42815
P15149	QNHSTLDPNSPR	0.8275833	2	2.66313
P15149	TLQGTCGAPIDPSIYLSK	0.44919507	2	4.60939
P15149	TVSNVINSIVFGNR	0.82212701	2	3.2365
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.77324103**	**0.28636**	**3**
P15178	ALHHGIDLEK	1.34616071	3	3.30517
P15178	LEYCEALAMLR	1.8755418	2	2.95031
P15178	QMVKFAANINK+Oxidation(1	1.35977273		
P15429	**ENOB Beta_enolase**	**1.33219264**	**0.64361**	**6**
P15429	DATNVGDEGGFAPNILENNEALELLK	2.41827571	2	5.12995
P15429	FMIELDGTENK	1.46828488	2	3.28281
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	2.00787276	3	5.6371
P15429	IEEALGDK	7.860393	1	2.41668

P15429	TAIQAAGYPDK	5.48223902	2	2.97379
P15429	VNQIGSVTESIQACK	1.16956192	2	4.95931
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.33854241**	**3.3E-07**	**20**
P15650	AFVDSCLQLHETK	1.12891318	2	4.01376
P15650	AQDTAELFFEDVR	1.52087221	2	4.80286
P15650	AQDTAELFFEDVRLPASALLGEENK	1.4439126	3	5.32631
P15650	CIGAIAMTEPGAGSDLQGVR	1.45615426	2	6.35955
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6	1.5002189		
P15650	EQIEQFIPQMTAGK	1.28857339	2	4.98789
P15650	FFQEEVIPYHEEWEK	2.40046642	2	5.21064
P15650	GFYYLMQELPQER	1.57917443	2	4.14586
P15650	IFSSEHDIFR	1.17676034	2	3.04391
P15650	KFFQEEVIPYHEEWEK	1.50718892	2	5.14368
P15650	LDSASASMAK	1.16754902	2	2.50517
P15650	LDSASASMAK+Oxidation(7	1.4192073		
P15650	QGLLGINIAEK	1.178149	2	3.28884
P15650	RLDSASASMAK	1.25098956	2	3.38134
P15650	RLDSASASMAK+Oxidation(8	0.85448225		
P15650	SGSDWILNGSK	1.25500675	2	2.69857
P15650	TNICVTR	1.13336669	2	2.35139
P15650	TVAHIQTVQHK	1.07769884	2	2.91804
P15650	VQPIYGGTNEIMK	1.02228426	2	3.20376
P15650	VQPIYGGTNEIMK+Oxidation(11	1.33479565		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.35077364**	**0.00232**	**9**
P15651	ASSTANLIFEDCR	0.85948298	2	3.35461
P15651	EEGDSWVLNGTK	1.03256011	2	2.76697
P15651	ELVPIAAQLDK	1.05266778	2	2.9567
P15651	ELVPIAAQLDKEHLFPTSQVK	0.68143315	2	4.48841
P15651	GISAFLVPMPTPGLTLGK	1.66876115	2	3.62999
P15651	IGCFALSEPGNGSDAGAASTTAR	1.33305521	2	6.30175
P15651	IGIASQALGIAQASLDCAVK	2.40719254	3	4.96987
P15651	ITEIYEGTSEIQR	1.05531612	2	4.42685
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.28598212	4	4.96333
P15684	**AMPN Aminopeptidase N**	**0.92493463**	**0.28965**	**5**
P15684	ALGDTPAPNIDTTELVER	1.97816796	2	4.32479
P15684	AQIIHDSFNLASAGK	0.8812491	2	3.7072
P15684	LRSALACSNEVWILNR	1.98099357	2	2.30839
P15684	VVATTQMQAADAR	1.41919163	2	3.71342
P15684	YVEAVSPNR	0.88034886	2	2.46438
P15709	**ST2A1 Bile salt sulfotransferase**	**0.97447813**	**0.79534**	**2**
P15709	GNVLYGSWFEHIR	0.87405254	2	2.60428
P15709	NHFTVSQAEAFDK	1.61599123	1	3.75484
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**3.62571476**	**0.00588**	**3**
P15978	GYEQHAYDGR	3.56373303	2	2.4385
P15978	VEHEGLPEPLSQR	0.51220833	2	3.09697
P15978	YDSDAENPR	4.77518774	2	2.83425
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.61379854**	**6.3E-10**	**26**
P15999	AVDSLVPIGR	1.04760985	2	3.57164
P15999	EIVTNFLAGFEP	2.62537797	2	2.43216
P15999	EVAAFAQFGSDLDAATQQLLSR	1.6150195	2	6.61768
P15999	FESAFLSHVVSQHQSLLGNIR	1.61209435	2	6.0138
P15999	GIRPAINVGLSVSR	1.03191654	3	3.93396
P15999	GMSLNLEPDNVGVVVFGNDK	1.27202467	2	5.63109

P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1	1.40805459		
P15999	GYLDKLEPSK	0.99177235	1	2.82773
P15999	HALIIYDDLSK	1.48136407	2	2.7812
P15999	ILGADTSVDLEETGR	2.85481344	2	4.89381
P15999	LELAQYR	1.29791469	2	2.48399
P15999	LKEIVTNFLAGFEP	2.32857694	2	3.03922
P15999	LTDADAMK	1.08785883	2	2.66313
P15999	NVQAEEMVEFSSGLK	1.45109804	2	4.34027
P15999	QGQYSPMAIEEQVAVIYAGVR	1.27811516	3	5.25586
P15999	RLTDADAMK	1.23318994	2	2.92997
P15999	RSTVAQLVK	0.10721651	2	2.43216
P15999	RTGAIVDVPVGDELLGR	1.29166332	2	3.09896
P15999	STVAQLVK	1.42686987	2	2.52357
P15999	TGAIVDVPVGDELLGR	1.17341431	2	4.82722
P15999	TGTAEMSSILEER	1.01041763	2	4.37411
P15999	TGTAEMSSILEER+Oxidation(5	1.18303878		
P15999	TSIAIDTIINQK	1.20642172	2	4.61757
P15999	VLSIGDGIAR	1.02774435	2	2.91216
P15999	VVDALGNAIDGK	1.04610845	2	4.42404
P15999	VVDALGNAIDGKGPVGSK	1.038293	2	3.72534
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.34316128**	**0.01129**	**9**
P16036	ALYSNILGEENTYLWR	1.06925964	2	3.14802
P16036	EEGLNAFYK	1.06959222	1	2.61662
P16036	EKGSTASQVLQR	1.32910439	2	3.08548
P16036	FGFYEVFK	1.95023879	2	2.32737
P16036	GIFNGFSITLK	1.62227962	2	3.04245
P16036	GSTASQVLQR	1.18832148	2	3.07759
P16036	GWAPTLIGYSMQGLCK	1.14748209	2	2.79063
P16036	IQTQPGYANTLR	1.28960049	2	3.7901
P16036	MYKEEGLNAFYK	0.8579122	3	3.67296
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.20015318**	**0.49063**	**36**
P16086	ALINADELANDVAGAEALLDR	1.31672723	2	5.44427
P16086	ALSSEGKPYVTK	1.21289462	2	3.45721
P16086	DLASVQALLR	1.5688615	2	2.36186
P16086	DLSSVQTLLTK	1.3045603	2	3.14961
P16086	GNAMVEEGHFAAEDVK	1.29048848	2	4.10589
P16086	GVIDMGNSLIER	1.27206157	2	3.07557
P16086	HQAFEAELHANADR	1.62079522	2	2.91677
P16086	HQAFEAELSANQSR	0.63716028	2	4.25052
P16086	HQALQAEIAGHEPR	1.2085522	3	4.75946
P16086	HQEHKGEIDAHEDSFK	0.88196951	3	4.37673
P16086	HQLLEADISAHEDR	1.32254884	3	3.67163
P16086	KFEEFQTDLAAHEER	1.42256501	3	4.31921
P16086	LGDSHDLQR	1.28441307	2	3.20129
P16086	LGESQTLQQFSR	0.41479574	2	3.10756
P16086	LIQEQHPEEELIK	0.99737844	2	4.08782
P16086	LQQSHPLSANQIQVK	1.42735293	2	4.40617
P16086	LQTASDESYKDPTNIQSK	1.13995467	2	5.09226
P16086	LQVASDENYKDPTNLQGK	1.1104699	2	5.1868
P16086	LSDDNTIGQEEIQQR	1.66263597	2	4.07653
P16086	MQHNLEQQIQAR	2.21068887	2	3.36507
P16086	MQHNLEQQIQAR+Oxidation(0	0.90548589		
P16086	MTLVASEDYGDTLAAIQGLLK	1.12507056	2	3.79658
P16086	NQALNTDNYGHDLASVQALQR	1.21205123	2	6.16928
P16086	QFQDAGHFDAENIKK	1.16268815	2	2.84578
P16086	REELITNWEQIR	1.34130978	2	4.38016
P16086	SADESGQALLAAGHYASDEVR	1.46959136	2	4.57911

P16086	SLQQLAEER	1.09179883	2	2.86877
P16086	SQLLGSAHEVQR	0.5056016	2	3.29539
P16086	SSEEIESAFR	1.27797945	2	2.59749
P16086	SSLSSAQADFNQLAELDR	1.22619861	2	4.74207
P16086	TATDEAYKDPSNLQGK	1.21983143	2	4.35716
P16086	TKQEEVNAAWQR	1.61122171	2	3.4483
P16086	VLETAEDIQER	0.97823262	2	3.77127
P16086	VNDVCTNGQDLIK	1.0181453	2	3.16657
P16086	VNEVNQFAAK	1.27250616	2	2.56828
P16086	VNSLGETAQR	1.39548343	2	3.17674
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**0.95047777**	**0.91569**	**9**
P16232	EECALEIIK	1.10329688	1	2.06642
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8	1.86839258		
P16232	ETSGIILSQAAPK	0.9492329	2	3.13336
P16232	FALDGFFSTIR	1.34755268	2	2.99853
P16232	FVVEAGK	0.83618817	1	1.92354
P16232	KDEVYYDK	0.76698948	2	2.32476
P16232	MGAHVVLTAR	2.30586553	1	1.94936
P16232	MTQPLIASYSASK	1.05570746	2	3.41385
P16232	SSWTPLLLGNPGR	0.91731618	2	3.74862
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.61520683**	**0.07349**	**9**
P16290	ALPFWNEEIAPK	2.44960132	2	2.85574
P16290	AMEAVAAQGK	1.36508277	2	2.58411
P16290	AMEAVAAQGK+Oxidation(1	1.40441394		
P16290	HGESSWNQENR	5.38917733	2	3.95107
P16290	HNYYASISK	3.6479921	2	2.52029
P16290	HYGGLTGLNK	1.16167509	1	3.19366
P16290	SFDTPPPPMDEK	2.6131033	2	2.60675
P16290	TLWTILDVTDQMWVPVVR+Oxidation(11	3.17624168		
P16290	VLIAAHGNSLR	1.27329028	2	2.94739
P16303	**CES3 Carboxylesterase 3**	**0.84296707**	**0.5829**	**16**
P16303	AKEAAEEPSHWK	0.79276914	2	4.06837
P16303	DGASEEETNLSK	0.74256827	2	4.18626
P16303	EAAEEPSHWK	0.94405958	2	2.86087
P16303	ESYPFLPTVIDGVVLPK	0.83309169	2	4.15355
P16303	FAPPQPAEPWNFVK	0.38794457	1	2.33905
P16303	IGASTQAAQR	1.03279282	2	2.80827
P16303	LDLLGNPK	0.76433099	2	2.56699
P16303	MIPVVAEK	0.91082731	1	1.98532
P16303	QEFGWIIPTLMGYPLSEGK	1.36516105	2	2.57027
P16303	QKTEDELLETSLK	0.85241694	2	3.51366
P16303	SFNTVPYIVGINK	0.71113281	2	3.32145
P16303	TEDELLETSLK	0.72121481	2	3.86506
P16303	TPEEILAEK	1.35232399	2	2.64664
P16303	TTTSAVMVHCLR	0.53291268	2	3.07174
P16303	TVIGDHGDELFSVFGSPFLK	1.01173712	2	5.47958
P16303	YFGGTDDPAK	2.31366556	2	2.87755
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.45856422**	**0.81957**	**4**
P16332	GDVGMAGVAIDTVEDTK	1.47723948	2	4.29565
P16332	IDSGSEVIVGVNK	1.66008328	2	3.77944
P16332	NTQIIIQEESGIPK	1.15753381	2	3.59562
P16332	TGLQAGLTIDEFAPR	1.51418455	2	3.40072
P16409	**MYL3 Myosin light chain 3**	**1.36724393**	**0.91564**	**8**
P16409	AAPAPAAAPAAAPEPERPK	7.40801116	2	4.46803
P16409	ALGQNPTQAEVLR	2.38852226	2	3.74313

P16409	EGNGTVMGAELR	1.36903991	2	2.73079
P16409	IEFTPEQIEEFK	1.44994404	2	3.01994
P16409	LTEDEVEK	3.03769988	1	2.14643
P16409	MMDFETFLPMLQHISK	3.34323239	3	3.83165
P16409	NKDTGTYEDFVEGLR	1.64940295	2	3.451
P16409	VFDKEGNGTVMGAELR	1.10343595	2	4.11548
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.14623371**	**1.1E-12**	**18**
P16617	AHSSMVGVNLPQK	1.223716	3	4.06088
P16617	AHSSMVGVNLPQK+Oxidation(4	1.43301874		
P16617	ALESPERPFLAILGGAK	0.78562486	3	4.75942
P16617	DCVGSEVENACANPAAGTVILLENLR	1.46833147	3	6.49956
P16617	FCLDNGAK	1.17571437	1	1.96106
P16617	GCITIIGGGDTATCCAK	1.14156389	2	5.55183
P16617	IQLINNMLDK	1.47940123	2	3.03563
P16617	IQLINNMLDK+Oxidation(6	2.45361678		
P16617	ITLPVDFVTADK	1.69604244	2	2.74657
P16617	ITLPVDFVTADKFDENAK	1.85918697	2	4.78655
P16617	SVVLMSHLGRPDGVPMPDK	1.11453676	3	3.74741
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.41674311	4	4.76504
P16617	TGQATVASGIPAGWMGLDCGTESSK	1.1389777	2	5.03905
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.08002031	3	4.07681
P16617	VLNNMEIGTSLYDEEGAK	1.88459465	2	5.24542
P16617	VLPGVDALSNV	1.79031077	2	3.28639
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.16469201	3	4.835
P16617	YSLEPVAAELK	1.13204798	2	3.49632
P16638	**ACLY ATP_citrate synthase**	**1.4001899**	**9.9E-20**	**25**
P16638	AFDSGIIPMEFVNK	1.71157892	2	3.65403
P16638	AKPAMPQDSVPSPR	1.96156367	2	2.7421
P16638	DEPSVAAMVYPFTGDHK	1.09283064	2	2.95481
P16638	DLVSSLTSGLLTIGDR	1.35952153	2	3.70077
P16638	EAYPEEAYIADLDAK	1.12938259	2	3.62656
P16638	FGGALDAAAK	1.3988828	2	3.02035
P16638	GAIVPAQEVPPPTVPMDYSWAR	2.95212192	2	4.09636
P16638	GGPNYQEGLR	2.07923919	2	2.95829
P16638	GVTIIGPATVGGIKPGCFK	1.81184398	2	3.70465
P16638	HLLVHAPEDK	1.00560094	2	2.68079
P16638	HLLVHAPEDKK	1.71663389	2	3.46117
P16638	IGNTGGMLDNILASK	1.85364991	2	4.10394
P16638	LGLVGVNLSLDGVK	3.29024001	2	2.49956
P16638	LNAEDIK	1.4216168	1	1.94409
P16638	QHFPATPLLDYALEVEK	1.41434042	3	3.84036
P16638	RGGPNYQEGLR	2.08952384	2	3.3
P16638	SAYDSTMETMNYAQIR	1.95460643	2	2.93082
P16638	SGGMSNELNNIISR	1.16903139	2	3.65613
P16638	SMGFIGHYLDQK	1.16619211	2	2.91414
P16638	TIAIIAEGIPEALTR	1.63740553	2	4.98087
P16638	TTDGVYEGVAIGGDR	1.12576107	2	3.3363
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	2.0406894	3	3.45261
P16638	VDATADYICK	1.47413991	2	2.63092
P16638	WGDIEFPPPFGR	1.34249509	2	3.90479
P16638	YICTTSAIQNR	1.66145949	2	3.1424
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**1.03549269**	**2.1E-09**	**10**
P16970	DQVIYPDGKEDQK	1.52706178	2	2.82678
P16970	EGGWDSVQDWMDVLSGGEK	1.61233976	2	2.89161
P16970	FDHVPLATPNGDILIQDLSFEVR	1.18242313	3	4.14856
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.61260024	3	5.36746

P16970	GISDQVLK	1.46672017	1	1.94651
P16970	GYLDNVQLGHILER	0.92138733	2	3.56445
P16970	HLHSTHSELLEDYYQSGR	1.1174051	3	5.85202
P16970	ITELMQVLK	1.92766848	2	2.83461
P16970	KGISDQVLK	0.691498	2	2.51888
P16970	SGANVLICGPNGCGK	0.95654691	2	3.2054
P17074	**RS19 40S ribosomal protein S19**	**1.69028805**	**0.02579**	**5**
P17074	ELAPYDENWFYTR	1.43658813	2	2.95906
P17074	HKELAPYDENWFYTR	1.51356364	3	4.61017
P17074	LKVPEWVDTVK	1.9521256	3	3.3472
P17074	RVLQALEGLK	2.51184958	3	3.81539
P17074	VLQALEGLK	1.6246614	2	2.70721
P17077	**RL9 60S ribosomal protein L9**	**1.52276902**	**0.02321**	**8**
P17077	DFNHINVELSLLGK	2.15419458	2	3.0464
P17077	FLDGIYVSEK	1.28371813	2	3.12915
P17077	GTVQQPDE	27.0341601	1	2.03732
P17077	KFLDGIYVSEK	1.2123886	2	2.94164
P17077	SVYAHFPINVVIQENGSLVEIR	1.52302704	3	3.82579
P17077	TGVACSVSQAQK	1.21919761	2	3.50443
P17077	TICSHVQNMIK	1.5621145	2	3.17312
P17077	TILSNQTVDIPENVDITLK	1.22996507	2	4.8665
P17078	**RL35 60S ribosomal protein L35**	**1.28774928**	**0.0066**	**2**
P17078	QLDDLKVELSQLR	1.32352604	2	2.97702
P17078	VLTVINQTQK	1.2810953	2	2.92333
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.65330373**	**9.8E-05**	**5**
P17178	DHESTEGPGTGQDRPR	2.62486908	2	3.35757
P17178	SLAELPGPGTLR	1.82173604	2	2.61094
P17178	TNVNLASAPLLEQVMR	1.60459063	2	3.65578
P17178	VGCLEPSIPEDTATFIR	1.71301913	2	3.21551
P17178	YEVVLSPGMGEVK	1.51441424	2	3.42202
P17209	**MYL4 Myosin light chain 4**	**1.24216386**	**0.8585**	**2**
P17209	HVLATLGEK	2.67019326	1	2.64427
P17209	ITYGQCGDVLR	1.14687765	2	2.3725
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.62084515**	**0.9378**	**10**
P17425	ASAELFNQK	0.78337388	2	3.51042
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK	0.71395015	3	5.27687
P17425	ITASLCDLK	0.74483446	2	2.53664
P17425	LEDTYFDRDVEK	0.67667068	2	2.96751
P17425	MFLNDFLNDQNR	1.33846192	2	3.48395
P17425	NSIYSGLEAFGDVK	0.70928542	2	3.22585
P17425	NSLSYDCIGR	0.4155699	1	2.08573
P17425	TCVAPDVFAENMK	0.80418686	2	3.25146
P17425	VTQDATPGSALDK	0.58720437	2	3.6139
P17425	YTIGLGQAR	0.59150125	2	2.76626
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.33342204**	**0.10148**	**3**
P17426	FFQPTEMAAQDFFQR+Oxidation(6	1.31866086		
P17426	NADVELQQR	1.3300405	2	2.64205
P17426	VGGYILGEFGNLIAGDPR	1.39650851	2	3.94523
P17475	**A1AT Alpha_1_antiproteinase**	**2.23837624**	**9.9E-20**	**9**
P17475	AFHHLLQTLNRPDSELQLNTGNGLFVNK	0.6992794	3	4.54079
P17475	GTEAAGATVVEAVPMSLPPQVK	1.30114064	2	2.61991
P17475	MQHLEQTLTK	3.79801976	1	3.1274
P17475	MQHLEQTLTK+Oxidation(0	3.70143819		
P17475	NNYHSEAFSVNFADSEEAKK	3.48104402	3	5.07493
P17475	SAILYFPK	4.03507985	2	2.39516
P17475	TLLSSLGITR	3.80511091	2	2.98003

P17475	VFNNDADLSGITEDAPLK	2.23713342	2	5.83886
P17475	VINDYVEK	2.13346285	2	2.65176
P17702	**RL28 60S ribosomal protein L28**	**1.80160906**	**0.00013**	**2**
P17702	NCSSFLIK	1.80145649	2	2.42029
P17702	QTYSTEPNNLK	1.8016092	2	2.77923
P17712	**HXK4 Glucokinase**	**1.36816423**	**0.37913**	**2**
P17712	ASGAEGNNIVGLLR	1.11171197	2	2.30268
P17712	STPEGSEVGDFLSLDLGGTNFR	1.47491442	2	3.17647
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.25733859**	**6.3E-10**	**15**
P17764	EEQDKYAIGSYTR	1.20845349	2	3.48772
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.57891674	3	3.96508
P17764	EVYMGNVIQGGEGQAPTR	0.7187909	2	5.06654
P17764	FANEITPITISVK	1.51291937	2	4.12178
P17764	GKPDVVVKEDEEYK	1.25423024	2	3.72773
P17764	GKPDVVVKEDEEYKR	1.19011468	2	5.17298
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.78714812	2	4.96492
P17764	IHMGNCAENTAK	1.35632175	3	3.55753
P17764	IHMGNCAENTAK+Oxidation(2	1.31554405		
P17764	LEDLIVK	1.07179766	2	2.40383
P17764	LGTIAIQGAIEK	1.53095951	2	3.37283
P17764	QATLGAGLPIATPCTTVNK	1.12670286	2	4.63856
P17764	QGEFGLASICNGGGGASAVLIEK	1.06881094	2	5.11913
P17764	TPIGSFLGSLASQPATK	1.90126049	2	4.31948
P17764	VNVHGGAVSLGHPIGMSGAR	1.2809528	2	5.8808
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.152522**	**0.99999**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.19567885	3	5.54856
P17879	TTPSYVAFTDTER	1.08358372	2	3.62278
P17879	VEIIANDQGNR	6.36247401	2	3.76421
P17988	**ST1A1 Sulfotransferase 1A1**	**1.40207523**	**9.9E-20**	**4**
P17988	CPGVPSGLETLEETPAPR	2.11410062	2	4.23585
P17988	NTFTVAQNER	1.3866602	2	3.56406
P17988	SLPEETVDSIVHHTSFK	1.97841862	2	4.40445
P17988	THLPLSLLPQSLLDQK	2.62071755	2	4.71143
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.11840919**	**0.87499**	**29**
P18163	AELSVIFADKPEK	1.12958642	2	3.35532
P18163	ALEDLGR	0.85240856	2	2.33962
P18163	ALKPPCDLSMQSVEVTGTTEGVR	1.1717458	2	4.30022
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9	1.33984833		
P18163	CGVEIIGLK	1.05352826	2	2.87604
P18163	DGWLHTGDIGK	1.01482649	2	2.7965
P18163	GAMVTHQNIMNDCSGFIK	1.11024008	2	5.14771
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2	1.14195083		
P18163	GFQGSFEELCR	1.09394498	2	3.64198
P18163	GIAVHPELFSIDNGLLTPTLK	1.54620146	2	5.30351
P18163	GIQVSNDGPCLGSR	1.39233088	2	4.54336
P18163	IENIYLR	1.00669289	2	2.80915
P18163	IFGQANTSVK	1.09469081	2	2.8254
P18163	IIVIMDSYDNDLVER	1.70366828	2	5.06847
P18163	LLLEGVENK	1.11369048	2	3.34425
P18163	LLMDDLK	1.11008078	2	2.50697
P18163	LMITGAAPVSATVLTFLR	1.96080273	3	4.11402
P18163	LVDVEDMNYQAAK	0.91156588	2	4.64933
P18163	NAGLKPFEQVK	1.09031606	2	3.77725
P18163	NNSLWDK	1.03456053	2	2.49225
P18163	QVAEMAECIGSALIQK	1.16128838	2	5.53411
P18163	SAVLEDDKLLLYYYDDVR	2.08303769	3	3.61841

P18163	SQIDELYSTIK	0.86613699	2	3.61558
P18163	SQIDELYSTIKI	1.20475216	2	3.94699
P18163	TAEALDKDGWLHTGDIGK	1.08476503	2	5.25147
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	1.93845679	3	5.15537
P18163	TMYDGFQR	2.88212178	1	1.94556
P18163	VLQPTIFPVVPR	0.9632288	2	3.59794
P18163	WLLDFASK	1.25268146	2	2.56555
P18297	**SPRE Sepiapterin reductase**	**1.24591869**	**0.22952**	**5**
P18297	LGCAVCVLTGASR	1.32937218	2	3.03202
P18297	LLLINNAGTLGDVSK	1.22636136	2	3.89844
P18297	LNSEGELVDCGTSAQK	1.26109765	2	4.89868
P18297	TVVNISSLCALQPFK	1.39381398	2	3.27479
P18297	VLSYAPGPLDTNMQQLAR	0.84429127	2	3.44383
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.56737192**	**0.6812**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.56751572	2	5.49793
P18298	KIIVDTYGGWGAHGGGAFSGK	1.41876675	3	4.14974
P18298	YLDEDTIYHLQPSGR	1.42403922	2	4.7805
P18418	**CALR Calreticulin**	**1.04061654**	**0.98565**	**20**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	0.83811585	3	5.83845
P18418	CKDDEFTHLYTLIVRPDNTYEVK	0.93162806	3	4.92148
P18418	DMHGDSEYNIMFGPDICGPGTK	1.1471341	2	6.22996
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1	1.1897302		
P18418	EQFLDGDAWTNR	2.327718	2	3.17007
P18418	FYALSAR	1.75677669	2	2.38506
P18418	FYGDQEK	1.07639813	1	2.11905
P18418	FYGDQEKDK	1.14036779	1	2.92285
P18418	GQTLVVQFTVK	0.95882515	2	2.93733
P18418	HEQNIDCGGGYVK	1.15952384	2	4.4037
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	0.73392947	3	4.30204
P18418	IDNSQVESGSLEDDWDFLPPK	1.18926741	2	5.36384
P18418	IDNSQVESGSLEDDWDFLPPKK	3.10846952	3	4.88656
P18418	IKDPDAAKPEDWDER	1.43564656	2	4.368
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	1.89970993	3	5.51373
P18418	KVHVIFNYK	1.23580661	2	2.33979
P18418	LFPGGLDQK	1.18685609	2	2.37105
P18418	QIDNPDYK	1.13161499	1	2.09044
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.27876007	3	4.7888
P18418	VHVIFNYK	1.04903955	1	2.55527
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.35777744**	**0.05011**	**3**
P18420	AQPSQAADEPAEK	1.33447176	2	3.8529
P18420	IHQIEYAMEAVK	2.24545185	2	2.82726
P18420	NQYDNDVTVWSPQGR	1.67914369	2	2.99556
P18421	**PSB1 Proteasome subunit beta type_1**	**1.05162609**	**0.76301**	**4**
P18421	AGGSASAMLQPLLDNQVGFK	1.05076333	2	4.99356
P18421	AGGSASAMLQPLLDNQVGFK+Oxidation(7	3.77548412		
P18421	GAVYSFDPVGSYQR	1.30029845	2	3.00408
P18421	NMQNVEHVPLTLDR	1.19730383	2	3.64801
P18422	**PSA3 Proteasome subunit alpha type_3**	**1.45245419**	**1E-05**	**2**
P18422	AVENSSTAIGIR	1.45237416	2	3.23243
P18422	TEIEKLQMKEMTCR+Oxidation(10	3.04639481		
P18445	**RL27A 60S ribosomal protein L27a**	**1.18124605**	**0.49748**	**4**
P18445	LWTLVSEQTR	1.41605423	1	1.91416
P18445	NGVAPIIDVVR	1.54057342	1	2.15358
P18445	NQSFCPTVNLDK	1.18132012	2	3.29904
P18445	RNQSFCPTVNLDK	0.94132666	2	2.94568
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**1.49835399**	**0.03935**	**6**

P18484	FFQPTEMASQDFFQR	1.31808214	2	4.02479
P18484	FVNLFPEVK	1.52446275	2	2.83444
P18484	ILVAGDTMDSVK	1.26821469	2	2.74705
P18484	LTECLETILNK	1.39771696	2	2.42357
P18484	NNGVLFENQLLQIGLK	1.96863255	2	3.37997
P18484	THIETVINALK	0.70401023	2	2.8117
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**2.42175206**	**0.00837**	**4**
P18596	DIVPGDIVEVAVGDKVPADLR	4.36104506	2	3.38495
P18596	SLPSVETLGCTSVICSDK	2.53889845	2	4.61028
P18596	TGTLTTNQMSVCR	1.27530955	2	3.22655
P18596	VGEATETALTCLVEK	1.51403788	2	4.62514
P18757	**CGL Cystathionine gamma_lyase**	**1.00857089**	**1.8E-15**	**15**
P18757	AGDEVICMDEVYGGTNR	0.85899169	2	5.60928
P18757	ATLGISDTLIR	1.19071936	2	3.74076
P18757	AVVLPISLATTFK	0.84753833	3	4.28377
P18757	DLLEDLGQALK	1.25962339	2	3.35707
P18757	FLQNSLGAVPSPFDCYLCCR	2.71463655	2	3.91112
P18757	GTLQHAQVFLK	1.49148045	2	3.35526
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	2.36907248	3	4.42194
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	2.84398203	4	5.6156
P18757	LLEAAITPQTK	1.12237043	2	4.01647
P18757	LSVGLEDEKDLLEDLGQALK	1.42243126	3	6.35427
P18757	LVWIETPTNPTLK	1.19985609	2	3.88094
P18757	QCTGCPGMVSFYIK	1.93794036	2	3.72762
P18757	QDSPGQSSGFVYSR	1.21202439	2	3.85368
P18757	RVASEFGLK	1.53677859	2	2.49904
P18757	VIYPGLPSHPQHELAK	1.15868025	2	4.2341
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.32532217**	**0.00552**	**12**
P18886	ATNLTVSAVR	1.42361259	2	3.49467
P18886	ELHAHLLAQDK	1.80832997	2	3.65249
P18886	HSVGELQHMMAECSK	0.53566141	2	3.89476
P18886	LIFDGNEETLK	0.85102105	2	3.08487
P18886	QKLIFDGNEETLKK	1.3544115	2	2.33468
P18886	QYGQTVATYESCSTAAFK	1.48177622	2	3.69833
P18886	SEYNDQLTR	1.59933181	2	3.07104
P18886	TETIRPASIFTK	1.10425239	2	2.60541
P18886	TLQAGLLEPEVFHLNPSK	0.77980513	2	3.44897
P18886	TLSIDSIQFQR	1.60582794	2	3.0746
P18886	YILSDSSPVPEFPVAYLTSENR	1.38264347	2	5.31136
P18886	YLNAQKPLLDDSQFR	1.17697689	2	4.65914
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.07553185**	**6.3E-13**	**19**
P19112	AGGLATTGNEDILDIVPTEIHQK	1.12478048	3	6.45402
P19112	AGGTGEMTQLLNSLCTAIK	1.23778339	3	5.55676
P19112	APVIMGSTEDVQEFLEIYNK	2.27790222	2	4.97642
P19112	APVIMGSTEDVQEFLEIYNKDK	1.82954425	3	3.55884
P19112	DFDPAINEYIQR	1.87293812	2	4.02159
P19112	ESPVHSICDELF	3.09296577	2	2.35021
P19112	FPPDNSAPYGAR	1.07400591	2	2.77043
P19112	GNIYSINEGYAK	1.16356753	2	3.99729
P19112	KGNIYSINEGYAK	1.36870702	2	4.48673
P19112	KLDILSNDLVINMLK	1.49421982	2	4.76317
P19112	KTSANEPSEKDALQPGR	1.3483959	3	4.17629
P19112	LDILSNDLVINMLK	1.50246212	2	5.10375
P19112	LLYECNPIAYVMEK	1.60879835	2	4.45432
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.33293333	3	5.78643

P19112	SRPSLPLPQSR	1.06807877	2	3.35377
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.48567478	3	5.16979
P19112	TLVYGGIFLYPANK	1.04405236	2	3.8419
P19112	TLVYGGIFLYPANKK	0.89533109	2	2.9054
P19112	TSANEPSEKDALQPGR	1.19352801	2	4.4773
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**1.32051711**	**0.26217**	**3**
P19123	AAVEQLTEEQKNEFK	3.18974855	2	2.55913
P19123	GKSEEELSDLFR	1.24653514	2	2.58643
P19123	SEEELSDLFR	4.16235838	2	2.8364
P19132	**FRIH Ferritin heavy chain**	**1.27098643**	**0.19885**	**2**
P19132	QNYHQDSEAAINR	2.082081	2	2.88734
P19132	YFLHQSHEER	1.26874698	2	2.55777
P19225	**CP270 Cytochrome P450 2C70**	**1.19774471**	**0.41098**	**15**
P19225	ACIGEGLAR	1.50087202	2	2.64995
P19225	ASLNLSNPQDFIDYFLIK	1.75504717	2	3.1344
P19225	EALIDRGEEFSDK	1.67622191	2	3.25692
P19225	FDPGHFLDEK	1.18745649	2	2.46362
P19225	FILMEINR	1.78778429	2	2.63737
P19225	GTSVMACLTSALHDDKEFPNPEK	1.33315057	3	3.57707
P19225	IQEEITR	1.18074215	2	2.31765
P19225	IQEEVVYLLEALR	2.14106838	2	3.9269
P19225	KLPPGPTPLPIFGNILQVGVK	1.11174046	3	4.03319
P19225	KTTQDVEFR	1.34555647	2	2.30194
P19225	LPPGPTPLPIFGNILQVGVK	1.54820286	2	4.41558
P19225	NHMPYTDAVLHEIQR	1.37986262	3	3.82308
P19225	SDYFMAFSAGRR+Oxidation(4	0.96993716		
P19225	TTQDVEFR	1.21023987	2	2.43859
P19225	YIDFVPIPLPR	1.18798046	2	3.12531
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.04423841**	**0.58546**	**3**
P19234	DIEEIIDELR	7.62167138	2	3.61188
P19234	DTPENNPDTPFDFTPENYER	1.0296615	2	4.62126
P19234	FCCEPAGGLTSLTEPPK	1.41761586	2	3.13799
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.19615107**	**0.94736**	**9**
P19468	ASGELMTVAR	1.15624578	2	2.94006
P19468	CNQIANELCECPELLGSGFR	0.93512617	2	5.33809
P19468	IHLDDANESDHFENIQSTNWQTMR	0.92976054	3	5.0486
P19468	NTPSPFVETFPEDEEASK	1.14778722	2	4.59331
P19468	SLFFPDEAINK	1.12762561	2	2.60786
P19468	SRYDSIDSYLSK	0.77544357	2	2.70342
P19468	VQLLLNGGDVLETLQEK	1.30405448	2	4.6747
P19468	VVINVPIFK	2.15351303	2	2.69334
P19468	WGVISASVDDR	1.71027656	2	3.13825
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.07884104**	**0.97709**	**9**
P19488	AEMWLIR	1.21987578	2	2.89249
P19488	ANAIAWALAQIPQK	1.46465651	3	6.45927
P19488	FETFPTSVSK	0.98770353	1	1.90668
P19488	FETFPTSVSKDELEK	0.77201066	2	4.31848
P19488	GAAVTLNIR	1.27416106	2	2.56193
P19488	GHEVTVLKPSAYYVLDPK	0.82109199	2	4.53022
P19488	NWDPFYTEILGRPTTLAETMGK	1.55986779	2	4.86697
P19488	SDLFNALK	1.00537752	2	2.55647
P19488	TILDELVQR	0.95792879	2	3.39544
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**1.12413048**	**0.00502**	**10**
P19511	EGEHMINWVEK	1.38532157	2	2.32933

P19511	HVIQSISAQQEK	1.18297815	2	3.97659
P19511	HVIQSISAQQEKETIAK	1.28150356	3	4.75691
P19511	HYLFDVQR	1.10201537	2	2.68848
P19511	KEGEHMINWVEK	1.10266213	2	2.30447
P19511	LDYHISVQDMMR	1.52328503	3	4.55136
P19511	LNEEKIAQLEEIK	0.99359317	2	2.53071
P19511	NNIALALEVTYR	2.28991389	2	2.62271
P19511	YGASIGEFIDK	1.30776759	2	2.8361
P19511	YGASIGEFIDKLNEEK	3.93454496	2	3.47583
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.07565664**	**0.04821**	**13**
P19643	FIGGSGQVSER	1.40947376	2	3.31743
P19643	IISTTNGGQER	0.69945152	2	2.73166
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.75862142	3	4.63586
P19643	KFIGGSGQVSER	0.71175084	2	3.04442
P19643	KLCELYAK	0.49931096	2	2.52401
P19643	LERPVIHIDQTGENVVVK	1.1572215	2	5.29637
P19643	LLHDCGLSVVVLEAR	2.39700483	2	3.56399
P19643	TLNHEIYEAK	1.40117268	2	3.05249
P19643	TMDEMGQEIPSDAPWK	1.3714586	2	4.41484
P19643	VKLERPVIHIDQTGENVVVK	0.93715006	3	4.44664
P19643	VLNSQEALQPVHYEEK	1.29669861	2	4.6807
P19643	YVDLGGSYVGPTQNR	0.98407153	2	5.30995
P19643	YVISAIPPVLGMK	1.78256978	2	3.2598
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.39822183**	**0.00311**	**9**
P19804	DRPFFPGLVK	1.24824602	2	2.51363
P19804	EIGLWFKPEELIDYK	1.37558383	2	3.83056
P19804	GDFCIQVGR	1.20121194	2	3.31658
P19804	NIIHGSDSVESAEK	1.25556098	3	4.01611
P19804	NIIHGSDSVESAEKEIGLWFKPEELIDYK	1.49961391	4	4.8357
P19804	TFIAIKPDGVQR	1.16362003	2	2.94786
P19804	VMLGETNPADSKPGTIR	1.79166898	2	4.49908
P19804	VMLGETNPADSKPGTIR+Oxidation(1	1.40359003		
P19804	YMNSGPVVAMVWEGLNVVK	1.55080206	2	5.32369
P19814	**TGON3 Trans_Golgi network integral membrane protein TGN38**	**2.57641883**	**0.00576**	**2**
P19814	DSGSPTGGDSDNTTGGDSNK	2.54364318	2	4.74314
P19814	TSGGDSNKPTGSDNDKPTGGDSNKPTSK	4.31797058	4	4.65954
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.33430343**	**9.3E-07**	**2**
P19944	AAGVNVEPFWPGLFAK	1.91755298	2	2.94979
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.32579741	4	6.26471
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.64735183**	**9.9E-20**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.46455872	2	6.14348
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.01510097	3	4.84083
P19945	CFIVGADNVGSK	1.20354156	2	3.4121
P19945	GHLENNPALEK	1.21950159	2	3.68968
P19945	GNVGFVFTK	1.14234002	2	2.77154
P19945	GTIEILSDVQLIK	1.58765414	2	3.62435
P19945	IIQLLDDYPK	2.15250919	2	3.74527
P19945	NVASVCLQIGYPTVASVPHSIINGYK	1.56798686	3	4.19996
P19945	TSFFQALGITTK	1.67753184	2	4.16189
P19945	VLALSVETDYTFPLAEK	1.86792634	2	3.38682
P20059	**HEMO Hemopexin**	**1.03576413**	**0.00791**	**5**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.76263202	2	5.17846
P20059	FNPVTGEVPPR	1.06718929	2	2.65569
P20059	LFQEEFPGIPYPPDAAVECHR	1.37868674	3	4.34402
P20059	SGAQATWAELSWPHEK	0.70008418	2	3.12737

P20059	VDGALCLEK	1.78973439	2	2.54823
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**0.98272147**	**0.99093**	**6**
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	1.38307233	3	5.06436
P20070	LIDKEIISHDTR	1.25555292	3	4.14048
P20070	MSQYLENMNIGDTIEFR	0.79205625	2	4.42285
P20070	SSPAITLENPDIK	0.98266665	2	3.99659
P20070	SSPAITLENPDIKYPLR	1.2508269	2	3.88838
P20070	SVGMIAGGTGITPMLQVIR	1.15506949	2	4.46415
P20280	**RL21 60S ribosomal protein L21**	**1.16332359**	**0.96565**	**4**
P20280	HGVVPLATYMR	1.1139113	2	2.56905
P20280	KGDIVDIK	1.27552506	1	2.25277
P20280	TNGKEPELLEPIPYEFMA	1.09972639	2	3.6158
P20280	VYNVTQHAVGIIVNK	0.97355539	2	4.42374
P20673	**ARLY Argininosuccinate lyase**	**1.31636027**	**9E-10**	**16**
P20673	AEAECEVLFPGYTHLQR	1.39813605	2	4.92073
P20673	AEMQQILQGLDK	1.25154901	2	4.53292
P20673	AVVVAEMK	1.57762889	1	1.94993
P20673	EFNFVQLSDAYSTGSSLMPQK	2.04037408	2	5.80344
P20673	FNSSIAYDR	1.16275534	2	2.54475
P20673	HLWNVDLQGSK	1.2311186	1	3.30696
P20673	INVLPLGSGAIAGNPLGVDR	2.09090441	2	5.48454
P20673	KNPDSLELIR	1.03293518	2	2.61251
P20673	LKELIGEAAGK	1.55499342	2	3.19458
P20673	LYPNDEDIHTANER	56.7066278	2	3.91401
P20673	MAEDLILYGTK	1.09491134	2	3.70237
P20673	MAEDLILYGTK+Oxidation(0	1.4899454		
P20673	NDQVVTDLR	1.10316188	2	3.21711
P20673	SRNDQVVTDLR	1.38793354	2	2.88317
P20673	VAEEWAQGIFK	1.80856749	2	3.5697
P20673	VLIEAMVDR	1.42568743	2	2.75694
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.06295993**	**0.91739**	**6**
P20788	EIDQEAAVEVSQLR	1.08162596	2	4.2458
P20788	EIDQEAAVEVSQLRDPQHDLER	0.73202917	3	3.37509
P20788	ESLSGQAATRPLVATVGLNVPASVR	1.46314251	2	2.50068
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.04516589	3	4.80667
P20788	LSDIPEGK	1.34587468	1	2.02734
P20788	SGPFAPVLSATSR	1.0921133	2	2.8626
P20801	**TNNC2 Troponin C_ skeletal muscle**	**2.40098794**	**0.61935**	**4**
P20801	GKSEEELAECFR	4.26899073	2	3.24512
P20801	NADGYIDAEELAEIFR	1.27934818	2	4.82179
P20801	SEEELAECFR	2.15245069	2	3.2848
P20801	SYLSEEMIAEFK	2.00362438	2	2.67499
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.67526878**	**0.00258**	**3**
P20814	FDYEDKDFLNLIEK	2.18296636	3	3.99428
P20814	GTAVLTSLTSVLHDSK	1.57295088	2	3.73484
P20814	IKEHEESLDVSNPR	1.673742	2	4.69764
P20817	**CP4AE Cytochrome P450 4A14**	**0.85309399**	**0.94251**	**6**
P20817	ACQIAHEHTDGVIK	0.82278294	2	4.26931
P20817	AQLQNEEELQK	0.78059873	2	3.20137
P20817	AVEDLNNLTFFR	0.81099599	2	3.3195
P20817	HLDFLDILLFAK	1.05637736	2	3.81993
P20817	MRKAQLQNEEELQK+Oxidation(0	0.80714504		
P20817	VLLYDPDYVK	0.77838102	2	2.71002
P20852	**CP2A5 Cytochrome P450 2A5**	**1.05580328**	**0.76844**	**3**
P20852	DFIDSFLIR	1.66090868	2	2.31995
P20852	DPKFFSNPKDFNPK	1.61611922	2	2.538

P20852	EALVDQAEEFSGR	0.9340773	2	3.36968
P21213	**HUTH Histidine ammonia_lyase**	**1.68310996**	**1.3E-07**	**12**
P21213	ALDYLAIGVHELAAISER	1.72270844	3	4.06758
P21213	DIITTELNSATDNPMVFASR	1.83469927	2	4.21956
P21213	GETISGGNFHGEYPAK	1.36099959	2	4.13415
P21213	GEWLAVPCQDGK	1.19709596	2	2.46894
P21213	GYSGISLETLK	1.46385848	2	2.74128
P21213	LQELQVNLVR	1.71176812	2	3.17782
P21213	NKPDNGGFTSVDEVR	1.45568402	2	3.9932
P21213	SHSSGVGKPLSPER	1.27755265	2	4.37341
P21213	SLLDSDHHPSEIAESHR	1.31347016	3	4.82797
P21213	TVVYGITTGFGK	1.57338319	2	3.29553
P21213	VWEVAAPYIEK	1.54792023	2	2.41887
P21213	YIALDGDSLSTEDLVNLGK	1.68478369	2	5.15879
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.30506408**	**0.26699**	**9**
P21396	DVPAIEITHTFLER	1.3898717	2	3.37243
P21396	FVGGSGQVSEQIMGLLGDK	1.30271561	2	3.14002
P21396	IFSVTNGGQER	0.9889823	2	2.6415
P21396	INVLVLEAR	2.07082232	2	3.18034
P21396	KDIWVEEPESK	0.89573526	2	3.30015
P21396	KICELYAK	0.49931096	2	2.52401
P21396	VLGSQEALYPVHYEEK	1.13116755	2	4.45402
P21396	WVDVGGAYVGPTQNR	0.72483719	2	4.50637
P21396	YVISAIPPILTAK	1.34194841	2	2.94856
P21531	**RL3 60S ribosomal protein L3**	**1.74955327**	**1.1E-07**	**7**
P21531	AHLMEIQVNGGTVAEK	1.10853639	2	5.38146
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	1.62878427	3	5.28547
P21531	HGSLGFLPR	1.04230478	2	2.92632
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.76908851	2	5.13959
P21531	NNASTDYDLSDK	1.47238341	2	3.70017
P21531	SINPLGGFVHYGEVTNDFIMLK	2.03912538	2	3.63843
P21531	TVFAEHISDECK	1.64386478	2	3.99984
P21533	**RL6 60S ribosomal protein L6**	**1.43070043**	**2E-15**	**10**
P21533	AVDSQILPK	1.40618658	2	2.78786
P21533	FVIATSTK	1.25381826	1	2.22856
P21533	HLTDAYFK	1.42056327	2	2.56802
P21533	HQEGEIFDTEK	1.4761245	2	3.36501
P21533	HQEGEIFDTEKEK	1.37494931	2	4.19414
P21533	HQEGEIFDTEKEKYEITEQR	1.56594203	3	4.55576
P21533	QLGSGLLLVTGPLALNR	1.54455218	2	5.19689
P21533	SQFSLTNGMYPHK	1.1249245	2	3.3313
P21533	SSITPGTVLIILTGR	1.2579878	2	4.13516
P21533	YYPTEDVPR	3.02858418	1	1.99562
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**0.94342185**	**0.19002**	**6**
P21571	FEVLDKPQS	0.61800774	2	2.89692
P21571	FPTFNFEDPKFEVLDKPQS	1.38460587	3	3.32777
P21571	GEMDKFPTFNFEDPK	0.9897779	3	3.96244
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.52914632	3	3.83114
P21571	LASGGPVDTGPEYQQEVDR	1.26784131	2	5.31505
P21571	LASGGPVDTGPEYQQEVDRELFK	2.64133135	2	2.94897
P21643	**T23O Tryptophan 2_3_dioxygenase**	**6.97113295**	**9.9E-20**	**9**
P21643	AGTGGSSGYYYLR	5.06486423	2	2.93286
P21643	DNFEGDYNELLLK	1.95533386	2	3.59625
P21643	GGLIYGDYLQLEK	21.1107838	2	3.62728
P21643	GLEEEFLK	1.66291632	1	2.24592
P21643	ILNAQELQSEIK	12.301541	2	3.83426

P21643	KDSEEKEEQMAEFR	23.8093226	2	3.85829
P21643	NLSMEDNEEDGAQTGVNR	119.81509	2	6.06042
P21643	YNHVCMVHRMLGSK+Oxidation(5	1.93966637		
P21643	YNHVCMVHRMLGSK+Oxidation(9	1.64293996		
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.61897849**	**0.79712**	**2**
P21670	ATCIGNNSAAAVSMLK	1.20995892	2	3.41535
P21670	LLDEVFFSEK	1.62609173	2	3.375
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**1.27579496**	**0.99974**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	1.46120106	2	5.0123
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22	1.12367156		
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.29142891**	**0.24169**	**7**
P21913	CGPMVLDALIK	1.05093952	2	3.13622
P21913	CGPMVLDALIKIK	0.81849509	2	2.61755
P21913	CHTIMNCTQTCPK	1.28827989	2	4.48155
P21913	IDTDLGK	1.00884828	1	1.91315
P21913	IKNEIDSTLTFR	1.6088473	2	2.89163
P21913	LQDPFSLYR	1.87440089	2	2.76369
P21913	RIDTDLGK	1.23464051	2	2.58595
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.32184674**	**0.90192**	**6**
P21981	CDLEIQANGR	1.31907779	2	2.85641
P21981	DHHTADLCQEK	1.10586115	2	2.70764
P21981	KLVAEVSLK	2.22847941	2	2.45455
P21981	SEGTYCCGPVSVR	1.38288027	2	3.69216
P21981	VDLFPTDIGLHK	0.86336681	2	2.65927
P21981	YSGCLTESNLIK	1.13131891	2	3.55971
P22734	**COMT Catechol O_methyltransferase**	**1.60408348**	**5.3E-14**	**12**
P22734	AIYQGPSSPDKS	1.09060874	2	3.34702
P22734	EWAMNVGDAK	1.33651607	1	2.88443
P22734	GQIMDAVIR	1.14789816	2	2.9894
P22734	GQIMDAVIR+Oxidation(3	1.80233222		
P22734	GSSSFECTHYSSYLEYMK	6.22514206	2	4.43602
P22734	GTVLLADNVIVPGTPDFLAYVR	2.81395498	3	5.04401
P22734	KGTVLLADNVIVPGTPDFLAYVR	2.48670228	3	5.19426
P22734	KYDVDTLDMVFLDHWK	1.90639984	3	5.28126
P22734	VTILNGASQDLIPQLK	1.09217644	2	4.47632
P22734	YDVDTLDMVFLDHWK	2.5569021	2	4.49006
P22734	YLPDTLLLEK	1.46218182	2	3.00144
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.74384792	3	6.4661
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.49661736**	**0.06106**	**6**
P22789	EEDLILLTYPK	1.34091532	2	2.99747
P22789	ETLQNVCNK	2.61642235	2	2.35427
P22789	FVVKEEDLILLTYPK	3.54059572	3	3.4317
P22789	KLEPDELDLVLK	1.59280004	2	3.76198
P22789	LEPDELDLVLK	1.31220135	2	2.3574
P22789	NHFTVAQAEAFDK	1.91991213	2	3.44297
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.24183941**	**0.02529**	**23**
P22791	ASLDMFNK	1.12609861	2	2.79578
P22791	ASLDMFNKK	1.15107296	2	2.83551
P22791	DVGILALEVYFPAQYVDQTDLEK	2.20108199	3	5.66205
P22791	GLKLEETYTNK	3.82779493	2	2.84651
P22791	GLKLEETYTNKDVDK	1.28515085	3	3.37082
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.16324261	3	6.96637
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3	1.40681669		
P22791	IGAFSYGSGLAASFFSFR	1.6944794	2	3.2888

P22791	LEETYTNK	1.13241132	2	3.15436
P22791	LEETYTNKDVDK	1.23475729	2	4.12729
P22791	LEVGTETIIDK	0.83051122	2	3.78082
P22791	LMFNDFLSSSSDK	1.91579145	2	4.32502
P22791	LMFNDFLSSSSDK+Oxidation(1	2.35929289		
P22791	LMFNDFLSSSSDKQNNLYK	1.82457482	2	4.78452
P22791	LSIQCYLR	1.27925104	2	2.44313
P22791	LVSSVSDLPK	1.24429928	2	3.45192
P22791	MGFCSVQEDINSLCLTVVQR	1.22359981	2	4.1632
P22791	MSPEEFTEIMNQR	0.92374914	2	4.89085
P22791	MSPEEFTEIMNQR+Oxidation(0	1.40884201		
P22791	MSPEEFTEIMNQR+Oxidation(9	1.34546847		
P22791	TKLPWDAVGR	1.05368115	3	4.01192
P22791	VNFSPPGDTSNLFPGTWYLER	1.50568843	2	4.45927
P22791	YTVGLGQTR	1.13847242	2	3.44634
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.48891334**	**0.05099**	**10**
P22985	DEVTCVGHIIGAVVADTPEHAQR	1.07765986	3	3.8216
P22985	DGGCCGGSGNNPNCCMNQTK	1.43556505	2	5.7519
P22985	DPPANVQLFQEVPK	1.45775264	2	2.88138
P22985	LDPTFASATLLFQK	1.64784445	2	3.80933
P22985	NQPEPTVEEIENAFQGNLCR	1.49071795	2	5.0843
P22985	QLFQLDSPATPEK	0.83077449	2	3.4268
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.43213965	3	5.2065
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.3717475	3	5.30885
P22985	TLLRPEEILLSIEIPYSK	0.87618221	3	4.46445
P22985	TNLPSNTAFR	1.39576959	1	2.046
P23358	**RL12 60S ribosomal protein L12**	**1.12602802**	**0.00011**	**5**
P23358	CTGGEVGATSALAPK	1.33627374	2	4.13048
P23358	EILGTAQSVGCNVDGR	1.27661696	2	4.50077
P23358	HNGNITFDEIVNIAR	1.41199243	2	3.85397
P23358	HPHDIIDDINSGAVECPAS	0.90877315	2	4.55591
P23358	QAQIEVVPSASALIIK	2.13265793	2	3.84584
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.69142275**	**9.9E-20**	**10**
P23457	ALDGLNR	1.27918225	2	2.39259
P23457	ELTQVFEFQLASEDMK	2.09026478	2	4.13405
P23457	HFDSAYLYEVEEEVGQAIR	2.01218824	2	5.99956
P23457	MLDYCK	1.60124918	1	2.14713
P23457	SIGVSNFNCR	1.36556484	2	3.40528
P23457	SKDIILVSYCTLGSSR	0.93269808	2	4.44201
P23457	SPVLLDDPVLCAIAK	1.72959854	2	4.21325
P23457	VALNDGNFIPVLGFGTTVPEK	3.10191349	2	4.86066
P23457	YFDDHPNHPFTDE	1.64843508	2	4.19011
P23457	YKPVCNQVECHLYLNQSK	0.84999556	2	4.63768
P23514	**COPB Coatomer subunit beta**	**1.30971759**	**1.5E-10**	**8**
P23514	EAGELKPEEEITVGPVQK	0.83781558	2	4.08284
P23514	LVEKPSPLTLAPHDFANIK	1.68664602	3	3.72948
P23514	NFENLIPDAPELIHDFLVNEK	1.5687523	3	4.80343
P23514	TLQLALDLVSSR	1.30537374	2	3.4115
P23514	TNNVSEHEDTDKYR	1.05471023	2	3.81448
P23514	VLQDLVMDILR	1.68704962	2	3.52052
P23514	VLSECSPLMNDIFNK	1.37718792	2	2.86366
P23514	YEAAGTLVTLSSAPTAIK	1.46099332	2	5.29004
P23739	**SUIS Sucrase_isomaltase_ intestinal**	**1.00096067**	**0.99198**	**2**
P23739	LPGFGFNDQFIQISTR	0.99566132	2	2.4404
P23739	RMMTLNYPPVFSPELR+Oxidation(1	1.07457929		
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**1.04837277**	**0.00033**	**10**

P23965	ALQLGTLFPPAEALK	1.21125006	2	5.296
P23965	ATADNLIK	1.11922373	2	2.76712
P23965	AVQELWLR	1.37857933	2	2.72062
P23965	DNYVNTIGHR	1.30022003	2	2.67969
P23965	EGEAGIAVMK	1.14802367	1	2.00261
P23965	GVILTSERPGIFSAGLDLMEMYGR	1.89686761	3	5.49936
P23965	QREADIQNFTSFISR	1.06257891	2	3.04774
P23965	SLHVYLEK	0.90849112	1	2.1486
P23965	VGLVDEVVPEDQVHSK	0.97887908	2	4.8673
P23965	WFTIPDHSR	0.85707246	1	1.9616
P24049	**RL17 60S ribosomal protein L17**	**1.27766403**	**0.19779**	**4**
P24049	EQIVPKPEEEVAQK	1.32297646	2	3.8174
P24049	GLDVDSLVIEHIQVNK	1.46016755	2	4.39192
P24049	SAEFLLHMLK	2.14353146	2	2.84709
P24049	YSLDPENPTK	0.93097595	2	2.60598
P24050	**RS5 40S ribosomal protein S5**	**1.92218212**	**0.00607**	**5**
P24050	AQCPIVER	1.50471928	2	2.31387
P24050	QAVDVSPLR	5.22747736	2	2.31656
P24050	RQAVDVSPLR	1.92120482	2	2.33084
P24050	VNQAIWLLCTGAR	2.43582002	2	4.2079
P24050	WSTDDVQINDISLQDYIAVK	3.58493101	2	4.82144
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.47076029**	**0.89601**	**6**
P24090	ELACDDPETEHVALIAVDYLNK	1.55137579	2	4.2808
P24090	HAFSPVASVESASGEVLHSPK	1.26619275	3	6.05787
P24090	LGGEEVSVACK	1.34565299	2	3.71209
P24090	VGQPGDAGAAGPVAPLCPGR	1.14513056	2	5.20985
P24090	VLHAQCHSTPDSAEDVR	1.24663257	3	3.42023
P24090	VLHAQCHSTPDSAEDVRK	1.17251977	3	4.01869
P24268	**CATD Cathepsin D**	**1.37373504**	**6.5E-07**	**4**
P24268	AIGAVPLIQGEYMIPCEK	1.34684573	2	3.31334
P24268	DPTGQPGGELMLGGTDSR	0.90623588	2	4.73885
P24268	GGCEAIVDTGTSLLVGPVDEVK	0.99097104	3	3.50207
P24268	LGGQNYELHPEK	2.12686829	2	3.24573
P24329	**THTR Thiosulfate sulfurtransferase**	**1.0968467**	**0.00468**	**12**
P24329	EGHPVTSEPSRPEPAVFK	1.4242561	2	4.57323
P24329	FQLVDSR	0.84327646	2	2.38934
P24329	GSVNVPFMNFLTEDGFEK	1.82067503	2	3.25753
P24329	HVPGASFFDIEECR	1.34243934	2	4.10465
P24329	KVDLSQPLIATCR	1.01407007	2	4.65795
P24329	RFQLVDSR	0.88602044	2	2.49611
P24329	TVSVLNGGFR	1.10455758	2	2.91548
P24329	TYEQVLENLQSK	1.07863147	2	5.07622
P24329	VDLSQPLIATCR	1.05005035	2	3.73126
P24329	VLDASWYSPGTR	0.92579597	2	3.63676
P24329	WLAESIR	1.33609416	2	2.37692
P24329	YLGTQPEPDAVGLDSGHIR	1.12709027	3	4.79824
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.10511689**	**0.94829**	**9**
P24368	DKPLKDVIIVDCGK	1.13898772	3	3.82458
P24368	DTNGSQFFITTVK	1.31357023	2	3.83181
P24368	DVIIVDCGK	0.71948311	1	1.98992
P24368	HYGPGWVSMANAGK	1.80677043	2	4.00704
P24368	IEVEKPFAIAK	1.01922418	2	3.09217
P24368	IEVEKPFAIAKE	1.23730054	2	3.61651
P24368	TVDNFVALATGEK	0.92570285	2	4.10025
P24368	VLEGMDVVR	1.41762746	2	3.04046
P24368	VYFDFQIGDEPVGR	1.08636098	2	4.10535
P24457	**CP2DB Cytochrome P450 2D11**	**1.12230383**	**0.56256**	**2**

P24457	RFSVSTLR	0.69018948	2	2.564
P24457	SLEEWVTK	1.14787815	2	2.46066
P24470	**CP2CN Cytochrome P450 2C23**	**0.94929878**	**0.4793**	**12**
P24470	ACVGESLAR	1.19325596	2	2.75607
P24470	DLDIKPITTGIINLPPPYK	0.92473766	2	3.869
P24470	EALLQQGDEFLGR	1.10685895	2	2.69954
P24470	FGLLLLMK	2.16488907	2	3.08701
P24470	GTTVLPMLSSVMLDQK	1.1895209	2	3.98112
P24470	GYGLIFSNGER	0.87484987	2	3.7939
P24470	IEEEKDNLK	0.89976126	2	3.01472
P24470	LPPGPTPLPIIGNLLQLNLK	1.15808431	3	5.05692
P24470	RSLEERVQEEAR	1.09402448	2	2.49198
P24470	SEFHLENLAVCGSNLFTAGTETTSTTLR	1.48120913	3	3.78411
P24470	TFLNLMDLLNK	1.59861731	2	3.9953
P24470	YITLLPSSLPHAVVQDTK	0.67894836	2	4.58589
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**1.2005946**	**0.82467**	**8**
P24473	AGMATAQAQHLLNK	1.29513159	2	4.19168
P24473	DEDITESQNILSAAEK	0.87390813	2	5.84502
P24473	DSGNQPPAMVPHK	1.87476398	2	2.75497
P24473	FLTAVSMEQPEMLEK	1.01184426	2	4.87768
P24473	IWSRDEDITESQNILSAAEK	1.90785448	3	3.67963
P24473	MELLAYLLGEK	1.44771848	2	3.85944
P24473	QLFQVPMSVPK	0.81068798	2	2.55549
P24473	YGAFGLPTTVAHVDGK	0.92637896	2	4.04841
P25093	**FAAA Fumarylacetoacetase**	**1.26549268**	**2E-09**	**16**
P25093	AIDVGQGQTR	1.05983629	2	3.46433
P25093	AQEHIFGMVLMNDWSAR	2.76578708	2	3.85305
P25093	ASLQNLLSASQAQLR	1.00519853	2	4.88459
P25093	ASLQNLLSASQAQLRDDK	1.5614086	2	3.58822
P25093	ASSVVVSGTPIR	1.26661376	2	3.83348
P25093	DIQQWEYVPLGPFLGK	1.44323225	2	4.99227
P25093	FGEPIPISK	1.06999168	2	2.89393
P25093	GEGMSQAATICR	1.23430653	2	3.74885
P25093	GEGMSQAATICR+Oxidation(3	1.20676162		
P25093	GKENALLPNWLHLPVGYHGR	1.57850684	4	4.53415
P25093	HLFTGPVLSK	1.20514598	1	2.73185
P25093	HQHVFDETTLNSFMGLGQAAWK	1.17150608	2	5.42357
P25093	IGVAIGDQILDLSVIK	2.20685007	2	5.40393
P25093	SFGTTISPWVVPMDALMPFVVPNPK	1.15066353		
P25093	TFLLDGDEVIITGHCQGDGYR	1.14857546	2	5.0738
P25093	VGFGQCAGK	0.75879441	2	2.35363
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.30298201**	**0.35077**	**7**
P25113	ALPFWNEEIVPQIK	1.20376903	2	3.509
P25113	FSGWYDADLSPAGHEEAK	0.97913519	2	5.07037
P25113	FSGWYDADLSPAGHEEAKR	1.65732476	2	4.2297
P25113	HGESAWNLENR	1.34031007	2	3.78706
P25113	SYDVPPPPMEPDHPFYSNISK	2.02866847	2	3.80281
P25113	YADLTEDQLPSCESLK	0.94117936	2	5.3641
P25113	YADLTEDQLPSCESLKDTIAR	1.21980474	2	5.06723
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.20345897**	**0.0016**	**15**
P25235	EDQVIQLMNTIFSK	1.309479	2	3.88383
P25235	EETVLATVQALHTASHLSQQADLR	1.52646678	3	5.07798
P25235	FELDTSER	1.31376744	1	2.39473
P25235	FPEEEAPSTVLSQNLFTPK	0.92232245	2	3.8375
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.28456134	2	4.68701

P25235	KNFESLSEAFSVASAAAALSQNR	1.76712037	2	5.44087
P25235	LMDHVGTEPSIKEDQVIQLMNTIFSK	1.28853393	3	5.14101
P25235	LQVSSVLSQPLAQAAVK	1.6165053	2	5.8478
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.64627956	3	5.56416
P25235	NFESLSEAFSVASAAAALSQNR	1.95811998	3	4.90533
P25235	NIVEEIEDLVAR	1.20044506	3	4.6323
P25235	NPILWNVADVVIK	1.14400374	2	3.25738
P25235	TGQEVVFVAEPDNK	1.67762296	2	4.32545
P25235	YHVPVVVVPEGSASDTQEQAILR	1.13973293	3	6.39832
P25235	YIANTVELR	1.29518177	2	2.82702
P25318	**chain**	**1.12192004**	**0.6131**	**3**
P25318	GEKGFGMPGLPGLK+Oxidation(6	1.29714936		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(12	1.08647999		
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)Oxidation(9	1.08647999		
P25409	**ALAT1 Alanine aminotransferase 1**	**1.38748482**	**0.46526**	**3**
P25409	LTEQVFNEAPGIR	1.34315469	2	2.91472
P25409	VLCVINPGNPTGQVQTR	3.36049519	2	4.50118
P25409	VLTLDTMNPCVR	1.35951599	2	2.50242
P26039	**TLN1 Talin_1**	**1.12052427**	**0.11111**	**24**
P26039	ADAEGESDLENSR	1.50313558	2	3.62632
P26039	ADAEGESDLENSRK	1.26722333	2	3.20415
P26039	AGALQCSPSDVYTK	1.52845647	2	2.68833
P26039	ALEATTEHIR	1.30508172	2	2.36505
P26039	AQEACGPLEMDSALSVVQNLEK	1.46627041	2	4.49146
P26039	ASAGPQPLLVQSCK	1.13735225	2	2.87108
P26039	ASVPTIQDQASAMQLSQCAK	0.76860026	2	3.36574
P26039	AVAEQIPLLVQGVR	1.71815341	2	3.06253
P26039	EAAEGLRMATNAAAQNAIKK	1.20973097	2	2.65497
P26039	ILAQATSDLVNAIK	1.96385077	2	3.29756
P26039	LGAASLGAEDPETQVVLINAVK	2.09565765	2	4.27235
P26039	LLGEIAQGNENYAGIAAR	0.93819827	2	4.21337
P26039	LNEAAAGLNQAATELVQASR	1.27559072	2	5.11374
P26039	MATNAAAQNAIK	1.04224885	2	2.71029
P26039	NCGQMSEIEAK	1.37037235	2	2.94028
P26039	QFVQSAKEVANSTANLVK	1.23109142	2	2.39528
P26039	SNTSPEELGPLANQLTSDYGR	1.52244895	2	4.05546
P26039	TLAESALQLLYTAK	1.65242225	2	2.70907
P26039	TMLESAGGLIQTAR	1.22225587	2	2.61826
P26039	VGAIPANALDDGQWSQGLISAAR	1.01080517	2	5.05663
P26039	VGDDPAVWQLK	1.09130707	2	3.2794
P26039	VLGEAMTGISQNAK	1.12049267	2	3.32931
P26039	VLVQNAAGSQEK	1.30756296	2	3.15086
P26039	VVAPTISSPVCQEQLVEAGR	0.84123054	2	4.60903
P26043	**RADI Radixin**	**1.17186256**	**0.46494**	**11**
P26043	AFAAQEDLEK	1.13602019	2	3.02097
P26043	ALELEQER	1.13397662	2	2.47008
P26043	EIHKPGYLANDR	1.60056317	2	2.40559
P26043	FFPEDVSEELIQEITQR	1.50750111	3	4.0962
P26043	IQNWHEEHR	0.8749102	2	2.48059
P26043	KKEEEATEWQHK	1.14661604	3	4.19243
P26043	KTQNDVLHAENVK	1.25030845	2	5.06086
P26043	NQEQLAAELAEFTAK	1.36586785	2	5.10067
P26043	QLQALSSELAQAR	0.86200621	2	4.04214
P26043	RKPDTIEVQQMK	1.12892336	2	3.74671
P26043	TQNDVLHAENVK	1.19912076	2	4.11405

P26231	**CTNA1 Catenin alpha_1**	**1.18695428**	**6.1E-07**	**8**
P26231	LIEVANLACSISNNEEGVK	1.40385596	2	5.26296
P26231	LLEPLVTQVTTLVNTNSK	1.2584573	2	4.12106
P26231	NTSDVISAAK	1.35153605	2	2.39305
P26231	QIIVDPLSFSEER	1.28991559	2	2.88287
P26231	SAAGEFADDPCSSVK	1.23741125	2	4.39154
P26231	SDALNSAIDK	1.40241343	2	2.87703
P26231	TIADHCPDSACK	0.44771403	2	3.51977
P26231	VIHVVTSEMDNYEPGVYTEK	1.15637848	3	4.17196
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.09802211**	**0.81148**	**10**
P26284	AILAELTGR	1.0794351	2	2.6912
P26284	EEIQEVRSK	0.80515065	1	1.93804
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	1.50187689	3	6.51304
P26284	LEEGPPVTTVLTR	1.10142537	2	3.51335
P26284	MVNSNLASVEELK	1.14906376	2	2.91926
P26284	MVNSNLASVEELKEIDVEVR	1.0653174	2	4.36405
P26284	NFYGGNGIVGAQVPLGAGIALACK	1.51024535	2	4.20054
P26284	RGDFIPGLR	1.37925015	2	2.35812
P26284	TREEIQEVR	1.01834132	3	3.55589
P26284	VDGMDILCVR	1.42825173	2	3.43546
P26376	**IFM3 Interferon_induced transmembrane protein 3**	**0.91746563**	**0.93961**	**2**
P26376	IKEEYEVSELGAPHGSASVR	0.90525614	3	4.08259
P26376	KMVGDMTGAQAYASTAK+Oxidation(5	1.039261		
P26453	**BASI Basigin**	**1.4352512**	**0.20685**	**7**
P26453	GNINVEGPPR	1.41631671	2	3.4814
P26453	KSEHASEGEFVK	1.0945112	3	3.40795
P26453	RKPDQTLDEDDPGAAPLK	1.40569135	3	4.00201
P26453	SEASHPPVDEWVWFK	0.87803996	2	3.28807
P26453	SEHASEGEFVK	1.44640959	3	3.74149
P26453	SGEYSCIFLPEPVGR	1.60939464	2	3.61876
P26453	VLQEDTLPDLQMK	1.07095217	2	4.11576
P26516	**PSD7 26S proteasome non_ATPase regulatory subunit 7**	**1.483789**	**0.71217**	**2**
P26516	SVVALHNLINNK	2.00977857	2	2.76135
P26516	TFEHVTSEIGAEEAEEVGVEHLLR	1.32294602	3	4.49596
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.99155949**	**0.99978**	**7**
P26772	GGEIQPVSVK	1.15116862	2	3.46954
P26772	GGIMLPEK	1.11273985	2	2.66682
P26772	GGIMLPEK+Oxidation(3	1.16450775		
P26772	GKGGEIQPVSVK	0.97163545	2	3.41747
P26772	VLLPEYGGTK	0.92044591	2	2.37234
P26772	VLQATVVAVGSGGK	0.97383445	2	5.39118
P26772	VVLDDKDYFLFR	1.60443306	3	3.69212
P27139	**CAH2 Carbonic anhydrase 2**	**1.09742839**	**0.92183**	**4**
P27139	AVQHPDGLAVLGIFLK	1.63406929	2	3.98462
P27139	IGPASQGLQK	0.92195648	2	3.5178
P27139	ITEALHSIK	1.189555	2	2.45669
P27139	QSPVDIDTGTAQHDPSLQPLLICYDK	2.15218214	3	3.40572
P27321	**ICAL Calpastatin**	**1.26948091**	**0.03425**	**5**
P27321	GSDEVTASSAATGTSPR	2.69670653	2	4.2688
P27321	KGSDEVTASSAATGTSPR	1.27947003	2	5.21008
P27321	KVEEEVMNDQALQALSDSLGTR	1.68555007	3	3.67625
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	1.57115753	3	4.64595
P27321	SQSSEPPVIHEK	0.39956429	2	3.50463

P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.94545007**	**0.55389**	**6**
P27364	AVLAANGSILK	0.75546878	2	2.99302
P27364	ETILNDREEEHR	0.95273187	2	2.92913
P27364	GDIVDAQFLR	0.92428301	2	3.05994
P27364	IVQMLVQEK	1.17997015	2	2.61716
P27364	NGGTFHTCALR	0.50752199	2	2.6045
P27364	QTILDVNVK	0.90831945	2	2.38779
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.00841064**	**0.14509**	**6**
P27605	DLNHVCVISESGK	0.91200468	2	3.43581
P27605	FFADLLDYIK	1.69306292	2	3.54966
P27605	NVLIVEDIIDTGK	1.08937238	2	3.86119
P27605	SVGYRPDFVGFEIPDK	1.24887031	3	4.03102
P27605	SYCNDQSTGDIK	1.15112689	2	4.00832
P27605	VIGGDDLSTLTGK	0.7796974	2	4.36202
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.40264381**	**9.9E-20**	**17**
P27653	ASQAPSSFQLLYDLK	1.71822228	2	3.97226
P27653	AYTEEDLDLVEK	0.60687726	2	3.19383
P27653	GDILVVATGQPEMVK	3.76343758	2	2.5026
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.0379993	3	4.79251
P27653	IFHELTQTDK	1.82368838	3	3.47881
P27653	ITIGQAPTEK	1.75717696	2	2.43887
P27653	IYGADDIELLPEAQNK	2.6077973	2	4.99348
P27653	KITIGQAPTEK	1.46266729	2	2.86934
P27653	KVVGDVAYDEAK	1.41036473	2	3.70243
P27653	LDIDPETITWQR	1.3536408	2	3.82933
P27653	MHGGGPTVTAGLPLPK	0.87299212	2	3.81227
P27653	QGFGNLPICMAK	1.21878825	2	2.78848
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.45458547	3	5.59788
P27653	TDPAALTDDEINR	0.86725869	2	4.09686
P27653	THLSLSHNPEQK	1.4298358	2	3.85035
P27653	VVGDVAYDEAK	1.71475106	2	3.40638
P27653	YVVVTGITPTPLGEGK	1.36694433	2	4.82229
P27657	**LIPP Pancreatic triacylglycerol lipase**	**1.43852326**	**0.29426**	**2**
P27657	ATYTQATQNVR	1.16942923	2	2.96299
P27657	NILSQIVDIDGIWEGTR	1.44410971	2	2.93919
P27661	**H2AX Histone H2A.x**	**1.25420373**	**0.00383**	**3**
P27661	AGLQFPVGR	0.88487283	2	3.22539
P27661	HLQLAIR	1.31743561	2	2.71001
P27661	LLGGVTIAQGGVLPNIQAVLLPK	1.79580643	2	4.39413
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**1.48421079**	**0.59675**	**4**
P27768	ELEDMNQK	3.17739659	2	2.30775
P27768	IDAAEEEKYDMEVK	1.42117744	2	3.25216
P27768	SVMLQIAATELEK	1.30730961	2	2.92447
P27768	SVMLQIAATELEKEESR	1.5664557	2	3.68925
P27867	**DHSO Sorbitol dehydrogenase**	**1.06025005**	**0.11365**	**14**
P27867	AMGASQVVVIDLSASR	1.29800077	2	4.07644
P27867	AVEAFETAK	1.18161855	1	1.94922
P27867	EVGADFTIQVAK	1.53009136	2	3.15665
P27867	GENLSLVVHGPGDIR	1.02642185	2	3.81485
P27867	HSADFCYK	1.16306157	2	2.90614
P27867	IGDFVVK	1.32493682	2	2.47232
P27867	LENYPIPELGPNDVLLK	1.03439851	2	4.88393
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.36904409	3	4.1149
P27867	MHSVGICGSDVHYWEHGR	1.36782019	2	6.04524

P27867	MHSVGICGSDVHYWEHGR+Oxidation(0	1.33687784		
P27867	TLNVKPLVTHR	0.96257858	2	3.23657
P27867	VAIEPGVPR	1.97245439	1	2.18025
P27867	VLVCGAGPIGIVTLLVAK	1.75752586	3	5.74355
P27867	YCNTWPMAVSMLASK	1.50464527	2	3.3753
P27952	**RS2 40S ribosomal protein S2**	**1.49523455**	**0.00076**	**6**
P27952	AEDKEWIPVTK	1.98166578	2	3.39259
P27952	AFVAIGDYNGHVGLGVK	1.66173858	2	3.3435
P27952	GCTATLGNFAK	1.24660936	2	3.20058
P27952	GTGIVSAPVPK	1.26956056	2	2.4959
P27952	SLEEIYLFSLPIK	1.49529642	2	3.49273
P27952	TYSYLTPDLWK	1.30853639	2	3.26723
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.13530288**	**0.46769**	**26**
P28037	ADPLGLEAEK	1.07090335	2	2.42663
P28037	ANATEFGLASGVFTR	1.36461674	2	4.85761
P28037	AVQMGMSSVFFNK	1.65502875	2	3.35546
P28037	DLGEAALNEYLR	1.1687529	2	3.47982
P28037	ECEVLPDDTVSTLYNR	1.7288413	2	4.36165
P28037	EESFGPIMIISR	1.21684072	2	3.07562
P28037	EGHEVVGVFTIPDKDGK	1.18858494	2	4.56391
P28037	GNDKVPGAWTEACGQK	1.11799876	2	3.83084
P28037	GQALPEVVAK	1.24681251	2	2.96649
P28037	GSASSDLELTEAELATAEAVR	0.99244058	2	6.31158
P28037	GVVNILPGSGSLVGQR	1.04882097	2	4.82736
P28037	IGFTGSTEVGK	1.09708643	2	2.78719
P28037	ILPNVPEVEDSTDFFK	1.97465846	2	3.59059
P28037	INWDQPAEAIHNWIR	1.97068305	2	4.25018
P28037	IQGATIPINQARPNR	1.32648472	2	2.34545
P28037	KEGHEVVGVFTIPDKDGK	1.03393786	3	4.18843
P28037	KIGFTGSTEVGK	1.59325369	2	3.13217
P28037	KLVEYCQR	1.23887773	2	2.41092
P28037	LFVEESIHNQFVQK	1.10289962	2	4.45707
P28037	LIAEGTAPR	1.08850909	2	3.52205
P28037	LSDHPDVR	1.01907009	1	2.10967
P28037	NIQLEDGK	1.34188616	1	2.3031
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.56429145	3	4.4148
P28037	TDVAAPFGGFK	1.18237975	2	3.11586
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	1.37354656	3	5.27368
P28037	VVEEVEK	1.16491073	1	2.07731
P28064	**PSB8 Proteasome subunit beta type_8**	**1.0903478**	**0.99611**	**3**
P28064	ASAGSYIATIR	1.500937	2	2.77245
P28064	KGPGLYYVDDNGTR	1.01519183	2	2.84732
P28064	QDLSPEEAYDLAR	0.89142753	2	3.1804
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.45508348**	**1.1E-07**	**10**
P28480	AFHNEAQVNPER	1.42311172	2	3.61945
P28480	FATEAAITILR	1.44596334	2	3.22714
P28480	HGGYENAVHSGALDD	1.28834275	2	3.34447
P28480	ICDDELILIK	1.28232112	2	3.19386
P28480	LLEVEHPAAK	1.57683167	2	2.77535
P28480	MLVDDIGDVTITNDGATILK	1.18588585	2	2.34524
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.39863792	2	4.93783
P28480	SQNVMAAASIANIVK	1.76584827	2	4.6017
P28480	SSLGPVGLDK	1.18544911	2	2.41221
P28480	YINENLIINTDELGR	1.47953645	2	4.56631
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**1.18754613**	**0.96409**	**5**
P28492	ATGLQTSDPR	1.23977786	2	2.7969

P28492	GTPHSHQPQHSDHDASNSGMLPR	1.13921823	3	3.73105
P28492	MVQESSSGGLLDR	1.36092709	2	3.62209
P28492	SNPDLWGVSLCTVDGQR	1.10316068	2	4.07981
P28492	TALHVAAAEGHIDVVK	1.29256739	3	3.58745
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**1.23421735**	**0.8952**	**2**
P28650	LDILDVLSEIK	1.19061193	2	3.20016
P28650	VVDLLATDADIVSR	1.23431137	2	2.47061
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.12603368**	**0.98878**	**19**
P29147	AVLVTGCDSGFGFSLAK	0.99452434	2	5.64348
P29147	EVAEVNLWGTVR	1.78786256	2	2.42346
P29147	FGVEAFSDCLR	1.25131324	2	3.66929
P29147	GFLVFAGCLLK	0.9591419	2	3.7283
P29147	KMWDELPEVVR	0.97310116	2	3.34313
P29147	KMWDELPEVVR+Oxidation(1	1.40253306		
P29147	MANPARSPYCITK+Oxidation(0	1.0466666		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.09331913	3	5.65484
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0	1.45377584		
P29147	MQVMTHFPGAISDK	0.90204995	2	4.82906
P29147	MQVMTHFPGAISDK+Oxidation(0	1.00993047		
P29147	MQVMTHFPGAISDK+Oxidation(3	1.00993047		
P29147	MWDELPEVVR	1.36305294	2	3.41854
P29147	MWDELPEVVR+Oxidation(0	1.11537046		
P29147	TIQLNVCNSEEVEK	0.93501312	2	4.33444
P29147	VSVVEPGNFIAATSLYSPER	0.93817348	2	5.99969
P29147	VVNISSMLGR	1.18138239	2	3.92976
P29147	YEMHPLGVK	1.12281833	1	2.55044
P29147	YEMHPLGVK+Oxidation(2	1.5410613		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**1.05578461**	**0.17627**	**9**
P29266	DLGLAQDSATSTK	0.79456783	2	3.74448
P29266	EAGEQVASSPADVAEK	0.74115441	2	4.98183
P29266	GSLLIDSSTIDPSVSK	1.53374054	2	5.07553
P29266	HGYPLILYDVFPDVCK	1.50870744	2	5.13612
P29266	KGSLLIDSSTIDPSVSK	0.94852648	2	4.08563
P29266	MGAVFMDAPVSGGVGAAR	1.14490823	2	5.32116
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0	1.44250372		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5	1.44250372		
P29266	TPILLGSVAHQIYR	2.23422004	3	3.84981
P29314	**RS9 40S ribosomal protein S9**	**1.2728194**	**1.7E-05**	**9**
P29314	IEDFLER	1.17689259	2	2.65748
P29314	IGVLDEGK	0.78623707	2	2.62025
P29314	KGQGGAGAGDDEEED	1.21951305	2	3.23612
P29314	KQVVNIPSFIVR	1.1781472	2	2.53673
P29314	LDYILGLK	1.38092918	2	3.04203
P29314	LFEGNALLR	1.57806144	2	3.00147
P29314	LIGEYGLR	1.66763964	2	2.56291
P29314	QVVNIPSFIVR	1.26783933	2	2.66039
P29314	SRLDQELK	1.33065399	3	3.49595
P29315	**RINI Ribonuclease inhibitor**	**1.17390362**	**0.15653**	**7**
P29315	ASLQELDLGSNK	1.16781083	2	2.43099
P29315	ELVLSNNDFHEAGIHTLCQGLK	1.28736063	3	3.50612
P29315	LDDCGLTEVR	1.00743598	2	3.14918
P29315	LENCGITSANCK	1.05479234	2	3.61645
P29315	LSLQNCSLTEAGCGVLPDVLR	1.34513933	2	3.14955
P29315	SAIQANPALTELSLR	1.28053822	2	4.43585

P29315	TNELGDAGVGLVLQGLQNPTCK	1.34176413	2	5.34337
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.06177164**	**5.2E-13**	**11**
P29410	AMVASGSELGK	1.22003632	2	3.11276
P29410	AMVASGSELGK+Oxidation(1	1.260355		
P29410	AMVASGSELGKK	1.50781516	2	2.89378
P29410	AVLLGPPGAGK	0.97659221	2	2.60096
P29410	EAMKDDITGEPLIR	1.62507689	2	3.13877
P29410	LEAYHTQTTPLVEYYR	1.40512403	2	5.00483
P29410	LVSDEMVVELIEK	1.56900751	2	4.1976
P29410	NGFLLDGFPR	1.1689712	2	2.87766
P29410	NLETPSCK	1.00329228	2	2.33067
P29410	SYHEEFNPPK	0.97178686	3	3.44782
P29410	TRLEAYHTQTTPLVEYYR	1.45581555	3	3.52619
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**0.90391836**	**0.61109**	**6**
P29411	AYEAQTEPVLQYYQK	0.97993126	2	4.58133
P29411	GVLETFSGTETNK	1.09065566	2	2.87436
P29411	NLTQCSWLLDGFPR	1.47901389	2	3.82705
P29411	TVGIDDLTGEPLIQR	0.77286209	2	3.71508
P29411	VYNIEFNPPK	1.05741095	2	2.6067
P29411	VYQIDTVINLNVPFEVIK	1.33905828	2	3.29517
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**0.83003987**	**0.1796**	**2**
P29419	ELAEAEDVSIFK	0.8295139	2	3.43257
P29419	YSALILGMAYGAK	1.71872995	2	4.09777
P29457	**SERPH Serpin H1**	**1.21240718**	**0.57702**	**2**
P29457	GVVEVTHDLQK	1.18602078	2	3.15294
P29457	SALQSINEWASQTTDGK	1.96247431	2	2.5135
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.23565074**	**0.82531**	**4**
P30009	AEDGAAPSPSSETPK	1.1123985	2	3.65815
P30009	EAEAAEPEQPEQPEQPAAEEPR	0.56067607	2	3.92005
P30009	EAGEGAEAEGATADGAK	1.25611179	2	4.31611
P30009	GEAAAERPGEAAVASSPSK	1.2356799	2	4.56594
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**1.07539072**	**0.18986**	**3**
P30349	GSPMEISLPIALSK	1.14341953	2	3.05245
P30349	SLSNVIAHEISHSWTGNLVTNK	0.21900322	3	3.86572
P30349	SSALQWLTPEQTSGK	1.35519157	2	3.83139
P30427	**PLEC Plectin**	**1.12855794**	**0.25943**	**5**
P30427	LLEAAAQSSK	1.08997354	2	2.43488
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0	1.26011071		
P30427	SDQLTGLSLLPLSEK	1.99972039	2	2.51199
P30427	SKELAEQEAAR	1.08833176	2	2.92077
P30427	VLALPEPSPAAPTLR	1.08989123	2	2.9817
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.09418117**	**0.99778**	**7**
P30713	AQVHEYLGWHADNIR	0.8912218	2	4.9227
P30713	GQHLSEQFSQVNCLK	0.85500255	2	5.01445
P30713	NSMVLALQR	1.10561093	2	3.29761
P30713	TLPVPPPEAHASMMLR	1.2169819	2	2.59385
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	1.45982645	3	4.0839
P30713	VLGPLIGVQVPEEK	1.09265901	2	4.0583
P30713	YQVADHWYPADLQAR	1.18595988	2	4.66661
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.0324091**	**0.03074**	**2**
P30835	NEWGSLLEELVK	1.73069154	2	2.83908
P30835	VFANAPDSACVIGLR	0.42155659	2	2.56271
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.33891935**	**0.01407**	**9**
P30839	DILAAIAADLSK	1.33340123	2	3.05435
P30839	EKDILAAIAADLSK	1.08845218	2	4.26661

P30839	FDHILYTGNTAVGK	0.93157326	2	4.05788
P30839	HLTPVTLELGGK	1.55752895	3	3.42677
P30839	LQQLEALR	1.15973085	1	2.07449
P30839	NVEEAINFINDR	1.08830375	2	4.2853
P30839	VMQEEIFGPILPIVSVK	1.00264432	2	4.88933
P30839	VMQEEIFGPILPIVSVK+Oxidation(1	1.38984729		
P30839	YIAPTILTDVDPNSK	1.0320064	2	4.07383
P30904	**MIF Macrophage migration inhibitory factor**	**1.04657915**	**0.00074**	**2**
P30904	LHISPDR	0.85703851	1	2.0557
P30904	LLCGLLSDR	1.80622395	2	2.92955
P30999	**CTND1 Catenin delta_1**	**1.34946944**	**0.11637**	**3**
P30999	GYELLFQPEVVR	1.33465173	2	2.5908
P30999	HIEWESVLTNTAGCLR	1.47820212	2	2.80348
P30999	SLDNNYSTLNER	1.5862849	2	2.46552
P31000	**VIME Vimentin**	**0.85543525**	**0.35922**	**17**
P31000	DGQVINETSQHHDDLE	0.81268965	2	3.04076
P31000	ETNLESLPLVDTHSK	0.9360514	2	2.37687
P31000	FADLSEAANR	1.27545091	2	2.89052
P31000	ILLAELEQLK	1.55102962	2	2.8724
P31000	KLLEGEESR	1.02725179	2	3.06194
P31000	KVESLQEEIAFLK	1.20692923	2	3.96662
P31000	KVESLQEEIAFLKK	0.8194323	2	2.33484
P31000	LGDLYEEEMR	0.72234102	2	2.78672
P31000	LLEGEESR	0.69566806	2	2.80147
P31000	LQDEIQNMKEEMAR	0.79142269	2	3.66286
P31000	NLQEAEEWYK	0.91598508	2	2.88632
P31000	QDVDNASLAR	0.90164564	2	2.96533
P31000	QVQSLTCEVDALK	0.89112816	2	3.30043
P31000	RQVDQLTNDK	0.99430728	2	3.02392
P31000	SLYSSSPGGAYVTR	1.031387	2	2.86248
P31000	TNEKVELQELNDR	0.95541939	2	3.34615
P31000	VELQELNDR	0.76368442	2	2.99457
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**1.48004582**	**0.00023**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.14847321	2	5.95288
P31044	LYTLVLTDPDAPSR	1.8344271	2	4.93028
P31044	VDYGGVTVDELGK	0.8272559	2	4.82221
P31044	VLTPTQVMNRPSSISWDGLDPGK	1.9726613	3	4.78184
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.49054155	2	5.12574
P31044	YVWLVYEQEQPLNCDEPILSNK	1.52604074	2	5.61372
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.2405544**	**0.99926**	**18**
P31210	DELLTSLGK	1.2872969	2	2.79549
P31210	DIEALNK	1.29906366	1	2.55823
P31210	EEMKDIEALNK	1.65638103	2	3.31761
P31210	ENFQIFDFSLTK	1.22654994	2	3.34563
P31210	HIDGAYVYR	1.2046026	2	2.71516
P31210	IKENFQIFDFSLTK	1.35579533	2	4.35307
P31210	LWSTDHDPEMVRPALER	1.11458994	2	2.4929
P31210	NEHEVGEAIR	1.15266862	1	2.908
P31210	NPLWVNVSSPPLLK	1.56743765	2	4.37356
P31210	NPLWVNVSSPPLLKDELLTSLGK	1.52005548	3	4.9156
P31210	QLEVILNKPGLK	0.8033538	2	3.41556
P31210	REEIFYCGK	1.18139968	2	3.14858
P31210	RQLEVILNKPGLK	0.83014114	3	4.26637
P31210	SNLCATWEALEACK	1.15554572	2	4.40664
P31210	SNLCATWEALEACKDAGLVK	1.2374504	2	5.079
P31210	TAIDEGYR	1.10586104	2	2.57374

P31210	TQAQIVLR	1.38415037	2	3.02636
P31210	YKPVTNQVECHPYFTQTK	1.05181639	2	5.72203
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.00036591**	**0.13262**	**2**
P31230	GAEADQIIEYLK	1.95405838	2	2.98636
P31230	TVVSGLVNHVPLEQMQNR	0.88786747	3	3.53475
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.08833936**	**0.73258**	**6**
P31399	ANVDKPGLVDDFK	1.17692812	2	3.80185
P31399	IPVPEDKYTALVDAEEKEDVK	1.08321529	3	3.32943
P31399	NCAQFVTGSQAR	1.15987439	2	4.26891
P31399	NMIPFDQMTIDDLNEVFPETK	1.3780146	2	5.45486
P31399	SWNETFHTR	1.3087424	2	2.75927
P31399	YTALVDAEEKEDVK	0.96474242	2	3.77698
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.04631942**	**0.98898**	**5**
P32089	FIHDQTSSNPK	1.03617028	1	3.4529
P32089	GLSSLLYGSIPK	1.46465806	2	3.39515
P32089	NTLDCGVQILK	1.02827901	2	2.39629
P32089	SHGVLGLYR	1.0178191	1	2.02628
P32089	TQLQLDER	1.28741699	2	2.47254
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.07401598**	**0.98329**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	1.39784961	3	4.55885
P32198	GDTNPNIPKPTR	1.18231849	2	2.40292
P32198	MTALAQDFAVNLGPK	0.8644655	2	4.18235
P32198	SCTMESCNFVQAMMDPK	1.11723531	2	2.77267
P32198	TSPDAFIQLALQLAHYK	1.47342529	2	3.49923
P32198	YLESVRPLMK	1.0740466	2	2.32333
P32232	**CBS Cystathionine beta_synthase**	**1.18423161**	**9.9E-20**	**9**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	2.27156953	3	5.95485
P32232	ALGAEIVR	1.28759356	1	2.04501
P32232	CIIVMPEK	1.58980556	2	2.51768
P32232	FDSPESHVGVAWR	1.0830958	2	3.50131
P32232	NASNPLAHYDDTAEEILQQCDGK	1.66476375	2	5.66158
P32232	SNDDDSFAFAR	1.58378329	2	3.30077
P32232	VDMLVASAGTGGTITGIAR	1.73018643	2	4.62982
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	2.10744071	3	4.23577
P32232	VRPSDEVCK	1.15168319	3	3.75438
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.20373167**	**0.33634**	**11**
P32551	AVAFQNPQTR	1.24805783	2	3.35116
P32551	AVAQGNLSSADVQAAK	1.18040506	2	5.3487
P32551	GNNTTSLLSQSVAK	1.20395417	2	4.15908
P32551	IIENLHDVAYK	1.43157422	2	3.83772
P32551	ITSEELHYFVQNHFTSAR	1.43896856	3	4.04292
P32551	NALANPLYCPDYR	2.13289079	2	3.74444
P32551	RGNNTTSLLSQSVAK	1.16204767	2	3.30487
P32551	RWEVAALR	1.4199739	2	2.73014
P32551	SMTASGNLGHTPFLDEL	1.49452171	2	3.38016
P32551	TSAPGGVPLQPQELEFTK	1.0271097	2	4.04214
P32551	YENYNYLGTSHLLR	1.09642359	2	4.42947
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.54449231**	**9.9E-20**	**20**
P32755	AFEEEQALR	1.53138662	2	3.34721
P32755	DIAFEVEDCEHIVQK	1.82822345	2	4.08188
P32755	ENMDVLEELK	2.11857163	2	3.05278
P32755	EVVSHVIK	1.51003637	2	2.32575
P32755	FAVLQTYGDTTHTLVEK	1.59149717	2	5.25672

P32755	FLHFHSVTFWVGNAK	1.22756477	3	3.73515
P32755	FLPGFEAPTYK	1.63324987	2	2.7075
P32755	FWSVDDTQVHTEYSSLR	1.27331373	2	5.84082
P32755	GMEFLAVPSSYYR	2.30121376	2	3.28155
P32755	GNLTDLETNGVR	1.40520521	2	3.83297
P32755	HNHQGFGAGNFNSLFK	1.01392886	3	4.91846
P32755	ILVDYDEK	1.46792147	2	2.32865
P32755	IVFVLCSALNPWNK	1.68072828	2	2.96899
P32755	IVREPWVEEDKFGK	2.38716361	3	4.96986
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	2.52847868	3	7.34228
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK+Oxidation(20	2.63832631		
P32755	MGFEPLAYK	1.69723987	2	2.64896
P32755	SIVVANYEESIK	1.27620122	2	4.23279
P32755	SQIQEYVDYNGGAGVQHIALR	1.64929449	2	5.81498
P32755	TEDIITTIR	1.29976454	2	3.30782
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.00684484**	**0.98311**	**2**
P33124	ALRPTIFPVVPR	1.17795902	2	3.02346
P33124	IENIYIR	1.00669289	2	2.80915
P33273	**CP255 Cytochrome P450 2C55**	**0.92023717**	**0.41597**	**2**
P33273	FDYKDENFLNLMEK	0.91576338	3	4.88464
P33273	NFAEIK	1.45516058	1	1.90921
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.18371662**	**0.39542**	**26**
P34058	ADLINNLGTIAK	0.96691515	2	4.08765
P34058	EDQTEYLEER	1.10161861	2	3.55983
P34058	EGLELPEDEEEK	0.83329183	2	2.51252
P34058	EGLELPEDEEEKK	1.1066826	2	2.56271
P34058	EGLELPEDEEEKKK	1.43127632	2	3.1537
P34058	ELISNASDALDK	1.0996398	2	3.6059
P34058	FYEAFSK	1.40924616	1	1.95922
P34058	GVVDSEDLPLNISR	1.20725142	2	4.80619
P34058	HFSVEGQLEFR	1.25694561	2	2.66939
P34058	HLEINPDHPIVETLR	1.10046782	2	4.58497
P34058	HSQFIGYPITLYLEK	1.85501171	2	3.66626
P34058	IDIIPNPQER	1.03503311	2	3.05708
P34058	KHLEINPDHPIVETLR	1.30623193	2	4.83644
P34058	LGIHEDSTNR	1.21620809	2	2.90844
P34058	NPDDITQEEYGEFYK	0.99046885	2	4.96354
P34058	RAPFDLFENK	1.36427835	2	3.04066
P34058	RAPFDLFENKK	0.80349286	2	2.52583
P34058	SIYYITGESK	0.85893484	2	3.19449
P34058	SLTNDWEDHLAVK	1.15245959	2	4.32713
P34058	TLTLVDTGIGMTK	1.25291168	2	4.27911
P34058	TLTLVDTGIGMTK+Oxidation(10	1.77469366		
P34058	VILHLKEDQTEYLEER	1.35996971	3	4.04589
P34058	YESLTDPSK	1.16594231	1	2.70948
P34058	YESLTDPSKLDSGK	1.24717115	2	3.88405
P34058	YHTSQSGDEMTSLSEYVSR	1.33780693	2	5.48955
P34058	YIDQEELNK	2.00776547	2	3.48696
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.19790982**	**0.64223**	**7**
P34064	AIGSASEGAQSSLQEVYHK	0.99206795	2	4.51446
P34064	EELEEVIKDI	1.03335849	2	2.5477
P34064	GVNTFSPEGR	1.32438621	2	3.08947
P34064	ITSPLMEPSSIEK	1.17899092	2	2.61133
P34064	LNATNIELATVQPGQNFHMFTK	1.68049901	3	3.44823
P34064	SSLIILK	1.30186603	2	2.39765
P34064	STTLKEAIKSSLIILK	1.0231754	2	2.3154

P34067	**PSB4 Proteasome subunit beta type_4**	**1.11049106**	**0.85725**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.70771307	2	3.13328
P34067	TQNPMVTGTSVLGVK	1.03667427	2	3.35656
P34067	VNDSTMLGASGDYADFQYLK	1.51884608	2	4.49448
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.32299968**	**0.17059**	**2**
P35171	GGTSDALLYR	1.2167088	2	3.41543
P35171	LFQEDNGMPVHLK	1.32654587	2	4.38558
P35213	**1433B 14_3_3 protein beta/alpha**	**1.01813529**	**0.00821**	**7**
P35213	AVTEQGHELSNEER	1.22740532	2	4.48909
P35213	EKIEAELQDICSDVLELLDK	1.68994637	3	4.98565
P35213	QTTVSNSQQAYQEAFEISK	1.07635992	2	5.46302
P35213	TAFDEAIAELDTLNEESYK	0.99298813	2	4.81657
P35213	YDDMAAAMK	3.65356724	2	3.09257
P35213	YLILNATHAESK	1.59495905	2	3.58558
P35213	YLSEVASGDNK	0.95312008	2	3.04129
P35278	**RAB5C Ras_related protein Rab_5C**	**1.06684609**	**0.96502**	**4**
P35278	FEIWDTAGQER	0.87339588	2	3.16344
P35278	GVDLQESNPASR	1.23032083	2	2.70709
P35278	LVLLGESAVGK	1.30412787	2	2.75
P35278	NEPQNAAGAPGR	1.0518571	2	2.99653
P35427	**RL13A 60S ribosomal protein L13a**	**1.25772231**	**0.13946**	**2**
P35427	CEGINISGNFYR	1.40384493	2	3.14189
P35427	YQAVTATLEEK	1.24724414	2	3.1429
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**1.24571761**	**0.97637**	**2**
P35434	AQSELSGAADEAAR	1.30760654	2	4.66613
P35434	IEANEALVK	1.1215258	2	2.84138
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.48079986**	**0.00011**	**7**
P35435	GLCGAIHSSVAK	1.35486082	2	3.69161
P35435	HLIIGVSSDR	1.24228692	2	3.0661
P35435	NASDMIDK	1.64747744	2	2.35038
P35435	NDMAALTAAGK	1.49662098	2	3.94464
P35435	NDMAALTAAGK+Oxidation(2	1.7586923		
P35435	THSDQFLVSFK	0.83650092	1	3.03538
P35435	VYGTGSLALYEK	1.87722601	2	3.10062
P35559	**IDE Insulin_degrading enzyme**	**1.22764436**	**0.55611**	**4**
P35559	AIEDMTEEAFQK	1.0154441	2	3.13722
P35559	DREVNAVDSEHEK	1.25791035	3	3.57133
P35559	SNPGHYLGHLIGHEGPGSLLSELK	0.39694635	3	3.30114
P35559	YTLETRPNQEGIDVR	1.25852886	2	2.53031
P35565	**CALX Calnexin**	**0.87990973**	**0.99865**	**11**
P35565	AEEDEILNR	1.29449745	2	2.69464
P35565	EIEDPEDRKPEDWDERPK	1.80961188	3	3.33168
P35565	GSLSGWILSK	2.31059254	2	2.50193
P35565	KIPNPDFFEDLEPFR	1.09056477	3	4.29534
P35565	NKGDEEEEEEKLEEK	0.86656899	3	5.05456
P35565	TDAPQPDVK	1.10683657	2	2.38776
P35565	TDAPQPDVKDEEGKEEEK	0.91818331	3	4.36467
P35565	TSELNLDQFHDK	0.94956835	2	3.6907
P35565	VVDDWANDGWGLK	0.79723626	2	4.23063
P35565	VVDDWANDGWGLKK	0.56715615	2	2.80435
P35565	WEVDEMKETK	1.18091554	2	2.8193
P35571	**GPDM Glycerol_3_phosphate dehydrogenase_ mitochondrial**	**1.12202793**	**0.28069**	**2**
P35571	AITNLDVEQYR	0.49041928	2	2.71551

P35571	KQEELETATR	1.49286903	2	2.33559
P35704	**PRDX2 Peroxiredoxin_2**	**1.12209275**	**0.15763**	**5**
P35704	EGGLGPLNIPLLADVTK	1.21011577	2	3.47604
P35704	KEGGLGPLNIPLLADVTK	1.22919001	2	4.86094
P35704	NDEGIAYR	1.24348563	1	1.95971
P35704	QITVNDLPVGR	1.03664655	2	3.03412
P35704	SLSQNYGVLK	1.00400256	2	2.47037
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.93744948**	**0.02656**	**5**
P35738	AAVEQVPVEPYK	0.79234902	2	2.42939
P35738	GLLLSCIEDKNPCIFFEPK	1.5264669	2	3.66665
P35738	MNLFQSITSALDNSLAK	0.6734114	2	3.59215
P35738	SGDLFNCGSLTIR	0.72088674	2	3.01778
P35738	VCGYDTPFPHIFEPFYIPDK	1.23307063	3	3.49018
P35815	**PPM1B Protein phosphatase 1B**	**1.30842504**	**0.47359**	**2**
P35815	IQNAGGSVMIQR	1.30848402	2	2.82335
P35815	SGFALEPSVENVK	1.14469852	2	3.62746
P36201	**CRIP2 Cysteine_rich protein 2**	**0.8179628**	**0.4827**	**3**
P36201	ASSVTTFTGEPNMCPR	0.97369991	2	3.68081
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	0.7445164	3	6.47508
P36201	GVNTGAVGSYIYDKDPEGTVQP	0.85309427	2	4.31891
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**0.82609225**	**0.3826**	**11**
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.34270655	3	3.61061
P36365	ASLYNSVVSNSSK	0.65867058	2	2.92251
P36365	CCLEEGLEPTCFER	0.56824292	2	4.28105
P36365	FTEHVEEGR	0.86951512	2	3.02412
P36365	HSGFGLCYCK	1.09195246	2	3.24699
P36365	NLLPTPVVSWLISK	0.92777144	2	2.49186
P36365	SCDLGGLWR	0.79981464	2	2.76923
P36365	TQLREPVLNDELPGR	0.82637648	3	4.57949
P36365	VAIVGAGVSGLASIK	2.03128168	2	2.82332
P36365	VEDGQASLYK	0.92794722	2	3.46588
P36365	VLVVGMGNSGTDIAVEASHLAK	0.92865983	2	4.55916
P36506	**MP2K2 Dual specificity mitogen_activated protein kinase kinase 2**	**1.63348322**	**0.25576**	**2**
P36506	ISELGAGNGGVVTK	1.87994404	2	2.36098
P36506	KLEELDLDEQQR	1.48391526	2	3.03969
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.25960169**	**0.33396**	**8**
P36511	ANIIAWALAQIPQK	1.14945223	3	5.48749
P36511	FVNVWTYELPR	0.95953074	2	3.6615
P36511	FVTFPTSFSSHDLENFFTR	1.39863284	2	4.44904
P36511	GHEVTVLRPSAFVFLDPK	0.72591962	3	3.96885
P36511	IILEELVQK	1.23343462	2	3.53459
P36511	NAMWLSTIHHDQPTKPLDR	0.97559058	3	3.41859
P36511	SDLLNALEEVIDNPFYK	0.78631766	3	5.33736
P36511	TLGRPTTLAEIMGK	1.55997581	2	3.1035
P36536	**SAR1A GTP_binding protein SAR1a**	**1.32958706**	**0.36915**	**2**
P36536	IDRTDAISEEK	1.18688667	2	2.4917
P36536	VELNALMTDETISNVPILILGNK	1.61112618	3	5.66942
P36953	**AFAM Afamin**	**1.2281421**	**0.44999**	**2**
P36953	FTDSENVCQER	1.22724357	2	2.99725
P36953	SLAMVQQECK	1.79396705	2	2.75056
P36972	**APT Adenine phosphoribosyltransferase**	**1.23617887**	**0.00039**	**2**
P36972	IDYIAGLDSR	0.92358706	2	3.04337
P36972	SFPDFPIPGVLFR	1.23627584	2	3.25029
P37397	**CNN3 Calponin_3**	**1.13381783**	**0.91654**	**5**

P37397	AGQSVIGLQMGTNK	1.12796473	2	3.37461
P37397	LTLQPVDNSTISLQMGTNK	0.88399612	2	2.95356
P37397	MQTDKPFDQTTISLQMGTNK	1.25499664	3	3.55222
P37397	VNESSLNWPQLENIGNFIK	1.01416852	2	3.15147
P37397	YDQQAEEDLR	1.19445431	2	3.15414
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.19005103**	**0.53328**	**8**
P38650	DFPLNDLLSATELDKIR	1.62574673	2	2.38742
P38650	ILDDDTIITTLENLK	1.27501238	2	2.50648
P38650	QLQNISQAAAAGGAK	1.00491451	2	3.37664
P38650	VLLTTQGVDMISK	1.20794868	2	2.663
P38650	VLRPQVTAVAQQNQGEAPEPQDMK	1.18067284	3	5.4378
P38650	VQGLTVEQAEAVAR	1.17917541	2	3.27985
P38650	VQVALEELQDLK	1.35198445	2	3.02736
P38650	VTDFGDKVEDPTFLNQLQSGVNR	1.26429263	3	4.16205
P38652	**PGM1 Phosphoglucomutase_1**	**1.23558875**	**0.62228**	**17**
P38652	ADNFEYSDPVDGSISK	0.92118751	2	4.82459
P38652	AIGGIILTASHNPGGPNGDFGIK	1.18269136	2	5.7588
P38652	FFGNLMDASK	1.30886939	2	2.51639
P38652	FNISNGGPAPEAITDK	1.15847028	2	4.30233
P38652	INQDPQVMLAPLISIALK	1.14566373	3	4.60659
P38652	KQRVEDILK	0.98270786	1	2.02672
P38652	LSGTGSAGATIR	1.75624479	2	3.48021
P38652	LVIGQNGILSTPAVSCIIR	1.58581603	2	4.08125
P38652	NIFDFNALK	1.20457407	2	2.92314
P38652	QEATLVVGGDGR	1.27534714	2	3.20018
P38652	QQFDLENK	0.90802657	1	2.12824
P38652	SGEHDFGAAFDGDGDR	1.11832888	2	4.4598
P38652	SGEHDFGAAFDGDGDRNMILGK	1.56932957	3	3.7608
P38652	TIEEYAICPDLK	1.25802093	2	4.43188
P38652	TQAYPDQKPGTSGLR	0.9924518	2	3.4881
P38652	VFQGNANYAENFIQSIVSTVEPALR	1.33016314		
P38652	YDYEEVEAEGANK	1.0304275	2	5.18105
P38656	**LA Lupus La protein homolog**	**1.37837296**	**0.16619**	**2**
P38656	ITDDQQESLNK	2.14055144	2	4.19315
P38656	LDEGWVPLETMIK	1.31194845	2	2.99039
P38659	**PDIA4 Protein disulfide_isomerase A4**	**0.84455699**	**0.99874**	**22**
P38659	DLGLSESGEDVNAAILDESGKK	1.07516814	2	5.15013
P38659	DNDPPIAVAK	1.07511317	2	2.40049
P38659	EVSQPDWTPPPEVTLTLTK	0.97712726	2	3.55213
P38659	FDVSGYPTIK	0.99956312	2	3.49007
P38659	FDVSGYPTLK	0.99956312	2	3.49007
P38659	FHHTFSTEIAK	1.16871958	3	3.50149
P38659	FIDEHATK	1.13282752	2	2.46554
P38659	FIDEHATKR	0.84436743	2	2.55172
P38659	GQAVDYDGSR	0.99823084	2	2.66653
P38659	GRPFDYNGPR	1.22236883	2	2.87645
P38659	IDATSASMLASK	1.04525001	2	3.97559
P38659	IDATSASMLASK+Oxidation(7	0.78107942		
P38659	KGQAVDYDGSR	2.22637049	2	2.93026
P38659	MDATANDITNDR	0.71354681	2	3.95544
P38659	MHVMDVQGSTEASAIK	1.203724	2	4.62288
P38659	MHVMDVQGSTEASAIKDYVVK	1.05192927	3	4.59957
P38659	RFDVSGYPTLK	1.14731508	2	3.28803
P38659	RSPPIPLAK	2.01600095	2	2.40611
P38659	TFDAIVMDPK	0.93131411	2	3.53451
P38659	VDATEQTDLAK	1.25443322	2	4.12692
P38659	VEGFPTIYFAPSGDK	1.3202729	2	3.44627

P38659	YGIVDYMVEQSGPPSK	1.18581862	2	5.10871
P38718	**BR44 Brain protein 44**	**1.16661115**	**0.35977**	**2**
P38718	LRPLYNHPAGPR	1.17275863	2	2.82985
P38718	VELLLPK	0.66003388	1	2.22143
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**1.00131247**	**0.54656**	**5**
P38918	EEHFNGIALVEK	1.34441182	2	2.53456
P38918	FYAFNPLAGGLLTGR	1.40755126	2	4.63171
P38918	MDVTSSSASVR	0.91958871	2	3.58634
P38918	RMDVTSSSASVR	0.97654294	2	3.85364
P38918	TTYGPTAPSMISAAVR	1.00664419	2	3.96068
P38983	**RSSA 40S ribosomal protein SA**	**1.26563596**	**0.00014**	**8**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.46586626	3	5.86294
P38983	AIVAIENPADVSVISSR	1.51887685	2	4.80864
P38983	FAAATGATPIAGR	0.26269457	2	3.16064
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.40034536	3	3.62384
P38983	FTPGTFTNQIQAAFR	1.32265705	2	4.63599
P38983	KSDGIYIINLK	4.03886817	2	3.52242
P38983	SDGIYIINLK	1.31916644	2	3.02165
P38983	YVDIAIPCNNK	1.16678252	2	3.55075
P39032	**RL36 60S ribosomal protein L36**	**1.50679324**	**0.38797**	**2**
P39032	EELSNVLAAMR	1.42639494	2	2.40552
P39032	KREELSNVLAAMR	1.6814229	3	3.50914
P39052	**DYN2 Dynamin_2**	**1.2538252**	**0.43863**	**2**
P39052	ESSLILAVTPANMDLANSDALK	1.6004912	2	2.36734
P39052	NLVDSYVAIINK	1.10446444	2	3.11987
P40112	**PSB3 Proteasome subunit beta type_3**	**1.29213503**	**0.00789**	**2**
P40112	FGIQAQMVTTDFQK	1.99471941	2	3.43311
P40112	FGPYYTEPVIAGLDPK	1.27026645	2	3.09585
P40307	**PSB2 Proteasome subunit beta type_2**	**1.05980459**	**0.23616**	**3**
P40307	FILNLPTFSVR	2.08572806	2	3.28235
P40307	NGYELSPTAAANFTR	1.16530201	2	4.02458
P40307	VIDKDGIHNLENITFTK	1.04478845	2	4.03379
P41034	**TTPA Alpha_tocopherol transfer protein**	**2.13335355**	**1.5E-08**	**4**
P41034	AECPELSADLHPR	2.05924445	2	2.98702
P41034	AQEEGVPETPQPLTDAFLLR	2.2791408	2	3.71279
P41034	QLNEQPDHSPLVQPGLAELR	1.41936222	3	4.05484
P41034	VSLITSELIVQEVETQR	1.61991426	2	2.9696
P41123	**RL13 60S ribosomal protein L13**	**1.18215228**	**0.0009**	**3**
P41123	LATQLTGPVMPIR	3.13544861	2	3.12273
P41123	STESLQANVQR	1.17997826	2	3.88965
P41123	VDTWFNQPAR	1.22897606	2	3.46971
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**0.94002984**	**0.98233**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.63211706	2	4.24839
P41498	IELLGSYDPQK	0.95825775	2	3.22101
P41498	LVTDENVSDNWR	0.89871046	2	3.76149
P41542	**USO1 General vesicular transport factor p115**	**1.28749787**	**0.19539**	**14**
P41542	AWFEVGDENPGWSAQK	1.04891485	2	4.66609
P41542	CQNEQLQTAVTQQASQIQQHK	1.03011148	3	5.30596
P41542	EQDDLLVLLADQDQK	1.6014406	2	2.53703
P41542	GVMGGQSAGPQHTEAETIQK	1.32290919	2	4.35896
P41542	IVAFENAFER	1.15278797	2	3.05438
P41542	LQTENSELQQR	1.20328926	2	3.13897
P41542	LREEIEELR	1.13776581	2	2.72273
P41542	NNNSNQNFFK	0.8793275	2	2.71611
P41542	QLGPPVQQIILVSPMGVSK	2.08177063	2	4.0115

P41542	SHQVLLQSQLAEK	0.65509904	2	2.95188
P41542	SQLCSQSLEITR	1.17505168	2	3.36524
P41542	SVPVEGESELVTAAK	1.0742046	2	4.15425
P41542	TLEQHDNIVTHYK	1.00301096	2	3.904
P41542	VLVSPTNPPGATSSCQK	1.44689862	2	3.92053
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**0.73887273**	**0.00034**	**20**
P41562	ATDFVVPGPGK	1.01834783	2	3.63243
P41562	CATITPDEK	1.53877062	2	2.72004
P41562	DIFQEIYDK	1.6042234	1	2.39727
P41562	DLAACIK	0.77943715	1	1.90825
P41562	FKDIFQEIYDK	1.20587852	3	4.39488
P41562	GQETSTNPIASIFAWSR	1.33155048	2	4.79303
P41562	IHGGSVVEMQGDEMTR	1.62903581	2	5.30362
P41562	KIHGGSVVEMQGDEMTR	1.12372439	2	3.69044
P41562	LIDDMVAQAMK	1.02932482	2	4.45949
P41562	LIDDMVAQAMK+Oxidation(4	1.45749358		
P41562	LIDDMVAQAMK+Oxidation(9	0.88724053		
P41562	LILPYVELDLHSYDLGIENR	2.6772483	2	4.86949
P41562	LVTGWVKPIIIGR	1.09559081	2	3.24898
P41562	SDYLNTFEFMDK	1.53924966	2	4.46038
P41562	SDYLNTFEFMDK+Oxidation(9	3.67795002		
P41562	SEGGFIWACK	1.00044707	2	3.30598
P41562	SIEDFAHSSFQMALSK	1.08173558	2	5.08409
P41562	TVEAEAAHGTVTR	0.73114202	2	3.81893
P41562	VEITYTPK	1.05398911	2	2.45448
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.55384705	3	3.82442
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.24410287**	**0.03581**	**4**
P42123	DYSVTANSK	1.9597947	2	2.54543
P42123	IVADKDYSVTANSK	3.1686541	2	3.62665
P42123	SLADELALVDVLEDK	1.43931432	2	3.6337
P42123	VIGSGCNLDSAR	1.21516496	2	3.80732
P42228	**STAT4 Signal transducer and activator of transcription 4**	**0.97048884**	**0.4283**	**2**
P42228	FHSVEPYNK	1.87917012	1	1.91816
P42228	GDKGYVPSVFIPISTIR	0.92610546	2	2.73883
P42667	**SC11A Signal peptidase complex catalytic subunit SEC11A**	**1.1759308**	**0.78515**	**3**
P42667	GDLLFLTNR	1.17987889	2	2.43788
P42667	MLSLDFLDDVR	1.0013916	2	3.34428
P42667	VGEIVVFR	1.1809633	2	3.27065
P42676	**NEUL Neurolysin_ mitochondrial**	**1.04767346**	**0.00515**	**3**
P42676	AELGALPDDFIDSLEK	1.82517315	2	3.32762
P42676	NLILKPGGSLDGMDMLQNFLQR	1.49961545	3	4.1433
P42676	NLNEDDTSLVFSK	0.7669864	2	3.38772
P42930	**HSPB1 Heat shock protein beta_1**	**1.40974671**	**0.51072**	**2**
P42930	AQIGGPESEQSGAK	1.40885383	2	3.39337
P42930	VSLDVNHFAPEELTVK	2.70051225	2	2.58121
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.21677057**	**0.47231**	**10**
P42932	AIAGTGANVIVTGGK	1.23959547	2	2.75237
P42932	AVDDGVNTFK	1.48887515	2	2.51088
P42932	ELEVQHPAAK	1.63609212	2	2.85769
P42932	GEENLMDAQVK	1.31220374	2	3.58777
P42932	GSTDNLMDDIER	1.46168664	2	2.76197
P42932	HEKEDGAISTIVLR	5.11016324	2	2.92369
P42932	HFSGLEEAVYR	1.25056992	2	2.65739
P42932	NVGLDIEAEVPAVK	1.30090179	2	4.01113

P42932	QITSYGETCPGLEQYAIK	1.03080569	2	4.87195
P42932	TAEELMNFSK	1.14266954	2	2.58773
P43244	**MATR3 Matrin_3**	**1.15716042**	**0.14218**	**5**
P43244	ITPENLPQILLQLK	1.72791547	2	3.42861
P43244	NTHCSSLPHYQK	1.14866802	2	2.31662
P43244	TEEGPTLSYGR	1.07066615	2	2.55898
P43244	TENPAEGKEQEEK	1.03650887	2	3.38239
P43244	YQLLQLVEPFGVISNHLILNK	1.17820688	3	3.76019
P43274	**H14 Histone H1.4**	**1.3480857**	**0.98347**	**4**
P43274	ALAAAGYDVEK	1.35796985	2	3.86132
P43274	ALAAAGYDVEKNNSR	0.6027291	2	3.29513
P43274	SGVSLAALK	0.96206608	2	2.99182
P43274	SGVSLAALKK	0.79626463	2	2.68434
P43278	**H10 Histone H1.0**	**0.83841492**	**0.97165**	**2**
P43278	VGENADSQIK	0.83781972	2	3.4397
P43278	YSDMIVAAIQAEK	1.02410143	2	4.47286
P43883	**PLIN2 Perilipin_2**	**1.3274757**	**0.28049**	**2**
P43883	DSVASTVSGVVDK	1.32787719	2	2.35521
P43883	LEPQIAVANTYACK	0.39878407	2	3.94471
P45591	**COF2 Cofilin_2**	**1.47389489**	**0.11537**	**2**
P45591	HEWQVNGLDDIKDR	1.56390211	3	4.85484
P45591	QILVGDIGDTVEDPYTSFVK	1.45554431	2	3.86046
P45592	**COF1 Cofilin_1**	**1.36192656**	**0.80747**	**5**
P45592	EILVGDVGQTVDDPYTTFVK	1.12469815	2	5.11072
P45592	HELQANCYEEVK	1.08432948	2	3.83019
P45592	HELQANCYEEVKDR	1.40380759	3	5.62793
P45592	MLPDKDCR	1.37961982	2	2.33667
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.23552198	3	4.80309
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.31136583**	**0.12876**	**4**
P45878	GWDQGLLGMCEGEK	1.48882316	2	4.3016
P45878	KGDVLHMHYTGK	0.58753001	2	3.8757
P45878	KLVIPSELGYGER	1.58787067	2	2.74943
P45878	LVIPSELGYGER	1.31123707	2	2.79427
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.05104338**	**0.21284**	**17**
P45953	AMVENGGLVTSNPLR	0.895096	2	4.05193
P45953	AMVENGGLVTSNPLRV	1.17902864	2	4.19659
P45953	ASNTSEVYFDGVK	1.23210275	2	3.60534
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.99240827	3	5.12188
P45953	ENMASLQSNPQQQELFR	1.35554889	2	4.24987
P45953	FFEEVNDPAK	0.86459653	2	3.02512
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	0.83800705	3	5.58398
P45953	GIVNEQFLLQR	1.03670254	2	3.14125
P45953	IFEGTNDILR	1.76439092	2	3.14642
P45953	NDSLEKVEEDTLQGLK	1.28255581	2	3.64011
P45953	NPLGNVGLLIGEASK	1.6455587	2	3.70709
P45953	SFGGVTHGLPEK	1.44756287	2	2.60605
P45953	SFGGVTHGLPEKK	1.11854261	2	2.95757
P45953	SGELAVQALEQFATVVEAK	1.25780419	3	4.12116
P45953	SLSEGYPTAQHEK	1.30731917	2	3.42979
P45953	TGIGSGLSLSGIVHPELSR	1.19370635	3	4.60682
P45953	VEEDTLQGLK	0.77617467	2	2.76958
P46061	**RAGP1 Ran GTPase_activating protein 1**	**1.71136398**	**0.00599**	**2**
P46061	TAVLDAIDALMK	1.71756484	2	3.1766
P46061	VINLNDNTFTEK	1.64728272	2	2.51227
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.04096986**	**0.19215**	**4**

P46418	AILNYIATK	0.45840606	2	3.29148
P46418	SDGSLMFEQVPMVEIDGMK	1.07071172	2	4.38341
P46418	SHGQDYLVGNK	0.92113603	2	3.63771
P46418	VSNLPTVK	1.06321946	2	2.76883
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.78624724**	**0.21021**	**3**
P46425	ALPGHLKPFETLLSQNQGGK	0.78694022	2	4.16265
P46425	FEDGDLTLYQSNAILR	0.73802817	2	4.53322
P46425	MLLADQGQSWK	1.13058823	2	2.50915
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**0.91298871**	**0.01045**	**24**
P46462	AIANECQANFISIK	1.12899292	2	3.70608
P46462	EDEEESLNEVGYDDIGGCR	9.18904942	2	5.30883
P46462	ELQELVQYPVEHPDK	1.23184591	2	4.56693
P46462	ETVVEVPQVTWEDIGGLEDVK	0.95781293	2	4.47217
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.75752251	2	4.11236
P46462	EVDIGIPDATGR	0.99265153	2	2.73949
P46462	GDDLSTAILK	1.12409469	2	3.06045
P46462	GGNIGDGGGAADR	1.8697344	2	3.05514
P46462	GILLYGPPGTGK	1.05886999	2	2.85287
P46462	IVSQLLTLMDGLK	1.9876486	2	3.5126
P46462	KYEMFAQTLQQSR	1.40697598	2	4.05685
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	2.31286302	3	6.14338
P46462	LAGESESNLRKAFEEAEK	1.00392999	2	2.57452
P46462	LDQLIYIPLPDEK	1.19908235	2	4.50735
P46462	LEILQIHTK	0.81690888	2	2.82824
P46462	LGDVISIQPCPDVK	0.86595835	2	3.96911
P46462	LIVDEAINEDNSVVSLSQPK	1.29280308	2	5.45228
P46462	MDELQLFR	1.28087279	2	3.19064
P46462	MTNGFSGADLTEICQR	0.70396774	2	4.46241
P46462	NAPAIIFIDELDAIAPK	1.42745022	2	4.93198
P46462	QTNPSAMEVEEDDPVPEIR	0.83010523	2	4.39636
P46462	RSVSDNDIR	1.50079598	2	2.60967
P46462	VINQILTEMDGMSTK	1.4764416	2	4.59131
P46462	WALSQSNPSALR	1.86641111	2	3.45111
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**1.7708223**	**0.00061**	**5**
P46664	FIEDELQIPVK	1.11314649	2	3.15279
P46664	LDILDMFTEIK	1.75465792	2	3.26603
P46664	MCDLVSDFDGFSER	2.63596482	2	3.66236
P46664	VGIGAFPTEQDNEIGELLQTR	1.69351215	2	4.38233
P46664	VVDLLAQDADIVCR	2.40524129	2	3.51888
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.22516796**	**0.19399**	**4**
P46720	ESEHTDVHGSPQVENDGELK	1.69596184	3	3.74553
P46720	GIGETPIVPLGISYIEDFAK	1.43129654	2	3.80164
P46720	GVQHQLHVESK	0.69816843	2	3.02143
P46720	SENSPLYIGILEMGK	1.47095899	2	3.43931
P46844	**BIEA Biliverdin reductase A**	**0.7789026**	**0.99241**	**4**
P46844	FGVVVVGVGR	1.20556549	2	2.83465
P46844	GLLSWIEEK	1.26844417	2	2.5176
P46844	LLDQVSAEDLAAEK	0.46698483	2	4.65823
P46844	MTVQLETQNK	0.97292009	2	2.49603
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.23325775**	**0.67365**	**10**
P46953	AQGSVALSVTQDPACK	1.22106581	2	4.52156
P46953	ASFQPPVCNK	1.28711751	2	2.55939
P46953	DLGTQLAPIIQEFFHSEQYR	1.24881312	2	3.54777
P46953	FANTMGLVIER	1.24380043	2	3.56083
P46953	METELDGLR	1.02866174	2	2.74081

P46953	QDVDVWLWQLEGSSK	1.38879446	2	2.34734
P46953	QGEIFLLPAR	1.39412625	2	2.76677
P46953	RMETELDGLR	1.01493636	2	2.48808
P46953	TGKPNPDQLLK	1.23511126	3	3.58246
P46953	YYVGDTEDVLFEK	1.30715381	2	3.54466
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.17555896**	**0.02087**	**7**
P46978	FESVIHEFDPYFNYR	1.36466922	2	2.34324
P46978	FGQVYTEAK	1.59033906	2	2.72455
P46978	FHNWFDDR	1.47256588	2	2.54638
P46978	FYSLLDPSYAK	1.54963691	2	2.89661
P46978	NLDISRPDKK	1.42635981	2	2.41254
P46978	VGQAMASTEEK	0.86797057	2	3.17066
P46978	VGQAMASTEEK+Oxidation(4	1.7659658		
P47198	**RL22 60S ribosomal protein L22**	**1.43465123**	**0.09014**	**2**
P47198	AGNLGGGVVTIER	1.0707122	2	3.06414
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.9934935	3	5.5319
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.23323544**	**0.08091**	**4**
P47875	GFGFGQGAGALVHSE	1.51077754	2	3.15801
P47875	GLESTTLADKDGEIYCK	1.57807953	2	5.25659
P47875	HEEAPGHRPTTNPNASK	1.18553636	2	3.63392
P47875	NLDSTTVAVHGEEIYCK	1.20649699	2	4.72147
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.00697054**	**0.75128**	**3**
P47942	FQMPDQGMTSADDFFQGTK	0.79875876	2	4.07667
P47942	GLYDGPVCEVSVTPK	1.09183635	2	3.56534
P47942	SITIANQTNCPLYVTK	1.00430988	2	3.4281
P48004	**PSA7 Proteasome subunit alpha type_7**	**0.96476467**	**0.99906**	**2**
P48004	NYTDDAIETDDLTIK	0.94691059	2	4.54366
P48004	YVAEIEKEKEENEK	1.17785553	2	5.43228
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**1.42742597**	**0.02431**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	2.16784483	3	5.67617
P48024	TLTTVQGIADDYDK	1.36804406	2	3.66818
P48037	**ANXA6 Annexin A6**	**0.90253874**	**0.88395**	**20**
P48037	AANDFNPDADAK	1.0753059	2	3.55206
P48037	AINEAYKEDYHK	1.13162393	2	3.39675
P48037	ALIEILATR	1.2784997	2	3.21706
P48037	ALLALCGGED	1.78058738	1	2.15071
P48037	CLIEILASR	0.88019697	2	2.65755
P48037	DAFVAIVQSVK	1.30989422	2	3.82655
P48037	DLESDIIGDTSGHFQK	1.25355472	2	4.43676
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.0151383	2	5.15064
P48037	GELSGDFEK	1.51344573	1	2.18069
P48037	GFGSDKESILELITSR	1.12028783	2	4.27583
P48037	GIGTDEATIIDIITQR	0.99119143	2	4.26473
P48037	GSVHDFADFDANQDAEALYTAMK	1.06264364	3	4.13674
P48037	QRQEICQSYK	0.97953264	2	3.19726
P48037	SEIDLLNIR	1.57526632	2	3.07096
P48037	SEISGDLAR	1.27594068	2	2.34455
P48037	SELDMLDIR	0.65884348	2	2.96092
P48037	SLEDALSSDTSGHFK	1.26246358	2	3.67535
P48037	TNEQIHQLVAAYK	0.93152672	2	4.02279
P48037	TNYDIEHVIK	0.90083845	2	3.0886
P48037	TTGKPIEASIR	1.6904563	2	2.53742
P48500	**TPIS Triosephosphate isomerase**	**1.42625319**	**1.9E-11**	**15**
P48500	CLGELICTLNAAK	1.06987905	2	3.56666
P48500	CNVSEGVAQCTR	1.42272242	2	3.95579

P48500	DLGATWVVLGHSER	1.59205748	2	4.1648
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.36716661	4	5.94006
P48500	HIFGESDELIGQK	1.3439295	2	4.68053
P48500	IAVAAQNCYK	1.60494574	2	2.7012
P48500	IIYGGSVTGATCK	1.7290473	2	4.33989
P48500	LPADTEVVCAPPTAYIDFAR	1.96606518	2	4.41963
P48500	RHIFGESDELIGQK	1.30994886	2	4.41649
P48500	TATPQQAQEVHEK	1.18340015	2	3.63929
P48500	TATPQQAQEVHEKLR	0.8233386	2	2.39976
P48500	VNHALSEGLGVIACIGEK	1.81540689	2	5.67491
P48500	VTNGAFTGEISPGMIK	1.39223662	2	4.8655
P48500	VVFEQTK	1.29945888	1	1.93335
P48500	VVLAYEPVWAIGTGK	1.28182035	2	4.53242
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.82240208**	**2.5E-05**	**4**
P48508	ASTLHLQTGNLLNWGR	0.63245491	3	4.01161
P48508	EFPDVLECTMSHAVEK	0.80234994	2	3.59297
P48508	INPDEREEMK	0.97655213	2	2.64371
P48508	TLNEWSSQISPDLVR	0.70826766	2	4.68486
P48675	**DESM Desmin**	**2.17662346**	**0.55465**	**3**
P48675	NISEAEEWYKSK	1.35481723	2	2.32562
P48675	TSGGAGGLGSLR	2.11482804	2	2.70108
P48675	VSDLTQAANK	4.63181165	2	2.983
P48679	**LMNA Prelamin_A/C**	**1.15119979**	**0.99978**	**19**
P48679	AAYEAELGDAR	1.80287735	2	2.36502
P48679	AQHEDQVEQYK	0.94294304	2	3.04657
P48679	AQHEDQVEQYKK	1.23972958	2	4.33551
P48679	GSHCSSSGDPAEYNLR	1.4799388	2	3.95042
P48679	IDSLSAQLSQLQK	1.05425309	2	3.16959
P48679	ITESEEVVSR	1.04796132	2	3.1554
P48679	LEAALGEAK	1.24668829	2	2.31631
P48679	LKDLEALLNSK	1.09708038	2	2.86412
P48679	LQEKEDLQELNDR	1.26416622	2	4.2282
P48679	MQQQLDEYQELLDIK	1.26187666	2	4.55441
P48679	NIYSEELR	1.11494775	1	2.05941
P48679	NSNLVGAAHEELQQSR	0.95458132	2	4.71077
P48679	SGAQASSTPLSPTR	0.94132506	2	3.79115
P48679	SLETENAGLR	2.07680404	2	2.86808
P48679	SVGGSGGGSFGDNLVTR	0.88791114	2	3.58402
P48679	TALINATGEEVAMR	2.12067588	2	3.57683
P48679	TLEGELHDLR	1.92264162	2	2.4925
P48679	TVLCGTCGQPADK	1.07011396	2	3.44474
P48679	VAVEEVDEEGK	1.10148693	2	3.1088
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.36993604**	**1.2E-09**	**30**
P48721	AQFEGIVTDLIK	1.30355014	2	3.72062
P48721	ASNGDAWVEAHGK	1.48530698	2	3.81592
P48721	DAGQISGLNVLR	2.1671472	2	2.75738
P48721	DDIENMVK	1.76733156	1	2.02243
P48721	EQQIVIQSSGGLSK	1.14567154	2	3.86301
P48721	EQQIVIQSSGGLSKDDIENMVK	1.59422418	2	4.52976
P48721	ERVEAVNMAEGIIHDTETK	1.302151	3	5.56512
P48721	ETAENYLGHTAK	1.38879401	2	3.1378
P48721	GAVVGIDLGTTNSCVAVMEGK	1.87533026	2	5.38531
P48721	LFEMAYK	1.27475068	2	2.30513
P48721	LLGQFTLIGIPPAPR	2.19092285	2	3.73202
P48721	MEEFKDQLPADECNK	1.3975034	2	4.60724
P48721	MEEFKDQLPADECNK+Oxidation(0	2.18257617		

P48721	MKETAENYLGHTAK	1.06929865	2	4.30801
P48721	MKETAENYLGHTAK+Oxidation(0	1.02577922		
P48721	NAVITVPAYFNDSQR	1.15454539	2	3.46472
P48721	QAVTNPNNTFYATK	1.62020161	2	3.80291
P48721	RETGVDLTK	0.82151803	2	2.32814
P48721	RYDDPEVQK	1.14200249	2	3.23068
P48721	RYDDPEVQKDTK	1.07873276	2	3.78626
P48721	SDIGEVILVGGMTR	1.12814291	2	3.98357
P48721	SQVFSTAADGQTQVEIK	1.02016236	2	4.60531
P48721	STNGDTFLGGEDFDQALLR	1.91085583	2	6.07848
P48721	TTPSVVAFTPDGER	1.02441362	2	3.39462
P48721	VEAVNMAEGIIHDTETK	0.76439346	2	4.57309
P48721	VINEPTAAALAYGLDK	3.77548875	2	3.88297
P48721	VLENAEGAR	1.05986411	2	3.09374
P48721	VQQTVQDLFGR	0.99743387	2	3.72915
P48721	YDDPEVQK	1.40598731	2	2.35081
P48721	YDDPEVQKDTK	1.31924426	2	2.74901
P48998	**INVO Involucrin**	**1.06296653**	**0.80527**	**2**
P48998	ELLDQRLDQELVNK	0.9833341	2	2.32528
P48998	HKLENLTQKEK	1.17006654	1	1.93864
P49025	**CTRO Citron Rho_interacting kinase**	**1.07432355**	**0.89559**	**2**
P49025	LEEQLEK	1.13562997	1	2.01041
P49025	LMMNQLEEDLVSARR+Oxidation(1	1.03204508		
P49134	**ITB1 Integrin beta_1**	**0.88550586**	**0.97335**	**3**
P49134	CNCQSHGIPASPK	0.95251964	2	3.34812
P49134	FCECDNFNCDR	0.91354259	2	3.36757
P49134	GEFFNELVGQQR	0.87906137	2	2.88348
P49186	**MK09 Mitogen_activated protein kinase 9**	**1.19316762**	**0.67971**	**2**
P49186	DLLSKMLVIDPDK	0.71285905	1	1.97777
P49186	VIEQLGTPSAEFMK	1.19318632	2	2.60854
P49242	**RS3A 40S ribosomal protein S3a**	**1.69161731**	**3.1E-07**	**9**
P49242	ACQSIYPLHDVFVR	1.71862014	2	4.31543
P49242	ADGYEPPVQESV	1.05718415	1	2.08067
P49242	LIPDSIGKDIEK	1.28637412	2	2.51284
P49242	LITEDVQGK	4.17762737	2	2.56336
P49242	LMELHGEGGSSGK	1.4776776	2	3.5162
P49242	LMELHGEGGSSGK+Oxidation(1	1.21972506		
P49242	NCLTNFHGMDLTR	1.12624817	2	3.9812
P49242	TTDGYLLR	1.52128248	2	2.71638
P49242	VFEVSLADLQNDEVAFR	1.73117964	2	4.54017
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**1.38058317**	**0.9475**	**7**
P49432	EAINQGMDEELERDEK	2.3581776	2	3.71386
P49432	ILEDNSIPQVK	1.17845291	2	3.38225
P49432	IMEGPAFNFLDAPAVR	1.57346666	2	4.53161
P49432	IMEGPAFNFLDAPAVR+Oxidation(1	0.98567776		
P49432	TIRPMDIEAIEASVMK	1.42412196	3	4.4636
P49432	VFLLGEEVAQYDGAYK	1.23913851	2	4.2258
P49432	VTGADVPMPYAK	1.12492818	2	2.55439
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.94714224**	**6.8E-12**	**12**
P49889	CKEDALFNR	1.29855601	2	2.50345
P49889	FEEHYQQMK	0.95535602	2	2.98775
P49889	FEEHYQQMK+Oxidation(8	1.06366099		
P49889	FMEGQVPYGSWYDHVK	1.03419499	2	4.12992
P49889	IIQHTSFQEMK	0.70241619	2	2.88298
P49889	LIEFLER	0.95857161	2	2.47141
P49889	LIEFLERDPSAELVDR	1.03519927	3	5.17127

P49889	NEDLINGIK	0.72616817	2	3.08119
P49889	NNPCTNYSMLPETMIDLK	0.79659281	2	5.26169
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13	1.16078137		
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8	1.16078137		
P49889	SGSTWISEIVDMIYK	1.25675298	2	4.06547
P50137	**TKT Transketolase**	**1.23433955**	**5.7E-07**	**24**
P50137	AVELAANTK	0.8722844	1	2.09332
P50137	GITGIEDK	1.02402239	1	2.56275
P50137	GITGIEDKEAWHGKPLPK	1.20627092	3	3.60674
P50137	HQPTAIIAK	0.11996927	2	2.33053
P50137	IIALDGDTK	2.42504448	2	2.67016
P50137	ILATPPQEDAPSVDIANIR	1.18429197	2	4.80141
P50137	ISSDLDGHPVPK	1.19019992	2	3.37287
P50137	KISSDLDGHPVPK	1.10012008	2	3.84016
P50137	LAVSQVPR	1.44244985	2	2.36242
P50137	LAVSQVPRSGKPAELLK	2.43564686	2	2.58743
P50137	LDNLVAIFDINR	1.26308214	2	4.52468
P50137	LGQSDPAPLQHQVDVYQK	1.21813539	2	3.86
P50137	MFGIDKDAIVQAVK	1.1420219	2	4.85396
P50137	MFGIDKDAIVQAVK+Oxidation(0	1.12203533		
P50137	NMAEQIIQEIYSQVQSK	1.07135687	3	6.02296
P50137	NSTFSELFK	1.31803306	2	2.41564
P50137	QAFTDVATGSLGQGLGAACGMAYTGK	3.89639104	3	4.37783
P50137	SGKPAELLK	0.30945059	3	3.30089
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	1.48553931	3	4.59071
P50137	SVPMSTVFYPSDGVATEK	1.16897014	2	4.50025
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3	1.55726457		
P50137	TSRPENAIIYSNNEDFQVGQAK	1.03266105	3	5.89408
P50137	VLDPFTIKPLDK	1.11502771	2	3.24046
P50137	VLDPFTIKPLDKK	0.94106356	2	2.53447
P50169	**RDH3 Retinol dehydrogenase 3**	**1.09134289**	**0.59266**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	1.08518914	3	5.03017
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1	1.42660333		
P50169	FQDSYMK	1.11289875	1	1.98619
P50169	GLWGLVNNAGISVPVGPNEWMR	1.66285985	3	3.36717
P50169	KLWDQTTEEVK	1.56221215	2	3.05005
P50169	KLWDQTTEEVKEIYGEK	0.90824733	3	4.97876
P50169	LWDQTTEEVK	1.05233226	2	3.17013
P50169	LWDQTTEEVKEIYGEK	1.04136509	2	4.8106
P50169	MSLVGGGYCISK	1.09334994	2	4.05312
P50237	**ST1C1 Sulfotransferase 1C1**	**1.13360137**	**0.01208**	**12**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.96899215	3	5.27929
P50237	DISEEVLNK	0.80967064	1	2.4687
P50237	DLHLGEQDLQPETR	0.76034193	2	4.62826
P50237	EVNGILMSK	0.60875447	1	1.91602
P50237	FLEKDISEEVLNK	0.90021802	2	2.88934
P50237	HPFIEWTLPSPLNSGLDLANK	1.71354105	3	4.03658
P50237	IWNFQAKPDDLLIATYAK	1.97458401	3	3.67837
P50237	MKDLHLGEQDLQPETR	0.96831163	2	5.18946
P50237	MLPDPGTLGEYIEQFK	1.10339736	3	4.94631
P50237	MLPDPGTLGEYIEQFK+Oxidation(0	1.50539721		
P50237	THLPVHMLPPSFWK	3.38398557	3	3.71863
P50237	VLWGSWYDHVK	1.24153647	2	2.97803
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**0.92963615**	**0.45809**	**7**
P50398	FDLGQDVIDFTGHALALYR	1.47144186	3	4.61777
P50398	FQLLEGPPESMGR	1.21936484	2	3.95243

P50398	KQNDVFGEADQ	1.43412545	2	3.28881
P50398	NPYYGGESSSITPLEELYK	1.56959759	2	5.90962
P50398	QLICDPSYIPDR	0.72700869	2	3.01483
P50398	TDDYLDQPCLETINR	0.85731884	2	4.96161
P50398	TFEGVDPQTTSMR	1.01486291	2	3.38432
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**0.95921652**	**0.4937**	**15**
P50399	AYDATTHFETTCDDIK	1.13213439	2	4.12015
P50399	AYDATTHFETTCDDIKDIYK	1.41907384	3	6.22026
P50399	EIRPALELLEPIEQK	0.99060307	3	3.8109
P50399	EPEKEIRPALELLEPIEQK	1.19919426	3	3.42173
P50399	FDLGQDVIDFTGHSLALYR	0.9551331	3	4.04024
P50399	FKLPGQPPASMGR	1.52355155	2	2.6021
P50399	FVSISDLFVPK	1.27669744	2	3.26845
P50399	LSAIYGGTYMLNKPIEEIIVQNGK	3.07106368	3	4.58014
P50399	MLLFTEVTR	1.43121242	2	2.35783
P50399	MTGSEFDFEEMKR	1.13827349	2	3.63453
P50399	NTNDANSCQIIIPQNQVNR	0.87499972	2	4.37439
P50399	TDDYLDQPCCETINR	2.8378944	2	4.85099
P50399	TFEGVDPK	2.3228886	2	2.40487
P50399	VIEGSFVYK	1.09861682	2	2.33051
P50399	VLHMDQNPYYGGESASITPLEDLYK	1.23184986	2	5.5172
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.29330863**	**0.01446**	**7**
P50431	ALSDALTELGYK	0.92531833	2	4.08037
P50431	AVLEALGSCLNNK	1.03430962	2	4.27225
P50431	GLLEEDFQK	1.55615551	1	2.09667
P50431	IMGLDLPDGGHLTHGFMTDK	0.82766061	2	2.80099
P50431	IYQLQVLANCR	1.18615531	2	2.82082
P50431	VLEACSIACNK	1.29445346	2	4.01854
P50431	YSEGYPGQR	1.4911541	2	2.81589
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**1.10939151**	**0.03922**	**16**
P50475	ASEWVQQVSGLMDGK	1.1108377	2	4.47846
P50475	AVFDETYPDPVR	0.99033416	2	3.273
P50475	DIINEEEVQFLK	1.24484968	2	2.7119
P50475	ESDGVLKPLPK	1.61506413	2	2.379
P50475	GLEATDDSPK	1.70420116	2	2.70135
P50475	HNDLDDVGK	0.96303517	2	2.55703
P50475	ITCLCQVPQNAANR	1.17964651	2	3.826
P50475	IVAVTGAEAQK	1.36268214	2	2.57376
P50475	NVGCLQEALQLATSFAQLR	1.87238248	3	3.9414
P50475	QIWQNLGLDEAK	1.47212394	2	3.04844
P50475	RIVAVTGAEAQK	1.55776325	2	2.77359
P50475	SVLGDADQK	0.99434158	1	2.2071
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	1.62058441	3	3.67529
P50475	TITVALADGGRPDNTGR	0.99879485	2	3.03316
P50475	VDDSSEDKTEFTVK	1.29066419	2	4.06605
P50475	VGAEDTDGIDMAYR	1.0251923	2	3.87138
P50503	**F10A1 Hsc70_interacting protein**	**1.35132131**	**0.00054**	**6**
P50503	AIDLFTDAIK	1.4914891	2	2.74328
P50503	AIEINPDSAQPYK	1.3632046	2	3.53018
P50503	GAAIDALNDGELQK	1.23752144	2	3.71006
P50503	KGAAIDALNDGELQK	2.00301732	2	4.68558
P50503	LDYDEDASAMLR	0.98161887	2	3.3433
P50503	QDPSVLHTEEMR	1.03302315	2	2.31945
P50516	**VATA V_type proton ATPase catalytic subunit A**	**1.13756612**	**0.43715**	**2**
P50516	TALVANTSNMPVAAR	1.0993928	2	3.19536
P50516	VLDALFPCVQGGTTAIPGAFGCGK	1.85307273	2	3.31272

P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**1.50259009**	**0.03162**	**14**
P50554	GMCQLITMACGSCSNENAFK	1.44018862	2	4.55672
P50554	GNYLVDVDGNR	1.73536906	2	2.64162
P50554	GTFCSFDTPDEAIR	2.01831126	2	3.22422
P50554	HGCAFLVDEVQTGGGCTGK	1.21244545	2	6.11325
P50554	IDIPSFDWPIAPFPR	3.03064831	2	3.80431
P50554	IFNTWLGDPSK	1.80611037	2	3.00985
P50554	KHGCAFLVDEVQTGGGCTGK	1.31814702	2	5.03661
P50554	LVQQPQNASTFINRPALGILPPENFVDK	1.51888524	3	3.30369
P50554	MLDLYSQISSVPIGYNHPALAK	1.29920396	3	3.40676
P50554	NLLLAEVINIIK	1.57860358	3	5.32395
P50554	REDLLNNVAHAGK	1.25216705	3	3.6202
P50554	TLLTGLLDLQAQYPQFVSR	2.36208941	2	3.16171
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.27965132	2	4.021
P50554	VDFEFDYDGPLMK	1.37853721	2	4.04879
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.42141289**	**0.05932**	**2**
P50580	GDAMIMEETGK	1.1040597	2	2.66411
P50580	TIIQNPTDQQK	1.45625527	2	3.15499
P50878	**RL4 60S ribosomal protein L4**	**1.30071015**	**5.9E-10**	**11**
P50878	FCIWTESAFR	1.57683441	2	2.56805
P50878	KLDELYGTWR	1.38350128	2	2.97075
P50878	KLEAAAAALAAK	1.5285943	3	4.94121
P50878	LDELYGTWR	1.41177445	2	2.57116
P50878	LEAAAAALAAK	1.76593726	2	3.61069
P50878	NIPGITLLNVSK	1.4872226	1	2.69627
P50878	NVTLPAVFK	2.25395485	1	2.24195
P50878	RGPCIIYNEDNGIIK	0.90957008	2	2.99068
P50878	SGQGAFGNMCR	1.68632864	2	2.83619
P50878	SNYNLPMHK	1.41944576	2	2.63791
P50878	YAICSALAASALPALVMSK	2.62307866	2	2.54864
P51583	**PUR6 Multifunctional protein ADE2**	**1.09396081**	**0.98563**	**3**
P51583	ACGNFGIPCELR	1.09004666	2	2.60087
P51583	SWLPQNCTLVDMK	1.07643858	2	2.7441
P51583	VVVLMGSTSDLGHCEK	1.30922863	2	3.03931
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.14732912**	**1.2E-05**	**7**
P51635	ALEALVAK	1.60148421	2	2.82697
P51635	GLEVTAYSPLGSSDR	1.13886219	2	4.1147
P51635	HHPEDVEPAVR	1.14057324	3	3.58958
P51635	HIDCASVYGNETEIGEALK	0.98494005	2	6.04121
P51635	HIDCASVYGNETEIGEALKESVGAGK	1.13708319	3	6.26134
P51635	HPDEPVLLEEPVVLALAEK	1.79288814	3	6.06106
P51635	YIVPMITVDGK	1.12942884	2	2.32848
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.80242756**	**0.92524**	**17**
P51647	ANNTTYGLAAGVFTK	1.05007899	2	4.60145
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	1.10474192	3	3.66767
P51647	FPVLNPATEEVICHVEEGDK	0.23714866	3	3.82828
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.96036448	4	5.05052
P51647	IFINNEWHDSVSGK	1.19873979	2	4.28061
P51647	IFVEESVYDEFVR	0.83586609	2	4.22951
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	1.49639374	3	5.61166
P51647	IHGQTIPSDGDIFTFTR	1.38420853	3	4.28068
P51647	KFPVLNPATEEVICHVEEGDK	0.70564703	3	3.56804
P51647	KFPVLNPATEEVICHVEEGDKADVDK	1.35845386	4	4.87731
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	0.89733984	3	5.52338
P51647	LLLATIEAINGGK	4.86208423	2	4.19882
P51647	VAFTGSTQVGK	2.72233356	2	2.51871

P51647	VFANAYLSDLGGSIK	1.45352072	2	4.44487
P51647	YCAGWADK	1.16741575	2	2.48925
P51647	YVLGNPLTQGINQGPQIDK	0.81403773	2	5.22237
P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.92861436	2	3.88679
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**1.0973458**	**0.81918**	**9**
P51650	EVGEVLCTDPLVSK	2.98827211	2	3.77634
P51650	GIHDSFVTK	1.10847146	2	2.40437
P51650	HQSGGNFFEPTLLSNVTR	1.36609649	2	3.784
P51650	IITAESGKPLK	1.57870713	2	2.82229
P51650	ILLHHAANSVK	1.91684947	2	2.61054
P51650	LGTVADCGVPEAR	0.78799248	2	3.66227
P51650	VGNGFEEGTTQGPLINEK	0.88621695	2	4.61066
P51650	WLPTPATFPVYDPASGAK	0.94252656	2	3.54446
P51650	YGIDEYLEVK	1.64581363	2	2.90843
P51863	**VA0D1 V_type proton ATPase subunit d 1**	**1.03286797**	**0.6744**	**2**
P51863	ADDYEQVK	1.63016008	2	2.48969
P51863	LLFEGAGSNPGDK	1.02619536	2	3.05388
P51869	**CP4F4 Cytochrome P450 4F4**	**2.0693104**	**0.00066**	**4**
P51869	ALPSQHEDDILK	1.42560596	2	2.59484
P51869	NISLMTLDSLQK	1.48925759	2	3.52323
P51869	TLDFIDVLLLTK	2.16579756	2	3.61385
P51869	WQDLASGGSAR	1.2226242	2	3.17791
P51886	**LUM Lumican**	**0.88013478**	**0.43971**	**2**
P51886	NNQIDHIDEK	0.93209657	2	3.20646
P51886	SLQDLQLANNK	0.77371698	2	2.49798
P52296	**IMB1 Importin subunit beta_1**	**1.47165237**	**0.56401**	**7**
P52296	AAVENLPTFLVELSR	1.27470935	2	3.67735
P52296	GALQYLVPILTQTLTK	1.65004849	2	3.30453
P52296	GDQENVHPDVMLVQPR	1.43584772	2	2.9799
P52296	SNEILTAIIQGMR	1.47602508	2	2.9366
P52296	TVSPDRLELEAAQK	0.9052293	2	3.15176
P52296	VLANPGNSQVAR	1.19591257	2	3.05508
P52296	VQHQDALQISDVVMASLLR	1.46051439	2	2.88516
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.31637252**	**0.376**	**5**
P52303	KPTETQELVQQVLSLATQDSDNPDLR	1.52487067	3	3.34658
P52303	MEPLNNLQVAVK	1.47104995	2	2.53966
P52303	NINLIVQK	0.83926754	1	2.40891
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.35053068	3	3.69346
P52303	SQPDMAIMAVNTFVK	1.29257057	2	3.3392
P52504	**NDUS6 NADH dehydrogenase [ubiquinone] iron_sulfur protein 6_ mitochondrial**	**1.46249836**	**0.08472**	**2**
P52504	IIACDGGGGALGHPK	1.47463746	2	4.12379
P52504	VYINLDKETK	1.39283077	2	2.61759
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**0.97752706**	**0.84438**	**3**
P52555	FDTQYPYGEK	1.31699471	2	2.6502
P52555	ILDQGEDFPASELAR	0.97735811	2	5.05383
P52555	SLNILTAFR	2.55335618	2	2.34129
P52631	**STAT3 Signal transducer and activator of transcription 3**	**3.16503228**	**6.7E-09**	**3**
P52631	GLSIEQLTTLAEK	2.11611383	2	2.39859
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	3.20308374	3	4.60514
P52631	MQQLEQMLTALDQMR	1.80627244	2	2.44068
P52759	**UK114 Ribonuclease UK114**	**1.1140289**	**0.00193**	**7**
P52759	AAGCDFTNVVK	2.06631596	2	3.06297
P52759	AAYQVAALPK	0.67403301	2	2.67974

P52759	IEIEAIAVQGPFTTAGL	1.78534662	2	3.24048
P52759	NLGEILK	1.02180436	1	2.28774
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.29450824	2	4.52571
P52759	TTVLLADINDFGTVNEIYK	1.84423256	2	5.66671
P52759	TYFQGNLPAR	0.98400638	2	2.5079
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.36369321**	**0.3732**	**2**
P52845	CKEDAIFNR	1.29855601	2	2.50345
P52845	SGSTWIGEIVDMIYK	1.69912562	2	3.36445
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.35686952**	**9E-07**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	2.26155345	2	4.46841
P52847	FLAGNVAYGSWFDHVK	0.86680592	2	3.85498
P52847	IEEFQSRPCDIVIPTYPK	1.35308827	3	5.26857
P52847	IVHHTSFEVMK	0.83646568	2	3.05329
P52847	NYFTMTQSEK	1.16487918	2	2.92485
P52847	SGVELLK	1.51735197	2	2.33994
P52847	THLPIDLLPK	1.74626129	3	3.55572
P52847	TLDEHTLER	1.38379343	2	3.09245
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**0.84462987**	**9.9E-20**	**39**
P52873	ADEAYLIGR	1.15401152	2	2.80685
P52873	ADFAQACQDAGVR	0.92974686	2	4.47163
P52873	AEAEAQAEELSFPR	1.10948021	2	4.704
P52873	AGTHILCIK	1.66380218	2	2.71725
P52873	ALAVSDLNR	1.2374219	2	2.58356
P52873	AYSEALAAFGNGALFVEK	1.83396682	2	3.68999
P52873	AYVEANQMLGDLIK	1.47795251	2	4.70824
P52873	DAHQSLLATR	1.86997995	1	3.17389
P52873	DFTATFGPLDSLNTR	2.70102618	2	3.75664
P52873	DMAGLLKPAACTMLVSSLR	1.52247082	3	3.38815
P52873	ELIPNIPFQMLLR	1.74534396	2	2.84916
P52873	ENGVDAVHPGYGFLSER	1.40336544	2	2.96989
P52873	FIGPSPEVVR	1.1199169	2	2.43668
P52873	FLYECPWR	1.25053839	2	2.60596
P52873	GANAVGYTNYPDNVVFK	1.34021458	2	4.57553
P52873	GLAPVQAYLHIPDIIK	0.89975103	2	2.98051
P52873	GQIGAPMPGK	1.3418691	2	2.42727
P52873	GTPLDTEVPLER	0.84462922	2	3.65032
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	2.61163911	3	5.41622
P52873	HIEVQILGDQYGNILHLYER	1.86241321	3	7.00833
P52873	HYFIEVNSR	1.30220208	2	2.33898
P52873	IAEEFEVELER	1.36064916	2	3.24429
P52873	IEGRPGASLPPLNLK	0.94833955	2	3.4374
P52873	INGCAIQCR	1.79112001	2	3.25095
P52873	IVGDLAQFMVQNGLSR	1.901824	2	4.84208
P52873	LDNASAFQGAVISPHYDSLLVK	1.46580687	3	5.77047
P52873	LLHYLGHVMVNGPTTPIPVK	1.43156376	3	3.67751
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.49484395	4	6.50313
P52873	NHQGLLLMDTTFR	1.29054824	3	3.32054
P52873	QKADEAYLIGR	1.40027429	2	2.49514
P52873	QVGYENAGTVEFLVDK	1.71424928	2	3.77663
P52873	SSTAPVASPNVR	1.29104275	2	2.346
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.47630175	2	4.80542
P52873	TVAVYSEQDTGQMHR	1.73971491	2	4.56916
P52873	VFDYSEYWEGAR	1.579392	2	4.53713
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.2644817	2	4.12303
P52873	VVEIAPATHLDPQLR	1.51631345	2	4.23659
P52873	VVHSYEELEENYTR	1.22953596	2	5.23838

P52873	YSLEYYMGLAEELVR	1.72278111	3	4.51031
P52925	**HMGB2 High mobility group protein B2**	**1.37625086**	**0.8717**	**2**
P52925	KHPDSSVNFAEFSK	1.55154388	2	2.74042
P52925	SEHPGLSIGDTAK	1.16459141	2	2.84615
P52944	**PDLI1 PDZ and LIM domain protein 1**	**1.16715013**	**0.98158**	**5**
P52944	CGTGIVGVFVK	1.1904037	2	2.43476
P52944	GHFFVGDQIYCEK	1.11295585	2	3.78768
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	1.1535085	3	4.49917
P52944	TSASGEEANSRPSAQPHPSGGLIIDKESEVYK	1.23371441	3	5.01539
P52944	VTPPEGYDVVTVFPK	1.20511943	2	2.71025
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**2.08646795**	**1.7E-07**	**4**
P53395	LREELKPVALAR	2.01824269	2	2.6741
P53395	LSDIGEGIR	2.0862444	2	3.02368
P53395	RLAMENNIK	1.06908754	2	2.37853
P53395	SYLENPAFMLLDLK	2.23498737	2	4.60672
P53987	**MOT1 Monocarboxylate transporter 1**	**1.29564628**	**3.7E-06**	**5**
P53987	DGKEDETSTDVDEKPK	2.12362824	3	5.4891
P53987	DGKEDETSTDVDEKPKK	1.60732806	3	4.0479
P53987	EDETSTDVDEKPK	1.44134462	2	3.97638
P53987	ETQSPAPLQNSSGDPAEEESPV	32.4263693	2	5.04942
P53987	SDANTDLIGGSPK	1.27043745	2	4.13569
P54313	**GBB2 Guanine nucleotide_binding protein G(I)/G(S)/G(T) subunit beta_2**	**1.05544649**	**0.5141**	**2**
P54313	ACGDSTLTQITAGLDPVGR	1.67271797	2	3.99717
P54313	TFVSGACDASIK	1.02791263	2	2.7241
P54319	**PLAP Phospholipase A_2_activating protein**	**1.05582306**	**0.99053**	**3**
P54319	IGDVVGSSGANQQTSGK	1.05715855	2	4.65864
P54319	TGDLGDINAEQLPGR	1.17530763	2	4.13088
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.8464329	2	3.39071
P54822	**PUR8 Adenylosuccinate lyase**	**2.2759663**	**0.03334**	**2**
P54822	KVDIEVLSVLASLGASVHK	2.43636763	3	4.41643
P54822	VLSQQAAAVVK	1.2829027	2	2.85438
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.10309615**	**0.56252**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	1.59937343	3	4.89156
P54921	AIDIYEQVGTSAMDSPLLK	1.94767022	2	3.79316
P54921	IEEACEIYAR	0.76867083	2	2.75739
P54921	NSQSFFSGLFGGSSK	1.09972593	2	3.79222
P54921	YEELFPAFSDSR	1.73051787	2	2.62031
P55006	**RDH7 Retinol dehydrogenase 7**	**1.09477669**	**0.16139**	**11**
P55006	LETVILDVTK	5.90128208	2	3.51737
P55006	TESIVAATQWVK	1.08678757	2	4.08185
P55006	TNVTNMER	1.00063689	2	2.74532
P55006	TNVTNMER+Oxidation(5	0.74337945		
P55006	TSDRLETVILDVTK	1.33390884	3	4.58467
P55006	VAIIEPGGFK	1.06306422	2	2.38588
P55006	VLAACLTEK	1.20865765	2	3.07459
P55006	VVNIASTMGR	1.06718206	2	3.78917
P55006	VVNIASTMGR+Oxidation(7	1.23025307		
P55006	YGVEAFSDSLR	1.39271825	2	3.86489
P55006	YVFITGCDSGFGNLLAR	1.67622677	2	3.6655
P55051	**FABP7 Fatty acid_binding protein_ brain**	**0.9144992**	**0.52634**	**4**
P55051	ALGVGFATR	1.20358116	2	2.64514
P55051	LTDSQNFDEYMK	1.69110828	2	4.04984
P55051	QVGNVTKPTVIISQEGGK	0.91423277	3	4.12915
P55051	WDGKETNCVR	0.82173139	2	2.88639

P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.46423593**	**1.6E-09**	**6**
P55053	FDETTADGR	1.40079109	2	3.20589
P55053	KTETVCTFTDGALVQHQK	1.4137852	3	5.30947
P55053	LVESHGFEDYMK	1.37607517	2	3.42733
P55053	MGAMAKPDCIITLDGNNLTVK	1.60445078	2	4.1249
P55053	MVVECVMNNAICTR	1.52745085	2	3.84754
P55053	TETVCTFTDGALVQHQK	1.50092343	2	4.68317
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.04026534**	**0.2015**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.47692231	3	5.8671
P55159	IFFYDSENPPGSEVLR	0.86078174	2	6.21527
P55159	IQSILSEDPK	1.17630346	2	3.25976
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.97263749	3	4.07499
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	0.9479359	3	5.40814
P55159	VVADGFDFANGIGISLDGK	1.55476127	2	4.4463
P55159	YVYIAELLAHK	1.15459045	2	2.67735
P55260	**ANXA4 Annexin A4**	**1.37606912**	**0.30246**	**4**
P55260	AEIDMLDIPANFK	1.57744072	1	2.17768
P55260	GAGTDEGCLIEILASR	1.44343239	2	3.78345
P55260	GLGTDEDAIIGVLACR	1.30064723	2	3.90833
P55260	INQTYQQQYGR	1.16117036	2	3.61678
P55770	**NH2L1 NHP2_like protein 1**	**1.23554883**	**0.76501**	**2**
P55770	LLDLVQQSCNYK	1.35149782	2	3.89196
P55770	QQIQSIQQSIER	1.22922969	2	2.92991
P55937	**GOGA3 Golgin subfamily A member 3**	**1.43731164**	**0.48776**	**2**
P55937	LDSEMKELRQELIK+Oxidation(4	1.43996197		
P55937	QWYQQQLTLAQEAR	1.43550245	2	2.44317
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.31848066**	**0.82058**	**5**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.70886111	2	4.52467
P56399	IFQNAPTDPTQDFSTQVAK	1.02569401	2	4.19167
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.46587577	3	3.85841
P56399	KQEVQAWDGEVR	0.96472254	2	3.35561
P56399	SSENPNEVFR	1.30814573	2	2.45697
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**1.15508959**	**0.87889**	**4**
P56522	AGLLPSGPRPGYTAIQALLSDR	3.34723334	3	3.46841
P56522	LEGVGESTR	1.10459804	2	2.30893
P56522	TATEKPGVEEAAR	1.15345083	2	3.25808
P56522	TDITEVALGVLR	1.1572734	2	3.92462
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.29249776**	**0.06891**	**17**
P56574	ATDFVVDR	1.73479949	2	2.46367
P56574	CATITPDEAR	2.09036363	2	2.30452
P56574	DLAGCIHGLSNVK	1.52965095	2	2.50456
P56574	DQTNDQVTIDSALATQK	0.85610238	2	5.42566
P56574	FKDIFQEIFDK	1.2003898	2	3.43291
P56574	GKLDGNQDLIR	10.7014756	2	2.96892
P56574	IKVEKPVVEMDGDEMTR	1.6450463	3	3.47514
P56574	LDGNQDLIR	1.09094637	2	2.44979
P56574	LIDDMVAQVLK	4.03242177	2	4.05706
P56574	LNEHFLNTTDFLDTIK	1.49154767	2	4.56007
P56574	NILGGTVFR	1.1934515	2	2.78008
P56574	NILGGTVFREPIICK	5.20970753	2	3.00083
P56574	SSGGFVWACK	0.56194531	2	2.44972
P56574	TIEAEAAHGTVTR	1.17172895	2	3.92742
P56574	VCVQTVESGAMTK	1.21368724	2	3.86064
P56574	VEKPVVEMDGDEMTR	1.47810476	3	4.01855
P56574	YFDLGLPNR	1.2791573	2	2.52253

P56593	**CP2AC Cytochrome P450 2A12**	**0.94462344**	**0.72861**	**3**
P56593	MLQGTCGAPIDPTIYLSK	0.90308009	2	4.70444
P56593	NRQPQYEDHMK	1.02226095	3	4.13185
P56593	NRQPQYEDHMK+Oxidation(9	0.86897696		
P56656	**CP239 Cytochrome P450 2C39**	**0.89176708**	**0.94422**	**4**
P56656	EHQESLDVTNPR	0.89175099	2	3.68047
P56656	IKEHQESLDVTNPR	1.00940863	3	4.87248
P56656	NYLIPK	1.56559808	1	2.1687
P56656	VQEEIDHVIGR	1.41980029	2	3.6951
P56812	**PDCD5 Programmed cell death protein 5**	**0.96195445**	**1**	**3**
P56812	HGDPGDAAQQEAK	0.92858699	2	4.39695
P56812	NSILAQVLDQSAR	1.00751994	2	3.84585
P56812	VSEQGLIEILEK	0.97368492	2	3.3304
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**1.26326124**	**0.69132**	**8**
P57093	AISCHYGSSDCK	0.97506606	2	3.22801
P57093	IQDFQQNEELFR	1.40934946	2	3.57945
P57093	KFYEENGFLVIK	1.54563108	2	2.67677
P57093	MDYTRAGAR	0.61174425	2	2.5605
P57093	MYHGIQDYDPDSPR	1.65455834	2	2.98107
P57093	NLVSDDDIQR	1.25075919	2	2.42821
P57093	NNGCLVVLPGTHK	1.26030346	2	2.92034
P57093	YCALPQIVK	1.17970294	1	2.07252
P57113	**MAAI Maleylacetoacetate isomerase**	**1.25147902**	**5.3E-07**	**11**
P57113	AITSGFNALEK	1.25524563	2	3.41554
P57113	ALLALEAFQVSHPCR	1.54829073	2	4.12713
P57113	DGGQQFSEEFQTLNPMK	1.07761963	2	4.92675
P57113	FKVDLSPYPTISHINK	1.35820554	2	4.90249
P57113	GIDYEIVPINLIK	1.1657766	2	4.40449
P57113	IDGITIGQSLAILEYLEETRPIPR	1.41822632	3	4.18634
P57113	MISDLIASGIQPLQNLSVLK	1.46796404	2	5.43574
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0	2.31681684		
P57113	QVGQENQMPWAQK	1.07467855	2	3.8213
P57113	VDLSPYPTISHINK	1.14511215	2	3.78273
P57113	YCVGDEVSMADVCLAPQVANAER	1.86026048	3	6.55903
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.37712511**	**6.9E-07**	**3**
P57722	ESTGAQVQVAGDMLPNSTER	1.36140925	2	5.28909
P57722	INISEGNCPER	1.37591169	2	3.5385
P57722	LVVPASQCGSLIGK	1.49566385	2	2.59727
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**1.26167659**	**0.2062**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	1.26057508	3	4.67889
P58321	WLPLEANPEVTNQFLK	1.35767168	2	3.01776
P58389	**PTPA Serine/threonine_protein phosphatase 2A activator**	**1.09654094**	**0.84688**	**3**
P58389	FGSLLPIHPVTSG	0.87623214	2	2.40448
P58389	KEIHTVPDMGK	1.26976617	2	2.42018
P58389	WIDETPPVDQPSR	1.08416623	2	3.47848
P58751	**RELN Reelin**	**0.68922266**	**0.38582**	**2**
P58751	CGILSSGNNLFFNEDGLR	0.6843771	2	2.32494
P58751	QNYMMNFSRQHGLR	0.70023963	2	2.42773
P58775	**TPM2 Tropomyosin beta chain**	**1.10545721**	**0.53544**	**11**
P58775	AISEELDNALNDITSL	2.6147476	2	4.39084
P58775	ATDAEADVASLNR	3.97245532	2	4.23221
P58775	DAQEKLEQAEK	1.79803086	2	2.9043
P58775	KATDAEADVASLNR	2.2414089	2	4.0868
P58775	LDKENAIDR	2.16502467	2	3.08951
P58775	LKGTEDEVEK	3.79764805	2	2.85641

P58775	MELQEMQLK	0.98903137	2	2.98138
P58775	QLEEEQQALQK	3.04319812	2	3.55414
P58775	SLEAQADKYSTK	1.92326949	2	3.75664
P58775	TIDDLEDEVYAQK	0.58129704	2	3.9504
P58775	YSESVKDAQEK	0.47806513	2	3.09924
P59242	**CING Cingulin**	**1.49652921**	**0.0056**	**2**
P59242	LGQEQQALNR	1.93775888	2	2.79354
P59242	LQGLEQEAENK	1.44914416	2	2.96285
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.45024103**	**0.03733**	**2**
P59999	ELLLQPVTISR	1.45018528	2	3.02599
P59999	FMRFMMMR+Oxidation(4)Oxidation(5	1.61655163		
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.33108428**	**2.2E-10**	**4**
P60335	AITIAGVPQSVTECVK	1.34032187	2	3.52901
P60335	IITLTGPTNAIFK	2.17707241	2	2.90487
P60335	LVVPATQCGSLIGK	1.56689348	2	2.98914
P60335	VMTIPYQPMPASSPVICAGGQDR	1.26155012	3	4.4385
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.42419246**	**0.00063**	**6**
P60843	ATQALVLAPTR	1.11037198	1	1.95849
P60843	GFKDQIYDIFQK	1.41522044	3	3.88621
P60843	GVAINMVTEEDKR	1.343663	2	3.22981
P60843	KEELTLEGIR	1.42429985	2	2.35313
P60843	KGVAINMVTEEDKR	1.81547414	3	4.67023
P60843	LQMEAPHIIVGTPGR	1.30891502	3	3.87773
P60868	**RS20 40S ribosomal protein S20**	**1.38613432**	**8.3E-08**	**3**
P60868	DTGKTPVEPEVAIHR	1.65288266	3	4.41989
P60868	LIDLHSPSEIVK	1.37400817	2	3.13459
P60868	TPVEPEVAIHR	2.10497089	2	2.45865
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.17174743**	**0.28079**	**2**
P60901	AINQGGLTSVAVR	1.16800186	2	3.41184
P60901	LLDSSTVTHLFK	1.46397426	2	3.00812
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.14036745**	**0.96785**	**2**
P61087	GEIAGPPDTPYEGGR	1.35396077	2	3.20526
P61087	VDLVDENFTELR	1.13130048	2	3.50466
P61107	**RAB14 Ras_related protein Rab_14**	**1.14973117**	**0.44157**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	1.24387433	3	3.72783
P61107	NLTNPNTVIILIGNK	1.07463477	2	3.98962
P61107	SCLLHQFTEK	1.32385942	2	3.08708
P61107	STYNHLSSWLTDAR	1.06098457	2	3.31572
P61107	TGENVEDAFLEAAK	1.15887805	2	3.69374
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.14956557**	**0.2664**	**3**
P61222	GSELQNYFTK	1.35885165	2	2.34013
P61222	NTVANSPQTLLAGMNK	1.14361415	2	4.09023
P61222	VAETANEEEVKK	1.52973432	2	2.96918
P61314	**RL15 60S ribosomal protein L15**	**1.47014729**	**2.1E-14**	**5**
P61314	FFEVILIDPFHK	1.59327831	3	3.42168
P61314	GATYGKPVHHGVNQLK	1.52110561	2	4.38604
P61314	SLQSVAEER	1.38059956	2	2.79345
P61314	VLNSYWVGEDSTYK	1.41314498	2	4.08355
P61314	YIQELWR	1.51254328	2	2.61205
P61354	**RL27 60S ribosomal protein L27**	**1.47129241**	**0.58523**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	1.47133981	3	4.93704
P61354	VYNYNHLMPTR	1.34976834	2	3.01933
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.09247356**	**1**	**3**
P61459	AVGWNELEGR	1.05550243	2	3.19697
P61459	LDHHPEWFNVYNK	1.15247338	3	4.97846

P61459	LSAEERDQLLPNLR	1.14270335	3	4.32026
P61589	**RHOA Transforming protein RhoA**	**1.41566896**	**0.44926**	**4**
P61589	HFCPNVPIILVGNK	2.63481095	2	3.29609
P61589	HFCPNVPIILVGNKK	1.79076872	3	4.5125
P61589	MKQEPVKPEEGR	1.4298194	3	4.12111
P61589	MKQEPVKPEEGR+Oxidation(0	1.26828908		
P61751	**ARF4 ADP_ribosylation factor 4**	**1.7614227**	**1.9E-08**	**6**
P61751	ILMVGLDAAGK	1.9587136	2	2.89038
P61751	IQEGAAVLQK	1.33108304	2	2.94305
P61751	KQMRILMVGLDAAGK	1.41344997	2	2.37147
P61751	LGEIVTTIPTIGFNVETVEYK	1.49884815	3	4.25597
P61751	NICFTVWDVGGQDK	1.35091704	2	4.21744
P61751	QDLPNAMAISEMTDK	1.82620096	2	3.60782
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.15343371**	**0.99453**	**2**
P61805	ADFQGISPER	1.15343681	2	3.11042
P61805	FLEEYLSSTPQR	1.06045087	2	3.78181
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.22348913**	**0.48633**	**2**
P61924	GEDVPLTEQTVSQVLQSAK	1.21775791	2	4.62344
P61924	YYDDTYPSVK	1.44022233	2	2.4936
P61972	**NTF2 Nuclear transport factor 2**	**1.99750844**	**0.4699**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	3.45765848	3	4.2965
P61972	NINDAWVCTNDMFR	1.48755128	2	3.77299
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.28365536**	**9.9E-20**	**9**
P61980	GSDFDCELR	1.56105291	2	2.76896
P61980	GSYGDLGGPIITTQVTIPK	0.92454836	2	5.16481
P61980	IDEPLEGSEDR	1.90137562	2	3.67701
P61980	IILDLISESPIK	1.39533583	2	4.09562
P61980	IITITGTQDQIQNAQYLLQNSVK	1.3787989	3	7.09349
P61980	LFQECCPHSTDR	1.28216768	2	3.90689
P61980	NTDEMVELR	1.62590979	2	2.66511
P61980	RSRNTDEMVELR	1.19343917	2	2.50928
P61980	TDYNASVSVPDSSGPER	1.13354383	2	4.56336
P61983	**1433G 14_3_3 protein gamma**	**1.19041605**	**0.99993**	**4**
P61983	AYSEAHEISK	1.04917123	2	3.53049
P61983	NVTELNEPLSNEER	1.19993184	2	4.65729
P61983	TAFDDAIAELDTLNEDSYK	1.62134001	2	4.77342
P61983	YLAEVATGEK	1.18247317	2	3.08096
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**1.06663241**	**0.99806**	**5**
P62076	CIGKPGGSLDNSEQK	1.01516787	2	4.0928
P62076	KCIGKPGGSLDNSEQK	1.08453132	3	3.97799
P62076	LDPGAIMEQVK	0.84392617	2	2.94983
P62076	VQIAVANAQELLQR	1.0887723	2	5.01919
P62076	YMDAWNTVSR	1.07781431	2	3.08328
P62083	**RS7 40S ribosomal protein S7**	**1.60798917**	**9.9E-20**	**5**
P62083	AIIIFVPVPQLK	1.71124724	2	3.75935
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	2.1518051	3	5.18262
P62083	KAIIIFVPVPQLK	1.03909597	2	3.6696
P62083	TLTAVHDAILEDLVFPSEIVGK	1.63710546	2	5.1634
P62083	VETFSGVYK	1.07958226	2	2.32131
P62161	**CALM Calmodulin**	**1.2662836**	**0.9151**	**4**
P62161	DGNGYISAAELR	1.14215974	2	2.97082
P62161	EADIDGDGQVNYEEFVQMMTAK	2.63929003	2	5.22869
P62161	EAFSLFDKDGDGTITTK	1.16057102	2	4.71599

P62161	VFDKDGNGYISAAELR	1.08612233	2	4.96889
P62193	**PRS4 26S protease regulatory subunit 4**	**1.38724303**	**0.11313**	**4**
P62193	AICTEAGLMALRERR+Oxidation(8	4.09018285		
P62193	AVANQTSATFLR	1.29112995	2	3.0933
P62193	NQEQMKPLEEK	1.19093537	2	3.54506
P62193	TMLELLNQLDGFDSR	1.49279538	2	4.13625
P62198	**PRS8 26S protease regulatory subunit 8**	**1.43379703**	**0.00468**	**6**
P62198	EVIELPVKHPELFEALGIAQPK	1.37136235	3	4.38787
P62198	IAELMPGASGAEVK	1.19153736	2	3.16113
P62198	LEGGSGGDSEVQR	1.47386919	2	3.70943
P62198	LLREELQLLQEQGSYVGEVVR	1.51208208	3	3.99668
P62198	TMLELLNQLDGFEATK	2.08567461	2	3.71609
P62198	VHVTQEDFEMAVAK	0.97995312	2	3.13595
P62243	**RS8 40S ribosomal protein S8**	**1.27737679**	**9.9E-20**	**9**
P62243	ADGYVLEGK	2.48267479	2	3.16979
P62243	IIDVVYNASNNELVR	2.20616469	2	4.22857
P62243	ISSLLEEQFQQGK	1.75085581	2	4.23977
P62243	KYELGRPAANTK	1.44442091	2	3.58783
P62243	LDVGNFSWGSECCTR	1.24791925	2	3.96338
P62243	LTPEEEEILNK	1.19668456	2	3.0717
P62243	NCIVLIDSTPYR	1.55937287	2	3.47589
P62243	QWYESHYALPLGR	1.70801503	2	2.92363
P62243	YELGRPAANTK	0.8605631	2	2.9545
P62246	**RS15A 40S ribosomal protein S15a**	**1.30153217**	**1.7E-06**	**4**
P62246	HGYIGEFEIIDDHR	1.31780061	3	4.92148
P62246	IVVNLTGR	2.02553911	2	2.32918
P62246	MNVLADALK	1.43743172	2	2.73914
P62246	WQNNLLPSR	1.29608032	2	3.11739
P62250	**RS16 40S ribosomal protein S16**	**1.73644849**	**0.01319**	**6**
P62250	ALVAYYQK	2.69859166	1	2.23972
P62250	EIKDILIQYDR	1.13642282	2	2.61425
P62250	GGGHVAQIYAIR	1.8041962	2	3.07535
P62250	LLEPVLLLGK	1.68391223	2	2.80302
P62250	TLLVADPR	1.29730194	2	2.6086
P62250	VNGRPLEMIEPR	1.55224738	2	2.69585
P62260	**1433E 14_3_3 protein epsilon**	**1.19740022**	**1.7E-11**	**9**
P62260	AAFDDAIAELDTLSEESYK	1.32793037	2	6.03811
P62260	EENKGGEDKLK	1.71078003	2	2.70242
P62260	HLIPAANTGESK	1.25807359	2	3.1987
P62260	IISSIEQK	1.34296619	2	2.60819
P62260	LICCDILDVLDK	2.91055341	2	4.0564
P62260	YDEMVESMK	1.31903311	2	2.71077
P62260	YDEMVESMKK	2.08662318	2	2.67483
P62260	YLAEFATGNDR	0.7467003	2	2.94223
P62260	YLAEFATGNDRK	1.4679278	2	2.73987
P62268	**RS23 40S ribosomal protein S23**	**1.39601275**	**0.00944**	**2**
P62268	GHAVGDIPGVR	1.39721107	2	2.74766
P62268	KGHAVGDIPGVR	1.32050106	2	2.82558
P62271	**RS18 40S ribosomal protein S18**	**1.16030639**	**0.06238**	**6**
P62271	AGELTEDEVER	1.89058736	2	3.69618
P62271	LREDLER	1.22244178	1	2.21055
P62271	RAGELTEDEVER	0.79874637	2	3.10514
P62271	VITIMQNPR	1.15573534	2	2.83899
P62271	VLNTNIDGR	3.21967261	2	3.12737
P62271	YSQVLANGLDNK	1.36897552	2	4.04299
P62278	**RS13 40S ribosomal protein S13**	**1.15276097**	**0.06018**	**5**
P62278	GLAPDLPEDLYHLIK	1.41518756	2	3.09192

P62278	GLSQSALPYR	1.10686716	2	2.47847
P62278	GLTPSQIGVILR	1.06222011	2	2.98124
P62278	KGLTPSQIGVILR	1.20267714	3	3.89147
P62278	LILIESR	1.77542708	1	2.0731
P62329	**TYB4 Thymosin beta_4**	**0.93185058**	**0.98813**	**3**
P62329	ETIEQEKQAGES	1.26795368	2	2.44625
P62329	NPLPSKETIEQEK	1.00382312	2	2.73218
P62329	TETQEKNPLPSK	0.91003333	2	3.73931
P62332	**ARF6 ADP_ribosylation factor 6**	**1.58919357**	**0.33801**	**2**
P62332	FNVWDVGGQDK	1.58834459	2	3.02465
P62332	LGQSVTTIPTVGFNVETVTYK	1.66495421	2	2.67368
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.10190062**	**0.00089**	**5**
P62334	ADHDFVVQEDFMK	1.18643172	2	2.32383
P62334	ALQSVGQIVGEVLK	1.16646877	2	3.615
P62334	EVIELPLTNPELFQR	1.4824319	2	3.03575
P62334	HGEIDYEAIVK	0.55007081	2	3.53083
P62334	NVCTEAGMFAIR	1.10475944	2	2.76719
P62425	**RL7A 60S ribosomal protein L7a**	**1.10780957**	**0.157**	**11**
P62425	AGVNTVTTLVENK	1.25062851	2	4.02915
P62425	AGVNTVTTLVENKK	1.44839901	2	3.33457
P62425	HWGGNVLGPK	1.8291057	1	2.91587
P62425	KVVNPLFEK	1.4932191	2	2.36608
P62425	LKVPPAINQFTQALDR	1.93517984	3	4.29622
P62425	NFGIGQDIQPK	1.05040652	2	3.36864
P62425	TCTTVAFTQVNSEDK	1.25645332	2	3.35062
P62425	TCTTVAFTQVNSEDKGALAK	1.9759251	2	4.68271
P62425	TNYNDRYDEIR	1.33007417	2	2.35689
P62425	VAPAPAVVK	1.09653075	1	2.15337
P62425	VPPAINQFTQALDR	1.38136932	2	3.69734
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.78996196**	**9.9E-20**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.57321775	3	4.9869
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.60836317	4	5.25064
P62630	MDSTEPPYSQK	1.49195305	2	3.74136
P62630	MDSTEPPYSQK+Oxidation(0	1.79106456		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.35163642	5	5.93441
P62630	RYEEIVK	1.19315655	2	2.7394
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	0.82771318	3	5.20747
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14	1.40749836		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8	1.13319455		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.74686527	3	5.63393
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9	1.45793256		
P62630	YEEIVK	1.2752932	2	2.34163
P62630	YYVTIIDAPGHR	1.05828898	3	4.104
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.46676185**	**9.9E-20**	**7**
P62632	EHALLAYTLGVK	1.79475221	3	3.70318
P62632	IGGIGTVPVGR	1.62289584	2	3.54856
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.417772	3	4.56564
P62632	QLIVGVNK	1.33582331	1	2.43109
P62632	STTTGHLIYK	1.88556403	2	3.06981
P62632	THINIVVIGHVDSGK	0.86677388	2	5.39768
P62632	VETGILRPGMVVTFAPVNITTEVK	2.11374683	3	3.94433
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.39583778**	**0.0234**	**2**
P62634	CGETGHVAINCSK	1.35996294	2	4.45352
P62634	CYSCGEFGHIQK	1.46429174	2	3.37999

P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.28187025**	**0.22803**	**5**
P62703	FDTGNLCMVTGGANLGR	1.13609528	2	4.77984
P62703	GIPHLVTHDAR	1.4631776	2	2.74673
P62703	LSNIFVIGK	1.59048647	2	3.12328
P62703	TDITYPAGFMDVISIDK	1.70320012	2	4.94691
P62703	VNDTIQIDLETGK	1.99145354	2	4.548
P62718	**RL18A 60S ribosomal protein L18a**	**0.97650038**	**0.72424**	**2**
P62718	DLTTAGAVTQCYR	0.86155221	2	3.16364
P62718	SSGEIVYCGQVFEKSPLR	1.82498477	2	2.50862
P62752	**RL23A 60S ribosomal protein L23a**	**1.58952508**	**0.00126**	**7**
P62752	KLYDIDVAK	1.61053422	2	2.39104
P62752	LAPDYDALDVANK	1.11850882	2	3.71814
P62752	LDHYAIIK	1.33833878	2	2.52263
P62752	LYDIDVAK	1.15457658	1	1.98575
P62752	NKLDHYAIIK	1.41500381	3	3.39016
P62752	VNTLIRPDGEK	1.39501699	2	3.34056
P62752	VNTLIRPDGEKK	1.5395229	2	2.93046
P62755	**RS6 40S ribosomal protein S6**	**1.075886**	**3.2E-08**	**4**
P62755	LIEVDDER	0.98510243	2	3.07724
P62755	LNISFPATGCQK	1.18643674	2	2.85092
P62755	MATEVAADALGEEWK	1.70207869	2	4.78582
P62755	MATEVAADALGEEWK+Oxidation(0	1.07589216		
P62775	**MTPN Myotrophin**	**0.87622824**	**0.79079**	**3**
P62775	GPDGLTALEATDNQAIK	1.90973123	2	3.90549
P62775	HHITPLLSAVYEGHVSCVK	0.94775274	3	3.94215
P62775	NGDLDEVKDYVAK	0.87400493	2	3.19191
P62804	**H4 Histone H4**	**1.44282337**	**3.3E-16**	**9**
P62804	DAVTYTEHAK	1.78401126	2	3.01126
P62804	DNIQGITKPAIR	1.32731866	2	3.14164
P62804	ISGLIYEETR	2.13155102	2	3.97264
P62804	KTVTAMDVVYALK	1.83315067	3	4.77401
P62804	RISGLIYEETR	1.33044165	2	2.40331
P62804	TVTAMDVVYALK	1.39577241	2	3.90066
P62804	TVTAMDVVYALK+Oxidation(4	1.11120715		
P62804	VFLENVIR	1.27497119	2	3.26437
P62804	VFLENVIRDAVTYTEHAK	1.66535206	3	3.87555
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**0.82724222**	**0.22807**	**3**
P62815	AVVQVFEGTSGIDAK	0.75669788	2	3.64331
P62815	IYPEEMIQTGISAIDGMNSIAR	1.85907943	3	3.44089
P62815	SGQVLEVSGSK	1.23379595	2	2.81217
P62845	**RS15 40S ribosomal protein S15**	**1.3954775**	**0.35729**	**2**
P62845	DMIILPEMVGSMVGVYNGK	1.49526747	2	3.15847
P62845	KEAPPMEKPEVVK	1.39245645	3	4.03212
P62850	**RS24 40S ribosomal protein S24**	**1.44014488**	**0.02278**	**2**
P62850	KQMVIDVLHPGK	1.94875586	3	3.67591
P62850	TTGFGMIYDSLDYAK	1.39929438	2	4.00406
P62856	**RS26 40S ribosomal protein S26**	**1.24119313**	**0.03212**	**4**
P62856	DISEASVFDAYVLPK	1.19310265	2	3.11
P62856	FRPAGAAPRPPPKPM	0.97115518	2	2.73655
P62856	LHYCVSCAIHSK	1.48217273	3	3.33788
P62856	NIVEAAAVR	1.39403637	2	3.01359
P62859	**RS28 40S ribosomal protein S28**	**1.65739231**	**0.07892**	**2**
P62859	EGDVLTLLESER	1.67724128	2	3.53634
P62859	VEFMDDTSR	1.51930478	2	2.70491
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.57169767**	**1.5E-06**	**3**

P62870	ADDTFEALR	1.11368799	2	2.5475
P62870	LYKDDQLLDDGK	1.58065603	2	2.9807
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.82450676	3	4.52014
P62890	**RL30 60S ribosomal protein L30**	**1.51709843**	**0.13477**	**3**
P62890	LVILANNCPALR	1.37070199	2	3.06541
P62890	TGVHHYSGNNIELGTACGK	1.58165787	2	5.68993
P62890	VCTLAIIDPGDSDIIR	1.96493476	2	4.24025
P62898	**CYC Cytochrome c_ somatic**	**1.32781043**	**0.08335**	**7**
P62898	ADLIAYLK	1.1164528	2	3.12513
P62898	ADLIAYLKKATNE	0.72150354	2	2.46253
P62898	GITWGEDTLMEYLENPK	1.46545546	2	4.98805
P62898	GITWGEDTLMEYLENPKK	1.30224906	2	4.31643
P62898	KTGQAAGFSYTDANK	1.02417132	2	5.1925
P62898	TGPNLHGLFGR	0.91194013	2	3.37204
P62898	TGQAAGFSYTDANK	1.15619321	2	4.18944
P62902	**RL31 60S ribosomal protein L31**	**1.74673536**	**0.15096**	**2**
P62902	NLQTVNVDEN	1.00812544	1	2.41981
P62902	SAINEVVTR	1.92923078	2	3.05434
P62907	**RL10A 60S ribosomal protein L10a**	**1.26950097**	**1.6E-14**	**6**
P62907	AVDIPHMDIEALK	1.40991389	2	3.03815
P62907	AVDIPHMDIEALKK	1.17434712	2	3.07241
P62907	FSVCVLGDQQHCDEAK	1.46111464	2	4.12317
P62907	KYDAFLASESLIK	1.13055556	2	3.84331
P62907	VLCLAVAVGHVK	1.11110537	2	3.23442
P62907	YDAFLASESLIK	1.21489006	2	3.306
P62909	**RS3 40S ribosomal protein S3**	**1.19110058**	**9.9E-20**	**10**
P62909	AELNEFLTR	1.21783332	2	3.19437
P62909	DEILPTTPISEQK	1.31841006	2	3.3224
P62909	ELAEDGYSGVEVR	1.00648862	2	3.83229
P62909	ELTAVVQK	1.54744351	1	2.05135
P62909	FGFPEGSVELYAEK	4.13117927	2	3.56604
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.48281393	3	4.76127
P62909	GCEVVVSGK	1.27327573	2	2.41689
P62909	GGKPEPPAMPQPVPTA	1.51566057	2	4.07126
P62909	GLCAIAQAESLR	1.16682279	2	3.36026
P62909	TEIIILATR	1.65725406	2	3.28158
P62912	**RL32 60S ribosomal protein L32**	**1.53356705**	**3E-07**	**3**
P62912	ELEVLLMCNK	1.30960609	2	3.29667
P62912	GQILMPNIGYGSNK	1.25156477	2	3.15751
P62912	SYCAEIAHNVSSK	1.53521943	2	4.41383
P62914	**RL11 60S ribosomal protein L11**	**1.52191211**	**0.36443**	**2**
P62914	VLEQLTGQTPVFSK	1.52191467	2	4.42675
P62914	YDGIILPGK	1.22629947	2	3.05924
P62919	**RL8 60S ribosomal protein L8**	**1.44680245**	**3.1E-10**	**4**
P62919	ASGNYATVISHNPETK	1.43223112	2	4.43514
P62919	AVDFAER	1.52045491	1	1.97741
P62919	AVVGVVAGGGR	1.40936971	2	3.61877
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.56978799	3	5.37276
P62944	**AP2B1 AP_2 complex subunit beta**	**1.28785227**	**0.25077**	**3**
P62944	KPSETQELVQQVLSLATQDSDNPDLR	1.96715182	3	3.30468
P62944	LQNNNVYTIAK	1.22826201	2	2.40778
P62944	SQPDMAIMAVNSFVK	1.01714857	2	2.97341
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**1.0602113**	**0.98851**	**7**
P62959	AQVAQPGGDTIFGK	1.0369821	2	4.75212
P62959	CAADLGLK	1.25762756	2	2.52929
P62959	CLAFHDISPQAPTHFLVIPK	1.34116474	3	4.29055

P62959	HISQISVADDDDESLLGHLMIVGK	1.23719705	3	6.72587
P62959	IIFEDDR	1.38540706	2	2.59956
P62959	KHISQISVADDDDESLLGHLMIVGK	1.21271214	3	5.49068
P62959	MVVNEGADGGQSVYHIHLHVLGGR	1.05807998	3	4.37994
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.29884528**	**0.08404**	**6**
P62961	EDGNEEDKENQGDETQGQQPPQR	1.33567304	3	5.12613
P62961	GAEAANVTGPGGVPVQGSK	0.93766781	2	4.97392
P62961	NEGSESAPEGQAQQR	1.4667135	2	5.21107
P62961	NYQQNYQNSESGEK	1.11849584	2	4.82381
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	1.20193692	3	5.12922
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.75395769	3	5.12013
P62963	**PROF1 Profilin_1**	**1.37111643**	**0.32081**	**6**
P62963	CYEMASHLR	1.5675808	2	2.39401
P62963	DSLLQDGEFTMDLR	1.67697387	2	3.40966
P62963	DSPSVWAAVPGK	0.97813398	2	2.74058
P62963	SSFFVNGLTLGGQK	1.2271116	2	4.35779
P62963	STGGAPTFNVTVTMTAK	1.40121627	2	3.43468
P62963	TFVSITPAEVGVLVGK	1.23189499	2	4.63715
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**0.99558624**	**9.9E-20**	**25**
P63018	ARFEELNADLFR	1.49073714	3	3.73955
P63018	CNEIISWLDK	1.39476362	2	3.17904
P63018	DAGTIAGLNVLR	1.63355927	2	3.69132
P63018	FDDAVVQSDMK	1.20859657	2	3.871
P63018	FEELNADLFR	1.27429393	2	3.28983
P63018	FELTGIPPAPR	1.30390582	2	3.13579
P63018	HWPFMVVNDAGRPK	4.496166	3	3.51047
P63018	IINEPTAAAIAYGLDK	1.50031068	2	5.42855
P63018	IINEPTAAAIAYGLDKK	1.52614045	2	4.27956
P63018	LLQDFFNGK	1.94187346	2	2.69215
P63018	MKEIAEAYLGK	1.23790949	2	3.4522
P63018	MVNHFIAEFK	0.88266204	2	2.86187
P63018	NQTAEKEEFEHQQK	1.11277635	2	5.26832
P63018	NQVAMNPTNTVFDAK	1.10796805	2	4.97062
P63018	NQVAMNPTNTVFDAK+Oxidation(4	1.24710092		
P63018	NSLESYAFNMK	1.16251999	2	3.50634
P63018	RFDDAVVQSDMK	1.38372896	2	3.62859
P63018	SFYPEEVSSMVLTK	1.08540376	2	4.95721
P63018	SFYPEEVSSMVLTK+Oxidation(9	1.51495784		
P63018	SINPDEAVAYGAAVQAAILSGDK	1.83680422	2	5.93176
P63018	SQIHDIVLVGGSTR	1.11389559	2	4.46678
P63018	STAGDTHLGGEDFDNR	1.23795604	2	4.72993
P63018	TVTNAVVTVPAYFNDSQR	0.99528176	3	4.90088
P63018	VCNPIITK	1.33534906	2	2.53822
P63018	VQVEYKGETK	1.33091366	2	2.54376
P63029	**TCTP Translationally_controlled tumor protein**	**1.08774696**	**0.46391**	**3**
P63029	DLISHDELFSDIYK	1.68009705	2	3.90017
P63029	EIADGLCLEVEGK	1.08523147	2	3.26732
P63029	VKPFMTGAAEQIK	1.64650203	3	3.34117
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.09098197**	**0.99502**	**7**
P63036	ETTYYDVLGVKPNATQEELKK	1.11232726	3	3.56827
P63036	HYNGEAYEDDEHHPR	1.17841533	3	4.9599
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.46907616	3	4.00024
P63036	NVVHQLSVTLEDLYNGATR	1.03752792	2	4.05001
P63036	QISQAYEVLADSK	1.02950308	2	3.17226
P63036	TIVITSHPGQIVK	1.08871504	2	3.62617
P63036	VNFPENGFLSPDK	1.05857658	2	3.42163

P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.1789964**	**0.00044**	**36**
P63039	AAVEEGIVLGGGCALLR	1.18385823	2	5.38005
P63039	ALMLQGVDLLADAVAVTMGPK	0.90412224	3	6.58248
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(17	1.452382		
P63039	CEFQDAYVLLSEK	2.40792802	2	4.4081
P63039	CIPALDSLKPANEDQK	1.05624713	2	3.53513
P63039	DDAMLLK	1.3040282	1	1.99997
P63039	DIGNIISDAMK	0.78209856	2	3.37775
P63039	GIIDPTK	1.30737165	1	1.93064
P63039	GVMLAVDAVIAELK	1.66749498	2	4.53891
P63039	GVMLAVDAVIAELKK	1.33172671	2	4.63125
P63039	GYISPYFINTSK	1.42664664	2	3.09148
P63039	IGIEIIK	0.96880581	2	2.67976
P63039	IGIEIIKR	2.25449077	2	2.41996
P63039	ILQSSSEVGYDAMLGDFVNMVEK	2.3383742	3	5.09175
P63039	IQEITEQLDITTSEYEK	1.66492994	2	5.62386
P63039	IQEITEQLDITTSEYEKEK	1.28062452	2	5.26961
P63039	ISSVQSIVPALEIANAHR	2.42119268	2	4.32679
P63039	KISSVQSIVPALEIANAHR	1.80511897	3	4.38552
P63039	KPLVIIAEDVDGEALSTLVLNR	2.01450507	2	6.01495
P63039	LSDGVAVLK	1.20209406	2	2.96864
P63039	LVQDVANNTNEEAGDGTTTATVLAR	3.18260813	2	6.51714
P63039	NAGVEGSLIVEK	0.91470405	2	3.4122
P63039	QSKPVTTPEEIAQVATISANGDK	1.13419287	2	3.41524
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.25565069	3	4.84935
P63039	RGVMLAVDAVIAELKK	0.74482415	3	5.93169
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	1.71110587	3	5.14673
P63039	TLNDELEIIEGMK	0.69427816	2	4.79828
P63039	TLNDELEIIEGMK+Oxidation(11	2.47618801		
P63039	TVIIEQSWGSPK	1.03499298	2	4.42764
P63039	VGEVIVTK	1.22878087	2	3.24175
P63039	VGEVIVTKDDAMLLK	1.1160636	2	3.60917
P63039	VGGTSDVEVNEK	1.21242067	2	3.80371
P63039	VGGTSDVEVNEKK	1.34126993	2	3.73601
P63039	VGGTSDVEVNEKKDR	1.02635581	2	3.41717
P63039	VGLQVVAVK	1.38026959	2	3.09865
P63039	VTDALNATR	1.16933532	2	3.44299
P63092	**subunit alpha isoforms short**	**1.09928233**	**0.99826**	**2**
P63092	AFEPFYDEIKSKGALVK	1.12723832		
P63092	YTTPEDATPEPGEDPR	0.82532119		
P63102	**1433Z 14_3_3 protein zeta/delta**	**1.15958519**	**0.90957**	**10**
P63102	DICNDVLSLLEK	1.10292508	3	3.8173
P63102	EMQPTHPIR	1.75171752	2	2.32383
P63102	FLIPNASQPESK	1.03594617	2	2.90948
P63102	GIVDQSQQAYQEAFEISK	1.2995469	2	5.67016
P63102	KGIVDQSQQAYQEAFEISK	0.88045612	2	5.2667
P63102	SVTEQGAELSNEER	1.1760923	2	5.17422
P63102	TAFDEAIAELDTLSEESYK	1.73370903	3	4.63565
P63102	YDDMAACMK	1.15849872	2	2.52387
P63102	YLAEVAAGDDK	1.61225877	2	2.36058
P63102	YLAEVAAGDDKK	1.34458179	2	3.5155
P63159	**HMGB1 High mobility group protein B1**	**1.14523916**	**0.23527**	**6**
P63159	GEHPGLSIGDVAK	1.11003201	2	2.97856
P63159	GKFEDMAK	1.261929	1	2.01504
P63159	IKGEHPGLSIGDVAK	1.91820064	2	4.02613
P63159	KHPDASVNFSEFSK	1.50988779	3	4.19383
P63159	KLGEMWNNTAADDKQPYEK	1.26329316	3	4.61693

P63159	LGEMWNNTAADDKQPYEK	1.02089287	2	4.93213
P63174	**RL38 60S ribosomal protein L38**	**1.31897328**	**0.05399**	**2**
P63174	IEEIKDFLLTAR	1.40912579	2	3.03256
P63174	KIEEIKDFLLTAR	1.31870476	2	4.6024
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.22674997**	**2.8E-05**	**13**
P63245	DETNYGIPQR	1.01208479	2	2.52143
P63245	DGQAMLWDLNEGK	1.58358794	2	3.3529
P63245	FSPNSSNPIIVSCGWDK	1.32088812	2	4.22051
P63245	GHNGWVTQIATTPQFPDMILSASR	1.53421411	3	4.1962
P63245	HLYTLDGGDIINALCFSPNR	1.87015267	2	6.13431
P63245	IIVDELK	1.54824387	2	2.49785
P63245	IIVDELKQEVISTSSK	1.44728199	3	4.08416
P63245	IWDLEGK	1.29526176	2	2.36423
P63245	LWDLTTGTTTR	0.80558674	1	1.95773
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.29922459	3	5.39473
P63245	VWNLANCK	1.46892397	2	2.58687
P63245	VWQVTIGTR	0.86377351	2	2.86244
P63245	YWLCAATGPSIK	0.77005027	2	3.53412
P63259	**ACTG Actin_ cytoplasmic 2**	**1.15311502**	**0.46184**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.58584015	3	5.68872
P63259	DLYANTVLSGGTTMYPGIADR	0.82455522	2	6.0936
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13	1.52098559		
P63259	GYSFTTTAER	1.09566432	2	3.51666
P63259	KDLYANTVLSGGTTMYPGIADR	1.35774017	2	6.30012
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14	1.4003331		
P63259	QEYDESGPSIVHR	1.22846624	3	3.50643
P63259	VAPEEHPVLLTEAPLNPK	1.20762394	2	4.68066
P63324	**RS12 40S ribosomal protein S12**	**1.49729279**	**0.00112**	**4**
P63324	KVVGCSCVVVK	1.16928639	2	3.27817
P63324	LGEWVGLCK	1.69019356	2	3.16608
P63324	QAHLCVLASNCDEPMYVK	1.68958678	3	3.98918
P63324	VVGCSCVVVK	1.53906758	2	3.23924
P67779	**PHB Prohibitin**	**1.28188798**	**0.02688**	**11**
P67779	AAELIANSLATAGDGLIELR	1.245864	3	5.0684
P67779	AAIISAEGDSK	1.6034606	2	2.57841
P67779	DLQNVNITLR	0.99457384	2	3.24295
P67779	FDAGELITQR	0.94913491	2	3.72557
P67779	FGLALAVAGGVVNSALYNVDAGHR	1.68103395	3	3.37601
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.7494811	3	4.43454
P67779	IYTSIGEDYDER	1.1391142	2	3.50215
P67779	KLEAAEDIAYQLSR	1.21043504	2	4.64327
P67779	NVPVITGSK	1.06570701	1	2.28696
P67779	QVSDDLTER	0.85845338	2	2.45334
P67779	VLPSITTEILK	1.7754033	2	2.4025
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.31245454**	**1.8E-08**	**4**
P68037	ADLAEEYSK	4.07458748	2	2.38827
P68037	GQVCLPVISAENWKPATK	1.6621566	2	4.40799
P68037	IEINFPAEYPFKPPK	0.98293543	2	3.33293
P68037	TDQVIQSLIALVNDPQPEHPLR	1.38184721	2	5.28861
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.18851854**	**0.11179**	**5**
P68101	AGLNCSTETMPIK	1.27516475	2	3.12973
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.76542747	3	4.07829
P68101	HVAEVLEYTKDEQLESLFQR	0.95224594	3	4.00685
P68101	TEGLSVLNQAMAVIK	1.19097781	2	4.13596
P68101	VVTDTDETELAR	0.86095686	2	3.77996

P68136	**ACTS Actin_ alpha skeletal muscle**	**1.11985205**	**1.1E-16**	**18**
P68136	AGFAGDDAPR	1.80282153	2	3.46492
P68136	AVFPSIVGRPR	0.80089721	2	2.42247
P68136	DLYANNVMSGGTTMYPGIADR	3.31607982	2	4.72348
P68136	DSYVGDEAQSK	1.09413213	2	3.46228
P68136	DSYVGDEAQSKR	1.0217494	2	2.57108
P68136	EITALAPSTMK	1.19138449	2	2.98434
P68136	EITALAPSTMK+Oxidation(9	1.00999105		
P68136	GYSFVTTAER	1.78324688	2	3.72485
P68136	IWHHTFYNELR	2.55876215	2	2.96148
P68136	KDLYANNVMSGGTTMYPGIADR	3.90420323	2	5.14151
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14	1.20502782		
P68136	MQKEITALAPSTMK	2.3809414	2	3.51916
P68136	QEYDEAGPSIVHR	5.23675663	3	3.30013
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	3.26636203	3	6.09084
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28	4.38446162		
P68136	VAPEEHPTLLTEAPLNPK	2.13112881	2	4.24267
P68136	YPIEHGIITNWDDMEK	1.76148822	2	4.75753
P68136	YPIEHGIITNWDDMEK+Oxidation(13	2.04991822		
P68255	**1433T 14_3_3 protein theta**	**1.22969306**	**0.71055**	**7**
P68255	AVTEQGAELSNEER	1.055753	2	4.6872
P68255	SICTTVLELLDK	1.7797162	2	3.22655
P68255	TAFDEAIAELDTLNEDSYK	0.99437844	2	3.28603
P68255	VISSIEQK	1.07297529	2	2.60992
P68255	YLAEVACGDDR	0.77136951	2	2.35311
P68255	YLAEVACGDDRK	1.31683724	2	3.1614
P68255	YLIANATNPESK	1.53669593	2	3.17227
P68511	**1433F 14_3_3 protein eta**	**1.45149958**	**0.14916**	**5**
P68511	AVTELNEPLSNEDR	1.2444137	2	4.9965
P68511	ELETVCNDVLALLDK	1.35163601	2	3.5725
P68511	NCNDFQYESK	1.55448969	2	2.61677
P68511	NSVVEASEAAYK	1.65673858	2	2.8063
P68511	YLAEVASGEK	2.16181725	2	2.54534
P69897	**TBB5 Tubulin beta_5 chain**	**1.34016726**	**1.7E-12**	**4**
P69897	ALTVPELTQQVFDAK	1.3753057	2	3.27548
P69897	FWEVISDEHGIDPTGTYHGDSDLQLDR	1.54904934	3	4.5293
P69897	ISVYYNEATGGK	2.28200595	2	2.87951
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	2.08968871	2	5.17076
P70191	**TRAF5 TNF receptor_associated factor 5**	**0.99948253**	**0.82944**	**2**
P70191	SLRELNSVPICPVDK	0.53649331	2	2.34286
P70191	VTLMLLDQSGK	1.00706619	2	2.45972
P70372	**ELAV1 ELAV_like protein 1**	**1.19812103**	**0.64471**	**3**
P70372	SLFSSIGEVESAK	1.49542914	2	3.22271
P70372	TNLIVNYLPQNMTQEELR	0.9420388	2	3.54844
P70372	VLVDQTTGLSR	0.98509441	2	2.79901
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.26324929**	**0.61275**	**4**
P70470	ASFSQGPINSANR	1.44518919	2	3.09308
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.38938557	3	3.70286
P70470	GLVNPANVTFK	1.45397846	2	2.45555
P70470	VYEGMMHSSCQQEMMDVK	1.19450251	3	3.35158
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.83559075**	**6.9E-08**	**11**
P70473	ADVLLEPFR	0.82797864	2	3.33956
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	1.09646566	4	4.72753
P70473	DYGFSQEEIHQLHSDR	0.74196715	2	4.80469
P70473	GLGLESEELPSQMSIEDWPEMK	1.32866356	3	4.50279
P70473	GQNLLDGGAPFYTTYK	0.71005532	2	4.8595

P70473	GSFITDEEQHACPRPAPQLSR	0.72577131	3	4.29839
P70473	LGSVNHPSHLAR	1.33514631	2	3.31241
P70473	LQLGPETLR	0.81314072	2	2.40522
P70473	RDPSVGEHTVEVLK	0.93242558	3	4.24251
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.86448162	4	5.42512
P70473	TQAMGLWAQPR	0.90943852	2	3.47042
P70550	**RAB8B Ras_related protein Rab_8B**	**1.62222796**	**6.6E-05**	**2**
P70550	LLLIGDSGVGK	1.62810647	2	2.91201
P70550	NIEEHASSDVER	1.58242294	2	2.98077
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**1.1732398**	**0.96333**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	1.16007869	3	5.17034
P70552	VLGNNFYEYYVNDPPR	1.34680703	2	4.28155
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.89651615**	**0.98089**	**9**
P70580	EALKDEYDDLSDLTPAQQETLNDWDSQFTFK	0.94310144	3	5.38445
P70580	EGEEPTVYSDDEEPKDEAAR	0.87259268	2	4.59574
P70580	FYGPEGPYGVFAGR	0.92516557	2	4.53776
P70580	GDQPGASGDNDDDEPPPLPR	609.508951	2	4.99778
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.11992032	3	5.5517
P70580	KFYGPEGPYGVFAGR	0.68127912	2	3.9042
P70580	LLKEGEEPTVYSDDEEPKDEAAR	1.39403425	3	4.28539
P70580	RYDGVQDPR	1.10023573	1	2.08088
P70580	YDGVQDPR	0.95132797	2	2.87635
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.92220378**	**0.67272**	**9**
P70584	ASSTCQLTFENVK	1.25821787	2	2.89981
P70584	FAQEQIAPLVSTMDENSK	1.00392999	2	4.61998
P70584	IFDFQGLQHQVAHVATQLEAAR	1.54941162	3	6.06027
P70584	IGTIYEGTSNIQLNTIAK	1.15582769	2	4.50766
P70584	KFAQEQIAPLVSTMDENSK	0.78106606	2	6.00841
P70584	SGNYYVINGSK	1.27656696	2	3.36215
P70584	SVIQGLFQQGMMGIEVEAK	1.44323684	2	4.49709
P70584	VDASVALLCDIQNTVINK	1.36121595	2	4.87087
P70584	YYASEVAGLTTSK	0.92219362	2	4.22422
P70615	**LMNB1 Lamin_B1**	**1.1775566**	**0.68768**	**5**
P70615	ALYETELADAR	1.47969869	2	3.11991
P70615	KESDLSGAQIK	1.21225043	2	2.45197
P70615	LSSEMNTSTVNSAR	1.69294776	2	3.93546
P70615	NQNSWGTGEDVK	1.10954055	2	3.36962
P70615	SLEGDLEDLKDQIAQLEASLSAAK	1.17755413	3	3.62123
P70712	**KYNU Kynureninase**	**1.19956338**	**0.03068**	**11**
P70712	FKDCFYIPK	1.42131568	2	2.65154
P70712	IATELNCDPTDER	1.64645507	2	3.81566
P70712	IGAYGHEVGK	4.22316347	2	2.83386
P70712	LDEEDKLK	0.62380186	2	2.33185
P70712	LDEEDKLKR	1.40540042	2	2.68761
P70712	LLTAILDSTERN	1.79683779	2	3.30672
P70712	MEDILEVIEK	1.5166931	2	3.05429
P70712	TYLEEELDK	1.42572727	1	2.10386
P70712	TYLEEELDKWAK	1.08509077	2	2.73616
P70712	VAPVPLYNSFHDVYK	1.29792363	2	3.42916
P70712	YLNSGAGGLAGAFIHEK	1.51663714	2	4.45625
P80067	**CATC Dipeptidyl peptidase 1**	**1.30811616**	**0.00027**	**5**
P80067	GINFVSPVR	0.90781417	2	3.00439
P80067	GTDECAIESIAMAAIPIPK	1.21646919	2	5.13728
P80067	NSWGSQWGESGYFR	1.40146093	2	3.41384

P80067	RGTDECAIESIAMAAIPIPK	1.56580234	2	4.1065
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.50921988	3	5.78283
P80254	**DOPD D_dopachrome decarboxylase**	**1.28075932**	**0.00766**	**4**
P80254	FFPLEPWQIGK	1.06469297	2	2.78907
P80254	FLTEELSLDQDR	1.1283241	2	3.73394
P80254	LCAATATILDKPEDR	1.90810712	2	4.48946
P80254	STEPCAHLLISSIGVVGTAEQNR	1.01849629	2	5.49589
P80299	**HYES Epoxide hydrolase 2**	**1.04825186**	**0.97391**	**4**
P80299	ATEMGGILVGTPEDPK	1.43773159	2	3.47082
P80299	GHIEDCGHWTQIEKPAEVNQILIK	1.01244297	3	4.25433
P80299	TEIQNPSVTSK	1.04224885	2	2.65669
P80299	TSDDMGLLTVNK	1.23003541	2	3.20538
P80313	**TCPH T_complex protein 1 subunit eta**	**1.36230996**	**0.00121**	**6**
P80313	ATISNDGATILK	1.30750179	2	2.63486
P80313	EGTDSSQGIPQLVSNISACQVIAEAVR	3.74281016	3	4.1569
P80313	GGAEQFMEETER	1.17931087	2	3.14914
P80313	LLDVVHPAAK	1.38041541	2	2.54936
P80313	QLCDNAGFDATNILNK	0.73434853	2	3.84561
P80313	SQDAEVGDGTTSVTLLAAEFLK	2.104137	2	3.45923
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.24867272**	**0.00073**	**10**
P80317	ALQFLEQVK	2.65978679	2	2.70419
P80317	DGNVLLHEMQIQHPTASLIAK	1.39723007	3	4.66417
P80317	GIDPFSLDALAK	2.35730534	2	2.82951
P80317	HKSETDTSLIR	1.31663991	2	3.14319
P80317	IITEGFEAAK	1.29518177	2	2.53183
P80317	MLVSGAGDIK	0.64080353	2	2.34865
P80317	NAIDDGCVVPGAGAVEVALAEALIK	1.18716924	3	3.73285
P80317	TEVNSGFFYK	1.11927467	2	2.66682
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.08610193	2	4.71373
P80317	VLAQNSGFDLQETLVK	1.23222624	2	3.73282
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.92087136**	**0.58543**	**4**
P81155	LTFDTTFSPNTGK	2.14838254	2	3.5944
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.42017749	3	3.98552
P81155	VNNSSLIGVGYTQTLRPGVK	1.24532578	2	3.58643
P81155	YQLDPTASISAK	0.78167705	2	2.94988
P82198	**BGH3 Transforming growth factor_beta_induced protein ig_h3**	**1.09351613**	**0.7862**	**2**
P82198	MLTPPMGTVMDVLK+Oxidation(0)Oxidation(5	1.46440608		
P82198	SLQGDKLEVSSK	1.08840286	2	3.09666
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.07197644**	**0.82588**	**14**
P82995	DQVANSAFVER	1.14280772	2	2.6804
P82995	ELHINLIPNKQDR	0.86449574	2	2.8195
P82995	ELISNSSDALDK	1.07400724	2	2.92874
P82995	FYEQFSK	1.28483344	1	2.10674
P82995	HIYFITGETK	0.98129543	2	3.13323
P82995	HLEINPDHSIIETLR	1.12441824	2	4.68653
P82995	HSQFIGYPITLFVEK	2.41872458	3	3.72292
P82995	KHGLEVIYMIEPIDEYCVQQLK	1.73439057	3	3.33036
P82995	LGIHEDSQNR	1.1280954	1	3.11124
P82995	NPDDITNEEYGEFYK	0.97138884	2	5.08747
P82995	SLTNDWEEHLAVK	1.09627119	2	4.05766
P82995	TLTIVDTGIGMTK	1.25291168	2	4.27911
P82995	TLTIVDTGIGMTK+Oxidation(10	1.77469366		
P82995	YYTSASGDEMVSLK	1.50407929	2	3.13773
P83732	**RL24 60S ribosomal protein L24**	**1.41033109**	**3.4E-06**	**5**
P83732	AITGASLADIMAK	1.5096846	2	4.61999

P83732	CESAFLSK	1.40255092	2	2.36607
P83732	QINWTVLYR	2.18234078	2	2.59706
P83732	VELCSFSGYK	1.10783803	2	2.34048
P83732	VFQFLNAK	1.94132384	2	2.34652
P83868	**TEBP Prostaglandin E synthase 3**	**1.43728743**	**0.14516**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.76004511	3	4.05379
P83868	LTFSCLGGSDNFK	1.40995354	2	2.75563
P83883	**RL36A 60S ribosomal protein L36a**	**1.44145341**	**0.00562**	**2**
P83883	HFELGGDK	1.1869537	1	2.37839
P83883	LECVEPNCR	1.57210026	2	2.52478
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.27122003**	**0.4979**	**3**
P83941	AMLSGPGQFAENETNEVNFR	1.37249718	2	4.9483
P83941	LISSDGHEFIVK	1.37399007	2	2.40548
P83941	TYGGCEGPDAMYVK	1.24890894	2	3.82124
P84082	**ARF2 ADP_ribosylation factor 2**	**1.11741762**	**0.96554**	**4**
P84082	EELTRMLAEDELR+Oxidation(5	1.2978886		
P84082	MLAEDELR	0.72983266	2	2.60286
P84082	NISFTVWDVGGQDK	1.23543739	2	4.32412
P84082	QDLPNAMNAAEITDK	0.83396748	2	4.20599
P84083	**ARF5 ADP_ribosylation factor 5**	**1.08452484**	**0.57457**	**4**
P84083	DAVLLVFANK	1.27025624	2	4.12166
P84083	MLQEDELR	1.17529918	2	2.47275
P84083	QDMPNAMPVSELTDK	0.95668695	2	3.3521
P84083	VQESADELQK	1.08477286	2	3.07039
P84089	**ERH Enhancer of rudimentary homolog**	**1.12420127**	**0.8239**	**2**
P84089	ADTQTYQPYNK	1.12699821	2	2.60988
P84089	TYADYESVNECMEGVCK	1.09132143	2	4.88009
P84092	**AP2M1 AP_2 complex subunit mu**	**1.17369026**	**0.30336**	**3**
P84092	ISEENIK	1.26545361	1	1.94984
P84092	SNFKPSLLAQK	1.3905055	2	2.61487
P84092	VFEPKLNYSDHDVIK	1.1410505	2	2.74565
P84100	**RL19 60S ribosomal protein L19**	**1.26716855**	**0.1835**	**3**
P84100	ILMEHIHK	2.06894141	2	2.32009
P84100	LLADQAEAR	1.36570688	2	3.31571
P84100	VWLDPNETNEIANANSR	1.13214902	2	5.6317
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**0.86220015**	**0.20833**	**2**
P84104	NPPGFAFVEFEDPRDAADAVR	1.57666577	2	2.57823
P84104	VYVGNLGNNGNK	0.28137506	2	2.43126
P84245	**H33 Histone H3.3**	**1.43458634**	**0.44437**	**6**
P84245	DIQLAR	267.550905	1	2.10984
P84245	EIAQDFK	1.33376892	1	2.04089
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	2.04453532	4	4.91517
P84245	RVTIMPKDIQLAR+Oxidation(4	1.18547198		
P84245	STELLIR	1.07095295	2	2.60949
P84245	YRPGTVALR	0.89194241	2	2.38365
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.1472433**	**0.07763**	**4**
P84817	FQSEQAAGSVSK	1.10018585	2	3.05102
P84817	GIVLLEELLPK	1.443514	2	2.95042
P84817	GLLQTEPQNNQAK	1.16374055	2	3.69501
P84817	KFQSEQAAGSVSK	1.15293444	2	4.47906
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.99888659**	**0.52406**	**16**
P85834	AEAGDNLGALVR	1.03022543	2	3.70053
P85834	DKPHVNVGTIGHVDHGK	1.10451896	2	3.84595
P85834	DLEKPFLLPVESVYSIPGR	1.78614767	2	4.22639
P85834	GDECELLGHNK	1.12874066	2	2.87543
P85834	GEETPVIVGSALCALEQR	1.16581272	2	4.40429

P85834	GITINAAHVEYSTAAR	1.94819122	2	2.84616
P85834	GTVVTGTLER	1.09458028	2	2.84794
P85834	HYAHTDCPGHADYVK	0.98556394	3	5.00971
P85834	KGDECELLGHNK	1.05272797	3	4.43353
P85834	KYEEIDNAPEER	0.99887488	2	3.79296
P85834	LLDAVDTYIPVPTR	1.2173958	2	3.68734
P85834	QIGVEHVVVYVNK	1.03769074	2	2.96328
P85834	TIGTGLVTDVPAMTEEDK	1.63671854	2	4.34158
P85834	TIGTGLVTDVPAMTEEDKNIK	1.02465037	2	4.45657
P85834	TVVTGIEMFHK	0.50484863	2	2.34417
P85834	YEEIDNAPEER	0.61171831	2	3.34903
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.53265292**	**3E-14**	**11**
P85968	AGQAVDDFIEK	1.25124487	2	3.25126
P85968	CLSSLKEER	1.46949788	2	2.59507
P85968	FQDTDGKELLPK	1.52243356	2	3.43098
P85968	GILFVGSGVSGGEEGAR	1.14525273	2	4.65492
P85968	HEMLPANLIQAQR	1.31954134	2	3.19334
P85968	LVPLLDTGDIIIDGGNSEYR	3.60808301	2	5.25314
P85968	NPELQNLLLDDFFK	2.646614	2	4.43964
P85968	SAVDDCQDSWR	0.90449113	2	2.88359
P85968	TIFQAIAAK	0.93496926	2	2.69486
P85968	VGTGEPCCDWVGDEGAGHFVK	1.26474127	2	4.34917
P85968	YGPSLMPGGNK	1.35435172	2	2.48159
P85971	**6PGL 6_phosphogluconolactonase**	**1.68033012**	**0.02703**	**5**
P85971	DLPAATAPAGPASFAR	2.51308587	2	2.44906
P85971	ILEDQESALPAAMVQPR	0.85247701	2	4.80588
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.72432401	2	4.51289
P85971	TGALCWFLDEAAAR	1.85448547	2	3.57978
P85971	WTLGFCDER	1.12048496	2	2.58393
P85972	**VINC Vinculin**	**1.13171855**	**0.8443**	**15**
P85972	ALASQLQDSLK	1.15726316	2	2.60335
P85972	AQQVSQGLDVLTAK	1.06205599	2	4.30009
P85972	AVAGNISDPGLQK	1.0696741	2	3.35269
P85972	DPNASPGDAGEQAIR	1.01817664	2	2.36029
P85972	GNDIIAAAK	1.30775317	2	2.43386
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.58710333	3	5.11621
P85972	MLGQMTDQVADLR	1.17703626	2	3.52398
P85972	MSAEINEIIR	1.13890121	2	2.43627
P85972	MTGLVDEAIDTK	1.97925615	2	2.84285
P85972	QVATALQNLQTK	1.20668363	2	3.38661
P85972	SLLDASEEAIKK	1.10112613	2	2.73273
P85972	STVEGIQASVK	1.09291571	2	2.6099
P85972	VDQLAAQLADLAAR	1.26101393	2	3.26841
P85972	VLQLTSWDEDAWASK	0.99521298	2	3.26238
P85972	WIDNPTVDDR	1.30349129	2	2.97304
P85973	**PNPH Purine nucleoside phosphorylase**	**1.42855511**	**9.8E-06**	**13**
P85973	ASHQEVLEAGK	0.84408844	2	3.59789
P85973	DHINLPGFCGQNPLR	1.40474967	3	4.05178
P85973	ELQEGTYIMSAGPTFETVAESCLLR	3.5180218	2	5.21222
P85973	FEVGDIMLIR	1.23184827	2	3.79963
P85973	FHMYEGYSLSK	2.10432616	2	2.33016
P85973	HRPQVAVICGSGLGGLTAK	0.97241888	3	6.00344
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.74547648	3	3.77808
P85973	MLGADAVGMSTVPEVIVAR	1.43835769	2	5.9071
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0	1.96326471		
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(8	2.19773654		

P85973	VFGFSLITNK	1.52362249	2	3.13525
P85973	VFHLLGVDTLVVTNAAGGLNPK	2.37195377	2	5.39375
P85973	VVMDYNNLEK	1.2334504	2	2.4631
P86048	**RL10L 60S ribosomal protein L10_like**	**1.49454983**	**0.37359**	**6**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.52730495	3	6.04248
P86048	GAFGKPQGTVAR	1.51781523	2	2.82714
P86048	MLSCAGADR	1.36061944	2	2.36663
P86048	RLIPDGCGVK	1.06539322	2	2.31498
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.42915415	3	5.43705
P86048	VHIGQVIMSIR	8.04588488	2	3.01557
P86252		**1.00914639**	**0.6731**	**7**
P86252	ALELDPNLYR	1.19957673		
P86252	ANGFAELIPNAQLLQK	0.65780323		
P86252	CTSLGVNQGIYEEPK	0.79778674		
P86252	LGFQGAQDLANMFRFYALKPDR	1.46052221		
P86252	LIDDYGVEEEPAELPEGTSLTVDNK	1.61446219	2	4.02937
P86252	LIDDYGVEEEPAELPEGTSLTVDNKR	2.58442141	3	4.51811
P86252	VASDAQLELDKLDGELKK	1.59862316		
P97313	**PRKDC DNA_dependent protein kinase catalytic subunit**	**1.30238166**	**0.20889**	**3**
P97313	FHGVMKTLCLEVVLCR+Oxidation(4	1.30198642		
P97313	LCHDAFTENMVGESQLLEK	7.63095329	2	2.53486
P97313	QLFSSLFSGILKEMNK+Oxidation(13	1.85306573		
P97384	**ANX11 Annexin A11**	**0.92964075**	**0.02378**	**2**
P97384	GFGTDEQAIIDCLGSR	0.86949122	2	3.95441
P97384	SELDLLDIR	1.87433159	2	2.54409
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.03861763**	**0.12359**	**8**
P97519	FDGVMQAAR	1.79920974	2	2.83092
P97519	GFEEAVAAGAK	1.72988885	2	3.3043
P97519	GYVSCALGCPYEGK	1.04312342	2	3.86554
P97519	KNVNCSIEESFQR	1.32866907	2	3.74566
P97519	LIDMLSEAGLPVIEATSFVSPK	1.53534127	2	3.10489
P97519	LLEAGDFICQALNR	0.58238793	2	4.5365
P97519	NVNCSIEESFQR	0.94752087	2	3.39504
P97519	WVPQMADHSDVLK	0.73388926	2	2.95169
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**1.0807215**	**0.82091**	**7**
P97521	CLLQIQASSGK	1.0648513	2	2.60499
P97521	EEGVTSLYK	0.88018718	1	2.03939
P97521	KLYQEFGIR	1.58573106	2	2.32925
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.20557832	2	3.84684
P97521	LYQEFGIR	1.40014549	2	2.76219
P97521	SVHDLSVPR	1.37620536	3	3.55046
P97521	YSGTLDCAK	1.29309515	2	2.35282
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**0.98244255**	**0.9691**	**13**
P97524	ALHDHLGLR	0.60552202	2	2.33459
P97524	GEVGLLICK	0.99718611	2	2.33828
P97524	MKENYEFNGK	1.19394912	2	2.80226
P97524	SLLHCFQCCGAK	0.98680932	2	2.95297
P97524	TILHVFLEQAR	0.81294995	2	3.18124
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	1.09178375	3	5.69118
P97524	TYVPMTEDIYNAIIDK	0.87788788	3	4.79446
P97524	VDGVSADPIPESWR	1.25887733	2	2.8722
P97524	VLLASPELHEAVEEVLPTLK	0.97826467	3	4.92837
P97524	VTLMEEGFNPSVIK	1.93075511	2	4.18738
P97524	YDVEKDEPVR	1.0396136	2	2.89871

P97524	YLCNTPQKPNDR	1.16449179	2	3.21542
P97524	YNATVIQYIGELLR	0.82013443	2	3.48417
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.22975381**	**4.8E-06**	**10**
P97532	AFGHHSVSLLDGGFR	1.13368959	3	3.68447
P97532	ALVSAQWVAEALK	0.85630773	2	3.89037
P97532	AQPEHVISQGR	1.13860379	2	3.20836
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.61751771	3	6.45815
P97532	FQGTQPEPR	1.10376172	2	3.61153
P97532	HIPGAAFFDIDR	1.35799003	2	2.55749
P97532	LLDASWYLPK	1.69971975	2	3.73522
P97532	SPSEPAEFCAQLDPSFIK	1.2305226	2	2.95029
P97532	THEDILENLDAR	1.21255076	2	3.8751
P97532	YWLSQNLPISSGK	1.10153298	2	3.95519
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.11661835**	**0.03092**	**7**
P97536	AADIDQEVK	1.02587849	2	2.4843
P97536	EGPAVVGQFIQDVK	2.46764291	2	2.72115
P97536	FTISDHPQPIDPLLK	1.16003112	2	2.59571
P97536	ITSEALLVTQQLVK	1.50557025	2	3.15254
P97536	LGTLSALDILIK	2.8277983	2	2.45544
P97536	SVILEAFSSPSEEVK	1.7895701	2	2.88589
P97536	TYIQCIAAISR	1.10988809	2	3.45873
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.06442496**	**0.98507**	**16**
P97562	ATFADFCAQGAEICR	1.04076165	2	4.74954
P97562	CSAQTAADFR	1.16832762	2	2.93616
P97562	DFSLLPELHALSTGMK	0.8144789	2	2.82399
P97562	EAFLDLLPLIR	1.01177358	2	2.86014
P97562	ILEYQTQQQK	1.0757881	2	3.73719
P97562	KVESIIQSDPVFNLK	1.28197462	2	5.03614
P97562	LDKEPEIQR	1.06703673	3	3.40215
P97562	LFEWAQK	0.94246445	2	2.52092
P97562	LGTPQSNYLGMLVTR	1.54079118	2	3.37665
P97562	LSGLPTLVAR	1.61219495	2	2.52578
P97562	LTNILDGGLPNTVLR	1.24402775	2	4.49674
P97562	SGVDQHDAWNQTTVIHLQAAK	1.08859771	3	6.02312
P97562	SLEDHTPLPGITVGDIGPK	0.89150357	3	4.34066
P97562	SLGSDEQIAK	1.03921997	2	3.00689
P97562	VESIIQSDPVFNLK	1.08665951	2	4.26298
P97562	VLDGNVNLSLHGVAMNAIR	0.84392996	2	4.33949
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.08257108**	**0.19617**	**4**
P97576	ALADTENLR	1.9127671	2	2.58873
P97576	DLLEVADILEK	1.07850565	2	3.68469
P97576	EEVSNNNPHLK	1.56701234	2	3.04738
P97576	TLRPALVGVVK	0.95912455	3	3.54107
P97584	**PTGR1 Prostaglandin reductase 1**	**0.95223582**	**0.89001**	**6**
P97584	ALTDLMNWVSEGK	0.87125035	2	4.18498
P97584	GGETVLVNAAAGAVGSVVGQIAK	1.41775343	2	4.19693
P97584	HFEGFPTDSNFELR	1.02854494	2	3.78283
P97584	LKEGDSMMGEQVAR	1.17088104	2	3.77997
P97584	TGPCPPGPSPEVIIYQQLR	1.04190226	2	4.12981
P97584	YHEYITEGFEK	0.95409379	2	2.9319
P97608	**OPLA 5_oxoprolinase**	**1.25606724**	**0.91757**	**8**
P97608	AGDFGAAFVER	1.11230752	2	2.93049
P97608	GHTACADAYLTPTIQR	1.08829506	2	4.58662
P97608	GSILDPSPEAAVVGGNVLTSQR	1.34448472	2	4.96314
P97608	ISVGAEGPSMADTR+Oxidation(9	0.65164675		
P97608	ITDPEILESR	1.58017829	2	2.37036

P97608	LLSEDPANYADAPTEGIR	1.22404608	2	4.94868
P97608	SGLQLEDTPK	1.17173154	2	2.62954
P97608	TGDLLEIQQPVDLEALR	1.46968492	2	4.63633
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.37649199**	**6.9E-05**	**7**
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.49993417	3	3.97085
P97612	GTNCVTSYLTDCETQLSQAPR	1.12602882	2	4.94526
P97612	GYFGDIWDIILK	1.89858287	2	3.8686
P97612	NSVGLPVAVQCVALPWQEELCLR	2.4936356	3	3.81573
P97612	QGLLYGVPVSLK	1.06062672	2	2.85252
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	1.94632094	2	4.75659
P97612	VGYYETDNYTMPSPAMR	1.4102396	2	4.02943
P97690	**SMC3 Structural maintenance of chromosomes protein 3**	**1.19850236**	**0.63862**	**2**
P97690	KMVTKNDVMNLLESAGFSR+Oxidation(1	1.19863766		
P97690	NLEQYNKLDQDLNEVK	1.16841547	2	2.59066
P97697	**IMPA1 Inositol monophosphatase 1**	**1.47307573**	**0.00063**	**2**
P97697	SSPADLVTVTDQK	1.34163483	2	2.85215
P97697	VSQQEDITK	1.56840624	2	2.80689
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.0308602**	**0.01586**	**3**
P97700	AVVVNAAQLASYSQSK	1.02497298	2	4.98374
P97700	GIYTGLSAGLLR	1.24817506	2	2.9893
P97700	LTGADGTPPGFLLK	1.39075451	2	3.86219
P97834	**CSN1 COP9 signalosome complex subunit 1**	**2.20345137**	**0.24743**	**3**
P97834	EGSQGELTPANSQSR	1.67205222	2	2.88486
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(0	2.26934602		
P97834	MLDEMKDNLLLDMYLAPHVR+Oxidation(4	2.26934602		
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.83528047**	**0.1406**	**25**
P97852	AAVAVPSRPPDAVLR	0.92012749	2	2.30481
P97852	AVANYDSVEAGEK	0.97473003	2	3.81081
P97852	AYALAFAER	0.91029984	2	3.41125
P97852	CEAVIADILDK	0.92435156	2	2.56768
P97852	DTTSLNQAALYR	0.96451993	2	2.89049
P97852	FVYEGSADFSCLPTFGVIVAQK	1.78210436	2	3.68289
P97852	GALVVVNDLGGDFK	1.31579962	2	3.86066
P97852	GSSAADKVVEEIR	0.85637562	2	3.45239
P97852	HVLQQFADNDVSR	0.84432983	2	4.7001
P97852	ICDFSNASKPK	1.14199195	3	3.90532
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	0.95674766	3	5.6722
P97852	IDVVVNNAGILR	0.91664821	2	4.07432
P97852	ISDEDWDIIQR	1.31316338	2	3.69188
P97852	KNNIHCNTIAPNAGSR	0.79320021	2	5.0497
P97852	LGLLGLANTLVIEGR	1.63199745	2	3.62375
P97852	LNPQNAFFSGR	0.71913766	2	2.83874
P97852	NGSGEVYQGPAK	0.88846233	2	3.49526
P97852	NNIHCNTIAPNAGSR	0.81775251	2	4.6499
P97852	NQPMTPEAVR	0.84933323	2	2.35201
P97852	SIQESTGGIIEVLHK	0.82663836	2	4.16707
P97852	SLMSGGLAEVPGLSINFAK	1.04139522	2	4.57451
P97852	TALDTFGR	1.37213653	2	2.33081
P97852	VLHGEQYLELYKPLPR	0.86252191	2	5.01675
P97852	VNAVFEWHITK	0.8848187	2	3.16815
P97852	VVLVTGAGGGLGR	0.80818959	2	4.37584
P97874	**GAK Cyclin_G_associated kinase**	**1.07181405**	**0.50567**	**2**
P97874	AMVEEEITRNTTPMYR+Oxidation(13	3.06527865		
P97874	QELARDTDPFKLK	1.04356847	2	2.40881

Q00238	**ICAM1 Intercellular adhesion molecule 1**	**0.86732732**	**0.94132**	**2**
Q00238	LDTPDLLEVGTQQK	0.86622492	2	3.51144
Q00238	VELDPLPAWQQVGK	1.0457698	2	2.48009
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.53101013**	**0.33741**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	1.62365657	2	4.6329
Q00438	IIVENLFYPVTLDVLHQIFSK	1.50402895	3	4.3289
Q00438	KLPSDVTEGEVISLGLPFGK	1.41582222	2	4.36934
Q00438	NNQFQALLQYADPVSAQHAK	1.54869731	2	5.46689
Q00981	**UCHL1 Ubiquitin carboxyl_terminal hydrolase isozyme L1**	**1.20250946**	**0.46602**	**2**
Q00981	KQIEELK	1.41379197	2	2.35295
Q00981	MQLKPMEINPEMLNK+Oxidation(0	1.20175907		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.94681669**	**0.69737**	**3**
Q00PI9	AVEEQGDDQDSEK	1.35644905	2	3.98971
Q00PI9	EEAQPIVTKYK	1.75719888	1	1.97118
Q00PI9	SGDETPGSEAPGDK	1.98867427	2	3.24144
Q01177	**PLMN Plasminogen**	**0.89443697**	**0.95298**	**3**
Q01177	ILGSDVQQIAVTK	0.89322091	2	3.79419
Q01177	LVLEPNDADIALLK	0.86836258	2	2.81975
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	1.01031262	3	4.06154
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.09086349**	**0.48429**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	1.08245617	2	6.16508
Q01205	NDVITVQTPAFAESVTEGDVR	1.48176216	2	5.40729
Q01205	NVETMNYADIER	1.15846854	2	3.76866
Q01205	VEGGTPLFTLR	0.83208948	2	3.43586
Q01279	**EGFR Epidermal growth factor receptor**	**1.11254565**	**0.64778**	**2**
Q01279	NLQEILIGAVR	1.96794155	2	3.96008
Q01279	NYVVTDHGSCVR	0.96579131	2	2.69813
Q01405	**SC23A Protein transport protein Sec23A**	**1.30808805**	**1.8E-05**	**8**
Q01405	AETEEGPDVLR	1.40451354	2	3.22714
Q01405	AVLNPLCQVDYR	1.58099026	2	2.71889
Q01405	HFEALANR	0.98191408	1	2.021
Q01405	HLLQAPVDDAQEILHSR	1.29494883	3	5.49159
Q01405	MVVPVAALFTPLK	1.56558957	2	2.62188
Q01405	SGYQDMPEYENFR	0.15596923	2	3.09491
Q01405	SWHDIEKDNAK	1.33823136	2	3.13193
Q01405	YIDTEHGGSQAR	1.30407925	2	3.4385
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.99348547**	**0.89479**	**33**
Q02253	AEMEAAVAACK	1.32730276	2	4.01936
Q02253	AEMEAAVAACK+Oxidation(2	1.54026227		
Q02253	AEMEAAVAACKR	1.2453755	2	3.11029
Q02253	AFPAWADTSILSR	1.36712387	2	4.13204
Q02253	AISFVGSNQAGEYIFER	0.84844757	2	5.27586
Q02253	CMALSTAVLVGEAK	1.44664526	2	4.49299
Q02253	CMALSTAVLVGEAK+Oxidation(1	1.07897262		
Q02253	EEDATLSSPAVVMPTMGR	1.77611838	2	4.73156
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12	7.50263151		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15	7.50263151		
Q02253	EEIFGPVLVVLETETLDEAIK	0.95373584	2	3.30997
Q02253	ENTLNQLVGAAFGAAGQR	1.10755513	2	5.14734
Q02253	GDTNFYGK	1.09600093	2	2.61748
Q02253	GLQVVEHACSVTSLMLGETMPSITK	1.52854282	2	5.64712

Q02253	GYENGNFVGPTIISNVKPSMTCYK	1.18218992	3	3.85656
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.047052	2	5.39841
Q02253	KWLPELVER	1.73604125	3	3.3318
Q02253	LFIDGK	3.35856253	1	2.01425
Q02253	LITLEQGK	1.13156293	2	2.82319
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	0.87263332	3	4.35551
Q02253	NHGVVMPDANK	1.22322907	2	3.56681
Q02253	NHGVVMPDANK+Oxidation(5	1.1506875		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	1.43024727	3	6.13728
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5	1.29328782		
Q02253	QGIQFYTQLK	1.15762359	2	2.79436
Q02253	SDKWIDIHNPATNEVVGR	0.98074323	2	5.26877
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	1.09559967	2	5.47582
Q02253	TLADAEGDVFR	0.94687041	2	3.67223
Q02253	VCNLIDSGAK	1.09777741	2	3.39308
Q02253	VNAGDQPGADLGPLITPQAK	1.18681541	2	5.87971
Q02253	WIDIHNPATNEVVGR	0.88948327	2	4.89131
Q02253	WLPELVER	0.98586794	2	2.40156
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.80444067	3	3.527
Q02769	**FDFT Squalene synthase**	**0.72082965**	**0.01789**	**4**
Q02769	KLEDFVKPENVDVAVK	0.72085347	2	4.03598
Q02769	SFAAVIQALDGDIR	0.64939163	2	3.66306
Q02769	TQSLPNCQLISR	0.51210158	2	2.91068
Q02769	VVLEDFPTISLEFR	1.496223	2	3.28107
Q02874	**H2AY Core histone macro_H2A.1**	**1.1496872**	**0.48933**	**4**
Q02874	AASADSTTEGAPTDGFTVLSTK	1.10596082	2	4.1946
Q02874	GVTIASGGVLPNIHPELLAK	1.47610772	2	4.20125
Q02874	NCLALADDR	1.60765876	2	2.47509
Q02874	NGPLEVAGAAVSAGHGLPAK	0.92354769	2	2.81014
Q02974	**KHK Ketohexokinase**	**1.09738804**	**0.00087**	**8**
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.19209165	3	5.58082
Q02974	GGNASNSCTVLSLLGAR	1.32208055	2	4.72008
Q02974	GNSMQEALR	1.24279637	2	3.00488
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.89280167	3	5.85364
Q02974	IEQYNATQPLQQK	0.94546955	2	4.81642
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.49446746	3	6.50053
Q02974	TIILYDTNLPDVSAK	1.09582966	2	5.15103
Q02974	VSVEIEKPR	1.25233266	2	2.51895
Q03248	**BUP1 Beta_ureidopropionase**	**1.24147237**	**9.9E-20**	**15**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.22512502	2	6.14191
Q03248	EDLVLAPSSG	1.06395233	1	2.23347
Q03248	EKLPWTEFAESAEDGLTTR	1.12385551	2	4.72128
Q03248	ELAEAVKPNYSPNIVK	1.25295631	2	4.65263
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	3.38556963	3	3.49001
Q03248	HLPPDDLSQVK	1.08800363	2	2.52937
Q03248	HNMVVISPILER	1.29458576	2	3.08294
Q03248	HNMVVISPILER+Oxidation(2	1.39805162		
Q03248	IPLPTSAPVAEQVSALHK	2.208885	3	4.87513
Q03248	KHNMVVISPILER	1.025262	3	3.55404
Q03248	KHNMVVISPILER+Oxidation(3	0.9170842		
Q03248	NAAIANHCFTCALNR	1.48454382	2	4.68958
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.53097832	3	5.1116
Q03248	VGQEHYPNEFTSGDGK	1.85208534	2	4.35579
Q03248	VGQEHYPNEFTSGDGKK	1.32926034	3	4.79651
Q03336	**RGN Regucalcin**	**1.16860661**	**0.92673**	**16**
Q03336	CGESPVWEEASK	1.19346794	2	4.66944

Q03336	CLLFVDIPSK	1.19735476	2	3.42409
Q03336	DEQIPDGMCIDVEGK	0.92403687	2	4.44365
Q03336	DYSEMYVTCAR	1.88540901	2	3.2685
Q03336	FNDGKVDPAGR	1.00547067	2	3.0518
Q03336	HQGSLYSLFPDHSVK	1.20222258	3	4.89784
Q03336	KYFDQVDISNGLDWSLDHK	1.23334183	3	4.96737
Q03336	LWVACYNGGR	1.11449811	2	2.76679
Q03336	MEKDEQIPDGMCIDVEGK	0.95113575	2	5.0652
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0	0.97105227		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10	1.43095071		
Q03336	QSGGYVATIGTK	1.158398	2	2.78621
Q03336	VGVDAPVSSVALR	1.03000401	2	3.56801
Q03336	YFAGTMAEETAPAVLER	1.28166358	2	5.67048
Q03336	YFAGTMAEETAPAVLER+Oxidation(5	0.9001496		
Q03336	YFDQVDISNGLDWSLDHK	1.29840145	2	4.6959
Q03410	**SYCP1 Synaptonemal complex protein 1**	**1.17073071**	**0.38197**	**2**
Q03410	ATVDEAVKLQKEIDLR	0.98925174	2	2.46675
Q03410	LKMEQENTAILTDK	1.34713688	2	2.36828
Q03626	**MUG1 Murinoglobulin_1**	**1.06101263**	**0.76668**	**7**
Q03626	EDNSIHWERPQKPTK	0.67369798	2	2.6232
Q03626	EESSCIHSSCTAER	1.08565897	2	4.23187
Q03626	GGEFEMMPLGVNK	0.7465529	2	3.47751
Q03626	LTAQPAPSPEDLALSMGTIK	1.32411002	3	4.12259
Q03626	NLHPLNELFPLAYIEDPK	1.64508485	3	4.11805
Q03626	VQTVPLTCNNPK	1.06684477	2	2.96447
Q03626	VYHKEESSCIHSSCTAER	1.00462441	2	5.81911
Q04462	**SYVC Valyl_tRNA synthetase**	**1.26081107**	**0.98732**	**4**
Q04462	ALNPLEEWLR	0.99958972	2	2.33317
Q04462	ITPAHDQNDYEVGQR	1.26084845	2	3.68737
Q04462	LQQTEAELR	0.94760795	2	2.34132
Q04462	SVTQQPGSEITAPQK	1.1277706	2	3.54637
Q05982	**NDKA Nucleoside diphosphate kinase A**	**1.41882393**	**0.22169**	**2**
Q05982	EISLWFQPEELVDYK	1.54959978	2	2.85258
Q05982	FIQASEDLLK	1.38960422	2	2.36531
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.2344628**	**2.9E-10**	**8**
Q06647	FSPLTANLMNLLAENGR	1.88168799	2	4.31037
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.17133107	3	6.04703
Q06647	GQILNLEVK	0.92816249	2	2.73665
Q06647	LGNTQGVISAFSTIMSVHR	1.9094234	3	3.64138
Q06647	TDPSIMGGMIVR	1.25985266	2	3.32039
Q06647	TVLNSFLSK	1.05963578	2	2.72552
Q06647	VGQLLKDPK	1.77856999	1	2.1613
Q06647	VSLAVLNPYIK	1.42675955	2	3.58112
Q07071	**GCKR Glucokinase regulatory protein**	**1.54377932**	**5.9E-09**	**13**
Q07071	AAPISCHVQVAHEK	1.43126101	2	4.90169
Q07071	CIESLLQAIHFPQPLSDDVR	1.56508385	3	4.44121
Q07071	CLLEILR	1.99946897	2	2.52696
Q07071	GFLIGDHSDMFNQK	1.56527196	2	3.83192
Q07071	LLGQCDAEIFQEEGQIVPTYQR	4.01599686	2	5.03187
Q07071	LSAASSVCEVVR	2.32321347	2	2.792
Q07071	LYSESVLTTMLQVAGK	1.72272227	2	3.83555
Q07071	QEAFVLNPAIGPEGLSGSSR	1.63618566	2	4.86258
Q07071	TVDQGVVSSQR	1.51857212	2	3.56929
Q07071	VIPTALLSLLLR	2.84773634	2	2.96802
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.60871421	2	5.05545
Q07071	WVLNTVSTGAHVLLGK	2.85074415	2	3.4445
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.33292087	3	6.07007

Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**1.14281486**	**0.61433**	**9**
Q07116	AVDDSYNVQPDTVAPIWNLR	1.47150892	2	4.61876
Q07116	ETEAHVCFEGLDSDPTGTAYGASIPLAR	3.45911501	3	3.93677
Q07116	FVDLHPGGQSK	1.30941161	2	2.67693
Q07116	IGELNPEDR	0.97508318	2	2.4432
Q07116	LCDVLAQAGHR	0.67365637	2	3.24045
Q07116	LHVVGAPGGQSLSLSLDDLHK	1.86512536	3	3.70607
Q07116	MSPPLEASDPYSNDPMR	1.44722559	2	3.82777
Q07116	NHLPVPNLDPDTYR	1.04956411	2	2.66884
Q07116	VSVESEESYSHWQR	1.05881533	2	4.12602
Q07205	**IF5 Eukaryotic translation initiation factor 5**	**1.00869673**	**0.62537**	**3**
Q07205	AMGPLVLTEVLFDEK	1.3290083	2	3.67745
Q07205	LQDMLDGFIK	1.3244753	2	2.31177
Q07205	TVIVNMVDVAK	1.00519268	2	2.85976
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.64583124**	**0.01407**	**12**
Q07523	ALKEEKPTQSVPVSFPK	0.58139826	2	4.81859
Q07523	ALVITIDTPVLGNR	0.74305083	2	3.96141
Q07523	ASFCWNDLSLLQSITR	1.27616515	2	4.07296
Q07523	EDAELAMK	1.36112762	1	2.01864
Q07523	EEKPTQSVPVSFPK	0.80904036	2	3.76491
Q07523	EVLDILTAELHR	1.01033994	2	3.27532
Q07523	GEDGVKEVLDILTAELHR	0.99055991	3	5.12781
Q07523	HNVQGIVVSNHGGR	0.78127674	3	6.36064
Q07523	NQLNLEANILLK	0.79714638	2	3.88023
Q07523	QLDEVSASIDALR	0.71346965	2	3.11643
Q07523	TSWDFIEGEADDGITYSENIAAFK	1.07762516	3	3.30194
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	0.88752354	3	4.73957
Q07803	**EFGM Elongation factor G_ mitochondrial**	**1.66963357**	**0.21232**	**4**
Q07803	GIIDLIEER	1.67004876	2	2.86931
Q07803	LEFSDETFGANVPK	1.30347177	2	2.85278
Q07803	NYQGELKK	0.55999457	1	2.08622
Q07803	YQPCSPSTQEELVNK	2.63926377	2	3.09254
Q07936	**ANXA2 Annexin A2**	**0.98721468**	**0.77071**	**3**
Q07936	GLGTDEDSLIEIICSR	1.34674749	2	3.37049
Q07936	GVDEVTIVNILTNR	0.98554383	2	3.10122
Q07936	TNQELQEINR	1.43233598	2	2.95204
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.36280895**	**9.6E-05**	**3**
Q07984	FFDEESYSLLR	1.66180482	2	3.67008
Q07984	NNEDVSIIPPLFTVSVDHR	1.33123185	2	4.33862
Q07984	VQNMALYADVSGK	1.19687018	2	3.69997
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**1.33322295**	**0.97019**	**7**
Q08163	ALLVTASQCQQPAGNK	0.99784877	2	4.09057
Q08163	KEPALLELEGK	1.29839047	2	2.34322
Q08163	LEAVSHTSDMHCGYGDSPSK	1.34473809	3	5.07489
Q08163	NSLDCEIVSAK	1.1582354	2	3.07278
Q08163	SALFAQINQGESITHALK	1.3234462	2	4.18021
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	2.03502501	2	4.26463
Q08163	VENQENVSNLVIDDTELK	1.61230881	2	5.36006
Q08201	**MDR2 Multidrug resistance protein 2**	**1.62339354**	**0.41792**	**2**
Q08201	AKLSAAYLFSLFERQPLIDSYSR	1.56046062	2	2.5521
Q08201	FDTLVGDRGAQLSGGQK	1.9301454	2	2.53732
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.31846513**	**0.00834**	**6**
Q08415	ATLQAMDER	1.31068118	2	2.43284
Q08415	EQQHFGQPSSYFLQLPQAMELNR	1.3184537	3	5.71025
Q08415	ILVLNTPNNPLGK	2.04932664	2	3.26915

Q08415	LGASNDWQLDPAELASK	5.0923262	2	4.25427
Q08415	RLDGIDQNLWVEFGK	0.96195733	2	2.36245
Q08415	VGWVMGPDNIMK	1.22480273	2	2.45041
Q09073	**ADT2 ADP/ATP translocase 2**	**1.41921902**	**0.43517**	**7**
Q09073	AAYFGIYDTAK	1.37601895	2	2.42624
Q09073	DFLAGGVAAAISK	2.14547162	2	4.93099
Q09073	GLGDCLVK	1.44526591	2	2.80029
Q09073	GTDIMYTGTLDCWR	1.6488928	2	3.61974
Q09073	KGTDIMYTGTLDCWR	1.23744375	3	3.78966
Q09073	LLLQVQHASK	1.91579301	2	2.77317
Q09073	QIFLGGVDKR	1.19755698	2	2.39185
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.89961365**	**0.21373**	**9**
Q0D2L3	EAYQNILATGCIPLTLGGDHTITYPILQAVAK	1.6560936	3	4.13204
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	1.52442934	2	3.57721
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	1.10946427	3	3.53353
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	1.45976703	3	4.45837
Q0D2L3	SVDEGLLDSK	0.37622324	2	2.74482
Q0D2L3	SVDEGLLDSKR	1.10545214	2	3.14827
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.50060922	2	5.29579
Q0D2L3	VCSMMHLPLQSSPEGLDAAFVGVPLDTGTSNRPGAR	2.45770043	3	5.56457
Q0D2L3	VVLAEDCWMK	1.17701759	2	2.52312
Q0VAV2	**EXPH5 Exophilin_5**	**0.27166433**	**0.61111**	**4**
Q0VAV2	DMDVSVSKDEQLNK	0.90981822	2	2.32847
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1	0.26570061		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)Oxidation(7	0.64025061		
Q0VAV2	SLSDQDPGQEQREEK	1.11066756	2	2.48273
Q0VGK3	**GLCTK Glycerate kinase**	**1.15663097**	**0.43945**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	1.24036658	2	5.17847
Q0VGK3	GATIQELNTIR	1.92490882	2	2.80106
Q0VGK3	QLFDSAVGAVQPGPMLQR	1.03187686	2	3.58777
Q0ZHH6	**ATLA3 Atlastin_3**	**1.30248489**	**0.19775**	**7**
Q0ZHH6	ALASVLLQDHIR	1.72245002	2	2.61704
Q0ZHH6	EHQHEEIQNVR	1.31309306	2	3.39878
Q0ZHH6	EQLQTLIPYVLNPSK	1.34593749	2	2.76003
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	1.23394957	2	4.5233
Q0ZHH6	IYQGEDLPHPK	1.28888908	2	2.52423
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2	1.09074174		
Q0ZHH6	YQQELEEEITELYENFCK	1.49523385	2	5.27601
Q10728	**MYPT1 Protein phosphatase 1 regulatory subunit 12A**	**0.97775499**	**0.71143**	**2**
Q10728	EQENEEKDKEEK	1.3739383	2	2.32477
Q10728	SLLEMEKRER+Oxidation(4	0.91134302		
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**1.00299854**	**0.98207**	**27**
Q10758	AEAETMYQIK	1.24129163	2	3.32209
Q10758	AQYEEIANR	1.12341802	2	3.13165
Q10758	ATLEAAIADAEQR	0.98450982	2	4.70628
Q10758	DVDEAYMNKVELESR	0.7424441	2	3.44792
Q10758	ELQSQISDTSVVLSMDNSR	1.17119387	2	6.24015
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	1.07320229	2	4.99104
Q10758	KDVDEAYMNK	1.05635138	2	3.31882
Q10758	LEGLTDEINFLR	1.25003962	2	4.39292
Q10758	LESGMQNMSIHTK	1.4166346	2	3.87926
Q10758	LEVDPNIQAVR	1.14023319	2	3.69396
Q10758	LEVELGNMQGLVEDFK	1.33817718	2	5.05751
Q10758	LKLEVELGNMQGLVEDFK	1.36922851	3	3.52064
Q10758	LQAEIDALK	1.07642702	2	2.97322
Q10758	LVSESSDIMSK	1.27417113	2	3.49612

Q10758	QIHEEEIR	0.9338737	1	2.19595
Q10758	QLEALGQEK	1.03332576	1	2.16785
Q10758	RQLEALGQEK	0.98556912	2	2.57175
Q10758	SKTEISEMNR	1.32503921	3	3.76008
Q10758	SKTEISEMNR+Oxidation(7	1.25907605		
Q10758	SLDMDSIIAEVR	0.95092477	2	4.67944
Q10758	SNMDNMFESYINNLR	0.97658616	2	4.2057
Q10758	SRAEAETMYQIK	1.12336449	2	3.67364
Q10758	TEISEMNR	1.44106275	2	2.32093
Q10758	TEMENEFVLIK	1.08013578	2	3.60466
Q10758	TEMENEFVLIK+Oxidation(2	1.14508207		
Q10758	WSLLQQQK	0.86584707	2	3.00572
Q10758	YEELQTLAGK	0.96261958	2	3.60237
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**1.0497339**	**0.98425**	**2**
Q148W0	LGQSHFINWDLQMYYAEK+Oxidation(12	0.96343502		
Q148W0	TCEVIKDGRFK	1.05758052	1	2.296
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**1.43277864**	**0.76283**	**7**
Q14DH7	CVPGYNVMILDDNMQK	1.67350872	2	2.97358
Q14DH7	IAIIYDSPVTDTK	1.14256293	2	2.93041
Q14DH7	STLSALVNGKPYK	0.67726806	2	2.78172
Q14DH7	THFAASVADPER	1.40199776	2	3.66633
Q14DH7	VDDVINVAGHR	1.8412044	2	3.61651
Q14DH7	VLAEHGVAALFTAPTAIR	1.2863148	2	4.42953
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.11295846	2	3.42567
Q1H5H1	**SELT Selenoprotein T**	**1.4892424**	**0.25878**	**2**
Q1H5H1	IEGENYLPQPIYR	1.39627969	2	2.83603
Q1H5H1	LESGHLPSMQQLVQILDNEMK	1.53752868	3	3.98488
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**1.24979849**	**0.98863**	**11**
Q1HCL7	GSSYSGLLER	1.16528632	2	2.43481
Q1HCL7	LKPVIGVNTDPER	1.37229603	3	3.4647
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.3222491	3	5.23048
Q1HCL7	NVEHIIDSLRDEGIEVR	0.9769377	2	3.5436
Q1HCL7	QGNLTLPLNK	1.49094195	2	2.48926
Q1HCL7	SEASGPQLLPVR	1.1717592	2	3.10753
Q1HCL7	SEGHLCLPVR	0.80945278	2	2.77451
Q1HCL7	SSGLNLCTGTGSK	1.04078761	2	3.61795
Q1HCL7	VTNEYNESLLYSPEEPK	1.30909252	2	4.72269
Q1HCL7	YAELSEEDLK	1.33139234	2	2.77213
Q1HCL7	YTHSFPEALQK	1.43638039	2	2.49373
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.17698398**	**0.9169**	**7**
Q1JU68	AVEDIHGLFSLSK	2.27870503	2	3.19418
Q1JU68	EEEEQRRAEEQMLK	1.13118627	2	2.4563
Q1JU68	FNVLQYVVPEVK	1.44787184	2	3.40989
Q1JU68	ILQEHEQIK	1.20131414	2	2.3826
Q1JU68	KGPEADSEWR	0.96157826	2	2.61071
Q1JU68	LLDMDGIIVEK	0.77252677	2	3.01552
Q1JU68	NQLTAMSSVLAK	0.92194377	2	2.77784
Q29RW1	**MYH4 Myosin_4**	**1.19204539**	**0.66782**	**13**
Q29RW1	ANLMQAEIEELR	2.73410543	2	2.94908
Q29RW1	ELENEVENEQKR	3.6820001	2	3.10978
Q29RW1	GQDDLKEQLAMVER	1.3606615	2	2.87192
Q29RW1	LQDAEEHVEAVNSK	2.81080895	2	4.84159
Q29RW1	LQDLVDKLQTK	1.65297222	1	1.94186

Q29RW1	MEGDLNEMEIQLNHANR	1.42463241	2	4.04416
Q29RW1	MEIDDLASNMETVSK	6.67824273	2	4.33588
Q29RW1	NAYEESLDQLETLKR	3.16772375	2	4.01644
Q29RW1	SAETEKEMATMK	1.08057455	2	2.77454
Q29RW1	SELQASLEEAEASLEHEEGK	1.65289829	2	4.85812
Q29RW1	TEGGATVTVK	3.43206788	2	2.91739
Q29RW1	TKLEQQVDDLEGSLEQEK	1.02715731	2	4.93899
Q29RW1	TKLEQQVDDLEGSLEQEKK	2.56278794	3	4.62526
Q2PQA9	**KINH Kinesin_1 heavy chain**	**1.35782089**	**0.57983**	**4**
Q2PQA9	HVAVTNMNEHSSR	3.00031629	3	4.04124
Q2PQA9	MEENEKELAACQLR	1.52946504	2	2.35641
Q2PQA9	SAEVDSDDTGGSAAQK	1.2173927	2	5.21531
Q2PQA9	TGAEGAVLDEAK	1.26665503	2	2.42435
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**1.30538708**	**0.64623**	**6**
Q2TA68	AKNEILDEVISLSQVTPK	1.32141088	2	3.96823
Q2TA68	AVEVAWETLQDEFSR	1.28256646	2	2.3639
Q2TA68	GKEHDDIFDK	1.25668201	2	2.40361
Q2TA68	IDQLQEELLHTQLK	0.9984991	2	2.64901
Q2TA68	TSVLEMIAQAR	0.93011045	2	3.29925
Q2TA68	VVVVGDQSAGK	1.37349374	2	2.54199
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.43271631**	**0.00198**	**7**
Q2V057	ASIYGQFVAGETAEEVR	1.82996756	2	3.18024
Q2V057	EDCTQPDYEATSR	1.48084066	2	3.92341
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.27472306	3	3.60321
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.4878967	2	5.4459
Q2V057	SIPYGCLEEVIPYLIR	3.17903465	2	2.53174
Q2V057	SVTQLHGKEDCTQPDYEATSR	1.19410679	3	5.44921
Q2V057	TSEAWYEGNLSAMLHCVDLSR	1.42139474	2	3.45397
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.15789537**	**0.31845**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	1.09359175	3	4.74095
Q3B7D0	FGLFTPGSR	1.21192342	2	2.33909
Q3B7D0	HCDDSYTPQDK	1.61929923	2	3.78569
Q3B7D0	LEEDGDELAR	2.55392118	2	2.82395
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.11685175**	**0.99998**	**4**
Q3B7U9	SCSQVLEHQPDNIK	1.12124995	2	4.13734
Q3B7U9	TAEDGPDLEMLSGQER	1.07645651	2	4.21666
Q3B7U9	VDMTCEEEEELLQLK	1.12083431	2	4.14715
Q3B7U9	VLAQQGEYSEAIPILR	0.94371152	2	3.4743
Q3B8Q2	**IF4A3 Eukaryotic initiation factor 4A_III**	**1.22409747**	**0.82488**	**2**
Q3B8Q2	GIYAYGFEKPSAIQQR	1.22393915	2	4.58426
Q3B8Q2	GRDVIAQSQSGTGK	1.25246545	2	3.88809
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.16436105**	**0.34684**	**3**
Q3KRD8	ASFENNCEVGCFAK	1.16408486	2	2.43011
Q3KRD8	HGLLVPNNTTDQELQHIR	1.30661251	3	4.83218
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.451427	3	3.90298
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.20940137**	**0.47132**	**3**
Q3KRE0	GEGTGPPLPLPPAAQPGAESGGDR	1.22197029	2	3.66028
Q3KRE0	ISVLEALR	3.30768324	2	2.41864
Q3KRE0	QQQLLNEENLR	1.16828088	2	2.36425
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**1.12624478**	**0.39666**	**2**
Q3KRE8	ALTVPELTQQMFDSK	1.21276985	2	3.22134
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.43177361	3	5.05137
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**1.16396952**	**0.94453**	**2**

Q3MIB4	MEIIQVPGYTQEEK	1.16436454	2	3.72723
Q3MIB4	TVGVNNPVFLLDEVDK	1.05485667	2	2.44436
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**1.0755413**	**0.99576**	**6**
Q3MIE0	DGQEGIEAFIQK	1.07556157	2	2.76709
Q3MIE0	SDILHEAESEDLK	1.08742677	3	3.66626
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.15697927	2	4.73243
Q3MIE0	VALEMLFTGEPISAQEALR	0.86775803	2	3.66328
Q3MIE0	VIIISAEGPVFSSGHDLK	0.93740922	2	4.47785
Q3MIE0	VVPEEQLEEEATR	0.86099355	2	3.97194
Q3MIF4	**XYLB Xylulose kinase**	**0.91288326**	**0.34064**	**8**
Q3MIF4	CCLGWDFSTQQVK	1.76471303	2	3.20523
Q3MIF4	DLPEFGTQGGVHVHK	0.92934181	2	2.75126
Q3MIF4	FNADNMEVSAFPGDVEIR	1.27406913	2	4.45379
Q3MIF4	IHAEGLGYR	1.41695517	2	2.34742
Q3MIF4	IRDESASCSWNK	1.55534366	2	4.17306
Q3MIF4	VVAFTGDNPASLAGMR	0.9115016	2	3.87135
Q3MIF4	VWSQACLDACAPHLK	1.93103337	2	3.81145
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	2.1478324	2	5.27579
Q3SWS9	**JKIP1 Janus kinase and microtubule_interacting protein 1**	**1.29468663**	**0.61349**	**2**
Q3SWS9	LEMEENQLK+Oxidation(2	0.93856165		
Q3SWS9	VKTALLADAREEAR	1.29511307	2	2.38817
Q3T1I4	**PRRC1 Protein PRRC1**	**1.13254089**	**0.79435**	**2**
Q3T1I4	GQDDAPAGGIWGFIK	1.16992766	2	3.68292
Q3T1I4	WSGLLVTVGEVLEK	0.89446179	2	2.7461
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.2938088**	**0.00348**	**4**
Q3T1J1	EDLRLPEGDLGK	1.41192101	2	2.96803
Q3T1J1	EDLRLPEGDLGKEIEQK	1.41917422	2	4.25702
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.74440745	2	5.07142
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	2.35834695	3	4.24045
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.00486537**	**0.06615**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.12246921	3	4.02543
Q3T1K5	FTVTPSTTQVVGILK	1.36485749	2	4.08574
Q3T1K5	KVDGQQTIIACIESHQFQAK	1.04057751	3	3.77062
Q3TDQ1	**STT3B Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3B**	**1.18561095**	**0.63424**	**2**
Q3TDQ1	FGEMQLDFR	1.41317592	2	2.33488
Q3TDQ1	HLEEAFTSEHWLVR	1.18472304	3	4.07701
Q3U0D9	**HACE1 E3 ubiquitin_protein ligase HACE1**	**1.09613192**	**0.47413**	**2**
Q3U0D9	DSIFRSSCEIVSKANCAK	1.08246776	2	2.3169
Q3U0D9	MERAMEQLNRLTR	2.01237974	2	2.32771
Q3U0J8	**TBD2B TBC1 domain family member 2B**	**1.22613829**	**0.77878**	**2**
Q3U0J8	DTTDIISQHPNPSAEK	1.02369276	2	2.52619
Q3U0J8	QIELDLLRTLPNNK	1.2380639	2	2.5996
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.04360086**	**0.75989**	**2**
Q3UHR0	MQILQRKDTWAPK+Oxidation(0	1.50988309		
Q3UHR0	NLEEPGLLSR	1.04337687	2	2.36867
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.86265848**	**1.1E-06**	**3**
Q3ULJ0	GIDEGPDGLK	1.07545847	2	2.82018
Q3ULJ0	LGLMEMIAFAK	2.21697045	2	3.81507
Q3ULJ0	LTDIINNDHENVKYLPGHK	1.56088597	2	2.40201
Q3UMF0	**COBL1 Cordon_bleu protein_like 1**	**1.23531727**	**0.65411**	**2**

Q3UMF0	RAPLPPMPTSQGAAQGQERR+Oxidation(6	1.31045798		
Q3UMF0	SQGTSTYVQDR	1.22395546	2	2.39346
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.1915551**	**0.00057**	**18**
Q3UQ44	ALVGSENPPLTVIR	1.16427641	2	3.85569
Q3UQ44	AWVNQLETQTGEASK	1.08830376	2	5.20005
Q3UQ44	GVLLGIDDLQTNQFK	1.29964244	2	4.29391
Q3UQ44	HTDNTVQWLR	1.44603965	2	3.00362
Q3UQ44	KKGGEIEILNNTDNK	0.64225216	2	2.37617
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	2.14845762	3	4.71034
Q3UQ44	LGIAPQIQDLLGK	2.10814154	2	2.9931
Q3UQ44	LPYDVTTEQALTYPEVK	1.99096078	2	4.10466
Q3UQ44	LPYDVTTEQALTYPEVKNK	1.69460668	2	2.37227
Q3UQ44	LSAEEMDER	1.29661412	2	3.09178
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.20820722	2	5.23168
Q3UQ44	SKVDQVQDIVTGNPTVIK	1.0735437	2	4.99026
Q3UQ44	TALEEEIK	1.36412507	2	2.40717
Q3UQ44	TLDTLLLPTANIR	1.04075957	2	3.57865
Q3UQ44	VDFTEEEISNMR	1.65417068	2	3.95305
Q3UQ44	VDQVQDIVTGNPTVIK	1.01059587	2	5.09797
Q3UQ44	YGSIVDDER	1.2655749	2	2.45914
Q3UQ44	YQDILNEIAK	1.13604889	2	3.06104
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**1.67477392**	**0.33647**	**2**
Q3UV17	AQYEDIAQK	1.88575578	1	2.12442
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5	1.67339268		
Q3V0K9	**PLSI Plastin_1**	**1.16719353**	**0.99995**	**3**
Q3V0K9	AYFHLLNQIAPK	0.91327879	2	3.05478
Q3V0K9	KIENCNYAVELGK	1.003212	2	3.73083
Q3V0K9	QFVTPADVVSGNPK	1.22258625	2	3.30249
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.79115512**	**0.44576**	**2**
Q3V132	GNLANVIR	1.52387573	2	2.75501
Q3V132	YFPTQALNFAFK	2.16227834	2	3.40525
Q3ZAV8	**EDC4 Enhancer of mRNA_decapping protein 4**	**1.6410326**	**0.23955**	**2**
Q3ZAV8	SSHSTWPVDVSQIK	1.64606359	2	2.33053
Q3ZAV8	VISVSTSERTLLK	1.59506789	2	2.57487
Q497B0	**NIT2 Omega_amidase NIT2**	**1.19922849**	**0.44806**	**15**
Q497B0	ADLYSVESK	1.1905455	2	3.06079
Q497B0	AGTEETILYSDIDLK	1.35553176	2	3.73211
Q497B0	ASYVAWGHSTVVDPWGQVLTK	1.22022255	3	5.85666
Q497B0	AVDNQVYVATASPAR	0.88844899	2	4.68021
Q497B0	AVDNQVYVATASPARDEK	1.01724558	2	3.58641
Q497B0	ENSIYLIGGSIPEEDDGK	1.33058528	2	3.46068
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.02875465	3	4.96519
Q497B0	FAELAQIYAR	1.8755158	2	3.92586
Q497B0	IHLFDIDVPGK	1.17523922	3	3.4871
Q497B0	KIHLFDIDVPGK	1.08916864	3	4.73521
Q497B0	LALIQLQVSSIK	2.68465227	2	3.06932
Q497B0	LYNTCAVFGPDGNLLVK	1.17466721	2	4.1224
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.22931435	3	4.97485
Q497B0	TLSPGDSFSTFDTPYCR	1.20889244	2	4.7758
Q497B0	VGLGICYDMR	1.68879996	2	2.86102
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**0.94847659**	**0.79412**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.88796382	2	4.56128
Q498D5	FCNLALLLPIVTK	2.07743151	2	3.2297
Q498D5	GQLQILEK	0.90547781	1	2.059
Q498D5	LNELLTNVEELKEEIK	1.09602088	2	2.87154

Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**1.11906592**	**0.20532**	**2**
Q498U4	EEEPPEKVVDMASEK	0.44365463	2	2.3657
Q498U4	FGIVTSSAGTGTTEDTEAK	1.14242347	2	3.34286
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.25006836**	**0.01177**	**7**
Q499N5	GATLSHHNIVNNSNLIGQR	1.50309205	2	5.32955
Q499N5	GGENIYPAELEDFFHK	0.98705554	2	2.9767
Q499N5	SGETTTEEEIK	1.11852159	2	3.16073
Q499N5	TFETVGQDR	1.8611015	2	2.67236
Q499N5	TGDIASMDEQGFCR	1.1901509	2	3.72499
Q499N5	TVGECLDATAQR	2.30370398	2	2.90951
Q499N5	YIVFVEGYPLTVSGK	1.50405404	2	4.37984
Q4AEF8	**COPG Coatomer subunit gamma**	**1.23731613**	**0.47624**	**6**
Q4AEF8	FGAQNEEMLPSILVLLK	1.38583865	2	3.50185
Q4AEF8	SLPYNQPGTCYTLVALPK	1.05179074	2	2.44093
Q4AEF8	SSPEPVALTESETEYVIR	1.37172791	2	3.61256
Q4AEF8	TLEEAVGNIVK	1.07450336	2	2.64028
Q4AEF8	VVLEHEEVR	1.52387199	2	2.4354
Q4AEF8	VVVVQAISALCQK	3.08484959	2	2.46967
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.14752415**	**0.09825**	**5**
Q4FZT0	AEQINQAAGEASAVLAK	1.12573631	2	4.7049
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.5247805	2	5.54852
Q4FZT0	ATVLESEGTR	1.14741937	2	2.80368
Q4FZT0	DVQTTDTSIEELGR	1.88384119	2	2.9225
Q4FZT0	ILEPGLNVLIPVLDR	1.3074139	2	3.01991
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.15605573**	**0.98566**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	1.10228051	3	4.8805
Q4FZT9	FGGSGSQVDSAR	1.21808518	2	3.39619
Q4FZT9	SETELKDTYAR	1.24685623	2	3.04089
Q4FZT9	SGALLACGIVNSGVR	1.2157739	2	3.36753
Q4FZT9	SSTTSMTSVPKPLK	0.96846582	2	3.49787
Q4FZT9	TITGFQTHTTPVLLAHGER	1.11648175	3	3.92593
Q4FZT9	TPVQSQQPSATAPSGADEK	1.02241329	2	4.87975
Q4FZT9	VGQAVDVVGQAGKPK	0.90663964	2	3.46212
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.44573832**	**2E-07**	**4**
Q4FZX7	GDAGSADVQDLEK	3.41922755	2	3.4692
Q4FZX7	GNSLTLIDLPGHESLR	1.4054537	2	2.80888
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.90218558	2	4.84289
Q4FZX7	VGDGAGGAFQPYLDSLR	1.27281042	2	3.1283
Q4FZY0	**EFHD2 EF_hand domain_containing protein D2**	**1.17639478**	**0.53842**	**2**
Q4FZY0	KQAEEVK	1.16491073	1	1.94405
Q4FZY0	LSEIDVSTEGVK	1.90122102	2	2.59805
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.15072134**	**0.74208**	**6**
Q4G061	AEEEGGSDGSAAEAEPR	1.27109606	2	4.95918
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	5.43935206	3	5.01134
Q4G061	DRPQEADGIDSVIVVDNVPQVGPDR	1.96684079	3	3.5612
Q4G061	GTQGVVTNFEIFR	1.05325576	2	3.00808
Q4G061	IINDYYPEEDGK	1.34807075	2	2.86532
Q4G061	TEDAEEDAEARPEPEVR	0.5175204	3	3.61913
Q4G063	**CREL2 Cysteine_rich with EGF_like domain protein 2**	**1.53201375**	**0.33496**	**2**
Q4G063	ACCLPGTYGPDCK	1.44090936	2	3.03808
Q4G063	FNQGMANTAR	2.19472445	2	2.4181

Q4KLF8	**ARPC5 Actin_related protein 2/3 complex subunit 5**	**0.96818925**	**0.6605**	**2**
Q4KLF8	ALAAGGVGSIVR	0.78877107	2	2.84465
Q4KLF8	QGNMTAALQAALK	1.45934934	2	2.3489
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.41415143**	**0.00017**	**16**
Q4KLP0	ARPSVDHGLAR	0.84847324	2	3.06238
Q4KLP0	HAMVVCQNTDDVYIPLNHMDPNQK	1.76882935	3	5.71346
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.44278434	3	4.68575
Q4KLP0	LEELCPFPLDSLQQEMGK	1.56780163	3	5.42125
Q4KLP0	LLLESQEFDHFLATK	1.21779659	2	3.95675
Q4KLP0	LSAYGGITDIIIGMPHR	2.02327968	3	4.44434
Q4KLP0	LVTVYCEHGHK	1.58745658	2	2.36789
Q4KLP0	QQSQEDGDYSPNGSAQPGDK	1.98401134	2	2.63099
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.45358536	3	3.99712
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.28587059	3	5.02157
Q4KLP0	SSLYSSDIGK	1.37221431	2	2.83784
Q4KLP0	SVEVPEELQLHSHLLK	1.20159862	2	3.31004
Q4KLP0	WLLQSGLVILLPHGYDGAGPDHSSCR	1.17794925	3	3.36754
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.90228677	2	4.9568
Q4KLP0	YGGEGAESMMGFFHELLK	1.55474161	2	4.43611
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.65006813	3	4.56909
Q4KLZ6		**1.58324643**	**0.08906**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.38302871	2	4.91548
Q4KLZ6	AILEVLQTK	1.17824286	2	2.89094
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.61300328	2	3.61269
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	1.23971395	2	4.96248
Q4KLZ6	AVAQAGTAGTLLIVK	1.6855552	2	4.36264
Q4KLZ6	EGPTPASPAQVLSK	1.41346332	2	3.38581
Q4KLZ6	GLCGTILIHK	1.1696091	2	2.40148
Q4KLZ6	GVSLTLMLVDEPLLK	1.98788997	2	3.0735
Q4KLZ6	ISTTLIGLEEHLNALDR	2.58252264	2	3.60906
Q4KLZ6	LIDAETNAK	1.87703115	2	2.37296
Q4KLZ6	LNFGLAMEQAK	1.10754448	2	2.40456
Q4KLZ6	LSVLLLEK	2.13392543	2	2.60548
Q4KLZ6	MGGSSGALYGLFLTAAAQPLK	2.05776801	2	3.56324
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.72102625	3	5.90822
Q4KLZ6	VAGALAEEGMGLEEITK	2.11425414	2	4.53581
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	2.15039567	2	5.35237
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**0.92233255**	**0.43458**	**5**
Q4KM49	AFCEPGNVENNGVLSFVK	0.45680325	2	2.47295
Q4KM49	IDVGEAEPR	0.57998085	2	2.35082
Q4KM49	QVEPLDPPAGSAPGER	0.97681759	2	2.59556
Q4KM49	TVVSGLVQFVPK	1.54537133	2	3.06702
Q4KM49	VDAQFGGIDQR	0.42620535	2	3.12845
Q4KM73	**KCY UMP_CMP kinase**	**1.20271061**	**0.001**	**7**
Q4KM73	EMDQTMAANAQK	1.70152213	2	3.18346
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.43339864	3	4.59218
Q4KM73	IVPVEITISLLK	2.21570722	2	2.4975
Q4KM73	KNPDSQYGELIEK	1.22472642	2	3.80017
Q4KM73	NQDNLQGWNK	1.33340052	2	2.84177
Q4KM73	SVDEVFGDVMK	1.11811558	2	3.45938
Q4KM73	YGYTHLSAGELLR	1.02679919	3	4.27906
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.42565794**	**0.00404**	**5**
Q4KM74	DLQQYQSQAK	1.59021217	2	3.55237
Q4KM74	GEALSALDSK	1.47610823	2	2.85129
Q4KM74	IMVANIEEVLQR	1.15980342	2	2.78913

Q4KM74	NLGSINTELQDVQR	1.17152688	2	4.38384
Q4KM74	VADGLPLAASMQEDEQSGR	1.12152936	2	4.36481
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.02326185**	**0.63511**	**3**
Q4KMA2	IDIDPEETVK	1.01807586	2	2.75957
Q4KMA2	NFVVVMVTKPK	0.7597127	2	2.97463
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.28382349	2	4.24825
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.95588696**	**0.1239**	**6**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	1.35465462	3	3.56918
Q4QQW3	FLFDLNVDDGLAALGYSK	2.10416658	2	2.43737
Q4QQW3	HLETAEILGANIR	1.48798518	2	3.45891
Q4QQW3	IQDAGPVLADALR	0.67473546	2	2.9916
Q4QQW3	NLSQLPPVQIVMDSLSK	1.4410464	2	2.96438
Q4QQW3	TTDYAFEMAVSNIR	0.42819824	2	3.70436
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.65715263**	**0.00839**	**5**
Q4QRB4	AILVDLEPGTMDSVR	1.23442639	2	4.56213
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10	1.64473269		
Q4QRB4	EIVHIQAGQCGNQIGAK	2.86261165	2	4.93126
Q4QRB4	IMNTFSVVPSPK	1.31532377	2	4.1015
Q4QRB4	ISEQFTAMFR	1.62829494	2	3.37924
Q4V7C7	**ARP3 Actin_related protein 3**	**1.21780712**	**0.00799**	**6**
Q4V7C7	GVDDLDFFIGDEAIEKPTYATK	1.32341812	2	4.38781
Q4V7C7	KDYEEIGPSICR	1.05370185	2	3.66302
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.71835059	2	3.34781
Q4V7C7	LSEELSGGR	1.27932778	2	2.56612
Q4V7C7	NIVLSGGSTMFR	1.0549974	2	3.0931
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	1.36978784	3	5.24268
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**1.1977982**	**0.94111**	**6**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK	1.30519275	3	3.73339
Q4V8K1	QVFVCGNDSK	1.19164895	2	2.38265
Q4V8K1	SDVIVLAVHR	1.43636243	2	2.82238
Q4V8K1	TCADEFPLTVDSSEK	1.16436755	2	4.48802
Q4V8K1	TLGLTPLDQGSLVAAK	1.19417787	2	3.81118
Q4V8K1	VLIDVSNNQK	1.02537082	2	2.53512
Q501J6	**DDX17 Probable ATP_dependent RNA helicase DDX17**	**1.00173266**	**0.47322**	**2**
Q501J6	ELAQQVQQVADDYGK	0.64824659	2	3.12204
Q501J6	VLEEANQAINPK	1.0365925	2	2.62331
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**1.22341773**	**0.68537**	**4**
Q505J8	LQQVQAGQAEK	1.03981694	2	2.6754
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	1.77948418	3	4.59039
Q505J8	SLQALGEVIEAELR	1.22834044	2	3.7452
Q505J8	VVDSIEDEVQR	1.44612942	2	2.93538
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**1.07822799**	**0.80464**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	0.66991917	2	4.09343
Q561R9	ILIDTGEPSVPEYISCLK	1.07757139	2	3.79122
Q561R9	NISNDATYCIK	1.21069	2	2.95141
Q561R9	NNREEQIITVFR	0.77948926	2	2.69148
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.25357299**	**0.05024**	**6**
Q561S0	LLQYSDALEHLLSTGQGVVLER	2.62411852	3	3.76304
Q561S0	LTLPEYLPPHAVIYIDVPVSEIQSR	2.0067867	3	4.18579
Q561S0	VITVDGNICSGK	1.16022109	2	2.45809
Q561S0	VVEDIEYLNYNK	0.99935594	2	3.90041
Q561S0	YAPGYNADVGDK	0.7581802	2	2.66096
Q561S0	YGLLASILGDK	2.37366862	2	3.14905

Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.67050699**	**0.98265**	**5**
Q562C4	AQFSEVQLEWQPPPFK	0.85114818	2	4.51697
Q562C4	FIVAYGENMK	0.61589557	1	2.53391
Q562C4	HIGDGCHLTR	0.72169762	3	3.31753
Q562C4	VLQEVQR	0.62185039	2	2.54877
Q562C4	VTCVDPNPNFEK	0.84836806	2	3.60413
Q562C9	**MTND 1_2_dihydroxy_3_keto_5_methylthiopentene dioxygenase**	**1.21246638**	**0.66486**	**3**
Q562C9	GDMITLPAGIYHR	1.22436245	2	2.31988
Q562C9	LDADKYENDPELEQIR	1.10493448	2	4.20084
Q562C9	MFFEEHLHLDEEIR	3.76072757	2	2.4286
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.24259762**	**0.90916**	**11**
Q58FK9	AIILNTPHNPIGK	0.85108215	2	3.38963
Q58FK9	DSTLDAAEEIFR	1.35213953	2	3.19889
Q58FK9	DSTLDAAEEIFRTWNSR	1.27870463	2	2.3612
Q58FK9	IEGLDQNVWVEFTK	1.28062058	2	4.5557
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.25876608	3	4.48794
Q58FK9	MAGAVPVFIPLR	2.05221334	2	2.49665
Q58FK9	MDDPECYFNSLPK	0.82001751	2	4.18505
Q58FK9	RIEGLDQNVWVEFTK	1.08122656	2	3.72454
Q58FK9	RMDDPECYFNSLPK	0.98386012	2	2.76982
Q58FK9	SDEPYDYK	3.23169862	2	2.44851
Q58FK9	WTSSDWTFNPQELESK	0.89491063	2	5.06261
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.26018995**	**0.0588**	**3**
Q5BJQ0	AVLDSSPFLSEANAER	1.2446676	2	4.61341
Q5BJQ0	KMGGSFLICSKLK+Oxidation(1	1.85847706		
Q5BJQ0	TLNNDLGPHWR	1.47810191	2	2.5618
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.81003166**	**0.39612**	**25**
Q5BJY9	AQIFANSVDNAR	1.00877034	2	3.95999
Q5BJY9	AQYEQLAQK	0.99420941	2	3.47068
Q5BJY9	DAETTLLELR	2.14022461	2	2.94159
Q5BJY9	IREYLEK	1.20818859	2	2.40246
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	1.71977301	3	4.90783
Q5BJY9	KVVDDTNITR	0.98157668	2	3.07228
Q5BJY9	LEAEIATYR	0.99580414	2	3.28052
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	1.03442337	3	5.54595
Q5BJY9	LQLETEIEALKEELLFMK	1.96631364	2	5.04445
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	1.1797525	2	6.30482
Q5BJY9	NQNINLENNLGEVEAR	1.02529571	2	5.56496
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	0.98655959	3	5.18546
Q5BJY9	QSVESDIHGLR	1.17893293	2	2.85054
Q5BJY9	QSVESDIHGLRK	1.9692628	2	2.67645
Q5BJY9	QTQEYEALLNIK	1.12452751	2	3.52249
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.98298585	2	5.8958
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEKETMQDLNDR	1.04113239	3	4.34872
Q5BJY9	TLQTLEIDLDSMK	1.20693144	2	4.52038
Q5BJY9	VKLEAEIATYR	1.2464984	2	3.28103
Q5BJY9	VKYETELAMR	1.00427108	3	3.42398
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.45827623	2	5.27106
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.98774173	2	5.0705
Q5BJY9	VVDDTNITR	0.99674232	2	3.44837
Q5BJY9	YETELAMR	0.70614581	2	2.6174
Q5BJY9	YWSQQIEESTTVVTTK	1.191017	2	3.89621
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.54791589**	**3E-05**	**4**

Q5BK63	AVQHSNVVINLIGR	0.80619938	2	3.65763
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.44026486	3	6.06694
Q5BK63	NFDFEDVFVNIPR	2.21869406	2	3.85634
Q5BK63	WLSSEIEETKPAK	1.36866515	2	3.29303
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**1.38399024**	**0.5111**	**3**
Q5BK81	DVPYPPPLPPAVEAIQK	7.6970479	2	2.66155
Q5BK81	TGNVAEQLR	2.24156491	2	2.93323
Q5BK81	VEEVSLPDTINEGQVR	0.8856906	2	4.07436
Q5BQE6	**DHC24 Delta(24)_sterol reductase**	**1.11324455**	**0.87653**	**3**
Q5BQE6	LYEQHHVVQDMLVPMK	1.46081921	3	3.58048
Q5BQE6	QLGCQDAFPEVYDK	1.11318666	2	4.21588
Q5BQE6	YLFGWMVPPK	0.99515537	2	2.69534
Q5DTN8	**JKIP3 Janus kinase and microtubule_interacting protein 3**	**0.99426881**	**0.81963**	**2**
Q5DTN8	MKELQAVREALLR	1.65644286	2	2.32857
Q5DTN8	TREQLQAEIQRAQTR	0.98925174	2	2.98134
Q5DU56	**NLRC3 Protein NLRC3**	**1.08965293**	**0.40388**	**2**
Q5DU56	LTGLALGHLYR	1.39069078	2	2.36599
Q5DU56	TLEILDLR	1.04238443	2	2.50515
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.2605374**	**0.21274**	**2**
Q5EB77	NDIVNMLVGNK	1.26419853	2	3.46229
Q5EB77	TCDGVQCAFEELVEK	1.19627101	2	3.86545
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.45345884**	**0.33828**	**2**
Q5FVM4	MEELHNQEVQK	1.48891992	2	3.90704
Q5FVM4	RMEELHNQEVQK	1.40792873	3	4.28857
Q5FVQ4	**MLEC Malectin**	**1.20444027**	**0.96979**	**3**
Q5FVQ4	KEEEEEEEYDEGSNLKR	1.34978841	3	5.58868
Q5FVQ4	LSVQGEVSTFTGK	1.14877161	2	3.36708
Q5FVQ4	STPEDQILYQTER	1.24315812	2	4.69178
Q5FVR2	**TYPH Thymidine phosphorylase**	**1.02442031**	**0.12262**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10	1.09479826		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8	0.78590906		
Q5FVR2	FGGAAVFPDQEK	0.86400335	2	2.59456
Q5FVR2	KQEELLSPADGIVECVR	1.36547491	2	4.07112
Q5FVR2	VSLVLAPALAACGCK	1.02193701	2	3.05512
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.12420145**	**0.98655**	**3**
Q5FVR5	DEKENLFQSK	0.84085369	2	2.46325
Q5FVR5	ILFIVGENDQCLASK	1.15207897	2	3.73669
Q5FVR5	IQQPGIGVISVSK	1.11708019	2	3.3566
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**1.18612823**	**0.98468**	**3**
Q5FW57	AIDQEMFK	1.15976586	2	2.71364
Q5FW57	SSQMLQMLESSLR	1.38881075	2	4.10177
Q5FW57	VYGTVFHMNQGNPFK	1.60153794	2	3.73513
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.82070547**	**0.88189**	**8**
Q5I0C3	AGDALMVMIAMK	0.74934223	1	1.95855
Q5I0C3	HAPLVEFEEEEV	1.34266784	2	2.96482
Q5I0C3	IIEEAPAPGIDPEVR	0.78029517	2	3.86378
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	1.80483195	3	4.65818
Q5I0C3	QEGIIFIGPPSTAIR	0.91172961	2	2.49792
Q5I0C3	SEKEFQEQLESAR	1.08934906	2	3.47032
Q5I0C3	VFFSEGAQANR	1.51237798	2	2.44464
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	1.30013021	2	5.14113
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**1.03939415**	**0.82483**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	1.00362853	2	3.70615

Q5I0D1	HEEFEEGCK	1.08157092	2	2.87806
Q5I0D1	VTLAVSDLQK	1.22666338	2	2.49429
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**1.19667056**	**0.20664**	**2**
Q5I0D5	FRPGDEHHPEVR	1.17654245	3	3.65802
Q5I0D5	LGFDISEGEVTAPAPATCQILK	1.34645797	2	4.36325
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.4157246**	**0.36925**	**2**
Q5I0D7	GVNTDSGNVCR	1.37363604	2	3.1664
Q5I0D7	YAVDDVQYADEIASVLTSR	1.96668508	2	2.73932
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.40910538**	**0.52463**	**2**
Q5I0E7	QLVEQVEQIQK	1.00707457	2	3.5686
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.69229608	3	3.39444
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**1.30426497**	**0.00183**	**9**
Q5I0H9	DKNQDLCQQESVK	1.5384538	2	4.28053
Q5I0H9	FIEWMQNPEAPPPPEPTWEEQQTSVLHLVGDNFR	1.89678307	3	4.1226
Q5I0H9	GHTVLAGMNVYPPEFENIKEEYNVR	1.79165127	3	3.64914
Q5I0H9	GPPLWEEDPGAK	1.25169642	2	3.37593
Q5I0H9	GQGTICWVDCGDAESR	1.06316455	2	4.1044
Q5I0H9	NGEQQAVPALR	1.44461735	2	2.55593
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	3.02554938	3	4.12575
Q5I0H9	NQDLCQQESVK	0.96891486	2	3.42543
Q5I0H9	TELGFTSFIR	1.15571863	2	2.44762
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.46214363**	**0.25954**	**7**
Q5I0J9	HANLLVGSPSALADQTTER	1.30023344	2	5.78434
Q5I0J9	LDAAGGLQSLR	1.02656839	2	3.99282
Q5I0J9	LEGPLAAAHSSGPR	1.13527209	2	3.75329
Q5I0J9	LGQSLVSR	1.64250166	2	2.31063
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.76772934	2	3.38819
Q5I0J9	NSNTMAAAALAAPSLGFDR	1.07443713	2	4.63596
Q5I0J9	TVLYEGPVR	1.18957145	2	2.62407
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.59824887**	**0.00122**	**6**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	1.99497213	3	3.37932
Q5I0M2	DNHVVAAGSMEK	1.32704947	2	2.65586
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.66282139	3	4.80135
Q5I0M2	LYAEGDIPVPHAR	1.33438801	2	3.55439
Q5I0M2	VEVECSSLK	1.68509081	2	2.50724
Q5I0M2	YDLGGLVMVK	1.69273124	2	2.52426
Q5M7T9	**THNS2 Threonine synthase_like 2**	**1.6559186**	**4.6E-06**	**2**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	1.65592892	3	5.58988
Q5M7T9	LSEAVTSESVSDEAITQTMGR	1.41927137	2	4.48084
Q5M7U6	**ARP2 Actin_related protein 2**	**1.04423108**	**0.99982**	**5**
Q5M7U6	GYAFNHSADFETVR	0.9400406	2	4.00171
Q5M7U6	HLWDYTFGPEK	1.02347001	2	3.19684
Q5M7U6	ILLTEPPMNPTK	0.99991404	2	2.85151
Q5M7U6	SMLEVNYPMENGIVR	1.19860117	2	4.09419
Q5M7U6	VVVCDNGTGFVK	1.18000999	2	2.70943
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**1.43932382**	**0.97338**	**10**
Q5M7W5	AAVGLTGNDIATPPNK	2.30354796	2	3.48093
Q5M7W5	ATSPSTLVSTGSSSR	1.4411186	2	3.8683
Q5M7W5	EAETALPIEMDLAPPEDVALPK	1.08575189	2	3.08068
Q5M7W5	ESEGSPDTDAAPGPDTDVTLTK	0.91859392	2	4.18592
Q5M7W5	ETSGSQPPELCSGVSR	1.44051298	2	3.34701
Q5M7W5	NTAPPTEEETVPGK	1.53236495	2	2.58157
Q5M7W5	NTTPTGATPPAGMASTR	1.33214111	2	3.568
Q5M7W5	STLPVDEGSPLEK	1.26846112	2	2.47697

Q5M7W5	VGSLDNVGHLPAGGTVK	1.00548656	2	3.71376
Q5M7W5	VTEFNNVTPLSEEEVASIK	0.72361769	2	3.14494
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.45546322**	**0.03923**	**7**
Q5M875	ALTAELDTLGK	1.3827767	2	3.07804
Q5M875	IQNIQFEAIVGHR	1.64608351	3	4.2412
Q5M875	LWPVLEPDEVAR	1.29895683	2	2.49488
Q5M875	NSGHIVTVASVCGHR	1.95659156	2	4.50165
Q5M875	SLIDGILTNK	1.43691612	2	3.31113
Q5M875	SVAGQTVLITGAGHGIGR	1.13985589	2	4.09628
Q5M875	TSCLCPVFVNTGFTK	1.40007511	2	3.94863
Q5M9G3	**CAPR1 Caprin_1**	**1.14590941**	**0.05473**	**2**
Q5M9G3	LNQDQLDAVSK	1.58927172	2	3.17975
Q5M9G3	YQEVTNNLEFAK	1.12016493	2	3.03739
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.15584719**	**0.51864**	**2**
Q5M9I5	EEEEEELVDPLTTVR	1.15253105	2	4.23759
Q5M9I5	SQTEEDCTEELFDFLHAR	2.52926335	2	4.83109
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.12068888**	**0.87367**	**10**
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	1.77744185	2	4.99629
Q5PPL3	DPQLVPVLIDAAR	1.61032515	2	2.42473
Q5PPL3	GQVTGTDLINEVSK	0.87523019	2	4.0784
Q5PPL3	GVSTVFHCASPPSNSNNK	1.12595895	2	4.30668
Q5PPL3	GYAVNVFDVR	1.46571463	2	3.56783
Q5PPL3	ILTGLNYEAPK	1.18611338	2	3.58762
Q5PPL3	KGQVTGTDLINEVSK	1.23097309	2	4.41052
Q5PPL3	NGTEDLPYAMKPIDYYTETK	1.08794538	2	3.93677
Q5PPL3	NLVDFTFVENVVHGHILAAEHLSR	1.1994157	3	3.52041
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.14485556	2	5.41096
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.27911134**	**0.22227**	**7**
Q5PQT3	AINQEMFK	1.43136382	1	1.9529
Q5PQT3	AIQNLASIHSLQVK	0.97506128	2	4.04558
Q5PQT3	DPENCQEFLGSSEVINWK	2.02827615	2	5.29151
Q5PQT3	KLFPSLLDTK	1.06057266	2	2.71433
Q5PQT3	LSSLDVTHAALVNK	1.74272864	2	3.61602
Q5PQT3	MGGTVPQYR	1.53977053	2	2.56175
Q5PQT3	QHLQIQSSQSHLNK	1.36190027	2	3.39338
Q5PQX1	**TOIP1 Torsin_1A_interacting protein 1**	**1.25539149**	**0.90044**	**2**
Q5PQX1	LEQHSQQAQQQLSPATSGR	1.24280386	3	4.66536
Q5PQX1	SDFGNQSPSTSR	1.29029724	2	2.62768
Q5RJR2	**TWF1 Twinfilin_1**	**1.43244153**	**0.87438**	**2**
Q5RJR2	HQTLQGVAFPISR	1.12787617	2	3.02011
Q5RJR2	YLLSQSSPAPLTAAEEELR	1.53831247	2	4.32294
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**0.82441932**	**0.58424**	**5**
Q5RJR8	ATVLDLSCNK	0.79232445	2	2.81952
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	1.30841147	2	6.21131
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.07052024	2	4.05641
Q5RJR8	LQQLPADFGR	1.71313232	1	1.92139
Q5RJR8	WLDLKDNPLDPVLAK	1.22245996	2	2.67182
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.75745184**	**0.37733**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	3.39693732	3	4.753
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	1.41699565	3	4.76568
Q5RKI0	YAPSGFYIASGDISGK	1.2952735	2	4.53409
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.64286908**	**2.5E-11**	**5**
Q5RKI1	ELAQQIQK	1.64403585	1	2.28296

Q5RKI1	GIDVQQVSLVINYDLPTNR	2.3676182	2	3.61907
Q5RKI1	GYDVIAQAQSGTGK	1.4904021	2	5.13797
Q5RKI1	MFVLDEADEMLSR	2.21024657	2	4.4924
Q5RKI1	VLITTDLLAR	1.64458619	2	3.06854
Q5S6T3	**ISPD 2_C_methyl_D_erythritol 4_phosphate cytidylyltransferase_like protein**	**1.01409226**	**0.5174**	**2**
Q5S6T3	ISLAEAGATR	4.32622651	2	2.34198
Q5S6T3	MENLVWIRELAK	0.95836869	2	2.34806
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.28440211**	**0.95303**	**15**
Q5SGE0	AALDLEQVPSELAVTR	0.77211219	2	4.10799
Q5SGE0	CIANNQVETLEK	1.16420003	2	3.01274
Q5SGE0	GLDAIELSR	0.70094158	2	2.52148
Q5SGE0	HCVTMDTPAEK	1.32008874	2	2.96809
Q5SGE0	HDNAEDALNLK	1.63457202	2	3.64453
Q5SGE0	LIDYCK	2.03235096	1	1.93197
Q5SGE0	MEGANIQPNR	1.18060927	2	2.97081
Q5SGE0	SCGSLLPELSLAER	1.0695556	2	2.77297
Q5SGE0	SGSPGSNQALLLLR	1.15122838	2	2.88408
Q5SGE0	SGSQFDWALMR	1.45877266	2	2.39482
Q5SGE0	SSLSSSSPSAGDTVTEK	1.82435423	2	3.88544
Q5SGE0	SYVADKDVASAK	1.13309749	2	3.16469
Q5SGE0	TLLELIPELR	1.03334369	2	3.10069
Q5SGE0	TSQFTSSDLESTLEK	1.19799182	2	4.18987
Q5SGE0	VIEEQMEPALEK	1.0617274	2	3.11152
Q5SW19	**K0664 Protein KIAA0664**	**1.27110101**	**0.19899**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	0.774131	2	3.38476
Q5SW19	IGIGELITR	1.75039237	2	2.40003
Q5SW19	SVEGLQEGSVLR	1.24720497	2	2.73793
Q5SX40	**MYH1 Myosin_1**	**1.40319018**	**0.97959**	**86**
Q5SX40	AAYLQNLNSADLLK	3.08223924	2	3.44502
Q5SX40	ADIAESQVNK	5.633268	2	3.70484
Q5SX40	AEDEEEINAELTAK	3.65229633	2	4.21949
Q5SX40	AGLLGLLEEMR	0.3252825	2	4.26557
Q5SX40	AGLLGLLEEMRDDK	2.88338589	2	3.38575
Q5SX40	ALQEAHQQTLDDLQAEEDK	2.43410326	3	4.51196
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	2.99149688	3	6.77841
Q5SX40	ANLLQAEIEELR	3.83482902	2	3.71783
Q5SX40	ANSEVAQWR	1.29002548	2	2.87563
Q5SX40	DDKLAQLITR	2.1921784	2	2.35281
Q5SX40	DLEEATLQHEATAATLR	3.62109084	2	5.08514
Q5SX40	DTQLHLDDALR	2.4534304	2	2.8452
Q5SX40	EEQAEPDGTEVADK	0.47095254	2	3.38988
Q5SX40	EFEMSNLQSK	3.1170903	1	2.63379
Q5SX40	ELEGEVENEQK	0.42481107	2	2.88145
Q5SX40	ELEGEVENEQKR	5.38729583	2	3.02863
Q5SX40	ELTYQTEEDRK	1.49606138	2	3.1274
Q5SX40	EMANMKEEFEK	2.74409583	2	2.82398
Q5SX40	ENQSILITGESGAGK	5.46208792	2	4.10837
Q5SX40	EQYEEEQEAK	5.75649822	1	3.21304
Q5SX40	GQEDLKEQLAMVER	1.89035493	2	4.41943
Q5SX40	GSSFQTVSALFR	0.92705851	2	3.06736
Q5SX40	HADSVAELGEQIDNLQR	1.14941115	2	6.01742
Q5SX40	IAEQELLDASER	3.87625191	2	3.23326
Q5SX40	IEAQNKPFDAK	1.49647853	2	3.03745
Q5SX40	IEDEQALGMQLQK	4.04534159	2	4.60505
Q5SX40	IEDEQALGMQLQK+Oxidation(8	3.23239581		

Q5SX40	IEDMAMMTHLHEPAVLYNLK	2.54194389	3	4.30286
Q5SX40	IEELEEEIEAER	3.46859938	2	4.34576
Q5SX40	IKLEQQVDDLEGSLEQEK	3.72132206	2	5.11645
Q5SX40	IKLEQQVDDLEGSLEQEKK	1.30745693	3	4.10119
Q5SX40	IQHELEEAEER	2.70169316	2	3.69329
Q5SX40	IQHELEEAEERADIAESQVNK	2.74190939	3	3.88024
Q5SX40	IQLELNQVK	2.44273171	2	2.70493
Q5SX40	KIAEQELLDASER	3.16639839	2	3.82823
Q5SX40	KIQHELEEAEER	3.11114583	3	4.11516
Q5SX40	KKEFEMSNLQSK	4.31287112	2	3.86205
Q5SX40	KKLETDISQIQGEMEDIVQEAR	2.85360158	3	6.08285
Q5SX40	KLEDECSELK	2.35902342	2	2.91871
Q5SX40	KLEDECSELKK	1.5981391	2	4.02704
Q5SX40	KLETDISQIQGEMEDIVQEAR	2.88612144	2	5.64785
Q5SX40	KMEGDLNEMEIQLNHSNR	1.87491453	3	4.61326
Q5SX40	LAQESTMDVENDKQQLDEK	7.39657549	2	4.86328
Q5SX40	LDEAEQLALK	4.65759526	2	3.23504
Q5SX40	LEDECSELKK	4.12409927	2	3.32472
Q5SX40	LEEAGGATSAQIEMNK	0.99257126	2	5.15375
Q5SX40	LEQQVDDLEGSLEQEK	0.28670146	2	5.46536
Q5SX40	LEQQVDDLEGSLEQEKK	1.24137283	2	4.1631
Q5SX40	LETDISQIQGEMEDIVQEAR	1.49692767	2	5.19096
Q5SX40	LINELTAQR	1.77270155	2	3.14717
Q5SX40	LQDAEEHVEAVNAK	3.7003257	2	4.81502
Q5SX40	LQDLVDK	3.94062224	2	2.44684
Q5SX40	LQDLVDKLQSK	1.69188144	2	2.55319
Q5SX40	LQNEVEDLMIDVER	3.18447294	2	4.46346
Q5SX40	LQTESGEYSR	2.39322079	2	2.51991
Q5SX40	LTGAVMHYGNMK	1.71110593	2	2.67692
Q5SX40	MEGDLNEMEIQLNHSNR	1.56133299	2	4.73322
Q5SX40	MEGDLNEMEIQLNHSNRMAAEALR+Oxidation(0)Oxidation(17	1.25913223		
Q5SX40	MEIDDLASNMEVISK	13.9473598	2	4.95757
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	3.64707341	3	6.37659
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0	2.63358265		
Q5SX40	NDLQLQVQSEADSLADAEER	13.5607477	2	6.30669
Q5SX40	NKDPLNETVVGLYQK	3.42249434	2	4.69152
Q5SX40	NLQQEISDLTEQIAEGGK	2.76537266	2	6.02876
Q5SX40	NLQQEISDLTEQIAEGGKR	2.64698635	2	4.27337
Q5SX40	NLTEEMAGLDETIAK	2.94859249	2	4.78848
Q5SX40	QAEEAEEQSNVNLAK	6.78235022	2	4.41122
Q5SX40	QKYEETHAELEASQK	4.03520986	2	3.91191
Q5SX40	QLDEKDSLVSQLSR	2.11085198	2	3.19078
Q5SX40	QLEEEIK	1.13562997	1	2.20342
Q5SX40	QREEQAEPDGTEVADK	5.27873234	2	4.12469
Q5SX40	RDLEEATLQHEATAATLR	1.8406793	3	3.62924
Q5SX40	SAETEKEMANMKEEFEK	0.75979463	3	4.01588
Q5SX40	SELQAALEEAEASLEHEEGK	2.30400891	2	5.74997
Q5SX40	SSVFVVDAK	2.79335297	2	2.52796
Q5SX40	TKYETDAIQR	2.8167993	3	3.45201
Q5SX40	TLEDQVSELK	1.37590063	2	2.94919
Q5SX40	TNAACAALDK	2.77423736	1	1.98446
Q5SX40	TNAACAALDKK	1.88827542	2	2.98051
Q5SX40	VLNASAIPEGQFIDSK	2.95327319	2	4.29797
Q5SX40	VQLLHTQNTSLINTK	1.20864113	2	4.71032
Q5SX40	VRELEGEVENEQK	0.47294379	2	3.85636
Q5SX40	VRELEGEVENEQKR	2.28637301	3	4.14079

Q5SX40	VVESMQSTLDAEIR	1.63637956	2	3.74154
Q5SX40	YEETHAELEASQK	3.26193627	2	4.73862
Q5SX40	YETDAIQR	4.06508988	2	2.62035
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.21072969**	**0.99003**	**5**
Q5U206	DTDSEEEIR	1.76546387	2	2.83205
Q5U206	KMKDTDSEEEIR	1.22805146	3	3.41088
Q5U206	KMKDTDSEEEIR+Oxidation(1	1.74714059		
Q5U206	MKDTDSEEEIR	1.04978131	3	4.32711
Q5U206	MKDTDSEEEIR+Oxidation(0	1.07571089		
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.50181067**	**1.2E-05**	**4**
Q5U2Q7	GFGGIGGILR	1.43246281	2	2.75822
Q5U2Q7	LSVLGAITSVQQR	1.55712257	2	2.93988
Q5U2Q7	YFDEISQDTGK	1.97901655	2	2.53487
Q5U2Q7	YVLHCQGTEEEK	1.50617024	2	3.68392
Q5U2S3	**ZUFSP Zinc finger with UFM1_specific peptidase domain protein**	**1.13333777**	**0.70795**	**2**
Q5U2S3	QYGLDNSGGYKQQQLR	1.05845083	2	2.67702
Q5U2S3	TLCLLIFDPGCPSREMQKLLK+Oxidation(15	5.67390303		
Q5U2U0	**CLPX ATP_dependent Clp protease ATP_binding subunit clpX_like_ mitochondrial**	**1.57956419**	**0.70889**	**5**
Q5U2U0	LLEGTIVNVPEK	1.89703237	2	2.62449
Q5U2U0	QQAEVEK	1.16491073	1	1.91779
Q5U2U0	SGESNTHQDIEEK	1.56268644	2	3.60002
Q5U2U0	SGESNTHQDIEEKDR	1.61153362	3	4.32588
Q5U2U0	SNILLLGPTGSGK	1.45456494	2	2.37762
Q5U2V4	**PLBL1 Phospholipase B_like 1**	**1.85259222**	**0.05799**	**2**
Q5U2V4	IWEMGHCSALIK+Oxidation(3	14.9387213		
Q5U2V4	LGLDYSYDLAPR	1.42629591	2	2.51104
Q5U2Z7	**RHG24 Rho GTPase_activating protein 24**	**0.9315354**	**0.70914**	**2**
Q5U2Z7	EEEAGVKELTKQVK	0.88278013	2	2.3874
Q5U2Z7	FTMIEIKMRNAER+Oxidation(7	1.22762965		
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.21485882**	**0.49678**	**14**
Q5U300	AAVASLLQSVQVPEFTPK	1.2279999	3	3.67161
Q5U300	AENYDISPADR	0.83618396	2	3.19107
Q5U300	DNPGVVTCLDEAR	0.95400531	2	3.39997
Q5U300	FEVQGLQPNGEEMTLK	1.36984159	2	4.01965
Q5U300	IHVSDQELQSANASVDDSR	1.36031796	3	3.48724
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.42774399	2	4.71172
Q5U300	LDQPMTEIVSR	0.9523477	2	3.39489
Q5U300	LKSDTAAAAVR	1.42921595	2	2.82246
Q5U300	NEEDATELVTLAQAVNAR	2.7614067	3	4.68795
Q5U300	NFPNAIEHTLQWAR	1.38137378	2	3.40726
Q5U300	SLPASLAEPDFVMTDFAK	1.11891447	2	4.05759
Q5U300	SPPAVQQDNVDEDLIR	1.24284194	2	4.76979
Q5U300	SPPAVQQDNVDEDLIRK	1.07591043	3	3.32207
Q5U300	VVQGHQQLDSYK	1.39137732	2	3.42621
Q5U4E6	**GOGA4 Golgin subfamily A member 4**	**1.12255898**	**0.89895**	**3**
Q5U4E6	EFNTQLAQK	1.05279137	2	2.34942
Q5U4E6	EQAQQILTEKENVILQMR+Oxidation(16	1.05278947		
Q5U4E6	VQQCAKDTESQLSELR	4.44223796	2	2.31087
Q5XFW8	**SEC13 Protein SEC13 homolog**	**1.31352954**	**0.85254**	**4**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	1.39084631	2	3.45853
Q5XFW8	EEEDGQWKEEQK	1.3739383	2	2.75701
Q5XFW8	LEAHSDWVR	1.03161688	2	2.36868
Q5XFW8	NGGQILIADLR	1.32688939	2	2.48169

Q5XFX0	**TAGL2 Transgelin_2**	**1.0835768**	**0.07609**	**6**
Q5XFX0	DDGLFSGDPNWFPK	2.70661413	2	3.66492
Q5XFX0	NFSDNQLQEGK	1.55125389	2	3.15758
Q5XFX0	NVIGLQMGTNR	0.81768298	2	3.02612
Q5XFX0	QMEQISQFLQAAER	0.94813609	2	2.80307
Q5XFX0	TLMNLGGLAVAR	1.93990939	2	3.3582
Q5XFX0	YGINTTDIFQTVDLWEGK	1.43185916	2	4.73927
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.23378756**	**0.00225**	**11**
Q5XHY5	AEHDSILAEK	1.25402476	2	2.83885
Q5XHY5	FLGDIEIWNQAEK	1.47024839	2	3.76226
Q5XHY5	FMVDIDLDPGCTLNK	1.20166869	2	3.7564
Q5XHY5	GFQEVVTPNIFNSR	2.78735773	2	3.90931
Q5XHY5	LKAEHDSILAEK	1.06758089	2	3.34697
Q5XHY5	NELSGALTGLTR	1.47049052	2	3.20448
Q5XHY5	QLENSLNEFGEK	1.08205517	2	3.15633
Q5XHY5	QVMVVPVGPTCDEYAQK	1.57958226	2	3.66822
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.49237198	2	4.1517
Q5XHY5	VVWDLDRPLETDCTLELLK	2.73712297	2	3.88131
Q5XHY5	WELNPGDGAFYGPK	1.03685453	2	3.96393
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.33757146**	**0.24967**	**14**
Q5XHZ0	AFLEALQHQAETSSR	1.39893889	2	4.68455
Q5XHZ0	AQLLQPTLEINPR	1.04057201	2	3.72326
Q5XHZ0	EGIVTTAEQDIKEDIAK	1.0136502	2	2.32675
Q5XHZ0	ELISNASDALEK	0.62857772	2	2.70663
Q5XHZ0	FEDTSPAGER	2.71394562	2	2.49638
Q5XHZ0	GTITIQDTGIGMTK	1.07781801	2	3.56485
Q5XHZ0	GVVDSEDIPLNLSR	1.20725142	2	4.80619
Q5XHZ0	HLAEHSPYYEAMK	1.45170485	2	3.72621
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.10006758	3	4.05658
Q5XHZ0	NIYYLCAPNR	1.00161294	2	2.41473
Q5XHZ0	SDCKDFANESR	1.30300289	2	2.70157
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	1.49527138	3	3.64968
Q5XHZ0	YESSALPAGQLTSLSDYASR	2.9488309	2	5.63993
Q5XHZ0	YIAQAYDKPR	1.60762104	2	2.66106
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**0.90806093**	**0.75657**	**9**
Q5XI22	AGHFDKEIVPVHVSSR	1.356602	2	4.99351
Q5XI22	ELGLSPEK	1.36938994	1	1.95042
Q5XI22	HGSNLEAMSK	2.46946867	2	2.68347
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	1.36138015	3	5.21921
Q5XI22	MGEVPLADSILCDGLTDAFHNYHMGITAENVAK	1.34023824	3	4.07326
Q5XI22	MLKPLAQVVSWSQAGVEPSVMGVGPIPAIK	1.4056596	3	4.53659
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	0.58668391	2	5.42234
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	0.9208098	2	5.18503
Q5XI22	VNIDGGAIALGHPLGASGCR	1.02575635	2	5.44328
Q5XI29	**CPSF7 Cleavage and polyadenylation specificity factor subunit 7**	**1.07417089**	**0.63856**	**2**
Q5XI29	QNLSQFEAQAR	1.07400749	2	2.41633
Q5XI29	SIGVYDVVELK	1.35945192	2	2.36714
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.26817178**	**0.5361**	**8**
Q5XI32	GCWDSIHVVEVQEK	1.03564623	2	3.74296
Q5XI32	KLEVEANNAFDQYR	1.29808119	2	4.13815
Q5XI32	LEVEANNAFDQYR	1.00283087	2	3.75904
Q5XI32	LVEDMENK	1.59552129	2	2.66874
Q5XI32	NDLVEALK	1.06800027	2	2.40444
Q5XI32	SGSGTMNLGGSLTR	1.31006964	2	3.30343
Q5XI32	STLNEIYFGK	0.99986555	1	2.05758

Q5XI32	YDPPLEDGAMPSAR	0.8958874	2	3.58329
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.20977972**	**0.98261**	**3**
Q5XI60	ALDIAAGITR	0.95140526	2	3.26724
Q5XI60	HHVALDSAASQLSGR	1.27910385	2	4.60082
Q5XI60	NVATDALGALEAR	1.2232006	2	3.98321
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**0.9030718**	**0.9794**	**6**
Q5XI73	AEEYEFLTPMEEAPK	1.31748494	2	4.40899
Q5XI73	IDKTDYMVGSYGPR	1.19022565	2	3.98928
Q5XI73	SIQEIQELDKDDESLR	0.71018147	2	5.28958
Q5XI73	SIQEIQELDKDDESLRK	0.88814994	2	4.65383
Q5XI73	TDYMVGSYGPR	1.03509753	2	2.41423
Q5XI73	VAVSADPNVPNVIVTR	0.94235394	2	3.97865
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**0.96694855**	**0.0012**	**18**
Q5XI78	FGLEGCEVLIPALK	1.25959208	2	3.587
Q5XI78	FLDTAFDLDAFK	2.06792901	2	2.66043
Q5XI78	FLDTAFDLDAFKK	1.25393501	2	2.93743
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	1.12718344	3	5.9103
Q5XI78	ICEEAFTR	1.32716784	2	2.34013
Q5XI78	IEQLSPFPFDLLLK	1.62416141	2	3.32549
Q5XI78	LEAADEGSGDMK	0.9984792	2	3.51647
Q5XI78	LNVLANVIR	5.56311557	2	2.32154
Q5XI78	LVEDHLAVQSLIR	1.43901421	2	2.90109
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.81166892	2	5.5507
Q5XI78	NQGYYDYVKPR	1.14337938	2	2.37889
Q5XI78	NTNAGAPPGTAYQSPLSLSR	0.18671502	2	2.85357
Q5XI78	SSLATMAHAQSLVEAQPNVDK	1.0540404	3	4.4054
Q5XI78	TSFDEMLPGTHFQR	1.33234399	2	2.30849
Q5XI78	VIPEDGPAAQNPDK	1.27649635	2	2.94482
Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	1.5366096	3	4.24681
Q5XI78	YAELLVSQGVVNQPEYEEEISK	1.83242178	2	4.07064
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	1.68971315	3	3.93237
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**0.95420743**	**0.91757**	**6**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.8561207	2	3.94193
Q5XI95	FNIDPLITHTLTLSEANEAVQLMK	1.38080796	3	4.98578
Q5XI95	IIAVDINK	0.89414143	2	2.73793
Q5XI95	MVATGVCGTDIK	0.98848636	2	3.02144
Q5XI95	NNICTEIR	1.24392643	2	2.47322
Q5XI95	TVGATDCVDPR	1.89974034	2	2.82778
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.08827214**	**0.49007**	**6**
Q5XIC0	AAEMLLFGK	2.69449526	2	2.45247
Q5XIC0	ATQQDFENAMNQVK	0.91345397	2	4.27289
Q5XIC0	GILVTSEGGITK	1.08956647	2	3.45074
Q5XIC0	LHAVNEEECTTLR	1.31841914	2	3.85118
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.67566792	2	5.40824
Q5XIC0	WDAWNALGSLPK	0.90836549	2	3.69137
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.03705511**	**0.67059**	**2**
Q5XIC1	VAPSAVLGPNVSIGK	0.76227871	2	2.62822
Q5XIC1	VEGTPNDPNPNDPR	3.02040057	2	3.18967
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.16454327**	**0.72656**	**7**
Q5XIE6	AGIATHFVDSEK	1.05492163	2	3.11277
Q5XIE6	AVLIDKDQTPK	1.16587084	2	2.83667
Q5XIE6	GCAGVITLNRPK	1.33589524	2	2.91632

Q5XIE6	HTETAEVLLER	2.24476817	2	2.87884
Q5XIE6	INSCFSANTVEQILENLR	1.59147685	2	3.16181
Q5XIE6	LHVLEEELLALK	2.0345069	3	4.10167
Q5XIE6	WKPADLKDVTDEDLNSYFK	1.24600894	2	2.31577
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.13922449**	**0.40695**	**3**
Q5XIF3	DTQLITVDEK	0.91432152	2	2.48431
Q5XIF3	HGWSYDVEGR	1.43098212	2	2.88439
Q5XIF3	LDVTPLTGVPEEHIK	0.88966632	3	3.66129
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.15899192**	**0.00611**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	1.15702015	2	3.8446
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.31711307	2	5.22033
Q5XIF6	DVNAAIAAIK	1.80279971	2	3.10819
Q5XIF6	SIQFVDWCPTGFK	1.0557942	2	4.13838
Q5XIF6	TIGGGDDSFTTFFCETGAGK	2.60258106	2	2.78316
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.23347087**	**0.99222**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	1.25857111	2	4.39852
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.21971062	2	5.66521
Q5XIH7	**PHB2 Prohibitin_2**	**1.0474292**	**4.5E-05**	**10**
Q5XIH7	DLQMVNISLR	3.54919628	2	2.73049
Q5XIH7	FNASQLITQR	0.96181231	2	3.78161
Q5XIH7	IGGVQQDTILAEGLHFR	1.96310474	3	4.92463
Q5XIH7	IPWFQYPIIYDIR	1.83626709	2	2.4702
Q5XIH7	IVQAEGEAEAAK	1.26033758	2	4.05741
Q5XIH7	IYLTADNLVLNLQDESFTR	2.47124981	2	4.04246
Q5XIH7	LGLDYEER	0.83271621	2	2.46778
Q5XIH7	LLLGAGAVAYGVR	4.32304124	2	3.78403
Q5XIH7	VLPSIVNEVLK	1.25219346	1	2.29777
Q5XIH7	VLSRPNAQELPSMYQR	1.56836074	2	4.76181
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.42342947**	**8.1E-07**	**12**
Q5XIM9	DASLMVTNDGATILK	4.31664257	2	2.99152
Q5XIM9	EALLSSAVDHGSDEVK	1.70277789	2	4.25345
Q5XIM9	FWQDLMNIAGTTLSSK	1.72946583	2	3.4773
Q5XIM9	GATQQILDEAER	1.37952439	2	3.87399
Q5XIM9	GSGNLEAIHVIK	1.24039062	2	2.56925
Q5XIM9	HGINCFINR	0.80062415	2	2.65158
Q5XIM9	LIEEVMIGEDK	1.09804716	2	3.15561
Q5XIM9	MLPTIIADNAGYDSADLVAQLR	1.4438007	3	3.31328
Q5XIM9	NIGVDNPAAK	1.15719583	1	1.95384
Q5XIM9	SLHDALCVLAQTVK	1.45352072	2	3.89941
Q5XIM9	VAEIEHAEKEK	1.74594408	2	2.7948
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.92426668	2	4.35294
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.30743035**	**0.15377**	**10**
Q5XIN6	AAEVEGEQVDNK	1.47525759	2	3.87772
Q5XIN6	AMYLPDTLSPADQLK	1.24486084	2	2.46615
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.81931575	2	4.54462
Q5XIN6	FLQDTIEEMALK	1.56280967	2	3.03683
Q5XIN6	KLEEGGPVYSPPAQVVVK	1.31415526	2	3.72942
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	1.54000412	2	5.30412
Q5XIN6	LEEGGPVYSPPAQVVVK	0.82922336	2	3.39234
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.30328517	3	3.98203
Q5XIN6	LLELQSIGTNNFLR	1.39139891	2	3.46601
Q5XIN6	STLQTLPEIVAK	0.90021699	2	2.57672
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**1.23909118**	**0.79242**	**9**
Q5XIT9	AATGEEVSAEDLGGADLHCR	1.02074989	2	5.22438

Q5XIT9	ALVNQLHER	1.16148468	2	2.68444
Q5XIT9	ALYGDTLVTGFAR	1.20291434	2	3.5122
Q5XIT9	AQEIALQNR	1.28003276	2	2.57048
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.01673864	2	5.25139
Q5XIT9	LWDDGIIDPVDTR	1.21058836	2	3.53647
Q5XIT9	LYGEEEVPAGGIITGIGR	13.0570746	2	4.76527
Q5XIT9	RFEEEGNPYYSSAR	1.76696681	2	4.25401
Q5XIT9	VSGVECMIVANDATVK	1.15759828	2	3.39354
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**0.87944394**	**0.84446**	**2**
Q5XIU5	ALIDPSSGLPNR	0.88457282	2	2.7933
Q5XIU5	SGIITPIHEQWEK	0.83213333	2	3.03607
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.1243986**	**0.86584**	**3**
Q5XIU9	GLATFCLDK	1.23781932	2	2.80292
Q5XIU9	GLCSGPGAGEESPAATLPR	0.87307794	2	4.83923
Q5XIU9	VFDVTK	1.12658785	1	1.98739
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**0.97835474**	**0.86921**	**9**
Q60587	ALAMGYKPK	0.6983715	2	2.40505
Q60587	AMDSDWFAQNYMGR	0.61636219	2	3.15826
Q60587	AQDEGHLSDIVPFK	0.99052306	2	2.48664
Q60587	DFIYVSQDPK	0.60291945	2	2.79556
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	1.87497556	3	4.6773
Q60587	DNGIRPSSLEQMAK	0.97848246	2	3.64398
Q60587	DQLLLGPTYATPK	1.04406638	2	3.75995
Q60587	MMLDLNK	0.95325088	1	2.12756
Q60587	NIVVVEGVR	1.14493554	2	3.06333
Q60598	**SRC8 Src substrate cortactin**	**1.09879153**	**0.57527**	**3**
Q60598	NASTFEEVVQVPSAYQK	1.406511	2	3.54738
Q60598	TVQGSGHQEHINIHK	1.1311677	2	3.47368
Q60598	VDQSAVGFEYQGK	1.08868868	2	3.34599
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.56317557**	**0.04846**	**4**
Q60759	DILGGNGISDEYHVIR	1.36030703	2	3.86019
Q60759	DIVYEMGELGVLGPTIK	1.39471614	2	3.89685
Q60759	GYGCAGVSSVAYGLLTR	1.35817264	2	3.32187
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.63224748	3	5.09824
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**0.95180325**	**0.08381**	**3**
Q60817	DIELVMSQANVSR	1.49525821	2	3.41899
Q60817	IEDLSQQAQLAAAEK	1.37840099	2	4.676
Q60817	NILFVITKPDVYK	0.5721367	2	3.66666
Q60952	**CP250 Centrosome_associated protein CEP250**	**1.40845471**	**0.26844**	**2**
Q60952	GQIQDLKK	0.88361013	1	1.9552
Q60952	QQIDELQK	9.84842846	1	2.03522
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.98043205**	**0.99555**	**2**
Q61029	SELVANNVTLPAGEQR	1.16690079	2	4.56692
Q61029	YGVNPGPIVGTTR	0.97918269	2	2.71646
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.53527943**	**0.14639**	**2**
Q61035	ASAEQIEEEVTK	1.71161472	2	2.77658
Q61035	REDLVEEIR	1.50081414	2	2.46645
Q61043	**NIN Ninein**	**0.88855305**	**0.5404**	**3**
Q61043	NEITTLNEEDSISNLK	0.44272692	2	2.47405
Q61043	RQLQMAFDEEKAQLQEELR+Oxidation(4	0.77872512		
Q61043	SLENVLAEK	0.88936422	1	2.02442
Q61301	**CTNA2 Catenin alpha_2**	**1.5469888**	**0.1884**	**3**

Q61301	LLEPLVTQVTTLVNTSNK	1.25295698	2	3.82697
Q61301	TSVQTEDDQLIAGQSAR	1.22827836	2	5.00155
Q61301	WDDSGNDIIVLAK	1.64419463	2	3.0363
Q61335	**BAP31 B_cell receptor_associated protein 31**	**1.10187628**	**1**	**5**
Q61335	AENEALAMQK	1.10523222	2	3.41615
Q61335	KYMEENDQLK	1.14730773	2	2.63751
Q61335	KYMEENDQLKK	0.88166443	3	3.96824
Q61335	YMEENDQLK	1.18447387	2	2.74282
Q61335	YMEENDQLKK	0.94874364	2	2.90167
Q61545	**EWS RNA_binding protein EWS**	**0.97664877**	**0.62056**	**2**
Q61545	GDATVSYEDPPTAK	0.92138233	2	3.41173
Q61545	GGPGGPGGPGGPMGR	1.62868168	2	2.86395
Q61595	**KTN1 Kinectin**	**1.14852648**	**0.50486**	**2**
Q61595	TAEHEAAQQDLQSK	1.20503262	2	4.37952
Q61595	VEPVLVTK	0.37794739	2	2.35715
Q61655	**DD19A ATP_dependent RNA helicase DDX19A**	**1.2356443**	**0.30639**	**2**
Q61655	SNLVDNTNQVEVLQR	1.23301931	2	4.18284
Q61655	TSTTAEKTEEEEKEDR	1.86514312	3	3.98546
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**1.90293072**	**8.8E-07**	**6**
Q61656	ELAQQVQQVAAEYCR	0.93720846	2	2.8823
Q61656	GDGPICLVLAPTR	1.76565931	2	2.95587
Q61656	MLDMGFEPQIR	1.96476099	2	3.34645
Q61656	NFYQEHPDLAR	2.19941589	2	3.30726
Q61656	STCIYGGAPK	1.55435082	2	2.47578
Q61656	TAQEVDTYR	1.69731582	2	2.31755
Q61830	**MRC1 Macrophage mannose receptor 1**	**1.32195224**	**0.39509**	**3**
Q61830	LKLPWHEAETYCK	1.55593033	2	2.35084
Q61830	WTVDEQVQFTHWNADMPGR+Oxidation(15	2.21650757		
Q61830	YLNWLPGSPSSEPGK	1.27944808	2	2.62816
Q61941	**transhydrogenase_ mitochondrial**	**1.31141929**	**0.00116**	**13**
Q61941	AQYPIADLVK	1.23611223	2	2.47929
Q61941	DDFDFGTMSHVIR	1.41320731	2	2.52687
Q61941	EANSIVITPGYGLCAAK	1.49605453	2	3.83934
Q61941	FFTGQITAAGK	1.19112106	2	2.74212
Q61941	GITHIGYTDLPSR	0.92139686	2	3.74714
Q61941	ILIVGGGVAGLASAGAAK	1.93135005	2	3.90539
Q61941	KTTVLAMDQVPR	1.23273169	2	3.28874
Q61941	MATQASTLYSNNITK	1.15341412	2	4.72669
Q61941	QGFNVVVESGAGEASK	1.36968513	2	4.14883
Q61941	SLGAEPLEVDLK	1.31278681	2	3.51381
Q61941	TTVLAMDQVPR	1.32633261	2	2.57553
Q61941	TVAELEAEK	1.33153449	2	2.98057
Q61941	VTIAQGYDALSSMANISGYK	1.40903973	2	5.33168
Q61990	**PCBP2 Poly(rC)_binding protein 2**	**1.5754308**	**0.12686**	**2**
Q61990	AITIAGIPQSIIECVK	1.55992902	2	2.33291
Q61990	IITLAGPTNAIFK	3.24972941	2	2.54473
Q62009	**POSTN Periostin**	**1.92725664**	**0.20836**	**2**
Q62009	ISTGGGETGETLQKFLQK	1.11052608	2	2.52124
Q62009	TEGPAMTKIQIEGDPDFR	1.93088739	2	2.30993
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**2.2705879**	**3.5E-12**	**4**
Q62095	HVINFDLPSDIEEYVHR	2.35984874	3	4.44574
Q62095	SFLLDLLNATGK	2.27033802	2	4.17301
Q62095	VGNLGLATSFFNER	2.12415751	2	3.11215
Q62095	VGSTSENITQK	1.60211921	2	2.86075
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.45544879**	**0.05393**	**20**
Q62261	AKDEQSAVSMLK	1.24002651	2	2.47299

Q62261	ALVADSHPESER	1.36118433	2	3.19084
Q62261	DQNTVETLQR	1.05596053	2	2.99977
Q62261	EAEKLESEHPDQAQAILSR	4.19153689	3	3.84367
Q62261	EGMQLISEKPETEAVVKEK	1.41890598	2	2.34095
Q62261	EIEELQSQAQALSQEGK	0.69454556	2	3.78378
Q62261	FESLEPEMNNQASR	1.06003223	2	3.90479
Q62261	HLLGVEDLLQK	1.26810052	2	3.40903
Q62261	HQILEQAVEDYAETVHQLSK	1.34912442	3	5.53489
Q62261	ITDLYTDLR	1.15606747	2	2.43914
Q62261	LTTLELLEVR	2.60370177	2	2.91883
Q62261	LVSDGNINSDR	1.51900285	2	3.32429
Q62261	LVSQDNFGFDLPAVEAATK	3.59520333	2	3.17874
Q62261	SNAHYNLQNAFNLAEQHLGLTK	0.9071213	3	3.89783
Q62261	SQNIITDSSSLNAEAIR	0.97729082	2	5.24351
Q62261	TLETPAAQMEGFLNR	2.30077112	2	3.22523
Q62261	TQILAASYELHK	1.78309492	2	2.57199
Q62261	TQTAIASEDMPNTLTEAEK	1.36748287	2	5.21925
Q62261	VIESTQDLGNDLAGVMALQR	0.22466774	2	4.45921
Q62261	VLDNAIETEK	1.03318501	2	2.47117
Q62376	**RU17 U1 small nuclear ribonucleoprotein 70 kDa**	**1.15279193**	**0.39336**	**2**
Q62376	IERRQQEVETELK	0.49342449	2	2.30479
Q62376	RQQEVETELK	1.16555008	2	2.4842
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.17067662**	**0.88338**	**3**
Q62425	FYSVNVDYSK	1.17201623	2	2.84338
Q62425	KNNPEPWNK	1.01071558	2	2.54775
Q62425	LGPNEQYK	1.00846451	1	2.02545
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**1.44420598**	**0.29531**	**2**
Q62446	GWDEALLTMSK	1.70019556	2	2.47995
Q62446	SEETLDEGPPK	1.44170609	2	3.0409
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.07541562**	**7.4E-05**	**4**
Q62452	AMEIAEALGR	0.74928217	2	4.1044
Q62452	GAGVTLNVLEMTADDLENALK	1.14818901	2	5.39017
Q62452	WLPQNDLLGHPK	1.10434828	2	3.29481
Q62452	YTGTRPSNLAK	0.56709825	2	2.72087
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.10068337**	**0.08974**	**8**
Q62465	ACGLNFADLMGR	1.04042969	2	2.90657
Q62465	CLVLTGFGGYDK	0.77497062	2	2.92495
Q62465	ENGVTHPIDYHTTDYVDEIKK	1.40861346	3	3.54473
Q62465	GVDIVMDPLGGSDTAK	1.34025071	2	4.37029
Q62465	IDSVWPFEK	0.80530473	2	2.77437
Q62465	TVENVTVFGTASASK	0.98010001	2	3.5227
Q62465	VLLVPGPEKET	0.99066249	2	2.79258
Q62465	VVTYGMANLLTGPK	1.93764146	2	3.48565
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.37036481**	**0.02044**	**4**
Q62636	INVNEIFYDLVR	1.52209369	2	4.0262
Q62636	LVVLGSGGVGK	1.39074655	2	2.63694
Q62636	QWSNCAFLESSAK	0.91798529	2	2.54085
Q62636	VKDTDDVPMILVGNK	0.92609826	2	2.78135
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.79277558**	**0.9044**	**4**
Q62651	HVLHVQLNRPEK	1.32702624	2	3.79476
Q62651	MMADEALDSGLVSR	1.02284179	2	4.37672
Q62651	RIPEEVSDHNYESIQVTSAQK	0.90314398	3	5.60781

Q62651	SLVNELTFTAR	0.78125879	2	3.1926
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**1.35646642**	**3.6E-09**	**7**
Q62730	AVLVTGADSGFGHALAK	1.46083224	2	4.34994
Q62730	DIQHAICAK	1.90504289	2	2.39238
Q62730	EIQENYGQEYVHTQK	2.27083601	2	4.50491
Q62730	EMSNPDITPVLR	1.52489977	2	2.66544
Q62730	LSVLQMDVTKPEQIK	2.7254822	2	3.69452
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.92354769	3	4.60785
Q62730	VVTIHPGGFQTNIVGSQDSWDK	2.09445612	2	5.81526
Q62736	**CALD1 Non_muscle caldesmon**	**1.11013662**	**0.68177**	**14**
Q62736	ASGDKEAEGAPQVEAGK	1.24342741	2	4.85141
Q62736	ASGDKEAEGAPQVEAGKR	1.45046276	3	3.97246
Q62736	EEIERR	1.27007789	1	1.90469
Q62736	EFDPTITDGSLSVPSR	1.20453162	2	3.67397
Q62736	GGNLGENQIKDEK	1.17460521	2	3.47579
Q62736	GSVFSSPSASGTPNK	1.18553655	2	2.30513
Q62736	KVLEEEEQR	1.11974345	2	2.74377
Q62736	LEQYTNAIEGTK	1.10475606	2	3.37348
Q62736	MQNNSAENETAEGEEK	1.03247753	2	4.88519
Q62736	MQNNSAENETAEGEEKGESR	1.17006377	3	4.62822
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0	1.30489944		
Q62736	RGETESEEFEK	1.28912397	2	3.31606
Q62736	RRGETESEEFEK	1.54845989	2	2.89916
Q62736	VLEEEEQR	1.32131923	2	2.59837
Q62745	**CD81 CD81 antigen**	**1.1668906**	**0.88699**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.14059803	2	3.17297
Q62745	QFYDQALQQAVMDDDANNAK	1.80805595	2	5.03561
Q62769	**UN13B Protein unc_13 homolog B**	**0.94148567**	**0.39512**	**3**
Q62769	DHMVREETRNLTPK	0.94664658	2	2.58778
Q62769	ILSQRSNDEVAR	3.10454891	2	2.35181
Q62769	SNDEVAREFVK	0.63251123	1	1.93655
Q62770	**UN13C Protein unc_13 homolog C**	**1.54986964**	**0.46884**	**2**
Q62770	ENFPASNSERLQDLK	1.12412655	2	2.37452
Q62770	NLSMDETGLTILR	5.76046446	2	2.3763
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.60455878**	**0.43901**	**6**
Q62785	ANEEDEQEEGGDGASGDPK	1.35977164	2	5.57385
Q62785	ANEEDEQEEGGDGASGDPKK	1.46969988	3	3.51232
Q62785	GVEGLIDIENPNR	1.80426107	2	2.92045
Q62785	QKANEEDEQEEGGDGASGDPK	1.35122577	3	4.35504
Q62785	QKANEEDEQEEGGDGASGDPKK	1.89738543	3	3.43019
Q62785	YMKMHLAGKTEQAK	0.75392153	2	2.30757
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.09127693**	**0.72144**	**2**
Q62789	IILDELVQR	1.0425841	2	3.54343
Q62789	WIPQNDLLGHPK	1.10434828	2	3.29481
Q62812	**MYH9 Myosin_9**	**0.90433001**	**0.84487**	**68**
Q62812	ALEEAMEQK	1.17107012	2	3.29544
Q62812	ALELDSNLYR	1.07100731	2	3.28462
Q62812	ALEQQVEEMK	1.86104992	2	3.3023
Q62812	ALEQQVEEMKTQLEELEDELQATEDAK	1.32603195	3	3.39235
Q62812	ANLQIDQINTDLNLER	1.26017119	2	5.43453
Q62812	ASIAALEAK	1.24328156	2	2.68672
Q62812	ASREEILAQAK	2.00725524	2	2.98513
Q62812	CQYLQAEK	1.27134523	1	2.33016
Q62812	DFSALESQLQDTQELLQEENR	0.94606402	3	6.72677
Q62812	DLEAHIDTANK	1.31064048	2	3.46763
Q62812	DLGEELEALKTELEDTLDSTAAQQELR	1.18290526	3	4.49373

Q62812	DLQGRDEQSEEK	2.07584341	2	2.92571
Q62812	EEILAQAK	1.14676313	1	2.37493
Q62812	EEILAQAKENEK	1.17460521	2	2.34371
Q62812	ELEDATETADAMNR	0.89475257	2	4.42332
Q62812	ELETQISELQEDLESER	1.14509936	2	4.86494
Q62812	EMEAELEDERK	0.87909994	2	3.32527
Q62812	HEAMITDLEER	0.62575403	2	3.27159
Q62812	HEDELLAK	1.12643436	2	3.04689
Q62812	HSQAVEELAEQLEQTK	1.05650356	2	5.02092
Q62812	HSQAVEELAEQLEQTKR	1.17494826	3	5.65885
Q62812	IIGLDQVAGMSETALPGAFK	2.26197516	2	5.39499
Q62812	IMGIPEDEQMGLLR	1.42098505	2	2.61722
Q62812	IRELETQISELQEDLESER	1.21536796	2	5.4351
Q62812	KEEELQAALAR	1.15332534	3	3.3629
Q62812	KKVEAQLQELQVK	1.15703074	2	4.62047
Q62812	KLEEDQIIMEDQNCK	0.97579574	2	6.00955
Q62812	KLEGDSTDLSDQIAELQAQIAELK	1.49553761	2	5.57834
Q62812	KQELEEICHDLEAR	1.1691981	2	4.73266
Q62812	KVEAQLQELQVK	1.28844332	2	4.55015
Q62812	LDPHLVLDQLR	1.16147918	3	3.42147
Q62812	LEEDQIIMEDQNCK	0.87445827	2	4.99045
Q62812	LEGDSTDLSDQIAELQAQIAELK	1.48042883	3	5.22578
Q62812	LEVNLQAMK	0.90296917	2	2.63661
Q62812	LQEMESAVK	1.22773392	2	2.75338
Q62812	LQQELDDLLVDLDHQR	1.10699007	2	4.81848
Q62812	LQVELDSVTGLLNQSDSK	1.17971156	2	5.48712
Q62812	LTEMETMQSQLMAEK	1.49591455	2	4.97254
Q62812	MEDGVGCLETAEEAK	1.15794809	2	4.37249
Q62812	MQQNIQELEEQLEEEESAR	1.76334399	2	6.32211
Q62812	NAEQFKDQADK	1.38771531	2	3.45815
Q62812	NKHEAMITDLEER	1.50882834	3	4.10279
Q62812	NLPIYSEEIVDMYK	1.32681916	2	3.79672
Q62812	NMDPLNDNIATLLHQSSDK	1.09054009	2	4.94688
Q62812	NTDQASMPDNTAAQK	1.73565367	2	5.31293
Q62812	NTDQASMPDNTAAQK+Oxidation(6	1.83676128		
Q62812	QAQQERDELADEIANSSGK	1.19929216	3	4.19502
Q62812	QIATLHAQVTDMK	0.85206567	2	2.38453
Q62812	QLEEAEEEAQR	1.09597216	2	3.8772
Q62812	QSVSNLEK	1.14891885	2	2.47082
Q62812	QTLENERGELANEVK	0.78191284	2	3.38568
Q62812	RGDMPFVVTR	0.9840989	2	2.96735
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.02672766	3	5.75843
Q62812	RQLEEAEEEAQR	1.0077954	2	4.60045
Q62812	SMEAEMIQLQEELAAAER	1.20331008	3	4.33539
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1	2.11266923		
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)Oxidation(5	1.03155321		
Q62812	TDLLLEPYNK	1.10919316	2	3.41927
Q62812	TELEDTLDSTAAQQELR	0.71923826	2	5.33869
Q62812	TEMEDLMSSK	1.44470755	2	2.58969
Q62812	THEAQIQEMR	1.17658546	3	3.43686
Q62812	TQLEELEDELQATEDAK	1.35406287	2	6.59084
Q62812	VAEFTTDLMEEEEK	1.62119615	2	4.48055
Q62812	VEAQLQELQVK	0.55822282	2	3.48367
Q62812	VEDMAELTCLNEASVLHNLK	1.22897836	2	4.49972
Q62812	VISGVLQLGNIVFK	1.64083917	2	3.75795
Q62812	VSHLLGINVTDFTR	1.88397776	2	3.8123

Q62812	YEILTPNSIPK	0.94062511	2	3.13421
Q62824	**EXOC4 Exocyst complex component 4**	**0.92181446**	**0.86838**	**2**
Q62824	EDLDCDPEENSTLFMGILIQGLAR	1.19264194	2	2.31916
Q62824	SQTGVGDQTTQNTR	0.9205755	2	3.11758
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.3705555**	**0.93965**	**7**
Q62826	ADILEDKDGK	1.37106667	2	2.79058
Q62826	AFITNIPFDVK	1.46428784	2	3.24089
Q62826	GIGMGNLGPAGMGMEGIGFGINK	1.72594213	2	3.91876
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.10648411	2	5.02905
Q62826	INEILSNALK	1.73819385	2	2.61269
Q62826	MGPAMGPALGAGIER	1.1651661	2	2.75543
Q62826	MGPVMDRMATGLER+Oxidation(0)Oxidation(4)Oxidation(7	2.37737766		
Q62868	**ROCK2 Rho_associated protein kinase 2**	**1.08114387**	**0.5202**	**2**
Q62868	DEEISAAAIK	3.15589327	1	1.90037
Q62868	QENNHLMEMKMNLEK+Oxidation(6	1.07726633		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**0.89902805**	**0.13454**	**2**
Q62871	ADAEEEAATR	2.39615541	2	3.17089
Q62871	SVSTPSEAGSQDSGDGAVGSR	0.6620457	2	5.21896
Q62902	**LMAN1 Protein ERGIC_53**	**1.25973058**	**3.7E-07**	**7**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.14223862	2	4.15028
Q62902	GHPDLQGQPADDIFESIGDR	1.4906322	2	5.01564
Q62902	LVSGVQHPGSAGVYETTQHFMDIK	1.19982396	3	3.42386
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.0250776	3	6.36976
Q62902	RGAGTPGQPGQVSQQELDTVVR	1.26599121	3	4.45438
Q62902	YQEEFEHFQQELDK	1.31987677	2	5.31401
Q62902	YVSSLTEEISR	1.40603521	2	3.04648
Q62904	**DHB7 3_keto_steroid reductase**	**1.0406556**	**0.7471**	**3**
Q62904	MDVDEDTAEK	3.65352822	2	2.38957
Q62904	YATDLLNVALNR	1.02367384	2	2.57317
Q62904	YLSGTTGLGTNYVK	1.03043067	2	2.98828
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.83856083**	**0.0028**	**2**
Q62967	GLQVAPVLLSDELK	0.93715334	2	3.74149
Q62967	VYGVEGDLSEVAR	0.83191599	2	3.42081
Q62991	**SCFD1 Sec1 family domain_containing protein 1**	**1.20756833**	**0.12969**	**3**
Q62991	ALTDAGCNLSPLQYIK	2.33472838	2	2.90419
Q62991	FGQDIISPLLSVK	1.58718245	2	2.36116
Q62991	SLLDVISDPDAGTPEDK	0.93909059	2	2.86206
Q63041	**A1M Alpha_1_macroglobulin**	**0.83556532**	**0.81553**	**12**
Q63041	AEDITHNGIVYTPK	1.22467384	2	3.66851
Q63041	AEQGAYLGPLPYK	0.69139123	2	3.23818
Q63041	AESPVFVQTDKPIYKPGQTVK	0.733998	3	4.01247
Q63041	DTVVKPVIVEPEGIEK	1.03485567	2	3.75448
Q63041	GSIFNSGSHVLPLEQGK	1.06831954	2	4.07549
Q63041	KLQDQSNIQR	0.83624679	2	2.57123
Q63041	LIVYTILPNEELIADVQK	1.494381	2	2.99863
Q63041	LQDQSNIQR	0.72812386	2	2.9837
Q63041	QDLNDNDAYSVFQSIGLK	1.38487831	2	2.6273
Q63041	VNTLPLNFDK	0.75616016	2	2.74901
Q63041	YNILPEAEGEAPFTLK	0.92513848	2	4.90899
Q63041	YVVLVPSELYAGVPEK	1.00816103	2	3.00918
Q63060	**GLPK Glycerol kinase**	**1.38504599**	**5E-13**	**12**
Q63060	AGALEGVPISGCLGDQSAALVGQMCFQDGQAK	1.81065745	3	4.5678
Q63060	AVLGPLVGAVDQGTSSTR	1.37861913	2	5.19401
Q63060	CVFSEHGLLTTVAYK	1.1128928	2	4.28195

Q63060	DCGIPLSHLQVDGGMTSNK	1.35175491	2	4.43673
Q63060	EILQSVYECIEK	1.43652075	2	3.41925
Q63060	FEPQINAEESEIR	1.28632901	2	3.64244
Q63060	KVQEAVEENR	1.49356959	2	3.35223
Q63060	LGQLNIDISNIK	2.19648839	2	3.23066
Q63060	NTYGTGCFLLCNTGHK	0.88076742	2	3.81262
Q63060	SSSEIYGLMK	1.69122648	2	2.51534
Q63060	TAELLSHHQVEIK	1.59615199	2	3.45738
Q63060	VQEAVEENR	2.18542844	2	3.24487
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**1.06314735**	**0.31907**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.26609014	3	5.12988
Q63081	GESPVDYDGGR	2.14217938	2	2.85702
Q63081	GSFSEQGINEFLR	1.24011305	2	4.19658
Q63081	GSTAPVGGGSFPNITPR	0.99610708	2	4.87822
Q63081	HQSLGGQYGVQGFPTIK	1.42259624	2	5.07805
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.80264984	3	5.23477
Q63081	NLEPEWAAAATEVK	0.97304431	2	4.02494
Q63081	NSYLEVLLK	1.41613807	2	2.97378
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.02871443	3	5.02229
Q63081	TGEAIVDAALSALR	1.03662435	3	4.87508
Q63081	VGAVNADKHQSLGGQYGVQGFPTIK	1.03693372	3	4.60694
Q63083	**NUCB1 Nucleobindin_1**	**1.32027152**	**0.15954**	**3**
Q63083	LSQETEALGR	1.89272174	2	2.81855
Q63083	VNVPGSQAQLK	1.23093583	2	2.44025
Q63083	YLQEVINVLETDGHFR	1.3253026	3	4.11414
Q63108	**EST3 Liver carboxylesterase 3**	**1.06066518**	**0.9987**	**4**
Q63108	GGTSKEEINLSK	0.88668185	2	3.42736
Q63108	LDPMTATSLLK	1.43152002	2	2.50753
Q63108	QKTEEELLETTLK	1.22394177	2	3.50025
Q63108	SSFLLNLPEEAIPVAVEK	1.05903958	2	4.83555
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.29395726**	**0.00238**	**7**
Q63120	ACALLPDLEILPGGDMAEIGEK	2.65024688	2	4.82756
Q63120	HGEIQFNNYQVR	2.2395862	2	2.72902
Q63120	IVEYGSPEELLSNR	2.26440326	2	3.31796
Q63120	QSQSQDVLVLEEAK	1.75845475	2	2.56377
Q63120	YFAWEPSFQEQVQGIR	2.04383037	2	3.93459
Q63120	YLGGDDLDTSAIR	0.61368615	2	2.36148
Q63120	YRPELDLVLK	1.17651647	3	3.66308
Q63150	**DPYS Dihydropyrimidinase**	**1.15968226**	**0.15826**	**10**
Q63150	ALGKDDFTK	1.26787806	2	2.55283
Q63150	DQTCTPIPVKR	1.57487204	2	2.49283
Q63150	EIGAIAQVHAENGDLIAEGAK	1.59598824	2	4.999
Q63150	FVAVTSTNAAK	1.25162812	2	3.17668
Q63150	GSSLIEAFETWR	2.31613226	2	3.5411
Q63150	IAVGSDADIVIWDPEATR	2.05743483	2	3.26214
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	1.19048271	3	3.74974
Q63150	VVNDDFSQVADVLVEDGVVR	1.35017742	2	5.95564
Q63150	VVYEAGVFDVTAGHGK	1.35865735	2	4.20199
Q63150	VVYGEPIAAGLGTDGTQYWNK	1.50814895	2	5.8231
Q63228	**GMFB Glia maturation factor beta**	**1.72760802**	**0.23149**	**2**
Q63228	LVVLDEELEGVSPDELKDELPER	1.72781925	3	3.70804
Q63228	NTEDLTEEWLR	1.66015244	2	2.59946
Q63269	**ITPR3 Inositol 1_4_5_trisphosphate receptor type 3**	**0.7716863**	**9.8E-05**	**2**
Q63269	LLDGGNTEIQK	0.7699839	1	2.45957
Q63269	QKLMRDENILK+Oxidation(3	1.29714936		

Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.18941365**	**3.9E-10**	**19**
Q63270	AVEAGLNVKPYVK	0.90613185	2	2.96859
Q63270	AVLAESYER	1.27308374	2	2.6416
Q63270	DFSDSSQDPDFTQVVELDLK	1.9574375	2	3.66532
Q63270	FVEFFGPGVAQLSIADR	1.7641262	2	5.29679
Q63270	GFQVAPDHHNDHK	0.36985826	2	3.41537
Q63270	IDFEKEPLGVNAQGQQVFLK	1.11372389	3	6.12805
Q63270	IIPPGSGIIHQVNLEYLAR	1.42909938	2	2.52067
Q63270	KNDIENILNWSIMQHK	1.47854448	3	4.5379
Q63270	NCDEFLVK	1.04049071	2	2.32397
Q63270	NDIENILNWSIMQHK	1.30602131	2	2.51395
Q63270	NQDLEFER	1.30496951	1	2.69866
Q63270	QAPQTVHLPSGETLDVFDAAER	0.6154185	3	3.62427
Q63270	SIEVPFKPAR	0.84851998	2	2.54092
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.83417602	3	4.67185
Q63270	SPPFFESLTLDLQPPK	1.35381987	3	4.47541
Q63270	SWNALAAPSEK	1.17231353	2	2.60667
Q63270	TSLSPGSGVVTYYLR	1.27385481	2	3.54827
Q63270	VILQDFTGVPAVVDFAAMR	1.32214904	2	4.77858
Q63270	YQQAGLPLIVLAGK	1.0599112	2	3.55306
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**0.95415505**	**0.26195**	**18**
Q63276	AHGHFLFVVGEDDKNLNSK	1.16807274	2	6.07864
Q63276	ASEVGEVDLER	5.09618337	2	4.03287
Q63276	DDKGNLFNSQAFYR	0.94200547	2	3.3099
Q63276	GNLFNSQAFYR	0.77172606	2	2.67858
Q63276	LCHPYFPVEGK	1.14553169	3	3.5189
Q63276	LTAVPLSALVDEPVHIR	3.26877589	2	3.94814
Q63276	MPFVIPSINWGGEVIPHAAAQEHSWK	1.44480112	4	4.63693
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.97946433	3	4.23705
Q63276	QHLNPGFNSQL	0.98405182	2	3.50833
Q63276	QITATVLINGPNFVSSNPHVYR	1.1903688	3	4.77909
Q63276	TFEETADK	1.05149855	1	1.92101
Q63276	TFEETADKDSK	0.85249854	2	3.79436
Q63276	VDLEYFEEGVEFLLR	1.15582375	2	4.3345
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.76038388	3	5.15794
Q63276	VISSSLDSLILER	0.76854183	2	4.49398
Q63276	VTGLTPFQVVCLQASLK	1.18796702	3	5.2183
Q63276	WYVAPGVTR	0.78524214	1	2.12347
Q63276	YCFPIEK	1.00613312	2	2.57902
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.04149625**	**0.43917**	**26**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.49787169	3	6.02255
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.8894241	2	4.73007
Q63342	DGLLFGPYESQEK	1.81163493	2	2.71546
Q63342	EGQESPPSPPEWK	1.03399475	2	2.68183
Q63342	GGYDVEIR	1.37243864	2	2.63564
Q63342	GQDSTQLLDHLCANVIPK	1.22512945	2	4.10056
Q63342	IHELFPLLNMDK	1.1938573	2	2.75267
Q63342	IHYDSIK	1.21013146	1	2.36116
Q63342	IMNAGQEEGIDNFGTYALNALR	1.22743977	2	4.48295
Q63342	ISDIPVTAIR	1.18012425	2	3.336
Q63342	ITEHVEAAMEMVPVLK	1.65936669	2	4.64274
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.51791454	3	5.93332
Q63342	LEEETGQVVGFHQPGSIR	1.11820607	2	4.83796
Q63342	LNKPADFTGK	1.75282361	2	3.01995
Q63342	LTSEDLSDDVFK	0.81691297	2	4.03729

Q63342	NITDELGVLGVAGPYAR	1.87175959	2	4.77046
Q63342	NYPATIIQEPLVLTEPTR	1.40781333	2	4.47272
Q63342	REDSAALYER	0.48605629	2	2.65566
Q63342	TNWHATEQYIIEPEK	1.02562724	2	3.71256
Q63342	VGFTNISHMLTPR	1.00452135	2	3.11369
Q63342	VGVIDLSPFGK	1.20000045	2	3.52946
Q63342	VIGNTTSGSYSYSIQK	1.31523037	2	4.33565
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.94322943	3	4.30877
Q63342	WIEEAAVR	2.07918128	2	2.8172
Q63342	WTTTQYTEAK	1.03812564	2	2.72726
Q63342	YLSDWILHGEPPFDLIELDPNR	1.32724792	2	4.49836
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.17101167**	**0.78783**	**7**
Q63347	ALDEGDIALLK	1.2700345	2	2.819
Q63347	FDDGAGGDNEVQR	1.01031937	2	4.28376
Q63347	FVVDLSDQVAPTDIEEGMR	1.1368931	2	3.72301
Q63347	IINADSEDPK	1.17037256	2	3.20563
Q63347	QTLQSEQPLQVAR	1.17705093	2	3.67158
Q63347	QVEDDIQQLLK	1.36146058	2	2.98864
Q63347	TMLELINQLDGFDPR	1.00315202	2	3.01654
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.21261431**	**0.78553**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.40709412	2	5.70241
Q63362	KYTEQITSEK	1.21989592	2	2.72064
Q63362	TTGLVGLAVCDTPHER	1.1719676	2	4.25738
Q63362	YTEQITSEK	1.21317298	1	2.32351
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**1.14360373**	**0.30327**	**2**
Q63413	CIALAQLLVEQNFPAIAIHR	1.93733509	3	3.39219
Q63413	NCPHIVVGTPGR	1.0931743	2	2.98147
Q63429	**UBC Polyubiquitin_C**	**1.05294852**	**0.83143**	**3**
Q63429	ESTLHLVLR	0.801885	2	2.50406
Q63429	TITLEVEPSDTIENVK	1.07045198	2	4.85392
Q63429	TLSDYNIQK	1.18170831	2	2.68568
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**0.95665172**	**0.87927**	**10**
Q63448	ADWLDSEAPLAAYR	1.44921892	2	4.32425
Q63448	EIHALASAGKPLASWTAQR	0.9360083	2	4.57415
Q63448	GGYISGEQTGK	0.96123146	2	3.01199
Q63448	LGASLGSLSSGR	0.69992807	2	2.7108
Q63448	NLWAAVLQQSGVLER	0.98486442	2	4.51784
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.74179772	3	4.51586
Q63448	TIFLDLIELQR	1.82268613	2	2.51954
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.13118794	3	4.50697
Q63448	TTAHYDPATQEFILHSPDFEAAK	0.87131936	3	4.46822
Q63448	TVNFLEAYPGILGQK	1.12828268	2	5.11667
Q63507	**RL14 60S ribosomal protein L14**	**1.30610063**	**3.1E-09**	**3**
Q63507	CMQLTDFILK	0.81796205	2	2.75616
Q63507	LVAIVDVIDQNR	1.68209886	2	4.12323
Q63507	RFVEVGR	1.21248317	2	2.35885
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.52396351**	**0.4355**	**4**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.41329722	3	4.56427
Q63524	HEQEYMEVR	1.53739086	2	3.43714
Q63524	HEQEYMEVR+Oxidation(5	1.33754657		
Q63524	LEEMINELAVAMTAVK	1.146655	2	3.54257
Q63525	**NUDC Nuclear migration protein nudC**	**1.26497761**	**0.03313**	**4**
Q63525	GQAPVIDGELYNEVK	1.23846594	2	3.61122
Q63525	LVTSDPEINTK	1.41420814	2	2.43712
Q63525	VEESSWLIEDGK	1.18058489	2	2.41713

Q63525	WTQTLSELDLAVPFR	1.40816617	2	2.8311
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.07589216**	**0.06824**	**6**
Q63569	AMEVDERPTEQYSDIGGLDK	1.12613469	3	5.32753
Q63569	CTDDFNGAQCK	1.68727472	2	3.26109
Q63569	MNVSPDVNYEELAR	1.07589222	2	3.57539
Q63569	QTYFLPVIGLVDAEK	1.49246086	2	2.46088
Q63569	TMLELLNQLDGFQPNTQVK	0.6637626	2	3.92939
Q63569	VDILDPALLR	1.19889484	2	2.91082
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.16587024**	**0.91298**	**4**
Q63570	FDAQTGADR	1.2157437	2	2.73814
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.41179364	3	5.80839
Q63570	KDEQEHEFYK	1.16766191	2	3.42068
Q63570	RFDAQTGADR	1.06303092	2	3.01869
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.37869647**	**0.1571**	**4**
Q63584	ITDSAGHILYAK	1.51243172	2	3.73348
Q63584	LEDLSESIVNDFAYMK	1.76965439	2	3.58185
Q63584	NYEEIAK	1.29626313	1	2.40973
Q63584	RLEDLSESIVNDFAYMK	1.1595032	2	3.66917
Q63598	**PLST Plastin_3**	**1.32189007**	**0.98152**	**13**
Q63598	AESMLQQADK	1.21442534	2	3.42438
Q63598	ATDDIIVNWVNGTLSEAGK	1.35066601	2	5.11268
Q63598	AVGDGIVLCK	2.29631642	2	2.44519
Q63598	EGICALGGTSELSSEGTQHSYSEEEK	0.83186912	3	3.47384
Q63598	HVIPMNPNTDDLFK	1.03719389	2	3.03868
Q63598	IDINMSGFNETDDLKR	1.00768087	2	4.46001
Q63598	INNFSADIK	1.46183415	2	2.39374
Q63598	KLENCNYAVELGK	1.003212	2	3.73083
Q63598	NEALAALLR	0.93993528	2	2.61155
Q63598	TISSSLAVVDLIDAIQPGCINYDLVK	1.27024491	3	3.56522
Q63598	VYALPEDLVEVKPK	1.14739714	2	3.09043
Q63598	YPALTKPENQDIDWTLLEGETR	1.11914745	3	5.3709
Q63598	YTLNVMEDLGEGQK	0.83746585	2	3.6831
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.12024189**	**0.99964**	**8**
Q63610	IQVLQQQADDAEER	1.10828216	2	5.12508
Q63610	KIQVLQQQADDAEER	1.25126132	2	5.43538
Q63610	KLVIIEGDLER	0.81824155	2	3.22849
Q63610	LEKTIDDLEDKLK	2.1769859	2	2.71825
Q63610	LVIIEGDLER	1.23117875	2	2.94764
Q63610	MELQEIQLK	1.12386906	2	3.1234
Q63610	TIDDLEDKLK	0.88461573	2	2.6964
Q63610	YSQKEDKYEEEIK	1.48990027	2	4.94989
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.25176163**	**0.272**	**15**
Q63617	AANSLEAFIFETQDK	1.60868802	2	2.56057
Q63617	DAVITVPAFFNQAER	0.84828065	2	2.80569
Q63617	EGETPDEKESGDKSEAQKPNEK	1.19154308	3	3.99105
Q63617	FLGDSAAGMAIK	1.19112127	2	2.52277
Q63617	GQAGPEGVPPAPEEEKK	1.29747262	2	3.41887
Q63617	LIPEMDQIFTDVEMTTLEK	1.50079627	2	3.35289
Q63617	LYQPEYQEVSTEEQR	0.75674382	2	5.26585
Q63617	NINADEAAAMGAVYQAAALSK	1.26105187	2	5.32702
Q63617	SLAEDFAEQPIK	0.94817666	2	2.98217
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.77306817	3	3.43942
Q63617	TLGGLEMELR	1.17509182	2	2.9743
Q63617	TVLSANADHMAQIEGLMDDVDFK	1.4377717	3	3.88961
Q63617	VEFEELCADLFDR	2.048713	2	3.42113
Q63617	VESVFETLVEDSPEEESTLTK	1.47055587	2	4.01553

Q63617	VLQLINDNTATALSYGVFR	1.42004213	2	4.68982
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**1.09098767**	**0.22137**	**2**
Q63692	EGEEAGPGDPLLEAVPK	1.08918643	2	3.32555
Q63692	LGPGGLDPVEVYESLPEELQK	1.51990386	2	3.00766
Q63716	**PRDX1 Peroxiredoxin_1**	**1.14097006**	**0.23233**	**15**
Q63716	ADEGISFR	1.12680891	2	3.07918
Q63716	ATAVMPDGQFK	1.085045	2	2.87378
Q63716	GLFIIDDKGILR	1.39371673	2	2.86201
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.21674078	4	5.82243
Q63716	IGHPAPSFK	3.10184578	1	1.91633
Q63716	KQGGLGPMNIPLVSDPK	1.22306087	2	4.07012
Q63716	KQGGLGPMNIPLVSDPKR	0.86186914	3	3.81001
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.5308117	3	3.39142
Q63716	LVQAFQFTDK	1.66068991	2	3.29712
Q63716	QGGLGPMNIPLVSDPK	0.92608031	2	3.13924
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6	1.32571129		
Q63716	QITINDLPVGR	1.12698814	2	3.15417
Q63716	RTIAQDYGVLK	1.26760996	2	2.48117
Q63716	SVDEILR	1.14961854	2	2.48281
Q63716	TIAQDYGVLK	1.11881957	2	3.21053
Q63797	**PSME1 Proteasome activator complex subunit 1**	**1.27783794**	**0.01503**	**10**
Q63797	ISELDAFLK	1.19872886	2	2.36917
Q63797	ISELDAFLKEPALNEANLSNLK	1.71744239	2	5.35168
Q63797	KGDEDDKGPPCGPVNCNEK	1.28828932	3	4.81628
Q63797	KISELDAFLKEPALNEANLSNLK	1.33226693	3	5.88134
Q63797	LEGFQTQISK	1.20301586	2	2.71279
Q63797	NAYAVLYDIILK	2.33226859	2	3.55742
Q63797	QLVHELDEAEYQEIR	1.16862051	2	4.18508
Q63797	TENLLGSYFPK	1.39609556	2	3.49483
Q63797	VDVFREDLCSK	1.06153344	2	2.5216
Q63797	VFELMTSLHTK	0.99803551	2	3.04794
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.24365965**	**0.32268**	**4**
Q63798	AFYAELHHIISSNLEK	1.17991107	2	3.91519
Q63798	IEDGNDFGVAIQEK	1.60676592	2	4.04959
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.50627133	3	3.63328
Q63798	TKVEAFQTAISK	1.25717274	2	3.56125
Q63836	**SBP2 Selenium_binding protein 2**	**1.26056756**	**0.21445**	**3**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.60546073	2	5.34098
Q63836	IYVVDVGSEPR	1.10164584	2	3.82812
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.24242232	3	3.84383
Q63945	**SET Protein SET**	**0.98274633**	**0.81804**	**2**
Q63945	IDFYFDENPYFENK	1.67657569	2	4.27991
Q63945	LNEQASEEILK	0.96799579	2	3.16709
Q63965	**SFXN1 Sideroflexin_1**	**1.32352181**	**0.31813**	**5**
Q63965	NILLTNEQLENAR	1.25902796	2	4.38984
Q63965	QAITQVVISR	1.89933992	2	2.33622
Q63965	QGIVPAGLTENELWR	1.42827203	2	3.17632
Q63965	WDQSTFIGR	1.14884521	2	2.79195
Q63965	YAYDSAFHPDTGEK	1.53698088	2	4.28447
Q64012	**RALY RNA_binding protein Raly**	**1.33177634**	**0.53233**	**2**
Q64012	LEQIAEEQK	1.47510398	2	2.5215
Q64012	SNIDALLGR	1.17738629	2	2.35616
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**1.68425054**	**4.9E-09**	**19**
Q64057	AWNIWADIPAPK	1.85650645	2	3.80585
Q64057	DYEETIGK	1.59562158	1	1.92867
Q64057	EDNEGVFNGSWGGR	1.33331454	2	3.68846

Q64057	FKNEEEVFEWNNEVK	1.1608556	2	5.75616
Q64057	GAPTTSLVSIAVTK	1.09030165	2	5.00509
Q64057	GEVITTYCPANNEPIAR	1.19688472	2	5.00784
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	1.36138983	2	5.6004
Q64057	LFLHESIHDEVVDR	1.68429802	2	4.37684
Q64057	LVSLEMGK	1.83244038	2	2.44717
Q64057	NEEEVFEWNNEVK	1.32226432	2	4.5694
Q64057	QAVSMFVQAVEEAK	1.76454957	2	3.39187
Q64057	QAVSMFVQAVEEAKK	1.3570818	2	2.83807
Q64057	QGLSSSIFTK	1.88496367	2	2.75333
Q64057	QVALMVQER	1.30200354	2	2.51664
Q64057	STCTINYSTALPLAQGIK	1.40458351	2	4.87192
Q64057	VGNPWDPNILYGPLHTK	1.8074413	3	4.39954
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.4701379	3	6.07284
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1	2.51757147		
Q64057	VNLLSFTGSTQVGK	1.72903694	2	4.68843
Q64112	**IFIT2 Interferon_induced protein with tetratricopeptide repeats 2**	**1.15849473**	**0.70629**	**2**
Q64112	DPSAIDTLLR	1.02383218	2	2.55843
Q64112	NQAMALVEEALK	1.66029272	2	2.31053
Q64119	**MYL6 Myosin light polypeptide 6**	**1.17625721**	**0.04827**	**7**
Q64119	DQGTYEDYVEGLR	0.79904758	2	3.3784
Q64119	EGNGTVMGAEIR	1.36903991	2	2.73079
Q64119	HVLVTLGEK	1.20768794	2	2.57018
Q64119	ILYSQCGDVMR	1.23396524	2	2.91864
Q64119	NKDQGTYEDYVEGLR	1.17179371	2	4.14723
Q64119	VFDKEGNGTVMGAEIR	1.10343595	2	4.11548
Q64119	VLDFEHFLPMLQTVAK	1.26490232	2	4.78163
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**1.29778466**	**0.59456**	**2**
Q64122	DGFIDKEDLHDMLASLGK	1.29930331	2	5.23074
Q64122	LNGTDPEDVIR	1.05938656	2	2.60885
Q64176	**EST22 Liver carboxylesterase 22**	**0.84655907**	**0.05295**	**3**
Q64176	AISESGVALTAGLVK	0.9536582	2	4.58866
Q64176	EGYLQIGATTQQAQK	0.75392153	2	4.66931
Q64176	NFNTVPYIVGINK	0.99886767	2	3.46973
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.50813857**	**8.3E-05**	**7**
Q641Y0	ELGSECGIEFDEEK	1.39502281	2	4.04094
Q641Y0	NTLLIAGLQAR	1.80653709	2	3.42616
Q641Y0	SSLNPILFR	2.92194409	2	2.46711
Q641Y0	TADDPSLSLIK	1.02729902	2	2.57711
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.52413454	3	6.69727
Q641Y0	TLVLLDNLNVR	1.40607694	2	4.12485
Q641Y0	WVPFDGDDIQLEFVR	1.82500616	2	3.07863
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**0.99592294**	**0.86874**	**4**
Q641Y2	GSGIQWDLR	1.21135953	2	2.52462
Q641Y2	IDEVEEMLTNNR	0.9609991	2	3.86051
Q641Y2	IIEQCLNK	1.13299031	2	2.74819
Q641Y2	TQPYDVYDQVEFDVPIGSR	2.51838628	2	4.36947
Q641Z6	**EHD1 EH domain_containing protein 1**	**1.10403495**	**0.73606**	**2**
Q641Z6	LLDTVDDMLANDIAR	1.38911512	2	3.93503
Q641Z6	MQELLQTQDFSK	0.86549689	2	2.6241
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.18683226**	**0.90215**	**3**
Q64232	HYEVEIR	1.15100176	2	2.49738
Q64232	LCFLDKVEPQATISEIK	1.32431006	2	3.60549

Q64232	SLKDEDVLQK	1.18683225	2	3.56263
Q64240	**AMBP Protein AMBP**	**0.75920606**	**0.00079**	**2**
Q64240	AVLPQENEGSGSEPLITGTLK	0.76860298	2	4.17435
Q64240	TIAACNLPIVQGPCR	0.75766377	2	3.83851
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**1.42414766**	**0.20215**	**2**
Q642G4	GGDGQINEQVEK	1.42468455	2	2.88597
Q642G4	LLGPQEEGEGVVDVK	1.41849227	2	2.78095
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.0092659**	**0.99983**	**20**
Q64380	AIDSLSIEK	1.00033888	2	3.00798
Q64380	AYGIESHVLSPAETK	1.11167815	2	4.94827
Q64380	DGTMDPAGTCTTLTR	0.9587645	2	3.8829
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	2.16460881	3	5.3948
Q64380	DLYPLMNVDDLYGTLYVPR	1.18567378	2	3.87208
Q64380	FHHSLTDHPR	1.32058745	2	2.64953
Q64380	FYLLGADAR	1.05097773	2	2.64328
Q64380	GAQVIENCAVTGIR	1.17250454	2	3.78505
Q64380	HGLVNAGYR	1.02297257	2	2.68138
Q64380	IEGIQNMPNVR	0.94883635	2	3.19354
Q64380	LGVGGVVLLER	2.61901311	2	3.27762
Q64380	LQGDALSVGGYEANPIFWDEVSDK	2.87464262	2	4.20257
Q64380	NGDYALER	0.99733148	2	2.43571
Q64380	NYSVVFPHDEPLAGR	0.90847557	2	4.20826
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	1.50216491	3	4.07024
Q64380	RDPLHEELLGQGCVFQER	4.13156976	3	5.80591
Q64380	SDDSPLEAGLAFTCK	1.15881438	2	4.5192
Q64380	STVCGPESFTPDHKPLMGEAPELR	1.00696685	3	4.86359
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16	1.29094396		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	1.05433711	3	5.76771
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.10379737**	**0.08948**	**29**
Q64428	ADMVIEAVFEDLAVK	1.36430364	3	4.11034
Q64428	ALMGLYNGQVLCK	1.75585175	2	3.45997
Q64428	CLAPMMSEVIR	2.33313351	2	2.49765
Q64428	DGPGFYTTR	3.85140656	2	2.31759
Q64428	DSIFSNLIGQLDYK	1.28549082	2	3.05077
Q64428	DTTASAVAVGLK	1.27307062	2	3.7994
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.85243494	3	6.31415
Q64428	EVQSEFVEVMNEIWANDQIR	1.55189036	3	4.20686
Q64428	FGELALTK	1.14498553	2	3.02917
Q64428	FGGGSVELLK	1.09985149	2	3.18877
Q64428	FVDLYGAQK	1.02644564	2	3.02356
Q64428	GFYIYQSGSK	0.82990656	2	3.05216
Q64428	ILQEGVDPK	1.37546939	2	3.18369
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.22849435	4	5.43653
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.82547827	3	4.15068
Q64428	KYESAYGTQFTPCQLLR	1.83445103	2	4.70469
Q64428	LPAKPEVSSDEDIQYR	1.82611708	3	4.46949
Q64428	MGLVDQLVDPLGPGIK	0.94051027	2	5.08455
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0	1.07332973		
Q64428	MQLLEIITTDK	1.07672605	2	3.82033
Q64428	MQLLEIITTDK+Oxidation(0	1.66569234		
Q64428	MVGVPAAFDMMLTGR	1.97679525	2	3.3376
Q64428	NLNSEIDNILVNLR	1.16752694	2	4.41511
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	1.18763941	3	3.88604
Q64428	TGLEQGNDAGYLAESEK	1.01190759	2	5.10275
Q64428	TIEYLEEVAVNFAK	1.64586806	2	3.80416

Q64428	TVLGVPEVLLGILPGAGGTQR	1.14441219	3	4.7512
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	1.27426004	3	6.03005
Q64428	YESAYGTQFTPCQLLR	1.38629439	2	4.00735
Q64458	**CP2CT Cytochrome P450 2C29**	**0.89343465**	**8.9E-09**	**6**
Q64458	EHKESLDVTNPR	0.89175099	2	3.40956
Q64458	IKEHKESLDVTNPR	0.96189703	3	5.20486
Q64458	LPPGPTPLPIIGNFLQIDVK	2.36492749	3	4.98668
Q64458	VQEEAQCLVEELR	1.91821461	2	4.2021
Q64458	VQEEAQCLVEELRK	2.69563878	2	3.80194
Q64458	VQEEIDR	1.55781561	2	2.53091
Q64464	**CP3AD Cytochrome P450 3A13**	**1.03565992**	**0.49734**	**2**
Q64464	ALLSPTFTSGR	1.03993425	2	2.89316
Q64464	LQDEIDAALPNK	0.67598362	2	2.41455
Q64481	**CP3AG Cytochrome P450 3A16**	**1.09148265**	**0.36651**	**3**
Q64481	EMFPVIEQYGDILVK	1.82633209	2	2.40379
Q64481	GSIDPYVYLPFGNGPR	0.99609211	2	4.04317
Q64481	VLQNFSFQPCK	0.91894773	2	2.78413
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.40475752**	**0.02455**	**4**
Q64550	GHEVVVIAPEASIHIK	0.5678439	2	4.61325
Q64550	NMIIALTENFLCR	0.98059141	2	4.50404
Q64550	SVFDQDPFLLR	2.75056919	2	3.46737
Q64550	VVYSPYGSLATEILQK	0.87084215	2	4.9668
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**1.02311956**	**0.51164**	**3**
Q64560	ACVDSNENGDLGK	1.01467467	2	3.48793
Q64560	GTLIEAFPVLGGK	1.14585189	2	3.17228
Q64560	HEQISDLDR	1.4266056	2	2.59638
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.09125194**	**0.00798**	**15**
Q64563	AAVDCTVVGWGSCTVVGAK	4.31548597	2	2.595
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.40961092	3	5.72197
Q64563	ALGATDCLNPR	1.14595868	2	3.23274
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	1.17389475	3	6.05482
Q64563	FDLDLLVTHALPFDK	1.48680981	3	4.3007
Q64563	IIAIDINSEKFPK	0.98236451	2	3.06966
Q64563	INDAIDLMNQGK	1.38973083	2	4.1661
Q64563	KFDLDLLVTHALPFDK	1.12563631	3	5.28022
Q64563	LCLSPLTNLCGK	1.14613423	2	2.46615
Q64563	SVDSVPNLVTDYK	1.66649764	2	3.49291
Q64563	TDSPLCIEEIEVSPPK	1.5650222	2	4.11312
Q64563	VCLIGCGFTSGYGAAINTAK	0.46973543	2	4.88096
Q64563	VDDEANLER	1.45098108	2	3.09107
Q64563	VDEMNISTVDMILGR	1.18478076	2	4.06999
Q64563	VIATCVCPTDINATNPK	3.6559472	2	4.70127
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**1.10746642**	**0.33851**	**15**
Q64565	AYSNHTDIISFR	1.00671536	2	3.48409
Q64565	GGNFSQTFR	0.99543459	2	2.59794
Q64565	GGVCIADEVQTGFGR	0.7865866	2	4.04195
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.45464308	2	4.32601
Q64565	GLMVGIEMVQDK	1.51748547	2	3.37818
Q64565	HNMPPCDFSPEK	1.01594881	2	3.2347
Q64565	LSALLPEPLK	2.99385997	2	2.75202
Q64565	NSQEVGTYMLLK	0.8872169	2	3.31882
Q64565	SALTQHMER	1.90519118	2	2.52906
Q64565	SALTQHMER+Oxidation(6	1.73753728		
Q64565	TEVNQIHEDCK	1.01214161	2	3.29699
Q64565	TEVNQIHEDCKDMGLLVGR	1.06479167	2	5.24897
Q64565	VIFLVNSGSEANDLAMVMAR	1.9784042	2	3.16691

Q64565	YIEQFK	1.17311027	1	2.2579
Q64565	YQSLAYNHVLEIHK	2.1112786	2	3.95398
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**4.0916564**	**0.52052**	**9**
Q64578	AVGIVATTGVSTEIGK	5.93069212	2	3.42593
Q64578	DIVPGDIVEVAVGDKVPADIR	4.36104506	2	3.38495
Q64578	IGIFSENEEVADR	2.07113645	2	3.40337
Q64578	IRDQMAATEQDKTPLQQK	2.87395115	3	4.39291
Q64578	MNVFNTEVR	1.9995131	2	2.78718
Q64578	REEMVLDDSAK	2.52590087	2	2.76877
Q64578	TGTLTTNQMSVCK	4.00784195	2	3.44584
Q64578	VGEATETALTTLVEK	3.23699655	2	4.49547
Q64578	YGPNELPAEEGK	2.74477263	2	3.01092
Q64581	**CP3AI Cytochrome P450 3A18**	**0.68005297**	**0.64088**	**3**
Q64581	AITMSEDEEWKR	0.80518414	2	2.31719
Q64581	LAVIGVLQNFNIQPCEK	0.90139388	2	3.20531
Q64581	NPEYWLEPEEFNPER	0.60151964	2	3.86108
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.78781292**	**0.44225**	**10**
Q64591	ATAEEITSK	1.53271825	2	3.01701
Q64591	CDVRDPDMVHNTVLELIK	0.69707416	4	5.05214
Q64591	DPDMVHNTVLELIK	1.33790178	3	4.14183
Q64591	EEWDVIEGLIR	0.81982217	2	3.54377
Q64591	FFPPILKPMLPPNAFQGK	1.10273669	2	3.25908
Q64591	FNIIQPGPIK	0.54512057	2	2.89204
Q64591	NIDVLK	0.84202061	1	2.28936
Q64591	SLAAEWGR	0.97005843	2	2.37682
Q64591	VAFITGGGTGLGK	1.39323705	2	2.69071
Q64591	VTKEEWDVIEGLIR	1.09474365	3	4.9013
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.36323356**	**0.12051**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.2991255	2	4.48882
Q64602	DIISLAPGSPNPK	0.96395563	2	3.218
Q64602	EILLVPGNSFFVDNSAPSSFFR	1.79900041	2	3.48101
Q64602	FLYTIPNGNNPTGNSLTGDR	1.39968447	2	3.98845
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	2.63662151	3	6.46759
Q64602	SAVFTVENGSTIR	1.19753747	2	4.10521
Q64602	VLSQWKPEDSKDPTKR	1.26400537	3	4.14068
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.21020202**	**0.02463**	**14**
Q64611	AQGGQGLEWR	1.18484822	2	2.93961
Q64611	CHGSQASYLFQQDK	1.20812401	2	4.96056
Q64611	DVFGIVVDEAIR	1.25423345	2	3.07635
Q64611	FFNQLFSGLDPHALAGR	1.54824396	3	3.85355
Q64611	FYNVALDTGDK	1.01768869	2	3.10677
Q64611	GAAFLGLGTDSVR	1.33626561	2	3.24536
Q64611	GTMMIGYQPHGTR	1.25217979	2	2.87285
Q64611	IDQAFALTR	1.14106748	2	3.46272
Q64611	KGTMMIGYQPHGTR	1.45598388	3	3.97922
Q64611	LSQVAPVLK	1.49523418	2	2.30197
Q64611	QLLDLELQSQGESR	0.7533305	2	4.51638
Q64611	TLDGDPVAVEALLR	1.08093952	2	4.6021
Q64611	VCEWKEPEELK	1.11845397	3	3.7241
Q64611	YLVEEIK	0.98253931	1	2.40722
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**0.85406031**	**0.55214**	**2**
Q64638	VVFETGNYVK	0.66715279	1	2.05845
Q64638	YESLASELLQR	0.9832398	2	3.03348
Q64640	**ADK Adenosine kinase**	**1.268578**	**1.7E-05**	**11**

Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.28016815	3	7.1419
Q64640	AATFFGCIGIDK	1.21367477	2	3.33019
Q64640	AGHYAASVIIR	1.49803013	3	3.63438
Q64640	FGEILK	1.16146801	2	2.3522
Q64640	FKVEYHAGGSTQNSMK	1.28763447	2	4.10609
Q64640	HKELFDELVK	1.24389645	3	4.05358
Q64640	SLVANLAAANCYK	1.33547096	2	4.33123
Q64640	TGCTFPEKPDFH	1.68170255	2	2.74294
Q64640	VEYHAGGSTQNSMK	1.49444516	2	4.06014
Q64640	VEYHAGGSTQNSMK+Oxidation(12	1.39592743		
Q64640	YSLKPNDQILAEDK	1.30767207	3	4.25991
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.76027023**	**0.29147**	**8**
Q64654	EPAEDILQTLLDSTYK	1.04988087	2	3.82401
Q64654	GVAYDVPNAVFLEQK	0.87447593	2	4.32519
Q64654	NEDLNAEEVYGR	0.65222163	2	3.72399
Q64654	SGLNIAHFK	2.94387303	2	2.99592
Q64654	TFTYLLGSDAAALLFNSK	1.16547497	3	3.90519
Q64654	TVCGEDLPPLTYEQLK	0.56690317	2	4.42687
Q64654	YGPVFSFTMVGK	0.84307383	2	2.8097
Q64654	YLQDNPASGEK	0.90926989	2	2.79391
Q65Z40	**WAPL Wings apart_like protein homolog**	**1.04157699**	**0.77978**	**2**
Q65Z40	EKSISRIPEDNANK	1.02823804	2	2.58514
Q65Z40	LGQKRPNFKPDIQEIPK	1.28610094	2	2.39477
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.28561975**	**0.26402**	**5**
Q66H12	CNINCEEDPK	1.24272684	2	2.34034
Q66H12	INQDPLGIQGR	0.96168484	2	2.87806
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(0	1.78139883		
Q66H12	MTCMGYPGTTLDKVELDAATFAEWK+Oxidation(3	1.78139883		
Q66H12	TISPQNIDILQNPLLIK	1.5011384	2	3.43576
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**1.29678386**	**0.31066**	**2**
Q66H15	SLQGLAGEIVGEVR	1.32611122	2	3.3903
Q66H15	SQSLPNSLDYAQTSER	0.69265213	2	3.0147
Q66H45	**TTC36 Tetratricopeptide repeat protein 36**	**1.18198968**	**0.36859**	**2**
Q66H45	ALELQGVR	0.6776555	2	2.47311
Q66H45	LQGDVAGALEDLER	1.24025377	2	3.75276
Q66H71	**CPPED Calcineurin_like phosphoesterase domain_containing protein 1**	**0.87641796**	**0.10891**	**2**
Q66H71	LTEQAVEAINK	0.92504932	2	3.51174
Q66H71	SIDEDDDYFNLTK	0.71406613	2	2.98046
Q66H80	**COPD Coatomer subunit delta**	**1.74912741**	**5.3E-05**	**8**
Q66H80	GVQLQTHPNVDKK	1.48153199	2	3.51672
Q66H80	LFTAESLIGLK	1.79470885	2	3.02111
Q66H80	NSNILEDLETLR	1.91686098	2	3.51258
Q66H80	NTLEWCLPVIDAK	1.17322374	2	2.72746
Q66H80	SEGETIMSSNMGK	3.92152408	2	2.76797
Q66H80	TFTEMDSHEEK	0.9573143	2	2.65535
Q66H80	VAPAPARPSGPSK	1.45206525	2	2.54033
Q66H80	VTQVDGNSPVR	1.71299043	2	3.01899
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.28847205**	**0.03701**	**10**
Q66HA8	AGGIETIANEFSDR	1.38285812	2	2.94507
Q66HA8	FQEAEERPR	0.75828457	2	2.45946
Q66HA8	FVVQNVSAQK	1.319668	2	2.68755
Q66HA8	LKETAENNLK	1.27389778	2	2.58799
Q66HA8	NQQITHANNTVSSFK	1.34870943	2	4.7172
Q66HA8	RGPFELEAFYSDPQAVPYPEAK	1.66865697	3	3.78733
Q66HA8	SQFEELCAELLQK	1.06155976	2	2.60517

Q66HA8	SVLDAAQIVGLNCLR	1.66096905	2	3.70739
Q66HA8	VLGTAFDPFLGGK	1.10098604	2	2.98288
Q66HA8	YNHIDESEMK	0.97990367	2	2.50624
Q66HD0	**ENPL Endoplasmin**	**0.93977528**	**0.35294**	**27**
Q66HD0	DISTNYYASQK	1.20420274	2	3.16239
Q66HD0	EATEKEFEPLLNWMK	1.67559281	2	3.5056
Q66HD0	EEASDYLELDTIK	1.48269332	2	4.25037
Q66HD0	EEEAIQLDGLNASQIR	1.30373406	2	4.60118
Q66HD0	EFEPLLNWMK	1.44995849	2	2.90662
Q66HD0	EVEEDEYK	1.26613328	1	2.44448
Q66HD0	FQSSHHSTDITSLDQYVER	1.15433094	3	6.63283
Q66HD0	GLFDEYGSK	1.84920966	2	2.44932
Q66HD0	GVVDSDDLPLNVSR	0.9364012	2	5.15077
Q66HD0	KEAESSPFVER	1.14508295	2	3.50719
Q66HD0	KGYEVIYLTEPVDEYCIQALPEFDGKR	0.94963551	3	3.59155
Q66HD0	LGVIEDHSNR	1.30941253	2	3.11669
Q66HD0	LISLTDENALAGNEELTVK	1.88309711	2	5.42867
Q66HD0	LTESPCALVASQYGWSGNMER	2.22224518	2	5.48347
Q66HD0	MKEKQDK	0.6017598	1	1.92505
Q66HD0	NLLHVTDTGVGMTR	1.1181713	3	4.14452
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11	1.11269105		
Q66HD0	RVFITDDFHDMMPK	1.47151466	3	3.72948
Q66HD0	SGTSEFLNK	1.21394648	2	3.05282
Q66HD0	SGYLLPDTK	0.9467149	2	3.44509
Q66HD0	SILFVPTSAPR	1.28207522	2	3.5311
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	1.39014665	3	5.15407
Q66HD0	TETVEEPLEEDETAQEEK	0.91596892	2	5.27976
Q66HD0	TETVEEPLEEDETAQEEKEEADDEAAVEEEEEEKKPK	0.61188485	5	6.24007
Q66HD0	TFEINPR	1.19091391	2	2.73857
Q66HD0	VFITDDFHDMMPK	1.53776929	2	4.01099
Q66HD0	YNDTFWK	0.86931802	2	2.38363
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.30854996**	**0.00501**	**15**
Q66HF1	ALSEIAGITLPYDTLDQVR	0.80977318	3	3.93748
Q66HF1	AVTEGAQAVEEPSIC	1.20797088	2	2.80403
Q66HF1	DDGAAILAAVSSIAQK	1.24366331	2	4.35422
Q66HF1	DLLNKVDSDTLCTEEIFPNEGAGTDLR	2.75660011	3	4.26097
Q66HF1	FASEIAGVDDLGTTGR	1.6630833	2	4.58834
Q66HF1	GLLTYTSWEDALSR	1.16967307	2	3.6706
Q66HF1	GNDMQVGTYIEK	0.95533761	2	2.81418
Q66HF1	GWNILTNSEK	0.84762042	1	2.26339
Q66HF1	ILQDIASGNHEFSK	1.65236618	2	4.17614
Q66HF1	LGEVSPNLVR	1.25008385	2	3.00797
Q66HF1	LVDQEFLADPLVPPQLTIK	1.51555865	2	3.96118
Q66HF1	SATYVNTEGR	1.11188252	2	2.31744
Q66HF1	VAVTPPGLAR	0.72225795	2	2.53812
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	1.25478225	2	4.7317
Q66HF1	YDHLGDSPK	1.28840587	2	2.4766
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.57421791**	**7E-06**	**13**
Q66HF8	ADVDLAVR	0.53788898	2	2.36548
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	2.11593974	3	4.19254
Q66HF8	EEIFGPVQPLFK	1.39272925	2	3.2598
Q66HF8	IEEVIQR	3.29421829	2	2.30519
Q66HF8	KTFPTVNPTTGEVIGHVAEGDR	1.35749857	3	3.91188
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.38331976	3	4.16142
Q66HF8	LAPALATGNTVVMK	1.80388789	2	3.39251

Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.63034121	2	4.88567
Q66HF8	TFVEESIYHEFLER	1.06241022	2	4.46208
Q66HF8	VAEQTPLSALYLASLIK	2.94589007	2	3.00276
Q66HF8	VGNPFELDTQQGPQVDK	1.0612233	2	4.40022
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.34921399	2	4.49705
Q66HF8	YGLAAAVFTR	1.68968046	2	3.29539
Q66HG4	**GALM Aldose 1_epimerase**	**0.98581322**	**0.28554**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	1.45785029	2	4.50189
Q66HG4	TVFGELPSGGGAVEK	0.86563222	2	3.84872
Q66HG4	VSPDGEEGYPGELK	1.23184376	2	4.07073
Q66HG9	**MAVS Mitochondrial antiviral_signaling protein**	**1.40256597**	**0.88271**	**3**
Q66HG9	ICELPGLAEQVTR	1.67704136	2	2.76479
Q66HG9	STAATPSTVPTNIAPSK	1.19872411	2	3.17831
Q66HG9	TTLSSSSTGSAFAK	1.19032126	2	2.34491
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.17702576**	**3.2E-07**	**19**
Q66X93	ADDADEFGYSR	1.65822751	2	2.61315
Q66X93	ALLLPDHYLVTVMLSGIK	1.59193579	3	4.25504
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	0.9603204	3	6.06477
Q66X93	DTNGENIAESLVAEGLASR	2.08617546	2	4.34433
Q66X93	ETDGSETPEPFAAEAK	1.41848763	2	3.78974
Q66X93	FVDGEWYR	1.53692791	2	2.7819
Q66X93	GDVGLGLVK	1.25359406	2	2.57965
Q66X93	HFVDSHHQKPVNAIIEHVR	1.58781566	3	5.015
Q66X93	LEGDNIQDK	1.50874256	2	2.99266
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.62633889	2	5.73209
Q66X93	SAYYKPLLSAEEAAK	1.15069043	2	3.11338
Q66X93	SDISSHPPVEGAYAPR	1.31904381	3	4.41655
Q66X93	SSHYDELLAAEAR	1.30929976	2	4.0311
Q66X93	TCATVTIGGINIAEALVSK	1.12310549	2	3.49455
Q66X93	TDAVDSVVR	16.7338007	2	2.71306
Q66X93	VITEYLNAQESAK	1.16041782	2	3.92646
Q66X93	VMQVLNADAIVVK	2.02926384	2	4.10818
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.19044243	3	5.14646
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.87288914	3	4.53355
Q68FL6	**SYMC Methionyl_tRNA synthetase_ cytoplasmic**	**1.02110582**	**0.91715**	**3**
Q68FL6	ADKNQVAAEVAK	1.23542785	2	3.05545
Q68FL6	LENDQIENLR	0.902337	2	2.6913
Q68FL6	NNSELLNNLGNFINR	1.13141973	2	2.81915
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.84562543**	**0.00843**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.46926052	3	3.90271
Q68FP2	HNNWDLTPVK	1.2352832	2	3.2078
Q68FP2	IFLMDLNEPYPK	1.55492307	2	4.05185
Q68FP2	IQDPLSDNPR	1.28622566	2	3.0143
Q68FP2	KHNNWDLTPVK	0.8540244	2	2.49789
Q68FP2	LLIYNPEDPPGSEVLR	0.53135644	2	4.3891
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	1.24758468	3	4.59446
Q68FP2	YVYVADVTAK	0.9113101	1	2.99083
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.402857**	**0.07873**	**7**
Q68FQ0	GSNDMQYQHVIETLIGK	1.12506102	2	2.82305
Q68FQ0	GVIVDKDFSHPQMPK	1.34569285	2	2.80795
Q68FQ0	HKLDVTSVEDYK	2.00559708	2	3.63161
Q68FQ0	ISDNVLVDINNPEPLIQTAK	2.05177497	2	5.01982
Q68FQ0	LDVTSVEDYK	1.0694997	2	2.94363
Q68FQ0	SLHDALCVIR	1.50020374	2	2.69392
Q68FQ0	WVGGPEIELIAIATGGR	1.33041814	2	3.82036
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.08087253**	**6.9E-06**	**8**

Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.00571104	2	4.98693
Q68FR6	ALIAAQYSGAQIR	1.45391243	2	4.33745
Q68FR6	ILGLLDTHLK	1.91731212	2	2.51264
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.31735169	2	4.21749
Q68FR6	KLDPGSEETQTLVR	1.51970601	2	4.10036
Q68FR6	LDPGSEETQTLVR	1.15464244	2	3.54414
Q68FR6	STFVLDEFKR	1.18088335	2	2.52096
Q68FR6	WFLTCINQPQFR	0.98619537	2	3.35302
Q68FR9	**EF1D Elongation factor 1_delta**	**1.26967487**	**0.00017**	**6**
Q68FR9	ATAPQTQHVSPMR	1.3491451	2	3.30142
Q68FR9	ATAPQTQHVSPMR+Oxidation(11	0.9880986		
Q68FR9	FYEQMNGPVTAGSR	1.2696738	2	4.52624
Q68FR9	GVVQDLQQAISK	1.21339085	2	3.43811
Q68FR9	SIQLDGLVWGASK	1.36377385	2	3.25988
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.37598913	2	5.38088
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**1.13812564**	**0.28643**	**3**
Q68FS2	ATTADGSSILDR	2.78705777	2	2.32801
Q68FS2	NAAQVLVGIPLETGQK	0.89008954	2	2.98284
Q68FS2	QIQSLCFQVNNLLEK	1.57147556	2	2.40834
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.18442302**	**3.7E-09**	**17**
Q68FS4	ADMGGAATICSAIVSAAK	1.13920067	2	5.1015
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2	1.10785755		
Q68FS4	DKDDDVPQFTSAGENFNK	0.90439377	2	5.38146
Q68FS4	GITFDSGGISIK	1.24960679	2	3.18221
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.57857689	3	6.16995
Q68FS4	GVLFASGQNLAR	1.6431098	2	3.43383
Q68FS4	LFEASVETGDR	1.36673833	2	3.58747
Q68FS4	LHGSGDLEAWEK	1.75390611	2	2.95171
Q68FS4	LNLPINIIGLAPLCENMPSGK	2.09534479	2	5.04497
Q68FS4	QLMESPANEMTPTR	0.97472993	2	3.65393
Q68FS4	QVIDCQLADVNNLGK	1.71573851	2	4.72913
Q68FS4	SAGACTAAAFLR	1.11495326	2	3.88623
Q68FS4	SAGVDDQENWHEGK	1.00117381	2	3.97118
Q68FS4	SWIEEQEMGSFLSVAK	1.31410026	2	5.14901
Q68FS4	TFYGLHQDFPSVVVVGLGK	1.4996203	2	4.70411
Q68FS4	TIQVDNTDAEGR	1.01107517	2	4.1452
Q68FS4	TLIEFLLR	1.45757542	2	2.78993
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.15244531**	**0.99321**	**4**
Q68FT1	INDAMNMGHTAK	1.07725888	2	3.10169
Q68FT1	LNHVLEEEQK	1.19466924	2	3.40032
Q68FT1	STGEALVQGLMGAAVTLK	0.99373373	2	3.76337
Q68FT1	YTDQSGEEEEDYESEEQIQHR	1.00513602	3	4.68254
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.97949539**	**0.95281**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	0.8585568	2	3.80329
Q68FT3	ISQLDTQSPVTK	1.61001711	2	3.50086
Q68FT3	SLLLGTDVAENQK	0.84537247	2	3.4011
Q68FT3	TLGAQLPQYYEVLTAPISK	0.98322796	2	4.06975
Q68FT3	VFDCIEAYAPGFK	0.84626687	2	2.82351
Q68FT3	VLDQWFESEPLK	1.41488089	2	3.59083
Q68FT3	VQGVVLQGGEEVR	0.73264497	2	3.26104
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**0.98208967**	**9.9E-20**	**10**
Q68FT5	AGANIIGVNCR	1.2758358	2	3.62363
Q68FT5	AGLWTPEAVVEYPSAVR	1.27682084	3	4.09577
Q68FT5	AIAEELAPER	2.0967727	2	3.79623

Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.57384192	3	4.69201
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.78202511	3	4.66815
Q68FT5	FGPWTSLQTMK	1.91253535	2	2.51008
Q68FT5	GGFVDLPEYPFGLEPR	1.33648055	2	4.21859
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.8332924	2	2.67014
Q68FT5	REYWETLLPASGRPFCPSLSKPDA	0.37963633	3	3.66162
Q68FT5	YIGGCCGFEPYHIR	4.29307144	2	4.65506
Q68FT9	**SCLY Selenocysteine lyase**	**1.01199211**	**0.0587**	**6**
Q68FT9	AEVDLIVQDLK	1.25880194	2	3.90052
Q68FT9	CFHEQQTLQGR	1.13430061	2	2.76003
Q68FT9	NFRPGTENTPMIAGLGK	0.5989687	2	4.30324
Q68FT9	RVDVEDLGVDFLTIVGHK	1.3064638	3	5.33191
Q68FT9	TVDQISPEEGTRPHFITCTVEHDSIR	1.12507954	3	4.65663
Q68FT9	VLVHTDAAQALGK	1.19356831	3	3.31445
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**1.02125354**	**0.8759**	**13**
Q68FU3	AGDLGVDLTSK	0.82969168	2	3.49051
Q68FU3	EIDGGLETIR	1.53205793	2	2.33737
Q68FU3	EIIAVSCGPPQCQETIR	1.0934506	2	5.31334
Q68FU3	GIHVEVPGAEAENLGPLQVAR	1.5221042	2	5.84644
Q68FU3	HSMNPFCEIAVEEAVR	0.99942008	2	5.59787
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2	1.26468739		
Q68FU3	LKLPAVVTADLR	3.12671466	2	2.36035
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	3.18035021	3	5.73208
Q68FU3	RVIDFAVK	1.06781311	2	2.63964
Q68FU3	VDLLFLGK	0.99743202	2	2.73127
Q68FU3	VETTEDLVAK	0.80133422	2	3.56437
Q68FU3	VIDFAVK	0.83569091	2	2.42857
Q68FU3	VSVISVEEPPQR	1.01936298	2	3.56365
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.29618401**	**0.01732**	**10**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.72980897	3	6.01256
Q68FY0	IEEVDAQMVR	3.80970341	2	3.84492
Q68FY0	LCTSATESEVTR	1.61612167	2	2.85525
Q68FY0	NALISHLDGTTPVCEDIGR	1.04537015	2	4.56618
Q68FY0	NNGAGYFLEHLAFK	0.67959013	2	3.52426
Q68FY0	RIPLAEWESR	0.84232679	2	2.67835
Q68FY0	SGMFWLR	1.12400895	2	2.39729
Q68FY0	TDLTDYLSR	0.88963927	2	2.9454
Q68FY0	VVELLADIVQNISLEDSQIEK	1.35805105	3	5.36858
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.14056093	3	5.23737
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.88080898**	**0.03731**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.98942847	2	4.72678
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	1.52044764	3	4.0088
Q68G31	GESGGQTTPYDFYSR	0.99633432	2	3.96294
Q68G31	LQPTDSFSQSSCFGLR	1.17958214	2	3.55103
Q68G31	NVNSTLTFVTLSGELK	1.09061184	2	4.2573
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	1.58981944	3	5.774
Q68G31	VNTEPLPGIEK	0.73885963	2	2.64245
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.12442511**	**0.5321**	**2**
Q69Z23	GDPTRAEDQVLMRALR	0.98925174	2	2.41662
Q69Z23	YFIDLLMEK	2.83752409	1	2.0173
Q6A028	**SWP70 Switch_associated protein 70**	**4.05579485**	**0.01522**	**2**
Q6A028	FILEKVQDNFDK	4.52416992	1	1.91264
Q6A028	KGDILLDENCCVESLPDKDGK	2.84407337	2	2.3398

Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.24811052**	**0.59184**	**3**
Q6A0A9	LYEPDQLQELK	1.14950726	2	2.3939
Q6A0A9	SQGGVQPIPSQGGK	1.12163292	2	3.34622
Q6A0A9	VEGSSTASSGSQLAEGK	1.249722	2	4.23287
Q6AW69	**CGNL1 Cingulin_like protein 1**	**1.64141672**	**0.14851**	**2**
Q6AW69	NRRELAEMQTQLK+Oxidation(7	1.22518895		
Q6AW69	QDSAGPILDGAR	1.70466717	2	2.50615
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**0.93297652**	**0.98963**	**3**
Q6AXM8	FQEEENSLLHLK	0.93269587	2	3.70879
Q6AXM8	LFVYDPNHPPSSEVLR	0.99837168	2	2.46719
Q6AXM8	LVAEGFDSANGINISPDKK	1.09280672	2	3.53868
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**1.08818646**	**0.74176**	**4**
Q6AXS5	EETQPPVALKK	0.50072261	2	2.42261
Q6AXS5	FDQLFDDESDPFEVLK	1.07285456	2	5.29557
Q6AXS5	RFEKPLEEK	1.37401693	2	2.42124
Q6AXS5	SAAQAAAQTNSNAAGK	0.7934782	2	4.54963
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.9078073**	**0.6255**	**2**
Q6AXY0	FLQPGSQR	0.81249578	2	2.5621
Q6AXY0	YFPAFEK	0.97142862	1	2.00928
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.32225961**	**0.40846**	**4**
Q6AY09	ATENDIYNFFSPLNPMR	1.8207861	2	2.784
Q6AY09	GLPWSCSAEEVMR	1.72985041	2	2.94583
Q6AY09	HTGPNSPDTANDGFVR	1.20131979	2	4.17416
Q6AY09	STGEAFVQFASQEIAEK	1.22827875	2	3.92796
Q6AY20	**MPRD Cation_dependent mannose_6_phosphate receptor**	**1.23199529**	**0.85096**	**2**
Q6AY20	HTLAGNFNPVSEER	1.23491815	2	4.17523
Q6AY20	SCDLVGEKDKESK	1.22050859	2	3.68552
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.039288**	**0.153**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	2.07670291	3	4.01057
Q6AY30	ATLVLNCVGPYR	0.99155383	2	2.82379
Q6AY30	GGGVFTPGAAFSR	1.352248	2	2.36506
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.39279464	2	2.92966
Q6AY30	LQQVLEK	1.13943062	1	2.32071
Q6AY30	SVSNLKPVPVIGSK	0.9875066	2	3.79931
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.30838693**	**0.00264**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	1.66663212	2	4.55811
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.49226632	2	5.10541
Q6AY56	LISQIVSSITASLR	2.87198193	2	3.7551
Q6AY56	NLDIERPTYTNLNR	1.18698571	2	3.3133
Q6AY56	QLFHPEQLITGK	0.9131445	2	3.09159
Q6AY56	TIQFVDWCPTGFK	1.2241285	2	3.70063
Q6AY56	VGINYQPPTVVPGGDLAK	1.10251544	2	4.39579
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.91159436**	**0.84599**	**5**
Q6AY80	ALTSDILEEQR	1.42168227	2	3.24238
Q6AY80	EEPIHCTPSWYFQG	1.0932819	2	2.69827
Q6AY80	NDVTGALSNPEVFK	0.76745159	2	3.93004
Q6AY80	VLAPQISFGPEVSSEEQR	1.12287402	2	4.34197
Q6AY80	VLCQGFAFDVPGFYDSGFLK	1.50874935	2	2.80055
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**0.95371277**	**0.08746**	**3**
Q6AYG5	DVLETLWGGPANLEAIAK	1.40673005	2	4.05122
Q6AYG5	ILEQFPGGSIDLQK	0.62873664	2	3.41098

Q6AYG5	NTFCSGSDLNAVK	0.9967747	2	2.48237
Q6AYH5	**DCTN2 Dynactin subunit 2**	**1.45791406**	**0.12841**	**3**
Q6AYH5	ASVEDADTQNK	1.4894068	2	2.80982
Q6AYH5	VNALDLAVLDQVEAR	1.59172231	2	3.41295
Q6AYH5	WSPVASTLPELVQR	1.44304883	2	2.90362
Q6AYK6	**CYBP Calcyclin_binding protein**	**1.08743897**	**0.63404**	**2**
Q6AYK6	IYEDGDDDMKR	0.57194379	2	2.40685
Q6AYK6	WDYLTQVEK	2.90867985	2	2.60189
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.95742679**	**0.99734**	**4**
Q6AYQ8	IITLEEGDLILTGTPK	1.27283023	2	5.17019
Q6AYQ8	NLHHEVELGVLLGR	0.78487956	3	4.70732
Q6AYQ8	SFTSSCPVSAFVPK	0.92380859	2	3.98761
Q6AYQ8	STVLSEPVLFLKPSTAYAPEGSPVLMPAYCR	1.17440701	3	3.72354
Q6AYR8	**SCRN2 Secernin_2**	**1.19743564**	**0.81095**	**2**
Q6AYR8	GHQAALGLMDEQEQAQLR	1.10477077	3	4.30184
Q6AYR8	QEQQSLEQEGLEALR	1.19951477	2	3.88558
Q6AYS7	**ACY1A Aminoacylase_1A**	**1.45061725**	**0.03947**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	1.57956537	2	3.81153
Q6AYS7	ICTVQPNPDYGSAVTFLEER	5.24982969	2	4.57627
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.85347999**	**0.51189**	**3**
Q6AYS8	ALTDELAALGCTGVR	0.64079185	2	4.05791
Q6AYS8	FDAVVGYK	1.34609226	1	2.2866
Q6AYS8	SVAGEIVLITGAGHGIGR	0.80382869	2	4.02995
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.75384814**	**0.68321**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	0.84452756	2	3.43435
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.49034466	2	3.20889
Q6AYT9	NDDVINSSSYR	2.18202013	2	3.34475
Q6AYT9	TGVVMIPGISQLTQK	0.50715481	2	3.14431
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.24501898**	**5.3E-11**	**6**
Q6AYZ1	AVFVDLEPTVIDEVR	1.27875551	2	5.40966
Q6AYZ1	AYHEQLTVAEITNACFEPANQMVK	1.31596382	3	4.14551
Q6AYZ1	DVNAAIATIK	1.04034176	2	3.17294
Q6AYZ1	IHFPLATYAPVISAEK	2.49553525	2	3.79999
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	2.27447474	2	5.46006
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.10811117	2	4.70229
Q6DGG0	**PPID Peptidyl_prolyl cis_trans isomerase D**	**0.92838243**	**0.73329**	**4**
Q6DGG0	GTGPTTGKPLHFK	0.64852816	2	2.35666
Q6DGG0	IVLELFADIVPK	1.01050422	2	2.31037
Q6DGG0	MLENVEVNGEKPAK	1.32392075	2	3.70808
Q6DGG0	VFFDVDIGGER	1.43534817	2	2.83679
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**0.9219954**	**0.43197**	**6**
Q6DGG1	AVAIDLPGLGR	1.04339525	2	3.56435
Q6DGG1	FSSETWQNLGTLHR	1.31081761	2	3.63614
Q6DGG1	FSVLLLHGIR	2.25802863	2	3.08848
Q6DGG1	GYVPVAPICTDK	0.92127248	1	2.65398
Q6DGG1	INAADYAR	1.19685094	2	2.46774
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.62464226	2	5.38226
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.91335978**	**0.6808**	**2**
Q6EDY6	ELMESIK+Oxidation(2	1.66177502		
Q6EDY6	IENYLLR	0.90175462	2	2.45561
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.76910927**	**0.07854**	**2**
Q6GQP4	CDLSDIREVPLK	0.73179675	2	2.5344
Q6GQP4	CDLSDIREVPLKDAK	0.85878008	2	2.91608
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**1.40854429**	**0.10193**	**3**

Q6GQT1	ASVTVLGDILGSAMQNTQDLLK	1.16744004	2	2.35133
Q6GQT1	IQEEGTGVEETGK	23.2249401	2	3.72267
Q6GQT1	SSGSLLNNAMK	1.274608	2	3.09788
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**1.14356433**	**0.05587**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	1.06829654	2	3.87937
Q6I7R3	ILGIPVIITEQYPK	2.36578696	2	3.00799
Q6I7R3	YFGDIISVGQR	1.47754781	2	2.57839
Q6IE52	**MUG2 Murinoglobulin_2**	**1.09295958**	**0.99787**	**14**
Q6IE52	AHFSVMGDILSSAIK	1.04238202	2	3.67194
Q6IE52	HGIPFFVK	0.83675057	2	2.74722
Q6IE52	HTSSWLVTPK	0.85999016	2	2.80894
Q6IE52	LPSSEEEESLDINIEGAK	1.503804	2	2.88293
Q6IE52	MLIYTILPDGEVIADSVK	1.09223091	2	3.83604
Q6IE52	MLSGFIPLKPTVK	1.55388967	2	3.15561
Q6IE52	MLSGFIPLKPTVK+Oxidation(0	0.86159268		
Q6IE52	NLYPLKELVQDPK	1.63562424	1	2.04411
Q6IE52	QLSFSLSAEPIQGPYK	0.95121224	2	4.2773
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	1.11365184	3	3.65907
Q6IE52	VHLSFSPSQSLPASQTHMR	0.72225593	3	3.93723
Q6IE52	VKTVPLTCNNPK	1.07703433	2	2.96447
Q6IE52	VTASPQSLCGLR	2.35718384	2	2.50736
Q6IE52	YMVLVPSQLYTETPEK	0.89587134	2	3.72556
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**0.70466208**	**0.54995**	**2**
Q6IFW6	LENEIQTYR	1.00396146	2	2.34899
Q6IFW6	QSLEASLAETEGR	0.49566678	2	3.44501
Q6IFZ9	**K2C74 Keratin_ type II cytoskeletal 74**	**2.06256116**	**0.05323**	**2**
Q6IFZ9	FLEQQNQVLQTK	1.72403193	2	4.16948
Q6IFZ9	GDSALKDAWAKLDELEGALQQAK	6.05379838	3	3.60364
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.9628462**	**0.98389**	**4**
Q6IMF3	TNAENEFVTIK	1.77646329	2	2.75133
Q6IMF3	TNAENEFVTIKK	1.12990746	2	2.93977
Q6IMF3	WELLQQVDTSTR	1.12083958	2	3.61795
Q6IMF3	YEELQITAGK	0.96200514	2	3.46776
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**1.04140554**	**0.49614**	**7**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.87357227	3	5.46347
Q6IRK9	GEESAVMVVPR	1.31912469	2	2.82703
Q6IRK9	IVVYNQPYTDYGK	1.55998857	2	2.91765
Q6IRK9	LGLLVDTVGPR	1.58799074	2	2.98361
Q6IRK9	SVASFSIYSPHTGHQGYQDGVPK	0.83476598	3	3.45847
Q6IRK9	TYPDTDSFNTVAEITGSK	3.51257017	2	3.73194
Q6IRK9	VGAVASLIR	1.4697477	2	2.52945
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**1.02926977**	**0.77237**	**4**
Q6MGB5	AGVIGLTQTAAR	1.09894239	2	3.19555
Q6MGB5	CNSVLPGFIATPMTQK	2.09916387	2	2.34861
Q6MGB5	GSIINISSIVGK	1.74863847	2	2.7751
Q6MGB5	VGNIGQTNYASSK	0.99135324	2	2.76001
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.00891222**	**0.99982**	**3**
Q6NSR8	GIVYDTGGLSIK	0.95952168	2	2.36454
Q6NSR8	HNSPSAAHFITR	1.13681072	3	3.95459
Q6NSR8	TVEINNTDAEGR	1.01385384	2	2.9926
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.34692397**	**0.85917**	**3**
Q6NYB7	EFADSLGIPFLETSAK	1.25328187	2	3.79188
Q6NYB7	NATNVEQSFMTMAAEIK	1.86951006	2	5.09252
Q6NYB7	TITSSYYR	1.24010869	1	1.97861
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.46269749**	**0.00321**	**9**

Q6NZJ6	FMLQDVLDLR	1.63135672	2	2.79625
Q6NZJ6	GLPLVDDGGWNTVPISK	1.05372841	2	2.87266
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.22027229	3	3.35313
Q6NZJ6	IHNAENIQPGEQK	1.32070035	2	3.95514
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.67369585	3	3.56169
Q6NZJ6	KVEYTLGEESEAPGQR	1.41329422	2	4.75058
Q6NZJ6	LGIESTLER	1.24226138	2	2.4185
Q6NZJ6	LKEELEEAR	1.46021949	2	2.70229
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	1.10882963	3	4.99129
Q6P0K8	**PLAK Junction plakoglobin**	**1.34994454**	**0.49558**	**3**
Q6P0K8	LLNDEDPVVVTK	0.91099782	2	3.22565
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.52104201	3	3.62823
Q6P0K8	TMQNTSDLDTAR	1.25547066	2	3.25989
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.37545237**	**1.7E-10**	**14**
Q6P502	AMTGVEQWPYR	1.25205941	2	2.70722
Q6P502	AVAQALEVIPR	1.77914838	2	2.4506
Q6P502	DMMLNIINSSITTK	0.86332542	2	3.97657
Q6P502	EIQVQHPAAK	1.30383954	2	3.30226
Q6P502	GISDLAQHYLMR	1.59807604	2	3.04806
Q6P502	IVLLDSSLEYK	1.8750559	2	2.55909
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.78000766	3	4.09411
Q6P502	KGESQTDIEITR	1.37105467	2	3.27758
Q6P502	MLLDPMGGIVMTNDGNAILR	2.24984378	2	3.88515
Q6P502	NLQDAMQVCR	1.84452968	2	3.31944
Q6P502	NVLLDPQLVPGGGASEMAVAHALTEK	2.57178067	2	3.87082
Q6P502	TAVETAVLLLR	1.37038857	2	3.73921
Q6P502	TLIQNCGASTIR	1.40529076	2	3.34592
Q6P502	WSSLACNIALDAVK	1.42084791	2	3.7964
Q6P6M7	**selenium transferase**	**0.98615383**	**0.85203**	**4**
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.98372589**	**0.63198**	**14**
Q6P6R2	ALLNNSHYYHLAHGK	1.14717633	2	3.3111
Q6P6R2	ALTGGIAHLFK	1.15724264	2	2.63245
Q6P6R2	EANLAASFGKPINF	1.49569666	1	1.92902
Q6P6R2	IDVSVEAASGGK	3.00503148	2	3.03946
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.16032067	3	3.99356
Q6P6R2	IPNIFAIGDVVAGPMLAHK	1.65989056	3	3.50005
Q6P6R2	NETLGGTCLNVGCIPSK	0.82981712	2	5.16718
Q6P6R2	NQVTATTADGSTQVIGTK	1.05838975	2	5.63074
Q6P6R2	RPFTQNLGLEELGIELDPK	1.00454028	3	4.60339
Q6P6R2	SEEQLKEEGVEFK	1.04936148	2	3.53124
Q6P6R2	TNADTDGMVK	1.39389487	2	2.82534
Q6P6R2	TNADTDGMVK+Oxidation(7	1.95471773		
Q6P6R2	VCHAHPTLSEAFR	1.28731264	3	3.78274
Q6P6R2	VVHVNGFGK	1.73575895	3	3.45103
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.87461832**	**0.20861**	**6**
Q6P6S9	AAETHLIDYEK	1.40803975	2	2.66759
Q6P6S9	AQTLLLEVEEIFK	1.18775226	2	3.27033
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.75914513	2	4.39739
Q6P6S9	QGAETVQELLEVAK	0.74553528	2	3.14373
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	0.95649586	3	3.62794
Q6P6S9	WLEAEWIFGGVK	1.27657497	2	2.77027
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.33017477**	**1.4E-13**	**9**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2	0.97259642		
Q6P6V0	HFVALSTNTDK	1.45638562	1	3.25527
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.2941725	3	6.00124

Q6P6V0	MIPCDFLIPVQTQHPIR	2.24537529	2	2.42619
Q6P6V0	TFTTQETITNAETAK	1.40260628	2	4.75683
Q6P6V0	TLANLNPESSLFIIASK	1.20607644	3	5.20596
Q6P6V0	VDYQTGPIVWGEPGTNGQHAFYQLIHQGTK	1.62931915	3	4.02225
Q6P6V0	VFEGNRPTNSIVFTK	1.28550639	2	3.38279
Q6P6V0	VWFVSNIDGTHIAK	0.49213959	2	3.63236
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.20640718**	**0.32547**	**6**
Q6P7Q4	DFLLQQTMLR	1.4355251	2	3.38238
Q6P7Q4	FEELGVK	1.17182891	1	1.93778
Q6P7Q4	GFGHIGIAVPDVYEACK	1.30322732	2	4.0001
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.31285336	2	5.7382
Q6P7Q4	RFEELGVK	1.24470477	2	2.32368
Q6P7Q4	VLGLTLLQK	2.14975036	2	2.48099
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**0.94529603**	**0.46597**	**2**
Q6P7R8	GIFVQSVLPFFVATK	0.8161084	2	3.46805
Q6P7R8	LGEWAVVTGGTDGIGK	1.4354055	2	4.23867
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.14906273**	**0.05754**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	1.34086257	2	4.50998
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10	0.99779391		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.4798471	3	5.65801
Q6P9T8	EIVHLQAGQCGNQIGAK	2.86261165	2	4.93126
Q6P9T8	EVDEQMLNVQNK	8.62479852	2	4.47394
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	0.90579311	3	4.85032
Q6P9T8	INVYYNEATGGK	1.12762768	2	3.07603
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.53524226	3	6.60577
Q6P9T8	LHFFMPGFAPLTSR	1.60006068	2	3.26907
Q6P9T8	MSATFIGNSTAIQELFK	1.76555582	2	4.3316
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	1.49067165	3	5.80361
Q6P9T8	TAVCDIPPR	1.28425684	2	2.5009
Q6P9T8	YLTVAAVFR	1.84582685	2	2.68381
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.50633057**	**0.02567**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	1.42558991	3	3.73125
Q6P9U8	EGTGSTATSSSSTGGAVGK	1.51223323	2	4.27067
Q6PA06	**ATLA2 Atlastin_2**	**1.52393354**	**1.5E-06**	**5**
Q6PA06	AGLTDQVSHHAR	1.21595843	2	3.18057
Q6PA06	NLVPLLLAPENLVEK	1.60100238	2	3.02297
Q6PA06	QNQHEELQNVR	1.29858938	2	2.92974
Q6PA06	SMEQVCGGDKPYIAPSDLER	1.10417833	3	3.80321
Q6PA06	SMLQATAEANNLAAVAGAR	1.74586954	2	4.50093
Q6PCL9	**polymerase gamma**	**1.40414403**	**0.08933**	**2**
Q6PCL9	LTEILK	1.31107386		
Q6PCL9	QANNINMLKDGMK	1.49569666		
Q6PCU2	**VATE1 V_type proton ATPase subunit E 1**	**1.65097043**	**0.03431**	**2**
Q6PCU2	ARDDLITDLLNEAK	1.71277946	2	2.97243
Q6PCU2	LDLIAQQMMPEVR	1.23911416	2	2.56513
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.03199822**	**0.76419**	**2**
Q6PDM2	SHEGETAYIR	1.25656646	2	2.40953
Q6PDM2	TKDIEDVFYK	1.02185275	2	2.75332
Q6PDV7	**RL10 60S ribosomal protein L10**	**1.87184914**	**0.7146**	**2**
Q6PDV7	FNADEFEDMVAEK	2.44993871	2	3.81246
Q6PDV7	FNADEFEDMVAEKR	1.33809022	2	3.30423
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.28887818**	**0.3329**	**6**
Q6PEC1	AEDGENYAIK	1.33296331	2	2.6904
Q6PEC1	AEDGENYAIKK	1.31207423	2	2.47524
Q6PEC1	LEAAYTDLR	1.59903768	2	2.81162
Q6PEC1	MKAEDGENYAIK	0.20870108	2	2.79379

Q6PEC1	QAEILQESR	1.48142951	2	2.58364
Q6PEC1	QILESEKDLEEAEEYKEAR	1.24113603	3	4.09466
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.25758818**	**0.61143**	**3**
Q6PEC4	NDFTEEEEAQVR	1.4115903	2	3.45187
Q6PEC4	RTDDIPVWDQEFLK	1.1866197	2	3.02802
Q6PEC4	TDDIPVWDQEFLK	1.14555147	2	3.18925
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.34896647**	**0.45752**	**6**
Q6Q0N1	AVFQYIDENQDR	0.73882528	2	3.02616
Q6Q0N1	EGGSIPVTLTFQEATGK	1.04201217	2	2.76204
Q6Q0N1	LGGSVELVDIGK	1.02939784	2	3.58265
Q6Q0N1	MTEAAAADVQR	1.41665807	2	3.14374
Q6Q0N1	TGQEIPVNLR	1.36493993	2	2.57481
Q6Q0N1	TVFGVEPDLTR	1.39237285	2	2.39771
Q6RT24	**CENPE Centromere_associated protein E**	**1.16872569**	**0.30542**	**3**
Q6RT24	ENEDLKLK	1.35155486	2	2.32973
Q6RT24	MELENVNMKLQEK	1.13663201	2	2.55944
Q6RT24	NLQEYIDAQKSEKMK	1.33445316	2	2.40604
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.9273609**	**0.98703**	**2**
Q6SKG1	FDSTSILQTLSK	0.95743957	2	3.75613
Q6SKG1	TGTVLIPGTTQLTQK	0.90814456	2	2.85918
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.19420792**	**0.8753**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	2.13012886	2	4.64675
Q6TUG0	FQMTQEVVCDECPNVK	1.14949148	2	5.57842
Q6TUG0	KGEGLPNFDNNNIK	1.05714806	2	3.64917
Q6TUG0	TLEVEIEPGVR	1.3793789	2	3.1555
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.26442119**	**0.16751**	**19**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.25158866	2	5.09539
Q6UPE1	ALNEGGLQSIPK	0.89667497	2	3.36423
Q6UPE1	ASCDAQTYGIGLK	1.13131524	2	4.05393
Q6UPE1	DCTPIEYPKPDGQISFDLLSSVALSGTNHEHDQPAHLTLK	0.71343839	4	4.62569
Q6UPE1	FAEEADVVIVGAGPAGLSAAIR	2.03643271	2	3.08612
Q6UPE1	FCPAGVYEFVPLEQGDGFR	1.37953815	2	4.5225
Q6UPE1	GAPLNTPVTEDR	0.99438074	2	3.48264
Q6UPE1	GIATNDVGIQK	1.31323268	2	3.78917
Q6UPE1	HHPSIRPTLEGGK	0.46111996	2	2.4202
Q6UPE1	HHPSIRPTLEGGKR	1.32675486	2	2.82038
Q6UPE1	LQINAQNCVHCK	0.95846078	2	3.72339
Q6UPE1	NLSIYDGPEQR	0.88010112	2	3.14372
Q6UPE1	QLAAEQEKDIR	0.96785019	2	2.70154
Q6UPE1	QLTSENLQSK	1.053046	2	2.46372
Q6UPE1	SGSLAAEAIFK	0.86075042	2	3.14082
Q6UPE1	TAGLHVTEYEDNLK	1.32000997	2	3.97349
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	7.05672542	2	4.39
Q6UPE1	VDHTVGWPLDR	0.95420971	2	2.47605
Q6UPE1	VTIFAEGCHGHLAK	1.35950631	2	3.67792
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**1.16084009**	**0.26043**	**8**
Q6URK4	EDSVKPGAHLTVK	1.30531575	2	3.48456
Q6URK4	EDTEEYNLR	1.33513606	2	2.45323
Q6URK4	GFAFVTFDDHDTVDK	2.14385255	2	4.09519
Q6URK4	IETIEVMEDR	1.41721481	2	3.4034
Q6URK4	IFVGGIKEDTEEYNLR	1.85125256	2	4.2578
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	1.07499026	2	5.22703
Q6URK4	WGTLTDCVVMR	1.30676387	2	3.2414

Q6URK4	YHTINGHNCEVK	1.18063119	2	3.50797
Q6URW6	**MYH14 Myosin_14**	**1.01022981**	**0.99999**	**4**
Q6URW6	EDQSILCTGESGAGK	1.06993307	2	4.39641
Q6URW6	FDQLLAEEK	0.97456189	1	2.04082
Q6URW6	KFDQLLAEEK	1.28851355	2	2.83733
Q6URW6	QLLQANPILEAFGNAK	0.98026139	2	4.49156
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**1.07506595**	**0.73132**	**5**
Q6XQN1	AFAQQSLSR	1.73305172	2	2.49352
Q6XQN1	GSEVNVIGIGTNVVTCPK	1.02278941	2	4.22268
Q6XQN1	LDSGDLLQQAK	0.9986188	2	3.06168
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.15527169	2	5.03625
Q6XQN1	QLQNPAVYQVALSEK	1.84129299	2	3.83193
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.18554698**	**0.49597**	**2**
Q6ZPJ3	FRTTDIVIR	0.8358667	2	2.60035
Q6ZPJ3	NCAQGEGSMAKKVK	1.18792837	2	2.8212
Q6ZPV2	**INO80 DNA helicase INO80**	**0.85076254**	**0.42961**	**2**
Q6ZPV2	FIDVSPAEMANLMLQGLLAR+Oxidation(12	0.60938428		
Q6ZPV2	KLDEEMREAK+Oxidation(5	0.90684663		
Q6ZWR6	**SYNE1 Nesprin_1**	**0.91159956**	**0.67129**	**4**
Q6ZWR6	FGSITNQLLK	1.24538008	2	2.39879
Q6ZWR6	KDEIEGWSNSSLPK	0.72959659	2	2.52539
Q6ZWR6	LETILK	1.31107386	1	1.90074
Q6ZWR6	LKAKTDDLVHAK	0.93475349	2	2.31459
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.16544188**	**0.18485**	**2**
Q70FJ1	EDGGQPPPALPSEDLLK	0.66801015	2	2.74204
Q70FJ1	MDQITQSLCNLNK+Oxidation(0	1.54578762		
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.18844592**	**0.05839**	**5**
Q711G3	DCGTDVLDLWTLMQK	1.02539204	2	4.40866
Q711G3	DVEETKPELSLLGDGDH	0.90828505	2	4.13121
Q711G3	LNVAVGEYAK	1.16762549	2	2.76331
Q711G3	QHVPLDEYSANLR	2.07233441	2	2.63208
Q711G3	VILITPPPLCEAAWEK	1.71720138	2	2.73393
Q71LX4	**TLN2 Talin_2**	**1.12936205**	**0.47394**	**3**
Q71LX4	QEDVIATANLSR	1.42755248	1	1.97032
Q71LX4	QVAASTAQLLVACK	1.02723002	2	3.18949
Q71LX4	VMVTNVTSLLK	0.51794253	2	2.37738
Q71TY3	**RS27 40S ribosomal protein S27**	**1.88775036**	**0.03106**	**3**
Q71TY3	DLLHPSPEEEK	2.25306755	2	2.91667
Q71TY3	LTEGCSFR	1.56450998	2	2.38761
Q71TY3	LVQSPNSYFMDVK	1.27300136	2	2.80042
Q75N33	**SC16B Protein transport protein Sec16B**	**1.18416335**	**0.53085**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	1.03161074	2	3.67124
Q75N33	VLEPDWLVQLR	1.67669426	2	2.80606
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.05294687**	**0.639**	**6**
Q75Q39	NADLSTFYQNR	1.60016141	2	2.95816
Q75Q39	NREPLMPSPQFIK	0.99359317	2	2.82192
Q75Q39	QYMEEENYDK	#NUM!	1	1.94862
Q75Q39	SDEDKDKEGEALEVK	1.38726862	2	4.22832
Q75Q39	WKEVAQDCTK	0.82173139	2	2.33949
Q75Q39	YEQAIQCYTEAISLCPTEK	0.61086426	2	2.49781
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**2.00104919**	**0.69515**	**8**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	2.31335532	3	5.1377
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.39299456	2	4.99636
Q76MZ3	LSTIALALGVER	2.38342864	2	2.36096

Q76MZ3	LTQDQDVDVK	1.14816501	2	2.97982
Q76MZ3	QLSQSLLPAIVELAEDAK	1.90708507	3	4.13773
Q76MZ3	SALASVIMGLSPILGK	1.19765243	2	2.89103
Q76MZ3	SEIIPMFSNLASDEQDSVR	0.98669772	2	3.96919
Q76MZ3	VLELDNVK	1.22088443	2	2.5149
Q78IK4	**APOOL Apolipoprotein O_like**	**1.26938016**	**0.50459**	**2**
Q78IK4	EEEPKK	3.95458524	1	1.96138
Q78IK4	SESTSGTTQFIPDPK	1.15528684	2	2.42113
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**0.87678225**	**0.16997**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	0.88017144	3	5.66937
Q78P75	NFGSYVTHETK	1.36019475	2	2.92278
Q78P75	YNPTWHCIVGR	0.69476158	2	2.86639
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**1.16614909**	**0.00082**	**6**
Q791V5	EEGIVGFFAGLIPR	1.06327181	2	3.42882
Q791V5	GLFTGLTPR	1.19998841	2	2.58243
Q791V5	LCSGVLGTVVHGK	1.39745259	2	2.99564
Q791V5	SAATLITHPFHVITLR	1.18605375	3	3.56618
Q791V5	VLIQVGYEPLPPTIGR	1.18523003	2	4.18477
Q791V5	YCGLCDSIVTIYR	1.69809553	2	2.91509
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.39488673**	**0.23067**	**4**
Q794E4	ATENDIYNFFSPLNPVR	1.39767593	3	4.09186
Q794E4	HSGPNSADSANDGFVR	1.34516941	2	3.9465
Q794E4	ITGEAFVQFASQELAEK	0.99380894	2	2.71371
Q794E4	VHIEIGPDGR	1.39826447	2	2.7901
Q7M0E3	**DEST Destrin**	**1.79036766**	**0.05635**	**2**
Q7M0E3	HEYQANGPEDLNR	1.67291326	2	4.76629
Q7M0E3	HFVGMLPEKDCR	1.9306646	2	3.48551
Q7TMA5	**APOB Apolipoprotein B_100**	**0.88700679**	**0.94788**	**12**
Q7TMA5	ALEGKSDTVARLHTEK	1.44767081	2	2.41776
Q7TMA5	GFEPTLEALFGK	0.89927513	2	2.91823
Q7TMA5	IEGNLVFDPSSYLPK	1.1425015	2	2.99779
Q7TMA5	IEIDIPLPLGGK	0.46194718	2	2.77812
Q7TMA5	ITDNDVLIALDSAK	0.87823188	2	3.32554
Q7TMA5	KGTVATEMSTER	1.02699923	2	2.84147
Q7TMA5	LSISEQNAQR	0.81375839	2	2.74273
Q7TMA5	LSTSPFALNLTMLPK	1.07941442	1	1.90173
Q7TMA5	NFVASHIANILNSEELYVQDLK	0.80236648	3	3.84929
Q7TMA5	NLQHCDGFQPISTSVSPLALIK	1.21020716	3	3.79325
Q7TMA5	TILFDTFVNDVAPVEK	0.85022183	2	3.13251
Q7TMA5	VRSFTIDLLEIKAK	1.07941442	1	1.99944
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.09617881**	**0.90676**	**4**
Q7TNG8	AVVGSPHVSTASAVR	1.12424801	2	2.93918
Q7TNG8	AYSTDVCVPISR	1.15791341	2	3.38022
Q7TNG8	GSQGGLSQDFVEALK	0.96289311	2	3.6321
Q7TNG8	QLLQEEVGPVGVETMR	0.76934736	2	3.22962
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.0896642**	**0.73007**	**2**
Q7TP47	DLFEDELVPLFEK	1.9036872	2	3.27966
Q7TP47	NLANTVTEEILEK	1.10082558	2	3.68663
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.11702358**	**0.05979**	**4**
Q7TP48	ANPGFSMLDFLSDKPFIK	1.5155514	2	3.00243
Q7TP48	LENGEIETIAR	1.11240934	2	3.52103
Q7TP48	LLEYDTVTK	1.32471727	2	2.49107
Q7TP48	LLLSSETPIEGK	1.27510084	2	2.91197

Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.26422442**	**0.97929**	**8**
Q7TP52	AGVSVYGIIR	1.36758383	2	2.74656
Q7TP52	EDCSPADKPYIEEAR	1.0465322	2	3.71484
Q7TP52	KREDCSPADKPYIEEAR	1.16915641	3	4.21316
Q7TP52	LDYGGMGQEVQVEHIK	1.28212074	2	4.61124
Q7TP52	LKEHCIVNYQVK	1.51276896	2	4.07233
Q7TP52	NLIEWLNK	1.51275237	2	2.3561
Q7TP52	REDCSPADKPYIEEAR	1.17988375	3	3.69844
Q7TP52	TFSGQTHGFVHR	1.27078393	2	3.66039
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.24503517**	**0.98081**	**6**
Q7TPB1	ALIAGGGAPEIELALR	1.43470847	2	3.88185
Q7TPB1	ETLLNSATTSLNSK	1.50270013	2	3.31296
Q7TPB1	GDVTITNDGATILK	1.26838331	2	3.51737
Q7TPB1	SIHDALCVIR	1.50020374	2	2.69392
Q7TPB1	TGCNVLLIQK	0.88543347	2	2.60797
Q7TPB1	VIDPATATSVDLR	1.20372985	2	3.84164
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.28313824**	**0.01267**	**3**
Q7TPJ0	FLVGFTNK	1.70610256	2	2.48813
Q7TPJ0	GEDFPANNIVK	1.23390056	2	3.20333
Q7TPJ0	GTEDFIVESLDASFR	1.63507322	2	4.3717
Q7TQ20	**DNJC2 DnaJ homolog subfamily C member 2**	**0.92507355**	**0.74081**	**2**
Q7TQ20	MMEEVEKLCDR+Oxidation(0	0.96941353		
Q7TQ20	QIEEVNELMRK+Oxidation(8	0.90384538		
Q7TQ94	**NIT1 Nitrilase homolog 1**	**1.81709558**	**0.14905**	**2**
Q7TQ94	GQDWEQTQK	1.3862742	2	2.46455
Q7TQ94	NPAETLLLSEPLDGDLLGQYSQLAR	1.82288366	3	4.21868
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.13886455**	**0.91286**	**3**
Q7TQM4	AIWEAVQAYPK	0.88006653	2	2.56319
Q7TQM4	QDRPLPSTASDSTR	0.9288673	2	2.84504
Q7TQM4	TQCLEQAQR	1.14948467	2	2.88386
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.74047311**	**0.94265**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(1	0.77478362		
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(5	0.69319244		
Q80V31	**CE104 Centrosomal protein of 104 kDa**	**1.08772237**	**0.83043**	**2**
Q80V31	IDGSVLPTEAEVRAQK	1.02400562	2	2.55886
Q80V31	KLMEMPVGTQK+Oxidation(2)Oxidation(4	1.0892046		
Q80VM7	**ANR24 Ankyrin repeat domain_containing protein 24**	**1.44837201**	**0.35264**	**2**
Q80VM7	ADEVDVLAQAGLTGTVIR	0.98925174	2	2.68819
Q80VM7	QNQELLEK	9.84842846	1	2.01925
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.05775254**	**0.07902**	**13**
Q80W21	CLDAFPNLK	0.96069237	2	3.2003
Q80W21	CLDAFPNLKDFIAR	1.15731085	2	3.11884
Q80W21	FKLGLDFPNLPYLIDGSHK	1.02579069	3	5.07351
Q80W21	HNLCGETEEER	0.78993321	2	3.89162
Q80W21	IRVDILENQLMDNR	1.19125777	2	3.04944
Q80W21	ITQSNAILR	1.27542496	2	3.07713
Q80W21	KHNLCGETEEER	1.46262071	2	3.9986
Q80W21	KISDYMK	0.87840253	1	2.00136
Q80W21	LFLEYTDSSYEEK	0.26614574	2	4.04387
Q80W21	LGLDFPNLPYLIDGSHK	1.38247504	3	4.67577
Q80W21	LKPGYLEQLPGMMR	1.18945854	2	3.18071
Q80W21	LYSEFLGK	1.12637064	2	2.35592
Q80W21	VDILENQLMDNR	0.68695834	2	3.71466
Q80W93	**HYDIN Hydrocephalus_inducing protein**	**1.88579527**	**0.02255**	**3**
Q80W93	ELERLAKEMQEK+Oxidation(8	2.97700898		

Q80W93	LAKEMQEK	2.29585957	1	1.93259
Q80W93	LQTLDEDEYDALTAEEK	1.88387487	2	2.30161
Q80WS3	**FBLL1 rRNA/tRNA 2__O_methyltransferase fibrillarin_like protein 1**	**0.96062768**	**0.57147**	**3**
Q80WS3	DHAVVVGVYRPPPK	0.91260286	3	3.74093
Q80WS3	MKPAGGRGGWGWGGGK+Oxidation(0	1.06161233		
Q80WS3	TNIIPVLEDAR	1.43537433	2	2.40161
Q80X50	**UBP2L Ubiquitin_associated protein 2_like**	**1.21006495**	**0.1746**	**2**
Q80X50	IDLAVLLGK	1.17705931	2	3.14239
Q80X50	QRPQATAEQIR	1.5221617	2	2.51887
Q80X90	**FLNB Filamin_B**	**1.31970826**	**0.28808**	**11**
Q80X90	ADIEMPFDPSK	1.51377315	2	2.37343
Q80X90	FNDEHIPDSPYLVPVIAPSDDAR	1.68768739	3	3.64952
Q80X90	GAGIGGLGITVEGPSESK	1.40317993	2	3.8366
Q80X90	GEAGIPAEFSIWTR	1.29569792	2	2.31444
Q80X90	IGNLQTDLSDGLR	1.40633119	2	2.45996
Q80X90	ILAQDGEGQPIDIQMK	1.01772804	2	3.3675
Q80X90	TFEMSDFIVDTR	1.79075027	2	2.3016
Q80X90	VDIQTEDLEDGTCK	1.49343242	2	3.796
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.18629115	3	4.11054
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.3484478	3	3.47551
Q80X90	VVASGPGLEHGK	1.18483671	2	2.37975
Q80XC3	**US6NL USP6 N_terminal_like protein**	**1.14667152**	**0.84007**	**2**
Q80XC3	HYNHAAANQNSNAISNVRK	2.41250678	2	2.37964
Q80XC3	SVDEGSKNLK	1.13917001	2	2.41046
Q80XI3	**IF4G3 Eukaryotic translation initiation factor 4 gamma 3**	**1.63209961**	**0.00175**	**3**
Q80XI3	FLKITKPTIDEK	1.59506789	2	2.60857
Q80XI3	FMLQDVIDLR	1.63135672	2	2.79625
Q80XI3	NHDEESLECLCR	1.65338014	2	3.36872
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**1.04459491**	**0.52997**	**2**
Q80Y84	CDIGLLGLK	1.05194218	1	2.0753
Q80Y84	SSSEKNDCLRGK	0.63737519	1	1.93582
Q80YR7	**CLSPN Claspin**	**1.2145349**	**0.42951**	**2**
Q80YR7	GASFLPTAGFRSPSPGLFR	1.05721506	2	2.41257
Q80YR7	LEGASHAKPGEKLQMLK+Oxidation(14	1.27981408		
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.1909995**	**0.97337**	**2**
Q80Z25	ELEQEAERLEK	1.19093537	2	2.93997
Q80Z25	MIEESLK+Oxidation(0	1.23384897		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.61120138**	**0.00869**	**4**
Q80Z29	NAQLNMEQDVAPH	1.04514252	2	2.53487
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.54698352	2	3.78835
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.62027498	2	5.37929
Q80Z29	YLLETSGNLDGLEYK	1.59016294	2	4.55266
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**1.15505354**	**0.1847**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	1.82303596	2	2.62699
Q80Z36	YPEEQLK	0.6017598	1	2.09197
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.1741783**	**0.6047**	**5**
Q811D2	AQEDFDK	0.74110085	1	1.91143
Q811D2	LSGSEDSQQKVEEK	1.93192858	2	2.3696
Q811D2	NKDDLTPMLLAVK	1.37948375	2	2.4119
Q811D2	SADQLSEK	1.15989042	2	2.3079
Q811D2	SNLEEEARDLK	1.17539529	1	1.99484
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.04571517**	**0.44524**	**4**

Q811X6	EMKSLEQSGSLK+Oxidation(1	1.05758052		
Q811X6	IVDDQVILSSSSSCLLPSK	0.72703338	2	3.9303
Q811X6	LYDIEQQQITNALESIR	1.26375288	2	4.27153
Q811X6	TFGPVPEFSGDTVEK	1.54955062	2	2.8986
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**0.99459076**	**1.6E-07**	**10**
Q8BFZ3	CDVDIR	2.48700788	2	2.32686
Q8BFZ3	DLTDYLMK	1.23884677	1	2.21593
Q8BFZ3	HQGVMVGMGQK	1.65040444	3	3.63664
Q8BFZ3	HQGVMVGMGQK+Oxidation(4	1.18964955		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)Oxidation(7	1.54596327		
Q8BFZ3	HQGVMVGMGQK+Oxidation(7	1.04406661		
Q8BFZ3	SYELPDGQVITIGNER	0.98224345	3	5.23031
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.4087146	3	6.64004
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5	1.58293486		
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.20818023	3	4.32967
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**1.40965754**	**0.30373**	**6**
Q8BG32	LYDNLLEQNLIR	1.406937	2	3.3939
Q8BG32	TGQAAELGGLLK	1.18647878	2	3.1513
Q8BG32	TTANAIYCPPK	7.79235181	2	2.64396
Q8BG32	TYEAALETIQNMSK	1.37040685	2	2.37357
Q8BG32	VQIEHISSLIK	1.62983784	2	2.70242
Q8BG32	YQEALHLGSQLLR	1.29427715	2	2.50007
Q8BGD9	**IF4B Eukaryotic translation initiation factor 4B**	**1.207401**	**0.48905**	**2**
Q8BGD9	SQSSDTEQPSPTSGGGK	1.17974679	2	5.37759
Q8BGD9	VDVADQAQDKDRDDR	1.92468471	2	2.37885
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**1.21670425**	**0.20174**	**2**
Q8BGT5	LLEETGICVVPGSGFGQR	0.47336061	2	3.8384
Q8BGT5	VLCIINPGNPTGQVQSR	1.31750221	2	5.07928
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.22173712**	**0.41827**	**3**
Q8BGY2	KYEDICPSTHNMDVPNIK	1.22231863	3	4.79291
Q8BGY2	VHLVGIDIFTGK	1.46865481	3	3.74122
Q8BGY2	YEDICPSTHNMDVPNIK	1.21895435	2	3.88257
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.15852182**	**9.9E-20**	**8**
Q8BH00	ELLMLENFIGGK	1.35749845	2	3.59371
Q8BH00	ELNLPFGGMK	1.43016212	1	2.49095
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.07416944	3	5.3076
Q8BH00	ILCGEGVDQLSLPLR	1.53045763	3	4.95457
Q8BH00	ITQLSAPHCK	1.55396289	2	3.12905
Q8BH00	KLSLELGGK	1.18646244	1	2.25505
Q8BH00	NPAIIFEDANLEECIPATVR	1.57974945	2	5.0365
Q8BH00	SSFANQGEICLCTSR	1.5660372	2	3.90093
Q8BH18	**TM117 Transmembrane protein 117**	**1.59460769**	**0.323**	**2**
Q8BH18	FLKNEQGMENQDK	1.54578762	2	2.34406
Q8BH18	FLKNEQGMENQDK+Oxidation(7	1.73472913		
Q8BH59	**CMC1 Calcium_binding mitochondrial carrier protein Aralar1**	**1.51883392**	**0.04148**	**3**
Q8BH59	GLIPQLIGVAPEK	1.51856263	1	3.07248
Q8BH59	IAPLAEGALPYNLAELQR	1.66439539	2	2.85188
Q8BH59	YLGLYNDPNSNPK	1.20796533	2	3.11152
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.07590942**	**0.89659**	**11**
Q8BHN3	AEKDEPGAWEETFK	1.02688028	2	3.06362
Q8BHN3	DDNSVELTVAEGPYK	1.07589216	2	3.41011
Q8BHN3	LVAIVDPHIK	0.96823405	2	2.34349

Q8BHN3	MLDYLQGSGETPQTDIR	0.88002819	2	5.34461
Q8BHN3	REPWLLASQYQDAIR	1.727362	3	4.33095
Q8BHN3	SGGIERPFVLSR	1.08375108	2	2.4538
Q8BHN3	SIRPGLSPYR	0.9347132	2	2.3565
Q8BHN3	SLLLSVNAR	1.1521033	2	2.48766
Q8BHN3	VDSGYRVHEELRNHGLYVK	0.89472306	2	2.33052
Q8BHN3	VTEGGEPYR	1.46807007	2	2.40752
Q8BHN3	VVIMGAGKPAAVVLQTK	2.47407925	3	3.8582
Q8BI84	**MIA3 Melanoma inhibitory activity protein 3**	**1.62918872**	**0.27752**	**2**
Q8BI84	DDNISALTNCITQLNR	2.12183677	2	2.32124
Q8BI84	TQTAVSIVEEDLK	1.6070416	2	2.43565
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**1.44823289**	**0.10568**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.49569666	1	2.19315
Q8BIJ6	SCQTALAEILDVLVR	1.27062712	2	3.51358
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.05274195**	**0.9999**	**10**
Q8BJ64	ADSAYHPSCTCK	0.34558395	2	3.18561
Q8BJ64	AEVQTLVSR	1.22653576	2	2.88709
Q8BJ64	ELQPGSHVQSDK	1.04638552	2	3.07472
Q8BJ64	ELQPGSHVQSDKEIDAFVR	1.05165844	2	4.24555
Q8BJ64	GGDGPLHVSR	1.00319325	2	2.34865
Q8BJ64	HELGANMYR	0.93549942	2	2.34865
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	0.96048289	5	5.01656
Q8BJ64	TNHPLHQAFLQAAR	1.25756287	3	4.00004
Q8BJ64	VIGVENLR	1.03720982	2	2.74613
Q8BJ64	VLLLEAGPK	1.49329041	2	2.62868
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**1.21552934**	**0.1407**	**2**
Q8BJY1	GLTHPDDSVK	1.08655183	2	2.45672
Q8BJY1	TVAEIFGNSNYLR	2.97499777	2	2.48391
Q8BKC5	**IPO5 Importin_5**	**1.21627295**	**0.06415**	**2**
Q8BKC5	IFSIIAEGEMHEAIK	1.41246657	2	2.3325
Q8BKC5	VAAAESMPLLLECARVR+Oxidation(6	0.38046265		
Q8BKZ9	**ODPX Pyruvate dehydrogenase protein X component_ mitochondrial**	**1.01200084**	**0.77006**	**2**
Q8BKZ9	HSLDASQGTATGPR	1.00640665	2	3.94335
Q8BKZ9	VSVNDFIIR	2.6563922	2	3.05482
Q8BL66	**EEA1 Early endosome antigen 1**	**0.87580802**	**0.54406**	**2**
Q8BL66	MQAAVTELTAVKAQK	0.52490332	2	2.44298
Q8BL66	QESIKEITNLKDAK	1.62717475	2	2.30593
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.26149876**	**0.69332**	**2**
Q8BL97	NPPGFAFVEFEDPR	1.00946697	2	2.81618
Q8BL97	VYVGNLGTGAGK	1.28908569	2	2.56947
Q8BMA5	**NPAT Protein NPAT**	**1.00771641**	**0.99999**	**2**
Q8BMA5	AKETSNDVPTIMSSLWKK+Oxidation(11	1.07072707		
Q8BMA5	KKLPSSFPAGMDVDK+Oxidation(10	1.0065012		
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**1.31098296**	**0.16233**	**5**
Q8BP47	KEDGTFYEFGDDIPEAPER	0.87018976	2	4.40305
Q8BP47	LEDLVCDVVDR	1.22648304	2	2.81699
Q8BP47	LMTDTINEPILLCR	2.99398178	2	3.34017
Q8BP47	LTESVDVLMPNVGEIVGGSMR	1.31098267	2	2.9164
Q8BP47	YGTCPHGGYGLGLER	1.53853141	2	3.16098
Q8BTM8	**FLNA Filamin_A**	**1.06317043**	**0.73534**	**6**
Q8BTM8	AFGPGLQGGNAGSPAR	1.37302815	2	3.56198
Q8BTM8	ALGALVDSCAPGLCPDWDSWDASKPVNNAR	1.03316793	3	3.62483
Q8BTM8	ANLPQSFQVDTSK	1.13153214	2	2.44741
Q8BTM8	GAGTGGLGLAVEGPSEAK	0.9353496	2	3.72377
Q8BTM8	IVSPSGAAVPCK	1.45043006	2	2.41114

Q8BTM8	VEPGLGADNSVVR	1.66436057	2	2.86012
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**0.98755018**	**0.8424**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	0.90435074	2	3.13355
Q8BU33	LPNSLMGR+Oxidation(5	1.03450627		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.77995581	3	3.95851
Q8BWM0	**PGES2 Prostaglandin E synthase 2**	**1.11914023**	**0.65897**	**2**
Q8BWM0	AFLDFHSLPYQVVEVNPVR	1.06146753	3	3.52985
Q8BWM0	KVPILVAQEGDSLQQLNDSSVIISALK	1.15984006	3	4.62097
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**0.96456916**	**1**	**2**
Q8BWQ1	ADIWLIR	1.01053053	2	2.4481
Q8BWQ1	IHHDQPVKPLDR	0.94433509	3	3.51418
Q8BWR8	**RHPN2 Rhophilin_2**	**1.13552311**	**0.78393**	**2**
Q8BWR8	ETKEVDFSIVFK	1.12484131	2	2.53472
Q8BWR8	TGAENLLKVATNQK	1.1409016	2	2.48585
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**1.08675229**	**0.94468**	**2**
Q8BX70	ENALSELDVPFKVK	1.08665951	2	2.62614
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19	1.18290283		
Q8BY87	**UBP47 Ubiquitin carboxyl_terminal hydrolase 47**	**1.22634068**	**0.83564**	**2**
Q8BY87	AGGDSGNVDDDCER	1.53156066	2	3.49961
Q8BY87	QNIFDEMKK	1.08695208	2	2.43066
Q8BZI0	**AF1L1 Actin filament_associated protein 1_like 1**	**0.933658**	**0.87932**	**2**
Q8BZI0	IYDEVPYEK	0.95908237	1	2.0261
Q8BZI0	LSQEKQNSDSDSLGMNDSGSTLGRR	0.81486712	3	3.59391
Q8BZQ7	**ANC2 Anaphase_promoting complex subunit 2**	**0.97379655**	**0.40449**	**2**
Q8BZQ7	EIRNVELLK	1.05980483	2	2.41527
Q8BZQ7	QALEQFNQLSQVLHR	0.69000374	2	2.75226
Q8C6K9	**chain**	**0.97092037**	**0.79903**	**3**
Q8C6K9	NEHSFQVVGIQVR	0.97091318		
Q8C6K9	TMNPAFMGLDRATR+Oxidation(1)Oxidation(6	0.94983422		
Q8C6K9	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	1.41164368		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.06278808**	**0.01512**	**2**
Q8C7X2	FNVEDGEIVQQVR	0.93777922	2	3.98422
Q8C7X2	VMGDRSVLYK+Oxidation(1	2.75865654		
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.37522908**	**0.67364**	**3**
Q8CC88	FLPSLAQSALEK	1.07431662	2	2.44075
Q8CC88	HQATGELDDAK	1.43335014	2	3.4104
Q8CC88	VSSDQLSSENLTSAVGQK	1.47043522	2	3.20769
Q8CDI6	**CD158 Coiled_coil domain_containing protein 158**	**1.05230148**	**0.92936**	**3**
Q8CDI6	EKELSLEKEQNK	1.20394939	2	2.35146
Q8CDI6	EKVANMEVALDK+Oxidation(5	1.05964617		
Q8CDI6	ELDDRNMEVQRLEALLK	0.87938724	2	2.32278
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.20749672**	**0.91762**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	1.3688333	3	4.68694
Q8CFN2	WVPEITHHCPK	2.17279102	2	2.50773
Q8CFN2	YVECSALTQK	1.20692969	1	2.70188
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**0.9284189**	**0.04668**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	0.92135516	3	3.74259
Q8CG45	EHHFEAIALVEK	1.19917145	2	2.98795
Q8CG45	FFGNSWSETYR	1.14424956	2	3.00953
Q8CG45	FYAYNPLAGGLLTGK	1.29920542	2	4.36607
Q8CG45	MDASASAATVR	1.1207195	2	3.83804

Q8CG45	QVETELLPCLR	1.32184931	2	3.03559
Q8CG45	RMDASASAATVR	1.21919761	2	3.31487
Q8CG45	TTYGTSAPSMTSAALR	1.23332345	2	4.45599
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.25349746	3	5.4736
Q8CG45	WMYHHSQLQGTR	1.06267795	3	3.74459
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.02428454**	**0.98791**	**3**
Q8CG48	EEKLLEK	1.13562997	1	1.92741
Q8CG48	IKALNCEIEELER	1.06034098	2	2.43912
Q8CG48	KIKALNCEIEELER	1.02393046	2	2.64722
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.40650004**	**1.7E-07**	**11**
Q8CGC7	AIQGATSHHLGQNFSK	1.36914999	2	4.59959
Q8CGC7	DQDVEPGAPSMGAK	1.36546068	2	3.35812
Q8CGC7	DQVDSAVQELLQLK	1.65462625	2	4.15179
Q8CGC7	FVELPGAEMGK	2.1132689	2	2.5284
Q8CGC7	GDVSISVEEGKENLLR	1.36134677	2	4.00271
Q8CGC7	GSQFGQSCCLR	1.55076494	2	2.86139
Q8CGC7	KEENLAEWYSQVITK	0.92504778	2	4.46688
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.85203736	2	4.36456
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.29148577	2	4.86416
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.89438696	3	3.47052
Q8CGC7	VYEELLAIPVVR	1.86334692	2	3.42992
Q8CGN4	**BCOR BCL_6 corepressor**	**1.14218755**	**0.38852**	**3**
Q8CGN4	FLTDYLNDLQGR	0.97714757	1	1.94041
Q8CGN4	NWLLLSDVLK	3.71118097	2	2.52787
Q8CGN4	VCIELTGLHPKK	1.25681913	2	2.34277
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.05301978**	**0.98224**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(10	1.01080867		
Q8CHB8	DSGGQTLSPSWAAK	1.25735126	1	2.13864
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.54416007**	**0.0048**	**8**
Q8CHM7	DTSKPCLINIMIEPQSTR	1.31207983	3	4.75379
Q8CHM7	GAAYSHAEDSIR	1.4281051	2	3.37647
Q8CHM7	GVVPDNHPNCVGAAR	1.41426421	2	3.24663
Q8CHM7	GYFVQTPEELQDSLR	1.91604253	2	3.83254
Q8CHM7	LVELCNLPFLPTPMGK	1.2986752	2	4.48063
Q8CHM7	NCFIVSEGANTMDIGR	1.69909317	2	4.69397
Q8CHM7	NQEAMGAFQEFPQVEACR	1.17317636	2	6.43392
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	1.55143832	3	4.01666
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.82669416**	**0.07582**	**2**
Q8CIB5	GCEVTPDVNISGQK	0.78709368	2	3.51374
Q8CIB5	TSTILGDITSIPELADYIK	1.36351642	2	2.72138
Q8CIE6	**COPA Coatomer subunit alpha**	**1.35152395**	**1.5E-12**	**10**
Q8CIE6	ASNLENSTYDLYTIPK	1.68095187	2	4.13394
Q8CIE6	DADSQNPDAPEGK	1.41018393	2	4.01827
Q8CIE6	GITGVDLFGTTDAVVK	1.56117927	2	3.716
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.1758087	3	3.78069
Q8CIE6	LLELGPKPEVAQQTR	1.31895332	2	3.15225
Q8CIE6	QELILSNSEDK	1.73913999	2	2.62028
Q8CIE6	QQPLFVSGGDDYK	1.14223217	2	2.7117
Q8CIE6	SILLSVPLLVVDNK	1.49255914	2	4.00956
Q8CIE6	SSGLTAVWVAR	0.71089307	2	2.44891
Q8CIE6	TLDLPIYVTR	1.23944439	2	2.82687
Q8CJ27	**ASPM Abnormal spindle_like microcephaly_associated protein homolog**	**0.95768302**	**0.27957**	**2**
Q8CJ27	ALHHLLTYKHLSAILDALK	1.22161195	2	2.36556
Q8CJ27	FLSLRKTAIWIQR	0.71035457	2	2.63605
Q8CJ40	**CROCC Rootletin**	**1.35907695**	**0.0247**	**4**

Q8CJ40	DLLQLGGELVRTSR	1.18547198	2	2.42963
Q8CJ40	ELEERTGNLGRQR	1.71836301	2	2.40207
Q8CJ40	LRDQTAASAQAQEDAQR	1.74586954	2	2.3698
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9	1.37577066		
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.10453838**	**0.99547**	**4**
Q8JZN5	GIILVGNEEQK	1.0825938	2	2.41553
Q8JZN5	GSNTCEVHFENTR	1.11425664	2	4.52701
Q8JZN5	NLSEFGLIQEK	1.3497834	2	2.4622
Q8JZN5	SGNVTTVMETIGR	0.86038359	2	2.96583
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.08718898**	**0.82242**	**19**
Q8K009	AMVEAVQLIADGK	1.23479797	2	4.19427
Q8K009	ANNTEYGLASGVFTR	1.24961399	2	4.62549
Q8K009	DLGEEALNEYLK	1.29758529	2	3.77958
Q8K009	EESFGPIMVISK	1.65621551	2	3.05086
Q8K009	FLFPEGIK	0.72829739	2	2.45559
Q8K009	FQNGDIDGVLQR	1.07934695	2	3.21425
Q8K009	GVINIIPGSGGVAGQR	1.20537923	2	3.87897
Q8K009	HGSIIYHPSLLPR	1.1914984	2	4.36967
Q8K009	KLGFTGSTSVGK	1.51499525	2	2.49719
Q8K009	KVSLELGGK	0.6315245	1	2.03903
Q8K009	NGLVLFGNDGK	1.06564306	2	2.42723
Q8K009	NLQFEDGK	1.03918989	1	2.18625
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.47386695	3	4.02749
Q8K009	SCDVKPNDTVDSLYNR	3.59484497	2	4.48119
Q8K009	TDVAAPFGGMK+Oxidation(9	1.36440094		
Q8K009	TPQPEEGATYEGIQK	1.19598966	2	2.58287
Q8K009	VSYASLADVDR	1.35266069	2	2.91656
Q8K009	VVGVFTVPDKDGK	1.24468368	2	3.26216
Q8K009	YFAGWCDK	0.99671333	1	2.1003
Q8K1N2	**PHLB2 Pleckstrin homology_like domain family B member 2**	**0.78690707**	**0.7428**	**2**
Q8K1N2	EKENLCNLEKK	0.60153629	2	2.41911
Q8K1N2	LQEETSQRQKLIEK	1.11934719	2	2.38009
Q8K1Q0	**NMT1 Glycylpeptide N_tetradecanoyltransferase 1**	**1.05993887**	**0.68414**	**2**
Q8K1Q0	GNDMDSTQDQPVK	1.85658845	2	2.53111
Q8K1Q0	LGEVVNTHGPVEPDKDNIR	1.03117826	3	3.44455
Q8K1S6	**SPIR2 Protein spire homolog 2**	**1.60424178**	**0.0196**	**3**
Q8K1S6	ALFVETLELR	1.9266557	2	2.50528
Q8K1S6	DTADILLRR	1.57526632	2	2.31496
Q8K1S6	RDAFQSLQGPKWR	1.41124332	2	2.30447
Q8K2H2	**OTU6B OTU domain_containing protein 6B**	**1.0837833**	**0.99382**	**2**
Q8K2H2	EELEQLK	1.13562997	1	2.08084
Q8K2H2	EERIAEAEIENLSGAR	0.99389385	2	2.46803
Q8K2Z4	**CND1 Condensin complex subunit 1**	**1.64896192**	**0.02795**	**2**
Q8K2Z4	AIIDEFEQKLR	1.45391243	2	2.36961
Q8K2Z4	LLESFENMTSQTSLIDLDIGGK	1.95558825	2	2.44545
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**1.35917818**	**0.12807**	**2**
Q8K3J1	ILMWTELIR+Oxidation(2	1.9266557		
Q8K3J1	LCEAICPAQAITIEAEPR	1.29664462	3	4.90856
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.52324638**	**0.35128**	**6**
Q8K442	EDVQPLSQAFFK	1.63636457	2	2.89183
Q8K442	GQITAILGHSGAGK	1.28631643	2	3.74836

Q8K442	IDDFIHSLEQQNIALEVDAFGTR	1.35378217	3	4.09428
Q8K442	LTGVCPQCNVQFDFLTVR	1.95938806	2	2.83254
Q8K442	NTQNILVQNLSGGQK	1.18711418	2	2.96951
Q8K442	STLLNVLSGLCVPTK	1.56720497	2	3.79413
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.95644629**	**0.81878**	**12**
Q8K4C0	CCLEEGLEPVCFER	0.96882825	2	4.39759
Q8K4C0	FDHEMFGLKPK	1.17139381	2	3.32328
Q8K4C0	GYPIDILLSSR	1.24345775	2	3.27162
Q8K4C0	HSALGQHPTINDDLPNR	1.0633961	2	4.99735
Q8K4C0	IAVIGSGASGLTCIK	1.52787037	2	4.19835
Q8K4C0	KLPSQSEMMAEINK	0.94839584	2	3.8894
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.86804	3	4.74939
Q8K4C0	KTILTTEDR	0.86559204	2	2.80174
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	1.56208467	3	3.77859
Q8K4C0	SDDIGGLWR	1.05500305	2	3.02784
Q8K4C0	VFPPNLEKPTLAIIGLIQPLGAIMPISELQGR	1.47230909	4	5.0199
Q8K4C0	WATQVFK	1.56942585	1	1.9542
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.08692095**	**0.92775**	**3**
Q8K4T4	EVLNLTK	0.99943893	1	2.1182
Q8K4T4	IEELEETNKSLQK	1.70990316	2	2.558
Q8K4T4	IHELMNK	1.2273517	1	2.09297
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.08199158**	**0.9999**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	1.08202737	2	3.83324
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.02464354	2	5.80955
Q8K4Z5	**SF3A1 Splicing factor 3A subunit 1**	**1.60142043**	**0.12951**	**2**
Q8K4Z5	HKVSEFKEGK	1.57220281	2	2.30061
Q8K4Z5	IGEEEIQKPEEK	1.60178185	2	2.60164
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.16208852**	**0.99557**	**5**
Q8K586	FNVWDTAGQEK	1.17543862	2	3.31169
Q8K586	HLTGEFEK	1.08763151	1	2.04382
Q8K586	LVLVGDGGTGK	1.03742097	2	2.37278
Q8K586	NLQYYDISAK	1.10654231	1	2.13557
Q8K586	VCENIPIVLCGNK	1.09734692	2	3.72718
Q8K5B3	**MCFD2 Multiple coagulation factor deficiency protein 2 homolog**	**1.19489509**	**0.41324**	**2**
Q8K5B3	DDDKNNDGYIDYAEFAK	0.9409336	2	4.35357
Q8K5B3	STVHDQEHIMEHLEGVINQPEAEMSPQELQLHYFK	2.13722165	4	5.87028
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.99608864**	**0.40308**	**3**
Q8QZY1	VFSDEVQQQAQLSTIR	0.88150306	2	3.85333
Q8QZY1	VSGGPSLEQR	1.63328176	2	2.62712
Q8QZY1	VYEIQDIYENSWTK	1.54135503	2	3.92647
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**0.75892395**	**0.35813**	**6**
Q8R081	ASLNGADIYSGCCTLK	4.60366642	2	2.95599
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	0.99325111	3	5.0295
Q8R081	SDALETLGFLNHYQMK	1.2137923	2	3.68698
Q8R081	SKPGAAMVEMADGYAVDR	0.58590524	2	3.89393
Q8R081	SSSGLLEWDSK	0.85382121	2	2.32781
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	1.01768398	3	7.14297
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.14327878**	**0.96953**	**5**
Q8R0F9	FDNTYSLLHTK	1.05133127	2	3.13002
Q8R0F9	GSSHQVENEILFPGCVLR	1.0063698	2	4.7551
Q8R0F9	VCEMLLHECELQSQK	1.22853334	2	4.97628
Q8R0F9	VGYTAEVLLPDK	0.99090358	2	2.95609

Q8R0F9	VGYTAEVLLPDKACEEK	1.14672154	2	2.44847
Q8R0K2	**TRI31 E3 ubiquitin_protein ligase TRIM31**	**1.29137711**	**0.43481**	**2**
Q8R0K2	LQSSSMELLKDIKDALSR	1.26375288	2	2.552
Q8R0K2	QRLDEEESFLLSR	2.20662269	2	2.43184
Q8R164	**BPHL Valacyclovir hydrolase**	**1.05592275**	**0.04634**	**3**
Q8R164	FADEFNR	2.02482407	2	2.36687
Q8R164	FTLVAWDPR	1.36428241	2	2.98209
Q8R164	TDFAPQLQSLNK	1.05397024	2	3.728
Q8R1F5	**HYI Putative hydroxypyruvate isomerase**	**1.3773418**	**0.56078**	**2**
Q8R1F5	GDTVEGLSWLR	1.32686063	2	3.14266
Q8R1F5	GEMGLGAVPGR	1.86865711	2	2.53749
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**1.16845599**	**0.99242**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	1.55492753	2	4.48738
Q8R1V4	QLLDQVEQIQK	1.00707457	2	2.89605
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**1.17604159**	**0.78597**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	1.20797143	2	3.94613
Q8R3Q6	NCIAQTSAVVK	1.1739975	2	2.79186
Q8R491	**EHD3 EH domain_containing protein 3**	**1.3477068**	**0.02579**	**6**
Q8R491	ADQIETQQLMR	1.69143975	2	2.61221
Q8R491	GGAFEGTLQGPFGHGYGEGAGEGIDDAEWVVAR	4.58500076	3	4.333
Q8R491	LDISDEFSEVIK	1.62491302	2	3.63764
Q8R491	LFEAEEQDLFK	2.17623463	2	3.49502
Q8R491	MQDQLQAQDFSK	0.92857216	2	3.83833
Q8R491	QEETQRPVQMVK	1.39808161	2	2.7539
Q8VBU2	**NDRG2 Protein NDRG2**	**0.91573843**	**0.69361**	**6**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.88477369	3	5.11384
Q8VBU2	LDPTQTSFLK	1.20501016	1	2.08861
Q8VBU2	MADSGGQPQLTQPGK	1.31245823	2	3.1336
Q8VBU2	SLITHAPNLENIELYWNSYNNR	1.26462646	3	4.667
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.79597381	2	4.517
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.34088961	2	4.74081
Q8VC12	**HUTU Urocanate hydratase**	**1.13669728**	**0.00069**	**9**
Q8VC12	DHHDVSGTDSPFR	1.93700822	2	2.68359
Q8VC12	HQLVVGSQAR	0.97063582	2	2.91315
Q8VC12	LLALEFAQELR	2.90414632	2	3.96146
Q8VC12	LQYMDNIR	1.44586305	2	2.42834
Q8VC12	LVITNGMVIPNYSSR	1.51849772	2	3.82513
Q8VC12	MMLSWDVSNGVAR	1.31040498	2	3.17367
Q8VC12	VAIAVAINQAIASGK	2.82573705	2	4.00164
Q8VC12	VFVTSGLGGMSGAQAK	1.26476239	2	4.54127
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9	0.87705579		
Q8VDC1	**FYCO1 FYVE and coiled_coil domain_containing protein 1**	**1.19720207**	**0.53585**	**2**
Q8VDC1	GLELQVMQLQQEK	1.19725121	2	2.39016
Q8VDC1	MLVSRQGGQLQVEK+Oxidation(0	0.77476732		
Q8VDG5	**PPCS Phosphopantothenate__cysteine ligase**	**1.15651691**	**0.56475**	**2**
Q8VDG5	FLDNFSSGR	1.76412701	2	2.45637
Q8VDG5	LETDPDIIISR	1.05256255	2	2.58724
Q8VE11	**MTMR6 Myotubularin_related protein 6**	**0.73610172**	**0.49865**	**2**
Q8VE11	TMKGFMVLIEK+Oxidation(1	0.73610172		
Q8VE11	TMKGFMVLIEK+Oxidation(5	0.73610172		
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**1.20595507**	**0.97904**	**5**
Q8VED5	FLEQQNKVLETK	1.21375309	2	3.66851
Q8VED5	NKYEDEINK	1.08695208	2	2.95454
Q8VED5	NKYEDEINKR	1.03819485	3	3.33708

Q8VED5	NLDLDSIIAEVK	2.92656041	2	3.541
Q8VED5	YEDEINK	1.41271276	1	2.34168
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.11924765**	**0.01334**	**12**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.54126216	3	4.77499
Q8VEK3	FIEIAAR	1.51752122	1	1.90702
Q8VEK3	GYFEYIEENK	1.02837347	2	3.37234
Q8VEK3	LLEQYKEESK	1.38605724	2	3.26815
Q8VEK3	LLEQYKEESKK	1.25681913	2	3.66877
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	0.83591701	3	4.75506
Q8VEK3	NFILDQTNVSAAAQR	0.97594041	2	4.89524
Q8VEK3	NGQDLGVAFK	1.13463805	2	2.40092
Q8VEK3	TCNCETEDYGEK	1.26010914	2	3.57562
Q8VEK3	VSELKEELK	1.7668262	2	2.89193
Q8VEK3	VSELKEELKK	1.42519962	2	2.68919
Q8VEK3	YNILGTNTIMDK	1.35531757	2	3.656
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**1.11234768**	**0.96528**	**8**
Q8VHE9	ATVQSVLLDSAGR	1.12551246	2	3.86813
Q8VHE9	FLPLPLTQLLNK	0.79777875	2	3.22782
Q8VHE9	GATYGADHDLAR	1.14589576	2	3.26791
Q8VHE9	NLYSDLQALGSK	0.94539468	2	3.6197
Q8VHE9	RPPEPLVTDK	1.0710193	2	2.95453
Q8VHE9	RPPEPLVTDKEAR	1.15500242	3	4.20689
Q8VHE9	VESVTGGSPLTNQYYLAAHR	1.29247685	2	3.9792
Q8VHE9	VVAHGVSHAILLK	2.01158803	2	2.87402
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**1.28066174**	**0.05859**	**4**
Q8VHF5	AYAEGINR	1.18462709	2	2.51807
Q8VHF5	EGSSIGAIDSK	1.66024018	2	2.35077
Q8VHF5	GLVYETSVLDPDEGIR	2.18007815	2	4.34381
Q8VHF5	GYSIPECQK	1.40830908	2	2.80161
Q8VHK7	**HDGF Hepatoma_derived growth factor**	**1.26808121**	**0.32601**	**3**
Q8VHK7	GFSEGLWEIENNPTVK	0.55159157	2	3.70253
Q8VHK7	NSTPSEPDSGQGPPPEEEEGEEEAAKEEAEAQGVR	1.27397674	3	6.10673
Q8VHK7	SCAEEPEVEPEAHEGDGDKK	1.40473697	3	3.9406
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.53468573**	**0.00392**	**4**
Q8VHT6	FAHDFLFTPVEASLLAPQTK	3.78401963	2	4.36773
Q8VHT6	ILDLGSGSGR	1.07712693	2	2.90833
Q8VHT6	SLQNVHEEVISR	1.9724797	2	3.20885
Q8VHT6	TSADLQTNACVTPAK	1.37537973	2	3.87555
Q8VHX6	**FLNC Filamin_C**	**1.19663931**	**0.40991**	**3**
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.18790077	2	3.97345
Q8VHX6	IECDDKGDGSCDVR	1.46026432	2	3.44393
Q8VHX6	LIALLEVLSQK	3.08444665	2	2.62857
Q8VI04	**ASGL1 L_asparaginase**	**0.97267283**	**0.98619**	**5**
Q8VI04	DLSAGAVSAVRCIANPVK	0.98925174	2	2.35339
Q8VI04	FAADMGIPQTPAEK	0.9180047	2	3.44424
Q8VI04	GNLAYATSTGGIVNK	0.95485975	2	4.35895
Q8VI04	NSGTVGAVALDCK	1.25699357	2	3.29069
Q8VI04	TVDEAATLALDYMK	1.21780323	2	3.57368
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.03174807**	**0.47631**	**5**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.15619608	2	4.01386
Q8VID1	LAEDGAHVVISSR	1.15948403	2	3.70507
Q8VID1	NFAAELAPK	0.74082812	2	2.45876
Q8VID1	TALLGLTK	1.38436839	2	2.41564
Q8VID1	VNCLAPGLIK	1.79430752	2	2.51608
Q8VIF7	**SBP1 Selenium_binding protein 1**	**1.26945704**	**0.72503**	**11**

Q8VIF7	CGPGYATPLEAMK	0.81225686	2	3.10767
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.3534122	2	5.42326
Q8VIF7	GGFVLLDGETFEVK	1.69959064	2	3.90905
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	1.3797359	2	3.77977
Q8VIF7	HEIIQTLQMK	1.20498711	2	2.84595
Q8VIF7	HNIMVSTEWAAPNVFK	1.57429665	2	4.60945
Q8VIF7	LTGQIFLGGSIVK	1.24745183	2	3.01877
Q8VIF7	NEGGTWSVEK	1.0821465	2	3.16176
Q8VIF7	NTGIEAPDYLATVDVDPK	1.03544618	2	4.16405
Q8VIF7	QYDISNPK	1.08105573	1	2.11613
Q8VIF7	VIEPNEIHAK	1.27797891	2	2.96786
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**0.83659755**	**0.94023**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	0.82551081	2	3.2066
Q8VIJ6	MEELHSQEMQK	0.91314228	2	3.7953
Q8VIJ6	RMEELHSQEMQK	1.07528392	2	3.90017
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**0.88936583**	**0.52426**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	1.2439256	2	5.40929
Q91VA0	AILPFDLQIIDEK	1.14081815	2	3.85738
Q91VA0	GNILPPNTEGYIGIR	0.70691486	2	2.90914
Q91VA0	KVEFVSELPK	0.62349585	2	2.90151
Q91VA0	NKEFGQL	0.8858349	1	2.1487
Q91VA6	**PDIP2 Polymerase delta_interacting protein 2**	**0.96435824**	**0.79704**	**2**
Q91VA6	VLETVGVFEVPK	0.86233041	2	3.40001
Q91VA6	VTVIPFYMGMR+Oxidation(9	1.51584865		
Q91VM5	**RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1**	**1.31494756**	**0.34615**	**2**
Q91VM5	LFIGGLNTETNEK	1.05508778	2	2.79149
Q91VM5	VEQATKPSFESGR	1.31499256	2	3.93891
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.87834556**	**0.99503**	**2**
Q91VM9	IIAINVNDPEAEK	0.85091364	2	3.21823
Q91VM9	MEIATEEPLNPIK	1.13225339	2	4.43456
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**1.17951551**	**0.23902**	**6**
Q91W43	AGHQLQHDLFFDTLK	2.14210934	2	3.02957
Q91W43	DISLVHSMIPLGSCTMK	0.9127883	2	2.72649
Q91W43	EMLQALGLASIDELIEK	1.59553843	2	2.54451
Q91W43	IDDIYGDQHLVCTCPPMEVYESPFSEQK	1.3235371	3	4.43025
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	3.12992161	3	4.64839
Q91W43	VSFQPNSGAQGEYAGLATIR	1.49985264	2	5.20353
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.19738091**	**0.18288**	**3**
Q91W90	GTVLALTEK	1.60023468	2	2.39144
Q91W90	SFEDTIAQGITFVK	0.95056649	2	4.02806
Q91W90	VDCTQHYAVCSEHQVR	1.22037491	3	4.48855
Q91WL5	**CP4CA Cytochrome P450 4A12A**	**1.1909563**	**0.82152**	**2**
Q91WL5	FELLPDPTR	1.22820734	2	2.66626
Q91WL5	IQLQDEEELEK	1.19093537	2	2.48758
Q91X77	**CY250 Cytochrome P450 2C50**	**0.89206075**	**0.22437**	**5**
Q91X77	EHEESLDVTIPR	0.89175099	2	2.30784
Q91X77	IKEHEESLDVTIPR	1.04621256	3	3.66349
Q91X77	NFLLEK	0.72564532	1	2.10253
Q91X77	NYFIPK	0.80201682	1	1.92056
Q91X77	YALLLLLK	1.59788929	2	2.92146
Q91X78	**ERLN1 Erlin_1**	**1.07556098**	**0.63315**	**4**

Q91X78	DLNTMAPGLTIQAVR	0.94779616	2	3.44246
Q91X78	ISEIEDAAFLAR	1.07556161	2	2.9784
Q91X78	RISEIEDAAFLAREK	1.70670051	2	2.30733
Q91X78	SVQTTLQTDEVK	0.84309998	2	3.09624
Q91Y78	**UCHL3 Ubiquitin carboxyl_terminal hydrolase isozyme L3**	**1.10949351**	**0.99389**	**2**
Q91Y78	FLEESVAMSPEER	1.23149256	2	3.26073
Q91Y78	HLENYDAIR	1.10936466	2	2.58245
Q91Y81	**SEPT2 Septin_2**	**1.06614647**	**0.78442**	**4**
Q91Y81	ASIPFSVVGSNQLIEAK	1.27283018	2	2.66018
Q91Y81	ILDEIEEHSIK	1.05465374	2	2.65335
Q91Y81	KVENEDMNKDQILLEK	1.20074864	3	3.69238
Q91Y81	LTVVDTPGYGDAINSR	1.02194532	2	4.37815
Q91YP0	**L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial**	**1.0566123**	**0.8427**	**3**
Q91YP0	LIQQEDIK	1.13128873	2	2.40078
Q91YP0	LIVAVEQEEIPR	1.36112843	2	2.80304
Q91YP0	NAPSPAATSSLAISR	0.90897762	2	3.29706
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.30853781**	**0.02119**	**10**
Q91YT0	GAGAYICGEETALIESIEGK	1.6090403	2	2.57513
Q91YT0	GDARPAEIDSLWEISK	1.30353849	2	2.87714
Q91YT0	GEFYNEASNLQVAIR	1.38559574	2	3.55235
Q91YT0	GGAGFPTGLK	1.32961444	2	2.37067
Q91YT0	HFRPELEDR	1.57768149	2	2.33197
Q91YT0	KTSFGSLKDEDR	1.48032052	2	3.48027
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.85822838	3	4.19768
Q91YT0	LVEGCLVGGR	1.74937745	2	2.7434
Q91YT0	TSFGSLKDEDR	1.50666983	2	2.49589
Q91YT0	YLVVNADEGEPGTCK	1.06744046	2	4.94173
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.02331444**	**0.08617**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	1.29513035	3	6.77683
Q91Z53	LLDAAGANLR	0.96214215	2	3.26251
Q91Z53	NCVILPHIGSATYK	0.90912683	2	3.70573
Q91Z53	NTMSLLAANNLLAGLR	2.22515689	2	4.73976
Q91Z53	RLPEAIEEVK	0.93824804	3	3.30049
Q91Z53	VISTLSVGVDHLALDEIK	1.64218128	2	4.75026
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**1.09202283**	**0.46669**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	1.6870741	2	4.69947
Q91ZJ5	GGTLTQYEGK	1.07925582	2	2.37103
Q91ZJ5	GLPDNISSVLNK	1.40571919	2	3.37689
Q91ZJ5	GTVIIIANHGDR	1.27783094	2	3.00819
Q91ZJ5	IDIPPGAVLENK	1.64916108	2	2.87701
Q91ZJ5	IQRPPEDSIQPYEK	1.34396536	3	5.17817
Q91ZJ5	LNGGLGTSMGCK	1.71383179	2	2.96923
Q91ZJ5	LVEIAQVPK	1.3790758	2	3.45131
Q91ZJ5	NENTFLDLTVQQIEHLNK	1.19776681	2	5.0521
Q91ZJ5	RCEFVMEVTNK	0.9967747	2	2.37589
Q91ZJ5	RFESIPDMLELDHLTVSGDVTFGK	1.77550695	3	3.33507
Q91ZJ5	SFENSLGINVPR	1.08936659	2	3.44256
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	1.07177002	2	5.31327
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.14006904	2	4.49399
Q91ZU6	**DYST Dystonin**	**1.04524197**	**0.42616**	**2**
Q91ZU6	LDMLQQIATR+Oxidation(2	1.43661415		

Q91ZU6	SAETNIDQDITNLK	0.7847953	2	2.37363
Q91ZV0	**MIA2 Melanoma inhibitory activity protein 2**	**1.92991372**	**0.14171**	**2**
Q91ZV0	CGDLECETLISRVLALR	1.93153796	2	2.41905
Q91ZV0	KMLDQDDIVENDK+Oxidation(1	1.58671437		
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.01007155**	**0.82797**	**6**
Q91ZX7	CLQGACVVNK	1.4325964	2	2.43256
Q91ZX7	GCHVNECLSR	1.00330971	2	2.70352
Q91ZX7	ILQEDFTCR	0.92223202	2	2.4945
Q91ZX7	MYDAQQQQVGTNK	1.62078698	2	4.43759
Q91ZX7	TVLWPNGLSLDIPAGR	0.62536677	2	2.49056
Q91ZX7	VFFTDYGQIPK	0.99512177	2	3.27737
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.61808751**	**0.02097**	**2**
Q920A6	GLAEVSDIAEQVLNAVNK	1.62139853	3	5.64574
Q920A6	NTDGVNFYNILTK	1.45515866	2	2.91284
Q920D2	**DYR Dihydrofolate reductase**	**1.27340365**	**0.10231**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	1.57433179	2	4.6773
Q920D2	LIEQPELASK	1.03504089	2	3.00358
Q920D2	LLPEYPGVLSEIQEEK	1.38807724	2	3.70405
Q920D2	NGDLPWPLLR	1.22038486	2	3.2312
Q920F3	**KHDR2 KH domain_containing_ RNA_binding_ signal transduction_associated protein 2**	**1.11089509**	**0.34969**	**2**
Q920F3	LQEETGAKMSILGKGSMR+Oxidation(8	1.71821623		
Q920F3	MSHALEEIKK	1.10799504	1	2.2597
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**1.0939755**	**0.95926**	**5**
Q920F5	ADLLEAQALK	1.11642274	2	2.33896
Q920F5	EIAEVTGDPVHESLK	1.10427216	2	3.43761
Q920F5	ISECEAVHPVK	1.13169689	2	3.35816
Q920F5	LCSGLTASAMDELLR	0.79619211	2	2.30838
Q920F5	WLLGLLNVQGK	0.9901324	2	3.38123
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.1090023**	**0.82011**	**4**
Q920J4	AGCECLNESDEHGFDNCLR	1.13733946	3	4.03823
Q920J4	IDQYQGADAVGLEEK	0.99390283	2	4.82367
Q920J4	QHLENDPGSNEDTDIPK	1.47218573	2	2.38512
Q920J4	SEPTQALELTEDDIKEDGIVPLR	1.87017795	2	3.40548
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.07725917**	**0.91931**	**18**
Q920L2	ACALSIAESCRPGDK	0.87486792	2	2.87019
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.34227869	3	4.5069
Q920L2	ANAGEESVMNLDK	1.11212865	2	3.64589
Q920L2	GEGGILINSQGER	1.20371272	2	4.06212
Q920L2	GVIALCIEDGSIHR	1.17490647	2	3.35516
Q920L2	HTLSYVDTK	1.43141972	2	2.4893
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.1562608	3	6.76002
Q920L2	IDEYDYSKPIEGQQK	0.92599893	2	4.47603
Q920L2	KHTLSYVDTK	0.81564614	2	2.76582
Q920L2	NTIIATGGYGR	1.22987958	2	2.78549
Q920L2	SMQSHAAVFR	1.26829938	2	2.69007
Q920L2	TGHSLLHTLYGR	1.02096953	2	2.95551
Q920L2	TLNEADCATVPPAIR	1.07902904	2	3.69084
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.11175556	2	5.69867
Q920L2	VGSVLQEGCEK	1.20696461	2	3.54096
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	1.71391093	3	4.92184
Q920L2	VSQLYGDLQHLK	1.24408279	2	3.49626
Q920L2	VTLDYRPVIDK	1.03631299	2	2.97589

Q920P0	**DCXR L_xylulose reductase**	**1.03044832**	**0.96283**	**7**
Q920P0	ALTNHTVYCSTK	2.45701729	2	3.15117
Q920P0	AVVQVSQIVAR	1.23818871	2	3.16954
Q920P0	GVPGAIVNVSSQASQR	1.02632752	2	5.78407
Q920P0	SSMTTGSALPVDGGFLAT	1.1660594	2	2.85738
Q920P0	STVLALQAAGAQVVAVSR	1.13947643	2	3.9189
Q920P0	TREDLDSLVR	1.45582575	2	2.96284
Q920P0	VNAVNPTVVMTPMGR	1.5060403	2	3.44197
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.15223519**	**0.00024**	**5**
Q921F2	FGGNPGGFGNQGGFGNSR	1.11511521	2	4.41305
Q921F2	FTEYETQVK	1.44003714	2	2.63626
Q921F2	GISVHISNAEPK	0.86163951	2	2.52892
Q921F2	KDLKTGHSK	1.15116862	2	2.4425
Q921F2	TSDLIVLGLPWK	1.58694165	2	3.27269
Q921M3	**SF3B3 Splicing factor 3B subunit 3**	**1.00525588**	**0.88209**	**3**
Q921M3	FLAVGLVDNTVR	1.5433559	2	2.83468
Q921M3	LPPNTNDEVDEDPTGNK	0.88222056	2	2.6862
Q921M3	TVLDPVTGDLSDTR	1.02093332	2	2.66564
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.19456941**	**0.0005**	**7**
Q922F4	ALTVPELTQQMFDAK	1.39919752	2	3.98424
Q922F4	ALTVPELTQQMFDAK+Oxidation(10	1.20456038		
Q922F4	GHYTEGAELVDSVLDVVR	1.35699463	2	6.63607
Q922F4	IREEYPDR	1.31235919	2	2.97651
Q922F4	MASTFIGNSTAIQELFK	1.76555582	2	4.34616
Q922F4	NMMAACDPR	1.55922753	2	2.75148
Q922F4	NSSYFVEWIPNNVK	1.42707769	2	4.74812
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.0819437**	**0.99431**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4	1.08298155		
Q922J3	HEEILQNLQKMLADTEDK	1.06026302	2	2.33487
Q923D2		**1.35751935**	**0.88493**	**4**
Q923D2	HDLGHFMLR	1.15660778	3	3.3618
Q923D2	LQDVTDDHIR	1.35943454	2	3.16677
Q923D2	TGLTTLAQAVQAGYEVTVLVR	1.34955224	3	4.15661
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	1.50276611	3	4.19365
Q923K9	**A1CF APOBEC1 complementation factor**	**1.36412685**	**0.01838**	**3**
Q923K9	LAPQILEEICQK	2.54751792	2	2.90155
Q923K9	TGYSLVQENGQR	1.1695852	2	2.51915
Q923K9	VTEGVVDVIVYPSAADK	1.23222624	2	3.78576
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**1.06160987**	**0.00047**	**2**
Q923M1	SAVYPTSAVQMEAALK	1.36801717	2	4.21521
Q923M1	VISAEEALPGR	1.10234797	2	2.91798
Q923V8	**SEP15 15 kDa selenoprotein**	**1.1315391**	**0.41487**	**3**
Q923V8	GCCQEEAQFETK	1.19325221	2	4.15683
Q923V8	LLDDNGNIAEELSILK	1.13112894	2	4.0781
Q923V8	WNTDSVEEFLSEK	2.05411539	2	2.76854
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**2.33720772**	**0.11184**	**5**
Q924C3	AEYLHTWGGLLPVISK	2.37167655	3	3.91723
Q924C3	ELESPAAASLLAPMDLGEEPLEK	1.75002836	2	4.40713
Q924C3	GQPIWVTANHQEVR	1.45038755	2	3.3361
Q924C3	SGTYFWPGSDVEIDGILPDIYK	1.82235954	2	2.51833
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	1.69471728	2	3.87963
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**0.87718776**	**0.96892**	**14**
Q924S5	AGVTCIILPAENR	0.96320728	2	2.31455

Q924S5	AQLSATVLTLLIK	1.50473314	2	3.45383
Q924S5	AQSVLEEDHYGMEDVK	1.07273417	2	4.26816
Q924S5	EHQEALAVER	1.28307827	2	2.51945
Q924S5	ELGLEKDDKDAIEEK	1.49156224	2	3.74027
Q924S5	FSVGGMTDVAEIK	1.17644578	2	3.07037
Q924S5	GYQGDPSSALLELLDPEQNANFLDHYLDVPVDLSK	1.31515474	3	5.09929
Q924S5	HVMDVVDEELSK	0.84846603	2	3.62586
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.38168869	3	5.92571
Q924S5	MEMINVSGYVAQEK	1.16191316	2	2.66099
Q924S5	QLEVEPEGLEPEAENK	1.12722102	2	4.35001
Q924S5	QSDENLDLAR	1.272925	2	2.46775
Q924S5	TENPLVLIDEVDK	1.26281183	2	2.99689
Q924S5	VLEFIAVSQLR	1.23413925	2	2.77648
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**1.24849904**	**0.51608**	**2**
Q924W5	ELDMKEKELQEK	2.97700898	2	2.373
Q924W5	TKEQINQGEERLTELK	1.1473841	2	2.55773
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.37622061**	**1.3E-09**	**4**
Q99020	EYFGQFGEIEAIELPIDPK	2.40745289	2	3.56033
Q99020	FGEVVDCTIK	0.60849549	2	3.20895
Q99020	IFVGGLNPEATEEK	1.76826651	2	4.17422
Q99020	MFVGGLSWDTSK	1.51840823	2	2.55725
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**1.22988263**	**0.90488**	**2**
Q99068	EELKHFEAKIEK	1.17783124	2	2.43955
Q99068	HVESIGDPEHISR	1.23228265	3	4.12023
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.4673067**	**0.21869**	**3**
Q99JI4	GAEILEVLHSLPAVR	1.85938622	2	2.98469
Q99JI4	RLDEELEDAEK	1.8502948	2	3.18615
Q99JI4	VNEIVETNRPDSK	1.4562334	2	3.70418
Q99JW2	**ACY1 Aminoacylase_1**	**1.16425327**	**0.6712**	**3**
Q99JW2	FIEDTAAEK	1.16356347	2	2.69077
Q99JW2	SVSIQYLEAVR	1.74206054	2	2.56252
Q99JW2	TIHMTFVPDEEVGGHK	1.00714193	3	3.91934
Q99KK9	**SYHM Probable histidyl_tRNA synthetase_ mitochondrial**	**1.33805112**	**0.21143**	**2**
Q99KK9	IIAELWDAGIKAEMLYK+Oxidation(13	1.08400675		
Q99KK9	YDLTVPFAR	1.50992674	2	2.36435
Q99KN9	**EPN4 Clathrin interactor 1**	**1.04639793**	**0.96509**	**3**
Q99KN9	GEFKDEEETVTTK	1.03776068	2	3.58409
Q99KN9	HIHITQATETTTTR	1.21801229	2	3.35389
Q99KN9	IGSTIDDTISK	1.04638657	2	2.55054
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.89794466**	**0.95422**	**3**
Q99L04	ATAQEAQSLGGR	0.87824246	2	3.32304
Q99L04	CVPVVCDSSQESEVK	1.18451393	2	4.30699
Q99L04	GQVCVVTGASR	2.40437055	2	2.812
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.62297375**	**0.45594**	**5**
Q99LF4	GLGHQVATDALVAMEK	1.15968469	2	3.69262
Q99LF4	NLDFQDVLDK	1.75768583	2	3.08327
Q99LF4	NVTDVVNTCHDAGISK	1.39655797	2	4.33442
Q99LF4	NYNDELQFLDK	1.81771984	2	3.18358
Q99LF4	TNLDESDVQPVK	1.39863252	2	3.46662
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.44183105**	**0.07555**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11	1.44183105		

Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5	1.44183105		
Q99M73	**KRT84 Keratin_ type II cuticular Hb4**	**1.08816418**	**0.99875**	**2**
Q99M73	CKLADLEGALQQAKQDMAR	1.01925632	2	2.67274
Q99M73	EYQELMNVK	1.09181466	1	2.09333
Q99M87	**DNJA3 DnaJ homolog subfamily A member 3_ mitochondrial**	**0.94426583**	**0.44831**	**2**
Q99M87	GGPSVDPEELFR	1.31955118	2	2.3512
Q99M87	GSIITNPCVVCR	0.94426226	2	2.97703
Q99ML5	**PCYOX Prenylcysteine oxidase**	**1.34201854**	**0.17035**	**2**
Q99ML5	ELGLSSVPASGGLVGVYNGK	1.30687039	2	2.97188
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	1.36160452	3	4.82437
Q99MS0	**S14L2 SEC14_like protein 2**	**1.05349829**	**0.9998**	**6**
Q99MS0	AGEMTEVLPNQR	1.01724164	2	3.56896
Q99MS0	AGEMTEVLPNQR+Oxidation(3	1.29251108		
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	0.8994834	3	4.96753
Q99MS0	INYGGDIPK	1.01319556	2	2.41994
Q99MS0	QQYEHSVQISR	1.09634737	2	2.39323
Q99MS0	YNSHMVPEDGTLTCSEPGIYVLR	1.1148208	3	3.57075
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.97855935**	**0.99975**	**8**
Q99MZ8	GFSVVADTPELQR	0.86904826	2	3.64757
Q99MZ8	MGPSGGEGIEPER	1.02372455	2	3.35693
Q99MZ8	MGPSGGEGIEPERR	1.14201787	2	2.42232
Q99MZ8	QQSELQSQVR	1.00693413	2	2.98442
Q99MZ8	QSFTMVADTPENLR	0.88412812	2	3.56272
Q99MZ8	TGDTGMLPANYVEAI	1.62502642	1	2.20438
Q99MZ8	TQDQISNIK	1.00261766	2	2.70913
Q99MZ8	YHEEFEK	1.03173579	2	2.41015
Q99N27	**SNX1 Sorting nexin_1**	**1.2777092**	**0.31632**	**2**
Q99N27	LQEVECEEQR	0.98989222	2	2.49566
Q99N27	SLAMLGSSEDNTALSR	1.73023975	2	3.11309
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**1.41741627**	**0.38179**	**4**
Q99NA5	ENTEGEYSGIEHVIVDGVVQSIK	1.24824888	3	3.34318
Q99NA5	HMGLFDHAAK	2.16166474	3	3.41
Q99NA5	IEAACFATIK	1.33636596	2	2.61438
Q99NA5	NVTAIQGPGGK	1.39238757	2	2.54209
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**1.02615203**	**0.97862**	**2**
Q99NB7	GSISNTNVEALK	1.05947308	2	2.56565
Q99NB7	KGSISNTNVEALK	0.82806867	2	3.25764
Q99NB9	**SF3B1 Splicing factor 3B subunit 1**	**1.19973524**	**0.13904**	**3**
Q99NB9	EWMRICFELLELLK+Oxidation(2	0.50934919		
Q99NB9	GDTPGHATPGHGGATSSAR	1.87502571	3	3.77355
Q99NB9	WDQTADQTPGATPK	0.44756003	2	2.515
Q99P39	**NFS1 Cysteine desulfurase_ mitochondrial**	**1.17057125**	**0.62429**	**2**
Q99P39	AIGTDEDLAHSSIR	0.62697867	2	2.71838
Q99P39	VEALQSGGGQER	1.17479422	2	2.99854
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**1.0733277**	**0.67618**	**9**
Q99PF5	AINQQTGAFVEISR	1.24760959	2	3.49093
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	1.19564924	2	6.94084
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.97381233	2	4.96503
Q99PF5	IGQQPQQPGAPPQQDYTK	0.97219926	2	4.04874
Q99PF5	IINDLLQSLR	1.75812903	2	3.1882
Q99PF5	SVSLTGAPESVQK	0.96931349	2	2.56959
Q99PF5	VGGGIDVPVPR	0.98670864	2	3.21116
Q99PF5	VQISPDSGGLPER	0.91322689	2	2.48671
Q99PF5	VQQACEMVMDILR	1.3063192	2	2.34838
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.15100856**	**0.00108**	**20**

Q99PL5	AMEALALAER	0.70790955	2	2.93254
Q99PL5	DALNQATSQVESK	1.48829697	2	3.6129
Q99PL5	EAEETQNSLQAECDQYR	1.37941158	2	5.36002
Q99PL5	EHTSHLEAELEK	1.38846731	2	3.49551
Q99PL5	EQEIAAVQAR	1.90967228	2	2.48333
Q99PL5	GELESSDQVR	1.68507825	2	3.13698
Q99PL5	HLEDIVEK	1.68776284	2	2.38287
Q99PL5	HMAAASAECQNYAK	1.47656781	2	4.47872
Q99PL5	HMAAASAECQNYAK+Oxidation(1	1.24505127		
Q99PL5	IQEELEK	1.13562997	1	2.33836
Q99PL5	LIEILSEK	1.57022824	1	2.15009
Q99PL5	LKELESQVSCLEK	1.18555746	2	4.27782
Q99PL5	LLATEQEDAAVAK	1.03020433	2	3.70648
Q99PL5	LQQENSILR	0.90403867	2	2.67997
Q99PL5	LQSSEVEVK	1.46879751	2	2.73472
Q99PL5	QLLLESQSQLDEAK	0.75246629	2	2.3343
Q99PL5	TILAETEGMLK	2.03346487	2	2.78465
Q99PL5	TLQEQLENGPNTQLAR	1.07627309	2	5.0442
Q99PL5	TLVSTVGSMVFSEGEAQR	1.42403443	3	4.52774
Q99PL5	VEPAVSSIVNSIQVLASK	1.13140108	2	4.42531
Q99PP2		**1.19937437**	**1.5E-06**	**69**
Q99PP2	AAGSLLTDECR	1.02562367	2	2.99542
Q99PP2	ADSAEYSVMTTGGQSSAK	3.2528707		
Q99PP2	AEVSELPSVVR	1.0298733	2	3.11991
Q99PP2	ALLTPVAIAAGR	1.60946743		
Q99PP2	ASMMGQRASLLTAR+Oxidation(2)Oxidation(3	1.00025984		
Q99PP2	AVAENQPFLIEAMTYR	1.22671717	2	3.5909
Q99PP2	AVDEAADALLK	1.39523456	2	2.59679
Q99PP2	DQMVKNNHFTLK+Oxidation(2	0.89723472		
Q99PP2	EEKIEKK	1.07663854		
Q99PP2	EELEKMK	0.6017598	1	1.93655
Q99PP2	EIAGATPYITAAEEK	2.02167469	2	3.12933
Q99PP2	EKMNKPELFNGGEKK	1.9301454		
Q99PP2	ELDSITPDITPGWK	2.23626249	2	2.938
Q99PP2	EQVIESRRQMQAVK	1.01650881		
Q99PP2	FEFEQDLSEK	1.32722606	2	2.6752
Q99PP2	FFRPHFLQAPGDLTVQEGK	1.25791857		
Q99PP2	FKLINSTNIR	2.12489069		
Q99PP2	GIEQAVQSHAVAEEEAR	1.33817851	2	4.97611
Q99PP2	GNIYSLNEGYAK	1.16356753	2	3.99729
Q99PP2	GSAAAAATTSTREAEGAERR	1.16841547		
Q99PP2	GVYSEETLR	1.28388009	2	2.46495
Q99PP2	HFVTISSPLATQIPQAVGAAYAAK	0.91881015	2	4.91951
Q99PP2	HLQTYGEHYPLDHFDK	0.9150221	3	3.69136
Q99PP2	HVIHTVGPIAVGQPTASQAAELR	1.3312127	3	5.34375
Q99PP2	IENWPFSIKPTLR	1.22449994		
Q99PP2	IGHHSTSDDSSAYR	0.9300311	3	4.53531
Q99PP2	INLSNNK	1.4216168		
Q99PP2	KAMQEINYGPSPDNSIKLVR	1.57863187		
Q99PP2	KGNIYSLNEGYAK	1.36870702	2	4.48673
Q99PP2	KLQHELEEAEER	3.11114583	3	4.11516
Q99PP2	LEFIQPNVISGIPIYR	0.57640565	2	2.43712
Q99PP2	LFDDRLESIIQK	1.21375309		
Q99PP2	LGDAVEQGVINNSVLGYFIGR	1.66599346	2	3.79255
Q99PP2	LIEVEGPNSLGK	1.3365685		
Q99PP2	LKLVMNNFIYQTK	1.02758019		
Q99PP2	LMQVNDTLTSEDAGLR	0.66801015		

Q99PP2	LQHELEEAEER	2.70169316	2	3.69329
Q99PP2	LQHELEEAEERADIAESQVNK	2.74190939	3	3.88024
Q99PP2	MKKNMEQTVK+Oxidation(4	1.23834151		
Q99PP2	MNLQDELDELK	1.05195184	2	2.3215
Q99PP2	MNLQDELDELK+Oxidation(0	0.69770998		
Q99PP2	MQQVEASLQPETLK+Oxidation(0	1.47871722		
Q99PP2	MQQVEASLQPETLKK+Oxidation(0	2.31100767		
Q99PP2	NESGLDSGRSQR	0.86151764		
Q99PP2	NNGYAISTPTSEQYR	0.61206517	2	3.81349
Q99PP2	QGQIINPSEDPHLPQEEVLK	0.39146487	2	2.64279
Q99PP2	QRAEQETKLK	1.73563401		
Q99PP2	QTCLKTVVLLTDNK	1.07941442		
Q99PP2	QTITAQNAAVQAVK	1.39975491	2	3.96323
Q99PP2	QYLLNQGWWDEEQEK	0.76642976	2	3.43724
Q99PP2	RAALQAEIEELR	3.83482902	2	3.75052
Q99PP2	RFSTEVGSDCVSDNDR	2.8490313		
Q99PP2	SCYDLSCHAR	1.32759171	2	2.33992
Q99PP2	SCYLSSLDLLLEHR	0.93564016	2	2.63077
Q99PP2	SLEDALNQTATVTR	0.67943596	2	4.42391
Q99PP2	SMTLLNTMDR	1.39835545	2	2.75019
Q99PP2	SVDEVNYWDK	0.61678907	2	2.56256
Q99PP2	TAMDNSEIAGEK	1.71787707	2	2.41014
Q99PP2	TAMDNSEIAGEKK	1.71424918	2	2.50219
Q99PP2	TLHVEEVVPSVIEPSFGLGR	1.20374532	3	3.68518
Q99PP2	TSSAEMPTIPLGSAVEAIR	0.77482927	2	3.88487
Q99PP2	TWTAADMAAQITR+Oxidation(6	1.07463044		
Q99PP2	VDDSSGSIGR	1.67705376	2	2.86711
Q99PP2	VDGNDVFAVYNATK	0.56823619	2	2.85901
Q99PP2	VMEAFEQAER	0.53103354	2	3.28826
Q99PP2	VTMQNKISEATQEEDRL+Oxidation(2	1.00392999		
Q99PP2	VVSQYHELVVQAR	2.76153499	2	3.52323
Q99PP2	YNENHQHGK	0.92794863		
Q99PP2	YSTSSSSGVTAGK	1.00146341	2	2.89248
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**1.55051409**	**0.43431**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(10	1.55051409		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)Oxidation(9	1.55051409		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.31773903**	**0.47251**	**2**
Q9CPQ1	FGVAEPR	1.30534438	2	2.45255
Q9CPQ1	NYDSMKDFEEMR	1.33550846	2	3.76256
Q9CQ75	**NDUA2 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2**	**1.8253282**	**0.26056**	**2**
Q9CQ75	EIRVHLCQRSPGSQGVR	1.9412208	2	2.33404
Q9CQ75	TVSLNNLSADEVTR	1.32463349	2	2.41194
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**1.13324249**	**0.61852**	**2**
Q9CQS8	FYTEDSPGLK	1.11169264	2	2.43288
Q9CQS8	TTSAGTGGMWR	1.37471564	2	2.34406
Q9CQZ5	**NDUA6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6**	**1.43777723**	**0.23965**	**3**
Q9CQZ5	EVPNTVHLMQLDITVK	1.76785766	2	2.49098
Q9CQZ5	FFHETETPRPK	1.48914222	2	2.90883
Q9CQZ5	VVDLLVIK	1.33884245	2	2.93884
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**0.94955692**	**0.99955**	**2**
Q9CRB9	VAEELALEQAK	0.92467503	2	3.64654
Q9CRB9	YEYHPVCADLQTK	0.98939778	2	3.78162

Q9CTN4	**RHBT3 Rho_related BTB domain_containing protein 3**	**1.48201766**	**0.68411**	**2**
Q9CTN4	ELASMNLDIVDLLK	1.48335544	2	2.5715
Q9CTN4	LKDSGDVSDIIEK	1.35771132	2	2.46851
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**1.1650043**	**0.89476**	**2**
Q9CW42	DLLLPITPPATNPLLQCR	0.8903792	3	3.51864
Q9CW42	GLSVSEAECTAMGLR	1.18571673	2	3.90406
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**0.9945686**	**0.72975**	**4**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.1688518	2	4.46849
Q9CWH6	ALLEVVQSGGK	1.02330632	2	3.03472
Q9CWH6	LTVEDPVTVEYITR	1.55732698	2	4.0456
Q9CWH6	LYQTDPSGTYHAWK	0.9246923	2	2.89263
Q9CWK8	**SNX2 Sorting nexin_2**	**1.12817568**	**0.85622**	**4**
Q9CWK8	AVNTQALSGAGILR	1.22338851	2	3.21274
Q9CWK8	QQQFENLDQQLR	1.05841376	2	2.51612
Q9CWK8	WEDAQITLLK	1.17154405	2	2.47912
Q9CWK8	YLESLVQTQQQLIK	1.25932611	2	4.00882
Q9CWL2	**CASZ1 Zinc finger protein castor homolog 1**	**1.49569666**	**0.15156**	**2**
Q9CWL2	ISASKGLISPMMAR+Oxidation(10	1.49569666		
Q9CWL2	ISASKGLISPMMAR+Oxidation(11	1.49569666		
Q9CXS4	**CENPV Centromere protein V**	**2.04282064**	**0.00037**	**2**
Q9CXS4	LLLDTFEYQGLVK	2.05572187	2	3.90584
Q9CXS4	SNPGGFGIAPHCLDEGTVR	1.41110535	2	2.56592
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**1.2097535**	**0.74292**	**2**
Q9CYN2	LHDSLATER	0.93416957	2	2.6823
Q9CYN2	YVENFGLIDGR	1.48716991	2	2.8862
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**1.27635328**	**0.58772**	**2**
Q9CYW4	LEDILTGLGLR	1.02713634	2	4.38331
Q9CYW4	RLEDILTGLGLR	1.3084039	3	3.53366
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**0.94876908**	**0.99616**	**3**
Q9CZY3	LLEELEEGQK	0.96351393	1	2.98371
Q9CZY3	VNMSGVSSSNGVVDPR	0.87639934	2	3.10704
Q9CZY3	WTGMIIGPPR	1.01809342	2	2.86174
Q9D024	**CC47 Coiled_coil domain_containing protein 47**	**1.52278134**	**0.06812**	**3**
Q9D024	ERIMNEEDPEKQR	1.57937463	2	2.45902
Q9D024	IMQEEGQPLKLPDTK	0.73959866	2	3.19694
Q9D024	RLEEAALR	1.49921332	2	2.60542
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.37881922**	**1.9E-06**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	2.08834935	3	4.23743
Q9D0M3	GLLSSLDHTSIR	1.08579897	2	3.02922
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.60379654	3	5.55728
Q9D0M3	HLVGVCYTEEEAK	1.59671797	2	3.83048
Q9D0M3	LSDYFPKPYPNPEAAR	1.27208295	3	3.89529
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.35204593**	**0.00176**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.83455696	2	2.94313
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.45768844	2	4.73959
Q9D0S9	SLPADILYEDQQCLVFR	1.99016461	2	3.54147
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.19546626**	**0.00478**	**3**
Q9D172	GVEVTVGHEQEEGGK	1.01304779	2	4.07892
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.87833077	3	4.59366
Q9D172	NLSTFAVDGK	1.19521245	1	2.44705
Q9D180	**WDR65 WD repeat_containing protein 65**	**1.04264798**	**0.48438**	**2**

Q9D180	ERDLEALVR	0.71122202	2	2.56195
Q9D180	KNQELEK	1.13562997	1	2.17912
Q9D1M7	**FKB11 Peptidyl_prolyl cis_trans isomerase FKBP11**	**1.1998645**	**0.36085**	**2**
Q9D1M7	IIDTSLTRDPLVIELGQK	1.32692472	3	3.42869
Q9D1M7	QVIPGLEQSLLDMCVGEK	1.15371762	2	3.19027
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.16506818**	**0.12894**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0	3.05204139		
Q9D1Q6	NIIGYFEQK	1.19107484	1	2.37718
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.16255111	2	5.56591
Q9D1Q6	VDCDQHSDIAQR	1.12180175	2	3.62531
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.79484965**	**9.9E-20**	**5**
Q9D2U9	AMGIMNSFVNDIFER	2.3778107	2	5.12262
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1	1.67539964		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)Oxidation(4	1.3571525		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4	1.68516618		
Q9D2U9	LLLPGELAK	1.48793739	2	2.5265
Q9D417	**FBX24 F_box only protein 24**	**1.34029577**	**0.71333**	**2**
Q9D417	MKEIVGWMPLMAAQK+Oxidation(7	1.9301454		
Q9D417	RSCPSCGLEAGSEKK	1.33234399	2	2.4098
Q9D662	**SC23B Protein transport protein Sec23B**	**2.3004373**	**0.21926**	**2**
Q9D662	HLLQAPLDDAQEILQAR	1.76009092	3	3.98888
Q9D662	IDMNLTDLLGELQR	2.37788775	2	4.12283
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.6547897**	**0.0899**	**3**
Q9D6M3	GAAVNLTLVTPEK	1.88921302	2	3.3446
Q9D6M3	GVNEDTYSGFLDCAR	1.23426479	2	4.71079
Q9D6M3	NHGIAGLYK	1.62620326	1	2.21762
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.29811594**	**0.11133**	**11**
Q9D6Y9	CVAYAESHDQALVGDK	1.38398367	2	5.01181
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	1.24533259	3	3.30356
Q9D6Y9	FLNNFDR	1.44559226	2	2.40365
Q9D6Y9	GTHDLWDSR	1.42944019	2	2.74207
Q9D6Y9	GYESFGIHR	1.4484438	2	2.37497
Q9D6Y9	IVLDSDAAEYGGHQR	1.09115195	2	4.55543
Q9D6Y9	IYESHVGISSHEGK	1.34210235	2	4.5919
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.64768435	3	3.46496
Q9D6Y9	QFNLTDDDLLR	1.21702099	2	2.73187
Q9D6Y9	RQFNLTDDDLLR	1.19343917	2	3.20689
Q9D6Y9	WELYIPPK	1.54467105	2	2.5054
Q9D6Z1	**NOP56 Nucleolar protein 56**	**1.30600176**	**0.38668**	**2**
Q9D6Z1	ELNEEKLEK	1.24805783	2	2.44064
Q9D6Z1	IDCFSEVPTSVFGEK	1.51875291	2	2.53695
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**0.97179795**	**0.50811**	**6**
Q9D7B6	AVIFEDCAVPVANR	0.78644548	2	3.80757
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	2.4673867	2	4.50287
Q9D7B6	IGTEGQGFLIAMK	0.72617816	2	3.01147
Q9D7B6	TAAVALQEER	1.30418021	2	3.19025
Q9D7B6	TDVGGSGLSR	1.64038212	2	2.50662
Q9D7B6	VHQILEGSNEVMR	1.20925672	2	3.39504
Q9D7P6	**ISCU Iron_sulfur cluster assembly enzyme ISCU_ mitochondrial**	**1.01282262**	**0.90368**	**2**
Q9D7P6	NVGTGLVGAPACGDVMK	1.0113717	2	3.61298
Q9D7P6	VVDHYENPR	1.19260462	2	2.51709
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**1.35438695**	**0.33277**	**2**
Q9D7X8	ISDEMEDIIK	1.35896089	2	2.74569

Q9D7X8	SNISSLDEQEGVK	1.35434161	2	3.43341
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.5910071**	**5.3E-05**	**5**
Q9D819	GISCMNTTVSESPFK	1.51658026	2	5.1814
Q9D819	GQYISPFHDVPIYADK	1.54896452	2	3.20145
Q9D819	GQYISPFHDVPIYADKDVFHMVVEVPR	1.48706941	3	5.18851
Q9D819	VLGILAMIDEGETDWK	1.79043826	2	4.11798
Q9D819	YVANLFPYK	1.17956049	1	2.05646
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.22168422**	**0.30202**	**3**
Q9D880	TIALNQVEDVR	0.91890762	2	2.95796
Q9D880	TVLEHYALEDDPLEAFK	1.21175767	2	4.70519
Q9D880	VLLDLSAFLK	1.81226871	2	2.34876
Q9D8W5	**PSD12 26S proteasome non_ATPase regulatory subunit 12**	**1.79709395**	**0.06998**	**3**
Q9D8W5	LQEVIETLLSLEK	1.68714858	2	3.79144
Q9D8W5	TASDMVSTSR	1.80236506	2	2.34834
Q9D8W5	WSTLVEDYGVELR	2.76990663	2	3.12653
Q9DB15	**RM12 39S ribosomal protein L12_ mitochondrial**	**1.27995057**	**0.51974**	**3**
Q9DB15	KLVESLPQEIK	1.28731231	2	3.00219
Q9DB15	NYVQGINLVQAK	1.28731428	2	2.49881
Q9DB15	SEALAGAPLDNAPK	0.84184006	2	2.3292
Q9DBC0	**SELO Selenoprotein O**	**0.99935453**	**0.96346**	**2**
Q9DBC0	LGLIRVEK	0.95944797	2	2.30264
Q9DBC0	LLESPYHSEEEATGPEAVAR	1.06404872	3	3.36063
Q9DBG7	**SRPR Signal recognition particle receptor subunit alpha**	**1.38038548**	**0.0763**	**2**
Q9DBG7	GLVGSKSLSREDMESVLDK+Oxidation(12	1.29640095		
Q9DBG7	NQGFDVVLVDTAGR	1.44118933	2	2.91026
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.24725143**	**0.04981**	**2**
Q9DBH5	TPEEESIDWTK	0.83480353	2	2.47024
Q9DBH5	WSELAGCTADFR	1.25255345	2	3.36558
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**1.47987808**	**8.6E-05**	**4**
Q9DC70	LDDLINWAR	1.20082029	2	3.04387
Q9DC70	MAPALRKVYDQMPEPR+Oxidation(0)Oxidation(11	1.44305764		
Q9DC70	QADVMIVAGTLTNK	1.70180969	2	3.52124
Q9DC70	VYDQMPEPR	2.70576369	2	2.45812
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**1.29393439**	**0.32335**	**2**
Q9DCH4	FLMSLVNQVPK	1.49348124	2	2.76412
Q9DCH4	VIGLSSDLQQVGGASAR	1.15418086	2	4.69164
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.16381154**	**0.2474**	**2**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	3.08332419	3	4.31114
Q9DCM0	SLLPGCQSVISR	1.05147058	2	2.98589
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.58999802**	**8.2E-06**	**2**
Q9DCS9	AYDLVVDWPVTLVR	1.58926918	2	4.657
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.67026038	2	3.44819
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.29524174**	**0.07251**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.49791114	2	3.22539
Q9DCT2	ILTDYGFEGHPFR	1.76908338	2	2.80008
Q9DCT2	KFDLNSPWEAFPAYR	1.50960461	2	3.55867
Q9DCT2	SLADLTAVDVPTR	1.26392747	2	3.4189

Q9DCT2	VVAEPVELAQEFR	0.81490626	2	3.78415
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.35739705**	**1.1E-06**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	1.37454008	2	5.34437
Q9DCU9	LIEPNTAVTR	1.2194493	2	3.35929
Q9DCU9	TMDWFGYYGGPCR	1.37541238	2	3.6921
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.58425687**	**0.13162**	**2**
Q9EP75	DEDGKELSDEDIR	7.21399744	2	3.02796
Q9EP75	IFNDSTNIMHAK	1.57342654	2	3.67793
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.35299508**	**0.09887**	**10**
Q9EP89	EVWSEGLGYADVENR	1.14432473	2	3.83023
Q9EP89	FENSIESLR	0.68312809	2	2.75824
Q9EP89	GIIVSIICNMQSVGLNSTALK	1.13602914	3	3.96068
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	2.14807758	2	5.67587
Q9EP89	IKDEVGAPGIVVGVSVDGK	1.46011384	2	4.54509
Q9EP89	KNDFEQGELYLK	0.6647097	2	3.99431
Q9EP89	LDLDLPVQHYVPEFPEK	1.5403489	3	3.7387
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.54082943	3	3.98909
Q9EP89	LVNTPYVDNSYK	1.04992234	2	3.16289
Q9EP89	WAGGGFLSTVGDLLK	1.63761449	2	4.43359
Q9EPH2	**MRP MARCKS_related protein**	**1.19557994**	**0.14914**	**2**
Q9EPH2	AAATPESQEPQAK	1.31471352	2	2.44346
Q9EPH2	GDVTAEEAAGASPAK	0.86032767	2	3.30681
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.88613094**	**0.00033**	**10**
Q9EPH8	ALDTMNFDVIK	1.68786099	2	3.28561
Q9EPH8	GFGFVSFER	2.23353803	2	2.73177
Q9EPH8	GYGFVHFETQEAAER	1.44615413	2	3.29591
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	3.09661428	3	3.81052
Q9EPH8	KEFSPFGTITSAK	1.49221839	2	3.36882
Q9EPH8	NFGEDMDDER	17.8389681	2	2.56251
Q9EPH8	NLDDGIDDER	1.06608064	2	2.36495
Q9EPH8	SGVGNIFIK	1.44303427	2	2.76801
Q9EPH8	SKVDEAVAVLQAHQAK	1.41594854	2	5.10185
Q9EPH8	VDEAVAVLQAHQAK	1.79687239	2	2.85554
Q9EPJ0	**NUCKS Nuclear ubiquitous casein and cyclin_dependent kinases substrate**	**1.04682642**	**0.75639**	**2**
Q9EPJ0	NSQEDSEDSEEKDVK	1.03388547	2	3.54184
Q9EPJ0	TPSPKEEDEEAESPPEK	2.49207917	2	2.31661
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**4.39692909**	**9.9E-20**	**13**
Q9EQ76	ASIYQSVFTNSSK	2.59434534	2	3.1403
Q9EQ76	GTCILPSVNDMMDDIDEK	6.06673645	2	3.93977
Q9EQ76	ILCGTVSIKPNVK	0.90904661	2	3.00218
Q9EQ76	KEPVFNDELPAR	2.10034505	3	3.60438
Q9EQ76	LQEYITSFATEK	2.37833382	2	3.54957
Q9EQ76	NNEVTLYK	3.89970083	2	2.49475
Q9EQ76	NNLPTAISDWWYMK	2.57397849	2	2.50337
Q9EQ76	SCLEEGLEPTCFER	1.48367457	2	4.31256
Q9EQ76	SDDVGGLWK	2.55291912	2	2.92234
Q9EQ76	VAVIGAGVSGLAAIR	10.4937477	2	4.19912
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.30472053	3	3.69841
Q9EQ76	VWNDGYPWDMVVITR	2.28703961	2	3.88801
Q9EQ76	YIQFETLVTR	4.39060493	2	3.18684
Q9EQG6	**KDIS Kinase D_interacting substrate of 220 kDa**	**1.0725875**	**0.97267**	**2**
Q9EQG6	HLLAMGADVDQEGANSMTALIVAVK+Oxidation(4	1.97112014		
Q9EQG6	SSERPSLFQTDLKLK	1.02834195	2	2.32997

Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.13119283**	**0.4218**	**8**
Q9EQH3	HFHNTLEHLR	2.03811566	3	3.43914
Q9EQH3	IREDLPNLESSEETEQINK	1.49365858	2	5.51478
Q9EQH3	LFDIFSQQVATVIQSR	2.3142429	3	3.32909
Q9EQH3	LLDEAIQAVK	0.69494685	2	2.5808
Q9EQH3	LNLEHIATSSAVSK	1.33935658	2	4.2774
Q9EQH3	LSQLEGVNVER	1.1125553	2	3.01868
Q9EQH3	NIIIALIDR	1.48650268	2	2.41171
Q9EQH3	VLETTVEIFNK	1.31475885	2	2.87067
Q9EQS0	**TALDO Transaldolase**	**1.24349721**	**0.00018**	**6**
Q9EQS0	ALAGCDFLTISPK	1.23329326	2	3.30839
Q9EQS0	ILDWHVANTDKK	1.46889806	2	3.47564
Q9EQS0	LGGPQEEQIK	1.39883919	2	3.3097
Q9EQS0	LSSTWEGIQAGK	1.01956095	2	2.71191
Q9EQS0	SYEPQEDPGVK	1.01959106	2	2.82443
Q9EQS0	WLHNEDQMAVEK	1.23023941	2	3.75689
Q9EQS3	**MYCBP C_Myc_binding protein**	**1.42459987**	**0.25517**	**2**
Q9EQS3	LVQYEPPQEEK	1.43632676	2	2.47627
Q9EQS3	VLVALYEEPEKPTSALDFLK	1.2116557	3	3.44915
Q9EQW7	**KI13A Kinesin_like protein KIF13A**	**1.06961893**	**0.23048**	**3**
Q9EQW7	ADLTDSRALEKAVSR	1.27674769	3	3.3419
Q9EQW7	DETIAVPLEENSALPK	0.94664658	2	2.59086
Q9EQW7	VTQWAEER	1.34959473	2	2.43305
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.04285109**	**0.87967**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.16287764	2	4.34295
Q9EQX9	SNEAQAIETAR	1.03620878	2	3.37589
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.2508928	3	4.48138
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.32637953**	**0.00935**	**19**
Q9ER34	ADIANLAEEFK	1.1701468	2	3.56502
Q9ER34	CTTDHISAAGPWLK	1.40245411	2	4.01984
Q9ER34	DINQEVYNFLATAGAK	1.21807539	2	3.3442
Q9ER34	DLEDLQILIK	1.10511161	2	2.47384
Q9ER34	FKLEAPDADELPR	1.22617235	3	4.16928
Q9ER34	FNPETDFLTGK	1.63017387	1	2.48704
Q9ER34	GHLDNISNNLLIGAINIENGK	1.230733	2	5.80545
Q9ER34	IVYGHLDDPANQEIER	1.3500546	2	4.60139
Q9ER34	LNRPLTLSEK	1.44451398	2	2.4509
Q9ER34	LTGTLSGWTSPK	1.29794632	2	2.99456
Q9ER34	NAVTQEFGPVPDTAR	1.26087908	2	4.43713
Q9ER34	NTIVTSYNR	1.60473053	1	1.94905
Q9ER34	QGLLPLTFADPSDYNK	1.37757506	2	3.35535
Q9ER34	SDFDPGQDTYQHPPK	1.56143109	2	2.87933
Q9ER34	SQFTITPGSEQIR	1.12975998	2	3.91078
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	1.64547473	2	4.78304
Q9ER34	VDVSPTSQR	1.55430015	2	2.44661
Q9ER34	VGLIGSCTNSSYEDMGR	1.35787582	2	4.20039
Q9ER34	WVVIGDENYGEGSSR	1.1084773	2	4.41423
Q9ERU9	**RBP2 E3 SUMO_protein ligase RanBP2**	**1.25135705**	**0.50361**	**2**
Q9ERU9	EINSLRGQEK	1.16250815	2	2.61337
Q9ERU9	NLFRFGESTTGFNFSFK	1.25809152	2	2.32362
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**1.0815628**	**0.4242**	**5**
Q9ES21	HFDSQVIIYGK	1.07035174	2	2.79587
Q9ES21	LEEQDEFEK	1.06682464	2	2.75949
Q9ES21	TNVIQSLLAR	3.73737284	2	2.3946
Q9ES21	TQLGLVMDGFNSLLR	1.30725327	2	3.947
Q9ES21	VVTNQEGVFR	1.16436613	2	2.81056

Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.18977272**	**1.4E-05**	**14**
Q9ES38	ACQAAWALK	1.45391284	2	2.57269
Q9ES38	ADVWENFQQR	1.1706272	2	2.95416
Q9ES38	EGFDVGVIADPLYILDNK	1.30197226	2	5.37182
Q9ES38	GATAILVLPSK	1.15138197	2	3.20712
Q9ES38	HPPELFVDALEQQAQARPDQVALVCTGSEGCSITNR	1.36342249	4	4.54622
Q9ES38	IQDSLEITNTYK	1.39535567	2	3.81516
Q9ES38	LKEATIQEDK	1.49686498	2	2.83381
Q9ES38	LLAENIR	1.19922834	2	2.46671
Q9ES38	MLTPLELVQFDIETAEPVRDK	1.83488297	2	4.20163
Q9ES38	QGFCIPVETGKPGLLLTK	1.71400519	3	3.88201
Q9ES38	SISALSVFLGLAK	1.63018665	2	3.32014
Q9ES38	SLMPDVYQAVCEGTWK	0.91891872	2	3.90565
Q9ES38	YLCNVPGQPEDK	1.25165653	2	3.37767
Q9ES38	YLCNVPGQPEDKK	1.32529344	2	3.76698
Q9ESP1	**SDF2L Stromal cell_derived factor 2_like protein 1**	**0.89232186**	**0.77962**	**2**
Q9ESP1	ASAGLVTCGSVLK	0.89609105	2	3.59286
Q9ESP1	GQHEVHGMPSANAHNTWK	0.86382316	3	3.81913
Q9ESR9	**ABCA2 ATP_binding cassette sub_family A member 2**	**1.02744651**	**0.98143**	**2**
Q9ESR9	KEMDKMIEDLELSNK+Oxidation(2)Oxidation(5	1.11717869		
Q9ESR9	RHSLVQTLSGGMKR	1.02632752	2	2.36262
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.79917065**	**0.00161**	**2**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.39123924	2	4.14051
Q9EST6	SLDLFGCEVTNR	1.53529409	2	2.97743
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.43557428**	**0.23399**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.43565093	3	5.82827
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.39291946	3	4.50159
Q9ESW0	QGQGQLVTCSGAFK	1.23124652	2	2.36767
Q9HB97	**PARVA Alpha_parvin**	**0.99647622**	**0.53446**	**3**
Q9HB97	LNVAEVTQSEIAQK	0.89440116	2	4.31417
Q9HB97	QIQEEITGNTEALSGR	1.51469007	2	3.70708
Q9HB97	VLIDWINDVLVGER	1.75109418	2	2.3004
Q9JHL4	**DBNL Drebrin_like protein**	**0.52015478**	**0.29701**	**3**
Q9JHL4	AMSTTSVSSSQPGK	0.99237257	2	2.55232
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3	0.43304548		
Q9JHL4	TGELEQEVVSR	0.74535723	2	3.26564
Q9JHW0	**PSB7 Proteasome subunit beta type_7**	**1.16178197**	**0.4972**	**2**
Q9JHW0	ATEGMVVADK	1.0969221	2	2.57047
Q9JHW0	FRPDMEEEEAKK	1.41212076	3	3.81746
Q9JHZ9	**S38A3 Sodium_coupled neutral amino acid transporter 3**	**2.27980363**	**9.9E-20**	**3**
Q9JHZ9	AYEQLGYR	1.92884149	2	2.39203
Q9JHZ9	HLEGLLPVGMPTADTQR	2.76867755	2	3.9868
Q9JHZ9	MEIPRQTEMVELVPNGK+Oxidation(0)Oxidation(8	1.26288963		
Q9JI85	**NUCB2 Nucleobindin_2**	**1.03030823**	**0.9245**	**8**
Q9JI85	FQQGIAPSGPAGELK	1.1795553	2	3.1531
Q9JI85	HEEFKKYEMMK+Oxidation(8	0.59401402		
Q9JI85	HEEFKKYEMMK+Oxidation(9	0.59401402		
Q9JI85	LSQELDLVSHK	1.1896896	2	2.62893
Q9JI85	QEYQQAVQQLEQK	0.92847009	2	4.59552
Q9JI85	TRLDELK	0.99071745	1	2.01113
Q9JI85	VHNVEPVESAR	1.0278408	2	3.08007
Q9JI85	VYNPQNAEDDMIEMEEER	1.9653523	2	3.972
Q9JI91	**ACTN2 Alpha_actinin_2**	**2.23292992**	**0.00061**	**8**

Q9JI91	ETADTDTAEQVIASFR	1.60034926	2	3.06421
Q9JI91	GYEEWLLNEIR	2.33017675	2	3.4865
Q9JI91	HTNYTMEHIR	1.19404613	3	3.5452
Q9JI91	KHEAFESDLAAHQDR	1.65877188	2	5.36311
Q9JI91	MLDAEDIVNTPKPDER	1.22998515	2	3.2126
Q9JI91	QSILAIQNEVEK	1.88396593	2	2.72277
Q9JI91	SSIQITGALEDQMNQLK	1.47185711	2	3.08532
Q9JI91	TINEVETQILTR	1.65070193	2	3.14469
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.04201006**	**0.77187**	**7**
Q9JJ19	AVDPDSPAEASGLR	1.01395282	2	3.45978
Q9JJ19	IVEVNGVCMEGK	1.02417309	2	3.72394
Q9JJ19	LLVVDPETDEQLKK	1.21861787	2	2.85416
Q9JJ19	LVEPGSPAEK	0.75303353	2	2.7024
Q9JJ19	LVEVNGENVEK	0.93120688	2	3.04663
Q9JJ19	SEHTEPPAAADTK	1.33331877	2	3.32679
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	1.18361845	3	3.55325
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**1.45594109**	**0.33857**	**5**
Q9JJ40	AGVLADDHLIEVNGENVENASHEEVVEK	2.42997328	3	5.38256
Q9JJ40	GVFLTDITPQGVAMK	1.14214861	2	3.37839
Q9JJ40	IEKDTDGHLVR	1.52422014	2	3.19373
Q9JJ40	SGNSVTLLVLDGDSYEK	3.72325738	2	3.79667
Q9JJ40	VIEEGSPAEK	1.29626082	2	2.41843
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.32965966**	**0.87157**	**2**
Q9JJ46	HLTNAQSMLDNK	1.37300374	2	3.75976
Q9JJ46	VSVVPLGTGR	1.01614118	2	2.45105
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.35292473**	**0.29811**	**4**
Q9JJ54	FGDVVDCTLK	1.26807211	2	2.80834
Q9JJ54	IDASKNEEDEGHSNSSPR	1.65220215	3	4.66094
Q9JJ54	IFVGGLSPDTPEEK	1.87154033	2	4.03937
Q9JJ54	IFVGGLSPDTPEEKIR	1.96493476	2	2.40501
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.09652352**	**0.16474**	**4**
Q9JJ79	NCLEEWTKAAGLEK	1.08087497	2	2.65048
Q9JJ79	RASTAAAPLAAWVK	1.2880669	2	2.53825
Q9JJ79	TVLRGSGNLLR	1.36925348	2	2.46618
Q9JJ79	YVVQIGDK	1.41779644	1	2.30272
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.40121832**	**0.20242**	**2**
Q9JJU8	GDYDAFFEAR	1.40177363	2	3.18598
Q9JJU8	QQDVLCFLEANK	1.40121826	2	3.21735
Q9JJW3	**USMG5 Up_regulated during skeletal muscle growth protein 5**	**1.15467701**	**0.77381**	**2**
Q9JJW3	MAGPESDGQFQFTGIKK+Oxidation(0	2.1521498		
Q9JJW3	YFNSYTLTGR	1.1544612	2	2.80612
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.31174869**	**0.20905**	**4**
Q9JK38	GRVEDVVVSDECR	1.67847363	2	2.51818
Q9JK38	ITLECLPQNVGFYK	1.22608931	2	3.47628
Q9JK38	VEDVVVSDECR	1.39968369	2	3.36651
Q9JK38	VLGQLTETGVVSPEQFMK	1.33203497	2	4.63243
Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**1.14809956**	**0.6866**	**2**
Q9JK72	GDLGNVHAEASGR	1.31840669	2	3.22151

Q9JK72	SLVVDEGEDDLGR	1.13058699	2	3.02231
Q9JKJ9	**CP39A 24_hydroxycholesterol 7_alpha_hydroxylase**	**1.41848924**	**0.00788**	**2**
Q9JKJ9	TVLESISSVFGTAGK	1.2734732	2	3.33597
Q9JKJ9	TYDEGFEYGSQLPEWLLR	1.64267451	2	3.20149
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**2.24112576**	**0.548**	**4**
Q9JKS4	DFNMPLTISR	1.33045342	2	2.34284
Q9JKS4	DLAVDSASPVYQAVIK	0.86390669	2	3.59309
Q9JKS4	GAPAYNPTGPQVTPLAR	2.12796807	2	3.12809
Q9JKS4	TQSKPEDEADEWAR	3.570654	2	3.81607
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.1555488**	**0.52552**	**11**
Q9JLA3	AYNYVGQEVDGYHAFQTLTQIYNK	1.60234605	3	3.31771
Q9JLA3	FLFVDADQIVR	2.0287903	2	2.62032
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.26785651	3	6.0139
Q9JLA3	IEYQFFEDK	1.85720784	2	2.34456
Q9JLA3	ILETTTFFQR	1.97037006	2	2.8417
Q9JLA3	IVPEWQDYDQEIK	1.15550583	2	3.31969
Q9JLA3	LNIQPSETDYAVDIR	1.62183965	2	4.11147
Q9JLA3	TAAIANSMNYLTK	1.16280809	2	2.5771
Q9JLA3	VDALLSAQPK	1.40438804	2	2.7415
Q9JLA3	VEEDVASDLVMK	1.56067595	2	3.82461
Q9JLA3	VWQLQDLSFQTAAR	1.1882018	2	4.65391
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**0.92086956**	**0.70689**	**2**
Q9JLH7	GSDALTLLEYPETR	0.78604259	2	2.90587
Q9JLH7	KEEEGQAGAAEMR	0.9449612	2	3.70517
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.20868155**	**0.00096**	**18**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.9566214	2	4.75727
Q9JLJ3	ANDTTFGLAAGVFTR	1.23102407	2	4.92879
Q9JLJ3	CQVLLEAAR	1.26480423	2	3.30374
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.09570272	2	4.95438
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.26354089	3	3.39479
Q9JLJ3	EVNLAVENAK	1.4391089	2	3.15041
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.28993633	2	5.57225
Q9JLJ3	GIKPITLELGGK	0.86343236	3	3.96727
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	1.39652922	3	4.23865
Q9JLJ3	IGDPLLEDTR	1.20564859	2	3.7055
Q9JLJ3	MGPLINAPHLER	1.24482411	2	3.26442
Q9JLJ3	MGPLINAPHLER+Oxidation(0	1.28881785		
Q9JLJ3	RDEIAIMETINNGK	1.21101855	2	5.29883
Q9JLJ3	SPLIIFSDCNMK	1.75381167	2	2.60824
Q9JLJ3	VEPVDASGTEK	1.21111546	2	2.41424
Q9JLJ3	VSFTGSVPTGMK	1.23670624	2	3.10514
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10	1.27742933		
Q9JLJ3	VTIEYYSQLK	1.42126534	2	3.08449
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**1.39895116**	**0.16616**	**2**
Q9JLR1	IIEVGDTPK	1.4168157	2	2.66552
Q9JLR1	TWIEVSGSSAK	1.34387272	2	2.7547
Q9JLT0	**MYH10 Myosin_10**	**1.56660964**	**0.11616**	**2**
Q9JLT0	AGVLAHLEEER	1.49640287	2	3.4286
Q9JLT0	DAAGLESQLQDTQELLQEETR	1.80504578	2	3.18175
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**0.80234846**	**0.34004**	**2**
Q9JLZ1	LEAEAVPEVSEK	0.4611838	2	2.31979
Q9JLZ1	YEISSVPTFLFFK	1.69442383	2	2.58476

Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.94559159**	**0.90064**	**3**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	0.93249741	2	5.61671
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.74311365	3	4.47002
Q9JLZ3	SEVPGIFCAGADLK	1.08240792	2	2.95344
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**1.28622756**	**0.8407**	**15**
Q9JM53	AIASAAEGGSVPPIR	1.0148384	2	2.76764
Q9JM53	CLIATGGTPR	0.89251516	2	2.4216
Q9JM53	DGEQHEDLNEVAK	1.00952366	2	3.82964
Q9JM53	ILPEYLSNWTMEK	1.58614741	2	3.49459
Q9JM53	IMGLGLSPEEK	1.49124829	2	2.80551
Q9JM53	KSQASGIEVIQLFPEK	1.3498596	2	3.70989
Q9JM53	KVETDHIVTAVGLEPNVELAK	1.22217666	2	6.17864
Q9JM53	LNDGSQITFEK	1.21199891	2	3.50826
Q9JM53	SITVIGGGFLGSELACALGR	1.10789873	2	2.65708
Q9JM53	SQASGIEVIQLFPEK	1.05805769	2	4.13179
Q9JM53	TGGLEIDSDFGGFR	1.18683901	2	4.18675
Q9JM53	VETDHIVTAVGLEPNVELAK	1.09416713	2	5.18247
Q9JM53	VLIVSEDPELPYMRPPLSK	1.11387927	3	3.93852
Q9JM53	VMPNAIVQSVGVSGGK	1.29507837	2	4.28328
Q9JM53	VNAELQAR	1.26117656	2	2.60174
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**1.58698366**	**0.45874**	**2**
Q9JMA1	CTESEEEEVTK	1.49759376	2	3.69407
Q9JMA1	EKESVNAKVLK	2.72595327	2	2.37533
Q9JMD3	**PCTL PCTP_like protein**	**1.57015678**	**1.9E-09**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	1.3544115	2	4.66817
Q9JMD3	ESVQVPDDQDFR	1.08517006	2	2.83565
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.72384805	3	4.40511
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0	1.77591913		
Q9JMD3	SSQFLAPK	0.84294387	2	2.35623
Q9JMD3	WDSNVIETFDIAR	1.52183998	2	4.53405
Q9JME5	**AP3B2 AP_3 complex subunit beta_2**	**1.35358997**	**0.16234**	**2**
Q9JME5	DELVVAESVVVIK	2.06746452	2	2.51605
Q9JME5	LLQMQPAQHGEIIK	1.14602499	2	2.55969
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.06732743**	**0.87961**	**7**
Q9QVC8	ALELDSNNEK	1.22942959	2	2.63056
Q9QVC8	GEPNNVAGNQAQVK	1.04039976	2	3.85957
Q9QVC8	TEVAAGDHPTDAEMK	0.968466	2	3.66787
Q9QVC8	TQLAVCQQR	1.22716184	2	2.72842
Q9QVC8	VAENGAQSAPLPLEGVDISPK	0.94136158	2	3.92937
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	1.03331842	3	5.9155
Q9QVC8	VLQLYPSNK	0.74291435	2	2.33325
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.17991117**	**0.43638**	**3**
Q9QWN8	ALAQEDQSAGEVER	1.37347452	2	3.77066
Q9QWN8	FETLEPEMNALAAR	1.69407099	2	2.72911
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	1.1081994	3	4.22452
Q9QX79	**FETUB Fetuin_B**	**1.08398705**	**0.97511**	**3**
Q9QX79	GSIQHLPEQEEPEDSKGK	1.29882877	3	3.83006
Q9QX79	IFYETVHGQCK	1.08415201	2	2.38993
Q9QX79	NTAPTSSPSITAPR	0.99325288	2	3.15038
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**9.05393823**	**0.98022**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	9.57070731	2	3.67931
Q9QXG4	IGPIATPDYIQNAPGLPK	1.39156655	2	3.2977

Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.27367765**	**9.6E-08**	**32**
Q9QXQ0	ACLISLGYDVENDR	1.38841457	2	4.02405
Q9QXQ0	ACLISLGYDVENDRQGDAEFNR	1.42567781	3	3.85267
Q9QXQ0	AGTQIENIDEDFR	1.08874977	2	3.56221
Q9QXQ0	AGTQIENIDEDFRDGLK	1.20071429	2	4.2579
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.40196552	3	3.36847
Q9QXQ0	ASIHEAWTDGK	0.80777544	2	2.45294
Q9QXQ0	DDPVTNLNNAFEVAEK	1.55607986	2	3.60693
Q9QXQ0	ETTDTDTADQVIASFK	1.15562866	2	4.71037
Q9QXQ0	HRDYETATLSDIK	1.78923844	2	3.88742
Q9QXQ0	HRPELIEYDK	1.10220472	3	4.40283
Q9QXQ0	HTNYTMEHLR	1.19404613	3	3.5452
Q9QXQ0	ICDQWDNLGSLTHSR	1.27484069	2	4.59372
Q9QXQ0	INNVNKALDFIASK	0.98767521	2	2.30311
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.77213372	2	4.73469
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.6599358	2	4.42651
Q9QXQ0	LVSIGAEEIVDGNAK	1.65707835	2	3.15663
Q9QXQ0	MAPYQGPDAAPGALDYK	1.22490106	2	4.98175
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0	1.29131381		
Q9QXQ0	MLDAEDIVNTARPDEK	0.76319931	2	3.8771
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(0	0.95851989		
Q9QXQ0	MVSDINNGWQHLEQAEK	1.47918059	2	4.71801
Q9QXQ0	NFITAEELR	1.32996526	1	2.125
Q9QXQ0	NVNVQNFHISWK	0.32444356	2	2.34403
Q9QXQ0	QFASQANMVGPWIQTK	0.85112118	2	3.63946
Q9QXQ0	QLETIDQLHLEYAK	1.32664375	2	3.28057
Q9QXQ0	RDHALLEEQSK	1.21037705	3	3.88131
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	2.70808345	3	4.69341
Q9QXQ0	TINEVENQILTR	0.99488182	2	3.67342
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	2.18210428	3	5.40346
Q9QXQ0	VGWEQLLTTIAR	2.18710276	2	4.10189
Q9QXQ0	VLAGDKNFITAEELR	0.99219586	2	3.23279
Q9QXQ0	VLAVNQENEHLMEDYER	1.23405748	2	5.72971
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.10147281**	**0.9151**	**5**
Q9QXT0	ALVDELEWEIAR	1.41421013	2	3.58611
Q9QXT0	IDSDISGTLK	0.98900254	2	2.62545
Q9QXT0	INPDGSQSVVEVPYAR	1.08293072	2	3.66256
Q9QXT0	RTDLCDHALHR	1.30981084	3	3.92513
Q9QXT0	TDLCDHALHR	1.09318619	2	3.20789
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.02083166**	**9.9E-20**	**18**
Q9QXX4	DIMVTIRPHVLTPFVEECLVAAAGGTR	1.47285982	3	5.82647
Q9QXX4	DVEVTKEEFALAAQK	1.31423532	2	4.47879
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.33687766	2	5.96835
Q9QXX4	FGLYLPLFKPSASTSK	1.63579378	2	2.75989
Q9QXX4	GLLPQLLGVAPEK	1.51856263	1	3.07248
Q9QXX4	IAPLEEGMLPFNLAEAQR	2.34415632	2	5.23561
Q9QXX4	ITLPAPNPDHVGGYK	0.96093322	2	3.00412
Q9QXX4	KDVEVTKEEFALAAQK	1.13623766	2	5.62031
Q9QXX4	LQVAGEITTGPR	1.33303349	2	3.7317
Q9QXX4	LTVNDFVR	2.08910352	2	2.31738
Q9QXX4	NGEFFMSPHDFVTR	1.26733531	2	4.20744
Q9QXX4	NSFDCFK	1.23925489	1	1.9736
Q9QXX4	SSPQFGVTLLTYELLQR	1.87272494	2	3.8108
Q9QXX4	STGSFVGELMYK	1.63117004	2	3.43736
Q9QXX4	TVELLSGVVDQTK	1.47705289	2	4.51176
Q9QXX4	VSALSVVR	1.79433251	2	2.3056

Q9QXX4	YEGFFGLYR	1.36427538	2	2.74486
Q9QXX4	YLNIFGESQPNPK	0.99789679	2	4.43402
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**1.01564169**	**0.99717**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	0.94248846	2	4.57612
Q9QYU4	RAPAFLSADEVQDHLR	0.88334155	3	3.84162
Q9QYU4	SLGMAVEDLVAAK	0.85556263	2	3.76128
Q9QYU4	SSSLLIPPLEAALANFSK	1.06860511	2	2.89721
Q9QZ76	**MYG Myoglobin**	**1.91274029**	**0.63526**	**6**
Q9QZ76	GQHAAEIQPLAQSHATK	1.54384119	2	4.91335
Q9QZ76	HGCTVLTALGTILK	3.38823921	2	3.66195
Q9QZ76	KGQHAAEIQPLAQSHATK	8.8553711	3	5.45922
Q9QZ76	KKGQHAAEIQPLAQSHATK	4.58781505	3	4.50123
Q9QZ76	VEGDLAGHGQEVLISLFK	1.0341272	3	4.11227
Q9QZ76	YSGDFGADAQGAMSK	7.62221669	2	3.92959
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.20604133**	**0.90734**	**8**
Q9QZA2	ATLVKPTPVNVPISQK	1.24833305	2	3.26783
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.33237284	2	3.39303
Q9QZA2	HEGALETLLR	1.13648983	2	2.32565
Q9QZA2	LLDEEEATDNDLR	1.07130727	2	4.05015
Q9QZA2	MVPVSVQQSLAVFSQR	1.34792088	2	3.13145
Q9QZA2	NIQVSHQEFSK	1.32551898	2	3.35185
Q9QZA2	STAVVEQGGIQTVDQLIK	1.18933624	2	4.29954
Q9QZA2	TMQGSEVVNVLK	0.90844405	2	3.2771
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.36281715**	**0.00139**	**7**
Q9QZD8	GALVTVGQLSCYDQAK	1.17968438	2	5.08236
Q9QZD8	LFSGATMASSR	0.81407529	2	2.51429
Q9QZD8	MTGMALQVVR	1.54278213	2	2.78806
Q9QZD8	NYSHALDGLYR	1.14337808	2	2.83243
Q9QZD8	VHLQTQQEVK	1.2487954	2	3.04864
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.56572125	2	5.68047
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	1.44404314	3	3.5388
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.44432649**	**0.14624**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.64483274	2	4.11496
Q9QZH8	WFLQEDILEK	1.2465209	2	2.94973
Q9QZR9	**chain**	**0.88851526**	**0.33808**	**2**
Q9QZR9	EGPSGPFGALGQDGKDGPR	16.3783749		
Q9QZR9	GASGLLEMGPPGPMGMPGQK	0.78614544		
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.99310921**	**0.00046**	**5**
Q9QZU7	IDANNVAYTTGK	1.71147456	2	3.07129
Q9QZU7	MDDLTFDQK	2.40691555	2	2.55431
Q9QZU7	MNPGDVITFDNWR	2.00205953	2	2.80838
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.5320778	2	4.7948
Q9QZU7	SYEAGTEISR	1.91890074	2	2.75401
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**1.8393862**	**0.00041**	**2**
Q9QZX8	GIGETPIVPLGISYLDDFAK	1.8452601	2	3.48901
Q9QZX8	QFTDEGNPDSVNK	1.34032553	2	3.58281
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.86113395**	**0.34622**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	2.04452543	3	4.80459
Q9R063	ETDLLLDDSLVSLFGNR	2.06891509	2	4.02467
Q9R063	GVLFGVPGAFTPGCSK	1.14933862	2	4.19188
Q9R063	THLPGFVEQAGALK	1.06203852	3	4.48427
Q9R063	VGDTIPSVEVFEGEPGK	1.41061331	2	4.23487
Q9R063	VGDTIPSVEVFEGEPGKK	0.98559659	2	4.17005
Q9R063	VNLAELFK	1.10981106	2	2.56489

Q9R063	VQLLADPTGAFGK	0.84244363	2	3.55715
Q9R064	**GORS2 Golgi reassembly_stacking protein 2**	**0.97000816**	**0.25829**	**2**
Q9R064	ADTSSLTVDVMSPASK	0.95632813	2	4.27413
Q9R064	LYVYNTDTDNCR	1.79098374	2	2.53103
Q9R099	**TBL2 Transducin beta_like protein 2**	**1.29737433**	**0.00646**	**4**
Q9R099	ANVELDHATLVR	1.42228977	2	2.42379
Q9R099	FEEASTMPCR	0.96501051	2	2.66621
Q9R099	FLASCGDR	1.18716355	2	2.33993
Q9R099	LQQQLTQAQEALK	1.60589743	2	4.10972
Q9R0N0	**GALK1 Galactokinase**	**1.22917998**	**0.04732**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	1.57787266	3	4.46415
Q9R0N0	MEELEAGR	1.26103133	2	2.45974
Q9R0N0	RQCEEVAQALGK	0.97739962	2	3.20385
Q9R0N0	SLETSLVPLSDPK	1.25415927	2	3.28885
Q9R0N0	TDGLVSLLTTSK	1.25370197	2	3.80247
Q9R0N0	VEELLAEAR	1.14715837	2	3.11637
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.02847743**	**0.99785**	**6**
Q9R0T3	AEPSVAEYTVR	0.98754272	2	2.4658
Q9R0T3	ICSEVLQLEPDNVNALK	1.12723832	2	4.75959
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	0.90573134	3	5.65813
Q9R0T3	LIGSAEELIR	1.06824624	2	2.61684
Q9R0T3	LKNDNTEAFYK	1.40880129	2	2.6493
Q9R0T3	SNPSENEEKEAQSQLVK	1.01833059	2	5.15766
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.00621943**	**0.99111**	**4**
Q9R112	EGNALFTFPNTPVK	1.35546165	2	3.0399
Q9R112	STLSVIPSGVQWIQDR	1.41527331	2	2.79017
Q9R112	TAAAVAAQSGILDR	0.98095995	2	3.32618
Q9R112	VGAENVAIVEPSER	0.99287464	2	2.86908
Q9R172	**NOTC3 Neurogenic locus notch homolog protein 3**	**0.84808174**	**0.37198**	**2**
Q9R172	CTHQQPSREAACLCLPGWVGER	1.67982187	3	3.39699
Q9R172	YGGKCLDLVDK	0.786234	1	1.98789
Q9R1T3	**CATZ Cathepsin Z**	**1.42899072**	**0.36859**	**2**
Q9R1T3	HGIPDETCNNYQAK	1.45476013	2	3.86547
Q9R1T3	VGDYGSLSGR	1.29345432	2	2.82876
Q9R1T4	**SEPT6 Septin_6**	**1.146435**	**0.66412**	**2**
Q9R1T4	QMFVQRVKEK+Oxidation(1	0.95088262		
Q9R1T4	STLMDTLFNTK	1.80558683	2	2.87976
Q9R1T5	**ACY2 Aspartoacylase**	**1.61412718**	**0.4527**	**2**
Q9R1T5	EAFAKTTKLTLNAK	21.2293213	2	2.52017
Q9R1T5	VIPLGGDCTVYPVFVNEAAYYEK	1.59917189	3	3.58684
Q9R1T9	**KCNH4 Potassium voltage_gated channel subfamily H member 4**	**1.71123251**	**0.21355**	**2**
Q9R1T9	DGSAFWCLLDMMPIK+Oxidation(10	2.24246523		
Q9R1T9	KDGSAFWCLLDMMPIK+Oxidation(11)Oxidation(12	1.03120974		
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**1.51410134**	**0.03617**	**4**
Q9R1Z0	LCQNNFALGYK	1.43644599	2	2.40341
Q9R1Z0	LTLSALVDGK	2.36664619	2	2.30016
Q9R1Z0	LTVDTIFVPNTGK	1.24046861	2	2.96183
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	1.53738087	2	4.29561
Q9WTR8	**PHLP1 PH domain leucine_rich repeat protein phosphatase 1**	**1.372202**	**0.70025**	**2**
Q9WTR8	LEELEEIDISGNK	3.45087481	2	2.72164
Q9WTR8	LEELEEIDISGNKLK	1.27488193	2	2.39603

Q9WTT6	**GUAD Guanine deaminase**	**1.21519447**	**0.14601**	**10**
Q9WTT6	EIGNFEVGKDFDALLINPR	1.51988706	2	4.08246
Q9WTT6	ETTEESVKETER	1.21561465	2	3.16279
Q9WTT6	FQSTDVAEEVYTR	0.98287459	2	3.7186
Q9WTT6	FSLSCTETLMSELGNIAK	1.57526264	2	3.6433
Q9WTT6	GTFVHSTWTCPMEVLR	0.69204467	2	3.15965
Q9WTT6	IVFLEESSQQEK	1.080443	2	4.25337
Q9WTT6	NIEEVYVGGK	0.60424066	1	2.69527
Q9WTT6	NYTDVYDKNNLLTNK	0.91333563	2	4.41706
Q9WTT6	THDLYIQSHISENREEIEAVK	1.45942107	3	4.47567
Q9WTT6	VCMDLNNTVPEYK	1.11990241	2	3.61848
Q9WTT7	**BZW2 Basic leucine zipper and W2 domain_containing protein 2**	**1.27998068**	**0.67342**	**2**
Q9WTT7	AWMAEKDANSVTSSLR+Oxidation(2	1.3793145		
Q9WTT7	ELQERLSQECPIK	1.25363161	2	2.55037
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**1.13703934**	**0.99416**	**9**
Q9WU19	AIFVTVDTPYLGNR	0.93817504	2	4.25409
Q9WU19	AVFVGRPIIWGLAFQGEK	0.92249667	3	4.01176
Q9WU19	GVQDVLEILK	0.96483417	2	3.62784
Q9WU19	GVQDVLEILKEEFR	0.96891077	2	4.30141
Q9WU19	HGVDGILVSNHGAR	1.03073754	3	4.53181
Q9WU19	MKNFETNDLAFSPK+Oxidation(0	1.51658026		
Q9WU19	NFETNDLAFSPK	0.77731726	2	3.57137
Q9WU19	NVADIDLSTSVLGQR	1.96528704	2	4.94347
Q9WU19	VEVFLDGGVR	1.08792907	2	2.6852
Q9WU79	**PROD Proline dehydrogenase 1_ mitochondrial**	**1.27665891**	**0.79927**	**2**
Q9WU79	FTEEEEQQMK	1.49922763	2	3.11878
Q9WU79	HLVVPNVQTGQLEPLLSR	1.15667847	2	2.33994
Q9WU82	**CTNB1 Catenin beta_1**	**1.14023022**	**0.4383**	**5**
Q9WU82	HQEAEMAQNAVR	1.431735	2	3.40978
Q9WU82	LLNDEDQVVVNK	0.88544028	2	3.30851
Q9WU82	TMQNTNDVETAR	0.9565464	2	3.58624
Q9WU82	TMQNTNDVETAR+Oxidation(1	1.76726474		
Q9WU82	TSMGGTQQQFVEGVR	1.16064421	2	3.52761
Q9WUA2	**SYFB Phenylalanyl_tRNA synthetase beta chain**	**1.20985335**	**0.50068**	**3**
Q9WUA2	EMVRADLINKK	1.18147943	2	2.38823
Q9WUA2	KEMVRADLINK	1.18147943	2	2.36095
Q9WUA2	TYTIANQFPLNK	1.21118317	2	2.44837
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.26363785**	**0.00192**	**2**
Q9WUC4	LGGVEFNIDLPNKK	1.2203038	2	3.62919
Q9WUC4	VCIESEHSSDILLATLNK	1.37670719	2	5.74279
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**2.93471724**	**0.53773**	**3**
Q9WUH4	AIVAGDQNVEYK	3.09835427	2	2.67463
Q9WUH4	FCANTCVECR	2.60534463	2	2.71892
Q9WUH4	FVFHNEQVYCPDCAK	2.50263723	2	4.21178
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**1.32500635**	**0.22467**	**2**
Q9WUI1	ILDFGLAR	1.27588141	2	2.73213
Q9WUI1	QELNKTVWEVPQR	2.21149511	2	2.43044
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.51824446**	**0.93113**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(6	1.51211605		
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7	1.52147757		
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.86418928**	**0.36735**	**5**
Q9WUS0	AVILGPPGSGK	0.94619691	2	2.45807
Q9WUS0	GVLHQFSGTETNR	0.88962754	2	3.55004
Q9WUS0	TLVQAEALDR	0.83411758	2	2.82175
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.59578833	3	5.10579

Q9WUS0	YKDAAKPVIELYK	1.30739763	2	3.55925
Q9WUU8	**TNIP1 TNFAIP3_interacting protein 1**	**1.26033315**	**0.7041**	**2**
Q9WUU8	IFEEDFQRER	1.18938986	2	2.3264
Q9WUU8	QENEALK	1.27007789	1	2.29213
Q9WV85	**NDK3 Nucleoside diphosphate kinase 3**	**1.34890616**	**0.17819**	**3**
Q9WV85	LVKYMSSGPVVAMVWQGLDVVHASR+Oxidation(4)Oxidation(12	1.28325583		
Q9WV85	LVQASEELLR	1.5255987	2	2.70901
Q9WV85	TFLAVKPDGVQR	0.81798528	2	2.67797
Q9WVC0	**SEPT7 Septin_7**	**1.19585239**	**0.85697**	**3**
Q9WVC0	ADTLTPEECQQFK	0.83642831	2	2.85777
Q9WVC0	FEDYLNAESR	1.28715728	2	2.76163
Q9WVC0	NLEGYVGFANLPNQVYR	1.48056712	2	3.62276
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**2.55646473**	**4.4E-06**	**3**
Q9WVD5	DGPLGFYHGLSSTLLR	2.29306243	2	2.92424
Q9WVD5	LQTMYEMETSGK	3.63784732	2	3.12805
Q9WVD5	NEGITALYSGLKPTMIR	1.54599302	2	3.34505
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**1.5663253**	**0.43437**	**2**
Q9WVF7	AANMPDSELFELISENR	1.31096935	2	2.4759
Q9WVF7	MAWQWRGEFMPASR+Oxidation(0)Oxidation(9	4.68083153		
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**1.24049661**	**0.85063**	**13**
Q9WVK3	AGVYNLTK	1.19133612	2	2.52272
Q9WVK3	ASQPPSSSTQVTAIQCNIR	0.8649219	2	5.53707
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.10733236	3	6.29974
Q9WVK3	ELLHLGCNVVIASR	1.15606847	2	4.24377
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.21212049	2	5.48502
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12	3.03200015		
Q9WVK3	KEEEVNNLVK	0.96825986	3	4.01885
Q9WVK3	LTAAVDELR	1.29816408	2	3.18741
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.97438972	2	5.02034
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	1.01236085	3	3.75714
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.9464099	2	6.21111
Q9WVK3	TMALTWASSGVR	0.87438035	2	3.80029
Q9WVK3	TMALTWASSGVR+Oxidation(1	1.25230835		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.15134595**	**0.99538**	**17**
Q9WVK7	AADEFVEK	1.20546856	2	3.35121
Q9WVK7	DTPGFIVNR	1.49939599	2	2.70301
Q9WVK7	EDIDTAMK	1.00845154	1	2.15194
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.12376011	3	4.76593
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	1.11435819	3	5.48344
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(21	1.58519992		
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK+Oxidation(8	1.58677383		
Q9WVK7	GDASKEDIDTAMK	1.19059542	2	3.89158
Q9WVK7	GDASKEDIDTAMK+Oxidation(11	1.76217888		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	1.05977596	4	5.89555
Q9WVK7	KGIEESLK	1.17646842	2	2.4333
Q9WVK7	KGIEESLKR	1.1372298	2	2.42959
Q9WVK7	LKNELFQR	1.94255676	2	2.64532
Q9WVK7	LLVPYLIEAIR	0.93559163	2	2.75832
Q9WVK7	LVEVIK	1.08436374	2	2.41188
Q9WVK7	TFESLVDFCK	0.97126113	2	3.44328
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	1.24041525	3	6.05685

Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.07086769**	**0.99143**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	1.03458444	2	2.91434
Q9Z0N2	SFDVNKPGCEVDDLK	1.51779118	2	3.33122
Q9Z0N2	VGQEIEVRPGIVSK	1.07146353	2	3.25902
Q9Z0U5	**ADO Aldehyde oxidase**	**1.44812328**	**0.81339**	**17**
Q9Z0U5	EFQPLDPTQELIFPPELMR	1.43971824	2	2.62625
Q9Z0U5	ELSILYGGVGPTTIGAK	1.17733316	2	3.54661
Q9Z0U5	GEDMLITGGR	1.89051501	2	2.6167
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	1.27544762	2	4.60753
Q9Z0U5	GYESNINWEK	1.62882839	2	2.6265
Q9Z0U5	HATGEAIYCDDMPAVDR	2.03903836	2	2.70454
Q9Z0U5	HIQDIVAATLK	1.44339859	2	2.72739
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	1.78261181	3	3.68698
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	0.99827641	3	3.49852
Q9Z0U5	KLECGNVDEAFK	1.40025874	2	3.65669
Q9Z0U5	LVLDEVTLAGSAPGGK	1.9225316	2	3.72604
Q9Z0U5	MTWISPVTLEELVEAK	1.14538241	2	3.41583
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	1.82705361	2	3.09925
Q9Z0U5	NMASLGGHIVSR	1.52643981	2	3.17092
Q9Z0U5	QQNALAIVNSGMR	1.02412748	2	2.47314
Q9Z0U5	RLEPIISK	2.49300949	2	2.32455
Q9Z0U5	VVENNVDPEMMLLPYLR	2.12216173	2	2.83989
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**0.87867393**	**0.93027**	**5**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.78419562	3	5.18964
Q9Z0V5	GLFIIDDK	1.09943207	2	3.0266
Q9Z0V5	HGEVCPAGWKPGSETIIPDPAGK	0.86981119	3	3.55903
Q9Z0V5	QITLNDLPVGR	1.12698814	2	3.15417
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	1.13366621	3	5.6153
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**1.13358378**	**0.77259**	**5**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	1.12025022	3	5.43629
Q9Z0V6	GLFIIDPNGVIK	1.1113887	2	3.06107
Q9Z0V6	GTAVVNGEFK	1.2386496	2	2.72945
Q9Z0V6	HLSVNDLPVGR	1.10242269	2	2.58903
Q9Z0V6	NGGLGHMNITLLSDLTK	1.19496802	3	3.48105
Q9Z0W7	**CLIC4 Chloride intracellular channel protein 4**	**1.08063592**	**0.93235**	**3**
Q9Z0W7	DEFTNTCPSDKEVEIAYSDVAK	1.3068779	3	3.64276
Q9Z0W7	FLDGDEMTLADCNLLPK	1.30320892	2	4.24368
Q9Z0W7	NSRPEANEALER	1.05059402	3	4.29236
Q9Z142	**TMM33 Transmembrane protein 33**	**1.67972434**	**0.07134**	**2**
Q9Z142	ALLANALTSALR	1.50049842	2	3.75411
Q9Z142	LSTNQQNILK	1.75450254	2	2.43705
Q9Z1A6	**VIGLN Vigilin**	**1.2677286**	**2.7E-05**	**22**
Q9Z1A6	ASVITQVFHVPLEER	2.02474335	2	3.28023
Q9Z1A6	DLANIAEVEVSIPAK	5.15961668	2	2.54246
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	2.17156136	3	3.45362
Q9Z1A6	ELQAEQEDR	1.59820894	2	2.41051
Q9Z1A6	HEVLLISAEQDKR	1.22304987	3	4.51871
Q9Z1A6	ICLEIMQR	1.23546851	2	2.52203
Q9Z1A6	IDLPAENSNSETIVITGK	0.74969756	2	4.22862
Q9Z1A6	IEGDPQGVQQAK	1.24983289	2	3.46137
Q9Z1A6	IIFPAAEDKDQDLITIIGK	1.51542682	2	4.47798
Q9Z1A6	IQIPRPDDPSNQIK	1.34190952	2	2.50082
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.38143887	2	3.47024
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.18391024	2	4.77892
Q9Z1A6	LGQALTEVYAK	1.6738995	2	3.45592

Q9Z1A6	LQDLELK	1.13964548	1	2.39277
Q9Z1A6	LQTQASATVPIPK	1.17132918	2	3.64996
Q9Z1A6	LVGEIMQETGTR	1.36274637	2	3.51438
Q9Z1A6	MDYVEINIDHK	1.21500132	2	2.80396
Q9Z1A6	MVADLVENSYSISVPIFK	1.35826003	3	3.4058
Q9Z1A6	RCDIIVISGR	1.26564769	2	2.95816
Q9Z1A6	TGAHLELSLAK	1.20184324	3	3.80012
Q9Z1A6	TKDLIIEQR	1.43699726	2	2.67492
Q9Z1A6	VKELQAEQEDR	1.48435491	3	3.74886
Q9Z1J8	**S14L3 SEC14_like protein 3**	**1.64339232**	**0.01034**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	1.6060992	2	2.63266
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	1.58034219	3	4.35021
Q9Z1J8	GSSHQVEYEILFPGCVLR	1.83300796	2	4.8928
Q9Z1L0	**PK3CB Phosphatidylinositol_4_5_bisphosphate 3_kinase catalytic subunit beta isoform**	**0.99566545**	**0.85718**	**2**
Q9Z1L0	MARLCFAVYAVLDK+Oxidation(0	0.98428575		
Q9Z1L0	QPYYYPPFDK	4.36265281	1	1.94183
Q9Z1M9	**SMC1A Structural maintenance of chromosomes protein 1A**	**1.34453088**	**0.62056**	**3**
Q9Z1M9	EIKEKDSELNQK	1.21533703	2	2.56367
Q9Z1M9	IIDETMAQLQDLK	1.35484537	2	2.42764
Q9Z1M9	SGVISGGASDLKAKAR	1.4246429	2	2.33799
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**1.3153778**	**0.34985**	**2**
Q9Z1N1	YVGSMVADVHR	1.29299638	2	2.69828
Q9Z1N1	YVGSMVADVHR+Oxidation(4	1.38866005		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.14852116**	**0.37001**	**5**
Q9Z1P2	DYETATLSEIK	1.67379222	1	1.97016
Q9Z1P2	GISQEQMNEFR	0.95437544	2	2.8984
Q9Z1P2	ICDQWDNLGALTQK	1.10275325	2	4.1241
Q9Z1P2	IDQLEGDHQLIQEALIFDNK	1.37348108	3	3.91686
Q9Z1P2	MVSDINNAWGCLEQAEK	0.44469733	2	2.7107
Q9Z1W6	**LYRIC Protein LYRIC**	**1.22957638**	**0.96483**	**5**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.28304419	3	4.56793
Q9Z1W6	SSSQVPPMLQDTDKPK	1.70695479	2	3.41163
Q9Z1W6	SWQDELAQQAEEGSAR	1.20214505	2	5.682
Q9Z1W6	TELGLDLGLEPK	1.65730222	2	3.37922
Q9Z1W6	TLPPAISAEPSVTLSK	1.04486316	2	2.93514
Q9Z1Y3	**CADH2 Cadherin_2**	**1.4208425**	**0.41119**	**4**
Q9Z1Y3	FLEAGIYEVPIVITDSGNPPK	1.51601619	2	3.95178
Q9Z1Y3	IDPVNGQITTIAVLDR	1.31090629	2	3.92623
Q9Z1Y3	VCQCDSNGDCTDVDR	2.43931105	2	5.10662
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	1.47100755	3	3.59729
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.08200491**	**0.87036**	**3**
Q9Z270	FKGPFTDVVTTNLK	1.13173058	2	3.04318
Q9Z270	HEQILVLDPPSDLK	1.07781977	2	3.7484
Q9Z270	QDGPLPKPHSVSLNDTETR	2.08772998	3	3.40779
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**1.61585638**	**0.21991**	**2**
Q9Z2C8	SVGDGETVEFDVVEGEK	1.62741114	2	3.4501
Q9Z2C8	WFNVRNGYGFINRNDTK	1.51124827	2	2.30786
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**1.10615978**	**0.99972**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.6371902	2	5.00327
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.50776487	3	4.67838
Q9Z2I8	INFDDNAEFR	1.01308012	2	3.1599
Q9Z2I8	LEGTNVQEAQNILK	0.99359317	2	5.20132
Q9Z2I8	SENEPIENEAAR	1.01425515	2	4.19703

Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	1.23893898	2	6.15073
Q9Z2I8	SSGLPITSAVDLEDAAK	0.87212889	2	4.96308
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.90707566	2	2.70027
Q9Z2I8	VMVAEALDISR	1.300701	2	3.19775
Q9Z2I8	VVGELAQQMIGYNLATK	1.51396137	3	3.3922
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.24951756**	**0.00015**	**9**
Q9Z2I9	ALIADSGLK	1.15296536	1	2.15611
Q9Z2I9	AVSSQMIGQK	1.34932247	2	2.92479
Q9Z2I9	ICNQVLVCER	1.86006384	2	2.9847
Q9Z2I9	ILACDDLDEAAK	1.38731341	2	3.31227
Q9Z2I9	INFDSNSAYR	0.96047848	2	3.01595
Q9Z2I9	LSEIVTLAK	1.48123156	2	2.39499
Q9Z2I9	MGFPSNIVDSAAENMIK	0.85164289	2	4.20081
Q9Z2I9	SSDEAYAIAK	1.41628617	2	3.35545
Q9Z2I9	VQAILVNIFGGIMR	1.65663628	2	3.83501
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.09009483**	**3.5E-05**	**13**
Q9Z2L0	EHINLGCDVDFDIAGPSIR	2.5699186	2	3.12806
Q9Z2L0	KLETAVNLAWTAGNSNTR	1.01048635	2	5.44818
Q9Z2L0	LTFDSSFSPNTGK	1.08708635	2	3.72068
Q9Z2L0	LTFDSSFSPNTGKK	1.26905185	2	2.79907
Q9Z2L0	LTLSALLDGK	2.9778364	2	2.6867
Q9Z2L0	SENGLEFTSSGSANTETTK	1.39015347	2	3.76303
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	1.08605192	2	4.98805
Q9Z2L0	TKSENGLEFTSSGSANTETTK	0.60730509	3	3.5979
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	1.10019926	2	4.7374
Q9Z2L0	VTQSNFAVGYK	1.19196247	2	3.43257
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.94428029	2	4.91543
Q9Z2L0	WTEYGLTFTEK	1.58095887	1	2.90325
Q9Z2L0	YQVDPDACFSAK	1.28471673	2	3.3941
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.6008963**	**3.3E-16**	**6**
Q9Z2M4	AAVDAMTR	0.956097	2	2.32431
Q9Z2M4	GQVLQLHAGAAK	1.06960095	2	3.42674
Q9Z2M4	HLAVEWGPQNIR	0.97726261	2	3.49879
Q9Z2M4	LLEFESSSAK	0.63236206	2	2.30242
Q9Z2M4	VNSLAPGAISGTEGLR	0.58767269	2	3.83141
Q9Z2M4	VPPAVMAAVDQALK	1.82263401	2	3.34092
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**0.87282032**	**0.32889**	**3**
Q9Z2M7	IGVVGGSDFEK	1.40618462	2	2.35358
Q9Z2M7	LQEQLGNDVVEK	0.43641379	2	3.86212
Q9Z2M7	TVGYTVTAPEDTR	1.05497418	2	2.659
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.14778133**	**0.15139**	**17**
Q9Z2Q1	AQDGSNPLSLQDLIEK	1.12512345	2	3.42091
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.52662844	2	4.63233
Q9Z2Q1	CLSSATDPQTK	0.65235566	2	2.85184
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.17218305	2	3.4088
Q9Z2Q1	GGPGPLAGHPQVSR	0.62619545	2	3.11751
Q9Z2Q1	IDASQTDFEK	1.12384329	2	2.33075
Q9Z2Q1	IIAGDKEVVIAQK	1.2968653	2	3.03742
Q9Z2Q1	KIDASQTDFEK	1.17932896	2	2.51688
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.25622824	2	3.07342
Q9Z2Q1	QVQHILASASPSGR	1.57634932	2	3.27865
Q9Z2Q1	RQPVFISQVVTEK	0.48256312	2	3.7406
Q9Z2Q1	RQPVFISQVVTEKDFLSR	1.07796326	3	3.53808
Q9Z2Q1	TQPPEDISCIAWNR	1.08899858	2	2.96668
Q9Z2Q1	TTFEDLIQR	1.0096072	2	2.40678

Q9Z2Q1	VNFEEDSR	1.28849372	2	2.39294
Q9Z2Q1	VYSIMGGSIDGLR	1.27764178	2	2.80104
Q9Z2Q1	YLELLGYR	1.05799009	2	2.3738
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.17642498**	**0.91977**	**4**
Q9Z2Z8	AIECSYTSADGLK	1.20580371	2	3.40947
Q9Z2Z8	ASLADIWAK	1.38406722	2	2.35279
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.03818108	2	5.56653
Q9Z2Z8	GYLFPTSAEDCK	0.96281172	2	2.7939
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**1.04167143**	**0.99829**	**2**
Q9Z339	GSAPPGPVPEGQIR	1.04975416	2	3.15614
Q9Z339	LEALELNECIDHTPK	0.70023963	2	3.68915

Time point 12 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (12 h)**	**P-value (12 h)**	**Peptide number (12 h)**
Accession number	Peptide sequence	Peptide Ratio (12 h)	Charge state	Xcorr
A0FKI7	**ACBD5 Acyl_CoA_binding domain_containing protein 5**	**1.161504078**	**0.0664**	**3**
A0FKI7	LQEDMQNVLQR	1.810262011	2	2.585372
A0FKI7	RGGESEDISGVR	1.073827176	2	2.624462
A0FKI7	SSDLTSDLGNVLTSSNAK	0.964968775	2	3.258466
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**0.849199768**	**0.62852**	**2**
A2AAE1	SSRSLDQDSPSKK	0.84089735	2	2.660615
A2AAE1	TVDGNVNSMKRK	0.882498668	2	2.311105
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**0.914120228**	**0.31539**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	0.896677809	2	3.243532
A2ADY9	NPPLAEALLSGDLEK	0.84877232	2	3.426769
A2ADY9	VLVEQQQDR	0.99691041	2	2.469646
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.679899393**	**0.32448**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13)	0.67948714		
A2AGT5	IGSKENTKEGLAELYEYK	0.731169417	2	2.548419
A2AQP0	**MYH7B Myosin_7B**	**1.002290106**	**0.99505**	**13**
A2AQP0	AITDAAMMAEELK	1.522287774	2	2.93084
A2AQP0	AITDAAMMAEELKK	3.037879941	2	3.533626
A2AQP0	AITDAAMMAEELKK+Oxidation(6)	2.002530734		
A2AQP0	AITDAAMMAEELKK+Oxidation(7)	2.002530734	2	2.92241
A2AQP0	CNGVLEGIR	1.477574291	2	2.56169
A2AQP0	DIDDLELTLAK	1.625458009	2	3.795369
A2AQP0	ELEELSER	7.139843504	1	2.076466
A2AQP0	EQDTSAHLER	2.74660322	2	2.491106
A2AQP0	KDIDDLELTLAK	1.007549323	2	2.374543
A2AQP0	SIQELEK	0.995795173	2	2.393534
A2AQP0	TEELEEAK	2.064726245	2	2.364938
A2AQP0	VEDEQLVGVQLQK	2.713727121	2	2.320039
A2AQP0	VGNEYVTK	1.53272942	2	3.03588
A2ASS6	**TITIN Titin**	**0.89390551**	**0.96464**	**32**
A2ASS6	ACDALYPPGPPSNPK	1.82601052	2	2.53571
A2ASS6	AENRFGIGPPAETIQRTTAR	0.863714844	2	2.571583
A2ASS6	AGEDVQLLIPFK	1.373509535	2	2.586797
A2ASS6	APPIEPAPTPIAAPVTAPVVGK	4.616344651	2	4.506479
A2ASS6	ATGLIEGLDYQFR	0.886099648	2	2.990193
A2ASS6	ATLTWTPPLEDGGSPIK	0.94330042	2	2.316728
A2ASS6	ATNEVGSDTCACTVK	4.902925027	2	4.2124
A2ASS6	DGQELQIADRIKIQK	1.05563582	2	2.788064
A2ASS6	DPFDKPSQPGELEILSISK	1.007090686	3	3.67113
A2ASS6	GQSDPVTIGPLTVK	7.387717027	2	2.838985
A2ASS6	GYDEIPLEPNDKTEILK	2.034324138	2	2.419614
A2ASS6	IEALPSDISIDEGK	1.119238631	2	2.420704
A2ASS6	KGDGTQLACKVTGTPPIK	2.196236771	2	2.671027
A2ASS6	NAADNFSEPSESSGAITAR	5.186557922	2	3.984609
A2ASS6	NAADSVSEPSESTGPITVK	1.946413204	2	2.342911
A2ASS6	NAADSVSEPSESTGPITVKDDVEAPR	0.80290557	3	3.44918
A2ASS6	NAAGVFSEPSESTGAITAR	1.158592795	2	4.287962
A2ASS6	QEKIEGDLRAMLK+Oxidation(10)	1.218404367		
A2ASS6	QETEEIAASMVVVATAK	0.859651459	2	2.311084
A2ASS6	SAANLIVEEEDLR	1.035077778	2	2.596856

A2ASS6	VFAENEYGIGDPGETR	0.175515291	2	3.595248
A2ASS6	VGTGEPVETDSPVEAR	2.356753062	2	4.02984
A2ASS6	VIGSPNTPEGPLEYDDIQAR	2.429938323	2	3.607061
A2ASS6	VLACNAGGPGEPAEVPGTVK	5.597643482	2	3.04132
A2ASS6	VLAENEIGIGEPCETTEPVK	3.360487951	2	3.780295
A2ASS6	VLAENEYGIGLPAETAESVK	2.587881952	2	3.502002
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	1.561094695	3	3.598027
A2ASS6	VNAESTENNSLLTIK	1.897616139	2	3.736063
A2ASS6	VSGENEFGVGVPAETK	2.996992124	2	3.676018
A2ASS6	VSNVAGDNACSGILTVK	7.481464421	2	2.932786
A2ASS6	VSVLDVPGPPGPIEISNVSAEK	3.833592268	2	2.720303
A2ASS6	YGIGEPLDSEPETAR	1.70142205	2	3.220699
A2AU37	**RD21L Double_strand_break repair protein rad21_like protein 1**	**0.803416065**	**0.61164**	**2**
A2AU37	MKMTFRPGLVDLPK	0.538840229	1	2.065607
A2AU37	RGGVDMLLSTATQDLINDELK	1.082017606	2	2.361515
A2AWA9	**RBGP1 Rab GTPase_activating protein 1**	**0.811609917**	**0.08266**	**2**
A2AWA9	IVICVQQTANKELAIER	0.59570136	2	2.347069
A2AWA9	RLMELACNTKISQK+Oxidation(2)	1.105773298		
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.664084007**	**2.2E-16**	**11**
A2VCW9	AEGIVFNTQSTIK	1.624257735	2	2.755304
A2VCW9	AGGILQEDITEACLILGVK	1.783771868	2	3.923125
A2VCW9	AQEANMSLLDEVLK	1.473460963	2	4.386465
A2VCW9	GAQEVFNELPCEYVEPHELK	1.660199531	2	4.814317
A2VCW9	KTDGVYDPVEYEKYPER	1.403112269	3	3.912395
A2VCW9	KYDINTVNVTVGK	1.932840506	2	4.093321
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	1.475626737	3	4.090736
A2VCW9	QDAQSLLVPVK	1.007392849	2	2.666499
A2VCW9	REDVNAWER	1.785032982	2	3.088103
A2VCW9	SSVVPVEGCPELPHK	1.892139989	2	2.828781
A2VCW9	YDINTVNVTVGK	1.574742566	2	2.458222
A6H584	**chain**	**1.147082043**	**0.4063**	**7**
A6H584	FVNRAVFRMANGIDR+Oxidation(8)	0.759697548		
A6H584	NEHSFQVVGIQVR	1.057519023		
A6H584	QGDPGIEGPIGFPGPK	0.92020894		
A6H584	RGTQGYGPIGYDGQK	1.244569581		
A6H584	TMNPAFMGLDRATR+Oxidation(1)	0.611430019		
A6H584	YDVTDAVKVLK	0.749442848		
A6H584	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	0.949301345		
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**0.841518695**	**0.35703**	**12**
A7VJC2	GFGFVTFDDHDPVDK	0.98166342	2	3.113469
A7VJC2	GGGGNFGPGPGSNFR	0.947204821	2	3.529153
A7VJC2	GGNFGFGDSR	1.18466075	2	2.481533
A7VJC2	IDTIEIITDR	0.92491911	2	4.104054
A7VJC2	LFIGGLSFETTEESLR	1.239367495	2	3.873233
A7VJC2	LTDCVVMR	1.087333076	2	2.531387
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	1.133358014	2	6.311837
A7VJC2	NYYEQWGK	1.130334771	1	2.438159
A7VJC2	QEMQEVQSSR	0.880102716	2	3.014442
A7VJC2	QEMQEVQSSR+Oxidation(2)	1.013783028		
A7VJC2	TLETVPLER	1.300607714	2	2.316374
A7VJC2	YHTINGHNAEVR	0.898863389	2	3.443421
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.118894367**	**0.82301**	**2**
B0BN93	QMTDPNVALTFLEK	1.14344294	2	2.613935

B0BN93	SAWGQQPDLAANEAQLLR	0.999867037	2	4.055935
B0BN94	**F136A Protein FAM136A**	**1.242012932**	**0.77364**	**2**
B0BN94	CHAPLAQAQALVTSELER	1.365376215	2	3.155535
B0BN94	CSANCCEDNQASMQQVHQCIER	1.100219819	3	4.887235
B0BNE5	**ESTD S_formylglutathione hydrolase**	**0.987288875**	**4.1E-05**	**9**
B0BNE5	AFNGYLGPDQSK	1.028874565	2	3.454436
B0BNE5	AYDATCLVK	1.056469577	2	2.492888
B0BNE5	FAIYLPPQAESAK	1.383314346	2	3.34819
B0BNE5	LQEGYDHSYYFIATFITDHIR	1.071367756	3	3.807578
B0BNE5	MYSYVTEELPQLINANFPVDPQR	0.890848555	3	5.430045
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	0.985173444	2	5.709257
B0BNE5	SVSAFAPICNPVLCPWGK	0.9331954	2	4.041839
B0BNE5	SYSGPQIDILIDQGK	1.019536072	2	3.625741
B0BNE5	VFEHSSVELK	1.085338191	2	2.596017
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.646446978**	**0.04382**	**4**
B0BNN3	ADGLAIIGVLMK	0.298419055	2	3.155029
B0BNN3	GLLSSAEGEPAVPVLSNHRPPQPLK	0.185142458	3	3.38408
B0BNN3	HDSSLKPVSVSYNPATAK	0.842635055	3	4.418994
B0BNN3	VGPANPNLQK	0.33667985	2	2.923068
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.00257751**	**1**	**3**
B0K020	AMVNLQIQK	0.995339595	2	2.36063
B0K020	HNEETGDNVGPLIIK	1.097961342	2	5.499594
B0K020	VVHAFDMEDLGDK	0.893282017	3	3.474493
B2GUY2	**TFR2 Transferrin receptor protein 2**	**1.054784224**	**0.36708**	**2**
B2GUY2	MEQRWGLLRK	0.8046578	2	2.307011
B2GUY2	SAVGTAILLELVR	1.068672775	2	2.440598
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**0.912837692**	**0.60751**	**2**
B2GV24	TYDLPGDFLTQALTQR	0.905793723	2	3.170732
B2GV24	VNIVDLQQVINVDLTHIENR	0.918136146	3	3.333813
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**0.973266555**	**0.85959**	**2**
B2RX88	SISSVNVDQVRMRNEDR	0.967168779	2	2.660302
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(11)	0.887828291		
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.895580414**	**0.08314**	**6**
B2RYW9	ALAAQLPLIPR	0.964436606	2	2.40873
B2RYW9	ATDVMAYVAGFTVAHDVSAR	0.794605986	3	3.825161
B2RYW9	GETALSVAR	0.979588134	2	2.424387
B2RYW9	KGDEVQCEIEELGVIINK	0.845475321	2	5.030748
B2RYW9	TFDTFCPLGPALVTK	0.934309997	2	4.608132
B2RYW9	VNGEIVQSSNTNQMVFK	0.803595328	2	2.63537
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.226459792**	**0.69867**	**4**
B3DMA2	AVLTVTQYR	0.889502554	2	2.528278
B3DMA2	LDNIVFHPK	0.971731704	2	2.452926
B3DMA2	NLPDSDNEECLVHGDFK	1.021807504	2	3.163522
B3DMA2	SGQSNPTFFLQK	0.89029929	2	2.794599
B3GNI6	**SEP11 Septin_11**	**0.944936308**	**0.8077**	**3**
B3GNI6	AAAQLLQSQAQQSGAQQTK	0.877972613	3	3.423206
B3GNI6	FESDPATHNEPGVR	1.240126349	2	3.341409
B3GNI6	SYELQESNVR	0.960645404	2	3.007154
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.062809643**	**0.44789**	**3**
B5DFC8	GTEITHAVVIK	1.308759057	2	2.370891
B5DFC8	GTTEEICQIYLR	1.207157571	2	2.366318
B5DFC8	TEPTAQQNLALQLAEK	1.055383923	2	4.94246

D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**0.913862273**	**0.99503**	**2**
D3ZTX0	QCFYEDITQGTK	0.989019772	2	2.487056
D3ZTX0	SVIDYQTHFR	0.908283169	2	2.505766
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.004413427**	**0.96104**	**4**
D3ZW55	IDLPEYQGEPDEISIQK	0.978433511	2	4.673555
D3ZW55	KLEEVIQILGDKFPCTLVAQK	0.943522368	3	4.068567
D3ZW55	LKPEGLYQLLAGFEDK	1.117642792	3	3.523536
D3ZW55	LQEYFGVTDGAGDH	1.37253592	2	3.564531
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.045943253**	**0.61005**	**2**
D3ZZL9	ELNQKLTNKNSK	1.337338121	2	2.375901
D3ZZL9	IKCLQEESVVQCEELR	0.989325286	2	2.355404
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.165483708**	**0.53027**	**2**
D4A4T9	KEEDSDEIKIGTSCK	1.014888264	2	2.317466
D4A4T9	LSSGNEEDKKEEDSDEIK	1.173041962	3	4.327742
E9Q557	**DESP Desmoplakin**	**0.842795861**	**0.85555**	**2**
E9Q557	KQVQTSQKNTLR	0.835615469	1	2.113665
E9Q557	SQCTQVVQER	0.962912782	2	2.316055
F6YLP3	**selenium transferase**	**0.746616272**	**0.56775**	**3**
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**0.997265531**	**2.7E-15**	**8**
O08557	DENATLDGGDVLFTGR	0.733690129	2	3.3439
O08557	DYAVSTVPVADSLHLK	1.317813159	2	3.654308
O08557	GAEILADTFK	1.016833185	2	2.425145
O08557	GAEILADTFKDYAVSTVPVADSLHLK	0.857019478	3	3.715405
O08557	SFCSMAGPNLIAIGSSESAQK	0.898099343	2	4.946534
O08557	SQGEEVDFAR	1.078578533	2	2.82503
O08557	TPEEYPESAK	1.502035122	2	2.823317
O08557	VDGLLTCCSVFINK	1.009729794	2	3.501412
O08583	**THOC4 THO complex subunit 4**	**0.992734303**	**8.5E-07**	**2**
O08583	QQLSAEELDAQLDAYNAR	0.731786016	2	5.05844
O08583	SLGTADVHFER	1.016456085	2	2.512042
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.166590189**	**0.97677**	**13**
O08601	EDTTMYLLALK	0.848611751	2	2.368634
O08601	EFYSYENEPVGIENLK	3.885191177	2	4.147633
O08601	GCPSLAEHWKSIR	0.939233007	2	3.732044
O08601	GSFASNDIR	0.926336962	2	2.506254
O08601	MLSASGDPVSVVK	1.17428033	2	3.050823
O08601	MLSASGDPVSVVK+Oxidation(0)	0.983246781		
O08601	NALLPEGIPLLLK	0.896229307	1	2.379188
O08601	NILLSIGELPK	0.94791234	2	3.57962
O08601	REEILQILK	0.897260341	3	3.545714
O08601	SDSSIILQER	1.035421551	2	3.298037
O08601	SGSSSAYTGYVER	1.12772446	2	3.423101
O08601	SNLNIFQYIGK	1.167983433	2	3.61238
O08601	VKEFYSYENEPVGIENLK	0.925763561	2	2.879602
O08795	**GLU2B Glucosidase 2 subunit beta**	**1.377407907**	**0.0011**	**6**
O08795	ETVVTSTTEPSR	1.842596679	2	3.109632
O08795	KLWEEQQAAAK	1.008534238	2	2.921249
O08795	LWEEQQAAAK	1.070730433	2	3.331707
O08795	MPPYDEETQAIIDAAQEAR	1.01872311	2	3.128101
O08795	SLEDQVETLR	1.358113877	2	3.260869
O08795	YEQGTGCWQGPNR	1.111441728	2	4.040441

O08810	**U5S1 116 kDa U5 small nuclear ribonucleoprotein component**	**0.950270689**	**0.65844**	**2**
O08810	GGGQIIPTAR	1.159210081	2	2.632741
O08810	GLAEDIENEVVQITWNR	0.915790624	3	3.569975
O09158	**CP3AP Cytochrome P450 3A25**	**1.427774406**	**3.5E-06**	**3**
O09158	DVEINGVFIPK	2.92170601	2	3.153576
O09158	TLLSPTFTSGK	1.426944619	1	1.937561
O09158	VDFLQLMMNTQNSK	1.062886681	2	2.839521
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.491150564**	**9.9E-20**	**16**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.546570611	2	5.840227
O09171	AGPWTPEAAVEHPEAVR	1.673295324	2	5.082752
O09171	AGSNVMQTFTFYASEDK	1.695283867	2	2.91907
O09171	AGSNVMQTFTFYASEDKLENR	1.353168191	2	4.506721
O09171	EATTEQQLR	1.730800481	2	2.40755
O09171	GAAELMQQK	1.796743717	2	3.57105
O09171	GAAELMQQK+Oxidation(5)	1.834901069		
O09171	HGSWGSGLDMHTKPWIR	1.529059313	3	3.705908
O09171	IFHQQLEVFMK	1.335784461	2	2.756684
O09171	KEYWQNLR	1.634380108	3	3.805479
O09171	LNAGEVVIGDGGFVFALEK	1.49882825	3	6.242911
O09171	QGFIDLPEFPFGLEPR	1.386793423	2	5.351922
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.734706299	3	6.355076
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.529677504	3	6.552706
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9)	1.770592357		
O09171	VNEAACDIAR	1.602649166	2	4.035687
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.062206128**	**0.81787**	**10**
O09173	CFYNSDGDFLIVPQK	1.185371453	2	2.947672
O09173	FSVDVFEETR	1.061169702	2	3.188252
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	0.968683045	3	5.988619
O09173	LLIYTEFGK	1.189103254	1	2.054518
O09173	NCMSEFMGLIK	0.865947486	2	3.413135
O09173	QDVSPFNVVAWHGNYTPYK	0.980344109	2	3.647918
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	0.96581048	3	3.720453
O09173	SLRPGVAIADFVIFPPR	0.96136914	2	3.543944
O09173	TFRPPYYHR	1.254151798	3	3.340116
O09173	YISGFGNECASEDPR	1.273203497	2	3.992374
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**0.965683494**	**0.02503**	**19**
O35077	ANTIGISLIK	0.939637148	2	3.173305
O35077	DPAQGQLLK	1.07078656	2	2.412752
O35077	ELHSILQHK	1.442206198	1	2.950029
O35077	FCETTIGCK	1.003345796	2	2.629511
O35077	FCETTIGCKDPAQGQLLK	0.823692848	2	5.054601
O35077	GIDEGPNGLK	0.914313349	2	2.964919
O35077	GLVDKFPLFTAVYK	0.985333116	3	3.607473
O35077	ICDQLKGHLK	0.803307381	3	3.359608
O35077	ITVVQEVDTVEICGALK	0.860126941	3	4.424297
O35077	IVGSNASQLAHFDPR	1.034066385	2	3.143669
O35077	KLTEIINTQHENVK	0.96451699	2	5.103872
O35077	LISEVIGESLGIPMSVLMGANIASEVAEEK	0.652035034		
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	1.057486317	3	5.100658
O35077	LTEIINTQHENVK	0.925043289	2	4.516027
O35077	NIVAVGAGFCDGLGFGDNTK	0.89577549	2	5.425735
O35077	SIEQLEK	0.995795173	2	2.470503
O35077	VCIVGSGNWGSAIAK	0.941940881	2	4.706996

O35077	VCYEGQPVGEFICCLQNHPEHM	0.901815903	2	3.922442
O35077	VTMWVFEEDIGGR	0.844558395	2	3.467677
O35078	**OXDA D_amino_acid oxidase**	**0.793137622**	**0.33381**	**2**
O35078	GQIIQVEAPWIK	0.685993443	2	3.207431
O35078	SCCQLEPTLK	0.996107737	2	2.427518
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.93063701**	**0.22202**	**2**
O35094	KLEESDALQEAR	0.893229404	2	3.354514
O35094	TEMSEVLTEILR	0.95972764	2	3.566688
O35142	**COPB2 Coatomer subunit beta_**	**1.036477676**	**0.54702**	**4**
O35142	AAESLADPTEYENLFPGLK	0.99184377	2	3.363929
O35142	FELALQLGELK	1.133094631	2	3.043797
O35142	GSNNVALGYDEGSIIVK	0.876440188	2	3.587583
O35142	TFEVCDLPVR	1.040639016	2	2.770555
O35244	**PRDX6 Peroxiredoxin_6**	**0.943031645**	**0.99833**	**10**
O35244	DINAYNGAAPTEK	1.099095461	2	3.944559
O35244	DLAILLGMLDPAEKDEK	1.022804085	2	4.318313
O35244	FHDFLGDSWGILFSHPR	0.993767649	3	3.841123
O35244	GESVMVLPTLPEEEAK	0.918701077	2	3.181739
O35244	KGESVMVLPTLPEEEAK	0.955873693	2	4.874437
O35244	KGESVMVLPTLPEEEAK+Oxidation(5)	0.973169115		
O35244	LSILYPATTGR	1.150666543	2	2.876872
O35244	NFDEILR	0.861333	2	2.440198
O35244	VVDSLQLTASNPVATPVDWK	0.936193626	3	5.764417
O35244	VVFIFGPDKK	0.908797727	2	2.385901
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.964278751**	**1.5E-11**	**2**
O35469	DLGYEPLVSWEEAK	1.222583857	2	4.225851
O35469	TSEWIGTLVEQHR	0.739564263	2	3.485808
O35509	**RB11B Ras_related protein Rab_11B**	**1.083512586**	**0.97876**	**5**
O35509	AQIWDTAGQER	0.997759026	2	2.84259
O35509	GAVGALLVYDIAK	0.915202486	2	4.216823
O35509	HLTYENVER	0.949319456	2	3.010223
O35509	NEFNLESK	1.085156091	1	2.14975
O35509	VVLIGDSGVGK	1.02864764	2	2.704652
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**0.99868063**	**0.99395**	**2**
O35547	LERFEIPIK	0.999609363	2	2.679689
O35547	LSPEPWTPETGLVTDAFK	0.753729946	2	2.728541
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.006946008**	**0.70935**	**8**
O35567	AEVSNAIDQYVTGTIGEGEDLVK	0.822563548	2	4.408747
O35567	ALFEEVPELLTEAEK	0.972505456	2	3.774465
O35567	DGQVIGIGAGQQSR	1.124940472	2	3.168031
O35567	EVSDGIVAPGYEEEALK	1.091977188	2	4.171121
O35567	HVSPAGAAVGVPLSEDEAR	1.194361538	2	3.510359
O35567	RAEVSNAIDQYVTGTIGEGEDLVK	0.977218777	3	3.74148
O35567	SGVAYIVAPSGSTADK	1.024782117	2	3.097062
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.036211553	2	5.278191
O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**0.983785917**	**0.30105**	**2**
O35593	AVAVVVDPIQSVK	1.02934668	2	2.712783
O35593	VIDVFAMPQSGTGVSVEAVDPVFQAK	0.498631987	2	3.74656
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.1379977**	**1**	**2**
O35660	RYAMGDAPDYDR	1.119321203	2	3.130999
O35660	YAMGDAPDYDR+Oxidation(2)	1.096930699		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**1.092940773**	**0.99968**	**3**

O35760	AELGIPLEEVDLNEMNYLTR	0.967208798	2	4.26437
O35760	NCHLNENIDK	1.092884025	2	2.988859
O35760	NVTLNPDPNEIK	1.357558078	2	2.89706
O35763	**MOES Moesin**	**0.916717015**	**0.69467**	**2**
O35763	ALTSELANAR	0.917482721	2	3.170505
O35763	FYPEDVSEELIQDITQR	0.825291839	2	4.400842
O35783	**CALU Calumenin**	**1.112636837**	**0.93845**	**2**
O35783	HLVYESDQDKDGK	1.111005474	2	4.045784
O35783	VHNDAQNFDYDHDAFLGAEEAK	1.335332902	3	4.150329
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.125209689**	**0.96176**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	1.02614776	2	4.698423
O35796	AFVEFLTDEIK	0.943352129	2	3.625874
O35796	AFVEFLTDEIKEEK	1.01377983	2	3.572408
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.412292971	3	5.770348
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.026434153**	**0.09813**	**6**
O35814	ALDLDSSCK	0.993191346	2	2.366043
O35814	ALSAGNIDDALQCYSEAIK	0.969472738	2	5.29577
O35814	DCEECIQLEPTFIK	1.06955527	2	3.933009
O35814	ELIEQLQNKPSDLGTK	1.575324282	2	3.866702
O35814	LDPQNHVLYSNR	1.129539999	2	2.613568
O35814	LMDVGLIAIR	1.059116156	2	2.451773
O35820	**RCL Deoxyribonucleoside 5__monophosphate N_glycosidase**	**0.827229025**	**0.6023**	**2**
O35820	GGREDQALYAR	0.827007584	2	2.559
O35820	YFEAYLPQK	1.109768095	2	2.334074
O35821	**MBB1A Myb_binding protein 1A**	**1.407612461**	**0.00115**	**2**
O35821	ALDLIEVLVTK	1.292491832	2	3.055256
O35821	NVANVTPLTAQQR	1.616480175	2	3.027622
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**1.100131116**	**0.30421**	**2**
O35824	FDVQFPENNWINPDK	0.959259144	2	3.291251
O35824	NVLCSACSGQGGK	1.111861823	2	3.272644
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.175126379**	**0.01892**	**8**
O35826	DEAVGALHLIQAAK	1.213375879	2	3.47456
O35826	EVGAFGTPVINLGTR	1.159381928	2	2.864459
O35826	GEDEAAMVESVGLALVK	1.280340228	2	2.453385
O35826	IYGDGNAVPR	1.198311866	2	2.577689
O35826	SIDLQEPLQK	1.25218424	2	2.373598
O35826	TLVLFPNIDAGSK	0.987142254	2	3.097761
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.211926179	3	5.235929
O35826	VNPQEGVVLHSTK	1.255223133	2	2.547785
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.976038808**	**0.03412**	**5**
O35913	EGLQENVDGTENAK	1.615866422	2	3.668488
O35913	GASFVPAFFILR	1.088890739	2	2.699051
O35913	ILAGIPAPIYFGALIDR	1.153297116	2	2.415658
O35913	SLSGTYMNSMLTQIER	0.948358907	2	4.259255
O35913	SQTLNPTQDPSECVK	1.156924095	2	4.175505
O35923	**BRCA2 Breast cancer type 2 susceptibility protein homolog**	**0.683988326**	**0.51646**	**2**
O35923	AMKLFSDIENISEEPSTK	0.718466155	2	2.552217
O35923	SLLNEFDRIIESKGK	0.783095602	2	2.423902
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**0.918705367**	**0.00423**	**8**
O35952	ALLEVLGR	0.857067005	2	3.120642
O35952	FYEGTADEMYK	1.729197431	2	2.516407

O35952	HVEPGNTAVQEK	1.070079892	2	4.055639
O35952	LTTVLTTHHHWDHAGGNEK	0.997534232	3	3.913594
O35952	NAIGEPTVPSTLAEEFTYNPFMR	0.769727357	2	3.547781
O35952	TVQQHAGETDPVTTMR	0.934008571	2	5.104128
O35952	TVQQHAGETDPVTTMR+Oxidation(14)	0.938124174		
O35952	VTHLSTLEVGSLSVK	0.923735317	2	2.883583
O35987	**NSF1C NSFL1 cofactor p47**	**1.050570037**	**0.01131**	**6**
O35987	ASSSILINEAEPTTNIQIR	0.998225284	2	5.336307
O35987	EANLLNAVIVQR	1.383565648	2	3.370299
O35987	LGAAPEEESAYVAGER	1.202854481	2	4.021342
O35987	LGSTAPQVLNTSSPAQQAENEAK	1.142442097	2	3.968664
O35987	RGEVPAELR	2.637837237	2	2.471083
O35987	SYQDPSNAQFLESIR	0.997959452	2	4.488661
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.675294487**	**8.7E-05**	**3**
O54753	CSTNLSLVTDCMEHALTSK	2.791563333	3	3.395102
O54753	TWEATPEHIR	1.944257467	2	2.310511
O54753	YGVEAFSDVLR	1.517400812	2	2.727089
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**0.971165768**	**3.8E-06**	**2**
O54975	GSLTFEPLTLVPIQTK	0.981770186	2	4.041873
O54975	IENVVLVVPAK	0.82568763	2	2.895174
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.084418138**	**0.00278**	**5**
O55012	ATTLSNAVSSLASTGLSLTK	0.724602939	2	3.839085
O55012	ITAAQHSVTGSAVSK	1.479816324	2	4.302684
O55012	NTLFNLSNFLDK	1.113404939	2	2.540184
O55012	SGLQGYDMSTFIR	0.974644474	2	2.361617
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	1.061012785	3	5.658778
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.163983949**	**0.78141**	**6**
O55096	AGLLALEFYTPETANWR	0.995579375	2	3.922763
O55096	GEFEGFVAMVNK	0.898481968	2	3.075861
O55096	LASVLNTEPALDSELTSK	1.221661868	2	3.384279
O55096	NVSLGNVLAVAYATK	0.781855867	2	2.38712
O55096	SYEFQGNHFQVTR	0.840553308	2	3.819559
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.021975306	3	3.402171
O55125	**NIPS1 Protein NipSnap homolog 1**	**0.948494223**	**0.30691**	**4**
O55125	AGPNIYELR	1.005817482	2	3.04349
O55125	FSGGYPALMDCMNK	0.777340417	2	3.133015
O55125	GWDENVYYTVPLVR	1.118507456	2	3.458383
O55125	IQFHNVKPECLDAYNSLTEAVLPK	0.917892637	3	4.36804
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.199238096**	**0.80758**	**6**
O55171	ADAGGELDLAR	0.808250244	2	3.276752
O55171	DGLLDVVEALQSPLVDKK	1.181124235	2	5.071033
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.16863319	3	4.466774
O55171	GGELGLAMASFLK	1.158972781	2	3.847528
O55171	IEYFEEAVNYLR	1.008268095	2	4.191815
O55171	SCWDEPLSITVR	1.048438494	2	3.49113
O70127	**ABCBB Bile salt export pump**	**1.671349506**	**8.6E-06**	**8**
O70127	AGQITSEALSNIR	1.34427903	2	3.288379
O70127	AGSIADEVLSSIR	1.375988303	2	2.639027
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.440529031	3	4.16927
O70127	ILLLDEATSALDTESEK	1.479607475	2	4.181277
O70127	KFGEENHAFESDGSHNNDKK	1.324739993	3	3.933345
O70127	KPPINVYSEAGEK	2.241839848	2	3.316954
O70127	STALQLIQR	1.771087664	2	2.350636
O70127	YETNVGIQGSQLSR	0.929765539	2	3.46657

O70133	**DHX9 ATP_dependent RNA helicase A**	**1.210024797**	**0.923**	**2**
O70133	KMTPAYEIRAVGNK	0.833217268	2	2.565521
O70133	YPSPFFVFGEKIR	1.311039709	2	2.500704
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**0.942237741**	**0.01666**	**11**
O70199	EQIVVDLSHPGVSADDQVSR	1.097099755	2	5.671396
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	0.966463803	3	5.211238
O70199	IIDSLFNTVTDK	0.881249834	2	2.87754
O70199	IIDSLFNTVTDKK	0.815012756	2	3.543528
O70199	ILTTNTWSSELSK	0.952768941	2	3.342861
O70199	INAWNSPTLPIYEPGLK	0.984782236	2	3.728618
O70199	NLFFSTNIDDAIR	1.019657338	2	3.147455
O70199	VLDGLHNELQTIGFQIETIGK	0.833763272	2	5.335101
O70199	VLIGGDETPEGQR	1.057792131	2	3.616722
O70199	VTVVDVNEAR	1.004597412	2	3.363352
O70199	YWQQVIDMNDYQR	0.981858047	2	4.833843
O70251	**EF1B Elongation factor 1_beta**	**1.080597755**	**0.15338**	**4**
O70251	SIQADGLVWGSSK	1.108304835	2	3.765084
O70251	SSILLDVKPWDDETDMTK	1.09068289	2	4.20245
O70251	SSILLDVKPWDDETDMTKLEECVR	1.0756444	3	5.13022
O70251	TPAGLQVLNDYLADK	1.028713038	2	4.095759
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**0.939860005**	**2.6E-05**	**16**
O70351	GGIVGMTLPIAR	0.903068726	2	3.356582
O70351	GLVAVITGGASGLGLSTAK	0.878083203	2	4.690108
O70351	GVIINTASVAAFEGQVGQAAYSASK	0.970433925	3	4.100465
O70351	IDVAVNCAGIAVAIK	0.841689949	2	3.977468
O70351	KLGGNCIFAPANVTSEK	1.011919728	2	4.468948
O70351	KNQVHTLEDFQR	1.023054623	2	4.114242
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	0.911212152	3	4.315888
O70351	LGGNCIFAPANVTSEK	0.988809732	2	3.486175
O70351	LVAGVMGQNEPDQGGQR	1.152809425	2	5.227586
O70351	LVAGVMGQNEPDQGGQR+Oxidation(5)	0.817138708		
O70351	LVGQGATAVLLDVPNSEGETEAK	1.242492619	2	5.67453
O70351	NFLASQVPFPSR	0.912545633	2	4.559295
O70351	NQVHTLEDFQR	1.024535916	2	3.310391
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.015771887	2	5.040431
O70351	VINVNLIGTFNVIR	0.897403192	2	3.79679
O70351	VVTIAPGLFATPLLTTLPDK	0.977637085	2	5.420006
O70456	**1433S 14_3_3 protein sigma**	**1.153591065**	**3.1E-13**	**3**
O70456	DSTLIMQLLR	1.495600834	2	3.412398
O70456	DSTLIMQLLR+Oxidation(5)	1.177161527		
O70456	VLSSIEQK	0.937676151	2	3.254664
O70593	**SGTA Small glutamine_rich tetratricopeptide repeat_containing protein alpha**	**1.247174061**	**0.16874**	**2**
O70593	AIELNPANAVYFCNR	0.900964838	2	3.002361
O70593	TPPSEEDSAEAER	1.276227927	2	2.710049
O88202	**LPP60 60 kDa lysophospholipase**	**1.133830969**	**0.98868**	**2**
O88202	AAGAHLSPQELEDVGTELCR	1.031000993	3	3.690825
O88202	GVDVDACNEDGQSPLLLAVR	1.11509839	2	5.224089
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**1.038677524**	**0.95547**	**5**
O88428	GCTVWLTGLSGAGK	0.949802707	2	2.848485
O88428	GIHELFVPENK	1.144211292	2	2.611675
O88428	NLGFSAGDREENIR	1.070224695	2	3.361606
O88428	STNVVYQAHHVSR	0.906097495	2	3.474065
O88428	VLSMAPGLTSVEIIPFR	0.772685122	2	3.316246

O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**0.781814263**	**0.19494**	**2**
O88491	ENSEGAFGVLLPADAVQKAR	0.711927916	2	2.344276
O88491	SGKGEGLKLLNNMHEK	0.956850654	2	2.906617
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.059595035**	**0.85172**	**14**
O88600	AESEEMETSQAGSK	0.908640723	2	4.514785
O88600	AGGIETIANEYSDR	0.978481578	2	3.463859
O88600	FQESEERPK	0.405214006	2	2.328101
O88600	GCALQCAILSPAFK	0.898613293	2	4.046768
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	1.228835917	3	5.239132
O88600	LKETAESVLK	0.972714811	2	2.464055
O88600	MIMQDKLEK+Oxidation(0)	1.002383861		
O88600	MQVDQEEPHTEEQQPQTPAENK	1.067859524	3	4.74823
O88600	NFTTEQVTAMLLSK	0.911886272	2	3.705788
O88600	SNLAYDIVQLPTGLTGIK	1.021463028	2	4.945822
O88600	SVMDATQIAGLNCLR	0.903233993	2	2.889576
O88600	TSTVDLPIESQLLWQLDR	0.919051303	2	3.834906
O88600	VLATAFDTTLGGR	1.043317755	2	3.479396
O88600	WNSPAEEGSSDCEVFPK	0.839593739	2	3.414482
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**0.967779039**	**0.9739**	**21**
O88618	AFAACLGAIK	0.913004826	2	2.889683
O88618	AGEYEALPEK	1.009112972	2	2.863834
O88618	ALLDAAAFYCDK	1.033813952	2	3.467166
O88618	ALLDAAAFYCDKEK	0.800699998	2	3.33453
O88618	EAQELNLPVVGSQLVGLVPLK	1.21842987	3	4.043879
O88618	GVSMDECVLCAK	1.033808375	2	3.906974
O88618	IIEYLVPDSGPEQSLLDASLR	0.926225878	2	5.133275
O88618	ISSLLQEAK	1.130495208	2	2.711395
O88618	LAEELNVPVYLYGEAAQMPSR	0.931728143	2	4.975207
O88618	LAETVSQLWPALQELAQCGNLSCLSDLQVAAK	1.046240898	4	5.012574
O88618	LFVLEEEHR	1.087390257	2	2.766589
O88618	LGLDSLAPFDPK	0.308646517	2	3.640337
O88618	LIPPFHAASAQLTSLVDADAR	1.186700414	3	3.554824
O88618	MGALDVCPFIPVR	0.874720638	2	3.794453
O88618	MGALDVCPFIPVR+Oxidation(0)	0.905915472		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	0.920889636	3	4.505769
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	0.978996881	2	4.156594
O88618	TCALQEGLR	1.289390994	2	2.87365
O88618	TQAALVLGSLEAR	0.893162497	2	5.065959
O88618	TVYTFVGQPECVVEGALSAAR	1.034763839	2	4.854225
O88618	VQGIGWYLEEK	0.912379881	2	3.182912
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.085819826**	**0.98533**	**5**
O88637	GPPVFTQEER	1.071265947	2	2.73447
O88637	HKGPPVFTQEER	1.123729707	2	2.624393
O88637	TQGVSTTDLVGR	1.083230236	2	2.771423
O88637	WVDEVVPAAPYVTTLETLDK	0.946976156	2	3.142456
O88637	YVSEVVIGAPYSVTAELLNHFK	0.899257864	3	3.425522
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**0.916865984**	**0.99547**	**2**
O88656	ASSEGGAATGAGLDSLHK	0.905673894	2	4.384912
O88656	NSVSQISVLSGGK	0.979600281	2	2.447628
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**1.077127629**	**0.39107**	**2**
O88696	GQATDIAIQAEEIMK	1.036955908	2	3.618744
O88696	VLVHPPQDGEDEPELVQK	1.32825243	3	4.499228
O88746	**TOM1 Target of Myb protein 1**	**0.974916159**	**0.99999**	**3**

O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	1.004855487	3	5.876241
O88746	QQSTGAIPATQAR	0.966424049	2	2.614947
O88746	YEAPQTTDGLAGALDAR	0.999452467	2	4.199483
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.000908738**	**0.10192**	**4**
O88761	DTSEDIEELVEPVAAHGPK	1.082486712	2	3.818461
O88761	QCVENADLPEGEK	1.292851888	2	2.501987
O88761	TPEQCPSVVSLLSESYNPHVR	1.122681287	3	4.438766
O88761	TVGTPIASVPGSTNTGTVPGPEK	0.921551798	2	3.733288
O88767	**PARK7 Protein DJ_1**	**0.99800274**	**0.99998**	**6**
O88767	DVVICPDTSLEEAK	1.119495501	2	3.31286
O88767	GAEEMETVIPVDIMR	0.903339375	2	4.050001
O88767	GAEEMETVIPVDIMR+Oxidation(13)	0.990343266		
O88767	GLIAAICAGPTALLAHEVGFGCK	0.81453948	2	4.897345
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	0.986995729	2	4.723402
O88767	VTVAGLAGKDPVQCSR	1.007529289	2	4.445266
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**1.063367334**	**0.99135**	**2**
O88794	KKNEELGQLYR	1.074058968	2	2.779869
O88794	SSQIGAVVSR	1.060607938	2	2.89101
O88801	**HOME2 Homer protein homolog 2**	**0.831788805**	**0.52798**	**2**
O88801	EKEMELK	0.846016494	1	2.10689
O88801	EKNTQLK	0.792155665	1	2.020127
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.030798432**	**0.86228**	**15**
O88813	AILEDLQK	0.880081316	1	2.423197
O88813	ATMLIENVEK	1.086777774	2	2.370865
O88813	ATMLIENVEKDLTPGLK	1.164677665	2	2.451185
O88813	ATMLIENVEKDLTPGLK+Oxidation(2)	1.025386005		
O88813	FFQTQIK	0.846347258	1	1.991065
O88813	GLAVSDNGPCLGYR	0.910520753	2	3.810367
O88813	GSFEELCQNQCVK	0.991618398	2	4.287456
O88813	IGFFQGDIR	1.048025953	2	3.321431
O88813	LVQGVIFSCGGK	1.264826475	2	2.866491
O88813	NNDLILYYFSDAK	0.826345916	2	3.724621
O88813	SFLIGVVVPDPESLPSFAAK	0.842740928	2	4.330254
O88813	SIFVHPEPFSIENGLLTPTLK	0.883418733	2	3.032535
O88813	SRPILQVFVHGESLR	0.27881906	3	3.86181
O88813	TQEVLDKDGWLHTGDIGR	0.928040051	3	4.391942
O88813	TVILMDPFDDDLMK	0.828018504	2	3.128828
O88867	**KMO Kynurenine 3_monooxygenase**	**0.907110026**	**0.00519**	**4**
O88867	AVGLEDQIVSK	0.954719099	2	2.654234
O88867	DLLTAVESYPNAK	2.210197476	2	2.792644
O88867	NFPDAIPLMGEQALMR	0.999093894	2	2.862323
O88867	NFQVDVYEAR	1.222862981	2	2.888409
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.166987209**	**0.08761**	**4**
O88941	DLALPTLLNPK	1.17794013	2	2.529927
O88941	DQASEQLVGGQLTR	1.29083049	2	2.905201
O88941	LGPLLDVLADSR	0.977942555	2	3.293821
O88941	MDPSLFPPVPLFSGVPSR	0.911031349	2	2.71819
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**0.910234593**	**0.97676**	**2**
O88986	GTDELLGVMDQVTIINSTLGK	0.900265945	2	3.31637
O88986	HLDMADLEAK	0.975778454	2	2.315195
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**0.998896412**	**0.14736**	**8**
O88989	DLDVAVLVGSMPR	1.906935067	3	4.05575
O88989	ELTEEKETAFEFLSSA	1.091425296	2	3.703944
O88989	EVGVYEALKDDSWLK	1.435112991	2	3.752205
O88989	FVEGLPINDFSR	0.897345685	2	3.630882

O88989	GEFITTVQQR	1.039806128	2	4.270136
O88989	LGVTADDVK	1.146707162	2	2.85596
O88989	NVIIWGNHSSTQYPDVNHAK	0.961736809	2	5.619033
O88989	VIVVGNPANTNCLTASK	1.028818149	2	5.389115
O88990	**ACTN3 Alpha_actinin_3**	**0.819524534**	**4.4E-12**	**12**
O88990	AGTQIENIEEDFR	0.75909683	2	3.579388
O88990	CQAICDQWDNLGTLTQK	2.807224835	2	5.168026
O88990	CQLEINFNTLQTK	0.817267167	2	4.118224
O88990	FAIQDISVEETSAK	0.847682943	2	3.664222
O88990	GKEEMLNQHDYESASLQEVR	1.332230218	3	4.784576
O88990	GLSQEQLNEFR	2.821846105	2	2.608653
O88990	HEAFESDLAAHQDR	1.194349156	3	4.498434
O88990	RHEAFESDLAAHQDR	3.35066763	3	4.798569
O88990	SGNPYITLSSQDINNK	1.311377971	2	3.802952
O88990	VEHIAALAQELNELDYHEAASVNSR	1.128113335	3	4.124232
O88990	VGWEQLLTSIAR	0.924971356	2	2.563041
O88990	VLAVNQENEK	4.771921814	2	2.490795
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.658527852**	**0.00688**	**2**
O88994	CVLTTVDPDTGIIDR	0.657467129	2	4.111473
O88994	RQLQQVGTVSK	0.882406503	2	2.502644
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**0.918841865**	**0.90974**	**7**
O89000	EGGADGVTATNTVSGLMGLK	1.000446067	2	3.829697
O89000	GAVIVLGAGDTAFDCATSALR	0.854503481	2	2.314921
O89000	GMGLACGQDPELVR	1.095616306	2	3.188407
O89000	GTTSGPLYGPGQSSFLNIELISEK	0.814885483	2	3.519427
O89000	LTPNVTDIVSIAR	1.306597592	2	2.349785
O89000	QEYVGGLSTSEIPQFR	0.984785077	2	3.621115
O89000	TEQDETGNWVEDEEQIVR	0.999449256	2	4.719432
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.075637144**	**0.6033**	**2**
O89032	DDSDINTSKTGEVSKR	1.271675949	2	2.547387
O89032	EGWAPASYIDKRK	0.772191058	1	1.973449
O89046	**COR1B Coronin_1B**	**0.866492315**	**0.00067**	**3**
O89046	NDQCYEDIR	0.916257508	2	2.82929
O89046	NVLSDSKPAGYSR	0.870192961	2	3.129846
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.663712163	2	3.814561
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**0.948880752**	**0.76454**	**6**
O89049	IEQIEAGTPGR	1.284561427	2	3.420818
O89049	IEQIEAGTPGRLK	0.558564651	2	2.45242
O89049	LELTPVAIQAGR	1.026897586	2	2.66957
O89049	STNSEETIEDEFNTVLLAVGR	0.899949254	2	4.228694
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.949069163	3	4.035128
O89049	WGLGGTCVNVGCIPK	0.954449628	2	2.922061
P00173	**CYB5 Cytochrome b5**	**1.035453121**	**1**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	1.145362581	2	5.440202
P00173	FLEEHPGGEEVLR	0.950454238	2	4.331065
P00173	STWVILHHK	0.839140849	2	2.793056
P00173	TYIIGELHPDDR	1.024921934	2	4.244727
P00173	VYDLTK	0.993963104	1	2.135064
P00173	YYTLEEIQK	1.041747871	2	3.017815
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.737345753**	**9.9E-20**	**12**
P00388	DGALTQLNVAFSR	1.076570357	2	2.418118
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.617585755	3	4.795228
P00388	FAVFGLGNK	2.153050718	2	2.508693
P00388	GMSADPEEYDLADLSSLPEIDK	1.75114212	2	5.055513

P00388	GVATSWLR	2.122457804	2	2.336932
P00388	LEQLGAQR	1.852547395	2	2.640414
P00388	NIIVFYGSQTGTAEEFANR	1.275417843	2	3.17912
P00388	RSDEDYLYR	1.657309385	2	3.364368
P00388	SDEDYLYR	1.673252548	2	2.608301
P00388	SYENQKPPFDAK	1.748340733	2	3.25428
P00388	TALTYYLDITNPPR	1.191116452	2	2.506228
P00388	TNVLYELAQYASEPSEQEHLHK	1.798421286	3	3.685663
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.200244776**	**0.99562**	**5**
P00406	ILYMMDEINNPVLTVK	0.835535288	2	2.307731
P00406	LLEVDNR	1.171213408	2	2.52598
P00406	MLISSEDVLHSWAIPSLGLK	0.872212762	2	3.570268
P00406	VVLPMELPIR	1.034305065	2	2.680752
P00406	VVLPMELPIR+Oxidation(4)	1.013319578		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**0.857344371**	**0.01312**	**16**
P00481	FGMHLQAATPK	0.954914324	3	4.129622
P00481	GEYLPLLQGK	0.84116661	2	3.211051
P00481	GGNVLITDTWISMGQEDEK	0.748865059	2	4.995953
P00481	GGNVLITDTWISMGQEDEKK	0.669237599	2	4.640275
P00481	GLTLSWIGDGNNILHSIMMSAAK	0.787526039	2	4.19529
P00481	GYEPDPNIVK	0.925828029	2	2.69013
P00481	KPEEVDDEVFYSPR	1.779867421	2	3.52652
P00481	LQAFQGYQVTMK	1.009068184	2	3.839989
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	0.897222715	3	5.761353
P00481	QKGEYLPLLQGK	0.984957066	2	2.994097
P00481	SLGMIFEK	0.779141054	2	2.441405
P00481	SLVFPEAENR	0.957061353	2	2.649328
P00481	SLVFPEAENRK	0.874010587	2	2.95112
P00481	VLSSMTDAVLAR	0.835075651	2	3.980601
P00481	VLSSMTDAVLAR+Oxidation(4)	1.015072708		
P00481	YGKPVQSQVQLK	0.677278924	2	3.004725
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.770186285**	**1**	**2**
P00502	FIQSPEDLEK	0.778010095	2	2.587286
P00502	WLLAAAGVEFDEK	0.790985624	2	4.326678
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**0.90760071**	**1.4E-05**	**18**
P00507	ASAELALGENSEVLK	0.918155318	2	4.698341
P00507	DAGMQLQGYR	2.499218697	2	3.039075
P00507	DDNGKPYVLPSVR	1.084979131	2	2.740834
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.115772624	3	5.41396
P00507	EYLPIGGLADFCK	1.396899669	2	2.819358
P00507	FVTVQTISGTGALR	0.869876794	2	5.039452
P00507	HFIEQGINVCLCQSYAK	0.911702586	2	4.522585
P00507	IAATILTSPDLR	1.154990224	2	3.093737
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.034262644	3	4.310308
P00507	ISVAGVTSGNVGYLAHAIHQVTK	0.752721277	2	4.782934
P00507	KQWLQEVK	0.80774795	1	2.138605
P00507	MNLGVGAYR	0.939738023	2	2.934601
P00507	NLDKEYLPIGGLADFCK	0.894251911	2	5.338366
P00507	NMGLYGER	0.971204548	2	2.506797
P00507	TCGFDFSGALEDISK	0.956159825	2	4.821503
P00507	TQLVSNLK	0.945070301	2	2.961006
P00507	VGAFTVVCK	0.968922609	2	3.367226
P00507	VGASFLQR	1.010027995	2	3.004443
P00564	**KCRM Creatine kinase M_type**	**1.138870248**	**0.99965**	**11**
P00564	DLFDPIIQDR	0.923392202	2	2.490117

P00564	FEEILTR	2.786817817	2	2.469936
P00564	GGDDLDPNYVLSSR	0.879722974	2	4.798523
P00564	GQSIDDMIPAQK	3.868366357	2	3.37611
P00564	GTGGVDTAAVGAVFDISNADR	1.34914155	2	6.067082
P00564	LGSSEVEQVQLVVDGVK	2.903929705	2	4.918209
P00564	LSVEALNSLTGEFK	3.01736785	2	4.338848
P00564	RGTGGVDTAAVGAVFDISNADR	3.071859427	2	5.883774
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	2.824103467	3	5.872811
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR+Oxidation(1)	2.140111494		
P00564	TDLNHENLK	1.638987072	2	2.529152
P00787	**CATB Cathepsin B**	**0.953896288**	**0.9809**	**5**
P00787	GENHCGIESEIVAGIPR	0.955847329	2	4.52138
P00787	HEAGDVMGGHAIR	0.869167168	3	3.560832
P00787	HEAGDVMGGHAIR+Oxidation(6)	1.218754277		
P00787	MCEAGYSTSYKEDK	1.095340144	2	3.880888
P00787	NGPVEGAFTVFSDFLTYK	0.955334116	2	3.26154
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**0.990120678**	**0.12387**	**19**
P00884	ALQASALAAWGGK	0.987102232	2	4.860201
P00884	ATQEAFMK	1.083601049	2	2.609433
P00884	ATQEAFMK+Oxidation(6)	1.071361144		
P00884	ELLFSVDNSISQSIGGVILFHETLYQK	1.215823957	3	3.794712
P00884	ELSEIAQR	6.087707342	1	2.115321
P00884	ETTIQGLDGLSER	1.439519353	2	4.025199
P00884	GILAADESVGTMGNR	1.024596828	2	5.584123
P00884	GILAADESVGTMGNR+Oxidation(11)	1.041154498		
P00884	GIVVGIKLDQGGAPLAGTNK	1.216180274	2	3.465734
P00884	IKVENTEENR	1.306931948	2	2.478102
P00884	IKVENTEENRR	1.112620137	2	2.923598
P00884	ISDQCPSSLAIQENANALAR	0.967417714	2	6.218312
P00884	KELSEIAQR	1.092620677	2	2.843675
P00884	KYTPEQVAMATVTALHR	0.892806265	3	5.706024
P00884	KYTPEQVAMATVTALHR+Oxidation(8)	0.884624662		
P00884	LDQGGAPLAGTNK	0.985531032	2	4.596908
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.185369527	3	4.999493
P00884	YTPEQVAMATVTALHR	0.920701023	2	4.5543
P00884	YTPEQVAMATVTALHR+Oxidation(7)	0.945109333		
P01015	**ANGT Angiotensinogen**	**1.813612177**	**9.9E-20**	**3**
P01015	GSYNLQDLLAQAK	2.210197476	2	2.80368
P01015	SLDLSTDPVLAAQK	1.690747388	2	3.317123
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	1.677795514	2	3.915774
P01026	**CO3 Complement C3**	**1.250899188**	**3.9E-05**	**17**
P01026	AAVFNHFISDGVK	1.087311421	2	2.354795
P01026	ACEPGVDYVYK	1.175054202	2	2.57538
P01026	ADIGCTPGSGK	1.266066691	2	2.841699
P01026	DSCVGTLVVKGDPR	0.828977233	2	2.409441
P01026	EYVLPSFEVLVEPTEK	1.012932041	2	3.254046
P01026	IFTVDNNLLPVGK	1.124166648	2	3.105247
P01026	IGLQEVEVK	0.966911507	2	2.38234
P01026	RVPVVTQGSDAQALTQDDGVAK	1.163344259	3	5.53011
P01026	SGIPIVTSPYQIHFTK	1.820396556	2	3.209617
P01026	SGSDEVQAGQER	1.493834904	2	4.084831
P01026	SSVAVPYVIVPLK	1.007241769	2	3.151322
P01026	TVLTGATGHLNR	1.264146292	2	3.09662
P01026	VELKPGDNLNVNFHLR	1.03758306	3	5.341079
P01026	VHQFFNVGLIQPGSVK	1.328640763	3	3.971458
P01026	VLIEDGSGEAVLSR	1.229919625	2	4.530239

P01026	VPVVTQGSDAQALTQDDGVAK	1.367527648	2	5.903897
P01026	VTIKPAPETAK	1.357847617	2	2.535371
P01048	**KNT1 T_kininogen 1**	**0.469498126**	**0.64286**	**2**
P01048	FSVATQICNITPGK	0.806611706	2	2.843359
P01048	TELTADCETK	0.416388746	2	2.379227
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.328576632**	**9.9E-20**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.318455755	3	7.326679
P01946	FLASVSTVLTSK	0.208849573	2	3.902756
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.08827651	4	4.653927
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.25623372	4	6.330357
P01946	IGGHGGEYGEEALQR	0.339357127	3	4.870887
P01946	LRVDPVNFK	0.360022636	2	2.583225
P01946	MFAAFPTTK	0.401003591	2	2.745217
P01946	MFAAFPTTK+Oxidation(0)	0.21984389		
P01946	TYFSHIDVSPGSAQVK	0.324919613	2	5.175354
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.321367271**	**9.9E-20**	**4**
P02089	GTFASLSELHCDK	0.223774315	2	3.178641
P02089	LHVDPENFR	0.347199776	2	2.633535
P02089	YFDSFGDLSSASAIMGNPK	0.261744963	2	6.343416
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14)	0.226748891		
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.129145394**	**9.9E-20**	**9**
P02091	AAVNGLWGK	0.366308122	2	2.593747
P02091	EFTPCAQAAFQK	0.417870436	2	2.991656
P02091	GTFAHLSELHCDK	0.316574967	2	4.274859
P02091	GTFAHLSELHCDKLHVDPENFR	0.129071329	3	3.483479
P02091	KVINAFNDGLK	0.360221484	3	3.681827
P02091	LLGNMIVIVLGHHLGK	0.490778311	4	4.798428
P02091	VINAFNDGLK	0.31475729	2	2.89435
P02091	VNPDDVGGEALGR	0.304674254	2	4.027888
P02091	VVAGVASALAHK	0.486342289	2	3.613917
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.169083987**	**0.01778**	**6**
P02401	ILDSVGIEADDER	1.18902848	2	4.597485
P02401	KILDSVGIEADDER	1.423766154	2	3.830423
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.194252999	3	6.306197
P02401	NIEDVIAQGVGK	1.060266331	2	4.722207
P02401	VISELNGK	1.139940184	1	2.054207
P02401	YVASYLLAALGGNSNPSAK	1.10773671	2	4.930248
P02563	**MYH6 Myosin_6**	**1.0868585**	**0.67402**	**3**
P02563	DTQLQLDDAVR	0.931548551	2	2.676833
P02563	VKLEQQVDDLEGSLEQEK	2.295626223	2	5.157225
P02563	VKLEQQVDDLEGSLEQEKK	2.811530814	3	3.494292
P02564	**MYH7 Myosin_7**	**0.942780246**	**1**	**42**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.887440862	3	6.344643
P02564	ANDDLKENIAIVER	1.400177823	2	3.525035
P02564	AQLEFNQIK	2.386735079	1	1.958119
P02564	DLEEATLQHEATAAALR	1.941014657	2	5.202578
P02564	DTQIQLDDAVR	0.931548551	2	2.676833
P02564	EDQVMQQNPPK	2.172572831	2	3.244556
P02564	ELENELEAEQKR	2.555761518	2	2.882081
P02564	EQYEEETEAK	3.862439214	1	3.03225
P02564	GQNVQQVAYAIGALAK	1.512279675	2	3.759597
P02564	GTLEDQIIQANPALEAFGNAK	1.35968682	2	5.248735
P02564	IEDEQALGSQLQK	3.389120198	2	4.537066
P02564	IEELEEELEAER	2.329166246	2	4.26683
P02564	ILNPAAIPEGQFIDSR	2.848673595	2	2.547411
P02564	KLAEKDEEMEQAK	0.631288199	2	3.775279

P02564	KLAEQELIETSER	1.801072983	2	3.534202
P02564	KLEDECSELKR	3.511624301	3	3.445501
P02564	KVQHELDEAEER	3.06887793	2	3.541449
P02564	LAEQELIETSER	1.312461731	2	3.799828
P02564	LDEAEQIALK	1.663346653	2	3.962439
P02564	LEEAGGATSVQIEMNK	1.946445234	2	4.369197
P02564	LELDDVTSNMEQIIK	0.958288908	2	4.070542
P02564	LELQSALEEAEASLEHEEGK	0.899293098	2	4.138051
P02564	LLGSLDIDHNQYK	1.346212361	2	3.661696
P02564	LQDAEEAVEAVNAK	2.186607386	2	3.964658
P02564	LQNEIEDLMVDVER	2.036220379	2	3.89675
P02564	LTQESIMDLENDKQQLDER	4.367431239	2	4.551601
P02564	MDADLSQLQTEVEEAVQECR	0.86047162	2	5.235183
P02564	NDLQLQVQAEQDNLADAEER	3.41939206	2	5.463215
P02564	NLQEEISDLTEQLGSTGK	2.60643834	2	5.929419
P02564	NLTEEMAGLDEIIVK	1.3694187	2	4.750556
P02564	NNLLQAELEELR	2.884466023	2	3.388179
P02564	QAEEAEEQANTNLSK	2.73343311	2	4.975104
P02564	QKYEESQSELESSQK	2.091620912	2	3.39453
P02564	QREEQAEPDGTEEADK	3.279910984	2	2.931566
P02564	QREEQAEPDGTEEADKSAYLMGLNSADLLK	5.010110965	3	4.911406
P02564	SAYLMGLNSADLLK	1.433893252	2	2.545759
P02564	TLEDQMNEHR	2.542464901	2	2.651053
P02564	VQHELDEAEER	1.917037754	2	3.062501
P02564	VQHELDEAEERADIAESQVNK	7.725707732	3	3.587075
P02564	VQLLHSQNTSLINQK	3.189355192	2	3.987459
P02564	VRELENELEAEQKR	2.355286855	3	3.836714
P02564	VVDSLQTSLDAETR	2.788342934	2	4.193341
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**3.251080547**	**0.99767**	**13**
P02600	ALGTNPTNAEVK	1.956073622	2	3.536794
P02600	ALGTNPTNAEVKK	6.912132067	2	3.304775
P02600	DQGGYEDFVEGLR	0.457142359	2	3.560319
P02600	EQQEEFKEAFLLFDR	1.483528593	2	3.581992
P02600	IEFEQFLPMMQAISNNK	1.210314834	3	3.918038
P02600	ITLSQVGDVLR	4.018310956	2	3.239146
P02600	KIEFEQFLPMMQAISNNK	2.861095159	2	5.667635
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	1.989030857	4	5.266766
P02600	KPAAAAPAPAPAPAPAPAKPK	4.574888013	3	4.330929
P02600	KVLGNPSNEEMNAK	4.813214792	2	3.316699
P02600	KVLGNPSNEEMNAK+Oxidation(10)	11.0854208		
P02600	VLGNPSNEEMNAK	2.806761509	2	3.689341
P02600	VLGNPSNEEMNAK+Oxidation(9)	3.284837489		
P02625	**PRVA Parvalbumin alpha**	**2.683001624**	**0.91646**	**5**
P02625	AIGAFTAADSFDHK	2.654315242	2	3.38144
P02625	KVFHILDKDK	7.252740145	2	2.301836
P02625	SGFIEEDELGSILK	2.528407544	2	4.860672
P02625	TLMAAGDKDGDGK	4.804903316	2	3.183165
P02625	TLMAAGDKDGDGK+Oxidation(2)	2.652371355		
P02650	**APOE Apolipoprotein E**	**0.705703429**	**9.9E-20**	**11**
P02650	ELEEQLGPVAEETR	0.903440147	2	4.292765
P02650	GRLEEVGNQAR	0.704254033	2	3.512826
P02650	GWFEPLVEDMQR	0.777629774	2	3.443292
P02650	LEEVGNQAR	0.795566715	2	2.483841
P02650	LGADMEDLR	0.819820868	2	2.742156
P02650	LGPLVEQGR	0.75474128	2	2.766629
P02650	MEEQTQQIR	0.759917994	2	3.153938

P02650	NEVNTMLGQSTEELR	0.702617161	2	4.375723
P02650	SKMEEQTQQIR	0.742953429	2	3.23008
P02650	SKMEEQTQQIR+Oxidation(2)	1.201012662		
P02650	TANLGAGAAQPLR	0.675870757	2	3.67759
P02651	**APOA4 Apolipoprotein A_IV**	**0.926708382**	**0.90197**	**2**
P02651	TDVTQQLNTLFQDK	0.833639978	2	4.376289
P02651	VSTNIDQLQK	1.018611478	2	2.310643
P02680	**FIBG Fibrinogen gamma chain**	**1.277776901**	**2.4E-07**	**5**
P02680	LSIGDGQQHHMGGSK	1.653311938	2	2.716701
P02680	VAQLEAQCQEPCK	1.903084972	2	3.509436
P02680	VGPESDKYR	1.372800299	2	2.784405
P02680	YEALLLTHESSIR	1.271572349	2	3.894515
P02680	YLQDIYTSNK	1.564702082	2	2.442022
P02692	**FABPL Fatty acid_binding protein_ liver**	**0.904286451**	**9.9E-20**	**11**
P02692	AMGLPEDLIQK	0.884747597	2	3.725098
P02692	AMGLPEDLIQK+Oxidation(1)	0.838654143		
P02692	GVSEIVHEGK	0.909386928	2	3.410163
P02692	GVSEIVHEGKK	0.856738016	2	3.223191
P02692	SVTEFNGDTITNTMTLGDIVYK	0.803966929	2	5.532661
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13)	0.914232256		
P02692	SVTEFNGDTITNTMTLGDIVYKR	0.812816955	2	3.632193
P02692	VIHNEFTLGEECELETMTGEK	0.855702127	3	6.109758
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16)	0.921224853		
P02692	YQVQSQENFEPFMK	0.879248019	2	5.81941
P02692	YQVQSQENFEPFMK+Oxidation(12)	0.881650959		
P02696	**RET1 Retinol_binding protein 1**	**0.819377469**	**0.425**	**5**
P02696	ALDVNVALR	0.778865612	2	3.313287
P02696	CMTTVSWDGDKLQCVQK	0.638117307	2	4.672219
P02696	EFEEDLTGIDDR	0.930085366	2	2.46823
P02696	MLSNENFEEYLR	0.755895841	2	3.90598
P02696	MLSNENFEEYLR+Oxidation(0)	0.745665331		
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**0.822444088**	**0.37687**	**6**
P02706	DYQDFQHLDNENDHHQLQR	1.185772645	3	4.246231
P02706	FVQQHMGPLNTWIGLTDQNGPWK	1.551545508	3	3.500044
P02706	LVESQLEK	0.954586103	2	2.494918
P02706	SLSCQMAALR	0.861246947	2	2.700068
P02706	WVCETELGK	0.800414579	2	2.358272
P02706	WVDGTDYETGFK	0.772589175	2	3.173732
P02770	**ALBU Serum albumin**	**1.216122926**	**0.00059**	**24**
P02770	AADKDNCFATEGPNLVAR	1.595387781	2	4.97209
P02770	AETFTFHSDICTLPDKEK	1.492844768	2	4.504495
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.232613879	3	5.270844
P02770	CCSGSLVER	1.329163289	2	3.294529
P02770	CCTLPEAQR	1.186168794	2	3.199258
P02770	ECCHGDLLECADDR	1.408309846	2	3.626663
P02770	ECCHGDLLECADDRAELAK	1.237984179	2	5.189486
P02770	FKDLGEQHFK	1.27397989	3	4.290384
P02770	GLVLIAFSQYLQK	1.207613521	2	4.143642
P02770	INKECCHGDLLECADDRAELAK	1.728849701	3	4.70576
P02770	KQTALAELVK	1.239996743	3	4.082566
P02770	KYEATLEK	1.56891637	1	2.707031
P02770	LQACCDKPVLQK	1.25395578	2	4.323123
P02770	LVQEVTDFAK	1.253228162	2	3.589504
P02770	RHPDYSVSLLLR	1.245304045	3	5.342217
P02770	SIHTLFGDK	1.390489674	1	2.537309
P02770	TCVADENAENCDK	1.192413709	2	4.496723
P02770	TNCELYEK	1.151871774	2	2.896055

P02770	TVMGDFAQFVDK	1.176530759	2	3.728814
P02770	TVMGDFAQFVDK+Oxidation(2)	0.837268533		
P02770	YEATLEK	1.195662876	1	1.938763
P02770	YMCENQATISSK	1.189361768	2	4.095817
P02770	YMCENQATISSK+Oxidation(1)	1.24833748		
P02770	YNEVLTQCCTESDK	1.272090437	2	5.921127
P02803	**MT1 Metallothionein_1**	**21.1049952**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	12.7178822	2	5.284279
P02803	SCCSCCPVGCSK	22.53840198	2	3.903487
P04041	**GPX1 Glutathione peroxidase 1**	**0.758953382**	**9.9E-20**	**10**
P04041	FLVGPDGVPVR	0.807994676	2	3.482735
P04041	GLVVLGFPCNQFGHQENGK	0.722876969	2	4.365985
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.764157986	3	3.995894
P04041	NALPAPSDDPTALMTDPK	0.788511497	2	3.11904
P04041	NALPAPSDDPTALMTDPK+Oxidation(13)	0.950936297		
P04041	NDISWNFEK	0.743004266	2	2.94232
P04041	NEEILNSLK	0.777381627	1	2.388293
P04041	TIDIEPDIEALLSK	0.740836223	3	4.577692
P04041	YIIWSPVCR	0.794887281	2	3.110299
P04041	YVRPGGGFEPNFTLFEK	0.659058333	3	4.856639
P04167	**CP2B2 Cytochrome P450 2B2**	**2.117063725**	**8.1E-12**	**2**
P04167	GTIAVIEPIFK	2.113382483	2	2.713934
P04167	NLQEILDYIGHIVEK	1.441417984	2	3.720965
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.510791261**	**9.9E-20**	**18**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.75265723	2	4.185976
P04176	EDNIPQLEDVSQFLQTCTGFR	1.755308407	3	4.95246
P04176	FANQILSYGAELDADHPGFK	1.670075303	3	3.530921
P04176	FANQILSYGAELDADHPGFKDPVYR	1.155564213	4	5.037365
P04176	ILADSINSEVGILCNALQK	0.980694559	3	6.644315
P04176	LNKDEYEFFTYLDK	2.349635454	2	3.604046
P04176	LNKDEYEFFTYLDKR	1.053599853	3	3.818912
P04176	LRPVAGLLSSR	2.339730623	2	2.339522
P04176	NDIGATVHELSR	1.625237039	2	3.615365
P04176	NTVPWFPR	1.327086148	2	2.501236
P04176	QFADIAYNYR	1.222292554	2	2.545489
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.537655448	2	5.016753
P04176	TACQEYSVTEFQPLYYVAESFSDAK	1.017361982	2	4.733845
P04176	THACYEHNHIFPLLEK	1.795773435	2	4.667121
P04176	VEVLDNTQQLK	1.482932122	2	3.895681
P04176	VEYTEEEK	1.290946345	2	2.603281
P04176	VEYTEEEKQTWGTVFR	1.259957952	2	4.447991
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.266515724	3	4.716255
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**1.139041835**	**0.99503**	**8**
P04182	AFYNNVLGEYEEYITK	1.016365859	2	4.43028
P04182	DNGLLAKPTHGDIIR	1.088426709	2	2.581575
P04182	GLLNAIVIR	0.914146231	2	3.347982
P04182	KTEQGPPSSEYIFER	1.159680029	2	4.122945
P04182	TEQGPPSSEYIFER	1.140194612	2	4.149383
P04182	VLPMNTGVEAGETACK	1.090426906	2	4.296223
P04182	WLAVDHENVRPDIVLLGK	0.903275928	2	4.059553
P04182	YGAHNYHPLPVALER	0.750195623	2	3.614229
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.196866945**	**3.3E-11**	**5**
P04256	EDSQRPGAHLTVK	1.295921238	2	3.053057
P04256	GFAFVTFDDHDSVDK	1.186033984	2	2.902564
P04256	IEVIEIMTDR	1.0271231	2	3.408569

P04256	NQGGYGGSSSSSSYGSGR	1.143396638	2	4.936421
P04256	SESPKEPEQLR	1.044954013	2	2.362085
P04276	**VTDB Vitamin D_binding protein**	**1.20078732**	**6.5E-08**	**3**
P04276	SCESDAPFPVHPGTSECCTK	1.681420071	2	4.851318
P04276	VPTANLEDVLPLAEDLTEILSR	1.047343101		
P04276	YCSSQIDAEMR	1.420175477	2	2.46543
P04355	**MT2 Metallothionein_2**	**38.84861052**	**9.9E-20**	**3**
P04355	CSQGCICKEASDKCSCCA	2.137745456	3	3.632713
P04355	MDPNCSCATDGSCSCAGSCK	30.87228117	2	6.386932
P04355	SCCSCCPVGCAK	31.71648215	2	4.216469
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**2.785149336**	**0.99862**	**9**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.678149207	3	4.91573
P04466	GADPEDVITGAFK	3.070294242	2	4.345148
P04466	KQFLEELLTTQCDR	2.119900176	2	3.817376
P04466	LKGADPEDVITGAFK	2.785842432	2	3.765516
P04466	NEELDAMMK	3.709525401	1	2.322364
P04466	NICYVITHGDAK	1.608155931	2	3.073754
P04466	NICYVITHGDAKDQE	1.91838342	2	3.980803
P04466	NMWAAFPPDVGGNVDYK	1.486854115	2	2.915712
P04466	QFLEELLTTQCDR	3.565248448	2	4.005283
P04550	**PTMS Parathymosin**	**1.012894184**	**1**	**4**
P04550	RTAEEEDEADPKR	1.096673666	3	4.408648
P04550	SVEAAAELSAK	1.044207723	2	4.205069
P04550	TAEEEDEADPK	1.129619797	2	3.714639
P04550	TAEEEDEADPKR	1.085267561	3	3.740644
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.02056562**	**1.5E-06**	**17**
P04636	AGAGSATLSMAYAGAR	0.875811429	2	4.757953
P04636	AGAGSATLSMAYAGAR+Oxidation(9)	1.079831073		
P04636	ANTFVAELK	1.035895146	2	2.738801
P04636	EGVIECSFVQSK	1.655862165	1	3.060102
P04636	ETECTYFSTPLLLGK	2.347957394	2	3.758039
P04636	FVFSLVDAMNGK	0.872722213	2	4.290236
P04636	GCDVVVIPAGVPR	1.003628209	2	4.263672
P04636	GYLGPEQLPDCLK	0.94865864	2	4.307568
P04636	IFGVTTLDIVR	1.022079259	2	3.452798
P04636	IQEAGTEVVK	1.023241437	2	2.86749
P04636	LTLYDIAHTPGVAADLSHIETR	0.999576842	3	6.707665
P04636	MIAEAIPELK	0.972367895	2	3.056718
P04636	MIAEAIPELK+Oxidation(0)	0.945560748		
P04636	TIIPLISQCTPK	0.719382606	2	3.710312
P04636	VAVLGASGGIGQPLSLLLK	1.794781971	2	5.997471
P04636	VDFPQDQLATLTGR	0.886487224	2	4.760095
P04636	VNVPVIGGHAGK	1.13040863	2	3.61838
P04639	**APOA1 Apolipoprotein A_I**	**0.940634427**	**0.9999**	**5**
P04639	LQEQLGPVTQEFWANLEK	1.133284464	2	4.089848
P04639	NEMNKDLENVK	1.110892084	2	3.16358
P04639	QLNLNLLDNWDTLGSTVGR	0.873125904	2	4.298866
P04639	VKDFATVYVDAVK	0.950806845	2	2.832142
P04639	WNEEVEAYR	1.095500591	2	2.598564
P04642	**LDHA L_lactate dehydrogenase A chain**	**0.942746393**	**0.001**	**21**
P04642	DLADELALVDVIEDK	0.698791606	2	5.457942
P04642	DQLIVNLLK	1.142150358	2	2.928626
P04642	DQLIVNLLKEEQVPQNK	0.833872017	2	4.577693
P04642	EDVFLSVPCILGQNGISDVVK	0.867054645	2	4.660959
P04642	FIIPNVVK	0.786536744	2	2.382555
P04642	GEMMDLQHGSLFLK	0.775788347	2	3.94008

P04642	GEMMDLQHGSLFLK+Oxidation(2)	0.904280888		
P04642	GEMMDLQHGSLFLK+Oxidation(2)	0.832079176		
P04642	GEMMDLQHGSLFLK+Oxidation(3)	0.930027983	2	3.487276
P04642	KSADTLWGIQK	0.860407005	2	3.318448
P04642	LLIVSNPVDILTYVAWK	0.965083847	2	4.863012
P04642	NVNIFK	0.929674014	1	2.082439
P04642	QVVDSAYEVIK	0.818904963	2	3.502868
P04642	RVHPISTMIK	0.731522172	2	2.519708
P04642	RVHPISTMIK+Oxidation(7)	0.907065658		
P04642	SADTLWGIQK	0.887237226	2	3.934905
P04642	SLNPQLGTDADK	1.066526614	1	2.322855
P04642	SLNPQLGTDADKEQWK	0.971650479	2	4.857021
P04642	SLNPQLGTDADKEQWKDVHK	0.973023091	3	3.431161
P04642	VHPISTMIK+Oxidation(6)	1.156858458		
P04642	VTLTPDEEAR	0.974992161	2	2.741382
P04644	**RS17 40S ribosomal protein S17**	**0.912778347**	**0.62091**	**2**
P04644	LLDFGSLSNLQVTQPTVGMNFK	0.980299014	2	4.278763
P04644	VCEEIAIIPSK	1.062109117	2	2.866039
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.150389265**	**0.98887**	**11**
P04692	AISEELDHALNDMTSI	3.427952812	2	2.800011
P04692	GTEDELDKYSEALK	1.541360659	2	3.645583
P04692	GTEDELDKYSEALKDAQEK	5.713589755	2	4.108422
P04692	KLVIIESDLER	1.959555815	2	3.46125
P04692	LDKENALDR	2.836685604	2	2.785169
P04692	LKGTEDELDK	2.325073759	2	2.768812
P04692	LVIIESDLER	1.305733412	2	2.458196
P04692	MEIQEIQLK	1.053913363	2	3.021322
P04692	QLEDELVSLQK	3.828591011	2	2.855708
P04692	SIDDLEDELYAQK	0.766127694	2	4.23555
P04692	SKQLEDELVSLQK	1.183313804	2	3.335744
P04694	**ATTY Tyrosine aminotransferase**	**7.480229082**	**5.3E-06**	**5**
P04694	ILGPCTIVQGALK	5.083672034	2	2.672603
P04694	IQEFCEQHYHCAEGSQEECDK	21.15943387	3	4.451884
P04694	TACLVVNNPSNPCGSVFSK	10.49740066	2	4.933046
P04694	WDVRPSDMSNK	6.775863368	2	2.36815
P04694	YEPLANLSTNVPILSCGGLAK	34.25652149	2	3.429554
P04762	**CATA Catalase**	**1.006208144**	**9.9E-20**	**32**
P04762	APQKPDVLTTGGGNPIGDK	1.548335717	2	4.638016
P04762	DAMLFPSFIHSQK+Oxidation(2)	1.397093163		
P04762	DAQLFIQR	1.53048906	2	2.997428
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	0.848893015	4	4.567451
P04762	DPASDQMK	0.902781217	1	2.257921
P04762	DPASDQMK+Oxidation(6)	1.203144958		
P04762	DYPLIPVGK	0.95783707	1	2.244847
P04762	EAETFPFNPFDLTK	1.436842183	2	3.960579
P04762	FNSANEDNVTQVR	0.906626527	2	4.558928
P04762	FSTVAGESGSADTVR	1.0162357	2	5.280581
P04762	FSTVAGESGSADTVRDPR	0.77937742	2	2.307338
P04762	FYTEDGNWDLVGNNTPIFFIR	0.75812922	3	5.463285
P04762	GAGAFGYFEVTHDITR	0.819169748	2	4.783739
P04762	GPLLVQDVVFTDEMAHFDR	0.991623766	2	5.47609
P04762	HMNGYGSHTFK	0.856238292	3	4.108102
P04762	HMNGYGSHTFK+Oxidation(1)	1.039305585		
P04762	LAQEDPDYGLR	1.037866751	2	2.72948
P04762	LCENIANHLK	0.841999604	3	3.783859
P04762	LFAYPDTHR	1.051553541	2	2.914103

P04762	LGPNYLQIPVNCPYR	0.976835204	3	4.052971
P04762	LNIMTAGPR	0.962085924	2	3.145642
P04762	LNIMTAGPR+Oxidation(3)	1.11351126		
P04762	LVNANGEAVYCK	0.856810742	2	3.894319
P04762	NAIHTYVQAGSHIAAK	0.757504842	3	5.898609
P04762	NFTDVHPDYGAR	1.038685636	2	4.140734
P04762	NLPVEEAGR	0.881927974	1	2.323009
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	2.135186419	3	5.677136
P04762	RFNSANEDNVTQVR	0.890796517	2	4.521218
P04762	VFEHIGK	1.009714335	2	2.476162
P04762	VFEHIGKR	0.877510529	2	2.369051
P04762	VQALLDQYNSQKPK	0.937532805	2	4.940297
P04762	VWPHKDYPLIPVGK	0.731854143	2	3.481071
P04764	**ENOA Alpha_enolase**	**0.898139933**	**8.5E-05**	**14**
P04764	AGYTDQVVIGMDVAASEFYR	0.794929127	2	4.520521
P04764	DATNVGDEGGFAPNILENK	0.943493441	2	5.780879
P04764	FTATAGIQVVGDDLTVTNPK	0.887383662	2	5.306463
P04764	GNPTVEVDLYTAK	0.960645772	2	4.078547
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	0.810367914	3	6.15002
P04764	IDQLMIEMDGTENK	0.900126217	2	4.481691
P04764	IEEELGSK	0.893154559	2	2.321403
P04764	IGAEVYHNLK	1.068850937	2	3.209411
P04764	KLNVVEQEK	0.928396399	2	2.545506
P04764	LNVVEQEK	0.970157487	2	3.102386
P04764	LNVVEQEKIDQLMIEMDGTENK	0.84276229	3	4.648707
P04764	SCNCLLLK	1.156684158	2	2.981885
P04764	VNQIGSVTESLQACK	0.921830963	2	5.042507
P04764	YITPDQLADLYK	0.896307838	2	3.470566
P04785	**PDIA1 Protein disulfide_isomerase**	**0.838152452**	**4.1E-10**	**25**
P04785	DGVVLFK	1.421622883	2	2.440274
P04785	DHENIVIAK	1.214695333	2	2.75662
P04785	EADDIVNWLK	2.563319413	2	2.308766
P04785	HNQLPLVIEFTEQTAPK	0.915579079	3	5.686644
P04785	IKPHLMSQELPEDWDKQPVK	1.116994645	4	4.660788
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5)	1.212871412		
P04785	ILEFFGLK	0.958942368	2	3.074069
P04785	ILFIFIDSDHTDNQR	0.829843232	2	2.37653
P04785	LGETYKDHENIVIAK	0.990137955	3	4.736261
P04785	LITLEEEMTK	0.91291226	2	3.56582
P04785	LITLEEEMTK+Oxidation(7)	1.230771611		
P04785	LKAEGSEIR	1.194057749	1	2.096421
P04785	MDSTANEVEAVK	1.01511358	2	4.116548
P04785	MDSTANEVEAVK+Oxidation(0)	0.973384355		
P04785	NFEEVAFDEK	1.005601872	1	3.357725
P04785	NFEEVAFDEKK	1.039567051	2	3.736872
P04785	NNFEGEITK	0.99765783	2	2.534137
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	0.828212022	3	6.632107
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	0.802005587	3	6.390738
P04785	THILLFLPK	1.049071759	2	2.77799
P04785	TVIDYNGER	1.094517099	2	2.565073
P04785	VDATEESDLAQQYGVR	0.952607331	2	5.625583
P04785	VHSFPTLK	0.916249231	1	1.920658
P04785	YKPESDELTAEK	1.036735322	3	4.586089
P04785	YQLDKDGVVLFK	0.860318904	2	3.936726
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**0.983289149**	**0.71481**	**16**
P04797	GAAQNIIPASTGAAK	1.083873023	2	4.273346

P04797	IVSNASCTTNCLAPLAK	1.089421106	2	4.764961
P04797	LISWYDNEYGYSNR	1.255796514	2	4.061031
P04797	LVINGKPITIFQER	1.361745232	3	3.720879
P04797	RVIISAPSADAPMFVMGVNHEK	1.209494095	3	5.285765
P04797	RVIISAPSADAPMFVMGVNHEK+Oxidation(12)	0.655176515		
P04797	VGVNGFGR	1.176576376	2	2.578372
P04797	VIHDNFGIVEGLMTTVHAITATQK	0.99891177	3	7.493002
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12)	0.994265929		
P04797	VIISAPSADAPMFVMGVNHEK	0.887002179	2	4.64743
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11)	0.89192465		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14)	0.8777156		
P04797	VPTPNVSVVDLTCR	1.24860414	2	3.774345
P04797	VVDLMAYMASK	1.475516466	2	3.805506
P04797	VVDLMAYMASKE	1.391526084	2	2.766998
P04797	WGDAGAEYVVESTGVFTTMEK	1.03845158	2	5.567223
P04799	**CP1A2 Cytochrome P450 1A2**	**1.291125512**	**4.5E-06**	**6**
P04799	DFVENVTSGNAVDFFPVLR	1.108214241	2	3.760718
P04799	IGSTPVVVLSGLNTIK	1.604368848	2	3.059791
P04799	NSIQDITGALFK	1.287522024	2	3.475518
P04799	SMTFNPDSGPVWAAR	1.657730573	2	3.155394
P04799	TCEHVQAWPR	1.042431597	2	2.871635
P04799	TVQEHYQDFNK	1.291710825	2	3.458863
P04800	**CP3A1 Cytochrome P450 3A1**	**3.271034779**	**0.15425**	**2**
P04800	KLQEEIDR	1.520848109	2	2.31223
P04800	QGLLQPTKPIILK	3.314339518	2	2.387706
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.919881432**	**1**	**10**
P04903	DGNLMFDQVPMVEIDGMK	0.850171313	2	4.917635
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	0.963850154		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16)	0.944341432		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.965812961		
P04903	KDGNLMFDQVPMVEIDGMK	0.958153476	2	4.395597
P04903	LIQSPEDLEK	1.257645453	2	3.116575
P04903	LKKDGNLMFDQVPMVEIDGMK	0.917144053	2	2.692726
P04903	WLLAAAGVEFEEK	1.04854659	2	3.870257
P04903	YDLYGK	0.672190805	1	1.939573
P04903	YLPAFEK	0.960112149	1	2.002143
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.838323366**	**1.9E-05**	**9**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	1.093631724	3	5.295905
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	1.05606492	4	7.904847
P04904	LRNDGSLMFQQVPMVEIDGMK	0.882787708	2	3.804574
P04904	NDGSLMFQQVPMVEIDGMK	0.805298043	2	4.639302
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	0.868785926		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17)	0.877148156		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5)	0.861092697		
P04904	SHGQDYLVGNR	0.836122595	2	3.9099
P04904	WLLAAAGVEFEEQFLK	0.848533625	2	5.419931
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.065401267**	**0.0485**	**15**
P04905	ADIVENQVMDNR	1.195780824	2	4.293469
P04905	ADIVENQVMDNR+Oxidation(8)	1.017913262		
P04905	CLDAFPNLKDFLAR	1.193056719	2	2.693651
P04905	FKLGLDFPNLPYLIDGSR	0.937707525	3	4.854903
P04905	HHLCGETEEER	1.184897572	3	4.43464
P04905	IRADIVENQVMDNR	1.052437324	2	3.954945
P04905	ITQSNAIMR	1.133016948	2	3.089123
P04905	ITQSNAIMR+Oxidation(7)	1.203156309		
P04905	KHHLCGETEEER	1.414681672	3	3.686196
P04905	KITQSNAIMR	1.041638617	3	3.764464

P04905	KITQSNAIMR+Oxidation(8)	1.089824168		
P04905	LGLDFPNLPYLIDGSR	1.086164887	2	5.113865
P04905	MQLIMLCYNPDFEK	0.892572394	2	4.494752
P04905	VTYVDFLAYDILDQYHIFEPK	1.106060831	3	3.7413
P04905	YLSTPIFSK	0.964972319	2	2.708584
P04906	**GSTP1 Glutathione S_transferase P**	**0.959227087**	**0.99972**	**2**
P04906	EAALVDMVNDGVEDLR	0.984992163	2	4.733013
P04906	STCLYGQLPK	0.901006029	2	2.948133
P04937	**FINC Fibronectin**	**0.877643436**	**0.1246**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	1.573128899	2	3.529043
P04937	ITYGETGGNSPVQEFTVPGSK	0.855038873	2	2.655801
P04937	SSPVVIDASTAIDAPSNLR	0.952324214	2	2.466382
P04937	SYTITGLQPGTDYK	0.880324168	2	2.758991
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.131262102**	**0.98295**	**9**
P05065	ALANSLACQGK	1.505309901	2	2.964607
P05065	FSNEEIAMATVTALR	1.955176494	2	4.498697
P05065	GILAADESTGSIAK	1.813146254	2	4.228808
P05065	GVVPLAGTNGETTTQGLDGLSER	1.099912678	2	5.399199
P05065	IGEHTPSSLAIMENANVLAR	2.919578639	2	4.678485
P05065	KENLKAAQEEYIK	1.10777078	2	2.411307
P05065	LQSIGTENTEENR	3.055824383	2	3.80651
P05065	LQSIGTENTEENRR	3.184481209	2	2.521145
P05065	RLQSIGTENTEENR	3.184481209	2	4.08288
P05178	**CP2C6 Cytochrome P450 2C6**	**0.90162101**	**0.89162**	**9**
P05178	DQDFLNLMEK	1.119634332	2	2.581353
P05178	EALIDHGEEFAER	1.055780092	2	3.247572
P05178	FDYKDQDFLNLMEK	0.865432851	3	4.555609
P05178	FIDLIPTNLPHAVTCDIK	0.791965144	2	3.350196
P05178	GTTIITSLSSVLHDSK	0.825625152	2	3.75694
P05178	LPPGPIPLPIIGNIFQLNVK	0.952697756	3	3.520749
P05178	MCAGEGLAR	0.859990779	2	2.576167
P05178	NITQSLTSFSK	0.852007319	2	2.472451
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	0.822831792	3	4.718562
P05179	**CP2C7 Cytochrome P450 2C7**	**0.630409655**	**0.00319**	**7**
P05179	ACVGEGLAR	0.646572783	2	2.892647
P05179	FINFVPTNLPHAVTCDIK	0.830061273	2	2.656708
P05179	IEEHQESLDVTNPR	0.56740186	2	4.568703
P05179	KIEEHQESLDVTNPR	0.635202795	3	4.668203
P05179	KLPPGPTPLPIIGNFLQIDVK	0.353728707	3	5.507406
P05179	SDYFLPFSAGK	1.224914791	2	2.598929
P05179	VLTSLTSVLHDSK	0.610828817	2	3.416085
P05182	**CP2E1 Cytochrome P450 2E1**	**0.954994536**	**0.97629**	**14**
P05182	AKEHLQSLDINCAR	0.909424465	2	4.855285
P05182	DTVFQGYVIPK	1.376062841	2	2.820848
P05182	DVTDCLLIEMEK	1.55752536	2	3.026754
P05182	DVTDCLLIEMEKEK	1.014880324	2	2.489502
P05182	EHLQSLDINCAR	1.438028892	2	3.429089
P05182	FINLVPSNLPHEATR	1.004607789	2	3.822134
P05182	FKPEHFLNENGK	0.724412221	2	2.97678
P05182	GIIFNNGPTWK	1.03548693	2	2.414363
P05182	GQPFDPTFLIGCAPCNVIADILFNK	0.744570467		
P05182	GTVVIPTLDSLLYDSHEFPDPEK	0.926563355	2	4.885564
P05182	LDMPYMDAVVHEIQR	0.834056841	2	2.671844
P05182	LHEEIDR	1.069145527	1	1.958606
P05182	VCVGEGLAR	1.059413755	2	2.38397
P05182	YGLLILMK	1.17265299	2	3.088043
P05183	**CP3A2 Cytochrome P450 3A2**	**1.338352429**	**9.9E-20**	**10**

P05183	DIELDGLFIPK	2.478722571	2	4.140474
P05183	DSIAFFQK	1.425292076	1	2.182205
P05183	EMFPIIEQYGDILVK	1.196377044	2	3.951617
P05183	KDIELDGLFIPK	1.125627385	3	3.558479
P05183	KLQEEIDGALPSK	1.489434762	2	3.679556
P05183	LQEEIDGALPSK	1.46461661	2	4.103528
P05183	QAILEPEKPIVLK	0.842666847	2	3.283657
P05183	QEAETGKPVTMK	1.270636096	2	3.193538
P05183	QEAETGKPVTMK+Oxidation(10)	1.821139697		
P05183	VDFLQLMLNAHNNSK	1.051341494	2	3.709425
P05197	**EF2 Elongation factor 2**	**1.370342594**	**9.9E-20**	**31**
P05197	ALLELQLEPEELYQTFQR	1.171815547	2	5.471809
P05197	ARPFPDGLAEDIDKGEVSAR	1.256961825	3	6.160313
P05197	AYLPVNESFGFTADLR	1.075693431	2	3.876123
P05197	CELLYEGPPDDEAAMGIK	1.191592328	2	4.978745
P05197	CLYASVLTAQPR	1.846464603	2	2.461268
P05197	DLEEDHACIPIK	1.22563013	2	2.990952
P05197	DLEEDHACIPIKK	1.472895351	2	3.676381
P05197	EGIPALDNFLDK	1.093509668	2	2.648639
P05197	EGIPALDNFLDKL	2.932145701	2	3.578612
P05197	ETVSEESNVLCLSK	2.666121768	2	4.058276
P05197	GEGQLGAAER	1.145165596	2	3.360289
P05197	GHVFEESQVAGTPMFVVK	1.664519271	2	6.135114
P05197	GVQYLNEIK	2.168995979	2	2.342688
P05197	IWCFGPDGTGPNILTDITK	0.96227101	2	5.060048
P05197	KEDLYLKPIQR	0.808743344	2	3.303408
P05197	KIWCFGPDGTGPNILTDITK	1.174768153	2	4.830319
P05197	KVEDMMK+Oxidation(5)	1.365766143		
P05197	LDSEDKDKEGKPLLK	1.415811079	2	3.961259
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	1.027996097	3	5.989743
P05197	NMSVIAHVDHGK	1.215837891	2	3.947744
P05197	NMSVIAHVDHGK+Oxidation(1)	1.185188919		
P05197	STAISLFYELSENDLNFIK	1.551784318	3	4.766977
P05197	STLTDSLVCK	1.238539528	2	2.897322
P05197	TFCQLILDPIFK	1.160991489	2	4.199083
P05197	TGTITTFEHAHNMR	1.103859122	2	3.835143
P05197	VFDAIMNFR	0.984281444	2	2.826332
P05197	VFSGVVSTGLK	1.406162984	2	3.05037
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.043526808	3	3.652965
P05197	YEWDVAEAR	1.222376149	2	3.038956
P05197	YFDPANGK	1.230058594	1	2.037084
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.151998151	3	4.735874
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.182890583**	**0.99997**	**11**
P05369	ALYEELDLR	1.244052552	2	3.059262
P05369	EVLEYNTVGGK	1.888109569	2	3.069732
P05369	GLTVVQTFQELVEPR	1.11040604	3	3.864324
P05369	IKEVLEYNTVGGK	1.123515884	3	4.167077
P05369	QILEENYGQKDPEK	0.999181972	2	3.777578
P05369	QNFIQHFSQIVK	1.196309237	2	3.052457
P05369	SLIEQCSAPLPPSIFLELANK	0.955591671	3	5.298708
P05369	VGTDIQDNK	1.056360767	2	3.686793
P05369	VLTEDELGHPEK	1.429020657	2	2.720763
P05369	VLTEDELGHPEKGDAITR	1.359108948	2	4.569483
P05369	YEEDSYNR	0.959081246	2	2.345772
P05426	**RL7 60S ribosomal protein L7**	**1.010347817**	**0.65709**	**6**
P05426	AGNFYVPAEPK	1.115732278	2	2.672065
P05426	FGIICMEDLIHEIYTVGK	0.998841078	3	4.647248

P05426	IVEPYIAWGYPNLK	0.940955328	2	2.95143
P05426	SVNELIYK	1.155853239	2	2.795789
P05426	TTHFVEGGDAGNR	1.078510793	2	3.267327
P05426	TTHFVEGGDAGNREDQINR	0.995883724	2	4.565462
P05544	**SPA3L Serine protease inhibitor A3L**	**1.053650959**	**0.42409**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	0.918755457	2	4.603592
P05544	DSTMEEILEGLK	0.962654328	2	3.013456
P05544	IAELFSDLEER	0.936785323	2	2.875906
P05544	MQQVESSLQPETLK	0.844350723	2	4.215751
P05544	MQQVESSLQPETLK+Oxidation(0)	1.067614255		
P05544	VFSQQADLSR	1.243729936	2	2.576789
P05545	**SPA3K Serine protease inhibitor A3K**	**1.007445748**	**0.99872**	**8**
P05545	ALYQAEAFVADFK	1.004082497	2	2.884836
P05545	AVLDVDETGTEGAAATAVTAALK	1.031531355	2	5.443286
P05545	FSISTDYNLEEVLPELGIR	0.901936349	2	3.486674
P05545	IAELFSELDER	0.95688294	2	3.046522
P05545	IFSQQADLSR	0.910215159	2	2.580773
P05545	LSQPEDQAEINTGSALFIDK	0.679312591	2	4.84718
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	0.993043163	3	4.319727
P05545	NVVFSPLSISAALAILSLGAK	0.983427943		
P05765	**RS21 40S ribosomal protein S21**	**0.916967086**	**0.07658**	**3**
P05765	DHASIQMNVAEVDR	2.016389388	2	3.838672
P05765	MGESDDSILR	0.962492636	2	2.896264
P05765	TYGICGAIR	0.982144367	2	2.511735
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.986173496**	**0.00636**	**8**
P06214	AGADIIITYFAPQLLK	1.422103541	2	4.187796
P06214	AGCQVVAPSDMMDGR	1.132617096	2	3.463431
P06214	CVLIFGVPSR	0.995639063	2	2.835579
P06214	DEQGSAADSEDSPTIEAVR	0.941939773	2	5.506608
P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.886905484	3	4.583016
P06214	TAVLESMTAFR	0.882214671	2	2.95096
P06214	VPKDEQGSAADSEDSPTIEAVR	0.80518838	3	5.036238
P06214	YGVNQLEEMLRPLVEAGLR	0.872711938	3	4.589357
P06238	**A2MG Alpha_2_macroglobulin**	**1.567296352**	**0.00097**	**3**
P06238	FQVNNNNQLLLQR	15.83807511	2	3.072789
P06238	SESNMAIADVK	1.228515856	2	2.473328
P06238	VAVQLEASPDFLAAPEEK	1.730818352	2	3.442948
P06302	**PTMA Prothymosin alpha**	**0.94660031**	**0.99926**	**4**
P06302	EVVEEAENGR	0.961116248	2	2.345241
P06302	RVAEDDEDDDVETKK	1.007824797	3	5.884018
P06302	VAEDDEDDDVETK	1.135696408	2	3.862524
P06302	VAEDDEDDDVETKK	0.911732638	2	4.693449
P06399	**FIBA Fibrinogen alpha chain**	**1.195349012**	**0.01199**	**8**
P06399	AQQIQVLQK	1.420279073	2	2.649024
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	1.307427082	3	3.769013
P06399	GDFANANNFDNTFGQVSEDLR	1.28603532	2	5.694673
P06399	GDFANANNFDNTFGQVSEDLRR	1.063421803	3	3.303046
P06399	GLIDEANQDFTNR	1.382901763	2	3.657563
P06399	MADEAASEAHQEGDTR	1.415587203	2	4.116182
P06399	SQLQEGPPEWK	0.447015882	2	2.602514
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	1.299271541	2	4.672547
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.137877084**	**0.02454**	**5**
P06685	AVAGDASESALLK	1.170397861	2	3.160472
P06685	AVFQANQENLPILK	0.915455072	2	3.327251
P06685	EQPLDEELKDAFQNAYLELGGLGER	0.846931301	3	3.326185
P06685	LNIPVNQVNPR	1.164319465	2	3.032294

P06685	YEPAAVSEHGDKK	1.225074976	2	2.674323
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.094069715**	**0.9358**	**3**
P06687	DGPNALTPPPTTPEWVK	1.058936845	2	2.647821
P06687	GVGIISEGNETVEDIAAR	1.06491348	2	4.688804
P06687	QGAIVAVTGDGVNDSPALK	1.1382825	2	4.797959
P06757	**ADH1 Alcohol dehydrogenase 1**	**0.722947198**	**9.9E-20**	**18**
P06757	AAVLWEPHKPFTIEDIEVAPPK	0.690812879	3	5.449578
P06757	FPLEPLITHVLPFEK	0.644262205	3	4.512362
P06757	GAIFGGFK	0.704261253	2	2.344639
P06757	GALLDGTSR	0.788870974	2	2.859643
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.612928742	3	5.001085
P06757	HPESNLCCQTK	0.63291881	2	3.229142
P06757	ICKHPESNLCCQTK	1.240648225	3	4.133464
P06757	IDAAAPLDK	0.688624173	2	2.745425
P06757	IIAVDINKDK	0.494842322	2	2.719091
P06757	INEAFDLLR	0.755555898	2	3.581264
P06757	KFPLEPLITHVLPFEK	0.649957311	3	4.558144
P06757	LVADFMAK	0.719061794	2	2.60782
P06757	MVATGVCR	0.778069236	2	2.541071
P06757	MVATGVCR+Oxidation(0)	0.754692691		
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	0.721391644	4	7.670705
P06757	VCLIGCGFSTGYGSAVQVAK	0.700441396	2	6.181609
P06757	VIPLFSPQCGK	0.658501065	2	2.742628
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	0.642036768	2	5.143275
P06761	**GRP78 78 kDa glucose_regulated protein**	**0.991114018**	**9.9E-20**	**30**
P06761	AKFEELNMDLFR	0.982825289	3	4.246301
P06761	DAGTIAGLNVMR	1.708314975	2	3.492731
P06761	DNHLLGTFDLTGIPPAPR	1.113447144	2	4.246787
P06761	ELEEIVQPIISK	1.123160722	2	3.980221
P06761	FEELNMDLFR	0.848996087	2	3.484305
P06761	FEELNMDLFR+Oxidation(5)	0.906256121		
P06761	IEIESFFEGEDFSETLTR	0.814931984	2	5.272079
P06761	IEWLESHQDADIEDFK	1.017369948	2	5.687947
P06761	IEWLESHQDADIEDFKAK	0.778848144	3	4.164316
P06761	IINEPTAAAIAYGLDKR	1.008234516	2	4.466039
P06761	ITITNDQNR	1.042219434	2	2.664267
P06761	ITPSYVAFTPEGER	1.103244151	2	4.282418
P06761	KKELEEIVQPIISK	0.954472537	2	5.106496
P06761	KSDIDEIVLVGGSTR	0.976563619	2	4.544512
P06761	KSQIFSTASDNQPTVTIK	0.850990581	2	5.517912
P06761	LYGSGGPPPTGEEDTSEKDEL	1.374292977	2	5.698164
P06761	MKETAEAYLGK	0.946850314	2	2.697902
P06761	MKETAEAYLGK+Oxidation(0)	1.311362169		
P06761	NELESYAYSLK	1.001290597	2	3.670024
P06761	NQLTSNPENTVFDAK	1.029201426	2	5.121109
P06761	SDIDEIVLVGGSTR	1.072916086	1	3.508594
P06761	SQIFSTASDNQPTVTIK	0.981944949	2	5.298091
P06761	TFAPEEISAMVLTK	0.906631831	2	4.869541
P06761	TFAPEEISAMVLTK+Oxidation(9)	0.875525973		
P06761	TKPYIQVDIGGGQTK	0.966580954	3	4.631458
P06761	TWNDPSVQQDIK	0.980886246	2	4.014555
P06761	VLEDSDLK	0.86824792	1	2.116509
P06761	VLEDSDLKK	0.864003575	2	2.359615
P06761	VTHAVVTVPAYFNDAQR	0.966204735	2	5.056208
P06761	VYEGERPLTK	0.949078374	2	2.89851

P06866	**HPT Haptoglobin**	**2.135107507**	**9.9E-20**	**8**
P06866	ATDLKDWVQETMAK	1.293129139	3	3.817987
P06866	CELHYEK	2.490500461	2	2.345129
P06866	GAVSPVGVQPILNK	1.854590504	2	4.604812
P06866	KGAVSPVGVQPILNK	3.146850891	2	3.100904
P06866	LQTEGDGIYTLNSEK	2.957154815	2	4.254277
P06866	NQLVEIEK	2.118358953	1	2.335609
P06866	SCAVAEYGVYVR	1.810262011	2	3.115407
P06866	SVVDIGLIK	1.761754183	2	2.762702
P07150	**ANXA1 Annexin A1**	**0.827564231**	**0.72097**	**2**
P07150	GLGTDEDTLIEILTTR	0.827441777	2	4.279128
P07150	GVDEATIIDILTK	0.833813511	2	3.125175
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**0.966793232**	**0.00511**	**16**
P07153	ASSFVLALEPELESR	1.004133763	2	4.464863
P07153	AVTSEIAVLQSR	0.944966683	2	3.703603
P07153	FVDHVFDEQVIDSLTVK	0.893313921	2	4.142312
P07153	GEDEEDNNLEVR	1.042224233	2	3.73351
P07153	HFDETVNR	0.907155575	2	2.511789
P07153	IDHILDAL	1.407678672	2	2.312999
P07153	ISIVVETVYTHVLHPYPTQITQSEK	1.104215893	3	4.627875
P07153	LKTEGSDLCDR	0.955805916	3	3.412148
P07153	NIQVDSPYDISR	1.002022961	2	3.783175
P07153	NLVEQHIQDIVVHYTFNK	1.004374158	3	4.454648
P07153	SEDILDYGPFK	1.014217957	2	3.397948
P07153	TEGSDLCDR	1.026724716	2	2.33111
P07153	TILPAAAQDVYYR	1.415875607	2	3.295642
P07153	TVDLSSHLAK	0.929832183	2	2.59989
P07153	VHYENNSPFLTITSMTR	0.982389299	2	3.293406
P07153	VTAEVVLAHPGGGSTAR	1.164171375	2	4.467195
P07323	**ENOG Gamma_enolase**	**0.968304285**	**0.95962**	**4**
P07323	AAVPSGASTGIYEALELR	0.992631763	2	5.041862
P07323	FGANAILGVSLAVCK	0.917679248	2	3.509146
P07323	GNPTVEVDLHTAK	2.998431966	2	3.394585
P07323	SGETEDTFIADLVVGLCTGQIK	0.812573152	3	5.528365
P07335	**KCRB Creatine kinase B_type**	**1.004837442**	**0.85798**	**2**
P07335	FCTGLTQIETLFK	1.010594203	2	2.780213
P07335	GTGGVDTAAVGGVFDVSNADR	0.947569907	2	3.937548
P07338	**CTRB1 Chymotrypsinogen B**	**0.880099499**	**0.34389**	**2**
P07338	IVNGEDAIPGSWPWQVSLQDK	0.924795986	2	3.258435
P07338	LQQAALPIVSEADCK	0.795289965	2	2.696569
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.741278293**	**0.02871**	**2**
P07340	SYEAYVLNIIR	2.3347135	2	2.39268
P07340	YNPNVLPVQCTGK	1.409876502	2	2.604861
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**0.948154683**	**0.97863**	**13**
P07379	AINPENGFFGVAPGTSVK	1.224463576	2	4.712518
P07379	EEGWLAEHMLILGITNPEGK	1.200006931	2	4.018726
P07379	EVEEIDKYLEDQVNADLPYEIER	1.17110501	3	3.469648
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	0.98483148	3	4.941177
P07379	GLGDVNVEELFGISK	1.153263243	2	3.81999
P07379	IGIELTDSPYVVASMR	1.043711885	2	3.60867
P07379	MGTSVLEALGDGEFIK	0.996952221	2	3.713335
P07379	MGTSVLEALGDGEFIK+Oxidation(0)	1.165923534		
P07379	TVIITQEQR	1.196878777	2	2.663221

P07379	VECVGDDIAWMK	1.212998063	2	2.965854
P07379	VIQGSLDSLPQEVR	1.247177395	2	4.023687
P07379	YDNCWLALTDPR	0.984403564	2	2.502589
P07379	YLAAAFPSACGK	1.143137449	2	2.892146
P07483	**FABPH Fatty acid_binding protein_ heart**	**8.237540871**	**0.67722**	**3**
P07483	NFDDYMK	67.31185859	1	2.131093
P07483	QVASMTKPTTIIEK	1.306842405	2	3.407787
P07483	WDGQETTLTR	1.591100033	2	2.874666
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.142779564**	**0.02654**	**4**
P07632	DGVANVSIEDR	1.589326572	2	2.984033
P07632	GDGPVQGVIHFEQK	1.154798417	2	3.993328
P07632	HVGDLGNVAAGK	1.077724343	2	3.567435
P07632	VISLSGEHSIIGR	1.105176844	2	3.260971
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**1.300451178**	**0.99934**	**10**
P07633	AFDNDVDALCNLR	1.069854685	2	3.899174
P07633	AYNMLDIIHAVIDER	0.852235271	2	4.040467
P07633	GFVDDIIQPSSTR	1.143887074	2	4.086548
P07633	HLLGDTNYAWPTAEIAVMGAK	0.946354794	2	3.118145
P07633	ICCDLEVLASK	1.004136438	2	3.034343
P07633	IMDQAITVGAPVIGLNDSGGAR	0.964212319	2	4.458251
P07633	IQEGVESLAGYADIFLR	1.023776719	2	4.16819
P07633	LVPELDTVVPLESSK	0.909798447	2	3.496977
P07633	SVTNEDVTQEQLGGAK	1.097940142	2	5.273132
P07633	TVGIVGNQPNVASGCLDINSSVK	0.892265577	2	5.178185
P07687	**HYEP Epoxide hydrolase 1**	**1.243635357**	**9.9E-20**	**23**
P07687	DIELLYPYK	2.360989234	2	2.425642
P07687	DKEETLPLGDGWWGPGSKPSAK	1.39449635	3	5.489526
P07687	EDESIRPFK	1.776886807	2	2.671997
P07687	EDESIRPFKVETSDEEIKDLHQR	1.4562926	3	5.635212
P07687	ELEDGGLER	1.76580835	2	2.667474
P07687	ENLGQGIMVHK	1.930831001	2	2.750094
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.194312903	3	6.227268
P07687	FHYGFNSNYMK	1.408292442	2	2.565713
P07687	FLGYTEKDIELLYPYK	1.216031952	2	4.687556
P07687	GGHFAAFEEPK	1.284322799	2	3.494933
P07687	IEGLDIHFIHVKPPQLPSGR	1.160863144	3	3.675234
P07687	IIPLLTDPK	1.201984915	2	2.527847
P07687	KFVSLAELQ	1.32979681	2	2.861175
P07687	KQVEILNQYPHFK	1.214141885	3	4.834602
P07687	LLAQDIR	1.375381096	2	2.518207
P07687	QVEILNQYPHFK	1.18004781	2	3.747744
P07687	SEYRELEDGGLER	1.071957084	2	2.375244
P07687	SFYTMTPLLGQR	1.495137781	2	3.146075
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	1.116136809	3	6.466357
P07687	TKIEGLDIHFIHVKPPQLPSGR	2.811287249	3	3.882423
P07687	VETSDEEIK	1.07233933	2	2.475019
P07687	VETSDEEIKDLHQR	1.459645137	2	4.491154
P07687	VFVPTGFSAFPSELLHAPEK	1.125048427	2	4.739214
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**0.938602662**	**9.9E-20**	**96**
P07756	AADTIGYPVMIR	1.02805528	2	4.0677
P07756	AADTIGYPVMIR+Oxidation(9)	0.96221602		
P07756	AERPDGLILGMGGQTALNCGVELFK	0.874208343	3	7.097282
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10)	0.978306684		
P07756	AERPDGLILGMGGQTALNCGVELFKR	1.048869454	3	4.401909
P07756	AFAISGPFNVQFLVK	0.779283671	2	5.075504

P07756	AFAMTNQILVER	0.920232135	2	4.448738
P07756	AFAMTNQILVER+Oxidation(3)	0.930491426		
P07756	ALENNMSLDEIVK	0.909636014	2	4.58932
P07756	ALENNMSLDEIVK+Oxidation(5)	0.908625437		
P07756	AQTAHIVLEDGTK	0.84134762	2	4.512268
P07756	ATGYPLAFIAAK	0.855512306	2	3.061823
P07756	CEMASTGEVACFGEGIHTAFLK	0.843760488	3	5.364838
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2)	0.876758447		
P07756	CLGLTEAQTR	0.915832009	2	3.67824
P07756	DELGLNK	1.705573766	2	2.544711
P07756	DGSIDLVINLPNNNTK	1.165443067	2	5.461707
P07756	DILNMDK	1.557366511	1	1.952491
P07756	EIEYEVVR	1.906240603	2	2.302987
P07756	EPLFGISTGNIITGLAAGAK	0.952577729	3	5.735453
P07756	ETLMDLGTK	2.236594848	1	2.31788
P07756	EVEMDAVGK	2.995156827	1	2.211108
P07756	FLEEATR	0.973155074	2	2.498129
P07756	FLGVAEQLHNEGFK	0.867355096	2	4.680483
P07756	FVHDNYVIR	0.842293159	3	3.432724
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	0.842740167	3	6.349681
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15)	0.869033184		
P07756	GILIGIQQSFRPR	0.750518423	2	2.533752
P07756	GLNSESVTEETLR	1.014184183	2	4.852907
P07756	GNDVLVIECNLR	0.879357924	2	4.48727
P07756	GQILTMANPIIGNGGAPDTTAR	0.891909353	2	6.268684
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5)	0.933146709		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.731712957	3	4.852658
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(5)	0.831371857		
P07756	GQNQPVLNITNR	0.907556653	2	4.228017
P07756	GTTITSVLPKPALVASR	0.943912399	2	3.483668
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.205709081	3	6.620116
P07756	HLPTLEQPIIPSDYVAIK	0.920044881	2	5.619544
P07756	IALGIPLPEIK	1.056285109	2	3.277439
P07756	IAPSFAVESMEDALK	1.144674186	2	5.291159
P07756	IAPSFAVESMEDALK+Oxidation(9)	0.918278677		
P07756	IEFEGQSVDFVDPNK	0.970936774	2	5.163771
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	0.843786082	3	5.333523
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	0.850221329	3	5.431993
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	1.267211106	3	3.697894
P07756	IMGTSPLQIDR	1.237444536	2	3.292778
P07756	IMGTSPLQIDR+Oxidation(1)	1.160398799		
P07756	IMGTSPLQIDRAEDR	0.76618804	2	2.588139
P07756	KEPLFGISTGNIITGLAAGAK	0.795772667	2	5.245474
P07756	KTVVVNCNPETVSTDFDECDK	0.708132589	2	4.918505
P07756	LFAEAVQK	1.04106248	2	3.13731
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.100093166	3	4.976204
P07756	LRDADPILR	1.101877587	2	3.230293
P07756	LTSIDKWFLYK	1.008261455	2	2.576347
P07756	LYFEELSLER	1.339570047	2	3.584599
P07756	MCHPSVDGFTPR	0.925618817	3	4.969532
P07756	MCHPSVDGFTPR+Oxidation(0)	1.022714114		
P07756	MRDILNMDK	0.757982177	2	2.461464
P07756	MRDILNMDK+Oxidation(0)	1.088485485		

P07756	QADAVYFLPITPQFVTEVIK	1.767049404	3	5.233864
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	1.02861077	3	4.858395
P07756	QLFSDK	1.041617327	1	1.900032
P07756	QLFSDKLNEINEK	0.931976899	2	3.729779
P07756	QNLIAEVSTK	0.893414151	1	2.799965
P07756	RFLEEATR	0.926753407	2	2.67996
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.007224514	4	5.015932
P07756	RTAVDSGIALLTNFQVTK	0.825583265	2	5.020787
P07756	SAYALGGLGSGICPNK	1.010803282	2	5.041698
P07756	SAYALGGLGSGICPNKETLMDLGTK	0.820783651	2	4.381637
P07756	SFPFVSK	0.896945732	1	1.916722
P07756	SIFSAVLDELK	0.972521121	2	4.114195
P07756	SIFSAVLDELKVAQAPWK	0.874158829	3	4.520582
P07756	SLGQWLQEEK	0.903584541	2	3.976821
P07756	SVGEVMAIGR	0.921606965	2	3.471697
P07756	SVGEVMAIGR+Oxidation(5)	0.928483108		
P07756	TAVDSGIALLTNFQVTK	0.85496097	3	6.61693
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	0.876843851	3	4.429137
P07756	TFEESFQK	0.920757896	2	2.545689
P07756	TLGVDFIDVATK	0.841722303	2	4.220283
P07756	TSACFEPSLDYMVTK	1.030444939	2	4.78583
P07756	TSACFEPSLDYMVTK+Oxidation(11)	1.102384624		
P07756	TVLMNPNIASVQTNEVGLK	0.868807507	2	6.407845
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3)	0.893347453		
P07756	TVVVNCNPETVSTDFDECDK	0.606996179	2	5.703702
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	1.263008092	3	5.515955
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	0.898511248	3	7.505328
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22)	0.932189967		
P07756	VLGTSVESIMATEDR	0.941684975	2	4.789233
P07756	VLGTSVESIMATEDR+Oxidation(9)	0.997061393		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	0.868304383	2	5.947125
P07756	VMIGESVDEK	0.907848791	2	3.516449
P07756	VMIGESVDEK+Oxidation(1)	1.027251639		
P07756	VSQEHPVVLTK	0.995458168	2	3.684518
P07756	VVAVDCGIK	1.002205612	2	2.599414
P07756	YMESDGIK	0.870752143	2	2.42034
P07756	YMESDGIK+Oxidation(1)	0.898339561		
P07824	**ARGI1 Arginase_1**	**1.023368455**	**5.2E-14**	**16**
P07824	ANEQLAAVVAETQK	1.068967138	2	5.192086
P07824	DHGDLAFVDVPNDSPFQIVK	1.177101128	2	6.303233
P07824	DIVYIGLR	1.893414657	2	2.386336
P07824	DVDPGEHYIIK	3.894586361	2	3.361029
P07824	EGNHKPETDYLKPPK	1.497777068	2	2.689043
P07824	GKFPDVPGFSWVTPCISAK	0.961235881	3	4.963168
P07824	LKETEYNVR	1.237379584	3	3.347389
P07824	NGTISVVLGGDHSMAIGSISGHAR	0.975844245	3	4.418512
P07824	TGLLSGLDIMEVNPTLGK	1.064813478	2	5.853251
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9)	0.814220307		
P07824	TVNTAVALTLSCFGTK	1.35783776	2	5.269279
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	1.21666819	4	5.560514
P07824	VMEETFSYLLGR	1.54227204	2	3.957619
P07824	VMEETFSYLLGR+Oxidation(1)	1.488061704		
P07824	YFSMTEVDK	1.121669133	2	2.425884
P07824	YFSMTEVDKLGIGK+Oxidation(3)	1.042854923		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.785823958**	**9.9E-20**	**18**

P07871	AEELGLPILGVLR	0.819795016	2	4.265287
P07871	AEIVPVTTTVLDDK	0.855007301	2	4.420649
P07871	AEIVPVTTTVLDDKGDR	0.786176512	2	3.978006
P07871	AEIVPVTTTVLDDKGDRK	0.777044883	2	3.614794
P07871	DCLIPMGITSENVAER	1.146702831	2	2.878241
P07871	DCLIPMGITSENVAER+Oxidation(5)	1.265626804		
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.907906151	2	6.423011
P07871	GGFKDTTPDELLSAVLTAVLQDVK	0.503454573		
P07871	IAQFLSGIPETVPLSAVNR	1.036329228	2	2.836739
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.998754918	3	4.324794
P07871	QCSSGLQAVANIAGGIR	0.796668558	2	5.100989
P07871	QDAFALASQQK	0.81258934	2	3.421734
P07871	QKQDAFALASQQK	0.781298879	2	4.114099
P07871	QVVTLLNELK	0.777889329	2	2.596093
P07871	SKAEELGLPILGVLR	0.768147994	3	4.446339
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.722365553	3	4.855532
P07871	TITVSQDEGVRPSTTMEGLAK	0.755417137	2	4.59334
P07871	VNPLGGAIALGHPLGCTGAR	0.725915916	2	4.778697
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.902180386**	**0.03849**	**19**
P07872	AFTTWTANAGIEECR	1.148568528	2	4.044143
P07872	ASATFNPELITHILDGSPENTR	0.841387002	2	4.591238
P07872	ASEAHCHYVVVK	0.865696353	3	4.211193
P07872	EIENLILNDPDFQHEDYNFLTR	0.702595777	2	4.41354
P07872	EIGTHKPLPGITVGDIGPK	0.817510643	2	3.550845
P07872	EVAWNLTSVDLVR	1.171444187	2	3.762223
P07872	EYGISDPEEIMWFK	1.071530541	2	3.490992
P07872	FGYEEMDNGYLK	0.842415788	2	3.441206
P07872	GGDFLEGSIITGAQLSQVNAR	0.92618116	2	5.751139
P07872	GLETTATYDPK	0.993992254	2	3.20909
P07872	INESIGQGDLSELPELHALTAGLK	0.851496722	3	5.486875
P07872	LVEIAAK	0.880375453	1	2.060848
P07872	LVGGMVSYLNDLPSQR	1.56167381	2	3.367737
P07872	QSEPEPQILDFQTQQYK	0.866997408	2	4.729783
P07872	SFLVGNAAQSLSK	0.867713046	2	4.500191
P07872	TQEFILNSPTVTSIK	0.820481233	2	4.701035
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	0.888721011	3	5.792662
P07872	YAQVKPDGTYVKPLSNK	1.53603099	3	3.786342
P07872	YDGNVYENLFEWAK	1.02307571	2	5.278123
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**1.049013905**	**1**	**3**
P07895	AIWNVINWENVSQR	0.969179517	2	3.606142
P07895	GDVTTQVALQPALK	1.069789996	2	3.485644
P07895	HHATYVNNLNVTEEK	1.01294	2	4.625066
P07896	**ECHP Peroxisomal bifunctional enzyme**	**1.030052207**	**1**	**25**
P07896	ELSTVDLVVEAVFEDMNLK	1.077995261		
P07896	EWQSLAGPHGSK	1.573164392	2	2.903282
P07896	GGPMFYAASVGLPTVLEK	1.015712491	2	3.937281
P07896	GQGLTGPSLPPGTPVR	0.854893832	2	4.010396
P07896	GWYQYDKPLGR	1.018495162	2	2.935923
P07896	IFNKPVPSLPNMDSVFAEAIAK	0.948603146	3	4.068112
P07896	IGVVVGNCYGFVGNR	0.895025503	2	3.089379
P07896	IIDKPIEPR	1.034368866	2	2.637156
P07896	KGQGLTGPSLPPGTPVR	1.032507518	2	4.58959
P07896	KQYPGVLAPETCVR	0.90757163	2	3.759094
P07896	LCNPPVNAVSPTVIR	1.032984165	2	4.338208
P07896	LGILDAVVK	0.936015741	2	2.815678
P07896	LLEVIPSR	0.856474314	2	2.382654

P07896	LVAQGSPPLK	1.014141251	2	2.376482
P07896	QNPDIPQLEPSDYLR	0.868232773	2	3.774805
P07896	QYPGVLAPETCVR	0.938980488	2	3.287457
P07896	TASAQPVSSVGVLGLGTMGR	0.931093455	2	5.192828
P07896	TASAQPVSSVGVLGLGTMGR+Oxidation(17)	1.164951458		
P07896	TISKEEILER	0.940783041	2	2.684462
P07896	VGISVVAVESDPK	0.953537514	2	3.819666
P07896	VGLPEVTLGILPGAR	0.85378469	2	3.558491
P07896	VSDLAGLDVGWK	0.925964494	2	4.115533
P07896	YLSADEALR	0.992352136	2	2.657097
P07896	YSPLGDMLCEAGR	0.946483503	2	4.076702
P07896	YSSPTTIATVMSLSK	0.94274561	2	3.356931
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**1.082690947**	**0.06222**	**3**
P07953	IGGDSGLSAR	0.657028234	2	2.391631
P07953	NYEFFRPDNTEAQLIR	0.865973889	2	2.97137
P07953	TIQTAEALGVPYEQWK	1.107756566	2	2.963765
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.041547105**	**0.79796**	**5**
P08009	LCYNPDFEK	1.251332739	2	2.810278
P08009	LLLEYTDSSYEEK	1.062524202	2	4.815895
P08009	LLLEYTDSSYEEKR	0.974179117	2	3.835348
P08009	NQVFEATCLDAFPNLK	1.09593968	2	4.897267
P08009	SQWLNEK	1.02187942	2	2.651681
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.044263422**	**1**	**15**
P08010	FLSKPIFAK	1.086488305	1	1.932747
P08010	IRVDVLENQAMDTR	0.946493408	3	4.211671
P08010	ITYVDFLVYDVLDQHR	0.85727703	2	4.808164
P08010	KKPEYLEGLPEK	1.007264556	3	4.432535
P08010	KPEYLEGLPEK	1.104997328	2	3.712527
P08010	KYSMGDAPDYDR	0.957715571	2	3.585454
P08010	LFLEYTDTSYEDK	1.076346867	2	5.421856
P08010	LFLEYTDTSYEDKK	1.013749287	2	4.268782
P08010	LQLAMVCYSPDFER	1.130654529	2	4.804973
P08010	LQLAMVCYSPDFER+Oxidation(4)	1.114105205		
P08010	SQWLSEK	1.003493094	2	2.456386
P08010	VDVLENQAMDTR	0.967708871	2	4.666551
P08010	VDVLENQAMDTR+Oxidation(8)	0.976856178		
P08010	YSMGDAPDYDR	1.127518234	2	3.11258
P08010	YSMGDAPDYDR+Oxidation(2)	0.959922514		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.983759314**	**0.99989**	**7**
P08011	IYHTIAYLTPLPQPNR	0.986458547	2	4.815242
P08011	MMFLSSATAFQR	1.018758227	2	3.305546
P08011	MMFLSSATAFQR+Oxidation(0)	0.953289265		
P08011	MMFLSSATAFQR+Oxidation(0)	0.890652366		
P08011	MMFLSSATAFQR+Oxidation(1)	0.953289265	2	3.060802
P08011	VFANPEDCAGFGK	0.989800036	2	4.574967
P08011	VFANPEDCAGFGKGENAK	0.815781641	2	4.526186
P08081	**CLCA Clathrin light chain A**	**1.247931841**	**0.44885**	**2**
P08081	LEALDANSR	1.205116051	2	2.581615
P08081	WREEQTER	1.389236264	2	2.452036
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**0.867619244**	**0.55977**	**2**
P08290	EEQEFVVK	0.871515165	1	1.948143
P08290	WVDGTEYR	0.856937424	2	2.314624
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**0.911933684**	**0.17869**	**4**

P08461	AAPAAAAAAAPPGPR	0.913751036	2	2.623331
P08461	DVPLGTPLCIIVEK	1.382119311	2	3.141072
P08461	GLETIASDVVSLASK	0.890230779	2	3.905558
P08461	VAPTPAGVFIDIPISNIR	0.849747043	2	4.907052
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.033494634**	**1**	**9**
P08503	AFTGFIVEADTPGIHIGK	0.959675974	2	4.295234
P08503	ANWYFVLTR	0.925118189	2	2.624996
P08503	EEIIPVAPDYDK	1.351481634	2	3.288412
P08503	GITFEDVR	0.935108958	2	2.434762
P08503	IYQIYEGTAQIQR	1.008197479	2	4.972477
P08503	KGDEYVINGQK	1.022207181	2	4.340618
P08503	QEPGLGFSFELTEQQK	0.991857416	2	3.20518
P08503	SGEYPFPLIK	0.93524831	2	2.485406
P08503	TRPTVAAGAVGLAQR	0.860486079	2	4.462135
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**0.922967811**	**1**	**10**
P08541	DELQNHFIK	0.976387685	2	2.385172
P08541	FEIFSTSISK	1.064133596	2	2.437663
P08541	FEIFSTSISKDELQNHFIK	1.058420855	2	4.175125
P08541	FILPPSYVPVILSGLAGK	0.849535237	3	5.635575
P08541	GHEVTVLKPSAYFFLDPK	0.851671724	2	4.078653
P08541	HKEWDTFYSEILGRPTTVDETMSK	0.89892267	3	4.41874
P08541	LDFLSALEEVIDNPFYK	0.635974189		
P08541	LLDVWTYELPR	0.924225864	3	3.891724
P08541	NVMLLSTIHHDQPMKPLDR	0.915650545	3	3.617476
P08541	VEIWLIR	0.857772167	2	2.928756
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.064035241**	**0.11097**	**10**
P08542	EIINNPFYK	1.541603773	1	2.196939
P08542	FETFPTSVSKDELENYFIK	1.005884436	2	4.075817
P08542	FSPGYKIEKSSGR	1.523428227	2	2.337285
P08542	KWDPFYSEILGRPTTLAETMGK	0.967227239	2	3.950442
P08542	LVDVWTYELQR	0.842993403	2	3.510472
P08542	NAVWLSTIHHDQPMKPLDK	0.999619378	3	3.308901
P08542	NAVWLSTIHHDQPMKPLDK+Oxidation(13)	1.044020295		
P08542	SDLFNALKEIINNPFYK	0.908715949	2	2.328739
P08542	TPATLGPNTR	0.885592256	2	2.315405
P08542	WDPFYSEILGRPTTLAETMGK	0.872318179	2	3.456259
P08683	**CP2CB Cytochrome P450 2C11**	**1.158216241**	**9.9E-20**	**17**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	1.351979907	3	5.235713
P08683	EALVDLGEEFSGR	1.495263271	2	4.03007
P08683	EHQESLDKDNPR	0.56071824	2	4.110683
P08683	FDPGHFLDER	1.030580642	2	2.342104
P08683	FDYKDPTFLNLMHR	1.01176981	3	5.037016
P08683	FNENFR	1.199356568	1	1.979918
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	0.870309734	3	5.247375
P08683	GTNVIVSLSSILHDDKEFPNPEK	1.094120411	2	5.194221
P08683	ICAGEALAR	1.251143131	2	2.806861
P08683	LPPGPTPLPIIGNTLQIYMK	0.97295164	3	3.850737
P08683	NYVLEK	1.383769563	1	1.961482
P08683	SQMPYTDAVVHEIQR	1.177744144	2	4.255602
P08683	SQMPYTDAVVHEIQR+Oxidation(2)	1.317951719		
P08683	VKEHQESLDKDNPR	1.419414864	3	5.026835
P08683	VQEEIER	1.243537158	2	2.564214
P08683	YGLLLLLK	1.245236419	2	3.032969
P08683	YIDLVPTNLPHLVTR	1.009655294	2	4.177147
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**1.373206045**	**0.78464**	**3**

P08733	GADPEETILNAFK	1.212289628	2	3.500387
P08733	NEEIDEMIK	1.287593753	1	2.497734
P08733	NLVHIITHGEEKD	3.18769424	2	2.978891
P09006	**SPA3N Serine protease inhibitor A3N**	**2.238692717**	**9.4E-09**	**2**
P09034	**ASSY Argininosuccinate synthase**	**1.51714095**	**7.3E-05**	**15**
P09034	APNTPDVLEIEFK	1.178048557	2	3.341692
P09034	DGTTHSTSLDLFMYLNEVAGK	1.605987211	2	5.794582
P09034	EFVEEFIWPAVQSSALYEDR	1.443357642	3	5.624639
P09034	EQGYDVIAYLANIGQK	0.89934154	2	4.552794
P09034	FAELVYTGFWHSPECEFVR	1.561866676	2	5.14998
P09034	FELTCYSLAPQIK	1.644135119	2	4.274148
P09034	GRNDLMEYAK	1.238197402	2	3.060752
P09034	IDIVENR	1.203832103	2	2.499088
P09034	KVFIEDVSK	1.266706372	3	3.768346
P09034	NDLMEYAK	1.135185921	2	2.645692
P09034	SPWSMDENLMHISYEAGILENPK	1.229364277	3	5.353886
P09034	TQDPAKAPNTPDVLEIEFK	1.14491323	2	4.745066
P09034	TQDPAKAPNTPDVLEIEFKK	1.100694386	3	4.287529
P09034	VFIEDVSK	1.202249406	2	2.624222
P09034	VQVSVFK	1.364708441	2	2.407244
P09041	**PGK2 Phosphoglycerate kinase 2**	**0.993825931**	**0.97892**	**4**
P09041	FHVEEEGK	0.915883693	2	2.727597
P09041	LGDVYVNDAFGTAHR	1.036016948	3	4.076824
P09041	VDFNVPMK	0.898092863	1	2.068894
P09041	VSHVSTGGGASLELLEGK	1.021625387	2	5.654178
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.117289971**	**0.85859**	**2**
P09117	VLAAVYK	1.111522423	2	2.650187
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	2.078344691	3	3.621385
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.036141048**	**0.99551**	**2**
P09139	IGLLGYNATTENADR	1.04751685	2	3.32791
P09139	VLNAPPGISLISFNDK	0.965304861	2	3.049233
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**9.461306237**	**0.00119**	**4**
P09367	ALGVNTVGAQTLK	3.486165098	2	3.574248
P09367	AQLGLNELLK	11.57159782	1	2.009157
P09367	LGLPATIVVPSTTPALTIER	3.122781336	2	3.30031
P09367	MDSSQPSGSFK	4.577627216	2	2.311677
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.107935481**	**0.98622**	**13**
P09495	AEGDAAALNR	1.153026704	2	2.309447
P09495	EDKYEEEIK	1.801781942	1	2.631262
P09495	EENVGLHQTLDQTLNELNCI	1.037595862	2	4.936319
P09495	IQALQQQADDAEDR	1.214257335	2	4.655852
P09495	IQLVEEELDR	1.233165413	2	3.591852
P09495	IQLVEEELDRAQER	1.586536718	2	2.881613
P09495	KLVILEGELER	1.767489528	2	3.049757
P09495	LEEAEKAADESER	1.812138248	2	4.09306
P09495	LVILEGELER	2.150808548	2	3.334882
P09495	MEIQEMQLK	1.754096375	2	2.658723
P09495	RIQLVEEELDR	1.85092833	2	2.845778
P09495	YEEEIK	1.25642461	1	1.964746
P09495	YSEKEDKYEEEIK	0.855782501	2	4.182867
P09527	**RAB7A Ras_related protein Rab_7a**	**1.331743356**	**0.35291**	**5**
P09527	DPENFPFVVLGNK	1.19361831	2	3.528469
P09527	EAINVEQAFQTIAR	1.56463565	2	2.810843
P09527	GADCCVLVFDVTAPNTFK	1.069132326	2	4.124101
P09527	TLDSWRDEFLIQASPR	1.090695594	3	3.742782

P09527	VIILGDSGVGK	1.455935877	2	2.873304
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.129800978**	**0.1197**	**4**
P09605	GTGGVDTAAVADVYDISNIDR	2.115463563	2	4.784618
P09605	LSEMTEQDQQR	2.547433996	2	3.629936
P09605	LSEMTEQDQQR+Oxidation(3)	0.509783692		
P09605	SEVELVQIVIDGVNYLVDCEK	2.631843798		
P09606	**GLNA Glutamine synthetase**	**1.232605868**	**0.33448**	**6**
P09606	CIEEAIDK	1.148531547	2	2.849025
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.081849389	3	4.712731
P09606	LTGFHETSNINDFSAGVANR	1.210720714	2	6.077756
P09606	RLTGFHETSNINDFSAGVANR	0.951183408	3	5.081582
P09606	TCLLNETGDEPFQYK	1.476233204	2	5.31174
P09606	TCLLNETGDEPFQYKN	1.5815278	2	4.384977
P09811	**PYGL Glycogen phosphorylase_ liver form**	**0.897897659**	**9.9E-20**	**20**
P09811	DFSELEPDKFQNK	1.148599663	2	3.502312
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	0.873394391	3	4.714675
P09811	EGWQVEEADDWLR	0.911490642	2	3.823123
P09811	GIVGVENVAELK	0.823126606	2	3.090299
P09811	GIVGVENVAELKK	1.140142828	2	2.443712
P09811	HLQIIYEINQK	0.741219785	2	3.648097
P09811	IFVDIEK	0.796731757	1	2.082982
P09811	INPSSMFDVHVK	0.757408346	2	3.069651
P09811	LHSFVGDDIFLR	1.174483215	2	2.333138
P09811	LVIDQIDNGFFSPNQPDLFK	0.846373204	2	4.666643
P09811	LVTSVAEVVNNDPMVGSK	0.754778365	2	2.980352
P09811	TFAYTNHTVLPEALER	0.725460373	2	4.020741
P09811	VDDVAALDK	0.90108712	1	2.128051
P09811	VDDVAALDKK	0.748799665	2	3.11268
P09811	VFADYEAYVK	0.758349546	2	2.401982
P09811	VIPATDLSEQISTAGTEASGTGNMK	0.864137143	2	6.121733
P09811	VLYPNDNFFEGK	0.891889939	2	3.063613
P09811	VSQLYMNQK	1.337402736	2	3.091756
P09811	WLLLCNPGLADLIAEK	0.984824089	2	5.043386
P09811	YEYGIFNQK	0.746763181	2	2.569544
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**0.985737163**	**0.92003**	**12**
P09812	GLAGVENVSDLKK	1.600251146	2	3.034668
P09812	GYNAQEYYDRIPELR	15.90901186	2	2.770464
P09812	HLQIIYEINQR	3.437023723	2	2.916353
P09812	IGEEYISDLDQLR	2.340436248	2	3.854689
P09812	IGEEYISDLDQLRK	1.577380526	2	2.924317
P09812	LITAIGDVVNHDPAVGDR	2.534365652	2	3.605339
P09812	NLAENISR	0.911946578	1	2.473176
P09812	QIIEQLSSGFFSPK	1.588802298	2	3.258137
P09812	TNFDAFPDK	2.45598988	2	2.323047
P09812	VHINPNSLFDVQVK	0.983891317	2	2.808653
P09812	VIPAADLSEQISTAGTEASGTGNMK	2.560100707	2	5.036545
P09812	WLVLCNPGLAEVIAER	1.217492719	2	4.29391
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.026070844**	**0.70989**	**6**
P09875	ANVVASALAQIPQK	1.012865656	3	4.258505
P09875	FSGGLPLPPSYVPVVLSELSDR	0.998954975	3	4.645263
P09875	IILNELAQR	1.348940509	2	3.022376
P09875	SDLEYSFAK	1.339741545	2	2.507524
P09875	VDFSILSTTGLLTALK	1.026652503	2	4.534775
P09875	VFNEYSDVVENLCK	0.882396944	2	3.461263
P09895	**RL5 60S ribosomal protein L5**	**1.219343877**	**2.4E-14**	**5**
P09895	GAVDGGLSIPHSTK	1.184718225	2	4.376074
P09895	HIMGQNVADYMR	1.073389302	2	3.01488

P09895	NNVTPDMMEEMYK	1.272040771	2	3.352194
P09895	RFPGYDSESK	1.245153311	2	2.840241
P09895	YLMEEDEDAYKK	1.047432327	2	3.253284
P0C0S7	**H2AZ Histone H2A.Z**	**0.797794665**	**0.07782**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.79043073	2	3.751095
P0C0S7	GDEELDSLIK	0.790576608	2	3.518457
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.936414759**	**0.32258**	**17**
P0C2X9	AIEAAVLAR	0.937924997	2	2.968482
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.746001669	3	5.561224
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.858114298	2	4.758953
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	0.927905904	3	3.749143
P0C2X9	EEIFGPVLTVYVYPDEK	1.077374534	2	4.145845
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	1.014075203	2	5.184915
P0C2X9	KEWDLKPVADR	1.035216287	2	3.341376
P0C2X9	LYVPQSLWPQIK	1.171198549	2	3.266038
P0C2X9	NAAGNFYINDK	1.091399237	2	3.512446
P0C2X9	NFHFVHSSADVDSVVSGTLR	0.725266336	2	5.858699
P0C2X9	SAFEYGGQK	0.855212402	2	2.45889
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.855662923	3	5.720127
P0C2X9	STGSVVGQQPFGGAR	0.941691065	2	4.400449
P0C2X9	TVIQAEIDAAAELIDFFR	0.722218248		
P0C2X9	VANEPILAFTQGSPER	0.866501933	2	5.411601
P0C2X9	VGNPAEDFGTFFSAVIDAK	1.134857583	2	4.96786
P0C2X9	YQLSPFNHGHK	0.604631327	2	2.935117
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.318294131**	**2.9E-09**	**4**
P0C5H9	DRDVTFSPATIEEELIK	1.071443076	2	4.711087
P0C5H9	DVTFSPATIEEELIK	1.125138688	2	3.209631
P0C5H9	IINEVSKPLAHHIPVEK	1.373537093	3	3.812029
P0C5H9	ILDDWGEMCK	0.961592233	2	2.390073
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.100107372**	**8.7E-07**	**3**
P0C6F1	EDSVLGLQAFASWR	1.081330401	2	2.303156
P0C6F1	TMPLISDLR+Oxidation(1)	1.353572101		
P0C6F1	TMPLISDLRNPALR	1.073259554	2	2.396952
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.25641915**	**0.99744**	**12**
P10111	EGMSIVEAMER	1.274084693	2	2.990081
P10111	FEDENFILK	1.054470091	2	3.165493
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	0.977534201	3	5.952951
P10111	HTGPGILSMANAGPNTNGSQFFICTAK+Oxidation(8)	0.94823915		
P10111	IIPGFMCQGGDFTR	1.076699168	2	3.32359
P10111	ITISDCGQL	0.855554395	1	1.968194
P10111	KITISDCGQL	1.223019941	2	3.330281
P10111	SIYGEKFEDENFILK	0.962143403	2	4.425166
P10111	TEWLDGK	1.022322324	2	2.351271
P10111	VCFELFADK	1.071670374	2	3.320732
P10111	VCFELFADKVPK	1.014278827	2	3.857755
P10111	VKEGMSIVEAMER	1.021515798	2	3.000339
P10536	**RAB1B Ras_related protein Rab_1B**	**1.017798896**	**0.99434**	**3**
P10536	MGPGAASGGERPNLK	1.108188151	2	3.295355
P10536	NATNVEQAFMTMAAEIK+Oxidation(11)	0.918052662		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9)	0.918357869		
P10633	**CP2D1 Cytochrome P450 2D1**	**1.024123849**	**0.00131**	**4**
P10633	LVEESLTEVSGFIPEVLNTFPALLR	0.831066304		
P10633	SQGVILASYGPEWR	0.776380318	2	4.197389

P10633	TFMALLDNLLAENR	0.995988563	2	3.502585
P10633	YGDVFSLQK	1.291293963	2	2.84155
P10634	**CP2DQ Cytochrome P450 2D26**	**1.007408339**	**0.38408**	**17**
P10634	ACLGEPLAR	1.016933405	2	2.665581
P10634	AVSNVIASLVYAR	0.919386742	3	4.463062
P10634	DMTDAFLAEMQK	1.349367269	2	3.027043
P10634	EAEHPFNPSILLSK	1.845016934	2	3.082219
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	1.08194781	3	4.909128
P10634	FADIVPTNIPHMTSR	0.897894986	2	2.668834
P10634	FEYEDPFFNR	0.948629254	2	2.698626
P10634	FHPEHFLDAQGNFVK	1.030103541	2	4.805937
P10634	GNPESSFNDENLR	1.251296065	2	4.206139
P10634	GTTLIPNLSSVLK	0.917537366	2	2.545521
P10634	GTTLIPNLSSVLKDETVWEKPLR	1.003741072	2	4.334306
P10634	GVVLAPYGPEWR	0.924285607	2	3.436186
P10634	LNSFIALVDK	1.30344931	2	2.482055
P10634	RFEYEDPFFNR	0.998990548	3	4.071996
P10634	SLEQWVTEEAGHLCDTFAK	0.993634605	2	4.965187
P10634	SWDPAQPPR	0.994125981	2	2.653176
P10634	VHEEIDEVIGQVR	0.980958257	2	4.552141
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**0.99732936**	**2.3E-05**	**34**
P10719	AGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGR	1.235371119		
P10719	AHGGYSVFAGVGER	1.27224173	2	3.93031
P10719	AIAELGIYPAVDPLDSTSR	0.913147132	3	5.562542
P10719	DQEGQDVLLFIDNIFR	0.762253818		
P10719	EGNDLYHEMIESGVINLK	0.991328097	2	5.1579
P10719	FLSQPFQVAEVFTGHMGK	1.011775751	2	4.06247
P10719	FTQAGSEVSALLGR	0.934282309	2	4.842857
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	0.821411362	3	4.730116
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	0.785796421	3	4.720021
P10719	IGLFGGAGVGK	1.059316703	2	3.025123
P10719	IGLFGGAGVGKTVLIMELINNVAK	1.080099752	3	3.494787
P10719	ILQDYK	1.035204558	1	2.170173
P10719	IMDPNIVGSEHYDVAR	0.937424102	2	4.818998
P10719	IMDPNIVGSEHYDVAR+Oxidation(1)	1.066965119		
P10719	IMNVIGEPIDER	1.026049822	2	4.170508
P10719	IMNVIGEPIDER+Oxidation(1)	1.024757715		
P10719	IPSAVGYQPTLATDMGTMQER	1.042048948	2	4.837956
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14)	0.941615923		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17)	1.030786827		
P10719	LVLEVAQHLGESTVR	0.943239099	2	4.67961
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	0.997346248	3	4.985281
P10719	SLQDIIAILGMDELSEEDKLTVSR	0.759082195	3	5.441735
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10)	1.024749868		
P10719	TIAMDGTEGLVR	0.855484659	2	3.371756
P10719	TIAMDGTEGLVR+Oxidation(3)	0.951235562		
P10719	TREGNDLYHEMIESGVINLK	0.905346903	2	6.109365
P10719	TVLIMELINNVAK	0.776198371	2	4.571095
P10719	TVLIMELINNVAK+Oxidation(4)	0.842863018		
P10719	VALTGLTVAEYFR	1.108223196	2	4.072749
P10719	VALVYGQMNEPPGAR	1.039306835	2	4.363111
P10719	VALVYGQMNEPPGAR+Oxidation(7)	1.033495398		
P10719	VLDSGAPIK	1.001295169	2	3.028409
P10719	VLDSGAPIKIPVGPETLGR	0.890652268	3	4.761925
P10719	VVDLLAPYAK	0.85585365	2	3.03147
P10760	**SAHH Adenosylhomocysteinase**	**1.21924488**	**9.9E-20**	**18**
P10760	ALDIAENEMPGLMR	1.076489561	2	4.316842

P10760	ALDIAENEMPGLMR+Oxidation(12)	1.046733541		
P10760	ATDVMIAGK	1.085064838	2	2.824625
P10760	DGPLNMILDDGGDLTNLIHTK	1.130968417	2	5.419811
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5)	1.068978316		
P10760	EMYSASKPLK	1.732514625	2	2.495085
P10760	FDNLYGCR	1.280642896	2	2.861892
P10760	GETDEEYLWCIEQTLHFK	1.190799597	2	4.279146
P10760	GISEETTTGVHNLYK	1.248674241	2	4.13385
P10760	IILLAEGR	1.2866948	2	2.803187
P10760	KLDEAVAEAHLGK	1.295842765	3	5.16178
P10760	LDEAVAEAHLGK	1.295794386	2	3.852326
P10760	RATDVMIAGK	1.113915092	2	2.693585
P10760	SKFDNLYGCR	1.242069501	2	2.876086
P10760	VAVVAGYGDVGK	1.311548859	2	4.235604
P10760	VNIKPQVDR	1.191142441	2	2.919374
P10760	WLNENAVEK	1.251162001	2	3.16334
P10760	WSSCNIFSTQDHAAAAIAK	1.086565085	2	5.086745
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**0.880228591**	**0.71597**	**2**
P10818	HEEHERPEFVAYPHLR	1.10421726	3	3.320403
P10818	SRHEEHERPEFVAYPHLR	0.879204206	3	3.669015
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**0.945501968**	**0.00018**	**28**
P10860	ALASLMTYK	0.920859997	2	3.120529
P10860	CAVVDVPFGGAK	0.916074028	2	3.288343
P10860	CVGVGESDGSIWNPDGIDPK	0.94030584	2	5.151681
P10860	DDGSWEVIEGYR	1.391921367	2	4.09852
P10860	DIVHSGLAYTMER	1.695241413	2	3.319003
P10860	DIVHSGLAYTMER+Oxidation(10)	1.491773805		
P10860	DSNYHLLMSVQESLER	0.864641859	2	3.698667
P10860	DSNYHLLMSVQESLER+Oxidation(7)	1.430386227		
P10860	EDDPNFFK	1.111231295	1	2.06388
P10860	GASIVEDKLVEDLK	0.827142307	2	3.425748
P10860	GFIGPGIDVPAPDMSTGER	0.914027752	2	5.552316
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13)	0.928604939		
P10860	HGGTIPVVPTAEFQDR	0.94755354	2	4.468529
P10860	IIAEGANGPTTPEADK	1.018523106	2	5.261125
P10860	IIAEGANGPTTPEADKIFLER	0.923063483	3	4.6932
P10860	KGFIGPGIDVPAPDMSTGER	0.995042733	2	5.539396
P10860	KGFIGPGIDVPAPDMSTGER+Oxidation(14)	0.684855695		
P10860	LQHGSILGFPK	1.103404877	2	2.722525
P10860	MVEGFFDR	0.989088067	2	2.828782
P10860	MVEGFFDR+Oxidation(0)	1.036062898		
P10860	NLNHVSYGR	1.053136501	2	2.334039
P10860	NYTDNELEK	1.037273862	2	2.425296
P10860	RDDGSWEVIEGYR	0.919979071	2	4.242008
P10860	TAAYVNAIEK	0.943781579	2	3.602264
P10860	TFVVQGFGNVGLHSMR	0.808679699	2	3.998473
P10860	VYEGSILEADCDILIPAASEK	0.96521682	3	5.922235
P10860	YNLGLDLR	0.941471207	2	3.129853
P10860	YSTDVSVDEVK	0.898358599	2	3.187912
P10867	**GGLO L_gulonolactone oxidase**	**0.881372846**	**0.0744**	**7**
P10867	GDDILLSPCFQR	0.953257083	1	2.074422
P10867	GVQFQNWAK	1.155215221	2	2.407335
P10867	LDPTGMFLNSYLEK	0.775369179	2	4.415738
P10867	LDYWLAYETIMK	0.685177303	2	4.368528
P10867	NADVFQAAR	0.918499167	2	2.805848

P10867	TYGCSPEVYYQPTSVEEVR	0.977878826	2	4.904958
P10867	VVAHYPVEVR	1.045011983	2	2.796622
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.036183311**	**0.00869**	**4**
P10868	EHWIIECNDGVFQR	1.364025212	2	4.022839
P10868	WETPYMHSLAAAAASR	0.93188426	2	3.91216
P10868	YTDITAMFEETQVPALLEAGFQR	0.950678497	3	6.55796
P10868	YYAFPQMITPLVTK	0.758643689	2	3.481607
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.106450484**	**0.98845**	**2**
P10888	IQFNESFAEMNK	1.076552158	2	4.51784
P10888	SEDYALPSYVDR	1.082711774	2	4.045376
P11030	**ACBP Acyl_CoA_binding protein**	**1.010382585**	**0.57928**	**3**
P11030	QATVGDVNTDRPGLLDLK	1.028250634	3	3.652455
P11030	TQPTDEEMLFIYSHFK	2.065189687	2	4.393717
P11030	WDSWNK	1.098122382	1	2.037078
P11232	**THIO Thioredoxin**	**1.054189666**	**3.4E-05**	**2**
P11232	EAFQEALAAAGDK	1.861182099	2	4.316803
P11232	VGEFSGANK	1.024475785	2	2.959635
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**0.969893059**	**0.77907**	**5**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.403559356	3	6.728961
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	0.820487329	3	6.626053
P11240	GMNTLVGYDLVPEPK	0.9564332	2	3.662183
P11240	LNDFASAVR	0.96565542	2	3.261882
P11240	RLNDFASAVR	1.033150289	2	2.975237
P11348	**DHPR Dihydropteridine reductase**	**0.890977622**	**0.88055**	**11**
P11348	AALDGTPGMIGYGMAK	0.841503561	2	3.87694
P11348	EGGLLTLAGAK	0.982954562	2	3.123622
P11348	GAVHQLCQSLAGK	1.007000819	3	4.601231
P11348	MTDSFTEQADQVTAEVGK	0.982879112	2	5.547447
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0)	0.841560407		
P11348	NCDLMWK	0.907170776	1	2.080392
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	0.93217641	2	5.363461
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3)	0.871234741		
P11348	QSIWTSTISSHLATK	0.762040944	2	3.861891
P11348	RPNSGSLIQVVTTDGK	0.693150386	2	4.089117
P11348	VDAILCVAGGWAGGNAK	0.839540398	2	4.489226
P11442	**CLH Clathrin heavy chain 1**	**1.268263491**	**0.04161**	**37**
P11442	AFMTADLPNELIELLEK	0.826104043	3	4.596352
P11442	AHIAQLCEK	1.258347316	1	2.256866
P11442	ALEHFTDLYDIK	0.692699204	3	3.876439
P11442	CNEPAVWSQLAK	1.012350602	2	3.255463
P11442	EDKLECSEELGDLVK	0.958317616	2	2.716795
P11442	FDVNTSAVQVLIEHIGNLDR	0.935349104	3	3.624012
P11442	FNALFAQGNYSEAAK	0.94273882	2	4.576741
P11442	GQCDLELINVCNENSLFK	0.907710586	2	5.097107
P11442	GQFSTDELVAEVEK	1.055443027	2	4.289725
P11442	GQFSTDELVAEVEKR	0.970882708	2	3.647829
P11442	HELIEFR	1.236439564	2	2.349464
P11442	HSSLAGCQIINYR	0.922891843	2	2.713678
P11442	IHEGCEEPATHNALAK	1.054080747	2	5.305377
P11442	ISGETIFVTAPHEATAGIIGVNR	0.946920338	2	5.329196
P11442	IVLDNSVFSEHR	1.016877954	2	2.969058
P11442	IYIDSNNNPER	0.859502751	2	3.193036
P11442	KFDVNTSAVQVLIEHIGNLDR	0.926985586	3	5.637635
P11442	KFNALFAQGNYSEAAK	1.005557606	2	4.36682
P11442	LAELEEFINGPNNAHIQQVGDR	0.906591778	2	5.052642

P11442	LHIIEVGTPPTGNQPFPK	0.899926764	2	4.188672
P11442	LLYNNVSNFGR	0.907155629	2	2.340869
P11442	LPVVIGGLLDVDCSEDVIK	2.096779055	2	5.220828
P11442	LTDQLPLIIVCDR	0.880066907	2	3.240528
P11442	NLQNLLILTAIK	0.975031982	2	3.917333
P11442	NNLAGAEELFAR	1.245786483	2	3.534899
P11442	NNRPSEGPLQTR	0.975041157	3	4.19138
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.059316813	3	5.737468
P11442	SVDPTLALSVYLR	0.922581882	2	2.891626
P11442	SVNESLNNLFITEEDYQALR	1.00170183	3	5.126964
P11442	TLQIFNIEMK	0.899754356	2	2.889971
P11442	TSIDAYDNFDNISLAQR	1.070523988	2	4.362551
P11442	VGEQAQVVIIDMNDPSNPIR	0.841834105	2	4.622175
P11442	VIQCFAETGQVQK	1.002324251	2	4.629882
P11442	VSQPIEGHAASFAQFK	0.821964726	2	4.366082
P11442	WLLLTGISAQQNR	0.932411858	2	3.255105
P11442	YESLELCRPVLQQGR	0.963002325	2	2.676277
P11442	YIEIYVQK	1.183137449	1	2.369032
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.199114147**	**0.0193**	**6**
P11497	GGSWVVIDPTINPR	1.095592453	2	2.758224
P11497	GSVLEPEGTVEIK	1.477570843	2	2.699714
P11497	ITSENPDEGFKPSSGTVQELNFR	1.477583858	3	3.981685
P11497	TLRDPSLPLLELQDIMTSVSGR	1.113372383	3	3.361255
P11497	VNNADDFPNLFR	1.196398094	2	2.41684
P11497	VQQAELHTGSLPQIQSTALR	0.746406858	3	3.541937
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.907633169**	**0.98807**	**9**
P11507	DIVPGDIVEIAVGDKVPADIR	0.883162186	2	3.539428
P11507	IGIFGQDEDVTSK	0.907520624	2	3.386089
P11507	IRDEMVATEQER	1.28954209	2	3.106571
P11507	LDEFGEQLSK	1.512813644	2	2.823526
P11507	NAENAIEALK	1.152519027	2	2.339428
P11507	NAENAIEALKEYEPEMGK	1.593767239	2	3.939089
P11507	SEIGIAMGSGTAVAK	1.084559518	2	2.711593
P11507	TASEMVLADDNFSTIVAAVEEGR	1.321788457	3	4.803927
P11507	VDQSILTGESVSVIK	1.493679721	2	4.636975
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.022011951**	**1.1E-11**	**25**
P11598	DASVVGFFR	1.611666507	2	2.700565
P11598	DGEEAGAYDGPR	1.535183363	2	3.086436
P11598	DLLTAYYDVDYEK	1.218264107	2	3.241627
P11598	EATNPPIIQEEKPK	1.314053367	2	3.476962
P11598	EYDDNGEGITIFRPLHLANK	1.131465927	2	4.215931
P11598	FAHTNVESLVK	1.077809877	3	3.354488
P11598	FIQESIFGLCPHMTEDNKDLIQGK	0.881391936	3	5.034542
P11598	FISDKDASVVGFFR	1.075077675	2	4.289568
P11598	FLQEYFDGNLK	0.963546769	2	3.393449
P11598	FLQEYFDGNLKR	0.8950688	2	3.09834
P11598	FVMQEEFSR	0.928491749	2	2.5818
P11598	GFPTIYFSPANK	1.693691498	2	2.772385
P11598	IFRDGEEAGAYDGPR	1.027082089	2	3.647818
P11598	LAPEYEAAATR	1.078599074	2	3.441258
P11598	LNFAVASR	1.003355442	2	2.441781
P11598	LSKDPNIVIAK	1.034711653	3	3.790059
P11598	MDATANDVPSPYEVK	0.995603931	2	4.481105
P11598	MDATANDVPSPYEVK+Oxidation(0)	0.929645805		
P11598	QAGPASVPLR	1.598154656	2	2.547553
P11598	RLAPEYEAAATR	1.042619278	2	3.549448

P11598	SEPIPETNEGPVK	1.014630011	2	2.978814
P11598	TADGIVSHLK	1.152768214	2	2.906025
P11598	TFSHELSDFGLESTTGEIPVVAIR	0.878885269	2	6.226573
P11598	VDCTANTNTCNK	2.075977275	2	4.245453
P11598	YGVSGYPTLK	0.970446904	2	3.202235
P11711	**CP2A1 Cytochrome P450 2A1**	**0.885460795**	**4E-05**	**6**
P11711	GEQATYNTLFK	1.115784173	2	2.847202
P11711	GTDVFPILGSLMTDPK	0.8090805	2	3.653081
P11711	ILEEAGYLIK	0.953154887	2	2.726734
P11711	LEDINESPKPLGFTR	0.954988704	2	3.469052
P11711	TVSNVISSIVFGER	0.885430752	2	3.525805
P11711	VHEEIEQVIGR	1.250042253	2	3.209881
P11714	**CP2D9 Cytochrome P450 2D9**	**1.146391017**	**0.97448**	**2**
P11714	GNPESSFNDENLLMVVR	0.817604417	2	2.34788
P11714	VQQEIDEVIGQVR	1.066158342	2	4.841065
P11862	**GAS2 Growth arrest_specific protein 2**	**1.041728126**	**0.60327**	**2**
P11862	EIEQEETLSAPSPSPSPSSK	1.331014241	2	3.879451
P11862	LDNGALLCQLAATVQEK	1.017383541	2	4.086994
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**0.887875799**	**9.9E-20**	**23**
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.702683691	3	4.583633
P11884	EEIFGPVMQILK	1.255507754	2	3.797481
P11884	EEIFGPVMQILK+Oxidation(7)	1.271561092		
P11884	ELGEYGLQAYTEVK	1.390993805	2	4.45975
P11884	GYFIQPTVFGDVK	0.92978493	2	4.096813
P11884	HEPVGVCGQIIPWNFPLLMQAWK	0.844805057	3	4.190291
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.824666636	3	6.633285
P11884	LGPALATGNVVVMK	0.908724669	2	3.881171
P11884	LGPALATGNVVVMK+Oxidation(12)	0.946714318		
P11884	LLCGGGAAADR	1.098090343	2	3.536341
P11884	RVTLELGGK	1.016017521	2	2.744479
P11884	TEQGPQVDETQFK	0.937458783	2	4.756463
P11884	TFPTVNPSTGEVICQVAEGNK	0.983250939	2	4.97016
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.894269657	2	4.325205
P11884	TFVQEDVYDEFVER	0.867865681	2	5.176448
P11884	TIEEVVGR	0.868699501	2	3.001751
P11884	TIPIDGDFFSYTR	0.903478962	2	2.949207
P11884	VAEQTPLTALYVANLIK	0.973915287	3	5.245028
P11884	VAFTGSTEVGHLIQVAAGSSNLK	0.922643057	2	6.035166
P11884	VTLELGGK	0.942007253	1	1.966558
P11884	VVGNPFDSR	0.957208685	2	2.839046
P11884	YGLAAAVFTK	0.830925292	2	3.784074
P11884	YYAGWADK	0.889983906	2	2.577942
P11915	**NLTP Non_specific lipid_transfer protein**	**0.908912442**	**0.00417**	**24**
P11915	ADCTITMADSDLLALMTGK	0.781246331	2	5.697645
P11915	ADCTITMADSDLLALMTGK+Oxidation(15)	0.839394776		
P11915	ADCTITMADSDLLALMTGK+Oxidation(6)	0.837528008		
P11915	ANLIFK	0.975034698	2	2.363153
P11915	AVEIVAQEMVTDMPSTFEEK	0.897779964	2	4.274205
P11915	GHPLGATGLAQCAELCWQLR	0.973027094	3	3.727941
P11915	GSVLPDSDK	0.929936268	1	1.988598
P11915	GSVLPDSDKK	1.104966652	2	2.628221
P11915	HIDVLINK	0.895954798	2	2.858802
P11915	HSVNNPYSQFQDEYSLDEIMK	0.867963529	3	6.334317
P11915	KADCTITMADSDLLALMTGK	1.072259172	2	4.402377
P11915	KLEEEGEEFVK	0.955314742	2	4.491902
P11915	KLEEEGEEFVKK	0.941823151	3	4.443469

P11915	LEEEGEEFVK	1.071095807	2	2.693956
P11915	LEEEGEEFVKK	0.944144136	2	3.565766
P11915	LQSLQLQPDK	1.074626956	2	3.169401
P11915	MGFPEAASSFR	0.9393555	2	2.995764
P11915	MNPQSAFFQGK	0.963439486	2	3.250317
P11915	MNPQSAFFQGK+Oxidation(0)	0.820612173		
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	0.977502185	3	5.17075
P11915	THQISAAPTSSAGDGFK	1.033902697	2	4.404951
P11915	VFVVGVGMTK	0.957742952	2	2.556144
P11915	WVINPSGGLISK	0.931166393	2	3.308452
P11915	YGMSACPFAPQLFGSAGK	0.891061341	2	3.379063
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.061534057**	**0.9811**	**10**
P11980	AEGSDVANAVLDGADCIMLSGETAK	1.024353276	2	4.525784
P11980	AGKPVICATQMLESMIK	1.192161298	3	3.342162
P11980	DAVLDAWAEDVDLR	1.567927909	2	4.025075
P11980	GADYLVTEVENGGSLGSK	1.390447551	2	5.314896
P11980	GVNLPGAAVDLPAVSEK	1.194686343	2	3.770245
P11980	IYVDDGLISLQVK	1.578502102	2	3.697804
P11980	KGVNLPGAAVDLPAVSEK	3.062546208	2	3.643487
P11980	LDIDSAPITAR	1.797765754	2	3.20909
P11980	NTGIICTIGPASR	1.436791422	2	3.324592
P11980	VFLAQKMMIGRCNR+Oxidation(6)	0.949994846		
P12001	**RL18 60S ribosomal protein L18**	**0.91786925**	**0.00937**	**5**
P12001	GTVLLSGPR	1.256622696	2	2.931015
P12001	ILTFDQLALESPK	1.191235749	2	4.870775
P12001	TAVVVGTITDDVR	1.043561214	2	4.523719
P12001	TNRPPLSLSR	1.187214146	3	3.366225
P12001	TNSTFNQVVLK	0.9537977	2	3.176213
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**0.907507993**	**0.85486**	**9**
P12007	AQEIDQSNDFK	0.48942393	2	3.640245
P12007	FVQENLAPK	0.914114332	2	2.650152
P12007	FWITNGPDADVLVVYAK	0.977270784	2	3.653508
P12007	GSNTCELVFEDCK	1.050155754	2	4.458799
P12007	GSNTCELVFEDCKVPAANILSQESK	0.891134561	3	4.917409
P12007	GVYVLMSGLDLER	0.809243408	2	3.170815
P12007	IGQFQLMQGK	1.0977715	2	2.502737
P12007	LYEIGGGTSEVR	1.083647473	2	3.559751
P12007	TDLTAVPASR	0.919389717	2	2.963448
P12346	**TRFE Serotransferrin**	**1.075504199**	**9.9E-20**	**23**
P12346	ADRDQYELLCLDNTR	1.209434535	2	4.543229
P12346	ASDSSINWNNLK	1.320663654	2	3.270942
P12346	DGGGDVAFVK	1.198829058	2	3.113133
P12346	DLKQEDFQLLCPDGTK	1.119668203	2	4.446505
P12346	DQYELLCLDNTR	0.987055854	2	2.982026
P12346	EGVCPEGSIDSAPVK	2.324646348	2	3.489291
P12346	EGYNGYTGAFQCLVEK	1.113790038	2	3.528948
P12346	FDEFFSQGCAPGYK	1.220945543	2	4.345944
P12346	GDKDCTGNFCLFR	1.02631316	2	3.593474
P12346	GTDFQLNQLQGK	1.267551306	2	3.122989
P12346	GYYAVAVVK	1.262404103	2	2.79149
P12346	HQTVLENTNGK	1.039848613	2	2.579301
P12346	HTTIFEVLPQK	1.235516047	3	3.740234
P12346	KGTDFQLNQLQGK	1.476531521	2	3.59938
P12346	KTSYQDCIK	1.472540811	2	2.489622
P12346	LPEGTTYEEYLGAEYLQAVGNIR	0.866441801	2	4.675972
P12346	NGDGKEDLIWEILK	1.082942332	2	3.677605

P12346	QEDFQLLCPDGTK	1.319110555	2	3.582817
P12346	SKDFQLFGSPLGK	1.315226688	2	3.488945
P12346	TSYQDCIK	1.20802326	2	2.528939
P12346	VSTVLTAQK	1.31938207	2	2.616675
P12346	WCALSHQER	1.331752694	2	3.230942
P12346	WCAVSEHENTK	1.26325893	2	3.649519
P12711	**ADHX Alcohol dehydrogenase class_3**	**0.837954186**	**7.2E-06**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	0.862650164	3	5.782949
P12711	AFDLMHSGNSIR	0.977886947	2	2.502499
P12711	AGDTVIPLYIPQCGECK	0.86011325	2	4.027006
P12711	EFGATECINPQDFSK	1.365632301	2	4.189593
P12711	IDPSAPLDK	0.961521005	1	1.939675
P12711	IIGIDINK	0.763946342	2	2.371974
P12711	IIGIDINKDK	0.447414598	1	2.430563
P12711	VCLLGCGISTGYGAAVNTAK	0.89517661	2	5.521226
P12711	VDEFVTGNLSFDQINK	0.927921594	2	5.130754
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	0.84913066	2	4.143928
P12749	**RL26 60S ribosomal protein L26**	**1.225110241**	**1.8E-12**	**6**
P12749	DDEVQVVR	1.428529215	2	2.58808
P12749	FNPFVTSDR	1.134320598	2	2.363353
P12749	HFNAPSHIR	1.112670044	3	3.701633
P12749	KDDEVQVVR	1.232420293	2	3.385693
P12749	KIMSSPLSKELR+Oxidation(2)	1.033485949		
P12749	YVIYIER	0.986526455	1	1.919811
P12785	**FAS Fatty acid synthase**	**1.130640809**	**0.99218**	**44**
P12785	ACIDTALENLSTLK	1.174026798	2	4.915604
P12785	AGSDTELAAPK	1.104381766	2	3.247803
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.175204451	3	5.73813
P12785	DANLPAGSMAAVGLSWEECK	1.251969368	2	3.660444
P12785	DGGFLLMHTVLK	0.628701248	2	2.399549
P12785	DPETLLGYSMVGCQR	1.067082281	2	3.767768
P12785	EEEPEAMLPGAQPTLISAISK	1.008700815	2	3.315189
P12785	EQGVTFPSGEAQEQLIR	1.587148334	2	4.119235
P12785	FDASFFGVHPK	1.097087218	2	3.123435
P12785	FVFTPHVEPECLSESAILQK	1.303423899	2	4.565071
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	1.362716085	3	4.70531
P12785	GLESIINIIHSSLAEPR	1.103170279	2	4.76953
P12785	GNAGQSNYGFANSTMER	1.125377063	2	4.43746
P12785	GTNTGVWVGVSGSEASEALSR	0.971845045	2	3.539723
P12785	GVDLVLNSLAEEK	1.236977733	2	3.214894
P12785	GYDYGPHFQGVYEATLEGEQGK	1.560035573	3	3.763916
P12785	HFQLEQDKPEEQTAHAFVNVLTR	1.506406494	3	3.453434
P12785	LDPGSSELQK	1.095837684	2	2.378937
P12785	LFDHPEVPIPAESESVSR	1.070191285	2	4.0873
P12785	LLLPEDPLISGLLNSQALK	1.115725537	3	5.021595
P12785	LTPGCEAEAEAEAICFFIK	1.150302518	2	4.082347
P12785	MTVPGLEDLPQHGLPR	0.897284645	2	3.167776
P12785	QAQLNLSILLVNPEGPTLTR	1.041269809	2	4.554855
P12785	QQEQLVPTLEK	1.195910579	2	2.447166
P12785	QSPLLIGSTK	1.396873144	1	2.107911
P12785	RQQEQLVPTLEK	1.336387679	2	3.167008
P12785	SDEALKPLGVK	0.995106861	2	3.146637
P12785	SFDDSGNGYCR	0.985560664	2	3.1493
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.09554718	2	5.063999
P12785	SNMGHPEPASGLAALTK	1.106965148	2	3.647825
P12785	SNMGHPEPASGLAALTK+Oxidation(2)	1.144456483		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.321810312	2	5.068894

P12785	TMEAVQGLLEQGR	1.015595677	2	3.717564
P12785	TMEAVQGLLEQGR+Oxidation(1)	1.220546541		
P12785	VGDPQELNGITR	0.674379743	2	2.558468
P12785	VHLTGIDINPNALFPPVEFPVPR	1.080545534	2	5.039025
P12785	VLEALLPLK	1.25404411	2	2.357012
P12785	VLESDLVMNVYR	0.47258808	2	3.405668
P12785	VLLSLENGVWAPNLHFHNPNPEIPALLDGR	1.096670969	3	4.056353
P12785	VSVHIIEGDHR	1.264907473	2	2.753283
P12785	VTAIYIDPATHLQK	1.145980284	2	3.315601
P12785	VYATILNAGTNTDGCK	0.917181011	2	4.87661
P12785	VYQWEDPDSK	1.316794187	2	3.174712
P12785	WLSTSIPEAQWQSSLAR	1.015767192	2	2.372029
P12791	**CP2BA Cytochrome P450 2B10**	**1.325997955**	**6.1E-05**	**2**
P12791	IQEEAQCLVEELR	1.253805354	2	3.759812
P12791	IQEEAQCLVEELRK	1.185171203	2	3.544593
P12847	**MYH3 Myosin_3**	**0.851806315**	**0.98132**	**4**
P12847	IEAQNQPFDAK	2.809624814	2	2.748584
P12847	MKGTLEDQIISANPLLEAFGNAK	0.605245633	3	6.889268
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0)	2.161888183		
P12847	NALAHALQSSR	1.28155373	2	2.618051
P12928	**KPYR Pyruvate kinase isozymes R/L**	**0.828473155**	**0.98427**	**18**
P12928	AETSDVANAVLDGADCIMLSGETAK	0.757836372	2	5.386181
P12928	CCAAAIIVLTK	0.83121656	2	2.951444
P12928	CNLAGKPVVCATQMLESMITK	0.802394562	3	5.062019
P12928	EATESFATSPLSYRPVAIALDTK	1.282360055	3	4.059224
P12928	EPPEAIWADDVDR	0.897980348	2	2.440576
P12928	EPPEAIWADDVDRR	0.869839028	2	2.330976
P12928	GDLGIEIPAEK	0.897637524	2	3.103087
P12928	GSQVLVTVDPK	0.907256145	2	2.847728
P12928	GVNLPNTEVDLPGLSEQDLLDLR	0.769472452	2	5.44598
P12928	IGPEGLVTEVEHGGILGSR	0.804952456	2	4.779319
P12928	IYIDDGLISLVVQK	0.795744618	2	4.156784
P12928	KFDEILEVSDGIMVAR	0.81323027	3	3.386325
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	0.962141946	3	4.315272
P12928	LNFSHGSHEYHAESIANIR	0.870410147	3	4.181748
P12928	STSIIATIGPASR	0.814569744	2	3.579793
P12928	TGVLQGGPESEVEIVK	0.929090422	2	4.938263
P12928	TVWVDYHNITR	1.002371575	2	2.510377
P12928	VQFGIESGK	0.893294469	1	1.982685
P12938	**CP2D3 Cytochrome P450 2D3**	**0.861999182**	**0.30514**	**5**
P12938	DLTDAFLAEIEK	0.961174841	2	4.142829
P12938	FDYGDPDFIK	0.822630634	2	2.443841
P12938	GNPESSFNDANLR	1.021408915	2	4.309071
P12938	RFDYGDPDFIK	0.789567447	2	2.829973
P12938	TWDPDQPPR	0.861966881	2	2.43149
P12939	**CP2DA Cytochrome P450 2D10**	**1.245942515**	**3.3E-07**	**8**
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.266311837	3	5.298196
P12939	FEYEDPYLIR	1.667799543	2	2.409207
P12939	FGDIAPLNLPR	1.333050622	2	3.161536
P12939	ITSCDIEVQDFVIPK	1.365308714	2	4.545211
P12939	NLTDAFLAEVEK	1.151371359	2	4.136254
P12939	RFEYEDPYLIR	1.254911056	3	3.535597
P12939	SQGVVFASYGPEWR	1.087371983	2	3.59811
P12939	TTWDPAQPPR	1.353148664	2	2.433837
P13084	**NPM Nucleophosmin**	**1.452771507**	**0.12601**	**3**
P13084	MSVQPTVSLGGFEITPPVVLR	1.277613111	2	3.582177
P13084	MTDQEAIQDLWQWR	1.065536716	2	3.16819

P13084	VDNDENEHQLSLR	1.58201366	2	3.929126
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**0.988631104**	**0.99968**	**6**
P13086	LIGPNCPGIINPGECK	1.002718664	2	4.512835
P13086	MGHAGAIIAGGK	1.014228509	1	2.793092
P13086	MGHAGAIIAGGK+Oxidation(0)	1.051304371		
P13086	NIYIDK	0.939614372	1	1.971983
P13086	QGTFHSQQALEYGTK	0.951660549	2	2.841769
P13086	VICQGFTGK	0.968029728	2	2.308482
P13107	**CP2B3 Cytochrome P450 2B3**	**0.98971642**	**1**	**11**
P13107	ATLDPNAPR	1.011466882	2	2.326976
P13107	CLVEELK	0.972790273	1	2.00381
P13107	DFIDTFLLHMEK	1.102615169	2	3.009206
P13107	EVLDYIDHSVENHR	0.970561943	2	3.960704
P13107	FSDVSPMGLPCR	0.961352954	2	2.761684
P13107	FSDVSPMGLPCR+Oxidation(6)	0.973639939		
P13107	GIIAVLQPIMQEYGVSFVNEER	1.192552733	3	5.361229
P13107	LLDLLYR	1.129129324	2	2.488436
P13107	MCLGEGIAR	0.891558388	2	2.693204
P13107	QSVEDQIKEEAK	1.150392732	2	2.495909
P13107	SFIQLQEK	1.030332299	2	2.406467
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**2.680557992**	**9.9E-20**	**8**
P13221	ITWSNPPAQGAR	2.577013387	2	3.393543
P13221	IVATTLSNPELFK	2.13350976	2	3.639694
P13221	NFGLYNER	3.458518043	1	1.931059
P13221	NLDYVATSINEAVTK	2.264156077	2	4.887107
P13221	SCASQLVLGDNSPALR	2.929234127	2	5.405178
P13221	TDDSQPWVLPVVR	2.076831138	2	3.524652
P13221	VGGVQSLGGTGALR	1.325074094	2	2.393139
P13221	VGNLTVVGK	1.018380206	2	2.550872
P13255	**GNMT Glycine N_methyltransferase**	**1.441508467**	**6.5E-13**	**8**
P13255	AHMVTLDYTVQVPGAGR	1.080364004	2	4.934911
P13255	AWLLGLLR	1.462645606	2	2.789044
P13255	DITTSVLTVNNK	1.521251446	2	3.978507
P13255	LSYYPHCLASFTELVQEAFGGR	1.101218036	3	3.700447
P13255	NYDYILSTGCAPPGK	1.061608385	2	4.593596
P13255	SDLTKDITTSVLTVNNK	0.737508082	2	3.09809
P13255	SLGVAAEGIPDQYADGEAAR	1.151901986	2	5.755338
P13255	VWQLYIGDTR	0.74552155	2	2.605269
P13383	**NUCL Nucleolin**	**1.38917418**	**7.4E-05**	**8**
P13383	FGYVDFESAEDLEK	1.56572012	2	2.638528
P13383	GFGFVDFNSEEDAK	1.351561841	2	3.716178
P13383	GLSEDTTEETLK	0.966826278	2	2.904298
P13383	IEGSEPTTPFNLFIGNLNPNK	1.146841076	2	3.463486
P13383	NDLAAVDVR	1.485226222	2	2.431115
P13383	NLSFNITEDELK	1.331427185	2	2.777811
P13383	SEADAEKNLEEK	1.33006504	2	3.060445
P13383	SVSLYYTGEK	1.780676206	1	2.024874
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.984736919**	**0.99999**	**22**
P13437	AANEAGYFNEEMAPIEVK	0.956019838	2	5.24088
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11)	0.950696656		
P13437	DAEVVLCGGTESMSQSPYSVR	1.444166619	2	5.16125
P13437	DFTATDLTEFAAR	1.831125425	2	4.920811
P13437	DMDLIDVNEAFAPQFLAVQK	0.712890644	3	6.501692
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1)	1.068465054		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	1.020195852	3	5.731832
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	0.921566325	3	4.948078

P13437	GVFIVAAK	0.966316077	2	2.583429
P13437	ITAHLVHELR	1.468796255	2	3.024678
P13437	LCGSGFQSIVSGCQEICSK	1.272754921	2	5.477032
P13437	LEDTLWAGLTDQHVK	0.926544353	2	5.388068
P13437	RTPFGAYGGLLK	0.990366228	2	2.944408
P13437	SLDLDPSK	1.101461625	2	3.019894
P13437	TNVSGGAIALGHPLGGSGSR	0.994175157	2	6.242382
P13437	TPFGAYGGLLK	1.050324087	2	2.785176
P13437	VGVPTETGALTLNR	0.943432767	2	3.69551
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	0.890789661	2	5.95532
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14)	0.977356658		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	0.874926813	3	5.472631
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	0.993127545	3	3.586936
P13437	YAVGSACIGGGQGISLIIQNTA	0.973276624	2	2.477781
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.744338568**	**9.9E-20**	**8**
P13444	FVIGGPQGDAGVTGR	1.707297117	2	4.726541
P13444	HIGYDDSAK	1.869549082	2	2.825247
P13444	ICDQISDAVLDAHLK	1.844811325	2	5.156051
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.148617359	3	5.423157
P13444	SEFPWEVPK	1.511141074	2	2.541992
P13444	SGVLPWLRPDSK	1.004493492	2	3.107456
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.753562397	3	5.684929
P13444	TQVTVQYVQDNGAVIPVR	1.711738904	2	5.094707
P13471	**RS14 40S ribosomal protein S14**	**1.162801596**	**0.85483**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	1.248996993	2	5.853403
P13471	ELGITALHIK	1.326664994	2	2.416054
P13471	IEDVTPIPSDSTR	1.098142635	2	3.992328
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**1.489874161**	**1.7E-12**	**22**
P13601	ANNTPYGLAAGVFTK	1.669713084	2	4.254565
P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	1.642801954	3	3.305845
P13601	EEIFGPVQQIMK	1.867669821	2	3.81693
P13601	EMGEQGVYEYTELK	2.164545333	2	3.887575
P13601	FPVINPATEEVICHVEEGDK	1.033472301	3	4.09538
P13601	FPVINPATEEVICHVEEGDKADVDK	0.888100324	4	5.142944
P13601	GFFVQPTVFSNVTDEMR	1.718644587	2	4.312201
P13601	IAKEEIFGPVQQIMK	1.174848181	2	3.864847
P13601	IFINNEWHNSLNGK	1.453333947	2	3.500032
P13601	IFTHAYLLDTEVSIKALK	1.152402721	2	2.341056
P13601	IHGQTIPSDGDVFTYTR	1.369051658	2	4.627728
P13601	ILDLIESGK	1.123766239	2	2.729225
P13601	ILDLIESGKK	1.237086902	3	3.341717
P13601	KFPVINPATEEVICHVEEGDK	0.973636506	3	3.753911
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.970237613	4	4.866906
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	1.274719964	3	5.60002
P13601	LFVEESIYDEFVR	1.49567822	2	4.067123
P13601	VLLATMESMNAGK	1.731665663	2	3.981084
P13601	VSFTGSTEVGK	1.799446671	2	3.086549
P13601	YFAGWADK	1.374078624	1	2.056434
P13601	YVLGNPLDSGISQGPQIDK	1.613322441	2	4.961924
P13601	YVLGNPLDSGISQGPQIDKEQHAK	1.59884839	4	4.604517
P13697	**MAOX NADP_dependent malic enzyme**	**1.302776055**	**0.15454**	**5**
P13697	AECSAEECYK	1.324079793	1	2.810228
P13697	AIFASGSPFDPVTLPDGR	1.17170587	2	4.257449
P13697	GHIASVLNAWPEDVVK	1.010458969	2	3.816658
P13697	HINDSVFLTTAEVISQQVSDK	1.301332423	3	4.341857
P13697	NLEAIVQK	2.078590342	1	2.197101

P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**0.969019651**	**1.2E-08**	**14**
P13803	AAVDAGFVPNDMQVGQTGK	0.992843548	2	4.772173
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11)	0.931262981		
P13803	DPEAPIFQVADYGIVADLFK	1.000642337	2	5.355403
P13803	GLLPEELTPLILETQK	0.88082445	2	4.669336
P13803	GTSFEAAAASGGSASSEK	1.101979471	2	5.340793
P13803	LGGEVSCLVAGTK	0.905131203	2	4.711003
P13803	LLYDLADQLHAAVGASR	0.983348736	2	4.643563
P13803	LNVAPVSDIIEIK	1.015173814	3	4.717721
P13803	QFSYTHICAGASAFGK	0.797278165	2	3.163802
P13803	SDRPELTGAK	1.059425324	3	3.341209
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.797444003	3	7.038399
P13803	TIYAGNALCTVK	0.925256907	2	3.661068
P13803	VLVAQHDAYK	0.880328626	2	3.259243
P13803	VVQDLCK	0.893265128	2	2.751452
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**0.955544143**	**0.50028**	**3**
P13832	ATSNVFAMFDQSQIQEFK	0.883812122	2	4.652575
P13832	FTDEEVDELYR	0.99574636	2	3.499027
P13832	GNFNYIEFTR	1.025436831	2	2.628266
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.667666743**	**6.5E-12**	**5**
P14046	GDPIPNEQVLIK	0.608515088	2	3.181515
P14046	GMYESLPVVAVK	0.643278654	2	3.397591
P14046	ISLCHGNPTFSSETK	1.00582429	2	3.682433
P14046	QQNSYGGFSSTQDTVVALDALSK	0.569159705	2	4.142656
P14046	QSPGPCGSEVATVPETGR	0.649699467	2	3.336217
P14141	**CAH3 Carbonic anhydrase 3**	**1.002798398**	**3.7E-12**	**18**
P14141	EAPFNHFDPSCLFPACR	1.414352556	2	4.341764
P14141	EKGEFQILLDALDK	1.165048147	2	4.559532
P14141	EKGEFQILLDALDKIK	1.214118566	2	3.110992
P14141	EPMTVSSDQMAK	1.271344888	2	2.941079
P14141	EWGYASHNGPEHWHELYPIAK	1.287567385	3	4.517257
P14141	GDNQSPIELHTK	0.971615117	2	3.764329
P14141	GEFQILLDALDK	0.928569714	2	4.664411
P14141	GEFQILLDALDKIK	0.941443936	2	3.253896
P14141	GGPLSGPYR	1.023682674	2	2.956714
P14141	GKEAPFNHFDPSCLFPACR	0.773266051	3	3.525347
P14141	HDPSLQPWSVSYDPGSAK	0.909812877	3	5.572367
P14141	QFHLHWGSSDDHGSEHTVDGVK	1.083346932	2	4.643401
P14141	QPDGIAVVGIFLK	1.056753434	2	2.576633
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.939711885	3	5.701326
P14141	VVFDDTFDR	0.97983772	2	3.372337
P14141	YAAELHLVHWNPK	1.0211655	2	4.332443
P14141	YNTFGEALK	1.029351302	2	2.314709
P14141	YNTFGEALKQPDGIAVVGIFLK	0.895371906	3	6.01375
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.057425316**	**0.0429**	**7**
P14173	AGEGGGVIQGSASEATLVALLAAR	0.90715558	2	3.543346
P14173	ALIPTTAPQEPETYEDIIR	1.144789034	3	4.096662
P14173	GSNQLNETLLQR	1.125693845	2	2.866176
P14173	HSHQDSGLITDYR	1.059711567	3	3.633439
P14173	MLELPEAFLAGR	1.134442395	2	2.770898
P14173	QLQAASPELTQAALMEK	1.093379825	2	3.814373
P14173	TDLTEAFNMDPVYLR	1.068415041	2	3.676677
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**0.949571598**	**0.95453**	**15**
P14408	AAAEVNQEYGLDPK	1.204921355	2	4.467802
P14408	AIEMLGGELGSK	0.950141868	2	3.507025
P14408	IEYDTFGELK	0.9437493	2	3.542608

P14408	IEYDTFGELKVPTDK	0.776974654	2	3.649869
P14408	IYELAAGGTAVGTGLNTR	0.995697448	2	5.560617
P14408	KTAIELGYLTAEQFDEWVKPK	0.934935481	3	3.576987
P14408	LMNESLMLVTALNPHIGYDK	1.040337875	3	5.647627
P14408	LMNESLMLVTALNPHIGYDK+Oxidation(6)	1.013839976		
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.918283057	3	6.411434
P14408	SGLGELILPENEPGSSIMPGK	0.954100801	2	4.37712
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17)	0.939198953		
P14408	SKEFAQVIK	1.133978289	2	2.48217
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	0.990722045	3	4.20594
P14408	TAIELGYLTAEQFDEWVKPK	0.936286463	2	4.527267
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.210075251	3	6.005599
P14480	**FIBB Fibrinogen beta chain**	**1.541321794**	**9.9E-20**	**10**
P14480	AHYGGFTVQTEANK	2.003687542	2	2.906667
P14480	DNENVINEYSSILEDQK	1.156054678	2	3.269349
P14480	GFGNIATNEDTK	1.290476063	2	2.739107
P14480	GFGNIATNEDTKK	2.033509121	2	2.819092
P14480	IGPTELLIEMEDWK	1.783090061	2	3.57419
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.645676359	3	5.218724
P14480	LYIDETVNDNIPLNLR	1.450092157	2	3.006875
P14480	QTLLNHERPIK	2.384644153	2	2.747412
P14480	TENGGWTVIQNR	1.591490882	2	3.228431
P14480	YCGLPGEYWLGNDK	1.414312845	2	3.318062
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.936971525**	**0.08343**	**8**
P14604	AFAAGADIK	1.090715846	2	3.234199
P14604	AQFGQPEILLGTIPGAGGTQR	0.932332771	2	5.647284
P14604	FLSHWDHITR	0.983675253	2	3.129168
P14604	IFPVETLVEEAIQCAEK	0.971549667	2	5.81061
P14604	LFYSTFATDDR	1.375888619	2	2.726903
P14604	NSSVGLIQLNRPK	1.042190477	2	3.516642
P14604	SLAMEMVLTGDR	0.845439266	2	3.384629
P14604	TFQDCYSGK	1.026320448	2	2.788632
P14668	**ANXA5 Annexin A5**	**1.087296095**	**0.24397**	**3**
P14668	ETSGNLENLLLAVVK	1.120472126	2	3.481405
P14668	GLGTDEDSILNLLTAR	0.825991105	2	4.616629
P14668	GTVTDFSGFDGR	0.690392088	2	2.932259
P14669	**ANXA3 Annexin A3**	**0.778207802**	**7.8E-14**	**5**
P14669	GMGTDEDTLIEILTTR	0.817278555	2	3.150109
P14669	GTINNYPGFNPSVDAEAIR	0.77313784	2	4.933701
P14669	QYQEAYEQALK	0.778923129	2	2.551154
P14669	SEIDLLDIR	0.866707692	2	2.617257
P14669	TLINILTER	0.772337159	2	2.518674
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**0.989269391**	**0.76367**	**3**
P14685	AIQLEYSEAR	1.169672764	2	2.584062
P14685	LQLDSPEDAEFIVAK	1.053672723	2	3.861351
P14685	SVFPEQANNNEWAR	0.953604801	2	3.043399
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.074800572**	**0.99857**	**2**
P14740	LGTLEVEDQIEAAR	0.996092072	2	3.906668
P14740	VLEDNSALDK	1.131035137	2	2.860023
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.249936908**	**0.99999**	**12**
P14882	FLSDVYPDGFK	0.967599276	2	2.694512
P14882	FSSQEAASSFGDDR	1.212027204	2	3.318769
P14882	HGNALWLNER	1.252623464	2	2.597135
P14882	HIEIQVLGDK	1.034832968	2	2.397127
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	0.999723938	3	6.014308

P14882	LQVEHPVTECITGLDLVQEMILVAK	1.005186741	3	3.542439
P14882	MADEAVCVGPAPTSK	1.143944621	2	4.370352
P14882	MEDALDSYVIR	1.087234784	2	3.107002
P14882	SYLNMDAIMEAIK	1.021592649	2	3.150029
P14882	TGAQAVHPGYGFLSENK	1.054850159	2	4.045664
P14882	TVAIHSDVDASSVHVK	1.275473551	3	4.100473
P14882	VVEEAPSIFLDPETR	0.903037965	2	4.150364
P15083	**PIGR Polymeric immunoglobulin receptor**	**0.678459137**	**0.00016**	**4**
P15083	EIQNAGDQAQENR	0.933063877	2	3.655425
P15083	FSVLITGLR	0.66517799	2	2.667918
P15083	GVTGGSVAIVCPYNPK	0.798547592	2	4.329145
P15083	NNADLQVLEPEPELLYK	0.59570136	2	2.640825
P15149	**CP2A2 Cytochrome P450 2A2**	**0.907455341**	**0.00012**	**10**
P15149	DVQECILEEAGYLIK	1.031592574	3	4.597108
P15149	DVYSSITQLSER	1.125224984	2	2.426858
P15149	FSNLAPLGIPR	0.855173505	2	3.20416
P15149	GELPTFNILFK	0.906898135	2	2.417119
P15149	GTDVFPIIGSLMTEPK	0.846262006	2	3.933875
P15149	GYGFSLSNVEQAK	0.968997715	2	3.449176
P15149	NFIDSFLIR	0.944007883	1	2.565989
P15149	QNHSTLDPNSPR	1.009005659	2	3.029952
P15149	TLQGTCGAPIDPSIYLSK	0.886486181	2	4.209558
P15149	TVSNVINSIVFGNR	0.846050203	2	3.530468
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**0.896734839**	**0.95636**	**6**
P15178	FQTEIQTVNK	1.121333202	2	2.387757
P15178	GEEILSGAQR	0.968334729	2	2.91514
P15178	LEYCEALAMLR	0.887024603	2	2.931232
P15178	LPLQLDDAIRPEVEGEEDGR	1.122022645	3	3.89853
P15178	QMVKFAANINK+Oxidation(1)	0.908218531		
P15178	SNAYLAQSPQLYK	0.905320183	2	2.842947
P15429	**ENOB Beta_enolase**	**0.924466242**	**0.98853**	**7**
P15429	DATNVGDEGGFAPNILENNEALELLK	1.4240449	2	5.692757
P15429	FMIELDGTENK	2.30151031	2	2.341909
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	2.323764633	3	4.629873
P15429	IEEALGDK	4.64306954	1	2.36389
P15429	TAIQAAGYPDK	4.249985274	2	2.682114
P15429	VNQIGSVTESIQACK	0.921830963	2	5.042507
P15429	YNQLMRIEEALGDK	0.956435672	2	2.492086
P15473	**IBP3 Insulin_like growth factor_binding protein 3**	**0.901150992**	**0.79191**	**2**
P15473	EMEDTLNHLKFLNVLSPR	0.89328173	2	2.313431
P15473	MEVIIKGQARDSQR	1.039774558	2	2.312101
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.837681948**	**9.9E-20**	**20**
P15650	AFVDSCLQLHETK	0.898242004	2	4.137933
P15650	AQDTAELFFEDVR	0.963051751	2	4.809271
P15650	AQDTAELFFEDVRLPASALLGEENK	0.99539493	3	4.291989
P15650	CIGAIAMTEPGAGSDLQGVR	0.714809633	2	6.102579
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6)	0.77167463		
P15650	EQIEQFIPQMTAGK	1.745361212	2	4.990434
P15650	FFQEEVIPYHEEWEK	1.199547014	2	4.958344
P15650	GFYYLMQELPQER	0.804364919	2	3.911878
P15650	IFSSEHDIFR	1.034037583	2	2.987184
P15650	KFFQEEVIPYHEEWEK	0.963077394	3	5.007729
P15650	LDSASASMAK	0.841997403	2	2.63886
P15650	LPASALLGEENK	1.614701991	2	3.415677
P15650	LPASALLGEENKGFYYLMQELPQER	0.762881961	3	3.626521

P15650	QGLLGINIAEK	0.848719748	2	3.297413
P15650	RLDSASASMAK	0.787689772	2	3.485178
P15650	RLDSASASMAK+Oxidation(8)	0.961473318		
P15650	RSGSDWILNGSK	2.344838946	2	2.857289
P15650	SGSDWILNGSK	0.956783946	2	2.932576
P15650	VQPIYGGTNEIMK	0.82132507	2	3.250186
P15650	VQPIYGGTNEIMK+Oxidation(11)	0.87326078		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.797192875**	**9.9E-20**	**9**
P15651	ASSTANLIFEDCR	0.745924347	2	3.422934
P15651	EEGDSWVLNGTK	1.444718686	2	2.304456
P15651	ELVPIAAQLDK	1.212607598	1	1.956785
P15651	ELVPIAAQLDKEHLFPTSQVK	0.299071898	2	4.037627
P15651	GISAFLVPMPTPGLTLGK	1.080455572	2	2.510096
P15651	IGCFALSEPGNGSDAGAASTTAR	0.902712398	2	5.58182
P15651	IGIASQALGIAQASLDCAVK	0.801064205	2	4.930885
P15651	ITEIYEGTSEIQR	0.824869562	2	4.297855
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	0.787324821	4	4.912566
P15684	**AMPN Aminopeptidase N**	**1.394728152**	**4.1E-07**	**5**
P15684	ALGDTPAPNIDTTELVER	1.02418025	2	3.906228
P15684	AQIIHDSFNLASAGK	1.678885326	2	3.77442
P15684	ESALVFDPQSSSISNK	2.601242837	2	2.454454
P15684	VMAVDALASSHPLSSPANEVNTPAQISELFDSITYSK	1.453017058	3	3.823935
P15684	VVATTQMQAADAR	1.25380546	2	2.777344
P15709	**ST2A1 Bile salt sulfotransferase**	**1.039103441**	**0.0519**	**2**
P15709	GNVLYGSWFEHIR	1.132418899	2	3.04906
P15709	NHFTVSQAEAFDK	0.491598326	2	3.661526
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.018815467**	**0.74849**	**2**
P15978	VEHEGLPEPLSQR	1.042563462	2	3.271872
P15978	YDSDAENPR	0.659735342	2	2.722694
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**0.867625144**	**6.5E-11**	**24**
P15999	AVDSLVPIGR	0.902576837	2	3.494999
P15999	EIVTNFLAGFEP	3.718069367	2	2.409987
P15999	EVAAFAQFGSDLDAATQQLLSR	0.920369826	2	6.775969
P15999	FESAFLSHVVSQHQSLLGNIR	0.839800354	2	6.011279
P15999	GIRPAINVGLSVSR	0.931499732	3	3.626514
P15999	GMSLNLEPDNVGVVVFGNDK	0.881246226	2	5.684156
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1)	0.875310447		
P15999	GYLDKLEPSK	0.864785633	1	2.593194
P15999	ILGADTSVDLEETGR	1.095649868	2	5.006292
P15999	LELAQYR	0.905826829	2	2.693234
P15999	LKEIVTNFLAGFEP	1.184641317	2	3.256053
P15999	LTDADAMK	0.875488189	2	2.552619
P15999	LTDADAMK+Oxidation(6)	0.847043843		
P15999	LYCIYVAIGQK	1.233638933	2	2.409989
P15999	NVQAEEMVEFSSGLK	0.969810109	2	4.355209
P15999	QGQYSPMAIEEQVAVIYAGVR	1.056786944	3	5.223771
P15999	RTGAIVDVPVGDELLGR	0.877721623	2	2.85457
P15999	STVAQLVK	0.99584713	2	2.39713
P15999	TGAIVDVPVGDELLGR	0.889686497	2	4.928999
P15999	TGTAEMSSILEER	0.808003994	2	4.265776
P15999	TGTAEMSSILEER+Oxidation(5)	1.019832526		
P15999	TSIAIDTIINQK	0.879762592	2	4.391929
P15999	VLSIGDGIAR	0.905856065	2	3.160133
P15999	VVDALGNAIDGK	0.945003838	2	4.185841

P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.051269687**	**0.92892**	**7**
P16036	ALYSNILGEENTYLWR	1.051456144	2	3.331951
P16036	EEGLNAFYK	1.152143333	1	2.318203
P16036	FGFYEVFK	1.020536867	2	2.342442
P16036	GIFNGFSITLK	0.817723223	2	2.82009
P16036	GSTASQVLQR	1.052072114	2	2.970787
P16036	IQTQPGYANTLR	1.024885189	2	3.760676
P16036	MYKEEGLNAFYK	1.121787277	2	2.88434
P16086	**SPTA2 Spectrin alpha chain_ brain**	**0.995378269**	**0.07343**	**33**
P16086	ALINADELANDVAGAEALLDR	0.983408199	2	5.12341
P16086	ALSSEGKPYVTK	1.085069528	2	3.021644
P16086	DLSSVQTLLTK	1.045509026	2	2.781344
P16086	EAALTSEEVGADLEQVEVLQK	0.882679409	2	3.743141
P16086	GEIDAHEDSFK	0.97711355	2	2.405044
P16086	GVIDMGNSLIER	1.069288938	2	3.189369
P16086	HQAFEAELSANQSR	1.525085114	2	3.569421
P16086	HQEHKGEIDAHEDSFK	0.95696464	3	4.149324
P16086	HQLLEADISAHEDR	1.644113377	3	4.028481
P16086	KFEEFQTDLAAHEER	1.155434095	3	4.819622
P16086	LFGAAEVQR	1.208821845	2	2.582831
P16086	LGDSHDLQR	1.151485429	2	3.187368
P16086	LGESQTLQQFSR	1.001076728	2	3.238065
P16086	LIQEQHPEEELIK	0.970929759	2	3.524149
P16086	LQQSHPLSANQIQVK	1.543628231	2	3.946393
P16086	LQTASDESYKDPTNIQSK	1.134029185	2	4.325
P16086	LQVASDENYKDPTNLQGK	1.279099188	2	4.613623
P16086	LSDDNTIGQEEIQQR	1.036758243	2	4.238682
P16086	MTLVASEDYGDTLAAIQGLLK	0.941802589	2	3.162891
P16086	NQALNTDNYGHDLASVQALQR	1.036893383	3	4.873584
P16086	NTTGVTEEALK	0.999205715	2	2.350149
P16086	QFQDAGHFDAENIKK	0.792913771	2	2.580685
P16086	REELITNWEQIR	1.281381954	2	3.451416
P16086	SADESGQALLAAGHYASDEVR	1.043631064	3	3.639349
P16086	SLQQLAEER	0.93552503	2	2.761007
P16086	SQLLGSAHEVQR	0.378759191	2	3.21781
P16086	SSEEIESAFR	1.007659357	2	2.428163
P16086	SSLSSAQADFNQLAELDR	0.980633582	2	4.939239
P16086	TATDEAYKDPSNLQGK	1.06554267	2	3.581089
P16086	TKQEEVNAAWQR	1.110651728	2	3.027998
P16086	VLETAEDIQER	1.105177934	2	3.42193
P16086	VNDVCTNGQDLIK	1.175406408	2	3.177594
P16086	VNSLGETAQR	1.112039879	2	2.34579
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.413956779**	**6.3E-09**	**10**
P16232	EECALEIIK	2.144894414	1	1.97235
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(1)	1.007375904		
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8)	1.007375904		
P16232	ETSGIILSQAAPK	1.516497554	2	3.317542
P16232	FALDGFFSTIR	1.282858099	2	3.079359
P16232	KDEVYYDK	1.237692514	2	3.00259
P16232	MGAHVVLTAR	1.373515514	2	2.919173
P16232	MTQPLIASYSASK	1.307779952	2	3.380455
P16232	MTQPLIASYSASK+Oxidation(0)	1.926096579		
P16232	SSWTPLLLGNPGR	1.358390443	2	3.606695
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.026625622**	**0.97954**	**7**
P16290	AMEAVAAQGK	1.068596548	2	2.795687

P16290	AMEAVAAQGK+Oxidation(1)	0.918828413		
P16290	FLGDEETVR	2.126036372	2	2.669859
P16290	HGESSWNQENR	3.128641614	2	3.63271
P16290	HNYYASISK	1.159849015	2	2.369684
P16290	HYGGLTGLNK	1.313768814	1	2.924372
P16290	VLIAAHGNSLR	1.214168768	2	2.827607
P16303	**CES3 Carboxylesterase 3**	**0.956218836**	**0.00023**	**20**
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	0.960785385	3	3.861336
P16303	AKEAAEEPSHWK	0.980560712	2	4.250408
P16303	DGASEEETNLSK	1.261596841	2	4.197501
P16303	EAAEEPSHWK	1.715127615	2	2.927894
P16303	ENIPLQFSEDCLYLNVYTPADLTK	3.353763729	2	4.423151
P16303	ESYPFLPTVIDGVVLPK	1.31552736	2	4.154991
P16303	FAPPQPAEPWNFVK	0.796052931	2	2.551271
P16303	IGASTQAAQR	1.285866178	2	2.852261
P16303	KENIPLQFSEDCLYLNVYTPADLTK	1.606122618	2	4.658246
P16303	LDLLGNPK	1.055207746	2	2.495217
P16303	QEFGWIIPTLMGYPLSEGK	1.253545296	2	4.090944
P16303	QKTEDELLETSLK	1.19138767	3	3.701194
P16303	SFNTVPYIVGINK	1.911683911	2	3.375175
P16303	TEDELLETSLK	1.084999429	2	3.726542
P16303	TPEEILAEK	1.48091224	2	2.342819
P16303	TTTSAVMVHCLR	1.026294441	2	2.803672
P16303	TTTSAVMVHCLR+Oxidation(6)	0.938353725		
P16303	TVIGDHGDELFSVFGSPFLK	1.082820032	2	5.399829
P16303	YFGGTDDPAK	1.08873069	2	3.198878
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	0.920466806	3	3.579983
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.023300859**	**0.91619**	**7**
P16332	AAVQVLDDIEK	1.283865834	2	2.620392
P16332	AHCQTSGWSLTEQDPYNNIVR	1.044533952	3	5.170474
P16332	GDVGMAGVAIDTVEDTK	0.84810275	2	3.069168
P16332	IDSGSEVIVGVNK	1.142972219	2	3.577084
P16332	ILFDGIPLEK	0.98614792	2	2.318594
P16332	NTQIIIQEESGIPK	0.982769726	2	3.881436
P16332	TGLQAGLTIDEFAPR	1.017294782	2	3.439996
P16409	**MYL3 Myosin light chain 3**	**1.766806303**	**0.93364**	**6**
P16409	AAPAPAAAPAAAPEPERPK	3.012111358	2	4.281186
P16409	ALGQNPTQAEVLR	2.921960711	2	3.976088
P16409	DTGTYEDFVEGLR	2.067329942	2	3.297331
P16409	MMDFETFLPMLQHISK	1.16933665	2	2.926264
P16409	NKDTGTYEDFVEGLR	1.445365848	2	4.133505
P16409	VFDKEGNGTVMGAELR	2.701974062	2	3.517663
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.002998134**	**1**	**18**
P16617	AHSSMVGVNLPQK	1.092491162	3	4.083166
P16617	AHSSMVGVNLPQK+Oxidation(4)	1.361171706		
P16617	ALESPERPFLAILGGAK	1.086929306	3	4.525317
P16617	DCVGSEVENACANPAAGTVILLENLR	1.050429879	3	6.297062
P16617	FCLDNGAK	0.861235049	1	2.05084
P16617	GCITIIGGGDTATCCAK	1.051181123	2	5.566938
P16617	IQLINNMLDK	0.988918831	2	2.72171
P16617	IQLINNMLDK+Oxidation(6)	1.337311865		
P16617	ITLPVDFVTADKFDENAK	1.098879614	2	4.905708
P16617	QIVWNGPVGVFEWEAFAR	1.017071987	2	3.100346
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	0.876746695	4	4.691022
P16617	TGQATVASGIPAGWMGLDCGTESSK	0.93413591	2	4.736675
P16617	TGQATVASGIPAGWMGLDCGTESSKK	0.900335403	3	4.254049

P16617	VLNNMEIGTSLYDEEGAK	1.061290498	2	5.54474
P16617	VLNNMEIGTSLYDEEGAK+Oxidation(4)	0.941083012		
P16617	VLPGVDALSNV	1.09299051	2	2.735156
P16617	WNTEDKVSHVSTGGGASLELLEGK	0.883526272	3	4.855772
P16617	YSLEPVAAELK	0.968243344	2	3.618829
P16638	**ACLY ATP_citrate synthase**	**0.970228691**	**1**	**25**
P16638	AFDSGIIPMEFVNK	0.986150739	2	4.132862
P16638	AFDSGIIPMEFVNK+Oxidation(8)	0.868400644		
P16638	DEPSVAAMVYPFTGDHK	0.934910686	2	3.228929
P16638	DGVYILDLAAK	1.060479624	2	2.982784
P16638	DLVSSLTSGLLTIGDR	1.204184472	2	3.486832
P16638	EAYPEEAYIADLDAK	1.05343325	2	3.064889
P16638	FGGALDAAAK	0.939367469	2	2.458114
P16638	GAIVPAQEVPPPTVPMDYSWAR	0.944167127	2	4.228379
P16638	GGPNYQEGLR	1.013995903	2	2.718846
P16638	GVTIIGPATVGGIKPGCFK	0.881972465	2	2.852841
P16638	HLLVHAPEDK	0.978919773	2	2.664155
P16638	HLLVHAPEDKK	0.975255291	2	3.564683
P16638	IGNTGGMLDNILASK	0.953994399	2	3.65479
P16638	LGLVGVNLSLDGVK	1.145318283	2	2.830339
P16638	LNAEDIK	0.996827193	1	1.913635
P16638	QHFPATPLLDYALEVEK	0.994449864	3	4.445997
P16638	RGGPNYQEGLR	1.296069942	2	3.176728
P16638	SFDELGEIIQSVYEDLVAK	0.813916262		
P16638	SGGMSNELNNIISR	0.97043213	2	3.700621
P16638	TIAIIAEGIPEALTR	0.981436647	2	5.253416
P16638	TTDGVYEGVAIGGDR	1.198164334	2	3.421449
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	0.930705029	3	4.084336
P16638	VDATADYICK	1.06870536	2	2.470526
P16638	WGDIEFPPPFGR	0.955957197	2	3.933861
P16638	YICTTSAIQNR	0.938989952	2	2.813505
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.918058189**	**0.00028**	**5**
P16970	FDHVPLATPNGDILIQDLSFEVR	0.875268417	2	2.48301
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.739188957	3	4.97734
P16970	GYLDNVQLGHILER	0.864518928	2	3.446207
P16970	HLHSTHSELLEDYYQSGR	1.05719827	3	5.156248
P16970	SGANVLICGPNGCGK	0.844657012	2	3.116311
P17074	**RS19 40S ribosomal protein S19**	**1.011586186**	**0.98069**	**5**
P17074	DVNQQEFVR	0.650743536	2	2.368493
P17074	ELAPYDENWFYTR	0.735996131	2	2.484498
P17074	HKELAPYDENWFYTR	1.011570004	3	3.352571
P17074	RVLQALEGLK	1.16994358	3	3.319066
P17074	VLQALEGLK	1.017233111	2	2.717939
P17077	**RL9 60S ribosomal protein L9**	**0.995339162**	**1.1E-12**	**8**
P17077	DFNHINVELSLLGK	1.747507335	3	3.752424
P17077	FLDGIYVSEK	1.123227768	2	3.201822
P17077	GTVQQPDE	1.145172767	1	2.101096
P17077	KFLDGIYVSEK	1.179931645	2	2.726167
P17077	SVYAHFPINVVIQENGSLVEIR	1.1419688	3	3.74064
P17077	TGVACSVSQAQK	1.273216825	2	3.669527
P17077	TICSHVQNMIK	0.901587013	2	2.878561
P17077	TILSNQTVDIPENVDITLK	0.967064566	2	3.154075
P17078	**RL35 60S ribosomal protein L35**	**1.161858673**	**0.76008**	**2**
P17078	QLDDLKVELSQLR	1.018740242	2	2.586651
P17078	VLTVINQTQK	1.175356835	2	3.248564
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.276237624**	**0.00044**	**4**

P17178	DHESTEGPGTGQDRPR	4.777671359	2	2.52979
P17178	MLKPAEAALYTDALNEVISDFIAR	1.323485851	3	4.138936
P17178	VGCLEPSIPEDTATFIR	1.426830681	2	2.884553
P17178	YEVVLSPGMGEVK	1.102953244	2	3.745264
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.884125794**	**0.99995**	**15**
P17425	ASAELFNQK	0.951468141	2	3.109892
P17425	DKNSIYSGLEAFGDVK	1.257468421	2	3.026466
P17425	DVGIVALEIYFPSQYVDQAELEK	0.793924395	3	3.689102
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK+Oxidation(3)	0.755652991		
P17425	ITASLCDLK	0.922388663	1	1.942125
P17425	LEDTYFDRDVEK	0.820524378	2	2.920728
P17425	LPATSGEPESAVISNGEH	0.813040927	2	4.239635
P17425	MFLNDFLNDQNR	0.723582311	2	2.97792
P17425	MFLNDFLNDQNR+Oxidation(0)	0.440905485		
P17425	MGFCTDREDINSLCLTVVQK	0.791686951	3	4.179461
P17425	NSLSYDCIGR	1.149094639	2	2.872298
P17425	RPSTNDHSLDEGVGLVHSNTATEHIPSPAK	0.96243022	4	4.604982
P17425	TCVAPDVFAENMK	0.852302719	2	2.783931
P17425	VTQDATPGSALDK	0.731201961	2	3.805212
P17425	YTIGLGQAR	0.869177086	2	2.688532
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.106278946**	**0.65955**	**2**
P17426	NADVELQQR	1.10721925	2	2.807719
P17426	VGGYILGEFGNLIAGDPR	1.067681932	2	3.750861
P17475	**A1AT Alpha_1_antiproteinase**	**2.42733714**	**9.9E-20**	**5**
P17475	MQHLEQTLTK	1.978124038	2	3.007922
P17475	MQHLEQTLTK+Oxidation(0)	2.359819674		
P17475	TLLSSLGITR	2.271354747	2	3.155347
P17475	VFNNDADLSGITEDAPLK	1.632661583	2	5.7359
P17475	VINDYVEK	1.906240753	2	2.34795
P17702	**RL28 60S ribosomal protein L28**	**1.292666821**	**0.52075**	**2**
P17702	NCSSFLIK	1.219556432	2	2.415654
P17702	QTYSTEPNNLK	1.29700327	2	3.01876
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.110018243**	**0.70407**	**17**
P17764	EEQDKYAIGSYTR	1.270279148	2	3.561487
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.092249808	2	4.623279
P17764	EVYMGNVIQGGEGQAPTR	1.492007607	2	5.394138
P17764	EVYMGNVIQGGEGQAPTR+Oxidation(3)	2.042267751		
P17764	FANEITPITISVK	0.926478916	2	3.848681
P17764	GKPDVVVKEDEEYK	1.0115697	2	3.453354
P17764	GKPDVVVKEDEEYKR	0.928984919	2	5.075504
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.132386668	2	5.742885
P17764	IHMGNCAENTAK	1.081470072	2	3.178412
P17764	IHMGNCAENTAK+Oxidation(2)	0.899696619		
P17764	LEDLIVK	0.9999242	2	2.711647
P17764	LGTIAIQGAIEK	1.231556019	2	3.293019
P17764	QATLGAGLPIATPCTTVNK	1.06480839	2	4.624789
P17764	QGEFGLASICNGGGGASAVLIEK	1.001845663	2	4.942674
P17764	TPIGSFLGSLASQPATK	1.132126157	2	4.479323
P17764	VNVHGGAVSLGHPIGMSGAR	0.871764069	2	5.807877
P17764	VNVHGGAVSLGHPIGMSGAR+Oxidation(15)	1.131194991		
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.130683956**	**1**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	0.970180861	3	5.323452
P17879	TTPSYVAFTDTER	1.08745803	2	3.729563
P17879	VEIIANDQGNR	1.058121204	2	3.77198
P17988	**ST1A1 Sulfotransferase 1A1**	**1.378547636**	**9.9E-20**	**6**

P17988	CPGVPSGLETLEETPAPR	0.782649096	2	4.797564
P17988	ILEFLGR	1.344553259	2	2.344018
P17988	NTFTVAQNER	1.211045159	2	3.682426
P17988	SGTTWMSEILDMIYQGGK	0.976433873	2	4.986846
P17988	SLPEETVDSIVHHTSFK	1.253524106	2	4.56665
P17988	THLPLSLLPQSLLDQK	1.577265018	2	4.978549
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**0.896472154**	**9.9E-20**	**30**
P18163	AELSVIFADKPEK	0.79065497	2	3.141895
P18163	ALEDLGR	1.222368632	2	2.328306
P18163	ALKPPCDLSMQSVEVTGTTEGVR	0.887930349	2	4.535008
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9)	0.892845666		
P18163	CGVEIIGLK	0.792107994	2	2.879076
P18163	DGWLHTGDIGK	1.241523587	2	3.187433
P18163	GAMVTHQNIMNDCSGFIK	1.119907626	2	4.383051
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2)	0.878529095		
P18163	GFQGSFEELCR	0.820373525	2	3.625499
P18163	GIAVHPELFSIDNGLLTPTLK	0.950611809	2	5.813646
P18163	GIQVSNDGPCLGSR	0.926108088	2	4.508375
P18163	IENIYLR	0.870309749	2	2.95509
P18163	IFGQANTSVK	0.98337814	2	2.76034
P18163	IIVIMDSYDNDLVER	0.752126879	2	4.590707
P18163	LLLEGVENK	0.967002856	2	3.334471
P18163	LLMDDLK	0.936368431	2	2.434906
P18163	LMITGAAPVSATVLTFLR	0.666349057	2	3.52214
P18163	LVDVEDMNYQAAK	1.037455023	2	4.203762
P18163	LVDVEDMNYQAAK+Oxidation(6)	0.936707799		
P18163	NAGLKPFEQVK	0.96408304	2	3.831028
P18163	NNSLWDK	0.797069169	2	2.545614
P18163	QVAEMAECIGSALIQK	0.797169717	2	5.590154
P18163	QVAEMAECIGSALIQK+Oxidation(4)	0.905492632		
P18163	SAVLEDDKLLLYYYDDVR	1.669018933	3	4.165587
P18163	SQIDELYSTIK	0.861356992	2	3.657451
P18163	SQIDELYSTIKI	0.808420646	2	4.152328
P18163	TAEALDKDGWLHTGDIGK	0.838684356	2	5.108146
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	1.685443542	3	5.415393
P18163	VLQPTIFPVVPR	0.886017836	2	3.500982
P18163	WLLDFASK	0.828507022	2	2.381298
P18297	**SPRE Sepiapterin reductase**	**1.06856971**	**0.97392**	**4**
P18297	ALAPQLAGLLSPGSVLLLSAR	0.880891569	3	4.81566
P18297	LLLINNAGTLGDVSK	1.098927249	2	3.600589
P18297	LNSEGELVDCGTSAQK	1.203930461	2	4.78737
P18297	TVVNISSLCALQPFK	0.868993973	2	3.763449
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.682606794**	**1.1E-16**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	1.399087969	2	5.421152
P18298	KIIVDTYGGWGAHGGGAFSGK	1.373213002	3	3.46823
P18298	YLDEDTIYHLQPSGR	2.05377727	2	4.753562
P18418	**CALR Calreticulin**	**1.047607657**	**1**	**19**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	1.104436762	3	5.440219
P18418	CKDDEFTHLYTLIVRPDNTYEVK	1.081595265	3	4.856501
P18418	DMHGDSEYNIMFGPDICGPGTK	1.052384472	2	6.398684
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1)	1.053347766		
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(10)	1.053347766		
P18418	EQFLDGDAWTNR	1.590393617	2	3.022876
P18418	FYGDQEK	0.914191613	1	2.055975
P18418	FYGDQEKDK	0.967151072	1	2.776472
P18418	GQTLVVQFTVK	0.849637473	2	3.255028

P18418	HEQNIDCGGGYVK	0.925978785	2	4.420838
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	0.882961955	3	3.916787
P18418	IDNSQVESGSLEDDWDFLPPK	1.010162934	2	5.437834
P18418	IDNSQVESGSLEDDWDFLPPKK	0.925933311	2	4.899996
P18418	IKDPDAAKPEDWDER	1.234027615	2	4.383667
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	0.888333726	3	5.572803
P18418	LFPGGLDQK	1.059534233	1	2.052844
P18418	QIDNPDYK	0.925424692	1	2.290527
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	0.813496161	3	4.883288
P18418	VHVIFNYK	1.090984793	1	2.268359
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.120630528**	**0.2716**	**2**
P18420	AQPSQAADEPAEK	1.121429751	2	3.424672
P18420	NQYDNDVTVWSPQGR	1.030363504	2	3.629484
P18421	**PSB1 Proteasome subunit beta type_1**	**0.873148927**	**0.08926**	**3**
P18421	AGGSASAMLQPLLDNQVGFK	0.869625175	2	5.028276
P18421	GAVYSFDPVGSYQR	1.196852953	2	3.86107
P18421	NMQNVEHVPLTLDR	0.413096491	2	3.688417
P18445	**RL27A 60S ribosomal protein L27a**	**1.120474953**	**0.00102**	**2**
P18445	NQSFCPTVNLDK	1.150811259	2	3.352818
P18445	RNQSFCPTVNLDK	0.869624861	2	3.029666
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**0.773966081**	**0.0319**	**3**
P18484	LTECLETILNK	0.86210321	2	2.73545
P18484	NNGVLFENQLLQIGLK	0.702915016	2	3.254095
P18484	QLSNPQQEVQNIFK	1.28627247	2	3.409109
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.160035266**	**0.8933**	**5**
P18596	DIVPGDIVEVAVGDK	1.309576348	2	2.458181
P18596	DIVPGDIVEVAVGDKVPADLR	4.079039457	2	3.760574
P18596	SLPSVETLGCTSVICSDK	1.96208084	2	4.198058
P18596	TGTLTTNQMSVCR	1.004527624	2	2.415793
P18596	VGEATETALTCLVEK	1.155785057	2	4.386174
P18757	**CGL Cystathionine gamma_lyase**	**0.786845567**	**1**	**18**
P18757	AGDEVICMDEVYGGTNR	0.930580092	2	5.387766
P18757	AGDEVICMDEVYGGTNR+Oxidation(7)	1.156435479		
P18757	ATLGISDTLIR	0.893288849	2	3.54182
P18757	AVAALDGAK	1.257990993	2	2.670032
P18757	AVVLPISLATTFK	0.87660843	3	4.291078
P18757	DLLEDLGQALK	1.191148433	2	2.779878
P18757	FLQNSLGAVPSPFDCYLCCR	0.982785807	2	4.118407
P18757	GTLQHAQVFLK	1.076093273	2	3.069681
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.08439235	3	5.283734
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	1.171313385	4	5.448231
P18757	LLEAAITPQTK	1.023230945	2	3.884803
P18757	LSVGLEDEKDLLEDLGQALK	0.950947005	3	6.474934
P18757	LVWIETPTNPTLK	1.036565664	2	3.627706
P18757	QCTGCPGMVSFYIK	0.916263632	2	3.741347
P18757	QCTGCPGMVSFYIK+Oxidation(7)	0.92056726		
P18757	QDSPGQSSGFVYSR	1.049682304	2	3.700495
P18757	RVASEFGLK	1.224967995	2	2.585621
P18757	VIYPGLPSHPQHELAK	1.18168127	2	4.256135
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.154599364**	**0.78508**	**10**
P18886	ATNLTVSAVR	1.114845501	2	3.302066
P18886	ELHAHLLAQDK	1.714595841	2	3.009936
P18886	FFNEVFR	1.082586009	2	2.30748
P18886	LIFDGNEETLK	1.105826171	2	2.989042
P18886	QYGQTVATYESCSTAAFK	1.065779426	2	3.575184

P18886	SEYNDQLTR	1.21097511	2	2.673007
P18886	TETIRPASIFTK	1.37396849	2	2.583139
P18886	TLSIDSIQFQR	1.079008437	2	3.302003
P18886	YILSDSSPVPEFPVAYLTSENR	1.241869142	2	5.495711
P18886	YLNAQKPLLDDSQFR	1.087682882	2	4.368109
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**0.993463615**	**9.9E-20**	**18**
P19112	AGGLATTGNEDILDIVPTEIHQK	0.85800114	3	6.255063
P19112	AGGTGEMTQLLNSLCTAIK	0.80538494	2	5.363754
P19112	AGGTGEMTQLLNSLCTAIK+Oxidation(6)	0.810172326		
P19112	APVIMGSTEDVQEFLEIYNK	0.949346023	2	5.246606
P19112	DFDPAINEYIQR	1.346095969	2	3.916194
P19112	FPPDNSAPYGAR	0.902539911	2	2.553975
P19112	GNIYSINEGYAK	0.989239681	2	4.063055
P19112	KGNIYSINEGYAK	1.00396404	2	3.924677
P19112	KLDILSNDLVINMLK	0.794839355	2	6.077208
P19112	KTSANEPSEKDALQPGR	0.826458736	3	3.639435
P19112	LDILSNDLVINMLK	0.732856349	2	5.047803
P19112	LLYECNPIAYVMEK	1.078523947	2	4.267875
P19112	QAGIAQLYGIAGSTNVTGDQVK	0.869802574	3	6.084218
P19112	SRPSLPLPQSR	0.858475671	2	3.311398
P19112	SSYATCVLVSEEDTHAIIIEPEKR	0.957702125	3	5.78229
P19112	TLVYGGIFLYPANK	0.821210941	2	4.206293
P19112	TLVYGGIFLYPANKK	0.905778641	2	2.33301
P19112	TSANEPSEKDALQPGR	0.772966268	2	3.885636
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**1.089971606**	**0.92854**	**5**
P19123	AAVEQLTEEQK	1.258868602	2	2.861987
P19123	AAVEQLTEEQKNEFK	1.102815352	2	3.446536
P19123	GKSEEELSDLFR	1.02303009	2	2.570196
P19123	IDYDEFLEFMK	1.226180617	2	3.178984
P19123	SEEELSDLFR	2.698304961	2	2.930652
P19225	**CP270 Cytochrome P450 2C70**	**1.054486362**	**8.6E-09**	**14**
P19225	ACIGEGLAR	1.673436407	2	2.789742
P19225	ASLNLSNPQDFIDYFLIK	1.07114981	2	4.702113
P19225	EALIDRGEEFSDK	2.254384751	2	3.293825
P19225	FDPGHFLDEK	1.301693937	2	2.313699
P19225	FDYSDEK	1.396297497	1	1.99506
P19225	FILMEINR	1.490660394	2	2.33989
P19225	GTSVMACLTSALHDDKEFPNPEK	1.362746555	3	3.486035
P19225	IQEEITR	1.438073781	1	2.000205
P19225	IQEEVVYLLEALR	2.187935425	2	3.357499
P19225	LPPGPTPLPIFGNILQVGVK	0.970286268	3	4.910123
P19225	SDYFMAFSAGRR+Oxidation(4)	0.75113961		
P19225	SEFTMDNLIVTIGDLFGAGTETTSSTIK	0.680494457		
P19225	VSQGLGIVFSNGEIWK	1.663786895	2	3.348341
P19225	YIDFVPIPLPR	1.135882913	2	3.174598
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.202056779**	**0.44409**	**4**
P19234	AAAVLPVLDLAQR	1.701059356	2	2.355726
P19234	DIEEIIDELR	1.190410024	2	3.551643
P19234	DTPENNPDTPFDFTPENYER	1.018098608	2	4.397674
P19234	FCCEPAGGLTSLTEPPK	1.259426435	2	3.746825
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**0.903994533**	**0.39804**	**8**
P19468	ASGELMTVAR	0.911947574	2	2.696695
P19468	CNQIANELCECPELLGSGFR	0.978817221	2	5.099301
P19468	DKNTPSPFVETFPEDEEASK	0.943591066	3	3.43545

P19468	GYVSDIDCR	1.032233951	2	2.584268
P19468	NTPSPFVETFPEDEEASK	1.223664191	2	4.776046
P19468	SLFFPDEAINK	0.984877709	2	2.661707
P19468	VQLLLNGGDVLETLQEK	0.868007606	2	4.72091
P19468	WGVISASVDDR	0.869192541	2	3.256202
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**0.910114952**	**0.0006**	**9**
P19488	AEMWLIR	0.999208824	2	2.918362
P19488	ANAIAWALAQIPQK	0.894208962	3	5.953065
P19488	FETFPTSVSK	1.077076612	1	2.001886
P19488	FETFPTSVSKDELEK	0.610438612	2	3.394245
P19488	GAAVTLNIR	0.961106148	2	2.511322
P19488	GHEVTVLKPSAYYVLDPK	0.937416088	2	4.521748
P19488	NWDPFYTEILGRPTTLAETMGK	0.967120442	2	5.012445
P19488	SDLFNALK	1.056868677	2	2.764688
P19488	TILDELVQR	0.913108123	2	3.196654
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**0.953990166**	**0.99275**	**10**
P19511	HVIQSISAQQEK	0.937863025	2	3.994242
P19511	HVIQSISAQQEKETIAK	0.975946742	3	4.07216
P19511	HYLFDVQR	0.899399527	2	2.588789
P19511	LDYHISVQDMMR	0.805690491	3	4.311595
P19511	LGLIPEEFFQFLYPK	0.959366089	2	2.678539
P19511	LNEEKIAQLEEIK	1.016116375	2	2.530182
P19511	NNIALALEVTYR	0.868773115	2	2.350246
P19511	QIQDAINR	0.977718845	1	2.123898
P19511	YGASIGEFIDK	0.916264413	2	2.913744
P19511	YGASIGEFIDKLNEEK	0.969062833	2	3.847262
P19643	**AOFB Amine oxidase [flavin_containing] B**	**0.872817264**	**0.98719**	**12**
P19643	FIGGSGQVSER	0.881109636	2	3.244701
P19643	IISTTNGGQER	1.115525257	2	3.063423
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.103484364	3	4.6288
P19643	KFIGGSGQVSER	1.158301718	2	3.105097
P19643	LERPVIHIDQTGENVVVK	0.897372684	2	4.49568
P19643	LLHDCGLSVVVLEAR	1.088207077	2	3.440828
P19643	TLNHEIYEAK	0.999153321	2	2.814503
P19643	TMDEMGQEIPSDAPWK	0.987551203	2	4.181168
P19643	VLNSQEALQPVHYEEK	0.995440684	2	4.835337
P19643	YVDLGGSYVGPTQNR	0.926067245	2	5.324489
P19643	YVISAIPPVLGMK	0.815703888	2	2.931791
P19643	YVISAIPPVLGMK+Oxidation(11)	0.787763786		
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.118992148**	**3.6E-11**	**9**
P19804	DRPFFPGLVK	2.039442464	2	2.339988
P19804	EIGLWFKPEELIDYK	1.214739795	2	4.117491
P19804	GDFCIQVGR	1.066146951	2	3.198852
P19804	NIIHGSDSVESAEK	1.148708388	1	3.941249
P19804	TFIAIKPDGVQR	1.017541983	2	3.256384
P19804	VMLGETNPADSKPGTIR	1.148653311	2	3.896411
P19804	VMLGETNPADSKPGTIR+Oxidation(1)	1.157745129		
P19804	YMNSGPVVAMVWEGLNVVK	0.828949525	2	5.097666
P19804	YMNSGPVVAMVWEGLNVVK+Oxidation(1)	0.926024383		
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.078184976**	**0.53224**	**2**
P19944	AAGVNVEPFWPGLFAK	1.017009965	2	3.429322
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.083215941	3	5.706236
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.027519599**	**0.21155**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.035786281	2	6.02914
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.007283377	2	4.54503
P19945	CFIVGADNVGSK	0.95654906	2	3.674735

P19945	GHLENNPALEK	1.060476556	2	3.695569
P19945	GNVGFVFTK	1.0957721	2	2.793194
P19945	GTIEILSDVQLIK	1.071250708	2	3.363508
P19945	IIQLLDDYPK	1.287748344	2	3.639399
P19945	NVASVCLQIGYPTVASVPHSIINGYK	0.965242763	3	3.874542
P19945	TSFFQALGITTK	1.027859289	2	4.218082
P19945	VLALSVETDYTFPLAEK	0.962003182	2	3.940639
P20059	**HEMO Hemopexin**	**1.071016507**	**0.99465**	**7**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.195817387	2	4.612888
P20059	FNPVTGEVPPR	1.083750842	2	2.46482
P20059	GECQSEGVLFFQGNR	0.924611183	2	3.756286
P20059	GGNNLVSGYPK	1.129545445	2	2.539176
P20059	LFQEEFPGIPYPPDAAVECHR	1.130009703	3	3.750477
P20059	SGAQATWAELSWPHEK	1.044168064	3	3.545642
P20059	VDGALCLEK	1.069297028	2	2.64807
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**0.942927715**	**0.0958**	**9**
P20070	AVLKDPNDHTVCYLLFANQSEK	0.849044961	3	4.702319
P20070	DILLRPELEELR	1.194185097	2	2.552075
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	0.946306995	3	4.961462
P20070	LIDKEIISHDTR	1.296926762	2	3.734611
P20070	MSQYLENMNIGDTIEFR	1.044268284	2	3.5756
P20070	SSPAITLENPDIK	1.0561423	2	3.877282
P20070	SSPAITLENPDIKYPLR	0.734797337	2	3.847224
P20070	SVGMIAGGTGITPMLQVIR	0.911146462	2	5.092463
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(3)	1.052382949		
P20280	**RL21 60S ribosomal protein L21**	**1.003882425**	**0.10698**	**3**
P20280	KGDIVDIK	1.311876179	1	2.243574
P20280	TNGKEPELLEPIPYEFMA	1.134289844	2	3.014197
P20280	VYNVTQHAVGIIVNK	0.990260874	2	4.618709
P20650	**PPM1A Protein phosphatase 1A**	**1.091741198**	**0.52181**	**2**
P20650	SRLEVTDDLEK	0.734121658	2	2.316962
P20650	VCNEVVDTCLYK	1.091864726	2	2.536309
P20673	**ARLY Argininosuccinate lyase**	**1.11344437**	**1.4E-05**	**16**
P20673	AEAECEVLFPGYTHLQR	1.022354121	2	4.595074
P20673	AEMQQILQGLDK	1.013174442	2	4.501705
P20673	AEMQQILQGLDK+Oxidation(2)	1.191179818		
P20673	AVVVAEMK	1.214037484	2	2.380149
P20673	EFNFVQLSDAYSTGSSLMPQK	1.263212159	2	5.484978
P20673	ELIGEAAGK	2.252100101	1	1.932617
P20673	FNSSIAYDR	1.161398299	2	2.774706
P20673	HLWNVDLQGSK	1.159750619	1	3.161577
P20673	INVLPLGSGAIAGNPLGVDR	1.22974916	2	5.577091
P20673	LKELIGEAAGK	1.106875974	2	2.986611
P20673	LYPNDEDIHTANER	1.260981024	2	3.882632
P20673	MAEDLILYGTK	0.965796241	2	3.742563
P20673	MAEDLILYGTK+Oxidation(0)	1.101225455		
P20673	NDQVVTDLR	0.977107124	2	3.408863
P20673	SRNDQVVTDLR	0.95233361	2	2.630143
P20673	VAEEWAQGIFK	1.118892948	2	3.819015
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**0.95907489**	**1**	**5**
P20788	EIDQEAAVEVSQLR	1.207484556	2	4.250672
P20788	EIDQEAAVEVSQLRDPQHDLER	1.014785332	3	3.326869
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	0.895780009	3	4.294538
P20788	LSDIPEGK	1.042539992	1	2.021074
P20788	SGPFAPVLSATSR	1.011237944	2	3.031933
P20801	**TNNC2 Troponin C_ skeletal muscle**	**1.41766262**	**0.90726**	**5**

P20801	AAFDMFDADGGGDISVK	2.110480201	2	4.173479
P20801	GKSEEELAECFR	0.836028951	2	3.613492
P20801	NADGYIDAEELAEIFR	1.490808755	2	4.794307
P20801	SEEELAECFR	4.032417718	2	3.293289
P20801	SYLSEEMIAEFK	1.562412493	2	2.757431
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**0.896062008**	**0.9736**	**4**
P20814	FDYEDKDFLNLIEK	0.85674291	3	4.161927
P20814	GTAVLTSLTSVLHDSK	1.078643996	2	3.105676
P20814	IKEHEESLDVSNPR	0.99954292	3	4.048508
P20814	SDYFIPFSAGK	1.224914791	2	2.598929
P20817	**CP4AE Cytochrome P450 4A14**	**0.935696091**	**0.9912**	**8**
P20817	ACQIAHEHTDGVIK	1.044661531	2	3.977923
P20817	AQLQNEEELQK	0.881548296	2	3.546
P20817	AVEDLNNLTFFR	0.881794453	2	3.414963
P20817	EFQQVLTWVEK	1.037922453	2	2.656531
P20817	HLDFLDILLFAK	0.927430548	2	3.235344
P20817	MEDGKSLSDEDLR	0.955991155	2	2.391694
P20817	MRKAQLQNEEELQK+Oxidation(0)	0.982343645		
P20817	VLLYDPDYVK	0.917340955	2	2.382238
P20852	**CP2A5 Cytochrome P450 2A5**	**1.642255629**	**0.5101**	**2**
P20852	DFIDSFLIR	1.055493843	2	2.662069
P20852	EALVDQAEEFSGR	1.380391402	2	3.351563
P21213	**HUTH Histidine ammonia_lyase**	**0.666142658**	**1.3E-13**	**13**
P21213	ALDYLAIGVHELAAISER	0.581516963	2	4.196963
P21213	DIITTELNSATDNPMVFASR	0.669144351	2	4.286501
P21213	GETISGGNFHGEYPAK	0.636664126	2	3.827773
P21213	GEWLAVPCQDGK	0.417163894	2	2.516691
P21213	GQIEVAFR	0.285420615	2	2.39418
P21213	LQELQVNLVR	0.583575675	2	3.256324
P21213	NKPDNGGFTSVDEVR	0.691709195	2	3.614604
P21213	QADIVAALTLEVLK	0.551851736	2	2.613843
P21213	SHSSGVGKPLSPER	0.631319133	2	3.63549
P21213	SLLDSDHHPSEIAESHR	0.52349309	3	4.384646
P21213	TVVYGITTGFGK	0.602908351	2	3.594153
P21213	VWEVAAPYIEK	0.791552274	2	2.875035
P21213	YIALDGDSLSTEDLVNLGK	0.575365524	2	5.177346
P21396	**AOFA Amine oxidase [flavin_containing] A**	**0.93264364**	**0.83044**	**7**
P21396	DVPAIEITHTFLER	1.460366081	2	2.481183
P21396	IFSVTNGGQER	0.826406333	2	2.548023
P21396	INVLVLEAR	1.055990991	2	2.945532
P21396	KDIWVEEPESK	0.927628506	2	3.247698
P21396	VLGSQEALYPVHYEEK	0.947112228	2	3.882811
P21396	WVDVGGAYVGPTQNR	0.846475138	2	4.810678
P21396	YVISAIPPILTAK	0.710838358	2	2.905345
P21531	**RL3 60S ribosomal protein L3**	**1.290937798**	**4.7E-11**	**6**
P21531	AHLMEIQVNGGTVAEK	1.081377206	2	5.237579
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	1.197352433	3	5.929224
P21531	HGSLGFLPR	1.180190292	2	3.112545
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.109900505	2	4.770232
P21531	NNASTDYDLSDK	1.293258336	2	3.225097
P21531	TVFAEHISDECK	1.379887677	2	3.690672
P21533	**RL6 60S ribosomal protein L6**	**1.101066274**	**4.3E-06**	**8**
P21533	AVDSQILPK	1.085793012	2	2.75714
P21533	FVIATSTK	1.223160153	1	2.017998
P21533	HLTDAYFK	1.197987311	2	2.436034
P21533	HQEGEIFDTEK	1.33111344	2	3.32333
P21533	HQEGEIFDTEKEK	1.120878291	2	4.00106

P21533	QLGSGLLLVTGPLALNR	1.201140642	2	5.045406
P21533	SSITPGTVLIILTGR	1.073247056	2	3.891764
P21533	YYPTEDVPR	1.164378957	2	2.440053
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.007977348**	**0.40088**	**6**
P21571	FEVLDKPQS	1.024706831	2	2.93575
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	0.82467355	3	3.930324
P21571	GEMDKFPTFNFEDPKFEVLDKPQS+Oxidation(2)	0.78653035		
P21571	LASGGPVDTGPEYQQEVDR	1.320368744	2	5.28316
P21571	LASGGPVDTGPEYQQEVDRELFK	1.296514669	2	2.799888
P21571	RLASGGPVDTGPEYQQEVDR	0.879676305	3	4.52364
P21643	**T23O Tryptophan 2_3_dioxygenase**	**3.166348661**	**2E-10**	**2**
P21643	GGLIYGDYLQLEK	6.98605785	2	3.617439
P21643	ILNAQELQSEIK	2.318161854	2	3.652973
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.002056102**	**0.97203**	**4**
P21670	ATCIGNNSAAAVSMLK	1.044529148	2	2.812556
P21670	LLDEVFFSEK	1.01441689	2	3.597595
P21670	LNEDMACSVAGITSDANVLTNELR	1.252439789	3	3.446458
P21670	YLLQYQEPIPCEQLVTALCDIK	1.141976809	2	3.044539
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**0.761058627**	**9.9E-20**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	0.788561445	3	5.287484
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22)	0.830226919		
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**0.980034412**	**0.84388**	**6**
P21913	CGPMVLDALIKIK	0.741322403	2	2.4207
P21913	CHTIMNCTQTCPK	0.997039155	2	4.316717
P21913	CHTIMNCTQTCPK+Oxidation(4)	1.307148719		
P21913	IKNEIDSTLTFR	1.15564956	2	2.395818
P21913	LQDPFSLYR	1.158440649	2	2.753863
P21913	RIDTDLGK	0.992662296	2	2.437272
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**0.922762613**	**0.99859**	**5**
P21981	CDLEIQANGR	0.918164504	2	2.991685
P21981	LVVNFQCDK	0.903309419	2	2.676165
P21981	SEGTYCCGPVSVR	0.928644692	2	3.694467
P21981	WDNNYGDGISPMAWIGSVDILR	0.928275567	3	4.197842
P21981	YSGCLTESNLIK	0.931795844	2	3.566343
P22734	**COMT Catechol O_methyltransferase**	**0.798216619**	**0.99704**	**14**
P22734	AIYQGPSSPDK	1.125640082	2	2.362952
P22734	AIYQGPSSPDKS	0.748508002	2	3.150823
P22734	EWAMNVGDAK	2.845366847	1	2.769252
P22734	GQIMDAVIR	0.88525338	2	3.032671
P22734	GQIMDAVIR+Oxidation(3)	1.112655087		
P22734	GSSSFECTHYSSYLEYMK	2.388971421	2	4.563265
P22734	GTVLLADNVIVPGTPDFLAYVR	0.711478556	3	4.868077
P22734	KGTVLLADNVIVPGTPDFLAYVR	0.741458419	2	4.687739
P22734	KYDVDTLDMVFLDHWK	0.869791042	3	5.635423
P22734	VTILNGASQDLIPQLK	0.794990838	2	4.301364
P22734	VVDGLEK	0.831327081	2	2.380745
P22734	YDVDTLDMVFLDHWK	0.818629081	3	4.602151
P22734	YLPDTLLLEK	0.837483386	2	2.913932
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	0.785546814	3	6.094255
P22789	**ST2A2 Alcohol sulfotransferase A**	**0.777624628**	**0.53199**	**4**
P22789	EEDLILLTYPK	0.984726208	2	2.591067
P22789	ETLQNVCNK	1.039472453	1	2.011793
P22789	KLEPDELDLVLK	0.563955885	3	4.730116
P22789	NHFTVAQAEAFDK	0.664237735	2	3.43943

P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**0.894200683**	**0.99996**	**21**
P22791	ASLDMFNK	1.086424636	2	2.46946
P22791	ASLDMFNKK	0.981867068	2	2.525005
P22791	DVGILALEVYFPAQYVDQTDLEK	0.941098241	3	7.205613
P22791	GLKLEETYTNK	0.76632094	2	2.782672
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.011991441	3	7.034035
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3)	0.947423646		
P22791	IGAFSYGSGLAASFFSFR	0.949072286	2	3.879208
P22791	LEETYTNK	0.920012016	2	3.021606
P22791	LEETYTNKDVDK	0.945829756	2	4.108529
P22791	LEVGTETIIDK	1.053396676	2	3.733799
P22791	LMFNDFLSSSSDK	0.991982651	2	4.421253
P22791	LMFNDFLSSSSDK+Oxidation(1)	1.044270733		
P22791	LSIQCYLR	0.868464917	2	2.317
P22791	LVSSVSDLPK	1.191420715	2	3.49174
P22791	MGFCSVQEDINSLCLTVVQR	1.017824405	3	3.493203
P22791	MSPEEFTEIMNQR	0.933403754	2	4.656848
P22791	MSPEEFTEIMNQR+Oxidation(0)	0.939911618		
P22791	MSPEEFTEIMNQR+Oxidation(9)	0.993195003		
P22791	TKLPWDAVGR	0.954744877	3	3.950933
P22791	VNFSPPGDTSNLFPGTWYLER	0.872432648	2	5.053218
P22791	YTVGLGQTR	0.954994096	2	3.335884
P22985	**XDH Xanthine dehydrogenase/oxidase**	**0.826101088**	**0.98018**	**10**
P22985	DEVTCVGHIIGAVVADTPEHAQR	1.015515068	3	3.848655
P22985	DPPANVQLFQEVPK	0.992300744	2	3.843398
P22985	DQTVSLSPSLFNPEDFKPLDPTQEPIFPPELLR	1.093233184	3	3.389107
P22985	LDPTFASATLLFQK	0.914825171	2	4.018567
P22985	NQPEPTVEEIENAFQGNLCR	0.982579153	2	4.713365
P22985	QLFQLDSPATPEK	0.81650017	2	3.205284
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.008547169	3	5.768322
P22985	TGTVVALEVAHFSNGGNTEDLSR	0.840571486	3	4.624146
P22985	TLLRPEEILLSIEIPYSK	0.922918436	3	4.050619
P22985	TNLPSNTAFR	0.629246054	1	2.258965
P23358	**RL12 60S ribosomal protein L12**	**1.039885456**	**9.4E-05**	**7**
P23358	CTGGEVGATSALAPK	1.092648209	2	4.083876
P23358	EILGTAQSVGCNVDGR	1.964280734	2	4.437327
P23358	HNGNITFDEIVNIAR	1.060886803	2	4.24865
P23358	HPHDIIDDINSGAVECPAS	1.080559304	2	4.839104
P23358	IGPLGLSPK	1.283081988	2	2.539657
P23358	QAQIEVVPSASALIIK	1.176666223	2	3.876422
P23358	VGDDIAKATGDWKGLR	0.902205682	2	2.412156
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**0.896394992**	**0.92608**	**10**
P23457	ALDGLNR	0.908854019	2	2.557236
P23457	ELTQVFEFQLASEDMK	0.799657814	2	3.290043
P23457	HFDSAYLYEVEEEVGQAIR	1.072177268	2	6.166505
P23457	MLDYCK	0.783171605	1	1.974668
P23457	SIGVSNFNCR	0.892650756	2	3.290779
P23457	SKDIILVSYCTLGSSR	0.959571861	2	5.066266
P23457	SPVLLDDPVLCAIAK	0.976779929	2	3.925643
P23457	VALNDGNFIPVLGFGTTVPEK	0.957447063	2	5.186249
P23457	YFDDHPNHPFTDE	0.619717975	2	3.745184
P23457	YKPVCNQVECHLYLNQSK	2.017830025	2	4.67289
P23514	**COPB Coatomer subunit beta**	**1.076265551**	**0.72762**	**7**
P23514	EAGELKPEEEITVGPVQK	1.197555758	2	4.338065
P23514	EDIQSVMTEVR	1.074492813	2	2.941848
P23514	NFENLIPDAPELIHDFLVNEK	0.779380105	3	4.017214

P23514	TNNVSEHEDTDKYR	1.215626354	3	4.127946
P23514	VLQDLVMDILR	0.943322317	2	3.618531
P23514	VLSECSPLMNDIFNK	1.123976707	2	2.667123
P23514	YEAAGTLVTLSSAPTAIK	1.093105595	2	4.9897
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.991503389**	**0.99485**	**8**
P23965	ALQLGTLFPPAEALK	0.940826201	2	5.413283
P23965	AVQELWLR	1.028614867	2	2.60382
P23965	DNYVNTIGHR	1.186852569	2	3.032264
P23965	GVILTSERPGIFSAGLDLMEMYGR	0.885045808	3	6.201207
P23965	QREADIQNFTSFISR	1.068440507	2	2.700237
P23965	SLHVYLEK	0.901884206	1	2.312779
P23965	VGLVDEVVPEDQVHSK	0.938291175	2	4.73955
P23965	WFTIPDHSR	0.874546797	2	3.196717
P24049	**RL17 60S ribosomal protein L17**	**1.286286562**	**9.9E-20**	**3**
P24049	EQIVPKPEEEVAQK	1.691968535	2	3.547131
P24049	GLDVDSLVIEHIQVNK	1.114953473	2	4.686262
P24049	YSLDPENPTK	1.246851787	1	2.764604
P24050	**RS5 40S ribosomal protein S5**	**0.925565519**	**0.42712**	**4**
P24050	HAFEIIHLLTGENPLQVLVNAIINSGPR	0.738829091		
P24050	RQAVDVSPLR	1.184951488	2	2.364157
P24050	VNQAIWLLCTGAR	0.968101075	2	4.110164
P24050	WSTDDVQINDISLQDYIAVK	0.975983539	2	4.764235
P24063	**ITAL Integrin alpha_L**	**1.124615841**	**0.40161**	**2**
P24063	ASEAQVLVKVDLIHEK	1.120596293	2	2.400362
P24063	DFEKILEFMK	1.150895493	3	3.333261
P24090	**FETUA Alpha_2_HS_glycoprotein**	**0.67866596**	**9.9E-15**	**6**
P24090	AQNVPFPVSTLVEFVIAATDCTGQEVTDPAK	0.635258342		
P24090	ELACDDPETEHVALIAVDYLNK	0.640201591	2	4.181743
P24090	HAFSPVASVESASGEVLHSPK	0.863687632	3	5.960438
P24090	LGGEEVSVACK	0.697287563	2	3.692735
P24090	VGQPGDAGAAGPVAPLCPGR	0.679280787	2	5.089277
P24090	VLHAQCHSTPDSAEDVRK	0.625558329	3	4.009344
P24268	**CATD Cathepsin D**	**0.818415313**	**0.00024**	**4**
P24268	AIGAVPLIQGEYMIPCEK	0.817941075	2	3.479833
P24268	DPTGQPGGELMLGGTDSR	1.037358554	2	4.746852
P24268	GGCEAIVDTGTSLLVGPVDEVK	1.202270917	2	4.077839
P24268	LGGQNYELHPEK	0.938185709	2	2.911747
P24329	**THTR Thiosulfate sulfurtransferase**	**0.907477935**	**0.00468**	**12**
P24329	EGHPVTSEPSRPEPAVFK	1.276821121	2	4.698688
P24329	FQLVDSR	0.87931684	2	2.466033
P24329	GSVNVPFMNFLTEDGFEK	2.109647449	2	5.276097
P24329	HVPGASFFDIEECR	1.021543104	3	3.614053
P24329	KVDLSQPLIATCR	0.896501595	2	4.780231
P24329	RFQLVDSR	0.974939488	2	2.474419
P24329	TVSVLNGGFR	0.87772493	2	2.887061
P24329	TYEQVLENLQSK	0.884187568	2	5.085625
P24329	VDLSQPLIATCR	0.909933913	2	3.545904
P24329	VLDASWYSPGTR	0.876233183	2	3.735063
P24329	WLAESIR	0.908100583	2	2.359281
P24329	YLGTQPEPDAVGLDSGHIR	0.907842557	3	5.052375
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.154362276**	**0.91536**	**9**
P24368	DKPLKDVIIVDCGK	1.172841061	2	3.641815
P24368	DTNGSQFFITTVK	1.23175724	2	3.580475
P24368	DVIIVDCGK	1.172197084	1	1.990567
P24368	HYGPGWVSMANAGK	0.987455355	2	3.234995
P24368	IEVEKPFAIAK	1.061118142	2	3.292331

P24368	IEVEKPFAIAKE	1.01663629	2	3.558626
P24368	TVDNFVALATGEK	0.936784353	2	3.755565
P24368	VLEGMDVVR	1.018722312	2	2.775417
P24368	VYFDFQIGDEPVGR	0.912951664	2	4.321369
P24457	**CP2DB Cytochrome P450 2D11**	**1.185850392**	**0.56482**	**2**
P24457	RFSVSTLR	1.149220729	2	2.541351
P24457	SLEEWVTK	1.234814052	2	2.756786
P24470	**CP2CN Cytochrome P450 2C23**	**0.830742257**	**0.07793**	**10**
P24470	ACVGESLAR	0.916669533	2	2.52792
P24470	AQPFDPTFILACAPCNVICSILFNDR	0.734372451		
P24470	DLDIKPITTGIINLPPPYK	0.862131659	2	3.717576
P24470	EALLQQGDEFLGR	1.2570194	2	2.581231
P24470	GTTVLPMLSSVMLDQK	0.889524047	2	4.008655
P24470	GYGLIFSNGER	0.804085881	2	3.241366
P24470	IEEEKDNLK	0.858372946	1	2.898257
P24470	LPPGPTPLPIIGNLLQLNLK	0.870546853	2	3.49408
P24470	TFLNLMDLLNK	0.826805352	2	3.86456
P24470	YITLLPSSLPHAVVQDTK	0.777430519	2	3.412023
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.844438509**	**0.14369**	**9**
P24473	AGMATAQAQHLLNK	1.039398212	2	3.919411
P24473	AGMATAQAQHLLNK+Oxidation(2)	0.973103535		
P24473	DEDITESQNILSAAEK	1.016367533	2	5.743433
P24473	DSGNQPPAMVPHK	1.003870072	2	2.420162
P24473	FLTAVSMEQPEMLEK	0.77748117	2	4.188372
P24473	FLTAVSMEQPEMLEK+Oxidation(11)	0.830078826		
P24473	MELLAYLLGEK	0.843941615	2	4.110036
P24473	QLFQVPMSVPK	0.816228377	2	2.719655
P24473	YGAFGLPTTVAHVDGK	0.849695306	2	3.759221
P25093	**FAAA Fumarylacetoacetase**	**0.979983952**	**0.0244**	**17**
P25093	AIDVGQGQTR	1.002511138	2	3.408475
P25093	AQEHIFGMVLMNDWSAR	0.942497629	3	3.693632
P25093	AQEHIFGMVLMNDWSAR+Oxidation(7)	0.611181121		
P25093	ASLQNLLSASQAQLR	0.961429984	2	4.802083
P25093	ASLQNLLSASQAQLRDDK	0.867740587	2	3.145474
P25093	ASSVVVSGTPIR	0.958304834	2	3.595053
P25093	DIQQWEYVPLGPFLGK	1.44089065	2	4.832111
P25093	FGEPIPISK	0.967740047	2	2.87535
P25093	GEGMSQAATICR	0.963967705	2	3.657554
P25093	GEGMSQAATICR+Oxidation(3)	1.256828052		
P25093	GKENALLPNWLHLPVGYHGR	0.759614954	3	3.470478
P25093	HLFTGPVLSK	1.097585763	1	2.707079
P25093	HQHVFDETTLNSFMGLGQAAWK	0.856630507	2	5.374691
P25093	IGVAIGDQILDLSVIK	1.104194881	2	5.417109
P25093	IGVAIGDQILDLSVIKHLFTGPVLSK	0.974266836	3	3.952735
P25093	TFLLDGDEVIITGHCQGDGYR	0.967735575	2	5.027973
P25093	VGFGQCAGK	1.136265362	2	2.385562
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.005098207**	**0.99991**	**7**
P25113	ALPFWNEEIVPQIK	1.014043357	2	3.936657
P25113	FSGWYDADLSPAGHEEAK	0.859722309	2	4.953215
P25113	HGESAWNLENR	1.041583154	2	3.739516
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	0.90778887	3	3.463135
P25113	SYDVPPPPMEPDHPFYSNISK	0.913415754	2	4.318289
P25113	YADLTEDQLPSCESLK	0.956079773	2	5.490339
P25113	YADLTEDQLPSCESLKDTIAR	0.898366402	2	5.017619
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.050173306**	**0.99908**	**14**

P25235	DLLLAAVSEDSSVAQIYHAVAALSGFGLPLASHEALGALTAR	0.767538758		
P25235	EDQVIQLMNTIFSK	1.986882822	2	2.394762
P25235	EETVLATVQALHTASHLSQQADLR	1.109179885	3	4.313227
P25235	FELDTSER	0.982956737	1	2.048539
P25235	FPEEEAPSTVLSQNLFTPK	0.953036463	2	4.258036
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.025461973	2	4.523488
P25235	LQVSSVLSQPLAQAAVK	1.170132363	2	5.727839
P25235	LSKEETVLATVQALHTASHLSQQADLR	0.921513051	3	4.536286
P25235	NFESLSEAFSVASAAAALSQNR	0.954286056	3	5.480579
P25235	NIVEEIEDLVAR	0.956508273	3	4.683619
P25235	NPILWNVADVVIK	1.030290185	2	3.269099
P25235	TGQEVVFVAEPDNK	1.361148652	2	3.90921
P25235	YHVPVVVVPEGSASDTQEQAILR	0.918525708	3	6.531534
P25235	YIANTVELR	0.972684481	2	2.587934
P25409	**ALAT1 Alanine aminotransferase 1**	**1.391660225**	**0.0065**	**2**
P25409	LTEQVFNEAPGIR	1.316152913	2	3.48034
P25409	VLCVINPGNPTGQVQTR	1.923892853	2	4.639893
P25977	**UBF1 Nucleolar transcription factor 1**	**0.909025417**	**0.06677**	**2**
P25977	AKYAKLHPEMSNLDLTK	0.982661233	2	2.336063
P25977	ALKAMEMTWNNMEKK+Oxidation(11)	0.766891		
P26039	**TLN1 Talin_1**	**1.000386169**	**1.2E-10**	**22**
P26039	ADAEGESDLENSR	0.791438081	2	2.895252
P26039	ADAEGESDLENSRK	0.853268785	2	3.190112
P26039	AGALQCSPSDVYTK	1.227916986	2	2.655855
P26039	ASAGPQPLLVQSCK	0.993749273	2	3.023999
P26039	AVAEQIPLLVQGVR	0.990383616	2	3.555277
P26039	EAAEGLRMATNAAAQNAIKK	0.98064421	2	2.737611
P26039	ELMEEKKDEGTGTLR+Oxidation(2)	1.271675949		
P26039	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	0.845168356		
P26039	GVGAAATAVTQALNELLQHVK	0.94185703	3	3.591889
P26039	ILAQATSDLVNAIK	1.2709753	2	2.623954
P26039	LGAASLGAEDPETQVVLINAVK	0.901874323	2	4.412858
P26039	LLGEIAQGNENYAGIAAR	1.187127706	2	4.275113
P26039	LNEAAAGLNQAATELVQASR	0.871873469	2	5.238898
P26039	MVAAATNNLCEAANAAVQGHASQEK	1.152192698	3	3.432194
P26039	SNTSPEELGPLANQLTSDYGR	0.874859067	2	4.014234
P26039	TLAESALQLLYTAK	0.931751451	2	2.988723
P26039	TMLESAGGLIQTAR	0.576330363	2	2.631551
P26039	VGAIPANALDDGQWSQGLISAAR	0.927126814	2	4.517199
P26039	VGDDPAVWQLK	0.882498974	2	2.834435
P26039	VLGEAMTGISQNAK	1.051379049	2	2.791625
P26039	VLVQNAAGSQEK	0.960203767	2	2.514229
P26039	VVAPTISSPVCQEQLVEAGR	0.95811903	2	4.492325
P26043	**RADI Radixin**	**0.930599674**	**0.23691**	**10**
P26043	AFAAQEDLEK	1.277916231	2	2.558512
P26043	ALELEQER	0.991978694	1	1.927128
P26043	FFPEDVSEELIQEITQR	0.871906952	3	4.641557
P26043	IQNWHEEHR	1.172930551	2	2.512294
P26043	KKEEEATEWQHK	1.127065804	3	3.736757
P26043	KTQNDVLHAENVK	1.056672938	2	5.050867
P26043	NQEQLAAELAEFTAK	0.930579032	2	5.102746
P26043	QLQALSSELAQAR	1.044864272	2	3.757116
P26043	RKPDTIEVQQMK	0.872079507	2	3.868768
P26043	TQNDVLHAENVK	1.117756796	2	3.942393
P26231	**CTNA1 Catenin alpha_1**	**1.044418094**	**0.13947**	**10**
P26231	AEVQNLGGELVVSGVDSAMSLIQAAK	0.916073243	3	4.156018

P26231	AHVLAASVEQATENFLEK	0.597059874	2	2.36008
P26231	AVMDHVSDSFLETNVPLLVLIEAAK	0.972060529	3	3.537484
P26231	LIEVANLACSISNNEEGVK	1.073194764	2	4.894123
P26231	LLEPLVTQVTTLVNTNSK	0.888157331	2	4.011494
P26231	QIIVDPLSFSEER	1.039366226	2	2.683527
P26231	SAAGEFADDPCSSVK	1.000815461	2	4.052165
P26231	SDALNSAIDK	1.324177487	2	2.521385
P26231	TIADHCPDSACK	0.322527896	2	3.559316
P26231	VIHVVTSEMDNYEPGVYTEK	0.991019801	3	3.553701
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**0.908426326**	**0.86615**	**8**
P26284	AILAELTGR	0.900429509	2	2.572551
P26284	EEIQEVRSK	0.738925454	1	1.934391
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	0.720323235	3	6.632319
P26284	LEEGPPVTTVLTR	0.901698039	2	3.486447
P26284	MVNSNLASVEELKEIDVEVR	2.645664137	2	3.005507
P26284	RGDFIPGLR	1.089032657	2	2.708508
P26284	TREEIQEVR	0.875496846	3	3.489574
P26284	VDGMDILCVR	1.024094276	2	3.337078
P26453	**BASI Basigin**	**1.031142531**	**0.31909**	**7**
P26453	GNINVEGPPR	1.001812462	2	3.469563
P26453	KSEHASEGEFVK	0.844904054	2	2.864264
P26453	RKPDQTLDEDDPGAAPLK	1.100301374	3	4.149471
P26453	SEASHPPVDEWVWFK	0.982221025	3	3.926523
P26453	SEHASEGEFVK	1.178995803	3	3.543998
P26453	SGEYSCIFLPEPVGR	0.969127162	2	3.463887
P26453	VLQEDTLPDLQMK	1.026143853	2	4.353234
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.822274961**	**0.99987**	**7**
P26772	GGEIQPVSVK	1.019507047	2	3.260054
P26772	GGIMLPEK	0.661066524	2	2.330966
P26772	GGIMLPEK+Oxidation(3)	0.996475842		
P26772	GKGGEIQPVSVK	0.99098135	2	3.399598
P26772	VLLPEYGGTK	1.024235707	2	2.367303
P26772	VLQATVVAVGSGGK	1.027203109	2	5.511703
P26772	VVLDDKDYFLFR	0.901424015	3	3.403807
P27139	**CAH2 Carbonic anhydrase 2**	**0.706293458**	**0.24824**	**2**
P27139	IGPASQGLQK	0.709686612	2	2.541601
P27139	ITEALHSIK	0.696987753	2	2.426861
P27321	**ICAL Calpastatin**	**0.914537148**	**0.16754**	**4**
P27321	KGSDEVTASSAATGTSPR	1.138190374	2	4.842527
P27321	KVEEEVMNDQALQALSDSLGTR	0.85914749	3	3.571078
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	1.206964831	3	4.182306
P27321	SQSSEPPVIHEK	0.7588766	2	3.226077
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.875354876**	**0.04521**	**6**
P27364	AVLAANGSILK	0.873591625	2	2.891518
P27364	ETILNDREEEHR	1.201539092	2	2.920848
P27364	GDIVDAQFLR	0.822445775	2	2.993035
P27364	IVQMLVQEK	1.014267896	2	2.660714
P27364	NGGTFHTCALR	0.944488915	2	3.07916
P27364	QTILDVNVK	0.683432808	1	2.105358
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.062689557**	**9.8E-08**	**6**
P27605	DLNHVCVISESGK	1.460516256	2	3.692392
P27605	FFADLLDYIK	1.092523763	2	3.194604
P27605	NVLIVEDIIDTGK	1.006967477	2	4.105061
P27605	SVGYRPDFVGFEIPDK	0.974360197	3	3.809477

P27605	SYCNDQSTGDIK	1.096298334	2	3.961218
P27605	VIGGDDLSTLTGK	0.923249988	2	4.223195
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.450828288**	**4.9E-08**	**21**
P27653	ASQAPSSFQLLYDLK	1.401573927	2	4.174053
P27653	AYTEEDLDLVEK	0.945298993	2	3.028994
P27653	CTHWAEGGQGALALAQAVQR	1.035742422	2	5.196739
P27653	DVDGLTSINAGK	1.092496634	2	2.433334
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.100018256	3	5.084738
P27653	GVPTGFVLPIR	1.950841058	2	2.528205
P27653	IFHELTQTDK	1.352306043	3	3.613856
P27653	IYGADDIELLPEAQNK	1.241416625	2	5.288408
P27653	KITIGQAPTEK	1.511597944	2	2.911438
P27653	KVVGDVAYDEAK	1.453528371	2	3.886915
P27653	LDIDPETITWQR	1.362824075	2	4.084001
P27653	MHGGGPTVTAGLPLPK+Oxidation(0)	1.487169988		
P27653	QGFGNLPICMAK	0.964842023	2	3.162811
P27653	TADLDKEVNK	1.208851915	2	2.400633
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.177964875	3	4.611959
P27653	TDPAALTDDEINR	1.199793055	2	4.379691
P27653	THLSLSHNPEQK	1.234669476	2	3.832612
P27653	VLLSALDR	1.523228769	2	2.476872
P27653	VVGDVAYDEAK	1.2238992	2	3.727813
P27653	YSGLQPHVVVLVATVR	1.372355958	3	3.520746
P27653	YVVVTGITPTPLGEGK	1.218338698	2	4.88205
P27657	**LIPP Pancreatic triacylglycerol lipase**	**0.630616401**	**0.08234**	**2**
P27657	ATYTQATQNVR	0.631113139	2	2.520481
P27657	ITGLDAAEPYFQGTPEEVR	0.103023349	2	3.888477
P27661	**H2AX Histone H2A.x**	**0.90757701**	**0.0833**	**3**
P27661	AGLQFPVGR	0.894714604	2	3.193053
P27661	HLQLAIR	1.007131691	2	2.642278
P27661	LLGGVTIAQGGVLPNIQAVLLPK	0.891378349	3	4.717062
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**1.088883466**	**0.87052**	**3**
P27768	IDAAEEEKYDMEVK	2.599735728	2	3.716147
P27768	SVMLQIAATELEK	0.985343398	2	2.529842
P27768	SVMLQIAATELEKEESR	2.118161815	2	3.105138
P27867	**DHSO Sorbitol dehydrogenase**	**0.92070569**	**0.00327**	**14**
P27867	AMGASQVVVIDLSASR	0.967494825	2	4.037575
P27867	AVEAFETAK	0.875308268	2	2.990508
P27867	EVGADFTIQVAK	1.365434872	2	2.781494
P27867	GENLSLVVHGPGDIR	0.932745132	2	3.973934
P27867	HSADFCYK	0.951869808	2	2.814023
P27867	IGDFVVK	0.966236662	2	2.62791
P27867	LENYPIPELGPNDVLLK	0.923156919	2	4.792784
P27867	LPDSVTFEEGALIEPLSVGIYACR	0.846201183	2	4.750957
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0)	0.914716292		
P27867	TLNVKPLVTHR	0.907413648	2	3.259476
P27867	VAIEPGVPR	1.031063666	2	2.585423
P27867	VAIEPGVPREIDEFCKIGR	0.833135859	2	2.545574
P27867	VLVCGAGPIGIVTLLVAK	0.747278319	3	6.226439
P27867	YNLTPSIFFCATPPDDGNLCR	2.234394998	2	4.203186
P27952	**RS2 40S ribosomal protein S2**	**1.306920177**	**0.35506**	**7**
P27952	AEDKEWIPVTK	1.237236885	2	3.212702
P27952	AFVAIGDYNGHVGLGVK	1.217722159	2	3.788078
P27952	ATFDAISK	1.117182341	2	2.444848
P27952	GCTATLGNFAK	1.168766323	2	2.840331
P27952	GTGIVSAPVPK	1.084090221	2	2.449337

P27952	SLEEIYLFSLPIK	0.57122069	1	2.712297
P27952	TYSYLTPDLWK	0.997615694	2	2.706529
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**1.047389352**	**0.57426**	**26**
P28037	ADPLGLEAEK	1.123234707	2	2.822206
P28037	ANATEFGLASGVFTR	1.052704513	2	4.444672
P28037	AVQMGMSSVFFNK	1.024355736	2	3.511725
P28037	CPQSEEGATYEGIQK	0.805775647	2	4.314612
P28037	DLGEAALNEYLR	1.615049008	2	3.288827
P28037	ECEVLPDDTVSTLYNR	1.689214137	2	5.007122
P28037	EGHEVVGVFTIPDKDGK	1.101875594	2	4.51124
P28037	GNDKVPGAWTEACGQK	1.209958378	2	3.536968
P28037	GQALPEVVAK	1.029579659	2	2.596334
P28037	GSASSDLELTEAELATAEAVR	1.016401763	2	6.296675
P28037	GVVNILPGSGSLVGQR	0.973111184	2	4.944245
P28037	IGFTGSTEVGK	1.168529531	2	3.110392
P28037	ILPNVPEVEDSTDFFK	1.334165016	2	3.691142
P28037	INWDQPAEAIHNWIR	0.984655924	2	3.67751
P28037	KEGHEVVGVFTIPDKDGK	1.118769035	3	3.482716
P28037	KIGFTGSTEVGK	0.994784119	2	2.950796
P28037	KLVEYCQR	1.14018178	2	2.535579
P28037	LFVEESIHNQFVQK	1.045044387	2	4.598858
P28037	LIAEGTAPR	1.159999402	2	3.134685
P28037	LQAGTVFINTYNK	2.129373634	2	2.507685
P28037	LSDHPDVR	0.957500714	1	2.099179
P28037	NIQLEDGK	0.982873851	1	1.998016
P28037	TAACLAAGNTVVIKPAQVTPLTALK	0.912729163	3	4.426006
P28037	TDVAAPFGGFK	1.020774958	2	2.719699
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	1.101352417	3	6.586313
P28037	VVEEVEK	1.029127651	2	2.478464
P28064	**PSB8 Proteasome subunit beta type_8**	**0.904852657**	**0.88134**	**3**
P28064	ASAGSYIATIR	0.963796142	2	2.527466
P28064	QDLSPEEAYDLAR	0.844105611	2	3.116903
P28064	VESTDVSDLLHK	0.910074347	2	2.901866
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.119564516**	**0.28243**	**10**
P28480	AFHNEAQVNPER	1.150270694	2	3.419807
P28480	FATEAAITILR	0.99593015	2	3.260354
P28480	HGGYENAVHSGALDD	1.10427791	2	4.228732
P28480	ICDDELILIK	1.077170761	2	3.170019
P28480	LLEVEHPAAK	1.031786726	2	2.39514
P28480	MLVDDIGDVTITNDGATILK	0.930722873	2	4.338411
P28480	SLHDALCVVK	0.898299329	2	2.455453
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.094257428	2	4.637555
P28480	SQNVMAAASIANIVK	1.039583385	2	4.022607
P28480	YINENLIINTDELGR	0.997218889	2	4.484542
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.793505188**	**0.35576**	**3**
P28492	MVQESSSGGLLDR	0.772262257	2	3.222004
P28492	SNPDLWGVSLCTVDGQR	0.811134667	2	3.155111
P28492	TALHVAAAEGHIDVVK	0.780458435	3	3.5419
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**1.149874989**	**0.97745**	**3**
P28650	CQGGNNAGHTVVVDGK	1.320629018	2	3.70611
P28650	LDILDVLSEIK	1.224740549	2	3.153514
P28650	VGIGAFPTEQINEIGDLLQNR	1.060353148	3	3.803699
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**0.907905148**	**0.94384**	**20**
P29147	AVLVTGCDSGFGFSLAK	0.928460972	2	5.714079
P29147	EVAEVNLWGTVR	1.458609117	2	2.754992

P29147	FGVEAFSDCLR	0.996529285	2	3.706598
P29147	GFLVFAGCLLK	1.253874335	2	3.480829
P29147	KMWDELPEVVR	0.857347898	2	2.84792
P29147	KMWDELPEVVR+Oxidation(1)	0.843474067		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.07870014	3	5.449405
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0)	0.950376418		
P29147	MQVMTHFPGAISDK	1.034369203	2	4.578563
P29147	MQVMTHFPGAISDK+Oxidation(0)	1.075510944		
P29147	MQVMTHFPGAISDK+Oxidation(0)	0.8398298		
P29147	MQVMTHFPGAISDK+Oxidation(3)	0.802363788		
P29147	MWDELPEVVR	0.766956169	2	3.080644
P29147	MWDELPEVVR+Oxidation(0)	0.831685549		
P29147	TIQLNVCNSEEVEK	1.00202342	2	4.449669
P29147	VSVVEPGNFIAATSLYSPER	0.956988298	2	6.10183
P29147	VVNISSMLGR	1.012989318	2	3.961768
P29147	VVNISSMLGR+Oxidation(6)	1.038819341		
P29147	YEMHPLGVK	1.079413038	2	2.703852
P29147	YEMHPLGVK+Oxidation(2)	1.077108466		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**1.035446969**	**1.5E-06**	**8**
P29266	DLGLAQDSATSTK	1.008349821	2	4.0746
P29266	EAGEQVASSPADVAEK	1.21707293	2	4.741756
P29266	GSLLIDSSTIDPSVSK	0.845422137	2	4.769774
P29266	HGYPLILYDVFPDVCK	0.897373929	2	4.997539
P29266	KGSLLIDSSTIDPSVSK	0.955442432	2	4.659856
P29266	MGAVFMDAPVSGGVGAAR	1.209155403	2	4.789086
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0)	0.8379367		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5)	0.8379367		
P29314	**RS9 40S ribosomal protein S9**	**1.146973654**	**0.00476**	**9**
P29314	IEDFLER	1.097805559	2	2.829904
P29314	IGVLDEGK	1.143043516	2	2.395046
P29314	KGQGGAGAGDDEEED	0.852855057	2	4.175772
P29314	LDYILGLK	1.050126358	2	2.547796
P29314	LFEGNALLR	1.135616371	2	2.629325
P29314	LIGEYGLR	1.362693037	2	2.646587
P29314	QVVNIPSFIVR	1.147743012	2	2.454194
P29314	RLQTQVFK	1.282128869	2	2.301405
P29314	SRLDQELK	1.093176878	3	3.315833
P29315	**RINI Ribonuclease inhibitor**	**1.001673295**	**0.6789**	**6**
P29315	ASLQELDLGSNK	0.894955506	2	2.827818
P29315	ELHLNDNPLGDEGLK	0.946684348	2	2.926205
P29315	LDDCGLTEVR	0.897288473	2	2.926793
P29315	LENCGITSANCK	0.916144883	2	3.330049
P29315	SAIQANPALTELSLR	0.94419522	2	4.594812
P29315	TNELGDAGVGLVLQGLQNPTCK	0.91068512	2	5.286791
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**0.934668903**	**0.38553**	**10**
P29410	AMVASGSELGK	1.034480434	2	2.361654
P29410	AMVASGSELGKK	1.118331647	2	3.138547
P29410	AVLLGPPGAGK	1.110943805	2	2.709268
P29410	EAMKDDITGEPLIR	1.104276836	2	2.723557
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.161653487	3	6.222835
P29410	LEAYHTQTTPLVEYYR	0.962706931	2	5.400816
P29410	LVSDEMVVELIEK	0.931082572	2	4.143301
P29410	NGFLLDGFPR	0.870738084	2	3.35506
P29410	NLETPSCK	0.937135666	2	2.349375
P29410	SYHEEFNPPK	0.972368964	3	3.856591

P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**0.865177059**	**0.92233**	**8**
P29411	AYEAQTEPVLQYYQK	0.910621097	2	4.183173
P29411	EDDKPETVIK	1.29537721	2	2.633277
P29411	KGVLETFSGTETNK	0.857056884	2	3.050477
P29411	NLTQCSWLLDGFPR	0.838818413	2	3.339229
P29411	TLPQAEALDR	0.936839357	2	2.339847
P29411	TVGIDDLTGEPLIQR	0.886018676	2	3.351763
P29411	VYNIEFNPPK	0.888577653	2	3.155336
P29411	VYQIDTVINLNVPFEVIK	0.851939125	2	2.660056
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**1.065745357**	**2.4E-05**	**2**
P29419	ELAEAEDVSIFK	1.373436885	2	3.297797
P29419	YSALILGMAYGAK	0.894552451	2	4.087216
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**0.921295015**	**0.99989**	**3**
P30009	AEDGAAPSPSSETPK	0.895839312	2	3.924316
P30009	AEEPSEAVGEK	0.988411076	2	2.78907
P30009	GEAAAERPGEAAVASSPSK	0.886198404	2	4.547205
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**0.825743107**	**0.06975**	**4**
P30349	EEDLNSFSIEDLK	1.099042478	2	2.668863
P30349	SLSNVIAHEISHSWTGNLVTNK	0.688041265	3	4.175377
P30349	SSALQWLTPEQTSGK	0.897321307	2	2.99612
P30349	WEEAIPLALK	0.852403262	2	2.913596
P30427	**PLEC Plectin**	**0.904031157**	**0.70186**	**6**
P30427	AQAEAQQPVFNTLR	0.986484332	2	2.994362
P30427	AQVEQELTTLR	0.895357495	2	2.514488
P30427	LLDPEDVDVPQPDEK	0.811830853	2	3.726467
P30427	LQAEEVAQQK	1.002370202	2	2.398628
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0)	0.878579385		
P30427	VLALPEPSPAAPTLR	0.868243573	2	2.781167
P30713	**GSTT2 Glutathione S_transferase theta_2**	**0.975209459**	**4.4E-16**	**6**
P30713	AQVHEYLGWHADNIR	0.906514562	2	4.898557
P30713	GQHLSEQFSQVNCLK	0.836481845	2	4.794899
P30713	NSMVLALQR	0.865815711	2	2.868994
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.920058884	3	4.296496
P30713	VLGPLIGVQVPEEK	0.875523137	2	3.897211
P30713	YQVADHWYPADLQAR	0.738410081	2	4.862041
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.076529996**	**0.30007**	**2**
P30835	NEWGSLLEELVK	1.148149124	2	3.212283
P30835	VFANAPDSACVIGLR	0.474456336	2	2.403141
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.107442444**	**0.00023**	**10**
P30839	DILAAIAADLSK	1.282342061	2	3.030413
P30839	EKDILAAIAADLSK	1.37480076	2	4.115873
P30839	EKPLALYIFSHNNK	0.989432601	2	3.133023
P30839	FDHILYTGNTAVGK	1.032604544	2	3.935179
P30839	HLTPVTLELGGK	1.079776142	3	3.315098
P30839	NVEEAINFINDR	1.233330777	2	4.109665
P30839	QRFDHILYTGNTAVGK	1.04318541	2	2.83376
P30839	VMQEEIFGPILPIVSVK	0.861233762	2	4.425926
P30839	VMQEEIFGPILPIVSVK+Oxidation(1)	0.893803982		
P30839	YIAPTILTDVDPNSK	0.964644188	2	3.860017
P30904	**MIF Macrophage migration inhibitory factor**	**1.662522169**	**1E-06**	**2**
P30904	LHISPDR	1.290783948	1	2.018165
P30904	LLCGLLSDR	1.683705532	2	2.934856
P30999	**CTND1 Catenin delta_1**	**0.853764147**	**0.00562**	**3**
P30999	GYELLFQPEVVR	0.873967001	2	2.842425
P30999	QDVYGPQPQVR	1.198276089	2	2.43279

P30999	SQSSHSYDDSTLPLIDR	0.67791267	2	2.594846
P31000	**VIME Vimentin**	**0.789711655**	**1.9E-06**	**15**
P31000	DGQVINETSQHHDDLE	0.739113407	2	3.114833
P31000	FADLSEAANR	1.052612718	2	2.840343
P31000	ILLAELEQLK	0.82770082	2	3.222592
P31000	KLLEGEESR	0.914639388	2	2.730617
P31000	KVESLQEEIAFLK	0.714930877	2	3.975406
P31000	LGDLYEEEMR	0.931037818	2	2.336449
P31000	LLEGEESR	0.854954101	2	2.749329
P31000	LQEEMLQR	0.826676959	2	2.328545
P31000	NLQEAEEWYK	0.801783447	2	2.81154
P31000	QDVDNASLAR	0.772937879	2	2.805826
P31000	QVQSLTCEVDALK	0.863817194	2	3.541288
P31000	RQVDQLTNDK	0.816903313	2	2.516809
P31000	SLYSSSPGGAYVTR	0.894692273	2	2.809831
P31000	TNEKVELQELNDR	0.969001124	2	2.835557
P31000	VELQELNDR	1.064819419	2	2.587061
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**0.954942966**	**1.5E-08**	**7**
P31044	GNDISSGTVLSEYVGSGPPK	0.952709899	2	6.581267
P31044	KYHLGAPVAGTCFQAEWDDSVPK	0.871907072	3	3.775324
P31044	LYTLVLTDPDAPSR	1.235088593	2	4.267089
P31044	VDYGGVTVDELGK	0.951783959	2	4.858945
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.890047717	3	5.079072
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.540725303	2	5.398308
P31044	YVWLVYEQEQPLNCDEPILSNK	0.960933381	2	5.405777
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.163290203**	**0.10687**	**19**
P31210	DELLTSLGK	1.454720883	2	2.862387
P31210	DIEALNK	2.376879009	1	2.46768
P31210	EEMKDIEALNK	2.162583194	2	3.385076
P31210	ENFQIFDFSLTK	1.265871435	2	3.027293
P31210	HIDGAYVYR	1.143358363	2	2.939373
P31210	IKENFQIFDFSLTK	1.312465178	3	4.346778
P31210	LWSTDHDPEMVRPALER	1.17713618	3	3.668172
P31210	NEHEVGEAIR	1.124515721	2	3.07835
P31210	NPLWVNVSSPPLLK	1.263005469	2	4.442975
P31210	NPLWVNVSSPPLLKDELLTSLGK	0.929350657	3	5.236874
P31210	QLEVILNKPGLK	1.214852673	2	3.382973
P31210	REEIFYCGK	1.211110312	2	3.28525
P31210	RQLEVILNKPGLK	1.184565762	3	3.680693
P31210	SLGVSNFNR	1.107885486	2	2.376778
P31210	SNLCATWEALEACK	1.202733277	2	4.941665
P31210	SNLCATWEALEACKDAGLVK	1.114704171	2	5.145218
P31210	TAIDEGYR	1.19573807	2	2.436932
P31210	TQAQIVLR	1.212479731	2	3.036217
P31210	YKPVTNQVECHPYFTQTK	1.101323258	2	5.77276
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.060585503**	**0.02555**	**2**
P31230	GAEADQIIEYLK	1.059037855	2	3.477441
P31230	KEIEELK	1.438073781	1	1.999019
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**0.878544393**	**0.79916**	**7**
P31399	ANVDKPGLVDDFK	1.086399754	2	3.780981
P31399	KYPYWPHQPIENL	1.168250369	2	2.380995
P31399	NCAQFVTGSQAR	0.942766606	2	4.925229
P31399	NMIPFDQMTIDDLNEVFPETK	0.823044716	2	5.076017
P31399	SWNETFHTR	1.185657004	2	2.676055

P31399	TIDWVSFVEIMPQNQK	1.055355818	2	4.12896
P31399	YTALVDAEEKEDVK	1.020073672	2	3.638041
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.061207936**	**0.99636**	**6**
P32089	FIHDQTSSNPK	0.922156886	1	3.547732
P32089	GLSSLLYGSIPK	0.796122621	2	3.292212
P32089	GTYQGLTATVLK	0.852726518	2	2.628208
P32089	NTLDCGVQILK	0.890857006	2	2.497192
P32089	SHGVLGLYR	0.922966552	1	1.914029
P32089	TQLQLDER	1.062349155	2	2.918798
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**0.768486693**	**1.4E-06**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	0.874411839	2	4.595607
P32198	GDTNPNIPKPTR	0.872637161	2	2.501151
P32198	LSTSQTPQQQVELFDFEK	1.605861361	2	2.815178
P32198	MTALAQDFAVNLGPK	0.677016222	2	3.388431
P32198	MTALAQDFAVNLGPK+Oxidation(0)	0.841451256		
P32198	TSPDAFIQLALQLAHYK	0.793091943	2	3.259335
P32232	**CBS Cystathionine beta_synthase**	**1.229519527**	**9.9E-20**	**11**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.201265273	3	5.973728
P32232	ALGAEIVR	1.420677253	1	1.970291
P32232	CVVILPDSVR	1.159137176	2	2.467029
P32232	FDSPESHVGVAWR	1.165998554	2	3.785591
P32232	LKNEIPNSHILDQYR	1.437930849	3	3.346921
P32232	NASNPLAHYDDTAEEILQQCDGK	1.39342492	2	5.300978
P32232	SNDDDSFAFAR	1.45729091	2	3.32601
P32232	VDMLVASAGTGGTITGIAR	1.078251533	2	4.834332
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.275187904	3	3.979408
P32232	VRPSDEVCK	1.101365901	2	2.631969
P32232	VWISPDTPSR	1.177511614	2	2.367357
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.092508254**	**0.72847**	**13**
P32551	AVAFQNPQTR	1.094464939	2	3.220823
P32551	AVAQGNLSSADVQAAK	1.093465833	2	4.976707
P32551	GNNTTSLLSQSVAK	1.156182911	2	4.174992
P32551	IIENLHDVAYK	1.338848155	2	3.558061
P32551	ITSEELHYFVQNHFTSAR	0.822064944	3	3.873832
P32551	LPNGLVIASLENYAPLSR	1.340862403	2	4.686533
P32551	NALANPLYCPDYR	1.055598055	2	3.018948
P32551	RGNNTTSLLSQSVAK	1.757012712	2	3.279236
P32551	RWEVAALR	1.089910725	2	2.410336
P32551	SMTASGNLGHTPFLDEL	1.050241465	2	3.213099
P32551	SMTASGNLGHTPFLDEL+Oxidation(1)	0.808560125		
P32551	TSAPGGVPLQPQELEFTK	1.018562605	2	4.216162
P32551	YENYNYLGTSHLLR	0.884226444	2	4.273424
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.38248831**	**9.9E-20**	**17**
P32755	AFEEEQALR	1.446654588	2	3.559216
P32755	DIAFEVEDCEHIVQK	1.381597751	2	4.093562
P32755	ENMDVLEELK	2.309655064	2	2.845803
P32755	FAVLQTYGDTTHTLVEK	1.289748783	2	4.977412
P32755	FLPGFEAPTYK	1.223647937	1	2.402299
P32755	FWSVDDTQVHTEYSSLR	1.478030727	2	5.522952
P32755	GMEFLAVPSSYYR	1.546351354	2	3.59925
P32755	GNLTDLETNGVR	1.485555877	2	3.72886
P32755	HNHQGFGAGNFNSLFK	1.450282682	3	5.647913
P32755	ILVDYDEK	1.432019752	2	2.402559
P32755	IVFVLCSALNPWNK	1.369160821	2	3.657444

P32755	IVREPWVEEDKFGK	1.438604109	3	4.488583
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.466299394	3	7.771306
P32755	MGFEPLAYK	1.675427729	2	2.619258
P32755	SIVVANYEESIK	1.27266325	2	4.159398
P32755	SQIQEYVDYNGGAGVQHIALR	1.442564284	2	5.54957
P32755	TEDIITTIR	1.356983471	2	3.391608
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**0.860675301**	**0.00915**	**2**
P33124	ALRPTIFPVVPR	0.88818339	2	2.979572
P33124	IENIYIR	0.870309749	2	2.95509
P33273	**CP255 Cytochrome P450 2C55**	**0.963510847**	**0.94639**	**4**
P33273	DENFLNLMEK	1.042339975	2	2.312552
P33273	ELRHFSLMTLR	0.898072191	2	2.365308
P33273	FDYKDENFLNLMEK	0.865432851	3	4.522217
P33273	IQEEASCLVEELR	0.957720889	2	2.719774
P33274	**CP4F1 Cytochrome P450 4F1**	**1.172168013**	**0.34215**	**2**
P33274	ACNLVHEFTDAVIR	1.185941803	3	3.738177
P33274	TLPDQGLDEFLK	1.120499977	2	2.517616
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.103509881**	**0.88301**	**25**
P34058	ADLINNLGTIAK	0.965225095	2	4.18483
P34058	EDQTEYLEER	1.418301461	2	3.430418
P34058	EGLELPEDEEEK	0.693510742	2	2.541823
P34058	EGLELPEDEEEKKK	1.255463657	2	3.370606
P34058	ELISNASDALDK	1.931546356	2	3.384502
P34058	EQVANSAFVER	2.241252006	2	2.369812
P34058	GFEVVYMTEPIDEYCVQQLK	0.618817929	2	4.445317
P34058	GVVDSEDLPLNISR	1.043524545	2	4.912754
P34058	HFSVEGQLEFR	0.994720597	2	2.571582
P34058	HLEINPDHPIVETLR	1.06240251	2	4.582771
P34058	HSQFIGYPITLYLEK	1.160327991	2	4.129283
P34058	IDIIPNPQER	0.982490982	2	3.117871
P34058	KHLEINPDHPIVETLR	1.070226107	2	4.827516
P34058	LGIHEDSTNR	1.019637971	2	3.40681
P34058	NPDDITQEEYGEFYK	1.206182335	2	4.753683
P34058	RAPFDLFENK	1.028645048	2	2.811533
P34058	SIYYITGESK	0.999391731	2	3.040217
P34058	SLTNDWEDHLAVK	1.01367367	2	4.017478
P34058	TLTLVDTGIGMTK	0.982615738	2	4.082806
P34058	TLTLVDTGIGMTK+Oxidation(10)	1.012793231		
P34058	VILHLKEDQTEYLEER	1.099050769	3	3.719254
P34058	YESLTDPSK	1.070476665	2	2.642702
P34058	YESLTDPSKLDSGK	1.129952156	2	3.596219
P34058	YHTSQSGDEMTSLSEYVSR	1.077310416	2	5.552259
P34058	YIDQEELNK	1.009660179	2	3.487408
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.026710674**	**0.99896**	**3**
P34064	AIGSASEGAQSSLQEVYHK	1.236088038	2	4.718152
P34064	EELEEVIKDI	0.970999692	2	2.494571
P34064	GVNTFSPEGR	0.972207421	2	3.013032
P34067	**PSB4 Proteasome subunit beta type_4**	**0.88015795**	**0.37791**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	0.859192591	2	3.634493
P34067	TQNPMVTGTSVLGVK	0.878633554	2	2.837394
P34067	VNDSTMLGASGDYADFQYLK	0.928813732	2	4.302262
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.029680375**	**0.99943**	**2**
P35171	GGTSDALLYR	1.110033528	2	2.888413
P35171	LFQEDNGMPVHLK	1.059370507	2	3.616754
P35213	**1433B 14_3_3 protein beta/alpha**	**0.943828188**	**0.94742**	**6**
P35213	AVTEQGHELSNEER	1.063701109	2	4.544152

P35213	EKIEAELQDICSDVLELLDK	0.720638547	3	3.559023
P35213	QTTVSNSQQAYQEAFEISK	0.99841736	2	5.24455
P35213	TAFDEAIAELDTLNEESYK	0.856541474	2	4.837814
P35213	YLILNATHAESK	1.099353962	2	3.207704
P35213	YLSEVASGDNK	1.071369933	1	2.999391
P35278	**RAB5C Ras_related protein Rab_5C**	**0.885792105**	**0.49899**	**2**
P35278	GVDLQESNPASR	1.03673848	2	3.07112
P35278	NEPQNAAGAPGR	0.873465708	2	2.857707
P35427	**RL13A 60S ribosomal protein L13a**	**1.163805618**	**0.13093**	**2**
P35427	CEGINISGNFYR	1.02239002	2	3.313946
P35427	YQAVTATLEEK	1.142755399	2	3.434364
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**0.980709026**	**0.9998**	**2**
P35434	AQSELSGAADEAAR	1.002434332	2	4.591399
P35434	IEANEALVK	0.948744371	2	3.168806
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**0.975206047**	**1**	**7**
P35435	GLCGAIHSSVAK	1.017494481	2	3.798018
P35435	HLIIGVSSDR	0.911177114	2	2.786877
P35435	NASDMIDK	1.006919608	1	2.113865
P35435	NDMAALTAAGK	0.972392524	2	3.376471
P35435	NDMAALTAAGK+Oxidation(2)	0.889265749		
P35435	THSDQFLVSFK	0.891540673	2	3.339708
P35435	VYGTGSLALYEK	1.031669925	2	2.992851
P35565	**CALX Calnexin**	**1.294093084**	**3.9E-07**	**9**
P35565	AEEDEILNR	2.199288718	2	2.914994
P35565	KIPNPDFFEDLEPFR	1.002474965	3	3.99702
P35565	NKGDEEEEEEKLEEK	1.142991561	2	5.21963
P35565	SDTSTPPSPK	1.536603425	2	2.530315
P35565	TDAPQPDVK	1.004766526	2	2.343518
P35565	TDAPQPDVKDEEGKEEEK	1.037426261	2	3.868199
P35565	TSELNLDQFHDK	1.395428211	2	3.883714
P35565	VVDDWANDGWGLK	0.959984645	2	4.30863
P35565	VVDDWANDGWGLKK	0.91079743	2	2.767107
P35704	**PRDX2 Peroxiredoxin_2**	**0.973525209**	**0.99998**	**4**
P35704	EGGLGPLNIPLLADVTK	0.951624568	2	3.352696
P35704	KEGGLGPLNIPLLADVTK	0.892750139	2	4.256789
P35704	NDEGIAYR	0.958918361	2	2.392763
P35704	QITVNDLPVGR	0.973543855	2	2.69115
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.881477168**	**0.46409**	**5**
P35738	AAVEQVPVEPYK	1.030677989	2	2.660911
P35738	GLLLSCIEDKNPCIFFEPK	0.938876962	2	3.466292
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	0.89223987	3	4.104013
P35738	MNLFQSITSALDNSLAK	0.780416115	2	2.629858
P35738	SGDLFNCGSLTIR	0.881149233	2	2.892294
P35815	**PPM1B Protein phosphatase 1B**	**1.085071192**	**0.77845**	**2**
P35815	IQNAGGSVMIQR	0.957122979	2	3.083096
P35815	SGFALEPSVENVK	1.101809213	2	3.126184
P36201	**CRIP2 Cysteine_rich protein 2**	**1.064155674**	**0.65769**	**3**
P36201	ASSVTTFTGEPNMCPR	2.159338415	2	3.899054
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	0.812363339	3	6.951923
P36201	GVNTGAVGSYIYDKDPEGTVQP	0.939565565	2	4.259221
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**1.002039089**	**0.93344**	**11**
P36365	ALQSDYITYIDDLLTSINAKPDLR	0.967960803	3	3.499315
P36365	ASLYNSVVSNSSK	1.030722886	2	2.308056

P36365	CCLEEGLEPTCFER	1.041477744	2	4.114057
P36365	ENSVVFNNTPK	1.777951026	2	2.554125
P36365	FTEHVEEGR	0.874688132	2	3.131942
P36365	NLLPTPVVSWLISK	0.790179354	2	2.466439
P36365	SCDLGGLWR	1.068006484	2	2.766515
P36365	TQLREPVLNDELPGR	0.949766188	3	4.071889
P36365	VAIVGAGVSGLASIK	1.286227692	2	2.873965
P36365	VEDGQASLYK	1.022846459	2	3.531333
P36365	VLVVGMGNSGTDIAVEASHLAK	0.996219059	2	2.945758
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**0.947902223**	**1**	**7**
P36511	ANIIAWALAQIPQK	0.828940071	3	5.083358
P36511	FVNVWTYELPR	0.97922704	2	3.194323
P36511	FVTFPTSFSSHDLENFFTR	1.155460177	2	4.163317
P36511	GHEVTVLRPSAFVFLDPK	1.139020355	3	3.524342
P36511	IILEELVQK	1.00384014	2	3.283202
P36511	SDLLNALEEVIDNPFYK	0.667875588	2	5.231205
P36511	TLGRPTTLAEIMGK	1.107494696	3	3.614776
P36536	**SAR1A GTP_binding protein SAR1a**	**1.024957776**	**0.95056**	**2**
P36536	LVFLGLDNAGK	1.060492872	2	2.993917
P36536	VELNALMTDETISNVPILILGNK	0.935467885	3	4.625602
P36972	**APT Adenine phosphoribosyltransferase**	**0.862470903**	**0.05241**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	0.817558596	2	3.898834
P36972	IDYIAGLDSR	0.857423437	2	3.457277
P36972	SFPDFPIPGVLFR	0.887504849	2	3.550406
P37397	**CNN3 Calponin_3**	**1.229914618**	**0.01923**	**3**
P37397	AGQSVIGLQMGTNK	1.235298431	2	4.283856
P37397	VNESSLNWPQLENIGNFIK	0.966300739	2	3.378146
P37397	YDQQAEEDLR	1.318452349	2	3.259101
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**0.981690936**	**0.39368**	**8**
P38650	FGNPLLVQDVESYDPVLNPVLNR	0.90699799	2	4.533171
P38650	GWENHVEGQK	1.715127615	2	2.878756
P38650	ILDDDTIITTLENLK	0.932878863	2	2.694302
P38650	QLQNISQAAAAGGAK	0.923624212	2	3.302531
P38650	SSLQSQCLNEVLK	0.892264317	2	2.920714
P38650	VQGLTVEQAEAVAR	1.054301838	2	3.584492
P38650	VQVALEELQDLK	0.869763473	2	2.711881
P38650	VTDFGDKVEDPTFLNQLQSGVNR	0.901508358	3	4.068075
P38652	**PGM1 Phosphoglucomutase_1**	**1.014564343**	**0.99869**	**16**
P38652	ADNFEYSDPVDGSISK	0.991402368	2	4.70753
P38652	AIGGIILTASHNPGGPNGDFGIK	0.801091962	2	5.283345
P38652	FFGNLMDASK	0.949660364	2	2.307066
P38652	FNISNGGPAPEAITDK	0.919214453	2	4.284826
P38652	INQDPQVMLAPLISIALK	0.775345912	2	4.933863
P38652	KQRVEDILK	0.447414598	1	1.982547
P38652	LSGTGSAGATIR	1.153050514	2	3.631773
P38652	LSLCGEESFGTGSDHIR	1.018707673	2	3.557404
P38652	LVIGQNGILSTPAVSCIIR	0.942066631	2	3.736856
P38652	NIFDFNALK	0.871388024	1	1.940837
P38652	QEATLVVGGDGR	1.056167738	2	2.991833
P38652	QQFDLENK	1.027786249	1	2.155559
P38652	SGEHDFGAAFDGDGDR	1.074294654	2	4.443589
P38652	TIEEYAICPDLK	0.917843745	2	3.08145
P38652	TQAYPDQKPGTSGLR	1.000643978	2	3.362595
P38652	YDYEEVEAEGANK	0.941999778	2	5.05689
P38656	**LA Lupus La protein homolog**	**1.067962012**	**0.66674**	**2**
P38656	ITDDQQESLNK	1.067740304	2	3.934011
P38656	LDEGWVPLETMIK	0.859704114	2	2.450222

P38659	**PDIA4 Protein disulfide_isomerase A4**	**1.021861258**	**1E-08**	**20**
P38659	DLGLSESGEDVNAAILDESGKK	1.103584196	2	5.112491
P38659	DNDPPIAVAK	0.890190717	2	2.343389
P38659	EVSQPDWTPPPEVTLTLTK	1.03172638	2	3.761898
P38659	FDVSGYPTIK	0.851742357	2	3.355823
P38659	FDVSGYPTLK	0.851742357	2	3.355823
P38659	FIDEHATK	0.984819447	2	2.63242
P38659	FIDEHATKR	1.181054534	2	2.765029
P38659	GQAVDYDGSR	0.926266806	2	2.845011
P38659	IDATSASMLASK	0.857476147	2	3.587105
P38659	IDATSASMLASK+Oxidation(7)	1.036125376		
P38659	KGQAVDYDGSR	1.657894761	2	2.633599
P38659	MDATANDITNDR	0.902156673	2	3.987757
P38659	MHVMDVQGSTEASAIKDYVVK	0.787835745	3	3.720118
P38659	QLEPVYTSLGK	0.854681658	2	2.556856
P38659	RFDVSGYPTLK	1.024171116	2	3.158771
P38659	RSPPIPLAK	0.790843114	2	2.373942
P38659	TQEEIVAK	1.003661764	2	2.396427
P38659	VDATEQTDLAK	0.95184037	2	4.046705
P38659	VEGFPTIYFAPSGDK	1.272039785	2	3.444849
P38659	YGIVDYMVEQSGPPSK	0.962066538	2	4.651431
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**1.024730817**	**0.99863**	**7**
P38918	EEHFNGIALVEK	1.152474215	2	3.04461
P38918	FQLETSLK	1.193428471	1	1.943807
P38918	FYAFNPLAGGLLTGR	1.122278472	2	4.475383
P38918	MDVTSSSASVR	1.215648662	2	3.590468
P38918	QVETELFPCLR	0.971849515	2	2.492181
P38918	RMDVTSSSASVR	1.09652251	2	3.549952
P38918	TTYGPTAPSMISAAVR	0.866957415	2	3.746691
P38983	**RSSA 40S ribosomal protein SA**	**1.026777599**	**0.01336**	**9**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.181290752	3	5.82599
P38983	AIVAIENPADVSVISSR	1.045303395	2	5.649462
P38983	EHPWEVMPDLYFYRDPEEIEKEEQAAAEK	0.516000765	3	3.756177
P38983	FAAATGATPIAGR	1.258244699	2	3.043618
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.141140263	3	4.044478
P38983	FTPGTFTNQIQAAFR	1.014303213	2	4.441462
P38983	KSDGIYIINLK	0.530602265	2	3.2187
P38983	SDGIYIINLK	1.144058573	2	2.975475
P38983	YVDIAIPCNNK	1.026178857	1	3.025011
P39032	**RL36 60S ribosomal protein L36**	**1.092903809**	**0.72516**	**2**
P39032	EELSNVLAAMR	1.232015322	2	2.48169
P39032	KREELSNVLAAMR	1.04044674	2	3.831596
P39447	**ZO1 Tight junction protein ZO_1**	**0.724461208**	**0.67704**	**2**
P39447	GEEVTILAQK	0.38090541	2	2.478636
P39447	GGPAEGQLQENDR	1.011373578	2	2.914105
P40112	**PSB3 Proteasome subunit beta type_3**	**0.944267192**	**0.94042**	**2**
P40112	FGIQAQMVTTDFQK	0.870346722	2	3.4818
P40112	FGPYYTEPVIAGLDPK	0.946333573	2	3.492236
P40307	**PSB2 Proteasome subunit beta type_2**	**1.006526522**	**0.9941**	**3**
P40307	FILNLPTFSVR	1.153865069	2	3.013951
P40307	NGYELSPTAAANFTR	0.940662005	2	3.554812
P40307	VIDKDGIHNLENITFTK	0.928550523	3	4.734424
P40329	**SYRC Arginyl_tRNA synthetase_ cytoplasmic**	**0.847580461**	**0.50377**	**2**
P40329	LNDYVFSFDK	1.12916013	2	2.704495
P40329	SDGGYTYDTSDLAAIK	0.837597975	2	4.012593
P41034	**TTPA Alpha_tocopherol transfer protein**	**0.933506832**	**0.30459**	**6**

P41034	AECPELSADLHPR	0.63810853	2	2.969157
P41034	AIFDLEGWQISHAFQITPSVAK	0.727989593	2	4.617293
P41034	AQEEGVPETPQPLTDAFLLR	0.98463136	2	3.834833
P41034	GIHLINEPVIFHAVFSMIKPFLTEK	0.575325642	4	4.707664
P41034	QLNEQPDHSPLVQPGLAELR	0.872896719	3	3.960544
P41034	VSLITSELIVQEVETQR	1.013703754	3	3.797645
P41123	**RL13 60S ribosomal protein L13**	**1.014669514**	**7.6E-13**	**3**
P41123	LATQLTGPVMPIR	0.945157537	2	2.952143
P41123	STESLQANVQR	1.166418171	2	3.971032
P41123	VDTWFNQPAR	1.032784675	2	3.451286
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**0.903166607**	**0.99944**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.118110186	2	3.103318
P41498	IELLGSYDPQK	0.914807202	2	3.437858
P41498	LVTDENVSDNWR	1.171505434	2	3.796196
P41542	**USO1 General vesicular transport factor p115**	**1.144992802**	**0.2043**	**15**
P41542	AWFEVGDENPGWSAQK	0.812944173	2	4.63702
P41542	CQNEQLQTAVTQQASQIQQHK	1.040844083	3	4.119624
P41542	EQDLQLEELK	1.16277818	2	2.487828
P41542	IVAFENAFER	1.313117283	2	2.622846
P41542	LQTENSELQQR	1.00107254	2	3.125226
P41542	LREEIEELR	1.14290241	2	2.47305
P41542	NDGVLLLQALTR	0.965202851	2	3.437385
P41542	NNNSNQNFFK	0.959229681	2	2.490579
P41542	QLDSSNSTIAILQTEK	1.141522828	2	3.906002
P41542	QLGPPVQQIILVSPMGVSK	0.902474599	2	2.387461
P41542	QSEDLGSQFTEIFIK	1.076068519	2	3.539407
P41542	SQLCSQSLEITR	1.14369856	2	3.104682
P41542	SVPVEGESELVTAAK	1.059964382	2	3.69433
P41542	TLEQHDNIVTHYK	1.016629974	2	3.48302
P41542	VLVSPTNPPGATSSCQK	1.069994267	2	4.18065
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**0.873997178**	**2.9E-15**	**18**
P41562	ATDFVVPGPGK	0.912580217	2	3.607947
P41562	CATITPDEK	0.947791744	2	2.682965
P41562	DIFQEIYDK	1.049560328	1	2.473907
P41562	DLAACIK	2.206675605	1	2.002927
P41562	FKDIFQEIYDK	0.883075437	3	4.118649
P41562	GQETSTNPIASIFAWSR	0.725275911	2	4.963188
P41562	IHGGSVVEMQGDEMTR	1.16478858	2	4.612719
P41562	LIDDMVAQAMK	0.898911961	2	4.588535
P41562	LIDDMVAQAMK+Oxidation(4)	1.006722676		
P41562	LILPYVELDLHSYDLGIENR	0.992042016	2	4.69077
P41562	LVTGWVKPIIIGR	0.964319888	2	3.214007
P41562	SDYLNTFEFMDK	0.843296068	2	4.336756
P41562	SDYLNTFEFMDK+Oxidation(9)	0.909114548		
P41562	SEGGFIWACK	0.826041141	2	3.322345
P41562	SIEDFAHSSFQMALSK	0.815235231	2	4.935408
P41562	TVEAEAAHGTVTR	0.985149267	2	3.966763
P41562	VEITYTPK	0.856889546	2	2.764072
P41562	VTYLVHDFEEGGGVAMGMYNQDK	0.971640549	3	3.328084
P42123	**LDHB L_lactate dehydrogenase B chain**	**0.908911603**	**0.07521**	**6**
P42123	DYSVTANSK	1.429626218	2	2.453655
P42123	IVADKDYSVTANSK	2.27946584	2	3.983585
P42123	LIAPVADDETAVPNNK	1.711389869	2	2.5292
P42123	LKDDEVAQLR	1.776436392	2	2.565563
P42123	SLADELALVDVLEDK	1.246834969	2	3.594932

P42123	VIGSGCNLDSAR	0.938230933	2	3.926786
P42676	**NEUL Neurolysin_ mitochondrial**	**0.756701341**	**0.02178**	**4**
P42676	AELGALPDDFIDSLEK	0.756639851	2	3.013837
P42676	NLILKPGGSLDGMDMLQNFLQR	0.87956927	3	3.472996
P42676	NLNEDDTSLVFSK	0.90338444	2	3.120328
P42676	TRTEQLIAQTK	0.705694691	2	2.754903
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.093186012**	**0.04569**	**9**
P42932	AIAGTGANVIVTGGK	1.063018621	2	3.82366
P42932	AVDDGVNTFK	1.160143042	2	2.962775
P42932	EDGAISTIVLR	0.951825151	2	2.660331
P42932	ELEVQHPAAK	1.62746149	2	2.941638
P42932	GEENLMDAQVK	1.697231565	2	2.456546
P42932	HFSGLEEAVYR	1.23333359	2	2.724827
P42932	NVGLDIEAEVPAVK	1.159063179	2	3.07452
P42932	QITSYGETCPGLEQYAIK	1.129856429	2	4.595458
P42932	TAEELMNFSK	0.976845585	2	2.329487
P43244	**MATR3 Matrin_3**	**0.972837273**	**0.99519**	**3**
P43244	GDTDQASNILASFGLSAR	0.781389063	2	3.43647
P43244	ITPENLPQILLQLK	0.912254747	2	3.679196
P43244	TENPAEGKEQEEK	0.89820784	2	2.953317
P43274	**H14 Histone H1.4**	**0.905628522**	**0.85973**	**3**
P43274	ALAAAGYDVEK	0.918892672	2	3.611325
P43274	SGVSLAALK	1.07804008	2	2.922416
P43274	SGVSLAALKK	0.832890229	2	2.592466
P43276	**H15 Histone H1.5**	**0.906938181**	**0.07589**	**2**
P43276	ALAAGGYDVEK	0.657385329	2	2.551481
P43276	ATGPPVSELITK	0.957266847	2	2.551647
P43278	**H10 Histone H1.0**	**0.895687759**	**1E-10**	**2**
P43278	VGENADSQIK	0.906861545	2	3.519381
P43278	YSDMIVAAIQAEK	0.819911562	2	3.987155
P45591	**COF2 Cofilin_2**	**1.096902234**	**0.20323**	**4**
P45591	HEWQVNGLDDIKDR	1.21361041	3	4.205368
P45591	KEDLVFIFWAPESAPLK	1.434150919	3	3.570692
P45591	QIIVEEAK	1.058390625	2	2.355095
P45591	QILVGDIGDTVEDPYTSFVK	0.842388415	2	4.77419
P45592	**COF1 Cofilin_1**	**1.030394333**	**0.43591**	**4**
P45592	EILVGDVGQTVDDPYTTFVK	1.013326056	2	4.593636
P45592	HELQANCYEEVK	1.032633705	2	3.475245
P45592	HELQANCYEEVKDR	1.003714535	3	5.294194
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	0.762977498	3	4.866737
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.125269887**	**0.99397**	**4**
P45878	GWDQGLLGMCEGEK	0.953592176	2	3.979692
P45878	KLVIPSELGYGER	1.073646449	2	2.557052
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	1.141431505	3	4.399527
P45878	LVIPSELGYGER	1.079150575	2	2.659063
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.104089032**	**0.54499**	**18**
P45953	AMVENGGLVTSNPLR	0.944441482	2	3.433763
P45953	AMVENGGLVTSNPLRV	1.045759182	2	3.22963
P45953	AMVENGGLVTSNPLRV+Oxidation(1)	0.971304427		
P45953	ASNTSEVYFDGVK	1.093235484	2	3.711103
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.036251139	2	4.81055
P45953	ENMASLQSNPQQQELFR	1.3062705	2	4.292533
P45953	FFEEVNDPAK	0.979115563	2	3.128175
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	0.869824102	3	5.826537
P45953	GIVNEQFLLQR	0.8046578	2	3.425009

P45953	IFEGTNDILR	1.000255817	2	2.670158
P45953	NDSLEKVEEDTLQGLK	0.747165864	2	3.444993
P45953	NPLGNVGLLIGEASK	1.125507884	2	3.46002
P45953	SFGGVTHGLPEK	1.030584509	2	2.311799
P45953	SFGGVTHGLPEKK	0.997835477	2	3.009181
P45953	SGELAVQALEQFATVVEAK	0.900167678	3	4.776571
P45953	SLSEGYPTAQHEK	1.052107055	2	3.325535
P45953	TGIGSGLSLSGIVHPELSR	1.011717397	2	4.521201
P45953	VEEDTLQGLK	0.943542476	2	2.662334
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**1.210399719**	**0.99273**	**4**
P46418	AILNYIATK	1.290637153	2	3.308846
P46418	SDGSLMFEQVPMVEIDGMK	1.167259716	2	2.751177
P46418	SHGQDYLVGNK	1.342111402	2	3.13551
P46418	VSNLPTVK	0.960968615	2	2.892628
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.679895418**	**0.0057**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.687684579	3	3.971177
P46425	FEDGDLTLYQSNAILR	0.757877564	2	4.711096
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.018945213**	**0.67346**	**28**
P46462	AIANECQANFISIK	1.352741301	2	3.73597
P46462	EAVCIVLSDDTCSDEK	0.786736205	2	2.738125
P46462	ELQELVQYPVEHPDK	1.134514425	2	4.269449
P46462	ETVVEVPQVTWEDIGGLEDVK	0.945939815	2	3.017491
P46462	ETVVEVPQVTWEDIGGLEDVKR	1.031103035	2	4.063055
P46462	EVDIGIPDATGR	1.303178608	2	3.039968
P46462	GDDLSTAILK	0.964307896	2	3.058485
P46462	GGNIGDGGGAADR	1.310690327	2	3.975876
P46462	GILLYGPPGTGK	1.091565576	2	3.193771
P46462	GVLFYGPPGCGK	1.079774297	2	2.507306
P46462	IVSQLLTLMDGLK	1.216816899	2	3.058284
P46462	KYEMFAQTLQQSR	1.282279257	2	3.799582
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.026199291	3	6.18906
P46462	LAGESESNLRKAFEEAEK	1.079886096	2	2.605604
P46462	LDQLIYIPLPDEK	0.900033086	2	4.471232
P46462	LEILQIHTK	1.32191103	2	2.693849
P46462	LGDVISIQPCPDVK	1.017212754	2	4.263931
P46462	LIVDEAINEDNSVVSLSQPK	1.032883163	2	5.833801
P46462	MDELQLFR	0.883054706	2	3.037797
P46462	MDELQLFR+Oxidation(0)	1.011990262		
P46462	MTNGFSGADLTEICQR	0.87015931	2	4.227392
P46462	MTNGFSGADLTEICQR+Oxidation(0)	1.038946633		
P46462	NAPAIIFIDELDAIAPK	1.066612245	2	5.098776
P46462	QAAPCVLFFDELDSIAK	1.700879856	3	3.444426
P46462	QTNPSAMEVEEDDPVPEIR	1.012738312	2	4.645095
P46462	RSVSDNDIR	0.477395435	2	2.891446
P46462	VINQILTEMDGMSTK	0.986659381	2	4.552554
P46462	WALSQSNPSALR	1.006201614	2	3.169538
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**0.98838571**	**0.74941**	**4**
P46664	FIEDELQIPVK	0.993740777	2	3.050907
P46664	LDILDMFTEIK	0.820348903	2	3.409123
P46664	VGIGAFPTEQDNEIGELLQTR	0.934415954	2	4.399871
P46664	VVDLLAQDADIVCR	1.012901488	2	3.721214
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**0.963470315**	**0.20269**	**3**
P46720	ESEHTDVHGSPQVENDGELK	1.430794526	3	3.477867
P46720	GIGETPIVPLGISYIEDFAK	1.007119385	2	3.494571
P46720	SENSPLYIGILEMGK	0.924549759	2	3.739497

P46844	**BIEA Biliverdin reductase A**	**0.908100408**	**0.28543**	**3**
P46844	FGVVVVGVGR	1.044847342	2	2.753653
P46844	LLDQVSAEDLAAEK	0.99224857	2	4.371974
P46844	MTVQLETQNK	0.786951614	2	2.740632
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**0.957682757**	**0.03708**	**9**
P46953	AQGSVALSVTQDPACK	0.843583442	2	4.486174
P46953	ASFQPPVCNK	0.904618706	2	2.356057
P46953	DLGTQLAPIIQEFFHSEQYR	0.935223618	2	4.312824
P46953	FANTMGLVIER	1.150057388	2	2.608901
P46953	METELDGLR	0.874768952	2	2.619124
P46953	QDVDVWLWQLEGSSK	0.93558815	2	3.890494
P46953	QGEIFLLPAR	1.304096483	2	3.270734
P46953	TGKPNPDQLLK	0.874403762	3	3.827189
P46953	YYVGDTEDVLFEK	0.990624945	2	4.019377
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.058546964**	**0.97567**	**5**
P46978	FGQVYTEAK	1.063691308	2	2.695893
P46978	FYSLLDPSYAK	1.025870176	2	2.92425
P46978	NLDISRPDKK	1.094184503	2	2.797149
P46978	VGQAMASTEEK	1.003027652	2	3.402025
P46978	VGQAMASTEEK+Oxidation(4)	0.302084027		
P47198	**RL22 60S ribosomal protein L22**	**0.938963283**	**0.99999**	**2**
P47198	AGNLGGGVVTIER	0.947075273	2	3.527872
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.037568614	3	5.18702
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.08173587**	**1.6E-05**	**4**
P47875	GFGFGQGAGALVHSE	0.793757414	2	3.211263
P47875	GLESTTLADKDGEIYCK	0.914393873	2	5.188237
P47875	HEEAPGHRPTTNPNASK	0.988170063	3	3.810413
P47875	NLDSTTVAVHGEEIYCK	0.990974047	2	3.687725
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**1.109002552**	**0.74579**	**2**
P47942	GIQEEMEALVK	0.768690941	2	2.800728
P47942	GLYDGPVCEVSVTPK	1.073695014	2	3.635516
P48004	**PSA7 Proteasome subunit alpha type_7**	**0.997619194**	**0.52761**	**3**
P48004	GRDIVVLGVEK	1.113118694	2	2.658012
P48004	NYTDDAIETDDLTIK	0.95267373	2	4.550107
P48004	YVAEIEKEKEENEK	0.888433853	2	5.051441
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**1.416872191**	**9.9E-20**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.803161235	3	5.465962
P48024	TLTTVQGIADDYDK	1.406136683	2	3.168539
P48037	**ANXA6 Annexin A6**	**0.871880687**	**0.99995**	**19**
P48037	AANDFNPDADAK	1.139895544	2	3.350109
P48037	AINEAYKEDYHK	1.140676431	2	3.176689
P48037	ALIEILATR	0.988786891	2	3.34523
P48037	CLIEILASR	1.109617103	2	2.517637
P48037	DAFVAIVQSVK	1.581789821	2	3.004673
P48037	DLESDIIGDTSGHFQK	1.302268992	2	3.860751
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	0.8470147	2	4.935554
P48037	GELSGDFEK	1.024979848	1	2.101067
P48037	GFGSDKESILELITSR	0.909351366	2	4.219398
P48037	GIGTDEATIIDIITQR	1.158859003	2	4.058478
P48037	KTNYDIEHVIK	1.167426128	2	2.478091
P48037	QRQEICQSYK	0.995306783	2	4.016341
P48037	SEIDLLNIR	1.010339485	2	3.281227
P48037	SEISGDLAR	1.041066832	2	2.360828
P48037	SELDMLDIR	0.995151241	2	2.682776
P48037	SLEDALSSDTSGHFK	0.960421411	2	3.934227

P48037	TNEQIHQLVAAYK	0.988339054	2	3.982612
P48037	TNYDIEHVIK	1.067210808	2	3.250883
P48037	TTGKPIEASIR	0.928610062	2	2.501235
P48450	**ERG7 Lanosterol synthase**	**2.184324336**	**0.2924**	**2**
P48450	ILGIGPDDPDLVR	1.768108713	2	2.38531
P48450	SVQLPDGGWGLHIEDK	2.299705047	2	2.733079
P48500	**TPIS Triosephosphate isomerase**	**1.113610282**	**1.4E-05**	**13**
P48500	CNVSEGVAQCTR	1.035386215	2	3.708891
P48500	DLGATWVVLGHSER	1.659301018	2	3.686285
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	0.948755778	4	6.551955
P48500	HIFGESDELIGQK	1.146341278	2	4.016953
P48500	IAVAAQNCYK	1.193154465	2	2.697418
P48500	IIYGGSVTGATCK	1.260893228	2	4.642459
P48500	LPADTEVVCAPPTAYIDFAR	0.94369402	2	5.048263
P48500	RHIFGESDELIGQK	1.128832713	2	3.918656
P48500	TATPQQAQEVHEK	1.311824739	2	3.741127
P48500	VNHALSEGLGVIACIGEK	0.931725543	2	5.277333
P48500	VTNGAFTGEISPGMIK	1.063168276	2	5.160472
P48500	VTNGAFTGEISPGMIK+Oxidation(13)	1.068398297		
P48500	VVLAYEPVWAIGTGK	0.949215857	3	4.661988
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.911644038**	**0.18027**	**5**
P48508	ASTLHLQTGNLLNWGR	0.85708867	3	4.298683
P48508	EFPDVLECTMSHAVEK	0.996596913	2	3.725932
P48508	INPDEREEMK	0.826419545	2	2.568276
P48508	LFIVGSNSSSSTR	0.666857699	2	3.019517
P48508	TLNEWSSQISPDLVR	0.793154221	2	4.79794
P48675	**DESM Desmin**	**1.279169563**	**0.82119**	**3**
P48675	ADVDAATLAR	1.484094264	2	2.393958
P48675	FLEQQNAALAAEVNR	1.437728648	2	4.291257
P48675	VSDLTQAANK	1.876219459	2	2.988657
P48679	**LMNA Prelamin_A/C**	**0.908503413**	**9.5E-06**	**16**
P48679	AAYEAELGDAR	1.181866426	2	2.957789
P48679	AQHEDQVEQYK	1.038648576	2	3.065216
P48679	AQHEDQVEQYKK	1.153369505	3	3.937302
P48679	IDSLSAQLSQLQK	0.968909241	2	3.134309
P48679	ITESEEVVSR	0.84173058	2	3.229878
P48679	LKDLEALLNSK	0.98023591	2	2.741622
P48679	LQEKEDLQELNDR	0.990419528	2	4.39889
P48679	LRDLEDSLAR	0.798118156	2	2.468886
P48679	MQQQLDEYQELLDIK	1.013433573	2	4.396125
P48679	MQQQLDEYQELLDIK+Oxidation(0)	0.993976652		
P48679	NSNLVGAAHEELQQSR	0.884622395	2	4.365974
P48679	SGAQASSTPLSPTR	0.840707295	2	3.261025
P48679	SVGGSGGGSFGDNLVTR	0.811420865	2	3.984489
P48679	TALINATGEEVAMR	0.878395655	2	3.236383
P48679	TVLCGTCGQPADK	0.91498568	2	3.301952
P48679	VAVEEVDEEGK	1.22957921	2	2.930672
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**0.985483946**	**2.2E-16**	**28**
P48721	AQFEGIVTDLIK	1.010737937	2	3.776506
P48721	ASNGDAWVEAHGK	1.034426939	2	3.740872
P48721	DAGQISGLNVLR	0.977673462	2	3.569642
P48721	EQQIVIQSSGGLSK	1.510774387	2	3.759012
P48721	EQQIVIQSSGGLSKDDIENMVK	1.222794059	2	4.436788
P48721	ERVEAVNMAEGIIHDTETK	1.093812548	3	5.767061
P48721	ETAENYLGHTAK	1.584561426	2	3.59407
P48721	GAVVGIDLGTTNSCVAVMEGK	0.947797639	2	5.629698

P48721	LLGQFTLIGIPPAPR	1.197441883	2	3.079156
P48721	MEEFKDQLPADECNK	1.211789319	2	4.770112
P48721	MEEFKDQLPADECNK+Oxidation(0)	1.595014355		
P48721	MKETAENYLGHTAK	0.923536494	2	4.151165
P48721	MKETAENYLGHTAK+Oxidation(0)	1.136010567		
P48721	NAVITVPAYFNDSQR	1.150510172	2	3.569063
P48721	QAASSLQQASLK	1.738807068	2	2.993021
P48721	QAVTNPNNTFYATK	1.484807285	2	3.781953
P48721	RYDDPEVQK	1.197803682	2	2.92188
P48721	RYDDPEVQKDTK	1.058560312	2	3.766151
P48721	SDIGEVILVGGMTR	0.990635188	2	4.318917
P48721	SQVFSTAADGQTQVEIK	1.605605622	2	5.021915
P48721	STNGDTFLGGEDFDQALLR	1.066169807	2	5.616467
P48721	TTPSVVAFTPDGER	0.991281144	2	3.706936
P48721	VEAVNMAEGIIHDTETK	0.975614025	2	4.325917
P48721	VINEPTAAALAYGLDK	1.240844255	2	4.134956
P48721	VLENAEGAR	1.075250017	2	3.07982
P48721	VQQTVQDLFGR	1.022004265	2	3.446519
P48721	YDDPEVQK	0.962745356	2	2.465925
P48721	YDDPEVQKDTK	0.925277661	2	2.778764
P48725	**PCNT Pericentrin**	**0.9259075**	**0.66475**	**2**
P48725	EEVSGGNGPCRGSPGRGSLER	0.925763561	2	2.332365
P48725	VYQSLSTAVEGLLEMALDSSKQLEEAR	2.848483677	3	3.332243
P49134	**ITB1 Integrin beta_1**	**0.887016802**	**0.45527**	**4**
P49134	CNCQSHGIPASPK	0.818992752	2	3.655881
P49134	GEFFNELVGQQR	0.856873073	2	2.800832
P49134	RITSDFRIGFGSFVEK	0.883079624	2	2.359382
P49134	SAVTTVVNPK	0.887330308	2	2.437993
P49242	**RS3A 40S ribosomal protein S3a**	**1.080919922**	**0.00105**	**9**
P49242	ACQSIYPLHDVFVR	1.277205092	2	3.968821
P49242	ADGYEPPVQESV	1.145939201	2	2.353567
P49242	LIPDSIGKDIEK	1.128469871	2	2.508604
P49242	LITEDVQGK	1.107785597	2	2.744938
P49242	LMELHGEGGSSGK	1.030817084	2	3.458177
P49242	LMELHGEGGSSGK+Oxidation(1)	1.244643224		
P49242	NCLTNFHGMDLTR	0.972469209	2	3.800273
P49242	TTDGYLLR	1.138361076	2	3.069434
P49242	VFEVSLADLQNDEVAFR	0.957316723	2	4.274086
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.995878048**	**0.98519**	**6**
P49432	EAINQGMDEELERDEK	0.909532098	2	2.557161
P49432	ILEDNSIPQVK	1.011454967	2	3.077391
P49432	IMEGPAFNFLDAPAVR	1.016235687	2	4.222926
P49432	IMEGPAFNFLDAPAVR+Oxidation(1)	0.922557526		
P49432	TIRPMDIEAIEASVMK	0.901842595	3	4.404881
P49432	VFLLGEEVAQYDGAYK	1.140425341	2	3.539786
P49620	**DGKG Diacylglycerol kinase gamma**	**0.96552179**	**0.71331**	**2**
P49620	QGERILQKFHYLLNPK	3.380958974	2	2.496506
P49620	WGGGYEGGSLTKILK	0.930212058	2	2.344863
P49717	**MCM4 DNA replication licensing factor MCM4**	**0.741308051**	**0.00591**	**2**
P49717	GQSDTAITKDMFEEALR	0.42763819	2	2.312626
P49717	YQQLFEDIR	0.753638432	1	1.979849
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.561427002**	**9.9E-20**	**13**
P49889	CKEDALFNR	0.607438631	2	2.599116
P49889	FEEHYQQQMK	0.791577716	2	2.811329
P49889	FEEHYQQQMK+Oxidation(8)	1.157153053		
P49889	FMEGQVPYGSWYDHVK	0.722063529	2	3.767872

P49889	IIQHTSFQEMK	0.779948782	2	2.679441
P49889	LIEFLERDPSAELVDR	0.702592728	3	5.062951
P49889	NEDLINGIK	0.644275268	2	2.907812
P49889	NNPCTNYSMLPETMIDLK	0.514649755	2	4.478652
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13)	0.429741465		
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8)	0.429741465		
P49889	SFSEFVEK	0.688202953	2	2.374656
P49889	SGSTWISEIVDMIYK	0.439808161	2	4.562672
P49889	YWEDVETFLARPDDLLIVTYPK	1.164536408	3	4.197574
P50137	**TKT Transketolase**	**0.891498482**	**0.00205**	**23**
P50137	AVELAANTK	0.989047873	1	1.975096
P50137	GHAAPILYAVWAEAGFLPEAELLNLR	1.090755317	3	3.482074
P50137	GITGIEDK	1.03030955	1	2.330757
P50137	IIALDGDTK	1.489465991	2	2.456312
P50137	ILATPPQEDAPSVDIANIR	0.981043058	3	5.383316
P50137	ISSDLDGHPVPK	1.004185591	2	3.244202
P50137	KISSDLDGHPVPK	0.926121976	2	3.901942
P50137	LAVSQVPR	1.009900984	2	2.301791
P50137	LAVSQVPRSGKPAELLK	1.909745998	2	2.601427
P50137	LDNLVAIFDINR	0.961353686	2	4.3408
P50137	LGQSDPAPLQHQVDVYQK	1.1072011	2	4.031178
P50137	MFGIDKDAIVQAVK	0.825349516	2	4.396074
P50137	MFGIDKDAIVQAVK+Oxidation(0)	0.86417206		
P50137	NMAEQIIQEIYSQVQSK	0.788135549	3	5.850729
P50137	NMAEQIIQEIYSQVQSK+Oxidation(1)	0.762523814		
P50137	NSTFSELFK	0.98456288	2	2.396109
P50137	SGKPAELLK	1.092915737	3	3.400248
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	0.885531841	3	4.069691
P50137	SVPMSTVFYPSDGVATEK	0.907819837	2	4.290738
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3)	0.951364212		
P50137	TSRPENAIIYSNNEDFQVGQAK	0.930050184	3	6.319445
P50137	VLDPFTIKPLDK	1.074185328	2	3.029834
P50137	VLDPFTIKPLDKK	0.860142284	2	2.734724
P50169	**RDH3 Retinol dehydrogenase 3**	**1.003008672**	**0.04422**	**10**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	0.886929088	3	5.047653
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1)	0.880262074		
P50169	FQDSYMK	0.951056782	1	2.086136
P50169	GLWGLVNNAGISVPVGPNEWMR	0.87018359	2	3.715937
P50169	KLWDQTTEEVK	0.887261839	2	3.076902
P50169	KLWDQTTEEVKEIYGEK	0.922551889	3	4.721564
P50169	LWDQTTEEVK	1.096520877	2	3.255734
P50169	LWDQTTEEVKEIYGEK	0.91954956	2	5.144002
P50169	MSLVGGGYCISK	1.262640571	2	3.773761
P50169	MSLVGGGYCISK+Oxidation(0)	1.278345335		
P50237	**ST1C1 Sulfotransferase 1C1**	**0.825430875**	**2.2E-12**	**9**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.720548882	2	5.233977
P50237	DISEEVLNK	1.543766993	2	2.636224
P50237	DLHLGEQDLQPETR	1.162736897	2	4.309466
P50237	HPFIEWTLPSPLNSGLDLANK	0.318756432	3	3.322172
P50237	IWNFQAKPDDLLIATYAK	0.995891049	3	3.750057
P50237	MKDLHLGEQDLQPETR	0.995682804	2	3.980995
P50237	MLPDPGTLGEYIEQFK	0.787728356	3	4.699763
P50237	MLPDPGTLGEYIEQFK+Oxidation(0)	0.853370014		
P50237	VLWGSWYDHVK	1.298996762	2	3.119763
P50298	**ARY2 Arylamine N_acetyltransferase 2**	**0.871519513**	**0.87371**	**2**
P50298	FSYKDNIDLVEFK	0.976816337	2	2.683943

P50298	SLTEEEIEDVLK	0.864082692	2	2.767169
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**0.94090089**	**0.00662**	**8**
P50398	FDLGQDVIDFTGHALALYR	0.884751642	3	4.230884
P50398	FQLLEGPPESMGR	0.934911558	2	3.548142
P50398	KQNDVFGEADQ	1.057339875	2	2.635939
P50398	MLLYTEVTRYLDFK	0.961016013	2	2.34705
P50398	NPYYGGESSSITPLEELYK	0.862503184	2	5.448057
P50398	QLICDPSYIPDR	1.001927861	2	3.348272
P50398	TDDYLDQPCLETINR	1.028099761	2	5.167658
P50398	TFEGVDPQTTSMR	0.926534703	2	2.595511
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.040101495**	**0.99316**	**7**
P50399	AYDATTHFETTCDDIK	1.995270615	2	4.772915
P50399	AYDATTHFETTCDDIKDIYK	0.964478062	3	5.506894
P50399	EIRPALELLEPIEQK	1.078926038	3	3.93112
P50399	FDLGQDVIDFTGHSLALYR	1.121617239	3	4.703263
P50399	FVSISDLFVPK	0.833987719	2	3.141755
P50399	NTNDANSCQIIIPQNQVNR	1.091124075	2	4.221483
P50399	TDDYLDQPCCETINR	0.997107962	2	4.765975
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.218586785**	**0.40574**	**7**
P50431	ALSDALTELGYK	1.013369147	2	3.998201
P50431	AVLEALGSCLNNK	0.986549803	2	4.476895
P50431	GLLEEDFQK	0.88274865	2	2.358482
P50431	ISATSIFFESMPYK	1.328103346	2	3.510657
P50431	IYQLQVLANCR	0.858489525	2	2.690809
P50431	VLEACSIACNK	0.977754308	2	3.92667
P50431	YSEGYPGQR	1.150867458	2	2.772025
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**0.96794886**	**0.88566**	**14**
P50475	ASEWVQQVSGLMDGK	1.022601953	2	4.166582
P50475	AVFDETYPDPVR	1.010450376	2	3.268637
P50475	DIINEEEVQFLK	0.845791974	2	3.182424
P50475	GLEATDDSPK	0.966275883	2	2.590701
P50475	ITCLCQVPQNAANR	1.14242076	2	4.588664
P50475	IVAVTGAEAQK	1.084775047	2	2.752509
P50475	NVGCLQEALQLATSFAQLR	0.89541211	2	2.918587
P50475	QIWQNLGLDEAK	1.038436118	2	3.140088
P50475	RIVAVTGAEAQK	1.467579861	2	2.946728
P50475	SVLGDADQK	0.832730042	1	2.199129
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	1.202634937	3	4.02376
P50475	TITVALADGGRPDNTGR	1.096812272	2	3.0999
P50475	VDDSSEDKTEFTVK	1.27042841	2	3.751496
P50475	VGAEDTDGIDMAYR	1.059218557	2	3.851568
P50503	**F10A1 Hsc70_interacting protein**	**1.434091256**	**9.9E-20**	**6**
P50503	AIDLFTDAIK	1.312366111	2	2.900306
P50503	AIEINPDSAQPYK	1.547079509	2	3.461441
P50503	GAAIDALNDGELQK	1.497407843	2	3.666522
P50503	KGAAIDALNDGELQK	1.498604451	2	4.918941
P50503	LDYDEDASAMLR	1.19365366	2	3.564228
P50503	QDPSVLHTEEMR	1.735337777	2	2.5345
P50516	**VATA V_type proton ATPase catalytic subunit A**	**0.85809941**	**0.72088**	**3**
P50516	ADYAQLLEDMQNAFR	0.844044317	2	3.741143
P50516	TALVANTSNMPVAAR	0.997359255	2	3.594894
P50516	VLDALFPCVQGGTTAIPGAFGCGK	0.968240494	2	2.847148
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**0.906381697**	**0.8984**	**12**
P50554	GNYLVDVDGNR	1.068125566	1	2.183243
P50554	GTFCSFDTPDEAIR	1.256669079	2	3.756868

P50554	GVVLGGCGDK	0.970690583	2	2.304727
P50554	HGCAFLVDEVQTGGGCTGK	0.843494031	2	5.863329
P50554	IDIPSFDWPIAPFPR	0.774930215	2	3.742017
P50554	KHGCAFLVDEVQTGGGCTGK	1.179106196	3	3.70531
P50554	LVQQPQNASTFINRPALGILPPENFVDK	0.762106776	3	3.722294
P50554	NLLLAEVINIIK	0.818140163	3	4.942817
P50554	REDLLNNVAHAGK	1.329251867	2	2.360586
P50554	TLLTGLLDLQAQYPQFVSR	0.994550918	3	4.104712
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	0.915028474	2	3.462449
P50554	YPLEEFVTDNQQEEAR	0.942609311	2	3.006053
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.173172247**	**0.00054**	**4**
P50580	HELLQPFNVLYEK	1.033040823	2	2.964564
P50580	LVKPGNQNTQVTEAWNK	1.270970317	3	3.389173
P50580	SLVEASSSGVSVLSLCEK	0.977419071	2	2.49089
P50580	TIIQNPTDQQK	1.179397331	2	3.135452
P50878	**RL4 60S ribosomal protein L4**	**1.11632236**	**2.3E-05**	**11**
P50878	FCIWTESAFR	1.0540357	2	2.528991
P50878	KLDELYGTWR	1.119002749	2	3.157358
P50878	KLEAAAAALAAK	1.218821919	3	4.27761
P50878	LDELYGTWR	0.920783949	2	2.629948
P50878	LEAAAAALAAK	1.205853579	2	3.0964
P50878	NIPGITLLNVSK	1.070106398	2	3.293212
P50878	NVTLPAVFK	1.218448138	1	2.003755
P50878	RGPCIIYNEDNGIIK	1.103272016	2	3.468535
P50878	SGQGAFGNMCR	1.207699625	2	2.378578
P50878	SNYNLPMHK	1.178905857	2	2.562851
P50878	YAICSALAASALPALVMSK	1.316568652	2	3.499718
P51583	**PUR6 Multifunctional protein ADE2**	**1.107878031**	**0.26072**	**3**
P51583	ACGNFGIPCELR	1.097542941	2	2.64011
P51583	AEYEGDGIPTVFVAVAGR	1.212324082	2	3.204171
P51583	SWLPQNCTLVDMK	1.15369982	2	2.622981
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**0.819819435**	**6.3E-06**	**8**
P51635	ALEALVAK	0.910589872	2	2.527867
P51635	ALGLSNFSSR	1.111080213	2	2.806605
P51635	GLEVTAYSPLGSSDR	0.887625735	2	4.452848
P51635	HHPEDVEPAVR	0.947894144	3	3.740552
P51635	HIDCASVYGNETEIGEALK	0.714189517	2	5.929032
P51635	HIDCASVYGNETEIGEALKESVGAGK	1.0928502	3	6.122674
P51635	HPDEPVLLEEPVVLALAEK	1.026624697	3	6.084077
P51635	QLDALNK	0.972376616	1	2.300743
P51647	**AL1A1 Retinal dehydrogenase 1**	**1.101849744**	**1**	**17**
P51647	ANNTTYGLAAGVFTK	1.158039299	2	3.94088
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	1.057060061	3	3.890269
P51647	ELGEHGLYEYTELK	1.56126221	2	3.721067
P51647	FPVLNPATEEVICHVEEGDK	1.033472301	3	4.09538
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.888100324	4	5.142944
P51647	IFINNEWHDSVSGK	1.10356724	2	4.352702
P51647	IFVEESVYDEFVR	0.949011815	2	4.264873
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	0.979998832	4	5.756516
P51647	IHGQTIPSDGDIFTFTR	1.028129766	2	4.546439
P51647	KFPVLNPATEEVICHVEEGDK	0.973636506	3	3.753911
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.970237613	4	4.866906
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	1.002984994	3	3.774581
P51647	LLLATIEAINGGK	0.183980687	2	4.117346
P51647	VFANAYLSDLGGSIK	1.052470943	2	4.558314
P51647	YCAGWADK	1.007194266	1	2.056455
P51647	YVLGNPLTQGINQGPQIDK	1.03954213	2	5.026834

P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.969012969	2	3.508366
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.828009895**	**0.02532**	**7**
P51650	EVGEVLCTDPLVSK	0.916938871	2	3.806841
P51650	HQSGGNFFEPTLLSNVTR	1.02076289	2	3.581902
P51650	LGTVADCGVPEAR	0.846138713	2	3.434222
P51650	VGNGFEEGTTQGPLINEK	0.780310837	2	4.312137
P51650	VYGDIIYTSAK	0.816217532	2	2.664002
P51650	WLPTPATFPVYDPASGAK	0.857880268	2	3.764623
P51650	YGIDEYLEVK	0.880413607	2	3.085031
P51869	**CP4F4 Cytochrome P450 4F4**	**1.080958079**	**0.9943**	**2**
P51869	TLDFIDVLLLTK	1.10028396	2	3.61471
P51869	WQDLASGGSAR	1.070356816	2	2.53931
P51886	**LUM Lumican**	**0.986546931**	**0.78388**	**3**
P51886	ITNIPDEYFNR	0.498213672	2	2.333369
P51886	NNQIDHIDEK	1.104014728	2	3.094421
P51886	SLQDLQLANNK	0.940274111	2	2.69651
P52020	**ERG1 Squalene monooxygenase**	**1.057103372**	**0.66819**	**2**
P52020	DIPDLYDDAAIFQAK	0.777506476	2	2.466207
P52020	GVLLLGDAYNLR	1.209133299	2	2.967228
P52296	**IMB1 Importin subunit beta_1**	**0.952275654**	**0.97172**	**5**
P52296	AAVENLPTFLVELSR	0.889732577	2	3.41269
P52296	GALQYLVPILTQTLTK	0.912657535	2	2.446865
P52296	SNEILTAIIQGMR	0.951827163	2	3.146467
P52296	TVSPDRLELEAAQK	0.994073264	2	2.871838
P52296	VLANPGNSQVAR	1.108384951	2	3.595824
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.051056378**	**0.99971**	**4**
P52303	NINLIVQK	0.877224126	1	2.212781
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.017530063	3	3.917299
P52303	SQPDMAIMAVNTFVK	0.991674314	2	2.602387
P52303	YNDPIYVK	1.073809673	2	2.524617
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.099317139**	**0.99978**	**3**
P52555	ILDQGEDFPASELAR	1.095411514	2	4.81951
P52555	QGQDGLSGVK	1.028467321	2	2.465656
P52555	SLNILTAFR	1.045025349	2	2.811404
P52631	**STAT3 Signal transducer and activator of transcription 3**	**3.343733748**	**1.2E-12**	**3**
P52631	GLSIEQLTTLAEK	2.148524728	2	3.080907
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	3.352925174	3	3.380996
P52631	TQIQSVEPYTK	2.536034824	2	2.638862
P52734	**FGD1 FYVE_ RhoGEF and PH domain_containing protein 1**	**1.105368342**	**0.87015**	**2**
P52734	SLELQARTEEEKK	1.00620499	2	2.504863
P52734	TEEEKKDWVQAINSTLLK	1.11437284	2	2.353791
P52759	**UK114 Ribonuclease UK114**	**0.893189846**	**0.00686**	**8**
P52759	AAGCDFTNVVK	1.084504096	2	3.009787
P52759	AAYQVAALPK	1.158435901	2	2.641856
P52759	APAAIGAYSQAVLVDR	0.857703718	2	3.708164
P52759	IEIEAIAVQGPFTTAGL	0.712561023	2	3.513055
P52759	NLGEILK	0.908095872	2	2.380661
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	0.725856914	2	4.30302
P52759	TTVLLADINDFGTVNEIYK	0.890266727	2	4.875
P52759	TYFQGNLPAR	0.894784658	2	3.087487
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**0.560667495**	**4.3E-10**	**2**
P52845	CKEDAIFNR	0.607438631	2	2.599116
P52845	SGSTWIGEIVDMIYK	0.432123969	2	3.55171

P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.146216125**	**3.7E-05**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	1.260540581	2	5.013755
P52847	FLAGNVAYGSWFDHVK	1.111242758	2	3.503611
P52847	IEEFQSRPCDIVIPTYPK	1.109864282	3	4.805368
P52847	IVHHTSFEVMK	1.390395001	2	2.915155
P52847	NYFTMTQSEK	1.127199633	1	2.71535
P52847	SGTTWLSEIVDMVLNDGNVEK	0.962266609		
P52847	THLPIDLLPK	1.130442922	3	3.71345
P52847	TLDEHTLER	1.229838678	2	3.003373
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**0.971251823**	**7.4E-15**	**37**
P52873	ADEAYLIGR	0.872992888	2	2.946749
P52873	ADFAQACQDAGVR	0.904444862	2	4.476007
P52873	AEAEAQAEELSFPR	0.958959565	2	4.44045
P52873	AGTHILCIK	1.030875255	1	2.032533
P52873	ALAVSDLNR	0.906476446	2	2.604053
P52873	AYSEALAAFGNGALFVEK	0.770222927	2	3.705422
P52873	AYVEANQMLGDLIK	0.921299502	2	4.511999
P52873	DAHQSLLATR	1.538669357	1	3.117682
P52873	DFTATFGPLDSLNTR	1.351267418	2	4.286073
P52873	DMAGLLKPAACTMLVSSLR	0.971745498	2	3.075082
P52873	ELIPNIPFQMLLR	1.420973338	2	2.404148
P52873	ENGVDAVHPGYGFLSER	1.116018551	2	3.072159
P52873	FLYECPWR	0.876119158	2	2.606937
P52873	GANAVGYTNYPDNVVFK	1.057276378	2	4.332129
P52873	GLAPVQAYLHIPDIIK	0.837393188	2	2.95695
P52873	GTPLDTEVPLER	0.870413551	2	3.590704
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	0.830682006	2	5.941383
P52873	HGEEVTPEDVLSAAMYPDVFAQFK+Oxidation(14)	0.86782264		
P52873	HIEVQILGDQYGNILHLYER	0.829130273	3	4.759448
P52873	HYFIEVNSR	0.807853488	2	2.553222
P52873	IAEEFEVELER	0.81937761	2	3.287968
P52873	IEGRPGASLPPLNLK	0.803047547	2	3.610756
P52873	INGCAIQCR	0.92781767	2	2.843999
P52873	IVGDLAQFMVQNGLSR	0.816513557	2	5.297952
P52873	LDNASAFQGAVISPHYDSLLVK	0.893133051	3	5.832052
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	0.866964512	4	5.441233
P52873	NHQGLLLMDTTFR	1.214256748	2	3.355662
P52873	QKADEAYLIGR	0.945127266	3	3.43804
P52873	QVFFELNGQLR	0.810318667	2	2.771383
P52873	QVGYENAGTVEFLVDK	1.003056186	2	4.107854
P52873	SVVEFLQGYIGIPHGGFPEPFR	0.82659895	2	4.300785
P52873	TVAVYSEQDTGQMHR	0.951240345	2	4.34306
P52873	VFDYSEYWEGAR	0.75991993	2	4.571292
P52873	VSPSPVDPIVPVVPIGPPPAGFR	0.753417237	2	4.461032
P52873	VVEIAPATHLDPQLR	0.878713045	2	4.116382
P52873	VVHSYEELEENYTR	0.892525685	2	5.158436
P52873	YSLEYYMGLAEELVR	1.206928364	3	4.689162
P52944	**PDLI1 PDZ and LIM domain protein 1**	**0.849431934**	**0.4991**	**7**
P52944	AAIANLCIGDLITAIDGEDTSSMTHLEAQNK	0.877354396	3	4.367404
P52944	CGTGIVGVFVK	0.806880239	2	2.437644
P52944	GCVDNMTLTVSR	1.26545592	2	2.36246
P52944	GHFFVGDQIYCEK	0.981331207	2	3.517665
P52944	QSTSFLVLQEILESDGK	0.785372857	2	2.435704
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	1.0119457	3	3.953514
P52944	VTPPEGYDVVTVFPK	0.845807655	2	2.790221

P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.166827195**	**0.9003**	**3**
P53395	LSDIGEGIR	0.955413476	2	2.467001
P53395	LSEVVGSGK	0.947986123	2	2.343265
P53395	SYLENPAFMLLDLK	1.153030019	2	4.640735
P53987	**MOT1 Monocarboxylate transporter 1**	**1.077899628**	**0.00018**	**5**
P53987	DGKEDETSTDVDEKPK	1.521693574	3	5.626783
P53987	DGKEDETSTDVDEKPKK	1.79933806	3	3.870491
P53987	EDETSTDVDEKPK	1.569857271	2	3.100295
P53987	ETQSPAPLQNSSGDPAEEESPV	1.062972513	2	4.404111
P53987	SDANTDLIGGSPK	0.985327227	2	4.050053
P54319	**PLAP Phospholipase A_2_activating protein**	**1.028799071**	**0.99704**	**4**
P54319	GQTLGLGNTSFSDPFTGGGR	1.020286521	2	3.343384
P54319	IGDVVGSSGANQQTSGK	1.030449838	2	4.515548
P54319	TGDLGDINAEQLPGR	1.100002688	2	3.665746
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.928185281	2	2.871021
P54822	**PUR8 Adenylosuccinate lyase**	**0.975493112**	**0.99891**	**2**
P54822	KVDIEVLSVLASLGASVHK	0.97147046	3	4.43676
P54822	VLSQQAAAVVK	0.976840767	2	2.3284
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.070109233**	**0.88634**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	0.94072002	3	4.882149
P54921	HDAATCFVDAGNAFK	0.853492327	2	2.34596
P54921	IEEACEIYAR	1.137318331	2	2.711907
P54921	NSQSFFSGLFGGSSK	1.108634389	2	3.431803
P54921	YEELFPAFSDSR	0.945103852	2	2.893608
P55006	**RDH7 Retinol dehydrogenase 7**	**1.011265171**	**0.46087**	**11**
P55006	LETVILDVTK	1.053376324	2	3.238852
P55006	TESIVAATQWVK	0.963428948	2	3.939571
P55006	TNVTNMER	0.998924816	2	2.770482
P55006	TNVTNMER+Oxidation(5)	0.809860227		
P55006	TSDRLETVILDVTK	0.979126876	3	4.194678
P55006	VAIIEPGGFK	1.003355359	2	2.645862
P55006	VLAACLTEK	1.205664142	2	3.324537
P55006	VVNIASTMGR	0.96108673	2	3.654848
P55006	VVNIASTMGR+Oxidation(7)	1.036621608		
P55006	YGVEAFSDSLR	1.080834781	2	3.835497
P55006	YVFITGCDSGFGNLLAR	1.046906173	2	3.677321
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.334092557**	**0.26182**	**4**
P55051	ALGVGFATR	1.352552398	2	2.713905
P55051	LTDSQNFDEYMK	1.14744102	2	4.400812
P55051	LTDSQNFDEYMK+Oxidation(10)	1.711507692		
P55051	QVGNVTKPTVIISQEGGK	1.253465614	3	3.837464
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**0.821878038**	**0.2473**	**5**
P55053	FDETTADGR	0.755199665	2	2.961714
P55053	KTETVCTFTDGALVQHQK	1.076908343	3	5.080284
P55053	LVESHGFEDYMK	1.017870337	2	2.62493
P55053	MVVECVMNNAICTR	0.957041834	2	3.24547
P55053	TETVCTFTDGALVQHQK	1.111298192	2	4.305476
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.086569804**	**0.36351**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.126161866	3	5.518301
P55159	IFFYDSENPPGSEVLR	1.068003027	2	5.901761
P55159	IQSILSEDPK	1.188766803	2	3.088877
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.232730262	3	4.119244
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	0.910951666	3	3.966547
P55159	VVADGFDFANGIGISLDGK	0.882036714	2	4.085935
P55159	YVYIAELLAHK	0.956498752	2	2.879871

P55260	**ANXA4 Annexin A4**	**1.094834852**	**0.33777**	**5**
P55260	AEIDMLDIPANFK	0.901483247	1	2.213793
P55260	GAGTDEGCLIEILASR	0.905311971	2	3.410341
P55260	GLGTDEDAIIGVLACR	1.094104756	2	4.126154
P55260	INQTYQQQYGR	1.407333346	2	2.759853
P55260	SETSGSFEDALLAIVK	1.045869571	2	2.424878
P55770	**NH2L1 NHP2_like protein 1**	**1.115664064**	**0.59517**	**2**
P55770	LLDLVQQSCNYK	1.104983611	2	2.66762
P55770	QQIQSIQQSIER	1.115698491	2	3.012279
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.009694075**	**0.19284**	**6**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	0.896849488	2	4.222363
P56399	IFQNAPTDPTQDFSTQVAK	1.293398079	2	3.966633
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	0.968358698	3	3.431857
P56399	IVILPDYLEIAR	0.978516887	2	2.623757
P56399	KQEVQAWDGEVR	0.996221203	2	3.12834
P56399	VTSAVEALLSADSASR	1.038622285	2	2.768435
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**0.930053473**	**0.21433**	**3**
P56522	AVPTGDVEDLPCGLLLSSVGYK	0.723249515	2	4.420526
P56522	TATEKPGVEEAAR	0.868492741	2	3.177993
P56522	TDITEVALGVLR	0.931703425	2	4.048718
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.204860511**	**0.7948**	**14**
P56574	CATITPDEAR	1.155768861	2	2.304648
P56574	DLAGCIHGLSNVK	1.273784536	2	2.856535
P56574	DQTNDQVTIDSALATQK	1.204141496	2	5.04928
P56574	FKDIFQEIFDK	1.057325994	2	3.236313
P56574	GKLDGNQDLIR	1.519157011	2	2.809859
P56574	LDGNQDLIR	1.276425447	2	2.383461
P56574	LIDDMVAQVLK	1.146837026	2	4.314041
P56574	LNEHFLNTTDFLDTIK	1.179694622	2	4.724234
P56574	NILGGTVFR	0.87139068	2	2.351218
P56574	SSGGFVWACK	1.279412797	2	2.53247
P56574	TIEAEAAHGTVTR	1.034721206	2	4.098842
P56574	VCVQTVESGAMTK	1.218641831	2	3.096589
P56574	VEKPVVEMDGDEMTR	1.221494365	3	3.64442
P56574	YFDLGLPNR	0.966320911	2	2.535134
P56593	**CP2AC Cytochrome P450 2A12**	**1.260972249**	**0.47293**	**3**
P56593	MLQGTCGAPIDPTIYLSK	0.898580176	2	3.959047
P56593	NRQPQYEDHMK	1.407313172	3	3.826875
P56593	YLPGPQQQIIK	0.809278171	2	2.444141
P56656	**CP239 Cytochrome P450 2C39**	**0.92722284**	**0.00676**	**5**
P56656	EHQESLDVTNPR	1.384097258	2	3.381594
P56656	IKEHQESLDVTNPR	0.843063624	3	4.751965
P56656	NYLIPK	0.720349468	1	2.191697
P56656	SDHFMPFSAGKRVCAGEGLAR	0.90875747	2	2.390186
P56656	VQEEIDHVIGR	1.43853961	2	3.185246
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**1.924163975**	**9.9E-20**	**8**
P57093	AISCHYGSSDCK	1.811379217	2	3.384495
P57093	FYEENGFLVIK	1.846563645	2	2.588346
P57093	GDTVFFHPLLIHGSGR	2.512393856	3	3.538332
P57093	IQDFQQNEELFR	1.118422068	2	4.337041
P57093	KFYEENGFLVIK	1.908397167	2	3.388309
P57093	NLVSDDDIQR	2.514928935	1	2.865102
P57093	NNGCLVVLPGTHK	2.369192904	2	2.514804
P57093	YCALPQIVK	1.909364975	1	2.199789

P57113	**MAAI Maleylacetoacetate isomerase**	**0.85707436**	**3.3E-16**	**13**
P57113	AITSGFNALEK	1.00821539	2	3.292677
P57113	ALLALEAFQVSHPCR	0.79896274	2	4.283391
P57113	DGGQQFSEEFQTLNPMK	1.098620936	2	4.925333
P57113	FKVDLSPYPTISHINK	0.803722517	2	5.0818
P57113	GIDYEIVPINLIK	0.838214483	2	4.469725
P57113	IDGITIGQSLAILEYLEETRPIPR	0.776746277	3	3.965795
P57113	LLPQDPQK	0.991532445	1	2.099002
P57113	LLPQDPQKR	1.032790535	2	2.54798
P57113	MISDLIASGIQPLQNLSVLK	0.631644398	2	4.770432
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0)	0.893480836		
P57113	QVGQENQMPWAQK	0.960326509	2	3.890368
P57113	VDLSPYPTISHINK	0.841823633	2	3.469768
P57113	YCVGDEVSMADVCLAPQVANAER	0.794790078	3	6.312306
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.06529108**	**0.37504**	**3**
P57722	ESTGAQVQVAGDMLPNSTER	1.247443758	2	4.876122
P57722	INISEGNCPER	1.065259379	2	3.45471
P57722	LVVPASQCGSLIGK	1.303201809	2	2.617839
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**0.923465695**	**0.95662**	**3**
P58321	SQGQDVTSSVYFMK	0.923465014	2	2.381233
P58321	VTHETSAHEGQTEAPSIDEK	1.002367925	3	4.700929
P58321	WLPLEANPEVTNQFLK	0.953477369	2	3.48753
P58751	**RELN Reelin**	**0.950261314**	**0.63668**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**1.156676751**	**0.99952**	**12**
P58775	AISEELDNALNDITSL	4.440369462	2	4.401304
P58775	ATDAEADVASLNR	1.548975921	2	4.230064
P58775	CGDLEEELK	3.937842184	2	2.39582
P58775	DAQEKLEQAEK	1.333118336	2	2.569577
P58775	KATDAEADVASLNR	4.603771414	2	4.181209
P58775	LDKENAIDR	2.836685604	2	2.785169
P58775	LKGTEDEVEK	2.296091856	3	3.581951
P58775	MELQEMQLK	1.754096375	2	2.658723
P58775	QLEEEQQALQK	1.473798107	2	3.970421
P58775	SLEAQADKYSTK	3.469279601	2	3.347279
P58775	TIDDLEDEVYAQK	1.768139901	2	4.065521
P58775	YSESVKDAQEK	0.858214474	2	2.995986
P59242	**CING Cingulin**	**1.097514845**	**0.06502**	**2**
P59242	LGQEQQALNR	1.233692988	2	2.74131
P59242	LQGLEQEAENK	1.024063712	2	2.543168
P59279	**RAB2B Ras_related protein Rab_2B**	**1.024719286**	**0.86518**	**2**
P59279	GAAGALLVYDITR	0.880153501	2	2.996588
P59279	LQIWDTAGQESFR	1.029217354	2	3.677009
P59759	**MKL2 MKL/myocardin_like protein 2**	**0.973257926**	**0.85519**	**2**
P59759	LVEVLK	1.025692933	2	2.451511
P59759	QIEELK	0.759123921	1	2.071705
P59895	**NEK6 Serine/threonine_protein kinase Nek6**	**1.067348313**	**0.8995**	**2**
P59895	QDCVKEIGLLK	1.104997328	2	2.346838
P59895	TVALKKVQIFEMMDAK+Oxidation(11)	1.035600782		
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**0.915371747**	**0.04258**	**2**
P59999	AENFFILR	0.852366553	2	2.571273
P59999	ELLLQPVTISR	1.394155343	2	2.691309
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.018976693**	**0.02556**	**5**
P60335	AITIAGVPQSVTECVK	0.994155193	2	3.201518
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	1.014458097	4	5.41702
P60335	IITLTGPTNAIFK	1.059774417	2	2.666085

P60335	LVVPATQCGSLIGK	1.218216963	2	3.344987
P60335	VMTIPYQPMPASSPVICAGGQDR	1.003020107	2	3.636625
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.282694007**	**3.3E-08**	**5**
P60843	ATQALVLAPTR	1.504662254	1	2.350039
P60843	GFKDQIYDIFQK	1.078607087	2	3.521557
P60843	KEELTLEGIR	1.377146423	2	2.50622
P60843	KGVAINMVTEEDKR	1.499904415	3	4.088434
P60843	LQMEAPHIIVGTPGR	1.218572331	3	3.843683
P60868	**RS20 40S ribosomal protein S20**	**1.182060963**	**9.9E-08**	**3**
P60868	DTGKTPVEPEVAIHR	1.056417399	3	3.533911
P60868	LIDLHSPSEIVK	1.22469662	2	3.199862
P60868	VCADLIR	1.112292775	2	2.340431
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.164750956**	**0.47645**	**2**
P60901	AINQGGLTSVAVR	1.169582527	2	3.441447
P60901	LLDSSTVTHLFK	1.115912214	2	2.795613
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.220881586**	**0.0158**	**2**
P61087	GEIAGPPDTPYEGGR	1.437288632	2	3.669807
P61087	VDLVDENFTELR	1.018004155	2	3.483526
P61107	**RAB14 Ras_related protein Rab_14**	**0.982517446**	**0.94751**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	0.886566815	3	3.682695
P61107	LTSEPQPQR	0.988311832	2	2.562986
P61107	NLTNPNTVIILIGNK	0.859254961	2	3.227733
P61107	SCLLHQFTEK	1.274841274	2	2.967806
P61107	STYNHLSSWLTDAR	0.922101383	2	3.284862
P61203	**CSN2 COP9 signalosome complex subunit 2**	**0.804924681**	**0.90781**	**2**
P61203	NYDESGSPR	0.761699293	2	2.469565
P61203	WTNQLNSLNQAVVSK	0.996296583	2	2.980879
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.037955287**	**0.97672**	**4**
P61222	GTVGSILDR	1.129049067	2	2.328647
P61222	NTVANSPQTLLAGMNK	1.009142382	2	3.602403
P61222	NVEDLSGGELQR	1.190876687	2	2.921072
P61222	VAETANEEEVKK	1.127679891	2	2.620749
P61314	**RL15 60S ribosomal protein L15**	**1.026854913**	**0.00053**	**6**
P61314	FFEVILIDPFHK	0.996674626	3	3.4665
P61314	GATYGKPVHHGVNQLK	1.381985969	2	4.368115
P61314	SLQSVAEER	1.138775942	2	2.688399
P61314	SLQSVAEERAGR	1.067595394	2	2.482018
P61314	VLNSYWVGEDSTYK	1.092162849	2	4.257211
P61314	YIQELWR	1.124180588	2	2.665078
P61354	**RL27 60S ribosomal protein L27**	**1.383038234**	**0.00365**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	1.924835759	3	4.116739
P61354	YSVDIPLDK	1.034169515	2	2.416169
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.043167006**	**0.81437**	**4**
P61459	AVGWNELEGR	1.07422109	2	3.129657
P61459	DQLLPNLR	1.712745281	2	2.354288
P61459	LDHHPEWFNVYNK	1.107411337	3	4.774946
P61459	LSAEERDQLLPNLR	0.964044568	3	4.01652
P61589	**RHOA Transforming protein RhoA**	**1.022036091**	**0.94443**	**3**
P61589	LVIVGDGACGK	0.951950957	2	2.709564
P61589	MKQEPVKPEEGR	1.200651826	3	3.451423
P61589	MKQEPVKPEEGR+Oxidation(0)	0.938334461		
P61751	**ARF4 ADP_ribosylation factor 4**	**1.081629357**	**0.00034**	**4**
P61751	IQEGAAVLQK	1.204665154	2	2.885529
P61751	LGEIVTTIPTIGFNVETVEYK	0.993407888	3	5.029695
P61751	NICFTVWDVGGQDK	1.027414997	2	4.127611

P61751	QDLPNAMAISEMTDK	1.044805777	2	3.772226
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.06744834**	**1**	**2**
P61805	ADFQGISPER	1.12162211	2	2.940885
P61805	FLEEYLSSTPQR	1.009213394	2	3.698464
P61972	**NTF2 Nuclear transport factor 2**	**1.006024532**	**0.99048**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	0.964814161	3	4.044783
P61972	NINDAWVCTNDMFR	1.01348916	2	3.601073
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.004885518**	**0.99615**	**8**
P61980	GSDFDCELR	1.11137517	2	2.602711
P61980	GSYGDLGGPIITTQVTIPK	0.998558259	2	5.05323
P61980	IDEPLEGSEDR	1.197085626	2	3.460135
P61980	IILDLISESPIK	1.001962267	2	3.972289
P61980	IITITGTQDQIQNAQYLLQNSVK	0.978896915	3	7.045339
P61980	LFQECCPHSTDR	1.109376986	2	3.674992
P61980	TDYNASVSVPDSSGPER	1.192042754	2	4.231711
P61980	VVLIGGKPDR	1.021924498	2	2.517359
P61983	**1433G 14_3_3 protein gamma**	**1.111564299**	**0.01773**	**4**
P61983	AYSEAHEISK	1.038575085	2	3.239245
P61983	NVTELNEPLSNEER	1.231068928	2	4.937109
P61983	TAFDDAIAELDTLNEDSYK	0.837222507	2	5.16806
P61983	YLAEVATGEK	1.115490338	2	2.922291
P62046	**LRCH1 Leucine_rich repeat and calponin homology domain_containing protein 1**	**0.963980617**	**0.66648**	**2**
P62046	DRELDIAMIEQLR	0.991382042	2	2.586196
P62046	NLESIDPQFTIRRK	0.932951454	2	2.319091
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.986802803**	**1**	**5**
P62076	CIGKPGGSLDNSEQK	0.982474426	2	4.043394
P62076	KCIGKPGGSLDNSEQK	1.132506981	3	4.540523
P62076	LDPGAIMEQVK	0.94444009	2	3.22487
P62076	VQIAVANAQELLQR	1.009668593	2	4.958214
P62076	YMDAWNTVSR	0.940234349	2	2.757345
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**1.169549983**	**6.8E-05**	**2**
P62078	FIDTTLAITGR	0.74554279	2	2.79627
P62078	TENCLSSCVDR	1.224672431	2	2.918724
P62083	**RS7 40S ribosomal protein S7**	**1.025283396**	**0.98936**	**5**
P62083	AIIIFVPVPQLK	0.911366318	2	3.792275
P62083	DVNFEFPEFQL	2.32464672	2	2.404202
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.029157872	3	4.949751
P62083	KAIIIFVPVPQLK	0.950752466	2	3.807272
P62083	TLTAVHDAILEDLVFPSEIVGK	1.086833373	2	5.099612
P62161	**CALM Calmodulin**	**1.037522779**	**0.99332**	**3**
P62161	EADIDGDGQVNYEEFVQMMTAK	0.781527878	2	4.775527
P62161	EAFSLFDKDGDGTITTK	1.381964464	2	4.172574
P62161	VFDKDGNGYISAAELR	0.990448721	2	4.886259
P62193	**PRS4 26S protease regulatory subunit 4**	**0.977262722**	**0.99632**	**4**
P62193	APQETYADIGGLDNQIQEIK	1.176098744	2	4.969431
P62193	MGQSQSGGHGPGGGK+Oxidation(0)	1.059524535		
P62193	NQEQMKPLEEK	1.032833579	2	3.234378
P62193	TMLELLNQLDGFDSR	0.993510062	2	4.048751
P62198	**PRS8 26S protease regulatory subunit 8**	**1.056793383**	**0.99409**	**6**
P62198	EELQLLQEQGSYVGEVVR	0.912178151	2	2.487425
P62198	IAELMPGASGAEVK	1.130650635	2	2.429717

P62198	IEELQLIVNDK	1.04929074	2	3.005128
P62198	LEGGSGGDSEVQR	1.083736681	2	3.750051
P62198	LLREELQLLQEQGSYVGEVVR	1.06895998	3	4.049383
P62198	TMLELLNQLDGFEATK	1.045163993	2	3.626887
P62243	**RS8 40S ribosomal protein S8**	**1.136747948**	**9.9E-20**	**8**
P62243	ADGYVLEGK	1.181544385	2	2.817324
P62243	IIDVVYNASNNELVR	1.673870514	2	4.377695
P62243	ISSLLEEQFQQGK	1.19174764	2	3.991194
P62243	KYELGRPAANTK	1.165500415	2	3.317575
P62243	LDVGNFSWGSECCTR	1.092619694	2	3.792821
P62243	LTPEEEEILNK	1.055030918	2	3.369033
P62243	NCIVLIDSTPYR	1.230837429	2	3.883613
P62243	YELGRPAANTK	1.191480291	2	2.98953
P62246	**RS15A 40S ribosomal protein S15a**	**1.078856978**	**0.42328**	**3**
P62246	HGYIGEFEIIDDHR	1.082070978	2	4.955499
P62246	MNVLADALK	1.006915418	2	2.343958
P62246	WQNNLLPSR	1.095548812	2	3.000891
P62250	**RS16 40S ribosomal protein S16**	**1.225798467**	**0.74096**	**5**
P62250	ALVAYYQK	1.253690397	2	2.390972
P62250	EIKDILIQYDR	1.063709382	2	2.42965
P62250	GGGHVAQIYAIR	1.501243233	2	3.151434
P62250	LLEPVLLLGK	1.070439254	2	3.048643
P62250	TLLVADPR	1.114747546	2	2.715634
P62260	**1433E 14_3_3 protein epsilon**	**0.948980236**	**0.82466**	**8**
P62260	AAFDDAIAELDTLSEESYK	0.935963005	2	6.356453
P62260	AAFDDAIAELDTLSEESYKDSTLIMQLLR	1.19573193		
P62260	EENKGGEDKLK	1.781516833	2	2.743721
P62260	HLIPAANTGESK	0.967878189	1	3.152375
P62260	IISSIEQK	1.068682132	2	2.705436
P62260	LICCDILDVLDK	1.28014222	2	4.031466
P62260	YLAEFATGNDR	0.887816447	2	2.983791
P62260	YLAEFATGNDRK	0.985554097	2	2.836806
P62271	**RS18 40S ribosomal protein S18**	**0.862118962**	**1.7E-05**	**5**
P62271	AGELTEDEVER	1.158813445	2	3.734788
P62271	RAGELTEDEVER	0.33207228	2	3.485244
P62271	VITIMQNPR	1.043099979	2	2.878926
P62271	VLNTNIDGR	1.145925951	2	2.893923
P62271	YSQVLANGLDNK	1.170381943	2	4.14412
P62278	**RS13 40S ribosomal protein S13**	**1.117377673**	**0.43637**	**4**
P62278	GLAPDLPEDLYHLIK	1.096999709	2	2.972571
P62278	GLSQSALPYR	1.134099133	2	2.638877
P62278	KGLTPSQIGVILR	1.092158199	3	4.102226
P62278	LILIESR	1.687269418	2	2.332903
P62332	**ARF6 ADP_ribosylation factor 6**	**0.903426734**	**0.4066**	**2**
P62332	FNVWDVGGQDK	0.851615901	2	2.818628
P62332	LGQSVTTIPTVGFNVETVTYK	0.976861332	2	3.422548
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.000323431**	**0.00254**	**5**
P62334	ALQSVGQIVGEVLK	1.011872042	2	3.088
P62334	AVASQLDCNFLK	1.479606978	2	2.728567
P62334	EVIELPLTNPELFQR	1.486156586	2	3.398631
P62334	FSEGTSADR	1.021891507	2	2.522824
P62334	HGEIDYEAIVK	0.964622184	2	3.36691
P62425	**RL7A 60S ribosomal protein L7a**	**1.121355007**	**0.42456**	**12**
P62425	AGVNTVTTLVENK	1.109764425	2	4.043626
P62425	AGVNTVTTLVENKK	1.088057508	2	2.857599
P62425	HWGGNVLGPK	0.879767836	1	1.979264
P62425	KVVNPLFEK	1.549211264	2	2.537223

P62425	LKVPPAINQFTQALDR	1.139009029	3	4.502523
P62425	NFGIGQDIQPK	1.074936106	2	3.47069
P62425	QTATQLLK	1.197155397	2	2.382945
P62425	TCTTVAFTQVNSEDK	1.654386147	2	4.132649
P62425	TCTTVAFTQVNSEDKGALAK	2.013576978	2	3.93124
P62425	TNYNDRYDEIR	1.045941871	2	2.448781
P62425	VAPAPAVVK	1.271108543	1	2.162721
P62425	VPPAINQFTQALDR	1.006657344	2	3.522041
P62630	**EF1A1 Elongation factor 1_alpha 1**	**0.94931745**	**0.0001**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.092737619	3	5.326085
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.0531096	4	5.790313
P62630	MDSTEPPYSQK	0.983167156	2	3.581632
P62630	MDSTEPPYSQK+Oxidation(0)	1.082214574		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.050074724	5	6.546849
P62630	RYEEIVK	1.028167422	2	2.612775
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.065910422	3	5.107624
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14)	1.046005245		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8)	1.005401361		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.073130947	2	5.471049
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)	1.052203765		
P62630	YEEIVK	1.169288995	1	2.091926
P62630	YYVTIIDAPGHR	1.078915615	3	3.641772
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.146138676**	**9.9E-20**	**9**
P62632	EHALLAYTLGVK	1.944272341	3	4.062109
P62632	IGGIGTVPVGR	1.282714831	2	3.651441
P62632	MDSTEPAYSEK	2.287549362	2	2.305096
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	0.970693313	3	4.571581
P62632	QLIVGVNK	1.473298825	1	2.771101
P62632	QTVAVGVIK	1.205712519	1	2.245
P62632	STTTGHLIYK	1.07044711	2	3.250636
P62632	THINIVVIGHVDSGK	1.166181684	2	5.463567
P62632	VETGILRPGMVVTFAPVNITTEVK	1.877696459	3	3.592238
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.001805878**	**0.95204**	**2**
P62634	CGETGHVAINCSK	1.02059968	2	4.427821
P62634	CYSCGEFGHIQK	0.966834292	2	3.083513
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.031509827**	**1**	**6**
P62703	FDTGNLCMVTGGANLGR	1.100651382	2	4.970669
P62703	FDTGNLCMVTGGANLGR+Oxidation(7)	0.688009444		
P62703	GIPHLVTHDAR	1.120491992	2	2.608608
P62703	LSNIFVIGK	1.162480726	2	2.874052
P62703	TDITYPAGFMDVISIDK	1.024239191	2	4.585635
P62703	VNDTIQIDLETGK	1.042779109	2	3.755436
P62718	**RL18A 60S ribosomal protein L18a**	**1.167358007**	**0.00024**	**2**
P62718	DLTTAGAVTQCYR	1.482076064	2	3.037
P62718	SSGEIVYCGQVFEKSPLR	1.0750158	2	2.495971
P62752	**RL23A 60S ribosomal protein L23a**	**1.059812329**	**1.5E-07**	**6**
P62752	LAPDYDALDVANK	1.076837212	2	3.569261
P62752	LDHYAIIK	1.228017293	2	2.405123
P62752	LYDIDVAK	1.164677665	1	1.921885
P62752	NKLDHYAIIK	1.274728126	2	2.482819
P62752	VNTLIRPDGEK	1.267642629	2	3.084478
P62752	VNTLIRPDGEKK	1.433816682	2	2.83795
P62755	**RS6 40S ribosomal protein S6**	**1.102681431**	**0.42661**	**6**
P62755	DIPGLTDTTVPR	0.850180132	2	2.336389

P62755	EEAAEYAKLLAK	1.085017146	2	2.398875
P62755	LIEVDDER	1.088552179	2	2.785909
P62755	LNISFPATGCQK	1.067918944	2	3.125343
P62755	MATEVAADALGEEWK	1.188337166	2	4.356373
P62755	MATEVAADALGEEWK+Oxidation(0)	1.133856893		
P62775	**MTPN Myotrophin**	**1.027421833**	**0.99624**	**2**
P62775	GPDGLTALEATDNQAIK	1.10909859	2	3.706726
P62775	HHITPLLSAVYEGHVSCVK	1.010114497	3	3.61731
P62804	**H4 Histone H4**	**1.193949608**	**9.9E-20**	**9**
P62804	DAVTYTEHAK	3.255926374	2	3.091598
P62804	DNIQGITKPAIR	1.27161213	2	3.254271
P62804	ISGLIYEETR	1.137268912	2	3.773031
P62804	KTVTAMDVVYALK	1.035176907	2	3.023273
P62804	RISGLIYEETR	1.013229464	2	2.307495
P62804	TLYGFGG	0.546147588	1	1.95168
P62804	TVTAMDVVYALK	0.945190526	2	4.065288
P62804	TVTAMDVVYALK+Oxidation(4)	0.898864692		
P62804	VFLENVIR	0.888991302	2	3.015818
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**0.810645564**	**0.05455**	**3**
P62815	AVVQVFEGTSGIDAK	0.814568596	2	3.637273
P62815	IYPEEMIQTGISAIDGMNSIAR	0.554291389	2	2.450038
P62815	QIYPPINVLPSLSR	1.010304035	2	2.353211
P62832	**RL23 60S ribosomal protein L23**	**1.23986131**	**0.48762**	**2**
P62832	GSAITGPVAK	1.094175524	2	2.38306
P62832	ISLGLPVGAVINCADNTGAK	1.069741914	2	4.896225
P62853	**RS25 40S ribosomal protein S25**	**1.247155271**	**0.30684**	**2**
P62853	GGDAPAAGEDA	1.211682662	1	2.019867
P62853	LNNLVLFDK	1.249606276	2	3.052199
P62856	**RS26 40S ribosomal protein S26**	**1.119770931**	**0.07858**	**3**
P62856	DISEASVFDAYVLPK	1.44275932	2	3.269862
P62856	FRPAGAAPRPPPKPM	0.694882333	2	2.352892
P62856	NIVEAAAVR	1.112736911	2	2.92795
P62859	**RS28 40S ribosomal protein S28**	**1.54849274**	**0.0006**	**2**
P62859	EGDVLTLLESER	1.645641823	2	3.234688
P62859	VEFMDDTSR	1.453297619	2	2.597485
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**1.036878942**	**0.70725**	**2**
P62870	ADDTFEALR	0.995487666	2	2.583726
P62870	TLGECGFTSQTARPQAPATVGLAFR	1.143024561	3	3.421448
P62890	**RL30 60S ribosomal protein L30**	**1.174217403**	**0.31303**	**2**
P62890	TGVHHYSGNNIELGTACGK	1.184981714	2	5.654829
P62890	VCTLAIIDPGDSDIIR	1.171733308	2	4.219794
P62898	**CYC Cytochrome c_ somatic**	**1.06685941**	**0.99992**	**6**
P62898	ADLIAYLK	0.885498362	2	2.869547
P62898	GITWGEDTLMEYLENPK	1.049246032	2	4.962444
P62898	GITWGEDTLMEYLENPKK	1.037501187	2	4.559816
P62898	KTGQAAGFSYTDANK	0.939745676	2	4.752879
P62898	TGPNLHGLFGR	1.036069318	2	3.266914
P62898	TGQAAGFSYTDANK	1.133847313	2	4.271093
P62902	**RL31 60S ribosomal protein L31**	**1.100341013**	**8.3E-05**	**2**
P62902	NLQTVNVDEN	1.194485459	1	2.527725
P62902	SAINEVVTR	1.118805487	2	2.938576
P62907	**RL10A 60S ribosomal protein L10a**	**0.882283304**	**9.9E-20**	**6**
P62907	AVDIPHMDIEALK	1.070270977	2	2.814103
P62907	AVDIPHMDIEALKK	0.943062331	2	2.603906
P62907	FSVCVLGDQQHCDEAK	1.371396232	2	4.194169

P62907	KYDAFLASESLIK	0.800992994	2	4.006351
P62907	VLCLAVAVGHVK	0.661173391	3	3.895473
P62907	YDAFLASESLIK	1.075773382	2	3.453281
P62909	**RS3 40S ribosomal protein S3**	**1.08188644**	**4.8E-14**	**10**
P62909	AELNEFLTR	1.075864896	2	2.840172
P62909	DEILPTTPISEQK	1.081416406	2	3.703027
P62909	ELAEDGYSGVEVR	2.028198102	2	3.429917
P62909	ELTAVVQK	1.461036122	1	2.077975
P62909	FGFPEGSVELYAEK	1.309334858	2	4.053975
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.040316368	3	4.938177
P62909	GCEVVVSGK	1.193081858	2	2.772482
P62909	GGKPEPPAMPQPVPTA	1.241414541	2	3.54081
P62909	GLCAIAQAESLR	1.072932951	2	3.390461
P62909	TEIIILATR	1.081824948	2	3.178227
P62912	**RL32 60S ribosomal protein L32**	**1.259936948**	**9.9E-20**	**3**
P62912	ELEVLLMCNK	1.402974753	2	2.851244
P62912	GQILMPNIGYGSNK	0.886671317	2	2.932909
P62912	SYCAEIAHNVSSK	1.234769656	2	4.803632
P62914	**RL11 60S ribosomal protein L11**	**0.938925048**	**0.95969**	**2**
P62914	VLEQLTGQTPVFSK	1.068015144	2	4.411545
P62914	YDGIILPGK	1.057811027	2	2.816654
P62919	**RL8 60S ribosomal protein L8**	**1.115441089**	**9.9E-20**	**3**
P62919	ASGNYATVISHNPETK	1.287092678	2	4.673055
P62919	AVVGVVAGGGR	1.119512423	2	3.430963
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	0.776515331	3	4.549391
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.929603538**	**0.98959**	**7**
P62959	AQVAQPGGDTIFGK	0.95684528	2	4.618267
P62959	CAADLGLK	1.104778398	2	2.751844
P62959	CLAFHDISPQAPTHFLVIPK	0.975200799	3	4.2221
P62959	HISQISVADDDDESLLGHLMIVGK	0.862574399	3	6.730711
P62959	IIFEDDR	0.692426633	2	2.349279
P62959	KHISQISVADDDDESLLGHLMIVGK	0.858749114	3	5.558572
P62959	MVVNEGADGGQSVYHIHLHVLGGR	0.974934891	3	4.706339
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.379038271**	**9.9E-20**	**7**
P62961	AADPPAENSSAPEAEQGGAE	0.606979051	2	2.638389
P62961	EDGNEEDKENQGDETQGQQPPQR	1.164019672	3	5.125838
P62961	GAEAANVTGPGGVPVQGSK	1.591726209	2	5.013956
P62961	NEGSESAPEGQAQQR	1.598273763	2	5.307773
P62961	NYQQNYQNSESGEK	1.940094613	2	4.167553
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	1.235183303	3	5.04581
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.616076415	4	4.648341
P62963	**PROF1 Profilin_1**	**0.843200024**	**9.9E-20**	**6**
P62963	CYEMASHLR	0.758853202	2	2.749566
P62963	DSLLQDGEFTMDLR	1.121218891	2	3.313122
P62963	DSPSVWAAVPGK	1.350783932	2	2.935594
P62963	SSFFVNGLTLGGQK	0.841620131	2	4.577405
P62963	STGGAPTFNVTVTMTAK	0.858015684	2	3.025207
P62963	TFVSITPAEVGVLVGK	0.806031333	2	4.78787
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.260460668**	**9.9E-20**	**28**
P63018	ARFEELNADLFR	1.326698947	2	2.980095
P63018	CNEIISWLDK	0.852473037	2	3.059733
P63018	DAGTIAGLNVLR	2.358117247	2	3.742252
P63018	EIAEAYLGK	2.257299695	1	1.965855
P63018	FDDAVVQSDMK	1.182758527	2	3.937093
P63018	FEELNADLFR	1.136656966	2	3.179737

P63018	FELTGIPPAPR	1.487615568	2	3.183309
P63018	GTLDPVEK	1.168003723	1	2.014535
P63018	HWPFMVVNDAGRPK+Oxidation(4)	1.186220914		
P63018	IINEPTAAAIAYGLDK	1.139954859	2	5.129612
P63018	IINEPTAAAIAYGLDKK	1.133091206	2	4.717216
P63018	LLQDFFNGK	1.279363726	2	3.076245
P63018	MKEIAEAYLGK	0.788642452	2	2.883192
P63018	MKEIAEAYLGK+Oxidation(0)	1.395331415		
P63018	NQTAEKEEFEHQQK	1.300729178	2	4.88416
P63018	NQVAMNPTNTVFDAK	1.134543424	2	4.988507
P63018	NQVAMNPTNTVFDAK+Oxidation(4)	1.273197353		
P63018	NSLESYAFNMK	1.348294183	2	3.569918
P63018	QATKDAGTIAGLNVLR	0.817950848	2	2.450734
P63018	RFDDAVVQSDMK	1.272344689	2	3.578502
P63018	SFYPEEVSSMVLTK	1.12283619	2	4.940659
P63018	SFYPEEVSSMVLTK+Oxidation(9)	1.062905807		
P63018	SINPDEAVAYGAAVQAAILSGDK	1.158772849	2	6.059334
P63018	SQIHDIVLVGGSTR	1.238373142	2	4.924558
P63018	STAGDTHLGGEDFDNR	1.359013343	2	4.248702
P63018	TVTNAVVTVPAYFNDSQR	1.134975733	3	4.360116
P63018	VCNPIITK	1.216533226	2	2.301606
P63018	VQVEYKGETK	1.113581229	2	2.55106
P63029	**TCTP Translationally_controlled tumor protein**	**1.776826638**	**3.5E-08**	**3**
P63029	DLISHDELFSDIYK	2.068164725	2	3.755276
P63029	EIADGLCLEVEGK	1.548327344	2	3.338216
P63029	TEGAIDDSLIGGNASAEGPEGEGTESTVVTGVDIVMNHHLQETSFTK	1.468468958	4	4.588511
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**0.893982115**	**0.99173**	**6**
P63036	HYNGEAYEDDEHHPR	1.222674141	3	5.353754
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.145739946	3	4.491005
P63036	NVVHQLSVTLEDLYNGATR	1.207284027	2	4.116804
P63036	QISQAYEVLADSK	1.030334964	2	3.700417
P63036	TIVITSHPGQIVK	0.894571212	2	3.461507
P63036	VNFPENGFLSPDK	1.012504153	2	3.358402
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.136090343**	**1**	**33**
P63039	AAVEEGIVLGGGCALLR	0.933366114	2	5.253572
P63039	ALMLQGVDLLADAVAVTMGPK	0.638639343	3	5.283134
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(2)	0.794770357		
P63039	CEFQDAYVLLSEK	0.891146859	2	4.896836
P63039	CIPALDSLKPANEDQK	0.900365367	2	3.654528
P63039	DIGNIISDAMK	0.868843858	2	3.221639
P63039	GVMLAVDAVIAELK	0.998401812	2	3.839546
P63039	GVMLAVDAVIAELKK	1.024640275	2	4.479409
P63039	GYISPYFINTSK	1.22701273	2	3.029247
P63039	IGIEIIK	0.941545863	2	2.589458
P63039	ILQSSSEVGYDAMLGDFVNMVEK	1.021543004	2	4.979472
P63039	IQEITEQLDITTSEYEK	0.986943988	2	5.939842
P63039	IQEITEQLDITTSEYEKEK	0.924960514	2	5.061436
P63039	ISSVQSIVPALEIANAHR	1.090908538	2	4.255525
P63039	KISSVQSIVPALEIANAHR	0.838850644	3	4.550709
P63039	KPLVIIAEDVDGEALSTLVLNR	0.924151549	2	6.136534
P63039	LSDGVAVLK	1.067738277	2	3.098129
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.029091285	2	6.636322
P63039	NAGVEGSLIVEK	1.022658012	2	3.584287
P63039	QSKPVTTPEEIAQVATISANGDK	0.985803281	2	3.581943
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	0.875064345	3	4.842977
P63039	RGVMLAVDAVIAELKK	0.828232724	3	5.770705

P63039	TALLDAAGVASLLTTAEAVVTEIPK	0.957668334		
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	0.997979973	3	5.031567
P63039	TLNDELEIIEGMK	0.900653883	2	4.659017
P63039	TLNDELEIIEGMK+Oxidation(11)	0.955933931		
P63039	TVIIEQSWGSPK	0.958116381	2	4.378443
P63039	VGEVIVTK	0.940792426	2	2.938201
P63039	VGEVIVTKDDAMLLK	1.090595434	2	2.50118
P63039	VGGTSDVEVNEK	1.018846411	2	3.820652
P63039	VGGTSDVEVNEKK	1.10178638	2	3.518459
P63039	VGLQVVAVK	1.06141352	2	3.282634
P63039	VTDALNATR	0.969566213	2	3.571726
P63102	**1433Z 14_3_3 protein zeta/delta**	**0.983141461**	**0.97204**	**9**
P63102	DICNDVLSLLEK	1.631639263	3	3.680529
P63102	FLIPNASQPESK	0.990698608	2	3.36873
P63102	GIVDQSQQAYQEAFEISK	0.988731832	2	5.748536
P63102	GIVDQSQQAYQEAFEISKK	1.010795623	2	2.62193
P63102	KGIVDQSQQAYQEAFEISK	1.051697696	2	6.013041
P63102	SVTEQGAELSNEER	1.122496584	2	5.56115
P63102	TAFDEAIAELDTLSEESYK	1.000769933	2	5.686096
P63102	YDDMAACMK	1.021355256	2	2.451387
P63102	YLAEVAAGDDKK	0.964976613	2	3.611005
P63159	**HMGB1 High mobility group protein B1**	**0.982958647**	**1**	**4**
P63159	GEHPGLSIGDVAK	1.039851389	2	3.117338
P63159	IKGEHPGLSIGDVAK	0.976556674	2	3.950677
P63159	KHPDASVNFSEFSK	1.030366882	2	4.289649
P63159	LGEMWNNTAADDKQPYEK+Oxidation(3)	0.936859548		
P63174	**RL38 60S ribosomal protein L38**	**1.171222489**	**2.1E-06**	**4**
P63174	IEEIKDFLLTAR	1.016368082	3	3.361184
P63174	KIEEIKDFLLTAR	1.106005902	2	4.108852
P63174	YLYTLVITDK	1.397258385	2	2.896703
P63174	YLYTLVITDKEK	1.307506734	2	2.708998
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.2318204**	**0.00016**	**12**
P63245	DETNYGIPQR	1.830025306	2	2.940192
P63245	DGQAMLWDLNEGK	1.272061073	2	2.969844
P63245	FSPNSSNPIIVSCGWDK	1.159487174	2	4.112599
P63245	GHNGWVTQIATTPQFPDMILSASR	0.891374746	3	4.168629
P63245	HLYTLDGGDIINALCFSPNR	1.117635104	2	5.901755
P63245	IIVDELKQEVISTSSK	1.017340878	2	4.346048
P63245	LWDLTTGTTTR	0.920439921	2	2.589536
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.102622918	3	5.536952
P63245	VWNLANCK	1.161840242	2	2.67961
P63245	VWQVTIGTR	1.185227044	2	2.736893
P63245	YTVQDESHSEWVSCVR	1.243065664	2	4.654795
P63245	YWLCAATGPSIK	1.197976328	2	2.844509
P63259	**ACTG Actin_ cytoplasmic 2**	**0.945804764**	**0.9983**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.471165565	3	4.768364
P63259	DLYANTVLSGGTTMYPGIADR	1.290070386	2	6.086339
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13)	1.155938712		
P63259	GYSFTTTAER	0.932686888	2	3.353513
P63259	KDLYANTVLSGGTTMYPGIADR	0.934829686	2	6.449868
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.988714065		
P63259	QEYDESGPSIVHR	0.82622632	3	3.422786
P63259	VAPEEHPVLLTEAPLNPK	0.955979628	3	4.739213
P63324	**RS12 40S ribosomal protein S12**	**1.158440876**	**9.1E-06**	**4**
P63324	KVVGCSCVVVK	1.223603928	2	3.379607
P63324	LGEWVGLCK	0.999696317	2	2.847631

P63324	QAHLCVLASNCDEPMYVK	1.09898146	3	3.552733
P63324	VVGCSCVVVK	1.213299658	2	3.238082
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**1.095619791**	**0.26197**	**3**
P63331	CGNQAAIMELDDTLK	0.964053331	2	2.771279
P63331	NVVTIFSAPNYCYR	0.942113405	2	2.326139
P63331	YSFLQFDPAPR	1.106168837	2	3.419724
P67779	**PHB Prohibitin**	**1.003914961**	**1**	**12**
P67779	AAELIANSLATAGDGLIELR	0.939821828	3	4.217194
P67779	AAIISAEGDSK	1.057035321	2	2.481286
P67779	DLQNVNITLR	1.056672887	2	3.002888
P67779	FDAGELITQR	0.900361808	2	3.540552
P67779	FGLALAVAGGVVNSALYNVDAGHR	0.960725527	3	3.53134
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.037336594	4	4.84002
P67779	IYTSIGEDYDER	0.97682632	2	3.367364
P67779	KLEAAEDIAYQLSR	0.972174423	2	4.813692
P67779	NITYLPAGQSVLLQLPQ	0.981305635	3	3.430168
P67779	NVPVITGSK	0.944253378	1	2.277607
P67779	QVSDDLTER	1.048286347	2	2.416462
P67779	VLPSITTEILK	0.882100496	2	2.314491
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.008444526**	**1**	**3**
P68037	ADLAEEYSK	1.004097342	2	2.63813
P68037	GQVCLPVISAENWKPATK	0.984017493	2	3.764193
P68037	TDQVIQSLIALVNDPQPEHPLR	0.989351624	2	5.153215
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.177372575**	**0.1365**	**3**
P68101	AGLNCSTETMPIK	1.176393579	2	3.406359
P68101	TEGLSVLNQAMAVIK	1.030573517	2	3.985758
P68101	VVTDTDETELAR	1.173347922	2	3.305271
P68136	**ACTS Actin_ alpha skeletal muscle**	**1.82610607**	**1.3E-09**	**16**
P68136	AGFAGDDAPR	1.255986091	2	3.356367
P68136	AVFPSIVGRPR	1.133307313	2	2.6985
P68136	DLYANNVMSGGTTMYPGIADR	3.076201345	2	4.663561
P68136	DSYVGDEAQSK	3.434310888	2	3.540015
P68136	EITALAPSTMK	1.384855283	2	3.137859
P68136	EITALAPSTMK+Oxidation(9)	1.492574451		
P68136	GYSFVTTAER	1.644853268	2	3.958458
P68136	IWHHTFYNELR	1.502899673	2	2.690291
P68136	KDLYANNVMSGGTTMYPGIADR	2.198040214	2	5.034206
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14)	1.466391006		
P68136	QEYDEAGPSIVHR	2.617538352	2	3.163333
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	2.974348855	3	6.811887
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28)	1.323393536		
P68136	VAPEEHPTLLTEAPLNPK	1.68656183	2	4.392037
P68136	YPIEHGIITNWDDMEK	1.193974038	2	4.450612
P68136	YPIEHGIITNWDDMEK+Oxidation(13)	0.775739648		
P68255	**1433T 14_3_3 protein theta**	**0.965668856**	**1**	**6**
P68255	AVTEQGAELSNEER	0.869993584	2	4.632949
P68255	SICTTVLELLDK	1.035498534	2	3.100723
P68255	TAFDEAIAELDTLNEDSYK	0.882606182	2	4.80388
P68255	VISSIEQK	0.937676151	2	3.254664
P68255	YLAEVACGDDR	1.003844523	2	3.001915
P68255	YLIANATNPESK	0.97381279	2	2.822546
P68511	**1433F 14_3_3 protein eta**	**1.338751316**	**0.00912**	**4**
P68511	AVTELNEPLSNEDR	1.374785102	2	4.666099
P68511	ELETVCNDVLALLDK	0.910835104	2	3.471905

P68511	NCNDFQYESKVFYLK	1.078293962	2	2.347584
P68511	NSVVEASEAAYK	1.335713937	2	3.215416
P69897	**TBB5 Tubulin beta_5 chain**	**1.03091529**	**0.92259**	**3**
P69897	ALTVPELTQQVFDAK	0.879805188	2	3.496055
P69897	ISVYYNEATGGK	1.058071296	2	2.942208
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	0.96480677	2	5.354481
P70372	**ELAV1 ELAV_like protein 1**	**1.100575403**	**0.74014**	**2**
P70372	TNLIVNYLPQNMTQEELR	0.982841022	2	3.423189
P70372	VLVDQTTGLSR	1.128249382	2	2.41271
P70470	**LYPA1 Acyl_protein thioesterase 1**	**0.984351775**	**0.98044**	**2**
P70470	ASFSQGPINSANR	0.828881227	2	2.944511
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	0.985061712	3	4.041405
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.823394509**	**9E-09**	**11**
P70473	ADVLLEPFR	0.7250223	2	3.362092
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	0.659171482	4	5.201691
P70473	DYGFSQEEIHQLHSDR	0.920147211	2	4.859573
P70473	GLGLESEELPSQMSIEDWPEMK	0.673852077	3	4.846204
P70473	GQNLLDGGAPFYTTYK	0.793266359	2	5.439533
P70473	GSFITDEEQHACPRPAPQLSR	0.898264411	3	3.852139
P70473	LGSVNHPSHLAR	0.80573923	2	3.395815
P70473	LSGFGQSGIFSK	0.882498974	2	3.040418
P70473	RDPSVGEHTVEVLK	0.748414098	3	4.396935
P70473	TADGEFMAVGAIEPQFYTLLLK	0.949710791	3	4.134341
P70473	TQAMGLWAQPR	0.612264063	2	3.131624
P70550	**RAB8B Ras_related protein Rab_8B**	**1.165794241**	**0.16386**	**2**
P70550	LLLIGDSGVGK	1.154761353	2	2.78506
P70550	NIEEHASSDVER	1.392687406	2	2.307937
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**0.609241704**	**0.00025**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.661612772	3	4.136862
P70552	VLGNNFYEYYVNDPPR	0.58680251	2	3.368034
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.999178744**	**0.9995**	**6**
P70580	FYGPEGPYGVFAGR	0.908611879	2	4.010903
P70580	GDQPGASGDNDDDEPPPLPR	1.114855926	2	4.976551
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.16208794	3	5.030583
P70580	KFYGPEGPYGVFAGR	1.026763777	2	3.61088
P70580	RYDGVQDPR	0.903270227	1	2.152603
P70580	YDGVQDPR	1.053102484	2	2.837738
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.072994414**	**0.08817**	**8**
P70584	ASSTCQLTFENVK	1.148079758	2	3.288247
P70584	FAQEQIAPLVSTMDENSK	1.079886096	2	4.963452
P70584	IFDFQGLQHQVAHVATQLEAAR	1.022390595	3	6.144009
P70584	IGTIYEGTSNIQLNTIAK	1.049588459	2	4.556328
P70584	KFAQEQIAPLVSTMDENSK	0.846024757	2	5.804394
P70584	SGNYYVINGSK	0.92369228	2	2.883802
P70584	VDASVALLCDIQNTVINK	2.706199421	2	4.921355
P70584	YYASEVAGLTTSK	1.071020437	2	4.13797
P70587	**LRRC7 Leucine_rich repeat_containing protein 7**	**0.925938119**	**0.94426**	**2**
P70587	KESTDESEVDK	1.005395936	2	2.371924
P70587	SREQQPYEGNINK	0.924909006	2	2.487029
P70615	**LMNB1 Lamin_B1**	**0.798532653**	**3.7E-07**	**5**
P70615	ALYETELADAR	0.981225486	2	3.075354
P70615	KESDLSGAQIK	0.955942806	2	2.531164
P70615	LSSEMNTSTVNSAR	0.799762841	2	3.783771

P70615	NQNSWGTGEDVK	0.78761948	2	3.285865
P70615	SLEGDLEDLKDQIAQLEASLSAAK	0.727479944	3	4.62332
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**0.870332365**	**0.88657**	**2**
P70694	REDIFYTSK	0.884169736	2	3.131126
P70694	SIGVSNFNR	1.107885486	2	2.376778
P70712	**KYNU Kynureninase**	**0.896891785**	**0.98594**	**9**
P70712	IATELNCDPTDER	1.164863275	2	3.587585
P70712	IGAYGHEVGK	0.998316614	2	2.839433
P70712	LLTAILDSTERN	1.029344357	2	3.290477
P70712	LQLIPGVNGFR	0.883407301	2	2.524788
P70712	MEDILEVIEK	0.900353504	2	2.588513
P70712	TYLEEELDK	0.893121529	1	2.201579
P70712	TYLEEELDKWAK	0.629233478	2	2.55421
P70712	VAPVPLYNSFHDVYK	0.824168504	2	2.946423
P70712	YLNSGAGGLAGAFIHEK	1.991879196	2	4.307238
P80067	**CATC Dipeptidyl peptidase 1**	**0.93078782**	**0.28084**	**6**
P80067	GINFVSPVR	0.832605132	2	3.120631
P80067	GTDECAIESIAMAAIPIPK	0.886397712	3	4.523062
P80067	NQESCGSCYSFASLGMLEAR	0.763716086	2	3.400318
P80067	NSWGSQWGESGYFR	0.93516635	2	3.612549
P80067	RGTDECAIESIAMAAIPIPK	0.80880899	2	3.884704
P80067	YAQDFGVVEENCFPYTATDAPCKPK	0.845699008	3	5.995942
P80254	**DOPD D_dopachrome decarboxylase**	**2.306865831**	**1.2E-05**	**4**
P80254	FFPLEPWQIGK	1.448575291	2	2.443477
P80254	FLTEELSLDQDR	1.457057834	2	3.868703
P80254	LCAATATILDKPEDR	2.356226623	2	4.249262
P80254	STEPCAHLLISSIGVVGTAEQNR	1.765815625	2	5.097519
P80299	**HYES Epoxide hydrolase 2**	**0.98007776**	**0.38915**	**2**
P80299	ATEMGGILVGTPEDPK	0.797372263	2	3.675416
P80299	TEIQNPSVTSK	1.043105791	2	3.139398
P80313	**TCPH T_complex protein 1 subunit eta**	**1.231780746**	**0.23877**	**5**
P80313	ATISNDGATILK	1.157762207	2	2.597908
P80313	GGAEQFMEETER	1.140301606	2	2.978167
P80313	LLDVVHPAAK	1.239628903	2	2.571696
P80313	QLCDNAGFDATNILNK	1.01272811	2	3.29668
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.134220424	2	4.824515
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.101092078**	**0.85996**	**8**
P80317	ALQFLEQVK	1.186881449	2	2.799048
P80317	DGNVLLHEMQIQHPTASLIAK	1.045491301	3	4.370374
P80317	GIDPFSLDALAK	1.11888894	2	2.493104
P80317	NAIDDGCVVPGAGAVEVALAEALIK	0.896472786	3	4.183879
P80317	QADLYISEGLHPR	1.234509527	2	2.389749
P80317	TEVNSGFFYK	1.165585438	2	2.587647
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.005281241	2	5.435468
P80317	VLAQNSGFDLQETLVK	0.892176233	2	3.982014
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**1.130694759**	**0.69507**	**6**
P81155	LTFDTTFSPNTGK	1.146293846	2	3.205997
P81155	SNFAVGYR	1.175675044	2	2.440187
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.039467501	3	3.332845
P81155	VNNSSLIGVGYTQTLRPGVK	1.321150673	2	3.789334
P81155	WCEYGLTFTEK	1.16379712	2	2.609626
P81155	YQLDPTASISAK	1.074159082	2	3.235001
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.066908647**	**0.78836**	**17**
P82995	DQVANSAFVER	1.261722732	2	2.548248
P82995	ELHINLIPNKQDR	1.216264325	2	3.237441
P82995	ELISNSSDALDK	1.343200756	2	2.801405

P82995	FYEQFSK	0.960811879	1	2.258059
P82995	HGLEVIYMIEPIDEYCVQQLK	1.132340155	3	3.479845
P82995	HIYFITGETK	0.991033903	2	2.734051
P82995	HLEINPDHSIIETLR	1.036845465	2	4.453443
P82995	HSQFIGYPITLFVEK	1.726192021	2	3.751134
P82995	LGIHEDSQNR	0.898522241	3	3.456845
P82995	NPDDITNEEYGEFYK	1.193646579	2	5.141033
P82995	RAPFDLFENR	1.015302176	2	2.414553
P82995	SLTNDWEEHLAVK	0.997097811	2	4.009841
P82995	TDTGEPMGR	1.050382585	2	2.536737
P82995	TDTGEPMGR+Oxidation(6)	1.09330633		
P82995	TLTIVDTGIGMTK	0.982615738	2	4.082806
P82995	TLTIVDTGIGMTK+Oxidation(10)	1.012793231		
P82995	YYTSASGDEMVSLK	1.078012673	2	3.855253
P83732	**RL24 60S ribosomal protein L24**	**1.048463969**	**0.60559**	**3**
P83732	AITGASLADIMAK	1.047550843	2	4.100321
P83732	CESAFLSK	1.206572881	2	2.301211
P83732	VELCSFSGYK	1.126292137	2	2.373016
P83868	**TEBP Prostaglandin E synthase 3**	**1.258245097**	**0.01176**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.371307427	3	3.456263
P83868	LTFSCLGGSDNFK	1.258180536	2	2.963548
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.075745984**	**0.82758**	**2**
P83941	AMLSGPGQFAENETNEVNFR	0.957292049	2	4.484667
P83941	TYGGCEGPDAMYVK	1.118777497	2	2.820043
P84082	**ARF2 ADP_ribosylation factor 2**	**1.011656556**	**1**	**2**
P84082	NISFTVWDVGGQDK	0.871640143	2	4.573415
P84082	QDLPNAMNAAEITDK	1.014824737	2	4.238098
P84083	**ARF5 ADP_ribosylation factor 5**	**0.937972355**	**0.9994**	**3**
P84083	DAVLLVFANK	1.252304181	2	3.551579
P84083	QDMPNAMPVSELTDK	1.019696694	2	3.038013
P84083	VQESADELQK	0.964166264	2	3.120927
P84089	**ERH Enhancer of rudimentary homolog**	**1.102368699**	**0.93451**	**2**
P84089	ADTQTYQPYNK	1.240764856	2	2.845531
P84089	TYADYESVNECMEGVCK	1.0432791	2	4.376767
P84100	**RL19 60S ribosomal protein L19**	**0.786696744**	**0.00037**	**2**
P84100	LLADQAEAR	1.231605597	2	3.25748
P84100	VWLDPNETNEIANANSR	1.126351108	2	5.359803
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**0.948262726**	**0.7383**	**2**
P84104	AFGYYGPLR	0.948491816	2	2.326913
P84104	VYVGNLGNNGNK	0.941652483	2	2.312838
P84245	**H33 Histone H3.3**	**0.874393623**	**0.66997**	**5**
P84245	DIQLAR	1.584581648	1	1.954342
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	0.878367892	4	6.475613
P84245	RVTIMPKDIQLAR+Oxidation(4)	0.916650907		
P84245	STELLIR	0.934903222	2	2.396577
P84245	YRPGTVALR	0.976355533	2	2.390287
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.023208866**	**0.96495**	**4**
P84817	FQSEQAAGSVSK	1.043438044	2	2.661446
P84817	GIVLLEELLPK	0.888672106	2	2.47952
P84817	GLLQTEPQNNQAK	1.08678093	2	3.404764
P84817	KFQSEQAAGSVSK	0.918983611	2	4.3534
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.989237915**	**0.33173**	**16**
P85834	AEAGDNLGALVR	0.942962107	2	3.889097
P85834	DKPHVNVGTIGHVDHGK	1.684056544	3	3.862269
P85834	DLEKPFLLPVESVYSIPGR	1.3072488	2	4.01343
P85834	ELLTEFGYKGEETPVIVGSALCALEQR	0.915729326	3	3.830712

P85834	GDECELLGHNK	1.066863579	2	2.598526
P85834	GEETPVIVGSALCALEQR	0.942244344	2	4.514171
P85834	GITINAAHVEYSTAAR	2.356226623	2	3.56819
P85834	GTVVTGTLER	1.000243782	2	2.818779
P85834	HYAHTDCPGHADYVK	0.837237881	2	4.252855
P85834	KGDECELLGHNK	0.834147648	2	3.707256
P85834	KYEEIDNAPEER	0.962347037	2	3.770941
P85834	LLDAVDTYIPVPTR	0.833262624	2	3.810656
P85834	QIGVEHVVVYVNK	0.939168082	2	2.6654
P85834	TIGTGLVTDVPAMTEEDK	0.927425156	2	3.254942
P85834	TIGTGLVTDVPAMTEEDKNIK	2.256630223	2	3.503105
P85834	YEEIDNAPEER	0.991631451	2	3.4091
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.007560574**	**1**	**10**
P85968	AGQAVDDFIEK	0.996810013	2	3.314199
P85968	CLSSLKEER	0.975975775	2	2.625907
P85968	FQDTDGKELLPK	1.170300715	2	2.954648
P85968	GILFVGSGVSGGEEGAR	1.018511846	2	5.384297
P85968	HEMLPANLIQAQR	0.811744742	2	2.704418
P85968	LVPLLDTGDIIIDGGNSEYR	1.016381898	2	5.130198
P85968	NPELQNLLLDDFFK	0.912961948	2	4.459496
P85968	SAVDDCQDSWR	1.143220844	2	3.109797
P85968	VGTGEPCCDWVGDEGAGHFVK	0.879463831	2	4.455013
P85968	YGPSLMPGGNK	1.010095926	2	2.31253
P85971	**6PGL 6_phosphogluconolactonase**	**1.146838443**	**0.79949**	**5**
P85971	DLPAATAPAGPASFAR	1.147535374	2	3.196603
P85971	ILEDQESALPAAMVQPR	0.989086401	2	4.751103
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	0.906270736	2	4.655992
P85971	TGALCWFLDEAAAR	0.891656829	2	4.000999
P85971	WTLGFCDER	1.016158282	2	2.582484
P85972	**VINC Vinculin**	**0.8895162**	**4.2E-05**	**8**
P85972	AQQVSQGLDVLTAK	1.044146065	2	3.984172
P85972	AVAGNISDPGLQK	0.970663754	2	3.106084
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.805595072	3	5.229705
P85972	QVATALQNLQTK	0.982073725	2	2.989647
P85972	SLLDASEEAIKK	0.998104766	2	2.379302
P85972	STVEGIQASVK	0.910678083	2	2.444925
P85972	VDQLAAQLADLAAR	0.810021354	2	3.093156
P85972	VLQLTSWDEDAWASK	0.867188316	2	2.479235
P85973	**PNPH Purine nucleoside phosphorylase**	**0.855314135**	**0.95593**	**11**
P85973	ASHQEVLEAGK	0.975656213	2	3.443137
P85973	DHINLPGFCGQNPLR	1.076346169	3	4.061932
P85973	ELQEGTYIMSAGPTFETVAESCLLR	0.940677727	2	5.300961
P85973	FEVGDIMLIR	0.853820825	2	3.277911
P85973	HRPQVAVICGSGLGGLTAK	1.012582618	3	6.021018
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.043440214	3	4.416514
P85973	MLGADAVGMSTVPEVIVAR	0.857401918	2	4.660902
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0)	0.883023642		
P85973	VFGFSLITNK	0.807026408	2	3.361583
P85973	VFHLLGVDTLVVTNAAGGLNPK	0.901711457	2	5.22585
P85973	VVMDYNNLEK	0.843845833	2	2.637196
P86048	**RL10L 60S ribosomal protein L10_like**	**0.975782216**	**0.28529**	**5**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	0.729437709	3	4.144639
P86048	GAFGKPQGTVAR	1.187101058	2	2.540185
P86048	MLSCAGADR	1.044495674	2	2.322023
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.206284056	3	4.983397
P86048	VHIGQVIMSIR	0.95230223	2	2.800275

P86252		**0.942482888**	**0.74793**	**4**
P86252	AAGSLLTDECR	0.957163536	2	3.063311
P86252	ADSAEYSVMTTGGQSSAK	2.678410575	2	4.037457
P86252	AEVSELPSVVR	0.863426107	2	2.808608
P86252	AISGDLTAEEELER	0.852616917		
P86252	ALLTPVAIAAGR	0.996116026	2	2.515415
P86252	AMQEINYGPSPDNSIKLVR+Oxidation(1)	0.895231131		
P86252	ASMMGQRASLLTAR+Oxidation(2)	0.829371667		
P86252	AVAENQPFLIEAMTYR	1.098339612	2	4.512483
P86252	AVEIAHALCLTERQIK	0.836701185		
P86252	DQMVKNNHFTLK+Oxidation(2)	0.970026939		
P86252	EELEKMK	0.846016494	1	2.121805
P86252	EIAGATPYITAAEEK	1.363995336	2	3.062317
P86252	EKMNKPELFNGGEK+Oxidation(2)	1.13671599		
P86252	ELDSITPDITPGWK	0.845057753	2	3.436802
P86252	FFRPHFLQAPGDLTVQEGK	0.878579385		
P86252	FKLINSTNIR	0.808984383		
P86252	GENLVSMTVEGPPPK	1.440230306		
P86252	GIEQAVQSHAVAEEEAR	1.229711726	2	4.984147
P86252	GNIYSLNEGYAK	0.989239681	2	4.063055
P86252	GVYAVGDVCGK	0.97528908	1	2.256901
P86252	HLQTYGEHYPLDHFDK	0.585139031	3	3.382231
P86252	HVIHTVGPIAVGQPTASQAAELR	1.009584639	3	4.892754
P86252	IGHHSTSDDSSAYR	1.402129059	3	4.058208
P86252	KAMQEINYGPSPDNSIKLVR	0.813025352		
P86252	KGNIYSLNEGYAK	1.00396404	2	3.924677
P86252	KHTLIIEGATK	6.380388303	2	2.65277
P86252	KLQHELEEAEER	1.634400315	2	3.797122
P86252	KVVSDLDVIMSHLK	0.837706309		
P86252	LEFIQPNVISGIPIYR	0.870634776	2	2.797159
P86252	LFEEQLK	0.846016494		
P86252	LGDAVEQGVINNSVLGYFIGR	0.772798237	2	4.409735
P86252	LMQVNDTLTSEDAGLR	1.056055021		
P86252	LNNIYQNNLTK	1.1723929	2	2.995801
P86252	LQHELEEAEER	3.435080516	2	3.616211
P86252	MNLQDELDELK	0.989143131	2	2.48876
P86252	MNLQDELDELK+Oxidation(0)	0.90110873		
P86252	MQQVEASLQPETLK+Oxidation(0)	0.844350723		
P86252	NNGYAISTPTSEQYR	0.855205934	2	3.662744
P86252	QGQASAQGRAGSQGQAQGR	0.738097916		
P86252	QGQIINPSEDPHLPQEEVLK	0.833334581	2	2.993174
P86252	QTCLKTVVLLTDNK	0.538840229		
P86252	QTITAQNAAVQAVK	1.187804406	2	4.087745
P86252	QYLLNQGWWDEEQEK	1.042380076	2	3.815337
P86252	RAALQAEIEELR	2.315686808	2	3.95424
P86252	SEIQAEQDR	1.202505658	2	2.764528
P86252	SLEDALNQTATVTR	0.994144011	2	4.29333
P86252	SSSLLAKSPSK	0.712920514		
P86252	TLHVEEVVPSVIEPSFGLGR	1.091282398	3	3.684277
P86252	TSSAEMPTIPLGSAVEAIR	1.006952211	2	4.047329
P86252	TVNVVQFEPNK	1.137597288	2	2.448723
P86252	VDDSSGSIGR	1.379482873	2	2.619897
P86252	VDGNDVFAVYNATK	1.120701798	2	3.957363
P86252	VMEAFEQAER	0.894496167	2	3.415471
P86252	VVSQYHELVVQAR	2.983807429	2	3.593987
P86252	YNENHQHGK	1.075990455		
P86252	YSTSSSSGVTAGK	0.974945767	2	2.562317

P86252s	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	1.050785774	3	3.802206
P86252s	LEGDLKDLELQADSAVKGR	0.761724518		
P86252s	LIDDYGVEEEPAELPEGTSLTVDNKR	1.001378302	3	4.302517
P86252s	VASDAQLELDKLDGELKK	1.106335182		
P97384	**ANX11 Annexin A11**	**1.084889586**	**0.88375**	**2**
P97384	GFGTDEQAIIDCLGSR	1.113208741	2	4.320592
P97384	SELDLLDIR	0.866707692	2	2.617257
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**0.916557914**	**0.77877**	**7**
P97519	GFEEAVAAGAK	1.106399288	2	3.594613
P97519	GYVSCALGCPYEGK	0.974196194	2	4.214695
P97519	KNVNCSIEESFQR	1.161705377	2	3.293892
P97519	LIDMLSEAGLPVIEATSFVSPK	0.797535081	3	4.579722
P97519	LLEAGDFICQALNR	1.14272912	2	4.501926
P97519	NVNCSIEESFQR	1.099197379	2	3.655052
P97519	WVPQMADHSDVLK	0.968743559	2	2.797295
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**0.870103856**	**0.97475**	**7**
P97521	CLLQIQASSGK	0.727191128	1	2.917691
P97521	EEGVTSLYK	1.003679841	1	2.024671
P97521	KLYQEFGIR	1.036314505	2	2.533414
P97521	LQTQPPSLPGQPPMYSGTIDCFR	0.88728364	2	4.041005
P97521	LYQEFGIR	0.877946921	2	2.60825
P97521	SVHDLSVPR	0.877145151	2	2.594274
P97521	YSGTLDCAK	0.811792141	2	2.345995
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.032723104**	**0.80709**	**14**
P97524	GEVGLLICK	1.01050043	2	2.62281
P97524	ITELTPFFGYAGGK	1.113747408	2	2.924391
P97524	SEVTFTTPAVYIYTSGTTGLPK	1.485513164	2	2.995711
P97524	SLLHCFQCCGAK	0.972546355	2	2.73525
P97524	TILHVFLEQAR	0.826229712	3	3.314967
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	1.038169521	3	4.804519
P97524	TYVPMTEDIYNAIIDK	1.086391683	3	4.141877
P97524	VDGVSADPIPESWR	1.490928526	2	3.059649
P97524	VLLASPELHEAVEEVLPTLK	1.023565102	3	4.220395
P97524	VTLMEEGFNPSVIK	0.980779951	2	3.992028
P97524	YDVEKDEPVR	0.941553207	2	3.115143
P97524	YDVEKDEPVRDANGYCIK	1.339226582	3	3.612456
P97524	YLCNTPQKPNDR	1.112930591	2	3.058653
P97524	YNATVIQYIGELLR	1.122333638	2	4.166836
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.085061076**	**0.99983**	**9**
P97532	AFGHHSVSLLDGGFR	1.207698182	2	3.540091
P97532	ALVSAQWVAEALK	1.068134454	2	4.239162
P97532	AQPEHVISQGR	1.005540003	2	2.849282
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.084764036	3	6.738776
P97532	FQGTQPEPR	1.035929944	2	2.820221
P97532	LLDASWYLPK	1.101701871	2	3.828099
P97532	SPSEPAEFCAQLDPSFIK	0.307419802	2	3.001405
P97532	THEDILENLDAR	1.073355623	2	3.252385
P97532	YWLSQNLPISSGK	0.969567351	2	3.75554
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.015022075**	**0.69343**	**8**
P97536	AADIDQEVK	1.157822996	2	2.487307
P97536	EGPAVVGQFIQDVK	1.053519372	2	3.104601
P97536	FTISDHPQPIDPLLK	0.877052359	2	2.399117
P97536	ITSEALLVTQQLVK	0.918827652	2	2.703396
P97536	LTLIDPETLLPR	1.086014876	2	2.801983

P97536	SVILEAFSSPSEEVK	1.160891413	2	2.764555
P97536	TLEDPDLNVR	1.048496978	2	2.308181
P97536	TYIQCIAAISR	0.943622408	2	2.959081
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**0.985648152**	**0.98738**	**20**
P97562	ATASCTYEGENTVLYLQVAR	1.0827935	2	3.932951
P97562	ATFADFCAQGAEICR	1.206054188	2	4.969956
P97562	CSAQTAADFR	1.185013989	2	2.989659
P97562	DFSLLPELHALSTGMK	0.894329373	2	2.378968
P97562	EAFLDLLPLIR	1.081924294	2	2.878322
P97562	EELYEDAIQK	2.260355264	2	2.367866
P97562	FAEVLPDGTYQR	0.680020678	2	2.753202
P97562	HSPSFSVER	0.97230907	2	2.410936
P97562	ILEYQTQQQK	0.98752892	2	3.814326
P97562	KVESIIQSDPVFNLK	0.934319586	2	4.956357
P97562	LDKEPEIQR	1.075009389	2	2.698369
P97562	LFEWAQK	0.854829519	2	2.455192
P97562	LGTPQSNYLGMLVTR	0.978128623	2	3.51787
P97562	LTNILDGGLPNTVLR	1.03595774	2	4.660285
P97562	MGLEHIDNGFLQLNHVR	1.091132477	3	4.276673
P97562	SGVDQHDAWNQTTVIHLQAAK	0.927357132	3	6.127796
P97562	SLEDHTPLPGITVGDIGPK	0.945897851	3	4.6145
P97562	SLGSDEQIAK	1.029123287	2	2.630379
P97562	VESIIQSDPVFNLK	1.023286939	2	4.25094
P97562	VLDGNVNLSLHGVAMNAIR	0.775349528	2	3.217199
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.126434655**	**0.00321**	**3**
P97576	ALADTENLR	1.08007633	2	2.652947
P97576	DLLEVADILEK	1.902666177	2	3.208895
P97576	TLRPALVGVVK	1.20382419	2	2.532409
P97584	**PTGR1 Prostaglandin reductase 1**	**0.876793362**	**0.00488**	**5**
P97584	ALTDLMNWVSEGK	0.819098869	2	4.106936
P97584	GGETVLVNAAAGAVGSVVGQIAK	0.959074493	2	5.645947
P97584	HFEGFPTDSNFELR	0.841292986	2	3.738657
P97584	TGPCPPGPSPEVIIYQQLR	0.979252692	2	4.031363
P97584	YHEYITEGFEK	0.906708396	2	2.835616
P97608	**OPLA 5_oxoprolinase**	**1.171960073**	**0.74933**	**11**
P97608	AGDFGAAFVER	0.9843608	2	3.01052
P97608	GGPVTVTDANLVLGR	1.050185439	2	2.737121
P97608	GHTACADAYLTPTIQR	0.834250527	2	3.424024
P97608	GSILDPSPEAAVVGGNVLTSQR	1.190196106	2	4.799467
P97608	ISVGAEGPSMADTR	0.963252118	2	2.705291
P97608	ISVGAEGPSMADTR+Oxidation(9)	1.067796364		
P97608	ITDPEILESR	0.594336414	2	2.644432
P97608	LLSEDPANYADAPTEGIR	0.932042041	2	4.303636
P97608	SGLFVVGPESAGAHPGPACYR	0.985510046	2	3.774463
P97608	SGLQLEDTPK	1.414972209	2	2.505929
P97608	TGDLLEIQQPVDLEALR	0.927966625	2	4.335544
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**0.848187764**	**0.95629**	**7**
P97612	FMREVEQLMTPQK+Oxidation(8)	0.916413292		
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	0.938245581	3	4.687197
P97612	GTNCVTSYLTDCETQLSQAPR	0.894005989	2	4.940621
P97612	GYFGDIWDIILK	0.837487627	2	3.012081
P97612	LQSGELSPEAVFFTYLGK	1.032242736	2	4.712319
P97612	NSVGLPVAVQCVALPWQEELCLR	0.876657922	2	4.173378
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	0.738703803	2	4.759167
P97697	**IMPA1 Inositol monophosphatase 1**	**0.911849556**	**0.65833**	**2**
P97697	SLLVTELGSSR	0.908630249	2	2.370705
P97697	SSPADLVTVTDQK	1.070757847	2	2.782658

P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**1.013265344**	**0.7044**	**4**
P97700	AVVVNAAQLASYSQSK	0.86488282	2	4.764484
P97700	GIYTGLSAGLLR	0.904403801	2	2.838662
P97700	LGIYTVLFER	0.671868571	2	2.725049
P97700	LTGADGTPPGFLLK	1.015607881	2	3.152544
P97840	**LEG9 Galectin_9**	**1.648323182**	**1.6E-06**	**2**
P97840	NTQINNSWGPEER	1.485482215	2	2.45388
P97840	SINISGVVLPDAK	1.827735201	2	3.382073
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.971225258**	**9.9E-20**	**21**
P97852	AVANYDSVEAGEK	1.052600364	2	4.025462
P97852	AYALAFAER	1.034820873	2	3.573151
P97852	CEAVIADILDK	0.983531046	2	2.462658
P97852	DTTSLNQAALYR	2.665573139	2	2.474168
P97852	FVYEGSADFSCLPTFGVIVAQK	0.755230308	2	4.482731
P97852	GALVVVNDLGGDFK	0.965047921	2	4.382337
P97852	GSSAADKVVEEIR	0.972035083	2	2.719899
P97852	HVLQQFADNDVSR	0.982207592	2	4.46525
P97852	ICDFSNASKPK	0.915096723	3	3.767988
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	0.994354583	3	5.501728
P97852	IDVVVNNAGILR	0.866429647	2	3.404274
P97852	ISDEDWDIIQR	0.902266651	2	3.788776
P97852	KNNIHCNTIAPNAGSR	0.753475389	2	4.858433
P97852	LNPQNAFFSGR	1.006722676	2	2.634136
P97852	NGSGEVYQGPAK	0.990083654	2	3.084965
P97852	NNIHCNTIAPNAGSR	0.982731535	2	4.571816
P97852	SIQESTGGIIEVLHK	0.735484004	2	4.006524
P97852	SLMSGGLAEVPGLSINFAK	0.80756101	2	3.042466
P97852	VLHGEQYLELYKPLPR	0.75200003	2	4.40263
P97852	VNAVFEWHITK	1.092293106	2	2.518687
P97852	VVLVTGAGGGLGR	1.00926952	2	3.716695
Q00238	**ICAM1 Intercellular adhesion molecule 1**	**1.074910131**	**0.86975**	**2**
Q00238	LDTPDLLEVGTQQK	0.888348542	2	3.083777
Q00238	VELDPLPAWQQVGK	1.120802166	2	2.946469
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**0.914272158**	**0.99965**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	0.886415552	2	4.195621
Q00438	KLPSDVTEGEVISLGLPFGK	0.989986481	2	4.71256
Q00438	LSLDGQNIYNACCTLR	0.917654393	2	3.539298
Q00438	NNQFQALLQYADPVSAQHAK	0.967454804	2	5.648084
Q00780	**chain**	**0.890004053**	**2.1E-06**	**4**
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(3)	1.079101758		
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(5)	1.079101758		
Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.734043114		
Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.734043114		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**0.920951566**	**0.09145**	**3**
Q00PI9	AVEEQGDDQDSEK	0.741069867	2	3.826132
Q00PI9	EEAQPIVTKYK	1.603172322	1	1.944967
Q00PI9	SGDETPGSEAPGDK	0.593414894	2	2.854772
Q01177	**PLMN Plasminogen**	**0.741250078**	**6.3E-09**	**3**
Q01177	ILGSDVQQIAVTK	0.741708218	2	3.72667
Q01177	LVLEPNDADIALLK	0.80753705	2	2.585154

Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	0.697220224	3	4.320611
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**0.903692732**	**0.00589**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	0.878332123	2	6.318629
Q01205	NDVITVQTPAFAESVTEGDVR	1.011858922	2	5.202766
Q01205	NVETMNYADIER	0.899727691	2	3.414136
Q01205	VEGGTPLFTLR	0.878545533	2	3.219785
Q01405	**SC23A Protein transport protein Sec23A**	**1.023202637**	**0.83487**	**4**
Q01405	AETEEGPDVLR	1.045808465	2	2.906969
Q01405	AVLNPLCQVDYR	1.010940653	2	2.731359
Q01405	HLLQAPVDDAQEILHSR	1.150722478	3	5.625575
Q01405	YIDTEHGGSQAR	1.226622619	2	3.281142
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.908600146**	**9.9E-20**	**31**
Q02253	AEMEAAVAACK	0.945855114	2	3.806141
Q02253	AEMEAAVAACK+Oxidation(2)	0.989540635		
Q02253	AFPAWADTSILSR	0.944161785	2	4.002167
Q02253	AISFVGSNQAGEYIFER	0.919811556	2	5.175509
Q02253	CMALSTAVLVGEAK	0.938745544	2	4.501402
Q02253	CMALSTAVLVGEAK+Oxidation(1)	0.938449385		
Q02253	EEDATLSSPAVVMPTMGR	1.084217115	2	4.306534
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12)	0.984796696		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15)	0.851675059		
Q02253	EGASILLDGR	1.220536057	2	2.541578
Q02253	ENTLNQLVGAAFGAAGQR	1.05292088	2	5.499629
Q02253	GDTNFYGK	0.961005298	2	2.444874
Q02253	GLQVVEHACSVTSLMLGETMPSITK	0.605937893	2	5.593545
Q02253	GYENGNFVGPTIISNVKPSMTCYK	0.743320942	3	3.931876
Q02253	IVNDNPYGNGTAIFTTNGAIAR	0.805944829	2	5.41856
Q02253	LITLEQGK	0.987184909	2	2.815262
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.287349467	3	4.297335
Q02253	NHGVVMPDANK	1.03336323	1	3.367598
Q02253	NHGVVMPDANK+Oxidation(5)	0.994965366		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	0.839207159	3	6.170986
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5)	0.776611021		
Q02253	QGIQFYTQLK	0.919244624	2	2.723757
Q02253	SDKWIDIHNPATNEVVGR	0.779286775	2	5.280058
Q02253	TITSQWK	0.992006122	2	2.52672
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.791882934	2	5.272245
Q02253	TLADAEGDVFR	0.961405698	2	3.487832
Q02253	VCNLIDSGAK	1.006578899	2	3.481856
Q02253	VNAGDQPGADLGPLITPQAK	0.899022107	2	5.73663
Q02253	WIDIHNPATNEVVGR	0.782397306	2	4.919349
Q02253	WLPELVER	0.915004301	2	2.503947
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	0.847098184	3	4.01954
Q02769	**FDFT Squalene synthase**	**0.92672525**	**0.99998**	**4**
Q02769	KLEDFVKPENVDVAVK	1.118901532	3	4.031358
Q02769	SFAAVIQALDGDIR	0.921756351	2	3.208762
Q02769	TQSLPNCQLISR	1.128151201	2	2.720667
Q02769	VVLEDFPTISLEFR	1.078161634	2	3.461503
Q02874	**H2AY Core histone macro_H2A.1**	**0.915594092**	**8E-07**	**3**
Q02874	AASADSTTEGAPTDGFTVLSTK	1.219644757	2	4.435774
Q02874	GVTIASGGVLPNIHPELLAK	0.787814897	2	4.139748
Q02874	NGPLEVAGAAVSAGHGLPAK	0.751531656	2	3.318297

Q02974	**KHK Ketohexokinase**	**0.911181855**	**5.4E-05**	**9**
Q02974	FGCQVAGK	0.797408252	2	2.540273
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	0.863916138	3	5.735806
Q02974	GGNASNSCTVLSLLGAR	0.91167824	2	4.686769
Q02974	GNSMQEALR	0.976823701	2	3.038121
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.014269364	3	5.765394
Q02974	IEQYNATQPLQQK	0.963587405	2	4.874523
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.885306237	3	5.239995
Q02974	TIILYDTNLPDVSAK	0.82918477	2	5.020726
Q02974	VSVEIEKPR	0.941859145	2	2.374932
Q03248	**BUP1 Beta_ureidopropionase**	**1.055840106**	**0.00467**	**12**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.057893796	2	6.272588
Q03248	EKLPWTEFAESAEDGLTTR	1.176544744	3	4.716307
Q03248	ELAEAVKPNYSPNIVK	1.549367768	2	4.28682
Q03248	HNMVVISPILER	0.874282138	2	2.940649
Q03248	HNMVVISPILER+Oxidation(2)	0.969773377		
Q03248	IPLPTSAPVAEQVSALHK	1.135003343	3	4.797505
Q03248	KHNMVVISPILER	0.77440263	2	2.932451
Q03248	KHNMVVISPILER+Oxidation(3)	1.156563371		
Q03248	NAAIANHCFTCALNR	1.044417371	2	4.462059
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.167509414	3	5.643678
Q03248	VGQEHYPNEFTSGDGK	1.205715483	2	4.244584
Q03248	VGQEHYPNEFTSGDGKK	1.070110276	3	4.940723
Q03336	**RGN Regucalcin**	**0.846491419**	**9.9E-20**	**16**
Q03336	CGESPVWEEASK	0.872666617	2	4.676763
Q03336	CLLFVDIPSK	0.77157944	2	3.32637
Q03336	DEQIPDGMCIDVEGK	0.973481321	2	4.613037
Q03336	DYSEMYVTCAR	2.128480984	2	2.767431
Q03336	FNDGKVDPAGR	0.995099701	2	2.721576
Q03336	HQGSLYSLFPDHSVK	1.115666265	2	4.72393
Q03336	KYFDQVDISNGLDWSLDHK	0.881945715	3	5.688782
Q03336	LWVACYNGGR	0.771267509	2	2.983313
Q03336	MEKDEQIPDGMCIDVEGK	0.792275188	2	5.107283
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0)	0.756249513		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10)	0.756774459		
Q03336	QSGGYVATIGTK	0.902262111	2	2.891176
Q03336	VGVDAPVSSVALR	0.829632237	2	3.795334
Q03336	YFAGTMAEETAPAVLER	0.829948692	2	5.590406
Q03336	YFAGTMAEETAPAVLER+Oxidation(5)	0.811299459		
Q03336	YFDQVDISNGLDWSLDHK	0.862855528	3	4.381349
Q03410	**SYCP1 Synaptonemal complex protein 1**	**0.955896438**	**0.3159**	**2**
Q03410	ISEEKLLGEVEK	1.007549323	2	2.306461
Q03410	MEQENTAILTDKK+Oxidation(0)	0.848692673		
Q03626	**MUG1 Murinoglobulin_1**	**0.854187092**	**4E-07**	**6**
Q03626	EESSCIHSSCTAER	1.07695331	2	3.901366
Q03626	GGEFEMMPLGVNK	0.597254078	2	3.138592
Q03626	LTAQPAPSPEDLALSMGTIK	0.734023815	3	4.647064
Q03626	NLHPLNELFPLAYIEDPK	0.746825662	3	4.434322
Q03626	VQTVPLTCNNPK	0.664714628	2	2.902613
Q03626	VYHKEESSCIHSSCTAER	1.132885153	3	4.376818
Q04462	**SYVC Valyl_tRNA synthetase**	**0.939913845**	**0.96079**	**6**
Q04462	ADFPAGIPECGTDALR	1.012247981	2	2.420991
Q04462	ALNPLEEWLR	0.905154729	2	2.541792
Q04462	ITPAHDQNDYEVGQR	1.132856926	2	3.35845
Q04462	LQQTEAELR	1.000139191	2	2.360418
Q04462	SVTQQPGSEITAPQK	0.935751709	2	3.157324
Q04462	VQGSDSDEEVVVATTR	1.018205537	2	3.938783

Q05096	**MYO1B Myosin_Ib**	**0.763957033**	**0.025**	**2**
Q05096	LEDLATLIQK	0.735420151		
Q05096	NAMQIVGFSDPEAESVLEVVAAVLK	0.954361486		
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**0.990036665**	**0.94928**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(0)	0.933656685		
Q05144	YLECSALTQR	1.079413027	2	2.977731
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.271461722**	**0.98439**	**9**
Q06647	FSPLTANLMNLLAENGR	0.918298207	3	4.128219
Q06647	GEVPCTVTTAFPLDEAVLSELK	0.90483111	3	5.819669
Q06647	GQILNLEVK	1.074763844	2	2.480382
Q06647	LGNTQGVISAFSTIMSVHR	0.901187032	3	3.331209
Q06647	LVRPPVQVYGIEGR	1.218340273	3	3.537324
Q06647	TDPSIMGGMIVR	0.856011886	2	3.22957
Q06647	TVLNSFLSK	0.803420997	2	3.019607
Q06647	VSLAVLNPYIK	0.933670309	2	3.061923
Q06647	YATALYSAASK	1.502893628	2	3.433251
Q07071	**GCKR Glucokinase regulatory protein**	**0.988190729**	**0.78056**	**14**
Q07071	AAPISCHVQVAHEK	0.952903853	2	4.917322
Q07071	CLLEILR	0.988423583	2	2.620968
Q07071	GFLIGDHSDMFNQK	1.127381762	2	3.540482
Q07071	GLGQKPLYTYLIAGGDR	1.259695295	2	3.116616
Q07071	LLGQCDAEIFQEEGQIVPTYQR	1.523517696	2	5.07553
Q07071	LYSESVLTTMLQVAGK	0.998125969	2	2.609931
Q07071	NDPIEDWR	0.921932835	1	1.903314
Q07071	QEAFVLNPAIGPEGLSGSSR	0.641365964	2	3.052136
Q07071	STQALEDPPACGTLN	0.940949977	2	2.404625
Q07071	TVDQGVVSSQR	0.863992875	2	3.528949
Q07071	VIPTALLSLLLR	0.800058382	2	3.557179
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	0.919730266	2	5.32788
Q07071	WVLNTVSTGAHVLLGK	0.430248323	2	2.746226
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	0.964004522	3	5.562906
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.91973172**	**0.99965**	**7**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.947440476	2	4.616793
Q07116	FVDLHPGGQSK	1.261879289	2	2.438539
Q07116	LCDVLAQAGHR	0.877762468	2	2.992418
Q07116	MSPPLEASDPYSNDPMR	0.928974551	2	2.676604
Q07116	NHLPVPNLDPDTYR	0.963466181	2	2.479079
Q07116	VSVESEESYSHWQR	0.955447943	2	3.742706
Q07116	VVVPGVVGAR	0.903994476	2	2.441212
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.804903054**	**9.9E-20**	**10**
Q07523	ALKEEKPTQSVPVSFPK	0.841964473	3	4.584561
Q07523	ALVITIDTPVLGNR	0.812297743	2	4.477938
Q07523	ASFCWNDLSLLQSITR	0.785894636	2	4.09175
Q07523	EEKPTQSVPVSFPK	0.90263064	2	2.963409
Q07523	EVLDILTAELHR	1.211365892	2	3.241111
Q07523	GEDGVKEVLDILTAELHR	0.855066443	3	5.187481
Q07523	HNVQGIVVSNHGGR	0.745925838	3	6.118731
Q07523	NQLNLEANILLK	0.763802817	2	3.470214
Q07523	QLDEVSASIDALR	0.78394789	2	3.07338
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	0.963292244	3	4.638498
Q07803	**EFGM Elongation factor G_ mitochondrial**	**1.069977447**	**0.90997**	**3**
Q07803	GIIDLIEER	1.131261348	2	2.701093
Q07803	LEFSDETFGANVPK	0.982165297	2	3.698801
Q07803	YQPCSPSTQEELVNK	1.11903051	2	3.262235
Q07936	**ANXA2 Annexin A2**	**0.880402151**	**0.00626**	**2**
Q07936	GLGTDEDSLIEIICSR	0.880652585	2	3.027557

Q07936	GVDEVTIVNILTNR	0.777449162	2	4.110605
Q07984	**SSRD Translocon_associated protein subunit delta**	**0.989342331**	**1**	**3**
Q07984	FFDEESYSLLR	1.114843913	2	3.539228
Q07984	NNEDVSIIPPLFTVSVDHR	0.967913815	3	3.918537
Q07984	VQNMALYADVSGK	1.037484608	2	3.255476
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**0.957314573**	**0.00533**	**8**
Q08163	ALLVTASQCQQPAGNK	0.724522561	2	4.680972
Q08163	GAVPYVQAFDSLLANPVAEYLK	1.157579129	3	3.773344
Q08163	LEAVSHTSDMHCGYGDSPSK	1.051503866	3	4.858672
Q08163	LSDLLAPISEQIQEVITFR	1.023908889	2	3.428841
Q08163	NSLDCEIVSAK	0.9612065	2	3.08192
Q08163	SALFAQINQGESITHALK	0.797869651	2	3.81525
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	0.872487637	2	3.668366
Q08163	VENQENVSNLVIDDTELK	0.880088036	2	4.824555
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**0.969399394**	**0.25607**	**4**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	0.986222811	3	4.904198
Q08415	ILVLNTPNNPLGK	1.205127054	2	3.055063
Q08415	LGASNDWQLDPAELASK	0.787636901	2	3.342516
Q08415	RLDGIDQNLWVEFGK	0.87900746	2	2.932952
Q09073	**ADT2 ADP/ATP translocase 2**	**1.340299142**	**1.1E-14**	**7**
Q09073	DFLAGGVAAAISK	1.652276886	2	4.769534
Q09073	EQGVLSFWR	2.246596185	1	1.908197
Q09073	GLGDCLVK	0.969302817	2	2.582445
Q09073	GTDIMYTGTLDCWR	1.079364342	2	3.633347
Q09073	KGTDIMYTGTLDCWR	1.151740714	2	3.369285
Q09073	LLLQVQHASK	1.568152209	2	2.74865
Q09073	QIFLGGVDK	1.343405362	2	2.682165
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.896949713**	**0.99822**	**6**
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	0.823195946	2	3.742505
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	1.097443145	3	3.645275
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	0.825224783	3	4.635373
Q0D2L3	SVDEGLLDSK	1.194540286	2	2.982182
Q0D2L3	SVDEGLLDSKR	1.005963284	2	2.664193
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.05241575	2	5.410556
Q0VAV2	**EXPH5 Exophilin_5**	**1.033771087**	**0.96442**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1)	1.013302205		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)	0.739197467		
Q0VGK3	**GLCTK Glycerate kinase**	**0.8173414**	**4.6E-11**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	0.752601588	3	5.882719
Q0VGK3	GATIQELNTIR	0.892819946	2	2.921111
Q0VGK3	QLFDSAVGAVQPGPMLQR	1.730818352	2	3.81942
Q0ZHH6	**ATLA3 Atlastin_3**	**0.883188186**	**0.7861**	**4**
Q0ZHH6	EHGHSNWLGDPEEPLTGFSWR	1.104802224	3	4.070914
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	0.901561107	2	4.557232
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2)	1.196813514		
Q0ZHH6	YQQELEEEITELYENFCK	0.787417733	2	4.759522
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.844361054**	**2E-06**	**25**
Q10758	AEAETMYQIK	1.096778078	2	3.403797
Q10758	AQYEEIANR	0.920701762	2	3.051852
Q10758	ATLEAAIADAEQR	0.845700434	2	4.638978
Q10758	ELQSQISDTSVVLSMDNSR	1.185905001	2	5.746842
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	0.784423653	2	4.486948
Q10758	LEGLTDEINFLR	0.859344905	2	4.255579
Q10758	LESGMQNMSIHTK	0.728211936	2	3.778391
Q10758	LEVDPNIQAVR	0.890384176	2	3.735526

Q10758	LEVELGNMQGLVEDFK	0.875796592	2	5.06192
Q10758	LKLEVELGNMQGLVEDFK	0.960954108	3	4.004301
Q10758	LQAEIDALK	0.958487126	2	2.746445
Q10758	LVSESSDIMSK	1.06872878	2	3.012508
Q10758	QIHEEEIR	0.807165732	1	2.329552
Q10758	QLEALGQEK	0.815993188	1	2.260305
Q10758	RQLEALGQEK	1.013480562	2	2.326897
Q10758	SKTEISEMNR	0.807463121	3	3.435024
Q10758	SKTEISEMNR+Oxidation(7)	1.045300605		
Q10758	SLDMDSIIAEVR	0.880302154	2	4.583012
Q10758	SNMDNMFESYINNLR	0.945190361	2	4.085135
Q10758	SRAEAETMYQIK	1.049101309	2	3.519465
Q10758	TEISEMNR	0.981315092	2	2.487784
Q10758	TEMENEFVLIK	0.850228833	2	3.333536
Q10758	TEMENEFVLIK+Oxidation(2)	0.827224992		
Q10758	WSLLQQQK	1.092738045	2	2.915474
Q10758	YEELQTLAGK	0.909443461	2	3.700737
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**0.8574951**	**0.52215**	**2**
Q148W0	FMAASVASSNRDEALDK+Oxidation(1)	1.187613889		
Q148W0	TCEVIKDGRFK	0.854874817	1	2.209782
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.922172**	**0.05645**	**6**
Q14DH7	IAIIYDSPVTDTK	1.185337793	2	2.43253
Q14DH7	STLSALVNGKPYK	1.043523529	2	2.816439
Q14DH7	THFAASVADPER	0.835455191	2	3.603552
Q14DH7	VDDVINVAGHR	1.100435585	2	3.394854
Q14DH7	VLAEHGVAALFTAPTAIR	0.595660947	2	3.773319
Q14DH7	VTPTIEDPSIFGHIEEVLK	0.798927861	2	3.405083
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.972092737**	**0.54206**	**12**
Q1HCL7	ALNEVFIGESLSSR	0.77441289	2	3.101025
Q1HCL7	ASYYEISVDDGPWEK	0.961524075	2	3.25054
Q1HCL7	LKPVIGVNTDPER	0.965702069	3	3.598658
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	0.918284139	3	5.227853
Q1HCL7	NVEHIIDSLRDEGIEVR	0.774941065	2	3.463174
Q1HCL7	QGNLTLPLNK	0.829752332	2	3.024254
Q1HCL7	SEASGPQLLPVR	0.844646332	2	3.419453
Q1HCL7	SEGHLCLPVR	1.097549851	2	2.345104
Q1HCL7	SSGLNLCTGTGSK	0.896427224	2	3.592942
Q1HCL7	VTNEYNESLLYSPEEPK	0.985291811	2	4.44559
Q1HCL7	YEFEQQR	1.157512879	2	2.535376
Q1HCL7	YTHSFPEALQK	0.765533199	2	2.662583
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.062739208**	**0.2335**	**5**
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	1.46868819	3	3.472024
Q1JU68	FNVLQYVVPEVK	1.050015371	2	3.160152
Q1JU68	ILQEHEQIK	0.925661391	2	2.671459
Q1JU68	KGPEADSEWR	1.092419274	2	2.563402
Q1JU68	LLDMDGIIVEK	0.914764848	2	2.905599
Q29RW1	**MYH4 Myosin_4**	**1.043965641**	**0.9818**	**15**
Q29RW1	AGLLGTLEEMRDEK	0.999077241	2	2.416799
Q29RW1	ELENEVENEQK	2.69322476	2	2.420846
Q29RW1	ELENEVENEQKR	4.279683951	2	2.990504
Q29RW1	LINELSAQK	1.78432937	2	2.789417
Q29RW1	LQDAEEHVEAVNSK	4.063822616	2	4.478714
Q29RW1	LQDLVDKLQTK	0.962980426	1	2.103887

Q29RW1	MEGDLNEMEIQLNHANR	1.432639232	2	4.315431
Q29RW1	MEIDDLASNMETVSK	2.201821476	2	4.295159
Q29RW1	NAYEESLDQLETLK	1.300824611	2	4.811811
Q29RW1	NAYEESLDQLETLKR	3.812371201	2	3.791671
Q29RW1	QKYEETQAELEASQK	6.568259624	2	3.587818
Q29RW1	SELQASLEEAEASLEHEEGK	2.120696558	2	4.69357
Q29RW1	SNAACAALDK	2.132717356	2	2.313639
Q29RW1	TLEDQLSEVK	1.811821463	2	2.460041
Q29RW1	VAEQELLDASER	2.208186328	2	2.686498
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**1.32552493**	**0.02331**	**2**
Q2EMV9	LQEELTR	1.438073781	1	2.000205
Q2EMV9	VLVEFEKESLNIAGK	0.945743593	2	2.446773
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**0.937238762**	**0.20415**	**2**
Q2TA68	TSVLEMIAQAR	0.583360327	2	3.265171
Q2TA68	VIQHNALEDR	0.937641915	2	2.341963
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**0.915275692**	**0.95228**	**7**
Q2V057	EDCTQPDYEATSR	1.080785013	2	3.782402
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	0.954911864	2	4.489268
Q2V057	NLQLSCLSTEQNQHLQASLSR	0.854776303	2	5.577103
Q2V057	REQALLSQELWR	0.72463555	2	3.060992
Q2V057	SIPYGCLEEVIPYLIR	1.108330122	2	3.612137
Q2V057	SVTQLHGKEDCTQPDYEATSR	0.934156012	3	3.729579
Q2V057	TSEAWYEGNLSAMLHCVDLSR	0.986919301	2	2.737828
Q32Q06	**AP1M1 AP_1 complex subunit mu_1**	**0.886078893**	**0.25282**	**2**
Q32Q06	HNNLYLVATSK	1.364610902	2	2.411808
Q32Q06	MRVFLSGMPELR+Oxidation(0)	0.820745237		
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**0.939691477**	**0.86764**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	0.780121856	3	4.691477
Q3B7D0	HCDDSYTPQDK	0.845923421	2	3.089515
Q3B7D0	LEEDGDELAR	1.225090487	2	2.499826
Q3B7D0	TCAEAVVPSYVPIVK	1.105448947	2	3.190239
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**0.858628942**	**7.8E-05**	**4**
Q3B7U9	SCSQVLEHQPDNIK	0.846438621	2	4.108989
Q3B7U9	TAEDGPDLEMLSGQER	1.191237871	2	3.801841
Q3B7U9	VDMTCEEEEELLQLK	0.806601813	2	4.211577
Q3B7U9	VLAQQGEYSEAIPILR	0.734964849	2	3.131577
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.047247516**	**0.96581**	**3**
Q3KRD8	ASFENNCEVGCFAK	1.094769999	2	2.843504
Q3KRD8	HGLLVPNNTTDQELQHIR	0.986034993	3	4.840389
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	0.866955766	2	3.827856
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**0.981870416**	**0.43857**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	0.55420814	2	3.244584
Q3KRE0	ISVLEALR	1.092672323	2	2.364279
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**0.898899762**	**0.10748**	**2**
Q3KRE8	ALTVPELTQQMFDSK	0.89883034	2	3.316341
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.934626793	3	4.180816
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**0.582073351**	**0.00489**	**2**
Q3MIB4	MEIIQVPGYTQEEK	0.505343861	2	3.596625
Q3MIB4	TVGVNNPVFLLDEVDK	0.979973744	2	3.608235
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**0.911821707**	**0.94386**	**7**
Q3MIE0	DGQEGIEAFIQK	1.089361184	2	3.310794
Q3MIE0	KVALEMLFTGEPISAQEALR	0.992443623	3	3.504132

Q3MIE0	SDILHEAESEDLK	1.007757722	3	3.739595
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	0.884303682	2	4.646878
Q3MIE0	VALEMLFTGEPISAQEALR	0.824651949	2	3.375892
Q3MIE0	VIIISAEGPVFSSGHDLK	0.845875708	2	4.28749
Q3MIE0	VVPEEQLEEEATR	0.937449632	2	4.144634
Q3MIF4	**XYLB Xylulose kinase**	**0.860831903**	**1E-12**	**7**
Q3MIF4	AFHGLAGGTGVAFSEVVK	1.141522828	2	2.323471
Q3MIF4	CCLGWDFSTQQVK	0.910542785	2	2.942708
Q3MIF4	FNADNMEVSAFPGDVEIR	0.790284276	2	4.04073
Q3MIF4	IRDESASCSWNK	0.807908341	2	4.094701
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	1.053444979	2	4.378472
Q3MIF4	VVAFTGDNPASLAGMR	0.910561965	2	3.668159
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	0.997863822	2	5.297771
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.038969963**	**0.99998**	**4**
Q3T1J1	EDLRLPEGDLGK	1.141991494	2	2.813557
Q3T1J1	EDLRLPEGDLGKEIEQK	0.95808054	3	4.747553
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	0.98779035	3	5.738932
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.02961389	3	3.76142
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**0.967088011**	**0.85307**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	0.998842865	3	4.580015
Q3T1K5	FTVTPSTTQVVGILK	0.936517054	2	3.706344
Q3T1K5	LLLNNDNLLR	1.354768966	2	2.40651
Q3T1L0	**A16A1 Aldehyde dehydrogenase family 16 member A1**	**1.103239642**	**0.34291**	**2**
Q3T1L0	HGAAPTVAETEVELSVR	1.001957439	2	2.398283
Q3T1L0	VQDQGQTLQVTGLR	1.106625737	2	4.167922
Q3TLP5	**ECHD2 Enoyl_CoA hydratase domain_containing protein 2_ mitochondrial**	**0.874112713**	**0.9758**	**2**
Q3TLP5	ALALAQEILPQAPIAVR	0.888165589		
Q3TLP5	NALGNVFVSELLEALAQLR	0.866437459		
Q3U2P1	**SC24A Protein transport protein Sec24A**	**0.995671618**	**0.82508**	**2**
Q3U2P1	CTLTSVPQTQALLNK	0.959635721	2	3.598585
Q3U2P1	TLETQSALGPALQAAFK	0.9443123	2	3.11167
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**0.992231991**	**0.99994**	**2**
Q3ULJ0	GIDEGPDGLK	1.000237115	2	2.671374
Q3ULJ0	LGLMEMIAFAK	0.897079033	2	3.82464
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**0.946808769**	**0.99732**	**14**
Q3UQ44	ALVGSENPPLTVIR	1.021445486	2	3.997128
Q3UQ44	AWVNQLETQTGEASK	0.912372377	2	5.080618
Q3UQ44	GVLLGIDDLQTNQFK	1.050363312	2	4.791054
Q3UQ44	HTDNTVQWLR	1.323807132	2	2.848342
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.222914364	3	4.515428
Q3UQ44	LGIAPQIQDLLGK	1.184186176	2	2.73368
Q3UQ44	LPYDVTTEQALTYPEVK	1.138964468	2	4.329138
Q3UQ44	LSAEEMDER	0.97700078	2	2.698053
Q3UQ44	NPNAVLTCVDDSLSQEYQK	0.87927198	2	4.969876
Q3UQ44	TALEEEIK	1.086453707	1	2.005997
Q3UQ44	TLDTLLLPTANIR	0.837910899	2	2.55318
Q3UQ44	VDFTEEEISNMR	0.839346621	2	3.389883
Q3UQ44	VDQVQDIVTGNPTVIK	0.950041914	2	4.916214
Q3UQ44	YQDILNEIAK	0.976313853	2	2.605644
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**1.021955653**	**0.75422**	**3**
Q3UV17	AQYEDIAQK	1.48588292	1	2.129373
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5)	1.052730729		

Q3UV17	VDSLTDEINFLR	0.907457128	2	2.468676
Q3UZY0	**SFI1 Protein SFI1 homolog**	**1.548527214**	**0.01843**	**2**
Q3UZY0	EEWWVSQREWK	1.549750531	2	2.704753
Q3UZY0	MGRAQAAHFHSAQLLSR+Oxidation(0)	1.543137062		
Q3V036	**CCD27 Coiled_coil domain_containing protein 27**	**1.036849162**	**0.61385**	**2**
Q3V036	MDLISSERTIK+Oxidation(0)	0.736940118		
Q3V036	SSEGPPEEAAAAKLSRPSQSK	1.133737593	2	2.749781
Q3V0K9	**PLSI Plastin_1**	**1.104786024**	**0.98985**	**3**
Q3V0K9	AYFHLLNQIAPK	0.96551003	2	2.825564
Q3V0K9	KIENCNYAVELGK	1.127555578	2	3.923074
Q3V0K9	QFVTPADVVSGNPK	0.969059893	2	3.802747
Q3V132	**ADT4 ADP/ATP translocase 4**	**0.957943731**	**1**	**2**
Q3V132	GNLANVIR	1.091373886	2	2.726654
Q3V132	YFPTQALNFAFK	0.948519725	2	2.945507
Q497B0	**NIT2 Omega_amidase NIT2**	**1.012528436**	**0.82948**	**14**
Q497B0	AGTEETILYSDIDLK	1.03285296	2	4.27928
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.967077757	2	4.908471
Q497B0	AVDNQVYVATASPAR	0.939726213	2	4.960291
Q497B0	AVDNQVYVATASPARDEK	0.817149349	2	3.383258
Q497B0	ENSIYLIGGSIPEEDDGK	0.858067217	2	2.837044
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	0.877853639	3	4.478386
Q497B0	FAELAQIYAR	1.14555251	2	3.704595
Q497B0	IHLFDIDVPGK	0.964848629	2	2.833553
Q497B0	KIHLFDIDVPGK	0.862438153	3	4.682935
Q497B0	LALIQLQVSSIK	1.061348496	2	3.335123
Q497B0	LYNTCAVFGPDGNLLVK	1.089613467	2	4.455254
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	0.868670504	3	4.344718
Q497B0	TLSPGDSFSTFDTPYCR	1.039700844	2	4.702559
Q497B0	VGLGICYDMR	0.950187806	2	2.744405
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**0.72270768**	**0.17735**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.658864861	2	4.155301
Q498D5	FCNLALLLPIVTK	0.681618887	2	3.224146
Q498D5	LEECIQDELGVR	0.747448212	2	3.148288
Q498D5	LNELLTNVEELKEEIK	0.673249609	2	3.456348
Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**0.939512738**	**0.86265**	**2**
Q498U4	EEEPPEKVVDMASEK	0.999195053	2	2.594336
Q498U4	FGIVTSSAGTGTTEDTEAK	1.423707121	2	4.130384
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.515758046**	**0.18069**	**10**
Q499N5	GATLSHHNIVNNSNLIGQR	0.888312802	3	4.826545
Q499N5	GGENIYPAELEDFFHK	1.138787851	2	3.088278
Q499N5	GGVIAGSLAPPELIR	1.275726847	2	2.670899
Q499N5	LPDLTTVISVDAPLPGTLLLDEVVAAGGK	1.129753052		
Q499N5	SGETTTEEEIK	1.127845587	2	2.952603
Q499N5	TFETVGQDR	1.398155965	2	2.514926
Q499N5	TGDIASMDEQGFCR	1.589375935	2	3.680996
Q499N5	TVGECLDATAQR	1.746628289	2	3.140662
Q499N5	YHQGFLSCYDPINIQFTSGTTGNPK	1.141240217	3	4.664974
Q499N5	YIVFVEGYPLTVSGK	1.315325546	2	4.652744
Q4AEF8	**COPG Coatomer subunit gamma**	**0.943495004**	**0.02599**	**5**
Q4AEF8	FGAQNEEMLPSILVLLK	0.897477412	2	3.164956
Q4AEF8	QEIFQEQLAAVPEFQGLGPLFK	0.930556496	3	4.288921
Q4AEF8	SSPEPVALTESETEYVIR	1.186045915	2	3.99375
Q4AEF8	VVLEHEEVR	1.321244934	2	2.35103

Q4AEF8	VVVVQAISALCQK	1.521186458	2	2.306965
Q4FZT0	**STML2 Stomatin_like protein 2**	**0.955987352**	**0.55491**	**6**
Q4FZT0	AEQINQAAGEASAVLAK	0.988673231	2	4.799156
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	0.874919343	2	4.997075
Q4FZT0	ATVLESEGTR	1.007462672	2	2.770914
Q4FZT0	DVQTTDTSIEELGR	1.247415148	2	2.82636
Q4FZT0	ILEPGLNVLIPVLDR	0.929155458	2	3.655525
Q4FZT0	NTVILFVPQQEAWVVER	0.835413065	2	3.051839
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.143316249**	**1.1E-13**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	1.587859677	3	4.971573
Q4FZT9	FGGSGSQVDSAR	1.079357552	2	3.891086
Q4FZT9	GEAIEAILAALEVVSEPFR	1.009427757		
Q4FZT9	SETELKDTYAR	1.202217526	2	2.357594
Q4FZT9	SGALLACGIVNSGVR	1.266980567	2	3.677731
Q4FZT9	SSTTSMTSVPKPLK	0.978366968	2	2.582055
Q4FZT9	TITGFQTHTTPVLLAHGER	1.232514777	3	3.709084
Q4FZT9	TPVQSQQPSATAPSGADEK	1.145991293	2	4.440697
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.004465931**	**4.2E-06**	**5**
Q4FZX7	DTQTSITDSSAIYK	0.845513914	2	3.096941
Q4FZX7	GDAGSADVQDLEK	1.115518769	2	3.329109
Q4FZX7	GNSLTLIDLPGHESLR	1.11554	2	3.491884
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.564327196	2	4.616443
Q4FZX7	VGDGAGGAFQPYLDSLR	1.134877111	2	3.283015
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**0.950020673**	**0.76413**	**5**
Q4G061	AEEEGGSDGSAAEAEPR	0.918108518	2	4.84523
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	1.050274222	3	5.91656
Q4G061	GTQGVVTNFEIFR	1.012953567	2	2.819967
Q4G061	IINDYYPEEDGK	1.022094467	2	2.60998
Q4G061	TEDAEEDAEARPEPEVR	0.432334456	3	3.900955
Q4G069	**RMD1 Regulator of microtubule dynamics protein 1**	**1.159624943**	**0.49548**	**2**
Q4G069	IAEVLFANPPSSTYEEALK	0.567668966	2	2.488319
Q4G069	VLLYEALEYAK	1.160386503	2	2.565507
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.032090153**	**0.98971**	**13**
Q4KLP0	ARPSVDHGLAR	0.996771008	2	2.369559
Q4KLP0	LEELCPFPLDSLQQEMGK	0.932428015	2	5.123319
Q4KLP0	LLLESQEFDHFLATK	0.96253269	2	3.409804
Q4KLP0	LSAYGGITDIIIGMPHR	1.091115153	3	3.380409
Q4KLP0	LVTVYCEHGHK	1.525305305	2	2.845205
Q4KLP0	NGTNLDWATAETLALGSLLAQGFNVR	1.129314745		
Q4KLP0	QWGHNELDEPFFTNPVMYK	0.977110562	3	3.792775
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.04467451	3	5.151444
Q4KLP0	SSLYSSDIGK	1.090821044	2	2.693988
Q4KLP0	SVEVPEELQLHSHLLK	1.041418115	2	3.813759
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	0.926412018	2	4.926007
Q4KLP0	YGGEGAESMMGFFHELLK	0.749073947	2	4.407415
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.080749397	3	4.527272
Q4KLZ6		**0.896324512**	**4.6E-06**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	0.838193581	2	4.532551
Q4KLZ6	AILEVLQTK	0.733812703	2	2.713578
Q4KLZ6	ANTDLPAWSAAMDAGLK	0.782166703	2	3.889141
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	0.861700165	2	5.905149
Q4KLZ6	AVAQAGTAGTLLIVK	0.788725283	2	4.368645

Q4KLZ6	EGPTPASPAQVLSK	0.865198869	2	3.055923
Q4KLZ6	GLCGTILIHK	0.727381028	2	2.321606
Q4KLZ6	GVSLTLMLVDEPLLK	0.66062519	2	3.166383
Q4KLZ6	ISTTLIGLEEHLNALDR	0.978609811	2	3.941124
Q4KLZ6	LIDAETNAK	0.849540602	2	2.991795
Q4KLZ6	LNFGLAMEQAK	0.986887216	2	2.489008
Q4KLZ6	LSVLLLEK	0.995608826	2	2.801949
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	0.760378316	3	5.444092
Q4KLZ6	TMLDSLWAAAQELQAWK	0.710237481	2	4.337875
Q4KLZ6	VAGALAEEGMGLEEITK	0.948076634	2	3.692878
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	1.304052173	2	5.297269
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.004526888**	**0.51078**	**4**
Q4KM49	AFCEPGNVENNGVLSFVK	0.793131747	2	3.433717
Q4KM49	QVEPLDPPAGSAPGER	1.003985542	2	3.170385
Q4KM49	TVVSGLVQFVPK	1.005276866	2	3.228129
Q4KM49	VDAQFGGIDQR	1.129520672	2	2.940107
Q4KM73	**KCY UMP_CMP kinase**	**0.984753234**	**0.08677**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	0.902515491	2	4.499327
Q4KM73	IVPVEITISLLK	0.695848269	2	2.319888
Q4KM73	KNPDSQYGELIEK	1.077217192	2	3.669565
Q4KM73	NQDNLQGWNK	0.959699789	2	3.088647
Q4KM73	SVDEVFGDVMK	0.909931168	2	3.071751
Q4KM73	YGYTHLSAGELLR	0.749337279	3	4.39207
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.26083383**	**2.7E-12**	**4**
Q4KM74	DLQQYQSQAK	1.278254141	2	3.297288
Q4KM74	GEALSALDSK	1.285424986	2	2.557648
Q4KM74	NLGSINTELQDVQR	1.281381954	2	4.204613
Q4KM74	VADGLPLAASMQEDEQSGR	1.207481118	2	2.635653
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**0.915385489**	**0.99899**	**2**
Q4KMA2	NFVVVMVTKPK	0.772592146	2	2.839968
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.003005988	2	4.658129
Q4KSH7	**MP2K7 Dual specificity mitogen_activated protein kinase kinase 7**	**1.284877352**	**0.49678**	**2**
Q4KSH7	RSGNKEENK	1.228920111	1	1.989794
Q4KSH7	YNKLLEHSFIK	3.190335845	1	1.937529
Q4QQS8	**NUP85 Nuclear pore complex protein Nup85**	**0.885554299**	**0.0923**	**2**
Q4QQS8	LEEELSGK	0.896525512		
Q4QQS8	RFGDAASLLLSLMTSQIAPR+Oxidation(12)	0.557802931		
Q4QQV3	**F162A Protein FAM162A**	**0.949777056**	**1**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	0.966677175	2	4.118657
Q4QQV3	RHESLTSLNLER	0.968326102	3	4.249256
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.846151067**	**0.15238**	**5**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	1.001466374	3	3.7553
Q4QQW3	HLETAEILGANIR	0.843643316	2	3.415718
Q4QQW3	IQDAGPVLADALR	0.938401062	2	2.779708
Q4QQW3	NLSQLPPVQIVMDSLSK	0.844652275	2	2.61558
Q4QQW3	VEPTDGSFMDAIEFAK	1.016931738	2	2.668852
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**0.976172107**	**0.98803**	**6**
Q4QRB4	AILVDLEPGTMDSVR	0.899067133	2	4.907288
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10)	0.927804592		
Q4QRB4	EIVHIQAGQCGNQIGAK	1.200454566	2	5.043253
Q4QRB4	IMNTFSVVPSPK	1.04614141	2	3.418721
Q4QRB4	IMNTFSVVPSPK+Oxidation(1)	1.190063365		
Q4QRB4	ISEQFTAMFR	0.949610868	2	3.584484
Q4V7C7	**ARP3 Actin_related protein 3**	**0.936175187**	**0.65442**	**5**

Q4V7C7	KDYEEIGPSICR	1.078464552	2	3.647529
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	0.810868252	2	3.149663
Q4V7C7	LSEELSGGR	0.973453354	2	2.713385
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	0.841264332	3	3.668952
Q4V7C7	YSYVCPDLVK	1.134419551	2	2.364987
Q4V8F9	**HSDL2 Hydroxysteroid dehydrogenase_like protein 2**	**0.93726286**	**0.99053**	**3**
Q4V8F9	DEQQINSAVEK	0.909122858	2	3.098461
Q4V8F9	KVDIIADAAYSIFK	0.951229116	2	2.403412
Q4V8F9	SFTGNFIIDENILK	1.063307642	2	2.932067
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**1.022955141**	**0.99972**	**2**
Q4V8K1	TCADEFPLTVDSSEK	1.032368621	2	4.587189
Q4V8K1	TLGLTPLDQGSLVAAK	1.03084707	2	3.809314
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.968208945**	**0.7741**	**3**
Q505J8	LQQVQAGQAEK	1.049663332	2	2.513763
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	0.968813713	3	4.930496
Q505J8	SLQALGEVIEAELR	0.823410712	2	3.58163
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**0.869433887**	**0.63031**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	0.7489007	2	4.291328
Q561R9	ILIDTGEPSVPEYISCLK	0.890333433	2	3.363614
Q561R9	NISNDATYCIK	1.082188029	2	2.474453
Q561R9	NNREEQIITVFR	0.791225957	2	2.541478
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.142150515**	**0.92945**	**5**
Q561S0	LLQYSDALEHLLSTGQGVVLER	1.067016869	3	3.665848
Q561S0	VITVDGNICSGK	1.275042811	2	2.923081
Q561S0	VVEDIEYLNYNK	1.243047842	2	4.201758
Q561S0	YAPGYNADVGDK	1.10270546	2	2.675377
Q561S0	YGLLASILGDK	0.88995499	2	2.947858
Q562C4	**MET7B Methyltransferase_like protein 7B**	**1.108229005**	**0.96146**	**5**
Q562C4	AQFSEVQLEWQPPPFK	1.168715505	2	4.897835
Q562C4	FIVAYGENMK	1.167133976	2	2.720356
Q562C4	HIGDGCHLTR	1.009263062	3	3.406351
Q562C4	VLQEVQR	1.133358255	2	2.769327
Q562C4	VTCVDPNPNFEK	1.295267809	2	3.563125
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.464500879**	**1.2E-12**	**7**
Q58FK9	AIILNTPHNPIGK	1.921763767	2	3.220357
Q58FK9	DSTLDAAEEIFR	1.712386832	2	2.946199
Q58FK9	IEGLDQNVWVEFTK	1.390691457	2	4.713377
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.600946276	2	4.058285
Q58FK9	MDDPECYFNSLPK	1.368051322	2	3.673065
Q58FK9	RIEGLDQNVWVEFTK	1.518812266	2	3.940595
Q58FK9	WTSSDWTFNPQELESK	1.58711866	2	5.071333
Q5BJP3	**UFM1 Ubiquitin_fold modifier 1**	**0.996544269**	**0.58071**	**2**
Q5BJP3	VLSVPESTPFTAVLK	2.252804465	2	2.327214
Q5BJP3	VPAATSAIITNDGIGINPAQTAGNVFLK	1.008829057	3	4.359497
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.906003671**	**5.4E-13**	**27**
Q5BJY9	AQIFANSVDNAR	0.953753162	2	3.837768
Q5BJY9	AQYEQLAQK	0.914128877	2	3.286449
Q5BJY9	DAETTLLELR	2.707446235	2	2.805743
Q5BJY9	IREYLEK	0.991858962	3	3.354275
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	0.929380598	3	4.771309
Q5BJY9	KVVDDTNITR	0.958865874	2	3.025656
Q5BJY9	LEAEIATYR	0.914423276	2	3.009181
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.784783182	3	4.361937
Q5BJY9	LQLETEIEALK	1.258357623	2	2.899629
Q5BJY9	LQLETEIEALKEELLFMK	0.872003234	2	5.307376

Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.851271455	2	6.313861
Q5BJY9	NQNINLENNLGEVEAR	0.850447536	2	5.502141
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	0.919897618	3	5.128973
Q5BJY9	QSVESDIHGLR	1.093745233	2	2.649623
Q5BJY9	QSVESDIHGLRK	0.936986062	2	2.650688
Q5BJY9	QTQEYEALLNIK	0.881106763	2	3.452058
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.777927192	2	5.979166
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK+Oxidation(14)	0.885678902		
Q5BJY9	TLQTLEIDLDSMK	0.833629935	2	4.245171
Q5BJY9	TLQTLEIDLDSMK+Oxidation(11)	1.027605747		
Q5BJY9	VKLEAEIATYR	1.000312156	2	2.921019
Q5BJY9	VKYETELAMR	0.872300511	3	3.476688
Q5BJY9	VQMEQLNGVLLHLESELAQTR	0.880555345	3	5.1235
Q5BJY9	VRPASSAASVYAGAGGSGSR	1.540739571	2	5.635721
Q5BJY9	VVDDTNITR	0.944893326	2	3.336481
Q5BJY9	YETELAMR	0.909597021	2	2.751773
Q5BJY9	YWSQQIEESTTVVTTK	0.909308382	2	4.745063
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**0.909866528**	**0.99995**	**4**
Q5BK63	AVQHSNVVINLIGR	0.778053779	2	3.384199
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.004719219	3	5.333165
Q5BK63	NFDFEDVFVNIPR	0.924340871	2	3.990403
Q5BK63	WLSSEIEETKPAK	1.010426966	2	2.937504
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.936204732**	**0.59439**	**4**
Q5BK81	AILDGNGLEK	0.959582927	2	2.401326
Q5BK81	DVPYPPPLPPAVEAIQK	1.072783411	2	2.694816
Q5BK81	TGNVAEQLR	0.818159083	2	2.631785
Q5BK81	VEEVSLPDTINEGQVR	0.946391879	2	4.062984
Q5DTT3	**F208B Protein FAM208B**	**1.094456966**	**0.06106**	**2**
Q5DTT3	QGENIDKLMEYVKNK	1.605605622	2	2.326965
Q5DTT3	VSVPSEHSENLSFLEK	0.53194799	2	2.343685
Q5DW34	**EHMT1 Histone_lysine N_methyltransferase EHMT1**	**0.86427355**	**0.19874**	**2**
Q5DW34	TPLMEAAENNHLDAVKYLIK+Oxidation(3)	1.116062357		
Q5DW34	YDCVVLFLSRDSDVTLKNK	0.854297106	2	2.364569
Q5EB77	**RAB18 Ras_related protein Rab_18**	**0.911280289**	**0.7815**	**3**
Q5EB77	LDNWLNELETYCTR	1.287323551	2	2.888129
Q5EB77	NDIVNMLVGNK	0.847309396	2	3.08801
Q5EB77	TCDGVQCAFEELVEK	1.074872559	2	3.467986
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.667634919**	**0.03156**	**2**
Q5FVM4	MEELHNQEVQK	1.071850997	2	3.222231
Q5FVM4	MEELHNQEVQK+Oxidation(0)	1.769721398		
Q5FVQ4	**MLEC Malectin**	**0.86859582**	**1**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	0.918827017	3	5.539516
Q5FVQ4	STPEDQILYQTER	1.037449676	2	4.009935
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.866601858**	**0.24544**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10)	0.787320582		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8)	0.76174461		
Q5FVR2	DVTATVDSVPLITASILSK	1.353790111	2	2.499779
Q5FVR2	FGGAAVFPDQEK	0.630968121	2	2.329409
Q5FVR2	VSLVLAPALAACGCK	0.998608436	2	2.515367
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**0.928722146**	**0.98295**	**4**
Q5FVR5	DEKENLFQSK	0.833613967	2	2.501851
Q5FVR5	ILFIVGENDQCLASK	0.879288148	2	3.897016
Q5FVR5	IQQPGIGVISVSK	0.8241566	2	3.025784

Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	0.846945607	3	4.101441
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**1.099858103**	**0.50862**	**2**
Q5FW57	AIDQEMFK	1.134824195	1	1.990007
Q5FW57	SSQMLQMLESSLR	0.806781405	2	3.754406
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**0.722226885**	**0.33568**	**3**
Q5HZV9	AIENIDTLTNLESLFLGK	0.719618517	2	3.020503
Q5HZV9	ELDLYDNQIK	4.769208912	2	2.357517
Q5HZV9	ELDLYDNQIKK	2.717071414	2	2.40515
Q5HZY0	**UBXN4 UBX domain_containing protein 4**	**1.383995944**	**0.00381**	**2**
Q5HZY0	LPDGSSFTNQFPSDAPLEEAR	1.022176291	2	4.251848
Q5HZY0	NTELCETPTTSDPK	1.520857747	2	4.060839
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**0.97022238**	**0.46755**	**2**
Q5HZY2	EELDSLMTDETIANVPILILGNK	0.953532575	3	3.527583
Q5HZY2	IDRPEAISEER	1.321233829	2	2.671447
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.862079799**	**0.03243**	**6**
Q5I0C3	HAPLVEFEEEEV	0.86720844	2	2.939146
Q5I0C3	IIEEAPAPGIDPEVR	0.828571374	2	3.840908
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	0.827417211	3	3.407942
Q5I0C3	SEKEFQEQLESAR	1.029694393	2	3.20655
Q5I0C3	TNVDFLLR	0.885900234	2	2.382185
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	0.767057325	2	5.126723
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.954044932**	**0.45077**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	0.956906821	2	3.571954
Q5I0D1	HEEFEEGCK	0.869329313	2	2.560919
Q5I0D1	VTLAVSDLQK	0.774237854	2	2.323287
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**0.876573049**	**5.1E-05**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	1.003181208	3	3.789254
Q5I0D5	LGFDISEGEVTAPAPATCQILK	0.792362114	2	4.340418
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**0.8447016**	**0.00234**	**2**
Q5I0D7	GVNTDSGNVCR	1.024624079	2	2.417106
Q5I0D7	YAVDDVQYADEIASVLTSR	0.709723789	2	3.950121
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.080015791**	**0.89902**	**2**
Q5I0E7	QLVEQVEQIQK	0.981995584	2	3.741625
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	1.094687208	3	4.08146
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**0.978951019**	**0.99914**	**4**
Q5I0H9	DKNQDLCQQESVK	1.288592367	2	4.20531
Q5I0H9	GPPLWEEDPGAK	0.879689228	2	3.173129
Q5I0H9	GQGTICWVDCGDAESR	0.803436399	2	4.062721
Q5I0H9	NQDLCQQESVK	0.82880356	2	3.190464
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**0.949158373**	**0.9526**	**8**
Q5I0J9	HANLLVGSPSALADQTTER	0.896287619	2	5.469194
Q5I0J9	IIHESGVQILR	0.995452595	2	2.511107
Q5I0J9	LDAAGGLQSLR	0.878148915	2	3.761127
Q5I0J9	LEGPLAAAHSSGPR	1.011970752	2	3.35916
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.02027611	2	3.098477
Q5I0J9	NSNTMAAAALAAPSLGFDR	0.85347551	2	4.320286
Q5I0J9	TVLYEGPVR	0.998264309	2	2.834515
Q5I0J9	VGVVGYGR	1.026211143	2	2.343987
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.026576064**	**0.23943**	**5**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	0.869926525	3	4.324335
Q5I0M2	DNHVVAAGSMEK	1.334319061	2	2.84924
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.02474069	3	6.041539

Q5I0M2	LYAEGDIPVPHAR	0.93412121	2	2.951888
Q5I0M2	VEVECSSLK	1.021134848	2	2.662642
Q5I0P2	**GCSH Glycine cleavage system H protein_ mitochondrial**	**0.997975305**	**0.92389**	**2**
Q5I0P2	MTLSDPSELDELMSEEAYEK	0.981993313	2	5.214109
Q5I0P2	SCYEDGWLIK	0.937613907	2	2.306847
Q5M7T9	**THNS2 Threonine synthase_like 2**	**1.257787728**	**0.0284**	**3**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	1.25862996	3	5.418866
Q5M7T9	GDFSLCEVVR	1.219809584	2	2.529871
Q5M7T9	MGLPISLVVAVNR	1.052696786	2	2.547187
Q5M7U6	**ARP2 Actin_related protein 2**	**0.857665725**	**0.00099**	**5**
Q5M7U6	GYAFNHSADFETVR	0.779098118	2	3.77078
Q5M7U6	HLWDYTFGPEK	0.946705776	2	3.320496
Q5M7U6	KHMVFLGGAVLADIMK+Oxidation(2)	0.998186012		
Q5M7U6	LCYVGYNIEQEQK	1.739442526	2	2.396196
Q5M7U6	SMLEVNYPMENGIVR	0.815978038	2	3.193145
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.943280439**	**0.00021**	**7**
Q5M7W5	AAVGLTGNDIATPPNK	0.939814892	2	3.546937
Q5M7W5	ATSPSTLVSTGSSSR	0.835434518	2	3.649583
Q5M7W5	NTTPTGATPPAGMASTR	1.188390593	2	2.70681
Q5M7W5	STLPVDEGSPLEK	0.95757449	2	2.402106
Q5M7W5	TEFIPLLDGDEK	0.932704152	2	2.504158
Q5M7W5	VGSLDNVGHLPAGGTVK	1.004237885	2	3.369494
Q5M7W5	VTEFNNVTPLSEEEVASIK	1.04243119	2	3.169424
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.008529836**	**1**	**7**
Q5M875	ALTAELDTLGK	1.046874284	2	2.828357
Q5M875	IQNIQFEAIVGHR	0.808921884	3	3.523788
Q5M875	LWPVLEPDEVAR	1.015699895	2	2.400387
Q5M875	NSGHIVTVASVCGHR	0.976032732	2	4.399843
Q5M875	SLIDGILTNK	1.034492091	2	3.324672
Q5M875	SVAGQTVLITGAGHGIGR	0.971954472	2	4.027478
Q5M875	TSCLCPVFVNTGFTK	0.82419367	2	3.81641
Q5M9G3	**CAPR1 Caprin_1**	**1.265897549**	**0.04618**	**4**
Q5M9G3	LNQDQLDAVSK	1.277427571	2	3.254042
Q5M9G3	SSFSNTPNSGYTQSQFNAPR	0.467756998	2	3.801034
Q5M9G3	TVLELQYVLDK	1.38191888	2	2.437326
Q5M9G3	YQEVTNNLEFAK	1.135537386	2	2.742763
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.052737173**	**0.99879**	**2**
Q5M9I5	EEEEEELVDPLTTVR	0.987852841	2	2.678546
Q5M9I5	SQTEEDCTEELFDFLHAR	1.075171358	2	4.86154
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**1.133252808**	**1**	**9**
Q5PPL3	AVLDANDPKK	1.077095608	2	2.479386
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	1.042250506	2	4.930092
Q5PPL3	DPQLVPVLIDAAR	1.066849468	3	3.405301
Q5PPL3	GQVTGTDLINEVSK	1.040508411	2	3.785707
Q5PPL3	GVSTVFHCASPPSNSNNK	1.16503397	2	4.786042
Q5PPL3	GYAVNVFDVR	1.058943704	2	3.588144
Q5PPL3	ILTGLNYEAPK	1.208675611	2	2.863304
Q5PPL3	KGQVTGTDLINEVSK	1.041909309	2	4.079587
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.022935593	3	5.26558
Q5PQQ2	**WBP11 WW domain_binding protein 11**	**1.149652267**	**0.64213**	**4**
Q5PQQ2	KLEVEYEQK	6.591187209	1	2.173596
Q5PQQ2	LDEMEFNPVQQPQLNEKVLK+Oxidation(3)	1.527272407		
Q5PQQ2	RDEDMLYSPELAQR	1.01596514	2	2.325378

Q5PQQ2	STSSTKSGKFMNPTDQAR	1.034152705	2	2.471763
Q5PQR4	**RSRC2 Arginine/serine_rich coiled_coil protein 2**	**0.973911123**	**0.03844**	**2**
Q5PQR4	EKEMVEK+Oxidation(3)	1.13393557		
Q5PQR4	KEGDKSQSAEIWEK	0.417234391	2	2.543995
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**0.936582725**	**0.99317**	**6**
Q5PQT3	AIQNLASIHSLQVK	0.955590991	2	3.398991
Q5PQT3	DPENCQEFLGSSEVINWK	0.880810897	2	5.326753
Q5PQT3	FWLFGGNER	0.87744249	2	2.415078
Q5PQT3	GFPVYSHTDK	0.907995988	2	2.676879
Q5PQT3	LSSLDVTHAALVNK	1.048674061	2	3.241656
Q5PQT3	QHLQIQSSQSHLNK	1.277601522	2	3.480844
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.06656231**	**0.90967**	**6**
Q5RJR8	ATVLDLSCNK	1.063940553	2	3.114544
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	0.97275399	2	6.028548
Q5RJR8	HHEILQWVLQTDSQQ	0.875709427	2	3.239959
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.100644313	2	3.92303
Q5RJR8	LQQLPADFGR	1.278973355	2	2.354561
Q5RJR8	LSTLPSDFCGLTHLVK	0.82278047	2	3.183544
Q5RKH1	**PRP4B Serine/threonine_protein kinase PRP4 homolog**	**0.860301222**	**0.39576**	**2**
Q5RKH1	DLLDQILMLDPAKR+Oxidation(7)	0.750702287		
Q5RKH1	LAMDLKGKMPNK+Oxidation(2)	0.926704544		
Q5RKH6	**OS9 Protein OS_9**	**0.899560938**	**0.87229**	**3**
Q5RKH6	EQAILALTSTLDK	0.899473429	2	2.423348
Q5RKH6	LQESQSPELVQK	0.899550245	2	2.935137
Q5RKH6	QEQPGDDTTEAPQR	0.919079848	2	3.091011
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.012559816**	**0.99984**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.083161829	3	5.042492
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	0.982706935	3	4.643034
Q5RKI0	YAPSGFYIASGDISGK	0.999707133	2	4.312936
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.200094931**	**9.9E-20**	**5**
Q5RKI1	ELAQQIQK	1.692125453	1	2.229965
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.113840793	2	3.997807
Q5RKI1	GYDVIAQAQSGTGK	1.360185625	2	5.314204
Q5RKI1	MFVLDEADEMLSR	1.138446918	2	4.288107
Q5RKI1	VLITTDLLAR	1.01527245	2	3.487532
Q5S006	**LRRK2 Leucine_rich repeat serine/threonine_protein kinase 2**	**0.970468251**	**0.62545**	**2**
Q5S006	MPRITNLDASR+Oxidation(0)	0.705289833		
Q5S006	WLCKVMAQILTVK	0.972071127	2	2.334558
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.181768306**	**0.00063**	**16**
Q5SGE0	AALDLEQVPSELAVTR	1.026681355	2	4.194396
Q5SGE0	CIANNQVETLEK	1.189781396	2	2.88551
Q5SGE0	DVGEPVPFTEPPESFGFYIK	1.069489047	2	2.966461
Q5SGE0	GLDAIELSR	1.018191191	2	2.69324
Q5SGE0	HCVTMDTPAEK	1.064960955	2	3.008977
Q5SGE0	HDNAEDALNLK	1.246195927	2	3.565758
Q5SGE0	MEGANIQPNR	1.060031679	2	2.722537
Q5SGE0	SCGSLLPELSLAER	1.152410779	2	2.36615
Q5SGE0	SCGSLLPELSLAERTEFAHK	1.202882507	2	2.40415
Q5SGE0	SGSPGSNQALLLLR	1.243669426	2	2.828588
Q5SGE0	SSLSSSSPSAGDTVTEK	1.021823668	2	4.347086
Q5SGE0	SYVADKDVASAK	1.154812475	2	2.857055
Q5SGE0	TLLELIPELR	1.150721904	2	3.005342

Q5SGE0	TSQFTSSDLESTLEK	1.348069383	2	3.05048
Q5SGE0	VIEEQMEPALEK	1.118336951	2	2.92843
Q5SGE0	VYLQNEYR	1.243314664	2	2.451252
Q5SNZ0	**GRDN Girdin**	**0.99562514**	**0.44764**	**2**
Q5SNZ0	KVEILENEIIQEK	0.910911438	2	2.523196
Q5SNZ0	YNQLLKQKGQLEDLEK	0.829205835	2	2.643322
Q5SW19	**K0664 Protein KIAA0664**	**1.210023268**	**1.1E-06**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	0.942680592	2	2.93945
Q5SW19	IGIGELITR	1.462568761	2	2.917611
Q5SW19	SVEGLQEGSVLR	1.284991651	2	2.823326
Q5SX40	**MYH1 Myosin_1**	**1.114896768**	**1**	**95**
Q5SX40	AAYLQNLNSADLLK	1.090997505	2	3.658021
Q5SX40	ADIAESQVNK	1.103517044	2	4.055568
Q5SX40	AEDEEEINAELTAK	1.09556516	2	4.381058
Q5SX40	AGLLGLLEEMR	2.234620657	2	3.978479
Q5SX40	AGLLGLLEEMRDDK	2.090902779	2	3.335037
Q5SX40	ALQEAHQQTLDDLQAEEDK	2.555849046	2	5.756624
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	2.596350461	3	6.764009
Q5SX40	ANLLQAEIEELR	2.33304926	2	3.93121
Q5SX40	ANSEVAQWR	1.236351014	2	3.037319
Q5SX40	DLEEATLQHEATAATLR	3.300992093	2	4.96199
Q5SX40	DTQLHLDDALR	3.288869614	1	3.613188
Q5SX40	EEQAEPDGTEVADK	4.830731653	2	3.558584
Q5SX40	EFEMSNLQSK	2.454573062	1	2.543429
Q5SX40	ELEEISER	7.139843504	1	2.076466
Q5SX40	ELEGEVENEQK	4.394209225	2	2.69849
Q5SX40	ELEGEVENEQKR	6.010647342	2	3.285165
Q5SX40	ELTYQTEEDRK	3.523689324	2	3.095385
Q5SX40	ENQSILITGESGAGK	3.819238706	2	4.716943
Q5SX40	EQYEEEQEAK	3.604105803	1	3.199806
Q5SX40	GQEDLKEQLAMVER	2.988814676	2	4.443505
Q5SX40	GSSFQTVSALFR	1.693728181	2	3.03157
Q5SX40	HADSVAELGEQIDNLQR	2.436188471	2	5.959991
Q5SX40	IAEQELLDASER	3.017602672	2	3.778352
Q5SX40	IEAQNKPFDAK	2.809624814	2	2.748584
Q5SX40	IEDEQALGMQLQK	1.994306038	2	4.865421
Q5SX40	IEDEQALGMQLQK+Oxidation(8)	4.569097178		
Q5SX40	IEDMAMMTHLHEPAVLYNLK	1.167037947	3	4.340081
Q5SX40	IEELEEEIEAER	2.329166246	2	4.26683
Q5SX40	IKLEQQVDDLEGSLEQEK	3.165629548	2	5.140683
Q5SX40	IKLEQQVDDLEGSLEQEKK	4.401247926	2	5.21932
Q5SX40	INQQLDTK	1.68520903	1	2.172988
Q5SX40	IQHELEEAEER	3.435080516	2	3.616211
Q5SX40	IQLELNQVK	2.453451554	2	2.780883
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	3.84470158	3	7.394549
Q5SX40	KIAEQELLDASER	3.697220893	2	3.631049
Q5SX40	KIQHELEEAEER	1.634400315	2	3.797122
Q5SX40	KKEFEMSNLQSK	2.928492402	2	4.017015
Q5SX40	KKLETDISQIQGEMEDIVQEAR	1.364252756	3	5.967843
Q5SX40	KLEDECSELK	1.855943997	2	3.074796
Q5SX40	KLEDECSELKK	1.956122314	3	4.254461
Q5SX40	KLETDISQIQGEMEDIVQEAR	2.174334121	2	5.557512
Q5SX40	KMEGDLNEMEIQLNHSNR	1.530758647	3	4.224661
Q5SX40	KMEGDLNEMEIQLNHSNR+Oxidation(1)	1.68996793		
Q5SX40	LAQESTMDVENDKQQLDEK	6.434213661	2	4.648623
Q5SX40	LDEAEQLALK	1.663346653	2	3.962439
Q5SX40	LEDECSELK	1.247752284	2	2.378723

Q5SX40	LEDECSELKK	4.728246884	2	2.886516
Q5SX40	LEEAGGATSAQIEMNK	1.229038366	2	4.728858
Q5SX40	LEEAGGATSAQIEMNK+Oxidation(13)	1.032594091		
Q5SX40	LEQQVDDLEGSLEQEK	4.168673522	2	5.633994
Q5SX40	LEQQVDDLEGSLEQEKK	1.015997705	2	4.511164
Q5SX40	LETDISQIQGEMEDIVQEAR	1.154059633	2	5.562187
Q5SX40	LINELTAQR	2.312810325	2	2.947413
Q5SX40	LLGSIDIDHTQYK	1.47630553	2	3.481214
Q5SX40	LQDAEEHVEAVNAK	3.310406178	2	4.967914
Q5SX40	LQDLVDK	4.464186729	1	2.132548
Q5SX40	LQDLVDKLQSK	1.167755456	2	2.583841
Q5SX40	LQNEVEDLMIDVER	2.841295768	2	4.725507
Q5SX40	LQTESGEYSR	2.698383715	2	2.525086
Q5SX40	LYEQHLGK	2.109967271	2	2.32573
Q5SX40	MEGDLNEMEIQLNHSNR	1.597542487	2	4.659929
Q5SX40	MEIDDLASNMEVISK	4.718085282	2	5.13623
Q5SX40	MEIDDLASNMEVISK+Oxidation(0)	3.196379227		
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	0.595366629	3	6.71066
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0)	2.161888183		
Q5SX40	NDLQLQVQSEADSLADAEER	2.072308529	2	6.70725
Q5SX40	NKDPLNETVVGLYQK	2.799779271	2	4.822206
Q5SX40	NLQQEISDLTEQIAEGGK	2.458306586	2	6.905754
Q5SX40	NLQQEISDLTEQIAEGGKR	3.003353147	2	3.748134
Q5SX40	NLTEEMAGLDETIAK	2.294244473	2	4.854417
Q5SX40	NLTEEMAGLDETIAK+Oxidation(5)	1.995676357		
Q5SX40	QAEEAEEQSNVNLAK	4.949209096	2	4.537892
Q5SX40	QKYEETHAELEASQK	3.895319921	2	4.468509
Q5SX40	QLDEKDSLVSQLSR	0.961290758	2	3.07626
Q5SX40	QLEEEIK	1.438073781	1	2.149653
Q5SX40	QREEQAEPDGTEVADK	4.265142878	2	3.97609
Q5SX40	RANLLQAEIEELR	4.604468763	2	2.33789
Q5SX40	RDLEEATLQHEATAATLR	0.766409313	2	4.946259
Q5SX40	SAETEKEMANMK	1.065068404	2	3.064342
Q5SX40	SAETEKEMANMKEEFEK	13.4956891	2	4.918159
Q5SX40	SELQAALEEAEASLEHEEGK	4.131502877	2	6.020133
Q5SX40	SLSTELFK	2.203734087	2	2.412401
Q5SX40	SSVFVVDAK	5.783367557	1	2.125075
Q5SX40	TKYETDAIQR	1.143725897	3	3.493541
Q5SX40	TLEDQVSELK	1.621188781	2	3.506889
Q5SX40	TNAACAALDKK	4.275091062	2	3.200219
Q5SX40	VKELTYQTEEDRK	0.859609735	2	3.684565
Q5SX40	VLNASAIPEGQFIDSK	2.300788165	2	4.429382
Q5SX40	VQLLHTQNTSLINTK	2.227741675	2	4.620411
Q5SX40	VRELEGEVENEQKR	2.854410956	3	3.889015
Q5SX40	VVESMQSTLDAEIR	1.335515537	2	4.080634
Q5SX40	VVESMQSTLDAEIR+Oxidation(4)	1.678529058		
Q5SX40	YDKIEDMAMMTHLHEPAVLYNLK	0.794352318	3	4.390036
Q5SX40	YEETHAELEASQK	4.433653892	2	4.767837
Q5SX40	YETDAIQR	2.281704755	2	2.578749
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.081677629**	**0.62299**	**5**
Q5U206	DTDSEEEIR	1.345776153	2	2.707368
Q5U206	KMKDTDSEEEIR	0.492929354	2	2.306405
Q5U206	KMKDTDSEEEIR+Oxidation(1)	1.502543019		
Q5U206	MKDTDSEEEIR	0.919219524	2	3.104297
Q5U206	MKDTDSEEEIR+Oxidation(0)	1.205500232		
Q5U211	**SNX3 Sorting nexin_3**	**0.887203819**	**0.36306**	**2**
Q5U211	CLHMFLQDEIIDK	0.698807615	2	2.37173

Q5U211	GDDGIFDDNFIEER	1.068358192	2	2.842775
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.127140191**	**0.90157**	**3**
Q5U2Q7	LSVLGAITSVQQR	0.991676163	2	2.402318
Q5U2Q7	YFDEISQDTGK	1.349632284	2	2.682383
Q5U2Q7	YVLHCQGTEEEK	1.140245297	2	3.63262
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.005918284**	**0.17908**	**12**
Q5U300	AAVASLLQSVQVPEFTPK	0.963073759	3	3.715683
Q5U300	AENYDISPADR	1.049928845	2	2.99153
Q5U300	DNPGVVTCLDEAR	1.083506096	2	3.39023
Q5U300	FEVQGLQPNGEEMTLK	1.054170454	2	3.892946
Q5U300	IYDDDFFQNLDGVANALDNVDAR	0.78556146	2	4.449693
Q5U300	LDQPMTEIVSR	0.98793736	2	2.627829
Q5U300	MLQTSSVLVSGLR	0.941185843	2	2.372286
Q5U300	NEEDATELVTLAQAVNAR	0.907955023	2	4.557729
Q5U300	NFPNAIEHTLQWAR	1.121282577	2	3.440497
Q5U300	SLPASLAEPDFVMTDFAK	0.941989761	2	3.549592
Q5U300	SPPAVQQDNVDEDLIR	1.009104623	2	4.720029
Q5U300	VVQGHQQLDSYK	1.251390997	2	3.925257
Q5XFX0	**TAGL2 Transgelin_2**	**0.88290221**	**3.3E-05**	**4**
Q5XFX0	DDGLFSGDPNWFPK	0.831092056	2	3.560257
Q5XFX0	QMEQISQFLQAAER	0.733342482	2	3.099038
Q5XFX0	TLMNLGGLAVAR	0.987712384	2	3.554724
Q5XFX0	YGINTTDIFQTVDLWEGK	0.81692367	2	5.069996
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**0.979639483**	**0.9977**	**11**
Q5XHY5	AEHDSILAEK	0.95390885	2	2.597994
Q5XHY5	DQELYFFHELSPGSCFFLPK	1.703786843	3	3.418052
Q5XHY5	FLGDIEIWNQAEK	0.930435667	2	3.594064
Q5XHY5	FMVDIDLDPGCTLNK	0.839338135	2	2.976842
Q5XHY5	GFQEVVTPNIFNSR	0.964344465	2	3.122215
Q5XHY5	LKAEHDSILAEK	2.347741129	2	3.249691
Q5XHY5	NELSGALTGLTR	0.978990039	2	3.266307
Q5XHY5	QLENSLNEFGEK	1.086529139	2	3.185023
Q5XHY5	QVMVVPVGPTCDEYAQK	1.013544181	2	3.267956
Q5XHY5	TTPYQIACGISQGLADNTVVAK	0.975849595	2	4.226333
Q5XHY5	WELNPGDGAFYGPK	0.992931757	2	3.761512
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**0.996024345**	**0.83852**	**13**
Q5XHZ0	AFLEALQHQAETSSR	0.992182485	2	4.587068
Q5XHZ0	AQLLQPTLEINPR	1.04575607	2	3.477069
Q5XHZ0	EELVSNLGTIAR	0.994658205	2	2.55594
Q5XHZ0	ELISNASDALEK	1.264057473	2	3.58824
Q5XHZ0	FEDTSPAGER	1.223755235	2	2.767632
Q5XHZ0	GTITIQDTGIGMTK	0.977000135	2	3.493619
Q5XHZ0	GVVDSEDIPLNLSR	1.043524545	2	4.912754
Q5XHZ0	HLAEHSPYYEAMK	1.41280922	2	3.282081
Q5XHZ0	LDTHPAMVTVLEMGAAR	0.921838038	3	4.365638
Q5XHZ0	SDCKDFANESR	1.089544699	2	2.759222
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	1.152062535	3	3.615469
Q5XHZ0	YESSALPAGQLTSLSDYASR	0.938285873	2	5.707639
Q5XHZ0	YIAQAYDKPR	1.245561574	2	2.878207
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.163934602**	**0.99873**	**7**
Q5XI22	AGHFDKEIVPVHVSSR	1.041195792	2	4.251559
Q5XI22	HGSNLEAMSK	0.974257856	2	2.778616
Q5XI22	HGSNLEAMSK+Oxidation(7)	0.645903841		
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	1.322236166	3	4.880542

Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	1.124636253	2	4.888167
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	1.341191023	3	5.933632
Q5XI22	VNIDGGAIALGHPLGASGCR	1.136068484	2	5.820588
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.042244595**	**0.69877**	**7**
Q5XI32	KLEVEANNAFDQYR	1.019626888	2	4.473894
Q5XI32	LEVEANNAFDQYR	1.03510842	2	3.371792
Q5XI32	LVEDMENK	1.515710792	2	2.319997
Q5XI32	NLSDLIDLVPSLCEDLLSSVDQPLK	0.901392818		
Q5XI32	SGSGTMNLGGSLTR	0.971555594	2	2.868657
Q5XI32	STLNEIYFGK	0.829081988	2	2.610337
Q5XI32	YDPPLEDGAMPSAR	0.891994662	2	2.523153
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.525954479**	**1.3E-14**	**3**
Q5XI60	ALDIAAGITR	1.727648638	2	3.583572
Q5XI60	HHVALDSAASQLSGR	1.514115404	2	4.258485
Q5XI60	NVATDALGALEAR	1.772750259	2	3.819297
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.003608776**	**0.70224**	**6**
Q5XI73	AEEYEFLTPMEEAPK	0.897001241	2	4.365891
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	0.861667345	3	3.312611
Q5XI73	SIQEIQELDKDDESLR	0.534717216	2	4.934564
Q5XI73	SIQEIQELDKDDESLRK	0.877490852	2	4.319915
Q5XI73	TDYMVGSYGPR	0.883055165	2	2.67347
Q5XI73	VAVSADPNVPNVIVTR	1.009208934	2	4.454436
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**1.056545094**	**0.84216**	**15**
Q5XI78	FGLEGCEVLIPALK	1.223519586	2	3.408001
Q5XI78	FLDTAFDLDAFK	1.05562319	2	2.468751
Q5XI78	FLDTAFDLDAFKK	1.104960186	2	2.83962
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	0.827931545	3	4.433742
Q5XI78	ICEEAFTR	1.119429064	2	2.440774
Q5XI78	IEQLSPFPFDLLLK	1.107931088	2	3.613792
Q5XI78	LEAADEGSGDMK	0.962488269	2	2.423432
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.196309743	3	4.982562
Q5XI78	NTNAGAPPGTAYQSPLSLSR	1.059150531	2	4.521922
Q5XI78	SSLATMAHAQSLVEAQPNVDK	1.055787634	3	4.480308
Q5XI78	SWDIFFR	1.061546411	2	2.353437
Q5XI78	VIPEDGPAAQNPDK	1.317473999	2	3.079614
Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	0.857625735	3	4.211287
Q5XI78	YAELLVSQGVVNQPEYEEEISK	0.847204368	2	4.176691
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	1.067682322	3	3.80502
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**0.664680249**	**0.14382**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.59795285	2	3.88944
Q5XI95	IIAVDINK	0.766409596	2	2.875825
Q5XI95	MVATGVCGTDIK	0.835351015	2	3.224852
Q5XI95	NNICTEIR	0.802799521	2	2.461977
Q5XI95	TVGATDCVDPR	0.579896645	2	2.601793
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.033167878**	**0.01859**	**5**
Q5XIC0	ATQQDFENAMNQVK	0.824424859	2	4.765385
Q5XIC0	GILVTSEGGITK	0.965722388	2	3.844986
Q5XIC0	LHAVNEEECTTLR	0.901982213	2	3.651217
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	1.053423669	2	5.1551
Q5XIC0	WDAWNALGSLPK	0.826129745	2	3.596739
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**0.822129206**	**0.90743**	**5**
Q5XIE6	AGIATHFVDSEK	1.189792143	2	3.386729
Q5XIE6	AGQTLSQDLFR	1.037779191	2	2.382031

Q5XIE6	AVLIDKDQTPK	1.318005625	2	2.594764
Q5XIE6	INSCFSANTVEQILENLR	0.925919007	2	3.847363
Q5XIE6	LHVLEEELLALK	1.227919072	3	3.679724
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.031178061**	**0.9996**	**2**
Q5XIF3	HGWSYDVEGR	0.990146035	2	2.842702
Q5XIF3	LDVTPLTGVPEEHIK	1.047505059	3	3.608404
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.007768536**	**0.99474**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	1.010557729	2	3.760549
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.021563765	3	5.324975
Q5XIF6	DVNAAIAAIK	1.001302472	2	2.880304
Q5XIF6	SIQFVDWCPTGFK	0.948549905	2	4.34043
Q5XIF6	TIGGGDDSFTTFFCETGAGK	1.391457055	2	4.564332
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.215742971**	**0.70463**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	0.734049596	2	3.996675
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.209014993	2	5.894697
Q5XIH7	**PHB2 Prohibitin_2**	**0.895338903**	**0.85329**	**11**
Q5XIH7	AQVSLLIR	1.148296746	2	2.773294
Q5XIH7	DLQMVNISLR	1.07256814	2	3.193563
Q5XIH7	FNASQLITQR	0.868386561	2	3.687476
Q5XIH7	IGGVQQDTILAEGLHFR	0.948050298	3	4.425041
Q5XIH7	IPWFQYPIIYDIR	0.990266264	2	2.953961
Q5XIH7	IVQAEGEAEAAK	0.896884531	2	4.184361
Q5XIH7	IYLTADNLVLNLQDESFTR	0.958619158	2	4.575488
Q5XIH7	LGLDYEER	1.083676565	2	2.598001
Q5XIH7	LLLGAGAVAYGVR	1.247592832	2	3.493178
Q5XIH7	VLPSIVNEVLK	0.771002941	2	2.815963
Q5XIH7	VLSRPNAQELPSMYQR	1.050536096	2	3.836985
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.211037853**	**6.6E-11**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	1.50399608	2	4.211146
Q5XIM9	GATQQILDEAER	1.226044355	2	3.909883
Q5XIM9	GSGNLEAIHVIK	1.515838091	2	2.915132
Q5XIM9	HGINCFINR	1.161565772	2	2.540056
Q5XIM9	ILIANTGMDTDK	1.448690661	2	2.742394
Q5XIM9	LIEEVMIGEDK	1.124636568	2	3.128077
Q5XIM9	NIGVDNPAAK	1.032826359	1	2.026639
Q5XIM9	SLHDALCVLAQTVK	1.052470943	2	3.778103
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.174983342	2	4.557994
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.020205391**	**0.92971**	**6**
Q5XIN6	AAEVEGEQVDNK	1.012089466	2	4.005324
Q5XIN6	FLQDTIEEMALK	1.024189813	2	2.958354
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.951097497	2	5.473849
Q5XIN6	LEEGGPVYSPPAQVVVK	0.960244977	2	3.09571
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.185745549	3	4.42701
Q5XIN6	LLELQSIGTNNFLR	0.927223551	2	2.988791
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**0.869319889**	**0.7888**	**10**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.967586663	2	4.953421
Q5XIT9	ALVNQLHER	1.091502569	2	2.587605
Q5XIT9	ALYGDTLVTGFAR	0.925025102	2	3.679648
Q5XIT9	AQEIALQNR	0.804739942	2	2.627568
Q5XIT9	DRIDNLIDPGSPFLEFSQFAGYK	1.15070323	3	4.390281
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	0.94000089	3	4.436713
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.212516059	2	5.084144
Q5XIT9	LWDDGIIDPVDTR	0.903379105	2	3.265567
Q5XIT9	LYGEEEVPAGGIITGIGR	0.896540906	2	4.380058

Q5XIT9	QGTIFLAGPPLVK	1.09954839	2	2.46614
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**1.024481557**	**0.85711**	**2**
Q5XIU5	ALIDPSSGLPNR	1.030593597	2	2.540231
Q5XIU5	DPLSPFAVGGEDLDPFGCQR	0.9015553	2	2.728643
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**0.886763189**	**0.31973**	**3**
Q5XIU9	FYGPAGPYGIFAGR	0.893592548	2	2.765221
Q5XIU9	GLATFCLDK	1.096566803	2	2.848962
Q5XIU9	GLCSGPGAGEESPAATLPR	0.877928717	2	4.786752
Q5XKE0	**MYPC2 Myosin_binding protein C_ fast_type**	**0.879150069**	**0.58348**	**3**
Q5XKE0	LVVEISDPDLPLK	0.864154375	2	2.824512
Q5XKE0	SEDAGELDFSGLLK	2.356049842	2	3.418824
Q5XKE0	TSDNSIVVVAGNK	1.165290117	2	2.627337
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**1.15251665**	**0.98776**	**7**
Q60587	ALAMGYKPK	0.951584936	2	2.537009
Q60587	AQDEGHLSDIVPFK	1.08558867	2	3.040215
Q60587	DFIYVSQDPK	0.98036525	2	2.675435
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.899194925	3	4.630652
Q60587	DNGIRPSSLEQMAK	1.20516023	2	3.24394
Q60587	DQLLLGPTYATPK	1.334088231	2	3.72816
Q60587	NIVVVEGVR	0.955506618	2	2.859435
Q60598	**SRC8 Src substrate cortactin**	**1.490363953**	**0.41636**	**3**
Q60598	ENVFQEHQTLK	1.866262875	2	2.305964
Q60598	NASTFEEVVQVPSAYQK	1.058629545	2	3.476493
Q60598	VDQSAVGFEYQGK	1.139100891	2	3.031708
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.015083144**	**0.74569**	**4**
Q60759	DILGGNGISDEYHVIR	1.143024561	2	3.724004
Q60759	DIVYEMGELGVLGPTIK	1.178492328	2	2.378566
Q60759	GYGCAGVSSVAYGLLTR	1.051798062	2	3.495746
Q60759	HAMNLEAVNTYEGTHDIHALILGR	0.965612533	4	5.504468
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.166541735**	**1.2E-06**	**3**
Q60817	DIELVMSQANVSR	1.171336547	2	3.21888
Q60817	IEDLSQQAQLAAAEK	1.541366967	2	4.623466
Q60817	NILFVITKPDVYK	1.006380802	2	3.316381
Q60952	**CP250 Centrosome_associated protein CEP250**	**0.947124402**	**0.96061**	**2**
Q60952	AQVIESQRGQIQDLK	0.973397554	2	2.485214
Q60952	GQIQDLKK	0.880081316	1	1.926622
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.881999237**	**0.23854**	**3**
Q61029	SELVANNVTLPAGEQR	0.945684291	2	4.318009
Q61029	SSTPLPTVSSSAENTR	0.867774296	2	2.861665
Q61029	YGVNPGPIVGTTR	0.918369902	2	2.49091
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.323817419**	**0.31042**	**2**
Q61035	ASAEQIEEEVTK	1.373156897	2	3.13664
Q61035	REDLVEEIR	1.300422096	2	2.446332
Q61043	**NIN Ninein**	**0.929551137**	**0.64266**	**2**
Q61043	ERATAAAMKQEQEILER	2.25561267	2	2.347957
Q61043	NEITTLNEEDSISNLK	0.929534697	2	2.369422
Q61301	**CTNA2 Catenin alpha_2**	**0.926803509**	**0.00342**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	0.888157331	2	3.852325
Q61301	TSVQTEDDQLIAGQSAR	1.403125436	2	5.11628
Q61301	WDDSGNDIIVLAK	1.016087447	2	3.063114
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.928971926**	**0.89061**	**3**
Q61335	AENEALAMQK	0.947486613	2	3.189856

Q61335	AENEALAMQK+Oxidation(7)	0.890494407		
Q61335	YMEENDQLK	0.804308952	2	2.606822
Q61595	**KTN1 Kinectin**	**1.250970317**	**0.53625**	**3**
Q61595	EKNWEAMEALASTEK	1.234382234	2	2.303116
Q61595	TAEHEAAQQDLQSK	0.980977664	2	4.094522
Q61595	VEPVLVTK	1.2866948	2	2.391616
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**1.164751951**	**4.8E-12**	**5**
Q61656	ELAQQVQQVAAEYCR	3.102005376	2	3.525018
Q61656	GDGPICLVLAPTR	1.302255835	2	3.290333
Q61656	LIDFLECGK	1.544147673	2	2.377806
Q61656	MLDMGFEPQIR	0.98596479	2	2.734263
Q61656	WNLDELPK	1.592203583	2	2.339129
Q61789	**LAMA3 Laminin subunit alpha_3**	**0.88128229**	**0.2042**	**2**
Q61789	QLEEIK	0.759123921	1	2.071705
Q61789	RLQQVSPALNSLQQTLK	0.897934673	2	2.358094
Q61838	**A2M Alpha_2_macroglobulin**	**0.77070245**	**0.18268**	**2**
Q61838	QQNSHGGFSSTQDTVVALQALSK	0.764969466	3	3.40497
Q61838	TEVNTNHVLIYIEK	0.812374013	2	4.017232
Q61941	**transhydrogenase_ mitochondrial**	**0.999306219**	**0.99535**	**11**
Q61941	EANSIVITPGYGLCAAK	0.950930316	2	3.62171
Q61941	FGIHPVAGR	0.985986831	2	2.600293
Q61941	GITHIGYTDLPSR	0.939056031	3	3.492761
Q61941	ILIVGGGVAGLASAGAAK	1.042282097	2	4.986356
Q61941	KTTVLAMDQVPR	0.911373158	2	3.020321
Q61941	LGGLTAALGGAVGIMGLANGLR+Oxidation(14)	0.920000671		
Q61941	MATQASTLYSNNITK	1.2914382	2	4.302822
Q61941	QGFNVVVESGAGEASK	1.089983315	2	3.995804
Q61941	SLGAEPLEVDLK	0.871167192	2	3.072893
Q61941	TTVLAMDQVPR	0.88408037	2	3.108333
Q61941	VTIAQGYDALSSMANISGYK	0.954111056	2	5.16627
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.566200901**	**2.3E-10**	**7**
Q62095	DLLDLLVEAK	7.810258091	2	2.673614
Q62095	GCHLLVATPGR	1.967858985	2	2.422241
Q62095	HVINFDLPSDIEEYVHR	1.3900748	3	3.741286
Q62095	QYPISLVLAPTR	1.285044751	2	2.366513
Q62095	SFLLDLLNATGK	1.275057116	2	4.648483
Q62095	VGNLGLATSFFNER	1.892901578	2	3.054713
Q62095	VGSTSENITQK	1.786898053	2	2.719128
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.012880736**	**0.56574**	**17**
Q62261	ALVADSHPESER	1.035743917	2	3.214828
Q62261	EGMQLISEKPETEAVVK	1.003669613	2	2.633162
Q62261	EIEELQSQAQALSQEGK	1.183202178	2	4.620604
Q62261	EVDDLEQWIAER	1.162619595	2	2.469398
Q62261	EVVAGSHELGQDYEHVTMLQER	0.969032946	3	4.185279
Q62261	HQILEQAVEDYAETVHQLSK	0.5574596	3	4.062027
Q62261	ITDLYTDLR	1.06731078	2	2.601324
Q62261	IVSSNDVGHDEYSTQSLVK	1.113402591	3	3.53696
Q62261	LSDGNEYLFQAK	0.787260876	2	2.425565
Q62261	LVSDGNINSDR	1.163393973	2	3.226314
Q62261	LVSQDNFGFDLPAVEAATK	1.090111137	2	3.10879
Q62261	SNAHYNLQNAFNLAEQHLGLTK	1.001471995	3	3.701616
Q62261	SQNIITDSSSLNAEAIR	1.236284215	2	5.182074
Q62261	TLETPAAQMEGFLNR	0.882641869	2	3.75248
Q62261	TQTAIASEDMPNTLTEAEK	1.131991863	2	5.141212
Q62261	VIESTQDLGNDLAGVMALQR	0.920824487	3	4.310005
Q62261	VLDNAIETEK	0.980649619	2	2.523117

Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.102438677**	**0.99927**	**3**
Q62425	FYSVNVDYSK	1.115392261	2	2.875136
Q62425	KNNPEPWNK	1.085474633	2	2.46735
Q62425	LGPNEQYK	0.993377542	2	2.303015
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**0.999202064**	**0.95787**	**2**
Q62446	FLQDHGSDSFLAEHK	0.946321025	3	3.677244
Q62446	SEETLDEGPPK	1.057010698	2	3.49318
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**0.914641985**	**0.05023**	**5**
Q62452	AMEIAEALGR	1.069149448	2	3.802165
Q62452	GAGVTLNVLEMTADDLENALK	0.795435675	3	5.544568
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(10)	1.056148335		
Q62452	WLPQNDLLGHPK	0.949719718	2	3.141353
Q62452	YTGTRPSNLAK	1.343051024	2	2.621476
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.030044645**	**0.03938**	**6**
Q62465	ACGLNFADLMGR	0.988972201	2	3.002732
Q62465	CLVLTGFGGYDK	0.986846757	2	3.433311
Q62465	GVDIVMDPLGGSDTAK	1.004119125	2	4.022839
Q62465	IDSVWPFEK	0.883860242	1	1.947339
Q62465	TVENVTVFGTASASK	0.976876649	2	3.884974
Q62465	VLLVPGPEKET	0.822286046	2	2.681477
Q62468	**VILI Villin_1**	**1.068736595**	**0.7633**	**2**
Q62468	HEDCYILDQGGLKIFVWK	1.081557052	2	2.466425
Q62468	SGAMSQALNFIKAK	1.04941144	2	2.343069
Q62636	**RAP1B Ras_related protein Rap_1b**	**0.93099977**	**0.28458**	**3**
Q62636	INVNEIFYDLVR	0.796529623	2	3.998847
Q62636	QWSNCAFLESSAK	0.990567665	2	2.809093
Q62636	YDPTIEDSYR	0.780427097	2	2.369595
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.802231769**	**0.00029**	**7**
Q62651	HVLHVQLNRPEK	0.86972627	2	3.623407
Q62651	IPEEVSDHNYESIQVTSAQK	1.059046971	3	3.86903
Q62651	MMADEALDSGLVSR	1.084672952	2	3.596234
Q62651	MMADEALDSGLVSR+Oxidation(0)	0.833059933		
Q62651	MMADEALDSGLVSR+Oxidation(1)	0.833059933	2	3.352635
Q62651	RIPEEVSDHNYESIQVTSAQK	1.123230166	3	5.695125
Q62651	SLVNELTFTAR	0.706527619	2	3.470867
Q62717	**CAPS1 Calcium_dependent secretion activator 1**	**0.958335506**	**0.42048**	**2**
Q62717	IDELIEETVK	1.087272513	2	2.579759
Q62717	NCPDQDLKIK	0.794428871	1	1.930554
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**1.294936673**	**0.08673**	**4**
Q62730	AVLVTGADSGFGHALAK	1.294299491	2	4.166598
Q62730	EIQENYGQEYVHTQK	1.5134839	2	4.414559
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.751531656	3	4.516719
Q62730	VVTIHPGGFQTNIVGSQDSWDK	1.324631064	2	5.433097
Q62736	**CALD1 Non_muscle caldesmon**	**0.877768295**	**0.01277**	**12**
Q62736	ASGDKEAEGAPQVEAGK	0.853002879	2	4.556921
Q62736	ASGDKEAEGAPQVEAGKR	0.920504498	3	3.881339
Q62736	EEIERR	2.150410157	1	1.936645
Q62736	EFDPTITDGSLSVPSR	1.399150774	2	3.764091
Q62736	GETESEEFEK	0.929446176	2	2.755527
Q62736	GGNLGENQIKDEK	0.803164935	2	3.428121
Q62736	LEQYTNAIEGTK	0.739881375	2	3.908771
Q62736	MQNNSAENETAEGEEKGESR	0.70818354	3	4.421706

Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0)	0.841488089		
Q62736	NDDDEEEAAR	0.687317399	2	3.356249
Q62736	RGETESEEFEK	1.002092665	2	3.156646
Q62736	VLEEEEQR	1.011273242	2	2.471493
Q62745	**CD81 CD81 antigen**	**0.8283933**	**0.84524**	**2**
Q62745	NSLCPSSSNSFTQLLK	1.110589183	2	2.734691
Q62745	QFYDQALQQAVMDDDANNAK	0.739071576	2	5.214956
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.051751758**	**0.95189**	**3**
Q62785	ANEEDEQEEGGDGASGDPK	1.279174871	2	4.265042
Q62785	GVEGLIDIENPNR	1.041224493	2	2.859095
Q62785	KVTQLDLDGPK	1.003048466	2	2.811088
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**0.881233857**	**0.99639**	**2**
Q62789	IILDELVQR	0.86655821	2	3.580021
Q62789	WIPQNDLLGHPK	0.949719718	2	3.141353
Q62812	**MYH9 Myosin_9**	**0.892704147**	**0.00025**	**63**
Q62812	ALEEAMEQK	0.965179557	2	3.043352
Q62812	ALELDSNLYR	0.982274344	2	3.322808
Q62812	ALEQQVEEMK	1.009287567	2	2.959561
Q62812	ANLQIDQINTDLNLER	0.90970373	2	4.672554
Q62812	ASIAALEAK	0.925216089	2	2.564772
Q62812	ASREEILAQAK	1.088566939	2	2.888782
Q62812	CQYLQAEK	0.92359633	2	2.452314
Q62812	DELADEIANSSGK	1.264093387	2	2.848852
Q62812	DFSALESQLQDTQELLQEENR	0.916792363	3	5.59496
Q62812	DLEAHIDTANK	1.556418141	2	3.227349
Q62812	DLQGRDEQSEEK	0.396341398	2	3.219682
Q62812	EEILAQAK	1.039399418	1	2.314359
Q62812	EEILAQAKENEK	0.803164935	2	2.380374
Q62812	ELEDATETADAMNR	1.143810592	2	4.125894
Q62812	ELETQISELQEDLESER	0.921647189	2	3.977254
Q62812	HEAMITDLEER	0.888001525	2	3.125541
Q62812	HEDELLAK	0.889484646	2	2.814973
Q62812	HSQAVEELAEQLEQTK	0.914883688	2	4.944811
Q62812	HSQAVEELAEQLEQTKR	0.944970893	3	4.918312
Q62812	IIGLDQVAGMSETALPGAFK	0.972103879	2	5.328916
Q62812	IRELETQISELQEDLESER	1.03942096	3	3.549749
Q62812	KEEELQAALAR	0.994222724	2	3.150658
Q62812	KKVEAQLQELQVK	0.858732233	2	4.650298
Q62812	KLEEDQIIMEDQNCK	1.039183218	2	5.908616
Q62812	KLEGDSTDLSDQIAELQAQIAELK	0.890462601	2	5.83131
Q62812	KQELEEICHDLEAR	0.977018039	2	4.495746
Q62812	KVEAQLQELQVK	1.033384259	2	4.244519
Q62812	LEEDQIIMEDQNCK	0.919377774	2	4.514317
Q62812	LEGDSTDLSDQIAELQAQIAELK	0.802107753	2	3.573766
Q62812	LEVNLQAMK	0.821580371	2	2.709557
Q62812	LQEMESAVK	0.88299323	2	2.543259
Q62812	LQQELDDLLVDLDHQR	0.965337647	2	4.783808
Q62812	LQVELDSVTGLLNQSDSK	0.926236343	2	5.731694
Q62812	LTEMETMQSQLMAEK	0.912172032	2	3.787762
Q62812	MEDGVGCLETAEEAK	1.192982465	2	4.229836
Q62812	MQQNIQELEEQLEEEESAR	0.976163217	2	6.155732
Q62812	MQQNIQELEEQLEEEESAR+Oxidation(0)	0.952709075		
Q62812	NAEQFKDQADK	0.836138895	2	3.680455
Q62812	NLPIYSEEIVDMYK	1.035654147	2	3.213697
Q62812	NMDPLNDNIATLLHQSSDK	0.962459469	2	4.609973
Q62812	NTDQASMPDNTAAQK	0.937899444	2	5.421165

Q62812	NTDQASMPDNTAAQK+Oxidation(6)	1.101702439		
Q62812	QAQQERDELADEIANSSGK	1.035030558	3	4.37909
Q62812	QIATLHAQVTDMK	0.81270245	2	2.801854
Q62812	QLEEAEEEAQR	0.985578139	2	3.685886
Q62812	QNKELK	0.759123921	1	1.923305
Q62812	QSVSNLEK	1.028151933	2	2.601386
Q62812	QTLENERGELANEVK	1.102726932	2	2.913452
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	0.775270421	3	5.424296
Q62812	RQLEEAEEEAQR	0.932817668	2	4.352044
Q62812	SMEAEMIQLQEELAAAER	0.919669965	2	4.781615
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)	0.918786343		
Q62812	TDLLLEPYNK	0.807941169	2	2.848344
Q62812	TELEDTLDSTAAQQELR	0.912555759	2	5.294106
Q62812	THEAQIQEMR	0.872176774	2	3.26961
Q62812	THEAQIQEMR+Oxidation(8)	1.161619066		
Q62812	TQLEELEDELQATEDAK	0.882573995	2	5.893728
Q62812	VAEFTTDLMEEEEK	1.065974566	2	4.137895
Q62812	VEAQLQELQVK	0.809278171	2	3.695632
Q62812	VEDMAELTCLNEASVLHNLK	1.043879194	2	4.46499
Q62812	VISGVLQLGNIVFK	0.873449949	2	2.851271
Q62812	VSHLLGINVTDFTR	0.836811714	2	3.813626
Q62812	YEILTPNSIPK	0.939587184	2	3.011113
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**0.876069558**	**3.2E-05**	**5**
Q62826	ADILEDKDGK	1.011193485	2	2.699049
Q62826	AFITNIPFDVK	1.052428658	2	3.359712
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	0.776699553	2	4.819779
Q62826	INEILSNALK	0.814773183	2	2.69234
Q62826	MGPVMDRMATGLER+Oxidation(0)	0.922054278		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.041940708**	**0.79605**	**2**
Q62871	ADAEEEAATR	0.970630887	2	3.456928
Q62871	SVSTPSEAGSQDSGDGAVGSR	1.382738729	2	3.373426
Q62902	**LMAN1 Protein ERGIC_53**	**1.065903806**	**0.98567**	**6**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.118488883	2	4.302756
Q62902	GHPDLQGQPADDIFESIGDR	1.080307226	2	4.739892
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.028963779	3	4.969922
Q62902	RGAGTPGQPGQVSQQELDTVVR	1.014885973	3	4.417906
Q62902	YQEEFEHFQQELDK	1.096546899	2	4.730906
Q62902	YVSSLTEEISR	1.088953921	2	3.511666
Q62904	**DHB7 3_keto_steroid reductase**	**1.071385054**	**0.98788**	**2**
Q62904	YATDLLNVALNR	0.967166913	2	2.648441
Q62904	YLSGTTGLGTNYVK	1.174113747	2	2.93935
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.909627105**	**0.09073**	**2**
Q62967	GLQVAPVLLSDELK	0.812958366	2	2.815267
Q62967	VYGVEGDLSEVAR	1.55456585	2	3.137665
Q62975	**ZPI Protein Z_dependent protease inhibitor**	**0.92345351**	**0.57414**	**2**
Q62975	FKLNQRYEMHELLK	0.813997843	2	2.70348
Q62975	KMEVFFPKFK	0.962980426	1	2.060384
Q63041	**A1M Alpha_1_macroglobulin**	**0.649048476**	**8.3E-15**	**10**
Q63041	AEDITHNGIVYTPK	0.628714777	2	3.463758
Q63041	AEQGAYLGPLPYK	0.716920453	2	3.238444
Q63041	AESPVFVQTDKPIYKPGQTVK	0.619600556	3	4.738815
Q63041	DTVVKPVIVEPEGIEK	0.725029348	2	2.457087
Q63041	GSIFNSGSHVLPLEQGK	0.719046625	2	3.75082
Q63041	LQDQSNIQR	0.592441328	2	2.916166
Q63041	QDLNDNDAYSVFQSIGLK	1.014104956	2	2.785951

Q63041	QLNYQHSDGSYSTFGDR	0.659688452	2	2.645306
Q63041	YNILPEAEGEAPFTLK	0.676304764	2	4.984459
Q63041	YVVLVPSELYAGVPEK	0.647973697	2	3.074736
Q63060	**GLPK Glycerol kinase**	**0.91667327**	**0.07292**	**11**
Q63060	AVLGPLVGAVDQGTSSTR	0.849542088	2	5.297806
Q63060	CVFSEHGLLTTVAYK	0.843070397	2	4.015862
Q63060	DCGIPLSHLQVDGGMTSNK	1.242383468	2	3.790442
Q63060	EILQSVYECIEK	1.343766412	2	3.635431
Q63060	FEPQINAEESEIR	1.034369203	2	3.518729
Q63060	KAVLGPLVGAVDQGTSSTR	0.962035529	3	3.337056
Q63060	KVQEAVEENR	1.036051054	2	3.223442
Q63060	LGQLNIDISNIK	1.114197414	2	2.82469
Q63060	NTYGTGCFLLCNTGHK	0.902765791	2	4.149413
Q63060	TAELLSHHQVEIK	0.971316486	2	3.149246
Q63060	VQEAVEENR	0.945445369	2	3.041784
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**0.916688707**	**9.9E-20**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	0.869955344	3	5.50354
Q63081	GESPVDYDGGR	0.980678739	2	2.856317
Q63081	GSFSEQGINEFLR	1.02703951	2	4.267861
Q63081	GSTAPVGGGSFPNITPR	0.967757477	2	4.823972
Q63081	HQSLGGQYGVQGFPTIK	0.866968059	2	5.125422
Q63081	KDVVELTDDTFDK	1.031472298	2	4.115155
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.914410559	4	5.215255
Q63081	NLEPEWAAAATEVK	0.910281332	2	4.081563
Q63081	NSYLEVLLK	0.912804287	2	2.72928
Q63081	TCEEHQLCVVAVLPHILDTGATGR	0.891160857	3	4.550593
Q63081	TGEAIVDAALSALR	0.915148183	3	4.58711
Q63083	**NUCB1 Nucleobindin_1**	**0.911190361**	**0.88575**	**4**
Q63083	ADTGDAPVPAPAGDQK	1.009130194	2	3.463319
Q63083	ELQQAVLQMEQR	1.253507016	2	2.64502
Q63083	LSQETEALGR	0.943961989	2	2.828318
Q63083	VNVPGSQAQLK	0.911179128	2	2.550505
Q63089	**S22A1 Solute carrier family 22 member 1**	**0.88428056**	**0.04883**	**2**
Q63089	ENTIYLQVQTGK	0.89613876	2	2.317788
Q63089	GVALPETIEEAENLGR	0.865399826	2	3.10419
Q63108	**EST3 Liver carboxylesterase 3**	**0.981211545**	**0.54564**	**7**
Q63108	DFNTVPYIVGINK	1.595297923	2	2.677123
Q63108	GGTSKEEINLSK	0.892810388	2	3.540097
Q63108	LDPMTATSLLK	0.864271404	2	2.521205
Q63108	MKPSTVVGDHGDEIYSVFGAPILR	0.997132163	3	3.887483
Q63108	QKTEEELLETTLK	1.006848336	2	3.574369
Q63108	SSFLLNLPEEAIPVAVEK	0.859579203	2	4.645937
Q63108	TEEELLETTLK	1.05239955	2	2.499465
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**0.871680359**	**1.1E-16**	**6**
Q63120	ACALLPDLEILPGGDMAEIGEK	1.693337231	2	3.498795
Q63120	ISEYINVENEAPWVTDK	1.125113762	2	3.79597
Q63120	IVEYGSPEELLSNR	1.064926051	2	3.41682
Q63120	QSQSQDVLVLEEAK	1.169709355	2	3.266795
Q63120	YFAWEPSFQEQVQGIR	1.008327658	2	4.646604
Q63120	YRPELDLVLK	1.439397439	2	2.399018
Q63150	**DPYS Dihydropyrimidinase**	**1.011545801**	**0.9915**	**9**
Q63150	DQTCTPIPVK	1.452901001	2	2.448888
Q63150	EIGAIAQVHAENGDLIAEGAK	1.141039737	2	4.997487
Q63150	FVAVTSTNAAK	0.97430095	2	3.211935
Q63150	GEVITLKPR	1.07144225	2	2.399349
Q63150	GSSLIEAFETWR	1.013324228	2	3.06013

Q63150	MLALGITGPEGHELCRPEAVEAEATLR	0.993034035	3	3.627389
Q63150	VVNDDFSQVADVLVEDGVVR	1.00993405	2	5.589057
Q63150	VVYEAGVFDVTAGHGK	0.973690013	2	3.865458
Q63150	VVYGEPIAAGLGTDGTQYWNK	0.899524632	2	5.477098
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.043747449**	**3.5E-13**	**16**
Q63270	AVEAGLNVKPYVK	0.843034721	2	3.255152
Q63270	AVLAESYER	1.040195968	2	2.370706
Q63270	FVEFFGPGVAQLSIADR	0.872390284	2	5.201436
Q63270	GFQVAPDHHNDHK	2.093454579	2	3.251628
Q63270	IDFEKEPLGVNAQGQQVFLK	0.765593784	3	4.687419
Q63270	KNDIENILNWSIMQHK	0.814072816	3	4.652308
Q63270	NCDEFLVK	0.92233386	1	2.048974
Q63270	NQDLEFER	0.936168792	2	2.479582
Q63270	QAPQTVHLPSGETLDVFDAAER	0.735511431	3	3.701478
Q63270	SIEVPFKPAR	1.147991529	2	2.589269
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	0.859458918	3	5.093326
Q63270	SPPFFESLTLDLQPPK	1.048712986	3	3.88698
Q63270	SWNALAAPSEK	0.9156339	1	2.325432
Q63270	TSLSPGSGVVTYYLR	1.000071444	2	3.470172
Q63270	VILQDFTGVPAVVDFAAMR	0.874417009	3	4.483238
Q63270	YQQAGLPLIVLAGK	0.827180167	2	3.539708
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**0.785306253**	**3.2E-11**	**17**
Q63276	AHGHFLFVVGEDDKNLNSK	0.924287981	2	5.835223
Q63276	ASEVGEVDLER	0.833279649	2	3.869868
Q63276	DDKGNLFNSQAFYR	0.795876193	2	3.298659
Q63276	GNLFNSQAFYR	0.762806547	2	3.048615
Q63276	LCHPYFPVEGK	0.956176167	2	2.656939
Q63276	LTAVPLSALVDEPVHIR	1.504391902	2	4.111654
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	0.730920452	2	4.057826
Q63276	QHLNPGFNSQL	0.857106036	2	3.547451
Q63276	QITATVLINGPNFVSSNPHVYR	0.661727568	3	5.248504
Q63276	TFEETADK	0.922353568	1	1.975335
Q63276	TFEETADKDSK	0.776685852	2	3.926252
Q63276	VDLEYFEEGVEFLLR	0.745197824	3	4.795879
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	0.742659319	2	5.307502
Q63276	VISSSLDSLILER	0.781051628	2	3.537139
Q63276	VTGLTPFQVVCLQASLK	0.807122947	3	5.327432
Q63276	WYVAPGVTR	0.632267247	2	2.65423
Q63276	YCFPIEK	0.910085028	2	2.595945
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**0.863886434**	**0.97133**	**24**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	0.866798828	3	5.970218
Q63342	AWGSEMNCDTNPLEAGLDYFIK	0.842513496	2	4.50319
Q63342	DGLLFGPYESQEK	1.357981156	2	2.61695
Q63342	EGQESPPSPPEWK	1.357416589	2	2.676322
Q63342	GGYDVEIR	0.945362316	2	2.306157
Q63342	GQDSTQLLDHLCANVIPK	0.873899637	2	4.022426
Q63342	IMNAGQEEGIDNFGTYALNALR	0.525619094	2	4.875884
Q63342	ISDIPVTAIR	0.952416888	2	3.232371
Q63342	ITEHVEAAMEMVPVLK	0.916360059	2	3.927021
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	0.876038621	3	5.173427
Q63342	LEEETGQVVGFHQPGSIR	0.858133017	2	4.767273
Q63342	LNKPADFTGK	1.087527438	2	2.636228
Q63342	LTSEDLSDDVFK	1.004426755	2	4.147946
Q63342	NITDELGVLGVAGPYAR	0.845573355	2	4.831796
Q63342	NYPATIIQEPLVLTEPTR	0.949447302	2	4.1668

Q63342	REDSAALYER	0.710362782	2	3.230521
Q63342	SLAFAYVPVELSEVGQQVEVELLGK	0.727021031	3	4.972811
Q63342	TNWHATEQYIIEPEK	0.865188693	2	4.153389
Q63342	VGFTNISHMLTPR	1.093691331	2	2.402288
Q63342	VGVIDLSPFGK	0.843567571	2	3.399476
Q63342	VIGNTTSGSYSYSIQK	0.941491203	2	4.334137
Q63342	WIEEAAVR	1.002897819	2	2.761974
Q63342	WTTTQYTEAK	0.925092926	2	2.81355
Q63342	YLSDWILHGEPPFDLIELDPNR	0.771030935	3	4.346085
Q63347	**PRS7 26S protease regulatory subunit 7**	**0.909000231**	**0.88765**	**8**
Q63347	ALDEGDIALLK	1.042439037	2	3.094614
Q63347	ESDTGLAPPALWDLAADK	1.044900368	2	2.508094
Q63347	FDDGAGGDNEVQR	0.934918537	2	4.175218
Q63347	FVVDLSDQVAPTDIEEGMR	0.855317975	2	3.856356
Q63347	IINADSEDPK	1.090271027	2	3.047869
Q63347	QTLQSEQPLQVAR	0.992283613	2	4.001585
Q63347	QVEDDIQQLLK	1.063910795	2	2.441735
Q63347	TMLELINQLDGFDPR	0.789757698	2	2.964977
Q63355	**MYO1C Myosin_Ic**	**0.984246213**	**0.14933**	**2**
Q63355	MSLLQLVEILR	0.529986782	2	2.511883
Q63355	YMDVQFDFKGAPVGGHILSYLLEK+Oxidation(1)	1.827858052		
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**0.987820249**	**0.99051**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	1.015186774	2	6.6786
Q63362	KYTEQITSEK	1.024144385	2	2.426236
Q63362	TTGLVGLAVCDTPHER	0.905224549	2	3.476041
Q63362	YTEQITSEK	1.083484094	2	2.452557
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**1.299193315**	**0.85589**	**2**
Q63413	AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK	0.92827033	3	3.799471
Q63413	NCPHIVVGTPGR	1.406052366	2	3.049633
Q63429	**UBC Polyubiquitin_C**	**1.003213283**	**0.36321**	**3**
Q63429	ESTLHLVLR	2.144843392	2	2.427556
Q63429	TITLEVEPSDTIENVK	1.003114008	2	4.717163
Q63429	TLSDYNIQK	0.98106577	2	2.548782
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**0.804413251**	**1.6E-15**	**10**
Q63448	ADWLDSEAPLAAYR	0.866008843	2	4.247795
Q63448	DDAVALVDAIAPSDFVLGSPIGR	0.804335904	3	4.142456
Q63448	EIHALASAGKPLASWTAQR	0.802810043	2	4.096396
Q63448	GGYISGEQTGK	0.80458848	2	2.920685
Q63448	NLWAAVLQQSGVLER	0.67702294	2	4.46384
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.869529377	3	3.502545
Q63448	TIFLDLIELQR	0.835113848	2	3.38361
Q63448	TIFSTLENDPLFARPFGADLPLEK	0.728018664	3	4.512849
Q63448	TTAHYDPATQEFILHSPDFEAAK	0.741683617	3	4.542653
Q63448	TVNFLEAYPGILGQK	0.833414941	2	4.615621
Q63507	**RL14 60S ribosomal protein L14**	**1.053986704**	**0.975**	**3**
Q63507	ALVDGPCTR	1.205116051	2	2.415944
Q63507	CMQLTDFILK	0.950627206	2	2.551852
Q63507	LVAIVDVIDQNR	1.16468256	2	4.126261
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**0.979225729**	**0.08913**	**3**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	0.824417699	3	5.36974
Q63524	HEQEYMEVR	0.995862648	2	3.33628
Q63524	HEQEYMEVR+Oxidation(5)	1.304503784		
Q63525	**NUDC Nuclear migration protein nudC**	**1.026886237**	**0.58724**	**4**
Q63525	GQAPVIDGELYNEVK	1.025137007	2	3.454822
Q63525	LSDLDSETR	1.25542037	2	2.665147

Q63525	LVTSDPEINTK	1.177746429	2	2.395669
Q63525	VEESSWLIEDGK	1.041853624	2	3.01153
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.071249403**	**0.16995**	**5**
Q63569	AMEVDERPTEQYSDIGGLDK	1.358879445	3	3.656654
Q63569	CTDDFNGAQCK	0.919458495	2	3.332251
Q63569	MNVSPDVNYEELAR	1.189901749	2	3.309615
Q63569	MSTEEIVQR	1.016560999	2	2.404523
Q63569	QTYFLPVIGLVDAEK	1.227439897	2	2.730999
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.086894063**	**0.31989**	**4**
Q63570	GVLMYGPPGCGK+Oxidation(3)	1.079774297		
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.21566887	3	5.442052
Q63570	KDEQEHEFYK	1.411705034	2	2.956087
Q63570	RFDAQTGADR	1.045414156	2	2.609976
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**0.926108303**	**0.04109**	**4**
Q63584	ITDSAGHILYAK	0.975037374	2	3.314518
Q63584	LEDLSESIVNDFAYMK	0.865586126	2	2.92805
Q63584	NYEEIAK	0.926737799	1	2.266356
Q63584	RLEDLSESIVNDFAYMK	1.00478323	2	3.829109
Q63598	**PLST Plastin_3**	**1.096447593**	**0.99995**	**11**
Q63598	AESMLQQADK	0.951904495	2	2.879221
Q63598	ATDDIIVNWVNGTLSEAGK	0.922024872	3	4.949576
Q63598	AVGDGIVLCK	1.013706039	1	1.951555
Q63598	HVIPMNPNTDDLFK	0.879370018	2	2.782761
Q63598	IDINMSGFNETDDLKR	0.971421948	2	4.337924
Q63598	INNFSADIK	1.082851784	2	2.578387
Q63598	KLENCNYAVELGK	1.127555578	2	3.923074
Q63598	NEALAALLR	1.101730874	2	2.745475
Q63598	VYALPEDLVEVKPK	0.991051788	2	2.961497
Q63598	YPALTKPENQDIDWTLLEGETR	0.981038199	3	5.177026
Q63598	YTLNVMEDLGEGQK	1.044122463	2	3.698828
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.067880814**	**0.1518**	**8**
Q63610	EQAEAEVASLNR	1.805247179	2	2.865719
Q63610	IQVLQQQADDAEER	1.111389461	2	5.12711
Q63610	KIQVLQQQADDAEER	1.166536635	2	5.410338
Q63610	KLVIIEGDLER	1.133344524	2	2.77177
Q63610	LVIIEGDLER	0.997231964	2	2.482031
Q63610	MELQEIQLK	1.053913363	2	3.021322
Q63610	TIDDLEDKLK	0.844344285	2	2.861605
Q63610	YSQKEDKYEEEIK	1.618412158	2	4.677725
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**0.957447698**	**0.24331**	**16**
Q63617	AANSLEAFIFETQDK	0.864521314	2	3.303391
Q63617	DAVITVPAFFNQAER	1.02298543	2	2.333813
Q63617	EGETPDEKESGDKSEAQKPNEK	1.256692839	3	3.770401
Q63617	ESGDKSEAQKPNEK	1.197758735	2	2.348613
Q63617	FLGDSAAGMAIK	0.908478781	2	2.647946
Q63617	LEDLTLR	0.988363976	2	2.373968
Q63617	LGNTISSLFGGGTSSDAK	0.994285366	2	3.302428
Q63617	LIPEMDQIFTDVEMTTLEK	0.904305036	2	2.782573
Q63617	LYQPEYQEVSTEEQR	1.473561537	2	5.059073
Q63617	NINADEAAAMGAVYQAAALSK	0.933047401	2	2.993598
Q63617	SLAEDFAEQPIK	1.168018754	2	2.735234
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	0.803873444	3	3.91786
Q63617	TLGGLEMELR	0.994534505	2	2.306415
Q63617	VEFEELCADLFDR	1.070797135	2	3.89708
Q63617	VESVFETLVEDSPEEESTLTK	1.153388462	2	4.21553
Q63617	VLQLINDNTATALSYGVFR	0.97276343	2	2.947274

Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**0.981368652**	**0.97292**	**2**
Q63692	EGEEAGPGDPLLEAVPK	1.122904467	2	3.577682
Q63692	LGPGGLDPVEVYESLPEELQK	0.955004237	2	2.685598
Q63716	**PRDX1 Peroxiredoxin_1**	**1.004753721**	**0.99318**	**15**
Q63716	ADEGISFR	1.094616406	2	3.06872
Q63716	ATAVMPDGQFK	1.028277164	2	2.943845
Q63716	DISLSDYK	3.827283899	2	2.505138
Q63716	HGEVCPAGWKPGSDTIKPDVNK	1.101361773	4	6.228096
Q63716	IGHPAPSFK	1.63047055	1	1.932111
Q63716	KLNCQVIGASVDSHFCHLAWINTPK	2.172617403	4	4.572121
Q63716	KQGGLGPMNIPLVSDPK	0.657920426	2	4.135698
Q63716	LNCQVIGASVDSHFCHLAWINTPK	1.048656632	3	3.653662
Q63716	LVQAFQFTDK	1.209587657	2	3.532369
Q63716	QGGLGPMNIPLVSDPK	0.843922991	2	3.479512
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6)	0.909156995		
Q63716	QITINDLPVGR	0.97343716	2	3.308394
Q63716	RTIAQDYGVLK	1.415199597	2	2.532115
Q63716	SVDEILR	0.988104621	2	2.699282
Q63716	TIAQDYGVLK	1.03473603	2	3.247339
Q63768	**CRK Adapter molecule crk**	**1.13922747**	**0.58327**	**2**
Q63768	IGDQEFDSLPALLEFYK	1.066327479	2	3.292372
Q63768	VPNAYDKTALALEVGELVK	1.168835773	2	2.317183
Q63797	**PSME1 Proteasome activator complex subunit 1**	**0.919440971**	**0.8774**	**10**
Q63797	EPALNEANLSNLK	0.3673086	2	2.400531
Q63797	ISELDAFLK	0.961367434	2	2.819068
Q63797	ISELDAFLKEPALNEANLSNLK	0.847283938	3	6.055887
Q63797	KGDEDDKGPPCGPVNCNEK	1.01577285	3	4.801366
Q63797	KISELDAFLKEPALNEANLSNLK	0.913163306	3	5.733959
Q63797	LEGFQTQISK	1.007685262	2	3.01388
Q63797	NAYAVLYDIILK	1.231435093	2	2.883824
Q63797	QLVHELDEAEYQEIR	0.940928053	3	4.660054
Q63797	TENLLGSYFPK	0.980671822	2	3.60702
Q63797	VDVFREDLCSK	0.900007214	2	2.387007
Q63798	**PSME2 Proteasome activator complex subunit 2**	**0.986244656**	**0.99823**	**6**
Q63798	AFYAELHHIISSNLEK	0.941211118	2	3.978549
Q63798	IEDGNDFGVAIQEK	0.928126079	2	4.24792
Q63798	IISLSQLLQEDSLNVADLSSLR	1.096321002	2	2.33724
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.100297033	3	3.445489
Q63798	TKVEAFQTAISK	0.84544449	2	3.455294
Q63798	VEAFQTAISK	0.994424621	2	2.612056
Q63836	**SBP2 Selenium_binding protein 2**	**1.137004255**	**0.99215**	**5**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.090436577	3	5.46247
Q63836	GSFVLLDGETFEVK	1.060345416	2	2.446326
Q63836	IYVVDVGSEPR	1.167711389	2	3.959319
Q63836	LNPNFLVDFGK	1.024744386	2	2.730465
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.074800422	3	4.310116
Q63945	**SET Protein SET**	**1.040745085**	**0.94124**	**3**
Q63945	IDFYFDENPYFENK	1.040872047	2	3.856183
Q63945	LNEQASEEILK	1.040781096	2	2.725482
Q63945	VEVTEFEDIK	0.837575432	2	2.567454
Q63965	**SFXN1 Sideroflexin_1**	**1.064881495**	**0.99994**	**6**
Q63965	MSGEVPPNINIKEPR+Oxidation(0)	1.044135647		
Q63965	NILLTNEQLENAR	0.900214991	2	4.475253
Q63965	QAITQVVISR	1.123892979	2	2.43131
Q63965	QGIVPAGLTENELWR	1.004228806	2	2.972429
Q63965	WDQSTFIGR	0.907076499	2	2.833481
Q63965	YAYDSAFHPDTGEK	1.232269358	2	4.07131

Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**1.117180432**	**9.9E-20**	**17**
Q64057	AWNIWADIPAPK	0.765359149	2	3.94756
Q64057	EDNEGVFNGSWGGR	1.066262847	2	3.637798
Q64057	EGGTVVYGGK	0.815825933	2	2.454009
Q64057	FKNEEEVFEWNNEVK	0.749113089	2	5.458163
Q64057	GAPTTSLVSIAVTK	0.611399859	2	4.213446
Q64057	GEVITTYCPANNEPIAR	0.805873476	2	5.085406
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.778929089	2	5.649642
Q64057	LFLHESIHDEVVDR	0.889025953	2	4.218174
Q64057	NEEEVFEWNNEVK	0.870313977	2	4.541942
Q64057	QAVSMFVQAVEEAK	0.854482599	2	3.084381
Q64057	QGLSSSIFTK	0.936382068	2	2.567421
Q64057	QVALMVQER	0.878958184	2	2.302101
Q64057	STCTINYSTALPLAQGIK	1.104853989	2	4.678034
Q64057	VGNPWDPNILYGPLHTK	0.95583213	3	4.141422
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	0.817661914	3	6.092217
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1)	0.848812123		
Q64057	VNLLSFTGSTQVGK	0.783468391	2	4.875194
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**2.23072966**	**0.64068**	**2**
Q640L5	EVIDLGQELR	1.797765754	2	2.355314
Q640L5	SMQLSQLDMVLDQTKTELEKTTNSVK	2.848483677	3	3.601153
Q64119	**MYL6 Myosin light polypeptide 6**	**0.988435459**	**0.98524**	**6**
Q64119	DQGTYEDYVEGLR	1.248391575	2	3.351062
Q64119	HVLVTLGEK	1.162842698	1	2.293932
Q64119	ILYSQCGDVMR	1.129943151	2	2.688288
Q64119	NKDQGTYEDYVEGLR	1.117354634	2	4.194821
Q64119	VFDKEGNGTVMGAEIR	2.701974062	2	3.517663
Q64119	VLDFEHFLPMLQTVAK	0.940577428	2	4.943352
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**0.877325208**	**0.73598**	**2**
Q64122	DGFIDKEDLHDMLASLGK	0.88559715	2	4.722607
Q64122	LNGTDPEDVIR	1.145422008	2	2.886698
Q64176	**EST22 Liver carboxylesterase 22**	**0.863174576**	**0.0001**	**4**
Q64176	AISESGVALTAGLVK	0.858563152	2	3.887493
Q64176	EGYLQIGATTQQAQK	1.087495127	2	4.587856
Q64176	LDQMTAMSLLK+Oxidation(3)	1.102667832		
Q64176	NFNTVPYIVGINK	1.455330695	2	3.455234
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**0.979942803**	**0.96937**	**9**
Q641Y0	ELGSECGIEFDEEK	1.190629971	2	3.523845
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	1.350174158	4	6.983397
Q641Y0	NTLLIAGLQAR	0.974049872	2	3.819304
Q641Y0	SSLNPILFR	1.221790244	2	2.411361
Q641Y0	TADDPSLSLIK	0.792248827	2	2.714213
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	0.97825259	4	6.546318
Q641Y0	TLVLLDNLNVR	0.981089809	2	3.846589
Q641Y0	WVPFDGDDIQLEFVR	0.965428611	2	2.734822
Q641Y0	YSQTGNYELAVALSR	1.198726414	2	3.453722
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.05147571**	**0.84939**	**5**
Q641Y2	GSGIQWDLR	0.996655809	2	2.547239
Q641Y2	IDEVEEMLTNNR	1.180318794	2	3.631346
Q641Y2	IIEQCLNK	1.023955171	2	2.883131
Q641Y2	LYTEGYQVPPGATYTAIEAPK	0.985682017	2	2.946365

Q641Y2	TQPYDVYDQVEFDVPIGSR	1.253842104	2	3.992386
Q641Y8	**DDX1 ATP_dependent RNA helicase DDX1**	**1.041472182**	**0.86638**	**3**
Q641Y8	GDVRFLICTDVAAR	1.086109122	2	2.34389
Q641Y8	GHVDILAPTVQELAALEK	1.115453097	3	3.880937
Q641Y8	GSAFAIGSDGLCCQSR	1.035563042	2	3.700125
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.025561939**	**0.9993**	**4**
Q64232	HYEVEIR	0.986340807	2	2.311956
Q64232	LCFLDKVEPQATISEIK	1.051750857	2	4.690748
Q64232	SLKDEDVLQK	0.995613637	2	3.338138
Q64232	VEPQATISEIK	1.030230986	2	2.373876
Q64240	**AMBP Protein AMBP**	**0.757334521**	**9.9E-20**	**3**
Q64240	AFAELWAFDAAQGK	0.723193896	2	3.526134
Q64240	AVLPQENEGSGSEPLITGTLK	0.815759089	2	4.844437
Q64240	TIAACNLPIVQGPCR	0.727550618	2	3.263431
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**1.191949109**	**1.1E-12**	**2**
Q642G4	GGDGQINEQVEK	1.524900858	2	3.136687
Q642G4	LLGPQEEGEGVVDVK	1.14338177	2	3.42698
Q64303	**PAK2 Serine/threonine_protein kinase PAK 2**	**1.055843682**	**0.00341**	**2**
Q64303	NKIISIFSSTEK	0.733027069	2	2.805637
Q64303	SVIDPIPAPVGDSNVDSGAK	1.194160657	2	2.832949
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**0.730716201**	**9.9E-20**	**19**
Q64380	AYGIESHVLSPAETK	0.763382423	2	4.588248
Q64380	DGTMDPAGTCTTLTR	1.526039908	2	4.071686
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	0.713136225	3	5.652499
Q64380	DLYPLMNVDDLYGTLYVPR	0.774407993	2	2.564961
Q64380	EEAQGASVVPQGPSQPLPSTANVVVIGGGSLGCQTLYHLAK	0.766943416	3	3.592457
Q64380	FHHSLTDHPR	0.625378341	2	2.652392
Q64380	FYLLGADAR	0.839514834	2	2.683296
Q64380	GAQVIENCAVTGIR	0.991038139	2	4.177184
Q64380	HGLVNAGYR	0.844623916	2	2.575393
Q64380	IEGIQNMPNVR	0.710724029	2	3.324223
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.705021613	2	4.458218
Q64380	NGDYALER	0.869628322	2	2.310163
Q64380	NYSVVFPHDEPLAGR	0.697461906	2	3.984923
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.641224418	3	4.655502
Q64380	RDPLHEELLGQGCVFQER	0.826810626	3	5.591014
Q64380	SDDSPLEAGLAFTCK	1.005578089	2	2.657634
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.780114558	3	4.378253
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16)	0.820163221		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.709886194	3	5.090612
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**0.896658462**	**9.9E-20**	**29**
Q64428	ADMVIEAVFEDLAVK	0.790972727	2	3.967575
Q64428	ALMGLYNGQVLCK	0.955627675	2	3.308134
Q64428	DSIFSNLIGQLDYK	1.631219261	2	3.478514
Q64428	DTTASAVAVGLK	1.243087286	2	3.639003
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.976652811	3	5.405834
Q64428	EVQSEFVEVMNEIWANDQIR	0.828054365	3	4.221745
Q64428	FGELALTK	0.945951667	2	3.015374
Q64428	FGGGSVELLK	0.971199878	2	3.06003
Q64428	FVDLYGAQK	0.966361267	2	2.916451
Q64428	GFYIYQSGSK	0.982816352	2	2.835433
Q64428	ILQEGVDPK	1.009863392	2	3.290217
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	0.667210003	4	5.096561
Q64428	KTVLGVPEVLLGILPGAGGTQR	0.889276585	2	4.316564

Q64428	KYESAYGTQFTPCQLLR	1.079082123	2	5.012655
Q64428	LDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	0.928030053		
Q64428	LPAKPEVSSDEDIQYR	1.055914891	2	4.406058
Q64428	MGLVDQLVDPLGPGIK	0.866962653	2	5.015884
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0)	1.002970488		
Q64428	MQLLEIITTDK	0.843633068	2	3.931868
Q64428	MQLLEIITTDK+Oxidation(0)	0.877365785		
Q64428	MVGVPAAFDMMLTGR	0.990468107	2	3.256285
Q64428	NLNSEIDNILVNLR	0.819643787	2	4.710977
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	0.85465121	3	3.909349
Q64428	SPKPVVAAISGSCLGGGLELAIACQYR	0.893066276	3	3.641849
Q64428	TGLEQGNDAGYLAESEK	0.969929879	2	4.991644
Q64428	TIEYLEEVAVNFAK	0.945180594	3	4.20218
Q64428	TVLGVPEVLLGILPGAGGTQR	0.761119885	3	5.119709
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.882764323	3	6.421921
Q64428	YESAYGTQFTPCQLLR	0.966825215	2	4.808635
Q64458	**CP2CT Cytochrome P450 2C29**	**0.683814013**	**6.7E-16**	**6**
Q64458	EHKESLDVTNPR	1.384097258	2	3.291539
Q64458	IKEHKESLDVTNPR	0.825106867	3	5.073951
Q64458	LPPGPTPLPIIGNFLQIDVK	0.628312343	2	4.004734
Q64458	VQEEAQCLVEELR	0.548993616	2	4.387594
Q64458	VQEEAQCLVEELRK	0.561595618	2	3.858618
Q64458	VQEEIDR	0.783757813	2	2.410247
Q64481	**CP3AG Cytochrome P450 3A16**	**2.256974993**	**0.0013**	**3**
Q64481	EMFPVIEQYGDILVK	2.728067916	2	3.031672
Q64481	GSIDPYVYLPFGNGPR	2.274740352	2	3.931224
Q64481	VLQNFSFQPCK	1.841867415	2	2.78399
Q64541	**AT1A4 Sodium/potassium_transporting ATPase subunit alpha_4**	**0.918848882**	**0.45297**	**2**
Q64541	LIIVEGCQR	1.14715521	2	2.678524
Q64541	NLEAVETLGSTSTICSDK	0.917463311	2	3.080789
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.113373095**	**1**	**5**
Q64550	GHEVVVIAPEASIHIK	1.101944335	2	4.889272
Q64550	LLVIPIDGSHWLSMLGVIQQLQQK	0.925310298	3	4.470123
Q64550	NMIIALTENFLCR	1.0298695	2	4.349101
Q64550	SVFDQDPFLLR	1.153739308	2	3.184846
Q64550	VVYSPYGSLATEILQK	1.281419955	2	5.125023
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**0.853369108**	**0.88694**	**3**
Q64560	ACVDSNENGDLGK	0.750771628	2	3.433127
Q64560	DPVQVAAPSDHGVGIEPVFPENTENSEK	0.828427128	3	3.848384
Q64560	GTLIEAFPVLGGK	0.889313922	2	2.601735
Q64563	**ADH4 Alcohol dehydrogenase 4**	**1.261886271**	**0.89277**	**12**
Q64563	AAVDCTVVGWGSCTVVGAK	1.658632043	2	3.864539
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	1.226947853	3	5.246053
Q64563	ALGATDCLNPR	1.374407512	2	3.218276
Q64563	FDLDLLVTHALPFDK	1.045100953	3	4.313217
Q64563	INDAIDLMNQGK	1.020970899	2	3.396684
Q64563	KFDLDLLVTHALPFDK	1.156968991	3	4.829554
Q64563	SVDSVPNLVTDYK	1.157263432	2	4.373028
Q64563	TDSPLCIEEIEVSPPK	1.421211492	2	3.785296
Q64563	VCLIGCGFTSGYGAAINTAK	0.998065199	2	3.670304
Q64563	VDDEANLER	1.450232922	2	2.82535
Q64563	VDEMNISTVDMILGR	1.084012796	2	3.480024
Q64563	VIATCVCPTDINATNPK	1.247065087	2	4.754181
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**0.885226075**	**0.81715**	**13**
Q64565	AYSNHTDIISFR	0.933095753	2	3.370985

Q64565	GGNFSQTFR	1.045162523	2	2.504953
Q64565	GGVCIADEVQTGFGR	1.05795493	2	4.354096
Q64565	GIGNGFPMAAVVTTPEIASSLAK	0.945589459	2	4.637915
Q64565	LRDEFDIVGDVR	0.856075006	2	2.883657
Q64565	LSALLPEPLK	1.282199706	2	2.781003
Q64565	NSQEVGTYMLLK	0.754920586	2	2.85787
Q64565	SALTQHMER	1.175234916	2	2.530699
Q64565	SALTQHMER+Oxidation(6)	0.661665983		
Q64565	TEVNQIHEDCK	1.046479813	2	2.997313
Q64565	TEVNQIHEDCKDMGLLVGR	0.750391548	2	5.521994
Q64565	VIFLVNSGSEANDLAMVMAR	0.74728709	2	4.695429
Q64565	YIEQFK	0.880964737	1	2.15976
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**2.328279632**	**0.83594**	**8**
Q64578	AVGIVATTGVSTEIGK	3.645797895	2	3.473829
Q64578	DIVPGDIVEVAVGDKVPADIR	4.079039457	2	3.760574
Q64578	DQMAATEQDKTPLQQK	9.555829951	2	3.942774
Q64578	EFDDLPLAEQR	2.534795809	2	2.685803
Q64578	IGIFSENEEVADR	2.585437915	2	3.041716
Q64578	IRDQMAATEQDKTPLQQK	3.668764358	3	3.715467
Q64578	TGTLTTNQMSVCK	4.096893944	2	2.876467
Q64578	VGEATETALTTLVEK	1.347732149	2	4.784593
Q64581	**CP3AI Cytochrome P450 3A18**	**1.428370555**	**1.5E-10**	**5**
Q64581	AITMSEDEEWKR	1.001230692	2	2.311385
Q64581	EEAKGEPINMK	2.773758805	2	2.336759
Q64581	LAVIGVLQNFNIQPCEK	1.15856045	3	3.320505
Q64581	NPEYWLEPEEFNPER	1.841599108	2	4.133575
Q64581	TILSPTFTSGK	1.426944619	1	1.937561
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.875098979**	**0.99983**	**12**
Q64591	ATAEEITSK	0.876599901	2	2.906292
Q64591	CDVRDPDMVHNTVLELIK	0.924947613	4	4.873317
Q64591	DPDMVHNTVLELIK	0.922421485	3	3.74667
Q64591	EEWDVIEGLIR	1.199398109	2	3.740566
Q64591	FDGGEEVFLSGEFNSLKK	0.508596857	2	2.939223
Q64591	FNIIQPGPIK	0.78963807	2	2.670853
Q64591	LGTVEELANLATFLCSDYASWINGAVIR	1.168760584		
Q64591	NIDVLK	1.018927647	1	2.090248
Q64591	SLAAEWGR	0.928428666	2	2.670436
Q64591	VAFITGGGTGLGK	0.880753905	2	2.78525
Q64591	VAGHPDVVINNAAGNFISPSER	1.089091279	2	6.101136
Q64591	VTKEEWDVIEGLIR	0.925980392	3	4.784861
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.006983946**	**0.0427**	**10**
Q64602	ASFSQVTPAQMDLVFQR	0.858967406	2	4.207116
Q64602	DIISLAPGSPNPK	1.297781193	2	3.050683
Q64602	EILLVPGNSFFVDNSAPSSFFR	1.148740597	2	3.586128
Q64602	FLTATSLAR	0.822349846	2	2.406299
Q64602	FLYTIPNGNNPTGNSLTGDR	0.879843649	2	4.011209
Q64602	GLAEWHVPK	1.141522353	2	2.449018
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.044642001	3	5.774458
Q64602	SAVFTVENGSTIR	0.962319348	2	3.436837
Q64602	VGFITGPK	1.086221556	1	1.910192
Q64602	VLSQWKPEDSKDPTKR	1.092296083	3	3.659276
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**0.961611181**	**0.99858**	**11**
Q64611	AQGGQGLEWR	1.016139574	2	3.213446
Q64611	CHGSQASYLFQQDK	0.990310305	2	4.352719

Q64611	FFNQLFSGLDPHALAGR	0.948909497	3	4.201155
Q64611	FYNVALDTGDK	0.760812012	2	3.268161
Q64611	GAAFLGLGTDSVR	0.876375703	2	3.076898
Q64611	IDQAFALTR	0.956631872	2	3.061519
Q64611	MVVANPILVQADIDFLLGELER	0.735797853		
Q64611	QLLDLELQSQGESR	0.961158635	2	3.837628
Q64611	TLDGDPVAVEALLR	0.914390903	2	4.500065
Q64611	VCEWKEPEELK	0.931657434	3	3.697585
Q64611	YLVEEIK	0.966817285	1	2.391475
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**1.116644242**	**0.85786**	**3**
Q64638	GHQAVVLAPEVTVHIK	0.863031137	3	3.502925
Q64638	VVFETGNYVK	1.176048999	2	2.356892
Q64638	YESLASELLQR	0.996335868	2	3.197192
Q64640	**ADK Adenosine kinase**	**1.068970716**	**0.03453**	**12**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.271186208	3	6.765608
Q64640	AATFFGCIGIDK	0.7739456	2	3.045069
Q64640	AGHYAASVIIR	1.048653393	3	3.578603
Q64640	FGEILK	1.075213029	2	2.427885
Q64640	FKVEYHAGGSTQNSMK	1.485776845	2	3.026518
Q64640	HKELFDELVK	1.068549397	3	3.790277
Q64640	HLDLENNWMLVEK	0.929444483	2	3.788278
Q64640	SLVANLAAANCYK	0.975288141	2	4.737859
Q64640	VEAPEALSENVLFGMGNPLLDISAVVDKDFLDK	0.856170264		
Q64640	VEYHAGGSTQNSMK	1.031213969	2	4.050841
Q64640	VEYHAGGSTQNSMK+Oxidation(12)	1.289659963		
Q64640	YSLKPNDQILAEDK	1.103248718	3	4.959095
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.923704318**	**1**	**7**
Q64654	EPAEDILQTLLDSTYK	0.986915342	2	3.919968
Q64654	GVAYDVPNAVFLEQK	1.126614068	2	3.226981
Q64654	NEDLNAEEVYGR	1.071343469	2	4.106766
Q64654	SGLNIAHFK	1.082998838	2	2.966093
Q64654	TPQTVAGYTIPPGHQVCVSPTVNQR	1.181835847	3	3.94804
Q64654	TVCGEDLPPLTYEQLK	0.96960942	2	4.072863
Q64654	YLQDNPASGEK	1.003020941	2	2.61559
Q65CL1	**CTNA3 Catenin alpha_3**	**0.985276681**	**0.99938**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(0)	0.986150739		
Q65CL1	NLMNAVVQTVK	0.982640033	2	2.888613
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.021484291**	**0.92641**	**3**
Q66H12	CNINCEEDPK	0.813691014	2	2.711522
Q66H12	INQDPLGIQGR	0.81300239	2	3.109276
Q66H12	TISPQNIDILQNPLLIK	1.053613718	2	2.357762
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**0.888546231**	**0.19728**	**3**
Q66H15	AEELQPGFSK	0.914832431	2	2.655945
Q66H15	AIELQPEDPR	0.894609825	2	2.342432
Q66H15	SLQGLAGEIVGEVR	0.782446237	2	2.755211
Q66H80	**COPD Coatomer subunit delta**	**1.021798831**	**0.25027**	**5**
Q66H80	GVQLQTHPNVDKK	1.243672856	2	3.434421
Q66H80	LFTAESLIGLK	1.098482229	2	2.823047
Q66H80	NSNILEDLETLR	1.064746956	2	3.076531
Q66H80	NTLEWCLPVIDAK	1.024564726	2	2.858103
Q66H80	VTQVDGNSPVR	2.250313224	2	2.939242
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.040474857**	**0.11849**	**9**
Q66HA8	AGGIETIANEFSDR	1.133299478	2	2.851369
Q66HA8	FQEAEERPR	0.996690663	2	2.480205
Q66HA8	FVVQNVSAQK	0.958969224	2	2.387136
Q66HA8	IARFFGKDVSTTLNADEAVAR	0.698958125	2	2.317001

Q66HA8	NQQITHANNTVSSFK	1.317760346	2	4.570228
Q66HA8	SVLDAAQIVGLNCLR	1.068736962	2	3.456195
Q66HA8	TEEVSAIEIVGGATR	0.729075786	2	3.408049
Q66HA8	VLGTAFDPFLGGK	0.953621542	2	3.098852
Q66HA8	YNHIDESEMKKVEK	0.727826143	2	2.612902
Q66HD0	**ENPL Endoplasmin**	**0.967369857**	**0.84684**	**28**
Q66HD0	DISTNYYASQK	1.366112446	2	2.997864
Q66HD0	EATEKEFEPLLNWMK	1.261894703	2	2.830895
Q66HD0	EEASDYLELDTIK	1.023324033	2	4.207668
Q66HD0	EEEAIQLDGLNASQIR	1.049073308	2	4.398885
Q66HD0	EFEPLLNWMK	1.188840735	2	2.347774
Q66HD0	EVEEDEYK	1.172359586	1	2.658949
Q66HD0	FQSSHHSTDITSLDQYVER	1.036805029	3	5.646537
Q66HD0	GLFDEYGSK	0.999860162	2	2.463858
Q66HD0	GVVDSDDLPLNVSR	1.05059902	2	4.920107
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	1.273296977	3	3.963573
Q66HD0	KEAESSPFVER	1.16669354	2	3.173807
Q66HD0	LGVIEDHSNR	1.077062408	2	3.358554
Q66HD0	LISLTDENALAGNEELTVK	1.093251483	2	5.50101
Q66HD0	LTESPCALVASQYGWSGNMER	0.986943637	2	5.476592
Q66HD0	LTESPCALVASQYGWSGNMER+Oxidation(18)	0.865804052		
Q66HD0	NLLHVTDTGVGMTR	1.106690176	2	3.98749
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11)	1.074374105		
Q66HD0	SGTSEFLNK	0.985021446	2	3.201717
Q66HD0	SGYLLPDTK	1.032197376	2	3.216391
Q66HD0	SILFVPTSAPR	0.999759602	2	3.28606
Q66HD0	TDDEVVQR	1.051613625	2	3.312746
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	0.993772153	3	5.450044
Q66HD0	TETVEEPLEEDETAQEEK	1.226328301	2	5.23895
Q66HD0	TFEINPR	1.105272622	2	2.402784
Q66HD0	TVWDWELMNDIKPIWQRPSK	0.878893972	3	3.317456
Q66HD0	VFITDDFHDMMPK	0.994413197	2	3.840754
Q66HD0	YNDTFWK	1.033693388	1	2.101287
Q66HD0	YSQFINFPIYVWSSK	0.863893984	2	3.32529
Q66HD3	**NASP Nuclear autoantigenic sperm protein**	**1.048880672**	**0.5719**	**2**
Q66HD3	LSETKDGASVEEVK	0.92880983	2	2.430129
Q66HD3	QDTLMKVVEIEAEIDSEVK+Oxidation(4)	1.055967772		
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.036722138**	**0.49828**	**11**
Q66HF1	ALSEIAGITLPYDTLDQVR	0.999156576	2	5.15308
Q66HF1	AVTEGAQAVEEPSIC	1.121465814	2	3.185316
Q66HF1	DDGAAILAAVSSIAQK	1.077030415	2	4.513566
Q66HF1	FASEIAGVDDLGTTGR	1.343882434	2	4.085585
Q66HF1	FEAPLFNAR	0.990769878	2	2.660874
Q66HF1	GLLTYTSWEDALSR	0.950443474	2	3.590138
Q66HF1	ILQDIASGNHEFSK	1.395078689	2	4.192792
Q66HF1	LGEVSPNLVR	1.118884254	2	2.961337
Q66HF1	LVDQEFLADPLVPPQLTIK	0.950713861	2	3.110144
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	1.115390344	2	4.287465
Q66HF1	YDHLGDSPK	1.007482824	2	2.576717
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.028954783**	**2.2E-07**	**11**
Q66HF8	EEIFGPVQPLFK	1.254063106	2	3.039147
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	0.734482374	3	3.456821
Q66HF8	LAPALATGNTVVMK	0.937661644	2	3.299885
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.008677979	2	4.794425
Q66HF8	TFVEESIYHEFLER	0.854448207	2	3.741059

Q66HF8	VAEQTPLSALYLASLIK	1.247374447	2	3.606155
Q66HF8	VAFTGSTEVGHLIQK	0.701821403	2	3.271901
Q66HF8	VGNPFELDTQQGPQVDK	0.911598103	2	3.796599
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	0.906330414	2	4.495793
Q66HF8	YGLAAAVFTR	0.639633418	2	3.084833
Q66HF8	YNQLFINNEWHDAVSK	0.947885671	2	3.536329
Q66HG4	**GALM Aldose 1_epimerase**	**0.72573864**	**9.9E-20**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	0.763061247	2	4.37411
Q66HG4	TVFGELPSGGGAVEK	0.68099059	2	3.677706
Q66HG4	VSPDGEEGYPGELK	0.820126088	2	3.925192
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.116321361**	**7.3E-06**	**20**
Q66X93	ADDADEFGYSR	2.29736928	2	2.549358
Q66X93	ALLLPDHYLVTVMLSGIK	0.958878953	3	4.24561
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	0.944417735	3	4.316439
Q66X93	DTNGENIAESLVAEGLASR	1.068487459	2	5.025278
Q66X93	ETDGSETPEPFAAEAK	1.324821458	2	3.806101
Q66X93	GDVGLGLVK	1.111179381	2	2.43039
Q66X93	HFVDSHHQKPVNAIIEHVR	1.167466596	3	4.056577
Q66X93	LEGDNIQDK	1.017123008	2	2.860885
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.201051797	2	5.536663
Q66X93	SAYYKPLLSAEEAAK	1.126397472	2	3.223134
Q66X93	SDISSHPPVEGAYAPR	1.179760497	3	4.724852
Q66X93	SEAVVEYVFSGSR	1.106716153	2	3.347418
Q66X93	SSHYDELLAAEAR	1.19636155	2	3.529833
Q66X93	TCATVTIGGINIAEALVSK	0.942170796	2	3.512292
Q66X93	TDAVDSVVR	1.266985056	2	2.680137
Q66X93	VADISGDTQK	1.838206908	2	2.480506
Q66X93	VITEYLNAQESAK	1.121415275	2	3.843806
Q66X93	VMQVLNADAIVVK	0.962921766	2	2.878518
Q66X93	VSVTVDYIRPASPATETVPAFSER	0.933555058	3	5.622403
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.912929478	3	3.982018
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.875156668**	**0.01821**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.006240099	3	3.777817
Q68FP2	HNNWDLTPVK	0.861902851	2	2.977453
Q68FP2	IFLMDLNEPYPK	0.945634405	2	3.19641
Q68FP2	IQDPLSDNPR	0.923138225	2	3.127307
Q68FP2	LLIYNPEDPPGSEVLR	0.928867197	2	4.058468
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	0.928259841	3	4.768847
Q68FP2	VVAQGFSSANGITVSLDQK	0.791309391	2	3.367835
Q68FP2	YVYVADVTAK	0.882553486	1	3.0049
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**0.931878231**	**0.25038**	**6**
Q68FQ0	GSNDMQYQHVIETLIGK	1.099401434	2	3.139063
Q68FQ0	HKLDVTSVEDYK	1.11668192	2	3.201262
Q68FQ0	ISDNVLVDINNPEPLIQTAK	1.123243666	2	5.188832
Q68FQ0	LDVTSVEDYK	1.149650729	2	2.371968
Q68FQ0	SLHDALCVIR	0.747642091	2	2.481982
Q68FQ0	WVGGPEIELIAIATGGR	0.944989038	2	3.903633
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.154876122**	**0.04036**	**9**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.059341955	2	5.139385
Q68FR6	ALIAAQYSGAQIR	1.157280463	2	3.712908
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	1.038602554	2	4.251281
Q68FR6	ILGLLDTHLK	1.130870898	2	2.769705
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.12459977	3	3.806649
Q68FR6	KLDPGSEETQTLVR	1.118105263	2	3.863262
Q68FR6	LDPGSEETQTLVR	1.09182054	2	3.653568
Q68FR6	STFVLDEFKR	1.158212964	2	2.479879

Q68FR6	WFLTCINQPQFR	1.173359555	2	3.139211
Q68FR9	**EF1D Elongation factor 1_delta**	**1.070206536**	**0.01518**	**6**
Q68FR9	ATAPQTQHVSPMR	1.008132462	2	3.562022
Q68FR9	FYEQMNGPVTAGSR	1.179885248	2	4.418282
Q68FR9	GVVQDLQQAISK	1.040573974	2	3.754268
Q68FR9	SIQLDGLVWGASK	1.057969606	2	3.266758
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.149031482	2	5.518403
Q68FR9	VGTDLLEEEITK	1.146563708	2	3.484912
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**1.062166179**	**0.64361**	**3**
Q68FS2	NAAQVLVGIPLETGQK	0.926369977	2	2.691726
Q68FS2	QDLAQLMNSSGSHK	2.588498884	2	2.391995
Q68FS2	VISFEEQVASIR	0.92230949	2	2.425801
Q68FS4	**AMPL Cytosol aminopeptidase**	**0.922707479**	**2.2E-16**	**18**
Q68FS4	ADMGGAATICSAIVSAAK	0.823126231	2	5.504634
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2)	1.007207893		
Q68FS4	DKDDDVPQFTSAGENFNK	1.138581628	2	4.939332
Q68FS4	GITFDSGGISIK	0.97768996	2	3.304582
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	0.930875549	3	5.805487
Q68FS4	GVLFASGQNLAR	0.994495647	2	3.291774
Q68FS4	LFEASVETGDR	0.941073231	2	3.374507
Q68FS4	LHGSGDLEAWEK	1.024792403	2	3.650855
Q68FS4	LILADALCYAHTFNPK	1.015983365	2	3.985195
Q68FS4	LNLPINIIGLAPLCENMPSGK	0.963409253	2	5.039613
Q68FS4	QLMESPANEMTPTR	0.870748003	2	3.783976
Q68FS4	QVIDCQLADVNNLGK	0.938491555	2	4.979078
Q68FS4	SAGACTAAAFLR	0.959807973	2	3.502427
Q68FS4	SAGVDDQENWHEGK	0.991520215	2	3.748395
Q68FS4	SWIEEQEMGSFLSVAK	0.774876931	2	5.368445
Q68FS4	TFYGLHQDFPSVVVVGLGK	0.848341554	2	5.416978
Q68FS4	TIQVDNTDAEGR	0.882167754	2	3.795482
Q68FS4	TLIEFLLR	0.871105744	2	2.598734
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**0.902512633**	**0.99475**	**4**
Q68FT1	INDAMNMGHTAK	0.811737998	2	3.035889
Q68FT1	LNHVLEEEQK	0.922388783	3	3.434418
Q68FT1	STGEALVQGLMGAAVTLK	0.942057962	2	3.00385
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.931060812	3	4.689087
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.884509109**	**0.59032**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	0.849635834	2	3.570796
Q68FT3	ISQLDTQSPVTK	0.884474467	2	3.420857
Q68FT3	SLLLGTDVAENQK	0.768014859	2	3.939502
Q68FT3	TLGAQLPQYYEVLTAPISK	0.729891028	2	4.260234
Q68FT3	VFDCIEAYAPGFK	0.873422497	2	2.853969
Q68FT3	VLDQWFESEPLK	0.905915472	2	2.849102
Q68FT3	VQGVVLQGGEEVR	0.789453731	2	3.592483
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.043919633**	**9.9E-20**	**10**
Q68FT5	AGADVLQTFTFSAAEDR	1.849986208	2	2.655468
Q68FT5	AGANIIGVNCR	1.160348319	2	3.478096
Q68FT5	AGLWTPEAVVEYPSAVR	1.087837956	2	3.445393
Q68FT5	AIAEELAPER	1.756245229	2	3.778363
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.038044409	3	4.462389
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	0.973795847	3	4.075529
Q68FT5	FGPWTSLQTMK	0.834819288	2	2.814073
Q68FT5	GGFVDLPEYPFGLEPR	0.995948812	2	4.104311
Q68FT5	LDSGEVVVGDGGFLFTLEK	0.685905782	2	3.922539

Q68FT5	YIGGCCGFEPYHIR	2.148579114	2	4.710752
Q68FT9	**SCLY Selenocysteine lyase**	**1.14295824**	**0.70952**	**4**
Q68FT9	AEVDLIVQDLK	1.045241261	2	3.883864
Q68FT9	NFRPGTENTPMIAGLGK	0.891598513	2	3.349958
Q68FT9	RVDVEDLGVDFLTIVGHK	1.088294476	3	5.547755
Q68FT9	VLVHTDAAQALGK	1.230890492	2	2.473229
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.942779046**	**7.3E-10**	**11**
Q68FU3	AGDLGVDLTSK	0.952281258	2	3.636026
Q68FU3	EIIAVSCGPPQCQETIR	1.25031836	2	4.782104
Q68FU3	GIHVEVPGAEAENLGPLQVAR	0.462849185	2	6.043542
Q68FU3	HSMNPFCEIAVEEAVR	0.985922731	2	5.254708
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2)	0.903497376		
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	0.805717018	3	5.085751
Q68FU3	RVIDFAVK	1.000176319	2	2.804606
Q68FU3	VDLLFLGK	0.841610039	2	2.80443
Q68FU3	VETTEDLVAK	0.925808351	2	3.357481
Q68FU3	VIDFAVK	1.047376323	2	2.412454
Q68FU3	VSVISVEEPPQR	0.962979371	2	3.454462
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.028929866**	**0.99951**	**9**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.031706528	3	5.630429
Q68FY0	IEEVDAQMVR	1.068552572	2	3.606245
Q68FY0	LCTSATESEVTR	1.251598803	2	3.277986
Q68FY0	NALISHLDGTTPVCEDIGR	0.926382205	2	4.513545
Q68FY0	NNGAGYFLEHLAFK	0.945634293	2	3.371237
Q68FY0	RIPLAEWESR	1.253697099	2	2.604239
Q68FY0	TDLTDYLSR	1.112602009	2	2.820077
Q68FY0	VVELLADIVQNISLEDSQIEK	0.877847688	3	6.90851
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.161507854	2	4.962695
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.929493424**	**0.99912**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.903833693	2	4.670763
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	1.010641327	3	3.924644
Q68G31	GESGGQTTPYDFYSR	1.122702899	2	3.963842
Q68G31	LQPTDSFSQSSCFGLR	0.700612073	2	3.668367
Q68G31	NVNSTLTFVTLSGELK	0.926068301	2	4.288925
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	0.880739485	3	6.268124
Q68G31	VNTEPLPGIEK	1.057424028	2	2.412276
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.225465776**	**0.83943**	**2**
Q69Z23	MNILTNEMRRSLK+Oxidation(0)	1.301603531		
Q69Z23	YFIDLLMEK	1.414021275	1	2.141696
Q69ZH9	**RHG23 Rho GTPase_activating protein 23**	**0.785590791**	**0.00641**	**2**
Q69ZH9	LEPMDTIFVKNVK	0.710822661	2	2.43207
Q69ZH9	SRAEAEGPGAGTARACPR	1.024467431	2	2.380046
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.162397263**	**0.42939**	**2**
Q6A0A9	SQGGVQPIPSQGGK	1.469699019	2	3.095812
Q6A0A9	VEGSSTASSGSQLAEGK	1.012152486	2	4.280548
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.148879593**	**0.00248**	**3**
Q6AXM8	FQEEENSLLHLK	0.544972503	2	2.715732
Q6AXM8	LFVYDPNHPPSSEVLR	1.068097133	2	2.491378
Q6AXM8	WANVVYYSPEEVK	3.200998133	2	3.553181
Q6AXN3	**TMED5 Transmembrane emp24 domain_containing protein 5**	**1.342564984**	**0.24451**	**2**
Q6AXN3	LEDILESINSIK	1.168765282	2	3.850768
Q6AXN3	LEDILESINSIKSR	1.35612626	2	2.50144

Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.945634079**	**0.98569**	**3**
Q6AXS5	EETQPPVALKK	0.949186177	2	2.389626
Q6AXS5	FDQLFDDESDPFEVLK	0.938513564	2	4.3778
Q6AXS5	SAAQAAAQTNSNAAGK	1.087088979	2	4.432777
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.970627756**	**0.99913**	**2**
Q6AXY0	FLQPGSQR	0.970246946	2	2.420994
Q6AXY0	YFPAFEK	0.977527399	1	1.918532
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.05627764**	**0.90298**	**3**
Q6AY09	ATENDIYNFFSPLNPMR	0.884011603	2	2.689776
Q6AY09	HTGPNSPDTANDGFVR	1.046598888	2	4.401614
Q6AY09	STGEAFVQFASQEIAEK	1.08113703	2	4.386896
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**0.91278514**	**0.55889**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.061812871	3	4.399938
Q6AY30	ATLVLNCVGPYR	0.915021099	2	2.613501
Q6AY30	GGGVFTPGAAFSR	0.86057046	2	2.434473
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	0.708997165	2	4.231153
Q6AY30	LQQVLEK	1.083270969	1	2.015729
Q6AY30	SVSNLKPVPVIGSK	0.929050435	2	3.835439
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**0.977939767**	**0.95922**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	1.057153129	2	4.75739
Q6AY56	FDGALNVDLTEFQTNLVPYPR	0.926371728	2	4.999843
Q6AY56	LISQIVSSITASLR	1.002635744	2	3.415795
Q6AY56	NLDIERPTYTNLNR	0.976557731	2	3.190492
Q6AY56	QLFHPEQLITGK	0.691183665	2	2.417712
Q6AY56	TIQFVDWCPTGFK	0.930098881	2	3.786335
Q6AY56	VGINYQPPTVVPGGDLAK	0.978995732	2	4.529583
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.687093939**	**0.13342**	**3**
Q6AY80	NDVTGALSNPEVFK	0.621209417	2	3.854708
Q6AY80	VLAPQISFGPEVSSEEQR	0.622018643	2	4.37001
Q6AY80	VLCQGFAFDVPGFYDSGFLK	0.833994487	2	3.490055
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**1.075344954**	**0.99166**	**4**
Q6AYG5	DVLETLWGGPANLEAIAK	1.111640116	2	3.023892
Q6AYG5	ILEQFPGGSIDLQK	1.052842331	2	3.135883
Q6AYG5	NTFCSGSDLNAVK	0.948401426	2	2.587861
Q6AYG5	VIELENWTEGK	1.213075135	2	2.948895
Q6AYH5	**DCTN2 Dynactin subunit 2**	**0.968552355**	**0.59863**	**3**
Q6AYH5	ASVEDADTQNK	1.060743458	2	2.342033
Q6AYH5	VNALDLAVLDQVEAR	1.296177202	2	2.814499
Q6AYH5	WSPVASTLPELVQR	0.960117305	2	2.995299
Q6AYM2	**TEKT2 Tektin_2**	**1.177766473**	**0.57941**	**2**
Q6AYM2	RLEEDLR	1.208540582	1	1.947017
Q6AYM2	TNTMLLDTKCMDIR+Oxidation(3)	0.878170195		
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.777726076**	**9.9E-20**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	0.771081288	2	4.493897
Q6AYQ8	NLHHEVELGVLLGR	0.820059264	3	4.135174
Q6AYQ8	SFTSSCPVSAFVPK	0.761364171	2	4.080788
Q6AYR8	**SCRN2 Secernin_2**	**0.981108021**	**0.99867**	**2**
Q6AYR8	GLLTGEQTPAPQELGSLFQAFVER	1.009770045	3	4.153685
Q6AYR8	QEQQSLEQEGLEALR	0.984237874	2	4.008386
Q6AYS7	**ACY1A Aminoacylase_1A**	**0.884360175**	**0.08231**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	0.847667887	2	4.701358
Q6AYS7	ICTVQPNPDYGSAVTFLEER	1.399773034	2	4.517102
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.862968012**	**0.81162**	**4**

Q6AYS8	ALTDELAALGCTGVR	0.887026284	2	3.731156
Q6AYS8	FDAVVGYK	1.025042462	1	2.229856
Q6AYS8	MIFVPGSIALLTVLER	1.094239777	2	2.767705
Q6AYS8	SVAGEIVLITGAGHGIGR	0.86183297	2	3.983209
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.934860926**	**0.99164**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	0.976853454	2	4.369028
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.934454111	2	3.79195
Q6AYT9	NDDVINSSSYR	0.897615622	2	2.588251
Q6AYT9	TGVVMIPGISQLTQK	0.847908267	2	2.444242
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.051221591**	**0.53232**	**5**
Q6AYZ1	AVFVDLEPTVIDEVR	1.069838888	2	5.030551
Q6AYZ1	DVNAAIATIK	1.203823718	2	3.061604
Q6AYZ1	IHFPLATYAPVISAEK	1.256074235	2	3.413831
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.061249942	2	5.396956
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.077991669	2	4.837774
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.046972939**	**3.1E-09**	**7**
Q6DGG1	AVAIDLPGLGR	0.85677102	2	3.487673
Q6DGG1	FSSETWQNLGTLHR	0.874537903	2	3.45856
Q6DGG1	FSVLLLHGIR	0.928395546	2	2.6252
Q6DGG1	GYVPVAPICTDK	0.874336154	1	2.68742
Q6DGG1	INAADYAR	0.921875622	2	2.461321
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	0.949080762	2	4.987156
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK+Oxidation(12)	0.952698037		
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.871355979**	**0.11487**	**2**
Q6EDY6	IENYLLR	0.870309749	2	2.52352
Q6EDY6	SSDAHELGEGDEKKK	1.010324302	2	2.359173
Q6EJB6	**UT14B U3 small nucleolar RNA_associated protein 14 homolog B**	**0.984355285**	**0.42359**	**2**
Q6EJB6	ARMTERMSLK+Oxidation(2)	0.832409539		
Q6EJB6	EAAFSKTSQMLSR+Oxidation(9)	0.679403955		
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.850512868**	**0.04218**	**2**
Q6GQP4	CDLSDIREVPLK	0.689465692	2	2.391659
Q6GQP4	CDLSDIREVPLKDAK	0.917663759	2	2.737571
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**22.65174069**	**3.2E-05**	**2**
Q6GQT1	IQEEGTGVEETGK	23.10982326	2	3.796557
Q6GQT1	QLSFPLSSEPTQGSYK	3.413214217	2	2.817775
Q6GQT9	**NOMO1 Nodal modulator 1**	**0.989863446**	**0.99932**	**2**
Q6GQT9	SSIDSEPALVLGPLK	1.029477293	2	3.058939
Q6GQT9	VQVVVPEAETR	0.968290376	2	2.484355
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**0.912389187**	**0.00024**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	0.905571961	2	4.141586
Q6I7R3	ILGIPVIITEQYPK	1.066115327	2	3.054214
Q6I7R3	YFGDIISVGQR	0.924252494	2	2.864285
Q6IE47	**ISK6 Serine protease inhibitor Kazal_type 6**	**1.092774146**	**0.66343**	**2**
Q6IE47	CAFCKALEK	1.075990455	1	1.980058
Q6IE47	LFQINCGEFRDPK	1.570976179	2	2.410531
Q6IE52	**MUG2 Murinoglobulin_2**	**0.95173107**	**9.9E-20**	**14**
Q6IE52	AHFSVMGDILSSAIK	0.677016222	2	3.501241
Q6IE52	HTSSWLVTPK	0.68621009	2	2.674901
Q6IE52	LPSSEEEESLDINIEGAK	0.790846479	2	4.660444
Q6IE52	MLIYTILPDGEVIADSVK	0.744888307	2	3.812035
Q6IE52	MLSGFIPLKPTVK+Oxidation(0)	0.876441293		
Q6IE52	MNRIMQWQDVK+Oxidation(0)	0.770508875		

Q6IE52	NLYPLKELVQDPK	0.684926391	1	2.079934
Q6IE52	QLSFSLSAEPIQGPYK	0.518060454	2	4.087656
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	0.752766204	3	3.521737
Q6IE52	VHLSFSPSQSLPASQTHMR	0.745345878	3	3.414121
Q6IE52	VKTVPLTCNNPK	0.659540493	2	2.902613
Q6IE52	VTASPQSLCGLR	0.68599406	2	2.886737
Q6IE52	YMVLVPSQLYTETPEK	0.640248148	2	3.577462
Q6IE52	YMVLVPSQLYTETPEK+Oxidation(1)	0.729787297		
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.004053315**	**0.82986**	**2**
Q6IFW6	LENEIQTYR	1.194961565	2	2.517452
Q6IFW6	QSLEASLAETEGR	0.98244744	2	2.756063
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.894655661**	**0.95408**	**4**
Q6IMF3	TNAENEFVTIK	1.490322439	2	2.952923
Q6IMF3	TNAENEFVTIKK	0.440249309	2	2.426961
Q6IMF3	WELLQQVDTSTR	1.100286388	2	3.626365
Q6IMF3	YEELQITAGK	0.911750503	2	3.470391
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**1.017967306**	**0.83432**	**5**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.883109091	3	5.379867
Q6IRK9	GEESAVMVVPR	0.830458328	2	2.420935
Q6IRK9	IVVYNQPYTDYGK	1.324443109	2	3.371046
Q6IRK9	TYPDTDSFNTVAEITGSK	0.944946425	2	3.797605
Q6IRK9	VGAVASLIR	0.780035654	2	2.516366
Q6KCD5	**NIPBL Nipped_B_like protein**	**0.911046142**	**0.55108**	**2**
Q6KCD5	AFLISLLNLFDDTAK	0.423694559	2	2.598496
Q6KCD5	QNNTRSENTKARPETPK	1.198810737	2	2.566816
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.915598069**	**0.98877**	**4**
Q6MGB5	AGVIGLTQTAAR	0.873517658	2	3.334717
Q6MGB5	GSIINISSIVGK	0.889095342	2	2.581352
Q6MGB5	SALALVTGAGSGIGR	0.972643131	2	3.157082
Q6MGB5	VGNIGQTNYASSK	1.223159809	2	2.366945
Q6NS46	**RRP5 Protein RRP5 homolog**	**0.982889581**	**0.59644**	**2**
Q6NS46	GKQTKSTEVPR	0.88408037	2	2.678293
Q6NS46	IIDYSQMDELALLSLR	1.108996558	2	2.370475
Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.099234459**	**0.62217**	**2**
Q6NSR8	HNSPSAAHFITR	0.981093948	3	3.557373
Q6NSR8	TVEINNTDAEGR	0.855895055	2	2.693942
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**0.948273039**	**0.95365**	**3**
Q6NYB7	EFADSLGIPFLETSAK	1.366568099	2	3.616446
Q6NYB7	MGPGATAGGAEK	1.322015957	2	2.92138
Q6NYB7	NATNVEQSFMTMAAEIK	0.922211278	2	4.619451
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.189806931**	**2.3E-08**	**9**
Q6NZJ6	DLDFAKAKPRMDQYFNQMEK+Oxidation(10)	0.746585617		
Q6NZJ6	GLPLVDDGGWNTVPISK	1.029413781	2	2.949481
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.155500114	3	3.472805
Q6NZJ6	IHNAENIQPGEQK	1.188174391	2	4.175091
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.306185357	3	3.58037
Q6NZJ6	LGIESTLER	1.125484489	2	2.373941
Q6NZJ6	LKEELEEAR	1.243654269	2	2.673569
Q6NZJ6	QVTQLAIDTEER	1.182463853	2	2.854519
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.740881412	3	4.776618
Q6P0K8	**PLAK Junction plakoglobin**	**1.03926265**	**0.99393**	**2**
Q6P0K8	LLNDEDPVVVTK	1.108455026	2	2.979309
Q6P0K8	NLALCPANHAPLQEAAVIPR	0.935413361	3	3.684323
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.045355366**	**4.8E-13**	**8**
Q6P502	GISDLAQHYLMR	1.084726111	2	2.378875
Q6P502	IVLLDSSLEYK	0.900024048	2	2.679242

Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.082904553	3	3.686874
Q6P502	KGESQTDIEITR	1.234325057	2	3.182367
Q6P502	NLQDAMQVCR	1.323361949	2	2.802642
Q6P502	TAVETAVLLLR	1.064504274	2	3.385841
Q6P502	TLIQNCGASTIR	1.324354815	2	2.936961
Q6P502	WSSLACNIALDAVK	0.995244936	2	3.883981
Q6P5D3	**DHX57 Putative ATP_dependent RNA helicase DHX57**	**0.983090547**	**0.986**	**2**
Q6P5D3	ARHNRTAQEEVEEDLR	0.978097997	2	2.304696
Q6P5D3	QEETLALKSICGEK	0.995251273	2	2.324683
Q6P6M7	EMFVYLSTQLKK+Oxidation(1)	4.330702105		
Q6P6M7	SGDISAVQPK	0.970785403	2	2.305707
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	0.790490355	2	3.998195
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.928882039**	**1**	**12**
Q6P6R2	ALTGGIAHLFK	0.935984542	2	2.696993
Q6P6R2	EANLAASFGKPINF	0.905446457	1	2.056696
Q6P6R2	IDVSVEAASGGK	1.052926416	2	3.659001
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	0.922466849	3	4.130208
Q6P6R2	IPNIFAIGDVVAGPMLAHK	1.035122293	3	3.417117
Q6P6R2	NETLGGTCLNVGCIPSK	0.929534697	2	5.345018
Q6P6R2	NQVTATTADGSTQVIGTK	1.126716702	2	5.649474
Q6P6R2	RPFTQNLGLEELGIELDPK	1.032428244	3	4.214916
Q6P6R2	SEEQLKEEGVEFK	1.008238281	3	4.12924
Q6P6R2	TNADTDGMVK	0.900217481	2	2.824356
Q6P6R2	TNADTDGMVK+Oxidation(7)	0.962505731		
Q6P6R2	VCHAHPTLSEAFR	1.042274623	3	3.80575
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.953257818**	**0.97871**	**7**
Q6P6S9	AAETHLIDYEK	1.156053664	2	2.461366
Q6P6S9	AQTLLLEVEEIFK	1.063908857	2	3.8696
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.926198327	2	4.732957
Q6P6S9	QGAETVQELLEVAK	0.880614182	2	3.313205
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	0.891567517	3	3.851656
Q6P6S9	VEDFERKAR	0.696899291	2	2.442626
Q6P6S9	WLEAEWIFGGVK	0.891295484	2	3.082896
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.069630772**	**0.05961**	**8**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2)	1.187805488		
Q6P6V0	HFVALSTNTDK	1.080463128	2	2.721133
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	0.806082425	3	5.439646
Q6P6V0	MIPCDFLIPVQTQHPIR	0.791635737	2	3.133447
Q6P6V0	TFTTQETITNAETAK	1.104117707	2	5.115226
Q6P6V0	TLANLNPESSLFIIASK	0.820167949	3	4.964591
Q6P6V0	VFEGNRPTNSIVFTK	0.84467763	2	3.392012
Q6P6V0	VWFVSNIDGTHIAK	0.792994594	2	3.464535
Q6P7B0	**SYWC Tryptophanyl_tRNA synthetase_ cytoplasmic**	**1.054831373**	**0.98128**	**2**
Q6P7B0	ASEDFVDPWTVR	1.047185937	2	2.694035
Q6P7B0	TLIDVLQPLIAEHQAR	1.134330656	3	3.314078
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.127271376**	**0.48355**	**6**
Q6P7Q4	ATLELTHNWGTEDDETQSYHNGNSDPR	0.728925537	3	3.982593
Q6P7Q4	DFLLQQTMLR	1.084381324	2	3.317003
Q6P7Q4	FEELGVK	0.90283459	1	1.91717
Q6P7Q4	GFGHIGIAVPDVYEACK	0.929219217	2	3.455763
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	0.872859504	2	5.643552
Q6P7Q4	RFEELGVK	0.994869886	2	2.648204
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.147536737**	**0.00022**	**2**

Q6P7R8	GIFVQSVLPFFVATK	1.081975696	2	3.300225
Q6P7R8	LGEWAVVTGGTDGIGK	1.147737819	2	4.03946
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.215544261**	**1.2E-05**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	1.034876129	2	4.682413
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10)	1.034068734		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.313701421	3	5.302368
Q6P9T8	EIVHLQAGQCGNQIGAK	1.200454566	2	5.043253
Q6P9T8	EVDEQMLNVQNK	1.392096915	2	4.069465
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	0.896042025	3	5.632992
Q6P9T8	INVYYNEATGGK	1.029822164	2	3.468115
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.992520868	3	5.342913
Q6P9T8	LHFFMPGFAPLTSR	1.297416196	2	2.700942
Q6P9T8	MSATFIGNSTAIQELFK	0.91649274	2	3.974575
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	1.227504141	3	4.662916
Q6P9T8	TAVCDIPPR	1.025933783	2	2.500931
Q6P9T8	YLTVAAVFR	1.015846749	2	2.469502
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.265074268**	**8.2E-13**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	0.652446408	3	4.351461
Q6P9U8	EGTGSTATSSSSTGGAVGK	1.49635517	2	4.13056
Q6PA06	**ATLA2 Atlastin_2**	**1.265709446**	**0.00069**	**5**
Q6PA06	AGLTDQVSHHAR	1.055804504	2	3.34998
Q6PA06	NLVPLLLAPENLVEK	1.292489309	2	2.892005
Q6PA06	QNQHEELQNVR	1.253908859	2	2.731601
Q6PA06	SMEQVCGGDKPYIAPSDLER	1.315263355	3	3.485745
Q6PA06	SMLQATAEANNLAAVAGAR	1.192207862	2	4.490577
Q6PCL9	**polymerase gamma**	**0.973267758**	**0.93282**	**4**
Q6PCL9	ATDITPIPMSEGGISDMPKR	0.995883724		
Q6PCL9	LTEILK	1.008333081		
Q6PCL9	QANNINMLKDGMK	0.901483247		
Q6PCL9	WEMDDPRPIAKAER	1.096812272		
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.198817705**	**0.07706**	**2**
Q6PDM2	SHEGETAYIR	1.499072571	2	2.640331
Q6PDM2	VVVSGLPPSGSWQDLK	1.198543281	2	2.310523
Q6PDN3	**MYLK Myosin light chain kinase_ smooth muscle**	**0.888864192**	**0.74238**	**2**
Q6PDN3	LIDFGLAR	0.721752417	2	2.373367
Q6PDN3	VSMSEKNGMQILEIRGVTR	0.895231131	2	2.444653
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.062141937**	**0.94093**	**3**
Q6PEC1	LEAAYTDLR	1.067856293	2	3.178392
Q6PEC1	QILESEKDLEEAEEYKEAR	1.105172036	3	3.835938
Q6PEC1	RLEAAYTDLR	1.032893461	2	2.347981
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.229358518**	**0.0332**	**3**
Q6PEC4	NDFTEEEEAQVR	1.833788632	2	3.461069
Q6PEC4	TDDIPVWDQEFLK	1.18524296	2	3.122371
Q6PEC4	TVANMIKGKTPEEIR+Oxidation(4)	1.063334897		
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.095665862**	**0.21453**	**6**
Q6Q0N1	AVFQYIDENQDR	0.941691237	2	3.008107
Q6Q0N1	EGGSIPVTLTFQEATGK	1.117834053	2	2.612732
Q6Q0N1	LGGSVELVDIGK	1.377847365	2	3.731147
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	0.838800368	2	2.634509
Q6Q0N1	MTEAAAADVQR	1.111161265	2	2.602796
Q6Q0N1	TVFGVEPDLTR	1.065677205	2	2.547685
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.969708958**	**0.68916**	**3**
Q6SKG1	AFIVLNPDYK	0.954028154	2	2.790596
Q6SKG1	FDSTSILQTLSK	0.967233469	2	3.127405

Q6SKG1	TGTVLIPGTTQLTQK	1.23853635	2	2.935618
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**0.956194272**	**0.99997**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	0.968585781	2	4.513122
Q6TUG0	FQMTQEVVCDECPNVK	1.010931062	2	5.165411
Q6TUG0	KGEGLPNFDNNNIK	1.021008154	2	2.752147
Q6TUG0	TLEVEIEPGVR	0.937039392	2	3.227964
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.000302325**	**0.9928**	**16**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	0.926921083	2	4.313604
Q6UPE1	ALNEGGLQSIPK	0.915024113	2	3.159334
Q6UPE1	ASCDAQTYGIGLK	0.974269852	2	3.68383
Q6UPE1	FCPAGVYEFVPLEQGDGFR	0.880335073	2	4.946673
Q6UPE1	GAPLNTPVTEDR	0.918013111	2	3.449286
Q6UPE1	GIATNDVGIQK	0.937946281	2	3.562947
Q6UPE1	HHPSIRPTLEGGK	0.808041055	2	2.424297
Q6UPE1	LQINAQNCVHCK	1.11310282	2	3.729051
Q6UPE1	NLSIYDGPEQR	0.911492278	2	3.21672
Q6UPE1	QLAAEQEKDIR	0.845207166	2	2.804508
Q6UPE1	QLTSENLQSK	0.866387444	2	2.462073
Q6UPE1	SGSLAAEAIFK	0.888181101	2	3.355657
Q6UPE1	TAGLHVTEYEDNLK	1.138832174	2	3.880151
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	1.031873951	2	3.703534
Q6UPE1	VDHTVGWPLDR	0.871844155	2	2.646851
Q6UPE1	VTIFAEGCHGHLAK	0.841619292	2	3.383801
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**0.95793291**	**0.99997**	**7**
Q6URK4	EDSVKPGAHLTVK	1.028410833	2	3.369654
Q6URK4	EDTEEYNLR	1.338108787	2	2.342645
Q6URK4	GFAFVTFDDHDTVDK	0.844459402	2	4.251501
Q6URK4	IETIEVMEDR	0.93750569	2	3.391518
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	1.19035414	2	4.976744
Q6URK4	WGTLTDCVVMR	0.966629475	2	2.30274
Q6URK4	YHTINGHNCEVK	1.040332089	2	3.574183
Q6URW6	**MYH14 Myosin_14**	**0.987898229**	**0.98504**	**4**
Q6URW6	EDQSILCTGESGAGK	1.184476314	2	4.497694
Q6URW6	FDQLLAEEK	0.947509527	2	2.33667
Q6URW6	KFDQLLAEEK	1.093157248	2	2.579592
Q6URW6	QLLQANPILEAFGNAK	0.917951254	2	4.332239
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**1.059936972**	**0.99992**	**5**
Q6XQN1	GSEVNVIGIGTNVVTCPK	1.034215159	2	4.118571
Q6XQN1	LDSGDLLQQAK	1.030029789	2	2.949369
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.098473857	2	4.483629
Q6XQN1	QLQNPAVYQVALSEK	0.922953684	2	3.823194
Q6XQN1	VWLQGAQEPCTVKPAQVEPLLR	1.065952219	3	3.648148
Q6Y7W8	**PERQ2 PERQ amino acid_rich with GYF domain_containing protein 2**	**0.985368891**	**0.16286**	**2**
Q6Y7W8	AEEENRSENSLSAKVPSR	0.74763938	2	2.419723
Q6Y7W8	KDEPKAEQVEK	0.986133268	2	2.517178
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**0.881673923**	**0.48963**	**2**
Q6ZPJ3	FRTTDIVIR	0.861145263	2	2.451537
Q6ZPJ3	NCAQGEGSMAKKVK	1.002324251	2	2.563106
Q6ZPY5	**ZN507 Zinc finger protein 507**	**1.081641358**	**0.82996**	**2**
Q6ZPY5	CSLCGYVCSHPPSLK	1.132409364	2	2.341023
Q6ZPY5	IISSSPNK	0.977390821	2	2.352312
Q704S8	**CACP Carnitine O_acetyltransferase**	**0.986371158**	**0.63278**	**3**
Q704S8	ALQPIVSEEEWAHTK	1.166224313	2	2.495661
Q704S8	DKVNRESVNSIQK	1.183313804	2	2.333611

Q704S8	FNITPEIKNDIEK	0.974146324	2	3.187848
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**0.979857331**	**0.99398**	**5**
Q711G3	DCGTDVLDLWTLMQK	1.209463652	2	3.87297
Q711G3	DVEETKPELSLLGDGDH	1.029861269	2	3.449936
Q711G3	LNVAVGEYAK	0.976994578	2	3.027585
Q711G3	QHVPLDEYSANLR	0.953440716	2	2.562931
Q711G3	VILITPPPLCEAAWEK	0.854501242	2	2.646211
Q71TY3	**RS27 40S ribosomal protein S27**	**1.618213282**	**0.16188**	**2**
Q71TY3	DLLHPSPEEEK	1.626939151	2	2.327085
Q71TY3	LVQSPNSYFMDVK	1.184899809	2	2.86871
Q75N33	**SC16B Protein transport protein Sec16B**	**0.797219857**	**0.52265**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	1.08727397	2	3.800258
Q75N33	VLEPDWLVQLR	0.781982304	2	2.506728
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.033867114**	**0.6894**	**3**
Q75Q39	NADLSTFYQNR	1.054561268	2	2.573889
Q75Q39	NREPLMPSPQFIK	1.016116375	2	2.548639
Q75Q39	SDEDKDKEGEALEVK	1.29997138	2	4.165979
Q75WE7	**VWA5A von Willebrand factor A domain_containing protein 5A**	**0.934978945**	**0.51849**	**2**
Q75WE7	YTQETIEEAVER	1.130297472	2	2.552592
Q75WE7	YVQELPLESDGALR	0.777709626	2	2.61122
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**0.942772278**	**0.92515**	**7**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	0.994828014	3	4.354185
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	0.913887437	3	3.376251
Q76MZ3	IGPILDNSTLQSEVKPILEK	0.764829069	2	4.528924
Q76MZ3	LTQDQDVDVK	1.010267667	2	2.886872
Q76MZ3	QLSQSLLPAIVELAEDAK	0.987053	3	3.834573
Q76MZ3	SALASVIMGLSPILGK	0.85859346	2	3.083025
Q76MZ3	SEIIPMFSNLASDEQDSVR	0.955943188	2	3.855789
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**0.885475092**	**0.98757**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	1.03578367	2	5.674018
Q78P75	NFGSYVTHETK	1.139195663	2	2.710826
Q78P75	YNPTWHCIVGR	0.954364649	2	2.721489
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**0.906031684**	**0.23077**	**5**
Q791V5	EEGIVGFFAGLIPR	0.815951761	2	3.596333
Q791V5	GLFTGLTPR	0.908531857	2	2.801613
Q791V5	LCSGVLGTVVHGK	1.259818248	3	3.354568
Q791V5	VLIQVGYEPLPPTIGR	0.878664213	2	4.165522
Q791V5	YCGLCDSIVTIYR	0.899337139	2	2.932106
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.076447259**	**0.56129**	**4**
Q794E4	ATENDIYNFFSPLNPVR	1.098243555	3	4.899892
Q794E4	HSGPNSADSANDGFVR	1.021098982	2	4.180212
Q794E4	ITGEAFVQFASQELAEK	0.997704426	2	3.867411
Q794E4	VHIEIGPDGR	1.133728611	2	2.742947
Q7M0E3	**DEST Destrin**	**1.080182329**	**2.7E-09**	**2**
Q7M0E3	HEYQANGPEDLNR	1.146600939	2	4.373701
Q7M0E3	KEELMFFLWAPEQAPLK	0.898087692	2	3.834273
Q7TMA5	**APOB Apolipoprotein B_100**	**0.818585342**	**1.7E-12**	**12**
Q7TMA5	GFEPTLEALFGK	0.678879528	2	2.900756
Q7TMA5	GGINQVGLAFESTK	0.842660808	2	2.473005
Q7TMA5	IEGNLVFDPSSYLPK	0.77027346	2	3.489512
Q7TMA5	IEIDIPLPLGGK	0.895286146	2	3.085059
Q7TMA5	ITDNDVLIALDSAK	1.16217389	2	3.20563

Q7TMA5	KGTVATEMSTER	1.79415586	2	2.643985
Q7TMA5	LLQWEQSEQVK	0.943584348	2	2.433946
Q7TMA5	LSISEQNAQR	0.88769402	2	2.580496
Q7TMA5	NFVASHIANILNSEELYVQDLK	0.888053677	3	3.645085
Q7TMA5	NSVSTALEHTLSALLTPAEQTSSWK	0.614744798	3	3.35974
Q7TMA5	SVGFHLPSQEVQIPTFTIPK	0.873064275	3	3.525585
Q7TMA5	TILFDTFVNDVAPVEK	0.689652642	2	3.475433
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.123826036**	**0.03395**	**4**
Q7TNG8	AVVGSPHVSTASAVR	1.071283165	2	2.375283
Q7TNG8	AYSTDVCVPISR	1.300105152	2	3.702007
Q7TNG8	GSQGGLSQDFVEALK	1.110484061	2	3.741249
Q7TNG8	QLLQEEVGPVGVETMR	1.304822071	2	2.694601
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.074578464**	**0.56582**	**2**
Q7TP47	DLFEDELVPLFEK	1.351919	2	3.06382
Q7TP47	NLANTVTEEILEK	1.069480969	2	3.680556
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.015206452**	**0.22031**	**4**
Q7TP48	LENGEIETIAR	0.983026775	2	3.319412
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	1.024705097	3	3.358104
Q7TP48	LLEYDTVTK	0.911143242	2	2.358764
Q7TP48	LLLSSETPIEGK	1.941971233	2	2.989513
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**0.823372185**	**0.11711**	**7**
Q7TP52	AGVSVYGIIR	1.32979681	2	2.393999
Q7TP52	EDCSPADKPYIEEAR	1.010794506	2	3.540596
Q7TP52	KREDCSPADKPYIEEAR	0.834988353	2	4.624423
Q7TP52	LDYGGMGQEVQVEHIK	0.891598513	2	4.417758
Q7TP52	LKEHCIVNYQVK	0.701421295	2	3.824452
Q7TP52	NLIEWLNK	0.790921673	2	2.452743
Q7TP52	TFSGQTHGFVHR	0.83881514	2	3.603651
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.035191168**	**0.03565**	**11**
Q7TPB1	ALIAGGGAPEIELALR	1.075301251	2	4.126056
Q7TPB1	DIEREDIEFICK	1.485085629	2	2.380545
Q7TPB1	ETLLNSATTSLNSK	1.222071956	2	3.556609
Q7TPB1	GDVTITNDGATILK	0.847943085	2	3.287564
Q7TPB1	GIHPTIISESFQK	1.115650217	2	2.636964
Q7TPB1	IDDVVNTR	1.071978582	2	2.375369
Q7TPB1	LVIEEAER	1.873392938	1	1.946073
Q7TPB1	MIQDGKGDVTITNDGATILK+Oxidation(0)	0.821505221		
Q7TPB1	SIHDALCVIR	0.747642091	2	2.481982
Q7TPB1	TGCNVLLIQK	0.680630037	2	2.502972
Q7TPB1	VIDPATATSVDLR	1.046185127	2	3.38237
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.094201216**	**1**	**2**
Q7TPJ0	GEDFPANNIVK	0.975632843	2	3.022465
Q7TPJ0	GTEDFIVESLDASFR	0.985192606	2	4.092875
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**0.929998931**	**0.23719**	**2**
Q7TQM4	QDRPLPSTASDSTR	0.815299579	2	3.185305
Q7TQM4	TQCLEQAQR	0.930274264	2	3.019858
Q80TV8	**CLAP1 CLIP_associating protein 1**	**0.968657322**	**0.79796**	**2**
Q80TV8	MESCLAQVLQK	1.406052366	2	2.498413
Q80TV8	MGADLLGSVQAKVQK+Oxidation(0)	0.959446059		
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**1.009726892**	**4.1E-05**	**11**
Q80W21	CLDAFPNLK	0.889137762	2	3.183004
Q80W21	CLDAFPNLKDFIAR	1.193056719	2	2.693651

Q80W21	FKLGLDFPNLPYLIDGSHK	0.842082889	3	4.137031
Q80W21	HNLCGETEEER	1.000324197	2	3.825125
Q80W21	ITQSNAILR	1.141029842	2	3.149814
Q80W21	KHNLCGETEEER	1.109289388	3	4.447618
Q80W21	LFLEYTDSSYEEK	1.056846592	2	3.974284
Q80W21	LGLDFPNLPYLIDGSHK	0.982760264	2	4.7105
Q80W21	LKPGYLEQLPGMMR	0.755333455	2	2.619989
Q80W21	LYSEFLGK	1.056252492	2	2.314208
Q80W21	VDILENQLMDNR	0.967858363	2	3.693533
Q80X50	**UBP2L Ubiquitin_associated protein 2_like**	**0.954479875**	**0.8449**	**2**
Q80X50	IDLAVLLGK	0.954254811	2	3.387492
Q80X50	QRPQATAEQIR	1.088519978	2	2.33472
Q80X90	**FLNB Filamin_B**	**0.946240014**	**0.55984**	**9**
Q80X90	ADIEMPFDPSK	0.988223434	2	2.335035
Q80X90	AHGPGLEGGLVGKPAEFTIDTK	0.948304939	3	3.496061
Q80X90	GAGIGGLGITVEGPSESK	0.977996962	2	3.55208
Q80X90	GFLDGVYSFEYYPSTPGK	1.247073816	2	3.188443
Q80X90	IGNLQTDLSDGLR	1.173512331	2	2.38394
Q80X90	ILAQDGEGQPIDIQMK	0.942430567	2	3.852266
Q80X90	VDIQTEDLEDGTCK	1.064486392	2	3.917562
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.547080617	3	3.900689
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.017849964	2	3.887513
Q80YR5	**SAFB2 Scaffold attachment factor B2**	**0.949046902**	**0.65089**	**2**
Q80YR5	GSKMEEEGSEDNGLEEDSR	0.662742238	2	2.393886
Q80YR5	SEPVKEEGSELEQPFAQATSSVGPDR	1.01422003	3	4.219013
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.037300096**	**1**	**2**
Q80Z25	ELEQEAERLEK	1.032833579	2	2.939034
Q80Z25	MIEESLK+Oxidation(0)	1.05311388		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.119026437**	**0.02893**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.372715145	2	3.935778
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.27322815	5	4.608683
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.120436797	2	4.45121
Q80Z29	YLLETSGNLDGLEYK	1.155173841	2	4.222397
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**0.960228747**	**0.99703**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	1.007375904	2	2.729569
Q80Z36	YPEEQLK	0.908086209	2	2.33479
Q80ZF0	**chain**	**0.930102882**	**0.75058**	**2**
Q810B6	**ANFY1 Ankyrin repeat and FYVE domain_containing protein 1**	**1.12941358**	**0.45103**	**2**
Q810B6	QLDLELK	1.139983495	1	2.257823
Q810B6	RESGAAEQVDNKGR	0.862827335	1	1.925182
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.281299489**	**0.84434**	**2**
Q811D2	AQEDFDK	1.283881787	1	1.949182
Q811D2	LNMLSSKLDNEKQNK	0.931756063	2	2.336043
Q811X6	**CRYL1 Lambda_crystallin homolog**	**0.895647291**	**0.86469**	**3**
Q811X6	EMKSLEQSGSLK+Oxidation(1)	0.854874817		
Q811X6	IVDDQVILSSSSSCLLPSK	0.942829754	2	2.731198
Q811X6	TFGPVPEFSGDTVEK	0.6541976	2	3.012004
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.364563874**	**1**	**10**
Q8BFZ3	CDVDIR	0.972251391	1	2.001956
Q8BFZ3	DLTDYLMK	1.67384596	1	2.07498
Q8BFZ3	HQGVMVGMGQK	1.074655267	3	3.90187
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	1.267639394		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	1.143501965		

Q8BFZ3	HQGVMVGMGQK+Oxidation(7)	1.033058182		
Q8BFZ3	SYELPDGQVITIGNER	1.064596025	3	5.169834
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.066151376	3	6.937174
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)	1.047960743		
Q8BFZ3	VAPDEHPILLTEAPLNPK	0.956185313	3	4.210713
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**1.058634034**	**0.95384**	**5**
Q8BG32	LYDNLLEQNLIR	0.90304169	2	3.650634
Q8BG32	TGQAAELGGLLK	1.051031876	2	2.474134
Q8BG32	TTANAIYCPPK	1.084065741	2	3.076473
Q8BG32	TYEAALETIQNMSK	1.076421258	2	3.262693
Q8BG32	VQIEHISSLIK	1.112087456	2	3.159459
Q8BG79	**C19L2 CWF19_like protein 2**	**0.875413738**	**0.10811**	**2**
Q8BG79	KNQDSSGNLRSK	0.687361384	2	2.392182
Q8BG79	MWPVSSPRETLDMKAER+Oxidation(12)	0.930543116		
Q8BGC4	**ZADH2 Zinc_binding alcohol dehydrogenase domain_containing protein 2**	**1.466578724**	**0.62024**	**2**
Q8BGC4	DCPVPLPGDGDLLVR	1.461785029	2	2.343935
Q8BGC4	FVGINASDINYSAGR	2.882514123	2	3.814173
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**1.177007476**	**9.4E-13**	**3**
Q8BGT5	ILTLESMNPQVK	0.885043701	2	2.604494
Q8BGT5	LLEETGICVVPGSGFGQR	1.053439326	2	3.769341
Q8BGT5	VLCIINPGNPTGQVQSR	1.665784502	2	4.51233
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**0.970049922**	**0.99944**	**4**
Q8BGY2	KYEDICPSTHNMDVPNIK	1.095036666	3	4.350031
Q8BGY2	KYEDICPSTHNMDVPNIK+Oxidation(11)	1.082445531		
Q8BGY2	VHLVGIDIFTGK	0.980750683	1	3.36391
Q8BGY2	YEDICPSTHNMDVPNIK	0.913523408	2	4.045334
Q8BGY3	**LUZP2 Leucine zipper protein 2**	**0.797013322**	**0.22874**	**2**
Q8BGY3	DLQNENKSLK	1.087272513	2	2.312989
Q8BGY3	SLQEALQNQLK	0.73090149	2	2.477481
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**0.957677854**	**0.05445**	**9**
Q8BH00	ELLMLENFIGGK	1.506384755	2	3.387634
Q8BH00	ELNLPFGGMK	1.13054053	1	2.232169
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.003432004	3	5.092261
Q8BH00	ILCGEGVDQLSLPLR	1.013469034	2	4.385639
Q8BH00	ITQLSAPHCK	1.222199851	2	2.94709
Q8BH00	KLSLELGGK	0.959386523	1	2.004368
Q8BH00	NPAIIFEDANLEECIPATVR	0.908049499	3	5.344548
Q8BH00	SSFANQGEICLCTSR	1.888234605	2	4.445076
Q8BH00	TPVGIAGLISPWNLPLYLLTWK	0.880845032		
Q8BH69	**SPS1 Selenide_ water dikinase 1**	**0.810906806**	**0.17046**	**2**
Q8BH69	IIEVAPQVATQNVNPTPGATS	0.809564273	2	3.680098
Q8BH69	YGEGHQAWIIGIVEK	0.768534208	2	2.364937
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.090286854**	**0.99974**	**8**
Q8BHN3	AEKDEPGAWEETFK	1.148826108	2	3.427011
Q8BHN3	DDNSVELTVAEGPYK	1.155203569	2	3.638777
Q8BHN3	MLDYLQGSGETPQTDIR	0.979099009	2	4.764602
Q8BHN3	MLDYLQGSGETPQTDIR+Oxidation(0)	0.99891719		
Q8BHN3	REPWLLASQYQDAIR	0.933198229	3	3.755299
Q8BHN3	SGGIERPFVLSR	1.029539414	2	2.527569
Q8BHN3	SLLLSVNAR	0.933377348	2	2.420121
Q8BHN3	VTEGGEPYR	0.965044499	2	2.536797
Q8BI84	**MIA3 Melanoma inhibitory activity protein 3**	**0.846373003**	**0.04677**	**2**

Q8BI84	LQLESEREQNVK	0.117092676	2	2.342728
Q8BI84	TQTAVSIVEEDLK	0.862213907	2	2.619912
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**1.216560776**	**0.5673**	**2**
Q8BIJ6	DTVLLPQTSFPMK	0.901483247	1	2.230632
Q8BIJ6	SCQTALAEILDVLVR	0.874060245	2	3.898237
Q8BIJ7	**RUFY1 RUN and FYVE domain_containing protein 1**	**1.005355937**	**0.48866**	**2**
Q8BIJ7	EKDTSCLLQTELQQVEGLK	1.139664699	2	2.446253
Q8BIJ7	ELQDEKAELRK	0.855462794	2	2.445209
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**0.847211442**	**0.94558**	**7**
Q8BJ64	ADSAYHPSCTCK	1.598534384	2	3.403724
Q8BJ64	AEVQTLVSR	0.920253387	2	2.75354
Q8BJ64	ELQPGSHVQSDK	1.144226861	2	2.5352
Q8BJ64	ELQPGSHVQSDKEIDAFVR	1.064957003	2	4.11539
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.041154957	5	4.860238
Q8BJ64	TNHPLHQAFLQAAR	0.843353903	3	4.677282
Q8BJ64	VLLLEAGPK	0.923388873	2	2.930708
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**0.961964844**	**0.94684**	**2**
Q8BJY1	GLTHPDDSVK	0.950224027	2	2.487785
Q8BJY1	TVAEIFGNSNYLR	1.070576851	2	3.076345
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**0.95343311**	**0.425**	**2**
Q8BL97	NPPGFAFVEFEDPR	1.193789894	2	3.482625
Q8BL97	VYVGNLGTGAGK	0.921154087	2	2.359843
Q8BMJ2	**SYLC Leucyl_tRNA synthetase_ cytoplasmic**	**1.179002721**	**0.8223**	**3**
Q8BMJ2	QTGEGVGPQEYTLVK	1.227903771	2	2.366236
Q8BMJ2	SFITTDVNPYYDSFVR	1.02321639	2	3.315366
Q8BMJ2	STGNFLTLSQAVDK	1.198991958	2	2.974211
Q8BTM8	**FLNA Filamin_A**	**1.097580921**	**0.95939**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	0.840670797	2	3.789589
Q8BTM8	ANLPQSFQVDTSK	0.944058598	2	2.465197
Q8BTM8	GAGTGGLGLAVEGPSEAK	1.1047685	2	3.685926
Q8BTM8	IVSPSGAAVPCK	1.081923593	2	2.456903
Q8BTM8	VTAQGPGLEPSGNIANK	0.982703334	2	3.940563
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.038373933**	**0.0003**	**2**
Q8BTZ7	HHGQEGSILVTK	0.818880034	3	3.756291
Q8BTZ7	YGVVVCEADTGR	1.048441121	2	3.255346
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.019071967**	**0.99659**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	1.018908966	2	2.420279
Q8BU33	LPNSLMGR+Oxidation(5)	1.023629715		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.88339642	2	4.582908
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.178517812**	**0.99434**	**2**
Q8BWQ1	ADIWLIR	0.972812503	2	2.536914
Q8BWQ1	IHHDQPVKPLDR	1.248317402	3	3.50576
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**0.912573064**	**0.81946**	**2**
Q8BX70	ENALSELDVPFKVK	1.02211022	2	2.902301
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19)	0.860921554		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.258095213**	**0.00492**	**2**
Q8C7X2	FNVEDGEIVQQVR	1.007643884	2	3.270266
Q8C7X2	VMGDRSVLYK+Oxidation(1)	1.591372446		
Q8C8R3	**ANK2 Ankyrin_2**	**1.143477938**	**9.1E-13**	**2**
Q8C8R3	STSSSGRPGTSPTRESR	0.727826143	2	2.43608
Q8C8R3	TSTDFSEVIKQELEDNDK	1.729234938	2	2.613098

Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**0.793528533**	**0.54717**	**4**
Q8CC88	HQATGELDDAK	1.210989459	2	3.385847
Q8CC88	IILDNLQAK	1.174226727	2	2.302537
Q8CC88	NLADQGIINYPYSTR	1.334624135	2	3.190962
Q8CC88	VSSDQLSSENLTSAVGQK	0.788806845	2	3.489278
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**0.875157541**	**0.37796**	**2**
Q8CDM4	MEEESIDLIIKEQK	1.707760812	2	2.39728
Q8CDM4	VTCQHKMEEESIDLIIK	0.866371932	2	2.37989
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.100799282**	**0.01397**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	0.983393162	3	4.998273
Q8CFN2	WVPEITHHCPK	1.053149565	2	2.406111
Q8CFN2	YVECSALTQK	1.128805564	2	3.052529
Q8CFW1	**ANO2 Anoctamin_2**	**1.148876382**	**0.10682**	**2**
Q8CFW1	TEQTFEERLILK	1.19174764	2	2.368721
Q8CFW1	TKDIGIWFDILSGIGK	0.647973697	2	2.339453
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.117808842**	**0.00013**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	0.949451261	2	2.893334
Q8CG45	EHHFEAIALVEK	1.716478009	2	2.345078
Q8CG45	FFGNSWSETYR	1.111916732	2	2.817085
Q8CG45	FYAYNPLAGGLLTGK	0.972956609	2	4.537042
Q8CG45	MDASASAATVR	0.989719708	2	3.673352
Q8CG45	MDASASAATVR+Oxidation(0)	1.05475113		
Q8CG45	QVETELLPCLR	0.990083678	2	2.962501
Q8CG45	RMDASASAATVR	1.274890331	2	2.760439
Q8CG45	TTYGTSAPSMTSAALR	0.984554935	2	4.211116
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.102226126	3	5.550289
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**1.34640234**	**0.00068**	**2**
Q8CG48	EEKLLEK	1.438073781	1	1.965779
Q8CG48	IKALNCEIEELER	1.278472532	2	2.464792
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.031702587**	**3.9E-10**	**10**
Q8CGC7	AIQGATSHHLGQNFSK	1.144358144	2	4.479011
Q8CGC7	DQDVEPGAPSMGAK	1.276387297	2	3.14168
Q8CGC7	DQVDSAVQELLQLK	1.165950958	2	3.728001
Q8CGC7	GDVSISVEEGKENLLR	1.353892912	2	3.47736
Q8CGC7	KEENLAEWYSQVITK	1.079549617	2	4.356993
Q8CGC7	KGDIIQLQR	1.099351411	2	2.657011
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.052762351	2	4.380905
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.230161874	2	4.633912
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	1.077647287	3	3.47725
Q8CGC7	VYEELLAIPVVR	1.175269775	2	3.032671
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.070537298**	**0.99275**	**9**
Q8CHM7	DTSKPCLINIMIEPQSTR	0.991318688	2	3.494121
Q8CHM7	GAAYSHAEDSIR	0.620290949	2	3.43655
Q8CHM7	GVVPDNHPNCVGAAR	1.129022639	2	3.364092
Q8CHM7	GYFVQTPEELQDSLR	0.984089956	2	4.051752
Q8CHM7	LVELCNLPFLPTPMGK	1.092692617	2	4.265065
Q8CHM7	NCFIVSEGANTMDIGR	1.145012165	2	4.907655
Q8CHM7	NQEAMGAFQEFPQVEACR	1.132206488	2	6.103219
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	1.006700468	3	4.140991
Q8CHM7	YKECCMPPPLSLAETSAVR	1.301118154	2	2.369579
Q8CI17	**MB213 Protein mab_21_like 3**	**0.967182346**	**0.89425**	**2**
Q8CI17	QQISQTMEEVQK+Oxidation(6)	0.967637351		
Q8CI17	RQQISQTMEEVQK	0.966320526	2	2.3575

Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.934976598**	**0.42411**	**3**
Q8CIB5	GCEVTPDVNISGQK	0.97687428	2	3.165857
Q8CIB5	INQLYEQAK	0.888480163	2	2.969903
Q8CIB5	TSTILGDITSIPELADYIK	0.807909865	2	2.898173
Q8CIE6	**COPA Coatomer subunit alpha**	**1.095213917**	**0.99936**	**7**
Q8CIE6	ASNLENSTYDLYTIPK	1.125017485	2	3.797963
Q8CIE6	DADSQNPDAPEGK	1.630558043	2	3.2413
Q8CIE6	GITGVDLFGTTDAVVK	1.086109122	2	3.995919
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	1.007943988	2	3.641241
Q8CIE6	LLELGPKPEVAQQTR	1.098798534	2	3.470856
Q8CIE6	SILLSVPLLVVDNK	0.980779776	2	3.5948
Q8CIE6	TLDLPIYVTR	0.997506021	2	2.672677
Q8CJ40	**CROCC Rootletin**	**0.79916393**	**0.3586**	**4**
Q8CJ40	DLLQLGGELVRTSR	0.924812383	2	2.47817
Q8CJ40	ELEERTGNLGRQR	3.708500845	2	2.307867
Q8CJ40	LQEERRLLQER	1.074047017	2	2.359333
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9)	0.788236452		
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.107644821**	**0.23874**	**3**
Q8JZN5	GSNTCEVHFENTR	1.127893492	2	4.359045
Q8JZN5	NLSEFGLIQEK	0.999327255	2	3.107225
Q8JZN5	SGNVTTVMETIGR	0.974709001	2	2.505223
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**0.947994859**	**5.9E-11**	**16**
Q8K009	ADPLALAAEK	0.803107884	2	2.639571
Q8K009	AGFSVFWADDGLDTGPILLQR	0.845940291	2	3.867094
Q8K009	AMVEAVQLIADGK	0.624923985	2	3.769438
Q8K009	ANNTEYGLASGVFTR	0.739643972	2	4.734161
Q8K009	DLGEEALNEYLK	0.903524153	2	3.232624
Q8K009	EESFGPIMVISK	0.845080798	2	2.40331
Q8K009	FLFPEGIK	0.99497133	2	2.402335
Q8K009	FQNGDIDGVLQR	0.750606936	2	2.911394
Q8K009	GVINIIPGSGGVAGQR	0.744168854	2	3.957973
Q8K009	HGSIIYHPSLLPR	1.10966178	2	4.178293
Q8K009	LEAGTVFINTYNK	1.066428086	2	3.081229
Q8K009	NLQFEDGK	0.707147894	1	2.128599
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	0.654280928	3	3.709913
Q8K009	SCDVKPNDTVDSLYNR	0.934635642	2	4.433568
Q8K009	TPQPEEGATYEGIQK	0.932241369	2	3.200745
Q8K009	VVGVFTVPDKDGK	0.788484804	2	3.137646
Q8K1S6	**SPIR2 Protein spire homolog 2**	**1.209652826**	**0.07018**	**2**
Q8K1S6	ALFVETLELR	1.561095979	2	2.312166
Q8K1S6	DTADILLRR	1.010339485	2	2.424882
Q8K2F0	**BRD3 Bromodomain_containing protein 3**	**1.016676468**	**0.08082**	**2**
Q8K2F0	LNLPDYHKIIK	1.468138858	2	2.459141
Q8K2F0	QLSLDINRLPGEK	0.704041743	2	2.453372
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**0.9990478**	**0.99978**	**2**
Q8K3J1	LCEAICPAQAITIEAEPR	0.97747699	2	4.369447
Q8K3J1	YVNKKEQESEVDMK	1.02130546	2	2.317082
Q8K440	**ABC8B ATP_binding cassette sub_family A member 8_B**	**1.134245015**	**0.9609**	**3**
Q8K440	GEILGLLGHNGAGKSTSLK	0.920527932	2	2.313141
Q8K440	LMEMEQTLSSLRETEK+Oxidation(1)	1.087876363		
Q8K440	LMEMEQTLSSLRETEK+Oxidation(3)	1.11653707		
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.02507778**	**0.64613**	**5**

Q8K442	GQITAILGHSGAGK	1.517491617	2	3.506877
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	0.971900845	3	3.541419
Q8K442	LTGVCPQCNVQFDFLTVR	1.219688535	2	2.814696
Q8K442	NTQNILVQNLSGGQK	0.994002444	2	3.425331
Q8K442	STLLNVLSGLCVPTK	1.023708553	2	3.722986
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.984327409**	**0.99931**	**9**
Q8K4C0	FDHEMFGLKPK	1.222210746	2	2.921404
Q8K4C0	GYPIDILLSSR	0.925607493	2	3.06238
Q8K4C0	HSALGQHPTINDDLPNR	1.067368547	2	4.999358
Q8K4C0	IAVIGSGASGLTCIK	1.22750092	2	4.029736
Q8K4C0	KLPSQSEMMAEINK	1.052222876	2	3.820664
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	1.043056	3	4.587523
Q8K4C0	KTILTTEDR	0.97266641	2	2.560853
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	0.973273116	3	4.066142
Q8K4C0	SDDIGGLWR	0.962279452	2	2.813447
Q8K4G6		**0.993544587**	**0.60391**	**56**
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**0.970701274**	**0.45612**	**2**
Q8K4T4	FQPRAETQSMKIELK+Oxidation(9)	1.268287808		
Q8K4T4	IEELEETNKSLQK	0.961060802	2	2.406459
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**0.876120354**	**0.13037**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	0.882925565	2	4.19953
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	0.875506331	2	5.983057
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.073951769**	**0.89993**	**3**
Q8K586	FNVWDTAGQEK	1.035248229	2	3.033225
Q8K586	NLQYYDISAK	0.928758162	1	2.215826
Q8K586	VCENIPIVLCGNK	1.094326247	2	3.828304
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**1.124607378**	**0.84186**	**2**
Q8QZY1	KSEGEMDFLRSNPK	0.948146844	2	2.312369
Q8QZY1	VFSDEVQQQAQLSTIR	1.133205498	2	3.875024
Q8R066	**C1QT4 Complement C1q tumor necrosis factor_related protein 4**	**1.089603343**	**0.05592**	**2**
Q8R066	NRDEVQAMIYDDGASRR	0.964969465	2	2.326402
Q8R066	TLSVKLMKNR	1.417842474	2	2.413723
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.036304207**	**0.35127**	**5**
Q8R081	ASLNGADIYSGCCTLK	1.041735254	2	3.317305
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	1.148843795	3	5.179823
Q8R081	SDALETLGFLNHYQMK	0.977099887	2	2.988459
Q8R081	SSSGLLEWDSK	0.741269741	2	2.833583
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.791340103	3	7.479366
Q8R0F9	**S14L4 SEC14_like protein 4**	**1.019725774**	**0.3675**	**6**
Q8R0F9	FDNTYSLLHTK	1.591156676	2	3.068027
Q8R0F9	GSSHQVENEILFPGCVLR	1.254715246	2	5.072796
Q8R0F9	VCEMLLHECELQSQK	1.634055544	2	4.637535
Q8R0F9	VCEMLLHECELQSQK+Oxidation(3)	2.037816182		
Q8R0F9	VGYTAEVLLPDK	1.589846337	2	2.695363
Q8R0F9	VGYTAEVLLPDKACEEK	0.977015754	2	2.743185
Q8R164	**BPHL Valacyclovir hydrolase**	**0.997170152**	**0.9773**	**3**
Q8R164	FADEFNR	1.159011097	2	2.49064
Q8R164	QVSLLGWSDGGITALIAAAK	0.821004673	2	3.436995
Q8R164	TDFAPQLQSLNK	0.987558947	2	3.547161
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**0.981333225**	**1**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	0.979877793	2	3.550782

Q8R1V4	QLLDQVEQIQK	0.981995584	2	3.146686
Q8R3Q6	**CCD58 Coiled_coil domain_containing protein 58**	**1.133679776**	**0.74498**	**2**
Q8R3Q6	IVHELNTTVPTASFAGK	0.906524242	2	4.195305
Q8R3Q6	NCIAQTSAVVK	1.152508675	2	2.661136
Q8R491	**EHD3 EH domain_containing protein 3**	**0.945137607**	**1**	**5**
Q8R491	ADQIETQQLMR	0.950059333	2	2.79187
Q8R491	LDISDEFSEVIK	0.957060513	2	3.138056
Q8R491	LFEAEEQDLFK	0.933851332	2	3.6
Q8R491	MQDQLQAQDFSK	1.057504177	2	3.81479
Q8R491	QEETQRPVQMVK	0.934620593	2	2.529147
Q8VBU2	**NDRG2 Protein NDRG2**	**0.816015492**	**0.00937**	**7**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.813344127	3	4.767313
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK+Oxidation(3)	0.731437613		
Q8VBU2	LDPTQTSFLK	0.608936889	1	1.909294
Q8VBU2	MADSGGQPQLTQPGK	0.912846622	2	3.85656
Q8VBU2	SLITHAPNLENIELYWNSYNNR	1.026584609	3	4.776059
Q8VBU2	TASLTSAASIDGSR	1.057596174	2	3.109354
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.723438705	2	4.424169
Q8VC12	**HUTU Urocanate hydratase**	**1.027476958**	**0.99999**	**7**
Q8VC12	HQLVVGSQAR	1.052909594	2	3.096704
Q8VC12	LLALEFAQELR	1.062365072	2	3.781817
Q8VC12	LQYMDNIR	1.099826956	2	2.35022
Q8VC12	LVITNGMVIPNYSSR	1.065808155	2	3.353469
Q8VC12	VAIAVAINQAIASGK	0.846843038	2	3.664294
Q8VC12	VFVTSGLGGMSGAQAK	0.923263585	2	4.50862
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9)	1.020616386		
Q8VDG5	**PPCS Phosphopantothenate__cysteine ligase**	**1.210884938**	**0.47586**	**2**
Q8VDG5	FLDNFSSGR	1.104853746	2	2.483594
Q8VDG5	LETDPDIIISR	1.236888731	2	3.169044
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.901435992**	**0.46542**	**4**
Q8VED5	NKYEDEINK	0.889529839	2	2.761595
Q8VED5	NKYEDEINKR	0.882404157	3	3.440344
Q8VED5	NLDLDSIIAEVK	1.173155533	2	3.849866
Q8VED5	YEDEINK	0.899551906	1	2.480872
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**0.979423437**	**0.81086**	**9**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.029661576	3	4.495188
Q8VEK3	GYFEYIEENK	0.973392971	2	3.266571
Q8VEK3	LLEQYKEESK	1.00310808	2	3.166838
Q8VEK3	LLEQYKEESKK	0.87894101	2	3.383716
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	0.999389558	3	5.08896
Q8VEK3	NFILDQTNVSAAAQR	0.90068407	2	4.528125
Q8VEK3	TCNCETEDYGEK	1.048758774	2	3.385928
Q8VEK3	VSELKEELKK	1.158640004	2	2.42955
Q8VEK3	YNILGTNTIMDK	0.970033078	2	3.575292
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**1.122237304**	**0.94981**	**7**
Q8VHE9	ATVQSVLLDSAGR	1.112157284	2	3.539473
Q8VHE9	FLPLPLTQLLNK	1.599745983	2	2.857179
Q8VHE9	GATYGADHDLAR	1.24793394	2	3.173579
Q8VHE9	NLYSDLQALGSK	1.072259077	2	2.919394
Q8VHE9	RPPEPLVTDK	1.360457037	2	2.618397
Q8VHE9	VLVLEQHTK	1.559527641	2	2.387858
Q8VHE9	VVAHGVSHAILLK	0.9639291	2	2.420338
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.353902026**	**9.9E-20**	**4**
Q8VHT6	DCYVLSQLVGQK	1.312776345	2	2.967536
Q8VHT6	ILDLGSGSGR	0.917606499	2	2.688855

Q8VHT6	SLQNVHEEVISR	1.51054462	2	3.216307
Q8VHT6	TSADLQTNACVTPAK	1.447404732	2	3.84688
Q8VHX6	**FLNC Filamin_C**	**1.03811215**	**0.49451**	**3**
Q8VHX6	AFGPGLEGGLVNK	1.061802126	2	2.600145
Q8VHX6	GAGTGGLGLTVEGPCEAK	1.036947903	2	3.895885
Q8VHX6	LIALLEVLSQK	1.517486429	2	2.698955
Q8VI04	**ASGL1 L_asparaginase**	**0.874677433**	**0.66103**	**3**
Q8VI04	FAADMGIPQTPAEK	1.109311037	2	2.711102
Q8VI04	GNLAYATSTGGIVNK	0.874631469	2	4.287473
Q8VI04	TVDEAATLALDYMK	0.858093376	2	2.656144
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**0.941571415**	**0.04287**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	0.900782702	2	4.466636
Q8VID1	LAEDGAHVVISSR	3.206957361	2	3.700807
Q8VID1	NFAAELAPK	0.920027162	2	2.517546
Q8VID1	VNCLAPGLIK	1.037456184	2	2.540972
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.971330402**	**0.99953**	**10**
Q8VIF7	CGPGYATPLEAMK	1.084779917	2	3.467742
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.262962049	2	4.957894
Q8VIF7	GGFVLLDGETFEVK	1.044927222	2	4.192704
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	1.011866266	2	4.33114
Q8VIF7	HEIIQTLQMK	1.037394098	2	2.641031
Q8VIF7	HNIMVSTEWAAPNVFK	0.997318485	2	4.299456
Q8VIF7	LTGQIFLGGSIVK	0.790393288	2	3.003609
Q8VIF7	NEGGTWSVEK	1.107264991	2	2.886699
Q8VIF7	NTGIEAPDYLATVDVDPK	0.940287662	2	5.206403
Q8VIF7	VIEPNEIHAK	1.12303093	2	2.54865
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.088711926**	**0.93675**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	1.09299027	2	2.827186
Q8VIJ6	NLSPYVSNELLEEAFSQFGPIER	1.075571743	2	3.53484
Q8VIJ6	YGEPGEVFINK	0.98518395	2	2.798023
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**0.82241256**	**1**	**6**
Q91VA0	AFIVLNPEFLSHDQEQLIK	0.975288748	2	5.577048
Q91VA0	AILPFDLQIIDEK	0.911182134	2	3.773881
Q91VA0	GNILPPNTEGYIGIR	0.852743319	2	3.009643
Q91VA0	HNQGLAFR	0.839369804	2	2.323281
Q91VA0	KVEFVSELPK	0.912172589	2	2.873079
Q91VA0	NKEFGQL	1.086300622	1	2.108725
Q91VM5	**RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1**	**0.958306518**	**0.86586**	**2**
Q91VM5	LFIGGLNTETNEK	1.095537409	2	3.151284
Q91VM5	VEQATKPSFESGR	0.955016778	2	3.522907
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.781789231**	**2.1E-05**	**2**
Q91VM9	IIAINVNDPEAEK	0.935531495	2	3.251032
Q91VM9	MEIATEEPLNPIK	0.777792144	2	3.867111
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.769415174**	**0.0058**	**4**
Q91W43	AGHQLQHDLFFDTLK	0.760677143	2	2.411082
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	0.926817894	2	4.082502
Q91W43	VSFQPNSGAQGEYAGLATIR	0.790608878	2	4.778082
Q91W43	YGNIDVAHLK	0.767127752	3	3.490403
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**0.983074635**	**0.10029**	**2**
Q91W90	SFEDTIAQGITFVK	0.97787759	2	3.558086

Q91W90	VDCTQHYAVCSEHQVR	1.155665829	3	4.390991
Q91WL5	**CP4CA Cytochrome P450 4A12A**	**0.89800466**	**0.98914**	**3**
Q91WL5	FELLPDPTR	0.886928172	2	2.396487
Q91WL5	IQLQDEEELEK	1.032833579	2	2.35265
Q91WL5	VAVALTLLR	0.970387015	2	2.599054
Q91X77	**CY250 Cytochrome P450 2C50**	**0.913330646**	**0.4995**	**3**
Q91X77	IKEHEESLDVTIPR	0.876292536	3	3.601666
Q91X77	NFLLEK	0.828514468	1	2.107804
Q91X77	YALLLLLK	1.063466056	2	2.820367
Q91X78	**ERLN1 Erlin_1**	**1.114920689**	**0.02255**	**2**
Q91X78	ISEIEDAAFLAR	0.984776941	2	2.785827
Q91X78	SVQTTLQTDEVK	1.229351229	2	3.215433
Q91XE8	**TM205 Transmembrane protein 205**	**0.885851973**	**0.59246**	**2**
Q91XE8	HTFGLVQSK	0.884291664	2	2.48441
Q91XE8	MEKGEDPGSLIK+Oxidation(0)	1.912021529		
Q91XQ0	**DYH8 Dynein heavy chain 8_ axonemal**	**0.857334156**	**0.65072**	**2**
Q91XQ0	FRPEICDMVGNLVSVSR+Oxidation(7)	0.852683993		
Q91XQ0	SMTGIPNLQETLKEKQAR	1.078156055	2	2.585173
Q91XR8	**GPX42 Phospholipid hydroperoxide glutathione peroxidase_ nuclear**	**1.185620305**	**0.12232**	**2**
Q91XR8	TDVNYTQLVDLHAR	0.905595983	3	3.442171
Q91XR8	YGPMEEPQVIEK	1.194091814	2	2.519012
Q91Y81	**SEPT2 Septin_2**	**0.874289793**	**0.99777**	**2**
Q91Y81	ASIPFSVVGSNQLIEAK	0.800018177	2	3.384167
Q91Y81	LTVVDTPGYGDAINSR	0.87769852	2	4.060359
Q91YE2	**EGLN2 Egl nine homolog 2**	**0.990463746**	**0.9393**	**2**
Q91YE2	ERAAARDK	0.911946578	1	2.038808
Q91YE2	YQLASGQK	1.078307034	1	1.943258
Q91YP0	**L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial**	**0.903996884**	**0.76011**	**2**
Q91YP0	ISELSGCNPDPQIVPFR	0.861520486	2	3.158764
Q91YP0	NAPSPAATSSLAISR	1.022025704	2	3.44049
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.101522791**	**0.99989**	**9**
Q91YT0	GAGAYICGEETALIESIEGK	0.968500118	2	3.312476
Q91YT0	GDARPAEIDSLWEISK	1.021868952	2	3.21349
Q91YT0	GEFYNEASNLQVAIR	1.013941219	2	3.505469
Q91YT0	KTSFGSLKDEDR	1.031038268	2	3.271385
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.205509129	3	3.825422
Q91YT0	LVEGCLVGGR	1.066646942	2	2.59467
Q91YT0	QIEGHTICALGDGAAWPVQGLIR	0.970574594	3	3.540077
Q91YT0	TSFGSLKDEDR	1.122976921	2	2.614883
Q91YT0	YLVVNADEGEPGTCK	1.096224982	2	5.062545
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**0.816540506**	**0.70343**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	0.796052065	3	6.880455
Q91Z53	LLDAAGANLR	0.979090251	2	3.152913
Q91Z53	NCVILPHIGSATYK	0.832637046	2	3.619254
Q91Z53	NTMSLLAANNLLAGLR	0.784760307	2	4.523881
Q91Z53	RLPEAIEEVK	0.866922663	2	2.459644
Q91Z53	VISTLSVGVDHLALDEIK	1.044432631	2	4.234691
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**1.004753162**	**0.99998**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	0.912594866	3	4.776452
Q91ZJ5	FVQDLSK	0.848274532	1	1.990381
Q91ZJ5	GGTLTQYEGK	0.991756797	2	2.543858

Q91ZJ5	GLPDNISSVLNK	0.981680718	2	3.876582
Q91ZJ5	GTVIIIANHGDR	0.950838043	2	3.043601
Q91ZJ5	IDIPPGAVLENK	0.9601895	2	3.036104
Q91ZJ5	IQRPPEDSIQPYEK	1.030939419	3	4.487566
Q91ZJ5	LNGGLGTSMGCK	1.017463589	2	3.127034
Q91ZJ5	LQEQNAIDMEIIVNPK	1.032049945	2	2.489109
Q91ZJ5	LVEIAQVPK	1.042658218	2	3.35483
Q91ZJ5	NENTFLDLTVQQIEHLNK	0.887856771	2	5.244436
Q91ZJ5	SFENSLGINVPR	0.924195531	2	3.22864
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	0.87798623	3	5.508804
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	0.954571869	2	4.605159
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**0.843241661**	**0.71658**	**7**
Q91ZX7	AVTDEEPFLIFANR	0.809296967	2	2.499593
Q91ZX7	CLQGACVVNK	1.247047461	2	2.335465
Q91ZX7	GCHVNECLSR	1.019193496	2	2.629994
Q91ZX7	IETAAMDGTLR	1.426875406	2	2.327921
Q91ZX7	ILQEDFTCR	0.994435004	2	2.55975
Q91ZX7	LDGLCIPLR	1.058239893	2	2.458098
Q91ZX7	MYDAQQQQVGTNK	1.031281763	2	4.3498
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**0.890917437**	**0.88903**	**3**
Q920A6	DLDTVASDMMVLLK	0.959246652	2	3.320173
Q920A6	GLAEVSDIAEQVLNAVNK	0.887593728	3	4.870239
Q920A6	NTDGVNFYNILTK	1.21855017	2	2.944644
Q920D2	**DYR Dihydrofolate reductase**	**0.932307902**	**0.00847**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	0.804997691	2	4.390249
Q920D2	LIEQPELASK	0.81342733	2	2.521969
Q920D2	LLPEYPGVLSEIQEEK	0.932871278	2	3.67855
Q920D2	NGDLPWPLLR	0.772075854	2	3.038924
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**1.000684861**	**0.83902**	**4**
Q920F5	ADLLEAQALK	0.797408655	2	2.312699
Q920F5	EIAEVTGDPVHESLK	1.202774435	2	2.971857
Q920F5	ISECEAVHPVK	0.942619207	2	3.344306
Q920F5	WLLGLLNVQGK	0.854382935	2	3.616333
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**0.892407833**	**0.86801**	**19**
Q920L2	ACALSIAESCRPGDK	1.089705636	2	3.148103
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	0.836887172	3	4.823573
Q920L2	ANAGEESVMNLDK	1.038937283	2	4.005419
Q920L2	GEGGILINSQGER	0.963950818	2	4.334742
Q920L2	GSDWLGDQDAIHYMTEQAPASVVELENYGMPFSR	1.063373051	3	5.011825
Q920L2	GVIALCIEDGSIHR	0.910973294	2	3.499012
Q920L2	HTLSYVDTK	0.981231107	1	2.257205
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	0.88893568	3	6.994025
Q920L2	IDEYDYSKPIEGQQK	1.105974951	2	4.544931
Q920L2	KHTLSYVDTK	0.903415105	2	2.605049
Q920L2	LGANSLLDLVVFGR	1.083766496	2	3.403199
Q920L2	NTIIATGGYGR	1.000704793	2	2.80642
Q920L2	TGHSLLHTLYGR	0.808977823	2	2.343961
Q920L2	TLNEADCATVPPAIR	0.895034903	2	3.617169
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.092136912	3	3.426553
Q920L2	VGSVLQEGCEK	0.976518532	2	3.472378
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.877671245	3	4.009187
Q920L2	VSQLYGDLQHLK	0.974980248	3	3.451027
Q920L2	VTLDYRPVIDK	1.017968309	2	3.336547

Q920P0	**DCXR L_xylulose reductase**	**0.852062298**	**0.99832**	**6**
Q920P0	AVVQVSQIVAR	0.824124591	2	2.997207
Q920P0	GVPGAIVNVSSQASQR	0.941344131	2	5.490012
Q920P0	SSMTTGSALPVDGGFLAT	0.971243806	2	2.871311
Q920P0	STVLALQAAGAQVVAVSR	1.095356508	2	4.404534
Q920P0	TREDLDSLVR	0.969004422	2	3.042619
Q920P0	VNAVNPTVVMTPMGR	0.968978512	2	2.845801
Q921F2	**TADBP TAR DNA_binding protein 43**	**1.034015385**	**0.83487**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	1.013828938	2	4.071534
Q921F2	FTEYETQVK	1.070199224	2	2.674551
Q921F2	GISVHISNAEPK	1.249885052	2	2.664879
Q921F2	TSDLIVLGLPWK	1.068672775	2	3.12147
Q922F4	**TBB6 Tubulin beta_6 chain**	**0.978726723**	**0.99982**	**5**
Q922F4	ALTVPELTQQMFDAK	0.929831357	2	4.139413
Q922F4	GHYTEGAELVDSVLDVVR	1.00308319	2	6.669033
Q922F4	IREEYPDR	0.98547314	2	2.96996
Q922F4	MASTFIGNSTAIQELFK	0.91649274	2	3.833952
Q922F4	NSSYFVEWIPNNVK	1.045117193	2	4.782595
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.054600789**	**0.99396**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4)	1.023490813		
Q922J3	HEEILQNLQKMLADTEDK	1.064957003	2	2.564286
Q923D2		**0.919903881**	**0.61526**	**3**
Q923D2	LQDVTDDHIR	0.949995474	2	3.364575
Q923D2	TGLTTLAQAVQAGYEVTVLVR	0.801030843	3	4.281244
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.898106045	3	4.542738
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**1.217631442**	**0.66896**	**2**
Q923J6	FFFLSNDEMLEILSETKDPLR	1.287249569	2	2.412905
Q923J6	LEFLTNLDIK	0.808984383	1	2.099626
Q923K9	**A1CF APOBEC1 complementation factor**	**0.938266425**	**0.98136**	**2**
Q923K9	LAPQILEEICQK	0.982549995	2	2.33733
Q923K9	VTEGVVDVIVYPSAADK	0.919740644	2	3.581791
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**0.828511879**	**0.01014**	**2**
Q923M1	SAVYPTSAVQMEAALK	0.834820256	2	3.812218
Q923M1	VISAEEALPGR	0.867183771	2	3.128269
Q923V8	**SEP15 15 kDa selenoprotein**	**0.904993463**	**0.21557**	**3**
Q923V8	GCCQEEAQFETK	0.959669199	2	3.891757
Q923V8	LLDDNGNIAEELSILK	1.158009873	2	4.218528
Q923V8	WNTDSVEEFLSEK	0.849206819	2	2.954593
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**1.208456938**	**0.00371**	**5**
Q924C3	AEYLHTWGGLLPVISK	0.864612881	3	3.951748
Q924C3	GQPIWVTANHQEVR	0.820293846	2	2.925019
Q924C3	IEPLTFYLDPQWQLALNPSER	1.208521836	2	2.427873
Q924C3	SGTYFWPGSDVEIDGILPDIYK	0.570078754	2	3.438065
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	0.698476593	2	2.754629
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.022122084**	**0.93382**	**13**
Q924S5	AGVTCIILPAENR	1.046678077	2	2.623525
Q924S5	AQLSATVLTLLIK	1.336380736	2	3.864212
Q924S5	AQSVLEEDHYGMEDVK	1.198747234	2	4.259191
Q924S5	EHQEALAVER	1.001137157	2	2.877724
Q924S5	EVGDELGAKPQLEMVTEATSDTSK	0.854911066	3	3.453974
Q924S5	HVMDVVDEELSK	0.98476448	2	3.212523
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.147399766	3	6.188807
Q924S5	MEMINVSGYVAQEK	1.997245748	2	2.543144

Q924S5	NYLDWLTSIPWGR	0.769025537	2	2.883768
Q924S5	QLEVEPEGLEPEAENK	0.977675504	2	4.258727
Q924S5	QSDENLDLAR	0.885016863	2	2.818621
Q924S5	TENPLVLIDEVDK	0.948405482	2	2.778177
Q924S5	VLEFIAVSQLR	0.818822581	2	3.088209
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**0.969602005**	**0.99921**	**2**
Q924W5	ELDMKEKELQEK+Oxidation(3)	0.991961432		
Q924W5	TKEQINQGEERLTELK	0.962580667	2	2.455998
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**0.983070888**	**1.9E-13**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	1.037459877	2	2.95541
Q99020	FGEVVDCTIK	0.829800743	2	2.761502
Q99020	IFVGGLNPEATEEK	1.420037055	2	4.035909
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**0.848613954**	**0.6533**	**3**
Q99068	EELKHFEAKIEK	1.000104876	2	2.427901
Q99068	HLQDLSSR	0.84829449	2	2.337855
Q99068	HVESIGDPEHISR	1.110156805	3	3.373267
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.147180885**	**0.87362**	**4**
Q99JI4	GAEILEVLHSLPAVR	1.207532802	2	2.35956
Q99JI4	LDEELEDAEK	1.116619437	2	2.397714
Q99JI4	RLDEELEDAEK	1.21236713	2	2.910735
Q99JI4	VNEIVETNRPDSK	1.041902102	2	3.589453
Q99KN9	**EPN4 Clathrin interactor 1**	**0.994992009**	**0.68925**	**2**
Q99KN9	GEFKDEEETVTTK	1.142825819	2	3.05005
Q99KN9	HIHITQATETTTTR	0.968787641	3	3.387228
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.91148734**	**0.99954**	**2**
Q99L04	ATAQEAQSLGGR	0.914255868	2	3.64541
Q99L04	CVPVVCDSSQESEVK	0.911383947	2	3.399817
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**0.954727394**	**0.86536**	**4**
Q99LF4	GLGHQVATDALVAMEK	0.67368369	2	3.972651
Q99LF4	NVTDVVNTCHDAGISK	1.21169126	2	4.468873
Q99LF4	NYNDELQFLDK	0.945030327	2	2.920885
Q99LF4	TNLDESDVQPVK	0.96201831	2	3.316954
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.055967772**	**0.63423**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11)	1.055967772		
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5)	1.055967772		
Q99ML5	**PCYOX Prenylcysteine oxidase**	**0.846060863**	**0.34185**	**3**
Q99ML5	ELGLSSVPASGGLVGVYNGK	0.795694173	2	2.518651
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	0.923163482	3	4.483006
Q99ML5	YQSHDYAFSSVEK	0.956586407	2	2.882505
Q99MS0	**S14L2 SEC14_like protein 2**	**1.014474051**	**0.52859**	**5**
Q99MS0	AGEMTEVLPNQR	1.346001904	2	2.975658
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	0.611647024	2	3.191858
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.018782175	3	4.807725
Q99MS0	INYGGDIPK	1.042862192	2	2.504065
Q99MS0	QQYEHSVQISR	1.012812803	2	2.478615
Q99MW1	**STK31 Serine/threonine_protein kinase 31**	**0.965783929**	**0.8731**	**2**
Q99MW1	EVLLENYKALELK	0.821862527	2	2.304487
Q99MW1	QDQKLIEENEK	1.032833579	2	2.588887
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.882049709**	**0.1586**	**7**
Q99MZ8	GFSVVADTPELQR	0.821020715	2	3.381973
Q99MZ8	MGPSGGEGIEPER	0.997481927	2	3.194432
Q99MZ8	QQSELQSQVR	0.877923262	2	2.431894

Q99MZ8	QSFTMVADTPENLR	0.906307579	2	3.302576
Q99MZ8	TQDQISNIK	1.061112303	2	2.659462
Q99MZ8	YHEEFEK	0.860326684	1	2.215444
Q99MZ8	YKEEFEK	0.817724485	1	2.325076
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**1.009840612**	**0.72063**	**2**
Q99NA5	IEAACFATIK	0.885978997	2	2.315682
Q99NA5	NVTAIQGPGGK	1.196637301	2	2.437847
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**1.12901894**	**0.94088**	**3**
Q99NB7	GSISNTNVEALK	1.134780783	2	2.856956
Q99NB7	KGSISNTNVEALK	1.028166639	2	3.169024
Q99NB7	VHLKPVLLQTEQEQVEHR	1.006178685	3	3.845462
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**0.99989459**	**0.8418**	**8**
Q99PF5	AINQQTGAFVEISR	2.508169776	2	3.685945
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.949838515	2	6.111699
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.099945495	2	4.655235
Q99PF5	IGQQPQQPGAPPQQDYTK	1.424069602	2	3.685757
Q99PF5	IINDLLQSLR	0.991798347	2	2.696557
Q99PF5	SVSLTGAPESVQK	1.091882192	2	3.309307
Q99PF5	VGGGIDVPVPR	0.859405366	2	2.879406
Q99PF5	VQISPDSGGLPER	0.807192476	2	2.566416
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.210188688**	**4.4E-16**	**21**
Q99PL5	DALNQATSQVESK	1.663214106	2	3.758504
Q99PL5	EAEETQNSLQAECDQYR	1.323379297	2	5.467913
Q99PL5	EEITQLK	0.792155665	1	1.977029
Q99PL5	EHTSHLEAELEK	1.388954544	2	3.317014
Q99PL5	EQEIAAVQAR	1.862536844	2	2.379784
Q99PL5	ETSYEEALANQR	2.547637376	2	2.740476
Q99PL5	GELESSDQVR	1.276252978	2	3.153927
Q99PL5	HLEDIVEK	1.411866186	2	2.544025
Q99PL5	HMAAASAECQNYAK	0.823433041	2	4.461192
Q99PL5	HMAAASAECQNYAK+Oxidation(1)	1.486338727		
Q99PL5	IQEELEK	1.438073781	1	2.14268
Q99PL5	LKELESQVSCLEK	0.991573162	2	4.059691
Q99PL5	LLATEQEDAAVAK	1.261733245	2	4.539742
Q99PL5	LQQENSILR	1.206468665	2	2.829821
Q99PL5	LQSSEVEVK	1.082105025	2	2.524143
Q99PL5	LREAEETQNSLQAECDQYR	1.002297983	3	5.125143
Q99PL5	QLHLAEAQTK	1.262573538	2	2.327596
Q99PL5	TILAETEGMLK	1.048951656	2	3.038155
Q99PL5	TLQEQLENGPNTQLAR	1.069559441	2	4.824466
Q99PL5	TLVSTVGSMVFSEGEAQR	1.112113638	3	4.837025
Q99PL5	VEPAVSSIVNSIQVLASK	0.911461578	2	4.981925
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**0.891598513**	**0.89156**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.891598513		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.891598513		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.047604142**	**0.99884**	**2**
Q9CPQ1	FGVAEPR	1.047328677	2	2.345819
Q9CPQ1	NYDSMKDFEEMR	1.22444532	2	3.545067
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**1.067188005**	**0.53903**	**2**
Q9CQS8	FYTEDSPGLK	1.224073348	2	2.331386
Q9CQS8	TTSAGTGGMWR	1.030504865	2	2.3868
Q9CRB8	**MTFP1 Mitochondrial fission process protein 1**	**0.918642167**	**0.47052**	**2**
Q9CRB8	SVDFLLDSSLR	0.869170082	2	2.799437
Q9CRB8	YLGYANEVGEAFR	1.103349096	2	2.718529

Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.254630751**	**0.01164**	**2**
Q9CRB9	VAEELALEQAK	1.3586326	2	3.572165
Q9CRB9	YEYHPVCADLQTK	0.904666101	2	3.661733
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.942794096**	**0.03535**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	1.152811467	2	4.14524
Q9CW42	GLSVSEAECTAMGLR	0.826898614	2	3.313146
Q9CW42	LQQVGTVAQLWIYPIK	0.803286742	2	2.945435
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.051855409**	**0.93056**	**3**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.012524585	2	4.488051
Q9CWH6	ALLEVVQSGGK	0.878148915	2	3.431706
Q9CWH6	LTVEDPVTVEYITR	1.086672227	2	3.902525
Q9CWK8	**SNX2 Sorting nexin_2**	**0.950690484**	**0.96511**	**4**
Q9CWK8	AVNTQALSGAGILR	0.896753488	2	3.189193
Q9CWK8	QQQFENLDQQLR	0.961437907	2	2.818141
Q9CWK8	WEDAQITLLK	0.931244139	2	2.788138
Q9CWK8	YWEAFLPEAK	1.019207315	2	2.53179
Q9CXS4	**CENPV Centromere protein V**	**0.81083498**	**0.00354**	**2**
Q9CXS4	LLLDTFEYQGLVK	0.817924736	2	3.939583
Q9CXS4	SVVTEEFNGSDWER	0.809890474	2	3.769433
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**1.222909568**	**3E-05**	**2**
Q9CYN2	LHDSLATER	0.968025646	2	2.419529
Q9CYN2	YVENFGLIDGR	1.223899481	2	2.736593
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.844083458**	**0.27147**	**2**
Q9CYW4	LEDILTGLGLR	0.82552951	2	4.23748
Q9CYW4	RLEDILTGLGLR	0.643644214	2	3.281152
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**0.971750315**	**0.60071**	**2**
Q9CZY3	LLEELEEGQK	0.951812652	2	2.749477
Q9CZY3	VNMSGVSSSNGVVDPR	1.192760786	2	2.61564
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.027025383**	**0.9298**	**4**
Q9D0M3	GLLSSLDHTSIR	1.015197375	2	3.196044
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.095932324	3	5.915704
Q9D0M3	HLVGVCYTEEEAK	1.061173259	2	3.734705
Q9D0M3	LSDYFPKPYPNPEAAR	1.149300593	3	3.633964
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**0.800427954**	**0.22948**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	0.847364613	2	2.823217
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	0.996100181	2	5.156553
Q9D0S9	SLPADILYEDQQCLVFR	0.866938416	2	3.498697
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.046787538**	**1**	**4**
Q9D172	GVEVTVGHEQEEGGK	1.084215924	2	3.801411
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.050047903	2	4.62831
Q9D172	NLSTFAVDGK	0.983566719	1	2.622995
Q9D172	NVLAESAR	0.995547612	1	1.930207
Q9D180	**WDR65 WD repeat_containing protein 65**	**1.334104236**	**0.07131**	**2**
Q9D180	KNQELEK	1.438073781	1	2.122219
Q9D180	QIEPRENEIK	1.21358461	1	1.982005
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**0.921062187**	**9.9E-20**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0)	3.157682584		
Q9D1Q6	NIIGYFEQK	0.817061185	1	2.084002
Q9D1Q6	SNPVHEIQSLDEVTNLDR	0.879767351	2	5.255363
Q9D1Q6	VDCDQHSDIAQR	0.920548726	2	3.631815

Q9D2U9	**H2B3A Histone H2B type 3_A**	**0.90746924**	**0.03832**	**6**
Q9D2U9	AMGIMNSFVNDIFER	0.925080832	2	4.8175
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.839921256		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.903105181		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4)	0.903401424		
Q9D2U9	LLLPGELAK	0.982151198	2	2.640281
Q9D2U9	QVHPDTGISSK	0.997846953	2	2.37401
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.278910835**	**0.32924**	**3**
Q9D6M3	GAAVNLTLVTPEK	1.198751487	2	3.113856
Q9D6M3	GVNEDTYSGFLDCAR	1.47400855	2	4.846322
Q9D6M3	NHGIAGLYK	1.236380457	1	2.047149
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**0.825475705**	**0.7203**	**10**
Q9D6Y9	CSDGGIYCK	0.872591716	1	2.085543
Q9D6Y9	CVAYAESHDQALVGDK	0.963739225	2	5.011642
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	0.865096983	3	3.409191
Q9D6Y9	GTHDLWDSR	0.93504571	2	2.563571
Q9D6Y9	GYESFGIHR	0.862655053	2	2.45794
Q9D6Y9	IVLDSDAAEYGGHQR	1.191692445	2	4.534115
Q9D6Y9	IYESHVGISSHEGK	0.825361417	2	4.405342
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	0.676756174	3	3.363416
Q9D6Y9	QFNLTDDDLLR	0.793131094	2	2.494174
Q9D6Y9	RQFNLTDDDLLR	1.096902816	2	2.590854
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.045101472**	**0.01498**	**3**
Q9D7B6	AVIFEDCAVPVANR	0.916039558	2	4.067587
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	0.987617262	2	4.376923
Q9D7B6	VHQILEGSNEVMR	1.35202058	2	2.589013
Q9D7S7	**RL22L 60S ribosomal protein L22_like 1**	**1.592105391**	**1.4E-05**	**2**
Q9D7S7	FHLDLTHPVEDGIFDSGNFEQFLR	1.419947504	3	3.788766
Q9D7S7	TGNLGNVVHIER	3.835980963	2	2.476783
Q9D7W5	**MED8 Mediator of RNA polymerase II transcription subunit 8**	**1.15294891**	**0.21666**	**2**
Q9D7W5	NQVIIPLVLSPDRDEDLMR+Oxidation(17)	1.153630171		
Q9D7W5	QIQSLNKMCSNLLEK+Oxidation(7)	1.284787212		
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**0.853983975**	**0.00121**	**2**
Q9D7X8	ISDEMEDIIK	0.803027546	2	2.959699
Q9D7X8	SNISSLDEQEGVK	0.960523276	2	3.056067
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.048298154**	**0.37898**	**5**
Q9D819	GISCMNTTVSESPFK	0.835622015	2	4.502737
Q9D819	GQYISPFHDVPIYADK	1.093177192	2	3.77724
Q9D819	VLGILAMIDEGETDWK	1.031631449	2	4.000464
Q9D819	YKVPDGKPENEFAFNAEFK	0.865198722	2	3.641628
Q9D819	YVANLFPYK	0.933187547	1	1.93985
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**0.957536959**	**0.99976**	**2**
Q9D880	TIALNQVEDVR	0.890404458	2	2.934498
Q9D880	TVLEHYALEDDPLEAFK	0.975614844	2	5.039001
Q9DBA8	**HUTI Probable imidazolonepropionase**	**0.819487811**	**0.52198**	**4**
Q9DBA8	AGTTLVECK	0.944143057	2	2.600883
Q9DBA8	GVFDLDTTR	0.777850293	2	2.303739
Q9DBA8	QGDAIIINASR	1.105892496	2	2.671376
Q9DBA8	SGYGLNLETELK	1.013110763	2	2.36286
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.187698054**	**0.26887**	**3**
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	1.325342923	3	4.624665
Q9DBH5	TPEEESIDWTK	1.072343393	2	2.42645
Q9DBH5	WSELAGCTADFR	1.058979393	2	3.172407

Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**1.102571808**	**0.48988**	**2**
Q9DC70	LDDLINWAR	1.06433707	2	2.990906
Q9DC70	QADVMIVAGTLTNK	1.110663579	2	3.313989
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**1.137709911**	**0.01548**	**2**
Q9DCH4	IQDALSTVLQYAEDVLSGK	1.129134144		
Q9DCH4	VIGLSSDLQQVGGASAR	1.237419922		
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.130441579**	**0.98825**	**2**
Q9DCM0	SLLPGCQSVISR	1.004967186	2	3.202382
Q9DCM0	TDFQQGCAK	1.190119553	2	2.363618
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**0.975651695**	**0.99233**	**2**
Q9DCS9	AYDLVVDWPVTLVR	0.936451565	2	4.678904
Q9DCS9	TPAPSPQTSLPNPITYLTK	1.110024763	2	3.350693
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.018149312**	**4E-05**	**5**
Q9DCT2	FDLNSPWEAFPAYR	1.024139647	2	2.781314
Q9DCT2	ILTDYGFEGHPFR	0.833536936	2	2.639343
Q9DCT2	KFDLNSPWEAFPAYR	1.007702434	2	3.633706
Q9DCT2	SLADLTAVDVPTR	1.126334123	2	3.562822
Q9DCT2	VVAEPVELAQEFR	1.304219028	2	3.311777
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.032313199**	**0.98827**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	0.892603981	2	5.19591
Q9DCU9	LIEPNTAVTR	1.016390466	2	3.306714
Q9DCU9	TMDWFGYYGGPCR	1.099972082	2	3.402372
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.660350005**	**0.07788**	**2**
Q9EP75	DEDGKELSDEDIR	1.466267645	2	2.713569
Q9EP75	IFNDSTNIMHAK	1.660731348	2	3.303768
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**0.716355627**	**0.00012**	**10**
Q9EP89	FENSIESLR	0.860964584	2	2.828457
Q9EP89	GIIVSIICNMQSVGLNSTALK	0.735072062	3	3.732419
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	0.732180099	3	4.018808
Q9EP89	IKDEVGAPGIVVGVSVDGK	0.705199275	2	5.023402
Q9EP89	KNDFEQGELYLK	0.823635438	2	3.799617
Q9EP89	LDLDLPVQHYVPEFPEK	0.824819056	2	3.133782
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	0.885501098	3	3.666809
Q9EP89	LVNTPYVDNSYK	0.860772263	2	3.22032
Q9EP89	NDFEQGELYLK	0.483768953	2	2.911693
Q9EP89	WAGGGFLSTVGDLLK	0.708991836	2	4.316546
Q9EPH2	**MRP MARCKS_related protein**	**1.141610544**	**0.18393**	**2**
Q9EPH2	AAATPESQEPQAK	1.151702514	2	2.77378
Q9EPH2	GDVTAEEAAGASPAK	1.006332044	2	3.416121
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.275323199**	**6E-07**	**13**
Q9EPH8	ALDTMNFDVIK	1.154062762	2	3.303414
Q9EPH8	ALYDTFSAFGNILSCK	1.437526855	2	2.595096
Q9EPH8	FSPAGPILSIR	1.062218663	2	2.315148
Q9EPH8	GFGFVCFSSPEEATK	2.217282551	2	4.003506
Q9EPH8	GFGFVSFER	1.135788678	2	2.784455
Q9EPH8	GYGFVHFETQEAAER	1.383781086	2	3.121152
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	0.989480761	3	3.652498
Q9EPH8	KEFSPFGTITSAK	1.016934055	2	2.878023
Q9EPH8	NLDDGIDDER	1.015337428	2	2.848306
Q9EPH8	SGVGNIFIK	1.359750771	2	2.757515
Q9EPH8	SKVDEAVAVLQAHQAK	1.257287123	2	5.239744

Q9EPH8	SLGYAYVNFQQPADAER	1.116066353	2	3.651202
Q9EPH8	VDEAVAVLQAHQAK	1.399093646	2	3.149306
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.432657513**	**2.2E-09**	**12**
Q9EQ76	ASIYQSVFTNSSK	1.222284862	2	3.178519
Q9EQ76	GTCILPSVNDMMDDIDEK	1.492026151	2	3.594205
Q9EQ76	ILCGTVSIKPNVK	1.05419742	2	2.995908
Q9EQ76	KEPVFNDELPAR	1.264461864	2	3.221512
Q9EQ76	LQEYITSFATEK	1.856804281	2	4.073552
Q9EQ76	NNEVTLYK	2.30027803	2	2.452675
Q9EQ76	NNLPTAISDWWYMK	1.405977666	2	2.910594
Q9EQ76	SCLEEGLEPTCFER	1.443213049	2	4.589561
Q9EQ76	SDDVGGLWK	1.882690973	2	2.771746
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	1.299622146	3	5.19264
Q9EQ76	VWNDGYPWDMVVITR	1.127896238	2	4.133258
Q9EQ76	YIQFETLVTR	1.587798888	2	3.305302
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.049291111**	**0.77168**	**6**
Q9EQH3	ACAELHQNVNVK	1.186178633	2	3.704721
Q9EQH3	IREDLPNLESSEETEQINK	1.249833113	3	3.848196
Q9EQH3	LNLEHIATSSAVSK	0.979265773	2	3.521428
Q9EQH3	LSQLEGVNVER	1.00515823	2	2.980165
Q9EQH3	NIIIALIDR	0.940301027	2	2.318205
Q9EQH3	VLETTVEIFNK	1.048461299	2	2.707417
Q9EQH7	**NDST3 Bifunctional heparan sulfate N_deacetylase/N_sulfotransferase 3**	**0.853711177**	**0.75647**	**2**
Q9EQH7	KFALEHGIPTDMGYAVSPHHSGVYPVHVQLYEAWKK	0.852365316	3	3.349104
Q9EQH7	TTPATVMDEVQK+Oxidation(6)	0.927044133		
Q9EQN5	**SMBP2 DNA_binding protein SMUBP_2**	**0.938677123**	**0.81409**	**2**
Q9EQN5	CPTTSVRKPASAQESRQEAR	0.938752091	2	2.363061
Q9EQN5	KPSEKPLGSQVQPQHSSK	0.813990194	2	2.349717
Q9EQS0	**TALDO Transaldolase**	**1.153280927**	**8.9E-08**	**7**
Q9EQS0	ALAGCDFLTISPK	1.00811933	2	3.480733
Q9EQS0	EAGISKDRILIK	0.958844251	2	2.348685
Q9EQS0	ILDWHVANTDKK	1.334814313	2	3.206593
Q9EQS0	LGGPQEEQIK	1.210251548	2	3.0213
Q9EQS0	LSSTWEGIQAGK	1.119087222	2	2.837765
Q9EQS0	SYEPQEDPGVK	0.925472042	2	2.893496
Q9EQS0	WLHNEDQMAVEK	1.022191808	3	3.321831
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.01644733**	**0.99996**	**3**
Q9EQX9	LELFLPEEYPMAAPK	0.946754443	2	3.44018
Q9EQX9	SNEAQAIETAR	0.973542477	2	3.656157
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.064457722	3	4.342836
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.170218822**	**0.00025**	**23**
Q9ER34	ADIANLAEEFK	1.336825405	2	3.482643
Q9ER34	CTTDHISAAGPWLK	1.21956538	2	4.316233
Q9ER34	DINQEVYNFLATAGAK	0.982053289	2	4.141652
Q9ER34	DLEDLQILIK	1.48731359	2	2.503135
Q9ER34	FKLEAPDADELPR	1.001646895	3	4.274623
Q9ER34	FNPETDFLTGK	1.158450478	1	2.424444
Q9ER34	GHLDNISNNLLIGAINIENGK	1.123034604	2	5.606589
Q9ER34	IVYGHLDDPANQEIER	1.447760974	2	4.952315
Q9ER34	LEAPDADELPR	1.23344646	2	2.591181
Q9ER34	LNRPLTLSEK	1.706198262	2	2.44747
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	0.955926495	3	3.680157
Q9ER34	LTGTLSGWTSPK	1.459619982	2	2.58896
Q9ER34	NAVTQEFGPVPDTAR	1.248594965	2	4.557825

Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	1.008732811	3	4.41255
Q9ER34	NTIVTSYNR	1.158029419	2	2.376795
Q9ER34	QGLLPLTFADPSDYNK	1.174493012	2	3.443295
Q9ER34	SDFDPGQDTYQHPPK	1.25047525	2	2.455174
Q9ER34	SQFTITPGSEQIR	1.074163108	2	3.452129
Q9ER34	VAMQDATAQMAMLQFISSGLPK	0.883818227	2	2.373071
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	1.485555753	2	4.916017
Q9ER34	VDVSPTSQR	1.248203575	2	2.40706
Q9ER34	VGLIGSCTNSSYEDMGR	1.17312929	2	4.367917
Q9ER34	WVVIGDENYGEGSSR	1.171732144	2	4.51262
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.977661939**	**0.95559**	**3**
Q9ES21	LEEQDEFEK	1.253472389	2	2.818766
Q9ES21	TNVIQSLLAR	1.026483234	2	2.339262
Q9ES21	TQLGLVMDGFNSLLR	0.976877595	2	3.780588
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.061747952**	**0.99836**	**13**
Q9ES38	ACQAAWALK	1.33555204	2	2.536236
Q9ES38	ADVWENFQQR	1.025609352	2	3.01327
Q9ES38	EGFDVGVIADPLYILDNK	0.955605083	2	5.338932
Q9ES38	GATAILVLPSK	1.026124714	2	2.68855
Q9ES38	IQDSLEITNTYK	1.010344485	2	3.73132
Q9ES38	LKEATIQEDK	1.109673173	2	2.607008
Q9ES38	LLAENIR	1.375381096	2	2.398221
Q9ES38	MLTPLELVQFDIETAEPVRDK	0.92452553	2	4.282512
Q9ES38	QGFCIPVETGKPGLLLTK	1.084002642	3	3.666495
Q9ES38	SISALSVFLGLAK	0.641151903	2	3.4069
Q9ES38	SLMPDVYQAVCEGTWK	1.108185236	2	3.956059
Q9ES38	YLCNVPGQPEDK	1.110398962	2	3.328959
Q9ES38	YLCNVPGQPEDKK	0.902702115	2	2.494618
Q9ES53	**UFD1 Ubiquitin fusion degradation protein 1 homolog**	**0.942696137**	**0.18022**	**2**
Q9ES53	FQPQSPDFLDITNPK	1.188107049	2	2.49985
Q9ES53	FVAFSGEGQSLRKK	0.765732669	2	2.583275
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.963720591**	**0.99936**	**2**
Q9EST6	SLDLFGCEVTNR	0.963128779	2	3.098548
Q9EST6	TPAAVQELVLDNCK	0.977524838	2	3.456145
Q9ESV1	**LUZP1 Leucine zipper protein 1**	**0.883957781**	**0.21648**	**2**
Q9ESV1	EKLEEEENLTR	0.898922958	2	2.87248
Q9ESV1	RMADLEKLEEALSR	0.881196771	2	2.531142
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**0.853096113**	**0.82081**	**4**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.123242107	3	6.021239
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	0.879017592	3	3.961372
Q9ESW0	QGQGQLVTCSGAFK	1.065134031	2	2.899868
Q9ESW0	VTLGTQPTVLR	0.99869502	2	2.633499
Q9HB97	**PARVA Alpha_parvin**	**1.236021689**	**0.895**	**2**
Q9HB97	DLAEDLYDGQVLQK	1.514190072	2	3.101923
Q9HB97	LNVAEVTQSEIAQK	1.231857594	2	4.336986
Q9JHL4	**DBNL Drebrin_like protein**	**0.781034176**	**0.03594**	**4**
Q9JHL4	AMSTTSVSSSQPGK	0.778685236	2	2.585805
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3)	0.542663126		
Q9JHL4	TGELEQEVVSR	0.978486165	2	3.341404
Q9JHL4	VAGTGEGGLEELVEELNSGK	0.755061675	2	2.865452
Q9JI85	**NUCB2 Nucleobindin_2**	**1.278754903**	**0.14343**	**4**
Q9JI85	FQQGIAPSGPAGELK	1.170049837	2	2.733264
Q9JI85	QEYQQAVQQLEQK	1.100728957	2	4.3223
Q9JI85	QVIEVLETDPHFR	1.010270156	2	2.669342
Q9JI85	VHNVEPVESAR	1.288687999	2	2.918343

Q9JI91	**ACTN2 Alpha_actinin_2**	**1.081427237**	**0.96316**	**11**
Q9JI91	DQSLQEELAR	1.808802629	2	2.612214
Q9JI91	ETADTDTAEQVIASFR	1.743967994	2	3.933638
Q9JI91	GYEEWLLNEIR	1.143559431	3	3.371127
Q9JI91	HRPDLIDYSK	1.071986931	2	2.394802
Q9JI91	HTNYTMEHIR	1.125010907	3	3.40227
Q9JI91	HTNYTMEHIR+Oxidation(5)	1.15590658		
Q9JI91	KHEAFESDLAAHQDR	1.175865897	2	5.367726
Q9JI91	LEGDHQLIQEGLVFDNK	1.05020061	3	4.948175
Q9JI91	MLDAEDIVNTPKPDER	2.510535678	2	3.889498
Q9JI91	QSILAIQNEVEK	2.082947987	2	2.971831
Q9JI91	TINEVETQILTR	2.690073818	2	2.530003
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.163972057**	**9.9E-20**	**7**
Q9JJ19	AVDPDSPAEASGLR	1.887292552	2	3.683422
Q9JJ19	IVEVNGVCMEGK	1.457046563	2	3.225758
Q9JJ19	LLVVDPETDEQLKK	1.678446314	2	2.474663
Q9JJ19	LVEPGSPAEK	1.482310168	2	2.526153
Q9JJ19	LVEVNGENVEK	1.507166185	2	2.793793
Q9JJ19	SEHTEPPAAADTK	0.751024527	2	3.033579
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	1.008004732	3	3.674628
Q9JJ22	**ERAP1 Endoplasmic reticulum aminopeptidase 1**	**0.87379229**	**0.61919**	**2**
Q9JJ22	ASLINNAFQLVSIGK	0.918588289	2	2.522066
Q9JJ22	TQEFPHILTLIGR	0.842267352	2	2.578067
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**0.916264107**	**0.97799**	**3**
Q9JJ40	GVFLTDITPQGVAMK	0.968490699	2	2.415186
Q9JJ40	NGGDQTTLLVLDK	1.007549323	2	2.454234
Q9JJ40	SGNSVTLLVLDGDSYEK	0.882820889	2	4.384834
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.047868511**	**0.93442**	**3**
Q9JJ46	HLTNAQSMLDNK	0.94215743	2	3.52705
Q9JJ46	HLTNAQSMLDNK+Oxidation(7)	1.204533949		
Q9JJ46	VSVVPLGTGR	1.177015413	2	2.52231
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**0.975527906**	**0.4987**	**3**
Q9JJ54	FGDVVDCTLK	0.906958052	2	2.987431
Q9JJ54	IFVGGLSPDTPEEK	1.003469258	2	4.201118
Q9JJ54	IFVGGLSPDTPEEKIR	1.196778939	2	2.507551
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.018002896**	**0.93577**	**5**
Q9JJ79	ASDLKDLNSR	0.914159517	2	2.321454
Q9JJ79	ELMLERETLLAR+Oxidation(2)	0.937700516		
Q9JJ79	NCLEEWTKAAGLEK	1.053139825	2	2.420096
Q9JJ79	TVLRGSGNLLR	1.064504274	2	2.436831
Q9JJ79	YVVQIGDK	0.979244197	1	2.072972
Q9JJM9	**SEPT5 Septin_5**	**1.06115228**	**0.8166**	**2**
Q9JJM9	LIRMKDEELR	1.052880737	2	2.47511
Q9JJM9	MQEMLQKMK+Oxidation(3)	2.271045036		
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**0.777587315**	**0.01311**	**2**
Q9JJU8	GDYDAFFEAR	0.934851486	2	2.486322
Q9JJU8	QQDVLCFLEANK	0.838766533	2	3.280272
Q9JK11	**RTN4 Reticulon_4**	**1.104111871**	**0.52529**	**2**
Q9JK11	VDRKCLEDSLEQK	1.101057794	2	2.346146
Q9JK11	YSNSALGHVNSTIK	1.213525803	2	2.698704

Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**0.991223519**	**1**	**3**
Q9JK38	ITLECLPQNVGFYK	1.004948522	2	3.030867
Q9JK38	VEDVVVSDECR	1.00734793	2	3.536087
Q9JK38	VLGQLTETGVVSPEQFMK	0.948755147	2	4.170403
Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**0.830935985**	**0.762**	**2**
Q9JK72	GDLGNVHAEASGR	0.932479063	2	2.770985
Q9JK72	SLVVDEGEDDLGR	0.79502795	2	2.304827
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**2.569751737**	**0.60181**	**2**
Q9JKS4	GAPAYNPTGPQVTPLAR	2.390655147	2	3.930653
Q9JKS4	TQSKPEDEADEWAR	3.13307817	2	3.546019
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.029288773**	**0.99891**	**12**
Q9JLA3	AIWAALQTQTSNSAK	1.118554842	2	3.624517
Q9JLA3	FLFVDADQIVR	0.994042624	2	2.90383
Q9JLA3	FLSPLQQNLLK	0.98663335	2	2.385851
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	0.983291249	3	6.338928
Q9JLA3	IEYQFFEDK	1.040109751	2	2.520868
Q9JLA3	IVPEWQDYDQEIK	0.91329684	2	3.289206
Q9JLA3	LNIQPSETDYAVDIR	1.054382984	2	3.947537
Q9JLA3	TAAIANSMNYLTK	0.997285374	2	2.553551
Q9JLA3	VDALLSAQPK	1.036304338	2	3.003724
Q9JLA3	VEEDVASDLVMK	0.970956675	2	3.505897
Q9JLA3	VWQLQDLSFQTAAR	1.154839263	2	4.416657
Q9JLA3	YVLEPEISFTADNSFAK	1.35334035	2	3.714201
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**0.906180328**	**0.10676**	**3**
Q9JLH7	GSDALTLLEYPETR	0.853946585	2	2.47365
Q9JLH7	KEEEGQAGAAEMR+Oxidation(11)	0.79427596		
Q9JLH7	QYGITGDNVRRELLALVK	0.384103762	2	2.372433
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**0.986694308**	**0.84093**	**19**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	0.758555714	2	4.330059
Q9JLJ3	ANDTTFGLAAGVFTR	0.989808274	2	4.617095
Q9JLJ3	CQVLLEAAR	0.991621748	2	3.51146
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.019714981	2	4.632158
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	0.965451258	3	3.355614
Q9JLJ3	EVNLAVENAK	1.343809473	1	2.949497
Q9JLJ3	GALLANFLTQGQVCCNGTR	0.8830399	2	5.380242
Q9JLJ3	GIKPITLELGGK	1.007853826	3	3.972119
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	0.975358698	3	3.605326
Q9JLJ3	IGDPLLEDTR	0.930423306	2	4.013814
Q9JLJ3	MGPLINAPHLER	1.132534524	2	3.122439
Q9JLJ3	MGPLINAPHLER+Oxidation(0)	1.132857906		
Q9JLJ3	RDEIAIMETINNGK	1.02687328	2	5.36157
Q9JLJ3	SAPALACGNAMIFKPSPFTPVSALLLAEIYTK	0.867025699	3	3.459284
Q9JLJ3	SPLIIFSDCNMK	1.049304208	2	2.554181
Q9JLJ3	VEPVDASGTEK	0.980569362	1	2.24513
Q9JLJ3	VSFTGSVPTGMK	0.963391894	2	3.574542
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10)	0.983191366		
Q9JLJ3	VTIEYYSQLK	1.365843999	2	3.126212
Q9JLQ0	**CD2AP CD2_associated protein**	**0.870513285**	**0.1073**	**2**
Q9JLQ0	LQEEGWLEGELNGR	1.010324302	2	2.338794
Q9JLQ0	SNLEVEIAK	0.868785503	1	1.90647
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**0.964433392**	**0.36705**	**3**

Q9JLR1	GTLMELGISPIVTSGLIMQLLAGAK	1.061048754		
Q9JLR1	IIEVGDTPK	0.944293028	2	2.440527
Q9JLR1	TWIEVSGSSAK	1.222142705	2	2.667454
Q9JLT0	**MYH10 Myosin_10**	**1.147864971**	**0.00815**	**2**
Q9JLT0	AGVLAHLEEER	1.147887604	2	3.572839
Q9JLT0	KFDQLLAEEKGISAR	1.101708739	2	2.409313
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**0.67325414**	**0.11673**	**2**
Q9JLZ1	ELEASEELDTICPK	0.674398939	2	3.107807
Q9JLZ1	LEAEAVPEVSEK	0.185677554	2	2.494289
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.883501351**	**0.06532**	**4**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	0.883397536	2	5.713046
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.74673818	3	4.365326
Q9JLZ3	GIVVLGINR	0.951924739	2	2.852493
Q9JLZ3	SEVPGIFCAGADLK	0.898477512	2	2.937486
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**0.940338508**	**0.9988**	**15**
Q9JM53	AIASAAEGGSVPPIR	0.972413833	2	3.161554
Q9JM53	CLIATGGTPR	0.87820342	2	2.583949
Q9JM53	DGEQHEDLNEVAK	1.113099222	3	3.593656
Q9JM53	ILPEYLSNWTMEK	1.030994156	2	3.104879
Q9JM53	KSQASGIEVIQLFPEK	0.969092366	2	3.847722
Q9JM53	KVETDHIVTAVGLEPNVELAK	0.871626658	2	6.305777
Q9JM53	LNDGSQITFEK	0.886923128	2	3.346531
Q9JM53	SITVIGGGFLGSELACALGR	0.890460281	2	3.335269
Q9JM53	SQASGIEVIQLFPEK	0.944521951	2	4.461123
Q9JM53	TGGLEIDSDFGGFR	0.904586704	2	4.566465
Q9JM53	VETDHIVTAVGLEPNVELAK	0.935748552	2	5.21568
Q9JM53	VLIVSEDPELPYMRPPLSK	0.935396887	3	3.741368
Q9JM53	VMPNAIVQSVGVSGGK	0.915608296	2	4.041173
Q9JM53	VMPNAIVQSVGVSGGK+Oxidation(1)	0.908073833		
Q9JM53	VNAELQAR	0.9067375	2	2.486544
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**1.126680755**	**0.88954**	**2**
Q9JMA1	CTESEEEEVTK	1.095589178	2	3.621925
Q9JMA1	EKESVNAKVLK	1.289601659	2	2.315269
Q9JMD3	**PCTL PCTP_like protein**	**0.848047412**	**0.08327**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	0.825023778	2	4.894949
Q9JMD3	ESVQVPDDQDFR	2.262283995	2	2.362798
Q9JMD3	MECCDVPAETLYDVLHDIEYR	0.887596501	3	4.597589
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0)	0.934292717		
Q9JMD3	SCVITYLAQVDPK	0.988080422	2	3.148957
Q9JMD3	WDSNVIETFDIAR	0.853098481	2	4.318172
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**0.794385913**	**4E-09**	**5**
Q9QVC8	GEPNNVAGNQAQVK	0.906303439	2	4.135672
Q9QVC8	TEVAAGDHPTDAEMK	0.770942642	2	2.958541
Q9QVC8	TQLAVCQQR	0.813923253	2	2.493568
Q9QVC8	VAENGAQSAPLPLEGVDISPK	0.778563174	2	4.122159
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	0.841427903	3	5.068828
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.049685208**	**0.95297**	**2**
Q9QWN8	ALAQEDQSAGEVER	1.102321787	2	3.926124
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	1.04846535	3	4.347451
Q9QX74	**SHAN2 SH3 and multiple ankyrin repeat domains protein 2**	**0.784749459**	**0.87645**	**2**
Q9QX74	KNMLINIVDTAQQK+Oxidation(2)	0.962434072		
Q9QX74	SSSPASPENYVHPLTGR	0.781654971	2	2.590291

Q9QX79	**FETUB Fetuin_B**	**1.386421754**	**3E-06**	**2**
Q9QX79	GSIQHLPEQEEPEDSKGK	1.107919942	3	3.667366
Q9QX79	NTAPTSSPSITAPR	1.396591321	2	3.599302
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**0.982975764**	**0.47777**	**3**
Q9QXG4	AELGMNDSPSQSPPVK	1.335749272	2	3.721881
Q9QXG4	GATTNICYNVLDR	0.843889429	2	2.567111
Q9QXG4	IGPIATPDYIQNAPGLPK	1.444821969	2	3.047927
Q9QXH4	**ITAX Integrin alpha_X**	**0.9422774**	**0.8461**	**2**
Q9QXH4	GGSQMTFLVTFDVSPK+Oxidation(4)	1.102726932		
Q9QXH4	MLDFVKAVMSQLQRPSTR	0.937133657	2	2.396969
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**1.01944147**	**1**	**2**
Q9QXK3	SIATLAITTLLK	0.842030567	2	3.450824
Q9QXK3	SSEPVQLTEAETEYFVR	1.012686036	2	3.633356
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**0.997850804**	**0.00217**	**27**
Q9QXQ0	ACLISLGYDVENDR	1.001259632	2	4.069881
Q9QXQ0	AGTQIENIDEDFR	1.0239583	2	3.54526
Q9QXQ0	AGTQIENIDEDFRDGLK	1.015613183	2	4.207278
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.271669127	3	3.547238
Q9QXQ0	ASIHEAWTDGK	0.860414715	1	2.291869
Q9QXQ0	DDPVTNLNNAFEVAEK	0.894696577	2	3.080803
Q9QXQ0	ETTDTDTADQVIASFK	1.195264243	2	4.461416
Q9QXQ0	GISQEQMQEFR	1.237731852	2	3.158813
Q9QXQ0	HRDYETATLSDIK	1.308110288	2	3.519663
Q9QXQ0	HRPELIEYDK	1.048021187	3	4.139844
Q9QXQ0	HTNYTMEHLR	1.125010907	3	3.40227
Q9QXQ0	HTNYTMEHLR+Oxidation(5)	1.15590658		
Q9QXQ0	ICDQWDNLGSLTHSR	1.005573692	2	4.374999
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.917619067	2	4.513169
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.073483195	2	4.867167
Q9QXQ0	LVSIGAEEIVDGNAK	1.09254369	2	3.236647
Q9QXQ0	MAPYQGPDAAPGALDYK	0.985104295	2	4.62986
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0)	0.98014618		
Q9QXQ0	MLDAEDIVNTARPDEK	1.054391805	2	3.708212
Q9QXQ0	QFASQANMVGPWIQTK	0.818264235	2	3.828565
Q9QXQ0	QLETIDQLHLEYAK	0.993831236	2	2.964627
Q9QXQ0	RDHALLEEQSK	1.05661542	3	3.952373
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	0.917325792	3	5.32006
Q9QXQ0	TINEVENQILTR	1.119791287	2	3.677704
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	1.016378017	3	5.398366
Q9QXQ0	VGWEQLLTTIAR	0.818314045	2	4.047909
Q9QXQ0	VLAVNQENEHLMEDYER	1.28860089	2	5.049682
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**0.905918607**	**0.99754**	**5**
Q9QXT0	ALVDELEWEIAR	0.847143864	2	3.554797
Q9QXT0	IDSDISGTLK	0.995188556	2	2.319111
Q9QXT0	INPDGSQSVVEVPYAR	0.908473008	2	4.00082
Q9QXT0	RTDLCDHALHR	1.038932071	3	3.429007
Q9QXT0	TDLCDHALHR	1.022943384	2	2.862922
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**0.842232268**	**0.79951**	**16**
Q9QXX4	ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	1.098083845	3	4.904266
Q9QXX4	ASGDAARPFLLQLAESAYR	1.26084176	2	3.558573
Q9QXX4	DGSVPLLAEIFAGGCAGGSQVIFTNPLEIVK	0.928343259		
Q9QXX4	DVEVTKEEFALAAQK	1.140752294	2	4.388765
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	0.799795311	2	5.580944
Q9QXX4	GLLPQLLGVAPEK	0.928914735	2	2.995626
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.210473107	2	5.060184

Q9QXX4	ITLPAPNPDHVGGYK	1.081330401	2	2.346985
Q9QXX4	KDVEVTKEEFALAAQK	1.008241012	2	4.777228
Q9QXX4	LQVAGEITTGPR	1.07787734	2	3.503073
Q9QXX4	LTVNDFVR	0.858083998	2	2.434569
Q9QXX4	NGEFFMSPHDFVTR	0.867030255	2	3.661848
Q9QXX4	SSPQFGVTLLTYELLQR	1.131026731	2	3.966285
Q9QXX4	STGSFVGELMYK	0.861495623	2	2.463364
Q9QXX4	TVELLSGVVDQTK	0.942236608	2	4.298398
Q9QXX4	YLNIFGESQPNPK	0.905841366	2	4.405842
Q9QYU2	**EFTS Elongation factor Ts_ mitochondrial**	**0.94660181**	**0.78134**	**2**
Q9QYU2	ALETCGGDLK	1.172085624	2	2.420243
Q9QYU2	YGALVICQTPEQITNLEEVGR	0.849190674	2	4.676792
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.971947014**	**0.94909**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	0.921188805	2	3.723191
Q9QYU4	RAPAFLSADEVQDHLR	0.923992607	3	4.63598
Q9QYU4	SLGMAVEDLVAAK	0.811037335	2	3.143306
Q9QYU4	SSSLLIPPLEAALANFSK	0.943062733	2	3.088178
Q9QZ76	**MYG Myoglobin**	**1.038118013**	**0.98851**	**5**
Q9QZ76	GQHAAEIQPLAQSHATK	0.952091156	2	4.88546
Q9QZ76	HGCTVLTALGTILK	0.581376025	2	3.535485
Q9QZ76	KGQHAAEIQPLAQSHATK	1.686709781	3	5.712786
Q9QZ76	VEGDLAGHGQEVLISLFK	2.211231642	3	4.915684
Q9QZ76	YSGDFGADAQGAMSK	4.660828999	2	4.750554
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.096422854**	**0.90458**	**9**
Q9QZA2	ATLVKPTPVNVPISQK	0.965456399	2	3.703234
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	0.934901583	2	3.538852
Q9QZA2	FYNELTEILVR	0.937748485	2	2.943046
Q9QZA2	LLDEEEATDNDLR	1.046593458	2	3.466552
Q9QZA2	MVPVSVQQSLAVFSQR	1.024311165	2	2.676082
Q9QZA2	NIQVSHQEFSK	1.15724287	2	3.357834
Q9QZA2	NLATAYDNFVELVANLK	0.934541309	3	4.168279
Q9QZA2	STAVVEQGGIQTVDQLIK	1.104373462	2	4.235548
Q9QZA2	YYDQICSIEPK	1.051917397	2	2.345001
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**0.903501773**	**0.80916**	**5**
Q9QZD8	GALVTVGQLSCYDQAK	0.908048258	2	4.869442
Q9QZD8	NYSHALDGLYR	0.898156781	2	2.907637
Q9QZD8	VHLQTQQEVK	0.888119964	1	3.011795
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	0.860577749	2	5.651291
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	0.861792051	3	3.399382
Q9QZH8	**AAAD Arylacetamide deacetylase**	**0.94263122**	**0.97295**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.117856711	2	4.119337
Q9QZH8	WFLQEDILEK	0.908479592	2	3.349015
Q9QZK2	**BCAR3 Breast cancer anti_estrogen resistance protein 3**	**1.14739125**	**0.64938**	**2**
Q9QZK2	EGSLAEGRPDVVKR	1.054704959	2	2.649199
Q9QZK2	FSSDARTGEALR	1.413386679	2	2.317252
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.308565444**	**1.7E-07**	**6**
Q9QZU7	IDANNVAYTTGK	1.360603123	2	3.338987
Q9QZU7	IIELDDKGQVVR	1.571046611	2	2.543926
Q9QZU7	LLLEALDVNIR	1.081295062	2	2.857077
Q9QZU7	MNPGDVITFDNWR	1.294447576	2	3.172843
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.268944304	2	4.499276
Q9QZU7	SYEAGTEISR	1.333724971	2	2.836032
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**0.850557702**	**0.99895**	**3**

Q9QZX8	GIGETPIVPLGISYLDDFAK	0.91783607	2	3.048605
Q9QZX8	QEEQDPSNMTGFLR	1.00580013	2	2.354832
Q9QZX8	QFTDEGNPDSVNK	0.823936087	2	3.422201
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.937784258**	**0.01644**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	1.141886093	2	4.088025
Q9R063	ETDLLLDDSLVSLFGNR	0.757392294	2	4.151052
Q9R063	GVLFGVPGAFTPGCSK	0.922236319	2	4.193405
Q9R063	THLPGFVEQAGALK	0.860820115	3	4.748904
Q9R063	VGDTIPSVEVFEGEPGK	0.9820562	2	3.758513
Q9R063	VGDTIPSVEVFEGEPGKK	0.934428348	2	3.754559
Q9R063	VNLAELFK	0.912587679	2	2.852062
Q9R063	VQLLADPTGAFGK	1.008140233	2	3.996456
Q9R0N0	**GALK1 Galactokinase**	**0.916681971**	**0.24625**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	0.821084965	3	4.378198
Q9R0N0	QCEEVAQALGK	0.932697496	2	2.463462
Q9R0N0	RQCEEVAQALGK	0.896909086	2	3.03592
Q9R0N0	SLETSLVPLSDPK	0.850007473	2	3.204306
Q9R0N0	TDGLVSLLTTSK	0.912115349	2	3.433484
Q9R0N0	VEELLAEAR	0.978386332	2	3.157166
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.046793423**	**0.94819**	**6**
Q9R0T3	AEPSVAEYTVR	0.896736469	2	2.743583
Q9R0T3	FDDGEDPLDAETQQGGGSNPFHR	1.062159898	3	3.659253
Q9R0T3	ICSEVLQLEPDNVNALK	0.900711829	2	5.405903
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	0.81674593	3	5.490442
Q9R0T3	LIGSAEELIR	0.901604353	2	2.378122
Q9R0T3	SNPSENEEKEAQSQLVK	0.98132018	2	5.015873
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.036886872**	**0.98646**	**4**
Q9R112	EGNALFTFPNTPVK	1.11533455	2	2.707342
Q9R112	STLSVIPSGVQWIQDR	1.036534302	2	2.549031
Q9R112	TAAAVAAQSGILDR	1.197804046	2	2.791556
Q9R112	VGAENVAIVEPSER	0.992957954	2	2.867388
Q9R1T3	**CATZ Cathepsin Z**	**0.941311797**	**0.9936**	**2**
Q9R1T3	HGIPDETCNNYQAK	0.939175525	2	3.794746
Q9R1T3	VGDYGSLSGR	1.243194876	2	2.64976
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**1.095798879**	**0.19939**	**5**
Q9R1Z0	LCQNNFALGYK	1.404765781	2	2.526619
Q9R1Z0	LTLSALVDGK	1.374990864	2	2.720363
Q9R1Z0	LTVDTIFVPNTGK	1.036739242	2	3.499559
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	1.228347545	2	4.110036
Q9R1Z0	WNTDNTLGTEISWENK	0.891097271	2	2.896702
Q9R1Z8	**VINEX Vinexin**	**0.901014796**	**0.7216**	**2**
Q9R1Z8	LSAELDKDLR	0.90067497	3	3.522681
Q9R1Z8	MPDLQLDWTLEDPPK+Oxidation(0)	1.142812664		
Q9R257	**HEBP1 Heme_binding protein 1**	**1.06069731**	**0.43083**	**2**
Q9R257	FATVEVTDKPVDEALR	0.9285409	2	3.528544
Q9R257	NSLFGSVETWPWQVLSTGGK	1.142243174	2	3.863076
Q9WTT6	**GUAD Guanine deaminase**	**1.30488862**	**2.2E-05**	**10**
Q9WTT6	EIGNFEVGKDFDALLINPR	0.94985828	2	3.565097
Q9WTT6	ETTEESVKETER	1.313603554	2	3.253301
Q9WTT6	FQSTDVAEEVYTR	0.978881714	2	4.313101
Q9WTT6	FSLSCTETLMSELGNIAK	0.868303047	2	4.127766
Q9WTT6	GTFVHSTWTCPMEVLR	0.918936293	2	3.132769
Q9WTT6	IVFLEESSQQEK	1.041894666	2	3.919569
Q9WTT6	NIEEVYVGGK	0.864161558	1	2.790273
Q9WTT6	NYTDVYDKNNLLTNK	0.778045716	2	4.412564

Q9WTT6	THDLYIQSHISENREEIEAVK	0.887373739	3	3.755657
Q9WTT6	VCMDLNNTVPEYK	1.038226589	2	3.978439
Q9WTV5	**PSMD9 26S proteasome non_ATPase regulatory subunit 9**	**1.093479388**	**0.99282**	**2**
Q9WTV5	ADVDLYQVR	1.050496423	2	2.705196
Q9WTV5	RKEEIEAQIK	1.019522493	3	3.916663
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**0.879036164**	**9.9E-20**	**9**
Q9WU19	AIFVTVDTPYLGNR	0.964233094	2	4.592975
Q9WU19	AVFVGRPIIWGLAFQGEK	0.887522719	3	4.129823
Q9WU19	GVQDVLEILK	0.867859851	2	2.912539
Q9WU19	GVQDVLEILKEEFR	0.723625611	2	3.956644
Q9WU19	HGVDGILVSNHGAR	0.808643379	3	5.21556
Q9WU19	MKNFETNDLAFSPK+Oxidation(0)	0.835370516		
Q9WU19	NFETNDLAFSPK	0.76220449	2	3.410523
Q9WU19	NVADIDLSTSVLGQR	0.885321017	2	4.907847
Q9WU19	VEVFLDGGVR	0.85089691	2	2.95267
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**0.839300633**	**0.70977**	**2**
Q9WU49	GNVVPSPLPTR	0.92305513	2	2.462003
Q9WU49	LQAVEVVITHLAPGTK	0.837843605	2	3.991714
Q9WU65	**GLPK2 Glycerol kinase 2**	**0.848301574**	**0.11523**	**2**
Q9WU65	GIICGLTQFTNK	0.801088586	2	3.463225
Q9WU65	TGLPLSTYFSAVK	1.791614468	2	2.617165
Q9WU82	**CTNB1 Catenin beta_1**	**0.915978474**	**0.93368**	**3**
Q9WU82	HQEAEMAQNAVR	0.911684188	2	3.357732
Q9WU82	LLNDEDQVVVNK	0.965907422	2	3.253192
Q9WU82	TMQNTNDVETAR	0.837643739	2	3.417847
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**0.975243794**	**1E-09**	**3**
Q9WUC4	LGGVEFNIDLPNK	0.950988805	2	2.852182
Q9WUC4	LGGVEFNIDLPNKK	1.010731725	2	3.457079
Q9WUC4	VCIESEHSSDILLATLNK	1.233300554	2	5.705632
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**1.530234925**	**0.78272**	**2**
Q9WUH4	FCANTCVECR	1.324210833	2	2.999619
Q9WUH4	FVFHNEQVYCPDCAK	1.739230262	2	4.135421
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**0.867426642**	**0.80004**	**2**
Q9WUI1	ILDFGLAR	0.721752417	2	2.373367
Q9WUI1	QELNKTVWEVPQR	0.887542849	2	2.345996
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.979627963**	**0.99588**	**6**
Q9WUS0	AVILGPPGSGK	0.984647664	2	2.520515
Q9WUS0	GLLVPDHVITR	1.082560508	2	2.498282
Q9WUS0	GVLHQFSGTETNR	0.909473081	2	3.619946
Q9WUS0	TLVQAEALDR	0.963442149	2	2.901691
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.06577441	3	5.072241
Q9WUS0	YKDAAKPVIELYK	1.11439055	2	2.536824
Q9WV97	**TIM9 Mitochondrial import inner membrane translocase subunit Tim9**	**1.100596629**	**0.00203**	**2**
Q9WV97	FQEYHIQQNEALAAK	1.155931983	2	4.868166
Q9WV97	LTETCFLDCVK	0.831105006	2	2.385885
Q9WVC0	**SEPT7 Septin_7**	**1.156823045**	**0.92994**	**2**
Q9WVC0	ADTLTPEECQQFK	1.152779354	2	3.356287
Q9WVC0	NLEGYVGFANLPNQVYR	0.896632443	2	2.30755
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**1.582578516**	**2.1E-14**	**4**
Q9WVD5	DGPLGFYHGLSSTLLR	1.821056096	2	3.076921
Q9WVD5	LQTMYEMETSGK	1.971608917	2	2.377356
Q9WVD5	NEGITALYSGLKPTMIR	0.965614978	2	3.577058
Q9WVD5	SNPAIQAAIDLTAGAAGGTACVLTGQPFDTMK	1.635523302	3	4.556772

Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.847661225**	**9.9E-20**	**13**
Q9WVK3	AGVYNLTK	1.043415844	2	2.411403
Q9WVK3	ASQPPSSSTQVTAIQCNIR	0.924422333	2	5.47989
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	0.89928876	3	6.884837
Q9WVK3	ELLHLGCNVVIASR	1.40192713	2	3.852978
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	0.794480299	2	5.240016
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12)	0.895034678		
Q9WVK3	KEEEVNNLVK	0.903933262	3	4.183327
Q9WVK3	LTAAVDELR	1.048564095	2	3.131771
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.869783261	2	5.012838
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	0.880673182	3	3.334849
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.799318943	2	6.327176
Q9WVK3	TMALTWASSGVR	0.804171892	2	3.897732
Q9WVK3	TMALTWASSGVR+Oxidation(1)	0.831024624		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**0.919484476**	**0.73028**	**14**
Q9WVK7	AADEFVEK	1.145423826	2	3.132052
Q9WVK7	EDIDTAMK	1.09941309	1	1.983415
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.020452059	2	5.541116
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	0.915670518	3	5.373808
Q9WVK7	GDASKEDIDTAMK	0.989340188	3	3.850496
Q9WVK7	GDASKEDIDTAMK+Oxidation(11)	1.110825174		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.88609207	3	7.517247
Q9WVK7	KGIEESLK	1.053541971	1	2.137823
Q9WVK7	KGIEESLKR	1.047762508	2	2.348249
Q9WVK7	LKNELFQR	1.056881451	2	2.694453
Q9WVK7	LLVPYLIEAIR	0.872665539	2	2.555841
Q9WVK7	LVEVIK	1.025692933	2	2.451511
Q9WVK7	TFESLVDFCK	1.075551958	2	3.441023
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	0.92931284	3	6.204538
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.283292626**	**0.37183**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	1.033024381	2	3.306947
Q9Z0N2	SFDVNKPGCEVDDLK	1.225861069	2	3.454753
Q9Z0N2	VGQEIEVRPGIVSK	1.292225872	2	3.10233
Q9Z0U5	**ADO Aldehyde oxidase**	**0.862766632**	**1**	**17**
Q9Z0U5	CGLSPEQVR	1.125068241	2	2.48427
Q9Z0U5	CTGYRPIIDACK	0.842675034	2	2.621097
Q9Z0U5	DLEPLILTIEEAIQHK	0.829327812	2	3.289575
Q9Z0U5	EFQPLDPTQELIFPPELMR	0.804835634	2	3.069865
Q9Z0U5	ELSILYGGVGPTTIGAK	0.949989923	2	3.496761
Q9Z0U5	GEDMLITGGR	1.012825503	2	2.36863
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	0.766797192	2	4.614176
Q9Z0U5	GYESNINWEK	0.930674617	2	2.828918
Q9Z0U5	HIQDIVAATLK	0.755599861	2	2.447212
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	0.940084778	2	4.594275
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	0.707925907	3	3.380001
Q9Z0U5	KLECGNVDEAFK	0.777794829	2	3.549228
Q9Z0U5	LVLDEVTLAGSAPGGK	0.864308726	2	3.534112
Q9Z0U5	MTWISPVTLEELVEAK	0.900686084	2	3.203017
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	0.688330442	2	3.722775
Q9Z0U5	RLEPIISK	0.977354494	2	2.436527
Q9Z0U5	VVENNVDPEMMLLPYLR	0.869974672	2	3.864388
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**0.960679735**	**0.64081**	**4**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	1.743667319	2	5.433118
Q9Z0V5	GLFIIDDK	0.982068061	2	2.978997

Q9Z0V5	QITLNDLPVGR	0.97343716	2	3.308394
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	0.99529044	3	6.021302
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.958600648**	**0.99753**	**6**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	0.948182157	3	5.999172
Q9Z0V6	GLFIIDPNGVIK	0.935262106	2	3.068291
Q9Z0V6	GTAVVNGEFK	1.04484671	2	2.453907
Q9Z0V6	HLSVNDLPVGR	0.946277705	2	2.87021
Q9Z0V6	NGGLGHMNITLLSDLTK	1.057453176	2	2.817187
Q9Z0V6	SVEEPLRLVK	0.852403262	2	2.488593
Q9Z142	**TMM33 Transmembrane protein 33**	**0.885828964**	**0.71202**	**2**
Q9Z142	ALLANALTSALR	0.921943836	2	3.72164
Q9Z142	LSTNQQNILK	1.186203065	2	2.468726
Q9Z1A6	**VIGLN Vigilin**	**1.014617078**	**0.00058**	**22**
Q9Z1A6	ASVITQVFHVPLEER	1.434862062	2	2.88712
Q9Z1A6	DKFPEVIINFPDPAQK	1.660424964	3	4.04574
Q9Z1A6	DLANIAEVEVSIPAK	1.253723128	2	3.74732
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.047382405	3	3.519886
Q9Z1A6	ELQAEQEDR	1.301069542	2	2.50733
Q9Z1A6	GNSLQEILER	1.049431381	2	2.524348
Q9Z1A6	HEVLLISAEQDKR	1.123309741	3	4.274891
Q9Z1A6	IDLPAENSNSETIVITGK	0.982453026	2	4.628772
Q9Z1A6	IEGDPQGVQQAK	0.95824253	2	3.178707
Q9Z1A6	IIFPAAEDKDQDLITIIGK	0.998512498	2	3.236438
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.368822427	2	4.309167
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.00256333	2	4.52848
Q9Z1A6	LGQALTEVYAK	1.164455045	2	3.205396
Q9Z1A6	LQDLELK	1.139983495	1	2.320713
Q9Z1A6	LQTQASATVPIPK	1.007533423	2	3.530967
Q9Z1A6	LVGEIMQETGTR	1.132015121	2	3.385951
Q9Z1A6	MDYVEINIDHK	1.100266972	2	3.225439
Q9Z1A6	MVADLVENSYSISVPIFK	0.878140621	2	2.988643
Q9Z1A6	RCDIIVISGR	0.968825405	2	2.776778
Q9Z1A6	TEIVFTGEKEQLAQAVAR	0.918889315	2	4.179046
Q9Z1A6	TKDLIIEQR	1.166578973	2	2.525235
Q9Z1A6	VKELQAEQEDR	0.951039433	2	3.015939
Q9Z1J8	**S14L3 SEC14_like protein 3**	**0.859641783**	**0.85202**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.841043921	3	3.857328
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	0.989059049	3	3.815496
Q9Z1J8	GSSHQVEYEILFPGCVLR	0.939124667	2	4.619497
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**0.842867329**	**0.00862**	**2**
Q9Z1N1	YVGSMVADVHR	0.706952292	2	2.318095
Q9Z1N1	YVGSMVADVHR+Oxidation(4)	0.875189969		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**0.868582998**	**0.01555**	**3**
Q9Z1P2	DYETATLSEIK	1.223647937	1	2.080388
Q9Z1P2	ICDQWDNLGALTQK	0.748436977	2	3.898709
Q9Z1P2	KDDPLTNLNTAFDVAER	2.511242219	2	2.663866
Q9Z1W6	**LYRIC Protein LYRIC**	**0.878332796**	**0.89682**	**3**
Q9Z1W6	SWQDELAQQAEEGSAR	1.004116186	2	5.390511
Q9Z1W6	TELGLDLGLEPK	0.867534986	2	2.797747
Q9Z1W6	TLPPAISAEPSVTLSK	0.82541717	2	3.161659
Q9Z1Y3	**CADH2 Cadherin_2**	**0.884961474**	**0.39813**	**2**
Q9Z1Y3	IDPVNGQITTIAVLDR	0.882910219	2	3.495197
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	1.0114684	3	3.387642
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**1.005939065**	**0.94945**	**3**
Q9Z270	FKGPFTDVVTTNLK	0.865436867	2	2.602382

Q9Z270	HEQILVLDPPSDLK	0.996022975	2	4.187204
Q9Z270	QDGPLPKPHSVSLNDTETR	1.020097298	3	3.351138
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**0.914278211**	**0.21217**	**2**
Q9Z2C8	NDTKEDVFVHQTAIK	0.879925524	2	3.421593
Q9Z2C8	SVGDGETVEFDVVEGEK	1.128983146	2	3.689335
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.895571048**	**6.9E-06**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.72364563	2	4.563154
Q9Z2I8	GKGVFNSGLK	1.063948568	2	2.312438
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	0.84301443	3	4.77351
Q9Z2I8	INFDDNAEFR	0.838048232	2	3.207994
Q9Z2I8	LEGTNVQEAQNILK	1.016116375	2	5.226037
Q9Z2I8	SENEPIENEAAR	1.016002497	2	4.052405
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.862283016	2	5.999477
Q9Z2I8	SSGLPITSAVDLEDAAK	0.889993222	2	4.538201
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.897040726	2	2.952747
Q9Z2I8	VMVAEALDISR	0.968030665	2	3.318779
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**0.9293025**	**0.99999**	**8**
Q9Z2I9	ALIADSGLK	0.98101832	1	2.08293
Q9Z2I9	ICNQVLVCER	1.160248442	2	2.861273
Q9Z2I9	ILACDDLDEAAK	0.940504212	2	3.392226
Q9Z2I9	INFDSNSAYR	1.023339946	2	2.837421
Q9Z2I9	LSEIVTLAK	1.071988848	2	2.50533
Q9Z2I9	MGFPSNIVDSAAENMIK	1.033024158	2	2.828672
Q9Z2I9	SSDEAYAIAK	0.971674454	2	3.503048
Q9Z2I9	VQAILVNIFGGIMR	0.746740724	2	3.837887
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.078467275**	**0.99291**	**11**
Q9Z2L0	KLETAVNLAWTAGNSNTR	0.912043588	2	5.814874
Q9Z2L0	LTFDSSFSPNTGK	0.996430197	2	3.601147
Q9Z2L0	LTFDSSFSPNTGKK	1.028636511	2	2.553809
Q9Z2L0	LTLSALLDGK	1.321172863	2	2.493484
Q9Z2L0	SENGLEFTSSGSANTETTK	1.2668888	2	4.596782
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	0.978337118	3	5.105243
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	1.123328113	2	4.438754
Q9Z2L0	VTQSNFAVGYK	1.028149722	2	3.132606
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.008991896	2	4.545949
Q9Z2L0	WTEYGLTFTEK	1.167052598	2	2.902601
Q9Z2L0	YQVDPDACFSAK	1.07481551	2	3.553422
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.991287816**	**1**	**4**
Q9Z2M4	GQVLQLHAGAAK	1.273666585	2	3.187414
Q9Z2M4	HLAVEWGPQNIR	0.975770676	2	3.269214
Q9Z2M4	VNSLAPGAISGTEGLR	0.956869927	2	3.931054
Q9Z2M4	VPPAVMAAVDQALK	0.97817578	2	3.169947
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.042298069**	**0.86924**	**4**
Q9Z2M7	IGVVGGSDFEK	1.593545332	2	2.376433
Q9Z2M7	LQEQLGNDVVEK	1.070485356	2	3.491516
Q9Z2M7	TVGYTVTAPEDTR	1.055131613	2	2.519665
Q9Z2M7	YDYVFPENGLVAYK	0.882809847	2	3.340096
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**0.982905131**	**1**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	1.124177219	2	4.183478
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	0.971123801	2	4.623977
Q9Z2Q1	CLSSATDPQTK	0.874291357	2	2.623059
Q9Z2Q1	DQTLSPTIISGLHSIAR	1.055493914	2	3.423858
Q9Z2Q1	GGPGPLAGHPQVSR	0.907233754	2	3.098453
Q9Z2Q1	IDASQTDFEK	1.173371335	2	2.494619

Q9Z2Q1	IIAGDKEVVIAQK	0.991826844	2	2.537663
Q9Z2Q1	KIDASQTDFEK	1.003450207	2	3.043903
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	0.956534264	2	5.171887
Q9Z2Q1	QVQHILASASPSGR	0.974826433	2	2.912612
Q9Z2Q1	SSYEGQPLPK	0.967110728	2	2.477648
Q9Z2Q1	TQPPEDISCIAWNR	1.015713458	2	2.673215
Q9Z2Q1	TTFEDLIQR	1.044936365	2	2.34945
Q9Z2Q1	VYSIMGGSIDGLR	0.695549999	2	2.619166
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**1.349988345**	**0.74842**	**3**
Q9Z2Z8	AIECSYTSADGLK	1.563999327	2	3.996382
Q9Z2Z8	ASLADIWAK	1.436778732	2	2.651257
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	1.30264054	2	5.473073
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**0.943247769**	**0.89509**	**5**
Q9Z339	GSAPPGPVPEGQIR	0.943317342	2	3.326944
Q9Z339	LEALELNECIDHTPK	0.783664995	2	4.331292
Q9Z339	LEEAMANK	0.898977882	1	1.997001
Q9Z339	LEEAMANK+Oxidation(4)	0.696691721		
Q9Z339	LFPDDPYEKACQK	0.927285777	2	2.423779

Time point 18 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (18 h)**	**P-value (18 h)**	**Peptide number (18 h)**
Accession number	Peptide sequence	Peptide Ratio (18 h)	Charge state	Xcorr
A0FKI7	**ACBD5 Acyl_CoA_binding domain_containing protein 5**	**1.052205134**	**0.34537**	**3**
A0FKI7	LQEDMQNVLQR	**2.139102071**	2	2.585372
A0FKI7	RGGESEDISGVR	**1.043448039**	2	2.624462
A0FKI7	SSDLTSDLGNVLTSSNAK	**0.986319998**	2	3.258466
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**0.661052031**	**0.37661**	**2**
A2AAE1	SSRSLDQDSPSKK	**0.560473666**	2	2.660615
A2AAE1	TVDGNVNSMKRK	**0.81387359**	2	2.311105
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**0.947979336**	**0.00136**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	**1.004546319**	2	3.243532
A2ADY9	NPPLAEALLSGDLEK	**0.797773895**	2	3.426769
A2ADY9	VLVEQQQDR	**0.919943188**	2	2.469646
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.45086507**	**0.00164**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13)	**0.197541578**		
A2AGT5	IGSKENTKEGLAELYEYK	**0.599739329**	2	2.548419
A2AQP0	**MYH7B Myosin_7B**	**1.029720577**	**0.99992**	**13**
A2AQP0	AITDAAMMAEELK	**0.976184423**	2	2.93084
A2AQP0	AITDAAMMAEELKK	**0.9369823**	2	3.533626
A2AQP0	AITDAAMMAEELKK+Oxidation(6)	**0.915594871**		
A2AQP0	AITDAAMMAEELKK+Oxidation(7)	**0.915594871**	2	2.92241
A2AQP0	CNGVLEGIR	**0.783271973**	2	2.56169
A2AQP0	DIDDLELTLAK	**0.591972826**	2	3.795369
A2AQP0	ELEELSER	**1.267267823**	1	2.076466
A2AQP0	EQDTSAHLER	**1.350380815**	2	2.491106
A2AQP0	KDIDDLELTLAK	**1.000875638**	2	2.374543
A2AQP0	SIQELEK	**1.013481804**	2	2.393534
A2AQP0	TEELEEAK	**1.069985369**	2	2.364938
A2AQP0	VEDEQLVGVQLQK	**1.280925754**	2	2.320039
A2AQP0	VGNEYVTK	**1.008882669**	2	3.03588
A2ASS6	**TITIN Titin**	**1.045516194**	**0.17933**	**32**
A2ASS6	ACDALYPPGPPSNPK	**0.754211158**	2	2.53571
A2ASS6	AENRFGIGPPAETIQRTTAR	**0.878021582**	2	2.571583
A2ASS6	AGEDVQLLIPFK	**1.168877467**	2	2.586797
A2ASS6	APPIEPAPTPIAAPVTAPVVGK	**1.503151073**	2	4.506479
A2ASS6	ATGLIEGLDYQFR	**0.476732223**	2	2.990193
A2ASS6	ATLTWTPPLEDGGSPIK	**0.921152921**	2	2.316728
A2ASS6	ATNEVGSDTCACTVK	**1.166672552**	2	4.2124
A2ASS6	DGQELQIADRIKIQK	**1.356180803**	2	2.788064
A2ASS6	DPFDKPSQPGELEILSISK	**1.411397672**	3	3.67113
A2ASS6	GQSDPVTIGPLTVK	**1.683280108**	2	2.838985
A2ASS6	GYDEIPLEPNDKTEILK	**0.881981603**	2	2.419614
A2ASS6	IEALPSDISIDEGK	**2.483010738**	2	2.420704
A2ASS6	KGDGTQLACKVTGTPPIK	**0.349441136**	2	2.671027
A2ASS6	NAADNFSEPSESSGAITAR	**1.446437278**	2	3.984609
A2ASS6	NAADSVSEPSESTGPITVK	**1.021398993**	2	2.342911
A2ASS6	NAADSVSEPSESTGPITVKDDVEAPR	**0.828475657**	3	3.44918
A2ASS6	NAAGVFSEPSESTGAITAR	**1.058276062**	2	4.287962
A2ASS6	QEKIEGDLRAMLK+Oxidation(10)	**0.447118369**		
A2ASS6	QETEEIAASMVVVATAK	**0.735297951**	2	2.311084
A2ASS6	SAANLIVEEEDLR	**0.42159355**	2	2.596856

A2ASS6	VFAENEYGIGDPGETR	**0.16373374**	2	3.595248
A2ASS6	VGTGEPVETDSPVEAR	**1.010831848**	2	4.02984
A2ASS6	VIGSPNTPEGPLEYDDIQAR	**0.801060825**	2	3.607061
A2ASS6	VLACNAGGPGEPAEVPGTVK	**1.381611864**	2	3.04132
A2ASS6	VLAENEIGIGEPCETTEPVK	**2.075515182**	2	3.780295
A2ASS6	VLAENEYGIGLPAETAESVK	**0.881464189**	2	3.502002
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	**0.8101625**	3	3.598027
A2ASS6	VNAESTENNSLLTIK	**0.470149234**	2	3.736063
A2ASS6	VSGENEFGVGVPAETK	**1.795118632**	2	3.676018
A2ASS6	VSNVAGDNACSGILTVK	**3.61532595**	2	2.932786
A2ASS6	VSVLDVPGPPGPIEISNVSAEK	**1.785134481**	2	2.720303
A2ASS6	YGIGEPLDSEPETAR	**0.862961481**	2	3.220699
A2AU37	**RD21L Double_strand_break repair protein rad21_like protein 1**	**0.446023914**	**0.2496**	**2**
A2AU37	MKMTFRPGLVDLPK	**0.298849157**	1	2.065607
A2AU37	RGGVDMLLSTATQDLINDELK	**1.301541832**	2	2.361515
A2AWA9	**RBGP1 Rab GTPase_activating protein 1**	**0.753040132**	**0.36543**	**2**
A2AWA9	IVICVQQTANKELAIER	**0.763727191**	2	2.347069
A2AWA9	RLMELACNTKISQK+Oxidation(2)	**0.752155093**		
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.113271941**	**0.30609**	**11**
A2VCW9	AEGIVFNTQSTIK	**1.616230549**	2	2.755304
A2VCW9	AGGILQEDITEACLILGVK	**0.733041738**	2	3.923125
A2VCW9	AQEANMSLLDEVLK	**1.045074813**	2	4.386465
A2VCW9	GAQEVFNELPCEYVEPHELK	**1.203073316**	2	4.814317
A2VCW9	KTDGVYDPVEYEKYPER	**1.132749307**	3	3.912395
A2VCW9	KYDINTVNVTVGK	**1.404251284**	2	4.093321
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	**1.396068514**	3	4.090736
A2VCW9	QDAQSLLVPVK	**1.048637481**	2	2.666499
A2VCW9	REDVNAWER	**1.225863197**	2	3.088103
A2VCW9	SSVVPVEGCPELPHK	**1.238138192**	2	2.828781
A2VCW9	YDINTVNVTVGK	**0.90184009**	2	2.458222
A6H584	**chain**	**1.167445632**	**0.64034**	**7**
A6H584	FVNRAVFRMANGIDR+Oxidation(8)	**1.267228932**		
A6H584	NEHSFQVVGIQVR	**0.945915402**		
A6H584	QGDPGIEGPIGFPGPK	**0.823049638**		
A6H584	RGTQGYGPIGYDGQK	**1.512336291**		
A6H584	TMNPAFMGLDRATR+Oxidation(1)	**1.197675638**		
A6H584	YDVTDAVKVLK	**1.123256812**		
A6H584	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	**0.808119344**		
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**0.940539187**	**0.00055**	**12**
A7VJC2	GFGFVTFDDHDPVDK	**0.913321526**	2	3.113469
A7VJC2	GGGGNFGPGPGSNFR	**0.941448114**	2	3.529153
A7VJC2	GGNFGFGDSR	**0.504397803**	2	2.481533
A7VJC2	IDTIEIITDR	**0.833306132**	2	4.104054
A7VJC2	LFIGGLSFETTEESLR	**1.208085393**	2	3.873233
A7VJC2	LTDCVVMR	**0.828382157**	2	2.531387
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	**0.914438763**	2	6.311837
A7VJC2	NYYEQWGK	**0.902084994**	1	2.438159
A7VJC2	QEMQEVQSSR	**0.786347362**	2	3.014442
A7VJC2	QEMQEVQSSR+Oxidation(2)	**1.352986782**		
A7VJC2	TLETVPLER	**1.426245351**	2	2.316374
A7VJC2	YHTINGHNAEVR	**1.3156954**	2	3.443421
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.064126435**	**0.94222**	**2**
B0BN93	QMTDPNVALTFLEK	**1.134957106**	2	2.613935

B0BN93	SAWGQQPDLAANEAQLLR	**1.054308629**	2	4.055935
B0BN94	**F136A Protein FAM136A**	**0.937292468**	**0.99988**	**2**
B0BN94	CHAPLAQAQALVTSELER	**0.977849456**	2	3.155535
B0BN94	CSANCCEDNQASMQQVHQCIER	**0.877814909**	3	4.887235
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.001329174**	**0.00559**	**9**
B0BNE5	AFNGYLGPDQSK	**1.068747734**	2	3.454436
B0BNE5	AYDATCLVK	**1.096580425**	2	2.492888
B0BNE5	FAIYLPPQAESAK	**1.489652147**	2	3.34819
B0BNE5	LQEGYDHSYYFIATFITDHIR	**2.056340574**	3	3.807578
B0BNE5	MYSYVTEELPQLINANFPVDPQR	**0.985266975**	3	5.430045
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	**1.047359849**	2	5.709257
B0BNE5	SVSAFAPICNPVLCPWGK	**1.03341193**	2	4.041839
B0BNE5	SYSGPQIDILIDQGK	**1.221983611**	2	3.625741
B0BNE5	VFEHSSVELK	**0.916741432**	2	2.596017
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.685818556**	**0.71117**	**4**
B0BNN3	ADGLAIIGVLMK	**0.644505911**	2	3.155029
B0BNN3	GLLSSAEGEPAVPVLSNHRPPQPLK	**0.729987432**	3	3.38408
B0BNN3	HDSSLKPVSVSYNPATAK	**0.68939842**	3	4.418994
B0BNN3	VGPANPNLQK	**0.705284081**	2	2.923068
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**0.891246855**	**0.00414**	**3**
B0K020	AMVNLQIQK	**0.841577971**	2	2.36063
B0K020	HNEETGDNVGPLIIK	**0.832768223**	2	5.499594
B0K020	VVHAFDMEDLGDK	**0.891820721**	3	3.474493
B2GUY2	**TFR2 Transferrin receptor protein 2**	**1.223167784**	**0.11495**	**2**
B2GUY2	MEQRWGLLRK	**1.198949144**	2	2.307011
B2GUY2	SAVGTAILLELVR	**1.324663995**	2	2.440598
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.100177371**	**0.83605**	**2**
B2GV24	TYDLPGDFLTQALTQR	**1.09939197**	2	3.170732
B2GV24	VNIVDLQQVINVDLTHIENR	**0.903238924**	3	3.333813
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**0.838080551**	**0.95557**	**2**
B2RX88	SISSVNVDQVRMRNEDR	**0.832705649**	2	2.660302
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(11)	**0.923141425**		
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.769830913**	**8.9E-16**	**6**
B2RYW9	ALAAQLPLIPR	**0.777967726**	2	2.40873
B2RYW9	ATDVMAYVAGFTVAHDVSAR	**1.114801062**	3	3.825161
B2RYW9	GETALSVAR	**0.712168847**	2	2.424387
B2RYW9	KGDEVQCEIEELGVIINK	**0.717492914**	2	5.030748
B2RYW9	TFDTFCPLGPALVTK	**0.773575667**	2	4.608132
B2RYW9	VNGEIVQSSNTNQMVFK	**0.708393073**	2	2.63537
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**0.928958761**	**0.99017**	**4**
B3DMA2	AVLTVTQYR	**0.894725179**	2	2.528278
B3DMA2	LDNIVFHPK	**1.062034644**	2	2.452926
B3DMA2	NLPDSDNEECLVHGDFK	**1.107439394**	2	3.163522
B3DMA2	SGQSNPTFFLQK	**0.927671265**	2	2.794599
B3GNI6	**SEP11 Septin_11**	**0.947372005**	**0.01311**	**3**
B3GNI6	AAAQLLQSQAQQSGAQQTK	**1.207425924**	3	3.423206
B3GNI6	FESDPATHNEPGVR	**1.302644456**	2	3.341409
B3GNI6	SYELQESNVR	**0.772034336**	2	3.007154
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.299916125**	**2.1E-08**	**3**
B5DFC8	GTEITHAVVIK	**0.926416751**	2	2.370891
B5DFC8	GTTEEICQIYLR	**1.16109314**	2	2.366318
B5DFC8	TEPTAQQNLALQLAEK	**1.35626849**	2	4.94246

D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.04285872**	**0.69003**	**2**
D3ZTX0	QCFYEDITQGTK	**0.783946519**	2	2.487056
D3ZTX0	SVIDYQTHFR	**1.215077203**	2	2.505766
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.25980494**	**0.9162**	**4**
D3ZW55	IDLPEYQGEPDEISIQK	**1.029157933**	2	4.673555
D3ZW55	KLEEVIQILGDKFPCTLVAQK	**0.934460026**	3	4.068567
D3ZW55	LKPEGLYQLLAGFEDK	**1.287551872**	3	3.523536
D3ZW55	LQEYFGVTDGAGDH	**1.385790473**	2	3.564531
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.2062683**	**0.57141**	**2**
D3ZZL9	ELNQKLTNKNSK	**1.147278446**	2	2.375901
D3ZZL9	IKCLQEESVVQCEELR	**1.182722107**	2	2.355404
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.184550501**	**0.44535**	**2**
D4A4T9	KEEDSDEIKIGTSCK	**0.854126552**	2	2.317466
D4A4T9	LSSGNEEDKKEEDSDEIK	**1.185924704**	3	4.327742
E9Q557	**DESP Desmoplakin**	**0.756494509**	**0.38752**	**2**
E9Q557	KQVQTSQKNTLR	**0.678119938**	1	2.113665
E9Q557	SQCTQVVQER	**0.868925923**	2	2.316055
F6YLP3	**selenium transferase**	**1.112264616**	**0.82682**	**3**
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**0.885517409**	**9.9E-07**	**8**
O08557	DENATLDGGDVLFTGR	**0.667026443**	2	3.3439
O08557	DYAVSTVPVADSLHLK	**1.067580774**	2	3.654308
O08557	GAEILADTFK	**0.960090645**	2	2.425145
O08557	GAEILADTFKDYAVSTVPVADSLHLK	**0.801053076**	3	3.715405
O08557	SFCSMAGPNLIAIGSSESAQK	**0.747420444**	2	4.946534
O08557	SQGEEVDFAR	**0.806947554**	2	2.82503
O08557	TPEEYPESAK	**2.034987746**	2	2.823317
O08557	VDGLLTCCSVFINK	**1.078050759**	2	3.501412
O08583	**THOC4 THO complex subunit 4**	**0.722737651**	**2.6E-07**	**2**
O08583	QQLSAEELDAQLDAYNAR	**0.697631358**	2	5.05844
O08583	SLGTADVHFER	**0.863788392**	2	2.512042
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.193234243**	**0.1679**	**13**
O08601	EDTTMYLLALK	**0.877216409**	2	2.368634
O08601	EFYSYENEPVGIENLK	**1.357090867**	2	4.147633
O08601	GCPSLAEHWKSIR	**0.974991398**	2	3.732044
O08601	GSFASNDIR	**1.118577336**	2	2.506254
O08601	MLSASGDPVSVVK	**0.957107302**	2	3.050823
O08601	MLSASGDPVSVVK+Oxidation(0)	**0.904437521**		
O08601	NALLPEGIPLLLK	**1.204192113**	1	2.379188
O08601	NILLSIGELPK	**0.972301003**	2	3.57962
O08601	REEILQILK	**0.896799296**	3	3.545714
O08601	SDSSIILQER	**1.103633115**	2	3.298037
O08601	SGSSSAYTGYVER	**1.197191892**	2	3.423101
O08601	SNLNIFQYIGK	**1.125949765**	2	3.61238
O08601	VKEFYSYENEPVGIENLK	**1.127278508**	2	2.879602
O08795	**GLU2B Glucosidase 2 subunit beta**	**0.938407114**	**0.14324**	**6**
O08795	ETVVTSTTEPSR	**1.563059192**	2	3.109632
O08795	KLWEEQQAAAK	**0.967365365**	2	2.921249
O08795	LWEEQQAAAK	**0.802713046**	2	3.331707
O08795	MPPYDEETQAIIDAAQEAR	**0.945371082**	2	3.128101
O08795	SLEDQVETLR	**1.209623668**	2	3.260869
O08795	YEQGTGCWQGPNR	**1.1238668**	2	4.040441

O08810	**U5S1 116 kDa U5 small nuclear ribonucleoprotein component**	**1.015087021**	**0.10438**	**2**
O08810	GGGQIIPTAR	1.241941711	2	2.632741
O08810	GLAEDIENEVVQITWNR	0.686792156	3	3.569975
O09158	**CP3AP Cytochrome P450 3A25**	**1.314028893**	**0.99085**	**3**
O09158	DVEINGVFIPK	1.016835457	2	3.153576
O09158	TLLSPTFTSGK	1.156794817	1	1.937561
O09158	VDFLQLMMNTQNSK	1.018589614	2	2.839521
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**0.79412029**	**9.9E-20**	**16**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.811503481	2	5.840227
O09171	AGPWTPEAAVEHPEAVR	2.561704856	2	5.082752
O09171	AGSNVMQTFTFYASEDK	6.12039425	2	2.91907
O09171	AGSNVMQTFTFYASEDKLENR	17.45093416	2	4.506721
O09171	EATTEQQLR	1.294423188	2	2.40755
O09171	GAAELMQQK	2.176569434	2	3.57105
O09171	GAAELMQQK+Oxidation(5)	2.433986889		
O09171	HGSWGSGLDMHTKPWIR	3.596550966	3	3.705908
O09171	IFHQQLEVFMK	1.541958721	2	2.756684
O09171	KEYWQNLR	1.934805471	3	3.805479
O09171	LNAGEVVIGDGGFVFALEK	1.757169666	3	6.242911
O09171	QGFIDLPEFPFGLEPR	1.648059517	2	5.351922
O09171	QVADEGDALVAGGVSQTPSYLSCK	2.187970113	3	6.355076
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.821239631	3	6.552706
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9)	2.462221548		
O09171	VNEAACDIAR	1.933594026	2	4.035687
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.280828724**	**0.00014**	**10**
O09173	CFYNSDGDFLIVPQK	1.224805828	2	2.947672
O09173	FSVDVFEETR	1.417859777	2	3.188252
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.09397899	3	5.988619
O09173	LLIYTEFGK	1.536095941	1	2.054518
O09173	NCMSEFMGLIK	1.063801927	2	3.413135
O09173	QDVSPFNVVAWHGNYTPYK	1.41052999	2	3.647918
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	1.199911024	3	3.720453
O09173	SLRPGVAIADFVIFPPR	1.047915495	2	3.543944
O09173	TFRPPYYHR	1.3361239	3	3.340116
O09173	YISGFGNECASEDPR	1.493179678	2	3.992374
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.284000678**	**0.1477**	**19**
O35077	ANTIGISLIK	0.894096288	2	3.173305
O35077	DPAQGQLLK	1.499701492	2	2.412752
O35077	ELHSILQHK	1.491116082	1	2.950029
O35077	FCETTIGCK	1.11037561	2	2.629511
O35077	FCETTIGCKDPAQGQLLK	0.910048263	2	5.054601
O35077	GIDEGPNGLK	0.956613845	2	2.964919
O35077	GLVDKFPLFTAVYK	1.294252109	3	3.607473
O35077	ICDQLKGHLK	0.766003737	3	3.359608
O35077	ITVVQEVDTVEICGALK	0.805592035	3	4.424297
O35077	IVGSNASQLAHFDPR	1.208956836	2	3.143669
O35077	KLTEIINTQHENVK	0.890215936	2	5.103872
O35077	LISEVIGESLGIPMSVLMGANIASEVAEEK	0.747105573		
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	1.453944467	3	5.100658
O35077	LTEIINTQHENVK	0.916603246	2	4.516027
O35077	NIVAVGAGFCDGLGFGDNTK	0.967001649	2	5.425735
O35077	SIEQLEK	1.013481804	2	2.470503
O35077	VCIVGSGNWGSAIAK	0.916047791	2	4.706996

O35077	VCYEGQPVGEFICCLQNHPEHM	**0.999424325**	2	3.922442
O35077	VTMWVFEEDIGGR	**1.062478287**	2	3.467677
O35078	**OXDA D_amino_acid oxidase**	**0.727213055**	**0.08681**	**2**
O35078	GQIIQVEAPWIK	**0.625085145**	2	3.207431
O35078	SCCQLEPTLK	**0.995213562**	2	2.427518
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**1.003064328**	**2.5E-05**	**2**
O35094	KLEESDALQEAR	**0.820351722**	2	3.354514
O35094	TEMSEVLTEILR	**1.018005904**	2	3.566688
O35142	**COPB2 Coatomer subunit beta_**	**1.060685132**	**0.99983**	**4**
O35142	AAESLADPTEYENLFPGLK	**1.124355925**	2	3.363929
O35142	FELALQLGELK	**0.99701408**	2	3.043797
O35142	GSNNVALGYDEGSIIVK	**1.040219889**	2	3.587583
O35142	TFEVCDLPVR	**1.059370144**	2	2.770555
O35244	**PRDX6 Peroxiredoxin_6**	**1.128316243**	**0.52474**	**10**
O35244	DINAYNGAAPTEK	**0.893338994**	2	3.944559
O35244	DLAILLGMLDPAEKDEK	**1.023663414**	2	4.318313
O35244	FHDFLGDSWGILFSHPR	**0.7225943**	3	3.841123
O35244	GESVMVLPTLPEEEAK	**1.013758928**	2	3.181739
O35244	KGESVMVLPTLPEEEAK	**1.015009873**	2	4.874437
O35244	KGESVMVLPTLPEEEAK+Oxidation(5)	**1.190785841**		
O35244	LSILYPATTGR	**1.187910303**	2	2.876872
O35244	NFDEILR	**0.786307074**	2	2.440198
O35244	VVDSLQLTASNPVATPVDWK	**0.9684542**	3	5.764417
O35244	VVFIFGPDKK	**0.71566463**	2	2.385901
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.850445893**	**0.87902**	**2**
O35469	DLGYEPLVSWEEAK	**1.032439502**	2	4.225851
O35469	TSEWIGTLVEQHR	**0.818776495**	2	3.485808
O35509	**RB11B Ras_related protein Rab_11B**	**1.056600695**	**0.98591**	**5**
O35509	AQIWDTAGQER	**1.008927048**	2	2.84259
O35509	GAVGALLVYDIAK	**1.064217968**	2	4.216823
O35509	HLTYENVER	**0.957615073**	2	3.010223
O35509	NEFNLESK	**1.049200913**	1	2.14975
O35509	VVLIGDSGVGK	**1.053080685**	2	2.704652
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**0.608527427**	**2.5E-07**	**2**
O35547	LERFEIPIK	**0.581672981**	2	2.679689
O35547	LSPEPWTPETGLVTDAFK	**0.877062254**	2	2.728541
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.127820597**	**0.00883**	**8**
O35567	AEVSNAIDQYVTGTIGEGEDLVK	**0.835151059**	2	4.408747
O35567	ALFEEVPELLTEAEK	**1.20549037**	2	3.774465
O35567	DGQVIGIGAGQQSR	**0.919194678**	2	3.168031
O35567	EVSDGIVAPGYEEEALK	**0.945408435**	2	4.171121
O35567	HVSPAGAAVGVPLSEDEAR	**1.327276844**	2	3.510359
O35567	RAEVSNAIDQYVTGTIGEGEDLVK	**1.014065013**	3	3.74148
O35567	SGVAYIVAPSGSTADK	**1.166481831**	2	3.097062
O35567	VTVVCEPEDYGAVAAEMQGSGNK	**0.734666646**	2	5.278191
O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**0.782210252**	**0.07081**	**2**
O35593	AVAVVVDPIQSVK	**1.153567963**	2	2.712783
O35593	VIDVFAMPQSGTGVSVEAVDPVFQAK	**0.362164912**	2	3.74656
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**0.706688299**	**0.98075**	**2**
O35660	RYAMGDAPDYDR	**0.763036097**	2	3.130999
O35660	YAMGDAPDYDR+Oxidation(2)	**0.659048721**		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.857153796**	**1**	**3**

O35760	AELGIPLEEVDLNEMNYLTR	0.945987059	2	4.26437
O35760	NCHLNENIDK	0.749918381	2	2.988859
O35760	NVTLNPDPNEIK	0.871523298	2	2.89706
O35763	**MOES Moesin**	**0.738146059**	**2.8E-08**	**2**
O35763	ALTSELANAR	0.74501384	2	3.170505
O35763	FYPEDVSEELIQDITQR	0.658950556	2	4.400842
O35783	**CALU Calumenin**	**1.231530268**	**0.6078**	**2**
O35783	HLVYESDQDKDGK	1.236769876	2	4.045784
O35783	VHNDAQNFDYDHDAFLGAEEAK	0.854677032	3	4.150329
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.056365945**	**0.32795**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	1.016058905	2	4.698423
O35796	AFVEFLTDEIK	1.201550638	2	3.625874
O35796	AFVEFLTDEIKEEK	0.994515469	2	3.572408
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.541135439	3	5.770348
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.075418649**	**0.96034**	**6**
O35814	ALDLDSSCK	1.11148124	2	2.366043
O35814	ALSAGNIDDALQCYSEAIK	1.07452047	2	5.29577
O35814	DCEECIQLEPTFIK	0.952622692	2	3.933009
O35814	ELIEQLQNKPSDLGTK	1.073248061	2	3.866702
O35814	LDPQNHVLYSNR	2.314971629	2	2.613568
O35814	LMDVGLIAIR	0.985611661	2	2.451773
O35820	**RCL Deoxyribonucleoside 5__monophosphate N_glycosidase**	**1.025949717**	**0.83052**	**2**
O35820	GGREDQALYAR	1.01766043	2	2.559
O35820	YFEAYLPQK	1.096026454	2	2.334074
O35821	**MBB1A Myb_binding protein 1A**	**1.605676664**	**0.01618**	**2**
O35821	ALDLIEVLVTK	1.564746839	2	3.055256
O35821	NVANVTPLTAQQR	1.636918202	2	3.027622
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**0.794346625**	**0.02734**	**2**
O35824	FDVQFPENNWINPDK	0.535858608	2	3.291251
O35824	NVLCSACSGQGGK	1.126902393	2	3.272644
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**0.856821256**	**0.44842**	**8**
O35826	DEAVGALHLIQAAK	1.038983348	2	3.47456
O35826	EVGAFGTPVINLGTR	0.939552394	2	2.864459
O35826	GEDEAAMVESVGLALVK	1.188771944	2	2.453385
O35826	IYGDGNAVPR	0.710211185	2	2.577689
O35826	SIDLQEPLQK	0.912547343	2	2.373598
O35826	TLVLFPNIDAGSK	0.7846299	2	3.097761
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	0.770478776	3	5.235929
O35826	VNPQEGVVLHSTK	1.208824549	2	2.547785
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**1.10937315**	**7.4E-05**	**5**
O35913	EGLQENVDGTENAK	0.929684946	2	3.668488
O35913	GASFVPAFFILR	0.818886363	2	2.699051
O35913	ILAGIPAPIYFGALIDR	0.968270419	2	2.415658
O35913	SLSGTYMNSMLTQIER	0.646585867	2	4.259255
O35913	SQTLNPTQDPSECVK	0.677662708	2	4.175505
O35923	**BRCA2 Breast cancer type 2 susceptibility protein homolog**	**0.58044688**	**0.04679**	**2**
O35923	AMKLFSDIENISEEPSTK	0.63333495	2	2.552217
O35923	SLLNEFDRIIESKGK	0.580420809	2	2.423902
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**0.891127744**	**4.6E-07**	**8**
O35952	ALLEVLGR	0.790442146	2	3.120642
O35952	FYEGTADEMYK	0.695166139	2	2.516407

O35952	HVEPGNTAVQEK	1.079665736	2	4.055639
O35952	LTTVLTTHHHWDHAGGNEK	0.713827342	3	3.913594
O35952	NAIGEPTVPSTLAEEFTYNPFMR	0.898955239	2	3.547781
O35952	TVQQHAGETDPVTTMR	0.809407347	2	5.104128
O35952	TVQQHAGETDPVTTMR+Oxidation(14)	0.930482631		
O35952	VTHLSTLEVGSLSVK	0.713291842	2	2.883583
O35987	**NSF1C NSFL1 cofactor p47**	**1.112449712**	**0.11636**	**6**
O35987	ASSSILINEAEPTTNIQIR	0.897962563	2	5.336307
O35987	EANLLNAVIVQR	1.490420682	2	3.370299
O35987	LGAAPEEESAYVAGER	1.165393133	2	4.021342
O35987	LGSTAPQVLNTSSPAQQAENEAK	0.989216039	2	3.968664
O35987	RGEVPAELR	3.217380024	2	2.471083
O35987	SYQDPSNAQFLESIR	0.991953509	2	4.488661
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.735997713**	**0.0776**	**3**
O54753	CSTNLSLVTDCMEHALTSK	2.737127511	3	3.395102
O54753	TWEATPEHIR	1.905864726	2	2.310511
O54753	YGVEAFSDVLR	1.69606476	2	2.727089
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.066499943**	**0.43342**	**2**
O54975	GSLTFEPLTLVPIQTK	1.134261887	2	4.041873
O54975	IENVVLVVPAK	0.907581317	2	2.895174
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.114819764**	**0.93734**	**5**
O55012	ATTLSNAVSSLASTGLSLTK	1.169123432	2	3.839085
O55012	ITAAQHSVTGSAVSK	1.265730492	2	4.302684
O55012	NTLFNLSNFLDK	1.145497666	2	2.540184
O55012	SGLQGYDMSTFIR	1.189371515	2	2.361617
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	0.929662054	3	5.658778
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.194892996**	**0.77592**	**6**
O55096	AGLLALEFYTPETANWR	1.276608414	2	3.922763
O55096	GEFEGFVAMVNK	1.116928678	2	3.075861
O55096	LASVLNTEPALDSELTSK	1.386637195	2	3.384279
O55096	NVSLGNVLAVAYATK	1.089039845	2	2.38712
O55096	SYEFQGNHFQVTR	1.133364166	2	3.819559
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	1.057670998	3	3.402171
O55125	**NIPS1 Protein NipSnap homolog 1**	**0.969717395**	**0.84161**	**4**
O55125	AGPNIYELR	0.898560336	2	3.04349
O55125	FSGGYPALMDCMNK	0.978140838	2	3.133015
O55125	GWDENVYYTVPLVR	1.669342065	2	3.458383
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.159149514	3	4.36804
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**0.908213061**	**0.49601**	**6**
O55171	ADAGGELDLAR	0.75048238	2	3.276752
O55171	DGLLDVVEALQSPLVDKK	0.959461123	2	5.071033
O55171	DVQKPYVVELEVLDGHEPDGGQR	0.912858163	3	4.466774
O55171	GGELGLAMASFLK	0.767331058	2	3.847528
O55171	IEYFEEAVNYLR	0.932417752	2	4.191815
O55171	SCWDEPLSITVR	0.943689484	2	3.49113
O70127	**ABCBB Bile salt export pump**	**1.363487942**	**9.8E-06**	**8**
O70127	AGQITSEALSNIR	1.466428613	2	3.288379
O70127	AGSIADEVLSSIR	1.586927135	2	2.639027
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.337991445	3	4.16927
O70127	ILLLDEATSALDTESEK	1.352573812	2	4.181277
O70127	KFGEENHAFESDGSHNNDKK	0.919363725	3	3.933345
O70127	KPPINVYSEAGEK	2.426099388	2	3.316954
O70127	STALQLIQR	1.567065863	2	2.350636
O70127	YETNVGIQGSQLSR	1.122132032	2	3.46657

O70133	**DHX9 ATP_dependent RNA helicase A**	**1.014089659**	**0.50517**	**2**
O70133	KMTPAYEIRAVGNK	**0.698688669**	2	2.565521
O70133	YPSPFFVFGEKIR	**1.05824656**	2	2.500704
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**0.956238135**	**0.99918**	**11**
O70199	EQIVVDLSHPGVSADDQVSR	**0.941652355**	2	5.671396
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	**1.076840544**	3	5.211238
O70199	IIDSLFNTVTDK	**1.008459381**	2	2.87754
O70199	IIDSLFNTVTDKK	**0.923273566**	2	3.543528
O70199	ILTTNTWSSELSK	**1.262565504**	2	3.342861
O70199	INAWNSPTLPIYEPGLK	**1.040791177**	2	3.728618
O70199	NLFFSTNIDDAIR	**1.151599394**	2	3.147455
O70199	VLDGLHNELQTIGFQIETIGK	**0.907967298**	2	5.335101
O70199	VLIGGDETPEGQR	**0.997658483**	2	3.616722
O70199	VTVVDVNEAR	**0.962250321**	2	3.363352
O70199	YWQQVIDMNDYQR	**0.862538399**	2	4.833843
O70251	**EF1B Elongation factor 1_beta**	**1.130202121**	**2.2E-05**	**4**
O70251	SIQADGLVWGSSK	**1.049352227**	2	3.765084
O70251	SSILLDVKPWDDETDMTK	**1.001869888**	2	4.20245
O70251	SSILLDVKPWDDETDMTKLEECVR	**0.758614305**	3	5.13022
O70251	TPAGLQVLNDYLADK	**1.624573483**	2	4.095759
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**0.755201409**	**8.7E-09**	**16**
O70351	GGIVGMTLPIAR	**0.697403583**	2	3.356582
O70351	GLVAVITGGASGLGLSTAK	**0.797246842**	2	4.690108
O70351	GVIINTASVAAFEGQVGQAAYSASK	**1.173932076**	3	4.100465
O70351	IDVAVNCAGIAVAIK	**0.727137228**	2	3.977468
O70351	KLGGNCIFAPANVTSEK	**0.911558255**	2	4.468948
O70351	KNQVHTLEDFQR	**0.815387183**	2	4.114242
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	**0.894240124**	3	4.315888
O70351	LGGNCIFAPANVTSEK	**0.945971805**	2	3.486175
O70351	LVAGVMGQNEPDQGGQR	**0.863276894**	2	5.227586
O70351	LVAGVMGQNEPDQGGQR+Oxidation(5)	**0.610411813**		
O70351	LVGQGATAVLLDVPNSEGETEAK	**1.159443528**	2	5.67453
O70351	NFLASQVPFPSR	**0.837561772**	2	4.559295
O70351	NQVHTLEDFQR	**0.846293476**	2	3.310391
O70351	RLVGQGATAVLLDVPNSEGETEAK	**0.877013105**	2	5.040431
O70351	VINVNLIGTFNVIR	**0.770413502**	2	3.79679
O70351	VVTIAPGLFATPLLTTLPDK	**0.896468775**	2	5.420006
O70456	**1433S 14_3_3 protein sigma**	**1.301264591**	**3.2E-12**	**3**
O70456	DSTLIMQLLR	**1.555278708**	2	3.412398
O70456	DSTLIMQLLR+Oxidation(5)	**1.421197344**		
O70456	VLSSIEQK	**1.017683396**	2	3.254664
O70593	**SGTA Small glutamine_rich tetratricopeptide repeat_containing protein alpha**	**1.460731704**	**0.01411**	**2**
O70593	AIELNPANAVYFCNR	**1.226757245**	2	3.002361
O70593	TPPSEEDSAEAER	**1.486104341**	2	2.710049
O88202	**LPP60 60 kDa lysophospholipase**	**1.027331477**	**0.99718**	**2**
O88202	AAGAHLSPQELEDVGTELCR	**0.957591475**	3	3.690825
O88202	GVDVDACNEDGQSPLLLAVR	**0.962307238**	2	5.224089
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**0.867620383**	**0.971**	**5**
O88428	GCTVWLTGLSGAGK	**0.838167104**	2	2.848485
O88428	GIHELFVPENK	**1.008925332**	2	2.611675
O88428	NLGFSAGDREENIR	**0.874396703**	2	3.361606
O88428	STNVVYQAHHVSR	**0.916997217**	2	3.474065
O88428	VLSMAPGLTSVEIIPFR	**0.830035029**	2	3.316246

O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**0.745156412**	**0.00074**	**2**
O88491	ENSEGAFGVLLPADAVQKAR	**0.544641626**	2	2.344276
O88491	SGKGEGLKLLNNMHEK	**1.379042451**	2	2.906617
O88600	**HSP74 Heat shock 70 kDa protein 4**	**1.05628417**	**0.91478**	**14**
O88600	AESEEMETSQAGSK	**1.018018743**	2	4.514785
O88600	AGGIETIANEYSDR	**0.920448308**	2	3.463859
O88600	FQESEERPK	**0.324914988**	2	2.328101
O88600	GCALQCAILSPAFK	**0.980880952**	2	4.046768
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	**1.204910535**	3	5.239132
O88600	LKETAESVLK	**0.672384849**	2	2.464055
O88600	MIMQDKLEK+Oxidation(0)	**0.956823766**		
O88600	MQVDQEEPHTEEQQPQTPAENK	**1.215778655**	3	4.74823
O88600	NFTTEQVTAMLLSK	**1.061669756**	2	3.705788
O88600	SNLAYDIVQLPTGLTGIK	**1.035516915**	2	4.945822
O88600	SVMDATQIAGLNCLR	**0.820295658**	2	2.889576
O88600	TSTVDLPIESQLLWQLDR	**0.895282141**	2	3.834906
O88600	VLATAFDTTLGGR	**0.940323507**	2	3.479396
O88600	WNSPAEEGSSDCEVFPK	**0.730826424**	2	3.414482
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.145835095**	**1.8E-08**	**21**
O88618	AFAACLGAIK	**0.929053606**	2	2.889683
O88618	AGEYEALPEK	**1.053181116**	2	2.863834
O88618	ALLDAAAFYCDK	**1.410492307**	2	3.467166
O88618	ALLDAAAFYCDKEK	**0.901637003**	2	3.33453
O88618	EAQELNLPVVGSQLVGLVPLK	**1.350241841**	3	4.043879
O88618	GVSMDECVLCAK	**1.278743609**	2	3.906974
O88618	IIEYLVPDSGPEQSLLDASLR	**1.195223888**	2	5.133275
O88618	ISSLLQEAK	**1.279441659**	2	2.711395
O88618	LAEELNVPVYLYGEAAQMPSR	**1.38963452**	2	4.975207
O88618	LAETVSQLWPALQELAQCGNLSCLSDLQVAAK	**1.313044978**	4	5.012574
O88618	LFVLEEEHR	**0.722399629**	2	2.766589
O88618	LGLDSLAPFDPK	**1.027937816**	2	3.640337
O88618	LIPPFHAASAQLTSLVDADAR	**1.254192349**	3	3.554824
O88618	MGALDVCPFIPVR	**0.973784863**	2	3.794453
O88618	MGALDVCPFIPVR+Oxidation(0)	**0.79948126**		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	**1.296062491**	3	4.505769
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	**1.307474108**	2	4.156594
O88618	TCALQEGLR	**1.322006578**	2	2.87365
O88618	TQAALVLGSLEAR	**1.063141012**	2	5.065959
O88618	TVYTFVGQPECVVEGALSAAR	**2.205043027**	2	4.854225
O88618	VQGIGWYLEEK	**1.14667367**	2	3.182912
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.008214521**	**0.63208**	**5**
O88637	GPPVFTQEER	**1.028177344**	2	2.73447
O88637	HKGPPVFTQEER	**1.052898993**	2	2.624393
O88637	TQGVSTTDLVGR	**1.29631068**	2	2.771423
O88637	WVDEVVPAAPYVTTLETLDK	**1.068550278**	2	3.142456
O88637	YVSEVVIGAPYSVTAELLNHFK	**1.234762384**	3	3.425522
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**0.892723296**	**0.97543**	**2**
O88656	ASSEGGAATGAGLDSLHK	**0.891738412**	2	4.384912
O88656	NSVSQISVLSGGK	**1.067017439**	2	2.447628
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**0.970243273**	**0.99928**	**2**
O88696	GQATDIAIQAEEIMK	**0.945503359**	2	3.618744
O88696	VLVHPPQDGEDEPELVQK	**0.985049611**	3	4.499228
O88746	**TOM1 Target of Myb protein 1**	**0.925598231**	**0.64577**	**3**

O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	**0.908221321**	3	5.876241
O88746	QQSTGAIPATQAR	**1.186963371**	2	2.614947
O88746	YEAPQTTDGLAGALDAR	**1.048663405**	2	4.199483
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**0.792119108**	**0.7223**	**4**
O88761	DTSEDIEELVEPVAAHGPK	**0.80020931**	2	3.818461
O88761	QCVENADLPEGEK	**0.974445603**	2	2.501987
O88761	TPEQCPSVVSLLSESYNPHVR	**1.451399405**	3	4.438766
O88761	TVGTPIASVPGSTNTGTVPGPEK	**0.971461965**	2	3.733288
O88767	**PARK7 Protein DJ_1**	**0.860917226**	**3E-05**	**6**
O88767	DVVICPDTSLEEAK	**1.165077872**	2	3.31286
O88767	GAEEMETVIPVDIMR	**0.733155327**	2	4.050001
O88767	GAEEMETVIPVDIMR+Oxidation(13)	**0.749613971**		
O88767	GLIAAICAGPTALLAHEVGFGCK	**0.969031452**	2	4.897345
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	**0.868768467**	2	4.723402
O88767	VTVAGLAGKDPVQCSR	**0.76076478**	2	4.445266
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**0.842127751**	**0.58465**	**2**
O88794	KKNEELGQLYR	**1.098140563**	2	2.779869
O88794	SSQIGAVVSR	**0.840822116**	2	2.89101
O88801	**HOME2 Homer protein homolog 2**	**0.651788309**	**0.05382**	**2**
O88801	EKEMELK	**0.999574806**	1	2.10689
O88801	EKNTQLK	**0.42500871**	1	2.020127
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**0.911497097**	**0.0001**	**15**
O88813	AILEDLQK	**0.907294339**	1	2.423197
O88813	ATMLIENVEK	**0.99894775**	2	2.370865
O88813	ATMLIENVEKDLTPGLK	**1.069771844**	2	2.451185
O88813	ATMLIENVEKDLTPGLK+Oxidation(2)	**0.818417861**		
O88813	FFQTQIK	**0.774817907**	1	1.991065
O88813	GLAVSDNGPCLGYR	**0.889827403**	2	3.810367
O88813	GSFEELCQNQCVK	**0.836544109**	2	4.287456
O88813	IGFFQGDIR	**1.022118441**	2	3.321431
O88813	LVQGVIFSCGGK	**1.333939748**	2	2.866491
O88813	NNDLILYYFSDAK	**1.576295793**	2	3.724621
O88813	SFLIGVVVPDPESLPSFAAK	**0.70896247**	2	4.330254
O88813	SIFVHPEPFSIENGLLTPTLK	**1.762372671**	2	3.032535
O88813	SRPILQVFVHGESLR	**0.528757702**	3	3.86181
O88813	TQEVLDKDGWLHTGDIGR	**0.682176927**	3	4.391942
O88813	TVILMDPFDDDLMK	**0.696927193**	2	3.128828
O88867	**KMO Kynurenine 3_monooxygenase**	**0.91689247**	**4.3E-05**	**4**
O88867	AVGLEDQIVSK	**0.732596671**	2	2.654234
O88867	DLLTAVESYPNAK	**1.537726616**	2	2.792644
O88867	NFPDAIPLMGEQALMR	**0.977955521**	2	2.862323
O88867	NFQVDVYEAR	**0.969142886**	2	2.888409
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.021257797**	**0.83058**	**4**
O88941	DLALPTLLNPK	**1.061325692**	2	2.529927
O88941	DQASEQLVGGQLTR	**1.076221809**	2	2.905201
O88941	LGPLLDVLADSR	**0.950758625**	2	3.293821
O88941	MDPSLFPPVPLFSGVPSR	**0.984926137**	2	2.71819
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**0.635522697**	**0.07681**	**2**
O88986	GTDELLGVMDQVTIINSTLGK	**0.699064836**	2	3.31637
O88986	HLDMADLEAK	**0.530767878**	2	2.315195
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**0.935537646**	**0.83817**	**8**
O88989	DLDVAVLVGSMPR	**1.385851835**	3	4.05575
O88989	ELTEEKETAFEFLSSA	**1.810139783**	2	3.703944
O88989	EVGVYEALKDDSWLK	**1.219022729**	2	3.752205
O88989	FVEGLPINDFSR	**0.919030994**	2	3.630882

O88989	GEFITTVQQR	1.082357383	2	4.270136
O88989	LGVTADDVK	1.013959573	2	2.85596
O88989	NVIIWGNHSSTQYPDVNHAK	1.023078608	2	5.619033
O88989	VIVVGNPANTNCLTASK	1.092817458	2	5.389115
O88990	**ACTN3 Alpha_actinin_3**	**1.000553274**	**3.3E-05**	**12**
O88990	AGTQIENIEEDFR	0.902777712	2	3.579388
O88990	CQAICDQWDNLGTLTQK	0.689913888	2	5.168026
O88990	CQLEINFNTLQTK	1.093485292	2	4.118224
O88990	FAIQDISVEETSAK	0.769131979	2	3.664222
O88990	GKEEMLNQHDYESASLQEVR	1.028743603	3	4.784576
O88990	GLSQEQLNEFR	0.952156102	2	2.608653
O88990	HEAFESDLAAHQDR	1.124902822	3	4.498434
O88990	RHEAFESDLAAHQDR	0.836708232	3	4.798569
O88990	SGNPYITLSSQDINNK	1.188927996	2	3.802952
O88990	VEHIAALAQELNELDYHEAASVNSR	0.766436709	3	4.124232
O88990	VGWEQLLTSIAR	0.939267878	2	2.563041
O88990	VLAVNQENEK	1.327180737	2	2.490795
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.719992417**	**0.01067**	**2**
O88994	CVLTTVDPDTGIIDR	0.641893075	2	4.111473
O88994	RQLQQVGTVSK	0.840188799	2	2.502644
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**0.884966747**	**0.88406**	**7**
O89000	EGGADGVTATNTVSGLMGLK	0.919779494	2	3.829697
O89000	GAVIVLGAGDTAFDCATSALR	0.890217561	2	2.314921
O89000	GMGLACGQDPELVR	0.828608325	2	3.188407
O89000	GTTSGPLYGPGQSSFLNIELISEK	1.209405825	2	3.519427
O89000	LTPNVTDIVSIAR	1.148490984	2	2.349785
O89000	QEYVGGLSTSEIPQFR	0.921047401	2	3.621115
O89000	TEQDETGNWVEDEEQIVR	0.97098059	2	4.719432
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.221180871**	**0.02366**	**2**
O89032	DDSDINTSKTGEVSKR	1.31526441	2	2.547387
O89032	EGWAPASYIDKRK	0.944539148	1	1.973449
O89046	**COR1B Coronin_1B**	**0.891472646**	**6E-06**	**3**
O89046	NDQCYEDIR	0.823566862	2	2.82929
O89046	NVLSDSKPAGYSR	1.072948409	2	3.129846
O89046	SGVSTATAITDIPSGNLAGSGEAGK	0.54722603	2	3.814561
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.055705342**	**0.5054**	**6**
O89049	IEQIEAGTPGR	1.035110401	2	3.420818
O89049	IEQIEAGTPGRLK	1.097253527	2	2.45242
O89049	LELTPVAIQAGR	1.106780543	2	2.66957
O89049	STNSEETIEDEFNTVLLAVGR	1.130879551	2	4.228694
O89049	VVGFHVLGPNAGEVTQGFAAALK	0.879717882	3	4.035128
O89049	WGLGGTCVNVGCIPK	0.886505073	2	2.922061
P00173	**CYB5 Cytochrome b5**	**1.035885335**	**0.34418**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	0.933688785	2	5.440202
P00173	FLEEHPGGEEVLR	0.907499272	2	4.331065
P00173	STWVILHHK	0.730174022	2	2.793056
P00173	TYIIGELHPDDR	0.913819135	2	4.244727
P00173	VYDLTK	0.917014266	1	2.135064
P00173	YYTLEEIQK	0.932977192	2	3.017815
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.792868753**	**3E-14**	**12**
P00388	DGALTQLNVAFSR	0.844765033	2	2.418118
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.777278179	3	4.795228
P00388	FAVFGLGNK	2.259010656	2	2.508693
P00388	GMSADPEEYDLADLSSLPEIDK	1.584070265	2	5.055513

P00388	GVATSWLR	**1.924419959**	2	2.336932
P00388	LEQLGAQR	**1.708180173**	2	2.640414
P00388	NIIVFYGSQTGTAEEFANR	**2.340342155**	2	3.17912
P00388	RSDEDYLYR	**1.212042705**	2	3.364368
P00388	SDEDYLYR	**1.387061345**	2	2.608301
P00388	SYENQKPPFDAK	**1.537465615**	2	3.25428
P00388	TALTYYLDITNPPR	**1.112698712**	2	2.506228
P00388	TNVLYELAQYASEPSEQEHLHK	**2.528857259**	3	3.685663
P00406	**COX2 Cytochrome c oxidase subunit 2**	**0.879652459**	**0.11077**	**5**
P00406	ILYMMDEINNPVLTVK	**0.560962002**	2	2.307731
P00406	LLEVDNR	**1.090140293**	2	2.52598
P00406	MLISSEDVLHSWAIPSLGLK	**0.419475793**	2	3.570268
P00406	VVLPMELPIR	**0.789094165**	2	2.680752
P00406	VVLPMELPIR+Oxidation(4)	**1.27173405**		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**0.811553853**	**9.9E-20**	**16**
P00481	FGMHLQAATPK	**0.686665951**	3	4.129622
P00481	GEYLPLLQGK	**0.74025266**	2	3.211051
P00481	GGNVLITDTWISMGQEDEK	**0.79079298**	2	4.995953
P00481	GGNVLITDTWISMGQEDEKK	**0.85674307**	2	4.640275
P00481	GLTLSWIGDGNNILHSIMMSAAK	**0.818800361**	2	4.19529
P00481	GYEPDPNIVK	**0.800315747**	2	2.69013
P00481	KPEEVDDEVFYSPR	**1.239695032**	2	3.52652
P00481	LQAFQGYQVTMK	**0.842943651**	2	3.839989
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	**0.744891499**	3	5.761353
P00481	QKGEYLPLLQGK	**0.738372089**	2	2.994097
P00481	SLGMIFEK	**0.581647805**	2	2.441405
P00481	SLVFPEAENR	**0.839310776**	2	2.649328
P00481	SLVFPEAENRK	**0.733240036**	2	2.95112
P00481	VLSSMTDAVLAR	**0.686896485**	2	3.980601
P00481	VLSSMTDAVLAR+Oxidation(4)	**0.95382377**		
P00481	YGKPVQSQVQLK	**0.360824808**	2	3.004725
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.68033713**	**0.33959**	**2**
P00502	FIQSPEDLEK	**0.416852362**	2	2.587286
P00502	WLLAAAGVEFDEK	**0.683937631**	2	4.326678
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.061362787**	**9.9E-20**	**18**
P00507	ASAELALGENSEVLK	**0.884619266**	2	4.698341
P00507	DAGMQLQGYR	**1.59749452**	2	3.039075
P00507	DDNGKPYVLPSVR	**1.048667293**	2	2.740834
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	**1.521949756**	3	5.41396
P00507	EYLPIGGLADFCK	**1.109539801**	2	2.819358
P00507	FVTVQTISGTGALR	**0.819479888**	2	5.039452
P00507	HFIEQGINVCLCQSYAK	**0.765582361**	2	4.522585
P00507	IAATILTSPDLR	**1.643636647**	2	3.093737
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	**1.573377352**	3	4.310308
P00507	ISVAGVTSGNVGYLAHAIHQVTK	**0.496526373**	2	4.782934
P00507	KQWLQEVK	**0.507655833**	1	2.138605
P00507	MNLGVGAYR	**0.814749541**	2	2.934601
P00507	NLDKEYLPIGGLADFCK	**0.777434697**	2	5.338366
P00507	NMGLYGER	**0.802177016**	2	2.506797
P00507	TCGFDFSGALEDISK	**0.932330418**	2	4.821503
P00507	TQLVSNLK	**0.833465261**	2	2.961006
P00507	VGAFTVVCK	**0.929922324**	2	3.367226
P00507	VGASFLQR	**1.030824742**	2	3.004443
P00564	**KCRM Creatine kinase M_type**	**0.938875299**	**1**	**11**
P00564	DLFDPIIQDR	**1.445887648**	2	2.490117

P00564	FEEILTR	1.028520339	2	2.469936
P00564	GGDDLDPNYVLSSR	0.712971585	2	4.798523
P00564	GQSIDDMIPAQK	0.676921313	2	3.37611
P00564	GTGGVDTAAVGAVFDISNADR	0.886652516	2	6.067082
P00564	LGSSEVEQVQLVVDGVK	0.94853363	2	4.918209
P00564	LSVEALNSLTGEFK	1.005352908	2	4.338848
P00564	RGTGGVDTAAVGAVFDISNADR	0.895069693	2	5.883774
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	0.897349825	3	5.872811
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR+Oxidation(1)	0.983421126		
P00564	TDLNHENLK	1.103563569	2	2.529152
P00787	**CATB Cathepsin B**	**0.893644046**	**0.64852**	**5**
P00787	GENHCGIESEIVAGIPR	0.886492004	2	4.52138
P00787	HEAGDVMGGHAIR	0.895166841	3	3.560832
P00787	HEAGDVMGGHAIR+Oxidation(6)	1.335806433		
P00787	MCEAGYSTSYKEDK	1.136869028	2	3.880888
P00787	NGPVEGAFTVFSDFLTYK	1.485252985	2	3.26154
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.211253973**	**9.9E-20**	**19**
P00884	ALQASALAAWGGK	1.097341834	2	4.860201
P00884	ATQEAFMK	1.127588178	2	2.609433
P00884	ATQEAFMK+Oxidation(6)	1.472856227		
P00884	ELLFSVDNSISQSIGGVILFHETLYQK	2.287366326	3	3.794712
P00884	ELSEIAQR	3.635972447	1	2.115321
P00884	ETTIQGLDGLSER	1.358057093	2	4.025199
P00884	GILAADESVGTMGNR	0.990181935	2	5.584123
P00884	GILAADESVGTMGNR+Oxidation(11)	1.375384542		
P00884	GIVVGIKLDQGGAPLAGTNK	1.395878402	2	3.465734
P00884	IKVENTEENR	1.535970132	2	2.478102
P00884	IKVENTEENRR	2.251555549	2	2.923598
P00884	ISDQCPSSLAIQENANALAR	1.101132167	2	6.218312
P00884	KELSEIAQR	1.077121482	2	2.843675
P00884	KYTPEQVAMATVTALHR	0.858204152	3	5.706024
P00884	KYTPEQVAMATVTALHR+Oxidation(8)	0.987595718		
P00884	LDQGGAPLAGTNK	1.044456539	2	4.596908
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	2.218863099	3	4.999493
P00884	YTPEQVAMATVTALHR	0.937180044	2	4.5543
P00884	YTPEQVAMATVTALHR+Oxidation(7)	0.832835903		
P01015	**ANGT Angiotensinogen**	**1.537626526**	**2E-06**	**3**
P01015	GSYNLQDLLAQAK	1.537726616	2	2.80368
P01015	SLDLSTDPVLAAQK	1.262791565	2	3.317123
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	1.793605762	2	3.915774
P01026	**CO3 Complement C3**	**1.393987277**	**6E-05**	**17**
P01026	AAVFNHFISDGVK	1.246708804	2	2.354795
P01026	ACEPGVDYVYK	1.436121664	2	2.57538
P01026	ADIGCTPGSGK	1.25583878	2	2.841699
P01026	DSCVGTLVVKGDPR	0.874808536	2	2.409441
P01026	EYVLPSFEVLVEPTEK	1.104156501	2	3.254046
P01026	IFTVDNNLLPVGK	1.099001278	2	3.105247
P01026	IGLQEVEVK	0.961369681	2	2.38234
P01026	RVPVVTQGSDAQALTQDDGVAK	1.118963168	3	5.53011
P01026	SGIPIVTSPYQIHFTK	2.032653638	2	3.209617
P01026	SGSDEVQAGQER	1.748139626	2	4.084831
P01026	SSVAVPYVIVPLK	1.582155552	2	3.151322
P01026	TVLTGATGHLNR	1.154834647	2	3.09662
P01026	VELKPGDNLNVNFHLR	1.063219523	3	5.341079
P01026	VHQFFNVGLIQPGSVK	1.727194214	3	3.971458
P01026	VLIEDGSGEAVLSR	1.115532119	2	4.530239

P01026	VPVVTQGSDAQALTQDDGVAK	1.371018105	2	5.903897
P01026	VTIKPAPETAK	1.384258458	2	2.535371
P01048	**KNT1 T_kininogen 1**	**0.703176317**	**0.56454**	**2**
P01048	FSVATQICNITPGK	0.974495445	2	2.843359
P01048	TELTADCETK	0.290872829	2	2.379227
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.642327018**	**0.99997**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	0.767038806	3	7.326679
P01946	FLASVSTVLTSK	0.658351598	2	3.902756
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	0.653501964	4	4.653927
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.680597335	4	6.330357
P01946	IGGHGGEYGEEALQR	0.775512339	3	4.870887
P01946	LRVDPVNFK	0.678717159	2	2.583225
P01946	MFAAFPTTK	0.735487382	2	2.745217
P01946	MFAAFPTTK+Oxidation(0)	0.604522456		
P01946	TYFSHIDVSPGSAQVK	0.761251411	2	5.175354
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.680043587**	**0.99976**	**4**
P02089	GTFASLSELHCDK	0.783741157	2	3.178641
P02089	LHVDPENFR	0.734002845	2	2.633535
P02089	YFDSFGDLSSASAIMGNPK	0.67951808	2	6.343416
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14)	0.74933554		
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.532180514**	**0.96184**	**9**
P02091	AAVNGLWGK	2.052200395	2	2.593747
P02091	EFTPCAQAAFQK	0.835427186	2	2.991656
P02091	GTFAHLSELHCDK	0.870699823	2	4.274859
P02091	GTFAHLSELHCDKLHVDPENFR	0.492116816	3	3.483479
P02091	KVINAFNDGLK	0.842255012	3	3.681827
P02091	LLGNMIVIVLGHHLGK	0.699039662	4	4.798428
P02091	VINAFNDGLK	0.769959315	2	2.89435
P02091	VNPDDVGGEALGR	0.771520139	2	4.027888
P02091	VVAGVASALAHK	0.86455615	2	3.613917
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.159284681**	**1.9E-10**	**6**
P02401	ILDSVGIEADDER	1.048119614	2	4.597485
P02401	KILDSVGIEADDER	0.839905332	2	3.830423
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.101024253	3	6.306197
P02401	NIEDVIAQGVGK	1.054962239	2	4.722207
P02401	VISELNGK	1.131227052	1	2.054207
P02401	YVASYLLAALGGNSNPSAK	1.347103972	2	4.930248
P02563	**MYH6 Myosin_6**	**0.884353831**	**0.82802**	**3**
P02563	DTQLQLDDAVR	0.921073421	2	2.676833
P02563	VKLEQQVDDLEGSLEQEK	0.747432425	2	5.157225
P02563	VKLEQQVDDLEGSLEQEKK	0.959664615	3	3.494292
P02564	**MYH7 Myosin_7**	**0.933361276**	**0.99997**	**42**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.816705776	3	6.344643
P02564	ANDDLKENIAIVER	0.813628361	2	3.525035
P02564	AQLEFNQIK	0.934134422	1	1.958119
P02564	DLEEATLQHEATAAALR	0.700982552	2	5.202578
P02564	DTQIQLDDAVR	0.921073421	2	2.676833
P02564	EDQVMQQNPPK	1.065864718	2	3.244556
P02564	ELENELEAEQKR	0.96791497	2	2.882081
P02564	EQYEEETEAK	0.764322914	1	3.03225
P02564	GQNVQQVAYAIGALAK	0.684645365	2	3.759597
P02564	GTLEDQIIQANPALEAFGNAK	0.862764693	2	5.248735
P02564	IEDEQALGSQLQK	0.664611786	2	4.537066
P02564	IEELEEELEAER	0.598350202	2	4.26683
P02564	ILNPAAIPEGQFIDSR	0.95438712	2	2.547411
P02564	KLAEKDEEMEQAK	0.118299289	2	3.775279

P02564	KLAEQELIETSER	**0.846841777**	2	3.534202
P02564	KLEDECSELKR	**1.015218312**	3	3.445501
P02564	KVQHELDEAEER	**1.17404057**	2	3.541449
P02564	LAEQELIETSER	**0.550161681**	2	3.799828
P02564	LDEAEQIALK	**1.150637548**	2	3.962439
P02564	LEEAGGATSVQIEMNK	**1.000260259**	2	4.369197
P02564	LELDDVTSNMEQIIK	**0.958160074**	2	4.070542
P02564	LELQSALEEAEASLEHEEGK	**0.66328271**	2	4.138051
P02564	LLGSLDIDHNQYK	**0.643351439**	2	3.661696
P02564	LQDAEEAVEAVNAK	**1.142872478**	2	3.964658
P02564	LQNEIEDLMVDVER	**0.845335913**	2	3.89675
P02564	LTQESIMDLENDKQQLDER	**0.350264334**	2	4.551601
P02564	MDADLSQLQTEVEEAVQECR	**1.013957696**	2	5.235183
P02564	NDLQLQVQAEQDNLADAEER	**0.84129141**	2	5.463215
P02564	NLQEEISDLTEQLGSTGK	**0.831935727**	2	5.929419
P02564	NLTEEMAGLDEIIVK	**1.191271518**	2	4.750556
P02564	NNLLQAELEELR	**0.915241815**	2	3.388179
P02564	QAEEAEEQANTNLSK	**0.853288268**	2	4.975104
P02564	QKYEESQSELESSQK	**0.999576275**	2	3.39453
P02564	QREEQAEPDGTEEADK	**1.070534315**	2	2.931566
P02564	QREEQAEPDGTEEADKSAYLMGLNSADLLK	**2.033830798**	3	4.911406
P02564	SAYLMGLNSADLLK	**1.022204401**	2	2.545759
P02564	TLEDQMNEHR	**0.669873759**	2	2.651053
P02564	VQHELDEAEER	**0.928550733**	2	3.062501
P02564	VQHELDEAEERADIAESQVNK	**0.84047893**	3	3.587075
P02564	VQLLHSQNTSLINQK	**1.096090653**	2	3.987459
P02564	VRELENELEAEQKR	**0.504657997**	3	3.836714
P02564	VVDSLQTSLDAETR	**0.91747267**	2	4.193341
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**1.570514129**	**0.99999**	**13**
P02600	ALGTNPTNAEVK	**1.112340472**	2	3.536794
P02600	ALGTNPTNAEVKK	**1.145362893**	2	3.304775
P02600	DQGGYEDFVEGLR	**0.528115367**	2	3.560319
P02600	EQQEEFKEAFLLFDR	**0.682472283**	2	3.581992
P02600	IEFEQFLPMMQAISNNK	**0.955063938**	3	3.918038
P02600	ITLSQVGDVLR	**1.407615423**	2	3.239146
P02600	KIEFEQFLPMMQAISNNK	**1.02098425**	2	5.667635
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	**1.004866324**	4	5.266766
P02600	KPAAAAPAPAPAPAPAPAKPK	**2.416819765**	3	4.330929
P02600	KVLGNPSNEEMNAK	**0.764737391**	2	3.316699
P02600	KVLGNPSNEEMNAK+Oxidation(10)	**1.144327513**		
P02600	VLGNPSNEEMNAK	**1.168467742**	2	3.689341
P02600	VLGNPSNEEMNAK+Oxidation(9)	**1.06104363**		
P02625	**PRVA Parvalbumin alpha**	**0.831084944**	**1**	**5**
P02625	AIGAFTAADSFDHK	**1.013913956**	2	3.38144
P02625	KVFHILDKDK	**0.897668359**	2	2.301836
P02625	SGFIEEDELGSILK	**0.774525635**	2	4.860672
P02625	TLMAAGDKDGDGK	**0.845577494**	2	3.183165
P02625	TLMAAGDKDGDGK+Oxidation(2)	**1.130477392**		
P02650	**APOE Apolipoprotein E**	**0.897767623**	**0.05612**	**11**
P02650	ELEEQLGPVAEETR	**1.067493101**	2	4.292765
P02650	GRLEEVGNQAR	**0.836230881**	2	3.512826
P02650	GWFEPLVEDMQR	**0.91200704**	2	3.443292
P02650	LEEVGNQAR	**0.921578068**	2	2.483841
P02650	LGADMEDLR	**0.797752308**	2	2.742156
P02650	LGPLVEQGR	**1.206062914**	2	2.766629
P02650	MEEQTQQIR	**0.898925078**	2	3.153938

P02650	NEVNTMLGQSTEELR	**0.838701821**	2	4.375723
P02650	SKMEEQTQQIR	**0.727575637**	2	3.23008
P02650	SKMEEQTQQIR+Oxidation(2)	**1.787418728**		
P02650	TANLGAGAAQPLR	**0.926201244**	2	3.67759
P02651	**APOA4 Apolipoprotein A_IV**	**0.972518059**	**0.28507**	**2**
P02651	TDVTQQLNTLFQDK	**0.832699897**	2	4.376289
P02651	VSTNIDQLQK	**1.363366236**	2	2.310643
P02680	**FIBG Fibrinogen gamma chain**	**1.696532311**	**2E-07**	**5**
P02680	LSIGDGQQHHMGGSK	**1.16865329**	2	2.716701
P02680	VAQLEAQCQEPCK	**2.514435058**	2	3.509436
P02680	VGPESDKYR	**1.360171604**	2	2.784405
P02680	YEALLLTHESSIR	**1.435357858**	2	3.894515
P02680	YLQDIYTSNK	**1.687228475**	2	2.442022
P02692	**FABPL Fatty acid_binding protein_ liver**	**0.804250242**	**9.9E-20**	**11**
P02692	AMGLPEDLIQK	**0.768879171**	2	3.725098
P02692	AMGLPEDLIQK+Oxidation(1)	**0.83809312**		
P02692	GVSEIVHEGK	**0.825249424**	2	3.410163
P02692	GVSEIVHEGKK	**0.784789833**	2	3.223191
P02692	SVTEFNGDTITNTMTLGDIVYK	**0.833532817**	2	5.532661
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13)	**0.90185357**		
P02692	SVTEFNGDTITNTMTLGDIVYKR	**0.674479485**	2	3.632193
P02692	VIHNEFTLGEECELETMTGEK	**0.819401401**	3	6.109758
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16)	**0.855043435**		
P02692	YQVQSQENFEPFMK	**0.936212904**	2	5.81941
P02692	YQVQSQENFEPFMK+Oxidation(12)	**0.994229149**		
P02696	**RET1 Retinol_binding protein 1**	**0.955518502**	**0.99846**	**5**
P02696	ALDVNVALR	**0.923874984**	2	3.313287
P02696	CMTTVSWDGDKLQCVQK	**0.938848375**	2	4.672219
P02696	EFEEDLTGIDDR	**1.007030328**	2	2.46823
P02696	MLSNENFEEYLR	**0.722337818**	2	3.90598
P02696	MLSNENFEEYLR+Oxidation(0)	**0.994971438**		
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.009305324**	**0.40079**	**6**
P02706	DYQDFQHLDNENDHHQLQR	**1.117192325**	3	4.246231
P02706	FVQQHMGPLNTWIGLTDQNGPWK	**1.95344701**	3	3.500044
P02706	LVESQLEK	**1.077429471**	2	2.494918
P02706	SLSCQMAALR	**0.723373755**	2	2.700068
P02706	WVCETELGK	**0.818094781**	2	2.358272
P02706	WVDGTDYETGFK	**0.794445158**	2	3.173732
P02770	**ALBU Serum albumin**	**1.386046877**	**9.9E-20**	**24**
P02770	AADKDNCFATEGPNLVAR	**2.414100043**	2	4.97209
P02770	AETFTFHSDICTLPDKEK	**3.563040206**	2	4.504495
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	**1.536493956**	3	5.270844
P02770	CCSGSLVER	**1.311348658**	2	3.294529
P02770	CCTLPEAQR	**1.253844695**	2	3.199258
P02770	ECCHGDLLECADDR	**1.365239662**	2	3.626663
P02770	ECCHGDLLECADDRAELAK	**1.417526388**	2	5.189486
P02770	FKDLGEQHFK	**1.483260311**	3	4.290384
P02770	GLVLIAFSQYLQK	**1.709897855**	2	4.143642
P02770	INKECCHGDLLECADDRAELAK	**1.589978639**	3	4.70576
P02770	KQTALAELVK	**1.308803271**	3	4.082566
P02770	KYEATLEK	**1.936846312**	1	2.707031
P02770	LQACCDKPVLQK	**1.457021853**	2	4.323123
P02770	LVQEVTDFAK	**1.270800673**	2	3.589504
P02770	RHPDYSVSLLLR	**1.290712278**	3	5.342217
P02770	SIHTLFGDK	**1.51709036**	1	2.537309
P02770	TCVADENAENCDK	**1.285347617**	2	4.496723
P02770	TNCELYEK	**1.392313961**	2	2.896055

P02770	TVMGDFAQFVDK	1.174812096	2	3.728814
P02770	TVMGDFAQFVDK+Oxidation(2)	0.897802761		
P02770	YEATLEK	1.347296805	1	1.938763
P02770	YMCENQATISSK	1.365215148	2	4.095817
P02770	YMCENQATISSK+Oxidation(1)	1.564334353		
P02770	YNEVLTQCCTESDK	1.448647561	2	5.921127
P02803	**MT1 Metallothionein_1**	**8.637905145**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	1.259781935	2	5.284279
P02803	SCCSCCPVGCSK	8.580790777	2	3.903487
P04041	**GPX1 Glutathione peroxidase 1**	**0.638887094**	**9.9E-20**	**10**
P04041	FLVGPDGVPVR	0.714872383	2	3.482735
P04041	GLVVLGFPCNQFGHQENGK	0.609252136	2	4.365985
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	0.665608944	3	3.995894
P04041	NALPAPSDDPTALMTDPK	0.673094714	2	3.11904
P04041	NALPAPSDDPTALMTDPK+Oxidation(13)	0.744527322		
P04041	NDISWNFEK	0.622440212	2	2.94232
P04041	NEEILNSLK	0.656472448	1	2.388293
P04041	TIDIEPDIEALLSK	0.761111707	3	4.577692
P04041	YIIWSPVCR	0.720687444	2	3.110299
P04041	YVRPGGGFEPNFTLFEK	0.574270072	3	4.856639
P04167	**CP2B2 Cytochrome P450 2B2**	**1.275266272**	**0.92468**	**2**
P04167	GTIAVIEPIFK	1.453918347	2	2.713934
P04167	NLQEILDYIGHIVEK	1.183797834	2	3.720965
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.811862212**	**9.9E-20**	**18**
P04176	AYGAGLLSSFGELQYCLSDKPK	2.661509049	2	4.185976
P04176	EDNIPQLEDVSQFLQTCTGFR	2.041167584	3	4.95246
P04176	FANQILSYGAELDADHPGFK	3.382388402	3	3.530921
P04176	FANQILSYGAELDADHPGFKDPVYR	1.569672038	4	5.037365
P04176	ILADSINSEVGILCNALQK	0.804450787	3	6.644315
P04176	LNKDEYEFFTYLDK	10.36988259	2	3.604046
P04176	LNKDEYEFFTYLDKR	1.629314427	3	3.818912
P04176	LRPVAGLLSSR	1.484168336	2	2.339522
P04176	NDIGATVHELSR	1.666031202	2	3.615365
P04176	NTVPWFPR	1.389279594	2	2.501236
P04176	QFADIAYNYR	1.525284841	2	2.545489
P04176	SFAQFSQEIGLASLGAPDEYIEK	2.286972633	2	5.016753
P04176	TACQEYSVTEFQPLYYVAESFSDAK	9.080967008	2	4.733845
P04176	THACYEHNHIFPLLEK	1.699690891	2	4.667121
P04176	VEVLDNTQQLK	1.506054738	2	3.895681
P04176	VEYTEEEK	1.418361818	2	2.603281
P04176	VEYTEEEKQTWGTVFR	1.199486714	2	4.447991
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.723576669	3	4.716255
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.948928079**	**0.9956**	**8**
P04182	AFYNNVLGEYEEYITK	1.174226148	2	4.43028
P04182	DNGLLAKPTHGDIIR	1.00217339	2	2.581575
P04182	GLLNAIVIR	0.874977849	2	3.347982
P04182	KTEQGPPSSEYIFER	1.289891805	2	4.122945
P04182	TEQGPPSSEYIFER	1.082618648	2	4.149383
P04182	VLPMNTGVEAGETACK	0.826159881	2	4.296223
P04182	WLAVDHENVRPDIVLLGK	0.89070064	2	4.059553
P04182	YGAHNYHPLPVALER	0.62855323	2	3.614229
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**0.95249875**	**0.97734**	**5**
P04256	EDSQRPGAHLTVK	0.948525695	2	3.053057
P04256	GFAFVTFDDHDSVDK	1.048679015	2	2.902564
P04256	IEVIEIMTDR	0.882396283	2	3.408569
P04256	NQGGYGGSSSSSSYGSGR	1.104868555	2	4.936421

P04256	SESPKEPEQLR	**1.039310448**	2	2.362085
P04276	**VTDB Vitamin D_binding protein**	**1.133184135**	**0.00098**	**3**
P04276	SCESDAPFPVHPGTSECCTK	**1.410387912**	2	4.851318
P04276	VPTANLEDVLPLAEDLTEILSR	**1.156497184**		
P04276	YCSSQIDAEMR	**1.283585236**	2	2.46543
P04355	**MT2 Metallothionein_2**	**18.23845785**	**9.9E-20**	**3**
P04355	CSQGCICKEASDKCSCCA	**6.314216016**	3	3.632713
P04355	MDPNCSCATDGSCSCAGSCK	**5.239810964**	2	6.386932
P04355	SCCSCCPVGCAK	**14.51813197**	2	4.216469
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**1.095660819**	**0.99836**	**9**
P04466	AAAEGSSNVFSMFDQTQIQEFK	**1.049682303**	3	4.91573
P04466	GADPEDVITGAFK	**0.694764765**	2	4.345148
P04466	KQFLEELLTTQCDR	**0.751582652**	2	3.817376
P04466	LKGADPEDVITGAFK	**0.94468857**	2	3.765516
P04466	NEELDAMMK	**0.949614991**	1	2.322364
P04466	NICYVITHGDAK	**1.467754036**	2	3.073754
P04466	NICYVITHGDAKDQE	**0.687363728**	2	3.980803
P04466	NMWAAFPPDVGGNVDYK	**0.702432351**	2	2.915712
P04466	QFLEELLTTQCDR	**0.557547926**	2	4.005283
P04550	**PTMS Parathymosin**	**1.030265948**	**0.89957**	**4**
P04550	RTAEEEDEADPKR	**0.96304559**	3	4.408648
P04550	SVEAAAELSAK	**1.083587492**	2	4.205069
P04550	TAEEEDEADPK	**1.052543842**	2	3.714639
P04550	TAEEEDEADPKR	**1.348762283**	3	3.740644
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**0.966608695**	**8.2E-06**	**17**
P04636	AGAGSATLSMAYAGAR	**0.952600317**	2	4.757953
P04636	AGAGSATLSMAYAGAR+Oxidation(9)	**1.373504882**		
P04636	ANTFVAELK	**0.973109694**	2	2.738801
P04636	EGVIECSFVQSK	**1.132810918**	1	3.060102
P04636	ETECTYFSTPLLLGK	**3.907109486**	2	3.758039
P04636	FVFSLVDAMNGK	**0.877508585**	2	4.290236
P04636	GCDVVVIPAGVPR	**0.942350052**	2	4.263672
P04636	GYLGPEQLPDCLK	**0.917934307**	2	4.307568
P04636	IFGVTTLDIVR	**1.102747018**	2	3.452798
P04636	IQEAGTEVVK	**0.924661156**	2	2.86749
P04636	LTLYDIAHTPGVAADLSHIETR	**0.916918634**	3	6.707665
P04636	MIAEAIPELK	**0.894744834**	2	3.056718
P04636	MIAEAIPELK+Oxidation(0)	**1.064918529**		
P04636	TIIPLISQCTPK	**0.892861785**	2	3.710312
P04636	VAVLGASGGIGQPLSLLLK	**1.700343032**	2	5.997471
P04636	VDFPQDQLATLTGR	**0.808894877**	2	4.760095
P04636	VNVPVIGGHAGK	**0.903604239**	2	3.61838
P04639	**APOA1 Apolipoprotein A_I**	**1.169197841**	**0.00552**	**5**
P04639	LQEQLGPVTQEFWANLEK	**1.649943486**	2	4.089848
P04639	NEMNKDLENVK	**0.991138768**	2	3.16358
P04639	QLNLNLLDNWDTLGSTVGR	**1.266475524**	2	4.298866
P04639	VKDFATVYVDAVK	**2.049906731**	2	2.832142
P04639	WNEEVEAYR	**1.534960381**	2	2.598564
P04642	**LDHA L_lactate dehydrogenase A chain**	**0.961894076**	**0.02588**	**21**
P04642	DLADELALVDVIEDK	**0.894387133**	2	5.457942
P04642	DQLIVNLLK	**1.274623047**	2	2.928626
P04642	DQLIVNLLKEEQVPQNK	**0.971412322**	2	4.577693
P04642	EDVFLSVPCILGQNGISDVVK	**1.19151917**	2	4.660959
P04642	FIIPNVVK	**0.833964047**	2	2.382555
P04642	GEMMDLQHGSLFLK	**0.85858298**	2	3.94008
P04642	GEMMDLQHGSLFLK+Oxidation(2)	**1.450875254**		

P04642	GEMMDLQHGSLFLK+Oxidation(2)	**1.008885327**		
P04642	GEMMDLQHGSLFLK+Oxidation(3)	**1.033518112**	2	3.487276
P04642	KSADTLWGIQK	**1.191483722**	2	3.318448
P04642	LLIVSNPVDILTYVAWK	**1.582898652**	2	4.863012
P04642	NVNIFK	**1.162840461**	1	2.082439
P04642	QVVDSAYEVIK	**1.118734445**	2	3.502868
P04642	RVHPISTMIK	**0.992605402**	2	2.519708
P04642	RVHPISTMIK+Oxidation(7)	**1.315203409**		
P04642	SADTLWGIQK	**1.108446271**	2	3.934905
P04642	SLNPQLGTDADK	**1.57257836**	1	2.322855
P04642	SLNPQLGTDADKEQWK	**1.220465863**	2	4.857021
P04642	SLNPQLGTDADKEQWKDVHK	**0.790417971**	3	3.431161
P04642	VHPISTMIK+Oxidation(6)	**2.108777538**		
P04642	VTLTPDEEAR	**1.099403344**	2	2.741382
P04644	**RS17 40S ribosomal protein S17**	**1.100701202**	**0.99865**	**2**
P04644	LLDFGSLSNLQVTQPTVGMNFK	**1.082020052**	2	4.278763
P04644	VCEEIAIIPSK	**1.064960897**	2	2.866039
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.000690754**	**0.99999**	**11**
P04692	AISEELDHALNDMTSI	**1.196286461**	2	2.800011
P04692	GTEDELDKYSEALK	**1.016351492**	2	3.645583
P04692	GTEDELDKYSEALKDAQEK	**0.927506692**	2	4.108422
P04692	KLVIIESDLER	**0.994046509**	2	3.46125
P04692	LDKENALDR	**1.024994441**	2	2.785169
P04692	LKGTEDELDK	**1.272898971**	2	2.768812
P04692	LVIIESDLER	**0.911172763**	2	2.458196
P04692	MEIQEIQLK	**0.985217119**	2	3.021322
P04692	QLEDELVSLQK	**0.774235612**	2	2.855708
P04692	SIDDLEDELYAQK	**0.506793647**	2	4.23555
P04692	SKQLEDELVSLQK	**1.237520502**	2	3.335744
P04694	**ATTY Tyrosine aminotransferase**	**0.87856784**	**0.28444**	**5**
P04694	ILGPCTIVQGALK	**1.614394244**	2	2.672603
P04694	IQEFCEQHYHCAEGSQEECDK	**3.724452873**	3	4.451884
P04694	TACLVVNNPSNPCGSVFSK	**0.791704636**	2	4.933046
P04694	WDVRPSDMSNK	**1.100147555**	2	2.36815
P04694	YEPLANLSTNVPILSCGGLAK	**2.040714662**	2	3.429554
P04762	**CATA Catalase**	**1.009175472**	**9.9E-20**	**32**
P04762	APQKPDVLTTGGGNPIGDK	**4.112577441**	2	4.638016
P04762	DAMLFPSFIHSQK+Oxidation(2)	**1.674072004**		
P04762	DAQLFIQR	**1.134412095**	2	2.997428
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	**0.595137503**	4	4.567451
P04762	DPASDQMK	**0.990129735**	1	2.257921
P04762	DPASDQMK+Oxidation(6)	**1.625990572**		
P04762	DYPLIPVGK	**0.8341974**	1	2.244847
P04762	EAETFPFNPFDLTK	**1.050619013**	2	3.960579
P04762	FNSANEDNVTQVR	**0.682442928**	2	4.558928
P04762	FSTVAGESGSADTVR	**0.895244174**	2	5.280581
P04762	FSTVAGESGSADTVRDPR	**0.38233254**	2	2.307338
P04762	FYTEDGNWDLVGNNTPIFFIR	**1.162395944**	3	5.463285
P04762	GAGAFGYFEVTHDITR	**0.792670691**	2	4.783739
P04762	GPLLVQDVVFTDEMAHFDR	**1.592903934**	2	5.47609
P04762	HMNGYGSHTFK	**0.796265699**	3	4.108102
P04762	HMNGYGSHTFK+Oxidation(1)	**1.297094702**		
P04762	LAQEDPDYGLR	**1.451493688**	2	2.72948
P04762	LCENIANHLK	**0.761397008**	3	3.783859
P04762	LFAYPDTHR	**0.959770062**	2	2.914103
P04762	LGPNYLQIPVNCPYR	**0.964646165**	3	4.052971

P04762	LNIMTAGPR	**0.753318988**	2	3.145642
P04762	LNIMTAGPR+Oxidation(3)	**1.150030281**		
P04762	LVNANGEAVYCK	**0.890632607**	2	3.894319
P04762	NAIHTYVQAGSHIAAK	**0.653159959**	3	5.898609
P04762	NFTDVHPDYGAR	**0.738037339**	2	4.140734
P04762	NLPVEEAGR	**0.762576155**	1	2.323009
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	**3.348273814**	3	5.677136
P04762	RFNSANEDNVTQVR	**0.725500742**	2	4.521218
P04762	VFEHIGK	**0.914215736**	2	2.476162
P04762	VFEHIGKR	**0.817320473**	2	2.369051
P04762	VQALLDQYNSQKPK	**0.824301335**	2	4.940297
P04762	VWPHKDYPLIPVGK	**0.494150845**	2	3.481071
P04764	**ENOA Alpha_enolase**	**1.085433107**	**0.24366**	**14**
P04764	AGYTDQVVIGMDVAASEFYR	**0.816183386**	2	4.520521
P04764	DATNVGDEGGFAPNILENK	**1.004135796**	2	5.780879
P04764	FTATAGIQVVGDDLTVTNPK	**1.147676584**	2	5.306463
P04764	GNPTVEVDLYTAK	**1.377681584**	2	4.078547
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	**0.95307354**	3	6.15002
P04764	IDQLMIEMDGTENK	**0.945621033**	2	4.481691
P04764	IEEELGSK	**1.0490354**	2	2.321403
P04764	IGAEVYHNLK	**1.874713659**	2	3.209411
P04764	KLNVVEQEK	**1.435178698**	2	2.545506
P04764	LNVVEQEK	**1.119978977**	2	3.102386
P04764	LNVVEQEKIDQLMIEMDGTENK	**0.859170408**	3	4.648707
P04764	SCNCLLLK	**1.253186578**	2	2.981885
P04764	VNQIGSVTESLQACK	**1.098756489**	2	5.042507
P04764	YITPDQLADLYK	**0.995972699**	2	3.470566
P04785	**PDIA1 Protein disulfide_isomerase**	**0.961989315**	**0.49439**	**25**
P04785	DGVVLFK	**1.248741349**	2	2.440274
P04785	DHENIVIAK	**1.172108512**	2	2.75662
P04785	EADDIVNWLK	**1.22693759**	2	2.308766
P04785	HNQLPLVIEFTEQTAPK	**0.969414221**	3	5.686644
P04785	IKPHLMSQELPEDWDKQPVK	**0.875530074**	4	4.660788
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5)	**1.257596854**		
P04785	ILEFFGLK	**1.007763238**	2	3.074069
P04785	ILFIFIDSDHTDNQR	**0.934802041**	2	2.37653
P04785	LGETYKDHENIVIAK	**0.938292983**	3	4.736261
P04785	LITLEEEMTK	**0.880790421**	2	3.56582
P04785	LITLEEEMTK+Oxidation(7)	**1.215149354**		
P04785	LKAEGSEIR	**1.226963058**	1	2.096421
P04785	MDSTANEVEAVK	**0.937698291**	2	4.116548
P04785	MDSTANEVEAVK+Oxidation(0)	**1.063785139**		
P04785	NFEEVAFDEK	**0.914690846**	1	3.357725
P04785	NFEEVAFDEKK	**1.009821043**	2	3.736872
P04785	NNFEGEITK	**0.904816636**	2	2.534137
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	**1.011968352**	3	6.632107
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	**0.868355883**	3	6.390738
P04785	THILLFLPK	**1.015119889**	2	2.77799
P04785	TVIDYNGER	**0.810136717**	2	2.565073
P04785	VDATEESDLAQQYGVR	**0.844410805**	2	5.625583
P04785	VHSFPTLK	**0.812560909**	1	1.920658
P04785	YKPESDELTAEK	**1.00792385**	3	4.586089
P04785	YQLDKDGVVLFK	**0.915295204**	2	3.936726
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**0.873804009**	**3.3E-06**	**16**
P04797	GAAQNIIPASTGAAK	**1.273927941**	2	4.273346
P04797	IVSNASCTTNCLAPLAK	**1.146397214**	2	4.764961

P04797	LISWYDNEYGYSNR	**1.223179136**	2	4.061031
P04797	LVINGKPITIFQER	**1.388848936**	3	3.720879
P04797	RVIISAPSADAPMFVMGVNHEK	**1.591082884**	3	5.285765
P04797	RVIISAPSADAPMFVMGVNHEK+Oxidation(12)	**1.049290626**		
P04797	VGVNGFGR	**1.257194212**	2	2.578372
P04797	VIHDNFGIVEGLMTTVHAITATQK	**1.03149035**	3	7.493002
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12)	**1.282168736**		
P04797	VIISAPSADAPMFVMGVNHEK	**0.925567268**	2	4.64743
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11)	**1.152606062**		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14)	**1.152751967**		
P04797	VPTPNVSVVDLTCR	**3.174919107**	2	3.774345
P04797	VVDLMAYMASK	**4.179721262**	2	3.805506
P04797	VVDLMAYMASKE	**6.962146633**	2	2.766998
P04797	WGDAGAEYVVESTGVFTTMEK	**1.15004951**	2	5.567223
P04799	**CP1A2 Cytochrome P450 1A2**	**1.940091431**	**0.9727**	**6**
P04799	DFVENVTSGNAVDFFPVLR	**1.106363203**	2	3.760718
P04799	IGSTPVVVLSGLNTIK	**1.326966978**	2	3.059791
P04799	NSIQDITGALFK	**1.052471804**	2	3.475518
P04799	SMTFNPDSGPVWAAR	**1.968953562**	2	3.155394
P04799	TCEHVQAWPR	**0.492083869**	2	2.871635
P04799	TVQEHYQDFNK	**1.1802574**	2	3.458863
P04800	**CP3A1 Cytochrome P450 3A1**	**3.487680161**	**0.2291**	**2**
P04800	KLQEEIDR	**0.720800856**	2	2.31223
P04800	QGLLQPTKPIILK	**3.697512324**	2	2.387706
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.748155477**	**0.01379**	**10**
P04903	DGNLMFDQVPMVEIDGMK	**0.536287744**	2	4.917635
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	**0.800654304**		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16)	**0.808039929**		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	**0.79613045**		
P04903	KDGNLMFDQVPMVEIDGMK	**0.552892754**	2	4.395597
P04903	LIQSPEDLEK	**0.910588293**	2	3.116575
P04903	LKKDGNLMFDQVPMVEIDGMK	**1.162763859**	2	2.692726
P04903	WLLAAAGVEFEEK	**0.772454752**	2	3.870257
P04903	YDLYGK	**0.6394911**	1	1.939573
P04903	YLPAFEK	**0.782977872**	1	2.002143
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.908538089**	**0.14637**	**9**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	**1.195747661**	3	5.295905
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	**1.351799168**	4	7.904847
P04904	LRNDGSLMFQQVPMVEIDGMK	**1.011294162**	2	3.804574
P04904	NDGSLMFQQVPMVEIDGMK	**0.749451827**	2	4.639302
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	**0.918207664**		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17)	**0.926054581**		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5)	**0.908072808**		
P04904	SHGQDYLVGNR	**0.856590242**	2	3.9099
P04904	WLLAAAGVEFEEQFLK	**0.880430721**	2	5.419931
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**0.79593676**	**0.94472**	**15**
P04905	ADIVENQVMDNR	**0.958774245**	2	4.293469
P04905	ADIVENQVMDNR+Oxidation(8)	**1.077428054**		
P04905	CLDAFPNLKDFLAR	**0.764323397**	2	2.693651
P04905	FKLGLDFPNLPYLIDGSR	**0.875606261**	3	4.854903
P04905	HHLCGETEEER	**1.099681116**	3	4.43464
P04905	IRADIVENQVMDNR	**0.853677665**	2	3.954945
P04905	ITQSNAIMR	**1.014567342**	2	3.089123
P04905	ITQSNAIMR+Oxidation(7)	**1.221538568**		
P04905	KHHLCGETEEER	**1.431306324**	3	3.686196
P04905	KITQSNAIMR	**0.776727306**	3	3.764464
P04905	KITQSNAIMR+Oxidation(8)	**1.205510212**		

P04905	LGLDFPNLPYLIDGSR	**1.017735735**	2	5.113865
P04905	MQLIMLCYNPDFEK	**1.38628481**	2	4.494752
P04905	VTYVDFLAYDILDQYHIFEPK	**1.137854432**	3	3.7413
P04905	YLSTPIFSK	**0.96804733**	2	2.708584
P04906	**GSTP1 Glutathione S_transferase P**	**0.904956741**	**0.98835**	**2**
P04906	EAALVDMVNDGVEDLR	**0.884380223**	2	4.733013
P04906	STCLYGQLPK	**1.068991289**	2	2.948133
P04937	**FINC Fibronectin**	**1.111389954**	**0.12417**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	**1.73643825**	2	3.529043
P04937	ITYGETGGNSPVQEFTVPGSK	**1.033452385**	2	2.655801
P04937	SSPVVIDASTAIDAPSNLR	**1.146186422**	2	2.466382
P04937	SYTITGLQPGTDYK	**0.969934788**	2	2.758991
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**0.949901488**	**1**	**9**
P05065	ALANSLACQGK	**1.049081485**	2	2.964607
P05065	FSNEEIAMATVTALR	**0.958676689**	2	4.498697
P05065	GILAADESTGSIAK	**1.098818183**	2	4.228808
P05065	GVVPLAGTNGETTTQGLDGLSER	**1.056297945**	2	5.399199
P05065	IGEHTPSSLAIMENANVLAR	**1.154343504**	2	4.678485
P05065	KENLKAAQEEYIK	**1.03586175**	2	2.411307
P05065	LQSIGTENTEENR	**1.343188114**	2	3.80651
P05065	LQSIGTENTEENRR	**1.093467052**	2	2.521145
P05065	RLQSIGTENTEENR	**1.093467052**	2	4.08288
P05178	**CP2C6 Cytochrome P450 2C6**	**0.769325892**	**1.3E-08**	**9**
P05178	DQDFLNLMEK	**0.898658941**	2	2.581353
P05178	EALIDHGEEFAER	**0.628226912**	2	3.247572
P05178	FDYKDQDFLNLMEK	**0.655858115**	3	4.555609
P05178	FIDLIPTNLPHAVTCDIK	**0.581609704**	2	3.350196
P05178	GTTIITSLSSVLHDSK	**0.616770812**	2	3.75694
P05178	LPPGPIPLPIIGNIFQLNVK	**0.59406931**	3	3.520749
P05178	MCAGEGLAR	**0.661471084**	2	2.576167
P05178	NITQSLTSFSK	**0.634552413**	2	2.472451
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	**0.856127107**	3	4.718562
P05179	**CP2C7 Cytochrome P450 2C7**	**1.197399047**	**0.32555**	**7**
P05179	ACVGEGLAR	**1.36581818**	2	2.892647
P05179	FINFVPTNLPHAVTCDIK	**0.851683286**	2	2.656708
P05179	IEEHQESLDVTNPR	**1.091813738**	2	4.568703
P05179	KIEEHQESLDVTNPR	**1.627804489**	3	4.668203
P05179	KLPPGPTPLPIIGNFLQIDVK	**1.154197616**	3	5.507406
P05179	SDYFLPFSAGK	**3.429294722**	2	2.598929
P05179	VLTSLTSVLHDSK	**1.589692137**	2	3.416085
P05182	**CP2E1 Cytochrome P450 2E1**	**1.064178356**	**4.6E-14**	**14**
P05182	AKEHLQSLDINCAR	**0.592955883**	2	4.855285
P05182	DTVFQGYVIPK	**1.561450004**	2	2.820848
P05182	DVTDCLLIEMEK	**1.024791294**	2	3.026754
P05182	DVTDCLLIEMEKEK	**0.803017402**	2	2.489502
P05182	EHLQSLDINCAR	**1.02411978**	2	3.429089
P05182	FINLVPSNLPHEATR	**0.685485698**	2	3.822134
P05182	FKPEHFLNENGK	**0.744919474**	2	2.97678
P05182	GIIFNNGPTWK	**0.905649032**	2	2.414363
P05182	GQPFDPTFLIGCAPCNVIADILFNK	**0.927561932**		
P05182	GTVVIPTLDSLLYDSHEFPDPEK	**0.761343118**	2	4.885564
P05182	LDMPYMDAVVHEIQR	**0.788454148**	2	2.671844
P05182	LHEEIDR	**0.780556585**	1	1.958606
P05182	VCVGEGLAR	**0.905986212**	2	2.38397
P05182	YGLLILMK	**0.638576304**	2	3.088043
P05183	**CP3A2 Cytochrome P450 3A2**	**0.896035756**	**2.9E-06**	**10**
P05183	DIELDGLFIPK	**0.732985676**	2	4.140474

P05183	DSIAFFQK	2.351353357	1	2.182205
P05183	EMFPIIEQYGDILVK	0.857019136	2	3.951617
P05183	KDIELDGLFIPK	0.545139692	3	3.558479
P05183	KLQEEIDGALPSK	0.893598643	2	3.679556
P05183	LQEEIDGALPSK	0.801547373	2	4.103528
P05183	QAILEPEKPIVLK	0.858443081	2	3.283657
P05183	QEAETGKPVTMK	0.526318996	2	3.193538
P05183	QEAETGKPVTMK+Oxidation(10)	1.429946651		
P05183	VDFLQLMLNAHNNSK	0.557898274	2	3.709425
P05197	**EF2 Elongation factor 2**	**1.289247702**	**9.9E-20**	**31**
P05197	ALLELQLEPEELYQTFQR	1.636252784	2	5.471809
P05197	ARPFPDGLAEDIDKGEVSAR	1.294468636	3	6.160313
P05197	AYLPVNESFGFTADLR	1.283853342	2	3.876123
P05197	CELLYEGPPDDEAAMGIK	1.311770384	2	4.978745
P05197	CLYASVLTAQPR	4.393645116	2	2.461268
P05197	DLEEDHACIPIK	1.128183349	2	2.990952
P05197	DLEEDHACIPIKK	1.09881655	2	3.676381
P05197	EGIPALDNFLDK	0.975435811	2	2.648639
P05197	EGIPALDNFLDKL	3.674569372	2	3.578612
P05197	ETVSEESNVLCLSK	2.27152946	2	4.058276
P05197	GEGQLGAAER	1.287181248	2	3.360289
P05197	GHVFEESQVAGTPMFVVK	2.428310139	2	6.135114
P05197	GVQYLNEIK	4.930880982	2	2.342688
P05197	IWCFGPDGTGPNILTDITK	1.223826588	2	5.060048
P05197	KEDLYLKPIQR	1.30950929	2	3.303408
P05197	KIWCFGPDGTGPNILTDITK	1.166963753	2	4.830319
P05197	KVEDMMK+Oxidation(5)	1.900783944		
P05197	LDSEDKDKEGKPLLK	1.786052347	2	3.961259
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	1.12592897	3	5.989743
P05197	NMSVIAHVDHGK	1.43409096	2	3.947744
P05197	NMSVIAHVDHGK+Oxidation(1)	1.517606508		
P05197	STAISLFYELSENDLNFIK	3.028600199	3	4.766977
P05197	STLTDSLVCK	1.211665103	2	2.897322
P05197	TFCQLILDPIFK	1.709084922	2	4.199083
P05197	TGTITTFEHAHNMR	1.270005007	2	3.835143
P05197	VFDAIMNFR	1.004537169	2	2.826332
P05197	VFSGVVSTGLK	1.441645482	2	3.05037
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.181391042	3	3.652965
P05197	YEWDVAEAR	1.106821753	2	3.038956
P05197	YFDPANGK	1.247257341	1	2.037084
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.542554421	3	4.735874
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.23986095**	**0.99938**	**11**
P05369	ALYEELDLR	1.076655729	2	3.059262
P05369	EVLEYNTVGGK	0.56681029	2	3.069732
P05369	GLTVVQTFQELVEPR	1.164067484	3	3.864324
P05369	IKEVLEYNTVGGK	0.904009747	3	4.167077
P05369	QILEENYGQKDPEK	0.878713152	2	3.777578
P05369	QNFIQHFSQIVK	1.790974498	2	3.052457
P05369	SLIEQCSAPLPPSIFLELANK	0.974535377	3	5.298708
P05369	VGTDIQDNK	1.004386652	2	3.686793
P05369	VLTEDELGHPEK	1.424502948	2	2.720763
P05369	VLTEDELGHPEKGDAITR	1.068010973	2	4.569483
P05369	YEEDSYNR	1.013817994	2	2.345772
P05426	**RL7 60S ribosomal protein L7**	**1.207282707**	**0.01815**	**6**
P05426	AGNFYVPAEPK	1.190907076	2	2.672065
P05426	FGIICMEDLIHEIYTVGK	1.159746731	3	4.647248
P05426	IVEPYIAWGYPNLK	1.496930078	2	2.95143

P05426	SVNELIYK	**1.17065655**	2	2.795789
P05426	TTHFVEGGDAGNR	**1.119506298**	2	3.267327
P05426	TTHFVEGGDAGNREDQINR	**1.248009578**	2	4.565462
P05544	**SPA3L Serine protease inhibitor A3L**	**1.05683003**	**0.08999**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	**1.2087913**	2	4.603592
P05544	DSTMEEILEGLK	**0.686338418**	2	3.013456
P05544	IAELFSDLEER	**1.289692897**	2	2.875906
P05544	MQQVESSLQPETLK	**0.869542038**	2	4.215751
P05544	MQQVESSLQPETLK+Oxidation(0)	**0.812794426**		
P05544	VFSQQADLSR	**1.360505081**	2	2.576789
P05545	**SPA3K Serine protease inhibitor A3K**	**1.427866229**	**0.07293**	**8**
P05545	ALYQAEAFVADFK	**1.208252297**	2	2.884836
P05545	AVLDVDETGTEGAAATAVTAALK	**1.088259246**	2	5.443286
P05545	FSISTDYNLEEVLPELGIR	**1.235437454**	2	3.486674
P05545	IAELFSELDER	**1.517008543**	2	3.046522
P05545	IFSQQADLSR	**1.093547249**	2	2.580773
P05545	LSQPEDQAEINTGSALFIDK	**1.495926735**	2	4.84718
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	**1.617185306**	3	4.319727
P05545	NVVFSPLSISAALAILSLGAK	**1.05989729**		
P05765	**RS21 40S ribosomal protein S21**	**1.070121033**	**0.24229**	**3**
P05765	DHASIQMNVAEVDR	**1.336975759**	2	3.838672
P05765	MGESDDSILR	**1.038043183**	2	2.896264
P05765	TYGICGAIR	**1.000287047**	2	2.511735
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.819096924**	**1.4E-08**	**8**
P06214	AGADIIITYFAPQLLK	**3.335370705**	2	4.187796
P06214	AGCQVVAPSDMMDGR	**0.895722665**	2	3.463431
P06214	CVLIFGVPSR	**1.104898047**	2	2.835579
P06214	DEQGSAADSEDSPTIEAVR	**0.746292467**	2	5.506608
P06214	DIQEGADILMVKPGLPYLDMVQEVK	**0.886074339**	3	4.583016
P06214	TAVLESMTAFR	**0.736160602**	2	2.95096
P06214	VPKDEQGSAADSEDSPTIEAVR	**0.797512358**	3	5.036238
P06214	YGVNQLEEMLRPLVEAGLR	**0.808036486**	3	4.589357
P06238	**A2MG Alpha_2_macroglobulin**	**1.034283935**	**0.01341**	**3**
P06238	FQVNNNNQLLLQR	**6.617718418**	2	3.072789
P06238	SESNMAIADVK	**1.180968522**	2	2.473328
P06238	VAVQLEASPDFLAAPEEK	**1.033053971**	2	3.442948
P06302	**PTMA Prothymosin alpha**	**1.004630762**	**0.26899**	**4**
P06302	EVVEEAENGR	**1.000536256**	2	2.345241
P06302	RVAEDDEDDDVETKK	**1.353544689**	3	5.884018
P06302	VAEDDEDDDVETK	**1.236269226**	2	3.862524
P06302	VAEDDEDDDVETKK	**0.956460781**	2	4.693449
P06399	**FIBA Fibrinogen alpha chain**	**1.122439304**	**0.58085**	**8**
P06399	AQQIQVLQK	**1.440096555**	2	2.649024
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	**1.26417399**	3	3.769013
P06399	GDFANANNFDNTFGQVSEDLR	**1.088656394**	2	5.694673
P06399	GDFANANNFDNTFGQVSEDLRR	**0.983787191**	3	3.303046
P06399	GLIDEANQDFTNR	**1.227711916**	2	3.657563
P06399	MADEAASEAHQEGDTR	**1.254447058**	2	4.116182
P06399	SQLQEGPPEWK	**0.820522083**	2	2.602514
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	**1.364718462**	2	4.672547
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.282617808**	**0.46358**	**5**
P06685	AVAGDASESALLK	**1.251923288**	2	3.160472
P06685	AVFQANQENLPILK	**1.096486025**	2	3.327251
P06685	EQPLDEELKDAFQNAYLELGGLGER	**1.071649382**	3	3.326185
P06685	LNIPVNQVNPR	**0.785412688**	2	3.032294
P06685	YEPAAVSEHGDKK	**1.630168196**	2	2.674323

P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.021703014**	**0.99998**	**3**
P06687	DGPNALTPPPTTPEWVK	1.037685362	2	2.647821
P06687	GVGIISEGNETVEDIAAR	0.996760863	2	4.688804
P06687	QGAIVAVTGDGVNDSPALK	1.036302535	2	4.797959
P06757	**ADH1 Alcohol dehydrogenase 1**	**0.809542966**	**0.10912**	**18**
P06757	AAVLWEPHKPFTIEDIEVAPPK	0.857486742	3	5.449578
P06757	FPLEPLITHVLPFEK	1.229258353	3	4.512362
P06757	GAIFGGFK	0.818996653	2	2.344639
P06757	GALLDGTSR	0.990763926	2	2.859643
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	0.778710264	3	5.001085
P06757	HPESNLCCQTK	1.299899304	2	3.229142
P06757	ICKHPESNLCCQTK	2.229971384	3	4.133464
P06757	IDAAAPLDK	0.725707807	2	2.745425
P06757	IIAVDINKDK	0.609582826	2	2.719091
P06757	INEAFDLLR	0.915835009	2	3.581264
P06757	KFPLEPLITHVLPFEK	0.789775733	3	4.558144
P06757	LVADFMAK	0.820132302	2	2.60782
P06757	MVATGVCR	0.916966766	2	2.541071
P06757	MVATGVCR+Oxidation(0)	1.045848402		
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.042474672	4	7.670705
P06757	VCLIGCGFSTGYGSAVQVAK	0.784054432	2	6.181609
P06757	VIPLFSPQCGK	0.999020088	2	2.742628
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	0.733017299	2	5.143275
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.025169502**	**0.81314**	**30**
P06761	AKFEELNMDLFR	1.002193198	3	4.246301
P06761	DAGTIAGLNVMR	1.263457135	2	3.492731
P06761	DNHLLGTFDLTGIPPAPR	0.930032781	2	4.246787
P06761	ELEEIVQPIISK	0.949149627	2	3.980221
P06761	FEELNMDLFR	0.778536165	2	3.484305
P06761	FEELNMDLFR+Oxidation(5)	0.707934509		
P06761	IEIESFFEGEDFSETLTR	1.12233027	2	5.272079
P06761	IEWLESHQDADIEDFK	0.972772947	2	5.687947
P06761	IEWLESHQDADIEDFKAK	0.730029813	3	4.164316
P06761	IINEPTAAAIAYGLDKR	1.080378676	2	4.466039
P06761	ITITNDQNR	1.029745406	2	2.664267
P06761	ITPSYVAFTPEGER	1.277887091	2	4.282418
P06761	KKELEEIVQPIISK	0.888724256	2	5.106496
P06761	KSDIDEIVLVGGSTR	0.959686215	2	4.544512
P06761	KSQIFSTASDNQPTVTIK	1.136958327	2	5.517912
P06761	LYGSGGPPPTGEEDTSEKDEL	1.260008163	2	5.698164
P06761	MKETAEAYLGK	0.986909404	2	2.697902
P06761	MKETAEAYLGK+Oxidation(0)	1.268414161		
P06761	NELESYAYSLK	1.32741789	2	3.670024
P06761	NQLTSNPENTVFDAK	1.044069839	2	5.121109
P06761	SDIDEIVLVGGSTR	0.908060413	1	3.508594
P06761	SQIFSTASDNQPTVTIK	1.052219571	2	5.298091
P06761	TFAPEEISAMVLTK	0.899831496	2	4.869541
P06761	TFAPEEISAMVLTK+Oxidation(9)	1.023278478		
P06761	TKPYIQVDIGGGQTK	1.07330255	3	4.631458
P06761	TWNDPSVQQDIK	0.996582204	2	4.014555
P06761	VLEDSDLK	0.830340797	1	2.116509
P06761	VLEDSDLKK	0.911467051	2	2.359615
P06761	VTHAVVTVPAYFNDAQR	1.006596877	2	5.056208
P06761	VYEGERPLTK	0.999884701	2	2.89851
P06866	**HPT Haptoglobin**	**2.378214887**	**9.9E-20**	**8**

P06866	ATDLKDWVQETMAK	**1.563814952**	3	3.817987
P06866	CELHYEK	**4.06338212**	2	2.345129
P06866	GAVSPVGVQPILNK	**2.349537034**	2	4.604812
P06866	KGAVSPVGVQPILNK	**3.78336028**	2	3.100904
P06866	LQTEGDGIYTLNSEK	**3.346730074**	2	4.254277
P06866	NQLVEIEK	**2.387563883**	1	2.335609
P06866	SCAVAEYGVYVR	**2.139102071**	2	3.115407
P06866	SVVDIGLIK	**2.033805644**	2	2.762702
P07150	**ANXA1 Annexin A1**	**0.857175974**	**0.86984**	**2**
P07150	GLGTDEDTLIEILTTR	**0.852153139**	2	4.279128
P07150	GVDEATIIDILTK	**0.986049732**	2	3.125175
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.086970451**	**4.3E-05**	**16**
P07153	ASSFVLALEPELESR	**1.046976976**	2	4.464863
P07153	AVTSEIAVLQSR	**1.04894836**	2	3.703603
P07153	FVDHVFDEQVIDSLTVK	**0.779639726**	2	4.142312
P07153	GEDEEDNNLEVR	**0.848738609**	2	3.73351
P07153	HFDETVNR	**0.926670145**	2	2.511789
P07153	IDHILDAL	**1.475384804**	2	2.312999
P07153	ISIVVETVYTHVLHPYPTQITQSEK	**1.172686335**	3	4.627875
P07153	LKTEGSDLCDR	**0.848826319**	3	3.412148
P07153	NIQVDSPYDISR	**1.106649797**	2	3.783175
P07153	NLVEQHIQDIVVHYTFNK	**1.259989267**	3	4.454648
P07153	SEDILDYGPFK	**0.829715632**	2	3.397948
P07153	TEGSDLCDR	**0.9877805**	2	2.33111
P07153	TILPAAAQDVYYR	**1.709325505**	2	3.295642
P07153	TVDLSSHLAK	**0.833966279**	2	2.59989
P07153	VHYENNSPFLTITSMTR	**1.058477843**	2	3.293406
P07153	VTAEVVLAHPGGGSTAR	**1.06133303**	2	4.467195
P07323	**ENOG Gamma_enolase**	**1.141464393**	**0.07985**	**4**
P07323	AAVPSGASTGIYEALELR	**1.267298441**	2	5.041862
P07323	FGANAILGVSLAVCK	**0.959219884**	2	3.509146
P07323	GNPTVEVDLHTAK	**0.851993431**	2	3.394585
P07323	SGETEDTFIADLVVGLCTGQIK	**0.990586748**	3	5.528365
P07335	**KCRB Creatine kinase B_type**	**0.891633752**	**0.46892**	**2**
P07335	FCTGLTQIETLFK	**0.795505885**	2	2.780213
P07335	GTGGVDTAAVGGVFDVSNADR	**0.940172491**	2	3.937548
P07338	**CTRB1 Chymotrypsinogen B**	**0.800931499**	**0.22346**	**2**
P07338	IVNGEDAIPGSWPWQVSLQDK	**0.552196695**	2	3.258435
P07338	LQQAALPIVSEADCK	**0.845970424**	2	2.696569
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.183286993**	**0.03919**	**2**
P07340	SYEAYVLNIIR	**2.520220401**	2	2.39268
P07340	YNPNVLPVQCTGK	**1.102408405**	2	2.604861
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.147772724**	**0.99999**	**13**
P07379	AINPENGFFGVAPGTSVK	**1.027891441**	2	4.712518
P07379	EEGWLAEHMLILGITNPEGK	**1.356326909**	2	4.018726
P07379	EVEEIDKYLEDQVNADLPYEIER	**0.945123957**	3	3.469648
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	**1.048741826**	3	4.941177
P07379	GLGDVNVEELFGISK	**0.947619947**	2	3.81999
P07379	IGIELTDSPYVVASMR	**0.784284888**	2	3.60867
P07379	MGTSVLEALGDGEFIK	**0.884462975**	2	3.713335
P07379	MGTSVLEALGDGEFIK+Oxidation(0)	**1.072825614**		
P07379	TVIITQEQR	**0.945340758**	2	2.663221
P07379	VECVGDDIAWMK	**0.859311354**	2	2.965854

P07379	VIQGSLDSLPQEVR	**0.982568422**	2	4.023687
P07379	YDNCWLALTDPR	**0.819969021**	2	2.502589
P07379	YLAAAFPSACGK	**1.093946797**	2	2.892146
P07483	**FABPH Fatty acid_binding protein_ heart**	**1.676652621**	**0.39709**	**3**
P07483	NFDDYMK	**4.546798268**	1	2.131093
P07483	QVASMTKPTTIIEK	**0.504801692**	2	3.407787
P07483	WDGQETTLTR	**0.84982001**	2	2.874666
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.310795217**	**0.0333**	**4**
P07632	DGVANVSIEDR	**1.186142266**	2	2.984033
P07632	GDGPVQGVIHFEQK	**1.191723226**	2	3.993328
P07632	HVGDLGNVAAGK	**1.049981203**	2	3.567435
P07632	VISLSGEHSIIGR	**1.074895293**	2	3.260971
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.872411254**	**1.2E-11**	**10**
P07633	AFDNDVDALCNLR	**0.778513427**	2	3.899174
P07633	AYNMLDIIHAVIDER	**0.768615188**	2	4.040467
P07633	GFVDDIIQPSSTR	**1.025348154**	2	4.086548
P07633	HLLGDTNYAWPTAEIAVMGAK	**0.90988223**	2	3.118145
P07633	ICCDLEVLASK	**0.91235945**	2	3.034343
P07633	IMDQAITVGAPVIGLNDSGGAR	**0.624709394**	2	4.458251
P07633	IQEGVESLAGYADIFLR	**0.84837644**	2	4.16819
P07633	LVPELDTVVPLESSK	**0.762089854**	2	3.496977
P07633	SVTNEDVTQEQLGGAK	**0.864016654**	2	5.273132
P07633	TVGIVGNQPNVASGCLDINSSVK	**0.735654405**	2	5.178185
P07687	**HYEP Epoxide hydrolase 1**	**0.967592925**	**9.9E-20**	**23**
P07687	DIELLYPYK	**0.765141409**	2	2.425642
P07687	DKEETLPLGDGWWGPGSKPSAK	**0.946344983**	3	5.489526
P07687	EDESIRPFK	**1.265323455**	2	2.671997
P07687	EDESIRPFKVETSDEEIKDLHQR	**1.026422198**	3	5.635212
P07687	ELEDGGLER	**1.045078437**	2	2.667474
P07687	ENLGQGIMVHK	**0.957310189**	2	2.750094
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	**1.23998659**	3	6.227268
P07687	FHYGFNSNYMK	**0.582624019**	2	2.565713
P07687	FLGYTEKDIELLYPYK	**0.719214996**	2	4.687556
P07687	GGHFAAFEEPK	**0.822285989**	2	3.494933
P07687	IEGLDIHFIHVKPPQLPSGR	**1.579703346**	3	3.675234
P07687	IIPLLTDPK	**0.737359784**	2	2.527847
P07687	KFVSLAELQ	**1.025190831**	2	2.861175
P07687	KQVEILNQYPHFK	**0.756913333**	3	4.834602
P07687	LLAQDIR	**1.070339557**	2	2.518207
P07687	QVEILNQYPHFK	**0.727071898**	2	3.747744
P07687	SEYRELEDGGLER	**0.934021819**	2	2.375244
P07687	SFYTMTPLLGQR	**2.534725641**	2	3.146075
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	**0.833226545**	3	6.466357
P07687	TKIEGLDIHFIHVKPPQLPSGR	**4.531398825**	3	3.882423
P07687	VETSDEEIK	**0.947189244**	2	2.475019
P07687	VETSDEEIKDLHQR	**1.096524784**	2	4.491154
P07687	VFVPTGFSAFPSELLHAPEK	**1.109574878**	2	4.739214
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.187051873**	**9.9E-20**	**96**
P07756	AADTIGYPVMIR	**1.200444796**	2	4.0677
P07756	AADTIGYPVMIR+Oxidation(9)	**1.542219514**		
P07756	AERPDGLILGMGGQTALNCGVELFK	**0.969648995**	3	7.097282
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10)	**1.081771736**		
P07756	AERPDGLILGMGGQTALNCGVELFKR	**1.267799257**	3	4.401909
P07756	AFAISGPFNVQFLVK	**0.901156696**	2	5.075504
P07756	AFAMTNQILVER	**0.839670097**	2	4.448738

P07756	AFAMTNQILVER+Oxidation(3)	**1.053411167**		
P07756	ALENNMSLDEIVK	**0.908114836**	2	4.58932
P07756	ALENNMSLDEIVK+Oxidation(5)	**1.033728439**		
P07756	AQTAHIVLEDGTK	**0.912376704**	2	4.512268
P07756	ATGYPLAFIAAK	**0.880835619**	2	3.061823
P07756	CEMASTGEVACFGEGIHTAFLK	**0.874998176**	3	5.364838
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2)	**0.992913648**		
P07756	CLGLTEAQTR	**0.886423581**	2	3.67824
P07756	DELGLNK	**1.096448608**	2	2.544711
P07756	DGSIDLVINLPNNNTK	**1.05351477**	2	5.461707
P07756	DILNMDK	**1.007235478**	1	1.952491
P07756	EIEYEVVR	**1.215790813**	2	2.302987
P07756	EPLFGISTGNIITGLAAGAK	**1.201268447**	3	5.735453
P07756	ETLMDLGTK	**1.174219693**	1	2.31788
P07756	EVEMDAVGK	**1.578262713**	1	2.211108
P07756	FLEEATR	**0.793409651**	2	2.498129
P07756	FLGVAEQLHNEGFK	**0.936484897**	2	4.680483
P07756	FVHDNYVIR	**0.979317475**	3	3.432724
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	**0.953796097**	3	6.349681
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15)	**1.191744428**		
P07756	GILIGIQQSFRPR	**0.515314872**	2	2.533752
P07756	GLNSESVTEETLR	**1.176634058**	2	4.852907
P07756	GNDVLVIECNLR	**0.862696001**	2	4.48727
P07756	GQILTMANPIIGNGGAPDTTAR	**0.925373718**	2	6.268684
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5)	**1.078689223**		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	**0.633670156**	3	4.852658
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(5)	**0.825815097**		
P07756	GQNQPVLNITNR	**0.905728328**	2	4.228017
P07756	GTTITSVLPKPALVASR	**0.644781361**	2	3.483668
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	**2.610780642**	3	6.620116
P07756	HLPTLEQPIIPSDYVAIK	**1.029571197**	2	5.619544
P07756	IALGIPLPEIK	**1.177076652**	2	3.277439
P07756	IAPSFAVESMEDALK	**1.136947305**	2	5.291159
P07756	IAPSFAVESMEDALK+Oxidation(9)	**0.936612885**		
P07756	IEFEGQSVDFVDPNK	**0.913704567**	2	5.163771
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	**0.905346962**	3	5.333523
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	**0.802622099**	3	5.431993
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	**0.723391867**	3	3.697894
P07756	IMGTSPLQIDR	**1.078584394**	2	3.292778
P07756	IMGTSPLQIDR+Oxidation(1)	**1.392810868**		
P07756	IMGTSPLQIDRAEDR	**0.562954897**	2	2.588139
P07756	KEPLFGISTGNIITGLAAGAK	**0.626107304**	2	5.245474
P07756	KTVVVNCNPETVSTDFDECDK	**0.1635482**	2	4.918505
P07756	LFAEAVQK	**1.001965608**	2	3.13731
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	**1.222700387**	3	4.976204
P07756	LRDADPILR	**1.038242384**	2	3.230293
P07756	LTSIDKWFLYK	**0.779245978**	2	2.576347
P07756	LYFEELSLER	**1.930970097**	2	3.584599
P07756	MCHPSVDGFTPR	**0.80790128**	3	4.969532
P07756	MCHPSVDGFTPR+Oxidation(0)	**1.007733888**		
P07756	MRDILNMDK	**0.65774318**	2	2.461464
P07756	MRDILNMDK+Oxidation(0)	**1.095864379**		
P07756	QADAVYFLPITPQFVTEVIK	**3.381377484**	3	5.233864
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	**13.06482867**	3	4.858395

P07756	QLFSDK	**1.275255581**	1	1.900032
P07756	QLFSDKLNEINEK	**0.895150475**	2	3.729779
P07756	QNLIAEVSTK	**0.914040474**	1	2.799965
P07756	RFLEEATR	**0.851046262**	2	2.67996
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	**0.962860544**	4	5.015932
P07756	RTAVDSGIALLTNFQVTK	**0.945037922**	2	5.020787
P07756	SAYALGGLGSGICPNK	**1.253100342**	2	5.041698
P07756	SAYALGGLGSGICPNKETLMDLGTK	**0.790521245**	2	4.381637
P07756	SFPFVSK	**1.013263947**	1	1.916722
P07756	SIFSAVLDELK	**1.201079501**	2	4.114195
P07756	SIFSAVLDELKVAQAPWK	**0.756615471**	3	4.520582
P07756	SLGQWLQEEK	**0.872484685**	2	3.976821
P07756	SVGEVMAIGR	**0.853253983**	2	3.471697
P07756	SVGEVMAIGR+Oxidation(5)	**1.017518939**		
P07756	TAVDSGIALLTNFQVTK	**1.188251314**	3	6.61693
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	**0.917529585**	3	4.429137
P07756	TFEESFQK	**0.886396786**	2	2.545689
P07756	TLGVDFIDVATK	**0.851849446**	2	4.220283
P07756	TSACFEPSLDYMVTK	**1.067411102**	2	4.78583
P07756	TSACFEPSLDYMVTK+Oxidation(11)	**1.239429585**		
P07756	TVLMNPNIASVQTNEVGLK	**0.780874112**	2	6.407845
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3)	**0.880878562**		
P07756	TVVVNCNPETVSTDFDECDK	**0.613559155**	2	5.703702
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	**1.609996514**	3	5.515955
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	**0.954840644**	3	7.505328
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22)	**1.084766855**		
P07756	VLGTSVESIMATEDR	**0.903372208**	2	4.789233
P07756	VLGTSVESIMATEDR+Oxidation(9)	**1.040796984**		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	**0.809542217**	2	5.947125
P07756	VMIGESVDEK	**0.785380288**	2	3.516449
P07756	VMIGESVDEK+Oxidation(1)	**1.047573676**		
P07756	VSQEHPVVLTK	**1.100175868**	2	3.684518
P07756	VVAVDCGIK	**0.918026716**	2	2.599414
P07756	YMESDGIK	**0.810606672**	2	2.42034
P07756	YMESDGIK+Oxidation(1)	**0.930024733**		
P07824	**ARGI1 Arginase_1**	**1.506043257**	**9.9E-20**	**16**
P07824	ANEQLAAVVAETQK	**1.38294939**	2	5.192086
P07824	DHGDLAFVDVPNDSPFQIVK	**1.521838429**	2	6.303233
P07824	DIVYIGLR	**2.758799331**	2	2.386336
P07824	DVDPGEHYIIK	**2.079694782**	2	3.361029
P07824	EGNHKPETDYLKPPK	**1.913990208**	2	2.689043
P07824	GKFPDVPGFSWVTPCISAK	**1.203058073**	3	4.963168
P07824	LKETEYNVR	**1.509693137**	3	3.347389
P07824	NGTISVVLGGDHSMAIGSISGHAR	**1.095477418**	3	4.418512
P07824	TGLLSGLDIMEVNPTLGK	**1.33577605**	2	5.853251
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9)	**1.006555112**		
P07824	TVNTAVALTLSCFGTK	**1.794390886**	2	5.269279
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	**1.728167748**	4	5.560514
P07824	VMEETFSYLLGR	**5.001208075**	2	3.957619
P07824	VMEETFSYLLGR+Oxidation(1)	**5.759924831**		
P07824	YFSMTEVDK	**1.396654399**	2	2.425884
P07824	YFSMTEVDKLGIGK+Oxidation(3)	**1.072124161**		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.672016901**	**9.9E-20**	**18**
P07871	AEELGLPILGVLR	**0.737253151**	2	4.265287
P07871	AEIVPVTTTVLDDK	**0.77509407**	2	4.420649

P07871	AEIVPVTTTVLDDKGDR	0.707794878	2	3.978006
P07871	AEIVPVTTTVLDDKGDRK	0.599674309	2	3.614794
P07871	DCLIPMGITSENVAER	1.042093546	2	2.878241
P07871	DCLIPMGITSENVAER+Oxidation(5)	1.034698664		
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.758145077	2	6.423011
P07871	GGFKDTTPDELLSAVLTAVLQDVK	0.511557469		
P07871	IAQFLSGIPETVPLSAVNR	2.389725207	2	2.836739
P07871	LKPECLGDISVGNVLQPGAGAAMAR	0.485565697	3	4.324794
P07871	QCSSGLQAVANIAGGIR	0.616266624	2	5.100989
P07871	QDAFALASQQK	0.675905144	2	3.421734
P07871	QKQDAFALASQQK	0.636949715	2	4.114099
P07871	QVVTLLNELK	0.92374459	2	2.596093
P07871	SKAEELGLPILGVLR	0.623593806	3	4.446339
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.639921792	3	4.855532
P07871	TITVSQDEGVRPSTTMEGLAK	0.740434877	2	4.59334
P07871	VNPLGGAIALGHPLGCTGAR	0.590725726	2	4.778697
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.658977754**	**9.9E-20**	**19**
P07872	AFTTWTANAGIEECR	0.828997794	2	4.044143
P07872	ASATFNPELITHILDGSPENTR	0.680747912	2	4.591238
P07872	ASEAHCHYVVVK	0.780166769	3	4.211193
P07872	EIENLILNDPDFQHEDYNFLTR	0.944950104	2	4.41354
P07872	EIGTHKPLPGITVGDIGPK	0.652027498	2	3.550845
P07872	EVAWNLTSVDLVR	0.790698539	2	3.762223
P07872	EYGISDPEEIMWFK	0.823654859	2	3.490992
P07872	FGYEEMDNGYLK	0.610146019	2	3.441206
P07872	GGDFLEGSIITGAQLSQVNAR	0.570587132	2	5.751139
P07872	GLETTATYDPK	0.771509516	2	3.20909
P07872	INESIGQGDLSELPELHALTAGLK	0.655395289	3	5.486875
P07872	LVEIAAK	0.814519684	1	2.060848
P07872	LVGGMVSYLNDLPSQR	1.182119454	2	3.367737
P07872	QSEPEPQILDFQTQQYK	0.622765233	2	4.729783
P07872	SFLVGNAAQSLSK	0.627253956	2	4.500191
P07872	TQEFILNSPTVTSIK	0.681103631	2	4.701035
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	0.610129486	3	5.792662
P07872	YAQVKPDGTYVKPLSNK	2.758840306	3	3.786342
P07872	YDGNVYENLFEWAK	0.754690141	2	5.278123
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.955634066**	**0.99621**	**3**
P07895	AIWNVINWENVSQR	0.965226667	2	3.606142
P07895	GDVTTQVALQPALK	0.907565775	2	3.485644
P07895	HHATYVNNLNVTEEK	0.992309048	2	4.625066
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.924836413**	**5.6E-09**	**25**
P07896	ELSTVDLVVEAVFEDMNLK	1.255041229		
P07896	EWQSLAGPHGSK	1.672667306	2	2.903282
P07896	GGPMFYAASVGLPTVLEK	1.370607435	2	3.937281
P07896	GQGLTGPSLPPGTPVR	0.730285657	2	4.010396
P07896	GWYQYDKPLGR	0.830199746	2	2.935923
P07896	IFNKPVPSLPNMDSVFAEAIAK	0.679114163	3	4.068112
P07896	IGVVVGNCYGFVGNR	0.7393092	2	3.089379
P07896	IIDKPIEPR	0.702058078	2	2.637156
P07896	KGQGLTGPSLPPGTPVR	0.670720139	2	4.58959
P07896	KQYPGVLAPETCVR	0.52774928	2	3.759094
P07896	LCNPPVNAVSPTVIR	0.727408898	2	4.338208
P07896	LGILDAVVK	0.68697414	2	2.815678
P07896	LLEVIPSR	0.670234869	2	2.382654
P07896	LVAQGSPPLK	0.757617449	2	2.376482
P07896	QNPDIPQLEPSDYLR	0.672126513	2	3.774805

P07896	QYPGVLAPETCVR	**0.813508764**	2	3.287457
P07896	TASAQPVSSVGVLGLGTMGR	**1.023721233**	2	5.192828
P07896	TASAQPVSSVGVLGLGTMGR+Oxidation(17)	**1.096011082**		
P07896	TISKEEILER	**0.671625642**	2	2.684462
P07896	VGISVVAVESDPK	**0.72976081**	2	3.819666
P07896	VGLPEVTLGILPGAR	**0.673621027**	2	3.558491
P07896	VSDLAGLDVGWK	**0.670265139**	2	4.115533
P07896	YLSADEALR	**0.830114212**	2	2.657097
P07896	YSPLGDMLCEAGR	**0.665974323**	2	4.076702
P07896	YSSPTTIATVMSLSK	**0.970117896**	2	3.356931
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**0.959472682**	**0.00057**	**3**
P07953	IGGDSGLSAR	**0.580694483**	2	2.391631
P07953	NYEFFRPDNTEAQLIR	**0.818965618**	2	2.97137
P07953	TIQTAEALGVPYEQWK	**1.857310324**	2	2.963765
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**0.841634461**	**1.2E-14**	**5**
P08009	LCYNPDFEK	**0.819543096**	2	2.810278
P08009	LLLEYTDSSYEEK	**1.001928444**	2	4.815895
P08009	LLLEYTDSSYEEKR	**0.793955905**	2	3.835348
P08009	NQVFEATCLDAFPNLK	**0.534729189**	2	4.897267
P08009	SQWLNEK	**0.985645305**	2	2.651681
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**0.816908542**	**0.66566**	**15**
P08010	FLSKPIFAK	**0.52039072**	1	1.932747
P08010	IRVDVLENQAMDTR	**0.64085985**	3	4.211671
P08010	ITYVDFLVYDVLDQHR	**1.398640155**	2	4.808164
P08010	KKPEYLEGLPEK	**0.802639345**	3	4.432535
P08010	KPEYLEGLPEK	**0.924642675**	2	3.712527
P08010	KYSMGDAPDYDR	**0.616327931**	2	3.585454
P08010	LFLEYTDTSYEDK	**0.641440173**	2	5.421856
P08010	LFLEYTDTSYEDKK	**0.796036662**	2	4.268782
P08010	LQLAMVCYSPDFER	**1.036049661**	2	4.804973
P08010	LQLAMVCYSPDFER+Oxidation(4)	**1.193965933**		
P08010	SQWLSEK	**0.940182823**	2	2.456386
P08010	VDVLENQAMDTR	**0.741613415**	2	4.666551
P08010	VDVLENQAMDTR+Oxidation(8)	**0.943650644**		
P08010	YSMGDAPDYDR	**0.753788128**	2	3.11258
P08010	YSMGDAPDYDR+Oxidation(2)	**0.907929424**		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.931643702**	**0.90528**	**7**
P08011	IYHTIAYLTPLPQPNR	**0.90953909**	2	4.815242
P08011	MMFLSSATAFQR	**1.030334089**	2	3.305546
P08011	MMFLSSATAFQR+Oxidation(0)	**0.960079006**		
P08011	MMFLSSATAFQR+Oxidation(0)	**1.058622181**		
P08011	MMFLSSATAFQR+Oxidation(1)	**1.058622181**	2	3.060802
P08011	VFANPEDCAGFGK	**0.842644758**	2	4.574967
P08011	VFANPEDCAGFGKGENAK	**0.544380993**	2	4.526186
P08081	**CLCA Clathrin light chain A**	**1.324549594**	**0.11083**	**2**
P08081	LEALDANSR	**1.094792754**	2	2.581615
P08081	WREEQTER	**1.549478233**	2	2.452036
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**0.925758448**	**0.90098**	**2**
P08290	EEQEFVVK	**0.97610798**	1	1.948143
P08290	WVDGTEYR	**0.889245812**	2	2.314624
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.098621602**	**0.39829**	**4**
P08461	AAPAAAAAAPPGPR	**1.000398255**	2	2.623331
P08461	DVPLGTPLCIIVEK	**1.411271169**	2	3.141072

P08461	GLETIASDVVSLASK	0.917358548	2	3.905558
P08461	VAPTPAGVFIDIPISNIR	0.889998738	2	4.907052
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.882272965**	**7.6E-05**	**9**
P08503	AFTGFIVEADTPGIHIGK	0.777578386	2	4.295234
P08503	ANWYFVLTR	1.026917963	2	2.624996
P08503	EEIIPVAPDYDK	0.972356658	2	3.288412
P08503	GITFEDVR	0.842233653	2	2.434762
P08503	IYQIYEGTAQIQR	0.902871723	2	4.972477
P08503	KGDEYVINGQK	0.92394404	2	4.340618
P08503	QEPGLGFSFELTEQQK	0.847149265	2	3.20518
P08503	SGEYPFPLIK	0.793526191	2	2.485406
P08503	TRPTVAAGAVGLAQR	0.63214513	2	4.462135
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.061548919**	**0.48843**	**10**
P08541	DELQNHFIK	1.184295684	2	2.385172
P08541	FEIFSTSISK	1.432720158	2	2.437663
P08541	FEIFSTSISKDELQNHFIK	1.10069848	2	4.175125
P08541	FILPPSYVPVILSGLAGK	1.134825173	3	5.635575
P08541	GHEVTVLKPSAYFFLDPK	1.357531634	2	4.078653
P08541	HKEWDTFYSEILGRPTTVDETMSK	1.630085478	3	4.41874
P08541	LDFLSALEEVIDNPFYK	1.061906216		
P08541	LLDVWTYELPR	1.88691193	3	3.891724
P08541	NVMLLSTIHHDQPMKPLDR	1.042877252	3	3.617476
P08541	VEIWLIR	1.048472391	2	2.928756
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.078640221**	**0.98684**	**10**
P08542	EIINNPFYK	1.105617549	1	2.196939
P08542	FETFPTSVSKDELENYFIK	0.882359434	2	4.075817
P08542	FSPGYKIEKSSGR	1.465402558	2	2.337285
P08542	KWDPFYSEILGRPTTLAETMGK	1.002183373	2	3.950442
P08542	LVDVWTYELQR	1.050001258	2	3.510472
P08542	NAVWLSTIHHDQPMKPLDK	0.836643449	3	3.308901
P08542	NAVWLSTIHHDQPMKPLDK+Oxidation(13)	1.318403634		
P08542	SDLFNALKEIINNPFYK	0.908515224	2	2.328739
P08542	TPATLGPNTR	1.006386336	2	2.315405
P08542	WDPFYSEILGRPTTLAETMGK	1.04575211	2	3.456259
P08683	**CP2CB Cytochrome P450 2C11**	**0.777814018**	**0.06356**	**17**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	0.830103581	3	5.235713
P08683	EALVDLGEEFSGR	0.666435076	2	4.03007
P08683	EHQESLDKDNPR	0.443922753	2	4.110683
P08683	FDPGHFLDER	0.529872801	2	2.342104
P08683	FDYKDPTFLNLMHR	1.028931285	3	5.037016
P08683	FNENFR	0.737155092	1	1.979918
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	0.819796199	3	5.247375
P08683	GTNVIVSLSSILHDDKEFPNPEK	0.848122018	2	5.194221
P08683	ICAGEALAR	0.848883878	2	2.806861
P08683	LPPGPTPLPIIGNTLQIYMK	0.663347281	3	3.850737
P08683	NYVLEK	1.05350459	1	1.961482
P08683	SQMPYTDAVVHEIQR	0.757920657	2	4.255602
P08683	SQMPYTDAVVHEIQR+Oxidation(2)	0.964171376		
P08683	VKEHQESLDKDNPR	0.986574251	3	5.026835
P08683	VQEEIER	0.848691053	2	2.564214
P08683	YGLLLLLK	0.631222549	2	3.032969
P08683	YIDLVPTNLPHLVTR	0.508137777	2	4.177147
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**1.182782064**	**0.46334**	**3**
P08733	GADPEETILNAFK	0.689666022	2	3.500387
P08733	NEEIDEMIK	1.323924539	1	2.497734

P08733	NLVHIITHGEEKD	0.836892839	2	2.978891
P09006	**SPA3N Serine protease inhibitor A3N**	**1.285791321**	**0.00637**	**2**
P09034	**ASSY Argininosuccinate synthase**	**2.119770534**	**9.9E-20**	**15**
P09034	APNTPDVLEIEFK	2.120002132	2	3.341692
P09034	DGTTHSTSLDLFMYLNEVAGK	5.015613706	2	5.794582
P09034	EFVEEFIWPAVQSSALYEDR	1.96462244	3	5.624639
P09034	EQGYDVIAYLANIGQK	3.076588348	2	4.552794
P09034	FAELVYTGFWHSPECEFVR	8.550442809	2	5.14998
P09034	FELTCYSLAPQIK	3.907345591	2	4.274148
P09034	GRNDLMEYAK	1.653023545	2	3.060752
P09034	IDIVENR	1.291570431	2	2.499088
P09034	KVFIEDVSK	1.464515026	3	3.768346
P09034	NDLMEYAK	1.217377839	2	2.645692
P09034	SPWSMDENLMHISYEAGILENPK	2.913249308	3	5.353886
P09034	TQDPAKAPNTPDVLEIEFK	1.272163951	2	4.745066
P09034	TQDPAKAPNTPDVLEIEFKK	1.115668326	3	4.287529
P09034	VFIEDVSK	1.468199733	2	2.624222
P09034	VQVSVFK	1.762163121	2	2.407244
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.115801818**	**0.99761**	**4**
P09041	FHVEEEGK	0.983475335	2	2.727597
P09041	LGDVYVNDAFGTAHR	1.07608636	3	4.076824
P09041	VDFNVPMK	0.9189577	1	2.068894
P09041	VSHVSTGGGASLELLEGK	0.976023127	2	5.654178
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.174103943**	**0.66879**	**2**
P09117	VLAAVYK	1.192015669	2	2.650187
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	1.240346372	3	3.621385
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.3671771**	**0.12797**	**2**
P09139	IGLLGYNATTENADR	1.543559896	2	3.32791
P09139	VLNAPPGISLISFNDK	1.362013065	2	3.049233
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**3.508737536**	**0.00095**	**4**
P09367	ALGVNTVGAQTLK	2.358020491	2	3.574248
P09367	AQLGLNELLK	7.122631218	1	2.009157
P09367	LGLPATIVVPSTTPALTIER	2.345356972	2	3.30031
P09367	MDSSQPSGSFK	3.508161997	2	2.311677
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.003318568**	**0.79543**	**13**
P09495	AEGDAAALNR	1.259066578	2	2.309447
P09495	EDKYEEEIK	1.048005796	1	2.631262
P09495	EENVGLHQTLDQTLNELNCI	1.230688419	2	4.936319
P09495	IQALQQQADDAEDR	0.810778523	2	4.655852
P09495	IQLVEEELDR	0.868343321	2	3.591852
P09495	IQLVEEELDRAQER	0.818405971	2	2.881613
P09495	KLVILEGELER	1.160963304	2	3.049757
P09495	LEEAEKAADESER	0.60680554	2	4.09306
P09495	LVILEGELER	0.955758717	2	3.334882
P09495	MEIQEMQLK	0.735166933	2	2.658723
P09495	RIQLVEEELDR	1.042707767	2	2.845778
P09495	YEEEIK	0.955190376	1	1.964746
P09495	YSEKEDKYEEEIK	0.823424541	2	4.182867
P09527	**RAB7A Ras_related protein Rab_7a**	**1.289953406**	**0.28474**	**5**
P09527	DPENFPFVVLGNK	1.523655276	2	3.528469
P09527	EAINVEQAFQTIAR	1.245379489	2	2.810843
P09527	GADCCVLVFDVTAPNTFK	1.158592685	2	4.124101
P09527	TLDSWRDEFLIQASPR	0.605887363	3	3.742782
P09527	VIILGDSGVGK	1.235194193	2	2.873304
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.141612992**	**0.46659**	**4**

P09605	GTGGVDTAAVADVYDISNIDR	**0.954302689**	2	4.784618
P09605	LSEMTEQDQQR	**1.141569031**	2	3.629936
P09605	LSEMTEQDQQR+Oxidation(3)	**0.650643388**		
P09605	SEVELVQIVIDGVNYLVDCEK	**1.299978746**		
P09606	**GLNA Glutamine synthetase**	**0.840118077**	**0.00169**	**6**
P09606	CIEEAIDK	**0.916438935**	2	2.849025
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	**1.102089876**	3	4.712731
P09606	LTGFHETSNINDFSAGVANR	**1.262911318**	2	6.077756
P09606	RLTGFHETSNINDFSAGVANR	**0.850432516**	3	5.081582
P09606	TCLLNETGDEPFQYK	**1.674851838**	2	5.31174
P09606	TCLLNETGDEPFQYKN	**1.525904538**	2	4.384977
P09811	**PYGL Glycogen phosphorylase_ liver form**	**0.848993412**	**6.2E-10**	**20**
P09811	DFSELEPDKFQNK	**0.818788292**	2	3.502312
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	**0.766367221**	3	4.714675
P09811	EGWQVEEADDWLR	**0.804973584**	2	3.823123
P09811	GIVGVENVAELK	**0.856733277**	2	3.090299
P09811	GIVGVENVAELKK	**0.921494952**	2	2.443712
P09811	HLQIIYEINQK	**0.760867558**	2	3.648097
P09811	IFVDIEK	**0.857532364**	1	2.082982
P09811	INPSSMFDVHVK	**0.704112815**	2	3.069651
P09811	LHSFVGDDIFLR	**0.963747414**	2	2.333138
P09811	LVIDQIDNGFFSPNQPDLFK	**0.772574849**	2	4.666643
P09811	LVTSVAEVVNNDPMVGSK	**0.718736118**	2	2.980352
P09811	TFAYTNHTVLPEALER	**0.697489015**	2	4.020741
P09811	VDDVAALDK	**0.755408716**	1	2.128051
P09811	VDDVAALDKK	**0.739786646**	2	3.11268
P09811	VFADYEAYVK	**0.860073975**	2	2.401982
P09811	VIPATDLSEQISTAGTEASGTGNMK	**0.660531649**	2	6.121733
P09811	VLYPNDNFFEGK	**0.80288681**	2	3.063613
P09811	VSQLYMNQK	**2.175425961**	2	3.091756
P09811	WLLLCNPGLADLIAEK	**1.059638481**	2	5.043386
P09811	YEYGIFNQK	**0.831854085**	2	2.569544
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**0.910768504**	**0.6024**	**12**
P09812	GLAGVENVSDLKK	**0.799324664**	2	3.034668
P09812	GYNAQEYYDRIPELR	**0.256746731**	2	2.770464
P09812	HLQIIYEINQR	**2.399206252**	2	2.916353
P09812	IGEEYISDLDQLR	**0.877438826**	2	3.854689
P09812	IGEEYISDLDQLRK	**1.009869007**	2	2.924317
P09812	LITAIGDVVNHDPAVGDR	**1.080774235**	2	3.605339
P09812	NLAENISR	**0.811012174**	1	2.473176
P09812	QIIEQLSSGFFSPK	**1.241001382**	2	3.258137
P09812	TNFDAFPDK	**1.210451417**	2	2.323047
P09812	VHINPNSLFDVQVK	**0.766978792**	2	2.808653
P09812	VIPAADLSEQISTAGTEASGTGNMK	**1.581353477**	2	5.036545
P09812	WLVLCNPGLAEVIAER	**0.905581315**	2	4.29391
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**0.90144344**	**9.9E-20**	**6**
P09875	ANVVASALAQIPQK	**0.696702363**	3	4.258505
P09875	FSGGLPLPPSYVPVVLSELSDR	**1.156957283**	3	4.645263
P09875	IILNELAQR	**0.862076006**	2	3.022376
P09875	SDLEYSFAK	**1.259892325**	2	2.507524
P09875	VDFSILSTTGLLTALK	**0.688934966**	2	4.534775
P09875	VFNEYSDVVENLCK	**0.951336774**	2	3.461263
P09895	**RL5 60S ribosomal protein L5**	**1.100273403**	**0.00075**	**5**
P09895	GAVDGGLSIPHSTK	**1.11323736**	2	4.376074
P09895	HIMGQNVADYMR	**0.858278071**	2	3.01488
P09895	NNVTPDMMEEMYK	**1.037962827**	2	3.352194
P09895	RFPGYDSESK	**1.354879131**	2	2.840241

P09895	YLMEEDEDAYKK	**1.1421387**	2	3.253284
P0C0S7	**H2AZ Histone H2A.Z**	**0.466527805**	**0.18646**	**2**
P0C0S7	ATIAGGGVIPHIHK	**0.57027138**	2	3.751095
P0C0S7	GDEELDSLIK	**0.719745404**	2	3.518457
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.831047733**	**9.9E-20**	**17**
P0C2X9	AIEAAVLAR	**0.779135378**	2	2.968482
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	**0.558407083**	3	5.561224
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	**0.63460077**	2	4.758953
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	**0.872236546**	3	3.749143
P0C2X9	EEIFGPVLTVYVYPDEK	**1.034873463**	2	4.145845
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	**0.901671442**	2	5.184915
P0C2X9	KEWDLKPVADR	**0.758187783**	2	3.341376
P0C2X9	LYVPQSLWPQIK	**0.762865834**	2	3.266038
P0C2X9	NAAGNFYINDK	**1.257957174**	2	3.512446
P0C2X9	NFHFVHSSADVDSVVSGTLR	**0.836271804**	2	5.858699
P0C2X9	SAFEYGGQK	**0.763249961**	2	2.45889
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	**0.845033771**	3	5.720127
P0C2X9	STGSVVGQQPFGGAR	**0.757822335**	2	4.400449
P0C2X9	TVIQAEIDAAAELIDFFR	**0.780824555**		
P0C2X9	VANEPILAFTQGSPER	**0.893427514**	2	5.411601
P0C2X9	VGNPAEDFGTFFSAVIDAK	**3.316392858**	2	4.96786
P0C2X9	YQLSPFNHGHK	**0.809913805**	2	2.935117
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.013394459**	**0.95257**	**4**
P0C5H9	DRDVTFSPATIEEELIK	**1.006432599**	2	4.711087
P0C5H9	DVTFSPATIEEELIK	**1.011703512**	2	3.209631
P0C5H9	IINEVSKPLAHHIPVEK	**1.280122181**	3	3.812029
P0C5H9	ILDDWGEMCK	**1.040242287**	2	2.390073
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.185106088**	**4.7E-06**	**3**
P0C6F1	EDSVLGLQAFASWR	**0.933234031**	2	2.303156
P0C6F1	TMPLISDLR+Oxidation(1)	**1.412791745**		
P0C6F1	TMPLISDLRNPALR	**1.2624174**	2	2.396952
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.10180034**	**0.08592**	**12**
P10111	EGMSIVEAMER	**1.140866166**	2	2.990081
P10111	FEDENFILK	**1.048650852**	2	3.165493
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	**1.05571074**	3	5.952951
P10111	HTGPGILSMANAGPNTNGSQFFICTAK+Oxidation(8)	**1.005480594**		
P10111	IIPGFMCQGGDFTR	**0.956794528**	2	3.32359
P10111	ITISDCGQL	**0.813075311**	1	1.968194
P10111	KITISDCGQL	**1.122859747**	2	3.330281
P10111	SIYGEKFEDENFILK	**0.890009559**	2	4.425166
P10111	TEWLDGK	**0.910448538**	2	2.351271
P10111	VCFELFADK	**1.242553966**	2	3.320732
P10111	VCFELFADKVPK	**0.937108811**	2	3.857755
P10111	VKEGMSIVEAMER	**0.705709615**	2	3.000339
P10536	**RAB1B Ras_related protein Rab_1B**	**1.091952627**	**1**	**3**
P10536	MGPGAASGGERPNLK	**1.023645209**	2	3.295355
P10536	NATNVEQAFMTMAAEIK+Oxidation(11)	**1.097787151**		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9)	**1.104397933**		
P10633	**CP2D1 Cytochrome P450 2D1**	**0.989685486**	**0.65362**	**4**
P10633	LVEESLTEVSGFIPEVLNTFPALLR	**0.970786467**		
P10633	SQGVILASYGPEWR	**0.782387474**	2	4.197389
P10633	TFMALLDNLLAENR	**0.883214519**	2	3.502585
P10633	YGDVFSLQK	**1.1068099**	2	2.84155
P10634	**CP2DQ Cytochrome P450 2D26**	**0.792857782**	**9.9E-20**	**17**

P10634	ACLGEPLAR	**0.939262877**	2	2.665581
P10634	AVSNVIASLVYAR	**0.682228774**	3	4.463062
P10634	DMTDAFLAEMQK	**0.984205433**	2	3.027043
P10634	EAEHPFNPSILLSK	**1.167697559**	2	3.082219
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	**0.803591691**	3	4.909128
P10634	FADIVPTNIPHMTSR	**0.892801514**	2	2.668834
P10634	FEYEDPFFNR	**0.664639603**	2	2.698626
P10634	FHPEHFLDAQGNFVK	**0.827677052**	2	4.805937
P10634	GNPESSFNDENLR	**1.098623735**	2	4.206139
P10634	GTTLIPNLSSVLK	**0.716711033**	2	2.545521
P10634	GTTLIPNLSSVLKDETVWEKPLR	**0.557255403**	2	4.334306
P10634	GVVLAPYGPEWR	**0.730038527**	2	3.436186
P10634	LNSFIALVDK	**1.547475985**	2	2.482055
P10634	RFEYEDPFFNR	**0.838645509**	3	4.071996
P10634	SLEQWVTEEAGHLCDTFAK	**0.837408093**	2	4.965187
P10634	SWDPAQPPR	**0.796226029**	2	2.653176
P10634	VHEEIDEVIGQVR	**0.767454534**	2	4.552141
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**0.917581131**	**9.9E-20**	**34**
P10719	AGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGR	**1.440687823**		
P10719	AHGGYSVFAGVGER	**1.835862898**	2	3.93031
P10719	AIAELGIYPAVDPLDSTSR	**0.851654242**	3	5.562542
P10719	DQEGQDVLLFIDNIFR	**2.013856458**		
P10719	EGNDLYHEMIESGVINLK	**0.8738677**	2	5.1579
P10719	FLSQPFQVAEVFTGHMGK	**1.070032206**	2	4.06247
P10719	FTQAGSEVSALLGR	**0.914526416**	2	4.842857
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	**1.493068811**	3	4.730116
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	**2.01604741**	3	4.720021
P10719	IGLFGGAGVGK	**1.028057236**	2	3.025123
P10719	IGLFGGAGVGKTVLIMELINNVAK	**0.847142763**	3	3.494787
P10719	ILQDYK	**0.950522757**	1	2.170173
P10719	IMDPNIVGSEHYDVAR	**0.749790236**	2	4.818998
P10719	IMDPNIVGSEHYDVAR+Oxidation(1)	**1.019148676**		
P10719	IMNVIGEPIDER	**0.841591665**	2	4.170508
P10719	IMNVIGEPIDER+Oxidation(1)	**1.13400406**		
P10719	IPSAVGYQPTLATDMGTMQER	**1.651103851**	2	4.837956
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14)	**2.198542834**		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17)	**1.608687608**		
P10719	LVLEVAQHLGESTVR	**0.936169884**	2	4.67961
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	**1.048131699**	3	4.985281
P10719	SLQDIIAILGMDELSEEDKLTVSR	**0.690128312**	3	5.441735
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10)	**0.928734574**		
P10719	TIAMDGTEGLVR	**0.804835401**	2	3.371756
P10719	TIAMDGTEGLVR+Oxidation(3)	**0.948297116**		
P10719	TREGNDLYHEMIESGVINLK	**0.827281558**	2	6.109365
P10719	TVLIMELINNVAK	**0.893354455**	2	4.571095
P10719	TVLIMELINNVAK+Oxidation(4)	**1.087573698**		
P10719	VALTGLTVAEYFR	**1.597929939**	2	4.072749
P10719	VALVYGQMNEPPGAR	**1.015796692**	2	4.363111
P10719	VALVYGQMNEPPGAR+Oxidation(7)	**1.064204329**		
P10719	VLDSGAPIK	**0.966790219**	2	3.028409
P10719	VLDSGAPIKIPVGPETLGR	**0.76846952**	3	4.761925
P10719	VVDLLAPYAK	**0.858289108**	2	3.03147
P10760	**SAHH Adenosylhomocysteinase**	**1.249424427**	**9.9E-20**	**18**
P10760	ALDIAENEMPGLMR	**1.039736216**	2	4.316842
P10760	ALDIAENEMPGLMR+Oxidation(12)	**1.222385146**		
P10760	ATDVMIAGK	**1.02911258**	2	2.824625
P10760	DGPLNMILDDGGDLTNLIHTK	**1.201629458**	2	5.419811

P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5)	**1.193542418**		
P10760	EMYSASKPLK	**2.04407092**	2	2.495085
P10760	FDNLYGCR	**1.179942556**	2	2.861892
P10760	GETDEEYLWCIEQTLHFK	**1.425744493**	2	4.279146
P10760	GISEETTTGVHNLYK	**1.166175852**	2	4.13385
P10760	IILLAEGR	**1.477850476**	2	2.803187
P10760	KLDEAVAEAHLGK	**1.217135904**	3	5.16178
P10760	LDEAVAEAHLGK	**1.259845919**	2	3.852326
P10760	RATDVMIAGK	**1.160292499**	2	2.693585
P10760	SKFDNLYGCR	**1.254776241**	2	2.876086
P10760	VAVVAGYGDVGK	**1.534940851**	2	4.235604
P10760	VNIKPQVDR	**1.200785718**	2	2.919374
P10760	WLNENAVEK	**1.322085556**	2	3.16334
P10760	WSSCNIFSTQDHAAAAIAK	**1.15281856**	2	5.086745
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**0.831916297**	**0.00014**	**2**
P10818	HEEHERPEFVAYPHLR	**0.894986612**	3	3.320403
P10818	SRHEEHERPEFVAYPHLR	**0.551078016**	3	3.669015
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**0.902311003**	**0.00231**	**28**
P10860	ALASLMTYK	**0.893566798**	2	3.120529
P10860	CAVVDVPFGGAK	**1.044604445**	2	3.288343
P10860	CVGVGESDGSIWNPDGIDPK	**0.856640179**	2	5.151681
P10860	DDGSWEVIEGYR	**1.26903615**	2	4.09852
P10860	DIVHSGLAYTMER	**1.380571523**	2	3.319003
P10860	DIVHSGLAYTMER+Oxidation(10)	**1.503571513**		
P10860	DSNYHLLMSVQESLER	**0.84837372**	2	3.698667
P10860	DSNYHLLMSVQESLER+Oxidation(7)	**2.080804769**		
P10860	EDDPNFFK	**0.699257985**	1	2.06388
P10860	GASIVEDKLVEDLK	**0.7642439**	2	3.425748
P10860	GFIGPGIDVPAPDMSTGER	**0.836506137**	2	5.552316
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13)	**0.94997043**		
P10860	HGGTIPVVPTAEFQDR	**0.913904028**	2	4.468529
P10860	IIAEGANGPTTPEADK	**0.797697241**	2	5.261125
P10860	IIAEGANGPTTPEADKIFLER	**0.879545165**	3	4.6932
P10860	KGFIGPGIDVPAPDMSTGER	**0.792854763**	2	5.539396
P10860	KGFIGPGIDVPAPDMSTGER+Oxidation(14)	**0.774430691**		
P10860	LQHGSILGFPK	**0.773635799**	2	2.722525
P10860	MVEGFFDR	**0.763812235**	2	2.828782
P10860	MVEGFFDR+Oxidation(0)	**0.997470086**		
P10860	NLNHVSYGR	**1.013168154**	2	2.334039
P10860	NYTDNELEK	**0.848849691**	2	2.425296
P10860	RDDGSWEVIEGYR	**0.886266024**	2	4.242008
P10860	TAAYVNAIEK	**1.055721311**	2	3.602264
P10860	TFVVQGFGNVGLHSMR	**0.589802967**	2	3.998473
P10860	VYEGSILEADCDILIPAASEK	**0.860680192**	3	5.922235
P10860	YNLGLDLR	**0.920127607**	2	3.129853
P10860	YSTDVSVDEVK	**1.027927684**	2	3.187912
P10867	**GGLO L_gulonolactone oxidase**	**1.070552078**	**1**	**7**
P10867	GDDILLSPCFQR	**1.024942713**	1	2.074422
P10867	GVQFQNWAK	**1.061259773**	2	2.407335
P10867	LDPTGMFLNSYLEK	**0.809125139**	2	4.415738
P10867	LDYWLAYETIMK	**0.993862432**	2	4.368528
P10867	NADVFQAAR	**0.919045156**	2	2.805848
P10867	TYGCSPEVYYQPTSVEEVR	**1.073643319**	2	4.904958
P10867	VVAHYPVEVR	**1.047444345**	2	2.796622
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.056051841**	**0.26968**	**4**

P10868	EHWIIECNDGVFQR	1.333968572	2	4.022839
P10868	WETPYMHSLAAAAASR	1.523639885	2	3.91216
P10868	YTDITAMFEETQVPALLEAGFQR	0.990095316	3	6.55796
P10868	YYAFPQMITPLVTK	0.996701582	2	3.481607
P10888	COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial	0.952133402	1	2
P10888	IQFNESFAEMNK	0.946751944	2	4.51784
P10888	SEDYALPSYVDR	0.868701546	2	4.045376
P11030	ACBP Acyl_CoA_binding protein	1.228829343	1.5E-09	3
P11030	QATVGDVNTDRPGLLDLK	1.36285562	3	3.652455
P11030	TQPTDEEMLFIYSHFK	8.950117081	2	4.393717
P11030	WDSWNK	0.931194	1	2.037078
P11232	THIO Thioredoxin	1.111396614	0.99793	2
P11232	EAFQEALAAAGDK	1.346144778	2	4.316803
P11232	VGEFSGANK	1.027362062	2	2.959635
P11240	COX5A Cytochrome c oxidase subunit 5A_ mitochondrial	0.898139693	7.4E-09	5
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.243892421	3	6.728961
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.209456678	3	6.626053
P11240	GMNTLVGYDLVPEPK	0.797400898	2	3.662183
P11240	LNDFASAVR	0.902801975	2	3.261882
P11240	RLNDFASAVR	0.837883764	2	2.975237
P11348	DHPR Dihydropteridine reductase	0.840455036	0.02284	11
P11348	AALDGTPGMIGYGMAK	1.234324019	2	3.87694
P11348	EGGLLTLAGAK	0.914177251	2	3.123622
P11348	GAVHQLCQSLAGK	1.024784792	3	4.601231
P11348	MTDSFTEQADQVTAEVGK	0.769720155	2	5.547447
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0)	0.874314771		
P11348	NCDLMWK	0.679220469	1	2.080392
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	0.90572365	2	5.363461
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3)	0.846887861		
P11348	QSIWTSTISSHLATK	0.782008841	2	3.861891
P11348	RPNSGSLIQVVTTDGK	0.850552059	2	4.089117
P11348	VDAILCVAGGWAGGNAK	0.795156341	2	4.489226
P11442	CLH Clathrin heavy chain 1	1.122902943	0.83086	37
P11442	AFMTADLPNELIELLEK	0.884251208	3	4.596352
P11442	AHIAQLCEK	1.349177856	1	2.256866
P11442	ALEHFTDLYDIK	0.766118379	3	3.876439
P11442	CNEPAVWSQLAK	1.049445705	2	3.255463
P11442	EDKLECSEELGDLVK	1.008349595	2	2.716795
P11442	FDVNTSAVQVLIEHIGNLDR	0.936735213	3	3.624012
P11442	FNALFAQGNYSEAAK	1.083573449	2	4.576741
P11442	GQCDLELINVCNENSLFK	0.859798924	2	5.097107
P11442	GQFSTDELVAEVEK	0.905554652	2	4.289725
P11442	GQFSTDELVAEVEKR	0.971823749	2	3.647829
P11442	HELIEFR	1.263450029	2	2.349464
P11442	HSSLAGCQIINYR	0.86224356	2	2.713678
P11442	IHEGCEEPATHNALAK	1.028183121	2	5.305377
P11442	ISGETIFVTAPHEATAGIIGVNR	1.021074422	2	5.329196
P11442	IVLDNSVFSEHR	1.084543795	2	2.969058
P11442	IYIDSNNNPER	0.758324865	2	3.193036
P11442	KFDVNTSAVQVLIEHIGNLDR	0.814830297	3	5.637635
P11442	KFNALFAQGNYSEAAK	0.889491127	2	4.36682
P11442	LAELEEFINGPNNAHIQQVGDR	1.005752193	2	5.052642
P11442	LHIIEVGTPPTGNQPFPK	0.841853675	2	4.188672
P11442	LLYNNVSNFGR	1.470445328	2	2.340869
P11442	LPVVIGGLLDVDCSEDVIK	2.134945623	2	5.220828

P11442	LTDQLPLIIVCDR	**0.896919193**	2	3.240528
P11442	NLQNLLILTAIK	**0.677886139**	2	3.917333
P11442	NNLAGAEELFAR	**1.274001368**	2	3.534899
P11442	NNRPSEGPLQTR	**0.95352951**	3	4.19138
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	**1.098581917**	3	5.737468
P11442	SVDPTLALSVYLR	**0.877541685**	2	2.891626
P11442	SVNESLNNLFITEEDYQALR	**1.262212172**	3	5.126964
P11442	TLQIFNIEMK	**1.01609021**	2	2.889971
P11442	TSIDAYDNFDNISLAQR	**1.091597815**	2	4.362551
P11442	VGEQAQVVIIDMNDPSNPIR	**0.788319331**	2	4.622175
P11442	VIQCFAETGQVQK	**1.127156631**	2	4.629882
P11442	VSQPIEGHAASFAQFK	**0.846676905**	2	4.366082
P11442	WLLLTGISAQQNR	**0.889841565**	2	3.255105
P11442	YESLELCRPVLQQGR	**0.859926847**	2	2.676277
P11442	YIEIYVQK	**1.065032903**	1	2.369032
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.404099635**	**9.9E-20**	**6**
P11497	GGSWVVIDPTINPR	**1.634023776**	2	2.758224
P11497	GSVLEPEGTVEIK	**2.622724782**	2	2.699714
P11497	ITSENPDEGFKPSSGTVQELNFR	**1.951322092**	3	3.981685
P11497	TLRDPSLPLLELQDIMTSVSGR	**1.311614943**	3	3.361255
P11497	VNNADDFPNLFR	**1.522946285**	2	2.41684
P11497	VQQAELHTGSLPQIQSTALR	**0.923750538**	3	3.541937
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.991478681**	**0.92083**	**9**
P11507	DIVPGDIVEIAVGDKVPADIR	**0.632140457**	2	3.539428
P11507	IGIFGQDEDVTSK	**0.684382101**	2	3.386089
P11507	IRDEMVATEQER	**1.082732521**	2	3.106571
P11507	LDEFGEQLSK	**1.104109243**	2	2.823526
P11507	NAENAIEALK	**0.99118653**	2	2.339428
P11507	NAENAIEALKEYEPEMGK	**1.194555631**	2	3.939089
P11507	SEIGIAMGSGTAVAK	**1.011500003**	2	2.711593
P11507	TASEMVLADDNFSTIVAAVEEGR	**1.013538909**	3	4.803927
P11507	VDQSILTGESVSVIK	**0.930560081**	2	4.636975
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.004486257**	**1.7E-15**	**25**
P11598	DASVVGFFR	**1.01436971**	2	2.700565
P11598	DGEEAGAYDGPR	**1.066077059**	2	3.086436
P11598	DLLTAYYDVDYEK	**1.213330529**	2	3.241627
P11598	EATNPPIIQEEKPK	**1.1377572**	2	3.476962
P11598	EYDDNGEGITIFRPLHLANK	**1.130835552**	2	4.215931
P11598	FAHTNVESLVK	**1.386079386**	3	3.354488
P11598	FIQESIFGLCPHMTEDNKDLIQGK	**0.798129848**	3	5.034542
P11598	FISDKDASVVGFFR	**0.547768262**	2	4.289568
P11598	FLQEYFDGNLK	**0.868469305**	2	3.393449
P11598	FLQEYFDGNLKR	**0.775661523**	2	3.09834
P11598	FVMQEEFSR	**0.943373389**	2	2.5818
P11598	GFPTIYFSPANK	**3.14394765**	2	2.772385
P11598	IFRDGEEAGAYDGPR	**0.624668394**	2	3.647818
P11598	LAPEYEAAATR	**0.939122847**	2	3.441258
P11598	LNFAVASR	**1.089993419**	2	2.441781
P11598	LSKDPNIVIAK	**0.923440099**	3	3.790059
P11598	MDATANDVPSPYEVK	**0.881554495**	2	4.481105
P11598	MDATANDVPSPYEVK+Oxidation(0)	**1.118924837**		
P11598	QAGPASVPLR	**2.46638155**	2	2.547553
P11598	RLAPEYEAAATR	**0.843874544**	2	3.549448
P11598	SEPIPETNEGPVK	**0.968470195**	2	2.978814
P11598	TADGIVSHLK	**1.912845553**	2	2.906025
P11598	TFSHELSDFGLESTTGEIPVVAIR	**1.039612964**	2	6.226573

P11598	VDCTANTNTCNK	3.793858819	2	4.245453
P11598	YGVSGYPTLK	0.979130672	2	3.202235
P11711	**CP2A1 Cytochrome P450 2A1**	**0.822863716**	**9.9E-20**	**6**
P11711	GEQATYNTLFK	1.434381164	2	2.847202
P11711	GTDVFPILGSLMTDPK	0.721492659	2	3.653081
P11711	ILEEAGYLIK	0.820952592	2	2.726734
P11711	LEDINESPKPLGFTR	0.976761391	2	3.469052
P11711	TVSNVISSIVFGER	0.830062816	2	3.525805
P11711	VHEEIEQVIGR	0.903156312	2	3.209881
P11714	**CP2D9 Cytochrome P450 2D9**	**1.058371529**	**0.95327**	**2**
P11714	GNPESSFNDENLLMVVR	0.802584519	2	2.34788
P11714	VQQEIDEVIGQVR	0.967261139	2	4.841065
P11862	**GAS2 Growth arrest_specific protein 2**	**1.114206215**	**0.99637**	**2**
P11862	EIEQEETLSAPSPSPSPSSK	1.155635238	2	3.879451
P11862	LDNGALLCQLAATVQEK	0.96340793	2	4.086994
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**0.919271656**	**3.4E-08**	**23**
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	1.019734061	3	4.583633
P11884	EEIFGPVMQILK	1.079144412	2	3.797481
P11884	EEIFGPVMQILK+Oxidation(7)	1.063594663		
P11884	ELGEYGLQAYTEVK	1.250886143	2	4.45975
P11884	GYFIQPTVFGDVK	1.098996401	2	4.096813
P11884	HEPVGVCGQIIPWNFPLLMQAWK	0.858559166	3	4.190291
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.763436084	3	6.633285
P11884	LGPALATGNVVVMK	0.729862122	2	3.881171
P11884	LGPALATGNVVVMK+Oxidation(12)	0.829992055		
P11884	LLCGGGAAADR	1.018469734	2	3.536341
P11884	RVTLELGGK	0.75183183	2	2.744479
P11884	TEQGPQVDETQFK	0.844757111	2	4.756463
P11884	TFPTVNPSTGEVICQVAEGNK	1.074586429	2	4.97016
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.839149877	2	4.325205
P11884	TFVQEDVYDEFVER	0.835549473	2	5.176448
P11884	TIEEVVGR	0.725725773	2	3.001751
P11884	TIPIDGDFFSYTR	0.951550086	2	2.949207
P11884	VAEQTPLTALYVANLIK	1.30841735	3	5.245028
P11884	VAFTGSTEVGHLIQVAAGSSNLK	0.89336778	2	6.035166
P11884	VTLELGGK	0.781571123	1	1.966558
P11884	VVGNPFDSR	0.863471031	2	2.839046
P11884	YGLAAAVFTK	0.682892615	2	3.784074
P11884	YYAGWADK	0.802660682	2	2.577942
P11915	**NLTP Non_specific lipid_transfer protein**	**0.923668692**	**0.85123**	**24**
P11915	ADCTITMADSDLLALMTGK	0.845521165	2	5.697645
P11915	ADCTITMADSDLLALMTGK+Oxidation(15)	0.955185087		
P11915	ADCTITMADSDLLALMTGK+Oxidation(6)	0.937136071		
P11915	ANLIFK	1.010614573	2	2.363153
P11915	AVEIVAQEMVTDMPSTFEEK	0.878958182	2	4.274205
P11915	GHPLGATGLAQCAELCWQLR	0.846710677	3	3.727941
P11915	GSVLPDSDK	0.956597007	1	1.988598
P11915	GSVLPDSDKK	1.067241745	2	2.628221
P11915	HIDVLINK	0.832566751	2	2.858802
P11915	HSVNNPYSQFQDEYSLDEIMK	0.996672868	3	6.334317
P11915	KADCTITMADSDLLALMTGK	1.273294353	2	4.402377
P11915	KLEEEGEEFVK	0.98216275	2	4.491902
P11915	KLEEEGEEFVKK	0.934201571	3	4.443469
P11915	LEEEGEEFVK	0.916295354	2	2.693956
P11915	LEEEGEEFVKK	0.972252427	2	3.565766
P11915	LQSLQLQPDK	1.201814984	2	3.169401

P11915	MGFPEAASSFR	**0.87555992**	2	2.995764
P11915	MNPQSAFFQGK	**0.925672859**	2	3.250317
P11915	MNPQSAFFQGK+Oxidation(0)	**1.069219132**		
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	**0.937161173**	3	5.17075
P11915	THQISAAPTSSAGDGFK	**1.00586863**	2	4.404951
P11915	VFVVGVGMTK	**0.821829121**	2	2.556144
P11915	WVINPSGGLISK	**1.026660689**	2	3.308452
P11915	YGMSACPFAPQLFGSAGK	**1.428981497**	2	3.379063
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.033908623**	**0.92839**	**10**
P11980	AEGSDVANAVLDGADCIMLSGETAK	**0.909061546**	2	4.525784
P11980	AGKPVICATQMLESMIK	**0.738825097**	3	3.342162
P11980	DAVLDAWAEDVDLR	**0.907210203**	2	4.025075
P11980	GADYLVTEVENGGSLGSK	**0.792260678**	2	5.314896
P11980	GVNLPGAAVDLPAVSEK	**1.043045432**	2	3.770245
P11980	IYVDDGLISLQVK	**0.96272484**	2	3.697804
P11980	KGVNLPGAAVDLPAVSEK	**0.940429571**	2	3.643487
P11980	LDIDSAPITAR	**0.749549584**	2	3.20909
P11980	NTGIICTIGPASR	**0.889475034**	2	3.324592
P11980	VFLAQKMMIGRCNR+Oxidation(6)	**0.971771577**		
P12001	**RL18 60S ribosomal protein L18**	**1.096382254**	**0.15621**	**5**
P12001	GTVLLSGPR	**1.494731206**	2	2.931015
P12001	ILTFDQLALESPK	**1.222628695**	2	4.870775
P12001	TAVVVGTITDDVR	**1.13329032**	2	4.523719
P12001	TNRPPLSLSR	**1.113280508**	3	3.366225
P12001	TNSTFNQVVLK	**0.958537546**	2	3.176213
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**0.740121774**	**9.9E-20**	**9**
P12007	AQEIDQSNDFK	**0.855055844**	2	3.640245
P12007	FVQENLAPK	**0.74300204**	2	2.650152
P12007	FWITNGPDADVLVVYAK	**1.361214165**	2	3.653508
P12007	GSNTCELVFEDCK	**0.994509224**	2	4.458799
P12007	GSNTCELVFEDCKVPAANILSQESK	**0.727746526**	3	4.917409
P12007	GVYVLMSGLDLER	**0.776105083**	2	3.170815
P12007	IGQFQLMQGK	**1.155771885**	2	2.502737
P12007	LYEIGGGTSEVR	**0.854343478**	2	3.559751
P12007	TDLTAVPASR	**0.646942278**	2	2.963448
P12346	**TRFE Serotransferrin**	**1.199723428**	**9.9E-20**	**23**
P12346	ADRDQYELLCLDNTR	**1.242708254**	2	4.543229
P12346	ASDSSINWNNLK	**1.47799761**	2	3.270942
P12346	DGGGDVAFVK	**1.152680435**	2	3.113133
P12346	DLKQEDFQLLCPDGTK	**0.88294343**	2	4.446505
P12346	DQYELLCLDNTR	**1.630409607**	2	2.982026
P12346	EGVCPEGSIDSAPVK	**2.086399298**	2	3.489291
P12346	EGYNGYTGAFQCLVEK	**1.121931389**	2	3.528948
P12346	FDEFFSQGCAPGYK	**0.908466277**	2	4.345944
P12346	GDKDCTGNFCLFR	**1.269766353**	2	3.593474
P12346	GTDFQLNQLQGK	**1.388248091**	2	3.122989
P12346	GYYAVAVVK	**1.270518695**	2	2.79149
P12346	HQTVLENTNGK	**1.849408941**	2	2.579301
P12346	HTTIFEVLPQK	**1.288631901**	3	3.740234
P12346	KGTDFQLNQLQGK	**1.248223811**	2	3.59938
P12346	KTSYQDCIK	**1.651540149**	2	2.489622
P12346	LPEGTTYEEYLGAEYLQAVGNIR	**1.172365605**	2	4.675972
P12346	NGDGKEDLIWEILK	**1.117288922**	2	3.677605
P12346	QEDFQLLCPDGTK	**1.081085458**	2	3.582817
P12346	SKDFQLFGSPLGK	**2.065806419**	2	3.488945
P12346	TSYQDCIK	**1.233900092**	2	2.528939

P12346	VSTVLTAQK	1.467495417	2	2.616675
P12346	WCALSHQER	1.8891208	2	3.230942
P12346	WCAVSEHENTK	1.388442289	2	3.649519
P12711	**ADHX Alcohol dehydrogenase class_3**	**0.829620995**	**1.3E-05**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	0.897186963	3	5.782949
P12711	AFDLMHSGNSIR	0.831092229	2	2.502499
P12711	AGDTVIPLYIPQCGECK	0.885995111	2	4.027006
P12711	EFGATECINPQDFSK	1.024721102	2	4.189593
P12711	IDPSAPLDK	0.672840043	1	1.939675
P12711	IIGIDINK	0.887245242	2	2.371974
P12711	IIGIDINKDK	0.574871019	1	2.430563
P12711	VCLLGCGISTGYGAAVNTAK	0.749168624	2	5.521226
P12711	VDEFVTGNLSFDQINK	0.74710626	2	5.130754
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	0.810950308	2	4.143928
P12749	**RL26 60S ribosomal protein L26**	**1.126040613**	**0.58723**	**6**
P12749	DDEVQVVR	1.039531205	2	2.58808
P12749	FNPFVTSDR	1.090401308	2	2.363353
P12749	HFNAPSHIR	1.036646469	3	3.701633
P12749	KDDEVQVVR	1.222329459	2	3.385693
P12749	KIMSSPLSKELR+Oxidation(2)	1.245293174		
P12749	YVIYIER	1.125231451	1	1.919811
P12785	**FAS Fatty acid synthase**	**1.756669559**	**9.9E-20**	**44**
P12785	ACIDTALENLSTLK	1.923878054	2	4.915604
P12785	AGSDTELAAPK	1.705911082	2	3.247803
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.597688531	3	5.73813
P12785	DANLPAGSMAAVGLSWEECK	1.122254347	2	3.660444
P12785	DGGFLLMHTVLK	1.110301936	2	2.399549
P12785	DPETLLGYSMVGCQR	0.837349839	2	3.767768
P12785	EEEPEAMLPGAQPTLISAISK	1.156249333	2	3.315189
P12785	EQGVTFPSGEAQEQLIR	2.155197665	2	4.119235
P12785	FDASFFGVHPK	1.731169088	2	3.123435
P12785	FVFTPHVEPECLSESAILQK	2.873578539	2	4.565071
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	2.30472687	3	4.70531
P12785	GLESIINIIHSSLAEPR	1.086752698	2	4.76953
P12785	GNAGQSNYGFANSTMER	1.581828455	2	4.43746
P12785	GTNTGVWVGVSGSEASEALSR	1.221573797	2	3.539723
P12785	GVDLVLNSLAEEK	1.825083919	2	3.214894
P12785	GYDYGPHFQGVYEATLEGEQGK	2.673904998	3	3.763916
P12785	HFQLEQDKPEEQTAHAFVNVLTR	1.461511936	3	3.453434
P12785	LDPGSSELQK	1.834076211	2	2.378937
P12785	LFDHPEVPIPAESESVSR	1.569646963	2	4.0873
P12785	LLLPEDPLISGLLNSQALK	1.796286131	3	5.021595
P12785	LTPGCEAEAEAEAICFFIK	2.31643348	2	4.082347
P12785	MTVPGLEDLPQHGLPR	1.278210098	2	3.167776
P12785	QAQLNLSILLVNPEGPTLTR	1.774779679	2	4.554855
P12785	QQEQLVPTLEK	2.456945603	2	2.447166
P12785	QSPLLIGSTK	2.112537532	1	2.107911
P12785	RQQEQLVPTLEK	2.326940773	2	3.167008
P12785	SDEALKPLGVK	1.116383971	2	3.146637
P12785	SFDDSGNGYCR	1.905233532	2	3.1493
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.640459266	2	5.063999
P12785	SNMGHPEPASGLAALTK	1.341297632	2	3.647825
P12785	SNMGHPEPASGLAALTK+Oxidation(2)	1.956476987		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.488373694	2	5.068894
P12785	TMEAVQGLLEQGR	1.304540956	2	3.717564
P12785	TMEAVQGLLEQGR+Oxidation(1)	1.00168945		
P12785	VGDPQELNGITR	0.973145474	2	2.558468

P12785	VHLTGIDINPNALFPPVEFPVPR	**1.472694632**	2	5.039025
P12785	VLEALLPLK	**1.729494113**	2	2.357012
P12785	VLESDLVMNVYR	**0.578659327**	2	3.405668
P12785	VLLSLENGVWAPNLHFHNPNPEIPALLDGR	**1.167980344**	3	4.056353
P12785	VSVHIIEGDHR	**1.904426857**	2	2.753283
P12785	VTAIYIDPATHLQK	**1.665042025**	2	3.315601
P12785	VYATILNAGTNTDGCK	**1.379607219**	2	4.87661
P12785	VYQWEDPDSK	**2.237702841**	2	3.174712
P12785	WLSTSIPEAQWQSSLAR	**1.180870425**	2	2.372029
P12791	**CP2BA Cytochrome P450 2B10**	**0.930035158**	**0.48779**	**2**
P12791	IQEEAQCLVEELR	**0.916667428**	2	3.759812
P12791	IQEEAQCLVEELRK	**0.723901322**	2	3.544593
P12847	**MYH3 Myosin_3**	**0.996894541**	**0.98949**	**4**
P12847	IEAQNQPFDAK	**0.727935421**	2	2.748584
P12847	MKGTLEDQIISANPLLEAFGNAK	**0.858394216**	3	6.889268
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0)	**1.030718369**		
P12847	NALAHALQSSR	**0.792491972**	2	2.618051
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.165559041**	**9.5E-05**	**18**
P12928	AETSDVANAVLDGADCIMLSGETAK	**1.047561658**	2	5.386181
P12928	CCAAAIIVLTK	**0.821759407**	2	2.951444
P12928	CNLAGKPVVCATQMLESMITK	**0.869267274**	3	5.062019
P12928	EATESFATSPLSYRPVAIALDTK	**1.961936847**	3	4.059224
P12928	EPPEAIWADDVDR	**1.09100898**	2	2.440576
P12928	EPPEAIWADDVDRR	**1.021465277**	2	2.330976
P12928	GDLGIEIPAEK	**1.035957386**	2	3.103087
P12928	GSQVLVTVDPK	**1.205756114**	2	2.847728
P12928	GVNLPNTEVDLPGLSEQDLLDLR	**1.15814012**	2	5.44598
P12928	IGPEGLVTEVEHGGILGSR	**0.94539988**	2	4.779319
P12928	IYIDDGLISLVVQK	**1.193131511**	2	4.156784
P12928	KFDEILEVSDGIMVAR	**0.870487085**	3	3.386325
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	**1.3428816**	3	4.315272
P12928	LNFSHGSHEYHAESIANIR	**1.602802104**	3	4.181748
P12928	STSIIATIGPASR	**1.026482766**	2	3.579793
P12928	TGVLQGGPESEVEIVK	**1.594418546**	2	4.938263
P12928	TVWVDYHNITR	**1.385814544**	2	2.510377
P12928	VQFGIESGK	**1.068326733**	1	1.982685
P12938	**CP2D3 Cytochrome P450 2D3**	**0.851934911**	**0.00228**	**5**
P12938	DLTDAFLAEIEK	**0.94834043**	2	4.142829
P12938	FDYGDPDFIK	**0.847161681**	2	2.443841
P12938	GNPESSFNDANLR	**0.930137798**	2	4.309071
P12938	RFDYGDPDFIK	**0.646683897**	2	2.829973
P12938	TWDPDQPPR	**0.659224254**	2	2.43149
P12939	**CP2DA Cytochrome P450 2D10**	**1.268682337**	**0.19922**	**8**
P12939	AVQEVLVTHGEDTADRPPVPIFK	**1.048441671**	3	5.298196
P12939	FEYEDPYLIR	**1.213381258**	2	2.409207
P12939	FGDIAPLNLPR	**1.352646024**	2	3.161536
P12939	ITSCDIEVQDFVIPK	**1.044369511**	2	4.545211
P12939	NLTDAFLAEVEK	**0.921114708**	2	4.136254
P12939	RFEYEDPYLIR	**1.04512773**	3	3.535597
P12939	SQGVVFASYGPEWR	**3.991228691**	2	3.59811
P12939	TTWDPAQPPR	**1.230036838**	2	2.433837
P13084	**NPM Nucleophosmin**	**2.011700376**	**0.00237**	**3**
P13084	MSVQPTVSLGGFEITPPVVLR	**1.292095426**	2	3.582177
P13084	MTDQEAIQDLWQWR	**1.241688399**	2	3.16819
P13084	VDNDENEHQLSLR	**1.905817111**	2	3.929126
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**0.790350976**	**9.5E-05**	**6**

P13086	LIGPNCPGIINPGECK	**0.850692221**	2	4.512835
P13086	MGHAGAIIAGGK	**0.657798707**	1	2.793092
P13086	MGHAGAIIAGGK+Oxidation(0)	**0.972036722**		
P13086	NIYIDK	**0.884533267**	1	1.971983
P13086	QGTFHSQQALEYGTK	**0.736913781**	2	2.841769
P13086	VICQGFTGK	**0.777716629**	2	2.308482
P13107	**CP2B3 Cytochrome P450 2B3**	**1.247711278**	**0.40638**	**11**
P13107	ATLDPNAPR	**1.035426141**	2	2.326976
P13107	CLVEELK	**0.790058114**	1	2.00381
P13107	DFIDTFLLHMEK	**1.371201696**	2	3.009206
P13107	EVLDYIDHSVENHR	**1.183724486**	2	3.960704
P13107	FSDVSPMGLPCR	**1.28642405**	2	2.761684
P13107	FSDVSPMGLPCR+Oxidation(6)	**1.188409327**		
P13107	GIIAVLQPIMQEYGVSFVNEER	**1.945880637**	3	5.361229
P13107	LLDLLYR	**1.102451156**	2	2.488436
P13107	MCLGEGIAR	**0.764844918**	2	2.693204
P13107	QSVEDQIKEEAK	**1.065454543**	2	2.495909
P13107	SFIQLQEK	**0.997474552**	2	2.406467
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**2.675455813**	**9.9E-20**	**8**
P13221	ITWSNPPAQGAR	**2.6956808**	2	3.393543
P13221	IVATTLSNPELFK	**2.320167456**	2	3.639694
P13221	NFGLYNER	**3.564997057**	1	1.931059
P13221	NLDYVATSINEAVTK	**2.82299914**	2	4.887107
P13221	SCASQLVLGDNSPALR	**2.69299967**	2	5.405178
P13221	TDDSQPWVLPVVR	**2.172912206**	2	3.524652
P13221	VGGVQSLGGTGALR	**2.531183108**	2	2.393139
P13221	VGNLTVVGK	**0.889123768**	2	2.550872
P13255	**GNMT Glycine N_methyltransferase**	**0.999576448**	**0.9986**	**8**
P13255	AHMVTLDYTVQVPGAGR	**0.979189451**	2	4.934911
P13255	AWLLGLLR	**1.120273979**	2	2.789044
P13255	DITTSVLTVNNK	**1.218154473**	2	3.978507
P13255	LSYYPHCLASFTELVQEAFGGR	**1.038232901**	3	3.700447
P13255	NYDYILSTGCAPPGK	**1.032708771**	2	4.593596
P13255	SDLTKDITTSVLTVNNK	**1.052056741**	2	3.09809
P13255	SLGVAAEGIPDQYADGEAAR	**1.095227901**	2	5.755338
P13255	VWQLYIGDTR	**0.79198674**	2	2.605269
P13383	**NUCL Nucleolin**	**1.696734213**	**6.6E-05**	**8**
P13383	FGYVDFESAEDLEK	**1.813095635**	2	2.638528
P13383	GFGFVDFNSEEDAK	**1.677395962**	2	3.716178
P13383	GLSEDTTEETLK	**0.763858578**	2	2.904298
P13383	IEGSEPTTPFNLFIGNLNPNK	**1.018561151**	2	3.463486
P13383	NDLAAVDVR	**1.246352816**	2	2.431115
P13383	NLSFNITEDELK	**1.26192502**	2	2.777811
P13383	SEADAEKNLEEK	**2.38004366**	2	3.060445
P13383	SVSLYYTGEK	**3.642787907**	1	2.024874
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.850722421**	**9.9E-20**	**22**
P13437	AANEAGYFNEEMAPIEVK	**0.781113916**	2	5.24088
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11)	**0.957242521**		
P13437	DAEVVLCGGTESMSQSPYSVR	**1.079332498**	2	5.16125
P13437	DFTATDLTEFAAR	**1.095616778**	2	4.920811
P13437	DMDLIDVNEAFAPQFLAVQK	**0.972866475**	3	6.501692
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1)	**1.068045533**		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	**0.732400222**	3	5.731832
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	**0.695388634**	3	4.948078
P13437	GVFIVAAK	**0.806956991**	2	2.583429
P13437	ITAHLVHELR	**1.466755207**	2	3.024678
P13437	LCGSGFQSIVSGCQEICSK	**0.984489107**	2	5.477032

P13437	LEDTLWAGLTDQHVK	**0.788059866**	2	5.388068
P13437	RTPFGAYGGLLK	**0.896982409**	2	2.944408
P13437	SLDLDPSK	**0.777970868**	2	3.019894
P13437	TNVSGGAIALGHPLGGSGSR	**0.745202624**	2	6.242382
P13437	TPFGAYGGLLK	**0.86148698**	2	2.785176
P13437	VGVPTETGALTLNR	**0.815911494**	2	3.69551
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	**0.785397928**	2	5.95532
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14)	**0.882181228**		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	**0.66081049**	3	5.472631
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	**0.821365767**	3	3.586936
P13437	YAVGSACIGGGQGISLIIQNTA	**0.705492423**	2	2.477781
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**2.047177124**	**9.9E-20**	**8**
P13444	FVIGGPQGDAGVTGR	**1.799711066**	2	4.726541
P13444	HIGYDDSAK	**2.305241206**	2	2.825247
P13444	ICDQISDAVLDAHLK	**1.833052983**	2	5.156051
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	**1.354327557**	3	5.423157
P13444	SEFPWEVPK	**1.61824651**	2	2.541992
P13444	SGVLPWLRPDSK	**0.945488115**	2	3.107456
P13444	TCNVLVALEQQSPDIAQCVHLDR	**2.011888132**	3	5.684929
P13444	TQVTVQYVQDNGAVIPVR	**2.388445289**	2	5.094707
P13471	**RS14 40S ribosomal protein S14**	**1.123529025**	**0.01211**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	**1.814232436**	2	5.853403
P13471	ELGITALHIK	**1.677591589**	2	2.416054
P13471	IEDVTPIPSDSTR	**1.030909693**	2	3.992328
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.891027222**	**0.00145**	**22**
P13601	ANNTPYGLAAGVFTK	**1.131984639**	2	4.254565
P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	**0.824628051**	3	3.305845
P13601	EEIFGPVQQIMK	**1.010219735**	2	3.81693
P13601	EMGEQGVYEYTELK	**1.457795908**	2	3.887575
P13601	FPVINPATEEVICHVEEGDK	**0.732425275**	3	4.09538
P13601	FPVINPATEEVICHVEEGDKADVDK	**0.590695086**	4	5.142944
P13601	GFFVQPTVFSNVTDEMR	**5.203719624**	2	4.312201
P13601	IAKEEIFGPVQQIMK	**0.871155733**	2	3.864847
P13601	IFINNEWHNSLNGK	**1.27204641**	2	3.500032
P13601	IFTHAYLLDTEVSIKALK	**1.138027491**	2	2.341056
P13601	IHGQTIPSDGDVFTYTR	**1.104825312**	2	4.627728
P13601	ILDLIESGK	**0.762421359**	2	2.729225
P13601	ILDLIESGKK	**0.734975974**	3	3.341717
P13601	KFPVINPATEEVICHVEEGDK	**0.836600359**	3	3.753911
P13601	KFPVINPATEEVICHVEEGDKADVDK	**0.601143905**	4	4.866906
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	**0.661908697**	3	5.60002
P13601	LFVEESIYDEFVR	**0.996055405**	2	4.067123
P13601	VLLATMESMNAGK	**0.948328243**	2	3.981084
P13601	VSFTGSTEVGK	**1.145615774**	2	3.086549
P13601	YFAGWADK	**0.840945238**	1	2.056434
P13601	YVLGNPLDSGISQGPQIDK	**0.985741357**	2	4.961924
P13601	YVLGNPLDSGISQGPQIDKEQHAK	**1.077257625**	4	4.604517
P13697	**MAOX NADP_dependent malic enzyme**	**1.175564606**	**0.98501**	**5**
P13697	AECSAEECYK	**1.06508527**	1	2.810228
P13697	AIFASGSPFDPVTLPDGR	**0.88273732**	2	4.257449
P13697	GHIASVLNAWPEDVVK	**1.18054461**	2	3.816658
P13697	HINDSVFLTTAEVISQQVSDK	**1.288282754**	3	4.341857
P13697	NLEAIVQK	**1.095514677**	1	2.197101
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.024432157**	**9.9E-20**	**14**
P13803	AAVDAGFVPNDMQVGQTGK	**0.767888216**	2	4.772173

P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11)	**0.821160414**		
P13803	DPEAPIFQVADYGIVADLFK	**0.953179689**	2	5.355403
P13803	GLLPEELTPLILETQK	**0.89679486**	2	4.669336
P13803	GTSFEAAAASGGSASSEK	**0.95967033**	2	5.340793
P13803	LGGEVSCLVAGTK	**0.812048151**	2	4.711003
P13803	LLYDLADQLHAAVGASR	**0.755753169**	2	4.643563
P13803	LNVAPVSDIIEIK	**0.969564753**	3	4.717721
P13803	QFSYTHICAGASAFGK	**0.903525153**	2	3.163802
P13803	SDRPELTGAK	**0.941598411**	3	3.341209
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	**0.673416823**	3	7.038399
P13803	TIYAGNALCTVK	**0.792471107**	2	3.661068
P13803	VLVAQHDAYK	**0.893799062**	2	3.259243
P13803	VVQDLCK	**0.891056882**	2	2.751452
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.196398315**	**0.90599**	**3**
P13832	ATSNVFAMFDQSQIQEFK	**1.033736577**	2	4.652575
P13832	FTDEEVDELYR	**1.134805517**	2	3.499027
P13832	GNFNYIEFTR	**1.197609821**	2	2.628266
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.577755401**	**9.9E-20**	**5**
P14046	GDPIPNEQVLIK	**0.579576735**	2	3.181515
P14046	GMYESLPVVAVK	**0.513977216**	2	3.397591
P14046	ISLCHGNPTFSSETK	**0.790447567**	2	3.682433
P14046	QQNSYGGFSSTQDTVVALDALSK	**0.468406347**	2	4.142656
P14046	QSPGPCGSEVATVPETGR	**0.637907341**	2	3.336217
P14141	**CAH3 Carbonic anhydrase 3**	**0.777647641**	**9.9E-20**	**18**
P14141	EAPFNHFDPSCLFPACR	**0.941308101**	2	4.341764
P14141	EKGEFQILLDALDK	**0.851110278**	2	4.559532
P14141	EKGEFQILLDALDKIK	**0.520927114**	2	3.110992
P14141	EPMTVSSDQMAK	**1.15337025**	2	2.941079
P14141	EWGYASHNGPEHWHELYPIAK	**0.809062994**	3	4.517257
P14141	GDNQSPIELHTK	**0.687488197**	2	3.764329
P14141	GEFQILLDALDK	**0.838150089**	2	4.664411
P14141	GEFQILLDALDKIK	**0.632117885**	2	3.253896
P14141	GGPLSGPYR	**0.817841633**	2	2.956714
P14141	GKEAPFNHFDPSCLFPACR	**0.573780884**	3	3.525347
P14141	HDPSLQPWSVSYDPGSAK	**0.806565311**	3	5.572367
P14141	QFHLHWGSSDDHGSEHTVDGVK	**0.70683273**	2	4.643401
P14141	QPDGIAVVGIFLK	**0.889688085**	2	2.576633
P14141	SLFASAENEPPVPLVGNWRPPQPIK	**0.788907778**	3	5.701326
P14141	VVFDDTFDR	**0.651713242**	2	3.372337
P14141	YAAELHLVHWNPK	**1.152616459**	2	4.332443
P14141	YNTFGEALK	**0.818845299**	2	2.314709
P14141	YNTFGEALKQPDGIAVVGIFLK	**0.62002851**	3	6.01375
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**0.921429608**	**0.98641**	**7**
P14173	AGEGGGVIQGSASEATLVALLAAR	**0.993280425**	2	3.543346
P14173	ALIPTTAPQEPETYEDIIR	**0.894625105**	3	4.096662
P14173	GSNQLNETLLQR	**0.892727986**	2	2.866176
P14173	HSHQDSGLITDYR	**0.998257579**	3	3.633439
P14173	MLELPEAFLAGR	**0.816429724**	2	2.770898
P14173	QLQAASPELTQAALMEK	**0.873033358**	2	3.814373
P14173	TDLTEAFNMDPVYLR	**1.005192234**	2	3.676677
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**0.825993322**	**9.9E-20**	**15**
P14408	AAAEVNQEYGLDPK	**1.209750287**	2	4.467802
P14408	AIEMLGGELGSK	**0.810834992**	2	3.507025
P14408	IEYDTFGELK	**0.956457436**	2	3.542608
P14408	IEYDTFGELKVPTDK	**0.722641401**	2	3.649869
P14408	IYELAAGGTAVGTGLNTR	**0.89039211**	2	5.560617
P14408	KTAIELGYLTAEQFDEWVKPK	**0.860283442**	3	3.576987

P14408	LMNESLMLVTALNPHIGYDK	**0.818073181**	3	5.647627
P14408	LMNESLMLVTALNPHIGYDK+Oxidation(6)	**0.85344598**		
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	**0.809106128**	3	6.411434
P14408	SGLGELILPENEPGSSIMPGK	**0.719651532**	2	4.37712
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17)	**0.995654128**		
P14408	SKEFAQVIK	**1.218562091**	2	2.48217
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	**0.735271233**	3	4.20594
P14408	TAIELGYLTAEQFDEWVKPK	**0.74787044**	2	4.527267
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	**2.214922816**	3	6.005599
P14480	**FIBB Fibrinogen beta chain**	**1.68397676**	**9.9E-20**	**10**
P14480	AHYGGFTVQTEANK	**1.651486144**	2	2.906667
P14480	DNENVINEYSSILEDQK	**1.330859736**	2	3.269349
P14480	GFGNIATNEDTK	**1.344170537**	2	2.739107
P14480	GFGNIATNEDTKK	**1.749539052**	2	2.819092
P14480	IGPTELLIEMEDWK	**1.441323844**	2	3.57419
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	**1.561559457**	3	5.218724
P14480	LYIDETVNDNIPLNLR	**1.266267105**	2	3.006875
P14480	QTLLNHERPIK	**1.977778097**	2	2.747412
P14480	TENGGWTVIQNR	**1.342763364**	2	3.228431
P14480	YCGLPGEYWLGNDK	**1.197496534**	2	3.318062
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.899798018**	**9.9E-20**	**8**
P14604	AFAAGADIK	**0.838583075**	2	3.234199
P14604	AQFGQPEILLGTIPGAGGTQR	**0.833367982**	2	5.647284
P14604	FLSHWDHITR	**0.786159226**	2	3.129168
P14604	IFPVETLVEEAIQCAEK	**0.741295055**	2	5.81061
P14604	LFYSTFATDDR	**1.74262917**	2	2.726903
P14604	NSSVGLIQLNRPK	**0.842227842**	2	3.516642
P14604	SLAMEMVLTGDR	**0.63439499**	2	3.384629
P14604	TFQDCYSGK	**0.877594237**	2	2.788632
P14668	**ANXA5 Annexin A5**	**0.913273803**	**0.97174**	**3**
P14668	ETSGNLENLLLAVVK	**0.993527836**	2	3.481405
P14668	GLGTDEDSILNLLTAR	**0.834521126**	2	4.616629
P14668	GTVTDFSGFDGR	**0.712040475**	2	2.932259
P14669	**ANXA3 Annexin A3**	**0.718549614**	**9.9E-20**	**5**
P14669	GMGTDEDTLIEILTTR	**0.732890053**	2	3.150109
P14669	GTINNYPGFNPSVDAEAIR	**0.645142968**	2	4.933701
P14669	QYQEAYEQALK	**0.717970716**	2	2.551154
P14669	SEIDLLDIR	**0.822474935**	2	2.617257
P14669	TLINILTER	**0.646292833**	2	2.518674
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.037807597**	**0.79013**	**3**
P14685	AIQLEYSEAR	**1.393634164**	2	2.584062
P14685	LQLDSPEDAEFIVAK	**0.969250573**	2	3.861351
P14685	SVFPEQANNNEWAR	**1.077427121**	2	3.043399
P14740	**DPP4 Dipeptidyl peptidase 4**	**0.874683031**	**0.00321**	**2**
P14740	LGTLEVEDQIEAAR	**0.875579566**	2	3.906668
P14740	VLEDNSALDK	**0.914892669**	2	2.860023
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**0.89192051**	**0.88258**	**12**
P14882	FLSDVYPDGFK	**0.824016175**	2	2.694512
P14882	FSSQEAASSFGDDR	**0.871884216**	2	3.318769
P14882	HGNALWLNER	**1.120402042**	2	2.597135
P14882	HIEIQVLGDK	**0.887262658**	2	2.397127
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	**0.912610593**	3	6.014308
P14882	LQVEHPVTECITGLDLVQEMILVAK	**1.037187223**	3	3.542439
P14882	MADEAVCVGPAPTSK	**0.777510104**	2	4.370352
P14882	MEDALDSYVIR	**0.946318425**	2	3.107002

P14882	SYLNMDAIMEAIK	**0.896929074**	2	3.150029
P14882	TGAQAVHPGYGFLSENK	**1.021134536**	2	4.045664
P14882	TVAIHSDVDASSVHVK	**0.871084779**	3	4.100473
P14882	VVEEAPSIFLDPETR	**0.738029186**	2	4.150364
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.187831275**	**0.89621**	**4**
P15083	EIQNAGDQAQENR	**0.948632797**	2	3.655425
P15083	FSVLITGLR	**1.240590376**	2	2.667918
P15083	GVTGGSVAIVCPYNPK	**1.016956219**	2	4.329145
P15083	NNADLQVLEPEPELLYK	**0.763727191**	2	2.640825
P15149	**CP2A2 Cytochrome P450 2A2**	**0.631637576**	**9.9E-20**	**10**
P15149	DVQECILEEAGYLIK	**0.65547555**	3	4.597108
P15149	DVYSSITQLSER	**0.964182691**	2	2.426858
P15149	FSNLAPLGIPR	**0.697805749**	2	3.20416
P15149	GELPTFNILFK	**0.39876664**	2	2.417119
P15149	GTDVFPIIGSLMTEPK	**0.47594201**	2	3.933875
P15149	GYGFSLSNVEQAK	**0.630969105**	2	3.449176
P15149	NFIDSFLIR	**0.79195352**	1	2.565989
P15149	QNHSTLDPNSPR	**0.656700311**	2	3.029952
P15149	TLQGTCGAPIDPSIYLSK	**0.554428243**	2	4.209558
P15149	TVSNVINSIVFGNR	**0.68794923**	2	3.530468
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.060659846**	**0.08643**	**6**
P15178	FQTEIQTVNK	**1.242283278**	2	2.387757
P15178	GEEILSGAQR	**0.698432902**	2	2.91514
P15178	LEYCEALAMLR	**0.805895917**	2	2.931232
P15178	LPLQLDDAIRPEVEGEEDGR	**1.699445997**	3	3.89853
P15178	QMVKFAANINK+Oxidation(1)	**1.149205676**		
P15178	SNAYLAQSPQLYK	**1.137947373**	2	2.842947
P15429	**ENOB Beta_enolase**	**0.965745314**	**0.99999**	**7**
P15429	DATNVGDEGGFAPNILENNEALELLK	**0.860043041**	2	5.692757
P15429	FMIELDGTENK	**0.982174547**	2	2.341909
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	**0.721459268**	3	4.629873
P15429	IEEALGDK	**0.939518542**	1	2.36389
P15429	TAIQAAGYPDK	**1.01958724**	2	2.682114
P15429	VNQIGSVTESIQACK	**1.098756489**	2	5.042507
P15429	YNQLMRIEEALGDK	**0.954924599**	2	2.492086
P15473	**IBP3 Insulin_like growth factor_binding protein 3**	**0.71550193**	**0.04636**	**2**
P15473	EMEDTLNHLKFLNVLSPR	**0.524491059**	2	2.313431
P15473	MEVIIKGQARDSQR	**0.976075765**	2	2.312101
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.821290243**	**9.9E-20**	**20**
P15650	AFVDSCLQLHETK	**0.862179913**	2	4.137933
P15650	AQDTAELFFEDVR	**0.983574578**	2	4.809271
P15650	AQDTAELFFEDVRLPASALLGEENK	**1.012540809**	3	4.291989
P15650	CIGAIAMTEPGAGSDLQGVR	**0.685068758**	2	6.102579
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6)	**0.848213313**		
P15650	EQIEQFIPQMTAGK	**1.170717656**	2	4.990434
P15650	FFQEEVIPYHEEWEK	**1.996401953**	2	4.958344
P15650	GFYYLMQELPQER	**1.117657641**	2	3.911878
P15650	IFSSEHDIFR	**1.071627659**	2	2.987184
P15650	KFFQEEVIPYHEEWEK	**1.836703325**	3	5.007729
P15650	LDSASASMAK	**0.734226863**	2	2.63886
P15650	LPASALLGEENK	**0.828839675**	2	3.415677
P15650	LPASALLGEENKGFYYLMQELPQER	**0.950819101**	3	3.626521
P15650	QGLLGINIAEK	**0.817585617**	2	3.297413
P15650	RLDSASASMAK	**0.766897439**	2	3.485178
P15650	RLDSASASMAK+Oxidation(8)	**1.420420659**		

P15650	RSGSDWILNGSK	**1.246628161**	2	2.857289
P15650	SGSDWILNGSK	**0.963777339**	2	2.932576
P15650	VQPIYGGTNEIMK	**0.800029279**	2	3.250186
P15650	VQPIYGGTNEIMK+Oxidation(11)	**0.894506149**		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.814483787**	**0.05935**	**9**
P15651	ASSTANLIFEDCR	**0.979621925**	2	3.422934
P15651	EEGDSWVLNGTK	**0.61582046**	2	2.304456
P15651	ELVPIAAQLDK	**0.823492808**	1	1.956785
P15651	ELVPIAAQLDKEHLFPTSQVK	**0.803869278**	2	4.037627
P15651	GISAFLVPMPTPGLTLGK	**0.991138332**	2	2.510096
P15651	IGCFALSEPGNGSDAGAASTTAR	**0.777754369**	2	5.58182
P15651	IGIASQALGIAQASLDCAVK	**0.819828449**	2	4.930885
P15651	ITEIYEGTSEIQR	**0.813447333**	2	4.297855
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	**0.938169615**	4	4.912566
P15684	**AMPN Aminopeptidase N**	**1.080355881**	**0.34783**	**5**
P15684	ALGDTPAPNIDTTELVER	**0.881459431**	2	3.906228
P15684	AQIIHDSFNLASAGK	**1.110075338**	2	3.77442
P15684	ESALVFDPQSSSISNK	**1.602443717**	2	2.454454
P15684	VMAVDALASSHPLSSPANEVNTPAQISELFDSITYSK	**1.762124657**	3	3.823935
P15684	VVATTQMQAADAR	**1.248913843**	2	2.777344
P15709	**ST2A1 Bile salt sulfotransferase**	**1.126701648**	**0.67713**	**2**
P15709	GNVLYGSWFEHIR	**1.070843016**	2	3.04906
P15709	NHFTVSQAEAFDK	**1.360527767**	2	3.661526
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.186273814**	**0.25198**	**2**
P15978	VEHEGLPEPLSQR	**1.363617669**	2	3.271872
P15978	YDSDAENPR	**0.934906538**	2	2.722694
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.005253113**	**9.9E-20**	**24**
P15999	AVDSLVPIGR	**0.850993679**	2	3.494999
P15999	EIVTNFLAGFEP	**7.179584967**	2	2.409987
P15999	EVAAFAQFGSDLDAATQQLLSR	**1.056779237**	2	6.775969
P15999	FESAFLSHVVSQHQSLLGNIR	**0.815510572**	2	6.011279
P15999	GIRPAINVGLSVSR	**0.739999997**	3	3.626514
P15999	GMSLNLEPDNVGVVVFGNDK	**1.09653781**	2	5.684156
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1)	**0.944489477**		
P15999	GYLDKLEPSK	**0.605157912**	1	2.593194
P15999	ILGADTSVDLEETGR	**1.025882335**	2	5.006292
P15999	LELAQYR	**0.863537733**	2	2.693234
P15999	LKEIVTNFLAGFEP	**4.556708023**	2	3.256053
P15999	LTDADAMK	**0.897996922**	2	2.552619
P15999	LTDADAMK+Oxidation(6)	**0.930372581**		
P15999	LYCIYVAIGQK	**1.543662009**	2	2.409989
P15999	NVQAEEMVEFSSGLK	**1.832220956**	2	4.355209
P15999	QGQYSPMAIEEQVAVIYAGVR	**1.885876869**	3	5.223771
P15999	RTGAIVDVPVGDELLGR	**0.669229807**	2	2.85457
P15999	STVAQLVK	**0.823822075**	2	2.39713
P15999	TGAIVDVPVGDELLGR	**0.747709296**	2	4.928999
P15999	TGTAEMSSILEER	**0.804889718**	2	4.265776
P15999	TGTAEMSSILEER+Oxidation(5)	**0.964986021**		
P15999	TSIAIDTIINQK	**0.831362458**	2	4.391929
P15999	VLSIGDGIAR	**0.964526316**	2	3.160133
P15999	VVDALGNAIDGK	**0.86592944**	2	4.185841
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**0.855324603**	**0.99818**	**7**
P16036	ALYSNILGEENTYLWR	**1.037215309**	2	3.331951
P16036	EEGLNAFYK	**1.116176047**	1	2.318203
P16036	FGFYEVFK	**0.988282395**	2	2.342442

P16036	GIFNGFSITLK	**0.836552259**	2	2.82009
P16036	GSTASQVLQR	**0.968091951**	2	2.970787
P16036	IQTQPGYANTLR	**1.039055892**	2	3.760676
P16036	MYKEEGLNAFYK	**0.885287386**	2	2.88434
P16086	**SPTA2 Spectrin alpha chain_ brain**	**0.951915037**	**0.10607**	**33**
P16086	ALINADELANDVAGAEALLDR	**0.972502343**	2	5.12341
P16086	ALSSEGKPYVTK	**1.082036519**	2	3.021644
P16086	DLSSVQTLLTK	**0.972606816**	2	2.781344
P16086	EAALTSEEVGADLEQVEVLQK	**0.72392911**	2	3.743141
P16086	GEIDAHEDSFK	**0.916240963**	2	2.405044
P16086	GVIDMGNSLIER	**0.954973209**	2	3.189369
P16086	HQAFEAELSANQSR	**1.000972077**	2	3.569421
P16086	HQEHKGEIDAHEDSFK	**1.213114943**	3	4.149324
P16086	HQLLEADISAHEDR	**1.155539835**	3	4.028481
P16086	KFEEFQTDLAAHEER	**0.984911396**	3	4.819622
P16086	LFGAAEVQR	**1.084598036**	2	2.582831
P16086	LGDSHDLQR	**0.976672154**	2	3.187368
P16086	LGESQTLQQFSR	**0.437201409**	2	3.238065
P16086	LIQEQHPEEELIK	**1.111800248**	2	3.524149
P16086	LQQSHPLSANQIQVK	**1.015405489**	2	3.946393
P16086	LQTASDESYKDPTNIQSK	**0.669417104**	2	4.325
P16086	LQVASDENYKDPTNLQGK	**0.841587819**	2	4.613623
P16086	LSDDNTIGQEEIQQR	**1.02683583**	2	4.238682
P16086	MTLVASEDYGDTLAAIQGLLK	**1.026489646**	2	3.162891
P16086	NQALNTDNYGHDLASVQALQR	**1.036879988**	3	4.873584
P16086	NTTGVTEEALK	**0.822605043**	2	2.350149
P16086	QFQDAGHFDAENIKK	**0.641035215**	2	2.580685
P16086	REELITNWEQIR	**1.187065725**	2	3.451416
P16086	SADESGQALLAAGHYASDEVR	**0.805766664**	3	3.639349
P16086	SLQQLAEER	**0.864858592**	2	2.761007
P16086	SQLLGSAHEVQR	**0.535499543**	2	3.21781
P16086	SSEEIESAFR	**1.048614462**	2	2.428163
P16086	SSLSSAQADFNQLAELDR	**0.913745743**	2	4.939239
P16086	TATDEAYKDPSNLQGK	**0.951042319**	2	3.581089
P16086	TKQEEVNAAWQR	**1.416447818**	2	3.027998
P16086	VLETAEDIQER	**0.886991723**	2	3.42193
P16086	VNDVCTNGQDLIK	**1.209897864**	2	3.177594
P16086	VNSLGETAQR	**1.176845349**	2	2.34579
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.252460637**	**0.15356**	**10**
P16232	EECALEIIK	**1.642300038**	1	1.97235
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(1)	**0.762135369**		
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8)	**0.762135369**		
P16232	ETSGIILSQAAPK	**1.358971765**	2	3.317542
P16232	FALDGFFSTIR	**1.640375648**	2	3.079359
P16232	KDEVYYDK	**1.038933943**	2	3.00259
P16232	MGAHVVLTAR	**1.096455636**	2	2.919173
P16232	MTQPLIASYSASK	**1.186169808**	2	3.380455
P16232	MTQPLIASYSASK+Oxidation(0)	**3.229444951**		
P16232	SSWTPLLLGNPGR	**1.126483894**	2	3.606695
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.320047485**	**0.18122**	**7**
P16290	AMEAVAAQGK	**0.917013933**	2	2.795687
P16290	AMEAVAAQGK+Oxidation(1)	**1.316739663**		
P16290	FLGDEETVR	**0.692865414**	2	2.669859
P16290	HGESSWNQENR	**1.206362085**	2	3.63271
P16290	HNYYASISK	**1.110939948**	2	2.369684
P16290	HYGGLTGLNK	**1.551967184**	1	2.924372

P16290	VLIAAHGNSLR	**1.053583713**	2	2.827607
P16303	**CES3 Carboxylesterase 3**	**0.842853645**	**0.00025**	**20**
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	**0.89386655**	3	3.861336
P16303	AKEAAEEPSHWK	**0.695110891**	2	4.250408
P16303	DGASEEETNLSK	**0.745166616**	2	4.197501
P16303	EAAEEPSHWK	**1.111313381**	2	2.927894
P16303	ENIPLQFSEDCLYLNVYTPADLTK	**9.146940951**	2	4.423151
P16303	ESYPFLPTVIDGVVLPK	**0.948140274**	2	4.154991
P16303	FAPPQPAEPWNFVK	**0.940516152**	2	2.551271
P16303	IGASTQAAQR	**1.315324547**	2	2.852261
P16303	KENIPLQFSEDCLYLNVYTPADLTK	**5.14316818**	2	4.658246
P16303	LDLLGNPK	**0.882791034**	2	2.495217
P16303	QEFGWIIPTLMGYPLSEGK	**1.487029467**	2	4.090944
P16303	QKTEDELLETSLK	**0.830620948**	3	3.701194
P16303	SFNTVPYIVGINK	**2.225028988**	2	3.375175
P16303	TEDELLETSLK	**0.614355478**	2	3.726542
P16303	TPEEILAEK	**2.646499938**	2	2.342819
P16303	TTTSAVMVHCLR	**0.555408935**	2	2.803672
P16303	TTTSAVMVHCLR+Oxidation(6)	**0.92549329**		
P16303	TVIGDHGDELFSVFGSPFLK	**1.509835172**	2	5.399829
P16303	YFGGTDDPAK	**0.735321256**	2	3.198878
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	**0.706227441**	3	3.579983
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**0.97794848**	**0.4944**	**7**
P16332	AAVQVLDDIEK	**1.731828702**	2	2.620392
P16332	AHCQTSGWSLTEQDPYNNIVR	**1.262975692**	3	5.170474
P16332	GDVGMAGVAIDTVEDTK	**0.780119619**	2	3.069168
P16332	IDSGSEVIVGVNK	**0.878036565**	2	3.577084
P16332	ILFDGIPLEK	**0.99467298**	2	2.318594
P16332	NTQIIIQEESGIPK	**0.996468983**	2	3.881436
P16332	TGLQAGLTIDEFAPR	**0.950086946**	2	3.439996
P16409	**MYL3 Myosin light chain 3**	**0.863541159**	**0.99289**	**6**
P16409	AAPAPAAAPAAAPEPERPK	**0.82411539**	2	4.281186
P16409	ALGQNPTQAEVLR	**0.931438409**	2	3.976088
P16409	DTGTYEDFVEGLR	**0.969127033**	2	3.297331
P16409	MMDFETFLPMLQHISK	**0.863323075**	2	2.926264
P16409	NKDTGTYEDFVEGLR	**0.793437233**	2	4.133505
P16409	VFDKEGNGTVMGAELR	**0.970092036**	2	3.517663
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.007220541**	**0.25948**	**18**
P16617	AHSSMVGVNLPQK	**0.874704849**	3	4.083166
P16617	AHSSMVGVNLPQK+Oxidation(4)	**0.95835882**		
P16617	ALESPERPFLAILGGAK	**1.695965947**	3	4.525317
P16617	DCVGSEVENACANPAAGTVILLENLR	**0.99004029**	3	6.297062
P16617	FCLDNGAK	**0.818175753**	1	2.05084
P16617	GCITIIGGGDTATCCAK	**1.015689549**	2	5.566938
P16617	IQLINNMLDK	**0.789736876**	2	2.72171
P16617	IQLINNMLDK+Oxidation(6)	**1.478456165**		
P16617	ITLPVDFVTADKFDENAK	**1.005498141**	2	4.905708
P16617	QIVWNGPVGVFEWEAFAR	**1.018964936**	2	3.100346
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	**1.150801499**	4	4.691022
P16617	TGQATVASGIPAGWMGLDCGTESSK	**0.948045356**	2	4.736675
P16617	TGQATVASGIPAGWMGLDCGTESSKK	**0.982532389**	3	4.254049
P16617	VLNNMEIGTSLYDEEGAK	**0.907603717**	2	5.54474
P16617	VLNNMEIGTSLYDEEGAK+Oxidation(4)	**0.823938476**		
P16617	VLPGVDALSNV	**1.199853669**	2	2.735156
P16617	WNTEDKVSHVSTGGGASLELLEGK	**0.765972107**	3	4.855772
P16617	YSLEPVAAELK	**1.019190239**	2	3.618829

P16638	**ACLY ATP_citrate synthase**	**1.170193709**	**0.00069**	**25**
P16638	AFDSGIIPMEFVNK	**1.219102145**	2	4.132862
P16638	AFDSGIIPMEFVNK+Oxidation(8)	**0.824683603**		
P16638	DEPSVAAMVYPFTGDHK	**1.269132974**	2	3.228929
P16638	DGVYILDLAAK	**1.199945902**	2	2.982784
P16638	DLVSSLTSGLLTIGDR	**1.208427674**	2	3.486832
P16638	EAYPEEAYIADLDAK	**1.201994027**	2	3.064889
P16638	FGGALDAAAK	**1.06832144**	2	2.458114
P16638	GAIVPAQEVPPPTVPMDYSWAR	**1.124199077**	2	4.228379
P16638	GGPNYQEGLR	**1.544598581**	2	2.718846
P16638	GVTIIGPATVGGIKPGCFK	**1.027202825**	2	2.852841
P16638	HLLVHAPEDK	**0.834255805**	2	2.664155
P16638	HLLVHAPEDKK	**1.398566813**	2	3.564683
P16638	IGNTGGMLDNILASK	**1.055802651**	2	3.65479
P16638	LGLVGVNLSLDGVK	**1.074203922**	2	2.830339
P16638	LNAEDIK	**1.466630847**	1	1.913635
P16638	QHFPATPLLDYALEVEK	**1.11886233**	3	4.445997
P16638	RGGPNYQEGLR	**2.010908921**	2	3.176728
P16638	SFDELGEIIQSVYEDLVAK	**1.020305398**		
P16638	SGGMSNELNNIISR	**1.096510435**	2	3.700621
P16638	TIAIIAEGIPEALTR	**1.16605174**	2	5.253416
P16638	TTDGVYEGVAIGGDR	**1.38978788**	2	3.421449
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	**0.949704582**	3	4.084336
P16638	VDATADYICK	**0.857874947**	2	2.470526
P16638	WGDIEFPPPFGR	**1.135351387**	2	3.933861
P16638	YICTTSAIQNR	**1.157959201**	2	2.813505
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.903137699**	**0.01356**	**5**
P16970	FDHVPLATPNGDILIQDLSFEVR	**0.818808003**	2	2.48301
P16970	GIEGAQASPLIPGAGEIINADNIIK	**0.731024334**	3	4.97734
P16970	GYLDNVQLGHILER	**0.866538208**	2	3.446207
P16970	HLHSTHSELLEDYYQSGR	**0.903332227**	3	5.156248
P16970	SGANVLICGPNGCGK	**0.801705704**	2	3.116311
P17074	**RS19 40S ribosomal protein S19**	**0.993409512**	**0.88781**	**5**
P17074	DVNQQEFVR	**0.478760726**	2	2.368493
P17074	ELAPYDENWFYTR	**0.596302826**	2	2.484498
P17074	HKELAPYDENWFYTR	**1.031645001**	3	3.352571
P17074	RVLQALEGLK	**1.279894372**	3	3.319066
P17074	VLQALEGLK	**1.049516042**	2	2.717939
P17077	**RL9 60S ribosomal protein L9**	**1.146508666**	**5.6E-05**	**8**
P17077	DFNHINVELSLLGK	**1.347247218**	3	3.752424
P17077	FLDGIYVSEK	**1.089906129**	2	3.201822
P17077	GTVQQPDE	**1.201441588**	1	2.101096
P17077	KFLDGIYVSEK	**1.326254335**	2	2.726167
P17077	SVYAHFPINVVIQENGSLVEIR	**1.173463627**	3	3.74064
P17077	TGVACSVSQAQK	**1.307073492**	2	3.669527
P17077	TICSHVQNMIK	**0.859071429**	2	2.878561
P17077	TILSNQTVDIPENVDITLK	**0.876471062**	2	3.154075
P17078	**RL35 60S ribosomal protein L35**	**1.232785316**	**0.48063**	**2**
P17078	QLDDLKVELSQLR	**0.983833985**	2	2.586651
P17078	VLTVINQTQK	**1.277828099**	2	3.248564
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.308934416**	**6.8E-05**	**4**
P17178	DHESTEGPGTGQDRPR	**5.071100671**	2	2.52979
P17178	MLKPAEAALYTDALNEVISDFIAR	**1.599111076**	3	4.138936
P17178	VGCLEPSIPEDTATFIR	**1.450034267**	2	2.884553
P17178	YEVVLSPGMGEVK	**1.04995525**	2	3.745264

P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.982219975**	**0.99492**	**15**
P17425	ASAELFNQK	**1.197211243**	2	3.109892
P17425	DKNSIYSGLEAFGDVK	**1.534462091**	2	3.026466
P17425	DVGIVALEIYFPSQYVDQAELEK	**0.974243911**	3	3.689102
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK+Oxidation(3)	**0.964224948**		
P17425	ITASLCDLK	**0.881949828**	1	1.942125
P17425	LEDTYFDRDVEK	**0.843488251**	2	2.920728
P17425	LPATSGEPESAVISNGEH	**2.939749804**	2	4.239635
P17425	MFLNDFLNDQNR	**0.727225108**	2	2.97792
P17425	MFLNDFLNDQNR+Oxidation(0)	**0.913654452**		
P17425	MGFCTDREDINSLCLTVVQK	**1.053031659**	3	4.179461
P17425	NSLSYDCIGR	**1.095648118**	2	2.872298
P17425	RPSTNDHSLDEGVGLVHSNTATEHIPSPAK	**1.89556525**	4	4.604982
P17425	TCVAPDVFAENMK	**0.963765223**	2	2.783931
P17425	VTQDATPGSALDK	**0.827473711**	2	3.805212
P17425	YTIGLGQAR	**0.937648876**	2	2.688532
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.020383329**	**0.19954**	**2**
P17426	NADVELQQR	**1.196415534**	2	2.807719
P17426	VGGYILGEFGNLIAGDPR	**0.962710864**	2	3.750861
P17475	**A1AT Alpha_1_antiproteinase**	**1.203373451**	**9.9E-20**	**5**
P17475	MQHLEQTLTK	**1.723559972**	2	3.007922
P17475	MQHLEQTLTK+Oxidation(0)	**2.72128273**		
P17475	TLLSSLGITR	**2.406110039**	2	3.155347
P17475	VFNNDADLSGITEDAPLK	**1.312283154**	2	5.7359
P17475	VINDYVEK	**1.60042977**	2	2.34795
P17702	**RL28 60S ribosomal protein L28**	**1.785053311**	**2.8E-06**	**2**
P17702	NCSSFLIK	**1.14548158**	2	2.415654
P17702	QTYSTEPNNLK	**2.165051144**	2	3.01876
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.00481495**	**0.0002**	**17**
P17764	EEQDKYAIGSYTR	**0.98348814**	2	3.561487
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	**1.444022742**	2	4.623279
P17764	EVYMGNVIQGGEGQAPTR	**1.201290249**	2	5.394138
P17764	EVYMGNVIQGGEGQAPTR+Oxidation(3)	**1.9958673**		
P17764	FANEITPITISVK	**1.101243305**	2	3.848681
P17764	GKPDVVVKEDEEYK	**0.711705214**	2	3.453354
P17764	GKPDVVVKEDEEYKR	**0.996239487**	2	5.075504
P17764	IAAFADAAVDPIDFPLAPAYAVPK	**1.248487856**	2	5.742885
P17764	IHMGNCAENTAK	**0.974300959**	2	3.178412
P17764	IHMGNCAENTAK+Oxidation(2)	**0.950066766**		
P17764	LEDLIVK	**0.892105146**	2	2.711647
P17764	LGTIAIQGAIEK	**1.071445924**	2	3.293019
P17764	QATLGAGLPIATPCTTVNK	**0.944112075**	2	4.624789
P17764	QGEFGLASICNGGGGASAVLIEK	**0.834134035**	2	4.942674
P17764	TPIGSFLGSLASQPATK	**1.509930063**	2	4.479323
P17764	VNVHGGAVSLGHPIGMSGAR	**0.752841272**	2	5.807877
P17764	VNVHGGAVSLGHPIGMSGAR+Oxidation(15)	**1.464687318**		
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.456243991**	**9.9E-20**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	**1.253831091**	3	5.323452
P17879	TTPSYVAFTDTER	**1.61298764**	2	3.729563
P17879	VEIIANDQGNR	**1.049561472**	2	3.77198
P17988	**ST1A1 Sulfotransferase 1A1**	**1.79359279**	**9.9E-20**	**6**
P17988	CPGVPSGLETLEETPAPR	**1.906712056**	2	4.797564
P17988	ILEFLGR	**2.179686401**	2	2.344018
P17988	NTFTVAQNER	**1.74174143**	2	3.682426
P17988	SGTTWMSEILDMIYQGGK	**1.216495676**	2	4.986846

P17988	SLPEETVDSIVHHTSFK	**1.80153867**	2	4.56665
P17988	THLPLSLLPQSLLDQK	**2.122643543**	2	4.978549
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**0.895120061**	**9.9E-20**	**30**
P18163	AELSVIFADKPEK	**0.806228083**	2	3.141895
P18163	ALEDLGR	**1.475790879**	2	2.328306
P18163	ALKPPCDLSMQSVEVTGTTEGVR	**0.782791373**	2	4.535008
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9)	**0.989822337**		
P18163	CGVEIIGLK	**0.731100067**	2	2.879076
P18163	DGWLHTGDIGK	**1.061694954**	2	3.187433
P18163	GAMVTHQNIMNDCSGFIK	**1.198925131**	2	4.383051
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2)	**1.282159684**		
P18163	GFQGSFEELCR	**0.874914755**	2	3.625499
P18163	GIAVHPELFSIDNGLLTPTLK	**1.687135506**	2	5.813646
P18163	GIQVSNDGPCLGSR	**0.932495023**	2	4.508375
P18163	IENIYLR	**0.894360709**	2	2.95509
P18163	IFGQANTSVK	**0.936747832**	2	2.76034
P18163	IIVIMDSYDNDLVER	**0.737871888**	2	4.590707
P18163	LLLEGVENK	**0.956643346**	2	3.334471
P18163	LLMDDLK	**0.662751464**	2	2.434906
P18163	LMITGAAPVSATVLTFLR	**0.714665572**	2	3.52214
P18163	LVDVEDMNYQAAK	**1.087279822**	2	4.203762
P18163	LVDVEDMNYQAAK+Oxidation(6)	**1.051501831**		
P18163	NAGLKPFEQVK	**0.826025466**	2	3.831028
P18163	NNSLWDK	**0.664962001**	2	2.545614
P18163	QVAEMAECIGSALIQK	**0.656641046**	2	5.590154
P18163	QVAEMAECIGSALIQK+Oxidation(4)	**1.189419258**		
P18163	SAVLEDDKLLLYYYDDVR	**4.222851914**	3	4.165587
P18163	SQIDELYSTIK	**1.219801738**	2	3.657451
P18163	SQIDELYSTIKI	**1.361456626**	2	4.152328
P18163	TAEALDKDGWLHTGDIGK	**0.867103356**	2	5.108146
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	**15.67561443**	3	5.415393
P18163	VLQPTIFPVVPR	**0.793251115**	2	3.500982
P18163	WLLDFASK	**0.797011273**	2	2.381298
P18297	**SPRE Sepiapterin reductase**	**0.907965492**	**0.94757**	**4**
P18297	ALAPQLAGLLSPGSVLLLSAR	**0.847360575**	3	4.81566
P18297	LLLINNAGTLGDVSK	**1.000333858**	2	3.600589
P18297	LNSEGELVDCGTSAQK	**0.99599789**	2	4.78737
P18297	TVVNISSLCALQPFK	**0.896512168**	2	3.763449
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**2.362668279**	**9.9E-20**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	**1.351411445**	2	5.421152
P18298	KIIVDTYGGWGAHGGGAFSGK	**1.995659633**	3	3.46823
P18298	YLDEDTIYHLQPSGR	**2.721910794**	2	4.753562
P18418	**CALR Calreticulin**	**0.895662942**	**1**	**19**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	**1.007461301**	3	5.440219
P18418	CKDDEFTHLYTLIVRPDNTYEVK	**2.205997611**	3	4.856501
P18418	DMHGDSEYNIMFGPDICGPGTK	**0.734549637**	2	6.398684
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1)	**1.03199132**		
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(10)	**1.03199132**		
P18418	EQFLDGDAWTNR	**1.269099759**	2	3.022876
P18418	FYGDQEK	**0.871785793**	1	2.055975
P18418	FYGDQEKDK	**0.902994946**	1	2.776472
P18418	GQTLVVQFTVK	**1.119103161**	2	3.255028
P18418	HEQNIDCGGGYVK	**0.964631906**	2	4.420838
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	**0.724445219**	3	3.916787
P18418	IDNSQVESGSLEDDWDFLPPK	**0.975605611**	2	5.437834
P18418	IDNSQVESGSLEDDWDFLPPKK	**0.873695017**	2	4.899996

P18418	IKDPDAAKPEDWDER	**0.906006709**	2	4.383667
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	**0.895645545**	3	5.572803
P18418	LFPGGLDQK	**0.966073485**	1	2.052844
P18418	QIDNPDYK	**0.911895632**	1	2.290527
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	**0.950948681**	3	4.883288
P18418	VHVIFNYK	**0.990620417**	1	2.268359
P18420	**PSA1 Proteasome subunit alpha type_1**	**0.995406161**	**0.00038**	**2**
P18420	AQPSQAADEPAEK	**1.240563048**	2	3.424672
P18420	NQYDNDVTVWSPQGR	**0.955442479**	2	3.629484
P18421	**PSB1 Proteasome subunit beta type_1**	**1.009964956**	**0.05912**	**3**
P18421	AGGSASAMLQPLLDNQVGFK	**0.863976944**	2	5.028276
P18421	GAVYSFDPVGSYQR	**1.323776791**	2	3.86107
P18421	NMQNVEHVPLTLDR	**0.30177593**	2	3.688417
P18445	**RL27A 60S ribosomal protein L27a**	**1.164970037**	**0.14258**	**2**
P18445	NQSFCPTVNLDK	**1.152837846**	2	3.352818
P18445	RNQSFCPTVNLDK	**0.930457169**	2	3.029666
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**0.754327927**	**0.33924**	**3**
P18484	LTECLETILNK	**0.764525099**	2	2.73545
P18484	NNGVLFENQLLQIGLK	**0.93838641**	2	3.254095
P18484	QLSNPQQEVQNIFK	**0.753650992**	2	3.409109
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**0.953972506**	**0.93901**	**5**
P18596	DIVPGDIVEVAVGDK	**1.097752582**	2	2.458181
P18596	DIVPGDIVEVAVGDKVPADLR	**1.562783081**	2	3.760574
P18596	SLPSVETLGCTSVICSDK	**0.890151902**	2	4.198058
P18596	TGTLTTNQMSVCR	**0.943986753**	2	2.415793
P18596	VGEATETALTCLVEK	**1.023278455**	2	4.386174
P18757	**CGL Cystathionine gamma_lyase**	**0.938606204**	**0.17575**	**18**
P18757	AGDEVICMDEVYGGTNR	**0.627829823**	2	5.387766
P18757	AGDEVICMDEVYGGTNR+Oxidation(7)	**0.93732373**		
P18757	ATLGISDTLIR	**1.002273818**	2	3.54182
P18757	AVAALDGAK	**0.953581996**	2	2.670032
P18757	AVVLPISLATTFK	**1.008912637**	3	4.291078
P18757	DLLEDLGQALK	**0.752968973**	2	2.779878
P18757	FLQNSLGAVPSPFDCYLCCR	**1.224818375**	2	4.118407
P18757	GTLQHAQVFLK	**0.923039618**	2	3.069681
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	**1.159988441**	3	5.283734
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	**1.145798552**	4	5.448231
P18757	LLEAAITPQTK	**0.844555388**	2	3.884803
P18757	LSVGLEDEKDLLEDLGQALK	**0.818912413**	3	6.474934
P18757	LVWIETPTNPTLK	**0.861322358**	2	3.627706
P18757	QCTGCPGMVSFYIK	**0.734394523**	2	3.741347
P18757	QCTGCPGMVSFYIK+Oxidation(7)	**0.964278048**		
P18757	QDSPGQSSGFVYSR	**0.984633022**	2	3.700495
P18757	RVASEFGLK	**0.89126477**	2	2.585621
P18757	VIYPGLPSHPQHELAK	**0.772826098**	2	4.256135
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**0.950181541**	**0.97425**	**10**
P18886	ATNLTVSAVR	**0.98330863**	2	3.302066
P18886	ELHAHLLAQDK	**1.236200059**	2	3.009936
P18886	FFNEVFR	**0.919312725**	2	2.30748
P18886	LIFDGNEETLK	**1.009306848**	2	2.989042
P18886	QYGQTVATYESCSTAAFK	**1.042915934**	2	3.575184
P18886	SEYNDQLTR	**0.977397728**	2	2.673007
P18886	TETIRPASIFTK	**0.944795715**	2	2.583139
P18886	TLSIDSIQFQR	**0.942693402**	2	3.302003
P18886	YILSDSSPVPEFPVAYLTSENR	**1.2267427**	2	5.495711

P18886	YLNAQKPLLDDSQFR	0.952961304	2	4.368109
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**0.911365601**	**9.9E-20**	**18**
P19112	AGGLATTGNEDILDIVPTEIHQK	0.814049322	3	6.255063
P19112	AGGTGEMTQLLNSLCTAIK	0.976019945	2	5.363754
P19112	AGGTGEMTQLLNSLCTAIK+Oxidation(6)	0.800881777		
P19112	APVIMGSTEDVQEFLEIYNK	1.463429327	2	5.246606
P19112	DFDPAINEYIQR	1.280947308	2	3.916194
P19112	FPPDNSAPYGAR	1.012552212	2	2.553975
P19112	GNIYSINEGYAK	1.059533608	2	4.063055
P19112	KGNIYSINEGYAK	1.023460663	2	3.924677
P19112	KLDILSNDLVINMLK	0.794535361	2	6.077208
P19112	KTSANEPSEKDALQPGR	0.801745773	3	3.639435
P19112	LDILSNDLVINMLK	0.79493446	2	5.047803
P19112	LLYECNPIAYVMEK	1.574156687	2	4.267875
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.036498742	3	6.084218
P19112	SRPSLPLPQSR	0.826387525	2	3.311398
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.00489602	3	5.78229
P19112	TLVYGGIFLYPANK	0.889706414	2	4.206293
P19112	TLVYGGIFLYPANKK	0.770812934	2	2.33301
P19112	TSANEPSEKDALQPGR	0.835876111	2	3.885636
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**1.266708235**	**0.54952**	**5**
P19123	AAVEQLTEEQK	1.26255323	2	2.861987
P19123	AAVEQLTEEQKNEFK	1.14129846	2	3.446536
P19123	GKSEEELSDLFR	0.916705988	2	2.570196
P19123	IDYDEFLEFMK	1.267325521	2	3.178984
P19123	SEEELSDLFR	0.916011525	2	2.930652
P19225	**CP270 Cytochrome P450 2C70**	**1.286161932**	**1.4E-05**	**14**
P19225	ACIGEGLAR	0.905395568	2	2.789742
P19225	ASLNLSNPQDFIDYFLIK	1.325901472	2	4.702113
P19225	EALIDRGEEFSDK	1.208003235	2	3.293825
P19225	FDPGHFLDEK	0.808042689	2	2.313699
P19225	FDYSDEK	1.271328944	1	1.99506
P19225	FILMEINR	0.93988405	2	2.33989
P19225	GTSVMACLTSALHDDKEFPNPEK	0.714264659	3	3.486035
P19225	IQEEITR	0.953402333	1	2.000205
P19225	IQEEVVYLLEALR	3.924774684	2	3.357499
P19225	LPPGPTPLPIFGNILQVGVK	0.716738445	3	4.910123
P19225	SDYFMAFSAGRR+Oxidation(4)	0.835729138		
P19225	SEFTMDNLIVTIGDLFGAGTETTSSTIK	0.913432481		
P19225	VSQGLGIVFSNGEIWK	1.138254659	2	3.348341
P19225	YIDFVPIPLPR	0.819811426	2	3.174598
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.100793748**	**0.22987**	**4**
P19234	AAAVLPVLDLAQR	2.613892079	2	2.355726
P19234	DIEEIIDELR	0.992573697	2	3.551643
P19234	DTPENNPDTPFDFTPENYER	0.997847939	2	4.397674
P19234	FCCEPAGGLTSLTEPPK	1.147310605	2	3.746825
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.028846959**	**0.9862**	**8**
P19468	ASGELMTVAR	1.046317564	2	2.696695
P19468	CNQIANELCECPELLGSGFR	0.8731108	2	5.099301
P19468	DKNTPSPFVETFPEDEEASK	0.942847058	3	3.43545
P19468	GYVSDIDCR	0.791389279	2	2.584268
P19468	NTPSPFVETFPEDEEASK	1.234054242	2	4.776046
P19468	SLFFPDEAINK	1.010577105	2	2.661707
P19468	VQLLLNGGDVLETLQEK	1.01861009	2	4.72091

P19468	WGVISASVDDR	0.696748014	2	3.256202
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**0.949725347**	**0.91376**	**9**
P19488	AEMWLIR	0.798456717	2	2.918362
P19488	ANAIAWALAQIPQK	1.038219019	3	5.953065
P19488	FETFPTSVSK	0.960672712	1	2.001886
P19488	FETFPTSVSKDELEK	0.777371628	2	3.394245
P19488	GAAVTLNIR	0.933250157	2	2.511322
P19488	GHEVTVLKPSAYYVLDPK	1.123706226	2	4.521748
P19488	NWDPFYTEILGRPTTLAETMGK	0.967776817	2	5.012445
P19488	SDLFNALK	0.936332752	2	2.764688
P19488	TILDELVQR	0.684077901	2	3.196654
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**0.761657838**	**6.1E-12**	**10**
P19511	HVIQSISAQQEK	0.896695841	2	3.994242
P19511	HVIQSISAQQEKETIAK	0.632572131	3	4.07216
P19511	HYLFDVQR	0.878786172	2	2.588789
P19511	LDYHISVQDMMR	0.549571158	3	4.311595
P19511	LGLIPEEFFQFLYPK	1.110492532	2	2.678539
P19511	LNEEKIAQLEEIK	0.875516558	2	2.530182
P19511	NNIALALEVTYR	0.907087072	2	2.350246
P19511	QIQDAINR	0.833949861	1	2.123898
P19511	YGASIGEFIDK	1.306514657	2	2.913744
P19511	YGASIGEFIDKLNEEK	0.879546598	2	3.847262
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.199708414**	**0.52182**	**12**
P19643	FIGGSGQVSER	0.845564474	2	3.244701
P19643	IISTTNGGQER	1.165244109	2	3.063423
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.276720387	3	4.6288
P19643	KFIGGSGQVSER	1.103682876	2	3.105097
P19643	LERPVIHIDQTGENVVVK	0.83861712	2	4.49568
P19643	LLHDCGLSVVVLEAR	0.933515138	2	3.440828
P19643	TLNHEIYEAK	0.942676709	2	2.814503
P19643	TMDEMGQEIPSDAPWK	0.750928949	2	4.181168
P19643	VLNSQEALQPVHYEEK	1.000872013	2	4.835337
P19643	YVDLGGSYVGPTQNR	0.848474632	2	5.324489
P19643	YVISAIPPVLGMK	0.593172068	2	2.931791
P19643	YVISAIPPVLGMK+Oxidation(11)	0.702307493		
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.121752118**	**0.99869**	**9**
P19804	DRPFFPGLVK	1.290395369	2	2.339988
P19804	EIGLWFKPEELIDYK	1.131257052	2	4.117491
P19804	GDFCIQVGR	1.021213506	2	3.198852
P19804	NIIHGSDSVESAEK	1.133172337	1	3.941249
P19804	TFIAIKPDGVQR	1.045079367	2	3.256384
P19804	VMLGETNPADSKPGTIR	0.956722626	2	3.896411
P19804	VMLGETNPADSKPGTIR+Oxidation(1)	1.094459818		
P19804	YMNSGPVVAMVWEGLNVVK	0.859327157	2	5.097666
P19804	YMNSGPVVAMVWEGLNVVK+Oxidation(1)	0.823994419		
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.075101544**	**7.4E-05**	**2**
P19944	AAGVNVEPFWPGLFAK	1.646659456	2	3.429322
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.072663608	3	5.706236
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.021294677**	**5.4E-05**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.310708104	2	6.02914
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.084184976	2	4.54503
P19945	CFIVGADNVGSK	1.003120092	2	3.674735
P19945	GHLENNPALEK	1.086234217	2	3.695569
P19945	GNVGFVFTK	1.381488984	2	2.793194
P19945	GTIEILSDVQLIK	1.08001379	2	3.363508
P19945	IIQLLDDYPK	1.468730649	2	3.639399

P19945	NVASVCLQIGYPTVASVPHSIINGYK	0.858601362	3	3.874542
P19945	TSFFQALGITTK	1.245543111	2	4.218082
P19945	VLALSVETDYTFPLAEK	0.985107684	2	3.940639
P20059	**HEMO Hemopexin**	**1.836267417**	**0.0398**	**7**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	1.367748713	2	4.612888
P20059	FNPVTGEVPPR	1.157838332	2	2.46482
P20059	GECQSEGVLFFQGNR	0.918368572	2	3.756286
P20059	GGNNLVSGYPK	1.205149649	2	2.539176
P20059	LFQEEFPGIPYPPDAAVECHR	1.238137243	3	3.750477
P20059	SGAQATWAELSWPHEK	1.255166441	3	3.545642
P20059	VDGALCLEK	1.14690297	2	2.64807
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**0.899120007**	**0.45474**	**9**
P20070	AVLKDPNDHTVCYLLFANQSEK	9.809276696	3	4.702319
P20070	DILLRPELEELR	0.932288785	2	2.552075
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	0.58408575	3	4.961462
P20070	LIDKEIISHDTR	0.898652852	2	3.734611
P20070	MSQYLENMNIGDTIEFR	0.86969791	2	3.5756
P20070	SSPAITLENPDIK	0.903384732	2	3.877282
P20070	SSPAITLENPDIKYPLR	0.661827348	2	3.847224
P20070	SVGMIAGGTGITPMLQVIR	0.735066717	2	5.092463
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(3)	1.019598854		
P20280	**RL21 60S ribosomal protein L21**	**1.122034406**	**0.12988**	**3**
P20280	KGDIVDIK	1.382939732	1	2.243574
P20280	TNGKEPELLEPIPYEFMA	0.974415617	2	3.014197
P20280	VYNVTQHAVGIIVNK	1.00143829	2	4.618709
P20650	**PPM1A Protein phosphatase 1A**	**0.808286685**	**0.06873**	**2**
P20650	SRLEVTDDLEK	0.561462851	2	2.316962
P20650	VCNEVVDTCLYK	1.267100752	2	2.536309
P20673	**ARLY Argininosuccinate lyase**	**0.980094984**	**0.01508**	**16**
P20673	AEAECEVLFPGYTHLQR	1.233611702	2	4.595074
P20673	AEMQQILQGLDK	0.992218741	2	4.501705
P20673	AEMQQILQGLDK+Oxidation(2)	1.295037156		
P20673	AVVVAEMK	1.199355932	2	2.380149
P20673	EFNFVQLSDAYSTGSSLMPQK	1.278041627	2	5.484978
P20673	ELIGEAAGK	1.82417888	1	1.932617
P20673	FNSSIAYDR	1.467781451	2	2.774706
P20673	HLWNVDLQGSK	1.167558218	1	3.161577
P20673	INVLPLGSGAIAGNPLGVDR	1.371827099	2	5.577091
P20673	LKELIGEAAGK	1.203462824	2	2.986611
P20673	LYPNDEDIHTANER	1.19697174	2	3.882632
P20673	MAEDLILYGTK	1.035854493	2	3.742563
P20673	MAEDLILYGTK+Oxidation(0)	1.091831834		
P20673	NDQVVTDLR	0.914559955	2	3.408863
P20673	SRNDQVVTDLR	0.616304608	2	2.630143
P20673	VAEEWAQGIFK	1.446550359	2	3.819015
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**0.794004179**	**3.8E-06**	**5**
P20788	EIDQEAAVEVSQLR	1.069873241	2	4.250672
P20788	EIDQEAAVEVSQLRDPQHDLER	0.841888124	3	3.326869
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	0.729644974	3	4.294538
P20788	LSDIPEGK	0.924537545	1	2.021074
P20788	SGPFAPVLSATSR	0.828067378	2	3.031933
P20801	**TNNC2 Troponin C_ skeletal muscle**	**0.855041075**	**0.98278**	**5**
P20801	AAFDMFDADGGGDISVK	0.685894308	2	4.173479
P20801	GKSEEELAECFR	0.678172529	2	3.613492
P20801	NADGYIDAEELAEIFR	0.951548241	2	4.794307
P20801	SEEELAECFR	1.046988689	2	3.293289

P20801	SYLSEEMIAEFK	**0.849502775**	2	2.757431
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**0.909476828**	**0.07075**	**4**
P20814	FDYEDKDFLNLIEK	**0.764807533**	3	4.161927
P20814	GTAVLTSLTSVLHDSK	**0.805437469**	2	3.105676
P20814	IKEHEESLDVSNPR	**0.744293923**	3	4.048508
P20814	SDYFIPFSAGK	**3.429294722**	2	2.598929
P20817	**CP4AE Cytochrome P450 4A14**	**1.056078944**	**0.00655**	**8**
P20817	ACQIAHEHTDGVIK	**0.928908195**	2	3.977923
P20817	AQLQNEEELQK	**0.663842581**	2	3.546
P20817	AVEDLNNLTFFR	**0.748099975**	2	3.414963
P20817	EFQQVLTWVEK	**0.841868663**	2	2.656531
P20817	HLDFLDILLFAK	**1.09027006**	2	3.235344
P20817	MEDGKSLSDEDLR	**0.785418792**	2	2.391694
P20817	MRKAQLQNEEELQK+Oxidation(0)	**0.747168222**		
P20817	VLLYDPDYVK	**0.66984833**	2	2.382238
P20852	**CP2A5 Cytochrome P450 2A5**	**0.717831244**	**0.30254**	**2**
P20852	DFIDSFLIR	**0.612623781**	2	2.662069
P20852	EALVDQAEEFSGR	**0.872783092**	2	3.351563
P21213	**HUTH Histidine ammonia_lyase**	**0.676442359**	**4E-05**	**13**
P21213	ALDYLAIGVHELAAISER	**0.590202584**	2	4.196963
P21213	DIITTELNSATDNPMVFASR	**0.929517368**	2	4.286501
P21213	GETISGGNFHGEYPAK	**0.655105841**	2	3.827773
P21213	GEWLAVPCQDGK	**0.459995666**	2	2.516691
P21213	GQIEVAFR	**0.642752933**	2	2.39418
P21213	LQELQVNLVR	**0.630424401**	2	3.256324
P21213	NKPDNGGFTSVDEVR	**0.647160849**	2	3.614604
P21213	QADIVAALTLEVLK	**0.506393912**	2	2.613843
P21213	SHSSGVGKPLSPER	**0.925093179**	2	3.63549
P21213	SLLDSDHHPSEIAESHR	**0.670178002**	3	4.384646
P21213	TVVYGITTGFGK	**0.735991219**	2	3.594153
P21213	VWEVAAPYIEK	**0.920488241**	2	2.875035
P21213	YIALDGDSLSTEDLVNLGK	**0.608141538**	2	5.177346
P21396	**AOFA Amine oxidase [flavin_containing] A**	**0.828893663**	**0.00345**	**7**
P21396	DVPAIEITHTFLER	**1.110233343**	2	2.481183
P21396	IFSVTNGGQER	**0.627965323**	2	2.548023
P21396	INVLVLEAR	**0.833997712**	2	2.945532
P21396	KDIWVEEPESK	**0.779918244**	2	3.247698
P21396	VLGSQEALYPVHYEEK	**0.819102353**	2	3.882811
P21396	WVDVGGAYVGPTQNR	**0.715398538**	2	4.810678
P21396	YVISAIPPILTAK	**0.788990206**	2	2.905345
P21531	**RL3 60S ribosomal protein L3**	**1.398540751**	**1.9E-10**	**6**
P21531	AHLMEIQVNGGTVAEK	**0.957407719**	2	5.237579
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	**1.194672226**	3	5.929224
P21531	HGSLGFLPR	**1.002026872**	2	3.112545
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	**1.325449486**	2	4.770232
P21531	NNASTDYDLSDK	**1.286780333**	2	3.225097
P21531	TVFAEHISDECK	**1.423072327**	2	3.690672
P21533	**RL6 60S ribosomal protein L6**	**1.13997637**	**0.00036**	**8**
P21533	AVDSQILPK	**1.123450306**	2	2.75714
P21533	FVIATSTK	**1.361359377**	1	2.017998
P21533	HLTDAYFK	**1.068129179**	2	2.436034
P21533	HQEGEIFDTEK	**1.354691847**	2	3.32333
P21533	HQEGEIFDTEKEK	**1.163304127**	2	4.00106
P21533	QLGSGLLLVTGPLALNR	**1.303094835**	2	5.045406
P21533	SSITPGTVLIILTGR	**1.018507394**	2	3.891764
P21533	YYPTEDVPR	**1.174719297**	2	2.440053

P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**0.946778419**	**0.38215**	**6**
P21571	FEVLDKPQS	**0.864184787**	2	2.93575
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	**0.731445929**	3	3.930324
P21571	GEMDKFPTFNFEDPKFEVLDKPQS+Oxidation(2)	**0.764200529**		
P21571	LASGGPVDTGPEYQQEVDR	**1.132791807**	2	5.28316
P21571	LASGGPVDTGPEYQQEVDRELFK	**1.299570013**	2	2.799888
P21571	RLASGGPVDTGPEYQQEVDR	**1.102270231**	3	4.52364
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.270945214**	**4.7E-05**	**2**
P21643	GGLIYGDYLQLEK	**1.983347488**	2	3.617439
P21643	ILNAQELQSEIK	**1.224971001**	2	3.652973
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.575584895**	**0.17772**	**4**
P21670	ATCIGNNSAAAVSMLK	**1.190914803**	2	2.812556
P21670	LLDEVFFSEK	**1.157714365**	2	3.597595
P21670	LNEDMACSVAGITSDANVLTNELR	**1.22986169**	3	3.446458
P21670	YLLQYQEPIPCEQLVTALCDIK	**1.018517983**	2	3.044539
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**0.589945407**	**9.9E-20**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	**0.679855389**	3	5.287484
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22)	**0.788026453**		
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.049986222**	**0.56084**	**6**
P21913	CGPMVLDALIKIK	**0.806624066**	2	2.4207
P21913	CHTIMNCTQTCPK	**0.828550154**	2	4.316717
P21913	CHTIMNCTQTCPK+Oxidation(4)	**1.691740419**		
P21913	IKNEIDSTLTFR	**0.917681647**	2	2.395818
P21913	LQDPFSLYR	**1.205814853**	2	2.753863
P21913	RIDTDLGK	**0.897060269**	2	2.437272
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**0.977962163**	**0.99994**	**5**
P21981	CDLEIQANGR	**0.963482293**	2	2.991685
P21981	LVVNFQCDK	**1.072551267**	2	2.676165
P21981	SEGTYCCGPVSVR	**0.878756683**	2	3.694467
P21981	WDNNYGDGISPMAWIGSVDILR	**0.97658376**	3	4.197842
P21981	YSGCLTESNLIK	**0.992625525**	2	3.566343
P22734	**COMT Catechol O_methyltransferase**	**0.855646316**	**0.9657**	**14**
P22734	AIYQGPSSPDK	**1.301271976**	2	2.362952
P22734	AIYQGPSSPDKS	**0.860479832**	2	3.150823
P22734	EWAMNVGDAK	**1.117397676**	1	2.769252
P22734	GQIMDAVIR	**0.705395255**	2	3.032671
P22734	GQIMDAVIR+Oxidation(3)	**0.905020603**		
P22734	GSSSFECTHYSSYLEYMK	**53.28639645**	2	4.563265
P22734	GTVLLADNVIVPGTPDFLAYVR	**1.025907037**	3	4.868077
P22734	KGTVLLADNVIVPGTPDFLAYVR	**1.00523215**	2	4.687739
P22734	KYDVDTLDMVFLDHWK	**0.851381467**	3	5.635423
P22734	VTILNGASQDLIPQLK	**0.756817696**	2	4.301364
P22734	VVDGLEK	**0.904683504**	2	2.380745
P22734	YDVDTLDMVFLDHWK	**0.932598437**	3	4.602151
P22734	YLPDTLLLEK	**0.762703708**	2	2.913932
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	**0.912713133**	3	6.094255
P22789	**ST2A2 Alcohol sulfotransferase A**	**0.701092423**	**0.2258**	**4**
P22789	EEDLILLTYPK	**0.708475883**	2	2.591067
P22789	ETLQNVCNK	**1.609661378**	1	2.011793
P22789	KLEPDELDLVLK	**1.106081671**	3	4.730116
P22789	NHFTVAQAEAFDK	**0.550326452**	2	3.43943
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**0.935685333**	**0.93938**	**21**
P22791	ASLDMFNK	**0.99900049**	2	2.46946

P22791	ASLDMFNKK	**0.78152928**	2	2.525005
P22791	DVGILALEVYFPAQYVDQTDLEK	**1.02810189**	3	7.205613
P22791	GLKLEETYTNK	**0.596105147**	2	2.782672
P22791	GTHMENAYDFYKPNLASEYPLVDGK	**0.938660686**	3	7.034035
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3)	**1.144558389**		
P22791	IGAFSYGSGLAASFFSFR	**1.120052414**	2	3.879208
P22791	LEETYTNK	**0.893841567**	2	3.021606
P22791	LEETYTNKDVDK	**1.032543634**	2	4.108529
P22791	LEVGTETIIDK	**0.967621912**	2	3.733799
P22791	LMFNDFLSSSSDK	**0.707646557**	2	4.421253
P22791	LMFNDFLSSSSDK+Oxidation(1)	**0.985540997**		
P22791	LSIQCYLR	**0.663864292**	2	2.317
P22791	LVSSVSDLPK	**1.053030535**	2	3.49174
P22791	MGFCSVQEDINSLCLTVVQR	**1.104963234**	3	3.493203
P22791	MSPEEFTEIMNQR	**0.85793515**	2	4.656848
P22791	MSPEEFTEIMNQR+Oxidation(0)	**0.96628906**		
P22791	MSPEEFTEIMNQR+Oxidation(9)	**0.950255229**		
P22791	TKLPWDAVGR	**0.9025046**	3	3.950933
P22791	VNFSPPGDTSNLFPGTWYLER	**0.975819902**	2	5.053218
P22791	YTVGLGQTR	**0.889539954**	2	3.335884
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.047844331**	**0.609**	**10**
P22985	DEVTCVGHIIGAVVADTPEHAQR	**1.418537499**	3	3.848655
P22985	DPPANVQLFQEVPK	**1.468220576**	2	3.843398
P22985	DQTVSLSPSLFNPEDFKPLDPTQEPIFPPELLR	**1.019326057**	3	3.389107
P22985	LDPTFASATLLFQK	**1.378387413**	2	4.018567
P22985	NQPEPTVEEIENAFQGNLCR	**1.092672962**	2	4.713365
P22985	QLFQLDSPATPEK	**0.936565257**	2	3.205284
P22985	SVASIGGNIITASPISDLNPVFMASGAK	**1.124547525**	3	5.768322
P22985	TGTVVALEVAHFSNGGNTEDLSR	**1.018133016**	3	4.624146
P22985	TLLRPEEILLSIEIPYSK	**1.203509104**	3	4.050619
P22985	TNLPSNTAFR	**0.854364026**	1	2.258965
P23358	**RL12 60S ribosomal protein L12**	**1.159010797**	**0.00014**	**7**
P23358	CTGGEVGATSALAPK	**1.213056753**	2	4.083876
P23358	EILGTAQSVGCNVDGR	**1.454446836**	2	4.437327
P23358	HNGNITFDEIVNIAR	**1.167347744**	2	4.24865
P23358	HPHDIIDDINSGAVECPAS	**0.904266168**	2	4.839104
P23358	IGPLGLSPK	**0.850114972**	2	2.539657
P23358	QAQIEVVPSASALIIK	**1.580809395**	2	3.876422
P23358	VGDDIAKATGDWKGLR	**0.877036768**	2	2.412156
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.195024332**	**9.9E-20**	**10**
P23457	ALDGLNR	**1.076618198**	2	2.557236
P23457	ELTQVFEFQLASEDMK	**1.211386658**	2	3.290043
P23457	HFDSAYLYEVEEEVGQAIR	**2.919310528**	2	6.166505
P23457	MLDYCK	**0.908728332**	1	1.974668
P23457	SIGVSNFNCR	**1.077945893**	2	3.290779
P23457	SKDIILVSYCTLGSSR	**1.455773184**	2	5.066266
P23457	SPVLLDDPVLCAIAK	**1.797780635**	2	3.925643
P23457	VALNDGNFIPVLGFGTTVPEK	**1.622629228**	2	5.186249
P23457	YFDDHPNHPFTDE	**1.176150723**	2	3.745184
P23457	YKPVCNQVECHLYLNQSK	**5.645365944**	2	4.67289
P23514	**COPB Coatomer subunit beta**	**1.051208211**	**0.40726**	**7**
P23514	EAGELKPEEEITVGPVQK	**1.063124115**	2	4.338065
P23514	EDIQSVMTEVR	**0.908744055**	2	2.941848
P23514	NFENLIPDAPELIHDFLVNEK	**1.063830143**	3	4.017214
P23514	TNNVSEHEDTDKYR	**1.494346116**	3	4.127946
P23514	VLQDLVMDILR	**1.050316247**	2	3.618531
P23514	VLSECSPLMNDIFNK	**0.764540718**	2	2.667123

P23514	YEAAGTLVTLSSAPTAIK	**1.397077881**	2	4.9897
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.837485342**	**0.08622**	**8**
P23965	ALQLGTLFPPAEALK	**0.743849184**	2	5.413283
P23965	AVQELWLR	**0.799637974**	2	2.60382
P23965	DNYVNTIGHR	**1.103319724**	2	3.032264
P23965	GVILTSERPGIFSAGLDLMEMYGR	**0.783229311**	3	6.201207
P23965	QREADIQNFTSFISR	**0.867454854**	2	2.700237
P23965	SLHVYLEK	**0.875959757**	1	2.312779
P23965	VGLVDEVVPEDQVHSK	**0.769715286**	2	4.73955
P23965	WFTIPDHSR	**0.84956816**	2	3.196717
P24049	**RL17 60S ribosomal protein L17**	**1.251960496**	**1.1E-16**	**3**
P24049	EQIVPKPEEEVAQK	**1.594476955**	2	3.547131
P24049	GLDVDSLVIEHIQVNK	**1.008570108**	2	4.686262
P24049	YSLDPENPTK	**1.128484834**	1	2.764604
P24050	**RS5 40S ribosomal protein S5**	**0.955347715**	**0.84755**	**4**
P24050	HAFEIIHLLTGENPLQVLVNAIINSGPR	**0.955617838**		
P24050	RQAVDVSPLR	**1.085937483**	2	2.364157
P24050	VNQAIWLLCTGAR	**1.21169207**	2	4.110164
P24050	WSTDDVQINDISLQDYIAVK	**1.135905598**	2	4.764235
P24063	**ITAL Integrin alpha_L**	**1.106973842**	**0.88981**	**2**
P24063	ASEAQVLVKVDLIHEK	**1.013119388**	2	2.400362
P24063	DFEKILEFMK	**1.125677612**	3	3.333261
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.215809747**	**3.7E-10**	**6**
P24090	AQNVPFPVSTLVEFVIAATDCTGQEVTDPAK	**0.811383332**		
P24090	ELACDDPETEHVALIAVDYLNK	**1.000524649**	2	4.181743
P24090	HAFSPVASVESASGEVLHSPK	**1.221883955**	3	5.960438
P24090	LGGEEVSVACK	**0.642439148**	2	3.692735
P24090	VGQPGDAGAAGPVAPLCPGR	**0.704620341**	2	5.089277
P24090	VLHAQCHSTPDSAEDVRK	**0.74013996**	3	4.009344
P24268	**CATD Cathepsin D**	**0.82575938**	**0.00404**	**4**
P24268	AIGAVPLIQGEYMIPCEK	**0.821398389**	2	3.479833
P24268	DPTGQPGGELMLGGTDSR	**0.778650248**	2	4.746852
P24268	GGCEAIVDTGTSLLVGPVDEVK	**1.092888992**	2	4.077839
P24268	LGGQNYELHPEK	**0.969249957**	2	2.911747
P24329	**THTR Thiosulfate sulfurtransferase**	**0.786859915**	**2.4E-12**	**12**
P24329	EGHPVTSEPSRPEPAVFK	**0.967069832**	2	4.698688
P24329	FQLVDSR	**0.763198561**	2	2.466033
P24329	GSVNVPFMNFLTEDGFEK	**20.11334892**	2	5.276097
P24329	HVPGASFFDIEECR	**1.076048407**	3	3.614053
P24329	KVDLSQPLIATCR	**0.907530824**	2	4.780231
P24329	RFQLVDSR	**0.792940797**	2	2.474419
P24329	TVSVLNGGFR	**0.879850572**	2	2.887061
P24329	TYEQVLENLQSK	**0.789109134**	2	5.085625
P24329	VDLSQPLIATCR	**0.934747678**	2	3.545904
P24329	VLDASWYSPGTR	**0.762000108**	2	3.735063
P24329	WLAESIR	**0.836108091**	2	2.359281
P24329	YLGTQPEPDAVGLDSGHIR	**0.85094859**	3	5.052375
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**0.929033952**	**0.99972**	**9**
P24368	DKPLKDVIIVDCGK	**1.070802049**	2	3.641815
P24368	DTNGSQFFITTVK	**1.162166081**	2	3.580475
P24368	DVIIVDCGK	**0.6222505**	1	1.990567
P24368	HYGPGWVSMANAGK	**0.913417058**	2	3.234995
P24368	IEVEKPFAIAK	**1.042477904**	2	3.292331
P24368	IEVEKPFAIAKE	**0.753432063**	2	3.558626
P24368	TVDNFVALATGEK	**1.055940242**	2	3.755565
P24368	VLEGMDVVR	**0.93228703**	2	2.775417

P24368	VYFDFQIGDEPVGR	**0.902110311**	2	4.321369
P24457	**CP2DB Cytochrome P450 2D11**	**0.973514804**	**0.99598**	**2**
P24457	RFSVSTLR	**0.910858568**	2	2.541351
P24457	SLEEWVTK	**0.986737848**	2	2.756786
P24470	**CP2CN Cytochrome P450 2C23**	**0.580603025**	**9.9E-20**	**10**
P24470	ACVGESLAR	**0.594518927**	2	2.52792
P24470	AQPFDPTFILACAPCNVICSILFNDR	**0.543984462**		
P24470	DLDIKPITTGIINLPPPYK	**0.54575029**	2	3.717576
P24470	EALLQQGDEFLGR	**0.974517075**	2	2.581231
P24470	GTTVLPMLSSVMLDQK	**0.639595915**	2	4.008655
P24470	GYGLIFSNGER	**0.561266643**	2	3.241366
P24470	IEEEKDNLK	**0.713792227**	1	2.898257
P24470	LPPGPTPLPIIGNLLQLNLK	**0.846517881**	2	3.49408
P24470	TFLNLMDLLNK	**0.488170632**	2	3.86456
P24470	YITLLPSSLPHAVVQDTK	**0.421967845**	2	3.412023
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.745556423**	**2.1E-07**	**9**
P24473	AGMATAQAQHLLNK	**0.840687241**	2	3.919411
P24473	AGMATAQAQHLLNK+Oxidation(2)	**0.759907373**		
P24473	DEDITESQNILSAAEK	**0.94413451**	2	5.743433
P24473	DSGNQPPAMVPHK	**0.934259236**	2	2.420162
P24473	FLTAVSMEQPEMLEK	**0.629933187**	2	4.188372
P24473	FLTAVSMEQPEMLEK+Oxidation(11)	**0.979129462**		
P24473	MELLAYLLGEK	**1.23599174**	2	4.110036
P24473	QLFQVPMSVPK	**0.790263161**	2	2.719655
P24473	YGAFGLPTTVAHVDGK	**1.04455235**	2	3.759221
P25093	**FAAA Fumarylacetoacetase**	**1.002667307**	**0.45841**	**17**
P25093	AIDVGQGQTR	**1.043361737**	2	3.408475
P25093	AQEHIFGMVLMNDWSAR	**1.12349737**	3	3.693632
P25093	AQEHIFGMVLMNDWSAR+Oxidation(7)	**0.250239537**		
P25093	ASLQNLLSASQAQLR	**0.844582234**	2	4.802083
P25093	ASLQNLLSASQAQLRDDK	**0.808971613**	2	3.145474
P25093	ASSVVVSGTPIR	**1.01636061**	2	3.595053
P25093	DIQQWEYVPLGPFLGK	**1.369963949**	2	4.832111
P25093	FGEPIPISK	**0.991087581**	2	2.87535
P25093	GEGMSQAATICR	**0.921371897**	2	3.657554
P25093	GEGMSQAATICR+Oxidation(3)	**1.419123704**		
P25093	GKENALLPNWLHLPVGYHGR	**1.025367425**	3	3.470478
P25093	HLFTGPVLSK	**0.996204101**	1	2.707079
P25093	HQHVFDETTLNSFMGLGQAAWK	**0.887537541**	2	5.374691
P25093	IGVAIGDQILDLSVIK	**1.139198849**	2	5.417109
P25093	IGVAIGDQILDLSVIKHLFTGPVLSK	**1.216743354**	3	3.952735
P25093	TFLLDGDEVIITGHCQGDGYR	**0.841353903**	2	5.027973
P25093	VGFGQCAGK	**1.259360324**	2	2.385562
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.098899727**	**0.33525**	**7**
P25113	ALPFWNEEIVPQIK	**1.532879031**	2	3.936657
P25113	FSGWYDADLSPAGHEEAK	**0.793192445**	2	4.953215
P25113	HGESAWNLENR	**1.073812138**	2	3.739516
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	**0.995703303**	3	3.463135
P25113	SYDVPPPPMEPDHPFYSNISK	**1.162669744**	2	4.318289
P25113	YADLTEDQLPSCESLK	**1.061119127**	2	5.490339
P25113	YADLTEDQLPSCESLKDTIAR	**0.935084344**	2	5.017619
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.130435526**	**1.3E-14**	**14**
P25235	DLLLAAVSEDSSVAQIYHAVAALSGFGLPLASHEALGALTAR	**1.319413898**		
P25235	EDQVIQLMNTIFSK	**2.263595439**	2	2.394762

P25235	EETVLATVQALHTASHLSQQADLR	**1.014354994**	3	4.313227
P25235	FELDTSER	**0.904504722**	1	2.048539
P25235	FPEEEAPSTVLSQNLFTPK	**0.735592213**	2	4.258036
P25235	ISTEVGITNVDLSTVDKDQSIAPK	**0.909136197**	2	4.523488
P25235	LQVSSVLSQPLAQAAVK	**0.991448778**	2	5.727839
P25235	LSKEETVLATVQALHTASHLSQQADLR	**0.787807653**	3	4.536286
P25235	NFESLSEAFSVASAAAALSQNR	**1.049885528**	3	5.480579
P25235	NIVEEIEDLVAR	**0.97967234**	3	4.683619
P25235	NPILWNVADVVIK	**1.187734084**	2	3.269099
P25235	TGQEVVFVAEPDNK	**2.856992215**	2	3.90921
P25235	YHVPVVVVPEGSASDTQEQAILR	**1.08921652**	3	6.531534
P25235	YIANTVELR	**0.954879605**	2	2.587934
P25409	**ALAT1 Alanine aminotransferase 1**	**3.188861976**	**1.9E-11**	**2**
P25409	LTEQVFNEAPGIR	**2.537207748**	2	3.48034
P25409	VLCVINPGNPTGQVQTR	**5.841683759**	2	4.639893
P25977	**UBF1 Nucleolar transcription factor 1**	**0.933871737**	**0.37221**	**2**
P25977	AKYAKLHPEMSNLDLTK	**0.934145969**	2	2.336063
P25977	ALKAMEMTWNNMEKK+Oxidation(11)	**0.833345836**		
P26039	**TLN1 Talin_1**	**0.99421258**	**0.07034**	**22**
P26039	ADAEGESDLENSR	**1.054946729**	2	2.895252
P26039	ADAEGESDLENSRK	**0.639087735**	2	3.190112
P26039	AGALQCSPSDVYTK	**1.14534076**	2	2.655855
P26039	ASAGPQPLLVQSCK	**0.996350997**	2	3.023999
P26039	AVAEQIPLLVQGVR	**0.907590793**	2	3.555277
P26039	EAAEGLRMATNAAAQNAIKK	**0.793546854**	2	2.737611
P26039	ELMEEKKDEGTGTLR+Oxidation(2)	**1.31526441**		
P26039	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	**0.775047738**		
P26039	GVGAAATAVTQALNELLQHVK	**0.685610395**	3	3.591889
P26039	ILAQATSDLVNAIK	**1.180165117**	2	2.623954
P26039	LGAASLGAEDPETQVVLINAVK	**1.281012848**	2	4.412858
P26039	LLGEIAQGNENYAGIAAR	**0.97891709**	2	4.275113
P26039	LNEAAAGLNQAATELVQASR	**0.819835778**	2	5.238898
P26039	MVAAATNNLCEAANAAVQGHASQEK	**0.952831901**	3	3.432194
P26039	SNTSPEELGPLANQLTSDYGR	**0.934647544**	2	4.014234
P26039	TLAESALQLLYTAK	**1.071373029**	2	2.988723
P26039	TMLESAGGLIQTAR	**0.838491174**	2	2.631551
P26039	VGAIPANALDDGQWSQGLISAAR	**0.905924231**	2	4.517199
P26039	VGDDPAVWQLK	**0.961175111**	2	2.834435
P26039	VLGEAMTGISQNAK	**0.94788004**	2	2.791625
P26039	VLVQNAAGSQEK	**1.025557105**	2	2.514229
P26039	VVAPTISSPVCQEQLVEAGR	**0.826052472**	2	4.492325
P26043	**RADI Radixin**	**0.858570224**	**0.91954**	**10**
P26043	AFAAQEDLEK	**1.537800159**	2	2.558512
P26043	ALELEQER	**0.827572754**	1	1.927128
P26043	FFPEDVSEELIQEITQR	**0.927789137**	3	4.641557
P26043	IQNWHEEHR	**1.43814686**	2	2.512294
P26043	KKEEEATEWQHK	**1.302364049**	3	3.736757
P26043	KTQNDVLHAENVK	**0.919702217**	2	5.050867
P26043	NQEQLAAELAEFTAK	**0.880574237**	2	5.102746
P26043	QLQALSSELAQAR	**0.857791786**	2	3.757116
P26043	RKPDTIEVQQMK	**0.735521629**	2	3.868768
P26043	TQNDVLHAENVK	**1.069731004**	2	3.942393
P26231	**CTNA1 Catenin alpha_1**	**0.976817105**	**0.63942**	**10**
P26231	AEVQNLGGELVVSGVDSAMSLIQAAK	**0.857546575**	3	4.156018
P26231	AHVLAASVEQATENFLEK	**0.486728654**	2	2.36008
P26231	AVMDHVSDSFLETNVPLLVLIEAAK	**0.952394879**	3	3.537484
P26231	LIEVANLACSISNNEEGVK	**0.866664775**	2	4.894123

P26231	LLEPLVTQVTTLVNTNSK	**0.90265869**	2	4.011494
P26231	QIIVDPLSFSEER	**1.144388861**	2	2.683527
P26231	SAAGEFADDPCSSVK	**0.923226944**	2	4.052165
P26231	SDALNSAIDK	**1.189269259**	2	2.521385
P26231	TIADHCPDSACK	**0.384951649**	2	3.559316
P26231	VIHVVTSEMDNYEPGVYTEK	**1.015607451**	3	3.553701
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**0.958801579**	**0.10786**	**8**
P26284	AILAELTGR	**0.868232667**	2	2.572551
P26284	EEIQEVRSK	**0.626897853**	1	1.934391
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	**0.796812237**	3	6.632319
P26284	LEEGPPVTTVLTR	**0.862044173**	2	3.486447
P26284	MVNSNLASVEELKEIDVEVR	**0.910604165**	2	3.005507
P26284	RGDFIPGLR	**0.962128749**	2	2.708508
P26284	TREEIQEVR	**0.90443346**	3	3.489574
P26284	VDGMDILCVR	**0.840766645**	2	3.337078
P26453	**BASI Basigin**	**0.880612075**	**0.97578**	**7**
P26453	GNINVEGPPR	**1.059770156**	2	3.469563
P26453	KSEHASEGEFVK	**1.460818227**	2	2.864264
P26453	RKPDQTLDEDDPGAAPLK	**1.068388384**	3	4.149471
P26453	SEASHPPVDEWVWFK	**1.001971562**	3	3.926523
P26453	SEHASEGEFVK	**1.149318554**	3	3.543998
P26453	SGEYSCIFLPEPVGR	**0.935534199**	2	3.463887
P26453	VLQEDTLPDLQMK	**0.880479365**	2	4.353234
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**0.780112857**	**0.12447**	**7**
P26772	GGEIQPVSVK	**0.909278191**	2	3.260054
P26772	GGIMLPEK	**0.854395548**	2	2.330966
P26772	GGIMLPEK+Oxidation(3)	**0.965643463**		
P26772	GKGGEIQPVSVK	**0.580007179**	2	3.399598
P26772	VLLPEYGGTK	**0.953304288**	2	2.367303
P26772	VLQATVVAVGSGGK	**0.857674831**	2	5.511703
P26772	VVLDDKDYFLFR	**0.862891245**	3	3.403807
P27139	**CAH2 Carbonic anhydrase 2**	**0.737910284**	**0.3561**	**2**
P27139	IGPASQGLQK	**0.744949323**	2	2.541601
P27139	ITEALHSIK	**0.730583299**	2	2.426861
P27321	**ICAL Calpastatin**	**0.750711823**	**4.3E-15**	**4**
P27321	KGSDEVTASSAATGTSPR	**0.7091784**	2	4.842527
P27321	KVEEEVMNDQALQALSDSLGTR	**0.745467971**	3	3.571078
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	**0.99300882**	3	4.182306
P27321	SQSSEPPVIHEK	**0.460320497**	2	3.226077
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.866550369**	**0.8345**	**6**
P27364	AVLAANGSILK	**0.82182743**	2	2.891518
P27364	ETILNDREEEHR	**1.354954271**	2	2.920848
P27364	GDIVDAQFLR	**0.808666213**	2	2.993035
P27364	IVQMLVQEK	**0.876305126**	2	2.660714
P27364	NGGTFHTCALR	**0.813923133**	2	3.07916
P27364	QTILDVNVK	**0.706278627**	1	2.105358
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**1.093695851**	**0.34279**	**6**
P27605	DLNHVCVISESGK	**1.272180931**	2	3.692392
P27605	FFADLLDYIK	**1.092625042**	2	3.194604
P27605	NVLIVEDIIDTGK	**1.042272429**	2	4.105061
P27605	SVGYRPDFVGFEIPDK	**1.067121445**	3	3.809477
P27605	SYCNDQSTGDIK	**1.167236378**	2	3.961218
P27605	VIGGDDLSTLTGK	**1.153676756**	2	4.223195

P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.368997653**	**8E-07**	**21**
P27653	ASQAPSSFQLLYDLK	**1.655482967**	2	4.174053
P27653	AYTEEDLDLVEK	**1.128599739**	2	3.028994
P27653	CTHWAEGGQGALALAQAVQR	**1.091627917**	2	5.196739
P27653	DVDGLTSINAGK	**0.987616843**	2	2.433334
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	**1.064741168**	3	5.084738
P27653	GVPTGFVLPIR	**1.73367035**	2	2.528205
P27653	IFHELTQTDK	**1.231711836**	3	3.613856
P27653	IYGADDIELLPEAQNK	**1.060476158**	2	5.288408
P27653	KITIGQAPTEK	**1.447776035**	2	2.911438
P27653	KVVGDVAYDEAK	**1.562235463**	2	3.886915
P27653	LDIDPETITWQR	**1.236165351**	2	4.084001
P27653	MHGGGPTVTAGLPLPK+Oxidation(0)	**1.254915112**		
P27653	QGFGNLPICMAK	**0.91497371**	2	3.162811
P27653	TADLDKEVNK	**1.154167068**	2	2.400633
P27653	TADLDKEVNKGDILVVATGQPEMVK	**1.076659012**	3	4.611959
P27653	TDPAALTDDEINR	**1.218262305**	2	4.379691
P27653	THLSLSHNPEQK	**1.45064001**	2	3.832612
P27653	VLLSALDR	**1.460228696**	2	2.476872
P27653	VVGDVAYDEAK	**1.377968097**	2	3.727813
P27653	YSGLQPHVVVLVATVR	**1.549694686**	3	3.520746
P27653	YVVVTGITPTPLGEGK	**1.334452693**	2	4.88205
P27657	**LIPP Pancreatic triacylglycerol lipase**	**0.617139727**	**0.23439**	**2**
P27657	ATYTQATQNVR	**0.533003403**	2	2.520481
P27657	ITGLDAAEPYFQGTPEEVR	**0.588937218**	2	3.888477
P27661	**H2AX Histone H2A.x**	**0.79791338**	**0.011**	**3**
P27661	AGLQFPVGR	**0.885940439**	2	3.193053
P27661	HLQLAIR	**0.851595394**	2	2.642278
P27661	LLGGVTIAQGGVLPNIQAVLLPK	**0.773551463**	3	4.717062
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**0.814822704**	**0.63149**	**3**
P27768	IDAAEEEKYDMEVK	**0.511689996**	2	3.716147
P27768	SVMLQIAATELEK	**0.932572194**	2	2.529842
P27768	SVMLQIAATELEKEESR	**0.575439603**	2	3.105138
P27867	**DHSO Sorbitol dehydrogenase**	**1.011421032**	**0.00317**	**14**
P27867	AMGASQVVVIDLSASR	**0.877452294**	2	4.037575
P27867	AVEAFETAK	**0.76113922**	2	2.990508
P27867	EVGADFTIQVAK	**1.121020283**	2	2.781494
P27867	GENLSLVVHGPGDIR	**0.958838141**	2	3.973934
P27867	HSADFCYK	**1.028381322**	2	2.814023
P27867	IGDFVVK	**0.943675147**	2	2.62791
P27867	LENYPIPELGPNDVLLK	**1.017087846**	2	4.792784
P27867	LPDSVTFEEGALIEPLSVGIYACR	**1.01857557**	2	4.750957
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0)	**0.932740366**		
P27867	TLNVKPLVTHR	**0.673223415**	2	3.259476
P27867	VAIEPGVPR	**1.34437595**	2	2.585423
P27867	VAIEPGVPREIDEFCKIGR	**0.797818209**	2	2.545574
P27867	VLVCGAGPIGIVTLLVAK	**0.772296095**	3	6.226439
P27867	YNLTPSIFFCATPPDDGNLCR	**7.004895792**	2	4.203186
P27952	**RS2 40S ribosomal protein S2**	**1.184857865**	**0.74859**	**7**
P27952	AEDKEWIPVTK	**1.134735148**	2	3.212702
P27952	AFVAIGDYNGHVGLGVK	**1.287109792**	2	3.788078
P27952	ATFDAISK	**1.146152683**	2	2.444848
P27952	GCTATLGNFAK	**1.151974077**	2	2.840331
P27952	GTGIVSAPVPK	**1.143887617**	2	2.449337
P27952	SLEEIYLFSLPIK	**2.863213179**	1	2.712297
P27952	TYSYLTPDLWK	**1.099257737**	2	2.706529

P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**0.928852072**	**1**	**26**
P28037	ADPLGLEAEK	**1.014422177**	2	2.822206
P28037	ANATEFGLASGVFTR	**1.03475227**	2	4.444672
P28037	AVQMGMSSVFFNK	**0.921490614**	2	3.511725
P28037	CPQSEEGATYEGIQK	**1.394382322**	2	4.314612
P28037	DLGEAALNEYLR	**1.137603106**	2	3.288827
P28037	ECEVLPDDTVSTLYNR	**1.322606366**	2	5.007122
P28037	EGHEVVGVFTIPDKDGK	**1.083052157**	2	4.51124
P28037	GNDKVPGAWTEACGQK	**0.929261387**	2	3.536968
P28037	GQALPEVVAK	**0.954400337**	2	2.596334
P28037	GSASSDLELTEAELATAEAVR	**0.967251781**	2	6.296675
P28037	GVVNILPGSGSLVGQR	**0.925184971**	2	4.944245
P28037	IGFTGSTEVGK	**1.139075242**	2	3.110392
P28037	ILPNVPEVEDSTDFFK	**1.024788629**	2	3.691142
P28037	INWDQPAEAIHNWIR	**0.880048801**	2	3.67751
P28037	KEGHEVVGVFTIPDKDGK	**1.126922437**	3	3.482716
P28037	KIGFTGSTEVGK	**0.868507942**	2	2.950796
P28037	KLVEYCQR	**1.25752866**	2	2.535579
P28037	LFVEESIHNQFVQK	**0.85150664**	2	4.598858
P28037	LIAEGTAPR	**1.053931238**	2	3.134685
P28037	LQAGTVFINTYNK	**3.166633176**	2	2.507685
P28037	LSDHPDVR	**1.031530695**	1	2.099179
P28037	NIQLEDGK	**1.052074619**	1	1.998016
P28037	TAACLAAGNTVVIKPAQVTPLTALK	**0.774703229**	3	4.426006
P28037	TDVAAPFGGFK	**0.990109257**	2	2.719699
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	**0.91024023**	3	6.586313
P28037	VVEEVEK	**0.964597293**	2	2.478464
P28064	**PSB8 Proteasome subunit beta type_8**	**1.021886284**	**0.99873**	**3**
P28064	ASAGSYIATIR	**1.06915227**	2	2.527466
P28064	QDLSPEEAYDLAR	**0.987455797**	2	3.116903
P28064	VESTDVSDLLHK	**1.09913434**	2	2.901866
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.196766375**	**0.645**	**10**
P28480	AFHNEAQVNPER	**1.193310863**	2	3.419807
P28480	FATEAAITILR	**1.055373151**	2	3.260354
P28480	HGGYENAVHSGALDD	**1.396060989**	2	4.228732
P28480	ICDDELILIK	**1.085941226**	2	3.170019
P28480	LLEVEHPAAK	**1.127133974**	2	2.39514
P28480	MLVDDIGDVTITNDGATILK	**1.061982725**	2	4.338411
P28480	SLHDALCVVK	**0.962432003**	2	2.455453
P28480	SLLVIPNTLAVNAAQDSTDLVAK	**1.100861615**	2	4.637555
P28480	SQNVMAAASIANIVK	**1.026813371**	2	4.022607
P28480	YINENLIINTDELGR	**0.948386981**	2	4.484542
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.906004146**	**0.34197**	**3**
P28492	MVQESSSGGLLDR	**0.630624608**	2	3.222004
P28492	SNPDLWGVSLCTVDGQR	**0.942455529**	2	3.155111
P28492	TALHVAAAEGHIDVVK	**0.829532254**	3	3.5419
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**0.865393532**	**0.56855**	**3**
P28650	CQGGNNAGHTVVVDGK	**0.631517281**	2	3.70611
P28650	LDILDVLSEIK	**0.859948728**	2	3.153514
P28650	VGIGAFPTEQINEIGDLLQNR	**0.879052373**	3	3.803699
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**0.858340176**	**9.9E-20**	**20**
P29147	AVLVTGCDSGFGFSLAK	**0.654728183**	2	5.714079
P29147	EVAEVNLWGTVR	**1.19443072**	2	2.754992
P29147	FGVEAFSDCLR	**0.799749866**	2	3.706598
P29147	GFLVFAGCLLK	**0.998456083**	2	3.480829

P29147	KMWDELPEVVR	**0.76461493**	2	2.84792
P29147	KMWDELPEVVR+Oxidation(1)	**0.71570834**		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	**1.169922021**	3	5.449405
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0)	**1.080031127**		
P29147	MQVMTHFPGAISDK	**1.111304196**	2	4.578563
P29147	MQVMTHFPGAISDK+Oxidation(0)	**1.110908886**		
P29147	MQVMTHFPGAISDK+Oxidation(0)	**0.788639724**		
P29147	MQVMTHFPGAISDK+Oxidation(3)	**0.782643165**		
P29147	MWDELPEVVR	**0.431276718**	2	3.080644
P29147	MWDELPEVVR+Oxidation(0)	**0.699843219**		
P29147	TIQLNVCNSEEVEK	**0.778160161**	2	4.449669
P29147	VSVVEPGNFIAATSLYSPER	**0.81224887**	2	6.10183
P29147	VVNISSMLGR	**0.805693981**	2	3.961768
P29147	VVNISSMLGR+Oxidation(6)	**0.6962298**		
P29147	YEMHPLGVK	**0.821940494**	2	2.703852
P29147	YEMHPLGVK+Oxidation(2)	**0.801872587**		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.985054736**	**2.4E-10**	**8**
P29266	DLGLAQDSATSTK	**1.021073612**	2	4.0746
P29266	EAGEQVASSPADVAEK	**0.867968133**	2	4.741756
P29266	GSLLIDSSTIDPSVSK	**0.746704623**	2	4.769774
P29266	HGYPLILYDVFPDVCK	**0.877544962**	2	4.997539
P29266	KGSLLIDSSTIDPSVSK	**0.784409606**	2	4.659856
P29266	MGAVFMDAPVSGGVGAAR	**0.941444959**	2	4.789086
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0)	**0.97728543**		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5)	**0.97728543**		
P29314	**RS9 40S ribosomal protein S9**	**1.164599718**	**0.13375**	**9**
P29314	IEDFLER	**1.137794754**	2	2.829904
P29314	IGVLDEGK	**0.937765026**	2	2.395046
P29314	KGQGGAGAGDDEEED	**1.898809931**	2	4.175772
P29314	LDYILGLK	**1.183512967**	2	2.547796
P29314	LFEGNALLR	**1.127674702**	2	2.629325
P29314	LIGEYGLR	**1.462039232**	2	2.646587
P29314	QVVNIPSFIVR	**1.034977299**	2	2.454194
P29314	RLQTQVFK	**1.38718884**	2	2.301405
P29314	SRLDQELK	**1.089279743**	3	3.315833
P29315	**RINI Ribonuclease inhibitor**	**0.973315179**	**0.10981**	**6**
P29315	ASLQELDLGSNK	**0.992636862**	2	2.827818
P29315	ELHLNDNPLGDEGLK	**0.811305067**	2	2.926205
P29315	LDDCGLTEVR	**0.852120171**	2	2.926793
P29315	LENCGITSANCK	**0.9950535**	2	3.330049
P29315	SAIQANPALTELSLR	**1.048618489**	2	4.594812
P29315	TNELGDAGVGLVLQGLQNPTCK	**0.883525434**	2	5.286791
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.026323213**	**0.70727**	**10**
P29410	AMVASGSELGK	**0.993191944**	2	2.361654
P29410	AMVASGSELGKK	**0.964429502**	2	3.138547
P29410	AVLLGPPGAGK	**0.992634329**	2	2.709268
P29410	EAMKDDITGEPLIR	**1.311461601**	2	2.723557
P29410	GIHCAIDASQTPDVVFASILAAFSK	**1.513064774**	3	6.222835
P29410	LEAYHTQTTPLVEYYR	**1.083219923**	2	5.400816
P29410	LVSDEMVVELIEK	**0.9182419**	2	4.143301
P29410	NGFLLDGFPR	**0.927283502**	2	3.35506
P29410	NLETPSCK	**1.008510346**	2	2.349375
P29410	SYHEEFNPPK	**0.971631224**	3	3.856591
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**0.935663456**	**0.09967**	**8**

P29411	AYEAQTEPVLQYYQK	**0.980891798**	2	4.183173
P29411	EDDKPETVIK	**0.78622217**	2	2.633277
P29411	KGVLETFSGTETNK	**0.719188899**	2	3.050477
P29411	NLTQCSWLLDGFPR	**0.840090675**	2	3.339229
P29411	TLPQAEALDR	**0.916782507**	2	2.339847
P29411	TVGIDDLTGEPLIQR	**0.593296033**	2	3.351763
P29411	VYNIEFNPPK	**0.651907094**	2	3.155336
P29411	VYQIDTVINLNVPFEVIK	**0.83615161**	2	2.660056
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**1.090409486**	**0.99633**	**2**
P29419	ELAEAEDVSIFK	**1.125050645**	2	3.297797
P29419	YSALILGMAYGAK	**0.961801089**	2	4.087216
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.055062669**	**6.8E-06**	**3**
P30009	AEDGAAPSPSSETPK	**0.735229357**	2	3.924316
P30009	AEEPSEAVGEK	**1.030535918**	2	2.78907
P30009	GEAAAERPGEAAVASSPSK	**1.273043928**	2	4.547205
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**0.964871939**	**0.01077**	**4**
P30349	EEDLNSFSIEDLK	**2.32616697**	2	2.668863
P30349	SLSNVIAHEISHSWTGNLVTNK	**0.692499653**	3	4.175377
P30349	SSALQWLTPEQTSGK	**1.007437633**	2	2.99612
P30349	WEEAIPLALK	**1.272801244**	2	2.913596
P30427	**PLEC Plectin**	**0.80602341**	**0.76703**	**6**
P30427	AQAEAQQPVFNTLR	**1.030672629**	2	2.994362
P30427	AQVEQELTTLR	**0.857635079**	2	2.514488
P30427	LLDPEDVDVPQPDEK	**0.756758366**	2	3.726467
P30427	LQAEEVAQQK	**0.910779179**	2	2.398628
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0)	**0.900910922**		
P30427	VLALPEPSPAAPTLR	**0.935156105**	2	2.781167
P30713	**GSTT2 Glutathione S_transferase theta_2**	**1.024899897**	**7.7E-05**	**6**
P30713	AQVHEYLGWHADNIR	**1.073575926**	2	4.898557
P30713	GQHLSEQFSQVNCLK	**0.990334663**	2	4.794899
P30713	NSMVLALQR	**0.875256486**	2	2.868994
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	**1.316756786**	3	4.296496
P30713	VLGPLIGVQVPEEK	**0.811680063**	2	3.897211
P30713	YQVADHWYPADLQAR	**0.785445407**	2	4.862041
P30835	**K6PL 6_phosphofructokinase_ liver type**	**1.126470793**	**0.21664**	**2**
P30835	NEWGSLLEELVK	**1.163951099**	2	3.212283
P30835	VFANAPDSACVIGLR	**0.385257177**	2	2.403141
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**0.816199663**	**0.07179**	**10**
P30839	DILAAIAADLSK	**0.91590694**	2	3.030413
P30839	EKDILAAIAADLSK	**0.977708437**	2	4.115873
P30839	EKPLALYIFSHNNK	**1.293509292**	2	3.133023
P30839	FDHILYTGNTAVGK	**1.638640688**	2	3.935179
P30839	HLTPVTLELGGK	**0.963557099**	3	3.315098
P30839	NVEEAINFINDR	**1.355632453**	2	4.109665
P30839	QRFDHILYTGNTAVGK	**1.142864578**	2	2.83376
P30839	VMQEEIFGPILPIVSVK	**0.713630128**	2	4.425926
P30839	VMQEEIFGPILPIVSVK+Oxidation(1)	**0.955399096**		
P30839	YIAPTILTDVDPNSK	**0.972590677**	2	3.860017
P30904	**MIF Macrophage migration inhibitory factor**	**1.12430693**	**0.99851**	**2**
P30904	LHISPDR	**0.970150014**	1	2.018165
P30904	LLCGLLSDR	**1.166816841**	2	2.934856
P30999	**CTND1 Catenin delta_1**	**0.961900933**	**0.72033**	**3**
P30999	GYELLFQPEVVR	**0.832241355**	2	2.842425
P30999	QDVYGPQPQVR	**0.978009014**	2	2.43279
P30999	SQSSHSYDDSTLPLIDR	**0.961347925**	2	2.594846
P31000	**VIME Vimentin**	**0.765707147**	**1.7E-12**	**15**

P31000	DGQVINETSQHHDDLE	**0.783377264**	2	3.114833
P31000	FADLSEAANR	**1.105607869**	2	2.840343
P31000	ILLAELEQLK	**0.742362602**	2	3.222592
P31000	KLLEGEESR	**0.859766418**	2	2.730617
P31000	KVESLQEEIAFLK	**0.771770599**	2	3.975406
P31000	LGDLYEEEMR	**0.567220146**	2	2.336449
P31000	LLEGEESR	**0.748017058**	2	2.749329
P31000	LQEEMLQR	**0.658706861**	2	2.328545
P31000	NLQEAEEWYK	**0.749976636**	2	2.81154
P31000	QDVDNASLAR	**0.524235949**	2	2.805826
P31000	QVQSLTCEVDALK	**0.748854022**	2	3.541288
P31000	RQVDQLTNDK	**0.810196338**	2	2.516809
P31000	SLYSSSPGGAYVTR	**1.27716286**	2	2.809831
P31000	TNEKVELQELNDR	**0.985718212**	2	2.835557
P31000	VELQELNDR	**0.679215283**	2	2.587061
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**0.940476686**	**9.9E-20**	**7**
P31044	GNDISSGTVLSEYVGSGPPK	**0.917495794**	2	6.581267
P31044	KYHLGAPVAGTCFQAEWDDSVPK	**1.656772374**	3	3.775324
P31044	LYTLVLTDPDAPSR	**1.234138424**	2	4.267089
P31044	VDYGGVTVDELGK	**0.777044441**	2	4.858945
P31044	VLTPTQVMNRPSSISWDGLDPGK	**0.817823749**	3	5.079072
P31044	YHLGAPVAGTCFQAEWDDSVPK	**3.355344271**	2	5.398308
P31044	YVWLVYEQEQPLNCDEPILSNK	**1.270054568**	2	5.405777
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.047656766**	**0.99863**	**19**
P31210	DELLTSLGK	**0.9434171**	2	2.862387
P31210	DIEALNK	**1.170414223**	1	2.46768
P31210	EEMKDIEALNK	**1.108976955**	2	3.385076
P31210	ENFQIFDFSLTK	**1.220901898**	2	3.027293
P31210	HIDGAYVYR	**1.039839371**	2	2.939373
P31210	IKENFQIFDFSLTK	**1.305189842**	3	4.346778
P31210	LWSTDHDPEMVRPALER	**0.74179631**	3	3.668172
P31210	NEHEVGEAIR	**0.847191892**	2	3.07835
P31210	NPLWVNVSSPPLLK	**1.213755238**	2	4.442975
P31210	NPLWVNVSSPPLLKDELLTSLGK	**0.826471254**	3	5.236874
P31210	QLEVILNKPGLK	**0.903518151**	2	3.382973
P31210	REEIFYCGK	**1.411273554**	2	3.28525
P31210	RQLEVILNKPGLK	**0.749660141**	3	3.680693
P31210	SLGVSNFNR	**0.717128848**	2	2.376778
P31210	SNLCATWEALEACK	**0.87003392**	2	4.941665
P31210	SNLCATWEALEACKDAGLVK	**0.643151395**	2	5.145218
P31210	TAIDEGYR	**0.863984965**	2	2.436932
P31210	TQAQIVLR	**0.924439928**	2	3.036217
P31210	YKPVTNQVECHPYFTQTK	**1.058831475**	2	5.77276
P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.211373193**	**3.6E-07**	**2**
P31230	GAEADQIIEYLK	**1.233795988**	2	3.477441
P31230	KEIEELK	**0.953402333**	1	1.999019
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.087476604**	**0.5042**	**7**
P31399	ANVDKPGLVDDFK	**1.086831633**	2	3.780981
P31399	KYPYWPHQPIENL	**0.874499217**	2	2.380995
P31399	NCAQFVTGSQAR	**0.879274906**	2	4.925229
P31399	NMIPFDQMTIDDLNEVFPETK	**0.841733067**	2	5.076017
P31399	SWNETFHTR	**1.126896809**	2	2.676055
P31399	TIDWVSFVEIMPQNQK	**1.426880478**	2	4.12896
P31399	YTALVDAEEKEDVK	**1.129737406**	2	3.638041

P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.053375214**	**0.92342**	**6**
P32089	FIHDQTSSNPK	**1.25341659**	1	3.547732
P32089	GLSSLLYGSIPK	**0.735162044**	2	3.292212
P32089	GTYQGLTATVLK	**0.778249323**	2	2.628208
P32089	NTLDCGVQILK	**0.915180165**	2	2.497192
P32089	SHGVLGLYR	**0.477375101**	1	1.914029
P32089	TQLQLDER	**0.993702181**	2	2.918798
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**0.79519875**	**5.8E-07**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	**0.887731984**	2	4.595607
P32198	GDTNPNIPKPTR	**0.934896067**	2	2.501151
P32198	LSTSQTPQQQVELFDFEK	**2.209944517**	2	2.815178
P32198	MTALAQDFAVNLGPK	**0.670079328**	2	3.388431
P32198	MTALAQDFAVNLGPK+Oxidation(0)	**0.456994427**		
P32198	TSPDAFIQLALQLAHYK	**0.73693748**	2	3.259335
P32232	**CBS Cystathionine beta_synthase**	**2.060861316**	**9.9E-20**	**11**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	**1.455261165**	3	5.973728
P32232	ALGAEIVR	**1.920798275**	1	1.970291
P32232	CVVILPDSVR	**1.4884805**	2	2.467029
P32232	FDSPESHVGVAWR	**1.077695973**	2	3.785591
P32232	LKNEIPNSHILDQYR	**1.941807534**	3	3.346921
P32232	NASNPLAHYDDTAEEILQQCDGK	**1.95252162**	2	5.300978
P32232	SNDDDSFAFAR	**2.097282137**	2	3.32601
P32232	VDMLVASAGTGGTITGIAR	**1.338642422**	2	4.834332
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	**1.915083819**	3	3.979408
P32232	VRPSDEVCK	**1.775340248**	2	2.631969
P32232	VWISPDTPSR	**1.375412415**	2	2.367357
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**0.967049714**	**0.90612**	**13**
P32551	AVAFQNPQTR	**1.125369913**	2	3.220823
P32551	AVAQGNLSSADVQAAK	**0.926605314**	2	4.976707
P32551	GNNTTSLLSQSVAK	**0.984366971**	2	4.174992
P32551	IIENLHDVAYK	**1.271643363**	2	3.558061
P32551	ITSEELHYFVQNHFTSAR	**1.01448394**	3	3.873832
P32551	LPNGLVIASLENYAPLSR	**1.759175424**	2	4.686533
P32551	NALANPLYCPDYR	**0.983044365**	2	3.018948
P32551	RGNNTTSLLSQSVAK	**0.974686088**	2	3.279236
P32551	RWEVAALR	**1.091840391**	2	2.410336
P32551	SMTASGNLGHTPFLDEL	**0.880341544**	2	3.213099
P32551	SMTASGNLGHTPFLDEL+Oxidation(1)	**0.948751368**		
P32551	TSAPGGVPLQPQELEFTK	**0.873149491**	2	4.216162
P32551	YENYNYLGTSHLLR	**1.164471458**	2	4.273424
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.404431405**	**9.9E-20**	**17**
P32755	AFEEEQALR	**1.536584807**	2	3.559216
P32755	DIAFEVEDCEHIVQK	**1.395856168**	2	4.093562
P32755	ENMDVLEELK	**1.837848954**	2	2.845803
P32755	FAVLQTYGDTTHTLVEK	**1.54235509**	2	4.977412
P32755	FLPGFEAPTYK	**1.259150529**	1	2.402299
P32755	FWSVDDTQVHTEYSSLR	**3.070106439**	2	5.522952
P32755	GMEFLAVPSSYYR	**1.569783149**	2	3.59925
P32755	GNLTDLETNGVR	**1.57871179**	2	3.72886
P32755	HNHQGFGAGNFNSLFK	**1.462203752**	3	5.647913
P32755	ILVDYDEK	**1.627276987**	2	2.402559
P32755	IVFVLCSALNPWNK	**1.388997797**	2	3.657444
P32755	IVREPWVEEDKFGK	**1.465405299**	3	4.488583
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	**1.621208365**	3	7.771306

P32755	MGFEPLAYK	**1.653270698**	2	2.619258
P32755	SIVVANYEESIK	**1.320801677**	2	4.159398
P32755	SQIQEYVDYNGGAGVQHIALR	**1.564205092**	2	5.54957
P32755	TEDIITTIR	**1.416327943**	2	3.391608
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**0.880400757**	**0.39724**	**2**
P33124	ALRPTIFPVVPR	**0.801317024**	2	2.979572
P33124	IENIYIR	**0.894360709**	2	2.95509
P33273	**CP255 Cytochrome P450 2C55**	**0.769648872**	**0.43796**	**4**
P33273	DENFLNLMEK	**1.039979807**	2	2.312552
P33273	ELRHFSLMTLR	**1.117081759**	2	2.365308
P33273	FDYKDENFLNLMEK	**0.655858115**	3	4.522217
P33273	IQEEASCLVEELR	**1.208783506**	2	2.719774
P33274	**CP4F1 Cytochrome P450 4F1**	**1.30927757**	**0.05084**	**2**
P33274	ACNLVHEFTDAVIR	**1.234720377**	3	3.738177
P33274	TLPDQGLDEFLK	**1.847088494**	2	2.517616
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.086039168**	**0.58774**	**25**
P34058	ADLINNLGTIAK	**0.978928577**	2	4.18483
P34058	EDQTEYLEER	**1.300661181**	2	3.430418
P34058	EGLELPEDEEEK	**0.425246668**	2	2.541823
P34058	EGLELPEDEEEKKK	**1.270963165**	2	3.370606
P34058	ELISNASDALDK	**1.245236793**	2	3.384502
P34058	EQVANSAFVER	**1.589420419**	2	2.369812
P34058	GFEVVYMTEPIDEYCVQQLK	**2.285575443**	2	4.445317
P34058	GVVDSEDLPLNISR	**1.011721285**	2	4.912754
P34058	HFSVEGQLEFR	**1.01399068**	2	2.571582
P34058	HLEINPDHPIVETLR	**1.037703839**	2	4.582771
P34058	HSQFIGYPITLYLEK	**2.53575845**	2	4.129283
P34058	IDIIPNPQER	**1.016885244**	2	3.117871
P34058	KHLEINPDHPIVETLR	**0.988475458**	2	4.827516
P34058	LGIHEDSTNR	**1.01488291**	2	3.40681
P34058	NPDDITQEEYGEFYK	**1.481342914**	2	4.753683
P34058	RAPFDLFENK	**1.047899873**	2	2.811533
P34058	SIYYITGESK	**1.472741656**	2	3.040217
P34058	SLTNDWEDHLAVK	**1.029706698**	2	4.017478
P34058	TLTLVDTGIGMTK	**0.939529526**	2	4.082806
P34058	TLTLVDTGIGMTK+Oxidation(10)	**1.196655446**		
P34058	VILHLKEDQTEYLEER	**1.139267061**	3	3.719254
P34058	YESLTDPSK	**1.059424214**	2	2.642702
P34058	YESLTDPSKLDSGK	**1.039086473**	2	3.596219
P34058	YHTSQSGDEMTSLSEYVSR	**1.121564134**	2	5.552259
P34058	YIDQEELNK	**0.934364304**	2	3.487408
P34064	**PSA5 Proteasome subunit alpha type_5**	**0.990851323**	**0.99126**	**3**
P34064	AIGSASEGAQSSLQEVYHK	**0.989656275**	2	4.718152
P34064	EELEEVIKDI	**0.814026674**	2	2.494571
P34064	GVNTFSPEGR	**1.065590823**	2	3.013032
P34067	**PSB4 Proteasome subunit beta type_4**	**0.84671025**	**0.00922**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	**1.035530018**	2	3.634493
P34067	TQNPMVTGTSVLGVK	**0.802402802**	2	2.837394
P34067	VNDSTMLGASGDYADFQYLK	**0.900886729**	2	4.302262
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**0.936890411**	**0.9743**	**2**
P35171	GGTSDALLYR	**0.941956494**	2	2.888413
P35171	LFQEDNGMPVHLK	**0.889237489**	2	3.616754
P35213	**1433B 14_3_3 protein beta/alpha**	**1.149160645**	**3.6E-07**	**6**
P35213	AVTEQGHELSNEER	**1.594734593**	2	4.544152
P35213	EKIEAELQDICSDVLELLDK	**0.833522004**	3	3.559023
P35213	QTTVSNSQQAYQEAFEISK	**1.034646777**	2	5.24455

P35213	TAFDEAIAELDTLNEESYK	1.002415372	2	4.837814
P35213	YLILNATHAESK	1.149495358	2	3.207704
P35213	YLSEVASGDNK	1.0380996	1	2.999391
P35278	RAB5C Ras_related protein Rab_5C	0.9892917	0.9773	2
P35278	GVDLQESNPASR	1.052715682	2	3.07112
P35278	NEPQNAAGAPGR	0.915930109	2	2.857707
P35427	RL13A 60S ribosomal protein L13a	1.446218039	6.4E-12	2
P35427	CEGINISGNFYR	1.055038968	2	3.313946
P35427	YQAVTATLEEK	1.223767162	2	3.434364
P35434	ATPD ATP synthase subunit delta_ mitochondrial	0.904334241	0.28963	2
P35434	AQSELSGAADEAAR	0.892229076	2	4.591399
P35434	IEANEALVK	0.87108585	2	3.168806
P35435	ATPG ATP synthase subunit gamma_ mitochondrial	0.920754016	0.00746	7
P35435	GLCGAIHSSVAK	1.015306233	2	3.798018
P35435	HLIIGVSSDR	0.828536573	2	2.786877
P35435	NASDMIDK	0.84409674	1	2.113865
P35435	NDMAALTAAGK	0.884593223	2	3.376471
P35435	NDMAALTAAGK+Oxidation(2)	0.835169507		
P35435	THSDQFLVSFK	1.077151429	2	3.339708
P35435	VYGTGSLALYEK	1.210218826	2	2.992851
P35565	CALX Calnexin	0.889905213	0.52562	9
P35565	AEEDEILNR	1.553291612	2	2.914994
P35565	KIPNPDFFEDLEPFR	0.843616444	3	3.99702
P35565	NKGDEEEEEEKLEEK	1.097354397	2	5.21963
P35565	SDTSTPPSPK	1.751221739	2	2.530315
P35565	TDAPQPDVK	0.963373774	2	2.343518
P35565	TDAPQPDVKDEEGKEEEK	0.845554486	2	3.868199
P35565	TSELNLDQFHDK	1.221615603	2	3.883714
P35565	VVDDWANDGWGLK	0.828665319	2	4.30863
P35565	VVDDWANDGWGLKK	0.533866839	2	2.767107
P35704	PRDX2 Peroxiredoxin_2	1.015939778	0.99352	4
P35704	EGGLGPLNIPLLADVTK	1.106666718	2	3.352696
P35704	KEGGLGPLNIPLLADVTK	0.829284839	2	4.256789
P35704	NDEGIAYR	0.940986865	2	2.392763
P35704	QITVNDLPVGR	0.949943197	2	2.69115
P35738	ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial	0.866196485	0.15581	5
P35738	AAVEQVPVEPYK	1.004438583	2	2.660911
P35738	GLLLSCIEDKNPCIFFEPK	0.903597956	2	3.466292
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	0.854655552	3	4.104013
P35738	MNLFQSITSALDNSLAK	0.809532411	2	2.629858
P35738	SGDLFNCGSLTIR	0.860837044	2	2.892294
P35815	PPM1B Protein phosphatase 1B	0.81799831	0.37556	2
P35815	IQNAGGSVMIQR	0.778629269	2	3.083096
P35815	SGFALEPSVENVK	1.081075933	2	3.126184
P36201	CRIP2 Cysteine_rich protein 2	1.058037118	0.6383	3
P36201	ASSVTTFTGEPNMCPR	3.536631597	2	3.899054
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	0.991380698	3	6.951923
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.092039561	2	4.259221
P36365	FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1	0.91600014	9.9E-20	11
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.246482523	3	3.499315
P36365	ASLYNSVVSNSSK	1.564837287	2	2.308056
P36365	CCLEEGLEPTCFER	0.768066076	2	4.114057
P36365	ENSVVFNNTPK	1.916172225	2	2.554125
P36365	FTEHVEEGR	0.664674052	2	3.131942

P36365	NLLPTPVVSWLISK	0.601321479	2	2.466439
P36365	SCDLGGLWR	0.655658598	2	2.766515
P36365	TQLREPVLNDELPGR	0.652417807	3	4.071889
P36365	VAIVGAGVSGLASIK	1.160138165	2	2.873965
P36365	VEDGQASLYK	0.813772455	2	3.531333
P36365	VLVVGMGNSGTDIAVEASHLAK	0.813109839	2	2.945758
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.053034967**	**0.00717**	**7**
P36511	ANIIAWALAQIPQK	0.776217934	3	5.083358
P36511	FVNVWTYELPR	1.051348409	2	3.194323
P36511	FVTFPTSFSSHDLENFFTR	1.721871169	2	4.163317
P36511	GHEVTVLRPSAFVFLDPK	1.368753533	3	3.524342
P36511	IILEELVQK	0.930649525	2	3.283202
P36511	SDLLNALEEVIDNPFYK	0.954127692	2	5.231205
P36511	TLGRPTTLAEIMGK	0.917526257	3	3.614776
P36536	**SAR1A GTP_binding protein SAR1a**	**1.250348476**	**0.80284**	**2**
P36536	LVFLGLDNAGK	1.25104157	2	2.993917
P36536	VELNALMTDETISNVPILILGNK	0.986984897	3	4.625602
P36972	**APT Adenine phosphoribosyltransferase**	**0.901658244**	**0.66201**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	0.901211787	2	3.898834
P36972	IDYIAGLDSR	0.902057186	2	3.457277
P36972	SFPDFPIPGVLFR	0.920237555	2	3.550406
P37397	**CNN3 Calponin_3**	**0.910255812**	**0.84566**	**3**
P37397	AGQSVIGLQMGTNK	0.897783093	2	4.283856
P37397	VNESSLNWPQLENIGNFIK	0.819868554	2	3.378146
P37397	YDQQAEEDLR	1.101230456	2	3.259101
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.003682195**	**0.99746**	**8**
P38650	FGNPLLVQDVESYDPVLNPVLNR	0.921869416	2	4.533171
P38650	GWENHVEGQK	1.111313381	2	2.878756
P38650	ILDDDTIITTLENLK	1.010518609	2	2.694302
P38650	QLQNISQAAAAGGAK	1.120646082	2	3.302531
P38650	SSLQSQCLNEVLK	0.914003627	2	2.920714
P38650	VQGLTVEQAEAVAR	0.985266122	2	3.584492
P38650	VQVALEELQDLK	0.979282218	2	2.711881
P38650	VTDFGDKVEDPTFLNQLQSGVNR	0.842810304	3	4.068075
P38652	**PGM1 Phosphoglucomutase_1**	**0.792574323**	**0.15501**	**16**
P38652	ADNFEYSDPVDGSISK	0.75750392	2	4.70753
P38652	AIGGIILTASHNPGGPNGDFGIK	0.776573427	2	5.283345
P38652	FFGNLMDASK	0.697778377	2	2.307066
P38652	FNISNGGPAPEAITDK	1.046650694	2	4.284826
P38652	INQDPQVMLAPLISIALK	0.761925731	2	4.933863
P38652	KQRVEDILK	0.574871019	1	1.982547
P38652	LSGTGSAGATIR	1.008032394	2	3.631773
P38652	LSLCGEESFGTGSDHIR	1.343070489	2	3.557404
P38652	LVIGQNGILSTPAVSCIIR	0.787771385	2	3.736856
P38652	NIFDFNALK	0.835329438	1	1.940837
P38652	QEATLVVGGDGR	0.822187003	2	2.991833
P38652	QQFDLENK	0.846650801	1	2.155559
P38652	SGEHDFGAAFDGDGDR	0.982593407	2	4.443589
P38652	TIEEYAICPDLK	0.787475314	2	3.08145
P38652	TQAYPDQKPGTSGLR	0.895027119	2	3.362595
P38652	YDYEEVEAEGANK	0.683302689	2	5.05689
P38656	**LA Lupus La protein homolog**	**1.031053844**	**0.6626**	**2**
P38656	ITDDQQESLNK	0.993563757	2	3.934011
P38656	LDEGWVPLETMIK	0.817886759	2	2.450222
P38659	**PDIA4 Protein disulfide_isomerase A4**	**0.887374886**	**3.8E-11**	**20**
P38659	DLGLSESGEDVNAAILDESGKK	0.855079828	2	5.112491
P38659	DNDPPIAVAK	0.7488017	2	2.343389

P38659	EVSQPDWTPPPEVTLTLTK	0.970429707	2	3.761898
P38659	FDVSGYPTIK	0.83660661	2	3.355823
P38659	FDVSGYPTLK	0.83660661	2	3.355823
P38659	FIDEHATK	1.099726276	2	2.63242
P38659	FIDEHATKR	1.443687276	2	2.765029
P38659	GQAVDYDGSR	0.954125924	2	2.845011
P38659	IDATSASMLASK	0.892768428	2	3.587105
P38659	IDATSASMLASK+Oxidation(7)	0.806107641		
P38659	KGQAVDYDGSR	2.98539007	2	2.633599
P38659	MDATANDITNDR	0.717839585	2	3.987757
P38659	MHVMDVQGSTEASAIKDYVVK	0.543604891	3	3.720118
P38659	QLEPVYTSLGK	0.870667395	2	2.556856
P38659	RFDVSGYPTLK	1.006282217	2	3.158771
P38659	RSPPIPLAK	0.76755392	2	2.373942
P38659	TQEEIVAK	1.033644326	2	2.396427
P38659	VDATEQTDLAK	0.955317966	2	4.046705
P38659	VEGFPTIYFAPSGDK	2.056931891	2	3.444849
P38659	YGIVDYMVEQSGPPSK	1.104557984	2	4.651431
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.862623068**	**0.02156**	**7**
P38918	EEHFNGIALVEK	1.228286739	2	3.04461
P38918	FQLETSLK	0.894289887	1	1.943807
P38918	FYAFNPLAGGLLTGR	1.500622668	2	4.475383
P38918	MDVTSSSASVR	0.586583131	2	3.590468
P38918	QVETELFPCLR	0.717067414	2	2.492181
P38918	RMDVTSSSASVR	0.823173072	2	3.549952
P38918	TTYGPTAPSMISAAVR	0.637293413	2	3.746691
P38983	**RSSA 40S ribosomal protein SA**	**1.095096791**	**9.9E-20**	**9**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.459875557	3	5.82599
P38983	AIVAIENPADVSVISSR	1.028810969	2	5.649462
P38983	EHPWEVMPDLYFYRDPEEIEKEEQAAAEK	0.410483448	3	3.756177
P38983	FAAATGATPIAGR	1.362109942	2	3.043618
P38983	FLAAGTHLGGTNLDFQMEQYIYK	1.5406685	3	4.044478
P38983	FTPGTFTNQIQAAFR	0.977071738	2	4.441462
P38983	KSDGIYIINLK	0.366675357	2	3.2187
P38983	SDGIYIINLK	1.228049695	2	2.975475
P38983	YVDIAIPCNNK	1.016957588	1	3.025011
P39032	**RL36 60S ribosomal protein L36**	**1.157851796**	**0.22355**	**2**
P39032	EELSNVLAAMR	1.452915512	2	2.48169
P39032	KREELSNVLAAMR	0.910136785	2	3.831596
P39447	**ZO1 Tight junction protein ZO_1**	**0.667164189**	**0.21062**	**2**
P39447	GEEVTILAQK	0.578828715	2	2.478636
P39447	GGPAEGQLQENDR	0.675555885	2	2.914105
P40112	**PSB3 Proteasome subunit beta type_3**	**0.920702042**	**0.58669**	**2**
P40112	FGIQAQMVTTDFQK	1.243962638	2	3.4818
P40112	FGPYYTEPVIAGLDPK	0.840559543	2	3.492236
P40307	**PSB2 Proteasome subunit beta type_2**	**1.181161374**	**0.69769**	**3**
P40307	FILNLPTFSVR	1.310123956	2	3.013951
P40307	NGYELSPTAAANFTR	1.003023925	2	3.554812
P40307	VIDKDGIHNLENITFTK	1.169353016	3	4.734424
P40329	**SYRC Arginyl_tRNA synthetase_ cytoplasmic**	**1.195089223**	**0.64458**	**2**
P40329	LNDYVFSFDK	1.122251604	2	2.704495
P40329	SDGGYTYDTSDLAAIK	1.089962661	2	4.012593
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.051286234**	**0.34906**	**6**
P41034	AECPELSADLHPR	1.365070089	2	2.969157
P41034	AIFDLEGWQISHAFQITPSVAK	0.748596788	2	4.617293
P41034	AQEEGVPETPQPLTDAFLLR	1.428348482	2	3.834833

P41034	GIHLINEPVIFHAVFSMIKPFLTEK	0.801466335	4	4.707664
P41034	QLNEQPDHSPLVQPGLAELR	1.041047371	3	3.960544
P41034	VSLITSELIVQEVETQR	1.1002934	3	3.797645
P41123	**RL13 60S ribosomal protein L13**	**1.117533235**	**1.9E-11**	**3**
P41123	LATQLTGPVMPIR	1.118118681	2	2.952143
P41123	STESLQANVQR	1.117652583	2	3.971032
P41123	VDTWFNQPAR	1.353699177	2	3.451286
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.032100345**	**0.72736**	**3**
P41498	IDSAATSTYEVGNPPDYR	0.896800088	2	3.103318
P41498	IELLGSYDPQK	0.835848234	2	3.437858
P41498	LVTDENVSDNWR	0.836493847	2	3.796196
P41542	**USO1 General vesicular transport factor p115**	**1.062017389**	**0.91657**	**15**
P41542	AWFEVGDENPGWSAQK	0.999128652	2	4.63702
P41542	CQNEQLQTAVTQQASQIQQHK	1.039481449	3	4.119624
P41542	EQDLQLEELK	1.243042295	2	2.487828
P41542	IVAFENAFER	1.24279783	2	2.622846
P41542	LQTENSELQQR	1.070920149	2	3.125226
P41542	LREEIEELR	1.079082312	2	2.47305
P41542	NDGVLLLQALTR	1.163033892	2	3.437385
P41542	NNNSNQNFFK	0.85361997	2	2.490579
P41542	QLDSSNSTIAILQTEK	1.207059514	2	3.906002
P41542	QLGPPVQQIILVSPMGVSK	0.817992605	2	2.387461
P41542	QSEDLGSQFTEIFIK	1.251875842	2	3.539407
P41542	SQLCSQSLEITR	1.029598919	2	3.104682
P41542	SVPVEGESELVTAAK	1.084435628	2	3.69433
P41542	TLEQHDNIVTHYK	1.117236534	2	3.48302
P41542	VLVSPTNPPGATSSCQK	1.064550134	2	4.18065
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**0.902748575**	**9.2E-08**	**18**
P41562	ATDFVVPGPGK	0.964719312	2	3.607947
P41562	CATITPDEK	1.060611421	2	2.682965
P41562	DIFQEIYDK	0.828890294	1	2.473907
P41562	DLAACIK	1.629583602	1	2.002927
P41562	FKDIFQEIYDK	0.823091409	3	4.118649
P41562	GQETSTNPIASIFAWSR	1.052210487	2	4.963188
P41562	IHGGSVVEMQGDEMTR	0.839764214	2	4.612719
P41562	LIDDMVAQAMK	0.723901059	2	4.588535
P41562	LIDDMVAQAMK+Oxidation(4)	1.18630457		
P41562	LILPYVELDLHSYDLGIENR	1.067891624	2	4.69077
P41562	LVTGWVKPIIIGR	0.826947669	2	3.214007
P41562	SDYLNTFEFMDK	0.760674659	2	4.336756
P41562	SDYLNTFEFMDK+Oxidation(9)	0.971534427		
P41562	SEGGFIWACK	0.845942003	2	3.322345
P41562	SIEDFAHSSFQMALSK	0.795049194	2	4.935408
P41562	TVEAEAAHGTVTR	0.956010342	2	3.966763
P41562	VEITYTPK	0.88925275	2	2.764072
P41562	VTYLVHDFEEGGGVAMGMYNQDK	1.089520254	3	3.328084
P42123	**LDHB L_lactate dehydrogenase B chain**	**0.935020077**	**0.10172**	**6**
P42123	DYSVTANSK	1.570814591	2	2.453655
P42123	IVADKDYSVTANSK	1.188907639	2	3.983585
P42123	LIAPVADDETAVPNNK	1.380779296	2	2.5292
P42123	LKDDEVAQLR	0.664948256	2	2.565563
P42123	SLADELALVDVLEDK	0.688225546	2	3.594932
P42123	VIGSGCNLDSAR	0.939929314	2	3.926786
P42676	**NEUL Neurolysin_ mitochondrial**	**1.045439031**	**0.47719**	**4**
P42676	AELGALPDDFIDSLEK	0.82440735	2	3.013837

P42676	NLILKPGGSLDGMDMLQNFLQR	**1.047702668**	3	3.472996
P42676	NLNEDDTSLVFSK	**0.816240158**	2	3.120328
P42676	TRTEQLIAQTK	**0.944278083**	2	2.754903
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.268821151**	**0.08593**	**9**
P42932	AIAGTGANVIVTGGK	**1.118540689**	2	3.82366
P42932	AVDDGVNTFK	**1.245649878**	2	2.962775
P42932	EDGAISTIVLR	**0.890179412**	2	2.660331
P42932	ELEVQHPAAK	**1.487875239**	2	2.941638
P42932	GEENLMDAQVK	**1.106512183**	2	2.456546
P42932	HFSGLEEAVYR	**1.14775125**	2	2.724827
P42932	NVGLDIEAEVPAVK	**1.206937207**	2	3.07452
P42932	QITSYGETCPGLEQYAIK	**1.270151712**	2	4.595458
P42932	TAEELMNFSK	**0.996181875**	2	2.329487
P43244	**MATR3 Matrin_3**	**1.079620516**	**0.3722**	**3**
P43244	GDTDQASNILASFGLSAR	**1.170976063**	2	3.43647
P43244	ITPENLPQILLQLK	**0.791009602**	2	3.679196
P43244	TENPAEGKEQEEK	**1.448058021**	2	2.953317
P43274	**H14 Histone H1.4**	**0.725721804**	**1.3E-05**	**3**
P43274	ALAAAGYDVEK	**0.840569791**	2	3.611325
P43274	SGVSLAALK	**0.882708524**	2	2.922416
P43274	SGVSLAALKK	**0.341651869**	2	2.592466
P43276	**H15 Histone H1.5**	**0.835182641**	**0.13515**	**2**
P43276	ALAAGGYDVEK	**0.731893231**	2	2.551481
P43276	ATGPPVSELITK	**0.858665642**	2	2.551647
P43278	**H10 Histone H1.0**	**0.696397972**	**9.9E-20**	**2**
P43278	VGENADSQIK	**0.820490538**	2	3.519381
P43278	YSDMIVAAIQAEK	**0.683956082**	2	3.987155
P45591	**COF2 Cofilin_2**	**0.977403566**	**0.82835**	**4**
P45591	HEWQVNGLDDIKDR	**1.014574087**	3	4.205368
P45591	KEDLVFIFWAPESAPLK	**3.187645938**	3	3.570692
P45591	QIIVEEAK	**0.908170986**	2	2.355095
P45591	QILVGDIGDTVEDPYTSFVK	**0.904691857**	2	4.77419
P45592	**COF1 Cofilin_1**	**0.994118719**	**1**	**4**
P45592	EILVGDVGQTVDDPYTTFVK	**1.002515272**	2	4.593636
P45592	HELQANCYEEVK	**0.994111885**	2	3.475245
P45592	HELQANCYEEVKDR	**1.014521837**	3	5.294194
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	**1.027741435**	3	4.866737
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.173531439**	**0.53751**	**4**
P45878	GWDQGLLGMCEGEK	**0.726307173**	2	3.979692
P45878	KLVIPSELGYGER	**1.159899825**	2	2.557052
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	**1.411525126**	3	4.399527
P45878	LVIPSELGYGER	**0.955587472**	2	2.659063
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.995323377**	**0.0751**	**18**
P45953	AMVENGGLVTSNPLR	**0.952083139**	2	3.433763
P45953	AMVENGGLVTSNPLRV	**0.950498758**	2	3.22963
P45953	AMVENGGLVTSNPLRV+Oxidation(1)	**1.255731194**		
P45953	ASNTSEVYFDGVK	**1.257039309**	2	3.711103
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	**1.006682055**	2	4.81055
P45953	ENMASLQSNPQQQELFR	**1.109703352**	2	4.292533
P45953	FFEEVNDPAK	**0.84538842**	2	3.128175
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	**0.998322811**	3	5.826537
P45953	GIVNEQFLLQR	**1.198949144**	2	3.425009
P45953	IFEGTNDILR	**0.970409652**	2	2.670158
P45953	NDSLEKVEEDTLQGLK	**0.793337761**	2	3.444993
P45953	NPLGNVGLLIGEASK	**1.432494532**	2	3.46002
P45953	SFGGVTHGLPEK	**1.098432123**	2	2.311799

P45953	SFGGVTHGLPEKK	0.837916931	2	3.009181
P45953	SGELAVQALEQFATVVEAK	1.000941027	3	4.776571
P45953	SLSEGYPTAQHEK	1.041169102	2	3.325535
P45953	TGIGSGLSLSGIVHPELSR	0.936185593	2	4.521201
P45953	VEEDTLQGLK	0.990642614	2	2.662334
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**0.920436786**	**0.99241**	**4**
P46418	AILNYIATK	1.263827555	2	3.308846
P46418	SDGSLMFEQVPMVEIDGMK	0.823926101	2	2.751177
P46418	SHGQDYLVGNK	0.997066862	2	3.13551
P46418	VSNLPTVK	0.904709493	2	2.892628
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.746101004**	**2.7E-06**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.58908991	3	3.971177
P46425	FEDGDLTLYQSNAILR	0.775258592	2	4.711096
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**0.959472409**	**0.02807**	**28**
P46462	AIANECQANFISIK	3.565747987	2	3.73597
P46462	EAVCIVLSDDTCSDEK	0.55487341	2	2.738125
P46462	ELQELVQYPVEHPDK	0.999930012	2	4.269449
P46462	ETVVEVPQVTWEDIGGLEDVK	0.852978898	2	3.017491
P46462	ETVVEVPQVTWEDIGGLEDVKR	0.913302428	2	4.063055
P46462	EVDIGIPDATGR	1.131442919	2	3.039968
P46462	GDDLSTAILK	0.825027565	2	3.058485
P46462	GGNIGDGGGAADR	1.253963206	2	3.975876
P46462	GILLYGPPGTGK	1.013473006	2	3.193771
P46462	GVLFYGPPGCGK	1.449555786	2	2.507306
P46462	IVSQLLTLMDGLK	1.23089898	2	3.058284
P46462	KYEMFAQTLQQSR	0.767231833	2	3.799582
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	0.975963846	3	6.18906
P46462	LAGESESNLRKAFEEAEK	0.822169442	2	2.605604
P46462	LDQLIYIPLPDEK	0.95996485	2	4.471232
P46462	LEILQIHTK	0.963234764	2	2.693849
P46462	LGDVISIQPCPDVK	0.866643357	2	4.263931
P46462	LIVDEAINEDNSVVSLSQPK	0.870124964	2	5.833801
P46462	MDELQLFR	0.753375701	2	3.037797
P46462	MDELQLFR+Oxidation(0)	1.089561658		
P46462	MTNGFSGADLTEICQR	0.576612295	2	4.227392
P46462	MTNGFSGADLTEICQR+Oxidation(0)	1.180275025		
P46462	NAPAIIFIDELDAIAPK	1.26156776	2	5.098776
P46462	QAAPCVLFFDELDSIAK	3.508369926	3	3.444426
P46462	QTNPSAMEVEEDDPVPEIR	0.766660089	2	4.645095
P46462	RSVSDNDIR	0.590876862	2	2.891446
P46462	VINQILTEMDGMSTK	0.863997948	2	4.552554
P46462	WALSQSNPSALR	0.912727113	2	3.169538
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**0.994998496**	**0.67815**	**4**
P46664	FIEDELQIPVK	1.236028099	2	3.050907
P46664	LDILDMFTEIK	1.219519533	2	3.409123
P46664	VGIGAFPTEQDNEIGELLQTR	0.788888728	2	4.399871
P46664	VVDLLAQDADIVCR	0.813368406	2	3.721214
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.077599987**	**0.04234**	**3**
P46720	ESEHTDVHGSPQVENDGELK	1.523050379	3	3.477867
P46720	GIGETPIVPLGISYIEDFAK	0.923806282	2	3.494571
P46720	SENSPLYIGILEMGK	0.805661936	2	3.739497
P46844	**BIEA Biliverdin reductase A**	**0.801381465**	**0.49958**	**3**
P46844	FGVVVVGVGR	1.041750199	2	2.753653
P46844	LLDQVSAEDLAAEK	1.107560207	2	4.371974
P46844	MTVQLETQNK	0.799166683	2	2.740632
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.22983349**	**0.0035**	**9**

P46953	AQGSVALSVTQDPACK	**0.555055972**	2	4.486174
P46953	ASFQPPVCNK	**0.893655234**	2	2.356057
P46953	DLGTQLAPIIQEFFHSEQYR	**0.927597523**	2	4.312824
P46953	FANTMGLVIER	**0.836004337**	2	2.608901
P46953	METELDGLR	**0.888112789**	2	2.619124
P46953	QDVDVWLWQLEGSSK	**1.278537088**	2	3.890494
P46953	QGEIFLLPAR	**1.29123306**	2	3.270734
P46953	TGKPNPDQLLK	**0.877647935**	3	3.827189
P46953	YYVGDTEDVLFEK	**1.064279627**	2	4.019377
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.089627209**	**0.93402**	**5**
P46978	FGQVYTEAK	**1.096058181**	2	2.695893
P46978	FYSLLDPSYAK	**1.139945055**	2	2.92425
P46978	NLDISRPDKK	**1.17509923**	2	2.797149
P46978	VGQAMASTEEK	**1.081850772**	2	3.402025
P46978	VGQAMASTEEK+Oxidation(4)	**0.520994092**		
P47198	**RL22 60S ribosomal protein L22**	**1.179247067**	**0.90663**	**2**
P47198	AGNLGGGVVTIER	**0.915815612**	2	3.527872
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	**1.191504553**	3	5.18702
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**0.950038418**	**0.49881**	**4**
P47875	GFGFGQGAGALVHSE	**0.850145354**	2	3.211263
P47875	GLESTTLADKDGEIYCK	**0.88557785**	2	5.188237
P47875	HEEAPGHRPTTNPNASK	**1.539416235**	3	3.810413
P47875	NLDSTTVAVHGEEIYCK	**1.015418848**	2	3.687725
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**0.914404565**	**0.73975**	**2**
P47942	GIQEEMEALVK	**0.745648459**	2	2.800728
P47942	GLYDGPVCEVSVTPK	**0.900819138**	2	3.635516
P48004	**PSA7 Proteasome subunit alpha type_7**	**0.968867634**	**0.2283**	**3**
P48004	GRDIVVLGVEK	**1.200685231**	2	2.658012
P48004	NYTDDAIETDDLTIK	**0.961989377**	2	4.550107
P48004	YVAEIEKEKEENEK	**0.949241805**	2	5.051441
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**1.285943602**	**1.1E-14**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	**1.687801799**	3	5.465962
P48024	TLTTVQGIADDYDK	**1.285842159**	2	3.168539
P48037	**ANXA6 Annexin A6**	**0.780834357**	**0.00139**	**19**
P48037	AANDFNPDADAK	**1.046625023**	2	3.350109
P48037	AINEAYKEDYHK	**0.959144349**	2	3.176689
P48037	ALIEILATR	**0.905722784**	2	3.34523
P48037	CLIEILASR	**0.807130336**	2	2.517637
P48037	DAFVAIVQSVK	**1.248874913**	2	3.004673
P48037	DLESDIIGDTSGHFQK	**0.416221808**	2	3.860751
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	**1.033804716**	2	4.935554
P48037	GELSGDFEK	**0.825392525**	1	2.101067
P48037	GFGSDKESILELITSR	**0.780742926**	2	4.219398
P48037	GIGTDEATIIDIITQR	**1.222799026**	2	4.058478
P48037	KTNYDIEHVIK	**0.756236396**	2	2.478091
P48037	QRQEICQSYK	**0.776879645**	2	4.016341
P48037	SEIDLLNIR	**1.036273494**	2	3.281227
P48037	SEISGDLAR	**0.882872497**	2	2.360828
P48037	SELDMLDIR	**0.718152737**	2	2.682776
P48037	SLEDALSSDTSGHFK	**0.875440487**	2	3.934227
P48037	TNEQIHQLVAAYK	**0.819652928**	2	3.982612
P48037	TNYDIEHVIK	**0.927496317**	2	3.250883
P48037	TTGKPIEASIR	**0.757317506**	2	2.501235
P48450	**ERG7 Lanosterol synthase**	**0.808721584**	**0.54918**	**2**
P48450	ILGIGPDDPDLVR	**0.742400051**	2	2.38531

P48450	SVQLPDGGWGLHIEDK	0.900911796	2	2.733079
P48500	**TPIS Triosephosphate isomerase**	**1.059149683**	**1.4E-09**	**13**
P48500	CNVSEGVAQCTR	1.117496428	2	3.708891
P48500	DLGATWVVLGHSER	1.504056381	2	3.686285
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.013791548	4	6.551955
P48500	HIFGESDELIGQK	1.097730122	2	4.016953
P48500	IAVAAQNCYK	2.143708127	2	2.697418
P48500	IIYGGSVTGATCK	1.332408315	2	4.642459
P48500	LPADTEVVCAPPTAYIDFAR	1.794906069	2	5.048263
P48500	RHIFGESDELIGQK	1.113985535	2	3.918656
P48500	TATPQQAQEVHEK	1.570691888	2	3.741127
P48500	VNHALSEGLGVIACIGEK	0.978807261	2	5.277333
P48500	VTNGAFTGEISPGMIK	1.038880939	2	5.160472
P48500	VTNGAFTGEISPGMIK+Oxidation(13)	1.070231844		
P48500	VVLAYEPVWAIGTGK	1.019334931	3	4.661988
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.845436696**	**0.00038**	**5**
P48508	ASTLHLQTGNLLNWGR	0.875093943	3	4.298683
P48508	EFPDVLECTMSHAVEK	1.000493589	2	3.725932
P48508	INPDEREEMK	0.572771144	2	2.568276
P48508	LFIVGSNSSSSTR	1.025912868	2	3.019517
P48508	TLNEWSSQISPDLVR	0.821131628	2	4.79794
P48675	**DESM Desmin**	**0.872300377**	**0.82981**	**3**
P48675	ADVDAATLAR	0.765195192	2	2.393958
P48675	FLEQQNAALAAEVNR	0.901176566	2	4.291257
P48675	VSDLTQAANK	0.911943983	2	2.988657
P48679	**LMNA Prelamin_A/C**	**0.832006169**	**9.9E-20**	**16**
P48679	AAYEAELGDAR	1.149715898	2	2.957789
P48679	AQHEDQVEQYK	0.926568306	2	3.065216
P48679	AQHEDQVEQYKK	1.493486312	3	3.937302
P48679	IDSLSAQLSQLQK	0.833536022	2	3.134309
P48679	ITESEEVVSR	0.72580241	2	3.229878
P48679	LKDLEALLNSK	0.753498585	2	2.741622
P48679	LQEKEDLQELNDR	0.86592776	2	4.39889
P48679	LRDLEDSLAR	0.490925151	2	2.468886
P48679	MQQQLDEYQELLDIK	0.972769088	2	4.396125
P48679	MQQQLDEYQELLDIK+Oxidation(0)	1.013887569		
P48679	NSNLVGAAHEELQQSR	0.864095909	2	4.365974
P48679	SGAQASSTPLSPTR	0.777338794	2	3.261025
P48679	SVGGSGGGSFGDNLVTR	0.812828068	2	3.984489
P48679	TALINATGEEVAMR	0.751759195	2	3.236383
P48679	TVLCGTCGQPADK	0.816438717	2	3.301952
P48679	VAVEEVDEEGK	1.116909258	2	2.930672
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.040887388**	**9.9E-20**	**28**
P48721	AQFEGIVTDLIK	0.892147799	2	3.776506
P48721	ASNGDAWVEAHGK	1.044613145	2	3.740872
P48721	DAGQISGLNVLR	0.996519136	2	3.569642
P48721	EQQIVIQSSGGLSK	1.379740687	2	3.759012
P48721	EQQIVIQSSGGLSKDDIENMVK	0.842587567	2	4.436788
P48721	ERVEAVNMAEGIIHDTETK	1.009507604	3	5.767061
P48721	ETAENYLGHTAK	1.42073234	2	3.59407
P48721	GAVVGIDLGTTNSCVAVMEGK	0.834557126	2	5.629698
P48721	LLGQFTLIGIPPAPR	1.183774123	2	3.079156
P48721	MEEFKDQLPADECNK	0.862042963	2	4.770112
P48721	MEEFKDQLPADECNK+Oxidation(0)	1.028138491		
P48721	MKETAENYLGHTAK	0.998796142	2	4.151165
P48721	MKETAENYLGHTAK+Oxidation(0)	1.000450649		

P48721	NAVITVPAYFNDSQR	**1.159187154**	2	3.569063
P48721	QAASSLQQASLK	**4.803084134**	2	2.993021
P48721	QAVTNPNNTFYATK	**2.338410317**	2	3.781953
P48721	RYDDPEVQK	**1.087582125**	2	2.92188
P48721	RYDDPEVQKDTK	**1.207644998**	2	3.766151
P48721	SDIGEVILVGGMTR	**0.84254582**	2	4.318917
P48721	SQVFSTAADGQTQVEIK	**3.82863963**	2	5.021915
P48721	STNGDTFLGGEDFDQALLR	**0.994382167**	2	5.616467
P48721	TTPSVVAFTPDGER	**0.995844676**	2	3.706936
P48721	VEAVNMAEGIIHDTETK	**0.922248429**	2	4.325917
P48721	VINEPTAAALAYGLDK	**1.293114324**	2	4.134956
P48721	VLENAEGAR	**1.012310957**	2	3.07982
P48721	VQQTVQDLFGR	**0.929664473**	2	3.446519
P48721	YDDPEVQK	**0.946617319**	2	2.465925
P48721	YDDPEVQKDTK	**0.815391934**	2	2.778764
P48725	**PCNT Pericentrin**	**0.883936962**	**0.79471**	**2**
P48725	EEVSGGNGPCRGSPGRGSLER	**1.127278508**	2	2.332365
P48725	VYQSLSTAVEGLLEMALDSSKQLEEAR	**0.873025331**	3	3.332243
P49134	**ITB1 Integrin beta_1**	**0.999636335**	**7.3E-11**	**4**
P49134	CNCQSHGIPASPK	**0.649837129**	2	3.655881
P49134	GEFFNELVGQQR	**0.828986319**	2	2.800832
P49134	RITSDFRIGFGSFVEK	**0.912006666**	2	2.359382
P49134	SAVTTVVNPK	**0.897699523**	2	2.437993
P49242	**RS3A 40S ribosomal protein S3a**	**1.157219358**	**0.02113**	**9**
P49242	ACQSIYPLHDVFVR	**1.246052062**	2	3.968821
P49242	ADGYEPPVQESV	**1.352619011**	2	2.353567
P49242	LIPDSIGKDIEK	**1.083186041**	2	2.508604
P49242	LITEDVQGK	**1.026500046**	2	2.744938
P49242	LMELHGEGGSSGK	**0.984633565**	2	3.458177
P49242	LMELHGEGGSSGK+Oxidation(1)	**1.28892793**		
P49242	NCLTNFHGMDLTR	**1.159917843**	2	3.800273
P49242	TTDGYLLR	**1.22834301**	2	3.069434
P49242	VFEVSLADLQNDEVAFR	**1.121415713**	2	4.274086
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.818905825**	**0.27396**	**6**
P49432	EAINQGMDEELERDEK	**1.037459497**	2	2.557161
P49432	ILEDNSIPQVK	**0.890703338**	2	3.077391
P49432	IMEGPAFNFLDAPAVR	**0.924050599**	2	4.222926
P49432	IMEGPAFNFLDAPAVR+Oxidation(1)	**0.954145861**		
P49432	TIRPMDIEAIEASVMK	**0.747930317**	3	4.404881
P49432	VFLLGEEVAQYDGAYK	**1.103304533**	2	3.539786
P49620	**DGKG Diacylglycerol kinase gamma**	**0.882606078**	**0.64033**	**2**
P49620	QGERILQKFHYLLNPK	**0.882706943**	2	2.496506
P49620	WGGGYEGGSLTKILK	**0.848858587**	2	2.344863
P49717	**MCM4 DNA replication licensing factor MCM4**	**0.539875506**	**0.05085**	**2**
P49717	GQSDTAITKDMFEEALR	**0.334135993**	2	2.312626
P49717	YQQLFEDIR	**0.743955259**	1	1.979849
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.503701502**	**9.9E-20**	**13**
P49889	CKEDALFNR	**0.553911979**	2	2.599116
P49889	FEEHYQQQMK	**0.496400718**	2	2.811329
P49889	FEEHYQQQMK+Oxidation(8)	**0.75039191**		
P49889	FMEGQVPYGSWYDHVK	**1.239324052**	2	3.767872
P49889	IIQHTSFQEMK	**0.392223495**	2	2.679441
P49889	LIEFLERDPSAELVDR	**0.402062452**	3	5.062951
P49889	NEDLINGIK	**0.511192088**	2	2.907812
P49889	NNPCTNYSMLPETMIDLK	**0.538326423**	2	4.478652
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13)	**0.695221099**		

P49889	NNPCTNYSMLPETMIDLK+Oxidation(8)	**0.695221099**		
P49889	SFSEFVEK	**0.586445988**	2	2.374656
P49889	SGSTWISEIVDMIYK	**0.408842005**	2	4.562672
P49889	YWEDVETFLARPDDLLIVTYPK	**1.869427321**	3	4.197574
P50137	**TKT Transketolase**	**0.989965174**	**0.05168**	**23**
P50137	AVELAANTK	**0.949749291**	1	1.975096
P50137	GHAAPILYAVWAEAGFLPEAELLNLR	**1.762842129**	3	3.482074
P50137	GITGIEDK	**1.017174337**	1	2.330757
P50137	IIALDGDTK	**1.537534659**	2	2.456312
P50137	ILATPPQEDAPSVDIANIR	**1.047356637**	3	5.383316
P50137	ISSDLDGHPVPK	**0.92923651**	2	3.244202
P50137	KISSDLDGHPVPK	**0.823513267**	2	3.901942
P50137	LAVSQVPR	**0.985430447**	2	2.301791
P50137	LAVSQVPRSGKPAELLK	**1.833613598**	2	2.601427
P50137	LDNLVAIFDINR	**1.006593785**	2	4.3408
P50137	LGQSDPAPLQHQVDVYQK	**1.149236338**	2	4.031178
P50137	MFGIDKDAIVQAVK	**0.713063523**	2	4.396074
P50137	MFGIDKDAIVQAVK+Oxidation(0)	**0.969112734**		
P50137	NMAEQIIQEIYSQVQSK	**1.015764735**	3	5.850729
P50137	NMAEQIIQEIYSQVQSK+Oxidation(1)	**1.619107633**		
P50137	NSTFSELFK	**1.032730294**	2	2.396109
P50137	SGKPAELLK	**1.13410747**	3	3.400248
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	**0.800060336**	3	4.069691
P50137	SVPMSTVFYPSDGVATEK	**0.912402841**	2	4.290738
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3)	**1.074955631**		
P50137	TSRPENAIIYSNNEDFQVGQAK	**1.226212425**	3	6.319445
P50137	VLDPFTIKPLDK	**0.980885492**	2	3.029834
P50137	VLDPFTIKPLDKK	**0.838640432**	2	2.734724
P50169	**RDH3 Retinol dehydrogenase 3**	**0.961527659**	**0.00055**	**10**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	**0.819528678**	3	5.047653
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1)	**0.877439235**		
P50169	FQDSYMK	**0.700827921**	1	2.086136
P50169	GLWGLVNNAGISVPVGPNEWMR	**0.735156453**	2	3.715937
P50169	KLWDQTTEEVK	**0.80656745**	2	3.076902
P50169	KLWDQTTEEVKEIYGEK	**0.829994871**	3	4.721564
P50169	LWDQTTEEVK	**0.979288128**	2	3.255734
P50169	LWDQTTEEVKEIYGEK	**0.691191543**	2	5.144002
P50169	MSLVGGGYCISK	**0.971451185**	2	3.773761
P50169	MSLVGGGYCISK+Oxidation(0)	**1.319391755**		
P50237	**ST1C1 Sulfotransferase 1C1**	**0.826373198**	**6E-14**	**9**
P50237	AGTTWTQEIVDMIQNDGDVQK	**0.66417597**	2	5.233977
P50237	DISEEVLNK	**0.94229253**	2	2.636224
P50237	DLHLGEQDLQPETR	**0.820213178**	2	4.309466
P50237	HPFIEWTLPSPLNSGLDLANK	**2.339960139**	3	3.322172
P50237	IWNFQAKPDDLLIATYAK	**0.91447379**	3	3.750057
P50237	MKDLHLGEQDLQPETR	**0.788221876**	2	3.980995
P50237	MLPDPGTLGEYIEQFK	**0.577903263**	3	4.699763
P50237	MLPDPGTLGEYIEQFK+Oxidation(0)	**0.871466501**		
P50237	VLWGSWYDHVK	**1.068149917**	2	3.119763
P50298	**ARY2 Arylamine N_acetyltransferase 2**	**0.747341736**	**0.13424**	**2**
P50298	FSYKDNIDLVEFK	**0.603494826**	2	2.683943
P50298	SLTEEEIEDVLK	**1.050187852**	2	2.767169
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**0.854465497**	**0.03345**	**8**
P50398	FDLGQDVIDFTGHALALYR	**1.020341197**	3	4.230884
P50398	FQLLEGPPESMGR	**0.853919226**	2	3.548142
P50398	KQNDVFGEADQ	**0.933558299**	2	2.635939

P50398	MLLYTEVTRYLDFK	**0.994525562**	2	2.34705
P50398	NPYYGGESSSITPLEELYK	**1.141660102**	2	5.448057
P50398	QLICDPSYIPDR	**0.72845201**	2	3.348272
P50398	TDDYLDQPCLETINR	**0.808879282**	2	5.167658
P50398	TFEGVDPQTTSMR	**0.834957083**	2	2.595511
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.12288116**	**0.75279**	**7**
P50399	AYDATTHFETTCDDIK	**1.840183817**	2	4.772915
P50399	AYDATTHFETTCDDIKDIYK	**1.011302156**	3	5.506894
P50399	EIRPALELLEPIEQK	**1.057189153**	3	3.93112
P50399	FDLGQDVIDFTGHSLALYR	**1.672479833**	3	4.703263
P50399	FVSISDLFVPK	**1.214973254**	2	3.141755
P50399	NTNDANSCQIIIPQNQVNR	**1.062297183**	2	4.221483
P50399	TDDYLDQPCCETINR	**0.823114317**	2	4.765975
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**0.947682052**	**0.09302**	**7**
P50431	ALSDALTELGYK	**0.921606683**	2	3.998201
P50431	AVLEALGSCLNNK	**1.080975266**	2	4.476895
P50431	GLLEEDFQK	**0.817319989**	2	2.358482
P50431	ISATSIFFESMPYK	**1.136513983**	2	3.510657
P50431	IYQLQVLANCR	**0.705807461**	2	2.690809
P50431	VLEACSIACNK	**1.044449129**	2	3.92667
P50431	YSEGYPGQR	**1.39962357**	2	2.772025
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**0.888694994**	**0.97789**	**14**
P50475	ASEWVQQVSGLMDGK	**1.009642333**	2	4.166582
P50475	AVFDETYPDPVR	**0.893469981**	2	3.268637
P50475	DIINEEEVQFLK	**0.657536183**	2	3.182424
P50475	GLEATDDSPK	**1.028189881**	2	2.590701
P50475	ITCLCQVPQNAANR	**1.004207564**	2	4.588664
P50475	IVAVTGAEAQK	**1.196691836**	2	2.752509
P50475	NVGCLQEALQLATSFAQLR	**0.970117111**	2	2.918587
P50475	QIWQNLGLDEAK	**0.983038987**	2	3.140088
P50475	RIVAVTGAEAQK	**1.53159666**	2	2.946728
P50475	SVLGDADQK	**0.805740462**	1	2.199129
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	**0.865772075**	3	4.02376
P50475	TITVALADGGRPDNTGR	**1.094746145**	2	3.0999
P50475	VDDSSEDKTEFTVK	**1.126989282**	2	3.751496
P50475	VGAEDTDGIDMAYR	**0.810219877**	2	3.851568
P50503	**F10A1 Hsc70_interacting protein**	**1.4982614**	**9.9E-20**	**6**
P50503	AIDLFTDAIK	**1.286432868**	2	2.900306
P50503	AIEINPDSAQPYK	**1.698897479**	2	3.461441
P50503	GAAIDALNDGELQK	**1.415513138**	2	3.666522
P50503	KGAAIDALNDGELQK	**1.505265428**	2	4.918941
P50503	LDYDEDASAMLR	**1.211893741**	2	3.564228
P50503	QDPSVLHTEEMR	**1.290971025**	2	2.5345
P50516	**VATA V_type proton ATPase catalytic subunit A**	**1.048868754**	**0.78477**	**3**
P50516	ADYAQLLEDMQNAFR	**0.996560648**	2	3.741143
P50516	TALVANTSNMPVAAR	**1.141749663**	2	3.594894
P50516	VLDALFPCVQGGTTAIPGAFGCGK	**0.742030342**	2	2.847148
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**0.946919101**	**0.09139**	**12**
P50554	GNYLVDVDGNR	**0.870320015**	1	2.183243
P50554	GTFCSFDTPDEAIR	**0.722787569**	2	3.756868
P50554	GVVLGGCGDK	**0.86433304**	2	2.304727
P50554	HGCAFLVDEVQTGGGCTGK	**0.983065965**	2	5.863329
P50554	IDIPSFDWPIAPFPR	**0.671787684**	2	3.742017
P50554	KHGCAFLVDEVQTGGGCTGK	**0.905103746**	3	3.70531
P50554	LVQQPQNASTFINRPALGILPPENFVDK	**0.934094646**	3	3.722294

P50554	NLLLAEVINIIK	0.616312978	3	4.942817
P50554	REDLLNNVAHAGK	1.237100527	2	2.360586
P50554	TLLTGLLDLQAQYPQFVSR	0.770015002	3	4.104712
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	0.529958754	2	3.462449
P50554	YPLEEFVTDNQQEEAR	1.043291532	2	3.006053
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.175224639**	**0.10109**	**4**
P50580	HELLQPFNVLYEK	1.086732714	2	2.964564
P50580	LVKPGNQNTQVTEAWNK	1.304203136	3	3.389173
P50580	SLVEASSSGVSVLSLCEK	0.931384118	2	2.49089
P50580	TIIQNPTDQQK	1.175796748	2	3.135452
P50878	**RL4 60S ribosomal protein L4**	**1.780955673**	**9.9E-20**	**11**
P50878	FCIWTESAFR	1.000144052	2	2.528991
P50878	KLDELYGTWR	1.197361122	2	3.157358
P50878	KLEAAAAALAAK	1.115554763	3	4.27761
P50878	LDELYGTWR	0.953810001	2	2.629948
P50878	LEAAAAALAAK	1.401084479	2	3.0964
P50878	NIPGITLLNVSK	1.262273434	2	3.293212
P50878	NVTLPAVFK	1.284778897	1	2.003755
P50878	RGPCIIYNEDNGIIK	1.30273757	2	3.468535
P50878	SGQGAFGNMCR	1.08522292	2	2.378578
P50878	SNYNLPMHK	1.249669344	2	2.562851
P50878	YAICSALAASALPALVMSK	1.635025219	2	3.499718
P51583	**PUR6 Multifunctional protein ADE2**	**1.20953862**	**0.22779**	**3**
P51583	ACGNFGIPCELR	0.952069563	2	2.64011
P51583	AEYEGDGIPTVFVAVAGR	1.662140812	2	3.204171
P51583	SWLPQNCTLVDMK	1.2321004	2	2.622981
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**0.959787477**	**0.00567**	**8**
P51635	ALEALVAK	0.993333845	2	2.527867
P51635	ALGLSNFSSR	1.127284217	2	2.806605
P51635	GLEVTAYSPLGSSDR	0.902458936	2	4.452848
P51635	HHPEDVEPAVR	0.888620504	3	3.740552
P51635	HIDCASVYGNETEIGEALK	0.952624295	2	5.929032
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.632151987	3	6.122674
P51635	HPDEPVLLEEPVVLALAEK	1.475436707	3	6.084077
P51635	QLDALNK	1.075859499	1	2.300743
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.668638756**	**9.9E-20**	**17**
P51647	ANNTTYGLAAGVFTK	0.864068371	2	3.94088
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.772216674	3	3.890269
P51647	ELGEHGLYEYTELK	0.740773505	2	3.721067
P51647	FPVLNPATEEVICHVEEGDK	0.732425275	3	4.09538
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.590695086	4	5.142944
P51647	IFINNEWHDSVSGK	0.706271671	2	4.352702
P51647	IFVEESVYDEFVR	0.638619362	2	4.264873
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	0.699878206	4	5.756516
P51647	IHGQTIPSDGDIFTFTR	0.875734077	2	4.546439
P51647	KFPVLNPATEEVICHVEEGDK	0.836600359	3	3.753911
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.601143905	4	4.866906
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	0.665383064	3	3.774581
P51647	LLLATIEAINGGK	1.640707702	2	4.117346
P51647	VFANAYLSDLGGSIK	0.856242169	2	4.558314
P51647	YCAGWADK	0.697815476	1	2.056455
P51647	YVLGNPLTQGINQGPQIDK	0.735564618	2	5.026834
P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.653040066	2	3.508366
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.621241454**	**1.2E-12**	**7**
P51650	EVGEVLCTDPLVSK	1.068323459	2	3.806841
P51650	HQSGGNFFEPTLLSNVTR	0.545964538	2	3.581902

P51650	LGTVADCGVPEAR	**0.550505074**	2	3.434222
P51650	VGNGFEEGTTQGPLINEK	**0.769300931**	2	4.312137
P51650	VYGDIIYTSAK	**1.031795081**	2	2.664002
P51650	WLPTPATFPVYDPASGAK	**0.646580063**	2	3.764623
P51650	YGIDEYLEVK	**0.653828646**	2	3.085031
P51869	**CP4F4 Cytochrome P450 4F4**	**1.304274353**	**0.23353**	**2**
P51869	TLDFIDVLLLTK	**1.278768037**	2	3.61471
P51869	WQDLASGGSAR	**1.001036347**	2	2.53931
P51886	**LUM Lumican**	**0.956204983**	**0.96726**	**3**
P51886	ITNIPDEYFNR	**0.798181788**	2	2.333369
P51886	NNQIDHIDEK	**0.978732257**	2	3.094421
P51886	SLQDLQLANNK	**0.844168051**	2	2.69651
P52020	**ERG1 Squalene monooxygenase**	**1.065307083**	**0.87093**	**2**
P52020	DIPDLYDDAAIFQAK	**0.962882907**	2	2.466207
P52020	GVLLLGDAYNLR	**1.184377709**	2	2.967228
P52296	**IMB1 Importin subunit beta_1**	**0.915802903**	**0.95727**	**5**
P52296	AAVENLPTFLVELSR	**0.676489645**	2	3.41269
P52296	GALQYLVPILTQTLTK	**1.061226879**	2	2.446865
P52296	SNEILTAIIQGMR	**0.941908221**	2	3.146467
P52296	TVSPDRLELEAAQK	**1.0094762**	2	2.871838
P52296	VLANPGNSQVAR	**1.104974015**	2	3.595824
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.19122797**	**0.63793**	**4**
P52303	NINLIVQK	**0.919016382**	1	2.212781
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	**0.853351033**	3	3.917299
P52303	SQPDMAIMAVNTFVK	**0.839188721**	2	2.602387
P52303	YNDPIYVK	**1.195400357**	2	2.524617
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**0.921961295**	**0.95842**	**3**
P52555	ILDQGEDFPASELAR	**0.882051604**	2	4.81951
P52555	QGQDGLSGVK	**0.878787017**	2	2.465656
P52555	SLNILTAFR	**0.871329448**	2	2.811404
P52631	**STAT3 Signal transducer and activator of transcription 3**	**2.663109279**	**5.6E-08**	**3**
P52631	GLSIEQLTTLAEK	**1.74931978**	2	3.080907
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	**2.803489227**	3	3.380996
P52631	TQIQSVEPYTK	**2.141357782**	2	2.638862
P52734	**FGD1 FYVE_ RhoGEF and PH domain_containing protein 1**	**0.894835379**	**0.44041**	**2**
P52734	SLELQARTEEEKK	**1.257313656**	2	2.504863
P52734	TEEEKKDWVQAINSTLLK	**0.887069766**	2	2.353791
P52759	**UK114 Ribonuclease UK114**	**0.870939248**	**0.09077**	**8**
P52759	AAGCDFTNVVK	**1.410775065**	2	3.009787
P52759	AAYQVAALPK	**1.33109704**	2	2.641856
P52759	APAAIGAYSQAVLVDR	**1.107029769**	2	3.708164
P52759	IEIEAIAVQGPFTTAGL	**0.93317823**	2	3.513055
P52759	NLGEILK	**1.040862889**	2	2.380661
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	**0.789832988**	2	4.30302
P52759	TTVLLADINDFGTVNEIYK	**1.11390132**	2	4.875
P52759	TYFQGNLPAR	**1.073434145**	2	3.087487
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**0.698096092**	**4.3E-05**	**2**
P52845	CKEDAIFNR	**0.553911979**	2	2.599116
P52845	SGSTWIGEIVDMIYK	**0.739919059**	2	3.55171
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.267542315**	**6.8E-11**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	**1.653760204**	2	5.013755
P52847	FLAGNVAYGSWFDHVK	**1.278071861**	2	3.503611
P52847	IEEFQSRPCDIVIPTYPK	**1.134033055**	3	4.805368

P52847	IVHHTSFEVMK	**1.612908539**	2	2.915155
P52847	NYFTMTQSEK	**1.084976614**	1	2.71535
P52847	SGTTWLSEIVDMVLNDGNVEK	**1.227008229**		
P52847	THLPIDLLPK	**1.158569908**	3	3.71345
P52847	TLDEHTLER	**1.159717214**	2	3.003373
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.014965198**	**9.9E-20**	**37**
P52873	ADEAYLIGR	**0.810779116**	2	2.946749
P52873	ADFAQACQDAGVR	**0.73779225**	2	4.476007
P52873	AEAEAQAEELSFPR	**0.964031058**	2	4.44045
P52873	AGTHILCIK	**1.044234103**	1	2.032533
P52873	ALAVSDLNR	**0.925559254**	2	2.604053
P52873	AYSEALAAFGNGALFVEK	**0.830471087**	2	3.705422
P52873	AYVEANQMLGDLIK	**1.087508011**	2	4.511999
P52873	DAHQSLLATR	**1.537926247**	1	3.117682
P52873	DFTATFGPLDSLNTR	**1.220288347**	2	4.286073
P52873	DMAGLLKPAACTMLVSSLR	**0.701032468**	2	3.075082
P52873	ELIPNIPFQMLLR	**1.607273665**	2	2.404148
P52873	ENGVDAVHPGYGFLSER	**1.073049389**	2	3.072159
P52873	FLYECPWR	**0.920215271**	2	2.606937
P52873	GANAVGYTNYPDNVVFK	**1.594863416**	2	4.332129
P52873	GLAPVQAYLHIPDIIK	**0.987424708**	2	2.95695
P52873	GTPLDTEVPLER	**0.716829125**	2	3.590704
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	**0.95640837**	2	5.941383
P52873	HGEEVTPEDVLSAAMYPDVFAQFK+Oxidation(14)	**0.761012896**		
P52873	HIEVQILGDQYGNILHLYER	**0.885162886**	3	4.759448
P52873	HYFIEVNSR	**0.828860646**	2	2.553222
P52873	IAEEFEVELER	**0.885969332**	2	3.287968
P52873	IEGRPGASLPPLNLK	**0.745061034**	2	3.610756
P52873	INGCAIQCR	**1.121038062**	2	2.843999
P52873	IVGDLAQFMVQNGLSR	**0.943291722**	2	5.297952
P52873	LDNASAFQGAVISPHYDSLLVK	**0.862441215**	3	5.832052
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	**0.849358674**	4	5.441233
P52873	NHQGLLLMDTTFR	**1.279853503**	2	3.355662
P52873	QKADEAYLIGR	**0.925468725**	3	3.43804
P52873	QVFFELNGQLR	**1.020530046**	2	2.771383
P52873	QVGYENAGTVEFLVDK	**1.007864909**	2	4.107854
P52873	SVVEFLQGYIGIPHGGFPEPFR	**1.018579465**	2	4.300785
P52873	TVAVYSEQDTGQMHR	**1.145761131**	2	4.34306
P52873	VFDYSEYWEGAR	**0.812573112**	2	4.571292
P52873	VSPSPVDPIVPVVPIGPPPAGFR	**0.731965509**	2	4.461032
P52873	VVEIAPATHLDPQLR	**0.788860502**	2	4.116382
P52873	VVHSYEELEENYTR	**0.905837558**	2	5.158436
P52873	YSLEYYMGLAEELVR	**1.562402383**	3	4.689162
P52944	**PDLI1 PDZ and LIM domain protein 1**	**0.724429247**	**0.00147**	**7**
P52944	AAIANLCIGDLITAIDGEDTSSMTHLEAQNK	**0.759066361**	3	4.367404
P52944	CGTGIVGVFVK	**0.672845116**	2	2.437644
P52944	GCVDNMTLTVSR	**0.914482223**	2	2.36246
P52944	GHFFVGDQIYCEK	**0.858360567**	2	3.517665
P52944	QSTSFLVLQEILESDGK	**0.846739255**	2	2.435704
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	**0.802596771**	3	3.953514
P52944	VTPPEGYDVVTVFPK	**0.68969644**	2	2.790221
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.028364743**	**0.93372**	**3**
P53395	LSDIGEGIR	**0.89376389**	2	2.467001
P53395	LSEVVGSGK	**1.016104648**	2	2.343265
P53395	SYLENPAFMLLDLK	**1.188813362**	2	4.640735

P53987	**MOT1 Monocarboxylate transporter 1**	**1.19940342**	**2.4E-09**	**5**
P53987	DGKEDETSTDVDEKPK	**1.954815507**	3	5.626783
P53987	DGKEDETSTDVDEKPKK	**2.385472241**	3	3.870491
P53987	EDETSTDVDEKPK	**1.307209666**	2	3.100295
P53987	ETQSPAPLQNSSGDPAEEESPV	**0.991739923**	2	4.404111
P53987	SDANTDLIGGSPK	**1.068255536**	2	4.050053
P54319	**PLAP Phospholipase A_2_activating protein**	**0.966766181**	**0.99995**	**4**
P54319	GQTLGLGNTSFSDPFTGGGR	**0.996864223**	2	3.343384
P54319	IGDVVGSSGANQQTSGK	**0.98153479**	2	4.515548
P54319	TGDLGDINAEQLPGR	**0.948846213**	2	3.665746
P54319	YVPGTSGPSNTVQTADPFTGAGR	**0.96147483**	2	2.871021
P54822	**PUR8 Adenylosuccinate lyase**	**1.080317643**	**0.90313**	**2**
P54822	KVDIEVLSVLASLGASVHK	**0.972506122**	3	4.43676
P54822	VLSQQAAAVVK	**0.79579892**	2	2.3284
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.133202211**	**0.89719**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	**0.818558251**	3	4.882149
P54921	HDAATCFVDAGNAFK	**0.888574288**	2	2.34596
P54921	IEEACEIYAR	**1.133141572**	2	2.711907
P54921	NSQSFFSGLFGGSSK	**1.146431531**	2	3.431803
P54921	YEELFPAFSDSR	**0.879349163**	2	2.893608
P55006	**RDH7 Retinol dehydrogenase 7**	**1.094525292**	**0.22964**	**11**
P55006	LETVILDVTK	**0.947471848**	2	3.238852
P55006	TESIVAATQWVK	**0.879358708**	2	3.939571
P55006	TNVTNMER	**0.900430949**	2	2.770482
P55006	TNVTNMER+Oxidation(5)	**1.003081739**		
P55006	TSDRLETVILDVTK	**0.886612132**	3	4.194678
P55006	VAIIEPGGFK	**1.322504831**	2	2.645862
P55006	VLAACLTEK	**1.060590423**	2	3.324537
P55006	VVNIASTMGR	**0.801556017**	2	3.654848
P55006	VVNIASTMGR+Oxidation(7)	**0.980853164**		
P55006	YGVEAFSDSLR	**1.087564426**	2	3.835497
P55006	YVFITGCDSGFGNLLAR	**0.963117494**	2	3.677321
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.086161362**	**0.9985**	**4**
P55051	ALGVGFATR	**1.119733543**	2	2.713905
P55051	LTDSQNFDEYMK	**1.048750622**	2	4.400812
P55051	LTDSQNFDEYMK+Oxidation(10)	**1.514603677**		
P55051	QVGNVTKPTVIISQEGGK	**0.973720449**	3	3.837464
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.106535634**	**0.01257**	**5**
P55053	FDETTADGR	**0.729152844**	2	2.961714
P55053	KTETVCTFTDGALVQHQK	**0.906866048**	3	5.080284
P55053	LVESHGFEDYMK	**1.073899776**	2	2.62493
P55053	MVVECVMNNAICTR	**0.618465027**	2	3.24547
P55053	TETVCTFTDGALVQHQK	**1.124511761**	2	4.305476
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**0.853780225**	**0.00033**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	**1.427013155**	3	5.518301
P55159	IFFYDSENPPGSEVLR	**0.753548924**	2	5.901761
P55159	IQSILSEDPK	**1.07304829**	2	3.088877
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	**1.872587444**	3	4.119244
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	**0.772891357**	3	3.966547
P55159	VVADGFDFANGIGISLDGK	**0.851951682**	2	4.085935
P55159	YVYIAELLAHK	**1.17373933**	2	2.879871
P55260	**ANXA4 Annexin A4**	**0.820883354**	**0.59225**	**5**
P55260	AEIDMLDIPANFK	**0.891649499**	1	2.213793
P55260	GAGTDEGCLIEILASR	**0.898737206**	2	3.410341
P55260	GLGTDEDAIIGVLACR	**0.828892976**	2	4.126154
P55260	INQTYQQQYGR	**1.162635009**	2	2.759853
P55260	SETSGSFEDALLAIVK	**0.75915565**	2	2.424878

P55770	**NH2L1 NHP2_like protein 1**	**0.962837438**	**0.72987**	**2**
P55770	LLDLVQQSCNYK	**0.729678097**	2	2.66762
P55770	QQIQSIQQSIER	**0.987739857**	2	3.012279
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**0.909287253**	**0.67861**	**6**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	**0.754349129**	2	4.222363
P56399	IFQNAPTDPTQDFSTQVAK	**1.168082121**	2	3.966633
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	**1.317074218**	3	3.431857
P56399	IVILPDYLEIAR	**1.013091859**	2	2.623757
P56399	KQEVQAWDGEVR	**1.009276732**	2	3.12834
P56399	VTSAVEALLSADSASR	**0.950054468**	2	2.768435
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**0.850452295**	**3.7E-08**	**3**
P56522	AVPTGDVEDLPCGLLLSSVGYK	**0.836698298**	2	4.420526
P56522	TATEKPGVEEAAR	**0.862450874**	2	3.177993
P56522	TDITEVALGVLR	**0.732655188**	2	4.048718
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.020841283**	**0.84677**	**14**
P56574	CATITPDEAR	**1.30439894**	2	2.304648
P56574	DLAGCIHGLSNVK	**0.767902044**	2	2.856535
P56574	DQTNDQVTIDSALATQK	**1.122163168**	2	5.04928
P56574	FKDIFQEIFDK	**0.680184308**	2	3.236313
P56574	GKLDGNQDLIR	**0.93271316**	2	2.809859
P56574	LDGNQDLIR	**0.798993804**	2	2.383461
P56574	LIDDMVAQVLK	**0.72254841**	2	4.314041
P56574	LNEHFLNTTDFLDTIK	**1.080086013**	2	4.724234
P56574	NILGGTVFR	**0.869143092**	2	2.351218
P56574	SSGGFVWACK	**1.001761947**	2	2.53247
P56574	TIEAEAAHGTVTR	**1.165997422**	2	4.098842
P56574	VCVQTVESGAMTK	**0.972633059**	2	3.096589
P56574	VEKPVVEMDGDEMTR	**1.020553326**	3	3.64442
P56574	YFDLGLPNR	**1.220410449**	2	2.535134
P56593	**CP2AC Cytochrome P450 2A12**	**1.118313006**	**0.0254**	**3**
P56593	MLQGTCGAPIDPTIYLSK	**1.131024011**	2	3.959047
P56593	NRQPQYEDHMK	**0.984886105**	3	3.826875
P56593	YLPGPQQQIIK	**0.55591357**	2	2.444141
P56656	**CP239 Cytochrome P450 2C39**	**0.771742059**	**4.6E-05**	**5**
P56656	EHQESLDVTNPR	**0.887910563**	2	3.381594
P56656	IKEHQESLDVTNPR	**0.700711055**	3	4.751965
P56656	NYLIPK	**0.990692062**	1	2.191697
P56656	SDHFMPFSAGKRVCAGEGLAR	**0.981509927**	2	2.390186
P56656	VQEEIDHVIGR	**0.963037941**	2	3.185246
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**2.528730674**	**9.9E-20**	**8**
P57093	AISCHYGSSDCK	**2.992766353**	2	3.384495
P57093	FYEENGFLVIK	**1.730856931**	2	2.588346
P57093	GDTVFFHPLLIHGSGR	**4.739575675**	3	3.538332
P57093	IQDFQQNEELFR	**1.294689214**	2	4.337041
P57093	KFYEENGFLVIK	**1.977350558**	2	3.388309
P57093	NLVSDDDIQR	**2.237413768**	1	2.865102
P57093	NNGCLVVLPGTHK	**2.172273247**	2	2.514804
P57093	YCALPQIVK	**2.359859516**	1	2.199789
P57113	**MAAI Maleylacetoacetate isomerase**	**0.843702301**	**2.1E-10**	**13**
P57113	AITSGFNALEK	**0.922233165**	2	3.292677
P57113	ALLALEAFQVSHPCR	**0.827532935**	2	4.283391
P57113	DGGQQFSEEFQTLNPMK	**0.913032397**	2	4.925333
P57113	FKVDLSPYPTISHINK	**0.730539185**	2	5.0818
P57113	GIDYEIVPINLIK	**0.969904635**	2	4.469725
P57113	IDGITIGGQSLAILEYLEETRPIPR	**0.844134153**	3	3.965795

P57113	LLPQDPQK	**1.039265953**		1	2.099002
P57113	LLPQDPQKR	**0.902943848**		2	2.54798
P57113	MISDLIASGIQPLQNLSVLK	**0.694686591**		2	4.770432
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0)	**0.918754333**			
P57113	QVGQENQMPWAQK	**0.917057165**		2	3.890368
P57113	VDLSPYPTISHINK	**0.873646349**		2	3.469768
P57113	YCVGDEVSMADVCLAPQVANAER	**0.735548592**		3	6.312306
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.077704819**	**0.98941**		**3**
P57722	ESTGAQVQVAGDMLPNSTER	**0.954110107**		2	4.876122
P57722	INISEGNCPER	**1.06130517**		2	3.45471
P57722	LVVPASQCGSLIGK	**1.199695858**		2	2.617839
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**0.990689808**	**0.99898**		**3**
P58321	SQGQDVTSSVYFMK	**0.973489713**		2	2.381233
P58321	VTHETSAHEGQTEAPSIDEK	**0.93435203**		3	4.700929
P58321	WLPLEANPEVTNQFLK	**0.998624043**		2	3.48753
P58751	**RELN Reelin**	**1.026671755**	**0.86367**		**2**
P58775	**TPM2 Tropomyosin beta chain**	**1.244616976**	**0.9949**		**12**
P58775	AISEELDNALNDITSL	**0.805194316**		2	4.401304
P58775	ATDAEADVASLNR	**0.814310331**		2	4.230064
P58775	CGDLEEELK	**0.829446342**		2	2.39582
P58775	DAQEKLEQAEK	**0.603355148**		2	2.569577
P58775	KATDAEADVASLNR	**1.250977733**		2	4.181209
P58775	LDKENAIDR	**1.024994441**		2	2.785169
P58775	LKGTEDEVEK	**1.283613943**		3	3.581951
P58775	MELQEMQLK	**0.735166933**		2	2.658723
P58775	QLEEEQQALQK	**0.820360086**		2	3.970421
P58775	SLEAQADKYSTK	**0.815176207**		2	3.347279
P58775	TIDDLEDEVYAQK	**0.619757671**		2	4.065521
P58775	YSESVKDAQEK	**0.246849616**		2	2.995986
P59242	**CING Cingulin**	**0.845297497**	**0.48644**		**2**
P59242	LGQEQQALNR	**1.036857517**		2	2.74131
P59242	LQGLEQEAENK	**0.798310404**		2	2.543168
P59279	**RAB2B Ras_related protein Rab_2B**	**1.055415214**	**0.95295**		**2**
P59279	GAAGALLVYDITR	**1.090669595**		2	2.996588
P59279	LQIWDTAGQESFR	**1.069661248**		2	3.677009
P59759	**MKL2 MKL/myocardin_like protein 2**	**0.891250155**	**0.93548**		**2**
P59759	LVEVLK	**0.925677126**		2	2.451511
P59759	QIEELK	**0.851133662**		1	2.071705
P59895	**NEK6 Serine/threonine_protein kinase Nek6**	**1.020398327**	**0.90296**		**2**
P59895	QDCVKEIGLLK	**0.924642675**		2	2.346838
P59895	TVALKKVQIFEMMDAK+Oxidation(11)	**1.060144723**			
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.098918828**	**0.55507**		**2**
P59999	AENFFILR	**1.081788027**		2	2.571273
P59999	ELLLQPVTISR	**1.168510164**		2	2.691309
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.003814303**	**0.31629**		**5**
P60335	AITIAGVPQSVTECVK	**1.150573824**		2	3.201518
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	**1.092581158**		4	5.41702
P60335	IITLTGPTNAIFK	**0.917012098**		2	2.666085
P60335	LVVPATQCGSLIGK	**1.28082383**		2	3.344987
P60335	VMTIPYQPMPASSPVICAGGQDR	**0.775558984**		2	3.636625
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.134925175**	**0.26666**		**5**
P60843	ATQALVLAPTR	**1.197707538**		1	2.350039
P60843	GFKDQIYDIFQK	**1.094529876**		2	3.521557
P60843	KEELTLEGIR	**1.290376006**		2	2.50622
P60843	KGVAINMVTEEDKR	**1.142154057**		3	4.088434

P60843	LQMEAPHIIVGTPGR	**1.073975562**	3	3.843683
P60868	**RS20 40S ribosomal protein S20**	**0.961785909**	**0.05131**	**3**
P60868	DTGKTPVEPEVAIHR	**0.799373589**	3	3.533911
P60868	LIDLHSPSEIVK	**1.209443305**	2	3.199862
P60868	VCADLIR	**1.11925818**	2	2.340431
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.218049326**	**0.24852**	**2**
P60901	AINQGGLTSVAVR	**1.035293807**	2	3.441447
P60901	LLDSSTVTHLFK	**1.385656506**	2	2.795613
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.185930262**	**0.286**	**2**
P61087	GEIAGPPDTPYEGGR	**1.477210459**	2	3.669807
P61087	VDLVDENFTELR	**0.943914482**	2	3.483526
P61107	**RAB14 Ras_related protein Rab_14**	**0.87430387**	**0.68715**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	**1.019687246**	3	3.682695
P61107	LTSEPQPQR	**1.347664856**	2	2.562986
P61107	NLTNPNTVIILIGNK	**0.716030153**	2	3.227733
P61107	SCLLHQFTEK	**0.86222714**	2	2.967806
P61107	STYNHLSSWLTDAR	**1.039080539**	2	3.284862
P61203	**CSN2 COP9 signalosome complex subunit 2**	**0.673245311**	**0.41605**	**2**
P61203	NYDESGSPR	**0.56155526**	2	2.469565
P61203	WTNQLNSLNQAVVSK	**0.764301033**	2	2.980879
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**0.968906418**	**0.38482**	**4**
P61222	GTVGSILDR	**1.267046509**	2	2.328647
P61222	NTVANSPQTLLAGMNK	**0.965150552**	2	3.602403
P61222	NVEDLSGGELQR	**1.089545723**	2	2.921072
P61222	VAETANEEEVKK	**2.075974409**	2	2.620749
P61314	**RL15 60S ribosomal protein L15**	**1.175167759**	**2.5E-11**	**6**
P61314	FFEVILIDPFHK	**1.151469092**	3	3.4665
P61314	GATYGKPVHHGVNQLK	**1.791153499**	2	4.368115
P61314	SLQSVAEER	**1.130471204**	2	2.688399
P61314	SLQSVAEERAGR	**0.951126722**	2	2.482018
P61314	VLNSYWVGEDSTYK	**1.322399259**	2	4.257211
P61314	YIQELWR	**1.252227774**	2	2.665078
P61354	**RL27 60S ribosomal protein L27**	**2.845207846**	**0.00084**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	**3.114495627**	3	4.116739
P61354	YSVDIPLDK	**1.29763219**	2	2.416169
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.057398619**	**0.59285**	**4**
P61459	AVGWNELEGR	**1.080751765**	2	3.129657
P61459	DQLLPNLR	**1.606579808**	2	2.354288
P61459	LDHHPEWFNVYNK	**1.215244125**	3	4.774946
P61459	LSAEERDQLLPNLR	**0.997842022**	3	4.01652
P61589	**RHOA Transforming protein RhoA**	**1.052087372**	**0.04015**	**3**
P61589	LVIVGDGACGK	**0.887824835**	2	2.709564
P61589	MKQEPVKPEEGR	**1.659245365**	3	3.451423
P61589	MKQEPVKPEEGR+Oxidation(0)	**1.30350079**		
P61751	**ARF4 ADP_ribosylation factor 4**	**1.086062088**	**0.14646**	**4**
P61751	IQEGAAVLQK	**1.309478245**	2	2.885529
P61751	LGEIVTTIPTIGFNVETVEYK	**1.165912812**	3	5.029695
P61751	NICFTVWDVGGQDK	**0.918273368**	2	4.127611
P61751	QDLPNAMAISEMTDK	**0.858767541**	2	3.772226
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.235986403**	**1**	**2**
P61805	ADFQGISPER	**0.981822245**	2	2.940885
P61805	FLEEYLSSTPQR	**0.949267713**	2	3.698464
P61972	**NTF2 Nuclear transport factor 2**	**0.842800545**	**0.69023**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	**0.924808418**	3	4.044783

P61972	NINDAWVCTNDMFR	0.824072263	2	3.601073
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.303075881**	**0.99192**	**8**
P61980	GSDFDCELR	1.049173815	2	2.602711
P61980	GSYGDLGGPIITTQVTIPK	0.89794887	2	5.05323
P61980	IDEPLEGSEDR	0.957174748	2	3.460135
P61980	IILDLISESPIK	1.197091905	2	3.972289
P61980	IITITGTQDQIQNAQYLLQNSVK	0.914418886	3	7.045339
P61980	LFQECCPHSTDR	1.018033823	2	3.674992
P61980	TDYNASVSVPDSSGPER	1.077425094	2	4.231711
P61980	VVLIGGKPDR	0.915767484	2	2.517359
P61983	**1433G 14_3_3 protein gamma**	**1.028287248**	**1**	**4**
P61983	AYSEAHEISK	1.009510988	2	3.239245
P61983	NVTELNEPLSNEER	1.053848043	2	4.937109
P61983	TAFDDAIAELDTLNEDSYK	0.882854679	2	5.16806
P61983	YLAEVATGEK	1.007423282	2	2.922291
P62046	**LRCH1 Leucine_rich repeat and calponin homology domain_containing protein 1**	**0.929498583**	**0.26398**	**2**
P62046	DRELDIAMIEQLR	0.84764982	2	2.586196
P62046	NLESIDPQFTIRRK	1.014895921	2	2.319091
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.822909334**	**3.3E-16**	**5**
P62076	CIGKPGGSLDNSEQK	0.843661287	2	4.043394
P62076	KCIGKPGGSLDNSEQK	1.232340513	3	4.540523
P62076	LDPGAIMEQVK	0.80466499	2	3.22487
P62076	VQIAVANAQELLQR	0.935865488	2	4.958214
P62076	YMDAWNTVSR	0.702722279	2	2.757345
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**1.016415275**	**0.3358**	**2**
P62078	FIDTTLAITGR	0.771464142	2	2.79627
P62078	TENCLSSCVDR	1.115388672	2	2.918724
P62083	**RS7 40S ribosomal protein S7**	**1.045887062**	**0.99665**	**5**
P62083	AIIIFVPVPQLK	1.009827043	2	3.792275
P62083	DVNFEFPEFQL	2.715847251	2	2.404202
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	1.06755355	3	4.949751
P62083	KAIIIFVPVPQLK	0.743539829	2	3.807272
P62083	TLTAVHDAILEDLVFPSEIVGK	1.11469377	2	5.099612
P62161	**CALM Calmodulin**	**1.047276199**	**0.99368**	**3**
P62161	EADIDGDGQVNYEEFVQMMTAK	1.399923581	2	4.775527
P62161	EAFSLFDKDGDGTITTK	1.4246709	2	4.172574
P62161	VFDKDGNGYISAAELR	0.980118084	2	4.886259
P62193	**PRS4 26S protease regulatory subunit 4**	**1.195794844**	**0.13441**	**4**
P62193	APQETYADIGGLDNQIQEIK	2.068825119	2	4.969431
P62193	MGQSQSGGHGPGGGK+Oxidation(0)	1.08425212		
P62193	NQEQMKPLEEK	1.242382408	2	3.234378
P62193	TMLELLNQLDGFDSR	0.905121893	2	4.048751
P62198	**PRS8 26S protease regulatory subunit 8**	**1.036034077**	**0.99637**	**6**
P62198	EELQLLQEQGSYVGEVVR	0.964877612	2	2.487425
P62198	IAELMPGASGAEVK	0.839592528	2	2.429717
P62198	IEELQLIVNDK	1.030487306	2	3.005128
P62198	LEGGSGGDSEVQR	1.141492751	2	3.750051
P62198	LLREELQLLQEQGSYVGEVVR	0.858709594	3	4.049383
P62198	TMLELLNQLDGFEATK	1.079829691	2	3.626887
P62243	**RS8 40S ribosomal protein S8**	**1.095786735**	**9.9E-20**	**8**
P62243	ADGYVLEGK	1.067776617	2	2.817324
P62243	IIDVVYNASNNELVR	2.800060327	2	4.377695
P62243	ISSLLEEQFQQGK	1.335714469	2	3.991194

P62243	KYELGRPAANTK	**0.976816497**	2	3.317575
P62243	LDVGNFSWGSECCTR	**0.966772695**	2	3.792821
P62243	LTPEEEEILNK	**1.044393557**	2	3.369033
P62243	NCIVLIDSTPYR	**1.076038392**	2	3.883613
P62243	YELGRPAANTK	**0.893981769**	2	2.98953
P62246	**RS15A 40S ribosomal protein S15a**	**1.245055113**	**0.00019**	**3**
P62246	HGYIGEFEIIDDHR	**1.203931057**	2	4.955499
P62246	MNVLADALK	**0.957406852**	2	2.343958
P62246	WQNNLLPSR	**1.184827599**	2	3.000891
P62250	**RS16 40S ribosomal protein S16**	**1.499263948**	**0.03913**	**5**
P62250	ALVAYYQK	**1.580969401**	2	2.390972
P62250	EIKDILIQYDR	**1.017234604**	2	2.42965
P62250	GGGHVAQIYAIR	**1.919028069**	2	3.151434
P62250	LLEPVLLLGK	**1.195868049**	2	3.048643
P62250	TLLVADPR	**1.129438395**	2	2.715634
P62260	**1433E 14_3_3 protein epsilon**	**1.109207935**	**0.90284**	**8**
P62260	AAFDDAIAELDTLSEESYK	**0.959244626**	2	6.356453
P62260	AAFDDAIAELDTLSEESYKDSTLIMQLLR	**1.594114407**		
P62260	EENKGGEDKLK	**1.032628993**	2	2.743721
P62260	HLIPAANTGESK	**0.971939199**	1	3.152375
P62260	IISSIEQK	**1.048028569**	2	2.705436
P62260	LICCDILDVLDK	**1.368805897**	2	4.031466
P62260	YLAEFATGNDR	**0.969381806**	2	2.983791
P62260	YLAEFATGNDRK	**0.879367391**	2	2.836806
P62271	**RS18 40S ribosomal protein S18**	**0.961527402**	**4.1E-09**	**5**
P62271	AGELTEDEVER	**0.987888027**	2	3.734788
P62271	RAGELTEDEVER	**0.898129138**	2	3.485244
P62271	VITIMQNPR	**0.962541296**	2	2.878926
P62271	VLNTNIDGR	**1.056863255**	2	2.893923
P62271	YSQVLANGLDNK	**1.303979718**	2	4.14412
P62278	**RS13 40S ribosomal protein S13**	**1.197692444**	**0.00035**	**4**
P62278	GLAPDLPEDLYHLIK	**1.340606305**	2	2.972571
P62278	GLSQSALPYR	**1.144821784**	2	2.638877
P62278	KGLTPSQIGVILR	**0.863562319**	3	4.102226
P62278	LILIESR	**1.679474627**	2	2.332903
P62332	**ARF6 ADP_ribosylation factor 6**	**0.72167861**	**0.30586**	**2**
P62332	FNVWDVGGQDK	**0.596128672**	2	2.818628
P62332	LGQSVTTIPTVGFNVETVTYK	**1.058115649**	2	3.422548
P62334	**PRS10 26S protease regulatory subunit 10B**	**1.025627289**	**9E-06**	**5**
P62334	ALQSVGQIVGEVLK	**0.90297541**	2	3.088
P62334	AVASQLDCNFLK	**1.028248684**	2	2.728567
P62334	EVIELPLTNPELFQR	**1.502964311**	2	3.398631
P62334	FSEGTSADR	**1.184078445**	2	2.522824
P62334	HGEIDYEAIVK	**0.514375389**	2	3.36691
P62425	**RL7A 60S ribosomal protein L7a**	**1.201030037**	**0.00017**	**12**
P62425	AGVNTVTTLVENK	**1.157763631**	2	4.043626
P62425	AGVNTVTTLVENKK	**0.928808841**	2	2.857599
P62425	HWGGNVLGPK	**0.767014102**	1	1.979264
P62425	KVVNPLFEK	**1.388977598**	2	2.537223
P62425	LKVPPAINQFTQALDR	**1.311205707**	3	4.502523
P62425	NFGIGQDIQPK	**1.127790241**	2	3.47069
P62425	QTATQLLK	**1.214175862**	2	2.382945
P62425	TCTTVAFTQVNSEDK	**2.105555519**	2	4.132649
P62425	TCTTVAFTQVNSEDKGALAK	**2.565283588**	2	3.93124
P62425	TNYNDRYDEIR	**1.104628264**	2	2.448781
P62425	VAPAPAVVK	**1.362025653**	1	2.162721
P62425	VPPAINQFTQALDR	**1.111694368**	2	3.522041

P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.178317853**	**1.3E-12**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	**1.094791737**	3	5.326085
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	**1.031884471**	4	5.790313
P62630	MDSTEPPYSQK	**0.904039803**	2	3.581632
P62630	MDSTEPPYSQK+Oxidation(0)	**1.085865081**		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	**1.050818527**	5	6.546849
P62630	RYEEIVK	**0.937843231**	2	2.612775
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	**1.184446057**	3	5.107624
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14)	**1.251706354**		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8)	**1.27539925**		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	**0.888122065**	2	5.471049
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)	**1.128073497**		
P62630	YEEIVK	**1.251227935**	1	2.091926
P62630	YYVTIIDAPGHR	**1.23943366**	3	3.641772
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.147175212**	**9.9E-20**	**9**
P62632	EHALLAYTLGVK	**1.995576993**	3	4.062109
P62632	IGGIGTVPVGR	**1.371780804**	2	3.651441
P62632	MDSTEPAYSEK	**0.870259032**	2	2.305096
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	**0.9582687**	3	4.571581
P62632	QLIVGVNK	**1.367768767**	1	2.771101
P62632	QTVAVGVIK	**1.020075771**	1	2.245
P62632	STTTGHLIYK	**1.11381952**	2	3.250636
P62632	THINIVVIGHVDSGK	**1.171672666**	2	5.463567
P62632	VETGILRPGMVVTFAPVNITTEVK	**1.084096491**	3	3.592238
P62634	**CNBP Cellular nucleic acid_binding protein**	**0.979364987**	**0.62643**	**2**
P62634	CGETGHVAINCSK	**0.981895576**	2	4.427821
P62634	CYSCGEFGHIQK	**0.888042964**	2	3.083513
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**0.941947773**	**0.99064**	**6**
P62703	FDTGNLCMVTGGANLGR	**0.968299296**	2	4.970669
P62703	FDTGNLCMVTGGANLGR+Oxidation(7)	**0.488039445**		
P62703	GIPHLVTHDAR	**1.138842579**	2	2.608608
P62703	LSNIFVIGK	**1.053264058**	2	2.874052
P62703	TDITYPAGFMDVISIDK	**1.012972517**	2	4.585635
P62703	VNDTIQIDLETGK	**1.085472641**	2	3.755436
P62718	**RL18A 60S ribosomal protein L18a**	**1.29126675**	**0.00177**	**2**
P62718	DLTTAGAVTQCYR	**1.311431842**	2	3.037
P62718	SSGEIVYCGQVFEKSPLR	**0.998727409**	2	2.495971
P62752	**RL23A 60S ribosomal protein L23a**	**0.997540798**	**0.00269**	**6**
P62752	LAPDYDALDVANK	**1.04692018**	2	3.569261
P62752	LDHYAIIK	**1.080271809**	2	2.405123
P62752	LYDIDVAK	**1.069771844**	1	1.921885
P62752	NKLDHYAIIK	**1.041632341**	2	2.482819
P62752	VNTLIRPDGEK	**1.206617723**	2	3.084478
P62752	VNTLIRPDGEKK	**1.514262363**	2	2.83795
P62755	**RS6 40S ribosomal protein S6**	**1.035238811**	**0.87901**	**6**
P62755	DIPGLTDTTVPR	**0.758706679**	2	2.336389
P62755	EEAAEYAKLLAK	**1.017186019**	2	2.398875
P62755	LIEVDDER	**0.917670452**	2	2.785909
P62755	LNISFPATGCQK	**0.999150968**	2	3.125343
P62755	MATEVAADALGEEWK	**1.019479125**	2	4.356373
P62755	MATEVAADALGEEWK+Oxidation(0)	**1.121554222**		
P62775	**MTPN Myotrophin**	**1.075880412**	**0.25669**	**2**
P62775	GPDGLTALEATDNQAIK	**1.914597715**	2	3.706726
P62775	HHITPLLSAVYEGHVSCVK	**1.070941479**	3	3.61731

P62804	**H4 Histone H4**	**1.215690493**	**9.9E-20**	**9**
P62804	DAVTYTEHAK	**2.11021531**	2	3.091598
P62804	DNIQGITKPAIR	**1.009063425**	2	3.254271
P62804	ISGLIYEETR	**1.653223973**	2	3.773031
P62804	KTVTAMDVVYALK	**1.215586856**	2	3.023273
P62804	RISGLIYEETR	**0.775225297**	2	2.307495
P62804	TLYGFGG	**0.6225752**	1	1.95168
P62804	TVTAMDVVYALK	**1.106626842**	2	4.065288
P62804	TVTAMDVVYALK+Oxidation(4)	**1.285765265**		
P62804	VFLENVIR	**0.863879347**	2	3.015818
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**0.912023617**	**0.23588**	**3**
P62815	AVVQVFEGTSGIDAK	**0.772930801**	2	3.637273
P62815	IYPEEMIQTGISAIDGMNSIAR	**0.734829425**	2	2.450038
P62815	QIYPPINVLPSLSR	**0.913283643**	2	2.353211
P62832	**RL23 60S ribosomal protein L23**	**1.57638169**	**0.49571**	**2**
P62832	GSAITGPVAK	**3.245142167**	2	2.38306
P62832	ISLGLPVGAVINCADNTGAK	**1.063497953**	2	4.896225
P62853	**RS25 40S ribosomal protein S25**	**1.559170766**	**6.7E-05**	**2**
P62853	GGDAPAAGEDA	**1.280828066**	1	2.019867
P62853	LNNLVLFDK	**1.559126006**	2	3.052199
P62856	**RS26 40S ribosomal protein S26**	**1.138410878**	**0.56499**	**3**
P62856	DISEASVFDAYVLPK	**1.310172399**	2	3.269862
P62856	FRPAGAAPRPPPKPM	**0.777673947**	2	2.352892
P62856	NIVEAAAVR	**1.118484651**	2	2.92795
P62859	**RS28 40S ribosomal protein S28**	**1.608779478**	**0.02552**	**2**
P62859	EGDVLTLLESER	**1.591689488**	2	3.234688
P62859	VEFMDDTSR	**1.703367584**	2	2.597485
P62870	**ELOB Transcription elongation factor B polypeptide 2**	**0.935853293**	**0.94506**	**2**
P62870	ADDTFEALR	**0.819520384**	2	2.583726
P62870	TLGECGFTSQTARPQAPATVGLAFR	**1.003052394**	3	3.421448
P62890	**RL30 60S ribosomal protein L30**	**1.326565219**	**0.30106**	**2**
P62890	TGVHHYSGNNIELGTACGK	**1.190771051**	2	5.654829
P62890	VCTLAIIDPGDSDIIR	**1.331953345**	2	4.219794
P62898	**CYC Cytochrome c_ somatic**	**1.075922626**	**0.99997**	**6**
P62898	ADLIAYLK	**1.073331618**	2	2.869547
P62898	GITWGEDTLMEYLENPK	**1.073791106**	2	4.962444
P62898	GITWGEDTLMEYLENPKK	**0.905837507**	2	4.559816
P62898	KTGQAAGFSYTDANK	**1.17193923**	2	4.752879
P62898	TGPNLHGLFGR	**0.947121951**	2	3.266914
P62898	TGQAAGFSYTDANK	**1.157937175**	2	4.271093
P62902	**RL31 60S ribosomal protein L31**	**1.315298562**	**0.00085**	**2**
P62902	NLQTVNVDEN	**1.864410321**	1	2.527725
P62902	SAINEVVTR	**1.288414876**	2	2.938576
P62907	**RL10A 60S ribosomal protein L10a**	**1.278820272**	**4.7E-12**	**6**
P62907	AVDIPHMDIEALK	**0.981305342**	2	2.814103
P62907	AVDIPHMDIEALKK	**0.97456472**	2	2.603906
P62907	FSVCVLGDQQHCDEAK	**1.390164386**	2	4.194169
P62907	KYDAFLASESLIK	**1.165022733**	2	4.006351
P62907	VLCLAVAVGHVK	**0.887327019**	3	3.895473
P62907	YDAFLASESLIK	**1.203900658**	2	3.453281
P62909	**RS3 40S ribosomal protein S3**	**1.165279755**	**9.9E-20**	**10**
P62909	AELNEFLTR	**1.196541883**	2	2.840172
P62909	DEILPTTPISEQK	**1.192949433**	2	3.703027
P62909	ELAEDGYSGVEVR	**1.550801208**	2	3.429917
P62909	ELTAVVQK	**1.321900705**	1	2.077975

P62909	FGFPEGSVELYAEK	**2.609201006**	2	4.053975
P62909	FVDGLMIHSGDPVNYYVDTAVR	**1.282938731**	3	4.938177
P62909	GCEVVVSGK	**1.149814128**	2	2.772482
P62909	GGKPEPPAMPQPVPTA	**1.350911862**	2	3.54081
P62909	GLCAIAQAESLR	**1.050861124**	2	3.390461
P62909	TEIIILATR	**1.2537794**	2	3.178227
P62912	**RL32 60S ribosomal protein L32**	**1.220535891**	**1.1E-06**	**3**
P62912	ELEVLLMCNK	**1.32190045**	2	2.851244
P62912	GQILMPNIGYGSNK	**1.062993658**	2	2.932909
P62912	SYCAEIAHNVSSK	**1.218287768**	2	4.803632
P62914	**RL11 60S ribosomal protein L11**	**1.062097894**	**1**	**2**
P62914	VLEQLTGQTPVFSK	**1.110286785**	2	4.411545
P62914	YDGIILPGK	**1.046257391**	2	2.816654
P62919	**RL8 60S ribosomal protein L8**	**1.082678623**	**1.8E-09**	**3**
P62919	ASGNYATVISHNPETK	**1.35223751**	2	4.673055
P62919	AVVGVVAGGGR	**1.078593005**	2	3.430963
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	**0.806256777**	3	4.549391
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.899060826**	**0.07304**	**7**
P62959	AQVAQPGGDTIFGK	**0.937123273**	2	4.618267
P62959	CAADLGLK	**1.35380658**	2	2.751844
P62959	CLAFHDISPQAPTHFLVIPK	**1.038320111**	3	4.2221
P62959	HISQISVADDDDESLLGHLMIVGK	**0.760329174**	3	6.730711
P62959	IIFEDDR	**0.534346264**	2	2.349279
P62959	KHISQISVADDDDESLLGHLMIVGK	**0.822991407**	3	5.558572
P62959	MVVNEGADGGQSVYHIHLHVLGGR	**0.942741992**	3	4.706339
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**2.252583387**	**9.9E-20**	**7**
P62961	AADPPAENSSAPEAEQGGAE	**0.737551801**	2	2.638389
P62961	EDGNEEDKENQGDETQGQQPPQR	**0.962751188**	3	5.125838
P62961	GAEAANVTGPGGVPVQGSK	**1.654331997**	2	5.013956
P62961	NEGSESAPEGQAQQR	**2.715175103**	2	5.307773
P62961	NYQQNYQNSESGEK	**1.997835057**	2	4.167553
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	**1.354147051**	3	5.04581
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	**1.448182025**	4	4.648341
P62963	**PROF1 Profilin_1**	**0.983096667**	**0.93408**	**6**
P62963	CYEMASHLR	**0.919827579**	2	2.749566
P62963	DSLLQDGEFTMDLR	**0.971960437**	2	3.313122
P62963	DSPSVWAAVPGK	**1.407084454**	2	2.935594
P62963	SSFFVNGLTLGGQK	**0.869373824**	2	4.577405
P62963	STGGAPTFNVTVTMTAK	**0.957439866**	2	3.025207
P62963	TFVSITPAEVGVLVGK	**0.878863995**	2	4.78787
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.351388882**	**9.9E-20**	**28**
P63018	ARFEELNADLFR	**1.282075636**	2	2.980095
P63018	CNEIISWLDK	**0.714317419**	2	3.059733
P63018	DAGTIAGLNVLR	**2.068710433**	2	3.742252
P63018	EIAEAYLGK	**1.920172663**	1	1.965855
P63018	FDDAVVQSDMK	**1.073346165**	2	3.937093
P63018	FEELNADLFR	**1.058325851**	2	3.179737
P63018	FELTGIPPAPR	**1.054383587**	2	3.183309
P63018	GTLDPVEK	**1.204554804**	1	2.014535
P63018	HWPFMVVNDAGRPK+Oxidation(4)	**1.779014513**		
P63018	IINEPTAAAIAYGLDK	**1.235026795**	2	5.129612
P63018	IINEPTAAAIAYGLDKK	**1.076554143**	2	4.717216
P63018	LLQDFFNGK	**1.083017658**	2	3.076245
P63018	MKEIAEAYLGK	**0.714147883**	2	2.883192
P63018	MKEIAEAYLGK+Oxidation(0)	**1.374655665**		

P63018	NQTAEKEEFEHQQK	**1.600351533**	2	4.88416
P63018	NQVAMNPTNTVFDAK	**1.077581452**	2	4.988507
P63018	NQVAMNPTNTVFDAK+Oxidation(4)	**1.370577101**		
P63018	NSLESYAFNMK	**1.67921626**	2	3.569918
P63018	QATKDAGTIAGLNVLR	**0.844684991**	2	2.450734
P63018	RFDDAVVQSDMK	**0.958417348**	2	3.578502
P63018	SFYPEEVSSMVLTK	**1.061312831**	2	4.940659
P63018	SFYPEEVSSMVLTK+Oxidation(9)	**1.076671089**		
P63018	SINPDEAVAYGAAVQAAILSGDK	**1.272557422**	2	6.059334
P63018	SQIHDIVLVGGSTR	**1.188343182**	2	4.924558
P63018	STAGDTHLGGEDFDNR	**1.216993914**	2	4.248702
P63018	TVTNAVVTVPAYFNDSQR	**1.104147406**	3	4.360116
P63018	VCNPIITK	**1.014859081**	2	2.301606
P63018	VQVEYKGETK	**1.282904396**	2	2.55106
P63029	**TCTP Translationally_controlled tumor protein**	**2.063612777**	**1.5E-13**	**3**
P63029	DLISHDELFSDIYK	**2.7908693**	2	3.755276
P63029	EIADGLCLEVEGK	**1.81850219**	2	3.338216
P63029	TEGAIDDSLIGGNASAEGPEGEGTESTVVTGVDIVMNHHLQETSFTK	**3.090646456**	4	4.588511
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.16572371**	**9.7E-06**	**6**
P63036	HYNGEAYEDDEHHPR	**1.519038489**	3	5.353754
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	**1.416996953**	3	4.491005
P63036	NVVHQLSVTLEDLYNGATR	**1.113885938**	2	4.116804
P63036	QISQAYEVLADSK	**1.185931335**	2	3.700417
P63036	TIVITSHPGQIVK	**0.965638127**	2	3.461507
P63036	VNFPENGFLSPDK	**1.184728133**	2	3.358402
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.11171987**	**9.9E-20**	**33**
P63039	AAVEEGIVLGGGCALLR	**0.891234085**	2	5.253572
P63039	ALMLQGVDLLADAVAVTMGPK	**0.55827581**	3	5.283134
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(2)	**0.926718232**		
P63039	CEFQDAYVLLSEK	**1.045214426**	2	4.896836
P63039	CIPALDSLKPANEDQK	**0.745821303**	2	3.654528
P63039	DIGNIISDAMK	**0.852295232**	2	3.221639
P63039	GVMLAVDAVIAELK	**0.87574615**	2	3.839546
P63039	GVMLAVDAVIAELKK	**0.644534156**	2	4.479409
P63039	GYISPYFINTSK	**1.394803404**	2	3.029247
P63039	IGIEIIK	**0.953610067**	2	2.589458
P63039	ILQSSSEVGYDAMLGDFVNMVEK	**0.946574099**	2	4.979472
P63039	IQEITEQLDITTSEYEK	**0.875694249**	2	5.939842
P63039	IQEITEQLDITTSEYEKEK	**0.72754118**	2	5.061436
P63039	ISSVQSIVPALEIANAHR	**0.83979261**	2	4.255525
P63039	KISSVQSIVPALEIANAHR	**1.400188382**	3	4.550709
P63039	KPLVIIAEDVDGEALSTLVLNR	**0.973765185**	2	6.136534
P63039	LSDGVAVLK	**1.030204857**	2	3.098129
P63039	LVQDVANNTNEEAGDGTTTATVLAR	**0.931354308**	2	6.636322
P63039	NAGVEGSLIVEK	**0.988393578**	2	3.584287
P63039	QSKPVTTPEEIAQVATISANGDK	**0.946901911**	2	3.581943
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	**0.76000407**	3	4.842977
P63039	RGVMLAVDAVIAELKK	**0.623211238**	3	5.770705
P63039	TALLDAAGVASLLTTAEAVVTEIPK	**1.140761166**		
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	**0.999850038**	3	5.031567
P63039	TLNDELEIIEGMK	**0.73848497**	2	4.659017
P63039	TLNDELEIIEGMK+Oxidation(11)	**0.892939022**		
P63039	TVIIEQSWGSPK	**0.905082399**	2	4.378443
P63039	VGEVIVTK	**0.812785275**	2	2.938201
P63039	VGEVIVTKDDAMLLK	**0.570840213**	2	2.50118
P63039	VGGTSDVEVNEK	**0.914471703**	2	3.820652

P63039	VGGTSDVEVNEKK	**1.06954792**	2	3.518459
P63039	VGLQVVAVK	**0.882309579**	2	3.282634
P63039	VTDALNATR	**0.938081094**	2	3.571726
P63102	**1433Z 14_3_3 protein zeta/delta**	**0.922394286**	**0.11941**	**9**
P63102	DICNDVLSLLEK	**1.294991965**	3	3.680529
P63102	FLIPNASQPESK	**0.937986329**	2	3.36873
P63102	GIVDQSQQAYQEAFEISK	**0.797542538**	2	5.748536
P63102	GIVDQSQQAYQEAFEISKK	**0.813014524**	2	2.62193
P63102	KGIVDQSQQAYQEAFEISK	**0.79831234**	2	6.013041
P63102	SVTEQGAELSNEER	**1.301187196**	2	5.56115
P63102	TAFDEAIAELDTLSEESYK	**1.143708833**	2	5.686096
P63102	YDDMAACMK	**0.874219532**	2	2.451387
P63102	YLAEVAAGDDKK	**0.987454186**	2	3.611005
P63159	**HMGB1 High mobility group protein B1**	**0.801663405**	**3.7E-06**	**4**
P63159	GEHPGLSIGDVAK	**0.798039593**	2	3.117338
P63159	IKGEHPGLSIGDVAK	**0.737631012**	2	3.950677
P63159	KHPDASVNFSEFSK	**1.089325262**	2	4.289649
P63159	LGEMWNNTAADDKQPYEK+Oxidation(3)	**0.960599096**		
P63174	**RL38 60S ribosomal protein L38**	**1.64294449**	**0.00355**	**4**
P63174	IEEIKDFLLTAR	**1.070803103**	3	3.361184
P63174	KIEEIKDFLLTAR	**1.146701771**	2	4.108852
P63174	YLYTLVITDK	**1.711602115**	2	2.896703
P63174	YLYTLVITDKEK	**1.885527102**	2	2.708998
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.130301004**	**6.9E-11**	**12**
P63245	DETNYGIPQR	**1.312384847**	2	2.940192
P63245	DGQAMLWDLNEGK	**1.273975013**	2	2.969844
P63245	FSPNSSNPIIVSCGWDK	**1.100314556**	2	4.112599
P63245	GHNGWVTQIATTPQFPDMILSASR	**0.968895456**	3	4.168629
P63245	HLYTLDGGDIINALCFSPNR	**1.397088827**	2	5.901755
P63245	IIVDELKQEVISTSSK	**0.97202602**	2	4.346048
P63245	LWDLTTGTTTR	**0.754007697**	2	2.589536
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	**1.276865234**	3	5.536952
P63245	VWNLANCK	**1.165817557**	2	2.67961
P63245	VWQVTIGTR	**1.166107385**	2	2.736893
P63245	YTVQDESHSEWVSCVR	**1.186454196**	2	4.654795
P63245	YWLCAATGPSIK	**0.964234395**	2	2.844509
P63259	**ACTG Actin_ cytoplasmic 2**	**1.086860706**	**0.53487**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	**2.962773047**	3	4.768364
P63259	DLYANTVLSGGTTMYPGIADR	**1.140157747**	2	6.086339
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13)	**0.989968569**		
P63259	GYSFTTTAER	**1.007387305**	2	3.353513
P63259	KDLYANTVLSGGTTMYPGIADR	**0.988278485**	2	6.449868
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)	**1.152025664**		
P63259	QEYDESGPSIVHR	**0.976029756**	3	3.422786
P63259	VAPEEHPVLLTEAPLNPK	**1.03142738**	3	4.739213
P63324	**RS12 40S ribosomal protein S12**	**1.091761856**	**0.12812**	**4**
P63324	KVVGCSCVVVK	**0.96580338**	2	3.379607
P63324	LGEWVGLCK	**1.012030683**	2	2.847631
P63324	QAHLCVLASNCDEPMYVK	**1.313889302**	3	3.552733
P63324	VVGCSCVVVK	**1.258820305**	2	3.238082
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**1.00764625**	**0.7663**	**3**
P63331	CGNQAAIMELDDTLK	**0.923065903**	2	2.771279
P63331	NVVTIFSAPNYCYR	**1.221406605**	2	2.326139
P63331	YSFLQFDPAPR	**1.008623381**	2	3.419724
P67779	**PHB Prohibitin**	**1.022170545**	**0.99937**	**12**

P67779	AAELIANSLATAGDGLIELR	0.956379441	3	4.217194
P67779	AAIISAEGDSK	1.198929139	2	2.481286
P67779	DLQNVNITLR	1.010504971	2	3.002888
P67779	FDAGELITQR	0.796447137	2	3.540552
P67779	FGLALAVAGGVVNSALYNVDAGHR	0.991374315	3	3.53134
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.082468133	4	4.84002
P67779	IYTSIGEDYDER	1.266525861	2	3.367364
P67779	KLEAAEDIAYQLSR	1.078612103	2	4.813692
P67779	NITYLPAGQSVLLQLPQ	0.995666213	3	3.430168
P67779	NVPVITGSK	0.969841003	1	2.277607
P67779	QVSDDLTER	1.0373427	2	2.416462
P67779	VLPSITTEILK	0.798363783	2	2.314491
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.081006925**	**0.06379**	**3**
P68037	ADLAEEYSK	0.772519352	2	2.63813
P68037	GQVCLPVISAENWKPATK	0.952241944	2	3.764193
P68037	TDQVIQSLIALVNDPQPEHPLR	1.152285534	2	5.153215
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.27263808**	**0.3468**	**3**
P68101	AGLNCSTETMPIK	1.278086624	2	3.406359
P68101	TEGLSVLNQAMAVIK	0.924395624	2	3.985758
P68101	VVTDTDETELAR	1.284533434	2	3.305271
P68136	**ACTS Actin_ alpha skeletal muscle**	**1.363773379**	**9.9E-20**	**16**
P68136	AGFAGDDAPR	1.660413116	2	3.356367
P68136	AVFPSIVGRPR	0.627144487	2	2.6985
P68136	DLYANNVMSGGTTMYPGIADR	0.769168839	2	4.663561
P68136	DSYVGDEAQSK	2.174332144	2	3.540015
P68136	EITALAPSTMK	1.088270515	2	3.137859
P68136	EITALAPSTMK+Oxidation(9)	1.196095022		
P68136	GYSFVTTAER	1.158462921	2	3.958458
P68136	IWHHTFYNELR	2.864273582	2	2.690291
P68136	KDLYANNVMSGGTTMYPGIADR	0.902623513	2	5.034206
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14)	1.167628513		
P68136	QEYDEAGPSIVHR	0.886831251	2	3.163333
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	0.891245097	3	6.811887
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28)	1.036136905		
P68136	VAPEEHPTLLTEAPLNPK	1.0352389	2	4.392037
P68136	YPIEHGIITNWDDMEK	1.791944221	2	4.450612
P68136	YPIEHGIITNWDDMEK+Oxidation(13)	0.785802088		
P68255	**1433T 14_3_3 protein theta**	**1.04979856**	**0.99429**	**6**
P68255	AVTEQGAELSNEER	1.511518849	2	4.632949
P68255	SICTTVLELLDK	1.188006417	2	3.100723
P68255	TAFDEAIAELDTLNEDSYK	1.020997724	2	4.80388
P68255	VISSIEQK	1.017683396	2	3.254664
P68255	YLAEVACGDDR	1.088167537	2	3.001915
P68255	YLIANATNPESK	0.985399959	2	2.822546
P68511	**1433F 14_3_3 protein eta**	**0.791392408**	**9.9E-08**	**4**
P68511	AVTELNEPLSNEDR	1.552646456	2	4.666099
P68511	ELETVCNDVLALLDK	1.080617667	2	3.471905
P68511	NCNDFQYESKVFYLK	0.775089801	2	2.347584
P68511	NSVVEASEAAYK	1.295787894	2	3.215416
P69897	**TBB5 Tubulin beta_5 chain**	**1.236742918**	**0.01044**	**3**
P69897	ALTVPELTQQVFDAK	1.208738318	2	3.496055
P69897	ISVYYNEATGGK	1.493880427	2	2.942208
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	0.987480745	2	5.354481
P70372	**ELAV1 ELAV_like protein 1**	**0.970807144**	**0.19327**	**2**
P70372	TNLIVNYLPQNMTQEELR	0.698110964	2	3.423189

P70372	VLVDQTTGLSR	**1.01944553**	2	2.41271
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.212853933**	**0.35177**	**2**
P70470	ASFSQGPINSANR	**0.74794634**	2	2.944511
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	**1.237306242**	3	4.041405
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.81075722**	**9.9E-20**	**11**
P70473	ADVLLEPFR	**0.697004654**	2	3.362092
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	**0.648682773**	4	5.201691
P70473	DYGFSQEEIHQLHSDR	**0.829017997**	2	4.859573
P70473	GLGLESEELPSQMSIEDWPEMK	**0.688329881**	3	4.846204
P70473	GQNLLDGGAPFYTTYK	**0.825547218**	2	5.439533
P70473	GSFITDEEQHACPRPAPQLSR	**0.842038768**	3	3.852139
P70473	LGSVNHPSHLAR	**0.898056233**	2	3.395815
P70473	LSGFGQSGIFSK	**0.961175111**	2	3.040418
P70473	RDPSVGEHTVEVLK	**0.631848479**	3	4.396935
P70473	TADGEFMAVGAIEPQFYTLLLK	**1.325109092**	3	4.134341
P70473	TQAMGLWAQPR	**0.512576746**	2	3.131624
P70550	**RAB8B Ras_related protein Rab_8B**	**1.263206451**	**0.38141**	**2**
P70550	LLLIGDSGVGK	**1.280269014**	2	2.78506
P70550	NIEEHASSDVER	**1.085372697**	2	2.307937
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**1.144110956**	**0.99818**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	**0.94050288**	3	4.136862
P70552	VLGNNFYEYYVNDPPR	**1.155257854**	2	3.368034
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.965972564**	**0.37294**	**6**
P70580	FYGPEGPYGVFAGR	**0.87198907**	2	4.010903
P70580	GDQPGASGDNDDDEPPPLPR	**1.018639037**	2	4.976551
P70580	IVRGDQPGASGDNDDDEPPPLPR	**0.879855147**	3	5.030583
P70580	KFYGPEGPYGVFAGR	**0.957198364**	2	3.61088
P70580	RYDGVQDPR	**0.597587414**	1	2.152603
P70580	YDGVQDPR	**0.83787877**	2	2.837738
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.585118114**	**9.9E-20**	**8**
P70584	ASSTCQLTFENVK	**0.748217278**	2	3.288247
P70584	FAQEQIAPLVSTMDENSK	**0.822169442**	2	4.963452
P70584	IFDFQGLQHQVAHVATQLEAAR	**0.621039297**	3	6.144009
P70584	IGTIYEGTSNIQLNTIAK	**0.613552204**	2	4.556328
P70584	KFAQEQIAPLVSTMDENSK	**0.570671165**	2	5.804394
P70584	SGNYYVINGSK	**0.552460703**	2	2.883802
P70584	VDASVALLCDIQNTVINK	**0.681896519**	2	4.921355
P70584	YYASEVAGLTTSK	**0.802974433**	2	4.13797
P70587	**LRRC7 Leucine_rich repeat_containing protein 7**	**1.666707337**	**0.10392**	**2**
P70587	KESTDESEVDK	**1.900420589**	2	2.371924
P70587	SREQQPYEGNINK	**1.001688077**	2	2.487029
P70615	**LMNB1 Lamin_B1**	**1.028266753**	**0.00879**	**5**
P70615	ALYETELADAR	**1.03795192**	2	3.075354
P70615	KESDLSGAQIK	**0.951717838**	2	2.531164
P70615	LSSEMNTSTVNSAR	**0.767309973**	2	3.783771
P70615	NQNSWGTGEDVK	**0.743156118**	2	3.285865
P70615	SLEGDLEDLKDQIAQLEASLSAAK	**0.759877354**	3	4.62332
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**0.998045402**	**2.3E-07**	**2**
P70694	REDIFYTSK	**1.399582589**	2	3.131126
P70694	SIGVSNFNR	**0.717128848**	2	2.376778
P70712	**KYNU Kynureninase**	**1.245796696**	**0.51063**	**9**
P70712	IATELNCDPTDER	**0.90456339**	2	3.587585
P70712	IGAYGHEVGK	**1.352906788**	2	2.839433
P70712	LLTAILDSTERN	**1.208537864**	2	3.290477

P70712	LQLIPGVNGFR	**0.961178552**	2	2.524788
P70712	MEDILEVIEK	**1.115091695**	2	2.588513
P70712	TYLEEELDK	**1.226539968**	1	2.201579
P70712	TYLEEELDKWAK	**0.65321263**	2	2.55421
P70712	VAPVPLYNSFHDVYK	**1.045073987**	2	2.946423
P70712	YLNSGAGGLAGAFIHEK	**1.063236856**	2	4.307238
P80067	**CATC Dipeptidyl peptidase 1**	**0.768971225**	**1.1E-16**	**6**
P80067	GINFVSPVR	**0.790629278**	2	3.120631
P80067	GTDECAIESIAMAAIPIPK	**0.786386281**	3	4.523062
P80067	NQESCGSCYSFASLGMLEAR	**0.981163366**	2	3.400318
P80067	NSWGSQWGESGYFR	**0.769052095**	2	3.612549
P80067	RGTDECAIESIAMAAIPIPK	**0.620338485**	2	3.884704
P80067	YAQDFGVVEENCFPYTATDAPCKPK	**1.047026565**	3	5.995942
P80254	**DOPD D_dopachrome decarboxylase**	**1.217403281**	**0.00554**	**4**
P80254	FFPLEPWQIGK	**1.098382384**	2	2.443477
P80254	FLTEELSLDQDR	**1.073236714**	2	3.868703
P80254	LCAATATILDKPEDR	**3.438090724**	2	4.249262
P80254	STEPCAHLLISSIGVVGTAEQNR	**1.332259763**	2	5.097519
P80299	**HYES Epoxide hydrolase 2**	**0.96289601**	**0.99865**	**2**
P80299	ATEMGGILVGTPEDPK	**0.918499545**	2	3.675416
P80299	TEIQNPSVTSK	**1.03049645**	2	3.139398
P80313	**TCPH T_complex protein 1 subunit eta**	**1.049609169**	**0.73974**	**5**
P80313	ATISNDGATILK	**1.243415526**	2	2.597908
P80313	GGAEQFMEETER	**1.262285164**	2	2.978167
P80313	LLDVVHPAAK	**1.049295687**	2	2.571696
P80313	QLCDNAGFDATNILNK	**0.973948603**	2	3.29668
P80313	SQDAEVGDGTTSVTLLAAEFLK	**1.192336286**	2	4.824515
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.016947869**	**0.71159**	**8**
P80317	ALQFLEQVK	**1.166351057**	2	2.799048
P80317	DGNVLLHEMQIQHPTASLIAK	**1.031543878**	3	4.370374
P80317	GIDPFSLDALAK	**1.134026738**	2	2.493104
P80317	NAIDDGCVVPGAGAVEVALAEALIK	**0.919539233**	3	4.183879
P80317	QADLYISEGLHPR	**1.845843207**	2	2.389749
P80317	TEVNSGFFYK	**1.272097214**	2	2.587647
P80317	VATAQDDITGDGTTSNVLIIGELLK	**1.064819436**	2	5.435468
P80317	VLAQNSGFDLQETLVK	**0.93253119**	2	3.982014
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.999775721**	**0.99991**	**6**
P81155	LTFDTTFSPNTGK	**0.916117828**	2	3.205997
P81155	SNFAVGYR	**0.947187985**	2	2.440187
P81155	TGDFQLHTNVNNGTEFGGSIYQK	**0.949294206**	3	3.332845
P81155	VNNSSLIGVGYTQTLRPGVK	**1.043170317**	2	3.789334
P81155	WCEYGLTFTEK	**1.039458365**	2	2.609626
P81155	YQLDPTASISAK	**0.982338491**	2	3.235001
P82995	**HS90A Heat shock protein HSP 90_alpha**	**0.955985104**	**0.98177**	**17**
P82995	DQVANSAFVER	**1.133133403**	2	2.548248
P82995	ELHINLIPNKQDR	**1.179087362**	2	3.237441
P82995	ELISNSSDALDK	**1.166181514**	2	2.801405
P82995	FYEQFSK	**1.060947234**	1	2.258059
P82995	HGLEVIYMIEPIDEYCVQQLK	**1.432990774**	3	3.479845
P82995	HIYFITGETK	**1.261566209**	2	2.734051
P82995	HLEINPDHSIIETLR	**0.962593024**	2	4.453443
P82995	HSQFIGYPITLFVEK	**6.820303769**	2	3.751134
P82995	LGIHEDSQNR	**0.921760512**	3	3.456845
P82995	NPDDITNEEYGEFYK	**1.187809759**	2	5.141033
P82995	RAPFDLFENR	**1.023480734**	2	2.414553
P82995	SLTNDWEEHLAVK	**0.975837856**	2	4.009841

P82995	TDTGEPMGR	1.272712336	2	2.536737
P82995	TDTGEPMGR+Oxidation(6)	1.217146191		
P82995	TLTIVDTGIGMTK	0.939529526	2	4.082806
P82995	TLTIVDTGIGMTK+Oxidation(10)	1.196655446		
P82995	YYTSASGDEMVSLK	1.014996782	2	3.855253
P83732	**RL24 60S ribosomal protein L24**	**1.050451065**	**0.22061**	**3**
P83732	AITGASLADIMAK	1.043495346	2	4.100321
P83732	CESAFLSK	1.431596965	2	2.301211
P83732	VELCSFSGYK	1.596756373	2	2.373016
P83868	**TEBP Prostaglandin E synthase 3**	**1.359242765**	**0.04457**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.752126795	3	3.456263
P83868	LTFSCLGGSDNFK	1.216669532	2	2.963548
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**0.9572469**	**0.58135**	**2**
P83941	AMLSGPGQFAENETNEVNFR	0.955120257	2	4.484667
P83941	TYGGCEGPDAMYVK	1.200828975	2	2.820043
P84082	**ARF2 ADP_ribosylation factor 2**	**0.970776538**	**1**	**2**
P84082	NISFTVWDVGGQDK	0.889693006	2	4.573415
P84082	QDLPNAMNAAEITDK	0.919524709	2	4.238098
P84083	**ARF5 ADP_ribosylation factor 5**	**1.151237371**	**0.15029**	**3**
P84083	DAVLLVFANK	1.469805576	2	3.551579
P84083	QDMPNAMPVSELTDK	0.620635181	2	3.038013
P84083	VQESADELQK	0.999684767	2	3.120927
P84089	**ERH Enhancer of rudimentary homolog**	**1.048223891**	**0.99999**	**2**
P84089	ADTQTYQPYNK	1.018719752	2	2.845531
P84089	TYADYESVNECMEGVCK	1.128413806	2	4.376767
P84100	**RL19 60S ribosomal protein L19**	**1.01991007**	**0.27233**	**2**
P84100	LLADQAEAR	1.219314061	2	3.25748
P84100	VWLDPNETNEIANANSR	0.913954787	2	5.359803
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**1.028863085**	**0.7516**	**2**
P84104	AFGYYGPLR	0.950933373	2	2.326913
P84104	VYVGNLGNNGNK	1.062641426	2	2.312838
P84245	**H33 Histone H3.3**	**1.06016354**	**0.99888**	**5**
P84245	DIQLAR	0.912764156	1	1.954342
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	1.089601326	4	6.475613
P84245	RVTIMPKDIQLAR+Oxidation(4)	0.998364148		
P84245	STELLIR	0.865800729	2	2.396577
P84245	YRPGTVALR	1.005039768	2	2.390287
P84817	**FIS1 Mitochondrial fission 1 protein**	**0.962889876**	**0.09754**	**4**
P84817	FQSEQAAGSVSK	0.778926706	2	2.661446
P84817	GIVLLEELLPK	0.845061517	2	2.47952
P84817	GLLQTEPQNNQAK	1.04213032	2	3.404764
P84817	KFQSEQAAGSVSK	0.809946015	2	4.3534
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.812423973**	**7.1E-10**	**16**
P85834	AEAGDNLGALVR	0.822721636	2	3.889097
P85834	DKPHVNVGTIGHVDHGK	0.827410444	3	3.862269
P85834	DLEKPFLLPVESVYSIPGR	1.342711545	2	4.01343
P85834	ELLTEFGYKGEETPVIVGSALCALEQR	1.04637875	3	3.830712
P85834	GDECELLGHNK	1.015014819	2	2.598526
P85834	GEETPVIVGSALCALEQR	0.95919309	2	4.514171
P85834	GITINAAHVEYSTAAR	3.438090724	2	3.56819
P85834	GTVVTGTLER	0.883460849	2	2.818779
P85834	HYAHTDCPGHADYVK	1.43392749	2	4.252855
P85834	KGDECELLGHNK	0.685755641	2	3.707256
P85834	KYEEIDNAPEER	1.020995581	2	3.770941
P85834	LLDAVDTYIPVPTR	0.693474954	2	3.810656
P85834	QIGVEHVVVYVNK	1.100106404	2	2.6654

P85834	TIGTGLVTDVPAMTEEDK	**0.809925839**	2	3.254942
P85834	TIGTGLVTDVPAMTEEDKNIK	**0.825187203**	2	3.503105
P85834	YEEIDNAPEER	**0.743722193**	2	3.4091
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.138756178**	**0.71649**	**10**
P85968	AGQAVDDFIEK	**1.164976239**	2	3.314199
P85968	CLSSLKEER	**1.025731204**	2	2.625907
P85968	FQDTDGKELLPK	**0.929039838**	2	2.954648
P85968	GILFVGSGVSGGEEGAR	**1.84571076**	2	5.384297
P85968	HEMLPANLIQAQR	**0.804873975**	2	2.704418
P85968	LVPLLDTGDIIIDGGNSEYR	**0.884766527**	2	5.130198
P85968	NPELQNLLLDDFFK	**1.287502745**	2	4.459496
P85968	SAVDDCQDSWR	**1.14138793**	2	3.109797
P85968	VGTGEPCCDWVGDEGAGHFVK	**0.922768339**	2	4.455013
P85968	YGPSLMPGGNK	**1.086106637**	2	2.31253
P85971	**6PGL 6_phosphogluconolactonase**	**1.014504449**	**0.99996**	**5**
P85971	DLPAATAPAGPASFAR	**1.067836521**	2	3.196603
P85971	ILEDQESALPAAMVQPR	**0.918871588**	2	4.751103
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	**1.088947272**	2	4.655992
P85971	TGALCWFLDEAAAR	**1.092121646**	2	4.000999
P85971	WTLGFCDER	**0.990651533**	2	2.582484
P85972	**VINC Vinculin**	**0.816439146**	**0.02249**	**8**
P85972	AQQVSQGLDVLTAK	**0.971372615**	2	3.984172
P85972	AVAGNISDPGLQK	**0.891015559**	2	3.106084
P85972	KIDAAQNWLADPNGGPEGEEQIR	**0.739759937**	3	5.229705
P85972	QVATALQNLQTK	**0.849658207**	2	2.989647
P85972	SLLDASEEAIKK	**0.895027769**	2	2.379302
P85972	STVEGIQASVK	**0.874651826**	2	2.444925
P85972	VDQLAAQLADLAAR	**0.837831898**	2	3.093156
P85972	VLQLTSWDEDAWASK	**0.864047721**	2	2.479235
P85973	**PNPH Purine nucleoside phosphorylase**	**0.794066236**	**0.01211**	**11**
P85973	ASHQEVLEAGK	**0.94781904**	2	3.443137
P85973	DHINLPGFCGQNPLR	**0.909283524**	3	4.061932
P85973	ELQEGTYIMSAGPTFETVAESCLLR	**0.898009535**	2	5.300961
P85973	FEVGDIMLIR	**0.702308867**	2	3.277911
P85973	HRPQVAVICGSGLGGLTAK	**0.728856682**	3	6.021018
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	**1.164375158**	3	4.416514
P85973	MLGADAVGMSTVPEVIVAR	**0.599646771**	2	4.660902
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0)	**0.967549517**		
P85973	VFGFSLITNK	**0.970441219**	2	3.361583
P85973	VFHLLGVDTLVVTNAAGGLNPK	**0.924216341**	2	5.22585
P85973	VVMDYNNLEK	**0.802862883**	2	2.637196
P86048	**RL10L 60S ribosomal protein L10_like**	**1.173019291**	**0.84784**	**5**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	**0.917828639**	3	4.144639
P86048	GAFGKPQGTVAR	**1.030940829**	2	2.540185
P86048	MLSCAGADR	**1.087965659**	2	2.322023
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	**1.358757358**	3	4.983397
P86048	VHIGQVIMSIR	**0.82183528**	2	2.800275
P86252		**0.821494559**	**0.02006**	**4**
P86252	AAGSLLTDECR	**0.997374674**	2	3.063311
P86252	ADSAEYSVMTTGGQSSAK	**0.739851549**	2	4.037457
P86252	AEVSELPSVVR	**0.781390538**	2	2.808608
P86252	AISGDLTAEEELER	**1.525515431**		
P86252	ALLTPVAIAAGR	**0.852299764**	2	2.515415
P86252	AMQEINYGPSPDNSIKLVR+Oxidation(1)	**0.785272458**		
P86252	ASMMGQRASLLTAR+Oxidation(2)	**0.812337384**		
P86252	AVAENQPFLIEAMTYR	**0.974047147**	2	4.512483

P86252	AVEIAHALCLTERQIK	**0.856136595**		
P86252	DQMVKNNHFTLK+Oxidation(2)	**0.740575213**		
P86252	EELEKMK	**0.999574806**	1	2.121805
P86252	EIAGATPYITAAEEK	**1.063157231**	2	3.062317
P86252	EKMNKPELFNGGEK+Oxidation(2)	**1.268628151**		
P86252	ELDSITPDITPGWK	**0.704889119**	2	3.436802
P86252	FFRPHFLQAPGDLTVQEGK	**0.900910922**		
P86252	FKLINSTNIR	**0.727432135**		
P86252	GENLVSMTVEGPPPK	**0.935338234**		
P86252	GIEQAVQSHAVAEEEAR	**0.988755722**	2	4.984147
P86252	GNIYSLNEGYAK	**1.059533608**	2	4.063055
P86252	GVYAVGDVCGK	**0.661282539**	1	2.256901
P86252	HLQTYGEHYPLDHFDK	**1.084465681**	3	3.382231
P86252	HVIHTVGPIAVGQPTASQAAELR	**0.744767491**	3	4.892754
P86252	IGHHSTSDDSSAYR	**1.01975096**	3	4.058208
P86252	KAMQEINYGPSPDNSIKLVR	**0.841799172**		
P86252	KGNIYSLNEGYAK	**1.023460663**	2	3.924677
P86252	KHTLIIEGATK	**1.11830044**	2	2.65277
P86252	KLQHELEEAEER	**1.068793275**	2	3.797122
P86252	KVVSDLDVIMSHLK	**0.872058522**		
P86252	LEFIQPNVISGIPIYR	**0.65212584**	2	2.797159
P86252	LFEEQLK	**0.999574806**		
P86252	LGDAVEQGVINNSVLGYFIGR	**0.80493809**	2	4.409735
P86252	LMQVNDTLTSEDAGLR	**0.634966084**		
P86252	LNNIYQNNLTK	**1.106599925**	2	2.995801
P86252	LQHELEEAEER	**0.843887317**	2	3.616211
P86252	MNLQDELDELK	**0.472908432**	2	2.48876
P86252	MNLQDELDELK+Oxidation(0)	**0.97712135**		
P86252	MQQVEASLQPETLK+Oxidation(0)	**0.869542038**		
P86252	NNGYAISTPTSEQYR	**0.784855278**	2	3.662744
P86252	QGQASAQGRAGSQGQAQGR	**0.841738769**		
P86252	QGQIINPSEDPHLPQEEVLK	**0.441966694**	2	2.993174
P86252	QTCLKTVVLLTDNK	**0.298849157**		
P86252	QTITAQNAAVQAVK	**0.97803945**	2	4.087745
P86252	QYLLNQGWWDEEQEK	**0.670965302**	2	3.815337
P86252	RAALQAEIEELR	**0.931933902**	2	3.95424
P86252	SEIQAEQDR	**1.051376596**	2	2.764528
P86252	SLEDALNQTATVTR	**0.7850336**	2	4.29333
P86252	SSSLLAKSPSK	**0.824493274**		
P86252	TLHVEEVVPSVIEPSFGLGR	**1.031412027**	3	3.684277
P86252	TSSAEMPTIPLGSAVEAIR	**0.928070396**	2	4.047329
P86252	TVNVVQFEPNK	**1.674835401**	2	2.448723
P86252	VDDSSGSIGR	**1.258480204**	2	2.619897
P86252	VDGNDVFAVYNATK	**1.529135877**	2	3.957363
P86252	VMEAFEQAER	**0.558925441**	2	3.415471
P86252	VVSQYHELVVQAR	**2.094245664**	2	3.593987
P86252	YNENHQHGK	**1.029831245**		
P86252	YSTSSSSGVTAGK	**0.911835455**	2	2.562317
P86252s	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	**1.305253948**	3	3.802206
P86252s	LEGDLKDLELQADSAVKGR	**0.430365797**		
P86252s	LIDDYGVEEEPAELPEGTSLTVDNKR	**0.764742487**	3	4.302517
P86252s	VASDAQLELDKLDGELKK	**0.849392616**		
P97384	**ANX11 Annexin A11**	**0.908020169**	**0.85236**	**2**
P97384	GFGTDEQAIIDCLGSR	**0.814923764**	2	4.320592
P97384	SELDLLDIR	**0.822474935**	2	2.617257
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**0.880920701**	**0.99971**	**7**

P97519	GFEEAVAAGAK	**0.844685926**	2	3.594613
P97519	GYVSCALGCPYEGK	**0.993398624**	2	4.214695
P97519	KNVNCSIEESFQR	**1.086763021**	2	3.293892
P97519	LIDMLSEAGLPVIEATSFVSPK	**1.017765678**	3	4.579722
P97519	LLEAGDFICQALNR	**0.960648203**	2	4.501926
P97519	NVNCSIEESFQR	**0.995233014**	2	3.655052
P97519	WVPQMADHSDVLK	**0.85673751**	2	2.797295
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**0.767782395**	**0.00441**	**7**
P97521	CLLQIQASSGK	**0.733783865**	1	2.917691
P97521	EEGVTSLYK	**0.88807296**	1	2.024671
P97521	KLYQEFGIR	**0.697245534**	2	2.533414
P97521	LQTQPPSLPGQPPMYSGTIDCFR	**0.89517316**	2	4.041005
P97521	LYQEFGIR	**0.758649758**	2	2.60825
P97521	SVHDLSVPR	**0.805249885**	2	2.594274
P97521	YSGTLDCAK	**0.950918274**	2	2.345995
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.02076349**	**0.17086**	**14**
P97524	GEVGLLICK	**0.725717565**	2	2.62281
P97524	ITELTPFFGYAGGK	**1.321849892**	2	2.924391
P97524	SEVTFTTPAVYIYTSGTTGLPK	**5.944581651**	2	2.995711
P97524	SLLHCFQCCGAK	**0.917442026**	2	2.73525
P97524	TILHVFLEQAR	**0.948034913**	3	3.314967
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	**1.023083983**	3	4.804519
P97524	TYVPMTEDIYNAIIDK	**0.997088954**	3	4.141877
P97524	VDGVSADPIPESWR	**1.551498477**	2	3.059649
P97524	VLLASPELHEAVEEVLPTLK	**1.035343403**	3	4.220395
P97524	VTLMEEGFNPSVIK	**1.265176908**	2	3.992028
P97524	YDVEKDEPVR	**1.015066507**	2	3.115143
P97524	YDVEKDEPVRDANGYCIK	**1.233627835**	3	3.612456
P97524	YLCNTPQKPNDR	**1.287291758**	2	3.058653
P97524	YNATVIQYIGELLR	**0.872685394**	2	4.166836
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**0.924850228**	**2.4E-14**	**9**
P97532	AFGHHSVSLLDGGFR	**0.792158801**	2	3.540091
P97532	ALVSAQWVAEALK	**0.783073185**	2	4.239162
P97532	AQPEHVISQGR	**0.893210917**	2	2.849282
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	**1.288607062**	3	6.738776
P97532	FQGTQPEPR	**0.862711858**	2	2.820221
P97532	LLDASWYLPK	**0.989809874**	2	3.828099
P97532	SPSEPAEFCAQLDPSFIK	**0.823096175**	2	3.001405
P97532	THEDILENLDAR	**0.826535366**	2	3.252385
P97532	YWLSQNLPISSGK	**0.786724883**	2	3.75554
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.072829482**	**0.29449**	**8**
P97536	AADIDQEVK	**1.357327831**	2	2.487307
P97536	EGPAVVGQFIQDVK	**1.508479599**	2	3.104601
P97536	FTISDHPQPIDPLLK	**1.371355401**	2	2.399117
P97536	ITSEALLVTQQLVK	**0.787402304**	2	2.703396
P97536	LTLIDPETLLPR	**1.197241263**	2	2.801983
P97536	SVILEAFSSPSEEVK	**1.016457414**	2	2.764555
P97536	TLEDPDLNVR	**0.984709094**	2	2.308181
P97536	TYIQCIAAISR	**0.948286472**	2	2.959081
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.279095894**	**2.7E-11**	**20**
P97562	ATASCTYEGENTVLYLQVAR	**2.070200106**	2	3.932951
P97562	ATFADFCAQGAEICR	**1.441807425**	2	4.969956
P97562	CSAQTAADFR	**1.733196342**	2	2.989659
P97562	DFSLLPELHALSTGMK	**0.753033588**	2	2.378968
P97562	EAFLDLLPLIR	**1.020321135**	2	2.878322

P97562	EELYEDAIQK	**1.303625879**	2	2.367866
P97562	FAEVLPDGTYQR	**0.89595875**	2	2.753202
P97562	HSPSFSVER	**1.158626391**	2	2.410936
P97562	ILEYQTQQQK	**1.087692175**	2	3.814326
P97562	KVESIIQSDPVFNLK	**1.015382196**	2	4.956357
P97562	LDKEPEIQR	**1.100494724**	2	2.698369
P97562	LFEWAQK	**0.806464133**	2	2.455192
P97562	LGTPQSNYLGMLVTR	**1.077811109**	2	3.51787
P97562	LTNILDGGLPNTVLR	**1.214290352**	2	4.660285
P97562	MGLEHIDNGFLQLNHVR	**1.214859606**	3	4.276673
P97562	SGVDQHDAWNQTTVIHLQAAK	**1.310028785**	3	6.127796
P97562	SLEDHTPLPGITVGDIGPK	**1.090595484**	3	4.6145
P97562	SLGSDEQIAK	**1.105620751**	2	2.630379
P97562	VESIIQSDPVFNLK	**1.219273903**	2	4.25094
P97562	VLDGNVNLSLHGVAMNAIR	**0.62969815**	2	3.217199
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.297927953**	**0.84732**	**3**
P97576	ALADTENLR	**1.034632916**	2	2.652947
P97576	DLLEVADILEK	**1.455278841**	2	3.208895
P97576	TLRPALVGVVK	**1.03736439**	2	2.532409
P97584	**PTGR1 Prostaglandin reductase 1**	**0.633083698**	**9.9E-20**	**5**
P97584	ALTDLMNWVSEGK	**0.786759214**	2	4.106936
P97584	GGETVLVNAAAGAVGSVVGQIAK	**0.69279728**	2	5.645947
P97584	HFEGFPTDSNFELR	**0.634060886**	2	3.738657
P97584	TGPCPPGPSPEVIIYQQLR	**1.094130768**	2	4.031363
P97584	YHEYITEGFEK	**0.622594754**	2	2.835616
P97608	**OPLA 5_oxoprolinase**	**0.961837377**	**0.95556**	**11**
P97608	AGDFGAAFVER	**0.893441181**	2	3.01052
P97608	GGPVTVTDANLVLGR	**1.10441784**	2	2.737121
P97608	GHTACADAYLTPTIQR	**1.000693637**	2	3.424024
P97608	GSILDPSPEAAVVGGNVLTSQR	**1.036550359**	2	4.799467
P97608	ISVGAEGPSMADTR	**0.78120978**	2	2.705291
P97608	ISVGAEGPSMADTR+Oxidation(9)	**1.38608343**		
P97608	ITDPEILESR	**0.293131649**	2	2.644432
P97608	LLSEDPANYADAPTEGIR	**0.94000851**	2	4.303636
P97608	SGLFVVGPESAGAHPGPACYR	**0.701616046**	2	3.774463
P97608	SGLQLEDTPK	**1.112283288**	2	2.505929
P97608	TGDLLEIQQPVDLEALR	**1.015922743**	2	4.335544
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.09591365**	**0.8984**	**7**
P97612	FMREVEQLMTPQK+Oxidation(8)	**1.153379548**		
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	**0.852164451**	3	4.687197
P97612	GTNCVTSYLTDCETQLSQAPR	**1.191453903**	2	4.940621
P97612	GYFGDIWDIILK	**0.879606785**	2	3.012081
P97612	LQSGELSPEAVFFTYLGK	**1.229899099**	2	4.712319
P97612	NSVGLPVAVQCVALPWQEELCLR	**1.052623136**	2	4.173378
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	**1.315309714**	2	4.759167
P97697	**IMPA1 Inositol monophosphatase 1**	**1.089972542**	**0.03178**	**2**
P97697	SLLVTELGSSR	**0.801700612**	2	2.370705
P97697	SSPADLVTVTDQK	**1.391642446**	2	2.782658
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**0.766886235**	**0.0063**	**4**
P97700	AVVVNAAQLASYSQSK	**0.766328389**	2	4.764484
P97700	GIYTGLSAGLLR	**0.722799489**	2	2.838662
P97700	LGIYTVLFER	**0.81291103**	2	2.725049
P97700	LTGADGTPPGFLLK	**0.930577893**	2	3.152544
P97840	**LEG9 Galectin_9**	**2.266529077**	**9.9E-20**	**2**
P97840	NTQINNSWGPEER	**2.262297779**	2	2.45388
P97840	SINISGVVLPDAK	**2.785785865**	2	3.382073

P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.919743848**	**0.29726**	**21**
P97852	AVANYDSVEAGEK	**1.128342419**	2	4.025462
P97852	AYALAFAER	**1.091177115**	2	3.573151
P97852	CEAVIADILDK	**3.037654903**	2	2.462658
P97852	DTTSLNQAALYR	**1.509071865**	2	2.474168
P97852	FVYEGSADFSCLPTFGVIVAQK	**0.704093266**	2	4.482731
P97852	GALVVVNDLGGDFK	**1.543320624**	2	4.382337
P97852	GSSAADKVVEEIR	**0.89079706**	2	2.719899
P97852	HVLQQFADNDVSR	**1.069964203**	2	4.46525
P97852	ICDFSNASKPK	**1.167640786**	3	3.767988
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	**0.878923582**	3	5.501728
P97852	IDVVVNNAGILR	**0.840816733**	2	3.404274
P97852	ISDEDWDIIQR	**0.958236864**	2	3.788776
P97852	KNNIHCNTIAPNAGSR	**0.987906244**	2	4.858433
P97852	LNPQNAFFSGR	**1.18630457**	2	2.634136
P97852	NGSGEVYQGPAK	**1.296359137**	2	3.084965
P97852	NNIHCNTIAPNAGSR	**1.165950153**	2	4.571816
P97852	SIQESTGGIIEVLHK	**0.874342931**	2	4.006524
P97852	SLMSGGLAEVPGLSINFAK	**0.819112386**	2	3.042466
P97852	VLHGEQYLELYKPLPR	**0.898733849**	2	4.40263
P97852	VNAVFEWHITK	**1.317127725**	2	2.518687
P97852	VVLVTGAGGGLGR	**0.984730965**	2	3.716695
Q00238	**ICAM1 Intercellular adhesion molecule 1**	**1.005342281**	**0.99473**	**2**
Q00238	LDTPDLLEVGTQQK	**0.941660256**	2	3.083777
Q00238	VELDPLPAWQQVGK	**1.030163725**	2	2.946469
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.021306508**	**0.99902**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	**1.028990408**	2	4.195621
Q00438	KLPSDVTEGEVISLGLPFGK	**0.940122536**	2	4.71256
Q00438	LSLDGQNIYNACCTLR	**1.014240564**	2	3.539298
Q00438	NNQFQALLQYADPVSAQHAK	**1.051269921**	2	5.648084
Q00780	**chain**	**0.936737876**	**0.02299**	**4**
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(3)	**1.639835461**		
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(5)	**1.639835461**		
Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	**0.756198123**		
Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	**0.756198123**		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**0.997694057**	**0.18352**	**3**
Q00PI9	AVEEQGDDQDSEK	**1.025270833**	2	3.826132
Q00PI9	EEAQPIVTKYK	**1.871612936**	1	1.944967
Q00PI9	SGDETPGSEAPGDK	**0.757770821**	2	2.854772
Q01177	**PLMN Plasminogen**	**0.854745496**	**0.35189**	**3**
Q01177	ILGSDVQQIAVTK	**0.851135554**	2	3.72667
Q01177	LVLEPNDADIALLK	**0.871885547**	2	2.585154
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	**0.869384807**	3	4.320611
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**0.980283601**	**0.00165**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	**0.894513161**	2	6.318629
Q01205	NDVITVQTPAFAESVTEGDVR	**0.985816558**	2	5.202766
Q01205	NVETMNYADIER	**1.031209904**	2	3.414136
Q01205	VEGGTPLFTLR	**0.826418502**	2	3.219785

Q01405	**SC23A Protein transport protein Sec23A**	**1.179211274**	**2.1E-06**	**4**
Q01405	AETEEGPDVLR	**1.07449012**	2	2.906969
Q01405	AVLNPLCQVDYR	**1.048650314**	2	2.731359
Q01405	HLLQAPVDDAQEILHSR	**1.24808205**	3	5.625575
Q01405	YIDTEHGGSQAR	**1.601515637**	2	3.281142
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.952252149**	**9.9E-20**	**31**
Q02253	AEMEAAVAACK	**0.733054825**	2	3.806141
Q02253	AEMEAAVAACK+Oxidation(2)	**0.665687063**		
Q02253	AFPAWADTSILSR	**0.816377088**	2	4.002167
Q02253	AISFVGSNQAGEYIFER	**0.9987883**	2	5.175509
Q02253	CMALSTAVLVGEAK	**0.763853126**	2	4.501402
Q02253	CMALSTAVLVGEAK+Oxidation(1)	**0.964181466**		
Q02253	EEDATLSSPAVVMPTMGR	**0.653144222**	2	4.306534
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12)	**0.809591341**		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15)	**1.033985384**		
Q02253	EGASILLDGR	**0.944980124**	2	2.541578
Q02253	ENTLNQLVGAAFGAAGQR	**0.874003671**	2	5.499629
Q02253	GDTNFYGK	**0.886389758**	2	2.444874
Q02253	GLQVVEHACSVTSLMLGETMPSITK	**0.726790433**	2	5.593545
Q02253	GYENGNFVGPTIISNVKPSMTCYK	**0.760766509**	3	3.931876
Q02253	IVNDNPYGNGTAIFTTNGAIAR	**0.841116858**	2	5.41856
Q02253	LITLEQGK	**0.894394327**	2	2.815262
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	**1.878738831**	3	4.297335
Q02253	NHGVVMPDANK	**0.866455532**	1	3.367598
Q02253	NHGVVMPDANK+Oxidation(5)	**1.475755717**		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	**0.64246808**	3	6.170986
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5)	**0.750915779**		
Q02253	QGIQFYTQLK	**1.024237476**	2	2.723757
Q02253	SDKWIDIHNPATNEVVGR	**0.742671859**	2	5.280058
Q02253	TITSQWK	**0.852866008**	2	2.52672
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	**0.610031079**	2	5.272245
Q02253	TLADAEGDVFR	**0.615594733**	2	3.487832
Q02253	VCNLIDSGAK	**0.8543359**	2	3.481856
Q02253	VNAGDQPGADLGPLITPQAK	**0.772490006**	2	5.73663
Q02253	WIDIHNPATNEVVGR	**0.715047036**	2	4.919349
Q02253	WLPELVER	**0.689063039**	2	2.503947
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	**0.613028921**	3	4.01954
Q02769	**FDFT Squalene synthase**	**1.01118259**	**0.62915**	**4**
Q02769	KLEDFVKPENVDVAVK	**0.855122647**	3	4.031358
Q02769	SFAAVIQALDGDIR	**0.862262078**	2	3.208762
Q02769	TQSLPNCQLISR	**0.742755999**	2	2.720667
Q02769	VVLEDFPTISLEFR	**0.857131464**	2	3.461503
Q02874	**H2AY Core histone macro_H2A.1**	**0.938469177**	**0.00115**	**3**
Q02874	AASADSTTEGAPTDGFTVLSTK	**1.812971407**	2	4.435774
Q02874	GVTIASGGVLPNIHPELLAK	**0.824590296**	2	4.139748
Q02874	NGPLEVAGAAVSAGHGLPAK	**0.722418799**	2	3.318297
Q02974	**KHK Ketohexokinase**	**1.27726215**	**0.99938**	**9**
Q02974	FGCQVAGK	**2.947047697**	2	2.540273
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	**0.968198779**	3	5.735806
Q02974	GGNASNSCTVLSLLGAR	**1.059719464**	2	4.686769
Q02974	GNSMQEALR	**0.905492858**	2	3.038121
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	**0.909614552**	3	5.765394
Q02974	IEQYNATQPLQQK	**1.223089552**	2	4.874523
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	**1.125009263**	3	5.239995
Q02974	TIILYDTNLPDVSAK	**0.924392596**	2	5.020726

Q02974	VSVEIEKPR	**1.091051186**	2	2.374932
Q03248	**BUP1 Beta_ureidopropionase**	**1.129449093**	**9.9E-20**	**12**
Q03248	AHHDLGYFYGSSYVAAPDGSR	**1.411836338**	2	6.272588
Q03248	EKLPWTEFAESAEDGLTTR	**1.024602686**	3	4.716307
Q03248	ELAEAVKPNYSPNIVK	**1.151905527**	2	4.28682
Q03248	HNMVVISPILER	**0.592467208**	2	2.940649
Q03248	HNMVVISPILER+Oxidation(2)	**1.248615747**		
Q03248	IPLPTSAPVAEQVSALHK	**1.791592665**	3	4.797505
Q03248	KHNMVVISPILER	**0.894031679**	2	2.932451
Q03248	KHNMVVISPILER+Oxidation(3)	**0.931902717**		
Q03248	NAAIANHCFTCALNR	**1.122944677**	2	4.462059
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	**1.467495537**	3	5.643678
Q03248	VGQEHYPNEFTSGDGK	**1.195682306**	2	4.244584
Q03248	VGQEHYPNEFTSGDGKK	**1.056597767**	3	4.940723
Q03336	**RGN Regucalcin**	**0.685621179**	**9.9E-20**	**16**
Q03336	CGESPVWEEASK	**0.781766096**	2	4.676763
Q03336	CLLFVDIPSK	**1.000344163**	2	3.32637
Q03336	DEQIPDGMCIDVEGK	**0.776387865**	2	4.613037
Q03336	DYSEMYVTCAR	**1.328657162**	2	2.767431
Q03336	FNDGKVDPAGR	**0.785048965**	2	2.721576
Q03336	HQGSLYSLFPDHSVK	**1.323936865**	2	4.72393
Q03336	KYFDQVDISNGLDWSLDHK	**0.861715846**	3	5.688782
Q03336	LWVACYNGGR	**0.968219025**	2	2.983313
Q03336	MEKDEQIPDGMCIDVEGK	**0.71130221**	2	5.107283
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0)	**0.813249678**		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10)	**0.818307193**		
Q03336	QSGGYVATIGTK	**0.887094786**	2	2.891176
Q03336	VGVDAPVSSVALR	**0.85239572**	2	3.795334
Q03336	YFAGTMAEETAPAVLER	**0.815498516**	2	5.590406
Q03336	YFAGTMAEETAPAVLER+Oxidation(5)	**0.900051854**		
Q03336	YFDQVDISNGLDWSLDHK	**0.717884671**	3	4.381349
Q03410	**SYCP1 Synaptonemal complex protein 1**	**0.792274493**	**0.08435**	**2**
Q03410	ISEEKLLGEVEK	**1.000875638**	2	2.306461
Q03410	MEQENTAILTDKK+Oxidation(0)	**0.770774987**		
Q03626	**MUG1 Murinoglobulin_1**	**0.814699172**	**1.1E-05**	**6**
Q03626	EESSCIHSSCTAER	**0.976562428**	2	3.901366
Q03626	GGEFEMMPLGVNK	**0.616706401**	2	3.138592
Q03626	LTAQPAPSPEDLALSMGTIK	**0.638427827**	3	4.647064
Q03626	NLHPLNELFPLAYIEDPK	**1.206091788**	3	4.434322
Q03626	VQTVPLTCNNPK	**0.656956565**	2	2.902613
Q03626	VYHKEESSCIHSSCTAER	**0.971604366**	3	4.376818
Q04462	**SYVC Valyl_tRNA synthetase**	**1.1375738**	**0.74893**	**6**
Q04462	ADFPAGIPECGTDALR	**1.164239067**	2	2.420991
Q04462	ALNPLEEWLR	**1.011416563**	2	2.541792
Q04462	ITPAHDQNDYEVGQR	**1.162472897**	2	3.35845
Q04462	LQQTEAELR	**1.393136369**	2	2.360418
Q04462	SVTQQPGSEITAPQK	**0.898521227**	2	3.157324
Q04462	VQGSDSDEEVVVATTR	**0.870789329**	2	3.938783
Q05096	**MYO1B Myosin_Ib**	**1.175127447**	**4.1E-05**	**2**
Q05096	LEDLATLIQK	**0.677725717**		
Q05096	NAMQIVGFSDPEAESVLEVVAAVLK	**1.177144009**		
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**1.054429286**	**0.71938**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(0)	**0.851262294**		
Q05144	YLECSALTQR	**1.068859041**	2	2.977731
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**0.799360009**	**0.44324**	**9**
Q06647	FSPLTANLMNLLAENGR	**1.038627052**	3	4.128219

Q06647	GEVPCTVTTAFPLDEAVLSELK	**0.882204516**	3	5.819669
Q06647	GQILNLEVK	**1.056416822**	2	2.480382
Q06647	LGNTQGVISAFSTIMSVHR	**0.892290227**	3	3.331209
Q06647	LVRPPVQVYGIEGR	**2.621386758**	3	3.537324
Q06647	TDPSIMGGMIVR	**0.775294355**	2	3.22957
Q06647	TVLNSFLSK	**0.831319713**	2	3.019607
Q06647	VSLAVLNPYIK	**1.187413965**	2	3.061923
Q06647	YATALYSAASK	**7.519198722**	2	3.433251
Q07071	**GCKR Glucokinase regulatory protein**	**1.16465667**	**0.21442**	**14**
Q07071	AAPISCHVQVAHEK	**1.092193814**	2	4.917322
Q07071	CLLEILR	**1.143302087**	2	2.620968
Q07071	GFLIGDHSDMFNQK	**1.31542113**	2	3.540482
Q07071	GLGQKPLYTYLIAGGDR	**3.127000023**	2	3.116616
Q07071	LLGQCDAEIFQEEGQIVPTYQR	**1.891864135**	2	5.07553
Q07071	LYSESVLTTMLQVAGK	**1.054534989**	2	2.609931
Q07071	NDPIEDWR	**0.920568572**	1	1.903314
Q07071	QEAFVLNPAIGPEGLSGSSR	**0.423948238**	2	3.052136
Q07071	STQALEDPPACGTLN	**1.253549126**	2	2.404625
Q07071	TVDQGVVSSQR	**1.078127182**	2	3.528949
Q07071	VIPTALLSLLLR	**1.169761565**	2	3.557179
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	**1.202109712**	2	5.32788
Q07071	WVLNTVSTGAHVLLGK	**0.65024989**	2	2.746226
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	**1.249755596**	3	5.562906
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.731736883**	**0.02153**	**7**
Q07116	AVDDSYNVQPDTVAPIWNLR	**0.721732391**	2	4.616793
Q07116	FVDLHPGGQSK	**0.729677186**	2	2.438539
Q07116	LCDVLAQAGHR	**0.626211765**	2	2.992418
Q07116	MSPPLEASDPYSNDPMR	**0.691506421**	2	2.676604
Q07116	NHLPVPNLDPDTYR	**0.68091377**	2	2.479079
Q07116	VSVESEESYSHWQR	**0.926348419**	2	3.742706
Q07116	VVVPGVVGAR	**0.489538361**	2	2.441212
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.680677516**	**9.9E-20**	**10**
Q07523	ALKEEKPTQSVPVSFPK	**0.514258877**	3	4.584561
Q07523	ALVITIDTPVLGNR	**0.568627262**	2	4.477938
Q07523	ASFCWNDLSLLQSITR	**0.857050272**	2	4.09175
Q07523	EEKPTQSVPVSFPK	**0.742888809**	2	2.963409
Q07523	EVLDILTAELHR	**0.639474335**	2	3.241111
Q07523	GEDGVKEVLDILTAELHR	**0.664679601**	3	5.187481
Q07523	HNVQGIVVSNHGGR	**0.573260362**	3	6.118731
Q07523	NQLNLEANILLK	**0.560426561**	2	3.470214
Q07523	QLDEVSASIDALR	**0.515527739**	2	3.07338
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	**1.339471628**	3	4.638498
Q07803	**EFGM Elongation factor G_ mitochondrial**	**1.183853614**	**0.51359**	**3**
Q07803	GIIDLIEER	**1.43046424**	2	2.701093
Q07803	LEFSDETFGANVPK	**1.031227988**	2	3.698801
Q07803	YQPCSPSTQEELVNK	**1.278839149**	2	3.262235
Q07936	**ANXA2 Annexin A2**	**0.872080118**	**0.28665**	**2**
Q07936	GLGTDEDSLIEIICSR	**0.81218006**	2	3.027557
Q07936	GVDEVTIVNILTNR	**0.871465394**	2	4.110605
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.065054194**	**0.26197**	**3**
Q07984	FFDEESYSLLR	**1.197938297**	2	3.539228
Q07984	NNEDVSIIPPLFTVSVDHR	**0.993002902**	3	3.918537
Q07984	VQNMALYADVSGK	**1.320700672**	2	3.255476
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**0.921403572**	**0.10846**	**8**
Q08163	ALLVTASQCQQPAGNK	**0.789165616**	2	4.680972
Q08163	GAVPYVQAFDSLLANPVAEYLK	**1.221939991**	3	3.773344

Q08163	LEAVSHTSDMHCGYGDSPSK	**1.030183084**	3	4.858672
Q08163	LSDLLAPISEQIQEVITFR	**1.08368824**	2	3.428841
Q08163	NSLDCEIVSAK	**0.974081717**	2	3.08192
Q08163	SALFAQINQGESITHALK	**0.690305435**	2	3.81525
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	**0.867071702**	2	3.668366
Q08163	VENQENVSNLVIDDTELK	**0.838481431**	2	4.824555
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**0.979645867**	**0.94744**	**4**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	**1.086263535**	3	4.904198
Q08415	ILVLNTPNNPLGK	**1.024931695**	2	3.055063
Q08415	LGASNDWQLDPAELASK	**0.644659342**	2	3.342516
Q08415	RLDGIDQNLWVEFGK	**0.870305099**	2	2.932952
Q09073	**ADT2 ADP/ATP translocase 2**	**1.274355461**	**0.55938**	**7**
Q09073	DFLAGGVAAAISK	**1.329200577**	2	4.769534
Q09073	EQGVLSFWR	**2.007652125**	1	1.908197
Q09073	GLGDCLVK	**0.968366724**	2	2.582445
Q09073	GTDIMYTGTLDCWR	**1.247802074**	2	3.633347
Q09073	KGTDIMYTGTLDCWR	**0.907324517**	2	3.369285
Q09073	LLLQVQHASK	**0.788022013**	2	2.74865
Q09073	QIFLGGVDK	**0.871424259**	2	2.682165
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.887795382**	**0.43545**	**6**
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	**0.528724875**	2	3.742505
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	**0.880124821**	3	3.645275
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	**0.995939042**	3	4.635373
Q0D2L3	SVDEGLLDSK	**1.062505178**	2	2.982182
Q0D2L3	SVDEGLLDSKR	**0.808486324**	2	2.664193
Q0D2L3	VADLGNVNVNLYNLQDSCR	**1.220127512**	2	5.410556
Q0VAV2	**EXPH5 Exophilin_5**	**0.710735658**	**0.4987**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1)	**0.617334992**		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)	**0.48922017**		
Q0VGK3	**GLCTK Glycerate kinase**	**1.027774356**	**1.1E-16**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	**0.62383969**	3	5.882719
Q0VGK3	GATIQELNTIR	**0.829378311**	2	2.921111
Q0VGK3	QLFDSAVGAVQPGPMLQR	**1.033053971**	2	3.81942
Q0ZHH6	**ATLA3 Atlastin_3**	**1.178274896**	**0.92036**	**4**
Q0ZHH6	EHGHSNWLGDPEEPLTGFSWR	**1.003135283**	3	4.070914
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	**0.988801465**	2	4.557232
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2)	**1.252579236**		
Q0ZHH6	YQQELEEEITELYENFCK	**1.148543888**	2	4.759522
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.941278007**	**9.9E-20**	**25**
Q10758	AEAETMYQIK	**0.929599542**	2	3.403797
Q10758	AQYEEIANR	**0.846723893**	2	3.051852
Q10758	ATLEAAIADAEQR	**0.737808209**	2	4.638978
Q10758	ELQSQISDTSVVLSMDNSR	**1.030962499**	2	5.746842
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	**0.788047529**	2	4.486948
Q10758	LEGLTDEINFLR	**0.720379105**	2	4.255579
Q10758	LESGMQNMSIHTK	**0.652453581**	2	3.778391
Q10758	LEVDPNIQAVR	**0.843344513**	2	3.735526
Q10758	LEVELGNMQGLVEDFK	**0.785888618**	2	5.06192
Q10758	LKLEVELGNMQGLVEDFK	**0.965893452**	3	4.004301
Q10758	LQAEIDALK	**0.859551438**	2	2.746445
Q10758	LVSESSDIMSK	**0.729056489**	2	3.012508
Q10758	QIHEEEIR	**0.845347444**	1	2.329552
Q10758	QLEALGQEK	**0.725764283**	1	2.260305
Q10758	RQLEALGQEK	**1.019443963**	2	2.326897
Q10758	SKTEISEMNR	**0.790777864**	3	3.435024
Q10758	SKTEISEMNR+Oxidation(7)	**1.295014262**		

Q10758	SLDMDSIIAEVR	**0.710701407**	2	4.583012
Q10758	SNMDNMFESYINNLR	**1.335645506**	2	4.085135
Q10758	SRAEAETMYQIK	**0.790996618**	2	3.519465
Q10758	TEISEMNR	**0.858309385**	2	2.487784
Q10758	TEMENEFVLIK	**0.782321002**	2	3.333536
Q10758	TEMENEFVLIK+Oxidation(2)	**0.909468882**		
Q10758	WSLLQQQK	**0.968119232**	2	2.915474
Q10758	YEELQTLAGK	**0.818878197**	2	3.700737
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**0.782069313**	**0.00544**	**2**
Q148W0	FMAASVASSNRDEALDK+Oxidation(1)	**0.77554423**		
Q148W0	TCEVIKDGRFK	**0.782210252**	1	2.209782
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.910846529**	**0.01648**	**6**
Q14DH7	IAIIYDSPVTDTK	**1.028164434**	2	2.43253
Q14DH7	STLSALVNGKPYK	**0.889302279**	2	2.816439
Q14DH7	THFAASVADPER	**0.930082157**	2	3.603552
Q14DH7	VDDVINVAGHR	**0.785990757**	2	3.394854
Q14DH7	VLAEHGVAALFTAPTAIR	**0.73974241**	2	3.773319
Q14DH7	VTPTIEDPSIFGHIEEVLK	**0.810667026**	2	3.405083
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.824452357**	**2.9E-14**	**12**
Q1HCL7	ALNEVFIGESLSSR	**0.669526572**	2	3.101025
Q1HCL7	ASYYEISVDDGPWEK	**0.849784499**	2	3.25054
Q1HCL7	LKPVIGVNTDPER	**0.786174849**	3	3.598658
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	**0.725916032**	3	5.227853
Q1HCL7	NVEHIIDSLRDEGIEVR	**0.637036347**	2	3.463174
Q1HCL7	QGNLTLPLNK	**0.638332977**	2	3.024254
Q1HCL7	SEASGPQLLPVR	**0.900947736**	2	3.419453
Q1HCL7	SEGHLCLPVR	**0.738855932**	2	2.345104
Q1HCL7	SSGLNLCTGTGSK	**0.714197435**	2	3.592942
Q1HCL7	VTNEYNESLLYSPEEPK	**1.038940646**	2	4.44559
Q1HCL7	YEFEQQR	**0.975348657**	2	2.535376
Q1HCL7	YTHSFPEALQK	**0.697581318**	2	2.662583
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.039448007**	**0.00059**	**5**
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	**1.484211237**	3	3.472024
Q1JU68	FNVLQYVVPEVK	**1.249064776**	2	3.160152
Q1JU68	ILQEHEQIK	**0.908089307**	2	2.671459
Q1JU68	KGPEADSEWR	**0.816340511**	2	2.563402
Q1JU68	LLDMDGIIVEK	**0.850777598**	2	2.905599
Q29RW1	**MYH4 Myosin_4**	**0.823668075**	**0.70987**	**15**
Q29RW1	AGLLGTLEEMRDEK	**0.921767167**	2	2.416799
Q29RW1	ELENEVENEQK	**0.570960727**	2	2.420846
Q29RW1	ELENEVENEQKR	**0.476271392**	2	2.990504
Q29RW1	LINELSAQK	**0.711274266**	2	2.789417
Q29RW1	LQDAEEHVEAVNSK	**0.879390375**	2	4.478714
Q29RW1	LQDLVDKLQTK	**0.785816379**	1	2.103887
Q29RW1	MEGDLNEMEIQLNHANR	**0.664333959**	2	4.315431
Q29RW1	MEIDDLASNMETVSK	**0.817199519**	2	4.295159
Q29RW1	NAYEESLDQLETLK	**0.431473841**	2	4.811811
Q29RW1	NAYEESLDQLETLKR	**0.930082358**	2	3.791671
Q29RW1	QKYEETQAELEASQK	**1.29383619**	2	3.587818
Q29RW1	SELQASLEEAEASLEHEEGK	**0.82648331**	2	4.69357
Q29RW1	SNAACAALDK	**0.741374496**	2	2.313639
Q29RW1	TLEDQLSEVK	**0.692691768**	2	2.460041
Q29RW1	VAEQELLDASER	**0.766852965**	2	2.686498
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**0.954824607**	**0.9859**	**2**

Q2EMV9	LQEELTR	**0.953402333**	1	2.000205
Q2EMV9	VLVEFEKESLNIAGK	**0.969136229**	2	2.446773
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**0.720900684**	**0.37357**	**2**
Q2TA68	TSVLEMIAQAR	**0.705499367**	2	3.265171
Q2TA68	VIQHNALEDR	**0.837336298**	2	2.341963
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**0.839437834**	**0.07296**	**7**
Q2V057	EDCTQPDYEATSR	**0.831848915**	2	3.782402
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	**1.008964036**	2	4.489268
Q2V057	NLQLSCLSTEQNQHLQASLSR	**0.738043167**	2	5.577103
Q2V057	REQALLSQELWR	**0.968043873**	2	3.060992
Q2V057	SIPYGCLEEVIPYLIR	**1.666813378**	2	3.612137
Q2V057	SVTQLHGKEDCTQPDYEATSR	**0.643782727**	3	3.729579
Q2V057	TSEAWYEGNLSAMLHCVDLSR	**0.951981322**	2	2.737828
Q32Q06	**AP1M1 AP_1 complex subunit mu_1**	**0.866742051**	**0.54429**	**2**
Q32Q06	HNNLYLVATSK	**1.073561453**	2	2.411808
Q32Q06	MRVFLSGMPELR+Oxidation(0)	**0.803865811**		
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**0.854388393**	**0.24289**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	**0.774631834**	3	4.691477
Q3B7D0	HCDDSYTPQDK	**1.027952894**	2	3.089515
Q3B7D0	LEEDGDELAR	**0.915653617**	2	2.499826
Q3B7D0	TCAEAVVPSYVPIVK	**0.949930701**	2	3.190239
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**0.852554628**	**1.1E-15**	**4**
Q3B7U9	SCSQVLEHQPDNIK	**0.664848902**	2	4.108989
Q3B7U9	TAEDGPDLEMLSGQER	**1.226491093**	2	3.801841
Q3B7U9	VDMTCEEEEELLQLK	**0.837617564**	2	4.211577
Q3B7U9	VLAQQGEYSEAIPILR	**0.617588609**	2	3.131577
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**0.898864544**	**0.97925**	**3**
Q3KRD8	ASFENNCEVGCFAK	**1.151285047**	2	2.843504
Q3KRD8	HGLLVPNNTTDQELQHIR	**0.868125147**	3	4.840389
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	**0.882935725**	2	3.827856
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.059109225**	**0.37985**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	**0.744199773**	2	3.244584
Q3KRE0	ISVLEALR	**0.629983214**	2	2.364279
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**0.972560556**	**0.65279**	**2**
Q3KRE8	ALTVPELTQQMFDSK	**1.154707157**	2	3.316341
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**0.875395578**	3	4.180816
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**0.700492339**	**0.00053**	**2**
Q3MIB4	MEIIQVPGYTQEEK	**0.438828428**	2	3.596625
Q3MIB4	TVGVNNPVFLLDEVDK	**0.755918111**	2	3.608235
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**0.829248914**	**4.3E-08**	**7**
Q3MIE0	DGQEGIEAFIQK	**0.959652222**	2	3.310794
Q3MIE0	KVALEMLFTGEPISAQEALR	**1.559300294**	3	3.504132
Q3MIE0	SDILHEAESEDLK	**0.837240543**	3	3.739595
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	**1.065315181**	2	4.646878
Q3MIE0	VALEMLFTGEPISAQEALR	**0.953324515**	2	3.375892
Q3MIE0	VIIISAEGPVFSSGHDLK	**0.776254723**	2	4.28749
Q3MIE0	VVPEEQLEEEATR	**0.734754655**	2	4.144634
Q3MIF4	**XYLB Xylulose kinase**	**0.89659002**	**0.07009**	**7**
Q3MIF4	AFHGLAGGTGVAFSEVVK	**1.207059514**	2	2.323471
Q3MIF4	CCLGWDFSTQQVK	**0.897622443**	2	2.942708
Q3MIF4	FNADNMEVSAFPGDVEIR	**0.807012683**	2	4.04073
Q3MIF4	IRDESASCSWNK	**0.820261556**	2	4.094701
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	**1.419876353**	2	4.378472

Q3MIF4	VVAFTGDNPASLAGMR	**0.904466209**	2	3.668159
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	**0.893591551**	2	5.297771
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**0.931555199**	**0.21933**	**4**
Q3T1J1	EDLRLPEGDLGK	**0.59787663**	2	2.813557
Q3T1J1	EDLRLPEGDLGKEIEQK	**0.878221312**	3	4.747553
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	**1.159509066**	3	5.738932
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	**1.148839003**	3	3.76142
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**0.870816573**	**0.43524**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	**0.897330149**	3	4.580015
Q3T1K5	FTVTPSTTQVVGILK	**0.773373876**	2	3.706344
Q3T1K5	LLLNNDNLLR	**1.259496201**	2	2.40651
Q3T1L0	**A16A1 Aldehyde dehydrogenase family 16 member A1**	**1.291699365**	**1.4E-09**	**2**
Q3T1L0	HGAAPTVAETEVELSVR	**0.839913248**	2	2.398283
Q3T1L0	VQDQGQTLQVTGLR	**1.306052907**	2	4.167922
Q3TLP5	**ECHD2 Enoyl_CoA hydratase domain_containing protein 2_ mitochondrial**	**0.829597161**	**0.00344**	**2**
Q3TLP5	ALALAQEILPQAPIAVR	**0.678909362**		
Q3TLP5	NALGNVFVSELLEALAQLR	**0.93487253**		
Q3U2P1	**SC24A Protein transport protein Sec24A**	**0.91051108**	**0.75674**	**2**
Q3U2P1	CTLTSVPQTQALLNK	**0.6638936**	2	3.598585
Q3U2P1	TLETQSALGPALQAAFK	**0.887349871**	2	3.11167
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.032646948**	**1**	**2**
Q3ULJ0	GIDEGPDGLK	**0.885060377**	2	2.671374
Q3ULJ0	LGLMEMIAFAK	**1.032094604**	2	3.82464
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.02140774**	**1**	**14**
Q3UQ44	ALVGSENPPLTVIR	**1.053045759**	2	3.997128
Q3UQ44	AWVNQLETQTGEASK	**1.061387794**	2	5.080618
Q3UQ44	GVLLGIDDLQTNQFK	**1.120054331**	2	4.791054
Q3UQ44	HTDNTVQWLR	**1.320862555**	2	2.848342
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	**1.367677683**	3	4.515428
Q3UQ44	LGIAPQIQDLLGK	**1.134518208**	2	2.73368
Q3UQ44	LPYDVTTEQALTYPEVK	**1.20737961**	2	4.329138
Q3UQ44	LSAEEMDER	**1.00948724**	2	2.698053
Q3UQ44	NPNAVLTCVDDSLSQEYQK	**1.022883092**	2	4.969876
Q3UQ44	TALEEEIK	**0.966752254**	1	2.005997
Q3UQ44	TLDTLLLPTANIR	**0.887285677**	2	2.55318
Q3UQ44	VDFTEEEISNMR	**0.811032632**	2	3.389883
Q3UQ44	VDQVQDIVTGNPTVIK	**0.969882776**	2	4.916214
Q3UQ44	YQDILNEIAK	**0.974615338**	2	2.605644
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**1.072247231**	**0.35875**	**3**
Q3UV17	AQYEDIAQK	**1.695805756**	1	2.129373
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5)	**0.922395626**		
Q3UV17	VDSLTDEINFLR	**0.935429458**	2	2.468676
Q3UZY0	**SFI1 Protein SFI1 homolog**	**1.306696365**	**0.29644**	**2**
Q3UZY0	EEWWVSQREWK	**1.046216733**	2	2.704753
Q3UZY0	MGRAQAAHFHSAQLLSR+Oxidation(0)	**1.329655245**		
Q3V036	**CCD27 Coiled_coil domain_containing protein 27**	**0.819240479**	**0.21473**	**2**
Q3V036	MDLISSERTIK+Oxidation(0)	**0.505202486**		
Q3V036	SSEGPPEEAAAAKLSRPSQSK	**0.855731179**	2	2.749781
Q3V0K9	**PLSI Plastin_1**	**0.856731271**	**0.53367**	**3**
Q3V0K9	AYFHLLNQIAPK	**0.979834934**	2	2.825564
Q3V0K9	KIENCNYAVELGK	**1.139715645**	2	3.923074

Q3V0K9	QFVTPADVVSGNPK	0.858610784	2	3.802747
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.15175819**	**0.65017**	**2**
Q3V132	GNLANVIR	0.915116965	2	2.726654
Q3V132	YFPTQALNFAFK	1.253014404	2	2.945507
Q497B0	**NIT2 Omega_amidase NIT2**	**0.952262806**	**2E-12**	**14**
Q497B0	AGTEETILYSDIDLK	1.419700761	2	4.27928
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.827635432	2	4.908471
Q497B0	AVDNQVYVATASPAR	1.183416825	2	4.960291
Q497B0	AVDNQVYVATASPARDEK	1.001923655	2	3.383258
Q497B0	ENSIYLIGGSIPEEDDGK	0.947573461	2	2.837044
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	0.836398021	3	4.478386
Q497B0	FAELAQIYAR	1.40339346	2	3.704595
Q497B0	IHLFDIDVPGK	1.282937815	2	2.833553
Q497B0	KIHLFDIDVPGK	0.820233311	3	4.682935
Q497B0	LALIQLQVSSIK	0.914625329	2	3.335123
Q497B0	LYNTCAVFGPDGNLLVK	0.85774856	2	4.455254
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	0.889163293	3	4.344718
Q497B0	TLSPGDSFSTFDTPYCR	1.194747241	2	4.702559
Q497B0	VGLGICYDMR	1.067489309	2	2.744405
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**0.765200178**	**0.19298**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.816647446	2	4.155301
Q498D5	FCNLALLLPIVTK	0.531621247	2	3.224146
Q498D5	LEECIQDELGVR	0.827401976	2	3.148288
Q498D5	LNELLTNVEELKEEIK	0.784155935	2	3.456348
Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**1.11995653**	**0.52922**	**2**
Q498U4	EEEPPEKVVDMASEK	0.879567736	2	2.594336
Q498U4	FGIVTSSAGTGTTEDTEAK	1.113183366	2	4.130384
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.331097981**	**0.01902**	**10**
Q499N5	GATLSHHNIVNNSNLIGQR	0.762995213	3	4.826545
Q499N5	GGENIYPAELEDFFHK	1.046673885	2	3.088278
Q499N5	GGVIAGSLAPPELIR	1.065759241	2	2.670899
Q499N5	LPDLTTVISVDAPLPGTLLLDEVVAAGGK	0.897014876		
Q499N5	SGETTTEEEIK	1.124135123	2	2.952603
Q499N5	TFETVGQDR	1.178480672	2	2.514926
Q499N5	TGDIASMDEQGFCR	1.22790738	2	3.680996
Q499N5	TVGECLDATAQR	1.353315699	2	3.140662
Q499N5	YHQGFLSCYDPINIQFTSGTTGNPK	1.034618069	3	4.664974
Q499N5	YIVFVEGYPLTVSGK	1.428025745	2	4.652744
Q4AEF8	**COPG Coatomer subunit gamma**	**1.006211157**	**0.06292**	**5**
Q4AEF8	FGAQNEEMLPSILVLLK	0.983937446	2	3.164956
Q4AEF8	QEIFQEQLAAVPEFQGLGPLFK	1.026597899	3	4.288921
Q4AEF8	SSPEPVALTESETEYVIR	1.33539393	2	3.99375
Q4AEF8	VVLEHEEVR	1.351343887	2	2.35103
Q4AEF8	VVVVQAISALCQK	0.838498943	2	2.306965
Q4FZT0	**STML2 Stomatin_like protein 2**	**0.87800346**	**0.01807**	**6**
Q4FZT0	AEQINQAAGEASAVLAK	0.873904869	2	4.799156
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.060394564	2	4.997075
Q4FZT0	ATVLESEGTR	0.954500323	2	2.770914
Q4FZT0	DVQTTDTSIEELGR	1.077596936	2	2.82636
Q4FZT0	ILEPGLNVLIPVLDR	0.89121143	2	3.655525
Q4FZT0	NTVILFVPQQEAWVVER	1.188998654	2	3.051839
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.146304205**	**0.85737**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	1.318350406	3	4.971573

Q4FZT9	FGGSGSQVDSAR	**1.080552096**	2	3.891086
Q4FZT9	GEAIEAILAALEVVSEPFR	**0.494043188**		
Q4FZT9	SETELKDTYAR	**0.819401221**	2	2.357594
Q4FZT9	SGALLACGIVNSGVR	**0.96906587**	2	3.677731
Q4FZT9	SSTTSMTSVPKPLK	**0.816832402**	2	2.582055
Q4FZT9	TITGFQTHTTPVLLAHGER	**1.3470051**	3	3.709084
Q4FZT9	TPVQSQQPSATAPSGADEK	**1.174290534**	2	4.440697
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.360980306**	**9.9E-20**	**5**
Q4FZX7	DTQTSITDSSAIYK	**0.799154855**	2	3.096941
Q4FZX7	GDAGSADVQDLEK	**0.931846503**	2	3.329109
Q4FZX7	GNSLTLIDLPGHESLR	**1.135960704**	2	3.491884
Q4FZX7	SAAPSTLDSSSTAPAQLGK	**2.045513618**	2	4.616443
Q4FZX7	VGDGAGGAFQPYLDSLR	**1.378615492**	2	3.283015
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**0.992959475**	**0.51686**	**5**
Q4G061	AEEEGGSDGSAAEAEPR	**1.036784046**	2	4.84523
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	**0.209460913**	3	5.91656
Q4G061	GTQGVVTNFEIFR	**0.950316516**	2	2.819967
Q4G061	IINDYYPEEDGK	**0.878074106**	2	2.60998
Q4G061	TEDAEEDAEARPEPEVR	**0.863836023**	3	3.900955
Q4G069	**RMD1 Regulator of microtubule dynamics protein 1**	**1.077177835**	**0.97257**	**2**
Q4G069	IAEVLFANPPSSTYEEALK	**0.853669368**	2	2.488319
Q4G069	VLLYEALEYAK	**1.081963188**	2	2.565507
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**0.835686284**	**0.6128**	**13**
Q4KLP0	ARPSVDHGLAR	**1.130907312**	2	2.369559
Q4KLP0	LEELCPFPLDSLQQEMGK	**0.853091303**	2	5.123319
Q4KLP0	LLLESQEFDHFLATK	**0.973604306**	2	3.409804
Q4KLP0	LSAYGGITDIIIGMPHR	**1.027336592**	3	3.380409
Q4KLP0	LVTVYCEHGHK	**2.531953668**	2	2.845205
Q4KLP0	NGTNLDWATAETLALGSLLAQGFNVR	**1.163306548**		
Q4KLP0	QWGHNELDEPFFTNPVMYK	**1.053444016**	3	3.792775
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	**0.895185292**	3	5.151444
Q4KLP0	SSLYSSDIGK	**1.023399047**	2	2.693988
Q4KLP0	SVEVPEELQLHSHLLK	**0.856070659**	2	3.813759
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	**0.826773874**	2	4.926007
Q4KLP0	YGGEGAESMMGFFHELLK	**0.850332466**	2	4.407415
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	**1.250802299**	3	4.527272
Q4KLZ6		**1.098406741**	**0.31629**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	**1.236028585**	2	4.532551
Q4KLZ6	AILEVLQTK	**1.201557953**	2	2.713578
Q4KLZ6	ANTDLPAWSAAMDAGLK	**0.956493414**	2	3.889141
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	**0.857758024**	2	5.905149
Q4KLZ6	AVAQAGTAGTLLIVK	**1.164879547**	2	4.368645
Q4KLZ6	EGPTPASPAQVLSK	**1.324967161**	2	3.055923
Q4KLZ6	GLCGTILIHK	**0.96292877**	2	2.321606
Q4KLZ6	GVSLTLMLVDEPLLK	**1.235327727**	2	3.166383
Q4KLZ6	ISTTLIGLEEHLNALDR	**1.413773718**	2	3.941124
Q4KLZ6	LIDAETNAK	**1.194803897**	2	2.991795
Q4KLZ6	LNFGLAMEQAK	**0.875792654**	2	2.489008
Q4KLZ6	LSVLLLEK	**1.498914691**	2	2.801949
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	**1.190608984**	3	5.444092
Q4KLZ6	TMLDSLWAAAQELQAWK	**0.861721323**	2	4.337875
Q4KLZ6	VAGALAEEGMGLEEITK	**1.200294667**	2	3.692878
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	**1.156019795**	2	5.297269

Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.186449614**	**0.3134**	**4**
Q4KM49	AFCEPGNVENNGVLSFVK	**0.71164403**	2	3.433717
Q4KM49	QVEPLDPPAGSAPGER	**1.115576676**	2	3.170385
Q4KM49	TVVSGLVQFVPK	**1.013280763**	2	3.228129
Q4KM49	VDAQFGGIDQR	**1.369659336**	2	2.940107
Q4KM73	**KCY UMP_CMP kinase**	**1.131665491**	**0.99953**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	**1.068284389**	2	4.499327
Q4KM73	IVPVEITISLLK	**0.718131369**	2	2.319888
Q4KM73	KNPDSQYGELIEK	**1.122211537**	2	3.669565
Q4KM73	NQDNLQGWNK	**0.977259229**	2	3.088647
Q4KM73	SVDEVFGDVMK	**0.858372602**	2	3.071751
Q4KM73	YGYTHLSAGELLR	**0.853832453**	3	4.39207
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.314089364**	**3.1E-05**	**4**
Q4KM74	DLQQYQSQAK	**1.234656148**	2	3.297288
Q4KM74	GEALSALDSK	**1.21954398**	2	2.557648
Q4KM74	NLGSINTELQDVQR	**1.187065725**	2	4.204613
Q4KM74	VADGLPLAASMQEDEQSGR	**1.02858121**	2	2.635653
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**0.898400901**	**0.12532**	**2**
Q4KMA2	NFVVVMVTKPK	**0.776091939**	2	2.839968
Q4KMA2	QIIQQNPSLLPALLQQIGR	**0.849684841**	2	4.658129
Q4KSH7	**MP2K7 Dual specificity mitogen_activated protein kinase kinase 7**	**0.981410424**	**0.66684**	**2**
Q4KSH7	RSGNKEENK	**1.18794702**	1	1.989794
Q4KSH7	YNKLLEHSFIK	**0.693205046**	1	1.937529
Q4QQS8	**NUP85 Nuclear pore complex protein Nup85**	**1.054217111**	**0.04455**	**2**
Q4QQS8	LEEELSGK	**1.057089488**		
Q4QQS8	RFGDAASLLLSLMTSQIAPR+Oxidation(12)	**0.526712903**		
Q4QQV3	**F162A Protein FAM162A**	**0.89706887**	**0.90889**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	**0.911512457**	2	4.118657
Q4QQV3	RHESLTSLNLER	**0.879040166**	3	4.249256
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.86693134**	**0.00584**	**5**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	**1.389718222**	3	3.7553
Q4QQW3	HLETAEILGANIR	**0.8619178**	2	3.415718
Q4QQW3	IQDAGPVLADALR	**0.860709406**	2	2.779708
Q4QQW3	NLSQLPPVQIVMDSLSK	**0.851127458**	2	2.61558
Q4QQW3	VEPTDGSFMDAIEFAK	**0.840248116**	2	2.668852
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.220785782**	**0.13604**	**6**
Q4QRB4	AILVDLEPGTMDSVR	**0.791895907**	2	4.907288
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10)	**0.960078666**		
Q4QRB4	EIVHIQAGQCGNQIGAK	**1.229780363**	2	5.043253
Q4QRB4	IMNTFSVVPSPK	**1.162015586**	2	3.418721
Q4QRB4	IMNTFSVVPSPK+Oxidation(1)	**1.479058613**		
Q4QRB4	ISEQFTAMFR	**1.234697302**	2	3.584484
Q4V7C7	**ARP3 Actin_related protein 3**	**0.99853127**	**0.99986**	**5**
Q4V7C7	KDYEEIGPSICR	**0.925970318**	2	3.647529
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	**1.013429181**	2	3.149663
Q4V7C7	LSEELSGGR	**0.997827817**	2	2.713385
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	**0.978568857**	3	3.668952
Q4V7C7	YSYVCPDLVK	**1.039492623**	2	2.364987
Q4V8F9	**HSDL2 Hydroxysteroid dehydrogenase_like protein 2**	**0.908800317**	**0.6498**	**3**
Q4V8F9	DEQQINSAVEK	**1.142960759**	2	3.098461
Q4V8F9	KVDIIADAAYSIFK	**0.845468825**	2	2.403412
Q4V8F9	SFTGNFIIDENILK	**0.865430939**	2	2.932067
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**0.88488657**	**0.18253**	**2**

Q4V8K1	TCADEFPLTVDSSEK	**0.825162297**	2	4.587189
Q4V8K1	TLGLTPLDQGSLVAAK	**0.865005052**	2	3.809314
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.827989827**	**1.7E-05**	**3**
Q505J8	LQQVQAGQAEK	**1.150358155**	2	2.513763
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	**0.848849305**	3	4.930496
Q505J8	SLQALGEVIEAELR	**0.580750325**	2	3.58163
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**0.7643751**	**0.01188**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	**0.652038802**	2	4.291328
Q561R9	ILIDTGEPSVPEYISCLK	**0.861191013**	2	3.363614
Q561R9	NISNDATYCIK	**0.856322806**	2	2.474453
Q561R9	NNREEQIITVFR	**0.527122396**	2	2.541478
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.291478942**	**0.89836**	**5**
Q561S0	LLQYSDALEHLLSTGQGVVLER	**1.106603916**	3	3.665848
Q561S0	VITVDGNICSGK	**0.87887619**	2	2.923081
Q561S0	VVEDIEYLNYNK	**1.387615731**	2	4.201758
Q561S0	YAPGYNADVGDK	**1.069055512**	2	2.675377
Q561S0	YGLLASILGDK	**0.816762818**	2	2.947858
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.778458241**	**0.89448**	**5**
Q562C4	AQFSEVQLEWQPPPFK	**0.832032411**	2	4.897835
Q562C4	FIVAYGENMK	**0.768760035**	2	2.720356
Q562C4	HIGDGCHLTR	**0.572401435**	3	3.406351
Q562C4	VLQEVQR	**0.717013345**	2	2.769327
Q562C4	VTCVDPNPNFEK	**0.982132067**	2	3.563125
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**0.915185036**	**1**	**7**
Q58FK9	AIILNTPHNPIGK	**0.748645846**	2	3.220357
Q58FK9	DSTLDAAEEIFR	**0.935715864**	2	2.946199
Q58FK9	IEGLDQNVWVEFTK	**0.913833377**	2	4.713377
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	**1.102015404**	2	4.058285
Q58FK9	MDDPECYFNSLPK	**0.799549025**	2	3.673065
Q58FK9	RIEGLDQNVWVEFTK	**0.874572894**	2	3.940595
Q58FK9	WTSSDWTFNPQELESK	**0.812876584**	2	5.071333
Q5BJP3	**UFM1 Ubiquitin_fold modifier 1**	**1.285982589**	**0.00159**	**2**
Q5BJP3	VLSVPESTPFTAVLK	**3.0515471**	2	2.327214
Q5BJP3	VPAATSAIITNDGIGINPAQTAGNVFLK	**1.280088776**	3	4.359497
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.746421217**	**9.9E-20**	**27**
Q5BJY9	AQIFANSVDNAR	**1.052087379**	2	3.837768
Q5BJY9	AQYEQLAQK	**0.86715459**	2	3.286449
Q5BJY9	DAETTLLELR	**1.616728887**	2	2.805743
Q5BJY9	IREYLEK	**0.829973161**	3	3.354275
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	**0.809507874**	3	4.771309
Q5BJY9	KVVDDTNITR	**0.781424027**	2	3.025656
Q5BJY9	LEAEIATYR	**0.875895868**	2	3.009181
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	**0.662287247**	3	4.361937
Q5BJY9	LQLETEIEALK	**1.127455354**	2	2.899629
Q5BJY9	LQLETEIEALKEELLFMK	**1.342083744**	2	5.307376
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	**0.700187399**	2	6.313861
Q5BJY9	NQNINLENNLGEVEAR	**0.834475783**	2	5.502141
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	**1.056479265**	3	5.128973
Q5BJY9	QSVESDIHGLR	**0.842839248**	2	2.649623
Q5BJY9	QSVESDIHGLRK	**0.827620589**	2	2.650688
Q5BJY9	QTQEYEALLNIK	**0.810802818**	2	3.452058
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	**0.652076502**	2	5.979166
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK+Oxidation(14)	**0.93729513**		
Q5BJY9	TLQTLEIDLDSMK	**0.75313529**	2	4.245171
Q5BJY9	TLQTLEIDLDSMK+Oxidation(11)	**0.982179325**		
Q5BJY9	VKLEAEIATYR	**0.868573041**	2	2.921019

Q5BJY9	VKYETELAMR	**0.675745451**	3	3.476688
Q5BJY9	VQMEQLNGVLLHLESELAQTR	**0.860695358**	3	5.1235
Q5BJY9	VRPASSAASVYAGAGGSGSR	**1.49363735**	2	5.635721
Q5BJY9	VVDDTNITR	**0.822048287**	2	3.336481
Q5BJY9	YETELAMR	**0.745699013**	2	2.751773
Q5BJY9	YWSQQIEESTTVVTTK	**1.077391691**	2	4.745063
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**0.924722471**	**0.99997**	**4**
Q5BK63	AVQHSNVVINLIGR	**0.950681224**	2	3.384199
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	**0.997897104**	3	5.333165
Q5BK63	NFDFEDVFVNIPR	**0.994143943**	2	3.990403
Q5BK63	WLSSEIEETKPAK	**1.092866652**	2	2.937504
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.929834063**	**0.95143**	**4**
Q5BK81	AILDGNGLEK	**0.957081123**	2	2.401326
Q5BK81	DVPYPPPLPPAVEAIQK	**0.834410376**	2	2.694816
Q5BK81	TGNVAEQLR	**0.891238651**	2	2.631785
Q5BK81	VEEVSLPDTINEGQVR	**0.949214599**	2	4.062984
Q5DTT3	**F208B Protein FAM208B**	**1.150734453**	**1E-09**	**2**
Q5DTT3	QGENIDKLMEYVKNK	**3.82863963**	2	2.326965
Q5DTT3	VSVPSEHSENLSFLEK	**0.345864304**	2	2.343685
Q5DW34	**EHMT1 Histone_lysine N_methyltransferase EHMT1**	**1.032719302**	**0.08692**	**2**
Q5DW34	TPLMEAAENNHLDAVKYLIK+Oxidation(3)	**1.14693737**		
Q5DW34	YDCVVLFLSRDSDVTLKNK	**0.631634678**	2	2.364569
Q5EB77	**RAB18 Ras_related protein Rab_18**	**0.923073679**	**0.24799**	**3**
Q5EB77	LDNWLNELETYCTR	**1.643245495**	2	2.888129
Q5EB77	NDIVNMLVGNK	**0.690360841**	2	3.08801
Q5EB77	TCDGVQCAFEELVEK	**0.951930942**	2	3.467986
Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.677409788**	**0.0109**	**2**
Q5FVM4	MEELHNQEVQK	**0.824542063**	2	3.222231
Q5FVM4	MEELHNQEVQK+Oxidation(0)	**2.145803264**		
Q5FVQ4	**MLEC Malectin**	**0.996119217**	**0.99983**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	**1.330140814**	3	5.539516
Q5FVQ4	STPEDQILYQTER	**0.841364895**	2	4.009935
Q5FVR2	**TYPH Thymidine phosphorylase**	**1.271132135**	**0.00047**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10)	**0.646199393**		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8)	**0.673529055**		
Q5FVR2	DVTATVDSVPLITASILSK	**1.47241781**	2	2.499779
Q5FVR2	FGGAAVFPDQEK	**0.614919741**	2	2.329409
Q5FVR2	VSLVLAPALAACGCK	**0.799779385**	2	2.515367
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.098922739**	**0.85609**	**4**
Q5FVR5	DEKENLFQSK	**0.848522416**	2	2.501851
Q5FVR5	ILFIVGENDQCLASK	**0.814925831**	2	3.897016
Q5FVR5	IQQPGIGVISVSK	**0.981376977**	2	3.025784
Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	**1.173561327**	3	4.101441
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.695552532**	**4E-06**	**2**
Q5FW57	AIDQEMFK	**0.919542461**	1	1.990007
Q5FW57	SSQMLQMLESSLR	**0.54994187**	2	3.754406
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**0.933488919**	**0.67166**	**3**
Q5HZV9	AIENIDTLTNLESLFLGK	**0.756785816**	2	3.020503
Q5HZV9	ELDLYDNQIK	**0.984540861**	2	2.357517
Q5HZV9	ELDLYDNQIKK	**0.943523047**	2	2.40515
Q5HZY0	**UBXN4 UBX domain_containing protein 4**	**1.667119386**	**0.0331**	**2**
Q5HZY0	LPDGSSFTNQFPSDAPLEEAR	**1.573570086**	2	4.251848

Q5HZY0	NTELCETPTTSDPK	**1.503224391**	2	4.060839
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**0.992480901**	**0.93834**	**2**
Q5HZY2	EELDSLMTDETIANVPILILGNK	**0.907624592**	3	3.527583
Q5HZY2	IDRPEAISEER	**1.190507424**	2	2.671447
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.780097805**	**5.6E-16**	**6**
Q5I0C3	HAPLVEFEEEEV	**0.783630002**	2	2.939146
Q5I0C3	IIEEAPAPGIDPEVR	**0.661474535**	2	3.840908
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	**0.686675444**	3	3.407942
Q5I0C3	SEKEFQEQLESAR	**0.750654529**	2	3.20655
Q5I0C3	TNVDFLLR	**0.85942329**	2	2.382185
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	**0.70519218**	2	5.126723
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.822702521**	**0.32117**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	**0.810920581**	2	3.571954
Q5I0D1	HEEFEEGCK	**0.785611649**	2	2.560919
Q5I0D1	VTLAVSDLQK	**0.947265794**	2	2.323287
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**0.761597831**	**0.00466**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	**0.808254448**	3	3.789254
Q5I0D5	LGFDISEGEVTAPAPATCQILK	**0.759928459**	2	4.340418
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**0.910826732**	**0.37139**	**2**
Q5I0D7	GVNTDSGNVCR	**1.150626239**	2	2.417106
Q5I0D7	YAVDDVQYADEIASVLTSR	**0.874809281**	2	3.950121
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**0.952307554**	**0.97155**	**2**
Q5I0E7	QLVEQVEQIQK	**0.95246713**	2	3.741625
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	**0.960344923**	3	4.08146
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**0.748514602**	**0.15617**	**4**
Q5I0H9	DKNQDLCQQESVK	**0.97068377**	2	4.20531
Q5I0H9	GPPLWEEDPGAK	**0.884842409**	2	3.173129
Q5I0H9	GQGTICWVDCGDAESR	**0.873490913**	2	4.062721
Q5I0H9	NQDLCQQESVK	**0.747984716**	2	3.190464
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**0.985295535**	**0.66883**	**8**
Q5I0J9	HANLLVGSPSALADQTTER	**1.054081611**	2	5.469194
Q5I0J9	IIHESGVQILR	**0.928800687**	2	2.511107
Q5I0J9	LDAAGGLQSLR	**0.959482096**	2	3.761127
Q5I0J9	LEGPLAAAHSSGPR	**0.892057735**	2	3.35916
Q5I0J9	MAGSVPPALQLEDLTTLEER	**0.933872124**	2	3.098477
Q5I0J9	NSNTMAAAALAAPSLGFDR	**0.752081811**	2	4.320286
Q5I0J9	TVLYEGPVR	**1.057845141**	2	2.834515
Q5I0J9	VGVVGYGR	**0.918408561**	2	2.343987
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.090667565**	**0.00648**	**5**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	**0.951961437**	3	4.324335
Q5I0M2	DNHVVAAGSMEK	**1.298965401**	2	2.84924
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	**1.064423917**	3	6.041539
Q5I0M2	LYAEGDIPVPHAR	**1.189891255**	2	2.951888
Q5I0M2	VEVECSSLK	**1.085661415**	2	2.662642
Q5I0P2	**GCSH Glycine cleavage system H protein_ mitochondrial**	**1.012917237**	**0.81139**	**2**
Q5I0P2	MTLSDPSELDELMSEEAYEK	**0.701365929**	2	5.214109
Q5I0P2	SCYEDGWLIK	**1.355779077**	2	2.306847
Q5M7T9	**THNS2 Threonine synthase_like 2**	**1.12266047**	**0.00791**	**3**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	**1.118762204**	3	5.418866
Q5M7T9	GDFSLCEVVR	**1.176324217**	2	2.529871
Q5M7T9	MGLPISLVVAVNR	**1.679311585**	2	2.547187
Q5M7U6	**ARP2 Actin_related protein 2**	**1.112411011**	**0.45792**	**5**

Q5M7U6	GYAFNHSADFETVR	0.910385629	2	3.77078
Q5M7U6	HLWDYTFGPEK	0.993493392	2	3.320496
Q5M7U6	KHMVFLGGAVLADIMK+Oxidation(2)	0.881532595		
Q5M7U6	LCYVGYNIEQEQK	1.482303154	2	2.396196
Q5M7U6	SMLEVNYPMENGIVR	0.665028574	2	3.193145
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.88501475**	**0.00905**	**7**
Q5M7W5	AAVGLTGNDIATPPNK	0.84758762	2	3.546937
Q5M7W5	ATSPSTLVSTGSSSR	0.841843455	2	3.649583
Q5M7W5	NTTPTGATPPAGMASTR	0.880928385	2	2.70681
Q5M7W5	STLPVDEGSPLEK	0.832329315	2	2.402106
Q5M7W5	TEFIPLLDGDEK	0.76910602	2	2.504158
Q5M7W5	VGSLDNVGHLPAGGTVK	0.785897468	2	3.369494
Q5M7W5	VTEFNNVTPLSEEEVASIK	0.866140242	2	3.169424
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.222820382**	**0.90241**	**7**
Q5M875	ALTAELDTLGK	1.301567627	2	2.828357
Q5M875	IQNIQFEAIVGHR	1.049009179	3	3.523788
Q5M875	LWPVLEPDEVAR	1.04879957	2	2.400387
Q5M875	NSGHIVTVASVCGHR	1.023058621	2	4.399843
Q5M875	SLIDGILTNK	1.262836863	2	3.324672
Q5M875	SVAGQTVLITGAGHGIGR	1.121207385	2	4.027478
Q5M875	TSCLCPVFVNTGFTK	1.323108009	2	3.81641
Q5M9G3	**CAPR1 Caprin_1**	**1.296945688**	**0.00268**	**4**
Q5M9G3	LNQDQLDAVSK	1.405116527	2	3.254042
Q5M9G3	SSFSNTPNSGYTQSQFNAPR	0.200674414	2	3.801034
Q5M9G3	TVLELQYVLDK	1.608655747	2	2.437326
Q5M9G3	YQEVTNNLEFAK	1.23120088	2	2.742763
Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**1.096907955**	**0.56357**	**2**
Q5M9I5	EEEEEELVDPLTTVR	0.792894894	2	2.678546
Q5M9I5	SQTEEDCTEELFDFLHAR	1.489750646	2	4.86154
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**0.990668898**	**0.96117**	**9**
Q5PPL3	AVLDANDPKK	1.111396721	2	2.479386
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	0.891865395	2	4.930092
Q5PPL3	DPQLVPVLIDAAR	1.110222117	3	3.405301
Q5PPL3	GQVTGTDLINEVSK	0.917489929	2	3.785707
Q5PPL3	GVSTVFHCASPPSNSNNK	1.432661991	2	4.786042
Q5PPL3	GYAVNVFDVR	1.031809612	2	3.588144
Q5PPL3	ILTGLNYEAPK	1.168200809	2	2.863304
Q5PPL3	KGQVTGTDLINEVSK	0.88407971	2	4.079587
Q5PPL3	VQFFIGDLCNQQDLYPALK	1.119276494	3	5.26558
Q5PQQ2	**WBP11 WW domain_binding protein 11**	**0.820286377**	**0.02713**	**4**
Q5PQQ2	KLEVEYEQK	0.180149797	1	2.173596
Q5PQQ2	LDEMEFNPVQQPQLNEKVLK+Oxidation(3)	2.200473561		
Q5PQQ2	RDEDMLYSPELAQR	0.961433146	2	2.325378
Q5PQQ2	STSSTKSGKFMNPTDQAR	1.187935811	2	2.471763
Q5PQR4	**RSRC2 Arginine/serine_rich coiled_coil protein 2**	**0.936448492**	**0.84269**	**2**
Q5PQR4	EKEMVEK+Oxidation(3)	0.936546525		
Q5PQR4	KEGDKSQSAEIWEK	0.758329921	2	2.543995
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**0.889403384**	**0.57687**	**6**
Q5PQT3	AIQNLASIHSLQVK	0.790678289	2	3.398991
Q5PQT3	DPENCQEFLGSSEVINWK	0.885846074	2	5.326753
Q5PQT3	FWLFGGNER	0.853316923	2	2.415078
Q5PQT3	GFPVYSHTDK	1.268377517	2	2.676879
Q5PQT3	LSSLDVTHAALVNK	1.199086566	2	3.241656

Q5PQT3	QHLQIQSSQSHLNK	**0.849489929**	2	3.480844
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**0.970285376**	**0.99973**	**6**
Q5RJR8	ATVLDLSCNK	**1.002071097**	2	3.114544
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	**0.927126218**	2	6.028548
Q5RJR8	HHEILQWVLQTDSQQ	**0.921728915**	2	3.239959
Q5RJR8	LDGNELDLSLSDLNEVPVK	**0.966033357**	2	3.92303
Q5RJR8	LQQLPADFGR	**1.133880094**	2	2.354561
Q5RJR8	LSTLPSDFCGLTHLVK	**0.96780502**	2	3.183544
Q5RKH1	**PRP4B Serine/threonine_protein kinase PRP4 homolog**	**0.83501916**	**0.2064**	**2**
Q5RKH1	DLLDQILMLDPAKR+Oxidation(7)	**1.19626366**		
Q5RKH1	LAMDLKGKMPNK+Oxidation(2)	**0.800353706**		
Q5RKH6	**OS9 Protein OS_9**	**0.924661577**	**0.95443**	**3**
Q5RKH6	EQAILALTSTLDK	**1.060082356**	2	2.423348
Q5RKH6	LQESQSPELVQK	**0.972604798**	2	2.935137
Q5RKH6	QEQPGDDTTEAPQR	**0.843269404**	2	3.091011
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.015087006**	**0.73761**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	**1.176925931**	3	5.042492
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	**0.994102906**	3	4.643034
Q5RKI0	YAPSGFYIASGDISGK	**1.010502727**	2	4.312936
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.191914897**	**0.00011**	**5**
Q5RKI1	ELAQQIQK	**1.463241895**	1	2.229965
Q5RKI1	GIDVQQVSLVINYDLPTNR	**1.322287581**	2	3.997807
Q5RKI1	GYDVIAQAQSGTGK	**1.230551147**	2	5.314204
Q5RKI1	MFVLDEADEMLSR	**1.079376402**	2	4.288107
Q5RKI1	VLITTDLLAR	**1.034777046**	2	3.487532
Q5S006	**LRRK2 Leucine_rich repeat serine/threonine_protein kinase 2**	**0.803722078**	**0.45564**	**2**
Q5S006	MPRITNLDASR+Oxidation(0)	**0.748211297**		
Q5S006	WLCKVMAQILTVK	**0.862827278**	2	2.334558
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.046721556**	**0.84176**	**16**
Q5SGE0	AALDLEQVPSELAVTR	**0.907856555**	2	4.194396
Q5SGE0	CIANNQVETLEK	**1.099027482**	2	2.88551
Q5SGE0	DVGEPVPFTEPPESFGFYIK	**1.017424503**	2	2.966461
Q5SGE0	GLDAIELSR	**0.853002974**	2	2.69324
Q5SGE0	HCVTMDTPAEK	**0.991267606**	2	3.008977
Q5SGE0	HDNAEDALNLK	**1.058029986**	2	3.565758
Q5SGE0	MEGANIQPNR	**0.867235549**	2	2.722537
Q5SGE0	SCGSLLPELSLAER	**0.996108367**	2	2.36615
Q5SGE0	SCGSLLPELSLAERTEFAHK	**1.894333448**	2	2.40415
Q5SGE0	SGSPGSNQALLLLR	**1.122793657**	2	2.828588
Q5SGE0	SSLSSSSPSAGDTVTEK	**0.89283794**	2	4.347086
Q5SGE0	SYVADKDVASAK	**0.916846716**	2	2.857055
Q5SGE0	TLLELIPELR	**1.052156779**	2	3.005342
Q5SGE0	TSQFTSSDLESTLEK	**1.264547675**	2	3.05048
Q5SGE0	VIEEQMEPALEK	**1.159196445**	2	2.92843
Q5SGE0	VYLQNEYR	**1.331667176**	2	2.451252
Q5SNZ0	**GRDN Girdin**	**1.269628891**	**0.66565**	**2**
Q5SNZ0	KVEILENEIIQEK	**1.090139403**	2	2.523196
Q5SNZ0	YNQLLKQKGQLEDLEK	**0.8914111**	2	2.643322
Q5SW19	**K0664 Protein KIAA0664**	**1.170425287**	**0.00337**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	**0.886338434**	2	2.93945
Q5SW19	IGIGELITR	**1.536098166**	2	2.917611
Q5SW19	SVEGLQEGSVLR	**1.177639966**	2	2.823326
Q5SX40	**MYH1 Myosin_1**	**1.149828094**	**1**	**95**

Q5SX40	AAYLQNLNSADLLK	**0.348624445**	2	3.658021
Q5SX40	ADIAESQVNK	**0.978779848**	2	4.055568
Q5SX40	AEDEEEINAELTAK	**0.894083347**	2	4.381058
Q5SX40	AGLLGLLEEMR	**0.866165744**	2	3.978479
Q5SX40	AGLLGLLEEMRDDK	**1.04104619**	2	3.335037
Q5SX40	ALQEAHQQTLDDLQAEEDK	**1.355597495**	2	5.756624
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	**0.700472582**	3	6.764009
Q5SX40	ANLLQAEIEELR	**0.936466195**	2	3.93121
Q5SX40	ANSEVAQWR	**0.809620259**	2	3.037319
Q5SX40	DLEEATLQHEATAATLR	**1.120004805**	2	4.96199
Q5SX40	DTQLHLDDALR	**1.159773218**	1	3.613188
Q5SX40	EEQAEPDGTEVADK	**0.675708289**	2	3.558584
Q5SX40	EFEMSNLQSK	**1.005884828**	1	2.543429
Q5SX40	ELEEISER	**1.267267823**	1	2.076466
Q5SX40	ELEGEVENEQK	**0.732480342**	2	2.69849
Q5SX40	ELEGEVENEQKR	**1.249977037**	2	3.285165
Q5SX40	ELTYQTEEDRK	**1.429248435**	2	3.095385
Q5SX40	ENQSILITGESGAGK	**1.097674018**	2	4.716943
Q5SX40	EQYEEEQEAK	**1.154272904**	1	3.199806
Q5SX40	GQEDLKEQLAMVER	**0.839815989**	2	4.443505
Q5SX40	GSSFQTVSALFR	**0.980705184**	2	3.03157
Q5SX40	HADSVAELGEQIDNLQR	**0.905160225**	2	5.959991
Q5SX40	IAEQELLDASER	**0.710304647**	2	3.778352
Q5SX40	IEAQNKPFDAK	**0.727935421**	2	2.748584
Q5SX40	IEDEQALGMQLQK	**0.619339007**	2	4.865421
Q5SX40	IEDEQALGMQLQK+Oxidation(8)	**1.121656812**		
Q5SX40	IEDMAMMTHLHEPAVLYNLK	**0.650004816**	3	4.340081
Q5SX40	IEELEEEIEAER	**0.598350202**	2	4.26683
Q5SX40	IKLEQQVDDLEGSLEQEK	**1.215752306**	2	5.140683
Q5SX40	IKLEQQVDDLEGSLEQEKK	**1.059292197**	2	5.21932
Q5SX40	INQQLDTK	**1.666561112**	1	2.172988
Q5SX40	IQHELEEAEER	**0.843887317**	2	3.616211
Q5SX40	IQLELNQVK	**0.98281913**	2	2.780883
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	**0.667130767**	3	7.394549
Q5SX40	KIAEQELLDASER	**0.918904042**	2	3.631049
Q5SX40	KIQHELEEAEER	**1.068793275**	2	3.797122
Q5SX40	KKEFEMSNLQSK	**0.742917144**	2	4.017015
Q5SX40	KKLETDISQIQGEMEDIVQEAR	**0.79413104**	3	5.967843
Q5SX40	KLEDECSELK	**0.768179636**	2	3.074796
Q5SX40	KLEDECSELKK	**1.002510496**	3	4.254461
Q5SX40	KLETDISQIQGEMEDIVQEAR	**1.010178214**	2	5.557512
Q5SX40	KMEGDLNEMEIQLNHSNR	**1.14618005**	3	4.224661
Q5SX40	KMEGDLNEMEIQLNHSNR+Oxidation(1)	**0.965025362**		
Q5SX40	LAQESTMDVENDKQQLDEK	**0.681165269**	2	4.648623
Q5SX40	LDEAEQLALK	**1.150637548**	2	3.962439
Q5SX40	LEDECSELK	**0.377332919**	2	2.378723
Q5SX40	LEDECSELKK	**0.958780455**	2	2.886516
Q5SX40	LEEAGGATSAQIEMNK	**0.736234055**	2	4.728858
Q5SX40	LEEAGGATSAQIEMNK+Oxidation(13)	**0.783587977**		
Q5SX40	LEQQVDDLEGSLEQEK	**0.805142035**	2	5.633994
Q5SX40	LEQQVDDLEGSLEQEKK	**0.94138724**	2	4.511164
Q5SX40	LETDISQIQGEMEDIVQEAR	**1.000850332**	2	5.562187
Q5SX40	LINELTAQR	**0.904273831**	2	2.947413
Q5SX40	LLGSIDIDHTQYK	**1.812561531**	2	3.481214
Q5SX40	LQDAEEHVEAVNAK	**1.054391459**	2	4.967914
Q5SX40	LQDLVDK	**0.861983619**	1	2.132548
Q5SX40	LQDLVDKLQSK	**0.996044213**	2	2.583841

Q5SX40	LQNEVEDLMIDVER	0.846288212	2	4.725507
Q5SX40	LQTESGEYSR	1.11085558	2	2.525086
Q5SX40	LYEQHLGK	1.024720068	2	2.32573
Q5SX40	MEGDLNEMEIQLNHSNR	0.501356107	2	4.659929
Q5SX40	MEIDDLASNMEVISK	0.426301348	2	5.13623
Q5SX40	MEIDDLASNMEVISK+Oxidation(0)	1.150033637		
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	0.85415294	3	6.71066
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0)	1.030718369		
Q5SX40	NDLQLQVQSEADSLADAEER	0.63782569	2	6.70725
Q5SX40	NKDPLNETVVGLYQK	1.006328504	2	4.822206
Q5SX40	NLQQEISDLTEQIAEGGK	1.043479441	2	6.905754
Q5SX40	NLQQEISDLTEQIAEGGKR	0.858140958	2	3.748134
Q5SX40	NLTEEMAGLDETIAK	0.868361104	2	4.854417
Q5SX40	NLTEEMAGLDETIAK+Oxidation(5)	0.648689714		
Q5SX40	QAEEAEEQSNVNLAK	0.968359361	2	4.537892
Q5SX40	QKYEETHAELEASQK	0.813532281	2	4.468509
Q5SX40	QLDEKDSLVSQLSR	0.894437876	2	3.07626
Q5SX40	QLEEEIK	0.953402333	1	2.149653
Q5SX40	QREEQAEPDGTEVADK	1.083049513	2	3.97609
Q5SX40	RANLLQAEIEELR	1.101642462	2	2.33789
Q5SX40	RDLEEATLQHEATAATLR	0.220142646	2	4.946259
Q5SX40	SAETEKEMANMK	1.310919556	2	3.064342
Q5SX40	SAETEKEMANMKEEFEK	#NUM!	2	4.918159
Q5SX40	SELQAALEEAEASLEHEEGK	0.994666797	2	6.020133
Q5SX40	SLSTELFK	1.093562205	2	2.412401
Q5SX40	SSVFVVDAK	1.001710757	1	2.125075
Q5SX40	TKYETDAIQR	1.102643805	3	3.493541
Q5SX40	TLEDQVSELK	0.601753287	2	3.506889
Q5SX40	TNAACAALDKK	1.811273605	2	3.200219
Q5SX40	VKELTYQTEEDRK	0.680920165	2	3.684565
Q5SX40	VLNASAIPEGQFIDSK	0.91898018	2	4.429382
Q5SX40	VQLLHTQNTSLINTK	0.675352909	2	4.620411
Q5SX40	VRELEGEVENEQKR	0.832206661	3	3.889015
Q5SX40	VVESMQSTLDAEIR	0.892088914	2	4.080634
Q5SX40	VVESMQSTLDAEIR+Oxidation(4)	1.142974241		
Q5SX40	YDKIEDMAMMTHLHEPAVLYNLK	0.628209431	3	4.390036
Q5SX40	YEETHAELEASQK	1.057967405	2	4.767837
Q5SX40	YETDAIQR	0.940382761	2	2.578749
Q5U206	**CALL3 Calmodulin_like protein 3**	**0.853755356**	**7.3E-06**	**5**
Q5U206	DTDSEEEIR	1.347656947	2	2.707368
Q5U206	KMKDTDSEEEIR	0.510738483	2	2.306405
Q5U206	KMKDTDSEEEIR+Oxidation(1)	2.041016806		
Q5U206	MKDTDSEEEIR	0.836741045	2	3.104297
Q5U206	MKDTDSEEEIR+Oxidation(0)	1.370771759		
Q5U211	**SNX3 Sorting nexin_3**	**0.847474792**	**0.34773**	**2**
Q5U211	CLHMFLQDEIIDK	0.67704088	2	2.37173
Q5U211	GDDGIFDDNFIEER	1.100746179	2	2.842775
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.162733739**	**0.67023**	**3**
Q5U2Q7	LSVLGAITSVQQR	0.867912815	2	2.402318
Q5U2Q7	YFDEISQDTGK	1.191853343	2	2.682383
Q5U2Q7	YVLHCQGTEEEK	1.273241894	2	3.63262
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**0.954573761**	**0.91983**	**12**
Q5U300	AAVASLLQSVQVPEFTPK	1.20042746	3	3.715683
Q5U300	AENYDISPADR	0.921438633	2	2.99153
Q5U300	DNPGVVTCLDEAR	1.057073123	2	3.39023

Q5U300	FEVQGLQPNGEEMTLK	**0.929791118**	2	3.892946
Q5U300	IYDDDFFQNLDGVANALDNVDAR	**0.808042728**	2	4.449693
Q5U300	LDQPMTEIVSR	**1.041775366**	2	2.627829
Q5U300	MLQTSSVLVSGLR	**0.957799943**	2	2.372286
Q5U300	NEEDATELVTLAQAVNAR	**0.84666434**	2	4.557729
Q5U300	NFPNAIEHTLQWAR	**1.099720371**	2	3.440497
Q5U300	SLPASLAEPDFVMTDFAK	**0.959898592**	2	3.549592
Q5U300	SPPAVQQDNVDEDLIR	**0.918824078**	2	4.720029
Q5U300	VVQGHQQLDSYK	**1.112995676**	2	3.925257
Q5XFX0	**TAGL2 Transgelin_2**	**0.890427376**	**0.02343**	**4**
Q5XFX0	DDGLFSGDPNWFPK	**0.765766976**	2	3.560257
Q5XFX0	QMEQISQFLQAAER	**0.629647215**	2	3.099038
Q5XFX0	TLMNLGGLAVAR	**0.649658912**	2	3.554724
Q5XFX0	YGINTTDIFQTVDLWEGK	**0.813786345**	2	5.069996
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**0.965319249**	**0.28495**	**11**
Q5XHY5	AEHDSILAEK	**1.160600712**	2	2.597994
Q5XHY5	DQELYFFHELSPGSCFFLPK	**1.57301292**	3	3.418052
Q5XHY5	FLGDIEIWNQAEK	**1.011610573**	2	3.594064
Q5XHY5	FMVDIDLDPGCTLNK	**0.643129175**	2	2.976842
Q5XHY5	GFQEVVTPNIFNSR	**1.105988466**	2	3.122215
Q5XHY5	LKAEHDSILAEK	**2.934340836**	2	3.249691
Q5XHY5	NELSGALTGLTR	**0.897096008**	2	3.266307
Q5XHY5	QLENSLNEFGEK	**1.234962944**	2	3.185023
Q5XHY5	QVMVVPVGPTCDEYAQK	**0.955895446**	2	3.267956
Q5XHY5	TTPYQIACGISQGLADNTVVAK	**1.134212091**	2	4.226333
Q5XHY5	WELNPGDGAFYGPK	**1.015557026**	2	3.761512
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**0.956845328**	**0.87608**	**13**
Q5XHZ0	AFLEALQHQAETSSR	**0.935894135**	2	4.587068
Q5XHZ0	AQLLQPTLEINPR	**0.821917311**	2	3.477069
Q5XHZ0	EELVSNLGTIAR	**1.005732721**	2	2.55594
Q5XHZ0	ELISNASDALEK	**1.28661011**	2	3.58824
Q5XHZ0	FEDTSPAGER	**1.014254891**	2	2.767632
Q5XHZ0	GTITIQDTGIGMTK	**0.875990439**	2	3.493619
Q5XHZ0	GVVDSEDIPLNLSR	**1.011721285**	2	4.912754
Q5XHZ0	HLAEHSPYYEAMK	**1.244870443**	2	3.282081
Q5XHZ0	LDTHPAMVTVLEMGAAR	**0.822326404**	3	4.365638
Q5XHZ0	SDCKDFANESR	**1.079397073**	2	2.759222
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	**1.124142626**	3	3.615469
Q5XHZ0	YESSALPAGQLTSLSDYASR	**0.902976082**	2	5.707639
Q5XHZ0	YIAQAYDKPR	**1.002730677**	2	2.878207
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**0.960509939**	**0.331**	**7**
Q5XI22	AGHFDKEIVPVHVSSR	**0.608117207**	2	4.251559
Q5XI22	HGSNLEAMSK	**1.316497375**	2	2.778616
Q5XI22	HGSNLEAMSK+Oxidation(7)	**0.78996006**		
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	**1.055806835**	3	4.880542
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	**0.866793644**	2	4.888167
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	**1.540861052**	3	5.933632
Q5XI22	VNIDGGAIALGHPLGASGCR	**0.906017715**	2	5.820588
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.11928811**	**0.8269**	**7**
Q5XI32	KLEVEANNAFDQYR	**0.920558701**	2	4.473894
Q5XI32	LEVEANNAFDQYR	**0.912418224**	2	3.371792
Q5XI32	LVEDMENK	**2.280204691**	2	2.319997
Q5XI32	NLSDLIDLVPSLCEDLLSSVDQPLK	**0.87775518**		
Q5XI32	SGSGTMNLGGSLTR	**0.910906451**	2	2.868657
Q5XI32	STLNEIYFGK	**0.905223202**	2	2.610337
Q5XI32	YDPPLEDGAMPSAR	**0.873954326**	2	2.523153

Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.411907582**	**0.0027**	**3**
Q5XI60	ALDIAAGITR	**1.48516776**	2	3.583572
Q5XI60	HHVALDSAASQLSGR	**1.40363325**	2	4.258485
Q5XI60	NVATDALGALEAR	**1.015543102**	2	3.819297
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**0.91997923**	**0.04644**	**6**
Q5XI73	AEEYEFLTPMEEAPK	**0.837223301**	2	4.365891
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	**0.862772534**	3	3.312611
Q5XI73	SIQEIQELDKDDESLR	**0.52135122**	2	4.934564
Q5XI73	SIQEIQELDKDDESLRK	**0.929505807**	2	4.319915
Q5XI73	TDYMVGSYGPR	**0.903208138**	2	2.67347
Q5XI73	VAVSADPNVPNVIVTR	**1.232612247**	2	4.454436
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**0.866315023**	**0.99996**	**15**
Q5XI78	FGLEGCEVLIPALK	**1.091776747**	2	3.408001
Q5XI78	FLDTAFDLDAFK	**1.173224692**	2	2.468751
Q5XI78	FLDTAFDLDAFKK	**0.989578652**	2	2.83962
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	**0.931189571**	3	4.433742
Q5XI78	ICEEAFTR	**1.167805688**	2	2.440774
Q5XI78	IEQLSPFPFDLLLK	**1.035419217**	2	3.613792
Q5XI78	LEAADEGSGDMK	**0.863408709**	2	2.423432
Q5XI78	NITLSLVANPSHLEAADPVVMGK	**1.01399362**	3	4.982562
Q5XI78	NTNAGAPPGTAYQSPLSLSR	**1.154036563**	2	4.521922
Q5XI78	SSLATMAHAQSLVEAQPNVDK	**0.970261908**	3	4.480308
Q5XI78	SWDIFFR	**0.922212857**	2	2.353437
Q5XI78	VIPEDGPAAQNPDK	**1.168479041**	2	3.079614
Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	**1.029714775**	3	4.211287
Q5XI78	YAELLVSQGVVNQPEYEEEISK	**0.911303645**	2	4.176691
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	**1.090168076**	3	3.80502
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**0.928350917**	**0.00496**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	**0.472913992**	2	3.88944
Q5XI95	IIAVDINK	**0.927495929**	2	2.875825
Q5XI95	MVATGVCGTDIK	**0.722324924**	2	3.224852
Q5XI95	NNICTEIR	**0.549716855**	2	2.461977
Q5XI95	TVGATDCVDPR	**0.466129756**	2	2.601793
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**0.867180697**	**0.29377**	**5**
Q5XIC0	ATQQDFENAMNQVK	**0.802855301**	2	4.765385
Q5XIC0	GILVTSEGGITK	**0.853856479**	2	3.844986
Q5XIC0	LHAVNEEECTTLR	**0.848050502**	2	3.651217
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	**0.883849574**	2	5.1551
Q5XIC0	WDAWNALGSLPK	**0.814125871**	2	3.596739
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**0.876421715**	**0.93803**	**5**
Q5XIE6	AGIATHFVDSEK	**1.044490029**	2	3.386729
Q5XIE6	AGQTLSQDLFR	**1.012032765**	2	2.382031
Q5XIE6	AVLIDKDQTPK	**0.883115265**	2	2.594764
Q5XIE6	INSCFSANTVEQILENLR	**0.827217932**	2	3.847363
Q5XIE6	LHVLEEELLALK	**0.875864307**	3	3.679724
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.030833305**	**1**	**2**
Q5XIF3	HGWSYDVEGR	**1.037463165**	2	2.842702
Q5XIF3	LDVTPLTGVPEEHIK	**1.005309411**	3	3.608404
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.03481545**	**0.77785**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	**1.042376098**	2	3.760549
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	**1.071499573**	3	5.324975
Q5XIF6	DVNAAIAAIK	**1.041944437**	2	2.880304
Q5XIF6	SIQFVDWCPTGFK	**1.067795996**	2	4.34043

Q5XIF6	TIGGGDDSFTTFFCETGAGK	2.135267293	2	4.564332
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**0.94409476**	**0.99883**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	0.845575493	2	3.996675
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.007914776	2	5.894697
Q5XIH7	**PHB2 Prohibitin_2**	**0.974572218**	**0.17159**	**11**
Q5XIH7	AQVSLLIR	0.918858576	2	2.773294
Q5XIH7	DLQMVNISLR	1.348900864	2	3.193563
Q5XIH7	FNASQLITQR	0.921267323	2	3.687476
Q5XIH7	IGGVQQDTILAEGLHFR	1.059909628	3	4.425041
Q5XIH7	IPWFQYPIIYDIR	0.974515163	2	2.953961
Q5XIH7	IVQAEGEAEAAK	0.979474817	2	4.184361
Q5XIH7	IYLTADNLVLNLQDESFTR	1.216696914	2	4.575488
Q5XIH7	LGLDYEER	0.640956859	2	2.598001
Q5XIH7	LLLGAGAVAYGVR	1.528971602	2	3.493178
Q5XIH7	VLPSIVNEVLK	0.81241701	2	2.815963
Q5XIH7	VLSRPNAQELPSMYQR	0.964473228	2	3.836985
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.368670183**	**1E-05**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	1.621556759	2	4.211146
Q5XIM9	GATQQILDEAER	1.367961732	2	3.909883
Q5XIM9	GSGNLEAIHVIK	1.785668212	2	2.915132
Q5XIM9	HGINCFINR	1.423387358	2	2.540056
Q5XIM9	ILIANTGMDTDK	1.517732828	2	2.742394
Q5XIM9	LIEEVMIGEDK	0.984565115	2	3.128077
Q5XIM9	NIGVDNPAAK	1.066116357	1	2.026639
Q5XIM9	SLHDALCVLAQTVK	0.856242169	2	3.778103
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.224688458	2	4.557994
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**0.908811005**	**0.00205**	**6**
Q5XIN6	AAEVEGEQVDNK	1.009115296	2	4.005324
Q5XIN6	FLQDTIEEMALK	0.921867435	2	2.958354
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.702841582	2	5.473849
Q5XIN6	LEEGGPVYSPPAQVVVK	0.798200048	2	3.09571
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.078706402	3	4.42701
Q5XIN6	LLELQSIGTNNFLR	0.775423926	2	2.988791
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**0.852211363**	**0.36004**	**10**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.748010425	2	4.953421
Q5XIT9	ALVNQLHER	0.923589165	2	2.587605
Q5XIT9	ALYGDTLVTGFAR	0.920900207	2	3.679648
Q5XIT9	AQEIALQNR	0.809023507	2	2.627568
Q5XIT9	DRIDNLIDPGSPFLEFSQFAGYK	1.209452535	3	4.390281
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	0.92218431	3	4.436713
Q5XIT9	LGTQPDSGSSTYQENYEQMK	0.725209882	2	5.084144
Q5XIT9	LWDDGIIDPVDTR	0.638432297	2	3.265567
Q5XIT9	LYGEEEVPAGGIITGIGR	0.766340263	2	4.380058
Q5XIT9	QGTIFLAGPPLVK	0.826069506	2	2.46614
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**0.957762879**	**0.92695**	**2**
Q5XIU5	ALIDPSSGLPNR	0.933407053	2	2.540231
Q5XIU5	DPLSPFAVGGEDLDPFGCQR	0.966618881	2	2.728643
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**1.17269393**	**0.22356**	**3**
Q5XIU9	FYGPAGPYGIFAGR	1.033500523	2	2.765221
Q5XIU9	GLATFCLDK	1.184910197	2	2.848962
Q5XIU9	GLCSGPGAGEESPAATLPR	0.838580953	2	4.786752
Q5XKE0	**MYPC2 Myosin_binding protein C_ fast_type**	**0.844358475**	**0.39815**	**3**
Q5XKE0	LVVEISDPDLPLK	0.698491583	2	2.824512
Q5XKE0	SEDAGELDFSGLLK	1.280410466	2	3.418824

Q5XKE0	TSDNSIVVVAGNK	**0.852208439**	2	2.627337
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**0.891137703**	**0.00941**	**7**
Q60587	ALAMGYKPK	**0.875257192**	2	2.537009
Q60587	AQDEGHLSDIVPFK	**1.238508903**	2	3.040215
Q60587	DFIYVSQDPK	**0.953336752**	2	2.675435
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	**0.780676458**	3	4.630652
Q60587	DNGIRPSSLEQMAK	**0.849092689**	2	3.24394
Q60587	DQLLLGPTYATPK	**1.031737908**	2	3.72816
Q60587	NIVVVEGVR	**0.919061957**	2	2.859435
Q60598	**SRC8 Src substrate cortactin**	**0.865219723**	**0.91609**	**3**
Q60598	ENVFQEHQTLK	**1.286635461**	2	2.305964
Q60598	NASTFEEVVQVPSAYQK	**1.546440651**	2	3.476493
Q60598	VDQSAVGFEYQGK	**0.855420802**	2	3.031708
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.032499042**	**0.35809**	**4**
Q60759	DILGGNGISDEYHVIR	**1.003052394**	2	3.724004
Q60759	DIVYEMGELGVLGPTIK	**1.119091482**	2	2.378566
Q60759	GYGCAGVSSVAYGLLTR	**1.185314119**	2	3.495746
Q60759	HAMNLEAVNTYEGTHDIHALILGR	**0.991618489**	4	5.504468
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.178457447**	**0.23364**	**3**
Q60817	DIELVMSQANVSR	**1.089423212**	2	3.21888
Q60817	IEDLSQQAQLAAAEK	**1.289943617**	2	4.623466
Q60817	NILFVITKPDVYK	**1.229842447**	2	3.316381
Q60952	**CP250 Centrosome_associated protein CEP250**	**0.889530238**	**0.52515**	**2**
Q60952	AQVIESQRGQIQDLK	**0.835565974**	2	2.485214
Q60952	GQIQDLKK	**0.907294339**	1	1.926622
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.800136617**	**3.2E-07**	**3**
Q61029	SELVANNVTLPAGEQR	**0.772670156**	2	4.318009
Q61029	SSTPLPTVSSSAENTR	**0.912599677**	2	2.861665
Q61029	YGVNPGPIVGTTR	**0.781664045**	2	2.49091
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.088034887**	**0.97044**	**2**
Q61035	ASAEQIEEEVTK	**1.02083256**	2	3.13664
Q61035	REDLVEEIR	**1.059062644**	2	2.446332
Q61043	**NIN Ninein**	**0.844061869**	**0.42082**	**2**
Q61043	ERATAAAMKQEQEILER	**0.879530555**	2	2.347957
Q61043	NEITTLNEEDSISNLK	**0.83985724**	2	2.369422
Q61301	**CTNA2 Catenin alpha_2**	**0.881166969**	**0.00558**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	**0.90265869**	2	3.852325
Q61301	TSVQTEDDQLIAGQSAR	**1.463023569**	2	5.11628
Q61301	WDDSGNDIIVLAK	**0.869037757**	2	3.063114
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.763187484**	**0.51679**	**3**
Q61335	AENEALAMQK	**0.846477258**	2	3.189856
Q61335	AENEALAMQK+Oxidation(7)	**0.899135668**		
Q61335	YMEENDQLK	**0.699091838**	2	2.606822
Q61595	**KTN1 Kinectin**	**1.402568798**	**0.14035**	**3**
Q61595	EKNWEAMEALASTEK	**0.645689713**	2	2.303116
Q61595	TAEHEAAQQDLQSK	**0.978212693**	2	4.094522
Q61595	VEPVLVTK	**1.477850476**	2	2.391616
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**0.923857006**	**0.0461**	**5**
Q61656	ELAQQVQQVAAEYCR	**1.876529625**	2	3.525018
Q61656	GDGPICLVLAPTR	**0.905968446**	2	3.290333
Q61656	LIDFLECGK	**1.181060938**	2	2.377806
Q61656	MLDMGFEPQIR	**0.75837971**	2	2.734263

Q61656	WNLDELPK	**1.290670245**	2	2.339129
Q61789	**LAMA3 Laminin subunit alpha_3**	**0.886850129**	**0.9343**	**2**
Q61789	QLEEIK	**0.851133662**	1	2.071705
Q61789	RLQQVSPALNSLQQTLK	**0.99325752**	2	2.358094
Q61838	**A2M Alpha_2_macroglobulin**	**0.928534112**	**0.99897**	**2**
Q61838	QQNSHGGFSSTQDTVVALQALSK	**0.991662301**	3	3.40497
Q61838	TEVNTNHVLIYIEK	**0.919048666**	2	4.017232
Q61941	**transhydrogenase_ mitochondrial**	**1.006881088**	**0.56793**	**11**
Q61941	EANSIVITPGYGLCAAK	**0.998395442**	2	3.62171
Q61941	FGIHPVAGR	**0.800363647**	2	2.600293
Q61941	GITHIGYTDLPSR	**0.925866073**	3	3.492761
Q61941	ILIVGGGVAGLASAGAAK	**0.940908335**	2	4.986356
Q61941	KTTVLAMDQVPR	**0.832693477**	2	3.020321
Q61941	LGGLTAALGGAVGIMGLANGLR+Oxidation(14)	**0.918689984**		
Q61941	MATQASTLYSNNITK	**1.575573948**	2	4.302822
Q61941	QGFNVVVESGAGEASK	**1.038317873**	2	3.995804
Q61941	SLGAEPLEVDLK	**0.915201809**	2	3.072893
Q61941	TTVLAMDQVPR	**0.821656102**	2	3.108333
Q61941	VTIAQGYDALSSMANISGYK	**0.816948522**	2	5.16627
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.655015392**	**2.4E-05**	**7**
Q62095	DLLDLLVEAK	**2.500824688**	2	2.673614
Q62095	GCHLLVATPGR	**1.220083217**	2	2.422241
Q62095	HVINFDLPSDIEEYVHR	**1.59684205**	3	3.741286
Q62095	QYPISLVLAPTR	**1.270101327**	2	2.366513
Q62095	SFLLDLLNATGK	**1.394669666**	2	4.648483
Q62095	VGNLGLATSFFNER	**1.33926269**	2	3.054713
Q62095	VGSTSENITQK	**1.655021673**	2	2.719128
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.067951112**	**0.92267**	**17**
Q62261	ALVADSHPESER	**1.112346165**	2	3.214828
Q62261	EGMQLISEKPETEAVVK	**0.816669272**	2	2.633162
Q62261	EIEELQSQAQALSQEGK	**1.162511292**	2	4.620604
Q62261	EVDDLEQWIAER	**0.82309479**	2	2.469398
Q62261	EVVAGSHELGQDYEHVTMLQER	**0.679599537**	3	4.185279
Q62261	HQILEQAVEDYAETVHQLSK	**0.786040162**	3	4.062027
Q62261	ITDLYTDLR	**0.943478155**	2	2.601324
Q62261	IVSSNDVGHDEYSTQSLVK	**0.947699708**	3	3.53696
Q62261	LSDGNEYLFQAK	**0.856198979**	2	2.425565
Q62261	LVSDGNINSDR	**1.219373205**	2	3.226314
Q62261	LVSQDNFGFDLPAVEAATK	**1.175694395**	2	3.10879
Q62261	SNAHYNLQNAFNLAEQHLGLTK	**1.100865297**	3	3.701616
Q62261	SQNIITDSSSLNAEAIR	**0.976910096**	2	5.182074
Q62261	TLETPAAQMEGFLNR	**1.61298562**	2	3.75248
Q62261	TQTAIASEDMPNTLTEAEK	**1.096300151**	2	5.141212
Q62261	VIESTQDLGNDLAGVMALQR	**0.25052384**	3	4.310005
Q62261	VLDNAIETEK	**0.756577272**	2	2.523117
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.26579325**	**0.00097**	**3**
Q62425	FYSVNVDYSK	**1.308896042**	2	2.875136
Q62425	KNNPEPWNK	**0.91632306**	2	2.46735
Q62425	LGPNEQYK	**1.177129575**	2	2.303015
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**1.111542421**	**0.75584**	**2**
Q62446	FLQDHGSDSFLAEHK	**1.099061022**	3	3.677244
Q62446	SEETLDEGPPK	**1.119315702**	2	3.49318
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**0.826208293**	**1.7E-14**	**5**
Q62452	AMEIAEALGR	**0.720460723**	2	3.802165
Q62452	GAGVTLNVLEMTADDLENALK	**0.712380308**	3	5.544568
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(10)	**1.05313379**		

Q62452	WLPQNDLLGHPK	**0.877131703**	2	3.141353
Q62452	YTGTRPSNLAK	**0.907986826**	2	2.621476
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**0.800041917**	**2.1E-07**	**6**
Q62465	ACGLNFADLMGR	**0.797381879**	2	3.002732
Q62465	CLVLTGFGGYDK	**1.09020416**	2	3.433311
Q62465	GVDIVMDPLGGSDTAK	**0.801174315**	2	4.022839
Q62465	IDSVWPFEK	**0.799672779**	1	1.947339
Q62465	TVENVTVFGTASASK	**1.093668536**	2	3.884974
Q62465	VLLVPGPEKET	**0.7221742**	2	2.681477
Q62468	**VILI Villin_1**	**1.125853032**	**0.04813**	**2**
Q62468	HEDCYILDQGGLKIFVWK	**1.12446017**	2	2.466425
Q62468	SGAMSQALNFIKAK	**1.331162709**	2	2.343069
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.150304571**	**0.4574**	**3**
Q62636	INVNEIFYDLVR	**1.214152168**	2	3.998847
Q62636	QWSNCAFLESSAK	**1.145799161**	2	2.809093
Q62636	YDPTIEDSYR	**0.459384058**	2	2.369595
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.751834132**	**0.04104**	**7**
Q62651	HVLHVQLNRPEK	**0.708713119**	2	3.623407
Q62651	IPEEVSDHNYESIQVTSAQK	**1.124660251**	3	3.86903
Q62651	MMADEALDSGLVSR	**0.927976374**	2	3.596234
Q62651	MMADEALDSGLVSR+Oxidation(0)	**0.902771684**		
Q62651	MMADEALDSGLVSR+Oxidation(1)	**0.902771684**	2	3.352635
Q62651	RIPEEVSDHNYESIQVTSAQK	**0.832349569**	3	5.695125
Q62651	SLVNELTFTAR	**0.745888769**	2	3.470867
Q62717	**CAPS1 Calcium_dependent secretion activator 1**	**0.823691521**	**0.47698**	**2**
Q62717	IDELIEETVK	**0.856286929**	2	2.579759
Q62717	NCPDQDLKIK	**0.816002976**	1	1.930554
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**0.476379337**	**9.9E-20**	**4**
Q62730	AVLVTGADSGFGHALAK	**0.457278525**	2	4.166598
Q62730	EIQENYGQEYVHTQK	**0.50529327**	2	4.414559
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	**0.722418799**	3	4.516719
Q62730	VVTIHPGGFQTNIVGSQDSWDK	**0.422494851**	2	5.433097
Q62736	**CALD1 Non_muscle caldesmon**	**0.952508524**	**0.97282**	**12**
Q62736	ASGDKEAEGAPQVEAGK	**0.938814663**	2	4.556921
Q62736	ASGDKEAEGAPQVEAGKR	**0.891330321**	3	3.881339
Q62736	EEIERR	**1.48049833**	1	1.936645
Q62736	EFDPTITDGSLSVPSR	**1.045400526**	2	3.764091
Q62736	GETESEEFEK	**0.819970214**	2	2.755527
Q62736	GGNLGENQIKDEK	**0.851393209**	2	3.428121
Q62736	LEQYTNAIEGTK	**1.028609636**	2	3.908771
Q62736	MQNNSAENETAEGEEKGESR	**1.108630585**	3	4.421706
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0)	**1.404735177**		
Q62736	NDDDEEEAAR	**1.253631395**	2	3.356249
Q62736	RGETESEEFEK	**1.059151314**	2	3.156646
Q62736	VLEEEEQR	**0.993644681**	2	2.471493
Q62745	**CD81 CD81 antigen**	**0.911999788**	**0.95904**	**2**
Q62745	NSLCPSSSNSFTQLLK	**0.815123836**	2	2.734691
Q62745	QFYDQALQQAVMDDDANNAK	**0.819669356**	2	5.214956
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**0.872912483**	**0.83643**	**3**
Q62785	ANEEDEQEEGGDGASGDPK	**0.916281493**	2	4.265042
Q62785	GVEGLIDIENPNR	**0.920697943**	2	2.859095
Q62785	KVTQLDLDGPK	**1.001835047**	2	2.811088
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.118823856**	**0.37814**	**2**
Q62789	IILDELVQR	**0.842423968**	2	3.580021

Q62789	WIPQNDLLGHPK	**0.877131703**	2	3.141353
Q62812	**MYH9 Myosin_9**	**0.970537938**	**1.3E-09**	**63**
Q62812	ALEEAMEQK	**0.781549122**	2	3.043352
Q62812	ALELDSNLYR	**0.95960642**	2	3.322808
Q62812	ALEQQVEEMK	**1.018667464**	2	2.959561
Q62812	ANLQIDQINTDLNLER	**0.79750583**	2	4.672554
Q62812	ASIAALEAK	**0.936986121**	2	2.564772
Q62812	ASREEILAQAK	**1.346501806**	2	2.888782
Q62812	CQYLQAEK	**1.064267888**	2	2.452314
Q62812	DELADEIANSSGK	**1.447182005**	2	2.848852
Q62812	DFSALESQLQDTQELLQEENR	**0.909125143**	3	5.59496
Q62812	DLEAHIDTANK	**1.124525446**	2	3.227349
Q62812	DLQGRDEQSEEK	**0.459440555**	2	3.219682
Q62812	EEILAQAK	**0.918312967**	1	2.314359
Q62812	EEILAQAKENEK	**0.851393209**	2	2.380374
Q62812	ELEDATETADAMNR	**1.052670226**	2	4.125894
Q62812	ELETQISELQEDLESER	**0.841837933**	2	3.977254
Q62812	HEAMITDLEER	**0.848198851**	2	3.125541
Q62812	HEDELLAK	**0.946696607**	2	2.814973
Q62812	HSQAVEELAEQLEQTK	**0.809549142**	2	4.944811
Q62812	HSQAVEELAEQLEQTKR	**0.954676142**	3	4.918312
Q62812	IIGLDQVAGMSETALPGAFK	**1.114941566**	2	5.328916
Q62812	IRELETQISELQEDLESER	**0.995290987**	3	3.549749
Q62812	KEEELQAALAR	**0.929837933**	2	3.150658
Q62812	KKVEAQLQELQVK	**0.652015392**	2	4.650298
Q62812	KLEEDQIIMEDQNCK	**1.042044374**	2	5.908616
Q62812	KLEGDSTDLSDQIAELQAQIAELK	**0.868344571**	2	5.83131
Q62812	KQELEEICHDLEAR	**0.949898545**	2	4.495746
Q62812	KVEAQLQELQVK	**0.996096932**	2	4.244519
Q62812	LEEDQIIMEDQNCK	**0.990409638**	2	4.514317
Q62812	LEGDSTDLSDQIAELQAQIAELK	**0.845589276**	2	3.573766
Q62812	LEVNLQAMK	**0.977775373**	2	2.709557
Q62812	LQEMESAVK	**0.792024214**	2	2.543259
Q62812	LQQELDDLLVDLDHQR	**0.748318252**	2	4.783808
Q62812	LQVELDSVTGLLNQSDSK	**0.863190201**	2	5.731694
Q62812	LTEMETMQSQLMAEK	**0.915570831**	2	3.787762
Q62812	MEDGVGCLETAEEAK	**0.930080388**	2	4.229836
Q62812	MQQNIQELEEQLEEEESAR	**0.905822819**	2	6.155732
Q62812	MQQNIQELEEQLEEEESAR+Oxidation(0)	**0.832921732**		
Q62812	NAEQFKDQADK	**1.105516644**	2	3.680455
Q62812	NLPIYSEEIVDMYK	**1.186871964**	2	3.213697
Q62812	NMDPLNDNIATLLHQSSDK	**0.944336783**	2	4.609973
Q62812	NTDQASMPDNTAAQK	**0.796039771**	2	5.421165
Q62812	NTDQASMPDNTAAQK+Oxidation(6)	**1.576383063**		
Q62812	QAQQERDELADEIANSSGK	**1.044390992**	3	4.37909
Q62812	QIATLHAQVTDMK	**0.572421552**	2	2.801854
Q62812	QLEEAEEEAQR	**1.00203018**	2	3.685886
Q62812	QNKELK	**0.851133662**	1	1.923305
Q62812	QSVSNLEK	**1.006454005**	2	2.601386
Q62812	QTLENERGELANEVK	**0.952206901**	2	2.913452
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	**0.894585938**	3	5.424296
Q62812	RQLEEAEEEAQR	**0.86603788**	2	4.352044
Q62812	SMEAEMIQLQEELAAAER	**0.954681596**	2	4.781615
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)	**0.972149825**		
Q62812	TDLLLEPYNK	**0.824293229**	2	2.848344
Q62812	TELEDTLDSTAAQQELR	**0.813628387**	2	5.294106
Q62812	THEAQIQEMR	**0.760061379**	2	3.26961

Q62812	THEAQIQEMR+Oxidation(8)	**1.821104094**		
Q62812	TQLEELEDELQATEDAK	**0.898130925**	2	5.893728
Q62812	VAEFTTDLMEEEEK	**0.991649442**	2	4.137895
Q62812	VEAQLQELQVK	**0.55591357**	2	3.695632
Q62812	VEDMAELTCLNEASVLHNLK	**0.943070959**	2	4.46499
Q62812	VISGVLQLQGNIVFK	**1.002280473**	2	2.851271
Q62812	VSHLLGINVTDFTR	**0.930332021**	2	3.813626
Q62812	YEILTPNSIPK	**0.878907227**	2	3.011113
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.181713674**	**0.00035**	**5**
Q62826	ADILEDKDGK	**0.865777814**	2	2.699049
Q62826	AFITNIPFDVK	**1.220312109**	2	3.359712
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	**0.777762105**	2	4.819779
Q62826	INEILSNALK	**0.79216795**	2	2.69234
Q62826	MGPVMDRMATGLER+Oxidation(0)	**0.823999476**		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.213997179**	**0.84224**	**2**
Q62871	ADAEEEAATR	**0.976804616**	2	3.456928
Q62871	SVSTPSEAGSQDSGDGAVGSR	**1.345053535**	2	3.373426
Q62902	**LMAN1 Protein ERGIC_53**	**0.996276194**	**0.00741**	**6**
Q62902	GAGTPGQPGQVSQQELDTVVR	**1.179522856**	2	4.302756
Q62902	GHPDLQGQPADDIFESIGDR	**1.087461516**	2	4.739892
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	**1.300117252**	3	4.969922
Q62902	RGAGTPGQPGQVSQQELDTVVR	**1.055492546**	3	4.417906
Q62902	YQEEFEHFQQELDK	**1.255655017**	2	4.730906
Q62902	YVSSLTEEISR	**1.175821058**	2	3.511666
Q62904	**DHB7 3_keto_steroid reductase**	**0.883821803**	**0.90962**	**2**
Q62904	YATDLLNVALNR	**0.883574381**	2	2.648441
Q62904	YLSGTTGLGTNYVK	**0.897259272**	2	2.93935
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.798319988**	**0.00018**	**2**
Q62967	GLQVAPVLLSDELK	**0.569439338**	2	2.815267
Q62967	VYGVEGDLSEVAR	**0.88158452**	2	3.137665
Q62975	**ZPI Protein Z_dependent protease inhibitor**	**0.724034851**	**0.01892**	**2**
Q62975	FKLNQRYEMHELLK	**0.710771985**	2	2.70348
Q62975	KMEVFFPKFK	**0.785816379**	1	2.060384
Q63041	**A1M Alpha_1_macroglobulin**	**0.847992822**	**0.36775**	**10**
Q63041	AEDITHNGIVYTPK	**0.744162774**	2	3.463758
Q63041	AEQGAYLGPLPYK	**0.729157493**	2	3.238444
Q63041	AESPVFVQTDKPIYKPGQTVK	**0.751777941**	3	4.738815
Q63041	DTVVKPVIVEPEGIEK	**0.869036867**	2	2.457087
Q63041	GSIFNSGSHVLPLEQGK	**0.634736349**	2	3.75082
Q63041	LQDQSNIQR	**0.78760439**	2	2.916166
Q63041	QDLNDNDAYSVFQSIGLK	**1.61792108**	2	2.785951
Q63041	QLNYQHSDGSYSTFGDR	**0.976218005**	2	2.645306
Q63041	YNILPEAEGEAPFTLK	**0.844802289**	2	4.984459
Q63041	YVVLVPSELYAGVPEK	**0.929104163**	2	3.074736
Q63060	**GLPK Glycerol kinase**	**1.315270973**	**0.00767**	**11**
Q63060	AVLGPLVGAVDQGTSSTR	**1.15632209**	2	5.297806
Q63060	CVFSEHGLLTTVAYK	**1.177752273**	2	4.015862
Q63060	DCGIPLSHLQVDGGMTSNK	**1.378560151**	2	3.790442
Q63060	EILQSVYECIEK	**1.413691207**	2	3.635431
Q63060	FEPQINAEESEIR	**1.111304196**	2	3.518729
Q63060	KAVLGPLVGAVDQGTSSTR	**0.93541102**	3	3.337056
Q63060	KVQEAVEENR	**1.918010323**	2	3.223442
Q63060	LGQLNIDISNIK	**1.364593767**	2	2.82469
Q63060	NTYGTGCFLLCNTGHK	**0.988575091**	2	4.149413
Q63060	TAELLSHHQVEIK	**1.279537204**	2	3.149246

Q63060	VQEAVEENR	**1.280974966**	2	3.041784
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**0.95348804**	**2.7E-06**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	**1.058876416**	3	5.50354
Q63081	GESPVDYDGGR	**0.840969326**	2	2.856317
Q63081	GSFSEQGINEFLR	**0.991185679**	2	4.267861
Q63081	GSTAPVGGGSFPNITPR	**0.932568861**	2	4.823972
Q63081	HQSLGGQYGVQGFPTIK	**0.816831132**	2	5.125422
Q63081	KDVVELTDDTFDK	**0.976224598**	2	4.115155
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	**0.877218661**	4	5.215255
Q63081	NLEPEWAAAATEVK	**0.868541977**	2	4.081563
Q63081	NSYLEVLLK	**0.869717646**	2	2.72928
Q63081	TCEEHQLCVVAVLPHILDTGATGR	**0.788173382**	3	4.550593
Q63081	TGEAIVDAALSALR	**0.874889595**	3	4.58711
Q63083	**NUCB1 Nucleobindin_1**	**1.196292122**	**0.15741**	**4**
Q63083	ADTGDAPVPAPAGDQK	**1.199807907**	2	3.463319
Q63083	ELQQAVLQMEQR	**1.465730107**	2	2.64502
Q63083	LSQETEALGR	**1.079833841**	2	2.828318
Q63083	VNVPGSQAQLK	**0.943736796**	2	2.550505
Q63089	**S22A1 Solute carrier family 22 member 1**	**1.180154237**	**0.96913**	**2**
Q63089	ENTIYLQVQTGK	**0.963732181**	2	2.317788
Q63089	GVALPETIEEAENLGR	**1.037381721**	2	3.10419
Q63108	**EST3 Liver carboxylesterase 3**	**0.771597065**	**2.4E-06**	**7**
Q63108	DFNTVPYIVGINK	**2.838530197**	2	2.677123
Q63108	GGTSKEEINLSK	**0.739818569**	2	3.540097
Q63108	LDPMTATSLLK	**0.906803996**	2	2.521205
Q63108	MKPSTVVGDHGDEIYSVFGAPILR	**0.972199377**	3	3.887483
Q63108	QKTEEELLETTLK	**0.824075408**	2	3.574369
Q63108	SSFLLNLPEEAIPVAVEK	**0.771625682**	2	4.645937
Q63108	TEEELLETTLK	**0.851866051**	2	2.499465
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.299209987**	**0.00243**	**6**
Q63120	ACALLPDLEILPGGDMAEIGEK	**1.596323494**	2	3.498795
Q63120	ISEYINVENEAPWVTDK	**1.529844687**	2	3.79597
Q63120	IVEYGSPEELLSNR	**0.946001085**	2	3.41682
Q63120	QSQSQDVLVLEEAK	**1.144368101**	2	3.266795
Q63120	YFAWEPSFQEQVQGIR	**1.333266634**	2	4.646604
Q63120	YRPELDLVLK	**1.818626781**	2	2.399018
Q63150	**DPYS Dihydropyrimidinase**	**0.934817863**	**0.84203**	**9**
Q63150	DQTCTPIPVK	**1.169030142**	2	2.448888
Q63150	EIGAIAQVHAENGDLIAEGAK	**1.114908346**	2	4.997487
Q63150	FVAVTSTNAAK	**0.980808997**	2	3.211935
Q63150	GEVITLKPR	**0.93253884**	2	2.399349
Q63150	GSSLIEAFETWR	**0.937254**	2	3.06013
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	**0.771679537**	3	3.627389
Q63150	VVNDDFSQVADVLVEDGVVR	**0.930380977**	2	5.589057
Q63150	VVYEAGVFDVTAGHGK	**1.095933176**	2	3.865458
Q63150	VVYGEPIAAGLGTDGTQYWNK	**0.929692573**	2	5.477098
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**0.816929526**	**1.7E-07**	**16**
Q63270	AVEAGLNVKPYVK	**0.7870147**	2	3.255152
Q63270	AVLAESYER	**0.856404193**	2	2.370706
Q63270	FVEFFGPGVAQLSIADR	**1.282241827**	2	5.201436
Q63270	GFQVAPDHHNDHK	**2.652147425**	2	3.251628
Q63270	IDFEKEPLGVNAQGQQVFLK	**0.947449339**	3	4.687419
Q63270	KNDIENILNWSIMQHK	**0.813076301**	3	4.652308
Q63270	NCDEFLVK	**0.940442133**	1	2.048974
Q63270	NQDLEFER	**0.720682921**	2	2.479582
Q63270	QAPQTVHLPSGETLDVFDAAER	**0.483249442**	3	3.701478

Q63270	SIEVPFKPAR	**0.971830809**	2	2.589269
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	**1.081689697**	3	5.093326
Q63270	SPPFFESLTLDLQPPK	**1.172773094**	3	3.88698
Q63270	SWNALAAPSEK	**0.89599186**	1	2.325432
Q63270	TSLSPGSGVVTYYLR	**1.021829971**	2	3.470172
Q63270	VILQDFTGVPAVVDFAAMR	**1.277594253**	3	4.483238
Q63270	YQQAGLPLIVLAGK	**0.740670491**	2	3.539708
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.181522112**	**0.00029**	**17**
Q63276	AHGHFLFVVGEDDKNLNSK	**1.861430624**	2	5.835223
Q63276	ASEVGEVDLER	**1.01604592**	2	3.869868
Q63276	DDKGNLFNSQAFYR	**0.901941124**	2	3.298659
Q63276	GNLFNSQAFYR	**1.08816689**	2	3.048615
Q63276	LCHPYFPVEGK	**0.855862994**	2	2.656939
Q63276	LTAVPLSALVDEPVHIR	**0.942633482**	2	4.111654
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	**1.645856128**	2	4.057826
Q63276	QHLNPGFNSQL	**1.064215256**	2	3.547451
Q63276	QITATVLINGPNFVSSNPHVYR	**0.934696611**	3	5.248504
Q63276	TFEETADK	**1.159577112**	1	1.975335
Q63276	TFEETADKDSK	**1.049046672**	2	3.926252
Q63276	VDLEYFEEGVEFLLR	**1.297139038**	3	4.795879
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	**1.062653134**	2	5.307502
Q63276	VISSSLDSLILER	**0.264819011**	2	3.537139
Q63276	VTGLTPFQVVCLQASLK	**1.215499325**	3	5.327432
Q63276	WYVAPGVTR	**0.831604105**	2	2.65423
Q63276	YCFPIEK	**1.01697267**	2	2.595945
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.065578371**	**0.94622**	**24**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	**0.869974978**	3	5.970218
Q63342	AWGSEMNCDTNPLEAGLDYFIK	**0.901385711**	2	4.50319
Q63342	DGLLFGPYESQEK	**1.119038254**	2	2.61695
Q63342	EGQESPPSPPEWK	**1.023164553**	2	2.676322
Q63342	GGYDVEIR	**0.739005852**	2	2.306157
Q63342	GQDSTQLLDHLCANVIPK	**0.814694189**	2	4.022426
Q63342	IMNAGQEEGIDNFGTYALNALR	**0.801838565**	2	4.875884
Q63342	ISDIPVTAIR	**0.864370751**	2	3.232371
Q63342	ITEHVEAAMEMVPVLK	**0.917894466**	2	3.927021
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	**0.813446146**	3	5.173427
Q63342	LEEETGQVVGFHQPGSIR	**0.82221005**	2	4.767273
Q63342	LNKPADFTGK	**1.018593693**	2	2.636228
Q63342	LTSEDLSDDVFK	**0.82449212**	2	4.147946
Q63342	NITDELGVLGVAGPYAR	**0.760385434**	2	4.831796
Q63342	NYPATIIQEPLVLTEPTR	**0.926987644**	2	4.1668
Q63342	REDSAALYER	**0.786397634**	2	3.230521
Q63342	SLAFAYVPVELSEVGQQVEVELLGK	**1.458699174**	3	4.972811
Q63342	TNWHATEQYIIEPEK	**1.18751916**	2	4.153389
Q63342	VGFTNISHMLTPR	**1.181567962**	2	2.402288
Q63342	VGVIDLSPFGK	**0.737743895**	2	3.399476
Q63342	VIGNTTSGSYSYSIQK	**1.069380368**	2	4.334137
Q63342	WIEEAAVR	**1.124252857**	2	2.761974
Q63342	WTTTQYTEAK	**0.889024023**	2	2.81355
Q63342	YLSDWILHGEPPFDLIELDPNR	**0.787940764**	3	4.346085
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.071892083**	**0.95961**	**8**
Q63347	ALDEGDIALLK	**1.060919397**	2	3.094614
Q63347	ESDTGLAPPALWDLAADK	**1.023337582**	2	2.508094
Q63347	FDDGAGGDNEVQR	**1.096544819**	2	4.175218
Q63347	FVVDLSDQVAPTDIEEGMR	**0.809589742**	2	3.856356

Q63347	IINADSEDPK	**1.02496961**	2	3.047869
Q63347	QTLQSEQPLQVAR	**0.979188113**	2	4.001585
Q63347	QVEDDIQQLLK	**0.962966338**	2	2.441735
Q63347	TMLELINQLDGFDPR	**0.808952837**	2	2.964977
Q63355	**MYO1C Myosin_Ic**	**0.449245719**	**0.04838**	**2**
Q63355	MSLLQLVEILR	**0.428850996**	2	2.511883
Q63355	YMDVQFDFKGAPVGGHILSYLLEK+Oxidation(1)	**0.690365499**		
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.038027301**	**0.99914**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	**1.022839789**	2	6.6786
Q63362	KYTEQITSEK	**0.969244764**	2	2.426236
Q63362	TTGLVGLAVCDTPHER	**1.027977438**	2	3.476041
Q63362	YTEQITSEK	**1.086307401**	2	2.452557
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**0.739694388**	**0.30234**	**2**
Q63413	AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK	**0.529673341**	3	3.799471
Q63413	NCPHIVVGTPGR	**0.869503826**	2	3.049633
Q63429	**UBC Polyubiquitin_C**	**1.046506035**	**0.86426**	**3**
Q63429	ESTLHLVLR	**1.60296961**	2	2.427556
Q63429	TITLEVEPSDTIENVK	**1.041554259**	2	4.717163
Q63429	TLSDYNIQK	**1.017611848**	2	2.548782
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**0.968981304**	**0.013**	**10**
Q63448	ADWLDSEAPLAAYR	**0.876993946**	2	4.247795
Q63448	DDAVALVDAIAPSDFVLGSPIGR	**0.838375337**	3	4.142456
Q63448	EIHALASAGKPLASWTAQR	**0.706685637**	2	4.096396
Q63448	GGYISGEQTGK	**0.939662334**	2	2.920685
Q63448	NLWAAVLQQSGVLER	**0.84312952**	2	4.46384
Q63448	QFGPTDKEEIPVLEYPLQQWR	**0.832447963**	3	3.502545
Q63448	TIFLDLIELQR	**1.01295583**	2	3.38361
Q63448	TIFSTLENDPLFARPFGADLPLEK	**0.823822747**	3	4.512849
Q63448	TTAHYDPATQEFILHSPDFEAAK	**1.095430972**	3	4.542653
Q63448	TVNFLEAYPGILGQK	**1.099789807**	2	4.615621
Q63507	**RL14 60S ribosomal protein L14**	**1.319415425**	**0.99203**	**3**
Q63507	ALVDGPCTR	**1.094792754**	2	2.415944
Q63507	CMQLTDFILK	**0.852002025**	2	2.551852
Q63507	LVAIVDVIDQNR	**0.996773835**	2	4.126261
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.053879658**	**0.98735**	**3**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	**0.919126937**	3	5.36974
Q63524	HEQEYMEVR	**1.071155736**	2	3.33628
Q63524	HEQEYMEVR+Oxidation(5)	**0.934787416**		
Q63525	**NUDC Nuclear migration protein nudC**	**1.150364776**	**0.65724**	**4**
Q63525	GQAPVIDGELYNEVK	**1.154966248**	2	3.454822
Q63525	LSDLDSETR	**1.031453044**	2	2.665147
Q63525	LVTSDPEINTK	**1.143503957**	2	2.395669
Q63525	VEESSWLIEDGK	**0.936281392**	2	3.01153
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.081143314**	**0.46305**	**5**
Q63569	AMEVDERPTEQYSDIGGLDK	**1.473896012**	3	3.656654
Q63569	CTDDFNGAQCK	**0.889465209**	2	3.332251
Q63569	MNVSPDVNYEELAR	**1.072062729**	2	3.309615
Q63569	MSTEEIVQR	**0.999919607**	2	2.404523
Q63569	QTYFLPVIGLVDAEK	**1.206694506**	2	2.730999
Q63570	**PRS6B 26S protease regulatory subunit 6B**	**1.234347504**	**0.12256**	**4**
Q63570	GVLMYGPPGCGK+Oxidation(3)	**1.449555786**		
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	**1.671573012**	3	5.442052
Q63570	KDEQEHEFYK	**1.286723538**	2	2.956087
Q63570	RFDAQTGADR	**1.099776524**	2	2.609976

Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**0.987897418**	**0.99939**	**4**
Q63584	ITDSAGHILYAK	**1.028245036**	2	3.314518
Q63584	LEDLSESIVNDFAYMK	**0.966649357**	2	2.92805
Q63584	NYEEIAK	**1.021727486**	1	2.266356
Q63584	RLEDLSESIVNDFAYMK	**0.948032911**	2	3.829109
Q63598	**PLST Plastin_3**	**0.807572058**	**0.81047**	**11**
Q63598	AESMLQQADK	**0.906198869**	2	2.879221
Q63598	ATDDIIVNWVNGTLSEAGK	**0.769763364**	3	4.949576
Q63598	AVGDGIVLCK	**1.083749509**	1	1.951555
Q63598	HVIPMNPNTDDLFK	**0.742480577**	2	2.782761
Q63598	IDINMSGFNETDDLKR	**0.849405019**	2	4.337924
Q63598	INNFSADIK	**1.178670926**	2	2.578387
Q63598	KLENCNYAVELGK	**1.139715645**	2	3.923074
Q63598	NEALAALLR	**1.005945045**	2	2.745475
Q63598	VYALPEDLVEVKPK	**0.951761763**	2	2.961497
Q63598	YPALTKPENQDIDWTLLEGETR	**0.910990216**	3	5.177026
Q63598	YTLNVMEDLGEGQK	**1.233282043**	2	3.698828
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**0.985622772**	**0.93371**	**8**
Q63610	EQAEAEVASLNR	**1.395068763**	2	2.865719
Q63610	IQVLQQQADDAEER	**0.971951071**	2	5.12711
Q63610	KIQVLQQQADDAEER	**1.043290205**	2	5.410338
Q63610	KLVIIEGDLER	**0.965291869**	2	2.77177
Q63610	LVIIEGDLER	**0.853797338**	2	2.482031
Q63610	MELQEIQLK	**0.985217119**	2	3.021322
Q63610	TIDDLEDKLK	**0.714652064**	2	2.861605
Q63610	YSQKEDKYEEEIK	**0.920229659**	2	4.677725
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.060900201**	**0.00307**	**16**
Q63617	AANSLEAFIFETQDK	**0.865270806**	2	3.303391
Q63617	DAVITVPAFFNQAER	**0.970900413**	2	2.333813
Q63617	EGETPDEKESGDKSEAQKPNEK	**1.550392947**	3	3.770401
Q63617	ESGDKSEAQKPNEK	**0.821844983**	2	2.348613
Q63617	FLGDSAAGMAIK	**0.845000448**	2	2.647946
Q63617	LEDLTLR	**1.023061089**	2	2.373968
Q63617	LGNTISSLFGGGTSSDAK	**0.749103252**	2	3.302428
Q63617	LIPEMDQIFTDVEMTTLEK	**0.944160699**	2	2.782573
Q63617	LYQPEYQEVSTEEQR	**1.490865124**	2	5.059073
Q63617	NINADEAAAMGAVYQAAALSK	**1.146479017**	2	2.993598
Q63617	SLAEDFAEQPIK	**1.13477278**	2	2.735234
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	**0.892220865**	3	3.91786
Q63617	TLGGLEMELR	**0.85611828**	2	2.306415
Q63617	VEFEELCADLFDR	**0.866577146**	2	3.89708
Q63617	VESVFETLVEDSPEEESTLTK	**1.504571037**	2	4.21553
Q63617	VLQLINDNTATALSYGVFR	**1.189228608**	2	2.947274
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**0.885781063**	**0.87591**	**2**
Q63692	EGEEAGPGDPLLEAVPK	**0.950261317**	2	3.577682
Q63692	LGPGGLDPVEVYESLPEELQK	**1.029633647**	2	2.685598
Q63716	**PRDX1 Peroxiredoxin_1**	**1.139888418**	**8E-08**	**15**
Q63716	ADEGISFR	**1.037488956**	2	3.06872
Q63716	ATAVMPDGQFK	**0.973680711**	2	2.943845
Q63716	DISLSDYK	**1.943713007**	2	2.505138
Q63716	HGEVCPAGWKPGSDTIKPDVNK	**1.013416054**	4	6.228096
Q63716	IGHPAPSFK	**2.218505044**	1	1.932111
Q63716	KLNCQVIGASVDSHFCHLAWINTPK	**9.047404299**	4	4.572121
Q63716	KQGGLGPMNIPLVSDPK	**0.885778079**	2	4.135698
Q63716	LNCQVIGASVDSHFCHLAWINTPK	**1.302013798**	3	3.653662
Q63716	LVQAFQFTDK	**2.068270604**	2	3.532369

Q63716	QGGLGPMNIPLVSDPK	0.582517491	2	3.479512
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6)	1.082828394		
Q63716	QITINDLPVGR	0.958007309	2	3.308394
Q63716	RTIAQDYGVLK	1.025038195	2	2.532115
Q63716	SVDEILR	0.891832373	2	2.699282
Q63716	TIAQDYGVLK	1.064552536	2	3.247339
Q63768	**CRK Adapter molecule crk**	**1.03740205**	**0.71996**	**2**
Q63768	IGDQEFDSLPALLEFYK	0.900773919	2	3.292372
Q63768	VPNAYDKTALALEVGELVK	1.169420492	2	2.317183
Q63797	**PSME1 Proteasome activator complex subunit 1**	**0.928564484**	**1.1E-06**	**10**
Q63797	EPALNEANLSNLK	0.860166251	2	2.400531
Q63797	ISELDAFLK	0.928572956	2	2.819068
Q63797	ISELDAFLKEPALNEANLSNLK	0.746431094	3	6.055887
Q63797	KGDEDDKGPPCGPVNCNEK	0.904545747	3	4.801366
Q63797	KISELDAFLKEPALNEANLSNLK	0.850545704	3	5.733959
Q63797	LEGFQTQISK	1.042677861	2	3.01388
Q63797	NAYAVLYDIILK	1.773361083	2	2.883824
Q63797	QLVHELDEAEYQEIR	0.949880783	3	4.660054
Q63797	TENLLGSYFPK	0.937176947	2	3.60702
Q63797	VDVFREDLCSK	0.79548186	2	2.387007
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.0768253**	**0.8922**	**6**
Q63798	AFYAELHHIISSNLEK	1.008559382	2	3.978549
Q63798	IEDGNDFGVAIQEK	0.853195321	2	4.24792
Q63798	IISLSQLLQEDSLNVADLSSLR	1.429727039	2	2.33724
Q63798	KIISLSQLLQEDSLNVADLSSLR	0.926930888	3	3.445489
Q63798	TKVEAFQTAISK	0.997354245	2	3.455294
Q63798	VEAFQTAISK	1.126077672	2	2.612056
Q63836	**SBP2 Selenium_binding protein 2**	**0.963231143**	**0.12221**	**5**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.045825456	3	5.46247
Q63836	GSFVLLDGETFEVK	0.935122975	2	2.446326
Q63836	IYVVDVGSEPR	0.887640635	2	3.959319
Q63836	LNPNFLVDFGK	0.733377321	2	2.730465
Q63836	LNPNFLVDFGKEPLGPALAHELR	0.748404588	3	4.310116
Q63945	**SET Protein SET**	**1.016497616**	**0.74475**	**3**
Q63945	IDFYFDENPYFENK	1.016497628	2	3.856183
Q63945	LNEQASEEILK	0.972305165	2	2.725482
Q63945	VEVTEFEDIK	0.660572431	2	2.567454
Q63965	**SFXN1 Sideroflexin_1**	**1.182662572**	**0.00513**	**6**
Q63965	MSGEVPPNINIKEPR+Oxidation(0)	0.858239394		
Q63965	NILLTNEQLENAR	0.816939	2	4.475253
Q63965	QAITQVVISR	0.851227322	2	2.43131
Q63965	QGIVPAGLTENELWR	0.404607787	2	2.972429
Q63965	WDQSTFIGR	1.061069248	2	2.833481
Q63965	YAYDSAFHPDTGEK	1.16024532	2	4.07131
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**0.860750216**	**9.9E-20**	**17**
Q64057	AWNIWADIPAPK	0.719605845	2	3.94756
Q64057	EDNEGVFNGSWGGR	0.871707896	2	3.637798
Q64057	EGGTVVYGGK	1.08741823	2	2.454009
Q64057	FKNEEEVFEWNNEVK	0.717040274	2	5.458163
Q64057	GAPTTSLVSIAVTK	0.542363853	2	4.213446
Q64057	GEVITTYCPANNEPIAR	0.767759243	2	5.085406
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.68772596	2	5.649642
Q64057	LFLHESIHDEVVDR	0.839893973	2	4.218174
Q64057	NEEEVFEWNNEVK	0.809055117	2	4.541942
Q64057	QAVSMFVQAVEEAK	0.84089447	2	3.084381
Q64057	QGLSSSIFTK	0.770521208	2	2.567421

Q64057	QVALMVQER	**0.661894581**	2	2.302101
Q64057	STCTINYSTALPLAQGIK	**1.980679108**	2	4.678034
Q64057	VGNPWDPNILYGPLHTK	**0.972606169**	3	4.141422
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	**0.672239081**	3	6.092217
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1)	**0.746255699**		
Q64057	VNLLSFTGSTQVGK	**1.221766783**	2	4.875194
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**0.866489645**	**0.7401**	**2**
Q640L5	EVIDLGQELR	**0.749549584**	2	2.355314
Q640L5	SMQLSQLDMVLDQTKTELEKTTNSVK	**0.873025331**	3	3.601153
Q64119	**MYL6 Myosin light polypeptide 6**	**0.842509984**	**0.11428**	**6**
Q64119	DQGTYEDYVEGLR	**1.001161799**	2	3.351062
Q64119	HVLVTLGEK	**0.906195678**	1	2.293932
Q64119	ILYSQCGDVMR	**1.185605985**	2	2.688288
Q64119	NKDQGTYEDYVEGLR	**0.891201944**	2	4.194821
Q64119	VFDKEGNGTVMGAEIR	**0.970092036**	2	3.517663
Q64119	VLDFEHFLPMLQTVAK	**0.814465388**	2	4.943352
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**0.89846189**	**0.16635**	**2**
Q64122	DGFIDKEDLHDMLASLGK	**0.810241401**	2	4.722607
Q64122	LNGTDPEDVIR	**1.07643433**	2	2.886698
Q64176	**EST22 Liver carboxylesterase 22**	**0.764806407**	**9.9E-20**	**4**
Q64176	AISESGVALTAGLVK	**0.781593479**	2	3.887493
Q64176	EGYLQIGATTQQAQK	**0.77384127**	2	4.587856
Q64176	LDQMTAMSLLK+Oxidation(3)	**0.776582795**		
Q64176	NFNTVPYIVGINK	**2.991926069**	2	3.455234
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**0.826736182**	**0.85826**	**9**
Q641Y0	ELGSECGIEFDEEK	**1.02138879**	2	3.523845
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	**1.892189906**	4	6.983397
Q641Y0	NTLLIAGLQAR	**0.965312407**	2	3.819304
Q641Y0	SSLNPILFR	**1.604032006**	2	2.411361
Q641Y0	TADDPSLSLIK	**0.73248569**	2	2.714213
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	**1.01748277**	4	6.546318
Q641Y0	TLVLLDNLNVR	**0.951216182**	2	3.846589
Q641Y0	WVPFDGDDIQLEFVR	**0.926343095**	2	2.734822
Q641Y0	YSQTGNYELAVALSR	**0.957128764**	2	3.453722
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**0.82874557**	**0.96964**	**5**
Q641Y2	GSGIQWDLR	**0.95482871**	2	2.547239
Q641Y2	IDEVEEMLTNNR	**0.860186562**	2	3.631346
Q641Y2	IIEQCLNK	**0.888836044**	2	2.883131
Q641Y2	LYTEGYQVPPGATYTAIEAPK	**1.162099019**	2	2.946365
Q641Y2	TQPYDVYDQVEFDVPIGSR	**1.120665439**	2	3.992386
Q641Y8	**DDX1 ATP_dependent RNA helicase DDX1**	**1.09821277**	**0.17613**	**3**
Q641Y8	GDVRFLICTDVAAR	**1.104322496**	2	2.34389
Q641Y8	GHVDILAPTVQELAALEK	**0.99264387**	3	3.880937
Q641Y8	GSAFAIGSDGLCCQSR	**1.219477925**	2	3.700125
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**0.80207872**	**0.01487**	**4**
Q64232	HYEVEIR	**0.80310215**	2	2.311956
Q64232	LCFLDKVEPQATISEIK	**0.808392094**	2	4.690748
Q64232	SLKDEDVLQK	**0.787330556**	2	3.338138
Q64232	VEPQATISEIK	**0.941662287**	2	2.373876
Q64240	**AMBP Protein AMBP**	**0.75766764**	**9.9E-20**	**3**
Q64240	AFAELWAFDAAQGK	**0.85701645**	2	3.526134
Q64240	AVLPQENEGSGSEPLITGTLK	**0.829291106**	2	4.844437

Q64240	TIAACNLPIVQGPCR	**0.706765176**	2	3.263431
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**1.838283264**	**8.3E-09**	**2**
Q642G4	GGDGQINEQVEK	**1.894816746**	2	3.136687
Q642G4	LLGPQEEGEGVVDVK	**1.127721849**	2	3.42698
Q64303	**PAK2 Serine/threonine_protein kinase PAK 2**	**0.863751052**	**0.97075**	**2**
Q64303	NKIISIFSSTEK	**0.851544532**	2	2.805637
Q64303	SVIDPIPAPVGDSNVDSGAK	**0.970820679**	2	2.832949
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.09325893**	**9.9E-20**	**19**
Q64380	AYGIESHVLSPAETK	**0.78072804**	2	4.588248
Q64380	DGTMDPAGTCTTLTR	**0.893321524**	2	4.071686
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	**0.97006523**	3	5.652499
Q64380	DLYPLMNVDDLYGTLYVPR	**0.771551339**	2	2.564961
Q64380	EEAQGASVVPQGPSQPLPSTANVVVIGGGSLGCQTLYHLAK	**0.748557344**	3	3.592457
Q64380	FHHSLTDHPR	**1.486147081**	2	2.652392
Q64380	FYLLGADAR	**0.926943858**	2	2.683296
Q64380	GAQVIENCAVTGIR	**1.056623168**	2	4.177184
Q64380	HGLVNAGYR	**0.82149185**	2	2.575393
Q64380	IEGIQNMPNVR	**0.640149759**	2	3.324223
Q64380	LQGDALSVGGYEANPIFWDEVSDK	**0.514188134**	2	4.458218
Q64380	NGDYALER	**1.068005323**	2	2.310163
Q64380	NYSVVFPHDEPLAGR	**0.660393596**	2	3.984923
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	**0.620160852**	3	4.655502
Q64380	RDPLHEELLGQGCVFQER	**0.666590582**	3	5.591014
Q64380	SDDSPLEAGLAFTCK	**1.141929585**	2	2.657634
Q64380	STVCGPESFTPDHKPLMGEAPELR	**0.657427878**	3	4.378253
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16)	**0.850805675**		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	**0.695140019**	3	5.090612
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**0.902630895**	**9.9E-20**	**29**
Q64428	ADMVIEAVFEDLAVK	**0.731168713**	2	3.967575
Q64428	ALMGLYNGQVLCK	**0.869231962**	2	3.308134
Q64428	DSIFSNLIGQLDYK	**1.482748729**	2	3.478514
Q64428	DTTASAVAVGLK	**1.021240686**	2	3.639003
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	**1.28217709**	3	5.405834
Q64428	EVQSEFVEVMNEIWANDQIR	**0.924420222**	3	4.221745
Q64428	FGELALTK	**0.902860674**	2	3.015374
Q64428	FGGGSVELLK	**0.945306601**	2	3.06003
Q64428	FVDLYGAQK	**0.928149764**	2	2.916451
Q64428	GFYIYQSGSK	**1.40759158**	2	2.835433
Q64428	ILQEGVDPK	**0.802347631**	2	3.290217
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	**0.788852887**	4	5.096561
Q64428	KTVLGVPEVLLGILPGAGGTQR	**0.828689458**	2	4.316564
Q64428	KYESAYGTQFTPCQLLR	**0.934057705**	2	5.012655
Q64428	LDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	**0.938070149**		
Q64428	LPAKPEVSSDEDIQYR	**1.698258873**	2	4.406058
Q64428	MGLVDQLVDPLGPGIK	**0.737782496**	2	5.015884
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0)	**0.87776552**		
Q64428	MQLLEIITTDK	**0.730058964**	2	3.931868
Q64428	MQLLEIITTDK+Oxidation(0)	**0.87132044**		
Q64428	MVGVPAAFDMMLTGR	**0.822404493**	2	3.256285
Q64428	NLNSEIDNILVNLR	**0.861696192**	2	4.710977
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	**0.74556901**	3	3.909349
Q64428	SPKPVVAAISGSCLGGGLELAIACQYR	**0.919249005**	3	3.641849
Q64428	TGLEQGNDAGYLAESEK	**1.0033062**	2	4.991644
Q64428	TIEYLEEVAVNFAK	**0.939623818**	3	4.20218
Q64428	TVLGVPEVLLGILPGAGGTQR	**0.742492328**	3	5.119709

Q64428	TVQQLAILGAGLMGAGIAQVSVDK	**0.730729695**	3	6.421921
Q64428	YESAYGTQFTPCQLLR	**0.871378481**	2	4.808635
Q64458	**CP2CT Cytochrome P450 2C29**	**0.800519767**	**0.00012**	**6**
Q64458	EHKESLDVTNPR	**0.887910563**	2	3.291539
Q64458	IKEHKESLDVTNPR	**0.65535438**	3	5.073951
Q64458	LPPGPTPLPIIGNFLQIDVK	**1.027132893**	2	4.004734
Q64458	VQEEAQCLVEELR	**1.644052485**	2	4.387594
Q64458	VQEEAQCLVEELRK	**1.224549856**	2	3.858618
Q64458	VQEEIDR	**0.911983556**	2	2.410247
Q64481	**CP3AG Cytochrome P450 3A16**	**2.533094857**	**0.26452**	**3**
Q64481	EMFPVIEQYGDILVK	**2.797247262**	2	3.031672
Q64481	GSIDPYVYLPFGNGPR	**2.159387167**	2	3.931224
Q64481	VLQNFSFQPCK	**2.610681195**	2	2.78399
Q64541	**AT1A4 Sodium/potassium_transporting ATPase subunit alpha_4**	**0.929011277**	**0.80905**	**2**
Q64541	LIIVEGCQR	**0.927632055**	2	2.678524
Q64541	NLEAVETLGSTSTICSDK	**0.94349035**	2	3.080789
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**0.847892861**	**0.86657**	**5**
Q64550	GHEVVVIAPEASIHIK	**0.649426627**	2	4.889272
Q64550	LLVIPIDGSHWLSMLGVIQQLQQK	**0.768450566**	3	4.470123
Q64550	NMIIALTENFLCR	**0.860858983**	2	4.349101
Q64550	SVFDQDPFLLR	**0.861882656**	2	3.184846
Q64550	VVYSPYGSLATEILQK	**0.895206013**	2	5.125023
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**0.86365226**	**0.912**	**3**
Q64560	ACVDSNENGDLGK	**0.877177445**	2	3.433127
Q64560	DPVQVAAPSDHGVGIEPVFPENTENSEK	**0.961645939**	3	3.848384
Q64560	GTLIEAFPVLGGK	**0.836513196**	2	2.601735
Q64563	**ADH4 Alcohol dehydrogenase 4**	**0.909862017**	**0.00018**	**12**
Q64563	AAVDCTVVGWGSCTVVGAK	**0.528222616**	2	3.864539
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	**0.567605044**	3	5.246053
Q64563	ALGATDCLNPR	**0.711377574**	2	3.218276
Q64563	FDLDLLVTHALPFDK	**0.701600923**	3	4.313217
Q64563	INDAIDLMNQGK	**0.736509482**	2	3.396684
Q64563	KFDLDLLVTHALPFDK	**0.660779728**	3	4.829554
Q64563	SVDSVPNLVTDYK	**0.576079275**	2	4.373028
Q64563	TDSPLCIEEIEVSPPK	**0.98620068**	2	3.785296
Q64563	VCLIGCGFTSGYGAAINTAK	**0.469519077**	2	3.670304
Q64563	VDDEANLER	**0.688203709**	2	2.82535
Q64563	VDEMNISTVDMILGR	**0.63099365**	2	3.480024
Q64563	VIATCVCPTDINATNPK	**0.598690984**	2	4.754181
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**0.813556083**	**6.6E-13**	**13**
Q64565	AYSNHTDIISFR	**0.965233642**	2	3.370985
Q64565	GGNFSQTFR	**0.879045736**	2	2.504953
Q64565	GGVCIADEVQTGFGR	**0.767847957**	2	4.354096
Q64565	GIGNGFPMAAVVTTPEIASSLAK	**0.721991893**	2	4.637915
Q64565	LRDEFDIVGDVR	**0.805868213**	2	2.883657
Q64565	LSALLPEPLK	**1.027962841**	2	2.781003
Q64565	NSQEVGTYMLLK	**0.452862275**	2	2.85787
Q64565	SALTQHMER	**0.898691903**	2	2.530699
Q64565	SALTQHMER+Oxidation(6)	**1.026736462**		
Q64565	TEVNQIHEDCK	**0.816664412**	2	2.997313
Q64565	TEVNQIHEDCKDMGLLVGR	**0.535359006**	2	5.521994
Q64565	VIFLVNSGSEANDLAMVMAR	**0.810042614**	2	4.695429
Q64565	YIEQFK	**0.695121326**	1	2.15976
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**0.841282176**	**0.95108**	**8**

Q64578	AVGIVATTGVSTEIGK	**0.775326027**	2	3.473829
Q64578	DIVPGDIVEVAVGDKVPADIR	**1.562783081**	2	3.760574
Q64578	DQMAATEQDKTPLQQK	**9.195704499**	2	3.942774
Q64578	EFDDLPLAEQR	**0.718559416**	2	2.685803
Q64578	IGIFSENEEVADR	**0.920611102**	2	3.041716
Q64578	IRDQMAATEQDKTPLQQK	**0.712303481**	3	3.715467
Q64578	TGTLTTNQMSVCK	**0.833449488**	2	2.876467
Q64578	VGEATETALTTLVEK	**1.088090631**	2	4.784593
Q64581	**CP3AI Cytochrome P450 3A18**	**2.211494165**	**0.40931**	**5**
Q64581	AITMSEDEEWKR	**1.029567894**	2	2.311385
Q64581	EEAKGEPINMK	**2.566748118**	2	2.336759
Q64581	LAVIGVLQNFNIQPCEK	**1.067813022**	3	3.320505
Q64581	NPEYWLEPEEFNPER	**1.12026822**	2	4.133575
Q64581	TILSPTFTSGK	**1.156794817**	1	1.937561
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**1.048255138**	**9.9E-20**	**12**
Q64591	ATAEEITSK	**1.064515208**	2	2.906292
Q64591	CDVRDPDMVHNTVLELIK	**0.578560891**	4	4.873317
Q64591	DPDMVHNTVLELIK	**0.885658929**	3	3.74667
Q64591	EEWDVIEGLIR	**0.860503475**	2	3.740566
Q64591	FDGGEEVFLSGEFNSLKK	**0.823566467**	2	2.939223
Q64591	FNIIQPGPIK	**0.677141244**	2	2.670853
Q64591	LGTVEELANLATFLCSDYASWINGAVIR	**1.21904131**		
Q64591	NIDVLK	**0.675659927**	1	2.090248
Q64591	SLAAEWGR	**0.751761796**	2	2.670436
Q64591	VAFITGGGTGLGK	**1.000812463**	2	2.78525
Q64591	VAGHPDVVINNAAGNFISPSER	**0.908578499**	2	6.101136
Q64591	VTKEEWDVIEGLIR	**0.599716008**	3	4.784861
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**0.949576636**	**0.54515**	**10**
Q64602	ASFSQVTPAQMDLVFQR	**0.832478331**	2	4.207116
Q64602	DIISLAPGSPNPK	**1.040785069**	2	3.050683
Q64602	EILLVPGNSFFVDNSAPSSFFR	**1.00979961**	2	3.586128
Q64602	FLTATSLAR	**0.658734739**	2	2.406299
Q64602	FLYTIPNGNNPTGNSLTGDR	**0.915938993**	2	4.011209
Q64602	GLAEWHVPK	**0.963980632**	2	2.449018
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	**0.91148197**	3	5.774458
Q64602	SAVFTVENGSTIR	**0.941552728**	2	3.436837
Q64602	VGFITGPK	**1.021391038**	1	1.910192
Q64602	VLSQWKPEDSKDPTKR	**0.92575737**	3	3.659276
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.140050467**	**0.98984**	**11**
Q64611	AQGGQGLEWR	**1.117621917**	2	3.213446
Q64611	CHGSQASYLFQQDK	**1.89315399**	2	4.352719
Q64611	FFNQLFSGLDPHALAGR	**2.044449177**	3	4.201155
Q64611	FYNVALDTGDK	**0.922561053**	2	3.268161
Q64611	GAAFLGLGTDSVR	**0.018497687**	2	3.076898
Q64611	IDQAFALTR	**1.246615965**	2	3.061519
Q64611	MVVANPILVQADIDFLLGELER	**1.066163911**		
Q64611	QLLDLELQSQGESR	**0.759841334**	2	3.837628
Q64611	TLDGDPVAVEALLR	**0.905850769**	2	4.500065
Q64611	VCEWKEPEELK	**1.06198065**	3	3.697585
Q64611	YLVEEIK	**1.278091087**	1	2.391475
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**0.876776739**	**0.80058**	**3**
Q64638	GHQAVVLAPEVTVHIK	**0.710662612**	3	3.502925
Q64638	VVFETGNYVK	**0.760335116**	2	2.356892
Q64638	YESLASELLQR	**0.923999699**	2	3.197192
Q64640	**ADK Adenosine kinase**	**1.110468936**	**9.9E-20**	**12**

Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.422857756	3	6.765608
Q64640	AATFFGCIGIDK	0.571838567	2	3.045069
Q64640	AGHYAASVIIR	0.974805667	3	3.578603
Q64640	FGEILK	1.169843392	2	2.427885
Q64640	FKVEYHAGGSTQNSMK	1.308937292	2	3.026518
Q64640	HKELFDELVK	1.191535232	3	3.790277
Q64640	HLDLENNWMLVEK	1.076232259	2	3.788278
Q64640	SLVANLAAANCYK	1.094214045	2	4.737859
Q64640	VEAPEALSENVLFGMGNPLLDISAVVDKDFLDK	0.78596085		
Q64640	VEYHAGGSTQNSMK	1.31549386	2	4.050841
Q64640	VEYHAGGSTQNSMK+Oxidation(12)	3.080015008		
Q64640	YSLKPNDQILAEDK	1.250614422	3	4.959095
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.692689065**	**0.4185**	**7**
Q64654	EPAEDILQTLLDSTYK	0.936327448	2	3.919968
Q64654	GVAYDVPNAVFLEQK	0.868620833	2	3.226981
Q64654	NEDLNAEEVYGR	0.806256018	2	4.106766
Q64654	SGLNIAHFK	0.960692905	2	2.966093
Q64654	TPQTVAGYTIPPGHQVCVSPTVNQR	0.864218661	3	3.94804
Q64654	TVCGEDLPPLTYEQLK	0.567706317	2	4.072863
Q64654	YLQDNPASGEK	0.686860908	2	2.61559
Q65CL1	**CTNA3 Catenin alpha_3**	**1.063001857**	**0.42125**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(0)	1.219102145		
Q65CL1	NLMNAVVQTVK	0.612288712	2	2.888613
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.01235857**	**0.48347**	**3**
Q66H12	CNINCEEDPK	0.565162544	2	2.711522
Q66H12	INQDPLGIQGR	0.723878761	2	3.109276
Q66H12	TISPQNIDILQNPLLIK	1.013952738	2	2.357762
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**0.770584004**	**0.07889**	**3**
Q66H15	AEELQPGFSK	0.860376842	2	2.655945
Q66H15	AIELQPEDPR	0.799785803	2	2.342432
Q66H15	SLQGLAGEIVGEVR	0.669157821	2	2.755211
Q66H80	**COPD Coatomer subunit delta**	**1.075127603**	**0.99485**	**5**
Q66H80	GVQLQTHPNVDKK	1.180253084	2	3.434421
Q66H80	LFTAESLIGLK	1.225872585	2	2.823047
Q66H80	NSNILEDLETLR	1.050603267	2	3.076531
Q66H80	NTLEWCLPVIDAK	0.924953377	2	2.858103
Q66H80	VTQVDGNSPVR	1.134901745	2	2.939242
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.124928712**	**0.1318**	**9**
Q66HA8	AGGIETIANEFSDR	1.309423129	2	2.851369
Q66HA8	FQEAEERPR	0.741159911	2	2.480205
Q66HA8	FVVQNVSAQK	0.963379432	2	2.387136
Q66HA8	IARFFGKDVSTTLNADEAVAR	0.671378323	2	2.317001
Q66HA8	NQQITHANNTVSSFK	1.252217479	2	4.570228
Q66HA8	SVLDAAQIVGLNCLR	0.954275685	2	3.456195
Q66HA8	TEEVSAIEIVGGATR	0.799810196	2	3.408049
Q66HA8	VLGTAFDPFLGGK	1.016773866	2	3.098852
Q66HA8	YNHIDESEMKKVEK	0.708304399	2	2.612902
Q66HD0	**ENPL Endoplasmin**	**1.090951645**	**0.24053**	**28**
Q66HD0	DISTNYYASQK	2.608858204	2	2.997864
Q66HD0	EATEKEFEPLLNWMK	1.015623441	2	2.830895
Q66HD0	EEASDYLELDTIK	0.890481967	2	4.207668
Q66HD0	EEEAIQLDGLNASQIR	0.714604859	2	4.398885
Q66HD0	EFEPLLNWMK	1.32201862	2	2.347774
Q66HD0	EVEEDEYK	1.032547789	1	2.658949
Q66HD0	FQSSHHSTDITSLDQYVER	1.110268635	3	5.646537
Q66HD0	GLFDEYGSK	0.793711812	2	2.463858

Q66HD0	GVVDSDDLPLNVSR	**0.929681309**	2	4.920107
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	**2.26630665**	3	3.963573
Q66HD0	KEAESSPFVER	**1.115931446**	2	3.173807
Q66HD0	LGVIEDHSNR	**1.136804315**	2	3.358554
Q66HD0	LISLTDENALAGNEELTVK	**0.922928935**	2	5.50101
Q66HD0	LTESPCALVASQYGWSGNMER	**0.964479231**	2	5.476592
Q66HD0	LTESPCALVASQYGWSGNMER+Oxidation(18)	**0.89002386**		
Q66HD0	NLLHVTDTGVGMTR	**1.058618226**	2	3.98749
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11)	**1.1446661**		
Q66HD0	SGTSEFLNK	**1.076018177**	2	3.201717
Q66HD0	SGYLLPDTK	**1.034915429**	2	3.216391
Q66HD0	SILFVPTSAPR	**1.084783236**	2	3.28606
Q66HD0	TDDEVVQR	**0.984944169**	2	3.312746
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	**0.902449151**	3	5.450044
Q66HD0	TETVEEPLEEDETAQEEK	**2.736042927**	2	5.23895
Q66HD0	TFEINPR	**1.031130857**	2	2.402784
Q66HD0	TVWDWELMNDIKPIWQRPSK	**0.979571234**	3	3.317456
Q66HD0	VFITDDFHDMMPK	**0.851061418**	2	3.840754
Q66HD0	YNDTFWK	**1.022836029**	1	2.101287
Q66HD0	YSQFINFPIYVWSSK	**0.71436567**	2	3.32529
Q66HD3	**NASP Nuclear autoantigenic sperm protein**	**1.026049092**	**0.60413**	**2**
Q66HD3	LSETKDGASVEEVK	**1.025777862**	2	2.430129
Q66HD3	QDTLMKVVEIEAEIDSEVK+Oxidation(4)	**1.163763482**		
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.197519843**	**0.52694**	**11**
Q66HF1	ALSEIAGITLPYDTLDQVR	**0.970207616**	2	5.15308
Q66HF1	AVTEGAQAVEEPSIC	**0.970740486**	2	3.185316
Q66HF1	DDGAAILAAVSSIAQK	**0.823464818**	2	4.513566
Q66HF1	FASEIAGVDDLGTTGR	**1.4551068**	2	4.085585
Q66HF1	FEAPLFNAR	**0.984228485**	2	2.660874
Q66HF1	GLLTYTSWEDALSR	**0.945108423**	2	3.590138
Q66HF1	ILQDIASGNHEFSK	**1.231552817**	2	4.192792
Q66HF1	LGEVSPNLVR	**1.024642006**	2	2.961337
Q66HF1	LVDQEFLADPLVPPQLTIK	**0.973356842**	2	3.110144
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	**1.024123147**	2	4.287465
Q66HF1	YDHLGDSPK	**1.013109025**	2	2.576717
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**0.617215229**	**5.7E-08**	**11**
Q66HF8	EEIFGPVQPLFK	**1.082802001**	2	3.039147
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	**0.50974372**	3	3.456821
Q66HF8	LAPALATGNTVVMK	**0.826768091**	2	3.299885
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	**0.623372076**	2	4.794425
Q66HF8	TFVEESIYHEFLER	**0.65066617**	2	3.741059
Q66HF8	VAEQTPLSALYLASLIK	**1.559296876**	2	3.606155
Q66HF8	VAFTGSTEVGHLIQK	**0.655166242**	2	3.271901
Q66HF8	VGNPFELDTQQGPQVDK	**0.977347859**	2	3.796599
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	**0.577232239**	2	4.495793
Q66HF8	YGLAAAVFTR	**0.710776716**	2	3.084833
Q66HF8	YNQLFINNEWHDAVSK	**0.980889925**	2	3.536329
Q66HG4	**GALM Aldose 1_epimerase**	**0.813585671**	**9.9E-20**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	**0.742268777**	2	4.37411
Q66HG4	TVFGELPSGGGAVEK	**0.711845504**	2	3.677706
Q66HG4	VSPDGEEGYPGELK	**0.786074198**	2	3.925192
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.365503924**	**2.9E-05**	**20**
Q66X93	ADDADEFGYSR	**2.708704921**	2	2.549358
Q66X93	ALLLPDHYLVTVMLSGIK	**0.849537604**	3	4.24561

Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	**1.012605493**	3	4.316439
Q66X93	DTNGENIAESLVAEGLASR	**1.080001339**	2	5.025278
Q66X93	ETDGSETPEPFAAEAK	**1.399196744**	2	3.806101
Q66X93	GDVGLGLVK	**1.139213638**	2	2.43039
Q66X93	HFVDSHHQKPVNAIIEHVR	**0.81045528**	3	4.056577
Q66X93	LEGDNIQDK	**1.152091164**	2	2.860885
Q66X93	NLPGLVQEGEPFSEEATLFTK	**1.539848862**	2	5.536663
Q66X93	SAYYKPLLSAEEAAK	**1.155042485**	2	3.223134
Q66X93	SDISSHPPVEGAYAPR	**1.083572152**	3	4.724852
Q66X93	SEAVVEYVFSGSR	**1.644365851**	2	3.347418
Q66X93	SSHYDELLAAEAR	**1.201561792**	2	3.529833
Q66X93	TCATVTIGGINIAEALVSK	**0.839325644**	2	3.512292
Q66X93	TDAVDSVVR	**1.250297794**	2	2.680137
Q66X93	VADISGDTQK	**1.086754319**	2	2.480506
Q66X93	VITEYLNAQESAK	**1.452742053**	2	3.843806
Q66X93	VMQVLNADAIVVK	**1.027105006**	2	2.878518
Q66X93	VSVTVDYIRPASPATETVPAFSER	**1.106654873**	3	5.622403
Q66X93	VWAHYEEQPVEEVMPVLEEK	**1.265892181**	3	3.982018
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.801517264**	**1.5E-05**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	**1.440931927**	3	3.777817
Q68FP2	HNNWDLTPVK	**0.741119489**	2	2.977453
Q68FP2	IFLMDLNEPYPK	**0.812298859**	2	3.19641
Q68FP2	IQDPLSDNPR	**0.881214594**	2	3.127307
Q68FP2	LLIYNPEDPPGSEVLR	**0.862498033**	2	4.058468
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	**0.873990819**	3	4.768847
Q68FP2	VVAQGFSSANGITVSLDQK	**0.626801628**	2	3.367835
Q68FP2	YVYVADVTAK	**0.877249434**	1	3.0049
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.172117817**	**0.35215**	**6**
Q68FQ0	GSNDMQYQHVIETLIGK	**1.352262774**	2	3.139063
Q68FQ0	HKLDVTSVEDYK	**0.80356531**	2	3.201262
Q68FQ0	ISDNVLVDINNPEPLIQTAK	**1.224109077**	2	5.188832
Q68FQ0	LDVTSVEDYK	**1.01294205**	2	2.371968
Q68FQ0	SLHDALCVIR	**0.846390782**	2	2.481982
Q68FQ0	WVGGPEIELIAIATGGR	**1.146052963**	2	3.903633
Q68FR6	**EF1G Elongation factor 1_gamma**	**0.887507185**	**3.5E-08**	**9**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	**1.015747065**	2	5.139385
Q68FR6	ALIAAQYSGAQIR	**1.473333034**	2	3.712908
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	**1.564493945**	2	4.251281
Q68FR6	ILGLLDTHLK	**1.063555381**	2	2.769705
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	**1.146063998**	3	3.806649
Q68FR6	KLDPGSEETQTLVR	**1.182086305**	2	3.863262
Q68FR6	LDPGSEETQTLVR	**0.961787656**	2	3.653568
Q68FR6	STFVLDEFKR	**1.05335417**	2	2.479879
Q68FR6	WFLTCINQPQFR	**0.889800436**	2	3.139211
Q68FR9	**EF1D Elongation factor 1_delta**	**0.957004927**	**0.99846**	**6**
Q68FR9	ATAPQTQHVSPMR	**0.786938661**	2	3.562022
Q68FR9	FYEQMNGPVTAGSR	**1.058303077**	2	4.418282
Q68FR9	GVVQDLQQAISK	**1.057589752**	2	3.754268
Q68FR9	SIQLDGLVWGASK	**0.94019504**	2	3.266758
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	**1.060484513**	2	5.518403
Q68FR9	VGTDLLEEEITK	**1.106402692**	2	3.484912
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**0.868538978**	**0.32661**	**3**
Q68FS2	NAAQVLVGIPLETGQK	**0.47928109**	2	2.691726
Q68FS2	QDLAQLMNSSGSHK	**0.771717278**	2	2.391995
Q68FS2	VISFEEQVASIR	**0.871443901**	2	2.425801
Q68FS4	**AMPL Cytosol aminopeptidase**	**0.896406889**	**9.9E-20**	**18**
Q68FS4	ADMGGAATICSAIVSAAK	**0.747434782**	2	5.504634

Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2)	**0.961785712**		
Q68FS4	DKDDDVPQFTSAGENFNK	**0.95916871**	2	4.939332
Q68FS4	GITFDSGGISIK	**0.983824216**	2	3.304582
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	**1.575363848**	3	5.805487
Q68FS4	GVLFASGQNLAR	**0.950098665**	2	3.291774
Q68FS4	LFEASVETGDR	**0.949642918**	2	3.374507
Q68FS4	LHGSGDLEAWEK	**0.841224371**	2	3.650855
Q68FS4	LILADALCYAHTFNPK	**1.240728842**	2	3.985195
Q68FS4	LNLPINIIGLAPLCENMPSGK	**1.161632121**	2	5.039613
Q68FS4	QLMESPANEMTPTR	**0.768570237**	2	3.783976
Q68FS4	QVIDCQLADVNNLGK	**0.758138177**	2	4.979078
Q68FS4	SAGACTAAAFLR	**0.956124118**	2	3.502427
Q68FS4	SAGVDDQENWHEGK	**0.923631159**	2	3.748395
Q68FS4	SWIEEQEMGSFLSVAK	**0.841097971**	2	5.368445
Q68FS4	TFYGLHQDFPSVVVVGLGK	**0.731962619**	2	5.416978
Q68FS4	TIQVDNTDAEGR	**0.834635008**	2	3.795482
Q68FS4	TLIEFLLR	**0.877753968**	2	2.598734
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**0.796995797**	**0.00192**	**4**
Q68FT1	INDAMNMGHTAK	**0.501682325**	2	3.035889
Q68FT1	LNHVLEEEQK	**0.828563151**	3	3.434418
Q68FT1	STGEALVQGLMGAAVTLK	**0.814195683**	2	3.00385
Q68FT1	YTDQSGEEEEDYESEEQIQHR	**0.866805192**	3	4.689087
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.720644479**	**0.05008**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	**0.712934221**	2	3.570796
Q68FT3	ISQLDTQSPVTK	**0.855237313**	2	3.420857
Q68FT3	SLLLGTDVAENQK	**0.647339224**	2	3.939502
Q68FT3	TLGAQLPQYYEVLTAPISK	**0.647170744**	2	4.260234
Q68FT3	VFDCIEAYAPGFK	**0.767956066**	2	2.853969
Q68FT3	VLDQWFESEPLK	**0.79948126**	2	2.849102
Q68FT3	VQGVVLQGGEEVR	**0.725039767**	2	3.592483
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.232800365**	**9.9E-20**	**10**
Q68FT5	AGADVLQTFTFSAAEDR	**3.657756338**	2	2.655468
Q68FT5	AGANIIGVNCR	**1.085295187**	2	3.478096
Q68FT5	AGLWTPEAVVEYPSAVR	**1.283667842**	2	3.445393
Q68FT5	AIAEELAPER	**2.123600737**	2	3.778363
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	**1.01380623**	3	4.462389
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	**0.976323507**	3	4.075529
Q68FT5	FGPWTSLQTMK	**0.877331275**	2	2.814073
Q68FT5	GGFVDLPEYPFGLEPR	**1.117188214**	2	4.104311
Q68FT5	LDSGEVVVGDGGFLFTLEK	**0.694211344**	2	3.922539
Q68FT5	YIGGCCGFEPYHIR	**3.683229134**	2	4.710752
Q68FT9	**SCLY Selenocysteine lyase**	**1.089354458**	**0.01096**	**4**
Q68FT9	AEVDLIVQDLK	**0.841919361**	2	3.883864
Q68FT9	NFRPGTENTPMIAGLGK	**0.7015674**	2	3.349958
Q68FT9	RVDVEDLGVDFLTIVGHK	**1.365316027**	3	5.547755
Q68FT9	VLVHTDAAQALGK	**0.841950945**	2	2.473229
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.822893761**	**0.00038**	**11**
Q68FU3	AGDLGVDLTSK	**0.80867219**	2	3.636026
Q68FU3	EIIAVSCGPPQCQETIR	**1.042580342**	2	4.782104
Q68FU3	GIHVEVPGAEAENLGPLQVAR	**0.510994311**	2	6.043542
Q68FU3	HSMNPFCEIAVEEAVR	**0.864328165**	2	5.254708
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2)	**1.0952742**		
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	**0.695727752**	3	5.085751

Q68FU3	RVIDFAVK	**0.796368121**	2	2.804606
Q68FU3	VDLLFLGK	**1.179461926**	2	2.80443
Q68FU3	VETTEDLVAK	**0.793719453**	2	3.357481
Q68FU3	VIDFAVK	**0.954453329**	2	2.412454
Q68FU3	VSVISVEEPPQR	**0.903150992**	2	3.454462
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.042685174**	**0.00022**	**9**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	**0.781855669**	3	5.630429
Q68FY0	IEEVDAQMVR	**0.832702811**	2	3.606245
Q68FY0	LCTSATESEVTR	**1.022191281**	2	3.277986
Q68FY0	NALISHLDGTTPVCEDIGR	**0.785545415**	2	4.513545
Q68FY0	NNGAGYFLEHLAFK	**0.749846954**	2	3.371237
Q68FY0	RIPLAEWESR	**0.909885975**	2	2.604239
Q68FY0	TDLTDYLSR	**0.734622305**	2	2.820077
Q68FY0	VVELLADIVQNISLEDSQIEK	**0.881800917**	3	6.90851
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	**1.056413948**	2	4.962695
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.92986174**	**0.87976**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	**0.779693235**	2	4.670763
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	**0.927733238**	3	3.924644
Q68G31	GESGGQTTPYDFYSR	**1.026047385**	2	3.963842
Q68G31	LQPTDSFSQSSCFGLR	**0.555224479**	2	3.668367
Q68G31	NVNSTLTFVTLSGELK	**1.022524672**	2	4.288925
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	**0.883042638**	3	6.268124
Q68G31	VNTEPLPGIEK	**1.083002058**	2	2.412276
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**0.782455086**	**0.77191**	**2**
Q69Z23	MNILTNEMRRSLK+Oxidation(0)	**0.723829878**		
Q69Z23	YFIDLLMEK	**0.859993936**	1	2.141696
Q69ZH9	**RHG23 Rho GTPase_activating protein 23**	**1.050839773**	**0.057**	**2**
Q69ZH9	LEPMDTIFVKNVK	**0.703878833**	2	2.43207
Q69ZH9	SRAEAEGPGAGTARACPR	**1.157077891**	2	2.380046
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**0.918665819**	**0.54566**	**2**
Q6A0A9	SQGGVQPIPSQGGK	**0.7113138**	2	3.095812
Q6A0A9	VEGSSTASSGSQLAEGK	**1.041323388**	2	4.280548
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.043088309**	**0.00163**	**3**
Q6AXM8	FQEEENSLLHLK	**0.482999268**	2	2.715732
Q6AXM8	LFVYDPNHPPSSEVLR	**0.693518203**	2	2.491378
Q6AXM8	WANVVYYSPEEVK	**3.333862154**	2	3.553181
Q6AXN3	**TMED5 Transmembrane emp24 domain_containing protein 5**	**0.768794927**	**0.96417**	**2**
Q6AXN3	LEDILESINSIK	**1.059517899**	2	3.850768
Q6AXN3	LEDILESINSIKSR	**0.912511982**	2	2.50144
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.889845054**	**0.95193**	**3**
Q6AXS5	EETQPPVALKK	**1.020938256**	2	2.389626
Q6AXS5	FDQLFDDESDPFEVLK	**1.047409998**	2	4.3778
Q6AXS5	SAAQAAAQTNSNAAGK	**1.495401372**	2	4.432777
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.858116969**	**0.33144**	**2**
Q6AXY0	FLQPGSQR	**0.856837351**	2	2.420994
Q6AXY0	YFPAFEK	**0.910391774**	1	1.918532
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**0.988080177**	**0.15789**	**3**
Q6AY09	ATENDIYNFFSPLNPMR	**1.203873926**	2	2.689776
Q6AY09	HTGPNSPDTANDGFVR	**0.956806051**	2	4.401614
Q6AY09	STGEAFVQFASQEIAEK	**1.555116092**	2	4.386896
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**0.863702791**	**0.66367**	**6**

Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	**1.008370929**	3	4.399938
Q6AY30	ATLVLNCVGPYR	**0.959079164**	2	2.613501
Q6AY30	GGGVFTPGAAFSR	**0.863766665**	2	2.434473
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	**0.828151502**	2	4.231153
Q6AY30	LQQVLEK	**0.982002892**	1	2.015729
Q6AY30	SVSNLKPVPVIGSK	**0.718996663**	2	3.835439
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.057883706**	**0.92097**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	**0.932903684**	2	4.75739
Q6AY56	FDGALNVDLTEFQTNLVPYPR	**1.044554739**	2	4.999843
Q6AY56	LISQIVSSITASLR	**0.95391142**	2	3.415795
Q6AY56	NLDIERPTYTNLNR	**1.060803391**	2	3.190492
Q6AY56	QLFHPEQLITGK	**0.792044926**	2	2.417712
Q6AY56	TIQFVDWCPTGFK	**1.217874003**	2	3.786335
Q6AY56	VGINYQPPTVVPGGDLAK	**0.922947444**	2	4.529583
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.94765334**	**0.99868**	**3**
Q6AY80	NDVTGALSNPEVFK	**0.830642603**	2	3.854708
Q6AY80	VLAPQISFGPEVSSEEQR	**0.938496875**	2	4.37001
Q6AY80	VLCQGFAFDVPGFYDSGFLK	**1.053063865**	2	3.490055
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**0.88650142**	**0.45014**	**4**
Q6AYG5	DVLETLWGGPANLEAIAK	**0.808934337**	2	3.023892
Q6AYG5	ILEQFPGGSIDLQK	**0.757646646**	2	3.135883
Q6AYG5	NTFCSGSDLNAVK	**0.816481474**	2	2.587861
Q6AYG5	VIELENWTEGK	**0.978042175**	2	2.948895
Q6AYH5	**DCTN2 Dynactin subunit 2**	**1.159471991**	**0.78636**	**3**
Q6AYH5	ASVEDADTQNK	**1.348063612**	2	2.342033
Q6AYH5	VNALDLAVLDQVEAR	**1.175348221**	2	2.814499
Q6AYH5	WSPVASTLPELVQR	**1.091918203**	2	2.995299
Q6AYM2	**TEKT2 Tektin_2**	**0.403788344**	**0.19399**	**1**
Q6AYM2	RLEEDLR	**0.988244943**	1	1.947017
Q6AYM2	TNTMLLDTKCMDIR+Oxidation(3)	**0.293541909**		
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.745737431**	**9.9E-20**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	**0.600250202**	2	4.493897
Q6AYQ8	NLHHEVELGVLLGR	**0.816839001**	3	4.135174
Q6AYQ8	SFTSSCPVSAFVPK	**0.630731497**	2	4.080788
Q6AYR8	**SCRN2 Secernin_2**	**0.823609863**	**0.01898**	**2**
Q6AYR8	GLLTGEQTPAPQELGSLFQAFVER	**1.779727221**	3	4.153685
Q6AYR8	QEQQSLEQEGLEALR	**0.79756418**	2	4.008386
Q6AYS7	**ACY1A Aminoacylase_1A**	**2.940586991**	**0.00487**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	**1.040332888**	2	4.701358
Q6AYS7	ICTVQPNPDYGSAVTFLEER	**2.013898276**	2	4.517102
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.829074624**	**0.49414**	**4**
Q6AYS8	ALTDELAALGCTGVR	**0.715418028**	2	3.731156
Q6AYS8	FDAVVGYK	**1.092851878**	1	2.229856
Q6AYS8	MIFVPGSIALLTVLER	**0.763236976**	2	2.767705
Q6AYS8	SVAGEIVLITGAGHGIGR	**0.792970778**	2	3.983209
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.801241543**	**0.87285**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	**0.56836601**	2	4.369028
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	**0.68884059**	2	3.79195
Q6AYT9	NDDVINSSSYR	**0.830145007**	2	2.588251
Q6AYT9	TGVVMIPGISQLTQK	**0.810274847**	2	2.444242
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.150548786**	**0.39858**	**5**
Q6AYZ1	AVFVDLEPTVIDEVR	**1.154564316**	2	5.030551
Q6AYZ1	DVNAAIATIK	**1.030745591**	2	3.061604
Q6AYZ1	IHFPLATYAPVISAEK	**0.974165194**	2	3.413831

Q6AYZ1	TIGGGDDSFNTFFSETGAGK	**1.337464768**	2	5.396956
Q6AYZ1	VGINYQPPTVVPGGDLAR	**1.182685552**	2	4.837774
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.160255922**	**3.5E-08**	**7**
Q6DGG1	AVAIDLPGLGR	**0.862423191**	2	3.487673
Q6DGG1	FSSETWQNLGTLHR	**0.990707789**	2	3.45856
Q6DGG1	FSVLLLHGIR	**1.094138058**	2	2.6252
Q6DGG1	GYVPVAPICTDK	**0.814462623**	1	2.68742
Q6DGG1	INAADYAR	**0.933415528**	2	2.461321
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	**1.368416961**	2	4.987156
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK+Oxidation(12)	**1.46482647**		
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.894339245**	**0.57857**	**2**
Q6EDY6	IENYLLR	**0.894360709**	2	2.52352
Q6EDY6	SSDAHELGEGDEKKK	**0.874680361**	2	2.359173
Q6EJB6	**UT14B U3 small nucleolar RNA_associated protein 14 homolog B**	**0.95758274**	**0.15128**	**2**
Q6EJB6	ARMTERMSLK+Oxidation(2)	**0.993366629**		
Q6EJB6	EAAFSKTSQMLSR+Oxidation(9)	**0.380657774**		
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.62469207**	**0.00112**	**2**
Q6GQP4	CDLSDIREVPLK	**0.555130426**	2	2.391659
Q6GQP4	CDLSDIREVPLKDAK	**0.79654167**	2	2.737571
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**7.186929045**	**7E-05**	**2**
Q6GQT1	IQEEGTGVEETGK	**7.289577113**	2	3.796557
Q6GQT1	QLSFPLSSEPTQGSYK	**1.677015304**	2	2.817775
Q6GQT9	**NOMO1 Nodal modulator 1**	**0.922295289**	**0.9669**	**2**
Q6GQT9	SSIDSEPALVLGPLK	**0.923945823**	2	3.058939
Q6GQT9	VQVVVPEAETR	**0.919950155**	2	2.484355
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**0.737525607**	**0.9254**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	**0.86493214**	2	4.141586
Q6I7R3	ILGIPVIITEQYPK	**0.875980055**	2	3.054214
Q6I7R3	YFGDIISVGQR	**0.952055732**	2	2.864285
Q6IE47	**ISK6 Serine protease inhibitor Kazal_type 6**	**0.93882775**	**0.94156**	**2**
Q6IE47	CAFCKALEK	**1.029831245**	1	1.980058
Q6IE47	LFQINCGEFRDPK	**0.907736334**	2	2.410531
Q6IE52	**MUG2 Murinoglobulin_2**	**0.683723995**	**7.8E-14**	**14**
Q6IE52	AHFSVMGDILSSAIK	**0.670079328**	2	3.501241
Q6IE52	HTSSWLVTPK	**0.541806311**	2	2.674901
Q6IE52	LPSSEEEESLDINIEGAK	**0.828645612**	2	4.660444
Q6IE52	MLIYTILPDGEVIADSVK	**0.783733985**	2	3.812035
Q6IE52	MLSGFIPLKPTVK+Oxidation(0)	**0.892391036**		
Q6IE52	MNRIMQWQDVK+Oxidation(0)	**0.478308501**		
Q6IE52	NLYPLKELVQDPK	**0.778121285**	1	2.079934
Q6IE52	QLSFSLSAEPIQGPYK	**0.67136564**	2	4.087656
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	**0.823003911**	3	3.521737
Q6IE52	VHLSFSPSQSLPASQTHMR	**0.530780309**	3	3.414121
Q6IE52	VKTVPLTCNNPK	**0.651147239**	2	2.902613
Q6IE52	VTASPQSLCGLR	**0.735655112**	2	2.886737
Q6IE52	YMVLVPSQLYTETPEK	**0.6397755**	2	3.577462
Q6IE52	YMVLVPSQLYTETPEK+Oxidation(1)	**0.761605421**		
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**0.899534913**	**0.41615**	**2**
Q6IFW6	LENEIQTYR	**1.370182512**	2	2.517452
Q6IFW6	QSLEASLAETEGR	**0.555883597**	2	2.756063
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.797889004**	**0.16112**	**4**
Q6IMF3	TNAENEFVTIK	**1.133571781**	2	2.952923
Q6IMF3	TNAENEFVTIKK	**0.300295858**	2	2.426961

Q6IMF3	WELLQQVDTSTR	0.824738861	2	3.626365
Q6IMF3	YEELQITAGK	0.823610667	2	3.470391
Q6IRK9	PGCP Plasma glutamate carboxypeptidase	0.808817057	0.25932	5
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.941453213	3	5.379867
Q6IRK9	GEESAVMVVPR	0.688578196	2	2.420935
Q6IRK9	IVVYNQPYTDYGK	1.865465822	2	3.371046
Q6IRK9	TYPDTDSFNTVAEITGSK	0.86892419	2	3.797605
Q6IRK9	VGAVASLIR	0.702819671	2	2.516366
Q6KCD5	NIPBL Nipped_B_like protein	0.739791547	0.4647	2
Q6KCD5	AFLISLLNLFDDTAK	0.804663039	2	2.598496
Q6KCD5	QNNTRSENTKARPETPK	0.539427378	2	2.566816
Q6MGB5	DHB8 Estradiol 17_beta_dehydrogenase 8	0.878429915	0.35418	4
Q6MGB5	AGVIGLTQTAAR	0.786440276	2	3.334717
Q6MGB5	GSIINISSIVGK	0.693697797	2	2.581352
Q6MGB5	SALALVTGAGSGIGR	1.060819248	2	3.157082
Q6MGB5	VGNIGQTNYASSK	1.464833373	2	2.366945
Q6NS46	RRP5 Protein RRP5 homolog	0.836385426	0.47523	2
Q6NS46	GKQTKSTEVPR	0.821656102	2	2.678293
Q6NS46	IIDYSQMDELALLSLR	0.961597533	2	2.370475
Q6NSR8	PEPL1 Probable aminopeptidase NPEPL1	0.965181388	0.04623	2
Q6NSR8	HNSPSAAHFITR	0.973571507	3	3.557373
Q6NSR8	TVEINNTDAEGR	0.670940946	2	2.693942
Q6NYB7	RAB1A Ras_related protein Rab_1A	1.311026652	0.22527	3
Q6NYB7	EFADSLGIPFLETSAK	1.316545471	2	3.616446
Q6NYB7	MGPGATAGGAEK	2.149298297	2	2.92138
Q6NYB7	NATNVEQSFMTMAAEIK	1.134973363	2	4.619451
Q6NZJ6	IF4G1 Eukaryotic translation initiation factor 4 gamma 1	0.902522448	1.8E-07	9
Q6NZJ6	DLDFAKAKPRMDQYFNQMEK+Oxidation(10)	0.8808238		
Q6NZJ6	GLPLVDDGGWNTVPISK	0.971126108	2	2.949481
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.170494116	3	3.472805
Q6NZJ6	IHNAENIQPGEQK	1.220044419	2	4.175091
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.456105089	3	3.58037
Q6NZJ6	LGIESTLER	1.041885226	2	2.373941
Q6NZJ6	LKEELEEAR	1.15888686	2	2.673569
Q6NZJ6	QVTQLAIDTEER	1.273743038	2	2.854519
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.761718605	3	4.776618
Q6P0K8	PLAK Junction plakoglobin	0.864046758	0.38999	2
Q6P0K8	LLNDEDPVVVTK	0.856343815	2	2.979309
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.118628923	3	3.684323
Q6P502	TCPG T_complex protein 1 subunit gamma	1.088212546	0.01187	8
Q6P502	GISDLAQHYLMR	1.087491593	2	2.378875
Q6P502	IVLLDSSLEYK	1.077635248	2	2.679242
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.12483079	3	3.686874
Q6P502	KGESQTDIEITR	1.422925964	2	3.182367
Q6P502	NLQDAMQVCR	1.12371736	2	2.802642
Q6P502	TAVETAVLLLR	1.175169532	2	3.385841
Q6P502	TLIQNCGASTIR	1.325873671	2	2.936961
Q6P502	WSSLACNIALDAVK	1.038861933	2	3.883981
Q6P5D3	DHX57 Putative ATP_dependent RNA helicase DHX57	0.97685357	0.97909	2
Q6P5D3	ARHNRTAQEEVEEDLR	0.994780359	2	2.304696
Q6P5D3	QEETLALKSICGEK	0.969634576	2	2.324683
Q6P6M7	EMFVYLSTQLKK+Oxidation(1)	0.574017228		
Q6P6M7	SGDISAVQPK	1.113094829	2	2.305707
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	1.119328912	2	3.998195

Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.800492336**	**0.0083**	**12**
Q6P6R2	ALTGGIAHLFK	**0.846389004**	2	2.696993
Q6P6R2	EANLAASFGKPINF	**0.824279004**	1	2.056696
Q6P6R2	IDVSVEAASGGK	**0.821298448**	2	3.659001
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	**0.825188385**	3	4.130208
Q6P6R2	IPNIFAIGDVVAGPMLAHK	**1.71389008**	3	3.417117
Q6P6R2	NETLGGTCLNVGCIPSK	**0.83985724**	2	5.345018
Q6P6R2	NQVTATTADGSTQVIGTK	**0.835008328**	2	5.649474
Q6P6R2	RPFTQNLGLEELGIELDPK	**1.124006153**	3	4.214916
Q6P6R2	SEEQLKEEGVEFK	**0.877374641**	3	4.12924
Q6P6R2	TNADTDGMVK	**0.78319327**	2	2.824356
Q6P6R2	TNADTDGMVK+Oxidation(7)	**1.085124286**		
Q6P6R2	VCHAHPTLSEAFR	**0.693296216**	3	3.80575
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.867310023**	**0.66716**	**7**
Q6P6S9	AAETHLIDYEK	**0.81987171**	2	2.461366
Q6P6S9	AQTLLLEVEEIFK	**0.868694222**	2	3.8696
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	**1.114778124**	2	4.732957
Q6P6S9	QGAETVQELLEVAK	**0.853059468**	2	3.313205
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	**0.884787435**	3	3.851656
Q6P6S9	VEDFERKAR	**0.764695652**	2	2.442626
Q6P6S9	WLEAEWIFGGVK	**0.830404317**	2	3.082896
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.095475742**	**0.60155**	**8**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2)	**0.509762106**		
Q6P6V0	HFVALSTNTDK	**1.107157238**	2	2.721133
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	**1.007462967**	3	5.439646
Q6P6V0	MIPCDFLIPVQTQHPIR	**0.63919351**	2	3.133447
Q6P6V0	TFTTQETITNAETAK	**1.156435175**	2	5.115226
Q6P6V0	TLANLNPESSLFIIASK	**1.108973825**	3	4.964591
Q6P6V0	VFEGNRPTNSIVFTK	**1.115223515**	2	3.392012
Q6P6V0	VWFVSNIDGTHIAK	**0.969593929**	2	3.464535
Q6P7B0	**SYWC Tryptophanyl_tRNA synthetase_ cytoplasmic**	**1.058849477**	**0.97149**	**2**
Q6P7B0	ASEDFVDPWTVR	**1.08008908**	2	2.694035
Q6P7B0	TLIDVLQPLIAEHQAR	**0.89179066**	3	3.314078
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.185669654**	**0.01228**	**6**
Q6P7Q4	ATLELTHNWGTEDDETQSYHNGNSDPR	**1.45573362**	3	3.982593
Q6P7Q4	DFLLQQTMLR	**1.158838241**	2	3.317003
Q6P7Q4	FEELGVK	**0.900902573**	1	1.91717
Q6P7Q4	GFGHIGIAVPDVYEACK	**1.018105091**	2	3.455763
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	**0.972548328**	2	5.643552
Q6P7Q4	RFEELGVK	**1.162804025**	2	2.648204
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.162943083**	**0.19269**	**2**
Q6P7R8	GIFVQSVLPFFVATK	**1.14247536**	2	3.300225
Q6P7R8	LGEWAVVTGGTDGIGK	**1.228634174**	2	4.03946
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**0.907928886**	**7.8E-06**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	**0.93655098**	2	4.682413
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10)	**1.040673174**		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**1.109101522**	3	5.302368
Q6P9T8	EIVHLQAGQCGNQIGAK	**1.229780363**	2	5.043253
Q6P9T8	EVDEQMLNVQNK	**1.223276305**	2	4.069465
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	**1.052016141**	3	5.632992
Q6P9T8	INVYYNEATGGK	**1.430228909**	2	3.468115
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**0.971338277**	3	5.342913
Q6P9T8	LHFFMPGFAPLTSR	**1.505887827**	2	2.700942
Q6P9T8	MSATFIGNSTAIQELFK	**1.143236011**	2	3.974575

Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	**0.904384322**	3	4.662916
Q6P9T8	TAVCDIPPR	**0.862522116**	2	2.500931
Q6P9T8	YLTVAAVFR	**0.911403388**	2	2.469502
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.382934584**	**7.1E-09**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	**1.066740287**	3	4.351461
Q6P9U8	EGTGSTATSSSSTGGAVGK	**1.410549347**	2	4.13056
Q6PA06	**ATLA2 Atlastin_2**	**1.124061065**	**0.01458**	**5**
Q6PA06	AGLTDQVSHHAR	**0.899051283**	2	3.34998
Q6PA06	NLVPLLLAPENLVEK	**1.496868709**	2	2.892005
Q6PA06	QNQHEELQNVR	**1.142301459**	2	2.731601
Q6PA06	SMEQVCGGDKPYIAPSDLER	**1.487423611**	3	3.485745
Q6PA06	SMLQATAEANNLAAVAGAR	**1.049435107**	2	4.490577
Q6PCL9	**polymerase gamma**	**1.065204373**	**0.46653**	**4**
Q6PCL9	ATDITPIPMSEGGISDMPKR	**1.248009578**		
Q6PCL9	LTEILK	**0.821815249**		
Q6PCL9	QANNINMLKDGMK	**0.891649499**		
Q6PCL9	WEMDDPRPIAKAER	**1.094746145**		
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.299148575**	**0.27167**	**2**
Q6PDM2	SHEGETAYIR	**1.299159826**	2	2.640331
Q6PDM2	VVVSGLPPSGSWQDLK	**1.050317331**	2	2.310523
Q6PDN3	**MYLK Myosin light chain kinase_ smooth muscle**	**1.277784346**	**0.63548**	**2**
Q6PDN3	LIDFGLAR	**1.296755375**	2	2.373367
Q6PDN3	VSMSEKNGMQILEIRGVTR	**0.785272458**	2	2.444653
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.060638896**	**0.00172**	**3**
Q6PEC1	LEAAYTDLR	**1.165153058**	2	3.178392
Q6PEC1	QILESEKDLEEAEEYKEAR	**1.328580348**	3	3.835938
Q6PEC1	RLEAAYTDLR	**1.042788392**	2	2.347981
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.174625652**	**0.88343**	**3**
Q6PEC4	NDFTEEEEAQVR	**1.397857237**	2	3.461069
Q6PEC4	TDDIPVWDQEFLK	**1.099204904**	2	3.122371
Q6PEC4	TVANMIKGKTPEEIR+Oxidation(4)	**1.11166815**		
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.256216806**	**1.4E-08**	**6**
Q6Q0N1	AVFQYIDENQDR	**0.525690692**	2	3.008107
Q6Q0N1	EGGSIPVTLTFQEATGK	**1.470262884**	2	2.612732
Q6Q0N1	LGGSVELVDIGK	**1.357592561**	2	3.731147
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	**0.91285442**	2	2.634509
Q6Q0N1	MTEAAAADVQR	**1.238121474**	2	2.602796
Q6Q0N1	TVFGVEPDLTR	**1.142807538**	2	2.547685
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.735729911**	**0.23831**	**3**
Q6SKG1	AFIVLNPDYK	**0.749359546**	2	2.790596
Q6SKG1	FDSTSILQTLSK	**0.755283538**	2	3.127405
Q6SKG1	TGTVLIPGTTQLTQK	**0.694706884**	2	2.935618
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**0.993821045**	**0.98703**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	**0.913313976**	2	4.513122
Q6TUG0	FQMTQEVVCDECPNVK	**1.068539269**	2	5.165411
Q6TUG0	KGEGLPNFDNNNIK	**1.141366574**	2	2.752147
Q6TUG0	TLEVEIEPGVR	**0.952621706**	2	3.227964
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**0.845441734**	**2.1E-07**	**16**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	**0.931333996**	2	4.313604
Q6UPE1	ALNEGGLQSIPK	**0.91599465**	2	3.159334
Q6UPE1	ASCDAQTYGIGLK	**0.980803153**	2	3.68383
Q6UPE1	FCPAGVYEFVPLEQGDGFR	**0.741348976**	2	4.946673
Q6UPE1	GAPLNTPVTEDR	**0.844769122**	2	3.449286
Q6UPE1	GIATNDVGIQK	**0.831882939**	2	3.562947

Q6UPE1	HHPSIRPTLEGGK	**0.735967444**	2	2.424297
Q6UPE1	LQINAQNCVHCK	**0.92761424**	2	3.729051
Q6UPE1	NLSIYDGPEQR	**0.876253367**	2	3.21672
Q6UPE1	QLAAEQEKDIR	**0.767469133**	2	2.804508
Q6UPE1	QLTSENLQSK	**0.793671997**	2	2.462073
Q6UPE1	SGSLAAEAIFK	**0.767580988**	2	3.355657
Q6UPE1	TAGLHVTEYEDNLK	**0.87100077**	2	3.880151
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	**0.878493225**	2	3.703534
Q6UPE1	VDHTVGWPLDR	**0.785731695**	2	2.646851
Q6UPE1	VTIFAEGCHGHLAK	**0.564103748**	2	3.383801
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**0.878755391**	**0.01246**	**7**
Q6URK4	EDSVKPGAHLTVK	**0.82397743**	2	3.369654
Q6URK4	EDTEEYNLR	**0.875935142**	2	2.342645
Q6URK4	GFAFVTFDDHDTVDK	**0.665337751**	2	4.251501
Q6URK4	IETIEVMEDR	**0.834196142**	2	3.391518
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	**1.016450323**	2	4.976744
Q6URK4	WGTLTDCVVMR	**0.84572987**	2	2.30274
Q6URK4	YHTINGHNCEVK	**1.76732362**	2	3.574183
Q6URW6	**MYH14 Myosin_14**	**1.223097788**	**0.92724**	**4**
Q6URW6	EDQSILCTGESGAGK	**1.24878319**	2	4.497694
Q6URW6	FDQLLAEEK	**0.935381891**	2	2.33667
Q6URW6	KFDQLLAEEK	**0.929574065**	2	2.579592
Q6URW6	QLLQANPILEAFGNAK	**0.870512048**	2	4.332239
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.560720801**	**2.9E-05**	**5**
Q6XQN1	GSEVNVIGIGTNVVTCPK	**0.422621818**	2	4.118571
Q6XQN1	LDSGDLLQQAK	**0.931065885**	2	2.949369
Q6XQN1	LYLQQGQPYEPLPSLEESR	**0.377153285**	2	4.483629
Q6XQN1	QLQNPAVYQVALSEK	**0.607581133**	2	3.823194
Q6XQN1	VWLQGAQEPCTVKPAQVEPLLR	**0.345423256**	3	3.648148
Q6Y7W8	**PERQ2 PERQ amino acid_rich with GYF domain_containing protein 2**	**0.720441477**	**0.07026**	**2**
Q6Y7W8	AEEENRSENSLSAKVPSR	**0.704740488**	2	2.419723
Q6Y7W8	KDEPKAEQVEK	**0.977452035**	2	2.517178
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**0.901418918**	**0.49903**	**2**
Q6ZPJ3	FRTTDIVIR	**0.900801765**	2	2.451537
Q6ZPJ3	NCAQGEGSMAKKVK	**1.127156631**	2	2.563106
Q6ZPY5	**ZN507 Zinc finger protein 507**	**1.139790313**	**0.40759**	**2**
Q6ZPY5	CSLCGYVCSHPPSLK	**1.212420201**	2	2.341023
Q6ZPY5	IISSSPNK	**0.898978129**	2	2.352312
Q704S8	**CACP Carnitine O_acetyltransferase**	**0.963888076**	**0.70311**	**3**
Q704S8	ALQPIVSEEEWAHTK	**0.946376755**	2	2.495661
Q704S8	DKVNRESVNSIQK	**1.237520502**	2	2.333611
Q704S8	FNITPEIKNDIEK	**0.904755769**	2	3.187848
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.121651783**	**0.96371**	**5**
Q711G3	DCGTDVLDLWTLMQK	**1.155516541**	2	3.87297
Q711G3	DVEETKPELSLLGDGDH	**0.954390121**	2	3.449936
Q711G3	LNVAVGEYAK	**1.144402502**	2	3.027585
Q711G3	QHVPLDEYSANLR	**0.919220723**	2	2.562931
Q711G3	VILITPPPLCEAAWEK	**0.824485592**	2	2.646211
Q71TY3	**RS27 40S ribosomal protein S27**	**1.377268777**	**0.22376**	**2**
Q71TY3	DLLHPSPEEEK	**1.377391269**	2	2.327085
Q71TY3	LVQSPNSYFMDVK	**1.342100986**	2	2.86871
Q75N33	**SC16B Protein transport protein Sec16B**	**0.970365828**	**0.68167**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	**0.277075664**	2	3.800258
Q75N33	VLEPDWLVQLR	**0.987183464**	2	2.506728

Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**0.967797748**	**0.13573**	**3**
Q75Q39	NADLSTFYQNR	**0.988249249**	2	2.573889
Q75Q39	NREPLMPSPQFIK	**0.875516558**	2	2.548639
Q75Q39	SDEDKDKEGEALEVK	**1.349262453**	2	4.165979
Q75WE7	**VWA5A von Willebrand factor A domain_containing protein 5A**	**0.932062416**	**0.52586**	**2**
Q75WE7	YTQETIEEAVER	**1.002033793**	2	2.552592
Q75WE7	YVQELPLESDGALR	**0.611045224**	2	2.61122
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**0.937614447**	**0.14114**	**7**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	**1.087238055**	3	4.354185
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	**1.161138184**	3	3.376251
Q76MZ3	IGPILDNSTLQSEVKPILEK	**0.943022903**	2	4.528924
Q76MZ3	LTQDQDVDVK	**1.307700171**	2	2.886872
Q76MZ3	QLSQSLLPAIVELAEDAK	**0.988367713**	3	3.834573
Q76MZ3	SALASVIMGLSPILGK	**0.786430301**	2	3.083025
Q76MZ3	SEIIPMFSNLASDEQDSVR	**0.719514347**	2	3.855789
Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**0.899415681**	**0.97295**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	**0.700719419**	2	5.674018
Q78P75	NFGSYVTHETK	**0.950634127**	2	2.710826
Q78P75	YNPTWHCIVGR	**0.872686645**	2	2.721489
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**0.90916266**	**0.47467**	**5**
Q791V5	EEGIVGFFAGLIPR	**1.700676477**	2	3.596333
Q791V5	GLFTGLTPR	**0.902965631**	2	2.801613
Q791V5	LCSGVLGTVVHGK	**0.794241908**	3	3.354568
Q791V5	VLIQVGYEPLPPTIGR	**0.883501723**	2	4.165522
Q791V5	YCGLCDSIVTIYR	**1.10826701**	2	2.932106
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.15110047**	**0.28941**	**4**
Q794E4	ATENDIYNFFSPLNPVR	**1.357346281**	3	4.899892
Q794E4	HSGPNSADSANDGFVR	**1.024114955**	2	4.180212
Q794E4	ITGEAFVQFASQELAEK	**0.70954974**	2	3.867411
Q794E4	VHIEIGPDGR	**0.969317988**	2	2.742947
Q7M0E3	**DEST Destrin**	**1.188759018**	**3.6E-05**	**2**
Q7M0E3	HEYQANGPEDLNR	**1.273103022**	2	4.373701
Q7M0E3	KEELMFFLWAPEQAPLK	**0.875592619**	2	3.834273
Q7TMA5	**APOB Apolipoprotein B_100**	**0.953740627**	**0.09046**	**12**
Q7TMA5	GFEPTLEALFGK	**1.033439112**	2	2.900756
Q7TMA5	GGINQVGLAFESTK	**1.098551058**	2	2.473005
Q7TMA5	IEGNLVFDPSSYLPK	**0.942838814**	2	3.489512
Q7TMA5	IEIDIPLPLGGK	**1.658575909**	2	3.085059
Q7TMA5	ITDNDVLIALDSAK	**0.811424049**	2	3.20563
Q7TMA5	KGTVATEMSTER	**0.381839731**	2	2.643985
Q7TMA5	LLQWEQSEQVK	**0.844318236**	2	2.433946
Q7TMA5	LSISEQNAQR	**1.125736942**	2	2.580496
Q7TMA5	NFVASHIANILNSEELYVQDLK	**1.169326691**	3	3.645085
Q7TMA5	NSVSTALEHTLSALLTPAEQTSSWK	**0.756794691**	3	3.35974
Q7TMA5	SVGFHLPSQEVQIPTFTIPK	**0.709191498**	3	3.525585
Q7TMA5	TILFDTFVNDVAPVEK	**0.976352252**	2	3.475433
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**0.853414257**	**0.0515**	**4**
Q7TNG8	AVVGSPHVSTASAVR	**0.510670141**	2	2.375283
Q7TNG8	AYSTDVCVPISR	**0.852284211**	2	3.702007
Q7TNG8	GSQGGLSQDFVEALK	**1.021307268**	2	3.741249
Q7TNG8	QLLQEEVGPVGVETMR	**0.568943812**	2	2.694601

Q7TP47	HNRPQ Heterogeneous nuclear ribonucleoprotein Q	1.086314525	0.24794	2
Q7TP47	DLFEDELVPLFEK	1.460964208	2	3.06382
Q7TP47	NLANTVTEEILEK	1.012098918	2	3.680556
Q7TP48	APMAP Adipocyte plasma membrane_associated protein	0.982911176	0.01562	4
Q7TP48	LENGEIETIAR	0.988663373	2	3.319412
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	1.139617195	3	3.358104
Q7TP48	LLEYDTVTK	0.936082358	2	2.358764
Q7TP48	LLLSSETPIEGK	2.061485189	2	2.989513
Q7TP52	CMBL Carboxymethylenebutenolidase homolog	0.82202863	0.00062	7
Q7TP52	AGVSVYGIIR	1.025190831	2	2.393999
Q7TP52	EDCSPADKPYIEEAR	0.916069372	2	3.540596
Q7TP52	KREDCSPADKPYIEEAR	0.84659243	2	4.624423
Q7TP52	LDYGGMGQEVQVEHIK	0.7015674	2	4.417758
Q7TP52	LKEHCIVNYQVK	0.863554589	2	3.824452
Q7TP52	NLIEWLNK	0.841648731	2	2.452743
Q7TP52	TFSGQTHGFVHR	0.720973288	2	3.603651
Q7TPB1	TCPD T_complex protein 1 subunit delta	0.831447746	9.9E-20	11
Q7TPB1	ALIAGGGAPEIELALR	1.023511379	2	4.126056
Q7TPB1	DIEREDIEFICK	1.589529848	2	2.380545
Q7TPB1	ETLLNSATTSLNSK	1.306824992	2	3.556609
Q7TPB1	GDVTITNDGATILK	0.655384725	2	3.287564
Q7TPB1	GIHPTIISESFQK	1.267468906	2	2.636964
Q7TPB1	IDDVVNTR	1.005760412	2	2.375369
Q7TPB1	LVIEEAER	1.327826983	1	1.946073
Q7TPB1	MIQDGKGDVTITNDGATILK+Oxidation(0)	0.87333294		
Q7TPB1	SIHDALCVIR	0.846390782	2	2.481982
Q7TPB1	TGCNVLLIQK	0.81279708	2	2.502972
Q7TPB1	VIDPATATSVDLR	1.081374267	2	3.38237
Q7TPJ0	SSRA Translocon_associated protein subunit alpha	1.129895239	0.79155	2
Q7TPJ0	GEDFPANNIVK	1.07859048	2	3.022465
Q7TPJ0	GTEDFIVESLDASFR	1.104603904	2	4.092875
Q7TQM4	SOAT2 Sterol O_acyltransferase 2	1.103604196	0.46853	2
Q7TQM4	QDRPLPSTASDSTR	0.9172552	2	3.185305
Q7TQM4	TQCLEQAQR	1.091894384	2	3.019858
Q80TV8	CLAP1 CLIP_associating protein 1	1.127128837	0.89552	2
Q80TV8	MESCLAQVLQK	0.869503826	2	2.498413
Q80TV8	MGADLLGSVQAKVQK+Oxidation(0)	1.18019088		
Q80W21	GSTM7 Glutathione S_transferase Mu 7	0.89131408	1.8E-10	11
Q80W21	CLDAFPNLK	0.782007485	2	3.183004
Q80W21	CLDAFPNLKDFIAR	0.764323397	2	2.693651
Q80W21	FKLGLDFPNLPYLIDGSHK	0.85347492	3	4.137031
Q80W21	HNLCGETEEER	0.938382986	2	3.825125
Q80W21	ITQSNAILR	0.95812866	2	3.149814
Q80W21	KHNLCGETEEER	0.790116262	3	4.447618
Q80W21	LFLEYTDSSYEEK	0.642022134	2	3.974284
Q80W21	LGLDFPNLPYLIDGSHK	0.949439229	2	4.7105
Q80W21	LKPGYLEQLPGMMR	0.258646858	2	2.619989
Q80W21	LYSEFLGK	1.053652137	2	2.314208
Q80W21	VDILENQLMDNR	0.511526008	2	3.693533
Q80X50	UBP2L Ubiquitin_associated protein 2_like	0.809651225	4.6E-06	2
Q80X50	IDLAVLLGK	0.812290922	2	3.387492
Q80X50	QRPQATAEQIR	0.79674814	2	2.33472
Q80X90	FLNB Filamin_B	0.981449665	0.82296	9
Q80X90	ADIEMPFDPSK	1.140479764	2	2.335035

Q80X90	AHGPGLEGGLVGKPAEFTIDTK	**0.989720532**	3	3.496061
Q80X90	GAGIGGLGITVEGPSESK	**0.979893896**	2	3.55208
Q80X90	GFLDGVYSFEYYPSTPGK	**1.973936745**	2	3.188443
Q80X90	IGNLQTDLSDGLR	**1.128568945**	2	2.38394
Q80X90	ILAQDGEGQPIDIQMK	**0.981304592**	2	3.852266
Q80X90	VDIQTEDLEDGTCK	**0.918093607**	2	3.917562
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	**1.227742439**	3	3.900689
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	**1.112839591**	2	3.887513
Q80YR5	**SAFB2 Scaffold attachment factor B2**	**1.001918274**	**0.44167**	**2**
Q80YR5	GSKMEEEGSEDNGLEEDSR	**0.733340665**	2	2.393886
Q80YR5	SEPVKEEGSELEQPFAQATSSVGPDR	**1.25583799**	3	4.219013
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.234812757**	**0.99929**	**2**
Q80Z25	ELEQEAERLEK	**1.242382408**	2	2.939034
Q80Z25	MIEESLK+Oxidation(0)	**1.114344388**		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.353091568**	**0.00035**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	**1.375146861**	2	3.935778
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	**2.459075286**	5	4.608683
Q80Z29	VIQGDGVDINTLQEIVEGMK	**1.09683744**	2	4.45121
Q80Z29	YLLETSGNLDGLEYK	**1.234117048**	2	4.222397
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**0.93216535**	**0.92715**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	**0.762135369**	2	2.729569
Q80Z36	YPEEQLK	**1.038977955**	2	2.33479
Q80ZF0	**chain**	**0.975049063**	**0.87775**	**2**
Q810B6	**ANFY1 Ankyrin repeat and FYVE domain_containing protein 1**	**1.005094384**	**0.3149**	**2**
Q810B6	QLDLELK	**1.074832562**	1	2.257823
Q810B6	RESGAAEQVDNKGR	**0.480942312**	1	1.925182
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**0.806121832**	**0.68645**	**2**
Q811D2	AQEDFDK	**0.763059445**	1	1.949182
Q811D2	LNMLSSKLDNEKQNK	**0.842554488**	2	2.336043
Q811X6	**CRYL1 Lambda_crystallin homolog**	**0.614816411**	**0.40301**	**3**
Q811X6	EMKSLEQSGSLK+Oxidation(1)	**0.782210252**		
Q811X6	IVDDQVILSSSSSCLLPSK	**0.961280169**	2	2.731198
Q811X6	TFGPVPEFSGDTVEK	**0.466813073**	2	3.012004
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**0.990160299**	**0.65197**	**10**
Q8BFZ3	CDVDIR	**0.779329916**	1	2.001956
Q8BFZ3	DLTDYLMK	**0.738120389**	1	2.07498
Q8BFZ3	HQGVMVGMGQK	**0.846695985**	3	3.90187
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	**1.508234074**		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	**1.002329615**		
Q8BFZ3	HQGVMVGMGQK+Oxidation(7)	**0.968087311**		
Q8BFZ3	SYELPDGQVITIGNER	**0.991697927**	3	5.169834
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	**1.012290329**	3	6.937174
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)	**1.224323106**		
Q8BFZ3	VAPDEHPILLTEAPLNPK	**1.034078848**	3	4.210713
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**0.953488957**	**0.76286**	**5**
Q8BG32	LYDNLLEQNLIR	**0.876178652**	2	3.650634
Q8BG32	TGQAAELGGLLK	**1.151233142**	2	2.474134
Q8BG32	TTANAIYCPPK	**1.130981396**	2	3.076473
Q8BG32	TYEAALETIQNMSK	**0.953771249**	2	3.262693
Q8BG32	VQIEHISSLIK	**0.825066682**	2	3.159459
Q8BG79	**C19L2 CWF19_like protein 2**	**0.710334599**	**0.03301**	**2**
Q8BG79	KNQDSSGNLRSK	**0.651336718**	2	2.392182

Q8BG79	MWPVSSPRETLDMKAER+Oxidation(12)	0.871690663		
Q8BGC4	ZADH2 Zinc_binding alcohol dehydrogenase domain_containing protein 2	0.724721146	0.70942	2
Q8BGC4	DCPVPLPGDGDLLVR	0.690457963	2	2.343935
Q8BGC4	FVGINASDINYSAGR	1.20438201	2	3.814173
Q8BGT5	ALAT2 Alanine aminotransferase 2	0.929827283	9.9E-20	3
Q8BGT5	ILTLESMNPQVK	0.905782189	2	2.604494
Q8BGT5	LLEETGICVVPGSGFGQR	0.972540714	2	3.769341
Q8BGT5	VLCIINPGNPTGQVQSR	1.623887869	2	4.51233
Q8BGY2	IF5A2 Eukaryotic translation initiation factor 5A_2	1.074130428	1	4
Q8BGY2	KYEDICPSTHNMDVPNIK	1.032467949	3	4.350031
Q8BGY2	KYEDICPSTHNMDVPNIK+Oxidation(11)	1.054407671		
Q8BGY2	VHLVGIDIFTGK	1.048486425	1	3.36391
Q8BGY2	YEDICPSTHNMDVPNIK	0.956601372	2	4.045334
Q8BGY3	LUZP2 Leucine zipper protein 2	0.829234418	0.01901	2
Q8BGY3	DLQNENKSLK	0.856286929	2	2.312989
Q8BGY3	SLQEALQNQLK	0.467717637	2	2.477481
Q8BH00	AL8A1 Aldehyde dehydrogenase family 8 member A1	1.035661807	7.4E-15	9
Q8BH00	ELLMLENFIGGK	1.473122822	2	3.387634
Q8BH00	ELNLPFGGMK	1.052317657	1	2.232169
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.028307706	3	5.092261
Q8BH00	ILCGEGVDQLSLPLR	1.033244657	2	4.385639
Q8BH00	ITQLSAPHCK	1.269089771	2	2.94709
Q8BH00	KLSLELGGK	0.70556921	1	2.004368
Q8BH00	NPAIIFEDANLEECIPATVR	0.927155626	3	5.344548
Q8BH00	SSFANQGEICLCTSR	3.155665909	2	4.445076
Q8BH00	TPVGIAGLISPWNLPLYLLTWK	1.058280463		
Q8BH69	SPS1 Selenide_ water dikinase 1	0.6963467	0.14833	2
Q8BH69	IIEVAPQVATQNVNPTPGATS	0.814512513	2	3.680098
Q8BH69	YGEGHQAWIIGIVEK	0.63108414	2	2.364937
Q8BHN3	GANAB Neutral alpha_glucosidase AB	0.912837124	0.9719	8
Q8BHN3	AEKDEPGAWEETFK	0.945001674	2	3.427011
Q8BHN3	DDNSVELTVAEGPYK	1.260999303	2	3.638777
Q8BHN3	MLDYLQGSGETPQTDIR	0.796746666	2	4.764602
Q8BHN3	MLDYLQGSGETPQTDIR+Oxidation(0)	1.1223557		
Q8BHN3	REPWLLASQYQDAIR	0.835274372	3	3.755299
Q8BHN3	SGGIERPFVLSR	0.978121961	2	2.527569
Q8BHN3	SLLLSVNAR	0.987371503	2	2.420121
Q8BHN3	VTEGGEPYR	0.912195545	2	2.536797
Q8BI84	MIA3 Melanoma inhibitory activity protein 3	0.813707156	0.3289	2
Q8BI84	LQLESEREQNVK	0.21614526	2	2.342728
Q8BI84	TQTAVSIVEEDLK	0.915669338	2	2.619912
Q8BIJ6	SYIM Isoleucyl_tRNA synthetase_ mitochondrial	0.730218127	9.4E-08	2
Q8BIJ6	DTVLLPQTSFPMK	0.891649499	1	2.230632
Q8BIJ6	SCQTALAEILDVLVR	0.687568033	2	3.898237
Q8BIJ7	RUFY1 RUN and FYVE domain_containing protein 1	0.854998959	0.06058	2
Q8BIJ7	EKDTSCLLQTELQQVEGLK	0.867993897	2	2.446253
Q8BIJ7	ELQDEKAELRK	0.651149208	2	2.445209
Q8BJ64	CHDH Choline dehydrogenase_ mitochondrial	0.863269298	0.00264	7
Q8BJ64	ADSAYHPSCTCK	3.897893631	2	3.403724
Q8BJ64	AEVQTLVSR	0.963525272	2	2.75354
Q8BJ64	ELQPGSHVQSDK	1.112037286	2	2.5352
Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.832232906	2	4.11539
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	0.96169435	5	4.860238

Q8BJ64	TNHPLHQAFLQAAR	**0.740339075**	3	4.677282
Q8BJ64	VLLLEAGPK	**0.890257873**	2	2.930708
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**0.898663849**	**0.18422**	**2**
Q8BJY1	GLTHPDDSVK	**0.881729431**	2	2.487785
Q8BJY1	TVAEIFGNSNYLR	**1.450511461**	2	3.076345
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.024688314**	**1**	**2**
Q8BL97	NPPGFAFVEFEDPR	**1.026841653**	2	3.482625
Q8BL97	VYVGNLGTGAGK	**0.995980114**	2	2.359843
Q8BMJ2	**SYLC Leucyl_tRNA synthetase_ cytoplasmic**	**1.048965192**	**0.70783**	**3**
Q8BMJ2	QTGEGVGPQEYTLVK	**1.137270385**	2	2.366236
Q8BMJ2	SFITTDVNPYYDSFVR	**1.046209353**	2	3.315366
Q8BMJ2	STGNFLTLSQAVDK	**0.773195938**	2	2.974211
Q8BTM8	**FLNA Filamin_A**	**0.887146664**	**0.78649**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	**0.832721997**	2	3.789589
Q8BTM8	ANLPQSFQVDTSK	**0.987123611**	2	2.465197
Q8BTM8	GAGTGGLGLAVEGPSEAK	**0.887424048**	2	3.685926
Q8BTM8	IVSPSGAAVPCK	**0.88687034**	2	2.456903
Q8BTM8	VTAQGPGLEPSGNIANK	**0.942057984**	2	3.940563
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.14547927**	**0.90802**	**2**
Q8BTZ7	HHGQEGSILVTK	**1.053828774**	3	3.756291
Q8BTZ7	YGVVVCEADTGR	**1.13813893**	2	3.255346
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**0.965126368**	**0.88501**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	**1.015488471**	2	2.420279
Q8BU33	LPNSLMGR+Oxidation(5)	**0.82322699**		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	**0.953470659**	2	4.582908
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**1.092162679**	**0.14272**	**2**
Q8BWQ1	ADIWLIR	**0.804809652**	2	2.536914
Q8BWQ1	IHHDQPVKPLDR	**1.206249821**	3	3.50576
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**1.141593804**	**1.2E-05**	**2**
Q8BX70	ENALSELDVPFKVK	**1.217304284**	2	2.902301
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19)	**0.800172874**		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.496686494**	**6.5E-10**	**2**
Q8C7X2	FNVEDGEIVQQVR	**1.043748101**	2	3.270266
Q8C7X2	VMGDRSVLYK+Oxidation(1)	**2.430761696**		
Q8C8R3	**ANK2 Ankyrin_2**	**1.051227339**	**3.4E-08**	**2**
Q8C8R3	STSSSGRPGTSPTRESR	**0.708304399**	2	2.43608
Q8C8R3	TSTDFSEVIKQELEDNDK	**1.549965022**	2	2.613098
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.246118793**	**0.64239**	**4**
Q8CC88	HQATGELDDAK	**1.246185374**	2	3.385847
Q8CC88	IILDNLQAK	**0.999628035**	2	2.302537
Q8CC88	NLADQGIINYPYSTR	**1.400304448**	2	3.190962
Q8CC88	VSSDQLSSENLTSAVGQK	**0.762032641**	2	3.489278
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**1.074536112**	**0.12469**	**2**
Q8CDM4	MEEESIDLIIKEQK	**1.144101394**	2	2.39728
Q8CDM4	VTCQHKMEEESIDLIIK	**0.715696703**	2	2.37989
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.010561881**	**0.73834**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	**0.876263553**	3	4.998273
Q8CFN2	WVPEITHHCPK	**0.902631225**	2	2.406111
Q8CFN2	YVECSALTQK	**1.124440378**	2	3.052529
Q8CFW1	**ANO2 Anoctamin_2**	**1.134049364**	**0.24977**	**2**
Q8CFW1	TEQTFEERLILK	**1.335714469**	2	2.368721
Q8CFW1	TKDIGIWFDILSGIGK	**0.929104163**	2	2.339453

Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.144744823**	**0.00077**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	**0.60065556**	2	2.893334
Q8CG45	EHHFEAIALVEK	**1.668075186**	2	2.345078
Q8CG45	FFGNSWSETYR	**0.933400628**	2	2.817085
Q8CG45	FYAYNPLAGGLLTGK	**1.111145432**	2	4.537042
Q8CG45	MDASASAATVR	**0.913509732**	2	3.673352
Q8CG45	MDASASAATVR+Oxidation(0)	**0.876161119**		
Q8CG45	QVETELLPCLR	**0.915617364**	2	2.962501
Q8CG45	RMDASASAATVR	**1.306412702**	2	2.760439
Q8CG45	TTYGTSAPSMTSAALR	**0.929765878**	2	4.211116
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	**1.725498455**	3	5.550289
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**0.934551113**	**0.96241**	**2**
Q8CG48	EEKLLEK	**0.953402333**	1	1.965779
Q8CG48	IKALNCEIEELER	**0.861063743**	2	2.464792
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.15541052**	**9.6E-06**	**10**
Q8CGC7	AIQGATSHHLGQNFSK	**1.197467167**	2	4.479011
Q8CGC7	DQDVEPGAPSMGAK	**0.956957387**	2	3.14168
Q8CGC7	DQVDSAVQELLQLK	**0.93854016**	2	3.728001
Q8CGC7	GDVSISVEEGKENLLR	**1.370944143**	2	3.47736
Q8CGC7	KEENLAEWYSQVITK	**1.233404776**	2	4.356993
Q8CGC7	KGDIIQLQR	**1.042922068**	2	2.657011
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	**1.123767466**	2	4.380905
Q8CGC7	SQGSGLSSGGAGEGQGPK	**1.350964589**	2	4.633912
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	**1.051730554**	3	3.47725
Q8CGC7	VYEELLAIPVVR	**1.28993025**	2	3.032671
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.211785422**	**7E-05**	**9**
Q8CHM7	DTSKPCLINIMIEPQSTR	**0.94520858**	2	3.494121
Q8CHM7	GAAYSHAEDSIR	**2.598060684**	2	3.43655
Q8CHM7	GVVPDNHPNCVGAAR	**1.553769353**	2	3.364092
Q8CHM7	GYFVQTPEELQDSLR	**1.056064917**	2	4.051752
Q8CHM7	LVELCNLPFLPTPMGK	**1.173388147**	2	4.265065
Q8CHM7	NCFIVSEGANTMDIGR	**1.140969945**	2	4.907655
Q8CHM7	NQEAMGAFQEFPQVEACR	**1.299685331**	2	6.103219
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	**1.045075349**	3	4.140991
Q8CHM7	YKECCMPPPLSLAETSAVR	**0.587694078**	2	2.369579
Q8CI17	**MB213 Protein mab_21_like 3**	**0.944144592**	**0.83127**	**2**
Q8CI17	QQISQTMEEVQK+Oxidation(6)	**0.976912626**		
Q8CI17	RQQISQTMEEVQK	**0.925012964**	2	2.3575
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.752659283**	**0.01498**	**3**
Q8CIB5	GCEVTPDVNISGQK	**0.730258523**	2	3.165857
Q8CIB5	INQLYEQAK	**0.878586773**	2	2.969903
Q8CIB5	TSTILGDITSIPELADYIK	**0.821496611**	2	2.898173
Q8CIE6	**COPA Coatomer subunit alpha**	**1.131070416**	**0.09762**	**7**
Q8CIE6	ASNLENSTYDLYTIPK	**1.529805144**	2	3.797963
Q8CIE6	DADSQNPDAPEGK	**1.096623217**	2	3.2413
Q8CIE6	GITGVDLFGTTDAVVK	**1.104322496**	2	3.995919
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	**0.856167425**	2	3.641241
Q8CIE6	LLELGPKPEVAQQTR	**1.126972382**	2	3.470856
Q8CIE6	SILLSVPLLVVDNK	**1.133962455**	2	3.5948
Q8CIE6	TLDLPIYVTR	**1.166892563**	2	2.672677
Q8CJ40	**CROCC Rootletin**	**0.879831491**	**0.88292**	**4**
Q8CJ40	DLLQLGGELVRTSR	**1.005972484**	2	2.47817
Q8CJ40	ELEERTGNLGRQR	**1.672041894**	2	2.307867
Q8CJ40	LQEERRLLQER	**0.870760109**	2	2.359333
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9)	**0.912296979**		

Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.01817219**	**0.88036**	**3**
Q8JZN5	GSNTCEVHFENTR	**1.092650807**	2	4.359045
Q8JZN5	NLSEFGLIQEK	**0.913819129**	2	3.107225
Q8JZN5	SGNVTTVMETIGR	**1.02547234**	2	2.505223
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.035583407**	**0.02895**	**16**
Q8K009	ADPLALAAEK	**0.971400478**	2	2.639571
Q8K009	AGFSVFWADDGLDTGPILLQR	**0.895124193**	2	3.867094
Q8K009	AMVEAVQLIADGK	**0.798088805**	2	3.769438
Q8K009	ANNTEYGLASGVFTR	**0.795308588**	2	4.734161
Q8K009	DLGEEALNEYLK	**0.942149838**	2	3.232624
Q8K009	EESFGPIMVISK	**1.083395712**	2	2.40331
Q8K009	FLFPEGIK	**0.881746585**	2	2.402335
Q8K009	FQNGDIDGVLQR	**0.906987163**	2	2.911394
Q8K009	GVINIIPGSGGVAGQR	**0.805726973**	2	3.957973
Q8K009	HGSIIYHPSLLPR	**0.912699881**	2	4.178293
Q8K009	LEAGTVFINTYNK	**1.2592886**	2	3.081229
Q8K009	NLQFEDGK	**0.740681487**	1	2.128599
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	**0.733194797**	3	3.709913
Q8K009	SCDVKPNDTVDSLYNR	**1.002013686**	2	4.433568
Q8K009	TPQPEEGATYEGIQK	**1.081018512**	2	3.200745
Q8K009	VVGVFTVPDKDGK	**0.871890999**	2	3.137646
Q8K1S6	**SPIR2 Protein spire homolog 2**	**1.383696395**	**0.10032**	**2**
Q8K1S6	ALFVETLELR	**1.622256173**	2	2.312166
Q8K1S6	DTADILLRR	**1.036273494**	2	2.424882
Q8K2F0	**BRD3 Bromodomain_containing protein 3**	**0.820439509**	**0.70385**	**2**
Q8K2F0	LNLPDYHKIIK	**1.355917393**	2	2.459141
Q8K2F0	QLSLDINRLPGEK	**0.820438854**	2	2.453372
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**0.875835384**	**0.81972**	**2**
Q8K3J1	LCEAICPAQAITIEAEPR	**0.880149963**	2	4.369447
Q8K3J1	YVNKKEQESEVDMK	**0.902437032**	2	2.317082
Q8K440	**ABC8B ATP_binding cassette sub_family A member 8_B**	**0.950549036**	**0.85667**	**3**
Q8K440	GEILGLLGHNGAGKSTSLK	**0.849112861**	2	2.313141
Q8K440	LMEMEQTLSSLRETEK+Oxidation(1)	**1.187065409**		
Q8K440	LMEMEQTLSSLRETEK+Oxidation(3)	**1.185668333**		
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**0.912268192**	**0.87508**	**5**
Q8K442	GQITAILGHSGAGK	**1.494939952**	2	3.506877
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	**0.914216311**	3	3.541419
Q8K442	LTGVCPQCNVQFDFLTVR	**1.302655026**	2	2.814696
Q8K442	NTQNILVQNLSGGQK	**0.90714207**	2	3.425331
Q8K442	STLLNVLSGLCVPTK	**0.961381167**	2	3.722986
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.785827422**	**9.9E-20**	**9**
Q8K4C0	FDHEMFGLKPK	**0.808300692**	2	2.921404
Q8K4C0	GYPIDILLSSR	**0.774464332**	2	3.06238
Q8K4C0	HSALGQHPTINDDLPNR	**0.710187792**	2	4.999358
Q8K4C0	IAVIGSGASGLTCIK	**0.797294421**	2	4.029736
Q8K4C0	KLPSQSEMMAEINK	**0.773208443**	2	3.820664
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	**0.769088452**	3	4.587523
Q8K4C0	KTILTTEDR	**0.74262732**	2	2.560853
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	**0.603527353**	3	4.066142
Q8K4C0	SDDIGGLWR	**0.662716721**	2	2.813447
Q8K4G6		**0.828108616**	**3.9E-06**	**56**

Q8K4T4	FLIP1 Filamin_A_interacting protein 1	1.260272252	0.10865	2
Q8K4T4	FQPRAETQSMKIELK+Oxidation(9)	**1.595478011**		
Q8K4T4	IEELEETNKSLQK	**1.216745005**	2	2.406459
Q8K4Z3	AIBP Apolipoprotein A_I_binding protein	0.782614383	0.00032	2
Q8K4Z3	GNPSGIQPDLLISLTAPK	**0.920569753**	2	4.19953
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	**0.77052926**	2	5.983057
Q8K586	RANT GTP_binding nuclear protein Ran_ testis_specific isoform	1.216003252	2.4E-05	3
Q8K586	FNVWDTAGQEK	**1.03637909**	2	3.033225
Q8K586	NLQYYDISAK	**1.195261867**	1	2.215826
Q8K586	VCENIPIVLCGNK	**1.325708433**	2	3.828304
Q8QZY1	EIF3L Eukaryotic translation initiation factor 3 subunit L	1.199705784	0.62856	2
Q8QZY1	KSEGEMDFLRSNPK	**0.953544712**	2	2.312369
Q8QZY1	VFSDEVQQQAQLSTIR	**1.200835551**	2	3.875024
Q8R066	C1QT4 Complement C1q tumor necrosis factor_related protein 4	1.536957791	0.04548	2
Q8R066	NRDEVQAMIYDDGASRR	**1.129559207**	2	2.326402
Q8R066	TLSVKLMKNR	**1.538007979**	2	2.413723
Q8R081	HNRPL Heterogeneous nuclear ribonucleoprotein L	0.926154703	0.00018	5
Q8R081	ASLNGADIYSGCCTLK	**1.398394244**	2	3.317305
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	**0.922734395**	3	5.179823
Q8R081	SDALETLGFLNHYQMK	**0.724023251**	2	2.988459
Q8R081	SSSGLLEWDSK	**0.649081005**	2	2.833583
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	**0.848482327**	3	7.479366
Q8R0F9	S14L4 SEC14_like protein 4	1.106906325	0.54997	6
Q8R0F9	FDNTYSLLHTK	**1.258163945**	2	3.068027
Q8R0F9	GSSHQVENEILFPGCVLR	**0.869853986**	2	5.072796
Q8R0F9	VCEMLLHECELQSQK	**0.77208304**	2	4.637535
Q8R0F9	VCEMLLHECELQSQK+Oxidation(3)	**0.903766432**		
Q8R0F9	VGYTAEVLLPDK	**1.058595522**	2	2.695363
Q8R0F9	VGYTAEVLLPDKACEEK	**0.652183023**	2	2.743185
Q8R164	BPHL Valacyclovir hydrolase	0.691100992	0.27792	3
Q8R164	FADEFNR	**0.818598333**	2	2.49064
Q8R164	QVSLLGWSDGGITALIAAAK	**0.748011395**	2	3.436995
Q8R164	TDFAPQLQSLNK	**0.814983499**	2	3.547161
Q8R1V4	TMED4 Transmembrane emp24 domain_containing protein 4	0.959952326	0.99998	2
Q8R1V4	CFIEEIPDETMVIGNYR	**1.020310497**	2	3.550782
Q8R1V4	QLLDQVEQIQK	**0.95246713**	2	3.146686
Q8R3Q6	CCD58 Coiled_coil domain_containing protein 58	0.895576217	0.28186	2
Q8R3Q6	IVHELNTTVPTASFAGK	**0.976860568**	2	4.195305
Q8R3Q6	NCIAQTSAVVK	**0.868855159**	2	2.661136
Q8R491	EHD3 EH domain_containing protein 3	0.913343752	0.85341	5
Q8R491	ADQIETQQLMR	**0.785869324**	2	2.79187
Q8R491	LDISDEFSEVIK	**0.934438667**	2	3.138056
Q8R491	LFEAEEQDLFK	**0.840739439**	2	3.6
Q8R491	MQDQLQAQDFSK	**1.057863041**	2	3.81479
Q8R491	QEETQRPVQMVK	**0.784702432**	2	2.529147
Q8VBU2	NDRG2 Protein NDRG2	0.86533573	3.4E-07	7
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	**0.755100013**	3	4.767313
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK+Oxidation(3)	**0.843730602**		
Q8VBU2	LDPTQTSFLK	**0.570171783**	1	1.909294
Q8VBU2	MADSGGQPQLTQPGK	**1.493580833**	2	3.85656
Q8VBU2	SLITHAPNLENIELYWNSYNNR	**0.99482346**	3	4.776059

Q8VBU2	TASLTSAASIDGSR	**1.429336077**	2	3.109354
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	**0.999771829**	2	4.424169
Q8VC12	**HUTU Urocanate hydratase**	**0.859021409**	**0.00485**	**7**
Q8VC12	HQLVVGSQAR	**0.87135034**	2	3.096704
Q8VC12	LLALEFAQELR	**0.96920184**	2	3.781817
Q8VC12	LQYMDNIR	**0.941606645**	2	2.35022
Q8VC12	LVITNGMVIPNYSSR	**0.756528813**	2	3.353469
Q8VC12	VAIAVAINQAIASGK	**1.299994298**	2	3.664294
Q8VC12	VFVTSGLGGMSGAQAK	**0.69453647**	2	4.50862
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9)	**0.790431471**		
Q8VDG5	**PPCS Phosphopantothenate__cysteine ligase**	**1.394918831**	**0.05319**	**2**
Q8VDG5	FLDNFSSGR	**1.293240151**	2	2.483594
Q8VDG5	LETDPDIIISR	**1.407513587**	2	3.169044
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.879038585**	**0.02217**	**4**
Q8VED5	NKYEDEINK	**0.749568368**	2	2.761595
Q8VED5	NKYEDEINKR	**0.7847122**	3	3.440344
Q8VED5	NLDLDSIIAEVK	**0.893144418**	2	3.849866
Q8VED5	YEDEINK	**1.086360644**	1	2.480872
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.136763558**	**0.20086**	**9**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	**1.119610015**	3	4.495188
Q8VEK3	GYFEYIEENK	**1.028128599**	2	3.266571
Q8VEK3	LLEQYKEESK	**1.318409847**	2	3.166838
Q8VEK3	LLEQYKEESKK	**1.161702739**	2	3.383716
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	**0.805552542**	3	5.08896
Q8VEK3	NFILDQTNVSAAAQR	**0.76726865**	2	4.528125
Q8VEK3	TCNCETEDYGEK	**1.099279783**	2	3.385928
Q8VEK3	VSELKEELKK	**0.98308385**	2	2.42955
Q8VEK3	YNILGTNTIMDK	**0.865069392**	2	3.575292
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.743629831**	**1.3E-05**	**7**
Q8VHE9	ATVQSVLLDSAGR	**0.856716066**	2	3.539473
Q8VHE9	FLPLPLTQLLNK	**0.756216829**	2	2.857179
Q8VHE9	GATYGADHDLAR	**1.073666374**	2	3.173579
Q8VHE9	NLYSDLQALGSK	**0.700128729**	2	2.919394
Q8VHE9	RPPEPLVTDK	**0.811568124**	2	2.618397
Q8VHE9	VLVLEQHTK	**0.763652379**	2	2.387858
Q8VHE9	VVAHGVSHAILLK	**0.621113753**	2	2.420338
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.586178714**	**9.9E-20**	**4**
Q8VHT6	DCYVLSQLVGQK	**1.406996547**	2	2.967536
Q8VHT6	ILDLGSGSGR	**0.848692789**	2	2.688855
Q8VHT6	SLQNVHEEVISR	**2.219191657**	2	3.216307
Q8VHT6	TSADLQTNACVTPAK	**1.958897346**	2	3.84688
Q8VHX6	**FLNC Filamin_C**	**0.946894403**	**0.43566**	**3**
Q8VHX6	AFGPGLEGGLVNK	**1.073844905**	2	2.600145
Q8VHX6	GAGTGGLGLTVEGPCEAK	**0.936722801**	2	3.895885
Q8VHX6	LIALLEVLSQK	**1.481632905**	2	2.698955
Q8VI04	**ASGL1 L_asparaginase**	**0.830353526**	**0.17816**	**3**
Q8VI04	FAADMGIPQTPAEK	**1.243453827**	2	2.711102
Q8VI04	GNLAYATSTGGIVNK	**0.888890367**	2	4.287473
Q8VI04	TVDEAATLALDYMK	**0.759611509**	2	2.656144
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**0.998757835**	**0.22591**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	**0.647922131**	2	4.466636
Q8VID1	LAEDGAHVVISSR	**2.120228188**	2	3.700807
Q8VID1	NFAAELAPK	**0.935900955**	2	2.517546
Q8VID1	VNCLAPGLIK	**1.044657781**	2	2.540972
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.846161555**	**0.5427**	**10**

Q8VIF7	CGPGYATPLEAMK	0.844555406	2	3.467742
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.028786962	2	4.957894
Q8VIF7	GGFVLLDGETFEVK	0.910543549	2	4.192704
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.806063137	2	4.33114
Q8VIF7	HEIIQTLQMK	0.938340955	2	2.641031
Q8VIF7	HNIMVSTEWAAPNVFK	0.865618059	2	4.299456
Q8VIF7	LTGQIFLGGSIVK	0.68632595	2	3.003609
Q8VIF7	NEGGTWSVEK	0.871540102	2	2.886699
Q8VIF7	NTGIEAPDYLATVDVDPK	0.912417407	2	5.206403
Q8VIF7	VIEPNEIHAK	0.76598106	2	2.54865
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.029829843**	**0.63777**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	0.976009606	2	2.827186
Q8VIJ6	NLSPYVSNELLEEAFSQFGPIER	0.968926243	2	3.53484
Q8VIJ6	YGEPGEVFINK	1.179571484	2	2.798023
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**0.788194621**	**0.79634**	**6**
Q91VA0	AFIVLNPEFLSHDQEQLIK	0.797104507	2	5.577048
Q91VA0	AILPFDLQIIDEK	0.818292911	2	3.773881
Q91VA0	GNILPPNTEGYIGIR	0.789172314	2	3.009643
Q91VA0	HNQGLAFR	0.875979292	2	2.323281
Q91VA0	KVEFVSELPK	0.912960219	2	2.873079
Q91VA0	NKEFGQL	0.874468988	1	2.108725
Q91VM5	**RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1**	**1.023286571**	**0.82044**	**2**
Q91VM5	LFIGGLNTETNEK	1.154471486	2	3.151284
Q91VM5	VEQATKPSFESGR	1.019481317	2	3.522907
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.944185591**	**0.94437**	**2**
Q91VM9	IIAINVNDPEAEK	0.93999533	2	3.251032
Q91VM9	MEIATEEPLNPIK	1.128820846	2	3.867111
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.866274495**	**0.59824**	**4**
Q91W43	AGHQLQHDLFFDTLK	0.876606985	2	2.411082
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	0.838161372	2	4.082502
Q91W43	VSFQPNSGAQGEYAGLATIR	0.857979617	2	4.778082
Q91W43	YGNIDVAHLK	0.838429677	3	3.490403
Q91W90	**TXND5 Thioredoxin domain_containing protein 5**	**1.129608447**	**0.00194**	**2**
Q91W90	SFEDTIAQGITFVK	0.888119432	2	3.558086
Q91W90	VDCTQHYAVCSEHQVR	1.458424782	3	4.390991
Q91WL5	**CP4CA Cytochrome P450 4A12A**	**1.017973323**	**0.26761**	**3**
Q91WL5	FELLPDPTR	0.650730058	2	2.396487
Q91WL5	IQLQDEEELEK	1.242382408	2	2.35265
Q91WL5	VAVALTLLR	1.304827285	2	2.599054
Q91X77	**CY250 Cytochrome P450 2C50**	**0.769066071**	**1.9E-15**	**3**
Q91X77	IKEHEESLDVTIPR	0.741990479	3	3.601666
Q91X77	NFLLEK	0.497808922	1	2.107804
Q91X77	YALLLLLK	0.780068264	2	2.820367
Q91X78	**ERLN1 Erlin_1**	**0.95426392**	**0.90377**	**2**
Q91X78	ISEIEDAAFLAR	0.950300903	2	2.785827
Q91X78	SVQTTLQTDEVK	0.997265546	2	3.215433
Q91XE8	**TM205 Transmembrane protein 205**	**0.841831482**	**0.97446**	**2**
Q91XE8	HTFGLVQSK	0.840876149	2	2.48441
Q91XE8	MEKGEDPGSLIK+Oxidation(0)	0.987389649		
Q91XQ0	**DYH8 Dynein heavy chain 8_ axonemal**	**0.871821746**	**0.4592**	**2**
Q91XQ0	FRPEICDMVGNLVSVSR+Oxidation(7)	1.014777627		

Q91XQ0	SMTGIPNLQETLKEKQAR	**0.527301244**	2	2.585173
Q91XR8	**GPX42 Phospholipid hydroperoxide glutathione peroxidase_ nuclear**	**0.903690434**	**0.50624**	**2**
Q91XR8	TDVNYTQLVDLHAR	**0.748766942**	3	3.442171
Q91XR8	YGPMEEPQVIEK	**0.995556101**	2	2.519012
Q91Y81	**SEPT2 Septin_2**	**0.663894869**	**0.00023**	**2**
Q91Y81	ASIPFSVVGSNQLIEAK	**0.807811675**	2	3.384167
Q91Y81	LTVVDTPGYGDAINSR	**0.655081168**	2	4.060359
Q91YE2	**EGLN2 Egl nine homolog 2**	**0.701685872**	**0.02973**	**2**
Q91YE2	ERAAARDK	**0.811012174**	1	2.038808
Q91YE2	YQLASGQK	**0.48250898**	1	1.943258
Q91YP0	**L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial**	**0.9190226**	**0.56532**	**2**
Q91YP0	ISELSGCNPDPQIVPFR	**0.957865559**	2	3.158764
Q91YP0	NAPSPAATSSLAISR	**0.910862269**	2	3.44049
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**0.948390506**	**0.99533**	**9**
Q91YT0	GAGAYICGEETALIESIEGK	**0.769143851**	2	3.312476
Q91YT0	GDARPAEIDSLWEISK	**0.906835629**	2	3.21349
Q91YT0	GEFYNEASNLQVAIR	**1.023726807**	2	3.505469
Q91YT0	KTSFGSLKDEDR	**1.027139789**	2	3.271385
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	**0.989821587**	3	3.825422
Q91YT0	LVEGCLVGGR	**1.056800604**	2	2.59467
Q91YT0	QIEGHTICALGDGAAWPVQGLIR	**0.800782828**	3	3.540077
Q91YT0	TSFGSLKDEDR	**1.124396137**	2	2.614883
Q91YT0	YLVVNADEGEPGTCK	**0.984204215**	2	5.062545
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**0.739963346**	**0.26234**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	**0.869272823**	3	6.880455
Q91Z53	LLDAAGANLR	**0.922252668**	2	3.152913
Q91Z53	NCVILPHIGSATYK	**0.638141073**	2	3.619254
Q91Z53	NTMSLLAANNLLAGLR	**0.794873867**	2	4.523881
Q91Z53	RLPEAIEEVK	**0.764586862**	2	2.459644
Q91Z53	VISTLSVGVDHLALDEIK	**1.028287321**	2	4.234691
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**0.554091116**	**9.9E-20**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	**0.700211892**	3	4.776452
Q91ZJ5	FVQDLSK	**0.489497676**	1	1.990381
Q91ZJ5	GGTLTQYEGK	**0.625624809**	2	2.543858
Q91ZJ5	GLPDNISSVLNK	**0.600815995**	2	3.876582
Q91ZJ5	GTVIIIANHGDR	**0.558670031**	2	3.043601
Q91ZJ5	IDIPPGAVLENK	**0.624248595**	2	3.036104
Q91ZJ5	IQRPPEDSIQPYEK	**0.614258869**	3	4.487566
Q91ZJ5	LNGGLGTSMGCK	**0.665077277**	2	3.127034
Q91ZJ5	LQEQNAIDMEIIVNPK	**1.255186878**	2	2.489109
Q91ZJ5	LVEIAQVPK	**0.622838841**	2	3.35483
Q91ZJ5	NENTFLDLTVQQIEHLNK	**0.534641184**	2	5.244436
Q91ZJ5	SFENSLGINVPR	**0.609005621**	2	3.22864
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	**0.569160431**	3	5.508804
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	**0.784025811**	2	4.605159
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.137347212**	**0.35499**	**7**
Q91ZX7	AVTDEEPFLIFANR	**1.112181391**	2	2.499593
Q91ZX7	CLQGACVVNK	**1.342329263**	2	2.335465
Q91ZX7	GCHVNECLSR	**0.923665401**	2	2.629994
Q91ZX7	IETAAMDGTLR	**1.334430833**	2	2.327921

Q91ZX7	ILQEDFTCR	**0.896040632**	2	2.55975
Q91ZX7	LDGLCIPLR	**1.191452437**	2	2.458098
Q91ZX7	MYDAQQQQVGTNK	**1.110264498**	2	4.3498
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.082948273**	**0.24869**	**3**
Q920A6	DLDTVASDMMVLLK	**0.902892071**	2	3.320173
Q920A6	GLAEVSDIAEQVLNAVNK	**0.815285594**	3	4.870239
Q920A6	NTDGVNFYNILTK	**1.539848402**	2	2.944644
Q920D2	**DYR Dihydrofolate reductase**	**0.910324177**	**0.52965**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	**0.798354237**	2	4.390249
Q920D2	LIEQPELASK	**0.819067141**	2	2.521969
Q920D2	LLPEYPGVLSEIQEEK	**0.993298757**	2	3.67855
Q920D2	NGDLPWPLLR	**0.906656985**	2	3.038924
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.959176821**	**0.99992**	**4**
Q920F5	ADLLEAQALK	**1.062044452**	2	2.312699
Q920F5	EIAEVTGDPVHESLK	**0.979285242**	2	2.971857
Q920F5	ISECEAVHPVK	**0.916396954**	2	3.344306
Q920F5	WLLGLLNVQGK	**1.020435106**	2	3.616333
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**0.928684498**	**9.9E-20**	**19**
Q920L2	ACALSIAESCRPGDK	**0.97726112**	2	3.148103
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	**0.792628424**	3	4.823573
Q920L2	ANAGEESVMNLDK	**0.864108475**	2	4.005419
Q920L2	GEGGILINSQGER	**0.784986076**	2	4.334742
Q920L2	GSDWLGDQDAIHYMTEQAPASVVELENYGMPFSR	**2.768249865**	3	5.011825
Q920L2	GVIALCIEDGSIHR	**0.999419455**	2	3.499012
Q920L2	HTLSYVDTK	**1.251867173**	1	2.257205
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	**0.731084898**	3	6.994025
Q920L2	IDEYDYSKPIEGQQK	**0.613309671**	2	4.544931
Q920L2	KHTLSYVDTK	**1.223585964**	2	2.605049
Q920L2	LGANSLLDLVVFGR	**1.070396636**	2	3.403199
Q920L2	NTIIATGGYGR	**0.872421446**	2	2.80642
Q920L2	TGHSLLHTLYGR	**0.720114821**	2	2.343961
Q920L2	TLNEADCATVPPAIR	**0.815209436**	2	3.617169
Q920L2	TYFSCTSAHTSTGDGTAMVTR	**1.112433706**	3	3.426553
Q920L2	VGSVLQEGCEK	**0.891254917**	2	3.472378
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	**0.716353469**	3	4.009187
Q920L2	VSQLYGDLQHLK	**0.672669578**	3	3.451027
Q920L2	VTLDYRPVIDK	**0.932980394**	2	3.336547
Q920P0	**DCXR L_xylulose reductase**	**0.896187557**	**1.9E-06**	**6**
Q920P0	AVVQVSQIVAR	**0.755668433**	2	2.997207
Q920P0	GVPGAIVNVSSQASQR	**0.830764633**	2	5.490012
Q920P0	SSMTTGSALPVDGGFLAT	**0.902592992**	2	2.871311
Q920P0	STVLALQAAGAQVVAVSR	**1.240266879**	2	4.404534
Q920P0	TREDLDSLVR	**0.751272925**	2	3.042619
Q920P0	VNAVNPTVVMTPMGR	**0.908230797**	2	2.845801
Q921F2	**TADBP TAR DNA_binding protein 43**	**0.904225384**	**2E-07**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	**0.811406979**	2	4.071534
Q921F2	FTEYETQVK	**0.929529977**	2	2.674551
Q921F2	GISVHISNAEPK	**0.970993442**	2	2.664879
Q921F2	TSDLIVLGLPWK	**1.324663995**	2	3.12147
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.042646379**	**0.75468**	**5**
Q922F4	ALTVPELTQQMFDAK	**1.219513242**	2	4.139413
Q922F4	GHYTEGAELVDSVLDVVR	**0.98340527**	2	6.669033
Q922F4	IREEYPDR	**0.873637278**	2	2.96996
Q922F4	MASTFIGNSTAIQELFK	**1.143236011**	2	3.833952

Q922F4	NSSYFVEWIPNNVK	**1.112965891**	2	4.782595
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**0.999356444**	**0.41292**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4)	**0.999664385**		
Q922J3	HEEILQNLQKMLADTEDK	**0.832232906**	2	2.564286
Q923D2		**0.867954541**	**0.27203**	**3**
Q923D2	LQDVTDDHIR	**0.954611261**	2	3.364575
Q923D2	TGLTTLAQAVQAGYEVTVLVR	**0.756153571**	3	4.281244
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	**0.939937245**	3	4.542738
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**0.888417414**	**0.89329**	**2**
Q923J6	FFFLSNDEMLEILSETKDPLR	**0.894645611**	2	2.412905
Q923J6	LEFLTNLDIK	**0.727432135**	1	2.099626
Q923K9	**A1CF APOBEC1 complementation factor**	**0.908652333**	**0.93763**	**2**
Q923K9	LAPQILEEICQK	**1.011096349**	2	2.33733
Q923K9	VTEGVVDVIVYPSAADK	**0.840058499**	2	3.581791
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**0.85994103**	**1.1E-05**	**2**
Q923M1	SAVYPTSAVQMEAALK	**0.710365627**	2	3.812218
Q923M1	VISAEEALPGR	**0.841764852**	2	3.128269
Q923V8	**SEP15 15 kDa selenoprotein**	**0.999962367**	**0.74303**	**3**
Q923V8	GCCQEEAQFETK	**0.902109344**	2	3.891757
Q923V8	LLDDNGNIAEELSILK	**1.108819427**	2	4.218528
Q923V8	WNTDSVEEFLSEK	**0.964768317**	2	2.954593
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**0.92509709**	**0.48478**	**5**
Q924C3	AEYLHTWGGLLPVISK	**0.817581224**	3	3.951748
Q924C3	GQPIWVTANHQEVR	**0.941147141**	2	2.925019
Q924C3	IEPLTFYLDPQWQLALNPSER	**1.216344353**	2	2.427873
Q924C3	SGTYFWPGSDVEIDGILPDIYK	**0.778135061**	2	3.438065
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	**0.840511582**	2	2.754629
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**0.940253049**	**0.7057**	**13**
Q924S5	AGVTCIILPAENR	**0.996446801**	2	2.623525
Q924S5	AQLSATVLTLLIK	**1.356553545**	2	3.864212
Q924S5	AQSVLEEDHYGMEDVK	**1.031267536**	2	4.259191
Q924S5	EHQEALAVER	**0.828917986**	2	2.877724
Q924S5	EVGDELGAKPQLEMVTEATSDTSK	**1.739531586**	3	3.453974
Q924S5	HVMDVVDEELSK	**0.791900628**	2	3.212523
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	**1.041698399**	3	6.188807
Q924S5	MEMINVSGYVAQEK	**1.169817873**	2	2.543144
Q924S5	NYLDWLTSIPWGR	**0.742768633**	2	2.883768
Q924S5	QLEVEPEGLEPEAENK	**0.919190716**	2	4.258727
Q924S5	QSDENLDLAR	**0.712226617**	2	2.818621
Q924S5	TENPLVLIDEVDK	**0.875894465**	2	2.778177
Q924S5	VLEFIAVSQLR	**0.906221368**	2	3.088209
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**0.954806791**	**0.35808**	**2**
Q924W5	ELDMKEKELQEK+Oxidation(3)	**1.04809778**		
Q924W5	TKEQINQGEERLTELK	**0.765199708**	2	2.455998
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**0.985589223**	**5.3E-07**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	**1.239113234**	2	2.95541
Q99020	FGEVVDCTIK	**0.658706046**	2	2.761502
Q99020	IFVGGLNPEATEEK	**1.301583187**	2	4.035909
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**0.988668818**	**0.15052**	**3**
Q99068	EELKHFEAKIEK	**1.030838124**	2	2.427901

Q99068	HLQDLSSR	**0.798917681**	2	2.337855
Q99068	HVESIGDPEHISR	**1.914411385**	3	3.373267
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**0.838195913**	**0.08949**	**4**
Q99JI4	GAEILEVLHSLPAVR	**1.073939219**	2	2.35956
Q99JI4	LDEELEDAEK	**1.147875506**	2	2.397714
Q99JI4	RLDEELEDAEK	**1.036214085**	2	2.910735
Q99JI4	VNEIVETNRPDSK	**1.295588134**	2	3.589453
Q99KN9	**EPN4 Clathrin interactor 1**	**1.016926222**	**0.92811**	**2**
Q99KN9	GEFKDEEETVTTK	**1.101027356**	2	3.05005
Q99KN9	HIHITQATETTTTR	**0.993581183**	3	3.387228
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.860485652**	**0.92942**	**2**
Q99L04	ATAQEAQSLGGR	**0.828150903**	2	3.64541
Q99L04	CVPVVCDSSQESEVK	**0.904240537**	2	3.399817
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.005743545**	**0.80613**	**4**
Q99LF4	GLGHQVATDALVAMEK	**0.650332992**	2	3.972651
Q99LF4	NVTDVVNTCHDAGISK	**1.095857447**	2	4.468873
Q99LF4	NYNDELQFLDK	**1.069706324**	2	2.920885
Q99LF4	TNLDESDVQPVK	**0.92793654**	2	3.316954
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.163763482**	**0.29598**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11)	**1.163763482**		
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5)	**1.163763482**		
Q99ML5	**PCYOX Prenylcysteine oxidase**	**0.979848725**	**0.76084**	**3**
Q99ML5	ELGLSSVPASGGLVGVYNGK	**0.776965033**	2	2.518651
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	**1.01069789**	3	4.483006
Q99ML5	YQSHDYAFSSVEK	**0.975082685**	2	2.882505
Q99MS0	**S14L2 SEC14_like protein 2**	**0.881312374**	**0.99533**	**5**
Q99MS0	AGEMTEVLPNQR	**0.833783219**	2	2.975658
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	**0.939541212**	2	3.191858
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	**0.842928679**	3	4.807725
Q99MS0	INYGGDIPK	**0.95738793**	2	2.504065
Q99MS0	QQYEHSVQISR	**1.075283984**	2	2.478615
Q99MW1	**STK31 Serine/threonine_protein kinase 31**	**1.089929799**	**0.37791**	**2**
Q99MW1	EVLLENYKALELK	**0.572850067**	2	2.304487
Q99MW1	QDQKLIEENEK	**1.242382408**	2	2.588887
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.894586203**	**0.32148**	**7**
Q99MZ8	GFSVVADTPELQR	**0.897638422**	2	3.381973
Q99MZ8	MGPSGGEGIEPER	**0.933016381**	2	3.194432
Q99MZ8	QQSELQSQVR	**0.928619795**	2	2.431894
Q99MZ8	QSFTMVADTPENLR	**0.881289729**	2	3.302576
Q99MZ8	TQDQISNIK	**1.144311725**	2	2.659462
Q99MZ8	YHEEFEK	**0.770626469**	1	2.215444
Q99MZ8	YKEEFEK	**0.600474497**	1	2.325076
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**1.308409568**	**0.67493**	**2**
Q99NA5	IEAACFATIK	**1.322383335**	2	2.315682
Q99NA5	NVTAIQGPGGK	**1.014952918**	2	2.437847
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**0.934038671**	**0.99767**	**3**
Q99NB7	GSISNTNVEALK	**1.046900298**	2	2.856956
Q99NB7	KGSISNTNVEALK	**0.781965101**	2	3.169024
Q99NB7	VHLKPVLLQTEQEQVEHR	**1.036133565**	3	3.845462
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**0.902118432**	**0.30456**	**8**
Q99PF5	AINQQTGAFVEISR	**0.911646792**	2	3.685945
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	**0.803635591**	2	6.111699
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	**0.921921051**	2	4.655235
Q99PF5	IGQQPQQPGAPPQQDYTK	**1.010913686**	2	3.685757

Q99PF5	IINDLLQSLR	0.83894379	2	2.696557
Q99PF5	SVSLTGAPESVQK	0.852372187	2	3.309307
Q99PF5	VGGGIDVPVPR	0.821605732	2	2.879406
Q99PF5	VQISPDSGGLPER	1.032821325	2	2.566416
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.190836408**	**0.00013**	**21**
Q99PL5	DALNQATSQVESK	1.387906647	2	3.758504
Q99PL5	EAEETQNSLQAECDQYR	1.342775524	2	5.467913
Q99PL5	EEITQLK	0.42500871	1	1.977029
Q99PL5	EHTSHLEAELEK	1.245567961	2	3.317014
Q99PL5	EQEIAAVQAR	1.375529629	2	2.379784
Q99PL5	ETSYEEALANQR	1.723171702	2	2.740476
Q99PL5	GELESSDQVR	1.3473972	2	3.153927
Q99PL5	HLEDIVEK	1.157875948	2	2.544025
Q99PL5	HMAAASAECQNYAK	0.713585538	2	4.461192
Q99PL5	HMAAASAECQNYAK+Oxidation(1)	1.826742176		
Q99PL5	IQEELEK	0.953402333	1	2.14268
Q99PL5	LKELESQVSCLEK	0.89392198	2	4.059691
Q99PL5	LLATEQEDAAVAK	1.148009451	2	4.539742
Q99PL5	LQQENSILR	1.002429747	2	2.829821
Q99PL5	LQSSEVEVK	0.949828225	2	2.524143
Q99PL5	LREAEETQNSLQAECDQYR	0.905218087	3	5.125143
Q99PL5	QLHLAEAQTK	1.185866259	2	2.327596
Q99PL5	TILAETEGMLK	1.009695326	2	3.038155
Q99PL5	TLQEQLENGPNTQLAR	0.865227474	2	4.824466
Q99PL5	TLVSTVGSMVFSEGEAQR	1.222738869	3	4.837025
Q99PL5	VEPAVSSIVNSIQVLASK	1.148240238	2	4.981925
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**0.7015674**	**1E-05**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.7015674		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.7015674		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**0.941704473**	**0.99081**	**2**
Q9CPQ1	FGVAEPR	0.953675164	2	2.345819
Q9CPQ1	NYDSMKDFEEMR	0.706129924	2	3.545067
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**1.213717121**	**0.76202**	**2**
Q9CQS8	FYTEDSPGLK	1.202628816	2	2.331386
Q9CQS8	TTSAGTGGMWR	0.905772361	2	2.3868
Q9CRB8	**MTFP1 Mitochondrial fission process protein 1**	**0.995391373**	**0.75792**	**2**
Q9CRB8	SVDFLLDSSLR	0.894899394	2	2.799437
Q9CRB8	YLGYANEVGEAFR	1.064941936	2	2.718529
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.236844178**	**0.00255**	**2**
Q9CRB9	VAEELALEQAK	1.251070732	2	3.572165
Q9CRB9	YEYHPVCADLQTK	0.990775723	2	3.661733
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.750620794**	**9.9E-05**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	0.867708082	2	4.14524
Q9CW42	GLSVSEAECTAMGLR	0.718647965	2	3.313146
Q9CW42	LQQVGTVAQLWIYPIK	0.745080332	2	2.945435
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.084744807**	**0.00937**	**3**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.285669237	2	4.488051
Q9CWH6	ALLEVVQSGGK	0.959482096	2	3.431706
Q9CWH6	LTVEDPVTVEYITR	1.191508048	2	3.902525
Q9CWK8	**SNX2 Sorting nexin_2**	**0.954980206**	**0.37535**	**4**
Q9CWK8	AVNTQALSGAGILR	0.873196846	2	3.189193
Q9CWK8	QQQFENLDQQLR	0.843077675	2	2.818141
Q9CWK8	WEDAQITLLK	0.968949267	2	2.788138
Q9CWK8	YWEAFLPEAK	1.209972567	2	2.53179

Q9CXS4	**CENPV Centromere protein V**	**0.939126497**	**0.77733**	**2**
Q9CXS4	LLLDTFEYQGLVK	**0.94001446**	2	3.939583
Q9CXS4	SVVTEEFNGSDWER	**0.918094561**	2	3.769433
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**1.032763075**	**0.99999**	**2**
Q9CYN2	LHDSLATER	**1.047163197**	2	2.419529
Q9CYN2	YVENFGLIDGR	**1.02000853**	2	2.736593
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.979881131**	**0.01385**	**2**
Q9CYW4	LEDILTGLGLR	**0.624497051**	2	4.23748
Q9CYW4	RLEDILTGLGLR	**2.587974235**	2	3.281152
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.042634904**	**0.7559**	**2**
Q9CZY3	LLEELEEGQK	**1.008967427**	2	2.749477
Q9CZY3	VNMSGVSSSNGVVDPR	**1.246065282**	2	2.61564
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.036207609**	**1.8E-05**	**4**
Q9D0M3	GLLSSLDHTSIR	**0.917659372**	2	3.196044
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	**1.476889986**	3	5.915704
Q9D0M3	HLVGVCYTEEEAK	**1.036324717**	2	3.734705
Q9D0M3	LSDYFPKPYPNPEAAR	**1.050961067**	3	3.633964
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.161817198**	**0.00033**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	**0.964782824**	2	2.823217
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	**0.953506545**	2	5.156553
Q9D0S9	SLPADILYEDQQCLVFR	**0.79270308**	2	3.498697
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**0.91799459**	**0.9989**	**4**
Q9D172	GVEVTVGHEQEEGGK	**0.986643126**	2	3.801411
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	**0.867415507**	2	4.62831
Q9D172	NLSTFAVDGK	**1.006870574**	1	2.622995
Q9D172	NVLAESAR	**0.928858416**	1	1.930207
Q9D180	**WDR65 WD repeat_containing protein 65**	**0.878767039**	**0.50276**	**2**
Q9D180	KNQELEK	**0.953402333**	1	2.122219
Q9D180	QIEPRENEIK	**0.618439668**	1	1.982005
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**0.894078886**	**9.9E-20**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0)	**3.444410806**		
Q9D1Q6	NIIGYFEQK	**0.808248018**	1	2.084002
Q9D1Q6	SNPVHEIQSLDEVTNLDR	**0.849594063**	2	5.255363
Q9D1Q6	VDCDQHSDIAQR	**1.023978937**	2	3.631815
Q9D2U9	**H2B3A Histone H2B type 3_A**	**0.996472926**	**0.11078**	**6**
Q9D2U9	AMGIMNSFVNDIFER	**0.854858576**	2	4.8175
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	**0.921303513**		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	**0.997937874**		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4)	**0.987918196**		
Q9D2U9	LLLPGELAK	**0.961037882**	2	2.640281
Q9D2U9	QVHPDTGISSK	**0.981600243**	2	2.37401
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.498283063**	**0.26529**	**3**
Q9D6M3	GAAVNLTLVTPEK	**1.267351623**	2	3.113856
Q9D6M3	GVNEDTYSGFLDCAR	**1.368599987**	2	4.846322
Q9D6M3	NHGIAGLYK	**1.746869268**	1	2.047149
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.031936422**	**0.96974**	**10**
Q9D6Y9	CSDGGIYCK	**0.902504183**	1	2.085543
Q9D6Y9	CVAYAESHDQALVGDK	**0.919577908**	2	5.011642
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	**1.440515016**	3	3.409191
Q9D6Y9	GTHDLWDSR	**0.630286752**	2	2.563571
Q9D6Y9	GYESFGIHR	**0.972600575**	2	2.45794
Q9D6Y9	IVLDSDAAEYGGHQR	**0.764312912**	2	4.534115

Q9D6Y9	IYESHVGISSHEGK	**1.065300634**	2	4.405342
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	**1.051761603**	3	3.363416
Q9D6Y9	QFNLTDDDLLR	**0.772308514**	2	2.494174
Q9D6Y9	RQFNLTDDDLLR	**1.038848002**	2	2.590854
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**0.989215623**	**0.05756**	**3**
Q9D7B6	AVIFEDCAVPVANR	**0.976392875**	2	4.067587
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	**0.868523479**	2	4.376923
Q9D7B6	VHQILEGSNEVMR	**1.544323653**	2	2.589013
Q9D7S7	**RL22L 60S ribosomal protein L22_like 1**	**2.023477947**	**0.0002**	**2**
Q9D7S7	FHLDLTHPVEDGIFDSGNFEQFLR	**1.692580641**	3	3.788766
Q9D7S7	TGNLGNVVHIER	**4.054903688**	2	2.476783
Q9D7W5	**MED8 Mediator of RNA polymerase II transcription subunit 8**	**1.541197038**	**0.0182**	**2**
Q9D7W5	NQVIIPLVLSPDRDEDLMR+Oxidation(17)	**1.263982968**		
Q9D7W5	QIQSLNKMCSNLLEK+Oxidation(7)	**1.816165798**		
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**0.954839318**	**0.0003**	**2**
Q9D7X8	ISDEMEDIIK	**0.757896515**	2	2.959699
Q9D7X8	SNISSLDEQEGVK	**1.003299221**	2	3.056067
Q9D819	**IPYR Inorganic pyrophosphatase**	**0.855166916**	**0.76688**	**5**
Q9D819	GISCMNTTVSESPFK	**0.838559102**	2	4.502737
Q9D819	GQYISPFHDVPIYADK	**1.347731434**	2	3.77724
Q9D819	VLGILAMIDEGETDWK	**1.000040222**	2	4.000464
Q9D819	YKVPDGKPENEFAFNAEFK	**1.064169513**	2	3.641628
Q9D819	YVANLFPYK	**1.076287183**	1	1.93985
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**0.673022996**	**0.83597**	**2**
Q9D880	TIALNQVEDVR	**0.655778928**	2	2.934498
Q9D880	TVLEHYALEDDPLEAFK	**1.016672793**	2	5.039001
Q9DBA8	**HUTI Probable imidazolonepropionase**	**0.805945647**	**0.199**	**4**
Q9DBA8	AGTTLVECK	**0.810406443**	2	2.600883
Q9DBA8	GVFDLDTTR	**0.920279865**	2	2.303739
Q9DBA8	QGDAIIINASR	**0.732415246**	2	2.671376
Q9DBA8	SGYGLNLETELK	**0.797501033**	2	2.36286
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.032969092**	**0.11834**	**3**
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	**1.514789641**	3	4.624665
Q9DBH5	TPEEESIDWTK	**0.951762283**	2	2.42645
Q9DBH5	WSELAGCTADFR	**1.012920451**	2	3.172407
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**0.813087424**	**0.61444**	**2**
Q9DC70	LDDLINWAR	**0.72681036**	2	2.990906
Q9DC70	QADVMIVAGTLTNK	**1.009610196**	2	3.313989
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**1.170798116**	**0.27945**	**2**
Q9DCH4	IQDALSTVLQYAEDVLSGK	**1.100783767**		
Q9DCH4	VIGLSSDLQQVGGASAR	**1.161059326**		
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**0.947941126**	**0.83501**	**2**
Q9DCM0	SLLPGCQSVISR	**0.884514933**	2	3.202382
Q9DCM0	TDFQQGCAK	**1.087278135**	2	2.363618
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**0.939226744**	**0.11165**	**2**
Q9DCS9	AYDLVVDWPVTLVR	**0.925024376**	2	4.678904
Q9DCS9	TPAPSPQTSLPNPITYLTK	**1.430398735**	2	3.350693
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**0.942503208**	**0.00011**	**5**
Q9DCT2	FDLNSPWEAFPAYR	**0.941838024**	2	2.781314

Q9DCT2	ILTDYGFEGHPFR	**0.693742244**	2	2.639343
Q9DCT2	KFDLNSPWEAFPAYR	**0.840104208**	2	3.633706
Q9DCT2	SLADLTAVDVPTR	**0.911269713**	2	3.562822
Q9DCT2	VVAEPVELAQEFR	**0.402795034**	2	3.311777
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**0.870471558**	**1.1E-05**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	**0.802170689**	2	5.19591
Q9DCU9	LIEPNTAVTR	**0.870935788**	2	3.306714
Q9DCU9	TMDWFGYYGGPCR	**1.141911215**	2	3.402372
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.505898193**	**0.21864**	**2**
Q9EP75	DEDGKELSDEDIR	**2.626126939**	2	2.713569
Q9EP75	IFNDSTNIMHAK	**1.504660998**	2	3.303768
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**0.633898668**	**8.3E-05**	**10**
Q9EP89	FENSIESLR	**0.823802841**	2	2.828457
Q9EP89	GIIVSIICNMQSVGLNSTALK	**0.746393355**	3	3.732419
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	**0.81064508**	3	4.018808
Q9EP89	IKDEVGAPGIVVGVSVDGK	**0.578728835**	2	5.023402
Q9EP89	KNDFEQGELYLK	**0.968494258**	2	3.799617
Q9EP89	LDLDLPVQHYVPEFPEK	**0.786436655**	2	3.133782
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	**1.082381437**	3	3.666809
Q9EP89	LVNTPYVDNSYK	**1.366409482**	2	3.22032
Q9EP89	NDFEQGELYLK	**1.201147171**	2	2.911693
Q9EP89	WAGGGFLSTVGDLLK	**0.940811818**	2	4.316546
Q9EPH2	**MRP MARCKS_related protein**	**0.809676709**	**0.41247**	**2**
Q9EPH2	AAATPESQEPQAK	**1.150156899**	2	2.77378
Q9EPH2	GDVTAEEAAGASPAK	**0.786406697**	2	3.416121
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.14742428**	**0.00201**	**13**
Q9EPH8	ALDTMNFDVIK	**1.226022756**	2	3.303414
Q9EPH8	ALYDTFSAFGNILSCK	**1.916612315**	2	2.595096
Q9EPH8	FSPAGPILSIR	**0.745435604**	2	2.315148
Q9EPH8	GFGFVCFSSPEEATK	**17.00060762**	2	4.003506
Q9EPH8	GFGFVSFER	**1.06428449**	2	2.784455
Q9EPH8	GYGFVHFETQEAAER	**1.507418604**	2	3.121152
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	**1.153989738**	3	3.652498
Q9EPH8	KEFSPFGTITSAK	**0.978013413**	2	2.878023
Q9EPH8	NLDDGIDDER	**0.82249807**	2	2.848306
Q9EPH8	SGVGNIFIK	**1.318771727**	2	2.757515
Q9EPH8	SKVDEAVAVLQAHQAK	**1.111213858**	2	5.239744
Q9EPH8	SLGYAYVNFQQPADAER	**1.259295676**	2	3.651202
Q9EPH8	VDEAVAVLQAHQAK	**1.389377949**	2	3.149306
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.900361647**	**9.9E-20**	**12**
Q9EQ76	ASIYQSVFTNSSK	**1.090633007**	2	3.178519
Q9EQ76	GTCILPSVNDMMDDIDEK	**1.455622135**	2	3.594205
Q9EQ76	ILCGTVSIKPNVK	**0.962518503**	2	2.995908
Q9EQ76	KEPVFNDELPAR	**1.091862725**	2	3.221512
Q9EQ76	LQEYITSFATEK	**3.02202122**	2	4.073552
Q9EQ76	NNEVTLYK	**3.223010145**	2	2.452675
Q9EQ76	NNLPTAISDWWYMK	**1.811154482**	2	2.910594
Q9EQ76	SCLEEGLEPTCFER	**1.448249438**	2	4.589561
Q9EQ76	SDDVGGLWK	**2.031804195**	2	2.771746
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	**1.723878694**	3	5.19264
Q9EQ76	VWNDGYPWDMVVITR	**1.264652657**	2	4.133258
Q9EQ76	YIQFETLVTR	**2.485982938**	2	3.305302
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**0.952630089**	**0.9084**	**6**

Q9EQH3	ACAELHQNVNVK	**1.036659836**	2	3.704721
Q9EQH3	IREDLPNLESSEETEQINK	**1.108164098**	3	3.848196
Q9EQH3	LNLEHIATSSAVSK	**0.791888984**	2	3.521428
Q9EQH3	LSQLEGVNVER	**1.0473152**	2	2.980165
Q9EQH3	NIIIALIDR	**0.805739812**	2	2.318205
Q9EQH3	VLETTVEIFNK	**0.933995599**	2	2.707417
Q9EQH7	**NDST3 Bifunctional heparan sulfate N_deacetylase/N_sulfotransferase 3**	**0.807877629**	**0.34389**	**2**
Q9EQH7	KFALEHGIPTDMGYAVSPHHSGVYPVHVQLYEAWKK	**0.648816833**	3	3.349104
Q9EQH7	TTPATVMDEVQK+Oxidation(6)	**0.893676541**		
Q9EQN5	**SMBP2 DNA_binding protein SMUBP_2**	**0.703814232**	**0.228**	**2**
Q9EQN5	CPTTSVRKPASAQESRQEAR	**0.66440897**	2	2.363061
Q9EQN5	KPSEKPLGSQVQPQHSSK	**0.709832321**	2	2.349717
Q9EQS0	**TALDO Transaldolase**	**0.832398183**	**0.39091**	**7**
Q9EQS0	ALAGCDFLTISPK	**0.835541913**	2	3.480733
Q9EQS0	EAGISKDRILIK	**0.822371864**	2	2.348685
Q9EQS0	ILDWHVANTDKK	**0.93117284**	2	3.206593
Q9EQS0	LGGPQEEQIK	**1.07972477**	2	3.0213
Q9EQS0	LSSTWEGIQAGK	**1.113618255**	2	2.837765
Q9EQS0	SYEPQEDPGVK	**0.890084494**	2	2.893496
Q9EQS0	WLHNEDQMAVEK	**0.88481983**	3	3.321831
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.062273652**	**0.09687**	**3**
Q9EQX9	LELFLPEEYPMAAPK	**0.953608671**	2	3.44018
Q9EQX9	SNEAQAIETAR	**1.099564715**	2	3.656157
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	**1.322033489**	3	4.342836
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.034768606**	**0.00354**	**23**
Q9ER34	ADIANLAEEFK	**1.237013487**	2	3.482643
Q9ER34	CTTDHISAAGPWLK	**1.062050718**	2	4.316233
Q9ER34	DINQEVYNFLATAGAK	**0.872095915**	2	4.141652
Q9ER34	DLEDLQILIK	**1.712410368**	2	2.503135
Q9ER34	FKLEAPDADELPR	**1.022918082**	3	4.274623
Q9ER34	FNPETDFLTGK	**0.948700278**	1	2.424444
Q9ER34	GHLDNISNNLLIGAINIENGK	**0.903509826**	2	5.606589
Q9ER34	IVYGHLDDPANQEIER	**1.815268711**	2	4.952315
Q9ER34	LEAPDADELPR	**1.359136675**	2	2.591181
Q9ER34	LNRPLTLSEK	**1.257299008**	2	2.44747
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	**1.01543831**	3	3.680157
Q9ER34	LTGTLSGWTSPK	**1.132720618**	2	2.58896
Q9ER34	NAVTQEFGPVPDTAR	**1.015529104**	2	4.557825
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	**1.1041568**	3	4.41255
Q9ER34	NTIVTSYNR	**1.252577238**	2	2.376795
Q9ER34	QGLLPLTFADPSDYNK	**1.09626401**	2	3.443295
Q9ER34	SDFDPGQDTYQHPPK	**1.094858309**	2	2.455174
Q9ER34	SQFTITPGSEQIR	**0.943511891**	2	3.452129
Q9ER34	VAMQDATAQMAMLQFISSGLPK	**1.097493451**	2	2.373071
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	**1.461961672**	2	4.916017
Q9ER34	VDVSPTSQR	**1.058101053**	2	2.40706
Q9ER34	VGLIGSCTNSSYEDMGR	**0.966856928**	2	4.367917
Q9ER34	WVVIGDENYGEGSSR	**0.977203196**	2	4.51262
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.924395615**	**0.99857**	**3**
Q9ES21	LEEQDEFEK	**0.94058185**	2	2.818766
Q9ES21	TNVIQSLLAR	**1.099461572**	2	2.339262
Q9ES21	TQLGLVMDGFNSLLR	**0.955729964**	2	3.780588
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.069159993**	**0.95346**	**13**
Q9ES38	ACQAAWALK	**1.077118897**	2	2.536236
Q9ES38	ADVWENFQQR	**1.041683438**	2	3.01327
Q9ES38	EGFDVGVIADPLYILDNK	**1.125812365**	2	5.338932

Q9ES38	GATAILVLPSK	**1.053979722**	2	2.68855
Q9ES38	IQDSLEITNTYK	**1.190995025**	2	3.73132
Q9ES38	LKEATIQEDK	**1.236654825**	2	2.607008
Q9ES38	LLAENIR	**1.070339557**	2	2.398221
Q9ES38	MLTPLELVQFDIETAEPVRDK	**0.897926012**	2	4.282512
Q9ES38	QGFCIPVETGKPGLLLTK	**0.884272966**	3	3.666495
Q9ES38	SISALSVFLGLAK	**0.393329518**	2	3.4069
Q9ES38	SLMPDVYQAVCEGTWK	**1.361962221**	2	3.956059
Q9ES38	YLCNVPGQPEDK	**1.202772699**	2	3.328959
Q9ES38	YLCNVPGQPEDKK	**0.895273034**	2	2.494618
Q9ES53	**UFD1 Ubiquitin fusion degradation protein 1 homolog**	**0.878745983**	**0.23884**	**2**
Q9ES53	FQPQSPDFLDITNPK	**0.868017154**	2	2.49985
Q9ES53	FVAFSGEGQSLRKK	**0.680862317**	2	2.583275
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.920002984**	**0.20512**	**2**
Q9EST6	SLDLFGCEVTNR	**0.910606007**	2	3.098548
Q9EST6	TPAAVQELVLDNCK	**1.099645218**	2	3.456145
Q9ESV1	**LUZP1 Leucine zipper protein 1**	**0.847696125**	**0.13587**	**2**
Q9ESV1	EKLEEEENLTR	**0.904994491**	2	2.87248
Q9ESV1	RMADLEKLEEALSR	**0.719832495**	2	2.531142
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.155876246**	**0.95601**	**4**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	**1.159045918**	3	6.021239
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	**1.14568511**	3	3.961372
Q9ESW0	QGQGQLVTCSGAFK	**0.970427705**	2	2.899868
Q9ESW0	VTLGTQPTVLR	**0.903337829**	2	2.633499
Q9HB97	**PARVA Alpha_parvin**	**0.962591061**	**0.95074**	**2**
Q9HB97	DLAEDLYDGQVLQK	**1.197424471**	2	3.101923
Q9HB97	LNVAEVTQSEIAQK	**0.932085885**	2	4.336986
Q9JHL4	**DBNL Drebrin_like protein**	**0.898330499**	**0.00014**	**4**
Q9JHL4	AMSTTSVSSSQPGK	**0.646406421**	2	2.585805
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3)	**0.249775579**		
Q9JHL4	TGELEQEVVSR	**1.060753536**	2	3.341404
Q9JHL4	VAGTGEGGLEELVEELNSGK	**0.737434643**	2	2.865452
Q9JI85	**NUCB2 Nucleobindin_2**	**1.083538706**	**0.45897**	**4**
Q9JI85	FQQGIAPSGPAGELK	**1.437682197**	2	2.733264
Q9JI85	QEYQQAVQQLEQK	**1.0871034**	2	4.3223
Q9JI85	QVIEVLETDPHFR	**0.911143878**	2	2.669342
Q9JI85	VHNVEPVESAR	**1.062990642**	2	2.918343
Q9JI91	**ACTN2 Alpha_actinin_2**	**1.241148396**	**0.82844**	**11**
Q9JI91	DQSLQEELAR	**1.051486384**	2	2.612214
Q9JI91	ETADTDTAEQVIASFR	**0.722956248**	2	3.933638
Q9JI91	GYEEWLLNEIR	**1.282367868**	3	3.371127
Q9JI91	HRPDLIDYSK	**0.753735162**	2	2.394802
Q9JI91	HTNYTMEHIR	**1.787058401**	3	3.40227
Q9JI91	HTNYTMEHIR+Oxidation(5)	**1.460473261**		
Q9JI91	KHEAFESDLAAHQDR	**0.889584653**	2	5.367726
Q9JI91	LEGDHQLIQEGLVFDNK	**0.862590149**	3	4.948175
Q9JI91	MLDAEDIVNTPKPDER	**0.739323375**	2	3.889498
Q9JI91	QSILAIQNEVEK	**1.063375637**	2	2.971831
Q9JI91	TINEVETQILTR	**1.095895157**	2	2.530003
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.079965042**	**0.52392**	**7**
Q9JJ19	AVDPDSPAEASGLR	**1.335247811**	2	3.683422
Q9JJ19	IVEVNGVCMEGK	**1.034666835**	2	3.225758
Q9JJ19	LLVVDPETDEQLKK	**1.082580315**	2	2.474663
Q9JJ19	LVEPGSPAEK	**1.152827656**	2	2.526153

Q9JJ19	LVEVNGENVEK	**2.236656791**	2	2.793793
Q9JJ19	SEHTEPPAAADTK	**0.691613033**	2	3.033579
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	**1.069366832**	3	3.674628
Q9JJ22	**ERAP1 Endoplasmic reticulum aminopeptidase 1**	**1.002990725**	**0.83922**	**2**
Q9JJ22	ASLINNAFQLVSIGK	**1.051793221**	2	2.522066
Q9JJ22	TQEFPHILTLIGR	**0.884522547**	2	2.578067
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**1.136250939**	**0.97039**	**3**
Q9JJ40	GVFLTDITPQGVAMK	**1.008186198**	2	2.415186
Q9JJ40	NGGDQTTLLVLDK	**1.000875638**	2	2.454234
Q9JJ40	SGNSVTLLVLDGDSYEK	**1.168141373**	2	4.384834
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.032833089**	**0.02582**	**3**
Q9JJ46	HLTNAQSMLDNK	**0.739088909**	2	3.52705
Q9JJ46	HLTNAQSMLDNK+Oxidation(7)	**1.030765173**		
Q9JJ46	VSVVPLGTGR	**0.871810111**	2	2.52231
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.063889363**	**0.63839**	**3**
Q9JJ54	FGDVVDCTLK	**0.873373304**	2	2.987431
Q9JJ54	IFVGGLSPDTPEEK	**1.005656922**	2	4.201118
Q9JJ54	IFVGGLSPDTPEEKIR	**1.329535434**	2	2.507551
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.080302006**	**0.41664**	**5**
Q9JJ79	ASDLKDLNSR	**1.082302045**	2	2.321454
Q9JJ79	ELMLERETLLAR+Oxidation(2)	**1.541952446**		
Q9JJ79	NCLEEWTKAAGLEK	**0.82001682**	2	2.420096
Q9JJ79	TVLRGSGNLLR	**1.175169532**	2	2.436831
Q9JJ79	YVVQIGDK	**0.885455782**	1	2.072972
Q9JJM9	**SEPT5 Septin_5**	**0.969133217**	**0.94876**	**2**
Q9JJM9	LIRMKDEELR	**0.961700093**	2	2.47511
Q9JJM9	MQEMLQKMK+Oxidation(3)	**1.166539143**		
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**0.96978918**	**0.99939**	**2**
Q9JJU8	GDYDAFFEAR	**0.760344767**	2	2.486322
Q9JJU8	QQDVLCFLEANK	**1.00008017**	2	3.280272
Q9JK11	**RTN4 Reticulon_4**	**1.089034236**	**0.23084**	**2**
Q9JK11	VDRKCLEDSLEQK	**1.089223031**	2	2.346146
Q9JK11	YSNSALGHVNSTIK	**0.562622052**	2	2.698704
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.23448971**	**0.99398**	**3**
Q9JK38	ITLECLPQNVGFYK	**1.159871007**	2	3.030867
Q9JK38	VEDVVVSDECR	**0.977922572**	2	3.536087
Q9JK38	VLGQLTETGVVSPEQFMK	**0.98167779**	2	4.170403
Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**1.02540329**	**0.89157**	**2**
Q9JK72	GDLGNVHAEASGR	**1.102012724**	2	2.770985
Q9JK72	SLVVDEGEDDLGR	**1.020877406**	2	2.304827
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**0.728706745**	**0.72703**	**2**
Q9JKS4	GAPAYNPTGPQVTPLAR	**0.982140367**	2	3.930653
Q9JKS4	TQSKPEDEADEWAR	**0.540669683**	2	3.546019
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**0.860915606**	**0.92977**	**12**
Q9JLA3	AIWAALQTQTSNSAK	**1.984490251**	2	3.624517
Q9JLA3	FLFVDADQIVR	**1.073529071**	2	2.90383
Q9JLA3	FLSPLQQNLLK	**0.951511141**	2	2.385851
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	**0.952029766**	3	6.338928
Q9JLA3	IEYQFFEDK	**1.147211161**	2	2.520868
Q9JLA3	IVPEWQDYDQEIK	**0.839020863**	2	3.289206

Q9JLA3	LNIQPSETDYAVDIR	**0.962716043**	2	3.947537
Q9JLA3	TAAIANSMNYLTK	**0.951080582**	2	2.553551
Q9JLA3	VDALLSAQPK	**0.929868118**	2	3.003724
Q9JLA3	VEEDVASDLVMK	**0.686931965**	2	3.505897
Q9JLA3	VWQLQDLSFQTAAR	**0.980708697**	2	4.416657
Q9JLA3	YVLEPEISFTADNSFAK	**1.159566858**	2	3.714201
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**0.734719446**	**0.28328**	**3**
Q9JLH7	GSDALTLLEYPETR	**0.822689934**	2	2.47365
Q9JLH7	KEEEGQAGAAEMR+Oxidation(11)	**0.840314393**		
Q9JLH7	QYGITGDNVRRELLALVK	**0.795745157**	2	2.372433
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.00363224**	**0.65185**	**19**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	**0.897988643**	2	4.330059
Q9JLJ3	ANDTTFGLAAGVFTR	**1.093942279**	2	4.617095
Q9JLJ3	CQVLLEAAR	**1.019004041**	2	3.51146
Q9JLJ3	EQGATVLCGGEPYAPEDPK	**1.025923659**	2	4.632158
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	**0.956725584**	3	3.355614
Q9JLJ3	EVNLAVENAK	**1.184950662**	1	2.949497
Q9JLJ3	GALLANFLTQGQVCCNGTR	**1.06958716**	2	5.380242
Q9JLJ3	GIKPITLELGGK	**1.068876595**	3	3.972119
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	**0.958928209**	3	3.605326
Q9JLJ3	IGDPLLEDTR	**0.955038731**	2	4.013814
Q9JLJ3	MGPLINAPHLER	**1.073738445**	2	3.122439
Q9JLJ3	MGPLINAPHLER+Oxidation(0)	**1.072319993**		
Q9JLJ3	RDEIAIMETINNGK	**1.064301671**	2	5.36157
Q9JLJ3	SAPALACGNAMIFKPSPFTPVSALLLAEIYTK	**0.9337961**	3	3.459284
Q9JLJ3	SPLIIFSDCNMK	**1.235452855**	2	2.554181
Q9JLJ3	VEPVDASGTEK	**0.798364277**	1	2.24513
Q9JLJ3	VSFTGSVPTGMK	**1.007759983**	2	3.574542
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10)	**1.099593171**		
Q9JLJ3	VTIEYYSQLK	**2.593396642**	2	3.126212
Q9JLQ0	**CD2AP CD2_associated protein**	**0.800970657**	**0.14363**	**2**
Q9JLQ0	LQEEGWLEGELNGR	**0.874680361**	2	2.338794
Q9JLQ0	SNLEVEIAK	**0.646385144**	1	1.90647
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**1.075667117**	**0.15898**	**3**
Q9JLR1	GTLMELGISPIVTSGLIMQLLAGAK	**0.884567445**		
Q9JLR1	IIEVGDTPK	**0.843077062**	2	2.440527
Q9JLR1	TWIEVSGSSAK	**1.284387433**	2	2.667454
Q9JLT0	**MYH10 Myosin_10**	**0.975672814**	**0.476**	**2**
Q9JLT0	AGVLAHLEEER	**1.085525679**	2	3.572839
Q9JLT0	KFDQLLAEEKGISAR	**0.685637913**	2	2.409313
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**0.795640529**	**0.63471**	**2**
Q9JLZ1	ELEASEELDTICPK	**0.789903211**	2	3.107807
Q9JLZ1	LEAEAVPEVSEK	**0.828915239**	2	2.494289
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.812440312**	**1.7E-06**	**4**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	**0.752446364**	2	5.713046
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	**0.735081155**	3	4.365326
Q9JLZ3	GIVVLGINR	**0.757439107**	2	2.852493
Q9JLZ3	SEVPGIFCAGADLK	**0.873262758**	2	2.937486
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**0.856835651**	**9.6E-13**	**15**
Q9JM53	AIASAAEGGSVPPIR	**0.967410956**	2	3.161554
Q9JM53	CLIATGGTPR	**0.7555654**	2	2.583949
Q9JM53	DGEQHEDLNEVAK	**1.014658304**	3	3.593656

Q9JM53	ILPEYLSNWTMEK	**0.923862625**	2	3.104879
Q9JM53	KSQASGIEVIQLFPEK	**0.950806597**	2	3.847722
Q9JM53	KVETDHIVTAVGLEPNVELAK	**0.880053046**	2	6.305777
Q9JM53	LNDGSQITFEK	**0.801749868**	2	3.346531
Q9JM53	SITVIGGGFLGSELACALGR	**0.712232413**	2	3.335269
Q9JM53	SQASGIEVIQLFPEK	**0.855039678**	2	4.461123
Q9JM53	TGGLEIDSDFGGFR	**0.885693426**	2	4.566465
Q9JM53	VETDHIVTAVGLEPNVELAK	**0.774542517**	2	5.21568
Q9JM53	VLIVSEDPELPYMRPPLSK	**0.867744935**	3	3.741368
Q9JM53	VMPNAIVQSVGVSGGK	**0.748850803**	2	4.041173
Q9JM53	VMPNAIVQSVGVSGGK+Oxidation(1)	**0.972648254**		
Q9JM53	VNAELQAR	**0.81753378**	2	2.486544
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**0.745274407**	**0.81218**	**2**
Q9JMA1	CTESEEEEVTK	**0.942687755**	2	3.621925
Q9JMA1	EKESVNAKVLK	**0.513926848**	2	2.315269
Q9JMD3	**PCTL PCTP_like protein**	**0.943380804**	**0.9584**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	**0.914326106**	2	4.894949
Q9JMD3	ESVQVPDDQDFR	**1.554292876**	2	2.362798
Q9JMD3	MECCDVPAETLYDVLHDIEYR	**1.12285185**	3	4.597589
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0)	**1.205135106**		
Q9JMD3	SCVITYLAQVDPK	**1.870395156**	2	3.148957
Q9JMD3	WDSNVIETFDIAR	**1.012132578**	2	4.318172
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**1.026733566**	**0.60045**	**5**
Q9QVC8	GEPNNVAGNQAQVK	**1.030321807**	2	4.135672
Q9QVC8	TEVAAGDHPTDAEMK	**0.794629564**	2	2.958541
Q9QVC8	TQLAVCQQR	**0.896891741**	2	2.493568
Q9QVC8	VAENGAQSAPLPLEGVDISPK	**0.941344255**	2	4.122159
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	**0.732938601**	3	5.068828
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**0.901972037**	**0.9874**	**2**
Q9QWN8	ALAQEDQSAGEVER	**0.919099659**	2	3.926124
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	**0.892648889**	3	4.347451
Q9QX74	**SHAN2 SH3 and multiple ankyrin repeat domains protein 2**	**0.493813002**	**0.08001**	**2**
Q9QX74	KNMLINIVDTAQQK+Oxidation(2)	**1.177606474**		
Q9QX74	SSSPASPENYVHPLTGR	**0.49983655**	2	2.590291
Q9QX79	**FETUB Fetuin_B**	**1.019934408**	**0.98259**	**2**
Q9QX79	GSIQHLPEQEEPEDSKGK	**1.04742256**	3	3.667366
Q9QX79	NTAPTSSPSITAPR	**1.016731926**	2	3.599302
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**0.961490164**	**0.62675**	**3**
Q9QXG4	AELGMNDSPSQSPPVK	**0.8053517**	2	3.721881
Q9QXG4	GATTNICYNVLDR	**2.189143599**	2	2.567111
Q9QXG4	IGPIATPDYIQNAPGLPK	**1.028143828**	2	3.047927
Q9QXH4	**ITAX Integrin alpha_X**	**0.801771784**	**0.48261**	**2**
Q9QXH4	GGSQMTFLVTFDVSPK+Oxidation(4)	**0.952206901**		
Q9QXH4	MLDFVKAVMSQLQRPSTR	**0.772099106**	2	2.396969
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**1.031195224**	**1**	**2**
Q9QXK3	SIATLAITTLLK	**0.971532872**	2	3.450824
Q9QXK3	SSEPVQLTEAETEYFVR	**1.050291772**	2	3.633356
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**0.967552373**	**0.83078**	**27**
Q9QXQ0	ACLISLGYDVENDR	**1.05909548**	2	4.069881
Q9QXQ0	AGTQIENIDEDFR	**1.159328535**	2	3.54526
Q9QXQ0	AGTQIENIDEDFRDGLK	**1.076967461**	2	4.207278
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	**1.273470007**	3	3.547238
Q9QXQ0	ASIHEAWTDGK	**1.117031029**	1	2.291869
Q9QXQ0	DDPVTNLNNAFEVAEK	**0.859582502**	2	3.080803
Q9QXQ0	ETTDTDTADQVIASFK	**0.897095122**	2	4.461416

Q9QXQ0	GISQEQMQEFR	**1.151623776**	2	3.158813
Q9QXQ0	HRDYETATLSDIK	**1.244168917**	2	3.519663
Q9QXQ0	HRPELIEYDK	**1.012774957**	3	4.139844
Q9QXQ0	HTNYTMEHLR	**1.787058401**	3	3.40227
Q9QXQ0	HTNYTMEHLR+Oxidation(5)	**1.460473261**		
Q9QXQ0	ICDQWDNLGSLTHSR	**0.978729741**	2	4.374999
Q9QXQ0	KDDPVTNLNNAFEVAEK	**0.931275727**	2	4.513169
Q9QXQ0	LSGSNPYTSVTPQIINSK	**1.436198717**	2	4.867167
Q9QXQ0	LVSIGAEEIVDGNAK	**1.074628312**	2	3.236647
Q9QXQ0	MAPYQGPDAAPGALDYK	**0.904440091**	2	4.62986
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0)	**1.180575247**		
Q9QXQ0	MLDAEDIVNTARPDEK	**0.84113588**	2	3.708212
Q9QXQ0	QFASQANMVGPWIQTK	**0.932481276**	2	3.828565
Q9QXQ0	QLETIDQLHLEYAK	**0.877890838**	2	2.964627
Q9QXQ0	RDHALLEEQSK	**1.078652596**	3	3.952373
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	**1.064395123**	3	5.32006
Q9QXQ0	TINEVENQILTR	**1.145429868**	2	3.677704
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	**1.426798737**	3	5.398366
Q9QXQ0	VGWEQLLTTIAR	**0.884936434**	2	4.047909
Q9QXQ0	VLAVNQENEHLMEDYER	**1.253481011**	2	5.049682
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**0.911221875**	**0.86966**	**5**
Q9QXT0	ALVDELEWEIAR	**0.757822002**	2	3.554797
Q9QXT0	IDSDISGTLK	**0.815858736**	2	2.319111
Q9QXT0	INPDGSQSVVEVPYAR	**0.928217788**	2	4.00082
Q9QXT0	RTDLCDHALHR	**1.047618797**	3	3.429007
Q9QXT0	TDLCDHALHR	**1.001616612**	2	2.862922
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**0.891258113**	**1.9E-12**	**16**
Q9QXX4	ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	**1.038862689**	3	4.904266
Q9QXX4	ASGDAARPFLLQLAESAYR	**1.261197586**	2	3.558573
Q9QXX4	DGSVPLLAEIFAGGCAGGSQVIFTNPLEIVK	**1.061957122**		
Q9QXX4	DVEVTKEEFALAAQK	**0.845551829**	2	4.388765
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	**0.628167472**	2	5.580944
Q9QXX4	GLLPQLLGVAPEK	**0.844496027**	2	2.995626
Q9QXX4	IAPLEEGMLPFNLAEAQR	**1.289067457**	2	5.060184
Q9QXX4	ITLPAPNPDHVGGYK	**0.933234031**	2	2.346985
Q9QXX4	KDVEVTKEEFALAAQK	**0.839513114**	2	4.777228
Q9QXX4	LQVAGEITTGPR	**0.851913223**	2	3.503073
Q9QXX4	LTVNDFVR	**0.635323503**	2	2.434569
Q9QXX4	NGEFFMSPHDFVTR	**0.905991417**	2	3.661848
Q9QXX4	SSPQFGVTLLTYELLQR	**1.394076681**	2	3.966285
Q9QXX4	STGSFVGELMYK	**0.711304165**	2	2.463364
Q9QXX4	TVELLSGVVDQTK	**0.987443756**	2	4.298398
Q9QXX4	YLNIFGESQPNPK	**0.867955679**	2	4.405842
Q9QYU2	**EFTS Elongation factor Ts_ mitochondrial**	**0.906591852**	**0.99914**	**2**
Q9QYU2	ALETCGGDLK	**0.870520598**	2	2.420243
Q9QYU2	YGALVICQTPEQITNLEEVGR	**0.964121517**	2	4.676792
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.773799635**	**0.01037**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	**0.896195548**	2	3.723191
Q9QYU4	RAPAFLSADEVQDHLR	**0.671044098**	3	4.63598
Q9QYU4	SLGMAVEDLVAAK	**0.773693747**	2	3.143306
Q9QYU4	SSSLLIPPLEAALANFSK	**0.463764482**	2	3.088178
Q9QZ76	**MYG Myoglobin**	**1.284375691**	**0.9922**	**5**
Q9QZ76	GQHAAEIQPLAQSHATK	**0.956845712**	2	4.88546
Q9QZ76	HGCTVLTALGTILK	**0.714996631**	2	3.535485
Q9QZ76	KGQHAAEIQPLAQSHATK	**0.865890836**	3	5.712786

Q9QZ76	VEGDLAGHGQEVLISLFK	**1.189692112**	3	4.915684
Q9QZ76	YSGDFGADAQGAMSK	**0.817328899**	2	4.750554
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**0.97889249**	**0.99914**	**9**
Q9QZA2	ATLVKPTPVNVPISQK	**0.942322111**	2	3.703234
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	**1.031286467**	2	3.538852
Q9QZA2	FYNELTEILVR	**0.828706247**	2	2.943046
Q9QZA2	LLDEEEATDNDLR	**1.137935434**	2	3.466552
Q9QZA2	MVPVSVQQSLAVFSQR	**1.088974446**	2	2.676082
Q9QZA2	NIQVSHQEFSK	**1.219462302**	2	3.357834
Q9QZA2	NLATAYDNFVELVANLK	**1.105346258**	3	4.168279
Q9QZA2	STAVVEQGGIQTVDQLIK	**0.969405949**	2	4.235548
Q9QZA2	YYDQICSIEPK	**0.980590583**	2	2.345001
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**0.790015573**	**0.10149**	**5**
Q9QZD8	GALVTVGQLSCYDQAK	**0.913587764**	2	4.869442
Q9QZD8	NYSHALDGLYR	**1.034293191**	2	2.907637
Q9QZD8	VHLQTQQEVK	**0.768369953**	1	3.011795
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	**0.808866249**	2	5.651291
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	**0.81255231**	3	3.399382
Q9QZH8	**AAAD Arylacetamide deacetylase**	**0.907051615**	**0.99678**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	**1.004647996**	2	4.119337
Q9QZH8	WFLQEDILEK	**0.906218769**	2	3.349015
Q9QZK2	**BCAR3 Breast cancer anti_estrogen resistance protein 3**	**0.974575059**	**0.66277**	**2**
Q9QZK2	EGSLAEGRPDVVKR	**0.929703827**	2	2.649199
Q9QZK2	FSSDARTGEALR	**1.307904077**	2	2.317252
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.849522307**	**2.7E-08**	**6**
Q9QZU7	IDANNVAYTTGK	**1.606979586**	2	3.338987
Q9QZU7	IIELDDKGQVVR	**1.574688069**	2	2.543926
Q9QZU7	LLLEALDVNIR	**1.356838891**	2	2.857077
Q9QZU7	MNPGDVITFDNWR	**1.334231764**	2	3.172843
Q9QZU7	QTVTGGDSEIVDGFNVCQK	**1.123651095**	2	4.499276
Q9QZU7	SYEAGTEISR	**1.749322135**	2	2.836032
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**0.823936325**	**0.83786**	**3**
Q9QZX8	GIGETPIVPLGISYLDDFAK	**1.044967475**	2	3.048605
Q9QZX8	QEEQDPSNMTGFLR	**1.236627954**	2	2.354832
Q9QZX8	QFTDEGNPDSVNK	**0.840555308**	2	3.422201
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.983222119**	**2.3E-14**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	**1.611822253**	2	4.088025
Q9R063	ETDLLLDDSLVSLFGNR	**0.961131474**	2	4.151052
Q9R063	GVLFGVPGAFTPGCSK	**0.816581957**	2	4.193405
Q9R063	THLPGFVEQAGALK	**0.734012071**	3	4.748904
Q9R063	VGDTIPSVEVFEGEPGK	**0.939617181**	2	3.758513
Q9R063	VGDTIPSVEVFEGEPGKK	**0.802167151**	2	3.754559
Q9R063	VNLAELFK	**0.846104707**	2	2.852062
Q9R063	VQLLADPTGAFGK	**0.768971423**	2	3.996456
Q9R0N0	**GALK1 Galactokinase**	**0.929066989**	**0.99949**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	**0.941448099**	3	4.378198
Q9R0N0	QCEEVAQALGK	**0.934777579**	2	2.463462
Q9R0N0	RQCEEVAQALGK	**0.853542665**	2	3.03592
Q9R0N0	SLETSLVPLSDPK	**0.900282894**	2	3.204306
Q9R0N0	TDGLVSLLTTSK	**1.01000175**	2	3.433484
Q9R0N0	VEELLAEAR	**0.932038921**	2	3.157166
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**0.871560067**	**0.97149**	**6**
Q9R0T3	AEPSVAEYTVR	**0.90512395**	2	2.743583
Q9R0T3	FDDGEDPLDAETQQGGGSNPFHR	**0.864823357**	3	3.659253

Q9R0T3	ICSEVLQLEPDNVNALK	**1.063064301**	2	5.405903
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	**0.880551765**	3	5.490442
Q9R0T3	LIGSAEELIR	**0.830490656**	2	2.378122
Q9R0T3	SNPSENEEKEAQSQLVK	**0.848641512**	2	5.015873
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.066048765**	**0.83328**	**4**
Q9R112	EGNALFTFPNTPVK	**1.25894843**	2	2.707342
Q9R112	STLSVIPSGVQWIQDR	**0.940293859**	2	2.549031
Q9R112	TAAAVAAQSGILDR	**1.118014319**	2	2.791556
Q9R112	VGAENVAIVEPSER	**0.995485889**	2	2.867388
Q9R1T3	**CATZ Cathepsin Z**	**1.006079623**	**1**	**2**
Q9R1T3	HGIPDETCNNYQAK	**0.997336596**	2	3.794746
Q9R1T3	VGDYGSLSGR	**0.992672824**	2	2.64976
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**1.26685736**	**0.18338**	**5**
Q9R1Z0	LCQNNFALGYK	**1.47232967**	2	2.526619
Q9R1Z0	LTLSALVDGK	**1.602905243**	2	2.720363
Q9R1Z0	LTVDTIFVPNTGK	**1.034807327**	2	3.499559
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	**0.957010844**	2	4.110036
Q9R1Z0	WNTDNTLGTEISWENK	**1.059934946**	2	2.896702
Q9R1Z8	**VINEX Vinexin**	**0.936306903**	**0.78104**	**2**
Q9R1Z8	LSAELDKDLR	**0.897036383**	3	3.522681
Q9R1Z8	MPDLQLDWTLEDPPK+Oxidation(0)	**1.10726101**		
Q9R257	**HEBP1 Heme_binding protein 1**	**1.10416094**	**0.08701**	**2**
Q9R257	FATVEVTDKPVDEALR	**1.106845527**	2	3.528544
Q9R257	NSLFGSVETWPWQVLSTGGK	**1.256481746**	2	3.863076
Q9WTT6	**GUAD Guanine deaminase**	**1.010840632**	**0.01229**	**10**
Q9WTT6	EIGNFEVGKDFDALLINPR	**0.971919395**	2	3.565097
Q9WTT6	ETTEESVKETER	**1.529067252**	2	3.253301
Q9WTT6	FQSTDVAEEVYTR	**1.06057556**	2	4.313101
Q9WTT6	FSLSCTETLMSELGNIAK	**1.035933783**	2	4.127766
Q9WTT6	GTFVHSTWTCPMEVLR	**0.669048623**	2	3.132769
Q9WTT6	IVFLEESSQQEK	**1.47647953**	2	3.919569
Q9WTT6	NIEEVYVGGK	**1.131269062**	1	2.790273
Q9WTT6	NYTDVYDKNNLLTNK	**0.649395433**	2	4.412564
Q9WTT6	THDLYIQSHISENREEIEAVK	**1.315292446**	3	3.755657
Q9WTT6	VCMDLNNTVPEYK	**0.728526961**	2	3.978439
Q9WTV5	**PSMD9 26S proteasome non_ATPase regulatory subunit 9**	**0.923169081**	**0.90665**	**2**
Q9WTV5	ADVDLYQVR	**1.170665873**	2	2.705196
Q9WTV5	RKEEIEAQIK	**1.045874995**	3	3.916663
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**0.879652977**	**3.9E-05**	**9**
Q9WU19	AIFVTVDTPYLGNR	**1.060741635**	2	4.592975
Q9WU19	AVFVGRPIIWGLAFQGEK	**0.897824869**	3	4.129823
Q9WU19	GVQDVLEILK	**0.79386573**	2	2.912539
Q9WU19	GVQDVLEILKEEFR	**0.676840053**	2	3.956644
Q9WU19	HGVDGILVSNHGAR	**0.814597085**	3	5.21556
Q9WU19	MKNFETNDLAFSPK+Oxidation(0)	**0.839095236**		
Q9WU19	NFETNDLAFSPK	**0.825923046**	2	3.410523
Q9WU19	NVADIDLSTSVLGQR	**0.862704452**	2	4.907847
Q9WU19	VEVFLDGGVR	**0.963304157**	2	2.95267
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**0.884865644**	**0.32393**	**2**
Q9WU49	GNVVPSPLPTR	**0.651465038**	2	2.462003
Q9WU49	LQAVEVVITHLAPGTK	**0.91182722**	2	3.991714
Q9WU65	**GLPK2 Glycerol kinase 2**	**1.033374584**	**0.66113**	**2**
Q9WU65	GIICGLTQFTNK	**1.031437016**	2	3.463225
Q9WU65	TGLPLSTYFSAVK	**4.643059594**	2	2.617165

Q9WU82	**CTNB1 Catenin beta_1**	**0.893520144**	**0.04137**	**3**
Q9WU82	HQEAEMAQNAVR	**0.764847311**	2	3.357732
Q9WU82	LLNDEDQVVVNK	**1.029799458**	2	3.253192
Q9WU82	TMQNTNDVETAR	**0.880851284**	2	3.417847
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**0.978754802**	**4.1E-05**	**3**
Q9WUC4	LGGVEFNIDLPNK	**0.796938739**	2	2.852182
Q9WUC4	LGGVEFNIDLPNKK	**1.102190474**	2	3.457079
Q9WUC4	VCIESEHSSDILLATLNK	**1.134800644**	2	5.705632
Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**1.077215675**	**0.89375**	**2**
Q9WUH4	FCANTCVECR	**1.071749173**	2	2.999619
Q9WUH4	FVFHNEQVYCPDCAK	**1.197688796**	2	4.135421
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**1.295081723**	**0.51283**	**2**
Q9WUI1	ILDFGLAR	**1.296755375**	2	2.373367
Q9WUI1	QELNKTVWEVPQR	**0.587431941**	2	2.345996
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.916937985**	**0.06026**	**6**
Q9WUS0	AVILGPPGSGK	**0.788970081**	2	2.520515
Q9WUS0	GLLVPDHVITR	**0.778334742**	2	2.498282
Q9WUS0	GVLHQFSGTETNR	**0.921940764**	2	3.619946
Q9WUS0	TLVQAEALDR	**0.812862902**	2	2.901691
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	**1.150142543**	3	5.072241
Q9WUS0	YKDAAKPVIELYK	**0.594836477**	2	2.536824
Q9WV97	**TIM9 Mitochondrial import inner membrane translocase subunit Tim9**	**0.8835623**	**0.06782**	**2**
Q9WV97	FQEYHIQQNEALAAK	**0.859949991**	2	4.868166
Q9WV97	LTETCFLDCVK	**1.007291832**	2	2.385885
Q9WVC0	**SEPT7 Septin_7**	**0.945508552**	**0.71634**	**2**
Q9WVC0	ADTLTPEECQQFK	**0.991064805**	2	3.356287
Q9WVC0	NLEGYVGFANLPNQVYR	**0.759061498**	2	2.30755
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**1.310557753**	**4.8E-06**	**4**
Q9WVD5	DGPLGFYHGLSSTLLR	**1.393703505**	2	3.076921
Q9WVD5	LQTMYEMETSGK	**1.687590234**	2	2.377356
Q9WVD5	NEGITALYSGLKPTMIR	**0.826205695**	2	3.577058
Q9WVD5	SNPAIQAAIDLTAGAAGGTACVLTGQPFDTMK	**1.697329992**	3	4.556772
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.961202816**	**9.2E-12**	**13**
Q9WVK3	AGVYNLTK	**0.989728856**	2	2.411403
Q9WVK3	ASQPPSSSTQVTAIQCNIR	**0.862686707**	2	5.47989
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	**0.834249212**	3	6.884837
Q9WVK3	ELLHLGCNVVIASR	**1.037385842**	2	3.852978
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	**1.03957261**	2	5.240016
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12)	**1.241411329**		
Q9WVK3	KEEEVNNLVK	**0.864487826**	3	4.183327
Q9WVK3	LTAAVDELR	**1.170917601**	2	3.131771
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	**0.754637983**	2	5.012838
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	**0.749817916**	3	3.334849
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	**0.850952412**	2	6.327176
Q9WVK3	TMALTWASSGVR	**0.694435728**	2	3.897732
Q9WVK3	TMALTWASSGVR+Oxidation(1)	**0.961815913**		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**0.806786327**	**0.00273**	**14**
Q9WVK7	AADEFVEK	**0.936196094**	2	3.132052
Q9WVK7	EDIDTAMK	**0.939441584**	1	1.983415
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	**1.218269549**	2	5.541116
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	**0.824646161**	3	5.373808
Q9WVK7	GDASKEDIDTAMK	**0.759018826**	3	3.850496
Q9WVK7	GDASKEDIDTAMK+Oxidation(11)	**0.863245739**		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	**0.728489567**	3	7.517247

Q9WVK7	KGIEESLK	**0.993094323**	1	2.137823
Q9WVK7	KGIEESLKR	**0.815014115**	2	2.348249
Q9WVK7	LKNELFQR	**0.807183346**	2	2.694453
Q9WVK7	LLVPYLIEAIR	**0.969650447**	2	2.555841
Q9WVK7	LVEVIK	**0.925677126**	2	2.451511
Q9WVK7	TFESLVDFCK	**0.852179883**	2	3.441023
Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	**0.788560843**	3	6.204538
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.254293658**	**0.22826**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	**1.280463215**	2	3.306947
Q9Z0N2	SFDVNKPGCEVDDLK	**1.154722101**	2	3.454753
Q9Z0N2	VGQEIEVRPGIVSK	**1.263483957**	2	3.10233
Q9Z0U5	**ADO Aldehyde oxidase**	**0.818416838**	**0.92352**	**17**
Q9Z0U5	CGLSPEQVR	**0.926591003**	2	2.48427
Q9Z0U5	CTGYRPIIDACK	**0.599777435**	2	2.621097
Q9Z0U5	DLEPLILTIEEAIQHK	**0.715724117**	2	3.289575
Q9Z0U5	EFQPLDPTQELIFPPELMR	**0.906180377**	2	3.069865
Q9Z0U5	ELSILYGGVGPTTIGAK	**0.971089369**	2	3.496761
Q9Z0U5	GEDMLITGGR	**1.124349625**	2	2.36863
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	**0.906137143**	2	4.614176
Q9Z0U5	GYESNINWEK	**0.852151637**	2	2.828918
Q9Z0U5	HIQDIVAATLK	**0.8435997**	2	2.447212
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	**0.771315092**	2	4.594275
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	**0.846966292**	3	3.380001
Q9Z0U5	KLECGNVDEAFK	**0.833924593**	2	3.549228
Q9Z0U5	LVLDEVTLAGSAPGGK	**0.751191616**	2	3.534112
Q9Z0U5	MTWISPVTLEELVEAK	**1.096416363**	2	3.203017
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	**0.61492849**	2	3.722775
Q9Z0U5	RLEPIISK	**0.646033416**	2	2.436527
Q9Z0U5	VVENNVDPEMMLLPYLR	**0.75246472**	2	3.864388
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**0.999939417**	**3.4E-05**	**4**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	**2.692280403**	2	5.433118
Q9Z0V5	GLFIIDDK	**0.968113613**	2	2.978997
Q9Z0V5	QITLNDLPVGR	**0.958007309**	2	3.308394
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	**1.446587582**	3	6.021302
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.992092634**	**0.29986**	**6**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	**0.859298615**	3	5.999172
Q9Z0V6	GLFIIDPNGVIK	**0.880874875**	2	3.068291
Q9Z0V6	GTAVVNGEFK	**0.931685021**	2	2.453907
Q9Z0V6	HLSVNDLPVGR	**0.763002303**	2	2.87021
Q9Z0V6	NGGLGHMNITLLSDLTK	**0.979159039**	2	2.817187
Q9Z0V6	SVEEPLRLVK	**1.272801244**	2	2.488593
Q9Z142	**TMM33 Transmembrane protein 33**	**1.150214682**	**0.79389**	**2**
Q9Z142	ALLANALTSALR	**1.015729479**	2	3.72164
Q9Z142	LSTNQQNILK	**1.250395441**	2	2.468726
Q9Z1A6	**VIGLN Vigilin**	**1.264180779**	**0.00985**	**22**
Q9Z1A6	ASVITQVFHVPLEER	**1.470903062**	2	2.88712
Q9Z1A6	DKFPEVIINFPDPAQK	**1.245832498**	3	4.04574
Q9Z1A6	DLANIAEVEVSIPAK	**1.089396313**	2	3.74732
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	**1.009816374**	3	3.519886
Q9Z1A6	ELQAEQEDR	**1.487686269**	2	2.50733
Q9Z1A6	GNSLQEILER	**1.018933486**	2	2.524348
Q9Z1A6	HEVLLISAEQDKR	**1.634913735**	3	4.274891
Q9Z1A6	IDLPAENSNSETIVITGK	**0.944013251**	2	4.628772
Q9Z1A6	IEGDPQGVQQAK	**1.083311932**	2	3.178707
Q9Z1A6	IIFPAAEDKDQDLITIIGK	**1.12165584**	2	3.236438

Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	0.984827716	2	4.309167
Q9Z1A6	IVGELEQMVSEDVPLDHR	0.931936896	2	4.52848
Q9Z1A6	LGQALTEVYAK	1.5923168	2	3.205396
Q9Z1A6	LQDLELK	1.074832562	1	2.320713
Q9Z1A6	LQTQASATVPIPK	0.917458189	2	3.530967
Q9Z1A6	LVGEIMQETGTR	0.86869399	2	3.385951
Q9Z1A6	MDYVEINIDHK	0.982151097	2	3.225439
Q9Z1A6	MVADLVENSYSISVPIFK	1.03019156	2	2.988643
Q9Z1A6	RCDIIVISGR	1.122942589	2	2.776778
Q9Z1A6	TEIVFTGEKEQLAQAVAR	1.320046659	2	4.179046
Q9Z1A6	TKDLIIEQR	0.951633795	2	2.525235
Q9Z1A6	VKELQAEQEDR	0.93384858	2	3.015939
Q9Z1J8	**S14L3 SEC14_like protein 3**	**0.902876025**	**0.92713**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.933549555	3	3.857328
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	0.923531095	3	3.815496
Q9Z1J8	GSSHQVEYEILFPGCVLR	0.802865647	2	4.619497
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**0.96254784**	**0.52447**	**2**
Q9Z1N1	YVGSMVADVHR	0.860295068	2	2.318095
Q9Z1N1	YVGSMVADVHR+Oxidation(4)	0.967805033		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**1.123966453**	**0.00836**	**3**
Q9Z1P2	DYETATLSEIK	1.259150529	1	2.080388
Q9Z1P2	ICDQWDNLGALTQK	0.636235212	2	3.898709
Q9Z1P2	KDDPLTNLNTAFDVAER	2.038670836	2	2.663866
Q9Z1W6	**LYRIC Protein LYRIC**	**0.949722856**	**0.01004**	**3**
Q9Z1W6	SWQDELAQQAEEGSAR	0.595632734	2	5.390511
Q9Z1W6	TELGLDLGLEPK	0.805987817	2	2.797747
Q9Z1W6	TLPPAISAEPSVTLSK	0.792688639	2	3.161659
Q9Z1Y3	**CADH2 Cadherin_2**	**0.731279251**	**1.6E-06**	**2**
Q9Z1Y3	IDPVNGQITTIAVLDR	0.7244733	2	3.495197
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	0.888215979	3	3.387642
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**0.884957348**	**0.07522**	**3**
Q9Z270	FKGPFTDVVTTNLK	0.86227838	2	2.602382
Q9Z270	HEQILVLDPPSDLK	0.897591396	2	4.187204
Q9Z270	QDGPLPKPHSVSLNDTETR	0.823541229	3	3.351138
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**1.161438426**	**0.58437**	**2**
Q9Z2C8	NDTKEDVFVHQTAIK	0.844985214	2	3.421593
Q9Z2C8	SVGDGETVEFDVVEGEK	1.217605549	2	3.689335
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.831620412**	**9.9E-20**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	0.76035817	2	4.563154
Q9Z2I8	GKGVFNSGLK	0.694537073	2	2.312438
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.551619126	3	4.77351
Q9Z2I8	INFDDNAEFR	0.849761803	2	3.207994
Q9Z2I8	LEGTNVQEAQNILK	0.875516558	2	5.226037
Q9Z2I8	SENEPIENEAAR	0.964383655	2	4.052405
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.744629682	2	5.999477
Q9Z2I8	SSGLPITSAVDLEDAAK	0.747755903	2	4.538201
Q9Z2I8	SSGLPITSAVDLEDAAKK	1.550919803	2	2.952747
Q9Z2I8	VMVAEALDISR	0.831487264	2	3.318779
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**0.810600875**	**0.26386**	**8**
Q9Z2I9	ALIADSGLK	0.703841632	1	2.08293
Q9Z2I9	ICNQVLVCER	1.028503366	2	2.861273
Q9Z2I9	ILACDDLDEAAK	0.824365893	2	3.392226
Q9Z2I9	INFDSNSAYR	0.789815357	2	2.837421
Q9Z2I9	LSEIVTLAK	0.902815956	2	2.50533

Q9Z2I9	MGFPSNIVDSAAENMIK	**0.789970916**	2	2.828672
Q9Z2I9	SSDEAYAIAK	**0.821616081**	2	3.503048
Q9Z2I9	VQAILVNIFGGIMR	**0.582006154**	2	3.837887
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**0.959346307**	**0.92104**	**11**
Q9Z2L0	KLETAVNLAWTAGNSNTR	**0.874151416**	2	5.814874
Q9Z2L0	LTFDSSFSPNTGK	**0.834067169**	2	3.601147
Q9Z2L0	LTFDSSFSPNTGKK	**0.831200424**	2	2.553809
Q9Z2L0	LTLSALLDGK	**1.450529815**	2	2.493484
Q9Z2L0	SENGLEFTSSGSANTETTK	**1.193977605**	2	4.596782
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	**0.892049235**	3	5.105243
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	**0.901433811**	2	4.438754
Q9Z2L0	VTQSNFAVGYK	**1.008849493**	2	3.132606
Q9Z2L0	WNTDNTLGTEITVEDQLAR	**0.782332994**	2	4.545949
Q9Z2L0	WTEYGLTFTEK	**1.092281117**	2	2.902601
Q9Z2L0	YQVDPDACFSAK	**0.995660142**	2	3.553422
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.672591001**	**0.82841**	**4**
Q9Z2M4	GQVLQLHAGAAK	**0.760251723**	2	3.187414
Q9Z2M4	HLAVEWGPQNIR	**0.822093837**	2	3.269214
Q9Z2M4	VNSLAPGAISGTEGLR	**0.890046616**	2	3.931054
Q9Z2M4	VPPAVMAAVDQALK	**0.695030387**	2	3.169947
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.024652862**	**0.3691**	**4**
Q9Z2M7	IGVVGGSDFEK	**1.513948877**	2	2.376433
Q9Z2M7	LQEQLGNDVVEK	**1.202023245**	2	3.491516
Q9Z2M7	TVGYTVTAPEDTR	**1.041668408**	2	2.519665
Q9Z2M7	YDYVFPENGLVAYK	**0.82021905**	2	3.340096
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.043228121**	**0.99806**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	**0.90667282**	2	4.183478
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	**0.936232937**	2	4.623977
Q9Z2Q1	CLSSATDPQTK	**0.986231946**	2	2.623059
Q9Z2Q1	DQTLSPTIISGLHSIAR	**0.820062353**	2	3.423858
Q9Z2Q1	GGPGPLAGHPQVSR	**0.932288609**	2	3.098453
Q9Z2Q1	IDASQTDFEK	**0.882768678**	2	2.494619
Q9Z2Q1	IIAGDKEVVIAQK	**1.259765677**	2	2.537663
Q9Z2Q1	KIDASQTDFEK	**0.961763976**	2	3.043903
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	**1.135123533**	2	5.171887
Q9Z2Q1	QVQHILASASPSGR	**0.961223318**	2	2.912612
Q9Z2Q1	SSYEGQPLPK	**0.917503272**	2	2.477648
Q9Z2Q1	TQPPEDISCIAWNR	**0.911520976**	2	2.673215
Q9Z2Q1	TTFEDLIQR	**0.906065546**	2	2.34945
Q9Z2Q1	VYSIMGGSIDGLR	**1.321890215**	2	2.619166
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**0.849001411**	**0.99903**	**3**
Q9Z2Z8	AIECSYTSADGLK	**1.055643077**	2	3.996382
Q9Z2Z8	ASLADIWAK	**0.968866624**	2	2.651257
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	**0.828393566**	2	5.473073
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**0.724064674**	**0.25424**	**5**
Q9Z339	GSAPPGPVPEGQIR	**0.869016419**	2	3.326944
Q9Z339	LEALELNECIDHTPK	**0.481265441**	2	4.331292
Q9Z339	LEEAMANK	**0.876029525**	1	1.997001
Q9Z339	LEEAMANK+Oxidation(4)	**0.901988134**		
Q9Z339	LFPDDPYEKACQK	**0.573307857**	2	2.423779

Time point 30 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (30 h)**	**P-value (30 h)**	**Peptide number (30 h)**
Accession number	Peptide sequence	Peptide Ratio (30 h)	Charge state	Xcorr
A0FKI7	**ACBD5 Acyl_CoA_binding domain_containing protein 5**	**1.233493631**	**0.374245**	**3**
A0FKI7	LQEDMQNVLQR	**1.362416334**	2	2.58537
A0FKI7	RGGESEDISGVR	**0.810416735**	2	2.62446
A0FKI7	SSDLTSDLGNVLTSSNAK	**0.937875476**	2	3.25847
A2AAE1	**K1109 Uncharacterized protein KIAA1109**	**0.93954708**	**0.916348**	**2**
A2AAE1	SSRSLDQDSPSKK	**1.109327688**	2	2.66062
A2AAE1	TVDGNVNSMKRK	**0.93813753**	2	2.3111
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.042710034**	**0.000789**	**3**
A2ADY9	IDFSSIAVPGTSNPQQR	**1.070928465**	2	3.24353
A2ADY9	NPPLAEALLSGDLEK	**0.811907222**	2	3.42677
A2ADY9	VLVEQQQDR	**0.87215474**	2	2.46965
A2AGT5	**CKAP5 Cytoskeleton_associated protein 5**	**0.133495128**	**3.61E-05**	**2**
A2AGT5	DQVLAMLEKAKANMPSKPAAPAK+Oxidation(13)	**0.042441998**		
A2AGT5	IGSKENTKEGLAELYEYK	**0.490131439**	2	2.54842
A2AQP0	**MYH7B Myosin_7B**	**1.009209047**	**6.26E-05**	**13**
A2AQP0	AITDAAMMAEELK	**0.830789138**	2	2.93084
A2AQP0	AITDAAMMAEELKK	**0.369399251**	2	3.53363
A2AQP0	AITDAAMMAEELKK+Oxidation(6)	**1.009933756**		
A2AQP0	AITDAAMMAEELKK+Oxidation(7)	**1.009933756**	2	2.92241
A2AQP0	CNGVLEGIR	**0.684060364**	2	2.56169
A2AQP0	DIDDLELTLAK	**0.123793864**	2	3.79537
A2AQP0	ELEELSER	**0.047080241**	1	2.07647
A2AQP0	EQDTSAHLER	**1.032917024**	2	2.49111
A2AQP0	KDIDDLELTLAK	**1.070588276**	2	2.37454
A2AQP0	SIQELEK	**0.98278714**	2	2.39353
A2AQP0	TEELEEAK	**0.109643871**	2	2.36494
A2AQP0	VEDEQLVGVQLQK	**0.094536383**	2	2.32004
A2AQP0	VGNEYVTK	**0.633873801**	2	3.03588
A2ASS6	**TITIN Titin**	**0.495520316**	**0.012054**	**32**
A2ASS6	ACDALYPPGPPSNPK	**0.822524262**	2	2.53571
A2ASS6	AENRFGIGPPAETIQRTTAR	**0.896281099**	2	2.57158
A2ASS6	AGEDVQLLIPFK	**1.06633351**	2	2.5868
A2ASS6	APPIEPAPTPIAAPVTAPVVGK	**0.077393223**	2	4.50648
A2ASS6	ATGLIEGLDYQFR	**0.574741775**	2	2.99019
A2ASS6	ATLTWTPPLEDGGSPIK	**0.951820817**	2	2.31673
A2ASS6	ATNEVGSDTCACTVK	**0.079617973**	2	4.2124
A2ASS6	DGQELQIADRIKIQK	**1.196146556**	2	2.78806
A2ASS6	DPFDKPSQPGELEILSISK	**1.213828559**	3	3.67113
A2ASS6	GQSDPVTIGPLTVK	**0.917537205**	2	2.83899
A2ASS6	GYDEIPLEPNDKTEILK	**0.389085494**	2	2.41961
A2ASS6	IEALPSDISIDEGK	**0.175781923**	2	2.4207
A2ASS6	KGDGTQLACKVTGTPPIK	**0.031752067**	2	2.67103
A2ASS6	NAADNFSEPSESSGAITAR	**0.360687648**	2	3.98461
A2ASS6	NAADSVSEPSESTGPITVK	**0.323413092**	2	2.34291
A2ASS6	NAADSVSEPSESTGPITVKDDVEAPR	**1.168465638**	3	3.44918
A2ASS6	NAAGVFSEPSESTGAITAR	**1.460359484**	2	4.28796
A2ASS6	QEKIEGDLRAMLK+Oxidation(10)	**0.357498675**		
A2ASS6	QETEEIAASMVVVATAK	**1.176219598**	2	2.31108
A2ASS6	SAANLIVEEEDLR	**0.515691834**	2	2.59686

A2ASS6	VFAENEYGIGDPGETR	**0.074800878**	2	3.59525
A2ASS6	VGTGEPVETDSPVEAR	**0.074692782**	2	4.02984
A2ASS6	VIGSPNTPEGPLEYDDIQAR	**1.360815275**	2	3.60706
A2ASS6	VLACNAGGPGEPAEVPGTVK	**0.136171828**	2	3.04132
A2ASS6	VLAENEIGIGEPCETTEPVK	**0.822524262**	2	3.7803
A2ASS6	VLAENEYGIGLPAETAESVK	**0.404532452**	2	3.502
A2ASS6	VLDRPGPPEGPLAVSDVTSEK	**0.895997466**	3	3.59803
A2ASS6	VNAESTENNSLLTIK	**0.595612046**	2	3.73606
A2ASS6	VSGENEFGVGVPAETK	**1.123206539**	2	3.67602
A2ASS6	VSNVAGDNACSGILTVK	**1.238715741**	2	2.93279
A2ASS6	VSVLDVPGPPGPIEISNVSAEK	**0.665914937**	2	2.7203
A2ASS6	YGIGEPLDSEPETAR	**0.694097015**	2	3.2207
A2AU37	**RD21L Double_strand_break repair protein rad21_like protein 1**	**1.286273387**	**0.307271**	**2**
A2AU37	MKMTFRPGLVDLPK	**0.512638137**	1	2.06561
A2AU37	RGGVDMLLSTATQDLINDELK	**1.302621251**	2	2.36152
A2AWA9	**RBGP1 Rab GTPase_activating protein 1**	**0.610049492**	**0.069283**	**2**
A2AWA9	IVICVQQTANKELAIER	**0.603158824**	2	2.34707
A2AWA9	RLMELACNTKISQK+Oxidation(2)	**0.705389357**		
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.353747872**	**9.9E-20**	**11**
A2VCW9	AEGIVFNTQSTIK	**1.954368594**	2	2.7553
A2VCW9	AGGILQEDITEACLILGVK	**1.006474307**	2	3.92313
A2VCW9	AQEANMSLLDEVLK	**1.396689154**	2	4.38646
A2VCW9	GAQEVFNELPCEYVEPHELK	**1.427664045**	2	4.81432
A2VCW9	KTDGVYDPVEYEKYPER	**1.396279467**	3	3.9124
A2VCW9	KYDINTVNVTVGK	**1.678511909**	2	4.09332
A2VCW9	LQSLVESQDLVISLLPYVLHPVVAK	**1.915164567**	3	4.09074
A2VCW9	QDAQSLLVPVK	**1.178686783**	2	2.6665
A2VCW9	REDVNAWER	**1.712085833**	2	3.0881
A2VCW9	SSVVPVEGCPELPHK	**1.564824937**	2	2.82878
A2VCW9	YDINTVNVTVGK	**1.355986043**	2	2.45822
A6H584	**chain**	**0.852076289**	**0.029862**	**7**
A6H584	FVNRAVFRMANGIDR+Oxidation(8)	**0.975439617**		
A6H584	NEHSFQVVGIQVR	**0.850963103**		
A6H584	QGDPGIEGPIGFPGPK	**1.138985404**		
A6H584	RGTQGYGPIGYDGQK	**1.953601173**		
A6H584	TMNPAFMGLDRATR+Oxidation(1)	**1.481114698**		
A6H584	YDVTDAVKVLK	**0.997345107**		
A6H584	YLIVVTDGHPLEGYKEPCGGLEDAVNEAK	**0.617405993**		
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**0.964172263**	**1.92E-05**	**12**
A7VJC2	GFGFVTFDDHDPVDK	**1.006512515**	2	3.11347
A7VJC2	GGGGNFGPGPGSNFR	**1.147431494**	2	3.52915
A7VJC2	GGNFGFGDSR	**1.182890887**	2	2.48153
A7VJC2	IDTIEIITDR	**0.920680334**	2	4.10405
A7VJC2	LFIGGLSFETTEESLR	**1.970746869**	2	3.87323
A7VJC2	LTDCVVMR	**0.678993611**	2	2.53139
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	**0.935279587**	2	6.31184
A7VJC2	NYYEQWGK	**1.013687242**	1	2.43816
A7VJC2	QEMQEVQSSR	**0.811449718**	2	3.01444
A7VJC2	QEMQEVQSSR+Oxidation(2)	**1.203599516**		
A7VJC2	TLETVPLER	**1.365372743**	2	2.31637
A7VJC2	YHTINGHNAEVR	**1.479921318**	2	3.44342
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.096444392**	**0.922462**	**2**
B0BN93	QMTDPNVALTFLEK	**1.09774679**	2	2.61394

B0BN93	SAWGQQPDLAANEAQLLR	**0.991171804**	2	4.05594
B0BN94	**F136A Protein FAM136A**	**1.250206289**	**0.999136**	**2**
B0BN94	CHAPLAQAQALVTSELER	**0.929928243**	2	3.15553
B0BN94	CSANCCEDNQASMQQVHQCIER	**1.037552834**	3	4.88723
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.082804575**	**1.52E-13**	**9**
B0BNE5	AFNGYLGPDQSK	**1.368509797**	2	3.45444
B0BNE5	AYDATCLVK	**1.113883066**	2	2.49289
B0BNE5	FAIYLPPQAESAK	**1.684448534**	2	3.34819
B0BNE5	LQEGYDHSYYFIATFITDHIR	**1.792444061**	3	3.80758
B0BNE5	MYSYVTEELPQLINANFPVDPQR	**1.014661029**	3	5.43004
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	**1.049688503**	2	5.70926
B0BNE5	SVSAFAPICNPVLCPWGK	**1.122189102**	2	4.04184
B0BNE5	SYSGPQIDILIDQGK	**1.098170141**	2	3.62574
B0BNE5	VFEHSSVELK	**1.152933671**	2	2.59602
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.523068439**	**0.302661**	**4**
B0BNN3	ADGLAIIGVLMK	**0.55817952**	2	3.15503
B0BNN3	GLLSSAEGEPAVPVLSNHRPPQPLK	**0.181566395**	3	3.38408
B0BNN3	HDSSLKPVSVSYNPATAK	**0.902631531**	3	4.41899
B0BNN3	VGPANPNLQK	**0.412293651**	2	2.92307
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**0.899493773**	**0.998891**	**3**
B0K020	AMVNLQIQK	**0.906006113**	2	2.36063
B0K020	HNEETGDNVGPLIIK	**1.059681131**	2	5.49959
B0K020	VVHAFDMEDLGDK	**0.869984417**	3	3.47449
B2GUY2	**TFR2 Transferrin receptor protein 2**	**1.536683675**	**0.059819**	**2**
B2GUY2	MEQRWGLLRK	**1.550852876**	2	2.30701
B2GUY2	SAVGTAILLELVR	**1.248079705**	2	2.4406
B2GV24	**UFL1 E3 UFM1_protein ligase 1**	**1.106049964**	**0.779027**	**2**
B2GV24	TYDLPGDFLTQALTQR	**1.055765995**	2	3.17073
B2GV24	VNIVDLQQVINVDLTHIENR	**1.052833144**	3	3.33381
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**0.833122177**	**0.920364**	**2**
B2RX88	SISSVNVDQVRMRNEDR	**0.807604596**	2	2.6603
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(11)	**0.98874865**		
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.936591149**	**0.634788**	**6**
B2RYW9	ALAAQLPLIPR	**0.94593879**	2	2.40873
B2RYW9	ATDVMAYVAGFTVAHDVSAR	**1.163284629**	3	3.82516
B2RYW9	GETALSVAR	**0.925039984**	2	2.42439
B2RYW9	KGDEVQCEIEELGVIINK	**0.86857019**	2	5.03075
B2RYW9	TFDTFCPLGPALVTK	**0.932257693**	2	4.60813
B2RYW9	VNGEIVQSSNTNQMVFK	**0.969187413**	2	2.63537
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.052428832**	**0.998541**	**4**
B3DMA2	AVLTVTQYR	**1.011456395**	2	2.52828
B3DMA2	LDNIVFHPK	**1.006031034**	2	2.45293
B3DMA2	NLPDSDNEECLVHGDFK	**1.103765825**	2	3.16352
B3DMA2	SGQSNPTFFLQK	**1.154860524**	2	2.7946
B3GNI6	**SEP11 Septin_11**	**1.18197436**	**0.779837**	**3**
B3GNI6	AAAQLLQSQAQQSGAQQTK	**1.079029452**	3	3.42321
B3GNI6	FESDPATHNEPGVR	**1.440662578**	2	3.34141
B3GNI6	SYELQESNVR	**0.952044917**	2	3.00715
B5DFC8	**EIF3C Eukaryotic translation initiation factor 3 subunit C**	**1.17574591**	**0.022219**	**3**
B5DFC8	GTEITHAVVIK	**1.059208961**	2	2.37089
B5DFC8	GTTEEICQIYLR	**1.124524409**	2	2.36632
B5DFC8	TEPTAQQNLALQLAEK	**1.197362971**	2	4.94246

D3ZTX0	**TMED7 Transmembrane emp24 domain_containing protein 7**	**1.101086307**	**0.08158**	**2**
D3ZTX0	QCFYEDITQGTK	**0.774703195**	2	2.48706
D3ZTX0	SVIDYQTHFR	**1.282415138**	2	2.50577
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.141452398**	**0.732141**	**4**
D3ZW55	IDLPEYQGEPDEISIQK	**1.01721701**	2	4.67356
D3ZW55	KLEEVIQILGDKFPCTLVAQK	**1.054531088**	3	4.06857
D3ZW55	LKPEGLYQLLAGFEDK	**1.691602863**	3	3.52354
D3ZW55	LQEYFGVTDGAGDH	**1.268693869**	2	3.56453
D3ZZL9	**GCC2 GRIP and coiled_coil domain_containing protein 2**	**1.235609577**	**0.079694**	**2**
D3ZZL9	ELNQKLTNKNSK	**1.179883111**	2	2.3759
D3ZZL9	IKCLQEESVVQCEELR	**1.237110574**	2	2.3554
D4A4T9	**CHRD1 Cysteine and histidine_rich domain_containing protein 1**	**1.218179278**	**0.011423**	**2**
D4A4T9	KEEDSDEIKIGTSCK	**1.31537508**	2	2.31747
D4A4T9	LSSGNEEDKKEEDSDEIK	**1.205629435**	3	4.32774
E9Q557	**DESP Desmoplakin**	**0.835044732**	**0.167606**	**2**
E9Q557	KQVQTSQKNTLR	**1.180906704**	1	2.11367
E9Q557	SQCTQVVQER	**0.679045684**	2	2.31605
F6YLP3	**selenium transferase**	**0.260334699**	**0.4188**	**3**
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**1.271239092**	**9.9E-20**	**8**
O08557	DENATLDGGDVLFTGR	**0.792449198**	2	3.3439
O08557	DYAVSTVPVADSLHLK	**1.341691696**	2	3.65431
O08557	GAEILADTFK	**1.153808577**	2	2.42515
O08557	GAEILADTFKDYAVSTVPVADSLHLK	**1.079734434**	3	3.7154
O08557	SFCSMAGPNLIAIGSSESAQK	**0.842602092**	2	4.94653
O08557	SQGEEVDFAR	**1.18894073**	2	2.82503
O08557	TPEEYPESAK	**3.106857558**	2	2.82332
O08557	VDGLLTCCSVFINK	**1.560224182**	2	3.50141
O08583	**THOC4 THO complex subunit 4**	**0.782337241**	**2.05E-07**	**2**
O08583	QQLSAEELDAQLDAYNAR	**0.705781804**	2	5.05844
O08583	SLGTADVHFER	**1.000650105**	2	2.51204
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.32095983**	**1.54E-13**	**13**
O08601	EDTTMYLLALK	**0.826556276**	2	2.36863
O08601	EFYSYENEPVGIENLK	**1.379777565**	2	4.14763
O08601	GCPSLAEHWKSIR	**1.2883043**	2	3.73204
O08601	GSFASNDIR	**1.189168466**	2	2.50625
O08601	MLSASGDPVSVVK	**1.087356381**	2	3.05082
O08601	MLSASGDPVSVVK+Oxidation(0)	**1.111867302**		
O08601	NALLPEGIPLLLK	**1.176930561**	1	2.37919
O08601	NILLSIGELPK	**1.136986961**	2	3.57962
O08601	REEILQILK	**1.108351631**	3	3.54571
O08601	SDSSIILQER	**1.24012625**	2	3.29804
O08601	SGSSSAYTGYVER	**1.317058312**	2	3.4231
O08601	SNLNIFQYIGK	**3.445220696**	2	3.61238
O08601	VKEFYSYENEPVGIENLK	**1.194363523**	2	2.8796
O08795	**GLU2B Glucosidase 2 subunit beta**	**0.907597605**	**0.861406**	**6**
O08795	ETVVTSTTEPSR	**1.143909317**	2	3.10963
O08795	KLWEEQQAAAK	**0.905724686**	2	2.92125
O08795	LWEEQQAAAK	**1.051243171**	2	3.33171
O08795	MPPYDEETQAIIDAAQEAR	**0.916652056**	2	3.1281
O08795	SLEDQVETLR	**1.26964912**	2	3.26087
O08795	YEQGTGCWQGPNR	**1.079727167**	2	4.04044

O08810	**U5S1 116 kDa U5 small nuclear ribonucleoprotein component**	**1.198738349**	**0.74022**	**2**
O08810	GGGQIIPTAR	**1.227321622**	2	2.63274
O08810	GLAEDIENEVVQITWNR	**0.971352497**	3	3.56997
O09158	**CP3AP Cytochrome P450 3A25**	**1.76203603**	**0.096184**	**3**
O09158	DVEINGVFIPK	**1.851295404**	2	3.15358
O09158	TLLSPTFTSGK	**1.137495428**	1	1.93756
O09158	VDFLQLMMNTQNSK	**1.4451854**	2	2.83952
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**2.395749784**	**9.9E-20**	**16**
O09171	AGAAIVGVNCHFDPSTSLQTIK	**1.740223987**	2	5.84023
O09171	AGPWTPEAAVEHPEAVR	**2.148905257**	2	5.08275
O09171	AGSNVMQTFTFYASEDK	**1.663238817**	2	2.91907
O09171	AGSNVMQTFTFYASEDKLENR	**4.140952136**	2	4.50672
O09171	EATTEQQLR	**1.23956357**	2	2.40755
O09171	GAAELMQQK	**1.901055226**	2	3.57105
O09171	GAAELMQQK+Oxidation(5)	**2.465898778**		
O09171	HGSWGSGLDMHTKPWIR	**1.245537849**	3	3.70591
O09171	IFHQQLEVFMK	**1.484482547**	2	2.75668
O09171	KEYWQNLR	**1.759769014**	3	3.80548
O09171	LNAGEVVIGDGGFVFALEK	**1.89606887**	3	6.24291
O09171	QGFIDLPEFPFGLEPR	**1.678504576**	2	5.35192
O09171	QVADEGDALVAGGVSQTPSYLSCK	**2.111869083**	3	6.35508
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	**1.677487081**	3	6.55271
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9)	**2.511136543**		
O09171	VNEAACDIAR	**1.743404503**	2	4.03569
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.304510081**	**1.33E-15**	**10**
O09173	CFYNSDGDFLIVPQK	**1.370859196**	2	2.94767
O09173	FSVDVFEETR	**1.472247468**	2	3.18825
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	**1.311682705**	3	5.98862
O09173	LLIYTEFGK	**1.939443816**	1	2.05452
O09173	NCMSEFMGLIK	**1.240393782**	2	3.41313
O09173	QDVSPFNVVAWHGNYTPYK	**1.514582057**	2	3.64792
O09173	QGGFLPGGGSLHSAMTPHGPDADCFEK	**1.141488337**	3	3.72045
O09173	SLRPGVAIADFVIFPPR	**1.092593509**	2	3.54394
O09173	TFRPPYYHR	**1.775571904**	3	3.34012
O09173	YISGFGNECASEDPR	**1.878110521**	2	3.99237
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.016461225**	**2.49E-07**	**19**
O35077	ANTIGISLIK	**1.082950709**	2	3.1733
O35077	DPAQGQLLK	**1.777318182**	2	2.41275
O35077	ELHSILQHK	**1.305011933**	1	2.95003
O35077	FCETTIGCK	**1.113137069**	2	2.62951
O35077	FCETTIGCKDPAQGQLLK	**1.073460794**	2	5.0546
O35077	GIDEGPNGLK	**0.984925484**	2	2.96492
O35077	GLVDKFPLFTAVYK	**1.533995919**	3	3.60747
O35077	ICDQLKGHLK	**0.768940152**	3	3.35961
O35077	ITVVQEVDTVEICGALK	**0.814698229**	3	4.4243
O35077	IVGSNASQLAHFDPR	**1.688239683**	2	3.14367
O35077	KLTEIINTQHENVK	**0.957434754**	2	5.10387
O35077	LISEVIGESLGIPMSVLMGANIASEVAEEK	**0.812517598**		
O35077	LPPNVVAVPDVVQAATGADILVFVVPHQFIGK	**1.559477622**	3	5.10066
O35077	LTEIINTQHENVK	**0.943210745**	2	4.51603
O35077	NIVAVGAGFCDGLGFGDNTK	**1.050529971**	2	5.42573
O35077	SIEQLEK	**0.98278714**	2	2.4705
O35077	VCIVGSGNWGSAIAK	**1.046211443**	2	4.707

O35077	VCYEGQPVGEFICCLQNHPEHM	**1.048044892**	2	3.92244
O35077	VTMWVFEEDIGGR	**1.275575177**	2	3.46768
O35078	**OXDA D_amino_acid oxidase**	**1.077444615**	**0.975563**	**2**
O35078	GQIIQVEAPWIK	**0.883930785**	2	3.20743
O35078	SCCQLEPTLK	**1.108423666**	2	2.42752
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.964660987**	**0.99993**	**2**
O35094	KLEESDALQEAR	**0.935947176**	2	3.35451
O35094	TEMSEVLTEILR	**1.037584184**	2	3.56669
O35142	**COPB2 Coatomer subunit beta_**	**1.02274495**	**0.807017**	**4**
O35142	AAESLADPTEYENLFPGLK	**1.188143207**	2	3.36393
O35142	FELALQLGELK	**1.021291896**	2	3.0438
O35142	GSNNVALGYDEGSIIVK	**1.206563154**	2	3.58758
O35142	TFEVCDLPVR	**0.932559489**	2	2.77056
O35244	**PRDX6 Peroxiredoxin_6**	**1.104550189**	**0.006052**	**10**
O35244	DINAYNGAAPTEK	**1.099148887**	2	3.94456
O35244	DLAILLGMLDPAEKDEK	**1.037018511**	2	4.31831
O35244	FHDFLGDSWGILFSHPR	**1.012390031**	3	3.84112
O35244	GESVMVLPTLPEEEAK	**0.922074486**	2	3.18174
O35244	KGESVMVLPTLPEEEAK	**0.922838745**	2	4.87444
O35244	KGESVMVLPTLPEEEAK+Oxidation(5)	**1.155218921**		
O35244	LSILYPATTGR	**1.420294628**	2	2.87687
O35244	NFDEILR	**0.846637493**	2	2.4402
O35244	VVDSLQLTASNPVATPVDWK	**0.971068993**	3	5.76442
O35244	VVFIFGPDKK	**1.828973397**	2	2.3859
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**1.151277359**	**0.987976**	**2**
O35469	DLGYEPLVSWEEAK	**1.379937406**	2	4.22585
O35469	TSEWIGTLVEQHR	**1.003291086**	2	3.48581
O35509	**RB11B Ras_related protein Rab_11B**	**1.055670496**	**0.601745**	**5**
O35509	AQIWDTAGQER	**0.983073742**	2	2.84259
O35509	GAVGALLVYDIAK	**1.040853757**	2	4.21682
O35509	HLTYENVER	**0.941427267**	2	3.01022
O35509	NEFNLESK	**1.216281756**	1	2.14975
O35509	VVLIGDSGVGK	**1.255314062**	2	2.70465
O35547	**ACSL4 Long_chain_fatty_acid__CoA ligase 4**	**0.816561206**	**0.122324**	**2**
O35547	LERFEIPIK	**0.817134643**	2	2.67969
O35547	LSPEPWTPETGLVTDAFK	**0.389248153**	2	2.72854
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**1.013532838**	**0.171356**	**8**
O35567	AEVSNAIDQYVTGTIGEGEDLVK	**0.927146668**	2	4.40875
O35567	ALFEEVPELLTEAEK	**1.189103938**	2	3.77446
O35567	DGQVIGIGAGQQSR	**0.990547346**	2	3.16803
O35567	EVSDGIVAPGYEEEALK	**0.951393227**	2	4.17112
O35567	HVSPAGAAVGVPLSEDEAR	**1.46666345**	2	3.51036
O35567	RAEVSNAIDQYVTGTIGEGEDLVK	**1.21839164**	3	3.74148
O35567	SGVAYIVAPSGSTADK	**1.151255906**	2	3.09706
O35567	VTVVCEPEDYGAVAAEMQGSGNK	**0.779833935**	2	5.27819
O35593	**PSDE 26S proteasome non_ATPase regulatory subunit 14**	**1.104914689**	**0.075304**	**2**
O35593	AVAVVVDPIQSVK	**1.110185477**	2	2.71278
O35593	VIDVFAMPQSGTGVSVEAVDPVFQAK	**0.403307006**	2	3.74656
O35660	**GSTM6 Glutathione S_transferase Mu 6**	**1.057648086**	**0.982535**	**2**
O35660	RYAMGDAPDYDR	**0.958855253**	2	3.131
O35660	YAMGDAPDYDR+Oxidation(2)	**1.380557964**		
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.577796804**	**0.137159**	**3**

O35760	AELGIPLEEVDLNEMNYLTR	**0.63648493**	2	4.26437
O35760	NCHLNENIDK	**0.499172302**	2	2.98886
O35760	NVTLNPDPNEIK	**0.56801018**	2	2.89706
O35763	**MOES Moesin**	**1.001792701**	**0.679269**	**2**
O35763	ALTSELANAR	**0.999249706**	2	3.17051
O35763	FYPEDVSEELIQDITQR	**0.7649495**	2	4.40084
O35783	**CALU Calumenin**	**0.969021522**	**0.978341**	**2**
O35783	HLVYESDQDKDGK	**0.981560914**	2	4.04578
O35783	VHNDAQNFDYDHDAFLGAEEAK	**0.820007619**	3	4.15033
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.342746801**	**1.43E-08**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	**1.039026251**	2	4.69842
O35796	AFVEFLTDEIK	**1.275684088**	2	3.62587
O35796	AFVEFLTDEIKEEK	**1.052940796**	2	3.57241
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	**1.730255856**	3	5.77035
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.079279688**	**0.843488**	**6**
O35814	ALDLDSSCK	**1.244369854**	2	2.36604
O35814	ALSAGNIDDALQCYSEAIK	**1.037267689**	2	5.29577
O35814	DCEECIQLEPTFIK	**0.964675838**	2	3.93301
O35814	ELIEQLQNKPSDLGTK	**1.113373558**	2	3.8667
O35814	LDPQNHVLYSNR	**2.44697274**	2	2.61357
O35814	LMDVGLIAIR	**1.032836536**	2	2.45177
O35820	**RCL Deoxyribonucleoside 5__monophosphate N_glycosidase**	**1.055918911**	**0.894824**	**2**
O35820	GGREDQALYAR	**0.900082513**	2	2.559
O35820	YFEAYLPQK	**1.061779515**	2	2.33407
O35821	**MBB1A Myb_binding protein 1A**	**1.089703417**	**0.969959**	**2**
O35821	ALDLIEVLVTK	**1.092075613**	2	3.05526
O35821	NVANVTPLTAQQR	**0.952884585**	2	3.02762
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**1.07583383**	**0.198217**	**2**
O35824	FDVQFPENNWINPDK	**0.555872143**	2	3.29125
O35824	NVLCSACSGQGGK	**1.076484553**	2	3.27264
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.04163181**	**0.74186**	**8**
O35826	DEAVGALHLIQAAK	**1.05920049**	2	3.47456
O35826	EVGAFGTPVINLGTR	**1.16095603**	2	2.86446
O35826	GEDEAAMVESVGLALVK	**1.139593919**	2	2.45338
O35826	IYGDGNAVPR	**0.917967272**	2	2.57769
O35826	SIDLQEPLQK	**1.077302274**	2	2.3736
O35826	TLVLFPNIDAGSK	**0.886566514**	2	3.09776
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	**0.853573937**	3	5.23593
O35826	VNPQEGVVLHSTK	**1.280336086**	2	2.54779
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.875837851**	**0.058043**	**5**
O35913	EGLQENVDGTENAK	**1.052741085**	2	3.66849
O35913	GASFVPAFFILR	**1.354504697**	2	2.69905
O35913	ILAGIPAPIYFGALIDR	**1.979186648**	2	2.41566
O35913	SLSGTYMNSMLTQIER	**0.778648049**	2	4.25926
O35913	SQTLNPTQDPSECVK	**0.874940101**	2	4.1755
O35923	**BRCA2 Breast cancer type 2 susceptibility protein homolog**	**0.741550678**	**0.026724**	**2**
O35923	AMKLFSDIENISEEPSTK	**0.71804696**	2	2.55222
O35923	SLLNEFDRIIESKGK	**0.675847885**	2	2.4239
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**0.916047838**	**0.999999**	**8**
O35952	ALLEVLGR	**1.004935913**	2	3.12064

O35952	FYEGTADEMYK	**0.894604037**	2	2.51641
O35952	HVEPGNTAVQEK	**1.232512384**	2	4.05564
O35952	LTTVLTTHHHWDHAGGNEK	**1.302812451**	3	3.91359
O35952	NAIGEPTVPSTLAEEFTYNPFMR	**1.017292011**	2	3.54778
O35952	TVQQHAGETDPVTTMR	**0.956132301**	2	5.10413
O35952	TVQQHAGETDPVTTMR+Oxidation(14)	**1.043256245**		
O35952	VTHLSTLEVGSLSVK	**1.123774525**	2	2.88358
O35987	**NSF1C NSFL1 cofactor p47**	**0.972953102**	**2.27E-05**	**6**
O35987	ASSSILINEAEPTTNIQIR	**0.945056791**	2	5.33631
O35987	EANLLNAVIVQR	**1.419873452**	2	3.3703
O35987	LGAAPEEESAYVAGER	**1.112535634**	2	4.02134
O35987	LGSTAPQVLNTSSPAQQAENEAK	**1.289569037**	2	3.96866
O35987	RGEVPAELR	**2.93578189**	2	2.47108
O35987	SYQDPSNAQFLESIR	**1.056907271**	2	4.48866
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.608165101**	**0.035772**	**3**
O54753	CSTNLSLVTDCMEHALTSK	**1.73279515**	3	3.3951
O54753	TWEATPEHIR	**1.580446626**	2	2.31051
O54753	YGVEAFSDVLR	**1.438534949**	2	2.72709
O54975	**XPP1 Xaa_Pro aminopeptidase 1**	**1.117571001**	**0.316197**	**2**
O54975	GSLTFEPLTLVPIQTK	**1.12149705**	2	4.04187
O54975	IENVVLVVPAK	**0.971668129**	2	2.89517
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.058419562**	**0.274915**	**5**
O55012	ATTLSNAVSSLASTGLSLTK	**0.947900417**	2	3.83908
O55012	ITAAQHSVTGSAVSK	**1.464593615**	2	4.30268
O55012	NTLFNLSNFLDK	**1.074558155**	2	2.54018
O55012	SGLQGYDMSTFIR	**1.211884291**	2	2.36162
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	**0.94436296**	3	5.65878
O55096	**DPP3 Dipeptidyl peptidase 3**	**1.026808474**	**0.014799**	**6**
O55096	AGLLALEFYTPETANWR	**1.219149414**	2	3.92276
O55096	GEFEGFVAMVNK	**1.112191455**	2	3.07586
O55096	LASVLNTEPALDSELTSK	**2.163195737**	2	3.38428
O55096	NVSLGNVLAVAYATK	**1.023353606**	2	2.38712
O55096	SYEFQGNHFQVTR	**1.239055023**	2	3.81956
O55096	VLLEAGEGLVTVTPTTGSDGRPDAR	**1.02826569**	3	3.40217
O55125	**NIPS1 Protein NipSnap homolog 1**	**1.173629315**	**1.29E-09**	**4**
O55125	AGPNIYELR	**1.071694409**	2	3.04349
O55125	FSGGYPALMDCMNK	**1.10699748**	2	3.13302
O55125	GWDENVYYTVPLVR	**1.682188822**	2	3.45838
O55125	IQFHNVKPECLDAYNSLTEAVLPK	**1.741790454**	3	4.36804
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.141346279**	**0.989002**	**6**
O55171	ADAGGELDLAR	**0.93081466**	2	3.27675
O55171	DGLLDVVEALQSPLVDKK	**1.159437979**	2	5.07103
O55171	DVQKPYVVELEVLDGHEPDGGQR	**0.909676326**	3	4.46677
O55171	GGELGLAMASFLK	**1.076762348**	2	3.84753
O55171	IEYFEEAVNYLR	**1.114116537**	2	4.19181
O55171	SCWDEPLSITVR	**0.965385003**	2	3.49113
O70127	**ABCBB Bile salt export pump**	**1.411652578**	**6.91E-07**	**8**
O70127	AGQITSEALSNIR	**1.275414383**	2	3.28838
O70127	AGSIADEVLSSIR	**1.522557619**	2	2.63903
O70127	ILDNLSMVIKPGETTALVGSSGAGK	**1.413868306**	3	4.16927
O70127	ILLLDEATSALDTESEK	**1.60718601**	2	4.18128
O70127	KFGEENHAFESDGSHNNDKK	**1.056350766**	3	3.93335
O70127	KPPINVYSEAGEK	**2.292530983**	2	3.31695
O70127	STALQLIQR	**1.495465874**	2	2.35064

O70127	YETNVGIQGSQLSR	1.156610491	2	3.46657
O70133	**DHX9 ATP_dependent RNA helicase A**	**0.783378743**	**0.000131**	**2**
O70133	KMTPAYEIRAVGNK	0.532097388	2	2.56552
O70133	YPSPFFVFGEKIR	1.041470411	2	2.5007
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**1.134439018**	**9.9E-20**	**11**
O70199	EQIVVDLSHPGVSADDQVSR	1.044536324	2	5.6714
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	1.374974718	3	5.21124
O70199	IIDSLFNTVTDK	1.078538347	2	2.87754
O70199	IIDSLFNTVTDKK	1.11681453	2	3.54353
O70199	ILTTNTWSSELSK	1.668849302	2	3.34286
O70199	INAWNSPTLPIYEPGLK	1.377335121	2	3.72862
O70199	NLFFSTNIDDAIR	1.365677505	2	3.14745
O70199	VLDGLHNELQTIGFQIETIGK	1.05004829	2	5.3351
O70199	VLIGGDETPEGQR	1.116920137	2	3.61672
O70199	VTVVDVNEAR	0.995708599	2	3.36335
O70199	YWQQVIDMNDYQR	0.925731235	2	4.83384
O70251	**EF1B Elongation factor 1_beta**	**1.109462111**	**0.001282**	**4**
O70251	SIQADGLVWGSSK	1.124069374	2	3.76508
O70251	SSILLDVKPWDDETDMTK	0.950548539	2	4.20245
O70251	SSILLDVKPWDDETDMTKLEECVR	0.945444015	3	5.13022
O70251	TPAGLQVLNDYLADK	1.77731112	2	4.09576
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.138528732**	**9.9E-20**	**16**
O70351	GGIVGMTLPIAR	0.83034066	2	3.35658
O70351	GLVAVITGGASGLGLSTAK	1.035266154	2	4.69011
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.319436015	3	4.10047
O70351	IDVAVNCAGIAVAIK	0.903098756	2	3.97747
O70351	KLGGNCIFAPANVTSEK	1.145014568	2	4.46895
O70351	KNQVHTLEDFQR	1.077271469	2	4.11424
O70351	LGDPAEYAHLVQMVIENPFLNGEVIR	1.259930164	3	4.31589
O70351	LGGNCIFAPANVTSEK	1.436572992	2	3.48617
O70351	LVAGVMGQNEPDQGGQR	1.315032253	2	5.22759
O70351	LVAGVMGQNEPDQGGQR+Oxidation(5)	1.065335978		
O70351	LVGQGATAVLLDVPNSEGETEAK	1.766103936	2	5.67453
O70351	NFLASQVPFPSR	1.008959037	2	4.55929
O70351	NQVHTLEDFQR	1.020272158	2	3.31039
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.165444979	2	5.04043
O70351	VINVNLIGTFNVIR	1.159453813	2	3.79679
O70351	VVTIAPGLFATPLLTTLPDK	1.234711674	2	5.42001
O70456	**1433S 14_3_3 protein sigma**	**1.09202373**	**1.05E-08**	**3**
O70456	DSTLIMQLLR	1.386113183	2	3.4124
O70456	DSTLIMQLLR+Oxidation(5)	1.406006181		
O70456	VLSSIEQK	1.095836557	2	3.25466
O70593	**SGTA Small glutamine_rich tetratricopeptide repeat_containing protein alpha**	**1.236628682**	**0.10566**	**2**
O70593	AIELNPANAVYFCNR	1.552103322	2	3.00236
O70593	TPPSEEDSAEAER	1.193826847	2	2.71005
O88202	**LPP60 60 kDa lysophospholipase**	**1.050194728**	**0.044655**	**2**
O88202	AAGAHLSPQELEDVGTELCR	1.164322368	3	3.69083
O88202	GVDVDACNEDGQSPLLLAVR	1.158537285	2	5.22409
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**0.915158767**	**0.995972**	**5**
O88428	GCTVWLTGLSGAGK	0.915037145	2	2.84848
O88428	GIHELFVPENK	1.030698954	2	2.61167
O88428	NLGFSAGDREENIR	1.014312024	2	3.36161
O88428	STNVVYQAHHVSR	1.209724943	2	3.47406
O88428	VLSMAPGLTSVEIIPFR	0.851268436	2	3.31625

O88491	**NSD1 Histone_lysine N_methyltransferase_ H3 lysine_36 and H4 lysine_20 specific**	**0.527041429**	**4.04E-06**	**2**
O88491	ENSEGAFGVLLPADAVQKAR	**0.45617646**	2	2.34428
O88491	SGKGEGLKLLNNMHEK	**1.657438563**	2	2.90662
O88600	**HSP74 Heat shock 70 kDa protein 4**	**0.885656652**	**0.35649**	**14**
O88600	AESEEMETSQAGSK	**0.853260696**	2	4.51478
O88600	AGGIETIANEYSDR	**1.059196641**	2	3.46386
O88600	FQESEERPK	**0.527861241**	2	2.3281
O88600	GCALQCAILSPAFK	**0.98496649**	2	4.04677
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	**1.267650601**	3	5.23913
O88600	LKETAESVLK	**0.769515566**	2	2.46405
O88600	MIMQDKLEK+Oxidation(0)	**0.923436278**		
O88600	MQVDQEEPHTEEQQPQTPAENK	**1.224375726**	3	4.74823
O88600	NFTTEQVTAMLLSK	**0.929885681**	2	3.70579
O88600	SNLAYDIVQLPTGLTGIK	**1.099035445**	2	4.94582
O88600	SVMDATQIAGLNCLR	**0.948054201**	2	2.88958
O88600	TSTVDLPIESQLLWQLDR	**0.965028703**	2	3.83491
O88600	VLATAFDTTLGGR	**1.098423123**	2	3.4794
O88600	WNSPAEEGSSDCEVFPK	**0.800595833**	2	3.41448
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.26529763**	**9.9E-20**	**21**
O88618	AFAACLGAIK	**0.979497979**	2	2.88968
O88618	AGEYEALPEK	**1.174736366**	2	2.86383
O88618	ALLDAAAFYCDK	**1.374366893**	2	3.46717
O88618	ALLDAAAFYCDKEK	**0.878009286**	2	3.33453
O88618	EAQELNLPVVGSQLVGLVPLK	**1.462756055**	3	4.04388
O88618	GVSMDECVLCAK	**1.167980036**	2	3.90697
O88618	IIEYLVPDSGPEQSLLDASLR	**1.238992702**	2	5.13328
O88618	ISSLLQEAK	**1.682225339**	2	2.71139
O88618	LAEELNVPVYLYGEAAQMPSR	**1.605478106**	2	4.97521
O88618	LAETVSQLWPALQELAQCGNLSCLSDLQVAAK	**1.617788076**	4	5.01257
O88618	LFVLEEEHR	**0.663479076**	2	2.76659
O88618	LGLDSLAPFDPK	**1.253402195**	2	3.64034
O88618	LIPPFHAASAQLTSLVDADAR	**1.611456723**	3	3.55482
O88618	MGALDVCPFIPVR	**0.972224744**	2	3.79445
O88618	MGALDVCPFIPVR+Oxidation(0)	**0.929093885**		
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	**1.442938265**	3	4.50577
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	**1.388626809**	2	4.15659
O88618	TCALQEGLR	**1.567167636**	2	2.87365
O88618	TQAALVLGSLEAR	**1.05647854**	2	5.06596
O88618	TVYTFVGQPECVVEGALSAAR	**2.43314298**	2	4.85422
O88618	VQGIGWYLEEK	**1.198670513**	2	3.18291
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.214693286**	**0.005601**	**5**
O88637	GPPVFTQEER	**1.147930144**	2	2.73447
O88637	HKGPPVFTQEER	**1.105811992**	2	2.62439
O88637	TQGVSTTDLVGR	**1.138494211**	2	2.77142
O88637	WVDEVVPAAPYVTTLETLDK	**1.267597853**	2	3.14246
O88637	YVSEVVIGAPYSVTAELLNHFK	**1.150274202**	3	3.42552
O88656	**ARC1B Actin_related protein 2/3 complex subunit 1B**	**0.915028906**	**0.966104**	**2**
O88656	ASSEGGAATGAGLDSLHK	**0.915010245**	2	4.38491
O88656	NSVSQISVLSGGK	**0.950521921**	2	2.44763
O88696	**CLPP Putative ATP_dependent Clp protease proteolytic subunit_ mitochondrial**	**0.957760336**	**0.628432**	**2**
O88696	GQATDIAIQAEEIMK	**1.001256771**	2	3.61874
O88696	VLVHPPQDGEDEPELVQK	**1.078529077**	3	4.49923
O88746	**TOM1 Target of Myb protein 1**	**1.045535399**	**0.646704**	**3**

O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	**0.893015125**	3	5.87624
O88746	QQSTGAIPATQAR	**1.066424064**	2	2.61495
O88746	YEAPQTTDGLAGALDAR	**1.063262619**	2	4.19948
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.612473989**	**0.022862**	**4**
O88761	DTSEDIEELVEPVAAHGPK	**0.901131259**	2	3.81846
O88761	QCVENADLPEGEK	**1.051571239**	2	2.50199
O88761	TPEQCPSVVSLLSESYNPHVR	**1.614824592**	3	4.43877
O88761	TVGTPIASVPGSTNTGTVPGPEK	**1.086563799**	2	3.73329
O88767	**PARK7 Protein DJ_1**	**0.967810718**	**0.045308**	**6**
O88767	DVVICPDTSLEEAK	**1.465147142**	2	3.31286
O88767	GAEEMETVIPVDIMR	**0.893431646**	2	4.05
O88767	GAEEMETVIPVDIMR+Oxidation(13)	**0.711491626**		
O88767	GLIAAICAGPTALLAHEVGFGCK	**0.990304297**	2	4.89735
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	**0.994979091**	2	4.7234
O88767	VTVAGLAGKDPVQCSR	**0.828937678**	2	4.44527
O88794	**PNPO Pyridoxine_5__phosphate oxidase**	**1.231261037**	**0.174264**	**2**
O88794	KKNEELGQLYR	**1.408270961**	2	2.77987
O88794	SSQIGAVVSR	**0.87208974**	2	2.89101
O88801	**HOME2 Homer protein homolog 2**	**0.90339461**	**0.043642**	**2**
O88801	EKEMELK	**0.967277009**	1	2.10689
O88801	EKNTQLK	**0.39734663**	1	2.02013
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**0.935312038**	**5.66E-15**	**15**
O88813	AILEDLQK	**0.966799316**	1	2.4232
O88813	ATMLIENVEK	**0.978532365**	2	2.37086
O88813	ATMLIENVEKDLTPGLK	**1.139076829**	2	2.45119
O88813	ATMLIENVEKDLTPGLK+Oxidation(2)	**0.91721163**		
O88813	FFQTQIK	**0.760990978**	1	1.99106
O88813	GLAVSDNGPCLGYR	**0.882819823**	2	3.81037
O88813	GSFEELCQNQCVK	**0.952703892**	2	4.28746
O88813	IGFFQGDIR	**1.581841934**	2	3.32143
O88813	LVQGVIFSCGGK	**1.804070857**	2	2.86649
O88813	NNDLILYYFSDAK	**0.928966447**	2	3.72462
O88813	SFLIGVVVPDPESLPSFAAK	**0.817355119**	2	4.33025
O88813	SIFVHPEPFSIENGLLTPTLK	**1.620397594**	2	3.03253
O88813	SRPILQVFVHGESLR	**1.845436224**	3	3.86181
O88813	TQEVLDKDGWLHTGDIGR	**0.769712708**	3	4.39194
O88813	TVILMDPFDDDLMK	**0.715331996**	2	3.12883
O88867	**KMO Kynurenine 3_monooxygenase**	**0.973761795**	**0.407914**	**4**
O88867	AVGLEDQIVSK	**0.884654972**	2	2.65423
O88867	DLLTAVESYPNAK	**1.009585248**	2	2.79264
O88867	NFPDAIPLMGEQALMR	**1.081203466**	2	2.86232
O88867	NFQVDVYEAR	**0.940607118**	2	2.88841
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**1.284789253**	**8.92E-06**	**4**
O88941	DLALPTLLNPK	**1.122761716**	2	2.52993
O88941	DQASEQLVGGQLTR	**1.267416527**	2	2.9052
O88941	LGPLLDVLADSR	**1.311057268**	2	3.29382
O88941	MDPSLFPPVPLFSGVPSR	**1.094270067**	2	2.71819
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**1.017591602**	**0.607502**	**2**
O88986	GTDELLGVMDQVTIINSTLGK	**1.055643897**	2	3.31637
O88986	HLDMADLEAK	**0.788628707**	2	2.3152
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.21859756**	**9.9E-20**	**8**
O88989	DLDVAVLVGSMPR	**1.513174255**	3	4.05575
O88989	ELTEEKETAFEFLSSA	**2.590805296**	2	3.70394
O88989	EVGVYEALKDDSWLK	**1.418949667**	2	3.7522
O88989	FVEGLPINDFSR	**1.107967707**	2	3.63088

O88989	GEFITTVQQR	**1.207270934**	2	4.27014
O88989	LGVTADDVK	**1.420812608**	2	2.85596
O88989	NVIIWGNHSSTQYPDVNHAK	**1.317991938**	2	5.61903
O88989	VIVVGNPANTNCLTASK	**1.362235095**	2	5.38911
O88990	**ACTN3 Alpha_actinin_3**	**1.096579154**	**4.45E-13**	**12**
O88990	AGTQIENIEEDFR	**0.87822979**	2	3.57939
O88990	CQAICDQWDNLGTLTQK	**0.390751406**	2	5.16803
O88990	CQLEINFNTLQTK	**1.131147027**	2	4.11822
O88990	FAIQDISVEETSAK	**0.686511146**	2	3.66422
O88990	GKEEMLNQHDYESASLQEVR	**1.012315637**	3	4.78458
O88990	GLSQEQLNEFR	**0.323125269**	2	2.60865
O88990	HEAFESDLAAHQDR	**0.786391282**	3	4.49843
O88990	RHEAFESDLAAHQDR	**0.09175148**	3	4.79857
O88990	SGNPYITLSSQDINNK	**0.798392683**	2	3.80295
O88990	VEHIAALAQELNELDYHEAASVNSR	**1.336864508**	3	4.12423
O88990	VGWEQLLTSIAR	**0.815814535**	2	2.56304
O88990	VLAVNQENEK	**0.144924968**	2	2.4908
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.716641017**	**0.529983**	**2**
O88994	CVLTTVDPDTGIIDR	**0.71420254**	2	4.11147
O88994	RQLQQVGTVSK	**0.745204585**	2	2.50264
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**1.047611567**	**0.55128**	**7**
O89000	EGGADGVTATNTVSGLMGLK	**0.895995969**	2	3.8297
O89000	GAVIVLGAGDTAFDCATSALR	**1.420081761**	2	2.31492
O89000	GMGLACGQDPELVR	**1.138537127**	2	3.18841
O89000	GTTSGPLYGPGQSSFLNIELISEK	**1.368991956**	2	3.51943
O89000	LTPNVTDIVSIAR	**1.468129763**	2	2.34979
O89000	QEYVGGLSTSEIPQFR	**1.034451187**	2	3.62112
O89000	TEQDETGNWVEDEEQIVR	**1.023755135**	2	4.71943
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**1.241436323**	**0.325688**	**2**
O89032	DDSDINTSKTGEVSKR	**1.392997292**	2	2.54739
O89032	EGWAPASYIDKRK	**1.026880815**	1	1.97345
O89046	**COR1B Coronin_1B**	**1.235096068**	**1.16E-07**	**3**
O89046	NDQCYEDIR	**0.941630915**	2	2.82929
O89046	NVLSDSKPAGYSR	**1.278097043**	2	3.12985
O89046	SGVSTATAITDIPSGNLAGSGEAGK	**0.596673147**	2	3.81456
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.239425581**	**0.059684**	**6**
O89049	IEQIEAGTPGR	**0.978294174**	2	3.42082
O89049	IEQIEAGTPGRLK	**0.924742019**	2	2.45242
O89049	LELTPVAIQAGR	**1.194920023**	2	2.66957
O89049	STNSEETIEDEFNTVLLAVGR	**1.155547987**	2	4.22869
O89049	VVGFHVLGPNAGEVTQGFAAALK	**0.967422146**	3	4.03513
O89049	WGLGGTCVNVGCIPK	**0.78848918**	2	2.92206
P00173	**CYB5 Cytochrome b5**	**1.007457734**	**0.999996**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	**1.056220013**	2	5.4402
P00173	FLEEHPGGEEVLR	**0.985002787**	2	4.33106
P00173	STWVILHHK	**0.931797279**	2	2.79306
P00173	TYIIGELHPDDR	**1.018828437**	2	4.24473
P00173	VYDLTK	**0.954186212**	1	2.13506
P00173	YYTLEEIQK	**1.039063104**	2	3.01781
P00388	**NCPR NADPH__cytochrome P450 reductase**	**2.32817399**	**9.9E-20**	**12**
P00388	DGALTQLNVAFSR	**0.748372451**	2	2.41812
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	**1.689625908**	3	4.79523
P00388	FAVFGLGNK	**2.170571585**	2	2.50869
P00388	GMSADPEEYDLADLSSLPEIDK	**1.328371862**	2	5.05551

P00388	GVATSWLR	**1.624050511**	2	2.33693
P00388	LEQLGAQR	**1.607323423**	2	2.64041
P00388	NIIVFYGSQTGTAEEFANR	**2.459279961**	2	3.17912
P00388	RSDEDYLYR	**1.295663107**	2	3.36437
P00388	SDEDYLYR	**1.604062066**	2	2.6083
P00388	SYENQKPPFDAK	**1.666356645**	2	3.25428
P00388	TALTYYLDITNPPR	**1.302804245**	2	2.50623
P00388	TNVLYELAQYASEPSEQEHLHK	**2.376665122**	3	3.68566
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.126193869**	**0.022216**	**5**
P00406	ILYMMDEINNPVLTVK	**0.557097266**	2	2.30773
P00406	LLEVDNR	**1.349301256**	2	2.52598
P00406	MLISSEDVLHSWAIPSLGLK	**0.500055332**	2	3.57027
P00406	VVLPMELPIR	**1.051283476**	2	2.68075
P00406	VVLPMELPIR+Oxidation(4)	**1.546664376**		
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**0.968478266**	**2.03E-09**	**16**
P00481	FGMHLQAATPK	**1.041204897**	3	4.12962
P00481	GEYLPLLQGK	**0.877568094**	2	3.21105
P00481	GGNVLITDTWISMGQEDEK	**1.354117583**	2	4.99595
P00481	GGNVLITDTWISMGQEDEKK	**1.476837308**	2	4.64028
P00481	GLTLSWIGDGNNILHSIMMSAAK	**1.397339796**	2	4.19529
P00481	GYEPDPNIVK	**0.988238231**	2	2.69013
P00481	KPEEVDDEVFYSPR	**3.262545503**	2	3.52652
P00481	LQAFQGYQVTMK	**1.620546512**	2	3.83999
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	**1.242414162**	3	5.76135
P00481	QKGEYLPLLQGK	**1.162584341**	2	2.9941
P00481	SLGMIFEK	**0.757714382**	2	2.4414
P00481	SLVFPEAENR	**1.070681708**	2	2.64933
P00481	SLVFPEAENRK	**1.102807769**	2	2.95112
P00481	VLSSMTDAVLAR	**0.975960879**	2	3.9806
P00481	VLSSMTDAVLAR+Oxidation(4)	**1.34416321**		
P00481	YGKPVQSQVQLK	**0.310169973**	2	3.00472
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.889531422**	**1**	**2**
P00502	FIQSPEDLEK	**0.697253224**	2	2.58729
P00502	WLLAAAGVEFDEK	**0.782122783**	2	4.32668
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**1.071401982**	**7.77E-16**	**18**
P00507	ASAELALGENSEVLK	**1.100581871**	2	4.69834
P00507	DAGMQLQGYR	**1.454926767**	2	3.03907
P00507	DDNGKPYVLPSVR	**1.143568366**	2	2.74083
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	**2.164076177**	3	5.41396
P00507	EYLPIGGLADFCK	**1.13908381**	2	2.81936
P00507	FVTVQTISGTGALR	**0.971082711**	2	5.03945
P00507	HFIEQGINVCLCQSYAK	**0.987004727**	2	4.52258
P00507	IAATILTSPDLR	**3.362646075**	2	3.09374
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	**1.985367243**	3	4.31031
P00507	ISVAGVTSGNVGYLAHAIHQVTK	**1.30326586**	2	4.78293
P00507	KQWLQEVK	**0.97870118**	1	2.13861
P00507	MNLGVGAYR	**0.931526501**	2	2.9346
P00507	NLDKEYLPIGGLADFCK	**1.069751909**	2	5.33837
P00507	NMGLYGER	**0.933683952**	2	2.5068
P00507	TCGFDFSGALEDISK	**1.169391234**	2	4.8215
P00507	TQLVSNLK	**0.977634933**	2	2.96101
P00507	VGAFTVVCK	**1.13839158**	2	3.36723
P00507	VGASFLQR	**1.405710082**	2	3.00444
P00564	**KCRM Creatine kinase M_type**	**0.757251259**	**9.9E-20**	**11**
P00564	DLFDPIIQDR	**0.825048982**	2	2.49012

P00564	FEEILTR	0.096886286	2	2.46994
P00564	GGDDLDPNYVLSSR	0.095616615	2	4.79852
P00564	GQSIDDMIPAQK	0.022094855	2	3.37611
P00564	GTGGVDTAAVGAVFDISNADR	0.081733294	2	6.06708
P00564	LGSSEVEQVQLVVDGVK	0.124564155	2	4.91821
P00564	LSVEALNSLTGEFK	0.204146082	2	4.33885
P00564	RGTGGVDTAAVGAVFDISNADR	0.109891318	2	5.88377
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	0.101164572	3	5.87281
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR+Oxidation(1)	0.173413785		
P00564	TDLNHENLK	0.528970444	2	2.52915
P00787	**CATB Cathepsin B**	**1.189942824**	**0.002645**	**5**
P00787	GENHCGIESEIVAGIPR	1.156148789	2	4.52138
P00787	HEAGDVMGGHAIR	1.037447715	3	3.56083
P00787	HEAGDVMGGHAIR+Oxidation(6)	1.828301615		
P00787	MCEAGYSTSYKEDK	1.196359924	2	3.88089
P00787	NGPVEGAFTVFSDFLTYK	1.546199669	2	3.26154
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.25176293**	**9.9E-20**	**19**
P00884	ALQASALAAWGGK	1.293584383	2	4.8602
P00884	ATQEAFMK	1.181162478	2	2.60943
P00884	ATQEAFMK+Oxidation(6)	1.799296586		
P00884	ELLFSVDNSISQSIGGVILFHETLYQK	2.241439678	3	3.79471
P00884	ELSEIAQR	3.203456624	1	2.11532
P00884	ETTIQGLDGLSER	1.401499599	2	4.0252
P00884	GILAADESVGTMGNR	1.139110949	2	5.58412
P00884	GILAADESVGTMGNR+Oxidation(11)	1.48777494		
P00884	GIVVGIKLDQGGAPLAGTNK	1.194803567	2	3.46573
P00884	IKVENTEENR	1.499772529	2	2.4781
P00884	IKVENTEENRR	1.267741598	2	2.9236
P00884	ISDQCPSSLAIQENANALAR	1.17555975	2	6.21831
P00884	KELSEIAQR	0.591359401	2	2.84368
P00884	KYTPEQVAMATVTALHR	1.031249434	3	5.70602
P00884	KYTPEQVAMATVTALHR+Oxidation(8)	1.341647793		
P00884	LDQGGAPLAGTNK	1.2336705	2	4.59691
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	2.088994786	3	4.99949
P00884	YTPEQVAMATVTALHR	1.062488712	2	4.5543
P00884	YTPEQVAMATVTALHR+Oxidation(7)	0.809841709		
P01015	**ANGT Angiotensinogen**	**1.031415572**	**0.467465**	**3**
P01015	GSYNLQDLLAQAK	1.009585248	2	2.80368
P01015	SLDLSTDPVLAAQK	1.049680419	2	3.31712
P01015	STCAQLENPSVETLPEPTFEPVPIQAK	0.243682552	2	3.91577
P01026	**CO3 Complement C3**	**1.099496295**	**0.356344**	**17**
P01026	AAVFNHFISDGVK	1.22940009	2	2.35479
P01026	ACEPGVDYVYK	0.871163597	2	2.57538
P01026	ADIGCTPGSGK	0.984395737	2	2.8417
P01026	DSCVGTLVVKGDPR	0.808250319	2	2.40944
P01026	EYVLPSFEVLVEPTEK	0.942212868	2	3.25405
P01026	IFTVDNNLLPVGK	0.931226291	2	3.10525
P01026	IGLQEVEVK	1.131859479	2	2.38234
P01026	RVPVVTQGSDAQALTQDDGVAK	1.166708358	3	5.53011
P01026	SGIPIVTSPYQIHFTK	1.516371106	2	3.20962
P01026	SGSDEVQAGQER	1.293918483	2	4.08483
P01026	SSVAVPYVIVPLK	1.649342992	2	3.15132
P01026	TVLTGATGHLNR	1.075865142	2	3.09662
P01026	VELKPGDNLNVNFHLR	1.160891613	3	5.34108
P01026	VHQFFNVGLIQPGSVK	1.585876303	3	3.97146
P01026	VLIEDGSGEAVLSR	1.074145817	2	4.53024

P01026	VPVVTQGSDAQALTQDDGVAK	**1.273705585**	2	5.9039
P01026	VTIKPAPETAK	**0.986932504**	2	2.53537
P01048	**KNT1 T_kininogen 1**	**0.57883875**	**0.3504**	**2**
P01048	FSVATQICNITPGK	**0.623690738**	2	2.84336
P01048	TELTADCETK	**0.332211177**	2	2.37923
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.53023819**	**7.46E-12**	**9**
P01946	AADHVEDLPGALSTLSDLHAHK	**0.450847031**	3	7.32668
P01946	FLASVSTVLTSK	**0.373500995**	2	3.90276
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDK	**0.46613773**	4	4.65393
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	**0.453926576**	4	6.33036
P01946	IGGHGGEYGEEALQR	**0.344973636**	3	4.87089
P01946	LRVDPVNFK	**0.565622853**	2	2.58322
P01946	MFAAFPTTK	**0.479367214**	2	2.74522
P01946	MFAAFPTTK+Oxidation(0)	**0.397118027**		
P01946	TYFSHIDVSPGSAQVK	**0.497237771**	2	5.17535
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.36749882**	**2.85E-06**	**4**
P02089	GTFASLSELHCDK	**0.42569313**	2	3.17864
P02089	LHVDPENFR	**0.445806385**	2	2.63354
P02089	YFDSFGDLSSASAIMGNPK	**0.338193842**	2	6.34342
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14)	**0.292200669**		
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.519341304**	**0.000244**	**9**
P02091	AAVNGLWGK	**0.770967069**	2	2.59375
P02091	EFTPCAQAAFQK	**0.460018932**	2	2.99166
P02091	GTFAHLSELHCDK	**0.507268649**	2	4.27486
P02091	GTFAHLSELHCDKLHVDPENFR	**0.436553553**	3	3.48348
P02091	KVINAFNDGLK	**0.460522845**	3	3.68183
P02091	LLGNMIVIVLGHHLGK	**0.506376984**	4	4.79843
P02091	VINAFNDGLK	**0.450843537**	2	2.89435
P02091	VNPDDVGGEALGR	**0.312721903**	2	4.02789
P02091	VVAGVASALAHK	**0.49849401**	2	3.61392
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.396641139**	**9.9E-20**	**6**
P02401	ILDSVGIEADDER	**1.408270706**	2	4.59749
P02401	KILDSVGIEADDER	**1.473566327**	2	3.83042
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	**1.470287791**	3	6.3062
P02401	NIEDVIAQGVGK	**1.130240782**	2	4.72221
P02401	VISELNGK	**1.211178188**	1	2.05421
P02401	YVASYLLAALGGNSNPSAK	**1.512823934**	2	4.93025
P02563	**MYH6 Myosin_6**	**0.721770191**	**0.117644**	**3**
P02563	DTQLQLDDAVR	**0.929548779**	2	2.67683
P02563	VKLEQQVDDLEGSLEQEK	**0.311258303**	2	5.15723
P02563	VKLEQQVDDLEGSLEQEKK	**0.253008924**	3	3.49429
P02564	**MYH7 Myosin_7**	**0.406781096**	**9.9E-20**	**42**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	**0.055520002**	3	6.34464
P02564	ANDDLKENIAIVER	**0.286848929**	2	3.52503
P02564	AQLEFNQIK	**0.176394886**	1	1.95812
P02564	DLEEATLQHEATAAALR	**0.250198736**	2	5.20258
P02564	DTQIQLDDAVR	**0.929548779**	2	2.67683
P02564	EDQVMQQNPPK	**0.595808942**	2	3.24456
P02564	ELENELEAEQKR	**0.299564229**	2	2.88208
P02564	EQYEEETEAK	**0.257216453**	1	3.03225
P02564	GQNVQQVAYAIGALAK	**0.369337329**	2	3.7596
P02564	GTLEDQIIQANPALEAFGNAK	**0.577596457**	2	5.24874
P02564	IEDEQALGSQLQK	**0.246845055**	2	4.53707
P02564	IEELEEELEAER	**0.05757179**	2	4.26683
P02564	ILNPAAIPEGQFIDSR	**0.201283378**	2	2.54741
P02564	KLAEKDEEMEQAK	**0.192113206**	2	3.77528

P02564	KLAEQELIETSER	**0.434726838**	2	3.5342
P02564	KLEDECSELKR	**0.215966486**	3	3.4455
P02564	KVQHELDEAEER	**0.092361136**	2	3.54145
P02564	LAEQELIETSER	**0.582678314**	2	3.79983
P02564	LDEAEQIALK	**0.146736204**	2	3.96244
P02564	LEEAGGATSVQIEMNK	**0.853511142**	2	4.3692
P02564	LELDDVTSNMEQIIK	**0.712751047**	2	4.07054
P02564	LELQSALEEAEASLEHEEGK	**0.932517329**	2	4.13805
P02564	LLGSLDIDHNQYK	**0.380525593**	2	3.6617
P02564	LQDAEEAVEAVNAK	**0.428640638**	2	3.96466
P02564	LQNEIEDLMVDVER	**0.267132975**	2	3.89675
P02564	LTQESIMDLENDKQQLDER	**0.179173466**	2	4.5516
P02564	MDADLSQLQTEVEEAVQECR	**0.720001348**	2	5.23518
P02564	NDLQLQVQAEQDNLADAEER	**0.312275687**	2	5.46321
P02564	NLQEEISDLTEQLGSTGK	**0.244788628**	2	5.92942
P02564	NLTEEMAGLDEIIVK	**1.364368423**	2	4.75056
P02564	NNLLQAELEELR	**0.418814141**	2	3.38818
P02564	QAEEAEEQANTNLSK	**0.052101974**	2	4.9751
P02564	QKYEESQSELESSQK	**0.492618133**	2	3.39453
P02564	QREEQAEPDGTEEADK	**0.155720804**	2	2.93157
P02564	QREEQAEPDGTEEADKSAYLMGLNSADLLK	**0.276702963**	3	4.91141
P02564	SAYLMGLNSADLLK	**0.613918006**	2	2.54576
P02564	TLEDQMNEHR	**0.435296831**	2	2.65105
P02564	VQHELDEAEER	**0.969960172**	2	3.0625
P02564	VQHELDEAEERADIAESQVNK	**0.441911039**	3	3.58708
P02564	VQLLHSQNTSLINQK	**0.057587288**	2	3.98746
P02564	VRELENELEAEQKR	**0.486417252**	3	3.83671
P02564	VVDSLQTSLDAETR	**0.311394007**	2	4.19334
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**0.340949566**	**5.22E-15**	**13**
P02600	ALGTNPTNAEVK	**0.085109028**	2	3.53679
P02600	ALGTNPTNAEVKK	**0.154107615**	2	3.30477
P02600	DQGGYEDFVEGLR	**0.083122802**	2	3.56032
P02600	EQQEEFKEAFLLFDR	**1.391007807**	2	3.58199
P02600	IEFEQFLPMMQAISNNK	**0.315316716**	3	3.91804
P02600	ITLSQVGDVLR	**0.113391631**	2	3.23915
P02600	KIEFEQFLPMMQAISNNK	**0.293411066**	2	5.66763
P02600	KIEFEQFLPMMQAISNNKDQGGYEDFVEGLR	**0.391091258**	4	5.26677
P02600	KPAAAAPAPAPAPAPAPAKPK	**#NUM!**	3	4.33093
P02600	KVLGNPSNEEMNAK	**0.026885005**	2	3.3167
P02600	KVLGNPSNEEMNAK+Oxidation(10)	**#NUM!**		
P02600	VLGNPSNEEMNAK	**0.066378376**	2	3.68934
P02600	VLGNPSNEEMNAK+Oxidation(9)	**0.171291866**		
P02625	**PRVA Parvalbumin alpha**	**0.327890243**	**1.62E-05**	**5**
P02625	AIGAFTAADSFDHK	**0.24323789**	2	3.38144
P02625	KVFHILDKDK	**0.303487383**	2	2.30184
P02625	SGFIEEDELGSILK	**0.225962215**	2	4.86067
P02625	TLMAAGDKDGDGK	**0.117273558**	2	3.18317
P02625	TLMAAGDKDGDGK+Oxidation(2)	**0.454948741**		
P02650	**APOE Apolipoprotein E**	**1.315143202**	**0.534639**	**11**
P02650	ELEEQLGPVAEETR	**1.188575809**	2	4.29276
P02650	GRLEEVGNQAR	**1.113027098**	2	3.51283
P02650	GWFEPLVEDMQR	**1.044390736**	2	3.44329
P02650	LEEVGNQAR	**1.042977987**	2	2.48384
P02650	LGADMEDLR	**0.934882123**	2	2.74216
P02650	LGPLVEQGR	**1.377495179**	2	2.76663
P02650	MEEQTQQIR	**0.818197096**	2	3.15394

P02650	NEVNTMLGQSTEELR	**1.041278717**		2	4.37572
P02650	SKMEEQTQQIR	**0.837996389**		2	3.23008
P02650	SKMEEQTQQIR+Oxidation(2)	**1.566698199**			
P02650	TANLGAGAAQPLR	**1.054991533**		2	3.67759
P02651	**APOA4 Apolipoprotein A_IV**	**0.753025404**	**0.285178**	**2**	
P02651	TDVTQQLNTLFQDK	**0.654076268**		2	4.37629
P02651	VSTNIDQLQK	**0.950733198**		2	2.31064
P02680	**FIBG Fibrinogen gamma chain**	**0.984179062**	**0.686481**	**5**	
P02680	LSIGDGQQHHMGGSK	**0.673214267**		2	2.7167
P02680	VAQLEAQCQEPCK	**1.617732338**		2	3.50944
P02680	VGPESDKYR	**0.963264474**		2	2.7844
P02680	YEALLLTHESSIR	**0.985569585**		2	3.89451
P02680	YLQDIYTSNK	**1.079425942**		2	2.44202
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.103633238**	**4.76E-13**	**11**	
P02692	AMGLPEDLIQK	**0.917629087**		2	3.7251
P02692	AMGLPEDLIQK+Oxidation(1)	**1.15271137**			
P02692	GVSEIVHEGK	**0.977388031**		2	3.41016
P02692	GVSEIVHEGKK	**0.979474301**		2	3.22319
P02692	SVTEFNGDTITNTMTLGDIVYK	**1.021725521**		2	5.53266
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13)	**1.039685764**			
P02692	SVTEFNGDTITNTMTLGDIVYKR	**0.770956132**		2	3.63219
P02692	VIHNEFTLGEECELETMTGEK	**1.00993871**		3	6.10976
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16)	**1.180633018**			
P02692	YQVQSQENFEPFMK	**1.163373857**		2	5.81941
P02692	YQVQSQENFEPFMK+Oxidation(12)	**1.446352886**			
P02696	**RET1 Retinol_binding protein 1**	**0.942057803**	**0.049225**	**5**	
P02696	ALDVNVALR	**0.782072483**		2	3.31329
P02696	CMTTVSWDGDKLQCVQK	**0.5016474**		2	4.67222
P02696	EFEEDLTGIDDR	**0.679848462**		2	2.46823
P02696	MLSNENFEEYLR	**0.543126498**		2	3.90598
P02696	MLSNENFEEYLR+Oxidation(0)	**0.960254084**			
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.136133582**	**0.571854**	**6**	
P02706	DYQDFQHLDNENDHHQLQR	**1.623704183**		3	4.24623
P02706	FVQQHMGPLNTWIGLTDQNGPWK	**1.338407714**		3	3.50004
P02706	LVESQLEK	**1.234916579**		2	2.49492
P02706	SLSCQMAALR	**0.900946802**		2	2.70007
P02706	WVCETELGK	**0.897203892**		2	2.35827
P02706	WVDGTDYETGFK	**0.954828292**		2	3.17373
P02770	**ALBU Serum albumin**	**1.044314935**	**5.31E-12**	**24**	
P02770	AADKDNCFATEGPNLVAR	**1.533050004**		2	4.97209
P02770	AETFTFHSDICTLPDKEK	**2.655643403**		2	4.5045
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	**0.801096665**		3	5.27084
P02770	CCSGSLVER	**0.700430461**		2	3.29453
P02770	CCTLPEAQR	**0.657343396**		2	3.19926
P02770	ECCHGDLLECADDR	**0.769475882**		2	3.62666
P02770	ECCHGDLLECADDRAELAK	**0.660522916**		2	5.18949
P02770	FKDLGEQHFK	**0.816848134**		3	4.29038
P02770	GLVLIAFSQYLQK	**1.043626824**		2	4.14364
P02770	INKECCHGDLLECADDRAELAK	**0.381417**		3	4.70576
P02770	KQTALAELVK	**0.820162769**		3	4.08257
P02770	KYEATLEK	**0.585321071**		1	2.70703
P02770	LQACCDKPVLQK	**0.845882954**		2	4.32312
P02770	LVQEVTDFAK	**0.730323611**		2	3.5895
P02770	RHPDYSVSLLLR	**0.770258835**		3	5.34222
P02770	SIHTLFGDK	**0.741118573**		1	2.53731
P02770	TCVADENAENCDK	**0.811235262**		2	4.49672
P02770	TNCELYEK	**0.838309435**		2	2.89605

P02770	TVMGDFAQFVDK	**0.575734083**	2	3.72881
P02770	TVMGDFAQFVDK+Oxidation(2)	**0.801306884**		
P02770	YEATLEK	**0.615578947**	1	1.93876
P02770	YMCENQATISSK	**0.661009048**	2	4.09582
P02770	YMCENQATISSK+Oxidation(1)	**0.869423086**		
P02770	YNEVLTQCCTESDK	**0.751392639**	2	5.92113
P02803	**MT1 Metallothionein_1**	**4.256216337**	**9.9E-20**	**2**
P02803	MDPNCSCSTGGSCTCSSSCGCK	**2.778829284**	2	5.28428
P02803	SCCSCCPVGCSK	**4.036206351**	2	3.90349
P04041	**GPX1 Glutathione peroxidase 1**	**0.798883024**	**1.12E-05**	**10**
P04041	FLVGPDGVPVR	**0.821668001**	2	3.48274
P04041	GLVVLGFPCNQFGHQENGK	**0.912085967**	2	4.36598
P04041	GLVVLGFPCNQFGHQENGKNEEILNSLK	**0.819357239**	3	3.99589
P04041	NALPAPSDDPTALMTDPK	**0.7786429**	2	3.11904
P04041	NALPAPSDDPTALMTDPK+Oxidation(13)	**1.212273944**		
P04041	NDISWNFEK	**0.767831384**	2	2.94232
P04041	NEEILNSLK	**0.887857816**	1	2.38829
P04041	TIDIEPDIEALLSK	**0.99037764**	3	4.57769
P04041	YIIWSPVCR	**0.819022121**	2	3.1103
P04041	YVRPGGGFEPNFTLFEK	**0.789330039**	3	4.85664
P04167	**CP2B2 Cytochrome P450 2B2**	**1.260078964**	**0.062912**	**2**
P04167	GTIAVIEPIFK	**1.261168877**	2	2.71393
P04167	NLQEILDYIGHIVEK	**1.258631096**	2	3.72097
P04176	**PH4H Phenylalanine_4_hydroxylase**	**2.250472863**	**9.9E-20**	**18**
P04176	AYGAGLLSSFGELQYCLSDKPK	**3.079409497**	2	4.18598
P04176	EDNIPQLEDVSQFLQTCTGFR	**2.309157925**	3	4.95246
P04176	FANQILSYGAELDADHPGFK	**2.853175088**	3	3.53092
P04176	FANQILSYGAELDADHPGFKDPVYR	**1.485652535**	4	5.03737
P04176	ILADSINSEVGILCNALQK	**0.874819009**	3	6.64431
P04176	LNKDEYEFFTYLDK	**12.10942275**	2	3.60405
P04176	LNKDEYEFFTYLDKR	**2.039078133**	3	3.81891
P04176	LRPVAGLLSSR	**2.180388581**	2	2.33952
P04176	NDIGATVHELSR	**1.616435751**	2	3.61536
P04176	NTVPWFPR	**1.265873692**	2	2.50124
P04176	QFADIAYNYR	**1.532989225**	2	2.54549
P04176	SFAQFSQEIGLASLGAPDEYIEK	**1.91386243**	2	5.01675
P04176	TACQEYSVTEFQPLYYVAESFSDAK	**4.841320338**	2	4.73385
P04176	THACYEHNHIFPLLEK	**1.612225418**	2	4.66712
P04176	VEVLDNTQQLK	**1.357285328**	2	3.89568
P04176	VEYTEEEK	**1.315260609**	2	2.60328
P04176	VEYTEEEKQTWGTVFR	**1.200401005**	2	4.44799
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	**1.776581594**	3	4.71625
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.910067209**	**0.975711**	**8**
P04182	AFYNNVLGEYEEYITK	**1.05935258**	2	4.43028
P04182	DNGLLAKPTHGDIIR	**1.058833923**	2	2.58157
P04182	GLLNAIVIR	**0.928971655**	2	3.34798
P04182	KTEQGPPSSEYIFER	**1.120977892**	2	4.12294
P04182	TEQGPPSSEYIFER	**0.971487029**	2	4.14938
P04182	VLPMNTGVEAGETACK	**0.777734331**	2	4.29622
P04182	WLAVDHENVRPDIVLLGK	**0.64424682**	2	4.05955
P04182	YGAHNYHPLPVALER	**0.679193117**	2	3.61423
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**1.017317449**	**0.007537**	**5**
P04256	EDSQRPGAHLTVK	**1.017380943**	2	3.05306
P04256	GFAFVTFDDHDSVDK	**1.102014029**	2	2.90256
P04256	IEVIEIMTDR	**0.900961035**	2	3.40857

P04256	NQGGYGGSSSSSSYGSGR	**1.333547727**	2	4.93642
P04256	SESPKEPEQLR	**1.041228611**	2	2.36209
P04276	**VTDB Vitamin D_binding protein**	**1.146322757**	**0.243526**	**3**
P04276	SCESDAPFPVHPGTSECCTK	**0.961189272**	2	4.85132
P04276	VPTANLEDVLPLAEDLTEILSR	**1.227272493**		
P04276	YCSSQIDAEMR	**1.009355647**	2	2.46543
P04355	**MT2 Metallothionein_2**	**3.14521159**	**9.9E-20**	**3**
P04355	CSQGCICKEASDKCSCCA	**2.151272709**	3	3.63271
P04355	MDPNCSCATDGSCSCAGSCK	**1.297532565**	2	6.38693
P04355	SCCSCCPVGCAK	**7.54359113**	2	4.21647
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**0.143829276**	**5.36E-12**	**9**
P04466	AAAEGSSNVFSMFDQTQIQEFK	**0.414718107**	3	4.91573
P04466	GADPEDVITGAFK	**0.084671802**	2	4.34515
P04466	KQFLEELLTTQCDR	**0.155757402**	2	3.81738
P04466	LKGADPEDVITGAFK	**0.266161733**	2	3.76552
P04466	NEELDAMMK	**0.02367322**	1	2.32236
P04466	NICYVITHGDAK	**0.273405101**	2	3.07375
P04466	NICYVITHGDAKDQE	**0.11329065**	2	3.9808
P04466	NMWAAFPPDVGGNVDYK	**0.275834466**	2	2.91571
P04466	QFLEELLTTQCDR	**0.163555996**	2	4.00528
P04550	**PTMS Parathymosin**	**1.142292878**	**2.98E-09**	**4**
P04550	RTAEEEDEADPKR	**1.355335071**	3	4.40865
P04550	SVEAAAELSAK	**1.136462143**	2	4.20507
P04550	TAEEEDEADPK	**1.044309143**	2	3.71464
P04550	TAEEEDEADPKR	**1.311523237**	3	3.74064
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**1.163387337**	**9.9E-20**	**17**
P04636	AGAGSATLSMAYAGAR	**1.174213312**	2	4.75795
P04636	AGAGSATLSMAYAGAR+Oxidation(9)	**1.7635472**		
P04636	ANTFVAELK	**1.192692932**	2	2.7388
P04636	EGVIECSFVQSK	**1.317925864**	1	3.0601
P04636	ETECTYFSTPLLLGK	**3.528177467**	2	3.75804
P04636	FVFSLVDAMNGK	**1.136384578**	2	4.29024
P04636	GCDVVVIPAGVPR	**1.092202824**	2	4.26367
P04636	GYLGPEQLPDCLK	**1.030961848**	2	4.30757
P04636	IFGVTTLDIVR	**1.381819138**	2	3.4528
P04636	IQEAGTEVVK	**1.002777004**	2	2.86749
P04636	LTLYDIAHTPGVAADLSHIETR	**1.165083774**	3	6.70767
P04636	MIAEAIPELK	**0.886709638**	2	3.05672
P04636	MIAEAIPELK+Oxidation(0)	**1.323072682**		
P04636	TIIPLISQCTPK	**1.678869251**	2	3.71031
P04636	VAVLGASGGIGQPLSLLLK	**1.357284078**	2	5.99747
P04636	VDFPQDQLATLTGR	**0.882325982**	2	4.7601
P04636	VNVPVIGGHAGK	**1.161633919**	2	3.61838
P04639	**APOA1 Apolipoprotein A_I**	**1.039454444**	**0.991291**	**5**
P04639	LQEQLGPVTQEFWANLEK	**1.320081078**	2	4.08985
P04639	NEMNKDLENVK	**0.913297359**	2	3.16358
P04639	QLNLNLLDNWDTLGSTVGR	**1.025363379**	2	4.29887
P04639	VKDFATVYVDAVK	**1.176640837**	2	2.83214
P04639	WNEEVEAYR	**0.9883429**	2	2.59856
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.068400441**	**5.15E-10**	**21**
P04642	DLADELALVDVIEDK	**1.074357596**	2	5.45794
P04642	DQLIVNLLK	**1.185417912**	2	2.92863
P04642	DQLIVNLLKEEQVPQNK	**0.947469915**	2	4.57769
P04642	EDVFLSVPCILGQNGISDVVK	**1.3323684**	2	4.66096
P04642	FIIPNVVK	**0.883678889**	2	2.38255
P04642	GEMMDLQHGSLFLK	**0.785731002**	2	3.94008

P04642	GEMMDLQHGSLFLK+Oxidation(2)	**1.821556626**		
P04642	GEMMDLQHGSLFLK+Oxidation(2)	**1.141579734**		
P04642	GEMMDLQHGSLFLK+Oxidation(3)	**1.152474717**	2	3.48728
P04642	KSADTLWGIQK	**1.21920039**	2	3.31845
P04642	LLIVSNPVDILTYVAWK	**1.53029756**	2	4.86301
P04642	NVNIFK	**1.121059331**	1	2.08244
P04642	QVVDSAYEVIK	**1.037464246**	2	3.50287
P04642	RVHPISTMIK	**1.159273813**	2	2.51971
P04642	RVHPISTMIK+Oxidation(7)	**1.15207831**		
P04642	SADTLWGIQK	**1.136223055**	2	3.93491
P04642	SLNPQLGTDADK	**1.098983586**	1	2.32285
P04642	SLNPQLGTDADKEQWK	**1.20851561**	2	4.85702
P04642	SLNPQLGTDADKEQWKDVHK	**0.989402682**	3	3.43116
P04642	VHPISTMIK+Oxidation(6)	**1.893072866**		
P04642	VTLTPDEEAR	**1.126613555**	2	2.74138
P04644	**RS17 40S ribosomal protein S17**	**1.371167421**	**0.296442**	**2**
P04644	LLDFGSLSNLQVTQPTVGMNFK	**1.302994516**	2	4.27876
P04644	VCEEIAIIPSK	**1.104881853**	2	2.86604
P04692	**TPM1 Tropomyosin alpha_1 chain**	**0.457827681**	**2.25E-08**	**11**
P04692	AISEELDHALNDMTSI	**0.310507183**	2	2.80001
P04692	GTEDELDKYSEALK	**0.453365367**	2	3.64558
P04692	GTEDELDKYSEALKDAQEK	**0.426542887**	2	4.10842
P04692	KLVIIESDLER	**0.574348777**	2	3.46125
P04692	LDKENALDR	**0.130832287**	2	2.78517
P04692	LKGTEDELDK	**0.199768969**	2	2.76881
P04692	LVIIESDLER	**0.599054411**	2	2.4582
P04692	MEIQEIQLK	**0.761633797**	2	3.02132
P04692	QLEDELVSLQK	**0.174645451**	2	2.85571
P04692	SIDDLEDELYAQK	**0.021948099**	2	4.23555
P04692	SKQLEDELVSLQK	**1.194185739**	2	3.33574
P04694	**ATTY Tyrosine aminotransferase**	**1.137569532**	**0.808444**	**5**
P04694	ILGPCTIVQGALK	**1.64573741**	2	2.6726
P04694	IQEFCEQHYHCAEGSQEECDK	**1.070351263**	3	4.45188
P04694	TACLVVNNPSNPCGSVFSK	**0.674869036**	2	4.93305
P04694	WDVRPSDMSNK	**0.983234627**	2	2.36815
P04694	YEPLANLSTNVPILSCGGLAK	**1.33418286**	2	3.42955
P04762	**CATA Catalase**	**0.990602047**	**9.9E-20**	**32**
P04762	APQKPDVLTTGGGNPIGDK	**5.624901778**	2	4.63802
P04762	DAMLFPSFIHSQK+Oxidation(2)	**1.869836949**		
P04762	DAQLFIQR	**1.047616399**	2	2.99743
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	**0.671636069**	4	4.56745
P04762	DPASDQMK	**0.788639829**	1	2.25792
P04762	DPASDQMK+Oxidation(6)	**1.620780919**		
P04762	DYPLIPVGK	**0.766933216**	1	2.24485
P04762	EAETFPFNPFDLTK	**1.031366525**	2	3.96058
P04762	FNSANEDNVTQVR	**0.831262601**	2	4.55893
P04762	FSTVAGESGSADTVR	**0.819534406**	2	5.28058
P04762	FSTVAGESGSADTVRDPR	**0.488632893**	2	2.30734
P04762	FYTEDGNWDLVGNNTPIFFIR	**1.37716776**	3	5.46329
P04762	GAGAFGYFEVTHDITR	**0.748143704**	2	4.78374
P04762	GPLLVQDVVFTDEMAHFDR	**1.563254252**	2	5.47609
P04762	HMNGYGSHTFK	**0.725896046**	3	4.1081
P04762	HMNGYGSHTFK+Oxidation(1)	**0.957509101**		
P04762	LAQEDPDYGLR	**1.018984533**	2	2.72948
P04762	LCENIANHLK	**0.789231152**	3	3.78386
P04762	LFAYPDTHR	**1.091916244**	2	2.9141

P04762	LGPNYLQIPVNCPYR	**1.024721359**	3	4.05297
P04762	LNIMTAGPR	**0.861234299**	2	3.14564
P04762	LNIMTAGPR+Oxidation(3)	**1.258884214**		
P04762	LVNANGEAVYCK	**1.100444903**	2	3.89432
P04762	NAIHTYVQAGSHIAAK	**0.703657227**	3	5.89861
P04762	NFTDVHPDYGAR	**0.878468285**	2	4.14073
P04762	NLPVEEAGR	**0.771313619**	1	2.32301
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	**2.072787832**	3	5.67714
P04762	RFNSANEDNVTQVR	**0.722670547**	2	4.52122
P04762	VFEHIGK	**0.899645962**	2	2.47616
P04762	VFEHIGKR	**0.632338562**	2	2.36905
P04762	VQALLDQYNSQKPK	**0.846782204**	2	4.9403
P04762	VWPHKDYPLIPVGK	**0.611204838**	2	3.48107
P04764	**ENOA Alpha_enolase**	**1.053611317**	**9.9E-20**	**14**
P04764	AGYTDQVVIGMDVAASEFYR	**0.951035743**	2	4.52052
P04764	DATNVGDEGGFAPNILENK	**1.098709818**	2	5.78088
P04764	FTATAGIQVVGDDLTVTNPK	**1.171684032**	2	5.30646
P04764	GNPTVEVDLYTAK	**1.519825573**	2	4.07855
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	**1.023763249**	3	6.15002
P04764	IDQLMIEMDGTENK	**0.984982505**	2	4.48169
P04764	IEEELGSK	**1.070351263**	2	2.3214
P04764	IGAEVYHNLK	**2.309547264**	2	3.20941
P04764	KLNVVEQEK	**0.48819134**	2	2.54551
P04764	LNVVEQEK	**1.165215577**	2	3.10239
P04764	LNVVEQEKIDQLMIEMDGTENK	**1.026569131**	3	4.64871
P04764	SCNCLLLK	**1.163758182**	2	2.98189
P04764	VNQIGSVTESLQACK	**0.809959656**	2	5.04251
P04764	YITPDQLADLYK	**1.001315651**	2	3.47057
P04785	**PDIA1 Protein disulfide_isomerase**	**1.054969489**	**9.9E-20**	**25**
P04785	DGVVLFK	**1.158649022**	2	2.44027
P04785	DHENIVIAK	**1.257697325**	2	2.75662
P04785	EADDIVNWLK	**1.239775964**	2	2.30877
P04785	HNQLPLVIEFTEQTAPK	**1.116920481**	3	5.68664
P04785	IKPHLMSQELPEDWDKQPVK	**1.134349096**	4	4.66079
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5)	**1.579324902**		
P04785	ILEFFGLK	**1.222059462**	2	3.07407
P04785	ILFIFIDSDHTDNQR	**1.015074775**	2	2.37653
P04785	LGETYKDHENIVIAK	**1.110546974**	3	4.73626
P04785	LITLEEEMTK	**0.976178513**	2	3.56582
P04785	LITLEEEMTK+Oxidation(7)	**1.351345847**		
P04785	LKAEGSEIR	**0.960650936**	1	2.09642
P04785	MDSTANEVEAVK	**0.969177913**	2	4.11655
P04785	MDSTANEVEAVK+Oxidation(0)	**1.233858212**		
P04785	NFEEVAFDEK	**1.102305192**	1	3.35772
P04785	NFEEVAFDEKK	**1.128972461**	2	3.73687
P04785	NNFEGEITK	**0.978572117**	2	2.53414
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	**1.178066771**	3	6.63211
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	**1.077837034**	3	6.39074
P04785	THILLFLPK	**1.182929875**	2	2.77799
P04785	TVIDYNGER	**0.976756244**	2	2.56507
P04785	VDATEESDLAQQYGVR	**1.072427596**	2	5.62558
P04785	VHSFPTLK	**1.020962878**	1	1.92066
P04785	YKPESDELTAEK	**1.132756515**	3	4.58609
P04785	YQLDKDGVVLFK	**1.029257208**	2	3.93673
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**0.958823635**	**9.9E-20**	**16**
P04797	GAAQNIIPASTGAAK	**1.198504464**	2	4.27335

P04797	IVSNASCTTNCLAPLAK	**1.260447021**	2	4.76496
P04797	LISWYDNEYGYSNR	**2.094238293**	2	4.06103
P04797	LVINGKPITIFQER	**2.16908592**	3	3.72088
P04797	RVIISAPSADAPMFVMGVNHEK	**1.440297115**	3	5.28576
P04797	RVIISAPSADAPMFVMGVNHEK+Oxidation(12)	**1.078349729**		
P04797	VGVNGFGR	**1.303283118**	2	2.57837
P04797	VIHDNFGIVEGLMTTVHAITATQK	**1.09622391**	3	7.493
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12)	**1.406547733**		
P04797	VIISAPSADAPMFVMGVNHEK	**0.895433214**	2	4.64743
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11)	**1.170342547**		
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14)	**1.163409121**		
P04797	VPTPNVSVVDLTCR	**4.229550015**	2	3.77434
P04797	VVDLMAYMASK	**3.252594959**	2	3.80551
P04797	VVDLMAYMASKE	**3.110256575**	2	2.767
P04797	WGDAGAEYVVESTGVFTTMEK	**1.115479379**	2	5.56722
P04799	**CP1A2 Cytochrome P450 1A2**	**1.045830254**	**0.894987**	**6**
P04799	DFVENVTSGNAVDFFPVLR	**1.018150588**	2	3.76072
P04799	IGSTPVVVLSGLNTIK	**1.266493664**	2	3.05979
P04799	NSIQDITGALFK	**0.761656849**	2	3.47552
P04799	SMTFNPDSGPVWAAR	**1.759259694**	2	3.15539
P04799	TCEHVQAWPR	**0.629036385**	2	2.87164
P04799	TVQEHYQDFNK	**0.915471071**	2	3.45886
P04800	**CP3A1 Cytochrome P450 3A1**	**3.148515806**	**0.32378**	**2**
P04800	KLQEEIDR	**0.761542332**	2	2.31223
P04800	QGLLQPTKPIILK	**3.440994238**	2	2.38771
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**1.265492639**	**0.023221**	**10**
P04903	DGNLMFDQVPMVEIDGMK	**0.620037772**	2	4.91763
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	**0.887183258**		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16)	**0.922741837**		
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	**0.877138526**		
P04903	KDGNLMFDQVPMVEIDGMK	**0.7247424**	2	4.3956
P04903	LIQSPEDLEK	**1.2424338**	2	3.11657
P04903	LKKDGNLMFDQVPMVEIDGMK	**1.290698242**	2	2.69273
P04903	WLLAAAGVEFEEK	**1.018604393**	2	3.87026
P04903	YDLYGK	**0.699503948**	1	1.93957
P04903	YLPAFEK	**0.85406805**	1	2.00214
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.910092328**	**5.22E-13**	**9**
P04904	ADVYLVQVLYHVEELDPSALANFPLLK	**1.279053383**	3	5.29591
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK	**1.660906985**	4	7.90485
P04904	LRNDGSLMFQQVPMVEIDGMK	**1.234883415**	2	3.80457
P04904	NDGSLMFQQVPMVEIDGMK	**0.793572459**	2	4.6393
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	**0.970194559**		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17)	**0.97285218**		
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5)	**0.964162197**		
P04904	SHGQDYLVGNR	**0.907698355**	2	3.9099
P04904	WLLAAAGVEFEEQFLK	**0.996314755**	2	5.41993
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**1.249857347**	**9.9E-20**	**15**
P04905	ADIVENQVMDNR	**0.900941657**	2	4.29347
P04905	ADIVENQVMDNR+Oxidation(8)	**1.144370523**		
P04905	CLDAFPNLKDFLAR	**0.973881502**	2	2.69365
P04905	FKLGLDFPNLPYLIDGSR	**0.998684075**	3	4.8549
P04905	HHLCGETEEER	**1.111420481**	3	4.43464
P04905	IRADIVENQVMDNR	**1.034036522**	2	3.95495
P04905	ITQSNAIMR	**1.069152481**	2	3.08912
P04905	ITQSNAIMR+Oxidation(7)	**1.430199175**		
P04905	KHHLCGETEEER	**1.34810337**	3	3.6862
P04905	KITQSNAIMR	**0.871333371**	3	3.76446

P04905	KITQSNAIMR+Oxidation(8)	0.92986218		
P04905	LGLDFPNLPYLIDGSR	1.367645022	2	5.11387
P04905	MQLIMLCYNPDFEK	1.59779523	2	4.49475
P04905	VTYVDFLAYDILDQYHIFEPK	1.139535757	3	3.7413
P04905	YLSTPIFSK	1.006612106	2	2.70858
P04906	**GSTP1 Glutathione S_transferase P**	**1.08330181**	**0.973791**	**2**
P04906	EAALVDMVNDGVEDLR	1.073444697	2	4.73301
P04906	STCLYGQLPK	1.083790067	2	2.94813
P04937	**FINC Fibronectin**	**0.962018935**	**0.928739**	**4**
P04937	FTQVSPTTLTAQWTAPSVK	1.332355893	2	3.52904
P04937	ITYGETGGNSPVQEFTVPGSK	0.964982964	2	2.6558
P04937	SSPVVIDASTAIDAPSNLR	0.907780843	2	2.46638
P04937	SYTITGLQPGTDYK	0.933423169	2	2.75899
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**0.469668781**	**9.9E-20**	**9**
P05065	ALANSLACQGK	0.435167211	2	2.96461
P05065	FSNEEIAMATVTALR	0.374960526	2	4.4987
P05065	GILAADESTGSIAK	0.341414629	2	4.22881
P05065	GVVPLAGTNGETTTQGLDGLSER	0.492019778	2	5.3992
P05065	IGEHTPSSLAIMENANVLAR	0.362453302	2	4.67849
P05065	KENLKAAQEEYIK	1.240761883	2	2.41131
P05065	LQSIGTENTEENR	0.424511322	2	3.80651
P05065	LQSIGTENTEENRR	0.34133662	2	2.52114
P05065	RLQSIGTENTEENR	0.34133662	2	4.08288
P05178	**CP2C6 Cytochrome P450 2C6**	**0.743236991**	**0.004037**	**9**
P05178	DQDFLNLMEK	0.643900362	2	2.58135
P05178	EALIDHGEEFAER	1.174031844	2	3.24757
P05178	FDYKDQDFLNLMEK	0.85343156	3	4.55561
P05178	FIDLIPTNLPHAVTCDIK	0.658418121	2	3.3502
P05178	GTTIITSLSSVLHDSK	0.789263068	2	3.75694
P05178	LPPGPIPLPIIGNIFQLNVK	0.888561195	3	3.52075
P05178	MCAGEGLAR	0.643531909	2	2.57617
P05178	NITQSLTSFSK	0.904607151	2	2.47245
P05178	TNGSPCDPTFILGCAPCNVICSIIFQNR	0.953713443	3	4.71856
P05179	**CP2C7 Cytochrome P450 2C7**	**0.99691467**	**0.888304**	**7**
P05179	ACVGEGLAR	1.133772511	2	2.89265
P05179	FINFVPTNLPHAVTCDIK	0.777431403	2	2.65671
P05179	IEEHQESLDVTNPR	0.931826844	2	4.5687
P05179	KIEEHQESLDVTNPR	1.339651372	3	4.6682
P05179	KLPPGPTPLPIIGNFLQIDVK	1.11323076	3	5.50741
P05179	SDYFLPFSAGK	1.666031759	2	2.59893
P05179	VLTSLTSVLHDSK	1.368430617	2	3.41608
P05182	**CP2E1 Cytochrome P450 2E1**	**0.971859969**	**0.067899**	**14**
P05182	AKEHLQSLDINCAR	0.701165072	2	4.85529
P05182	DTVFQGYVIPK	1.396765848	2	2.82085
P05182	DVTDCLLIEMEK	1.001541319	2	3.02675
P05182	DVTDCLLIEMEKEK	0.965543539	2	2.4895
P05182	EHLQSLDINCAR	1.153115576	2	3.42909
P05182	FINLVPSNLPHEATR	0.790115878	2	3.82213
P05182	FKPEHFLNENGK	0.869127979	2	2.97678
P05182	GIIFNNGPTWK	1.092563549	2	2.41436
P05182	GQPFDPTFLIGCAPCNVIADILFNK	0.989719659		
P05182	GTVVIPTLDSLLYDSHEFPDPEK	0.861797637	2	4.88556
P05182	LDMPYMDAVVHEIQR	0.853122217	2	2.67184
P05182	LHEEIDR	0.867897599	1	1.95861
P05182	VCVGEGLAR	1.072994676	2	2.38397
P05182	YGLLILMK	0.762321777	2	3.08804
P05183	**CP3A2 Cytochrome P450 3A2**	**1.060390421**	**0.295697**	**10**

P05183	DIELDGLFIPK	**1.320279742**	2	4.14047
P05183	DSIAFFQK	**2.192463982**	1	2.18221
P05183	EMFPIIEQYGDILVK	**1.05434216**	2	3.95162
P05183	KDIELDGLFIPK	**0.892477872**	3	3.55848
P05183	KLQEEIDGALPSK	**1.1133718**	2	3.67956
P05183	LQEEIDGALPSK	**1.075763685**	2	4.10353
P05183	QAILEPEKPIVLK	**1.093310138**	2	3.28366
P05183	QEAETGKPVTMK	**0.664421177**	2	3.19354
P05183	QEAETGKPVTMK+Oxidation(10)	**1.422880866**		
P05183	VDFLQLMLNAHNNSK	**0.803834955**	2	3.70943
P05197	**EF2 Elongation factor 2**	**1.250913187**	**9.9E-20**	**31**
P05197	ALLELQLEPEELYQTFQR	**1.596886147**	2	5.47181
P05197	ARPFPDGLAEDIDKGEVSAR	**1.279234273**	3	6.16031
P05197	AYLPVNESFGFTADLR	**1.186227698**	2	3.87612
P05197	CELLYEGPPDDEAAMGIK	**0.836185773**	2	4.97875
P05197	CLYASVLTAQPR	**2.773320216**	2	2.46127
P05197	DLEEDHACIPIK	**1.059082849**	2	2.99095
P05197	DLEEDHACIPIKK	**1.036903495**	2	3.67638
P05197	EGIPALDNFLDK	**0.847330614**	2	2.64864
P05197	EGIPALDNFLDKL	**4.022166534**	2	3.57861
P05197	ETVSEESNVLCLSK	**1.863968321**	2	4.05828
P05197	GEGQLGAAER	**1.260658929**	2	3.36029
P05197	GHVFEESQVAGTPMFVVK	**2.285101857**	2	6.13511
P05197	GVQYLNEIK	**4.537289495**	2	2.34269
P05197	IWCFGPDGTGPNILTDITK	**1.436180106**	2	5.06005
P05197	KEDLYLKPIQR	**1.191195905**	2	3.30341
P05197	KIWCFGPDGTGPNILTDITK	**1.269496417**	2	4.83032
P05197	KVEDMMK+Oxidation(5)	**1.91768676**		
P05197	LDSEDKDKEGKPLLK	**1.453465456**	2	3.96126
P05197	LMEPIYLVEIQCPEQVVGGIYGVLNR	**1.151719234**	3	5.98974
P05197	NMSVIAHVDHGK	**1.462100521**	2	3.94774
P05197	NMSVIAHVDHGK+Oxidation(1)	**1.251117017**		
P05197	STAISLFYELSENDLNFIK	**2.57013685**	3	4.76698
P05197	STLTDSLVCK	**1.175140935**	2	2.89732
P05197	TFCQLILDPIFK	**1.40921015**	2	4.19908
P05197	TGTITTFEHAHNMR	**1.385860583**	2	3.83514
P05197	VFDAIMNFR	**0.740278105**	2	2.82633
P05197	VFSGVVSTGLK	**1.441558104**	2	3.05037
P05197	WLPAGDALLQMITIHLPSPVTAQK	**1.337800638**	3	3.65297
P05197	YEWDVAEAR	**1.17342185**	2	3.03896
P05197	YFDPANGK	**1.219294382**	1	2.03708
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	**1.616262823**	3	4.73587
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.051651434**	**0.999685**	**11**
P05369	ALYEELDLR	**0.998179925**	2	3.05926
P05369	EVLEYNTVGGK	**1.101098881**	2	3.06973
P05369	GLTVVQTFQELVEPR	**1.234955995**	3	3.86432
P05369	IKEVLEYNTVGGK	**0.94162653**	3	4.16708
P05369	QILEENYGQKDPEK	**0.914321616**	2	3.77758
P05369	QNFIQHFSQIVK	**2.204771659**	2	3.05246
P05369	SLIEQCSAPLPPSIFLELANK	**0.883731163**	3	5.29871
P05369	VGTDIQDNK	**0.969526898**	2	3.68679
P05369	VLTEDELGHPEK	**1.127147598**	2	2.72076
P05369	VLTEDELGHPEKGDAITR	**1.046462518**	2	4.56948
P05369	YEEDSYNR	**0.953320804**	2	2.34577
P05426	**RL7 60S ribosomal protein L7**	**1.290401504**	**9.9E-20**	**6**
P05426	AGNFYVPAEPK	**1.325732022**	2	2.67206
P05426	FGIICMEDLIHEIYTVGK	**1.398140232**	3	4.64725

P05426	IVEPYIAWGYPNLK	1.481842498	2	2.95143
P05426	SVNELIYK	1.189621564	2	2.79579
P05426	TTHFVEGGDAGNR	1.467123868	2	3.26733
P05426	TTHFVEGGDAGNREDQINR	1.41700664	2	4.56546
P05544	**SPA3L Serine protease inhibitor A3L**	**1.188722862**	**0.000722**	**6**
P05544	AVLDVDETGTEATAATGVATVIR	1.073505012	2	4.60359
P05544	DSTMEEILEGLK	1.028059823	2	3.01346
P05544	IAELFSDLEER	1.303434701	2	2.87591
P05544	MQQVESSLQPETLK	0.792684697	2	4.21575
P05544	MQQVESSLQPETLK+Oxidation(0)	0.759554282		
P05544	VFSQQADLSR	1.573478536	2	2.57679
P05545	**SPA3K Serine protease inhibitor A3K**	**1.553211027**	**5.66E-05**	**8**
P05545	ALYQAEAFVADFK	1.494697227	2	2.88484
P05545	AVLDVDETGTEGAAATAVTAALK	1.161218513	2	5.44329
P05545	FSISTDYNLEEVLPELGIR	1.358526099	2	3.48667
P05545	IAELFSELDER	1.625369491	2	3.04652
P05545	IFSQQADLSR	1.181454574	2	2.58077
P05545	LSQPEDQAEINTGSALFIDK	1.691844837	2	4.84718
P05545	LSQPEDQAEINTGSALFIDKEQPILSEFQEK	2.443602434	3	4.31973
P05545	NVVFSPLSISAALAILSLGAK	1.41088802		
P05765	**RS21 40S ribosomal protein S21**	**1.032794957**	**0.999395**	**3**
P05765	DHASIQMNVAEVDR	1.054343288	2	3.83867
P05765	MGESDDSILR	1.075053016	2	2.89626
P05765	TYGICGAIR	1.042351336	2	2.51174
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.934216002**	**0.070982**	**8**
P06214	AGADIIITYFAPQLLK	1.684321256	2	4.1878
P06214	AGCQVVAPSDMMDGR	0.898882442	2	3.46343
P06214	CVLIFGVPSR	1.210912849	2	2.83558
P06214	DEQGSAADSEDSPTIEAVR	0.979817083	2	5.50661
P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.954323183	3	4.58302
P06214	TAVLESMTAFR	0.815266974	2	2.95096
P06214	VPKDEQGSAADSEDSPTIEAVR	0.88543855	3	5.03624
P06214	YGVNQLEEMLRPLVEAGLR	0.911848202	3	4.58936
P06238	**A2MG Alpha_2_macroglobulin**	**1.063923661**	**0.050995**	**3**
P06238	FQVNNNNQLLLQR	3.1801399	2	3.07279
P06238	SESNMAIADVK	1.301857174	2	2.47333
P06238	VAVQLEASPDFLAAPEEK	0.789482421	2	3.44295
P06302	**PTMA Prothymosin alpha**	**0.821003464**	**0.685637**	**4**
P06302	EVVEEAENGR	1.028491863	2	2.34524
P06302	RVAEDDEDDDVETKK	0.968466969	3	5.88402
P06302	VAEDDEDDDVETK	0.911827394	2	3.86252
P06302	VAEDDEDDDVETKK	0.73787585	2	4.69345
P06399	**FIBA Fibrinogen alpha chain**	**0.724926243**	**0.004001**	**8**
P06399	AQQIQVLQK	0.828325589	2	2.64902
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.696500784	3	3.76901
P06399	GDFANANNFDNTFGQVSEDLR	0.725892057	2	5.69467
P06399	GDFANANNFDNTFGQVSEDLRR	0.696132349	3	3.30305
P06399	GLIDEANQDFTNR	1.103029329	2	3.65756
P06399	MADEAASEAHQEGDTR	0.616877584	2	4.11618
P06399	SQLQEGPPEWK	0.497559786	2	2.60251
P06399	TSDSDIFTDIENPSSHVPEFSSSSK	0.527960297	2	4.67255
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.298205934**	**9.97E-14**	**5**
P06685	AVAGDASESALLK	1.405929133	2	3.16047
P06685	AVFQANQENLPILK	1.174230906	2	3.32725
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.292826375	3	3.32619
P06685	LNIPVNQVNPR	1.334764313	2	3.03229

P06685	YEPAAVSEHGDKK	**1.432321178**	2	2.67432
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.129015396**	**0.10987**	**3**
P06687	DGPNALTPPPTTPEWVK	**0.997390758**	2	2.64782
P06687	GVGIISEGNETVEDIAAR	**1.147725303**	2	4.6888
P06687	QGAIVAVTGDGVNDSPALK	**1.145870861**	2	4.79796
P06757	**ADH1 Alcohol dehydrogenase 1**	**0.814794245**	**1**	**18**
P06757	AAVLWEPHKPFTIEDIEVAPPK	**0.962157899**	3	5.44958
P06757	FPLEPLITHVLPFEK	**1.326034797**	3	4.51236
P06757	GAIFGGFK	**0.835522121**	2	2.34464
P06757	GALLDGTSR	**1.013384607**	2	2.85964
P06757	GKPIHHFISTSTFSQYTVVDDIAVAK	**1.237357058**	3	5.00109
P06757	HPESNLCCQTK	**3.143547944**	2	3.22914
P06757	ICKHPESNLCCQTK	**1.412943716**	3	4.13346
P06757	IDAAAPLDK	**0.824370514**	2	2.74542
P06757	IIAVDINKDK	**0.794170247**	2	2.71909
P06757	INEAFDLLR	**0.998744242**	2	3.58126
P06757	KFPLEPLITHVLPFEK	**0.859188492**	3	4.55814
P06757	LVADFMAK	**0.993899889**	2	2.60782
P06757	MVATGVCR	**0.803252896**	2	2.54107
P06757	MVATGVCR+Oxidation(0)	**1.000047696**		
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	**0.9331557**	4	7.6707
P06757	VCLIGCGFSTGYGSAVQVAK	**0.893056603**	2	6.18161
P06757	VIPLFSPQCGK	**0.990060935**	2	2.74263
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	**0.791399032**	2	5.14327
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.113400061**	**9.9E-20**	**30**
P06761	AKFEELNMDLFR	**1.083623924**	3	4.2463
P06761	DAGTIAGLNVMR	**1.112219426**	2	3.49273
P06761	DNHLLGTFDLTGIPPAPR	**1.069833423**	2	4.24679
P06761	ELEEIVQPIISK	**0.98223223**	2	3.98022
P06761	FEELNMDLFR	**0.857471596**	2	3.48431
P06761	FEELNMDLFR+Oxidation(5)	**0.780014597**		
P06761	IEIESFFEGEDFSETLTR	**0.99504038**	2	5.27208
P06761	IEWLESHQDADIEDFK	**0.906986543**	2	5.68795
P06761	IEWLESHQDADIEDFKAK	**0.771135767**	3	4.16432
P06761	IINEPTAAAIAYGLDKR	**1.258722198**	2	4.46604
P06761	ITITNDQNR	**1.09243547**	2	2.66427
P06761	ITPSYVAFTPEGER	**1.329210264**	2	4.28242
P06761	KKELEEIVQPIISK	**1.056284358**	2	5.1065
P06761	KSDIDEIVLVGGSTR	**1.092483774**	2	4.54451
P06761	KSQIFSTASDNQPTVTIK	**1.121945087**	2	5.51791
P06761	LYGSGGPPPTGEEDTSEKDEL	**1.804959339**	2	5.69816
P06761	MKETAEAYLGK	**1.013070398**	2	2.6979
P06761	MKETAEAYLGK+Oxidation(0)	**1.489289777**		
P06761	NELESYAYSLK	**1.664998104**	2	3.67002
P06761	NQLTSNPENTVFDAK	**1.101374096**	2	5.12111
P06761	SDIDEIVLVGGSTR	**1.033930009**	1	3.50859
P06761	SQIFSTASDNQPTVTIK	**1.113300991**	2	5.29809
P06761	TFAPEEISAMVLTK	**0.928940019**	2	4.86954
P06761	TFAPEEISAMVLTK+Oxidation(9)	**1.272756476**		
P06761	TKPYIQVDIGGGQTK	**1.306363845**	3	4.63146
P06761	TWNDPSVQQDIK	**1.047375641**	2	4.01456
P06761	VLEDSDLK	**1.052099508**	1	2.11651
P06761	VLEDSDLKK	**0.919383576**	2	2.35961
P06761	VTHAVVTVPAYFNDAQR	**1.139155305**	2	5.05621
P06761	VYEGERPLTK	**1.037675493**	2	2.89851

P06866	**HPT Haptoglobin**	**1.582577035**	**1.39E-11**	**8**
P06866	ATDLKDWVQETMAK	**1.218739153**	3	3.81799
P06866	CELHYEK	**1.751492102**	2	2.34513
P06866	GAVSPVGVQPILNK	**1.199463844**	2	4.60481
P06866	KGAVSPVGVQPILNK	**2.109910583**	2	3.1009
P06866	LQTEGDGIYTLNSEK	**1.666221099**	2	4.25428
P06866	NQLVEIEK	**1.297524617**	1	2.33561
P06866	SCAVAEYGVYVR	**1.362416334**	2	3.11541
P06866	SVVDIGLIK	**1.079164965**	2	2.7627
P07150	**ANXA1 Annexin A1**	**0.990966468**	**0.985938**	**2**
P07150	GLGTDEDTLIEILTTR	**0.983805458**	2	4.27913
P07150	GVDEATIIDILTK	**1.155197586**	2	3.12517
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.567512656**	**8.43E-10**	**16**
P07153	ASSFVLALEPELESR	**1.249048396**	2	4.46486
P07153	AVTSEIAVLQSR	**0.045741544**	2	3.7036
P07153	FVDHVFDEQVIDSLTVK	**1.010961609**	2	4.14231
P07153	GEDEEDNNLEVR	**1.237846912**	2	3.73351
P07153	HFDETVNR	**1.029539642**	2	2.51179
P07153	IDHILDAL	**2.348307121**	2	2.313
P07153	ISIVVETVYTHVLHPYPTQITQSEK	**1.409342162**	3	4.62788
P07153	LKTEGSDLCDR	**1.176551962**	3	3.41215
P07153	NIQVDSPYDISR	**1.324807547**	2	3.78317
P07153	NLVEQHIQDIVVHYTFNK	**1.551546064**	3	4.45465
P07153	SEDILDYGPFK	**1.200456195**	2	3.39795
P07153	TEGSDLCDR	**1.209316518**	2	2.33111
P07153	TILPAAAQDVYYR	**2.211828**	2	3.29564
P07153	TVDLSSHLAK	**1.012473**	2	2.59989
P07153	VHYENNSPFLTITSMTR	**1.208649314**	2	3.29341
P07153	VTAEVVLAHPGGGSTAR	**1.278501156**	2	4.4672
P07323	**ENOG Gamma_enolase**	**1.197612961**	**0.189461**	**4**
P07323	AAVPSGASTGIYEALELR	**1.192006033**	2	5.04186
P07323	FGANAILGVSLAVCK	**1.021963902**	2	3.50915
P07323	GNPTVEVDLHTAK	**0.433042992**	2	3.39459
P07323	SGETEDTFIADLVVGLCTGQIK	**1.096420431**	3	5.52837
P07335	**KCRB Creatine kinase B_type**	**1.029123755**	**0.35392**	**2**
P07335	FCTGLTQIETLFK	**0.755049139**	2	2.78021
P07335	GTGGVDTAAVGGVFDVSNADR	**1.040453748**	2	3.93755
P07338	**CTRB1 Chymotrypsinogen B**	**1.285254751**	**0.076747**	**2**
P07338	IVNGEDAIPGSWPWQVSLQDK	**0.555899378**	2	3.25844
P07338	LQQAALPIVSEADCK	**1.312458649**	2	2.69657
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.127540693**	**0.010932**	**2**
P07340	SYEAYVLNIIR	**2.406910031**	2	2.39268
P07340	YNPNVLPVQCTGK	**1.002355012**	2	2.60486
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.174929828**	**0.999903**	**13**
P07379	AINPENGFFGVAPGTSVK	**1.066602485**	2	4.71252
P07379	EEGWLAEHMLILGITNPEGK	**1.549663376**	2	4.01873
P07379	EVEEIDKYLEDQVNADLPYEIER	**0.81386427**	3	3.46965
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	**0.959693541**	3	4.94118
P07379	GLGDVNVEELFGISK	**1.174605075**	2	3.81999
P07379	IGIELTDSPYVVASMR	**0.875744992**	2	3.60867
P07379	MGTSVLEALGDGEFIK	**0.904352452**	2	3.71333
P07379	MGTSVLEALGDGEFIK+Oxidation(0)	**1.22511994**		
P07379	TVIITQEQR	**1.047156105**	2	2.66322

P07379	VECVGDDIAWMK	**0.970697497**	2	2.96585
P07379	VIQGSLDSLPQEVR	**1.124553832**	2	4.02369
P07379	YDNCWLALTDPR	**0.991582827**	2	2.50259
P07379	YLAAAFPSACGK	**1.186816655**	2	2.89215
P07483	**FABPH Fatty acid_binding protein_ heart**	**0.377527882**	**0.048016**	**3**
P07483	NFDDYMK	**2.548197589**	1	2.13109
P07483	QVASMTKPTTIIEK	**0.011993677**	2	3.40779
P07483	WDGQETTLTR	**0.759587535**	2	2.87467
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.155620349**	**1.52E-14**	**4**
P07632	DGVANVSIEDR	**1.331034426**	2	2.98403
P07632	GDGPVQGVIHFEQK	**1.348846895**	2	3.99333
P07632	HVGDLGNVAAGK	**1.169080969**	2	3.56743
P07632	VISLSGEHSIIGR	**1.38090984**	2	3.26097
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**1.108165081**	**3.11E-05**	**10**
P07633	AFDNDVDALCNLR	**1.330584247**	2	3.89917
P07633	AYNMLDIIHAVIDER	**1.093458397**	2	4.04047
P07633	GFVDDIIQPSSTR	**1.609026016**	2	4.08655
P07633	HLLGDTNYAWPTAEIAVMGAK	**1.005204227**	2	3.11814
P07633	ICCDLEVLASK	**1.23904184**	2	3.03434
P07633	IMDQAITVGAPVIGLNDSGGAR	**0.841720403**	2	4.45825
P07633	IQEGVESLAGYADIFLR	**1.198514441**	2	4.16819
P07633	LVPELDTVVPLESSK	**1.123369889**	2	3.49698
P07633	SVTNEDVTQEQLGGAK	**1.305790377**	2	5.27313
P07633	TVGIVGNQPNVASGCLDINSSVK	**0.99200433**	2	5.17818
P07687	**HYEP Epoxide hydrolase 1**	**1.321025181**	**1.11E-16**	**23**
P07687	DIELLYPYK	**0.812547537**	2	2.42564
P07687	DKEETLPLGDGWWGPGSKPSAK	**1.10097334**	3	5.48953
P07687	EDESIRPFK	**1.343796305**	2	2.672
P07687	EDESIRPFKVETSDEEIKDLHQR	**1.177489456**	3	5.63521
P07687	ELEDGGLER	**1.186150904**	2	2.66747
P07687	ENLGQGIMVHK	**0.980458826**	2	2.75009
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	**1.635213669**	3	6.22727
P07687	FHYGFNSNYMK	**1.02238413**	2	2.56571
P07687	FLGYTEKDIELLYPYK	**0.885477975**	2	4.68756
P07687	GGHFAAFEEPK	**0.976086367**	2	3.49493
P07687	IEGLDIHFIHVKPPQLPSGR	**1.90146409**	3	3.67523
P07687	IIPLLTDPK	**0.976202808**	2	2.52785
P07687	KFVSLAELQ	**1.326164217**	2	2.86118
P07687	KQVEILNQYPHFK	**0.83709081**	3	4.8346
P07687	LLAQDIR	**1.170106651**	2	2.51821
P07687	QVEILNQYPHFK	**0.863625795**	2	3.74774
P07687	SEYRELEDGGLER	**1.583681089**	2	2.37524
P07687	SFYTMTPLLGQR	**2.312410968**	2	3.14608
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	**0.959131312**	3	6.46636
P07687	TKIEGLDIHFIHVKPPQLPSGR	**3.619310122**	3	3.88242
P07687	VETSDEEIK	**0.881869584**	2	2.47502
P07687	VETSDEEIKDLHQR	**1.083955545**	2	4.49115
P07687	VFVPTGFSAFPSELLHAPEK	**1.17363291**	2	4.73921
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.543538199**	**9.9E-20**	**96**
P07756	AADTIGYPVMIR	**1.485941195**	2	4.0677
P07756	AADTIGYPVMIR+Oxidation(9)	**2.164753672**		
P07756	AERPDGLILGMGGQTALNCGVELFK	**1.262710368**	3	7.09728
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10)	**1.361495261**		
P07756	AERPDGLILGMGGQTALNCGVELFKR	**1.799437517**	3	4.40191

P07756	AFAISGPFNVQFLVK	**1.112799198**	2	5.0755
P07756	AFAMTNQILVER	**1.03725565**	2	4.44874
P07756	AFAMTNQILVER+Oxidation(3)	**1.374711538**		
P07756	ALENNMSLDEIVK	**1.050029262**	2	4.58932
P07756	ALENNMSLDEIVK+Oxidation(5)	**1.278277366**		
P07756	AQTAHIVLEDGTK	**0.979727603**	2	4.51227
P07756	ATGYPLAFIAAK	**2.231977895**	2	3.06182
P07756	CEMASTGEVACFGEGIHTAFLK	**1.125013204**	3	5.36484
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2)	**1.299942549**		
P07756	CLGLTEAQTR	**1.005303001**	2	3.67824
P07756	DELGLNK	**1.255793311**	2	2.54471
P07756	DGSIDLVINLPNNNTK	**1.280131006**	2	5.46171
P07756	DILNMDK	**1.196017632**	1	1.95249
P07756	EIEYEVVR	**1.380784626**	2	2.30299
P07756	EPLFGISTGNIITGLAAGAK	**1.509510373**	3	5.73545
P07756	ETLMDLGTK	**1.2036278**	1	2.31788
P07756	EVEMDAVGK	**1.508984275**	1	2.21111
P07756	FLEEATR	**0.945470699**	2	2.49813
P07756	FLGVAEQLHNEGFK	**1.249427926**	2	4.68048
P07756	FVHDNYVIR	**1.569393118**	3	3.43272
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	**1.193104927**	3	6.34968
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15)	**1.607886145**		
P07756	GILIGIQQSFRPR	**0.505471251**	2	2.53375
P07756	GLNSESVTEETLR	**1.282183297**	2	4.85291
P07756	GNDVLVIECNLR	**1.087986765**	2	4.48727
P07756	GQILTMANPIIGNGGAPDTTAR	**0.988619321**	2	6.26868
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5)	**1.328202615**		
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	**0.825356356**	3	4.85266
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK+Oxidation(5)	**1.092573365**		
P07756	GQNQPVLNITNR	**1.102197124**	2	4.22802
P07756	GTTITSVLPKPALVASR	**0.970174515**	2	3.48367
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	**2.602456205**	3	6.62012
P07756	HLPTLEQPIIPSDYVAIK	**1.179418739**	2	5.61954
P07756	IALGIPLPEIK	**1.839165063**	2	3.27744
P07756	IAPSFAVESMEDALK	**1.850411155**	2	5.29116
P07756	IAPSFAVESMEDALK+Oxidation(9)	**1.007165488**		
P07756	IEFEGQSVDFVDPNK	**1.010587508**	2	5.16377
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	**1.278014012**	3	5.33352
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	**1.167212715**	3	5.43199
P07756	ILESDRKEPLFGISTGNIITGLAAGAK	**1.180929732**	3	3.69789
P07756	IMGTSPLQIDR	**1.847158947**	2	3.29278
P07756	IMGTSPLQIDR+Oxidation(1)	**2.599361085**		
P07756	IMGTSPLQIDRAEDR	**0.600331971**	2	2.58814
P07756	KEPLFGISTGNIITGLAAGAK	**0.833198774**	2	5.24547
P07756	KTVVVNCNPETVSTDFDECDK	**0.274410796**	2	4.91851
P07756	LFAEAVQK	**1.170917394**	2	3.13731
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	**1.676310027**	3	4.9762
P07756	LRDADPILR	**1.374530621**	2	3.23029
P07756	LTSIDKWFLYK	**0.816295894**	2	2.57635
P07756	LYFEELSLER	**1.637410238**	2	3.5846
P07756	MCHPSVDGFTPR	**0.865789971**	3	4.96953
P07756	MCHPSVDGFTPR+Oxidation(0)	**1.280902196**		
P07756	MRDILNMDK	**0.725544773**	2	2.46146

P07756	MRDILNMDK+Oxidation(0)	**1.394598795**		
P07756	QADAVYFLPITPQFVTEVIK	**2.692853354**	3	5.23386
P07756	QIDTLAAEYPSVTNYLYVTYNGQEHDIK	**6.897428515**	3	4.8584
P07756	QLFSDK	**1.280368969**	1	1.90003
P07756	QLFSDKLNEINEK	**1.194592635**	2	3.72978
P07756	QNLIAEVSTK	**1.199887369**	1	2.79997
P07756	RFLEEATR	**1.21581384**	2	2.67996
P07756	RGAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	**1.303365393**	4	5.01593
P07756	RTAVDSGIALLTNFQVTK	**1.314486982**	2	5.02079
P07756	SAYALGGLGSGICPNK	**1.476817426**	2	5.0417
P07756	SAYALGGLGSGICPNKETLMDLGTK	**1.07893769**	2	4.38164
P07756	SFPFVSK	**1.313911006**	1	1.91672
P07756	SIFSAVLDELK	**1.427375351**	2	4.11419
P07756	SIFSAVLDELKVAQAPWK	**1.419703908**	3	4.52058
P07756	SLGQWLQEEK	**1.095523969**	2	3.97682
P07756	SVGEVMAIGR	**1.058671519**	2	3.4717
P07756	SVGEVMAIGR+Oxidation(5)	**1.363755922**		
P07756	TAVDSGIALLTNFQVTK	**1.597131151**	3	6.61693
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	**1.215197709**	3	4.42914
P07756	TFEESFQK	**1.108768709**	2	2.54569
P07756	TLGVDFIDVATK	**1.138200246**	2	4.22028
P07756	TSACFEPSLDYMVTK	**1.123697014**	2	4.78583
P07756	TSACFEPSLDYMVTK+Oxidation(11)	**1.426508805**		
P07756	TVLMNPNIASVQTNEVGLK	**0.908550986**	2	6.40784
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3)	**1.133448545**		
P07756	TVVVNCNPETVSTDFDECDK	**0.469651228**	2	5.7037
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	**1.752311275**	3	5.51595
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	**1.102321269**	3	7.50533
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22)	**1.390696386**		
P07756	VLGTSVESIMATEDR	**1.138528988**	2	4.78923
P07756	VLGTSVESIMATEDR+Oxidation(9)	**1.398834367**		
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	**1.069280347**	2	5.94713
P07756	VMIGESVDEK	**0.929083227**	2	3.51645
P07756	VMIGESVDEK+Oxidation(1)	**1.361816927**		
P07756	VSQEHPVVLTK	**1.212408768**	2	3.68452
P07756	VVAVDCGIK	**1.064400129**	2	2.59941
P07756	YMESDGIK	**1.035438722**	2	2.42034
P07756	YMESDGIK+Oxidation(1)	**1.285737769**		
P07824	**ARGI1 Arginase_1**	**1.244517199**	**9.9E-20**	**16**
P07824	ANEQLAAVVAETQK	**1.369564603**	2	5.19209
P07824	DHGDLAFVDVPNDSPFQIVK	**1.569381987**	2	6.30323
P07824	DIVYIGLR	**2.793190301**	2	2.38634
P07824	DVDPGEHYIIK	**1.959096123**	2	3.36103
P07824	EGNHKPETDYLKPPK	**1.748389561**	2	2.68904
P07824	GKFPDVPGFSWVTPCISAK	**1.453137597**	3	4.96317
P07824	LKETEYNVR	**1.555722536**	3	3.34739
P07824	NGTISVVLGGDHSMAIGSISGHAR	**1.16862812**	3	4.41851
P07824	TGLLSGLDIMEVNPTLGK	**1.411357715**	2	5.85325
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9)	**1.078117082**		
P07824	TVNTAVALTLSCFGTK	**1.619532053**	2	5.26928
P07824	VHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLK	**2.009972144**	4	5.56051
P07824	VMEETFSYLLGR	**5.007591296**	2	3.95762
P07824	VMEETFSYLLGR+Oxidation(1)	**4.715682659**		
P07824	YFSMTEVDK	**1.402595628**	2	2.42588

P07824	YFSMTEVDKLGIGK+Oxidation(3)	**1.128605717**		
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.794063594**	**9.9E-20**	**18**
P07871	AEELGLPILGVLR	**0.857715422**	2	4.26529
P07871	AEIVPVTTTVLDDK	**0.822799871**	2	4.42065
P07871	AEIVPVTTTVLDDKGDR	**0.749056045**	2	3.97801
P07871	AEIVPVTTTVLDDKGDRK	**0.763637826**	2	3.61479
P07871	DCLIPMGITSENVAER	**1.060152733**	2	2.87824
P07871	DCLIPMGITSENVAER+Oxidation(5)	**0.919466249**		
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	**0.885641016**	2	6.42301
P07871	GGFKDTTPDELLSAVLTAVLQDVK	**0.815416886**		
P07871	IAQFLSGIPETVPLSAVNR	**2.996945707**	2	2.83674
P07871	LKPECLGDISVGNVLQPGAGAAMAR	**0.640166983**	3	4.32479
P07871	QCSSGLQAVANIAGGIR	**0.71355524**	2	5.10099
P07871	QDAFALASQQK	**0.764842328**	2	3.42173
P07871	QKQDAFALASQQK	**0.657190956**	2	4.1141
P07871	QVVTLLNELK	**1.135562099**	2	2.59609
P07871	SKAEELGLPILGVLR	**0.634879818**	3	4.44634
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	**0.731038489**	3	4.85553
P07871	TITVSQDEGVRPSTTMEGLAK	**0.71549921**	2	4.59334
P07871	VNPLGGAIALGHPLGCTGAR	**0.677651035**	2	4.7787
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.863062877**	**9.9E-20**	**19**
P07872	AFTTWTANAGIEECR	**0.701436522**	2	4.04414
P07872	ASATFNPELITHILDGSPENTR	**0.748349146**	2	4.59124
P07872	ASEAHCHYVVVK	**0.887964985**	3	4.21119
P07872	EIENLILNDPDFQHEDYNFLTR	**0.960384545**	2	4.41354
P07872	EIGTHKPLPGITVGDIGPK	**0.744767344**	2	3.55084
P07872	EVAWNLTSVDLVR	**0.632168354**	2	3.76222
P07872	EYGISDPEEIMWFK	**0.787801112**	2	3.49099
P07872	FGYEEMDNGYLK	**0.682687712**	2	3.44121
P07872	GGDFLEGSIITGAQLSQVNAR	**0.691729098**	2	5.75114
P07872	GLETTATYDPK	**0.776299984**	2	3.20909
P07872	INESIGQGDLSELPELHALTAGLK	**0.77135101**	3	5.48688
P07872	LVEIAAK	**0.798120467**	1	2.06085
P07872	LVGGMVSYLNDLPSQR	**1.322835032**	2	3.36774
P07872	QSEPEPQILDFQTQQYK	**0.66145615**	2	4.72978
P07872	SFLVGNAAQSLSK	**0.729890503**	2	4.50019
P07872	TQEFILNSPTVTSIK	**0.732814068**	2	4.70104
P07872	TSNHAIVLAQLITQGECYGLHAFVVPIR	**0.7019441**	3	5.79266
P07872	YAQVKPDGTYVKPLSNK	**2.579217825**	3	3.78634
P07872	YDGNVYENLFEWAK	**0.728659055**	2	5.27812
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**1.070111553**	**0.937554**	**3**
P07895	AIWNVINWENVSQR	**1.062992124**	2	3.60614
P07895	GDVTTQVALQPALK	**0.957977417**	2	3.48564
P07895	HHATYVNNLNVTEEK	**1.167978534**	2	4.62507
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.988080038**	**9.9E-20**	**25**
P07896	ELSTVDLVVEAVFEDMNLK	**1.325901704**		
P07896	EWQSLAGPHGSK	**1.653148236**	2	2.90328
P07896	GGPMFYAASVGLPTVLEK	**1.018135118**	2	3.93728
P07896	GQGLTGPSLPPGTPVR	**0.568890082**	2	4.0104
P07896	GWYQYDKPLGR	**0.648891515**	2	2.93592
P07896	IFNKPVPSLPNMDSVFAEAIAK	**0.839525817**	3	4.06811
P07896	IGVVVGNCYGFVGNR	**0.972736711**	2	3.08938
P07896	IIDKPIEPR	**0.811962333**	2	2.63716
P07896	KGQGLTGPSLPPGTPVR	**0.578338469**	2	4.58959
P07896	KQYPGVLAPETCVR	**0.42920983**	2	3.75909
P07896	LCNPPVNAVSPTVIR	**0.801922484**	2	4.33821

P07896	LGILDAVVK	0.750158242	2	2.81568
P07896	LLEVIPSR	0.74207523	2	2.38265
P07896	LVAQGSPPLK	0.872273867	2	2.37648
P07896	QNPDIPQLEPSDYLR	0.469852239	2	3.7748
P07896	QYPGVLAPETCVR	0.655280632	2	3.28746
P07896	TASAQPVSSVGVLGLGTMGR	0.763563022	2	5.19283
P07896	TASAQPVSSVGVLGLGTMGR+Oxidation(17)	1.010960311		
P07896	TISKEEILER	0.569725846	2	2.68446
P07896	VGISVVAVESDPK	0.623262171	2	3.81967
P07896	VGLPEVTLGILPGAR	0.590586444	2	3.55849
P07896	VSDLAGLDVGWK	0.628523905	2	4.11553
P07896	YLSADEALR	0.79316483	2	2.6571
P07896	YSPLGDMLCEAGR	0.507931186	2	4.0767
P07896	YSSPTTIATVMSLSK	1.129316465	2	3.35693
P07953	**F261 6_phosphofructo_2_kinase/fructose_2_6_biphosphatase 1**	**1.054215415**	**0.256437**	**3**
P07953	IGGDSGLSAR	0.775998756	2	2.39163
P07953	NYEFFRPDNTEAQLIR	1.015642712	2	2.97137
P07953	TIQTAEALGVPYEQWK	1.539332698	2	2.96376
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.331778525**	**1.18E-07**	**5**
P08009	LCYNPDFEK	1.760803147	2	2.81028
P08009	LLLEYTDSSYEEK	1.205176363	2	4.8159
P08009	LLLEYTDSSYEEKR	1.096608582	2	3.83535
P08009	NQVFEATCLDAFPNLK	0.796241877	2	4.89727
P08009	SQWLNEK	1.073401153	2	2.65168
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.819324936**	**9.9E-20**	**15**
P08010	FLSKPIFAK	1.243399397	1	1.93275
P08010	IRVDVLENQAMDTR	1.105752126	3	4.21167
P08010	ITYVDFLVYDVLDQHR	1.940522504	2	4.80816
P08010	KKPEYLEGLPEK	1.078362521	3	4.43253
P08010	KPEYLEGLPEK	1.829472172	2	3.71253
P08010	KYSMGDAPDYDR	1.103474637	2	3.58545
P08010	LFLEYTDTSYEDK	1.250069326	2	5.42186
P08010	LFLEYTDTSYEDKK	1.336264847	2	4.26878
P08010	LQLAMVCYSPDFER	1.966733368	2	4.80497
P08010	LQLAMVCYSPDFER+Oxidation(4)	1.95836109		
P08010	SQWLSEK	1.183318151	2	2.45639
P08010	VDVLENQAMDTR	1.060281789	2	4.66655
P08010	VDVLENQAMDTR+Oxidation(8)	1.333320489		
P08010	YSMGDAPDYDR	1.431936409	2	3.11258
P08010	YSMGDAPDYDR+Oxidation(2)	1.480042038		
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.960009986**	**0.075086**	**7**
P08011	IYHTIAYLTPLPQPNR	1.535911013	2	4.81524
P08011	MMFLSSATAFQR	1.147126511	2	3.30555
P08011	MMFLSSATAFQR+Oxidation(0)	0.971719471		
P08011	MMFLSSATAFQR+Oxidation(0)	1.42679367		
P08011	MMFLSSATAFQR+Oxidation(1)	1.42679367	2	3.0608
P08011	VFANPEDCAGFGK	0.995329782	2	4.57497
P08011	VFANPEDCAGFGKGENAK	0.800788303	2	4.52619
P08081	**CLCA Clathrin light chain A**	**1.222579828**	**0.56836**	**2**
P08081	LEALDANSR	1.145883048	2	2.58161
P08081	WREEQTER	1.337667801	2	2.45204
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**1.05595524**	**0.954546**	**2**
P08290	EEQEFVVK	1.063410829	1	1.94814
P08290	WVDGTEYR	1.032561655	2	2.31462

P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.08074206**	**0.007451**	**4**
P08461	AAPAAAAAAPPGPR	**0.993138582**	2	2.62333
P08461	DVPLGTPLCIIVEK	**1.400026751**	2	3.14107
P08461	GLETIASDVVSLASK	**1.033983228**	2	3.90556
P08461	VAPTPAGVFIDIPISNIR	**1.107988045**	2	4.90705
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.903982001**	**0.014391**	**9**
P08503	AFTGFIVEADTPGIHIGK	**0.862546804**	2	4.29523
P08503	ANWYFVLTR	**1.122930094**	2	2.625
P08503	EEIIPVAPDYDK	**1.021753988**	2	3.28841
P08503	GITFEDVR	**1.015854912**	2	2.43476
P08503	IYQIYEGTAQIQR	**1.168865198**	2	4.97248
P08503	KGDEYVINGQK	**1.02552038**	2	4.34062
P08503	QEPGLGFSFELTEQQK	**0.876784296**	2	3.20518
P08503	SGEYPFPLIK	**0.859283949**	2	2.48541
P08503	TRPTVAAGAVGLAQR	**0.828214531**	2	4.46213
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**2.398625022**	**2.63E-10**	**10**
P08541	DELQNHFIK	**1.541307701**	2	2.38517
P08541	FEIFSTSISK	**1.399558555**	2	2.43766
P08541	FEIFSTSISKDELQNHFIK	**1.056122319**	2	4.17513
P08541	FILPPSYVPVILSGLAGK	**1.628620726**	3	5.63558
P08541	GHEVTVLKPSAYFFLDPK	**2.971325518**	2	4.07865
P08541	HKEWDTFYSEILGRPTTVDETMSK	**1.666468292**	3	4.41874
P08541	LDFLSALEEVIDNPFYK	**1.338963371**		
P08541	LLDVWTYELPR	**2.54838404**	3	3.89172
P08541	NVMLLSTIHHDQPMKPLDR	**1.082289973**	3	3.61748
P08541	VEIWLIR	**1.111228799**	2	2.92876
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.194956725**	**0.000367**	**10**
P08542	EIINNPFYK	**1.306057939**	1	2.19694
P08542	FETFPTSVSKDELENYFIK	**1.1257167**	2	4.07582
P08542	FSPGYKIEKSSGR	**1.106900883**	2	2.33728
P08542	KWDPFYSEILGRPTTLAETMGK	**1.077681003**	2	3.95044
P08542	LVDVWTYELQR	**1.443948542**	2	3.51047
P08542	NAVWLSTIHHDQPMKPLDK	**1.529639092**	3	3.3089
P08542	NAVWLSTIHHDQPMKPLDK+Oxidation(13)	**1.731055938**		
P08542	SDLFNALKEIINNPFYK	**0.784706432**	2	2.32874
P08542	TPATLGPNTR	**1.082213384**	2	2.31541
P08542	WDPFYSEILGRPTTLAETMGK	**1.320184286**	2	3.45626
P08683	**CP2CB Cytochrome P450 2C11**	**0.724938661**	**5.47E-13**	**17**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	**0.83125868**	3	5.23571
P08683	EALVDLGEEFSGR	**0.746953523**	2	4.03007
P08683	EHQESLDKDNPR	**0.263283695**	2	4.11068
P08683	FDPGHFLDER	**0.597908891**	2	2.3421
P08683	FDYKDPTFLNLMHR	**0.874026434**	3	5.03702
P08683	FNENFR	**0.715556166**	1	1.97992
P08683	GAPFDPTFILGCAPCNVICSIIFQNR	**1.001358595**	3	5.24738
P08683	GTNVIVSLSSILHDDKEFPNPEK	**0.942203454**	2	5.19422
P08683	ICAGEALAR	**0.958554128**	2	2.80686
P08683	LPPGPTPLPIIGNTLQIYMK	**1.282415295**	3	3.85074
P08683	NYVLEK	**0.844246473**	1	1.96148
P08683	SQMPYTDAVVHEIQR	**0.709988522**	2	4.2556
P08683	SQMPYTDAVVHEIQR+Oxidation(2)	**1.067823431**		
P08683	VKEHQESLDKDNPR	**0.703585634**	3	5.02683
P08683	VQEEIER	**0.808907551**	2	2.56421
P08683	YGLLLLLK	**0.864838962**	2	3.03297

P08683	YIDLVPTNLPHLVTR	**0.582001723**	2	4.17715
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**0.752599469**	**0.122483**	**3**
P08733	GADPEETILNAFK	**0.788782619**	2	3.50039
P08733	NEEIDEMIK	**1.319103907**	1	2.49773
P08733	NLVHIITHGEEKD	**0.064246963**	2	2.97889
P09006	**SPA3N Serine protease inhibitor A3N**	**0.88683301**	**0.656843**	**2**
P09034	**ASSY Argininosuccinate synthase**	**2.940243244**	**9.9E-20**	**15**
P09034	APNTPDVLEIEFK	**3.118899971**	2	3.34169
P09034	DGTTHSTSLDLFMYLNEVAGK	**6.464044743**	2	5.79458
P09034	EFVEEFIWPAVQSSALYEDR	**2.701458608**	3	5.62464
P09034	EQGYDVIAYLANIGQK	**2.89308192**	2	4.55279
P09034	FAELVYTGFWHSPECEFVR	**4.943831879**	2	5.14998
P09034	FELTCYSLAPQIK	**4.855056138**	2	4.27415
P09034	GRNDLMEYAK	**2.096862546**	2	3.06075
P09034	IDIVENR	**1.608097469**	2	2.49909
P09034	KVFIEDVSK	**1.884436175**	3	3.76835
P09034	NDLMEYAK	**1.369717487**	2	2.64569
P09034	SPWSMDENLMHISYEAGILENPK	**3.996593895**	3	5.35389
P09034	TQDPAKAPNTPDVLEIEFK	**1.739317766**	2	4.74507
P09034	TQDPAKAPNTPDVLEIEFKK	**1.694365643**	3	4.28753
P09034	VFIEDVSK	**1.979590951**	2	2.62422
P09034	VQVSVFK	**2.177774482**	2	2.40724
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.149630849**	**0.000129**	**4**
P09041	FHVEEEGK	**0.962319448**	2	2.7276
P09041	LGDVYVNDAFGTAHR	**1.156050477**	3	4.07682
P09041	VDFNVPMK	**1.008024921**	1	2.06889
P09041	VSHVSTGGGASLELLEGK	**0.97677208**	2	5.65418
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.284612821**	**0.000117**	**2**
P09117	VLAAVYK	**1.301773089**	2	2.65019
P09117	YASICQQNGIVPIVEPEILPDGDHDLKR	**0.202390857**	3	3.62138
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.83229075**	**0.001221**	**2**
P09139	IGLLGYNATTENADR	**1.809865342**	2	3.32791
P09139	VLNAPPGISLISFNDK	**1.832905219**	2	3.04923
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**10.38315206**	**8.43E-06**	**4**
P09367	ALGVNTVGAQTLK	**7.218248837**	2	3.57425
P09367	AQLGLNELLK	**22.90820989**	1	2.00916
P09367	LGLPATIVVPSTTPALTIER	**5.858267091**	2	3.30031
P09367	MDSSQPSGSFK	**8.955643638**	2	2.31168
P09495	**TPM4 Tropomyosin alpha_4 chain**	**0.552307659**	**9.9E-20**	**13**
P09495	AEGDAAALNR	**1.108365916**	2	2.30945
P09495	EDKYEEEIK	**0.422831267**	1	2.63126
P09495	EENVGLHQTLDQTLNELNCI	**1.938026691**	2	4.93632
P09495	IQALQQQADDAEDR	**1.288750347**	2	4.65585
P09495	IQLVEEELDR	**0.553576122**	2	3.59185
P09495	IQLVEEELDRAQER	**0.674804888**	2	2.88161
P09495	KLVILEGELER	**0.38355685**	2	3.04976
P09495	LEEAEKAADESER	**0.399966918**	2	4.09306
P09495	LVILEGELER	**0.419257243**	2	3.33488
P09495	MEIQEMQLK	**0.261431617**	2	2.65872
P09495	RIQLVEEELDR	**0.631573829**	2	2.84578
P09495	YEEEIK	**0.618500123**	1	1.96475
P09495	YSEKEDKYEEEIK	**0.951775625**	2	4.18287
P09527	**RAB7A Ras_related protein Rab_7a**	**1.151236224**	**0.027802**	**5**
P09527	DPENFPFVVLGNK	**1.476750408**	2	3.52847

P09527	EAINVEQAFQTIAR	0.560451592	2	2.81084
P09527	GADCCVLVFDVTAPNTFK	1.211251808	2	4.1241
P09527	TLDSWRDEFLIQASPR	0.684082476	3	3.74278
P09527	VIILGDSGVGK	1.074265691	2	2.8733
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**0.755281917**	**0.093876**	**4**
P09605	GTGGVDTAAVADVYDISNIDR	0.735558389	2	4.78462
P09605	LSEMTEQDQQR	0.444210813	2	3.62994
P09605	LSEMTEQDQQR+Oxidation(3)	0.755936656		
P09605	SEVELVQIVIDGVNYLVDCEK	0.616922099		
P09606	**GLNA Glutamine synthetase**	**1.236431054**	**1.52E-13**	**6**
P09606	CIEEAIDK	1.066981074	2	2.84903
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.108405906	3	4.71273
P09606	LTGFHETSNINDFSAGVANR	1.38378552	2	6.07776
P09606	RLTGFHETSNINDFSAGVANR	0.979611444	3	5.08158
P09606	TCLLNETGDEPFQYK	1.498427068	2	5.31174
P09606	TCLLNETGDEPFQYKN	1.9821986	2	4.38498
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.251044888**	**0.008588**	**20**
P09811	DFSELEPDKFQNK	1.335921735	2	3.50231
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.041126949	3	4.71468
P09811	EGWQVEEADDWLR	1.055903894	2	3.82312
P09811	GIVGVENVAELK	1.023896369	2	3.0903
P09811	GIVGVENVAELKK	1.824238743	2	2.44371
P09811	HLQIIYEINQK	0.912176612	2	3.6481
P09811	IFVDIEK	1.133073901	1	2.08298
P09811	INPSSMFDVHVK	0.950645559	2	3.06965
P09811	LHSFVGDDIFLR	2.012653661	2	2.33314
P09811	LVIDQIDNGFFSPNQPDLFK	1.211244226	2	4.66664
P09811	LVTSVAEVVNNDPMVGSK	0.897211722	2	2.98035
P09811	TFAYTNHTVLPEALER	1.043599991	2	4.02074
P09811	VDDVAALDK	1.083830909	1	2.12805
P09811	VDDVAALDKK	1.060153005	2	3.11268
P09811	VFADYEAYVK	1.256690362	2	2.40198
P09811	VIPATDLSEQISTAGTEASGTGNMK	0.927807641	2	6.12173
P09811	VLYPNDNFFEGK	0.943633774	2	3.06361
P09811	VSQLYMNQK	2.348456212	2	3.09176
P09811	WLLLCNPGLADLIAEK	1.299169336	2	5.04339
P09811	YEYGIFNQK	1.096956227	2	2.56954
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**0.3513872**	**0.294345**	**12**
P09812	GLAGVENVSDLKK	0.779345176	2	3.03467
P09812	GYNAQEYYDRIPELR	#NUM!	2	2.77046
P09812	HLQIIYEINQR	1.517431791	2	2.91635
P09812	IGEEYISDLDQLR	0.595137507	2	3.85469
P09812	IGEEYISDLDQLRK	0.758802042	2	2.92432
P09812	LITAIGDVVNHDPAVGDR	0.350494657	2	3.60534
P09812	NLAENISR	0.889638535	1	2.47318
P09812	QIIEQLSSGFFSPK	0.61787135	2	3.25814
P09812	TNFDAFPDK	0.090670343	2	2.32305
P09812	VHINPNSLFDVQVK	0.884236892	2	2.80865
P09812	VIPAADLSEQISTAGTEASGTGNMK	0.553352305	2	5.03654
P09812	WLVLCNPGLAEVIAER	0.862846941	2	4.29391
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**1.119221568**	**3.44E-06**	**6**
P09875	ANVVASALAQIPQK	0.914315312	3	4.25851
P09875	FSGGLPLPPSYVPVVLSELSDR	1.868185964	3	4.64526
P09875	IILNELAQR	1.287892379	2	3.02238
P09875	SDLEYSFAK	1.415450601	2	2.50752
P09875	VDFSILSTTGLLTALK	1.009672448	2	4.53477
P09875	VFNEYSDVVENLCK	1.127499516	2	3.46126

P09895	**RL5 60S ribosomal protein L5**	**1.15035306**	**1.24E-06**	**5**
P09895	GAVDGGLSIPHSTK	**1.127199171**	2	4.37607
P09895	HIMGQNVADYMR	**0.775048487**	2	3.01488
P09895	NNVTPDMMEEMYK	**0.987130234**	2	3.35219
P09895	RFPGYDSESK	**1.349919467**	2	2.84024
P09895	YLMEEDEDAYKK	**1.271452496**	2	3.25328
P0C0S7	**H2AZ Histone H2A.Z**	**0.86006473**	**0.730578**	**2**
P0C0S7	ATIAGGGVIPHIHK	**0.862048258**	2	3.75109
P0C0S7	GDEELDSLIK	**0.771973823**	2	3.51846
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**1.112522878**	**9.9E-20**	**17**
P0C2X9	AIEAAVLAR	**0.996653142**	2	2.96848
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	**1.026960745**	3	5.56122
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	**1.044479958**	2	4.75895
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	**1.156654355**	3	3.74914
P0C2X9	EEIFGPVLTVYVYPDEK	**1.058305306**	2	4.14585
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	**1.057774538**	2	5.18492
P0C2X9	KEWDLKPVADR	**0.997543768**	2	3.34138
P0C2X9	LYVPQSLWPQIK	**1.655612032**	2	3.26604
P0C2X9	NAAGNFYINDK	**1.708220156**	2	3.51245
P0C2X9	NFHFVHSSADVDSVVSGTLR	**1.31187237**	2	5.8587
P0C2X9	SAFEYGGQK	**1.140182105**	2	2.45889
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	**1.125798032**	3	5.72013
P0C2X9	STGSVVGQQPFGGAR	**1.014190664**	2	4.40045
P0C2X9	TVIQAEIDAAAELIDFFR	**0.937478707**		
P0C2X9	VANEPILAFTQGSPER	**1.224136535**	2	5.4116
P0C2X9	VGNPAEDFGTFFSAVIDAK	**2.151079977**	2	4.96786
P0C2X9	YQLSPFNHGHK	**1.611747923**	2	2.93512
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.093115286**	**0.124954**	**4**
P0C5H9	DRDVTFSPATIEEELIK	**1.079700813**	2	4.71109
P0C5H9	DVTFSPATIEEELIK	**1.093648593**	2	3.20963
P0C5H9	IINEVSKPLAHHIPVEK	**1.248219379**	3	3.81203
P0C5H9	ILDDWGEMCK	**1.061838944**	2	2.39007
P0C6F1	**DYH2 Dynein heavy chain 2_ axonemal**	**1.346849151**	**0.002473**	**3**
P0C6F1	EDSVLGLQAFASWR	**1.280323467**	2	2.30316
P0C6F1	TMPLISDLR+Oxidation(1)	**1.606802515**		
P0C6F1	TMPLISDLRNPALR	**1.296876687**	2	2.39695
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**1.278943029**	**2.02E-08**	**12**
P10111	EGMSIVEAMER	**1.154733723**	2	2.99008
P10111	FEDENFILK	**1.084965327**	2	3.16549
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	**1.527582814**	3	5.95295
P10111	HTGPGILSMANAGPNTNGSQFFICTAK+Oxidation(8)	**1.203456308**		
P10111	IIPGFMCQGGDFTR	**1.045536597**	2	3.32359
P10111	ITISDCGQL	**1.124886536**	1	1.96819
P10111	KITISDCGQL	**1.37810485**	2	3.33028
P10111	SIYGEKFEDENFILK	**0.906003397**	2	4.42517
P10111	TEWLDGK	**1.023279483**	2	2.35127
P10111	VCFELFADK	**1.304466435**	2	3.32073
P10111	VCFELFADKVPK	**1.16519037**	2	3.85775
P10111	VKEGMSIVEAMER	**1.007687892**	2	3.00034
P10536	**RAB1B Ras_related protein Rab_1B**	**1.134643446**	**0.985491**	**3**
P10536	MGPGAASGGERPNLK	**0.836669284**	2	3.29535
P10536	NATNVEQAFMTMAAEIK+Oxidation(11)	**1.121139879**		
P10536	NATNVEQAFMTMAAEIK+Oxidation(9)	**1.126100422**		

P10633	**CP2D1 Cytochrome P450 2D1**	**0.974649729**	**0.249665**	**4**
P10633	LVEESLTEVSGFIPEVLNTFPALLR	**0.949586744**		
P10633	SQGVILASYGPEWR	**1.054737344**	2	4.19739
P10633	TFMALLDNLLAENR	**0.862440132**	2	3.50258
P10633	YGDVFSLQK	**0.967668941**	2	2.84155
P10634	**CP2DQ Cytochrome P450 2D26**	**0.986080778**	**0.000282**	**17**
P10634	ACLGEPLAR	**1.000143274**	2	2.66558
P10634	AVSNVIASLVYAR	**0.92545627**	3	4.46306
P10634	DMTDAFLAEMQK	**1.171054908**	2	3.02704
P10634	EAEHPFNPSILLSK	**1.122175625**	2	3.08222
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	**0.9343876**	3	4.90913
P10634	FADIVPTNIPHMTSR	**0.863677658**	2	2.66883
P10634	FEYEDPFFNR	**0.834254024**	2	2.69863
P10634	FHPEHFLDAQGNFVK	**0.874403105**	2	4.80594
P10634	GNPESSFNDENLR	**0.97241554**	2	4.20614
P10634	GTTLIPNLSSVLK	**0.887621178**	2	2.54552
P10634	GTTLIPNLSSVLKDETVWEKPLR	**0.638348375**	2	4.33431
P10634	GVVLAPYGPEWR	**0.840238564**	2	3.43619
P10634	LNSFIALVDK	**2.693027979**	2	2.48206
P10634	RFEYEDPFFNR	**0.953913583**	3	4.072
P10634	SLEQWVTEEAGHLCDTFAK	**1.012864456**	2	4.96519
P10634	SWDPAQPPR	**0.895534439**	2	2.65318
P10634	VHEEIDEVIGQVR	**0.915211073**	2	4.55214
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.123465896**	**9.9E-20**	**34**
P10719	AGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGR	**1.337632218**		
P10719	AHGGYSVFAGVGER	**2.088258895**	2	3.93031
P10719	AIAELGIYPAVDPLDSTSR	**0.998147434**	3	5.56254
P10719	DQEGQDVLLFIDNIFR	**6.285313546**		
P10719	EGNDLYHEMIESGVINLK	**1.063379188**	2	5.1579
P10719	FLSQPFQVAEVFTGHMGK	**1.516238846**	2	4.06247
P10719	FTQAGSEVSALLGR	**1.101257822**	2	4.84286
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	**2.072493505**	3	4.73012
P10719	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR	**3.757446388**	3	4.72002
P10719	IGLFGGAGVGK	**1.568404306**	2	3.02512
P10719	IGLFGGAGVGKTVLIMELINNVAK	**1.105204409**	3	3.49479
P10719	ILQDYK	**1.146543862**	1	2.17017
P10719	IMDPNIVGSEHYDVAR	**1.022778228**	2	4.819
P10719	IMDPNIVGSEHYDVAR+Oxidation(1)	**1.715485771**		
P10719	IMNVIGEPIDER	**1.299489335**	2	4.17051
P10719	IMNVIGEPIDER+Oxidation(1)	**1.807651362**		
P10719	IPSAVGYQPTLATDMGTMQER	**1.765664113**	2	4.83796
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14)	**2.345008716**		
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17)	**1.868478335**		
P10719	LVLEVAQHLGESTVR	**1.250594729**	2	4.67961
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	**1.156701602**	3	4.98528
P10719	SLQDIIAILGMDELSEEDKLTVSR	**1.001101178**	3	5.44174
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10)	**1.10684848**		
P10719	TIAMDGTEGLVR	**0.988149097**	2	3.37176
P10719	TIAMDGTEGLVR+Oxidation(3)	**1.326862748**		
P10719	TREGNDLYHEMIESGVINLK	**0.991329882**	2	6.10936
P10719	TVLIMELINNVAK	**0.978096402**	2	4.5711
P10719	TVLIMELINNVAK+Oxidation(4)	**1.264381322**		
P10719	VALTGLTVAEYFR	**2.441307832**	2	4.07275
P10719	VALVYGQMNEPPGAR	**1.006382616**	2	4.36311
P10719	VALVYGQMNEPPGAR+Oxidation(7)	**1.272810067**		
P10719	VLDSGAPIK	**1.105450158**	2	3.02841

P10719	VLDSGAPIKIPVGPETLGR	**1.018699011**	3	4.76193
P10719	VVDLLAPYAK	**1.036179833**	2	3.03147
P10760	**SAHH Adenosylhomocysteinase**	**1.268481768**	**9.9E-20**	**18**
P10760	ALDIAENEMPGLMR	**1.003570859**	2	4.31684
P10760	ALDIAENEMPGLMR+Oxidation(12)	**1.346617616**		
P10760	ATDVMIAGK	**1.090644592**	2	2.82463
P10760	DGPLNMILDDGGDLTNLIHTK	**1.452963179**	2	5.41981
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5)	**1.331151189**		
P10760	EMYSASKPLK	**1.818729541**	2	2.49508
P10760	FDNLYGCR	**1.292737775**	2	2.86189
P10760	GETDEEYLWCIEQTLHFK	**1.657245838**	2	4.27915
P10760	GISEETTTGVHNLYK	**1.265667877**	2	4.13385
P10760	IILLAEGR	**1.993760062**	2	2.80319
P10760	KLDEAVAEAHLGK	**1.326222433**	3	5.16178
P10760	LDEAVAEAHLGK	**1.27526148**	2	3.85233
P10760	RATDVMIAGK	**1.201787504**	2	2.69358
P10760	SKFDNLYGCR	**1.417662478**	2	2.87609
P10760	VAVVAGYGDVGK	**1.618199852**	2	4.2356
P10760	VNIKPQVDR	**1.317033318**	2	2.91937
P10760	WLNENAVEK	**1.338282624**	2	3.16334
P10760	WSSCNIFSTQDHAAAAIAK	**1.357844097**	2	5.08674
P10818	**CX6A1 Cytochrome c oxidase subunit 6A1_ mitochondrial**	**0.888914236**	**0.681125**	**2**
P10818	HEEHERPEFVAYPHLR	**1.058929637**	3	3.3204
P10818	SRHEEHERPEFVAYPHLR	**0.877775328**	3	3.66902
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**1.10623**	**9.9E-20**	**28**
P10860	ALASLMTYK	**1.295828506**	2	3.12053
P10860	CAVVDVPFGGAK	**1.25423348**	2	3.28834
P10860	CVGVGESDGSIWNPDGIDPK	**0.863050606**	2	5.15168
P10860	DDGSWEVIEGYR	**1.489837308**	2	4.09852
P10860	DIVHSGLAYTMER	**1.427871156**	2	3.319
P10860	DIVHSGLAYTMER+Oxidation(10)	**1.582065131**		
P10860	DSNYHLLMSVQESLER	**0.92797736**	2	3.69867
P10860	DSNYHLLMSVQESLER+Oxidation(7)	**1.983568958**		
P10860	EDDPNFFK	**1.170926126**	1	2.06388
P10860	GASIVEDKLVEDLK	**1.219132729**	2	3.42575
P10860	GFIGPGIDVPAPDMSTGER	**0.950944926**	2	5.55232
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13)	**0.940816127**		
P10860	HGGTIPVVPTAEFQDR	**1.093254256**	2	4.46853
P10860	IIAEGANGPTTPEADK	**1.051662995**	2	5.26113
P10860	IIAEGANGPTTPEADKIFLER	**1.091835805**	3	4.6932
P10860	KGFIGPGIDVPAPDMSTGER	**0.943206344**	2	5.5394
P10860	KGFIGPGIDVPAPDMSTGER+Oxidation(14)	**0.972416379**		
P10860	LQHGSILGFPK	**1.348184868**	2	2.72253
P10860	MVEGFFDR	**0.935106891**	2	2.82878
P10860	MVEGFFDR+Oxidation(0)	**1.431976959**		
P10860	NLNHVSYGR	**0.485388419**	2	2.33404
P10860	NYTDNELEK	**1.119110952**	2	2.4253
P10860	RDDGSWEVIEGYR	**1.299061484**	2	4.24201
P10860	TAAYVNAIEK	**1.323140889**	2	3.60226
P10860	TFVVQGFGNVGLHSMR	**0.679151636**	2	3.99847
P10860	VYEGSILEADCDILIPAASEK	**1.108221984**	3	5.92223
P10860	YNLGLDLR	**1.146669**	2	3.12985
P10860	YSTDVSVDEVK	**1.381710499**	2	3.18791
P10867	**GGLO L_gulonolactone oxidase**	**0.746338753**	**3.57E-11**	**7**
P10867	GDDILLSPCFQR	**0.839746343**	1	2.07442

P10867	GVQFQNWAK	1.210024	2	2.40734
P10867	LDPTGMFLNSYLEK	0.683709015	2	4.41574
P10867	LDYWLAYETIMK	0.935017541	2	4.36853
P10867	NADVFQAAR	0.72899776	2	2.80585
P10867	TYGCSPEVYYQPTSVEEVR	0.784663522	2	4.90496
P10867	VVAHYPVEVR	0.830914423	2	2.79662
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**0.869072243**	**0.145975**	**4**
P10868	EHWIIECNDGVFQR	1.060563861	2	4.02284
P10868	WETPYMHSLAAAAASR	1.648747079	2	3.91216
P10868	YTDITAMFEETQVPALLEAGFQR	1.101437329	3	6.55796
P10868	YYAFPQMITPLVTK	0.866583172	2	3.48161
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.245537203**	**7.9E-07**	**2**
P10888	IQFNESFAEMNK	1.255896448	2	4.51784
P10888	SEDYALPSYVDR	1.292723707	2	4.04538
P11030	**ACBP Acyl_CoA_binding protein**	**1.579267249**	**9.9E-20**	**3**
P11030	QATVGDVNTDRPGLLDLK	1.521786342	3	3.65245
P11030	TQPTDEEMLFIYSHFK	7.441122412	2	4.39372
P11030	WDSWNK	1.063773763	1	2.03708
P11232	**THIO Thioredoxin**	**1.186785643**	**0.014447**	**2**
P11232	EAFQEALAAAGDK	1.630245905	2	4.3168
P11232	VGEFSGANK	1.045030735	2	2.95964
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**0.96439652**	**4.56E-12**	**5**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.194573476	3	6.72896
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	2.065732351	3	6.62605
P11240	GMNTLVGYDLVPEPK	0.899110697	2	3.66218
P11240	LNDFASAVR	1.019948572	2	3.26188
P11240	RLNDFASAVR	1.017220755	2	2.97524
P11348	**DHPR Dihydropteridine reductase**	**1.124110119**	**0.000884**	**11**
P11348	AALDGTPGMIGYGMAK	1.232725328	2	3.87694
P11348	EGGLLTLAGAK	1.157282768	2	3.12362
P11348	GAVHQLCQSLAGK	1.17537585	3	4.60123
P11348	MTDSFTEQADQVTAEVGK	1.049681857	2	5.54745
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0)	1.261430441		
P11348	NCDLMWK	0.812584555	1	2.08039
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	0.994181975	2	5.36346
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3)	1.226540367		
P11348	QSIWTSTISSHLATK	0.927048275	2	3.86189
P11348	RPNSGSLIQVVTTDGK	1.003117063	2	4.08912
P11348	VDAILCVAGGWAGGNAK	0.932769503	2	4.48923
P11442	**CLH Clathrin heavy chain 1**	**0.972999309**	**1.1E-07**	**37**
P11442	AFMTADLPNELIELLEK	1.039330528	3	4.59635
P11442	AHIAQLCEK	0.97065037	1	2.25687
P11442	ALEHFTDLYDIK	0.971712558	3	3.87644
P11442	CNEPAVWSQLAK	1.055860295	2	3.25546
P11442	EDKLECSEELGDLVK	0.959989564	2	2.71679
P11442	FDVNTSAVQVLIEHIGNLDR	1.048612289	3	3.62401
P11442	FNALFAQGNYSEAAK	1.154907713	2	4.57674
P11442	GQCDLELINVCNENSLFK	0.894526018	2	5.09711
P11442	GQFSTDELVAEVEK	0.93348066	2	4.28972
P11442	GQFSTDELVAEVEKR	1.008114354	2	3.64783
P11442	HELIEFR	1.540635651	2	2.34946
P11442	HSSLAGCQIINYR	0.972496366	2	2.71368
P11442	IHEGCEEPATHNALAK	1.155060194	2	5.30538
P11442	ISGETIFVTAPHEATAGIIGVNR	1.164164454	2	5.3292
P11442	IVLDNSVFSEHR	1.586409607	2	2.96906

P11442	IYIDSNNNPER	**1.249410716**	2	3.19304
P11442	KFDVNTSAVQVLIEHIGNLDR	**0.906802542**	3	5.63764
P11442	KFNALFAQGNYSEAAK	**1.246260213**	2	4.36682
P11442	LAELEEFINGPNNAHIQQVGDR	**0.91466234**	2	5.05264
P11442	LHIIEVGTPPTGNQPFPK	**0.953753435**	2	4.18867
P11442	LLYNNVSNFGR	**1.591952435**	2	2.34087
P11442	LPVVIGGLLDVDCSEDVIK	**1.522221328**	2	5.22083
P11442	LTDQLPLIIVCDR	**0.971336857**	2	3.24053
P11442	NLQNLLILTAIK	**0.792844838**	2	3.91733
P11442	NNLAGAEELFAR	**1.26880539**	2	3.5349
P11442	NNRPSEGPLQTR	**0.996646984**	3	4.19138
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	**1.196395792**	3	5.73747
P11442	SVDPTLALSVYLR	**0.969449115**	2	2.89163
P11442	SVNESLNNLFITEEDYQALR	**1.44772793**	3	5.12696
P11442	TLQIFNIEMK	**0.983083788**	2	2.88997
P11442	TSIDAYDNFDNISLAQR	**0.968772755**	2	4.36255
P11442	VGEQAQVVIIDMNDPSNPIR	**0.918840546**	2	4.62218
P11442	VIQCFAETGQVQK	**1.162815747**	2	4.62988
P11442	VSQPIEGHAASFAQFK	**1.0745069**	2	4.36608
P11442	WLLLTGISAQQNR	**1.068145848**	2	3.25511
P11442	YESLELCRPVLQQGR	**0.551504749**	2	2.67628
P11442	YIEIYVQK	**1.289529861**	1	2.36903
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.547311588**	**3.99E-09**	**6**
P11497	GGSWVVIDPTINPR	**1.54733896**	2	2.75822
P11497	GSVLEPEGTVEIK	**1.830824699**	2	2.69971
P11497	ITSENPDEGFKPSSGTVQELNFR	**1.572063998**	3	3.98168
P11497	TLRDPSLPLLELQDIMTSVSGR	**1.337103327**	3	3.36126
P11497	VNNADDFPNLFR	**1.270076571**	2	2.41684
P11497	VQQAELHTGSLPQIQSTALR	**0.854348685**	3	3.54194
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.818492491**	**7.93E-05**	**9**
P11507	DIVPGDIVEIAVGDKVPADIR	**0.626462604**	2	3.53943
P11507	IGIFGQDEDVTSK	**0.923520458**	2	3.38609
P11507	IRDEMVATEQER	**1.022815696**	2	3.10657
P11507	LDEFGEQLSK	**0.903936392**	2	2.82353
P11507	NAENAIEALK	**0.606535677**	2	2.33943
P11507	NAENAIEALKEYEPEMGK	**0.75490214**	2	3.93909
P11507	SEIGIAMGSGTAVAK	**1.027067075**	2	2.71159
P11507	TASEMVLADDNFSTIVAAVEEGR	**0.693773478**	3	4.80393
P11507	VDQSILTGESVSVIK	**0.510702382**	2	4.63697
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.183497102**	**9.9E-20**	**25**
P11598	DASVVGFFR	**1.24358327**	2	2.70056
P11598	DGEEAGAYDGPR	**1.364548456**	2	3.08644
P11598	DLLTAYYDVDYEK	**1.36917592**	2	3.24163
P11598	EATNPPIIQEEKPK	**1.174444757**	2	3.47696
P11598	EYDDNGEGITIFRPLHLANK	**1.065544017**	2	4.21593
P11598	FAHTNVESLVK	**1.208391692**	3	3.35449
P11598	FIQESIFGLCPHMTEDNKDLIQGK	**0.845156274**	3	5.03454
P11598	FISDKDASVVGFFR	**1.492026575**	2	4.28957
P11598	FLQEYFDGNLK	**0.948784522**	2	3.39345
P11598	FLQEYFDGNLKR	**1.003978775**	2	3.09834
P11598	FVMQEEFSR	**1.251342724**	2	2.5818
P11598	GFPTIYFSPANK	**2.326950462**	2	2.77238
P11598	IFRDGEEAGAYDGPR	**0.91057948**	2	3.64782
P11598	LAPEYEAAATR	**1.105420715**	2	3.44126
P11598	LNFAVASR	**1.527178346**	2	2.44178
P11598	LSKDPNIVIAK	**1.191129352**	3	3.79006

P11598	MDATANDVPSPYEVK	**0.952172857**	2	4.48111
P11598	MDATANDVPSPYEVK+Oxidation(0)	**1.282921139**		
P11598	QAGPASVPLR	**2.228502974**	2	2.54755
P11598	RLAPEYEAAATR	**0.993965967**	2	3.54945
P11598	SEPIPETNEGPVK	**1.065382505**	2	2.97881
P11598	TADGIVSHLK	**2.406329206**	2	2.90603
P11598	TFSHELSDFGLESTTGEIPVVAIR	**1.288796851**	2	6.22657
P11598	VDCTANTNTCNK	**3.241778022**	2	4.24545
P11598	YGVSGYPTLK	**1.143568769**	2	3.20224
P11711	**CP2A1 Cytochrome P450 2A1**	**0.862692881**	**2.17E-05**	**6**
P11711	GEQATYNTLFK	**1.202579621**	2	2.8472
P11711	GTDVFPILGSLMTDPK	**0.749465051**	2	3.65308
P11711	ILEEAGYLIK	**0.8771372**	2	2.72673
P11711	LEDINESPKPLGFTR	**0.969236557**	2	3.46905
P11711	TVSNVISSIVFGER	**0.886972092**	2	3.5258
P11711	VHEEIEQVIGR	**0.862468197**	2	3.20988
P11714	**CP2D9 Cytochrome P450 2D9**	**0.844243947**	**1.76E-10**	**2**
P11714	GNPESSFNDENLLMVVR	**0.826757279**	2	2.34788
P11714	VQQEIDEVIGQVR	**0.851055**	2	4.84107
P11862	**GAS2 Growth arrest_specific protein 2**	**1.156093843**	**0.779964**	**2**
P11862	EIEQEETLSAPSPSPSPSSK	**1.23395424**	2	3.87945
P11862	LDNGALLCQLAATVQEK	**1.093531402**	2	4.08699
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**1.016152759**	**9.9E-20**	**23**
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	**0.587101704**	3	4.58363
P11884	EEIFGPVMQILK	**1.106227749**	2	3.79748
P11884	EEIFGPVMQILK+Oxidation(7)	**1.125699387**		
P11884	ELGEYGLQAYTEVK	**1.323363597**	2	4.45975
P11884	GYFIQPTVFGDVK	**1.305765552**	2	4.09681
P11884	HEPVGVCGQIIPWNFPLLMQAWK	**0.989744953**	3	4.19029
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	**0.922631949**	3	6.63329
P11884	LGPALATGNVVVMK	**0.985645224**	2	3.88117
P11884	LGPALATGNVVVMK+Oxidation(12)	**1.491613646**		
P11884	LLCGGGAAADR	**1.371063052**	2	3.53634
P11884	RVTLELGGK	**0.909494799**	2	2.74448
P11884	TEQGPQVDETQFK	**0.990413205**	2	4.75646
P11884	TFPTVNPSTGEVICQVAEGNK	**1.017990675**	2	4.97016
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	**0.916522603**	2	4.32521
P11884	TFVQEDVYDEFVER	**1.0291148**	2	5.17645
P11884	TIEEVVGR	**0.908160683**	2	3.00175
P11884	TIPIDGDFFSYTR	**1.215455189**	2	2.94921
P11884	VAEQTPLTALYVANLIK	**1.641156622**	3	5.24503
P11884	VAFTGSTEVGHLIQVAAGSSNLK	**1.125585166**	2	6.03517
P11884	VTLELGGK	**0.898362231**	1	1.96656
P11884	VVGNPFDSR	**1.003989671**	2	2.83905
P11884	YGLAAAVFTK	**0.95624304**	2	3.78407
P11884	YYAGWADK	**0.99404439**	2	2.57794
P11915	**NLTP Non_specific lipid_transfer protein**	**0.8343029**	**4.44E-16**	**24**
P11915	ADCTITMADSDLLALMTGK	**1.142042071**	2	5.69764
P11915	ADCTITMADSDLLALMTGK+Oxidation(15)	**1.115075471**		
P11915	ADCTITMADSDLLALMTGK+Oxidation(6)	**1.113203847**		
P11915	ANLIFK	**1.176170197**	2	2.36315
P11915	AVEIVAQEMVTDMPSTFEEK	**0.955907948**	2	4.2742
P11915	GHPLGATGLAQCAELCWQLR	**0.909879054**	3	3.72794
P11915	GSVLPDSDK	**1.037795661**	1	1.9886
P11915	GSVLPDSDKK	**1.139514401**	2	2.62822
P11915	HIDVLINK	**0.87349564**	2	2.8588

P11915	HSVNNPYSQFQDEYSLDEIMK	0.929337306	3	6.33432
P11915	KADCTITMADSDLLALMTGK	1.643680582	2	4.40238
P11915	KLEEEGEEFVK	1.188976459	2	4.4919
P11915	KLEEEGEEFVKK	1.156161707	3	4.44347
P11915	LEEEGEEFVK	1.201688237	2	2.69396
P11915	LEEEGEEFVKK	1.221465191	2	3.56577
P11915	LQSLQLQPDK	1.654321722	2	3.1694
P11915	MGFPEAASSFR	0.990056432	2	2.99576
P11915	MNPQSAFFQGK	1.077616615	2	3.25032
P11915	MNPQSAFFQGK+Oxidation(0)	1.279813454		
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.199723175	3	5.17075
P11915	THQISAAPTSSAGDGFK	1.08691653	2	4.40495
P11915	VFVVGVGMTK	1.017433788	2	2.55614
P11915	WVINPSGGLISK	1.131766672	2	3.30845
P11915	YGMSACPFAPQLFGSAGK	1.304732364	2	3.37906
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**0.598891147**	**0.00016**	**10**
P11980	AEGSDVANAVLDGADCIMLSGETAK	0.581837233	2	4.52578
P11980	AGKPVICATQMLESMIK	0.713608382	3	3.34216
P11980	DAVLDAWAEDVDLR	0.898381054	2	4.02507
P11980	GADYLVTEVENGGSLGSK	0.782128085	2	5.3149
P11980	GVNLPGAAVDLPAVSEK	0.981257156	2	3.77025
P11980	IYVDDGLISLQVK	0.427875062	2	3.6978
P11980	KGVNLPGAAVDLPAVSEK	0.652418368	2	3.64349
P11980	LDIDSAPITAR	0.574795623	2	3.20909
P11980	NTGIICTIGPASR	0.471039948	2	3.32459
P11980	VFLAQKMMIGRCNR+Oxidation(6)	1.246801721		
P12001	**RL18 60S ribosomal protein L18**	**1.437307182**	**1.11E-16**	**5**
P12001	GTVLLSGPR	1.433050438	2	2.93101
P12001	ILTFDQLALESPK	1.436336385	2	4.87078
P12001	TAVVVGTITDDVR	1.30900529	2	4.52372
P12001	TNRPPLSLSR	1.307015259	3	3.36622
P12001	TNSTFNQVVLK	1.152078577	2	3.17621
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.002657321**	**2.12E-13**	**9**
P12007	AQEIDQSNDFK	0.235447544	2	3.64025
P12007	FVQENLAPK	1.031299464	2	2.65015
P12007	FWITNGPDADVLVVYAK	1.615891729	2	3.65351
P12007	GSNTCELVFEDCK	1.347855583	2	4.4588
P12007	GSNTCELVFEDCKVPAANILSQESK	1.121892503	3	4.91741
P12007	GVYVLMSGLDLER	1.075428012	2	3.17081
P12007	IGQFQLMQGK	1.159379503	2	2.50274
P12007	LYEIGGGTSEVR	1.180038655	2	3.55975
P12007	TDLTAVPASR	1.018995	2	2.96345
P12346	**TRFE Serotransferrin**	**1.048892766**	**6.97E-13**	**23**
P12346	ADRDQYELLCLDNTR	1.132444541	2	4.54323
P12346	ASDSSINWNNLK	1.159459162	2	3.27094
P12346	DGGGDVAFVK	1.269473737	2	3.11313
P12346	DLKQEDFQLLCPDGTK	0.853740393	2	4.4465
P12346	DQYELLCLDNTR	0.512028983	2	2.98203
P12346	EGVCPEGSIDSAPVK	1.553845232	2	3.48929
P12346	EGYNGYTGAFQCLVEK	1.060218357	2	3.52895
P12346	FDEFFSQGCAPGYK	0.992335249	2	4.34594
P12346	GDKDCTGNFCLFR	0.933968779	2	3.59347
P12346	GTDFQLNQLQGK	1.020880008	2	3.12299
P12346	GYYAVAVVK	1.071307193	2	2.79149
P12346	HQTVLENTNGK	0.603587986	2	2.5793
P12346	HTTIFEVLPQK	1.001603576	3	3.74023

P12346	KGTDFQLNQLQGK	**1.070129123**	2	3.59938
P12346	KTSYQDCIK	**1.212644874**	2	2.48962
P12346	LPEGTTYEEYLGAEYLQAVGNIR	**1.132666864**	2	4.67597
P12346	NGDGKEDLIWEILK	**0.909377722**	2	3.67761
P12346	QEDFQLLCPDGTK	**1.158211917**	2	3.58282
P12346	SKDFQLFGSPLGK	**1.436210427**	2	3.48895
P12346	TSYQDCIK	**1.037197277**	2	2.52894
P12346	VSTVLTAQK	**0.956062907**	2	2.61668
P12346	WCALSHQER	**1.729764951**	2	3.23094
P12346	WCAVSEHENTK	**1.120263539**	2	3.64952
P12711	**ADHX Alcohol dehydrogenase class_3**	**0.814875191**	**0.999991**	**10**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	**0.960161371**	3	5.78295
P12711	AFDLMHSGNSIR	**0.953847307**	2	2.5025
P12711	AGDTVIPLYIPQCGECK	**0.974282805**	2	4.02701
P12711	EFGATECINPQDFSK	**1.064513779**	2	4.18959
P12711	IDPSAPLDK	**0.85666436**	1	1.93967
P12711	IIGIDINK	**1.004820814**	2	2.37197
P12711	IIGIDINKDK	**0.752315339**	1	2.43056
P12711	VCLLGCGISTGYGAAVNTAK	**1.014551396**	2	5.52123
P12711	VDEFVTGNLSFDQINK	**0.852078873**	2	5.13075
P12711	VEPGSTCAVFGLGGVGLAVIMGCK	**0.903502925**	2	4.14393
P12749	**RL26 60S ribosomal protein L26**	**1.387992183**	**0.018027**	**6**
P12749	DDEVQVVR	**1.428795173**	2	2.58808
P12749	FNPFVTSDR	**1.165679446**	2	2.36335
P12749	HFNAPSHIR	**1.164612727**	3	3.70163
P12749	KDDEVQVVR	**1.159473853**	2	3.38569
P12749	KIMSSPLSKELR+Oxidation(2)	**1.507016162**		
P12749	YVIYIER	**1.280967601**	1	1.91981
P12785	**FAS Fatty acid synthase**	**1.518284687**	**9.9E-20**	**44**
P12785	ACIDTALENLSTLK	**1.851439422**	2	4.9156
P12785	AGSDTELAAPK	**1.559856385**	2	3.2478
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	**1.394477584**	3	5.73813
P12785	DANLPAGSMAAVGLSWEECK	**0.882781412**	2	3.66044
P12785	DGGFLLMHTVLK	**1.334726016**	2	2.39955
P12785	DPETLLGYSMVGCQR	**0.685546173**	2	3.76777
P12785	EEEPEAMLPGAQPTLISAISK	**1.17919687**	2	3.31519
P12785	EQGVTFPSGEAQEQLIR	**1.952780038**	2	4.11924
P12785	FDASFFGVHPK	**1.519799486**	2	3.12343
P12785	FVFTPHVEPECLSESAILQK	**2.640009605**	2	4.56507
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	**1.947623575**	3	4.70531
P12785	GLESIINIIHSSLAEPR	**1.361246862**	2	4.76953
P12785	GNAGQSNYGFANSTMER	**1.379698437**	2	4.43746
P12785	GTNTGVWVGVSGSEASEALSR	**1.094173977**	2	3.53972
P12785	GVDLVLNSLAEEK	**1.562654437**	2	3.21489
P12785	GYDYGPHFQGVYEATLEGEQGK	**1.66730917**	3	3.76392
P12785	HFQLEQDKPEEQTAHAFVNVLTR	**1.677066201**	3	3.45343
P12785	LDPGSSELQK	**1.767328765**	2	2.37894
P12785	LFDHPEVPIPAESESVSR	**1.261214552**	2	4.0873
P12785	LLLPEDPLISGLLNSQALK	**2.476806655**	3	5.02159
P12785	LTPGCEAEAEAEAICFFIK	**2.803680401**	2	4.08235
P12785	MTVPGLEDLPQHGLPR	**1.24581403**	2	3.16778
P12785	QAQLNLSILLVNPEGPTLTR	**1.760120276**	2	4.55486
P12785	QQEQLVPTLEK	**1.730230802**	2	2.44717
P12785	QSPLLIGSTK	**1.727305981**	1	2.10791
P12785	RQQEQLVPTLEK	**1.474747066**	2	3.16701
P12785	SDEALKPLGVK	**1.043547038**	2	3.14664
P12785	SFDDSGNGYCR	**2.048994996**	2	3.1493

P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.520198018	2	5.064
P12785	SNMGHPEPASGLAALTK	1.136931584	2	3.64783
P12785	SNMGHPEPASGLAALTK+Oxidation(2)	1.768371345		
P12785	TGGTYGEDLGADYNLSQVCDGK	1.471704964	2	5.06889
P12785	TMEAVQGLLEQGR	1.073786779	2	3.71756
P12785	TMEAVQGLLEQGR+Oxidation(1)	1.318444833		
P12785	VGDPQELNGITR	1.277800722	2	2.55847
P12785	VHLTGIDINPNALFPPVEFPVPR	1.398993242	2	5.03902
P12785	VLEALLPLK	1.584411606	2	2.35701
P12785	VLESDLVMNVYR	1.155519652	2	3.40567
P12785	VLLSLENGVWAPNLHFHNPNPEIPALLDGR	1.257073657	3	4.05635
P12785	VSVHIIEGDHR	1.751662451	2	2.75328
P12785	VTAIYIDPATHLQK	1.507050669	2	3.3156
P12785	VYATILNAGTNTDGCK	1.236103663	2	4.87661
P12785	VYQWEDPDSK	1.641244006	2	3.17471
P12785	WLSTSIPEAQWQSSLAR	1.170940698	2	2.37203
P12791	**CP2BA Cytochrome P450 2B10**	**0.720107138**	**1E-11**	**2**
P12791	IQEEAQCLVEELR	0.773891442	2	3.75981
P12791	IQEEAQCLVEELRK	0.739730359	2	3.54459
P12847	**MYH3 Myosin_3**	**0.214323417**	**8.2E-09**	**4**
P12847	IEAQNQPFDAK	0.146298106	2	2.74858
P12847	MKGTLEDQIISANPLLEAFGNAK	0.124544241	3	6.88927
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0)	0.278469011		
P12847	NALAHALQSSR	0.327352583	2	2.61805
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.214028182**	**9.9E-20**	**18**
P12928	AETSDVANAVLDGADCIMLSGETAK	1.106388019	2	5.38618
P12928	CCAAAIIVLTK	0.834064783	2	2.95144
P12928	CNLAGKPVVCATQMLESMITK	1.001912586	3	5.06202
P12928	EATESFATSPLSYRPVAIALDTK	1.834648087	3	4.05922
P12928	EPPEAIWADDVDR	1.154794194	2	2.44058
P12928	EPPEAIWADDVDRR	1.228036089	2	2.33098
P12928	GDLGIEIPAEK	0.81251215	2	3.10309
P12928	GSQVLVTVDPK	1.20438475	2	2.84773
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.193732256	2	5.44598
P12928	IGPEGLVTEVEHGGILGSR	1.021961017	2	4.77932
P12928	IYIDDGLISLVVQK	1.243613906	2	4.15678
P12928	KFDEILEVSDGIMVAR	0.953625462	3	3.38633
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.394615404	3	4.31527
P12928	LNFSHGSHEYHAESIANIR	2.230631786	3	4.18175
P12928	STSIIATIGPASR	0.023228198	2	3.57979
P12928	TGVLQGGPESEVEIVK	1.106133246	2	4.93826
P12928	TVWVDYHNITR	1.976630072	2	2.51038
P12928	VQFGIESGK	1.051233523	1	1.98269
P12938	**CP2D3 Cytochrome P450 2D3**	**1.177156804**	**0.244595**	**5**
P12938	DLTDAFLAEIEK	0.894226091	2	4.14283
P12938	FDYGDPDFIK	0.602990445	2	2.44384
P12938	GNPESSFNDANLR	0.992679695	2	4.30907
P12938	RFDYGDPDFIK	0.81032097	2	2.82997
P12938	TWDPDQPPR	0.669186904	2	2.43149
P12939	**CP2DA Cytochrome P450 2D10**	**0.874060372**	**9.9E-20**	**8**
P12939	AVQEVLVTHGEDTADRPPVPIFK	0.746103703	3	5.2982
P12939	FEYEDPYLIR	0.804194678	2	2.40921
P12939	FGDIAPLNLPR	1.062669705	2	3.16154
P12939	ITSCDIEVQDFVIPK	0.849226034	2	4.54521
P12939	NLTDAFLAEVEK	0.872677911	2	4.13625
P12939	RFEYEDPYLIR	0.845819274	3	3.5356
P12939	SQGVVFASYGPEWR	0.960579513	2	3.59811

P12939	TTWDPAQPPR	**0.77586371**	2	2.43384
P13084	**NPM Nucleophosmin**	**1.996039722**	**0.000109**	**3**
P13084	MSVQPTVSLGGFEITPPVVLR	**1.388571858**	2	3.58218
P13084	MTDQEAIQDLWQWR	**1.122590976**	2	3.16819
P13084	VDNDENEHQLSLR	**1.968585431**	2	3.92913
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**1.21935178**	**1.66E-10**	**6**
P13086	LIGPNCPGIINPGECK	**1.297833621**	2	4.51283
P13086	MGHAGAIIAGGK	**0.773331898**	1	2.79309
P13086	MGHAGAIIAGGK+Oxidation(0)	**0.807300085**		
P13086	NIYIDK	**1.114584962**	1	1.97198
P13086	QGTFHSQQALEYGTK	**0.896522053**	2	2.84177
P13086	VICQGFTGK	**0.993945965**	2	2.30848
P13107	**CP2B3 Cytochrome P450 2B3**	**1.21340678**	**2.99E-06**	**11**
P13107	ATLDPNAPR	**0.932514301**	2	2.32698
P13107	CLVEELK	**0.795441871**	1	2.00381
P13107	DFIDTFLLHMEK	**1.313461211**	2	3.00921
P13107	EVLDYIDHSVENHR	**1.104304256**	2	3.9607
P13107	FSDVSPMGLPCR	**1.117580742**	2	2.76168
P13107	FSDVSPMGLPCR+Oxidation(6)	**1.209257785**		
P13107	GIIAVLQPIMQEYGVSFVNEER	**2.31690718**	3	5.36123
P13107	LLDLLYR	**0.858962033**	2	2.48844
P13107	MCLGEGIAR	**0.669395985**	2	2.6932
P13107	QSVEDQIKEEAK	**0.951444464**	2	2.49591
P13107	SFIQLQEK	**1.30890939**	2	2.40647
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**3.274003528**	**9.9E-20**	**8**
P13221	ITWSNPPAQGAR	**3.54452953**	2	3.39354
P13221	IVATTLSNPELFK	**3.340336066**	2	3.63969
P13221	NFGLYNER	**3.660673322**	1	1.93106
P13221	NLDYVATSINEAVTK	**3.300773501**	2	4.88711
P13221	SCASQLVLGDNSPALR	**3.368405441**	2	5.40518
P13221	TDDSQPWVLPVVR	**2.189259845**	2	3.52465
P13221	VGGVQSLGGTGALR	**1.31216157**	2	2.39314
P13221	VGNLTVVGK	**1.157345311**	2	2.55087
P13255	**GNMT Glycine N_methyltransferase**	**1.310199567**	**1.53E-06**	**8**
P13255	AHMVTLDYTVQVPGAGR	**1.178280983**	2	4.93491
P13255	AWLLGLLR	**1.353705831**	2	2.78904
P13255	DITTSVLTVNNK	**1.522118108**	2	3.97851
P13255	LSYYPHCLASFTELVQEAFGGR	**1.468020941**	3	3.70045
P13255	NYDYILSTGCAPPGK	**1.460406686**	2	4.5936
P13255	SDLTKDITTSVLTVNNK	**1.149025141**	2	3.09809
P13255	SLGVAAEGIPDQYADGEAAR	**1.352167615**	2	5.75534
P13255	VWQLYIGDTR	**1.10905156**	2	2.60527
P13383	**NUCL Nucleolin**	**1.231794983**	**0.005411**	**8**
P13383	FGYVDFESAEDLEK	**1.506229929**	2	2.63853
P13383	GFGFVDFNSEEDAK	**1.683261997**	2	3.71618
P13383	GLSEDTTEETLK	**0.775941671**	2	2.9043
P13383	IEGSEPTTPFNLFIGNLNPNK	**1.086869461**	2	3.46349
P13383	NDLAAVDVR	**1.045410964**	2	2.43111
P13383	NLSFNITEDELK	**1.141750794**	2	2.77781
P13383	SEADAEKNLEEK	**1.203380855**	2	3.06045
P13383	SVSLYYTGEK	**4.079851877**	1	2.02487
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.964885645**	**9.9E-20**	**22**
P13437	AANEAGYFNEEMAPIEVK	**0.900897412**	2	5.24088
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11)	**1.259571623**		
P13437	DAEVVLCGGTESMSQSPYSVR	**1.241477846**	2	5.16125
P13437	DFTATDLTEFAAR	**1.670712365**	2	4.92081

P13437	DMDLIDVNEAFAPQFLAVQK	**1.423033167**	3	6.50169
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1)	**1.307901487**		
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	**0.87422693**	3	5.73183
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	**0.888568671**	3	4.94808
P13437	GVFIVAAK	**0.928536874**	2	2.58343
P13437	ITAHLVHELR	**2.517833415**	2	3.02468
P13437	LCGSGFQSIVSGCQEICSK	**1.565909049**	2	5.47703
P13437	LEDTLWAGLTDQHVK	**1.006689841**	2	5.38807
P13437	RTPFGAYGGLLK	**1.60399455**	2	2.94441
P13437	SLDLDPSK	**1.027952413**	2	3.01989
P13437	TNVSGGAIALGHPLGGSGSR	**0.864679231**	2	6.24238
P13437	TPFGAYGGLLK	**0.957405657**	2	2.78518
P13437	VGVPTETGALTLNR	**1.028766639**	2	3.69551
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	**1.019509047**	2	5.95532
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR+Oxidation(14)	**1.164844272**		
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	**1.086775348**	3	5.47263
P13437	VVGYFVSGCDPAIMGIGPVPAITGALKK	**0.713147898**	3	3.58694
P13437	YAVGSACIGGGQGISLIIQNTA	**0.834328649**	2	2.47778
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**2.250517263**	**9.9E-20**	**8**
P13444	FVIGGPQGDAGVTGR	**1.693303055**	2	4.72654
P13444	HIGYDDSAK	**1.959052248**	2	2.82525
P13444	ICDQISDAVLDAHLK	**1.834823702**	2	5.15605
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	**0.89936968**	3	5.42316
P13444	SEFPWEVPK	**1.543103994**	2	2.54199
P13444	SGVLPWLRPDSK	**1.08770169**	2	3.10746
P13444	TCNVLVALEQQSPDIAQCVHLDR	**1.945856907**	3	5.68493
P13444	TQVTVQYVQDNGAVIPVR	**2.322227563**	2	5.09471
P13471	**RS14 40S ribosomal protein S14**	**1.355097077**	**0.009091**	**3**
P13471	ADRDESSPYAAMLAAQDVAQR	**1.680727018**	2	5.8534
P13471	ELGITALHIK	**1.675602614**	2	2.41605
P13471	IEDVTPIPSDSTR	**1.294856786**	2	3.99233
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**1.16094965**	**2.22E-16**	**22**
P13601	ANNTPYGLAAGVFTK	**0.601582097**	2	4.25457
P13601	EAGFPPGVVNVVPGYGSTAGAAISSHMDIDK	**0.463608903**	3	3.30585
P13601	EEIFGPVQQIMK	**0.734566788**	2	3.81693
P13601	EMGEQGVYEYTELK	**0.375882791**	2	3.88757
P13601	FPVINPATEEVICHVEEGDK	**0.996983204**	3	4.09538
P13601	FPVINPATEEVICHVEEGDKADVDK	**0.73894982**	4	5.14294
P13601	GFFVQPTVFSNVTDEMR	**2.256466442**	2	4.3122
P13601	IAKEEIFGPVQQIMK	**0.779966703**	2	3.86485
P13601	IFINNEWHNSLNGK	**1.437562595**	2	3.50003
P13601	IFTHAYLLDTEVSIKALK	**1.422570576**	2	2.34106
P13601	IHGQTIPSDGDVFTYTR	**0.701060259**	2	4.62773
P13601	ILDLIESGK	**0.575867636**	2	2.72922
P13601	ILDLIESGKK	**0.687191791**	3	3.34172
P13601	KFPVINPATEEVICHVEEGDK	**0.970585947**	3	3.75391
P13601	KFPVINPATEEVICHVEEGDKADVDK	**0.644086349**	4	4.86691
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	**0.267596138**	3	5.60002
P13601	LFVEESIYDEFVR	**0.489323593**	2	4.06712
P13601	VLLATMESMNAGK	**0.453338107**	2	3.98108
P13601	VSFTGSTEVGK	**0.578761208**	2	3.08655
P13601	YFAGWADK	**0.785405504**	1	2.05643
P13601	YVLGNPLDSGISQGPQIDK	**0.440691726**	2	4.96192
P13601	YVLGNPLDSGISQGPQIDKEQHAK	**0.453555109**	4	4.60452
P13697	**MAOX NADP_dependent malic enzyme**	**1.279822936**	**0.644327**	**5**

P13697	AECSAEECYK	**1.572535967**	1	2.81023
P13697	AIFASGSPFDPVTLPDGR	**1.051594328**	2	4.25745
P13697	GHIASVLNAWPEDVVK	**0.980702894**	2	3.81666
P13697	HINDSVFLTTAEVISQQVSDK	**1.301627862**	3	4.34186
P13697	NLEAIVQK	**1.415441455**	1	2.1971
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**1.025188004**	**8.15E-10**	**14**
P13803	AAVDAGFVPNDMQVGQTGK	**0.953674272**	2	4.77217
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11)	**1.081790992**		
P13803	DPEAPIFQVADYGIVADLFK	**1.162751774**	2	5.3554
P13803	GLLPEELTPLILETQK	**1.098425021**	2	4.66934
P13803	GTSFEAAAASGGSASSEK	**1.28774512**	2	5.34079
P13803	LGGEVSCLVAGTK	**1.015517402**	2	4.711
P13803	LLYDLADQLHAAVGASR	**1.220208321**	2	4.64356
P13803	LNVAPVSDIIEIK	**1.391606917**	3	4.71772
P13803	QFSYTHICAGASAFGK	**1.525676335**	2	3.1638
P13803	SDRPELTGAK	**0.935864557**	3	3.34121
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	**0.986717058**	3	7.0384
P13803	TIYAGNALCTVK	**1.146336628**	2	3.66107
P13803	VLVAQHDAYK	**1.126207591**	2	3.25924
P13803	VVQDLCK	**0.954867731**	2	2.75145
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.248159131**	**3.93E-06**	**3**
P13832	ATSNVFAMFDQSQIQEFK	**1.24789488**	2	4.65257
P13832	FTDEEVDELYR	**0.982720846**	2	3.49903
P13832	GNFNYIEFTR	**1.377550717**	2	2.62827
P14046	**A1I3 Alpha_1_inhibitor 3**	**0.707957331**	**1.07E-05**	**5**
P14046	GDPIPNEQVLIK	**0.711340077**	2	3.18152
P14046	GMYESLPVVAVK	**0.692238353**	2	3.39759
P14046	ISLCHGNPTFSSETK	**1.113896858**	2	3.68243
P14046	QQNSYGGFSSTQDTVVALDALSK	**0.674239673**	2	4.14266
P14046	QSPGPCGSEVATVPETGR	**0.7094303**	2	3.33622
P14141	**CAH3 Carbonic anhydrase 3**	**1.038103059**	**0.265292**	**18**
P14141	EAPFNHFDPSCLFPACR	**1.112706271**	2	4.34176
P14141	EKGEFQILLDALDK	**0.97815569**	2	4.55953
P14141	EKGEFQILLDALDKIK	**0.618769288**	2	3.11099
P14141	EPMTVSSDQMAK	**1.742699402**	2	2.94108
P14141	EWGYASHNGPEHWHELYPIAK	**0.962901749**	3	4.51726
P14141	GDNQSPIELHTK	**0.991345103**	2	3.76433
P14141	GEFQILLDALDK	**0.975043647**	2	4.66441
P14141	GEFQILLDALDKIK	**0.868060206**	2	3.2539
P14141	GGPLSGPYR	**0.972326959**	2	2.95671
P14141	GKEAPFNHFDPSCLFPACR	**0.80060859**	3	3.52535
P14141	HDPSLQPWSVSYDPGSAK	**1.043616745**	3	5.57237
P14141	QFHLHWGSSDDHGSEHTVDGVK	**0.864279509**	2	4.6434
P14141	QPDGIAVVGIFLK	**1.462138016**	2	2.57663
P14141	SLFASAENEPPVPLVGNWRPPQPIK	**0.946098316**	3	5.70133
P14141	VVFDDTFDR	**0.513108245**	2	3.37234
P14141	YAAELHLVHWNPK	**1.51974003**	2	4.33244
P14141	YNTFGEALK	**0.994614485**	2	2.31471
P14141	YNTFGEALKQPDGIAVVGIFLK	**0.920657636**	3	6.01375
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.078424008**	**0.076798**	**7**
P14173	AGEGGGVIQGSASEATLVALLAAR	**0.998826248**	2	3.54335
P14173	ALIPTTAPQEPETYEDIIR	**0.968255325**	3	4.09666
P14173	GSNQLNETLLQR	**1.158580146**	2	2.86618
P14173	HSHQDSGLITDYR	**1.041211601**	3	3.63344
P14173	MLELPEAFLAGR	**0.918546303**	2	2.7709
P14173	QLQAASPELTQAALMEK	**0.947115319**	2	3.81437

P14173	TDLTEAFNMDPVYLR	1.144419961	2	3.67668
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.137272471**	**4.44E-16**	**15**
P14408	AAAEVNQEYGLDPK	1.39348379	2	4.4678
P14408	AIEMLGGELGSK	0.921830298	2	3.50702
P14408	IEYDTFGELK	1.027472559	2	3.54261
P14408	IEYDTFGELKVPTDK	1.130464694	2	3.64987
P14408	IYELAAGGTAVGTGLNTR	1.002059682	2	5.56062
P14408	KTAIELGYLTAEQFDEWVKPK	1.089554889	3	3.57699
P14408	LMNESLMLVTALNPHIGYDK	1.239945836	3	5.64763
P14408	LMNESLMLVTALNPHIGYDK+Oxidation(6)	1.421816848		
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	1.115853756	3	6.41143
P14408	SGLGELILPENEPGSSIMPGK	0.91079349	2	4.37712
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17)	1.060742018		
P14408	SKEFAQVIK	1.112926657	2	2.48217
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	0.902228904	3	4.20594
P14408	TAIELGYLTAEQFDEWVKPK	0.933737723	2	4.52727
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	2.213035	3	6.0056
P14480	**FIBB Fibrinogen beta chain**	**1.200567939**	**0.731238**	**10**
P14480	AHYGGFTVQTEANK	0.871154231	2	2.90667
P14480	DNENVINEYSSILEDQK	1.349555138	2	3.26935
P14480	GFGNIATNEDTK	1.107483955	2	2.73911
P14480	GFGNIATNEDTKK	1.070245452	2	2.81909
P14480	IGPTELLIEMEDWK	0.949000013	2	3.57419
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	0.943218657	3	5.21872
P14480	LYIDETVNDNIPLNLR	0.950412316	2	3.00687
P14480	QTLLNHERPIK	1.013155155	2	2.74741
P14480	TENGGWTVIQNR	0.887178995	2	3.22843
P14480	YCGLPGEYWLGNDK	0.779483672	2	3.31806
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**1.069103158**	**2.81E-07**	**8**
P14604	AFAAGADIK	1.142087326	2	3.2342
P14604	AQFGQPEILLGTIPGAGGTQR	0.994202219	2	5.64728
P14604	FLSHWDHITR	1.044089712	2	3.12917
P14604	IFPVETLVEEAIQCAEK	1.224050836	2	5.81061
P14604	LFYSTFATDDR	1.593658849	2	2.7269
P14604	NSSVGLIQLNRPK	1.161344792	2	3.51664
P14604	SLAMEMVLTGDR	0.763313649	2	3.38463
P14604	TFQDCYSGK	1.166692386	2	2.78863
P14668	**ANXA5 Annexin A5**	**1.050597773**	**0.998332**	**3**
P14668	ETSGNLENLLLAVVK	1.053757943	2	3.48141
P14668	GLGTDEDSILNLLTAR	0.935573128	2	4.61663
P14668	GTVTDFSGFDGR	0.86475472	2	2.93226
P14669	**ANXA3 Annexin A3**	**0.697713044**	**9.9E-20**	**5**
P14669	GMGTDEDTLIEILTTR	0.834282129	2	3.15011
P14669	GTINNYPGFNPSVDAEAIR	0.640678515	2	4.9337
P14669	QYQEAYEQALK	0.723618593	2	2.55115
P14669	SEIDLLDIR	0.708381388	2	2.61726
P14669	TLINILTER	0.754014758	2	2.51867
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.078594589**	**6.44E-05**	**3**
P14685	AIQLEYSEAR	1.032268526	2	2.58406
P14685	LQLDSPEDAEFIVAK	1.072519478	2	3.86135
P14685	SVFPEQANNNEWAR	1.210083562	2	3.0434
P14740	**DPP4 Dipeptidyl peptidase 4**	**0.976221051**	**1**	**2**
P14740	LGTLEVEDQIEAAR	0.9383111	2	3.90667
P14740	VLEDNSALDK	1.154362323	2	2.86002
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**1.216953815**	**4.62E-05**	**12**

P14882	FLSDVYPDGFK	**1.122204562**	2	2.69451
P14882	FSSQEAASSFGDDR	**1.318630574**	2	3.31877
P14882	HGNALWLNER	**1.434423966**	2	2.59714
P14882	HIEIQVLGDK	**1.189482543**	2	2.39713
P14882	LHDEDHTVVASNNGPTFNVEVDGSK	**1.079717337**	3	6.01431
P14882	LQVEHPVTECITGLDLVQEMILVAK	**1.236352613**	3	3.54244
P14882	MADEAVCVGPAPTSK	**0.998180862**	2	4.37035
P14882	MEDALDSYVIR	**1.20588414**	2	3.107
P14882	SYLNMDAIMEAIK	**1.262917738**	2	3.15003
P14882	TGAQAVHPGYGFLSENK	**1.344281731**	2	4.04566
P14882	TVAIHSDVDASSVHVK	**1.182112444**	3	4.10047
P14882	VVEEAPSIFLDPETR	**0.953339769**	2	4.15036
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.105328951**	**0.143748**	**4**
P15083	EIQNAGDQAQENR	**1.079103067**	2	3.65543
P15083	FSVLITGLR	**1.400391728**	2	2.66792
P15083	GVTGGSVAIVCPYNPK	**1.109575641**	2	4.32915
P15083	NNADLQVLEPEPELLYK	**0.603158824**	2	2.64082
P15149	**CP2A2 Cytochrome P450 2A2**	**0.703041173**	**9.9E-20**	**10**
P15149	DVQECILEEAGYLIK	**0.695713949**	3	4.59711
P15149	DVYSSITQLSER	**1.236834344**	2	2.42686
P15149	FSNLAPLGIPR	**0.707863234**	2	3.20416
P15149	GELPTFNILFK	**0.501835126**	2	2.41712
P15149	GTDVFPIIGSLMTEPK	**0.524985404**	2	3.93387
P15149	GYGFSLSNVEQAK	**0.732351214**	2	3.44918
P15149	NFIDSFLIR	**0.746761469**	1	2.56599
P15149	QNHSTLDPNSPR	**0.712324076**	2	3.02995
P15149	TLQGTCGAPIDPSIYLSK	**0.602316279**	2	4.20956
P15149	TVSNVINSIVFGNR	**0.728243333**	2	3.53047
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.267283986**	**8.85E-06**	**6**
P15178	FQTEIQTVNK	**1.119908838**	2	2.38776
P15178	GEEILSGAQR	**0.87961836**	2	2.91514
P15178	LEYCEALAMLR	**0.795794415**	2	2.93123
P15178	LPLQLDDAIRPEVEGEEDGR	**1.248554064**	3	3.89853
P15178	QMVKFAANINK+Oxidation(1)	**1.507859139**		
P15178	SNAYLAQSPQLYK	**1.332145879**	2	2.84295
P15429	**ENOB Beta_enolase**	**1.00745795**	**6.01E-07**	**7**
P15429	DATNVGDEGGFAPNILENNEALELLK	**0.419401073**	2	5.69276
P15429	FMIELDGTENK	**0.431240758**	2	2.34191
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	**0.354334329**	3	4.62987
P15429	IEEALGDK	**0.068413783**	1	2.36389
P15429	TAIQAAGYPDK	**0.174534009**	2	2.68211
P15429	VNQIGSVTESIQACK	**0.809959656**	2	5.04251
P15429	YNQLMRIEEALGDK	**1.505069535**	2	2.49209
P15473	**IBP3 Insulin_like growth factor_binding protein 3**	**0.77186931**	**0.296606**	**2**
P15473	EMEDTLNHLKFLNVLSPR	**0.762227247**	2	2.31343
P15473	MEVIIKGQARDSQR	**1.110110001**	2	2.3121
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.122948701**	**9.9E-20**	**20**
P15650	AFVDSCLQLHETK	**1.087492353**	2	4.13793
P15650	AQDTAELFFEDVR	**1.119596599**	2	4.80927
P15650	AQDTAELFFEDVRLPASALLGEENK	**1.140661206**	3	4.29199
P15650	CIGAIAMTEPGAGSDLQGVR	**0.721362826**	2	6.10258
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6)	**1.064669855**		
P15650	EQIEQFIPQMTAGK	**1.190422576**	2	4.99043
P15650	FFQEEVIPYHEEWEK	**2.479823591**	2	4.95834
P15650	GFYYLMQELPQER	**1.169183313**	2	3.91188

P15650	IFSSEHDIFR	**1.41962977**	2	2.98718
P15650	KFFQEEVIPYHEEWEK	**2.232379667**	3	5.00773
P15650	LDSASASMAK	**0.832704298**	2	2.63886
P15650	LPASALLGEENK	**1.472192426**	2	3.41568
P15650	LPASALLGEENKGFYYLMQELPQER	**1.303057454**	3	3.62652
P15650	QGLLGINIAEK	**0.950595206**	2	3.29741
P15650	RLDSASASMAK	**0.828810727**	2	3.48518
P15650	RLDSASASMAK+Oxidation(8)	**1.121046142**		
P15650	RSGSDWILNGSK	**1.477360366**	2	2.85729
P15650	SGSDWILNGSK	**1.062010482**	2	2.93258
P15650	VQPIYGGTNEIMK	**0.912708059**	2	3.25019
P15650	VQPIYGGTNEIMK+Oxidation(11)	**1.073567749**		
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.161222697**	**0.000316**	**9**
P15651	ASSTANLIFEDCR	**0.932778475**	2	3.42293
P15651	EEGDSWVLNGTK	**0.869163017**	2	2.30446
P15651	ELVPIAAQLDK	**1.038085047**	1	1.95679
P15651	ELVPIAAQLDKEHLFPTSQVK	**0.537116292**	2	4.03763
P15651	GISAFLVPMPTPGLTLGK	**1.082305821**	2	2.5101
P15651	IGCFALSEPGNGSDAGAASTTAR	**1.24571827**	2	5.58182
P15651	IGIASQALGIAQASLDCAVK	**1.187489756**	2	4.93089
P15651	ITEIYEGTSEIQR	**0.980064524**	2	4.29785
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	**1.319061002**	4	4.91257
P15684	**AMPN Aminopeptidase N**	**1.322115411**	**0.03746**	**5**
P15684	ALGDTPAPNIDTTELVER	**0.8480968**	2	3.90623
P15684	AQIIHDSFNLASAGK	**1.294822323**	2	3.77442
P15684	ESALVFDPQSSSISNK	**1.605608346**	2	2.45445
P15684	VMAVDALASSHPLSSPANEVNTPAQISELFDSITYSK	**1.531248205**	3	3.82394
P15684	VVATTQMQAADAR	**1.32384355**	2	2.77734
P15709	**ST2A1 Bile salt sulfotransferase**	**1.356145153**	**0.764152**	**2**
P15709	GNVLYGSWFEHIR	**1.183074192**	2	3.04906
P15709	NHFTVSQAEAFDK	**1.497615454**	2	3.66153
P15978	**HA11 Class I histocompatibility antigen_ Non_RT1.A alpha_1 chain**	**1.110128288**	**0.996401**	**2**
P15978	VEHEGLPEPLSQR	**1.103088849**	2	3.27187
P15978	YDSDAENPR	**1.115689201**	2	2.72269
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.109540853**	**9.9E-20**	**24**
P15999	AVDSLVPIGR	**1.048909201**	2	3.495
P15999	EIVTNFLAGFEP	**7.553209576**	2	2.40999
P15999	EVAAFAQFGSDLDAATQQLLSR	**1.693930875**	2	6.77597
P15999	FESAFLSHVVSQHQSLLGNIR	**1.251124524**	2	6.01128
P15999	GIRPAINVGLSVSR	**1.266479192**	3	3.62651
P15999	GMSLNLEPDNVGVVVFGNDK	**1.401469296**	2	5.68416
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1)	**1.263907592**		
P15999	GYLDKLEPSK	**0.770583739**	1	2.59319
P15999	ILGADTSVDLEETGR	**1.36703226**	2	5.00629
P15999	LELAQYR	**1.115303361**	2	2.69323
P15999	LKEIVTNFLAGFEP	**3.824898159**	2	3.25605
P15999	LTDADAMK	**0.955294339**	2	2.55262
P15999	LTDADAMK+Oxidation(6)	**1.312519197**		
P15999	LYCIYVAIGQK	**1.406119762**	2	2.40999
P15999	NVQAEEMVEFSSGLK	**1.757894226**	2	4.35521
P15999	QGQYSPMAIEEQVAVIYAGVR	**2.026812193**	3	5.22377
P15999	RTGAIVDVPVGDELLGR	**0.809966899**	2	2.85457
P15999	STVAQLVK	**1.033013921**	2	2.39713
P15999	TGAIVDVPVGDELLGR	**0.908099859**	2	4.929

P15999	TGTAEMSSILEER	**0.873978022**	2	4.26578
P15999	TGTAEMSSILEER+Oxidation(5)	**1.034150278**		
P15999	TSIAIDTIINQK	**1.007375163**	2	4.39193
P15999	VLSIGDGIAR	**1.071677682**	2	3.16013
P15999	VVDALGNAIDGK	**1.168281438**	2	4.18584
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.221596076**	**1.11E-16**	**7**
P16036	ALYSNILGEENTYLWR	**1.232244749**	2	3.33195
P16036	EEGLNAFYK	**1.229338425**	1	2.3182
P16036	FGFYEVFK	**1.021675405**	2	2.34244
P16036	GIFNGFSITLK	**1.050200138**	2	2.82009
P16036	GSTASQVLQR	**1.082064773**	2	2.97079
P16036	IQTQPGYANTLR	**1.269102174**	2	3.76068
P16036	MYKEEGLNAFYK	**1.086549574**	2	2.88434
P16086	**SPTA2 Spectrin alpha chain_ brain**	**1.006854687**	**0.073277**	**33**
P16086	ALINADELANDVAGAEALLDR	**1.159141274**	2	5.12341
P16086	ALSSEGKPYVTK	**1.322025406**	2	3.02164
P16086	DLSSVQTLLTK	**1.038468183**	2	2.78134
P16086	EAALTSEEVGADLEQVEVLQK	**0.940118835**	2	3.74314
P16086	GEIDAHEDSFK	**1.081265222**	2	2.40504
P16086	GVIDMGNSLIER	**0.988547773**	2	3.18937
P16086	HQAFEAELSANQSR	**1.135978673**	2	3.56942
P16086	HQEHKGEIDAHEDSFK	**1.154847069**	3	4.14932
P16086	HQLLEADISAHEDR	**1.122743726**	3	4.02848
P16086	KFEEFQTDLAAHEER	**1.145997982**	3	4.81962
P16086	LFGAAEVQR	**1.249388677**	2	2.58283
P16086	LGDSHDLQR	**1.091879505**	2	3.18737
P16086	LGESQTLQQFSR	**0.841656898**	2	3.23806
P16086	LIQEQHPEEELIK	**1.341181147**	2	3.52415
P16086	LQQSHPLSANQIQVK	**1.713638729**	2	3.94639
P16086	LQTASDESYKDPTNIQSK	**1.075013277**	2	4.325
P16086	LQVASDENYKDPTNLQGK	**1.462379489**	2	4.61362
P16086	LSDDNTIGQEEIQQR	**1.140559267**	2	4.23868
P16086	MTLVASEDYGDTLAAIQGLLK	**0.996019825**	2	3.16289
P16086	NQALNTDNYGHDLASVQALQR	**1.113247322**	3	4.87358
P16086	NTTGVTEEALK	**1.064072023**	2	2.35015
P16086	QFQDAGHFDAENIKK	**0.808943351**	2	2.58068
P16086	REELITNWEQIR	**1.183033935**	2	3.45142
P16086	SADESGQALLAAGHYASDEVR	**0.83867358**	3	3.63935
P16086	SLQQLAEER	**1.011709288**	2	2.76101
P16086	SQLLGSAHEVQR	**1.414107457**	2	3.21781
P16086	SSEEIESAFR	**0.930245721**	2	2.42816
P16086	SSLSSAQADFNQLAELDR	**1.004042306**	2	4.93924
P16086	TATDEAYKDPSNLQGK	**1.18838095**	2	3.58109
P16086	TKQEEVNAAWQR	**0.839169355**	2	3.028
P16086	VLETAEDIQER	**1.015618471**	2	3.42193
P16086	VNDVCTNGQDLIK	**1.12975086**	2	3.17759
P16086	VNSLGETAQR	**1.233010961**	2	2.34579
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**1.28168956**	**9.9E-20**	**10**
P16232	EECALEIIK	**1.816365544**	1	1.97235
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(1)	**0.986888411**		
P16232	EMAYHLSKMGAHVVLTAR+Oxidation(8)	**0.986888411**		
P16232	ETSGIILSQAAPK	**1.334428722**	2	3.31754
P16232	FALDGFFSTIR	**1.668591049**	2	3.07936
P16232	KDEVYYDK	**1.101372055**	2	3.00259
P16232	MGAHVVLTAR	**1.21517904**	2	2.91917

P16232	MTQPLIASYSASK	**1.935311302**	2	3.38045
P16232	MTQPLIASYSASK+Oxidation(0)	**3.818748307**		
P16232	SSWTPLLLGNPGR	**1.320753536**	2	3.60669
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.288622443**	**4.74E-10**	**7**
P16290	AMEAVAAQGK	**0.870062923**	2	2.79569
P16290	AMEAVAAQGK+Oxidation(1)	**1.320030742**		
P16290	FLGDEETVR	**0.593474195**	2	2.66986
P16290	HGESSWNQENR	**0.50773264**	2	3.63271
P16290	HNYYASISK	**0.259024037**	2	2.36968
P16290	HYGGLTGLNK	**1.512400191**	1	2.92437
P16290	VLIAAHGNSLR	**1.330659287**	2	2.82761
P16303	**CES3 Carboxylesterase 3**	**1.069297223**	**9.9E-20**	**20**
P16303	AISESGVVLTSALITTDSKPIANLIATLSGCK	**1.000793583**	3	3.86134
P16303	AKEAAEEPSHWK	**0.824344774**	2	4.25041
P16303	DGASEEETNLSK	**1.09943646**	2	4.1975
P16303	EAAEEPSHWK	**1.360061495**	2	2.92789
P16303	ENIPLQFSEDCLYLNVYTPADLTK	**5.067960175**	2	4.42315
P16303	ESYPFLPTVIDGVVLPK	**1.113859556**	2	4.15499
P16303	FAPPQPAEPWNFVK	**1.143382355**	2	2.55127
P16303	IGASTQAAQR	**1.069872778**	2	2.85226
P16303	KENIPLQFSEDCLYLNVYTPADLTK	**3.767519069**	2	4.65825
P16303	LDLLGNPK	**1.049680348**	2	2.49522
P16303	QEFGWIIPTLMGYPLSEGK	**1.515989756**	2	4.09094
P16303	QKTEDELLETSLK	**1.036288767**	3	3.70119
P16303	SFNTVPYIVGINK	**2.493958093**	2	3.37518
P16303	TEDELLETSLK	**0.764195258**	2	3.72654
P16303	TPEEILAEK	**3.657654191**	2	2.34282
P16303	TTTSAVMVHCLR	**1.028611898**	2	2.80367
P16303	TTTSAVMVHCLR+Oxidation(6)	**0.972552897**		
P16303	TVIGDHGDELFSVFGSPFLK	**1.946940815**	2	5.39983
P16303	YFGGTDDPAK	**1.009463767**	2	3.19888
P16303	YVNLEGFAQPVAVFLGIPFAKPPLGSLR	**0.956600888**	3	3.57998
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.150293493**	**1.28E-07**	**7**
P16332	AAVQVLDDIEK	**2.047482854**	2	2.62039
P16332	AHCQTSGWSLTEQDPYNNIVR	**1.296198635**	3	5.17047
P16332	GDVGMAGVAIDTVEDTK	**0.952564778**	2	3.06917
P16332	IDSGSEVIVGVNK	**1.225390323**	2	3.57708
P16332	ILFDGIPLEK	**1.246721367**	2	2.31859
P16332	NTQIIIQEESGIPK	**1.224868428**	2	3.88144
P16332	TGLQAGLTIDEFAPR	**0.907013622**	2	3.44
P16409	**MYL3 Myosin light chain 3**	**0.486082377**	**1.7E-05**	**6**
P16409	AAPAPAAAPAAAPEPERPK	**0.041861104**	2	4.28119
P16409	ALGQNPTQAEVLR	**0.047638842**	2	3.97609
P16409	DTGTYEDFVEGLR	**0.701299507**	2	3.29733
P16409	MMDFETFLPMLQHISK	**0.771983863**	2	2.92626
P16409	NKDTGTYEDFVEGLR	**0.605274855**	2	4.1335
P16409	VFDKEGNGTVMGAELR	**0.263571228**	2	3.51766
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.165894754**	**9.9E-20**	**18**
P16617	AHSSMVGVNLPQK	**1.055783789**	3	4.08317
P16617	AHSSMVGVNLPQK+Oxidation(4)	**0.902005313**		
P16617	ALESPERPFLAILGGAK	**2.156343705**	3	4.52532
P16617	DCVGSEVENACANPAAGTVILLENLR	**1.119654671**	3	6.29706
P16617	FCLDNGAK	**0.843522521**	1	2.05084
P16617	GCITIIGGGDTATCCAK	**1.068772577**	2	5.56694
P16617	IQLINNMLDK	**0.882006893**	2	2.72171
P16617	IQLINNMLDK+Oxidation(6)	**1.954702108**		

P16617	ITLPVDFVTADKFDENAK	**1.426385675**	2	4.90571
P16617	QIVWNGPVGVFEWEAFAR	**1.180546075**	2	3.10035
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	**1.165987981**	4	4.69102
P16617	TGQATVASGIPAGWMGLDCGTESSK	**0.853170307**	2	4.73668
P16617	TGQATVASGIPAGWMGLDCGTESSKK	**0.88697081**	3	4.25405
P16617	VLNNMEIGTSLYDEEGAK	**0.995550016**	2	5.54474
P16617	VLNNMEIGTSLYDEEGAK+Oxidation(4)	**1.048079375**		
P16617	VLPGVDALSNV	**1.236310503**	2	2.73516
P16617	WNTEDKVSHVSTGGGASLELLEGK	**0.889048741**	3	4.85577
P16617	YSLEPVAAELK	**1.023369652**	2	3.61883
P16638	**ACLY ATP_citrate synthase**	**1.336584569**	**3.11E-15**	**25**
P16638	AFDSGIIPMEFVNK	**1.399948068**	2	4.13286
P16638	AFDSGIIPMEFVNK+Oxidation(8)	**0.939970417**		
P16638	DEPSVAAMVYPFTGDHK	**1.3091288**	2	3.22893
P16638	DGVYILDLAAK	**1.030747684**	2	2.98278
P16638	DLVSSLTSGLLTIGDR	**1.115513344**	2	3.48683
P16638	EAYPEEAYIADLDAK	**1.164764539**	2	3.06489
P16638	FGGALDAAAK	**1.161935264**	2	2.45811
P16638	GAIVPAQEVPPPTVPMDYSWAR	**1.191667236**	2	4.22838
P16638	GGPNYQEGLR	**1.498204413**	2	2.71885
P16638	GVTIIGPATVGGIKPGCFK	**1.229183754**	2	2.85284
P16638	HLLVHAPEDK	**1.049260671**	2	2.66416
P16638	HLLVHAPEDKK	**1.191706846**	2	3.56468
P16638	IGNTGGMLDNILASK	**1.341027625**	2	3.65479
P16638	LGLVGVNLSLDGVK	**1.793470697**	2	2.83034
P16638	LNAEDIK	**1.509021368**	1	1.91364
P16638	QHFPATPLLDYALEVEK	**1.155340351**	3	4.446
P16638	RGGPNYQEGLR	**2.144712848**	2	3.17673
P16638	SFDELGEIIQSVYEDLVAK	**1.166842043**		
P16638	SGGMSNELNNIISR	**1.304461685**	2	3.70062
P16638	TIAIIAEGIPEALTR	**1.145958822**	2	5.25342
P16638	TTDGVYEGVAIGGDR	**1.317646274**	2	3.42145
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	**0.99202485**	3	4.08434
P16638	VDATADYICK	**0.941676254**	2	2.47053
P16638	WGDIEFPPPFGR	**1.253862948**	2	3.93386
P16638	YICTTSAIQNR	**1.274843556**	2	2.8135
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.826602541**	**2.69E-11**	**5**
P16970	FDHVPLATPNGDILIQDLSFEVR	**0.80922831**	2	2.48301
P16970	GIEGAQASPLIPGAGEIINADNIIK	**0.750335635**	3	4.97734
P16970	GYLDNVQLGHILER	**0.823876304**	2	3.44621
P16970	HLHSTHSELLEDYYQSGR	**0.840337926**	3	5.15625
P16970	SGANVLICGPNGCGK	**0.847861567**	2	3.11631
P17074	**RS19 40S ribosomal protein S19**	**1.100632984**	**0.746691**	**5**
P17074	DVNQQEFVR	**0.402950565**	2	2.36849
P17074	ELAPYDENWFYTR	**0.600205197**	2	2.4845
P17074	HKELAPYDENWFYTR	**1.080197201**	3	3.35257
P17074	RVLQALEGLK	**1.201840992**	3	3.31907
P17074	VLQALEGLK	**1.167343041**	2	2.71794
P17077	**RL9 60S ribosomal protein L9**	**1.162805105**	**8.71E-08**	**8**
P17077	DFNHINVELSLLGK	**0.038880998**	3	3.75242
P17077	FLDGIYVSEK	**1.156451942**	2	3.20182
P17077	GTVQQPDE	**1.399451086**	1	2.1011
P17077	KFLDGIYVSEK	**1.382255515**	2	2.72617
P17077	SVYAHFPINVVIQENGSLVEIR	**1.460094734**	3	3.74064
P17077	TGVACSVSQAQK	**1.161184455**	2	3.66953
P17077	TICSHVQNMIK	**0.827190222**	2	2.87856

P17077	TILSNQTVDIPENVDITLK	**0.978009009**	2	3.15407
P17078	**RL35 60S ribosomal protein L35**	**1.273007452**	**0.178145**	**2**
P17078	QLDDLKVELSQLR	**1.043512654**	2	2.58665
P17078	VLTVINQTQK	**1.275375723**	2	3.24856
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**0.902540499**	**2.62E-05**	**4**
P17178	DHESTEGPGTGQDRPR	**3.632317883**	2	2.52979
P17178	MLKPAEAALYTDALNEVISDFIAR	**1.324434609**	3	4.13894
P17178	VGCLEPSIPEDTATFIR	**1.414002958**	2	2.88455
P17178	YEVVLSPGMGEVK	**1.141875651**	2	3.74526
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.484625667**	**1.47E-05**	**15**
P17425	ASAELFNQK	**0.554613123**	2	3.10989
P17425	DKNSIYSGLEAFGDVK	**1.158349416**	2	3.02647
P17425	DVGIVALEIYFPSQYVDQAELEK	**1.327398136**	3	3.6891
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK+Oxidation(3)	**0.495673171**		
P17425	ITASLCDLK	**0.935235408**	1	1.94212
P17425	LEDTYFDRDVEK	**0.551692753**	2	2.92073
P17425	LPATSGEPESAVISNGEH	**0.913436368**	2	4.23964
P17425	MFLNDFLNDQNR	**0.523420203**	2	2.97792
P17425	MFLNDFLNDQNR+Oxidation(0)	**0.550625057**		
P17425	MGFCTDREDINSLCLTVVQK	**0.518022103**	3	4.17946
P17425	NSLSYDCIGR	**0.501529468**	2	2.8723
P17425	RPSTNDHSLDEGVGLVHSNTATEHIPSPAK	**1.141530387**	4	4.60498
P17425	TCVAPDVFAENMK	**0.466101712**	2	2.78393
P17425	VTQDATPGSALDK	**0.449274435**	2	3.80521
P17425	YTIGLGQAR	**0.428931655**	2	2.68853
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.269614148**	**8.66E-07**	**2**
P17426	NADVELQQR	**1.264819164**	2	2.80772
P17426	VGGYILGEFGNLIAGDPR	**1.270946981**	2	3.75086
P17475	**A1AT Alpha_1_antiproteinase**	**0.932760743**	**0.293689**	**5**
P17475	MQHLEQTLTK	**0.949202756**	2	3.00792
P17475	MQHLEQTLTK+Oxidation(0)	**1.514843602**		
P17475	TLLSSLGITR	**1.074159911**	2	3.15535
P17475	VFNNDADLSGITEDAPLK	**0.947647218**	2	5.7359
P17475	VINDYVEK	**1.070527143**	2	2.34795
P17702	**RL28 60S ribosomal protein L28**	**1.912941852**	**9.9E-20**	**2**
P17702	NCSSFLIK	**1.167488117**	2	2.41565
P17702	QTYSTEPNNLK	**2.342227861**	2	3.01876
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.203683686**	**9.9E-20**	**17**
P17764	EEQDKYAIGSYTR	**1.198247046**	2	3.56149
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	**1.707106055**	2	4.62328
P17764	EVYMGNVIQGGEGQAPTR	**1.579390066**	2	5.39414
P17764	EVYMGNVIQGGEGQAPTR+Oxidation(3)	**2.426941099**		
P17764	FANEITPITISVK	**1.153690913**	2	3.84868
P17764	GKPDVVVKEDEEYK	**0.980411117**	2	3.45335
P17764	GKPDVVVKEDEEYKR	**1.02544511**	2	5.0755
P17764	IAAFADAAVDPIDFPLAPAYAVPK	**2.196116579**	2	5.74289
P17764	IHMGNCAENTAK	**1.27344277**	2	3.17841
P17764	IHMGNCAENTAK+Oxidation(2)	**1.247297731**		
P17764	LEDLIVK	**1.08856773**	2	2.71165
P17764	LGTIAIQGAIEK	**1.617609686**	2	3.29302
P17764	QATLGAGLPIATPCTTVNK	**1.060155416**	2	4.62479
P17764	QGEFGLASICNGGGGASAVLIEK	**1.04219662**	2	4.94267
P17764	TPIGSFLGSLASQPATK	**1.700537569**	2	4.47932
P17764	VNVHGGAVSLGHPIGMSGAR	**0.733457987**	2	5.80788

P17764	VNVHGGAVSLGHPIGMSGAR+Oxidation(15)	**1.673706209**		
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.601451708**	**9.9E-20**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	**1.322787911**	3	5.32345
P17879	TTPSYVAFTDTER	**1.637763691**	2	3.72956
P17879	VEIIANDQGNR	**1.160590515**	2	3.77198
P17988	**ST1A1 Sulfotransferase 1A1**	**1.742022933**	**9.9E-20**	**6**
P17988	CPGVPSGLETLEETPAPR	**1.937209213**	2	4.79756
P17988	ILEFLGR	**2.18567723**	2	2.34402
P17988	NTFTVAQNER	**1.828178476**	2	3.68243
P17988	SGTTWMSEILDMIYQGGK	**1.262380334**	2	4.98685
P17988	SLPEETVDSIVHHTSFK	**1.949014423**	2	4.56665
P17988	THLPLSLLPQSLLDQK	**1.957899408**	2	4.97855
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.138998416**	**9.9E-20**	**30**
P18163	AELSVIFADKPEK	**1.011406758**	2	3.14189
P18163	ALEDLGR	**1.943748043**	2	2.32831
P18163	ALKPPCDLSMQSVEVTGTTEGVR	**0.924760014**	2	4.53501
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9)	**1.230299905**		
P18163	CGVEIIGLK	**0.898627199**	2	2.87908
P18163	DGWLHTGDIGK	**1.100110072**	2	3.18743
P18163	GAMVTHQNIMNDCSGFIK	**1.210681102**	2	4.38305
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2)	**1.508710995**		
P18163	GFQGSFEELCR	**1.014089933**	2	3.6255
P18163	GIAVHPELFSIDNGLLTPTLK	**2.134928017**	2	5.81365
P18163	GIQVSNDGPCLGSR	**0.998637194**	2	4.50838
P18163	IENIYLR	**0.963498534**	2	2.95509
P18163	IFGQANTSVK	**1.084983899**	2	2.76034
P18163	IIVIMDSYDNDLVER	**0.998551972**	2	4.59071
P18163	LLLEGVENK	**1.131758204**	2	3.33447
P18163	LLMDDLK	**1.00841596**	2	2.43491
P18163	LMITGAAPVSATVLTFLR	**1.147058864**	2	3.52214
P18163	LVDVEDMNYQAAK	**0.96063502**	2	4.20376
P18163	LVDVEDMNYQAAK+Oxidation(6)	**1.460769334**		
P18163	NAGLKPFEQVK	**1.108701621**	2	3.83103
P18163	NNSLWDK	**0.814360687**	2	2.54561
P18163	QVAEMAECIGSALIQK	**0.824419522**	2	5.59015
P18163	QVAEMAECIGSALIQK+Oxidation(4)	**1.3493284**		
P18163	SAVLEDDKLLLYYYDDVR	**5.173535749**	3	4.16559
P18163	SQIDELYSTIK	**1.441842134**	2	3.65745
P18163	SQIDELYSTIKI	**1.69341447**	2	4.15233
P18163	TAEALDKDGWLHTGDIGK	**1.114966683**	2	5.10815
P18163	TKPKPPEPEDLAIICFTSGTTGNPK	**7.217752933**	3	5.41539
P18163	VLQPTIFPVVPR	**1.031221978**	2	3.50098
P18163	WLLDFASK	**0.955552201**	2	2.3813
P18297	**SPRE Sepiapterin reductase**	**0.993289502**	**0.000299**	**4**
P18297	ALAPQLAGLLSPGSVLLLSAR	**1.07256505**	3	4.81566
P18297	LLLINNAGTLGDVSK	**1.099914261**	2	3.60059
P18297	LNSEGELVDCGTSAQK	**1.294393482**	2	4.78737
P18297	TVVNISSLCALQPFK	**1.047070094**	2	3.76345
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**2.175216584**	**9.9E-20**	**3**
P18298	IIVDTYGGWGAHGGGAFSGK	**1.624590352**	2	5.42115
P18298	KIIVDTYGGWGAHGGGAFSGK	**2.529147281**	3	3.46823
P18298	YLDEDTIYHLQPSGR	**2.400722269**	2	4.75356
P18418	**CALR Calreticulin**	**0.960942897**	**0.00734**	**19**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	**1.389477511**	3	5.44022
P18418	CKDDEFTHLYTLIVRPDNTYEVK	**2.433021556**	3	4.8565
P18418	DMHGDSEYNIMFGPDICGPGTK	**0.829539217**	2	6.39868

P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1)	1.111599001		
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(10)	1.111599001		
P18418	EQFLDGDAWTNR	0.920506086	2	3.02288
P18418	FYGDQEK	0.954782696	1	2.05597
P18418	FYGDQEKDK	0.971874319	1	2.77647
P18418	GQTLVVQFTVK	1.287082201	2	3.25503
P18418	HEQNIDCGGGYVK	0.967274473	2	4.42084
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	0.845340887	3	3.91679
P18418	IDNSQVESGSLEDDWDFLPPK	0.950835717	2	5.43783
P18418	IDNSQVESGSLEDDWDFLPPKK	0.931804445	2	4.9
P18418	IKDPDAAKPEDWDER	1.164020642	2	4.38367
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	0.874979417	3	5.5728
P18418	LFPGGLDQK	1.252636007	1	2.05284
P18418	QIDNPDYK	0.998621729	1	2.29053
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.179568935	3	4.88329
P18418	VHVIFNYK	1.176964015	1	2.26836
P18420	PSA1 Proteasome subunit alpha type_1	1.063607691	0.004156	2
P18420	AQPSQAADEPAEK	1.263993698	2	3.42467
P18420	NQYDNDVTVWSPQGR	1.001713811	2	3.62948
P18421	PSB1 Proteasome subunit beta type_1	1.162577762	0.009167	3
P18421	AGGSASAMLQPLLDNQVGFK	1.004129728	2	5.02828
P18421	GAVYSFDPVGSYQR	1.407533181	2	3.86107
P18421	NMQNVEHVPLTLDR	0.279847441	2	3.68842
P18445	RL27A 60S ribosomal protein L27a	1.310738401	3.65E-07	2
P18445	NQSFCPTVNLDK	1.272061152	2	3.35282
P18445	RNQSFCPTVNLDK	0.854907115	2	3.02967
P18484	AP2A2 AP_2 complex subunit alpha_2	0.705058575	1.43E-08	3
P18484	LTECLETILNK	0.95650714	2	2.73545
P18484	NNGVLFENQLLQIGLK	0.877544021	2	3.2541
P18484	QLSNPQQEVQNIFK	0.477219119	2	3.40911
P18596	AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	0.87341681	0.000963	5
P18596	DIVPGDIVEVAVGDK	0.980986949	2	2.45818
P18596	DIVPGDIVEVAVGDKVPADLR	1.597758322	2	3.76057
P18596	SLPSVETLGCTSVICSDK	0.482881894	2	4.19806
P18596	TGTLTTNQMSVCR	1.175904422	2	2.41579
P18596	VGEATETALTCLVEK	0.89745144	2	4.38617
P18757	CGL Cystathionine gamma_lyase	0.943196339	0.000689	18
P18757	AGDEVICMDEVYGGTNR	0.522278899	2	5.38777
P18757	AGDEVICMDEVYGGTNR+Oxidation(7)	0.947159893		
P18757	ATLGISDTLIR	1.017704622	2	3.54182
P18757	AVAALDGAK	0.819609364	2	2.67003
P18757	AVVLPISLATTFK	1.153224977	3	4.29108
P18757	DLLEDLGQALK	0.529096866	2	2.77988
P18757	FLQNSLGAVPSPFDCYLCCR	1.501855631	2	4.11841
P18757	GTLQHAQVFLK	0.977840445	2	3.06968
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.467810822	3	5.28373
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	1.514233983	4	5.44823
P18757	LLEAAITPQTK	0.888566015	2	3.8848
P18757	LSVGLEDEKDLLEDLGQALK	0.919247464	3	6.47493
P18757	LVWIETPTNPTLK	0.923798083	2	3.62771
P18757	QCTGCPGMVSFYIK	0.849349185	2	3.74135
P18757	QCTGCPGMVSFYIK+Oxidation(7)	1.22688687		
P18757	QDSPGQSSGFVYSR	1.236550568	2	3.7005
P18757	RVASEFGLK	1.06038741	2	2.58562
P18757	VIYPGLPSHPQHELAK	0.810306523	2	4.25614

P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.305144869**	**7.92E-08**	**10**
P18886	ATNLTVSAVR	**1.184647776**	2	3.30207
P18886	ELHAHLLAQDK	**1.456197337**	2	3.00994
P18886	FFNEVFR	**1.115667074**	2	2.30748
P18886	LIFDGNEETLK	**1.129951243**	2	2.98904
P18886	QYGQTVATYESCSTAAFK	**1.425511641**	2	3.57518
P18886	SEYNDQLTR	**1.295329465**	2	2.67301
P18886	TETIRPASIFTK	**1.404257849**	2	2.58314
P18886	TLSIDSIQFQR	**1.191352548**	2	3.302
P18886	YILSDSSPVPEFPVAYLTSENR	**1.683263972**	2	5.49571
P18886	YLNAQKPLLDDSQFR	**1.122340815**	2	4.36811
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.075895143**	**9.9E-20**	**18**
P19112	AGGLATTGNEDILDIVPTEIHQK	**0.96826533**	3	6.25506
P19112	AGGTGEMTQLLNSLCTAIK	**1.13293783**	2	5.36375
P19112	AGGTGEMTQLLNSLCTAIK+Oxidation(6)	**1.060869042**		
P19112	APVIMGSTEDVQEFLEIYNK	**1.736309243**	2	5.24661
P19112	DFDPAINEYIQR	**1.169800325**	2	3.91619
P19112	FPPDNSAPYGAR	**1.115765156**	2	2.55398
P19112	GNIYSINEGYAK	**1.209333133**	2	4.06306
P19112	KGNIYSINEGYAK	**1.225402057**	2	3.92468
P19112	KLDILSNDLVINMLK	**0.962131771**	2	6.07721
P19112	KTSANEPSEKDALQPGR	**1.054062205**	3	3.63943
P19112	LDILSNDLVINMLK	**1.021724613**	2	5.0478
P19112	LLYECNPIAYVMEK	**2.031882181**	2	4.26788
P19112	QAGIAQLYGIAGSTNVTGDQVK	**1.15724285**	3	6.08422
P19112	SRPSLPLPQSR	**0.99390814**	2	3.3114
P19112	SSYATCVLVSEEDTHAIIIEPEKR	**1.21370261**	3	5.78229
P19112	TLVYGGIFLYPANK	**1.014263828**	2	4.20629
P19112	TLVYGGIFLYPANKK	**0.823536097**	2	2.33301
P19112	TSANEPSEKDALQPGR	**1.022048697**	2	3.88564
P19123	**TNNC1 Troponin C_ slow skeletal and cardiac muscles**	**1.117277412**	**0.313683**	**5**
P19123	AAVEQLTEEQK	**1.108676035**	2	2.86199
P19123	AAVEQLTEEQKNEFK	**1.275515652**	2	3.44654
P19123	GKSEEELSDLFR	**1.113396546**	2	2.5702
P19123	IDYDEFLEFMK	**0.830588654**	2	3.17898
P19123	SEEELSDLFR	**0.493499925**	2	2.93065
P19225	**CP270 Cytochrome P450 2C70**	**0.883285083**	**9.9E-20**	**14**
P19225	ACIGEGLAR	**0.838964175**	2	2.78974
P19225	ASLNLSNPQDFIDYFLIK	**1.28355179**	2	4.70211
P19225	EALIDRGEEFSDK	**1.425613379**	2	3.29382
P19225	FDPGHFLDEK	**0.818529947**	2	2.3137
P19225	FDYSDEK	**1.148358376**	1	1.99506
P19225	FILMEINR	**0.828418565**	2	2.33989
P19225	GTSVMACLTSALHDDKEFPNPEK	**0.739857205**	3	3.48604
P19225	IQEEITR	**0.829165347**	1	2.0002
P19225	IQEEVVYLLEALR	**2.880222135**	2	3.3575
P19225	LPPGPTPLPIFGNILQVGVK	**0.869541807**	3	4.91012
P19225	SDYFMAFSAGRR+Oxidation(4)	**0.888906188**		
P19225	SEFTMDNLIVTIGDLFGAGTETTSSTIK	**0.892118686**		
P19225	VSQGLGIVFSNGEIWK	**1.455657329**	2	3.34834
P19225	YIDFVPIPLPR	**0.916399172**	2	3.1746
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**1.322969694**	**0.134125**	**4**
P19234	AAAVLPVLDLAQR	**2.801044469**	2	2.35573
P19234	DIEEIIDELR	**1.307015055**	2	3.55164

P19234	DTPENNPDTPFDFTPENYER	**1.168545702**	2	4.39767
P19234	FCCEPAGGLTSLTEPPK	**1.442178288**	2	3.74682
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**1.056805478**	**0.049585**	**8**
P19468	ASGELMTVAR	**1.165167997**	2	2.6967
P19468	CNQIANELCECPELLGSGFR	**0.842490898**	2	5.0993
P19468	DKNTPSPFVETFPEDEEASK	**0.838511911**	3	3.43545
P19468	GYVSDIDCR	**0.991990696**	2	2.58427
P19468	NTPSPFVETFPEDEEASK	**1.079914009**	2	4.77605
P19468	SLFFPDEAINK	**0.953175414**	2	2.66171
P19468	VQLLLNGGDVLETLQEK	**1.061185578**	2	4.72091
P19468	WGVISASVDDR	**0.792192485**	2	3.2562
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.174623722**	**1.11E-07**	**9**
P19488	AEMWLIR	**0.930162204**	2	2.91836
P19488	ANAIAWALAQIPQK	**1.152581698**	3	5.95307
P19488	FETFPTSVSK	**1.170151293**	1	2.00189
P19488	FETFPTSVSKDELEK	**0.971259846**	2	3.39425
P19488	GAAVTLNIR	**1.179871117**	2	2.51132
P19488	GHEVTVLKPSAYYVLDPK	**1.509146187**	2	4.52175
P19488	NWDPFYTEILGRPTTLAETMGK	**1.08199653**	2	5.01245
P19488	SDLFNALK	**1.109961619**	2	2.76469
P19488	TILDELVQR	**1.050255167**	2	3.19665
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**0.953659311**	**0.000268**	**10**
P19511	HVIQSISAQQEK	**1.097629123**	2	3.99424
P19511	HVIQSISAQQEKETIAK	**0.925118634**	3	4.07216
P19511	HYLFDVQR	**0.989513745**	2	2.58879
P19511	LDYHISVQDMMR	**0.665274747**	3	4.31159
P19511	LGLIPEEFFQFLYPK	**1.737923621**	2	2.67854
P19511	LNEEKIAQLEEIK	**1.070428607**	2	2.53018
P19511	NNIALALEVTYR	**1.047004066**	2	2.35025
P19511	QIQDAINR	**1.047606518**	1	2.1239
P19511	YGASIGEFIDK	**1.392898759**	2	2.91374
P19511	YGASIGEFIDKLNEEK	**1.211155584**	2	3.84726
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.025153774**	**3.31E-08**	**12**
P19643	FIGGSGQVSER	**1.123554725**	2	3.2447
P19643	IISTTNGGQER	**1.377015009**	2	3.06342
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	**1.261102186**	3	4.6288
P19643	KFIGGSGQVSER	**1.404531247**	2	3.1051
P19643	LERPVIHIDQTGENVVVK	**1.068089369**	2	4.49568
P19643	LLHDCGLSVVVLEAR	**1.399988295**	2	3.44083
P19643	TLNHEIYEAK	**1.173589568**	2	2.8145
P19643	TMDEMGQEIPSDAPWK	**0.808788828**	2	4.18117
P19643	VLNSQEALQPVHYEEK	**1.214611803**	2	4.83534
P19643	YVDLGGSYVGPTQNR	**1.197137445**	2	5.32449
P19643	YVISAIPPVLGMK	**0.741507296**	2	2.93179
P19643	YVISAIPPVLGMK+Oxidation(11)	**0.955177624**		
P19804	**NDKB Nucleoside diphosphate kinase B**	**1.175015051**	**9.9E-20**	**9**
P19804	DRPFFPGLVK	**1.41134867**	2	2.33999
P19804	EIGLWFKPEELIDYK	**1.247675963**	2	4.11749
P19804	GDFCIQVGR	**1.120430855**	2	3.19885
P19804	NIIHGSDSVESAEK	**1.248158796**	1	3.94125
P19804	TFIAIKPDGVQR	**1.23447472**	2	3.25638
P19804	VMLGETNPADSKPGTIR	**1.074085214**	2	3.89641
P19804	VMLGETNPADSKPGTIR+Oxidation(1)	**1.165046148**		
P19804	YMNSGPVVAMVWEGLNVVK	**1.266015116**	2	5.09767
P19804	YMNSGPVVAMVWEGLNVVK+Oxidation(1)	**0.712244601**		
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.041499956**	**0.00789**	**2**

P19944	AAGVNVEPFWPGLFAK	**2.002242518**	2	3.42932
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	**1.047769309**	3	5.70624
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.281289473**	**9.9E-20**	**10**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	**1.296351429**	2	6.02914
P19945	AGAIAPCEVTVPAQNTGLGPEK	**1.005375888**	2	4.54503
P19945	CFIVGADNVGSK	**1.102568129**	2	3.67474
P19945	GHLENNPALEK	**1.105652973**	2	3.69557
P19945	GNVGFVFTK	**1.872004913**	2	2.79319
P19945	GTIEILSDVQLIK	**1.297141482**	2	3.36351
P19945	IIQLLDDYPK	**1.909678089**	2	3.6394
P19945	NVASVCLQIGYPTVASVPHSIINGYK	**1.258388945**	3	3.87454
P19945	TSFFQALGITTK	**1.303646682**	2	4.21808
P19945	VLALSVETDYTFPLAEK	**0.92857749**	2	3.94064
P20059	**HEMO Hemopexin**	**0.864752891**	**0.300135**	**7**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	**1.080610814**	2	4.61289
P20059	FNPVTGEVPPR	**0.755885132**	2	2.46482
P20059	GECQSEGVLFFQGNR	**0.875884493**	2	3.75629
P20059	GGNNLVSGYPK	**0.711894348**	2	2.53918
P20059	LFQEEFPGIPYPPDAAVECHR	**0.824093041**	3	3.75048
P20059	SGAQATWAELSWPHEK	**1.016064799**	3	3.54564
P20059	VDGALCLEK	**0.876926264**	2	2.64807
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.062811925**	**0.255548**	**9**
P20070	AVLKDPNDHTVCYLLFANQSEK	**2.436438816**	3	4.70232
P20070	DILLRPELEELR	**0.845354569**	2	2.55208
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	**0.838430539**	3	4.96146
P20070	LIDKEIISHDTR	**0.943131773**	2	3.73461
P20070	MSQYLENMNIGDTIEFR	**1.082423946**	2	3.5756
P20070	SSPAITLENPDIK	**0.966455983**	2	3.87728
P20070	SSPAITLENPDIKYPLR	**0.713375358**	2	3.84722
P20070	SVGMIAGGTGITPMLQVIR	**0.774854258**	2	5.09246
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(3)	**1.182952132**		
P20280	**RL21 60S ribosomal protein L21**	**1.495423188**	**2.83E-08**	**3**
P20280	KGDIVDIK	**1.571462235**	1	2.24357
P20280	TNGKEPELLEPIPYEFMA	**1.002491583**	2	3.0142
P20280	VYNVTQHAVGIIVNK	**1.094975865**	2	4.61871
P20650	**PPM1A Protein phosphatase 1A**	**0.87811021**	**0.030112**	**2**
P20650	SRLEVTDDLEK	**0.62830381**	2	2.31696
P20650	VCNEVVDTCLYK	**1.399658549**	2	2.53631
P20673	**ARLY Argininosuccinate lyase**	**1.36066593**	**9.9E-20**	**16**
P20673	AEAECEVLFPGYTHLQR	**1.271060254**	2	4.59507
P20673	AEMQQILQGLDK	**1.064120528**	2	4.5017
P20673	AEMQQILQGLDK+Oxidation(2)	**1.513327016**		
P20673	AVVVAEMK	**1.244963493**	2	2.38015
P20673	EFNFVQLSDAYSTGSSLMPQK	**1.324259371**	2	5.48498
P20673	ELIGEAAGK	**2.400093942**	1	1.93262
P20673	FNSSIAYDR	**1.81780063**	2	2.77471
P20673	HLWNVDLQGSK	**1.250621512**	1	3.16158
P20673	INVLPLGSGAIAGNPLGVDR	**1.377482143**	2	5.57709
P20673	LKELIGEAAGK	**1.359315008**	2	2.98661
P20673	LYPNDEDIHTANER	**1.405534166**	2	3.88263
P20673	MAEDLILYGTK	**1.195422607**	2	3.74256
P20673	MAEDLILYGTK+Oxidation(0)	**1.182850632**		
P20673	NDQVVTDLR	**1.101152524**	2	3.40886
P20673	SRNDQVVTDLR	**1.182470982**	2	2.63014
P20673	VAEEWAQGIFK	**1.580851483**	2	3.81901

P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.118565734**	**0.887636**	**5**
P20788	EIDQEAAVEVSQLR	**1.1272284**	2	4.25067
P20788	EIDQEAAVEVSQLRDPQHDLER	**0.974230965**	3	3.32687
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	**1.106583984**	3	4.29454
P20788	LSDIPEGK	**1.166656408**	1	2.02107
P20788	SGPFAPVLSATSR	**1.052460848**	2	3.03193
P20801	**TNNC2 Troponin C_ skeletal muscle**	**0.490033944**	**0.008984**	**5**
P20801	AAFDMFDADGGGDISVK	**0.620055571**	2	4.17348
P20801	GKSEEELAECFR	**0.470715686**	2	3.61349
P20801	NADGYIDAEELAEIFR	**0.440555124**	2	4.79431
P20801	SEEELAECFR	**0.136584548**	2	3.29329
P20801	SYLSEEMIAEFK	**0.808596085**	2	2.75743
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**0.980399486**	**0.60236**	**4**
P20814	FDYEDKDFLNLIEK	**0.996575189**	3	4.16193
P20814	GTAVLTSLTSVLHDSK	**1.021264383**	2	3.10568
P20814	IKEHEESLDVSNPR	**0.922350865**	3	4.04851
P20814	SDYFIPFSAGK	**1.666031759**	2	2.59893
P20817	**CP4AE Cytochrome P450 4A14**	**0.976646715**	**0.99541**	**8**
P20817	ACQIAHEHTDGVIK	**1.015681321**	2	3.97792
P20817	AQLQNEEELQK	**0.87752011**	2	3.546
P20817	AVEDLNNLTFFR	**0.935303057**	2	3.41496
P20817	EFQQVLTWVEK	**0.839596034**	2	2.65653
P20817	HLDFLDILLFAK	**1.18206487**	2	3.23534
P20817	MEDGKSLSDEDLR	**0.742850785**	2	2.39169
P20817	MRKAQLQNEEELQK+Oxidation(0)	**0.995097407**		
P20817	VLLYDPDYVK	**0.917503526**	2	2.38224
P20852	**CP2A5 Cytochrome P450 2A5**	**1.009505275**	**0.999479**	**2**
P20852	DFIDSFLIR	**0.956054509**	2	2.66207
P20852	EALVDQAEEFSGR	**0.991903894**	2	3.35156
P21213	**HUTH Histidine ammonia_lyase**	**1.02296085**	**0.997054**	**13**
P21213	ALDYLAIGVHELAAISER	**0.949220134**	2	4.19696
P21213	DIITTELNSATDNPMVFASR	**1.443953176**	2	4.2865
P21213	GETISGGNFHGEYPAK	**0.96390764**	2	3.82777
P21213	GEWLAVPCQDGK	**0.659258338**	2	2.51669
P21213	GQIEVAFR	**0.388560755**	2	2.39418
P21213	LQELQVNLVR	**1.096690003**	2	3.25632
P21213	NKPDNGGFTSVDEVR	**1.070324318**	2	3.6146
P21213	QADIVAALTLEVLK	**0.976148677**	2	2.61384
P21213	SHSSGVGKPLSPER	**1.056097256**	2	3.63549
P21213	SLLDSDHHPSEIAESHR	**0.837350196**	3	4.38465
P21213	TVVYGITTGFGK	**1.058561861**	2	3.59415
P21213	VWEVAAPYIEK	**1.231381004**	2	2.87503
P21213	YIALDGDSLSTEDLVNLGK	**1.089660983**	2	5.17735
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.051459951**	**0.111777**	**7**
P21396	DVPAIEITHTFLER	**1.35661283**	2	2.48118
P21396	IFSVTNGGQER	**0.748617284**	2	2.54802
P21396	INVLVLEAR	**1.064152625**	2	2.94553
P21396	KDIWVEEPESK	**0.756730186**	2	3.2477
P21396	VLGSQEALYPVHYEEK	**0.998778383**	2	3.88281
P21396	WVDVGGAYVGPTQNR	**0.889791956**	2	4.81068
P21396	YVISAIPPILTAK	**0.996953772**	2	2.90534
P21531	**RL3 60S ribosomal protein L3**	**1.113595873**	**0.091209**	**6**
P21531	AHLMEIQVNGGTVAEK	**0.953100012**	2	5.23758
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	**1.086350759**	3	5.92922
P21531	HGSLGFLPR	**1.072210246**	2	3.11254
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	**1.230277125**	2	4.77023

P21531	NNASTDYDLSDK	**1.231308554**	2	3.2251
P21531	TVFAEHISDECK	**1.276340759**	2	3.69067
P21533	**RL6 60S ribosomal protein L6**	**1.259392758**	**0.001157**	**8**
P21533	AVDSQILPK	**1.119945033**	2	2.75714
P21533	FVIATSTK	**1.262020108**	1	2.018
P21533	HLTDAYFK	**1.118338293**	2	2.43603
P21533	HQEGEIFDTEK	**1.347139646**	2	3.32333
P21533	HQEGEIFDTEKEK	**1.109412999**	2	4.00106
P21533	QLGSGLLLVTGPLALNR	**1.300166603**	2	5.04541
P21533	SSITPGTVLIILTGR	**1.189019838**	2	3.89176
P21533	YYPTEDVPR	**1.277207978**	2	2.44005
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.099255846**	**3.51E-12**	**6**
P21571	FEVLDKPQS	**1.116503165**	2	2.93575
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	**1.108243038**	3	3.93032
P21571	GEMDKFPTFNFEDPKFEVLDKPQS+Oxidation(2)	**0.921148411**		
P21571	LASGGPVDTGPEYQQEVDR	**2.339526192**	2	5.28316
P21571	LASGGPVDTGPEYQQEVDRELFK	**1.746409279**	2	2.79989
P21571	RLASGGPVDTGPEYQQEVDR	**1.191955919**	3	4.52364
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.394779991**	**0.0008**	**2**
P21643	GGLIYGDYLQLEK	**1.347433037**	2	3.61744
P21643	ILNAQELQSEIK	**1.442069364**	2	3.65297
P21670	**PSA4 Proteasome subunit alpha type_4**	**1.656361573**	**0.000736**	**4**
P21670	ATCIGNNSAAAVSMLK	**1.595829708**	2	2.81256
P21670	LLDEVFFSEK	**1.610948033**	2	3.59759
P21670	LNEDMACSVAGITSDANVLTNELR	**1.3005079**	3	3.44646
P21670	YLLQYQEPIPCEQLVTALCDIK	**1.210706599**	2	3.04454
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**0.724668657**	**9.9E-20**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	**0.756200003**	3	5.28748
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22)	**0.96363961**		
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.360332715**	**3.28E-10**	**6**
P21913	CGPMVLDALIKIK	**0.725384567**	2	2.4207
P21913	CHTIMNCTQTCPK	**0.894585687**	2	4.31672
P21913	CHTIMNCTQTCPK+Oxidation(4)	**1.568667632**		
P21913	IKNEIDSTLTFR	**1.360598567**	2	2.39582
P21913	LQDPFSLYR	**1.635638278**	2	2.75386
P21913	RIDTDLGK	**1.138731993**	2	2.43727
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.269043723**	**0.014809**	**5**
P21981	CDLEIQANGR	**1.045204915**	2	2.99168
P21981	LVVNFQCDK	**1.976999402**	2	2.67616
P21981	SEGTYCCGPVSVR	**1.071319707**	2	3.69447
P21981	WDNNYGDGISPMAWIGSVDILR	**1.532449638**	3	4.19784
P21981	YSGCLTESNLIK	**1.279619818**	2	3.56634
P22734	**COMT Catechol O_methyltransferase**	**0.912667239**	**0.987366**	**14**
P22734	AIYQGPSSPDK	**1.349209936**	2	2.36295
P22734	AIYQGPSSPDKS	**0.986667133**	2	3.15082
P22734	EWAMNVGDAK	**0.928817469**	1	2.76925
P22734	GQIMDAVIR	**0.707223488**	2	3.03267
P22734	GQIMDAVIR+Oxidation(3)	**1.097704912**		
P22734	GSSSFECTHYSSYLEYMK	**10.01197199**	2	4.56326
P22734	GTVLLADNVIVPGTPDFLAYVR	**1.277380402**	3	4.86808
P22734	KGTVLLADNVIVPGTPDFLAYVR	**1.246449977**	2	4.68774
P22734	KYDVDTLDMVFLDHWK	**0.87138034**	3	5.63542
P22734	VTILNGASQDLIPQLK	**0.815038322**	2	4.30136

P22734	VVDGLEK	**0.93350772**	2	2.38074
P22734	YDVDTLDMVFLDHWK	**0.929574028**	3	4.60215
P22734	YLPDTLLLEK	**0.745028866**	2	2.91393
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	**0.966738512**	3	6.09426
P22789	**ST2A2 Alcohol sulfotransferase A**	**0.697184977**	**0.69204**	**4**
P22789	EEDLILLTYPK	**0.843335422**	2	2.59107
P22789	ETLQNVCNK	**1.378639815**	1	2.01179
P22789	KLEPDELDLVLK	**0.925832654**	3	4.73012
P22789	NHFTVAQAEAFDK	**0.61936031**	2	3.43943
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.260671288**	**9.9E-20**	**21**
P22791	ASLDMFNK	**1.047630703**	2	2.46946
P22791	ASLDMFNKK	**0.914354233**	2	2.52501
P22791	DVGILALEVYFPAQYVDQTDLEK	**1.147262173**	3	7.20561
P22791	GLKLEETYTNK	**0.936977039**	2	2.78267
P22791	GTHMENAYDFYKPNLASEYPLVDGK	**0.938290291**	3	7.03403
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3)	**1.204145877**		
P22791	IGAFSYGSGLAASFFSFR	**1.337318736**	2	3.87921
P22791	LEETYTNK	**1.149213069**	2	3.02161
P22791	LEETYTNKDVDK	**1.220926644**	2	4.10853
P22791	LEVGTETIIDK	**1.100647261**	2	3.7338
P22791	LMFNDFLSSSSDK	**1.58347167**	2	4.42125
P22791	LMFNDFLSSSSDK+Oxidation(1)	**1.822713703**		
P22791	LSIQCYLR	**1.999099173**	2	2.317
P22791	LVSSVSDLPK	**1.275073151**	2	3.49174
P22791	MGFCSVQEDINSLCLTVVQR	**1.557541622**	3	3.4932
P22791	MSPEEFTEIMNQR	**0.946690141**	2	4.65685
P22791	MSPEEFTEIMNQR+Oxidation(0)	**1.101088948**		
P22791	MSPEEFTEIMNQR+Oxidation(9)	**1.181356716**		
P22791	TKLPWDAVGR	**1.113635708**	3	3.95093
P22791	VNFSPPGDTSNLFPGTWYLER	**1.236611261**	2	5.05322
P22791	YTVGLGQTR	**1.088096338**	2	3.33588
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.32479003**	**9.9E-20**	**10**
P22985	DEVTCVGHIIGAVVADTPEHAQR	**1.141669087**	3	3.84866
P22985	DPPANVQLFQEVPK	**1.467764679**	2	3.8434
P22985	DQTVSLSPSLFNPEDFKPLDPTQEPIFPPELLR	**1.126268872**	3	3.38911
P22985	LDPTFASATLLFQK	**1.618796843**	2	4.01857
P22985	NQPEPTVEEIENAFQGNLCR	**0.81697529**	2	4.71336
P22985	QLFQLDSPATPEK	**1.026873296**	2	3.20528
P22985	SVASIGGNIITASPISDLNPVFMASGAK	**1.35509128**	3	5.76832
P22985	TGTVVALEVAHFSNGGNTEDLSR	**1.147640279**	3	4.62415
P22985	TLLRPEEILLSIEIPYSK	**1.373370612**	3	4.05062
P22985	TNLPSNTAFR	**0.824943261**	1	2.25897
P23358	**RL12 60S ribosomal protein L12**	**1.108820957**	**0.048484**	**7**
P23358	CTGGEVGATSALAPK	**1.125314878**	2	4.08388
P23358	EILGTAQSVGCNVDGR	**1.414886801**	2	4.43733
P23358	HNGNITFDEIVNIAR	**1.124850855**	2	4.24865
P23358	HPHDIIDDINSGAVECPAS	**1.013939083**	2	4.8391
P23358	IGPLGLSPK	**1.490418583**	2	2.53966
P23358	QAQIEVVPSASALIIK	**1.383604281**	2	3.87642
P23358	VGDDIAKATGDWKGLR	**0.938537663**	2	2.41216
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**4.943423064**	**9.9E-20**	**10**
P23457	ALDGLNR	**1.131631023**	2	2.55724
P23457	ELTQVFEFQLASEDMK	**1.385477256**	2	3.29004
P23457	HFDSAYLYEVEEEVGQAIR	**3.683268832**	2	6.1665
P23457	MLDYCK	**1.036521724**	1	1.97467
P23457	SIGVSNFNCR	**1.176188493**	2	3.29078

P23457	SKDIILVSYCTLGSSR	**1.599379637**	2	5.06627
P23457	SPVLLDDPVLCAIAK	**2.771584797**	2	3.92564
P23457	VALNDGNFIPVLGFGTTVPEK	**2.000437819**	2	5.18625
P23457	YFDDHPNHPFTDE	**1.97376703**	2	3.74518
P23457	YKPVCNQVECHLYLNQSK	**5.479153618**	2	4.67289
P23514	**COPB Coatomer subunit beta**	**1.066053945**	**0.002993**	**7**
P23514	EAGELKPEEEITVGPVQK	**1.180025405**	2	4.33807
P23514	EDIQSVMTEVR	**1.021180431**	2	2.94185
P23514	NFENLIPDAPELIHDFLVNEK	**1.121105474**	3	4.01721
P23514	TNNVSEHEDTDKYR	**1.262186452**	3	4.12795
P23514	VLQDLVMDILR	**1.016020465**	2	3.61853
P23514	VLSECSPLMNDIFNK	**0.81928935**	2	2.66712
P23514	YEAAGTLVTLSSAPTAIK	**1.653500274**	2	4.9897
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**1.071193009**	**0.996054**	**8**
P23965	ALQLGTLFPPAEALK	**0.880295462**	2	5.41328
P23965	AVQELWLR	**0.974206218**	2	2.60382
P23965	DNYVNTIGHR	**1.166936244**	2	3.03226
P23965	GVILTSERPGIFSAGLDLMEMYGR	**1.05979382**	3	6.20121
P23965	QREADIQNFTSFISR	**1.219431657**	2	2.70024
P23965	SLHVYLEK	**1.114145892**	1	2.31278
P23965	VGLVDEVVPEDQVHSK	**1.013507512**	2	4.73955
P23965	WFTIPDHSR	**0.899115443**	2	3.19672
P24049	**RL17 60S ribosomal protein L17**	**1.055400121**	**9.28E-09**	**3**
P24049	EQIVPKPEEEVAQK	**1.46179289**	2	3.54713
P24049	GLDVDSLVIEHIQVNK	**1.105911673**	2	4.68626
P24049	YSLDPENPTK	**1.0209424**	1	2.7646
P24050	**RS5 40S ribosomal protein S5**	**1.233669511**	**0.001232**	**4**
P24050	HAFEIIHLLTGENPLQVLVNAIINSGPR	**0.911496467**		
P24050	RQAVDVSPLR	**1.17957038**	2	2.36416
P24050	VNQAIWLLCTGAR	**1.328107029**	2	4.11016
P24050	WSTDDVQINDISLQDYIAVK	**1.487873004**	2	4.76424
P24063	**ITAL Integrin alpha_L**	**1.122431026**	**0.355694**	**2**
P24063	ASEAQVLVKVDLIHEK	**1.109432001**	2	2.40036
P24063	DFEKILEFMK	**1.300017901**	3	3.33326
P24090	**FETUA Alpha_2_HS_glycoprotein**	**0.749071166**	**9.9E-20**	**6**
P24090	AQNVPFPVSTLVEFVIAATDCTGQEVTDPAK	**0.770573072**		
P24090	ELACDDPETEHVALIAVDYLNK	**1.168228602**	2	4.18174
P24090	HAFSPVASVESASGEVLHSPK	**0.813325409**	3	5.96044
P24090	LGGEEVSVACK	**0.557085879**	2	3.69273
P24090	VGQPGDAGAAGPVAPLCPGR	**0.539482043**	2	5.08928
P24090	VLHAQCHSTPDSAEDVRK	**0.811649205**	3	4.00934
P24268	**CATD Cathepsin D**	**1.124464024**	**0.000389**	**4**
P24268	AIGAVPLIQGEYMIPCEK	**0.970116433**	2	3.47983
P24268	DPTGQPGGELMLGGTDSR	**0.951859422**	2	4.74685
P24268	GGCEAIVDTGTSLLVGPVDEVK	**1.258178654**	2	4.07784
P24268	LGGQNYELHPEK	**1.451734153**	2	2.91175
P24329	**THTR Thiosulfate sulfurtransferase**	**1.03031041**	**3.33E-16**	**12**
P24329	EGHPVTSEPSRPEPAVFK	**1.206236705**	2	4.69869
P24329	FQLVDSR	**1.029970692**	2	2.46603
P24329	GSVNVPFMNFLTEDGFEK	**9.062795605**	2	5.2761
P24329	HVPGASFFDIEECR	**1.313501934**	3	3.61405
P24329	KVDLSQPLIATCR	**1.101186129**	2	4.78023
P24329	RFQLVDSR	**1.195018617**	2	2.47442
P24329	TVSVLNGGFR	**1.023476518**	2	2.88706
P24329	TYEQVLENLQSK	**1.022612326**	2	5.08563
P24329	VDLSQPLIATCR	**1.098475245**	2	3.5459

P24329	VLDASWYSPGTR	**0.990946293**	2	3.73506
P24329	WLAESIR	**1.051750196**	2	2.35928
P24329	YLGTQPEPDAVGLDSGHIR	**1.06361912**	3	5.05237
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.139334983**	**0.000138**	**9**
P24368	DKPLKDVIIVDCGK	**1.114005989**	2	3.64182
P24368	DTNGSQFFITTVK	**1.323903476**	2	3.58047
P24368	DVIIVDCGK	**1.173057436**	1	1.99057
P24368	HYGPGWVSMANAGK	**1.008141286**	2	3.235
P24368	IEVEKPFAIAK	**1.144290292**	2	3.29233
P24368	IEVEKPFAIAKE	**1.201722924**	2	3.55863
P24368	TVDNFVALATGEK	**1.314324166**	2	3.75557
P24368	VLEGMDVVR	**1.045446738**	2	2.77542
P24368	VYFDFQIGDEPVGR	**1.102169251**	2	4.32137
P24457	**CP2DB Cytochrome P450 2D11**	**0.937578817**	**0.902315**	**2**
P24457	RFSVSTLR	**1.025261049**	2	2.54135
P24457	SLEEWVTK	**0.910472508**	2	2.75679
P24470	**CP2CN Cytochrome P450 2C23**	**0.583177838**	**9.9E-20**	**10**
P24470	ACVGESLAR	**0.683381772**	2	2.52792
P24470	AQPFDPTFILACAPCNVICSILFNDR	**0.844395076**		
P24470	DLDIKPITTGIINLPPPYK	**0.598774094**	2	3.71758
P24470	EALLQQGDEFLGR	**0.757905756**	2	2.58123
P24470	GTTVLPMLSSVMLDQK	**0.633288549**	2	4.00865
P24470	GYGLIFSNGER	**0.716746139**	2	3.24137
P24470	IEEEKDNLK	**0.738624315**	1	2.89826
P24470	LPPGPTPLPIIGNLLQLNLK	**0.797642652**	2	3.49408
P24470	TFLNLMDLLNK	**0.526168582**	2	3.86456
P24470	YITLLPSSLPHAVVQDTK	**0.4881478**	2	3.41202
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.754023725**	**2.2E-14**	**9**
P24473	AGMATAQAQHLLNK	**0.977009316**	2	3.91941
P24473	AGMATAQAQHLLNK+Oxidation(2)	**1.124173395**		
P24473	DEDITESQNILSAAEK	**0.914489499**	2	5.74343
P24473	DSGNQPPAMVPHK	**0.961322911**	2	2.42016
P24473	FLTAVSMEQPEMLEK	**0.716402872**	2	4.18837
P24473	FLTAVSMEQPEMLEK+Oxidation(11)	**1.032513506**		
P24473	MELLAYLLGEK	**1.78608601**	2	4.11004
P24473	QLFQVPMSVPK	**0.945577108**	2	2.71966
P24473	YGAFGLPTTVAHVDGK	**1.20621172**	2	3.75922
P25093	**FAAA Fumarylacetoacetase**	**1.109736205**	**9.9E-20**	**17**
P25093	AIDVGQGQTR	**1.077975931**	2	3.40848
P25093	AQEHIFGMVLMNDWSAR	**1.169546878**	3	3.69363
P25093	AQEHIFGMVLMNDWSAR+Oxidation(7)	**0.191588941**		
P25093	ASLQNLLSASQAQLR	**0.917661017**	2	4.80208
P25093	ASLQNLLSASQAQLRDDK	**0.83402054**	2	3.14547
P25093	ASSVVVSGTPIR	**1.085004937**	2	3.59505
P25093	DIQQWEYVPLGPFLGK	**1.485660947**	2	4.83211
P25093	FGEPIPISK	**1.066420526**	2	2.87535
P25093	GEGMSQAATICR	**1.033158627**	2	3.65755
P25093	GEGMSQAATICR+Oxidation(3)	**1.728344222**		
P25093	GKENALLPNWLHLPVGYHGR	**1.962366646**	3	3.47048
P25093	HLFTGPVLSK	**1.143063219**	1	2.70708
P25093	HQHVFDETTLNSFMGLGQAAWK	**1.113899683**	2	5.37469
P25093	IGVAIGDQILDLSVIK	**1.615531929**	2	5.41711
P25093	IGVAIGDQILDLSVIKHLFTGPVLSK	**1.024248148**	3	3.95273
P25093	TFLLDGDEVIITGHCQGDGYR	**0.890999497**	2	5.02797
P25093	VGFGQCAGK	**1.108153904**	2	2.38556
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.09456108**	**9.9E-20**	**7**
P25113	ALPFWNEEIVPQIK	**2.041917421**	2	3.93666

P25113	FSGWYDADLSPAGHEEAK	0.94235131	2	4.95321
P25113	HGESAWNLENR	1.183241652	2	3.73952
P25113	HLEGLSEEAIMELNLPTGIPIVYELDK	1.111940398	3	3.46314
P25113	SYDVPPPPMEPDHPFYSNISK	1.323021514	2	4.31829
P25113	YADLTEDQLPSCESLK	1.21402303	2	5.49034
P25113	YADLTEDQLPSCESLKDTIAR	1.061310151	2	5.01762
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.118479758**	**9.9E-20**	**14**
P25235	DLLLAAVSEDSSVAQIYHAVAALSGFGLPLASHEALGALTAR	1.696288001		
P25235	EDQVIQLMNTIFSK	2.334843058	2	2.39476
P25235	EETVLATVQALHTASHLSQQADLR	1.099182293	3	4.31323
P25235	FELDTSER	1.005464437	1	2.04854
P25235	FPEEEAPSTVLSQNLFTPK	0.846528721	2	4.25804
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.156764817	2	4.52349
P25235	LQVSSVLSQPLAQAAVK	1.43569606	2	5.72784
P25235	LSKEETVLATVQALHTASHLSQQADLR	0.955131898	3	4.53629
P25235	NFESLSEAFSVASAAAALSQNR	1.205098317	3	5.48058
P25235	NIVEEIEDLVAR	1.1259139	3	4.68362
P25235	NPILWNVADVVIK	1.353709883	2	3.2691
P25235	TGQEVVFVAEPDNK	2.541222637	2	3.90921
P25235	YHVPVVVVPEGSASDTQEQAILR	1.283338675	3	6.53153
P25235	YIANTVELR	1.098392187	2	2.58793
P25409	**ALAT1 Alanine aminotransferase 1**	**5.036209807**	**4.79E-13**	**2**
P25409	LTEQVFNEAPGIR	3.781844008	2	3.48034
P25409	VLCVINPGNPTGQVQTR	9.333101519	2	4.63989
P25977	**UBF1 Nucleolar transcription factor 1**	**1.072911087**	**0.883958**	**2**
P25977	AKYAKLHPEMSNLDLTK	1.072995221	2	2.33606
P25977	ALKAMEMTWNNMEKK+Oxidation(11)	0.994301647		
P26039	**TLN1 Talin_1**	**0.981033453**	**1.16E-11**	**22**
P26039	ADAEGESDLENSR	1.028733437	2	2.89525
P26039	ADAEGESDLENSRK	1.005626325	2	3.19011
P26039	AGALQCSPSDVYTK	1.101938773	2	2.65585
P26039	ASAGPQPLLVQSCK	0.946409365	2	3.024
P26039	AVAEQIPLLVQGVR	0.862476179	2	3.55528
P26039	EAAEGLRMATNAAAQNAIKK	0.861645462	2	2.73761
P26039	ELMEEKKDEGTGTLR+Oxidation(2)	1.392997292		
P26039	GTEWVDPEDPTVIAENELLGAAAAIEAAAK	0.76269553		
P26039	GVGAAATAVTQALNELLQHVK	0.799429584	3	3.59189
P26039	ILAQATSDLVNAIK	1.706297405	2	2.62395
P26039	LGAASLGAEDPETQVVLINAVK	1.522199849	2	4.41286
P26039	LLGEIAQGNENYAGIAAR	1.284762865	2	4.27511
P26039	LNEAAAGLNQAATELVQASR	0.865042774	2	5.2389
P26039	MVAAATNNLCEAANAAVQGHASQEK	0.988037108	3	3.43219
P26039	SNTSPEELGPLANQLTSDYGR	0.984675442	2	4.01423
P26039	TLAESALQLLYTAK	1.159786911	2	2.98872
P26039	TMLESAGGLIQTAR	0.512895482	2	2.63155
P26039	VGAIPANALDDGQWSQGLISAAR	0.929716806	2	4.5172
P26039	VGDDPAVWQLK	1.430026994	2	2.83443
P26039	VLGEAMTGISQNAK	0.788163975	2	2.79163
P26039	VLVQNAAGSQEK	0.992482061	2	2.51423
P26039	VVAPTISSPVCQEQLVEAGR	0.818363454	2	4.49232
P26043	**RADI Radixin**	**1.095838324**	**0.646099**	**10**
P26043	AFAAQEDLEK	1.461374718	2	2.55851
P26043	ALELEQER	0.936823133	1	1.92713
P26043	FFPEDVSEELIQEITQR	1.130202285	3	4.64156

P26043	IQNWHEEHR	**0.741091114**	2	2.51229
P26043	KKEEEATEWQHK	**0.851406545**	3	3.73676
P26043	KTQNDVLHAENVK	**1.080204958**	2	5.05087
P26043	NQEQLAAELAEFTAK	**1.077016938**	2	5.10275
P26043	QLQALSSELAQAR	**0.988363672**	2	3.75712
P26043	RKPDTIEVQQMK	**0.828975797**	2	3.86877
P26043	TQNDVLHAENVK	**1.166051118**	2	3.94239
P26231	**CTNA1 Catenin alpha_1**	**0.981181148**	**0.001317**	**10**
P26231	AEVQNLGGELVVSGVDSAMSLIQAAK	**1.050317231**	3	4.15602
P26231	AHVLAASVEQATENFLEK	**0.65363364**	2	2.36008
P26231	AVMDHVSDSFLETNVPLLVLIEAAK	**1.205451209**	3	3.53748
P26231	LIEVANLACSISNNEEGVK	**0.974464834**	2	4.89412
P26231	LLEPLVTQVTTLVNTNSK	**1.033009067**	2	4.01149
P26231	QIIVDPLSFSEER	**1.213133103**	2	2.68353
P26231	SAAGEFADDPCSSVK	**1.238249182**	2	4.05216
P26231	SDALNSAIDK	**1.265299217**	2	2.52139
P26231	TIADHCPDSACK	**0.688648569**	2	3.55932
P26231	VIHVVTSEMDNYEPGVYTEK	**1.053461811**	3	3.5537
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.051461478**	**0.969915**	**8**
P26284	AILAELTGR	**0.972291069**	2	2.57255
P26284	EEIQEVRSK	**0.672532097**	1	1.93439
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	**0.992455674**	3	6.63232
P26284	LEEGPPVTTVLTR	**0.943618114**	2	3.48645
P26284	MVNSNLASVEELKEIDVEVR	**0.539919468**	2	3.00551
P26284	RGDFIPGLR	**1.129285772**	2	2.70851
P26284	TREEIQEVR	**1.063407655**	3	3.48957
P26284	VDGMDILCVR	**0.893576355**	2	3.33708
P26453	**BASI Basigin**	**1.108383304**	**0.103231**	**7**
P26453	GNINVEGPPR	**1.160013335**	2	3.46956
P26453	KSEHASEGEFVK	**1.157163042**	2	2.86426
P26453	RKPDQTLDEDDPGAAPLK	**1.221326897**	3	4.14947
P26453	SEASHPPVDEWVWFK	**1.015823687**	3	3.92652
P26453	SEHASEGEFVK	**1.235886162**	3	3.544
P26453	SGEYSCIFLPEPVGR	**1.078735925**	2	3.46389
P26453	VLQEDTLPDLQMK	**0.892285372**	2	4.35323
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**1.202958931**	**0.918987**	**7**
P26772	GGEIQPVSVK	**1.05835306**	2	3.26005
P26772	GGIMLPEK	**0.814851031**	2	2.33097
P26772	GGIMLPEK+Oxidation(3)	**1.397032779**		
P26772	GKGGEIQPVSVK	**0.920509083**	2	3.3996
P26772	VLLPEYGGTK	**1.14170716**	2	2.3673
P26772	VLQATVVAVGSGGK	**1.082673404**	2	5.5117
P26772	VVLDDKDYFLFR	**1.0985239**	3	3.40381
P27139	**CAH2 Carbonic anhydrase 2**	**0.842844217**	**0.587593**	**2**
P27139	IGPASQGLQK	**0.818693963**	2	2.5416
P27139	ITEALHSIK	**0.845206998**	2	2.42686
P27321	**ICAL Calpastatin**	**0.835281055**	**8.99E-13**	**4**
P27321	KGSDEVTASSAATGTSPR	**0.825667494**	2	4.84253
P27321	KVEEEVMNDQALQALSDSLGTR	**0.741471817**	3	3.57108
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	**1.262297393**	3	4.18231
P27321	SQSSEPPVIHEK	**0.430020555**	2	3.22608
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**1.083510505**	**0.988885**	**6**
P27364	AVLAANGSILK	**1.107820818**	2	2.89152
P27364	ETILNDREEEHR	**1.245273315**	2	2.92085

P27364	GDIVDAQFLR	**1.041670253**	2	2.99304
P27364	IVQMLVQEK	**1.319263261**	2	2.66071
P27364	NGGTFHTCALR	**1.010318994**	2	3.07916
P27364	QTILDVNVK	**0.973695144**	1	2.10536
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**0.924061891**	**0.000267**	**6**
P27605	DLNHVCVISESGK	**1.260375037**	2	3.69239
P27605	FFADLLDYIK	**1.268175403**	2	3.1946
P27605	NVLIVEDIIDTGK	**1.209624298**	2	4.10506
P27605	SVGYRPDFVGFEIPDK	**0.930141848**	3	3.80948
P27605	SYCNDQSTGDIK	**1.273956401**	2	3.96122
P27605	VIGGDDLSTLTGK	**1.174133518**	2	4.22319
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**1.55640674**	**9.9E-20**	**21**
P27653	ASQAPSSFQLLYDLK	**1.85660266**	2	4.17405
P27653	AYTEEDLDLVEK	**1.126001939**	2	3.02899
P27653	CTHWAEGGQGALALAQAVQR	**1.13168488**	2	5.19674
P27653	DVDGLTSINAGK	**1.004553714**	2	2.43333
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	**1.055254075**	3	5.08474
P27653	GVPTGFVLPIR	**1.688359707**	2	2.52821
P27653	IFHELTQTDK	**1.357019508**	3	3.61386
P27653	IYGADDIELLPEAQNK	**1.399975681**	2	5.28841
P27653	KITIGQAPTEK	**1.749552284**	2	2.91144
P27653	KVVGDVAYDEAK	**1.706364735**	2	3.88691
P27653	LDIDPETITWQR	**1.314023268**	2	4.084
P27653	MHGGGPTVTAGLPLPK+Oxidation(0)	**1.533765021**		
P27653	QGFGNLPICMAK	**0.942411115**	2	3.16281
P27653	TADLDKEVNK	**1.569590047**	2	2.40063
P27653	TADLDKEVNKGDILVVATGQPEMVK	**1.108813402**	3	4.61196
P27653	TDPAALTDDEINR	**1.287024219**	2	4.37969
P27653	THLSLSHNPEQK	**1.398411664**	2	3.83261
P27653	VLLSALDR	**1.549573996**	2	2.47687
P27653	VVGDVAYDEAK	**1.449932896**	2	3.72781
P27653	YSGLQPHVVVLVATVR	**2.400753642**	3	3.52075
P27653	YVVVTGITPTPLGEGK	**1.422147792**	2	4.88205
P27657	**LIPP Pancreatic triacylglycerol lipase**	**0.738851755**	**0.129291**	**2**
P27657	ATYTQATQNVR	**0.472238113**	2	2.52048
P27657	ITGLDAAEPYFQGTPEEVR	**0.293134274**	2	3.88848
P27661	**H2AX Histone H2A.x**	**1.256704126**	**0.999674**	**3**
P27661	AGLQFPVGR	**0.993742237**	2	3.19305
P27661	HLQLAIR	**0.999146568**	2	2.64228
P27661	LLGGVTIAQGGVLPNIQAVLLPK	**1.106964536**	3	4.71706
P27768	**TNNI2 Troponin I_ fast skeletal muscle**	**0.443320035**	**0.408236**	**3**
P27768	IDAAEEEKYDMEVK	**0.25891202**	2	3.71615
P27768	SVMLQIAATELEK	**0.854565256**	2	2.52984
P27768	SVMLQIAATELEKEESR	**0.646061144**	2	3.10514
P27867	**DHSO Sorbitol dehydrogenase**	**0.965446695**	**1.45E-10**	**14**
P27867	AMGASQVVVIDLSASR	**0.8358365**	2	4.03758
P27867	AVEAFETAK	**0.94128947**	2	2.99051
P27867	EVGADFTIQVAK	**1.013299724**	2	2.78149
P27867	GENLSLVVHGPGDIR	**0.975212614**	2	3.97393
P27867	HSADFCYK	**0.984808661**	2	2.81402
P27867	IGDFVVK	**0.948059112**	2	2.62791
P27867	LENYPIPELGPNDVLLK	**0.990643094**	2	4.79278
P27867	LPDSVTFEEGALIEPLSVGIYACR	**1.114643841**	2	4.75096
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0)	**1.145933951**		
P27867	TLNVKPLVTHR	**0.956333912**	2	3.25948

P27867	VAIEPGVPR	**1.470945799**	2	2.58542
P27867	VAIEPGVPREIDEFCKIGR	**0.770932617**	2	2.54557
P27867	VLVCGAGPIGIVTLLVAK	**1.159371099**	3	6.22644
P27867	YNLTPSIFFCATPPDDGNLCR	**2.977344105**	2	4.20319
P27952	**RS2 40S ribosomal protein S2**	**1.177752904**	**0.317749**	**7**
P27952	AEDKEWIPVTK	**1.201587222**	2	3.2127
P27952	AFVAIGDYNGHVGLGVK	**1.354857991**	2	3.78808
P27952	ATFDAISK	**1.155458704**	2	2.44485
P27952	GCTATLGNFAK	**1.227728226**	2	2.84033
P27952	GTGIVSAPVPK	**1.212020345**	2	2.44934
P27952	SLEEIYLFSLPIK	**0.821699855**	1	2.7123
P27952	TYSYLTPDLWK	**1.095021443**	2	2.70653
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**0.915736489**	**0.059894**	**26**
P28037	ADPLGLEAEK	**1.040276829**	2	2.82221
P28037	ANATEFGLASGVFTR	**1.031962561**	2	4.44467
P28037	AVQMGMSSVFFNK	**1.024965762**	2	3.51173
P28037	CPQSEEGATYEGIQK	**1.431139577**	2	4.31461
P28037	DLGEAALNEYLR	**1.152842955**	2	3.28883
P28037	ECEVLPDDTVSTLYNR	**1.006711146**	2	5.00712
P28037	EGHEVVGVFTIPDKDGK	**1.050216563**	2	4.51124
P28037	GNDKVPGAWTEACGQK	**0.896333561**	2	3.53697
P28037	GQALPEVVAK	**0.918446074**	2	2.59633
P28037	GSASSDLELTEAELATAEAVR	**0.899811811**	2	6.29668
P28037	GVVNILPGSGSLVGQR	**0.908668751**	2	4.94424
P28037	IGFTGSTEVGK	**1.240464524**	2	3.11039
P28037	ILPNVPEVEDSTDFFK	**1.212955138**	2	3.69114
P28037	INWDQPAEAIHNWIR	**0.916458666**	2	3.67751
P28037	KEGHEVVGVFTIPDKDGK	**0.998609179**	3	3.48272
P28037	KIGFTGSTEVGK	**0.783279931**	2	2.9508
P28037	KLVEYCQR	**1.365660598**	2	2.53558
P28037	LFVEESIHNQFVQK	**0.932386323**	2	4.59886
P28037	LIAEGTAPR	**1.021380344**	2	3.13468
P28037	LQAGTVFINTYNK	**1.888010153**	2	2.50769
P28037	LSDHPDVR	**0.911481743**	1	2.09918
P28037	NIQLEDGK	**1.084974624**	1	1.99802
P28037	TAACLAAGNTVVIKPAQVTPLTALK	**1.05375164**	3	4.42601
P28037	TDVAAPFGGFK	**0.909670567**	2	2.7197
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	**1.003354728**	3	6.58631
P28037	VVEEVEK	**1.110737237**	2	2.47846
P28064	**PSB8 Proteasome subunit beta type_8**	**1.243193037**	**0.975496**	**3**
P28064	ASAGSYIATIR	**1.219763342**	2	2.52747
P28064	QDLSPEEAYDLAR	**0.888278938**	2	3.1169
P28064	VESTDVSDLLHK	**0.956414394**	2	2.90187
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.317524541**	**0.009759**	**10**
P28480	AFHNEAQVNPER	**1.357803385**	2	3.41981
P28480	FATEAAITILR	**0.969782093**	2	3.26035
P28480	HGGYENAVHSGALDD	**1.344152286**	2	4.22873
P28480	ICDDELILIK	**0.903422424**	2	3.17002
P28480	LLEVEHPAAK	**0.988026426**	2	2.39514
P28480	MLVDDIGDVTITNDGATILK	**1.170146396**	2	4.33841
P28480	SLHDALCVVK	**0.918721317**	2	2.45545
P28480	SLLVIPNTLAVNAAQDSTDLVAK	**1.103600318**	2	4.63755
P28480	SQNVMAAASIANIVK	**0.963679792**	2	4.02261
P28480	YINENLIINTDELGR	**0.913941378**	2	4.48454
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.902965769**	**0.984144**	**3**
P28492	MVQESSSGGLLDR	**0.991190039**	2	3.222

P28492	SNPDLWGVSLCTVDGQR	**0.885726002**	2	3.15511
P28492	TALHVAAAEGHIDVVK	**0.985295328**	3	3.5419
P28650	**PURA1 Adenylosuccinate synthetase isozyme 1**	**0.717797367**	**0.006552**	**3**
P28650	CQGGNNAGHTVVVDGK	**0.523382952**	2	3.70611
P28650	LDILDVLSEIK	**0.666057417**	2	3.15351
P28650	VGIGAFPTEQINEIGDLLQNR	**0.963950745**	3	3.8037
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**1.145809554**	**9.9E-20**	**20**
P29147	AVLVTGCDSGFGFSLAK	**0.939095398**	2	5.71408
P29147	EVAEVNLWGTVR	**1.125134366**	2	2.75499
P29147	FGVEAFSDCLR	**1.328997356**	2	3.7066
P29147	GFLVFAGCLLK	**1.704012183**	2	3.48083
P29147	KMWDELPEVVR	**1.013716067**	2	2.84792
P29147	KMWDELPEVVR+Oxidation(1)	**1.094406383**		
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	**2.522632588**	3	5.4494
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0)	**2.255727659**		
P29147	MQVMTHFPGAISDK	**1.247490366**	2	4.57856
P29147	MQVMTHFPGAISDK+Oxidation(0)	**1.290040093**		
P29147	MQVMTHFPGAISDK+Oxidation(0)	**1.177866236**		
P29147	MQVMTHFPGAISDK+Oxidation(3)	**1.422074468**		
P29147	MWDELPEVVR	**0.564266843**	2	3.08064
P29147	MWDELPEVVR+Oxidation(0)	**0.997451213**		
P29147	TIQLNVCNSEEVEK	**1.02823351**	2	4.44967
P29147	VSVVEPGNFIAATSLYSPER	**1.026673178**	2	6.10183
P29147	VVNISSMLGR	**1.099191396**	2	3.96177
P29147	VVNISSMLGR+Oxidation(6)	**1.089412289**		
P29147	YEMHPLGVK	**0.965326654**	2	2.70385
P29147	YEMHPLGVK+Oxidation(2)	**1.250567721**		
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.998390101**	**4.59E-05**	**8**
P29266	DLGLAQDSATSTK	**1.296294979**	2	4.0746
P29266	EAGEQVASSPADVAEK	**1.154748835**	2	4.74176
P29266	GSLLIDSSTIDPSVSK	**0.858967677**	2	4.76977
P29266	HGYPLILYDVFPDVCK	**1.109767087**	2	4.99754
P29266	KGSLLIDSSTIDPSVSK	**0.946519636**	2	4.65986
P29266	MGAVFMDAPVSGGVGAAR	**0.769949214**	2	4.78909
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0)	**1.164878456**		
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5)	**1.164878456**		
P29314	**RS9 40S ribosomal protein S9**	**1.686369559**	**1.67E-07**	**9**
P29314	IEDFLER	**1.179187979**	2	2.8299
P29314	IGVLDEGK	**1.043342424**	2	2.39505
P29314	KGQGGAGAGDDEEED	**3.142467519**	2	4.17577
P29314	LDYILGLK	**1.205060293**	2	2.5478
P29314	LFEGNALLR	**1.198016953**	2	2.62933
P29314	LIGEYGLR	**1.6974016**	2	2.64659
P29314	QVVNIPSFIVR	**0.981896037**	2	2.45419
P29314	RLQTQVFK	**0.641956773**	2	2.3014
P29314	SRLDQELK	**1.161822125**	3	3.31583
P29315	**RINI Ribonuclease inhibitor**	**0.943477061**	**0.602259**	**6**
P29315	ASLQELDLGSNK	**0.56103435**	2	2.82782
P29315	ELHLNDNPLGDEGLK	**0.853488796**	2	2.9262
P29315	LDDCGLTEVR	**0.769173122**	2	2.92679
P29315	LENCGITSANCK	**0.943520601**	2	3.33005
P29315	SAIQANPALTELSLR	**0.977387343**	2	4.59481
P29315	TNELGDAGVGLVLQGLQNPTCK	**0.916967696**	2	5.28679
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.12560595**	**1.83E-13**	**10**

P29410	AMVASGSELGK	1.026231725	2	2.36165
P29410	AMVASGSELGKK	0.98238005	2	3.13855
P29410	AVLLGPPGAGK	1.089368508	2	2.70927
P29410	EAMKDDITGEPLIR	1.526461632	2	2.72356
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.863698976	3	6.22284
P29410	LEAYHTQTTPLVEYYR	1.242871979	2	5.40082
P29410	LVSDEMVVELIEK	1.079287768	2	4.1433
P29410	NGFLLDGFPR	0.947014649	2	3.35506
P29410	NLETPSCK	1.013237365	2	2.34937
P29410	SYHEEFNPPK	0.978435107	3	3.85659
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**1.033299364**	**0.527361**	**8**
P29411	AYEAQTEPVLQYYQK	1.180418731	2	4.18317
P29411	EDDKPETVIK	0.790327959	2	2.63328
P29411	KGVLETFSGTETNK	0.841300624	2	3.05048
P29411	NLTQCSWLLDGFPR	0.914786438	2	3.33923
P29411	TLPQAEALDR	1.065268033	2	2.33985
P29411	TVGIDDLTGEPLIQR	0.753493318	2	3.35176
P29411	VYNIEFNPPK	0.858847231	2	3.15534
P29411	VYQIDTVINLNVPFEVIK	1.010967909	2	2.66006
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**1.274241931**	**0.357289**	**2**
P29419	ELAEAEDVSIFK	1.216268945	2	3.2978
P29419	YSALILGMAYGAK	1.105247821	2	4.08722
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**0.988450157**	**0.912252**	**3**
P30009	AEDGAAPSPSSETPK	0.8975259	2	3.92432
P30009	AEEPSEAVGEK	1.074149986	2	2.78907
P30009	GEAAAERPGEAAVASSPSK	0.982369729	2	4.5472
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**0.906849476**	**0.521034**	**4**
P30349	EEDLNSFSIEDLK	1.653405978	2	2.66886
P30349	SLSNVIAHEISHSWTGNLVTNK	0.709079149	3	4.17538
P30349	SSALQWLTPEQTSGK	0.952767417	2	2.99612
P30349	WEEAIPLALK	0.937375828	2	2.9136
P30427	**PLEC Plectin**	**0.979060823**	**0.981512**	**6**
P30427	AQAEAQQPVFNTLR	1.046340967	2	2.99436
P30427	AQVEQELTTLR	0.991315414	2	2.51449
P30427	LLDPEDVDVPQPDEK	0.919475183	2	3.72647
P30427	LQAEEVAQQK	1.074215124	2	2.39863
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0)	1.080698275		
P30427	VLALPEPSPAAPTLR	0.928067116	2	2.78117
P30713	**GSTT2 Glutathione S_transferase theta_2**	**0.948508332**	**1.8E-09**	**6**
P30713	AQVHEYLGWHADNIR	1.297204179	2	4.89856
P30713	GQHLSEQFSQVNCLK	1.090321858	2	4.7949
P30713	NSMVLALQR	0.93151252	2	2.86899
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	1.54918766	3	4.2965
P30713	VLGPLIGVQVPEEK	0.952301119	2	3.89721
P30713	YQVADHWYPADLQAR	0.79733099	2	4.86204
P30835	**K6PL 6_phosphofructokinase_ liver type**	**0.93681811**	**0.437109**	**2**
P30835	NEWGSLLEELVK	0.958498622	2	3.21228
P30835	VFANAPDSACVIGLR	0.353976784	2	2.40314
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**1.113548506**	**7.45E-07**	**10**
P30839	DILAAIAADLSK	1.073618902	2	3.03041
P30839	EKDILAAIAADLSK	1.005812523	2	4.11587
P30839	EKPLALYIFSHNNK	0.913257502	2	3.13302
P30839	FDHILYTGNTAVGK	1.726486218	2	3.93518
P30839	HLTPVTLELGGK	1.003863399	3	3.3151
P30839	NVEEAINFINDR	1.817240472	2	4.10967

P30839	QRFDHILYTGNTAVGK	**1.874810105**	2	2.83376
P30839	VMQEEIFGPILPIVSVK	**0.78245227**	2	4.42593
P30839	VMQEEIFGPILPIVSVK+Oxidation(1)	**1.118995435**		
P30839	YIAPTILTDVDPNSK	**0.989081848**	2	3.86002
P30904	**MIF Macrophage migration inhibitory factor**	**1.405306983**	**7.89E-08**	**2**
P30904	LHISPDR	**0.999517403**	1	2.01816
P30904	LLCGLLSDR	**1.855014977**	2	2.93486
P30999	**CTND1 Catenin delta_1**	**1.180587482**	**0.883368**	**3**
P30999	GYELLFQPEVVR	**0.997844038**	2	2.84242
P30999	QDVYGPQPQVR	**1.180587918**	2	2.43279
P30999	SQSSHSYDDSTLPLIDR	**1.076699096**	2	2.59485
P31000	**VIME Vimentin**	**1.144115168**	**6.7E-13**	**15**
P31000	DGQVINETSQHHDDLE	**0.824208636**	2	3.11483
P31000	FADLSEAANR	**1.206098647**	2	2.84034
P31000	ILLAELEQLK	**0.815748841**	2	3.22259
P31000	KLLEGEESR	**0.896433887**	2	2.73062
P31000	KVESLQEEIAFLK	**0.797865278**	2	3.97541
P31000	LGDLYEEEMR	**0.647249553**	2	2.33645
P31000	LLEGEESR	**0.846493734**	2	2.74933
P31000	LQEEMLQR	**0.536835051**	2	2.32855
P31000	NLQEAEEWYK	**0.716210955**	2	2.81154
P31000	QDVDNASLAR	**0.631053095**	2	2.80583
P31000	QVQSLTCEVDALK	**0.908971595**	2	3.54129
P31000	RQVDQLTNDK	**0.696145573**	2	2.51681
P31000	SLYSSSPGGAYVTR	**1.598565944**	2	2.80983
P31000	TNEKVELQELNDR	**0.893575312**	2	2.83556
P31000	VELQELNDR	**0.625560376**	2	2.58706
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**1.035538204**	**9.9E-20**	**7**
P31044	GNDISSGTVLSEYVGSGPPK	**1.025811188**	2	6.58127
P31044	KYHLGAPVAGTCFQAEWDDSVPK	**1.12153684**	3	3.77532
P31044	LYTLVLTDPDAPSR	**1.51291284**	2	4.26709
P31044	VDYGGVTVDELGK	**0.885979736**	2	4.85895
P31044	VLTPTQVMNRPSSISWDGLDPGK	**0.887328635**	3	5.07907
P31044	YHLGAPVAGTCFQAEWDDSVPK	**2.233888883**	2	5.39831
P31044	YVWLVYEQEQPLNCDEPILSNK	**1.326883441**	2	5.40578
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**1.753343632**	**8.51E-08**	**19**
P31210	DELLTSLGK	**1.580361402**	2	2.86239
P31210	DIEALNK	**1.41153355**	1	2.46768
P31210	EEMKDIEALNK	**1.157905857**	2	3.38508
P31210	ENFQIFDFSLTK	**1.220749099**	2	3.02729
P31210	HIDGAYVYR	**1.324950569**	2	2.93937
P31210	IKENFQIFDFSLTK	**2.287756849**	3	4.34678
P31210	LWSTDHDPEMVRPALER	**1.250239516**	3	3.66817
P31210	NEHEVGEAIR	**1.143514967**	2	3.07835
P31210	NPLWVNVSSPPLLK	**1.526913266**	2	4.44298
P31210	NPLWVNVSSPPLLKDELLTSLGK	**1.177550079**	3	5.23687
P31210	QLEVILNKPGLK	**1.285029943**	2	3.38297
P31210	REEIFYCGK	**1.636623271**	2	3.28525
P31210	RQLEVILNKPGLK	**1.103742608**	3	3.68069
P31210	SLGVSNFNR	**0.823623608**	2	2.37678
P31210	SNLCATWEALEACK	**0.887964939**	2	4.94167
P31210	SNLCATWEALEACKDAGLVK	**0.77047026**	2	5.14522
P31210	TAIDEGYR	**1.205900493**	2	2.43693
P31210	TQAQIVLR	**1.195955033**	2	3.03622
P31210	YKPVTNQVECHPYFTQTK	**1.568235532**	2	5.77276

P31230	**AIMP1 Aminoacyl tRNA synthase complex_interacting multifunctional protein 1**	**1.236051746**	**0.000441**	**2**
P31230	GAEADQIIEYLK	**1.245078906**	2	3.47744
P31230	KEIEELK	**0.829165347**	1	1.99902
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.400959747**	**3.24E-12**	**7**
P31399	ANVDKPGLVDDFK	**1.147375265**	2	3.78098
P31399	KYPYWPHQPIENL	**1.161153561**	2	2.381
P31399	NCAQFVTGSQAR	**1.077722326**	2	4.92523
P31399	NMIPFDQMTIDDLNEVFPETK	**1.048089202**	2	5.07602
P31399	SWNETFHTR	**1.192928**	2	2.67606
P31399	TIDWVSFVEIMPQNQK	**1.948205458**	2	4.12896
P31399	YTALVDAEEKEDVK	**1.415593864**	2	3.63804
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.052847554**	**0.412215**	**6**
P32089	FIHDQTSSNPK	**1.261791471**	1	3.54773
P32089	GLSSLLYGSIPK	**0.916870225**	2	3.29221
P32089	GTYQGLTATVLK	**1.084948217**	2	2.62821
P32089	NTLDCGVQILK	**1.13557196**	2	2.49719
P32089	SHGVLGLYR	**0.871478156**	1	1.91403
P32089	TQLQLDER	**1.09375005**	2	2.9188
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**0.814176647**	**0.00028**	**6**
P32198	ELEQQMQQILDDPSEPQPGEAK	**0.783425028**	2	4.59561
P32198	GDTNPNIPKPTR	**1.015165852**	2	2.50115
P32198	LSTSQTPQQQVELFDFEK	**3.176275898**	2	2.81518
P32198	MTALAQDFAVNLGPK	**0.737815733**	2	3.38843
P32198	MTALAQDFAVNLGPK+Oxidation(0)	**0.482860376**		
P32198	TSPDAFIQLALQLAHYK	**0.792645447**	2	3.25934
P32232	**CBS Cystathionine beta_synthase**	**1.424705906**	**9.9E-20**	**11**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	**1.501670829**	3	5.97373
P32232	ALGAEIVR	**1.696460841**	1	1.97029
P32232	CVVILPDSVR	**1.432354644**	2	2.46703
P32232	FDSPESHVGVAWR	**1.380080502**	2	3.78559
P32232	LKNEIPNSHILDQYR	**2.646204616**	3	3.34692
P32232	NASNPLAHYDDTAEEILQQCDGK	**1.799974263**	2	5.30098
P32232	SNDDDSFAFAR	**2.288582781**	2	3.32601
P32232	VDMLVASAGTGGTITGIAR	**1.302910902**	2	4.83433
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	**2.13829661**	3	3.97941
P32232	VRPSDEVCK	**1.569677834**	2	2.63197
P32232	VWISPDTPSR	**1.491373311**	2	2.36736
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.149732056**	**5.55E-16**	**13**
P32551	AVAFQNPQTR	**1.464649126**	2	3.22082
P32551	AVAQGNLSSADVQAAK	**1.126317573**	2	4.97671
P32551	GNNTTSLLSQSVAK	**1.327578571**	2	4.17499
P32551	IIENLHDVAYK	**1.577796499**	2	3.55806
P32551	ITSEELHYFVQNHFTSAR	**1.217414356**	3	3.87383
P32551	LPNGLVIASLENYAPLSR	**2.027149499**	2	4.68653
P32551	NALANPLYCPDYR	**0.675943276**	2	3.01895
P32551	RGNNTTSLLSQSVAK	**1.048880853**	2	3.27924
P32551	RWEVAALR	**1.151966609**	2	2.41034
P32551	SMTASGNLGHTPFLDEL	**1.158158294**	2	3.2131
P32551	SMTASGNLGHTPFLDEL+Oxidation(1)	**1.243355794**		
P32551	TSAPGGVPLQPQELEFTK	**1.027222254**	2	4.21616
P32551	YENYNYLGTSHLLR	**2.055367982**	2	4.27342
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.921392042**	**9.9E-20**	**17**
P32755	AFEEEQALR	**1.618334633**	2	3.55922

P32755	DIAFEVEDCEHIVQK	1.365182132	2	4.09356
P32755	ENMDVLEELK	1.991451013	2	2.8458
P32755	FAVLQTYGDTTHTLVEK	1.671892101	2	4.97741
P32755	FLPGFEAPTYK	1.404721676	1	2.4023
P32755	FWSVDDTQVHTEYSSLR	3.430592051	2	5.52295
P32755	GMEFLAVPSSYYR	1.905145868	2	3.59925
P32755	GNLTDLETNGVR	1.58174356	2	3.72886
P32755	HNHQGFGAGNFNSLFK	1.83249683	3	5.64791
P32755	ILVDYDEK	1.875790541	2	2.40256
P32755	IVFVLCSALNPWNK	1.642872034	2	3.65744
P32755	IVREPWVEEDKFGK	1.813631382	3	4.48858
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.857905843	3	7.77131
P32755	MGFEPLAYK	1.872824556	2	2.61926
P32755	SIVVANYEESIK	1.534677671	2	4.1594
P32755	SQIQEYVDYNGGAGVQHIALR	1.829604653	2	5.54957
P32755	TEDIITTIR	1.610932646	2	3.39161
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**0.964803966**	**1**	**2**
P33124	ALRPTIFPVVPR	1.025262677	2	2.97957
P33124	IENIYIR	0.963498534	2	2.95509
P33273	**CP255 Cytochrome P450 2C55**	**1.38493716**	**0.121878**	**4**
P33273	DENFLNLMEK	1.123085108	2	2.31255
P33273	ELRHFSLMTLR	1.275130515	2	2.36531
P33273	FDYKDENFLNLMEK	0.85343156	3	4.52222
P33273	IQEEASCLVEELR	1.450211475	2	2.71977
P33274	**CP4F1 Cytochrome P450 4F1**	**1.449199909**	**0.000249**	**2**
P33274	ACNLVHEFTDAVIR	1.417315994	3	3.73818
P33274	TLPDQGLDEFLK	1.929312353	2	2.51762
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.27458827**	**6E-14**	**25**
P34058	ADLINNLGTIAK	1.016945315	2	4.18483
P34058	EDQTEYLEER	1.31260608	2	3.43042
P34058	EGLELPEDEEEK	0.716657704	2	2.54182
P34058	EGLELPEDEEEKKK	1.155254689	2	3.37061
P34058	ELISNASDALDK	1.461506156	2	3.3845
P34058	EQVANSAFVER	1.340892319	2	2.36981
P34058	GFEVVYMTEPIDEYCVQQLK	0.943238582	2	4.44532
P34058	GVVDSEDLPLNISR	1.03388055	2	4.91275
P34058	HFSVEGQLEFR	1.127693567	2	2.57158
P34058	HLEINPDHPIVETLR	1.013573107	2	4.58277
P34058	HSQFIGYPITLYLEK	3.843154529	2	4.12928
P34058	IDIIPNPQER	0.975785212	2	3.11787
P34058	KHLEINPDHPIVETLR	1.073524648	2	4.82752
P34058	LGIHEDSTNR	1.116963379	2	3.40681
P34058	NPDDITQEEYGEFYK	1.350742605	2	4.75368
P34058	RAPFDLFENK	0.994580564	2	2.81153
P34058	SIYYITGESK	1.749392398	2	3.04022
P34058	SLTNDWEDHLAVK	0.991730071	2	4.01748
P34058	TLTLVDTGIGMTK	0.837169641	2	4.08281
P34058	TLTLVDTGIGMTK+Oxidation(10)	1.166992983		
P34058	VILHLKEDQTEYLEER	1.252196203	3	3.71925
P34058	YESLTDPSK	1.122902439	2	2.6427
P34058	YESLTDPSKLDSGK	1.174184772	2	3.59622
P34058	YHTSQSGDEMTSLSEYVSR	1.163135866	2	5.55226
P34058	YIDQEELNK	0.956804198	2	3.48741
P34064	**PSA5 Proteasome subunit alpha type_5**	**1.065971237**	**0.821661**	**3**
P34064	AIGSASEGAQSSLQEVYHK	1.062134066	2	4.71815
P34064	EELEEVIKDI	0.757358137	2	2.49457
P34064	GVNTFSPEGR	1.066002586	2	3.01303

P34067	**PSB4 Proteasome subunit beta type_4**	**1.276876407**	**0.846499**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	**1.188059712**	2	3.63449
P34067	TQNPMVTGTSVLGVK	**0.90393345**	2	2.83739
P34067	VNDSTMLGASGDYADFQYLK	**1.044465441**	2	4.30226
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.035040071**	**0.01316**	**2**
P35171	GGTSDALLYR	**1.198280751**	2	2.88841
P35171	LFQEDNGMPVHLK	**1.120117168**	2	3.61675
P35213	**1433B 14_3_3 protein beta/alpha**	**1.020371028**	**0.934824**	**6**
P35213	AVTEQGHELSNEER	**1.256429993**	2	4.54415
P35213	EKIEAELQDICSDVLELLDK	**1.03341666**	3	3.55902
P35213	QTTVSNSQQAYQEAFEISK	**0.946595416**	2	5.24455
P35213	TAFDEAIAELDTLNEESYK	**1.060024272**	2	4.83781
P35213	YLILNATHAESK	**0.811702151**	2	3.2077
P35213	YLSEVASGDNK	**1.064987258**	1	2.99939
P35278	**RAB5C Ras_related protein Rab_5C**	**0.979628458**	**0.709349**	**2**
P35278	GVDLQESNPASR	**1.026451672**	2	3.07112
P35278	NEPQNAAGAPGR	**0.869973529**	2	2.85771
P35427	**RL13A 60S ribosomal protein L13a**	**1.293340383**	**3.93E-14**	**2**
P35427	CEGINISGNFYR	**1.06520565**	2	3.31395
P35427	YQAVTATLEEK	**1.288246568**	2	3.43436
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**1.039243463**	**1**	**2**
P35434	AQSELSGAADEAAR	**1.066652712**	2	4.5914
P35434	IEANEALVK	**0.984508502**	2	3.16881
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.178993484**	**1.21E-06**	**7**
P35435	GLCGAIHSSVAK	**1.147240304**	2	3.79802
P35435	HLIIGVSSDR	**1.031655663**	2	2.78688
P35435	NASDMIDK	**1.042435481**	1	2.11387
P35435	NDMAALTAAGK	**0.951942145**	2	3.37647
P35435	NDMAALTAAGK+Oxidation(2)	**1.136144175**		
P35435	THSDQFLVSFK	**1.828381533**	2	3.33971
P35435	VYGTGSLALYEK	**1.732998591**	2	2.99285
P35565	**CALX Calnexin**	**0.930414324**	**0.945319**	**9**
P35565	AEEDEILNR	**0.871211895**	2	2.91499
P35565	KIPNPDFFEDLEPFR	**0.916910326**	3	3.99702
P35565	NKGDEEEEEEKLEEK	**1.049722829**	2	5.21963
P35565	SDTSTPPSPK	**0.94731679**	2	2.53032
P35565	TDAPQPDVK	**0.918222377**	2	2.34352
P35565	TDAPQPDVKDEEGKEEEK	**0.883045645**	2	3.8682
P35565	TSELNLDQFHDK	**1.142180647**	2	3.88371
P35565	VVDDWANDGWGLK	**0.92191258**	2	4.30863
P35565	VVDDWANDGWGLKK	**1.088212503**	2	2.76711
P35704	**PRDX2 Peroxiredoxin_2**	**1.019619747**	**0.498063**	**4**
P35704	EGGLGPLNIPLLADVTK	**1.142598797**	2	3.3527
P35704	KEGGLGPLNIPLLADVTK	**0.901948656**	2	4.25679
P35704	NDEGIAYR	**0.996492078**	2	2.39276
P35704	QITVNDLPVGR	**0.903881917**	2	2.69115
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.970590809**	**0.796843**	**5**
P35738	AAVEQVPVEPYK	**0.96208587**	2	2.66091
P35738	GLLLSCIEDKNPCIFFEPK	**0.759900702**	2	3.46629
P35738	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	**0.994521862**	3	4.10401
P35738	MNLFQSITSALDNSLAK	**0.86068145**	2	2.62986
P35738	SGDLFNCGSLTIR	**0.975406554**	2	2.89229
P35815	**PPM1B Protein phosphatase 1B**	**1.161124384**	**0.064956**	**2**

P35815	IQNAGGSVMIQR	0.828980951	2	3.0831
P35815	SGFALEPSVENVK	1.199249865	2	3.12618
P36201	**CRIP2 Cysteine_rich protein 2**	**1.343478852**	**0.000249**	**3**
P36201	ASSVTTFTGEPNMCPR	3.925137561	2	3.89905
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.319107978	3	6.95192
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.348325304	2	4.25922
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**0.915175626**	**0.013245**	**11**
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.588780044	3	3.49931
P36365	ASLYNSVVSNSSK	1.851639775	2	2.30806
P36365	CCLEEGLEPTCFER	0.763835977	2	4.11406
P36365	ENSVVFNNTPK	1.59766289	2	2.55412
P36365	FTEHVEEGR	0.916151723	2	3.13194
P36365	NLLPTPVVSWLISK	0.866911255	2	2.46644
P36365	SCDLGGLWR	0.762354573	2	2.76652
P36365	TQLREPVLNDELPGR	0.897557105	3	4.07189
P36365	VAIVGAGVSGLASIK	1.452099593	2	2.87397
P36365	VEDGQASLYK	0.885102344	2	3.53133
P36365	VLVVGMGNSGTDIAVEASHLAK	0.940190077	2	2.94576
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.258702293**	**1.67E-05**	**7**
P36511	ANIIAWALAQIPQK	1.244755997	3	5.08336
P36511	FVNVWTYELPR	1.090713559	2	3.19432
P36511	FVTFPTSFSSHDLENFFTR	1.928606798	2	4.16332
P36511	GHEVTVLRPSAFVFLDPK	1.77180349	3	3.52434
P36511	IILEELVQK	1.017944611	2	3.2832
P36511	SDLLNALEEVIDNPFYK	1.075703933	2	5.23121
P36511	TLGRPTTLAEIMGK	0.987329941	3	3.61478
P36536	**SAR1A GTP_binding protein SAR1a**	**1.761925751**	**0.020785**	**2**
P36536	LVFLGLDNAGK	1.762812601	2	2.99392
P36536	VELNALMTDETISNVPILILGNK	1.219833821	3	4.6256
P36972	**APT Adenine phosphoribosyltransferase**	**1.219785162**	**1.32E-05**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	0.91280822	2	3.89883
P36972	IDYIAGLDSR	0.929689843	2	3.45728
P36972	SFPDFPIPGVLFR	1.221331005	2	3.55041
P37397	**CNN3 Calponin_3**	**0.925354347**	**0.011634**	**3**
P37397	AGQSVIGLQMGTNK	0.853000458	2	4.28386
P37397	VNESSLNWPQLENIGNFIK	0.753598871	2	3.37815
P37397	YDQQAEEDLR	0.694367306	2	3.2591
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**0.959325912**	**0.873134**	**8**
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.035333426	2	4.53317
P38650	GWENHVEGQK	1.360061495	2	2.87876
P38650	ILDDDTIITTLENLK	0.878547357	2	2.6943
P38650	QLQNISQAAAAGGAK	0.896754641	2	3.30253
P38650	SSLQSQCLNEVLK	1.040859241	2	2.92071
P38650	VQGLTVEQAEAVAR	0.99173421	2	3.58449
P38650	VQVALEELQDLK	1.032743992	2	2.71188
P38650	VTDFGDKVEDPTFLNQLQSGVNR	0.884285506	3	4.06808
P38652	**PGM1 Phosphoglucomutase_1**	**1.152762056**	**0.98277**	**16**
P38652	ADNFEYSDPVDGSISK	0.881870637	2	4.70753
P38652	AIGGIILTASHNPGGPNGDFGIK	0.952138541	2	5.28334
P38652	FFGNLMDASK	0.886115485	2	2.30707
P38652	FNISNGGPAPEAITDK	1.158717901	2	4.28483
P38652	INQDPQVMLAPLISIALK	1.061364727	2	4.93386
P38652	KQRVEDILK	0.752315339	1	1.98255
P38652	LSGTGSAGATIR	1.377069767	2	3.63177
P38652	LSLCGEESFGTGSDHIR	1.572082061	2	3.5574
P38652	LVIGQNGILSTPAVSCIIR	1.178553782	2	3.73686

P38652	NIFDFNALK	**0.911216295**	1	1.94084
P38652	QEATLVVGGDGR	**1.04751969**	2	2.99183
P38652	QQFDLENK	**0.929042838**	1	2.15556
P38652	SGEHDFGAAFDGDGDR	**1.027913173**	2	4.44359
P38652	TIEEYAICPDLK	**0.984124704**	2	3.08145
P38652	TQAYPDQKPGTSGLR	**0.995437007**	2	3.3626
P38652	YDYEEVEAEGANK	**0.698111296**	2	5.05689
P38656	**LA Lupus La protein homolog**	**1.163120544**	**0.171502**	**2**
P38656	ITDDQQESLNK	**1.141128195**	2	3.93401
P38656	LDEGWVPLETMIK	**0.67959655**	2	2.45022
P38659	**PDIA4 Protein disulfide_isomerase A4**	**0.836639303**	**0.000555**	**20**
P38659	DLGLSESGEDVNAAILDESGKK	**0.979153349**	2	5.11249
P38659	DNDPPIAVAK	**0.747662726**	2	2.34339
P38659	EVSQPDWTPPPEVTLTLTK	**1.112803652**	2	3.7619
P38659	FDVSGYPTIK	**0.946752943**	2	3.35582
P38659	FDVSGYPTLK	**0.946752943**	2	3.35582
P38659	FIDEHATK	**1.094202487**	2	2.63242
P38659	FIDEHATKR	**1.309858366**	2	2.76503
P38659	GQAVDYDGSR	**1.085157589**	2	2.84501
P38659	IDATSASMLASK	**1.154834137**	2	3.5871
P38659	IDATSASMLASK+Oxidation(7)	**1.197292755**		
P38659	KGQAVDYDGSR	**2.118959951**	2	2.6336
P38659	MDATANDITNDR	**0.897208774**	2	3.98776
P38659	MHVMDVQGSTEASAIKDYVVK	**0.822630758**	3	3.72012
P38659	QLEPVYTSLGK	**1.050409964**	2	2.55686
P38659	RFDVSGYPTLK	**1.170934207**	2	3.15877
P38659	RSPPIPLAK	**1.187965894**	2	2.37394
P38659	TQEEIVAK	**1.019898462**	2	2.39643
P38659	VDATEQTDLAK	**1.142108651**	2	4.0467
P38659	VEGFPTIYFAPSGDK	**1.549629313**	2	3.44485
P38659	YGIVDYMVEQSGPPSK	**1.757308205**	2	4.65143
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.686281488**	**9.9E-20**	**7**
P38918	EEHFNGIALVEK	**0.963848039**	2	3.04461
P38918	FQLETSLK	**1.00221383**	1	1.94381
P38918	FYAFNPLAGGLLTGR	**1.809134963**	2	4.47538
P38918	MDVTSSSASVR	**0.744091409**	2	3.59047
P38918	QVETELFPCLR	**0.742711844**	2	2.49218
P38918	RMDVTSSSASVR	**0.686132944**	2	3.54995
P38918	TTYGPTAPSMISAAVR	**0.564167298**	2	3.74669
P38983	**RSSA 40S ribosomal protein SA**	**1.060699118**	**9.9E-20**	**9**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	**1.463856704**	3	5.82599
P38983	AIVAIENPADVSVISSR	**1.088169377**	2	5.64946
P38983	EHPWEVMPDLYFYRDPEEIEKEEQAAAEK	**0.709575839**	3	3.75618
P38983	FAAATGATPIAGR	**1.452332234**	2	3.04362
P38983	FLAAGTHLGGTNLDFQMEQYIYK	**1.971483289**	3	4.04448
P38983	FTPGTFTNQIQAAFR	**0.95068694**	2	4.44146
P38983	KSDGIYIINLK	**0.447891566**	2	3.2187
P38983	SDGIYIINLK	**1.105723061**	2	2.97548
P38983	YVDIAIPCNNK	**1.30666838**	1	3.02501
P39032	**RL36 60S ribosomal protein L36**	**1.127374324**	**0.736208**	**2**
P39032	EELSNVLAAMR	**0.866933254**	2	2.48169
P39032	KREELSNVLAAMR	**1.169237909**	2	3.8316
P39447	**ZO1 Tight junction protein ZO_1**	**0.64302424**	**0.020366**	**2**
P39447	GEEVTILAQK	**0.622014843**	2	2.47864
P39447	GGPAEGQLQENDR	**0.649026947**	2	2.91411
P40112	**PSB3 Proteasome subunit beta type_3**	**1.069493332**	**0.511469**	**2**

P40112	FGIQAQMVTTDFQK	**1.203625367**	2	3.4818
P40112	FGPYYTEPVIAGLDPK	**1.062495192**	2	3.49224
P40307	**PSB2 Proteasome subunit beta type_2**	**1.140669969**	**0.649241**	**3**
P40307	FILNLPTFSVR	**1.337191547**	2	3.01395
P40307	NGYELSPTAAANFTR	**1.091315246**	2	3.55481
P40307	VIDKDGIHNLENITFTK	**1.170833172**	3	4.73442
P40329	**SYRC Arginyl_tRNA synthetase_ cytoplasmic**	**1.188331879**	**0.045845**	**2**
P40329	LNDYVFSFDK	**1.289069393**	2	2.7045
P40329	SDGGYTYDTSDLAAIK	**1.043521306**	2	4.01259
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.273750148**	**0.00019**	**6**
P41034	AECPELSADLHPR	**1.511565902**	2	2.96916
P41034	AIFDLEGWQISHAFQITPSVAK	**0.507894166**	2	4.61729
P41034	AQEEGVPETPQPLTDAFLLR	**1.4639685**	2	3.83483
P41034	GIHLINEPVIFHAVFSMIKPFLTEK	**1.140375662**	4	4.70766
P41034	QLNEQPDHSPLVQPGLAELR	**1.024912901**	3	3.96054
P41034	VSLITSELIVQEVETQR	**1.150090094**	3	3.79764
P41123	**RL13 60S ribosomal protein L13**	**1.21655366**	**8.07E-07**	**3**
P41123	LATQLTGPVMPIR	**1.229761956**	2	2.95214
P41123	STESLQANVQR	**1.139279177**	2	3.97103
P41123	VDTWFNQPAR	**1.459202144**	2	3.45129
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**0.798630977**	**0.797136**	**3**
P41498	IDSAATSTYEVGNPPDYR	**1.180231251**	2	3.10332
P41498	IELLGSYDPQK	**0.899890609**	2	3.43786
P41498	LVTDENVSDNWR	**0.869953353**	2	3.7962
P41542	**USO1 General vesicular transport factor p115**	**1.126546064**	**0.000513**	**15**
P41542	AWFEVGDENPGWSAQK	**0.93235824**	2	4.63702
P41542	CQNEQLQTAVTQQASQIQQHK	**1.08964476**	3	4.11962
P41542	EQDLQLEELK	**1.227744329**	2	2.48783
P41542	IVAFENAFER	**1.456315427**	2	2.62285
P41542	LQTENSELQQR	**1.102707649**	2	3.12523
P41542	LREEIEELR	**1.07571057**	2	2.47305
P41542	NDGVLLLQALTR	**1.259461237**	2	3.43739
P41542	NNNSNQNFFK	**0.942375531**	2	2.49058
P41542	QLDSSNSTIAILQTEK	**1.010670628**	2	3.906
P41542	QLGPPVQQIILVSPMGVSK	**0.736836108**	2	2.38746
P41542	QSEDLGSQFTEIFIK	**1.2734304**	2	3.53941
P41542	SQLCSQSLEITR	**1.106617879**	2	3.10468
P41542	SVPVEGESELVTAAK	**1.112682**	2	3.69433
P41542	TLEQHDNIVTHYK	**1.174171772**	2	3.48302
P41542	VLVSPTNPPGATSSCQK	**1.119641899**	2	4.18065
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**1.003943384**	**2.22E-16**	**18**
P41562	ATDFVVPGPGK	**1.160225435**	2	3.60795
P41562	CATITPDEK	**1.231912374**	2	2.68297
P41562	DIFQEIYDK	**0.985373746**	1	2.47391
P41562	DLAACIK	**1.774170801**	1	2.00293
P41562	FKDIFQEIYDK	**0.993552607**	3	4.11865
P41562	GQETSTNPIASIFAWSR	**1.306922564**	2	4.96319
P41562	IHGGSVVEMQGDEMTR	**0.987164422**	2	4.61272
P41562	LIDDMVAQAMK	**0.819606716**	2	4.58853
P41562	LIDDMVAQAMK+Oxidation(4)	**1.524558431**		
P41562	LILPYVELDLHSYDLGIENR	**1.621144646**	2	4.69077
P41562	LVTGWVKPIIIGR	**1.306741149**	2	3.21401
P41562	SDYLNTFEFMDK	**0.906282752**	2	4.33676
P41562	SDYLNTFEFMDK+Oxidation(9)	**1.186615261**		
P41562	SEGGFIWACK	**0.932545194**	2	3.32235

P41562	SIEDFAHSSFQMALSK	**1.058949857**	2	4.93541
P41562	TVEAEAAHGTVTR	**1.052313067**	2	3.96676
P41562	VEITYTPK	**1.076138435**	2	2.76407
P41562	VTYLVHDFEEGGGVAMGMYNQDK	**1.4790168**	3	3.32808
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.085315121**	**0.000125**	**6**
P42123	DYSVTANSK	**1.407245961**	2	2.45365
P42123	IVADKDYSVTANSK	**0.295516123**	2	3.98358
P42123	LIAPVADDETAVPNNK	**0.568063041**	2	2.5292
P42123	LKDDEVAQLR	**0.272204697**	2	2.56556
P42123	SLADELALVDVLEDK	**0.485258725**	2	3.59493
P42123	VIGSGCNLDSAR	**1.11838995**	2	3.92679
P42676	**NEUL Neurolysin_ mitochondrial**	**1.124358455**	**0.600318**	**4**
P42676	AELGALPDDFIDSLEK	**0.898133992**	2	3.01384
P42676	NLILKPGGSLDGMDMLQNFLQR	**1.146175243**	3	3.473
P42676	NLNEDDTSLVFSK	**0.992350184**	2	3.12033
P42676	TRTEQLIAQTK	**1.269937723**	2	2.7549
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.097839649**	**0.001181**	**9**
P42932	AIAGTGANVIVTGGK	**1.029246456**	2	3.82366
P42932	AVDDGVNTFK	**1.138080425**	2	2.96277
P42932	EDGAISTIVLR	**0.867664943**	2	2.66033
P42932	ELEVQHPAAK	**1.309334521**	2	2.94164
P42932	GEENLMDAQVK	**0.92297774**	2	2.45655
P42932	HFSGLEEAVYR	**1.164679372**	2	2.72483
P42932	NVGLDIEAEVPAVK	**1.248125419**	2	3.07452
P42932	QITSYGETCPGLEQYAIK	**1.241861433**	2	4.59546
P42932	TAEELMNFSK	**1.133723936**	2	2.32949
P43244	**MATR3 Matrin_3**	**1.140425165**	**0.98897**	**3**
P43244	GDTDQASNILASFGLSAR	**1.116511838**	2	3.43647
P43244	ITPENLPQILLQLK	**0.963317088**	2	3.6792
P43244	TENPAEGKEQEEK	**1.303086426**	2	2.95332
P43274	**H14 Histone H1.4**	**0.962477687**	**1**	**3**
P43274	ALAAAGYDVEK	**0.940891113**	2	3.61133
P43274	SGVSLAALK	**1.159153296**	2	2.92242
P43274	SGVSLAALKK	**0.91425697**	2	2.59247
P43276	**H15 Histone H1.5**	**0.876776983**	**0.358746**	**2**
P43276	ALAAGGYDVEK	**0.760622465**	2	2.55148
P43276	ATGPPVSELITK	**0.984184457**	2	2.55165
P43278	**H10 Histone H1.0**	**0.882568927**	**3.12E-08**	**2**
P43278	VGENADSQIK	**0.911517049**	2	3.51938
P43278	YSDMIVAAIQAEK	**0.811157954**	2	3.98716
P45591	**COF2 Cofilin_2**	**1.51272871**	**0.360731**	**4**
P45591	HEWQVNGLDDIKDR	**1.068188302**	3	4.20537
P45591	KEDLVFIFWAPESAPLK	**2.672900195**	3	3.57069
P45591	QIIVEEAK	**0.935035551**	2	2.3551
P45591	QILVGDIGDTVEDPYTSFVK	**1.026638658**	2	4.77419
P45592	**COF1 Cofilin_1**	**1.010719893**	**0.934144**	**4**
P45592	EILVGDVGQTVDDPYTTFVK	**1.003931997**	2	4.59364
P45592	HELQANCYEEVK	**1.003755317**	2	3.47524
P45592	HELQANCYEEVKDR	**1.149730634**	3	5.29419
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	**1.190885322**	3	4.86674
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.40978632**	**0.003356**	**4**
P45878	GWDQGLLGMCEGEK	**0.708465548**	2	3.97969
P45878	KLVIPSELGYGER	**1.452041979**	2	2.55705
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	**1.49844606**	3	4.39953
P45878	LVIPSELGYGER	**1.270331352**	2	2.65906

P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.219105818**	**9.9E-20**	**18**
P45953	AMVENGGLVTSNPLR	1.050374986	2	3.43376
P45953	AMVENGGLVTSNPLRV	1.135580676	2	3.22963
P45953	AMVENGGLVTSNPLRV+Oxidation(1)	1.38569516		
P45953	ASNTSEVYFDGVK	1.901121938	2	3.7111
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.206620974	2	4.81055
P45953	ENMASLQSNPQQQELFR	1.230426593	2	4.29253
P45953	FFEEVNDPAK	0.973423086	2	3.12818
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.012924242	3	5.82654
P45953	GIVNEQFLLQR	1.550852876	2	3.42501
P45953	IFEGTNDILR	1.215362558	2	2.67016
P45953	NDSLEKVEEDTLQGLK	0.945445095	2	3.44499
P45953	NPLGNVGLLIGEASK	1.445203414	2	3.46002
P45953	SFGGVTHGLPEK	1.229819632	2	2.3118
P45953	SFGGVTHGLPEKK	0.998887654	2	3.00918
P45953	SGELAVQALEQFATVVEAK	1.278791916	3	4.77657
P45953	SLSEGYPTAQHEK	1.234175201	2	3.32553
P45953	TGIGSGLSLSGIVHPELSR	1.200810509	2	4.5212
P45953	VEEDTLQGLK	1.053390404	2	2.66233
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**0.953249722**	**0.19233**	**4**
P46418	AILNYIATK	2.901834247	2	3.30885
P46418	SDGSLMFEQVPMVEIDGMK	0.824859334	2	2.75118
P46418	SHGQDYLVGNK	0.858449567	2	3.13551
P46418	VSNLPTVK	0.929136485	2	2.89263
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.895666352**	**0.005804**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.651202093	3	3.97118
P46425	FEDGDLTLYQSNAILR	0.911996699	2	4.7111
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**1.093312501**	**9.9E-20**	**28**
P46462	AIANECQANFISIK	4.062615923	2	3.73597
P46462	EAVCIVLSDDTCSDEK	0.484935617	2	2.73813
P46462	ELQELVQYPVEHPDK	1.06685762	2	4.26945
P46462	ETVVEVPQVTWEDIGGLEDVK	0.899194015	2	3.01749
P46462	ETVVEVPQVTWEDIGGLEDVKR	0.917441602	2	4.06306
P46462	EVDIGIPDATGR	1.083050685	2	3.03997
P46462	GDDLSTAILK	0.904181256	2	3.05848
P46462	GGNIGDGGGAADR	1.366159474	2	3.97588
P46462	GILLYGPPGTGK	1.088891158	2	3.19377
P46462	GVLFYGPPGCGK	1.530226612	2	2.50731
P46462	IVSQLLTLMDGLK	1.573719714	2	3.05828
P46462	KYEMFAQTLQQSR	0.641030454	2	3.79958
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.134319155	3	6.18906
P46462	LAGESESNLRKAFEEAEK	0.902875305	2	2.6056
P46462	LDQLIYIPLPDEK	1.090043003	2	4.47123
P46462	LEILQIHTK	1.19793898	2	2.69385
P46462	LGDVISIQPCPDVK	1.072750888	2	4.26393
P46462	LIVDEAINEDNSVVSLSQPK	0.9592869	2	5.8338
P46462	MDELQLFR	0.854945034	2	3.0378
P46462	MDELQLFR+Oxidation(0)	1.279568646		
P46462	MTNGFSGADLTEICQR	0.577955996	2	4.22739
P46462	MTNGFSGADLTEICQR+Oxidation(0)	1.489171978		
P46462	NAPAIIFIDELDAIAPK	1.868504274	2	5.09878
P46462	QAAPCVLFFDELDSIAK	3.971127831	3	3.44443
P46462	QTNPSAMEVEEDDPVPEIR	0.812294763	2	4.6451
P46462	RSVSDNDIR	0.580568821	2	2.89145
P46462	VINQILTEMDGMSTK	0.941030365	2	4.55255

P46462	WALSQSNPSALR	1.050985966	2	3.16954
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**0.909525916**	**0.784498**	**4**
P46664	FIEDELQIPVK	1.095566776	2	3.05091
P46664	LDILDMFTEIK	1.101818681	2	3.40912
P46664	VGIGAFPTEQDNEIGELLQTR	0.968654135	2	4.39987
P46664	VVDLLAQDADIVCR	0.820948839	2	3.72121
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**0.921317789**	**0.041317**	**3**
P46720	ESEHTDVHGSPQVENDGELK	1.424179343	3	3.47787
P46720	GIGETPIVPLGISYIEDFAK	1.148531429	2	3.49457
P46720	SENSPLYIGILEMGK	0.886235153	2	3.7395
P46844	**BIEA Biliverdin reductase A**	**0.794194079**	**0.331156**	**3**
P46844	FGVVVVGVGR	1.072300724	2	2.75365
P46844	LLDQVSAEDLAAEK	0.724667148	2	4.37197
P46844	MTVQLETQNK	0.79229578	2	2.74063
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**0.94181372**	**0.973189**	**9**
P46953	AQGSVALSVTQDPACK	0.385567782	2	4.48617
P46953	ASFQPPVCNK	0.938555169	2	2.35606
P46953	DLGTQLAPIIQEFFHSEQYR	1.043126882	2	4.31282
P46953	FANTMGLVIER	1.036187831	2	2.6089
P46953	METELDGLR	0.894886355	2	2.61912
P46953	QDVDVWLWQLEGSSK	1.244287534	2	3.89049
P46953	QGEIFLLPAR	0.959845132	2	3.27073
P46953	TGKPNPDQLLK	0.889274233	3	3.82719
P46953	YYVGDTEDVLFEK	0.965013823	2	4.01938
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.296401562**	**0.075798**	**5**
P46978	FGQVYTEAK	1.3265264	2	2.69589
P46978	FYSLLDPSYAK	1.307789046	2	2.92425
P46978	NLDISRPDKK	1.503675051	2	2.79715
P46978	VGQAMASTEEK	1.324437212	2	3.40203
P46978	VGQAMASTEEK+Oxidation(4)	0.512516861		
P47198	**RL22 60S ribosomal protein L22**	**1.49993244**	**0.001688**	**2**
P47198	AGNLGGGVVTIER	1.059150965	2	3.52787
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.529300182	3	5.18702
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**0.917229956**	**0.618361**	**4**
P47875	GFGFGQGAGALVHSE	0.883886631	2	3.21126
P47875	GLESTTLADKDGEIYCK	1.085297399	2	5.18824
P47875	HEEAPGHRPTTNPNASK	0.92636226	3	3.81041
P47875	NLDSTTVAVHGEEIYCK	1.114828098	2	3.68772
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**0.878042852**	**0.87026**	**2**
P47942	GIQEEMEALVK	0.848854498	2	2.80073
P47942	GLYDGPVCEVSVTPK	0.878241661	2	3.63552
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.124052381**	**0.789713**	**3**
P48004	GRDIVVLGVEK	1.150160859	2	2.65801
P48004	NYTDDAIETDDLTIK	0.960418291	2	4.55011
P48004	YVAEIEKEKEENEK	1.12883683	2	5.05144
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**0.941842979**	**0.007366**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.378128602	3	5.46596
P48024	TLTTVQGIADDYDK	0.93929246	2	3.16854
P48037	**ANXA6 Annexin A6**	**0.883610336**	**0.996932**	**19**
P48037	AANDFNPDADAK	1.403245845	2	3.35011
P48037	AINEAYKEDYHK	1.06904435	2	3.17669
P48037	ALIEILATR	1.017458563	2	3.34523
P48037	CLIEILASR	1.126099717	2	2.51764
P48037	DAFVAIVQSVK	1.490744597	2	3.00467

P48037	DLESDIIGDTSGHFQK	0.645083682	2	3.86075
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.263331991	2	4.93555
P48037	GELSGDFEK	0.882611785	1	2.10107
P48037	GFGSDKESILELITSR	0.944782646	2	4.2194
P48037	GIGTDEATIIDIITQR	1.289691217	2	4.05848
P48037	KTNYDIEHVIK	0.931127558	2	2.47809
P48037	QRQEICQSYK	1.024183544	2	4.01634
P48037	SEIDLLNIR	1.225994123	2	3.28123
P48037	SEISGDLAR	1.024439227	2	2.36083
P48037	SELDMLDIR	0.74037328	2	2.68278
P48037	SLEDALSSDTSGHFK	1.076500814	2	3.93423
P48037	TNEQIHQLVAAYK	0.985280665	2	3.98261
P48037	TNYDIEHVIK	0.984838604	2	3.25088
P48037	TTGKPIEASIR	1.057219097	2	2.50123
P48450	**ERG7 Lanosterol synthase**	**1.184289341**	**0.470089**	**2**
P48450	ILGIGPDDPDLVR	0.897449783	2	2.38531
P48450	SVQLPDGGWGLHIEDK	2.318539945	2	2.73308
P48500	**TPIS Triosephosphate isomerase**	**1.137497926**	**9.9E-20**	**13**
P48500	CNVSEGVAQCTR	1.035096383	2	3.70889
P48500	DLGATWVVLGHSER	1.340864189	2	3.68629
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	0.958063479	4	6.55196
P48500	HIFGESDELIGQK	1.020548211	2	4.01695
P48500	IAVAAQNCYK	2.057419088	2	2.69742
P48500	IIYGGSVTGATCK	1.387734503	2	4.64246
P48500	LPADTEVVCAPPTAYIDFAR	1.465909541	2	5.04826
P48500	RHIFGESDELIGQK	1.163735033	2	3.91866
P48500	TATPQQAQEVHEK	1.479159881	2	3.74113
P48500	VNHALSEGLGVIACIGEK	0.981122305	2	5.27733
P48500	VTNGAFTGEISPGMIK	1.082066862	2	5.16047
P48500	VTNGAFTGEISPGMIK+Oxidation(13)	1.270863555		
P48500	VVLAYEPVWAIGTGK	1.010486019	3	4.66199
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.80355606**	**0.005328**	**5**
P48508	ASTLHLQTGNLLNWGR	0.835608148	3	4.29868
P48508	EFPDVLECTMSHAVEK	1.232030381	2	3.72593
P48508	INPDEREEMK	0.566525319	2	2.56828
P48508	LFIVGSNSSSSTR	0.926100342	2	3.01952
P48508	TLNEWSSQISPDLVR	0.81555604	2	4.79794
P48675	**DESM Desmin**	**0.548989567**	**0.014302**	**3**
P48675	ADVDAATLAR	0.801514595	2	2.39396
P48675	FLEQQNAALAAEVNR	0.589749728	2	4.29126
P48675	VSDLTQAANK	0.355639494	2	2.98866
P48679	**LMNA Prelamin_A/C**	**0.955529705**	**4.33E-15**	**16**
P48679	AAYEAELGDAR	1.278864376	2	2.95779
P48679	AQHEDQVEQYK	0.99340813	2	3.06522
P48679	AQHEDQVEQYKK	0.920256113	3	3.9373
P48679	IDSLSAQLSQLQK	0.934953394	2	3.13431
P48679	ITESEEVVSR	0.744777319	2	3.22988
P48679	LKDLEALLNSK	0.745626206	2	2.74162
P48679	LQEKEDLQELNDR	0.966712999	2	4.39889
P48679	LRDLEDSLAR	0.65324837	2	2.46889
P48679	MQQQLDEYQELLDIK	1.110680393	2	4.39612
P48679	MQQQLDEYQELLDIK+Oxidation(0)	1.044078537		
P48679	NSNLVGAAHEELQQSR	0.826193984	2	4.36597
P48679	SGAQASSTPLSPTR	0.807296772	2	3.26103
P48679	SVGGSGGGSFGDNLVTR	1.093142635	2	3.98449
P48679	TALINATGEEVAMR	0.819923013	2	3.23638

P48679	TVLCGTCGQPADK	**0.836459478**	2	3.30195
P48679	VAVEEVDEEGK	**1.232519751**	2	2.93067
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**1.925393702**	**9.9E-20**	**28**
P48721	AQFEGIVTDLIK	**1.048546778**	2	3.77651
P48721	ASNGDAWVEAHGK	**1.242637112**	2	3.74087
P48721	DAGQISGLNVLR	**1.055607319**	2	3.56964
P48721	EQQIVIQSSGGLSK	**1.367382846**	2	3.75901
P48721	EQQIVIQSSGGLSKDDIENMVK	**1.056657916**	2	4.43679
P48721	ERVEAVNMAEGIIHDTETK	**1.080766211**	3	5.76706
P48721	ETAENYLGHTAK	**1.435479527**	2	3.59407
P48721	GAVVGIDLGTTNSCVAVMEGK	**0.855150273**	2	5.6297
P48721	LLGQFTLIGIPPAPR	**1.819704551**	2	3.07916
P48721	MEEFKDQLPADECNK	**0.937554876**	2	4.77011
P48721	MEEFKDQLPADECNK+Oxidation(0)	**1.429195058**		
P48721	MKETAENYLGHTAK	**1.041599104**	2	4.15117
P48721	MKETAENYLGHTAK+Oxidation(0)	**1.318507968**		
P48721	NAVITVPAYFNDSQR	**1.283742007**	2	3.56906
P48721	QAASSLQQASLK	**6.865283564**	2	2.99302
P48721	QAVTNPNNTFYATK	**2.438808149**	2	3.78195
P48721	RYDDPEVQK	**1.202803167**	2	2.92188
P48721	RYDDPEVQKDTK	**1.240503407**	2	3.76615
P48721	SDIGEVILVGGMTR	**0.922617386**	2	4.31892
P48721	SQVFSTAADGQTQVEIK	**2.415297203**	2	5.02191
P48721	STNGDTFLGGEDFDQALLR	**1.14467192**	2	5.61647
P48721	TTPSVVAFTPDGER	**1.104914051**	2	3.70694
P48721	VEAVNMAEGIIHDTETK	**0.894597153**	2	4.32592
P48721	VINEPTAAALAYGLDK	**1.39852499**	2	4.13496
P48721	VLENAEGAR	**1.097651071**	2	3.07982
P48721	VQQTVQDLFGR	**1.078783399**	2	3.44652
P48721	YDDPEVQK	**1.065955519**	2	2.46592
P48721	YDDPEVQKDTK	**1.054996133**	2	2.77876
P48725	**PCNT Pericentrin**	**1.07263168**	**0.080687**	**2**
P48725	EEVSGGNGPCRGSPGRGSLER	**1.194363523**	2	2.33237
P48725	VYQSLSTAVEGLLEMALDSSKQLEEAR	**0.037594831**	3	3.33224
P49134	**ITB1 Integrin beta_1**	**0.836013387**	**3.1E-05**	**4**
P49134	CNCQSHGIPASPK	**0.769187758**	2	3.65588
P49134	GEFFNELVGQQR	**0.749001287**	2	2.80083
P49134	RITSDFRIGFGSFVEK	**1.183866983**	2	2.35938
P49134	SAVTTVVNPK	**0.991477142**	2	2.43799
P49242	**RS3A 40S ribosomal protein S3a**	**1.29711819**	**3.08E-08**	**9**
P49242	ACQSIYPLHDVFVR	**1.327342302**	2	3.96882
P49242	ADGYEPPVQESV	**1.283008789**	2	2.35357
P49242	LIPDSIGKDIEK	**1.196063171**	2	2.5086
P49242	LITEDVQGK	**1.024204621**	2	2.74494
P49242	LMELHGEGGSSGK	**0.941267015**	2	3.45818
P49242	LMELHGEGGSSGK+Oxidation(1)	**1.401930639**		
P49242	NCLTNFHGMDLTR	**1.317220813**	2	3.80027
P49242	TTDGYLLR	**1.21026181**	2	3.06943
P49242	VFEVSLADLQNDEVAFR	**1.186218263**	2	4.27409
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.870921154**	**0.78134**	**6**
P49432	EAINQGMDEELERDEK	**0.868628511**	2	2.55716
P49432	ILEDNSIPQVK	**1.130153492**	2	3.07739
P49432	IMEGPAFNFLDAPAVR	**1.004723984**	2	4.22293
P49432	IMEGPAFNFLDAPAVR+Oxidation(1)	**1.087246502**		
P49432	TIRPMDIEAIEASVMK	**0.83853127**	3	4.40488
P49432	VFLLGEEVAQYDGAYK	**1.038757765**	2	3.53979

P49620	**DGKG Diacylglycerol kinase gamma**	**0.380511433**	**0.115121**	**2**
P49620	QGERILQKFHYLLNPK	**0.202805104**	2	2.49651
P49620	WGGGYEGGSLTKILK	**0.956246735**	2	2.34486
P49717	**MCM4 DNA replication licensing factor MCM4**	**0.745029369**	**0.003847**	**2**
P49717	GQSDTAITKDMFEEALR	**0.70797129**	2	2.31263
P49717	YQQLFEDIR	**0.745048268**	1	1.97985
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.684218515**	**9.9E-20**	**13**
P49889	CKEDALFNR	**0.421995697**	2	2.59912
P49889	FEEHYQQQMK	**0.482706743**	2	2.81133
P49889	FEEHYQQQMK+Oxidation(8)	**0.726265352**		
P49889	FMEGQVPYGSWYDHVK	**1.150708081**	2	3.76787
P49889	IIQHTSFQEMK	**0.57627299**	2	2.67944
P49889	LIEFLERDPSAELVDR	**0.416516305**	3	5.06295
P49889	NEDLINGIK	**0.50656451**	2	2.90781
P49889	NNPCTNYSMLPETMIDLK	**0.468612914**	2	4.47865
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13)	**0.656147986**		
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8)	**0.656147986**		
P49889	SFSEFVEK	**0.551974494**	2	2.37466
P49889	SGSTWISEIVDMIYK	**0.391983328**	2	4.56267
P49889	YWEDVETFLARPDDLLIVTYPK	**1.408939393**	3	4.19757
P50137	**TKT Transketolase**	**0.866030541**	**3.33E-12**	**23**
P50137	AVELAANTK	**0.972694622**	1	1.9751
P50137	GHAAPILYAVWAEAGFLPEAELLNLR	**1.432886196**	3	3.48207
P50137	GITGIEDK	**1.025444704**	1	2.33076
P50137	IIALDGDTK	**1.513186192**	2	2.45631
P50137	ILATPPQEDAPSVDIANIR	**1.134785848**	3	5.38332
P50137	ISSDLDGHPVPK	**0.924994399**	2	3.2442
P50137	KISSDLDGHPVPK	**0.934473339**	2	3.90194
P50137	LAVSQVPR	**1.071805859**	2	2.30179
P50137	LAVSQVPRSGKPAELLK	**1.547887734**	2	2.60143
P50137	LDNLVAIFDINR	**0.932724159**	2	4.3408
P50137	LGQSDPAPLQHQVDVYQK	**1.269104045**	2	4.03118
P50137	MFGIDKDAIVQAVK	**0.681205152**	2	4.39607
P50137	MFGIDKDAIVQAVK+Oxidation(0)	**1.077297655**		
P50137	NMAEQIIQEIYSQVQSK	**1.118477712**	3	5.85073
P50137	NMAEQIIQEIYSQVQSK+Oxidation(1)	**1.36234777**		
P50137	NSTFSELFK	**0.930823167**	2	2.39611
P50137	SGKPAELLK	**0.620631876**	3	3.40025
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	**0.865364326**	3	4.06969
P50137	SVPMSTVFYPSDGVATEK	**0.798678304**	2	4.29074
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3)	**1.139168745**		
P50137	TSRPENAIIYSNNEDFQVGQAK	**1.311272289**	3	6.31945
P50137	VLDPFTIKPLDK	**1.064829297**	2	3.02983
P50137	VLDPFTIKPLDKK	**0.910123605**	2	2.73472
P50169	**RDH3 Retinol dehydrogenase 3**	**0.902390149**	**4.64E-10**	**10**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	**0.699270186**	3	5.04765
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1)	**0.926571903**		
P50169	FQDSYMK	**0.719949664**	1	2.08614
P50169	GLWGLVNNAGISVPVGPNEWMR	**0.970870588**	2	3.71594
P50169	KLWDQTTEEVK	**0.727048186**	2	3.0769
P50169	KLWDQTTEEVKEIYGEK	**0.794933948**	3	4.72156
P50169	LWDQTTEEVK	**0.845778161**	2	3.25573
P50169	LWDQTTEEVKEIYGEK	**0.833238283**	2	5.144
P50169	MSLVGGGYCISK	**0.892501305**	2	3.77376
P50169	MSLVGGGYCISK+Oxidation(0)	**0.988079792**		
P50237	**ST1C1 Sulfotransferase 1C1**	**1.016742644**	**1.37E-09**	**9**

P50237	AGTTWTQEIVDMIQNDGDVQK	0.782001924	2	5.23398
P50237	DISEEVLNK	1.063213565	2	2.63622
P50237	DLHLGEQDLQPETR	1.145338065	2	4.30947
P50237	HPFIEWTLPSPLNSGLDLANK	0.376888074	3	3.32217
P50237	IWNFQAKPDDLLIATYAK	1.589745645	3	3.75006
P50237	MKDLHLGEQDLQPETR	0.884720043	2	3.98099
P50237	MLPDPGTLGEYIEQFK	0.770915595	3	4.69976
P50237	MLPDPGTLGEYIEQFK+Oxidation(0)	1.156396709		
P50237	VLWGSWYDHVK	1.089443005	2	3.11976
P50298	**ARY2 Arylamine N_acetyltransferase 2**	**0.904994015**	**0.669495**	**2**
P50298	FSYKDNIDLVEFK	0.796960694	2	2.68394
P50298	SLTEEEIEDVLK	0.961093702	2	2.76717
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**0.876032216**	**0.001883**	**8**
P50398	FDLGQDVIDFTGHALALYR	1.426344225	3	4.23088
P50398	FQLLEGPPESMGR	0.842487114	2	3.54814
P50398	KQNDVFGEADQ	0.874184341	2	2.63594
P50398	MLLYTEVTRYLDFK	1.358082552	2	2.34705
P50398	NPYYGGESSSITPLEELYK	1.24025153	2	5.44806
P50398	QLICDPSYIPDR	0.869907895	2	3.34827
P50398	TDDYLDQPCLETINR	1.029513567	2	5.16766
P50398	TFEGVDPQTTSMR	0.938515854	2	2.59551
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**0.982825914**	**1.99E-07**	**7**
P50399	AYDATTHFETTCDDIK	1.296167239	2	4.77291
P50399	AYDATTHFETTCDDIKDIYK	1.084756204	3	5.50689
P50399	EIRPALELLEPIEQK	0.992325281	3	3.93112
P50399	FDLGQDVIDFTGHSLALYR	1.898011521	3	4.70326
P50399	FVSISDLFVPK	1.273325552	2	3.14176
P50399	NTNDANSCQIIIPQNQVNR	1.000958092	2	4.22148
P50399	TDDYLDQPCCETINR	1.131560194	2	4.76597
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.04760277**	**6.57E-08**	**7**
P50431	ALSDALTELGYK	0.990828721	2	3.9982
P50431	AVLEALGSCLNNK	1.169212097	2	4.47689
P50431	GLLEEDFQK	0.886167397	2	2.35848
P50431	ISATSIFFESMPYK	1.66297881	2	3.51066
P50431	IYQLQVLANCR	0.745112883	2	2.69081
P50431	VLEACSIACNK	1.1101358	2	3.92667
P50431	YSEGYPGQR	0.84327464	2	2.77202
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**0.972429415**	**0.930049**	**14**
P50475	ASEWVQQVSGLMDGK	0.921328415	2	4.16658
P50475	AVFDETYPDPVR	1.046514047	2	3.26864
P50475	DIINEEEVQFLK	0.644188601	2	3.18242
P50475	GLEATDDSPK	1.023211176	2	2.5907
P50475	ITCLCQVPQNAANR	0.971268263	2	4.58866
P50475	IVAVTGAEAQK	1.254071252	2	2.75251
P50475	NVGCLQEALQLATSFAQLR	1.016727888	2	2.91859
P50475	QIWQNLGLDEAK	0.973979721	2	3.14009
P50475	RIVAVTGAEAQK	1.189081879	2	2.94673
P50475	SVLGDADQK	0.866373852	1	2.19913
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	1.031532155	3	4.02376
P50475	TITVALADGGRPDNTGR	1.04725548	2	3.0999
P50475	VDDSSEDKTEFTVK	1.551119584	2	3.7515
P50475	VGAEDTDGIDMAYR	0.894553544	2	3.85157
P50503	**F10A1 Hsc70_interacting protein**	**1.327262475**	**9.9E-20**	**6**
P50503	AIDLFTDAIK	1.273482567	2	2.90031
P50503	AIEINPDSAQPYK	1.567135493	2	3.46144
P50503	GAAIDALNDGELQK	1.46081746	2	3.66652

P50503	KGAAIDALNDGELQK	1.462850824	2	4.91894
P50503	LDYDEDASAMLR	0.966138307	2	3.56423
P50503	QDPSVLHTEEMR	1.163215779	2	2.5345
P50516	**VATA V_type proton ATPase catalytic subunit A**	**1.068298255**	**0.973462**	**3**
P50516	ADYAQLLEDMQNAFR	0.872629324	2	3.74114
P50516	TALVANTSNMPVAAR	1.018856056	2	3.59489
P50516	VLDALFPCVQGGTTAIPGAFGCGK	0.977392213	2	2.84715
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**1.715667953**	**8.61E-06**	**12**
P50554	GNYLVDVDGNR	1.460612209	1	2.18324
P50554	GTFCSFDTPDEAIR	1.702378492	2	3.75687
P50554	GVVLGGCGDK	1.292408954	2	2.30473
P50554	HGCAFLVDEVQTGGGCTGK	1.435554514	2	5.86333
P50554	IDIPSFDWPIAPFPR	1.277115746	2	3.74202
P50554	KHGCAFLVDEVQTGGGCTGK	1.601497379	3	3.70531
P50554	LVQQPQNASTFINRPALGILPPENFVDK	2.053631635	3	3.72229
P50554	NLLLAEVINIIK	1.221162936	3	4.94282
P50554	REDLLNNVAHAGK	1.440296862	2	2.36059
P50554	TLLTGLLDLQAQYPQFVSR	1.360087172	3	4.10471
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	0.948458227	2	3.46245
P50554	YPLEEFVTDNQQEEAR	1.122240835	2	3.00605
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.157395493**	**0.036727**	**4**
P50580	HELLQPFNVLYEK	1.139482978	2	2.96456
P50580	LVKPGNQNTQVTEAWNK	1.467118085	3	3.38917
P50580	SLVEASSSGVSVLSLCEK	1.187454798	2	2.49089
P50580	TIIQNPTDQQK	1.148276519	2	3.13545
P50878	**RL4 60S ribosomal protein L4**	**1.334499764**	**9.9E-20**	**11**
P50878	FCIWTESAFR	1.035278527	2	2.52899
P50878	KLDELYGTWR	1.214454264	2	3.15736
P50878	KLEAAAAALAAK	1.216054549	3	4.27761
P50878	LDELYGTWR	0.946314523	2	2.62995
P50878	LEAAAAALAAK	1.359116816	2	3.0964
P50878	NIPGITLLNVSK	1.428833118	2	3.29321
P50878	NVTLPAVFK	1.32702152	1	2.00375
P50878	RGPCIIYNEDNGIIK	1.322080653	2	3.46853
P50878	SGQGAFGNMCR	1.073447204	2	2.37858
P50878	SNYNLPMHK	1.279185053	2	2.56285
P50878	YAICSALAASALPALVMSK	1.747958298	2	3.49972
P51583	**PUR6 Multifunctional protein ADE2**	**0.977859865**	**0.88342**	**3**
P51583	ACGNFGIPCELR	0.977456019	2	2.64011
P51583	AEYEGDGIPTVFVAVAGR	1.259264513	2	3.20417
P51583	SWLPQNCTLVDMK	1.077566619	2	2.62298
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**1.077873403**	**4.59E-14**	**8**
P51635	ALEALVAK	1.102650881	2	2.52787
P51635	ALGLSNFSSR	1.573253193	2	2.80661
P51635	GLEVTAYSPLGSSDR	1.042294267	2	4.45285
P51635	HHPEDVEPAVR	1.072949889	3	3.74055
P51635	HIDCASVYGNETEIGEALK	1.078018627	2	5.92903
P51635	HIDCASVYGNETEIGEALKESVGAGK	1.184240901	3	6.12267
P51635	HPDEPVLLEEPVVLALAEK	1.85510489	3	6.08408
P51635	QLDALNK	1.143871478	1	2.30074
P51647	**AL1A1 Retinal dehydrogenase 1**	**1.139650198**	**9.9E-20**	**17**
P51647	ANNTTYGLAAGVFTK	1.022892632	2	3.94088
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.986296394	3	3.89027
P51647	ELGEHGLYEYTELK	1.055735426	2	3.72107
P51647	FPVLNPATEEVICHVEEGDK	0.996983204	3	4.09538
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.73894982	4	5.14294

P51647	IFINNEWHDSVSGK	**1.296128563**	2	4.3527
P51647	IFVEESVYDEFVR	**0.949791281**	2	4.26487
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	**1.240580363**	4	5.75652
P51647	IHGQTIPSDGDIFTFTR	**1.338064978**	2	4.54644
P51647	KFPVLNPATEEVICHVEEGDK	**0.970585947**	3	3.75391
P51647	KFPVLNPATEEVICHVEEGDKADVDK	**0.644086349**	4	4.86691
P51647	KYVLGNPLTQGINQGPQIDKEQHDK	**0.997315345**	3	3.77458
P51647	LLLATIEAINGGK	**4.84896386**	2	4.11735
P51647	VFANAYLSDLGGSIK	**1.363206659**	2	4.55831
P51647	YCAGWADK	**0.945011853**	1	2.05645
P51647	YVLGNPLTQGINQGPQIDK	**0.931357939**	2	5.02683
P51647	YVLGNPLTQGINQGPQIDKEQHDK	**0.941222073**	2	3.50837
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.959935038**	**7.82E-07**	**7**
P51650	EVGEVLCTDPLVSK	**1.620016792**	2	3.80684
P51650	HQSGGNFFEPTLLSNVTR	**1.082719929**	2	3.5819
P51650	LGTVADCGVPEAR	**0.954994963**	2	3.43422
P51650	VGNGFEEGTTQGPLINEK	**0.989698938**	2	4.31214
P51650	VYGDIIYTSAK	**1.525986933**	2	2.664
P51650	WLPTPATFPVYDPASGAK	**0.944591953**	2	3.76462
P51650	YGIDEYLEVK	**0.804551799**	2	3.08503
P51869	**CP4F4 Cytochrome P450 4F4**	**1.330601732**	**7.01E-05**	**2**
P51869	TLDFIDVLLLTK	**1.395937287**	2	3.61471
P51869	WQDLASGGSAR	**1.214558431**	2	2.53931
P51886	**LUM Lumican**	**0.628655273**	**0.00064**	**3**
P51886	ITNIPDEYFNR	**0.550607331**	2	2.33337
P51886	NNQIDHIDEK	**0.626064147**	2	3.09442
P51886	SLQDLQLANNK	**0.997914247**	2	2.69651
P52020	**ERG1 Squalene monooxygenase**	**0.938626557**	**0.907443**	**2**
P52020	DIPDLYDDAAIFQAK	**1.064587289**	2	2.46621
P52020	GVLLLGDAYNLR	**0.87987063**	2	2.96723
P52296	**IMB1 Importin subunit beta_1**	**1.249087323**	**0.003521**	**5**
P52296	AAVENLPTFLVELSR	**0.570768038**	2	3.41269
P52296	GALQYLVPILTQTLTK	**0.92282253**	2	2.44686
P52296	SNEILTAIIQGMR	**0.99398967**	2	3.14647
P52296	TVSPDRLELEAAQK	**1.105475425**	2	2.87184
P52296	VLANPGNSQVAR	**1.251385259**	2	3.59582
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.122238669**	**0.365218**	**4**
P52303	NINLIVQK	**0.742160291**	1	2.21278
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	**0.862140512**	3	3.9173
P52303	SQPDMAIMAVNTFVK	**1.076723628**	2	2.60239
P52303	YNDPIYVK	**1.685804269**	2	2.52462
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.057611976**	**0.990743**	**3**
P52555	ILDQGEDFPASELAR	**1.055530708**	2	4.81951
P52555	QGQDGLSGVK	**0.922350504**	2	2.46566
P52555	SLNILTAFR	**1.005285071**	2	2.8114
P52631	**STAT3 Signal transducer and activator of transcription 3**	**1.713420251**	**1.99E-05**	**3**
P52631	GLSIEQLTTLAEK	**1.349688481**	2	3.08091
P52631	LLQTAATAAQQGGQANHPTAAVVTEK	**2.06980918**	3	3.381
P52631	TQIQSVEPYTK	**2.32815347**	2	2.63886
P52734	**FGD1 FYVE_ RhoGEF and PH domain_containing protein 1**	**1.219979486**	**0.483166**	**2**
P52734	SLELQARTEEEKK	**1.353556018**	2	2.50486
P52734	TEEEKKDWVQAINSTLLK	**1.121365474**	2	2.35379
P52759	**UK114 Ribonuclease UK114**	**1.077327673**	**0.002928**	**8**

P52759	AAGCDFTNVVK	**1.943570427**	2	3.00979
P52759	AAYQVAALPK	**1.346133737**	2	2.64186
P52759	APAAIGAYSQAVLVDR	**1.260249316**	2	3.70816
P52759	IEIEAIAVQGPFTTAGL	**1.155284001**	2	3.51306
P52759	NLGEILK	**1.103054009**	2	2.38066
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	**1.035466463**	2	4.30302
P52759	TTVLLADINDFGTVNEIYK	**1.224425526**	2	4.875
P52759	TYFQGNLPAR	**1.113913309**	2	3.08749
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**0.757124044**	**4.4E-05**	**2**
P52845	CKEDAIFNR	**0.421995697**	2	2.59912
P52845	SGSTWIGEIVDMIYK	**0.743419078**	2	3.55171
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.370216635**	**9.9E-20**	**8**
P52847	DNPLVNYTHLPTEIMDHSK	**1.918828193**	2	5.01376
P52847	FLAGNVAYGSWFDHVK	**1.623823617**	2	3.50361
P52847	IEEFQSRPCDIVIPTYPK	**1.238680192**	3	4.80537
P52847	IVHHTSFEVMK	**1.735361212**	2	2.91515
P52847	NYFTMTQSEK	**1.103324404**	1	2.71535
P52847	SGTTWLSEIVDMVLNDGNVEK	**1.365729679**		
P52847	THLPIDLLPK	**1.214310589**	3	3.71345
P52847	TLDEHTLER	**1.17511507**	2	3.00337
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.055871018**	**9.9E-20**	**37**
P52873	ADEAYLIGR	**0.97988554**	2	2.94675
P52873	ADFAQACQDAGVR	**0.957235741**	2	4.47601
P52873	AEAEAQAEELSFPR	**1.072541955**	2	4.44045
P52873	AGTHILCIK	**1.461200358**	1	2.03253
P52873	ALAVSDLNR	**1.021562069**	2	2.60405
P52873	AYSEALAAFGNGALFVEK	**1.02903254**	2	3.70542
P52873	AYVEANQMLGDLIK	**1.21534792**	2	4.512
P52873	DAHQSLLATR	**1.530718961**	1	3.11768
P52873	DFTATFGPLDSLNTR	**1.271331501**	2	4.28607
P52873	DMAGLLKPAACTMLVSSLR	**1.055763451**	2	3.07508
P52873	ELIPNIPFQMLLR	**1.83858389**	2	2.40415
P52873	ENGVDAVHPGYGFLSER	**1.395361977**	2	3.07216
P52873	FLYECPWR	**1.061123111**	2	2.60694
P52873	GANAVGYTNYPDNVVFK	**2.609389812**	2	4.33213
P52873	GLAPVQAYLHIPDIIK	**1.323257607**	2	2.95695
P52873	GTPLDTEVPLER	**0.831416722**	2	3.5907
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	**1.206182487**	2	5.94138
P52873	HGEEVTPEDVLSAAMYPDVFAQFK+Oxidation(14)	**1.080259829**		
P52873	HIEVQILGDQYGNILHLYER	**1.090204425**	3	4.75945
P52873	HYFIEVNSR	**1.027787722**	2	2.55322
P52873	IAEEFEVELER	**1.011309844**	2	3.28797
P52873	IEGRPGASLPPLNLK	**1.018617724**	2	3.61076
P52873	INGCAIQCR	**1.322346725**	2	2.844
P52873	IVGDLAQFMVQNGLSR	**1.306347881**	2	5.29795
P52873	LDNASAFQGAVISPHYDSLLVK	**0.966312773**	3	5.83205
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	**0.964595514**	4	5.44123
P52873	NHQGLLLMDTTFR	**1.511395319**	2	3.35566
P52873	QKADEAYLIGR	**1.152252717**	3	3.43804
P52873	QVFFELNGQLR	**1.314313426**	2	2.77138
P52873	QVGYENAGTVEFLVDK	**1.215844237**	2	4.10785
P52873	SVVEFLQGYIGIPHGGFPEPFR	**1.408671303**	2	4.30079
P52873	TVAVYSEQDTGQMHR	**1.288885079**	2	4.34306
P52873	VFDYSEYWEGAR	**0.931572603**	2	4.57129
P52873	VSPSPVDPIVPVVPIGPPPAGFR	**0.898412207**	2	4.46103
P52873	VVEIAPATHLDPQLR	**0.936863875**	2	4.11638

P52873	VVHSYEELEENYTR	1.060406422	2	5.15844
P52873	YSLEYYMGLAEELVR	2.110564159	3	4.68916
P52944	**PDLI1 PDZ and LIM domain protein 1**	**0.917696625**	**0.739287**	**7**
P52944	AAIANLCIGDLITAIDGEDTSSMTHLEAQNK	0.957114869	3	4.3674
P52944	CGTGIVGVFVK	0.857959219	2	2.43764
P52944	GCVDNMTLTVSR	0.954028465	2	2.36246
P52944	GHFFVGDQIYCEK	1.028500108	2	3.51767
P52944	QSTSFLVLQEILESDGK	1.034705014	2	2.4357
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	0.900686353	3	3.95351
P52944	VTPPEGYDVVTVFPK	0.814400777	2	2.79022
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.555990905**	**9.61E-07**	**3**
P53395	LSDIGEGIR	1.237588494	2	2.467
P53395	LSEVVGSGK	1.05012332	2	2.34327
P53395	SYLENPAFMLLDLK	1.553568711	2	4.64073
P53987	**MOT1 Monocarboxylate transporter 1**	**0.970257278**	**0.000164**	**5**
P53987	DGKEDETSTDVDEKPK	1.489253379	3	5.62678
P53987	DGKEDETSTDVDEKPKK	2.274681796	3	3.87049
P53987	EDETSTDVDEKPK	1.289179769	2	3.10029
P53987	ETQSPAPLQNSSGDPAEEESPV	0.946464708	2	4.40411
P53987	SDANTDLIGGSPK	1.099398086	2	4.05005
P54319	**PLAP Phospholipase A_2_activating protein**	**1.120919323**	**0.337191**	**4**
P54319	GQTLGLGNTSFSDPFTGGGR	0.860291417	2	3.34338
P54319	IGDVVGSSGANQQTSGK	1.123513272	2	4.51555
P54319	TGDLGDINAEQLPGR	1.025791205	2	3.66575
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.89372202	2	2.87102
P54822	**PUR8 Adenylosuccinate lyase**	**0.961095991**	**0.945656**	**2**
P54822	KVDIEVLSVLASLGASVHK	0.971385001	3	4.43676
P54822	VLSQQAAAVVK	0.826724137	2	2.3284
P54921	**SNAA Alpha_soluble NSF attachment protein**	**1.255506507**	**1.2E-14**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	0.957593289	3	4.88215
P54921	HDAATCFVDAGNAFK	1.08612384	2	2.34596
P54921	IEEACEIYAR	0.976897276	2	2.71191
P54921	NSQSFFSGLFGGSSK	1.260417975	2	3.4318
P54921	YEELFPAFSDSR	0.90144342	2	2.89361
P55006	**RDH7 Retinol dehydrogenase 7**	**0.940784918**	**0.000701**	**11**
P55006	LETVILDVTK	0.916202364	2	3.23885
P55006	TESIVAATQWVK	0.93526536	2	3.93957
P55006	TNVTNMER	0.809682621	2	2.77048
P55006	TNVTNMER+Oxidation(5)	0.75204507		
P55006	TSDRLETVILDVTK	0.915006173	3	4.19468
P55006	VAIIEPGGFK	1.265470506	2	2.64586
P55006	VLAACLTEK	1.085290543	2	3.32454
P55006	VVNIASTMGR	0.874915599	2	3.65485
P55006	VVNIASTMGR+Oxidation(7)	1.089370947		
P55006	YGVEAFSDSLR	1.097667783	2	3.8355
P55006	YVFITGCDSGFGNLLAR	1.183867796	2	3.67732
P55051	**FABP7 Fatty acid_binding protein_ brain**	**1.158195664**	**0.410452**	**4**
P55051	ALGVGFATR	1.262468505	2	2.71391
P55051	LTDSQNFDEYMK	1.148281979	2	4.40081
P55051	LTDSQNFDEYMK+Oxidation(10)	1.673272931		
P55051	QVGNVTKPTVIISQEGGK	0.910358894	3	3.83746
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.196538014**	**0.136928**	**5**
P55053	FDETTADGR	1.154392797	2	2.96171
P55053	KTETVCTFTDGALVQHQK	1.289649532	3	5.08028
P55053	LVESHGFEDYMK	1.228325153	2	2.62493

P55053	MVVECVMNNAICTR	**0.928182364**	2	3.24547
P55053	TETVCTFTDGALVQHQK	**1.541942066**	2	4.30548
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**1.377676015**	**9.9E-20**	**7**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	**1.872531807**	3	5.5183
P55159	IFFYDSENPPGSEVLR	**0.971389376**	2	5.90176
P55159	IQSILSEDPK	**1.257781098**	2	3.08888
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	**1.971327883**	3	4.11924
P55159	VLSFDTLVDNISVDPVTGDLWVGCHPNGMR	**1.010397196**	3	3.96655
P55159	VVADGFDFANGIGISLDGK	**0.947222463**	2	4.08594
P55159	YVYIAELLAHK	**1.546034008**	2	2.87987
P55260	**ANXA4 Annexin A4**	**0.899385094**	**0.333809**	**5**
P55260	AEIDMLDIPANFK	**0.914470555**	1	2.21379
P55260	GAGTDEGCLIEILASR	**1.054331522**	2	3.41034
P55260	GLGTDEDAIIGVLACR	**0.903903035**	2	4.12615
P55260	INQTYQQQYGR	**1.912586831**	2	2.75985
P55260	SETSGSFEDALLAIVK	**0.944111069**	2	2.42488
P55770	**NH2L1 NHP2_like protein 1**	**1.02604295**	**0.997577**	**2**
P55770	LLDLVQQSCNYK	**1.032985515**	2	2.66762
P55770	QQIQSIQQSIER	**1.025931862**	2	3.01228
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.070803361**	**0.01056**	**6**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	**0.900203442**	2	4.22236
P56399	IFQNAPTDPTQDFSTQVAK	**1.457936522**	2	3.96663
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	**1.135324616**	3	3.43186
P56399	IVILPDYLEIAR	**1.202972115**	2	2.62376
P56399	KQEVQAWDGEVR	**1.090971639**	2	3.12834
P56399	VTSAVEALLSADSASR	**1.361788658**	2	2.76844
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**0.94344934**	**0.003155**	**3**
P56522	AVPTGDVEDLPCGLLLSSVGYK	**1.446320032**	2	4.42053
P56522	TATEKPGVEEAAR	**1.027672234**	2	3.17799
P56522	TDITEVALGVLR	**0.926215776**	2	4.04872
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.158905482**	**0.060697**	**14**
P56574	CATITPDEAR	**1.377239951**	2	2.30465
P56574	DLAGCIHGLSNVK	**1.055192084**	2	2.85653
P56574	DQTNDQVTIDSALATQK	**1.163423688**	2	5.04928
P56574	FKDIFQEIFDK	**0.837123395**	2	3.23631
P56574	GKLDGNQDLIR	**1.118436064**	2	2.80986
P56574	LDGNQDLIR	**1.023494642**	2	2.38346
P56574	LIDDMVAQVLK	**0.84833966**	2	4.31404
P56574	LNEHFLNTTDFLDTIK	**1.363932629**	2	4.72423
P56574	NILGGTVFR	**1.051627019**	2	2.35122
P56574	SSGGFVWACK	**1.185521587**	2	2.53247
P56574	TIEAEAAHGTVTR	**1.044527799**	2	4.09884
P56574	VCVQTVESGAMTK	**1.057083127**	2	3.09659
P56574	VEKPVVEMDGDEMTR	**1.040919726**	3	3.64442
P56574	YFDLGLPNR	**1.602967854**	2	2.53513
P56593	**CP2AC Cytochrome P450 2A12**	**1.06804975**	**0.364695**	**3**
P56593	MLQGTCGAPIDPTIYLSK	**1.076769315**	2	3.95905
P56593	NRQPQYEDHMK	**1.108317389**	3	3.82688
P56593	YLPGPQQQIIK	**0.715254725**	2	2.44414
P56656	**CP239 Cytochrome P450 2C39**	**0.909941053**	**0.483113**	**5**
P56656	EHQESLDVTNPR	**0.869286138**	2	3.38159
P56656	IKEHQESLDVTNPR	**0.823873164**	3	4.75197
P56656	NYLIPK	**0.890117001**	1	2.1917
P56656	SDHFMPFSAGKRVCAGEGLAR	**1.273182557**	2	2.39019
P56656	VQEEIDHVIGR	**1.241333898**	2	3.18525

P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**1.245401057**	**0.011706**	**8**
P57093	AISCHYGSSDCK	**0.998148787**	2	3.3845
P57093	FYEENGFLVIK	**1.100287658**	2	2.58835
P57093	GDTVFFHPLLIHGSGR	**2.234020245**	3	3.53833
P57093	IQDFQQNEELFR	**1.353592743**	2	4.33704
P57093	KFYEENGFLVIK	**1.192086015**	2	3.38831
P57093	NLVSDDDIQR	**1.318321599**	1	2.8651
P57093	NNGCLVVLPGTHK	**0.914243934**	2	2.5148
P57093	YCALPQIVK	**1.426771627**	1	2.19979
P57113	**MAAI Maleylacetoacetate isomerase**	**1.121063909**	**1.88E-12**	**13**
P57113	AITSGFNALEK	**1.119172901**	2	3.29268
P57113	ALLALEAFQVSHPCR	**1.045548881**	2	4.28339
P57113	DGGQQFSEEFQTLNPMK	**1.088815291**	2	4.92533
P57113	FKVDLSPYPTISHINK	**0.912005249**	2	5.0818
P57113	GIDYEIVPINLIK	**1.094944956**	2	4.46973
P57113	IDGITIGQSLAILEYLEETRPIPR	**1.023784388**	3	3.9658
P57113	LLPQDPQK	**1.237270203**	1	2.099
P57113	LLPQDPQKR	**1.284572597**	2	2.54798
P57113	MISDLIASGIQPLQNLSVLK	**1.021455819**	2	4.77043
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0)	**1.283306121**		
P57113	QVGQENQMPWAQK	**1.144809211**	2	3.89037
P57113	VDLSPYPTISHINK	**1.074965697**	2	3.46977
P57113	YCVGDEVSMADVCLAPQVANAER	**0.879070834**	3	6.31231
P57722	**PCBP3 Poly(rC)_binding protein 3**	**1.151391488**	**0.000906**	**3**
P57722	ESTGAQVQVAGDMLPNSTER	**1.060028454**	2	4.87612
P57722	INISEGNCPER	**1.15102381**	2	3.45471
P57722	LVVPASQCGSLIGK	**1.416528311**	2	2.61784
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**0.982331452**	**0.99889**	**3**
P58321	SQGQDVTSSVYFMK	**1.026522733**	2	2.38123
P58321	VTHETSAHEGQTEAPSIDEK	**1.005870377**	3	4.70093
P58321	WLPLEANPEVTNQFLK	**0.9572978**	2	3.48753
P58751	**RELN Reelin**	**0.91001487**	**0.836367**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**0.288700157**	**4.4E-13**	**12**
P58775	AISEELDNALNDITSL	**0.279447912**	2	4.4013
P58775	ATDAEADVASLNR	**0.143889009**	2	4.23006
P58775	CGDLEEELK	**0.134115015**	2	2.39582
P58775	DAQEKLEQAEK	**0.410795398**	2	2.56958
P58775	KATDAEADVASLNR	**0.331099522**	2	4.18121
P58775	LDKENAIDR	**0.130832287**	2	2.78517
P58775	LKGTEDEVEK	**0.20085829**	3	3.58195
P58775	MELQEMQLK	**0.261431617**	2	2.65872
P58775	QLEEEQQALQK	**0.121283005**	2	3.97042
P58775	SLEAQADKYSTK	**0.065570772**	2	3.34728
P58775	TIDDLEDEVYAQK	**0.019097428**	2	4.06552
P58775	YSESVKDAQEK	**0.161170423**	2	2.99599
P59242	**CING Cingulin**	**0.918145881**	**0.080859**	**2**
P59242	LGQEQQALNR	**1.202883039**	2	2.74131
P59242	LQGLEQEAENK	**0.903486604**	2	2.54317
P59279	**RAB2B Ras_related protein Rab_2B**	**1.006362784**	**0.999873**	**2**
P59279	GAAGALLVYDITR	**1.006275472**	2	2.99659
P59279	LQIWDTAGQESFR	**1.002839051**	2	3.67701
P59759	**MKL2 MKL/myocardin_like protein 2**	**1.090500438**	**0.84948**	**2**
P59759	LVEVLK	**1.17131375**	2	2.45151
P59759	QIEELK	**0.947690672**	1	2.0717
P59895	**NEK6 Serine/threonine_protein kinase Nek6**	**1.160197151**	**0.500035**	**2**

P59895	QDCVKEIGLLK	**1.829472172**	2	2.34684
P59895	TVALKKVQIFEMMDAK+Oxidation(11)	**1.160194357**		
P59999	**ARPC4 Actin_related protein 2/3 complex subunit 4**	**1.096410131**	**0.790329**	**2**
P59999	AENFFILR	**1.126473978**	2	2.57127
P59999	ELLLQPVTISR	**1.08394101**	2	2.69131
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.147770971**	**9.9E-20**	**5**
P60335	AITIAGVPQSVTECVK	**1.108338998**	2	3.20152
P60335	CSDAAGYPHATHDLEGPPLDAYSIQGQHTISPLDLAK	**1.173388505**	4	5.41702
P60335	IITLTGPTNAIFK	**1.433267742**	2	2.66608
P60335	LVVPATQCGSLIGK	**1.51068185**	2	3.34499
P60335	VMTIPYQPMPASSPVICAGGQDR	**0.62580303**	2	3.63662
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.186452311**	**0.748468**	**5**
P60843	ATQALVLAPTR	**1.183336381**	1	2.35004
P60843	GFKDQIYDIFQK	**1.042332442**	2	3.52156
P60843	KEELTLEGIR	**1.178920788**	2	2.50622
P60843	KGVAINMVTEEDKR	**0.978466551**	3	4.08843
P60843	LQMEAPHIIVGTPGR	**1.221128383**	3	3.84368
P60868	**RS20 40S ribosomal protein S20**	**1.297798941**	**0.000555**	**3**
P60868	DTGKTPVEPEVAIHR	**0.929736062**	3	3.53391
P60868	LIDLHSPSEIVK	**1.36725004**	2	3.19986
P60868	VCADLIR	**1.201787042**	2	2.34043
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.228545621**	**0.095942**	**2**
P60901	AINQGGLTSVAVR	**1.176093349**	2	3.44145
P60901	LLDSSTVTHLFK	**1.423723863**	2	2.79561
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.129031119**	**0.020841**	**2**
P61087	GEIAGPPDTPYEGGR	**1.510413796**	2	3.66981
P61087	VDLVDENFTELR	**1.11703315**	2	3.48353
P61107	**RAB14 Ras_related protein Rab_14**	**0.859264307**	**0.701855**	**5**
P61107	IYQNIQDGSLDLNAAESGVQHKPSAPQGGR	**1.26313951**	3	3.6827
P61107	LTSEPQPQR	**1.184493084**	2	2.56299
P61107	NLTNPNTVIILIGNK	**1.101089152**	2	3.22773
P61107	SCLLHQFTEK	**0.854929123**	2	2.96781
P61107	STYNHLSSWLTDAR	**1.026455734**	2	3.28486
P61203	**CSN2 COP9 signalosome complex subunit 2**	**0.550418874**	**0.175769**	**2**
P61203	NYDESGSPR	**0.397589643**	2	2.46957
P61203	WTNQLNSLNQAVVSK	**0.626991804**	2	2.98088
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.113420014**	**0.423653**	**4**
P61222	GTVGSILDR	**1.135808074**	2	2.32865
P61222	NTVANSPQTLLAGMNK	**0.998609143**	2	3.6024
P61222	NVEDLSGGELQR	**0.972718053**	2	2.92107
P61222	VAETANEEEVKK	**2.264270006**	2	2.62075
P61314	**RL15 60S ribosomal protein L15**	**1.261150995**	**4.52E-06**	**6**
P61314	FFEVILIDPFHK	**0.995214005**	3	3.4665
P61314	GATYGKPVHHGVNQLK	**1.480171286**	2	4.36812
P61314	SLQSVAEER	**1.192066436**	2	2.6884
P61314	SLQSVAEERAGR	**1.075634409**	2	2.48202
P61314	VLNSYWVGEDSTYK	**1.346693744**	2	4.25721
P61314	YIQELWR	**1.233610008**	2	2.66508
P61354	**RL27 60S ribosomal protein L27**	**2.549156094**	**8.29E-10**	**2**
P61354	NIDDGTSDRPYSHALVAGIDR	**2.5039423**	3	4.11674
P61354	YSVDIPLDK	**2.304064745**	2	2.41617
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.338861819**	**1.09E-13**	**4**
P61459	AVGWNELEGR	**1.093332935**	2	3.12966
P61459	DQLLPNLR	**1.118898133**	2	2.35429

P61459	LDHHPEWFNVYNK	**1.33227989**	3	4.77495
P61459	LSAEERDQLLPNLR	**1.056256195**	3	4.01652
P61589	**RHOA Transforming protein RhoA**	**1.271765838**	**0.000748**	**3**
P61589	LVIVGDGACGK	**1.123069771**	2	2.70956
P61589	MKQEPVKPEEGR	**1.547809129**	3	3.45142
P61589	MKQEPVKPEEGR+Oxidation(0)	**1.381440514**		
P61751	**ARF4 ADP_ribosylation factor 4**	**1.179064635**	**3.23E-06**	**4**
P61751	IQEGAAVLQK	**1.189097353**	2	2.88553
P61751	LGEIVTTIPTIGFNVETVEYK	**1.213350186**	3	5.0297
P61751	NICFTVWDVGGQDK	**1.089771803**	2	4.12761
P61751	QDLPNAMAISEMTDK	**0.848559729**	2	3.77223
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.198699774**	**0.999486**	**2**
P61805	ADFQGISPER	**1.132674118**	2	2.94088
P61805	FLEEYLSSTPQR	**1.248791784**	2	3.69846
P61972	**NTF2 Nuclear transport factor 2**	**0.874029703**	**0.975146**	**2**
P61972	IQHSITAQDHQPTPDSCIISMVVGQLK	**0.895292511**	3	4.04478
P61972	NINDAWVCTNDMFR	**0.878378368**	2	3.60107
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**1.115797108**	**2.06E-05**	**8**
P61980	GSDFDCELR	**1.24093953**	2	2.60271
P61980	GSYGDLGGPIITTQVTIPK	**0.914194816**	2	5.05323
P61980	IDEPLEGSEDR	**1.202466625**	2	3.46014
P61980	IILDLISESPIK	**1.18712594**	2	3.97229
P61980	IITITGTQDQIQNAQYLLQNSVK	**1.102050598**	3	7.04534
P61980	LFQECCPHSTDR	**1.29520127**	2	3.67499
P61980	TDYNASVSVPDSSGPER	**1.25877924**	2	4.23171
P61980	VVLIGGKPDR	**0.965437161**	2	2.51736
P61983	**1433G 14_3_3 protein gamma**	**0.925887743**	**0.999993**	**4**
P61983	AYSEAHEISK	**0.991148198**	2	3.23924
P61983	NVTELNEPLSNEER	**1.075341827**	2	4.93711
P61983	TAFDDAIAELDTLNEDSYK	**0.960358807**	2	5.16806
P61983	YLAEVATGEK	**1.090567418**	2	2.92229
P62046	**LRCH1 Leucine_rich repeat and calponin homology domain_containing protein 1**	**0.909771435**	**0.165355**	**2**
P62046	DRELDIAMIEQLR	**0.910318888**	2	2.5862
P62046	NLESIDPQFTIRRK	**0.853197987**	2	2.31909
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**1.071473543**	**0.054095**	**5**
P62076	CIGKPGGSLDNSEQK	**0.974699443**	2	4.04339
P62076	KCIGKPGGSLDNSEQK	**1.407705347**	3	4.54052
P62076	LDPGAIMEQVK	**0.966998859**	2	3.22487
P62076	VQIAVANAQELLQR	**1.109643045**	2	4.95821
P62076	YMDAWNTVSR	**0.85303024**	2	2.75734
P62078	**TIM8B Mitochondrial import inner membrane translocase subunit Tim8 B**	**1.457619947**	**3.49E-11**	**2**
P62078	FIDTTLAITGR	**0.91418252**	2	2.79627
P62078	TENCLSSCVDR	**1.736624877**	2	2.91872
P62083	**RS7 40S ribosomal protein S7**	**1.197305701**	**0.683498**	**5**
P62083	AIIIFVPVPQLK	**1.004404946**	2	3.79227
P62083	DVNFEFPEFQL	**3.734053285**	2	2.4042
P62083	IVKPNGEKPDEFESGISQALLELEMNSDLK	**1.157132287**	3	4.94975
P62083	KAIIIFVPVPQLK	**1.166429105**	2	3.80727
P62083	TLTAVHDAILEDLVFPSEIVGK	**1.153716457**	2	5.09961
P62161	**CALM Calmodulin**	**1.212748502**	**0.085415**	**3**
P62161	EADIDGDGQVNYEEFVQMMTAK	**1.385954413**	2	4.77553

P62161	EAFSLFDKDGDGTITTK	1.453238814	2	4.17257
P62161	VFDKDGNGYISAAELR	1.165533523	2	4.88626
P62193	**PRS4 26S protease regulatory subunit 4**	**1.058280849**	**0.301036**	**4**
P62193	APQETYADIGGLDNQIQEIK	1.818892437	2	4.96943
P62193	MGQSQSGGHGPGGGK+Oxidation(0)	0.982417098		
P62193	NQEQMKPLEEK	1.489921744	2	3.23438
P62193	TMLELLNQLDGFDSR	0.991281282	2	4.04875
P62198	**PRS8 26S protease regulatory subunit 8**	**1.130995391**	**0.137876**	**6**
P62198	EELQLLQEQGSYVGEVVR	1.080408804	2	2.48743
P62198	IAELMPGASGAEVK	0.163485812	2	2.42972
P62198	IEELQLIVNDK	1.062612895	2	3.00513
P62198	LEGGSGGDSEVQR	1.181133493	2	3.75005
P62198	LLREELQLLQEQGSYVGEVVR	1.150462693	3	4.04938
P62198	TMLELLNQLDGFEATK	1.058309333	2	3.62689
P62243	**RS8 40S ribosomal protein S8**	**1.151352885**	**9.9E-20**	**8**
P62243	ADGYVLEGK	1.1182142	2	2.81732
P62243	IIDVVYNASNNELVR	2.132850714	2	4.37769
P62243	ISSLLEEQFQQGK	1.596693818	2	3.99119
P62243	KYELGRPAANTK	1.083246	2	3.31757
P62243	LDVGNFSWGSECCTR	1.05857029	2	3.79282
P62243	LTPEEEEILNK	1.164459906	2	3.36903
P62243	NCIVLIDSTPYR	1.124818789	2	3.88361
P62243	YELGRPAANTK	0.924176169	2	2.98953
P62246	**RS15A 40S ribosomal protein S15a**	**1.174965419**	**0.136512**	**3**
P62246	HGYIGEFEIIDDHR	1.154373575	2	4.9555
P62246	MNVLADALK	0.929030618	2	2.34396
P62246	WQNNLLPSR	1.252900199	2	3.00089
P62250	**RS16 40S ribosomal protein S16**	**1.474372091**	**4.22E-07**	**5**
P62250	ALVAYYQK	1.711579775	2	2.39097
P62250	EIKDILIQYDR	1.143566823	2	2.42965
P62250	GGGHVAQIYAIR	1.806057827	2	3.15143
P62250	LLEPVLLLGK	1.323562934	2	3.04864
P62250	TLLVADPR	1.117941774	2	2.71563
P62260	**1433E 14_3_3 protein epsilon**	**1.090464032**	**3.77E-15**	**8**
P62260	AAFDDAIAELDTLSEESYK	1.009218338	2	6.35645
P62260	AAFDDAIAELDTLSEESYKDSTLIMQLLR	1.77899134		
P62260	EENKGGEDKLK	0.97913698	2	2.74372
P62260	HLIPAANTGESK	0.975708327	1	3.15237
P62260	IISSIEQK	1.230390154	2	2.70544
P62260	LICCDILDVLDK	2.027126757	2	4.03147
P62260	YLAEFATGNDR	1.001522299	2	2.98379
P62260	YLAEFATGNDRK	1.029538395	2	2.83681
P62271	**RS18 40S ribosomal protein S18**	**1.024350605**	**5.55E-16**	**5**
P62271	AGELTEDEVER	1.008371175	2	3.73479
P62271	RAGELTEDEVER	0.283623736	2	3.48524
P62271	VITIMQNPR	0.620553961	2	2.87893
P62271	VLNTNIDGR	1.296176163	2	2.89392
P62271	YSQVLANGLDNK	1.243798119	2	4.14412
P62278	**RS13 40S ribosomal protein S13**	**1.241157226**	**0.002674**	**4**
P62278	GLAPDLPEDLYHLIK	1.474710879	2	2.97257
P62278	GLSQSALPYR	1.015001473	2	2.63888
P62278	KGLTPSQIGVILR	1.299244032	3	4.10223
P62278	LILIESR	2.058289263	2	2.3329
P62332	**ARF6 ADP_ribosylation factor 6**	**1.104921522**	**0.096601**	**2**
P62332	FNVWDVGGQDK	0.84109932	2	2.81863
P62332	LGQSVTTIPTVGFNVETVTYK	1.147571705	2	3.42255
P62334	**PRS10 26S protease regulatory subunit 10B**	**0.851274987**	**0.000194**	**5**

P62334	ALQSVGQIVGEVLK	0.936435859	2	3.088
P62334	AVASQLDCNFLK	0.776148233	2	2.72857
P62334	EVIELPLTNPELFQR	1.428929604	2	3.39863
P62334	FSEGTSADR	1.096377834	2	2.52282
P62334	HGEIDYEAIVK	0.447825478	2	3.36691
P62425	**RL7A 60S ribosomal protein L7a**	**1.227489481**	**2.22E-16**	**12**
P62425	AGVNTVTTLVENK	1.222578134	2	4.04363
P62425	AGVNTVTTLVENKK	0.977669362	2	2.8576
P62425	HWGGNVLGPK	0.964981193	1	1.97926
P62425	KVVNPLFEK	1.529968329	2	2.53722
P62425	LKVPPAINQFTQALDR	1.600695838	3	4.50252
P62425	NFGIGQDIQPK	1.172165949	2	3.47069
P62425	QTATQLLK	1.136903532	2	2.38295
P62425	TCTTVAFTQVNSEDK	2.424487624	2	4.13265
P62425	TCTTVAFTQVNSEDKGALAK	3.5211451	2	3.93124
P62425	TNYNDRYDEIR	1.27048651	2	2.44878
P62425	VAPAPAVVK	1.384538998	1	2.16272
P62425	VPPAINQFTQALDR	1.269275696	2	3.52204
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.214738381**	**9.9E-20**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.131754515	3	5.32608
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.060451198	4	5.79031
P62630	MDSTEPPYSQK	0.891969076	2	3.58163
P62630	MDSTEPPYSQK+Oxidation(0)	1.10251218		
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.207896413	5	6.54685
P62630	RYEEIVK	0.892795376	2	2.61278
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.286894281	3	5.10762
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14)	1.334972569		
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8)	1.345599079		
P62630	VETGVLKPGMVVTFAPVNVTTEVK	0.912543866	2	5.47105
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)	1.212866791		
P62630	YEEIVK	1.286502193	1	2.09193
P62630	YYVTIIDAPGHR	1.219644306	3	3.64177
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.085601997**	**9.9E-20**	**9**
P62632	EHALLAYTLGVK	1.766749681	3	4.06211
P62632	IGGIGTVPVGR	1.621767182	2	3.65144
P62632	MDSTEPAYSEK	0.339446656	2	2.3051
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.048122967	3	4.57158
P62632	QLIVGVNK	1.42276466	1	2.7711
P62632	QTVAVGVIK	1.224715605	1	2.245
P62632	STTTGHLIYK	1.095708362	2	3.25064
P62632	THINIVVIGHVDSGK	1.183095045	2	5.46357
P62632	VETGILRPGMVVTFAPVNITTEVK	0.229386536	3	3.59224
P62634	**CNBP Cellular nucleic acid_binding protein**	**1.065027126**	**0.949702**	**2**
P62634	CGETGHVAINCSK	1.058499082	2	4.42782
P62634	CYSCGEFGHIQK	1.05330331	2	3.08351
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.071856324**	**0.055567**	**6**
P62703	FDTGNLCMVTGGANLGR	0.960922024	2	4.97067
P62703	FDTGNLCMVTGGANLGR+Oxidation(7)	0.308953183		
P62703	GIPHLVTHDAR	1.130481408	2	2.60861
P62703	LSNIFVIGK	1.580849212	2	2.87405
P62703	TDITYPAGFMDVISIDK	1.010524425	2	4.58564
P62703	VNDTIQIDLETGK	1.201467023	2	3.75544
P62718	**RL18A 60S ribosomal protein L18a**	**1.434377602**	**0.00037**	**2**
P62718	DLTTAGAVTQCYR	1.447009669	2	3.037

P62718	SSGEIVYCGQVFEKSPLR	1.162832149	2	2.49597
P62752	RL23A 60S ribosomal protein L23a	1.138859348	4.5E-12	6
P62752	LAPDYDALDVANK	1.145943017	2	3.56926
P62752	LDHYAIIK	1.115693901	2	2.40512
P62752	LYDIDVAK	1.139076829	1	1.92189
P62752	NKLDHYAIIK	1.319037728	2	2.48282
P62752	VNTLIRPDGEK	1.431910308	2	3.08448
P62752	VNTLIRPDGEKK	1.526936418	2	2.83795
P62755	RS6 40S ribosomal protein S6	1.043444839	0.840172	6
P62755	DIPGLTDTTVPR	0.810330921	2	2.33639
P62755	EEAAEYAKLLAK	1.189543452	2	2.39887
P62755	LIEVDDER	1.008230845	2	2.78591
P62755	LNISFPATGCQK	1.125597127	2	3.12534
P62755	MATEVAADALGEEWK	1.043332748	2	4.35637
P62755	MATEVAADALGEEWK+Oxidation(0)	1.191732185		
P62775	MTPN Myotrophin	1.37452291	0.000611	2
P62775	GPDGLTALEATDNQAIK	2.064910144	2	3.70673
P62775	HHITPLLSAVYEGHVSCVK	1.225015884	3	3.61731
P62804	H4 Histone H4	1.047847029	9.9E-20	9
P62804	DAVTYTEHAK	1.832369846	2	3.0916
P62804	DNIQGITKPAIR	1.014053685	2	3.25427
P62804	ISGLIYEETR	2.009334047	2	3.77303
P62804	KTVTAMDVVYALK	0.937358167	2	3.02327
P62804	RISGLIYEETR	0.919568834	2	2.30749
P62804	TLYGFGG	1.06287128	1	1.95168
P62804	TVTAMDVVYALK	0.97719542	2	4.06529
P62804	TVTAMDVVYALK+Oxidation(4)	1.248908469		
P62804	VFLENVIR	0.98307482	2	3.01582
P62815	VATB2 V_type proton ATPase subunit B_ brain isoform	0.912919967	0.096223	3
P62815	AVVQVFEGTSGIDAK	0.935215916	2	3.63727
P62815	IYPEEMIQTGISAIDGMNSIAR	0.586124296	2	2.45004
P62815	QIYPPINVLPSLSR	0.929737934	2	2.35321
P62832	RL23 60S ribosomal protein L23	1.389025511	9.9E-20	2
P62832	GSAITGPVAK	0.354571425	2	2.38306
P62832	ISLGLPVGAVINCADNTGAK	1.329311577	2	4.89623
P62853	RS25 40S ribosomal protein S25	2.118621769	9.9E-20	2
P62853	GGDAPAAGEDA	1.705456598	1	2.01987
P62853	LNNLVLFDK	2.153419006	2	3.0522
P62856	RS26 40S ribosomal protein S26	1.0693746	0.202385	3
P62856	DISEASVFDAYVLPK	1.392111513	2	3.26986
P62856	FRPAGAAPRPPPKPM	0.660309437	2	2.35289
P62856	NIVEAAAVR	1.097592433	2	2.92795
P62859	RS28 40S ribosomal protein S28	1.693632523	3.95E-07	2
P62859	EGDVLTLLESER	1.553768083	2	3.23469
P62859	VEFMDDTSR	1.391765066	2	2.59748
P62870	ELOB Transcription elongation factor B polypeptide 2	0.932915941	0.932125	2
P62870	ADDTFEALR	0.930838525	2	2.58373
P62870	TLGECGFTSQTARPQAPATVGLAFR	0.945344509	3	3.42145
P62890	RL30 60S ribosomal protein L30	1.472096409	7.99E-07	2
P62890	TGVHHYSGNNIELGTACGK	1.246322893	2	5.65483
P62890	VCTLAIIDPGDSDIIR	1.476698674	2	4.21979
P62898	CYC Cytochrome c_ somatic	1.153346858	2.43E-08	6
P62898	ADLIAYLK	1.193456257	2	2.86955
P62898	GITWGEDTLMEYLENPK	1.127158427	2	4.96244
P62898	GITWGEDTLMEYLENPKK	1.009232338	2	4.55982

P62898	KTGQAAGFSYTDANK	1.398157285	2	4.75288
P62898	TGPNLHGLFGR	1.171627768	2	3.26691
P62898	TGQAAGFSYTDANK	1.318119678	2	4.27109
P62902	**RL31 60S ribosomal protein L31**	**2.675894142**	**1.1E-14**	**2**
P62902	NLQTVNVDEN	2.643409951	1	2.52772
P62902	SAINEVVTR	1.337750185	2	2.93858
P62907	**RL10A 60S ribosomal protein L10a**	**1.360612439**	**6.29E-09**	**6**
P62907	AVDIPHMDIEALK	1.145791681	2	2.8141
P62907	AVDIPHMDIEALKK	1.082413564	2	2.60391
P62907	FSVCVLGDQQHCDEAK	1.444916374	2	4.19417
P62907	KYDAFLASESLIK	1.195779011	2	4.00635
P62907	VLCLAVAVGHVK	1.240981859	3	3.89547
P62907	YDAFLASESLIK	1.291111327	2	3.45328
P62909	**RS3 40S ribosomal protein S3**	**1.210815427**	**9.9E-20**	**10**
P62909	AELNEFLTR	1.223264168	2	2.84017
P62909	DEILPTTPISEQK	1.281485422	2	3.70303
P62909	ELAEDGYSGVEVR	1.631864922	2	3.42992
P62909	ELTAVVQK	1.310416864	1	2.07797
P62909	FGFPEGSVELYAEK	2.873774095	2	4.05397
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.245101636	3	4.93818
P62909	GCEVVVSGK	1.111682805	2	2.77248
P62909	GGKPEPPAMPQPVPTA	1.475968724	2	3.54081
P62909	GLCAIAQAESLR	1.079143549	2	3.39046
P62909	TEIIILATR	1.224086616	2	3.17823
P62912	**RL32 60S ribosomal protein L32**	**1.203107874**	**0.053763**	**3**
P62912	ELEVLLMCNK	1.214795936	2	2.85124
P62912	GQILMPNIGYGSNK	1.322792165	2	2.93291
P62912	SYCAEIAHNVSSK	1.171413293	2	4.80363
P62914	**RL11 60S ribosomal protein L11**	**1.140032575**	**0.451809**	**2**
P62914	VLEQLTGQTPVFSK	1.132736786	2	4.41155
P62914	YDGIILPGK	1.144384845	2	2.81665
P62919	**RL8 60S ribosomal protein L8**	**1.230243749**	**2.96E-10**	**3**
P62919	ASGNYATVISHNPETK	1.337184739	2	4.67305
P62919	AVVGVVAGGGR	1.069530069	2	3.43096
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	0.727679519	3	4.54939
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**1.093260153**	**0.029461**	**7**
P62959	AQVAQPGGDTIFGK	1.06040815	2	4.61827
P62959	CAADLGLK	1.341678202	2	2.75184
P62959	CLAFHDISPQAPTHFLVIPK	1.154040963	3	4.2221
P62959	HISQISVADDDDESLLGHLMIVGK	0.738445645	3	6.73071
P62959	IIFEDDR	0.670689691	2	2.34928
P62959	KHISQISVADDDDESLLGHLMIVGK	0.695072588	3	5.55857
P62959	MVVNEGADGGQSVYHIHLHVLGGR	1.073176462	3	4.70634
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.402187792**	**7.35E-10**	**7**
P62961	AADPPAENSSAPEAEQGGAE	0.693529504	2	2.63839
P62961	EDGNEEDKENQGDETQGQQPPQR	1.043295979	3	5.12584
P62961	GAEAANVTGPGGVPVQGSK	1.317985137	2	5.01396
P62961	NEGSESAPEGQAQQR	1.417052367	2	5.30777
P62961	NYQQNYQNSESGEK	2.192645367	2	4.16755
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	1.502083134	3	5.04581
P62961	RPQYSNPPVQGEVMEGADNQGAGEQGRPVR	1.245372353	4	4.64834
P62963	**PROF1 Profilin_1**	**1.048260348**	**0.797993**	**6**
P62963	CYEMASHLR	0.836531362	2	2.74957
P62963	DSLLQDGEFTMDLR	1.029114544	2	3.31312
P62963	DSPSVWAAVPGK	1.524071663	2	2.93559

P62963	SSFFVNGLTLGGQK	**0.996025541**	2	4.57741
P62963	STGGAPTFNVTVTMTAK	**0.999675884**	2	3.02521
P62963	TFVSITPAEVGVLVGK	**0.79400484**	2	4.78787
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.257482862**	**9.9E-20**	**28**
P63018	ARFEELNADLFR	**1.164653268**	2	2.98009
P63018	CNEIISWLDK	**0.776200704**	2	3.05973
P63018	DAGTIAGLNVLR	**1.59715915**	2	3.74225
P63018	EIAEAYLGK	**1.638770812**	1	1.96586
P63018	FDDAVVQSDMK	**1.000950066**	2	3.93709
P63018	FEELNADLFR	**0.975071984**	2	3.17974
P63018	FELTGIPPAPR	**0.85209508**	2	3.18331
P63018	GTLDPVEK	**1.146826113**	1	2.01453
P63018	HWPFMVVNDAGRPK+Oxidation(4)	**1.88102939**		
P63018	IINEPTAAAIAYGLDK	**1.311323778**	2	5.12961
P63018	IINEPTAAAIAYGLDKK	**1.066771949**	2	4.71722
P63018	LLQDFFNGK	**1.342590303**	2	3.07625
P63018	MKEIAEAYLGK	**0.874054888**	2	2.88319
P63018	MKEIAEAYLGK+Oxidation(0)	**1.619463062**		
P63018	NQTAEKEEFEHQQK	**1.318350054**	2	4.88416
P63018	NQVAMNPTNTVFDAK	**1.02174591**	2	4.98851
P63018	NQVAMNPTNTVFDAK+Oxidation(4)	**1.360006659**		
P63018	NSLESYAFNMK	**1.701403023**	2	3.56992
P63018	QATKDAGTIAGLNVLR	**1.032100459**	2	2.45073
P63018	RFDDAVVQSDMK	**0.997019842**	2	3.5785
P63018	SFYPEEVSSMVLTK	**0.958197139**	2	4.94066
P63018	SFYPEEVSSMVLTK+Oxidation(9)	**1.018853346**		
P63018	SINPDEAVAYGAAVQAAILSGDK	**1.384102362**	2	6.05933
P63018	SQIHDIVLVGGSTR	**1.181190953**	2	4.92456
P63018	STAGDTHLGGEDFDNR	**1.238506769**	2	4.2487
P63018	TVTNAVVTVPAYFNDSQR	**1.104017146**	3	4.36012
P63018	VCNPIITK	**1.071879782**	2	2.30161
P63018	VQVEYKGETK	**1.220790502**	2	2.55106
P63029	**TCTP Translationally_controlled tumor protein**	**1.585789652**	**1.06E-05**	**3**
P63029	DLISHDELFSDIYK	**2.167843329**	2	3.75528
P63029	EIADGLCLEVEGK	**1.428289919**	2	3.33822
P63029	TEGAIDDSLIGGNASAEGPEGEGTESTVVTGVDIVMNHHLQETSFTK	**1.950471717**	4	4.58851
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.11272639**	**0.001129**	**6**
P63036	HYNGEAYEDDEHHPR	**1.544012083**	3	5.35375
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	**1.336746403**	3	4.49101
P63036	NVVHQLSVTLEDLYNGATR	**1.085946595**	2	4.1168
P63036	QISQAYEVLADSK	**1.152841416**	2	3.70042
P63036	TIVITSHPGQIVK	**0.988771611**	2	3.46151
P63036	VNFPENGFLSPDK	**1.111964333**	2	3.3584
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.249933038**	**9.9E-20**	**33**
P63039	AAVEEGIVLGGGCALLR	**1.058687502**	2	5.25357
P63039	ALMLQGVDLLADAVAVTMGPK	**1.177641303**	3	5.28313
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(2)	**1.111291083**		
P63039	CEFQDAYVLLSEK	**1.115010613**	2	4.89684
P63039	CIPALDSLKPANEDQK	**0.978924019**	2	3.65453
P63039	DIGNIISDAMK	**1.006441011**	2	3.22164
P63039	GVMLAVDAVIAELK	**1.049403481**	2	3.83955
P63039	GVMLAVDAVIAELKK	**0.904372922**	2	4.47941
P63039	GYISPYFINTSK	**1.601581847**	2	3.02925
P63039	IGIEIIK	**1.158501458**	2	2.58946
P63039	ILQSSSEVGYDAMLGDFVNMVEK	**1.559640578**	2	4.97947

P63039	IQEITEQLDITTSEYEK	**0.938291384**	2	5.93984
P63039	IQEITEQLDITTSEYEKEK	**0.903319157**	2	5.06144
P63039	ISSVQSIVPALEIANAHR	**1.338303989**	2	4.25552
P63039	KISSVQSIVPALEIANAHR	**1.342376376**	3	4.55071
P63039	KPLVIIAEDVDGEALSTLVLNR	**1.313207522**	2	6.13653
P63039	LSDGVAVLK	**1.233272618**	2	3.09813
P63039	LVQDVANNTNEEAGDGTTTATVLAR	**1.259101386**	2	6.63632
P63039	NAGVEGSLIVEK	**1.216665674**	2	3.58429
P63039	QSKPVTTPEEIAQVATISANGDK	**1.01399751**	2	3.58194
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	**0.987831861**	3	4.84298
P63039	RGVMLAVDAVIAELKK	**0.875338186**	3	5.7707
P63039	TALLDAAGVASLLTTAEAVVTEIPK	**1.196282743**		
P63039	TALLDAAGVASLLTTAEAVVTEIPKEEK	**1.114826423**	3	5.03157
P63039	TLNDELEIIEGMK	**0.887779685**	2	4.65902
P63039	TLNDELEIIEGMK+Oxidation(11)	**1.124704445**		
P63039	TVIIEQSWGSPK	**1.126460517**	2	4.37844
P63039	VGEVIVTK	**1.065387372**	2	2.9382
P63039	VGEVIVTKDDAMLLK	**0.599197946**	2	2.50118
P63039	VGGTSDVEVNEK	**1.127712518**	2	3.82065
P63039	VGGTSDVEVNEKK	**1.300095442**	2	3.51846
P63039	VGLQVVAVK	**1.244569462**	2	3.28263
P63039	VTDALNATR	**1.050371554**	2	3.57173
P63102	**1433Z 14_3_3 protein zeta/delta**	**1.299313964**	**0.767437**	**9**
P63102	DICNDVLSLLEK	**1.510646161**	3	3.68053
P63102	FLIPNASQPESK	**1.064293721**	2	3.36873
P63102	GIVDQSQQAYQEAFEISK	**0.849475041**	2	5.74854
P63102	GIVDQSQQAYQEAFEISKK	**1.019483911**	2	2.62193
P63102	KGIVDQSQQAYQEAFEISK	**0.980707131**	2	6.01304
P63102	SVTEQGAELSNEER	**1.206808292**	2	5.56115
P63102	TAFDEAIAELDTLSEESYK	**1.237943777**	2	5.6861
P63102	YDDMAACMK	**0.886132379**	2	2.45139
P63102	YLAEVAAGDDKK	**1.169660982**	2	3.611
P63159	**HMGB1 High mobility group protein B1**	**0.992183127**	**0.004304**	**4**
P63159	GEHPGLSIGDVAK	**0.917068162**	2	3.11734
P63159	IKGEHPGLSIGDVAK	**0.998554029**	2	3.95068
P63159	KHPDASVNFSEFSK	**1.246840438**	2	4.28965
P63159	LGEMWNNTAADDKQPYEK+Oxidation(3)	**1.217175887**		
P63174	**RL38 60S ribosomal protein L38**	**1.296118877**	**0.001476**	**4**
P63174	IEEIKDFLLTAR	**0.96233855**	3	3.36118
P63174	KIEEIKDFLLTAR	**1.197796783**	2	4.10885
P63174	YLYTLVITDK	**1.35338924**	2	2.8967
P63174	YLYTLVITDKEK	**1.810211723**	2	2.709
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.018247566**	**5.98E-05**	**12**
P63245	DETNYGIPQR	**1.777445897**	2	2.94019
P63245	DGQAMLWDLNEGK	**1.254977539**	2	2.96984
P63245	FSPNSSNPIIVSCGWDK	**1.041631836**	2	4.1126
P63245	GHNGWVTQIATTPQFPDMILSASR	**0.938821689**	3	4.16863
P63245	HLYTLDGGDIINALCFSPNR	**1.457728902**	2	5.90175
P63245	IIVDELKQEVISTSSK	**1.054704479**	2	4.34605
P63245	LWDLTTGTTTR	**1.032383892**	2	2.58954
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	**1.403665253**	3	5.53695
P63245	VWNLANCK	**1.122314264**	2	2.67961
P63245	VWQVTIGTR	**1.181895657**	2	2.73689
P63245	YTVQDESHSEWVSCVR	**1.303851936**	2	4.65479
P63245	YWLCAATGPSIK	**0.880075838**	2	2.84451
P63259	**ACTG Actin_ cytoplasmic 2**	**1.128400712**	**0.009066**	**8**

P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	**4.29578862**	3	4.76836
P63259	DLYANTVLSGGTTMYPGIADR	**1.178986254**	2	6.08634
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13)	**1.012272844**		
P63259	GYSFTTTAER	**1.043069537**	2	3.35351
P63259	KDLYANTVLSGGTTMYPGIADR	**0.96316569**	2	6.44987
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)	**1.239726552**		
P63259	QEYDESGPSIVHR	**0.901153847**	3	3.42279
P63259	VAPEEHPVLLTEAPLNPK	**1.103812677**	3	4.73921
P63324	**RS12 40S ribosomal protein S12**	**1.178504301**	**0.384839**	**4**
P63324	KVVGCSCVVVK	**1.097461838**	2	3.37961
P63324	LGEWVGLCK	**1.12650475**	2	2.84763
P63324	QAHLCVLASNCDEPMYVK	**1.249894147**	3	3.55273
P63324	VVGCSCVVVK	**1.119952592**	2	3.23808
P63331	**PP2AA Serine/threonine_protein phosphatase 2A catalytic subunit alpha isoform**	**1.084605135**	**0.328932**	**3**
P63331	CGNQAAIMELDDTLK	**0.935541969**	2	2.77128
P63331	NVVTIFSAPNYCYR	**0.782406243**	2	2.32614
P63331	YSFLQFDPAPR	**1.086338128**	2	3.41972
P67779	**PHB Prohibitin**	**1.003776048**	**0.024323**	**12**
P67779	AAELIANSLATAGDGLIELR	**0.968682284**	3	4.21719
P67779	AAIISAEGDSK	**1.231208236**	2	2.48129
P67779	DLQNVNITLR	**1.041532467**	2	3.00289
P67779	FDAGELITQR	**0.833648843**	2	3.54055
P67779	FGLALAVAGGVVNSALYNVDAGHR	**1.024537529**	3	3.53134
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	**1.173417972**	4	4.84002
P67779	IYTSIGEDYDER	**2.143905845**	2	3.36736
P67779	KLEAAEDIAYQLSR	**1.14384705**	2	4.81369
P67779	NITYLPAGQSVLLQLPQ	**1.063916305**	3	3.43017
P67779	NVPVITGSK	**0.907230375**	1	2.27761
P67779	QVSDDLTER	**0.96185425**	2	2.41646
P67779	VLPSITTEILK	**0.819406396**	2	2.31449
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.314929471**	**4.52E-08**	**3**
P68037	ADLAEEYSK	**0.839523806**	2	2.63813
P68037	GQVCLPVISAENWKPATK	**0.906718893**	2	3.76419
P68037	TDQVIQSLIALVNDPQPEHPLR	**1.27609653**	2	5.15322
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.293134321**	**0.031783**	**3**
P68101	AGLNCSTETMPIK	**1.288367277**	2	3.40636
P68101	TEGLSVLNQAMAVIK	**0.914766624**	2	3.98576
P68101	VVTDTDETELAR	**1.279264758**	2	3.30527
P68136	**ACTS Actin_ alpha skeletal muscle**	**1.09760797**	**9.9E-20**	**16**
P68136	AGFAGDDAPR	**1.428330045**	2	3.35637
P68136	AVFPSIVGRPR	**0.83930766**	2	2.6985
P68136	DLYANNVMSGGTTMYPGIADR	**0.291774294**	2	4.66356
P68136	DSYVGDEAQSK	**1.629058901**	2	3.54001
P68136	EITALAPSTMK	**0.880478758**	2	3.13786
P68136	EITALAPSTMK+Oxidation(9)	**1.042216602**		
P68136	GYSFVTTAER	**0.135106059**	2	3.95846
P68136	IWHHTFYNELR	**3.643422957**	2	2.69029
P68136	KDLYANNVMSGGTTMYPGIADR	**0.114270137**	2	5.03421
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14)	**0.44973999**		
P68136	QEYDEAGPSIVHR	**0.14447372**	2	3.16333
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	**0.094722873**	3	6.81189
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28)	**0.188902796**		
P68136	VAPEEHPTLLTEAPLNPK	**0.098658494**	2	4.39204
P68136	YPIEHGIITNWDDMEK	**1.757715799**	2	4.45061

P68136	YPIEHGIITNWDDMEK+Oxidation(13)	0.935747316		
P68255	**1433T 14_3_3 protein theta**	**1.058297798**	**0.998768**	**6**
P68255	AVTEQGAELSNEER	0.946121467	2	4.63295
P68255	SICTTVLELLDK	1.178792518	2	3.10072
P68255	TAFDEAIAELDTLNEDSYK	0.958385644	2	4.80388
P68255	VISSIEQK	1.095836557	2	3.25466
P68255	YLAEVACGDDR	0.784341786	2	3.00191
P68255	YLIANATNPESK	0.959961592	2	2.82255
P68511	**1433F 14_3_3 protein eta**	**0.835727697**	**0.432008**	**4**
P68511	AVTELNEPLSNEDR	1.361264153	2	4.6661
P68511	ELETVCNDVLALLDK	1.107974942	2	3.4719
P68511	NCNDFQYESKVFYLK	0.829655821	2	2.34758
P68511	NSVVEASEAAYK	1.26819552	2	3.21542
P69897	**TBB5 Tubulin beta_5 chain**	**1.582232063**	**2.5E-09**	**3**
P69897	ALTVPELTQQVFDAK	1.272072215	2	3.49605
P69897	ISVYYNEATGGK	1.745745189	2	2.94221
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.373849905	2	5.35448
P70372	**ELAV1 ELAV_like protein 1**	**0.872107413**	**0.783528**	**2**
P70372	TNLIVNYLPQNMTQEELR	0.847109615	2	3.42319
P70372	VLVDQTTGLSR	0.962735112	2	2.41271
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.31734052**	**0.010047**	**2**
P70470	ASFSQGPINSANR	2.221440086	2	2.94451
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.294997659	3	4.0414
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.950478982**	**6.87E-11**	**11**
P70473	ADVLLEPFR	0.815214404	2	3.36209
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	0.766061084	4	5.20169
P70473	DYGFSQEEIHQLHSDR	0.989640502	2	4.85957
P70473	GLGLESEELPSQMSIEDWPEMK	0.720853233	3	4.8462
P70473	GQNLLDGGAPFYTTYK	0.818114358	2	5.43953
P70473	GSFITDEEQHACPRPAPQLSR	0.933918729	3	3.85214
P70473	LGSVNHPSHLAR	1.324871751	2	3.39581
P70473	LSGFGQSGIFSK	1.430026994	2	3.04042
P70473	RDPSVGEHTVEVLK	0.784096076	3	4.39693
P70473	TADGEFMAVGAIEPQFYTLLLK	1.562766771	3	4.13434
P70473	TQAMGLWAQPR	0.702876837	2	3.13162
P70550	**RAB8B Ras_related protein Rab_8B**	**1.117869063**	**9.9E-20**	**2**
P70550	LLLIGDSGVGK	1.599899891	2	2.78506
P70550	NIEEHASSDVER	0.789943159	2	2.30794
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**0.87419546**	**0.015819**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.568556868	3	4.13686
P70552	VLGNNFYEYYVNDPPR	0.901875299	2	3.36803
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**1.138249827**	**0.551866**	**6**
P70580	FYGPEGPYGVFAGR	1.092994039	2	4.0109
P70580	GDQPGASGDNDDDEPPPLPR	1.098345042	2	4.97655
P70580	IVRGDQPGASGDNDDDEPPPLPR	1.135237782	3	5.03058
P70580	KFYGPEGPYGVFAGR	1.186951052	2	3.61088
P70580	RYDGVQDPR	0.757044201	1	2.1526
P70580	YDGVQDPR	0.903034107	2	2.83774
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.914480358**	**9.9E-20**	**8**
P70584	ASSTCQLTFENVK	1.100513468	2	3.28825
P70584	FAQEQIAPLVSTMDENSK	0.902875305	2	4.96345
P70584	IFDFQGLQHQVAHVATQLEAAR	0.96085005	3	6.14401
P70584	IGTIYEGTSNIQLNTIAK	0.890809417	2	4.55633
P70584	KFAQEQIAPLVSTMDENSK	0.66988264	2	5.80439

P70584	SGNYYVINGSK	**0.812220049**	2	2.8838
P70584	VDASVALLCDIQNTVINK	**0.275570165**	2	4.92136
P70584	YYASEVAGLTTSK	**1.059234064**	2	4.13797
P70587	**LRRC7 Leucine_rich repeat_containing protein 7**	**0.861182391**	**0.31781**	**2**
P70587	KESTDESEVDK	**1.612996463**	2	2.37192
P70587	SREQQPYEGNINK	**0.840936821**	2	2.48703
P70615	**LMNB1 Lamin_B1**	**0.842150096**	**0.256055**	**5**
P70615	ALYETELADAR	**1.137216415**	2	3.07535
P70615	KESDLSGAQIK	**0.995503832**	2	2.53116
P70615	LSSEMNTSTVNSAR	**0.836700916**	2	3.78377
P70615	NQNSWGTGEDVK	**0.721843545**	2	3.28587
P70615	SLEGDLEDLKDQIAQLEASLSAAK	**0.87044781**	3	4.62332
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**1.170120593**	**2.98E-11**	**2**
P70694	REDIFYTSK	**1.40102464**	2	3.13113
P70694	SIGVSNFNR	**0.823623608**	2	2.37678
P70712	**KYNU Kynureninase**	**1.158324437**	**9.66E-10**	**9**
P70712	IATELNCDPTDER	**0.802601921**	2	3.58759
P70712	IGAYGHEVGK	**1.508540728**	2	2.83943
P70712	LLTAILDSTERN	**1.519147835**	2	3.29048
P70712	LQLIPGVNGFR	**1.275429449**	2	2.52479
P70712	MEDILEVIEK	**1.061195565**	2	2.58851
P70712	TYLEEELDK	**1.425827559**	1	2.20158
P70712	TYLEEELDKWAK	**0.876154918**	2	2.55421
P70712	VAPVPLYNSFHDVYK	**1.160426786**	2	2.94642
P70712	YLNSGAGGLAGAFIHEK	**0.56221618**	2	4.30724
P80067	**CATC Dipeptidyl peptidase 1**	**1.15023159**	**1.36E-07**	**6**
P80067	GINFVSPVR	**1.312786639**	2	3.12063
P80067	GTDECAIESIAMAAIPIPK	**1.20628439**	3	4.52306
P80067	NQESCGSCYSFASLGMLEAR	**1.56206449**	2	3.40032
P80067	NSWGSQWGESGYFR	**1.135318718**	2	3.61255
P80067	RGTDECAIESIAMAAIPIPK	**0.956185975**	2	3.8847
P80067	YAQDFGVVEENCFPYTATDAPCKPK	**1.722645044**	3	5.99594
P80254	**DOPD D_dopachrome decarboxylase**	**1.252589562**	**3.33E-16**	**4**
P80254	FFPLEPWQIGK	**1.223549721**	2	2.44348
P80254	FLTEELSLDQDR	**1.182549822**	2	3.8687
P80254	LCAATATILDKPEDR	**3.202989809**	2	4.24926
P80254	STEPCAHLLISSIGVVGTAEQNR	**1.169957726**	2	5.09752
P80299	**HYES Epoxide hydrolase 2**	**1.130173812**	**0.979637**	**2**
P80299	ATEMGGILVGTPEDPK	**0.859561413**	2	3.67542
P80299	TEIQNPSVTSK	**1.083269801**	2	3.1394
P80313	**TCPH T_complex protein 1 subunit eta**	**1.201991322**	**0.046132**	**5**
P80313	ATISNDGATILK	**1.125250141**	2	2.59791
P80313	GGAEQFMEETER	**1.312113201**	2	2.97817
P80313	LLDVVHPAAK	**1.102660262**	2	2.5717
P80313	QLCDNAGFDATNILNK	**0.961935659**	2	3.29668
P80313	SQDAEVGDGTTSVTLLAAEFLK	**1.447644955**	2	4.82451
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.245140693**	**0.214187**	**8**
P80317	ALQFLEQVK	**1.176526927**	2	2.79905
P80317	DGNVLLHEMQIQHPTASLIAK	**0.984933394**	3	4.37037
P80317	GIDPFSLDALAK	**1.260399331**	2	2.4931
P80317	NAIDDGCVVPGAGAVEVALAEALIK	**1.041265532**	3	4.18388
P80317	QADLYISEGLHPR	**2.360480686**	2	2.38975
P80317	TEVNSGFFYK	**1.347059423**	2	2.58765
P80317	VATAQDDITGDGTTSNVLIIGELLK	**1.031141477**	2	5.43547
P80317	VLAQNSGFDLQETLVK	**1.03341314**	2	3.98201

P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**1.072065159**	**0.733024**	**6**
P81155	LTFDTTFSPNTGK	**1.07182143**	2	3.206
P81155	SNFAVGYR	**1.074421633**	2	2.44019
P81155	TGDFQLHTNVNNGTEFGGSIYQK	**1.049828849**	3	3.33285
P81155	VNNSSLIGVGYTQTLRPGVK	**0.997302777**	2	3.78933
P81155	WCEYGLTFTEK	**1.07213418**	2	2.60963
P81155	YQLDPTASISAK	**1.201041153**	2	3.235
P82995	**HS90A Heat shock protein HSP 90_alpha**	**1.155406675**	**1.78E-11**	**17**
P82995	DQVANSAFVER	**1.144077911**	2	2.54825
P82995	ELHINLIPNKQDR	**1.405644758**	2	3.23744
P82995	ELISNSSDALDK	**1.169092929**	2	2.8014
P82995	FYEQFSK	**1.201498339**	1	2.25806
P82995	HGLEVIYMIEPIDEYCVQQLK	**1.440649316**	3	3.47984
P82995	HIYFITGETK	**1.560488834**	2	2.73405
P82995	HLEINPDHSIIETLR	**0.945140607**	2	4.45344
P82995	HSQFIGYPITLFVEK	**7.759776629**	2	3.75113
P82995	LGIHEDSQNR	**1.031194836**	3	3.45684
P82995	NPDDITNEEYGEFYK	**1.367365626**	2	5.14103
P82995	RAPFDLFENR	**1.173410769**	2	2.41455
P82995	SLTNDWEEHLAVK	**1.011211513**	2	4.00984
P82995	TDTGEPMGR	**1.15025613**	2	2.53674
P82995	TDTGEPMGR+Oxidation(6)	**1.435047579**		
P82995	TLTIVDTGIGMTK	**0.837169641**	2	4.08281
P82995	TLTIVDTGIGMTK+Oxidation(10)	**1.166992983**		
P82995	YYTSASGDEMVSLK	**1.099699219**	2	3.85525
P83732	**RL24 60S ribosomal protein L24**	**1.060808585**	**0.076301**	**3**
P83732	AITGASLADIMAK	**1.044714762**	2	4.10032
P83732	CESAFLSK	**1.468590387**	2	2.30121
P83732	VELCSFSGYK	**2.369091579**	2	2.37302
P83868	**TEBP Prostaglandin E synthase 3**	**1.902330777**	**1.03E-07**	**2**
P83868	HLNEIDLFHCIDPNDSK	**3.672095919**	3	3.45626
P83868	LTFSCLGGSDNFK	**1.750328865**	2	2.96355
P83941	**ELOC Transcription elongation factor B polypeptide 1**	**1.020144594**	**0.900795**	**2**
P83941	AMLSGPGQFAENETNEVNFR	**0.965426207**	2	4.48467
P83941	TYGGCEGPDAMYVK	**1.075849212**	2	2.82004
P84082	**ARF2 ADP_ribosylation factor 2**	**0.983513315**	**1**	**2**
P84082	NISFTVWDVGGQDK	**0.219304258**	2	4.57342
P84082	QDLPNAMNAAEITDK	**1.018617787**	2	4.2381
P84083	**ARF5 ADP_ribosylation factor 5**	**1.035740846**	**2.33E-07**	**3**
P84083	DAVLLVFANK	**1.931995808**	2	3.55158
P84083	QDMPNAMPVSELTDK	**0.580303156**	2	3.03801
P84083	VQESADELQK	**1.092442095**	2	3.12093
P84089	**ERH Enhancer of rudimentary homolog**	**1.380442787**	**0.168141**	**2**
P84089	ADTQTYQPYNK	**1.465627833**	2	2.84553
P84089	TYADYESVNECMEGVCK	**1.236721165**	2	4.37677
P84100	**RL19 60S ribosomal protein L19**	**1.061182987**	**0.01606**	**2**
P84100	LLADQAEAR	**1.292205077**	2	3.25748
P84100	VWLDPNETNEIANANSR	**1.056301015**	2	5.3598
P84104	**SRSF3 Serine/arginine_rich splicing factor 3**	**1.096692169**	**0.380847**	**2**
P84104	AFGYYGPLR	**1.192364478**	2	2.32691
P84104	VYVGNLGNNGNK	**1.083440848**	2	2.31284
P84245	**H33 Histone H3.3**	**1.116253463**	**0.914941**	**5**
P84245	DIQLAR	**1.164935663**	1	1.95434
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	**1.174905679**	4	6.47561
P84245	RVTIMPKDIQLAR+Oxidation(4)	**1.14286161**		

P84245	STELLIR	**1.035924274**	2	2.39658
P84245	YRPGTVALR	**1.122311667**	2	2.39029
P84817	**FIS1 Mitochondrial fission 1 protein**	**0.988766101**	**0.082856**	**4**
P84817	FQSEQAAGSVSK	**0.764312039**	2	2.66145
P84817	GIVLLEELLPK	**0.98135013**	2	2.47952
P84817	GLLQTEPQNNQAK	**1.120828423**	2	3.40476
P84817	KFQSEQAAGSVSK	**0.927020804**	2	4.3534
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**1.132978776**	**9.9E-20**	**16**
P85834	AEAGDNLGALVR	**1.083023782**	2	3.8891
P85834	DKPHVNVGTIGHVDHGK	**0.75451429**	3	3.86227
P85834	DLEKPFLLPVESVYSIPGR	**1.507764041**	2	4.01343
P85834	ELLTEFGYKGEETPVIVGSALCALEQR	**1.119177254**	3	3.83071
P85834	GDECELLGHNK	**1.160476569**	2	2.59853
P85834	GEETPVIVGSALCALEQR	**1.142440133**	2	4.51417
P85834	GITINAAHVEYSTAAR	**3.202989809**	2	3.56819
P85834	GTVVTGTLER	**1.201732896**	2	2.81878
P85834	HYAHTDCPGHADYVK	**1.56861631**	2	4.25285
P85834	KGDECELLGHNK	**1.050813578**	2	3.70726
P85834	KYEEIDNAPEER	**1.558936282**	2	3.77094
P85834	LLDAVDTYIPVPTR	**0.99315655**	2	3.81066
P85834	QIGVEHVVVYVNK	**1.00854967**	2	2.6654
P85834	TIGTGLVTDVPAMTEEDK	**0.920473171**	2	3.25494
P85834	TIGTGLVTDVPAMTEEDKNIK	**0.603993667**	2	3.50311
P85834	YEEIDNAPEER	**1.282736934**	2	3.4091
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.016322891**	**9.9E-20**	**10**
P85968	AGQAVDDFIEK	**1.342163695**	2	3.3142
P85968	CLSSLKEER	**1.066405024**	2	2.62591
P85968	FQDTDGKELLPK	**1.117486047**	2	2.95465
P85968	GILFVGSGVSGGEEGAR	**1.812420276**	2	5.3843
P85968	HEMLPANLIQAQR	**0.816657912**	2	2.70442
P85968	LVPLLDTGDIIIDGGNSEYR	**1.366862175**	2	5.1302
P85968	NPELQNLLLDDFFK	**1.669282667**	2	4.4595
P85968	SAVDDCQDSWR	**1.271915586**	2	3.1098
P85968	VGTGEPCCDWVGDEGAGHFVK	**0.980612695**	2	4.45501
P85968	YGPSLMPGGNK	**1.070568208**	2	2.31253
P85971	**6PGL 6_phosphogluconolactonase**	**1.160108346**	**0.148283**	**5**
P85971	DLPAATAPAGPASFAR	**1.098433547**	2	3.1966
P85971	ILEDQESALPAAMVQPR	**1.036938341**	2	4.7511
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	**1.245410258**	2	4.65599
P85971	TGALCWFLDEAAAR	**1.059941981**	2	4.001
P85971	WTLGFCDER	**1.137057455**	2	2.58248
P85972	**VINC Vinculin**	**1.034436844**	**0.001246**	**8**
P85972	AQQVSQGLDVLTAK	**1.035010081**	2	3.98417
P85972	AVAGNISDPGLQK	**1.040523969**	2	3.10608
P85972	KIDAAQNWLADPNGGPEGEEQIR	**0.784789179**	3	5.2297
P85972	QVATALQNLQTK	**0.928071023**	2	2.98965
P85972	SLLDASEEAIKK	**1.049439136**	2	2.3793
P85972	STVEGIQASVK	**0.934985453**	2	2.44492
P85972	VDQLAAQLADLAAR	**0.820355778**	2	3.09316
P85972	VLQLTSWDEDAWASK	**1.28005522**	2	2.47923
P85973	**PNPH Purine nucleoside phosphorylase**	**0.930376317**	**8.55E-11**	**11**
P85973	ASHQEVLEAGK	**0.953093964**	2	3.44314
P85973	DHINLPGFCGQNPLR	**1.000005443**	3	4.06193
P85973	ELQEGTYIMSAGPTFETVAESCLLR	**1.019558278**	2	5.30096
P85973	FEVGDIMLIR	**0.787546692**	2	3.27791
P85973	HRPQVAVICGSGLGGLTAK	**0.894082384**	3	6.02102

P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	**1.517442541**		3	4.41651
P85973	MLGADAVGMSTVPEVIVAR	**0.691172941**		2	4.6609
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0)	**0.996653283**			
P85973	VFGFSLITNK	**1.174380133**		2	3.36158
P85973	VFHLLGVDTLVVTNAAGGLNPK	**1.141190245**		2	5.22585
P85973	VVMDYNNLEK	**0.904669611**		2	2.6372
P86048	**RL10L 60S ribosomal protein L10_like**	**1.222927782**	**0.292994**		**5**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	**0.951369275**		3	4.14464
P86048	GAFGKPQGTVAR	**1.239872817**		2	2.54019
P86048	MLSCAGADR	**0.924733425**		2	2.32202
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	**1.309060511**		3	4.9834
P86048	VHIGQVIMSIR	**0.966918334**		2	2.80028
P86252		**1.126217012**	**0.066766**		**4**
P86252	AAGSLLTDECR	**1.1185871**		2	3.06331
P86252	ADSAEYSVMTTGGQSSAK	**0.240965479**		2	4.03746
P86252	AEVSELPSVVR	**0.890049754**		2	2.80861
P86252	AISGDLTAEEELER	**0.961382309**			
P86252	ALLTPVAIAAGR	**0.821235657**		2	2.51542
P86252	AMQEINYGPSPDNSIKLVR+Oxidation(1)	**0.761359239**			
P86252	ASMMGQRASLLTAR+Oxidation(2)	**1.029955017**			
P86252	AVAENQPFLIEAMTYR	**0.997456351**		2	4.51248
P86252	AVEIAHALCLTERQIK	**0.973251469**			
P86252	DQMVKNNHFTLK+Oxidation(2)	**0.855441582**			
P86252	EELEKMK	**0.967277009**		1	2.1218
P86252	EIAGATPYITAAEEK	**1.098780799**		2	3.06232
P86252	EKMNKPELFNGGEK+Oxidation(2)	**1.499552925**			
P86252	ELDSITPDITPGWK	**0.879408868**		2	3.4368
P86252	FFRPHFLQAPGDLTVQEGK	**1.080698275**			
P86252	FKLINSTNIR	**0.870845632**			
P86252	GENLVSMTVEGPPPK	**1.014566383**			
P86252	GIEQAVQSHAVAEEEAR	**1.16986166**		2	4.98415
P86252	GNIYSLNEGYAK	**1.209333133**		2	4.06306
P86252	GVYAVGDVCGK	**0.467855173**		1	2.2569
P86252	HLQTYGEHYPLDHFDK	**0.358503272**		3	3.38223
P86252	HVIHTVGPIAVGQPTASQAAELR	**0.91622006**		3	4.89275
P86252	IGHHSTSDDSSAYR	**0.981401429**		3	4.05821
P86252	KAMQEINYGPSPDNSIKLVR	**1.137274722**			
P86252	KGNIYSLNEGYAK	**1.225402057**		2	3.92468
P86252	KHTLIIEGATK	**#NUM!**		2	2.65277
P86252	KLQHELEEAEER	**0.136135018**		2	3.79712
P86252	KVVSDLDVIMSHLK	**1.078986878**			
P86252	LEFIQPNVISGIPIYR	**0.740195542**		2	2.79716
P86252	LFEEQLK	**0.967277009**			
P86252	LGDAVEQGVINNSVLGYFIGR	**1.078183176**		2	4.40974
P86252	LMQVNDTLTSEDAGLR	**0.545961113**			
P86252	LNNIYQNNLTK	**1.037038687**		2	2.9958
P86252	LQHELEEAEER	**0.052687648**		2	3.61621
P86252	MNLQDELDELK	**0.866268377**		2	2.48876
P86252	MNLQDELDELK+Oxidation(0)	**1.241181567**			
P86252	MQQVEASLQPETLK+Oxidation(0)	**0.792684697**			
P86252	NNGYAISTPTSEQYR	**0.898558603**		2	3.66274
P86252	QGQASAQGRAGSQGQAQGR	**0.998451209**			
P86252	QGQIINPSEDPHLPQEEVLK	**0.533932355**		2	2.99317
P86252	QTCLKTVVLLTDNK	**0.512638137**			
P86252	QTITAQNAAVQAVK	**1.083622663**		2	4.08774
P86252	QYLLNQGWWDEEQEK	**0.458780737**		2	3.81534
P86252	RAALQAEIEELR	**0.053541218**		2	3.95424

P86252	SEIQAEQDR	1.166163626	2	2.76453
P86252	SLEDALNQTATVTR	1.142753995	2	4.29333
P86252	SSSLLAKSPSK	0.985825165		
P86252	TLHVEEVVPSVIEPSFGLGR	1.025569241	3	3.68428
P86252	TSSAEMPTIPLGSAVEAIR	1.003601219	2	4.04733
P86252	TVNVVQFEPNK	2.060424564	2	2.44872
P86252	VDDSSGSIGR	1.265944106	2	2.6199
P86252	VDGNDVFAVYNATK	1.448263696	2	3.95736
P86252	VMEAFEQAER	0.653043313	2	3.41547
P86252	VVSQYHELVVQAR	1.756738018	2	3.59399
P86252	YNENHQHGK	1.238458384		
P86252	YSTSSSSGVTAGK	0.695944909	2	2.56232
P86252s	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	1.052219044	3	3.80221
P86252s	LEGDLKDLELQADSAVKGR	0.482065954		
P86252s	LIDDYGVEEEPAELPEGTSLTVDNKR	0.769219983	3	4.30252
P86252s	VASDAQLELDKLDGELKK	1.134462381		
P97384	**ANX11 Annexin A11**	**0.833422059**	**0.344878**	**2**
P97384	GFGTDEQAIIDCLGSR	0.878984567	2	4.32059
P97384	SELDLLDIR	0.708381388	2	2.61726
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.162589327**	**0.046095**	**7**
P97519	GFEEAVAAGAK	1.149735046	2	3.59461
P97519	GYVSCALGCPYEGK	1.163266671	2	4.21469
P97519	KNVNCSIEESFQR	1.289559315	2	3.29389
P97519	LIDMLSEAGLPVIEATSFVSPK	1.283848239	3	4.57972
P97519	LLEAGDFICQALNR	1.32306409	2	4.50193
P97519	NVNCSIEESFQR	1.133562508	2	3.65505
P97519	WVPQMADHSDVLK	0.87184533	2	2.7973
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**1.131776671**	**0.033167**	**7**
P97521	CLLQIQASSGK	0.938444793	1	2.91769
P97521	EEGVTSLYK	0.899421487	1	2.02467
P97521	KLYQEFGIR	1.096656153	2	2.53341
P97521	LQTQPPSLPGQPPMYSGTIDCFR	1.195371445	2	4.04101
P97521	LYQEFGIR	1.209768553	2	2.60825
P97521	SVHDLSVPR	1.011117709	2	2.59427
P97521	YSGTLDCAK	1.126300614	2	2.34599
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**1.117404688**	**0.463889**	**14**
P97524	GEVGLLICK	0.92064823	2	2.62281
P97524	ITELTPFFGYAGGK	1.510551746	2	2.92439
P97524	SEVTFTTPAVYIYTSGTTGLPK	3.358391889	2	2.99571
P97524	SLLHCFQCCGAK	1.127436851	2	2.73525
P97524	TILHVFLEQAR	0.973051998	3	3.31497
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	0.942243248	3	4.80452
P97524	TYVPMTEDIYNAIIDK	1.122851629	3	4.14188
P97524	VDGVSADPIPESWR	1.193771705	2	3.05965
P97524	VLLASPELHEAVEEVLPTLK	1.096316001	3	4.22039
P97524	VTLMEEGFNPSVIK	1.103251784	2	3.99203
P97524	YDVEKDEPVR	1.09156874	2	3.11514
P97524	YDVEKDEPVRDANGYCIK	0.960328141	3	3.61246
P97524	YLCNTPQKPNDR	1.122463237	2	3.05865
P97524	YNATVIQYIGELLR	1.921995785	2	4.16684
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.210165035**	**1.17E-13**	**9**
P97532	AFGHHSVSLLDGGFR	1.028324887	2	3.54009
P97532	ALVSAQWVAEALK	1.13068441	2	4.23916
P97532	AQPEHVISQGR	0.937798082	2	2.84928
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	1.627428165	3	6.73878

P97532	FQGTQPEPR	**1.034778298**	2	2.82022
P97532	LLDASWYLPK	**1.284801824**	2	3.8281
P97532	SPSEPAEFCAQLDPSFIK	**0.539851764**	2	3.00141
P97532	THEDILENLDAR	**1.045004387**	2	3.25239
P97532	YWLSQNLPISSGK	**0.997350274**	2	3.75554
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.09296203**	**0.185445**	**8**
P97536	AADIDQEVK	**1.451800673**	2	2.48731
P97536	EGPAVVGQFIQDVK	**1.949395127**	2	3.1046
P97536	FTISDHPQPIDPLLK	**1.261318063**	2	2.39912
P97536	ITSEALLVTQQLVK	**0.990605013**	2	2.7034
P97536	LTLIDPETLLPR	**1.516112531**	2	2.80198
P97536	SVILEAFSSPSEEVK	**0.98445327**	2	2.76456
P97536	TLEDPDLNVR	**1.02766982**	2	2.30818
P97536	TYIQCIAAISR	**1.043646189**	2	2.95908
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.232975088**	**8.77E-10**	**20**
P97562	ATASCTYEGENTVLYLQVAR	**1.730821387**	2	3.93295
P97562	ATFADFCAQGAEICR	**1.382652947**	2	4.96996
P97562	CSAQTAADFR	**1.675343526**	2	2.98966
P97562	DFSLLPELHALSTGMK	**0.681880556**	2	2.37897
P97562	EAFLDLLPLIR	**1.121012762**	2	2.87832
P97562	EELYEDAIQK	**1.046980227**	2	2.36787
P97562	FAEVLPDGTYQR	**0.865572548**	2	2.7532
P97562	HSPSFSVER	**1.066618126**	2	2.41094
P97562	ILEYQTQQQK	**1.085295212**	2	3.81433
P97562	KVESIIQSDPVFNLK	**0.874803001**	2	4.95636
P97562	LDKEPEIQR	**1.08090055**	2	2.69837
P97562	LFEWAQK	**0.866597256**	2	2.45519
P97562	LGTPQSNYLGMLVTR	**1.269343273**	2	3.51787
P97562	LTNILDGGLPNTVLR	**1.248275094**	2	4.66028
P97562	MGLEHIDNGFLQLNHVR	**1.00191479**	3	4.27667
P97562	SGVDQHDAWNQTTVIHLQAAK	**1.022017909**	3	6.1278
P97562	SLEDHTPLPGITVGDIGPK	**0.931529238**	3	4.6145
P97562	SLGSDEQIAK	**1.052335708**	2	2.63038
P97562	VESIIQSDPVFNLK	**0.939698706**	2	4.25094
P97562	VLDGNVNLSLHGVAMNAIR	**0.764427561**	2	3.2172
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.37617021**	**0.11852**	**3**
P97576	ALADTENLR	**1.167846827**	2	2.65295
P97576	DLLEVADILEK	**1.519240443**	2	3.2089
P97576	TLRPALVGVVK	**1.223478124**	2	2.53241
P97584	**PTGR1 Prostaglandin reductase 1**	**0.951165689**	**1.01E-06**	**5**
P97584	ALTDLMNWVSEGK	**1.099590801**	2	4.10694
P97584	GGETVLVNAAAGAVGSVVGQIAK	**0.938868989**	2	5.64595
P97584	HFEGFPTDSNFELR	**0.788886208**	2	3.73866
P97584	TGPCPPGPSPEVIIYQQLR	**1.516590557**	2	4.03136
P97584	YHEYITEGFEK	**0.827583191**	2	2.83562
P97608	**OPLA 5_oxoprolinase**	**0.993653213**	**0.74092**	**11**
P97608	AGDFGAAFVER	**1.050851087**	2	3.01052
P97608	GGPVTVTDANLVLGR	**1.02221086**	2	2.73712
P97608	GHTACADAYLTPTIQR	**1.102866391**	2	3.42402
P97608	GSILDPSPEAAVVGGNVLTSQR	**0.975525104**	2	4.79947
P97608	ISVGAEGPSMADTR	**1.041799047**	2	2.70529
P97608	ISVGAEGPSMADTR+Oxidation(9)	**1.303131483**		
P97608	ITDPEILESR	**0.207872677**	2	2.64443
P97608	LLSEDPANYADAPTEGIR	**1.066408155**	2	4.30364
P97608	SGLFVVGPESAGAHPGPACYR	**0.599528172**	2	3.77446
P97608	SGLQLEDTPK	**1.206217288**	2	2.50593

P97608	TGDLLEIQQPVDLEALR	**0.893849411**	2	4.33554
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.221023922**	**0.00017**	**7**
P97612	FMREVEQLMTPQK+Oxidation(8)	**1.302456565**		
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	**0.890521543**	3	4.6872
P97612	GTNCVTSYLTDCETQLSQAPR	**1.3641199**	2	4.94062
P97612	GYFGDIWDIILK	**1.011518493**	2	3.01208
P97612	LQSGELSPEAVFFTYLGK	**1.613149706**	2	4.71232
P97612	NSVGLPVAVQCVALPWQEELCLR	**1.159550295**	2	4.17338
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	**1.660416265**	2	4.75917
P97697	**IMPA1 Inositol monophosphatase 1**	**1.371528743**	**0.798969**	**2**
P97697	SLLVTELGSSR	**1.026933738**	2	2.3707
P97697	SSPADLVTVTDQK	**1.45527029**	2	2.78266
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**0.971744018**	**0.360231**	**4**
P97700	AVVVNAAQLASYSQSK	**0.929429493**	2	4.76448
P97700	GIYTGLSAGLLR	**0.900972443**	2	2.83866
P97700	LGIYTVLFER	**0.856293597**	2	2.72505
P97700	LTGADGTPPGFLLK	**1.134448866**	2	3.15254
P97840	**LEG9 Galectin_9**	**2.686499158**	**0.000243**	**2**
P97840	NTQINNSWGPEER	**2.059743145**	2	2.45388
P97840	SINISGVVLPDAK	**2.69454812**	2	3.38207
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**1.013016789**	**9.86E-08**	**21**
P97852	AVANYDSVEAGEK	**1.334185094**	2	4.02546
P97852	AYALAFAER	**1.299941163**	2	3.57315
P97852	CEAVIADILDK	**1.015442434**	2	2.46266
P97852	DTTSLNQAALYR	**1.5299694**	2	2.47417
P97852	FVYEGSADFSCLPTFGVIVAQK	**0.837520173**	2	4.48273
P97852	GALVVVNDLGGDFK	**1.434078601**	2	4.38234
P97852	GSSAADKVVEEIR	**1.025982431**	2	2.7199
P97852	HVLQQFADNDVSR	**1.092751297**	2	4.46525
P97852	ICDFSNASKPK	**1.336385847**	3	3.76799
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	**0.98737909**	3	5.50173
P97852	IDVVVNNAGILR	**0.917070918**	2	3.40427
P97852	ISDEDWDIIQR	**0.8334273**	2	3.78878
P97852	KNNIHCNTIAPNAGSR	**0.819603842**	2	4.85843
P97852	LNPQNAFFSGR	**1.524558431**	2	2.63414
P97852	NGSGEVYQGPAK	**1.439620113**	2	3.08497
P97852	NNIHCNTIAPNAGSR	**1.031855875**	2	4.57182
P97852	SIQESTGGIIEVLHK	**0.854489815**	2	4.00652
P97852	SLMSGGLAEVPGLSINFAK	**0.933231254**	2	3.04247
P97852	VLHGEQYLELYKPLPR	**1.012576966**	2	4.40263
P97852	VNAVFEWHITK	**1.649722148**	2	2.51869
P97852	VVLVTGAGGGLGR	**0.974706926**	2	3.71669
Q00238	**ICAM1 Intercellular adhesion molecule 1**	**0.817197211**	**0.303633**	**2**
Q00238	LDTPDLLEVGTQQK	**1.016695269**	2	3.08378
Q00238	VELDPLPAWQQVGK	**0.811923848**	2	2.94647
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.1403604**	**0.003503**	**4**
Q00438	IAIPGLAGAGNSVLLVSNLNPER	**1.526076763**	2	4.19562
Q00438	KLPSDVTEGEVISLGLPFGK	**1.06283075**	2	4.71256
Q00438	LSLDGQNIYNACCTLR	**1.015228506**	2	3.5393
Q00438	NNQFQALLQYADPVSAQHAK	**1.176056487**	2	5.64808
Q00780	**chain**	**0.922418917**	**0.011088**	**4**
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(3)	**2.1635855**		
Q00780	AGPMGMAGPKGPMGPMGPKGIGPYGQPGPK+Oxidation(5)	**2.1635855**		

Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	**0.863219625**		
Q00780	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	**0.863219625**		
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**1.541407217**	**0.170865**	**3**
Q00PI9	AVEEQGDDQDSEK	**1.139290326**	2	3.82613
Q00PI9	EEAQPIVTKYK	**2.322612529**	1	1.94497
Q00PI9	SGDETPGSEAPGDK	**1.180478459**	2	2.85477
Q01177	**PLMN Plasminogen**	**1.108598699**	**0.781332**	**3**
Q01177	ILGSDVQQIAVTK	**1.115671728**	2	3.72667
Q01177	LVLEPNDADIALLK	**0.994196571**	2	2.58515
Q01177	STELCAGHLAGGIDSCQGDSGGPLVCFEK	**0.816448316**	3	4.32061
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.116785642**	**0.975177**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	**1.108247405**	2	6.31863
Q01205	NDVITVQTPAFAESVTEGDVR	**1.137315077**	2	5.20277
Q01205	NVETMNYADIER	**1.322201289**	2	3.41414
Q01205	VEGGTPLFTLR	**1.089224355**	2	3.21978
Q01405	**SC23A Protein transport protein Sec23A**	**1.12112462**	**1.26E-11**	**4**
Q01405	AETEEGPDVLR	**1.079975967**	2	2.90697
Q01405	AVLNPLCQVDYR	**1.118217452**	2	2.73136
Q01405	HLLQAPVDDAQEILHSR	**1.23974541**	3	5.62557
Q01405	YIDTEHGGSQAR	**1.613267507**	2	3.28114
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.919779589**	**9.9E-20**	**31**
Q02253	AEMEAAVAACK	**0.888601848**	2	3.80614
Q02253	AEMEAAVAACK+Oxidation(2)	**1.184711083**		
Q02253	AFPAWADTSILSR	**1.0364832**	2	4.00217
Q02253	AISFVGSNQAGEYIFER	**1.336111594**	2	5.17551
Q02253	CMALSTAVLVGEAK	**0.865314462**	2	4.5014
Q02253	CMALSTAVLVGEAK+Oxidation(1)	**1.289554859**		
Q02253	EEDATLSSPAVVMPTMGR	**0.709971286**	2	4.30653
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12)	**0.775777778**		
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15)	**1.3278745**		
Q02253	EGASILLDGR	**0.727106164**	2	2.54158
Q02253	ENTLNQLVGAAFGAAGQR	**0.996723376**	2	5.49963
Q02253	GDTNFYGK	**1.070042554**	2	2.44487
Q02253	GLQVVEHACSVTSLMLGETMPSITK	**0.901866446**	2	5.59355
Q02253	GYENGNFVGPTIISNVKPSMTCYK	**0.787334736**	3	3.93188
Q02253	IVNDNPYGNGTAIFTTNGAIAR	**1.182610507**	2	5.41856
Q02253	LITLEQGK	**1.166523494**	2	2.81526
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	**3.273005395**	3	4.29733
Q02253	NHGVVMPDANK	**0.967584675**	1	3.3676
Q02253	NHGVVMPDANK+Oxidation(5)	**1.205069056**		
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	**0.823993119**	3	6.17099
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5)	**1.078677792**		
Q02253	QGIQFYTQLK	**1.440464981**	2	2.72376
Q02253	SDKWIDIHNPATNEVVGR	**1.091108751**	2	5.28006
Q02253	TITSQWK	**0.976429562**	2	2.52672
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	**0.650743953**	2	5.27224
Q02253	TLADAEGDVFR	**0.874937824**	2	3.48783
Q02253	VCNLIDSGAK	**1.009362519**	2	3.48186
Q02253	VNAGDQPGADLGPLITPQAK	**0.899536693**	2	5.73663

Q02253	WIDIHNPATNEVVGR	0.956270845	2	4.91935
Q02253	WLPELVER	0.815406891	2	2.50395
Q02253	YAHMVDVGQVGVNVPIPVPLPMFSFTGSR	1.089470553	3	4.01954
Q02769	**FDFT Squalene synthase**	**0.907541218**	**0.086693**	**4**
Q02769	KLEDFVKPENVDVAVK	0.66432978	3	4.03136
Q02769	SFAAVIQALDGDIR	0.704149376	2	3.20876
Q02769	TQSLPNCQLISR	0.598667403	2	2.72067
Q02769	VVLEDFPTISLEFR	0.905142317	2	3.4615
Q02874	**H2AY Core histone macro_H2A.1**	**0.93471462**	**0.272436**	**3**
Q02874	AASADSTTEGAPTDGFTVLSTK	1.551703497	2	4.43577
Q02874	GVTIASGGVLPNIHPELLAK	0.906771758	2	4.13975
Q02874	NGPLEVAGAAVSAGHGLPAK	0.844788666	2	3.3183
Q02974	**KHK Ketohexokinase**	**1.033023887**	**0.536251**	**9**
Q02974	FGCQVAGK	1.123786162	2	2.54027
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.000562884	3	5.73581
Q02974	GGNASNSCTVLSLLGAR	1.041819617	2	4.68677
Q02974	GNSMQEALR	0.941510546	2	3.03812
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.978388248	3	5.76539
Q02974	IEQYNATQPLQQK	1.325666618	2	4.87452
Q02974	RGVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.028740555	3	5.23999
Q02974	TIILYDTNLPDVSAK	0.944797045	2	5.02073
Q02974	VSVEIEKPR	1.10318589	2	2.37493
Q03248	**BUP1 Beta_ureidopropionase**	**1.225702188**	**9.9E-20**	**12**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.460698667	2	6.27259
Q03248	EKLPWTEFAESAEDGLTTR	1.051810663	3	4.71631
Q03248	ELAEAVKPNYSPNIVK	1.209603737	2	4.28682
Q03248	HNMVVISPILER	1.170703487	2	2.94065
Q03248	HNMVVISPILER+Oxidation(2)	1.430694499		
Q03248	IPLPTSAPVAEQVSALHK	1.715730925	3	4.7975
Q03248	KHNMVVISPILER	0.142927623	2	2.93245
Q03248	KHNMVVISPILER+Oxidation(3)	1.230022494		
Q03248	NAAIANHCFTCALNR	1.229511769	2	4.46206
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.394144525	3	5.64368
Q03248	VGQEHYPNEFTSGDGK	1.10585445	2	4.24458
Q03248	VGQEHYPNEFTSGDGKK	1.049796114	3	4.94072
Q03336	**RGN Regucalcin**	**0.982514739**	**2.49E-13**	**16**
Q03336	CGESPVWEEASK	0.982252747	2	4.67676
Q03336	CLLFVDIPSK	1.241910149	2	3.32637
Q03336	DEQIPDGMCIDVEGK	0.870691768	2	4.61304
Q03336	DYSEMYVTCAR	1.345905073	2	2.76743
Q03336	FNDGKVDPAGR	0.932362715	2	2.72158
Q03336	HQGSLYSLFPDHSVK	1.382745088	2	4.72393
Q03336	KYFDQVDISNGLDWSLDHK	1.085941649	3	5.68878
Q03336	LWVACYNGGR	1.341115484	2	2.98331
Q03336	MEKDEQIPDGMCIDVEGK	0.863007916	2	5.10728
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0)	1.13461793		
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10)	1.134354035		
Q03336	QSGGYVATIGTK	0.985724965	2	2.89118
Q03336	VGVDAPVSSVALR	0.928426876	2	3.79533
Q03336	YFAGTMAEETAPAVLER	0.841658894	2	5.59041
Q03336	YFAGTMAEETAPAVLER+Oxidation(5)	1.025428867		
Q03336	YFDQVDISNGLDWSLDHK	0.90770395	3	4.38135
Q03410	**SYCP1 Synaptonemal complex protein 1**	**1.065649863**	**0.005612**	**2**
Q03410	ISEEKLLGEVEK	1.070588276	2	2.30646
Q03410	MEQENTAILTDKK+Oxidation(0)	0.555119579		
Q03626	**MUG1 Murinoglobulin_1**	**0.883103259**	**0.000358**	**6**
Q03626	EESSCIHSSCTAER	1.085306851	2	3.90137

Q03626	GGEFEMMPLGVNK	**0.487059899**	2	3.13859
Q03626	LTAQPAPSPEDLALSMGTIK	**0.904884401**	3	4.64706
Q03626	NLHPLNELFPLAYIEDPK	**1.467334918**	3	4.43432
Q03626	VQTVPLTCNNPK	**0.840069613**	2	2.90261
Q03626	VYHKEESSCIHSSCTAER	**1.187643315**	3	4.37682
Q04462	**SYVC Valyl_tRNA synthetase**	**1.27730106**	**0.335167**	**6**
Q04462	ADFPAGIPECGTDALR	**1.335057337**	2	2.42099
Q04462	ALNPLEEWLR	**1.049538004**	2	2.54179
Q04462	ITPAHDQNDYEVGQR	**1.400921515**	2	3.35845
Q04462	LQQTEAELR	**1.480903748**	2	2.36042
Q04462	SVTQQPGSEITAPQK	**0.977391028**	2	3.15732
Q04462	VQGSDSDEEVVVATTR	**0.903899736**	2	3.93878
Q05096	**MYO1B Myosin_Ib**	**0.772004637**	**0.004116**	**2**
Q05096	LEDLATLIQK	**0.708611743**		
Q05096	NAMQIVGFSDPEAESVLEVVAAVLK	**1.158110369**		
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**1.170588703**	**0.578415**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(0)	**0.877566221**		
Q05144	YLECSALTQR	**1.150257368**	2	2.97773
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.069789734**	**0.000649**	**9**
Q06647	FSPLTANLMNLLAENGR	**1.430915365**	3	4.12822
Q06647	GEVPCTVTTAFPLDEAVLSELK	**1.059815162**	3	5.81967
Q06647	GQILNLEVK	**1.442240327**	2	2.48038
Q06647	LGNTQGVISAFSTIMSVHR	**1.592390403**	3	3.33121
Q06647	LVRPPVQVYGIEGR	**3.026757103**	3	3.53732
Q06647	TDPSIMGGMIVR	**0.758294879**	2	3.22957
Q06647	TVLNSFLSK	**1.1759052**	2	3.01961
Q06647	VSLAVLNPYIK	**1.644811634**	2	3.06192
Q06647	YATALYSAASK	**3.145191925**	2	3.43325
Q07071	**GCKR Glucokinase regulatory protein**	**1.274211107**	**4.22E-07**	**14**
Q07071	AAPISCHVQVAHEK	**1.305615632**	2	4.91732
Q07071	CLLEILR	**1.370120987**	2	2.62097
Q07071	GFLIGDHSDMFNQK	**1.360255014**	2	3.54048
Q07071	GLGQKPLYTYLIAGGDR	**3.873878899**	2	3.11662
Q07071	LLGQCDAEIFQEEGQIVPTYQR	**2.997405834**	2	5.07553
Q07071	LYSESVLTTMLQVAGK	**1.592592762**	2	2.60993
Q07071	NDPIEDWR	**1.256469057**	1	1.90331
Q07071	QEAFVLNPAIGPEGLSGSSR	**2.125976048**	2	3.05214
Q07071	STQALEDPPACGTLN	**1.301942899**	2	2.40463
Q07071	TVDQGVVSSQR	**1.256886583**	2	3.52895
Q07071	VIPTALLSLLLR	**1.375825891**	2	3.55718
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	**1.443609681**	2	5.32788
Q07071	WVLNTVSTGAHVLLGK	**0.97503468**	2	2.74623
Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	**1.286041168**	3	5.56291
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**1.04352799**	**0.97387**	**7**
Q07116	AVDDSYNVQPDTVAPIWNLR	**1.040205636**	2	4.61679
Q07116	FVDLHPGGQSK	**1.198245582**	2	2.43854
Q07116	LCDVLAQAGHR	**0.896954889**	2	2.99242
Q07116	MSPPLEASDPYSNDPMR	**0.760978937**	2	2.6766
Q07116	NHLPVPNLDPDTYR	**0.982395976**	2	2.47908
Q07116	VSVESEESYSHWQR	**1.100412838**	2	3.74271
Q07116	VVVPGVVGAR	**0.863556492**	2	2.44121
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**1.244445584**	**9.9E-20**	**10**
Q07523	ALKEEKPTQSVPVSFPK	**0.604720849**	3	4.58456
Q07523	ALVITIDTPVLGNR	**0.708573671**	2	4.47794
Q07523	ASFCWNDLSLLQSITR	**1.101752681**	2	4.09175
Q07523	EEKPTQSVPVSFPK	**0.901197559**	2	2.96341

Q07523	EVLDILTAELHR	**0.829290405**	2	3.24111
Q07523	GEDGVKEVLDILTAELHR	**0.805182891**	3	5.18748
Q07523	HNVQGIVVSNHGGR	**0.707940207**	3	6.11873
Q07523	NQLNLEANILLK	**0.708617779**	2	3.47021
Q07523	QLDEVSASIDALR	**0.703587942**	2	3.07338
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	**1.908464557**	3	4.6385
Q07803	**EFGM Elongation factor G_ mitochondrial**	**1.170889203**	**0.045423**	**3**
Q07803	GIIDLIEER	**1.492559537**	2	2.70109
Q07803	LEFSDETFGANVPK	**1.148592092**	2	3.6988
Q07803	YQPCSPSTQEELVNK	**1.171656941**	2	3.26223
Q07936	**ANXA2 Annexin A2**	**1.119152217**	**0.00626**	**2**
Q07936	GLGTDEDSLIEIICSR	**0.798163596**	2	3.02756
Q07936	GVDEVTIVNILTNR	**0.811115993**	2	4.11061
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.220540907**	**0.058573**	**3**
Q07984	FFDEESYSLLR	**1.254537186**	2	3.53923
Q07984	NNEDVSIIPPLFTVSVDHR	**1.178379343**	3	3.91854
Q07984	VQNMALYADVSGK	**1.168138442**	2	3.25548
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**0.829454502**	**0.000198**	**8**
Q08163	ALLVTASQCQQPAGNK	**0.741373624**	2	4.68097
Q08163	GAVPYVQAFDSLLANPVAEYLK	**1.096987518**	3	3.77334
Q08163	LEAVSHTSDMHCGYGDSPSK	**0.94584785**	3	4.85867
Q08163	LSDLLAPISEQIQEVITFR	**1.192806673**	2	3.42884
Q08163	NSLDCEIVSAK	**0.972789285**	2	3.08192
Q08163	SALFAQINQGESITHALK	**0.432587022**	2	3.81525
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	**0.972467593**	2	3.66837
Q08163	VENQENVSNLVIDDTELK	**0.842683798**	2	4.82456
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.293359737**	**0.046879**	**4**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	**1.142103202**	3	4.9042
Q08415	ILVLNTPNNPLGK	**1.297295493**	2	3.05506
Q08415	LGASNDWQLDPAELASK	**0.421953839**	2	3.34252
Q08415	RLDGIDQNLWVEFGK	**1.01696224**	2	2.93295
Q09073	**ADT2 ADP/ATP translocase 2**	**1.131891877**	**1.22E-10**	**7**
Q09073	DFLAGGVAAAISK	**1.382225892**	2	4.76953
Q09073	EQGVLSFWR	**1.779613281**	1	1.9082
Q09073	GLGDCLVK	**1.059063685**	2	2.58245
Q09073	GTDIMYTGTLDCWR	**1.381221761**	2	3.63335
Q09073	KGTDIMYTGTLDCWR	**1.066989496**	2	3.36929
Q09073	LLLQVQHASK	**1.48687944**	2	2.74865
Q09073	QIFLGGVDK	**0.982821634**	2	2.68216
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**1.256106772**	**2.07E-05**	**6**
Q0D2L3	EESLMLGTVNPSTGALPFQSLR	**0.968446528**	2	3.74251
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	**0.971972699**	3	3.64527
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	**1.327413061**	3	4.63537
Q0D2L3	SVDEGLLDSK	**1.212899087**	2	2.98218
Q0D2L3	SVDEGLLDSKR	**1.174547635**	2	2.66419
Q0D2L3	VADLGNVNVNLYNLQDSCR	**1.325023757**	2	5.41056
Q0VAV2	**EXPH5 Exophilin_5**	**0.828281823**	**0.978205**	**2**
Q0VAV2	DMDVSVSKDEQLNK+Oxidation(1)	**1.154331001**		
Q0VAV2	GMAKNDPMELQTPR+Oxidation(1)	**0.809131804**		
Q0VGK3	**GLCTK Glycerate kinase**	**0.843557537**	**0.004855**	**3**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	**0.779800392**	3	5.88272
Q0VGK3	GATIQELNTIR	**1.016536073**	2	2.92111
Q0VGK3	QLFDSAVGAVQPGPMLQR	**0.789482421**	2	3.81942
Q0ZHH6	**ATLA3 Atlastin_3**	**0.938673343**	**0.528128**	**4**
Q0ZHH6	EHGHSNWLGDPEEPLTGFSWR	**0.900539503**	3	4.07091

Q0ZHH6	GGSDPETTGIQIWSEVFTVK	**1.119851527**	2	4.55723
Q0ZHH6	LAMDEIFQKPFQTLMFLVR+Oxidation(2)	**1.272731857**		
Q0ZHH6	YQQELEEEITELYENFCK	**1.167744287**	2	4.75952
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**1.120155227**	**0.000145**	**25**
Q10758	AEAETMYQIK	**0.928906739**	2	3.4038
Q10758	AQYEEIANR	**0.922508643**	2	3.05185
Q10758	ATLEAAIADAEQR	**0.868894912**	2	4.63898
Q10758	ELQSQISDTSVVLSMDNSR	**0.991073381**	2	5.74684
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	**1.005792277**	2	4.48695
Q10758	LEGLTDEINFLR	**0.883825801**	2	4.25558
Q10758	LESGMQNMSIHTK	**0.688475368**	2	3.77839
Q10758	LEVDPNIQAVR	**1.008837941**	2	3.73553
Q10758	LEVELGNMQGLVEDFK	**0.950022196**	2	5.06192
Q10758	LKLEVELGNMQGLVEDFK	**1.271520228**	3	4.0043
Q10758	LQAEIDALK	**1.021429448**	2	2.74644
Q10758	LVSESSDIMSK	**0.90577985**	2	3.01251
Q10758	QIHEEEIR	**0.895938362**	1	2.32955
Q10758	QLEALGQEK	**0.788019687**	1	2.26031
Q10758	RQLEALGQEK	**1.197675979**	2	2.3269
Q10758	SKTEISEMNR	**0.91486181**	3	3.43502
Q10758	SKTEISEMNR+Oxidation(7)	**0.845226005**		
Q10758	SLDMDSIIAEVR	**0.87708913**	2	4.58301
Q10758	SNMDNMFESYINNLR	**1.649348922**	2	4.08514
Q10758	SRAEAETMYQIK	**0.998542297**	2	3.51947
Q10758	TEISEMNR	**0.846278801**	2	2.48778
Q10758	TEMENEFVLIK	**0.852426113**	2	3.33354
Q10758	TEMENEFVLIK+Oxidation(2)	**0.946791822**		
Q10758	WSLLQQQK	**1.068743562**	2	2.91547
Q10758	YEELQTLAGK	**0.877296902**	2	3.70074
Q148W0	**AT8B1 Probable phospholipid_transporting ATPase IC**	**0.869559382**	**0.384883**	**2**
Q148W0	FMAASVASSNRDEALDK+Oxidation(1)	**0.540143221**		
Q148W0	TCEVIKDGRFK	**0.882806323**	1	2.20978
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.911799167**	**0.224391**	**6**
Q14DH7	IAIIYDSPVTDTK	**1.537202219**	2	2.43253
Q14DH7	STLSALVNGKPYK	**0.901516979**	2	2.81644
Q14DH7	THFAASVADPER	**1.080695347**	2	3.60355
Q14DH7	VDDVINVAGHR	**1.064079158**	2	3.39485
Q14DH7	VLAEHGVAALFTAPTAIR	**1.189806235**	2	3.77332
Q14DH7	VTPTIEDPSIFGHIEEVLK	**0.909159056**	2	3.40508
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.813933321**	**5.04E-07**	**12**
Q1HCL7	ALNEVFIGESLSSR	**0.641892156**	2	3.10102
Q1HCL7	ASYYEISVDDGPWEK	**1.018244004**	2	3.25054
Q1HCL7	LKPVIGVNTDPER	**1.099108645**	3	3.59866
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	**0.873534346**	3	5.22785
Q1HCL7	NVEHIIDSLRDEGIEVR	**0.733944359**	2	3.46317
Q1HCL7	QGNLTLPLNK	**0.894884306**	2	3.02425
Q1HCL7	SEASGPQLLPVR	**0.948043381**	2	3.41945
Q1HCL7	SEGHLCLPVR	**0.907717667**	2	2.3451
Q1HCL7	SSGLNLCTGTGSK	**0.819151887**	2	3.59294
Q1HCL7	VTNEYNESLLYSPEEPK	**1.085574679**	2	4.44559
Q1HCL7	YEFEQQR	**1.133199167**	2	2.53538
Q1HCL7	YTHSFPEALQK	**1.076104471**	2	2.66258
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.110932596**	**2.84E-11**	**5**

Q1JU68	EQPEKEPELQQYVPQLQNNTILR	**1.22606734**	3	3.47202
Q1JU68	FNVLQYVVPEVK	**1.244705625**	2	3.16015
Q1JU68	ILQEHEQIK	**0.873032991**	2	2.67146
Q1JU68	KGPEADSEWR	**0.809181623**	2	2.5634
Q1JU68	LLDMDGIIVEK	**0.799441387**	2	2.9056
Q29RW1	**MYH4 Myosin_4**	**0.214947341**	**0.003937**	**15**
Q29RW1	AGLLGTLEEMRDEK	**0.803451786**	2	2.4168
Q29RW1	ELENEVENEQK	**0.851190822**	2	2.42085
Q29RW1	ELENEVENEQKR	**0.118726977**	2	2.9905
Q29RW1	LINELSAQK	**0.738776045**	2	2.78942
Q29RW1	LQDAEEHVEAVNSK	**0.234461516**	2	4.47871
Q29RW1	LQDLVDKLQTK	**0.86453421**	1	2.10389
Q29RW1	MEGDLNEMEIQLNHANR	**0.344853227**	2	4.31543
Q29RW1	MEIDDLASNMETVSK	**0.557268528**	2	4.29516
Q29RW1	NAYEESLDQLETLK	**0.103473164**	2	4.81181
Q29RW1	NAYEESLDQLETLKR	**0.069013163**	2	3.79167
Q29RW1	QKYEETQAELEASQK	**0.596945739**	2	3.58782
Q29RW1	SELQASLEEAEASLEHEEGK	**0.299066494**	2	4.69357
Q29RW1	SNAACAALDK	**0.685646851**	2	2.31364
Q29RW1	TLEDQLSEVK	**0.446125411**	2	2.46004
Q29RW1	VAEQELLDASER	**0.766929055**	2	2.6865
Q2EMV9	**PAR14 Poly [ADP_ribose] polymerase 14**	**0.83254781**	**0.564355**	**2**
Q2EMV9	LQEELTR	**0.829165347**	1	2.0002
Q2EMV9	VLVEFEKESLNIAGK	**0.903381279**	2	2.44677
Q2TA68	**OPA1 Dynamin_like 120 kDa protein_ mitochondrial**	**1.199333257**	**0.084823**	**2**
Q2TA68	TSVLEMIAQAR	**0.598393559**	2	3.26517
Q2TA68	VIQHNALEDR	**1.201058389**	2	2.34196
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.151412583**	**4.45E-06**	**7**
Q2V057	EDCTQPDYEATSR	**1.059331241**	2	3.7824
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	**1.306738949**	2	4.48927
Q2V057	NLQLSCLSTEQNQHLQASLSR	**1.049441876**	2	5.5771
Q2V057	REQALLSQELWR	**1.161891864**	2	3.06099
Q2V057	SIPYGCLEEVIPYLIR	**2.412472268**	2	3.61214
Q2V057	SVTQLHGKEDCTQPDYEATSR	**0.840330532**	3	3.72958
Q2V057	TSEAWYEGNLSAMLHCVDLSR	**0.926264963**	2	2.73783
Q32Q06	**AP1M1 AP_1 complex subunit mu_1**	**1.114443002**	**0.377636**	**2**
Q32Q06	HNNLYLVATSK	**1.271951215**	2	2.41181
Q32Q06	MRVFLSGMPELR+Oxidation(0)	**1.088777135**		
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.133527807**	**0.977789**	**4**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	**1.077005117**	3	4.69148
Q3B7D0	HCDDSYTPQDK	**0.997855148**	2	3.08951
Q3B7D0	LEEDGDELAR	**1.146491814**	2	2.49983
Q3B7D0	TCAEAVVPSYVPIVK	**1.166966188**	2	3.19024
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**1.008909915**	**3.36E-10**	**4**
Q3B7U9	SCSQVLEHQPDNIK	**0.760375834**	2	4.10899
Q3B7U9	TAEDGPDLEMLSGQER	**1.444323456**	2	3.80184
Q3B7U9	VDMTCEEEEELLQLK	**0.888988984**	2	4.21158
Q3B7U9	VLAQQGEYSEAIPILR	**0.718861743**	2	3.13158
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**1.116667076**	**0.353232**	**3**
Q3KRD8	ASFENNCEVGCFAK	**1.17483404**	2	2.8435
Q3KRD8	HGLLVPNNTTDQELQHIR	**1.089233238**	3	4.84039
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	**0.761430649**	2	3.82786
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**0.449457065**	**0.346307**	**2**

Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	**0.820923146**	2	3.24458
Q3KRE0	ISVLEALR	**0.810863977**	2	2.36428
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**0.994237855**	**7.16E-10**	**2**
Q3KRE8	ALTVPELTQQMFDSK	**1.431256312**	2	3.31634
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**1.005732741**	3	4.18082
Q3MIB4	**LONP2 Lon protease homolog 2_ peroxisomal**	**0.572274536**	**0.000782**	**2**
Q3MIB4	MEIIQVPGYTQEEK	**0.572907486**	2	3.59663
Q3MIB4	TVGVNNPVFLLDEVDK	**0.559484381**	2	3.60823
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**1.068047652**	**0.00015**	**7**
Q3MIE0	DGQEGIEAFIQK	**1.081370887**	2	3.31079
Q3MIE0	KVALEMLFTGEPISAQEALR	**2.188506147**	3	3.50413
Q3MIE0	SDILHEAESEDLK	**1.173200385**	3	3.7396
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	**1.687058582**	2	4.64688
Q3MIE0	VALEMLFTGEPISAQEALR	**1.017394507**	2	3.37589
Q3MIE0	VIIISAEGPVFSSGHDLK	**0.966946311**	2	4.28749
Q3MIE0	VVPEEQLEEEATR	**1.052626771**	2	4.14463
Q3MIF4	**XYLB Xylulose kinase**	**0.923718994**	**0.749507**	**7**
Q3MIF4	AFHGLAGGTGVAFSEVVK	**1.010670628**	2	2.32347
Q3MIF4	CCLGWDFSTQQVK	**0.999362904**	2	2.94271
Q3MIF4	FNADNMEVSAFPGDVEIR	**0.904860608**	2	4.04073
Q3MIF4	IRDESASCSWNK	**0.901438921**	2	4.0947
Q3MIF4	SAPQPSLAATPNPGASQVYAALLPR	**0.99827188**	2	4.37847
Q3MIF4	VVAFTGDNPASLAGMR	**1.04302396**	2	3.66816
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	**1.13013775**	2	5.29777
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.31457535**	**0.084888**	**4**
Q3T1J1	EDLRLPEGDLGK	**0.967114277**	2	2.81356
Q3T1J1	EDLRLPEGDLGKEIEQK	**1.006363607**	3	4.74755
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	**1.331647925**	3	5.73893
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	**1.374182375**	3	3.76142
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.164566169**	**0.390583**	**3**
Q3T1K5	FIIHAPPGEFNEVFNDVR	**1.000021469**	3	4.58001
Q3T1K5	FTVTPSTTQVVGILK	**0.807654719**	2	3.70634
Q3T1K5	LLLNNDNLLR	**1.354296085**	2	2.40651
Q3T1L0	**A16A1 Aldehyde dehydrogenase family 16 member A1**	**1.219678886**	**0.000236**	**2**
Q3T1L0	HGAAPTVAETEVELSVR	**0.910043015**	2	2.39828
Q3T1L0	VQDQGQTLQVTGLR	**1.220765678**	2	4.16792
Q3TLP5	**ECHD2 Enoyl_CoA hydratase domain_containing protein 2_ mitochondrial**	**1.065472278**	**0.842244**	**2**
Q3TLP5	ALALAQEILPQAPIAVR	**0.950977879**		
Q3TLP5	NALGNVFVSELLEALAQLR	**1.139623718**		
Q3U2P1	**SC24A Protein transport protein Sec24A**	**0.992105904**	**0.561423**	**2**
Q3U2P1	CTLTSVPQTQALLNK	**0.509288289**	2	3.59858
Q3U2P1	TLETQSALGPALQAAFK	**1.001178829**	2	3.11167
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**0.967664335**	**0.015267**	**2**
Q3ULJ0	GIDEGPDGLK	**0.908999796**	2	2.67137
Q3ULJ0	LGLMEMIAFAK	**1.364262184**	2	3.82464
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.143569089**	**1.03E-07**	**14**
Q3UQ44	ALVGSENPPLTVIR	**1.100143934**	2	3.99713
Q3UQ44	AWVNQLETQTGEASK	**1.127891504**	2	5.08062
Q3UQ44	GVLLGIDDLQTNQFK	**1.258107711**	2	4.79105
Q3UQ44	HTDNTVQWLR	**1.507170068**	2	2.84834

Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.949031715	3	4.51543
Q3UQ44	LGIAPQIQDLLGK	1.724474936	2	2.73368
Q3UQ44	LPYDVTTEQALTYPEVK	1.189684044	2	4.32914
Q3UQ44	LSAEEMDER	1.095101133	2	2.69805
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.020534105	2	4.96988
Q3UQ44	TALEEEIK	1.12237965	1	2.006
Q3UQ44	TLDTLLLPTANIR	0.923201739	2	2.55318
Q3UQ44	VDFTEEEISNMR	0.972718323	2	3.38988
Q3UQ44	VDQVQDIVTGNPTVIK	1.01841597	2	4.91621
Q3UQ44	YQDILNEIAK	1.140738356	2	2.60564
Q3UV17	**K22O Keratin_ type II cytoskeletal 2 oral**	**1.124450634**	**0.236414**	**3**
Q3UV17	AQYEDIAQK	0.464137594	1	2.12937
Q3UV17	KQNTNMQTSIAEAEQR+Oxidation(5)	1.081922799		
Q3UV17	VDSLTDEINFLR	1.042181647	2	2.46868
Q3UZY0	**SFI1 Protein SFI1 homolog**	**1.201045188**	**0.28911**	**2**
Q3UZY0	EEWWVSQREWK	0.785733889	2	2.70475
Q3UZY0	MGRAQAAHFHSAQLLSR+Oxidation(0)	1.525527382		
Q3V036	**CCD27 Coiled_coil domain_containing protein 27**	**0.905206761**	**0.41755**	**2**
Q3V036	MDLISSERTIK+Oxidation(0)	0.626943989		
Q3V036	SSEGPPEEAAAAKLSRPSQSK	0.944248148	2	2.74978
Q3V0K9	**PLSI Plastin_1**	**0.955202176**	**0.997877**	**3**
Q3V0K9	AYFHLLNQIAPK	1.055795565	2	2.82556
Q3V0K9	KIENCNYAVELGK	1.012253907	2	3.92307
Q3V0K9	QFVTPADVVSGNPK	0.911456375	2	3.80275
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.253770622**	**0.00611**	**2**
Q3V132	GNLANVIR	1.135697023	2	2.72665
Q3V132	YFPTQALNFAFK	1.501722444	2	2.94551
Q497B0	**NIT2 Omega_amidase NIT2**	**1.074159484**	**2.19E-06**	**14**
Q497B0	AGTEETILYSDIDLK	1.354138466	2	4.27928
Q497B0	ASYVAWGHSTVVDPWGQVLTK	1.086640072	2	4.90847
Q497B0	AVDNQVYVATASPAR	1.304495096	2	4.96029
Q497B0	AVDNQVYVATASPARDEK	1.195258721	2	3.38326
Q497B0	ENSIYLIGGSIPEEDDGK	0.956601608	2	2.83704
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	0.897099193	3	4.47839
Q497B0	FAELAQIYAR	1.504261032	2	3.70459
Q497B0	IHLFDIDVPGK	1.616796893	2	2.83355
Q497B0	KIHLFDIDVPGK	0.879465117	3	4.68294
Q497B0	LALIQLQVSSIK	1.219618117	2	3.33512
Q497B0	LYNTCAVFGPDGNLLVK	0.948070652	2	4.45525
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.006899129	3	4.34472
Q497B0	TLSPGDSFSTFDTPYCR	1.319265346	2	4.70256
Q497B0	VGLGICYDMR	1.094727856	2	2.74441
Q498D5	**RMD2 Regulator of microtubule dynamics protein 2**	**0.872673866**	**0.748507**	**4**
Q498D5	AYGDMYDLSTNTQEK	0.876794937	2	4.1553
Q498D5	FCNLALLLPIVTK	0.587364265	2	3.22415
Q498D5	LEECIQDELGVR	0.96852542	2	3.14829
Q498D5	LNELLTNVEELKEEIK	0.807451043	2	3.45635
Q498U4	**SARNP SAP domain_containing ribonucleoprotein**	**1.132368021**	**0.320881**	**2**
Q498U4	EEEPPEKVVDMASEK	0.900418989	2	2.59434
Q498U4	FGIVTSSAGTGTTEDTEAK	1.213701865	2	4.13038
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.610344692**	**2.78E-15**	**10**
Q499N5	GATLSHHNIVNNSNLIGQR	0.714318448	3	4.82655
Q499N5	GGENIYPAELEDFFHK	1.260964156	2	3.08828

Q499N5	GGVIAGSLAPPELIR	**1.255612121**	2	2.6709
Q499N5	LPDLTTVISVDAPLPGTLLLDEVVAAGGK	**1.32772256**		
Q499N5	SGETTTEEEIK	**1.096734907**	2	2.9526
Q499N5	TFETVGQDR	**1.340301334**	2	2.51493
Q499N5	TGDIASMDEQGFCR	**1.568714195**	2	3.681
Q499N5	TVGECLDATAQR	**1.404360881**	2	3.14066
Q499N5	YHQGFLSCYDPINIQFTSGTTGNPK	**1.518086579**	3	4.66497
Q499N5	YIVFVEGYPLTVSGK	**1.704095542**	2	4.65274
Q4AEF8	**COPG Coatomer subunit gamma**	**1.093664699**	**0.477036**	**5**
Q4AEF8	FGAQNEEMLPSILVLLK	**0.942014991**	2	3.16496
Q4AEF8	QEIFQEQLAAVPEFQGLGPLFK	**1.126877507**	3	4.28892
Q4AEF8	SSPEPVALTESETEYVIR	**1.15246602**	2	3.99375
Q4AEF8	VVLEHEEVR	**1.354118383**	2	2.35103
Q4AEF8	VVVVQAISALCQK	**0.720423943**	2	2.30696
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.097573172**	**0.008283**	**6**
Q4FZT0	AEQINQAAGEASAVLAK	**1.060705381**	2	4.79916
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	**1.166804325**	2	4.99707
Q4FZT0	ATVLESEGTR	**1.15684726**	2	2.77091
Q4FZT0	DVQTTDTSIEELGR	**0.813253651**	2	2.82636
Q4FZT0	ILEPGLNVLIPVLDR	**1.161692624**	2	3.65553
Q4FZT0	NTVILFVPQQEAWVVER	**1.425576898**	2	3.05184
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.078220235**	**1.11E-08**	**8**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	**1.614782577**	3	4.97157
Q4FZT9	FGGSGSQVDSAR	**1.260276734**	2	3.89109
Q4FZT9	GEAIEAILAALEVVSEPFR	**0.9899007**		
Q4FZT9	SETELKDTYAR	**0.848195276**	2	2.35759
Q4FZT9	SGALLACGIVNSGVR	**1.086896746**	2	3.67773
Q4FZT9	SSTTSMTSVPKPLK	**1.063935131**	2	2.58205
Q4FZT9	TITGFQTHTTPVLLAHGER	**1.484769674**	3	3.70908
Q4FZT9	TPVQSQQPSATAPSGADEK	**1.284516776**	2	4.4407
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.538078478**	**9.9E-20**	**5**
Q4FZX7	DTQTSITDSSAIYK	**1.074217631**	2	3.09694
Q4FZX7	GDAGSADVQDLEK	**1.203893974**	2	3.32911
Q4FZX7	GNSLTLIDLPGHESLR	**1.257630957**	2	3.49188
Q4FZX7	SAAPSTLDSSSTAPAQLGK	**1.858918423**	2	4.61644
Q4FZX7	VGDGAGGAFQPYLDSLR	**1.515139366**	2	3.28302
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.078195789**	**0.003362**	**5**
Q4G061	AEEEGGSDGSAAEAEPR	**0.780473141**	2	4.84523
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	**0.143643228**	3	5.91656
Q4G061	GTQGVVTNFEIFR	**1.087548954**	2	2.81997
Q4G061	IINDYYPEEDGK	**0.657746431**	2	2.60998
Q4G061	TEDAEEDAEARPEPEVR	**0.231405549**	3	3.90095
Q4G069	**RMD1 Regulator of microtubule dynamics protein 1**	**1.082043834**	**0.939863**	**2**
Q4G069	IAEVLFANPPSSTYEEALK	**1.255148879**	2	2.48832
Q4G069	VLLYEALEYAK	**1.081885566**	2	2.56551
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.485234404**	**1.47E-09**	**13**
Q4KLP0	ARPSVDHGLAR	**0.834711076**	2	2.36956
Q4KLP0	LEELCPFPLDSLQQEMGK	**1.121404197**	2	5.12332
Q4KLP0	LLLESQEFDHFLATK	**1.493754328**	2	3.4098
Q4KLP0	LSAYGGITDIIIGMPHR	**1.557352879**	3	3.38041
Q4KLP0	LVTVYCEHGHK	**3.662906907**	2	2.8452

Q4KLP0	NGTNLDWATAETLALGSLLAQGFNVR	1.235485772		
Q4KLP0	QWGHNELDEPFFTNPVMYK	1.227597663	3	3.79277
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.152965948	3	5.15144
Q4KLP0	SSLYSSDIGK	1.431985368	2	2.69399
Q4KLP0	SVEVPEELQLHSHLLK	1.206779731	2	3.81376
Q4KLP0	WQGLVQPAACVTTWDTGVPLELLR	1.264040578	2	4.92601
Q4KLP0	YGGEGAESMMGFFHELLK	1.019202287	2	4.40741
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.469170255	3	4.52727
Q4KLZ6		**1.241693679**	**4.02E-08**	**16**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.130503634	2	4.53255
Q4KLZ6	AILEVLQTK	1.247918653	2	2.71358
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.135126752	2	3.88914
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	1.012009841	2	5.90515
Q4KLZ6	AVAQAGTAGTLLIVK	1.250605079	2	4.36865
Q4KLZ6	EGPTPASPAQVLSK	1.29224374	2	3.05592
Q4KLZ6	GLCGTILIHK	1.099546164	2	2.32161
Q4KLZ6	GVSLTLMLVDEPLLK	1.144046303	2	3.16638
Q4KLZ6	ISTTLIGLEEHLNALDR	2.081548664	2	3.94112
Q4KLZ6	LIDAETNAK	1.144385666	2	2.9918
Q4KLZ6	LNFGLAMEQAK	0.846708962	2	2.48901
Q4KLZ6	LSVLLLEK	1.873828434	2	2.80195
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.234321882	3	5.44409
Q4KLZ6	TMLDSLWAAAQELQAWK	1.064028222	2	4.33787
Q4KLZ6	VAGALAEEGMGLEEITK	1.439960394	2	3.69288
Q4KLZ6	VALLSGGGSGHEPAHAGFIGK	1.349589744	2	5.29727
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**0.943984059**	**0.774882**	**4**
Q4KM49	AFCEPGNVENNGVLSFVK	0.934579518	2	3.43372
Q4KM49	QVEPLDPPAGSAPGER	1.083618807	2	3.17038
Q4KM49	TVVSGLVQFVPK	0.900193076	2	3.22813
Q4KM49	VDAQFGGIDQR	1.284692843	2	2.94011
Q4KM73	**KCY UMP_CMP kinase**	**0.980297753**	**0.000445**	**6**
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.278091419	2	4.49933
Q4KM73	IVPVEITISLLK	0.940497119	2	2.31989
Q4KM73	KNPDSQYGELIEK	1.065156343	2	3.66957
Q4KM73	NQDNLQGWNK	0.969140058	2	3.08865
Q4KM73	SVDEVFGDVMK	0.874774507	2	3.07175
Q4KM73	YGYTHLSAGELLR	0.855399051	3	4.39207
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.184466839**	**1.2E-05**	**4**
Q4KM74	DLQQYQSQAK	1.424624762	2	3.29729
Q4KM74	GEALSALDSK	1.316125792	2	2.55765
Q4KM74	NLGSINTELQDVQR	1.183033935	2	4.20461
Q4KM74	VADGLPLAASMQEDEQSGR	0.719115035	2	2.63565
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.007057619**	**0.999715**	**2**
Q4KMA2	NFVVVMVTKPK	0.800215544	2	2.83997
Q4KMA2	QIIQQNPSLLPALLQQIGR	0.927523192	2	4.65813
Q4KSH7	**MP2K7 Dual specificity mitogen_activated protein kinase kinase 7**	**0.964992875**	**0.11814**	**2**
Q4KSH7	RSGNKEENK	1.323758938	1	1.98979
Q4KSH7	YNKLLEHSFIK	0.109529384	1	1.93753
Q4QQS8	**NUP85 Nuclear pore complex protein Nup85**	**1.07436098**	**0.950745**	**2**
Q4QQS8	LEEELSGK	1.080162134		
Q4QQS8	RFGDAASLLLSLMTSQIAPR+Oxidation(12)	0.862714592		
Q4QQV3	**F162A Protein FAM162A**	**1.215316301**	**0.970475**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	1.133676754	2	4.11866
Q4QQV3	RHESLTSLNLER	1.065065846	3	4.24926

Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**1.10874963**	**0.694023**	**5**
Q4QQW3	AANLYACSPHSEFLDYVNAPIGK	**1.668086781**	3	3.7553
Q4QQW3	HLETAEILGANIR	**0.739275561**	2	3.41572
Q4QQW3	IQDAGPVLADALR	**1.035492705**	2	2.77971
Q4QQW3	NLSQLPPVQIVMDSLSK	**1.074993265**	2	2.61558
Q4QQW3	VEPTDGSFMDAIEFAK	**1.02134482**	2	2.66885
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.220692142**	**9.9E-20**	**6**
Q4QRB4	AILVDLEPGTMDSVR	**0.761875194**	2	4.90729
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10)	**1.147194362**		
Q4QRB4	EIVHIQAGQCGNQIGAK	**1.213909466**	2	5.04325
Q4QRB4	IMNTFSVVPSPK	**1.74175998**	2	3.41872
Q4QRB4	IMNTFSVVPSPK+Oxidation(1)	**2.064781091**		
Q4QRB4	ISEQFTAMFR	**1.582226055**	2	3.58448
Q4V7C7	**ARP3 Actin_related protein 3**	**1.103410695**	**0.113482**	**5**
Q4V7C7	KDYEEIGPSICR	**1.027833819**	2	3.64753
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	**1.366885412**	2	3.14966
Q4V7C7	LSEELSGGR	**1.144070491**	2	2.71338
Q4V7C7	TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK	**0.967607991**	3	3.66895
Q4V7C7	YSYVCPDLVK	**1.422784025**	2	2.36499
Q4V8F9	**HSDL2 Hydroxysteroid dehydrogenase_like protein 2**	**1.048997431**	**0.934748**	**3**
Q4V8F9	DEQQINSAVEK	**1.051484556**	2	3.09846
Q4V8F9	KVDIIADAAYSIFK	**0.962255624**	2	2.40341
Q4V8F9	SFTGNFIIDENILK	**0.870630991**	2	2.93207
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**0.81904082**	**0.004879**	**2**
Q4V8K1	TCADEFPLTVDSSEK	**0.929829749**	2	4.58719
Q4V8K1	TLGLTPLDQGSLVAAK	**0.78868587**	2	3.80931
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**1.008239187**	**0.018872**	**3**
Q505J8	LQQVQAGQAEK	**1.285148681**	2	2.51376
Q505J8	RLEVADGGLDSAELATQLGVEHQAVVGAVK	**0.935539678**	3	4.9305
Q505J8	SLQALGEVIEAELR	**0.790524151**	2	3.58163
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**0.939383417**	**0.770799**	**4**
Q561R9	ANIIYPGHGPVIHNAEAK	**0.713773312**	2	4.29133
Q561R9	ILIDTGEPSVPEYISCLK	**0.988478867**	2	3.36361
Q561R9	NISNDATYCIK	**1.054767068**	2	2.47445
Q561R9	NNREEQIITVFR	**0.74776345**	2	2.54148
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**0.979322709**	**2.17E-05**	**5**
Q561S0	LLQYSDALEHLLSTGQGVVLER	**0.778867405**	3	3.66585
Q561S0	VITVDGNICSGK	**1.010688231**	2	2.92308
Q561S0	VVEDIEYLNYNK	**1.949683706**	2	4.20176
Q561S0	YAPGYNADVGDK	**1.664466499**	2	2.67538
Q561S0	YGLLASILGDK	**1.228715984**	2	2.94786
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.911632573**	**0.989557**	**5**
Q562C4	AQFSEVQLEWQPPPFK	**1.250267807**	2	4.89783
Q562C4	FIVAYGENMK	**1.158482249**	2	2.72036
Q562C4	HIGDGCHLTR	**1.27261786**	3	3.40635
Q562C4	VLQEVQR	**0.936979679**	2	2.76933
Q562C4	VTCVDPNPNFEK	**1.369262112**	2	3.56313
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.203142204**	**0.994024**	**7**
Q58FK9	AIILNTPHNPIGK	**1.509210647**	2	3.22036
Q58FK9	DSTLDAAEEIFR	**1.260205859**	2	2.9462
Q58FK9	IEGLDQNVWVEFTK	**1.199827181**	2	4.71338
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	**1.642289312**	2	4.05828

Q58FK9	MDDPECYFNSLPK	1.088647307	2	3.67307
Q58FK9	RIEGLDQNVWVEFTK	1.105355492	2	3.9406
Q58FK9	WTSSDWTFNPQELESK	1.08120583	2	5.07133
Q5BJP3	**UFM1 Ubiquitin_fold modifier 1**	**2.712981495**	**3.38E-06**	**2**
Q5BJP3	VLSVPESTPFTAVLK	2.761068142	2	2.32721
Q5BJP3	VPAATSAIITNDGIGINPAQTAGNVFLK	1.251162106	3	4.3595
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.985092554**	**9.9E-20**	**27**
Q5BJY9	AQIFANSVDNAR	1.224735811	2	3.83777
Q5BJY9	AQYEQLAQK	0.957497578	2	3.28645
Q5BJY9	DAETTLLELR	1.338440065	2	2.80574
Q5BJY9	IREYLEK	0.984277283	3	3.35428
Q5BJY9	KNHEEEVQGLEAQIASSGLTVEVDAPK	0.818823587	3	4.77131
Q5BJY9	KVVDDTNITR	0.891400061	2	3.02566
Q5BJY9	LEAEIATYR	0.920830917	2	3.00918
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.711339167	3	4.36194
Q5BJY9	LQLETEIEALK	1.138769196	2	2.89963
Q5BJY9	LQLETEIEALKEELLFMK	1.693807676	2	5.30738
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.830552501	2	6.31386
Q5BJY9	NQNINLENNLGEVEAR	0.869548715	2	5.50214
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	1.341767107	3	5.12897
Q5BJY9	QSVESDIHGLR	0.87981196	2	2.64962
Q5BJY9	QSVESDIHGLRK	1.035032596	2	2.65069
Q5BJY9	QTQEYEALLNIK	0.860002677	2	3.45206
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.657811858	2	5.97917
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK+Oxidation(14)	1.090644421		
Q5BJY9	TLQTLEIDLDSMK	0.820079144	2	4.24517
Q5BJY9	TLQTLEIDLDSMK+Oxidation(11)	1.075483999		
Q5BJY9	VKLEAEIATYR	1.058967701	2	2.92102
Q5BJY9	VKYETELAMR	0.776583005	3	3.47669
Q5BJY9	VQMEQLNGVLLHLESELAQTR	1.012501515	3	5.1235
Q5BJY9	VRPASSAASVYAGAGGSGSR	1.567841443	2	5.63572
Q5BJY9	VVDDTNITR	0.881226157	2	3.33648
Q5BJY9	YETELAMR	0.761857345	2	2.75177
Q5BJY9	YWSQQIEESTTVVTTK	1.190246061	2	4.74506
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.196899928**	**0.048212**	**4**
Q5BK63	AVQHSNVVINLIGR	1.101011866	2	3.3842
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.332787602	3	5.33316
Q5BK63	NFDFEDVFVNIPR	1.227284573	2	3.9904
Q5BK63	WLSSEIEETKPAK	1.426335285	2	2.9375
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.955917917**	**0.84207**	**4**
Q5BK81	AILDGNGLEK	1.151097607	2	2.40133
Q5BK81	DVPYPPPLPPAVEAIQK	0.958498082	2	2.69482
Q5BK81	TGNVAEQLR	0.934237498	2	2.63178
Q5BK81	VEEVSLPDTINEGQVR	0.872931315	2	4.06298
Q5DTT3	**F208B Protein FAM208B**	**0.890929246**	**0.00533**	**2**
Q5DTT3	QGENIDKLMEYVKNK	2.415297203	2	2.32696
Q5DTT3	VSVPSEHSENLSFLEK	0.328636542	2	2.34369
Q5DW34	**EHMT1 Histone_lysine N_methyltransferase EHMT1**	**1.156284231**	**0.300483**	**2**
Q5DW34	TPLMEAAENNHLDAVKYLIK+Oxidation(3)	1.602089311		
Q5DW34	YDCVVLFLSRDSDVTLKNK	1.046803411	2	2.36457
Q5EB77	**RAB18 Ras_related protein Rab_18**	**0.819270395**	**0.006462**	**3**
Q5EB77	LDNWLNELETYCTR	1.893377189	2	2.88813
Q5EB77	NDIVNMLVGNK	0.719140688	2	3.08801
Q5EB77	TCDGVQCAFEELVEK	0.826410664	2	3.46799

Q5FVM4	**NONO Non_POU domain_containing octamer_binding protein**	**1.779271588**	**0.008856**	**2**
Q5FVM4	MEELHNQEVQK	**0.824719711**	2	3.22223
Q5FVM4	MEELHNQEVQK+Oxidation(0)	**2.082294366**		
Q5FVQ4	**MLEC Malectin**	**1.28205231**	**0.974873**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	**1.441761831**	3	5.53952
Q5FVQ4	STPEDQILYQTER	**1.057573507**	2	4.00993
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.711172473**	**0.004629**	**5**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10)	**0.714669725**		
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8)	**0.722850293**		
Q5FVR2	DVTATVDSVPLITASILSK	**1.458356888**	2	2.49978
Q5FVR2	FGGAAVFPDQEK	**0.887910393**	2	2.32941
Q5FVR2	VSLVLAPALAACGCK	**0.744023903**	2	2.51537
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.449263744**	**0.008884**	**4**
Q5FVR5	DEKENLFQSK	**0.930472279**	2	2.50185
Q5FVR5	ILFIVGENDQCLASK	**0.947710289**	2	3.89702
Q5FVR5	IQQPGIGVISVSK	**1.287582064**	2	3.02578
Q5FVR5	VLLEEDLDYFEEAANFLLAHPK	**1.530227754**	3	4.10144
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.883039967**	**0.956273**	**2**
Q5FW57	AIDQEMFK	**1.05152549**	1	1.99001
Q5FW57	SSQMLQMLESSLR	**0.83942162**	2	3.75441
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**0.72275347**	**0.037465**	**3**
Q5HZV9	AIENIDTLTNLESLFLGK	**0.760623759**	2	3.0205
Q5HZV9	ELDLYDNQIK	**0.214176242**	2	2.35752
Q5HZV9	ELDLYDNQIKK	**0.059073363**	2	2.40515
Q5HZY0	**UBXN4 UBX domain_containing protein 4**	**1.392091764**	**0.000893**	**2**
Q5HZY0	LPDGSSFTNQFPSDAPLEEAR	**1.480206846**	2	4.25185
Q5HZY0	NTELCETPTTSDPK	**1.53312678**	2	4.06084
Q5HZY2	**SAR1B GTP_binding protein SAR1b**	**1.149610177**	**0.809604**	**2**
Q5HZY2	EELDSLMTDETIANVPILILGNK	**1.149234084**	3	3.52758
Q5HZY2	IDRPEAISEER	**1.15692961**	2	2.67145
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**1.003540367**	**0.843366**	**6**
Q5I0C3	HAPLVEFEEEEV	**0.914117161**	2	2.93915
Q5I0C3	IIEEAPAPGIDPEVR	**0.90159523**	2	3.84091
Q5I0C3	IYAEDPDNNFMPGAGPLVHLSTPPPDMSTR	**0.771571762**	3	3.40794
Q5I0C3	SEKEFQEQLESAR	**1.176489101**	2	3.20655
Q5I0C3	TNVDFLLR	**1.16679271**	2	2.38219
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	**0.879640189**	2	5.12672
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.838782069**	**0.416405**	**3**
Q5I0D1	ESQSILTPLVSLDTPGK	**0.786004497**	2	3.57195
Q5I0D1	HEEFEEGCK	**0.896753973**	2	2.56092
Q5I0D1	VTLAVSDLQK	**0.807460683**	2	2.32329
Q5I0D5	**LHPP Phospholysine phosphohistidine inorganic pyrophosphate phosphatase**	**0.898085599**	**0.568092**	**2**
Q5I0D5	AFQVLMELENPVLISLGK	**1.116687238**	3	3.78925
Q5I0D5	LGFDISEGEVTAPAPATCQILK	**0.894803256**	2	4.34042
Q5I0D7	**PEPD Xaa_Pro dipeptidase**	**1.014733608**	**0.425607**	**2**
Q5I0D7	GVNTDSGNVCR	**1.237188203**	2	2.41711
Q5I0D7	YAVDDVQYADEIASVLTSR	**1.036358488**	2	3.95012
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**1.009443182**	**0.323239**	**2**
Q5I0E7	QLVEQVEQIQK	**1.08296257**	2	3.74162
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	**1.186251833**	3	4.08146

Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**0.959878788**	**0.410653**	**4**
Q5I0H9	DKNQDLCQQESVK	**1.041994553**	2	4.20531
Q5I0H9	GPPLWEEDPGAK	**1.032148272**	2	3.17313
Q5I0H9	GQGTICWVDCGDAESR	**1.150321965**	2	4.06272
Q5I0H9	NQDLCQQESVK	**0.757970748**	2	3.19046
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.035061219**	**0.002516**	**8**
Q5I0J9	HANLLVGSPSALADQTTER	**1.156079553**	2	5.46919
Q5I0J9	IIHESGVQILR	**1.019412638**	2	2.51111
Q5I0J9	LDAAGGLQSLR	**1.208201673**	2	3.76113
Q5I0J9	LEGPLAAAHSSGPR	**0.847273876**	2	3.35916
Q5I0J9	MAGSVPPALQLEDLTTLEER	**1.260871456**	2	3.09848
Q5I0J9	NSNTMAAAALAAPSLGFDR	**0.74401459**	2	4.32029
Q5I0J9	TVLYEGPVR	**1.052110659**	2	2.83451
Q5I0J9	VGVVGYGR	**1.034478988**	2	2.34399
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.006024607**	**0.974002**	**5**
Q5I0M2	CSGIASAAATAVEVATSTGWAGHVAGTR	**0.97093418**	3	4.32434
Q5I0M2	DNHVVAAGSMEK	**1.068753823**	2	2.84924
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	**1.002423223**	3	6.04154
Q5I0M2	LYAEGDIPVPHAR	**1.038892444**	2	2.95189
Q5I0M2	VEVECSSLK	**1.054532807**	2	2.66264
Q5I0P2	**GCSH Glycine cleavage system H protein_ mitochondrial**	**0.816446912**	**0.912482**	**2**
Q5I0P2	MTLSDPSELDELMSEEAYEK	**0.816223449**	2	5.21411
Q5I0P2	SCYEDGWLIK	**0.909155481**	2	2.30685
Q5M7T9	**THNS2 Threonine synthase_like 2**	**1.274464218**	**0.000544**	**3**
Q5M7T9	FPEAVQAAGLTPETPAEILALEHK	**1.279912522**	3	5.41887
Q5M7T9	GDFSLCEVVR	**1.193545935**	2	2.52987
Q5M7T9	MGLPISLVVAVNR	**1.368185792**	2	2.54719
Q5M7U6	**ARP2 Actin_related protein 2**	**0.955554699**	**0.636547**	**5**
Q5M7U6	GYAFNHSADFETVR	**1.033347189**	2	3.77078
Q5M7U6	HLWDYTFGPEK	**1.135633865**	2	3.3205
Q5M7U6	KHMVFLGGAVLADIMK+Oxidation(2)	**0.920150964**		
Q5M7U6	LCYVGYNIEQEQK	**1.460636326**	2	2.3962
Q5M7U6	SMLEVNYPMENGIVR	**0.811904858**	2	3.19314
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.920222329**	**5.47E-07**	**7**
Q5M7W5	AAVGLTGNDIATPPNK	**0.889739238**	2	3.54694
Q5M7W5	ATSPSTLVSTGSSSR	**0.823200455**	2	3.64958
Q5M7W5	NTTPTGATPPAGMASTR	**0.937692201**	2	2.70681
Q5M7W5	STLPVDEGSPLEK	**0.904576833**	2	2.40211
Q5M7W5	TEFIPLLDGDEK	**0.587190147**	2	2.50416
Q5M7W5	VGSLDNVGHLPAGGTVK	**0.849286415**	2	3.36949
Q5M7W5	VTEFNNVTPLSEEEVASIK	**1.17271529**	2	3.16942
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.338424399**	**0.235297**	**7**
Q5M875	ALTAELDTLGK	**1.333294617**	2	2.82836
Q5M875	IQNIQFEAIVGHR	**1.55428943**	3	3.52379
Q5M875	LWPVLEPDEVAR	**1.264507668**	2	2.40039
Q5M875	NSGHIVTVASVCGHR	**1.135795195**	2	4.39984
Q5M875	SLIDGILTNK	**1.330514515**	2	3.32467
Q5M875	SVAGQTVLITGAGHGIGR	**1.443208869**	2	4.02748
Q5M875	TSCLCPVFVNTGFTK	**1.347810963**	2	3.81641
Q5M9G3	**CAPR1 Caprin_1**	**1.092866113**	**0.112434**	**4**
Q5M9G3	LNQDQLDAVSK	**1.122157744**	2	3.25404
Q5M9G3	SSFSNTPNSGYTQSQFNAPR	**0.204131774**	2	3.80103
Q5M9G3	TVLELQYVLDK	**1.294360675**	2	2.43733
Q5M9G3	YQEVTNNLEFAK	**1.110502481**	2	2.74276

Q5M9I5	**QCR6 Cytochrome b_c1 complex subunit 6_ mitochondrial**	**0.799411443**	**2.87E-05**	**2**
Q5M9I5	EEEEEELVDPLTTVR	**0.680096508**	2	2.67855
Q5M9I5	SQTEEDCTEELFDFLHAR	**2.284605224**	2	4.86154
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**0.945421135**	**2.61E-14**	**9**
Q5PPL3	AVLDANDPKK	**0.822677841**	2	2.47939
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	**0.904930592**	2	4.93009
Q5PPL3	DPQLVPVLIDAAR	**0.925692889**	3	3.4053
Q5PPL3	GQVTGTDLINEVSK	**0.91235788**	2	3.78571
Q5PPL3	GVSTVFHCASPPSNSNNK	**1.570338253**	2	4.78604
Q5PPL3	GYAVNVFDVR	**1.130191376**	2	3.58814
Q5PPL3	ILTGLNYEAPK	**1.281501858**	2	2.8633
Q5PPL3	KGQVTGTDLINEVSK	**0.976561118**	2	4.07959
Q5PPL3	VQFFIGDLCNQQDLYPALK	**1.265120976**	3	5.26558
Q5PQQ2	**WBP11 WW domain_binding protein 11**	**0.774828435**	**0.041173**	**4**
Q5PQQ2	KLEVEYEQK	**0.122798162**	1	2.1736
Q5PQQ2	LDEMEFNPVQQPQLNEKVLK+Oxidation(3)	**2.8794979**		
Q5PQQ2	RDEDMLYSPELAQR	**1.35151292**	2	2.32538
Q5PQQ2	STSSTKSGKFMNPTDQAR	**0.754211878**	2	2.47176
Q5PQR4	**RSRC2 Arginine/serine_rich coiled_coil protein 2**	**1.275475684**	**0.000335**	**2**
Q5PQR4	EKEMVEK+Oxidation(3)	**1.275496284**		
Q5PQR4	KEGDKSQSAEIWEK	**0.582875041**	2	2.54399
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.449703359**	**3.35E-09**	**6**
Q5PQT3	AIQNLASIHSLQVK	**0.988248998**	2	3.39899
Q5PQT3	DPENCQEFLGSSEVINWK	**1.131545226**	2	5.32675
Q5PQT3	FWLFGGNER	**1.106296196**	2	2.41508
Q5PQT3	GFPVYSHTDK	**1.470020746**	2	2.67688
Q5PQT3	LSSLDVTHAALVNK	**1.858161896**	2	3.24166
Q5PQT3	QHLQIQSSQSHLNK	**1.15054726**	2	3.48084
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.082655191**	**0.169321**	**6**
Q5RJR8	ATVLDLSCNK	**1.04142297**	2	3.11454
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	**1.134782731**	2	6.02855
Q5RJR8	HHEILQWVLQTDSQQ	**1.180782461**	2	3.23996
Q5RJR8	LDGNELDLSLSDLNEVPVK	**1.013427135**	2	3.92303
Q5RJR8	LQQLPADFGR	**1.710704602**	2	2.35456
Q5RJR8	LSTLPSDFCGLTHLVK	**1.042709229**	2	3.18354
Q5RKH1	**PRP4B Serine/threonine_protein kinase PRP4 homolog**	**1.037451266**	**0.484149**	**2**
Q5RKH1	DLLDQILMLDPAKR+Oxidation(7)	**1.026540499**		
Q5RKH1	LAMDLKGKMPNK+Oxidation(2)	**0.96635821**		
Q5RKH6	**OS9 Protein OS_9**	**1.194694622**	**0.044471**	**3**
Q5RKH6	EQAILALTSTLDK	**1.133484775**	2	2.42335
Q5RKH6	LQESQSPELVQK	**1.246199377**	2	2.93514
Q5RKH6	QEQPGDDTTEAPQR	**1.388332065**	2	3.09101
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**0.978359743**	**0.940541**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	**0.903020749**	3	5.04249
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	**0.840298418**	3	4.64303
Q5RKI0	YAPSGFYIASGDISGK	**1.040645999**	2	4.31294
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.134626348**	**0.007594**	**5**
Q5RKI1	ELAQQIQK	**1.261271263**	1	2.22996
Q5RKI1	GIDVQQVSLVINYDLPTNR	**1.127568048**	2	3.99781
Q5RKI1	GYDVIAQAQSGTGK	**1.081221179**	2	5.3142
Q5RKI1	MFVLDEADEMLSR	**1.12439139**	2	4.28811
Q5RKI1	VLITTDLLAR	**0.906250817**	2	3.48753

Q5S006	**LRRK2 Leucine_rich repeat serine/threonine_protein kinase 2**	**0.901098948**	**0.394095**	**2**
Q5S006	MPRITNLDASR+Oxidation(0)	**1.060768902**		
Q5S006	WLCKVMAQILTVK	**0.900512072**	2	2.33456
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**1.037826122**	**0.000691**	**16**
Q5SGE0	AALDLEQVPSELAVTR	**1.033929903**	2	4.1944
Q5SGE0	CIANNQVETLEK	**1.03564529**	2	2.88551
Q5SGE0	DVGEPVPFTEPPESFGFYIK	**1.378733174**	2	2.96646
Q5SGE0	GLDAIELSR	**0.972642095**	2	2.69324
Q5SGE0	HCVTMDTPAEK	**1.130882949**	2	3.00898
Q5SGE0	HDNAEDALNLK	**1.236147565**	2	3.56576
Q5SGE0	MEGANIQPNR	**0.970156549**	2	2.72254
Q5SGE0	SCGSLLPELSLAER	**1.048982703**	2	2.36615
Q5SGE0	SCGSLLPELSLAERTEFAHK	**0.899853871**	2	2.40415
Q5SGE0	SGSPGSNQALLLLR	**1.474647377**	2	2.82859
Q5SGE0	SSLSSSSPSAGDTVTEK	**0.979742591**	2	4.34709
Q5SGE0	SYVADKDVASAK	**1.144696577**	2	2.85706
Q5SGE0	TLLELIPELR	**1.14616679**	2	3.00534
Q5SGE0	TSQFTSSDLESTLEK	**1.403519322**	2	3.05048
Q5SGE0	VIEEQMEPALEK	**1.184711293**	2	2.92843
Q5SGE0	VYLQNEYR	**1.556431057**	2	2.45125
Q5SNZ0	**GRDN Girdin**	**1.155108035**	**0.414025**	**2**
Q5SNZ0	KVEILENEIIQEK	**1.175570957**	2	2.5232
Q5SNZ0	YNQLLKQKGQLEDLEK	**1.051290811**	2	2.64332
Q5SW19	**K0664 Protein KIAA0664**	**1.100186924**	**3.65E-07**	**3**
Q5SW19	GLEMDPIDCTPPEYILPGSR	**0.667464803**	2	2.93945
Q5SW19	IGIGELITR	**1.644552632**	2	2.91761
Q5SW19	SVEGLQEGSVLR	**1.213174549**	2	2.82333
Q5SX40	**MYH1 Myosin_1**	**0.362067268**	**9.9E-20**	**95**
Q5SX40	AAYLQNLNSADLLK	**0.050277683**	2	3.65802
Q5SX40	ADIAESQVNK	**0.109136572**	2	4.05557
Q5SX40	AEDEEEINAELTAK	**0.338228949**	2	4.38106
Q5SX40	AGLLGLLEEMR	**0.075781505**	2	3.97848
Q5SX40	AGLLGLLEEMRDDK	**0.773579245**	2	3.33504
Q5SX40	ALQEAHQQTLDDLQAEEDK	**1.284724061**	2	5.75662
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	**0.033869197**	3	6.76401
Q5SX40	ANLLQAEIEELR	**0.050116452**	2	3.93121
Q5SX40	ANSEVAQWR	**0.460522008**	2	3.03732
Q5SX40	DLEEATLQHEATAATLR	**0.084313598**	2	4.96199
Q5SX40	DTQLHLDDALR	**0.69841731**	1	3.61319
Q5SX40	EEQAEPDGTEVADK	**0.075460254**	2	3.55858
Q5SX40	EFEMSNLQSK	**0.711383947**	1	2.54343
Q5SX40	ELEEISER	**0.047080241**	1	2.07647
Q5SX40	ELEGEVENEQK	**0.186344741**	2	2.69849
Q5SX40	ELEGEVENEQKR	**0.057264667**	2	3.28517
Q5SX40	ELTYQTEEDRK	**0.328212564**	2	3.09538
Q5SX40	ENQSILITGESGAGK	**0.220640748**	2	4.71694
Q5SX40	EQYEEEQEAK	**0.093712955**	1	3.19981
Q5SX40	GQEDLKEQLAMVER	**0.346874213**	2	4.44351
Q5SX40	GSSFQTVSALFR	**0.600732091**	2	3.03157
Q5SX40	HADSVAELGEQIDNLQR	**0.082460666**	2	5.95999
Q5SX40	IAEQELLDASER	**0.113346848**	2	3.77835
Q5SX40	IEAQNKPFDAK	**0.146298106**	2	2.74858
Q5SX40	IEDEQALGMQLQK	**0.012006654**	2	4.86542
Q5SX40	IEDEQALGMQLQK+Oxidation(8)	**0.268954495**		
Q5SX40	IEDMAMMTHLHEPAVLYNLK	**0.584065656**	3	4.34008

Q5SX40	IEELEEEIEAER	**0.05757179**	2	4.26683
Q5SX40	IKLEQQVDDLEGSLEQEK	**0.036480146**	2	5.14068
Q5SX40	IKLEQQVDDLEGSLEQEKK	**0.083391034**	2	5.21932
Q5SX40	INQQLDTK	**#NUM!**	1	2.17299
Q5SX40	IQHELEEAEER	**0.052687648**	2	3.61621
Q5SX40	IQLELNQVK	**0.384812516**	2	2.78088
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	**0.447385541**	3	7.39455
Q5SX40	KIAEQELLDASER	**0.260519789**	2	3.63105
Q5SX40	KIQHELEEAEER	**0.136135018**	2	3.79712
Q5SX40	KKEFEMSNLQSK	**#NUM!**	2	4.01701
Q5SX40	KKLETDISQIQGEMEDIVQEAR	**0.377512107**	3	5.96784
Q5SX40	KLEDECSELK	**0.403114042**	2	3.0748
Q5SX40	KLEDECSELKK	**0.073054056**	3	4.25446
Q5SX40	KLETDISQIQGEMEDIVQEAR	**0.158956363**	2	5.55751
Q5SX40	KMEGDLNEMEIQLNHSNR	**0.108001364**	3	4.22466
Q5SX40	KMEGDLNEMEIQLNHSNR+Oxidation(1)	**1.430277031**		
Q5SX40	LAQESTMDVENDKQQLDEK	**0.042915091**	2	4.64862
Q5SX40	LDEAEQLALK	**0.146736204**	2	3.96244
Q5SX40	LEDECSELK	**0.270754866**	2	2.37872
Q5SX40	LEDECSELKK	**0.208763259**	2	2.88652
Q5SX40	LEEAGGATSAQIEMNK	**0.591918619**	2	4.72886
Q5SX40	LEEAGGATSAQIEMNK+Oxidation(13)	**0.411794186**		
Q5SX40	LEQQVDDLEGSLEQEK	**0.081417847**	2	5.63399
Q5SX40	LEQQVDDLEGSLEQEKK	**0.214566878**	2	4.51116
Q5SX40	LETDISQIQGEMEDIVQEAR	**0.306184504**	2	5.56219
Q5SX40	LINELTAQR	**0.129257621**	2	2.94741
Q5SX40	LLGSIDIDHTQYK	**0.152230993**	2	3.48121
Q5SX40	LQDAEEHVEAVNAK	**0.096642476**	2	4.96791
Q5SX40	LQDLVDK	**0.065583388**	1	2.13255
Q5SX40	LQDLVDKLQSK	**1.080376921**	2	2.58384
Q5SX40	LQNEVEDLMIDVER	**0.167386523**	2	4.72551
Q5SX40	LQTESGEYSR	**0.12437485**	2	2.52509
Q5SX40	LYEQHLGK	**0.49384284**	2	2.32573
Q5SX40	MEGDLNEMEIQLNHSNR	**0.109766367**	2	4.65993
Q5SX40	MEIDDLASNMEVISK	**0.165973895**	2	5.13623
Q5SX40	MEIDDLASNMEVISK+Oxidation(0)	**0.647794499**		
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	**0.124716712**	3	6.71066
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0)	**0.278469011**		
Q5SX40	NDLQLQVQSEADSLADAEER	**0.055049798**	2	6.70725
Q5SX40	NKDPLNETVVGLYQK	**0.069830452**	2	4.82221
Q5SX40	NLQQEISDLTEQIAEGGK	**0.197303272**	2	6.90575
Q5SX40	NLQQEISDLTEQIAEGGKR	**0.155032236**	2	3.74813
Q5SX40	NLTEEMAGLDETIAK	**0.055375398**	2	4.85442
Q5SX40	NLTEEMAGLDETIAK+Oxidation(5)	**0.213927411**		
Q5SX40	QAEEAEEQSNVNLAK	**0.067489446**	2	4.53789
Q5SX40	QKYEETHAELEASQK	**0.065752071**	2	4.46851
Q5SX40	QLDEKDSLVSQLSR	**0.442744656**	2	3.07626
Q5SX40	QLEEEIK	**0.829165347**	1	2.14965
Q5SX40	QREEQAEPDGTEVADK	**0.050620473**	2	3.97609
Q5SX40	RANLLQAEIEELR	**0.109289086**	2	2.33789
Q5SX40	RDLEEATLQHEATAATLR	**0.101790586**	2	4.94626
Q5SX40	SAETEKEMANMK	**0.922711533**	2	3.06434
Q5SX40	SAETEKEMANMKEEFEK	**#NUM!**	2	4.91816
Q5SX40	SELQAALEEAEASLEHEEGK	**0.142903968**	2	6.02013
Q5SX40	SLSTELFK	**0.065371971**	2	2.4124
Q5SX40	SSVFVVDAK	**0.073693431**	1	2.12507
Q5SX40	TKYETDAIQR	**0.133450028**	3	3.49354

Q5SX40	TLEDQVSELK	**0.47041251**	2	3.50689
Q5SX40	TNAACAALDKK	**0.091089859**	2	3.20022
Q5SX40	VKELTYQTEEDRK	**0.581743935**	2	3.68456
Q5SX40	VLNASAIPEGQFIDSK	**0.071310856**	2	4.42938
Q5SX40	VQLLHTQNTSLINTK	**0.002908265**	2	4.62041
Q5SX40	VRELEGEVENEQKR	**0.29637152**	3	3.88902
Q5SX40	VVESMQSTLDAEIR	**0.121649262**	2	4.08063
Q5SX40	VVESMQSTLDAEIR+Oxidation(4)	**0.908374473**		
Q5SX40	YDKIEDMAMMTHLHEPAVLYNLK	**0.599734838**	3	4.39004
Q5SX40	YEETHAELEASQK	**0.058102235**	2	4.76784
Q5SX40	YETDAIQR	**0.279890336**	2	2.57875
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.035245213**	**1.07E-10**	**5**
Q5U206	DTDSEEEIR	**1.37096718**	2	2.70737
Q5U206	KMKDTDSEEEIR	**0.4708499**	2	2.3064
Q5U206	KMKDTDSEEEIR+Oxidation(1)	**1.85070942**		
Q5U206	MKDTDSEEEIR	**0.91836162**	2	3.1043
Q5U206	MKDTDSEEEIR+Oxidation(0)	**1.684536188**		
Q5U211	**SNX3 Sorting nexin_3**	**1.105592849**	**0.959114**	**2**
Q5U211	CLHMFLQDEIIDK	**0.90509958**	2	2.37173
Q5U211	GDDGIFDDNFIEER	**0.967629045**	2	2.84278
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.314053971**	**2.89E-08**	**3**
Q5U2Q7	LSVLGAITSVQQR	**1.142222674**	2	2.40232
Q5U2Q7	YFDEISQDTGK	**1.165297861**	2	2.68238
Q5U2Q7	YVLHCQGTEEEK	**1.315486234**	2	3.63262
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.236986518**	**0.001454**	**12**
Q5U300	AAVASLLQSVQVPEFTPK	**1.124690598**	3	3.71568
Q5U300	AENYDISPADR	**0.988838452**	2	2.99153
Q5U300	DNPGVVTCLDEAR	**1.21027056**	2	3.39023
Q5U300	FEVQGLQPNGEEMTLK	**0.994231165**	2	3.89295
Q5U300	IYDDDFFQNLDGVANALDNVDAR	**0.922449416**	2	4.44969
Q5U300	LDQPMTEIVSR	**0.929058956**	2	2.62783
Q5U300	MLQTSSVLVSGLR	**0.836678325**	2	2.37229
Q5U300	NEEDATELVTLAQAVNAR	**0.924733278**	2	4.55773
Q5U300	NFPNAIEHTLQWAR	**1.122412595**	2	3.4405
Q5U300	SLPASLAEPDFVMTDFAK	**0.976977054**	2	3.54959
Q5U300	SPPAVQQDNVDEDLIR	**0.917293914**	2	4.72003
Q5U300	VVQGHQQLDSYK	**1.302538903**	2	3.92526
Q5XFX0	**TAGL2 Transgelin_2**	**0.892454702**	**0.350254**	**4**
Q5XFX0	DDGLFSGDPNWFPK	**0.936694509**	2	3.56026
Q5XFX0	QMEQISQFLQAAER	**0.905467628**	2	3.09904
Q5XFX0	TLMNLGGLAVAR	**0.58840428**	2	3.55472
Q5XFX0	YGINTTDIFQTVDLWEGK	**0.874543354**	2	5.07
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**0.976410885**	**0.141291**	**11**
Q5XHY5	AEHDSILAEK	**0.912069723**	2	2.59799
Q5XHY5	DQELYFFHELSPGSCFFLPK	**1.521151277**	3	3.41805
Q5XHY5	FLGDIEIWNQAEK	**0.854797179**	2	3.59406
Q5XHY5	FMVDIDLDPGCTLNK	**0.562633269**	2	2.97684
Q5XHY5	GFQEVVTPNIFNSR	**0.392668656**	2	3.12222
Q5XHY5	LKAEHDSILAEK	**2.882100228**	2	3.24969
Q5XHY5	NELSGALTGLTR	**1.110366807**	2	3.26631
Q5XHY5	QLENSLNEFGEK	**0.976410334**	2	3.18502
Q5XHY5	QVMVVPVGPTCDEYAQK	**0.929983574**	2	3.26796
Q5XHY5	TTPYQIACGISQGLADNTVVAK	**0.962575916**	2	4.22633
Q5XHY5	WELNPGDGAFYGPK	**0.829109893**	2	3.76151

Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.073938135**	**0.002446**	**13**
Q5XHZ0	AFLEALQHQAETSSR	**1.188476953**	2	4.58707
Q5XHZ0	AQLLQPTLEINPR	**1.082069603**	2	3.47707
Q5XHZ0	EELVSNLGTIAR	**0.87800675**	2	2.55594
Q5XHZ0	ELISNASDALEK	**1.272594138**	2	3.58824
Q5XHZ0	FEDTSPAGER	**1.219374982**	2	2.76763
Q5XHZ0	GTITIQDTGIGMTK	**1.119332618**	2	3.49362
Q5XHZ0	GVVDSEDIPLNLSR	**1.03388055**	2	4.91275
Q5XHZ0	HLAEHSPYYEAMK	**1.335091219**	2	3.28208
Q5XHZ0	LDTHPAMVTVLEMGAAR	**0.910982824**	3	4.36564
Q5XHZ0	SDCKDFANESR	**1.255638971**	2	2.75922
Q5XHZ0	VCEGQVLPEMEIHLQTDAEK	**1.16858022**	3	3.61547
Q5XHZ0	YESSALPAGQLTSLSDYASR	**1.165405082**	2	5.70764
Q5XHZ0	YIAQAYDKPR	**1.380622279**	2	2.87821
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**1.119518484**	**2.71E-10**	**7**
Q5XI22	AGHFDKEIVPVHVSSR	**0.589765812**	2	4.25156
Q5XI22	HGSNLEAMSK	**1.100792365**	2	2.77862
Q5XI22	HGSNLEAMSK+Oxidation(7)	**0.191688031**		
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	**1.29999142**	3	4.88054
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	**0.885985094**	2	4.88817
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	**1.603979617**	3	5.93363
Q5XI22	VNIDGGAIALGHPLGASGCR	**0.908448515**	2	5.82059
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**1.16738762**	**0.614958**	**7**
Q5XI32	KLEVEANNAFDQYR	**0.975457475**	2	4.47389
Q5XI32	LEVEANNAFDQYR	**1.085144893**	2	3.37179
Q5XI32	LVEDMENK	**1.7688468**	2	2.32
Q5XI32	NLSDLIDLVPSLCEDLLSSVDQPLK	**1.126054376**		
Q5XI32	SGSGTMNLGGSLTR	**0.89451603**	2	2.86866
Q5XI32	STLNEIYFGK	**1.129370779**	2	2.61034
Q5XI32	YDPPLEDGAMPSAR	**0.790157803**	2	2.52315
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.370259373**	**2.23E-08**	**3**
Q5XI60	ALDIAAGITR	**1.288666907**	2	3.58357
Q5XI60	HHVALDSAASQLSGR	**1.401423**	2	4.25848
Q5XI60	NVATDALGALEAR	**1.125694076**	2	3.8193
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.247723438**	**1.22E-12**	**6**
Q5XI73	AEEYEFLTPMEEAPK	**0.740596353**	2	4.36589
Q5XI73	LTLVCSTAPGPLELDLTGDLESFKK	**1.13037047**	3	3.31261
Q5XI73	SIQEIQELDKDDESLR	**0.518708115**	2	4.93456
Q5XI73	SIQEIQELDKDDESLRK	**0.907741101**	2	4.31992
Q5XI73	TDYMVGSYGPR	**0.875114779**	2	2.67347
Q5XI73	VAVSADPNVPNVIVTR	**1.2703621**	2	4.45444
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**1.132559644**	**1.05E-09**	**15**
Q5XI78	FGLEGCEVLIPALK	**1.135883088**	2	3.408
Q5XI78	FLDTAFDLDAFK	**1.112365176**	2	2.46875
Q5XI78	FLDTAFDLDAFKK	**0.983255533**	2	2.83962
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	**0.974121199**	3	4.43374
Q5XI78	ICEEAFTR	**1.182144517**	2	2.44077
Q5XI78	IEQLSPFPFDLLLK	**1.19346494**	2	3.61379
Q5XI78	LEAADEGSGDMK	**0.781759897**	2	2.42343
Q5XI78	NITLSLVANPSHLEAADPVVMGK	**0.993394683**	3	4.98256
Q5XI78	NTNAGAPPGTAYQSPLSLSR	**1.243444486**	2	4.52192
Q5XI78	SSLATMAHAQSLVEAQPNVDK	**1.01757259**	3	4.48031
Q5XI78	SWDIFFR	**1.018326093**	2	2.35344
Q5XI78	VIPEDGPAAQNPDK	**1.276423488**	2	3.07961

Q5XI78	VVNAPIFHVNSDDPEAVMYVCK	**1.181624146**	3	4.21129
Q5XI78	YAELLVSQGVVNQPEYEEEISK	**0.83722485**	2	4.17669
Q5XI78	YAELLVSQGVVNQPEYEEEISKYDK	**0.989703488**	3	3.80502
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**1.023249671**	**0.885002**	**5**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	**0.666168135**	2	3.88944
Q5XI95	IIAVDINK	**0.992343959**	2	2.87583
Q5XI95	MVATGVCGTDIK	**0.706550474**	2	3.22485
Q5XI95	NNICTEIR	**0.927084751**	2	2.46198
Q5XI95	TVGATDCVDPR	**0.823372055**	2	2.60179
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**1.114192691**	**0.999982**	**5**
Q5XIC0	ATQQDFENAMNQVK	**0.987998981**	2	4.76539
Q5XIC0	GILVTSEGGITK	**1.099342115**	2	3.84499
Q5XIC0	LHAVNEEECTTLR	**1.165525498**	2	3.65122
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	**1.134362996**	2	5.1551
Q5XIC0	WDAWNALGSLPK	**0.942353594**	2	3.59674
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**1.294014321**	**0.017346**	**5**
Q5XIE6	AGIATHFVDSEK	**1.110609386**	2	3.38673
Q5XIE6	AGQTLSQDLFR	**1.120424135**	2	2.38203
Q5XIE6	AVLIDKDQTPK	**1.197007055**	2	2.59476
Q5XIE6	INSCFSANTVEQILENLR	**1.238448511**	2	3.84736
Q5XIE6	LHVLEEELLALK	**1.296246376**	3	3.67972
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.155669528**	**3.98E-05**	**2**
Q5XIF3	HGWSYDVEGR	**1.179065513**	2	2.8427
Q5XIF3	LDVTPLTGVPEEHIK	**1.13929762**	3	3.6084
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.168062729**	**2.51E-05**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	**1.186294994**	2	3.76055
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	**1.032227265**	3	5.32497
Q5XIF6	DVNAAIAAIK	**1.264011416**	2	2.8803
Q5XIF6	SIQFVDWCPTGFK	**1.182840605**	2	4.34043
Q5XIF6	TIGGGDDSFTTFFCETGAGK	**3.565485705**	2	4.56433
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**0.845167712**	**0.93048**	**2**
Q5XIG4	SVPLAATSMLITQGLISK	**0.776783629**	2	3.99668
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	**1.028334804**	2	5.8947
Q5XIH7	**PHB2 Prohibitin_2**	**1.096555534**	**1.36E-07**	**11**
Q5XIH7	AQVSLLIR	**1.072516115**	2	2.77329
Q5XIH7	DLQMVNISLR	**1.433294633**	2	3.19356
Q5XIH7	FNASQLITQR	**1.001728342**	2	3.68748
Q5XIH7	IGGVQQDTILAEGLHFR	**1.153985476**	3	4.42504
Q5XIH7	IPWFQYPIIYDIR	**0.975443209**	2	2.95396
Q5XIH7	IVQAEGEAEAAK	**0.981630341**	2	4.18436
Q5XIH7	IYLTADNLVLNLQDESFTR	**1.605149843**	2	4.57549
Q5XIH7	LGLDYEER	**0.624604542**	2	2.598
Q5XIH7	LLLGAGAVAYGVR	**2.044926459**	2	3.49318
Q5XIH7	VLPSIVNEVLK	**0.928941563**	2	2.81596
Q5XIH7	VLSRPNAQELPSMYQR	**1.170356619**	2	3.83698
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.381471742**	**9.9E-20**	**9**
Q5XIM9	EALLSSAVDHGSDEVK	**1.356870447**	2	4.21115
Q5XIM9	GATQQILDEAER	**1.287435809**	2	3.90988
Q5XIM9	GSGNLEAIHVIK	**1.55436599**	2	2.91513
Q5XIM9	HGINCFINR	**1.724937506**	2	2.54006
Q5XIM9	ILIANTGMDTDK	**1.852864578**	2	2.74239
Q5XIM9	LIEEVMIGEDK	**1.151692593**	2	3.12808
Q5XIM9	NIGVDNPAAK	**1.052633984**	1	2.02664
Q5XIM9	SLHDALCVLAQTVK	**1.363206659**	2	3.7781

Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.238411576	2	4.55799
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.268275846**	**0.000231**	**6**
Q5XIN6	AAEVEGEQVDNK	1.32586952	2	4.00532
Q5XIN6	FLQDTIEEMALK	1.072506137	2	2.95835
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.923714817	2	5.47385
Q5XIN6	LEEGGPVYSPPAQVVVK	0.957898407	2	3.09571
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.39137696	3	4.42701
Q5XIN6	LLELQSIGTNNFLR	0.926153771	2	2.98879
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**1.099379212**	**0.987347**	**10**
Q5XIT9	AATGEEVSAEDLGGADLHCR	1.090534694	2	4.95342
Q5XIT9	ALVNQLHER	1.16239902	2	2.5876
Q5XIT9	ALYGDTLVTGFAR	1.043522172	2	3.67965
Q5XIT9	AQEIALQNR	1.132876797	2	2.62757
Q5XIT9	DRIDNLIDPGSPFLEFSQFAGYK	1.25329391	3	4.39028
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.086821036	3	4.43671
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.205185313	2	5.08414
Q5XIT9	LWDDGIIDPVDTR	0.867566655	2	3.26557
Q5XIT9	LYGEEEVPAGGIITGIGR	1.035648284	2	4.38006
Q5XIT9	QGTIFLAGPPLVK	2.424755086	2	2.46614
Q5XIU5	**PSMF1 Proteasome inhibitor PI31 subunit**	**1.059533712**	**0.867511**	**2**
Q5XIU5	ALIDPSSGLPNR	1.074671999	2	2.54023
Q5XIU5	DPLSPFAVGGEDLDPFGCQR	0.931637235	2	2.72864
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**0.916214974**	**6.97E-07**	**3**
Q5XIU9	FYGPAGPYGIFAGR	1.122699515	2	2.76522
Q5XIU9	GLATFCLDK	1.353092899	2	2.84896
Q5XIU9	GLCSGPGAGEESPAATLPR	0.913346779	2	4.78675
Q5XKE0	**MYPC2 Myosin_binding protein C_ fast_type**	**0.911666357**	**0.9294**	**3**
Q5XKE0	LVVEISDPDLPLK	0.893763964	2	2.82451
Q5XKE0	SEDAGELDFSGLLK	0.946018234	2	3.41882
Q5XKE0	TSDNSIVVVAGNK	0.92557865	2	2.62734
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**1.084744456**	**0.719696**	**7**
Q60587	ALAMGYKPK	0.814894675	2	2.53701
Q60587	AQDEGHLSDIVPFK	1.266163954	2	3.04021
Q60587	DFIYVSQDPK	1.143942142	2	2.67543
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.892114272	3	4.63065
Q60587	DNGIRPSSLEQMAK	1.055852658	2	3.24394
Q60587	DQLLLGPTYATPK	1.100880576	2	3.72816
Q60587	NIVVVEGVR	1.029288213	2	2.85943
Q60598	**SRC8 Src substrate cortactin**	**0.996045319**	**0.202409**	**3**
Q60598	ENVFQEHQTLK	1.807751563	2	2.30596
Q60598	NASTFEEVVQVPSAYQK	1.164526599	2	3.47649
Q60598	VDQSAVGFEYQGK	0.991181375	2	3.03171
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**1.219395008**	**2.97E-07**	**4**
Q60759	DILGGNGISDEYHVIR	0.945344509	2	3.724
Q60759	DIVYEMGELGVLGPTIK	1.354223463	2	2.37857
Q60759	GYGCAGVSSVAYGLLTR	1.078940706	2	3.49575
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.219458888	4	5.50447
Q60817	**NACA Nascent polypeptide_associated complex subunit alpha**	**1.19776234**	**1.88E-06**	**3**
Q60817	DIELVMSQANVSR	1.22721629	2	3.21888
Q60817	IEDLSQQAQLAAAEK	1.293102388	2	4.62347
Q60817	NILFVITKPDVYK	1.302252639	2	3.31638

Q60952	**CP250 Centrosome_associated protein CEP250**	**0.942597208**	**0.806042**	**2**	
Q60952	AQVIESQRGQIQDLK	**0.90025944**		2	2.48521
Q60952	GQIQDLKK	**0.966799316**		1	1.92662
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.89549068**	**0.84898**	**3**	
Q61029	SELVANNVTLPAGEQR	**0.895401453**		2	4.31801
Q61029	SSTPLPTVSSSAENTR	**0.911207693**		2	2.86167
Q61029	YGVNPGPIVGTTR	**0.863831401**		2	2.49091
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.071813199**	**0.053893**	**2**	
Q61035	ASAEQIEEEVTK	**1.001966347**		2	3.13664
Q61035	REDLVEEIR	**1.484302658**		2	2.44633
Q61043	**NIN Ninein**	**0.901242101**	**0.324759**	**2**	
Q61043	ERATAAAMKQEQEILER	**0.364327326**		2	2.34796
Q61043	NEITTLNEEDSISNLK	**0.974839087**		2	2.36942
Q61301	**CTNA2 Catenin alpha_2**	**1.181010768**	**0.504254**	**3**	
Q61301	LLEPLVTQVTTLVNTSNK	**1.033009067**		2	3.85232
Q61301	TSVQTEDDQLIAGQSAR	**1.345232253**		2	5.11628
Q61301	WDDSGNDIIVLAK	**0.92749058**		2	3.06311
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.971197983**	**0.997068**	**3**	
Q61335	AENEALAMQK	**0.987234957**		2	3.18986
Q61335	AENEALAMQK+Oxidation(7)	**1.040648835**			
Q61335	YMEENDQLK	**1.087679341**		2	2.60682
Q61595	**KTN1 Kinectin**	**1.117847115**	**0.015579**	**3**	
Q61595	EKNWEAMEALASTEK	**0.617982904**		2	2.30312
Q61595	TAEHEAAQQDLQSK	**1.133699297**		2	4.09452
Q61595	VEPVLVTK	**1.993760062**		2	2.39162
Q61656	**DDX5 Probable ATP_dependent RNA helicase DDX5**	**0.849219147**	**0.005294**	**5**	
Q61656	ELAQQVQQVAAEYCR	**1.640290159**		2	3.52502
Q61656	GDGPICLVLAPTR	**0.833303265**		2	3.29033
Q61656	LIDFLECGK	**1.025346259**		2	2.37781
Q61656	MLDMGFEPQIR	**0.77111283**		2	2.73426
Q61656	WNLDELPK	**1.160908456**		2	2.33913
Q61789	**LAMA3 Laminin subunit alpha_3**	**0.92759088**	**0.615076**	**2**	
Q61789	QLEEIK	**0.947690672**		1	2.0717
Q61789	RLQQVSPALNSLQQTLK	**0.921828953**		2	2.35809
Q61838	**A2M Alpha_2_macroglobulin**	**1.039571481**	**0.986774**	**2**	
Q61838	QQNSHGGFSSTQDTVVALQALSK	**0.945719226**		3	3.40497
Q61838	TEVNTNHVLIYIEK	**1.05639716**		2	4.01723
Q61941	**transhydrogenase_ mitochondrial**	**1.057092293**	**0.706392**	**11**	
Q61941	EANSIVITPGYGLCAAK	**1.05407803**		2	3.62171
Q61941	FGIHPVAGR	**0.969757872**		2	2.60029
Q61941	GITHIGYTDLPSR	**0.949212144**		3	3.49276
Q61941	ILIVGGGVAGLASAGAAK	**1.353021974**		2	4.98636
Q61941	KTTVLAMDQVPR	**0.975156908**		2	3.02032
Q61941	LGGLTAALGGAVGIMGLANGLR+Oxidation(14)	**0.944868692**			
Q61941	MATQASTLYSNNITK	**1.553733385**		2	4.30282
Q61941	QGFNVVVESGAGEASK	**1.114689453**		2	3.9958
Q61941	SLGAEPLEVDLK	**1.065491515**		2	3.07289
Q61941	TTVLAMDQVPR	**0.937933502**		2	3.10833
Q61941	VTIAQGYDALSSMANISGYK	**0.96509285**		2	5.16627
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.164387502**	**0.138331**	**7**	
Q62095	DLLDLLVEAK	**2.214351319**		2	2.67361
Q62095	GCHLLVATPGR	**1.20808322**		2	2.42224
Q62095	HVINFDLPSDIEEYVHR	**1.290650759**		3	3.74129
Q62095	QYPISLVLAPTR	**0.963394607**		2	2.36651
Q62095	SFLLDLLNATGK	**1.092572116**		2	4.64848

Q62095	VGNLGLATSFFNER	**1.556115132**	2	3.05471
Q62095	VGSTSENITQK	**1.440013238**	2	2.71913
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**1.141986569**	**0.568433**	**17**
Q62261	ALVADSHPESER	**1.156430926**	2	3.21483
Q62261	EGMQLISEKPETEAVVK	**0.940774754**	2	2.63316
Q62261	EIEELQSQAQALSQEGK	**1.220068278**	2	4.6206
Q62261	EVDDLEQWIAER	**0.802771872**	2	2.4694
Q62261	EVVAGSHELGQDYEHVTMLQER	**0.854149315**	3	4.18528
Q62261	HQILEQAVEDYAETVHQLSK	**0.818488633**	3	4.06203
Q62261	ITDLYTDLR	**1.108082099**	2	2.60132
Q62261	IVSSNDVGHDEYSTQSLVK	**1.257620733**	3	3.53696
Q62261	LSDGNEYLFQAK	**1.079034392**	2	2.42557
Q62261	LVSDGNINSDR	**1.175629703**	2	3.22631
Q62261	LVSQDNFGFDLPAVEAATK	**1.120646904**	2	3.10879
Q62261	SNAHYNLQNAFNLAEQHLGLTK	**1.273237055**	3	3.70162
Q62261	SQNIITDSSSLNAEAIR	**0.952222698**	2	5.18207
Q62261	TLETPAAQMEGFLNR	**1.6016895**	2	3.75248
Q62261	TQTAIASEDMPNTLTEAEK	**1.089798435**	2	5.14121
Q62261	VIESTQDLGNDLAGVMALQR	**0.294072858**	3	4.31
Q62261	VLDNAIETEK	**0.767187371**	2	2.52312
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.623768249**	**9.9E-20**	**3**
Q62425	FYSVNVDYSK	**1.637917323**	2	2.87514
Q62425	KNNPEPWNK	**0.801245267**	2	2.46735
Q62425	LGPNEQYK	**1.565177152**	2	2.30301
Q62446	**FKBP3 Peptidyl_prolyl cis_trans isomerase FKBP3**	**1.297667774**	**0.155412**	**2**
Q62446	FLQDHGSDSFLAEHK	**1.306463657**	3	3.67724
Q62446	SEETLDEGPPK	**1.155654921**	2	3.49318
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.23763669**	**0.012848**	**5**
Q62452	AMEIAEALGR	**0.900823705**	2	3.80217
Q62452	GAGVTLNVLEMTADDLENALK	**0.978698337**	3	5.54457
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(10)	**1.373021329**		
Q62452	WLPQNDLLGHPK	**1.049555488**	2	3.14135
Q62452	YTGTRPSNLAK	**0.5997532**	2	2.62148
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**1.174187986**	**0.369392**	**6**
Q62465	ACGLNFADLMGR	**0.957397227**	2	3.00273
Q62465	CLVLTGFGGYDK	**1.145120817**	2	3.43331
Q62465	GVDIVMDPLGGSDTAK	**0.896726771**	2	4.02284
Q62465	IDSVWPFEK	**0.876499098**	1	1.94734
Q62465	TVENVTVFGTASASK	**1.257126191**	2	3.88497
Q62465	VLLVPGPEKET	**0.920398097**	2	2.68148
Q62468	**VILI Villin_1**	**1.227665304**	**0.00968**	**2**
Q62468	HEDCYILDQGGLKIFVWK	**1.226300097**	2	2.46643
Q62468	SGAMSQALNFIKAK	**1.573757049**	2	2.34307
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.28189281**	**0.176812**	**3**
Q62636	INVNEIFYDLVR	**1.583922978**	2	3.99885
Q62636	QWSNCAFLESSAK	**1.18671919**	2	2.80909
Q62636	YDPTIEDSYR	**0.663734634**	2	2.3696
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**1.00113669**	**0.997838**	**7**
Q62651	HVLHVQLNRPEK	**0.996300221**	2	3.62341
Q62651	IPEEVSDHNYESIQVTSAQK	**1.311696794**	3	3.86903
Q62651	MMADEALDSGLVSR	**1.038316244**	2	3.59623
Q62651	MMADEALDSGLVSR+Oxidation(0)	**1.070193807**		
Q62651	MMADEALDSGLVSR+Oxidation(1)	**1.070193807**	2	3.35263

Q62651	RIPEEVSDHNYESIQVTSAQK	0.928589982	3	5.69513
Q62651	SLVNELTFTAR	0.989632787	2	3.47087
Q62717	**CAPS1 Calcium_dependent secretion activator 1**	**1.201890612**	**0.530993**	**2**
Q62717	IDELIEETVK	1.138487596	2	2.57976
Q62717	NCPDQDLKIK	1.279470627	1	1.93055
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**0.66496509**	**9.27E-14**	**4**
Q62730	AVLVTGADSGFGHALAK	0.531128265	2	4.1666
Q62730	EIQENYGQEYVHTQK	0.706423442	2	4.41456
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.844788666	3	4.51672
Q62730	VVTIHPGGFQTNIVGSQDSWDK	0.413803702	2	5.4331
Q62736	**CALD1 Non_muscle caldesmon**	**1.004024102**	**0.005372**	**12**
Q62736	ASGDKEAEGAPQVEAGK	0.969619174	2	4.55692
Q62736	ASGDKEAEGAPQVEAGKR	1.166445507	3	3.88134
Q62736	EEIERR	1.464631589	1	1.93664
Q62736	EFDPTITDGSLSVPSR	1.020327538	2	3.76409
Q62736	GETESEEFEK	1.142462604	2	2.75553
Q62736	GGNLGENQIKDEK	1.139538442	2	3.42812
Q62736	LEQYTNAIEGTK	1.415881238	2	3.90877
Q62736	MQNNSAENETAEGEEKGESR	1.026611632	3	4.42171
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0)	1.473166227		
Q62736	NDDDEEEAAR	1.774855768	2	3.35625
Q62736	RGETESEEFEK	1.239818044	2	3.15665
Q62736	VLEEEEQR	1.130070877	2	2.47149
Q62745	**CD81 CD81 antigen**	**0.743287677**	**0.618716**	**2**
Q62745	NSLCPSSSNSFTQLLK	0.811851682	2	2.73469
Q62745	QFYDQALQQAVMDDDANNAK	0.732615834	2	5.21496
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.000972949**	**0.573456**	**3**
Q62785	ANEEDEQEEGGDGASGDPK	0.881039791	2	4.26504
Q62785	GVEGLIDIENPNR	1.131218545	2	2.8591
Q62785	KVTQLDLDGPK	1.241587451	2	2.81109
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**1.076199614**	**0.999906**	**2**
Q62789	IILDELVQR	1.057066474	2	3.58002
Q62789	WIPQNDLLGHPK	1.049555488	2	3.14135
Q62812	**MYH9 Myosin_9**	**0.927304591**	**0.00517**	**63**
Q62812	ALEEAMEQK	0.926075043	2	3.04335
Q62812	ALELDSNLYR	1.002723432	2	3.32281
Q62812	ALEQQVEEMK	0.911364626	2	2.95956
Q62812	ANLQIDQINTDLNLER	0.885772711	2	4.67255
Q62812	ASIAALEAK	1.038008889	2	2.56477
Q62812	ASREEILAQAK	1.273126072	2	2.88878
Q62812	CQYLQAEK	1.068930626	2	2.45231
Q62812	DELADEIANSSGK	1.141261161	2	2.84885
Q62812	DFSALESQLQDTQELLQEENR	1.06111674	3	5.59496
Q62812	DLEAHIDTANK	1.174913252	2	3.22735
Q62812	DLQGRDEQSEEK	0.470712638	2	3.21968
Q62812	EEILAQAK	1.041881531	1	2.31436
Q62812	EEILAQAKENEK	1.139538442	2	2.38037
Q62812	ELEDATETADAMNR	1.038473724	2	4.12589
Q62812	ELETQISELQEDLESER	0.940134435	2	3.97725
Q62812	HEAMITDLEER	0.921796727	2	3.12554
Q62812	HEDELLAK	0.902498922	2	2.81497
Q62812	HSQAVEELAEQLEQTK	0.878497171	2	4.94481
Q62812	HSQAVEELAEQLEQTKR	1.068428209	3	4.91831
Q62812	IIGLDQVAGMSETALPGAFK	1.071561457	2	5.32892
Q62812	IRELETQISELQEDLESER	1.036464316	3	3.54975

Q62812	KEEELQAALAR	1.024643493	2	3.15066
Q62812	KKVEAQLQELQVK	0.753502844	2	4.6503
Q62812	KLEEDQIIMEDQNCK	0.97809756	2	5.90862
Q62812	KLEGDSTDLSDQIAELQAQIAELK	0.966530421	2	5.83131
Q62812	KQELEEICHDLEAR	1.030747122	2	4.49575
Q62812	KVEAQLQELQVK	1.175860155	2	4.24452
Q62812	LEEDQIIMEDQNCK	1.103626036	2	4.51432
Q62812	LEGDSTDLSDQIAELQAQIAELK	0.934697321	2	3.57377
Q62812	LEVNLQAMK	1.024716919	2	2.70956
Q62812	LQEMESAVK	0.910080379	2	2.54326
Q62812	LQQELDDLLVDLDHQR	0.911652427	2	4.78381
Q62812	LQVELDSVTGLLNQSDSK	0.996177832	2	5.73169
Q62812	LTEMETMQSQLMAEK	0.703018438	2	3.78776
Q62812	MEDGVGCLETAEEAK	1.032443689	2	4.22984
Q62812	MQQNIQELEEQLEEEESAR	0.823571628	2	6.15573
Q62812	MQQNIQELEEQLEEEESAR+Oxidation(0)	0.74489128		
Q62812	NAEQFKDQADK	1.38280406	2	3.68046
Q62812	NLPIYSEEIVDMYK	1.346323165	2	3.2137
Q62812	NMDPLNDNIATLLHQSSDK	0.912089317	2	4.60997
Q62812	NTDQASMPDNTAAQK	0.939853174	2	5.42116
Q62812	NTDQASMPDNTAAQK+Oxidation(6)	1.911045851		
Q62812	QAQQERDELADEIANSSGK	1.100530048	3	4.37909
Q62812	QIATLHAQVTDMK	0.779082792	2	2.80185
Q62812	QLEEAEEEAQR	1.076390434	2	3.68589
Q62812	QNKELK	0.947690672	1	1.92331
Q62812	QSVSNLEK	1.085741139	2	2.60139
Q62812	QTLENERGELANEVK	1.196283187	2	2.91345
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	0.950286604	3	5.4243
Q62812	RQLEEAEEEAQR	0.978180677	2	4.35204
Q62812	SMEAEMIQLQEELAAAER	1.046432826	2	4.78161
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)	1.177115716		
Q62812	TDLLLEPYNK	0.923639569	2	2.84834
Q62812	TELEDTLDSTAAQQELR	0.88859186	2	5.29411
Q62812	THEAQIQEMR	0.737563154	2	3.26961
Q62812	THEAQIQEMR+Oxidation(8)	1.634061766		
Q62812	TQLEELEDELQATEDAK	0.818899401	2	5.89373
Q62812	VAEFTTDLMEEEEK	0.97795747	2	4.1379
Q62812	VEAQLQELQVK	0.715254725	2	3.69563
Q62812	VEDMAELTCLNEASVLHNLK	1.0994942	2	4.46499
Q62812	VISGVLQLGNIVFK	1.126958954	2	2.85127
Q62812	VSHLLGINVTDFTR	1.074592732	2	3.81363
Q62812	YEILTPNSIPK	0.909184644	2	3.01111
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**0.981720587**	**1.26E-06**	**5**
Q62826	ADILEDKDGK	0.886746678	2	2.69905
Q62826	AFITNIPFDVK	1.363750001	2	3.35971
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	1.022138766	2	4.81978
Q62826	INEILSNALK	0.986823559	2	2.69234
Q62826	MGPVMDRMATGLER+Oxidation(0)	0.963552021		
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.201490189**	**0.180177**	**2**
Q62871	ADAEEEAATR	1.201407198	2	3.45693
Q62871	SVSTPSEAGSQDSGDGAVGSR	1.37848491	2	3.37343
Q62902	**LMAN1 Protein ERGIC_53**	**1.104343979**	**7.26E-06**	**6**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.064862538	2	4.30276
Q62902	GHPDLQGQPADDIFESIGDR	1.025632827	2	4.73989
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.27072139	3	4.96992

Q62902	RGAGTPGQPGQVSQQELDTVVR	1.41031625	3	4.41791
Q62902	YQEEFEHFQQELDK	1.294988279	2	4.73091
Q62902	YVSSLTEEISR	1.172319652	2	3.51167
Q62904	**DHB7 3_keto_steroid reductase**	**0.703840979**	**0.048345**	**2**
Q62904	YATDLLNVALNR	0.635870123	2	2.64844
Q62904	YLSGTTGLGTNYVK	1.263879134	2	2.93935
Q62967	**MVD1 Diphosphomevalonate decarboxylase**	**0.850064565**	**0.000808**	**2**
Q62967	GLQVAPVLLSDELK	0.709868645	2	2.81527
Q62967	VYGVEGDLSEVAR	0.855927504	2	3.13766
Q62975	**ZPI Protein Z_dependent protease inhibitor**	**0.875434316**	**0.677822**	**2**
Q62975	FKLNQRYEMHELLK	0.888540245	2	2.70348
Q62975	KMEVFFPKFK	0.86453421	1	2.06038
Q63041	**A1M Alpha_1_macroglobulin**	**0.711131553**	**5.13E-07**	**10**
Q63041	AEDITHNGIVYTPK	0.63596513	2	3.46376
Q63041	AEQGAYLGPLPYK	0.595715707	2	3.23844
Q63041	AESPVFVQTDKPIYKPGQTVK	0.689966084	3	4.73882
Q63041	DTVVKPVIVEPEGIEK	0.66893146	2	2.45709
Q63041	GSIFNSGSHVLPLEQGK	0.761298735	2	3.75082
Q63041	LQDQSNIQR	0.686043126	2	2.91617
Q63041	QDLNDNDAYSVFQSIGLK	1.694365607	2	2.78595
Q63041	QLNYQHSDGSYSTFGDR	1.038404494	2	2.64531
Q63041	YNILPEAEGEAPFTLK	0.707033727	2	4.98446
Q63041	YVVLVPSELYAGVPEK	0.815434332	2	3.07474
Q63060	**GLPK Glycerol kinase**	**1.330701455**	**7.4E-11**	**11**
Q63060	AVLGPLVGAVDQGTSSTR	1.283960005	2	5.29781
Q63060	CVFSEHGLLTTVAYK	1.06006695	2	4.01586
Q63060	DCGIPLSHLQVDGGMTSNK	1.459679869	2	3.79044
Q63060	EILQSVYECIEK	1.301441069	2	3.63543
Q63060	FEPQINAEESEIR	1.247490366	2	3.51873
Q63060	KAVLGPLVGAVDQGTSSTR	1.158123496	3	3.33706
Q63060	KVQEAVEENR	1.479820018	2	3.22344
Q63060	LGQLNIDISNIK	1.774353804	2	2.82469
Q63060	NTYGTGCFLLCNTGHK	1.393287959	2	4.14941
Q63060	TAELLSHHQVEIK	1.297263937	2	3.14925
Q63060	VQEAVEENR	1.090848225	2	3.04178
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**0.995914565**	**0.010157**	**11**
Q63081	ALDLFSDNAPPPELLEIINEDIAK	1.238167635	3	5.50354
Q63081	GESPVDYDGGR	1.058549501	2	2.85632
Q63081	GSFSEQGINEFLR	1.08798968	2	4.26786
Q63081	GSTAPVGGGSFPNITPR	1.034762191	2	4.82397
Q63081	HQSLGGQYGVQGFPTIK	0.945358762	2	5.12542
Q63081	KDVVELTDDTFDK	0.986479072	2	4.11515
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	0.980157242	4	5.21526
Q63081	NLEPEWAAAATEVK	0.966069625	2	4.08156
Q63081	NSYLEVLLK	0.99399948	2	2.72928
Q63081	TCEEHQLCVVAVLPHILDTGATGR	0.891002799	3	4.55059
Q63081	TGEAIVDAALSALR	0.986236628	3	4.58711
Q63083	**NUCB1 Nucleobindin_1**	**1.138049109**	**0.938128**	**4**
Q63083	ADTGDAPVPAPAGDQK	1.203973919	2	3.46332
Q63083	ELQQAVLQMEQR	1.184656913	2	2.64502
Q63083	LSQETEALGR	1.09442029	2	2.82832
Q63083	VNVPGSQAQLK	0.942072232	2	2.55051
Q63089	**S22A1 Solute carrier family 22 member 1**	**0.906248366**	**0.300789**	**2**
Q63089	ENTIYLQVQTGK	1.103011051	2	2.31779
Q63089	GVALPETIEEAENLGR	0.953226853	2	3.10419
Q63108	**EST3 Liver carboxylesterase 3**	**0.906022874**	**9.9E-20**	**7**
Q63108	DFNTVPYIVGINK	2.403451171	2	2.67712

Q63108	GGTSKEEINLSK	0.797772241	2	3.5401
Q63108	LDPMTATSLLK	0.786896924	2	2.5212
Q63108	MKPSTVVGDHGDEIYSVFGAPILR	0.95997082	3	3.88748
Q63108	QKTEEELLETTLK	0.921761836	2	3.57437
Q63108	SSFLLNLPEEAIPVAVEK	0.736743052	2	4.64594
Q63108	TEEELLETTLK	0.848878707	2	2.49946
Q63120	MRP2 Canalicular multispecific organic anion transporter 1	1.044950643	1.11E-16	6
Q63120	ACALLPDLEILPGGDMAEIGEK	1.489249986	2	3.49879
Q63120	ISEYINVENEAPWVTDK	1.362551364	2	3.79597
Q63120	IVEYGSPEELLSNR	1.094673993	2	3.41682
Q63120	QSQSQDVLVLEEAK	1.033091602	2	3.26679
Q63120	YFAWEPSFQEQVQGIR	1.239340755	2	4.6466
Q63120	YRPELDLVLK	1.857960795	2	2.39902
Q63150	DPYS Dihydropyrimidinase	0.989615052	0.597851	9
Q63150	DQTCTPIPVK	1.44393001	2	2.44889
Q63150	EIGAIAQVHAENGDLIAEGAK	1.046236652	2	4.99749
Q63150	FVAVTSTNAAK	1.071801156	2	3.21194
Q63150	GEVITLKPR	1.129750797	2	2.39935
Q63150	GSSLIEAFETWR	1.016736833	2	3.06013
Q63150	MLALGITGPEGHELCRPEAVEAEATLR	0.846979098	3	3.62739
Q63150	VVNDDFSQVADVLVEDGVVR	1.041150707	2	5.58906
Q63150	VVYEAGVFDVTAGHGK	1.200254608	2	3.86546
Q63150	VVYGEPIAAGLGTDGTQYWNK	1.018940126	2	5.4771
Q63270	ACOC Cytoplasmic aconitate hydratase	1.02980423	7.11E-13	16
Q63270	AVEAGLNVKPYVK	1.025423828	2	3.25515
Q63270	AVLAESYER	1.029653299	2	2.37071
Q63270	FVEFFGPGVAQLSIADR	1.393921422	2	5.20144
Q63270	GFQVAPDHHNDHK	3.004894579	2	3.25163
Q63270	IDFEKEPLGVNAQGQQVFLK	0.937890146	3	4.68742
Q63270	KNDIENILNWSIMQHK	0.900339674	3	4.65231
Q63270	NCDEFLVK	0.979463349	1	2.04897
Q63270	NQDLEFER	0.874355279	2	2.47958
Q63270	QAPQTVHLPSGETLDVFDAAER	0.736465966	3	3.70148
Q63270	SIEVPFKPAR	1.079956752	2	2.58927
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.373068057	3	5.09333
Q63270	SPPFFESLTLDLQPPK	1.325500813	3	3.88698
Q63270	SWNALAAPSEK	1.019380674	1	2.32543
Q63270	TSLSPGSGVVTYYLR	1.769523168	2	3.47017
Q63270	VILQDFTGVPAVVDFAAMR	1.504837585	3	4.48324
Q63270	YQQAGLPLIVLAGK	1.052292811	2	3.53971
Q63276	BAAT Bile acid_CoA:amino acid N_acyltransferase	1.022527891	4.03E-09	17
Q63276	AHGHFLFVVGEDDKNLNSK	2.649855987	2	5.83522
Q63276	ASEVGEVDLER	0.939020222	2	3.86987
Q63276	DDKGNLFNSQAFYR	1.030466668	2	3.29866
Q63276	GNLFNSQAFYR	1.151683325	2	3.04861
Q63276	LCHPYFPVEGK	1.315148695	2	2.65694
Q63276	LTAVPLSALVDEPVHIR	1.376884934	2	4.11165
Q63276	NWTLLSYPGAGHLIEPPYSPLCSASR	1.666311591	2	4.05783
Q63276	QHLNPGFNSQL	1.125875483	2	3.54745
Q63276	QITATVLINGPNFVSSNPHVYR	0.9515338	3	5.2485
Q63276	TFEETADK	0.993861214	1	1.97533
Q63276	TFEETADKDSK	1.00249207	2	3.92625
Q63276	VDLEYFEEGVEFLLR	1.349434593	3	4.79588
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.145050719	2	5.3075
Q63276	VISSSLDSLILER	0.656779649	2	3.53714

Q63276	VTGLTPFQVVCLQASLK	**1.479140333**	3	5.32743
Q63276	WYVAPGVTR	**0.754198595**	2	2.65423
Q63276	YCFPIEK	**1.076826781**	2	2.59594
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.024997922**	**0.756094**	**24**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	**0.949861826**	3	5.97022
Q63342	AWGSEMNCDTNPLEAGLDYFIK	**1.113354016**	2	4.50319
Q63342	DGLLFGPYESQEK	**1.175825363**	2	2.61695
Q63342	EGQESPPSPPEWK	**1.028843961**	2	2.67632
Q63342	GGYDVEIR	**0.882802481**	2	2.30616
Q63342	GQDSTQLLDHLCANVIPK	**0.978878403**	2	4.02243
Q63342	IMNAGQEEGIDNFGTYALNALR	**1.209648903**	2	4.87588
Q63342	ISDIPVTAIR	**1.100057427**	2	3.23237
Q63342	ITEHVEAAMEMVPVLK	**0.979049321**	2	3.92702
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	**1.031005228**	3	5.17343
Q63342	LEEETGQVVGFHQPGSIR	**1.047355488**	2	4.76727
Q63342	LNKPADFTGK	**1.35996773**	2	2.63623
Q63342	LTSEDLSDDVFK	**1.265817249**	2	4.14795
Q63342	NITDELGVLGVAGPYAR	**0.980722102**	2	4.8318
Q63342	NYPATIIQEPLVLTEPTR	**1.19462959**	2	4.1668
Q63342	REDSAALYER	**1.668259765**	2	3.23052
Q63342	SLAFAYVPVELSEVGQQVEVELLGK	**1.854616845**	3	4.97281
Q63342	TNWHATEQYIIEPEK	**1.339511682**	2	4.15339
Q63342	VGFTNISHMLTPR	**1.243957095**	2	2.40229
Q63342	VGVIDLSPFGK	**0.949687842**	2	3.39948
Q63342	VIGNTTSGSYSYSIQK	**1.336059029**	2	4.33414
Q63342	WIEEAAVR	**1.331371414**	2	2.76197
Q63342	WTTTQYTEAK	**0.980375509**	2	2.81355
Q63342	YLSDWILHGEPPFDLIELDPNR	**1.126619466**	3	4.34608
Q63347	**PRS7 26S protease regulatory subunit 7**	**1.038576935**	**0.835927**	**8**
Q63347	ALDEGDIALLK	**1.015837261**	2	3.09461
Q63347	ESDTGLAPPALWDLAADK	**1.247246**	2	2.50809
Q63347	FDDGAGGDNEVQR	**1.120452177**	2	4.17522
Q63347	FVVDLSDQVAPTDIEEGMR	**1.194966264**	2	3.85636
Q63347	IINADSEDPK	**1.002667214**	2	3.04787
Q63347	QTLQSEQPLQVAR	**0.951622147**	2	4.00159
Q63347	QVEDDIQQLLK	**1.075268921**	2	2.44174
Q63347	TMLELINQLDGFDPR	**0.803564416**	2	2.96498
Q63355	**MYO1C Myosin_Ic**	**0.202673745**	**0.459599**	**2**
Q63355	MSLLQLVEILR	**0.90501781**	2	2.51188
Q63355	YMDVQFDFKGAPVGGHILSYLLEK+Oxidation(1)	**0.180934128**		
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.164570028**	**1.54E-05**	**4**
Q63362	KLENLLQGGEVEEVILQAEK	**1.224363935**	2	6.6786
Q63362	KYTEQITSEK	**1.077239092**	2	2.42624
Q63362	TTGLVGLAVCDTPHER	**1.112023953**	2	3.47604
Q63362	YTEQITSEK	**1.220539179**	2	2.45256
Q63413	**DX39B Spliceosome RNA helicase Ddx39b**	**1.080111025**	**0.284286**	**2**
Q63413	AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK	**0.41378103**	3	3.79947
Q63413	NCPHIVVGTPGR	**1.127516315**	2	3.04963
Q63429	**UBC Polyubiquitin_C**	**1.017894729**	**0.606206**	**3**
Q63429	ESTLHLVLR	**1.417797618**	2	2.42756
Q63429	TITLEVEPSDTIENVK	**1.017577279**	2	4.71716
Q63429	TLSDYNIQK	**1.163137369**	2	2.54878
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.037206121**	**0.153752**	**10**
Q63448	ADWLDSEAPLAAYR	**0.962373394**	2	4.2478
Q63448	DDAVALVDAIAPSDFVLGSPIGR	**1.039997582**	3	4.14246

Q63448	EIHALASAGKPLASWTAQR	0.757806795	2	4.0964
Q63448	GGYISGEQTGK	0.930859147	2	2.92069
Q63448	NLWAAVLQQSGVLER	0.921313324	2	4.46384
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.883597148	3	3.50254
Q63448	TIFLDLIELQR	1.033695566	2	3.38361
Q63448	TIFSTLENDPLFARPFGADLPLEK	0.971766612	3	4.51285
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.109303653	3	4.54265
Q63448	TVNFLEAYPGILGQK	1.122920896	2	4.61562
Q63507	RL14 60S ribosomal protein L14	1.375813368	0.000407	3
Q63507	ALVDGPCTR	1.145883048	2	2.41594
Q63507	CMQLTDFILK	0.828632725	2	2.55185
Q63507	LVAIVDVIDQNR	1.410016344	2	4.12626
Q63524	TMED2 Transmembrane emp24 domain_containing protein 2	1.087774636	0.92542	3
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.003295619	3	5.36974
Q63524	HEQEYMEVR	1.025969035	2	3.33628
Q63524	HEQEYMEVR+Oxidation(5)	1.166829191		
Q63525	NUDC Nuclear migration protein nudC	1.124576806	0.080337	4
Q63525	GQAPVIDGELYNEVK	1.124756089	2	3.45482
Q63525	LSDLDSETR	0.233850352	2	2.66515
Q63525	LVTSDPEINTK	1.161677188	2	2.39567
Q63525	VEESSWLIEDGK	0.91510045	2	3.01153
Q63569	PRS6A 26S protease regulatory subunit 6A	0.984697439	0.018466	5
Q63569	AMEVDERPTEQYSDIGGLDK	1.561062556	3	3.65665
Q63569	CTDDFNGAQCK	0.956724358	2	3.33225
Q63569	MNVSPDVNYEELAR	1.04897765	2	3.30961
Q63569	MSTEEIVQR	0.886564059	2	2.40452
Q63569	QTYFLPVIGLVDAEK	1.18577896	2	2.731
Q63570	PRS6B 26S protease regulatory subunit 6B	1.487607611	0.036543	4
Q63570	GVLMYGPPGCGK+Oxidation(3)	1.530226612		
Q63570	IQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR	1.651532602	3	5.44205
Q63570	KDEQEHEFYK	1.323974021	2	2.95609
Q63570	RFDAQTGADR	1.239859598	2	2.60998
Q63584	TMEDA Transmembrane emp24 domain_containing protein 10	0.992092707	0.000685	4
Q63584	ITDSAGHILYAK	1.521712112	2	3.31452
Q63584	LEDLSESIVNDFAYMK	1.084645114	2	2.92805
Q63584	NYEEIAK	0.981795465	1	2.26636
Q63584	RLEDLSESIVNDFAYMK	1.030035437	2	3.82911
Q63598	PLST Plastin_3	0.958929505	0.79533	11
Q63598	AESMLQQADK	0.971694594	2	2.87922
Q63598	ATDDIIVNWVNGTLSEAGK	0.951297124	3	4.94958
Q63598	AVGDGIVLCK	1.026870319	1	1.95156
Q63598	HVIPMNPNTDDLFK	0.764747919	2	2.78276
Q63598	IDINMSGFNETDDLKR	0.944283359	2	4.33792
Q63598	INNFSADIK	1.461436116	2	2.57839
Q63598	KLENCNYAVELGK	1.012253907	2	3.92307
Q63598	NEALAALLR	0.976409484	2	2.74548
Q63598	VYALPEDLVEVKPK	0.944023157	2	2.9615
Q63598	YPALTKPENQDIDWTLLEGETR	0.959426709	3	5.17703
Q63598	YTLNVMEDLGEGQK	1.07666669	2	3.69883
Q63610	TPM3 Tropomyosin alpha_3 chain	1.314428243	9.9E-20	8
Q63610	EQAEAEVASLNR	1.58011329	2	2.86572
Q63610	IQVLQQQADDAEER	1.321276707	2	5.12711
Q63610	KIQVLQQQADDAEER	1.317609731	2	5.41034
Q63610	KLVIIEGDLER	1.010374262	2	2.77177
Q63610	LVIIEGDLER	0.85378103	2	2.48203

Q63610	MELQEIQLK	**0.761633797**	2	3.02132
Q63610	TIDDLEDKLK	**1.185609351**	2	2.86161
Q63610	YSQKEDKYEEEIK	**0.757057189**	2	4.67772
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**0.985094027**	**8.41E-05**	**16**
Q63617	AANSLEAFIFETQDK	**0.983104276**	2	3.30339
Q63617	DAVITVPAFFNQAER	**1.120666047**	2	2.33381
Q63617	EGETPDEKESGDKSEAQKPNEK	**1.606382853**	3	3.7704
Q63617	ESGDKSEAQKPNEK	**0.896016797**	2	2.34861
Q63617	FLGDSAAGMAIK	**1.017306572**	2	2.64795
Q63617	LEDLTLR	**1.080353625**	2	2.37397
Q63617	LGNTISSLFGGGTSSDAK	**1.094909973**	2	3.30243
Q63617	LIPEMDQIFTDVEMTTLEK	**0.993809686**	2	2.78257
Q63617	LYQPEYQEVSTEEQR	**1.679869812**	2	5.05907
Q63617	NINADEAAAMGAVYQAAALSK	**1.100771468**	2	2.9936
Q63617	SLAEDFAEQPIK	**1.174514702**	2	2.73523
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	**1.021268187**	3	3.91786
Q63617	TLGGLEMELR	**1.045469139**	2	2.30642
Q63617	VEFEELCADLFDR	**0.769953929**	2	3.89708
Q63617	VESVFETLVEDSPEEESTLTK	**1.216042916**	2	4.21553
Q63617	VLQLINDNTATALSYGVFR	**1.451339389**	2	2.94727
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**1.013002412**	**0.122706**	**2**
Q63692	EGEEAGPGDPLLEAVPK	**0.833596694**	2	3.57768
Q63692	LGPGGLDPVEVYESLPEELQK	**0.908776732**	2	2.6856
Q63716	**PRDX1 Peroxiredoxin_1**	**1.221949736**	**9.9E-20**	**15**
Q63716	ADEGISFR	**1.188304645**	2	3.06872
Q63716	ATAVMPDGQFK	**0.971626957**	2	2.94384
Q63716	DISLSDYK	**1.621735593**	2	2.50514
Q63716	HGEVCPAGWKPGSDTIKPDVNK	**1.12869737**	4	6.2281
Q63716	IGHPAPSFK	**3.171498014**	1	1.93211
Q63716	KLNCQVIGASVDSHFCHLAWINTPK	**5.063921637**	4	4.57212
Q63716	KQGGLGPMNIPLVSDPK	**1.341239919**	2	4.1357
Q63716	LNCQVIGASVDSHFCHLAWINTPK	**1.684779751**	3	3.65366
Q63716	LVQAFQFTDK	**3.45460511**	2	3.53237
Q63716	QGGLGPMNIPLVSDPK	**0.738928727**	2	3.47951
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6)	**1.403742824**		
Q63716	QITINDLPVGR	**1.019713037**	2	3.30839
Q63716	RTIAQDYGVLK	**1.192999444**	2	2.53211
Q63716	SVDEILR	**1.072757696**	2	2.69928
Q63716	TIAQDYGVLK	**1.143738341**	2	3.24734
Q63768	**CRK Adapter molecule crk**	**1.120516025**	**0.207031**	**2**
Q63768	IGDQEFDSLPALLEFYK	**1.063090531**	2	3.29237
Q63768	VPNAYDKTALALEVGELVK	**1.343974699**	2	2.31718
Q63797	**PSME1 Proteasome activator complex subunit 1**	**1.214852228**	**3.09E-13**	**10**
Q63797	EPALNEANLSNLK	**0.565041253**	2	2.40053
Q63797	ISELDAFLK	**0.873605246**	2	2.81907
Q63797	ISELDAFLKEPALNEANLSNLK	**0.842032942**	3	6.05589
Q63797	KGDEDDKGPPCGPVNCNEK	**0.952392863**	3	4.80137
Q63797	KISELDAFLKEPALNEANLSNLK	**0.987725068**	3	5.73396
Q63797	LEGFQTQISK	**0.985662538**	2	3.01388
Q63797	NAYAVLYDIILK	**1.548149915**	2	2.88382
Q63797	QLVHELDEAEYQEIR	**0.964557004**	3	4.66005
Q63797	TENLLGSYFPK	**0.870819647**	2	3.60702
Q63797	VDVFREDLCSK	**0.92466143**	2	2.38701
Q63798	**PSME2 Proteasome activator complex subunit 2**	**1.036953593**	**0.539433**	**6**
Q63798	AFYAELHHIISSNLEK	**1.196629802**	2	3.97855

Q63798	IEDGNDFGVAIQEK	0.928218606	2	4.24792
Q63798	IISLSQLLQEDSLNVADLSSLR	1.654536979	2	2.33724
Q63798	KIISLSQLLQEDSLNVADLSSLR	1.050150064	3	3.44549
Q63798	TKVEAFQTAISK	0.959595144	2	3.45529
Q63798	VEAFQTAISK	0.96940484	2	2.61206
Q63836	**SBP2 Selenium_binding protein 2**	**1.233698344**	**1.44E-05**	**5**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.279747394	3	5.46247
Q63836	GSFVLLDGETFEVK	1.135999166	2	2.44633
Q63836	IYVVDVGSEPR	1.198570741	2	3.95932
Q63836	LNPNFLVDFGK	1.022884927	2	2.73046
Q63836	LNPNFLVDFGKEPLGPALAHELR	1.206295169	3	4.31012
Q63945	**SET Protein SET**	**1.041084504**	**0.677577**	**3**
Q63945	IDFYFDENPYFENK	1.095148288	2	3.85618
Q63945	LNEQASEEILK	1.040881867	2	2.72548
Q63945	VEVTEFEDIK	0.654028281	2	2.56745
Q63965	**SFXN1 Sideroflexin_1**	**1.172702454**	**0.072232**	**6**
Q63965	MSGEVPPNINIKEPR+Oxidation(0)	0.80857193		
Q63965	NILLTNEQLENAR	1.039322802	2	4.47525
Q63965	QAITQVVISR	0.795345856	2	2.43131
Q63965	QGIVPAGLTENELWR	0.590096334	2	2.97243
Q63965	WDQSTFIGR	1.44121792	2	2.83348
Q63965	YAYDSAFHPDTGEK	1.375238198	2	4.07131
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**0.905111676**	**9.9E-20**	**17**
Q64057	AWNIWADIPAPK	0.892103686	2	3.94756
Q64057	EDNEGVFNGSWGGR	0.961934397	2	3.6378
Q64057	EGGTVVYGGK	1.424575637	2	2.45401
Q64057	FKNEEEVFEWNNEVK	1.020347548	2	5.45816
Q64057	GAPTTSLVSIAVTK	0.865108188	2	4.21345
Q64057	GEVITTYCPANNEPIAR	1.027086724	2	5.08541
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.901212679	2	5.64964
Q64057	LFLHESIHDEVVDR	1.482967362	2	4.21817
Q64057	NEEEVFEWNNEVK	0.883825304	2	4.54194
Q64057	QAVSMFVQAVEEAK	1.048209737	2	3.08438
Q64057	QGLSSSIFTK	1.137583247	2	2.56742
Q64057	QVALMVQER	0.815419898	2	2.3021
Q64057	STCTINYSTALPLAQGIK	2.32334905	2	4.67803
Q64057	VGNPWDPNILYGPLHTK	1.179852472	3	4.14142
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	0.791743491	3	6.09222
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1)	0.890157286		
Q64057	VNLLSFTGSTQVGK	1.711225176	2	4.87519
Q640L5	**CCD18 Coiled_coil domain_containing protein 18**	**0.455681889**	**0.089025**	**2**
Q640L5	EVIDLGQELR	0.574795623	2	2.35531
Q640L5	SMQLSQLDMVLDQTKTELEKTTNSVK	0.037594831	3	3.60115
Q64119	**MYL6 Myosin light polypeptide 6**	**1.039915158**	**0.280748**	**6**
Q64119	DQGTYEDYVEGLR	1.380945541	2	3.35106
Q64119	HVLVTLGEK	0.970094518	1	2.29393
Q64119	ILYSQCGDVMR	1.660893736	2	2.68829
Q64119	NKDQGTYEDYVEGLR	0.941982871	2	4.19482
Q64119	VFDKEGNGTVMGAEIR	0.263571228	2	3.51766
Q64119	VLDFEHFLPMLQTVAK	0.941141341	2	4.94335
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**0.843552657**	**0.922666**	**2**
Q64122	DGFIDKEDLHDMLASLGK	0.872685719	2	4.72261
Q64122	LNGTDPEDVIR	1.110382013	2	2.8867
Q64176	**EST22 Liver carboxylesterase 22**	**0.796763387**	**9.9E-20**	**4**

Q64176	AISESGVALTAGLVK	**0.727611824**	2	3.88749
Q64176	EGYLQIGATTQQAQK	**0.977822249**	2	4.58786
Q64176	LDQMTAMSLLK+Oxidation(3)	**0.699318721**		
Q64176	NFNTVPYIVGINK	**2.665034265**	2	3.45523
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.120951655**	**0.442756**	**9**
Q641Y0	ELGSECGIEFDEEK	**1.355372797**	2	3.52384
Q641Y0	GVGMVADPDNPLVLDILTGSSTSYSFFPDKPITQYPHAVGR	**3.370244939**	4	6.9834
Q641Y0	NTLLIAGLQAR	**1.151744625**	2	3.8193
Q641Y0	SSLNPILFR	**1.783483129**	2	2.41136
Q641Y0	TADDPSLSLIK	**0.913738338**	2	2.71421
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	**1.149474239**	4	6.54632
Q641Y0	TLVLLDNLNVR	**1.109591684**	2	3.84659
Q641Y0	WVPFDGDDIQLEFVR	**1.000533933**	2	2.73482
Q641Y0	YSQTGNYELAVALSR	**1.029918505**	2	3.45372
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.206948733**	**0.353863**	**5**
Q641Y2	GSGIQWDLR	**1.041555104**	2	2.54724
Q641Y2	IDEVEEMLTNNR	**1.126749575**	2	3.63135
Q641Y2	IIEQCLNK	**1.232186474**	2	2.88313
Q641Y2	LYTEGYQVPPGATYTAIEAPK	**1.885252249**	2	2.94636
Q641Y2	TQPYDVYDQVEFDVPIGSR	**1.37809616**	2	3.99239
Q641Y8	**DDX1 ATP_dependent RNA helicase DDX1**	**1.047863226**	**0.580783**	**3**
Q641Y8	GDVRFLICTDVAAR	**1.038962803**	2	2.34389
Q641Y8	GHVDILAPTVQELAALEK	**0.99346814**	3	3.88094
Q641Y8	GSAFAIGSDGLCCQSR	**1.1656615**	2	3.70012
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**1.172186836**	**0.010436**	**4**
Q64232	HYEVEIR	**0.712364119**	2	2.31196
Q64232	LCFLDKVEPQATISEIK	**0.98451433**	2	4.69075
Q64232	SLKDEDVLQK	**0.913374595**	2	3.33814
Q64232	VEPQATISEIK	**0.932305124**	2	2.37388
Q64240	**AMBP Protein AMBP**	**1.005218702**	**0.995145**	**3**
Q64240	AFAELWAFDAAQGK	**1.097385761**	2	3.52613
Q64240	AVLPQENEGSGSEPLITGTLK	**1.008394864**	2	4.84444
Q64240	TIAACNLPIVQGPCR	**0.890588806**	2	3.26343
Q642G4	**PEX14 Peroxisomal membrane protein PEX14**	**1.600859328**	**1.44E-10**	**2**
Q642G4	GGDGQINEQVEK	**1.611829914**	2	3.13669
Q642G4	LLGPQEEGEGVVDVK	**1.307402375**	2	3.42698
Q64303	**PAK2 Serine/threonine_protein kinase PAK 2**	**1.020901152**	**0.990145**	**2**
Q64303	NKIISIFSSTEK	**1.021291228**	2	2.80564
Q64303	SVIDPIPAPVGDSNVDSGAK	**0.953089589**	2	2.83295
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.106395551**	**0.477462**	**19**
Q64380	AYGIESHVLSPAETK	**1.012916533**	2	4.58825
Q64380	DGTMDPAGTCTTLTR	**1.258764776**	2	4.07169
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	**1.398509271**	3	5.6525
Q64380	DLYPLMNVDDLYGTLYVPR	**0.93221961**	2	2.56496
Q64380	EEAQGASVVPQGPSQPLPSTANVVVIGGGSLGCQTLYHLAK	**1.058701502**	3	3.59246
Q64380	FHHSLTDHPR	**0.945457316**	2	2.65239
Q64380	FYLLGADAR	**1.121809665**	2	2.6833
Q64380	GAQVIENCAVTGIR	**1.353891852**	2	4.17718
Q64380	HGLVNAGYR	**1.06434193**	2	2.57539
Q64380	IEGIQNMPNVR	**0.863615869**	2	3.32422
Q64380	LQGDALSVGGYEANPIFWDEVSDK	**0.740618642**	2	4.45822

Q64380	NGDYALER	1.036028074	2	2.31016
Q64380	NYSVVFPHDEPLAGR	0.931894787	2	3.98492
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.883024472	3	4.6555
Q64380	RDPLHEELLGQGCVFQER	0.934672468	3	5.59101
Q64380	SDDSPLEAGLAFTCK	1.324421351	2	2.65763
Q64380	STVCGPESFTPDHKPLMGEAPELR	0.833860169	3	4.37825
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16)	1.181483498		
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.898296027	3	5.09061
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**1.192626319**	**0.004225**	**29**
Q64428	ADMVIEAVFEDLAVK	0.820936026	2	3.96758
Q64428	ALMGLYNGQVLCK	0.968114051	2	3.30813
Q64428	DSIFSNLIGQLDYK	1.644773955	2	3.47851
Q64428	DTTASAVAVGLK	1.163531352	2	3.639
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	1.568553534	3	5.40583
Q64428	EVQSEFVEVMNEIWANDQIR	1.14648902	3	4.22174
Q64428	FGELALTK	1.062479812	2	3.01537
Q64428	FGGGSVELLK	1.250881122	2	3.06003
Q64428	FVDLYGAQK	1.167414768	2	2.91645
Q64428	GFYIYQSGSK	2.300338361	2	2.83543
Q64428	ILQEGVDPK	1.034413953	2	3.29022
Q64428	KLDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.026003492	4	5.09656
Q64428	KTVLGVPEVLLGILPGAGGTQR	1.059366769	2	4.31656
Q64428	KYESAYGTQFTPCQLLR	1.073525444	2	5.01266
Q64428	LDALTTGFGFPVGAATLADEVGIDVAQHVAEDLGK	1.152592688		
Q64428	LPAKPEVSSDEDIQYR	2.153582456	2	4.40606
Q64428	MGLVDQLVDPLGPGIK	0.844546789	2	5.01588
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0)	1.056572949		
Q64428	MQLLEIITTDK	0.844793443	2	3.93187
Q64428	MQLLEIITTDK+Oxidation(0)	1.097941319		
Q64428	MVGVPAAFDMMLTGR	0.962845511	2	3.25629
Q64428	NLNSEIDNILVNLR	1.039256416	2	4.71098
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	0.922460633	3	3.90935
Q64428	SPKPVVAAISGSCLGGGLELAIACQYR	1.192851293	3	3.64185
Q64428	TGLEQGNDAGYLAESEK	1.163882334	2	4.99164
Q64428	TIEYLEEVAVNFAK	1.139556375	3	4.20218
Q64428	TVLGVPEVLLGILPGAGGTQR	1.009565923	3	5.11971
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.956104449	3	6.42192
Q64428	YESAYGTQFTPCQLLR	1.116724293	2	4.80864
Q64458	**CP2CT Cytochrome P450 2C29**	**0.953346647**	**0.314954**	**6**
Q64458	EHKESLDVTNPR	0.869286138	2	3.29154
Q64458	IKEHKESLDVTNPR	0.782828699	3	5.07395
Q64458	LPPGPTPLPIIGNFLQIDVK	1.017327084	2	4.00473
Q64458	VQEEAQCLVEELR	1.016294176	2	4.38759
Q64458	VQEEAQCLVEELRK	1.118909327	2	3.85862
Q64458	VQEEIDR	0.901812743	2	2.41025
Q64481	**CP3AG Cytochrome P450 3A16**	**2.86945485**	**0.000257**	**3**
Q64481	EMFPVIEQYGDILVK	2.290617708	2	3.03167
Q64481	GSIDPYVYLPFGNGPR	2.886167937	2	3.93122
Q64481	VLQNFSFQPCK	3.625279025	2	2.78399
Q64541	**AT1A4 Sodium/potassium_transporting ATPase subunit alpha_4**	**1.208885949**	**0.195273**	**2**
Q64541	LIIVEGCQR	1.208892614	2	2.67852
Q64541	NLEAVETLGSTSTICSDK	1.200944207	2	3.08079
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.167806002**	**0.100582**	**5**
Q64550	GHEVVVIAPEASIHIK	1.222423387	2	4.88927
Q64550	LLVIPIDGSHWLSMLGVIQQLQQK	1.379389227	3	4.47012

Q64550	NMIIALTENFLCR	**1.150159617**	2	4.3491
Q64550	SVFDQDPFLLR	**1.261767058**	2	3.18485
Q64550	VVYSPYGSLATEILQK	**1.455689254**	2	5.12502
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**0.681540784**	**0.962264**	**3**
Q64560	ACVDSNENGDLGK	**0.828200153**	2	3.43313
Q64560	DPVQVAAPSDHGVGIEPVFPENTENSEK	**0.756211381**	3	3.84838
Q64560	GTLIEAFPVLGGK	**0.975854905**	2	2.60173
Q64563	**ADH4 Alcohol dehydrogenase 4**	**0.87417127**	**0.967533**	**12**
Q64563	AAVDCTVVGWGSCTVVGAK	**1.088804121**	2	3.86454
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	**0.731569014**	3	5.24605
Q64563	ALGATDCLNPR	**0.839900899**	2	3.21828
Q64563	FDLDLLVTHALPFDK	**0.866128827**	3	4.31322
Q64563	INDAIDLMNQGK	**0.966759874**	2	3.39668
Q64563	KFDLDLLVTHALPFDK	**0.852295447**	3	4.82955
Q64563	SVDSVPNLVTDYK	**0.642715619**	2	4.37303
Q64563	TDSPLCIEEIEVSPPK	**1.104200694**	2	3.7853
Q64563	VCLIGCGFTSGYGAAINTAK	**0.855020777**	2	3.6703
Q64563	VDDEANLER	**0.889407454**	2	2.82535
Q64563	VDEMNISTVDMILGR	**0.70664067**	2	3.48002
Q64563	VIATCVCPTDINATNPK	**0.756347177**	2	4.75418
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**0.956921862**	**2.7E-08**	**13**
Q64565	AYSNHTDIISFR	**1.142137124**	2	3.37099
Q64565	GGNFSQTFR	**1.063293768**	2	2.50495
Q64565	GGVCIADEVQTGFGR	**1.027947405**	2	4.3541
Q64565	GIGNGFPMAAVVTTPEIASSLAK	**1.010515218**	2	4.63791
Q64565	LRDEFDIVGDVR	**1.082876061**	2	2.88366
Q64565	LSALLPEPLK	**1.866409542**	2	2.781
Q64565	NSQEVGTYMLLK	**0.331452307**	2	2.85787
Q64565	SALTQHMER	**1.518109768**	2	2.5307
Q64565	SALTQHMER+Oxidation(6)	**1.302458071**		
Q64565	TEVNQIHEDCK	**1.092094759**	2	2.99731
Q64565	TEVNQIHEDCKDMGLLVGR	**0.93857903**	2	5.52199
Q64565	VIFLVNSGSEANDLAMVMAR	**1.04616358**	2	4.69543
Q64565	YIEQFK	**0.816458409**	1	2.15976
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**0.563811743**	**0.004195**	**8**
Q64578	AVGIVATTGVSTEIGK	**0.059722112**	2	3.47383
Q64578	DIVPGDIVEVAVGDKVPADIR	**1.597758322**	2	3.76057
Q64578	DQMAATEQDKTPLQQK	**#NUM!**	2	3.94277
Q64578	EFDDLPLAEQR	**1.077791664**	2	2.6858
Q64578	IGIFSENEEVADR	**0.483927336**	2	3.04172
Q64578	IRDQMAATEQDKTPLQQK	**#NUM!**	3	3.71547
Q64578	TGTLTTNQMSVCK	**0.224780076**	2	2.87647
Q64578	VGEATETALTTLVEK	**0.191478967**	2	4.78459
Q64581	**CP3AI Cytochrome P450 3A18**	**1.60428494**	**7E-07**	**5**
Q64581	AITMSEDEEWKR	**1.24028888**	2	2.31139
Q64581	EEAKGEPINMK	**1.854275647**	2	2.33676
Q64581	LAVIGVLQNFNIQPCEK	**1.489051679**	3	3.32051
Q64581	NPEYWLEPEEFNPER	**1.641389696**	2	4.13357
Q64581	TILSPTFTSGK	**1.137495428**	1	1.93756
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.835065559**	**0.09237**	**12**
Q64591	ATAEEITSK	**0.838119959**	2	2.90629
Q64591	CDVRDPDMVHNTVLELIK	**0.755633144**	4	4.87332
Q64591	DPDMVHNTVLELIK	**0.858685831**	3	3.74667
Q64591	EEWDVIEGLIR	**1.127825553**	2	3.74057

Q64591	FDGGEEVFLSGEFNSLKK	**1.357682749**	2	2.93922
Q64591	FNIIQPGPIK	**1.268165323**	2	2.67085
Q64591	LGTVEELANLATFLCSDYASWINGAVIR	**1.812782995**		
Q64591	NIDVLK	**1.047287433**	1	2.09025
Q64591	SLAAEWGR	**0.988371123**	2	2.67044
Q64591	VAFITGGGTGLGK	**1.189290805**	2	2.78525
Q64591	VAGHPDVVINNAAGNFISPSER	**2.666574981**	2	6.10114
Q64591	VTKEEWDVIEGLIR	**0.854206724**	3	4.78486
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**1.356492718**	**2.55E-15**	**10**
Q64602	ASFSQVTPAQMDLVFQR	**1.176044347**	2	4.20712
Q64602	DIISLAPGSPNPK	**1.419659588**	2	3.05068
Q64602	EILLVPGNSFFVDNSAPSSFFR	**1.200941398**	2	3.58613
Q64602	FLTATSLAR	**0.913654059**	2	2.4063
Q64602	FLYTIPNGNNPTGNSLTGDR	**1.350950684**	2	4.01121
Q64602	GLAEWHVPK	**1.309059285**	2	2.44902
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	**1.330291**	3	5.77446
Q64602	SAVFTVENGSTIR	**1.378625827**	2	3.43684
Q64602	VGFITGPK	**1.495211925**	1	1.91019
Q64602	VLSQWKPEDSKDPTKR	**1.361295382**	3	3.65928
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**0.891750199**	**0.091017**	**11**
Q64611	AQGGQGLEWR	**0.890657846**	2	3.21345
Q64611	CHGSQASYLFQQDK	**2.003345489**	2	4.35272
Q64611	FFNQLFSGLDPHALAGR	**2.043497273**	3	4.20116
Q64611	FYNVALDTGDK	**1.165638079**	2	3.26816
Q64611	GAAFLGLGTDSVR	**0.479466808**	2	3.0769
Q64611	IDQAFALTR	**0.998946892**	2	3.06152
Q64611	MVVANPILVQADIDFLLGELER	**0.983831765**		
Q64611	QLLDLELQSQGESR	**0.82087764**	2	3.83763
Q64611	TLDGDPVAVEALLR	**0.857209275**	2	4.50006
Q64611	VCEWKEPEELK	**0.790510735**	3	3.69759
Q64611	YLVEEIK	**0.922497671**	1	2.39147
Q64638	**UD15 UDP_glucuronosyltransferase 1_5**	**1.074153678**	**0.997957**	**3**
Q64638	GHQAVVLAPEVTVHIK	**0.997257429**	3	3.50293
Q64638	VVFETGNYVK	**1.048320476**	2	2.35689
Q64638	YESLASELLQR	**1.090808056**	2	3.19719
Q64640	**ADK Adenosine kinase**	**1.184043357**	**9.9E-20**	**12**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	**1.632003634**	3	6.76561
Q64640	AATFFGCIGIDK	**0.603499996**	2	3.04507
Q64640	AGHYAASVIIR	**1.084576464**	3	3.5786
Q64640	FGEILK	**1.116232601**	2	2.42788
Q64640	FKVEYHAGGSTQNSMK	**1.224840487**	2	3.02652
Q64640	HKELFDELVK	**1.316259621**	3	3.79028
Q64640	HLDLENNWMLVEK	**1.075543734**	2	3.78828
Q64640	SLVANLAAANCYK	**1.182203528**	2	4.73786
Q64640	VEAPEALSENVLFGMGNPLLDISAVVDKDFLDK	**0.891384594**		
Q64640	VEYHAGGSTQNSMK	**1.288212822**	2	4.05084
Q64640	VEYHAGGSTQNSMK+Oxidation(12)	**1.862085895**		
Q64640	YSLKPNDQILAEDK	**1.326373473**	3	4.9591
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.816702597**	**2.01E-07**	**7**
Q64654	EPAEDILQTLLDSTYK	**0.870990766**	2	3.91997
Q64654	GVAYDVPNAVFLEQK	**0.717383681**	2	3.22698
Q64654	NEDLNAEEVYGR	**0.707754598**	2	4.10677
Q64654	SGLNIAHFK	**1.029586418**	2	2.96609
Q64654	TPQTVAGYTIPPGHQVCVSPTVNQR	**0.667063853**	3	3.94804
Q64654	TVCGEDLPPLTYEQLK	**0.45344429**	2	4.07286
Q64654	YLQDNPASGEK	**0.477258939**	2	2.61559

Q65CL1	**CTNA3 Catenin alpha_3**	**1.216584694**	**0.12984**	**2**
Q65CL1	MISESGSRMDVLAR+Oxidation(0)	1.399948068		
Q65CL1	NLMNAVVQTVK	0.765130613	2	2.88861
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**1.083067804**	**0.99617**	**3**
Q66H12	CNINCEEDPK	0.957710495	2	2.71152
Q66H12	INQDPLGIQGR	1.128538393	2	3.10928
Q66H12	TISPQNIDILQNPLLIK	1.072779658	2	2.35776
Q66H15	**RMD3 Regulator of microtubule dynamics protein 3**	**0.817165022**	**0.80773**	**3**
Q66H15	AEELQPGFSK	0.941485137	2	2.65595
Q66H15	AIELQPEDPR	0.979940377	2	2.34243
Q66H15	SLQGLAGEIVGEVR	0.750706177	2	2.75521
Q66H80	**COPD Coatomer subunit delta**	**1.015648384**	**4.42E-05**	**5**
Q66H80	GVQLQTHPNVDKK	1.162188503	2	3.43442
Q66H80	LFTAESLIGLK	1.300833599	2	2.82305
Q66H80	NSNILEDLETLR	1.133803352	2	3.07653
Q66H80	NTLEWCLPVIDAK	0.85940388	2	2.8581
Q66H80	VTQVDGNSPVR	0.564204332	2	2.93924
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.078810602**	**0.583046**	**9**
Q66HA8	AGGIETIANEFSDR	1.077300535	2	2.85137
Q66HA8	FQEAEERPR	0.788566243	2	2.4802
Q66HA8	FVVQNVSAQK	0.947796407	2	2.38714
Q66HA8	IARFFGKDVSTTLNADEAVAR	0.740776776	2	2.317
Q66HA8	NQQITHANNTVSSFK	1.333661963	2	4.57023
Q66HA8	SVLDAAQIVGLNCLR	1.013074564	2	3.4562
Q66HA8	TEEVSAIEIVGGATR	0.763221941	2	3.40805
Q66HA8	VLGTAFDPFLGGK	1.020854254	2	3.09885
Q66HA8	YNHIDESEMKKVEK	0.857132708	2	2.6129
Q66HD0	**ENPL Endoplasmin**	**1.068949444**	**5.34E-09**	**28**
Q66HD0	DISTNYYASQK	1.82666932	2	2.99786
Q66HD0	EATEKEFEPLLNWMK	1.419217596	2	2.83089
Q66HD0	EEASDYLELDTIK	0.94602412	2	4.20767
Q66HD0	EEEAIQLDGLNASQIR	0.629445416	2	4.39888
Q66HD0	EFEPLLNWMK	1.215936571	2	2.34777
Q66HD0	EVEEDEYK	1.073034547	1	2.65895
Q66HD0	FQSSHHSTDITSLDQYVER	1.26995761	3	5.64654
Q66HD0	GLFDEYGSK	1.084683562	2	2.46386
Q66HD0	GVVDSDDLPLNVSR	0.98206329	2	4.92011
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	1.701758505	3	3.96357
Q66HD0	KEAESSPFVER	1.187090753	2	3.17381
Q66HD0	LGVIEDHSNR	1.140830764	2	3.35855
Q66HD0	LISLTDENALAGNEELTVK	1.230150614	2	5.50101
Q66HD0	LTESPCALVASQYGWSGNMER	1.043075408	2	5.47659
Q66HD0	LTESPCALVASQYGWSGNMER+Oxidation(18)	1.455782394		
Q66HD0	NLLHVTDTGVGMTR	0.972555974	2	3.98749
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11)	1.219361327		
Q66HD0	SGTSEFLNK	1.143696064	2	3.20172
Q66HD0	SGYLLPDTK	1.102245658	2	3.21639
Q66HD0	SILFVPTSAPR	0.982593483	2	3.28606
Q66HD0	TDDEVVQR	1.057761673	2	3.31275
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	0.831878511	3	5.45004
Q66HD0	TETVEEPLEEDETAQEEK	1.503085554	2	5.23895
Q66HD0	TFEINPR	1.086776951	2	2.40278
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.156532116	3	3.31746
Q66HD0	VFITDDFHDMMPK	0.955889034	2	3.84075
Q66HD0	YNDTFWK	1.175156884	1	2.10129
Q66HD0	YSQFINFPIYVWSSK	0.69545046	2	3.32529

Q66HD3	**NASP Nuclear autoantigenic sperm protein**	**1.21793927**	**0.207094**	**2**
Q66HD3	LSETKDGASVEEVK	1.210675622	2	2.43013
Q66HD3	QDTLMKVVEIEAEIDSEVK+Oxidation(4)	1.259272035		
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.20456748**	**3.94E-08**	**11**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.202698784	2	5.15308
Q66HF1	AVTEGAQAVEEPSIC	1.1988135	2	3.18532
Q66HF1	DDGAAILAAVSSIAQK	1.065128517	2	4.51357
Q66HF1	FASEIAGVDDLGTTGR	1.538867412	2	4.08559
Q66HF1	FEAPLFNAR	1.08110616	2	2.66087
Q66HF1	GLLTYTSWEDALSR	1.186573762	2	3.59014
Q66HF1	ILQDIASGNHEFSK	1.393810506	2	4.19279
Q66HF1	LGEVSPNLVR	1.484850043	2	2.96134
Q66HF1	LVDQEFLADPLVPPQLTIK	1.109582127	2	3.11014
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.927073686	2	4.28746
Q66HF1	YDHLGDSPK	1.411021471	2	2.57672
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.567632229**	**1.45E-05**	**11**
Q66HF8	EEIFGPVQPLFK	1.108148196	2	3.03915
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.444862708	3	3.45682
Q66HF8	LAPALATGNTVVMK	1.514966371	2	3.29989
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.302678945	2	4.79442
Q66HF8	TFVEESIYHEFLER	0.980820593	2	3.74106
Q66HF8	VAEQTPLSALYLASLIK	3.60237015	2	3.60616
Q66HF8	VAFTGSTEVGHLIQK	2.638105499	2	3.2719
Q66HF8	VGNPFELDTQQGPQVDK	0.992282253	2	3.7966
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.313597553	2	4.49579
Q66HF8	YGLAAAVFTR	1.064990566	2	3.08483
Q66HF8	YNQLFINNEWHDAVSK	2.169825166	2	3.53633
Q66HG4	**GALM Aldose 1_epimerase**	**0.739887426**	**9.9E-20**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	0.799086062	2	4.37411
Q66HG4	TVFGELPSGGGAVEK	0.739616464	2	3.67771
Q66HG4	VSPDGEEGYPGELK	0.872722337	2	3.92519
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.393495333**	**9.9E-20**	**20**
Q66X93	ADDADEFGYSR	2.148005836	2	2.54936
Q66X93	ALLLPDHYLVTVMLSGIK	1.007044325	3	4.24561
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.208055835	3	4.31644
Q66X93	DTNGENIAESLVAEGLASR	1.148837861	2	5.02528
Q66X93	ETDGSETPEPFAAEAK	1.726663148	2	3.8061
Q66X93	GDVGLGLVK	1.26194591	2	2.43039
Q66X93	HFVDSHHQKPVNAIIEHVR	1.124456753	3	4.05658
Q66X93	LEGDNIQDK	1.122515213	2	2.86089
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.881528312	2	5.53666
Q66X93	SAYYKPLLSAEEAAK	1.421382408	2	3.22313
Q66X93	SDISSHPPVEGAYAPR	1.017644763	3	4.72485
Q66X93	SEAVVEYVFSGSR	1.929613878	2	3.34742
Q66X93	SSHYDELLAAEAR	1.350443069	2	3.52983
Q66X93	TCATVTIGGINIAEALVSK	0.897305871	2	3.51229
Q66X93	TDAVDSVVR	1.196870788	2	2.68014
Q66X93	VADISGDTQK	0.72148834	2	2.48051
Q66X93	VITEYLNAQESAK	1.583523685	2	3.84381
Q66X93	VMQVLNADAIVVK	1.098810994	2	2.87852
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.325311862	3	5.6224
Q66X93	VWAHYEEQPVEEVMPVLEEK	1.116708477	3	3.98202
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.939089706**	**4.25E-06**	**8**
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.683173749	3	3.77782

Q68FP2	HNNWDLTPVK	**0.910679624**	2	2.97745
Q68FP2	IFLMDLNEPYPK	**0.90189384**	2	3.19641
Q68FP2	IQDPLSDNPR	**1.105438067**	2	3.12731
Q68FP2	LLIYNPEDPPGSEVLR	**1.272457819**	2	4.05847
Q68FP2	VIQLGTLVDNLTVDPATGDILAGCHPNPMK	**1.098899152**	3	4.76885
Q68FP2	VVAQGFSSANGITVSLDQK	**0.688490519**	2	3.36783
Q68FP2	YVYVADVTAK	**0.933763413**	1	3.0049
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**1.074532307**	**9.85E-05**	**6**
Q68FQ0	GSNDMQYQHVIETLIGK	**1.480554006**	2	3.13906
Q68FQ0	HKLDVTSVEDYK	**0.683496629**	2	3.20126
Q68FQ0	ISDNVLVDINNPEPLIQTAK	**1.251236899**	2	5.18883
Q68FQ0	LDVTSVEDYK	**1.041601389**	2	2.37197
Q68FQ0	SLHDALCVIR	**1.047024807**	2	2.48198
Q68FQ0	WVGGPEIELIAIATGGR	**1.219764615**	2	3.90363
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.179073422**	**5.08E-13**	**9**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	**0.963222235**	2	5.13939
Q68FR6	ALIAAQYSGAQIR	**1.51339343**	2	3.71291
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	**1.663453216**	2	4.25128
Q68FR6	ILGLLDTHLK	**1.332475033**	2	2.7697
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	**1.278795227**	3	3.80665
Q68FR6	KLDPGSEETQTLVR	**1.177989861**	2	3.86326
Q68FR6	LDPGSEETQTLVR	**1.139945614**	2	3.65357
Q68FR6	STFVLDEFKR	**1.103266548**	2	2.47988
Q68FR6	WFLTCINQPQFR	**1.112202786**	2	3.13921
Q68FR9	**EF1D Elongation factor 1_delta**	**1.091122484**	**1.95E-06**	**6**
Q68FR9	ATAPQTQHVSPMR	**1.109674373**	2	3.56202
Q68FR9	FYEQMNGPVTAGSR	**1.108966298**	2	4.41828
Q68FR9	GVVQDLQQAISK	**1.120860993**	2	3.75427
Q68FR9	SIQLDGLVWGASK	**1.056628486**	2	3.26676
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	**1.230818908**	2	5.5184
Q68FR9	VGTDLLEEEITK	**1.242345407**	2	3.48491
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**1.013052745**	**0.648993**	**3**
Q68FS2	NAAQVLVGIPLETGQK	**0.504993609**	2	2.69173
Q68FS2	QDLAQLMNSSGSHK	**1.305023876**	2	2.392
Q68FS2	VISFEEQVASIR	**1.015856142**	2	2.4258
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.054274745**	**9.9E-20**	**18**
Q68FS4	ADMGGAATICSAIVSAAK	**0.809407971**	2	5.50463
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2)	**1.002950256**		
Q68FS4	DKDDDVPQFTSAGENFNK	**1.218512412**	2	4.93933
Q68FS4	GITFDSGGISIK	**1.1682508**	2	3.30458
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	**1.755599058**	3	5.80549
Q68FS4	GVLFASGQNLAR	**2.107805416**	2	3.29177
Q68FS4	LFEASVETGDR	**1.048260769**	2	3.37451
Q68FS4	LHGSGDLEAWEK	**0.981635311**	2	3.65086
Q68FS4	LILADALCYAHTFNPK	**1.483611291**	2	3.98519
Q68FS4	LNLPINIIGLAPLCENMPSGK	**1.697205117**	2	5.03961
Q68FS4	QLMESPANEMTPTR	**0.797859049**	2	3.78398
Q68FS4	QVIDCQLADVNNLGK	**0.945814678**	2	4.97908
Q68FS4	SAGACTAAAFLR	**1.085034844**	2	3.50243
Q68FS4	SAGVDDQENWHEGK	**1.107726782**	2	3.74839
Q68FS4	SWIEEQEMGSFLSVAK	**0.995465469**	2	5.36845
Q68FS4	TFYGLHQDFPSVVVVGLGK	**0.918967408**	2	5.41698
Q68FS4	TIQVDNTDAEGR	**0.998451931**	2	3.79548
Q68FS4	TLIEFLLR	**1.005758635**	2	2.59873
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**1.133163903**	**0.221794**	**4**
Q68FT1	INDAMNMGHTAK	**0.117034936**	2	3.03589

Q68FT1	LNHVLEEEQK	1.133990391	3	3.43442
Q68FT1	STGEALVQGLMGAAVTLK	1.059225212	2	3.00385
Q68FT1	YTDQSGEEEEDYESEEQIQHR	1.066846418	3	4.68909
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**1.112653184**	**0.062155**	**7**
Q68FT3	HVIGGAAVTEEIIPGFK	1.322208336	2	3.5708
Q68FT3	ISQLDTQSPVTK	1.53148603	2	3.42086
Q68FT3	SLLLGTDVAENQK	1.262067651	2	3.9395
Q68FT3	TLGAQLPQYYEVLTAPISK	1.117748745	2	4.26023
Q68FT3	VFDCIEAYAPGFK	1.051811968	2	2.85397
Q68FT3	VLDQWFESEPLK	0.929093885	2	2.8491
Q68FT3	VQGVVLQGGEEVR	1.385817079	2	3.59248
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.325870993**	**9.9E-20**	**10**
Q68FT5	AGADVLQTFTFSAAEDR	5.102560172	2	2.65547
Q68FT5	AGANIIGVNCR	1.114283678	2	3.4781
Q68FT5	AGLWTPEAVVEYPSAVR	1.2040235	2	3.44539
Q68FT5	AIAEELAPER	1.915442637	2	3.77836
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.324921861	3	4.46239
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.012588529	3	4.07553
Q68FT5	FGPWTSLQTMK	0.94441685	2	2.81407
Q68FT5	GGFVDLPEYPFGLEPR	1.129559347	2	4.10431
Q68FT5	LDSGEVVVGDGGFLFTLEK	0.884028058	2	3.92254
Q68FT5	YIGGCCGFEPYHIR	4.027528661	2	4.71075
Q68FT9	**SCLY Selenocysteine lyase**	**0.925618562**	**1.61E-10**	**4**
Q68FT9	AEVDLIVQDLK	0.773394132	2	3.88386
Q68FT9	NFRPGTENTPMIAGLGK	0.940823635	2	3.34996
Q68FT9	RVDVEDLGVDFLTIVGHK	1.28950368	3	5.54775
Q68FT9	VLVHTDAAQALGK	0.915410626	2	2.47323
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.979794116**	**8.2E-10**	**11**
Q68FU3	AGDLGVDLTSK	1.130890814	2	3.63603
Q68FU3	EIIAVSCGPPQCQETIR	1.220929775	2	4.7821
Q68FU3	GIHVEVPGAEAENLGPLQVAR	1.140987621	2	6.04354
Q68FU3	HSMNPFCEIAVEEAVR	0.939336993	2	5.25471
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2)	1.318235544		
Q68FU3	QAIDDDCNQTGQMTAGLLDWPQGTFASQVTLEGDKVK	0.948947233	3	5.08575
Q68FU3	RVIDFAVK	1.028431496	2	2.80461
Q68FU3	VDLLFLGK	1.547324913	2	2.80443
Q68FU3	VETTEDLVAK	0.947936475	2	3.35748
Q68FU3	VIDFAVK	1.144361924	2	2.41245
Q68FU3	VSVISVEEPPQR	1.11813816	2	3.45446
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.413974288**	**0.000406**	**9**
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.168473476	3	5.63043
Q68FY0	IEEVDAQMVR	0.941505295	2	3.60625
Q68FY0	LCTSATESEVTR	1.49682898	2	3.27799
Q68FY0	NALISHLDGTTPVCEDIGR	1.024618376	2	4.51354
Q68FY0	NNGAGYFLEHLAFK	1.069371462	2	3.37124
Q68FY0	RIPLAEWESR	1.361103732	2	2.60424
Q68FY0	TDLTDYLSR	1.345854059	2	2.82008
Q68FY0	VVELLADIVQNISLEDSQIEK	1.237003999	3	6.90851
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.342019341	2	4.9627
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.972872997**	**0.384377**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	1.028449171	2	4.67076

Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	0.94210418	3	3.92464
Q68G31	GESGGQTTPYDFYSR	1.431586413	2	3.96384
Q68G31	LQPTDSFSQSSCFGLR	0.735155599	2	3.66837
Q68G31	NVNSTLTFVTLSGELK	1.26289768	2	4.28893
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	0.912890244	3	6.26812
Q68G31	VNTEPLPGIEK	1.267598286	2	2.41228
Q69Z23	**DYH17 Dynein heavy chain 17_ axonemal**	**1.15144757**	**0.439698**	**2**
Q69Z23	MNILTNEMRRSLK+Oxidation(0)	0.629929042		
Q69Z23	YFIDLLMEK	1.31544975	1	2.1417
Q69ZH9	**RHG23 Rho GTPase_activating protein 23**	**1.041330326**	**0.094063**	**2**
Q69ZH9	LEPMDTIFVKNVK	0.783048054	2	2.43207
Q69ZH9	SRAEAEGPGAGTARACPR	1.050297794	2	2.38005
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.140649583**	**0.019052**	**2**
Q6A0A9	SQGGVQPIPSQGGK	1.190586036	2	3.09581
Q6A0A9	VEGSSTASSGSQLAEGK	1.138591886	2	4.28055
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**1.673156576**	**0.003706**	**3**
Q6AXM8	FQEEENSLLHLK	0.512764122	2	2.71573
Q6AXM8	LFVYDPNHPPSSEVLR	1.037667716	2	2.49138
Q6AXM8	WANVVYYSPEEVK	5.197907331	2	3.55318
Q6AXN3	**TMED5 Transmembrane emp24 domain_containing protein 5**	**1.148792829**	**0.580115**	**2**
Q6AXN3	LEDILESINSIK	1.631123691	2	3.85077
Q6AXN3	LEDILESINSIKSR	0.855009157	2	2.50144
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.814260182**	**0.426127**	**3**
Q6AXS5	EETQPPVALKK	0.780160608	2	2.38963
Q6AXS5	FDQLFDDESDPFEVLK	0.806010993	2	4.3778
Q6AXS5	SAAQAAAQTNSNAAGK	0.627515217	2	4.43278
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.889608152**	**0.501227**	**2**
Q6AXY0	FLQPGSQR	0.886002236	2	2.42099
Q6AXY0	YFPAFEK	0.904864977	1	1.91853
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.195530102**	**0.070116**	**3**
Q6AY09	ATENDIYNFFSPLNPMR	1.372948095	2	2.68978
Q6AY09	HTGPNSPDTANDGFVR	1.045288514	2	4.40161
Q6AY09	STGEAFVQFASQEIAEK	1.319330964	2	4.3869
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**1.127888247**	**0.307267**	**6**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	1.096295133	3	4.39994
Q6AY30	ATLVLNCVGPYR	1.128702004	2	2.6135
Q6AY30	GGGVFTPGAAFSR	0.924534531	2	2.43447
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.060777398	2	4.23115
Q6AY30	LQQVLEK	1.240967014	1	2.01573
Q6AY30	SVSNLKPVPVIGSK	0.97147194	2	3.83544
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.167498382**	**3.87E-08**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	1.116849726	2	4.75739
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.345034408	2	4.99984
Q6AY56	LISQIVSSITASLR	1.334548226	2	3.41579
Q6AY56	NLDIERPTYTNLNR	1.228374834	2	3.19049
Q6AY56	QLFHPEQLITGK	0.870027128	2	2.41771
Q6AY56	TIQFVDWCPTGFK	1.359761612	2	3.78633
Q6AY56	VGINYQPPTVVPGGDLAK	1.018043452	2	4.52958
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**1.326906917**	**0.879107**	**3**
Q6AY80	NDVTGALSNPEVFK	1.138980597	2	3.85471
Q6AY80	VLAPQISFGPEVSSEEQR	1.411363792	2	4.37001
Q6AY80	VLCQGFAFDVPGFYDSGFLK	1.188656628	2	3.49006

Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**0.856586554**	**0.700621**	**4**
Q6AYG5	DVLETLWGGPANLEAIAK	**0.91150826**	2	3.02389
Q6AYG5	ILEQFPGGSIDLQK	**0.837252586**	2	3.13588
Q6AYG5	NTFCSGSDLNAVK	**0.855561807**	2	2.58786
Q6AYG5	VIELENWTEGK	**1.247062014**	2	2.94889
Q6AYH5	**DCTN2 Dynactin subunit 2**	**0.947801334**	**0.590732**	**3**
Q6AYH5	ASVEDADTQNK	**0.727909526**	2	2.34203
Q6AYH5	VNALDLAVLDQVEAR	**1.194927369**	2	2.8145
Q6AYH5	WSPVASTLPELVQR	**0.878966583**	2	2.9953
Q6AYM2	**TEKT2 Tektin_2**	**0.572479873**	**0.150719**	**2**
Q6AYM2	RLEEDLR	**1.282155155**	1	1.94702
Q6AYM2	TNTMLLDTKCMDIR+Oxidation(3)	**0.555951432**		
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.981356959**	**1**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	**0.934438649**	2	4.4939
Q6AYQ8	NLHHEVELGVLLGR	**1.039873238**	3	4.13517
Q6AYQ8	SFTSSCPVSAFVPK	**0.912048236**	2	4.08079
Q6AYR8	**SCRN2 Secernin_2**	**0.881132181**	**0.066854**	**2**
Q6AYR8	GLLTGEQTPAPQELGSLFQAFVER	**1.46773961**	3	4.15368
Q6AYR8	QEQQSLEQEGLEALR	**0.862749312**	2	4.00839
Q6AYS7	**ACY1A Aminoacylase_1A**	**1.393735592**	**6.02E-08**	**2**
Q6AYS7	EMNLTLEPEIFPAATDSR	**0.965268287**	2	4.70136
Q6AYS7	ICTVQPNPDYGSAVTFLEER	**2.650892285**	2	4.5171
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**1.240828366**	**7.33E-05**	**4**
Q6AYS8	ALTDELAALGCTGVR	**0.972807689**	2	3.73116
Q6AYS8	FDAVVGYK	**1.308155077**	1	2.22986
Q6AYS8	MIFVPGSIALLTVLER	**1.124450123**	2	2.76771
Q6AYS8	SVAGEIVLITGAGHGIGR	**0.975119969**	2	3.98321
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.415182549**	**0.132387**	**4**
Q6AYT9	AFIVLSPAYVSHDPEALTR	**0.408411358**	2	4.36903
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	**0.365955183**	2	3.79195
Q6AYT9	NDDVINSSSYR	**0.657783889**	2	2.58825
Q6AYT9	TGVVMIPGISQLTQK	**0.701764105**	2	2.44424
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.314054233**	**9.9E-20**	**5**
Q6AYZ1	AVFVDLEPTVIDEVR	**1.283390529**	2	5.03055
Q6AYZ1	DVNAAIATIK	**1.179290311**	2	3.0616
Q6AYZ1	IHFPLATYAPVISAEK	**1.480092284**	2	3.41383
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	**1.604084041**	2	5.39696
Q6AYZ1	VGINYQPPTVVPGGDLAR	**1.307142979**	2	4.83777
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**1.300974382**	**5.93E-11**	**7**
Q6DGG1	AVAIDLPGLGR	**0.943813503**	2	3.48767
Q6DGG1	FSSETWQNLGTLHR	**1.143804924**	2	3.45856
Q6DGG1	FSVLLLHGIR	**1.091141424**	2	2.6252
Q6DGG1	GYVPVAPICTDK	**0.924237003**	1	2.68742
Q6DGG1	INAADYAR	**1.046604631**	2	2.46132
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	**1.581360173**	2	4.98716
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK+Oxidation(12)	**1.841805928**		
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.963631091**	**0.996816**	**2**
Q6EDY6	IENYLLR	**0.963498534**	2	2.52352
Q6EDY6	SSDAHELGEGDEKKK	**0.977987836**	2	2.35917
Q6EJB6	**UT14B U3 small nucleolar RNA_associated protein 14 homolog B**	**0.925859851**	**0.805017**	**2**
Q6EJB6	ARMTERMSLK+Oxidation(2)	**0.931944877**		
Q6EJB6	EAAFSKTSQMLSR+Oxidation(9)	**0.85760159**		

Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.690412277**	**0.044707**	**2**
Q6GQP4	CDLSDIREVPLK	**0.689231268**	2	2.39166
Q6GQP4	CDLSDIREVPLKDAK	**1.060319268**	2	2.73757
Q6GQT1	**A2MP Alpha_2_macroglobulin_P**	**3.114525902**	**1.91E-05**	**2**
Q6GQT1	IQEEGTGVEETGK	**3.922209309**	2	3.79656
Q6GQT1	QLSFPLSSEPTQGSYK	**1.416579966**	2	2.81778
Q6GQT9	**NOMO1 Nodal modulator 1**	**1.061544625**	**0.99121**	**2**
Q6GQT9	SSIDSEPALVLGPLK	**1.081741522**	2	3.05894
Q6GQT9	VQVVVPEAETR	**1.03635184**	2	2.48435
Q6I7R3	**ISOC1 Isochorismatase domain_containing protein 1**	**0.883739185**	**8.13E-07**	**3**
Q6I7R3	GLGSTVQEIDLTGVK	**0.882224948**	2	4.14159
Q6I7R3	ILGIPVIITEQYPK	**1.538382875**	2	3.05421
Q6I7R3	YFGDIISVGQR	**1.005421974**	2	2.86428
Q6IE47	**ISK6 Serine protease inhibitor Kazal_type 6**	**1.214369185**	**0.415613**	**2**
Q6IE47	CAFCKALEK	**1.238458384**	1	1.98006
Q6IE47	LFQINCGEFRDPK	**0.915279278**	2	2.41053
Q6IE52	**MUG2 Murinoglobulin_2**	**0.846239368**	**0.003086**	**14**
Q6IE52	AHFSVMGDILSSAIK	**0.737815733**	2	3.50124
Q6IE52	HTSSWLVTPK	**0.782131702**	2	2.6749
Q6IE52	LPSSEEEESLDINIEGAK	**1.015378295**	2	4.66044
Q6IE52	MLIYTILPDGEVIADSVK	**0.849154556**	2	3.81204
Q6IE52	MLSGFIPLKPTVK+Oxidation(0)	**1.177315302**		
Q6IE52	MNRIMQWQDVK+Oxidation(0)	**0.301964985**		
Q6IE52	NLYPLKELVQDPK	**0.890030738**	1	2.07993
Q6IE52	QLSFSLSAEPIQGPYK	**0.873939826**	2	4.08766
Q6IE52	QQNSHGGFSSTQDTVVALDALSK	**0.981741466**	3	3.52174
Q6IE52	VHLSFSPSQSLPASQTHMR	**0.847079811**	3	3.41412
Q6IE52	VKTVPLTCNNPK	**0.835599432**	2	2.90261
Q6IE52	VTASPQSLCGLR	**0.937124722**	2	2.88674
Q6IE52	YMVLVPSQLYTETPEK	**0.69298586**	2	3.57746
Q6IE52	YMVLVPSQLYTETPEK+Oxidation(1)	**0.813637702**		
Q6IFW6	**K1C10 Keratin_ type I cytoskeletal 10**	**1.139090649**	**0.393062**	**2**
Q6IFW6	LENEIQTYR	**1.476408595**	2	2.51745
Q6IFW6	QSLEASLAETEGR	**0.902620515**	2	2.75606
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.875814539**	**0.035201**	**4**
Q6IMF3	TNAENEFVTIK	**0.527446829**	2	2.95292
Q6IMF3	TNAENEFVTIKK	**0.096985362**	2	2.42696
Q6IMF3	WELLQQVDTSTR	**0.706859363**	2	3.62636
Q6IMF3	YEELQITAGK	**0.882965169**	2	3.47039
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**0.991825199**	**0.617332**	**5**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	**1.051543839**	3	5.37987
Q6IRK9	GEESAVMVVPR	**0.783643558**	2	2.42094
Q6IRK9	IVVYNQPYTDYGK	**1.570196483**	2	3.37105
Q6IRK9	TYPDTDSFNTVAEITGSK	**0.99375996**	2	3.79761
Q6IRK9	VGAVASLIR	**0.890473906**	2	2.51637
Q6KCD5	**NIPBL Nipped_B_like protein**	**0.929268941**	**0.239422**	**2**
Q6KCD5	AFLISLLNLFDDTAK	**1.723559944**	2	2.5985
Q6KCD5	QNNTRSENTKARPETPK	**0.529069814**	2	2.56682
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.932278328**	**0.142074**	**4**
Q6MGB5	AGVIGLTQTAAR	**0.922671385**	2	3.33472
Q6MGB5	GSIINISSIVGK	**1.076378192**	2	2.58135
Q6MGB5	SALALVTGAGSGIGR	**1.26376336**	2	3.15708
Q6MGB5	VGNIGQTNYASSK	**2.451410665**	2	2.36694
Q6NS46	**RRP5 Protein RRP5 homolog**	**0.989466669**	**0.80087**	**2**
Q6NS46	GKQTKSTEVPR	**0.937933502**	2	2.67829
Q6NS46	IIDYSQMDELALLSLR	**1.193760946**	2	2.37047

Q6NSR8	**PEPL1 Probable aminopeptidase NPEPL1**	**1.179046472**	**0.55102**	**2**
Q6NSR8	HNSPSAAHFITR	0.753075341	3	3.55737
Q6NSR8	TVEINNTDAEGR	0.83743817	2	2.69394
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.348870774**	**0.456471**	**3**
Q6NYB7	EFADSLGIPFLETSAK	1.654372413	2	3.61645
Q6NYB7	MGPGATAGGAEK	0.807886943	2	2.92138
Q6NYB7	NATNVEQSFMTMAAEIK	1.152880455	2	4.61945
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.137217952**	**6.53E-06**	**9**
Q6NZJ6	DLDFAKAKPRMDQYFNQMEK+Oxidation(10)	0.798899686		
Q6NZJ6	GLPLVDDGGWNTVPISK	0.982591229	2	2.94948
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.289529845	3	3.4728
Q6NZJ6	IHNAENIQPGEQK	1.179075072	2	4.17509
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.365782182	3	3.58037
Q6NZJ6	LGIESTLER	0.992433172	2	2.37394
Q6NZJ6	LKEELEEAR	1.095286759	2	2.67357
Q6NZJ6	QVTQLAIDTEER	1.22229513	2	2.85452
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.837363822	3	4.77662
Q6P0K8	**PLAK Junction plakoglobin**	**0.948398458**	**0.822338**	**2**
Q6P0K8	LLNDEDPVVVTK	0.947436377	2	2.97931
Q6P0K8	NLALCPANHAPLQEAAVIPR	1.329225128	3	3.68432
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.088423796**	**6.96E-11**	**8**
Q6P502	GISDLAQHYLMR	1.080381918	2	2.37887
Q6P502	IVLLDSSLEYK	1.369433034	2	2.67924
Q6P502	IVSRPEELREDDVGTGAGLLEIK	1.520259973	3	3.68687
Q6P502	KGESQTDIEITR	1.254969333	2	3.18237
Q6P502	NLQDAMQVCR	1.362429737	2	2.80264
Q6P502	TAVETAVLLLR	1.225254914	2	3.38584
Q6P502	TLIQNCGASTIR	1.211623447	2	2.93696
Q6P502	WSSLACNIALDAVK	1.1280813	2	3.88398
Q6P5D3	**DHX57 Putative ATP_dependent RNA helicase DHX57**	**1.08171337**	**0.44522**	**2**
Q6P5D3	ARHNRTAQEEVEEDLR	1.082679323	2	2.3047
Q6P5D3	QEETLALKSICGEK	0.830660141	2	2.32468
Q6P6M7	EMFVYLSTQLKK+Oxidation(1)	0.011652527		
Q6P6M7	SGDISAVQPK	1.522267232	2	2.30571
Q6P6M7	SMVTAGFEPVVIENVLEGDELR	1.010382979	2	3.99819
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**1.061712144**	**2.86E-06**	**12**
Q6P6R2	ALTGGIAHLFK	1.214407411	2	2.69699
Q6P6R2	EANLAASFGKPINF	0.927266938	1	2.0567
Q6P6R2	IDVSVEAASGGK	1.101705274	2	3.659
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.150714037	3	4.13021
Q6P6R2	IPNIFAIGDVVAGPMLAHK	1.955776414	3	3.41712
Q6P6R2	NETLGGTCLNVGCIPSK	0.974839087	2	5.34502
Q6P6R2	NQVTATTADGSTQVIGTK	1.193179015	2	5.64947
Q6P6R2	RPFTQNLGLEELGIELDPK	1.43685115	3	4.21492
Q6P6R2	SEEQLKEEGVEFK	1.002053116	3	4.12924
Q6P6R2	TNADTDGMVK	0.836785436	2	2.82436
Q6P6R2	TNADTDGMVK+Oxidation(7)	1.139977569		
Q6P6R2	VCHAHPTLSEAFR	1.330230067	3	3.80575
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.917862707**	**0.00845**	**7**
Q6P6S9	AAETHLIDYEK	1.193000166	2	2.46137
Q6P6S9	AQTLLLEVEEIFK	0.973584244	2	3.8696
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.906818268	2	4.73296
Q6P6S9	QGAETVQELLEVAK	0.750870563	2	3.31321

Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	**1.006207507**	3	3.85166
Q6P6S9	VEDFERKAR	**0.986122136**	2	2.44263
Q6P6S9	WLEAEWIFGGVK	**0.798132862**	2	3.0829
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**0.89537961**	**0.353484**	**8**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2)	**0.802736062**		
Q6P6V0	HFVALSTNTDK	**1.241266392**	2	2.72113
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	**0.894521275**	3	5.43965
Q6P6V0	MIPCDFLIPVQTQHPIR	**0.661475456**	2	3.13345
Q6P6V0	TFTTQETITNAETAK	**1.094832349**	2	5.11523
Q6P6V0	TLANLNPESSLFIIASK	**1.28004165**	3	4.96459
Q6P6V0	VFEGNRPTNSIVFTK	**1.356420595**	2	3.39201
Q6P6V0	VWFVSNIDGTHIAK	**1.171175933**	2	3.46453
Q6P7B0	**SYWC Tryptophanyl_tRNA synthetase_ cytoplasmic**	**1.042814447**	**0.994996**	**2**
Q6P7B0	ASEDFVDPWTVR	**1.043576194**	2	2.69403
Q6P7B0	TLIDVLQPLIAEHQAR	**0.946995198**	3	3.31408
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.119203128**	**8.52E-07**	**6**
Q6P7Q4	ATLELTHNWGTEDDETQSYHNGNSDPR	**1.357499216**	3	3.98259
Q6P7Q4	DFLLQQTMLR	**1.260626544**	2	3.317
Q6P7Q4	FEELGVK	**0.841559896**	1	1.91717
Q6P7Q4	GFGHIGIAVPDVYEACK	**1.231177162**	2	3.45576
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	**1.08712715**	2	5.64355
Q6P7Q4	RFEELGVK	**1.162667016**	2	2.6482
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.324815339**	**6.25E-05**	**2**
Q6P7R8	GIFVQSVLPFFVATK	**1.801324724**	2	3.30023
Q6P7R8	LGEWAVVTGGTDGIGK	**1.322924038**	2	4.03946
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.779395366**	**9.9E-20**	**13**
Q6P9T8	AVLVDLEPGTMDSVR	**0.980558719**	2	4.68241
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10)	**1.247811335**		
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**1.287430331**	3	5.30237
Q6P9T8	EIVHLQAGQCGNQIGAK	**1.213909466**	2	5.04325
Q6P9T8	EVDEQMLNVQNK	**1.188270002**	2	4.06947
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	**1.276366534**	3	5.63299
Q6P9T8	INVYYNEATGGK	**1.746761966**	2	3.46812
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	**1.201028466**	3	5.34291
Q6P9T8	LHFFMPGFAPLTSR	**2.237979137**	2	2.70094
Q6P9T8	MSATFIGNSTAIQELFK	**1.62655944**	2	3.97457
Q6P9T8	SGPFGQIFRPDNFVFGQSGAGNNWAK	**1.767923454**	3	4.66292
Q6P9T8	TAVCDIPPR	**1.039394093**	2	2.50093
Q6P9T8	YLTVAAVFR	**1.09162861**	2	2.4695
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**1.196013817**	**5.36E-05**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	**1.345266105**	3	4.35146
Q6P9U8	EGTGSTATSSSSTGGAVGK	**1.194069879**	2	4.13056
Q6PA06	**ATLA2 Atlastin_2**	**1.196714929**	**0.373826**	**5**
Q6PA06	AGLTDQVSHHAR	**1.022694319**	2	3.34998
Q6PA06	NLVPLLLAPENLVEK	**1.290349279**	2	2.892
Q6PA06	QNQHEELQNVR	**1.003376901**	2	2.7316
Q6PA06	SMEQVCGGDKPYIAPSDLER	**1.280326904**	3	3.48575
Q6PA06	SMLQATAEANNLAAVAGAR	**1.129223385**	2	4.49058
Q6PCL9	**polymerase gamma**	**0.922722113**	**0.582133**	**4**
Q6PCL9	ATDITPIPMSEGGISDMPKR	**1.41700664**		
Q6PCL9	LTEILK	**1.092495256**		
Q6PCL9	QANNINMLKDGMK	**0.914470555**		
Q6PCL9	WEMDDPRPIAKAER	**1.04725548**		
Q6PDM2	**SRSF1 Serine/arginine_rich splicing factor 1**	**1.273308982**	**0.023228**	**2**
Q6PDM2	SHEGETAYIR	**1.364030339**	2	2.64033

Q6PDM2	VVVSGLPPSGSWQDLK	**1.263831743**	2	2.31052
Q6PDN3	**MYLK Myosin light chain kinase_ smooth muscle**	**1.004543125**	**0.493154**	**2**
Q6PDN3	LIDFGLAR	**1.391616697**	2	2.37337
Q6PDN3	VSMSEKNGMQILEIRGVTR	**0.761359239**	2	2.44465
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.218909259**	**2.6E-08**	**3**
Q6PEC1	LEAAYTDLR	**1.187802329**	2	3.17839
Q6PEC1	QILESEKDLEEAEEYKEAR	**1.501720312**	3	3.83594
Q6PEC1	RLEAAYTDLR	**1.11475289**	2	2.34798
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.254204172**	**0.00224**	**3**
Q6PEC4	NDFTEEEEAQVR	**1.495253509**	2	3.46107
Q6PEC4	TDDIPVWDQEFLK	**1.194707184**	2	3.12237
Q6PEC4	TVANMIKGKTPEEIR+Oxidation(4)	**1.237471265**		
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.251929504**	**3.89E-07**	**6**
Q6Q0N1	AVFQYIDENQDR	**0.683431798**	2	3.00811
Q6Q0N1	EGGSIPVTLTFQEATGK	**1.315753626**	2	2.61273
Q6Q0N1	LGGSVELVDIGK	**1.330223138**	2	3.73115
Q6Q0N1	LVPDMIPEVVSEQVSSYLSK	**1.181797654**	2	2.63451
Q6Q0N1	MTEAAAADVQR	**1.098531399**	2	2.6028
Q6Q0N1	TVFGVEPDLTR	**1.074081152**	2	2.54768
Q6SKG1	**ACSM3 Acyl_coenzyme A synthetase ACSM3_ mitochondrial**	**0.920353903**	**0.040108**	**3**
Q6SKG1	AFIVLNPDYK	**0.864068727**	2	2.7906
Q6SKG1	FDSTSILQTLSK	**1.033256673**	2	3.1274
Q6SKG1	TGTVLIPGTTQLTQK	**0.982685342**	2	2.93562
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.316185705**	**1.38E-08**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	**1.161866085**	2	4.51312
Q6TUG0	FQMTQEVVCDECPNVK	**1.324578752**	2	5.16541
Q6TUG0	KGEGLPNFDNNNIK	**1.316083666**	2	2.75215
Q6TUG0	TLEVEIEPGVR	**1.06867526**	2	3.22796
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**0.942633224**	**0.792996**	**16**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	**1.233156671**	2	4.3136
Q6UPE1	ALNEGGLQSIPK	**1.102811322**	2	3.15933
Q6UPE1	ASCDAQTYGIGLK	**1.204489801**	2	3.68383
Q6UPE1	FCPAGVYEFVPLEQGDGFR	**0.949261189**	2	4.94667
Q6UPE1	GAPLNTPVTEDR	**0.992254122**	2	3.44929
Q6UPE1	GIATNDVGIQK	**1.021565357**	2	3.56295
Q6UPE1	HHPSIRPTLEGGK	**0.967993254**	2	2.4243
Q6UPE1	LQINAQNCVHCK	**1.280008894**	2	3.72905
Q6UPE1	NLSIYDGPEQR	**1.046105879**	2	3.21672
Q6UPE1	QLAAEQEKDIR	**1.108779381**	2	2.80451
Q6UPE1	QLTSENLQSK	**0.980397985**	2	2.46207
Q6UPE1	SGSLAAEAIFK	**0.855636874**	2	3.35566
Q6UPE1	TAGLHVTEYEDNLK	**1.088083599**	2	3.88015
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	**1.051192009**	2	3.70353
Q6UPE1	VDHTVGWPLDR	**0.998624516**	2	2.64685
Q6UPE1	VTIFAEGCHGHLAK	**0.781966101**	2	3.3838
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**0.958240653**	**0.244071**	**7**
Q6URK4	EDSVKPGAHLTVK	**0.970864772**	2	3.36965
Q6URK4	EDTEEYNLR	**1.102264984**	2	2.34265
Q6URK4	GFAFVTFDDHDTVDK	**0.330090239**	2	4.2515
Q6URK4	IETIEVMEDR	**0.927932953**	2	3.39152
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	**1.10781345**	2	4.97674
Q6URK4	WGTLTDCVVMR	**0.921241903**	2	2.30274

Q6URK4	YHTINGHNCEVK	1.672082177	2	3.57418
Q6URW6	**MYH14 Myosin_14**	**1.081014418**	**0.999987**	**4**
Q6URW6	EDQSILCTGESGAGK	0.978772002	2	4.49769
Q6URW6	FDQLLAEEK	0.983119795	2	2.33667
Q6URW6	KFDQLLAEEK	1.050680297	2	2.57959
Q6URW6	QLLQANPILEAFGNAK	0.944024351	2	4.33224
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.993265943**	**0.517495**	**5**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.746655887	2	4.11857
Q6XQN1	LDSGDLLQQAK	1.130459538	2	2.94937
Q6XQN1	LYLQQGQPYEPLPSLEESR	1.665710042	2	4.48363
Q6XQN1	QLQNPAVYQVALSEK	1.345105738	2	3.82319
Q6XQN1	VWLQGAQEPCTVKPAQVEPLLR	1.222994129	3	3.64815
Q6Y7W8	**PERQ2 PERQ amino acid_rich with GYF domain_containing protein 2**	**0.811241163**	**0.2546**	**2**
Q6Y7W8	AEEENRSENSLSAKVPSR	0.755533798	2	2.41972
Q6Y7W8	KDEPKAEQVEK	0.902090887	2	2.51718
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.141420929**	**0.012722**	**2**
Q6ZPJ3	FRTTDIVIR	0.813534578	2	2.45154
Q6ZPJ3	NCAQGEGSMAKKVK	1.162815747	2	2.56311
Q6ZPY5	**ZN507 Zinc finger protein 507**	**1.039498297**	**0.113589**	**2**
Q6ZPY5	CSLCGYVCSHPPSLK	1.439752063	2	2.34102
Q6ZPY5	IISSSPNK	1.037445614	2	2.35231
Q704S8	**CACP Carnitine O_acetyltransferase**	**1.203940035**	**0.018987**	**3**
Q704S8	ALQPIVSEEEWAHTK	0.729168966	2	2.49566
Q704S8	DKVNRESVNSIQK	1.194185739	2	2.33361
Q704S8	FNITPEIKNDIEK	1.388417115	2	3.18785
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.085626711**	**0.949333**	**5**
Q711G3	DCGTDVLDLWTLMQK	1.227249905	2	3.87297
Q711G3	DVEETKPELSLLGDGDH	1.003209588	2	3.44994
Q711G3	LNVAVGEYAK	1.107487279	2	3.02758
Q711G3	QHVPLDEYSANLR	1.126831509	2	2.56293
Q711G3	VILITPPPLCEAAWEK	0.798295023	2	2.64621
Q71TY3	**RS27 40S ribosomal protein S27**	**1.538103734**	**4.55E-06**	**2**
Q71TY3	DLLHPSPEEEK	1.223107145	2	2.32708
Q71TY3	LVQSPNSYFMDVK	1.753885518	2	2.86871
Q75N33	**SC16B Protein transport protein Sec16B**	**1.016220119**	**0.911192**	**2**
Q75N33	NLLTGEIPLNVDTPAQIVEK	1.424169347	2	3.80026
Q75N33	VLEPDWLVQLR	1.009892727	2	2.50673
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.084653308**	**0.45912**	**3**
Q75Q39	NADLSTFYQNR	1.343777828	2	2.57389
Q75Q39	NREPLMPSPQFIK	1.070428607	2	2.54864
Q75Q39	SDEDKDKEGEALEVK	1.262910448	2	4.16598
Q75WE7	**VWA5A von Willebrand factor A domain_containing protein 5A**	**0.90116096**	**0.38214**	**2**
Q75WE7	YTQETIEEAVER	0.965742721	2	2.55259
Q75WE7	YVQELPLESDGALR	0.594609114	2	2.61122
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.026264398**	**0.980058**	**7**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.032548556	3	4.35419
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	1.213658377	3	3.37625
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.056229614	2	4.52892
Q76MZ3	LTQDQDVDVK	0.896427514	2	2.88687
Q76MZ3	QLSQSLLPAIVELAEDAK	1.034646554	3	3.83457
Q76MZ3	SALASVIMGLSPILGK	0.864185377	2	3.08302
Q76MZ3	SEIIPMFSNLASDEQDSVR	0.827823405	2	3.85579

Q78P75	**DYL2 Dynein light chain 2_ cytoplasmic**	**0.714641032**	**0.999847**	**3**
Q78P75	NADMSEDMQQDAVDCATQAMEK	**0.642281342**	2	5.67402
Q78P75	NFGSYVTHETK	**0.910000698**	2	2.71083
Q78P75	YNPTWHCIVGR	**1.084418541**	2	2.72149
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**0.984548803**	**1.27E-06**	**5**
Q791V5	EEGIVGFFAGLIPR	**1.785774383**	2	3.59633
Q791V5	GLFTGLTPR	**0.972686753**	2	2.80161
Q791V5	LCSGVLGTVVHGK	**1.513048787**	3	3.35457
Q791V5	VLIQVGYEPLPPTIGR	**1.017729888**	2	4.16552
Q791V5	YCGLCDSIVTIYR	**1.166300983**	2	2.93211
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.498606859**	**8.05E-05**	**4**
Q794E4	ATENDIYNFFSPLNPVR	**1.571718029**	3	4.89989
Q794E4	HSGPNSADSANDGFVR	**1.085998294**	2	4.18021
Q794E4	ITGEAFVQFASQELAEK	**0.926396624**	2	3.86741
Q794E4	VHIEIGPDGR	**1.088056682**	2	2.74295
Q7M0E3	**DEST Destrin**	**1.299207831**	**1.56E-13**	**2**
Q7M0E3	HEYQANGPEDLNR	**1.357448605**	2	4.3737
Q7M0E3	KEELMFFLWAPEQAPLK	**0.917873006**	2	3.83427
Q7TMA5	**APOB Apolipoprotein B_100**	**0.909923927**	**8.4E-08**	**12**
Q7TMA5	GFEPTLEALFGK	**0.883021799**	2	2.90076
Q7TMA5	GGINQVGLAFESTK	**1.05769721**	2	2.473
Q7TMA5	IEGNLVFDPSSYLPK	**0.749348135**	2	3.48951
Q7TMA5	IEIDIPLPLGGK	**0.964677188**	2	3.08506
Q7TMA5	ITDNDVLIALDSAK	**1.040996905**	2	3.20563
Q7TMA5	KGTVATEMSTER	**0.436195674**	2	2.64399
Q7TMA5	LLQWEQSEQVK	**0.967498262**	2	2.43395
Q7TMA5	LSISEQNAQR	**1.06364654**	2	2.5805
Q7TMA5	NFVASHIANILNSEELYVQDLK	**0.874852211**	3	3.64509
Q7TMA5	NSVSTALEHTLSALLTPAEQTSSWK	**0.754171218**	3	3.35974
Q7TMA5	SVGFHLPSQEVQIPTFTIPK	**0.638684471**	3	3.52559
Q7TMA5	TILFDTFVNDVAPVEK	**0.824739262**	2	3.47543
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.161248147**	**0.000765**	**4**
Q7TNG8	AVVGSPHVSTASAVR	**0.87136462**	2	2.37528
Q7TNG8	AYSTDVCVPISR	**1.390567408**	2	3.70201
Q7TNG8	GSQGGLSQDFVEALK	**1.163587824**	2	3.74125
Q7TNG8	QLLQEEVGPVGVETMR	**0.953693236**	2	2.6946
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**0.912372131**	**0.026075**	**2**
Q7TP47	DLFEDELVPLFEK	**1.565739727**	2	3.06382
Q7TP47	NLANTVTEEILEK	**0.86683563**	2	3.68056
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.091232989**	**0.265881**	**4**
Q7TP48	LENGEIETIAR	**1.097537545**	2	3.31941
Q7TP48	LFENQLNGPESIVNIGDVLFTGTADGR	**1.095782087**	3	3.3581
Q7TP48	LLEYDTVTK	**1.018920852**	2	2.35876
Q7TP48	LLLSSETPIEGK	**1.923571554**	2	2.98951
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**1.015038786**	**0.942294**	**7**
Q7TP52	AGVSVYGIIR	**1.326164217**	2	2.394
Q7TP52	EDCSPADKPYIEEAR	**1.182896533**	2	3.5406
Q7TP52	KREDCSPADKPYIEEAR	**1.018945175**	2	4.62442
Q7TP52	LDYGGMGQEVQVEHIK	**0.940823635**	2	4.41776
Q7TP52	LKEHCIVNYQVK	**1.547977548**	2	3.82445
Q7TP52	NLIEWLNK	**1.008217688**	2	2.45274
Q7TP52	TFSGQTHGFVHR	**1.073523785**	2	3.60365

Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.108595636**	**6.55E-09**	**11**
Q7TPB1	ALIAGGGAPEIELALR	**1.129882354**	2	4.12606
Q7TPB1	DIEREDIEFICK	**1.386188884**	2	2.38054
Q7TPB1	ETLLNSATTSLNSK	**1.253140198**	2	3.55661
Q7TPB1	GDVTITNDGATILK	**0.730980146**	2	3.28756
Q7TPB1	GIHPTIISESFQK	**1.084510408**	2	2.63696
Q7TPB1	IDDVVNTR	**1.166089942**	2	2.37537
Q7TPB1	LVIEEAER	**1.394145917**	1	1.94607
Q7TPB1	MIQDGKGDVTITNDGATILK+Oxidation(0)	**0.864815833**		
Q7TPB1	SIHDALCVIR	**1.047024807**	2	2.48198
Q7TPB1	TGCNVLLIQK	**0.854382248**	2	2.50297
Q7TPB1	VIDPATATSVDLR	**1.156775364**	2	3.38237
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.309201401**	**1.15E-10**	**2**
Q7TPJ0	GEDFPANNIVK	**1.285394973**	2	3.02246
Q7TPJ0	GTEDFIVESLDASFR	**1.294489574**	2	4.09288
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**1.018273719**	**0.97323**	**2**
Q7TQM4	QDRPLPSTASDSTR	**0.981354935**	2	3.18531
Q7TQM4	TQCLEQAQR	**0.969282034**	2	3.01986
Q80TV8	**CLAP1 CLIP_associating protein 1**	**1.51936609**	**0.059455**	**2**
Q80TV8	MESCLAQVLQK	**1.127516315**	2	2.49841
Q80TV8	MGADLLGSVQAKVQK+Oxidation(0)	**1.530296976**		
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**0.978978844**	**9.9E-20**	**11**
Q80W21	CLDAFPNLK	**0.920094454**	2	3.183
Q80W21	CLDAFPNLKDFIAR	**0.973881502**	2	2.69365
Q80W21	FKLGLDFPNLPYLIDGSHK	**0.93613923**	3	4.13703
Q80W21	HNLCGETEEER	**1.038401705**	2	3.82512
Q80W21	ITQSNAILR	**1.314285639**	2	3.14981
Q80W21	KHNLCGETEEER	**0.42042139**	3	4.44762
Q80W21	LFLEYTDSSYEEK	**1.237447739**	2	3.97428
Q80W21	LGLDFPNLPYLIDGSHK	**1.368120615**	2	4.7105
Q80W21	LKPGYLEQLPGMMR	**0.716324965**	2	2.61999
Q80W21	LYSEFLGK	**1.278307734**	2	2.31421
Q80W21	VDILENQLMDNR	**0.68381413**	2	3.69353
Q80X50	**UBP2L Ubiquitin_associated protein 2_like**	**1.029815619**	**0.900193**	**2**
Q80X50	IDLAVLLGK	**1.035308746**	2	3.38749
Q80X50	QRPQATAEQIR	**0.899608116**	2	2.33472
Q80X90	**FLNB Filamin_B**	**1.2284177**	**6.01E-05**	**9**
Q80X90	ADIEMPFDPSK	**1.145897732**	2	2.33503
Q80X90	AHGPGLEGGLVGKPAEFTIDTK	**1.067937783**	3	3.49606
Q80X90	GAGIGGLGITVEGPSESK	**1.153842028**	2	3.55208
Q80X90	GFLDGVYSFEYYPSTPGK	**1.827605559**	2	3.18844
Q80X90	IGNLQTDLSDGLR	**1.351560452**	2	2.38394
Q80X90	ILAQDGEGQPIDIQMK	**0.977761067**	2	3.85227
Q80X90	VDIQTEDLEDGTCK	**1.094027106**	2	3.91756
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	**1.210374561**	3	3.90069
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	**1.478458745**	2	3.88751
Q80YR5	**SAFB2 Scaffold attachment factor B2**	**0.879430823**	**0.621996**	**2**
Q80YR5	GSKMEEEGSEDNGLEEDSR	**0.786058669**	2	2.39389
Q80YR5	SEPVKEEGSELEQPFAQATSSVGPDR	**1.163323065**	3	4.21901
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.408294363**	**0.830793**	**2**
Q80Z25	ELEQEAERLEK	**1.489921744**	2	2.93903
Q80Z25	MIEESLK+Oxidation(0)	**1.233596647**		
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.096632814**	**0.714746**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	**1.079851835**	2	3.93578

Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	**2.320353458**	5	4.60868
Q80Z29	VIQGDGVDINTLQEIVEGMK	**1.039597604**	2	4.45121
Q80Z29	YLLETSGNLDGLEYK	**1.044725661**	2	4.2224
Q80Z36	**ZHX3 Zinc fingers and homeoboxes protein 3**	**1.010227226**	**0.999999**	**2**
Q80Z36	FPYPTKAELCYLTVVTK	**0.986888411**	2	2.72957
Q80Z36	YPEEQLK	**1.003459123**	2	2.33479
Q80ZF0	**chain**	**1.033148753**	**0.594973**	**2**
Q810B6	**ANFY1 Ankyrin repeat and FYVE domain_containing protein 1**	**1.095358368**	**0.280933**	**2**
Q810B6	QLDLELK	**1.105622809**	1	2.25782
Q810B6	RESGAAEQVDNKGR	**0.484811635**	1	1.92518
Q811D2	**ANR26 Ankyrin repeat domain_containing protein 26**	**1.112811535**	**0.951338**	**2**
Q811D2	AQEDFDK	**1.116754655**	1	1.94918
Q811D2	LNMLSSKLDNEKQNK	**1.078152913**	2	2.33604
Q811X6	**CRYL1 Lambda_crystallin homolog**	**0.718089908**	**0.795091**	**3**
Q811X6	EMKSLEQSGSLK+Oxidation(1)	**0.882806323**		
Q811X6	IVDDQVILSSSSSCLLPSK	**1.091017115**	2	2.7312
Q811X6	TFGPVPEFSGDTVEK	**0.487141168**	2	3.012
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.115226228**	**1.38E-13**	**10**
Q8BFZ3	CDVDIR	**0.846851895**	1	2.00196
Q8BFZ3	DLTDYLMK	**0.855605198**	1	2.07498
Q8BFZ3	HQGVMVGMGQK	**0.684350817**	3	3.90187
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	**1.00838872**		
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	**0.825829919**		
Q8BFZ3	HQGVMVGMGQK+Oxidation(7)	**0.821128163**		
Q8BFZ3	SYELPDGQVITIGNER	**0.869423876**	3	5.16983
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	**0.94073454**	3	6.93717
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)	**1.152488441**		
Q8BFZ3	VAPDEHPILLTEAPLNPK	**1.108324671**	3	4.21071
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**0.939825226**	**0.053554**	**5**
Q8BG32	LYDNLLEQNLIR	**0.891454119**	2	3.65063
Q8BG32	TGQAAELGGLLK	**1.268484756**	2	2.47413
Q8BG32	TTANAIYCPPK	**1.203206697**	2	3.07647
Q8BG32	TYEAALETIQNMSK	**1.039163938**	2	3.26269
Q8BG32	VQIEHISSLIK	**0.899651872**	2	3.15946
Q8BG79	**C19L2 CWF19_like protein 2**	**0.673782658**	**0.056234**	**2**
Q8BG79	KNQDSSGNLRSK	**0.622771744**	2	2.39218
Q8BG79	MWPVSSPRETLDMKAER+Oxidation(12)	**1.022310983**		
Q8BGC4	**ZADH2 Zinc_binding alcohol dehydrogenase domain_containing protein 2**	**0.713221405**	**0.509442**	**2**
Q8BGC4	DCPVPLPGDGDLLVR	**0.94601266**	2	2.34394
Q8BGC4	FVGINASDINYSAGR	**0.378549751**	2	3.81417
Q8BGT5	**ALAT2 Alanine aminotransferase 2**	**1.35416347**	**0.000147**	**3**
Q8BGT5	ILTLESMNPQVK	**1.063729789**	2	2.60449
Q8BGT5	LLEETGICVVPGSGFGQR	**1.24939834**	2	3.76934
Q8BGT5	VLCIINPGNPTGQVQSR	**1.371805025**	2	4.51233
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.182798755**	**0.236961**	**4**
Q8BGY2	KYEDICPSTHNMDVPNIK	**1.099230531**	3	4.35003
Q8BGY2	KYEDICPSTHNMDVPNIK+Oxidation(11)	**1.188544326**		
Q8BGY2	VHLVGIDIFTGK	**1.151897364**	1	3.36391
Q8BGY2	YEDICPSTHNMDVPNIK	**0.931826158**	2	4.04533
Q8BGY3	**LUZP2 Leucine zipper protein 2**	**0.599340809**	**0.035169**	**2**
Q8BGY3	DLQNENKSLK	**1.138487596**	2	2.31299

Q8BGY3	SLQEALQNQLK	**0.548366834**	2	2.47748
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.129428418**	**9.9E-20**	**9**
Q8BH00	ELLMLENFIGGK	**1.483877237**	2	3.38763
Q8BH00	ELNLPFGGMK	**0.706727141**	1	2.23217
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	**1.243105842**	3	5.09226
Q8BH00	ILCGEGVDQLSLPLR	**1.141364962**	2	4.38564
Q8BH00	ITQLSAPHCK	**1.345702271**	2	2.94709
Q8BH00	KLSLELGGK	**0.822318075**	1	2.00437
Q8BH00	NPAIIFEDANLEECIPATVR	**1.039536903**	3	5.34455
Q8BH00	SSFANQGEICLCTSR	**3.466373848**	2	4.44508
Q8BH00	TPVGIAGLISPWNLPLYLLTWK	**1.202804654**		
Q8BH69	**SPS1 Selenide_ water dikinase 1**	**0.931885214**	**0.35169**	**2**
Q8BH69	IIEVAPQVATQNVNPTPGATS	**1.015984112**	2	3.6801
Q8BH69	YGEGHQAWIIGIVEK	**0.623223535**	2	2.36494
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.052445629**	**0.846992**	**8**
Q8BHN3	AEKDEPGAWEETFK	**1.147535198**	2	3.42701
Q8BHN3	DDNSVELTVAEGPYK	**1.420568991**	2	3.63878
Q8BHN3	MLDYLQGSGETPQTDIR	**0.855538076**	2	4.7646
Q8BHN3	MLDYLQGSGETPQTDIR+Oxidation(0)	**1.245439931**		
Q8BHN3	REPWLLASQYQDAIR	**0.988018503**	3	3.7553
Q8BHN3	SGGIERPFVLSR	**1.046120976**	2	2.52757
Q8BHN3	SLLLSVNAR	**1.172532104**	2	2.42012
Q8BHN3	VTEGGEPYR	**1.029190402**	2	2.5368
Q8BI84	**MIA3 Melanoma inhibitory activity protein 3**	**0.112853548**	**0.264135**	**2**
Q8BI84	LQLESEREQNVK	**0.050949539**	2	2.34273
Q8BI84	TQTAVSIVEEDLK	**0.921161157**	2	2.61991
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**0.888336992**	**0.007918**	**2**
Q8BIJ6	DTVLLPQTSFPMK	**0.914470555**	1	2.23063
Q8BIJ6	SCQTALAEILDVLVR	**0.779270478**	2	3.89824
Q8BIJ7	**RUFY1 RUN and FYVE domain_containing protein 1**	**0.903766833**	**0.503628**	**2**
Q8BIJ7	EKDTSCLLQTELQQVEGLK	**1.028381992**	2	2.44625
Q8BIJ7	ELQDEKAELRK	**0.831018542**	2	2.44521
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.026466658**	**0.135179**	**7**
Q8BJ64	ADSAYHPSCTCK	**3.014344099**	2	3.40372
Q8BJ64	AEVQTLVSR	**0.950578158**	2	2.75354
Q8BJ64	ELQPGSHVQSDK	**1.179783927**	2	2.5352
Q8BJ64	ELQPGSHVQSDKEIDAFVR	**1.042910847**	2	4.11539
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	**2.497027589**	5	4.86024
Q8BJ64	TNHPLHQAFLQAAR	**0.901059085**	3	4.67728
Q8BJ64	VLLLEAGPK	**1.044815875**	2	2.93071
Q8BJY1	**PSMD5 26S proteasome non_ATPase regulatory subunit 5**	**1.10958997**	**0.004991**	**2**
Q8BJY1	GLTHPDDSVK	**0.971850815**	2	2.48779
Q8BJY1	TVAEIFGNSNYLR	**2.354621366**	2	3.07635
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.107932458**	**0.693728**	**2**
Q8BL97	NPPGFAFVEFEDPR	**1.117290365**	2	3.48263
Q8BL97	VYVGNLGTGAGK	**1.057801804**	2	2.35984
Q8BMJ2	**SYLC Leucyl_tRNA synthetase_ cytoplasmic**	**0.889338842**	**0.089506**	**3**
Q8BMJ2	QTGEGVGPQEYTLVK	**1.482220343**	2	2.36624
Q8BMJ2	SFITTDVNPYYDSFVR	**0.891864573**	2	3.31537
Q8BMJ2	STGNFLTLSQAVDK	**0.705055744**	2	2.97421
Q8BTM8	**FLNA Filamin_A**	**0.935041761**	**0.207545**	**5**
Q8BTM8	AFGPGLQGGNAGSPAR	**0.724858978**	2	3.78959
Q8BTM8	ANLPQSFQVDTSK	**0.934862383**	2	2.4652

Q8BTM8	GAGTGGLGLAVEGPSEAK	**0.937954789**	2	3.68593
Q8BTM8	IVSPSGAAVPCK	**1.11854937**	2	2.4569
Q8BTM8	VTAQGPGLEPSGNIANK	**1.016384925**	2	3.94056
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.096337807**	**0.005911**	**2**
Q8BTZ7	HHGQEGSILVTK	**1.009681984**	3	3.75629
Q8BTZ7	YGVVVCEADTGR	**1.331998278**	2	3.25535
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**1.034218519**	**0.822034**	**3**
Q8BU33	AAVETLGVPCFLGGMSR	**1.109271899**	2	2.42028
Q8BU33	LPNSLMGR+Oxidation(5)	**0.973071245**		
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	**1.167530146**	2	4.58291
Q8BWQ1	**UD2A3 UDP_glucuronosyltransferase 2A3**	**0.987241062**	**0.476844**	**2**
Q8BWQ1	ADIWLIR	**0.977452159**	2	2.53691
Q8BWQ1	IHHDQPVKPLDR	**1.387201102**	3	3.50576
Q8BX70	**VP13C Vacuolar protein sorting_associated protein 13C**	**0.955500719**	**0.927443**	**2**
Q8BX70	ENALSELDVPFKVK	**0.93996531**	2	2.9023
Q8BX70	TVLQADSPQHDVEILKPVNMLLCIQR+Oxidation(19)	**1.105757338**		
Q8C7X2	**K0090 Uncharacterized protein KIAA0090**	**1.161774178**	**9.9E-20**	**2**
Q8C7X2	FNVEDGEIVQQVR	**1.053664556**	2	3.27027
Q8C7X2	VMGDRSVLYK+Oxidation(1)	**3.656667491**		
Q8C8R3	**ANK2 Ankyrin_2**	**1.101689219**	**0.000847**	**2**
Q8C8R3	STSSSGRPGTSPTRESR	**0.857132708**	2	2.43608
Q8C8R3	TSTDFSEVIKQELEDNDK	**1.415673886**	2	2.6131
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.492575467**	**0.003157**	**4**
Q8CC88	HQATGELDDAK	**1.563253899**	2	3.38585
Q8CC88	IILDNLQAK	**1.103326411**	2	2.30254
Q8CC88	NLADQGIINYPYSTR	**1.468551191**	2	3.19096
Q8CC88	VSSDQLSSENLTSAVGQK	**0.773915357**	2	3.48928
Q8CDM4	**CCD73 Coiled_coil domain_containing protein 73**	**0.856139661**	**0.215327**	**2**
Q8CDM4	MEEESIDLIIKEQK	**0.699941815**	2	2.39728
Q8CDM4	VTCQHKMEEESIDLIIK	**0.865445451**	2	2.37989
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.217583529**	**0.000282**	**3**
Q8CFN2	NVFDEAILAALEPPEPK	**1.112408264**	3	4.99827
Q8CFN2	WVPEITHHCPK	**0.969145516**	2	2.40611
Q8CFN2	YVECSALTQK	**1.216936818**	2	3.05253
Q8CFW1	**ANO2 Anoctamin_2**	**1.152441779**	**0.026165**	**2**
Q8CFW1	TEQTFEERLILK	**1.596693818**	2	2.36872
Q8CFW1	TKDIGIWFDILSGIGK	**0.815434332**	2	2.33945
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.250185975**	**2.71E-14**	**10**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	**0.627391007**	2	2.89333
Q8CG45	EHHFEAIALVEK	**1.729049363**	2	2.34508
Q8CG45	FFGNSWSETYR	**0.982862465**	2	2.81709
Q8CG45	FYAYNPLAGGLLTGK	**1.599324773**	2	4.53704
Q8CG45	MDASASAATVR	**1.009318623**	2	3.67335
Q8CG45	MDASASAATVR+Oxidation(0)	**1.225494035**		
Q8CG45	QVETELLPCLR	**1.072987471**	2	2.9625
Q8CG45	RMDASASAATVR	**1.162486317**	2	2.76044
Q8CG45	TTYGTSAPSMTSAALR	**0.975455469**	2	4.21112
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	**1.944101041**	3	5.55029
Q8CG48	**SMC2 Structural maintenance of chromosomes protein 2**	**0.716348579**	**0.036353**	**2**

Q8CG48	EEKLLEK	0.829165347	1	1.96578
Q8CG48	IKALNCEIEELER	0.739455667	2	2.46479
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.285744777**	**8.13E-10**	**10**
Q8CGC7	AIQGATSHHLGQNFSK	1.315727193	2	4.47901
Q8CGC7	DQDVEPGAPSMGAK	1.271752109	2	3.14168
Q8CGC7	DQVDSAVQELLQLK	1.192159457	2	3.728
Q8CGC7	GDVSISVEEGKENLLR	1.218783384	2	3.47736
Q8CGC7	KEENLAEWYSQVITK	0.977141456	2	4.35699
Q8CGC7	KGDIIQLQR	1.491054984	2	2.65701
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.252073068	2	4.38091
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.322882638	2	4.63391
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	1.075087553	3	3.47725
Q8CGC7	VYEELLAIPVVR	1.232726381	2	3.03267
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.236758795**	**0.115556**	**9**
Q8CHM7	DTSKPCLINIMIEPQSTR	0.912274069	2	3.49412
Q8CHM7	GAAYSHAEDSIR	0.608904204	2	3.43655
Q8CHM7	GVVPDNHPNCVGAAR	1.357374629	2	3.36409
Q8CHM7	GYFVQTPEELQDSLR	1.15886737	2	4.05175
Q8CHM7	LVELCNLPFLPTPMGK	1.361327851	2	4.26507
Q8CHM7	NCFIVSEGANTMDIGR	1.068847984	2	4.90765
Q8CHM7	NQEAMGAFQEFPQVEACR	1.083917067	2	6.10322
Q8CHM7	SSIYGRPGACYIDVPADLVTLQESTTSIK	0.9886117	3	4.14099
Q8CHM7	YKECCMPPPLSLAETSAVR	0.65599677	2	2.36958
Q8CI17	**MB213 Protein mab_21_like 3**	**0.875124962**	**0.281417**	**2**
Q8CI17	QQISQTMEEVQK+Oxidation(6)	1.22913744		
Q8CI17	RQQISQTMEEVQK	0.874495556	2	2.3575
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.869573686**	**0.813422**	**3**
Q8CIB5	GCEVTPDVNISGQK	0.819978773	2	3.16586
Q8CIB5	INQLYEQAK	1.030840067	2	2.9699
Q8CIB5	TSTILGDITSIPELADYIK	0.908197486	2	2.89817
Q8CIE6	**COPA Coatomer subunit alpha**	**1.226356336**	**0.000503**	**7**
Q8CIE6	ASNLENSTYDLYTIPK	1.509274482	2	3.79796
Q8CIE6	DADSQNPDAPEGK	1.275103213	2	3.2413
Q8CIE6	GITGVDLFGTTDAVVK	1.038962803	2	3.99592
Q8CIE6	GVNWAAFHPTMPLIVSGADDR	0.857353563	2	3.64124
Q8CIE6	LLELGPKPEVAQQTR	1.238046402	2	3.47086
Q8CIE6	SILLSVPLLVVDNK	1.221390752	2	3.5948
Q8CIE6	TLDLPIYVTR	1.030773952	2	2.67268
Q8CJ40	**CROCC Rootletin**	**1.000007837**	**0.771018**	**4**
Q8CJ40	DLLQLGGELVRTSR	1.137970647	2	2.47817
Q8CJ40	ELEERTGNLGRQR	1.688396498	2	2.30787
Q8CJ40	LQEERRLLQER	0.897311765	2	2.35933
Q8CJ40	QQQAEHATTMAVEK+Oxidation(9)	1.0082515		
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**1.346263924**	**9.9E-20**	**3**
Q8JZN5	GSNTCEVHFENTR	1.349216967	2	4.35905
Q8JZN5	NLSEFGLIQEK	1.036683594	2	3.10723
Q8JZN5	SGNVTTVMETIGR	0.862597773	2	2.50522
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**0.928900131**	**0.977764**	**16**
Q8K009	ADPLALAAEK	1.1696277	2	2.63957
Q8K009	AGFSVFWADDGLDTGPILLQR	1.251245118	2	3.86709
Q8K009	AMVEAVQLIADGK	1.037127466	2	3.76944
Q8K009	ANNTEYGLASGVFTR	0.855394224	2	4.73416
Q8K009	DLGEEALNEYLK	1.060620196	2	3.23262
Q8K009	EESFGPIMVISK	1.050124721	2	2.40331
Q8K009	FLFPEGIK	0.906433903	2	2.40233

Q8K009	FQNGDIDGVLQR	**1.068506107**	2	2.91139
Q8K009	GVINIIPGSGGVAGQR	**0.921505072**	2	3.95797
Q8K009	HGSIIYHPSLLPR	**1.006725922**	2	4.17829
Q8K009	LEAGTVFINTYNK	**1.209711256**	2	3.08123
Q8K009	NLQFEDGK	**0.912885444**	1	2.1286
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	**0.996695168**	3	3.70991
Q8K009	SCDVKPNDTVDSLYNR	**1.086984412**	2	4.43357
Q8K009	TPQPEEGATYEGIQK	**1.472096608**	2	3.20075
Q8K009	VVGVFTVPDKDGK	**1.059593706**	2	3.13765
Q8K1S6	**SPIR2 Protein spire homolog 2**	**1.418151882**	**0.126231**	**2**
Q8K1S6	ALFVETLELR	**1.421628136**	2	2.31217
Q8K1S6	DTADILLRR	**1.225994123**	2	2.42488
Q8K2F0	**BRD3 Bromodomain_containing protein 3**	**0.560758325**	**0.001194**	**2**
Q8K2F0	LNLPDYHKIIK	**0.159099914**	2	2.45914
Q8K2F0	QLSLDINRLPGEK	**0.560765573**	2	2.45337
Q8K3J1	**NDUS8 NADH dehydrogenase [ubiquinone] iron_sulfur protein 8_ mitochondrial**	**1.007291314**	**0.969744**	**2**
Q8K3J1	LCEAICPAQAITIEAEPR	**1.017733662**	2	4.36945
Q8K3J1	YVNKKEQESEVDMK	**0.758919562**	2	2.31708
Q8K440	**ABC8B ATP_binding cassette sub_family A member 8_B**	**1.001644413**	**0.975549**	**3**
Q8K440	GEILGLLGHNGAGKSTSLK	**1.023089962**	2	2.31314
Q8K440	LMEMEQTLSSLRETEK+Oxidation(1)	**0.728752226**		
Q8K440	LMEMEQTLSSLRETEK+Oxidation(3)	**0.822384261**		
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**1.066123213**	**0.990789**	**5**
Q8K442	GQITAILGHSGAGK	**1.2519217**	2	3.50688
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	**1.059239985**	3	3.54142
Q8K442	LTGVCPQCNVQFDFLTVR	**1.153898722**	2	2.8147
Q8K442	NTQNILVQNLSGGQK	**1.002223226**	2	3.42533
Q8K442	STLLNVLSGLCVPTK	**1.107628777**	2	3.72299
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.753643814**	**8.77E-15**	**9**
Q8K4C0	FDHEMFGLKPK	**0.600192792**	2	2.9214
Q8K4C0	GYPIDILLSSR	**0.76401865**	2	3.06238
Q8K4C0	HSALGQHPTINDDLPNR	**0.777179016**	2	4.99936
Q8K4C0	IAVIGSGASGLTCIK	**1.296534983**	2	4.02974
Q8K4C0	KLPSQSEMMAEINK	**0.777403336**	2	3.82066
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	**0.837674463**	3	4.58752
Q8K4C0	KTILTTEDR	**0.757503141**	2	2.56085
Q8K4C0	QQVDVFDGVLVCTGHHTDPHLPLDSFPGIEK	**0.638367655**	3	4.06614
Q8K4C0	SDDIGGLWR	**0.747376034**	2	2.81345
Q8K4G6		**0.829061948**	**1.56E-09**	**56**
Q8K4T4	**FLIP1 Filamin_A_interacting protein 1**	**1.316864849**	**0.069627**	**2**
Q8K4T4	FQPRAETQSMKIELK+Oxidation(9)	**1.247455415**		
Q8K4T4	IEELEETNKSLQK	**1.324398071**	2	2.40646
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**0.980492724**	**0.002618**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	**1.110027988**	2	4.19953
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	**0.915094022**	2	5.98306
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.207985974**	**0.000296**	**3**
Q8K586	FNVWDTAGQEK	**1.285496711**	2	3.03322
Q8K586	NLQYYDISAK	**1.503761657**	1	2.21583
Q8K586	VCENIPIVLCGNK	**1.187823982**	2	3.8283
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**1.196296617**	**0.533472**	**2**
Q8QZY1	KSEGEMDFLRSNPK	**0.964353088**	2	2.31237

Q8QZY1	VFSDEVQQQAQLSTIR	1.200170216	2	3.87502
Q8R066	C1QT4 Complement C1q tumor necrosis factor_related protein 4	1.277121695	0.13065	2
Q8R066	NRDEVQAMIYDDGASRR	1.066861899	2	2.3264
Q8R066	TLSVKLMKNR	1.369678758	2	2.41372
Q8R081	HNRPL Heterogeneous nuclear ribonucleoprotein L	1.152633356	8.82E-10	5
Q8R081	ASLNGADIYSGCCTLK	1.738025897	2	3.31731
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	1.030890787	3	5.17982
Q8R081	SDALETLGFLNHYQMK	0.952966767	2	2.98846
Q8R081	SSSGLLEWDSK	0.706466294	2	2.83358
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.740606441	3	7.47937
Q8R0F9	S14L4 SEC14_like protein 4	1.09158152	9.36E-07	6
Q8R0F9	FDNTYSLLHTK	1.592170255	2	3.06803
Q8R0F9	GSSHQVENEILFPGCVLR	0.960460793	2	5.0728
Q8R0F9	VCEMLLHECELQSQK	0.902447384	2	4.63753
Q8R0F9	VCEMLLHECELQSQK+Oxidation(3)	1.590943361		
Q8R0F9	VGYTAEVLLPDK	1.113319898	2	2.69536
Q8R0F9	VGYTAEVLLPDKACEEK	0.749555387	2	2.74318
Q8R164	BPHL Valacyclovir hydrolase	1.014628328	0.951831	3
Q8R164	FADEFNR	1.006463148	2	2.49064
Q8R164	QVSLLGWSDGGITALIAAAK	0.975937869	2	3.437
Q8R164	TDFAPQLQSLNK	1.069695451	2	3.54716
Q8R1V4	TMED4 Transmembrane emp24 domain_containing protein 4	1.033635613	0.977436	2
Q8R1V4	CFIEEIPDETMVIGNYR	0.939387539	2	3.55078
Q8R1V4	QLLDQVEQIQK	1.08296257	2	3.14669
Q8R3Q6	CCD58 Coiled_coil domain_containing protein 58	1.042965757	0.659921	2
Q8R3Q6	IVHELNTTVPTASFAGK	1.234612297	2	4.1953
Q8R3Q6	NCIAQTSAVVK	1.042497273	2	2.66114
Q8R491	EHD3 EH domain_containing protein 3	0.971590658	0.999996	5
Q8R491	ADQIETQQLMR	0.870267763	2	2.79187
Q8R491	LDISDEFSEVIK	1.357091937	2	3.13806
Q8R491	LFEAEEQDLFK	0.963505293	2	3.6
Q8R491	MQDQLQAQDFSK	0.942265933	2	3.81479
Q8R491	QEETQRPVQMVK	0.992156458	2	2.52915
Q8VBU2	NDRG2 Protein NDRG2	0.985453164	3.47E-06	7
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.780134836	3	4.76731
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK+Oxidation(3)	0.892170069		
Q8VBU2	LDPTQTSFLK	0.813810796	1	1.90929
Q8VBU2	MADSGGQPQLTQPGK	1.32567221	2	3.85656
Q8VBU2	SLITHAPNLENIELYWNSYNNR	1.499911362	3	4.77606
Q8VBU2	TASLTSAASIDGSR	1.585154701	2	3.10935
Q8VBU2	TLSQSSESGTLPSGPPGHTMEVSC	0.993915792	2	4.42417
Q8VC12	HUTU Urocanate hydratase	1.118253058	8.17E-11	7
Q8VC12	HQLVVGSQAR	0.979302889	2	3.0967
Q8VC12	LLALEFAQELR	1.7164658	2	3.78182
Q8VC12	LQYMDNIR	1.273460733	2	2.35022
Q8VC12	LVITNGMVIPNYSSR	1.308804362	2	3.35347
Q8VC12	VAIAVAINQAIASGK	1.378411483	2	3.66429
Q8VC12	VFVTSGLGGMSGAQAK	0.995601191	2	4.50862
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9)	1.206713589		
Q8VDG5	PPCS Phosphopantothenate__cysteine ligase	1.430248874	0.000154	2
Q8VDG5	FLDNFSSGR	1.453558988	2	2.48359
Q8VDG5	LETDPDIIISR	1.423274348	2	3.16904
Q8VED5	K2C79 Keratin_ type II cytoskeletal 79	0.826093422	1.82E-05	4

Q8VED5	NKYEDEINK	0.817039539	2	2.7616
Q8VED5	NKYEDEINKR	0.85057223	3	3.44034
Q8VED5	NLDLDSIIAEVK	0.702199516	2	3.84987
Q8VED5	YEDEINK	1.026876447	1	2.48087
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.075305245**	**3.8E-07**	**9**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.231823104	3	4.49519
Q8VEK3	GYFEYIEENK	0.883666614	2	3.26657
Q8VEK3	LLEQYKEESK	1.318620312	2	3.16684
Q8VEK3	LLEQYKEESKK	1.163739854	2	3.38372
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.002141954	3	5.08896
Q8VEK3	NFILDQTNVSAAAQR	0.839542798	2	4.52812
Q8VEK3	TCNCETEDYGEK	1.239761715	2	3.38593
Q8VEK3	VSELKEELKK	1.190329476	2	2.42955
Q8VEK3	YNILGTNTIMDK	0.85659825	2	3.57529
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.654433767**	**2.65E-10**	**7**
Q8VHE9	ATVQSVLLDSAGR	0.784144131	2	3.53947
Q8VHE9	FLPLPLTQLLNK	0.884953261	2	2.85718
Q8VHE9	GATYGADHDLAR	1.164995158	2	3.17358
Q8VHE9	NLYSDLQALGSK	0.728529167	2	2.91939
Q8VHE9	RPPEPLVTDK	0.771251946	2	2.6184
Q8VHE9	VLVLEQHTK	0.856611287	2	2.38786
Q8VHE9	VVAHGVSHAILLK	0.857311862	2	2.42034
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.639858967**	**1.21E-12**	**4**
Q8VHT6	DCYVLSQLVGQK	1.378893764	2	2.96754
Q8VHT6	ILDLGSGSGR	0.445435997	2	2.68886
Q8VHT6	SLQNVHEEVISR	1.68144728	2	3.21631
Q8VHT6	TSADLQTNACVTPAK	1.651861122	2	3.84688
Q8VHX6	**FLNC Filamin_C**	**0.957549975**	**0.532259**	**3**
Q8VHX6	AFGPGLEGGLVNK	1.091716909	2	2.60014
Q8VHX6	GAGTGGLGLTVEGPCEAK	0.957498924	2	3.89588
Q8VHX6	LIALLEVLSQK	1.541380421	2	2.69896
Q8VI04	**ASGL1 L_asparaginase**	**1.009323446**	**0.571922**	**3**
Q8VI04	FAADMGIPQTPAEK	1.266588814	2	2.7111
Q8VI04	GNLAYATSTGGIVNK	0.966705857	2	4.28747
Q8VI04	TVDEAATLALDYMK	1.025854617	2	2.65614
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.042854225**	**0.309281**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	0.986106544	2	4.46664
Q8VID1	LAEDGAHVVISSR	2.470862848	2	3.70081
Q8VID1	NFAAELAPK	1.010132221	2	2.51755
Q8VID1	VNCLAPGLIK	0.659782352	2	2.54097
Q8VIF7	**SBP1 Selenium_binding protein 1**	**1.034486672**	**0.889006**	**10**
Q8VIF7	CGPGYATPLEAMK	0.969307503	2	3.46774
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	1.304516123	2	4.95789
Q8VIF7	GGFVLLDGETFEVK	1.056992578	2	4.1927
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.822703943	2	4.33114
Q8VIF7	HEIIQTLQMK	1.053025902	2	2.64103
Q8VIF7	HNIMVSTEWAAPNVFK	0.874014685	2	4.29946
Q8VIF7	LTGQIFLGGSIVK	1.054311971	2	3.00361
Q8VIF7	NEGGTWSVEK	1.146722881	2	2.8867
Q8VIF7	NTGIEAPDYLATVDVDPK	1.150739893	2	5.2064
Q8VIF7	VIEPNEIHAK	0.888843442	2	2.54865
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.109708918**	**0.850908**	**3**
Q8VIJ6	FGQGGAGPVGGQGPR	1.000354029	2	2.82719
Q8VIJ6	NLSPYVSNELLEEAFSQFGPIER	0.936470287	2	3.53484

Q8VIJ6	YGEPGEVFINK	**1.317024808**	2	2.79802
Q91VA0	ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial	0.791748321	0.920392	6
Q91VA0	AFIVLNPEFLSHDQEQLIK	**0.887853057**	2	5.57705
Q91VA0	AILPFDLQIIDEK	**0.842718873**	2	3.77388
Q91VA0	GNILPPNTEGYIGIR	**0.846104333**	2	3.00964
Q91VA0	HNQGLAFR	**0.605429759**	2	2.32328
Q91VA0	KVEFVSELPK	**1.100698422**	2	2.87308
Q91VA0	NKEFGQL	**0.897414803**	1	2.10873
Q91VM5	RBMXL Heterogeneous nuclear ribonucleoprotein G_like 1	1.110993338	0.002179	2
Q91VM5	LFIGGLNTETNEK	**1.624566271**	2	3.15128
Q91VM5	VEQATKPSFESGR	**1.109327772**	2	3.52291
Q91VM9	IPYR2 Inorganic pyrophosphatase 2_ mitochondrial	1.205081641	0.062323	2
Q91VM9	IIAINVNDPEAEK	**1.238954227**	2	3.25103
Q91VM9	MEIATEEPLNPIK	**1.129761054**	2	3.86711
Q91W43	GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial	1.002166973	0.942004	4
Q91W43	AGHQLQHDLFFDTLK	**1.117309528**	2	2.41108
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	**0.973120569**	2	4.0825
Q91W43	VSFQPNSGAQGEYAGLATIR	**0.947779725**	2	4.77808
Q91W43	YGNIDVAHLK	**0.993940628**	3	3.4904
Q91W90	TXND5 Thioredoxin domain_containing protein 5	1.092797548	0.578129	2
Q91W90	SFEDTIAQGITFVK	**1.058754232**	2	3.55809
Q91W90	VDCTQHYAVCSEHQVR	**1.101092829**	3	4.39099
Q91WL5	CP4CA Cytochrome P450 4A12A	0.95080438	0.458983	3
Q91WL5	FELLPDPTR	**0.791839228**	2	2.39649
Q91WL5	IQLQDEEELEK	**1.489921744**	2	2.35265
Q91WL5	VAVALTLLR	**1.295023265**	2	2.59905
Q91X77	CY250 Cytochrome P450 2C50	0.784215308	1.54E-08	3
Q91X77	IKEHEESLDVTIPR	**0.887466246**	3	3.60167
Q91X77	NFLLEK	**0.582662677**	1	2.1078
Q91X77	YALLLLLK	**0.970444444**	2	2.82037
Q91X78	ERLN1 Erlin_1	1.217723409	0.151478	2
Q91X78	ISEIEDAAFLAR	**0.857163407**	2	2.78583
Q91X78	SVQTTLQTDEVK	**1.239441487**	2	3.21543
Q91XE8	TM205 Transmembrane protein 205	0.873508517	0.93777	2
Q91XE8	HTFGLVQSK	**0.872681443**	2	2.48441
Q91XE8	MEKGEDPGSLIK+Oxidation(0)	**0.903278306**		
Q91XQ0	DYH8 Dynein heavy chain 8_ axonemal	0.940664024	0.562531	2
Q91XQ0	FRPEICDMVGNLVSVSR+Oxidation(7)	**0.9406694**		
Q91XQ0	SMTGIPNLQETLKEKQAR	**0.682161447**	2	2.58517
Q91XR8	GPX42 Phospholipid hydroperoxide glutathione peroxidase_ nuclear	1.011709887	0.988524	2
Q91XR8	TDVNYTQLVDLHAR	**1.111563459**	3	3.44217
Q91XR8	YGPMEEPQVIEK	**1.010594765**	2	2.51901
Q91Y81	SEPT2 Septin_2	0.846430547	0.756645	2
Q91Y81	ASIPFSVVGSNQLIEAK	**1.090907992**	2	3.38417
Q91Y81	LTVVDTPGYGDAINSR	**0.790522187**	2	4.06036
Q91YE2	EGLN2 Egl nine homolog 2	0.650914042	0.025183	2
Q91YE2	ERAAARDK	**0.889638535**	1	2.03881
Q91YE2	YQLASGQK	**0.508328141**	1	1.94326
Q91YP0	L2HDH L_2_hydroxyglutarate dehydrogenase_ mitochondrial	1.050765692	0.694911	2
Q91YP0	ISELSGCNPDPQIVPFR	**0.859469177**	2	3.15876

Q91YP0	NAPSPAATSSLAISR	**1.059091496**	2	3.44049
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.015046576**	**0.403368**	**9**
Q91YT0	GAGAYICGEETALIESIEGK	**1.045518867**	2	3.31248
Q91YT0	GDARPAEIDSLWEISK	**1.040194327**	2	3.21349
Q91YT0	GEFYNEASNLQVAIR	**1.143098449**	2	3.50547
Q91YT0	KTSFGSLKDEDR	**1.121564536**	2	3.27139
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	**1.507456841**	3	3.82542
Q91YT0	LVEGCLVGGR	**1.376765**	2	2.59467
Q91YT0	QIEGHTICALGDGAAWPVQGLIR	**0.958498979**	3	3.54008
Q91YT0	TSFGSLKDEDR	**1.216018824**	2	2.61488
Q91YT0	YLVVNADEGEPGTCK	**1.204992078**	2	5.06254
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**1.012697823**	**0.019884**	**6**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	**1.109111254**	3	6.88045
Q91Z53	LLDAAGANLR	**0.968252054**	2	3.15291
Q91Z53	NCVILPHIGSATYK	**1.049939636**	2	3.61925
Q91Z53	NTMSLLAANNLLAGLR	**0.962774323**	2	4.52388
Q91Z53	RLPEAIEEVK	**0.825833891**	2	2.45964
Q91Z53	VISTLSVGVDHLALDEIK	**1.362559068**	2	4.23469
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**0.754456219**	**9.9E-20**	**14**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	**0.953728637**	3	4.77645
Q91ZJ5	FVQDLSK	**0.683256853**	1	1.99038
Q91ZJ5	GGTLTQYEGK	**0.894756576**	2	2.54386
Q91ZJ5	GLPDNISSVLNK	**0.794913229**	2	3.87658
Q91ZJ5	GTVIIIANHGDR	**0.816647896**	2	3.0436
Q91ZJ5	IDIPPGAVLENK	**0.805138746**	2	3.0361
Q91ZJ5	IQRPPEDSIQPYEK	**0.836114008**	3	4.48757
Q91ZJ5	LNGGLGTSMGCK	**0.936840071**	2	3.12703
Q91ZJ5	LQEQNAIDMEIIVNPK	**1.588227789**	2	2.48911
Q91ZJ5	LVEIAQVPK	**0.840965676**	2	3.35483
Q91ZJ5	NENTFLDLTVQQIEHLNK	**0.787947664**	2	5.24444
Q91ZJ5	SFENSLGINVPR	**0.854891842**	2	3.22864
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	**0.77591316**	3	5.5088
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	**1.172716335**	2	4.60516
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**0.938186361**	**0.759825**	**7**
Q91ZX7	AVTDEEPFLIFANR	**1.281892937**	2	2.49959
Q91ZX7	CLQGACVVNK	**0.986436493**	2	2.33547
Q91ZX7	GCHVNECLSR	**0.933884716**	2	2.62999
Q91ZX7	IETAAMDGTLR	**1.017763744**	2	2.32792
Q91ZX7	ILQEDFTCR	**0.982189**	2	2.55975
Q91ZX7	LDGLCIPLR	**1.178477802**	2	2.4581
Q91ZX7	MYDAQQQQVGTNK	**0.973937925**	2	4.3498
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**1.129892061**	**8.28E-07**	**3**
Q920A6	DLDTVASDMMVLLK	**1.238669165**	2	3.32017
Q920A6	GLAEVSDIAEQVLNAVNK	**1.035148425**	3	4.87024
Q920A6	NTDGVNFYNILTK	**1.869815068**	2	2.94464
Q920D2	**DYR Dihydrofolate reductase**	**1.050698927**	**0.06787**	**4**
Q920D2	IMQEFESDTFFPEIDLEK	**0.817833751**	2	4.39025
Q920D2	LIEQPELASK	**0.889556031**	2	2.52197
Q920D2	LLPEYPGVLSEIQEEK	**1.169613221**	2	3.67855
Q920D2	NGDLPWPLLR	**0.827449922**	2	3.03892

Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.96669215**	**0.992803**	**4**
Q920F5	ADLLEAQALK	**1.127847422**	2	2.3127
Q920F5	EIAEVTGDPVHESLK	**0.923800125**	2	2.97186
Q920F5	ISECEAVHPVK	**1.025960528**	2	3.34431
Q920F5	WLLGLLNVQGK	**1.104374592**	2	3.61633
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**1.190619029**	**0.00481**	**19**
Q920L2	ACALSIAESCRPGDK	**1.194236603**	2	3.1481
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	**1.123559317**	3	4.82357
Q920L2	ANAGEESVMNLDK	**0.966581162**	2	4.00542
Q920L2	GEGGILINSQGER	**0.974084109**	2	4.33474
Q920L2	GSDWLGDQDAIHYMTEQAPASVVELENYGMPFSR	**2.584853193**	3	5.01183
Q920L2	GVIALCIEDGSIHR	**1.292998258**	2	3.49901
Q920L2	HTLSYVDTK	**1.445003783**	1	2.2572
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	**1.028474816**	3	6.99403
Q920L2	IDEYDYSKPIEGQQK	**1.067935639**	2	4.54493
Q920L2	KHTLSYVDTK	**1.069998289**	2	2.60505
Q920L2	LGANSLLDLVVFGR	**1.420072461**	2	3.4032
Q920L2	NTIIATGGYGR	**0.973256142**	2	2.80642
Q920L2	TGHSLLHTLYGR	**0.809254385**	2	2.34396
Q920L2	TLNEADCATVPPAIR	**0.992137803**	2	3.61717
Q920L2	TYFSCTSAHTSTGDGTAMVTR	**1.279455497**	3	3.42655
Q920L2	VGSVLQEGCEK	**1.104045695**	2	3.47238
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	**0.897974122**	3	4.00919
Q920L2	VSQLYGDLQHLK	**1.089827307**	3	3.45103
Q920L2	VTLDYRPVIDK	**1.192031758**	2	3.33655
Q920P0	**DCXR L_xylulose reductase**	**0.945980991**	**0.999999**	**6**
Q920P0	AVVQVSQIVAR	**1.04271509**	2	2.99721
Q920P0	GVPGAIVNVSSQASQR	**0.977066418**	2	5.49001
Q920P0	SSMTTGSALPVDGGFLAT	**1.014535751**	2	2.87131
Q920P0	STVLALQAAGAQVVAVSR	**0.968490836**	2	4.40453
Q920P0	TREDLDSLVR	**0.902580931**	2	3.04262
Q920P0	VNAVNPTVVMTPMGR	**0.878140486**	2	2.8458
Q921F2	**TADBP TAR DNA_binding protein 43**	**0.960610696**	**0.17567**	**4**
Q921F2	FGGNPGGFGNQGGFGNSR	**0.949075615**	2	4.07153
Q921F2	FTEYETQVK	**1.094222937**	2	2.67455
Q921F2	GISVHISNAEPK	**1.101260089**	2	2.66488
Q921F2	TSDLIVLGLPWK	**1.248079705**	2	3.12147
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.054588814**	**9.9E-20**	**5**
Q922F4	ALTVPELTQQMFDAK	**1.490701701**	2	4.13941
Q922F4	GHYTEGAELVDSVLDVVR	**1.103263074**	2	6.66903
Q922F4	IREEYPDR	**1.002330808**	2	2.96996
Q922F4	MASTFIGNSTAIQELFK	**1.62655944**	2	3.83395
Q922F4	NSSYFVEWIPNNVK	**1.108090381**	2	4.78259
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.080781237**	**0.699165**	**2**
Q922J3	EMETMQAKLMK+Oxidation(4)	**1.109067164**		
Q922J3	HEEILQNLQKMLADTEDK	**1.042910847**	2	2.56429
Q923D2		**1.053470445**	**0.997878**	**3**
Q923D2	LQDVTDDHIR	**0.963684827**	2	3.36458
Q923D2	TGLTTLAQAVQAGYEVTVLVR	**0.936043686**	3	4.28124
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	**1.101727601**	3	4.54274
Q923J6	**DYH12 Dynein heavy chain 12_ axonemal**	**0.938685924**	**0.984779**	**2**
Q923J6	FFFLSNDEMLEILSETKDPLR	**0.94475463**	2	2.4129
Q923J6	LEFLTNLDIK	**0.870845632**	1	2.09963
Q923K9	**A1CF APOBEC1 complementation factor**	**1.269367365**	**0.066195**	**2**

Q923K9	LAPQILEEICQK	**1.270736327**	2	2.33733
Q923K9	VTEGVVDVIVYPSAADK	**0.693697687**	2	3.58179
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**0.907582586**	**0.832215**	**2**
Q923M1	SAVYPTSAVQMEAALK	**0.828455237**	2	3.81222
Q923M1	VISAEEALPGR	**0.962326288**	2	3.12827
Q923V8	**SEP15 15 kDa selenoprotein**	**1.185888763**	**0.001265**	**3**
Q923V8	GCCQEEAQFETK	**1.102248777**	2	3.89176
Q923V8	LLDDNGNIAEELSILK	**1.253301628**	2	4.21853
Q923V8	WNTDSVEEFLSEK	**1.175092965**	2	2.95459
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**0.986987557**	**0.930626**	**5**
Q924C3	AEYLHTWGGLLPVISK	**1.07579838**	3	3.95175
Q924C3	GQPIWVTANHQEVR	**0.972824259**	2	2.92502
Q924C3	IEPLTFYLDPQWQLALNPSER	**1.332405367**	2	2.42787
Q924C3	SGTYFWPGSDVEIDGILPDIYK	**0.943987169**	2	3.43807
Q924C3	SVSSDLGCTCDPSIVPIMDFEK	**0.972346218**	2	2.75463
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**1.15414832**	**0.594825**	**13**
Q924S5	AGVTCIILPAENR	**1.036166622**	2	2.62353
Q924S5	AQLSATVLTLLIK	**0.844477665**	2	3.86421
Q924S5	AQSVLEEDHYGMEDVK	**1.09301763**	2	4.25919
Q924S5	EHQEALAVER	**0.947808028**	2	2.87772
Q924S5	EVGDELGAKPQLEMVTEATSDTSK	**1.399720457**	3	3.45397
Q924S5	HVMDVVDEELSK	**1.071375531**	2	3.21252
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	**1.292595438**	3	6.18881
Q924S5	MEMINVSGYVAQEK	**1.477910734**	2	2.54314
Q924S5	NYLDWLTSIPWGR	**0.905608554**	2	2.88377
Q924S5	QLEVEPEGLEPEAENK	**1.007005337**	2	4.25873
Q924S5	QSDENLDLAR	**0.95254272**	2	2.81862
Q924S5	TENPLVLIDEVDK	**1.045403414**	2	2.77818
Q924S5	VLEFIAVSQLR	**1.338832033**	2	3.08821
Q924W5	**SMC6 Structural maintenance of chromosomes protein 6**	**0.932773285**	**0.950973**	**2**
Q924W5	ELDMKEKELQEK+Oxidation(3)	**1.049044365**		
Q924W5	TKEQINQGEERLTELK	**0.929976676**	2	2.456
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**1.080326754**	**9.9E-20**	**3**
Q99020	EYFGQFGEIEAIELPIDPK	**1.166277765**	2	2.95541
Q99020	FGEVVDCTIK	**0.609602946**	2	2.7615
Q99020	IFVGGLNPEATEEK	**1.661558973**	2	4.03591
Q99068	**AMRP Alpha_2_macroglobulin receptor_associated protein**	**1.130018204**	**0.138202**	**3**
Q99068	EELKHFEAKIEK	**1.125128897**	2	2.4279
Q99068	HLQDLSSR	**0.895619597**	2	2.33785
Q99068	HVESIGDPEHISR	**2.004114032**	3	3.37327
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.151619863**	**0.446368**	**4**
Q99JI4	GAEILEVLHSLPAVR	**1.045525495**	2	2.35956
Q99JI4	LDEELEDAEK	**1.385397474**	2	2.39771
Q99JI4	RLDEELEDAEK	**1.207910644**	2	2.91073
Q99JI4	VNEIVETNRPDSK	**1.116171438**	2	3.58945
Q99KN9	**EPN4 Clathrin interactor 1**	**1.316701598**	**0.233003**	**2**
Q99KN9	GEFKDEEETVTTK	**1.321553108**	2	3.05005
Q99KN9	HIHITQATETTTTR	**1.048787574**	3	3.38723
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.966306722**	**0.933715**	**2**

Q99L04	ATAQEAQSLGGR	0.891041987	2	3.64541
Q99L04	CVPVVCDSSQESEVK	0.990828646	2	3.39982
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.012991891**	**0.879826**	**4**
Q99LF4	GLGHQVATDALVAMEK	0.667490801	2	3.97265
Q99LF4	NVTDVVNTCHDAGISK	1.138887766	2	4.46887
Q99LF4	NYNDELQFLDK	1.109342879	2	2.92088
Q99LF4	TNLDESDVQPVK	1.071796524	2	3.31695
Q99LH1	**NOG2 Nucleolar GTP_binding protein 2**	**1.259272035**	**0.176633**	**2**
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(11)	1.259272035		
Q99LH1	GGEPDMLTVSKMVLNDWQR+Oxidation(5)	1.259272035		
Q99ML5	**PCYOX Prenylcysteine oxidase**	**1.11829301**	**0.595663**	**3**
Q99ML5	ELGLSSVPASGGLVGVYNGK	1.021773792	2	2.51865
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	1.092787782	3	4.48301
Q99ML5	YQSHDYAFSSVEK	1.260716731	2	2.88251
Q99MS0	**S14L2 SEC14_like protein 2**	**1.148877279**	**0.179519**	**5**
Q99MS0	AGEMTEVLPNQR	0.927511729	2	2.97566
Q99MS0	CGYDLDGCPVWYDIIGPLDAK	0.803749509	2	3.19186
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.149772385	3	4.80772
Q99MS0	INYGGDIPK	1.442974883	2	2.50406
Q99MS0	QQYEHSVQISR	1.054768588	2	2.47861
Q99MW1	**STK31 Serine/threonine_protein kinase 31**	**0.954055941**	**0.753699**	**2**
Q99MW1	EVLLENYKALELK	0.847578098	2	2.30449
Q99MW1	QDQKLIEENEK	1.489921744	2	2.58889
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.902672765**	**0.565355**	**7**
Q99MZ8	GFSVVADTPELQR	0.899713065	2	3.38197
Q99MZ8	MGPSGGEGIEPER	0.852320251	2	3.19443
Q99MZ8	QQSELQSQVR	1.047565757	2	2.43189
Q99MZ8	QSFTMVADTPENLR	1.010957117	2	3.30258
Q99MZ8	TQDQISNIK	1.211630856	2	2.65946
Q99MZ8	YHEEFEK	1.008735683	1	2.21544
Q99MZ8	YKEEFEK	0.802346736	1	2.32508
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**1.06152519**	**0.672487**	**2**
Q99NA5	IEAACFATIK	1.365347272	2	2.31568
Q99NA5	NVTAIQGPGGK	1.041940028	2	2.43785
Q99NB7	**ACO12 Acyl_coenzyme A thioesterase 12**	**1.23739648**	**0.385368**	**3**
Q99NB7	GSISNTNVEALK	1.147515009	2	2.85696
Q99NB7	KGSISNTNVEALK	0.986998412	2	3.16902
Q99NB7	VHLKPVLLQTEQEQVEHR	1.314921528	3	3.84546
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**1.048559322**	**0.305848**	**8**
Q99PF5	AINQQTGAFVEISR	0.398125577	2	3.68595
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.926893725	2	6.1117
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	1.154194422	2	4.65524
Q99PF5	IGQQPQQPGAPPQQDYTK	1.434956282	2	3.68576
Q99PF5	IINDLLQSLR	1.031506721	2	2.69656
Q99PF5	SVSLTGAPESVQK	0.916027781	2	3.30931
Q99PF5	VGGGIDVPVPR	1.025219054	2	2.87941
Q99PF5	VQISPDSGGLPER	0.941966581	2	2.56642
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**1.321191427**	**9.9E-20**	**21**
Q99PL5	DALNQATSQVESK	1.534804726	2	3.7585
Q99PL5	EAEETQNSLQAECDQYR	1.404310115	2	5.46791
Q99PL5	EEITQLK	0.39734663	1	1.97703
Q99PL5	EHTSHLEAELEK	1.35406359	2	3.31701
Q99PL5	EQEIAAVQAR	1.45323786	2	2.37978
Q99PL5	ETSYEEALANQR	1.532417643	2	2.74048
Q99PL5	GELESSDQVR	1.514229574	2	3.15393

Q99PL5	HLEDIVEK	**1.207014419**	2	2.54403
Q99PL5	HMAAASAECQNYAK	**0.954576501**	2	4.46119
Q99PL5	HMAAASAECQNYAK+Oxidation(1)	**1.922204432**		
Q99PL5	IQEELEK	**0.829165347**	1	2.14268
Q99PL5	LKELESQVSCLEK	**2.069263066**	2	4.05969
Q99PL5	LLATEQEDAAVAK	**1.359117966**	2	4.53974
Q99PL5	LQQENSILR	**1.338045133**	2	2.82982
Q99PL5	LQSSEVEVK	**1.206483973**	2	2.52414
Q99PL5	LREAEETQNSLQAECDQYR	**1.203869032**	3	5.12514
Q99PL5	QLHLAEAQTK	**1.087073993**	2	2.3276
Q99PL5	TILAETEGMLK	**1.053719127**	2	3.03816
Q99PL5	TLQEQLENGPNTQLAR	**1.219011203**	2	4.82447
Q99PL5	TLVSTVGSMVFSEGEAQR	**1.731868932**	3	4.83702
Q99PL5	VEPAVSSIVNSIQVLASK	**1.339281919**	2	4.98192
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**0.940823635**	**0.999966**	**2**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	**0.940823635**		
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	**0.940823635**		
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.058651206**	**0.991218**	**2**
Q9CPQ1	FGVAEPR	**1.061566223**	2	2.34582
Q9CPQ1	NYDSMKDFEEMR	**0.96744036**	2	3.54507
Q9CQS8	**SC61B Protein transport protein Sec61 subunit beta**	**1.292093496**	**0.487528**	**2**
Q9CQS8	FYTEDSPGLK	**1.279124213**	2	2.33139
Q9CQS8	TTSAGTGGMWR	**0.89155591**	2	2.3868
Q9CRB8	**MTFP1 Mitochondrial fission process protein 1**	**1.001276879**	**0.996282**	**2**
Q9CRB8	SVDFLLDSSLR	**1.027849329**	2	2.79944
Q9CRB8	YLGYANEVGEAFR	**0.940114874**	2	2.71853
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.168867726**	**0.512607**	**2**
Q9CRB9	VAEELALEQAK	**1.290874867**	2	3.57217
Q9CRB9	YEYHPVCADLQTK	**1.1152258**	2	3.66173
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**1.033664625**	**0.877255**	**3**
Q9CW42	DLLLPITPPATNPLLQCR	**1.122290822**	2	4.14524
Q9CW42	GLSVSEAECTAMGLR	**0.938304207**	2	3.31315
Q9CW42	LQQVGTVAQLWIYPIK	**0.732169885**	2	2.94543
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.238750314**	**9.9E-20**	**3**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	**1.18466191**	2	4.48805
Q9CWH6	ALLEVVQSGGK	**1.208201673**	2	3.43171
Q9CWH6	LTVEDPVTVEYITR	**1.390856494**	2	3.90252
Q9CWK8	**SNX2 Sorting nexin_2**	**1.117528658**	**0.954291**	**4**
Q9CWK8	AVNTQALSGAGILR	**1.050738235**	2	3.18919
Q9CWK8	QQQFENLDQQLR	**0.85248031**	2	2.81814
Q9CWK8	WEDAQITLLK	**1.035678455**	2	2.78814
Q9CWK8	YWEAFLPEAK	**1.182157171**	2	2.53179
Q9CXS4	**CENPV Centromere protein V**	**1.151742725**	**0.71955**	**2**
Q9CXS4	LLLDTFEYQGLVK	**1.185235779**	2	3.93958
Q9CXS4	SVVTEEFNGSDWER	**0.925667718**	2	3.76943
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**1.205592965**	**0.000623**	**2**
Q9CYN2	LHDSLATER	**0.91655104**	2	2.41953
Q9CYN2	YVENFGLIDGR	**1.208675454**	2	2.73659
Q9CYW4	**HDHD3 Haloacid dehalogenase_like hydrolase domain_containing protein 3**	**0.810504529**	**0.364743**	**2**
Q9CYW4	LEDILTGLGLR	**0.817999293**	2	4.23748
Q9CYW4	RLEDILTGLGLR	**2.100582175**	2	3.28115
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**1.183513753**	**0.782872**	**2**

Q9CZY3	LLEELEEGQK	**1.310207588**	2	2.74948
Q9CZY3	VNMSGVSSSNGVVDPR	**1.125693818**	2	2.61564
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.087824698**	**9.9E-20**	**4**
Q9D0M3	GLLSSLDHTSIR	**1.261228944**	2	3.19604
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	**2.146677002**	3	5.9157
Q9D0M3	HLVGVCYTEEEAK	**1.257547335**	2	3.73471
Q9D0M3	LSDYFPKPYPNPEAAR	**1.445861327**	3	3.63396
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.254855625**	**1.42E-10**	**3**
Q9D0S9	DVAPQAPVHFLVIPR	**1.130315187**	2	2.82322
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	**1.34842937**	2	5.15655
Q9D0S9	SLPADILYEDQQCLVFR	**1.000039528**	2	3.4987
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.170750924**	**5.61E-05**	**4**
Q9D172	GVEVTVGHEQEEGGK	**1.143976914**	2	3.80141
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	**1.375693107**	2	4.62831
Q9D172	NLSTFAVDGK	**1.297676021**	1	2.62299
Q9D172	NVLAESAR	**0.998966729**	1	1.93021
Q9D180	**WDR65 WD repeat_containing protein 65**	**0.481077864**	**0.087689**	**2**
Q9D180	KNQELEK	**0.829165347**	1	2.12222
Q9D180	QIEPRENEIK	**0.464102523**	1	1.98201
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.178298025**	**7.77E-16**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0)	**5.277154927**		
Q9D1Q6	NIIGYFEQK	**0.996837195**	1	2.084
Q9D1Q6	SNPVHEIQSLDEVTNLDR	**0.922276986**	2	5.25536
Q9D1Q6	VDCDQHSDIAQR	**1.048435433**	2	3.63182
Q9D2U9	**H2B3A Histone H2B type 3_A**	**1.06965058**	**0.014693**	**6**
Q9D2U9	AMGIMNSFVNDIFER	**1.021381341**	2	4.8175
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	**1.132997552**		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	**1.177141297**		
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4)	**1.165337224**		
Q9D2U9	LLLPGELAK	**1.135232071**	2	2.64028
Q9D2U9	QVHPDTGISSK	**0.964224986**	2	2.37401
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.32343352**	**0.00666**	**3**
Q9D6M3	GAAVNLTLVTPEK	**1.431474301**	2	3.11386
Q9D6M3	GVNEDTYSGFLDCAR	**1.606705101**	2	4.84632
Q9D6M3	NHGIAGLYK	**2.161818281**	1	2.04715
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**0.948756125**	**0.790566**	**10**
Q9D6Y9	CSDGGIYCK	**0.904503116**	1	2.08554
Q9D6Y9	CVAYAESHDQALVGDK	**0.990775217**	2	5.01164
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	**1.695594608**	3	3.40919
Q9D6Y9	GTHDLWDSR	**0.870627131**	2	2.56357
Q9D6Y9	GYESFGIHR	**0.978684454**	2	2.45794
Q9D6Y9	IVLDSDAAEYGGHQR	**1.207897114**	2	4.53412
Q9D6Y9	IYESHVGISSHEGK	**1.022616473**	2	4.40534
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	**2.12272163**	3	3.36342
Q9D6Y9	QFNLTDDDLLR	**0.803413027**	2	2.49417
Q9D6Y9	RQFNLTDDDLLR	**1.320983961**	2	2.59085
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.009972664**	**0.231854**	**3**
Q9D7B6	AVIFEDCAVPVANR	**1.009770656**	2	4.06759
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	**0.859021318**	2	4.37692
Q9D7B6	VHQILEGSNEVMR	**1.39607229**	2	2.58901
Q9D7S7	**RL22L 60S ribosomal protein L22_like 1**	**1.312332999**	**0.003395**	**2**
Q9D7S7	FHLDLTHPVEDGIFDSGNFEQFLR	**1.216138306**	3	3.78877
Q9D7S7	TGNLGNVVHIER	**2.841984426**	2	2.47678

Q9D7W5	**MED8 Mediator of RNA polymerase II transcription subunit 8**	**1.575929217**	**1.21E-06**	**2**
Q9D7W5	NQVIIPLVLSPDRDEDLMR+Oxidation(17)	**1.490227616**		
Q9D7W5	QIQSLNKMCSNLLEK+Oxidation(7)	**1.266305212**		
Q9D7X8	**GGCT Gamma_glutamylcyclotransferase**	**0.932473701**	**0.007413**	**2**
Q9D7X8	ISDEMEDIIK	**0.78266724**	2	2.9597
Q9D7X8	SNISSLDEQEGVK	**0.950035255**	2	3.05607
Q9D819	**IPYR Inorganic pyrophosphatase**	**0.966394352**	**0.000306**	**5**
Q9D819	GISCMNTTVSESPFK	**0.940924085**	2	4.50274
Q9D819	GQYISPFHDVPIYADK	**1.323298139**	2	3.77724
Q9D819	VLGILAMIDEGETDWK	**1.47983984**	2	4.00046
Q9D819	YKVPDGKPENEFAFNAEFK	**1.05462047**	2	3.64163
Q9D819	YVANLFPYK	**0.840984693**	1	1.93985
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.098084738**	**0.837314**	**2**
Q9D880	TIALNQVEDVR	**1.180912519**	2	2.9345
Q9D880	TVLEHYALEDDPLEAFK	**1.072092377**	2	5.039
Q9DBA8	**HUTI Probable imidazolonepropionase**	**0.90538641**	**0.519636**	**4**
Q9DBA8	AGTTLVECK	**1.121122523**	2	2.60088
Q9DBA8	GVFDLDTTR	**0.816799024**	2	2.30374
Q9DBA8	QGDAIIINASR	**1.197336478**	2	2.67138
Q9DBA8	SGYGLNLETELK	**1.100813359**	2	2.36286
Q9DBH5	**LMAN2 Vesicular integral_membrane protein VIP36**	**1.206778668**	**0.005478**	**3**
Q9DBH5	LPTGYYFGASAGTGDLSDNHDIISIK	**1.660533058**	3	4.62467
Q9DBH5	TPEEESIDWTK	**1.262214836**	2	2.42645
Q9DBH5	WSELAGCTADFR	**1.195890903**	2	3.17241
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**1.162490829**	**0.570292**	**2**
Q9DC70	LDDLINWAR	**0.870678433**	2	2.99091
Q9DC70	QADVMIVAGTLTNK	**1.259005878**	2	3.31399
Q9DCH4	**EIF3F Eukaryotic translation initiation factor 3 subunit F**	**1.032628393**	**0.007593**	**2**
Q9DCH4	IQDALSTVLQYAEDVLSGK	**1.115985599**		
Q9DCH4	VIGLSSDLQQVGGASAR	**1.075519572**		
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.119468381**	**0.622275**	**2**
Q9DCM0	SLLPGCQSVISR	**1.126120428**	2	3.20238
Q9DCM0	TDFQQGCAK	**1.291571435**	2	2.36362
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.407456549**	**0.00063**	**2**
Q9DCS9	AYDLVVDWPVTLVR	**1.078296076**	2	4.6789
Q9DCS9	TPAPSPQTSLPNPITYLTK	**1.817724502**	2	3.35069
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**0.975432699**	**2.01E-10**	**5**
Q9DCT2	FDLNSPWEAFPAYR	**0.970767052**	2	2.78131
Q9DCT2	ILTDYGFEGHPFR	**0.724520923**	2	2.63934
Q9DCT2	KFDLNSPWEAFPAYR	**1.036392587**	2	3.63371
Q9DCT2	SLADLTAVDVPTR	**1.247216165**	2	3.56282
Q9DCT2	VVAEPVELAQEFR	**0.703815061**	2	3.31178
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**1.132046338**	**5.61E-09**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	**1.306796494**	2	5.19591
Q9DCU9	LIEPNTAVTR	**1.095022803**	2	3.30671
Q9DCU9	TMDWFGYYGGPCR	**1.720840045**	2	3.40237
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.530854732**	**0.014659**	**2**
Q9EP75	DEDGKELSDEDIR	**0.998095981**	2	2.71357
Q9EP75	IFNDSTNIMHAK	**1.59072219**	2	3.30377

Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.090640292**	**3.53E-14**	**10**
Q9EP89	FENSIESLR	**1.022323383**	2	2.82846
Q9EP89	GIIVSIICNMQSVGLNSTALK	**1.054570898**	3	3.73242
Q9EP89	IFHDLDMLTTVQEENEPVIYNR	**0.986881935**	3	4.01881
Q9EP89	IKDEVGAPGIVVGVSVDGK	**0.877645202**	2	5.0234
Q9EP89	KNDFEQGELYLK	**1.435397833**	2	3.79962
Q9EP89	LDLDLPVQHYVPEFPEK	**1.23535473**	2	3.13378
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	**1.197743062**	3	3.66681
Q9EP89	LVNTPYVDNSYK	**2.555831446**	2	3.22032
Q9EP89	NDFEQGELYLK	**1.628527575**	2	2.91169
Q9EP89	WAGGGFLSTVGDLLK	**1.077183868**	2	4.31655
Q9EPH2	**MRP MARCKS_related protein**	**1.255062861**	**0.001181**	**2**
Q9EPH2	AAATPESQEPQAK	**1.263017714**	2	2.77378
Q9EPH2	GDVTAEEAAGASPAK	**0.786984985**	2	3.41612
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**2.278805831**	**0.000241**	**13**
Q9EPH8	ALDTMNFDVIK	**1.076054266**	2	3.30341
Q9EPH8	ALYDTFSAFGNILSCK	**2.322055721**	2	2.5951
Q9EPH8	FSPAGPILSIR	**0.774941392**	2	2.31515
Q9EPH8	GFGFVCFSSPEEATK	**3.896913363**	2	4.00351
Q9EPH8	GFGFVSFER	**1.115761704**	2	2.78446
Q9EPH8	GYGFVHFETQEAAER	**1.400711691**	2	3.12115
Q9EPH8	ITGMLLEIDNSELLHMLESPESLR	**1.296917934**	3	3.6525
Q9EPH8	KEFSPFGTITSAK	**1.036867199**	2	2.87802
Q9EPH8	NLDDGIDDER	**0.742107914**	2	2.84831
Q9EPH8	SGVGNIFIK	**1.153770273**	2	2.75752
Q9EPH8	SKVDEAVAVLQAHQAK	**1.259653338**	2	5.23974
Q9EPH8	SLGYAYVNFQQPADAER	**1.515427149**	2	3.6512
Q9EPH8	VDEAVAVLQAHQAK	**1.125046251**	2	3.14931
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.57911832**	**9.9E-20**	**12**
Q9EQ76	ASIYQSVFTNSSK	**1.514556744**	2	3.17852
Q9EQ76	GTCILPSVNDMMDDIDEK	**1.969143484**	2	3.5942
Q9EQ76	ILCGTVSIKPNVK	**1.508098081**	2	2.99591
Q9EQ76	KEPVFNDELPAR	**1.608323677**	2	3.22151
Q9EQ76	LQEYITSFATEK	**4.160085703**	2	4.07355
Q9EQ76	NNEVTLYK	**3.271585017**	2	2.45267
Q9EQ76	NNLPTAISDWWYMK	**2.008906469**	2	2.91059
Q9EQ76	SCLEEGLEPTCFER	**1.027385647**	2	4.58956
Q9EQ76	SDDVGGLWK	**2.935103522**	2	2.77175
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	**2.311074901**	3	5.19264
Q9EQ76	VWNDGYPWDMVVITR	**1.640235265**	2	4.13326
Q9EQ76	YIQFETLVTR	**3.056859826**	2	3.3053
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.263547071**	**0.555995**	**6**
Q9EQH3	ACAELHQNVNVK	**0.937806727**	2	3.70472
Q9EQH3	IREDLPNLESSEETEQINK	**1.189667922**	3	3.8482
Q9EQH3	LNLEHIATSSAVSK	**0.981990704**	2	3.52143
Q9EQH3	LSQLEGVNVER	**1.181643269**	2	2.98017
Q9EQH3	NIIIALIDR	**0.936425427**	2	2.31821
Q9EQH3	VLETTVEIFNK	**1.145568025**	2	2.70742
Q9EQH7	**NDST3 Bifunctional heparan sulfate N_deacetylase/N_sulfotransferase 3**	**1.055767759**	**0.554285**	**2**
Q9EQH7	KFALEHGIPTDMGYAVSPHHSGVYPVHVQLYEAWKK	**1.36465723**	3	3.3491
Q9EQH7	TTPATVMDEVQK+Oxidation(6)	**0.931281029**		
Q9EQN5	**SMBP2 DNA_binding protein SMUBP_2**	**0.635579268**	**0.578354**	**2**
Q9EQN5	CPTTSVRKPASAQESRQEAR	**0.878754475**	2	2.36306

Q9EQN5	KPSEKPLGSQVQPQHSSK	**0.550584163**	2	2.34972
Q9EQS0	**TALDO Transaldolase**	**1.199268353**	**7.91E-11**	**7**
Q9EQS0	ALAGCDFLTISPK	**1.001552761**	2	3.48073
Q9EQS0	EAGISKDRILIK	**0.994506132**	2	2.34868
Q9EQS0	ILDWHVANTDKK	**1.074382331**	2	3.20659
Q9EQS0	LGGPQEEQIK	**1.302269455**	2	3.0213
Q9EQS0	LSSTWEGIQAGK	**1.303283253**	2	2.83777
Q9EQS0	SYEPQEDPGVK	**0.946490971**	2	2.8935
Q9EQS0	WLHNEDQMAVEK	**0.832620967**	3	3.32183
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.125758593**	**0.001627**	**3**
Q9EQX9	LELFLPEEYPMAAPK	**0.910580383**	2	3.44018
Q9EQX9	SNEAQAIETAR	**1.127234428**	2	3.65616
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	**1.241977603**	3	4.34284
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.15246287**	**1.05E-12**	**23**
Q9ER34	ADIANLAEEFK	**1.089195681**	2	3.48264
Q9ER34	CTTDHISAAGPWLK	**1.030648243**	2	4.31623
Q9ER34	DINQEVYNFLATAGAK	**1.48817157**	2	4.14165
Q9ER34	DLEDLQILIK	**1.618001419**	2	2.50314
Q9ER34	FKLEAPDADELPR	**1.088471955**	3	4.27462
Q9ER34	FNPETDFLTGK	**1.105183954**	1	2.42444
Q9ER34	GHLDNISNNLLIGAINIENGK	**1.037291894**	2	5.60659
Q9ER34	IVYGHLDDPANQEIER	**2.206679916**	2	4.95232
Q9ER34	LEAPDADELPR	**1.225190457**	2	2.59118
Q9ER34	LNRPLTLSEK	**1.492326373**	2	2.44747
Q9ER34	LQLLEPFDKWDGKDLEDLQILIK	**1.183335033**	3	3.68016
Q9ER34	LTGTLSGWTSPK	**1.1627162**	2	2.58896
Q9ER34	NAVTQEFGPVPDTAR	**1.104065288**	2	4.55782
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	**1.43398722**	3	4.41255
Q9ER34	NTIVTSYNR	**1.181177002**	2	2.3768
Q9ER34	QGLLPLTFADPSDYNK	**1.126226123**	2	3.4433
Q9ER34	SDFDPGQDTYQHPPK	**1.156725879**	2	2.45517
Q9ER34	SQFTITPGSEQIR	**0.983963968**	2	3.45213
Q9ER34	VAMQDATAQMAMLQFISSGLPK	**1.705716463**	2	2.37307
Q9ER34	VAVPSTIHCDHLIEAQLGGEK	**1.573182749**	2	4.91602
Q9ER34	VDVSPTSQR	**1.146589654**	2	2.40706
Q9ER34	VGLIGSCTNSSYEDMGR	**0.954676088**	2	4.36792
Q9ER34	WVVIGDENYGEGSSR	**1.147283993**	2	4.51262
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.973872249**	**0.999689**	**3**
Q9ES21	LEEQDEFEK	**0.988270617**	2	2.81877
Q9ES21	TNVIQSLLAR	**1.048071573**	2	2.33926
Q9ES21	TQLGLVMDGFNSLLR	**0.973871336**	2	3.78059
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**1.136301659**	**0.294097**	**13**
Q9ES38	ACQAAWALK	**1.112334025**	2	2.53624
Q9ES38	ADVWENFQQR	**1.13907996**	2	3.01327
Q9ES38	EGFDVGVIADPLYILDNK	**1.209353074**	2	5.33893
Q9ES38	GATAILVLPSK	**1.132663041**	2	2.68855
Q9ES38	IQDSLEITNTYK	**1.094267971**	2	3.73132
Q9ES38	LKEATIQEDK	**1.247277595**	2	2.60701
Q9ES38	LLAENIR	**1.170106651**	2	2.39822
Q9ES38	MLTPLELVQFDIETAEPVRDK	**0.909435095**	2	4.28251
Q9ES38	QGFCIPVETGKPGLLLTK	**0.859566233**	3	3.6665
Q9ES38	SISALSVFLGLAK	**0.780532415**	2	3.4069
Q9ES38	SLMPDVYQAVCEGTWK	**1.510730832**	2	3.95606
Q9ES38	YLCNVPGQPEDK	**1.146213783**	2	3.32896
Q9ES38	YLCNVPGQPEDKK	**0.982773675**	2	2.49462
Q9ES53	**UFD1 Ubiquitin fusion degradation protein 1 homolog**	**1.084575399**	**0.297163**	**2**

Q9ES53	FQPQSPDFLDITNPK	**1.112369902**	2	2.49985
Q9ES53	FVAFSGEGQSLRKK	**0.772868849**	2	2.58327
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.99264803**	**0.818442**	**2**
Q9EST6	SLDLFGCEVTNR	**0.955619665**	2	3.09855
Q9EST6	TPAAVQELVLDNCK	**1.166606016**	2	3.45614
Q9ESV1	**LUZP1 Leucine zipper protein 1**	**0.811104898**	**0.053156**	**2**
Q9ESV1	EKLEEEENLTR	**0.999598211**	2	2.87248
Q9ESV1	RMADLEKLEEALSR	**0.72657335**	2	2.53114
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**0.986849489**	**2.67E-06**	**4**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	**1.294310417**	3	6.02124
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	**1.500537306**	3	3.96137
Q9ESW0	QGQGQLVTCSGAFK	**1.265982851**	2	2.89987
Q9ESW0	VTLGTQPTVLR	**1.016330016**	2	2.6335
Q9HB97	**PARVA Alpha_parvin**	**0.876704856**	**0.445874**	**2**
Q9HB97	DLAEDLYDGQVLQK	**0.676516115**	2	3.10192
Q9HB97	LNVAEVTQSEIAQK	**0.877952687**	2	4.33699
Q9JHL4	**DBNL Drebrin_like protein**	**0.988970471**	**0.01746**	**4**
Q9JHL4	AMSTTSVSSSQPGK	**0.774977323**	2	2.58581
Q9JHL4	ERAMSTTSVSSSQPGKLR+Oxidation(3)	**0.133149914**		
Q9JHL4	TGELEQEVVSR	**1.201405802**	2	3.3414
Q9JHL4	VAGTGEGGLEELVEELNSGK	**1.051696053**	2	2.86545
Q9JI85	**NUCB2 Nucleobindin_2**	**1.25051023**	**3E-13**	**4**
Q9JI85	FQQGIAPSGPAGELK	**1.464684744**	2	2.73326
Q9JI85	QEYQQAVQQLEQK	**1.260839001**	2	4.3223
Q9JI85	QVIEVLETDPHFR	**0.990583056**	2	2.66934
Q9JI85	VHNVEPVESAR	**1.253177584**	2	2.91834
Q9JI91	**ACTN2 Alpha_actinin_2**	**0.958877068**	**0.032255**	**11**
Q9JI91	DQSLQEELAR	**1.669762759**	2	2.61221
Q9JI91	ETADTDTAEQVIASFR	**0.617732094**	2	3.93364
Q9JI91	GYEEWLLNEIR	**1.081338357**	3	3.37113
Q9JI91	HRPDLIDYSK	**1.825754028**	2	2.3948
Q9JI91	HTNYTMEHIR	**0.956589421**	3	3.40227
Q9JI91	HTNYTMEHIR+Oxidation(5)	**1.487652903**		
Q9JI91	KHEAFESDLAAHQDR	**0.647090543**	2	5.36773
Q9JI91	LEGDHQLIQEGLVFDNK	**0.785910906**	3	4.94817
Q9JI91	MLDAEDIVNTPKPDER	**1.110472152**	2	3.8895
Q9JI91	QSILAIQNEVEK	**0.196346129**	2	2.97183
Q9JI91	TINEVETQILTR	**0.699251341**	2	2.53
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**0.976321403**	**0.782355**	**7**
Q9JJ19	AVDPDSPAEASGLR	**1.017492311**	2	3.68342
Q9JJ19	IVEVNGVCMEGK	**0.948138366**	2	3.22576
Q9JJ19	LLVVDPETDEQLKK	**1.282811966**	2	2.47466
Q9JJ19	LVEPGSPAEK	**0.97744519**	2	2.52615
Q9JJ19	LVEVNGENVEK	**2.664821997**	2	2.79379
Q9JJ19	SEHTEPPAAADTK	**0.389911811**	2	3.03358
Q9JJ19	VTPSQEHLDGPLPEPFSNGEIQK	**0.822500848**	3	3.67463
Q9JJ22	**ERAP1 Endoplasmic reticulum aminopeptidase 1**	**1.11332784**	**0.773183**	**2**
Q9JJ22	ASLINNAFQLVSIGK	**1.171159035**	2	2.52207
Q9JJ22	TQEFPHILTLIGR	**1.06864635**	2	2.57807
Q9JJ40	**NHRF3 Na(_)/H(_) exchange regulatory cofactor NHE_RF3**	**1.075684233**	**0.190226**	**3**
Q9JJ40	GVFLTDITPQGVAMK	**1.016307563**	2	2.41519
Q9JJ40	NGGDQTTLLVLDK	**1.070588276**	2	2.45423
Q9JJ40	SGNSVTLLVLDGDSYEK	**1.376380502**	2	4.38483

Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**0.842317559**	**0.05096**	**3**
Q9JJ46	HLTNAQSMLDNK	**0.84313863**	2	3.52705
Q9JJ46	HLTNAQSMLDNK+Oxidation(7)	**1.248406406**		
Q9JJ46	VSVVPLGTGR	**1.186345655**	2	2.52231
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**1.410083253**	**0.005733**	**3**
Q9JJ54	FGDVVDCTLK	**0.984556744**	2	2.98743
Q9JJ54	IFVGGLSPDTPEEK	**1.235331756**	2	4.20112
Q9JJ54	IFVGGLSPDTPEEKIR	**1.472532728**	2	2.50755
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.188054532**	**0.341905**	**5**
Q9JJ79	ASDLKDLNSR	**1.107392416**	2	2.32145
Q9JJ79	ELMLERETLLAR+Oxidation(2)	**1.869712434**		
Q9JJ79	NCLEEWTKAAGLEK	**1.126028833**	2	2.4201
Q9JJ79	TVLRGSGNLLR	**1.225254914**	2	2.43683
Q9JJ79	YVVQIGDK	**0.917744714**	1	2.07297
Q9JJM9	**SEPT5 Septin_5**	**0.888964662**	**0.01683**	**2**
Q9JJM9	LIRMKDEELR	**1.70145891**	2	2.47511
Q9JJM9	MQEMLQKMK+Oxidation(3)	**0.464459156**		
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.27424174**	**0.588277**	**2**
Q9JJU8	GDYDAFFEAR	**0.910816208**	2	2.48632
Q9JJU8	QQDVLCFLEANK	**1.07546863**	2	3.28027
Q9JK11	**RTN4 Reticulon_4**	**1.232922995**	**0.009923**	**2**
Q9JK11	VDRKCLEDSLEQK	**1.262201434**	2	2.34615
Q9JK11	YSNSALGHVNSTIK	**0.469202024**	2	2.6987
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.163772296**	**0.287479**	**3**
Q9JK38	ITLECLPQNVGFYK	**1.666556102**	2	3.03087
Q9JK38	VEDVVVSDECR	**1.189970226**	2	3.53609
Q9JK38	VLGQLTETGVVSPEQFMK	**1.214559247**	2	4.1704
Q9JK72	**CCS Copper chaperone for superoxide dismutase**	**1.411033451**	**0.034231**	**2**
Q9JK72	GDLGNVHAEASGR	**1.414550681**	2	2.77098
Q9JK72	SLVVDEGEDDLGR	**1.350782854**	2	2.30483
Q9JKS4	**LDB3 LIM domain_binding protein 3**	**0.233531254**	**0.139929**	**2**
Q9JKS4	GAPAYNPTGPQVTPLAR	**0.130477821**	2	3.93065
Q9JKS4	TQSKPEDEADEWAR	**0.27969417**	2	3.54602
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.305665881**	**0.093708**	**12**
Q9JLA3	AIWAALQTQTSNSAK	**1.630205854**	2	3.62452
Q9JLA3	FLFVDADQIVR	**1.178251058**	2	2.90383
Q9JLA3	FLSPLQQNLLK	**1.070146183**	2	2.38585
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	**1.138687209**	3	6.33893
Q9JLA3	IEYQFFEDK	**1.125488951**	2	2.52087
Q9JLA3	IVPEWQDYDQEIK	**0.930726886**	2	3.28921
Q9JLA3	LNIQPSETDYAVDIR	**1.103744473**	2	3.94754
Q9JLA3	TAAIANSMNYLTK	**1.216697617**	2	2.55355
Q9JLA3	VDALLSAQPK	**1.159874508**	2	3.00372
Q9JLA3	VEEDVASDLVMK	**0.839216213**	2	3.5059
Q9JLA3	VWQLQDLSFQTAAR	**1.177224711**	2	4.41666
Q9JLA3	YVLEPEISFTADNSFAK	**1.489606125**	2	3.7142
Q9JLH7	**CK5P3 CDK5 regulatory subunit_associated protein 3**	**0.814533468**	**0.212403**	**3**
Q9JLH7	GSDALTLLEYPETR	**0.923711383**	2	2.47365
Q9JLH7	KEEEGQAGAAEMR+Oxidation(11)	**0.711201091**		

Q9JLH7	QYGITGDNVRRELLALVK	**0.997859154**	2	2.37243
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.255452234**	**9.9E-20**	**19**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	**1.059424506**	2	4.33006
Q9JLJ3	ANDTTFGLAAGVFTR	**1.112440499**	2	4.61709
Q9JLJ3	CQVLLEAAR	**1.015573954**	2	3.51146
Q9JLJ3	EQGATVLCGGEPYAPEDPK	**1.147356057**	2	4.63216
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	**1.095591813**	3	3.35561
Q9JLJ3	EVNLAVENAK	**1.124399577**	1	2.9495
Q9JLJ3	GALLANFLTQGQVCCNGTR	**1.182281982**	2	5.38024
Q9JLJ3	GIKPITLELGGK	**1.357317307**	3	3.97212
Q9JLJ3	HGYYMTPCILTNCTDDMTCVK	**0.806049245**	3	3.60533
Q9JLJ3	IGDPLLEDTR	**1.137683487**	2	4.01381
Q9JLJ3	MGPLINAPHLER	**1.067483904**	2	3.12244
Q9JLJ3	MGPLINAPHLER+Oxidation(0)	**1.204915503**		
Q9JLJ3	RDEIAIMETINNGK	**1.118586734**	2	5.36157
Q9JLJ3	SAPALACGNAMIFKPSPFTPVSALLLAEIYTK	**1.094126341**	3	3.45928
Q9JLJ3	SPLIIFSDCNMK	**1.042491637**	2	2.55418
Q9JLJ3	VEPVDASGTEK	**1.044686846**	1	2.24513
Q9JLJ3	VSFTGSVPTGMK	**1.170635101**	2	3.57454
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10)	**1.405166065**		
Q9JLJ3	VTIEYYSQLK	**3.00613188**	2	3.12621
Q9JLQ0	**CD2AP CD2_associated protein**	**1.07749025**	**0.737269**	**2**
Q9JLQ0	LQEEGWLEGELNGR	**0.977987836**	2	2.33879
Q9JLQ0	SNLEVEIAK	**1.117237135**	1	1.90647
Q9JLR1	**S61A2 Protein transport protein Sec61 subunit alpha isoform 2**	**1.037688051**	**0.587304**	**3**
Q9JLR1	GTLMELGISPIVTSGLIMQLLAGAK	**1.176690598**		
Q9JLR1	IIEVGDTPK	**0.88333768**	2	2.44053
Q9JLR1	TWIEVSGSSAK	**1.216055344**	2	2.66745
Q9JLT0	**MYH10 Myosin_10**	**1.116699414**	**7.58E-08**	**2**
Q9JLT0	AGVLAHLEEER	**1.165810017**	2	3.57284
Q9JLT0	KFDQLLAEEKGISAR	**0.574962279**	2	2.40931
Q9JLZ1	**GLRX3 Glutaredoxin_3**	**0.748476736**	**0.271255**	**2**
Q9JLZ1	ELEASEELDTICPK	**0.753829684**	2	3.10781
Q9JLZ1	LEAEAVPEVSEK	**0.195840715**	2	2.49429
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.922062531**	**0.158081**	**4**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	**0.860984568**	2	5.71305
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	**0.917822701**	3	4.36533
Q9JLZ3	GIVVLGINR	**0.982881384**	2	2.85249
Q9JLZ3	SEVPGIFCAGADLK	**0.940213535**	2	2.93749
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**1.009306519**	**0.920498**	**15**
Q9JM53	AIASAAEGGSVPPIR	**1.120738332**	2	3.16155
Q9JM53	CLIATGGTPR	**0.814359608**	2	2.58395
Q9JM53	DGEQHEDLNEVAK	**1.425485092**	3	3.59366
Q9JM53	ILPEYLSNWTMEK	**1.064552314**	2	3.10488
Q9JM53	KSQASGIEVIQLFPEK	**1.200707252**	2	3.84772
Q9JM53	KVETDHIVTAVGLEPNVELAK	**0.979159008**	2	6.30578
Q9JM53	LNDGSQITFEK	**1.025564263**	2	3.34653
Q9JM53	SITVIGGGFLGSELACALGR	**0.840436636**	2	3.33527
Q9JM53	SQASGIEVIQLFPEK	**0.96645551**	2	4.46112
Q9JM53	TGGLEIDSDFGGFR	**1.126706544**	2	4.56646
Q9JM53	VETDHIVTAVGLEPNVELAK	**0.978824324**	2	5.21568
Q9JM53	VLIVSEDPELPYMRPPLSK	**1.007078213**	3	3.74137
Q9JM53	VMPNAIVQSVGVSGGK	**0.874786476**	2	4.04117

Q9JM53	VMPNAIVQSVGVSGGK+Oxidation(1)	**1.270167067**		
Q9JM53	VNAELQAR	**1.056412894**	2	2.48654
Q9JMA1	**UBP14 Ubiquitin carboxyl_terminal hydrolase 14**	**0.92123082**	**0.82396**	**2**
Q9JMA1	CTESEEEEVTK	**0.900555009**	2	3.62192
Q9JMA1	EKESVNAKVLK	**0.668751951**	2	2.31527
Q9JMD3	**PCTL PCTP_like protein**	**1.130547886**	**0.009933**	**6**
Q9JMD3	AVSIQTGYLIQSTGPK	**1.04313409**	2	4.89495
Q9JMD3	ESVQVPDDQDFR	**2.004426017**	2	2.3628
Q9JMD3	MECCDVPAETLYDVLHDIEYR	**1.218823013**	3	4.59759
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0)	**1.255144715**		
Q9JMD3	SCVITYLAQVDPK	**1.530867366**	2	3.14896
Q9JMD3	WDSNVIETFDIAR	**1.221299105**	2	4.31817
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**0.937262379**	**0.144601**	**5**
Q9QVC8	GEPNNVAGNQAQVK	**0.972488792**	2	4.13567
Q9QVC8	TEVAAGDHPTDAEMK	**0.712637289**	2	2.95854
Q9QVC8	TQLAVCQQR	**0.780363706**	2	2.49357
Q9QVC8	VAENGAQSAPLPLEGVDISPK	**0.852020838**	2	4.12216
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	**0.908585651**	3	5.06883
Q9QWN8	**SPTN2 Spectrin beta chain_ brain 2**	**1.083567774**	**0.348306**	**2**
Q9QWN8	ALAQEDQSAGEVER	**1.219463447**	2	3.92612
Q9QWN8	VGELTQEANALAAGHPAQAPAINTR	**1.034979405**	3	4.34745
Q9QX74	**SHAN2 SH3 and multiple ankyrin repeat domains protein 2**	**0.372356858**	**0.013859**	**2**
Q9QX74	KNMLINIVDTAQQK+Oxidation(2)	**1.202452424**		
Q9QX74	SSSPASPENYVHPLTGR	**0.415411857**	2	2.59029
Q9QX79	**FETUB Fetuin_B**	**0.909057479**	**0.558011**	**2**
Q9QX79	GSIQHLPEQEEPEDSKGK	**0.814022854**	3	3.66737
Q9QX79	NTAPTSSPSITAPR	**0.929298886**	2	3.5993
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**0.977849238**	**0.038844**	**3**
Q9QXG4	AELGMNDSPSQSPPVK	**0.887729352**	2	3.72188
Q9QXG4	GATTNICYNVLDR	**2.580117396**	2	2.56711
Q9QXG4	IGPIATPDYIQNAPGLPK	**1.342750065**	2	3.04793
Q9QXH4	**ITAX Integrin alpha_X**	**0.909389804**	**0.631572**	**2**
Q9QXH4	GGSQMTFLVTFDVSPK+Oxidation(4)	**1.196283187**		
Q9QXH4	MLDFVKAVMSQLQRPSTR	**0.89543945**	2	2.39697
Q9QXK3	**COPG2 Coatomer subunit gamma_2**	**0.925633403**	**0.95297**	**2**
Q9QXK3	SIATLAITTLLK	**1.114573603**	2	3.45082
Q9QXK3	SSEPVQLTEAETEYFVR	**0.920406639**	2	3.63336
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.161579201**	**2.43E-09**	**27**
Q9QXQ0	ACLISLGYDVENDR	**1.062287677**	2	4.06988
Q9QXQ0	AGTQIENIDEDFR	**1.066873655**	2	3.54526
Q9QXQ0	AGTQIENIDEDFRDGLK	**1.047679449**	2	4.20728
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	**1.322711246**	3	3.54724
Q9QXQ0	ASIHEAWTDGK	**0.858412609**	1	2.29187
Q9QXQ0	DDPVTNLNNAFEVAEK	**1.06348255**	2	3.0808
Q9QXQ0	ETTDTDTADQVIASFK	**0.963323919**	2	4.46142
Q9QXQ0	GISQEQMQEFR	**1.16165349**	2	3.15881
Q9QXQ0	HRDYETATLSDIK	**1.405770377**	2	3.51966
Q9QXQ0	HRPELIEYDK	**1.166868095**	3	4.13984
Q9QXQ0	HTNYTMEHLR	**0.956589421**	3	3.40227
Q9QXQ0	HTNYTMEHLR+Oxidation(5)	**1.487652903**		
Q9QXQ0	ICDQWDNLGSLTHSR	**1.014532901**	2	4.375
Q9QXQ0	KDDPVTNLNNAFEVAEK	**0.93698146**	2	4.51317
Q9QXQ0	LSGSNPYTSVTPQIINSK	**1.664428537**	2	4.86717

Q9QXQ0	LVSIGAEEIVDGNAK	**1.368625168**	2	3.23665
Q9QXQ0	MAPYQGPDAAPGALDYK	**0.896513202**	2	4.62986
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0)	**1.29569818**		
Q9QXQ0	MLDAEDIVNTARPDEK	**0.914190715**	2	3.70821
Q9QXQ0	QFASQANMVGPWIQTK	**0.979964246**	2	3.82857
Q9QXQ0	QLETIDQLHLEYAK	**0.99393142**	2	2.96463
Q9QXQ0	RDHALLEEQSK	**1.11524653**	3	3.95237
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	**1.14846245**	3	5.32006
Q9QXQ0	TINEVENQILTR	**1.099364629**	2	3.6777
Q9QXQ0	VEQIAAIAQELNELDYYDSHNVNTR	**1.443205542**	3	5.39837
Q9QXQ0	VGWEQLLTTIAR	**1.022882957**	2	4.04791
Q9QXQ0	VLAVNQENEHLMEDYER	**1.327581841**	2	5.04968
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**0.874705071**	**0.981909**	**5**
Q9QXT0	ALVDELEWEIAR	**0.836446004**	2	3.5548
Q9QXT0	IDSDISGTLK	**0.858016238**	2	2.31911
Q9QXT0	INPDGSQSVVEVPYAR	**1.009996004**	2	4.00082
Q9QXT0	RTDLCDHALHR	**1.027682388**	3	3.42901
Q9QXT0	TDLCDHALHR	**1.049439647**	2	2.86292
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**0.94184759**	**0.009042**	**16**
Q9QXX4	ASFANEDGQVSPGSLLLAGAIAGMPAASLVTPADVIK	**1.206561628**	3	4.90427
Q9QXX4	ASGDAARPFLLQLAESAYR	**1.228817909**	2	3.55857
Q9QXX4	DGSVPLLAEIFAGGCAGGSQVIFTNPLEIVK	**1.250702697**		
Q9QXX4	DVEVTKEEFALAAQK	**1.012824931**	2	4.38876
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	**0.89689806**	2	5.58094
Q9QXX4	GLLPQLLGVAPEK	**1.034031898**	2	2.99563
Q9QXX4	IAPLEEGMLPFNLAEAQR	**1.439698121**	2	5.06018
Q9QXX4	ITLPAPNPDHVGGYK	**1.280323467**	2	2.34699
Q9QXX4	KDVEVTKEEFALAAQK	**0.942372773**	2	4.77723
Q9QXX4	LQVAGEITTGPR	**1.061265706**	2	3.50307
Q9QXX4	LTVNDFVR	**0.920714865**	2	2.43457
Q9QXX4	NGEFFMSPHDFVTR	**0.927112159**	2	3.66185
Q9QXX4	SSPQFGVTLLTYELLQR	**2.104293242**	2	3.96628
Q9QXX4	STGSFVGELMYK	**0.889123734**	2	2.46336
Q9QXX4	TVELLSGVVDQTK	**1.142338133**	2	4.2984
Q9QXX4	YLNIFGESQPNPK	**1.044800241**	2	4.40584
Q9QYU2	**EFTS Elongation factor Ts_ mitochondrial**	**0.861808692**	**0.530172**	**2**
Q9QYU2	ALETCGGDLK	**1.009746952**	2	2.42024
Q9QYU2	YGALVICQTPEQITNLEEVGR	**0.800905632**	2	4.67679
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.810036113**	**0.370272**	**4**
Q9QYU4	GFLGVMPAYSAAEDALTTK	**0.967584657**	2	3.72319
Q9QYU4	RAPAFLSADEVQDHLR	**0.797358063**	3	4.63598
Q9QYU4	SLGMAVEDLVAAK	**0.658742807**	2	3.14331
Q9QYU4	SSSLLIPPLEAALANFSK	**0.839483902**	2	3.08818
Q9QZ76	**MYG Myoglobin**	**0.159669858**	**5.21E-07**	**5**
Q9QZ76	GQHAAEIQPLAQSHATK	**0.295959155**	2	4.88546
Q9QZ76	HGCTVLTALGTILK	**0.405111147**	2	3.53548
Q9QZ76	KGQHAAEIQPLAQSHATK	**0.031700795**	3	5.71279
Q9QZ76	VEGDLAGHGQEVLISLFK	**0.171341446**	3	4.91568
Q9QZ76	YSGDFGADAQGAMSK	**0.045681138**	2	4.75055
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.054461962**	**0.043201**	**9**
Q9QZA2	ATLVKPTPVNVPISQK	**0.946505919**	2	3.70323
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	**0.975750492**	2	3.53885
Q9QZA2	FYNELTEILVR	**0.749635599**	2	2.94305
Q9QZA2	LLDEEEATDNDLR	**1.273103118**	2	3.46655

Q9QZA2	MVPVSVQQSLAVFSQR	**1.157913668**	2	2.67608
Q9QZA2	NIQVSHQEFSK	**1.321868548**	2	3.35783
Q9QZA2	NLATAYDNFVELVANLK	**1.196601702**	3	4.16828
Q9QZA2	STAVVEQGGIQTVDQLIK	**0.975930048**	2	4.23555
Q9QZA2	YYDQICSIEPK	**1.033761233**	2	2.345
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.001391807**	**0.873083**	**5**
Q9QZD8	GALVTVGQLSCYDQAK	**0.981417616**	2	4.86944
Q9QZD8	NYSHALDGLYR	**1.157484019**	2	2.90764
Q9QZD8	VHLQTQQEVK	**0.864012684**	1	3.0118
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	**1.053812411**	2	5.65129
Q9QZD8	WYFGGLASCGAACCTHPLDLLK	**0.980759286**	3	3.39938
Q9QZH8	**AAAD Arylacetamide deacetylase**	**0.877790886**	**0.861778**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	**1.04604297**	2	4.11934
Q9QZH8	WFLQEDILEK	**0.87689034**	2	3.34902
Q9QZK2	**BCAR3 Breast cancer anti_estrogen resistance protein 3**	**0.844291571**	**0.000826**	**2**
Q9QZK2	EGSLAEGRPDVVKR	**0.853730409**	2	2.6492
Q9QZK2	FSSDARTGEALR	**1.229223954**	2	2.31725
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.411471385**	**8.86E-11**	**6**
Q9QZU7	IDANNVAYTTGK	**1.925619589**	2	3.33899
Q9QZU7	IIELDDKGQVVR	**1.629998022**	2	2.54393
Q9QZU7	LLLEALDVNIR	**1.304457407**	2	2.85708
Q9QZU7	MNPGDVITFDNWR	**1.286116715**	2	3.17284
Q9QZU7	QTVTGGDSEIVDGFNVCQK	**1.032045453**	2	4.49928
Q9QZU7	SYEAGTEISR	**1.543777725**	2	2.83603
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**1.57954112**	**0.000541**	**3**
Q9QZX8	GIGETPIVPLGISYLDDFAK	**0.999015083**	2	3.0486
Q9QZX8	QEEQDPSNMTGFLR	**1.335376835**	2	2.35483
Q9QZX8	QFTDEGNPDSVNK	**0.976586618**	2	3.4222
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.929069485**	**9.9E-20**	**8**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	**2.243469116**	2	4.08803
Q9R063	ETDLLLDDSLVSLFGNR	**1.201847174**	2	4.15105
Q9R063	GVLFGVPGAFTPGCSK	**0.898322196**	2	4.19341
Q9R063	THLPGFVEQAGALK	**0.883667697**	3	4.7489
Q9R063	VGDTIPSVEVFEGEPGK	**0.959665399**	2	3.75851
Q9R063	VGDTIPSVEVFEGEPGKK	**0.893858786**	2	3.75456
Q9R063	VNLAELFK	**0.941881864**	2	2.85206
Q9R063	VQLLADPTGAFGK	**0.999499758**	2	3.99646
Q9R0N0	**GALK1 Galactokinase**	**1.086662962**	**0.999996**	**6**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	**1.090636479**	3	4.3782
Q9R0N0	QCEEVAQALGK	**1.029408332**	2	2.46346
Q9R0N0	RQCEEVAQALGK	**1.097968175**	2	3.03592
Q9R0N0	SLETSLVPLSDPK	**1.021186641**	2	3.20431
Q9R0N0	TDGLVSLLTTSK	**1.060195739**	2	3.43348
Q9R0N0	VEELLAEAR	**1.0879993**	2	3.15717
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.378658362**	**8.26E-07**	**6**
Q9R0T3	AEPSVAEYTVR	**1.083322106**	2	2.74358
Q9R0T3	FDDGEDPLDAETQQGGGSNPFHR	**1.030604703**	3	3.65925
Q9R0T3	ICSEVLQLEPDNVNALK	**1.429865981**	2	5.4059
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	**1.069975873**	3	5.49044
Q9R0T3	LIGSAEELIR	**1.182447178**	2	2.37812
Q9R0T3	SNPSENEEKEAQSQLVK	**1.118656577**	2	5.01587
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.328499319**	**0.109674**	**4**
Q9R112	EGNALFTFPNTPVK	**1.404858605**	2	2.70734
Q9R112	STLSVIPSGVQWIQDR	**1.069314815**	2	2.54903

Q9R112	TAAAVAAQSGILDR	**1.30096816**	2	2.79156
Q9R112	VGAENVAIVEPSER	**1.146842228**	2	2.86739
Q9R1T3	**CATZ Cathepsin Z**	**1.087543838**	**0.999985**	**2**
Q9R1T3	HGIPDETCNNYQAK	**1.096206798**	2	3.79475
Q9R1T3	VGDYGSLSGR	**1.089670823**	2	2.64976
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**1.09059002**	**6.24E-08**	**5**
Q9R1Z0	LCQNNFALGYK	**1.746096032**	2	2.52662
Q9R1Z0	LTLSALVDGK	**2.351925895**	2	2.72036
Q9R1Z0	LTVDTIFVPNTGK	**1.128195859**	2	3.49956
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	**1.193393845**	2	4.11004
Q9R1Z0	WNTDNTLGTEISWENK	**0.946290571**	2	2.8967
Q9R1Z8	**VINEX Vinexin**	**0.994297787**	**0.472788**	**2**
Q9R1Z8	LSAELDKDLR	**0.9918582**	3	3.52268
Q9R1Z8	MPDLQLDWTLEDPPK+Oxidation(0)	**1.707305526**		
Q9R257	**HEBP1 Heme_binding protein 1**	**1.191684688**	**0.001954**	**2**
Q9R257	FATVEVTDKPVDEALR	**1.194869528**	2	3.52854
Q9R257	NSLFGSVETWPWQVLSTGGK	**1.249928778**	2	3.86308
Q9WTT6	**GUAD Guanine deaminase**	**1.328117896**	**2.15E-08**	**10**
Q9WTT6	EIGNFEVGKDFDALLINPR	**1.114628851**	2	3.5651
Q9WTT6	ETTEESVKETER	**1.349358151**	2	3.2533
Q9WTT6	FQSTDVAEEVYTR	**1.33648219**	2	4.3131
Q9WTT6	FSLSCTETLMSELGNIAK	**1.258165124**	2	4.12777
Q9WTT6	GTFVHSTWTCPMEVLR	**0.642040484**	2	3.13277
Q9WTT6	IVFLEESSQQEK	**1.687459582**	2	3.91957
Q9WTT6	NIEEVYVGGK	**1.244847541**	1	2.79027
Q9WTT6	NYTDVYDKNNLLTNK	**0.611927324**	2	4.41256
Q9WTT6	THDLYIQSHISENREEIEAVK	**1.543276904**	3	3.75566
Q9WTT6	VCMDLNNTVPEYK	**0.950964978**	2	3.97844
Q9WTV5	**PSMD9 26S proteasome non_ATPase regulatory subunit 9**	**1.386986441**	**0.202408**	**2**
Q9WTV5	ADVDLYQVR	**1.407829392**	2	2.7052
Q9WTV5	RKEEIEAQIK	**1.027874877**	3	3.91666
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**0.81122868**	**2.25E-12**	**9**
Q9WU19	AIFVTVDTPYLGNR	**1.071991105**	2	4.59297
Q9WU19	AVFVGRPIIWGLAFQGEK	**1.197634392**	3	4.12982
Q9WU19	GVQDVLEILK	**0.82943696**	2	2.91254
Q9WU19	GVQDVLEILKEEFR	**0.731109117**	2	3.95664
Q9WU19	HGVDGILVSNHGAR	**0.806447267**	3	5.21556
Q9WU19	MKNFETNDLAFSPK+Oxidation(0)	**0.935967762**		
Q9WU19	NFETNDLAFSPK	**0.797968501**	2	3.41052
Q9WU19	NVADIDLSTSVLGQR	**0.863650922**	2	4.90785
Q9WU19	VEVFLDGGVR	**1.009442978**	2	2.95267
Q9WU49	**CHSP1 Calcium_regulated heat stable protein 1**	**0.997952301**	**0.815857**	**2**
Q9WU49	GNVVPSPLPTR	**0.85149735**	2	2.462
Q9WU49	LQAVEVVITHLAPGTK	**1.022367395**	2	3.99171
Q9WU65	**GLPK2 Glycerol kinase 2**	**1.26504781**	**0.012139**	**2**
Q9WU65	GIICGLTQFTNK	**1.167682313**	2	3.46323
Q9WU65	TGLPLSTYFSAVK	**3.452101204**	2	2.61716
Q9WU82	**CTNB1 Catenin beta_1**	**0.91221282**	**0.181471**	**3**
Q9WU82	HQEAEMAQNAVR	**0.86301471**	2	3.35773
Q9WU82	LLNDEDQVVVNK	**1.109340556**	2	3.25319
Q9WU82	TMQNTNDVETAR	**0.862172972**	2	3.41785
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.337282252**	**9.9E-20**	**3**
Q9WUC4	LGGVEFNIDLPNK	**1.01074104**	2	2.85218
Q9WUC4	LGGVEFNIDLPNKK	**1.241346464**	2	3.45708
Q9WUC4	VCIESEHSSDILLATLNK	**1.404993105**	2	5.70563

Q9WUH4	**FHL1 Four and a half LIM domains protein 1**	**0.158976376**	**0.089785**	**2**
Q9WUH4	FCANTCVECR	**0.15862014**	2	2.99962
Q9WUH4	FVFHNEQVYCPDCAK	**0.606317664**	2	4.13542
Q9WUI1	**MK11 Mitogen_activated protein kinase 11**	**1.313880909**	**0.666404**	**2**
Q9WUI1	ILDFGLAR	**1.391616697**	2	2.37337
Q9WUI1	QELNKTVWEVPQR	**0.743524834**	2	2.346
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**1.11577441**	**0.004563**	**6**
Q9WUS0	AVILGPPGSGK	**0.851204869**	2	2.52052
Q9WUS0	GLLVPDHVITR	**0.893599094**	2	2.49828
Q9WUS0	GVLHQFSGTETNR	**1.365170132**	2	3.61995
Q9WUS0	TLVQAEALDR	**0.927796452**	2	2.90169
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	**1.156105856**	3	5.07224
Q9WUS0	YKDAAKPVIELYK	**0.752367516**	2	2.53682
Q9WV97	**TIM9 Mitochondrial import inner membrane translocase subunit Tim9**	**0.974298204**	**0.933679**	**2**
Q9WV97	FQEYHIQQNEALAAK	**0.931204816**	2	4.86817
Q9WV97	LTETCFLDCVK	**0.974752979**	2	2.38588
Q9WVC0	**SEPT7 Septin_7**	**1.103632161**	**0.988745**	**2**
Q9WVC0	ADTLTPEECQQFK	**1.109013878**	2	3.35629
Q9WVC0	NLEGYVGFANLPNQVYR	**1.064601171**	2	2.30755
Q9WVD5	**ORNT1 Mitochondrial ornithine transporter 1**	**1.453356868**	**4.94E-08**	**4**
Q9WVD5	DGPLGFYHGLSSTLLR	**1.462056708**	2	3.07692
Q9WVD5	LQTMYEMETSGK	**1.777033112**	2	2.37736
Q9WVD5	NEGITALYSGLKPTMIR	**0.875519373**	2	3.57706
Q9WVD5	SNPAIQAAIDLTAGAAGGTACVLTGQPFDTMK	**1.699886285**	3	4.55677
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.888897183**	**9.9E-20**	**13**
Q9WVK3	AGVYNLTK	**0.938478037**	2	2.4114
Q9WVK3	ASQPPSSSTQVTAIQCNIR	**0.892358908**	2	5.47989
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	**1.070915387**	3	6.88484
Q9WVK3	ELLHLGCNVVIASR	**0.973690568**	2	3.85298
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	**1.270370987**	2	5.24002
Q9WVK3	INFLVNNAGGQFMAPAEDITAK+Oxidation(12)	**1.811348982**		
Q9WVK3	KEEEVNNLVK	**0.869373085**	3	4.18333
Q9WVK3	LTAAVDELR	**1.330827477**	2	3.13177
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	**0.857226292**	2	5.01284
Q9WVK3	NFTIPDHDNWPVGAGDSSFIKK	**0.811762037**	3	3.33485
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	**0.943351121**	2	6.32718
Q9WVK3	TMALTWASSGVR	**0.820250741**	2	3.89773
Q9WVK3	TMALTWASSGVR+Oxidation(1)	**1.317460435**		
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**1.095339277**	**9.9E-20**	**14**
Q9WVK7	AADEFVEK	**1.25343869**	2	3.13205
Q9WVK7	EDIDTAMK	**1.069641123**	1	1.98342
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	**1.811921651**	2	5.54112
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	**1.141111154**	3	5.37381
Q9WVK7	GDASKEDIDTAMK	**1.081577854**	3	3.8505
Q9WVK7	GDASKEDIDTAMK+Oxidation(11)	**1.172378713**		
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	**0.902697768**	3	7.51725
Q9WVK7	KGIEESLK	**1.300255524**	1	2.13782
Q9WVK7	KGIEESLKR	**1.154618069**	2	2.34825
Q9WVK7	LKNELFQR	**1.337528093**	2	2.69445
Q9WVK7	LLVPYLIEAIR	**1.548474968**	2	2.55584
Q9WVK7	LVEVIK	**1.17131375**	2	2.45151
Q9WVK7	TFESLVDFCK	**1.148603234**	2	3.44102

Q9WVK7	TLSSLSTSTDAASVVHSTDLVVEAIVENLK	**1.10757259**	3	6.20454
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**1.239596673**	**3.74E-06**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	**1.424845239**	2	3.30695
Q9Z0N2	SFDVNKPGCEVDDLK	**0.937979316**	2	3.45475
Q9Z0N2	VGQEIEVRPGIVSK	**1.265399092**	2	3.10233
Q9Z0U5	**ADO Aldehyde oxidase**	**0.279999004**	**0.000653**	**17**
Q9Z0U5	CGLSPEQVR	**0.807892157**	2	2.48427
Q9Z0U5	CTGYRPIIDACK	**0.435608717**	2	2.6211
Q9Z0U5	DLEPLILTIEEAIQHK	**0.620679578**	2	3.28957
Q9Z0U5	EFQPLDPTQELIFPPELMR	**0.818326758**	2	3.06986
Q9Z0U5	ELSILYGGVGPTTIGAK	**0.907518889**	2	3.49676
Q9Z0U5	GEDMLITGGR	**0.795848831**	2	2.36863
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	**0.865056611**	2	4.61418
Q9Z0U5	GYESNINWEK	**0.597508525**	2	2.82892
Q9Z0U5	HIQDIVAATLK	**0.613112133**	2	2.44721
Q9Z0U5	HLDSDLNPLLAVGNCTLNLLSK	**0.667919358**	2	4.59427
Q9Z0U5	KCPDSDLKPQEVLVSVNIPCSR	**0.582136417**	3	3.38
Q9Z0U5	KLECGNVDEAFK	**0.617509226**	2	3.54923
Q9Z0U5	LVLDEVTLAGSAPGGK	**0.509072248**	2	3.53411
Q9Z0U5	MTWISPVTLEELVEAK	**1.045840015**	2	3.20302
Q9Z0U5	NHPEPSLDQLTDALGGNLCR	**0.274763716**	2	3.72277
Q9Z0U5	RLEPIISK	**0.325867285**	2	2.43653
Q9Z0U5	VVENNVDPEMMLLPYLR	**0.716439566**	2	3.86439
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**1.146359038**	**0.050801**	**4**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	**1.985889578**	2	5.43312
Q9Z0V5	GLFIIDDK	**1.049269778**	2	2.979
Q9Z0V5	QITLNDLPVGR	**1.019713037**	2	3.30839
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	**1.198273694**	3	6.0213
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**1.105752121**	**0.990989**	**6**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	**1.008327361**	3	5.99917
Q9Z0V6	GLFIIDPNGVIK	**1.101155926**	2	3.06829
Q9Z0V6	GTAVVNGEFK	**1.163500698**	2	2.45391
Q9Z0V6	HLSVNDLPVGR	**1.010963793**	2	2.87021
Q9Z0V6	NGGLGHMNITLLSDLTK	**1.037471397**	2	2.81719
Q9Z0V6	SVEEPLRLVK	**0.937375828**	2	2.48859
Q9Z142	**TMM33 Transmembrane protein 33**	**1.253800445**	**0.010213**	**2**
Q9Z142	ALLANALTSALR	**1.324510184**	2	3.72164
Q9Z142	LSTNQQNILK	**1.732289515**	2	2.46873
Q9Z1A6	**VIGLN Vigilin**	**1.666456835**	**9.9E-20**	**22**
Q9Z1A6	ASVITQVFHVPLEER	**1.370280592**	2	2.88712
Q9Z1A6	DKFPEVIINFPDPAQK	**1.500338944**	3	4.04574
Q9Z1A6	DLANIAEVEVSIPAK	**1.338417776**	2	3.74732
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	**1.192817354**	3	3.51989
Q9Z1A6	ELQAEQEDR	**1.084777842**	2	2.50733
Q9Z1A6	GNSLQEILER	**1.001375986**	2	2.52435
Q9Z1A6	HEVLLISAEQDKR	**1.879071098**	3	4.27489
Q9Z1A6	IDLPAENSNSETIVITGK	**1.006790556**	2	4.62877
Q9Z1A6	IEGDPQGVQQAK	**1.133000622**	2	3.17871
Q9Z1A6	IIFPAAEDKDQDLITIIGK	**1.224610029**	2	3.23644
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	**1.316985604**	2	4.30917
Q9Z1A6	IVGELEQMVSEDVPLDHR	**0.988695303**	2	4.52848
Q9Z1A6	LGQALTEVYAK	**2.161942514**	2	3.2054
Q9Z1A6	LQDLELK	**1.105622809**	1	2.32071
Q9Z1A6	LQTQASATVPIPK	**1.050276497**	2	3.53097
Q9Z1A6	LVGEIMQETGTR	**1.031916416**	2	3.38595

Q9Z1A6	MDYVEINIDHK	**0.939872323**	2	3.22544
Q9Z1A6	MVADLVENSYSISVPIFK	**1.187495375**	2	2.98864
Q9Z1A6	RCDIIVISGR	**0.962394597**	2	2.77678
Q9Z1A6	TEIVFTGEKEQLAQAVAR	**1.433894039**	2	4.17905
Q9Z1A6	TKDLIIEQR	**1.157784966**	2	2.52524
Q9Z1A6	VKELQAEQEDR	**1.160386287**	2	3.01594
Q9Z1J8	**S14L3 SEC14_like protein 3**	**0.964391445**	**0.773652**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	**1.065413135**	3	3.85733
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	**1.122689099**	3	3.8155
Q9Z1J8	GSSHQVEYEILFPGCVLR	**0.820120747**	2	4.6195
Q9Z1N1	**F16P2 Fructose_1_6_bisphosphatase isozyme 2**	**1.267462831**	**0.034873**	**2**
Q9Z1N1	YVGSMVADVHR	**0.709649482**	2	2.31809
Q9Z1N1	YVGSMVADVHR+Oxidation(4)	**1.3002999**		
Q9Z1P2	**ACTN1 Alpha_actinin_1**	**0.995760514**	**0.56658**	**3**
Q9Z1P2	DYETATLSEIK	**1.404721676**	1	2.08039
Q9Z1P2	ICDQWDNLGALTQK	**0.832190841**	2	3.89871
Q9Z1P2	KDDPLTNLNTAFDVAER	**0.861175774**	2	2.66387
Q9Z1W6	**LYRIC Protein LYRIC**	**0.960971364**	**0.999194**	**3**
Q9Z1W6	SWQDELAQQAEEGSAR	**0.875552839**	2	5.39051
Q9Z1W6	TELGLDLGLEPK	**0.947948019**	2	2.79775
Q9Z1W6	TLPPAISAEPSVTLSK	**0.974503988**	2	3.16166
Q9Z1Y3	**CADH2 Cadherin_2**	**0.736643604**	**2.96E-07**	**2**
Q9Z1Y3	IDPVNGQITTIAVLDR	**0.73640533**	2	3.4952
Q9Z1Y3	YSVTGPGADQPPTGIFIINPISGQLSVTKPLDR	**0.919385642**	3	3.38764
Q9Z270	**VAPA Vesicle_associated membrane protein_associated protein A**	**0.877957225**	**0.297139**	**3**
Q9Z270	FKGPFTDVVTTNLK	**0.862734631**	2	2.60238
Q9Z270	HEQILVLDPPSDLK	**0.943221182**	2	4.1872
Q9Z270	QDGPLPKPHSVSLNDTETR	**0.866102617**	3	3.35114
Q9Z2C8	**YBOX2 Y_box_binding protein 2**	**1.006468415**	**0.988932**	**2**
Q9Z2C8	NDTKEDVFVHQTAIK	**1.029278504**	2	3.42159
Q9Z2C8	SVGDGETVEFDVVEGEK	**0.994295672**	2	3.68933
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**1.025293076**	**0.138831**	**10**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	**0.806956796**	2	4.56315
Q9Z2I8	GKGVFNSGLK	**0.709159725**	2	2.31244
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	**1.652515437**	3	4.77351
Q9Z2I8	INFDDNAEFR	**1.208862421**	2	3.20799
Q9Z2I8	LEGTNVQEAQNILK	**1.070428607**	2	5.22604
Q9Z2I8	SENEPIENEAAR	**1.222237019**	2	4.05241
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	**0.991727442**	2	5.99948
Q9Z2I8	SSGLPITSAVDLEDAAK	**0.930511641**	2	4.5382
Q9Z2I8	SSGLPITSAVDLEDAAKK	**1.172207321**	2	2.95275
Q9Z2I8	VMVAEALDISR	**0.7987979**	2	3.31878
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.083103914**	**0.029864**	**8**
Q9Z2I9	ALIADSGLK	**0.998342814**	1	2.08293
Q9Z2I9	ICNQVLVCER	**1.553651116**	2	2.86127
Q9Z2I9	ILACDDLDEAAK	**1.272089611**	2	3.39223
Q9Z2I9	INFDSNSAYR	**1.303173869**	2	2.83742
Q9Z2I9	LSEIVTLAK	**1.261647582**	2	2.50533
Q9Z2I9	MGFPSNIVDSAAENMIK	**1.105752409**	2	2.82867
Q9Z2I9	SSDEAYAIAK	**1.116086526**	2	3.50305
Q9Z2I9	VQAILVNIFGGIMR	**0.689383447**	2	3.83789
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.034800438**	**0.000378**	**11**
Q9Z2L0	KLETAVNLAWTAGNSNTR	**1.087434219**	2	5.81487

Q9Z2L0	LTFDSSFSPNTGK	**1.18824356**	2	3.60115
Q9Z2L0	LTFDSSFSPNTGKK	**1.140050826**	2	2.55381
Q9Z2L0	LTLSALLDGK	**2.2544649**	2	2.49348
Q9Z2L0	SENGLEFTSSGSANTETTK	**1.072663767**	2	4.59678
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	**0.973483086**	3	5.10524
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	**0.97446329**	2	4.43875
Q9Z2L0	VTQSNFAVGYK	**1.226293607**	2	3.13261
Q9Z2L0	WNTDNTLGTEITVEDQLAR	**0.831717644**	2	4.54595
Q9Z2L0	WTEYGLTFTEK	**1.115568148**	2	2.9026
Q9Z2L0	YQVDPDACFSAK	**1.124200975**	2	3.55342
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.847029943**	**0.49754**	**4**
Q9Z2M4	GQVLQLHAGAAK	**0.774209709**	2	3.18741
Q9Z2M4	HLAVEWGPQNIR	**0.831380876**	2	3.26921
Q9Z2M4	VNSLAPGAISGTEGLR	**0.918118381**	2	3.93105
Q9Z2M4	VPPAVMAAVDQALK	**0.659492151**	2	3.16995
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.147663267**	**0.266612**	**4**
Q9Z2M7	IGVVGGSDFEK	**1.526345063**	2	2.37643
Q9Z2M7	LQEQLGNDVVEK	**1.181008294**	2	3.49152
Q9Z2M7	TVGYTVTAPEDTR	**1.200814018**	2	2.51966
Q9Z2M7	YDYVFPENGLVAYK	**0.942790767**	2	3.3401
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**0.926117928**	**0.000152**	**14**
Q9Z2Q1	AQDGSNPLSLQDLIEK	**0.82982271**	2	4.18348
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	**0.986404714**	2	4.62398
Q9Z2Q1	CLSSATDPQTK	**1.437138259**	2	2.62306
Q9Z2Q1	DQTLSPTIISGLHSIAR	**0.762775878**	2	3.42386
Q9Z2Q1	GGPGPLAGHPQVSR	**1.364835172**	2	3.09845
Q9Z2Q1	IDASQTDFEK	**1.000786738**	2	2.49462
Q9Z2Q1	IIAGDKEVVIAQK	**1.499294391**	2	2.53766
Q9Z2Q1	KIDASQTDFEK	**1.083429493**	2	3.0439
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	**1.50894219**	2	5.17189
Q9Z2Q1	QVQHILASASPSGR	**0.774852494**	2	2.91261
Q9Z2Q1	SSYEGQPLPK	**1.064402188**	2	2.47765
Q9Z2Q1	TQPPEDISCIAWNR	**0.915521947**	2	2.67321
Q9Z2Q1	TTFEDLIQR	**0.997626609**	2	2.34945
Q9Z2Q1	VYSIMGGSIDGLR	**1.06967857**	2	2.61917
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**0.913657862**	**0.830674**	**3**
Q9Z2Z8	AIECSYTSADGLK	**1.124631783**	2	3.99638
Q9Z2Z8	ASLADIWAK	**1.131021571**	2	2.65126
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	**0.924999227**	2	5.47307
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**0.977677149**	**0.363332**	**5**
Q9Z339	GSAPPGPVPEGQIR	**0.995925282**	2	3.32694
Q9Z339	LEALELNECIDHTPK	**0.528538489**	2	4.33129
Q9Z339	LEEAMANK	**0.82395151**	1	1.997
Q9Z339	LEEAMANK+Oxidation(4)	**0.780747785**		
Q9Z339	LFPDDPYEKACQK	**0.698230128**	2	2.42378

Time point 48 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (48 h)**	**P-value (48 h)**	**Peptide number (48 h)**
Accession number	Peptide sequence	Peptide Ratio (48 h)	Charge state	Xcorr
A0JPQ8	**ALKMO Alkylglycerol monooxygenase**	**0.782783733**	**1.8E-05**	**2**
A0JPQ8	LDDILTSMSAGVVSR	0.888046972	2	3.103714
A0JPQ8	SITHLASGSWK	0.748284777	2	2.597277
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**0.790122049**	**0.19342**	**2**
A2ADY9	NPPLAEALLSGDLEK	0.987819156	2	2.802645
A2ADY9	VLVEQQQDR	0.782319224	2	2.473169
A2AJL3	**FGGY FGGY carbohydrate kinase domain_containing protein**	**0.89747444**	**0.02815**	**3**
A2AJL3	GHGLTCEGQPVTSR	0.88890454	2	3.513079
A2AJL3	MSKVGKVVFPEHADK	0.793626702	2	2.39486
A2AJL3	YQVFLRMVEHQK	1.022906621	2	2.355281
A2AL36	**CNTRL Centriolin**	**0.881711725**	**0.7279**	**2**
A2AL36	LEVLNLSYNLIVK	0.882930261	2	2.434449
A2AL36	NQDKLNK	0.784436213	1	1.981636
A2APV2	**FMNL2 Formin_like protein 2**	**1.123235367**	**4.8E-07**	**2**
A2APV2	QAEEENELRKK	0.888549395	2	2.314742
A2APV2	QEQALMEK	2.423063848	1	2.011945
A2AQP0	**MYH7B Myosin_7B**	**0.877121314**	**0.64728**	**6**
A2AQP0	AITDAAMMAEELKK	0.979923998	2	3.03906
A2AQP0	DIDDLELTLAK	0.605412737	2	3.715271
A2AQP0	ELEELSER	0.670878278	1	2.061783
A2AQP0	HDCDLLR	0.503184494	2	2.386008
A2AQP0	TEELEEAK	0.861303647	2	2.635581
A2AQP0	VGNEYVTK	0.522255052	2	2.447743
A2ASS6	**TITIN Titin**	**1.077369979**	**0.91544**	**3**
A2ASS6	AENRFGIGPPAETIQRTTAR	0.989987795	2	2.684622
A2ASS6	APPIEPAPTPIAAPVTAPVVGK	0.732489639	2	3.892599
A2ASS6	RAPEPKPEFHVHEPGK	1.06404207	2	2.335221
A2AWL7	**MGAP MAX gene_associated protein**	**0.727299466**	**0.01454**	**3**
A2AWL7	ADVSLTTLLTAQASLK	0.814115494	1	2.094304
A2AWL7	ELIEDLKSLR	0.726236223	2	2.393612
A2AWL7	TDQGILVTNRDARALLSR	1.002968983	2	2.425015
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**0.791974414**	**0.5961**	**10**
A2VCW9	AEGIVFNTQSTIK	0.959152213	2	2.554884
A2VCW9	AGGILQEDITEACLILGVK	0.706057391	2	2.723447
A2VCW9	AQEANMSLLDEVLK	0.966319332	2	3.453885
A2VCW9	GAQEVFNELPCEYVEPHELK	0.843644187	2	4.532718

A2VCW9	KTDGVYDPVEYEKYPER	0.920144314	3	3.403803
A2VCW9	KYDINTVNVTVGK	0.834114105	2	3.70572
A2VCW9	QDAQSLLVPVK	0.948042843	2	2.695295
A2VCW9	REDVNAWER	0.962745761	2	2.776835
A2VCW9	SSVVPVEGCPELPHK	1.208145809	2	2.872846
A2VCW9	YDINTVNVTVGK	0.471231735	2	2.748539
A6H584	**chain**	**0.831944876**	**6.6E-05**	**2**
A6H584	FVNRAVFRMANGIDR+Oxidation(8)	0.761688435	2	2.594594
A6H584	NEHSFQVVGIQVR	0.829780604	2	2.512545
A6N6J5	**WDR35 WD repeat_containing protein 35**	**0.911526527**	**0.05089**	**2**
A6N6J5	LMYKIADEEAKK+Oxidation(1)	0.934926771	1	2.063617
A6N6J5	MYLDMDRRDLAIGLR+Oxidation(0)	0.698304716		2.339869
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.073066422**	**9.9E-20**	**10**
A7VJC2	GFGFVTFDDHDPVDK	1.130809333	2	3.842601
A7VJC2	GGGGNFGPGPGSNFR	0.921043398	2	2.646938
A7VJC2	GGNFGFGDSR	1.112834907	2	2.503038
A7VJC2	IDTIEIITDR	0.88774095	2	3.669585
A7VJC2	LTDCVVMR	0.51809589	2	2.433177
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	1.345458108	2	5.335678
A7VJC2	NYYEQWGK	0.851413137	2	2.347835
A7VJC2	QEMQEVQSSR	0.784636061	2	3.406555
A7VJC2	QEMQEVQSSR+Oxidation(2)	0.999412941	2	2.683985
A7VJC2	YHTINGHNAEVR	1.186140944	2	3.531202
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**0.997386475**	**0.95914**	**2**
B0BN93	QMTDPNVALTFLEK	1.065942583	2	2.714635
B0BN93	SAWGQQPDLAANEAQLLR	0.989499735	2	3.926875
B0BNA7	**EIF3I Eukaryotic translation initiation factor 3 subunit I**	**1.094140759**	**0.36459**	**3**
B0BNA7	HVLTGSADNSCR	0.816652011	2	3.058871
B0BNA7	MKPILLQGHERSITQIK+Oxidation(0)	1.471154596	2	2.366361
B0BNA7	SYSSGGEDGYVR	0.049200948	2	2.652438
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.202652941**	**9.9E-20**	**9**
B0BNE5	AFNGYLGPDQSK	1.046438843	2	2.916703
B0BNE5	AYDATCLVK	0.982445768	2	2.583571
B0BNE5	FAIYLPPQAESAK	1.273821051	2	2.893025
B0BNE5	MYSYVTEELPQLINANFPVDPQR	0.902812911	3	5.243639
B0BNE5	MYSYVTEELPQLINANFPVDPQR+Oxidation(0)	0.759048327	3	3.467616
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	0.873714309	2	5.552814
B0BNE5	SVSAFAPICNPVLCPWGK	0.867580926	2	4.51576
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	1.037358963	3	4.875159
B0BNE5	VFEHSSVELK	0.852161613	2	2.465598
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.661909792**	**0.29289**	**2**

B0BNN3	HDSSLKPVSVSYNPATAK	0.697856732	3	4.369028
B0BNN3	VGPANPNLQK	0.631695038	2	3.027961
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**0.875251096**	**8.7E-08**	**2**
B0K020	HNEETGDNVGPLIIK	0.875155713	2	5.542022
B0K020	VVHAFDMEDLGDK	0.897207822	3	4.252344
B2GUZ5	**CAZA1 F_actin_capping protein subunit alpha_1**	**0.875399022**	**0.10294**	**2**
B2GUZ5	EASDPQPEDVDGGLK	0.895951342	2	3.455634
B2GUZ5	FTITPPTAQVVGVLK	0.875337745	2	2.742404
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**1.054745167**	**0.76229**	**2**
B2RX88	SISSVNVDQVRMRNEDR	1.038182327	2	2.492404
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(11)	1.165334899	2	2.315852
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.878828432**	**4.3E-05**	**2**
B2RYW9	KGDEVQCEIEELGVIINK	0.887375034	2	4.624022
B2RYW9	TFDTFCPLGPALVTK	0.888498533	2	4.502189
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**1.106327496**	**0.09847**	**3**
B3DMA2	NLPDSDNEECLVHGDFK	1.211679192	2	3.132008
B3DMA2	RGQEVLTRVK	0.911541821	1	1.944883
B3DMA2	SLEAYLNQHLPGFGSDHR	1.165328273	3	3.307983
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**0.979709146**	**0.93043**	**4**
D3ZW55	IDLPEYQGEPDEISIQK	0.982469698	2	4.382393
D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.062729561	3	3.474637
D3ZW55	LKPEGLYQLLAGFEDK	1.100920151	3	3.526954
D3ZW55	LQEYFGVTDGAGDH	0.896876584	2	2.586045
E9Q557	**DESP Desmoplakin**	**0.668250887**	**0.00016**	**2**
E9Q557	KQVQTSQKNTLR	0.632173664	1	1.975029
E9Q557	SQCTQVVQER	0.66960768	2	2.584484
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**0.737820186**	**9.9E-20**	**9**
O08557	DENATLDGGDVLFTGR	0.773748956	2	3.200306
O08557	DYAVSTVPVADSLHLK	0.714582016	2	3.480199
O08557	GAEILADTFK	0.903438565	1	2.28705
O08557	GAEILADTFKDYAVSTVPVADSLHLK	0.844612119	3	3.89538
O08557	KEVDMMK+Oxidation(5)	0.529985306	1	1.985766
O08557	SFCSMAGPNLIAIGSSESAQK	0.71275277	2	4.443517
O08557	SQGEEVDFAR	0.6947175	2	2.932321
O08557	TPEEYPESAK	2.494234835	2	2.639826
O08557	VDGLLTCCSVFINK	1.182434862	2	3.017703
O08583	**THOC4 THO complex subunit 4**	**0.738810053**	**0.01004**	**2**
O08583	QQLSAEELDAQLDAYNAR	0.806617706	2	4.45257
O08583	SLGTADVHFER	0.830676869	2	2.535738

O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.256500085**	**9.9E-20**	**14**
O08601	EFYSYENEPVGIENLK	1.358055445	2	4.345022
O08601	GCPSLAEHWKSIR	1.193467618	2	3.54183
O08601	GHTTGLSLNNER	1.004251321	2	2.572468
O08601	GSFASNDIR	1.158492672	2	2.341599
O08601	MLSASGDPVSVVK	1.301708436	2	2.828194
O08601	NALLPEGIPLLLK	1.419660756	2	2.996096
O08601	NILLSIGELPK	1.044612429	2	4.041634
O08601	REEILQILK	1.14707874	2	2.519599
O08601	SDSSIILQER	1.064633149	2	3.022267
O08601	SGSSSAYTGYVER	1.23368329	2	3.536287
O08601	SNLNIFQYIGK	2.459060238	2	3.366102
O08601	VKEFYSYENEPVGIENLK	1.328574966	2	3.084463
O08601	YAEAGEGPVSHLATTVLQR	0.932190761	2	3.057607
O08601	YMLTVVQDILHFEMPASK+Oxidation(1)	1.088787772	2	2.428269
O08795	**GLU2B Glucosidase 2 subunit beta**	**0.951352021**	**0.76258**	**6**
O08795	ETVVTSTTEPSR	0.869888085	2	2.585464
O08795	KLWEEQQAAAK	0.891177711	2	3.314636
O08795	LWEEQQAAAK	0.954126926	2	3.06576
O08795	MPPYDEETQAIIDAAQEAR	0.92500894	2	4.31299
O08795	SLEDQVETLR	0.90009068	2	2.71696
O08795	YEQGTGCWQGPNR	0.994491487	2	3.874403
O08810	**U5S1 116 kDa U5 small nuclear ribonucleoprotein component**	**1.163411369**	**5E-05**	**2**
O08810	GGGQIIPTAR	1.175340011	2	2.785345
O08810	GLAEDIENEVVQITWNR	0.982263618	2	2.571165
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**2.133514567**	**9.9E-20**	**11**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.719804516	2	5.991273
O09171	AGPWTPEAAVEHPEAVR	1.978128423	2	5.073842
O09171	GAAELMQQK	1.795116383	2	3.7103
O09171	GAAELMQQK+Oxidation(5)	2.058612321	2	2.852686
O09171	KEYWQNLR	1.816404934	3	3.644898
O09171	LNAGEVVIGDGGFVFALEK	1.894738766	3	6.398526
O09171	QGFIDLPEFPFGLEPR	1.515439461	2	4.981332
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.799037037	3	6.089988
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	2.028981263	3	6.485535
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9)	1.776898556	4	6.060964
O09171	VNEAACDIAR	1.48032656	2	4.051086
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.155726252**	**9.9E-20**	**8**
O09173	CFYNSDGDFLIVPQK	1.636010231	2	3.612749
O09173	FSVDVFEETR	1.127167556	2	3.344777
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.132043961	3	5.003122

O09173	NCMSEFMGLIK	1.509064335	2	3.069097
O09173	QDVSPFNVVAWHGNYTPYK	1.475176502	2	3.37068
O09173	SLRPGVAIADFVIFPPR	1.105206816	3	3.513262
O09173	WKPFEIPK	1.231897253	2	2.416594
O09173	YISGFGNECASEDPR	2.205032093	2	4.403421
O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.147469392**	**1.3E-15**	**17**
O35077	ANTIGISLIK	1.108184195	2	3.043336
O35077	DPAQGQLLK	2.438130474	2	2.776202
O35077	ELHSILQHK	0.980148983	2	2.7721
O35077	FCETTIGCK	1.048233107	2	2.649421
O35077	FCETTIGCKDPAQGQLLK	1.185931486	2	4.936999
O35077	GIDEGPNGLK	1.109227761	2	2.339913
O35077	GLVDKFPLFTAVYK	1.775614941	2	2.83968
O35077	ICDQLKGHLK	0.734757181	2	2.568439
O35077	ITVVQEVDTVEICGALK	0.939223604	2	3.303079
O35077	IVGSNASQLAHFDPR	1.435357173	2	3.078059
O35077	KLTEIINTQHENVK	1.162397	2	5.001655
O35077	LTEIINTQHENVK	1.093494481	2	4.699396
O35077	NIVAVGAGFCDGLGFGDNTK	1.14164969	2	4.347475
O35077	SIEQLEK	1.019161032	2	2.327023
O35077	VCIVGSGNWGSAIAK	1.03489373	2	4.056345
O35077	VCYEGQPVGEFICCLQNHPEHM	1.198692842	2	3.820814
O35077	VTMWVFEEDIGGR	1.374914295	2	3.456358
O35078	**OXDA D_amino_acid oxidase**	**0.548939744**	**4.6E-07**	**2**
O35078	GQIIQVEAPWIK	0.476607774	2	2.9603
O35078	SCCQLEPTLK	0.672880649	2	2.36446
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.913386484**	**0.83216**	**3**
O35094	ILDISNVDLAMGK	0.968121191	2	2.886078
O35094	KLEESDALQEAR	0.908425493	2	3.413502
O35094	TEMSEVLTEILR	0.930094138	2	3.071975
O35142	**COPB2 Coatomer subunit beta_**	**1.148833213**	**1.1E-16**	**3**
O35142	AAESLADPTEYENLFPGLK	1.400092166	2	3.931186
O35142	FELALQLGELK	0.986342968	2	3.173294
O35142	GSNNVALGYDEGSIIVK	0.967371272	2	3.083227
O35244	**PRDX6 Peroxiredoxin_6**	**0.923504506**	**0.13968**	**10**
O35244	DFTPVCTTELGR	0.764936744	2	2.310607
O35244	DINAYNGAAPTEK	1.042484127	2	3.917353
O35244	DLAILLGMLDPAEKDEK	0.818627869	2	3.800843
O35244	GESVMVLPTLPEEEAK	1.05144318	2	3.034328
O35244	KGESVMVLPTLPEEEAK	1.013583801	2	4.926247
O35244	KGESVMVLPTLPEEEAK+Oxidation(5)	0.722439078	2	3.066444
O35244	LSILYPATTGR	1.009571058	2	2.436024

O35244	NFDEILR	0.904214896	1	2.04712
O35244	VVDSLQLTASNPVATPVDWK	0.910002744	2	5.015574
O35244	VVFIFGPDKK	1.239057394	2	2.342576
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.637227165**	**8.9E-16**	**2**
O35469	DLGYEPLVSWEEAK	0.627796245	2	4.20855
O35469	TSEWIGTLVEQHR	0.647038894	2	3.472775
O35509	**RB11B Ras_related protein Rab_11B**	**1.048966761**	**0.64533**	**4**
O35509	AQIWDTAGQER	0.961817887	2	2.747673
O35509	GAVGALLVYDIAK	1.063655032	2	3.745607
O35509	NEFNLESK	0.869383945	1	2.138716
O35509	VVLIGDSGVGK	0.913348397	2	2.402392
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**0.903269317**	**0.09801**	**7**
O35567	AEVSNAIDQYVTGTIGEGEDLVK	0.928734556	2	3.300903
O35567	ALFEEVPELLTEAEK	0.943294114	2	3.600438
O35567	DGQVIGIGAGQQSR	0.289765737	2	3.344449
O35567	EVSDGIVAPGYEEEALK	0.967894692	2	3.719402
O35567	HVSPAGAAVGVPLSEDEAR	0.895463517	2	4.173394
O35567	SGVAYIVAPSGSTADK	1.007850953	2	2.794787
O35567	VTVVCEPEDYGAVAAEMQGSGNK	0.746681191	2	5.161515
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.379024902**	**1.1E-05**	**3**
O35760	AELGIPLEEVDLNEMNYLTR	0.315420568	2	4.356061
O35760	NCHLNENIDK	0.210371979	2	3.005208
O35760	NVTLNPDPNEIK	0.46937728	2	3.356026
O35763	**MOES Moesin**	**0.887259556**	**0.21388**	**2**
O35763	ALTSELANAR	0.878827613	2	2.773598
O35763	FYPEDVSEELIQDITQR	0.982323349	2	2.871101
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**1.075057481**	**0.23275**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	0.981988003	2	4.763177
O35796	AFVEFLTDEIK	0.890625996	2	2.612067
O35796	AFVEFLTDEIKEEK	1.079674424	2	3.542451
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.536387422	3	5.098336
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**0.909170467**	**0.56506**	**3**
O35814	ALSAGNIDDALQCYSEAIK	0.997415989	2	5.097708
O35814	DCEECIQLEPTFIK	0.901185739	2	4.123972
O35814	ELIEQLQNKPSDLGTK	0.909151624	2	4.201553
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**0.914711753**	**0.79646**	**2**
O35824	FDVQFPENNWINPDK	0.961507685	2	3.322567
O35824	NVLCSACSGQGGK	0.913905029	2	3.073852
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.3045819**	**0.01258**	**5**
O35826	DEAVGALHLIQAAK	1.189443524	2	2.8906

O35826	IYGDGNAVPR	1.165236268	2	2.331684
O35826	SIDLQEPLQK	1.092054821	2	2.567137
O35826	TLVLFPNIDAGSK	1.121294528	2	3.030975
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.340157462	3	4.703054
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.412396807**	**9.9E-20**	**3**
O35913	EGLQENVDGTENAK	0.348113724	2	3.1736
O35913	SLSGTYMNSMLTQIER	0.86400873	2	3.078519
O35913	SQTLNPTQDPSECVK	0.400972996	2	4.190156
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**0.972990384**	**0.07581**	**7**
O35952	ALLEVLGR	0.922358236	2	2.902776
O35952	FYEGTADEMYK	1.030570706	2	2.494801
O35952	HVEPGNTAVQEK	0.95972816	3	3.865855
O35952	LTTVLTTHHHWDHAGGNEK	1.066126676	3	3.462862
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.006929046	2	3.8837
O35952	TVQQHAGETDPVTTMR	0.824999488	2	4.674879
O35952	TVQQHAGETDPVTTMR+Oxidation(14)	0.909485956	2	3.419782
O35987	**NSF1C NSFL1 cofactor p47**	**0.877207112**	**8.5E-08**	**4**
O35987	ASSSILINEAEPTTNIQIR	0.800048197	2	5.176984
O35987	EANLLNAVIVQR	0.973610042	2	3.168115
O35987	LGAAPEEESAYVAGER	0.920791458	2	4.011843
O35987	SYQDPSNAQFLESIR	0.915686644	2	3.99571
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.306157557**	**0.1596**	**2**
O54753	TWEATPEHIR	1.341222416	2	2.63641
O54753	YGVEAFSDVLR	1.275678696	2	2.658061
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.061426122**	**0.1205**	**5**
O55012	ATTLSNAVSSLASTGLSLTK	1.297083739	2	3.741146
O55012	ITAAQHSVTGSAVSK	1.004942882	2	4.19213
O55012	LVSDDLDSSLANLVGNLGIGNGTTK	0.805644808	3	3.978628
O55012	NTLFNLSNFLDK	1.137227908	2	2.773794
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	1.029432044	3	4.797277
O55096	**DPP3 Dipeptidyl peptidase 3**	**0.986083923**	**0.15966**	**4**
O55096	AGLLALEFYTPETANWR	1.130310034	2	4.366669
O55096	LASVLNTEPALDSELTSK	1.3280734	2	4.123619
O55096	NVSLGNVLAVAYATK	1.079894575	2	2.455905
O55096	SYEFQGNHFQVTR	0.948198399	2	3.557676
O55125	**NIPS1 Protein NipSnap homolog 1**	**0.969180812**	**2.1E-07**	**3**
O55125	AGPNIYELR	0.858300753	2	3.047142
O55125	GWDENVYYTVPLVR	1.473291748	2	3.002901
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.069690208	3	4.677287
O55148	**GAS7 Growth arrest_specific protein 7**	**0.677467653**	**0.0011**	**2**
O55148	EMSEFIRERIK	0.677082147	2	2.370407

O55148	QKDLEMKTQQLEIK+Oxidation(5)	0.892278822	2	2.482962
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**1.015618095**	**0.02893**	**6**
O55171	ADAGGELDLAR	1.150953518	2	2.353116
O55171	DGLLDVVEALQSPLVDKK	0.794073055	2	5.491057
O55171	DVQKPYVVELEVLDGHEPDGGQR	1.025955662	3	4.412811
O55171	GGELGLAMASFLK	0.81326556	2	3.634328
O55171	IEYFEEAVNYLR	1.0540763	2	4.026573
O55171	SCWDEPLSITVR	0.92621105	2	3.483399
O70127	**ABCBB Bile salt export pump**	**1.053255038**	**0.48691**	**4**
O70127	AGQITSEALSNIR	1.050443378	2	3.328748
O70127	AGSIADEVLSSIR	1.034590501	2	2.620444
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.249616142	3	3.433631
O70127	ILLLDEATSALDTESEK	0.996911891	2	3.856109
O70133	**DHX9 ATP_dependent RNA helicase A**	**0.971608196**	**0.00022**	**2**
O70133	KMTPAYEIRAVGNK	0.535536991	2	2.456806
O70133	YPSPFFVFGEKIR	1.078298133	2	2.510429
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**0.832155706**	**9.9E-20**	**11**
O70199	EQIVVDLSHPGVSADDQVSR	0.842055779	2	5.703694
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	0.881357943	3	6.006451
O70199	IIDSLFNTVTDK	0.860848473	2	2.712534
O70199	IIDSLFNTVTDKK	0.913242918	2	3.002607
O70199	ILTTNTWSSELSK	1.027295107	2	3.036883
O70199	INAWNSPTLPIYEPGLK	0.958461385	2	3.573433
O70199	NLFFSTNIDDAIR	1.054945411	2	3.184908
O70199	VLDGLHNELQTIGFQIETIGK	0.899179488	2	5.593967
O70199	VLIGGDETPEGQR	0.795854335	2	2.974247
O70199	VTVVDVNEAR	0.783824243	2	3.117615
O70199	YWQQVIDMNDYQR	0.781777783	2	4.336303
O70251	**EF1B Elongation factor 1_beta**	**1.102658151**	**2.2E-16**	**4**
O70251	SIQADGLVWGSSK	1.024596254	2	3.660266
O70251	SSILLDVKPWDDETDMTK	1.074923911	2	4.175203
O70251	SSILLDVKPWDDETDMTKLEECVR	0.996359368	3	4.29966
O70251	TPAGLQVLNDYLADK	1.857233008	2	3.955662
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**0.855909505**	**9.9E-20**	**18**
O70351	EVQAALTLAK	0.820929214	2	2.538556
O70351	GGIVGMTLPIAR	0.915322481	2	3.458628
O70351	GGIVGMTLPIAR+Oxidation(5)	0.674557695	2	3.152612
O70351	GLVAVITGGASGLGLSTAK	0.892604427	2	4.581475
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.474501079	2	3.718291
O70351	IDVAVNCAGIAVAIK	0.872147932	2	3.133094
O70351	KLGGNCIFAPANVTSEK	0.903193598	2	4.475845
O70351	KNQVHTLEDFQR	0.829835184	2	3.97714

O70351	LGGNCIFAPANVTSEK	0.919767297	2	3.3499
O70351	LGGNCIFAPANVTSEKEVQAALTLAK	1.265771512	3	3.416527
O70351	LVAGVMGQNEPDQGGQR	0.952697607	2	5.195188
O70351	LVGQGATAVLLDVPNSEGETEAK	1.105892008	2	4.822373
O70351	NFLASQVPFPSR	0.832963417	2	4.469247
O70351	NQVHTLEDFQR	0.823662885	3	3.41504
O70351	RLVGQGATAVLLDVPNSEGETEAK	0.975745861	3	5.05846
O70351	RLVGQGATAVLLDVPNSEGETEAKK	0.883437943	3	3.556714
O70351	VINVNLIGTFNVIR	1.069697129	2	3.348824
O70351	VVTIAPGLFATPLLTTLPDK	0.918979088	2	3.335507
O70456	**1433S 14_3_3 protein sigma**	**0.925783575**	**0.91858**	**4**
O70456	DSTLIMQLLR	1.067570891	2	3.275568
O70456	DSTLIMQLLR+Oxidation(5)	0.816109132	2	2.830377
O70456	VLSSIEQK	0.924561712	2	2.326001
O70456	YEDMAAFMKSAVEK+Oxidation(3)	0.938682203		2.33081
O88202	**LPP60 60 kDa lysophospholipase**	**0.964007107**	**0.89226**	**3**
O88202	AAGAHLSPQELEDVGTELCR	0.960960955	3	3.908411
O88202	DYSGQTPLHVAAR	1.120907324	2	2.658682
O88202	GVDVDACNEDGQSPLLLAVR	0.901098225	2	4.969258
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**0.794320175**	**2.7E-05**	**3**
O88428	GCTVWLTGLSGAGK	0.738522578	2	2.937469
O88428	IHESAGLPFFEIFVDAPLNICESR	1.059918088	3	3.768689
O88428	NLGFSAGDREENIR	0.794309741	2	3.011832
O88600	**HSP74 Heat shock 70 kDa protein 4**	**0.893659238**	**0.09384**	**15**
O88600	AESEEMETSQAGSK	0.84651757	2	4.483815
O88600	AESEEMETSQAGSK+Oxidation(5)	1.242359916	2	3.917899
O88600	AFSDPFVEAEK	0.928896491	2	2.525365
O88600	AGGIETIANEYSDR	0.873735313	2	3.487802
O88600	EFSITDVVPYPISLR	0.925577374	2	2.52834
O88600	ELSTTLNADEAVTR	0.850744699	2	2.351924
O88600	GCALQCAILSPAFK	0.918200797	2	3.429054
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	0.911441553	3	4.69788
O88600	MIMQDKLEK+Oxidation(0)	0.933287083	2	2.399258
O88600	NFTTEQVTAMLLSK	0.968090215	2	3.455726
O88600	NKEDQYEHLDAADMTK	0.98328986	3	3.488273
O88600	SNLAYDIVQLPTGLTGIK	0.874642373	2	4.433111
O88600	TSTVDLPIESQLLWQLDR	0.982678648	2	4.16192
O88600	VLATAFDTTLGGR	0.864978337	2	3.384554
O88600	WNSPAEEGSSDCEVFPK	0.922850156	2	3.408425
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.202164393**	**9.9E-20**	**20**
O88618	AFAACLGAIK	1.287897008	2	2.74629
O88618	AGEYEALPEK	1.182985883	2	2.92188

O88618	ALLDAAAFYCDK	1.337275999	2	3.932776
O88618	ALLDAAAFYCDKEK	0.843271476	2	3.828817
O88618	EAQELNLPVVGSQLVGLVPLK	1.176606298	3	4.36034
O88618	GVSMDECVLCAK	1.380283929	2	3.835449
O88618	IIEYLVPDSGPEQSLLDASLR	1.187673155	2	4.950724
O88618	ISSLLQEAK	1.288817397	1	2.103034
O88618	KVQGIGWYLEEK	1.195705179	2	2.636844
O88618	LAEELNVPVYLYGEAAQMPSR	1.629096151	2	5.020977
O88618	LFVLEEEHR	1.170360347	2	2.808884
O88618	LGLDSLAPFDPK	1.356031442	2	3.810372
O88618	MGALDVCPFIPVR	1.564772568	2	3.357251
O88618	MGALDVCPFIPVR+Oxidation(0)	1.334281254	2	2.673084
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.344107217	3	4.293399
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.286027682	2	3.910404
O88618	TCALQEGLR	1.454084934	2	2.742219
O88618	TQAALVLGSLEAR	1.118191766	2	5.055916
O88618	TVYTFVGQPECVVEGALSAAR	2.018302164	2	4.336102
O88618	VQGIGWYLEEK	1.157113912	2	3.421891
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.253722402**	**0.15235**	**6**
O88637	GPPVFTQEER	0.953698983	2	2.555979
O88637	HKGPPVFTQEER	0.99257761	2	3.018238
O88637	TEIVPDRDGSDPYEEPK	1.18560299	2	2.751698
O88637	TQGVSTTDLVGR	0.950395431	2	2.927661
O88637	WVDEVVPAAPYVTTLETLDK	1.293021903	2	2.939858
O88637	YVSEVVIGAPYSVTAELLNHFK	1.359662257	3	3.323131
O88746	**TOM1 Target of Myb protein 1**	**0.956025502**	**0.80117**	**2**
O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	0.946671858	3	5.489599
O88746	QQSTGAIPATQAR	1.487570301	2	2.396017
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**0.953603372**	**0.45314**	**2**
O88761	DTSEDIEELVEPVAAHGPK	0.993242004	2	3.394719
O88761	TVGTPIASVPGSTNTGTVPGPEK	0.921288763	2	3.185826
O88767	**PARK7 Protein DJ_1**	**0.965912139**	**0.01841**	**6**
O88767	DVVICPDTSLEEAK	1.046915559	2	3.046035
O88767	GAEEMETVIPVDIMR	1.125929509	2	4.128756
O88767	GAEEMETVIPVDIMR+Oxidation(13)	0.874557073	2	2.961041
O88767	GLIAAICAGPTALLAHEVGFGCK	0.610306191	2	4.94179
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	0.840123475	2	4.540389
O88767	VTVAGLAGKDPVQCSR	0.990429977	2	3.952677
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**1.269905259**	**9.9E-20**	**8**
O88813	AILEDLQK	0.734569554	1	1.91715
O88813	GLAVSDNGPCLGYR	0.867926979	2	2.992224
O88813	GSFEELCQNQCVK	0.818157693	2	4.384674

O88813	IGFFQGDIR	1.13209992	2	2.667367
O88813	SFLIGVVVPDPESLPSFAAK	0.705543273	2	3.873984
O88813	SIFVHPEPFSIENGLLTPTLK	1.330827362	3	3.7044
O88813	SRPILQVFVHGESLR	1.216920783	3	3.789805
O88813	TQEVLDKDGWLHTGDIGR	0.829397952	3	3.328365
O88867	**KMO Kynurenine 3_monooxygenase**	**0.566040856**	**9.9E-20**	**4**
O88867	AVGLEDQIVSK	0.618730711	1	2.467244
O88867	FNNDLSVCLPEFSR	0.966302383	2	3.629586
O88867	NFPDAIPLMGEQALMR	0.913893085	2	2.517786
O88867	NFQVDVYEAR	0.70945661	2	2.58554
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**0.855837174**	**0.15378**	**3**
O88941	DLALPTLLNPK	0.819501246	2	2.300483
O88941	LGPLLDVLADSR	0.891481542	2	2.796738
O88941	MDPSLFPPVPLFSGVPSR	0.854717091	2	2.480091
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**0.883355702**	**0.65487**	**2**
O88986	GTDELLGVMDQVTIINSTLGK	0.919361584	2	3.388648
O88986	VQISAVHSEEDIDR	1.038617079	2	3.542248
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.179478535**	**9.9E-20**	**8**
O88989	DLDVAVLVGSMPR	1.126029273	3	3.972061
O88989	ELTEEKETAFEFLSSA	1.095454861	2	3.727441
O88989	EVGVYEALKDDSWLK	1.19879789	2	3.820338
O88989	FVEGLPINDFSR	1.1616238	2	3.29685
O88989	GEFITTVQQR	1.142416718	2	3.988533
O88989	LGVTADDVK	1.178537343	2	2.815489
O88989	NVIIWGNHSSTQYPDVNHAK	1.231455434	2	5.757
O88989	VIVVGNPANTNCLTASK	1.172968893	2	5.171251
O88990	**ACTN3 Alpha_actinin_3**	**0.904749739**	**0.56675**	**5**
O88990	AGTQIENIEEDFR	0.620695739	2	3.064051
O88990	CQLEINFNTLQTK	0.960506789	2	4.113487
O88990	FAIQDISVEETSAK	0.866633941	2	4.190232
O88990	GLSQEQLNEFR	0.517570853	2	2.415922
O88990	HEAFESDLAAHQDR	1.00269941	3	4.298998
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.739452008**	**7.1E-05**	**2**
O88994	CVLTTVDPDTGIIDR	0.742018657	2	4.302613
O88994	QLQQVGTVSK	0.743348429	2	2.365731
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**0.944880335**	**0.00326**	**5**
O89000	EGGADGVTATNTVSGLMGLK	0.785620246	2	2.706854
O89000	GTTSGPLYGPGQSSFLNIELISEK	1.432806108	2	4.059982
O89000	LTPNVTDIVSIAR	0.526615428	2	2.551821
O89000	QEYVGGLSTSEIPQFR	0.892872703	2	3.520966
O89000	TEQDETGNWVEDEEQIVR	1.033961658	2	4.562162

O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**0.894402476**	**0.00805**	**2**
O89032	EGWAPASYIDKRK	0.687311457	1	1.963272
O89032	MLAYCVQDATVVDVEK	1.073968717	2	2.455116
O89046	**COR1B Coronin_1B**	**0.908303235**	**0.0203**	**2**
O89046	NDQCYEDIR	0.893375622	2	3.014926
O89046	NVLSDSKPAGYSR	0.983142089	2	3.323968
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**0.831458407**	**1.4E-05**	**5**
O89049	IEQIEAGTPGR	0.871987353	2	3.358
O89049	IEQIEAGTPGRLK	2.071222196	2	2.371856
O89049	LELTPVAIQAGR	0.92614829	2	2.740657
O89049	STNSEETIEDEFNTVLLAVGR	1.136601606	3	3.442827
O89049	WGLGGTCVNVGCIPK	0.806451961	2	3.069563
P00173	**CYB5 Cytochrome b5**	**0.656144453**	**9.9E-20**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	0.581924595	2	5.380463
P00173	FLEEHPGGEEVLR	0.651389877	2	4.176721
P00173	STWVILHHK	0.703628378	2	2.737279
P00173	TYIIGELHPDDR	0.720338515	2	3.875772
P00173	VYDLTK	0.634628251	1	2.132261
P00173	YYTLEEIQK	0.672409451	2	3.096185
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.196431224**	**1E-06**	**7**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.167729568	3	4.976091
P00388	GMSADPEEYDLADLSSLPEIDK	1.339712115	2	4.67908
P00388	LEQLGAQR	1.142010079	2	2.328925
P00388	RSDEDYLYR	1.210627186	2	3.232828
P00388	SDEDYLYR	1.121142289	2	2.38762
P00388	SYENQKPPFDAK	1.167383457	2	3.016846
P00388	TNVLYELAQYASEPSEQEHLHK	1.346413954	3	3.58361
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.017545835**	**0.91969**	**2**
P00406	LLEVDNR	0.977819292	2	2.549215
P00406	VVLPMELPIR	1.036538003	2	2.333756
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**0.887781467**	**9.9E-20**	**14**
P00481	FGMHLQAATPK	0.844055848	3	3.457302
P00481	GEYLPLLQGK	0.792893547	2	3.048455
P00481	GGNVLITDTWISMGQEDEK	1.128015723	2	4.531702
P00481	GGNVLITDTWISMGQEDEKK	1.192687752	2	4.63328
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.106899775	2	4.128619
P00481	GYEPDPNIVK	0.816951247	2	2.755304
P00481	LQAFQGYQVTMK	1.144049715	2	3.417808
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.127401922	3	5.728715
P00481	QKGEYLPLLQGK	0.846629557	2	3.19065
P00481	SLVFPEAENR	0.823558061	2	2.472008
P00481	SLVFPEAENRK	0.825778093	2	2.886991

P00481	VLSSMTDAVLAR	0.90763888	2	3.718466
P00481	VLSSMTDAVLAR+Oxidation(4)	0.897547104	2	2.771189
P00481	YGKPVQSQVQLK	0.392464316	2	2.816904
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.683941773**	**0.00164**	**2**
P00502	FIQSPEDLEK	0.639520849	2	2.787801
P00502	WLLAAAGVEFDEK	0.724604259	2	4.417922
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**0.810756723**	**9.9E-20**	**17**
P00507	ASAELALGENSEVLK	0.881828221	2	4.827941
P00507	DAGMQLQGYR	0.812049225	2	2.318431
P00507	DDNGKPYVLPSVR	0.857287626	2	3.32851
P00507	DDNGKPYVLPSVRKAEAQIAGK	0.794816236	2	2.383237
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.449517068	3	4.835541
P00507	FVTVQTISGTGALR	0.895301977	2	5.156823
P00507	HFIEQGINVCLCQSYAK	0.842379836	2	3.690485
P00507	IAATILTSPDLR	2.494150096	2	3.057026
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.432944728	3	4.326439
P00507	KQWLQEVK	0.942888196	1	2.113429
P00507	MNLGVGAYR	0.936578961	2	2.931424
P00507	NLDKEYLPIGGLADFCK	0.815154258	2	5.364047
P00507	NMGLYGER	0.853354552	1	2.19264
P00507	TCGFDFSGALEDISK	0.871848112	2	4.694676
P00507	TQLVSNLK	0.77836168	2	2.681593
P00507	VGAFTVVCK	0.956202319	2	3.125698
P00507	VGASFLQR	1.127098682	2	2.972824
P00564	**KCRM Creatine kinase M_type**	**0.722411411**	**0.25945**	**11**
P00564	DLFDPIIQDR	0.685400324	2	2.474128
P00564	FEEILTR	0.955079303	2	2.447623
P00564	GGDDLDPNYVLSSR	0.523451133	2	4.179605
P00564	GQSIDDMIPAQK	0.561534989	2	2.862451
P00564	GTGGVDTAAVGAVFDISNADR	0.54773613	2	5.894311
P00564	LGSSEVEQVQLVVDGVK	0.623884153	2	3.651853
P00564	LSVEALNSLTGEFK	0.62723141	2	3.74195
P00564	RGTGGVDTAAVGAVFDISNADR	0.440356193	2	4.173407
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	0.65875494	3	6.009603
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR+Oxidation(1)	0.5428977	4	4.558091
P00564	TDLNHENLK	0.57480519	2	2.638885
P00787	**CATB Cathepsin B**	**1.11070883**	**0.00102**	**4**
P00787	GENHCGIESEIVAGIPR	1.108936361	2	4.23511
P00787	HEAGDVMGGHAIR	1.040237514	3	3.887353
P00787	MCEAGYSTSYKEDK	1.044215055	2	3.726816
P00787	NGPVEGAFTVFSDFLTYK	1.407259516	2	3.620009
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.326175357**	**9.9E-20**	**18**

P00884	ALQASALAAWGGK	1.38269549	2	4.720711
P00884	ATQEAFMK	1.11453451	2	2.674007
P00884	ATQEAFMK+Oxidation(6)	1.817438177	1	2.216407
P00884	ELLFSVDNSISQSIGGVILFHETLYQK	2.265081793	3	4.121828
P00884	ELSEIAQR	1.055735688	1	2.175398
P00884	ETTIQGLDGLSER	1.175470534	2	3.702198
P00884	GILAADESVGTMGNR	1.252892588	2	5.43682
P00884	GILAADESVGTMGNR+Oxidation(11)	1.359542215	2	5.102598
P00884	IKVENTEENR	1.176906067	2	3.155527
P00884	IKVENTEENRR	0.986501143	2	3.163885
P00884	ISDQCPSSLAIQENANALAR	1.311426976	2	6.46809
P00884	KELSEIAQR	1.387751553	3	3.5845
P00884	KYTPEQVAMATVTALHR	1.59297331	3	6.008464
P00884	KYTPEQVAMATVTALHR+Oxidation(8)	1.08323583	3	4.797522
P00884	LDQGGAPLAGTNK	1.235552691	2	4.56857
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.94335856	3	5.047423
P00884	YTPEQVAMATVTALHR	1.520837368	2	4.71481
P00884	YTPEQVAMATVTALHR+Oxidation(7)	1.101418378	2	4.170346
P01015	**ANGT Angiotensinogen**	**0.891044615**	**0.1169**	**2**
P01015	GSYNLQDLLAQAK	0.648657453	2	2.340241
P01015	SLDLSTDPVLAAQK	1.470753596	2	2.691788
P01026	**CO3 Complement C3**	**0.915827526**	**0.02127**	**12**
P01026	ADIGCTPGSGK	0.87097673	2	2.412773
P01026	DSCVGTLVVKGDPR	0.915480882	2	2.360075
P01026	EYVLPSFEVLVEPTEK	1.071646562	2	4.084051
P01026	IFTVDNNLLPVGK	1.015617808	2	2.768405
P01026	RVPVVTQGSDAQALTQDDGVAK	0.897249933	2	4.88799
P01026	SGSDEVQAGQER	1.394831929	2	4.232399
P01026	SSVAVPYVIVPLK	1.679084423	2	2.451176
P01026	TVLTGATGHLNR	1.015973826	2	2.754661
P01026	VELKPGDNLNVNFHLR	1.062015343	3	4.973259
P01026	VHQFFNVGLIQPGSVK	1.462491399	3	3.570119
P01026	VLIEDGSGEAVLSR	1.110039133	2	3.524881
P01026	VLMDGVRPSSPEALVGK	1.091569767	2	2.648866
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.80880026**	**0.93054**	**8**
P01946	AADHVEDLPGALSTLSDLHAHK	0.874854707	3	7.351187
P01946	FLASVSTVLTSK	0.703761224	2	3.998177
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	1.046168084	6	4.989113
P01946	IGGHGGEYGEEALQR	0.831421971	3	5.073644
P01946	LRVDPVNFK	0.960309828	2	2.466158
P01946	MFAAFPTTK	0.99488251	2	2.492434
P01946	MFAAFPTTK+Oxidation(0)	0.558380777	2	2.698089

P01946	TYFSHIDVSPGSAQVK	0.862136951	2	5.197578
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.591430637**	**0.97259**	**4**
P02089	GTFASLSELHCDK	0.749892385	2	3.219352
P02089	LHVDPENFR	0.707408625	2	2.49771
P02089	YFDSFGDLSSASAIMGNPK	0.684958203	2	6.628827
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14)	0.700097551	2	5.571102
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.924719059**	**0.32843**	**9**
P02091	AAVNGLWGK	5.896612401	2	2.768222
P02091	EFTPCAQAAFQK	0.645177428	2	3.1865
P02091	GTFAHLSELHCDK	0.800993219	2	4.261004
P02091	GTFAHLSELHCDKLHVDPENFR	0.847350634	3	3.838347
P02091	KVINAFNDGLK	0.749126039	3	3.87784
P02091	LLGNMIVIVLGHHLGK	0.997479581	2	2.705111
P02091	VINAFNDGLK	0.738364759	2	2.924035
P02091	VNPDDVGGEALGR	0.746758033	2	4.073515
P02091	VVAGVASALAHK	0.699010005	2	3.487201
P02401	**RLA2 60S acidic ribosomal protein P2**	**1.023754342**	**6.9E-11**	**6**
P02401	ILDSVGIEADDER	1.169178762	2	4.746322
P02401	KILDSVGIEADDER	0.950275784	2	3.847073
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	0.937877597	3	5.837322
P02401	NIEDVIAQGVGK	1.013753227	2	4.606312
P02401	VISELNGK	1.053955146	1	2.011276
P02401	YVASYLLAALGGNSNPSAK	1.323692984	2	5.091392
P02563	**MYH6 Myosin_6**	**1.050516672**	**0.9269**	**2**
P02563	DTQLQLDDAVR	1.054400281	2	2.630583
P02563	VKLEQQVDDLEGSLEQEKK	0.865620688	3	3.693087
P02564	**MYH7 Myosin_7**	**0.99446024**	**5.1E-06**	**32**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	0.623222235	3	4.514825
P02564	ANDDLKENIAIVER	0.716933153	2	3.468239
P02564	DLEEATLQHEATAAALR	0.47065913	2	4.960937
P02564	DTQIQLDDAVR	1.054400281	2	2.630583
P02564	DVFVPDDKEEFVK	1.650520843	2	2.586309
P02564	ELENELEAEQK	1.176900432	2	2.33688
P02564	EQYEEETEAK	0.576108295	2	2.386412
P02564	GQNVQQVAYAIGALAK	0.885060078	2	3.430654
P02564	GTLEDQIIQANPALEAFGNAK	0.808023786	2	5.284353
P02564	IEDEQALGSQLQK	0.57414946	2	4.413587
P02564	IEELEEELEAER	0.667633219	2	3.778149
P02564	ILNPAAIPEGQFIDSR	0.649640163	2	2.835299
P02564	KLEDECSELKR	0.589844696	3	3.494481
P02564	KVQHELDEAEER	0.646221274	2	3.602796
P02564	LAEQELIETSER	0.668563234	2	3.214802
P02564	LDEAEQIALK	0.646495347	2	3.592026

P02564	LELDDVTSNMEQIIK	0.855437224	2	3.785596
P02564	LQDAEEAVEAVNAK	0.846278548	2	4.40889
P02564	LQNEIEDLMVDVER	0.832761595	2	2.971473
P02564	LTQESIMDLENDKQQLDER	0.986736552	3	3.585778
P02564	MDADLSQLQTEVEEAVQECR	0.847951007	2	4.245785
P02564	NAYEESLEHLETFK	0.735828284	2	2.850118
P02564	NLQEEISDLTEQLGSTGK	0.695405197	2	5.525924
P02564	NLTEEMAGLDEIIVK	1.036092638	2	3.703064
P02564	NNLLQAELEELR	0.686246034	2	3.453353
P02564	QAEEAEEQANTNLSK	0.645699149	2	4.896638
P02564	QKYEESQSELESSQK	0.822115564	2	3.415476
P02564	TLEDQMNEHR	0.602925386	2	2.643172
P02564	VKEMTERLEDEEEMNAELTAK	0.539132546	2	2.322104
P02564	VQHELDEAEER	0.980477258	3	3.38028
P02564	VQLLHSQNTSLINQK	0.713167557	2	3.943206
P02564	VVDSLQTSLDAETR	0.669758716	2	3.643353
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**0.826955312**	**0.82494**	**11**
P02600	ALGTNPTNAEVK	0.589733349	2	3.272845
P02600	ALGTNPTNAEVKK	0.625123303	2	3.038026
P02600	DQGGYEDFVEGLR	0.574504882	2	3.97068
P02600	IDLSAIK	0.552316526	2	2.328373
P02600	IEFEQFLPMMQAISNNK	0.944271306	2	3.650124
P02600	ITLSQVGDVLR	0.759886504	2	3.509644
P02600	KIEFEQFLPMMQAISNNK	0.667283222	2	5.380936
P02600	KPAAAAPAPAPAPAPAPAKPK	8.420704119	3	3.368535
P02600	KVLGNPSNEEMNAK	0.805008349	2	3.280922
P02600	VLGNPSNEEMNAK	0.588970715	2	3.570217
P02600	VLGNPSNEEMNAK+Oxidation(9)	0.622412034	2	2.807169
P02625	**PRVA Parvalbumin alpha**	**0.680013868**	**0.05208**	**4**
P02625	AIGAFTAADSFDHK	0.696656645	2	2.418355
P02625	SGFIEEDELGSILK	0.469080056	2	3.936534
P02625	TLMAAGDKDGDGK	0.444549565	2	2.916943
P02625	TLMAAGDKDGDGK+Oxidation(2)	0.657615935	2	3.023445
P02650	**APOE Apolipoprotein E**	**1.20305418**	**0.01971**	**12**
P02650	ELEEQLGPVAEETR	1.207350966	2	4.597376
P02650	GRLEEVGNQAR	1.005151208	2	3.622802
P02650	GWFEPLVEDMQR	1.02410494	2	3.141609
P02650	LEEVGNQAR	0.997627729	2	2.813071
P02650	LGADMEDLR	1.187949514	2	2.606182
P02650	LGPLVEQGR	1.238405129	2	2.444969
P02650	LQAEIFQAR	1.726698564	2	2.321469
P02650	MEEQTQQIR	0.997795039	2	2.542813

P02650	NEVNTMLGQSTEELR	1.091757471	2	4.403859
P02650	SKMEEQTQQIR	0.936749981	2	3.396561
P02650	SKMEEQTQQIR+Oxidation(2)	1.47519696	2	2.96943
P02650	TANLGAGAAQPLR	1.338474121	2	3.192875
P02680	**FIBG Fibrinogen gamma chain**	**0.902001522**	**0.00746**	**4**
P02680	VAQLEAQCQEPCK	2.396936359	2	2.751341
P02680	VGPESDKYR	0.353516587	2	2.841702
P02680	YEALLLTHESSIR	1.176309534	2	3.545323
P02680	YLQDIYTSNK	0.833241163	2	2.444826
P02692	**FABPL Fatty acid_binding protein_ liver**	**1.226062955**	**9.9E-20**	**12**
P02692	AMGLPEDLIQK	1.194503581	2	3.60376
P02692	AMGLPEDLIQK+Oxidation(1)	1.083962114	2	3.746587
P02692	GVSEIVHEGK	1.010246338	2	3.32548
P02692	GVSEIVHEGKK	1.011818097	2	3.203617
P02692	MVTTFK+Oxidation(0)	1.101088852	1	1.995837
P02692	SVTEFNGDTITNTMTLGDIVYK	1.148424229	3	5.727576
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13)	1.272436463	2	5.240052
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.229096292	2	3.57648
P02692	VIHNEFTLGEECELETMTGEK	1.100752618	3	6.170149
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16)	1.039054654	3	5.800786
P02692	YQVQSQENFEPFMK	1.213667835	2	5.80917
P02692	YQVQSQENFEPFMK+Oxidation(12)	1.37853711	2	5.223806
P02696	**RET1 Retinol_binding protein 1**	**0.812167166**	**0.46066**	**6**
P02696	ALDVNVALR	0.908604741	2	3.025125
P02696	CMTTVSWDGDKLQCVQK	1.331455235	2	3.762113
P02696	EFEEDLTGIDDR	0.770480519	2	2.472834
P02696	EFEEDLTGIDDRK	0.751692824	2	2.854273
P02696	MLSNENFEEYLR	1.048541253	2	3.328781
P02696	MLSNENFEEYLR+Oxidation(0)	0.819629272	2	3.18666
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.160099367**	**1.5E-07**	**4**
P02706	DYQDFQHLDNENDHHQLQR	1.597352468	3	4.487172
P02706	LVESQLEK	1.044983921	2	2.472374
P02706	SLSCQMAALR	1.21626297	2	2.636677
P02706	WVDGTDYETGFK	0.928480899	2	3.029561
P02770	**ALBU Serum albumin**	**1.226742568**	**2.2E-08**	**22**
P02770	AADKDNCFATEGPNLVAR	3.017738229	2	4.315941
P02770	AETFTFHSDICTLPDKEK	4.621938841	2	4.11612
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.173581772	2	5.148039
P02770	CCSGSLVER	0.898387761	2	2.704192
P02770	CCTLPEAQR	1.142470916	2	3.029857
P02770	ECCHGDLLECADDR	1.403051023	2	3.676816
P02770	ECCHGDLLECADDRAELAK	1.285640049	2	5.085512
P02770	FKDLGEQHFK	1.099875148	3	4.184365

P02770	GLVLIAFSQYLQK	1.476191082	2	3.644505
P02770	KQTALAELVK	1.24776651	3	4.133866
P02770	KYEATLEK	1.668142648	1	2.969912
P02770	LQACCDKPVLQK	1.104723998	2	4.164047
P02770	LVQEVTDFAK	1.281045362	2	3.271222
P02770	RHPDYSVSLLLR	1.424489978	3	5.089334
P02770	SIHTLFGDK	1.164827562	1	2.361022
P02770	TCVADENAENCDK	0.980960553	2	4.416258
P02770	TNCELYEK	1.115280423	2	2.757627
P02770	TVMGDFAQFVDK	1.147178147	2	2.893559
P02770	TVMGDFAQFVDK+Oxidation(2)	0.64012046	2	2.440962
P02770	YMCENQATISSK	1.117469434	2	4.211557
P02770	YMCENQATISSK+Oxidation(1)	1.142731284	2	3.545055
P02770	YNEVLTQCCTESDK	1.286337454	2	5.671119
P02803	**MT1 Metallothionein_1**	**2.231205543**	**9.9E-20**	**2**
P04041	**GPX1 Glutathione peroxidase 1**	**0.832531284**	**9.9E-20**	**9**
P04041	FLVGPDGVPVR	0.753561278	2	3.521695
P04041	GLVVLGFPCNQFGHQENGK	0.817454843	2	4.207802
P04041	NALPAPSDDPTALMTDPK	0.892481987	2	3.254999
P04041	NALPAPSDDPTALMTDPK+Oxidation(13)	0.762654185	2	2.701529
P04041	NDISWNFEK	0.776718673	2	2.777018
P04041	NEEILNSLK	0.785158643	2	2.475482
P04041	TIDIEPDIEALLSK	0.96516444	3	4.35711
P04041	YIIWSPVCR	0.956489498	2	2.467424
P04041	YVRPGGGFEPNFTLFEK	0.820266744	3	4.412416
P04167	**CP2B2 Cytochrome P450 2B2**	**0.452373384**	**9.9E-20**	**2**
P04167	GTIAVIEPIFK	0.301692883	2	2.61487
P04167	NLQEILDYIGHIVEK	0.56644012	2	3.802533
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.040439533**	**1.4E-05**	**14**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.567883375	3	3.509964
P04176	EDNIPQLEDVSQFLQTCTGFR	1.108986679	3	4.76325
P04176	FANQILSYGAELDADHPGFKDPVYR	1.565172331	3	4.492066
P04176	ILADSINSEVGILCNALQK	0.899195367	2	5.058584
P04176	LRPVAGLLSSR	1.693083539	2	2.500345
P04176	NDIGATVHELSR	0.950372819	2	3.690542
P04176	QFADIAYNYR	0.986204614	2	2.48142
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.097753316	2	4.38874
P04176	TACQEYSVTEFQPLYYVAESFSDAK	2.552232846	2	4.999586
P04176	THACYEHNHIFPLLEK	1.000227206	2	4.497329
P04176	VEVLDNTQQLK	0.944694858	2	3.546311
P04176	VEYTEEEK	0.926297129	2	2.738826
P04176	VEYTEEEKQTWGTVFR	0.980863715	2	3.762657
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.125509909	3	3.553357

P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**0.699794436**	**0.67593**	**6**
P04182	AFYNNVLGEYEEYITK	0.96467925	2	4.36976
P04182	GLLNAIVIR	0.835073059	2	2.790879
P04182	KTEQGPPSSEYIFER	0.922768345	2	3.934419
P04182	TEQGPPSSEYIFER	0.880811955	2	3.553824
P04182	VLPMNTGVEAGETACK	0.790561439	2	4.93869
P04182	WLAVDHENVRPDIVLLGK	0.684011254	2	4.381255
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**0.724546084**	**2.1E-11**	**5**
P04256	EDSQRPGAHLTVK	0.721098161	2	3.326706
P04256	IEVIEIMTDR	0.844915759	2	3.410411
P04256	MSKSESPKEPEQLR	0.982517937	2	2.398291
P04256	NQGGYGGSSSSSSYGSGR	0.953808425	2	4.695726
P04256	SESPKEPEQLR	0.846296744	2	2.513839
P04355	**MT2 Metallothionein_2**	**1.650888106**	**9.9E-20**	**2**
P04462		**0.80486731**	**9.9E-20**	**53**
P04462	AEVSELPSVVR	0.780952032	2	2.896098
P04462	ALLTPVAIAAGR	0.534242928	2	2.333061
P04462	ASMMGQRASLLTAR+Oxidation(2)	0.93720808		2.391548
P04462	AVAENQPFLIEAMTYR	0.877830497	2	3.972772
P04462	AVDEAADALLK	0.943851009	2	2.313546
P04462	AVEIAHALCLTERQIK	0.935016935	2	2.495136
P04462	DEELSCSVLELK	1.260761396	2	2.718766
P04462	DQMVKNNHFTLK+Oxidation(2)	0.721224304	2	2.445719
P04462	EELEKMK	0.866839663	1	1.909279
P04462	EIAGATPYITAAEEK	1.074088974	2	2.761628
P04462	EKMNKPELFNGGEKK	0.905775815	2	2.353093
P04462	ELDSITPDITPGWK	0.805980602	2	2.581837
P04462	FDQPKLKPKSDPK	0.914918753	2	2.301082
P04462	FFRPHFLQAPGDLTVQEGK	0.956967957	2	2.815243
P04462	FKLINSTNIR	0.741061577	1	1.908701
P04462	GIEQAVQSHAVAEEEAR	0.943952153	2	4.835969
P04462	GNIYSLNEGYAK	0.970721687	2	4.136878
P04462	GVYSEETLR	0.862872142	2	2.316339
P04462	HLQTYGEHYPLDHFDK	0.674523262	3	3.563968
P04462	HVIHTVGPIAVGQPTASQAAELR	0.739873931	3	4.171026
P04462	IEEMEKMLK+Oxidation(3)	0.673962983		1.983708
P04462	IGHHSTSDDSSAYR	1.051037794	3	4.201075
P04462	KAMQEINYGPSPDNSIKLVR	1.04716337	2	2.506249
P04462	KGNIYSLNEGYAK	1.110916279	2	4.005682
P04462	KLQHELEEAEER	0.729169944	3	4.042257
P04462	KVVSDLDVIMSHLK	0.933117125	2	2.613068
P04462	LEFIQPNVISGIPIYR	0.839223448	2	2.609355

P04462	LGDAVEQGVINNSVLGYFIGR	0.785570455	2	3.638799
P04462	LKLVMNNFIYQTK	1.029904788	2	2.42867
P04462	LNNIYQNNLTK	0.645088684	2	3.044884
P04462	LQHELEEAEER	0.599819255	2	3.572844
P04462	MNLQDELDELK	0.689111308	2	2.550207
P04462	MNLQDELDELK+Oxidation(0)	0.914669931	2	2.535447
P04462	NNGYAISTPTSEQYR	0.683778182	2	3.766916
P04462	QGQIINPSEDPHLPQEEVLK	0.479717828	2	2.555086
P04462	QRAEQETKLK	0.825473493	1	1.933957
P04462	QTITAQNAAVQAVK	0.855519646	2	4.554351
P04462	QYLLNQGWWDEEQEK	0.61583425	2	3.395736
P04462	RAALQAEIEELR	0.564380789	2	3.884
P04462	SEIQAEQDR	0.998694949	2	2.81657
P04462	SLEDALNQTATVTR	0.893258256	2	3.768177
P04462	SSSLLAKSPSK	1.144638373	2	2.352131
P04462	SVDEVNYWDK	0.757772093	2	2.535414
P04462	TNTGEDGQYFLK	0.690002291	2	2.316733
P04462	TSSAEMPTIPLGSAVEAIR	1.013083138	2	2.764965
P04462	TVNVVQFEPNK	0.792271298	2	2.378318
P04462	VDDSSGSIGR	1.24491141	2	2.670649
P04462	VDGNDVFAVYNATK	0.807079283	2	2.333353
P04462	VMEAFEQAER	0.634328737	2	3.053269
P04462	VSCSDNEFTQALTAAIPPESLTR	1.087099285	2	2.707381
P04462	VVSQYHELVVQAR	1.000793416	2	3.398304
P04462	YNENHQHGK	0.84284156	1	1.944025
P04462	YSTSSSSGVTAGK	0.453937595	2	2.864262
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**1.053022009**	**0.89888**	**7**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.092332063	2	4.804173
P04466	GADPEDVITGAFK	0.821298549	2	4.064617
P04466	KQFLEELLTTQCDR	0.502078077	2	3.56261
P04466	LKGADPEDVITGAFK	0.703875469	2	2.970653
P04466	NEELDAMMK	0.539438396	1	1.962136
P04466	NICYVITHGDAK	0.840230134	2	2.748763
P04466	QFLEELLTTQCDR	0.634319775	2	3.344339
P04550	**PTMS Parathymosin**	**1.03695269**	**1**	**4**
P04550	RTAEEEDEADPKR	0.984904178	3	4.261044
P04550	SVEAAAELSAK	0.970313926	2	3.703344
P04550	TAEEEDEADPK	0.984558175	2	3.671567
P04550	TAEEEDEADPKR	0.856604282	2	3.693547
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**0.884897843**	**9.9E-20**	**18**
P04636	AGAGSATLSMAYAGAR	1.181148142	2	4.690838
P04636	AGAGSATLSMAYAGAR+Oxidation(9)	1.044787635	2	3.679585

P04636	ANTFVAELK	1.029337774	2	2.644075
P04636	EGVIECSFVQSK	0.90749781	2	3.213264
P04636	ETECTYFSTPLLLGK	1.496530241	2	4.086312
P04636	FVFSLVDAMNGK	0.97856923	2	4.395347
P04636	GCDVVVIPAGVPR	0.892739582	2	4.376228
P04636	GYLGPEQLPDCLK	0.889687542	2	4.118331
P04636	IFGVTTLDIVR	1.086434688	2	3.698292
P04636	IQEAGTEVVK	0.864880419	2	2.962223
P04636	ITPFEEK	0.978039834	1	2.038932
P04636	LTLYDIAHTPGVAADLSHIETR	1.034821477	3	6.652123
P04636	MIAEAIPELK	1.198884332	2	2.721385
P04636	MIAEAIPELK+Oxidation(0)	0.808071867	2	2.922395
P04636	TIIPLISQCTPK	1.398930901	2	3.304041
P04636	VAVLGASGGIGQPLSLLLK	1.748381648	2	6.152614
P04636	VDFPQDQLATLTGR	0.874120178	2	4.605517
P04636	VNVPVIGGHAGK	0.777314245	1	2.294416
P04639	**APOA1 Apolipoprotein A_I**	**1.047103893**	**0.22825**	**6**
P04639	AKPALDDLGQGLMPVLEAWK	0.91121377	2	3.665092
P04639	LQEQLGPVTQEFWANLEK	1.462182492	2	4.550619
P04639	MRVNADALR+Oxidation(0)	0.890618297	2	2.52142
P04639	NEMNKDLENVK	1.146439763	2	3.238451
P04639	QLNLNLLDNWDTLGSTVGR	1.260618152	2	3.695431
P04639	WNEEVEAYR	1.359445283	2	2.794666
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.738830371**	**9.9E-20**	**16**
P04642	DLADELALVDVIEDK	1.138365324	2	5.270331
P04642	DLADELALVDVIEDKLK	1.114931184	2	3.357955
P04642	DQLIVNLLK	1.143129921	2	3.083397
P04642	DQLIVNLLKEEQVPQNK	1.426737138	2	4.861084
P04642	EDVFLSVPCILGQNGISDVVK	1.298473276	2	4.757306
P04642	FIIPNVVK	1.159069511	2	2.441001
P04642	GEMMDLQHGSLFLK	1.978859596	2	3.295779
P04642	GEMMDLQHGSLFLK+Oxidation(2)	1.360785372	2	2.317598
P04642	KSADTLWGIQK	1.504432402	2	3.08222
P04642	NVNIFK	1.153392009	1	2.200892
P04642	QVVDSAYEVIK	1.117555621	2	3.276128
P04642	RVHPISTMIK+Oxidation(7)	1.170424165	2	2.574553
P04642	SADTLWGIQK	1.134856799	2	3.829739
P04642	SLNPQLGTDADK	1.281169327	2	2.530431
P04642	SLNPQLGTDADKEQWK	1.080452779	2	4.835642
P04642	VTLTPDEEAR	1.087756176	2	2.876729
P04644	**RS17 40S ribosomal protein S17**	**1.055945665**	**0.00016**	**2**
P04644	LLDFGSLSNLQVTQPTVGMNFK	0.767225145	2	3.691715
P04644	VCEEIAIIPSK	1.057089498	2	2.94859

P04692	**TPM1 Tropomyosin alpha_1 chain**	**0.98786497**	**0.50384**	**9**
P04692	AISEELDHALNDMTSI	0.843235461	2	2.978607
P04692	GTEDELDKYSEALK	0.683254715	2	3.734473
P04692	KLVIIESDLER	0.756934434	2	3.125696
P04692	LDKENALDR	0.562523675	1	2.07886
P04692	LKGTEDELDK	0.750010256	2	2.760479
P04692	LVIIESDLER	0.765555523	2	2.661328
P04692	MEIQEIQLK	1.143859348	2	3.095226
P04692	QLEDELVSLQK	0.700938924	2	2.815211
P04692	SIDDLEDELYAQK	0.621143127	2	4.125755
P04694	**ATTY Tyrosine aminotransferase**	**1.047281926**	**0.46216**	**2**
P04762	**CATA Catalase**	**0.811494756**	**9.9E-20**	**30**
P04762	APQKPDVLTTGGGNPIGDK	30.92664287	2	4.500637
P04762	DAMLFPSFIHSQK+Oxidation(2)	0.758601345	2	2.73084
P04762	DAQLFIQR	0.727285186	2	2.999761
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	0.921671881	4	4.963597
P04762	DPASDQMK	1.026844423	1	2.033577
P04762	DPASDQMK+Oxidation(6)	1.590644317	2	2.498649
P04762	DYPLIPVGK	0.593615947	1	2.220763
P04762	EAETFPFNPFDLTK	0.684512604	2	4.295611
P04762	FNSANEDNVTQVR	0.742580627	2	4.709685
P04762	FSTVAGESGSADTVR	0.707773768	2	5.172873
P04762	FSTVAGESGSADTVRDPR	0.709458608	2	2.387699
P04762	FYTEDGNWDLVGNNTPIFFIR	1.023379226	3	5.883046
P04762	GAGAFGYFEVTHDITR	0.77276061	2	4.966301
P04762	GPLLVQDVVFTDEMAHFDR	1.67703876	2	5.740359
P04762	HMNGYGSHTFK	0.732834207	3	4.35929
P04762	HMNGYGSHTFK+Oxidation(1)	0.549764131	3	3.371254
P04762	LCENIANHLK	0.75373725	3	3.715064
P04762	LFAYPDTHR	0.770494094	2	2.90744
P04762	LGPNYLQIPVNCPYR	0.793253087	2	4.220779
P04762	LNIMTAGPR	0.770434814	2	3.082374
P04762	LNIMTAGPR+Oxidation(3)	0.970178631	2	2.343095
P04762	LVNANGEAVYCK	0.881894154	2	3.710603
P04762	NAIHTYVQAGSHIAAK	0.751329974	3	5.575508
P04762	NFTDVHPDYGAR	0.689618322	2	3.966133
P04762	NLPVEEAGR	0.62882095	1	2.260276
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	0.913106764	3	5.153251
P04762	RFNSANEDNVTQVR	0.70333201	2	4.574307
P04762	VFEHIGK	0.721446639	2	2.337086
P04762	VQALLDQYNSQKPK	0.726395063	2	4.945196
P04762	VWPHKDYPLIPVGK	0.678879681	2	3.707886

P04764	**ENOA Alpha_enolase**	**1.11866896**	**9.9E-20**	**14**
P04764	AGYTDQVVIGMDVAASEFYR	1.088782593	2	4.92137
P04764	DATNVGDEGGFAPNILENK	1.153535459	2	5.932173
P04764	FTATAGIQVVGDDLTVTNPK	1.222445811	2	4.792741
P04764	GNPTVEVDLYTAK	1.261354471	2	3.732408
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.093200279	3	6.473549
P04764	IDQLMIEMDGTENK	1.051719166	2	4.08548
P04764	IEEELGSK	1.029679477	2	2.498997
P04764	IGAEVYHNLK	2.275045082	2	3.091447
P04764	KLNVVEQEKIDQLMIEMDGTENK	1.010558882	3	4.750028
P04764	LNVVEQEK	1.030216903	2	2.373953
P04764	LNVVEQEKIDQLMIEMDGTENK	1.105955533	3	4.531311
P04764	SCNCLLLK	1.215563068	2	2.7912
P04764	VNQIGSVTESLQACK	1.01769791	2	5.138294
P04764	YITPDQLADLYK	1.017283718	2	3.458865
P04785	**PDIA1 Protein disulfide_isomerase**	**1.031297744**	**0.00024**	**24**
P04785	DHENIVIAK	0.884523512	2	2.903607
P04785	EADDIVNWLK	0.899823926	2	2.550138
P04785	HNQLPLVIEFTEQTAPK	1.030928082	2	5.355382
P04785	IKPHLMSQELPEDWDKQPVK	1.567062767	3	4.098238
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5)	0.943913868	3	3.511862
P04785	ILEFFGLK	1.237755034	2	2.808483
P04785	LGETYKDHENIVIAK	0.955760102	3	4.901206
P04785	LITLEEEMTK	1.071318134	2	3.55391
P04785	LITLEEEMTK+Oxidation(7)	0.888468543	2	2.555605
P04785	LKAEGSEIR	0.952413981	1	2.029341
P04785	LLDFIK	1.039243018	2	2.318328
P04785	MDSTANEVEAVK	0.927280809	2	4.130782
P04785	MDSTANEVEAVK+Oxidation(0)	0.924703265	2	3.793992
P04785	NFEEVAFDEK	0.897847875	2	3.011442
P04785	NFEEVAFDEKK	1.048302532	2	3.836338
P04785	NNFEGEITK	0.914561368	2	2.541124
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.057685171	3	6.620689
P04785	SVSDYDGK	2.136513688	1	1.901072
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.067441886	3	6.359739
P04785	THILLFLPK	1.174996003	2	2.655397
P04785	TVIDYNGER	0.971994337	2	2.639384
P04785	VDATEESDLAQQYGVR	0.922011935	2	5.721469
P04785	YKPESDELTAEK	0.930909717	3	3.935783
P04785	YQLDKDGVVLFK	1.045004059	2	3.979755
P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.283494586**	**9.9E-20**	**16**
P04797	GAAQNIIPASTGAAK	1.349641359	2	3.97963

P04797	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	1.066476777	3	3.961292
P04797	IVSNASCTTNCLAPLAK	1.143002449	2	4.76052
P04797	LISWYDNEYGYSNR	1.791217827	2	4.002328
P04797	LVINGKPITIFQER	1.639816122	3	4.524602
P04797	RVIISAPSADAPMFVMGVNHEK	1.501148121	3	5.016223
P04797	RVIISAPSADAPMFVMGVNHEK+Oxidation(12)	1.051330916	3	3.334367
P04797	VGVNGFGR	1.212369444	2	2.555681
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.230837356	3	7.995553
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12)	1.010638385	3	5.515219
P04797	VIISAPSADAPMFVMGVNHEK	1.461405249	2	4.440995
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11)	1.032862459	2	3.773929
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14)	1.032862459	2	3.58297
P04797	VPTPNVSVVDLTCR	5.817299599	2	3.134006
P04797	VVDLMAYMASK	1.943688268	2	3.149484
P04797	WGDAGAEYVVESTGVFTTMEK	1.278745757	2	5.464219
P04799	**CP1A2 Cytochrome P450 1A2**	**0.841863737**	**9.9E-20**	**4**
P04799	DFVENVTSGNAVDFFPVLR	1.013034002	2	3.114676
P04799	NSIQDITGALFK	0.676857005	2	3.349116
P04799	TVQEHYQDFNK	0.724737236	2	3.145325
P04799	VDLTPSYGLTMKPR	1.010801055	2	2.696079
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**0.642969792**	**9.9E-20**	**11**
P04903	DGNLMFDQVPMVEIDGMK	0.538303746	2	4.69398
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	0.591953855	2	4.149191
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	0.629937186		3.267055
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16)	0.602257238	2	3.539623
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.586148819	2	4.345055
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.617556401		2.386288
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.62511169		3.067009
P04903	KDGNLMFDQVPMVEIDGMK	0.811801309	2	4.007364
P04903	LIQSPEDLEK	0.521880394	2	2.834623
P04903	WLLAAAGVEFEEK	0.604339877	2	3.453865
P04903	YLPAFEK	0.600284819	1	1.992623
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.860261129**	**9.9E-20**	**8**
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK+Oxidation(4)	1.01395715	3	4.012702
P04904	NDGSLMFQQVPMVEIDGMK	0.913292584	2	4.790801
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	0.915451074	2	4.203456
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	1.034820441		2.30344
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17)	0.9426707	2	3.563113
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5)	0.900421155	2	4.342117
P04904	SHGQDYLVGNR	0.658753285	2	4.152242
P04904	WLLAAAGVEFEEQFLK	0.859732668	2	5.496327
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**0.911036416**	**9.9E-20**	**15**
P04905	ADIVENQVMDNR	0.769756663	2	4.201423

P04905	ADIVENQVMDNR+Oxidation(8)	0.691402371	2	3.801505
P04905	CLDAFPNLKDFLAR	1.007894266	2	3.252597
P04905	FKLGLDFPNLPYLIDGSR	1.295068519	3	4.251013
P04905	HHLCGETEEER	0.748361826	3	4.251129
P04905	IRADIVENQVMDNR	0.935327248	2	3.830147
P04905	ITQSNAIMR	0.729820081	2	3.029274
P04905	ITQSNAIMR+Oxidation(7)	0.832005821	2	2.791954
P04905	KHHLCGETEEER	0.887662307	3	3.393924
P04905	KITQSNAIMR	0.573925942	3	3.394994
P04905	KITQSNAIMR+Oxidation(8)	0.767448869	3	3.426098
P04905	LGLDFPNLPYLIDGSR	0.874547497	2	5.021028
P04905	MQLIMLCYNPDFEK	1.408877829	2	3.943282
P04905	VTYVDFLAYDILDQYHIFEPK	1.010280102	2	2.358567
P04905	YLSTPIFSK	0.872855131	2	2.659886
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**0.747309836**	**9.6E-05**	**7**
P05065	ALANSLACQGK	0.601709546	2	2.804791
P05065	FSNEEIAMATVTALR	0.587772671	2	4.306746
P05065	GILAADESTGSIAK	0.595050137	2	3.769952
P05065	GVVPLAGTNGETTTQGLDGLSER	0.805234403	2	5.347676
P05065	IGEHTPSSLAIMENANVLAR	0.355551365	2	4.546356
P05065	LQSIGTENTEENR	0.699181782	2	3.644312
P05065	RLQSIGTENTEENRR	0.596967819	3	3.420047
P05178	**CP2C6 Cytochrome P450 2C6**	**0.544653602**	**9.9E-20**	**6**
P05178	EALIDHGEEFAER	0.51768954	2	3.191398
P05178	EFPDPEIFDPGHFLDGNGK	0.564805973	2	2.531093
P05178	FDYKDQDFLNLMEK	0.656937497	3	3.583379
P05178	FIDLIPTNLPHAVTCDIK	0.512389119	2	3.144115
P05178	GTTIITSLSSVLHDSK	0.562899855	2	3.326177
P05178	NITQSLTSFSK	0.477102496	2	2.71881
P05179	**CP2C7 Cytochrome P450 2C7**	**2.824244557**	**9.9E-20**	**6**
P05179	ACVGEGLAR	2.052748365	2	2.916955
P05179	FINFVPTNLPHAVTCDIK	2.885770796	2	2.735643
P05179	IEEHQESLDVTNPR	2.754793235	2	4.59598
P05179	KIEEHQESLDVTNPR	2.735669132	2	4.981664
P05179	KLPPGPTPLPIIGNFLQIDVK	1.111371182	3	4.914122
P05179	VLTSLTSVLHDSK	3.263563543	2	2.95063
P05182	**CP2E1 Cytochrome P450 2E1**	**0.598010147**	**9.9E-20**	**12**
P05182	AKEHLQSLDINCAR	0.517211498	2	4.361197
P05182	DIDLSPVTVGFGSIPPQFK	0.457932877	2	3.000239
P05182	DRLDMPYMDAVVHEIQR	0.660158287	3	4.822714
P05182	DVTDCLLIEMEKEK	0.824054802	2	3.072663
P05182	EHLQSLDINCAR	0.685965596	2	3.079947
P05182	FINLVPSNLPHEATR	0.519703015	2	3.792022

P05182	FKPEHFLNENGK	0.580269932	2	2.82957
P05182	GTVVIPTLDSLLYDSHEFPDPEK	0.532126642	2	4.595514
P05182	LHEEIDR	0.392279836	1	1.968576
P05182	VCVGEGLAR	0.452221655	2	2.654427
P05182	YGLLILMK	0.420585845	2	2.891523
P05182	YSDYFK	0.448789445	1	1.909776
P05183	**CP3A2 Cytochrome P450 3A2**	**0.533911268**	**9.9E-20**	**10**
P05183	AVSVAKDEEWK	0.608714015	2	2.533993
P05183	DIELDGLFIPK	0.435890165	2	3.211535
P05183	EMFPIIEQYGDILVK	0.514712983	2	3.840974
P05183	KDIELDGLFIPK	0.43613064	3	3.319833
P05183	KLQEEIDGALPSK	0.519450967	2	2.332375
P05183	LQEEIDGALPSK	0.557902977	2	3.616447
P05183	QAILEPEKPIVLK	0.732364003	2	2.707572
P05183	QEAETGKPVTMK	0.427091697	2	3.488245
P05183	QEAETGKPVTMK+Oxidation(10)	0.439759709	2	3.038292
P05183	VDFLQLMLNAHNNSK	0.799218755	2	3.272521
P05197	**EF2 Elongation factor 2**	**1.181017857**	**9.9E-20**	**26**
P05197	ALLELQLEPEELYQTFQR	1.475803388	3	5.219496
P05197	ARPFPDGLAEDIDKGEVSAR	1.199279842	3	6.457891
P05197	AYLPVNESFGFTADLR	1.224149081	2	3.797352
P05197	CELLYEGPPDDEAAMGIK	1.111659541	2	3.331444
P05197	DLEEDHACIPIK	0.887747727	2	3.394294
P05197	DLEEDHACIPIKK	0.799878846	2	3.232989
P05197	EGIPALDNFLDK	0.674034834	2	2.579429
P05197	EGIPALDNFLDKL	1.267475388	2	3.762114
P05197	ETVSEESNVLCLSK	1.255107384	2	3.945892
P05197	GEGQLGAAER	1.105179176	2	3.248317
P05197	GHVFEESQVAGTPMFVVK	2.142594001	2	5.28469
P05197	IWCFGPDGTGPNILTDITK	0.882355083	2	4.981177
P05197	KEDLYLKPIQR	1.592028271	2	3.118764
P05197	KIWCFGPDGTGPNILTDITK	1.068796761	2	4.651132
P05197	KVEDMMK+Oxidation(4)	1.317965085	2	2.319535
P05197	KVEDMMK+Oxidation(5)	1.152040043	2	2.499585
P05197	LDSEDKDKEGKPLLK	1.084825987	2	3.408827
P05197	NMSVIAHVDHGK	0.996089008	2	3.170857
P05197	NMSVIAHVDHGK+Oxidation(1)	1.030900357	2	3.329734
P05197	STLTDSLVCK	1.032734731	2	2.880196
P05197	TFCQLILDPIFK	1.137086335	2	3.962596
P05197	VFSGVVSTGLK	1.127397681	2	2.428678
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.046604448	2	4.039077
P05197	YEWDVAEAR	1.077315859	2	3.001606
P05197	YFDPANGK	1.119270826	1	1.93718

P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.392172173	2	4.512369
P05369	**FPPS Farnesyl pyrophosphate synthase**	**1.177196647**	**9.9E-20**	**11**
P05369	ALYEELDLR	0.56621436	2	2.807233
P05369	EVLEYNTVGGK	0.424256128	2	2.821494
P05369	GLTVVQTFQELVEPR	0.539610186	2	3.816673
P05369	IKEVLEYNTVGGK	0.42206665	3	4.128438
P05369	QILEENYGQK	0.477552057	2	2.325033
P05369	QILEENYGQKDPEK	0.711251449	2	3.887293
P05369	QNFIQHFSQIVK	1.627852277	2	2.615097
P05369	SLIEQCSAPLPPSIFLELANK	0.489093382	3	5.140446
P05369	VGTDIQDNK	0.51529892	2	3.74066
P05369	VLTEDELGHPEK	0.434602455	2	2.650776
P05369	VLTEDELGHPEKGDAITR	0.445585199	2	4.682343
P05426	**RL7 60S ribosomal protein L7**	**1.139700261**	**1.8E-08**	**5**
P05426	AGNFYVPAEPK	1.193591039	2	2.710742
P05426	FGIICMEDLIHEIYTVGK	1.195564818	2	4.472468
P05426	KKVPAVPETLK	0.916653592	2	2.852211
P05426	TTHFVEGGDAGNR	1.283603481	2	2.856936
P05426	TTHFVEGGDAGNREDQINR	1.207342526	2	4.646428
P05544	**SPA3L Serine protease inhibitor A3L**	**0.902055218**	**9.9E-20**	**5**
P05544	AVLDVDETGTEATAATGVATVIR	2.101472319	2	4.975397
P05544	DSTMEEILEGLK	1.265762862	2	2.945675
P05544	IAELFSDLEER	0.644547697	2	2.72042
P05544	MQQVESSLQPETLK	0.484207681	2	2.580659
P05544	VFSQQADLSR	1.259559276	2	2.486998
P05545	**SPA3K Serine protease inhibitor A3K**	**1.696470177**	**9.9E-20**	**4**
P05545	ALYQAEAFVADFK	1.376898718	2	3.263059
P05545	AVLDVDETGTEGAAATAVTAALK	1.669812655	2	5.447422
P05545	FSISTDYNLEEVLPELGIR	1.736418251	2	3.139796
P05545	IAELFSELDER	2.300012155	2	3.035587
P05765	**RS21 40S ribosomal protein S21**	**1.065644726**	**0.90961**	**3**
P05765	DHASIQMNVAEVDR	0.881465814	2	3.314806
P05765	MGESDDSILR	1.09542077	2	2.979936
P05765	TYGICGAIR	0.96450828	2	3.055099
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.91912573**	**9.9E-20**	**5**
P06214	AGCQVVAPSDMMDGR	0.858800029	2	3.135767
P06214	DEQGSAADSEDSPTIEAVR	0.724004281	2	5.837516
P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.74486838	3	4.646149
P06214	VPKDEQGSAADSEDSPTIEAVR	0.899486573	2	5.730658
P06214	YGVNQLEEMLRPLVEAGLR	0.777182253	3	4.402484
P06302	**PTMA Prothymosin alpha**	**0.723596486**	**0.00017**	**3**
P06302	RVAEDDEDDDVETKK	0.715008625	2	5.029138
P06302	VAEDDEDDDVETK	0.791181575	2	3.484566

P06302	VAEDDEDDDVETKK	0.722557984	2	4.58238
P06399	**FIBA Fibrinogen alpha chain**	**0.868894583**	**0.5093**	**6**
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.776383347	3	3.873089
P06399	GDFANANNFDNTFGQVSEDLR	0.925639172	2	5.696483
P06399	GDKELLIGNEK	0.798606337	2	2.610721
P06399	GLIDEANQDFTNR	0.992013226	2	3.149817
P06399	MADEAASEAHQEGDTR	0.619773942	2	4.165961
P06399	SQLQEGPPEWK	0.804000363	2	2.814613
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.204727729**	**0.00375**	**4**
P06685	AVAGDASESALLK	1.104633703	2	3.005242
P06685	AVFQANQENLPILK	1.255187015	2	3.744137
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.079722792	3	3.598522
P06685	LNIPVNQVNPR	1.0651028	2	3.032067
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.11335881**	**0.78208**	**3**
P06687	DGPNALTPPPTTPEWVK	1.113742743	2	2.775795
P06687	GVGIISEGNETVEDIAAR	1.045700442	2	4.460113
P06687	QGAIVAVTGDGVNDSPALK	1.02980814	2	4.809303
P06757	**ADH1 Alcohol dehydrogenase 1**	**1.036543024**	**1.5E-09**	**16**
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.05384762	3	5.584548
P06757	FPLEPLITHVLPFEK	1.565695331	3	4.604165
P06757	GAIFGGFK	1.013452541	2	2.571701
P06757	GALLDGTSR	1.012389062	2	2.846235
P06757	HPESNLCCQTK	0.914358604	2	3.48851
P06757	IDAAAPLDK	0.813340415	2	2.803414
P06757	IIAVDINKDK	0.855930381	2	2.82971
P06757	INEAFDLLR	0.879927044	2	3.66088
P06757	KFPLEPLITHVLPFEK	0.954516423	3	4.759876
P06757	KFPLEPLITHVLPFEKINEAFDLLR	1.511420977	4	4.651751
P06757	MVATGVCR	0.836270244	2	2.490382
P06757	MVATGVCR+Oxidation(0)	0.750806287	2	2.364064
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.011275509	4	8.223295
P06757	VCLIGCGFSTGYGSAVQVAK	0.958127683	2	6.304361
P06757	VIPLFSPQCGK	0.922307858	2	2.627984
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.033369563	2	5.246611
P06761	**GRP78 78 kDa glucose_regulated protein**	**0.972407264**	**9.9E-20**	**30**
P06761	AKFEELNMDLFR	1.1789131	3	4.000876
P06761	DAGTIAGLNVMR	0.864618986	2	3.539682
P06761	DAGTIAGLNVMR+Oxidation(10)	1.241580705	2	2.876609
P06761	DNHLLGTFDLTGIPPAPR	0.97216682	2	4.745848
P06761	ELEEIVQPIISK	0.93352152	2	4.292752
P06761	FEELNMDLFR	0.989800578	2	3.583015

P06761	IEIESFFEGEDFSETLTR	1.124932791	2	5.094069
P06761	IEWLESHQDADIEDFK	1.041811572	2	5.497417
P06761	IEWLESHQDADIEDFKAK	1.132994657	2	2.319761
P06761	IINEPTAAAIAYGLDKR	1.24064212	2	4.230218
P06761	ITITNDQNR	0.979111784	2	2.584057
P06761	ITPSYVAFTPEGER	1.306142682	2	3.82739
P06761	KKELEEIVQPIISK	0.96767068	2	4.576622
P06761	KSDIDEIVLVGGSTR	1.135538521	2	4.275836
P06761	KSQIFSTASDNQPTVTIK	1.168762192	2	5.160884
P06761	LTPEEIER	0.970200779	1	1.921797
P06761	LYGSGGPPPTGEEDTSEKDEL	1.17000003	2	5.206133
P06761	MKETAEAYLGK	1.099280589	2	3.15425
P06761	MKETAEAYLGK+Oxidation(0)	1.055309334	2	2.718362
P06761	NELESYAYSLK	1.519753419	2	3.620304
P06761	NQLTSNPENTVFDAK	1.048962152	2	5.224015
P06761	SDIDEIVLVGGSTR	1.026273203	2	3.790836
P06761	SQIFSTASDNQPTVTIK	1.120150817	2	5.463784
P06761	TFAPEEISAMVLTK	1.046026339	2	4.78528
P06761	TFAPEEISAMVLTK+Oxidation(9)	0.789150844	2	3.497714
P06761	TKPYIQVDIGGGQTK	1.236156019	3	4.150956
P06761	TWNDPSVQQDIK	0.919493604	2	3.875259
P06761	VLEDSDLK	0.944889493	2	2.399711
P06761	VTHAVVTVPAYFNDAQR	1.042409587	2	4.913645
P06761	VYEGERPLTK	0.936787602	2	2.983136
P06866	**HPT Haptoglobin**	**0.97187965**	**0.06596**	**6**
P06866	ATDLKDWVQETMAK	1.185540829	2	2.794498
P06866	CELHYEK	1.082562045	2	2.360535
P06866	GAVSPVGVQPILNK	1.172718551	2	3.992347
P06866	LQTEGDGIYTLNSEK	1.308740589	2	4.313381
P06866	NQLVEIEK	0.97187782	1	2.706881
P06866	SCAVAEYGVYVR	0.65786868	2	3.060879
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.119970359**	**9.9E-20**	**10**
P07153	ASSFVLALEPELESR	1.151594314	2	4.230242
P07153	AVTSEIAVLQSR	1.39021375	2	3.844038
P07153	FVDHVFDEQVIDSLTVK	1.057914482	2	4.620297
P07153	GEDEEDNNLEVR	1.037533702	2	3.593437
P07153	HFDETVNR	0.925143277	2	2.756773
P07153	LKTEGSDLCDR	0.996047931	3	3.332665
P07153	NIQVDSPYDISR	1.239756464	2	3.379521
P07153	NLVEQHIQDIVVHYTFNK	1.442130018	3	4.884934
P07153	SEDILDYGPFK	1.081405851	2	3.437104

P07153	VTAEVVLAHPGGGSTAR	1.00064833	2	4.662031
P07323	**ENOG Gamma_enolase**	**1.152158358**	**9.9E-20**	**3**
P07323	AAVPSGASTGIYEALELR	1.419786985	2	5.053947
P07323	GNPTVEVDLHTAK	0.560798582	2	2.768125
P07323	SGETEDTFIADLVVGLCTGQIK	1.075075902	3	4.838418
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.415631541**	**0.01681**	**2**
P07340	SYEAYVLNIIR	2.027484508	2	2.647027
P07340	VAPPGLTQIPQIQK	0.977566039	2	2.462261
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.059650215**	**0.99967**	**11**
P07379	AINPENGFFGVAPGTSVK	0.865115668	2	3.495231
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	1.045328941	3	4.411446
P07379	GLGDVNVEELFGISK	1.141158158	2	3.965836
P07379	IGIELTDSPYVVASMR	1.100160674	2	3.354997
P07379	MGTSVLEALGDGEFIK	1.06840261	2	3.555865
P07379	MGTSVLEALGDGEFIK+Oxidation(0)	0.868234227	2	3.858835
P07379	TVIITQEQR	1.056221223	2	2.51903
P07379	VECVGDDIAWMK	1.005088103	2	2.709002
P07379	VIQGSLDSLPQEVR	1.038054554	2	4.142714
P07379	YLAAAFPSACGK	0.868592322	2	2.782071
P07379	YLEDQVNADLPYEIER	0.696347675	2	2.824774
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.106696364**	**0.0472**	**4**
P07632	DGVANVSIEDR	0.848759237	1	2.790324
P07632	GDGPVQGVIHFEQK	1.045333454	2	3.611964
P07632	HVGDLGNVAAGK	0.866719829	2	3.921211
P07632	VISLSGEHSIIGR	1.107480474	2	3.291776
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.838086785**	**9.9E-20**	**9**
P07633	AFDNDVDALCNLR	0.942463394	2	3.667088
P07633	AYNMLDIIHAVIDER	0.857820635	2	3.719673
P07633	GFVDDIIQPSSTR	0.928297225	2	3.372567
P07633	ICCDLEVLASK	0.786010021	2	2.851033
P07633	IMDQAITVGAPVIGLNDSGGAR	0.827346599	2	3.999461
P07633	IQEGVESLAGYADIFLR	0.854936668	2	4.286613
P07633	LVPELDTVVPLESSK	0.821847277	2	3.790625
P07633	SVTNEDVTQEQLGGAK	0.799992317	2	4.810746
P07633	TVGIVGNQPNVASGCLDINSSVK	0.765504046	2	4.496482
P07687	**HYEP Epoxide hydrolase 1**	**0.552723526**	**9.9E-20**	**19**
P07687	DIELLYPYK	0.442016451	1	2.358648
P07687	DKEETLPLGDGWWGPGSKPSAK	0.576163676	3	5.292636
P07687	EDESIRPFK	0.528338911	2	2.608094
P07687	EDESIRPFKVETSDEEIKDLHQR	0.667778487	3	5.760001
P07687	ENLGQGIMVHK	0.612792804	2	2.472392

P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	1.127823503	3	6.627189
P07687	FLGYTEK	0.502580574	1	1.956717
P07687	FLGYTEKDIELLYPYK	0.59431837	3	4.553707
P07687	GGHFAAFEEPK	0.590092948	2	3.467359
P07687	IIPLLTDPK	0.616483904	2	2.410017
P07687	KFVSLAELQ	0.702574214	2	2.731006
P07687	KQVEILNQYPHFK	0.531853912	3	4.617214
P07687	LLAQDIR	0.732314252	2	2.416731
P07687	QVEILNQYPHFK	0.529554645	3	3.636613
P07687	SEYRELEDGGLER	0.734687429	3	3.533217
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	0.612861364	3	6.292448
P07687	VETSDEEIK	0.592803828	2	2.469301
P07687	VETSDEEIKDLHQR	0.473482953	2	4.614288
P07687	VFVPTGFSAFPSELLHAPEK	0.785185162	2	4.369045
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**0.996368563**	**9.9E-20**	**87**
P07756	AADTIGYPVMIR	1.935705144	2	3.680625
P07756	AADTIGYPVMIR+Oxidation(9)	2.062428341	2	3.20642
P07756	AERPDGLILGMGGQTALNCGVELFK	0.923273946	3	6.517022
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10)	0.873770602	3	4.976897
P07756	AFAISGPFNVQFLVK	1.407588809	2	4.983434
P07756	AFAMTNQILVER	1.026847983	2	4.268549
P07756	AFAMTNQILVER+Oxidation(3)	0.922974101	2	3.758468
P07756	ALENNMSLDEIVK	0.95750965	2	4.662439
P07756	ALENNMSLDEIVK+Oxidation(5)	1.008064692	2	3.920368
P07756	AQTAHIVLEDGTK	0.917126532	2	4.268498
P07756	ATGYPLAFIAAK	2.178990172	2	3.306113
P07756	CEMASTGEVACFGEGIHTAFLK	0.985989476	3	4.869245
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2)	0.902428024	3	5.680539
P07756	CLGLTEAQTR	0.863029274	2	3.629699
P07756	DELGLNK	0.81084367	1	2.22431
P07756	DGSIDLVINLPNNNTK	0.997814169	2	5.477794
P07756	DILNMDK	0.891990819	1	1.94096
P07756	EIEYEVVR	0.931803868	1	2.17758
P07756	EPLFGISTGNIITGLAAGAK	1.62972151	2	5.763889
P07756	ETLMDLGTK	0.958912579	1	2.180815
P07756	EVEMDAVGK	0.836691089	1	2.075444
P07756	FLEEATR	0.948690667	2	2.609583
P07756	FLGVAEQLHNEGFK	1.070421009	2	4.738251
P07756	FVHDNYVIR	1.454879381	3	3.497327
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.080355888	3	5.972341
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15)	1.173667937	4	5.223215

P07756	GILIGIQQSFRPR	1.110042827	2	2.397679
P07756	GLNSESVTEETLR	1.0223895	2	4.907218
P07756	GNDVLVIECNLR	0.920085209	2	4.24574
P07756	GQILTMANPIIGNGGAPDTTAR	0.998824193	2	5.985503
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5)	0.946809478	2	5.423976
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	0.97037282	3	4.161013
P07756	GQNQPVLNITNR	0.926499726	2	4.321795
P07756	GTTITSVLPKPALVASR	1.108293755	2	3.25384
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.885956639	3	6.388122
P07756	HLPTLEQPIIPSDYVAIK	1.07461924	2	5.594483
P07756	IAPSFAVESMEDALK	1.192800709	2	5.045006
P07756	IAPSFAVESMEDALK+Oxidation(9)	0.875111101	2	2.608332
P07756	IEFEGQSVDFVDPNK	1.00384314	2	5.2604
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	1.092829057	3	5.282569
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.051199852	3	5.73916
P07756	IMGTSPLQIDR	1.574153968	2	2.654036
P07756	IMGTSPLQIDR+Oxidation(1)	1.054429816	2	2.965294
P07756	IMGTSPLQIDRAEDR	0.671975793	2	2.420063
P07756	KEPLFGISTGNIITGLAAGAK	0.952261342	2	5.483893
P07756	KTVVVNCNPETVSTDFDECDK	0.290520172	2	4.652337
P07756	LFAEAVQK	0.974315222	2	2.893215
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.085199271	4	4.88679
P07756	LRDADPILR	1.038862623	2	3.017129
P07756	LTSIDKWFLYK	0.830404699	2	2.769411
P07756	LYFEELSLER	1.319183286	2	3.535903
P07756	MCHPSVDGFTPR	1.299607383	3	4.752268
P07756	MCHPSVDGFTPR+Oxidation(0)	0.837507354	3	4.039312
P07756	QADAVYFLPITPQFVTEVIK	2.262636315	3	5.01443
P07756	QLFSDKLNEINEK	1.025004824	2	3.655469
P07756	QNLIAEVSTK	1.022073768	2	2.792892
P07756	RFLEEATR	0.885738548	2	2.807172
P07756	RTAVDSGIALLTNFQVTK	0.806488119	2	4.169274
P07756	SAYALGGLGSGICPNK	1.571781823	2	4.938928
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.227971232	2	4.220071
P07756	SFPFVSK	1.131820627	1	2.069431
P07756	SIFSAVLDELK	1.050952835	2	3.978276
P07756	SIFSAVLDELKVAQAPWK	1.723471782	3	3.53515
P07756	SLGQWLQEEK	1.018749951	2	4.102468
P07756	SVGEVMAIGR	0.96019306	2	3.7593
P07756	SVGEVMAIGR+Oxidation(5)	0.918244009	2	2.999075
P07756	TAVDSGIALLTNFQVTK	1.193699063	3	6.090451
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	1.59795572	3	4.010033
P07756	TFEESFQK	0.937535979	2	2.52637

P07756	TLGVDFIDVATK	1.111374962	2	4.108807
P07756	TSACFEPSLDYMVTK	1.186290749	2	4.76156
P07756	TSACFEPSLDYMVTK+Oxidation(11)	1.199125143	2	3.979743
P07756	TVLMNPNIASVQTNEVGLK	1.012692281	2	6.304126
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3)	0.983193407	2	6.057572
P07756	TVVVNCNPETVSTDFDECDK	0.469113002	2	5.781158
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	1.235413676	3	5.225307
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	1.092220618	3	7.247942
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22)	0.998894279	3	6.767986
P07756	VLGTSVESIMATEDR	0.997866893	2	4.828372
P07756	VLGTSVESIMATEDR+Oxidation(9)	0.969742918	2	4.342385
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	0.981315263	2	5.322717
P07756	VMIGESVDEK	0.99163063	2	3.486611
P07756	VMIGESVDEK+Oxidation(1)	0.94048051	2	3.037011
P07756	VSQEHPVVLTK	1.033963204	2	3.90386
P07756	VVAVDCGIK	0.917071904	2	2.39105
P07756	YMESDGIK	0.859766508	2	2.714977
P07756	YMESDGIK+Oxidation(1)	0.975666261	1	2.240093
P07824	**ARGI1 Arginase_1**	**1.182970156**	**9.9E-20**	**15**
P07824	ANEQLAAVVAETQK	1.334592706	2	5.331029
P07824	DHGDLAFVDVPNDSPFQIVK	1.337002055	2	6.87653
P07824	DIVYIGLR	1.980459187	2	2.730463
P07824	DVDPGEHYIIK	1.5366364	2	3.097352
P07824	EGLYITEEIYK	1.331126637	2	2.448736
P07824	EGNHKPETDYLKPPK	1.43510413	2	2.800012
P07824	GKFPDVPGFSWVTPCISAK	1.299034165	3	4.703111
P07824	LKETEYNVR	1.4173107	3	3.665861
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.553371839	3	4.400733
P07824	TGLLSGLDIMEVNPTLGK	1.311922368	2	5.808201
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9)	1.121086659	2	4.683285
P07824	TVNTAVALTLSCFGTK	1.281911017	2	4.7521
P07824	VMEETFSYLLGR	4.212936344	2	3.254689
P07824	YFSMTEVDK	1.415934885	1	2.271957
P07824	YFSMTEVDKLGIGK+Oxidation(3)	1.190073731	2	2.461653
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.761294626**	**9.9E-20**	**15**
P07871	AEELGLPILGVLR	0.752505365	2	4.44025
P07871	AEIVPVTTTVLDDK	0.777013003	2	4.127613
P07871	AEIVPVTTTVLDDKGDR	0.796147228	2	4.026548
P07871	AEIVPVTTTVLDDKGDRK	0.819618943	2	3.594028
P07871	DCLIPMGITSENVAER	0.77927032	2	3.586517
P07871	DCLIPMGITSENVAER+Oxidation(5)	0.688426265	2	2.93319
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.737891335	2	6.097786

P07871	IAQFLSGIPETVPLSAVNR	1.910515319	2	2.60835
P07871	QCSSGLQAVANIAGGIR	0.671975793	2	4.323938
P07871	QDAFALASQQK	0.648353078	2	3.332845
P07871	QKQDAFALASQQK	0.682938481	2	4.120291
P07871	SKAEELGLPILGVLR	0.731301026	3	4.248923
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.662496921	2	4.314189
P07871	TITVSQDEGVRPSTTMEGLAK	0.812502179	2	4.274511
P07871	VNPLGGAIALGHPLGCTGAR	0.693007777	2	4.961459
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.604936181**	**9.9E-20**	**16**
P07872	AFTTWTANAGIEECR	0.637237596	2	4.101248
P07872	ASATFNPELITHILDGSPENTR	0.607044162	2	4.748636
P07872	ASEAHCHYVVVK	0.717270229	3	4.156458
P07872	EIENLILNDPDFQHEDYNFLTR	0.735646792	2	4.455253
P07872	EIGTHKPLPGITVGDIGPK	0.525257427	3	4.113584
P07872	EVAWNLTSVDLVR	0.633426182	2	3.40482
P07872	EYGISDPEEIMWFK	0.730519468	2	3.361959
P07872	FGYEEMDNGYLK	0.615352967	2	3.598197
P07872	GGDFLEGSIITGAQLSQVNAR	0.647818242	2	5.157513
P07872	GLETTATYDPK	0.575832473	2	3.399365
P07872	INESIGQGDLSELPELHALTAGLK	0.582995322	3	5.308318
P07872	LVEIAAK	0.644252367	1	2.024047
P07872	QSEPEPQILDFQTQQYK	0.579186076	2	4.76811
P07872	SFLVGNAAQSLSK	0.546559383	2	3.853845
P07872	TQEFILNSPTVTSIK	0.60374175	2	4.890968
P07872	YDGNVYENLFEWAK	0.530360764	2	4.628086
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.681899248**	**1.1E-16**	**3**
P07895	AIWNVINWENVSQR	0.966565894	2	3.905118
P07895	GDVTTQVALQPALK	0.743608303	2	3.442553
P07895	HHATYVNNLNVTEEK	0.974799812	2	4.214888
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.679837814**	**9.9E-20**	**21**
P07896	GQGLTGPSLPPGTPVR	0.433809784	2	4.07126
P07896	GWYQYDKPLGR	0.464387643	2	2.747777
P07896	IFNKPVPSLPNMDSVFAEAIAK	0.558611926	3	3.579067
P07896	IGVVVGNCYGFVGNR	0.751071607	2	2.436362
P07896	IIDKPIEPR	0.422682601	2	2.424396
P07896	KGQGLTGPSLPPGTPVR	0.518196876	2	3.895568
P07896	KQYPGVLAPETCVR	0.489668283	2	3.732141
P07896	LCNPPVNAVSPTVIR	0.405864507	2	4.303395
P07896	LGILDAVVK	0.579572745	2	2.912469
P07896	LLEVIPSR	0.508866823	2	2.728523
P07896	QNPDIPQLEPSDYLR	0.441397963	2	3.800498
P07896	QYPGVLAPETCVR	0.460783106	2	3.592969

P07896	TASAQPVSSVGVLGLGTMGR	0.821874567	2	4.612984
P07896	TASAQPVSSVGVLGLGTMGR+Oxidation(17)	0.583434727	2	4.032934
P07896	TISKEEILER	0.426773314	2	2.867023
P07896	VGISVVAVESDPK	0.478394868	2	3.330619
P07896	VGLPEVTLGILPGAR	0.525736669	2	3.348469
P07896	VSDLAGLDVGWK	0.443433843	2	4.216769
P07896	YLSADEALR	0.612234306	2	2.551209
P07896	YSPLGDMLCEAGR	0.403474257	2	4.309145
P07896	YSSPTTIATVMSLSK	1.143168453	2	3.43817
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**0.788252295**	**9.9E-20**	**5**
P08009	LCYNPDFEK	0.860065038	2	2.790956
P08009	LLLEYTDSSYEEK	0.8015663	2	4.840567
P08009	LLLEYTDSSYEEKR	0.83159951	2	3.827513
P08009	NQVFEATCLDAFPNLK	0.471053936	2	4.525417
P08009	SQWLNEK	0.846043298	2	2.638976
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**1.037283692**	**9.9E-20**	**15**
P08010	CLDAFPNLKDFVAR	1.142536977	2	2.454325
P08010	IRVDVLENQAMDTR	0.902046557	3	4.282445
P08010	ITYVDFLVYDVLDQHR	1.409434449	2	5.045181
P08010	KKPEYLEGLPEK	0.767399815	3	4.417502
P08010	KPEYLEGLPEK	1.614704325	2	3.48164
P08010	KYSMGDAPDYDR	0.700066078	2	3.328475
P08010	LFLEYTDTSYEDK	0.843911852	2	5.117995
P08010	LFLEYTDTSYEDKK	0.793453042	2	4.403938
P08010	LQLAMVCYSPDFER	0.759454214	2	3.519673
P08010	LQLAMVCYSPDFER+Oxidation(4)	0.740979276	2	3.345862
P08010	SQWLSEK	0.897934947	2	2.418023
P08010	VDVLENQAMDTR	0.734824003	2	4.481347
P08010	VDVLENQAMDTR+Oxidation(8)	0.788149113	2	4.034321
P08010	YSMGDAPDYDR	0.924619466	2	2.942543
P08010	YSMGDAPDYDR+Oxidation(2)	1.09744256	2	2.717192
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**0.951125745**	**0.00082**	**4**
P08011	IYHTIAYLTPLPQPNR	1.280040597	2	5.720207
P08011	MMFLSSATAFQR+Oxidation(0)	0.886872937		2.551465
P08011	VFANPEDCAGFGK	0.905478718	2	4.692748
P08011	VFANPEDCAGFGKGENAK	0.875474574	2	4.422501
P08122	**chain**	**1.488027044**	**0.01205**	**3**
P08122	DEKSLAYPEGK	1.739482986	2	2.415499
P08122	DGAPGFPGTEGAKGNRGFPGLR	1.539824089	2	2.327391
P08122	GPAGRFGPDGPPGQPGIEGLAGPLGR	0.532498413	2	2.506688
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**1.005387085**	**0.99479**	**2**
P08290	DFQDIQQLDSEENDHQLIGDEEQGSHVQNLR	1.027587672	3	6.282168
P08290	EEQEFVVK	0.976915054	1	1.934371

P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**1.102635825**	**0.00714**	**5**
P08461	AAPAAAAAAPPGPR	0.953930073	2	3.043614
P08461	DVPLGTPLCIIVEK	1.028665641	2	3.02493
P08461	DVPVGSIICITVEKPQDIEAFK	1.388877322	2	4.096044
P08461	GLETIASDVVSLASK	1.067448359	2	4.202191
P08461	VAPTPAGVFIDIPISNIR	1.118909777	2	4.787501
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.85170936**	**9.9E-20**	**7**
P08503	AFTGFIVEADTPGIHIGK	0.913258503	2	4.224313
P08503	EEIIPVAPDYDK	0.84818542	2	3.041528
P08503	IYQIYEGTAQIQR	0.956280686	2	4.951216
P08503	KGDEYVINGQK	0.843949165	2	3.615403
P08503	QEPGLGFSFELTEQQK	0.843282065	2	2.6851
P08503	SGEYPFPLIK	0.884702661	2	2.577549
P08503	TRPTVAAGAVGLAQR	0.888168828	2	4.177897
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**1.782670548**	**9.9E-20**	**9**
P08541	DELQNHFIK	1.500182403	2	2.641715
P08541	FEIFSTSISKDELQNHFIK	1.8143857	3	3.555882
P08541	FILPPSYVPVILSGLAGK	1.857221612	3	5.915164
P08541	GAAVSLNIR	4.564188519	2	2.376905
P08541	GHEVTVLKPSAYFFLDPK	3.415224096	3	4.328868
P08541	HKEWDTFYSEILGRPTTVDETMSK	2.034429502	3	4.633792
P08541	LLDVWTYELPR	2.874620196	2	3.849134
P08541	SYWDLK	1.48043887	2	2.333124
P08541	VEIWLIR	1.463835824	2	2.762574
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.225538456**	**0.09267**	**6**
P08542	EIINNPFYK	0.754630735	1	2.102288
P08542	FETFPTSVSKDELENYFIK	0.877710457	2	4.066194
P08542	KWDPFYSEILGRPTTLAETMGK	1.052224494	2	4.043206
P08542	LVDVWTYELQR	1.132872709	2	3.346584
P08542	NAVWLSTIHHDQPMKPLDK	1.374882727	3	3.679787
P08542	WDPFYSEILGRPTTLAETMGK	1.015304456	2	4.084558
P08649	**CO4 Complement C4**	**1.522679874**	**0.00412**	**2**
P08649	SLEIPGSSDPNVIPDGDFSSFVR	1.496175256	2	3.15712
P08649	VTASEPLETLGSEGALSPGGVASLLR	1.373478686	2	2.96551
P08661	**MBL2 Mannose_binding protein C**	**1.276486457**	**8.5E-07**	**2**
P08661	ALCSELQGTVATPR	0.507119458	2	2.540499
P08661	TENVFEDLTGNR	1.307751482	2	2.778531
P08683	**CP2CB Cytochrome P450 2C11**	**0.854340891**	**9.9E-20**	**14**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	0.652385169	3	4.986457
P08683	EALVDLGEEFSGR	0.900287041	2	3.715386
P08683	EHQESLDKDNPR	0.448360259	2	3.995445

P08683	FDYKDPTFLNLMHR	1.015424609	3	4.861142
P08683	GTNVIVSLSSILHDDKEFPNPEK	0.793217513	2	5.097614
P08683	ICAGEALAR	0.668503141	2	3.120892
P08683	LPPGPTPLPIIGNTLQIYMK	1.050614526	2	3.282207
P08683	NYVLEK	0.569887586	1	2.064391
P08683	SQMPYTDAVVHEIQR	0.86163382	2	3.94216
P08683	SQMPYTDAVVHEIQR+Oxidation(2)	0.564244453	2	3.698865
P08683	VKEHQESLDKDNPR	0.6371402	3	5.024151
P08683	VQEEIER	0.653457387	2	2.626162
P08683	YGLLLLLK	0.789005661	2	3.188956
P08683	YIDLVPTNLPHLVTR	0.689350129	2	4.036538
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**0.691271133**	**0.53312**	**2**
P08733	GADPEETILNAFK	0.745391906	2	2.589054
P08733	NLVHIITHGEEKD	0.572257306	2	3.34575
P09034	**ASSY Argininosuccinate synthase**	**1.566916746**	**9.9E-20**	**16**
P09034	APNTPDVLEIEFK	4.109606077	2	3.470396
P09034	DGTTHSTSLDLFMYLNEVAGK	4.255113394	2	5.926031
P09034	EFVEEFIWPAVQSSALYEDR	1.828746266	3	5.715837
P09034	EQGYDVIAYLANIGQK	1.974363665	2	2.338559
P09034	FAELVYTGFWHSPECEFVR	2.654553403	2	4.042085
P09034	FELTCYSLAPQIK	2.741540782	2	4.260776
P09034	GRNDLMEYAK	1.780932881	2	3.017917
P09034	GRNDLMEYAK+Oxidation(5)	1.514410692	2	2.580156
P09034	IDIVENR	1.397041579	2	2.407131
P09034	KVFIEDVSK	1.356582003	3	3.3453
P09034	NDLMEYAK	1.572782883	2	2.535101
P09034	SPWSMDENLMHISYEAGILENPK	3.069702968	3	5.76887
P09034	TQDPAKAPNTPDVLEIEFK	1.874610979	2	4.880405
P09034	TQDPAKAPNTPDVLEIEFKK	2.224905	3	4.427262
P09034	VFIEDVSK	1.385324165	2	2.915686
P09034	VQVSVFK	1.896706495	1	2.054684
P09041	**PGK2 Phosphoglycerate kinase 2**	**0.99724231**	**0.73185**	**3**
P09041	FHVEEEGK	0.902061697	1	2.437882
P09041	LGDVYVNDAFGTAHR	1.065865862	3	4.282952
P09041	VSHVSTGGGASLELLEGK	1.039059135	2	5.660918
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.314408715**	**7.8E-06**	**2**
P09117	VLAAVYK	1.280599156	2	2.642177
P09117	YSPEEIAMATVTALR	0.587772671	2	2.432623
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.395241324**	**6.2E-10**	**2**
P09139	IGLLGYNATTENADR	1.220565094	2	3.363694
P09139	VLNAPPGISLISFNDK	1.724614162	2	2.799011

P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**3.779887845**	**2.1E-06**	**3**
P09456	**KAP0 cAMP_dependent protein kinase type I_alpha regulatory subunit**	**0.823707309**	**0.57762**	**2**
P09456	FERVLGPCSDILK	0.464468959	2	2.378657
P09456	LTVADALEPVQFEDGQK	0.987227373	2	3.832369
P09495	**TPM4 Tropomyosin alpha_4 chain**	**0.876507581**	**8.1E-09**	**13**
P09495	AEGDAAALNR	0.698785256	2	2.374294
P09495	EDKYEEEIK	0.673962983	1	2.929529
P09495	EENVGLHQTLDQTLNELNCI	0.996396108	2	4.957961
P09495	IQALQQQADDAEDR	0.870386598	2	4.400271
P09495	IQLVEEELDR	0.807569943	2	3.422169
P09495	IQLVEEELDRAQER	0.790868451	2	2.689069
P09495	KLVILEGELER	0.605479824	3	3.483312
P09495	LEEAEKAADESER	0.788165399	2	3.91638
P09495	LVILEGELER	0.672429097	2	2.7667
P09495	MEIQEMQLK	0.555694174	2	2.62533
P09495	RIQLVEEELDR	0.752517055	2	2.714399
P09495	YEEEIK	0.945818772	1	1.920169
P09495	YSEKEDKYEEEIK	0.644556315	2	4.203413
P09527	**RAB7A Ras_related protein Rab_7a**	**1.002344674**	**1.2E-07**	**3**
P09527	GADCCVLVFDVTAPNTFK	1.34259613	2	4.524641
P09527	TLDSWRDEFLIQASPR	0.914207111	2	2.362259
P09527	VIILGDSGVGK	0.943911122	2	2.711331
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.025333849**	**0.99936**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	1.025228289	2	3.999739
P09605	LSEMTEQDQQR	1.096369423	2	2.874059
P09606	**GLNA Glutamine synthetase**	**1.094338038**	**0.27379**	**5**
P09606	CIEEAIDK	0.694119014	2	2.527206
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	0.857739638	2	4.375358
P09606	LTGFHETSNINDFSAGVANR	0.900354651	2	5.788212
P09606	TCLLNETGDEPFQYK	0.884341497	2	4.971614
P09606	TCLLNETGDEPFQYKN	1.286935644	2	4.625268
P09811	**PYGL Glycogen phosphorylase_ liver form**	**1.056557407**	**0.02283**	**19**
P09811	DFSELEPDKFQNK	1.144050408	2	3.505346
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.157781069	3	4.938773
P09811	DLSQLTK	0.903073482	1	2.098884
P09811	EGWQVEEADDWLR	1.033457055	2	3.320076
P09811	GIVGVENVAELK	1.005668157	2	3.06156
P09811	GIVGVENVAELKK	1.483857966	2	2.888785
P09811	HLQIIYEINQK	1.016050661	2	3.447671
P09811	INPSSMFDVHVK	1.397571522	2	2.696436
P09811	LVIDQIDNGFFSPNQPDLFK	1.055872077	3	4.572525
P09811	LVTSVAEVVNNDPMVGSK	0.97552475	2	2.812567

P09811	MSLIEEEGGKR	1.053770237	2	2.746151
P09811	TFAYTNHTVLPEALER	1.154879191	2	3.722688
P09811	VDDVAALDK	0.944536274	2	2.348524
P09811	VDDVAALDKK	0.957610194	3	3.46648
P09811	VFADYEAYVK	1.15781619	1	2.222671
P09811	VIPATDLSEQISTAGTEASGTGNMK	1.096113407	2	6.075753
P09811	VLYPNDNFFEGK	0.970806268	2	3.109377
P09811	WLLLCNPGLADLIAEK	1.037735924	3	4.911973
P09811	YEYGIFNQK	1.102638583	1	2.453062
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**0.903007682**	**0.80443**	**2**
P09812	NLAENISR	0.955053174	1	2.530401
P09812	QIIEQLSSGFFSPK	0.845900956	2	3.639601
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**0.589053395**	**9.9E-20**	**6**
P09875	ANVVASALAQIPQK	0.532794706	3	4.091683
P09875	ESSINFEIYSVPLSK	1.174186482	2	2.705749
P09875	FSGGLPLPPSYVPVVLSELSDR	1.089837081	3	4.734142
P09875	IILNELAQR	0.527426279	2	2.856291
P09875	SDLEYSFAK	0.542471221	2	2.395199
P09875	VDFSILSTTGLLTALK	0.604005109	2	4.404573
P09895	**RL5 60S ribosomal protein L5**	**1.114649018**	**0.00013**	**4**
P09895	GAVDGGLSIPHSTK	1.217465264	2	4.19612
P09895	NNVTPDMMEEMYK	0.951699712	2	2.960209
P09895	RFPGYDSESK	1.230822514	2	2.701289
P09895	YLMEEDEDAYKK	1.020543388	2	3.067264
P0C0S7	**H2AZ Histone H2A.Z**	**0.738606273**	**9.9E-20**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.737014078	2	3.202504
P0C0S7	GDEELDSLIK	0.77213337	2	3.062839
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.879250179**	**9.9E-20**	**15**
P0C2X9	AIEAAVLAR	0.820239255	2	2.352923
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.790304642	3	5.343075
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.726862615	2	4.437436
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	0.854668598	3	3.734577
P0C2X9	EEIFGPVLTVYVYPDEK	0.59993192	2	3.140964
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	0.901757238	2	5.176111
P0C2X9	KEWDLKPVADR	0.696543629	2	3.050462
P0C2X9	LYVPQSLWPQIK	1.044972148	2	3.338728
P0C2X9	NAAGNFYINDK	2.096271692	2	2.880473
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.128782114	2	5.136427
P0C2X9	SAFEYGGQK	0.8670243	2	2.538263
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.81504009	3	5.119821
P0C2X9	STGSVVGQQPFGGAR	0.785367671	2	4.450132
P0C2X9	VANEPILAFTQGSPER	1.049003534	2	5.37271

P0C2X9	YQLSPFNHGHK	1.324228791	2	2.923884
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.113682085**	**0.63138**	**5**
P0C5H9	DRDVTFSPATIEEELIK	0.988966025	2	4.510808
P0C5H9	DVTFSPATIEEELIK	0.989830296	2	3.17285
P0C5H9	IINEVSKPLAHHIPVEK	1.019826818	3	3.657366
P0C5H9	ILDDWGEMCK	0.882331275	2	2.978632
P0C5H9	QIDLSTVDLKK	0.82952972	2	2.881731
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**0.89547846**	**9.9E-20**	**10**
P10111	EGMSIVEAMER	0.858531463	2	2.636749
P10111	FEDENFILK	0.87848946	2	3.355982
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.158363082	3	6.148696
P10111	IIPGFMCQGGDFTR	1.001327126	2	2.596653
P10111	KITISDCGQL	1.252274021	2	3.193159
P10111	SIYGEKFEDENFILK	0.960069801	2	4.399764
P10111	TEWLDGK	0.860240629	2	2.31304
P10111	VCFELFADK	1.158124925	2	3.410765
P10111	VCFELFADKVPK	1.040393486	3	3.827482
P10111	VKEGMSIVEAMER	1.218900433	2	2.81733
P10536	**RAB1B Ras_related protein Rab_1B**	**1.102898197**	**1.3E-06**	**3**
P10536	MGPGAASGGERPNLK	0.623081938	2	3.372909
P10536	NATNVEQAFMTMAAEIK+Oxidation(11)	1.146795883	2	3.436903
P10536	NATNVEQAFMTMAAEIK+Oxidation(9)	1.146795883	2	3.864061
P10633	**CP2D1 Cytochrome P450 2D1**	**0.806783761**	**9.9E-20**	**3**
P10633	SQGVILASYGPEWR	0.280392792	2	4.284493
P10633	TFMALLDNLLAENR	0.85721592	2	3.540455
P10633	YGDVFSLQK	0.815009473	2	2.794618
P10634	**CP2DQ Cytochrome P450 2D26**	**0.886817519**	**9.9E-20**	**17**
P10634	ACLGEPLAR	0.911802629	2	2.427033
P10634	AVSNVIASLVYAR	0.871792262	2	4.104393
P10634	DMTDAFLAEMQK	0.850322628	2	4.188449
P10634	EAEHPFNPSILLSK	0.774876534	2	2.325527
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	0.905660818	3	5.507686
P10634	FADIVPTNIPHMTSR	0.951987888	2	3.651089
P10634	FEYEDPFFNR	0.739300138	2	2.544244
P10634	FHPEHFLDAQGNFVK	0.870692409	2	4.282539
P10634	GNPESSFNDENLR	1.059803097	2	4.275727
P10634	GTTLIPNLSSVLK	0.625265288	2	2.31188
P10634	GTTLIPNLSSVLKDETVWEKPLR	0.727795085	2	4.028404
P10634	GVVLAPYGPEWR	0.686493048	2	3.504254
P10634	LNSFIALVDK	1.167611713	2	2.872913
P10634	RFEYEDPFFNR	0.836888246	3	3.30915
P10634	SLEQWVTEEAGHLCDTFAK	0.837182834	2	4.550595

P10634	SWDPAQPPR	0.801415731	2	2.502202
P10634	VHEEIDEVIGQVR	0.761421398	2	4.197106
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**0.984520327**	**9.9E-20**	**30**
P10719	AHGGYSVFAGVGER	1.432177019	2	4.065657
P10719	AIAELGIYPAVDPLDSTSR	0.981135294	2	4.975537
P10719	EGNDLYHEMIESGVINLK	0.966294563	2	4.918588
P10719	FLSQPFQVAEVFTGHMGK	1.380293337	2	3.847488
P10719	FTQAGSEVSALLGR	0.981272721	2	4.665462
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	1.520606609	3	5.209855
P10719	IGLFGGAGVGK	0.918301557	2	2.918162
P10719	ILQDYK	0.940211573	1	2.187932
P10719	IMDPNIVGSEHYDVAR	1.28506572	2	4.603392
P10719	IMDPNIVGSEHYDVAR+Oxidation(1)	0.795434334	2	4.095851
P10719	IMNVIGEPIDER	1.219945817	2	3.491669
P10719	IMNVIGEPIDER+Oxidation(1)	0.876901749	2	3.415983
P10719	IPSAVGYQPTLATDMGTMQER	2.797998277	2	5.111052
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14)	2.177110908	2	3.608154
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17)	2.177110908	2	4.286513
P10719	LVLEVAQHLGESTVR	0.995605924	2	4.672349
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	1.006419193	3	4.665442
P10719	SLQDIIAILGMDELSEEDKLTVSR	0.978801354	4	5.212303
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10)	0.981955286	3	4.015153
P10719	TIAMDGTEGLVR	0.996224468	2	3.406317
P10719	TIAMDGTEGLVR+Oxidation(3)	0.810236505	2	3.015239
P10719	TREGNDLYHEMIESGVINLK	1.038173278	2	6.026246
P10719	TVLIMELINNVAK	0.98449298	2	4.684461
P10719	TVLIMELINNVAK+Oxidation(4)	0.767365076	2	3.20977
P10719	VALTGLTVAEYFR	2.474423692	2	3.786068
P10719	VALVYGQMNEPPGAR	0.977994079	2	4.220304
P10719	VALVYGQMNEPPGAR+Oxidation(7)	0.816945725	2	2.857463
P10719	VLDSGAPIK	0.910596446	2	2.831918
P10719	VLDSGAPIKIPVGPETLGR	0.9604924	3	5.111969
P10719	VVDLLAPYAK	0.987240215	2	3.106712
P10760	**SAHH Adenosylhomocysteinase**	**1.088440701**	**9.9E-20**	**16**
P10760	ALDIAENEMPGLMR	1.27891187	2	4.341905
P10760	ATDVMIAGK	0.904747767	1	1.903281
P10760	DGPLNMILDDGGDLTNLIHTK	1.151644375	2	5.656613
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5)	0.986210891	3	4.402835
P10760	FDNLYGCR	1.07042746	2	2.686306
P10760	GETDEEYLWCIEQTLHFK	1.366113794	2	4.415736
P10760	GISEETTTGVHNLYK	1.060137105	2	4.166504
P10760	IILLAEGR	1.326821332	2	2.407276
P10760	KLDEAVAEAHLGK	1.060032359	3	4.995537

P10760	LDEAVAEAHLGK	1.12847927	2	3.796467
P10760	RATDVMIAGK	1.253074634	2	2.664023
P10760	SKFDNLYGCR	1.192580218	2	2.863877
P10760	VAVVAGYGDVGK	1.43567503	2	3.681723
P10760	VNIKPQVDR	0.949308815	2	2.749049
P10760	WLNENAVEK	1.137965509	2	2.826216
P10760	WSSCNIFSTQDHAAAAIAK	1.515164442	2	5.056983
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**1.188724036**	**9.9E-20**	**29**
P10860	ALASLMTYK	1.172161398	2	3.065789
P10860	CAVVDVPFGGAK	1.134008047	2	3.000407
P10860	CVGVGESDGSIWNPDGIDPK	0.812891666	2	5.176046
P10860	DDGSWEVIEGYR	0.850004078	2	3.892668
P10860	DIVHSGLAYTMER	1.00866955	2	3.375663
P10860	DIVHSGLAYTMER+Oxidation(10)	0.978417108	2	2.427266
P10860	DSNYHLLMSVQESLER	0.94420026	2	3.107387
P10860	EDDPNFFK	1.219127657	1	2.125179
P10860	GASIVEDKLVEDLK	1.248131143	2	3.133823
P10860	GFIGPGIDVPAPDMSTGER	0.926049255	2	5.333733
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13)	0.96634359	2	4.891709
P10860	HGGTIPVVPTAEFQDR	0.959648041	2	4.668546
P10860	IIAEGANGPTTPEADK	0.870457319	2	5.121608
P10860	IIAEGANGPTTPEADKIFLER	0.88225997	2	4.643274
P10860	KGFIGPGIDVPAPDMSTGER	0.910651742	2	4.980026
P10860	KGFIGPGIDVPAPDMSTGER+Oxidation(14)	0.721050426	2	4.141381
P10860	LQHGSILGFPK	0.737202259	2	2.739726
P10860	MVEGFFDR	1.221434383	2	2.718354
P10860	MVEGFFDR+Oxidation(0)	0.849486742	2	2.742622
P10860	NLNHVSYGR	1.087139058	2	2.367163
P10860	NYTDNELEK	0.870864071	2	2.487782
P10860	RDDGSWEVIEGYR	1.000181888	2	4.263594
P10860	RFTMELAK	0.944383099	2	2.320582
P10860	TAAYVNAIEK	1.313244097	2	3.337825
P10860	TFVVQGFGNVGLHSMR	1.212094444	2	4.02515
P10860	TFVVQGFGNVGLHSMR+Oxidation(14)	0.858095351	2	2.86318
P10860	VYEGSILEADCDILIPAASEK	0.950959248	3	6.09714
P10860	YNLGLDLR	0.934086819	2	3.250304
P10860	YSTDVSVDEVK	1.160937858	2	3.554041
P10867	**GGLO L_gulonolactone oxidase**	**0.920802348**	**4.1E-10**	**6**
P10867	GDDILLSPCFQR	0.794705594	1	2.016634
P10867	LDPTGMFLNSYLEK	0.782547026	2	4.23529
P10867	LDYWLAYETIMK	1.036322907	2	3.978343
P10867	NADVFQAAR	0.960306259	2	2.753819

P10867	TYGCSPEVYYQPTSVEEVR	0.875214986	2	4.83521
P10867	VVAHYPVEVR	0.84759204	2	2.777461
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**0.993669401**	**0.3888**	**4**
P10868	EHWIIECNDGVFQR	0.879033397	2	4.501667
P10868	ENICTEVMALVPPADCR	1.034415746	2	2.364018
P10868	YTDITAMFEETQVPALLEAGFQR	1.051981739	3	4.620678
P10868	YYAFPQMITPLVTK	0.651269115	2	2.74588
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**0.937586126**	**0.00011**	**4**
P10888	DYPLPDVAHVK	0.811842268	2	2.559607
P10888	IQFNESFAEMNK	1.088850449	2	3.635572
P10888	SEDYALPSYVDR	0.974640114	2	3.797805
P10888	VNPIQGFSAK	1.075383982	1	1.952887
P11030	**ACBP Acyl_CoA_binding protein**	**1.980955908**	**9.9E-20**	**4**
P11030	QATVGDVNTDRPGLLDLK	2.138729162	2	3.490846
P11030	TQPTDEEMLFIYSHFK	5.816601365	2	4.208907
P11030	TYVEKVEELK	1.188415672	2	2.32323
P11030	WDSWNK	1.147920272	1	2.045096
P11232	**THIO Thioredoxin**	**0.99751479**	**0.55871**	**2**
P11232	EAFQEALAAAGDK	0.916815056	2	4.004786
P11232	VGEFSGANK	1.178565137	2	2.777322
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**0.915967332**	**0.03314**	**5**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.333672467	3	6.361889
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.071824103	3	7.085
P11240	GMNTLVGYDLVPEPK	0.952316372	2	3.678948
P11240	LNDFASAVR	0.856569315	2	3.213717
P11240	RLNDFASAVR	0.904996057	2	2.736662
P11348	**DHPR Dihydropteridine reductase**	**1.070902412**	**9.9E-20**	**10**
P11348	AALDGTPGMIGYGMAK	1.191479408	2	3.553158
P11348	EGGLLTLAGAK	0.901005165	2	2.729009
P11348	GAVHQLCQSLAGK	1.427750096	2	3.859145
P11348	MTDSFTEQADQVTAEVGK	1.077337284	2	5.362756
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0)	0.765734052	2	5.750066
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	0.978531195	2	5.519856
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3)	0.770576526	2	3.925415
P11348	QSIWTSTISSHLATK	0.944944383	2	3.472125
P11348	RPNSGSLIQVVTTDGK	1.815210089	2	3.710833
P11348	VDAILCVAGGWAGGNAK	0.87121291	2	4.051018
P11442	**CLH Clathrin heavy chain 1**	**1.030742368**	**9.9E-20**	**31**
P11442	AHIAQLCEK	0.863934348	1	2.225108
P11442	ALEHFTDLYDIK	0.925448973	3	3.993561
P11442	AVDVFFPPEAQNDFPVAMQISEK	0.863168605	2	2.670698
P11442	FDVNTSAVQVLIEHIGNLDR	0.954675897	3	4.110577

P11442	FNALFAQGNYSEAAK	0.967617953	2	4.359346
P11442	GQCDLELINVCNENSLFK	0.903014845	2	5.226171
P11442	GQFSTDELVAEVEK	0.849323745	2	4.152606
P11442	GQFSTDELVAEVEKR	0.944987286	2	3.466628
P11442	IHEGCEEPATHNALAK	0.885199364	2	5.201392
P11442	ISGETIFVTAPHEATAGIIGVNR	1.109180767	2	5.213744
P11442	IYIDSNNNPER	1.068313018	2	3.234654
P11442	KFDVNTSAVQVLIEHIGNLDR	0.989273368	3	5.845061
P11442	KFNALFAQGNYSEAAK	1.028484343	2	4.171444
P11442	LAELEEFINGPNNAHIQQVGDR	1.020356059	2	4.959493
P11442	LHIIEVGTPPTGNQPFPK	1.039398167	2	4.297172
P11442	LPVVIGGLLDVDCSEDVIK	1.218047317	2	4.082672
P11442	LTDQLPLIIVCDR	0.963286725	2	3.094154
P11442	MAVRNNLAGAEELFARK+Oxidation(0)	1.12538154	2	2.321327
P11442	NLQNLLILTAIK	0.927165348	2	4.212542
P11442	NNLAGAEELFAR	0.938083555	2	4.02265
P11442	NNRPSEGPLQTR	0.844568717	3	4.098942
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.111748543	3	6.500882
P11442	SVDPTLALSVYLR	1.028058128	2	2.989966
P11442	SVNESLNNLFITEEDYQALR	1.399513669	2	4.496438
P11442	TLQIFNIEMK	1.174469571	2	2.79051
P11442	TSIDAYDNFDNISLAQR	0.986487035	2	4.244446
P11442	VDKLDASESLR	0.923719797	2	2.451727
P11442	VGEQAQVVIIDMNDPSNPIR	0.921676337	2	4.076597
P11442	VIQCFAETGQVQK	0.971266584	2	4.102799
P11442	VSQPIEGHAASFAQFK	1.22690617	2	4.236613
P11442	WLLLTGISAQQNR	1.10909362	2	2.963931
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.859106486**	**9.9E-20**	**5**
P11497	GGSWVVIDPTINPR	2.188642243	2	2.932549
P11497	GSVLEPEGTVEIK	2.22555038	2	2.648114
P11497	ITSENPDEGFKPSSGTVQELNFR	1.986277705	3	4.01538
P11497	TLRDPSLPLLELQDIMTSVSGR	1.74628239	3	3.953701
P11497	VQQAELHTGSLPQIQSTALR	0.608984125	3	3.620199
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**0.880110811**	**0.01588**	**6**
P11507	DIVPGDIVEIAVGDKVPADIR	1.132530869	2	2.799578
P11507	IGIFGQDEDVTSK	0.95424416	2	2.971655
P11507	IRDEMVATEQER	0.822532517	2	3.15128
P11507	LDEFGEQLSK	0.769792282	2	2.328009
P11507	TASEMVLADDNFSTIVAAVEEGR	0.780673436	3	3.712789
P11507	VDQSILTGESVSVIK	0.659306655	2	4.106581
P11598	**PDIA3 Protein disulfide_isomerase A3**	**0.891620342**	**9.9E-20**	**25**
P11598	DASVVGFFR	0.876592116	2	2.375275

P11598	DGEEAGAYDGPR	0.77584288	2	3.303884
P11598	DLFSDGHSEFLK	0.923138774	2	2.512794
P11598	EATNPPIIQEEKPK	0.853887129	2	3.656388
P11598	ELNDFISYLQR	0.905113195	2	2.653127
P11598	EYDDNGEGITIFRPLHLANK	0.975902168	2	4.478251
P11598	FAHTNVESLVK	2.381635076	2	2.696245
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.003885506	3	4.865358
P11598	FISDKDASVVGFFR	0.85230316	2	4.226071
P11598	FLQEYFDGNLK	0.871281577	2	3.50307
P11598	FLQEYFDGNLKR	1.025013291	2	3.137863
P11598	FVMQEEFSR	1.343699662	2	2.679884
P11598	IFRDGEEAGAYDGPR	0.862874601	2	3.278626
P11598	LAPEYEAAATR	0.90098829	2	3.231463
P11598	LNFAVASR	1.243013198	2	2.449139
P11598	LSKDPNIVIAK	0.815059355	3	4.016501
P11598	MDATANDVPSPYEVK	1.126185161	2	4.288888
P11598	MDATANDVPSPYEVK+Oxidation(0)	0.935065935	2	4.161642
P11598	QAGPASVPLRTEDEFK	1.443709178	2	2.45539
P11598	RLAPEYEAAATR	0.807998649	2	3.823626
P11598	SEPIPETNEGPVK	0.952447524	2	3.184956
P11598	TFLDAGHK	0.884456666	2	2.591974
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.163187269	2	5.957503
P11598	VDCTANTNTCNK	1.021441983	2	4.254447
P11598	YGVSGYPTLK	0.874063876	2	3.078152
P11610	**CD1D2 Antigen_presenting glycoprotein CD1d2**	**0.686258212**	**0.00466**	**2**
P11610	DIQELVKMMSPK+Oxidation(7)	0.686258212	2	2.577317
P11610	DIQELVKMMSPK+Oxidation(8)	0.686258212	2	2.446759
P11711	**CP2A1 Cytochrome P450 2A1**	**0.985180527**	**9.9E-20**	**6**
P11711	GEQATYNTLFK	1.07691559	2	2.626914
P11711	GTDVFPILGSLMTDPK	0.777622036	2	3.343952
P11711	ILEEAGYLIK	0.738948249	2	2.31033
P11711	LEDINESPKPLGFTR	1.068014665	2	3.505904
P11711	TVSNVISSIVFGER	0.803872388	2	3.580146
P11711	VHEEIEQVIGR	0.739123226	2	3.021977
P11714	**CP2D9 Cytochrome P450 2D9**	**0.824055216**	**9.9E-20**	**2**
P11714	GNPESSFNDENLLMVVR	0.94420026	2	2.675455
P11714	VQQEIDEVIGQVR	0.821312154	2	4.8384
P11862	**GAS2 Growth arrest_specific protein 2**	**0.824901674**	**8.6E-06**	**2**
P11862	EIEQEETLSAPSPSPSPSSK	1.11256323	2	4.0178
P11862	LDNGALLCQLAATVQEK	0.804826697	2	3.864927
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**0.916336704**	**9.9E-20**	**24**
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.905146538	3	4.275989

P11884	EEIFGPVMQILK	0.842568585	2	3.422286
P11884	EEIFGPVMQILK+Oxidation(7)	0.635843057	2	2.85709
P11884	ELGEYGLQAYTEVK	0.910450753	2	4.4711
P11884	GYFIQPTVFGDVK	0.973638754	2	4.077297
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.892759629	3	6.42725
P11884	LGPALATGNVVVMK	1.015805454	2	3.415183
P11884	LGPALATGNVVVMK+Oxidation(12)	0.748698854	2	3.623517
P11884	LLCGGGAAADR	0.898887639	2	3.321157
P11884	RVTLELGGK	0.704691305	2	2.782523
P11884	TEQGPQVDETQFK	0.808862032	2	4.575071
P11884	TEQGPQVDETQFKK	0.908385624	2	2.914654
P11884	TFPTVNPSTGEVICQVAEGNK	1.055914624	2	5.100505
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.864250204	2	4.254928
P11884	TFVQEDVYDEFVER	0.845128831	2	5.242601
P11884	TIEEVVGR	0.774115903	2	2.916169
P11884	TIPIDGDFFSYTR	0.966864081	2	2.795919
P11884	VAEQTPLTALYVANLIK	1.900196667	3	4.935835
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.240073646	2	6.182978
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	2.089505247	3	3.44299
P11884	VTLELGGK	0.755936681	1	1.970304
P11884	VVGNPFDSR	0.863980318	2	2.823668
P11884	YGLAAAVFTK	0.914225371	2	3.548285
P11884	YYAGWADK	0.841008721	1	1.949049
P11915	**NLTP Non_specific lipid_transfer protein**	**1.285107112**	**0.00013**	**19**
P11915	ADCTITMADSDLLALMTGK	1.07817013	2	5.559618
P11915	ADCTITMADSDLLALMTGK+Oxidation(15)	1.105977196	2	2.756225
P11915	ADCTITMADSDLLALMTGK+Oxidation(6)	1.114501001	2	4.308211
P11915	ANLIFK	1.088969319	2	2.34476
P11915	GSVLPDSDKK	1.803560417	2	2.505759
P11915	HIDVLINK	0.823725808	2	2.749436
P11915	HSVNNPYSQFQDEYSLDEIMK	1.032164232	2	5.439923
P11915	KADCTITMADSDLLALMTGK	1.237971314	2	3.96418
P11915	KLEEEGEEFVK	1.068355076	2	4.335941
P11915	KLEEEGEEFVKK	1.043387934	3	4.562216
P11915	LEEEGEEFVK	1.060048428	1	2.315851
P11915	LEEEGEEFVKK	1.094042916	2	3.482084
P11915	LQSLQLQPDK	1.131952765	2	3.415481
P11915	MNPQSAFFQGK	1.281916649	2	3.237615
P11915	MNPQSAFFQGK+Oxidation(0)	0.886981695	2	3.086328
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	1.153581805	3	5.733031
P11915	THQISAAPTSSAGDGFK	0.957251425	2	4.436141
P11915	WVINPSGGLISK	1.04667962	2	2.887324
P11915	YGMSACPFAPQLFGSAGK	1.249353664	2	2.810792

P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**0.945636846**	**7.4E-05**	**3**
P11980	GVNLPGAAVDLPAVSEK	0.947054868	2	3.701762
P11980	LDIDSAPITAR	0.825163796	2	2.959845
P11980	NTGIICTIGPASR	0.594398835	2	3.307356
P12001	**RL18 60S ribosomal protein L18**	**1.142625056**	**5.1E-13**	**5**
P12001	GTVLLSGPR	1.714261998	2	2.458262
P12001	ILTFDQLALESPK	1.165080868	2	4.994026
P12001	TAVVVGTITDDVR	1.137501553	2	4.343031
P12001	TNRPPLSLSR	0.959927044	3	3.447801
P12001	TNSTFNQVVLK	1.157090807	2	2.804724
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.005203961**	**0.24995**	**8**
P12007	AQEIDQSNDFK	0.678166813	2	3.351934
P12007	FVQENLAPK	0.874850897	2	2.753386
P12007	FWITNGPDADVLVVYAK	1.172110531	2	3.743194
P12007	GSNTCELVFEDCK	1.093689357	2	4.426341
P12007	GSNTCELVFEDCKVPAANILSQESK	1.007508816	3	5.050405
P12007	GVYVLMSGLDLER	1.048878256	2	3.100017
P12007	LYEIGGGTSEVR	0.930346314	2	3.549193
P12007	TDLTAVPASR	0.968655955	2	3.05182
P12336	**GTR2 Solute carrier family 2_ facilitated glucose transporter member 2**	**0.958613038**	**0.4989**	**2**
P12336	SFDEIAAEFR	0.956485096	2	3.018036
P12336	VSVIQLFTDPNYR	1.107998511	2	2.379023
P12346	**TRFE Serotransferrin**	**0.860290852**	**1.5E-05**	**21**
P12346	ADRDQYELLCLDNTR	1.174370286	2	4.40271
P12346	ASDSSINWNNLK	1.151457872	2	3.294673
P12346	DGGGDVAFVK	1.009701282	2	2.987252
P12346	DLKQEDFQLLCPDGTK	0.847020497	2	4.123101
P12346	EGVCPEGSIDSAPVK	1.095585037	2	3.429128
P12346	EGYNGYTGAFQCLVEK	0.861381749	2	2.949091
P12346	FDEFFSQGCAPGYK	1.020912148	2	4.198772
P12346	GDKDCTGNFCLFR	1.071547497	3	3.556913
P12346	GTDFQLNQLQGK	1.075123739	2	3.108733
P12346	GYYAVAVVK	1.157531546	2	3.295123
P12346	HTTIFEVLPQK	1.130419863	3	3.629882
P12346	KGTDFQLNQLQGK	0.974870052	3	3.943759
P12346	KTSYQDCIK	1.179724531	2	2.59595
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.003916294	2	4.711076
P12346	NGDGKEDLIWEILK	1.250846322	2	3.660434
P12346	QEDFQLLCPDGTK	0.9368152	2	2.818405
P12346	SKDFQLFGSPLGK	1.402013599	2	2.910552
P12346	TSYQDCIK	1.0657996	2	2.449548
P12346	VSTVLTAQK	1.006573701	2	2.73783

P12346	WCALSHQER	1.269727438	2	2.951264
P12346	WCAVSEHENTK	1.004446086	2	3.584677
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**1.005966304**	**0.06633**	**2**
P12368	NISHYEEQLVK	0.832763164	2	2.692959
P12368	NLDQEQLSQVLDAMFEK	1.049490499	2	4.106575
P12711	**ADHX Alcohol dehydrogenase class_3**	**0.879368863**	**9.9E-20**	**9**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	0.990675519	3	5.694255
P12711	AGDTVIPLYIPQCGECK	0.94420026	2	3.926112
P12711	AKEFGATECINPQDFSK	0.861493878	2	3.872194
P12711	EFGATECINPQDFSK	0.753040043	2	4.631954
P12711	IDPSAPLDK	0.825863935	1	2.06998
P12711	IIGIDINK	0.83191972	1	2.0943
P12711	IIGIDINKDK	0.863145493	2	2.557337
P12711	VCLLGCGISTGYGAAVNTAK	1.061545634	2	5.676191
P12711	VDEFVTGNLSFDQINK	0.806920057	2	4.892179
P12749	**RL26 60S ribosomal protein L26**	**1.045084336**	**0.41942**	**5**
P12749	DDEVQVVR	1.112239448	2	2.52155
P12749	FNPFVTSDR	1.01285158	2	2.663767
P12749	HFNAPSHIR	1.235046237	3	3.726597
P12749	KDDEVQVVR	0.962345137	2	3.171065
P12749	KIMSSPLSKELR+Oxidation(2)	1.16157581	2	2.47963
P12785	**FAS Fatty acid synthase**	**1.623226243**	**9.9E-20**	**42**
P12785	ACIDTALENLSTLK	2.022986488	2	4.567935
P12785	AEAVVAVLLTK	2.173127188	2	3.179349
P12785	AGSDTELAAPK	1.308582028	2	3.618582
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.692550421	3	5.675735
P12785	DHKDNLEFFLTNLGK	1.004061833	2	2.599478
P12785	DPETLLGYSMVGCQR	1.379971412	2	2.802916
P12785	EEEPEAMLPGAQPTLISAISK	1.156594308	2	3.875578
P12785	EQGVTFPSGEAQEQLIR	2.105996149	2	4.220711
P12785	FDASFFGVHPK	1.674957741	2	3.215391
P12785	FVFTPHVEPECLSESAILQK	1.893860654	2	4.428057
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	1.772955458	3	5.994374
P12785	GLESIINIIHSSLAEPR	1.168928395	2	4.303549
P12785	GNAGQSNYGFANSTMER	2.111173825	2	4.32393
P12785	GVDLVLNSLAEEK	2.028070093	2	3.670864
P12785	GYDYGPHFQGVYEATLEGEQGK	2.573001082	3	3.571103
P12785	LDPGSSELQK	1.630450161	2	2.54974
P12785	LFDHPEVPIPAESESVSR	2.233395	2	4.032842
P12785	LLLPEDPLISGLLNSQALK	2.238066667	3	4.889594
P12785	LTPGCEAEAEAEAICFFIK	1.624809166	2	3.92684
P12785	MTVPGLEDLPQHGLPR	1.882759906	2	3.501285

P12785	QAQLNLSILLVNPEGPTLTR	2.298720957	2	4.502846
P12785	QFVDAEHSK	0.612388284	2	2.367275
P12785	QQEQLVPTLEK	2.149835918	2	2.438782
P12785	RQQEQLVPTLEK	2.622188696	2	2.920692
P12785	RVYATILNAGTNTDGCK	0.461050572	2	2.482786
P12785	SDEALKPLGVK	2.143358779	2	3.055589
P12785	SFDDSGNGYCR	1.879925016	2	2.34025
P12785	SLSLSLEETPVVFENVTFHQATILPR	1.689722047	3	4.473696
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.9761019	2	5.397772
P12785	SNMGHPEPASGLAALTK	1.87714995	2	2.964784
P12785	SNMGHPEPASGLAALTK+Oxidation(2)	1.330429794	2	3.261074
P12785	TGGTYGEDLGADYNLSQVCDGK	1.978988723	2	4.993083
P12785	TMEAVQGLLEQGR	1.768706608	2	3.776312
P12785	TMEAVQGLLEQGR+Oxidation(1)	1.026837293	2	3.412564
P12785	VGDPQELNGITR	1.337685244	2	3.44143
P12785	VHLTGIDINPNALFPPVEFPVPR	1.798320632	2	4.635872
P12785	VLEALLPLK	2.174244734	2	2.824419
P12785	VLESDLVMNVYR	0.417461464	2	2.991359
P12785	VSVHIIEGDHR	1.98894113	2	2.796365
P12785	VTAIYIDPATHLQK	2.048703573	2	3.415653
P12785	VYATILNAGTNTDGCK	1.342037717	2	4.135136
P12785	VYQWEDPDSK	2.021268899	2	2.944968
P12791	**CP2BA Cytochrome P450 2B10**	**0.652443866**	**9.9E-20**	**2**
P12791	IQEEAQCLVEELR	0.562422039	2	4.399037
P12791	IQEEAQCLVEELRK	0.658032857	2	3.638347
P12847	**MYH3 Myosin_3**	**0.660260447**	**0.38035**	**4**
P12847	GTLEDQIISANPLLEAFGNAK	0.654221588	2	2.985037
P12847	MKGTLEDQIISANPLLEAFGNAK	0.601457787	3	6.321391
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0)	0.638321372	3	4.847859
P12847	NLTEELAGLDETIAK	0.769172734	2	2.35153
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.700969368**	**9.9E-20**	**18**
P12928	AAVIAVTR	2.959103014	2	2.556177
P12928	AETSDVANAVLDGADCIMLSGETAK	1.828839062	2	5.585162
P12928	CCAAAIIVLTK	1.040665309	2	2.54685
P12928	CNLAGKPVVCATQMLESMITK	1.432588949	3	4.973665
P12928	EATESFATSPLSYRPVAIALDTK	2.438996799	2	4.367115
P12928	EPPEAIWADDVDRR	1.943606927	2	2.450483
P12928	GDLGIEIPAEK	1.517727993	2	2.783844
P12928	GSQVLVTVDPK	1.854812313	2	3.141994
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.996107543	2	5.024025
P12928	IGPEGLVTEVEHGGILGSR	1.955440576	2	5.255551
P12928	IYIDDGLISLVVQK	2.054829607	2	4.394081
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	2.292007951	3	4.636216

P12928	RVQFGIESGK	0.941493249	2	2.404479
P12928	STSIIATIGPASR	1.163841796	2	3.722901
P12928	TGVLQGGPESEVEIVK	2.080255296	2	4.759411
P12928	TVWVDYHNITR	1.55204257	2	2.417079
P12928	VGDLVIVVTGWRPGSGYTNIMR	1.559300406	3	3.592625
P12928	VQFGIESGK	1.87556739	1	1.995212
P12938	**CP2D3 Cytochrome P450 2D3**	**0.685978444**	**9.9E-20**	**4**
P12938	DLTDAFLAEIEK	0.715367923	2	4.418019
P12938	FDYGDPDFIK	0.586992393	2	2.573801
P12938	GNPESSFNDANLR	0.749043936	2	4.395343
P12938	RFDYGDPDFIK	0.690002291	2	2.882139
P12939	**CP2DA Cytochrome P450 2D10**	**1.563517955**	**3.9E-11**	**8**
P12939	ALCNVIASLIFAR	1.066522401	2	2.393466
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.189582257	3	5.430445
P12939	FEYEDPYLIR	1.210690132	2	3.15457
P12939	FGDIAPLNLPR	1.564478156	2	3.287056
P12939	ITSCDIEVQDFVIPK	1.094308211	2	4.189401
P12939	NLTDAFLAEVEK	0.969360177	2	4.177208
P12939	RFEYEDPYLIR	1.076661289	3	3.654486
P12939	TTWDPAQPPR	1.133390234	2	2.765743
P13084	**NPM Nucleophosmin**	**0.952660231**	**0.9929**	**2**
P13084	MTDQEAIQDLWQWR	0.932076034	2	2.979163
P13084	VDNDENEHQLSLR	1.115235025	2	3.988224
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**0.968848126**	**0.05767**	**3**
P13086	LIGPNCPGIINPGECK	1.062343736	2	4.147032
P13086	MGHAGAIIAGGK	0.562281223	2	2.800292
P13086	QGTFHSQQALEYGTK	0.860223992	2	2.824051
P13107	**CP2B3 Cytochrome P450 2B3**	**1.313689253**	**1.3E-09**	**7**
P13107	DFIDTFLLHMEK	1.178012278	2	3.227979
P13107	EIDQVIGSQR	0.802755753	2	2.348132
P13107	EVLDYIDHSVENHR	0.890936892	2	3.74617
P13107	FSDVSPMGLPCR+Oxidation(6)	1.079554604	2	2.504637
P13107	GIIAVLQPIMQEYGVSFVNEER	1.788028738	3	6.515994
P13107	QSVEDQIKEEAK	0.980606105	2	2.684267
P13107	SFIQLQEK	1.026379397	2	2.552451
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**1.344056375**	**9.9E-20**	**6**
P13221	ITWSNPPAQGAR	1.245114532	2	3.563991
P13221	IVATTLSNPELFK	1.49175641	2	3.42102
P13221	NLDYVATSINEAVTK	1.441087611	2	4.615786
P13221	SCASQLVLGDNSPALR	2.037513985	2	4.449885
P13221	TDDSQPWVLPVVR	1.641332465	2	3.439863
P13221	VGGVQSLGGTGALR	2.282680313	2	2.601021

P13255	**GNMT Glycine N_methyltransferase**	**0.851029377**	**1.7E-05**	**7**
P13255	AHMVTLDYTVQVPGAGR	1.075559024	2	4.604633
P13255	AWLLGLLR	1.280901422	2	2.625663
P13255	DITTSVLTVNNK	0.866228415	2	3.786759
P13255	NIASMVRPGGLLVIDHR+Oxidation(4)	0.762088395	3	3.855249
P13255	NYDYILSTGCAPPGK	0.855894865	2	4.506861
P13255	SDLTKDITTSVLTVNNK	0.918830462	2	2.980359
P13255	SLGVAAEGIPDQYADGEAAR	0.85729024	2	5.395795
P13383	**NUCL Nucleolin**	**1.040633482**	**0.00018**	**4**
P13383	GFGFVDFNSEEDAK	1.075149303	2	3.38593
P13383	GLSEDTTEETLK	0.820398633	2	2.895458
P13383	IEGSEPTTPFNLFIGNLNPNK	0.746322082	2	2.738306
P13383	SEADAEKNLEEK	1.111383695	2	3.019146
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.673166051**	**9.9E-20**	**21**
P13437	AANEAGYFNEEMAPIEVK	0.722122156	2	5.320649
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11)	0.70182412	2	5.116405
P13437	DAEVVLCGGTESMSQSPYSVR	0.735925619	2	5.069211
P13437	DAEVVLCGGTESMSQSPYSVR+Oxidation(12)	1.134465846	2	3.187351
P13437	DFTATDLTEFAAR	0.649366026	2	4.038708
P13437	DMDLIDVNEAFAPQFLAVQK	0.770799372	3	6.025092
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1)	0.761821325	2	4.510396
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.618186085	2	5.597886
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	0.565093126	3	4.512787
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK+Oxidation(11)	0.543988888	3	3.536056
P13437	FGLDLK	0.691118139	2	2.342524
P13437	GVFIVAAK	0.718738815	2	2.466823
P13437	ITAHLVHELR	1.197299628	2	2.97402
P13437	LCGSGFQSIVSGCQEICSK	0.739209357	2	5.140188
P13437	LEDTLWAGLTDQHVK	0.655267881	2	5.061839
P13437	RTPFGAYGGLLK	1.099372073	2	2.532732
P13437	SLDLDPSK	0.658557953	2	2.896674
P13437	TNVSGGAIALGHPLGGSGSR	0.63013327	2	6.089171
P13437	VGVPTETGALTLNR	0.701867709	2	3.781097
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	0.591179413	2	6.129364
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	0.576524758	3	4.847097
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.186336515**	**9.9E-20**	**8**
P13444	FVIGGPQGDAGVTGR	1.178112664	2	4.819842
P13444	HIGYDDSAK	1.482643722	2	2.784954
P13444	ICDQISDAVLDAHLK	1.25207034	3	5.106026
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	0.764693863	3	6.60046
P13444	SEFPWEVPK	1.21379382	2	2.45008
P13444	SGVLPWLRPDSK	1.095093653	2	2.91682

P13444	TCNVLVALEQQSPDIAQCVHLDR	1.477338779	3	5.009028
P13444	TQVTVQYVQDNGAVIPVR	1.734630341	2	4.753774
P13471	**RS14 40S ribosomal protein S14**	**0.950331062**	**4E-10**	**4**
P13471	ADRDESSPYAAMLAAQDVAQR	1.356169761	2	5.671414
P13471	DESSPYAAMLAAQDVAQR	1.41844539	2	3.34797
P13471	ELGITALHIK	1.321274854	2	2.468617
P13471	IEDVTPIPSDSTR	0.947355973	2	3.741135
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.856396522**	**9.9E-20**	**15**
P13601	EEIFGPVQQIMK	0.539773904	2	3.427416
P13601	EMGEQGVYEYTELK	0.578330149	2	3.301206
P13601	FPVINPATEEVICHVEEGDKADVDK	0.567921631	4	5.153451
P13601	IAKEEIFGPVQQIMK	0.804505497	2	3.111602
P13601	IHGQTIPSDGDVFTYTR	0.842530249	2	3.818355
P13601	ILDLIESGK	0.529256313	2	3.254489
P13601	ILDLIESGKK	0.582374893	3	3.543305
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.646699853	3	3.639653
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	0.38254716	3	4.515509
P13601	LFVEESIYDEFVR	0.600734856	2	3.725007
P13601	VLLATMESMNAGK	0.892359893	2	2.861511
P13601	VSFTGSTEVGK	0.478586084	2	2.355322
P13601	YFAGWADK	0.666926181	1	2.091618
P13601	YVLGNPLDSGISQGPQIDK	0.537677496	2	4.852623
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.495491054	2	4.208746
P13697	**MAOX NADP_dependent malic enzyme**	**1.123189154**	**0.26808**	**5**
P13697	AECSAEECYK	1.234809332	2	3.034678
P13697	AIFASGSPFDPVTLPDGR	1.117495899	2	4.281984
P13697	GHIASVLNAWPEDVVK	1.082783951	2	2.842623
P13697	HINDSVFLTTAEVISQQVSDK	1.093528439	3	4.09601
P13697	ILGLGDLGCNGMGIPVGK	0.682602827	2	2.385633
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**0.919274499**	**9.9E-20**	**13**
P13803	AAVDAGFVPNDMQVGQTGK	0.953396589	2	4.388618
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11)	0.824846805	2	3.848487
P13803	GLLPEELTPLILETQK	0.982067088	2	4.514587
P13803	GTSFEAAAASGGSASSEK	0.89801427	2	5.165604
P13803	LGGEVSCLVAGTK	0.877500108	2	4.511054
P13803	LLYDLADQLHAAVGASR	0.960249213	2	5.123318
P13803	LNVAPVSDIIEIK	1.073812863	3	4.649651
P13803	QFSYTHICAGASAFGK	1.144487022	2	2.853104
P13803	SDRPELTGAK	0.804201928	3	3.402157
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.866376628	3	7.171578
P13803	TIYAGNALCTVK	0.942545905	2	3.519764
P13803	VLVAQHDAYK	0.856302851	2	3.373696

P13803	VVQDLCK	0.835837324	2	2.617921
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.061059179**	**0.80662**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.113440917	2	4.967342
P13832	FTDEEVDELYR	1.066484896	2	3.428142
P13832	GNFNYIEFTR	1.007929809	2	2.524019
P14046	**A1I3 Alpha_1_inhibitor 3**	**1.068968731**	**0.35047**	**7**
P14046	FSIDTNGISDYSLNIK	1.532973753	2	2.319447
P14046	GDPIPNEQVLIK	0.983773673	2	2.48965
P14046	GMYESLPVVAVK	0.93966102	2	3.092848
P14046	GMYESLPVVAVK+Oxidation(1)	0.718511298	2	2.80014
P14046	ISLCHGNPTFSSETK	1.689488088	2	3.183662
P14046	QQNSYGGFSSTQDTVVALDALSK	1.238286159	2	4.10768
P14046	QSPGPCGSEVATVPETGR	1.02655486	2	3.606339
P14141	**CAH3 Carbonic anhydrase 3**	**0.742825401**	**9.9E-20**	**17**
P14141	EAPFNHFDPSCLFPACR	0.696659865	2	4.100217
P14141	EKGEFQILLDALDK	0.695316511	2	4.344332
P14141	EPMTVSSDQMAK	2.051864778	2	2.640788
P14141	EWGYASHNGPEHWHELYPIAK	0.627888613	3	4.798904
P14141	GDNQSPIELHTK	0.720962115	2	3.510344
P14141	GEFQILLDALDK	0.666996776	2	4.750772
P14141	GEFQILLDALDKIK	0.808646504	2	3.009718
P14141	GGPLSGPYR	0.746688992	2	2.979345
P14141	GKEAPFNHFDPSCLFPACR	0.948322421	2	3.885133
P14141	HDPSLQPWSVSYDPGSAK	0.822137496	3	5.333054
P14141	QFHLHWGSSDDHGSEHTVDGVK	0.58250057	2	4.545606
P14141	QPDGIAVVGIFLK	1.101297387	2	2.695477
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.67665215	3	5.762795
P14141	VVFDDTFDR	0.720169557	2	3.278795
P14141	YAAELHLVHWNPK	1.302148527	2	4.10161
P14141	YNTFGEALK	0.68911862	2	2.520147
P14141	YNTFGEALKQPDGIAVVGIFLK	0.662343948	3	5.951661
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**0.887234697**	**0.38895**	**7**
P14173	AGEGGGVIQGSASEATLVALLAAR	1.08907129	2	5.286902
P14173	ALIPTTAPQEPETYEDIIR	0.886742356	2	3.482483
P14173	GSNQLNETLLQR	0.905041365	2	2.884965
P14173	HSHQDSGLITDYR	1.013207591	3	3.682444
P14173	MLELPEAFLAGR	1.244914156	2	2.630818
P14173	QLQAASPELTQAALMEK	0.953805513	2	3.703033
P14173	TDLTEAFNMDPVYLR	1.070739444	2	3.543494
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**1.062664856**	**9.9E-20**	**11**
P14408	AAAEVNQEYGLDPK	1.197859764	2	4.286795
P14408	AIEMLGGELGSK	0.807230805	2	3.942955
P14408	IEYDTFGELKVPTDK	1.17708116	2	3.038985

P14408	IYELAAGGTAVGTGLNTR	0.765691525	2	5.519475
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.734893237	3	5.992123
P14408	SGLGELILPENEPGSSIMPGK	0.701151876	2	4.608185
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17)	0.604421323	2	3.069037
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	0.866032709	3	4.381575
P14408	TAIELGYLTAEQFDEWVKPK	0.783192149	2	4.936927
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.309849664	3	6.252834
P14408	YYGAQTVR	0.73670688	2	2.503474
P14480	**FIBB Fibrinogen beta chain**	**1.127207348**	**0.97811**	**6**
P14480	AHYGGFTVQTEANK	1.019681405	2	2.368666
P14480	GFGNIATNEDTKK	0.96099159	2	2.922162
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	1.270321845	3	4.756452
P14480	LYIDETVNDNIPLNLR	1.14412982	2	2.547414
P14480	TENGGWTVIQNR	1.017010216	2	3.484118
P14480	YCGLPGEYWLGNDK	0.990189316	2	3.244504
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.710224648**	**9.9E-20**	**7**
P14604	AFAAGADIK	0.820836778	2	3.132133
P14604	AQFGQPEILLGTIPGAGGTQR	0.88397276	2	5.729046
P14604	FLSHWDHITR	0.866272766	2	3.012297
P14604	IFPVETLVEEAIQCAEK	0.822171843	2	5.632178
P14604	NSSVGLIQLNRPK	0.9186589	2	3.513586
P14668	**ANXA5 Annexin A5**	**0.795990247**	**3.8E-06**	**5**
P14668	EFRKNFATSLYSMIK	0.941097683	2	2.39026
P14668	ETSGNLENLLLAVVK	0.746245593	2	3.33549
P14668	GAGTDDHTLIR	0.804482355	2	2.714598
P14668	GLGTDEDSILNLLTAR	0.778488253	2	3.956472
P14668	GTVTDFSGFDGR	0.815928734	2	2.568354
P14669	**ANXA3 Annexin A3**	**0.678757998**	**9.9E-20**	**6**
P14669	GMGTDEDTLIEILTTR	0.69698552	2	3.128846
P14669	GTINNYPGFNPSVDAEAIR	0.65260223	2	4.623111
P14669	KDAQTLYDAGEKK	0.537733937	3	3.763871
P14669	QYQEAYEQALK	0.609154901	2	2.781823
P14669	SEIDLLDIR	0.833213639	2	2.996954
P14669	WGTDEDKFTEILCLR	0.851218816	3	3.485553
P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**0.950023039**	**0.99023**	**2**
P14685	LQLDSPEDAEFIVAK	0.945501703	2	4.041518
P14685	SVFPEQANNNEWAR	1.037391665	2	3.144493
P14740	**DPP4 Dipeptidyl peptidase 4**	**1.068954153**	**0.00368**	**3**
P14740	FRPAEPHFTSDGSSFYK	0.900272976	2	2.723209
P14740	LGTLEVEDQIEAAR	1.091040022	2	3.550217
P14740	VLEDNSALDK	1.188568884	2	2.689943
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**0.797462156**	**9.9E-20**	**11**

P14882	EIGYPVMIKASAGGGGK+Oxidation(6)	0.886344257	2	2.40752
P14882	FLSDVYPDGFK	0.871170071	2	2.927598
P14882	FSSQEAASSFGDDR	1.095287828	2	2.918512
P14882	HGNALWLNER	1.268862473	2	2.932504
P14882	HKQEDIPISGWAVECR	0.822924843	3	3.520111
P14882	MADEAVCVGPAPTSK	1.061196846	2	3.967639
P14882	MEDALDSYVIR	0.852011095	2	3.033719
P14882	SYLNMDAIMEAIK	0.825321036	2	2.336533
P14882	TGAQAVHPGYGFLSENK	0.916236535	2	4.035578
P14882	TVAIHSDVDASSVHVK	0.882211586	3	3.441371
P14882	VVEEAPSIFLDPETR	0.788200958	2	3.535632
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**0.689471303**	**4.7E-09**	**2**
P14942	KPPPDGHYVDVVR	0.689000689	2	2.70752
P14942	YFPVFEK	0.727904769	1	1.917878
P15083	**PIGR Polymeric immunoglobulin receptor**	**0.959109012**	**0.79686**	**3**
P15083	EIQNAGDQAQENR	1.027857468	2	3.988016
P15083	GVTGGSVAIVCPYNPK	1.074075819	2	3.744797
P15083	NNADLQVLEPEPELLYK	0.819054683	2	3.005404
P15149	**CP2A2 Cytochrome P450 2A2**	**0.590829885**	**9.9E-20**	**10**
P15149	DVQECILEEAGYLIK	0.54191649	3	5.151561
P15149	DVYSSITQLSER	0.84735425	2	3.068344
P15149	FSNLAPLGIPR	0.709663657	2	3.200616
P15149	GELPTFNILFK	0.481827301	2	2.704638
P15149	GTDVFPIIGSLMTEPK	0.508852443	3	3.723542
P15149	GYGFSLSNVEQAK	0.542276912	2	3.437746
P15149	NFIDSFLIR	0.733679678	2	2.456583
P15149	QNHSTLDPNSPR	0.629955012	2	2.967593
P15149	TLQGTCGAPIDPSIYLSK	0.60043735	2	4.725547
P15149	TVSNVINSIVFGNR	0.672029687	2	3.465978
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**0.966950951**	**0.11715**	**2**
P15178	GEEILSGAQR	0.914096124	2	2.731855
P15178	QMVKFAANINK+Oxidation(1)	1.193242781	2	2.354814
P15429	**ENOB Beta_enolase**	**1.015669513**	**0.23402**	**5**
P15429	DATNVGDEGGFAPNILENNEALELLK	0.681931365	2	4.984734
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	0.576002977	3	5.20497
P15429	IEEALGDK	0.473754588	1	2.115771
P15429	TAIQAAGYPDK	0.668758455	2	2.748728
P15429	VNQIGSVTESIQACK	1.01769791	2	5.138294
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.914624514**	**9.9E-20**	**21**
P15650	AFVDSCLQLHETK	1.048179896	2	4.120894
P15650	AQDTAELFFEDVR	1.20958844	2	4.868296
P15650	AQDTAELFFEDVRLPASALLGEENK	1.175214362	3	4.400803

P15650	CIGAIAMTEPGAGSDLQGVR	0.946059392	2	6.15964
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6)	0.873464194	2	5.639467
P15650	EQIEQFIPQMTAGK	0.880007249	2	5.021329
P15650	FFQEEVIPYHEEWEK	1.697928515	2	4.744329
P15650	GFYYLMQELPQER	1.168343866	2	2.976159
P15650	GFYYLMQELPQER+Oxidation(5)	0.989065508	2	2.654932
P15650	IFSSEHDIFR	1.091833506	2	2.841255
P15650	KFFQEEVIPYHEEWEK	1.693111829	2	4.771874
P15650	LDSASASMAK	0.747497021	2	2.419462
P15650	LDSASASMAK+Oxidation(7)	1.017473467	2	2.441253
P15650	LPASALLGEENK	1.948224187	2	3.335713
P15650	LPASALLGEENKGFYYLMQELPQER	3.231819738	3	3.968267
P15650	QGLLGINIAEK	0.964543997	2	3.282512
P15650	RLDSASASMAK	0.841388269	2	2.968098
P15650	RLDSASASMAK+Oxidation(8)	0.948508037	2	2.792291
P15650	SGSDWILNGSK	1.01109904	2	2.978194
P15650	VQPIYGGTNEIMK	1.05086051	2	3.55062
P15650	VQPIYGGTNEIMK+Oxidation(11)	0.952000287	2	3.060328
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.976995753**	**7.2E-11**	**7**
P15651	ASSTANLIFEDCR	1.127575139	2	3.427588
P15651	EEGDSWVLNGTK	0.780373982	2	2.719931
P15651	ELVPIAAQLDKEHLFPTSQVK	0.834905648	2	4.545294
P15651	IGCFALSEPGNGSDAGAASTTAR	1.153810975	2	5.904689
P15651	IGIASQALGIAQASLDCAVK	1.049448844	2	4.640051
P15651	ITEIYEGTSEIQR	0.842888537	2	4.286483
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.002430836	4	4.808429
P15684	**AMPN Aminopeptidase N**	**0.774880843**	**0.03253**	**3**
P15684	ALGDTPAPNIDTTELVER	1.011384783	2	3.738566
P15684	AQIIHDSFNLASAGK	0.709270646	2	3.4102
P15684	VVATTQMQAADAR	0.759507896	2	3.267232
P15709	**ST2A1 Bile salt sulfotransferase**	**0.922164842**	**1.9E-08**	**2**
P15709	GNVLYGSWFEHIR	0.799080632	2	2.979803
P15709	NHFTVSQAEAFDK	1.735466704	2	3.691901
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.283060406**	**9.9E-20**	**23**
P15999	AVDSLVPIGR	0.956840042	2	3.483189
P15999	EVAAFAQFGSDLDAATQQLLSR	1.347060613	2	6.425317
P15999	FESAFLSHVVSQHQSLLGNIR	1.30275723	3	5.923397
P15999	GIRPAINVGLSVSR	1.15532929	2	3.028062
P15999	GMSLNLEPDNVGVVVFGNDK	1.530124332	2	4.958539
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1)	1.031587185	2	3.553315
P15999	GYLDKLEPSK	0.880064776	2	2.443049
P15999	HALIIYDDLSK	2.37469691	2	2.469416

P15999	ILGADTSVDLEETGR	1.129222374	2	5.076817
P15999	LELAQYR	1.001345883	2	2.741239
P15999	LKEIVTNFLAGFEP	1.675408992	2	2.361426
P15999	LYCIYVAIGQK	0.993860331	2	2.495288
P15999	NVQAEEMVEFSSGLK	1.797686379	2	4.414446
P15999	QGQYSPMAIEEQVAVIYAGVR	1.545193931	3	4.951071
P15999	RLTDADAMK	0.769629685	2	2.335885
P15999	RTGAIVDVPVGDELLGR	1.129490306	2	3.097045
P15999	STVAQLVK	0.929811362	2	2.32218
P15999	TGAIVDVPVGDELLGR	0.941215557	2	4.58103
P15999	TGTAEMSSILEER	1.012809832	2	4.267123
P15999	TGTAEMSSILEER+Oxidation(5)	0.918046463	2	3.368952
P15999	TSIAIDTIINQK	0.948717077	2	4.340858
P15999	VLSIGDGIAR	1.027812396	2	3.242816
P15999	VVDALGNAIDGK	0.97615578	2	4.311783
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.038044811**	**0.66851**	**8**
P16036	ALYSNILGEENTYLWR	1.054799988	2	2.720075
P16036	EEGLNAFYK	1.021288601	1	2.080782
P16036	EKGSTASQVLQR	1.018703959	2	3.086685
P16036	FGFYEVFK	1.032038234	1	1.99456
P16036	GIFNGFSITLK	1.248713195	2	2.693912
P16036	GSTASQVLQR	0.934022777	2	3.043684
P16036	IQTQPGYANTLR	1.051926253	2	3.262573
P16036	MYKEEGLNAFYK+Oxidation(0)	0.840310218	2	2.675498
P16086	**SPTA2 Spectrin alpha chain_ brain**	**0.886579538**	**9.9E-20**	**28**
P16086	ALINADELANDVAGAEALLDR	0.882412865	3	4.296778
P16086	ALSSEGKPYVTK	0.8813243	2	3.245813
P16086	CNSLEEIKALREAHDAFR	1.778565359	2	2.580237
P16086	DVTGAEALLER	1.50702113	2	2.526131
P16086	GVIDMGNSLIER	0.818584048	2	2.942995
P16086	HQALQAEIAGHEPR	0.760587826	3	3.430938
P16086	KFEEFQTDLAAHEER	0.794802595	2	4.444002
P16086	LFGAAEVQR	0.810351555	2	2.352936
P16086	LGDSHDLQR	0.774061937	2	3.01277
P16086	LGESQTLQQFSR	0.963128978	2	3.248273
P16086	LIQEQHPEEELIK	0.979566296	2	2.851206
P16086	LQQSHPLSANQIQVK	0.919495825	2	3.670163
P16086	LQTASDESYKDPTNIQSK	0.791672762	2	5.07851
P16086	LQVASDENYKDPTNLQGK	0.81100252	2	4.902934
P16086	LSDDNTIGQEEIQQR	0.618459693	2	4.335981
P16086	MQHNLEQQIQAR+Oxidation(0)	0.64352731	2	2.622746
P16086	NQALNTDNYGHDLASVQALQR	0.902611616	2	5.815003
P16086	NTTGVTEEALK	0.933308425	2	2.414636

P16086	QFQDAGHFDAENIKK	0.827021079	2	2.517598
P16086	SADESGQALLAAGHYASDEVR	1.086095134	2	5.218959
P16086	SLQQLAEER	0.881078643	2	2.612935
P16086	SQLLGSAHEVQR	0.849604743	2	3.259055
P16086	SSLSSAQADFNQLAELDR	0.88506767	2	5.19909
P16086	TATDEAYKDPSNLQGK	0.820144503	2	3.813399
P16086	TKQEEVNAAWQR	1.104723998	2	3.067427
P16086	VLETAEDIQER	0.900599314	2	2.832828
P16086	VNDVCTNGQDLIK	0.907924742	2	2.661409
P16086	VNSLGETAQR	0.772659091	2	2.592139
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**0.597168319**	**9.9E-20**	**6**
P16232	EECALEIIK	0.564957043	1	2.280206
P16232	ETSGIILSQAAPK	0.527132783	2	3.553055
P16232	FALDGFFSTIR	1.243871426	2	2.726427
P16232	KDEVYYDK	0.485799448	1	2.554527
P16232	MTQPLIASYSASK	1.329064817	2	2.555568
P16232	SSWTPLLLGNPGR	0.502088923	2	3.50762
P16290	**PGAM2 Phosphoglycerate mutase 2**	**0.996794854**	**1.4E-05**	**4**
P16290	AMEAVAAQGK	0.807778256	2	2.501416
P16290	AMEAVAAQGK+Oxidation(1)	0.729048652	2	3.032785
P16290	HYGGLTGLNK	1.397372882	1	2.834015
P16290	VLIAAHGNSLR	0.918612658	2	2.509124
P16303	**CES3 Carboxylesterase 3**	**0.584636642**	**9.9E-20**	**13**
P16303	AKEAAEEPSHWK	0.547626793	2	3.94873
P16303	DGASEEETNLSK	0.510931306	2	4.300706
P16303	ESYPFLPTVIDGVVLPK	0.501750383	2	4.295737
P16303	LDLLGNPK	0.628867014	2	2.394383
P16303	MIPVVAEK	0.531078626	1	1.945731
P16303	QEFGWIIPTLMGYPLSEGK	0.884258769	2	3.86512
P16303	QKTEDELLETSLK	0.474100615	2	3.44549
P16303	SFNTVPYIVGINK	1.149379262	2	2.593274
P16303	TEDELLETSLK	0.509440319	2	3.628978
P16303	TPEEILAEK	1.598745532	2	2.331626
P16303	TTTSAVMVHCLR	0.638977446	2	2.495851
P16303	TVIGDHGDELFSVFGSPFLK	0.779458727	2	5.554857
P16303	YFGGTDDPAK	0.489861892	2	3.07163
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.066770784**	**0.53058**	**4**
P16332	AHCQTSGWSLTEQDPYNNIVR	1.286032489	3	4.286276
P16332	IDSGSEVIVGVNK	1.07867268	2	3.52451
P16332	NTQIIIQEESGIPK	1.069113906	2	3.882507
P16332	TGLQAGLTIDEFAPR	0.989764249	2	3.046561
P16409	**MYL3 Myosin light chain 3**	**0.764664853**	**0.59748**	**6**

P16409	AAPAPAAAPAAAPEPERPK	0.628221783	2	4.312579
P16409	ALGQNPTQAEVLR	0.571841189	2	3.855235
P16409	DTGTYEDFVEGLR	0.61442519	2	3.066713
P16409	IEFTPEQIEEFK	0.771097097	2	2.467093
P16409	NKDTGTYEDFVEGLR	0.90331797	2	3.401169
P16409	VFDKEGNGTVMGAELR	0.617977076	2	3.817748
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.002165852**	**9.9E-20**	**19**
P16617	AHSSMVGVNLPQK	1.028517599	2	3.507665
P16617	AHSSMVGVNLPQK+Oxidation(4)	0.769377159	2	2.815743
P16617	ALESPERPFLAILGGAK	1.765940629	3	4.454042
P16617	DCVGSEVENACANPAAGTVILLENLR	1.038299744	3	5.924394
P16617	FCLDNGAK	0.859683365	1	2.02842
P16617	GCITIIGGGDTATCCAK	0.97215405	2	5.307636
P16617	IQLINNMLDK	0.971024319	2	2.334903
P16617	IQLINNMLDK+Oxidation(6)	1.480632174	2	2.456831
P16617	ITLPVDFVTADK	1.081852342	2	2.338421
P16617	ITLPVDFVTADKFDENAK	1.464093226	2	4.660302
P16617	QIVWNGPVGVFEWEAFAR	0.759245897	2	3.046033
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.733870254	4	4.705709
P16617	TGQATVASGIPAGWMGLDCGTESSK	1.000832174	2	4.72055
P16617	TGQATVASGIPAGWMGLDCGTESSKK	1.062270633	3	4.142533
P16617	VLNNMEIGTSLYDEEGAK	1.179088364	2	4.841942
P16617	VLNNMEIGTSLYDEEGAK+Oxidation(4)	0.773517771	2	2.670293
P16617	VLPGVDALSNV	1.135423064	2	2.402672
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.133710354	3	4.544102
P16617	YSLEPVAAELK	0.990758912	2	2.974669
P16638	**ACLY ATP_citrate synthase**	**1.476541905**	**9.9E-20**	**20**
P16638	AFDSGIIPMEFVNK	1.494591037	2	3.475564
P16638	AFDSGIIPMEFVNK+Oxidation(8)	0.776565195	2	3.198521
P16638	DEPSVAAMVYPFTGDHK	1.406448973	2	3.526136
P16638	DGVYILDLAAK	1.253686335	2	2.329798
P16638	DLVSSLTSGLLTIGDR	1.286271626	2	3.744618
P16638	EAYPEEAYIADLDAK	1.426970892	2	3.246348
P16638	FGGALDAAAK	1.290080966	2	2.725577
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.483577339	2	4.050598
P16638	GGPNYQEGLR	1.714729698	2	2.955005
P16638	GVTIIGPATVGGIKPGCFK	1.295416349	2	3.400007
P16638	IGNTGGMLDNILASK	1.296423466	2	3.594409
P16638	LGLVGVNLSLDGVK	1.486538583	2	2.499125
P16638	LLVGVDEK	1.458244101	2	2.316245
P16638	RGGPNYQEGLR	2.315043174	2	3.296581
P16638	SGGMSNELNNIISR	1.150462148	2	3.332389
P16638	TIAIIAEGIPEALTR	1.375696049	2	4.547411

P16638	TTDGVYEGVAIGGDR	1.427745711	2	2.817966
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	1.551546115	3	3.649698
P16638	WGDIEFPPPFGR	1.097340835	2	3.9985
P16638	YICTTSAIQNR	1.460286364	2	2.998045
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.951455559**	**0.03992**	**7**
P16970	EGGWDSVQDWMDVLSGGEK	0.974750566	2	3.994806
P16970	FDHVPLATPNGDILIQDLSFEVR	1.211830128	3	4.00784
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.936486793	3	4.559751
P16970	GYLDNVQLGHILER	0.942568852	2	3.372169
P16970	HLHSTHSELLEDYYQSGR	0.857877018	3	4.73919
P16970	IANPDQLLTQDVEK	1.090643503	2	3.170719
P16970	SGANVLICGPNGCGK	0.924361049	2	3.454221
P17077	**RL9 60S ribosomal protein L9**	**0.985923207**	**0.00049**	**7**
P17077	FLDGIYVSEK	1.048512786	2	3.36401
P17077	GTVQQPDE	1.067093382	1	2.050989
P17077	KFLDGIYVSEK	1.120452924	2	2.477501
P17077	SVYAHFPINVVIQENGSLVEIR	1.105458973	3	3.385095
P17077	TGVACSVSQAQK	0.911502378	2	3.086485
P17077	TICSHVQNMIK	0.8499735	2	2.912883
P17077	TILSNQTVDIPENVDITLK	0.865871762	2	3.928612
P17078	**RL35 60S ribosomal protein L35**	**1.019808608**	**0.98813**	**2**
P17078	QLDDLKVELSQLR	0.95617888	2	2.415821
P17078	VLTVINQTQK	1.029791775	2	2.976694
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**1.375055895**	**1.2E-05**	**3**
P17178	MLKPAEAALYTDALNEVISDFIAR	1.536736807	3	3.718913
P17178	VGCLEPSIPEDTATFIR	1.430809859	2	3.063416
P17178	YEVVLSPGMGEVK	1.098943707	2	3.234018
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.23690726**	**9.9E-20**	**10**
P17425	ASAELFNQK	0.271354603	2	3.010036
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK+Oxidation(3)	0.142919393	3	4.794155
P17425	LEDTYFDRDVEK	0.209526773	2	2.828492
P17425	MFLNDFLNDQNR	0.362858953	2	2.619775
P17425	MFLNDFLNDQNR+Oxidation(0)	0.186142175	2	3.408628
P17425	NSLSYDCIGR	0.198935138	2	2.674054
P17425	RPSTNDHSLDEGVGLVHSNTATEHIPSPAK	0.537459474	4	4.652402
P17425	TCVAPDVFAENMK	0.256749039	2	2.468074
P17425	VTQDATPGSALDK	0.243946677	2	3.925191
P17425	YTIGLGQAR	0.249144095	2	2.61365
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**0.977787509**	**0.3818**	**3**
P17426	FVCKNSGVLFENQLLQIGVK	2.120858885	2	2.30254
P17426	NADVELQQR	1.062237565	2	2.643287
P17426	VGGYILGEFGNLIAGDPR	0.869584068	2	3.426387

P17475	**A1AT Alpha_1_antiproteinase**	**1.357697188**	**0.00123**	**6**
P17475	IVDLMK+Oxidation(4)	1.153392009	1	2.05017
P17475	MQHLEQTLTK	0.974961094	2	2.317177
P17475	NNYHSEAFSVNFADSEEAKK	1.973347017	3	4.351598
P17475	TLLSSLGITR	1.418790285	2	2.988697
P17475	VFNNDADLSGITEDAPLK	1.430947304	2	5.460659
P17475	VINDYVEK	1.399578729	1	2.190601
P17712	**HXK4 Glucokinase**	**1.298333019**	**0.00423**	**4**
P17712	ASGAEGNNIVGLLR	1.442578795	2	2.905324
P17712	LETHEEASVK	1.005452951	2	2.516607
P17712	STPEGSEVGDFLSLDLGGTNFR	1.300352159	2	4.221118
P17712	VGEGEAGQWSVK	1.219810316	2	3.033377
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.018874546**	**9.9E-20**	**16**
P17764	EEQDKYAIGSYTR	0.811544552	2	3.54635
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	1.125624077	3	3.389439
P17764	EVYMGNVIQGGEGQAPTR	1.098094595	2	4.751221
P17764	FANEITPITISVK	1.279713472	2	3.718861
P17764	GKPDVVVKEDEEYK	0.893675606	2	3.238362
P17764	GKPDVVVKEDEEYKR	0.845554923	2	4.575419
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.318977721	2	3.887921
P17764	IHMGNCAENTAK	0.529326774	2	3.197745
P17764	IHMGNCAENTAK+Oxidation(2)	0.979259757	2	3.029543
P17764	LEDLIVK	0.781749815	1	2.186316
P17764	LGTIAIQGAIEK	1.021776552	2	2.886348
P17764	QATLGAGLPIATPCTTVNK	0.910497082	2	4.639103
P17764	QGEFGLASICNGGGGASAVLIEK	0.843289435	2	4.761388
P17764	TPIGSFLGSLASQPATK	2.782148171	2	3.997275
P17764	VNVHGGAVSLGHPIGMSGAR	0.00611849	3	3.649167
P17764	VNVHGGAVSLGHPIGMSGAR+Oxidation(15)	0.747868291	3	3.311255
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.292500545**	**9.9E-20**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.163638599	3	4.659195
P17879	TTPSYVAFTDTER	1.502801667	2	3.697904
P17879	VEIIANDQGNR	1.035450822	2	3.804797
P17988	**ST1A1 Sulfotransferase 1A1**	**1.794669421**	**9.9E-20**	**4**
P17988	CPGVPSGLETLEETPAPR	1.842224035	2	4.924014
P17988	NTFTVAQNER	1.872008757	2	3.46223
P17988	SLPEETVDSIVHHTSFK	1.903932331	2	4.345303
P17988	THLPLSLLPQSLLDQK	2.013438996	2	4.724508
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**0.897364938**	**9.9E-20**	**23**
P18163	AELSVIFADKPEK	0.938772262	2	3.355863
P18163	ALKPPCDLSMQSVEVTGTTEGVR	0.905747344	2	4.492323
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9)	0.672625553	3	3.657052

P18163	CGVEIIGLK	0.814026231	2	3.078706
P18163	DGWLHTGDIGK	0.75876791	2	2.870425
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2)	1.74187799	3	3.737926
P18163	GFQGSFEELCR	0.987293783	2	3.200496
P18163	GIAVHPELFSIDNGLLTPTLK	1.836531564	2	5.668026
P18163	GIQVSNDGPCLGSR	0.866900614	2	4.577071
P18163	IENIYLR	0.87230799	2	2.844885
P18163	IFGQANTSVK	0.995569304	2	2.403597
P18163	IIVIMDSYDNDLVER	0.92732573	2	4.295888
P18163	LLLEGVENK	0.859972807	2	3.229224
P18163	LVDVEDMNYQAAK	1.052032256	2	4.505102
P18163	LVDVEDMNYQAAK+Oxidation(6)	0.869328575	2	3.408411
P18163	NAGLKPFEQVK	0.919276391	2	3.573082
P18163	NNSLWDK	0.877099824	2	2.6721
P18163	QVAEMAECIGSALIQK	0.829049128	2	5.345551
P18163	SQIDELYSTIK	0.970071533	2	3.579922
P18163	SQIDELYSTIKI	1.139707447	2	3.953763
P18163	TAEALDKDGWLHTGDIGK	1.10494462	2	5.248548
P18163	VLQPTIFPVVPR	0.880213385	2	3.635252
P18163	WLLDFASK	0.923522249	2	2.331704
P18297	**SPRE Sepiapterin reductase**	**0.880919756**	**2.7E-13**	**4**
P18297	ALAPQLAGLLSPGSVLLLSAR	0.902618634	3	4.804233
P18297	LNSEGELVDCGTSAQK	0.878356823	2	4.74238
P18297	TVVNISSLCALQPFK	1.180277831	2	2.699671
P18297	VLSYAPGPLDTNMQQLAR	0.863349879	2	2.489656
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.732696686**	**9.9E-20**	**2**
P18298	IIVDTYGGWGAHGGGAFSGK	0.926663647	2	5.277245
P18298	YLDEDTIYHLQPSGR	1.749557335	2	4.526864
P18418	**CALR Calreticulin**	**0.95903948**	**1.2E-05**	**19**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	0.876926036	3	5.909367
P18418	CKDDEFTHLYTLIVRPDNTYEVK	2.293685809	4	4.899911
P18418	DMHGDSEYNIMFGPDICGPGTK	1.046601436	2	5.851804
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1)	0.962226078	3	3.706678
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(10)	0.962226078	3	3.4793
P18418	EQFLDGDAWTNR	0.909026826	2	3.085924
P18418	FYGDQEK	1.017568825	1	1.956502
P18418	FYGDQEKDK	0.93799377	1	2.911206
P18418	GQTLVVQFTVK	1.194277785	2	3.328699
P18418	HEQNIDCGGGYVK	0.921790348	2	4.507418
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.115406725	3	4.041546
P18418	IDNSQVESGSLEDDWDFLPPK	0.890853927	2	5.156468
P18418	IDNSQVESGSLEDDWDFLPPKK	0.987252126	2	4.713474

P18418	IKDPDAAKPEDWDER	0.944460705	2	4.244777
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	0.961231565	3	4.973885
P18418	LFPGGLDQK	1.00026129	1	2.188573
P18418	QIDNPDYK	0.923942613	1	2.174539
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	0.998540368	3	5.726543
P18418	VHVIFNYK	1.484431731	1	2.323422
P18420	**PSA1 Proteasome subunit alpha type_1**	**1.124316938**	**0.01664**	**3**
P18420	AQPSQAADEPAEK	0.960592593	2	3.734879
P18420	ETLPAEQDLTTK	0.992326831	2	2.429116
P18420	NQYDNDVTVWSPQGR	1.14780841	2	3.650851
P18421	**PSB1 Proteasome subunit beta type_1**	**1.037594147**	**1.9E-05**	**2**
P18421	AGGSASAMLQPLLDNQVGFK	1.115015773	3	4.45752
P18421	GAVYSFDPVGSYQR	0.823615793	2	3.662261
P18445	**RL27A 60S ribosomal protein L27a**	**0.892730456**	**0.57801**	**2**
P18445	NGVAPIIDVVR	1.101428207	2	2.648369
P18445	NQSFCPTVNLDK	1.013053064	2	2.979494
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**1.018622392**	**0.40817**	**5**
P18484	FVNLFPEVK	0.905421408	2	2.75243
P18484	KGPSTVTDLEETKR	1.032215214	3	3.398864
P18484	NNGVLFENQLLQIGLK	1.156754227	2	3.264172
P18484	QLSNPQQEVQNIFK	0.703730574	2	3.386905
P18484	THIETVINALK	0.898491798	2	2.313368
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**0.86350277**	**0.1123**	**3**
P18596	DIVPGDIVEVAVGDKVPADLR	0.504793526	2	3.056824
P18596	SLPSVETLGCTSVICSDK	0.749778563	2	4.127248
P18596	VGEATETALTCLVEK	0.883899059	2	4.184026
P18757	**CGL Cystathionine gamma_lyase**	**0.809682328**	**9.9E-20**	**16**
P18757	AGDEVICMDEVYGGTNR	0.680028342	2	5.110285
P18757	AGDEVICMDEVYGGTNR+Oxidation(7)	0.509689372	2	3.875361
P18757	ATLGISDTLIR	0.954918672	2	3.614049
P18757	AVAALDGAK	1.220244815	2	2.354638
P18757	AVVLPISLATTFK	0.855714976	3	4.006486
P18757	FLQNSLGAVPSPFDCYLCCR	0.946640166	2	3.392103
P18757	GTLQHAQVFLK	0.792609627	2	2.757927
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.006064855	3	4.275409
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	0.893907457	4	4.960689
P18757	LLEAAITPQTK	0.68147935	2	3.876265
P18757	LSVGLEDEKDLLEDLGQALK	0.783488597	3	6.233472
P18757	LVWIETPTNPTLK	0.772869327	2	3.674063
P18757	QCTGCPGMVSFYIK	0.903825917	2	3.756606
P18757	QDSPGQSSGFVYSR	0.928918459	2	3.906448
P18757	RVASEFGLK	0.719484214	2	2.624012

P18757	VIYPGLPSHPQHELAK	0.67266255	2	3.89286
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.011075526**	**0.11384**	**11**
P18886	ATNLTVSAVR	1.079724702	2	3.174745
P18886	ELHAHLLAQDK	1.187461848	2	2.862761
P18886	LIFDGNEETLK	1.064796414	2	2.686887
P18886	QKLIFDGNEETLKK	0.990105301	2	2.400264
P18886	QYGQTVATYESCSTAAFK	1.060374512	2	4.113565
P18886	SEYNDQLTR	1.227518712	2	2.846058
P18886	TETIRPASIFTK	1.179963021	2	2.456772
P18886	TLQAGLLEPEVFHLNPSK	6.786883246	2	3.467111
P18886	TLSIDSIQFQR	1.102700803	2	3.167564
P18886	YILSDSSPVPEFPVAYLTSENR	1.098834805	2	5.204724
P18886	YLNAQKPLLDDSQFR	0.985431562	2	3.833109
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.026676397**	**1.9E-15**	**18**
P19112	AGGLATTGNEDILDIVPTEIHQK	0.943808783	3	6.205876
P19112	AGGTGEMTQLLNSLCTAIK	1.044832312	2	5.324265
P19112	AGGTGEMTQLLNSLCTAIK+Oxidation(6)	0.96937903	2	3.365777
P19112	APVIMGSTEDVQEFLEIYNK	1.670407225	2	5.043897
P19112	APVIMGSTEDVQEFLEIYNKDK	1.427919503	3	3.673533
P19112	DFDPAINEYIQR	0.913150887	2	3.826979
P19112	FPPDNSAPYGAR	1.027598157	2	2.599811
P19112	GNIYSINEGYAK	0.970721687	2	4.136878
P19112	KGNIYSINEGYAK	1.110916279	2	4.005682
P19112	KLDILSNDLVINMLK	1.006377105	2	5.296142
P19112	KTSANEPSEKDALQPGR	0.97999279	3	4.054168
P19112	LDILSNDLVINMLK	0.889759625	2	4.916448
P19112	LLYECNPIAYVMEK	1.549740441	2	4.132447
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.13299001	3	5.948756
P19112	SRPSLPLPQSR	0.89510283	2	3.412651
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.052608733	3	5.305854
P19112	TLVYGGIFLYPANK	0.992437339	2	3.763001
P19112	TSANEPSEKDALQPGR	0.974947088	2	3.707755
P19225	**CP270 Cytochrome P450 2C70**	**0.595596909**	**9.9E-20**	**9**
P19225	ACIGEGLAR	0.478304501	2	2.609738
P19225	ASLNLSNPQDFIDYFLIK	1.051187137	2	3.836382
P19225	EALIDRGEEFSDK	0.840310218	2	3.022806
P19225	IQEEVVYLLEALR	1.225558471	2	2.782215
P19225	KLPPGPTPLPIFGNILQVGVK	0.781914825	3	3.490888
P19225	KTTQDVEFR	0.63364385	2	2.329356
P19225	LPPGPTPLPIFGNILQVGVK	0.599441307	2	4.955725
P19225	SDYFMAFSAGRR+Oxidation(4)	1.03943125	1	1.960647
P19225	YIDFVPIPLPR	0.588749059	2	3.09975

P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**0.944161546**	**0.09007**	**4**
P19234	DIEEIIDELR	0.868241142	2	3.417425
P19234	DTPENNPDTPFDFTPENYER	1.237591223	2	4.255522
P19234	FCCEPAGGLTSLTEPPK	1.061039012	2	2.859828
P19234	YHIQVCTTTPCMLR	0.867814687	2	2.470977
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**0.894976625**	**6.5E-05**	**6**
P19468	CNQIANELCECPELLGSGFR	0.786301263	2	5.12767
P19468	EATSVLGEHQALCTITSFPR	0.729441736	2	3.726954
P19468	LDFLIPLSKVDENMK	0.80305042	2	2.465782
P19468	NTPSPFVETFPEDEEASK	0.896879777	2	4.421264
P19468	SLFFPDEAINK	0.775027692	2	2.62129
P19468	VQLLLNGGDVLETLQEK	0.924331746	2	4.816894
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**1.277722308**	**9.9E-20**	**7**
P19488	ANAIAWALAQIPQK	1.284237251	3	6.17779
P19488	EVINNPFYK	0.698080133	1	2.293064
P19488	FETFPTSVSKDELEK	0.505058659	2	3.871589
P19488	GHEVTVLKPSAYYVLDPK	1.243881502	3	4.398683
P19488	NWDPFYTEILGRPTTLAETMGK	1.052224494	2	4.819016
P19488	SDLFNALK	0.765694725	2	2.792472
P19488	TILDELVQR	0.852375046	2	3.154758
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**0.952646783**	**9.9E-20**	**8**
P19511	HVIQSISAQQEK	0.875761403	2	3.883437
P19511	HVIQSISAQQEKETIAK	1.092972903	3	4.015398
P19511	HYLFDVQR	0.887609474	2	2.448481
P19511	LDYHISVQDMMR	0.867951613	3	3.99332
P19511	LNEEKIAQLEEIK	0.838744386	2	2.691797
P19511	RKEGEHMINWVEK	0.587053537	2	2.522641
P19511	YGASIGEFIDK	1.186303014	2	2.91781
P19511	YGASIGEFIDKLNEEK	1.013774783	2	3.603116
P19643	**AOFB Amine oxidase [flavin_containing] B**	**0.941430173**	**0.13179**	**11**
P19643	FIGGSGQVSER	0.955520577	2	3.213182
P19643	IISTTNGGQER	1.024532476	2	2.826758
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.072037235	3	5.007388
P19643	KFIGGSGQVSER	0.970871055	2	2.957022
P19643	LERPVIHIDQTGENVVVK	0.890881428	3	5.090734
P19643	TLNHEIYEAK	0.854061813	2	2.991459
P19643	TMDEMGQEIPSDAPWK	0.840378243	2	3.219276
P19643	VLNSQEALQPVHYEEK	0.83411875	2	4.567133
P19643	YVDLGGSYVGPTQNR	0.96487515	2	4.191937
P19643	YVISAIPPVLGMK	0.838568882	2	3.154932
P19643	YVISAIPPVLGMK+Oxidation(11)	0.828698859	2	2.445378

P19686	**GCYA3 Guanylate cyclase soluble subunit alpha_3**	**0.838367506**	**0.00098**	**2**
P19686	DLAILQLGNGIR	0.867752991	2	2.707774
P19686	MMELSNEVMSPHGEPIK+Oxidation(8)	0.813308089	2	2.725073
P19804	**NDKB Nucleoside diphosphate kinase B**	**0.903082203**	**0.05815**	**8**
P19804	DRPFFPGLVK	0.847305671	2	2.425309
P19804	EIGLWFKPEELIDYK	0.960118634	2	3.92629
P19804	GDFCIQVGR	0.924380689	2	3.35049
P19804	NIIHGSDSVESAEK	0.906732098	1	3.903108
P19804	TFIAIKPDGVQR	1.037262423	2	2.888211
P19804	VMLGETNPADSKPGTIR	1.062651856	2	4.021312
P19804	VMLGETNPADSKPGTIR+Oxidation(1)	0.875613042	2	4.237875
P19804	YMNSGPVVAMVWEGLNVVK	1.237466133	2	4.930645
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.441047372**	**3.6E-08**	**2**
P19944	AAGVNVEPFWPGLFAK	3.437601421	2	2.75832
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.041655493	4	6.738688
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.597441307**	**9.9E-20**	**9**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	1.169334773	2	5.7766
P19945	AGAIAPCEVTVPAQNTGLGPEK	1.025165892	3	4.389659
P19945	CFIVGADNVGSK	0.99406959	2	3.240243
P19945	GHLENNPALEK	0.955102387	2	3.544275
P19945	GNVGFVFTK	1.613631793	2	2.714267
P19945	GTIEILSDVQLIK	1.184123092	2	3.061765
P19945	IIQLLDDYPK	0.848457658	2	3.829477
P19945	TSFFQALGITTK	1.265331847	2	3.998346
P19945	VLALSVETDYTFPLAEK	1.368363159	2	2.458873
P20059	**HEMO Hemopexin**	**0.987369074**	**0.99868**	**6**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	0.965482975	2	4.417696
P20059	FNPVTGEVPPR	1.015890448	2	2.458191
P20059	GECQSEGVLFFQGNR	0.920199081	2	3.786537
P20059	GGNNLVSGYPK	1.046497564	2	2.37534
P20059	LFQEEFPGIPYPPDAAVECHR	0.980846533	3	3.653296
P20059	SGAQATWAELSWPHEK	0.857975477	3	3.481474
P20069	**MPPA Mitochondrial_processing peptidase subunit alpha**	**1.01716962**	**0.76833**	**2**
P20069	HGGICDCQTSR	1.191303395	2	2.809563
P20069	LTDEEIEMTR	0.857886455	2	2.948157
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**0.738927082**	**9.9E-20**	**8**
P20070	DILLRPELEELR	0.751070535	2	2.555241
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	0.955631831	3	5.77773
P20070	LIDKEIISHDTR	0.747340137	3	3.510535
P20070	MSQYLENMNIGDTIEFR	1.07326684	2	3.922734
P20070	SSPAITLENPDIK	0.85956318	2	4.063457

P20070	SSPAITLENPDIKYPLR	0.965527703	2	3.401949
P20070	SVGMIAGGTGITPMLQVIR	0.924397418	2	4.375447
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(3)	0.826046401	2	2.445809
P20280	**RL21 60S ribosomal protein L21**	**0.961602269**	**0.19972**	**3**
P20280	KGDIVDIK	1.027625432	1	1.902305
P20280	TNGKEPELLEPIPYEFMA	0.711100166	2	2.941762
P20280	VYNVTQHAVGIIVNK	1.01768805	2	4.299368
P20673	**ARLY Argininosuccinate lyase**	**0.842978524**	**9.9E-20**	**15**
P20673	AEAECEVLFPGYTHLQR	0.993590521	2	4.250517
P20673	AEMQQILQGLDK	0.867261701	2	3.796751
P20673	AEMQQILQGLDK+Oxidation(2)	0.693965659	2	3.152582
P20673	EFNFVQLSDAYSTGSSLMPQK	0.865312135	2	5.648998
P20673	FNSSIAYDR	1.256558156	2	2.594378
P20673	HLWNVDLQGSK	0.821375207	1	3.219474
P20673	INVLPLGSGAIAGNPLGVDR	0.820432432	2	4.918809
P20673	KNPDSLELIR	0.852787892	2	2.437332
P20673	LKELIGEAAGK	0.817366221	2	2.816648
P20673	LYPNDEDIHTANER	0.809803777	2	3.830434
P20673	MAEDLILYGTK	0.896095925	2	3.499142
P20673	MAEDLILYGTK+Oxidation(0)	0.767304362	2	2.462548
P20673	NDQVVTDLR	0.852167289	2	3.438023
P20673	SRNDQVVTDLR	0.806868009	2	2.774558
P20673	VAEEWAQGIFK	1.576295927	2	3.292243
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**0.94662274**	**0.93803**	**3**
P20788	EIDQEAAVEVSQLR	1.078298133	2	4.344078
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	0.89714199	3	4.560709
P20788	SGPFAPVLSATSR	0.960854883	2	2.951125
P20801	**TNNC2 Troponin C_ skeletal muscle**	**0.737540365**	**0.04414**	**3**
P20801	GKSEEELAECFR	1.263776074	2	3.045792
P20801	NADGYIDAEELAEIFR	0.535053775	2	4.487903
P20801	SEEELAECFR	0.589020119	2	2.834992
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.143357386**	**0.46952**	**3**
P20814	FDYEDKDFLNLIEK	1.144811358	3	3.6812
P20814	GTAVLTSLTSVLHDSK	1.101231286	2	3.312654
P20814	IKEHEESLDVSNPR	1.099192945	3	3.851848
P20817	**CP4AE Cytochrome P450 4A14**	**0.52264498**	**9.9E-20**	**6**
P20817	ACQIAHEHTDGVIK	0.296858334	2	3.812618
P20817	AQLQNEEELQK	0.346712437	2	3.390829
P20817	AVEDLNNLTFFR	0.579757762	2	3.261478
P20817	EFQQVLTWVEK	0.434667249	2	2.708119
P20817	MRKAQLQNEEELQK+Oxidation(0)	0.692493415	2	2.911014
P20817	VLLYDPDYVK	0.287884804	2	2.830228

P20852	**CP2A5 Cytochrome P450 2A5**	**0.85740009**	**0.00917**	**2**
P20852	DFIDSFLIR	1.395241817	2	2.503233
P20852	EALVDQAEEFSGR	0.85214124	2	3.405679
P21213	**HUTH Histidine ammonia_lyase**	**0.829715958**	**0.01547**	**10**
P21213	DIITTELNSATDNPMVFASR	1.15414476	2	2.984238
P21213	GETISGGNFHGEYPAK	0.815493044	2	3.872245
P21213	LQELQVNLVR	0.810773738	2	3.047903
P21213	NKPDNGGFTSVDEVR	0.843210639	2	3.415476
P21213	SHSSGVGKPLSPER	0.796920629	2	4.093087
P21213	SLLDSDHHPSEIAESHR	0.800734836	3	4.532636
P21213	TVVYGITTGFGK	0.967124898	2	2.900258
P21213	VQDAYTLR	0.677398754	2	2.382204
P21213	VWEVAAPYIEK	0.871412941	2	2.363071
P21213	YIALDGDSLSTEDLVNLGK	0.808782758	2	4.672546
P21396	**AOFA Amine oxidase [flavin_containing] A**	**0.867248702**	**0.05422**	**6**
P21396	DVPAIEITHTFLER	0.970815807	2	3.175891
P21396	INVLVLEAR	1.094981439	2	3.143784
P21396	KDIWVEEPESK	0.938635251	2	3.257481
P21396	VLGSQEALYPVHYEEK	0.816898874	2	3.902416
P21396	WVDVGGAYVGPTQNR	0.962058379	2	4.235851
P21396	YVISAIPPILTAK	0.939454263	2	2.539017
P21531	**RL3 60S ribosomal protein L3**	**1.175997285**	**0.00067**	**6**
P21531	AHLMEIQVNGGTVAEK	1.443996622	2	3.868234
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	1.139981992	3	5.461251
P21531	HGSLGFLPR	1.224444923	2	2.690915
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.136221021	2	4.055512
P21531	NNASTDYDLSDK	0.993381183	2	3.308354
P21531	TVFAEHISDECK	1.120368017	2	3.121855
P21533	**RL6 60S ribosomal protein L6**	**1.115553792**	**0.91989**	**6**
P21533	HQEGEIFDTEK	1.081895339	2	3.254101
P21533	HQEGEIFDTEKEK	1.073744802	2	3.92587
P21533	HQEGEIFDTEKEKYEITEQR	1.054360904	3	3.790874
P21533	QLGSGLLLVTGPLALNR	1.131481867	2	4.894071
P21533	SSITPGTVLIILTGR	1.105406443	2	4.068552
P21533	YYPTEDVPR	1.020774987	1	2.097651
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.337138065**	**3.6E-07**	**6**
P21571	FEVLDKPQS	1.090521007	2	3.110434
P21571	GEMDKFPTFNFEDPK	1.270089397	3	3.706997
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	1.215656329	3	3.425504
P21571	LASGGPVDTGPEYQQEVDR	1.349831684	2	5.132745
P21571	LASGGPVDTGPEYQQEVDRELFK	1.048672708	2	2.481417
P21571	RLASGGPVDTGPEYQQEVDR	1.006861512	3	4.111584

P21643	**T23O Tryptophan 2_3_dioxygenase**	**0.991106726**	**0.68465**	**2**
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**0.740688706**	**9.9E-20**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	0.80518205	3	5.876086
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22)	0.63733672	3	4.064589
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**0.95183037**	**2.4E-14**	**7**
P21913	CGPMVLDALIKIK	0.874757754	2	2.420953
P21913	CHTIMNCTQTCPK	0.670774102	2	4.29317
P21913	CHTIMNCTQTCPK+Oxidation(4)	0.932675017	2	3.799774
P21913	IKNEIDSTLTFR	0.958531193	2	2.441281
P21913	LQDPFSLYR	1.254499543	2	2.600857
P21913	NEIDSTLTFR	0.907085132	2	2.356488
P21913	RIDTDLGK	0.921995945	2	2.542453
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.08957124**	**9.9E-20**	**4**
P21981	CDLEIQANGR	1.029108506	2	3.265766
P21981	DLYLENPEIK	0.938330824	2	2.698296
P21981	SEGTYCCGPVSVR	1.199598312	2	3.559674
P21981	YSGCLTESNLIK	1.456864173	2	3.056011
P22734	**COMT Catechol O_methyltransferase**	**1.030519304**	**0.82543**	**12**
P22734	AIYQGPSSPDKS	0.987941154	2	2.976692
P22734	EWAMNVGDAK	1.164350259	1	2.622914
P22734	GQIMDAVIR	0.997342689	2	2.33831
P22734	GQIMDAVIR+Oxidation(3)	0.748888784	2	2.549821
P22734	GTVLLADNVIVPGTPDFLAYVR	1.056670286	3	4.706006
P22734	KGTVLLADNVIVPGTPDFLAYVR	1.108574561	2	4.686999
P22734	KYDVDTLDMVFLDHWK	1.127852706	3	4.872995
P22734	VTILNGASQDLIPQLK	0.796274646	2	4.35623
P22734	VVDGLEK	0.841398088	2	2.439012
P22734	YDVDTLDMVFLDHWK	0.954396207	3	4.28956
P22734	YLPDTLLLEK	0.798524498	1	2.671151
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.075523575	3	5.968641
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.781909139**	**9.9E-20**	**4**
P22789	EEDLILLTYPK	1.678736248	2	2.32095
P22789	ETLQNVCNK	1.781169086	1	2.278391
P22789	KLEPDELDLVLK	2.044622592	3	3.908028
P22789	NHFTVAQAEAFDK	1.869986101	2	3.714982
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**1.065604966**	**9.9E-20**	**19**
P22791	ASLDMFNK	0.973301164	2	2.900562
P22791	ASLDMFNKK	1.003085282	2	2.516715
P22791	GLKLEETYTNK	1.125191204	2	2.99163
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.143328538	3	6.625047
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3)	0.874049364	3	5.792192

P22791	IGAFSYGSGLAASFFSFR	1.170793095	2	3.081395
P22791	LEETYTNK	1.009548069	2	2.876606
P22791	LEETYTNKDVDK	1.0557844	2	4.315097
P22791	LEVGTETIIDK	0.936236662	2	3.730953
P22791	LMFNDFLSSSSDK	1.56228794	2	4.133887
P22791	LMFNDFLSSSSDK+Oxidation(1)	0.986983997	2	4.027191
P22791	LVSSVSDLPK	1.016437417	2	3.617191
P22791	MGFCSVQEDINSLCLTVVQR	1.22843942	2	3.115784
P22791	MSPEEFTEIMNQR	0.999979596	2	4.830764
P22791	MSPEEFTEIMNQR+Oxidation(0)	0.914100299	2	4.046988
P22791	MSPEEFTEIMNQR+Oxidation(9)	0.896488743	2	3.320335
P22791	TKLPWDAVGR	0.928454916	3	4.027096
P22791	VNFSPPGDTSNLFPGTWYLER	0.96810801	2	5.051207
P22791	YTVGLGQTR	0.952979046	2	3.297619
P22985	**XDH Xanthine dehydrogenase/oxidase**	**0.960802667**	**4.5E-06**	**8**
P22985	DEVTCVGHIIGAVVADTPEHAQR	0.692096662	3	3.67183
P22985	ITSIDTSEAK	1.010387413	1	1.901069
P22985	LDPTFASATLLFQK	1.287037892	2	3.834048
P22985	NQPEPTVEEIENAFQGNLCR	0.655356751	2	4.903424
P22985	QLFQLDSPATPEK	0.946909264	2	3.002655
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.061547126	3	5.622664
P22985	TGTVVALEVAHFSNGGNTEDLSR	1.194941201	3	4.899419
P22985	TNLPSNTAFR	0.673482069	1	2.074683
P23358	**RL12 60S ribosomal protein L12**	**1.143974367**	**9.9E-20**	**5**
P23358	CTGGEVGATSALAPK	0.924026681	2	3.826294
P23358	EILGTAQSVGCNVDGR	0.889631679	2	4.811029
P23358	HNGNITFDEIVNIAR	1.076265132	2	4.095088
P23358	HPHDIIDDINSGAVECPAS	1.229581707	2	4.104812
P23358	QAQIEVVPSASALIIK	1.854347379	2	3.920141
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.82745496**	**9.9E-20**	**8**
P23457	ALDGLNR	1.163426813	2	2.438368
P23457	ELTQVFEFQLASEDMK	1.399436368	2	3.493985
P23457	HFDSAYLYEVEEEVGQAIR	2.2898546	2	5.92174
P23457	MLDYCK	1.098640874	1	1.912286
P23457	SIGVSNFNCR	1.196585876	2	3.468887
P23457	SPVLLDDPVLCAIAK	4.566406681	2	4.037699
P23457	VALNDGNFIPVLGFGTTVPEK	3.262043029	2	4.853246
P23457	YFDDHPNHPFTDE	2.392578018	2	4.194535
P23514	**COPB Coatomer subunit beta**	**1.369201902**	**0.00115**	**5**
P23514	EAGELKPEEEITVGPVQK	1.047962736	2	4.515505
P23514	NFENLIPDAPELIHDFLVNEK	1.002150945	3	4.453954
P23514	TNNVSEHEDTDKYR	1.42775313	2	4.329954
P23514	VLQDLVMDILR	1.063904541	2	3.000511

P23514	YEAAGTLVTLSSAPTAIK	1.359938665	2	4.795408
P23591	**FCL GDP_L_fucose synthase**	**1.109595578**	**0.02753**	**2**
P23591	DADLTDAAQTQALFQK	1.004508123	2	3.370487
P23591	VVADGAGLPGEEWVFVSSK	1.112246734	2	3.738948
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.863503665**	**3.3E-11**	**7**
P23965	ALQLGTLFPPAEALK	0.802074425	2	4.767969
P23965	DNYVNTIGHR	0.870467441	2	2.761271
P23965	GVILTSERPGIFSAGLDLMEMYGR	0.902055424	3	5.552876
P23965	QREADIQNFTSFISR	0.981167434	2	2.664509
P23965	SLHVYLEK	0.787947577	2	2.317596
P23965	VGLVDEVVPEDQVHSK	0.860537966	2	4.537124
P23965	WFTIPDHSR	0.904770747	2	3.175083
P24049	**RL17 60S ribosomal protein L17**	**1.032803697**	**1.1E-16**	**3**
P24049	EQIVPKPEEEVAQK	1.038684942	2	3.656812
P24049	GLDVDSLVIEHIQVNK	1.048673762	2	4.557854
P24049	YSLDPENPTK	0.738684966	1	2.731305
P24090	**FETUA Alpha_2_HS_glycoprotein**	**1.123560192**	**0.14542**	**6**
P24090	ELACDDPETEHVALIAVDYLNK	1.383368237	2	4.732122
P24090	HAFSPVASVESASGEVLHSPK	1.329784628	3	5.555621
P24090	LGGEEVSVACK	0.996748354	2	3.379126
P24090	QQAEHAVEGDCDFHILK	1.249298671	3	3.350752
P24090	VGQPGDAGAAGPVAPLCPGR	1.009612192	2	4.789919
P24090	VLHAQCHSTPDSAEDVRK	0.785191179	3	3.469405
P24268	**CATD Cathepsin D**	**1.296919618**	**6.4E-14**	**3**
P24268	AIGAVPLIQGEYMIPCEK	1.097568084	2	3.126006
P24268	DPTGQPGGELMLGGTDSR	1.224078458	2	3.821466
P24268	LGGQNYELHPEK	1.373320329	2	2.992856
P24329	**THTR Thiosulfate sulfurtransferase**	**0.916339206**	**9.9E-20**	**12**
P24329	EGHPVTSEPSRPEPAVFK	0.759065762	2	4.902783
P24329	FQLVDSR	0.899057466	2	2.615088
P24329	GSVNVPFMNFLTEDGFEK	3.101697705	2	3.526677
P24329	HVPGASFFDIEECR	1.09689438	2	3.435706
P24329	KVDLSQPLIATCR	0.923716869	2	4.1364
P24329	RFQLVDSR	0.961685109	2	2.378201
P24329	TVSVLNGGFR	0.919201469	2	3.164131
P24329	TYEQVLENLQSK	0.848948547	2	5.030221
P24329	VDLSQPLIATCR	0.965902056	2	3.835733
P24329	VLDASWYSPGTR	0.881672051	2	3.726613
P24329	WLAESIR	0.830756095	2	2.3667
P24329	YLGTQPEPDAVGLDSGHIR	0.917893434	3	4.784273
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**1.042697663**	**0.38104**	**8**
P24368	DKPLKDVIIVDCGK	0.950951051	2	3.778208

P24368	DTNGSQFFITTVK	0.896030354	2	4.035002
P24368	HYGPGWVSMANAGK	0.976869997	2	3.272851
P24368	IEVEKPFAIAK	0.952490733	2	3.182014
P24368	IEVEKPFAIAKE	0.704033162	2	3.05273
P24368	TVDNFVALATGEK	1.103626123	2	3.548785
P24368	VLEGMDVVR	0.992121084	2	2.676821
P24368	VYFDFQIGDEPVGR	0.957522286	2	3.809759
P24457	**CP2DB Cytochrome P450 2D11**	**0.957532224**	**0.45646**	**2**
P24457	RFSVSTLR	0.9398215	2	2.827209
P24457	SLEEWVTK	1.192843165	2	2.65561
P24470	**CP2CN Cytochrome P450 2C23**	**0.566110907**	**9.9E-20**	**7**
P24470	ACVGESLAR	0.390516483	2	2.462858
P24470	DLDIKPITTGIINLPPPYK	0.434274836	3	3.783337
P24470	EALLQQGDEFLGR	0.474776056	2	2.554503
P24470	GYGLIFSNGER	0.538130366	2	3.616805
P24470	IEEEKDNLK	0.516254355	1	2.924379
P24470	TFLNLMDLLNK	0.495313776	2	3.605686
P24470	YITLLPSSLPHAVVQDTK	0.43431959	2	3.168617
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.98796306**	**9.9E-20**	**7**
P24473	AGMATAQAQHLLNK	1.097260969	2	3.884553
P24473	DEDITESQNILSAAEK	1.006856066	2	5.431086
P24473	DSGNQPPAMVPHK	0.783996618	2	2.32207
P24473	FLTAVSMEQPEMLEK	0.808666122	2	3.986013
P24473	IWSRDEDITESQNILSAAEK	0.95766211	3	3.432733
P24473	MELLAYLLGEK	1.562497765	2	3.946337
P24473	YGAFGLPTTVAHVDGK	1.253367472	2	3.820304
P25093	**FAAA Fumarylacetoacetase**	**0.948790216**	**2.4E-14**	**14**
P25093	AIDVGQGQTR	0.950105643	2	3.544541
P25093	ASLQNLLSASQAQLR	1.132864375	2	4.662778
P25093	ASLQNLLSASQAQLRDDK	1.191048477	2	3.00562
P25093	ASSVVVSGTPIR	1.063224346	2	3.444203
P25093	DIQQWEYVPLGPFLGK	0.945286738	2	4.641189
P25093	FGEPIPISK	1.048965063	2	2.8973
P25093	GEGMSQAATICR	0.925257364	2	3.610839
P25093	GEGMSQAATICR+Oxidation(3)	0.89982806	2	2.902142
P25093	GKENALLPNWLHLPVGYHGR	2.422531843	3	3.332737
P25093	HLFTGPVLSK	0.91216727	1	2.471161
P25093	HQHVFDETTLNSFMGLGQAAWK	1.153047519	2	5.510929
P25093	IGVAIGDQILDLSVIK	1.102464401	2	5.532544
P25093	TFLLDGDEVIITGHCQGDGYR	0.982762183	2	5.016442
P25093	VGFGQCAGK	1.10314418	1	1.938651
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.086651147**	**9.9E-20**	**6**
P25113	ALPFWNEEIVPQIK	1.671620458	2	3.885508

P25113	FSGWYDADLSPAGHEEAK	1.102499086	2	4.730966
P25113	HGESAWNLENR	0.991124265	2	3.787521
P25113	SYDVPPPPMEPDHPFYSNISK	1.349003442	2	4.296752
P25113	YADLTEDQLPSCESLK	1.085928475	2	5.347072
P25113	YADLTEDQLPSCESLKDTIAR	1.08169221	2	5.011707
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.078126216**	**9.9E-20**	**13**
P25235	EDQVIQLMNTIFSK	1.194259566	2	3.260694
P25235	EETVLATVQALHTASHLSQQADLR	1.035548517	3	5.238063
P25235	FELDTSER	0.998888544	1	2.006508
P25235	FPEEEAPSTVLSQNLFTPK	0.719956622	2	3.908512
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.057319598	2	4.62573
P25235	LQVSSVLSQPLAQAAVK	1.126846099	2	4.861084
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.208953185	3	5.428406
P25235	NFESLSEAFSVASAAAALSQNR	1.138683124	3	4.314542
P25235	NIVEEIEDLVAR	0.927653156	3	4.727786
P25235	NPILWNVADVVIK	1.565856292	2	2.375684
P25235	TGQEVVFVAEPDNK	1.661212141	2	3.878228
P25235	YHVPVVVVPEGSASDTQEQAILR	1.27489091	3	5.422436
P25235	YIANTVELR	0.976456489	2	2.660456
P25318	**chain**	**0.830551839**	**0.0758**	**2**
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.831396322		2.549597
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.831396322		2.656323
P25409	**ALAT1 Alanine aminotransferase 1**	**2.839443038**	**9.9E-20**	**3**
P25409	AWALDIAELR	2.741784653	2	2.566194
P25409	LTEQVFNEAPGIR	2.836109535	2	3.577941
P25409	VLCVINPGNPTGQVQTR	11.34879176	2	4.273516
P26039	**TLN1 Talin_1**	**1.095272959**	**9.9E-20**	**14**
P26039	AGALQCSPSDVYTK	0.831196522	2	2.631141
P26039	AQEACGPLEMDSALSVVQNLEK	0.895914376	2	3.791391
P26039	ASAGPQPLLVQSCK	0.98680767	2	2.53924
P26039	AVAEQIPLLVQGVR	0.830115363	2	3.405003
P26039	EAAEGLRMATNAAAQNAIKK	0.899195367	2	2.80724
P26039	GVGAAATAVTQALNELLQHVK	0.847512123	3	4.448515
P26039	LGAASLGAEDPETQVVLINAVK	1.024101986	2	3.583176
P26039	LLGEIAQGNENYAGIAAR	0.942220518	2	3.791129
P26039	LNEAAAGLNQAATELVQASR	0.80548062	2	5.264231
P26039	SNTSPEELGPLANQLTSDYGR	0.98806422	2	3.966097
P26039	VGAIPANALDDGQWSQGLISAAR	0.732298616	2	4.508985
P26039	VGDDPAVWQLK	0.805918064	2	3.131146
P26039	VLVQNAAGSQEK	0.819643934	2	2.837111

P26039	VVAPTISSPVCQEQLVEAGR	0.757930693	2	4.751945
P26043	**RADI Radixin**	**0.929838264**	**1.6E-07**	**10**
P26043	AFAAQEDLEK	0.978590635	2	2.364146
P26043	ALELEQER	0.87723358	1	1.95868
P26043	FFPEDVSEELIQEITQR	0.88343833	3	4.111061
P26043	KKEEEATEWQHK	1.448011863	3	4.274758
P26043	KTQNDVLHAENVK	0.85291472	2	4.926212
P26043	NQEQLAAELAEFTAK	0.888384461	2	4.915983
P26043	QLQALSSELAQAR	0.893988231	2	3.362348
P26043	RKPDTIEVQQMK	0.775346622	2	3.707477
P26043	RKPDTIEVQQMK+Oxidation(10)	1.043734275	2	2.481065
P26043	TQNDVLHAENVK	0.946035398	2	3.586342
P26231	**CTNA1 Catenin alpha_1**	**1.272413151**	**0.02017**	**7**
P26231	AVMDHVSDSFLETNVPLLVLIEAAK	0.861733679	3	3.645379
P26231	IAEQVASFQEEK	1.560483962	2	2.650308
P26231	LIEVANLACSISNNEEGVK	0.922232806	2	3.859952
P26231	LLEPLVTQVTTLVNTNSK	0.9256918	2	3.725083
P26231	QIIVDPLSFSEER	0.871428027	2	2.48735
P26231	SAAGEFADDPCSSVK	0.964442744	2	4.018402
P26231	TIADHCPDSACK	0.185626318	2	3.07811
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**1.084405253**	**0.01005**	**7**
P26284	AILAELTGR	1.166519532	2	2.625057
P26284	EEIQEVRSK	0.454121802	1	1.96172
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	0.977507631	3	6.477973
P26284	LEEGPPVTTVLTR	0.925553922	2	3.605208
P26284	RGDFIPGLR	1.076676011	2	2.703109
P26284	TREEIQEVR	1.144809684	2	2.887303
P26284	VDGMDILCVR	0.911587861	2	3.258418
P26453	**BASI Basigin**	**1.053346044**	**5.8E-10**	**6**
P26453	GNINVEGPPR	1.062649968	2	3.349427
P26453	RKPDQTLDEDDPGAAPLK	1.145303686	3	3.755076
P26453	SEASHPPVDEWVWFK	1.108738272	3	3.895804
P26453	SEHASEGEFVK	1.08351109	2	3.006014
P26453	SGEYSCIFLPEPVGR	1.184842232	2	3.158765
P26453	VLQEDTLPDLQMK	0.853391415	2	4.106281
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**1.086190147**	**9.9E-20**	**6**
P26772	GGEIQPVSVK	0.915821217	2	3.378433
P26772	GGIMLPEK+Oxidation(3)	0.886507231	2	2.462898
P26772	GKGGEIQPVSVK	0.886468445	2	3.086954
P26772	VLLPEYGGTK	0.966840888	1	2.106637
P26772	VLQATVVAVGSGGK	0.853911526	2	5.086327
P26772	VVLDDKDYFLFR	1.086388229	3	3.629462

P27139	**CAH2 Carbonic anhydrase 2**	**0.966355146**	**0.94867**	**2**
P27139	AVQHPDGLAVLGIFLK	1.060168842	2	3.225291
P27139	IGPASQGLQK	0.785728652	2	3.130773
P27321	**ICAL Calpastatin**	**0.872731758**	**3.9E-07**	**3**
P27321	KGSDEVTASSAATGTSPR	0.757823561	2	5.018596
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	0.898691624	3	4.317224
P27321	SQSSEPPVIHEK	0.883419123	2	3.173701
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.729428645**	**9.9E-20**	**5**
P27364	AVLAANGSILK	0.620009809	2	2.738403
P27364	ETILNDREEEHR	0.566984695	2	2.73543
P27364	GDIVDAQFLR	0.680284899	2	3.126318
P27364	NGGTFHTCALR	0.76352499	2	2.573438
P27364	QTILDVNVK	0.594004425	1	2.178942
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**0.918194051**	**9.9E-20**	**6**
P27605	DLNHVCVISESGK	0.759700727	2	3.508493
P27605	FFADLLDYIK	0.783834801	2	3.455498
P27605	NVLIVEDIIDTGK	0.895052209	2	3.797857
P27605	SVGYRPDFVGFEIPDK	0.748314906	3	3.572189
P27605	SYCNDQSTGDIK	0.772999889	2	3.959823
P27605	VIGGDDLSTLTGK	1.547164028	2	3.18914
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**0.896947624**	**9.9E-20**	**17**
P27653	ASQAPSSFQLLYDLK	1.612934965	2	4.304605
P27653	AYTEEDLDLVEK	0.956665279	2	2.506304
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	0.976607503	3	3.778933
P27653	IFHELTQTDK	0.834015383	2	2.848661
P27653	ITIGQAPTEK	0.847840507	2	2.478407
P27653	IYGADDIELLPEAQNK	1.196019323	2	5.256581
P27653	KITIGQAPTEK	0.899931108	2	3.180773
P27653	KVVGDVAYDEAK	0.900082348	2	3.819021
P27653	LDIDPETITWQR	0.973372621	2	3.634663
P27653	MHGGGPTVTAGLPLPK+Oxidation(0)	0.751167621	2	3.622405
P27653	QGFGNLPICMAK	0.777365211	2	3.272857
P27653	TADLDKEVNKGDILVVATGQPEMVK	1.042572355	3	4.162988
P27653	TDPAALTDDEINR	0.890257477	2	4.335786
P27653	THLSLSHNPEQK	0.781364178	2	3.818975
P27653	VVGDVAYDEAK	0.757001327	2	3.356091
P27653	YSGLQPHVVVLVATVR	1.095653994	3	3.306831
P27653	YVVVTGITPTPLGEGK	0.900951584	2	4.213294
P27657	**LIPP Pancreatic triacylglycerol lipase**	**0.507067687**	**0.03487**	**2**
P27657	ATYTQATQNVR	0.330026655	2	2.498478
P27657	ITGLDAAEPYFQGTPEEVR	0.534083446	2	2.510916

P27661	**H2AX Histone H2A.x**	**0.811734458**	**0.0051**	**3**
P27661	AGLQFPVGR	0.943603573	2	3.232769
P27661	HLQLAIR	0.898633237	2	2.606043
P27661	LLGGVTIAQGGVLPNIQAVLLPK	0.795035564	3	4.100216
P27867	**DHSO Sorbitol dehydrogenase**	**0.841593799**	**9.9E-20**	**13**
P27867	AMGASQVVVIDLSASR	0.982448744	2	4.117572
P27867	AVEAFETAK	0.737699685	2	3.017348
P27867	EVGADFTIQVAK	0.818387223	2	2.64929
P27867	GENLSLVVHGPGDIR	0.78183454	3	3.80431
P27867	HSADFCYK	0.879559875	2	2.849999
P27867	IGDFVVK	0.851077334	2	2.543508
P27867	LENYPIPELGPNDVLLK	0.856554645	2	4.854634
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.445580709	2	4.725988
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0)	0.753241734	3	3.885855
P27867	TLNVKPLVTHR	0.809254524	2	3.171689
P27867	VAIEPGVPR	1.804454292	2	2.40722
P27867	VAIEPGVPREIDEFCKIGR	0.802940096	2	2.346937
P27867	VLVCGAGPIGIVTLLVAK	1.09227872	2	5.423267
P27952	**RS2 40S ribosomal protein S2**	**1.081133434**	**0.75856**	**5**
P27952	AEDKEWIPVTK	1.065372388	3	3.351241
P27952	AFVAIGDYNGHVGLGVK	1.222700823	2	4.068855
P27952	GCTATLGNFAK	1.046443205	2	2.80629
P27952	GTGIVSAPVPK	1.074099759	2	2.777031
P27952	TYSYLTPDLWK	0.929893587	2	2.592995
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**0.9577316**	**9.9E-20**	**25**
P28037	ADPLGLEAEK	0.740998059	2	2.537892
P28037	ANATEFGLASGVFTR	0.834976373	2	4.166287
P28037	AVQMGMSSVFFNK	0.976065806	2	2.86603
P28037	CPQSEEGATYEGIQK	6.761375896	2	4.593695
P28037	DLGEAALNEYLR	0.61059925	2	3.65357
P28037	ECEVLPDDTVSTLYNR	0.917679609	2	3.884767
P28037	EGHEVVGVFTIPDKDGK	0.760410244	2	4.851215
P28037	GNDKVPGAWTEACGQK	0.692337035	2	3.554529
P28037	GQALPEVVAK	0.743211391	2	2.522965
P28037	GSASSDLELTEAELATAEAVR	0.738264447	2	6.496266
P28037	GVVNILPGSGSLVGQR	0.754578199	2	4.847268
P28037	IGFTGSTEVGK	0.830625638	2	3.001848
P28037	ILPNVPEVEDSTDFFK	0.853713876	2	3.851798
P28037	INWDQPAEAIHNWIR	0.679464607	2	3.830847
P28037	IQGATIPINQARPNR	0.737596238	2	2.338132
P28037	KEGHEVVGVFTIPDKDGK	0.714822174	3	3.377346
P28037	KIGFTGSTEVGK	0.770697668	2	2.822243

P28037	KLVEYCQR	0.915205291	2	2.424565
P28037	LFVEESIHNQFVQK	0.742667032	2	4.41216
P28037	LIAEGTAPR	0.747452511	2	2.494098
P28037	LSDHPDVR	0.602017117	1	2.126725
P28037	NIQLEDGK	0.742042962	1	2.324163
P28037	TAACLAAGNTVVIKPAQVTPLTALK	0.829903432	3	4.181655
P28037	TDVAAPFGGFK	0.698442276	2	3.014616
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	0.787584431	2	5.165753
P28064	**PSB8 Proteasome subunit beta type_8**	**1.196124716**	**0.0193**	**3**
P28064	ASAGSYIATIR	1.091159372	2	2.871835
P28064	QDLSPEEAYDLAR	1.195489531	2	2.907834
P28064	VESTDVSDLLHK	1.338056938	2	2.391079
P28480	**TCPA T_complex protein 1 subunit alpha**	**1.031113174**	**0.92427**	**8**
P28480	AFHNEAQVNPER	0.918648807	2	3.47714
P28480	FATEAAITILR	0.986122662	2	2.725515
P28480	HGGYENAVHSGALDD	1.03659766	2	3.717347
P28480	ICDDELILIK	1.013908335	2	2.553008
P28480	LLEVEHPAAK	0.994775905	2	2.467425
P28480	SLLVIPNTLAVNAAQDSTDLVAK	0.964112296	2	4.153254
P28480	SQNVMAAASIANIVK	1.178899825	2	3.53311
P28480	YINENLIINTDELGR	1.056031653	2	4.68646
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**0.700509764**	**0.00625**	**3**
P28492	ATGLQTSDPR	0.585129922	2	2.446856
P28492	LSLNEEGIPHNPMVNAGAIVVSSLIK	0.822286217	3	4.755651
P28492	SNPDLWGVSLCTVDGQR	0.759861262	2	2.585394
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**0.838832515**	**9.9E-20**	**16**
P29147	AVLVTGCDSGFGFSLAK	0.713416358	2	5.554809
P29147	FGVEAFSDCLR	0.969897198	2	3.360998
P29147	GFLVFAGCLLK	1.113850394	2	3.253101
P29147	KMWDELPEVVR	0.986078753	2	2.486331
P29147	MANPARSPYCITK+Oxidation(0)	0.769736825	2	2.419892
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	2.042626456	3	4.856522
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0)	1.579203405	3	4.830182
P29147	MQVMTHFPGAISDK	1.34774363	2	3.575988
P29147	MQVMTHFPGAISDK+Oxidation(0)	0.967453592	2	2.789985
P29147	MQVMTHFPGAISDK+Oxidation(3)	0.967453592	2	2.969607
P29147	MWDELPEVVR	0.758621422	2	2.469376
P29147	MWDELPEVVR+Oxidation(0)	0.583075587	2	3.227258
P29147	TIQLNVCNSEEVEK	0.78786716	2	4.425793
P29147	VSVVEPGNFIAATSLYSPER	0.864945241	2	6.258769
P29147	VVNISSMLGR	0.797462028	2	3.755153
P29147	YEMHPLGVK	0.989020932	2	2.541778

P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.658606761**	**9.9E-20**	**8**
P29266	DLGLAQDSATSTK	0.635679804	2	3.853251
P29266	EAGEQVASSPADVAEK	0.623870605	2	4.755892
P29266	GSLLIDSSTIDPSVSK	0.643343792	2	4.462354
P29266	HGYPLILYDVFPDVCK	0.870824093	2	5.174333
P29266	KGSLLIDSSTIDPSVSK	0.787035098	2	4.369253
P29266	MGAVFMDAPVSGGVGAAR	0.736496601	2	4.601884
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0)	0.7108454	2	4.194208
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5)	0.7108454	2	3.241668
P29314	**RS9 40S ribosomal protein S9**	**1.047064079**	**0.15353**	**5**
P29314	IEDFLER	1.042784853	2	2.367025
P29314	KGQGGAGAGDDEEED	1.680426224	2	3.59923
P29314	LDYILGLK	1.108249789	2	2.655722
P29314	LFEGNALLR	1.03996786	2	2.967017
P29314	SRLDQELK	1.060605975	2	2.367792
P29315	**RINI Ribonuclease inhibitor**	**0.854193457**	**0.00268**	**5**
P29315	ASLQELDLGSNK	0.995644001	2	2.486231
P29315	LDDCGLTEVR	0.878383067	2	3.147821
P29315	LENCGITSANCK	0.906957289	2	3.021734
P29315	SAIQANPALTELSLR	0.989866265	2	4.202729
P29315	TNELGDAGVGLVLQGLQNPTCK	0.870603556	2	5.245348
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**0.827604827**	**0.00135**	**10**
P29410	AMVASGSELGK	0.89593243	2	2.628889
P29410	AMVASGSELGKK	0.756444655	2	2.626502
P29410	AVLLGPPGAGK	0.920338195	2	2.463969
P29410	EAMKDDITGEPLIR	1.689066461	2	2.434501
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.479239115	3	4.303236
P29410	LEAYHTQTTPLVEYYR	1.091029301	2	4.824097
P29410	LVSDEMVVELIEK	1.055561972	2	4.344147
P29410	NGFLLDGFPR	0.918336214	2	2.989437
P29410	NLETPSCK	0.821245972	1	2.011531
P29410	SYHEEFNPPK	1.135021018	3	3.319961
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**0.874145247**	**1.7E-12**	**4**
P29411	AYEAQTEPVLQYYQK	1.005113015	2	5.003166
P29411	EDDKPETVIK	0.69161679	2	2.602765
P29411	TVGIDDLTGEPLIQR	0.875265607	2	3.526627
P29411	VYNIEFNPPK	1.232713933	2	2.670184
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**1.187138434**	**0.49894**	**2**
P29419	ELAEAEDVSIFK	0.927445688	1	3.322429
P29419	YSALILGMAYGAK	1.189203635	2	3.441234
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**0.978576527**	**1.4E-06**	**2**

P30009	AEDGAAPSPSSETPK	0.78000016	2	3.614277
P30009	GEAAAERPGEAAVASSPSK	0.976660808	2	4.379532
P30276	**CCNB2 G2/mitotic_specific cyclin_B2**	**0.82724477**	**0.0419**	**2**
P30276	AVLEEIGNK	0.906655563	1	2.067325
P30276	FELGRPLPLHFLRR	0.686261777	2	2.473225
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**0.912127932**	**0.00075**	**2**
P30349	SLSNVIAHEISHSWTGNLVTNK	0.925679255	3	4.445697
P30349	SSALQWLTPEQTSGK	0.808738321	2	3.212433
P30427	**PLEC Plectin**	**0.853883907**	**0.01547**	**6**
P30427	AQVEQELTTLR	0.823691839	2	2.671062
P30427	LLDPEDVDVPQPDEK	0.805618658	2	3.320221
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0)	0.956967957	2	2.398796
P30427	SDQLTGLSLLPLSEK	0.858755053	2	2.842379
P30427	SQVEEELFSVR	1.57946168	2	2.342756
P30427	YLYGTGSVAGVYLPGSR	1.310530787	2	2.548097
P30713	**GSTT2 Glutathione S_transferase theta_2**	**0.802434938**	**9.9E-20**	**5**
P30713	AQVHEYLGWHADNIR	0.616672463	2	4.520831
P30713	GQHLSEQFSQVNCLK	0.807089691	2	4.767452
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.699737912	3	3.411608
P30713	VLGPLIGVQVPEEK	0.719178016	2	3.932847
P30713	YQVADHWYPADLQAR	0.640189849	2	4.563135
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**0.717258663**	**9.9E-20**	**9**
P30839	DILAAIAADLSK	0.618073212	2	2.672379
P30839	EKDILAAIAADLSK	0.691270832	2	3.696078
P30839	FDHILYTGNTAVGK	1.039072532	2	3.502771
P30839	HLTPVTLELGGK	0.747206859	2	2.926935
P30839	NVEEAINFINDR	1.352212913	2	3.958345
P30839	QRFDHILYTGNTAVGK	1.388255738	2	3.036983
P30839	VMQEEIFGPILPIVSVK	0.688409907	3	4.321095
P30839	VMQEEIFGPILPIVSVK+Oxidation(1)	0.681041994	2	4.660519
P30839	YIAPTILTDVDPNSK	0.791666663	2	4.326329
P30904	**MIF Macrophage migration inhibitory factor**	**0.889333852**	**0.11651**	**2**
P30904	LHISPDR	0.587056689	1	2.044309
P30904	LLCGLLSDR	0.918006319	2	2.545451
P31000	**VIME Vimentin**	**0.772417409**	**9.9E-20**	**14**
P31000	DGQVINETSQHHDDLE	0.786420128	2	3.242346
P31000	ETNLESLPLVDTHSK	0.746175207	2	2.628909
P31000	FADLSEAANR	1.040280145	2	2.734737
P31000	KLLEGEESR	0.777850428	2	2.663265
P31000	KVESLQEEIAFLK	0.762964671	2	3.768827
P31000	LGDLYEEEMR	0.632378327	2	2.365065
P31000	LLEGEESR	0.735464475	2	2.65074
P31000	NLQEAEEWYK	0.656801906	2	2.788474

P31000	QDVDNASLAR	0.696814398	2	2.536479
P31000	QVQSLTCEVDALK	0.751452216	2	3.32225
P31000	RQVDQLTNDK	0.485562149	2	2.661426
P31000	SLYSSSPGGAYVTR	1.023284234	2	2.379948
P31000	TNEKVELQELNDR	0.730197654	2	2.444677
P31000	VELQELNDR	0.600143187	2	2.715927
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**0.901210087**	**9.9E-20**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	0.870502955	2	6.045561
P31044	LYTLVLTDPDAPSR	1.071335246	2	4.438648
P31044	VDYGGVTVDELGK	0.852086559	2	4.49212
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.809024789	3	4.849732
P31044	YHLGAPVAGTCFQAEWDDSVPK	1.334561821	2	5.339462
P31044	YVWLVYEQEQPLNCDEPILSNK	1.00752023	2	5.233539
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**0.596396778**	**9.9E-20**	**17**
P31210	DELLTSLGK	0.50627741	2	2.58049
P31210	DIEALNK	0.434136487	1	2.473548
P31210	EEMKDIEALNK	0.72373088	2	3.369206
P31210	ENFQIFDFSLTK	0.814524814	2	3.191303
P31210	HIDGAYVYR	0.733745015	2	3.212218
P31210	IKENFQIFDFSLTK	0.923894803	2	3.900281
P31210	NEHEVGEAIR	0.616165557	2	3.092601
P31210	NPLWVNVSSPPLLK	0.870855045	2	4.308712
P31210	NPLWVNVSSPPLLKDELLTSLGK	0.729812711	3	4.685515
P31210	QLEVILNKPGLK	0.522757864	2	3.322124
P31210	REEIFYCGK	0.663634054	2	2.962653
P31210	SLGVSNFNR	0.601113186	2	2.583139
P31210	SNLCATWEALEACK	0.559406881	2	4.387854
P31210	SNLCATWEALEACKDAGLVK	0.587985257	2	4.710383
P31210	TAIDEGYR	0.694180565	2	2.615649
P31210	TQAQIVLR	0.651783184	2	3.086223
P31210	YKPVTNQVECHPYFTQTK	0.971393311	2	5.051595
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**0.931448372**	**8.2E-12**	**8**
P31399	ANVDKPGLVDDFK	0.931629021	2	3.520016
P31399	NCAQFVTGSQAR	0.982156778	2	4.753046
P31399	NMIPFDQMTIDDLNEVFPETK	0.856676467	2	4.98344
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(1)	0.919124583	2	4.069884
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(7)	1.003814379	2	3.937582
P31399	SWNETFHTR	0.949066013	2	2.606356
P31399	TIDWVSFVEIMPQNQK	1.629507704	3	3.514287
P31399	YTALVDAEEKEDVK	1.221230653	2	3.4593
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.028373061**	**0.62981**	**5**
P32089	FIHDQTSSNPK	1.014522565	1	3.601469

P32089	GLSSLLYGSIPK	1.133045683	2	3.065092
P32089	GTYQGLTATVLK	0.910197131	2	2.439975
P32089	SHGVLGLYR	0.971751651	1	2.097722
P32089	TQLQLDER	1.069624658	2	2.617077
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**0.966494512**	**0.51174**	**4**
P32198	ELEQQMQQILDDPSEPQPGEAK	0.999488091	2	4.372175
P32198	GDTNPNIPKPTR	0.97756986	2	2.493103
P32198	MTALAQDFAVNLGPK	0.893043815	2	3.257622
P32198	MTALAQDFAVNLGPK+Oxidation(0)	0.475946355	2	3.76634
P32232	**CBS Cystathionine beta_synthase**	**1.085576415**	**9.9E-20**	**8**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.332336754	3	5.924621
P32232	FDSPESHVGVAWR	1.001090945	2	3.468556
P32232	LKNEIPNSHILDQYR	1.088456427	3	3.4666
P32232	NASNPLAHYDDTAEEILQQCDGK	1.563261622	2	5.384356
P32232	SNDDDSFAFAR	1.426665526	2	3.369449
P32232	VDMLVASAGTGGTITGIAR	1.219047058	2	4.329044
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.565834958	3	4.195805
P32232	VRPSDEVCK	1.557849261	2	2.50546
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**0.947286759**	**9.9E-20**	**10**
P32551	AVAFQNPQTR	1.736076459	2	2.795251
P32551	AVAQGNLSSADVQAAK	0.938632697	2	4.782523
P32551	GNNTTSLLSQSVAK	1.073287751	2	4.215866
P32551	IIENLHDVAYK	0.991766812	2	3.696033
P32551	LPNGLVIASLENYAPLSR	0.960920164	3	3.429788
P32551	RGNNTTSLLSQSVAK	0.827365499	2	2.962132
P32551	SMTASGNLGHTPFLDEL	1.192313398	2	3.16481
P32551	SMTASGNLGHTPFLDEL+Oxidation(1)	0.846990844	2	3.374429
P32551	TSAPGGVPLQPQELEFTK	0.924636043	2	3.575655
P32551	YENYNYLGTSHLLR	1.704388965	2	4.000422
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.047379965**	**9.9E-20**	**16**
P32755	AFEEEQALR	1.291062299	2	3.364861
P32755	DIAFEVEDCEHIVQK	1.271329492	2	3.294794
P32755	FAVLQTYGDTTHTLVEK	1.452375259	2	5.073117
P32755	FLPGFEAPTYK	1.248940328	2	2.513811
P32755	FWSVDDTQVHTEYSSLR	2.061090106	2	5.547904
P32755	GMEFLAVPSSYYR	1.276603855	2	3.045526
P32755	GNLTDLETNGVR	1.13098371	2	3.61468
P32755	HNHQGFGAGNFNSLFK	1.372228319	3	4.997241
P32755	ILVDYDEK	1.167016365	2	2.872032
P32755	IVFVLCSALNPWNK	1.247270921	2	3.05992
P32755	IVREPWVEEDKFGK	1.263886816	3	4.246857
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.468417478	3	7.495541

P32755	MGFEPLAYK	2.148512642	2	2.343648
P32755	SIVVANYEESIK	1.331344782	2	4.151486
P32755	SQIQEYVDYNGGAGVQHIALR	1.447740888	2	5.488542
P32755	TEDIITTIR	1.241221489	2	3.402628
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**0.877421127**	**7.6E-10**	**2**
P33124	ALRPTIFPVVPR	0.885446946	2	3.077216
P33124	IENIYIR	0.87230799	2	2.844885
P33273	**CP255 Cytochrome P450 2C55**	**0.876281048**	**0.00172**	**2**
P33273	ELRHFSLMTLR	0.987893666	2	2.317363
P33273	FDYKDENFLNLMEK	0.656937497	3	3.544454
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.061094461**	**9.9E-20**	**24**
P34058	ADLINNLGTIAK	0.901563149	2	4.10553
P34058	EDQTEYLEER	0.986141101	2	3.341141
P34058	EGLELPEDEEEKKK	0.873689246	2	3.142198
P34058	ELISNASDALDK	0.830038877	2	3.637251
P34058	ELISNASDALDKIR	0.46416099	2	2.986531
P34058	GVVDSEDLPLNISR	0.970841494	2	4.749973
P34058	HLEINPDHPIVETLR	0.905352745	2	4.418153
P34058	HSQFIGYPITLYLEK	2.197809083	2	3.801575
P34058	IDIIPNPQER	0.871023839	2	2.967128
P34058	KHLEINPDHPIVETLR	0.920739881	2	3.266825
P34058	LGIHEDSTNR	0.813608362	2	3.296876
P34058	NPDDITQEEYGEFYK	1.537208602	2	4.884945
P34058	RAPFDLFENK	1.076144059	2	2.91025
P34058	RAPFDLFENKK	0.689831425	2	2.33402
P34058	SIYYITGESK	1.446356002	2	3.095205
P34058	SLTNDWEDHLAVK	1.113949235	2	3.89272
P34058	TLTLVDTGIGMTK	0.966270251	2	3.865714
P34058	TLTLVDTGIGMTK+Oxidation(10)	0.75674364	2	3.918484
P34058	VFIMDSCDELIPEYLNFIR	1.399981311	2	2.859722
P34058	VILHLKEDQTEYLEER	0.836009351	3	4.219722
P34058	YESLTDPSK	0.964237289	2	2.846514
P34058	YESLTDPSKLDSGK	0.959894241	2	3.66766
P34058	YHTSQSGDEMTSLSEYVSR	1.066763288	2	5.429961
P34058	YIDQEELNK	0.928217347	2	3.631156
P34067	**PSB4 Proteasome subunit beta type_4**	**0.999618029**	**0.32812**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	1.033963905	2	3.442951
P34067	TQNPMVTGTSVLGVK	0.891601924	2	2.542739
P34067	VNDSTMLGASGDYADFQYLK	1.107332167	2	4.18301
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.061434269**	**0.15944**	**3**
P35171	GGTSDALLYR	0.946367621	2	3.280332
P35171	LFQEDNGMPVHLK	1.181086954	2	3.831196

P35171	LFQEDNGMPVHLK+Oxidation(7)	0.796796511	2	2.694282
P35213	**1433B 14_3_3 protein beta/alpha**	**0.930465886**	**0.99963**	**5**
P35213	AVTEQGHELSNEER	1.133714979	2	4.567863
P35213	EKIEAELQDICSDVLELLDK	1.038094658	3	4.375509
P35213	QTTVSNSQQAYQEAFEISK	0.938165006	2	5.247869
P35213	TAFDEAIAELDTLNEESYK	0.959808221	2	5.310199
P35213	YLSEVASGDNK	0.93849232	1	3.129529
P35233	**PTN2 Tyrosine_protein phosphatase non_receptor type 2**	**0.849277469**	**0.45382**	**2**
P35233	CAQYWPTDDREMVFK+Oxidation(11)	1.066677167	2	2.362753
P35233	KRWLYWQPILTK	0.814115494	1	2.099688
P35278	**RAB5C Ras_related protein Rab_5C**	**0.892347778**	**0.01824**	**2**
P35278	FEIWDTAGQER	0.944581542	2	2.665885
P35278	GVDLQESNPASR	0.86566173	2	2.903585
P35427	**RL13A 60S ribosomal protein L13a**	**1.006595692**	**1**	**2**
P35427	CEGINISGNFYR	0.965726342	2	2.716946
P35427	YQAVTATLEEK	0.977023497	2	2.984513
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**0.903503401**	**0.00101**	**2**
P35434	AQSELSGAADEAAR	0.894770586	2	4.638041
P35434	IEANEALVK	0.941149915	2	3.304008
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**0.955067501**	**6.2E-06**	**6**
P35435	GLCGAIHSSVAK	0.952494555	2	3.697511
P35435	HLIIGVSSDR	0.921036591	2	2.912915
P35435	NASDMIDK	0.943594092	1	2.103876
P35435	NDMAALTAAGK	1.013813885	2	3.343344
P35435	THSDQFLVSFK	1.489143582	2	3.129928
P35435	VYGTGSLALYEK	1.339777091	2	2.874933
P35565	**CALX Calnexin**	**1.104828246**	**9.9E-20**	**8**
P35565	AEEDEILNR	0.793722083	2	2.593971
P35565	GSLSGWILSK	0.685096584	2	2.31165
P35565	KIPNPDFFEDLEPFR	1.062646054	3	4.4728
P35565	NKGDEEEEEEKLEEK	0.8844703	2	4.701201
P35565	TDAPQPDVKDEEGKEEEK	0.79821724	3	3.755375
P35565	TSELNLDQFHDK	0.721419208	2	3.647979
P35565	VVDDWANDGWGLK	0.733254734	2	3.884987
P35565	VVDDWANDGWGLKK	0.827433075	2	3.454346
P35704	**PRDX2 Peroxiredoxin_2**	**0.862294664**	**0.00047**	**5**
P35704	EGGLGPLNIPLLADVTK	0.872066978	2	2.897059
P35704	KEGGLGPLNIPLLADVTK	0.850841311	2	4.292226
P35704	NDEGIAYR	0.875588576	1	2.075346
P35704	QITVNDLPVGR	0.863383082	2	2.804196
P35704	SLSQNYGVLK	0.764135067	2	2.413411

P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.711227476**	**0.00337**	**2**
P35738	AAVEQVPVEPYK	0.722386455	2	2.31245
P35738	GLLLSCIEDKNPCIFFEPK	0.497504535	2	2.817338
P36201	**CRIP2 Cysteine_rich protein 2**	**1.222036235**	**0.21551**	**3**
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.133577462	3	6.76126
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.236830332	2	4.431647
P36201	VYFAEKVTSLGK	0.89198005	2	2.46953
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**0.6355393**	**9.9E-20**	**9**
P36365	ALQSDYITYIDDLLTSINAKPDLR	1.243434469	3	3.734042
P36365	ASLYNSVVSNSSK	1.097882043	2	2.977118
P36365	ENSVVFNNTPK	0.829261515	2	2.457228
P36365	FTEHVEEGR	0.533960558	2	2.888665
P36365	NLLPTPVVSWLISK	0.568612937	2	2.303929
P36365	SCDLGGLWR	0.553906638	2	2.828578
P36365	TQLREPVLNDELPGR	0.967745529	2	2.943776
P36365	VEDGQASLYK	0.643229702	2	3.304549
P36365	VLVVGMGNSGTDIAVEASHLAK	0.899512469	2	2.480818
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**0.789217867**	**9.9E-20**	**6**
P36511	ANIIAWALAQIPQK	1.010681218	3	4.376067
P36511	FVNVWTYELPR	1.212575305	2	2.781586
P36511	FVTFPTSFSSHDLENFFTR	1.727318944	2	3.88148
P36511	GHEVTVLRPSAFVFLDPK	1.674688401	2	2.961723
P36511	IILEELVQK	0.785027591	2	3.401037
P36511	TLGRPTTLAEIMGK	0.96403099	2	2.582662
P36972	**APT Adenine phosphoribosyltransferase**	**0.810217757**	**3.5E-05**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	0.831458433	2	2.781977
P36972	IDYIAGLDSR	0.966367318	1	2.294043
P36972	SFPDFPIPGVLFR	0.804292595	2	3.144978
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**0.862763779**	**0.19974**	**7**
P38650	EALELTDTGLLSGSEER	0.851310001	2	2.408808
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.107018938	3	3.392615
P38650	ILDDDTIITTLENLK	1.136510804	2	2.352604
P38650	QLQNISQAAAAGGAK	1.051945309	2	2.80931
P38650	SSLQSQCLNEVLK	0.835052229	2	3.112075
P38650	VQGLTVEQAEAVAR	1.002526677	2	3.092907
P38650	VQVALEELQDLK	0.845434847	2	2.64115
P38652	**PGM1 Phosphoglucomutase_1**	**0.761708222**	**9.9E-20**	**16**
P38652	ADNFEYSDPVDGSISK	0.893737315	2	4.863481
P38652	AIGGIILTASHNPGGPNGDFGIK	0.996175504	2	5.27492
P38652	FNISNGGPAPEAITDK	1.039668516	2	4.241812
P38652	IDAMHGVVGPYVK	0.418340426	2	3.118982
P38652	INQDPQVMLAPLISIALK	1.089548212	2	4.728986

P38652	KQRVEDILK	0.871919262	1	2.053016
P38652	LSGTGSAGATIR	0.755375589	2	2.67467
P38652	LSLCGEESFGTGSDHIR	1.8061292	2	3.243306
P38652	LVIGQNGILSTPAVSCIIR	1.042817471	2	3.554147
P38652	NIFDFNALK	0.854653325	1	2.10787
P38652	QEATLVVGGDGR	0.848604858	2	3.020263
P38652	SFVGKQFSANDK	1.01088209	1	2.061254
P38652	SGEHDFGAAFDGDGDR	0.866915997	2	4.39383
P38652	TIEEYAICPDLK	0.852688669	2	2.92078
P38652	TQAYPDQKPGTSGLR	0.689846865	2	3.706978
P38652	YDYEEVEAEGANK	1.014160652	2	4.936046
P38656	**LA Lupus La protein homolog**	**0.854576919**	**0.7358**	**3**
P38656	GSIFAVFDSIQSAK	0.994809856	2	2.355625
P38656	ITDDQQESLNK	0.808033704	2	3.98058
P38656	LDEGWVPLETMIK	1.436754111	2	2.94786
P38659	**PDIA4 Protein disulfide_isomerase A4**	**1.050004762**	**9.9E-20**	**18**
P38659	DLGLSESGEDVNAAILDESGKK	1.266762402	2	4.996846
P38659	EVSQPDWTPPPEVTLTLTK	1.051020037	2	3.436537
P38659	FDVSGYPTIK	1.048373202	2	3.294147
P38659	FDVSGYPTLK	1.048373202	2	3.294147
P38659	FIDEHATK	1.116343845	2	2.471492
P38659	FIDEHATKR	1.464476444	2	2.572917
P38659	GQAVDYDGSR	0.587993427	2	2.425307
P38659	GRPFDYNGPR	1.089027252	2	2.928123
P38659	IDATSASMLASK	1.076454335	2	3.497406
P38659	IDATSASMLASK+Oxidation(7)	1.153935672	2	3.211757
P38659	KGQAVDYDGSR	1.549389289	2	2.432132
P38659	MDATANDITNDR	1.087642227	2	3.830023
P38659	QLEPVYTSLGK	0.944766889	2	2.466219
P38659	RFDVSGYPTLK	1.261302879	2	3.064691
P38659	RSPPIPLAK	1.415549993	2	2.489756
P38659	VDATEQTDLAK	1.035747189	2	3.952965
P38659	VEGFPTIYFAPSGDK	1.12352125	2	3.234595
P38659	YGIVDYMVEQSGPPSK	1.640956276	2	4.401173
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.472749262**	**9.9E-20**	**4**
P38918	FYAFNPLAGGLLTGR	0.722301032	2	4.32189
P38918	MDVTSSSASVR	0.413360163	2	3.494018
P38918	RMDVTSSSASVR	0.47256532	2	2.923885
P38918	TTYGPTAPSMISAAVR	0.618925131	2	3.539783
P38983	**RSSA 40S ribosomal protein SA**	**1.168906413**	**9.9E-20**	**6**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.258088221	3	5.735627
P38983	AIVAIENPADVSVISSR	1.012500293	2	5.555783

P38983	FTPGTFTNQIQAAFR	1.177759807	2	4.701433
P38983	KSDGIYIINLK	1.816223922	2	2.86672
P38983	SDGIYIINLK	0.995416383	2	2.92307
P38983	YVDIAIPCNNK	1.230625686	2	3.330445
P40307	**PSB2 Proteasome subunit beta type_2**	**0.959610391**	**0.03431**	**2**
P40307	FILNLPTFSVR	1.296383546	2	2.639387
P40307	NGYELSPTAAANFTR	0.954471334	2	3.289738
P40329	**SYRC Arginyl_tRNA synthetase_ cytoplasmic**	**0.943809963**	**0.00091**	**2**
P40329	EENLKLK	1.188478976	1	1.945611
P40329	SDGGYTYDTSDLAAIK	0.863091937	2	3.691032
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.097577084**	**3.4E-05**	**6**
P41034	AECPELSADLHPR	0.958609723	2	2.48415
P41034	AIFDLEGWQISHAFQITPSVAK	1.126726904	2	4.575449
P41034	AQEEGVPETPQPLTDAFLLR	1.340198709	2	3.387881
P41034	QLNEQPDHSPLVQPGLAELR	1.089564094	3	3.394094
P41034	SEDYLSSISETIQ	1.528838835	2	2.320954
P41034	VSLITSELIVQEVETQR	1.254725878	2	3.539463
P41123	**RL13 60S ribosomal protein L13**	**1.051846794**	**0.00641**	**3**
P41123	LATQLTGPVMPIR	1.450243223	2	2.460745
P41123	STESLQANVQR	0.953423065	2	3.925001
P41123	VDTWFNQPAR	1.044099679	2	3.551446
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.029102741**	**9.7E-09**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.029205948	2	4.773513
P41498	IELLGSYDPQK	0.822205178	2	3.738861
P41498	LVTDENVSDNWR	0.821936933	2	3.450277
P41542	**USO1 General vesicular transport factor p115**	**1.00378872**	**0.61231**	**13**
P41542	AWFEVGDENPGWSAQK	0.889878059	2	4.029699
P41542	CQNEQLQTAVTQQASQIQQHK	0.915246572	3	4.865631
P41542	EQDDLLVLLADQDQK	1.135533991	2	2.685091
P41542	LQTENSELQQR	1.022748988	2	2.818101
P41542	LREEIEELR	0.923387648	2	2.413286
P41542	NDGVLLLQALTR	1.185521482	2	3.841659
P41542	NNNSNQNFFK	0.981707283	2	2.519103
P41542	QLDSSNSTIAILQTEK	0.971781845	2	3.483702
P41542	QSEDLGSQFTEIFIK	1.021467326	2	3.196417
P41542	SQLCSQSLEITR	1.030413394	2	3.122802
P41542	SVPVEGESELVTAAK	1.004716359	2	3.754909
P41542	TLEQHDNIVTHYK	0.919044935	2	3.23454
P41542	VLVSPTNPPGATSSCQK	0.980971649	2	3.267832
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**0.920930206**	**1.4E-13**	**16**
P41562	ATDFVVPGPGK	1.026018325	2	3.371049
P41562	CATITPDEK	1.269056016	2	2.586768

P41562	DIFQEIYDK	0.80730674	1	2.461578
P41562	FKDIFQEIYDK	0.952347124	3	4.430447
P41562	GQETSTNPIASIFAWSR	1.300744149	2	5.114202
P41562	IIWELIK	1.009571101	2	2.565112
P41562	LIDDMVAQAMK	0.957906126	2	3.525281
P41562	LIDDMVAQAMK+Oxidation(9)	0.822626481	2	2.333398
P41562	LILPYVELDLHSYDLGIENR	1.382507601	3	3.663644
P41562	LVTGWVKPIIIGR	1.236536028	3	4.029403
P41562	SDYLNTFEFMDK	0.954676625	2	4.081991
P41562	SDYLNTFEFMDK+Oxidation(9)	0.756879045	2	2.984837
P41562	SEGGFIWACK	0.906580429	2	3.31787
P41562	SIEDFAHSSFQMALSK	1.032038042	2	4.400452
P41562	TVEAEAAHGTVTR	0.864989056	2	3.549238
P41562	VEITYTPK	0.99115264	2	2.537252
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.104937168**	**0.93777**	**4**
P42123	DYSVTANSK	1.188974691	2	2.657978
P42123	LIAPVADDETAVPNNK	0.832617854	2	3.368857
P42123	SLADELALVDVLEDK	0.990256075	2	3.423537
P42123	VIGSGCNLDSAR	1.053708351	2	3.751447
P42676	**NEUL Neurolysin_ mitochondrial**	**1.151188465**	**0.27259**	**2**
P42676	AELGALPDDFIDSLEK	0.917526254	2	2.411804
P42676	TRTEQLIAQTK	1.239954594	2	3.176306
P42932	**TCPQ T_complex protein 1 subunit theta**	**1.028263765**	**6E-14**	**6**
P42932	AIAGTGANVIVTGGK	0.916777909	2	4.0802
P42932	AVDDGVNTFK	1.237558845	2	2.82986
P42932	ELEVQHPAAK	0.935650923	2	2.792686
P42932	GEENLMDAQVK	0.942580451	2	3.011295
P42932	NVGLDIEAEVPAVK	1.013700033	2	3.987832
P42932	QITSYGETCPGLEQYAIK	0.890961874	2	4.780943
P43244	**MATR3 Matrin_3**	**0.922713908**	**0.38329**	**3**
P43244	GNLGAGNGNLQGPR	0.8035721	2	2.364426
P43244	ITPENLPQILLQLK	0.923165907	2	3.461252
P43244	TEEGPTLSYGR	0.951443785	2	2.474397
P43274	**H14 Histone H1.4**	**0.771620762**	**9.9E-20**	**3**
P43274	ALAAAGYDVEK	0.823475222	2	3.529053
P43274	SGVSLAALK	0.768749198	2	3.148955
P43274	SGVSLAALKK	0.702477156	2	2.665961
P43276	**H15 Histone H1.5**	**0.795327341**	**0.02004**	**2**
P43276	ALAAGGYDVEK	1.033821173	2	2.350067
P43276	ATGPPVSELITK	0.670955516	2	2.349495
P43278	**H10 Histone H1.0**	**0.802863931**	**2E-15**	**2**
P43278	VGENADSQIK	0.781376884	2	3.525041
P43278	YSDMIVAAIQAEK	0.831912384	2	3.523097

P45591	**COF2 Cofilin_2**	**0.873314401**	**0.00015**	**2**
P45591	HEWQVNGLDDIKDR	0.878390578	3	4.240893
P45591	QILVGDIGDTVEDPYTSFVK	0.881533155	2	4.529437
P45592	**COF1 Cofilin_1**	**0.960187524**	**0.98424**	**3**
P45592	EILVGDVGQTVDDPYTTFVK	1.03288569	2	4.651553
P45592	HELQANCYEEVKDR	0.899618037	3	4.697182
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	1.031168968	3	3.663724
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**0.917879364**	**0.09268**	**4**
P45878	GWDQGLLGMCEGEK	0.909727528	2	3.932311
P45878	KLVIPSELGYGER	1.237615679	2	2.568548
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	1.253971784	3	4.288064
P45878	LVIPSELGYGER	0.866100647	2	2.538596
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.694816715**	**9.9E-20**	**17**
P45953	AMVENGGLVTSNPLR	1.267234216	2	2.644194
P45953	AMVENGGLVTSNPLRV	1.374067545	2	3.191954
P45953	ASNTSEVYFDGVK	1.741770041	2	4.164312
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	1.036428329	2	4.906074
P45953	ENMASLQSNPQQQELFR	0.855278505	2	4.452009
P45953	FFEEVNDPAK	1.628194239	2	2.425761
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	1.064592704	3	6.283577
P45953	GIVNEQFLLQR	1.418215345	2	2.983571
P45953	IFEGTNDILR	1.054551071	2	2.804143
P45953	NDSLEKVEEDTLQGLK	1.072412898	2	3.597562
P45953	NPLGNVGLLIGEASK	3.406102131	2	3.554903
P45953	SFGGVTHGLPEK	1.015364796	2	2.898193
P45953	SFGGVTHGLPEKK	1.357053495	2	2.80309
P45953	SGELAVQALEQFATVVEAK	1.244453868	3	5.000384
P45953	SLSEGYPTAQHEK	1.183582821	2	3.24165
P45953	TGIGSGLSLSGIVHPELSR	1.091966793	3	4.582042
P45953	VEEDTLQGLK	1.021642484	2	2.622389
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**0.788855555**	**1.7E-06**	**3**
P46418	AILNYIATK	1.27221254	2	3.088582
P46418	SHGQDYLVGNK	0.480068699	2	3.000169
P46418	VSNLPTVK	0.887554309	2	2.602988
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.749808172**	**4.9E-07**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.756821831	3	3.988088
P46425	FEDGDLTLYQSNAILR	0.697986455	2	4.071139
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**0.962688527**	**9.9E-20**	**23**
P46462	AIANECQANFISIK	0.711343575	2	3.107888
P46462	ELQELVQYPVEHPDK	0.959934854	2	4.370066
P46462	ETVVEVPQVTWEDIGGLEDVK	0.868047028	2	3.183033

P46462	ETVVEVPQVTWEDIGGLEDVKR	0.951580822	2	4.288118
P46462	EVDIGIPDATGR	0.773123374	2	2.644801
P46462	GDDLSTAILK	0.939063832	2	3.025616
P46462	GGNIGDGGGAADR	0.961922496	2	3.323622
P46462	GILLYGPPGTGK	0.849712169	2	3.177064
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.095818547	3	6.838257
P46462	LAGESESNLRKAFEEAEK	0.641347428	2	2.347341
P46462	LDQLIYIPLPDEK	0.891972953	2	4.265564
P46462	LEILQIHTK	0.908469784	1	2.338802
P46462	LGDVISIQPCPDVK	0.829227394	2	4.103157
P46462	LIVDEAINEDNSVVSLSQPK	0.885388146	2	5.61971
P46462	MDELQLFR	0.874257011	2	2.488086
P46462	MTNGFSGADLTEICQR+Oxidation(0)	0.88884492	2	3.871679
P46462	NAPAIIFIDELDAIAPK	1.007692403	2	4.68887
P46462	QAAPCVLFFDELDSIAK	2.110208185	2	3.46075
P46462	QTNPSAMEVEEDDPVPEIR	0.889195892	2	4.405373
P46462	RSVSDNDIR	0.890618297	2	2.929654
P46462	VINQILTEMDGMSTK	0.925501438	2	3.543642
P46462	VINQILTEMDGMSTK+Oxidation(8)	0.544606486	2	2.371827
P46462	WALSQSNPSALR	1.467193598	2	3.000924
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**0.882769727**	**0.00126**	**4**
P46664	FIEDELQIPVK	0.796059258	2	3.074489
P46664	LDILDMFTEIK	0.862119055	2	3.706762
P46664	VGIGAFPTEQDNEIGELLQTR	3.221570886	2	4.044451
P46664	VVDLLAQDADIVCR	1.048471897	2	3.733903
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**0.989270659**	**0.68804**	**3**
P46720	ESEHTDVHGSPQVENDGELK	0.799558152	3	3.442421
P46720	GIGETPIVPLGISYIEDFAK	0.997767861	2	3.360147
P46720	SENSPLYIGILEMGK	1.020929506	2	2.917818
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**1.01950422**	**0.00751**	**6**
P46953	AQGSVALSVTQDPACK	0.437921094	2	4.242898
P46953	DLGTQLAPIIQEFFHSEQYR	1.071921587	2	3.985065
P46953	QDVDVWLWQLEGSSK	0.891935457	2	3.473176
P46953	QGEIFLLPAR	1.045472195	2	3.036579
P46953	TGKPNPDQLLK	0.799219893	3	3.797587
P46953	YYVGDTEDVLFEK	0.869032294	2	3.572612
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.268586071**	**3.8E-10**	**6**
P46978	FESVIHEFDPYFNYR	1.219231983	3	3.823313
P46978	FGQVYTEAK	1.262719898	2	2.417142
P46978	FYSLLDPSYAK	1.183757372	2	3.287693
P46978	NLDISRPDKK	1.158185547	2	2.54968

P46978	VGQAMASTEEK	0.953078702	2	3.243232
P46978	VGQAMASTEEK+Oxidation(4)	1.753442582	2	3.256992
P47198	**RL22 60S ribosomal protein L22**	**1.099779315**	**0.14885**	**2**
P47198	AGNLGGGVVTIER	0.969788248	2	2.974918
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.262388672	3	5.092321
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.076071065**	**2.7E-06**	**3**
P47875	GFGFGQGAGALVHSE	0.766936	2	3.154712
P47875	GLESTTLADKDGEIYCK	1.061113509	2	4.748627
P47875	NLDSTTVAVHGEEIYCK	1.161675846	2	4.802594
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**0.872145528**	**9.9E-20**	**2**
P47942	GLYDGPVCEVSVTPK	0.736847628	2	3.093186
P47942	SITIANQTNCPLYVTK	0.792497016	2	3.285084
P48004	**PSA7 Proteasome subunit alpha type_7**	**1.22417055**	**1.5E-05**	**3**
P48004	GRDIVVLGVEK	1.224190457	2	2.658371
P48004	NYTDDAIETDDLTIK	1.114795184	2	3.898742
P48004	YVAEIEKEKEENEK	0.545527031	2	4.991709
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**0.862243761**	**0.11159**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.028892818	3	4.827719
P48024	TLTTVQGIADDYDK	0.832014102	2	3.23139
P48037	**ANXA6 Annexin A6**	**0.754015544**	**9.9E-20**	**15**
P48037	AANDFNPDADAK	1.008263848	2	3.017251
P48037	AINEAYKEDYHK	0.865523677	2	3.124152
P48037	DAFVAIVQSVK	0.483144338	2	2.893611
P48037	DLESDIIGDTSGHFQK	0.77767666	2	4.106172
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	0.594336275	2	4.670141
P48037	GELSGDFEK	0.78831508	1	2.066452
P48037	GFGSDKESILELITSR	0.823183124	2	3.964816
P48037	GIGTDEATIIDIITQR	0.677422401	2	4.325992
P48037	QRQEICQSYK	0.48369419	2	2.950975
P48037	SEIDLLNIR	0.908159854	2	3.122379
P48037	SEISGDLAR	0.76120121	2	2.358965
P48037	SLEDALSSDTSGHFK	0.819442719	2	3.819912
P48037	TNEQIHQLVAAYK	0.788249971	2	4.021069
P48037	TNYDIEHVIK	0.706437495	2	3.291972
P48037	TTGKPIEASIR	0.743313327	2	2.627642
P48500	**TPIS Triosephosphate isomerase**	**1.15006292**	**2.3E-05**	**12**
P48500	CNVSEGVAQCTR	0.928755224	2	3.618832
P48500	DLGATWVVLGHSER	0.919770419	2	3.137172
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	1.014905044	4	6.585271
P48500	HIFGESDELIGQK	1.077050818	2	4.071792
P48500	IIYGGSVTGATCK	1.009404244	2	3.885525
P48500	LPADTEVVCAPPTAYIDFAR	5.047593397	2	5.215746
P48500	RHIFGESDELIGQK	0.998556938	2	3.306357

P48500	TATPQQAQEVHEK	1.025617208	2	3.74413
P48500	VNHALSEGLGVIACIGEK	1.081929518	2	5.461014
P48500	VTNGAFTGEISPGMIK	1.038595235	2	4.798406
P48500	VTNGAFTGEISPGMIK+Oxidation(13)	0.792453771	2	3.605269
P48500	VVLAYEPVWAIGTGK	1.029304013	2	3.815034
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.675051156**	**9.9E-20**	**5**
P48508	ASTLHLQTGNLLNWGR	0.850783094	3	4.032835
P48508	EFPDVLECTMSHAVEK	0.629572893	2	3.144341
P48508	INPDEREEMK+Oxidation(8)	0.019488896	2	2.325667
P48508	QFDIQLLTHNDPK	0.80915358	2	3.050974
P48508	TLNEWSSQISPDLVR	0.673444009	2	5.12403
P48675	**DESM Desmin**	**0.551993108**	**0.01376**	**2**
P48675	TSGGAGGLGSLR	0.553288703	2	2.414954
P48675	VSDLTQAANK	0.537162658	2	2.921501
P48679	**LMNA Prelamin_A/C**	**0.660164712**	**9.9E-20**	**16**
P48679	AASGSGAQVGGSISSGSSASSVTVTR	0.924629416	2	3.671845
P48679	AAYEAELGDAR	1.200634887	2	2.624554
P48679	AQHEDQVEQYKK	0.986162884	2	3.912194
P48679	GSHCSSSGDPAEYNLR	0.994058098	2	4.053654
P48679	IDSLSAQLSQLQK	0.65749394	2	3.087513
P48679	ITESEEVVSR	0.772039075	2	3.15237
P48679	LKDLEALLNSK	0.906990535	2	2.796626
P48679	LQEKEDLQELNDR	0.791705542	2	4.151368
P48679	MQQQLDEYQELLDIK	1.015246799	2	4.5597
P48679	MQQQLDEYQELLDIK+Oxidation(0)	0.898293571	2	4.325635
P48679	NSNLVGAAHEELQQSR	0.953498819	2	3.740095
P48679	SGAQASSTPLSPTR	0.71144503	2	3.02487
P48679	SVGGSGGGSFGDNLVTR	0.890335713	2	3.541551
P48679	TALINATGEEVAMR	0.896040402	2	3.193204
P48679	TLEGELHDLR	0.891429769	2	2.547167
P48679	TVLCGTCGQPADK	0.801005091	2	3.277341
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**0.950447644**	**9.9E-20**	**26**
P48721	AQFEGIVTDLIK	0.923737644	2	3.774691
P48721	ASNGDAWVEAHGK	1.072446955	2	3.859415
P48721	DAGQISGLNVLR	1.054708487	2	3.703007
P48721	EQQIVIQSSGGLSK	0.931401932	2	4.047725
P48721	ERVEAVNMAEGIIHDTETK	1.073837467	3	4.912172
P48721	ETAENYLGHTAK	0.865712365	2	3.363572
P48721	GAVVGIDLGTTNSCVAVMEGK	0.909635818	2	4.480857
P48721	LLGQFTLIGIPPAPR	1.175283103	2	3.151826
P48721	MEEFKDQLPADECNK	1.100866418	2	4.160893
P48721	MEEFKDQLPADECNK+Oxidation(0)	0.889733187	2	3.611344

P48721	MKETAENYLGHTAK	0.983052691	3	3.635689
P48721	MKETAENYLGHTAK+Oxidation(0)	1.053179017	2	3.818745
P48721	NAVITVPAYFNDSQR	0.990121565	2	3.474062
P48721	QAASSLQQASLK	10.72971584	2	2.44278
P48721	QAVTNPNNTFYATK	2.338679879	2	3.574663
P48721	RYDDPEVQK	0.904907264	2	2.519009
P48721	RYDDPEVQKDTK	1.270379103	2	3.761296
P48721	SDIGEVILVGGMTR	0.901822493	2	3.92496
P48721	SQVFSTAADGQTQVEIK	1.587126825	2	4.809871
P48721	STNGDTFLGGEDFDQALLR	1.006688213	2	5.63714
P48721	TTPSVVAFTPDGER	0.966753606	2	3.780604
P48721	VEAVNMAEGIIHDTETK	0.943017997	2	4.539736
P48721	VINEPTAAALAYGLDK	1.115910548	2	3.396526
P48721	VLENAEGAR	0.878514525	2	3.029504
P48721	VQQTVQDLFGR	0.964284735	2	3.855745
P48721	YDDPEVQKDTK	0.809583365	2	2.823376
P49134	**ITB1 Integrin beta_1**	**0.858338878**	**1.2E-12**	**4**
P49134	CNCQSHGIPASPK	0.712699501	2	3.541617
P49134	GEFFNELVGQQR	0.869733435	2	2.876316
P49134	RITSDFRIGFGSFVEK	1.221584243	2	2.436207
P49134	SAVTTVVNPK	0.869529879	2	2.533628
P49242	**RS3A 40S ribosomal protein S3a**	**0.832333817**	**4.4E-07**	**8**
P49242	ACQSIYPLHDVFVR	1.259005752	2	3.648771
P49242	ADGYEPPVQESV	1.300226663	1	1.927423
P49242	LITEDVQGK	1.087390759	2	2.713486
P49242	LMELHGEGGSSGK	0.934785714	2	3.472215
P49242	LMELHGEGGSSGK+Oxidation(1)	1.138714622	2	3.344761
P49242	NCLTNFHGMDLTR	1.300759388	2	3.24013
P49242	TTDGYLLR	1.057048012	2	2.678319
P49242	VFEVSLADLQNDEVAFR	1.142534056	2	4.102216
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.973854603**	**0.31724**	**5**
P49432	ILEDNSIPQVK	1.01421684	2	3.548146
P49432	IMEGPAFNFLDAPAVR	0.999968642	2	4.309427
P49432	IMEGPAFNFLDAPAVR+Oxidation(1)	0.843553084	2	3.159256
P49432	TIRPMDIEAIEASVMK	1.250410692	3	4.084547
P49432	VFLLGEEVAQYDGAYK	1.02510506	2	3.581576
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.735161929**	**9.9E-20**	**12**
P49889	CKEDALFNR	0.632797969	2	2.675025
P49889	FEEHYQQQMK	0.503427964	2	2.640038
P49889	FMEGQVPYGSWYDHVK	1.027149441	2	3.460742
P49889	IIQHTSFQEMK	0.759507896	2	2.770547
P49889	LIEFLER	0.574537056	2	2.500275

P49889	LIEFLERDPSAELVDR	0.591985192	3	5.067487
P49889	NEDLINGIK	0.695083916	2	3.060859
P49889	NNPCTNYSMLPETMIDLK	0.802122373	2	5.616404
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13)	0.697129441	2	3.532263
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8)	0.697743058	2	4.641748
P49889	SFSEFVEK	0.706390693	2	2.343769
P49889	SGSTWISEIVDMIYK	0.789420777	3	4.737951
P50137	**TKT Transketolase**	**1.084581008**	**9.9E-20**	**20**
P50137	AVELAANTK	0.966966288	1	1.990582
P50137	GHAAPILYAVWAEAGFLPEAELLNLR	1.085112277	3	3.386425
P50137	GITGIEDK	0.86127832	1	2.502842
P50137	IIALDGDTK	0.948543879	2	2.749874
P50137	ILATPPQEDAPSVDIANIR	0.965959688	2	4.655358
P50137	ISSDLDGHPVPK	0.964964647	2	3.208534
P50137	KISSDLDGHPVPK	0.927801382	2	4.507701
P50137	LAVSQVPRSGKPAELLK	1.760726701	2	2.687505
P50137	LDNLVAIFDINR	0.887787268	2	3.643674
P50137	LGQSDPAPLQHQVDVYQK	1.072175771	2	4.093204
P50137	MFGIDKDAIVQAVK	1.110016161	2	3.792723
P50137	MFGIDKDAIVQAVK+Oxidation(0)	0.767073645	2	4.540049
P50137	NMAEQIIQEIYSQVQSK	1.013417427	3	6.019146
P50137	NMAEQIIQEIYSQVQSK+Oxidation(1)	1.136020485	3	3.808042
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	0.920109726	4	5.049379
P50137	SVPMSTVFYPSDGVATEK	1.016707527	2	4.517802
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3)	0.754373691	2	3.420105
P50137	TSRPENAIIYSNNEDFQVGQAK	1.265549875	3	5.640935
P50137	VLDPFTIKPLDK	0.927732851	2	3.202904
P50137	VLDPFTIKPLDKK	1.010452281	2	2.84944
P50169	**RDH3 Retinol dehydrogenase 3**	**0.966551174**	**9.9E-20**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	0.892975454	3	5.588794
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1)	0.771826991	4	5.061027
P50169	FQDSYMK	0.865810193	1	1.943887
P50169	KLWDQTTEEVK	0.889943947	2	3.06398
P50169	KLWDQTTEEVKEIYGEK	0.836402792	3	4.003571
P50169	LWDQTTEEVK	0.760812927	2	3.160588
P50169	LWDQTTEEVKEIYGEK	0.836001862	2	4.882746
P50169	MSLVGGGYCISK	1.042511173	2	3.437164
P50169	MSLVGGGYCISK+Oxidation(0)	0.745883746	2	2.630288
P50237	**ST1C1 Sulfotransferase 1C1**	**0.699999504**	**9.9E-20**	**6**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.729592135	2	5.319674
P50237	DISEEVLNK	0.65117787	1	2.493851
P50237	DLHLGEQDLQPETR	0.608295574	2	4.453965

P50237	MLPDPGTLGEYIEQFK	0.68940165	3	4.957333
P50237	MLPDPGTLGEYIEQFK+Oxidation(0)	0.675165341	2	3.01235
P50237	VLWGSWYDHVK	0.721543529	2	2.684813
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**0.901200683**	**4E-14**	**7**
P50398	FDLGQDVIDFTGHALALYR	1.040661301	3	4.637975
P50398	FQLLEGPPESMGR	1.087828175	2	3.092113
P50398	KQNDVFGEADQ	0.894549696	2	2.667857
P50398	NPYYGGESSSITPLEELYK	1.299934409	2	5.317774
P50398	QLICDPSYIPDR	0.816315691	2	3.116746
P50398	TDDYLDQPCLETINR	0.945199748	2	4.476079
P50398	TFEGVDPQTTSMR	0.91060377	2	2.468359
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.222190973**	**6.9E-11**	**6**
P50399	AYDATTHFETTCDDIKDIYK	1.149043932	3	5.264831
P50399	EIRPALELLEPIEQK	1.066003136	3	3.684567
P50399	FDLGQDVIDFTGHSLALYR	1.193723133	3	4.212861
P50399	FVSISDLFVPK	1.37998643	2	3.578496
P50399	NTNDANSCQIIIPQNQVNR	1.034354625	2	4.148934
P50399	TDDYLDQPCCETINR	1.265889692	2	4.829153
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.104657806**	**6.5E-05**	**5**
P50431	ALSDALTELGYK	1.097811769	2	3.727576
P50431	AVLEALGSCLNNK	1.132155745	2	3.978404
P50431	GLLEEDFQK	1.064627015	1	2.024469
P50431	NLDYAR	1.55118253	1	1.91591
P50431	VLEACSIACNK	1.0523858	2	3.222268
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**0.908653741**	**9.9E-20**	**14**
P50475	ASEWVQQVSGLMDGK	0.927294137	2	4.025017
P50475	AVFDETYPDPVR	0.956506892	2	3.449162
P50475	DIINEEEVQFLK	0.875184263	2	3.231427
P50475	ESDGVLKPLPK	0.614670083	2	2.490954
P50475	GLEATDDSPK	0.905960039	1	2.022873
P50475	ITCLCQVPQNAANR	0.946132314	2	4.364578
P50475	IVAVTGAEAQK	0.85300023	2	2.599305
P50475	NVGCLQEALQLATSFAQLR	0.818390051	2	3.89468
P50475	RIVAVTGAEAQK	0.82400778	2	3.120742
P50475	SVLGDADQK	0.662066131	1	2.14714
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	0.753460386	3	3.504322
P50475	TITVALADGGRPDNTGR	0.997771832	2	2.962601
P50475	VDDSSEDKTEFTVK	1.771171658	2	3.317425
P50475	VGAEDTDGIDMAYR	0.993521687	2	3.362617
P50503	**F10A1 Hsc70_interacting protein**	**1.493834548**	**9.9E-20**	**4**
P50503	AIDLFTDAIK	1.120243174	1	2.155436
P50503	AIEINPDSAQPYK	1.494410724	2	2.806139

P50503	GAAIDALNDGELQK	1.347012267	2	3.756278
P50503	KGAAIDALNDGELQK	1.475634816	2	4.472068
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**0.984133606**	**0.47849**	**9**
P50554	GNYLVDVDGNR	1.074790874	1	2.123013
P50554	GTFCSFDTPDEAIR	0.808649204	2	3.424258
P50554	HGCAFLVDEVQTGGGCTGK	1.613922125	2	4.551401
P50554	IDIPSFDWPIAPFPR	0.979599693	2	3.735508
P50554	NLLLAEVINIIK	0.97145096	3	4.543061
P50554	REDLLNNVAHAGK	0.888044183	2	2.459017
P50554	TLLTGLLDLQAQYPQFVSR	1.106367528	3	4.103565
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.234934686	2	3.763388
P50554	VDFEFDYDGPLMK	0.147244174	2	2.472927
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.017208076**	**0.81971**	**2**
P50580	HELLQPFNVLYEK	1.121824015	2	2.709095
P50580	TIIQNPTDQQK	1.009361247	2	3.093803
P50878	**RL4 60S ribosomal protein L4**	**1.196807681**	**0.02304**	**7**
P50878	KLDELYGTWR	1.061758506	2	2.624
P50878	KLEAAAAALAAK	1.079455711	2	3.140327
P50878	LDELYGTWR	0.975606829	2	2.63756
P50878	LEAAAAALAAK	1.083420944	2	3.056212
P50878	NIPGITLLNVSK	1.126997649	1	2.559685
P50878	RGPCIIYNEDNGIIK	1.285191886	2	3.177149
P50878	SGQGAFGNMCR	0.914374487	2	2.871396
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**0.866058234**	**9.9E-20**	**7**
P51635	ALEALVAK	0.930568083	2	2.599603
P51635	GLEVTAYSPLGSSDR	0.881840097	2	3.991508
P51635	HHPEDVEPAVR	0.819947128	3	3.747267
P51635	HIDCASVYGNETEIGEALK	1.063442384	2	5.983953
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.55317655	3	5.31116
P51635	HPDEPVLLEEPVVLALAEK	1.419316889	3	5.813315
P51635	YIVPMITVDGK	0.852908909	2	2.303903
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.684159042**	**9.9E-20**	**14**
P51647	ANNTTYGLAAGVFTK	0.75171431	2	4.584049
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.663613989	3	3.976219
P51647	ELGEHGLYEYTELK	0.665277027	2	3.464188
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.567921631	4	5.153451
P51647	IFINNEWHDSVSGK	0.716338231	2	4.259348
P51647	IFVEESVYDEFVR	0.679788625	2	4.160798
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	0.721303713	3	4.807703
P51647	IHGQTIPSDGDIFTFTR	0.806843865	2	3.832752
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.646699853	3	3.639653
P51647	LLLATIEAINGGK	1.757718054	2	3.321141

P51647	VFANAYLSDLGGSIK	0.714629862	2	4.133256
P51647	YCAGWADK	0.566096104	1	1.959455
P51647	YVLGNPLTQGINQGPQIDK	0.56555094	2	4.880556
P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.68300981	2	3.724341
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**0.950053078**	**9.9E-20**	**9**
P51650	EVGEVLCTDPLVSK	0.773386434	2	3.826193
P51650	GIHDSFVTK	0.748637847	1	1.928905
P51650	HQSGGNFFEPTLLSNVTR	1.234497211	2	3.628136
P51650	IITAESGKPLK	0.839989561	2	2.456952
P51650	LGTVADCGVPEAR	0.73707893	2	3.294676
P51650	VGNGFEEGTTQGPLINEK	0.826447628	2	4.743298
P51650	VYGDIIYTSAK	0.864520638	2	2.545814
P51650	WLPTPATFPVYDPASGAK	0.730631597	2	2.788122
P51650	YGIDEYLEVK	0.79775655	2	2.944673
P51869	**CP4F4 Cytochrome P450 4F4**	**1.104489685**	**0.56427**	**4**
P51869	ALPSQHEDDILK	1.044656399	2	2.652307
P51869	NISLMTLDSLQK	0.917027076	2	2.902648
P51869	TLDFIDVLLLTK	1.283910474	2	2.870393
P51869	WQDLASGGSAR	1.065491601	2	2.551827
P51886	**LUM Lumican**	**0.666805086**	**3.2E-08**	**2**
P51886	NNQIDHIDEK	0.66618448	2	3.321613
P51886	SLQDLQLANNK	0.676715244	2	3.090912
P52296	**IMB1 Importin subunit beta_1**	**0.886714969**	**0.14399**	**4**
P52296	AAVENLPTFLVELSR	0.889717374	2	2.59822
P52296	SNEILTAIIQGMR	0.881671381	2	2.729624
P52296	TVSPDRLELEAAQK	0.885779434	2	2.528145
P52296	VLANPGNSQVAR	0.926544709	2	3.188617
P52303	**AP1B1 AP_1 complex subunit beta_1**	**1.103674967**	**0.49035**	**3**
P52303	NINLIVQK	1.092727863	1	2.214321
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	0.961857036	3	4.008987
P52303	YNDPIYVK	1.13461766	2	2.489667
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**0.896979277**	**0.08951**	**3**
P52555	ILDQGEDFPASELAR	0.890355099	2	4.530788
P52555	QGQDGLSGVK	0.953199715	2	2.463145
P52555	SLNILTAFR	0.94248848	2	2.767022
P52759	**UK114 Ribonuclease UK114**	**1.384794867**	**9.9E-20**	**7**
P52759	AAGCDFTNVVK	4.471955866	2	2.816199
P52759	APAAIGAYSQAVLVDR	1.599718418	2	3.940127
P52759	IEIEAIAVQGPFTTAGL	1.414215956	1	3.480948
P52759	NLGEILK	1.099632852	1	2.2241
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.26026377	2	3.924372
P52759	TTVLLADINDFGTVNEIYK	1.337426469	2	5.191224

P52759	TYFQGNLPAR	1.066596841	2	2.975194
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**1.033681117**	**0.0017**	**2**
P52845	CKEDAIFNR	0.632797969	2	2.675025
P52845	SGSTWIGEIVDMIYK	1.035994141	2	4.485991
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.011465304**	**2E-05**	**6**
P52847	DNPLVNYTHLPTEIMDHSK	1.60912746	2	4.162657
P52847	FLAGNVAYGSWFDHVK	1.145558766	2	2.590621
P52847	IEEFQSRPCDIVIPTYPK	0.976668011	3	4.40213
P52847	NYFTMTQSEK	0.984094413	1	2.682984
P52847	THLPIDLLPK	1.052014685	3	3.403651
P52847	TLDEHTLER	0.986999752	2	2.978592
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.251078217**	**9.9E-20**	**32**
P52873	ADEAYLIGR	1.248009687	2	2.84
P52873	ADFAQACQDAGVR	1.094696996	2	4.147135
P52873	AEAEAQAEELSFPR	1.099521881	2	4.389189
P52873	AGTHILCIK	1.597404777	2	2.666861
P52873	ALAVSDLNR	1.074722202	2	2.747462
P52873	AYSEALAAFGNGALFVEK	1.310166015	2	4.018583
P52873	AYVEANQMLGDLIK	1.142336924	2	4.586826
P52873	DAHQSLLATR	1.095684288	1	3.140144
P52873	DFTATFGPLDSLNTR	0.937447218	2	4.263984
P52873	DMAGLLKPAACTMLVSSLR	1.283638943	2	2.965591
P52873	ELIPNIPFQMLLR	2.150124761	2	2.342536
P52873	ENGVDAVHPGYGFLSER	1.176130573	2	2.864562
P52873	FLYECPWR	1.353423507	1	2.14017
P52873	GANAVGYTNYPDNVVFK	1.787215994	2	4.378192
P52873	GTPLDTEVPLER	1.053417402	2	3.598784
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.244737737	2	5.651723
P52873	HIEVQILGDQYGNILHLYER	1.327352555	3	5.405817
P52873	HYFIEVNSR	1.284600275	2	2.721821
P52873	IAEEFEVELER	1.028981388	2	3.249185
P52873	IEGRPGASLPPLNLK	1.104029228	2	3.601726
P52873	INGCAIQCR	1.214257819	2	2.436433
P52873	IVGDLAQFMVQNGLSR	1.235915775	2	4.012462
P52873	LDNASAFQGAVISPHYDSLLVK	1.17298164	3	5.610799
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.125419535	4	4.612874
P52873	QVGYENAGTVEFLVDK	1.276998922	2	3.76786
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.627454291	2	4.178076
P52873	TVAVYSEQDTGQMHR	1.110662948	2	4.050876
P52873	VFDYSEYWEGAR	1.109259713	2	4.57888
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.020605343	2	4.328311
P52873	VVEIAPATHLDPQLR	1.217549423	2	4.871254

P52873	VVHSYEELEENYTR	1.238082994	2	5.107137
P52873	YSLEYYMGLAEELVR	1.315436021	3	4.436421
P52944	**PDLI1 PDZ and LIM domain protein 1**	**0.808505674**	**7.8E-06**	**4**
P52944	GHFFVGDQIYCEK	0.743524907	2	3.484726
P52944	QSTSFLVLQEILESDGK	1.03732223	2	2.357588
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	0.719582995	3	4.285783
P52944	VTPPEGYDVVTVFPK	0.741523488	2	2.732184
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**1.003757511**	**0.42079**	**3**
P53395	LSDIGEGIR	1.170181591	2	2.359381
P53395	LSEVVGSGK	1.707790108	1	2.035837
P53395	SYLENPAFMLLDLK	1.096981732	2	4.02904
P53987	**MOT1 Monocarboxylate transporter 1**	**1.213000573**	**2.2E-11**	**4**
P53987	DGKEDETSTDVDEKPK	1.412946278	3	5.227687
P53987	DGKEDETSTDVDEKPKK	1.125912012	3	3.695066
P53987	ETQSPAPLQNSSGDPAEEESPV	1.090018988	2	4.738933
P53987	SDANTDLIGGSPK	1.313335881	2	3.755585
P54319	**PLAP Phospholipase A_2_activating protein**	**0.947881948**	**0.83996**	**4**
P54319	GQTLGLGNTSFSDPFTGGGR	0.90343702	2	3.289221
P54319	IGDVVGSSGANQQTSGK	0.958353841	2	4.176491
P54319	TGDLGDINAEQLPGR	0.696831282	2	3.798121
P54319	YVPGTSGPSNTVQTADPFTGAGR	0.964265101	2	3.300346
P54921	**SNAA Alpha_soluble NSF attachment protein**	**0.987990022**	**0.38847**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	1.034923304	3	3.738202
P54921	AIDIYEQVGTSAMDSPLLK	1.044617972	2	3.402037
P54921	HDAATCFVDAGNAFK	0.927381009	2	2.519862
P54921	NSQSFFSGLFGGSSK	1.009893893	2	3.248611
P54921	YEELFPAFSDSR	0.921961244	2	2.617752
P55006	**RDH7 Retinol dehydrogenase 7**	**0.813217577**	**9.9E-20**	**11**
P55006	LETVILDVTK	0.845865874	2	2.95732
P55006	TESIVAATQWVK	0.759375113	2	3.960156
P55006	TNVTNMER	0.799694832	2	2.307278
P55006	TNVTNMER+Oxidation(5)	0.951975723	2	2.451325
P55006	TSDRLETVILDVTK	0.929012402	3	4.423671
P55006	VAIIEPGGFK	1.913887477	2	2.340947
P55006	VLAACLTEK	0.999899516	2	2.795191
P55006	VVNIASTMGR	0.8128587	2	3.49625
P55006	VVNIASTMGR+Oxidation(7)	0.76916688	2	2.670018
P55006	YGVEAFSDSLR	0.998198705	2	3.487123
P55006	YVFITGCDSGFGNLLAR	0.935663472	2	3.777071
P55051	**FABP7 Fatty acid_binding protein_ brain**	**0.953529079**	**0.05521**	**2**
P55051	LTDSQNFDEYMK	0.547179722	2	4.029449

P55051	QVGNVTKPTVIISQEGGK	0.79641804	3	3.866259
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**1.181914097**	**2E-08**	**4**
P55053	KTETVCTFTDGALVQHQK	1.146636864	3	4.391692
P55053	LVESHGFEDYMK	1.087862567	2	2.831761
P55053	MGAMAKPDCIITLDGNNLTVK	1.05605074	3	3.339383
P55053	TETVCTFTDGALVQHQK	1.259841679	2	4.515117
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**0.909783916**	**9.9E-20**	**6**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.625895127	3	5.337626
P55159	IFFYDSENPPGSEVLR	0.72252364	2	5.41295
P55159	IQSILSEDPK	0.72824268	2	3.127617
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	1.073971179	3	4.074294
P55159	VVADGFDFANGIGISLDGK	0.679285706	2	4.61414
P55159	YVYIAELLAHK	1.060144052	2	2.950297
P55260	**ANXA4 Annexin A4**	**0.965428945**	**0.0005**	**6**
P55260	AEIDMLDIPANFK	1.034169968	1	2.135097
P55260	GAGTDEGCLIEILASR	1.020201061	2	3.608621
P55260	GLGTDDSTLIR	0.845618066	2	2.897763
P55260	GLGTDEDAIIGVLACR	0.843096557	2	3.246096
P55260	KAMKGLGTDEDAIIGVLACR+Oxidation(2)	0.719956622	2	2.443936
P55260	SETSGSFEDALLAIVK	0.741224525	2	2.771432
P55770	**NH2L1 NHP2_like protein 1**	**0.859695357**	**1E-07**	**2**
P55770	LLDLVQQSCNYK	0.822483158	2	3.002731
P55770	QQIQSIQQSIER	0.868093945	2	2.728797
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.057400319**	**0.44216**	**3**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	1.006548057	2	4.514318
P56399	IFQNAPTDPTQDFSTQVAK	1.062683597	2	3.631502
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.109930462	3	4.091649
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**0.933541768**	**4.1E-05**	**4**
P56522	AVPTGDVEDLPCGLLLSSVGYK	1.480552526	2	4.13537
P56522	NVINTFTQTAR	1.142336814	2	2.527487
P56522	TATEKPGVEEAAR	0.860513619	2	3.124709
P56522	TDITEVALGVLR	0.862631261	2	3.461328
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**0.970876094**	**0.28102**	**10**
P56574	ATDFVVDR	1.073344648	2	2.579669
P56574	CATITPDEAR	1.145831711	2	2.333228
P56574	DQTNDQVTIDSALATQK	1.062157583	2	5.504167
P56574	GKLDGNQDLIR	0.88421504	2	3.107996
P56574	LDGNQDLIR	0.760496052	2	2.354269
P56574	LIDDMVAQVLK	0.907781115	2	4.076313
P56574	LNEHFLNTTDFLDTIK	1.021549092	3	3.493211
P56574	NILGGTVFR	0.88771622	2	2.503284
P56574	SSGGFVWACK	0.908636693	2	2.524999

P56574	TIEAEAAHGTVTR	0.847074614	2	3.851521
P56593	**CP2AC Cytochrome P450 2A12**	**0.987743373**	**0.13718**	**3**
P56593	MLQGTCGAPIDPTIYLSK	1.020122688	2	3.941405
P56593	MLQGTCGAPIDPTIYLSK+Oxidation(0)	0.961674638	2	3.070265
P56593	NRQPQYEDHMK	0.510292272	3	3.414096
P56656	**CP239 Cytochrome P450 2C39**	**0.624902786**	**9.9E-20**	**5**
P56656	EHQESLDVTNPR	0.415292638	2	3.374147
P56656	IKEHQESLDVTNPR	0.447152703	2	5.080953
P56656	NYLIPK	1.258822163	1	1.984186
P56656	VCAGEGLAR	2.052748365	2	2.395042
P56656	VQEEIDHVIGR	0.882004527	2	2.704765
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.924443923**	**0.00373**	**3**
P57093	AISCHYGSSDCK	0.95453047	2	3.075678
P57093	IQDFQQNEELFR	0.989724155	2	4.037259
P57093	NLVSDDDIQR	0.746032505	1	2.509339
P57113	**MAAI Maleylacetoacetate isomerase**	**0.937069622**	**0.94034**	**12**
P57113	AITSGFNALEK	0.937753142	2	3.321912
P57113	ALLALEAFQVSHPCR	1.123560277	2	4.438662
P57113	DGGQQFSEEFQTLNPMK	0.864609333	2	4.853898
P57113	DGGQQFSEEFQTLNPMK+Oxidation(15)	1.052756196	2	2.388199
P57113	FKVDLSPYPTISHINK	0.920516503	3	4.894072
P57113	GIDYEIVPINLIK	0.954740919	2	4.254309
P57113	IDGITIGQSLAILEYLEETRPIPR	1.012404989	3	3.833765
P57113	MISDLIASGIQPLQNLSVLK	0.932236698	2	4.552726
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0)	0.963270083	2	5.442207
P57113	QVGQENQMPWAQK	0.960450097	2	3.621455
P57113	VDLSPYPTISHINK	0.933117125	2	3.729605
P57113	YCVGDEVSMADVCLAPQVANAER	0.954556743	2	5.953649
P57722	**PCBP3 Poly(rC)_binding protein 3**	**0.959646004**	**0.2671**	**2**
P57722	ESTGAQVQVAGDMLPNSTER	0.877419749	2	4.827143
P57722	INISEGNCPER	0.959868344	2	3.359262
P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**0.913760413**	**0.00073**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	0.849491628	2	4.409287
P58321	WLPLEANPEVTNQFLK	0.848790445	2	3.534853
P58751	**RELN Reelin**	**0.91912573**	**0.74673**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**0.5581202**	**0.63456**	**10**
P58775	AISEELDNALNDITSL	0.55895368	2	4.330544
P58775	ATDAEADVASLNR	0.661025492	2	3.800955
P58775	CGDLEEELK	0.560867532	2	2.829835
P58775	KATDAEADVASLNR	0.599682777	2	4.325458
P58775	LDKENAIDR	0.562523675	1	2.07886
P58775	LKGTEDEVEK	0.685573634	3	3.548062

P58775	MELQEMQLK	0.555694174	2	2.62533
P58775	QLEEEQQALQK	0.561075153	2	3.973254
P58775	SLEAQADKYSTK	0.504681714	2	3.141567
P58775	TIDDLEDEVYAQK	0.6815055	2	3.713794
P59279	**RAB2B Ras_related protein Rab_2B**	**1.115561087**	**6.3E-06**	**2**
P59279	LQIWDTAGQESFR	1.048804242	2	3.15208
P59279	SYYRGAAGALLVYDITR	2.07125417	2	2.799156
P60335	**PCBP1 Poly(rC)_binding protein 1**	**0.885269827**	**0.05154**	**2**
P60335	AITIAGVPQSVTECVK	0.899941012	2	3.131236
P60335	LVVPATQCGSLIGK	0.856271692	2	3.075226
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**0.978879627**	**0.778**	**4**
P60843	ATQALVLAPTR	0.959286562	1	2.280616
P60843	GFKDQIYDIFQK	0.995562676	2	3.336825
P60843	KGVAINMVTEEDKR	1.251180145	3	3.479564
P60843	LQMEAPHIIVGTPGR	1.05959203	3	3.392213
P60868	**RS20 40S ribosomal protein S20**	**1.127253968**	**0.00037**	**2**
P60868	DTGKTPVEPEVAIHR	0.685780547	3	4.153121
P60868	LIDLHSPSEIVK	1.108871433	2	3.01281
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.044219518**	**0.27749**	**2**
P60901	AINQGGLTSVAVR	1.04318341	2	3.506802
P60901	LLDSSTVTHLFK	1.377183808	2	2.568946
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.079748539**	**0.30744**	**2**
P61087	GEIAGPPDTPYEGGR	1.096294339	2	3.526207
P61087	VDLVDENFTELR	1.043417646	2	2.600815
P61107	**RAB14 Ras_related protein Rab_14**	**1.13874612**	**0.40672**	**3**
P61107	NLTNPNTVIILIGNK	1.13040164	2	3.901582
P61107	SCLLHQFTEK	1.456618997	2	2.937956
P61107	STYNHLSSWLTDAR	0.936180211	2	2.547968
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**1.097207602**	**0.5637**	**2**
P61222	NTVANSPQTLLAGMNK	1.131439438	2	2.889657
P61222	NVEDLSGGELQR	0.961130352	2	2.935363
P61314	**RL15 60S ribosomal protein L15**	**0.979161786**	**0.99798**	**5**
P61314	FFEVILIDPFHK	1.086729787	3	3.832217
P61314	GATYGKPVHHGVNQLK	1.058250782	2	4.288197
P61314	SLQSVAEER	0.958748507	2	2.900325
P61314	VLNSYWVGEDSTYK	1.05796756	2	3.176862
P61314	YIQELWR	0.991800828	2	2.322099
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**0.976216569**	**0.08609**	**3**
P61459	AVGWNELEGR	0.909986972	2	2.810389
P61459	LDHHPEWFNVYNK	0.99101426	3	4.894184
P61459	LSAEERDQLLPNLR	1.035487123	3	4.089849
P61589	**RHOA Transforming protein RhoA**	**0.561119036**	**0.02794**	**2**

P61589	MKQEPVKPEEGR	0.550989316	3	3.570173
P61589	MKQEPVKPEEGR+Oxidation(0)	0.62519636	2	2.968805
P61751	**ARF4 ADP_ribosylation factor 4**	**1.085128735**	**0.35451**	**3**
P61751	IQEGAAVLQK	1.103297664	2	2.487654
P61751	LGEIVTTIPTIGFNVETVEYK	1.045095763	3	4.825347
P61751	NICFTVWDVGGQDK	1.292267485	2	3.550783
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.135127258**	**4.7E-06**	**2**
P61805	ADFQGISPER	1.103580374	2	2.659112
P61805	FLEEYLSSTPQR	1.169951545	2	3.697941
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.068105803**	**0.00055**	**2**
P61924	GEDVPLTEQTVSQVLQSAK	1.123900726	2	3.793215
P61924	YYDDTYPSVK	0.954177678	2	2.778639
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**0.865981966**	**9.9E-20**	**7**
P61980	GSDFDCELR	0.927117636	2	2.636313
P61980	GSYGDLGGPIITTQVTIPK	0.859819062	2	4.77486
P61980	IDEPLEGSEDR	0.824506754	2	3.353453
P61980	IILDLISESPIK	0.864229068	2	4.13629
P61980	IITITGTQDQIQNAQYLLQNSVK	0.904643878	3	5.279976
P61980	LFQECCPHSTDR	1.001308255	2	3.455653
P61980	TDYNASVSVPDSSGPER	0.997253699	2	4.407461
P61983	**1433G 14_3_3 protein gamma**	**0.959227699**	**0.00042**	**4**
P61983	AYSEAHEISK	0.701995916	2	3.420109
P61983	NVTELNEPLSNEER	0.845684504	2	4.89528
P61983	TAFDDAIAELDTLNEDSYK	0.885305833	2	4.363809
P61983	YLAEVATGEK	1.110112359	2	2.812194
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.80241771**	**9.9E-20**	**4**
P62076	CIGKPGGSLDNSEQK	0.715151299	2	3.951298
P62076	KCIGKPGGSLDNSEQK	0.805360583	3	3.960309
P62076	LDPGAIMEQVK	0.81592225	2	2.842101
P62076	VQIAVANAQELLQR	0.875261375	2	4.204293
P62083	**RS7 40S ribosomal protein S7**	**1.213289765**	**1.4E-08**	**3**
P62083	AIIIFVPVPQLK	1.119814645	2	3.730995
P62083	KAIIIFVPVPQLK	1.109963263	2	3.730429
P62083	TLTAVHDAILEDLVFPSEIVGK	1.066255505	2	5.252037
P62161	**CALM Calmodulin**	**1.218574289**	**9.9E-20**	**3**
P62161	EADIDGDGQVNYEEFVQMMTAK	1.50167548	2	4.766891
P62161	EAFSLFDKDGDGTITTK	1.480839978	2	4.053777
P62161	VFDKDGNGYISAAELR	1.099644756	2	4.872018
P62198	**PRS8 26S protease regulatory subunit 8**	**0.945368941**	**0.82146**	**3**
P62198	IEELQLIVNDK	1.099546228	2	2.74543

P62198	LEGGSGGDSEVQR	0.936737585	2	3.444813
P62198	TMLELLNQLDGFEATK	1.080653466	2	3.124863
P62243	**RS8 40S ribosomal protein S8**	**1.087074171**	**7.1E-14**	**9**
P62243	ADGYVLEGK	0.997570961	2	2.825637
P62243	IIDVVYNASNNELVR	1.333077792	2	3.630523
P62243	ISSLLEEQFQQGK	1.43426168	2	3.625464
P62243	KYELGRPAANTK	0.884653709	2	3.51506
P62243	LDVGNFSWGSECCTR	1.120821844	2	3.431524
P62243	LTPEEEEILNK	0.977367602	2	3.142258
P62243	NCIVLIDSTPYR	1.087864822	2	3.130186
P62243	QWYESHYALPLGR	1.213154778	2	2.338182
P62243	YELGRPAANTK	0.937966049	2	2.771123
P62246	**RS15A 40S ribosomal protein S15a**	**1.227432855**	**9.9E-20**	**3**
P62246	HGYIGEFEIIDDHR	1.210785401	3	4.614569
P62246	IVVNLTGR	1.142876947	2	2.463518
P62246	WQNNLLPSR	1.084450613	2	2.588881
P62250	**RS16 40S ribosomal protein S16**	**1.564675295**	**1.4E-11**	**4**
P62250	ALVAYYQK	1.441108401	1	2.00934
P62250	GGGHVAQIYAIR	1.569701084	2	3.048078
P62250	LLEPVLLLGK	1.210283176	2	2.754758
P62250	TLLVADPR	1.050349374	2	2.462845
P62260	**1433E 14_3_3 protein epsilon**	**1.241168813**	**0.01421**	**4**
P62260	AAFDDAIAELDTLSEESYK	1.043545477	2	5.830258
P62260	HLIPAANTGESK	0.846715352	2	2.347728
P62260	LICCDILDVLDK	1.264813616	2	3.575559
P62260	YLAEFATGNDRK	1.025170883	2	2.656211
P62271	**RS18 40S ribosomal protein S18**	**1.004517051**	**0.90305**	**5**
P62271	AGELTEDEVER	1.018416324	2	3.224936
P62271	LREDLER	0.909288259	1	2.007337
P62271	RAGELTEDEVER	1.152176311	2	3.316751
P62271	VLNTNIDGR	1.034068365	2	2.825207
P62271	YSQVLANGLDNK	1.077590168	1	3.509498
P62278	**RS13 40S ribosomal protein S13**	**1.063521034**	**3.5E-05**	**4**
P62278	GLAPDLPEDLYHLIK	1.29398648	2	2.912847
P62278	GLSQSALPYR	1.376156995	1	2.03685
P62278	GLTPSQIGVILR	1.060852861	2	2.547945
P62278	KGLTPSQIGVILR	1.09900628	2	2.664007
P62332	**ARF6 ADP_ribosylation factor 6**	**0.889339651**	**0.84859**	**2**
P62332	FNVWDVGGQDK	0.889314422	2	3.058421
P62332	LGQSVTTIPTVGFNVETVTYK	1.14166532	2	2.508281
P62334	**PRS10 26S protease regulatory subunit 10B**	**0.847767833**	**0.04895**	**4**
P62334	ALQSVGQIVGEVLK	1.249154728	2	3.435363
P62334	EVIELPLTNPELFQR	1.103694319	2	3.3984

P62334	HGEIDYEAIVK	0.733663064	2	2.527072
P62334	IHIDLPNEQAR	0.831830371	2	2.43277
P62425	**RL7A 60S ribosomal protein L7a**	**1.030597115**	**5.4E-09**	**9**
P62425	AGVNTVTTLVENK	0.994218556	2	4.150034
P62425	AGVNTVTTLVENKK	1.098591768	2	2.919873
P62425	NFGIGQDIQPK	1.057272002	2	3.540219
P62425	TCTTVAFTQVNSEDK	2.251072893	2	3.852014
P62425	TCTTVAFTQVNSEDKGALAK	3.011234067	2	4.344961
P62425	TNYNDRYDEIR	1.010961151	2	2.319822
P62425	VAPAPAVVK	1.063639145	1	1.959166
P62425	VPPAINQFTQALDR	1.140579852	2	3.791949
P62425	VVNPLFEK	1.79122781	1	1.906892
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.092031522**	**9.9E-20**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.048406583	3	4.87193
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.172303956	4	5.139885
P62630	MDSTEPPYSQK	0.696533777	2	3.812725
P62630	MDSTEPPYSQK+Oxidation(0)	0.764946175	2	3.037074
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.205738016	5	6.666904
P62630	RYEEIVK	0.77789691	2	2.379981
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.227126998	3	5.267326
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14)	1.223519283	3	4.483494
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8)	1.304252778	3	4.080794
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.032046856	2	5.370109
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)	0.978365268	3	5.045857
P62630	YEEIVK	0.998978855	1	2.17746
P62630	YYVTIIDAPGHR	1.010709356	3	3.617086
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.049213767**	**5E-15**	**8**
P62632	EHALLAYTLGVK	1.274386361	1	3.541148
P62632	IGGIGTVPVGR	1.310945888	2	3.508736
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.079090864	3	5.187576
P62632	QLIVGVNK	0.962156351	1	2.770817
P62632	QTVAVGVIK	0.931997593	1	2.064388
P62632	STTTGHLIYK	0.884411798	2	2.89936
P62632	THINIVVIGHVDSGK	1.024235052	2	4.844553
P62632	VETGILRPGMVVTFAPVNITTEVK	1.356955568	3	3.668497
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**0.9658268**	**0.10776**	**6**
P62703	FDTGNLCMVTGGANLGR	0.891219329	2	4.629406
P62703	FDTGNLCMVTGGANLGR+Oxidation(7)	0.417072259	2	4.258345
P62703	GIPHLVTHDAR	1.064262218	2	2.489572
P62703	LSNIFVIGK	0.881092989	2	2.465869
P62703	TDITYPAGFMDVISIDK	0.94669545	2	3.833196

P62703	VNDTIQIDLETGK	1.071512123	2	3.771943
P62718	**RL18A 60S ribosomal protein L18a**	**0.945534021**	**0.97849**	**2**
P62718	DLTTAGAVTQCYR	0.905747797	2	3.01477
P62718	SSGEIVYCGQVFEKSPLR	1.008490367	2	2.468338
P62752	**RL23A 60S ribosomal protein L23a**	**1.094821612**	**0.98666**	**5**
P62752	LAPDYDALDVANK	1.002301971	2	3.853549
P62752	LDHYAIIK	0.992166661	2	2.644187
P62752	NKLDHYAIIK	1.089627294	2	2.799782
P62752	VNTLIRPDGEK	1.076408494	2	2.819718
P62752	VNTLIRPDGEKK	1.148203206	2	2.868132
P62755	**RS6 40S ribosomal protein S6**	**0.93331041**	**0.03349**	**5**
P62755	DIPGLTDTTVPR	0.885806864	2	2.636167
P62755	LIEVDDER	1.036065631	2	2.735853
P62755	LNISFPATGCQK	0.966060696	2	2.997941
P62755	MATEVAADALGEEWK	1.25098659	2	3.750048
P62755	MATEVAADALGEEWK+Oxidation(0)	0.832311112	2	4.359123
P62804	**H4 Histone H4**	**0.77436451**	**9.9E-20**	**7**
P62804	DAVTYTEHAK	0.750863772	2	3.033608
P62804	DNIQGITKPAIR	0.715281694	2	3.422492
P62804	ISGLIYEETR	2.049203029	2	3.327663
P62804	RISGLIYEETR	0.984261833	2	2.418411
P62804	TVTAMDVVYALK	0.984855294	2	3.989232
P62804	TVTAMDVVYALK+Oxidation(4)	0.734805	2	3.227666
P62804	VFLENVIR	0.821132772	2	3.250706
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**0.76432275**	**0.0418**	**2**
P62815	AVVQVFEGTSGIDAK	0.603506325	2	3.220275
P62815	QIYPPINVLPSLSR	1.465504429	2	2.385887
P62853	**RS25 40S ribosomal protein S25**	**1.204359237**	**0.10947**	**2**
P62853	GGDAPAAGEDA	0.951755342	1	2.022215
P62853	LNNLVLFDK	1.231224194	2	2.808513
P62856	**RS26 40S ribosomal protein S26**	**1.002017743**	**0.90366**	**2**
P62856	DISEASVFDAYVLPK	1.085082691	2	3.402821
P62856	NIVEAAAVR	0.997161831	2	2.879097
P62890	**RL30 60S ribosomal protein L30**	**1.171612693**	**0.00107**	**2**
P62890	TGVHHYSGNNIELGTACGK	1.101247259	2	5.557289
P62890	VCTLAIIDPGDSDIIR	1.194344022	2	3.717555
P62898	**CYC Cytochrome c_ somatic**	**1.084687834**	**0.00038**	**6**
P62898	ADLIAYLK	1.048094088	2	2.777083
P62898	GITWGEDTLMEYLENPK	1.025102804	2	4.882487
P62898	GITWGEDTLMEYLENPKK	1.000532708	2	4.334102
P62898	KTGQAAGFSYTDANK	1.329070871	2	4.891124
P62898	TGPNLHGLFGR	1.035883547	2	3.253972

P62898	TGQAAGFSYTDANK	1.153415438	2	4.15838
P62902	**RL31 60S ribosomal protein L31**	**1.093276291**	**3E-11**	**2**
P62902	NLQTVNVDEN	2.486806853	1	2.291409
P62902	SAINEVVTR	1.064005079	2	3.117265
P62907	**RL10A 60S ribosomal protein L10a**	**1.03991103**	**0.94457**	**5**
P62907	AVDIPHMDIEALK	0.961139122	2	2.328678
P62907	AVDIPHMDIEALKK	1.024867514	2	2.630583
P62907	FSVCVLGDQQHCDEAK	1.051685274	2	3.922549
P62907	KYDAFLASESLIK	1.101924775	2	3.713563
P62907	YDAFLASESLIK	1.191375204	2	3.747255
P62909	**RS3 40S ribosomal protein S3**	**1.187617798**	**9.9E-20**	**10**
P62909	AELNEFLTR	1.092988732	2	2.86139
P62909	DEILPTTPISEQK	0.979584401	2	3.755286
P62909	ELAEDGYSGVEVR	0.969464721	2	3.424266
P62909	ELTAVVQK	0.920860047	2	2.31501
P62909	FGFPEGSVELYAEK	1.881697947	2	3.344488
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.293938407	3	4.015665
P62909	GCEVVVSGK	1.151974659	2	2.496615
P62909	GGKPEPPAMPQPVPTA	1.289321271	2	3.735763
P62909	GLCAIAQAESLR	1.100286681	2	3.160312
P62909	TEIIILATR	1.136449566	2	2.796017
P62912	**RL32 60S ribosomal protein L32**	**1.117896165**	**0.55639**	**2**
P62912	ELEVLLMCNK	1.163092512	2	2.53029
P62912	SYCAEIAHNVSSK	1.096760379	2	4.365849
P62914	**RL11 60S ribosomal protein L11**	**0.997827767**	**1**	**2**
P62914	VLEQLTGQTPVFSK	1.026346763	2	4.050513
P62914	YDGIILPGK	0.997422677	2	2.923451
P62919	**RL8 60S ribosomal protein L8**	**1.150784988**	**6.1E-09**	**3**
P62919	ASGNYATVISHNPETK	1.203815714	2	4.458452
P62919	AVVGVVAGGGR	1.018179161	2	3.559927
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.146870798	3	4.887388
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.914673028**	**1.8E-07**	**3**
P62959	AQVAQPGGDTIFGK	0.911609298	2	4.586193
P62959	CLAFHDISPQAPTHFLVIPK	1.080407289	3	4.566719
P62959	KHISQISVADDDDESLLGHLMIVGK	0.889170799	3	4.151852
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**0.918837394**	**1.1E-07**	**4**
P62961	EDGNEEDKENQGDETQGQQPPQR	0.915646512	3	5.166607
P62961	GAEAANVTGPGGVPVQGSK	1.133403046	2	5.049645
P62961	NEGSESAPEGQAQQR	1.062346232	2	4.989835
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	1.707420297	3	5.495861
P62963	**PROF1 Profilin_1**	**0.961062573**	**0.77842**	**4**
P62963	DSPSVWAAVPGK	1.130875073	1	2.205153

P62963	SSFFVNGLTLGGQK	0.949231214	2	4.52821
P62963	STGGAPTFNVTVTMTAK	0.862616675	2	2.630649
P62963	TFVSITPAEVGVLVGK	0.96309425	2	4.500277
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**1.218548072**	**9.9E-20**	**22**
P63018	ARFEELNADLFR	1.080645137	3	3.623376
P63018	CNEIISWLDK	0.858577622	2	3.137303
P63018	DAGTIAGLNVLR	0.935617664	2	3.597985
P63018	FDDAVVQSDMK	0.934728551	2	3.706823
P63018	FEELNADLFR	0.8789756	2	3.100222
P63018	FELTGIPPAPR	0.702896306	2	3.134699
P63018	IINEPTAAAIAYGLDK	1.140822008	2	4.749603
P63018	IINEPTAAAIAYGLDKK	1.293230787	2	4.554169
P63018	LLQDFFNGK	1.181134187	2	2.676929
P63018	NQTAEKEEFEHQQK	0.896574185	2	5.247122
P63018	NQVAMNPTNTVFDAK	1.067013445	2	4.506462
P63018	NQVAMNPTNTVFDAK+Oxidation(4)	0.903024884	2	4.271168
P63018	NSLESYAFNMK	1.952559232	2	3.245868
P63018	QATKDAGTIAGLNVLR	0.930846734	2	2.441626
P63018	RFDDAVVQSDMK	0.943379758	2	2.749187
P63018	SFYPEEVSSMVLTK	1.00287981	2	4.13757
P63018	SFYPEEVSSMVLTK+Oxidation(9)	0.790028724	2	2.898052
P63018	SINPDEAVAYGAAVQAAILSGDK	1.405769198	2	6.276466
P63018	SQIHDIVLVGGSTR	0.98285541	2	4.961404
P63018	STAGDTHLGGEDFDNR	0.943165667	2	4.426495
P63018	TVTNAVVTVPAYFNDSQR	0.912344622	2	4.084924
P63018	VCNPIITK	1.034636397	2	2.402173
P63029	**TCTP Translationally_controlled tumor protein**	**1.396882099**	**3.2E-12**	**2**
P63029	DLISHDELFSDIYK	1.396980456	2	3.55469
P63029	EIADGLCLEVEGK	1.112730199	2	3.257479
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.02302458**	**0.1698**	**6**
P63036	HYNGEAYEDDEHHPR	1.15187404	3	4.903773
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.041193636	3	3.763417
P63036	NVVHQLSVTLEDLYNGATR	1.061309207	2	5.875858
P63036	QISQAYEVLADSK	0.828887053	2	3.607974
P63036	TIVITSHPGQIVK	1.025997189	2	2.927377
P63036	VNFPENGFLSPDK	0.99165195	2	2.93688
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**1.174059414**	**9.9E-20**	**28**
P63039	AAVEEGIVLGGGCALLR	0.979374134	3	5.979507
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(17)	1.02119806	3	3.316453
P63039	CEFQDAYVLLSEK	1.400345275	2	4.692977
P63039	CIPALDSLKPANEDQK	0.901626056	2	3.313151
P63039	DDAMLLKGKGDK+Oxidation(3)	1.201329803	2	2.409225
P63039	DIGNIISDAMK	0.896520717	2	3.61682

P63039	GVMLAVDAVIAELKK	0.941472141	2	4.303885
P63039	GYISPYFINTSK	1.241885591	2	3.636939
P63039	ILQSSSEVGYDAMLGDFVNMVEK	1.062798819	2	4.968976
P63039	IQEITEQLDITTSEYEK	0.908506073	2	5.602526
P63039	IQEITEQLDITTSEYEKEK	0.784301467	2	5.163188
P63039	ISSVQSIVPALEIANAHR	1.064237895	2	4.091499
P63039	KISSVQSIVPALEIANAHR	1.77562915	3	3.309232
P63039	KPLVIIAEDVDGEALSTLVLNR	1.428948765	2	5.915522
P63039	LSDGVAVLK	1.099389291	2	2.698312
P63039	LVQDVANNTNEEAGDGTTTATVLAR	0.93867291	2	6.638293
P63039	NAGVEGSLIVEK	1.051112458	2	3.466503
P63039	QSKPVTTPEEIAQVATISANGDK	0.959495289	2	3.82041
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	1.006285049	3	5.26728
P63039	RGVMLAVDAVIAELKK	1.173205896	3	4.546206
P63039	TLNDELEIIEGMK	0.92493467	2	4.584354
P63039	TLNDELEIIEGMK+Oxidation(11)	0.850618864	2	3.494438
P63039	TVIIEQSWGSPK	0.873237316	2	4.458215
P63039	VGEVIVTK	0.892397866	2	2.981123
P63039	VGGTSDVEVNEK	0.94859429	2	3.840807
P63039	VGGTSDVEVNEKK	1.2467311	2	3.070491
P63039	VGLQVVAVK	0.945354208	2	3.452997
P63039	VTDALNATR	0.828384748	2	3.477735
P63088	**PP1G Serine/threonine_protein phosphatase PP1_gamma catalytic subunit**	**0.919054508**	**0.14239**	**2**
P63088	EIFLSQPILLELEAPLK	1.277062155	2	3.069157
P63088	TFTDCFNCLPIAAIVDEK	0.89086918	2	3.346401
P63095	**subunit alpha isoforms short**	**1.24244723**	**0.01452**	**2**
P63095	AFEPFYDEIKSKGALVK	1.184491295	2	2.79722
P63095	YTTPEDATPEPGEDPR	1.234253713	2	2.930989
P63102	**1433Z 14_3_3 protein zeta/delta**	**0.887078207**	**0.00152**	**7**
P63102	DICNDVLSLLEK	0.935714887	3	3.909975
P63102	FLIPNASQPESK	0.902966295	2	3.024502
P63102	GIVDQSQQAYQEAFEISK	0.870247316	2	5.716891
P63102	KGIVDQSQQAYQEAFEISK	0.918521015	2	5.324616
P63102	SVTEQGAELSNEER	1.013273237	2	4.96664
P63102	TAFDEAIAELDTLSEESYK	0.926492686	2	5.780411
P63102	YLAEVAAGDDKK	0.977358334	2	2.927513
P63159	**HMGB1 High mobility group protein B1**	**0.790584994**	**3.9E-09**	**3**
P63159	GEHPGLSIGDVAK	0.858788151	2	3.055941
P63159	IKGEHPGLSIGDVAK	0.777578685	3	3.715823
P63159	KHPDASVNFSEFSK	0.854161258	2	3.878653
P63174	**RL38 60S ribosomal protein L38**	**0.960324492**	**0.03229**	**2**
P63174	KIEEIKDFLLTAR	0.969582039	3	3.977749

P63174	YLYTLVITDKEK	1.576993416	2	2.324197
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.061449076**	**5.8E-07**	**8**
P63245	DGQAMLWDLNEGK	1.088303722	2	2.420337
P63245	FSPNSSNPIIVSCGWDK	1.05725437	2	4.539513
P63245	HLYTLDGGDIINALCFSPNR	1.048322731	2	5.68484
P63245	IIVDELKQEVISTSSK	1.056515966	2	4.002417
P63245	LWDLTTGTTTR	1.114032078	1	2.155001
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.227805825	3	5.232193
P63245	VWQVTIGTR	1.205217296	2	2.740269
P63245	YTVQDESHSEWVSCVR	1.142538816	2	4.208179
P63259	**ACTG Actin_ cytoplasmic 2**	**0.940974064**	**9.9E-20**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	2.612616132	3	4.296569
P63259	DLYANTVLSGGTTMYPGIADR	0.909133564	2	5.75515
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13)	0.779209117	2	4.154263
P63259	GYSFTTTAER	0.944210526	2	3.226637
P63259	KDLYANTVLSGGTTMYPGIADR	0.981168704	2	5.747538
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.775248025	3	4.135125
P63259	QEYDESGPSIVHR	0.813477244	3	3.515571
P63259	VAPEEHPVLLTEAPLNPK	0.915041494	2	4.488511
P63324	**RS12 40S ribosomal protein S12**	**1.012615424**	**0.99878**	**3**
P63324	KVVGCSCVVVK	0.970082938	2	2.720434
P63324	LGEWVGLCK	1.080373745	1	2.251585
P63324	VVGCSCVVVK	0.982163273	2	2.358621
P67779	**PHB Prohibitin**	**1.020200179**	**9.9E-20**	**9**
P67779	AAELIANSLATAGDGLIELR	0.947053932	3	5.031523
P67779	AAIISAEGDSK	1.702452757	2	2.455832
P67779	DLQNVNITLR	0.903718032	2	3.269057
P67779	FDAGELITQR	0.869108203	2	3.833949
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.214771391	3	4.148261
P67779	IYTSIGEDYDER	1.406661376	2	3.078731
P67779	KLEAAEDIAYQLSR	0.842308536	2	4.402473
P67779	NVPVITGSK	0.84614277	1	2.205909
P67779	VLPSITTEILK	0.940552853	2	2.34398
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.103866029**	**0.00232**	**3**
P68037	ADLAEEYSK	0.978182333	2	2.562334
P68037	GQVCLPVISAENWKPATK	1.06733618	2	3.007381
P68037	TDQVIQSLIALVNDPQPEHPLR	1.129817435	2	4.950209
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.032251107**	**0.64082**	**3**
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.779626697	3	3.446582
P68101	TEGLSVLNQAMAVIK	1.075511179	2	3.869827
P68101	VVTDTDETELAR	1.022197578	2	2.384977
P68136	**ACTS Actin_ alpha skeletal muscle**	**0.753069839**	**9.9E-20**	**15**

P68136	AGFAGDDAPR	1.210729853	2	3.215099
P68136	AVFPSIVGRPR	0.852466795	2	2.534182
P68136	DLYANNVMSGGTTMYPGIADR	0.719953849	2	4.446043
P68136	DSYVGDEAQSK	0.723795224	2	3.620298
P68136	EITALAPSTMK	0.768210768	2	3.009278
P68136	EITALAPSTMK+Oxidation(9)	0.685226247	2	2.858631
P68136	GYSFVTTAER	0.773535696	2	3.37831
P68136	KDLYANNVMSGGTTMYPGIADR	0.609287938	2	5.461151
P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14)	0.795115831	3	3.684181
P68136	QEYDEAGPSIVHR	0.54887948	2	2.957687
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	0.646560814	3	6.362449
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28)	0.609871217	3	4.602742
P68136	VAPEEHPTLLTEAPLNPK	0.603069503	2	4.435998
P68136	YPIEHGIITNWDDMEK	2.099104326	2	4.566063
P68136	YPIEHGIITNWDDMEK+Oxidation(13)	0.914459278	2	3.459258
P68255	**1433T 14_3_3 protein theta**	**0.925783577**	**0.99697**	**4**
P68255	AVTEQGAELSNEER	1.055080618	2	4.713728
P68255	SICTTVLELLDK	1.097415578	2	3.252977
P68255	TAFDEAIAELDTLNEDSYK	0.926859732	2	4.265424
P68255	VISSIEQK	0.924561712	2	2.326001
P68511	**1433F 14_3_3 protein eta**	**1.202074082**	**0.0002**	**3**
P68511	AVTELNEPLSNEDR	1.194031581	2	4.50381
P68511	ELETVCNDVLALLDK	1.1999923	2	3.276484
P68511	NSVVEASEAAYK	1.251330774	2	2.634066
P69735		**1.037448504**	**0.01231**	**6**
P69735	AKMEENPPVK+Oxidation(2)	0.955269385	1	1.944668
P69735	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	0.903874418	3	3.74464
P69735	EDEVQLLVEK	0.770468782	1	1.911271
P69735	GEPKLPAMDKPGGK+Oxidation(7)	1.032649155	2	2.312405
P69735	LIDDYGVEEEPAELPEGTSLTVDNKR	0.837870485	3	4.684844
P69735	QFDKMQAQLK	1.075324395	2	2.564309
P69897	**TBB5 Tubulin beta_5 chain**	**1.379116064**	**0.00012**	**3**
P69897	ALTVPELTQQVFDAK	1.175515987	2	2.305296
P69897	ISVYYNEATGGK	1.387412852	2	2.895912
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.300864464	2	4.921106
P70372	**ELAV1 ELAV_like protein 1**	**0.852089263**	**0.03018**	**3**
P70372	SLFSSIGEVESAK	0.903019281	2	3.548909
P70372	TNLIVNYLPQNMTQEELR	1.255914324	2	2.981827
P70372	VLVDQTTGLSR	0.845762703	2	2.815492
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.10027816**	**6.2E-11**	**2**
P70470	ASFSQGPINSANR	0.20142522	2	2.809319
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.111004634	3	3.534775

P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.926738777**	**9.9E-20**	**12**
P70473	ADVLLEPFR	0.686864905	2	3.403222
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	0.68966912	5	5.02812
P70473	DYGFSQEEIHQLHSDR	0.592071932	2	4.88701
P70473	GLGLESEELPSQMSIEDWPEMK	0.601438233	3	4.702718
P70473	GQNLLDGGAPFYTTYK	0.703530114	2	4.894444
P70473	LGSVNHPSHLAR	0.841568689	2	2.850481
P70473	LQLGPETLR	0.66842412	2	2.30093
P70473	LSGFGQSGIFSK	0.992503626	2	2.417526
P70473	RDPSVGEHTVEVLK	0.603642525	3	4.293209
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.762314482	5	4.788177
P70473	TADGEFMAVGAIEPQFYTLLLK	1.245505372	3	3.965599
P70473	TQAMGLWAQPR	0.753520422	2	2.810474
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**0.901817983**	**0.98064**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	0.860048758	3	3.703463
P70552	VLGNNFYEYYVNDPPR	1.044979933	2	3.888212
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**0.774561181**	**9.9E-20**	**7**
P70580	EGEEPTVYSDDEEPKDEAAR	0.607831245	2	4.241246
P70580	FYGPEGPYGVFAGR	0.867036801	2	3.586624
P70580	GDQPGASGDNDDDEPPPLPR	0.641577337	2	4.952713
P70580	IVRGDQPGASGDNDDDEPPPLPR	0.723674085	3	4.237782
P70580	KFYGPEGPYGVFAGR	0.982571703	2	3.744595
P70580	RYDGVQDPR	0.586173567	1	2.328986
P70580	YDGVQDPR	0.714932567	2	2.544315
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.544170063**	**9.9E-20**	**8**
P70584	ASSTCQLTFENVK	0.58988148	2	3.128057
P70584	FAQEQIAPLVSTMDENSK	0.641347428	2	4.062275
P70584	IFDFQGLQHQVAHVATQLEAAR	0.522387015	3	6.086495
P70584	IGTIYEGTSNIQLNTIAK	0.58564462	2	4.336423
P70584	KFAQEQIAPLVSTMDENSK	0.648274107	2	5.470951
P70584	SGNYYVINGSK	0.500521654	2	3.121269
P70584	VDASVALLCDIQNTVINK	0.510900275	2	4.673234
P70584	YYASEVAGLTTSK	0.594320235	2	3.57634
P70615	**LMNB1 Lamin_B1**	**0.720796226**	**0.00955**	**3**
P70615	ALYETELADAR	0.871550551	2	3.113181
P70615	LSSEMNTSTVNSAR	0.691271318	2	2.702589
P70615	MLSDKEREMAEIR+Oxidation(0)	0.990307941		2.380429
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**0.924951032**	**9.9E-20**	**2**
P70694	REDIFYTSK	1.411030209	2	2.979534
P70694	SIGVSNFNR	0.601113186	2	2.583139
P70712	**KYNU Kynureninase**	**1.690377062**	**9.9E-20**	**8**

P70712	IATELNCDPTDER	0.913655687	2	3.821668
P70712	IGAYGHEVGK	1.528134546	2	2.490699
P70712	LDEEDKLKR	1.279935248	2	2.515281
P70712	LLTAILDSTERN	1.203610681	2	3.295213
P70712	TYLEEELDK	1.291040822	1	2.038702
P70712	TYLEEELDKWAK	1.294077146	2	2.403753
P70712	VAPVPLYNSFHDVYK	1.88651099	2	3.105412
P70712	YLNSGAGGLAGAFIHEK	1.676340902	2	4.078792
P80067	**CATC Dipeptidyl peptidase 1**	**0.962419223**	**1.4E-11**	**4**
P80067	GTDECAIESIAMAAIPIPK	0.942911638	3	4.953782
P80067	NSWGSQWGESGYFR	0.875777593	2	3.494132
P80067	RGTDECAIESIAMAAIPIPK	0.968997064	2	3.657653
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.508779095	3	4.700295
P80254	**DOPD D_dopachrome decarboxylase**	**0.436777385**	**9.9E-20**	**4**
P80254	FFPLEPWQIGK	0.480815936	2	2.519263
P80254	FLTEELSLDQDR	0.429927045	2	3.545529
P80254	LCAATATILDKPEDR	0.941930335	2	4.564787
P80254	STEPCAHLLISSIGVVGTAEQNR	0.477010689	2	5.317988
P80299	**HYES Epoxide hydrolase 2**	**0.862868648**	**0.03472**	**2**
P80299	GHIEDCGHWTQIEKPAEVNQILIK	0.935714447	3	4.837795
P80299	TEIQNPSVTSK	0.861602691	2	2.913949
P80313	**TCPH T_complex protein 1 subunit eta**	**1.093241197**	**0.00218**	**6**
P80313	ATISNDGATILK	0.949630816	2	2.545905
P80313	EGTDSSQGIPQLVSNISACQVIAEAVR	0.959265943	3	3.729476
P80313	GGAEQFMEETER	1.114747562	2	2.906068
P80313	LLDVVHPAAK	1.008257371	2	2.322724
P80313	QLCDNAGFDATNILNK	0.874735125	2	3.917185
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.183677226	2	5.250331
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.032669075**	**0.47795**	**8**
P80317	ALQFLEQVK	1.050573871	2	2.737882
P80317	DGNVLLHEMQIQHPTASLIAK	1.101904198	3	4.114798
P80317	GIDPFSLDALAK	1.140144388	2	2.430478
P80317	HKSETDTSLIR	0.980445641	2	2.300486
P80317	NAIDDGCVVPGAGAVEVALAEALIK	0.902492368	3	5.683143
P80317	TEVNSGFFYK	1.233905087	2	2.488636
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.075476176	2	4.929206
P80317	VLAQNSGFDLQETLVK	0.996693036	2	3.877496
P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**0.936195455**	**0.00123**	**4**
P81155	LTFDTTFSPNTGK	0.833775535	2	3.17595
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.000744204	3	3.545638
P81155	VNNSSLIGVGYTQTLRPGVK	0.949607274	2	3.622474
P81155	YQLDPTASISAK	0.923853086	1	3.00689

P82995	**HS90A Heat shock protein HSP 90_alpha**	**0.976628376**	**9.9E-20**	**13**
P82995	ELHINLIPNKQDR	0.978857173	2	3.032042
P82995	ELISNSSDALDK	0.939486096	2	2.835321
P82995	HIYFITGETK	1.261558585	2	2.404857
P82995	HLEINPDHSIIETLR	0.90728155	2	4.003802
P82995	HSQFIGYPITLFVEK	4.371271955	2	2.904588
P82995	LGIHEDSQNR	0.185901849	3	3.470865
P82995	NPDDITNEEYGEFYK	1.657525797	2	4.723327
P82995	RAPFDLFENR	1.142845304	2	2.921669
P82995	SLTNDWEEHLAVK	1.125276301	2	4.105975
P82995	TLTIVDTGIGMTK	0.966270251	2	3.865714
P82995	TLTIVDTGIGMTK+Oxidation(10)	0.75674364	2	3.918484
P82995	VFIMDNCEELIPEYLNFIR	1.420260633	3	3.487977
P82995	YYTSASGDEMVSLK	1.039131949	2	3.292574
P83868	**TEBP Prostaglandin E synthase 3**	**1.219575058**	**0.02227**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.875941856	3	3.527152
P83868	LTFSCLGGSDNFK	1.004500307	2	2.528601
P83883	**RL36A 60S ribosomal protein L36a**	**1.013134209**	**0.74647**	**2**
P83883	HFELGGDK	0.891636683	1	2.020567
P83883	LECVEPNCR	1.055296304	2	2.528824
P84082	**ARF2 ADP_ribosylation factor 2**	**1.021566738**	**0.99809**	**2**
P84082	NISFTVWDVGGQDK	1.032798976	2	3.989875
P84082	QDLPNAMNAAEITDK	0.944720595	2	4.20974
P84083	**ARF5 ADP_ribosylation factor 5**	**0.936179223**	**0.00018**	**3**
P84083	DAVLLVFANK	1.764792249	2	3.058684
P84083	QDMPNAMPVSELTDK+Oxidation(2)	1.143795952		2.717098
P84083	VQESADELQK	0.828354751	2	2.59998
P84100	**RL19 60S ribosomal protein L19**	**1.020426515**	**1**	**2**
P84100	LLADQAEAR	1.017090805	2	3.335081
P84100	VWLDPNETNEIANANSR	1.020641413	2	5.162014
P84245	**H33 Histone H3.3**	**0.878439185**	**0.00566**	**4**
P84245	DIQLAR	0.706925801	1	1.976937
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	0.728423882	3	6.785794
P84245	RVTIMPKDIQLAR+Oxidation(4)	0.97532219	1	1.915773
P84245	STELLIR	0.887553176	2	2.457721
P84817	**FIS1 Mitochondrial fission 1 protein**	**0.906275717**	**0.00062**	**4**
P84817	FQSEQAAGSVSK	0.680352984	2	2.549486
P84817	GIVLLEELLPK	0.906270191	2	2.658628
P84817	GLLQTEPQNNQAK	0.971259782	2	3.539327
P84817	KFQSEQAAGSVSK	1.065461805	2	3.499165
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.875300278**	**0.01419**	**14**
P85834	AEAGDNLGALVR	0.962325651	2	3.413235
P85834	DKPHVNVGTIGHVDHGK	0.698659485	2	3.494962

P85834	DLEKPFLLPVESVYSIPGR	1.22231496	2	4.129338
P85834	GDECELLGHNK	0.926585026	2	2.575683
P85834	GEETPVIVGSALCALEQR	1.040185899	2	4.288355
P85834	GITINAAHVEYSTAAR	0.941930335	2	4.019041
P85834	GTVVTGTLER	0.932551105	2	2.645546
P85834	HYAHTDCPGHADYVK	1.436806061	2	4.116796
P85834	KGDECELLGHNK	0.914979198	3	3.86336
P85834	KYEEIDNAPEER	1.055706094	2	3.667236
P85834	LLDAVDTYIPVPTR	0.917430829	2	3.227089
P85834	TIGTGLVTDVPAMTEEDK	0.929348241	2	3.403549
P85834	TIGTGLVTDVPAMTEEDKNIK	1.074761274	2	4.004584
P85834	YEEIDNAPEER	1.029899249	2	3.331055
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.29732584**	**9.9E-20**	**8**
P85968	AGQAVDDFIEK	1.384446724	2	3.103558
P85968	CLSSLKEER	1.089918934	2	2.423365
P85968	FQDTDGKELLPK	1.151320404	2	3.030175
P85968	GILFVGSGVSGGEEGAR	1.535144864	2	4.725883
P85968	LVPLLDTGDIIIDGGNSEYR	1.215145786	2	5.26126
P85968	NPELQNLLLDDFFK	2.099421679	2	4.66022
P85968	SAVDDCQDSWR	1.15356943	2	2.506865
P85968	VGTGEPCCDWVGDEGAGHFVK	1.126547338	3	4.650394
P85971	**6PGL 6_phosphogluconolactonase**	**1.020777561**	**0.00066**	**5**
P85971	DLPAATAPAGPASFAR	0.829780604	2	2.545995
P85971	ILEDQESALPAAMVQPR	0.984565019	2	4.233101
P85971	LPIPDSQVLTIDPALPVEDAAEDYAR	1.208025209	2	4.756588
P85971	TGALCWFLDEAAAR	1.129383813	2	3.85347
P85971	WTLGFCDER	1.195805155	2	2.493023
P85972	**VINC Vinculin**	**0.903962435**	**9.9E-20**	**6**
P85972	ALASQLQDSLK	0.78605164	2	2.322105
P85972	AQQVSQGLDVLTAK	0.887128532	2	4.203481
P85972	AVAGNISDPGLQK	0.753336564	2	3.268168
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.762503839	3	5.293891
P85972	QVATALQNLQTK	1.00017853	2	3.118102
P85972	WIDNPTVDDR	0.749877558	2	2.729185
P85973	**PNPH Purine nucleoside phosphorylase**	**0.85719183**	**9.9E-20**	**10**
P85973	ASHQEVLEAGK	0.817430789	2	3.805377
P85973	DHINLPGFCGQNPLR	0.770182418	2	3.52973
P85973	ELQEGTYIMSAGPTFETVAESCLLR	0.914817822	2	5.170015
P85973	HRPQVAVICGSGLGGLTAK	0.73480193	3	5.794366
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.145657185	3	4.307453
P85973	MLGADAVGMSTVPEVIVAR	0.844198633	2	4.222852
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0)	0.877014084	2	5.281503

P85973	MLGADAVGMSTVPEVIVAR+Oxidation(8)	0.877014084	2	3.416082
P85973	VFGFSLITNK	1.217640471	2	2.472141
P85973	VFHLLGVDTLVVTNAAGGLNPK	0.896046383	2	4.924625
P86048	**RL10L 60S ribosomal protein L10_like**	**1.214506915**	**0.00049**	**2**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.195562778	3	6.149157
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.282186827	3	4.872549
P97313	**PRKDC DNA_dependent protein kinase catalytic subunit**	**0.90108229**	**0.83702**	**2**
P97313	FHGVMKTLCLEVVLCR+Oxidation(4)	0.911698658	2	2.307758
P97313	LCHDAFTENMVGESQLLEK	0.781520375	2	2.55094
P97384	**ANX11 Annexin A11**	**0.879271166**	**0.03592**	**2**
P97384	GFGTDEQAIIDCLGSR	0.89698519	2	3.615065
P97384	SELDLLDIR	0.833213639	2	2.996954
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**1.040539757**	**0.14285**	**7**
P97519	EVSIFGAASELFTR	0.943953416	2	2.976622
P97519	GFEEAVAAGAK	0.921053921	2	3.453538
P97519	GYVSCALGCPYEGK	0.978272668	2	4.112865
P97519	KNVNCSIEESFQR	1.076982202	2	3.457658
P97519	LLEAGDFICQALNR	1.068028194	2	4.46894
P97519	NVNCSIEESFQR	0.824506366	2	3.62254
P97519	WVPQMADHSDVLK	0.949936757	2	2.315388
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**0.852191242**	**3.5E-05**	**4**
P97521	CLLQIQASSGK	0.753943459	2	3.040649
P97521	LQTQPPSLPGQPPMYSGTIDCFR	0.853454961	2	3.700874
P97521	SVHDLSVPR	0.813081653	2	2.354771
P97521	YSGTLDCAK	0.945300661	2	2.453932
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**0.866301572**	**0.23151**	**11**
P97524	GEVGLLICK	0.719651264	2	2.340047
P97524	IQDTIEITGTFK	1.035266361	2	2.811436
P97524	TILHVFLEQAR	0.883279629	2	2.943198
P97524	TSNTNGVDTVLDK	0.944585154	2	2.706554
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	0.965554742	3	4.738248
P97524	TYVPMTEDIYNAIIDK	1.031851316	2	2.785213
P97524	VLLASPELHEAVEEVLPTLK	0.86745687	3	4.212831
P97524	VTLMEEGFNPSVIK	1.05320129	2	3.952802
P97524	YDVEKDEPVR	0.974186104	2	2.744646
P97524	YLCNTPQKPNDR	1.006637172	2	2.826348
P97524	YNATVIQYIGELLR	2.022633643	2	3.582401
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**0.996545585**	**9.9E-20**	**9**
P97532	AFGHHSVSLLDGGFR	0.910263552	2	3.222543
P97532	ALVSAQWVAEALK	1.189419243	2	3.222246
P97532	AQPEHVISQGR	0.754287435	1	2.677281

P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	0.992524876	3	6.650425
P97532	FQGTQPEPR	0.803842068	2	3.337012
P97532	LLDASWYLPK	1.114499987	2	3.353261
P97532	SPSEPAEFCAQLDPSFIK	0.707616035	2	2.845774
P97532	THEDILENLDAR	0.809923975	2	3.673381
P97532	YWLSQNLPISSGK	0.821632875	2	3.394027
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**0.944678619**	**0.00041**	**5**
P97536	AADIDQEVK	1.540341098	2	2.445155
P97536	AVAALLTIPEAEK	0.985181066	2	2.982876
P97536	EGPAVVGQFIQDVK	0.95931605	2	2.412363
P97536	ITSEALLVTQQLVK	0.930059026	2	2.634743
P97536	SVILEAFSSPSEEVK	1.104102972	2	2.473804
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.173013517**	**9.9E-20**	**17**
P97562	ATFADFCAQGAEICR	1.30033743	2	4.850674
P97562	CSAQTAADFR	2.123765545	2	3.085899
P97562	DFSLLPELHALSTGMK	1.198094814	2	2.340362
P97562	EAFLDLLPLIR	1.146038578	2	2.727204
P97562	FAEVLPDGTYQR	2.995724707	2	2.453399
P97562	HSPSFSVER	1.017219603	2	2.428501
P97562	ILEYQTQQQK	1.090596042	2	3.83991
P97562	KVESIIQSDPVFNLK	1.130275348	2	4.786794
P97562	LDKEPEIQR	1.002136328	2	3.244909
P97562	LGTPQSNYLGMLVTR	1.164414569	2	2.535848
P97562	LTNILDGGLPNTVLR	1.179555391	2	4.597988
P97562	MGLEHIDNGFLQLNHVR	1.359997695	3	4.828183
P97562	MGLEHIDNGFLQLNHVR+Oxidation(0)	0.946576505	3	3.619441
P97562	SGVDQHDAWNQTTVIHLQAAK	1.199846535	3	6.059176
P97562	SLEDHTPLPGITVGDIGPK	1.061032926	3	4.702854
P97562	SLGSDEQIAK	1.016569559	2	3.049968
P97562	VESIIQSDPVFNLK	1.034682039	2	4.591491
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**1.000661625**	**0.98195**	**2**
P97576	ATQSVPKEEVSNNNPHLK	0.950478911	3	3.407987
P97576	DLLEVADILEK	1.00071109	2	3.055806
P97584	**PTGR1 Prostaglandin reductase 1**	**0.753406402**	**9.9E-20**	**5**
P97584	ALTDLMNWVSEGK	0.688873092	2	4.130702
P97584	GGETVLVNAAAGAVGSVVGQIAK	0.789938419	2	5.008087
P97584	HFEGFPTDSNFELR	0.67931574	2	3.695263
P97584	TGPCPPGPSPEVIIYQQLR	1.212212469	2	4.300282
P97584	YHEYITEGFEK	0.654999776	2	2.851187
P97608	**OPLA 5_oxoprolinase**	**1.241491925**	**3.6E-09**	**7**
P97608	AGDFGAAFVER	1.043888206	2	3.00888
P97608	GSILDPSPEAAVVGGNVLTSQR	0.79675399	2	4.885572

P97608	ISVGAEGPSMADTR	0.739346518	2	2.714082
P97608	ISVGAEGPSMADTR+Oxidation(9)	1.145378079	2	2.466193
P97608	LEEQCVDALQVQGFPR	1.197877121	2	3.049272
P97608	LLSEDPANYADAPTEGIR	1.032336387	2	2.839118
P97608	TGDLLEIQQPVDLEALR	0.796309168	2	4.829195
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.165028561**	**0.00056**	**4**
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.10073339	3	3.591303
P97612	GTNCVTSYLTDCETQLSQAPR	1.181689096	2	4.879849
P97612	NSVGLPVAVQCVALPWQEELCLR	1.123332481	2	4.063348
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	2.194512676	2	4.87486
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**0.808221103**	**9.9E-20**	**3**
P97700	AVVVNAAQLASYSQSK	0.782329618	2	4.311816
P97700	GIYTGLSAGLLR	0.851653067	2	2.622166
P97700	LTGADGTPPGFLLK	0.851150032	2	3.422353
P97840	**LEG9 Galectin_9**	**1.867885111**	**9.9E-20**	**3**
P97840	FEEGGYVVCNTK	0.88951295	2	3.237333
P97840	NTQINNSWGPEER	2.876304485	2	2.723046
P97840	SINISGVVLPDAK	2.547201767	2	3.433416
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.960654875**	**9.9E-20**	**18**
P97852	AVANYDSVEAGEK	1.022125279	2	3.929727
P97852	AYALAFAER	1.061715701	2	3.263891
P97852	DTTSLNQAALYR	0.866941176	2	3.229864
P97852	FVYEGSADFSCLPTFGVIVAQK	0.890091146	2	2.947545
P97852	GALVVVNDLGGDFK	1.607178649	2	4.200909
P97852	GSSAADKVVEEIR	0.865927186	2	2.397472
P97852	HVLQQFADNDVSR	0.855237179	2	4.407331
P97852	ICDFSNASKPK	0.890602858	2	3.254502
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	0.903224721	3	5.58683
P97852	IDVVVNNAGILR	0.87153721	2	3.944085
P97852	ISDEDWDIIQR	0.751114833	2	4.123106
P97852	KNNIHCNTIAPNAGSR	0.743379334	2	4.658937
P97852	NGSGEVYQGPAK	1.209471386	2	3.576514
P97852	NNIHCNTIAPNAGSR	0.764262884	2	4.358411
P97852	SIQESTGGIIEVLHK	0.979628644	2	4.30546
P97852	SLMSGGLAEVPGLSINFAK	0.807996299	2	3.511303
P97852	VLHGEQYLELYKPLPR	1.151453873	2	3.994061
P97852	VVLVTGAGGGLGR	0.887174325	2	3.597025
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.122217687**	**0.83777**	**3**
Q00438	KLPSDVTEGEVISLGLPFGK	1.018437297	2	4.227991
Q00438	LSLDGQNIYNACCTLR	1.099326225	2	3.753609
Q00438	NNQFQALLQYADPVSAQHAK	1.079044609	2	5.375885

Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**0.96868927**	**1.5E-09**	**2**
Q00PI9	AVEEQGDDQDSEK	0.429011366	2	3.897223
Q00PI9	EEAQPIVTKYK	1.766051501	1	1.984461
Q01177	**PLMN Plasminogen**	**0.931964384**	**0.1213**	**3**
Q01177	CTTPPPPPGPTYQCLK	0.881478701	2	2.537731
Q01177	ILGSDVQQIAVTK	0.94172605	2	3.478179
Q01177	LVLEPNDADIALLK	1.157513906	2	2.814899
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.090941339**	**6.7E-16**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	0.950681962	2	6.292093
Q01205	NDVITVQTPAFAESVTEGDVR	1.089614812	2	5.237657
Q01205	NVETMNYADIER	1.102437125	2	3.539021
Q01205	VEGGTPLFTLR	1.008539122	2	3.126445
Q01279	**EGFR Epidermal growth factor receptor**	**1.00839656**	**0.61034**	**2**
Q01279	NLQEILIGAVR	1.018697771	2	3.523454
Q01279	NYVVTDHGSCVR	0.657220616	2	2.721021
Q01405	**SC23A Protein transport protein Sec23A**	**1.234105675**	**2.6E-05**	**4**
Q01405	AETEEGPDVLR	0.517541848	2	3.104984
Q01405	AVLNPLCQVDYR	1.023095842	2	2.917633
Q01405	HLLQAPVDDAQEILHSR	1.224957997	3	5.489069
Q01405	YIDTEHGGSQAR	1.355807623	2	3.128011
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.790799584**	**9.9E-20**	**29**
Q02253	AEMEAAVAACK	0.822756999	2	3.756109
Q02253	AEMEAAVAACK+Oxidation(2)	0.878156451	2	2.369361
Q02253	AEMEAAVAACKR	0.931620684	2	2.441915
Q02253	AFPAWADTSILSR	0.906198595	2	4.043441
Q02253	AISFVGSNQAGEYIFER	1.02807779	2	5.210232
Q02253	CMALSTAVLVGEAK	0.972755426	2	4.284485
Q02253	CMALSTAVLVGEAK+Oxidation(1)	0.721024979	2	3.390106
Q02253	EEDATLSSPAVVMPTMGR	0.658541859	2	4.364034
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12)	0.680062655	2	2.658854
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15)	0.680062655	2	2.994363
Q02253	EGASILLDGR	0.609139695	2	2.5253
Q02253	ENTLNQLVGAAFGAAGQR	0.706009437	2	5.265094
Q02253	GLQVVEHACSVTSLMLGETMPSITK	0.920943206	2	3.128989
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.011512093	2	5.46838
Q02253	LFIDGK	0.802269111	1	1.98009
Q02253	LITLEQGK	0.834583183	2	2.542436
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.812536861	3	4.534876
Q02253	NHGVVMPDANK	0.666982321	1	3.37557
Q02253	NHGVVMPDANK+Oxidation(5)	0.869560902	2	3.133326

Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	0.747787933	3	5.583002
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5)	0.654853869	3	4.536937
Q02253	QGIQFYTQLK	1.381239275	2	2.633466
Q02253	SDKWIDIHNPATNEVVGR	0.934817455	2	5.003437
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.720331112	2	5.229124
Q02253	TLADAEGDVFR	0.797394144	2	3.557268
Q02253	VCNLIDSGAK	0.775203517	2	3.419867
Q02253	VNAGDQPGADLGPLITPQAK	0.78538064	2	5.872653
Q02253	WIDIHNPATNEVVGR	0.854945724	2	4.806534
Q02253	WLPELVER	0.707701586	1	2.047425
Q02769	**FDFT Squalene synthase**	**1.038306616**	**0.00034**	**3**
Q02769	KLEDFVKPENVDVAVK	1.179240347	2	4.008185
Q02769	TQSLPNCQLISR	0.260756416	2	2.373805
Q02769	VVLEDFPTISLEFR	0.482053553	2	3.191253
Q02874	**H2AY Core histone macro_H2A.1**	**1.045474004**	**4.4E-13**	**2**
Q02874	AASADSTTEGAPTDGFTVLSTK	1.462722517	2	3.90074
Q02874	GVTIASGGVLPNIHPELLAK	0.839483799	2	3.725696
Q02974	**KHK Ketohexokinase**	**1.068689603**	**4E-13**	**7**
Q02974	CGLQGFDGIV	1.086639411	1	1.931799
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.030959808	3	5.789862
Q02974	GGNASNSCTVLSLLGAR	1.274109199	2	4.769522
Q02974	GNSMQEALR	0.896208819	2	2.796444
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	1.076385592	3	5.776125
Q02974	IEQYNATQPLQQK	1.22017294	2	4.823329
Q02974	TIILYDTNLPDVSAK	1.057888466	2	4.160303
Q03070	**CHIO Beta_chimaerin**	**0.765428659**	**2.3E-06**	**2**
Q03248	**BUP1 Beta_ureidopropionase**	**0.970909297**	**9.9E-20**	**12**
Q03248	AHHDLGYFYGSSYVAAPDGSR	1.137221058	2	6.31155
Q03248	EDLVLAPSSG	0.780898314	1	2.16939
Q03248	EKLPWTEFAESAEDGLTTR	0.865451288	3	5.420652
Q03248	ELAEAVKPNYSPNIVK	0.806367987	2	3.999628
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	0.829364435	3	3.450475
Q03248	HNMVVISPILER+Oxidation(2)	0.759577473	3	3.323118
Q03248	IPLPTSAPVAEQVSALHK	2.327940296	3	4.736858
Q03248	KHNMVVISPILER+Oxidation(3)	0.789175991	2	2.854398
Q03248	NAAIANHCFTCALNR	1.116599573	2	4.615192
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.312718004	3	4.766819
Q03248	VGQEHYPNEFTSGDGK	1.093395904	2	4.202857
Q03248	VGQEHYPNEFTSGDGKK	1.000462983	3	4.390571
Q03336	**RGN Regucalcin**	**0.785329189**	**9.9E-20**	**16**
Q03336	CGESPVWEEASK	0.837209433	2	4.634557
Q03336	CLLFVDIPSK	1.089598939	2	3.587068

Q03336	DEQIPDGMCIDVEGK	0.86032315	2	3.844223
Q03336	DYSEMYVTCAR	0.855820491	2	3.533961
Q03336	FNDGKVDPAGR	0.927783754	2	3.094414
Q03336	HQGSLYSLFPDHSVK	1.186305911	2	4.67337
Q03336	KYFDQVDISNGLDWSLDHK	0.758245017	3	5.102449
Q03336	LWVACYNGGR	1.628194239	2	2.36953
Q03336	MEKDEQIPDGMCIDVEGK	1.151179734	2	4.941734
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0)	0.818526183	2	4.421831
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10)	0.813069756	2	2.582642
Q03336	QSGGYVATIGTK	0.843776624	2	2.832511
Q03336	VGVDAPVSSVALR	0.947335316	2	3.732556
Q03336	YFAGTMAEETAPAVLER	0.958344117	2	5.615844
Q03336	YFAGTMAEETAPAVLER+Oxidation(5)	0.869205346	2	5.258267
Q03336	YFDQVDISNGLDWSLDHK	0.832720789	3	4.203415
Q03626	**MUG1 Murinoglobulin_1**	**1.007067407**	**5.7E-08**	**7**
Q03626	EESSCIHSSCTAER	0.956202458	2	4.015704
Q03626	FQVDNSNR	0.93198053	1	2.28701
Q03626	GGEFEMMPLGVNK	0.96339725	2	2.409217
Q03626	LTAQPAPSPEDLALSMGTIK	1.167240894	2	3.480268
Q03626	NLHPLNELFPLAYIEDPK	1.755197776	3	4.353296
Q03626	VQTVPLTCNNPK	1.045953132	2	3.028707
Q03626	VYHKEESSCIHSSCTAER	0.795025959	3	4.322114
Q04462	**SYVC Valyl_tRNA synthetase**	**0.866259068**	**1.5E-05**	**2**
Q04462	ALNPLEEWLR	0.977083663	2	2.618196
Q04462	SVTQQPGSEITAPQK	0.861431186	2	3.727619
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**0.878741432**	**0.00216**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(0)	0.872380797	2	2.594978
Q05144	YLECSALTQR	0.927145315	2	2.628647
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.027446984**	**0.24158**	**5**
Q06647	FSPLTANLMNLLAENGR	1.252820232	3	3.963166
Q06647	GEVPCTVTTAFPLDEAVLSELK	0.987110883	3	5.991828
Q06647	GQILNLEVK	1.03221577	2	2.615952
Q06647	LGNTQGVISAFSTIMSVHR	1.393121057	3	3.541844
Q06647	TDPSIMGGMIVR	0.96531454	2	2.301752
Q07071	**GCKR Glucokinase regulatory protein**	**1.359502652**	**9.9E-20**	**8**
Q07071	AAPISCHVQVAHEK	1.326297725	2	4.98641
Q07071	LLGQCDAEIFQEEGQIVPTYQR	2.238377865	2	2.985001
Q07071	QEAFVLNPAIGPEGLSGSSR	1.455430294	2	4.102199
Q07071	STQALEDPPACGTLN	1.409127538	2	2.646906
Q07071	TVDQGVVSSQR	1.258875487	2	3.20456
Q07071	VIPTALLSLLLR	1.453318013	2	2.589844
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	1.331735417	2	5.320509

Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.413431066	3	5.388371
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**1.014664031**	**0.19413**	**6**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.925596257	2	4.816015
Q07116	FVDLHPGGQSK	1.200633903	2	2.821556
Q07116	IGELNPEDR	0.942905359	2	2.325684
Q07116	LHVVGAPGGQSLSLSLDDLHK	0.900526043	3	3.886066
Q07116	NHLPVPNLDPDTYR	0.871757083	2	2.47862
Q07116	VSVESEESYSHWQR	0.986586164	2	3.830728
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.817014129**	**9.9E-20**	**11**
Q07523	ALKEEKPTQSVPVSFPK	0.631303873	2	4.133059
Q07523	ALVITIDTPVLGNR	0.691749819	2	4.480488
Q07523	ASFCWNDLSLLQSITR	0.891950319	2	4.316896
Q07523	EEKPTQSVPVSFPK	0.670689475	2	3.173342
Q07523	EVLDILTAELHR	0.742187321	2	3.358614
Q07523	GEDGVKEVLDILTAELHR	0.748449743	3	5.201115
Q07523	HNVQGIVVSNHGGR	0.687211225	3	5.9516
Q07523	NQLNLEANILLK	0.773696824	2	3.470469
Q07523	QLDEVSASIDALR	0.602678571	2	3.484373
Q07523	TSWDFIEGEADDGITYSENIAAFK	0.786970759	3	3.543399
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	1.407574824	3	3.989794
Q07936	**ANXA2 Annexin A2**	**0.642364641**	**4.9E-10**	**2**
Q07936	GLGTDEDSLIEIICSR	0.777802093	2	2.932078
Q07936	GVDEVTIVNILTNR	0.617834998	2	3.449976
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.172128195**	**1.6E-06**	**2**
Q07984	FFDEESYSLLR	1.31384182	2	3.224594
Q07984	NNEDVSIIPPLFTVSVDHR	1.138907077	3	3.842327
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**0.992723242**	**0.00565**	**5**
Q08163	ALLVTASQCQQPAGNK	0.745910074	2	4.613036
Q08163	LEAVSHTSDMHCGYGDSPSK	0.887540337	3	4.2197
Q08163	SALFAQINQGESITHALK	1.045078375	2	4.037986
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	0.972296832	2	3.930781
Q08163	VENQENVSNLVIDDTELK	0.889019505	2	4.953146
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.177434169**	**0.10025**	**3**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	1.128908612	3	4.526573
Q08415	ILVLNTPNNPLGK	1.380558708	2	2.832564
Q08415	LGASNDWQLDPAELASK	0.496295577	2	3.293769
Q09073	**ADT2 ADP/ATP translocase 2**	**1.31088002**	**5.5E-05**	**7**
Q09073	AAYFGIYDTAK	1.57583845	2	2.480694
Q09073	DFLAGGVAAAISK	0.976730823	2	4.675204
Q09073	GLGDCLVK	1.038139276	2	2.623147
Q09073	GTDIMYTGTLDCWR	1.308052615	2	3.479454
Q09073	LLLQVQHASK	1.303791136	2	2.476515

Q09073	QIFLGGVDK	1.269088091	2	2.503343
Q09073	QIFLGGVDKR	1.494616499	2	2.571011
Q09199	**B4GN2 Beta_1_4 N_acetylgalactosaminyltransferase 2**	**0.874724497**	**0.26393**	**2**
Q09199	MKYKFQDAYNQK+Oxidation(0)	0.968515127	2	3.007985
Q09199	QQTVPKLYDPGPER	0.872768475	2	2.309048
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.950346898**	**2.8E-15**	**5**
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	0.755563291	3	3.741223
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	1.003938841	3	3.913607
Q0D2L3	SVDEGLLDSK	0.715955408	1	1.903493
Q0D2L3	SVDEGLLDSKR	0.884400418	2	2.748976
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.41137168	2	5.483888
Q0VGK3	**GLCTK Glycerate kinase**	**0.781099065**	**0.01554**	**4**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	0.720132054	3	5.455039
Q0VGK3	GATIQELNTIR	0.938271914	2	3.501949
Q0VGK3	QLFDSAVGAVQPGPMLQR	0.884890447	2	2.399611
Q0VGK3	VAAACLTSSTAERPLEEEAK	1.055576811	3	3.379326
Q0ZHH6	**ATLA3 Atlastin_3**	**1.016480792**	**0.51165**	**4**
Q0ZHH6	EHGHSNWLGDPEEPLTGFSWR	1.035058655	3	4.163634
Q0ZHH6	EQLQTLIPYVLNPSK	1.176936779	2	2.875535
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	0.876413323	2	4.574502
Q0ZHH6	YQQELEEEITELYENFCK	1.024699851	2	5.473967
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.767122829**	**9.9E-20**	**23**
Q10758	AEAETMYQIK	0.744304658	2	3.217112
Q10758	AQYEEIANR	0.797289582	2	3.317327
Q10758	ATLEAAIADAEQR	0.796992864	2	4.673237
Q10758	ELQSQISDTSVVLSMDNSR	0.846276947	2	6.021467
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	0.745339132	2	4.456502
Q10758	LEGLTDEINFLR	0.845309521	2	4.172653
Q10758	LESGMQNMSIHTK	0.775685192	2	3.791135
Q10758	LEVDPNIQAVR	0.800382548	2	3.754794
Q10758	LEVELGNMQGLVEDFK	0.738204618	2	4.838166
Q10758	LKLEVELGNMQGLVEDFK	0.978312267	3	3.924508
Q10758	LQAEIDALK	0.760016852	2	2.71283
Q10758	LVSESSDIMSK	0.748383117	2	3.276882
Q10758	QIHEEEIR	0.676612362	1	2.260443
Q10758	RQLEALGQEK	0.65625577	2	2.342144
Q10758	SKTEISEMNR	0.703806761	3	3.435878
Q10758	SKTEISEMNR+Oxidation(7)	0.79369188	3	3.316963
Q10758	SLDMDSIIAEVR	0.788229019	2	4.385111
Q10758	SNMDNMFESYINNLR	1.726074577	2	3.930996
Q10758	SRAEAETMYQIK	0.791870098	2	3.419209
Q10758	TEMENEFVLIK	0.792065392	2	3.704112

Q10758	TEMENEFVLIK+Oxidation(2)	0.611201823	2	2.607109
Q10758	WSLLQQQK	0.747025744	2	2.621778
Q10758	YEELQTLAGK	0.733966358	2	3.533819
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.770541955**	**9.9E-20**	**4**
Q14DH7	STLSALVNGKPYK	0.806612282	2	2.8071
Q14DH7	THFAASVADPER	0.747531015	2	3.363013
Q14DH7	VDDVINVAGHR	0.503049104	2	3.013592
Q14DH7	VTPTIEDPSIFGHIEEVLK	1.001907391	2	3.448131
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.642119726**	**9.9E-20**	**10**
Q1HCL7	ALNEVFIGESLSSR	0.730319126	2	2.597473
Q1HCL7	ASYYEISVDDGPWEK	0.998427741	2	3.469481
Q1HCL7	LKPVIGVNTDPER	0.808762956	2	2.842851
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	0.818743174	3	3.944955
Q1HCL7	NVEHIIDSLRDEGIEVR	0.696306815	2	2.637195
Q1HCL7	QGNLTLPLNK	0.641627412	2	2.576342
Q1HCL7	SEASGPQLLPVR	0.823374377	2	3.095424
Q1HCL7	SEGHLCLPVR	0.522830313	2	2.406078
Q1HCL7	SSGLNLCTGTGSK	0.630946687	2	3.354122
Q1HCL7	VTNEYNESLLYSPEEPK	0.870770234	2	4.72075
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.005942164**	**0.01403**	**5**
Q1JU68	EEEEQRRAEEQMLK	0.863835455	2	2.594255
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	0.944222203	3	3.709209
Q1JU68	FNVLQYVVPEVK	1.276900435	2	3.468587
Q1JU68	ILQEHEQIK	0.96163498	2	2.484971
Q1JU68	MPAYFQRPENALK	1.186506212	2	2.501138
Q29RW1	**MYH4 Myosin_4**	**0.961384371**	**0.06128**	**5**
Q29RW1	LQDAEEHVEAVNSK	0.102146639	2	4.558672
Q29RW1	NAYEESLDQLETLK	0.886350217	2	4.672459
Q29RW1	NAYEESLDQLETLKR	0.605426467	2	3.788425
Q29RW1	TLEDQLSEVK	0.599293994	1	1.938447
Q29RW1	VKNLTEEMAGLDENIVKLTK+Oxidation(7)	1.138007295	2	2.487515
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.007801815**	**0.08682**	**5**
Q2V057	EDCTQPDYEATSR	0.966330431	2	3.190851
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.194252835	3	3.583256
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.187823411	2	5.547729
Q2V057	REQALLSQELWR	0.989259339	2	3.067287
Q2V057	SIPYGCLEEVIPYLIR	1.717088296	2	2.365288
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**1.062069834**	**0.51385**	**3**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	1.101910657	3	3.806794
Q3B7D0	HCDDSYTPQDK	1.406912041	2	2.985642
Q3B7D0	LEEDGDELAR	1.032338442	2	2.450053

Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**0.844934976**	**9.9E-20**	**4**
Q3B7U9	SCSQVLEHQPDNIK	0.594153035	2	3.929116
Q3B7U9	TAEDGPDLEMLSGQER	0.845044723	2	3.198392
Q3B7U9	VDMTCEEEEELLQLK	0.971919623	2	3.349041
Q3B7U9	VLAQQGEYSEAIPILR	0.712287272	2	3.627445
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**0.89042755**	**0.02415**	**2**
Q3KRD8	HGLLVPNNTTDQELQHIR	0.886153874	3	4.528344
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.023453534	3	4.264246
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.131687497**	**0.17772**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.213142373	2	3.390961
Q3KRE0	QEESVQKQEAIRR	0.931985111	2	2.44646
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**1.340398952**	**4.6E-11**	**2**
Q3KRE8	ALTVPELTQQMFDSK	1.27483158	2	3.126923
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.232332016	3	4.442835
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**0.902278656**	**9.9E-20**	**5**
Q3MIE0	DGQEGIEAFIQK	0.848550887	2	3.315477
Q3MIE0	SDILHEAESEDLK	0.791151178	2	3.217865
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.260024109	2	4.293262
Q3MIE0	VIIISAEGPVFSSGHDLK	0.943647935	2	4.24602
Q3MIE0	VVPEEQLEEEATR	0.707504542	2	3.862801
Q3MIF4	**XYLB Xylulose kinase**	**0.76417672**	**4.7E-09**	**6**
Q3MIF4	DLPEFGTQGGVHVHK	0.965906685	2	2.580442
Q3MIF4	FNADNMEVSAFPGDVEIR	0.864214757	2	3.543281
Q3MIF4	IRDESASCSWNK	0.754593835	2	4.038109
Q3MIF4	VVAFTGDNPASLAGMR	1.004279965	2	3.41045
Q3MIF4	VWSQACLDACAPHLK	1.071421336	2	3.482405
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	0.950955022	2	5.232971
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**1.102526291**	**0.00555**	**4**
Q3T1J1	EDLRLPEGDLGK	0.89198005	2	2.930072
Q3T1J1	EDLRLPEGDLGKEIEQK	1.188463995	2	3.861861
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.122402635	3	5.472258
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.143835713	3	3.902327
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.021521549**	**0.69733**	**2**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.079592379	3	3.792885
Q3T1K5	FTVTPSTTQVVGILK	0.965755201	2	3.448036
Q3U2P1	**SC24A Protein transport protein Sec24A**	**0.965588725**	**0.8582**	**2**
Q3U2P1	SVTASLSDAR	0.956644169	2	2.603142
Q3U2P1	TLETQSALGPALQAAFK	1.036580399	2	3.101465
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.00225234**	**0.99794**	**2**
Q3UHR0	MQILQRKDTWAPK+Oxidation(0)	1.009236588	2	2.321075

Q3UHR0	NLEEPGLLSR	1.002136328	2	2.323716
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.078451143**	**0.20655**	**2**
Q3ULJ0	GIDEGPDGLK	1.033421521	2	2.679812
Q3ULJ0	LGLMEMIAFAK	1.300475555	2	3.309729
Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.169547842**	**9.9E-20**	**13**
Q3UQ44	ALVGSENPPLTVIR	1.154367175	2	3.418619
Q3UQ44	AWVNQLETQTGEASK	0.995300741	2	5.008138
Q3UQ44	GVLLGIDDLQTNQFK	1.198669087	2	4.802857
Q3UQ44	HTDNTVQWLR	0.919400156	2	2.322217
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.520151916	3	4.136055
Q3UQ44	LGIAPQIQDLLGK	1.375845717	2	2.56322
Q3UQ44	LPYDVTTEQALTYPEVK	1.070460467	2	4.874897
Q3UQ44	LSAEEMDER	1.17495013	2	2.67249
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.291561503	2	4.945505
Q3UQ44	TALEEEIK	1.025688327	1	1.909055
Q3UQ44	TLDTLLLPTANIR	1.002218256	2	2.733276
Q3UQ44	VDQVQDIVTGNPTVIK	1.117587169	2	5.287315
Q3UQ44	YQDILNEIAK	1.077531291	2	2.58773
Q3UU35	**OVOS Ovostatin homolog**	**0.370256018**	**0.04455**	**2**
Q3UU35	EQQAKSLLSILDK	0.362899242	2	2.37259
Q3UU35	FSGPNNTPLVDK	0.625601028	2	2.364866
Q3V0K9	**PLSI Plastin_1**	**0.929146114**	**9.9E-20**	**3**
Q3V0K9	AYFHLLNQIAPK	1.309203768	2	2.663215
Q3V0K9	KIENCNYAVELGK	0.755916056	2	3.589231
Q3V0K9	QFVTPADVVSGNPK	0.734893119	2	3.499646
Q3V132	**ADT4 ADP/ATP translocase 4**	**0.925422083**	**0.40608**	**2**
Q3V132	GNLANVIR	0.919303444	2	2.646248
Q3V132	YFPTQALNFAFK	1.550145795	2	2.502429
Q497B0	**NIT2 Omega_amidase NIT2**	**1.128264047**	**9.9E-20**	**14**
Q497B0	ADLYSVESK	1.194491268	2	3.008034
Q497B0	AGTEETILYSDIDLK	1.408572707	2	3.699649
Q497B0	ASYVAWGHSTVVDPWGQVLTK	0.920295484	2	4.762712
Q497B0	AVDNQVYVATASPAR	1.297726721	2	4.74165
Q497B0	AVDNQVYVATASPARDEK	1.269964813	2	3.292629
Q497B0	ENSIYLIGGSIPEEDDGK	0.925051386	2	2.586455
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	1.101254552	3	4.024076
Q497B0	FAELAQIYAR	1.822768224	2	3.688807
Q497B0	IHLFDIDVPGK	1.113752823	2	2.809039
Q497B0	KIHLFDIDVPGK	1.113875184	3	4.679057
Q497B0	LALIQLQVSSIK	1.271735112	2	3.060254
Q497B0	LYNTCAVFGPDGNLLVK	0.957869175	2	4.117814
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	1.178908756	2	4.250361

Q497B0	TLSPGDSFSTFDTPYCR	1.486410747	2	4.699053
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.335222646**	**1.6E-13**	**7**
Q499N5	GATLSHHNIVNNSNLIGQR	1.227215254	2	4.682648
Q499N5	GGENIYPAELEDFFHK	1.126491104	2	2.742203
Q499N5	GGVIAGSLAPPELIR	1.207661971	2	2.785322
Q499N5	SGETTTEEEIK	0.939675623	2	3.294297
Q499N5	TGDIASMDEQGFCR	1.230367923	2	3.372527
Q499N5	TVGECLDATAQR	1.221254326	2	2.631075
Q499N5	YIVFVEGYPLTVSGK	1.366543055	2	4.147549
Q4AEF8	**COPG Coatomer subunit gamma**	**1.387856716**	**0.0003**	**4**
Q4AEF8	FGAQNEEMLPSILVLLK	1.092442159	2	4.009438
Q4AEF8	QEIFQEQLAAVPEFQGLGPLFK	1.456109424	2	3.801677
Q4AEF8	SSPEPVALTESETEYVIR	1.165623356	2	3.881681
Q4AEF8	TLEEAVGNIVK	0.845818962	2	2.43452
Q4FZT0	**STML2 Stomatin_like protein 2**	**0.896381936**	**1.4E-12**	**7**
Q4FZT0	AEQINQAAGEASAVLAK	0.85419056	2	5.218204
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	1.113994208	2	4.073671
Q4FZT0	ATVLESEGTR	1.072888241	2	2.572175
Q4FZT0	DVQTTDTSIEELGR	1.75876585	2	2.917351
Q4FZT0	ESLNANIVDAINQAADCWGIR	0.96530357	2	3.014851
Q4FZT0	ILEPGLNVLIPVLDR	0.857555891	2	2.651004
Q4FZT0	NTVILFVPQQEAWVVER	0.897364584	2	3.309701
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**0.915096062**	**0.00018**	**5**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.804161715	3	4.879641
Q4FZT9	FGGSGSQVDSAR	0.892543392	2	3.545676
Q4FZT9	SGALLACGIVNSGVR	0.904980537	2	3.538701
Q4FZT9	TPVQSQQPSATAPSGADEK	0.986243909	2	4.180166
Q4FZT9	VGQAVDVVGQAGKPK	1.360887293	2	2.717344
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.88580809**	**9.9E-20**	**4**
Q4FZX7	GDAGSADVQDLEK	1.204766199	2	3.076029
Q4FZX7	GNSLTLIDLPGHESLR	1.126703059	2	3.208313
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.891170532	2	4.373162
Q4FZX7	VGDGAGGAFQPYLDSLR	1.159320489	2	3.320086
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**0.997812822**	**0.44079**	**3**
Q4G061	AEEEGGSDGSAAEAEPR	0.856892556	2	4.599443
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	0.404183332	3	5.275448
Q4G061	GTQGVVTNFEIFR	0.983076451	2	3.065531
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.062343277**	**2E-08**	**9**
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.08247087	3	4.865601
Q4KLP0	LEELCPFPLDSLQQEMGK	0.954626748	2	4.992385

Q4KLP0	LLLESQEFDHFLATK	1.085063766	2	3.371296
Q4KLP0	LVTVYCEHGHK	1.235688565	2	2.367546
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.041435345	3	5.054205
Q4KLP0	SSLYSSDIGK	1.145076981	1	2.062884
Q4KLP0	SVEVPEELQLHSHLLK	1.163101868	2	3.52528
Q4KLP0	YGGEGAESMMGFFHELLK	1.282180263	3	4.722781
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	0.97851018	3	4.712882
Q4KLZ6		**1.209426991**	**9.9E-20**	**12**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.193582579	2	5.051637
Q4KLZ6	AILEVLQTK	1.667234945	2	3.141289
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.207756639	2	3.147828
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	1.085488645	2	5.352194
Q4KLZ6	AVAQAGTAGTLLIVK	1.624436033	2	3.992459
Q4KLZ6	EGPTPASPAQVLSK	1.250347254	1	3.086317
Q4KLZ6	ISTTLIGLEEHLNALDR	1.782213041	2	3.044081
Q4KLZ6	LIDAETNAK	1.249189014	2	2.538576
Q4KLZ6	LNFGLAMEQAK	0.580745001	2	2.756873
Q4KLZ6	LSVLLLEK	2.019691107	2	2.38109
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.324788721	3	5.413909
Q4KLZ6	VAGALAEEGMGLEEITK	1.95162309	2	4.002456
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.077761078**	**0.00355**	**6**
Q4KM49	AFCEPGNVENNGVLSFVK	0.961674638	2	3.160332
Q4KM49	IDVGEAEPR	1.113711285	2	2.331782
Q4KM49	QVEHPLLSGLLYPGLQALDEEYLK	1.180157041	3	3.43755
Q4KM49	QVEPLDPPAGSAPGER	0.880078714	2	2.731626
Q4KM49	TVVSGLVQFVPK	1.035221014	2	2.93474
Q4KM49	VDAQFGGIDQR	1.188770221	2	3.163657
Q4KM73	**KCY UMP_CMP kinase**	**1.00739412**	**8.7E-05**	**6**
Q4KM73	EMDQTMAANAQK+Oxidation(1)	0.716010355		2.546498
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.100589476	2	4.265735
Q4KM73	KNPDSQYGELIEK	1.125080617	2	4.059239
Q4KM73	NQDNLQGWNK	1.016211686	2	3.003123
Q4KM73	SVDEVFGDVMK	1.056704951	1	2.380033
Q4KM73	YGYTHLSAGELLR	1.135633044	3	4.363742
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.064520638**	**0.65341**	**3**
Q4KM74	DLQQYQSQAK	1.147263411	2	3.044678
Q4KM74	GEALSALDSK	1.005953067	2	2.943116
Q4KM74	NLGSINTELQDVQR	0.981155366	2	4.12268
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**0.907611509**	**0.00921**	**2**
Q4KMA2	IDIDPEETVK	0.955269385	1	2.552562
Q4KMA2	QIIQQNPSLLPALLQQIGR	0.871477441	2	4.851447
Q4LDD4	**ARAP1 Arf_GAP with Rho_GAP domain_ ANK repeat and PH domain_containing protein 1**	**1.160073589**	**0.07884**	**2**

Q4LDD4	LLDSLRQDAR	0.608461012	2	2.353717
Q4LDD4	LSSASVLGVRGSEQPDR	1.194344022	2	2.469859
Q4QQV3	**F162A Protein FAM162A**	**1.007622704**	**0.96662**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	0.937798324	2	3.691034
Q4QQV3	RHESLTSLNLER	1.029422281	3	3.913064
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.877226553**	**0.09815**	**3**
Q4QQW3	HLETAEILGANIR	0.813892712	2	2.340286
Q4QQW3	NLSQLPPVQIVMDSLSK	0.856157346	2	2.713561
Q4QQW3	VEPTDGSFMDAIEFAK	0.962299625	2	3.162513
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.09590979**	**1.3E-15**	**4**
Q4QRB4	AILVDLEPGTMDSVR	1.014012681	2	3.54907
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10)	1.009891706	2	3.759681
Q4QRB4	EIVHIQAGQCGNQIGAK	1.053556716	2	5.062567
Q4QRB4	ISEQFTAMFR	1.519435926	2	3.349626
Q4V7C7	**ARP3 Actin_related protein 3**	**0.804760951**	**0.01232**	**4**
Q4V7C7	KDYEEIGPSICR	0.931592729	2	3.179635
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.343477662	2	2.619276
Q4V7C7	LSEELSGGR	0.800694875	2	2.447011
Q4V7C7	YSYVCPDLVK	1.263887489	2	2.421438
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**0.804855425**	**7.2E-12**	**3**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK+Oxidation(0)	0.793687787	3	3.37502
Q4V8K1	SDVIVLAVHR	1.04023108	2	2.300995
Q4V8K1	TCADEFPLTVDSSEK	0.803032457	2	4.508103
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.782849521**	**0.05997**	**2**
Q505J8	LQQVQAGQAEK	0.782722456	2	2.700526
Q505J8	SLQALGEVIEAELR	0.824250244	2	3.162968
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**0.937800381**	**0.03221**	**3**
Q561R9	ANIIYPGHGPVIHNAEAK	1.094227732	2	4.073836
Q561R9	ILIDTGEPSVPEYISCLK	0.787770615	2	3.591895
Q561R9	NISNDATYCIK	0.927559407	2	2.508695
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.025448926**	**0.00037**	**3**
Q561S0	VITVDGNICSGK	0.994537719	2	3.297762
Q561S0	VVEDIEYLNYNK	1.327144225	2	3.91076
Q561S0	YGLLASILGDK	1.074295075	2	3.63839
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.762116187**	**0.6255**	**4**
Q562C4	AQFSEVQLEWQPPPFK	0.762125259	2	4.928831
Q562C4	HIGDGCHLTR	0.749127728	3	3.3981
Q562C4	VLQEVQR	0.617633279	1	1.904199
Q562C4	VTCVDPNPNFEK	0.855713625	2	3.530564
Q562C9	**MTND 1_2_dihydroxy_3_keto_5_methylthiopentene dioxygenase**	**0.917935445**	**0.59556**	**2**

Q562C9	LDADKYENDPELEQIR	0.939053547	2	3.771639
Q562C9	LDADKYENDPELEQIRK	0.899556274	3	3.791579
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**0.946152555**	**1**	**8**
Q58FK9	AIILNTPHNPIGK	0.878662511	2	3.31121
Q58FK9	ALSCLYGK	0.887567284	1	2.001167
Q58FK9	DSTLDAAEEIFR	0.806836153	2	3.075975
Q58FK9	IEGLDQNVWVEFTK	0.961508918	2	4.024992
Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.048943327	3	5.253339
Q58FK9	MDDPECYFNSLPK	1.016116455	2	3.726789
Q58FK9	RIEGLDQNVWVEFTK	0.943094016	2	4.387062
Q58FK9	WTSSDWTFNPQELESK	0.883613121	2	5.096912
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.362544715**	**9.9E-20**	**3**
Q5BJQ0	AVLDSSPFLSEANAER	1.372093295	2	4.842834
Q5BJQ0	MGGSFLICSKLK+Oxidation(0)	1.191375204	2	2.326127
Q5BJQ0	TLNNDLGPHWR	1.195360611	2	2.412748
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.788267555**	**9.9E-20**	**21**
Q5BJY9	AQIFANSVDNAR	0.902349706	2	3.212051
Q5BJY9	AQYEQLAQK	0.755034579	2	3.086969
Q5BJY9	DAETTLLELR	0.702176648	2	3.57211
Q5BJY9	KVVDDTNITR	0.781890662	2	3.023956
Q5BJY9	LEAEIATYR	0.725938671	2	2.958278
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.44099336	2	3.584319
Q5BJY9	LQLETEIEALK	0.71520487	2	2.334069
Q5BJY9	LQLETEIEALKEELLFMK	1.083966528	2	4.95938
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.760161899	2	5.931715
Q5BJY9	NQNINLENNLGEVEAR	0.807981189	2	5.395996
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	1.180416089	3	4.903996
Q5BJY9	QSVESDIHGLR	0.75960906	2	2.754449
Q5BJY9	QTQEYEALLNIK	0.79461647	2	3.818381
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.65260223	2	6.068655
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK+Oxidation(14)	0.923800505	2	4.624505
Q5BJY9	TLQTLEIDLDSMK	0.763629899	2	4.187773
Q5BJY9	VKLEAEIATYR	0.805107086	2	2.893545
Q5BJY9	VQMEQLNGVLLHLESELAQTR	0.857521406	2	5.028546
Q5BJY9	VRPASSAASVYAGAGGSGSR	1.530898053	2	4.959877
Q5BJY9	VVDDTNITR	0.758982939	2	3.512539
Q5BJY9	YWSQQIEESTTVVTK	0.99583832	2	4.240804
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.036730471**	**0.14877**	**3**
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.243073901	3	4.822174
Q5BK63	NFDFEDVFVNIPR	0.990534944	2	4.039148
Q5BK63	WLSSEIEETKPAK	1.180711619	2	2.549127
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.907667026**	**0.25437**	**2**

Q5BK81	VEEVSLPDTINEGQVR	0.907687381	2	4.297467
Q5EB77	**RAB18 Ras_related protein Rab_18**	**0.929459568**	**0.49487**	**2**
Q5EB77	LDNWLNELETYCTR	0.901980668	2	3.127669
Q5EB77	NDIVNMLVGNK	0.939250924	2	3.270662
Q5FVM6	**MTMRC Myotubularin_related protein 12**	**0.801231685**	**3.4E-06**	**3**
Q5FVM6	IVSGIIHHTQSPK	0.75649451	2	2.577226
Q5FVM6	LLEMMEEVQSLQEK+Oxidation(3)	7.303153383	2	2.730121
Q5FVM6	LLEMMEEVQSLQEK+Oxidation(4)	7.303153383	2	2.676554
Q5FVN1	**STBD1 Starch_binding domain_containing protein 1**	**0.815059967**	**0.36916**	**3**
Q5FVN1	DGGAEPLKDAPPGEAAAPGGGPGGGGSGGLSPEPSDR	0.839417322	3	5.407667
Q5FVN1	DLGNLTEAQR	0.758421258	2	2.491595
Q5FVN1	NSLVGGGWEVDGK	0.923074799	2	2.396076
Q5FVQ4	**MLEC Malectin**	**0.974827485**	**0.9992**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	0.976147758	3	5.364247
Q5FVQ4	STPEDQILYQTER	0.968515127	2	2.934954
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.867432681**	**0.68438**	**2**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10)	0.866891887	2	2.667907
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8)	0.871672313	2	2.406847
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.154430421**	**0.97447**	**3**
Q5FVR5	DEKENLFQSK	1.104635095	2	2.509888
Q5FVR5	ILFIVGENDQCLASK	1.102516029	2	3.519517
Q5FVR5	IQQPGIGVISVSK	1.198140754	2	2.765305
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.95604689**	**0.87236**	**2**
Q5FW57	AIDQEMFK	0.915133038	2	2.451717
Q5FW57	SSQMLQMLESSLR	0.956454796	2	3.603118
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**1.016711155**	**0.43647**	**2**
Q5HZV9	AIENIDTLTNLESLFLGK	1.034311686	2	2.587089
Q5HZV9	ELDLYDNQIKK	0.448089444	2	2.517656
Q5HZY0	**UBXN4 UBX domain_containing protein 4**	**0.90582657**	**0.12304**	**2**
Q5HZY0	LPDGSSFTNQFPSDAPLEEAR	1.10332075	2	4.452279
Q5HZY0	NTELCETPTTSDPK	0.896842841	2	3.906864
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.774215745**	**1.1E-16**	**4**
Q5I0C3	HAPLVEFEEEEV	0.878942621	2	2.60123
Q5I0C3	IIEEAPAPGIDPEVR	0.753198379	2	3.803097
Q5I0C3	SEKEFQEQLESAR	0.8536159	2	3.137144
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	0.957998678	2	5.250779
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.808682123**	**0.00032**	**2**
Q5I0D1	ESQSILTPLVSLDTPGK	0.805552935	2	3.625353
Q5I0D1	HEEFEEGCK	0.847174243	2	2.580274

Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**0.833756233**	**0.00337**	**2**
Q5I0E7	QLVEQVEQIQK	0.852294307	2	3.775221
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	0.769861068	3	3.45501
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**0.790293499**	**0.00107**	**7**
Q5I0H9	DKNQDLCQQESVK	0.777390497	2	4.364689
Q5I0H9	DVVHIDSEKDFR	0.720583145	2	2.411297
Q5I0H9	GPPLWEEDPGAK	0.861862417	2	2.991781
Q5I0H9	GQGTICWVDCGDAESR	1.026637429	2	3.933275
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.365704238	3	3.495957
Q5I0H9	NQDLCQQESVK	0.85834996	2	3.273687
Q5I0H9	TELGFTSFIR	1.237356957	2	2.815834
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**0.860441004**	**1.8E-07**	**6**
Q5I0J9	HANLLVGSPSALADQTTER	1.143850078	2	5.255484
Q5I0J9	LDAAGGLQSLR	0.984450021	2	3.734359
Q5I0J9	LEGPLAAAHSSGPR	0.858400802	2	3.401618
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.161323001	2	3.6543
Q5I0J9	NSNTMAAAALAAPSLGFDR	0.921633974	2	4.027501
Q5I0J9	NSNTMAAAALAAPSLGFDR+Oxidation(4)	0.803867431	2	2.830415
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.210452615**	**0.00702**	**3**
Q5I0M2	DNHVVAAGSMEK	0.978982006	2	2.52527
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.047977741	3	4.903224
Q5I0M2	LYAEGDIPVPHAR	1.213128925	2	3.497058
Q5I0P2	**GCSH Glycine cleavage system H protein_ mitochondrial**	**1.302727476**	**0.00472**	**2**
Q5I0P2	MTLSDPSELDELMSEEAYEK	1.291834564	2	4.969545
Q5I0P2	SCYEDGWLIK	1.969843944	2	2.601657
Q5M7U6	**ARP2 Actin_related protein 2**	**0.881244426**	**0.0012**	**3**
Q5M7U6	GYAFNHSADFETVR	0.959757902	2	3.553263
Q5M7U6	HLWDYTFGPEK	0.917445248	2	3.086746
Q5M7U6	KVVVCDNGTGFVK	0.569582638	2	2.481131
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.676994209**	**9.9E-20**	**7**
Q5M7W5	AAVGLTGNDIATPPNK	0.695774366	2	3.340347
Q5M7W5	ATSPSTLVSTGSSSR	0.677082147	2	3.850222
Q5M7W5	NTAPPTEEETVPGK	0.781352508	2	2.465443
Q5M7W5	NTTPTGATPPAGMASTR	0.580070209	2	2.775645
Q5M7W5	STLPVDEGSPLEK	0.790268667	2	2.50582
Q5M7W5	VGSLDNVGHLPAGGTVK	0.734268293	2	3.650003
Q5M7W5	VTEFNNVTPLSEEEVASIK	0.856870746	2	3.579927
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.416271219**	**9.9E-20**	**6**
Q5M875	ALTAELDTLGK	1.36873791	1	2.009573
Q5M875	IQNIQFEAIVGHR	1.779236678	3	3.427271
Q5M875	LWPVLEPDEVAR	1.219305602	2	2.750591

Q5M875	NSGHIVTVASVCGHR	1.034863752	2	2.891394
Q5M875	SVAGQTVLITGAGHGIGR	1.47104676	2	4.071236
Q5M875	TSCLCPVFVNTGFTK	1.256948008	2	3.548834
Q5M9G3	**CAPR1 Caprin_1**	**0.95608408**	**0.99574**	**2**
Q5M9G3	LNQDQLDAVSK	0.944851679	2	3.384257
Q5M9G3	YQEVTNNLEFAK	0.998746119	2	2.470774
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**0.790884008**	**2.9E-14**	**8**
Q5PPL3	AVLDANDPKK	0.556629604	2	2.31806
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	0.673152219	2	4.76149
Q5PPL3	GQVTGTDLINEVSK	0.606673389	2	3.782432
Q5PPL3	GVSTVFHCASPPSNSNNK	0.853842062	2	3.942226
Q5PPL3	GYAVNVFDVR	0.740352802	2	3.430586
Q5PPL3	ILTGLNYEAPK	0.572289894	2	2.786599
Q5PPL3	KGQVTGTDLINEVSK	0.578162464	2	4.616582
Q5PPL3	VQFFIGDLCNQQDLYPALK	0.874246808	2	5.284945
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**1.087095982**	**6.4E-13**	**4**
Q5PQT3	AIQNLASIHSLQVK	1.073584587	2	3.013428
Q5PQT3	DPENCQEFLGSSEVINWK	1.103392913	2	4.737935
Q5PQT3	LSSLDVTHAALVNK	1.794668796	2	3.05235
Q5PQT3	QHLQIQSSQSHLNK	0.667756451	2	3.550527
Q5RJR2	**TWF1 Twinfilin_1**	**0.947811606**	**0.43652**	**2**
Q5RJR2	HQTLQGVAFPISR	1.067787047	2	2.343112
Q5RJR2	YLLSQSSPAPLTAAEEELR	1.045295334	2	3.589548
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**0.862881802**	**0.01562**	**5**
Q5RJR8	ATVLDLSCNK	0.879884679	2	2.693558
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	0.868166577	2	5.996643
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.046636458	2	3.12499
Q5RJR8	LQQLPADFGR	1.00217615	2	2.631027
Q5RJR8	LSTLPSDFCGLTHLVK	1.111640734	2	2.397697
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**0.965190467**	**0.9651**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.101914862	3	4.83996
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	1.010186525	3	4.407589
Q5RKI0	YAPSGFYIASGDISGK	0.993769529	2	4.414797
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**0.995189931**	**9.3E-05**	**4**
Q5RKI1	ELAQQIQK	0.835188171	1	2.1123
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.209716062	2	4.482565
Q5RKI1	GYDVIAQAQSGTGK	0.981238269	2	5.122459
Q5RKI1	MFVLDEADEMLSR	1.179143481	2	3.713569
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**0.879228434**	**0.06059**	**11**
Q5SGE0	AALDLEQVPSELAVTR	0.986795908	2	3.787923
Q5SGE0	CIANNQVETLEK	0.894558574	2	2.865988

Q5SGE0	GLDAIELSR	0.954328628	2	2.447499
Q5SGE0	HCVTMDTPAEK	0.485077195	2	3.0397
Q5SGE0	HDNAEDALNLK	0.877813036	2	3.427001
Q5SGE0	MEGANIQPNR	0.943819135	2	2.653864
Q5SGE0	SCGSLLPELSLAER	1.039800116	2	2.491825
Q5SGE0	SGSPGSNQALLLLR	1.003202535	2	2.803065
Q5SGE0	SSLSSSSPSAGDTVTEK	0.847629473	2	4.045105
Q5SGE0	SYVADKDVASAK	0.792199392	2	2.457317
Q5SGE0	TLLELIPELR	0.874057691	2	2.732244
Q5SNZ0	**GRDN Girdin**	**1.20258312**	**0.0708**	**2**
Q5SNZ0	KVEILENEIIQEK	1.255187015	2	2.522902
Q5SNZ0	LEMENQSLTKTVEELR	0.948659451	2	2.364224
Q5SX40	**MYH1 Myosin_1**	**0.691186428**	**0.36181**	**69**
Q5SX40	AAYLQNLNSADLLK	0.464468959	2	4.368195
Q5SX40	ADIAESQVNK	0.535020147	2	3.509636
Q5SX40	AEDEEEINAELTAK	0.582706638	2	4.013975
Q5SX40	AGLLGLLEEMR	0.631591837	2	3.427724
Q5SX40	AGLLGLLEEMRDDK	0.929118669	2	3.17781
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	0.603332258	3	6.304634
Q5SX40	ANLLQAEIEELR	0.568112329	2	3.877061
Q5SX40	ANSEVAQWR	0.604273639	2	3.157691
Q5SX40	DLEEATLQHEATAATLR	0.633380714	2	4.855207
Q5SX40	DTQLHLDDALR	0.639288773	2	3.198178
Q5SX40	EEQAEPDGTEVADK	0.579252674	2	3.296257
Q5SX40	ELEEISER	0.670878278	1	2.061783
Q5SX40	ELEGEVENEQK	0.601489774	2	2.548838
Q5SX40	ELEGEVENEQKR	0.50333817	2	3.281485
Q5SX40	ELTYQTEEDRK	0.766573913	2	3.078153
Q5SX40	ENQSILITGESGAGK	0.598245468	2	4.181929
Q5SX40	EQYEEEQEAK	0.490011694	1	3.344578
Q5SX40	GQEDLKEQLAMVER	0.66612348	2	4.118229
Q5SX40	GSSFQTVSALFR	0.789627114	2	3.082216
Q5SX40	HADSVAELGEQIDNLQR	0.616691572	2	5.586379
Q5SX40	IAEQELLDASER	0.828152971	2	3.24455
Q5SX40	IEDEQALGMQLQK	0.56050939	2	4.091157
Q5SX40	IEELEEEIEAER	0.667633219	2	3.778149
Q5SX40	IKLEQQVDDLEGSLEQEK	0.689093831	2	5.024045
Q5SX40	IQHELEEAEER	0.599819255	2	3.572844
Q5SX40	IQLELNQVK	0.624582191	2	2.881454
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	0.57124329	3	6.363937
Q5SX40	KIAEQELLDASER	0.58105111	2	3.764159
Q5SX40	KIQHELEEAEER	0.729169944	3	4.042257
Q5SX40	KKLETDISQIQGEMEDIVQEAR	0.684417035	3	4.505655

Q5SX40	KLEDECSELK	0.575211164	2	2.719396
Q5SX40	KLEDECSELKK	0.470774491	3	4.916778
Q5SX40	KLETDISQIQGEMEDIVQEAR	0.621972475	2	5.625667
Q5SX40	LAQESTMDVENDKQQLDEK	0.781520375	2	4.905185
Q5SX40	LDEAEQLALK	0.646495347	2	3.592026
Q5SX40	LEEAGGATSAQIEMNK	1.060137105	2	3.566289
Q5SX40	LEQQVDDLEGSLEQEK	0.703751184	2	5.023464
Q5SX40	LEQQVDDLEGSLEQEKK	0.549892775	2	3.911954
Q5SX40	LETDISQIQGEMEDIVQEAR	0.656430471	2	5.370902
Q5SX40	LINELTAQR	0.628276175	2	3.130297
Q5SX40	LQDAEEHVEAVNAK	0.56273153	2	4.684793
Q5SX40	LQDLVDK	0.548316705	1	2.010559
Q5SX40	LQNEVEDLMIDVER	0.64892765	2	3.969707
Q5SX40	LQTESGEYSR	0.633634929	2	2.359988
Q5SX40	MEIDDLASNMEVISK	0.71001729	2	4.626048
Q5SX40	MEIDDLASNMEVISKSKGNLEK	0.970533883	2	2.312638
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	0.602710267	3	6.0546
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0)	0.638321372	3	4.774293
Q5SX40	NDLQLQVQSEADSLADAEER	0.594548657	2	6.228336
Q5SX40	NKDPLNETVVGLYQK	0.589027102	2	4.197359
Q5SX40	NLQQEISDLTEQIAEGGK	0.494116954	2	5.72428
Q5SX40	NLQQEISDLTEQIAEGGKR	0.658707964	2	4.700225
Q5SX40	NLTEEMAGLDETIAK	0.640347535	2	4.402757
Q5SX40	QAEEAEEQSNVNLAK	0.522383196	2	4.414633
Q5SX40	QKYEETHAELEASQK	0.599273695	2	4.124084
Q5SX40	QLDEKDSLVSQLSR	0.732243937	2	3.128924
Q5SX40	QREEQAEPDGTEVADK	0.51371621	2	3.992642
Q5SX40	SELQAALEEAEASLEHEEGK	0.718516659	2	5.396703
Q5SX40	SSVFVVDAK	0.518635934	2	2.690304
Q5SX40	TKYETDAIQR	0.545283011	3	3.586549
Q5SX40	TLEDQVSELK	0.653196618	2	2.866839
Q5SX40	TNAACAALDK	0.953391349	2	2.905536
Q5SX40	TNAACAALDKK	0.747128344	2	2.96631
Q5SX40	VLNASAIPEGQFIDSK	0.576238212	2	3.648799
Q5SX40	VQLLHTQNTSLINTK	0.615254843	2	4.968987
Q5SX40	VRELEGEVENEQK	1.048609081	2	2.58607
Q5SX40	VRELEGEVENEQKR	0.556663148	3	3.512467
Q5SX40	VVESMQSTLDAEIR	0.699531835	2	3.970633
Q5SX40	YETDAIQR	0.777464675	2	2.30081
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.116416188**	**0.00089**	**3**
Q5U206	DTDSEEEIR	1.034965206	2	2.85672
Q5U206	MKDTDSEEEIR	0.879181627	3	3.901918
Q5U206	MKDTDSEEEIR+Oxidation(0)	1.483079674	2	3.656955

Q5U211	**SNX3 Sorting nexin_3**	**0.840884413**	**0.0754**	**2**
Q5U211	CLHMFLQDEIIDK	0.724877889	2	2.512612
Q5U211	GDDGIFDDNFIEER	0.974356651	2	2.747305
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.020779379**	**1**	**3**
Q5U2Q7	GFGGIGGILR	0.984503931	2	2.726184
Q5U2Q7	YFDEISQDTGK	1.002762454	2	3.002523
Q5U2Q7	YVLHCQGTEEEK	1.056720824	2	3.457814
Q5U2Z3	**NP1L4 Nucleosome assembly protein 1_like 4**	**1.106427122**	**0.00116**	**2**
Q5U2Z3	LDNVSHTPSSYIETLPK	1.103008491	3	3.518448
Q5U2Z3	TYKMKSEPDK	2.232011314	1	2.307105
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**0.888995066**	**7.8E-09**	**10**
Q5U300	AAVASLLQSVQVPEFTPK	1.11140578	3	3.663842
Q5U300	AENYDISPADR	0.887482472	2	3.152476
Q5U300	DNPGVVTCLDEAR	0.878606156	2	3.134188
Q5U300	IYDDDFFQNLDGVANALDNVDAR	1.007152965	3	4.483192
Q5U300	LDQPMTEIVSR	1.174753723	2	2.745057
Q5U300	NEEDATELVTLAQAVNAR	1.058967123	2	4.585142
Q5U300	NFPNAIEHTLQWAR	1.250994938	2	2.329084
Q5U300	SLPASLAEPDFVMTDFAK	0.958252569	2	3.868164
Q5U300	SPPAVQQDNVDEDLIR	0.830151674	2	4.676074
Q5U300	VVQGHQQLDSYK	0.883451099	2	3.247773
Q5U312	**RAI14 Ankycorbin**	**0.978751666**	**0.03899**	**2**
Q5U312	ISQDADLKTPTK	0.611323465	2	2.351519
Q5U312	MHLLYAVQGQMDEDVQKVLK	1.240747617	2	2.524441
Q5U315	**RNA polymerase GLD2**	**1.102144335**	**0.92229**	**3**
Q5U315	KLDSAQQQCTEFLELIQQSLKDK	1.134417561	3	3.891707
Q5U315	QANNINMLKDGMK	1.034169968	1	2.101375
Q5U315	WEMDDPRPIAKAER	0.997771832	2	2.418452
Q5XFW8	**SEC13 Protein SEC13 homolog**	**0.962744437**	**0.98382**	**2**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	0.926964564	2	3.583376
Q5XFW8	NGGQILIADLR	1.063609411	2	2.930642
Q5XFX0	**TAGL2 Transgelin_2**	**0.885599367**	**9.9E-20**	**3**
Q5XFX0	DDGLFSGDPNWFPK	0.668791614	2	3.694493
Q5XFX0	NFSDNQLQEGK	0.756962983	2	2.939384
Q5XFX0	YGINTTDIFQTVDLWEGK	0.780638477	2	4.764005
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.031636804**	**8.7E-10**	**7**
Q5XHY5	AEHDSILAEK	0.902478159	2	2.757436
Q5XHY5	FLGDIEIWNQAEK	0.979449201	2	3.652484
Q5XHY5	GFQEVVTPNIFNSR	0.689313561	2	3.176931
Q5XHY5	QLENSLNEFGEK	1.044763039	2	3.057342
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.093640185	2	4.136822
Q5XHY5	VVWDLDRPLETDCTLELLK	1.882109575	2	3.955368

Q5XHY5	WELNPGDGAFYGPK	1.197493607	2	3.826979
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.09448057**	**0.29737**	**11**
Q5XHZ0	AFLEALQHQAETSSR	1.032252934	2	4.424129
Q5XHZ0	AQLLQPTLEINPR	0.967207611	2	3.769161
Q5XHZ0	EELVSNLGTIAR	0.948956228	2	2.380356
Q5XHZ0	FEDTSPAGER	0.987056558	2	2.828673
Q5XHZ0	GTITIQDTGIGMTK	0.848143698	2	3.354754
Q5XHZ0	GVVDSEDIPLNLSR	0.970841494	2	4.749973
Q5XHZ0	HLAEHSPYYEAMK	0.963908958	2	2.338017
Q5XHZ0	LDTHPAMVTVLEMGAAR	1.047859929	3	3.74412
Q5XHZ0	SDCKDFANESR	1.002005021	2	2.911949
Q5XHZ0	YESSALPAGQLTSLSDYASR	1.224527565	2	4.794215
Q5XHZ0	YIAQAYDKPR	1.030959018	2	2.602846
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**0.713993778**	**0.01229**	**5**
Q5XI22	AGHFDKEIVPVHVSSR	0.632054509	2	3.864826
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	0.781691506	3	4.468885
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	0.688371162	2	5.002166
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	0.850864357	3	4.572478
Q5XI22	VNIDGGAIALGHPLGASGCR	0.706240431	2	5.471931
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**0.892107694**	**0.18297**	**4**
Q5XI32	GCWDSIHVVEVQEK	0.733385861	2	3.061206
Q5XI32	KLEVEANNAFDQYR	0.889749843	2	4.07821
Q5XI32	LEVEANNAFDQYR	0.859381562	2	3.366152
Q5XI32	STLNEIYFGK	1.049541626	2	2.404682
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**0.979453252**	**0.29144**	**3**
Q5XI60	ALDIAAGITR	0.745188709	2	3.055067
Q5XI60	HHVALDSAASQLSGR	1.22837105	2	3.62374
Q5XI60	NVATDALGALEAR	0.677204062	2	4.190222
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.027542736**	**5.9E-09**	**3**
Q5XI73	AEEYEFLTPMEEAPK	0.944649379	2	4.381744
Q5XI73	SIQEIQELDKDDESLR	0.960660975	2	4.688811
Q5XI73	VAVSADPNVPNVIVTR	1.240422453	2	4.140522
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**1.170588092**	**1.5E-12**	**11**
Q5XI78	FGLEGCEVLIPALK	0.817974358	2	3.339713
Q5XI78	FLDTAFDLDAFKK	0.8227183	2	2.813032
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	0.817426839	3	4.39293
Q5XI78	ICEEAFTR	1.151355615	2	2.631347
Q5XI78	IEQLSPFPFDLLLK	1.069549915	2	3.813109
Q5XI78	LEAADEGSGDMK	0.88476365	2	3.323728
Q5XI78	LNVLANVIR	0.467052083	2	2.322634
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.260322889	3	4.674477

Q5XI78	NTNAGAPPGTAYQSPLSLSR	1.039256802	2	4.117846
Q5XI78	VIPEDGPAAQNPDK	0.93430133	2	3.188186
Q5XI78	YAELLVSQGVVNQPEYEEEISK	1.166305523	2	4.324884
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**0.635525086**	**1.7E-06**	**4**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.772420574	2	3.944797
Q5XI95	IIAVDINK	0.841817628	2	2.782745
Q5XI95	NNICTEIR	0.635211933	2	2.315088
Q5XI95	TVGATDCVDPR	0.549520326	2	2.721371
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**0.931264563**	**0.00136**	**5**
Q5XIC0	ATQQDFENAMNQVK	0.927125591	2	4.659765
Q5XIC0	GILVTSEGGITK	0.93274453	2	3.945824
Q5XIC0	LHAVNEEECTTLR	0.936496482	2	3.727828
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.939358668	2	4.540031
Q5XIC0	WDAWNALGSLPK	0.66274198	2	3.720134
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**0.988147739**	**0.9587**	**2**
Q5XIC1	NQQDGQLEESPGSWPGAGTIR	1.047195025	2	4.445496
Q5XIC1	VEGTPNDPNPNDPR	0.987753448	2	3.211919
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**0.845031802**	**0.00875**	**4**
Q5XIE6	AGIATHFVDSEK	0.821889868	2	3.386203
Q5XIE6	AGQTLSQDLFR	0.997104569	2	2.641332
Q5XIE6	AVLIDKDQTPK	0.786104907	2	2.390782
Q5XIE6	INSCFSANTVEQILENLR	0.904021434	2	4.054471
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.037768687**	**1**	**2**
Q5XIF3	HGWSYDVEGR	1.09236609	2	2.730582
Q5XIF3	LDVTPLTGVPEEHIK	1.037477226	2	3.477461
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**1.081246748**	**0.00431**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	1.042693019	2	3.903751
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.05343831	3	4.694045
Q5XIF6	DVNAAIAAIK	1.091499055	2	2.870887
Q5XIF6	SIQFVDWCPTGFK	0.954086314	2	3.779676
Q5XIF6	TIGGGDDSFTTFFCETGAGK	2.945608922	2	3.979545
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**0.912577692**	**0.54503**	**3**
Q5XIG4	SVPLAATSMLITQGLISK	0.86374566	2	3.562135
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	0.918595461	2	5.299726
Q5XIG4	YDSNVSGQSSFGTSPAADNIEKETLPR	0.929924803	3	3.842464
Q5XIH7	**PHB2 Prohibitin_2**	**0.917414006**	**1.1E-16**	**7**
Q5XIH7	DLQMVNISLR	2.355503822	2	2.914345
Q5XIH7	FNASQLITQR	0.937017921	2	3.941186
Q5XIH7	IGGVQQDTILAEGLHFR	1.370052428	3	4.669503
Q5XIH7	IVQAEGEAEAAK	0.856489848	2	4.236224
Q5XIH7	IYLTADNLVLNLQDESFTR	1.346195477	2	3.980792

Q5XIH7	LGLDYEER	1.048417039	1	2.509454
Q5XIH7	VLPSIVNEVLK	0.954359736	2	2.625473
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.081805347**	**3.2E-05**	**6**
Q5XIM9	EALLSSAVDHGSDEVK	1.098498023	2	4.034527
Q5XIM9	GATQQILDEAER	1.065707585	2	3.935396
Q5XIM9	GSGNLEAIHVIK	1.047642279	2	2.647833
Q5XIM9	NIGVDNPAAK	0.937885093	1	2.019505
Q5XIM9	SLHDALCVLAQTVK	0.71212259	2	3.246514
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.202492635	2	4.551359
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.178414044**	**1.5E-05**	**8**
Q5XIN6	AAEVEGEQVDNK	1.263948363	2	3.739089
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.99753418	2	4.535973
Q5XIN6	FLQDTIEEMALK	0.891017151	2	2.945608
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.869750977	2	5.347606
Q5XIN6	LEEGGPVYSPPAQVVVK	0.946326438	2	2.750551
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.072786795	3	4.064218
Q5XIN6	LLELQSIGTNNFLR	0.43302274	2	2.463132
Q5XIN6	STLQTLPEIVAK	0.958255159	2	2.31867
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**0.848558246**	**9.9E-20**	**8**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.87406684	2	4.724031
Q5XIT9	ALYGDTLVTGFAR	0.897636498	2	3.403098
Q5XIT9	AQEIALQNR	0.78519908	2	2.854755
Q5XIT9	DRIDNLIDPGSPFLEFSQFAGYK	1.435673893	3	4.576054
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.201213253	3	4.919759
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.063330737	2	5.123445
Q5XIT9	LWDDGIIDPVDTR	1.01834942	2	3.269868
Q5XIT9	LYGEEEVPAGGIITGIGR	0.809438639	2	4.309294
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**0.919766835**	**0.67657**	**2**
Q5XIU9	GLATFCLDK	0.995395457	2	2.73602
Q5XIU9	GLCSGPGAGEESPAATLPR	0.90740958	2	4.021212
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**0.792058428**	**9.9E-20**	**6**
Q60587	AQDEGHLSDIVPFK	1.14688981	2	3.189871
Q60587	DFIYVSQDPK	0.939675065	2	2.941574
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.890548771	3	4.119853
Q60587	DNGIRPSSLEQMAK	0.893322998	2	2.790373
Q60587	DQLLLGPTYATPK	0.773997247	2	3.408303
Q60587	NIVVVEGVR	0.821253824	2	2.838452
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**0.809460186**	**8.7E-13**	**4**
Q60759	DILGGNGISDEYHVIR	0.786904229	2	4.070438
Q60759	DIVYEMGELGVLGPTIK	0.768581319	2	3.513539

Q60759	GYGCAGVSSVAYGLLTR	1.465899102	2	3.352454
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.236139977	4	5.064039
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.797732484**	**6.7E-16**	**2**
Q61029	SELVANNVTLPAGEQR	0.797686595	2	4.07399
Q61029	SSTPLPTVSSSAENTR	0.826170204	2	2.933791
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**0.98580232**	**0.59102**	**2**
Q61035	ASAEQIEEEVTK	0.9856063	2	3.250256
Q61035	REDLVEEIR	1.186757306	2	2.355532
Q61092	**LAMC2 Laminin subunit gamma_2**	**0.913412623**	**0.0036**	**3**
Q61092	DRRQTSDQLLSR	1.103434633	2	2.414355
Q61092	LDDLKMTAER+Oxidation(5)	0.596899534	2	2.534703
Q61092	TKSLSQQLSLEGTQADIEADR	1.184093169	2	2.476654
Q61301	**CTNA2 Catenin alpha_2**	**0.966085861**	**0.92627**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	0.9256918	2	3.571844
Q61301	TSVQTEDDQLIAGQSAR	0.994590961	2	4.741488
Q61301	WDDSGNDIIVLAK	0.953615411	2	3.107732
Q61335	**BAP31 B_cell receptor_associated protein 31**	**0.729625367**	**2.2E-16**	**4**
Q61335	AENEALAMQK	0.722940759	2	3.474051
Q61335	AENEALAMQK+Oxidation(7)	0.832452673	2	2.302967
Q61335	KYMEENDQLKK+Oxidation(2)	0.346317311	3	3.774623
Q61335	YMEENDQLKK+Oxidation(1)	1.115407454	2	2.453544
Q61550	**RAD21 Double_strand_break repair protein rad21 homolog**	**1.244337408**	**0.20214**	**2**
Q61550	KLMMWKETGGVEK	1.244351979	2	2.333039
Q61550	TTIEESAMPPPPPQGVK+Oxidation(7)	0.908394944	2	2.38721
Q61595	**KTN1 Kinectin**	**0.977846653**	**0.96774**	**2**
Q61595	TAEHEAAQQDLQSK	0.995942401	2	3.309375
Q61595	VEPVLVTK	0.91169656	2	2.39416
Q61941	**transhydrogenase_ mitochondrial**	**0.956791973**	**0.86335**	**9**
Q61941	AISPDKDNFHFEVK	1.010204527	2	3.53288
Q61941	EANSIVITPGYGLCAAK	1.011114301	2	3.647742
Q61941	FGIHPVAGR	1.0233359	2	2.30262
Q61941	GITHIGYTDLPSR	1.065873798	2	3.65284
Q61941	KTTVLAMDQVPR	1.024289541	2	2.471188
Q61941	QGFNVVVESGAGEASK	0.951504649	2	4.350517
Q61941	SLGAEPLEVDLK	1.026132007	2	2.615309
Q61941	TTVLAMDQVPR	0.997240452	2	2.822897
Q61941	VTIAQGYDALSSMANISGYK	0.865567647	2	5.435009
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.160381551**	**0.70865**	**3**
Q62095	SFLLDLLNATGK	1.007038281	2	4.173364
Q62095	VGNLGLATSFFNER	1.372368222	2	2.346039
Q62095	VGSTSENITQK	1.172598328	2	3.030791
Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**0.854315107**	**1.1E-16**	**8**

Q62261	ALVADSHPESER	0.924223033	2	3.098406
Q62261	EAEKLESEHPDQAQAILSR	0.872979883	3	3.454188
Q62261	HLLGVEDLLQK	0.930886943	2	2.726887
Q62261	HQILEQAVEDYAETVHQLSK	0.745263773	3	4.118104
Q62261	LVSDGNINSDR	0.949380463	2	3.203244
Q62261	SQNIITDSSSLNAEAIR	0.79999093	2	5.260499
Q62261	TLETPAAQMEGFLNR	0.95644352	2	3.54291
Q62261	VIESTQDLGNDLAGVMALQR	0.669707164	2	3.339828
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.252626141**	**1.2E-07**	**2**
Q62425	FYSVNVDYSK	1.254254131	1	2.776693
Q62425	LGPNEQYK	1.194536948	2	2.373135
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**0.843224396**	**9.9E-20**	**5**
Q62452	AMEIAEALGR	0.598582062	2	3.270575
Q62452	GAGVTLNVLEMTADDLENALK	0.565857653	3	6.273658
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(10)	0.86423313	2	4.250556
Q62452	WLPQNDLLGHPK	0.849883666	2	2.968227
Q62452	YTGTRPSNLAK	0.513239063	2	2.797021
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**0.937138388**	**1.5E-10**	**6**
Q62465	ACGLNFADLMGR	0.86927048	2	2.843266
Q62465	CLVLTGFGGYDK	1.054062038	2	2.580568
Q62465	ENGVTHPIDYHTTDYVDEIKK	0.840352993	3	3.478638
Q62465	GVDIVMDPLGGSDTAK	0.756694286	2	4.321064
Q62465	TVENVTVFGTASASK	0.997293249	2	3.253728
Q62465	VLLVPGPEKET	0.802781646	2	2.514323
Q62468	**VILI Villin_1**	**1.236505231**	**5E-07**	**2**
Q62468	HEDCYILDQGGLKIFVWK	1.115749882	2	2.442375
Q62468	SGAMSQALNFIKAK	1.247998317	2	2.826864
Q62636	**RAP1B Ras_related protein Rap_1b**	**1.038049237**	**9.9E-20**	**2**
Q62636	INVNEIFYDLVR	2.330074777	2	4.085283
Q62636	VVGKEQGQNLAR	0.661618392	2	2.480749
Q62638	**GSLG1 Golgi apparatus protein 1**	**1.052183495**	**0.10244**	**2**
Q62638	LNDRIEMWSYAAK	1.196207171	2	2.35153
Q62638	NSELMDPKCKQMITK+Oxidation(4)	0.748887527	2	2.345784
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.700065492**	**9.9E-20**	**5**
Q62651	EVDVGLAADVGTLQR	0.627133877	2	3.486306
Q62651	HVLHVQLNRPEK	0.709740555	2	2.991192
Q62651	IPEEVSDHNYESIQVTSAQK	1.026013582	3	4.516869
Q62651	RIPEEVSDHNYESIQVTSAQK	0.663663572	3	4.822699
Q62651	SLVNELTFTAR	0.744700324	2	3.262189
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**0.709342508**	**0.01354**	**5**
Q62730	AVLVTGADSGFGHALAK	0.572406619	2	4.346628

Q62730	EIQENYGQEYVHTQK	0.870994466	2	4.256638
Q62730	LSVLQMDVTKPEQIK	0.851412276	2	2.853634
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	1.033218197	3	5.207445
Q62730	VVTIHPGGFQTNIVGSQDSWDK	0.674767813	2	5.410758
Q62736	**CALD1 Non_muscle caldesmon**	**1.096652518**	**0.00062**	**10**
Q62736	ASGDKEAEGAPQVEAGKR	0.903013878	3	4.066496
Q62736	EFDPTITDGSLSVPSR	0.863549846	2	3.426904
Q62736	GETESEEFEK	1.49570455	2	2.36579
Q62736	GGNLGENQIKDEK	0.945151774	2	3.272888
Q62736	LEQYTNAIEGTK	1.14922159	2	3.265606
Q62736	MQNNSAENETAEGEEKGESR	1.004731136	3	4.6323
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0)	1.264342153	3	4.788664
Q62736	NDDDEEEAAR	1.433775344	2	3.409209
Q62736	RGETESEEFEK	1.096944054	2	3.128067
Q62736	VLEEEEQR	0.992221999	1	1.957137
Q62745	**CD81 CD81 antigen**	**0.891626762**	**0.48367**	**2**
Q62745	NSLCPSSSNSFTQLLK	0.945313969	2	2.832131
Q62745	QFYDQALQQAVMDDDANNAK	0.894174235	2	4.5501
Q62769	**UN13B Protein unc_13 homolog B**	**0.897215235**	**0.00135**	**2**
Q62769	DHMVREETRNLTPK	0.644806852	2	2.483716
Q62769	SNDEVAREFVK	0.899206456	1	1.990039
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**1.09329615**	**0.53532**	**3**
Q62785	ANEEDEQEEGGDGASGDPK	0.794423779	2	4.125019
Q62785	GVEGLIDIENPNR	0.930072557	2	2.966767
Q62785	QYTSPEEIDAQLQAEK	1.109429597	2	3.377122
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**0.927739081**	**9.9E-20**	**2**
Q62789	IILDELVQR	1.552056474	2	3.509172
Q62789	WIPQNDLLGHPK	0.849883666	2	2.968227
Q62812	**MYH9 Myosin_9**	**0.87539372**	**9.9E-20**	**57**
Q62812	ALEEAMEQK	0.839325449	2	2.961576
Q62812	ALELDSNLYR	0.920737737	2	3.400318
Q62812	ALEQQVEEMK	0.886109176	2	2.937216
Q62812	ANLQIDQINTDLNLER	0.910102835	2	5.016233
Q62812	ASIAALEAK	0.864042293	2	2.602819
Q62812	ASREEILAQAK	1.064947918	2	2.706984
Q62812	CQYLQAEK	0.865381008	2	2.529243
Q62812	DFSALESQLQDTQELLQEENR	0.870521264	3	5.975073
Q62812	DLEAHIDTANK	0.837289307	2	3.415653
Q62812	DLQGRDEQSEEK	1.629258252	2	2.568952
Q62812	EEILAQAK	0.901014592	1	2.199077
Q62812	ELEDATETADAMNR	0.811376824	2	3.69872
Q62812	ELETQISELQEDLESER	0.800320245	2	3.899051

Q62812	HEDELLAK	0.806395153	2	3.100676
Q62812	HSQAVEELAEQLEQTK	0.883618017	2	4.962539
Q62812	HSQAVEELAEQLEQTKR	0.797560811	3	5.546907
Q62812	IAQLEEQLDNETK	0.996526705	2	4.016231
Q62812	IIGLDQVAGMSETALPGAFK	0.894885265	2	3.78374
Q62812	IRELETQISELQEDLESER	0.950980445	3	3.835921
Q62812	KEEELQAALAR	0.844272078	2	3.100376
Q62812	KKVEAQLQELQVK	0.835685457	2	4.661884
Q62812	KLEEDQIIMEDQNCK	0.87927825	2	5.658192
Q62812	KLEGDSTDLSDQIAELQAQIAELK	0.832968423	2	6.291564
Q62812	KQELEEICHDLEAR	0.947749237	2	4.281878
Q62812	KVEAQLQELQVK	0.916256453	2	4.211732
Q62812	LEEDQIIMEDQNCK	0.842297282	2	3.814162
Q62812	LEGDSTDLSDQIAELQAQIAELK	0.928357502	2	4.918293
Q62812	LQQELDDLLVDLDHQR	0.912971431	2	4.851518
Q62812	LQVELDSVTGLLNQSDSK	0.930592159	2	5.964386
Q62812	LTEMETMQSQLMAEK	1.038423159	2	3.324635
Q62812	MQQNIQELEEQLEEEESAR	1.001129591	2	6.003347
Q62812	MQQNIQELEEQLEEEESAR+Oxidation(0)	0.735840794	2	4.652771
Q62812	NAEQFKDQADK	1.198695225	2	3.689645
Q62812	NLPIYSEEIVDMYK	1.04761212	2	3.776233
Q62812	NMDPLNDNIATLLHQSSDK	0.971658327	2	4.427688
Q62812	NTDQASMPDNTAAQK	0.830544751	2	5.277442
Q62812	NTDQASMPDNTAAQK+Oxidation(6)	0.852670686	2	5.073442
Q62812	QAQQERDELADEIANSSGK	1.007167678	3	4.120313
Q62812	QIATLHAQVTDMK	1.224007983	2	2.680901
Q62812	QLEEAEEEAQR	0.920724628	2	3.270162
Q62812	QNKELK	0.958514551	1	2.191375
Q62812	QSVSNLEK	0.872384572	2	2.587089
Q62812	QTLENERGELANEVK	1.021903974	2	3.296558
Q62812	RGDMPFVVTR	0.853665823	2	2.330957
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	0.920009128	3	5.60279
Q62812	RQLEEAEEEAQR	0.87030987	2	4.41887
Q62812	SMEAEMIQLQEELAAAER	0.925526633	2	4.255435
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)	1.137640173		2.30145
Q62812	TDLLLEPYNK	1.00090775	2	3.193748
Q62812	TELEDTLDSTAAQQELR	0.948659451	2	4.911375
Q62812	THEAQIQEMR	0.711326687	2	3.151373
Q62812	THEAQIQEMR+Oxidation(8)	0.945053862	2	3.400297
Q62812	TQLEELEDELQATEDAK	0.86240593	2	6.109765
Q62812	VEAQLQELQVK	0.661813184	2	3.240036
Q62812	VEDMAELTCLNEASVLHNLK	0.936743535	2	4.395519
Q62812	VSHLLGINVTDFTR	1.046560005	2	3.709194

Q62812	YEILTPNSIPK	0.95538062	2	2.804184
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**1.091334012**	**0.4145**	**4**
Q62826	ADILEDKDGK	0.793777158	2	2.308204
Q62826	AFITNIPFDVK	1.185106945	2	3.198852
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	0.881319255	2	3.862215
Q62826	MGPVMDRMATGLER+Oxidation(0)	0.989544529	2	2.931424
Q62868	**ROCK2 Rho_associated protein kinase 2**	**0.618660369**	**0.0281**	**2**
Q62868	EENEEKTKLCK	0.375298421	2	2.367384
Q62868	LAEIMNRK+Oxidation(4)	0.629795611	1	2.053685
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**0.967720585**	**0.91642**	**2**
Q62871	ADAEEEAATR	0.967737373	2	3.278523
Q62871	SVSTPSEAGSQDSGDGAVGSR	0.910182586	2	4.732947
Q62902	**LMAN1 Protein ERGIC_53**	**1.199639086**	**1.1E-16**	**6**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.16317772	2	4.226358
Q62902	GHPDLQGQPADDIFESIGDR	1.010088205	2	4.890192
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.440162613	3	5.005457
Q62902	RGAGTPGQPGQVSQQELDTVVR	0.887669505	3	5.043847
Q62902	YQEEFEHFQQELDK	1.142348498	2	5.1436
Q62902	YVSSLTEEISR	0.921711953	2	3.400393
Q63041	**A1M Alpha_1_macroglobulin**	**0.832186559**	**2E-05**	**8**
Q63041	AEDITHNGIVYTPK	0.765094973	2	3.528978
Q63041	AEQGAYLGPLPYK	0.885518884	2	3.337096
Q63041	DTVVKPVIVEPEGIEK	0.956109847	2	3.123286
Q63041	GSIFNSGSHVLPLEQGK	0.79979351	2	3.697152
Q63041	LQDQSNIQR	0.760300173	2	3.068413
Q63041	QDLNDNDAYSVFQSIGLK	1.162157192	2	3.234031
Q63041	YNILPEAEGEAPFTLK	0.911944785	2	3.919297
Q63041	YVVLVPSELYAGVPEK	0.954116343	2	3.312874
Q63060	**GLPK Glycerol kinase**	**1.360197182**	**9.9E-20**	**10**
Q63060	AVLGPLVGAVDQGTSSTR	1.447209194	2	5.32653
Q63060	DCGIPLSHLQVDGGMTSNK	1.784081421	2	3.265332
Q63060	EILQSVYECIEK	1.287989652	2	3.872813
Q63060	FEPQINAEESEIR	1.501235012	2	3.483125
Q63060	KAVLGPLVGAVDQGTSSTR	0.857455123	3	3.501194
Q63060	KVQEAVEENR	1.156083267	2	3.320334
Q63060	LGQLNIDISNIK	1.425502067	2	3.029816
Q63060	NTYGTGCFLLCNTGHK	1.129520928	2	3.916847
Q63060	TAELLSHHQVEIK	1.377099633	2	3.170953
Q63060	VQEAVEENR	0.906049843	2	3.060728
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**0.95973911**	**5.6E-16**	**9**
Q63081	GESPVDYDGGR	0.916390176	2	2.944207
Q63081	GSFSEQGINEFLR	0.988568303	2	3.62426

Q63081	GSTAPVGGGSFPNITPR	0.959599242	2	4.28021
Q63081	HQSLGGQYGVQGFPTIK	0.806781124	2	5.043689
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	1.161534359	3	4.084782
Q63081	NLEPEWAAAATEVK	0.929629526	2	3.907022
Q63081	NSYLEVLLK	0.963411117	2	2.912807
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.179583604	3	4.690395
Q63081	TGEAIVDAALSALR	1.007373624	3	4.68916
Q63108	**EST3 Liver carboxylesterase 3**	**0.815228833**	**9.9E-20**	**5**
Q63108	DFNTVPYIVGINK	1.695748872	2	2.629604
Q63108	GGTSKEEINLSK	0.672956459	2	3.492644
Q63108	LDPMTATSLLK	0.776333523	2	3.059147
Q63108	QKTEEELLETTLK	0.81548542	2	3.580623
Q63108	SSFLLNLPEEAIPVAVEK	0.637815409	2	4.657144
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**0.855173685**	**0.38465**	**2**
Q63120	ACALLPDLEILPGGDMAEIGEK	0.9569102	2	2.965484
Q63120	YFAWEPSFQEQVQGIR	0.992174456	2	3.743453
Q63150	**DPYS Dihydropyrimidinase**	**0.767337541**	**9.9E-20**	**10**
Q63150	ALGKDDFTK	0.844672649	2	2.620963
Q63150	DQTCTPIPVK	0.687461619	1	2.120382
Q63150	DQTCTPIPVKR	0.734942114	2	2.633752
Q63150	EIGAIAQVHAENGDLIAEGAK	0.986517616	2	5.484122
Q63150	FVAVTSTNAAK	0.745865427	2	3.110895
Q63150	GEVITLKPR	0.789823575	2	2.314631
Q63150	GSSLIEAFETWR	0.759459089	2	2.994756
Q63150	VVNDDFSQVADVLVEDGVVR	0.689144788	2	5.240556
Q63150	VVYEAGVFDVTAGHGK	0.861868847	2	3.860447
Q63150	VVYGEPIAAGLGTDGTQYWNK	0.791476467	2	5.627224
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**0.852533392**	**1.2E-09**	**16**
Q63270	AVEAGLNVKPYVK	1.03155477	2	3.144447
Q63270	AVLAESYER	0.954245763	2	2.861386
Q63270	FVEFFGPGVAQLSIADR	1.189200499	2	4.411954
Q63270	GFQVAPDHHNDHK	0.637562248	2	3.037085
Q63270	IDFEKEPLGVNAQGQQVFLK	1.053108993	3	4.609636
Q63270	KNDIENILNWSIMQHK	1.202690824	3	3.82754
Q63270	NDIENILNWSIMQHK	1.103535822	2	2.457944
Q63270	NQDLEFER	0.863806295	2	2.373795
Q63270	QAPQTVHLPSGETLDVFDAAER	0.943032328	3	3.953301
Q63270	SIEVPFKPAR	1.003408194	2	2.428619
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.14756955	3	4.800594
Q63270	SPPFFESLTLDLQPPK	1.108256395	2	2.681449
Q63270	SWNALAAPSEK	0.85510574	1	2.604376
Q63270	TSLSPGSGVVTYYLR	1.313800989	2	2.912296

Q63270	VILQDFTGVPAVVDFAAMR	0.785449463	3	4.063266
Q63270	YQQAGLPLIVLAGK	0.920291508	2	3.213481
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.058847476**	**9.9E-20**	**13**
Q63276	AHGHFLFVVGEDDKNLNSK	2.08161357	2	5.967214
Q63276	ASEVGEVDLER	0.955244718	2	3.973317
Q63276	DDKGNLFNSQAFYR	0.961290675	3	3.421368
Q63276	GNLFNSQAFYR	1.179641159	2	2.760852
Q63276	LTAVPLSALVDEPVHIR	1.872169011	3	3.433373
Q63276	QHLNPGFNSQL	1.038602751	2	3.519397
Q63276	QITATVLINGPNFVSSNPHVYR	0.95256505	3	4.945737
Q63276	TFEETADKDSK	0.809682645	2	3.792937
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.057801372	2	5.234632
Q63276	VISSSLDSLILER	0.960141597	2	3.941213
Q63276	VTGLTPFQVVCLQASLK	1.215655385	3	3.647864
Q63276	WYVAPGVTR	0.63557938	2	2.74042
Q63276	YCFPIEK	0.896202013	2	2.541563
Q63279	**K1C19 Keratin_ type I cytoskeletal 19**	**0.857087147**	**0.02464**	**2**
Q63279	IVLQIDNAR	0.849585301	2	2.96024
Q63279	TIEDLRDKILGATIENSK	1.124281511	2	2.322479
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**0.726805363**	**9.9E-20**	**20**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	0.876548525	3	5.460544
Q63342	AWGSEMNCDTNPLEAGLDYFIK	0.902664931	2	4.50589
Q63342	EGQESPPSPPEWK	0.674449041	2	2.664611
Q63342	GQDSTQLLDHLCANVIPK	0.904207412	2	4.087729
Q63342	IMNAGQEEGIDNFGTYALNALR	1.765853079	2	4.735649
Q63342	ISDIPVTAIR	0.811505383	2	3.034938
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	0.880387785	3	6.029374
Q63342	LEEETGQVVGFHQPGSIR	0.722975192	2	4.586476
Q63342	LNKPADFTGK	0.746625053	1	2.530071
Q63342	LTSEDLSDDVFK	0.782158384	2	3.309136
Q63342	NITDELGVLGVAGPYAR	0.816973543	2	4.238839
Q63342	NYPATIIQEPLVLTEPTR	0.836217646	3	4.339882
Q63342	REDSAALYER	1.69564794	2	2.966743
Q63342	TNWHATEQYIIEPEK	1.008901317	2	4.071054
Q63342	VGVIDLSPFGK	0.846599525	2	3.630837
Q63342	VIGNTTSGSYSYSIQK	0.931831173	2	4.268919
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	0.774766896	3	4.255466
Q63342	WIEEAAVR	0.748407616	2	2.704669
Q63342	WTTTQYTEAK	0.815185229	2	2.307
Q63342	YLSDWILHGEPPFDLIELDPNR	0.622822606	3	4.064415
Q63347	**PRS7 26S protease regulatory subunit 7**	**0.89070306**	**1.7E-05**	**6**
Q63347	ALDEGDIALLK	0.868435727	2	2.810462

Q63347	FDDGAGGDNEVQR	0.859568591	2	3.575914
Q63347	IINADSEDPK	0.881487803	2	2.536339
Q63347	QTLQSEQPLQVAR	0.914954926	2	4.103676
Q63347	QVEDDIQQLLK	0.89299836	2	2.617951
Q63347	TMLELINQLDGFDPR	0.95621944	2	2.670878
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**0.943968353**	**0.81448**	**3**
Q63362	KLENLLQGGEVEEVILQAEK	0.925128913	2	4.675454
Q63362	TTGLVGLAVCDTPHER	0.945634661	2	4.07293
Q63362	YTEQITSEK	1.109994022	2	2.435438
Q63429	**UBC Polyubiquitin_C**	**0.96013455**	**0.9946**	**3**
Q63429	ESTLHLVLR	1.062381857	2	2.340466
Q63429	TITLEVEPSDTIENVK	0.95769122	2	4.723439
Q63429	TLSDYNIQK	1.005148088	2	2.496317
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.032123287**	**6.8E-07**	**9**
Q63448	ADWLDSEAPLAAYR	0.977505377	2	4.538589
Q63448	EIHALASAGKPLASWTAQR	0.741125125	2	4.218229
Q63448	GGYISGEQTGK	0.93190522	1	2.383697
Q63448	NLWAAVLQQSGVLER	1.110526592	2	4.0974
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.994979999	3	5.088423
Q63448	TIFLDLIELQR	1.01366447	2	3.467716
Q63448	TIFSTLENDPLFARPFGADLPLEK	1.029305414	3	4.336917
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.285037157	3	4.353027
Q63448	TVNFLEAYPGILGQK	1.065579285	2	4.949403
Q63493	**CD1D Antigen_presenting glycoprotein CD1d**	**1.273821051**	**0.00243**	**2**
Q63493	DIKEIVKMMSPK+Oxidation(7)	1.273821051	2	2.625995
Q63493	DIKEIVKMMSPK+Oxidation(8)	1.273821051	2	2.470165
Q63505	**TF3C1 General transcription factor 3C polypeptide 1**	**0.968925965**	**0.00131**	**2**
Q63505	NPNLEIPDTLQELFAKYR	1.308368722	2	2.547085
Q63505	YEEIDLETGILESRR	0.511500715	2	2.740065
Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**0.934381037**	**0.23093**	**2**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.103181836	3	5.033961
Q63524	HEQEYMEVR	0.877392834	2	2.811748
Q63525	**NUDC Nuclear migration protein nudC**	**0.942543266**	**0.70129**	**3**
Q63525	GQAPVIDGELYNEVK	0.944562199	2	3.080175
Q63525	LSDLDSETR	0.588050036	2	2.508842
Q63525	VEESSWLIEDGK	0.92178368	2	2.808433
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**1.103711078**	**0.05381**	**7**
Q63569	AMEVDERPTEQYSDIGGLDK	1.384327327	3	3.903711
Q63569	CTDDFNGAQCK	0.978209621	2	2.731547
Q63569	DSYLILETLPTEYDSR	1.086313587	2	3.403019
Q63569	MNVSPDVNYEELAR	1.011774033	2	3.032847

Q63569	QTYFLPVIGLVDAEK	1.097244221	2	2.697615
Q63569	TMLELLNQLDGFQPNTQVK	0.630679659	2	2.548872
Q63569	VDILDPALLR	0.900170618	2	2.392989
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.158043213**	**0.00012**	**4**
Q63584	ITDSAGHILYAK	1.182157122	2	3.577688
Q63584	LEDLSESIVNDFAYMK	0.996929643	2	3.55448
Q63584	NYEEIAK	0.859625678	1	2.233616
Q63584	RLEDLSESIVNDFAYMK	0.866513701	2	4.041759
Q63598	**PLST Plastin_3**	**0.772963924**	**9.9E-20**	**8**
Q63598	AESMLQQADK	0.738921026	2	2.731967
Q63598	ATDDIIVNWVNGTLSEAGK	0.856616532	2	4.556378
Q63598	IDINMSGFNETDDLKR	0.950375487	2	3.489283
Q63598	KLENCNYAVELGK	0.755916056	2	3.589231
Q63598	VDLNSNGFICDYELHELFK	1.00612261	2	4.036258
Q63598	VYALPEDLVEVKPK	0.906330709	2	3.189458
Q63598	YPALTKPENQDIDWTLLEGETR	0.709213668	3	5.640592
Q63598	YTLNVMEDLGEGQK	0.860351518	2	3.3985
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.075856364**	**3.1E-10**	**8**
Q63610	EQAEAEVASLNR	0.887293148	2	2.925125
Q63610	IQVLQQQADDAEER	1.180267328	2	4.820776
Q63610	KIQVLQQQADDAEER	1.050121083	2	5.400838
Q63610	KLVIIEGDLER	1.036809374	2	2.304484
Q63610	LVIIEGDLER	0.869619466	2	2.69653
Q63610	MELQEIQLK	1.143859348	2	3.095226
Q63610	TIDDLEDKLK	0.945849123	2	2.679843
Q63610	YSQKEDKYEEEIK	0.896608573	2	4.479173
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.102060954**	**2.6E-10**	**13**
Q63617	AANSLEAFIFETQDK	1.175758179	2	3.985163
Q63617	DAVITVPAFFNQAER	1.077332651	2	2.46626
Q63617	EGETPDEKESGDKSEAQKPNEK	0.986053396	3	3.869456
Q63617	FLGDSAAGMAIK	1.04012277	2	2.373202
Q63617	GQAGPEGVPPAPEEEKK	0.763001314	2	3.225506
Q63617	LGNTISSLFGGGTSSDAK	1.123492113	2	3.251617
Q63617	LYQPEYQEVSTEEQR	1.423393423	2	4.609168
Q63617	NINADEAAAMGAVYQAAALSK	1.147701805	2	4.64856
Q63617	SLAEDFAEQPIK	1.093691122	2	2.75734
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.103216887	3	3.80923
Q63617	VEFEELCADLFDR	1.042923915	2	3.391126
Q63617	VESVFETLVEDSPEEESTLTK	0.960347608	3	4.179318
Q63617	VLQLINDNTATALSYGVFR	1.122374237	2	4.001079
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**0.926889964**	**8.7E-05**	**2**
Q63692	EGEEAGPGDPLLEAVPK	0.685918527	2	3.824945

Q63692	LGPGGLDPVEVYESLPEELQK	1.076469898	2	2.775415
Q63716	**PRDX1 Peroxiredoxin_1**	**0.906323566**	**9.9E-20**	**15**
Q63716	ADEGISFR	0.923166441	2	3.137064
Q63716	ATAVMPDGQFK	0.932717957	2	2.775047
Q63716	ATAVMPDGQFK+Oxidation(4)	1.011031812	2	2.336777
Q63716	DISLSDYK	0.778630992	1	2.047317
Q63716	HGEVCPAGWKPGSDTIKPDVNK	0.909400067	3	6.00501
Q63716	IGHPAPSFK	3.364138837	1	2.04062
Q63716	KQGGLGPMNIPLVSDPK	1.215347356	2	3.263965
Q63716	KQGGLGPMNIPLVSDPK+Oxidation(7)	1.104420692	2	2.546925
Q63716	LVQAFQFTDK	2.067701264	2	2.895708
Q63716	QGGLGPMNIPLVSDPK	0.716982867	2	3.835082
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6)	0.790310529	2	3.256541
Q63716	QITINDLPVGR	0.834129924	2	3.085922
Q63716	RTIAQDYGVLK	0.895711588	2	2.572249
Q63716	SVDEILR	0.891276293	2	2.37259
Q63716	TIAQDYGVLK	0.890498161	2	3.392761
Q63787	**P85A Phosphatidylinositol 3_kinase regulatory subunit alpha**	**0.663236114**	**0.01395**	**2**
Q63787	MHGDYTLTLRKGGNNK+Oxidation(0)	0.613189423	2	2.30273
Q63787	SRISEIIDSR	1.230492482	1	2.038541
Q63797	**PSME1 Proteasome activator complex subunit 1**	**0.893408657**	**9.9E-20**	**8**
Q63797	ISELDAFLKEPALNEANLSNLK	0.843887699	2	5.316459
Q63797	KGDEDDKGPPCGPVNCNEK	0.864924241	3	4.315633
Q63797	KISELDAFLKEPALNEANLSNLK	0.896322794	3	4.833234
Q63797	LEGFQTQISK	0.8778904	2	2.741705
Q63797	NAYAVLYDIILK	1.948746169	2	4.119957
Q63797	QLVHELDEAEYQEIR	0.622047027	2	4.091653
Q63797	TENLLGSYFPK	0.89938539	2	3.420146
Q63797	VDVFREDLCSK	0.892367749	2	2.641342
Q63798	**PSME2 Proteasome activator complex subunit 2**	**0.97057775**	**0.13777**	**4**
Q63798	AFYAELHHIISSNLEK	0.920953476	3	3.500704
Q63798	IEDGNDFGVAIQEK	0.91082474	2	4.387158
Q63798	TKVEAFQTAISK	1.01687911	2	3.180129
Q63798	VEAFQTAISK	0.803990929	2	2.308157
Q63836	**SBP2 Selenium_binding protein 2**	**0.892918068**	**0.01091**	**4**
Q63836	GGSVQVLEDQELTCQPEPLVVK	0.983851549	3	5.653489
Q63836	IYVVDVGSEPR	0.852037002	2	3.227777
Q63836	LNPNFLVDFGK	0.320750897	2	2.410395
Q63836	LNPNFLVDFGKEPLGPALAHELR	0.873636606	3	4.400791
Q63965	**SFXN1 Sideroflexin_1**	**1.169376375**	**9.9E-20**	**6**
Q63965	MSGEVPPNINIK+Oxidation(0)	0.955277127	1	1.929551
Q63965	NILLTNEQLENAR	0.914918753	2	4.629127

Q63965	QAITQVVISR	1.893736554	2	2.611428
Q63965	QGIVPAGLTENELWR	0.931683846	2	2.904779
Q63965	WDQSTFIGR	0.881390334	2	2.574814
Q63965	YAYDSAFHPDTGEK	1.276901893	2	4.029942
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**0.884839721**	**9.9E-20**	**16**
Q64057	AWNIWADIPAPK	0.818380452	2	3.657171
Q64057	EDNEGVFNGSWGGR	0.810723501	2	3.541548
Q64057	FKNEEEVFEWNNEVK	1.04517947	2	5.351759
Q64057	GAPTTSLVSIAVTK	0.985403872	2	4.531024
Q64057	GEVITTYCPANNEPIAR	0.996763248	2	5.23091
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	1.027570183	2	5.731015
Q64057	LFLHESIHDEVVDR	0.960352323	2	2.861395
Q64057	NEEEVFEWNNEVK	1.029687062	2	4.374395
Q64057	QAVSMFVQAVEEAK	1.46042191	2	2.921363
Q64057	QGLSSSIFTK	1.233716236	2	2.567116
Q64057	QVALMVQER	0.9969406	2	2.460257
Q64057	STCTINYSTALPLAQGIK	1.843063408	2	3.989538
Q64057	VGNPWDPNILYGPLHTK	1.687614548	3	3.644227
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.295179274	3	5.514498
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1)	0.871933107	3	5.978415
Q64057	VNLLSFTGSTQVGK	1.645868886	2	4.538757
Q64060	**DDX4 Probable ATP_dependent RNA helicase DDX4**	**0.850322628**	**0.26566**	**2**
Q64060	MLDMGFGPEMKK+Oxidation(0)	0.850322628	2	2.429097
Q64060	MLDMGFGPEMKK+Oxidation(3)	0.850322628	2	2.323558
Q64119	**MYL6 Myosin light polypeptide 6**	**0.821233603**	**9.9E-20**	**5**
Q64119	DQGTYEDYVEGLR	0.807263595	2	3.353909
Q64119	HVLVTLGEK	0.839958585	2	2.390612
Q64119	NKDQGTYEDYVEGLR	0.887322784	2	4.31594
Q64119	VFDKEGNGTVMGAEIR	0.617977076	2	3.817748
Q64119	VLDFEHFLPMLQTVAK	0.857013587	3	4.493151
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**0.863277402**	**0.00089**	**2**
Q64122	DGFIDKEDLHDMLASLGK	0.84995077	2	4.822315
Q64122	LNGTDPEDVIR	0.8687169	2	2.601902
Q64176	**EST22 Liver carboxylesterase 22**	**0.573884289**	**9.9E-20**	**4**
Q64176	AISESGVALTAGLVK	0.64274869	2	4.237696
Q64176	EGYLQIGATTQQAQK	0.529189582	2	4.318136
Q64176	LDQMTAMSLLK+Oxidation(3)	0.60720067		2.517842
Q64176	NFNTVPYIVGINK	1.703743459	2	2.69482
Q641K1	**CBPC1 Cytosolic carboxypeptidase 1**	**1.603653178**	**0.0134**	**2**
Q641K1	GTLEYLMSNSPTAQSLR	1.608344396	2	2.337497
Q641K1	KDFGLPLTVLSCTK	1.551181402	2	2.378782

Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**0.996425261**	**0.07889**	**8**
Q641Y0	ELGSECGIEFDEEK	1.066930751	2	2.380695
Q641Y0	GFELTFK	0.966768992	2	2.546202
Q641Y0	NTLLIAGLQAR	1.043539836	2	3.613231
Q641Y0	SSLNPILFR	1.335748982	2	2.562171
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.189235734	3	6.583608
Q641Y0	TLVLLDNLNVR	0.922272689	2	3.461147
Q641Y0	WVPFDGDDIQLEFVR	0.976993998	2	3.254752
Q641Y0	YSQTGNYELAVALSR	1.02041397	2	3.221334
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**0.885679783**	**0.0002**	**3**
Q641Y2	IDEVEEMLTNNR	0.884928541	2	3.380239
Q641Y2	IIEQCLNK	0.899567765	2	2.361413
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.265356967	2	4.099835
Q641Y8	**DDX1 ATP_dependent RNA helicase DDX1**	**0.950038293**	**0.94349**	**2**
Q641Y8	GHVDILAPTVQELAALEK	0.937780019	3	3.461784
Q641Y8	GSAFAIGSDGLCCQSR	1.03546672	2	3.201665
Q641Z6	**EHD1 EH domain_containing protein 1**	**1.031821592**	**0.88521**	**2**
Q641Z6	KEMPNVFGKESK+Oxidation(2)	1.031647885	2	2.311286
Q641Z6	LLDTVDDMLANDIAR	1.043253801	2	2.670396
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**0.756567609**	**0.0001**	**3**
Q64232	LCFLDKVEPQATISEIK	0.929437927	2	4.085227
Q64232	SLKDEDVLQK	0.727410336	2	2.900389
Q64232	THPQWYPAR	0.741766378	2	2.529253
Q64240	**AMBP Protein AMBP**	**1.061760752**	**9.8E-07**	**3**
Q64240	AFAELWAFDAAQGK	1.061766763	2	3.825056
Q64240	AVLPQENEGSGSEPLITGTLK	0.74838038	2	4.345257
Q64240	TIAACNLPIVQGPCR	0.560396765	2	3.541959
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**1.008818761**	**9.9E-20**	**19**
Q64380	AIDSLSIEK	0.823911371	2	2.579655
Q64380	AYGIESHVLSPAETK	0.679267243	2	4.658861
Q64380	DGTMDPAGTCTTLTR	0.742937074	2	3.78573
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	0.980556053	3	5.715693
Q64380	DLYPLMNVDDLYGTLYVPR	0.841632267	2	2.618006
Q64380	EEAQGASVVPQGPSQPLPSTANVVVIGGGSLGCQTLYHLAK	0.922281297	3	4.303577
Q64380	FHHSLTDHPR	0.996826814	2	2.354779
Q64380	FYLLGADAR	0.835947331	2	2.840936
Q64380	GAQVIENCAVTGIR	1.688173255	2	4.328825
Q64380	HGLVNAGYR	0.845873561	2	2.515912
Q64380	IEGIQNMPNVR	0.6424503	2	2.808984
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.536637843	2	4.575271

Q64380	NYSVVFPHDEPLAGR	0.873847409	2	4.440866
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.861158779	3	4.749776
Q64380	RDPLHEELLGQGCVFQER	0.934883055	3	5.387558
Q64380	SDDSPLEAGLAFTCK	0.932746143	2	4.049664
Q64380	STVCGPESFTPDHKPLMGEAPELR	1.041000673	3	4.088438
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16)	0.647777135	3	3.937767
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.883650318	3	4.938793
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**0.885707538**	**9.9E-20**	**26**
Q64428	ADMVIEAVFEDLAVK	0.782301376	3	4.257564
Q64428	ADMVIEAVFEDLAVK+Oxidation(2)	0.658782854	2	2.660729
Q64428	ALMGLYNGQVLCK	0.926759991	2	2.647489
Q64428	DSIFSNLIGQLDYK	1.136867349	2	2.780998
Q64428	DTTASAVAVGLK	0.780751589	2	3.392498
Q64428	DTTVTGLGR	0.739007205	2	2.923759
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	1.333962458	3	5.401702
Q64428	EVQSEFVEVMNEIWANDQIR	0.808839232	3	5.767252
Q64428	FGELALTK	0.866604096	2	2.766047
Q64428	FGGGSVELLK	0.9033283	2	2.952074
Q64428	FVDLYGAQK	0.89711236	2	2.905365
Q64428	GFYIYQSGSK	1.425724967	1	2.113665
Q64428	ILQEGVDPK	0.844507846	2	2.659649
Q64428	KTVLGVPEVLLGILPGAGGTQR	0.977523059	2	3.766523
Q64428	LPAKPEVSSDEDIQYR	3.979567832	2	4.456141
Q64428	MGLVDQLVDPLGPGIK	0.833067129	2	4.5254
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0)	0.692713547	2	4.199664
Q64428	MQLLEIITTDK	0.904820692	2	3.89846
Q64428	MQLLEIITTDK+Oxidation(0)	0.635230674	2	2.916704
Q64428	MVGVPAAFDMMLTGR	0.91306684	2	2.885501
Q64428	NLNSEIDNILVNLR	0.893998254	2	4.575799
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	1.111738418	3	3.861304
Q64428	TGLEQGNDAGYLAESEK	0.956896846	2	5.074549
Q64428	TIEYLEEVAVNFAK	0.871917484	2	3.437444
Q64428	TVLGVPEVLLGILPGAGGTQR	0.891368121	3	4.910021
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.867313987	3	5.376739
Q64458	**CP2CT Cytochrome P450 2C29**	**1.313572933**	**9.9E-20**	**5**
Q64458	EHKESLDVTNPR	0.415292638	2	3.374147
Q64458	IKEHKESLDVTNPR	0.440799485	3	5.176611
Q64458	LPPGPTPLPIIGNFLQIDVK	2.410388868	3	4.461015
Q64458	VQEEAQCLVEELR	2.481281736	2	4.228667
Q64458	VQEEAQCLVEELRK	2.980590012	2	3.699624
Q64464	**CP3AD Cytochrome P450 3A13**	**0.553370858**	**9.1E-11**	**2**
Q64464	ALLSPTFTSGR	0.535026246	2	2.706029

Q64464	LQDEIDAALPNK	0.550203077	2	2.539172
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.037409205**	**9.9E-20**	**4**
Q64550	GHEVVVIAPEASIHIK	0.457063439	2	4.548394
Q64550	NMIIALTENFLCR	0.646667017	2	3.996836
Q64550	SVFDQDPFLLR	0.620619727	2	3.463125
Q64550	VVYSPYGSLATEILQK	0.55765552	3	4.38318
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**1.076016436**	**0.05798**	**4**
Q64560	ACVDSNENGDLGK	0.764143359	2	2.668589
Q64560	DPVQVAAPSDHGVGIEPVFPENTENSEK	1.464383428	3	4.169252
Q64560	GTLIEAFPVLGGK	1.07602762	2	3.035309
Q64560	HEQISDLDR	1.457283334	2	2.364944
Q64563	**ADH4 Alcohol dehydrogenase 4**	**0.875256569**	**9.9E-20**	**13**
Q64563	AAVDCTVVGWGSCTVVGAK	0.397753677	2	2.837254
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	0.475524676	3	4.209719
Q64563	ALGATDCLNPR	0.505855624	2	3.323163
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	0.587060937	3	3.962494
Q64563	FDLDLLVTHALPFDK	0.85253759	2	3.949098
Q64563	INDAIDLMNQGK	0.725684402	2	3.809342
Q64563	KFDLDLLVTHALPFDK	0.457352928	3	5.118972
Q64563	SVDSVPNLVTDYK	0.477775225	2	3.698997
Q64563	TDSPLCIEEIEVSPPK	0.516201497	2	4.000423
Q64563	VCLIGCGFTSGYGAAINTAK	0.618795595	2	4.414731
Q64563	VDDEANLER	0.472833862	2	2.611444
Q64563	VDEMNISTVDMILGR	0.552010071	2	3.653559
Q64563	VIATCVCPTDINATNPK	0.473722831	2	4.615272
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**1.008399747**	**0.0054**	**11**
Q64565	AYSNHTDIISFR	1.008149846	2	2.884983
Q64565	GGVCIADEVQTGFGR	0.822213327	2	4.103835
Q64565	GIGNGFPMAAVVTTPEIASSLAK	1.027340071	2	4.281126
Q64565	HNMPPCDFSPEK	0.973512946	2	2.35069
Q64565	LRDEFDIVGDVR	1.025641677	2	2.444882
Q64565	LSALLPEPLK	1.166277689	2	3.19558
Q64565	SALTQHMER	1.36093273	2	2.661439
Q64565	SALTQHMER+Oxidation(6)	0.879993174	2	2.692121
Q64565	TEVNQIHEDCK	0.90518862	2	2.923719
Q64565	TEVNQIHEDCKDMGLLVGR	0.954249815	2	5.304208
Q64565	YIEQFK	0.831810836	1	2.030674
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**0.827091315**	**0.38964**	**4**
Q64578	DIVPGDIVEVAVGDKVPADIR	0.504793526	2	3.056824
Q64578	IGIFSENEEVADR	0.734151986	2	2.792675
Q64578	VGEATETALTTLVEK	0.823426608	2	4.404289
Q64578	YGPNELPAEEGK	0.782762085	2	2.782587

Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.785304127**	**9.9E-20**	**8**
Q64591	ATAEEITSK	0.510971164	2	2.850521
Q64591	CDVRDPDMVHNTVLELIK	0.77559234	4	4.584389
Q64591	EEWDVIEGLIR	0.65157786	2	3.900975
Q64591	FNIIQPGPIK	1.12410104	2	2.755941
Q64591	NIDVLK	0.740947361	1	1.98223
Q64591	SLAAEWGR	0.830746059	2	2.648813
Q64591	VAGHPDVVINNAAGNFISPSER	0.893778327	2	6.153069
Q64591	VTKEEWDVIEGLIR	0.825699017	3	4.525304
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**0.957391272**	**0.99999**	**7**
Q64602	ASFSQVTPAQMDLVFQR	1.01361253	2	4.613951
Q64602	DIISLAPGSPNPK	1.038850574	2	3.049299
Q64602	EILLVPGNSFFVDNSAPSSFFR	0.95555813	3	3.503779
Q64602	FLYTIPNGNNPTGNSLTGDR	1.078437512	2	4.069632
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	0.980200214	3	5.654724
Q64602	SAVFTVENGSTIR	1.009524724	2	3.257262
Q64602	VLSQWKPEDSKDPTKR	0.72128705	3	4.20015
Q64604	**PTPRF Receptor_type tyrosine_protein phosphatase F**	**0.694847894**	**0.00208**	**2**
Q64604	DHPPIPITDLADNIERLK	0.672763042	2	2.311084
Q64604	RADEARPNTIDFGK	0.694981097	2	2.36615
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.074408725**	**5.9E-08**	**11**
Q64611	AQGGQGLEWR	0.945243676	2	2.950967
Q64611	CHGSQASYLFQQDK	1.847828876	2	4.934774
Q64611	DVFGIVVDEAIR	1.196056749	2	3.261277
Q64611	FFNQLFSGLDPHALAGR	1.81412036	3	3.9409
Q64611	FYNVALDTGDK	1.143067759	2	2.872342
Q64611	GAAFLGLGTDSVR	1.357353785	2	3.105682
Q64611	IDQAFALTR	1.095577072	2	3.173863
Q64611	QLLDLELQSQGESR	0.906173863	2	4.215693
Q64611	TLDGDPVAVEALLR	1.04961828	2	4.513156
Q64611	VCEWKEPEELK	1.112833412	3	3.460104
Q64611	YLVEEIK	0.912104754	1	2.292148
Q64640	**ADK Adenosine kinase**	**1.216668541**	**9.9E-20**	**10**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.397244492	3	7.077675
Q64640	AATFFGCIGIDK	0.720735032	2	2.956191
Q64640	AGHYAASVIIR	1.321311198	2	2.877637
Q64640	FGEILK	1.108928632	2	2.339075
Q64640	HKELFDELVK	1.091425027	3	3.548214
Q64640	HLDLENNWMLVEK	1.19143829	2	3.325822
Q64640	SLVANLAAANCYK	1.068533478	2	4.680538
Q64640	VEYHAGGSTQNSMK	1.029522819	2	3.783481

Q64640	VEYHAGGSTQNSMK+Oxidation(12)	1.109772754	2	4.034286
Q64640	YSLKPNDQILAEDK	1.254035053	3	4.247656
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.282869942**	**9.9E-20**	**5**
Q64654	EPAEDILQTLLDSTYK	0.517728041	2	3.142445
Q64654	GVAYDVPNAVFLEQK	0.391151015	2	3.279834
Q64654	NEDLNAEEVYGR	0.325500833	2	4.035079
Q64654	TVCGEDLPPLTYEQLK	0.25332945	2	4.147206
Q64654	YLQDNPASGEK	0.238694991	2	2.44868
Q64725	**KSYK Tyrosine_protein kinase SYK**	**0.92495437**	**0.58656**	**2**
Q64725	GMKGSEVTAMLEKGER+Oxidation(1)	0.92495437	2	2.413657
Q64725	GMKGSEVTAMLEKGER+Oxidation(9)	0.92495437	2	2.445394
Q65Z40	**WAPL Wings apart_like protein homolog**	**0.868317255**	**0.03993**	**2**
Q65Z40	EKSISRIPEDNANK	0.862591647	2	2.472019
Q65Z40	LGQKRPNFKPDIQEIPK	1.471154596	2	2.84779
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**0.751211779**	**3.8E-05**	**2**
Q66H12	INQDPLGIQGR	0.751196011	2	3.380789
Q66H12	TISPQNIDILQNPLLIK	0.860257839	2	2.469929
Q66H80	**COPD Coatomer subunit delta**	**0.893207433**	**0.4089**	**5**
Q66H80	GVQLQTHPNVDKK	0.888541215	2	3.546849
Q66H80	IEGLLAAFPK	0.825343477	2	2.425005
Q66H80	NSNILEDLETLR	0.94768035	2	3.345227
Q66H80	NTLEWCLPVIDAK	0.974586088	2	2.988647
Q66H80	VTQVDGNSPVR	0.785405168	2	2.907519
Q66HA8	**HS105 Heat shock protein 105 kDa**	**0.948258271**	**0.00038**	**6**
Q66HA8	AGGIETIANEFSDR	1.189850705	2	3.484196
Q66HA8	NQQITHANNTVSSFK	1.042571329	2	4.554781
Q66HA8	SVLDAAQIVGLNCLR	1.049139475	2	2.953448
Q66HA8	TEEVSAIEIVGGATR	0.915498856	2	2.915113
Q66HA8	VLGTAFDPFLGGK	1.023021946	2	3.077864
Q66HA8	YNHIDESEMKKVEK	0.751430136	2	2.323487
Q66HD0	**ENPL Endoplasmin**	**1.012086225**	**0.00052**	**22**
Q66HD0	DISTNYYASQK	1.487635423	2	3.080345
Q66HD0	EATEKEFEPLLNWMK	0.93240181	2	3.68222
Q66HD0	EEASDYLELDTIK	0.969499228	2	4.126424
Q66HD0	EEEAIQLDGLNASQIR	1.01757748	2	4.338768
Q66HD0	EVEEDEYK	0.87382254	1	2.548784
Q66HD0	FQSSHHSTDITSLDQYVER	1.022875872	2	5.877343
Q66HD0	GVVDSDDLPLNVSR	1.001654664	2	4.422697
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	1.437870611	3	3.710856
Q66HD0	KEAESSPFVER	1.082406718	2	3.024749
Q66HD0	LGVIEDHSNR	1.005765321	2	2.86495
Q66HD0	LISLTDENALAGNEELTVK	1.13763431	2	4.989111
Q66HD0	LTESPCALVASQYGWSGNMER	0.98918481	2	5.477437

Q66HD0	NLLHVTDTGVGMTR	1.125095	2	3.450425
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11)	0.767494029	2	3.222033
Q66HD0	SGTSEFLNK	1.070486901	2	3.149558
Q66HD0	SGYLLPDTK	0.992277755	2	3.222081
Q66HD0	SILFVPTSAPR	1.052683625	2	3.480984
Q66HD0	TDDEVVQR	0.947541188	2	3.286403
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	0.942705885	3	4.965813
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.072721351	3	3.440368
Q66HD0	VFITDDFHDMMPK	0.930074829	2	2.754229
Q66HD0	YNDTFWK	0.888159138	1	2.135209
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.041236998**	**1.9E-15**	**10**
Q66HF1	ALSEIAGITLPYDTLDQVR	0.87475679	2	4.925811
Q66HF1	DDGAAILAAVSSIAQK	0.895351198	2	4.883525
Q66HF1	FASEIAGVDDLGTTGR	1.579940164	2	4.182716
Q66HF1	GLLTYTSWEDALSR	1.180464707	2	3.863503
Q66HF1	ILQDIASGNHEFSK	1.00629049	2	3.804357
Q66HF1	LGEVSPNLVR	1.114402829	2	2.589068
Q66HF1	LVDQEFLADPLVPPQLTIK	0.975581947	3	3.589544
Q66HF1	SATYVNTEGR	0.999505355	2	2.344866
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	0.836682945	2	4.096296
Q66HF1	YDHLGDSPK	0.971602532	2	2.334139
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**0.8790273**	**6.7E-16**	**10**
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	1.060186864	3	3.30618
Q66HF8	EEIFGPVQPLFK	0.847426773	2	2.984644
Q66HF8	KTFPTVNPTTGEVIGHVAEGDR	1.033570654	3	4.187212
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.112643124	3	3.372763
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.300538241	2	4.389889
Q66HF8	TFVEESIYHEFLER	1.179934359	2	3.877968
Q66HF8	VAEQTPLSALYLASLIK	3.156066193	2	3.06982
Q66HF8	VAFTGSTEVGHLIQK	3.530446154	2	3.010205
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.056700241	2	4.422997
Q66HF8	YGLAAAVFTR	0.757403789	2	2.678922
Q66HG4	**GALM Aldose 1_epimerase**	**0.701144414**	**9.9E-20**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	0.795724515	2	3.565742
Q66HG4	TVFGELPSGGGAVEK	0.711916391	2	3.633665
Q66HG4	VSPDGEEGYPGELK	0.677999457	2	3.713943
Q66HG9	**MAVS Mitochondrial antiviral_signaling protein**	**0.929487823**	**0.60015**	**2**
Q66HG9	ICELPGLAEQVTR	1.003771244	2	2.656504
Q66HG9	STAATPSTVPTNIAPSK	0.936801332	2	2.384379
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.156418324**	**9.9E-20**	**18**
Q66X93	ALLLPDHYLVTVMLSGIK	0.857809539	3	3.846434

Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.147744868	3	5.459379
Q66X93	DTNGENIAESLVAEGLASR	1.100910638	2	5.080517
Q66X93	DVQIILESCHNQNILGTILHPNGNITELLLK	1.116056515	3	6.256713
Q66X93	ETDGSETPEPFAAEAK	1.533275988	2	3.47693
Q66X93	GDVGLGLVK	1.128286674	2	2.473064
Q66X93	LEGDNIQDK	1.118749947	2	2.603733
Q66X93	NLPGLVQEGEPFSEEATLFTK	2.457875531	2	5.638911
Q66X93	SAYYKPLLSAEEAAK	1.310995186	2	3.119321
Q66X93	SDISSHPPVEGAYAPR	0.966880097	3	4.065368
Q66X93	SEAVVEYVFSGSR	1.394305305	2	2.615828
Q66X93	SSHYDELLAAEAR	1.166455365	2	3.61264
Q66X93	TCATVTIGGINIAEALVSK	0.885501949	2	3.91251
Q66X93	TDAVDSVVR	1.074692563	2	2.512062
Q66X93	VADISGDTQK	0.810298868	2	2.412401
Q66X93	VITEYLNAQESAK	1.253661836	2	4.204988
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.278005039	3	4.683604
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.940236346	3	3.822192
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.823357789**	**9.9E-20**	**8**
Q68FP2	EIKPTEPQNCHLIEGLENGSEDIDILPSGLAFISTGLK	1.217027452	3	4.453087
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.279095782	3	3.34134
Q68FP2	HNNWDLTPVK	0.695610671	2	3.00581
Q68FP2	IFLMDLNEPYPK	0.860193085	2	2.822454
Q68FP2	IQDPLSDNPR	0.748987926	2	2.888701
Q68FP2	LLIYNPEDPPGSEVLR	0.874345324	2	3.911717
Q68FP2	VVAQGFSSANGITVSLDQK	0.78159519	2	3.561879
Q68FP2	YVYVADVTAK	0.678757758	1	2.96802
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**0.912952418**	**0.7291**	**3**
Q68FQ0	HKLDVTSVEDYK	0.902506849	2	3.560824
Q68FQ0	ISDNVLVDINNPEPLIQTAK	1.018973241	2	5.372161
Q68FQ0	WVGGPEIELIAIATGGR	1.059407272	2	3.523529
Q68FR6	**EF1G Elongation factor 1_gamma**	**1.339720055**	**0.0013**	**6**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.165878954	2	5.328891
Q68FR6	ALIAAQYSGAQIR	1.137772155	2	3.82993
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	1.78263039	2	3.983253
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.011430517	3	3.741212
Q68FR6	KLDPGSEETQTLVR	1.106022367	2	4.249683
Q68FR6	LDPGSEETQTLVR	1.108394377	2	3.326427
Q68FR9	**EF1D Elongation factor 1_delta**	**0.993416969**	**0.71337**	**6**
Q68FR9	ATAPQTQHVSPMR	0.869548997	2	3.254453
Q68FR9	FYEQMNGPVTAGSR	1.004520592	2	4.044384
Q68FR9	GVVQDLQQAISK	0.998824883	2	3.941365
Q68FR9	SIQLDGLVWGASK	0.923954553	2	3.069548
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	0.943960778	2	5.431731

Q68FR9	VGTDLLEEEITK	1.164897813	2	3.060036
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**0.66492463**	**0.58228**	**2**
Q68FS2	NAAQVLVGIPLETGQK	0.664961917	2	3.09318
Q68FS2	QDLAQLMNSSGSHK	0.596161635	2	2.850771
Q68FS4	**AMPL Cytosol aminopeptidase**	**0.900039401**	**9.9E-20**	**19**
Q68FS4	ADMGGAATICSAIVSAAK	0.894748879	2	4.936948
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2)	0.774819166	2	4.231163
Q68FS4	DKDDDVPQFTSAGENFNK	0.884119748	2	4.221
Q68FS4	GITFDSGGISIK	0.922672952	2	2.782814
Q68FS4	GLVLGIYSK	0.761267382	1	2.075235
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.311568275	3	6.037287
Q68FS4	GVLFASGQNLAR	1.325142445	2	3.067957
Q68FS4	LFEASVETGDR	0.885923993	2	2.742795
Q68FS4	LHGSGDLEAWEK	0.841826987	2	2.808017
Q68FS4	LNLPINIIGLAPLCENMPSGK	1.138344548	2	4.573497
Q68FS4	QLMESPANEMTPTR	0.81714182	2	3.887852
Q68FS4	QVIDCQLADVNNLGK	0.841807431	2	4.653482
Q68FS4	SAGACTAAAFLR	1.065124667	2	3.387338
Q68FS4	SAGVDDQENWHEGK	0.886115811	2	3.813685
Q68FS4	SAGVDDQENWHEGKENIR	1.085188661	3	3.410938
Q68FS4	SWIEEQEMGSFLSVAK	0.95028154	2	5.256531
Q68FS4	TFYGLHQDFPSVVVVGLGK	0.766983244	2	4.167919
Q68FS4	TIQVDNTDAEGR	0.861410711	2	3.817404
Q68FS4	TLIEFLLR	1.032940429	2	2.630566
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**0.891448649**	**0.00184**	**3**
Q68FT1	LNHVLEEEQK	0.872814368	2	3.194156
Q68FT1	STGEALVQGLMGAAVTLK	0.901949898	2	3.251091
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.91064168	3	4.994508
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.66048639**	**3.1E-07**	**6**
Q68FT3	ISQLDTQSPVTK	0.611323465	2	3.365757
Q68FT3	SLLLGTDVAENQK	0.659344866	2	3.491945
Q68FT3	TLGAQLPQYYEVLTAPISK	0.680419487	2	3.983496
Q68FT3	VFDCIEAYAPGFK	0.763705537	2	2.46249
Q68FT3	VLDQWFESEPLK	0.837172584	2	3.104494
Q68FT3	VQGVVLQGGEEVR	0.630581621	2	3.371186
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.276098002**	**9.9E-20**	**10**
Q68FT5	AGANIIGVNCR	1.226169447	2	3.750299
Q68FT5	AGLWTPEAVVEYPSAVR	1.201266255	2	4.480585
Q68FT5	AIAEELAPER	1.673079474	2	3.70167
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.093581122	3	4.236025
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.23256296	3	3.514765

Q68FT5	FGPWTSLQTMK	1.030938129	2	2.389893
Q68FT5	GFLPPASEK	2.343079502	1	1.906607
Q68FT5	GGFVDLPEYPFGLEPR	1.0725287	2	4.278891
Q68FT5	LDSGEVVVGDGGFLFTLEK	0.951269684	2	2.945224
Q68FT5	YIGGCCGFEPYHIR	2.946521307	2	4.420866
Q68FT9	**SCLY Selenocysteine lyase**	**0.670377966**	**9.9E-20**	**4**
Q68FT9	AEVDLIVQDLK	0.669868491	2	3.615599
Q68FT9	CFHEQQTLQGR	0.719375944	2	2.595431
Q68FT9	RVDVEDLGVDFLTIVGHK	0.979898503	3	5.676523
Q68FT9	VLVHTDAAQALGK	0.625272483	2	2.854839
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.894075748**	**9.9E-20**	**8**
Q68FU3	AGDLGVDLTSK	0.918487356	2	3.816684
Q68FU3	EIIAVSCGPPQCQETIR	0.88887552	2	4.803982
Q68FU3	GIHVEVPGAEAENLGPLQVAR	0.427877248	2	5.866375
Q68FU3	HSMNPFCEIAVEEAVR	1.361388835	2	4.739328
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2)	0.829222923	2	4.382783
Q68FU3	VDLLFLGK	1.251471972	2	2.803738
Q68FU3	VETTEDLVAK	0.79088559	2	3.278349
Q68FU3	VSVISVEEPPQR	0.881140029	2	3.440971
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.218623878**	**0.09245**	**11**
Q68FY0	EMQENDASMQNVVFDYLHATAFQGTPLAQAVEGPSENVR	1.888152033	3	4.4138
Q68FY0	EVESIGAHLNAYSTR	1.003847817	2	3.12697
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.163073085	3	5.211556
Q68FY0	IEEVDAQMVR	0.895455507	2	3.662644
Q68FY0	LCTSATESEVTR	1.103707499	2	2.983982
Q68FY0	NALISHLDGTTPVCEDIGR	0.939543569	2	4.192996
Q68FY0	NNGAGYFLEHLAFK	1.048761338	2	3.487449
Q68FY0	RIPLAEWESR	1.139123244	2	2.594026
Q68FY0	TDLTDYLSR	1.001757341	2	2.657713
Q68FY0	VVELLADIVQNISLEDSQIEK	0.971243175	3	5.977706
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.027532622	3	5.097607
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.727881617**	**9.9E-20**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.730650957	2	4.440315
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	0.780956523	3	3.64173
Q68G31	GESGGQTTPYDFYSR	0.898055347	2	3.915401
Q68G31	LQPTDSFSQSSCFGLR	0.808230421	2	3.267365
Q68G31	NVNSTLTFVTLSGELK	0.776329454	2	3.972027
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	0.852128294	3	4.928851
Q68G31	VNTEPLPGIEK	0.735787925	2	2.955717
Q69Z66	**MYSM1 Histone H2A deubiquitinase MYSM1**	**0.948588833**	**0.31329**	**3**
Q69Z66	KYTNSLQK	1.998235816	1	1.983686

Q69Z66	NSAELNEK	0.753336382	1	1.950879
Q69Z66	QTKTPERYLK	0.895711588	2	2.308583
Q6A000	**K0753 Uncharacterized protein KIAA0753**	**0.857525541**	**0.04085**	**2**
Q6A000	EIQEELDKLSPQK	0.838744386	2	2.355461
Q6A000	ILGSETSARLGDSK	0.863791056	2	2.551587
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**0.850523414**	**0.0008**	**2**
Q6A0A9	SQGGVQPIPSQGGK	2.335348917	2	2.665821
Q6A0A9	VEGSSTASSGSQLAEGK	0.850108702	2	4.217848
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**0.905846826**	**0.05548**	**2**
Q6AXM8	FQEEENSLLHLK	1.012560369	2	2.57851
Q6AXM8	LFVYDPNHPPSSEVLR	0.698304716	2	2.300478
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.817953121**	**1.8E-09**	**2**
Q6AXS5	FDQLFDDESDPFEVLK	0.841631213	2	4.72208
Q6AXS5	SAAQAAAQTNSNAAGK	1.78270606	2	4.594045
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.806823327**	**2.3E-05**	**2**
Q6AXY0	FLQPGSQR	0.759912483	2	2.452293
Q6AXY0	YFPAFEK	0.807780362	1	1.994576
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**1.178117924**	**0.01667**	**3**
Q6AY09	ATENDIYNFFSPLNPMR	1.514926085	2	2.522285
Q6AY09	HTGPNSPDTANDGFVR	0.972908802	2	4.611254
Q6AY09	STGEAFVQFASQEIAEK	1.477864182	2	3.943142
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**0.706470501**	**9.9E-20**	**4**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	0.83646598	3	3.828575
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.063087478	2	3.90887
Q6AY30	LQQVLEK	0.699151077	1	1.982102
Q6AY30	SVSNLKPVPVIGSK	0.702602059	2	3.210643
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.044256991**	**0.00381**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	0.841223354	2	4.09488
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.05707329	2	5.401331
Q6AY56	LISQIVSSITASLR	1.015246135	2	3.319748
Q6AY56	NLDIERPTYTNLNR	0.986297805	2	3.097337
Q6AY56	QLFHPEQLITGK	0.87772222	2	2.35307
Q6AY56	TIQFVDWCPTGFK	1.229649619	2	3.721541
Q6AY56	VGINYQPPTVVPGGDLAK	0.92920523	2	4.904021
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**0.837385877**	**0.56697**	**2**
Q6AY80	NDVTGALSNPEVFK	0.736137925	2	3.466573
Q6AY80	VLAPQISFGPEVSSEEQR	1.088578548	2	3.7164
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**0.659565589**	**1.4E-08**	**2**
Q6AYG5	DVLETLWGGPANLEAIAK	0.664885131	2	3.741493
Q6AYG5	ILEQFPGGSIDLQK	0.60209559	2	3.068047

Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.803361583**	**9.9E-20**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	0.750848253	2	3.71954
Q6AYQ8	NLHHEVELGVLLGR	0.835362975	3	4.703354
Q6AYQ8	SFTSSCPVSAFVPK	0.789081124	2	3.875191
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.893640934**	**6.2E-12**	**3**
Q6AYS8	ALTDELAALGCTGVR	0.698731815	2	3.576901
Q6AYS8	FDAVVGYK	0.631711866	1	2.097917
Q6AYS8	SVAGEIVLITGAGHGIGR	0.900830207	2	3.346679
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.651179325**	**0.43275**	**2**
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.608884988	2	3.12929
Q6AYT9	NDDVINSSSYR	0.797331943	2	3.377671
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.18588558**	**9.9E-20**	**5**
Q6AYZ1	AVFVDLEPTVIDEVR	1.215715334	2	5.318069
Q6AYZ1	DVNAAIATIK	0.982456157	2	3.211862
Q6AYZ1	IHFPLATYAPVISAEK	1.040847915	2	3.049576
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.708476106	2	5.430105
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.254318566	2	4.59305
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**0.961707056**	**9.9E-20**	**7**
Q6DGG1	AVAIDLPGLGR	0.796248778	2	3.33265
Q6DGG1	FSSETWQNLGTLHR	0.997225069	2	3.52961
Q6DGG1	FSVLLLHGIR	1.085679244	2	2.806667
Q6DGG1	GYVPVAPICTDK	0.75075496	2	3.010204
Q6DGG1	INAADYAR	0.814111211	2	2.372388
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.290073574	3	5.227358
Q6DGG1	VLVMEGAGHPCYLDKPDEWHTGLLDFLQELA	1.075760165	3	3.58092
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**0.872718101**	**0.00598**	**3**
Q6EDY6	ELMESIK+Oxidation(2)	0.952097314	1	1.950341
Q6EDY6	IENYLLR	0.872203111	2	2.572936
Q6EDY6	SSDAHELGEGDEKKK	0.794422338	2	2.432307
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**0.805440713**	**0.00331**	**2**
Q6GQP4	CDLSDIREVPLK	0.646478635	2	2.544029
Q6GQP4	CDLSDIREVPLKDAK	1.041411625	2	2.630132
Q6IE52	**MUG2 Murinoglobulin_2**	**1.071814903**	**0.0382**	**15**
Q6IE52	AHFSVMGDILSSAIK	0.991527732	2	3.28282
Q6IE52	GDPIPNEQVFIK	0.916596072	2	2.438287
Q6IE52	HGIPFFVK	1.883320068	2	2.545252
Q6IE52	HTSSWLVTPK	1.219840472	2	2.583892
Q6IE52	LPSSEEEESLDINIEGAK	1.38510345	2	4.964682
Q6IE52	MLIYTILPDGEVIADSVK	1.104330959	2	4.175538
Q6IE52	MLIYTILPDGEVIADSVK+Oxidation(0)	0.82314462	2	3.315023
Q6IE52	MLSGFIPLKPTVK+Oxidation(0)	1.053888199	2	2.587598

Q6IE52	NLYPLKELVQDPK	0.97532219	1	1.910462
Q6IE52	QLSFSLSAEPIQGPYK	1.26487708	2	4.064075
Q6IE52	VKTVPLTCNNPK	1.024268185	2	3.028707
Q6IE52	VLIVEPEGIKK	1.147233625	2	2.405734
Q6IE52	VTASPQSLCGLR	1.138986512	2	2.571673
Q6IE52	YMVLVPSQLYTETPEK	1.053547125	2	3.810358
Q6IE52	YMVLVPSQLYTETPEK+Oxidation(1)	0.81991548	2	3.261446
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.743984844**	**9.9E-20**	**3**
Q6IMF3	TNAENEFVTIK	0.685302786	2	2.502182
Q6IMF3	WELLQQVDTSTR	0.746078444	2	3.496271
Q6IMF3	YEELQITAGK	0.736917745	2	3.323662
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**0.994067062**	**3.2E-09**	**2**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	1.033814215	3	5.170481
Q6IRK9	TYPDTDSFNTVAEITGSK	0.740419749	2	4.380447
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.780398187**	**1.1E-07**	**3**
Q6MGB5	AGVIGLTQTAAR	0.778134032	2	3.482303
Q6MGB5	GSIINISSIVGK	0.758040666	2	2.479659
Q6MGB5	SALALVTGAGSGIGR	0.929247783	2	2.642201
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.22123156**	**0.0005**	**4**
Q6NYB7	EFADSLGIPFLETSAK	1.228839368	2	3.452065
Q6NYB7	MGPGATAGGAEK+Oxidation(0)	2.104140424	2	2.381153
Q6NYB7	NATNVEQSFMTMAAEIK	1.146795883	2	4.223239
Q6NYB7	RMGPGATAGGAEKSNVK	1.156419577	2	2.504136
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**0.936364745**	**0.97506**	**7**
Q6NZJ6	GLPLVDDGGWNTVPISK	0.929299214	2	2.762463
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.013047993	3	3.360265
Q6NZJ6	IHNAENIQPGEQK	0.944486152	2	4.330977
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.116985685	3	3.563276
Q6NZJ6	LKEELEEAR	0.934935789	2	2.530767
Q6NZJ6	QVTQLAIDTEER	0.999391179	2	3.241071
Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.971710215	3	4.13048
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**0.982902976**	**0.75307**	**6**
Q6P502	AVAQALEVIPR	0.981990144	2	2.51775
Q6P502	KGESQTDIEITR	1.199536096	2	2.419455
Q6P502	NLQDAMQVCR	0.945320865	2	2.982199
Q6P502	TAVETAVLLLR	1.07625267	2	3.398251
Q6P502	TLIQNCGASTIR	0.93792171	2	2.870304
Q6P502	WSSLACNIALDAVK	1.037090891	2	3.492018
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.779869501**	**9.9E-20**	**9**
Q6P6R2	IDVSVEAASGGK	0.853104861	2	3.584298
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	0.865051527	3	3.382485
Q6P6R2	NETLGGTCLNVGCIPSK	0.851310001	2	5.130776

Q6P6R2	NQVTATTADGSTQVIGTK	0.844532873	2	5.755962
Q6P6R2	RPFTQNLGLEELGIELDPK	1.734620141	3	4.766781
Q6P6R2	SEEQLKEEGVEFK	0.890707386	3	3.824153
Q6P6R2	TNADTDGMVK	0.729060732	2	2.601839
Q6P6R2	TNADTDGMVK+Oxidation(7)	0.957880861	2	2.797984
Q6P6R2	VCHAHPTLSEAFR	0.851755905	3	3.437882
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.708898528**	**3.1E-10**	**6**
Q6P6S9	AAETHLIDYEK	0.935213109	2	2.33201
Q6P6S9	AQTLLLEVEEIFK	0.706874082	2	3.065655
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.751185743	2	4.315549
Q6P6S9	QGAETVQELLEVAK	0.707737325	2	3.175282
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	0.644700973	3	3.498775
Q6P6S9	WLEAEWIFGGVK	0.674558765	2	2.481003
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.030137699**	**2.4E-11**	**7**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2)	0.927286767	2	2.715573
Q6P6V0	HFVALSTNTDK	1.150907312	2	2.64157
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.101937993	3	5.279137
Q6P6V0	TFTTQETITNAETAK	1.145542629	2	4.742327
Q6P6V0	TLANLNPESSLFIIASK	1.232823955	3	4.639544
Q6P6V0	VFEGNRPTNSIVFTK	1.286725455	2	2.973778
Q6P6V0	VWFVSNIDGTHIAK	1.33879507	2	3.655668
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**0.969244404**	**0.02927**	**3**
Q6P7Q4	DFLLQQTMLR	0.723578539	2	3.113421
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.03169664	2	5.517168
Q6P7Q4	RFEELGVK	0.969447925	2	2.496509
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**0.950387658**	**0.00206**	**2**
Q6P7R8	GIFVQSVLPFFVATK	1.522991831	2	2.799876
Q6P7R8	LGEWAVVTGGTDGIGK	0.819404389	2	3.532351
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.086881099**	**9.9E-20**	**11**
Q6P9T8	AVLVDLEPGTMDSVR	1.084049875	2	3.057495
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10)	0.889114255	2	3.907806
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	0.963513599	3	5.467319
Q6P9T8	EIVHLQAGQCGNQIGAK	1.053556716	2	5.062567
Q6P9T8	EVDEQMLNVQNK	0.897992761	2	4.346983
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	1.326183929	3	4.322352
Q6P9T8	INVYYNEATGGK	1.551847241	2	3.070583
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.007160904	3	6.148393
Q6P9T8	MSATFIGNSTAIQELFK	1.522026746	2	4.05878
Q6P9T8	TAVCDIPPR	1.124315101	2	2.595361
Q6P9T8	YLTVAAVFR	1.105521297	2	2.397625
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**0.990933963**	**0.15899**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	1.144964955	3	3.433859

Q6P9U8	EGTGSTATSSSSTGGAVGK	0.858321465	2	4.249612
Q6PA06	**ATLA2 Atlastin_2**	**1.067038316**	**0.99476**	**2**
Q6PA06	NLVPLLLAPENLVEK	1.069276568	2	3.07585
Q6PA06	QNQHEELQNVR	1.00307074	2	2.740132
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.130091161**	**8.7E-06**	**3**
Q6PEC1	LEAAYTDLR	0.985796198	2	2.862629
Q6PEC1	QAEILQESR	1.623630296	2	2.848119
Q6PEC1	RLEAAYTDLR	1.108583714	2	2.361752
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**1.01840189**	**0.50548**	**4**
Q6PEC4	NDFTEEEEAQVR	1.038963066	2	3.249994
Q6PEC4	RTDDIPVWDQEFLK	0.908342726	2	2.375908
Q6PEC4	TDDIPVWDQEFLK	1.010809872	2	2.532832
Q6PEC4	TVANMIKGKTPEEIR+Oxidation(4)	1.178398016	2	2.327264
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**0.958831271**	**7.1E-09**	**4**
Q6Q0N1	EGGSIPVTLTFQEATGK	1.317617873	2	2.673471
Q6Q0N1	LGGSVELVDIGK	0.847896575	2	2.941091
Q6Q0N1	MTEAAAADVQR	0.835025739	2	2.576043
Q6Q0N1	TVFGVEPDLTR	0.938330824	2	2.464374
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.149131678**	**2.9E-07**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.085168092	2	4.798786
Q6TUG0	FQMTQEVVCDECPNVK	1.468979068	2	4.662275
Q6TUG0	KGEGLPNFDNNNIK	1.421013818	2	2.883686
Q6TUG0	TLEVEIEPGVR	1.069551397	2	2.381402
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**1.090162735**	**9.9E-20**	**13**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.650519536	2	4.280781
Q6UPE1	ALNEGGLQSIPK	0.867395156	2	3.167406
Q6UPE1	ASCDAQTYGIGLK	1.188913075	2	3.477417
Q6UPE1	FCPAGVYEFVPLEQGDGFR	0.896509554	2	4.818525
Q6UPE1	GAPLNTPVTEDR	0.923677576	2	3.381248
Q6UPE1	GIATNDVGIQK	0.898522066	2	3.193973
Q6UPE1	LQINAQNCVHCK	0.914463492	2	3.188929
Q6UPE1	NLSIYDGPEQR	0.89407504	2	3.042401
Q6UPE1	QLTSENLQSK	0.835274398	2	2.591437
Q6UPE1	SGSLAAEAIFK	0.966890873	2	3.320204
Q6UPE1	TAGLHVTEYEDNLK	0.694981097	2	3.141437
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	0.935125915	2	3.761909
Q6UPE1	VTIFAEGCHGHLAK	0.650873208	2	3.184931
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**1.055325063**	**2.4E-06**	**7**
Q6URK4	EDSVKPGAHLTVK	0.805357067	2	3.459554
Q6URK4	GFAFVTFDDHDTVDK	1.035084101	2	3.842396
Q6URK4	IETIEVMEDR	0.865692236	2	3.402972
Q6URK4	IFVGGIKEDTEEYNLR	1.09710637	3	3.363607

Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	1.156555548	2	5.106761
Q6URK4	WGTLTDCVVMR	0.761807812	2	2.932795
Q6URK4	YHTINGHNCEVK	0.894094906	2	3.540127
Q6URW6	**MYH14 Myosin_14**	**0.903970871**	**9.9E-20**	**4**
Q6URW6	EDQSILCTGESGAGK	0.751527502	2	3.940934
Q6URW6	FDQLLAEEK	0.853955207	2	2.510147
Q6URW6	KFDQLLAEEK	0.905912147	2	2.886504
Q6URW6	QLLQANPILEAFGNAK	0.77783902	2	4.355002
Q6VGS5	**DAPLE Protein Daple**	**1.145576719**	**0.27931**	**2**
Q6VGS5	ELKTSLNNSQLELSR	1.1999923	2	2.302331
Q6VGS5	YGELEKENQQLSKK	1.037003576	2	2.324618
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.402875343**	**3.2E-10**	**4**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.40708541	2	4.090353
Q6XQN1	LDSGDLLQQAK	0.874963964	2	2.783299
Q6XQN1	LYLQQGQPYEPLPSLEESR	0.401772021	2	4.5337
Q6XQN1	QLQNPAVYQVALSEK	0.509758658	2	3.484419
Q6ZPF3	**TIAM2 T_lymphoma invasion and metastasis_inducing protein 2**	**1.108662702**	**0.23916**	**2**
Q6ZPF3	KMAELQLSVVSDPK+Oxidation(1)	1.075461693	2	2.302119
Q6ZPF3	STELEKDAQEGLAEFPDGLIK	1.234406663	2	2.408516
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**0.931059012**	**0.43275**	**3**
Q6ZPJ3	FLDDIKKLQENLK	0.951022628	2	2.384369
Q6ZPJ3	FRTTDIVIR	0.881355932	2	2.326805
Q6ZPJ3	NCAQGEGSMAKKVK	0.971266584	2	2.480072
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**0.7579203**	**0.00763**	**2**
Q70FJ1	LMKEKLEVQCQAEK+Oxidation(1)	0.759373527	2	2.509394
Q70FJ1	QRNTFAFAEK	0.72388404	1	1.952147
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**0.93751411**	**0.99367**	**4**
Q711G3	DCGTDVLDLWTLMQK	1.057844844	2	3.880005
Q711G3	DVEETKPELSLLGDGDH	0.944574521	2	3.432467
Q711G3	QHVPLDEYSANLR	1.011071078	2	2.585967
Q711G3	VILITPPPLCEAAWEK	0.922717506	2	2.633911
Q71LX4	**TLN2 Talin_2**	**0.825739818**	**0.04027**	**2**
Q71LX4	QEDVIATANLSR	0.817120929	2	2.950649
Q71LX4	QVAASTAQLLVACK	0.841736202	2	3.028237
Q75N33	**SC16B Protein transport protein Sec16B**	**1.198423194**	**0.00077**	**2**
Q75N33	EALEWAMK	2.423063848	1	1.947769
Q75N33	NLLTGEIPLNVDTPAQIVEK	1.081665578	2	4.311049
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.033224835**	**0.46265**	**2**
Q75Q39	NADLSTFYQNR	1.110760721	2	2.579278
Q75Q39	SDEDKDKEGEALEVK	1.006523605	2	3.685772
Q75WE7	**VWA5A von Willebrand factor A domain_containing protein 5A**	**0.834858568**	**0.07108**	**2**

Q75WE7	LDADLGGTEILTPLR	1.053330199	2	2.44487
Q75WE7	YVQELPLESDGALR	0.512686739	2	2.895805
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.028982874**	**0.06128**	**8**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	1.081083253	3	4.433817
Q76MZ3	DNTIEHLLPLFLAQLK	1.057372023	3	3.6036
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	1.06988061	3	3.862123
Q76MZ3	IGPILDNSTLQSEVKPILEK	0.972966208	2	4.53703
Q76MZ3	LTQDQDVDVK	0.872050643	2	2.622095
Q76MZ3	QLSQSLLPAIVELAEDAK	0.902832241	2	3.681839
Q76MZ3	SALASVIMGLSPILGK	1.042426357	2	3.252979
Q76MZ3	SEIIPMFSNLASDEQDSVR	0.719050304	2	3.544723
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**0.955905469**	**0.00038**	**5**
Q791V5	EEGIVGFFAGLIPR	1.783935194	2	3.865932
Q791V5	GLFTGLTPR	1.007115901	2	2.363672
Q791V5	SAATLITHPFHVITLR	1.213604879	3	3.535018
Q791V5	VLIQVGYEPLPPTIGR	0.971761415	2	4.156374
Q791V5	YCGLCDSIVTIYR	1.121910528	2	3.034861
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**1.239582993**	**3.9E-06**	**3**
Q794E4	ATENDIYNFFSPLNPVR	1.273983859	3	4.333314
Q794E4	HSGPNSADSANDGFVR	0.891410773	2	3.96095
Q794E4	VHIEIGPDGR	0.807680003	2	3.119194
Q7TMA5	**APOB Apolipoprotein B_100**	**0.656841389**	**2E-09**	**6**
Q7TMA5	GFEPTLEALFGK	0.813040718	2	2.874983
Q7TMA5	IEGNLVFDPSSYLPK	0.661907414	2	3.16996
Q7TMA5	IEIDIPLPLGGK	0.575609398	2	2.923283
Q7TMA5	ITDNDVLIALDSAK	1.022079956	2	3.138131
Q7TMA5	KGTVATEMSTER	0.51325617	2	2.704306
Q7TMA5	TILFDTFVNDVAPVEK	1.124439647	2	3.307117
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**0.813186685**	**2.8E-11**	**3**
Q7TNG8	AVVGSPHVSTASAVR	0.798555485	2	2.955059
Q7TNG8	AYSTDVCVPISR	0.773257919	2	3.091918
Q7TNG8	GSQGGLSQDFVEALK	0.839560493	2	3.502352
Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**0.908714928**	**0.00014**	**2**
Q7TP47	DLFEDELVPLFEK	1.32309026	2	3.208024
Q7TP47	NLANTVTEEILEK	0.908233452	2	3.661824
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**1.392611123**	**0.00294**	**4**
Q7TP48	GLFEVNPQK	1.01034149	1	2.123389
Q7TP48	LENGEIETIAR	1.001244734	2	3.027943
Q7TP48	LLEYDTVTK	1.028218575	2	2.413787
Q7TP48	LLLSSETPIEGK	1.415216483	2	2.854828

Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**0.922035893**	**3.4E-06**	**7**
Q7TP52	AGVSVYGIIR	0.702574214	2	2.591967
Q7TP52	EDCSPADKPYIEEAR	0.889523773	2	3.283609
Q7TP52	KREDCSPADKPYIEEAR	0.888309902	3	4.448145
Q7TP52	LDYGGMGQEVQVEHIK	0.998841983	2	4.537138
Q7TP52	LKEHCIVNYQVK	1.322894556	2	3.532428
Q7TP52	NLIEWLNK	0.81853345	1	2.51928
Q7TP52	TFSGQTHGFVHR	0.98345432	2	3.387561
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**0.932453675**	**0.1713**	**6**
Q7TPB1	AFADAMEVIPSTLAENAGLNPISTVTELR	0.914532396	3	3.384226
Q7TPB1	ALIAGGGAPEIELALR	1.12958094	2	3.546707
Q7TPB1	ETLLNSATTSLNSK	1.080006219	2	3.432967
Q7TPB1	GDVTITNDGATILK	1.025776882	2	3.445557
Q7TPB1	GIHPTIISESFQK	0.843896991	2	2.384657
Q7TPB1	VIDPATATSVDLR	0.903208446	2	3.341628
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.058557359**	**9.6E-06**	**2**
Q7TPJ0	GEDFPANNIVK	1.143934885	2	2.737093
Q7TPJ0	GTEDFIVESLDASFR	1.042822605	2	4.332164
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**0.834049936**	**0.0623**	**3**
Q7TQM4	AIWEAVQAYPK	0.865255124	2	2.336154
Q7TQM4	QDRPLPSTASDSTR	0.830639026	2	3.149165
Q7TQM4	TQCLEQAQR	0.341087925	2	2.629607
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.457523565**	**0.31765**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(1)	0.457523565	3	3.572107
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(5)	0.457523565	3	3.562283
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**0.818917095**	**9.9E-20**	**10**
Q80W21	CLDAFPNLK	0.746934668	2	3.148868
Q80W21	CLDAFPNLKDFIAR	1.007894266	2	3.252597
Q80W21	FKLGLDFPNLPYLIDGSHK	0.845446061	3	3.794268
Q80W21	HNLCGETEEER	0.841584972	2	3.997768
Q80W21	ITQSNAILR	0.77668174	2	3.11647
Q80W21	KHNLCGETEEER	0.609042093	3	4.130913
Q80W21	LFLEYTDSSYEEK	0.849492042	2	3.742438
Q80W21	LGLDFPNLPYLIDGSHK	0.873917519	3	4.35242
Q80W21	LYSEFLGK	0.840998593	1	2.429498
Q80W21	VDILENQLMDNR	0.537138265	2	3.503875
Q80W93	**HYDIN Hydrocephalus_inducing protein**	**1.53200863**	**9.3E-10**	**2**
Q80W93	FIVPVKAR	1.159069511	2	2.427654
Q80W93	LAKEMQEK	2.423063848	1	2.033756
Q80WE4	**KI20B Kinesin_like protein KIF20B**	**0.971877816**	**0.90379**	**2**
Q80WE4	ELLDLIEK	0.97187782	1	2.111984
Q80WE4	LNTGTMDDLDVLTR+Oxidation(5)	0.968515127	2	2.602783

Q80WP8	**GADL1 Glutamate decarboxylase_like protein 1**	**1.09724008**	**0.06884**	**3**
Q80WP8	ADSVAWNPHK	1.059935256	2	2.702766
Q80WP8	MLMAGIQCSALLVK+Oxidation(0)	0.778185726	2	2.428595
Q80WP8	MMKKGSLMLGYQPHR	1.329262749	2	2.493221
Q80X90	**FLNB Filamin_B**	**0.899287315**	**0.78821**	**6**
Q80X90	GAGIGGLGITVEGPSESK	1.072747289	2	3.662366
Q80X90	GEAGIPAEFSIWTR	1.005954022	2	2.588229
Q80X90	IGNLQTDLSDGLR	0.834172582	2	3.204597
Q80X90	VDIQTEDLEDGTCK	0.994513351	2	3.514197
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.05423413	2	4.965069
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	1.010872404	2	4.239129
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**0.829950058**	**0.23839**	**2**
Q80Y84	CDIGLLGLK	0.816119466	2	2.568292
Q80Y84	YRYTLDDLYPMMNALK+Oxidation(10)	1.001501656		2.304153
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**0.894867432**	**0.62282**	**2**
Q80Z25	MIEESLK+Oxidation(0)	0.940219522	2	2.369057
Q80Z25	RMIEESLK+Oxidation(1)	0.885738548	2	2.312514
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**1.065045753**	**0.11723**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.192409653	2	3.691751
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.404767642	5	4.812943
Q80Z29	VIQGDGVDINTLQEIVEGMK	1.010359679	2	4.506372
Q80Z29	YLLETSGNLDGLEYK	0.76120473	2	3.903606
Q811X6	**CRYL1 Lambda_crystallin homolog**	**0.868819683**	**0.58248**	**2**
Q811X6	LYDIEQQQITNALESIR	0.890904069	2	3.169236
Q811X6	TFGPVPEFSGDTVEK	0.992765507	2	3.107295
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**0.890224519**	**9.9E-20**	**9**
Q8BFZ3	CDVDIR	0.801986548	2	2.38123
Q8BFZ3	HQGVMVGMGQK	0.57222724	2	3.214974
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	0.749490196	3	3.499029
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	0.730872074		3.938262
Q8BFZ3	HQGVMVGMGQK+Oxidation(7)	0.785231621	3	3.314152
Q8BFZ3	SYELPDGQVITIGNER	0.860844684	2	5.051468
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.092836512	3	6.455184
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)	0.965634873	3	5.974591
Q8BFZ3	VAPDEHPILLTEAPLNPK	0.918144415	3	4.276495
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**0.836768769**	**2E-11**	**3**
Q8BG32	LYDNLLEQNLIR	0.83794295	2	3.633115
Q8BG32	TTANAIYCPPK	0.83715052	2	3.140503
Q8BG32	VQIEHISSLIK	0.687929976	2	2.794554
Q8BGT6	**MILK1 MICAL_like protein 1**	**0.837943885**	**0.19651**	**2**
Q8BGT6	EEEEDKMLETMIKK	0.836553332	2	2.339371

Q8BGT6	KDPPWITLVQTEPKK	0.945760621	2	2.347662
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.12570065**	**9.9E-20**	**5**
Q8BGY2	IVEMSTSK+Oxidation(3)	0.536520375	2	2.310062
Q8BGY2	KYEDICPSTHNMDVPNIK	1.210914558	3	4.160377
Q8BGY2	KYEDICPSTHNMDVPNIK+Oxidation(11)	0.901688992	3	3.411568
Q8BGY2	VHLVGIDIFTGK	1.21292884	2	3.402694
Q8BGY2	YEDICPSTHNMDVPNIK	1.003289722	2	3.760373
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.105244139**	**1E-15**	**10**
Q8BH00	DSYDFFTEIK	0.672873093	2	2.334916
Q8BH00	ELLMLENFIGGK	0.97228745	2	3.536484
Q8BH00	ELNLPFGGMK	0.919059814	1	2.291637
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.178289083	2	5.06076
Q8BH00	ILCGEGVDQLSLPLR	1.144079358	3	4.148017
Q8BH00	ITQLSAPHCK	1.06484006	2	2.815052
Q8BH00	KLSLELGGK	1.009760195	2	2.3087
Q8BH00	NPAIIFEDANLEECIPATVR	1.061042766	3	4.403743
Q8BH00	NQAGYFMLPTVITDIK	1.179901359	2	3.43048
Q8BH00	SSFANQGEICLCTSR	2.40119486	2	3.865173
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**0.916178282**	**0.07195**	**8**
Q8BHN3	AEKDEPGAWEETFK	0.889102975	2	2.916621
Q8BHN3	DDNSVELTVAEGPYK	1.002496285	2	3.228969
Q8BHN3	MLDYLQGSGETPQTDIR	1.082980167	2	4.773614
Q8BHN3	MLDYLQGSGETPQTDIR+Oxidation(0)	0.767431994	2	5.255156
Q8BHN3	REPWLLASQYQDAIR	0.948532092	3	3.601709
Q8BHN3	SGGIERPFVLSR	0.947199107	2	2.358219
Q8BHN3	SIRPGLSPYR	0.804696556	2	2.373337
Q8BHN3	THSDSKPYGPTSVGLDFSLPGMEHVYGIPEHADSLR	0.893528626	5	4.589782
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**0.921217426**	**0.22215**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.034169968	1	2.177176
Q8BIJ6	SCQTALAEILDVLVR	0.857465122	2	3.903869
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**0.830518524**	**4.9E-12**	**7**
Q8BJ64	ADSAYHPSCTCK	0.494971512	2	3.338553
Q8BJ64	AEVQTLVSR	0.828812609	2	2.461307
Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.791021231	2	4.100091
Q8BJ64	GGDGPLHVSR	0.802069683	2	2.438989
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	1.869492259	5	4.991092
Q8BJ64	TNHPLHQAFLQAAR	0.862231769	3	4.021713
Q8BJ64	VLLLEAGPK	0.8511819	2	2.649873
Q8BK64	**AHSA1 Activator of 90 kDa heat shock protein ATPase homolog 1**	**0.96686566**	**0.74468**	**2**
Q8BK64	ADATNVNNWHWTER	0.877216573	2	2.877216
Q8BK64	LDGEASINNR	1.065152266	2	2.63895

Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.000914717**	**0.53466**	**2**
Q8BL97	NPPGFAFVEFEDPR	0.935598227	2	2.491876
Q8BL97	VYVGNLGTGAGK	1.070821729	2	2.802097
Q8BMJ2	**SYLC Leucyl_tRNA synthetase_ cytoplasmic**	**0.879369572**	**0.60893**	**2**
Q8BMJ2	SFITTDVNPYYDSFVR	0.87962222	2	3.414272
Q8BMJ2	STGNFLTLSQAVDK	0.798140527	2	2.607379
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**0.892686397**	**7.9E-05**	**2**
Q8BP47	KEDGTFYEFGDDIPEAPER	1.420705504	2	4.32333
Q8BP47	LTESVDVLMPNVGEIVGGSMR	0.652415274	2	2.622137
Q8BQ33	**TICRR Treslin**	**0.972988445**	**0.31369**	**2**
Q8BQ33	MNTMSRSLK+Oxidation(0)	0.614779389	1	2.239679
Q8BQ33	QKMNTMSRSLK+Oxidation(2)	1.048302532		2.515048
Q8BTM8	**FLNA Filamin_A**	**0.828668737**	**9.9E-20**	**3**
Q8BTM8	AFGPGLQGGNAGSPAR	0.952034463	2	3.85674
Q8BTM8	GAGTGGLGLAVEGPSEAK	0.792002599	2	3.703381
Q8BTM8	GLVEPVDVVDNADGTQTVNYVPSR	0.515367211	2	5.163867
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**0.91761075**	**0.17086**	**2**
Q8BTZ7	HHGQEGSILVTK	0.936477864	3	3.35131
Q8BTZ7	YGVVVCEADTGR	0.899582379	2	2.772907
Q8BU14	**SEC62 Translocation protein SEC62**	**1.140187114**	**0.04826**	**2**
Q8BU14	AVECLLDSKWAK	1.174024504	2	2.489779
Q8BU14	IQEVGEPSKEEK	0.949202049	2	3.418259
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**0.783122042**	**1.6E-05**	**2**
Q8BU33	LPNSLMGR+Oxidation(5)	0.707997908	2	2.63353
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.922038627	2	5.112653
Q8BV79	**TRNK1 TPR and ankyrin repeat_containing protein 1**	**0.589001151**	**1.7E-05**	**2**
Q8BV79	LQLMSMDWPGQVPKRLLK+Oxidation(3)	0.589001151	2	2.456984
Q8BV79	LQLMSMDWPGQVPKRLLK+Oxidation(5)	0.589001151	2	2.394155
Q8BVE3	**VATH V_type proton ATPase subunit H**	**1.164994803**	**0.46382**	**2**
Q8BVE3	GAVDAAVPTNIIAAK	1.055686988	2	2.55597
Q8BVE3	QLQSEQPQTAAAR	1.167859975	2	2.412417
Q8C147	**DOCK8 Dedicator of cytokinesis protein 8**	**1.014334841**	**0.69714**	**2**
Q8C147	LNFASKLASAR	0.938093245	2	2.466516
Q8C147	RFMYTTPFTLEGRPR+Oxidation(2)	1.078695938	2	2.527167
Q8C8R3	**ANK2 Ankyrin_2**	**1.105749492**	**0.00932**	**2**
Q8C8R3	STSSSGRPGTSPTRESR	0.733062044	2	2.540637
Q8C8R3	TSTDFSEVIKQELEDNDK	1.11022255	2	2.983017
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**0.971112059**	**0.37004**	**3**
Q8CC88	HQATGELDDAK	0.629116864	2	3.35348
Q8CC88	NLADQGIINYPYSTR	1.123670432	2	2.992636
Q8CC88	VSSDQLSSENLTSAVGQK	0.949385293	2	3.602432

Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**0.900474976**	**0.0002**	**3**
Q8CFN2	DDPSTIEK	0.901813255	1	1.968742
Q8CFN2	NVFDEAILAALEPPEPK	0.928031364	3	5.090896
Q8CFN2	YVECSALTQK	0.816908295	2	2.892807
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**0.75888595**	**2.8E-15**	**9**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	0.932190761	2	2.640775
Q8CG45	EHHFEAIALVEK	0.883594262	2	2.688471
Q8CG45	FFGNSWSETYR	0.982527176	2	2.760707
Q8CG45	FYAYNPLAGGLLTGK	1.125918164	2	4.211129
Q8CG45	MDASASAATVR	0.757923751	2	3.724972
Q8CG45	QVETELLPCLR	0.784527517	2	2.679578
Q8CG45	RMDASASAATVR	0.926782799	2	2.490785
Q8CG45	TTYGTSAPSMTSAALR	0.886033717	2	4.256329
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.590288818	3	4.244577
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**1.015004711**	**0.00017**	**10**
Q8CGC7	AIQGATSHHLGQNFSK	1.065083822	2	4.108176
Q8CGC7	DQDVEPGAPSMGAK	0.825037834	2	3.082859
Q8CGC7	DQVDSAVQELLQLK	1.00906629	2	4.0168
Q8CGC7	GDVSISVEEGKENLLR	1.098805751	2	3.316414
Q8CGC7	GSQFGQSCCLR	1.070806214	2	2.365304
Q8CGC7	KEENLAEWYSQVITK	1.322546487	2	4.084888
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	0.93590634	2	4.219921
Q8CGC7	SQGSGLSSGGAGEGQGPK	0.991390314	2	4.89804
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.902514925	2	2.921504
Q8CGC7	VYEELLAIPVVR	1.061918781	2	2.78672
Q8CGN4	**BCOR BCL_6 corepressor**	**1.223702369**	**0.05237**	**2**
Q8CGN4	FLTDYLNDLQGR	0.980855808	1	2.003734
Q8CGN4	NWLLLSDVLK	1.316417826	2	2.496962
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**1.08762775**	**0.63637**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(10)	0.981167434	2	2.505867
Q8CHB8	DSGGQTLSPSWAAK	1.09646518	1	2.004535
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**0.996023365**	**0.85228**	**8**
Q8CHM7	DTSKPCLINIMIEPQSTR	1.065958566	2	3.478301
Q8CHM7	DTSKPCLINIMIEPQSTRK	1.028445619	2	2.320571
Q8CHM7	GAAYSHAEDSIR	0.048682141	2	3.295164
Q8CHM7	GVVPDNHPNCVGAAR	1.011406216	2	3.369596
Q8CHM7	GYFVQTPEELQDSLR	0.99031178	2	4.16779
Q8CHM7	LVELCNLPFLPTPMGK	0.996348088	2	4.131654
Q8CHM7	NCFIVSEGANTMDIGR	0.985072281	2	4.733199
Q8CHM7	NQEAMGAFQEFPQVEACR	1.141890512	2	4.908587
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.7042552**	**9.9E-20**	**2**
Q8CIB5	GCEVTPDVNISGQK	0.701529657	2	3.299987

Q8CIB5	TSTILGDITSIPELADYIK	0.830991095	2	3.079289
Q8CIE6	**COPA Coatomer subunit alpha**	**1.052475903**	**1.3E-08**	**6**
Q8CIE6	ASNLENSTYDLYTIPK	1.584555395	2	4.008404
Q8CIE6	DADSQNPDAPEGK	0.871443013	2	3.417788
Q8CIE6	GITGVDLFGTTDAVVK	1.058158878	2	2.702979
Q8CIE6	LLELGPKPEVAQQTR	1.008235754	2	2.595017
Q8CIE6	SILLSVPLLVVDNK	1.077460006	2	3.189211
Q8CIE6	TLDLPIYVTR	1.043542498	2	2.623641
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**0.891234701**	**0.00606**	**2**
Q8JZN5	GSNTCEVHFENTR	0.924807094	2	4.255743
Q8JZN5	NLSEFGLIQEK	0.880917332	2	3.136089
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**1.221642208**	**9.9E-20**	**16**
Q8K009	ADPLALAAEK	1.260532286	2	2.603598
Q8K009	AGFSVFWADDGLDTGPILLQR	1.561599637	2	2.350046
Q8K009	AMVEAVQLIADGK	1.638896864	2	3.677979
Q8K009	ANNTEYGLASGVFTR	0.673588097	2	4.742697
Q8K009	DLGEEALNEYLK	1.147105125	2	3.686132
Q8K009	FLFPEGIK	0.882670619	2	2.311523
Q8K009	FQNGDIDGVLQR	1.260217498	2	2.990376
Q8K009	GVINIIPGSGGVAGQR	1.21727026	2	2.779066
Q8K009	HGSIIYHPSLLPR	0.699269982	2	3.764791
Q8K009	NLQFEDGK	1.184643961	1	2.187108
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.687620965	3	3.445929
Q8K009	SCDVKPNDTVDSLYNR	1.408693104	2	4.634255
Q8K009	SPLIIFSDCDLEK	2.977418872	2	2.434675
Q8K009	TPQPEEGATYEGIQK	5.635393585	2	2.980946
Q8K009	VSYASLADVDR	1.459065695	2	3.613731
Q8K009	VVGVFTVPDKDGK	1.233368969	2	2.953269
Q8K2F0	**BRD3 Bromodomain_containing protein 3**	**1.180802611**	**0.01052**	**2**
Q8K2F0	KMDSREYPDAQGFAADIR	2.084252204	2	2.314347
Q8K2F0	QLSLDINRLPGEK	0.976211116	2	2.392806
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**0.873757916**	**0.85137**	**4**
Q8K442	GQITAILGHSGAGK	0.884951401	2	3.354488
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	0.934044014	3	3.615723
Q8K442	NTQNILVQNLSGGQK	0.748100319	2	2.648678
Q8K442	STLLNVLSGLCVPTK	0.913739651	2	3.203812
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.828133333**	**9.9E-20**	**9**
Q8K4C0	CCLEEGLEPVCFER	0.659470947	2	4.081275
Q8K4C0	EYKNPVEFTGK	0.642988505	2	2.327073
Q8K4C0	GYPIDILLSSR	0.576264799	2	3.55792
Q8K4C0	HSALGQHPTINDDLPNR	0.543273113	2	4.982573

Q8K4C0	IAVIGSGASGLTCIK	0.716828505	2	3.294501
Q8K4C0	KLPSQSEMMAEINK	0.606721703	2	3.64247
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.625147298	3	4.322129
Q8K4C0	KTILTTEDR	0.512180992	2	2.424112
Q8K4C0	SDDIGGLWR	0.534669108	2	2.91392
Q8K4Q0	**RPTOR Regulatory_associated protein of mTOR**	**1.098402512**	**0.01064**	**2**
Q8K4Q0	MPESVNVMQIVK+Oxidation(0)	0.842548771		2.337292
Q8K4Q0	QAQQVIQKGITR	1.538142975	1	2.120605
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**0.910619173**	**9.2E-06**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	0.850284345	2	4.118026
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	0.918715074	2	5.589459
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**1.075479733**	**0.27073**	**3**
Q8K586	FNVWDTAGQEK	1.111044167	2	3.005875
Q8K586	NLQYYDISAK	1.159366963	1	2.333461
Q8K586	VCENIPIVLCGNK	1.002296273	2	3.393962
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.988524364**	**0.84496**	**3**
Q8QZY1	QYEQQTYQVIPEVIK	1.084386435	2	2.673627
Q8QZY1	VFSDEVQQQAQLSTIR	0.979856191	2	4.068167
Q8QZY1	VYEIQDIYENSWTK	0.946428207	2	2.503316
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**1.213479198**	**3.3E-16**	**4**
Q8R081	ASLNGADIYSGCCTLK	1.489288894	2	3.507277
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	0.994932639	3	4.911361
Q8R081	SDALETLGFLNHYQMK	0.917118992	2	2.995269
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.802212185	3	7.470517
Q8R0F9	**S14L4 SEC14_like protein 4**	**0.84226998**	**0.00027**	**2**
Q8R0F9	FDNTYSLLHTK	0.897376604	2	2.903017
Q8R0F9	GSSHQVENEILFPGCVLR	0.649953652	2	5.486315
Q8R0K2	**TRI31 E3 ubiquitin_protein ligase TRIM31**	**0.906902515**	**0.18688**	**2**
Q8R0K2	AQVDLEKLKIHEEFK	0.908629509	2	2.465328
Q8R0K2	QRLDEEESFLLSR	0.557128264	2	2.412374
Q8R146	**APEH Acylamino_acid_releasing enzyme**	**0.795174809**	**1.2E-07**	**2**
Q8R146	GSTGFGQDSILSLPGNVGHQDVK	0.962868301	2	3.556288
Q8R146	QVLLSEPQEAAALYR	0.772780488	2	3.611272
Q8R164	**BPHL Valacyclovir hydrolase**	**0.923688432**	**9.9E-20**	**2**
Q8R164	QVSLLGWSDGGITALIAAAK	1.006998977	2	3.756064
Q8R164	TDFAPQLQSLNK	0.721642987	2	3.249377
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**0.855293989**	**0.04089**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	0.915650132	2	3.692452
Q8R1V4	QLLDQVEQIQK	0.852294307	2	3.239424
Q8R491	**EHD3 EH domain_containing protein 3**	**0.950753677**	**0.6991**	**3**
Q8R491	LDISDEFSEVIK	1.037139871	2	3.374796

Q8R491	LFEAEEQDLFK	0.947796429	2	3.123803
Q8R491	MQDQLQAQDFSK	0.845214315	2	3.12121
Q8VBU2	**NDRG2 Protein NDRG2**	**0.776345809**	**0.00524**	**6**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.852593528	3	4.637897
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK+Oxidation(3)	0.755829841	3	4.70909
Q8VBU2	LDPTQTSFLK	0.867997938	2	2.394476
Q8VBU2	MADSGGQPQLTQPGK	0.806496979	2	3.083048
Q8VBU2	TASLTSAASIDGSR	1.452723154	2	3.381552
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.198998113	2	3.55328
Q8VC12	**HUTU Urocanate hydratase**	**1.191826341**	**0.00021**	**6**
Q8VC12	HQLVVGSQAR	0.936787898	2	2.878387
Q8VC12	LLALEFAQELR	1.212056038	2	3.638972
Q8VC12	LVITNGMVIPNYSSR	1.160210759	2	2.743924
Q8VC12	VAIAVAINQAIASGK	2.250740714	2	2.991126
Q8VC12	VFVTSGLGGMSGAQAK	0.919877194	2	4.373806
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9)	0.91261499	2	2.726278
Q8VCD5	**MED17 Mediator of RNA polymerase II transcription subunit 17**	**0.724108018**	**0.13132**	**2**
Q8VCD5	EIFAQLSREAVQIK	0.814115494	1	2.10893
Q8VCD5	MELLMSALSPCLL+Oxidation(0)	0.723988224		2.325292
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.73380817**	**3E-08**	**4**
Q8VED5	NKYEDEINK	0.663704842	2	2.554667
Q8VED5	NKYEDEINKR	0.658376218	2	2.535197
Q8VED5	NLDLDSIIAEVK	0.660183164	2	2.760166
Q8VED5	YEDEINK	0.846694626	1	2.053252
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**0.978149083**	**3.7E-06**	**9**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	1.080385973	3	4.289993
Q8VEK3	GYFEYIEENK	1.015247377	2	3.316532
Q8VEK3	LLEQYKEESK	0.822806815	2	2.923428
Q8VEK3	LLEQYKEESKK	0.891637791	2	3.189782
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	0.967003551	3	4.986965
Q8VEK3	NFILDQTNVSAAAQR	0.869046243	2	4.662938
Q8VEK3	TCNCETEDYGEK	0.960389149	2	3.4796
Q8VEK3	VSELKEELKK	0.866751784	2	3.031257
Q8VEK3	YNILGTNTIMDK	0.936739831	2	3.624905
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.589555154**	**9.9E-20**	**4**
Q8VHE9	ATVQSVLLDSAGR	0.605576192	2	3.822774
Q8VHE9	GATYGADHDLAR	0.704009691	2	3.008013
Q8VHE9	NLYSDLQALGSK	0.573262362	2	3.072435
Q8VHE9	RPPEPLVTDK	0.580006872	2	2.970709
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**0.86609349**	**5.3E-10**	**3**
Q8VHF5	DILSNLIPK	0.849258354	2	2.420434
Q8VHF5	EGSSIGAIDSK	0.829134899	1	2.139305

Q8VHF5	GLVYETSVLDPDEGIR	0.866280178	2	4.023195
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.447924309**	**6E-06**	**3**
Q8VHT6	ILDLGSGSGR	0.854877986	2	2.962378
Q8VHT6	SLQNVHEEVISR	2.002366868	2	2.937655
Q8VHT6	TSADLQTNACVTPAK	1.656370226	2	3.497228
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**1.050189901**	**9.8E-06**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	1.050112907	2	4.487993
Q8VID1	LAEDGAHVVISSR	1.421478195	2	3.255774
Q8VID1	NFAAELAPK	0.809205848	2	2.59451
Q8VID1	VALVTASTDGIGLAIAR	2.394841564	2	2.989326
Q8VID6	**PDE11 Dual 3__5__cyclic_AMP and _GMP phosphodiesterase 11A**	**0.805011777**	**0.02263**	**2**
Q8VID6	MFMELGMVQKFK+Oxidation(0)	0.805011777	1	1.917717
Q8VID6	MFMELGMVQKFK+Oxidation(2)	0.805011777	1	1.906426
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.897440134**	**0.02369**	**8**
Q8VIF7	CGPGYATPLEAMK	0.742077955	2	3.234827
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	0.900096255	2	4.390937
Q8VIF7	GGFVLLDGETFEVK	0.892851875	2	3.940814
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.922202786	3	4.056978
Q8VIF7	NEGGTWSVEK	0.859925234	2	2.331684
Q8VIF7	NTGIEAPDYLATVDVDPK	0.842263789	2	5.022693
Q8VIF7	QYDISNPK	0.749544364	1	2.100129
Q8VIF7	VIEPNEIHAK	0.740793551	2	2.491315
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.110049098**	**0.01222**	**2**
Q8VIJ6	NLSPYVSNELLEEAFSQFGPIER	0.904822071	3	3.434645
Q8VIJ6	YGEPGEVFINK	1.156695512	2	2.69571
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**0.786326659**	**2.9E-06**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	0.899638626	2	5.306589
Q91VA0	AILPFDLQIIDEK	0.864069787	2	4.146455
Q91VA0	GNILPPNTEGYIGIR	0.808640791	2	2.922953
Q91VA0	HNQGLAFR	0.574924421	2	2.380603
Q91VA0	KVEFVSELPK	1.170490136	2	2.630617
Q91VA6	**PDIP2 Polymerase delta_interacting protein 2**	**1.011839024**	**0.98054**	**2**
Q91VA6	NHPWLELSDVHR	1.011827185	3	3.707343
Q91VA6	VLETVGVFEVPK	1.035779926	2	2.373256
Q91VH2	**SNX9 Sorting nexin_9**	**1.579598398**	**4.1E-07**	**2**
Q91VH2	GEQGLVPTDYVEILPNDGK	0.900132631	2	2.384259
Q91VH2	ITPQDKQTMVK+Oxidation(8)	1.773837283	1	2.10074
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.927668106**	**0.02036**	**2**
Q91VM9	IIAINVNDPEAEK	0.669017035	2	3.193566
Q91VM9	MEIATEEPLNPIK	1.074433848	2	3.632252

Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.736691013**	**0.00017**	**3**
Q91W43	IDDIYGDQHLVCTCPPMEVYESPFSEQK	0.727700953	3	3.697707
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	0.754454966	2	4.245063
Q91W43	VSFQPNSGAQGEYAGLATIR	0.873004655	2	4.526313
Q91X77	**CY250 Cytochrome P450 2C50**	**0.523834081**	**9.9E-20**	**3**
Q91X77	IKEHEESLDVTIPR	0.454450112	3	3.919033
Q91X77	NFLLEK	0.387952207	1	1.965251
Q91X77	YALLLLLK	0.865811011	2	2.597866
Q91X78	**ERLN1 Erlin_1**	**0.87490686**	**0.0212**	**2**
Q91X78	ISEIEDAAFLAR	0.926567189	2	3.67408
Q91X78	SVQTTLQTDEVK	0.87490414	2	3.416668
Q91Y81	**SEPT2 Septin_2**	**0.921137371**	**0.81586**	**2**
Q91Y81	ASIPFSVVGSNQLIEAK	1.1251192	2	2.700763
Q91Y81	LTVVDTPGYGDAINSR	0.919767297	2	3.797487
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.228153683**	**0.02158**	**8**
Q91YT0	GAGAYICGEETALIESIEGK	0.985292417	2	3.476463
Q91YT0	GDARPAEIDSLWEISK	0.783734933	2	3.091804
Q91YT0	GGAGFPTGLK	1.104883478	2	2.302608
Q91YT0	KTSFGSLKDEDR	1.243317819	2	3.030969
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.128277328	3	4.964741
Q91YT0	LVEGCLVGGR	0.855974138	2	2.44372
Q91YT0	TSFGSLKDEDR	1.054191173	2	2.551834
Q91YT0	YLVVNADEGEPGTCK	0.938682203	2	5.297962
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**0.905341278**	**9.9E-20**	**7**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	0.939963901	3	6.320993
Q91Z53	LLDAAGANLR	0.798351016	2	3.221628
Q91Z53	NCVILPHIGSATYK	1.016100711	2	3.315368
Q91Z53	NTMSLLAANNLLAGLR	0.831943044	2	3.664772
Q91Z53	NTMSLLAANNLLAGLR+Oxidation(2)	0.713300966	2	3.657813
Q91Z53	RLPEAIEEVK	0.831682653	2	2.64402
Q91Z53	VISTLSVGVDHLALDEIK	0.960776191	2	3.912876
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**0.660273843**	**9.9E-20**	**12**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	0.721967353	3	4.748354
Q91ZJ5	GGTLTQYEGK	0.58218526	2	2.493003
Q91ZJ5	GLPDNISSVLNK	0.578787284	2	3.269696
Q91ZJ5	GTVIIIANHGDR	0.566089888	2	3.200039
Q91ZJ5	IDIPPGAVLENK	0.628947128	2	2.740689
Q91ZJ5	IQRPPEDSIQPYEK	0.62340468	2	3.90405
Q91ZJ5	LQEQNAIDMEIIVNPK	0.883728157	2	3.344863
Q91ZJ5	LVEIAQVPK	0.610608477	2	3.378064

Q91ZJ5	NENTFLDLTVQQIEHLNK	0.615533787	2	5.33607
Q91ZJ5	SFENSLGINVPR	0.599969995	2	3.392874
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	0.64868117	2	4.7902
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	1.112367934	2	4.565436
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.209266066**	**0.11411**	**3**
Q91ZX7	AVTDEEPFLIFANR	1.218162736	2	2.613464
Q91ZX7	GCHVNECLSR	0.949038603	2	2.630216
Q91ZX7	MYDAQQQQVGTNK	0.690640939	2	4.146696
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**0.667283156**	**2.7E-06**	**2**
Q920A6	DLDTVASDMMVLLK	0.654041311	2	2.695241
Q920A6	GLAEVSDIAEQVLNAVNK	0.680764357	3	5.02439
Q920D2	**DYR Dihydrofolate reductase**	**1.147452954**	**0.02508**	**3**
Q920D2	LIEQPELASK	0.973016402	2	2.849247
Q920D2	LLPEYPGVLSEIQEEK	1.187217988	2	3.457096
Q920D2	NGDLPWPLLR	1.168870629	2	3.043258
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.832850127**	**0.25838**	**3**
Q920F5	EIAEVTGDPVHESLK	0.746194257	2	3.268419
Q920F5	ISECEAVHPVK	0.865059761	2	3.404402
Q920F5	WLLGLLNVQGK	1.081663739	2	3.261451
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.08410023**	**0.62897**	**2**
Q920J4	AGCECLNESDEHGFDNCLR	1.114239387	3	3.571455
Q920J4	IDQYQGADAVGLEEK	1.03150137	2	3.965451
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**0.988032071**	**8.1E-05**	**20**
Q920L2	AAFGLSEAGFNTACLTK	0.805615374	2	2.373381
Q920L2	ACALSIAESCRPGDK	0.976142969	2	2.873477
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.053347937	3	4.80377
Q920L2	ANAGEESVMNLDK	0.991124283	2	3.518165
Q920L2	DVVSRSMTLEIR+Oxidation(6)	0.942650288	2	2.365701
Q920L2	GEGGILINSQGER	0.961165912	2	3.956033
Q920L2	GVIALCIEDGSIHR	1.225433648	2	3.21592
Q920L2	HTLSYVDTK	1.143412482	2	2.309959
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	0.995973192	3	6.712187
Q920L2	IDEYDYSKPIEGQQK	0.887606953	2	4.472471
Q920L2	KHTLSYVDTK	0.106925343	2	2.608169
Q920L2	NTIIATGGYGR	0.953123472	2	3.000479
Q920L2	SMQSHAAVFR+Oxidation(1)	1.013489275	2	2.417603
Q920L2	TGHSLLHTLYGR	1.280863204	2	2.581045
Q920L2	TLNEADCATVPPAIR	0.894888274	2	3.639167
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.271022574	2	5.378039
Q920L2	VGSVLQEGCEK	0.957006626	2	3.691905
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.810604805	3	4.451532

Q920L2	VSQLYGDLQHLK	1.034055126	2	2.902638
Q920L2	VTLDYRPVIDK	0.898554781	2	2.953038
Q920P0	**DCXR L_xylulose reductase**	**0.703686277**	**9.9E-20**	**4**
Q920P0	AVVQVSQIVAR	0.751472807	2	3.100543
Q920P0	GVPGAIVNVSSQASQR	0.695070823	2	5.668148
Q920P0	STVLALQAAGAQVVAVSR	1.127584829	2	3.833537
Q920P0	TREDLDSLVR	0.676590911	2	2.799525
Q921F2	**TADBP TAR DNA_binding protein 43**	**0.946332003**	**0.00299**	**3**
Q921F2	FGGNPGGFGNQGGFGNSR	0.86547442	2	4.213485
Q921F2	KDLKTGHSK	0.916906947	2	2.480493
Q921F2	TSDLIVLGLPWK	0.951370799	2	3.120826
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.202902872**	**9.9E-20**	**5**
Q922F4	ALTVPELTQQMFDAK	1.292848135	2	4.033437
Q922F4	GHYTEGAELVDSVLDVVR	0.966456477	2	6.553408
Q922F4	IREEYPDR	0.993116667	2	2.636642
Q922F4	MASTFIGNSTAIQELFK	1.522026746	2	3.981064
Q922F4	NSSYFVEWIPNNVK	1.138301521	2	4.496965
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**1.030462127**	**0.02795**	**3**
Q922J3	EMETMQAKLMK+Oxidation(4)	1.048302532	2	2.55292
Q922J3	LQNELDTLKENNLK	0.793626702	2	2.316234
Q922J3	TASESISNLSEAGSVK	0.6486396	2	2.384444
Q923D2		**0.816574085**	**0.0005**	**3**
Q923D2	LQDVTDDHIR	0.813609474	2	3.232939
Q923D2	TGLTTLAQAVQAGYEVTVLVR	0.966853278	3	4.75114
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.953728437	3	4.619811
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**0.701610519**	**4.9E-05**	**2**
Q923M1	SAVYPTSAVQMEAALK	2.647563087	2	3.193392
Q923M1	VISAEEALPGR	0.701602092	2	2.429511
Q923V8	**SEP15 15 kDa selenoprotein**	**0.865737403**	**2.2E-10**	**3**
Q923V8	GCCQEEAQFETK	0.819315605	2	3.87992
Q923V8	LLDDNGNIAEELSILK	1.020339065	2	3.227501
Q923V8	WNTDSVEEFLSEK	1.448986954	2	3.260803
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**1.117215947**	**0.00149**	**2**
Q924C3	AEYLHTWGGLLPVISK	1.123831469	3	3.915133
Q924C3	SGTYFWPGSDVEIDGILPDIYK	1.005507511	2	4.208027
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**0.88786762**	**0.04053**	**8**
Q924S5	AQLSATVLTLLIK	1.311675842	2	2.643406
Q924S5	EHQEALAVER	0.73846315	2	2.493512
Q924S5	ELGLEKDDKDAIEEK	1.028857017	2	3.400943
Q924S5	HVMDVVDEELSK	0.991122393	2	2.449279

Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.185302202	3	5.975319
Q924S5	QLEVEPEGLEPEAENK	0.994728832	2	4.358443
Q924S5	QSDENLDLAR	0.815850836	2	2.492522
Q924S5	TENPLVLIDEVDK	0.986520826	2	3.306731
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**0.891014047**	**8E-06**	**2**
Q99020	FGEVVDCTIK	0.745030775	2	2.919915
Q99020	IFVGGLNPEATEEK	1.012099439	2	3.604638
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**0.942499325**	**0.96148**	**2**
Q99JI4	RLDEELEDAEK	0.945568208	2	2.953217
Q99JI4	VNEIVETNRPDSK	0.931113882	2	3.476076
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.876783035**	**0.98358**	**2**
Q99L04	ATAQEAQSLGGR	0.876204609	2	3.306137
Q99L04	CVPVVCDSSQESEVK	0.986586164	2	3.270591
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.076267332**	**0.99052**	**4**
Q99LF4	NLDFQDVLDK	0.967209762	2	2.731571
Q99LF4	NVTDVVNTCHDAGISK	1.026118891	2	4.2084
Q99LF4	NYNDELQFLDK	1.084593177	2	3.058101
Q99LF4	TNLDESDVQPVK	1.076312468	2	3.468498
Q99ML5	**PCYOX Prenylcysteine oxidase**	**0.910734145**	**0.30636**	**2**
Q99ML5	LLNQTLRENLK	0.909882407	2	2.401019
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	0.927776173	3	3.432255
Q99MR9	**PPR3A Protein phosphatase 1 regulatory subunit 3A**	**1.118544672**	**0.06432**	**2**
Q99MR9	DDLGANHPNVDDINK	1.125727038	2	2.443571
Q99MR9	SRSKEEPLLAPEENK	1.109679804	2	2.457809
Q99MS0	**S14L2 SEC14_like protein 2**	**1.087628554**	**0.19701**	**2**
Q99MS0	AGEMTEVLPNQR	0.86925634	2	3.111687
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.088198142	3	4.444666
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.889744722**	**1.2E-14**	**5**
Q99MZ8	GFSVVADTPELQR	0.753257964	2	3.588353
Q99MZ8	TGDTGMLPANYVEAI	1.089207043	1	2.078625
Q99MZ8	TQDQISNIK	1.004365819	2	2.460155
Q99MZ8	YHEEFEK	0.854799349	1	2.480466
Q99MZ8	YKEEFEK	0.925103066	1	2.229951
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**0.931552341**	**0.51408**	**2**
Q99NA5	ENTEGEYSGIEHVIVDGVVQSIK	0.812797015	2	4.050434
Q99NA5	NVTAIQGPGGK	0.931769076	2	2.589353
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**0.847826756**	**8.8E-08**	**5**
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.878608379	2	5.755085
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	0.718430819	2	4.311572
Q99PF5	IGQQPQQPGAPPQQDYTK	0.8324796	2	2.534653

Q99PF5	SVSLTGAPESVQK	0.849724771	2	3.304205
Q99PF5	VGGGIDVPVPR	0.739274419	2	2.397245
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**0.885015777**	**1.3E-11**	**20**
Q99PL5	AMEALALAER	1.271932927	2	2.394023
Q99PL5	DALNQATSQVESK	0.92197795	2	3.547411
Q99PL5	EAEETQNSLQAECDQYR	1.032084666	2	5.193424
Q99PL5	EHTSHLEAELEK	0.86922286	2	3.492528
Q99PL5	ELESQVSCLEK	0.87664476	2	2.580797
Q99PL5	GELESSDQVR	0.922065634	2	2.839402
Q99PL5	HMAAASAECQNYAK	0.832739965	2	4.177485
Q99PL5	HMAAASAECQNYAK+Oxidation(1)	1.036718742	2	4.407171
Q99PL5	LKELESQVSCLEK	1.013730799	2	3.503247
Q99PL5	LLATEQEDAAVAK	0.976121917	2	3.728318
Q99PL5	LQQENSILR	1.004874687	2	2.660317
Q99PL5	LQSSEVEVK	0.991261192	2	2.305017
Q99PL5	LREAEETQNSLQAECDQYR	0.985464705	3	4.046802
Q99PL5	QLHLAEAQTK	1.01416078	2	2.583905
Q99PL5	QLLLESQSQLDEAK	0.81658996	2	2.599088
Q99PL5	TILAETEGMLK	1.060525857	2	2.427948
Q99PL5	TILAETEGMLK+Oxidation(8)	1.060654646	2	2.314815
Q99PL5	TLQEQLENGPNTQLAR	0.981167434	2	5.447884
Q99PL5	TLVSTVGSMVFSEGEAQR	1.260972778	2	4.561435
Q99PL5	VEPAVSSIVNSIQVLASK	1.325253306	3	3.971125
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**0.998897728**	**0.98825**	**3**
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.998841983		2.435894
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.998841983		2.508493
Q99PV0	KGMLDPLEVHLLDFPNIVIK	1.077922887	2	2.334692
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**0.976322827**	**0.988**	**2**
Q9CPQ1	FGVAEPR	1.089477489	2	2.340449
Q9CPQ1	NYDSMKDFEEMR	0.965519337	2	3.295806
Q9CQZ5	**NDUA6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6**	**0.995087289**	**0.99479**	**2**
Q9CQZ5	FFHETETPRPK	1.014634994	2	2.859283
Q9CQZ5	VVDLLVIK	0.982268088	2	2.487111
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.053623013**	**0.941**	**2**
Q9CRB9	VAEELALEQAK	1.085683944	2	3.470028
Q9CRB9	YEYHPVCADLQTK	0.945033988	2	3.456891
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.933513377**	**0.44682**	**2**
Q9CW42	DLLLPITPPATNPLLQCR	0.867552648	2	4.031782
Q9CW42	GLSVSEAECTAMGLR	1.002464133	2	3.794089
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**0.965032724**	**2.9E-10**	**4**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.495328076	2	4.295112

Q9CWH6	ALLEVVQSGGK	1.233299112	2	3.026201
Q9CWH6	LTVEDPVTVEYITR	1.211298223	2	4.003379
Q9CWH6	LYQTDPSGTYHAWK	1.068477382	2	2.347267
Q9CWK8	**SNX2 Sorting nexin_2**	**1.018462607**	**0.88961**	**4**
Q9CWK8	AVNTQALSGAGILR	1.09114023	2	3.160701
Q9CWK8	QQQFENLDQQLR	0.995935379	2	2.690773
Q9CWK8	WEDAQITLLK	1.033910834	2	2.640582
Q9CWK8	YWEAFLPEAK	0.904828107	2	2.609057
Q9CXS4	**CENPV Centromere protein V**	**0.936223377**	**0.99608**	**2**
Q9CXS4	LLLDTFEYQGLVK	0.919413923	2	3.676038
Q9CXS4	SVVTEEFNGSDWER	0.984005053	2	3.546664
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**0.926186385**	**0.81973**	**2**
Q9CYN2	LHDSLATER	0.846525241	2	2.65284
Q9CYN2	YVENFGLIDGR	0.956432887	2	2.829926
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**0.913184745**	**0.49047**	**2**
Q9CZY3	LLEELEEGQK	0.802238328	2	2.42698
Q9CZY3	VNMSGVSSSNGVVDPR	0.965867155	2	2.910943
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.141368893**	**6.6E-15**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	1.126713623	3	3.559956
Q9D0M3	GLLSSLDHTSIR	1.090864041	2	2.888515
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.541234475	3	5.570314
Q9D0M3	HLVGVCYTEEEAK	0.970784247	2	3.58469
Q9D0M3	LSDYFPKPYPNPEAAR	1.033588133	3	3.499436
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**0.959326458**	**0.90675**	**2**
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.104379563	2	4.959614
Q9D0S9	SLPADILYEDQQCLVFR	0.940649777	2	3.445046
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**0.820067114**	**0.20357**	**4**
Q9D172	GVEVTVGHEQEEGGK	0.826264601	2	3.647312
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	0.874490382	3	4.529002
Q9D172	NLSTFAVDGK	1.017190384	1	2.444968
Q9D172	NVLAESAR	0.860387033	1	1.943514
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**0.97976903**	**1.1E-16**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0)	6.417905415	2	2.695593
Q9D1Q6	NIIGYFEQK	0.894350932	1	2.296551
Q9D1Q6	SNPVHEIQSLDEVTNLDR	0.912499191	2	4.967291
Q9D1Q6	VDCDQHSDIAQR	0.964908297	2	3.821754
Q9D2U9	**H2B3A Histone H2B type 3_A**	**0.923253774**	**0.01685**	**5**
Q9D2U9	AMGIMNSFVNDIFER	0.982076243	2	4.803142
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.950974081	2	4.48539
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.826612208		2.960929
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4)	0.936059312	2	3.665537

Q9D2U9	LLLPGELAK	0.909281607	2	2.53921
Q9D552	**SPT17 Spermatogenesis_associated protein 17**	**0.976137439**	**0.51865**	**3**
Q9D552	DINEVLEQR	0.97768896	2	2.541532
Q9D552	FENDAAVMIQSWFR	0.5968894	2	2.539365
Q9D552	MNLYNEMAVRIQR+Oxidation(0)	0.924883135	2	2.406679
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.385634919**	**4.2E-09**	**2**
Q9D6M3	GAAVNLTLVTPEK	1.560131509	2	3.443393
Q9D6M3	GVNEDTYSGFLDCAR	1.214775278	2	4.474363
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.027113959**	**6.9E-05**	**9**
Q9D6Y9	CSDGGIYCK	1.132355988	1	2.147859
Q9D6Y9	CVAYAESHDQALVGDK	0.965062502	2	4.355373
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	1.788238298	3	3.482711
Q9D6Y9	GTHDLWDSR	1.017970068	2	2.527989
Q9D6Y9	IVLDSDAAEYGGHQR	1.150540659	2	4.098411
Q9D6Y9	IYESHVGISSHEGK	0.876900427	2	3.068556
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.925989528	3	3.918929
Q9D6Y9	QFNLTDDDLLR	0.960159052	2	2.55812
Q9D6Y9	WELYIPPK	1.037478984	2	2.458507
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.032724664**	**0.34611**	**3**
Q9D7B6	AVIFEDCAVPVANR	0.908462344	2	3.642513
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	1.027278782	2	4.336489
Q9D7B6	VHQILEGSNEVMR	1.202075832	2	2.435715
Q9D819	**IPYR Inorganic pyrophosphatase**	**1.088637042**	**3.7E-10**	**4**
Q9D819	GISCMNTTVSESPFK	1.272937146	2	4.205544
Q9D819	GISCMNTTVSESPFK+Oxidation(4)	1.090086926	2	4.208474
Q9D819	VLGILAMIDEGETDWK	1.320030346	2	2.599179
Q9D819	YVANLFPYK	1.323922736	1	2.027217
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.513135151**	**0.00011**	**2**
Q9D880	TIALNQVEDVR	0.546040895	2	2.569459
Q9D880	TVLEHYALEDDPLEAFK	1.426469264	2	3.429388
Q9D8V0	**HM13 Minor histocompatibility antigen H13**	**1.043026754**	**0.10564**	**2**
Q9D8V0	EESTEASASKRLEK	1.186506212	2	2.734516
Q9D8V0	SSSDMPETITSR	1.042961204	2	2.806141
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**0.977946542**	**0.10586**	**2**
Q9DC70	LDDLINWAR	0.978877017	2	3.613633
Q9DC70	QADVMIVAGTLTNK	1.45370904	2	2.744044
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.042787521**	**0.95271**	**3**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.053071871	3	3.315753
Q9DCM0	SLLPGCQSVISR	1.026253851	2	3.339358
Q9DCM0	TDFQQGCAK	1.332298678	2	2.910632
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**0.988315731**	**0.05328**	**2**

Q9DCS9	AYDLVVDWPVTLVR	0.99303824	2	4.543563
Q9DCS9	TPAPSPQTSLPNPITYLTK	2.036284818	2	2.384007
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.084232024**	**0.29776**	**4**
Q9DCT2	FDLNSPWEAFPAYR	0.970573863	2	2.980884
Q9DCT2	KFDLNSPWEAFPAYR	0.891937399	2	3.493932
Q9DCT2	SLADLTAVDVPTR	1.084541348	2	3.670814
Q9DCT2	VVAEPVELAQEFR	0.47853957	2	3.31772
Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**0.876095712**	**9.9E-20**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	0.783769368	2	5.203297
Q9DCU9	LIEPNTAVTR	0.874490704	2	3.05442
Q9DCU9	TMDWFGYYGGPCR	1.431613895	2	3.064458
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**0.918467509**	**0.23428**	**2**
Q9EP75	DEDGKELSDEDIR	0.955587409	2	3.155837
Q9EP75	IFNDSTNIMHAK	0.828315998	2	3.003646
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**1.094362284**	**1.1E-16**	**7**
Q9EP89	EVWSEGLGYADVENR	0.906103348	2	3.553724
Q9EP89	FENSIESLR	0.939728698	2	2.494253
Q9EP89	IKDEVGAPGIVVGVSVDGK	0.852044437	2	4.804358
Q9EP89	KNDFEQGELYLK	1.333531347	2	2.347702
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.098233462	3	3.774042
Q9EP89	LVNTPYVDNSYK	1.308243649	2	3.073922
Q9EP89	WAGGGFLSTVGDLLK	1.765421972	2	4.588952
Q9EPE9	**AT131 Probable cation_transporting ATPase 13A1**	**0.953093429**	**0.30593**	**2**
Q9EPE9	MAVVGNAVPCGARPGGAR+Oxidation(0)	0.952697607	2	2.824174
Q9EPE9	VLALGYK	1.24758673	2	2.331106
Q9EPH2	**MRP MARCKS_related protein**	**0.990438929**	**0.00792**	**2**
Q9EPH2	AAATPESQEPQAK	0.991944232	2	2.423409
Q9EPH2	GDVTAEEAAGASPAK	0.698525273	2	2.695908
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**0.973723841**	**0.00038**	**5**
Q9EPH8	ALDTMNFDVIK	1.287276119	2	3.220999
Q9EPH8	EFSPFGTITSAK	0.871605499	2	2.52382
Q9EPH8	GFGFVSFER	1.01873779	2	2.559175
Q9EPH8	KEFSPFGTITSAK	0.875729078	2	2.583291
Q9EPH8	SKVDEAVAVLQAHQAK	0.963628185	2	5.093401
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.675553841**	**1.6E-15**	**12**
Q9EQ76	ASIYQSVFTNSSK	3.535488364	2	2.764112
Q9EQ76	GTCILPSVNDMMDDIDEK	2.083641275	2	4.043437
Q9EQ76	KEPVFNDELPAR	1.560609339	3	3.716878
Q9EQ76	LQEYITSFATEK	2.669061424	2	3.199283
Q9EQ76	NNEVTLYK	3.619313477	2	2.401145

Q9EQ76	NNLPTAISDWWYMK	1.675553721	2	2.860033
Q9EQ76	SCLEEGLEPTCFER	1.875736546	2	4.425112
Q9EQ76	SDDVGGLWK	2.435628129	2	2.712121
Q9EQ76	VAVIGAGVSGLAAIR	1.258591443	2	2.838715
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.500618486	3	3.86818
Q9EQ76	VWNDGYPWDMVVITR	1.320478557	2	3.954114
Q9EQ76	YIQFETLVTR	2.417949053	2	3.153888
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.029196951**	**0.54308**	**4**
Q9EQH3	IREDLPNLESSEETEQINK	1.020211297	2	5.477065
Q9EQH3	LNLEHIATSSAVSK	1.019722191	2	3.465947
Q9EQH3	LSQLEGVNVER	0.87052172	2	2.779352
Q9EQH3	VLETTVEIFNK	1.080215506	2	2.559355
Q9EQS0	**TALDO Transaldolase**	**0.997081886**	**0.48604**	**6**
Q9EQS0	ALAGCDFLTISPK	0.920079469	2	3.391461
Q9EQS0	ILDWHVANTDKK	1.029437736	2	3.083594
Q9EQS0	LGGPQEEQIK	1.114598165	2	2.810715
Q9EQS0	SYEPQEDPGVK	0.86359738	2	2.884957
Q9EQS0	VSTEVDAR	0.897288764	1	1.926685
Q9EQS0	WLHNEDQMAVEK	0.862765402	2	2.495158
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**0.890204601**	**0.21238**	**3**
Q9EQX9	LELFLPEEYPMAAPK	0.867086013	2	4.242614
Q9EQX9	SNEAQAIETAR	1.060756034	2	3.388136
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.070723282	3	4.304299
Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**0.987139129**	**1.6E-05**	**18**
Q9ER34	ADIANLAEEFK	0.926680264	2	3.016905
Q9ER34	CTTDHISAAGPWLK	0.907347177	2	3.915968
Q9ER34	DINQEVYNFLATAGAK	1.565727076	2	4.354849
Q9ER34	DLEDLQILIK	1.050458647	2	2.443531
Q9ER34	FKLEAPDADELPR	1.018169714	3	3.969935
Q9ER34	FNPETDFLTGK	1.048672708	1	2.270272
Q9ER34	GHLDNISNNLLIGAINIENGK	0.951145277	2	5.655514
Q9ER34	IVYGHLDDPANQEIER	1.535100238	2	4.65566
Q9ER34	LEAPDADELPR	1.02645416	2	2.513052
Q9ER34	LTGTLSGWTSPK	1.057279379	2	2.86316
Q9ER34	NAVTQEFGPVPDTAR	0.857840532	2	4.35867
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	1.130128915	3	4.07107
Q9ER34	QGLLPLTFADPSDYNK	1.008676353	2	3.347855
Q9ER34	SDFDPGQDTYQHPPK	1.025606413	2	2.668009
Q9ER34	SQFTITPGSEQIR	0.969475347	2	3.229641
Q9ER34	VDVSPTSQR	0.891244145	2	2.451645
Q9ER34	VGLIGSCTNSSYEDMGR	1.020246456	2	4.129498
Q9ER34	WVVIGDENYGEGSSR	1.128425521	2	4.312664

Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.894624059**	**0.00188**	**4**
Q9ES21	GSEKPLEQTFAK	0.80284873	2	2.576208
Q9ES21	LEEQDEFEK	0.722754826	2	2.504466
Q9ES21	TQLGLVMDGFNSLLR	0.985860402	2	3.156574
Q9ES21	VVTNQEGVFR	0.904996057	2	2.472775
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**0.810257557**	**2.2E-06**	**11**
Q9ES38	ACQAAWALK	0.920601616	2	2.36709
Q9ES38	ADVWENFQQR	0.928314151	2	3.144682
Q9ES38	EGFDVGVIADPLYILDNK	0.933389343	2	5.336772
Q9ES38	GATAILVLPSK	0.919534019	1	2.092693
Q9ES38	IQDSLEITNTYK	0.82220943	2	3.541666
Q9ES38	LKEATIQEDK	0.756045404	2	2.514682
Q9ES38	QGFCIPVETGKPGLLLTK	0.952706875	3	3.439604
Q9ES38	SISALSVFLGLAK	1.188329089	2	3.095566
Q9ES38	SLMPDVYQAVCEGTWK	0.845963544	2	3.852618
Q9ES38	YLCNVPGQPEDK	0.762398269	2	2.882055
Q9ES38	YLCNVPGQPEDKK	0.763003292	2	3.075578
Q9ES40	**PRAF3 PRA1 family protein 3**	**1.0000659**	**0.36187**	**2**
Q9ES40	AWDDFFPGSDR	1.011564445	2	2.762496
Q9ES40	LENKMEGIGLK	0.873150613	2	2.324797
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.944943628**	**0.07487**	**3**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.951087932	2	4.149755
Q9EST6	SLDLFGCEVTNR	0.898252002	2	2.684158
Q9EST6	TPAAVQELVLDNCK	1.491855944	2	3.611392
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.011312796**	**0.82031**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.026589633	3	5.805196
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.14574158	3	4.380011
Q9ESW0	QGQGQLVTCSGAFK	1.021598975	2	2.793206
Q9HB97	**PARVA Alpha_parvin**	**0.882150455**	**0.01057**	**2**
Q9HB97	LNVAEVTQSEIAQK	0.882161513	2	4.271971
Q9HB97	QIQEEITGNTEALSGR	0.830929501	2	2.477274
Q9JHL4	**DBNL Drebrin_like protein**	**1.210731233**	**2.2E-05**	**2**
Q9JHL4	AMSTTSVSSSQPGK	0.699744964	2	2.355576
Q9JHL4	TGELEQEVVSR	1.219810316	2	3.02602
Q9JI85	**NUCB2 Nucleobindin_2**	**1.157832436**	**6E-07**	**6**
Q9JI85	FQQGIAPSGPAGELK	1.25249069	2	2.923585
Q9JI85	LSQELDLVSHK	1.083071398	2	2.321695
Q9JI85	QEYQQAVQQLEQK	1.187210319	2	4.023011
Q9JI85	QVIEVLETDPHFR	1.014897606	2	2.431912
Q9JI85	TRLDELK	0.721420885	1	1.903174
Q9JI85	VHNVEPVESAR	1.085994752	2	2.676739
Q9JI91	**ACTN2 Alpha_actinin_2**	**0.859760351**	**0.03116**	**6**

Q9JI91	ETADTDTAEQVIASFR	0.859761085	2	3.00439
Q9JI91	GYEEWLLNEIR	0.844118922	2	3.775782
Q9JI91	HTNYTMEHIR	1.178138908	3	3.542534
Q9JI91	KHEAFESDLAAHQDR	0.743616709	2	5.401426
Q9JI91	QSILAIQNEVEK	0.534552229	2	2.808401
Q9JI91	TINEVETQILTR	0.777993504	2	2.673617
Q9JIL8	**RAD50 DNA repair protein RAD50**	**1.053129073**	**0.6638**	**2**
Q9JIL8	KEEQLSSYEDK	1.048302532	2	2.306278
Q9JIL8	MIELKTEILTK+Oxidation(0)	1.078170689	2	2.338447
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**0.980598843**	**9.9E-20**	**3**
Q9JJ19	AVDPDSPAEASGLR	0.738680249	2	3.159119
Q9JJ19	LVEVNGENVEK	0.685247029	2	2.426538
Q9JJ19	SEHTEPPAAADTK	1.862818237	2	3.02143
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**0.89833787**	**0.34675**	**2**
Q9JJ46	HLTNAQSMLDNK	0.933339697	2	3.14961
Q9JJ46	HLTNAQSMLDNK+Oxidation(7)	0.691783655	2	2.919941
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**0.805152076**	**1.1E-11**	**2**
Q9JJ54	FGDVVDCTLK	0.804789299	2	2.683613
Q9JJ54	IFVGGLSPDTPEEK	0.819611916	2	4.00692
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.064282686**	**0.82204**	**5**
Q9JJ79	DQIEVMKGNVKSR	0.898584748	2	2.313487
Q9JJ79	LVQSVHQSLAALSKVIR	0.561133881	2	2.629113
Q9JJ79	NCLEEWTKAAGLEK	1.066588493	2	2.560909
Q9JJ79	TVLRGSGNLLR	1.07625267	2	2.58366
Q9JJ79	YVVQIGDK	1.011261692	1	2.294213
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.006887144**	**0.64332**	**2**
Q9JJU8	GDYDAFFEAR	0.977896844	2	2.836132
Q9JJU8	QQDVLCFLEANK	1.076565283	2	3.314485
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**0.937096223**	**0.072**	**4**
Q9JK38	GRVEDVVVSDECR	0.837328789	2	3.032683
Q9JK38	ITLECLPQNVGFYK	1.255841241	2	3.012092
Q9JK38	VEDVVVSDECR	0.956194297	2	3.153153
Q9JK38	VLGQLTETGVVSPEQFMK	1.010494136	2	2.467033
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**0.939010539**	**0.3697**	**5**
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	0.904371569	3	5.820751
Q9JLA3	IVPEWQDYDQEIK	0.862331797	2	3.440546
Q9JLA3	LGIEGLSLHNILK	1.221625018	3	3.37365
Q9JLA3	LNIQPSETDYAVDIR	1.07810282	2	2.62119
Q9JLA3	VWQLQDLSFQTAAR	1.083049895	2	4.56084

Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.158410885**	**9.9E-20**	**17**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.431990013	2	3.896283
Q9JLJ3	ANDTTFGLAAGVFTR	1.187654029	2	4.752796
Q9JLJ3	CQVLLEAAR	0.943365861	2	3.123832
Q9JLJ3	EQGATVLCGGEPYAPEDPK	0.973622171	2	4.831931
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	1.039307573	3	3.403797
Q9JLJ3	EVNLAVENAK	0.826293431	1	2.863234
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.253258185	3	4.661617
Q9JLJ3	GIKPITLELGGK	0.966480084	3	4.028418
Q9JLJ3	IGDPLLEDTR	1.093497796	2	3.913923
Q9JLJ3	MGPLINAPHLER	1.066107941	2	3.084427
Q9JLJ3	MGPLINAPHLER+Oxidation(0)	0.867487789	2	2.823889
Q9JLJ3	RDEIAIMETINNGK	1.190073731	2	5.144137
Q9JLJ3	SAPALACGNAMIFKPSPFTPVSALLLAEIYTK	1.22894874	3	3.977435
Q9JLJ3	VEPVDASGTEK	0.903874357	2	2.312576
Q9JLJ3	VSFTGSVPTGMK	1.082532832	2	3.47068
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10)	0.937443944	2	2.656249
Q9JLJ3	VTIEYYSQLK	2.298576	2	2.911028
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.787191009**	**0.00223**	**4**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	0.854159329	2	4.932627
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.797361062	3	3.944791
Q9JLZ3	GIVVLGINR	0.945511843	2	2.873643
Q9JLZ3	SEVPGIFCAGADLK	0.781277628	2	2.603277
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**0.860457751**	**1E-12**	**14**
Q9JM53	AIASAAEGGSVPPIR	0.867943434	2	2.585572
Q9JM53	CLIATGGTPR	0.803867546	2	2.727941
Q9JM53	DGEQHEDLNEVAK	0.994011993	2	3.591244
Q9JM53	KSQASGIEVIQLFPEK	1.062835453	2	3.515223
Q9JM53	KVETDHIVTAVGLEPNVELAK	0.88504835	2	6.353092
Q9JM53	LNDGSQITFEK	0.931853236	2	3.377095
Q9JM53	SATEQSGTGIR	1.625648287	2	2.347409
Q9JM53	SITVIGGGFLGSELACALGR	1.091957042	2	3.041913
Q9JM53	SQASGIEVIQLFPEK	0.975701079	2	4.257881
Q9JM53	TGGLEIDSDFGGFR	0.867990209	2	3.857955
Q9JM53	VETDHIVTAVGLEPNVELAK	0.863940499	2	4.658452
Q9JM53	VLIVSEDPELPYMRPPLSK	0.919716503	2	2.695096
Q9JM53	VMPNAIVQSVGVSGGK	1.047477166	2	2.859402
Q9JM53	VMPNAIVQSVGVSGGK+Oxidation(1)	0.678759197	2	3.20344
Q9JMD3	**PCTL PCTP_like protein**	**1.027984539**	**0.99917**	**5**
Q9JMD3	AVSIQTGYLIQSTGPK	0.990105301	2	4.74025
Q9JMD3	ESVQVPDDQDFR	0.966888979	2	2.59228

Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.127539457	2	4.291899
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0)	1.041483256	3	3.768256
Q9JMD3	WDSNVIETFDIAR	1.025056543	2	4.048635
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**0.804526746**	**9.9E-20**	**5**
Q9QVC8	GEPNNVAGNQAQVK	0.702298254	2	3.734932
Q9QVC8	RGEAHLAVNDFDLAR	1.329846803	3	3.367903
Q9QVC8	TQLAVCQQR	0.673068386	2	2.467332
Q9QVC8	VAENGAQSAPLPLEGVDISPK	1.004059486	2	4.044621
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	0.826572128	3	5.934323
Q9QX79	**FETUB Fetuin_B**	**0.755267206**	**1.7E-05**	**2**
Q9QX79	GSIQHLPEQEEPEDSKGK	0.815979024	3	3.892594
Q9QX79	NTAPTSSPSITAPR	0.755263767	2	2.880602
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**0.775922746**	**0.34086**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	1.070032212	2	3.486866
Q9QXG4	IGPIATPDYIQNAPGLPK	0.647087554	2	2.847365
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**0.953545955**	**9.1E-05**	**25**
Q9QXQ0	ACLISLGYDVENDR	1.138105458	2	3.161388
Q9QXQ0	AGTQIENIDEDFR	1.146460882	2	3.37348
Q9QXQ0	AGTQIENIDEDFRDGLK	1.093558	2	4.409533
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.070427955	3	3.551919
Q9QXQ0	DDPVTNLNNAFEVAEK	0.820132657	2	2.906906
Q9QXQ0	ETTDTDTADQVIASFK	0.982338607	2	4.744575
Q9QXQ0	GISQEQMQEFR	1.064303634	2	3.000239
Q9QXQ0	HRDYETATLSDIK	1.120144405	2	3.743639
Q9QXQ0	HRPELIEYDK	0.984180592	3	3.963071
Q9QXQ0	HTNYTMEHLR	1.178138908	3	3.542534
Q9QXQ0	ICDQWDNLGSLTHSR	0.952583224	3	4.23142
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.966144246	3	4.841766
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.239974782	2	4.534512
Q9QXQ0	LVSIGAEEIVDGNAK	1.047548827	2	3.254972
Q9QXQ0	MAPYQGPDAAPGALDYK	1.068234836	2	4.422648
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0)	0.867814687	2	4.274773
Q9QXQ0	MLDAEDIVNTARPDEK	1.333499278	2	3.097188
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(0)	1.270973733	2	2.603706
Q9QXQ0	QFASQANMVGPWIQTK	1.106531167	2	3.232535
Q9QXQ0	RDHALLEEQSK	0.97422204	2	4.052082
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.116537508	3	4.500773
Q9QXQ0	TINEVENQILTR	0.715553428	2	3.616865
Q9QXQ0	VGWEQLLTTIAR	0.957959169	2	4.08855
Q9QXQ0	VLAGDKNFITAEELR	2.016383617	2	2.49605
Q9QXQ0	VLAVNQENEHLMEDYER	1.339755747	2	4.561548
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**0.968263489**	**0.00064**	**4**

Q9QXT0	ALVDELEWEIAR	0.867015103	2	4.078684
Q9QXT0	IDSDISGTLK	0.816129275	2	2.521428
Q9QXT0	INPDGSQSVVEVPYAR	0.989261342	2	3.942912
Q9QXT0	TDLCDHALHR	0.864343422	2	2.333884
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**0.922593945**	**9.9E-20**	**15**
Q9QXX4	ASGDAARPFLLQLAESAYR	1.228830523	3	4.441804
Q9QXX4	DVEVTKEEFALAAQK	0.944670251	2	4.440639
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	0.790397339	2	5.221288
Q9QXX4	GLLPQLLGVAPEK	0.926011567	2	3.049683
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.127399977	2	4.311089
Q9QXX4	ITLPAPNPDHVGGYK	1.551181402	2	2.350061
Q9QXX4	KDVEVTKEEFALAAQK	0.980953358	2	4.542936
Q9QXX4	LQVAGEITTGPR	0.86028186	2	3.464944
Q9QXX4	LTVNDFVR	1.104319167	2	2.592443
Q9QXX4	NGEFFMSPHDFVTR	1.206741911	2	3.614104
Q9QXX4	SSPQFGVTLLTYELLQR	1.789237369	2	4.179051
Q9QXX4	STGSFVGELMYK	0.990294608	2	2.773062
Q9QXX4	TVELLSGVVDQTK	0.85807254	2	4.100215
Q9QXX4	YEGFFGLYR	0.991147992	1	2.228602
Q9QXX4	YLNIFGESQPNPK	0.826775086	2	4.552802
Q9QY44	**ABCD2 ATP_binding cassette sub_family D member 2**	**1.282092349**	**0.00939**	**2**
Q9QY44	EGGWDAVMDWKDVLSGGEK+Oxidation(7)	1.116831147	2	2.742043
Q9QY44	VLKACSPKFGTLVAEEAHR	1.986436861	2	2.442595
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.88946568**	**0.01954**	**2**
Q9QYU4	GFLGVMPAYSAAEDALTTK	1.04943455	2	2.538795
Q9QYU4	SSSLLIPPLEAALANFSK	0.81156605	2	2.40248
Q9QZ09	**PHTF1 Putative homeodomain transcription factor 1**	**1.383559319**	**4E-06**	**2**
Q9QZ09	KMDMSVLEISGIIMSR+Oxidation(1)	0.782376975		2.786609
Q9QZ09	MGHIKPDLIDVDLIRGSTFAK+Oxidation(0)	1.391234944	2	2.433168
Q9QZ76	**MYG Myoglobin**	**0.791029705**	**0.998**	**4**
Q9QZ76	GQHAAEIQPLAQSHATK	0.908447484	2	5.104966
Q9QZ76	HGCTVLTALGTILK	0.775953322	2	3.089586
Q9QZ76	KGQHAAEIQPLAQSHATK	0.64398501	4	5.424273
Q9QZ76	VEGDLAGHGQEVLISLFK	0.673029793	3	5.314981
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.068964056**	**0.91526**	**7**
Q9QZA2	ATLVKPTPVNVPISQK	1.054197538	2	3.449319
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.089435731	2	3.211684
Q9QZA2	FYNELTEILVR	0.883581351	2	2.960599
Q9QZA2	LLDEEEATDNDLR	0.952033827	2	3.597755
Q9QZA2	NIQVSHQEFSK	1.030272801	2	3.024239

Q9QZA2	NLATAYDNFVELVANLK	1.017151675	3	3.589597
Q9QZA2	STAVVEQGGIQTVDQLIK	0.962033498	2	3.87014
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**0.925257866**	**0.11842**	**4**
Q9QZD8	GALVTVGQLSCYDQAK	0.877417137	2	3.824465
Q9QZD8	NYSHALDGLYR	0.980081474	2	2.725634
Q9QZD8	VHLQTQQEVK	0.840402555	1	2.760561
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	0.912362951	2	5.712021
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.157559789**	**7.5E-05**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.211179034	2	3.972656
Q9QZH8	WFLQEDILEK	1.107677204	2	3.350094
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.659583425**	**2E-14**	**5**
Q9QZU7	DNCQCSDCYLHSAK	1.570339541	2	2.909052
Q9QZU7	IDANNVAYTTGK	1.715712988	2	3.262721
Q9QZU7	IIELDDKGQVVR	1.28087573	2	2.425088
Q9QZU7	MNPGDVITFDNWR	1.049971139	2	2.57743
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.084038098	2	4.423891
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**1.335353732**	**3.5E-08**	**2**
Q9QZX8	GIGETPIVPLGISYLDDFAK	1.440395688	2	3.737144
Q9QZX8	QFTDEGNPDSVNK	1.267154364	2	3.410762
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.866118081**	**9.9E-20**	**9**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	1.093307065	2	3.7077
Q9R063	ETDLLLDDSLVSLFGNR	0.880398346	2	4.407073
Q9R063	GVLFGVPGAFTPGCSK	0.812414546	2	4.177969
Q9R063	KGVLFGVPGAFTPGCSK	0.868993198	2	3.106069
Q9R063	THLPGFVEQAGALK	0.779240653	3	3.977988
Q9R063	VGDTIPSVEVFEGEPGK	0.782246321	2	4.235331
Q9R063	VGDTIPSVEVFEGEPGKK	0.863852901	2	3.688788
Q9R063	VNLAELFK	0.865527823	2	2.82648
Q9R063	VQLLADPTGAFGK	0.871008224	2	4.035326
Q9R0N0	**GALK1 Galactokinase**	**0.823996903**	**0.06482**	**5**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	0.903481383	3	4.34018
Q9R0N0	RQCEEVAQALGK	0.965570382	2	2.818537
Q9R0N0	SLETSLVPLSDPK	0.785719477	2	2.694597
Q9R0N0	TDGLVSLLTTSK	0.853195813	2	3.598156
Q9R0N0	VEELLAEAR	0.829148584	2	2.656608
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.079834073**	**0.07892**	**5**
Q9R0T3	AEPSVAEYTVR	1.050533839	2	3.021717
Q9R0T3	FDDGEDPLDAETQQGGGSNPFHR	1.094506413	3	3.579365
Q9R0T3	ICSEVLQLEPDNVNALK	1.206205055	2	4.955377
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	1.036320577	3	5.367971
Q9R0T3	SNPSENEEKEAQSQLVK	0.924948007	2	4.646805
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.289867091**	**0.02608**	**4**

Q9R112	EGNALFTFPNTPVK	1.891802584	2	2.567956
Q9R112	STLSVIPSGVQWIQDR	1.44297228	2	2.391535
Q9R112	TAAAVAAQSGILDR	1.097132463	2	2.335433
Q9R112	VGAENVAIVEPSER	1.098023999	2	2.324897
Q9R1T3	**CATZ Cathepsin Z**	**0.839986149**	**0.02916**	**2**
Q9R1T3	HGIPDETCNNYQAK	0.840045291	2	3.900777
Q9R1T3	VGDYGSLSGR	0.811321793	2	2.552134
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**0.97220831**	**0.01502**	**3**
Q9R1Z0	LTLSALVDGK	1.845732153	2	2.63151
Q9R1Z0	LTVDTIFVPNTGK	0.922786984	2	3.086001
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	1.10031573	2	3.917221
Q9R257	**HEBP1 Heme_binding protein 1**	**1.207322923**	**0.00547**	**2**
Q9R257	FATVEVTDKPVDEALR	1.203123482	2	2.706884
Q9R257	NSLFGSVETWPWQVLSTGGK	1.190900525	2	3.743525
Q9WTR8	**PHLP1 PH domain leucine_rich repeat protein phosphatase 1**	**0.916317931**	**0.56756**	**2**
Q9WTR8	LEELEEIDISGNK	0.62146799	2	2.716123
Q9WTR8	LEELEEIDISGNKLK	0.921115125	2	2.316741
Q9WTT6	**GUAD Guanine deaminase**	**1.081122914**	**0.90632**	**7**
Q9WTT6	EIGNFEVGKDFDALLINPR	0.908287007	2	3.537149
Q9WTT6	ETTEESVKETER	0.940367549	2	3.239579
Q9WTT6	FQSTDVAEEVYTR	1.081388226	2	3.585751
Q9WTT6	IVFLEESSQQEK	1.123536161	2	3.757311
Q9WTT6	NIEEVYVGGK	1.259523917	1	1.932361
Q9WTT6	NYTDVYDKNNLLTNK	0.999013263	2	4.372304
Q9WTT6	VCMDLNNTVPEYK	1.108981665	2	3.7372
Q9WTV5	**PSMD9 26S proteasome non_ATPase regulatory subunit 9**	**0.973328541**	**0.08096**	**2**
Q9WTV5	ADVDLYQVR	1.625897879	2	2.620523
Q9WTV5	RKEEIEAQIK	0.840757395	3	3.329694
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**0.756111284**	**9.9E-20**	**7**
Q9WU19	AVFVGRPIIWGLAFQGEK	1.352652291	3	3.389856
Q9WU19	GVQDVLEILK	0.811070595	1	2.007855
Q9WU19	GVQDVLEILKEEFR	0.752491068	2	4.049794
Q9WU19	HGVDGILVSNHGAR	0.790532539	3	5.176381
Q9WU19	NFETNDLAFSPK	0.838354173	2	2.947986
Q9WU19	NVADIDLSTSVLGQR	0.80004956	2	4.974604
Q9WU19	VEVFLDGGVR	1.026103236	2	2.906112
Q9WU82	**CTNB1 Catenin beta_1**	**0.88637218**	**0.01285**	**4**
Q9WU82	AGDREDITEPAICALR	0.899748917	2	2.376073
Q9WU82	HQEAEMAQNAVR	0.858584079	2	3.240118
Q9WU82	LLNDEDQVVVNK	0.886247985	2	3.15532
Q9WU82	TMQNTNDVETAR	0.698899706	2	3.089158

Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**1.194798247**	**8.5E-08**	**4**
Q9WUC4	LGGVEFNIDLPNK	1.015225876	2	2.839043
Q9WUC4	LGGVEFNIDLPNKK	1.12409762	3	3.33666
Q9WUC4	VCIESEHSSDILLATLNK	1.191579417	2	5.479169
Q9WUC4	VLNKLGGVEFNIDLPNK	0.979070546	2	2.314406
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**0.896608573**	**0.8427**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(6)	0.896608573	2	2.31794
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7)	0.896608573	2	2.375822
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.741139096**	**9.9E-20**	**4**
Q9WUS0	AVILGPPGSGK	0.625129941	2	2.392797
Q9WUS0	GVLHQFSGTETNR	0.785798567	2	3.179753
Q9WUS0	TLVQAEALDR	0.623078341	2	2.751311
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	0.945333359	3	5.107171
Q9WVC0	**SEPT7 Septin_7**	**1.013707349**	**0.37183**	**2**
Q9WVC0	NLEGYVGFANLPNQVYR	0.86304829	2	3.740113
Q9WVC0	STLINSLFLTDLYSPEYPGPSHR	1.015340217	3	3.375935
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.605561952**	**0.00263**	**2**
Q9WVF7	AANMPDSELFELISENR	0.604164016	2	2.301883
Q9WVF7	MAWQWRGEFMPASR+Oxidation(0)	0.666268464		2.44538
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.852627342**	**9.9E-20**	**11**
Q9WVK3	AGVYNLTK	0.909779851	2	2.539975
Q9WVK3	ASQPPSSSTQVTAIQCNIR	0.883914871	2	5.49192
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	1.102620023	3	5.98571
Q9WVK3	ELLHLGCNVVIASR	0.805388898	2	3.905399
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	1.12661042	2	5.524289
Q9WVK3	KEEEVNNLVK	0.783666329	3	3.988356
Q9WVK3	LTAAVDELR	1.192745391	2	3.072181
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.709630965	2	5.143161
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.941703511	2	6.003706
Q9WVK3	TMALTWASSGVR	1.177758507	2	3.388549
Q9WVK3	TMALTWASSGVR+Oxidation(1)	0.758500019	2	2.938118
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**0.837777158**	**9.9E-20**	**12**
Q9WVK7	AADEFVEK	0.855000146	2	3.174679
Q9WVK7	DTPGFIVNR	0.745714748	2	2.32094
Q9WVK7	EDIDTAMK	0.646117298	1	2.161886
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.457319447	3	4.210552
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	0.658205126	3	5.341331
Q9WVK7	GDASKEDIDTAMK	0.716329013	2	3.471156
Q9WVK7	GDASKEDIDTAMK+Oxidation(11)	0.889884773	2	3.246618
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.824048672	4	5.136415
Q9WVK7	KGIEESLKR	0.78140976	2	2.786056

Q9WVK7	LKNELFQR	0.981722229	2	2.631053
Q9WVK7	LLVPYLIEAIR	1.339622016	2	2.447847
Q9WVK7	TFESLVDFCK	0.83491435	2	3.394188
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**0.930901573**	**0.97473**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	0.92128128	2	3.240149
Q9Z0N2	SFDVNKPGCEVDDLK	0.914753656	2	3.05022
Q9Z0N2	VGQEIEVRPGIVSK	0.940178272	2	3.05574
Q9Z0U5	**ADO Aldehyde oxidase**	**0.519512718**	**3E-12**	**8**
Q9Z0U5	CTGYRPIIDACK	0.354406356	2	2.665351
Q9Z0U5	DLEPLILTIEEAIQHK	1.173972347	2	2.789691
Q9Z0U5	ELSILYGGVGPTTIGAK	0.518375624	2	3.799639
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	0.51659794	2	4.603137
Q9Z0U5	KLECGNVDEAFK	0.488681465	2	3.42765
Q9Z0U5	LVLDEVTLAGSAPGGK	0.448183054	2	3.2858
Q9Z0U5	MTWISPVTLEELVEAK	0.668568908	2	3.200564
Q9Z0U5	VVENNVDPEMMLLPYLR	0.672797571	2	2.531185
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**0.870103479**	**1.2E-15**	**4**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.876707641	3	4.570931
Q9Z0V5	GLFIIDDK	0.994516199	2	3.118104
Q9Z0V5	QITLNDLPVGR	0.834129924	2	3.085922
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	1.008903493	3	5.810099
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.94753192**	**0.5885**	**4**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	1.028187202	3	6.444004
Q9Z0V6	GLFIIDPNGVIK	0.949176347	2	3.126246
Q9Z0V6	GTAVVNGEFK	0.983621806	2	2.407655
Q9Z0V6	HLSVNDLPVGR	0.874652357	2	2.800171
Q9Z122	**FADS2 Fatty acid desaturase 2**	**0.80949375**	**0.03884**	**2**
Q9Z122	AFHLDLDFVGK	0.829762883	3	3.605964
Q9Z122	HGIEYQEKPLLR	0.624757247	3	3.633338
Q9Z1A6	**VIGLN Vigilin**	**1.031054319**	**0.68449**	**17**
Q9Z1A6	ASVITQVFHVPLEER	1.155943192	2	2.957259
Q9Z1A6	DKFPEVIINFPDPAQK	0.89056615	3	3.477537
Q9Z1A6	DLANIAEVEVSIPAK	1.060837474	2	2.336405
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.084270532	2	3.174293
Q9Z1A6	GNSLQEILER	1.150068386	2	2.834247
Q9Z1A6	IDLPAENSNSETIVITGK	1.026803799	2	5.205644
Q9Z1A6	IEGDPQGVQQAK	1.018864441	2	3.600262
Q9Z1A6	IQIPRPDDPSNQIK	0.98310541	2	2.853973
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.263510071	2	2.723991
Q9Z1A6	IVGELEQMVSEDVPLDHR	1.04408496	2	3.993789
Q9Z1A6	LQDLELK	1.095353367	1	2.362921
Q9Z1A6	LQTQASATVPIPK	1.032982688	2	3.505463

Q9Z1A6	LVGEIMQETGTR	1.001634782	2	3.483627
Q9Z1A6	RCDIIVISGR	0.995325387	2	2.761325
Q9Z1A6	TGAHLELSLAK	1.194781118	3	3.41978
Q9Z1A6	TGVSVEIPPSDSISETVILR	1.108292971	2	2.634761
Q9Z1A6	VKELQAEQEDR	1.117814367	3	3.411653
Q9Z1J8	**S14L3 SEC14_like protein 3**	**0.836323956**	**0.00303**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.932246137	2	3.204896
Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	0.79697975	2	4.413899
Q9Z1J8	GSSHQVEYEILFPGCVLR	0.815637919	2	4.310538
Q9Z1M9	**SMC1A Structural maintenance of chromosomes protein 1A**	**0.953584499**	**0.70605**	**2**
Q9Z1M9	EIKEKDSELNQK	0.962291071	2	2.318438
Q9Z1M9	MDKVEDELKEK	0.921843158	2	2.365237
Q9Z1W6	**LYRIC Protein LYRIC**	**0.876389489**	**0.02656**	**3**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.034274494	3	3.473717
Q9Z1W6	SWQDELAQQAEEGSAR	0.86551282	2	5.594696
Q9Z1W6	TELGLDLGLEPK	0.916879157	2	3.013438
Q9Z269	**VAPB Vesicle_associated membrane protein_associated protein B**	**0.9740364**	**0.40184**	**2**
Q9Z269	TEAPVAAKPLTSPLDDAEVKK	0.832684951	3	3.455758
Q9Z269	VEQVLSLEPQHELK	0.975120903	2	3.784723
Q9Z277	**BAZ1B Tyrosine_protein kinase BAZ1B**	**0.855062407**	**2.5E-05**	**2**
Q9Z277	IHPLEKVDEEAVEK	0.527564305	2	2.451706
Q9Z277	LQKGGLGYMEGTSEFEARVISLEK	1.039703607	2	2.399335
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.824520477**	**9.9E-20**	**8**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	1.068430621	3	4.11281
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	1.226789382	2	4.60788
Q9Z2I8	INFDDNAEFR	0.981570898	2	3.195362
Q9Z2I8	LEGTNVQEAQNILK	0.838744386	2	5.071438
Q9Z2I8	SENEPIENEAAR	0.804876986	2	3.753941
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.843338829	2	5.947838
Q9Z2I8	SSGLPITSAVDLEDAAK	0.821921374	2	4.56245
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.785337538	2	3.544195
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.008043337**	**0.14419**	**6**
Q9Z2I9	ALIADSGLK	0.954192282	1	1.986279
Q9Z2I9	ILACDDLDEAAK	0.865466819	2	2.909318
Q9Z2I9	INFDSNSAYR	1.135415026	2	2.672813
Q9Z2I9	LSEIVTLAK	0.983520078	2	2.413548
Q9Z2I9	MGFPSNIVDSAAENMIK	1.025196787	2	2.775173
Q9Z2I9	SSDEAYAIAK	1.094639107	2	3.569951
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**0.81247315**	**4.1E-05**	**11**
Q9Z2L0	KLETAVNLAWTAGNSNTR	0.982574277	2	4.832703

Q9Z2L0	LTFDSSFSPNTGK	0.974891387	2	3.719875
Q9Z2L0	LTFDSSFSPNTGKK	0.909428679	2	2.848589
Q9Z2L0	SENGLEFTSSGSANTETTK	0.91523878	2	4.256815
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	0.848485758	3	5.04215
Q9Z2L0	TKSENGLEFTSSGSANTETTK	0.636252928	3	3.518906
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	0.890352997	2	4.44197
Q9Z2L0	VTQSNFAVGYK	0.997839865	2	2.804039
Q9Z2L0	WNTDNTLGTEITVEDQLAR	0.875375988	2	4.44851
Q9Z2L0	WTEYGLTFTEK	0.918099574	2	2.794506
Q9Z2L0	YQVDPDACFSAK	0.891000345	2	3.792374
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.684733193**	**1.1E-14**	**3**
Q9Z2M4	GQVLQLHAGAAK	0.913865528	2	2.949733
Q9Z2M4	HLAVEWGPQNIR	0.609445136	2	3.113725
Q9Z2M4	VNSLAPGAISGTEGLR	0.600750512	2	4.3013
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**0.864553815**	**0.01014**	**3**
Q9Z2M7	LQEQLGNDVVEK	0.790598103	2	3.597403
Q9Z2M7	TVGYTVTAPEDTR	1.109141211	2	2.689261
Q9Z2M7	YDYVFPENGLVAYK	0.991639573	2	3.186829
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**0.931753314**	**0.06318**	**12**
Q9Z2Q1	AQDGSNPLSLQDLIEK	1.067082328	2	4.14739
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	0.959228559	2	5.077232
Q9Z2Q1	CLSSATDPQTK	1.026769695	2	3.008002
Q9Z2Q1	DQTLSPTIISGLHSIAR	0.67330893	2	2.565691
Q9Z2Q1	GGPGPLAGHPQVSR	1.233882393	2	3.043104
Q9Z2Q1	KIDASQTDFEK	0.968725239	2	2.658661
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.315468879	2	3.63777
Q9Z2Q1	QVQHILASASPSGR	0.859858348	2	2.732763
Q9Z2Q1	SSYEGQPLPK	0.966686341	2	2.438343
Q9Z2Q1	TQPPEDISCIAWNR	0.921151656	2	3.071422
Q9Z2Q1	TTFEDLIQR	1.045898478	2	2.896065
Q9Z2Q1	VNFEEDSR	0.801940723	2	2.325756
Q9Z2U2	**ZN292 Zinc finger protein 292**	**0.952690892**	**0.51217**	**2**
Q9Z2U2	KLEVLSNNPDRTVLK	1.135995605	2	2.376967
Q9Z2U2	LINEDSTNAENQGNTTLK	0.904228468	2	2.699266
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**0.75741339**	**0.00169**	**4**
Q9Z2Z8	AIECSYTSADGLK	0.723829674	2	3.86921
Q9Z2Z8	ASLADIWAK	1.014991597	2	2.306351
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	0.7485868	2	4.896404
Q9Z2Z8	GYLFPTSAEDCK	0.797414081	2	2.370106
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**0.838808681**	**9.9E-20**	**2**
Q9Z339	GSAPPGPVPEGQIR	0.768471207	2	2.909402
Q9Z339	LEALELNECIDHTPK	0.839663093	2	4.100388

Time point 66 hours

Accession number	**Protein DESCRIPTION**	**Protein Ratio (66 h)**	**P-value (66 h)**	**Peptide number (66 h)**
Accession number	Peptide sequence	Peptide Ratio (66 h)	Charge state	Xcorr
A0JPQ8	**ALKMO Alkylglycerol monooxygenase**	**0.977039765**	**0.7258**	**2**
A0JPQ8	LDDILTSMSAGVVSR	1.08682981	2	3.10371
A0JPQ8	SITHLASGSWK	0.976568413	2	2.59728
A2ADY9	**DDI2 Protein DDI1 homolog 2**	**1.039565215**	**0.9987**	**2**
A2ADY9	NPPLAEALLSGDLEK	1.069951413	2	2.80264
A2ADY9	VLVEQQQDR	0.97052706	2	2.47317
A2AJL3	**FGGY FGGY carbohydrate kinase domain_containing protein**	**0.983261361**	**0.987**	**3**
A2AJL3	GHGLTCEGQPVTSR	0.976238127	2	3.51308
A2AJL3	MSKVGKVVFPEHADK	1.014926556	2	2.39486
A2AJL3	YQVFLRMVEHQK	1.022011431	2	2.35528
A2AL36	**CNTRL Centriolin**	**0.878483602**	**0.826**	**2**
A2AL36	LEVLNLSYNLIVK	0.878441228	2	2.43445
A2AL36	NQDKLNK	0.971867431	1	1.98164
A2APV2	**FMNL2 Formin_like protein 2**	**1.582510334**	**0.0036**	**2**
A2APV2	QAEEENELRKK	1.017582409	2	2.31474
A2APV2	QEQALMEK	2.349134844	1	2.01194
A2AQP0	**MYH7B Myosin_7B**	**1.275064355**	**0.9962**	**6**
A2AQP0	AITDAAMMAEELKK	1.234626899	2	3.03906
A2AQP0	DIDDLELTLAK	1.459878621	2	3.71527
A2AQP0	ELEELSER	1.299778758	1	2.06178
A2AQP0	HDCDLLR	1.112767778	2	2.38601
A2AQP0	TEELEEAK	1.132401558	2	2.63558
A2AQP0	VGNEYVTK	1.353596879	2	2.44774
A2ASS6	**TITIN Titin**	**1.173427039**	**0.3243**	**3**
A2ASS6	AENRFGIGPPAETIQRTTAR	1.169400505	2	2.68462
A2ASS6	APPIEPAPTPIAAPVTAPVVGK	1.344861157	2	3.8926
A2ASS6	RAPEPKPEFHVHEPGK	1.838102412	2	2.33522
A2AWL7	**MGAP MAX gene_associated protein**	**0.903390993**	**0.0544**	**3**
A2AWL7	ADVSLTTLLTAQASLK	0.904159748	1	2.0943
A2AWL7	ELIEDLKSLR	0.792759482	2	2.39361
A2AWL7	TDQGILVTNRDARALLSR	1.283274561	2	2.42502
A2VCW9	**AASS Alpha_aminoadipic semialdehyde synthase_ mitochondrial**	**1.174269325**	**0.425**	**10**
A2VCW9	AEGIVFNTQSTIK	1.040207567	2	2.55488
A2VCW9	AGGILQEDITEACLILGVK	1.021361374	2	2.72345
A2VCW9	AQEANMSLLDEVLK	1.185839058	2	3.45389
A2VCW9	GAQEVFNELPCEYVEPHELK	1.039326058	2	4.53272
A2VCW9	KTDGVYDPVEYEKYPER	1.240433164	3	3.4038
A2VCW9	KYDINTVNVTVGK	1.171806074	2	3.70572
A2VCW9	QDAQSLLVPVK	1.143696773	2	2.69529
A2VCW9	REDVNAWER	1.186279494	2	2.77684
A2VCW9	SSVVPVEGCPELPHK	1.215766068	2	2.87285
A2VCW9	YDINTVNVTVGK	0.773774731	2	2.74854
A6H584	**chain**	**0.852424902**	**0.4929**	**2**
A6H584	FVNRAVFRMANGIDR+Oxidation(8)	0.887451427	2	2.59459
A6H584	NEHSFQVVGIQVR	0.958491161	2	2.51254
A6N6J5	**WDR35 WD repeat_containing protein 35**	**0.838232804**	**0.437**	**2**
A6N6J5	LMYKIADEEAKK+Oxidation(1)	1.013449204	1	2.06362
A6N6J5	MYLDMDRRDLAIGLR+Oxidation(0)	0.835307774	2	2.33987
A7VJC2	**ROA2 Heterogeneous nuclear ribonucleoproteins A2/B1**	**1.001292763**	**0.0004**	**10**
A7VJC2	GFGFVTFDDHDPVDK	1.086853288	2	3.8426

A7VJC2	GGGGNFGPGPGSNFR	1.022598593	2	2.64694
A7VJC2	GGNFGFGDSR	1.146946781	2	2.50304
A7VJC2	IDTIEIITDR	0.955633852	2	3.66959
A7VJC2	LTDCVVMR	1.009920711	2	2.43318
A7VJC2	NMGGPYGGGNYGPGGSGGSGGYGGR	0.788414802	2	5.33568
A7VJC2	NYYEQWGK	0.892684543	2	2.34783
A7VJC2	QEMQEVQSSR	0.940004075	2	3.40655
A7VJC2	QEMQEVQSSR+Oxidation(2)	1.243987687	2	2.68398
A7VJC2	YHTINGHNAEVR	1.482971979	2	3.5312
B0BN93	**PSD13 26S proteasome non_ATPase regulatory subunit 13**	**1.089914056**	**0.9318**	**2**
B0BN93	QMTDPNVALTFLEK	1.036081415	2	2.71463
B0BN93	SAWGQQPDLAANEAQLLR	1.095874177	2	3.92688
B0BNA7	**EIF3I Eukaryotic translation initiation factor 3 subunit I**	**1.019717954**	**0.1554**	**3**
B0BNA7	HVLTGSADNSCR	1.404444176	2	3.05887
B0BNA7	MKPILLQGHERSITQIK+Oxidation(0)	1.007372121	2	2.36636
B0BNA7	SYSSGGEDGYVR	0.985307713	2	2.65244
B0BNE5	**ESTD S_formylglutathione hydrolase**	**1.045076159**	**0.0019**	**9**
B0BNE5	AFNGYLGPDQSK	1.125725997	2	2.9167
B0BNE5	AYDATCLVK	1.132111827	2	2.58357
B0BNE5	FAIYLPPQAESAK	1.191638734	2	2.89302
B0BNE5	MYSYVTEELPQLINANFPVDPQR	0.933637137	3	5.24364
B0BNE5	MYSYVTEELPQLINANFPVDPQR+Oxidation(0)	0.880564972	3	3.46762
B0BNE5	SGCQQAASEHGLVVIAPDTSPR	1.015675422	2	5.55281
B0BNE5	SVSAFAPICNPVLCPWGK	0.986217633	2	4.51576
B0BNE5	SYSGPQIDILIDQGKDDEFLSNGQLLPDNFIAACTEK	0.996872864	3	4.87516
B0BNE5	VFEHSSVELK	0.987474465	2	2.4656
B0BNN3	**CAH1 Carbonic anhydrase 1**	**0.457555666**	**0.0047**	**2**
B0BNN3	HDSSLKPVSVSYNPATAK	0.539151541	3	4.36903
B0BNN3	VGPANPNLQK	0.437919103	2	3.02796
B0K020	**CISD1 CDGSH iron_sulfur domain_containing protein 1**	**1.027171914**	**0.9789**	**2**
B0K020	HNEETGDNVGPLIIK	1.034414459	2	5.54202
B0K020	VVHAFDMEDLGDK	1.095867895	3	4.25234
B2GUZ5	**CAZA1 F_actin_capping protein subunit alpha_1**	**0.948327375**	**0.7822**	**2**
B2GUZ5	EASDPQPEDVDGGLK	0.95495972	2	3.45563
B2GUZ5	FTITPPTAQVVGVLK	0.942887989	2	2.7424
B2RX88	**CSPP1 Centrosome and spindle pole associated protein 1**	**1.538066585**	**2E-06**	**2**
B2RX88	SISSVNVDQVRMRNEDR	1.545190728	2	2.4924
B2RX88	SISSVNVDQVRMRNEDR+Oxidation(11)	1.503268032	2	2.31585
B2RYW9	**FAHD2 Fumarylacetoacetate hydrolase domain_containing protein 2**	**0.864051565**	**6E-07**	**2**
B2RYW9	KGDEVQCEIEELGVIINK	0.875010325	2	4.62402
B2RYW9	TFDTFCPLGPALVTK	0.862788015	2	4.50219
B3DMA2	**ACD11 Acyl_CoA dehydrogenase family member 11**	**0.794543883**	**0.0302**	**3**
B3DMA2	NLPDSDNEECLVHGDFK	0.957700042	2	3.13201
B3DMA2	RGQEVLTRVK	0.79432622	1	1.94488
B3DMA2	SLEAYLNQHLPGFGSDHR	1.057771867	3	3.30798
D3ZW55	**ITPA Inosine triphosphate pyrophosphatase**	**1.161723563**	**0.3045**	**4**
D3ZW55	IDLPEYQGEPDEISIQK	1.038149178	2	4.38239
D3ZW55	KLEEVIQILGDKFPCTLVAQK	1.174478101	3	3.47464
D3ZW55	LKPEGLYQLLAGFEDK	1.063991371	3	3.52695
D3ZW55	LQEYFGVTDGAGDH	0.891032404	2	2.58604
E9Q557	**DESP Desmoplakin**	**0.886607002**	**0.4281**	**2**
E9Q557	KQVQTSQKNTLR	0.861262607	1	1.97503
E9Q557	SQCTQVVQER	0.887263902	2	2.58448
O08557	**DDAH1 N(G)_N(G)_dimethylarginine dimethylaminohydrolase 1**	**0.955735985**	**3E-05**	**9**
O08557	DENATLDGGDVLFTGR	0.913355413	2	3.20031
O08557	DYAVSTVPVADSLHLK	0.931407019	2	3.4802

O08557	GAEILADTFK	0.903698697	1	2.28705
O08557	GAEILADTFKDYAVSTVPVADSLHLK	0.915278915	3	3.89538
O08557	KEVDMMK+Oxidation(5)	0.436501501	1	1.98577
O08557	SFCSMAGPNLIAIGSSESAQK	0.876152451	2	4.44352
O08557	SQGEEVDFAR	0.887238458	2	2.93232
O08557	TPEEYPESAK	1.66030248	2	2.63983
O08557	VDGLLTCCSVFINK	1.175914076	2	3.0177
O08583	**THOC4 THO complex subunit 4**	**0.981999568**	**0.8388**	**2**
O08583	QQLSAEELDAQLDAYNAR	0.914071858	2	4.45257
O08583	SLGTADVHFER	0.890626229	2	2.53574
O08601	**MTP Microsomal triglyceride transfer protein large subunit**	**1.026906686**	**0.2155**	**14**
O08601	EFYSYENEPVGIENLK	1.04375587	2	4.34502
O08601	GCPSLAEHWKSIR	1.013086186	2	3.54183
O08601	GHTTGLSLNNER	0.944260536	2	2.57247
O08601	GSFASNDIR	1.046644016	2	2.3416
O08601	MLSASGDPVSVVK	1.324998334	2	2.82819
O08601	NALLPEGIPLLLK	1.105822852	2	2.9961
O08601	NILLSIGELPK	0.952846908	2	4.04163
O08601	REEILQILK	0.938086477	2	2.5196
O08601	SDSSIILQER	0.887151344	2	3.02227
O08601	SGSSSAYTGYVER	1.04542791	2	3.53629
O08601	SNLNIFQYIGK	1.007554621	2	3.3661
O08601	VKEFYSYENEPVGIENLK	1.241406681	2	3.08446
O08601	YAEAGEGPVSHLATTVLQR	0.73117463	2	3.05761
O08601	YMLTVVQDILHFEMPASK+Oxidation(1)	1.187664869	2	2.42827
O08795	**GLU2B Glucosidase 2 subunit beta**	**1.109706152**	**2E-11**	**6**
O08795	ETVVTSTTEPSR	0.967857676	2	2.58546
O08795	KLWEEQQAAAK	1.101801409	2	3.31464
O08795	LWEEQQAAAK	1.146932854	2	3.06576
O08795	MPPYDEETQAIIDAAQEAR	1.286505683	2	4.31299
O08795	SLEDQVETLR	1.052976534	2	2.71696
O08795	YEQGTGCWQGPNR	1.241882348	2	3.8744
O08810	**U5S1 116 kDa U5 small nuclear ribonucleoprotein component**	**1.161949325**	**2E-08**	**2**
O08810	GGGQIIPTAR	1.184551743	2	2.78534
O08810	GLAEDIENEVVQITWNR	0.998953458	2	2.57116
O09171	**BHMT1 Betaine__homocysteine S_methyltransferase 1**	**1.560655511**	**1E-19**	**11**
O09171	AGAAIVGVNCHFDPSTSLQTIK	1.660777182	2	5.99127
O09171	AGPWTPEAAVEHPEAVR	1.939872425	2	5.07384
O09171	GAAELMQQK	1.812168062	2	3.7103
O09171	GAAELMQQK+Oxidation(5)	2.064328691	2	2.85269
O09171	KEYWQNLR	1.820580351	3	3.6449
O09171	LNAGEVVIGDGGFVFALEK	1.768762434	3	6.39853
O09171	QGFIDLPEFPFGLEPR	1.492365368	2	4.98133
O09171	QVADEGDALVAGGVSQTPSYLSCK	1.813676518	3	6.08999
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR	1.914878045	3	6.48554
O09171	TSGKPIAATMCIGPEGDLHGVSPGECAVR+Oxidation(9)	1.905952206	4	6.06096
O09171	VNEAACDIAR	1.577562345	2	4.05109
O09173	**HGD Homogentisate 1_2_dioxygenase**	**1.324751096**	**1E-19**	**8**
O09173	CFYNSDGDFLIVPQK	1.139976402	2	3.61275
O09173	FSVDVFEETR	1.379689224	2	3.34478
O09173	GYILEVYGVHFELPDLGPIGANGLANPR	1.49352711	3	5.00312
O09173	NCMSEFMGLIK	1.165638488	2	3.0691
O09173	QDVSPFNVVAWHGNYTPYK	1.295069152	2	3.37068
O09173	SLRPGVAIADFVIFPPR	1.339733991	3	3.51326
O09173	WKPFEIPK	1.335678762	2	2.41659
O09173	YISGFGNECASEDPR	1.409964759	2	4.40342

O35077	**GPDA Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic**	**1.133834653**	**4E-05**	**17**
O35077	ANTIGISLIK	1.093613029	2	3.04334
O35077	DPAQGQLLK	1.450559964	2	2.7762
O35077	ELHSILQHK	1.120635975	2	2.7721
O35077	FCETTIGCK	1.077539482	2	2.64942
O35077	FCETTIGCKDPAQGQLLK	0.977490006	2	4.937
O35077	GIDEGPNGLK	1.053076323	2	2.33991
O35077	GLVDKFPLFTAVYK	1.255490773	2	2.83968
O35077	ICDQLKGHLK	0.9804299	2	2.56844
O35077	ITVVQEVDTVEICGALK	1.148911955	2	3.30308
O35077	IVGSNASQLAHFDPR	1.482179473	2	3.07806
O35077	KLTEIINTQHENVK	0.943062215	2	5.00165
O35077	LTEIINTQHENVK	1.033355885	2	4.6994
O35077	NIVAVGAGFCDGLGFGDNTK	1.12340611	2	4.34747
O35077	SIEQLEK	1.0580032	2	2.32702
O35077	VCIVGSGNWGSAIAK	1.111599192	2	4.05635
O35077	VCYEGQPVGEFICCLQNHPEHM	1.270008835	2	3.82081
O35077	VTMWVFEEDIGGR	1.053537931	2	3.45636
O35078	**OXDA D_amino_acid oxidase**	**0.633930975**	**0.0038**	**2**
O35078	GQIIQVEAPWIK	0.596443286	2	2.9603
O35078	SCCQLEPTLK	0.840665236	2	2.36446
O35094	**TIM44 Mitochondrial import inner membrane translocase subunit TIM44**	**0.955390196**	**0.8869**	**3**
O35094	ILDISNVDLAMGK	0.955759123	2	2.88608
O35094	KLEESDALQEAR	0.955024375	2	3.4135
O35094	TEMSEVLTEILR	0.975778104	2	3.07197
O35142	**COPB2 Coatomer subunit beta_**	**1.146935069**	**0.0107**	**3**
O35142	AAESLADPTEYENLFPGLK	1.182378154	2	3.93119
O35142	FELALQLGELK	1.070700703	2	3.17329
O35142	GSNNVALGYDEGSIIVK	0.893795676	2	3.08323
O35244	**PRDX6 Peroxiredoxin_6**	**1.077632383**	**0.0687**	**10**
O35244	DFTPVCTTELGR	0.682499736	2	2.31061
O35244	DINAYNGAAPTEK	0.997801042	2	3.91735
O35244	DLAILLGMLDPAEKDEK	0.862072139	2	3.80084
O35244	GESVMVLPTLPEEEAK	1.123369064	2	3.03433
O35244	KGESVMVLPTLPEEEAK	1.009818481	2	4.92625
O35244	KGESVMVLPTLPEEEAK+Oxidation(5)	0.981274159	2	3.06644
O35244	LSILYPATTGR	1.136774941	2	2.43602
O35244	NFDEILR	0.933612953	1	2.04712
O35244	VVDSLQLTASNPVATPVDWK	1.038451467	2	5.01557
O35244	VVFIFGPDKK	1.106509325	2	2.34258
O35469	**3BHS6 3 beta_hydroxysteroid dehydrogenase/Delta 5___4_isomerase type 6**	**0.790907282**	**0.0044**	**2**
O35469	DLGYEPLVSWEEAK	0.787303388	2	4.20855
O35469	TSEWIGTLVEQHR	0.815073348	2	3.47278
O35509	**RB11B Ras_related protein Rab_11B**	**1.063034209**	**0.5426**	**4**
O35509	AQIWDTAGQER	1.09580322	2	2.74767
O35509	GAVGALLVYDIAK	1.07218662	2	3.74561
O35509	NEFNLESK	0.973434466	1	2.13872
O35509	VVLIGDSGVGK	1.063102635	2	2.40239
O35567	**PUR9 Bifunctional purine biosynthesis protein PURH**	**0.985217125**	**0.4789**	**7**
O35567	AEVSNAIDQYVTGTIGEGEDLVK	0.791445396	2	3.3009
O35567	ALFEEVPELLTEAEK	0.993782193	2	3.60044
O35567	DGQVIGIGAGQQSR	0.157464622	2	3.34445
O35567	EVSDGIVAPGYEEEALK	0.954540163	2	3.7194
O35567	HVSPAGAAVGVPLSEDEAR	0.93553221	2	4.17339

O35567	SGVAYIVAPSGSTADK	1.065786428	2	2.79479
O35567	VTVVCEPEDYGAVAAEMQGSGNK	1.019274763	2	5.16152
O35760	**IDI1 Isopentenyl_diphosphate Delta_isomerase 1**	**0.350496017**	**1E-05**	**3**
O35760	AELGIPLEEVDLNEMNYLTR	0.312230013	2	4.35606
O35760	NCHLNENIDK	0.206447321	2	3.00521
O35760	NVTLNPDPNEIK	0.570940021	2	3.35603
O35763	**MOES Moesin**	**1.000159387**	**0.9907**	**2**
O35763	ALTSELANAR	1.019482115	2	2.7736
O35763	FYPEDVSEELIQDITQR	0.939763902	2	2.8711
O35796	**C1QBP Complement component 1 Q subcomponent_binding protein_ mitochondrial**	**0.937558392**	**9E-12**	**4**
O35796	AEEQEPELTSTPNFVVEVTK	0.936464105	2	4.76318
O35796	AFVEFLTDEIK	0.853436395	2	2.61207
O35796	AFVEFLTDEIKEEK	1.03803288	2	3.54245
O35796	TLVLDCHYPEDEIGHEDEAESDIFSIK	1.516413076	3	5.09834
O35814	**STIP1 Stress_induced_phosphoprotein 1**	**1.055924431**	**0.9707**	**3**
O35814	ALSAGNIDDALQCYSEAIK	1.098434987	2	5.09771
O35814	DCEECIQLEPTFIK	1.036570237	2	4.12397
O35814	ELIEQLQNKPSDLGTK	0.960999236	2	4.20155
O35824	**DNJA2 DnaJ homolog subfamily A member 2**	**1.095235701**	**0.0304**	**2**
O35824	FDVQFPENNWINPDK	0.89643231	2	3.32257
O35824	NVLCSACSGQGGK	1.121739964	2	3.07385
O35826	**GLCNE Bifunctional UDP_N_acetylglucosamine 2_epimerase/N_acetylmannosamine kinase**	**1.319452582**	**0.0025**	**5**
O35826	DEAVGALHLIQAAK	1.33461357	2	2.8906
O35826	IYGDGNAVPR	1.203792315	2	2.33168
O35826	SIDLQEPLQK	1.257561655	2	2.56714
O35826	TLVLFPNIDAGSK	1.226225826	2	3.03097
O35826	TPLSDTLHLPVWVDNDGNCAAMAER	1.321034003	3	4.70305
O35913	**SO1A4 Solute carrier organic anion transporter family member 1A4**	**0.62625766**	**1E-19**	**3**
O35913	EGLQENVDGTENAK	0.622375187	2	3.1736
O35913	SLSGTYMNSMLTQIER	0.983799144	2	3.07852
O35913	SQTLNPTQDPSECVK	0.639609687	2	4.19016
O35952	**GLO2 Hydroxyacylglutathione hydrolase_ mitochondrial**	**1.035317231**	**0.3268**	**7**
O35952	ALLEVLGR	1.038568688	2	2.90278
O35952	FYEGTADEMYK	1.093293134	2	2.4948
O35952	HVEPGNTAVQEK	1.383086781	3	3.86585
O35952	LTTVLTTHHHWDHAGGNEK	1.222577298	3	3.46286
O35952	NAIGEPTVPSTLAEEFTYNPFMR	1.07234415	2	3.8837
O35952	TVQQHAGETDPVTTMR	1.015288317	2	4.67488
O35952	TVQQHAGETDPVTTMR+Oxidation(14)	0.960900456	2	3.41978
O35987	**NSF1C NSFL1 cofactor p47**	**0.866529739**	**0.0055**	**4**
O35987	ASSSILINEAEPTTNIQIR	0.866124533	2	5.17698
O35987	EANLLNAVIVQR	1.19242431	2	3.16812
O35987	LGAAPEEESAYVAGER	1.032071788	2	4.01184
O35987	SYQDPSNAQFLESIR	0.907603877	2	3.99571
O54753	**H17B6 17_beta_hydroxysteroid dehydrogenase type 6**	**1.284812237**	**0.2412**	**2**
O54753	TWEATPEHIR	1.361340751	2	2.63641
O54753	YGVEAFSDVLR	1.257136394	2	2.65806
O55012	**PICA Phosphatidylinositol_binding clathrin assembly protein**	**1.191010731**	**0.0018**	**5**
O55012	ATTLSNAVSSLASTGLSLTK	1.330184965	2	3.74115
O55012	ITAAQHSVTGSAVSK	1.251673641	2	4.19213
O55012	LVSDDLDSSLANLVGNLGIGNGTTK	1.053521706	3	3.97863
O55012	NTLFNLSNFLDK	1.013406908	2	2.77379
O55012	STNVAVDSGGGLLKPTVASQNQSLPVAK	1.093060425	3	4.79728
O55096	**DPP3 Dipeptidyl peptidase 3**	**0.974562412**	**0.0444**	**4**

O55096	AGLLALEFYTPETANWR	1.197184939	2	4.36667
O55096	LASVLNTEPALDSELTSK	1.229956753	2	4.12362
O55096	NVSLGNVLAVAYATK	1.055449119	2	2.45591
O55096	SYEFQGNHFQVTR	0.970112905	2	3.55768
O55125	**NIPS1 Protein NipSnap homolog 1**	**1.027909486**	**0.0207**	**3**
O55125	AGPNIYELR	0.992970575	2	3.04714
O55125	GWDENVYYTVPLVR	1.093964976	2	3.0029
O55125	IQFHNVKPECLDAYNSLTEAVLPK	1.293902019	3	4.67729
O55148	**GAS7 Growth arrest_specific protein 7**	**0.80684335**	**0.0899**	**2**
O55148	EMSEFIRERIK	0.806479485	2	2.37041
O55148	QKDLEMKTQQLEIK+Oxidation(5)	1.200959489	2	2.48296
O55171	**ACOT2 Acyl_coenzyme A thioesterase 2_ mitochondrial**	**0.931014511**	**1E-19**	**6**
O55171	ADAGGELDLAR	0.952380279	2	2.35312
O55171	DGLLDVVEALQSPLVDKK	0.624517457	2	5.49106
O55171	DVQKPYVVELEVLDGHEPDGGQR	0.943717773	3	4.41281
O55171	GGELGLAMASFLK	0.735400045	2	3.63433
O55171	IEYFEEAVNYLR	0.805793282	2	4.02657
O55171	SCWDEPLSITVR	0.764664048	2	3.4834
O70127	**ABCBB Bile salt export pump**	**0.970041496**	**0.9942**	**4**
O70127	AGQITSEALSNIR	0.973610923	2	3.32875
O70127	AGSIADEVLSSIR	0.928512998	2	2.62044
O70127	ILDNLSMVIKPGETTALVGSSGAGK	1.011836241	3	3.43363
O70127	ILLLDEATSALDTESEK	0.90952986	2	3.85611
O70133	**DHX9 ATP_dependent RNA helicase A**	**1.084675218**	**0.6544**	**2**
O70133	KMTPAYEIRAVGNK	0.890557819	2	2.45681
O70133	YPSPFFVFGEKIR	1.096820346	2	2.51043
O70199	**UGDH UDP_glucose 6_dehydrogenase**	**0.974840132**	**1E-19**	**11**
O70199	EQIVVDLSHPGVSADDQVSR	0.783215102	2	5.70369
O70199	IFDANTKPNLNLQVLSNPEFLAEGTAIK	0.955724383	3	6.00645
O70199	IIDSLFNTVTDK	0.964443495	2	2.71253
O70199	IIDSLFNTVTDKK	0.908125155	2	3.00261
O70199	ILTTNTWSSELSK	1.152307534	2	3.03688
O70199	INAWNSPTLPIYEPGLK	0.980900423	2	3.57343
O70199	NLFFSTNIDDAIR	1.007331594	2	3.18491
O70199	VLDGLHNELQTIGFQIETIGK	0.984891248	2	5.59397
O70199	VLIGGDETPEGQR	0.829223449	2	2.97425
O70199	VTVVDVNEAR	0.82202228	2	3.11762
O70199	YWQQVIDMNDYQR	0.923028964	2	4.3363
O70251	**EF1B Elongation factor 1_beta**	**1.142551256**	**1E-19**	**4**
O70251	SIQADGLVWGSSK	1.050255755	2	3.66027
O70251	SSILLDVKPWDDETDMTK	1.154325691	2	4.1752
O70251	SSILLDVKPWDDETDMTKLEECVR	0.934447499	3	4.29966
O70251	TPAGLQVLNDYLADK	1.347886154	2	3.95566
O70351	**HCD2 3_hydroxyacyl_CoA dehydrogenase type_2**	**1.268639369**	**2E-13**	**18**
O70351	EVQAALTLAK	0.972551404	2	2.53856
O70351	GGIVGMTLPIAR	0.954261882	2	3.45863
O70351	GGIVGMTLPIAR+Oxidation(5)	0.871840789	2	3.15261
O70351	GLVAVITGGASGLGLSTAK	1.072176142	2	4.58147
O70351	GVIINTASVAAFEGQVGQAAYSASK	1.514286666	2	3.71829
O70351	IDVAVNCAGIAVAIK	0.977069007	2	3.13309
O70351	KLGGNCIFAPANVTSEK	0.955711632	2	4.47584
O70351	KNQVHTLEDFQR	0.879733667	2	3.97714
O70351	LGGNCIFAPANVTSEK	1.072715633	2	3.3499
O70351	LGGNCIFAPANVTSEKEVQAALTLAK	1.116233012	3	3.41653
O70351	LVAGVMGQNEPDQGGQR	0.941000214	2	5.19519
O70351	LVGQGATAVLLDVPNSEGETEAK	1.337777475	2	4.82237
O70351	NFLASQVPFPSR	0.908976379	2	4.46925

O70351	NQVHTLEDFQR	0.908727011	3	3.41504
O70351	RLVGQGATAVLLDVPNSEGETEAK	1.036717598	3	5.05846
O70351	RLVGQGATAVLLDVPNSEGETEAKK	0.811301474	3	3.55671
O70351	VINVNLIGTFNVIR	1.093539534	2	3.34882
O70351	VVTIAPGLFATPLLTTLPDK	1.03662024	2	3.33551
O70456	**1433S 14_3_3 protein sigma**	**1.080590185**	**0.8679**	**4**
O70456	DSTLIMQLLR	1.070250168	2	3.27557
O70456	DSTLIMQLLR+Oxidation(5)	0.965188811	2	2.83038
O70456	VLSSIEQK	1.038211756	2	2.326
O70456	YEDMAAFMKSAVEK+Oxidation(3)	1.208087488	2	2.33081
O88202	**LPP60 60 kDa lysophospholipase**	**0.934189464**	**0.6057**	**3**
O88202	AAGAHLSPQELEDVGTELCR	0.973661843	3	3.90841
O88202	DYSGQTPLHVAAR	0.812895074	2	2.65868
O88202	GVDVDACNEDGQSPLLLAVR	1.128269583	2	4.96926
O88428	**PAPS2 Bifunctional 3__phosphoadenosine 5__phosphosulfate synthase 2**	**0.961377006**	**0.9994**	**3**
O88428	GCTVWLTGLSGAGK	0.929048292	2	2.93747
O88428	IHESAGLPFFEIFVDAPLNICESR	0.986149903	3	3.76869
O88428	NLGFSAGDREENIR	0.957288883	2	3.01183
O88600	**HSP74 Heat shock 70 kDa protein 4**	**0.924726033**	**0.2141**	**15**
O88600	AESEEMETSQAGSK	0.956625043	2	4.48381
O88600	AESEEMETSQAGSK+Oxidation(5)	1.474608351	2	3.9179
O88600	AFSDPFVEAEK	0.959940025	2	2.52537
O88600	AGGIETIANEYSDR	0.956457579	2	3.4878
O88600	EFSITDVVPYPISLR	1.021193438	2	2.52834
O88600	ELSTTLNADEAVTR	0.911072088	2	2.35192
O88600	GCALQCAILSPAFK	1.057260614	2	3.42905
O88600	HAEQNGPVDGQGDNPGTQAAEHGADTAVPSDGDK	1.075477155	3	4.69788
O88600	MIMQDKLEK+Oxidation(0)	1.073985341	2	2.39926
O88600	NFTTEQVTAMLLSK	1.14049144	2	3.45573
O88600	NKEDQYEHLDAADMTK	1.257328642	3	3.48827
O88600	SNLAYDIVQLPTGLTGIK	0.975005949	2	4.43311
O88600	TSTVDLPIESQLLWQLDR	1.06271907	2	4.16192
O88600	VLATAFDTTLGGR	0.893514685	2	3.38455
O88600	WNSPAEEGSSDCEVFPK	1.085362248	2	3.40843
O88618	**FTCD Formimidoyltransferase_cyclodeaminase**	**1.278577903**	**1E-19**	**20**
O88618	AFAACLGAIK	1.304764442	2	2.74629
O88618	AGEYEALPEK	1.271318095	2	2.92188
O88618	ALLDAAAFYCDK	1.413651887	2	3.93278
O88618	ALLDAAAFYCDKEK	1.140519204	2	3.82882
O88618	EAQELNLPVVGSQLVGLVPLK	1.13620343	3	4.36034
O88618	GVSMDECVLCAK	1.507287843	2	3.83545
O88618	IIEYLVPDSGPEQSLLDASLR	1.277613781	2	4.95072
O88618	ISSLLQEAK	1.267519423	1	2.10303
O88618	KVQGIGWYLEEK	1.216585336	2	2.63684
O88618	LAEELNVPVYLYGEAAQMPSR	1.456340275	2	5.02098
O88618	LFVLEEEHR	1.233132792	2	2.80888
O88618	LGLDSLAPFDPK	1.259892468	2	3.81037
O88618	MGALDVCPFIPVR	1.383729062	2	3.35725
O88618	MGALDVCPFIPVR+Oxidation(0)	1.259684369	2	2.67308
O88618	NLAQVSTNLLDFEVTALHTVYEEAR	1.547473039	3	4.2934
O88618	QAEWVPDFGPSSFVPSWGATVTGAR	1.180893311	2	3.9104
O88618	TCALQEGLR	1.662707868	2	2.74222
O88618	TQAALVLGSLEAR	1.14744042	2	5.05592
O88618	TVYTFVGQPECVVEGALSAAR	1.504458062	2	4.3361
O88618	VQGIGWYLEEK	1.288667465	2	3.42189
O88637	**PCY2 Ethanolamine_phosphate cytidylyltransferase**	**1.090604661**	**0.9848**	**6**

O88637	GPPVFTQEER	0.979812311	2	2.55598
O88637	HKGPPVFTQEER	0.984400615	2	3.01824
O88637	TEIVPDRDGSDPYEEPK	1.011155271	2	2.7517
O88637	TQGVSTTDLVGR	0.978914674	2	2.92766
O88637	WVDEVVPAAPYVTTLETLDK	1.086374209	2	2.93986
O88637	YVSEVVIGAPYSVTAELLNHFK	1.20720904	3	3.32313
O88746	**TOM1 Target of Myb protein 1**	**0.95380647**	**0.9751**	**2**
O88746	GDLSQHATPLPTPAVLPGDSPITPTPEQIGK	0.947977874	3	5.4896
O88746	QQSTGAIPATQAR	1.088127901	2	2.39602
O88761	**PSMD1 26S proteasome non_ATPase regulatory subunit 1**	**1.085444262**	**0.8128**	**2**
O88761	DTSEDIEELVEPVAAHGPK	1.016968309	2	3.39472
O88761	TVGTPIASVPGSTNTGTVPGPEK	1.085747418	2	3.18583
O88767	**PARK7 Protein DJ_1**	**1.676602542**	**7E-08**	**6**
O88767	DVVICPDTSLEEAK	1.016633309	2	3.04603
O88767	GAEEMETVIPVDIMR	1.04749498	2	4.12876
O88767	GAEEMETVIPVDIMR+Oxidation(13)	1.209088603	2	2.96104
O88767	GLIAAICAGPTALLAHEVGFGCK	0.698613889	2	4.94179
O88767	TQGPYDVVVLPGGNLGAQNLSESALVK	0.961162072	2	4.54039
O88767	VTVAGLAGKDPVQCSR	0.873997212	2	3.95268
O88813	**ACSL5 Long_chain_fatty_acid__CoA ligase 5**	**0.722056456**	**1E-19**	**8**
O88813	AILEDLQK	0.841094828	1	1.91715
O88813	GLAVSDNGPCLGYR	0.860745012	2	2.99222
O88813	GSFEELCQNQCVK	0.769597215	2	4.38467
O88813	IGFFQGDIR	1.182544648	2	2.66737
O88813	SFLIGVVVPDPESLPSFAAK	0.705807964	2	3.87398
O88813	SIFVHPEPFSIENGLLTPTLK	1.007430063	3	3.7044
O88813	SRPILQVFVHGESLR	0.81414948	3	3.78981
O88813	TQEVLDKDGWLHTGDIGR	0.862072863	3	3.32836
O88867	**KMO Kynurenine 3_monooxygenase**	**1.164929702**	**0.0823**	**4**
O88867	AVGLEDQIVSK	0.904683091	1	2.46724
O88867	FNNDLSVCLPEFSR	1.462139192	2	3.62959
O88867	NFPDAIPLMGEQALMR	0.939786041	2	2.51779
O88867	NFQVDVYEAR	1.016963129	2	2.58554
O88941	**MOGS Mannosyl_oligosaccharide glucosidase**	**0.899830782**	**0.3304**	**3**
O88941	DLALPTLLNPK	0.85026452	2	2.30048
O88941	LGPLLDVLADSR	0.948177861	2	2.79674
O88941	MDPSLFPPVPLFSGVPSR	0.884308774	2	2.48009
O88986	**KBL 2_amino_3_ketobutyrate coenzyme A ligase_ mitochondrial**	**0.948894482**	**0.1223**	**2**
O88986	GTDELLGVMDQVTIINSTLGK	0.902422849	2	3.38865
O88986	VQISAVHSEEDIDR	1.016623956	2	3.54225
O88989	**MDHC Malate dehydrogenase_ cytoplasmic**	**1.138357844**	**1E-19**	**8**
O88989	DLDVAVLVGSMPR	0.978952083	3	3.97206
O88989	ELTEEKETAFEFLSSA	1.127772012	2	3.72744
O88989	EVGVYEALKDDSWLK	1.029160115	2	3.82034
O88989	FVEGLPINDFSR	1.162221454	2	3.29685
O88989	GEFITTVQQR	1.133578174	2	3.98853
O88989	LGVTADDVK	1.240214806	2	2.81549
O88989	NVIIWGNHSSTQYPDVNHAK	1.178849693	2	5.757
O88989	VIVVGNPANTNCLTASK	1.153362003	2	5.17125
O88990	**ACTN3 Alpha_actinin_3**	**1.166111007**	**2E-05**	**5**
O88990	AGTQIENIEEDFR	1.087991188	2	3.06405
O88990	CQLEINFNTLQTK	1.14760315	2	4.11349
O88990	FAIQDISVEETSAK	0.958907067	2	4.19023
O88990	GLSQEQLNEFR	1.425369331	2	2.41592
O88990	HEAFESDLAAHQDR	1.449791507	3	4.299
O88994	**MOSC2 MOSC domain_containing protein 2_ mitochondrial**	**0.937426875**	**0.9999**	**2**
O88994	CVLTTVDPDTGIIDR	0.905060082	2	4.30261

O88994	QLQQVGTVSK	1.027533883	2	2.36573
O89000	**DPYD Dihydropyrimidine dehydrogenase [NADP_]**	**0.906224624**	**0.3649**	**5**
O89000	EGGADGVTATNTVSGLMGLK	0.832287956	2	2.70685
O89000	GTTSGPLYGPGQSSFLNIELISEK	1.113874704	2	4.05998
O89000	LTPNVTDIVSIAR	0.47273526	2	2.55182
O89000	QEYVGGLSTSEIPQFR	1.028395168	2	3.52097
O89000	TEQDETGNWVEDEEQIVR	1.182885329	2	4.56216
O89032	**SPD2A SH3 and PX domain_containing protein 2A**	**0.904814702**	**0.2903**	**2**
O89032	EGWAPASYIDKRK	0.901512109	1	1.96327
O89032	MLAYCVQDATVVDVEK	1.120635435	2	2.45512
O89046	**COR1B Coronin_1B**	**1.077396418**	**0.4297**	**2**
O89046	NDQCYEDIR	0.980281981	2	3.01493
O89046	NVLSDSKPAGYSR	1.100654867	2	3.32397
O89049	**TRXR1 Thioredoxin reductase 1_ cytoplasmic**	**1.006121695**	**0.6999**	**5**
O89049	IEQIEAGTPGR	1.030830177	2	3.358
O89049	IEQIEAGTPGRLK	0.470264912	2	2.37186
O89049	LELTPVAIQAGR	0.990508007	2	2.74066
O89049	STNSEETIEDEFNTVLLAVGR	1.049240188	3	3.44283
O89049	WGLGGTCVNVGCIPK	0.998586026	2	3.06956
P00173	**CYB5 Cytochrome b5**	**0.88514399**	**1E-19**	**6**
P00173	EQAGGDATENFEDVGHSTDAR	0.781123204	2	5.38046
P00173	FLEEHPGGEEVLR	0.853547403	2	4.17672
P00173	STWVILHHK	1.034535052	2	2.73728
P00173	TYIIGELHPDDR	0.910177731	2	3.87577
P00173	VYDLTK	0.838147773	1	2.13226
P00173	YYTLEEIQK	0.809257745	2	3.09618
P00388	**NCPR NADPH__cytochrome P450 reductase**	**1.216206847**	**1E-05**	**7**
P00388	DVQNTFYDIVAEFGPMEHTQAVDYVK	1.100100728	3	4.97609
P00388	GMSADPEEYDLADLSSLPEIDK	1.341514306	2	4.67908
P00388	LEQLGAQR	1.375009202	2	2.32892
P00388	RSDEDYLYR	1.328413562	2	3.23283
P00388	SDEDYLYR	1.316557288	2	2.38762
P00388	SYENQKPPFDAK	1.077826909	2	3.01685
P00388	TNVLYELAQYASEPSEQEHLHK	1.176383271	3	3.58361
P00406	**COX2 Cytochrome c oxidase subunit 2**	**1.129353547**	**0.0806**	**2**
P00406	LLEVDNR	1.184294509	2	2.54921
P00406	VVLPMELPIR	1.127455138	2	2.33376
P00481	**OTC Ornithine carbamoyltransferase_ mitochondrial**	**1.024987767**	**8E-11**	**14**
P00481	FGMHLQAATPK	0.966140865	3	3.4573
P00481	GEYLPLLQGK	0.982571065	2	3.04845
P00481	GGNVLITDTWISMGQEDEK	1.045723798	2	4.5317
P00481	GGNVLITDTWISMGQEDEKK	0.986341514	2	4.63328
P00481	GLTLSWIGDGNNILHSIMMSAAK	1.285373227	2	4.12862
P00481	GYEPDPNIVK	1.019249213	2	2.7553
P00481	LQAFQGYQVTMK	1.34140911	2	3.41781
P00481	LSTETGFALLGGHPSFLTTQDIHLGVNESLTDTAR	1.117633876	3	5.72871
P00481	QKGEYLPLLQGK	1.060689879	2	3.19065
P00481	SLVFPEAENR	1.056438611	2	2.47201
P00481	SLVFPEAENRK	1.03252082	2	2.88699
P00481	VLSSMTDAVLAR	1.053331785	2	3.71847
P00481	VLSSMTDAVLAR+Oxidation(4)	1.011847798	2	2.77119
P00481	YGKPVQSQVQLK	0.345153813	2	2.8169
P00502	**GSTA1 Glutathione S_transferase alpha_1**	**0.733494703**	**0.9999**	**2**
P00502	FIQSPEDLEK	0.768672388	2	2.7878
P00502	WLLAAAGVEFDEK	0.802509909	2	4.41792
P00507	**AATM Aspartate aminotransferase_ mitochondrial**	**0.998241179**	**4E-05**	**17**
P00507	ASAELALGENSEVLK	1.003411396	2	4.82794

P00507	DAGMQLQGYR	0.885203805	2	2.31843
P00507	DDNGKPYVLPSVR	0.984514928	2	3.32851
P00507	DDNGKPYVLPSVRKAEAQIAGK	0.839959682	2	2.38324
P00507	EGSSHNWQHITDQIGMFCFTGLKPEQVER	1.144279076	3	4.83554
P00507	FVTVQTISGTGALR	1.008228769	2	5.15682
P00507	HFIEQGINVCLCQSYAK	1.006927985	2	3.69049
P00507	IAATILTSPDLR	1.676843883	2	3.05703
P00507	IPEQSVLLLHACAHNPTGVDPRPEQWK	1.192137907	3	4.32644
P00507	KQWLQEVK	0.894088437	1	2.11343
P00507	MNLGVGAYR	1.115123937	2	2.93142
P00507	NLDKEYLPIGGLADFCK	0.935344658	2	5.36405
P00507	NMGLYGER	1.011535785	1	2.19264
P00507	TCGFDFSGALEDISK	0.948101214	2	4.69468
P00507	TQLVSNLK	0.948805306	2	2.68159
P00507	VGAFTVVCK	1.045116948	2	3.1257
P00507	VGASFLQR	1.193118128	2	2.97282
P00564	**KCRM Creatine kinase M_type**	**1.201539148**	**1**	**11**
P00564	DLFDPIIQDR	1.276272293	2	2.47413
P00564	FEEILTR	1.462333893	2	2.44762
P00564	GGDDLDPNYVLSSR	1.270534769	2	4.17961
P00564	GQSIDDMIPAQK	1.457512757	2	2.86245
P00564	GTGGVDTAAVGAVFDISNADR	1.308989431	2	5.89431
P00564	LGSSEVEQVQLVVDGVK	1.470800938	2	3.65185
P00564	LSVEALNSLTGEFK	1.312591091	2	3.74195
P00564	RGTGGVDTAAVGAVFDISNADR	1.193130946	2	4.17341
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR	1.198106017	3	6.0096
P00564	SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR+Oxidation(1)	1.315330111	4	4.55809
P00564	TDLNHENLK	1.079855908	2	2.63888
P00787	**CATB Cathepsin B**	**1.156419395**	**3E-07**	**4**
P00787	GENHCGIESEIVAGIPR	1.177198053	2	4.23511
P00787	HEAGDVMGGHAIR	1.162163558	3	3.88735
P00787	MCEAGYSTSYKEDK	1.224809384	2	3.72682
P00787	NGPVEGAFTVFSDFLTYK	1.192546046	2	3.62001
P00884	**ALDOB Fructose_bisphosphate aldolase B**	**1.385476054**	**1E-19**	**18**
P00884	ALQASALAAWGGK	1.587584483	2	4.72071
P00884	ATQEAFMK	1.189089917	2	2.67401
P00884	ATQEAFMK+Oxidation(6)	1.609721609	1	2.21641
P00884	ELLFSVDNSISQSIGGVILFHETLYQK	1.473021793	3	4.12183
P00884	ELSEIAQR	0.976850724	1	2.1754
P00884	ETTIQGLDGLSER	1.110384317	2	3.7022
P00884	GILAADESVGTMGNR	1.225740185	2	5.43682
P00884	GILAADESVGTMGNR+Oxidation(11)	1.394234857	2	5.1026
P00884	IKVENTEENR	1.49061219	2	3.15553
P00884	IKVENTEENRR	1.455178	2	3.16388
P00884	ISDQCPSSLAIQENANALAR	1.251781512	2	6.46809
P00884	KELSEIAQR	1.346947077	3	3.5845
P00884	KYTPEQVAMATVTALHR	1.367999581	3	6.00846
P00884	KYTPEQVAMATVTALHR+Oxidation(8)	1.484466917	3	4.79752
P00884	LDQGGAPLAGTNK	1.279005679	2	4.56857
P00884	YASICQQNGLVPIVEPEVLPDGDHDLEHCQYVSEK	1.39085073	3	5.04742
P00884	YTPEQVAMATVTALHR	1.508174577	2	4.71481
P00884	YTPEQVAMATVTALHR+Oxidation(7)	1.369805827	2	4.17035
P01015	**ANGT Angiotensinogen**	**0.73956745**	**0.12**	**2**
P01015	GSYNLQDLLAQAK	0.745397787	2	2.34024
P01015	SLDLSTDPVLAAQK	0.526879875	2	2.69179
P01026	**CO3 Complement C3**	**1.002709044**	**0.0691**	**12**
P01026	ADIGCTPGSGK	0.922144183	2	2.41277

P01026	DSCVGTLVVKGDPR	0.784267665	2	2.36007
P01026	EYVLPSFEVLVEPTEK	0.850477214	2	4.08405
P01026	IFTVDNNLLPVGK	0.973372197	2	2.7684
P01026	RVPVVTQGSDAQALTQDDGVAK	0.854654031	2	4.88799
P01026	SGSDEVQAGQER	1.448996697	2	4.2324
P01026	SSVAVPYVIVPLK	1.105576775	2	2.45118
P01026	TVLTGATGHLNR	0.941865073	2	2.75466
P01026	VELKPGDNLNVNFHLR	0.847555989	3	4.97326
P01026	VHQFFNVGLIQPGSVK	1.063607772	3	3.57012
P01026	VLIEDGSGEAVLSR	1.003671789	2	3.52488
P01026	VLMDGVRPSSPEALVGK	1.106347395	2	2.64887
P01946	**HBA Hemoglobin subunit alpha_1/2**	**0.439406131**	**1E-19**	**8**
P01946	AADHVEDLPGALSTLSDLHAHK	0.571431976	3	7.35119
P01946	FLASVSTVLTSK	0.431279939	2	3.99818
P01946	FLSHCLLVTLACHHPGDFTPAMHASLDKFLASVSTVLTSK	0.770133933	6	4.98911
P01946	IGGHGGEYGEEALQR	0.572221945	3	5.07364
P01946	LRVDPVNFK	0.485379064	2	2.46616
P01946	MFAAFPTTK	0.503010527	2	2.49243
P01946	MFAAFPTTK+Oxidation(0)	0.391143394	2	2.69809
P01946	TYFSHIDVSPGSAQVK	0.506990341	2	5.19758
P02089	**HBB2 Hemoglobin subunit beta_2**	**0.539177986**	**1E-19**	**4**
P02089	GTFASLSELHCDK	0.332506984	2	3.21935
P02089	LHVDPENFR	0.455002171	2	2.49771
P02089	YFDSFGDLSSASAIMGNPK	0.382230325	2	6.62883
P02089	YFDSFGDLSSASAIMGNPK+Oxidation(14)	0.419065493	2	5.5711
P02091	**HBB1 Hemoglobin subunit beta_1**	**0.644254961**	**1E-19**	**9**
P02091	AAVNGLWGK	1.245771683	2	2.76822
P02091	EFTPCAQAAFQK	0.400751519	2	3.1865
P02091	GTFAHLSELHCDK	0.542889873	2	4.261
P02091	GTFAHLSELHCDKLHVDPENFR	0.392660149	3	3.83835
P02091	KVINAFNDGLK	0.493657097	3	3.87784
P02091	LLGNMIVIVLGHHLGK	0.63074209	2	2.70511
P02091	VINAFNDGLK	0.49545302	2	2.92403
P02091	VNPDDVGGEALGR	0.484833564	2	4.07351
P02091	VVAGVASALAHK	0.489280445	2	3.4872
P02401	**RLA2 60S acidic ribosomal protein P2**	**0.999447142**	**3E-06**	**6**
P02401	ILDSVGIEADDER	1.266370297	2	4.74632
P02401	KILDSVGIEADDER	1.141676438	2	3.84707
P02401	LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK	1.287921827	3	5.83732
P02401	NIEDVIAQGVGK	1.003580431	2	4.60631
P02401	VISELNGK	1.046092301	1	2.01128
P02401	YVASYLLAALGGNSNPSAK	1.246865231	2	5.09139
P02563	**MYH6 Myosin_6**	**1.613888273**	**0.296**	**2**
P02563	DTQLQLDDAVR	1.456280404	2	2.63058
P02563	VKLEQQVDDLEGSLEQEKK	1.901282001	3	3.69309
P02564	**MYH7 Myosin_7**	**1.104747552**	**0.2386**	**32**
P02564	ALQEAHQQALDDLQAEEDKVNTLTK	1.158343025	3	4.51483
P02564	ANDDLKENIAIVER	1.210157581	2	3.46824
P02564	DLEEATLQHEATAAALR	1.015670279	2	4.96094
P02564	DTQIQLDDAVR	1.456280404	2	2.63058
P02564	DVFVPDDKEEFVK	1.397832563	2	2.58631
P02564	ELENELEAEQK	1.05907832	2	2.33688
P02564	EQYEEETEAK	1.47412684	2	2.38641
P02564	GQNVQQVAYAIGALAK	1.425247547	2	3.43065
P02564	GTLEDQIIQANPALEAFGNAK	1.08705397	2	5.28435
P02564	IEDEQALGSQLQK	1.451398456	2	4.41359
P02564	IEELEEELEAER	1.149533863	2	3.77815

P02564	ILNPAAIPEGQFIDSR	1.451573473	2	2.8353
P02564	KLEDECSELKR	1.148927118	3	3.49448
P02564	KVQHELDEAEER	1.085043736	2	3.6028
P02564	LAEQELIETSER	1.038548286	2	3.2148
P02564	LDEAEQIALK	1.264316219	2	3.59203
P02564	LELDDVTSNMEQIIK	1.135143282	2	3.7856
P02564	LQDAEEAVEAVNAK	1.324959363	2	4.40889
P02564	LQNEIEDLMVDVER	1.37483185	2	2.97147
P02564	LTQESIMDLENDKQQLDER	1.525647731	3	3.58578
P02564	MDADLSQLQTEVEEAVQECR	1.200341014	2	4.24579
P02564	NAYEESLEHLETFK	1.00502117	2	2.85012
P02564	NLQEEISDLTEQLGSTGK	1.083267449	2	5.52592
P02564	NLTEEMAGLDEIIVK	1.216096146	2	3.70306
P02564	NNLLQAELEELR	1.36510035	2	3.45335
P02564	QAEEAEEQANTNLSK	1.443863997	2	4.89664
P02564	QKYEESQSELESSQK	1.169960873	2	3.41548
P02564	TLEDQMNEHR	1.07065129	2	2.64317
P02564	VKEMTERLEDEEEMNAELTAK	1.387771294	2	2.3221
P02564	VQHELDEAEER	0.946037407	3	3.38028
P02564	VQLLHSQNTSLINQK	1.090250607	2	3.94321
P02564	VVDSLQTSLDAETR	1.120904547	2	3.64335
P02600	**MYL1 Myosin light chain 1/3_ skeletal muscle isoform**	**1.217321312**	**0.9828**	**11**
P02600	ALGTNPTNAEVK	1.225533727	2	3.27284
P02600	ALGTNPTNAEVKK	1.312012138	2	3.03803
P02600	DQGGYEDFVEGLR	1.643254597	2	3.97068
P02600	IDLSAIK	1.373974272	2	2.32837
P02600	IEFEQFLPMMQAISNNK	1.39030863	2	3.65012
P02600	ITLSQVGDVLR	2.030405938	2	3.50964
P02600	KIEFEQFLPMMQAISNNK	1.203968679	2	5.38094
P02600	KPAAAAPAPAPAPAPAPAKPK	6.232659665	3	3.36854
P02600	KVLGNPSNEEMNAK	1.01227467	2	3.28092
P02600	VLGNPSNEEMNAK	1.305534585	2	3.57022
P02600	VLGNPSNEEMNAK+Oxidation(9)	1.454308395	2	2.80717
P02625	**PRVA Parvalbumin alpha**	**1.082137771**	**0.433**	**4**
P02625	AIGAFTAADSFDHK	1.285369056	2	2.41835
P02625	SGFIEEDELGSILK	1.497666635	2	3.93653
P02625	TLMAAGDKDGDGK	0.878173509	2	2.91694
P02625	TLMAAGDKDGDGK+Oxidation(2)	1.486527682	2	3.02344
P02650	**APOE Apolipoprotein E**	**1.027671868**	**0.9699**	**12**
P02650	ELEEQLGPVAEETR	1.010668566	2	4.59738
P02650	GRLEEVGNQAR	0.927752081	2	3.6228
P02650	GWFEPLVEDMQR	0.897750333	2	3.14161
P02650	LEEVGNQAR	1.007503794	2	2.81307
P02650	LGADMEDLR	1.119338278	2	2.60618
P02650	LGPLVEQGR	1.150640197	2	2.44497
P02650	LQAEIFQAR	1.22158236	2	2.32147
P02650	MEEQTQQIR	0.909656617	2	2.54281
P02650	NEVNTMLGQSTEELR	0.995037983	2	4.40386
P02650	SKMEEQTQQIR	0.750452927	2	3.39656
P02650	SKMEEQTQQIR+Oxidation(2)	1.064458899	2	2.96943
P02650	TANLGAGAAQPLR	1.048956738	2	3.19287
P02680	**FIBG Fibrinogen gamma chain**	**0.925883784**	**0.9075**	**4**
P02680	VAQLEAQCQEPCK	1.158177415	2	2.75134
P02680	VGPESDKYR	0.301224198	2	2.8417
P02680	YEALLLTHESSIR	0.8441684	2	3.54532
P02680	YLQDIYTSNK	0.931886234	2	2.44483
P02692	**FABPL Fatty acid_binding protein_ liver**	**0.915977093**	**1E-19**	**12**

P02692	AMGLPEDLIQK	0.89143978	2	3.60376
P02692	AMGLPEDLIQK+Oxidation(1)	0.885062863	2	3.74659
P02692	GVSEIVHEGK	0.950515082	2	3.32548
P02692	GVSEIVHEGKK	0.837856293	2	3.20362
P02692	MVTTFK+Oxidation(0)	0.722150694	1	1.99584
P02692	SVTEFNGDTITNTMTLGDIVYK	0.860889466	3	5.72758
P02692	SVTEFNGDTITNTMTLGDIVYK+Oxidation(13)	1.041849996	2	5.24005
P02692	SVTEFNGDTITNTMTLGDIVYKR	1.065534381	2	3.57648
P02692	VIHNEFTLGEECELETMTGEK	0.908875122	3	6.17015
P02692	VIHNEFTLGEECELETMTGEK+Oxidation(16)	0.927575308	3	5.80079
P02692	YQVQSQENFEPFMK	0.895335828	2	5.80917
P02692	YQVQSQENFEPFMK+Oxidation(12)	0.938890716	2	5.22381
P02696	**RET1 Retinol_binding protein 1**	**0.915559835**	**0.9982**	**6**
P02696	ALDVNVALR	0.971240982	2	3.02512
P02696	CMTTVSWDGDKLQCVQK	0.787601594	2	3.76211
P02696	EFEEDLTGIDDR	0.862041875	2	2.47283
P02696	EFEEDLTGIDDRK	0.897751322	2	2.85427
P02696	MLSNENFEEYLR	0.949975132	2	3.32878
P02696	MLSNENFEEYLR+Oxidation(0)	0.989518878	2	3.18666
P02706	**ASGR1 Asialoglycoprotein receptor 1**	**1.170378402**	**0.2256**	**4**
P02706	DYQDFQHLDNENDHHQLQR	1.235768845	3	4.48717
P02706	LVESQLEK	1.173585241	2	2.47237
P02706	SLSCQMAALR	1.171040115	2	2.63668
P02706	WVDGTDYETGFK	1.006388114	2	3.02956
P02770	**ALBU Serum albumin**	**1.004097201**	**0.9993**	**22**
P02770	AADKDNCFATEGPNLVAR	1.390895552	2	4.31594
P02770	AETFTFHSDICTLPDKEK	1.749724221	2	4.11612
P02770	CCAEGDPPACYGTVLAEFQPLVEEPK	1.043517275	2	5.14804
P02770	CCSGSLVER	1.012638263	2	2.70419
P02770	CCTLPEAQR	0.985731181	2	3.02986
P02770	ECCHGDLLECADDR	1.073167473	2	3.67682
P02770	ECCHGDLLECADDRAELAK	0.95576197	2	5.08551
P02770	FKDLGEQHFK	0.910359714	3	4.18436
P02770	GLVLIAFSQYLQK	1.163387419	2	3.6445
P02770	KQTALAELVK	1.000615143	3	4.13387
P02770	KYEATLEK	0.874538324	1	2.96991
P02770	LQACCDKPVLQK	0.974648381	2	4.16405
P02770	LVQEVTDFAK	0.986370419	2	3.27122
P02770	RHPDYSVSLLLR	1.328090385	3	5.08933
P02770	SIHTLFGDK	0.939878077	1	2.36102
P02770	TCVADENAENCDK	0.909442671	2	4.41626
P02770	TNCELYEK	1.021388379	2	2.75763
P02770	TVMGDFAQFVDK	0.982192816	2	2.89356
P02770	TVMGDFAQFVDK+Oxidation(2)	0.762004349	2	2.44096
P02770	YMCENQATISSK	0.798475961	2	4.21156
P02770	YMCENQATISSK+Oxidation(1)	0.978794392	2	3.54505
P02770	YNEVLTQCCTESDK	1.059772253	2	5.67112
P02803	**MT1 Metallothionein_1**	**1.232305223**	**0.0097**	**2**
P04041	**GPX1 Glutathione peroxidase 1**	**0.794499317**	**1E-19**	**9**
P04041	FLVGPDGVPVR	0.789658695	2	3.5217
P04041	GLVVLGFPCNQFGHQENGK	0.819444281	2	4.2078
P04041	NALPAPSDDPTALMTDPK	0.875920749	2	3.255
P04041	NALPAPSDDPTALMTDPK+Oxidation(13)	0.902390982	2	2.70153
P04041	NDISWNFEK	0.81116324	2	2.77702
P04041	NEEILNSLK	0.842619526	2	2.47548
P04041	TIDIEPDIEALLSK	0.941732916	3	4.35711
P04041	YIIWSPVCR	0.908181867	2	2.46742

P04041	YVRPGGGFEPNFTLFEK	0.812358265	3	4.41242
P04167	**CP2B2 Cytochrome P450 2B2**	**0.848942192**	**1E-06**	**2**
P04167	GTIAVIEPIFK	0.784435824	2	2.61487
P04167	NLQEILDYIGHIVEK	0.549689911	2	3.80253
P04176	**PH4H Phenylalanine_4_hydroxylase**	**1.198690515**	**0.0054**	**14**
P04176	AYGAGLLSSFGELQYCLSDKPK	1.340369776	3	3.50996
P04176	EDNIPQLEDVSQFLQTCTGFR	1.118841746	3	4.76325
P04176	FANQILSYGAELDADHPGFKDPVYR	1.319607462	3	4.49207
P04176	ILADSINSEVGILCNALQK	0.955919449	2	5.05858
P04176	LRPVAGLLSSR	2.342655218	2	2.50035
P04176	NDIGATVHELSR	1.079148939	2	3.69054
P04176	QFADIAYNYR	1.108377126	2	2.48142
P04176	SFAQFSQEIGLASLGAPDEYIEK	1.075476174	2	4.38874
P04176	TACQEYSVTEFQPLYYVAESFSDAK	1.38258968	2	4.99959
P04176	THACYEHNHIFPLLEK	1.152186424	2	4.49733
P04176	VEVLDNTQQLK	1.041171536	2	3.54631
P04176	VEYTEEEK	1.174248898	2	2.73883
P04176	VEYTEEEKQTWGTVFR	0.958289297	2	3.76266
P04176	YCGFREDNIPQLEDVSQFLQTCTGFR	1.147016769	3	3.55336
P04182	**OAT Ornithine aminotransferase_ mitochondrial**	**1.007215536**	**0.3471**	**6**
P04182	AFYNNVLGEYEEYITK	0.950075567	2	4.36976
P04182	GLLNAIVIR	1.05204954	2	2.79088
P04182	KTEQGPPSSEYIFER	1.01916349	2	3.93442
P04182	TEQGPPSSEYIFER	0.960609268	2	3.55382
P04182	VLPMNTGVEAGETACK	0.965672812	2	4.93869
P04182	WLAVDHENVRPDIVLLGK	0.56895086	2	4.38126
P04256	**ROA1 Heterogeneous nuclear ribonucleoprotein A1**	**0.836686922**	**1E-08**	**5**
P04256	EDSQRPGAHLTVK	0.75147835	2	3.32671
P04256	IEVIEIMTDR	0.804044787	2	3.41041
P04256	MSKSESPKEPEQLR	0.981441354	2	2.39829
P04256	NQGGYGGSSSSSSYGSGR	0.906075339	2	4.69573
P04256	SESPKEPEQLR	0.877429308	2	2.51384
P04355	**MT2 Metallothionein_2**	**1.463556628**	**0.0724**	**2**
P04462		**0.811519386**	**6E-16**	**53**
P04462	AEVSELPSVVR	0.844227128	2	2.8961
P04462	ALLTPVAIAAGR	0.85629774	2	2.33306
P04462	ASMMGQRASLLTAR+Oxidation(2)	1.10080434	2	2.39155
P04462	AVAENQPFLIEAMTYR	1.185363104	2	3.97277
P04462	AVDEAADALLK	0.87988811	2	2.31355
P04462	AVEIAHALCLTERQIK	0.838870514	2	2.49514
P04462	DEELSCSVLELK	1.130476714	2	2.71877
P04462	DQMVKNNHFTLK+Oxidation(2)	0.935508335	2	2.44572
P04462	EELEKMK	0.865629988	1	1.90928
P04462	EIAGATPYITAAEEK	0.723700527	2	2.76163
P04462	EKMNKPELFNGGEKK	1.142081341	2	2.35309
P04462	ELDSITPDITPGWK	0.878001706	2	2.58184
P04462	FDQPKLKPKSDPK	1.090574969	2	2.30108
P04462	FFRPHFLQAPGDLTVQEGK	0.905419521	2	2.81524
P04462	FKLINSTNIR	1.675307345	1	1.9087
P04462	GIEQAVQSHAVAEEEAR	0.968523099	2	4.83597
P04462	GNIYSLNEGYAK	1.135678566	2	4.13688
P04462	GVYSEETLR	0.934921402	2	2.31634
P04462	HLQTYGEHYPLDHFDK	1.524181872	3	3.56397
P04462	HVIHTVGPIAVGQPTASQAAELR	0.908746287	3	4.17103
P04462	IEEMEKMLK+Oxidation(3)	0.983529762	1	1.98371
P04462	IGHHSTSDDSSAYR	2.468118223	3	4.20108
P04462	KAMQEINYGPSPDNSIKLVR	0.950830483	2	2.50625

P04462	KGNIYSLNEGYAK	1.140153195	2	4.00568
P04462	KLQHELEEAEER	1.27576202	3	4.04226
P04462	KVVSDLDVIMSHLK	1.052112926	2	2.61307
P04462	LEFIQPNVISGIPIYR	1.131076197	2	2.60935
P04462	LGDAVEQGVINNSVLGYFIGR	0.672277136	2	3.6388
P04462	LKLVMNNFIYQTK	1.189237955	2	2.42867
P04462	LNNIYQNNLTK	0.906455915	2	3.04488
P04462	LQHELEEAEER	1.465968865	2	3.57284
P04462	MNLQDELDELK	0.818465769	2	2.55021
P04462	MNLQDELDELK+Oxidation(0)	1.009872156	2	2.53545
P04462	NNGYAISTPTSEQYR	0.989286687	2	3.76692
P04462	QGQIINPSEDPHLPQEEVLK	0.768622489	2	2.55509
P04462	QRAEQETKLK	0.948756463	1	1.93396
P04462	QTITAQNAAVQAVK	0.811017782	2	4.55435
P04462	QYLLNQGWWDEEQEK	0.979937184	2	3.39574
P04462	RAALQAEIEELR	0.811473975	2	3.884
P04462	SEIQAEQDR	0.992147192	2	2.81657
P04462	SLEDALNQTATVTR	0.87004108	2	3.76818
P04462	SSSLLAKSPSK	1.185095278	2	2.35213
P04462	SVDEVNYWDK	1.30807979	2	2.53541
P04462	TNTGEDGQYFLK	0.799575203	2	2.31673
P04462	TSSAEMPTIPLGSAVEAIR	0.943186737	2	2.76497
P04462	TVNVVQFEPNK	0.866993555	2	2.37832
P04462	VDDSSGSIGR	1.324541187	2	2.67065
P04462	VDGNDVFAVYNATK	0.984380496	2	2.33335
P04462	VMEAFEQAER	0.910271378	2	3.05327
P04462	VSCSDNEFTQALTAAIPPESLTR	0.966773563	2	2.70738
P04462	VVSQYHELVVQAR	0.979536798	2	3.3983
P04462	YNENHQHGK	0.833509264	1	1.94403
P04462	YSTSSSSGVTAGK	0.469114285	2	2.86426
P04466	**MLRS Myosin regulatory light chain 2_ skeletal muscle isoform**	**1.585683196**	**0.9979**	**7**
P04466	AAAEGSSNVFSMFDQTQIQEFK	1.126129475	2	4.80417
P04466	GADPEDVITGAFK	1.475868778	2	4.06462
P04466	KQFLEELLTTQCDR	0.810472221	2	3.56261
P04466	LKGADPEDVITGAFK	1.172909331	2	2.97065
P04466	NEELDAMMK	1.127709774	1	1.96214
P04466	NICYVITHGDAK	1.524884396	2	2.74876
P04466	QFLEELLTTQCDR	1.205487769	2	3.34434
P04550	**PTMS Parathymosin**	**1.150493155**	**3E-09**	**4**
P04550	RTAEEEDEADPKR	1.368341347	3	4.26104
P04550	SVEAAAELSAK	1.130118826	2	3.70334
P04550	TAEEEDEADPK	1.345169563	2	3.67157
P04550	TAEEEDEADPKR	1.15288413	2	3.69355
P04636	**MDHM Malate dehydrogenase_ mitochondrial**	**0.841358593**	**1E-19**	**18**
P04636	AGAGSATLSMAYAGAR	1.077955222	2	4.69084
P04636	AGAGSATLSMAYAGAR+Oxidation(9)	1.105338408	2	3.67959
P04636	ANTFVAELK	1.061491903	2	2.64407
P04636	EGVIECSFVQSK	0.901749251	2	3.21326
P04636	ETECTYFSTPLLLGK	0.871654039	2	4.08631
P04636	FVFSLVDAMNGK	0.924778886	2	4.39535
P04636	GCDVVVIPAGVPR	0.869993521	2	4.37623
P04636	GYLGPEQLPDCLK	0.906786769	2	4.11833
P04636	IFGVTTLDIVR	1.252624881	2	3.69829
P04636	IQEAGTEVVK	0.935438569	2	2.96222
P04636	ITPFEEK	0.912207302	1	2.03893
P04636	LTLYDIAHTPGVAADLSHIETR	1.058217179	3	6.65212
P04636	MIAEAIPELK	0.947590951	2	2.72139

P04636	MIAEAIPELK+Oxidation(0)	0.978107064	2	2.92239
P04636	TIIPLISQCTPK	0.964656987	2	3.30404
P04636	VAVLGASGGIGQPLSLLLK	2.115090049	2	6.15261
P04636	VDFPQDQLATLTGR	0.973173595	2	4.60552
P04636	VNVPVIGGHAGK	0.73796227	1	2.29442
P04639	**APOA1 Apolipoprotein A_I**	**0.723761706**	**0.1384**	**6**
P04639	AKPALDDLGQGLMPVLEAWK	0.609324638	2	3.66509
P04639	LQEQLGPVTQEFWANLEK	0.8893875	2	4.55062
P04639	MRVNADALR+Oxidation(0)	0.47166987	2	2.52142
P04639	NEMNKDLENVK	0.677144834	2	3.23845
P04639	QLNLNLLDNWDTLGSTVGR	0.684601874	2	3.69543
P04639	WNEEVEAYR	0.817665862	2	2.79467
P04642	**LDHA L_lactate dehydrogenase A chain**	**1.04922394**	**2E-05**	**16**
P04642	DLADELALVDVIEDK	1.080016572	2	5.27033
P04642	DLADELALVDVIEDKLK	0.942131282	2	3.35795
P04642	DQLIVNLLK	1.116937733	2	3.0834
P04642	DQLIVNLLKEEQVPQNK	1.001407489	2	4.86108
P04642	EDVFLSVPCILGQNGISDVVK	1.069971618	2	4.75731
P04642	FIIPNVVK	1.063185912	2	2.441
P04642	GEMMDLQHGSLFLK	1.344284115	2	3.29578
P04642	GEMMDLQHGSLFLK+Oxidation(2)	0.896613122	2	2.3176
P04642	KSADTLWGIQK	1.22762387	2	3.08222
P04642	NVNIFK	1.142344049	1	2.20089
P04642	QVVDSAYEVIK	1.049814659	2	3.27613
P04642	RVHPISTMIK+Oxidation(7)	1.130199234	2	2.57455
P04642	SADTLWGIQK	1.123696437	2	3.82974
P04642	SLNPQLGTDADK	1.340611964	2	2.53043
P04642	SLNPQLGTDADKEQWK	1.085245021	2	4.83564
P04642	VTLTPDEEAR	1.093519283	2	2.87673
P04644	**RS17 40S ribosomal protein S17**	**0.935019285**	**0.7946**	**2**
P04644	LLDFGSLSNLQVTQPTVGMNFK	0.873369325	2	3.69171
P04644	VCEEIAIIPSK	1.013477177	2	2.94859
P04692	**TPM1 Tropomyosin alpha_1 chain**	**1.25056132**	**0.9996**	**9**
P04692	AISEELDHALNDMTSI	1.483349679	2	2.97861
P04692	GTEDELDKYSEALK	1.257680422	2	3.73447
P04692	KLVIIESDLER	1.186330619	2	3.1257
P04692	LDKENALDR	1.666157898	1	2.07886
P04692	LKGTEDELDK	1.476190077	2	2.76048
P04692	LVIIESDLER	0.97320155	2	2.66133
P04692	MEIQEIQLK	1.104689359	2	3.09523
P04692	QLEDELVSLQK	1.166660121	2	2.81521
P04692	SIDDLEDELYAQK	1.44862034	2	4.12576
P04694	**ATTY Tyrosine aminotransferase**	**0.937411042**	**0.9525**	**2**
P04762	**CATA Catalase**	**0.922529504**	**1E-19**	**30**
P04762	APQKPDVLTTGGGNPIGDK	2.981020261	2	4.50064
P04762	DAMLFPSFIHSQK+Oxidation(2)	0.916629968	2	2.73084
P04762	DAQLFIQR	0.817786775	2	2.99976
P04762	DGPMCMHDNQGGAPNYYPNSFSAPEQQGSALEHHSQCSADVK	1.033354783	4	4.9636
P04762	DPASDQMK	1.071057683	1	2.03358
P04762	DPASDQMK+Oxidation(6)	1.09640433	2	2.49865
P04762	DYPLIPVGK	0.789397068	1	2.22076
P04762	EAETFPFNPFDLTK	0.835422862	2	4.29561
P04762	FNSANEDNVTQVR	0.93721678	2	4.70968
P04762	FSTVAGESGSADTVR	0.958557285	2	5.17287
P04762	FSTVAGESGSADTVRDPR	0.889641238	2	2.3877
P04762	FYTEDGNWDLVGNNTPIFFIR	1.081799171	3	5.88305
P04762	GAGAFGYFEVTHDITR	0.929468868	2	4.9663

P04762	GPLLVQDVVFTDEMAHFDR	1.083000837	2	5.74036
P04762	HMNGYGSHTFK	0.873573081	3	4.35929
P04762	HMNGYGSHTFK+Oxidation(1)	0.880076528	3	3.37125
P04762	LCENIANHLK	0.98661931	3	3.71506
P04762	LFAYPDTHR	1.027948866	2	2.90744
P04762	LGPNYLQIPVNCPYR	1.181375372	2	4.22078
P04762	LNIMTAGPR	0.97857524	2	3.08237
P04762	LNIMTAGPR+Oxidation(3)	1.150006305	2	2.3431
P04762	LVNANGEAVYCK	1.056484091	2	3.7106
P04762	NAIHTYVQAGSHIAAK	0.932794783	3	5.57551
P04762	NFTDVHPDYGAR	0.863445096	2	3.96613
P04762	NLPVEEAGR	0.821621077	1	2.26028
P04762	NPANYFAEVEQMAFDPSNMPPGIEPSPDK	1.158317637	3	5.15325
P04762	RFNSANEDNVTQVR	0.836268969	2	4.57431
P04762	VFEHIGK	0.979798486	2	2.33709
P04762	VQALLDQYNSQKPK	0.894183016	2	4.9452
P04762	VWPHKDYPLIPVGK	0.832893046	2	3.70789
P04764	**ENOA Alpha_enolase**	**1.069038209**	**1E-19**	**14**
P04764	AGYTDQVVIGMDVAASEFYR	1.06007141	2	4.92137
P04764	DATNVGDEGGFAPNILENK	1.056363359	2	5.93217
P04764	FTATAGIQVVGDDLTVTNPK	1.213705779	2	4.79274
P04764	GNPTVEVDLYTAK	1.263375541	2	3.73241
P04764	HIADLAGNPEVILPVPAFNVINGGSHAGNK	1.030364662	3	6.47355
P04764	IDQLMIEMDGTENK	1.18412624	2	4.08548
P04764	IEEELGSK	1.073057065	2	2.499
P04764	IGAEVYHNLK	1.405755983	2	3.09145
P04764	KLNVVEQEKIDQLMIEMDGTENK	0.995390915	3	4.75003
P04764	LNVVEQEK	1.175005853	2	2.37395
P04764	LNVVEQEKIDQLMIEMDGTENK	1.016292676	3	4.53131
P04764	SCNCLLLK	1.276603211	2	2.7912
P04764	VNQIGSVTESLQACK	1.071418899	2	5.13829
P04764	YITPDQLADLYK	1.038954874	2	3.45887
P04785	**PDIA1 Protein disulfide_isomerase**	**0.916757098**	**0.7408**	**24**
P04785	DHENIVIAK	1.05619795	2	2.90361
P04785	EADDIVNWLK	0.797111316	2	2.55014
P04785	HNQLPLVIEFTEQTAPK	1.060701211	2	5.35538
P04785	IKPHLMSQELPEDWDKQPVK	1.140659204	3	4.09824
P04785	IKPHLMSQELPEDWDKQPVK+Oxidation(5)	1.09285396	3	3.51186
P04785	ILEFFGLK	1.283007776	2	2.80848
P04785	LGETYKDHENIVIAK	1.021827841	3	4.90121
P04785	LITLEEEMTK	1.029133375	2	3.55391
P04785	LITLEEEMTK+Oxidation(7)	1.146537201	2	2.55561
P04785	LKAEGSEIR	1.11122031	1	2.02934
P04785	LLDFIK	1.058012313	2	2.31833
P04785	MDSTANEVEAVK	1.013059184	2	4.13078
P04785	MDSTANEVEAVK+Oxidation(0)	0.996009123	2	3.79399
P04785	NFEEVAFDEK	1.046702009	2	3.01144
P04785	NFEEVAFDEKK	0.975525173	2	3.83634
P04785	NNFEGEITK	0.926780667	2	2.54112
P04785	QFLLAAEAVDDIPFGITSNSDVFSK	1.010324339	3	6.62069
P04785	SVSDYDGK	1.124396437	1	1.90107
P04785	TGPAATTLSDTAAAESLVDSSEVTVIGFFK	1.04773135	3	6.35974
P04785	THILLFLPK	1.101209887	2	2.6554
P04785	TVIDYNGER	1.037802634	2	2.63938
P04785	VDATEESDLAQQYGVR	0.995477829	2	5.72147
P04785	YKPESDELTAEK	1.015810841	3	3.93578
P04785	YQLDKDGVVLFK	0.996728412	2	3.97975

P04797	**G3P Glyceraldehyde_3_phosphate dehydrogenase**	**1.75190058**	**1E-19**	**16**
P04797	GAAQNIIPASTGAAK	1.222610548	2	3.97963
P04797	GILGYTEDQVVSCDFNSNSHSSTFDAGAGIALNDNFVK	1.020526082	3	3.96129
P04797	IVSNASCTTNCLAPLAK	1.176709771	2	4.76052
P04797	LISWYDNEYGYSNR	1.972737839	2	4.00233
P04797	LVINGKPITIFQER	1.531139172	3	4.5246
P04797	RVIISAPSADAPMFVMGVNHEK	1.07886451	3	5.01622
P04797	RVIISAPSADAPMFVMGVNHEK+Oxidation(12)	0.971709778	3	3.33437
P04797	VGVNGFGR	1.221828584	2	2.55568
P04797	VIHDNFGIVEGLMTTVHAITATQK	1.142675647	3	7.99555
P04797	VIHDNFGIVEGLMTTVHAITATQK+Oxidation(12)	1.195752934	3	5.51522
P04797	VIISAPSADAPMFVMGVNHEK	1.069754002	2	4.441
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(11)	1.173337166	2	3.77393
P04797	VIISAPSADAPMFVMGVNHEK+Oxidation(14)	1.173337166	2	3.58297
P04797	VPTPNVSVVDLTCR	1.908979662	2	3.13401
P04797	VVDLMAYMASK	1.119369384	2	3.14948
P04797	WGDAGAEYVVESTGVFTTMEK	1.14792402	2	5.46422
P04799	**CP1A2 Cytochrome P450 1A2**	**0.677969204**	**1E-19**	**4**
P04799	DFVENVTSGNAVDFFPVLR	0.844222766	2	3.11468
P04799	NSIQDITGALFK	0.571620934	2	3.34912
P04799	TVQEHYQDFNK	0.741861854	2	3.14533
P04799	VDLTPSYGLTMKPR	0.948007808	2	2.69608
P04903	**GSTA2 Glutathione S_transferase alpha_2**	**1.083412955**	**1E-19**	**11**
P04903	DGNLMFDQVPMVEIDGMK	0.699256953	2	4.69398
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	0.719744697	2	4.14919
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(10)	0.753980344	2	3.26706
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(16)	0.716964608	2	3.53962
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.716909248	2	4.34506
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.761705471	2	2.38629
P04903	DGNLMFDQVPMVEIDGMK+Oxidation(4)	0.738385411	2	3.06701
P04903	KDGNLMFDQVPMVEIDGMK	0.502512371	2	4.00736
P04903	LIQSPEDLEK	0.692123626	2	2.83462
P04903	WLLAAAGVEFEEK	0.747385351	2	3.45386
P04903	YLPAFEK	0.685157509	1	1.99262
P04904	**GSTA3 Glutathione S_transferase alpha_3**	**0.837612865**	**1E-19**	**8**
P04904	ALIDMYAEGVADLDEIVLHYPYIPPGEK+Oxidation(4)	0.967257578	3	4.0127
P04904	NDGSLMFQQVPMVEIDGMK	0.805509054	2	4.7908
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	0.85973184	2	4.20346
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(11)	1.003762852	2	2.30344
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(17)	0.851478172	2	3.56311
P04904	NDGSLMFQQVPMVEIDGMK+Oxidation(5)	0.857837973	2	4.34212
P04904	SHGQDYLVGNR	0.792933326	2	4.15224
P04904	WLLAAAGVEFEEQFLK	0.83490269	2	5.49633
P04905	**GSTM1 Glutathione S_transferase Mu 1**	**0.968372529**	**8E-16**	**15**
P04905	ADIVENQVMDNR	0.997837798	2	4.20142
P04905	ADIVENQVMDNR+Oxidation(8)	0.954615363	2	3.80151
P04905	CLDAFPNLKDFLAR	1.045493747	2	3.2526
P04905	FKLGLDFPNLPYLIDGSR	1.621993537	3	4.25101
P04905	HHLCGETEEER	1.402596213	3	4.25113
P04905	IRADIVENQVMDNR	0.919110872	2	3.83015
P04905	ITQSNAIMR	1.008075864	2	3.02927
P04905	ITQSNAIMR+Oxidation(7)	1.249752798	2	2.79195
P04905	KHHLCGETEEER	1.119685084	3	3.39392
P04905	KITQSNAIMR	0.956118807	3	3.39499
P04905	KITQSNAIMR+Oxidation(8)	1.204655998	3	3.4261
P04905	LGLDFPNLPYLIDGSR	1.066289059	2	5.02103
P04905	MQLIMLCYNPDFEK	0.836893825	2	3.94328

P04905	VTYVDFLAYDILDQYHIFEPK	0.754490669	2	2.35857
P04905	YLSTPIFSK	1.056797077	2	2.65989
P05065	**ALDOA Fructose_bisphosphate aldolase A**	**1.030390325**	**1**	**7**
P05065	ALANSLACQGK	1.208085309	2	2.80479
P05065	FSNEEIAMATVTALR	1.159486376	2	4.30675
P05065	GILAADESTGSIAK	1.117036754	2	3.76995
P05065	GVVPLAGTNGETTTQGLDGLSER	1.04495817	2	5.34768
P05065	IGEHTPSSLAIMENANVLAR	0.819898118	2	4.54636
P05065	LQSIGTENTEENR	1.321217402	2	3.64431
P05065	RLQSIGTENTEENRR	0.970107944	3	3.42005
P05178	**CP2C6 Cytochrome P450 2C6**	**0.664379598**	**1E-19**	**6**
P05178	EALIDHGEEFAER	0.65053373	2	3.1914
P05178	EFPDPEIFDPGHFLDGNGK	0.57923583	2	2.53109
P05178	FDYKDQDFLNLMEK	0.722302554	3	3.58338
P05178	FIDLIPTNLPHAVTCDIK	0.609566774	2	3.14412
P05178	GTTIITSLSSVLHDSK	0.699211252	2	3.32618
P05178	NITQSLTSFSK	0.690607134	2	2.71881
P05179	**CP2C7 Cytochrome P450 2C7**	**2.086434037**	**1E-19**	**6**
P05179	ACVGEGLAR	1.768459767	2	2.91695
P05179	FINFVPTNLPHAVTCDIK	1.948864995	2	2.73564
P05179	IEEHQESLDVTNPR	2.199409162	2	4.59598
P05179	KIEEHQESLDVTNPR	2.160780885	2	4.98166
P05179	KLPPGPTPLPIIGNFLQIDVK	1.230752184	3	4.91412
P05179	VLTSLTSVLHDSK	2.47202574	2	2.95063
P05182	**CP2E1 Cytochrome P450 2E1**	**0.900179805**	**2E-10**	**12**
P05182	AKEHLQSLDINCAR	0.723702006	2	4.3612
P05182	DIDLSPVTVGFGSIPPQFK	0.627495376	2	3.00024
P05182	DRLDMPYMDAVVHEIQR	0.699823249	3	4.82271
P05182	DVTDCLLIEMEKEK	0.960966056	2	3.07266
P05182	EHLQSLDINCAR	0.818157371	2	3.07995
P05182	FINLVPSNLPHEATR	0.701238281	2	3.79202
P05182	FKPEHFLNENGK	0.814305032	2	2.82957
P05182	GTVVIPTLDSLLYDSHEFPDPEK	0.690888123	2	4.59551
P05182	LHEEIDR	0.63014901	1	1.96858
P05182	VCVGEGLAR	0.72590669	2	2.65443
P05182	YGLLILMK	0.887293726	2	2.89152
P05182	YSDYFK	0.649219582	1	1.90978
P05183	**CP3A2 Cytochrome P450 3A2**	**0.95067739**	**3E-05**	**10**
P05183	AVSVAKDEEWK	1.248266369	2	2.53399
P05183	DIELDGLFIPK	0.892231531	2	3.21154
P05183	EMFPIIEQYGDILVK	0.999627229	2	3.84097
P05183	KDIELDGLFIPK	1.068370824	3	3.31983
P05183	KLQEEIDGALPSK	1.147773306	2	2.33237
P05183	LQEEIDGALPSK	1.089960968	2	3.61645
P05183	QAILEPEKPIVLK	1.458534396	2	2.70757
P05183	QEAETGKPVTMK	1.580819662	2	3.48824
P05183	QEAETGKPVTMK+Oxidation(10)	1.420689677	2	3.03829
P05183	VDFLQLMLNAHNNSK	1.114593611	2	3.27252
P05197	**EF2 Elongation factor 2**	**1.110068404**	**1E-19**	**26**
P05197	ALLELQLEPEELYQTFQR	1.219670883	3	5.2195
P05197	ARPFPDGLAEDIDKGEVSAR	1.113661673	3	6.45789
P05197	AYLPVNESFGFTADLR	1.135967675	2	3.79735
P05197	CELLYEGPPDDEAAMGIK	1.095532496	2	3.33144
P05197	DLEEDHACIPIK	0.993546813	2	3.39429
P05197	DLEEDHACIPIKK	0.90368634	2	3.23299
P05197	EGIPALDNFLDK	0.40788079	2	2.57943
P05197	EGIPALDNFLDKL	1.462662054	2	3.76211

P05197	ETVSEESNVLCLSK	1.159113305	2	3.94589
P05197	GEGQLGAAER	1.249768283	2	3.24832
P05197	GHVFEESQVAGTPMFVVK	1.365047043	2	5.28469
P05197	IWCFGPDGTGPNILTDITK	1.297307476	2	4.98118
P05197	KEDLYLKPIQR	1.303018503	2	3.11876
P05197	KIWCFGPDGTGPNILTDITK	1.021286644	2	4.65113
P05197	KVEDMMK+Oxidation(4)	1.000982968	2	2.31953
P05197	KVEDMMK+Oxidation(5)	0.935269214	2	2.49959
P05197	LDSEDKDKEGKPLLK	0.999462032	2	3.40883
P05197	NMSVIAHVDHGK	1.110076699	2	3.17086
P05197	NMSVIAHVDHGK+Oxidation(1)	1.131866868	2	3.32973
P05197	STLTDSLVCK	1.106224925	2	2.8802
P05197	TFCQLILDPIFK	1.213953286	2	3.9626
P05197	VFSGVVSTGLK	1.096492409	2	2.42868
P05197	WLPAGDALLQMITIHLPSPVTAQK	1.082723497	2	4.03908
P05197	YEWDVAEAR	1.159101705	2	3.00161
P05197	YFDPANGK	1.080253742	1	1.93718
P05197	YVEPIEDVPCGNIVGLVGVDQFLVK	1.218351913	2	4.51237
P05369	**FPPS Farnesyl pyrophosphate synthase**	**0.399765613**	**1E-19**	**11**
P05369	ALYEELDLR	0.515572687	2	2.80723
P05369	EVLEYNTVGGK	0.372975353	2	2.82149
P05369	GLTVVQTFQELVEPR	0.448840812	2	3.81667
P05369	IKEVLEYNTVGGK	0.37160084	3	4.12844
P05369	QILEENYGQK	0.472619062	2	2.32503
P05369	QILEENYGQKDPEK	0.543723045	2	3.88729
P05369	QNFIQHFSQIVK	0.871437454	2	2.6151
P05369	SLIEQCSAPLPPSIFLELANK	0.446584078	3	5.14045
P05369	VGTDIQDNK	0.483618018	2	3.74066
P05369	VLTEDELGHPEK	0.368572347	2	2.65078
P05369	VLTEDELGHPEKGDAITR	0.33158253	2	4.68234
P05426	**RL7 60S ribosomal protein L7**	**1.019434801**	**6E-05**	**5**
P05426	AGNFYVPAEPK	1.17950004	2	2.71074
P05426	FGIICMEDLIHEIYTVGK	1.209381301	2	4.47247
P05426	KKVPAVPETLK	0.768654318	2	2.85221
P05426	TTHFVEGGDAGNR	1.069720949	2	2.85694
P05426	TTHFVEGGDAGNREDQINR	1.018214559	2	4.64643
P05544	**SPA3L Serine protease inhibitor A3L**	**1.165154401**	**0.0006**	**5**
P05544	AVLDVDETGTEATAATGVATVIR	1.371875471	2	4.9754
P05544	DSTMEEILEGLK	1.139358972	2	2.94567
P05544	IAELFSDLEER	1.021044778	2	2.72042
P05544	MQQVESSLQPETLK	0.968410548	2	2.58066
P05544	VFSQQADLSR	1.161445112	2	2.487
P05545	**SPA3K Serine protease inhibitor A3K**	**1.165598161**	**0.0262**	**4**
P05545	ALYQAEAFVADFK	1.092997293	2	3.26306
P05545	AVLDVDETGTEGAAATAVTAALK	1.07146625	2	5.44742
P05545	FSISTDYNLEEVLPELGIR	1.247128279	2	3.1398
P05545	IAELFSELDER	1.467437118	2	3.03559
P05765	**RS21 40S ribosomal protein S21**	**1.125468113**	**0.4757**	**3**
P05765	DHASIQMNVAEVDR	1.059072798	2	3.31481
P05765	MGESDDSILR	1.079569264	2	2.97994
P05765	TYGICGAIR	1.13500197	2	3.0551
P06214	**HEM2 Delta_aminolevulinic acid dehydratase**	**0.665268712**	**1E-19**	**5**
P06214	AGCQVVAPSDMMDGR	0.762122143	2	3.13577
P06214	DEQGSAADSEDSPTIEAVR	0.728334897	2	5.83752
P06214	DIQEGADILMVKPGLPYLDMVQEVK	0.78779354	3	4.64615
P06214	VPKDEQGSAADSEDSPTIEAVR	0.772157696	2	5.73066
P06214	YGVNQLEEMLRPLVEAGLR	0.780207293	3	4.40248

P06302	**PTMA Prothymosin alpha**	**0.847861166**	**0.1348**	**3**
P06302	RVAEDDEDDDVETKK	0.801185681	2	5.02914
P06302	VAEDDEDDDVETK	1.095466925	2	3.48457
P06302	VAEDDEDDDVETKK	0.837588582	2	4.58238
P06399	**FIBA Fibrinogen alpha chain**	**0.830275353**	**0.0203**	**6**
P06399	EVVTSDDGSDCGDGMDLGLTHSFSGR	0.643222551	3	3.87309
P06399	GDFANANNFDNTFGQVSEDLR	0.717744068	2	5.69648
P06399	GDKELLIGNEK	0.954062457	2	2.61072
P06399	GLIDEANQDFTNR	0.923151003	2	3.14982
P06399	MADEAASEAHQEGDTR	0.616524953	2	4.16596
P06399	SQLQEGPPEWK	0.77852322	2	2.81461
P06685	**AT1A1 Sodium/potassium_transporting ATPase subunit alpha_1**	**1.103082206**	**0.2025**	**4**
P06685	AVAGDASESALLK	1.171383841	2	3.00524
P06685	AVFQANQENLPILK	1.102473227	2	3.74414
P06685	EQPLDEELKDAFQNAYLELGGLGER	1.013952351	3	3.59852
P06685	LNIPVNQVNPR	1.079357162	2	3.03207
P06687	**AT1A3 Sodium/potassium_transporting ATPase subunit alpha_3**	**1.118591457**	**0.0002**	**3**
P06687	DGPNALTPPPTTPEWVK	1.108026864	2	2.77579
P06687	GVGIISEGNETVEDIAAR	1.128107035	2	4.46011
P06687	QGAIVAVTGDGVNDSPALK	1.116734001	2	4.8093
P06757	**ADH1 Alcohol dehydrogenase 1**	**1.072169826**	**6E-12**	**16**
P06757	AAVLWEPHKPFTIEDIEVAPPK	1.221955607	3	5.58455
P06757	FPLEPLITHVLPFEK	1.441380361	3	4.60416
P06757	GAIFGGFK	1.093639301	2	2.5717
P06757	GALLDGTSR	1.1189688	2	2.84624
P06757	HPESNLCCQTK	0.80011559	2	3.48851
P06757	IDAAAPLDK	1.029981107	2	2.80341
P06757	IIAVDINKDK	1.041968318	2	2.82971
P06757	INEAFDLLR	1.11250077	2	3.66088
P06757	KFPLEPLITHVLPFEK	1.116937856	3	4.75988
P06757	KFPLEPLITHVLPFEKINEAFDLLR	1.519725633	4	4.65175
P06757	MVATGVCR	1.269558808	2	2.49038
P06757	MVATGVCR+Oxidation(0)	1.444041684	2	2.36406
P06757	SDDHAVSGSLFTPLPAVLGHEGAGIVESIGEGVTCVKPGDK	1.235332559	4	8.2233
P06757	VCLIGCGFSTGYGSAVQVAK	1.245621192	2	6.30436
P06757	VIPLFSPQCGK	1.101860899	2	2.62798
P06757	VTPGSTCAVFGLGGVGLSVVIGCK	1.402573317	2	5.24661
P06761	**GRP78 78 kDa glucose_regulated protein**	**1.23287665**	**1E-19**	**30**
P06761	AKFEELNMDLFR	1.165102723	3	4.00088
P06761	DAGTIAGLNVMR	0.942869535	2	3.53968
P06761	DAGTIAGLNVMR+Oxidation(10)	1.255240421	2	2.87661
P06761	DNHLLGTFDLTGIPPAPR	0.972010891	2	4.74585
P06761	ELEEIVQPIISK	0.960960425	2	4.29275
P06761	FEELNMDLFR	1.103205055	2	3.58301
P06761	IEIESFFEGEDFSETLTR	1.116481843	2	5.09407
P06761	IEWLESHQDADIEDFK	1.15391347	2	5.49742
P06761	IEWLESHQDADIEDFKAK	1.134965138	2	2.31976
P06761	IINEPTAAAIAYGLDKR	1.129495594	2	4.23022
P06761	ITITNDQNR	1.173160554	2	2.58406
P06761	ITPSYVAFTPEGER	1.252069129	2	3.82739
P06761	KKELEEIVQPIISK	0.933166486	2	4.57662
P06761	KSDIDEIVLVGGSTR	1.068139989	2	4.27584
P06761	KSQIFSTASDNQPTVTIK	1.134442323	2	5.16088
P06761	LTPEEIER	0.984238258	1	1.9218
P06761	LYGSGGPPPTGEEDTSEKDEL	1.425638336	2	5.20613
P06761	MKETAEAYLGK	1.096342627	2	3.15425
P06761	MKETAEAYLGK+Oxidation(0)	1.185042914	2	2.71836

P06761	NELESYAYSLK	1.235552849	2	3.6203
P06761	NQLTSNPENTVFDAK	1.081033364	2	5.22401
P06761	SDIDEIVLVGGSTR	1.131359996	2	3.79084
P06761	SQIFSTASDNQPTVTIK	1.050326785	2	5.46378
P06761	TFAPEEISAMVLTK	1.088253517	2	4.78528
P06761	TFAPEEISAMVLTK+Oxidation(9)	1.048573332	2	3.49771
P06761	TKPYIQVDIGGGQTK	1.107878988	3	4.15096
P06761	TWNDPSVQQDIK	1.055824557	2	3.87526
P06761	VLEDSDLK	1.082799986	2	2.39971
P06761	VTHAVVTVPAYFNDAQR	1.193052707	2	4.91365
P06761	VYEGERPLTK	1.037663564	2	2.98314
P06866	**HPT Haptoglobin**	**1.157414007**	**0.9981**	**6**
P06866	ATDLKDWVQETMAK	1.142373773	2	2.7945
P06866	CELHYEK	1.25294966	2	2.36053
P06866	GAVSPVGVQPILNK	1.042127245	2	3.99235
P06866	LQTEGDGIYTLNSEK	1.151486391	2	4.31338
P06866	NQLVEIEK	0.933339111	1	2.70688
P06866	SCAVAEYGVYVR	1.101068124	2	3.06088
P07153	**RPN1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 1**	**1.106653118**	**1E-19**	**10**
P07153	ASSFVLALEPELESR	1.096454857	2	4.23024
P07153	AVTSEIAVLQSR	1.318048874	2	3.84404
P07153	FVDHVFDEQVIDSLTVK	0.991160053	2	4.6203
P07153	GEDEEDNNLEVR	1.144023285	2	3.59344
P07153	HFDETVNR	0.915551966	2	2.75677
P07153	LKTEGSDLCDR	1.224843337	3	3.33266
P07153	NIQVDSPYDISR	1.269645943	2	3.37952
P07153	NLVEQHIQDIVVHYTFNK	0.866782301	3	4.88493
P07153	SEDILDYGPFK	1.091521427	2	3.4371
P07153	VTAEVVLAHPGGGSTAR	1.032794935	2	4.66203
P07323	**ENOG Gamma_enolase**	**1.122099668**	**1E-19**	**3**
P07323	AAVPSGASTGIYEALELR	1.322006368	2	5.05395
P07323	GNPTVEVDLHTAK	1.052881989	2	2.76812
P07323	SGETEDTFIADLVVGLCTGQIK	1.100044817	3	4.83842
P07340	**AT1B1 Sodium/potassium_transporting ATPase subunit beta_1**	**1.204008203**	**0.0063**	**2**
P07340	SYEAYVLNIIR	1.531751769	2	2.64703
P07340	VAPPGLTQIPQIQK	1.201891638	2	2.46226
P07379	**PCKGC Phosphoenolpyruvate carboxykinase_ cytosolic [GTP]**	**1.199880882**	**0.2155**	**11**
P07379	AINPENGFFGVAPGTSVK	0.963105276	2	3.49523
P07379	FVEGNAQLCQPEYIHICDGSEEEYGR	1.170236799	3	4.41145
P07379	GLGDVNVEELFGISK	1.271564465	2	3.96584
P07379	IGIELTDSPYVVASMR	1.067219867	2	3.355
P07379	MGTSVLEALGDGEFIK	1.069488125	2	3.55587
P07379	MGTSVLEALGDGEFIK+Oxidation(0)	1.318195671	2	3.85884
P07379	TVIITQEQR	1.234012414	2	2.51903
P07379	VECVGDDIAWMK	1.140735804	2	2.709
P07379	VIQGSLDSLPQEVR	1.278794402	2	4.14271
P07379	YLAAAFPSACGK	1.029329035	2	2.78207
P07379	YLEDQVNADLPYEIER	1.72971945	2	2.82477
P07632	**SODC Superoxide dismutase [Cu_Zn]**	**1.007717758**	**7E-08**	**4**
P07632	DGVANVSIEDR	0.962129224	1	2.79032
P07632	GDGPVQGVIHFEQK	1.171505127	2	3.61196
P07632	HVGDLGNVAAGK	0.96600425	2	3.92121
P07632	VISLSGEHSIIGR	1.166557394	2	3.29178
P07633	**PCCB Propionyl_CoA carboxylase beta chain_ mitochondrial**	**0.909220073**	**4E-05**	**9**
P07633	AFDNDVDALCNLR	1.26492815	2	3.66709
P07633	AYNMLDIIHAVIDER	0.910194073	2	3.71967

P07633	GFVDDIIQPSSTR	1.006967125	2	3.37257
P07633	ICCDLEVLASK	0.990433417	2	2.85103
P07633	IMDQAITVGAPVIGLNDSGGAR	1.005689144	2	3.99946
P07633	IQEGVESLAGYADIFLR	0.98469533	2	4.28661
P07633	LVPELDTVVPLESSK	1.024854117	2	3.79062
P07633	SVTNEDVTQEQLGGAK	0.938535693	2	4.81075
P07633	TVGIVGNQPNVASGCLDINSSVK	0.987629188	2	4.49648
P07687	**HYEP Epoxide hydrolase 1**	**0.77145065**	**1E-19**	**19**
P07687	DIELLYPYK	0.611779801	1	2.35865
P07687	DKEETLPLGDGWWGPGSKPSAK	0.702318886	3	5.29264
P07687	EDESIRPFK	0.772947662	2	2.60809
P07687	EDESIRPFKVETSDEEIKDLHQR	0.71606596	3	5.76
P07687	ENLGQGIMVHK	0.752753063	2	2.47239
P07687	ESGYLHIQATKPDTVGCALNDSPVGLAAYILEK	0.977760594	3	6.62719
P07687	FLGYTEK	0.634681884	1	1.95672
P07687	FLGYTEKDIELLYPYK	0.707210907	3	4.55371
P07687	GGHFAAFEEPK	0.776423668	2	3.46736
P07687	IIPLLTDPK	0.812129561	2	2.41002
P07687	KFVSLAELQ	0.843406607	2	2.73101
P07687	KQVEILNQYPHFK	0.709168964	3	4.61721
P07687	LLAQDIR	1.062656106	2	2.41673
P07687	QVEILNQYPHFK	0.761941987	3	3.63661
P07687	SEYRELEDGGLER	0.724377668	3	3.53322
P07687	SHGLSDEHVFEVICPSIPGYGYSEASSK	0.796782273	3	6.29245
P07687	VETSDEEIK	0.961707145	2	2.4693
P07687	VETSDEEIKDLHQR	0.69734889	2	4.61429
P07687	VFVPTGFSAFPSELLHAPEK	0.667741834	2	4.36904
P07756	**CPSM Carbamoyl_phosphate synthase [ammonia]_ mitochondrial**	**1.17519978**	**1E-19**	**87**
P07756	AADTIGYPVMIR	1.385794688	2	3.68063
P07756	AADTIGYPVMIR+Oxidation(9)	1.593874153	2	3.20642
P07756	AERPDGLILGMGGQTALNCGVELFK	1.153451487	3	6.51702
P07756	AERPDGLILGMGGQTALNCGVELFK+Oxidation(10)	1.15235617	3	4.9769
P07756	AFAISGPFNVQFLVK	1.829143933	2	4.98343
P07756	AFAMTNQILVER	1.142155335	2	4.26855
P07756	AFAMTNQILVER+Oxidation(3)	1.184146881	2	3.75847
P07756	ALENNMSLDEIVK	1.03958628	2	4.66244
P07756	ALENNMSLDEIVK+Oxidation(5)	1.125675426	2	3.92037
P07756	AQTAHIVLEDGTK	0.830137145	2	4.2685
P07756	ATGYPLAFIAAK	1.204488808	2	3.30611
P07756	CEMASTGEVACFGEGIHTAFLK	1.165278825	3	4.86925
P07756	CEMASTGEVACFGEGIHTAFLK+Oxidation(2)	1.160771896	3	5.68054
P07756	CLGLTEAQTR	1.075209089	2	3.6297
P07756	DELGLNK	0.984507324	1	2.22431
P07756	DGSIDLVINLPNNNTK	1.087067968	2	5.47779
P07756	DILNMDK	0.922601662	1	1.94096
P07756	EIEYEVVR	0.88644731	1	2.17758
P07756	EPLFGISTGNIITGLAAGAK	1.378759822	2	5.76389
P07756	ETLMDLGTK	0.963350855	1	2.18081
P07756	EVEMDAVGK	0.874482206	1	2.07544
P07756	FLEEATR	1.073378415	2	2.60958
P07756	FLGVAEQLHNEGFK	1.13283035	2	4.73825
P07756	FVHDNYVIR	1.317533403	3	3.49733
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK	1.280883052	3	5.97234
P07756	GAEVHLVPWNHDFTQMDYDGLLIAGGPGNPALAQPLIQNVK+Oxidation(15)	1.313218786	4	5.22321
P07756	GILIGIQQSFRPR	1.351103492	2	2.39768

P07756	GLNSESVTEETLR	1.235961753	2	4.90722
P07756	GNDVLVIECNLR	1.108939043	2	4.24574
P07756	GQILTMANPIIGNGGAPDTTAR	1.066400072	2	5.9855
P07756	GQILTMANPIIGNGGAPDTTAR+Oxidation(5)	1.071936145	2	5.42398
P07756	GQILTMANPIIGNGGAPDTTARDELGLNK	1.020265071	3	4.16101
P07756	GQNQPVLNITNR	1.066962207	2	4.32179
P07756	GTTITSVLPKPALVASR	1.148456029	2	3.25384
P07756	GYSFGHPSSVAGEVVFNTGLGGYSEALTDPAYK	1.367800133	3	6.38812
P07756	HLPTLEQPIIPSDYVAIK	1.120927231	2	5.59448
P07756	IAPSFAVESMEDALK	1.203647663	2	5.04501
P07756	IAPSFAVESMEDALK+Oxidation(9)	1.072777087	2	2.60833
P07756	IEFEGQSVDFVDPNK	1.181665057	2	5.2604
P07756	IEFEGQSVDFVDPNKQNLIAEVSTK	1.122380743	3	5.28257
P07756	ILDIYHQEACNGCIISVGGQIPNNLAVPLYK	1.321824195	3	5.73916
P07756	IMGTSPLQIDR	1.615623493	2	2.65404
P07756	IMGTSPLQIDR+Oxidation(1)	1.625737346	2	2.96529
P07756	IMGTSPLQIDRAEDR	0.70697663	2	2.42006
P07756	KEPLFGISTGNIITGLAAGAK	1.15222807	2	5.48389
P07756	KTVVVNCNPETVSTDFDECDK	0.404869634	2	4.65234
P07756	LFAEAVQK	1.157560154	2	2.89322
P07756	LFATEATSDWLNANNVPATPVAWPSQEGQNPSLSSIR	1.281843194	4	4.88679
P07756	LRDADPILR	1.154309832	2	3.01713
P07756	LTSIDKWFLYK	1.121350215	2	2.76941
P07756	LYFEELSLER	1.729631976	2	3.5359
P07756	MCHPSVDGFTPR	1.181207827	3	4.75227
P07756	MCHPSVDGFTPR+Oxidation(0)	1.125126641	3	4.03931
P07756	QADAVYFLPITPQFVTEVIK	1.72717222	3	5.01443
P07756	QLFSDKLNEINEK	1.023825147	2	3.65547
P07756	QNLIAEVSTK	1.225815639	2	2.79289
P07756	RFLEEATR	1.131891301	2	2.80717
P07756	RTAVDSGIALLTNFQVTK	1.200306516	2	4.16927
P07756	SAYALGGLGSGICPNK	1.377073234	2	4.93893
P07756	SAYALGGLGSGICPNKETLMDLGTK	1.185578407	2	4.22007
P07756	SFPFVSK	1.13191466	1	2.06943
P07756	SIFSAVLDELK	1.065165794	2	3.97828
P07756	SIFSAVLDELKVAQAPWK	1.493699044	3	3.53515
P07756	SLGQWLQEEK	1.113298612	2	4.10247
P07756	SVGEVMAIGR	1.11863	2	3.7593
P07756	SVGEVMAIGR+Oxidation(5)	1.170008126	2	2.99907
P07756	TAVDSGIALLTNFQVTK	1.223381808	3	6.09045
P07756	TAVDSGIALLTNFQVTKLFAEAVQK	1.779111085	3	4.01003
P07756	TFEESFQK	1.073388873	2	2.52637
P07756	TLGVDFIDVATK	1.138496578	2	4.10881
P07756	TSACFEPSLDYMVTK	1.153427232	2	4.76156
P07756	TSACFEPSLDYMVTK+Oxidation(11)	1.170312493	2	3.97974
P07756	TVLMNPNIASVQTNEVGLK	1.080053303	2	6.30413
P07756	TVLMNPNIASVQTNEVGLK+Oxidation(3)	1.093128136	2	6.05757
P07756	TVVVNCNPETVSTDFDECDK	0.693329813	2	5.78116
P07756	TVVVNCNPETVSTDFDECDKLYFEELSLER	1.249392047	3	5.22531
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK	1.236388518	3	7.24794
P07756	VISHAISEHVEDAGVHSGDATLMLPTQTISQGAIEK+Oxidation(22)	1.213701963	3	6.76799
P07756	VLGTSVESIMATEDR	1.113382792	2	4.82837
P07756	VLGTSVESIMATEDR+Oxidation(9)	1.161348304	2	4.34238
P07756	VLILGSGGLSIGQAGEFDYSGSQAVK	1.096200795	2	5.32272
P07756	VMIGESVDEK	1.129209755	2	3.48661
P07756	VMIGESVDEK+Oxidation(1)	1.1341978	2	3.03701
P07756	VSQEHPVVLTK	1.163951704	2	3.90386

P07756	VVAVDCGIK	1.14118096	2	2.39105
P07756	YMESDGIK	1.082840198	2	2.71498
P07756	YMESDGIK+Oxidation(1)	1.173790405	1	2.24009
P07824	**ARGI1 Arginase_1**	**1.319612785**	**1E-19**	**15**
P07824	ANEQLAAVVAETQK	1.372755078	2	5.33103
P07824	DHGDLAFVDVPNDSPFQIVK	1.232130709	2	6.87653
P07824	DIVYIGLR	1.240172081	2	2.73046
P07824	DVDPGEHYIIK	1.331007837	2	3.09735
P07824	EGLYITEEIYK	1.155561325	2	2.44874
P07824	EGNHKPETDYLKPPK	1.31979235	2	2.80001
P07824	GKFPDVPGFSWVTPCISAK	1.268415567	3	4.70311
P07824	LKETEYNVR	1.391767247	3	3.66586
P07824	NGTISVVLGGDHSMAIGSISGHAR	1.303903621	3	4.40073
P07824	TGLLSGLDIMEVNPTLGK	1.253828633	2	5.8082
P07824	TGLLSGLDIMEVNPTLGK+Oxidation(9)	1.218366695	2	4.68328
P07824	TVNTAVALTLSCFGTK	1.597351602	2	4.7521
P07824	VMEETFSYLLGR	1.675928561	2	3.25469
P07824	YFSMTEVDK	1.274236314	1	2.27196
P07824	YFSMTEVDKLGIGK+Oxidation(3)	1.118099728	2	2.46165
P07871	**THIKB 3_ketoacyl_CoA thiolase B_ peroxisomal**	**0.713513579**	**1E-19**	**15**
P07871	AEELGLPILGVLR	0.764517449	2	4.44025
P07871	AEIVPVTTTVLDDK	0.80322685	2	4.12761
P07871	AEIVPVTTTVLDDKGDR	0.659048752	2	4.02655
P07871	AEIVPVTTTVLDDKGDRK	0.724643726	2	3.59403
P07871	DCLIPMGITSENVAER	0.697170027	2	3.58652
P07871	DCLIPMGITSENVAER+Oxidation(5)	0.718704816	2	2.93319
P07871	DGGSTTAGNSSQVSDGAAAVLLAR	0.773102723	2	6.09779
P07871	IAQFLSGIPETVPLSAVNR	1.202117399	2	2.60835
P07871	QCSSGLQAVANIAGGIR	0.70697663	2	4.32394
P07871	QDAFALASQQK	0.72626031	2	3.33284
P07871	QKQDAFALASQQK	0.696884845	2	4.12029
P07871	SKAEELGLPILGVLR	0.689232928	3	4.24892
P07871	SYAVVGVPPDIMGIGPAYAIPAALQK	0.729453183	2	4.31419
P07871	TITVSQDEGVRPSTTMEGLAK	0.784777703	2	4.27451
P07871	VNPLGGAIALGHPLGCTGAR	0.651786025	2	4.96146
P07872	**ACOX1 Peroxisomal acyl_coenzyme A oxidase 1**	**0.614017235**	**1E-19**	**16**
P07872	AFTTWTANAGIEECR	0.669313322	2	4.10125
P07872	ASATFNPELITHILDGSPENTR	0.626972564	2	4.74864
P07872	ASEAHCHYVVVK	0.889922868	3	4.15646
P07872	EIENLILNDPDFQHEDYNFLTR	0.707610374	2	4.45525
P07872	EIGTHKPLPGITVGDIGPK	0.574092686	3	4.11358
P07872	EVAWNLTSVDLVR	0.588790283	2	3.40482
P07872	EYGISDPEEIMWFK	0.765203478	2	3.36196
P07872	FGYEEMDNGYLK	0.647207554	2	3.5982
P07872	GGDFLEGSIITGAQLSQVNAR	0.668157874	2	5.15751
P07872	GLETTATYDPK	0.665418011	2	3.39936
P07872	INESIGQGDLSELPELHALTAGLK	0.636115074	3	5.30832
P07872	LVEIAAK	0.706536672	1	2.02405
P07872	QSEPEPQILDFQTQQYK	0.612338842	2	4.76811
P07872	SFLVGNAAQSLSK	0.624747856	2	3.85384
P07872	TQEFILNSPTVTSIK	0.633677681	2	4.89097
P07872	YDGNVYENLFEWAK	0.608539867	2	4.62809
P07895	**SODM Superoxide dismutase [Mn]_ mitochondrial**	**0.918713173**	**1E-19**	**3**
P07895	AIWNVINWENVSQR	0.903222386	2	3.90512
P07895	GDVTTQVALQPALK	0.790096412	2	3.44255
P07895	HHATYVNNLNVTEEK	1.176364712	2	4.21489
P07896	**ECHP Peroxisomal bifunctional enzyme**	**0.772881361**	**1E-19**	**21**

P07896	GQGLTGPSLPPGTPVR	0.638412236	2	4.07126
P07896	GWYQYDKPLGR	0.548891366	2	2.74778
P07896	IFNKPVPSLPNMDSVFAEAIAK	0.828795144	3	3.57907
P07896	IGVVVGNCYGFVGNR	0.923959783	2	2.43636
P07896	IIDKPIEPR	0.633362837	2	2.4244
P07896	KGQGLTGPSLPPGTPVR	0.57699035	2	3.89557
P07896	KQYPGVLAPETCVR	0.643438051	2	3.73214
P07896	LCNPPVNAVSPTVIR	0.725604812	2	4.3034
P07896	LGILDAVVK	0.750416256	2	2.91247
P07896	LLEVIPSR	0.626718554	2	2.72852
P07896	QNPDIPQLEPSDYLR	0.654994034	2	3.8005
P07896	QYPGVLAPETCVR	0.695745109	2	3.59297
P07896	TASAQPVSSVGVLGLGTMGR	0.863785442	2	4.61298
P07896	TASAQPVSSVGVLGLGTMGR+Oxidation(17)	0.773647182	2	4.03293
P07896	TISKEEILER	0.555541491	2	2.86702
P07896	VGISVVAVESDPK	0.659730265	2	3.33062
P07896	VGLPEVTLGILPGAR	0.517012001	2	3.34847
P07896	VSDLAGLDVGWK	0.654596079	2	4.21677
P07896	YLSADEALR	0.695002056	2	2.55121
P07896	YSPLGDMLCEAGR	0.607009178	2	4.30915
P07896	YSSPTTIATVMSLSK	1.235494578	2	3.43817
P08009	**GSTM4 Glutathione S_transferase Yb_3**	**1.091168492**	**0.8641**	**5**
P08009	LCYNPDFEK	1.263906719	2	2.79096
P08009	LLLEYTDSSYEEK	1.038637684	2	4.84057
P08009	LLLEYTDSSYEEKR	1.046936109	2	3.82751
P08009	NQVFEATCLDAFPNLK	0.957209602	2	4.52542
P08009	SQWLNEK	1.067769624	2	2.63898
P08010	**GSTM2 Glutathione S_transferase Mu 2**	**0.976347253**	**0.5576**	**15**
P08010	CLDAFPNLKDFVAR	1.084127734	2	2.45433
P08010	IRVDVLENQAMDTR	1.01580497	3	4.28244
P08010	ITYVDFLVYDVLDQHR	1.194972894	2	5.04518
P08010	KKPEYLEGLPEK	0.924351132	3	4.4175
P08010	KPEYLEGLPEK	1.370837536	2	3.48164
P08010	KYSMGDAPDYDR	0.958778812	2	3.32848
P08010	LFLEYTDTSYEDK	1.053615862	2	5.118
P08010	LFLEYTDTSYEDKK	0.957098062	2	4.40394
P08010	LQLAMVCYSPDFER	0.990226444	2	3.51967
P08010	LQLAMVCYSPDFER+Oxidation(4)	1.106704579	2	3.34586
P08010	SQWLSEK	1.14721254	2	2.41802
P08010	VDVLENQAMDTR	0.979119011	2	4.48135
P08010	VDVLENQAMDTR+Oxidation(8)	1.034762894	2	4.03432
P08010	YSMGDAPDYDR	1.025376587	2	2.94254
P08010	YSMGDAPDYDR+Oxidation(2)	1.241147808	2	2.71719
P08011	**MGST1 Microsomal glutathione S_transferase 1**	**1.009685145**	**0.0003**	**4**
P08011	IYHTIAYLTPLPQPNR	0.948473804	2	5.72021
P08011	MMFLSSATAFQR+Oxidation(0)	1.049196288	2	2.55147
P08011	VFANPEDCAGFGK	1.005430881	2	4.69275
P08011	VFANPEDCAGFGKGENAK	0.809506297	2	4.4225
P08122	**chain**	**1.386491744**	**0.0175**	**3**
P08122	DEKSLAYPEGK	1.397576132	2	2.4155
P08122	DGAPGFPGTEGAKGNRGFPGLR	1.426531978	2	2.32739
P08122	GPAGRFGPDGPPGQPGIEGLAGPLGR	1.046337921	2	2.50669
P08290	**ASGR2 Asialoglycoprotein receptor 2**	**1.015765687**	**0.9614**	**2**
P08290	DFQDIQQLDSEENDHQLIGDEEQGSHVQNLR	1.07647039	3	6.28217
P08290	EEQEFVVK	0.975744465	1	1.93437
P08461	**ODP2 Dihydrolipoyllysine_residue acetyltransferase component of pyruvate dehydrogenase complex_ mitochondrial**	**0.959585289**	**0.0004**	**5**

P08461	AAPAAAAAAAPPGPR	0.80459977	2	3.04361
P08461	DVPLGTPLCIIVEK	0.950112249	2	3.02493
P08461	DVPVGSIICITVEKPQDIEAFK	0.706688132	2	4.09604
P08461	GLETIASDVVSLASK	0.874044407	2	4.20219
P08461	VAPTPAGVFIDIPISNIR	1.027826046	2	4.7875
P08503	**ACADM Medium_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.080050035**	**0.0041**	**7**
P08503	AFTGFIVEADTPGIHIGK	0.989827411	2	4.22431
P08503	EEIIPVAPDYDK	0.854993163	2	3.04153
P08503	IYQIYEGTAQIQR	1.066856998	2	4.95122
P08503	KGDEYVINGQK	0.932049433	2	3.6154
P08503	QEPGLGFSFELTEQQK	0.887555863	2	2.6851
P08503	SGEYPFPLIK	0.968516212	2	2.57755
P08503	TRPTVAAGAVGLAQR	0.976491703	2	4.1779
P08541	**UD2B2 UDP_glucuronosyltransferase 2B2**	**2.003205345**	**1E-19**	**9**
P08541	DELQNHFIK	1.924166689	2	2.64171
P08541	FEIFSTSISKDELQNHFIK	1.448763525	3	3.55588
P08541	FILPPSYVPVILSGLAGK	2.56778364	3	5.91516
P08541	GAAVSLNIR	3.239138601	2	2.3769
P08541	GHEVTVLKPSAYFFLDPK	2.126997171	3	4.32887
P08541	HKEWDTFYSEILGRPTTVDETMSK	1.609466506	3	4.63379
P08541	LLDVWTYELPR	2.56924966	2	3.84913
P08541	SYWDLK	1.751184258	2	2.33312
P08541	VEIWLIR	1.882540675	2	2.76257
P08542	**UDB17 UDP_glucuronosyltransferase 2B17**	**1.038813872**	**0.0002**	**6**
P08542	EIINNPFYK	0.828861631	1	2.10229
P08542	FETFPTSVSKDELENYFIK	1.045729047	2	4.06619
P08542	KWDPFYSEILGRPTTLAETMGK	1.442711705	2	4.04321
P08542	LVDVWTYELQR	1.170671628	2	3.34658
P08542	NAVWLSTIHHDQPMKPLDK	1.356197207	3	3.67979
P08542	WDPFYSEILGRPTTLAETMGK	1.162465049	2	4.08456
P08649	**CO4 Complement C4**	**1.060661369**	**0.9333**	**2**
P08649	SLEIPGSSDPNVIPDGDFSSFVR	1.126778966	2	3.15712
P08649	VTASEPLETLGSEGALSPGGVASLLR	1.119631384	2	2.96551
P08661	**MBL2 Mannose_binding protein C**	**0.889280217**	**0.7412**	**2**
P08661	ALCSELQGTVATPR	0.847113985	2	2.5405
P08661	TENVFEDLTGNR	1.031931473	2	2.77853
P08683	**CP2CB Cytochrome P450 2C11**	**0.96509295**	**0.0007**	**14**
P08683	DIDTTPAISGFGHLPPFYEACFIPVQR	0.829436194	3	4.98646
P08683	EALVDLGEEFSGR	1.011711186	2	3.71539
P08683	EHQESLDKDNPR	0.900743532	2	3.99545
P08683	FDYKDPTFLNLMHR	1.080554769	3	4.86114
P08683	GTNVIVSLSSILHDDKEFPNPEK	0.857679399	2	5.09761
P08683	ICAGEALAR	0.923731453	2	3.12089
P08683	LPPGPTPLPIIGNTLQIYMK	1.127077509	2	3.28221
P08683	NYVLEK	0.725528262	1	2.06439
P08683	SQMPYTDAVVHEIQR	0.910107257	2	3.94216
P08683	SQMPYTDAVVHEIQR+Oxidation(2)	0.79841571	2	3.69887
P08683	VKEHQESLDKDNPR	1.074518018	3	5.02415
P08683	VQEEIER	0.910504559	2	2.62616
P08683	YGLLLLLK	1.585987545	2	3.18896
P08683	YIDLVPTNLPHLVTR	0.827756189	2	4.03654
P08733	**MLRV Myosin regulatory light chain 2_ ventricular/cardiac muscle isoform**	**1.248097903**	**0.9166**	**2**
P08733	GADPEETILNAFK	1.258984819	2	2.58905
P08733	NLVHIITHGEEKD	1.183132503	2	3.34575
P09034	**ASSY Argininosuccinate synthase**	**1.647181805**	**1E-19**	**16**

P09034	APNTPDVLEIEFK	2.028774063	2	3.4704
P09034	DGTTHSTSLDLFMYLNEVAGK	2.267538855	2	5.92603
P09034	EFVEEFIWPAVQSSALYEDR	1.887086025	3	5.71584
P09034	EQGYDVIAYLANIGQK	1.989636856	2	2.33856
P09034	FAELVYTGFWHSPECEFVR	1.480715277	2	4.04209
P09034	FELTCYSLAPQIK	2.149241269	2	4.26078
P09034	GRNDLMEYAK	1.759695505	2	3.01792
P09034	GRNDLMEYAK+Oxidation(5)	1.792122568	2	2.58016
P09034	IDIVENR	1.528306936	2	2.40713
P09034	KVFIEDVSK	1.4277292	3	3.3453
P09034	NDLMEYAK	1.694517212	2	2.5351
P09034	SPWSMDENLMHISYEAGILENPK	1.694618975	3	5.76887
P09034	TQDPAKAPNTPDVLEIEFK	1.614458782	2	4.88041
P09034	TQDPAKAPNTPDVLEIEFKK	1.722395552	3	4.42726
P09034	VFIEDVSK	1.647901908	2	2.91569
P09034	VQVSVFK	1.766586147	1	2.05468
P09041	**PGK2 Phosphoglycerate kinase 2**	**1.039164564**	**1**	**3**
P09041	FHVEEEGK	1.000211082	1	2.43788
P09041	LGDVYVNDAFGTAHR	1.048317897	3	4.28295
P09041	VSHVSTGGGASLELLEGK	1.034117486	2	5.66092
P09117	**ALDOC Fructose_bisphosphate aldolase C**	**1.393948931**	**4E-10**	**2**
P09117	VLAAVYK	1.356682706	2	2.64218
P09117	YSPEEIAMATVTALR	1.159486376	2	2.43262
P09139	**SPYA Serine__pyruvate aminotransferase_ mitochondrial**	**1.440421193**	**9E-08**	**2**
P09139	IGLLGYNATTENADR	1.440276695	2	3.36369
P09139	VLNAPPGISLISFNDK	1.451390809	2	2.79901
P09367	**SDHL L_serine dehydratase/L_threonine deaminase**	**1.311843967**	**0.0121**	**3**
P09456	**KAP0 cAMP_dependent protein kinase type I_alpha regulatory subunit**	**1.038918681**	**0.0019**	**2**
P09456	FERVLGPCSDILK	0.318384202	2	2.37866
P09456	LTVADALEPVQFEDGQK	1.18594695	2	3.83237
P09495	**TPM4 Tropomyosin alpha_4 chain**	**1.148175661**	**0.0025**	**13**
P09495	AEGDAAALNR	0.817017445	2	2.37429
P09495	EDKYEEEIK	0.983529762	1	2.92953
P09495	EENVGLHQTLDQTLNELNCI	1.504950154	2	4.95796
P09495	IQALQQQADDAEDR	1.196069459	2	4.40027
P09495	IQLVEEELDR	1.11070041	2	3.42217
P09495	IQLVEEELDRAQER	0.973660038	2	2.68907
P09495	KLVILEGELER	1.251534268	3	3.48331
P09495	LEEAEKAADESER	1.086911598	2	3.91638
P09495	LVILEGELER	1.209965389	2	2.7667
P09495	MEIQEMQLK	0.80188551	2	2.62533
P09495	RIQLVEEELDR	1.005543478	2	2.7144
P09495	YEEEIK	1.199192222	1	1.92017
P09495	YSEKEDKYEEEIK	0.656693077	2	4.20341
P09527	**RAB7A Ras_related protein Rab_7a**	**1.46467339**	**2E-08**	**3**
P09527	GADCCVLVFDVTAPNTFK	1.437989983	2	4.52464
P09527	TLDSWRDEFLIQASPR	1.082971297	2	2.36226
P09527	VIILGDSGVGK	1.185495186	2	2.71133
P09605	**KCRS Creatine kinase S_type_ mitochondrial**	**1.37077605**	**0.8311**	**2**
P09605	GTGGVDTAAVADVYDISNIDR	1.32391193	2	3.99974
P09605	LSEMTEQDQQR	1.47678754	2	2.87406
P09606	**GLNA Glutamine synthetase**	**1.415919205**	**1E-19**	**5**
P09606	CIEEAIDK	1.164532215	2	2.52721
P09606	ITGTNAEVMPAQWEFQIGPCEGIR	1.367188699	2	4.37536
P09606	LTGFHETSNINDFSAGVANR	1.376395873	2	5.78821
P09606	TCLLNETGDEPFQYK	1.44614563	2	4.97161

P09606	TCLLNETGDEPFQYKN	2.146609784	2	4.62527
P09811	**PYGL Glycogen phosphorylase_ liver form**	**0.950240761**	**2E-08**	**19**
P09811	DFSELEPDKFQNK	0.868493139	2	3.50535
P09811	DGVGTVFDAFPDQVAIQLNDTHPALAIPELMR	1.018942318	3	4.93877
P09811	DLSQLTK	0.756731916	1	2.09888
P09811	EGWQVEEADDWLR	0.862938258	2	3.32008
P09811	GIVGVENVAELK	0.894644831	2	3.06156
P09811	GIVGVENVAELKK	1.053175314	2	2.88879
P09811	HLQIIYEINQK	0.923831612	2	3.44767
P09811	INPSSMFDVHVK	0.972985958	2	2.69644
P09811	LVIDQIDNGFFSPNQPDLFK	1.050455903	3	4.57253
P09811	LVTSVAEVVNNDPMVGSK	1.099932923	2	2.81257
P09811	MSLIEEEGGKR	1.093543736	2	2.74615
P09811	TFAYTNHTVLPEALER	0.959830248	2	3.72269
P09811	VDDVAALDK	0.979711014	2	2.34852
P09811	VDDVAALDKK	0.834882299	3	3.46648
P09811	VFADYEAYVK	0.802914285	1	2.22267
P09811	VIPATDLSEQISTAGTEASGTGNMK	0.935023471	2	6.07575
P09811	VLYPNDNFFEGK	0.9253168	2	3.10938
P09811	WLLLCNPGLADLIAEK	1.014496268	3	4.91197
P09811	YEYGIFNQK	1.085545142	1	2.45306
P09812	**PYGM Glycogen phosphorylase_ muscle form**	**0.897725192**	**0.0881**	**2**
P09812	NLAENISR	0.89805498	1	2.5304
P09812	QIIEQLSSGFFSPK	0.996042536	2	3.6396
P09875	**UD2B1 UDP_glucuronosyltransferase 2B1**	**0.680167333**	**1E-19**	**6**
P09875	ANVVASALAQIPQK	0.454791991	3	4.09168
P09875	ESSINFEIYSVPLSK	1.030681527	2	2.70575
P09875	FSGGLPLPPSYVPVVLSELSDR	0.6943977	3	4.73414
P09875	IILNELAQR	0.527722379	2	2.85629
P09875	SDLEYSFAK	0.553655327	2	2.3952
P09875	VDFSILSTTGLLTALK	0.606263846	2	4.40457
P09895	**RL5 60S ribosomal protein L5**	**1.114194151**	**0.4832**	**4**
P09895	GAVDGGLSIPHSTK	1.114380377	2	4.19612
P09895	NNVTPDMMEEMYK	0.900974809	2	2.96021
P09895	RFPGYDSESK	1.127914081	2	2.70129
P09895	YLMEEDEDAYKK	0.93795578	2	3.06726
P0C0S7	**H2AZ Histone H2A.Z**	**0.876436291**	**1E-19**	**2**
P0C0S7	ATIAGGGVIPHIHK	0.793448865	2	3.2025
P0C0S7	GDEELDSLIK	0.865010803	2	3.06284
P0C2X9	**AL4A1 Delta_1_pyrroline_5_carboxylate dehydrogenase_ mitochondrial**	**0.910529503**	**6E-06**	**15**
P0C2X9	AIEAAVLAR	1.017276912	2	2.35292
P0C2X9	ALNDLKDQTEAIPCVVGDEEVWTSDVR	0.916573745	3	5.34308
P0C2X9	DQTEAIPCVVGDEEVWTSDVR	0.830105596	2	4.43744
P0C2X9	EAGLPPNVIQFVPADGPTFGDTVTSSEHLCGINFTGSVPTFK	0.902121901	3	3.73458
P0C2X9	EEIFGPVLTVYVYPDEK	1.024858323	2	3.14096
P0C2X9	ETLQLVDSTTSYGLTGAVFAQDK	1.0430435	2	5.17611
P0C2X9	KEWDLKPVADR	0.894396195	2	3.05046
P0C2X9	LYVPQSLWPQIK	1.340825938	2	3.33873
P0C2X9	NAAGNFYINDK	1.387517163	2	2.88047
P0C2X9	NFHFVHSSADVDSVVSGTLR	1.125952576	2	5.13643
P0C2X9	SAFEYGGQK	1.011213532	2	2.53826
P0C2X9	SSPSLSILAGGQCNESVGYFVEPCIIESK	0.940789009	3	5.11982
P0C2X9	STGSVVGQQPFGGAR	0.944316635	2	4.45013
P0C2X9	VANEPILAFTQGSPER	1.084987728	2	5.37271
P0C2X9	YQLSPFNHGHK	1.303758227	2	2.92388
P0C5H9	**MANF Mesencephalic astrocyte_derived neurotrophic factor**	**1.124569727**	**0.9871**	**5**

P0C5H9	DRDVTFSPATIEEELIK	0.95560635	2	4.51081
P0C5H9	DVTFSPATIEEELIK	0.980978386	2	3.17285
P0C5H9	IINEVSKPLAHHIPVEK	1.126366077	3	3.65737
P0C5H9	ILDDWGEMCK	0.981307355	2	2.97863
P0C5H9	QIDLSTVDLKK	0.910460142	2	2.88173
P10111	**PPIA Peptidyl_prolyl cis_trans isomerase A**	**0.992473269**	**5E-12**	**10**
P10111	EGMSIVEAMER	0.842472728	2	2.63675
P10111	FEDENFILK	0.920213778	2	3.35598
P10111	HTGPGILSMANAGPNTNGSQFFICTAK	1.214412836	3	6.1487
P10111	IIPGFMCQGGDFTR	1.023335846	2	2.59665
P10111	KITISDCGQL	1.301982788	2	3.19316
P10111	SIYGEKFEDENFILK	0.801992348	2	4.39976
P10111	TEWLDGK	0.942679719	2	2.31304
P10111	VCFELFADK	1.14968609	2	3.41076
P10111	VCFELFADKVPK	0.978142785	3	3.82748
P10111	VKEGMSIVEAMER	1.058759837	2	2.81733
P10536	**RAB1B Ras_related protein Rab_1B**	**1.028140158**	**0.8582**	**3**
P10536	MGPGAASGGERPNLK	0.815929236	2	3.37291
P10536	NATNVEQAFMTMAAEIK+Oxidation(11)	1.027397157	2	3.4369
P10536	NATNVEQAFMTMAAEIK+Oxidation(9)	1.027397157	2	3.86406
P10633	**CP2D1 Cytochrome P450 2D1**	**0.988471082**	**6E-12**	**3**
P10633	SQGVILASYGPEWR	0.501114066	2	4.28449
P10633	TFMALLDNLLAENR	0.958270561	2	3.54045
P10633	YGDVFSLQK	0.990759279	2	2.79462
P10634	**CP2DQ Cytochrome P450 2D26**	**1.09839336**	**1E-19**	**17**
P10634	ACLGEPLAR	1.043018649	2	2.42703
P10634	AVSNVIASLVYAR	1.497882996	2	4.10439
P10634	DMTDAFLAEMQK	0.898914957	2	4.18845
P10634	EAEHPFNPSILLSK	0.865036012	2	2.32553
P10634	ELLVTYGEDTADRPLLPIYNHLGYGNK	0.991776287	3	5.50769
P10634	FADIVPTNIPHMTSR	0.871301364	2	3.65109
P10634	FEYEDPFFNR	1.127303457	2	2.54424
P10634	FHPEHFLDAQGNFVK	1.108147382	2	4.28254
P10634	GNPESSFNDENLR	1.153134264	2	4.27573
P10634	GTTLIPNLSSVLK	1.105686105	2	2.31188
P10634	GTTLIPNLSSVLKDETVWEKPLR	0.877150123	2	4.0284
P10634	GVVLAPYGPEWR	0.913994066	2	3.50425
P10634	LNSFIALVDK	1.204063215	2	2.87291
P10634	RFEYEDPFFNR	1.009121165	3	3.30915
P10634	SLEQWVTEEAGHLCDTFAK	1.028787188	2	4.5506
P10634	SWDPAQPPR	1.084526785	2	2.5022
P10634	VHEEIDEVIGQVR	0.994985968	2	4.19711
P10719	**ATPB ATP synthase subunit beta_ mitochondrial**	**1.251305201**	**3E-13**	**30**
P10719	AHGGYSVFAGVGER	0.934921885	2	4.06566
P10719	AIAELGIYPAVDPLDSTSR	1.017060295	2	4.97554
P10719	EGNDLYHEMIESGVINLK	0.930015505	2	4.91859
P10719	FLSQPFQVAEVFTGHMGK	1.183041506	2	3.84749
P10719	FTQAGSEVSALLGR	0.998817436	2	4.66546
P10719	GFQQILAGDYDHLPEQAFYMVGPIEEAVAK	1.292619965	3	5.20985
P10719	IGLFGGAGVGK	0.987826964	2	2.91816
P10719	ILQDYK	1.078438022	1	2.18793
P10719	IMDPNIVGSEHYDVAR	1.146628553	2	4.60339
P10719	IMDPNIVGSEHYDVAR+Oxidation(1)	0.970081239	2	4.09585
P10719	IMNVIGEPIDER	1.152518036	2	3.49167
P10719	IMNVIGEPIDER+Oxidation(1)	1.249892371	2	3.41598
P10719	IPSAVGYQPTLATDMGTMQER	1.50843574	2	5.11105
P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(14)	1.486698468	2	3.60815

P10719	IPSAVGYQPTLATDMGTMQER+Oxidation(17)	1.486698468	2	4.28651
P10719	LVLEVAQHLGESTVR	1.011618732	2	4.67235
P10719	QFAPIHAEAPEFIEMSVEQEILVTGIK	0.938608953	3	4.66544
P10719	SLQDIIAILGMDELSEEDKLTVSR	0.988083573	4	5.2123
P10719	SLQDIIAILGMDELSEEDKLTVSR+Oxidation(10)	1.074602906	3	4.01515
P10719	TIAMDGTEGLVR	0.991448056	2	3.40632
P10719	TIAMDGTEGLVR+Oxidation(3)	0.998773281	2	3.01524
P10719	TREGNDLYHEMIESGVINLK	0.986811236	2	6.02625
P10719	TVLIMELINNVAK	0.969965278	2	4.68446
P10719	TVLIMELINNVAK+Oxidation(4)	0.947267386	2	3.20977
P10719	VALTGLTVAEYFR	1.485213399	2	3.78607
P10719	VALVYGQMNEPPGAR	1.045515303	2	4.2203
P10719	VALVYGQMNEPPGAR+Oxidation(7)	1.037999086	2	2.85746
P10719	VLDSGAPIK	1.005906497	2	2.83192
P10719	VLDSGAPIKIPVGPETLGR	0.95852787	3	5.11197
P10719	VVDLLAPYAK	0.999334453	2	3.10671
P10760	**SAHH Adenosylhomocysteinase**	**1.139827856**	**3E-13**	**16**
P10760	ALDIAENEMPGLMR	1.184225206	2	4.34191
P10760	ATDVMIAGK	1.002826782	1	1.90328
P10760	DGPLNMILDDGGDLTNLIHTK	1.096152456	2	5.65661
P10760	DGPLNMILDDGGDLTNLIHTK+Oxidation(5)	1.028071475	3	4.40284
P10760	FDNLYGCR	1.136647502	2	2.68631
P10760	GETDEEYLWCIEQTLHFK	1.25074035	2	4.41574
P10760	GISEETTTGVHNLYK	1.084257212	2	4.1665
P10760	IILLAEGR	1.457490738	2	2.40728
P10760	KLDEAVAEAHLGK	1.100774496	3	4.99554
P10760	LDEAVAEAHLGK	1.199628466	2	3.79647
P10760	RATDVMIAGK	1.197698768	2	2.66402
P10760	SKFDNLYGCR	1.215761491	2	2.86388
P10760	VAVVAGYGDVGK	1.237332296	2	3.68172
P10760	VNIKPQVDR	1.030709758	2	2.74905
P10760	WLNENAVEK	1.129523502	2	2.82622
P10760	WSSCNIFSTQDHAAAAIAK	1.237969417	2	5.05698
P10860	**DHE3 Glutamate dehydrogenase 1_ mitochondrial**	**0.924603533**	**0.0053**	**29**
P10860	ALASLMTYK	1.251833456	2	3.06579
P10860	CAVVDVPFGGAK	1.228588537	2	3.00041
P10860	CVGVGESDGSIWNPDGIDPK	0.897905867	2	5.17605
P10860	DDGSWEVIEGYR	0.901368448	2	3.89267
P10860	DIVHSGLAYTMER	0.971538138	2	3.37566
P10860	DIVHSGLAYTMER+Oxidation(10)	1.050056396	2	2.42727
P10860	DSNYHLLMSVQESLER	0.980415016	2	3.10739
P10860	EDDPNFFK	1.226261316	1	2.12518
P10860	GASIVEDKLVEDLK	0.902094674	2	3.13382
P10860	GFIGPGIDVPAPDMSTGER	0.990934309	2	5.33373
P10860	GFIGPGIDVPAPDMSTGER+Oxidation(13)	1.018376353	2	4.89171
P10860	HGGTIPVVPTAEFQDR	1.020781411	2	4.66855
P10860	IIAEGANGPTTPEADK	0.995595761	2	5.12161
P10860	IIAEGANGPTTPEADKIFLER	0.843902682	2	4.64327
P10860	KGFIGPGIDVPAPDMSTGER	0.993915869	2	4.98003
P10860	KGFIGPGIDVPAPDMSTGER+Oxidation(14)	0.907002396	2	4.14138
P10860	LQHGSILGFPK	0.922317624	2	2.73973
P10860	MVEGFFDR	1.025882212	2	2.71835
P10860	MVEGFFDR+Oxidation(0)	0.980543903	2	2.74262
P10860	NLNHVSYGR	0.897739255	2	2.36716
P10860	NYTDNELEK	0.933031155	2	2.48778
P10860	RDDGSWEVIEGYR	1.059452013	2	4.26359
P10860	RFTMELAK	1.140146116	2	2.32058

P10860	TAAYVNAIEK	1.094839188	2	3.33783
P10860	TFVVQGFGNVGLHSMR	1.268009184	2	4.02515
P10860	TFVVQGFGNVGLHSMR+Oxidation(14)	0.833645998	2	2.86318
P10860	VYEGSILEADCDILIPAASEK	0.929435817	3	6.09714
P10860	YNLGLDLR	0.975424804	2	3.2503
P10860	YSTDVSVDEVK	1.000116849	2	3.55404
P10867	**GGLO L_gulonolactone oxidase**	**0.856430477**	**4E-06**	**6**
P10867	GDDILLSPCFQR	0.792857216	1	2.01663
P10867	LDPTGMFLNSYLEK	0.892500496	2	4.23529
P10867	LDYWLAYETIMK	1.000592693	2	3.97834
P10867	NADVFQAAR	0.885300121	2	2.75382
P10867	TYGCSPEVYYQPTSVEEVR	0.826061844	2	4.83521
P10867	VVAHYPVEVR	0.852518874	2	2.77746
P10868	**GAMT Guanidinoacetate N_methyltransferase**	**1.119088628**	**0.4553**	**4**
P10868	EHWIIECNDGVFQR	1.028519125	2	4.50167
P10868	ENICTEVMALVPPADCR	0.882276597	2	2.36402
P10868	YTDITAMFEETQVPALLEAGFQR	1.078807386	3	4.62068
P10868	YYAFPQMITPLVTK	0.716381747	2	2.74588
P10888	**COX41 Cytochrome c oxidase subunit 4 isoform 1_ mitochondrial**	**1.176713469**	**1E-19**	**4**
P10888	DYPLPDVAHVK	0.928201304	2	2.55961
P10888	IQFNESFAEMNK	1.194846355	2	3.63557
P10888	SEDYALPSYVDR	1.158536696	2	3.79781
P10888	VNPIQGFSAK	1.106946202	1	1.95289
P11030	**ACBP Acyl_CoA_binding protein**	**1.408525932**	**1E-16**	**4**
P11030	QATVGDVNTDRPGLLDLK	1.36609379	2	3.49085
P11030	TQPTDEEMLFIYSHFK	1.609264356	2	4.20891
P11030	TYVEKVEELK	0.919777255	2	2.32323
P11030	WDSWNK	1.031085728	1	2.0451
P11232	**THIO Thioredoxin**	**0.921771818**	**0.342**	**2**
P11232	EAFQEALAAAGDK	0.899950437	2	4.00479
P11232	VGEFSGANK	1.074726416	2	2.77732
P11240	**COX5A Cytochrome c oxidase subunit 5A_ mitochondrial**	**1.069591998**	**0.0402**	**5**
P11240	EIYPYVIQELRPTLNELGISTPEELGLDK	0.186500215	3	6.36189
P11240	EIYPYVIQELRPTLNELGISTPEELGLDKV	1.449206924	3	7.085
P11240	GMNTLVGYDLVPEPK	1.06035516	2	3.67895
P11240	LNDFASAVR	0.951363528	2	3.21372
P11240	RLNDFASAVR	1.071312423	2	2.73666
P11348	**DHPR Dihydropteridine reductase**	**1.119061763**	**2E-15**	**10**
P11348	AALDGTPGMIGYGMAK	1.074792842	2	3.55316
P11348	EGGLLTLAGAK	0.957605296	2	2.72901
P11348	GAVHQLCQSLAGK	1.38861815	2	3.85914
P11348	MTDSFTEQADQVTAEVGK	1.13225138	2	5.36276
P11348	MTDSFTEQADQVTAEVGK+Oxidation(0)	1.014854276	2	5.75007
P11348	NSGMPSGAAAIAVLPVTLDTPMNR	1.008416723	2	5.51986
P11348	NSGMPSGAAAIAVLPVTLDTPMNR+Oxidation(3)	0.970671139	2	3.92542
P11348	QSIWTSTISSHLATK	1.062369652	2	3.47213
P11348	RPNSGSLIQVVTTDGK	1.206301968	2	3.71083
P11348	VDAILCVAGGWAGGNAK	1.113468617	2	4.05102
P11442	**CLH Clathrin heavy chain 1**	**1.106366358**	**0.552**	**31**
P11442	AHIAQLCEK	1.056111801	1	2.22511
P11442	ALEHFTDLYDIK	0.958260509	3	3.99356
P11442	AVDVFFPPEAQNDFPVAMQISEK	1.016956004	2	2.6707
P11442	FDVNTSAVQVLIEHIGNLDR	1.034206979	3	4.11058
P11442	FNALFAQGNYSEAAK	0.986164879	2	4.35935
P11442	GQCDLELINVCNENSLFK	1.002042907	2	5.22617
P11442	GQFSTDELVAEVEK	1.015689312	2	4.15261
P11442	GQFSTDELVAEVEKR	0.877892152	2	3.46663

P11442	IHEGCEEPATHNALAK	1.111737842	2	5.20139
P11442	ISGETIFVTAPHEATAGIIGVNR	1.095526891	2	5.21374
P11442	IYIDSNNNPER	0.942925806	2	3.23465
P11442	KFDVNTSAVQVLIEHIGNLDR	1.049408486	3	5.84506
P11442	KFNALFAQGNYSEAAK	0.893032335	2	4.17144
P11442	LAELEEFINGPNNAHIQQVGDR	0.953569408	2	4.95949
P11442	LHIIEVGTPPTGNQPFPK	0.997407119	2	4.29717
P11442	LPVVIGGLLDVDCSEDVIK	1.076076529	2	4.08267
P11442	LTDQLPLIIVCDR	1.097766438	2	3.09415
P11442	MAVRNNLAGAEELFARK+Oxidation(0)	1.082461326	2	2.32133
P11442	NLQNLLILTAIK	1.116461572	2	4.21254
P11442	NNLAGAEELFAR	0.908260719	2	4.02265
P11442	NNRPSEGPLQTR	1.040322242	3	4.09894
P11442	RPLIDQVVQTALSETQDPEEVSVTVK	1.014986484	3	6.50088
P11442	SVDPTLALSVYLR	1.107101874	2	2.98997
P11442	SVNESLNNLFITEEDYQALR	1.072670544	2	4.49644
P11442	TLQIFNIEMK	1.122721503	2	2.79051
P11442	TSIDAYDNFDNISLAQR	1.079035645	2	4.24445
P11442	VDKLDASESLR	1.021992014	2	2.45173
P11442	VGEQAQVVIIDMNDPSNPIR	1.022798729	2	4.0766
P11442	VIQCFAETGQVQK	1.110137745	2	4.1028
P11442	VSQPIEGHAASFAQFK	1.064127948	2	4.23661
P11442	WLLLTGISAQQNR	1.213982951	2	2.96393
P11497	**ACACA Acetyl_CoA carboxylase 1**	**1.512981686**	**8E-14**	**5**
P11497	GGSWVVIDPTINPR	1.528852465	2	2.93255
P11497	GSVLEPEGTVEIK	1.698504305	2	2.64811
P11497	ITSENPDEGFKPSSGTVQELNFR	1.616964179	3	4.01538
P11497	TLRDPSLPLLELQDIMTSVSGR	1.333395394	3	3.9537
P11497	VQQAELHTGSLPQIQSTALR	0.947240566	3	3.6202
P11507	**AT2A2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2**	**1.004062419**	**1**	**6**
P11507	DIVPGDIVEIAVGDKVPADIR	1.00167254	2	2.79958
P11507	IGIFGQDEDVTSK	1.004794596	2	2.97166
P11507	IRDEMVATEQER	0.989713295	2	3.15128
P11507	LDEFGEQLSK	1.144813203	2	2.32801
P11507	TASEMVLADDNFSTIVAAVEEGR	1.009009168	3	3.71279
P11507	VDQSILTGESVSVIK	1.068077354	2	4.10658
P11598	**PDIA3 Protein disulfide_isomerase A3**	**1.003913368**	**2E-06**	**25**
P11598	DASVVGFFR	1.110047578	2	2.37527
P11598	DGEEAGAYDGPR	1.025456281	2	3.30388
P11598	DLFSDGHSEFLK	0.875566169	2	2.51279
P11598	EATNPPIIQEEKPK	0.93679067	2	3.65639
P11598	ELNDFISYLQR	0.922000014	2	2.65313
P11598	EYDDNGEGITIFRPLHLANK	1.002839434	2	4.47825
P11598	FAHTNVESLVK	1.266842022	2	2.69624
P11598	FIQESIFGLCPHMTEDNKDLIQGK	1.043579371	3	4.86536
P11598	FISDKDASVVGFFR	1.15736883	2	4.22607
P11598	FLQEYFDGNLK	1.023586315	2	3.50307
P11598	FLQEYFDGNLKR	1.041139043	2	3.13786
P11598	FVMQEEFSR	1.191884778	2	2.67988
P11598	IFRDGEEAGAYDGPR	0.941739676	2	3.27863
P11598	LAPEYEAAATR	1.009470663	2	3.23146
P11598	LNFAVASR	1.392635867	2	2.44914
P11598	LSKDPNIVIAK	1.041559401	3	4.0165
P11598	MDATANDVPSPYEVK	1.175164898	2	4.28889
P11598	MDATANDVPSPYEVK+Oxidation(0)	1.169596607	2	4.16164
P11598	QAGPASVPLRTEDEFK	0.970312204	2	2.45539
P11598	RLAPEYEAAATR	0.945630683	2	3.82363

P11598	SEPIPETNEGPVK	1.05875321	2	3.18496
P11598	TFLDAGHK	1.073705152	2	2.59197
P11598	TFSHELSDFGLESTTGEIPVVAIR	1.156609686	2	5.9575
P11598	VDCTANTNTCNK	2.127785209	2	4.25445
P11598	YGVSGYPTLK	1.037586671	2	3.07815
P11610	**CD1D2 Antigen_presenting glycoprotein CD1d2**	**0.86449973**	**0.353**	**2**
P11610	DIQELVKMMSPK+Oxidation(7)	0.86449973	2	2.57732
P11610	DIQELVKMMSPK+Oxidation(8)	0.86449973	2	2.44676
P11711	**CP2A1 Cytochrome P450 2A1**	**0.929455717**	**1E-19**	**6**
P11711	GEQATYNTLFK	0.935901891	2	2.62691
P11711	GTDVFPILGSLMTDPK	0.738046236	2	3.34395
P11711	ILEEAGYLIK	0.652055916	2	2.31033
P11711	LEDINESPKPLGFTR	0.929906983	2	3.5059
P11711	TVSNVISSIVFGER	0.694930479	2	3.58015
P11711	VHEEIEQVIGR	0.719305748	2	3.02198
P11714	**CP2D9 Cytochrome P450 2D9**	**0.913846831**	**0.9735**	**2**
P11714	GNPESSFNDENLLMVVR	0.980415016	2	2.67546
P11714	VQQEIDEVIGQVR	0.951066084	2	4.8384
P11862	**GAS2 Growth arrest_specific protein 2**	**1.054342483**	**0.4459**	**2**
P11862	EIEQEETLSAPSPSPSPSSK	1.144360778	2	4.0178
P11862	LDNGALLCQLAATVQEK	0.96220193	2	3.86493
P11884	**ALDH2 Aldehyde dehydrogenase_ mitochondrial**	**0.967381442**	**1E-19**	**24**
P11884	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK	0.196491249	3	4.27599
P11884	EEIFGPVMQILK	0.853597523	2	3.42229
P11884	EEIFGPVMQILK+Oxidation(7)	0.837613647	2	2.85709
P11884	ELGEYGLQAYTEVK	0.881049902	2	4.4711
P11884	GYFIQPTVFGDVK	0.873166869	2	4.0773
P11884	KTFPTVNPSTGEVICQVAEGNKEDVDK	0.855029951	3	6.42725
P11884	LGPALATGNVVVMK	0.999931719	2	3.41518
P11884	LGPALATGNVVVMK+Oxidation(12)	0.97750493	2	3.62352
P11884	LLCGGGAAADR	1.088475289	2	3.32116
P11884	RVTLELGGK	0.72670914	2	2.78252
P11884	TEQGPQVDETQFK	0.916428277	2	4.57507
P11884	TEQGPQVDETQFKK	0.82400489	2	2.91465
P11884	TFPTVNPSTGEVICQVAEGNK	1.251734967	2	5.1005
P11884	TFPTVNPSTGEVICQVAEGNKEDVDK	0.838289297	2	4.25493
P11884	TFVQEDVYDEFVER	0.917180542	2	5.2426
P11884	TIEEVVGR	0.867014684	2	2.91617
P11884	TIPIDGDFFSYTR	0.901561991	2	2.79592
P11884	VAEQTPLTALYVANLIK	1.104474063	3	4.93584
P11884	VAFTGSTEVGHLIQVAAGSSNLK	1.147353381	2	6.18298
P11884	VAFTGSTEVGHLIQVAAGSSNLKR	1.3335259	3	3.44299
P11884	VTLELGGK	0.741417245	1	1.9703
P11884	VVGNPFDSR	0.908326779	2	2.82367
P11884	YGLAAAVFTK	1.06133802	2	3.54829
P11884	YYAGWADK	0.789417932	1	1.94905
P11915	**NLTP Non_specific lipid_transfer protein**	**1.067507828**	**0.9987**	**19**
P11915	ADCTITMADSDLLALMTGK	1.045188679	2	5.55962
P11915	ADCTITMADSDLLALMTGK+Oxidation(15)	1.050619646	2	2.75623
P11915	ADCTITMADSDLLALMTGK+Oxidation(6)	1.053684988	2	4.30821
P11915	ANLIFK	1.118599627	2	2.34476
P11915	GSVLPDSDKK	1.113771121	2	2.50576
P11915	HIDVLINK	0.858889098	2	2.74944
P11915	HSVNNPYSQFQDEYSLDEIMK	0.986604701	2	5.43992
P11915	KADCTITMADSDLLALMTGK	0.998029192	2	3.96418
P11915	KLEEEGEEFVK	1.05042536	2	4.33594
P11915	KLEEEGEEFVKK	1.028760849	3	4.56222

P11915	LEEEGEEFVK	1.048970801	1	2.31585
P11915	LEEEGEEFVKK	0.968302854	2	3.48208
P11915	LQSLQLQPDK	1.159883638	2	3.41548
P11915	MNPQSAFFQGK	1.110759147	2	3.23762
P11915	MNPQSAFFQGK+Oxidation(0)	1.005251031	2	3.08633
P11915	SRPVFDFLTVLQCCPTSDGAAAAIVSSEEFVQK	0.833314258	3	5.73303
P11915	THQISAAPTSSAGDGFK	0.985704412	2	4.43614
P11915	WVINPSGGLISK	0.939249979	2	2.88732
P11915	YGMSACPFAPQLFGSAGK	0.942250625	2	2.81079
P11980	**KPYM Pyruvate kinase isozymes M1/M2**	**1.094545853**	**0.8485**	**3**
P11980	GVNLPGAAVDLPAVSEK	1.088681928	2	3.70176
P11980	LDIDSAPITAR	1.221719905	2	2.95984
P11980	NTGIICTIGPASR	0.939453144	2	3.30736
P12001	**RL18 60S ribosomal protein L18**	**1.179753791**	**1E-15**	**5**
P12001	GTVLLSGPR	1.321313429	2	2.45826
P12001	ILTFDQLALESPK	1.243751904	2	4.99403
P12001	TAVVVGTITDDVR	1.203053241	2	4.34303
P12001	TNRPPLSLSR	1.186688337	3	3.4478
P12001	TNSTFNQVVLK	1.128539183	2	2.80472
P12007	**IVD Isovaleryl_CoA dehydrogenase_ mitochondrial**	**1.127285414**	**0.0103**	**8**
P12007	AQEIDQSNDFK	0.832059576	2	3.35193
P12007	FVQENLAPK	1.007941681	2	2.75339
P12007	FWITNGPDADVLVVYAK	1.180352383	2	3.74319
P12007	GSNTCELVFEDCK	1.224943889	2	4.42634
P12007	GSNTCELVFEDCKVPAANILSQESK	0.972634956	3	5.05041
P12007	GVYVLMSGLDLER	0.98376663	2	3.10002
P12007	LYEIGGGTSEVR	1.109313286	2	3.54919
P12007	TDLTAVPASR	1.111437228	2	3.05182
P12336	**GTR2 Solute carrier family 2_ facilitated glucose transporter member 2**	**0.876801892**	**0.8587**	**2**
P12336	SFDEIAAEFR	0.906053932	2	3.01804
P12336	VSVIQLFTDPNYR	0.997390927	2	2.37902
P12346	**TRFE Serotransferrin**	**0.790967825**	**0.0516**	**21**
P12346	ADRDQYELLCLDNTR	0.960949413	2	4.40271
P12346	ASDSSINWNNLK	1.074019427	2	3.29467
P12346	DGGGDVAFVK	0.913331184	2	2.98725
P12346	DLKQEDFQLLCPDGTK	0.680933167	2	4.1231
P12346	EGVCPEGSIDSAPVK	0.94699394	2	3.42913
P12346	EGYNGYTGAFQCLVEK	0.787735661	2	2.94909
P12346	FDEFFSQGCAPGYK	0.738662588	2	4.19877
P12346	GDKDCTGNFCLFR	1.064895352	3	3.55691
P12346	GTDFQLNQLQGK	1.139407846	2	3.10873
P12346	GYYAVAVVK	0.97974789	2	3.29512
P12346	HTTIFEVLPQK	1.003061676	3	3.62988
P12346	KGTDFQLNQLQGK	1.078245906	3	3.94376
P12346	KTSYQDCIK	1.165096844	2	2.59595
P12346	LPEGTTYEEYLGAEYLQAVGNIR	1.087411181	2	4.71108
P12346	NGDGKEDLIWEILK	1.003201456	2	3.66043
P12346	QEDFQLLCPDGTK	0.865396685	2	2.81841
P12346	SKDFQLFGSPLGK	1.028217505	2	2.91055
P12346	TSYQDCIK	1.035269791	2	2.44955
P12346	VSTVLTAQK	1.104314162	2	2.73783
P12346	WCALSHQER	0.887345484	2	2.95126
P12346	WCAVSEHENTK	0.992067194	2	3.58468
P12368	**KAP2 cAMP_dependent protein kinase type II_alpha regulatory subunit**	**0.909886799**	**0.899**	**2**
P12368	NISHYEEQLVK	0.954457043	2	2.69296

P12368	NLDQEQLSQVLDAMFEK	0.915083465	2	4.10658
P12711	**ADHX Alcohol dehydrogenase class_3**	**1.035200201**	**2E-08**	**9**
P12711	AAVAWEAGKPLSIEEIEVAPPQAHEVR	0.997174129	3	5.69425
P12711	AGDTVIPLYIPQCGECK	0.980415016	2	3.92611
P12711	AKEFGATECINPQDFSK	0.909460603	2	3.87219
P12711	EFGATECINPQDFSK	0.763593575	2	4.63195
P12711	IDPSAPLDK	0.865706816	1	2.06998
P12711	IIGIDINK	1.152232025	1	2.0943
P12711	IIGIDINKDK	1.049169634	2	2.55734
P12711	VCLLGCGISTGYGAAVNTAK	1.065202619	2	5.67619
P12711	VDEFVTGNLSFDQINK	1.028829843	2	4.89218
P12749	**RL26 60S ribosomal protein L26**	**1.031045943**	**0.5172**	**5**
P12749	DDEVQVVR	1.229954635	2	2.52155
P12749	FNPFVTSDR	0.967403731	2	2.66377
P12749	HFNAPSHIR	1.305122076	3	3.7266
P12749	KDDEVQVVR	1.022086531	2	3.17106
P12749	KIMSSPLSKELR+Oxidation(2)	1.055240737	2	2.47963
P12785	**FAS Fatty acid synthase**	**1.166777222**	**5E-08**	**42**
P12785	ACIDTALENLSTLK	1.192628474	2	4.56794
P12785	AEAVVAVLLTK	1.301411372	2	3.17935
P12785	AGSDTELAAPK	1.15567961	2	3.61858
P12785	CPPGVVPACHNSEDTVTISGPQAAVNEFVEQLK	1.205476719	3	5.67573
P12785	DHKDNLEFFLTNLGK	1.013829374	2	2.59948
P12785	DPETLLGYSMVGCQR	1.024667886	2	2.80292
P12785	EEEPEAMLPGAQPTLISAISK	1.187848349	2	3.87558
P12785	EQGVTFPSGEAQEQLIR	1.178739471	2	4.22071
P12785	FDASFFGVHPK	1.004170209	2	3.21539
P12785	FVFTPHVEPECLSESAILQK	1.127053268	2	4.42806
P12785	GHALGETLACLPSEVQPGPSFLSQEEWESLFSR	1.297406497	3	5.99437
P12785	GLESIINIIHSSLAEPR	1.151234079	2	4.30355
P12785	GNAGQSNYGFANSTMER	1.339802961	2	4.32393
P12785	GVDLVLNSLAEEK	1.223375514	2	3.67086
P12785	GYDYGPHFQGVYEATLEGEQGK	1.811003042	3	3.5711
P12785	LDPGSSELQK	1.24556094	2	2.54974
P12785	LFDHPEVPIPAESESVSR	1.288779329	2	4.03284
P12785	LLLPEDPLISGLLNSQALK	1.468412489	3	4.88959
P12785	LTPGCEAEAEAEAICFFIK	1.080554476	2	3.92684
P12785	MTVPGLEDLPQHGLPR	1.207901606	2	3.50128
P12785	QAQLNLSILLVNPEGPTLTR	1.320069383	2	4.50285
P12785	QFVDAEHSK	0.673059035	2	2.36727
P12785	QQEQLVPTLEK	1.255359624	2	2.43878
P12785	RQQEQLVPTLEK	1.335986369	2	2.92069
P12785	RVYATILNAGTNTDGCK	0.778148266	2	2.48279
P12785	SDEALKPLGVK	1.199588473	2	3.05559
P12785	SFDDSGNGYCR	0.766441933	2	2.34025
P12785	SLSLSLEETPVVFENVTFHQATILPR	1.235454346	3	4.4737
P12785	SLYQPGGVAPESLEYIEAHGTGTK	1.148790401	2	5.39777
P12785	SNMGHPEPASGLAALTK	1.387227461	2	2.96478
P12785	SNMGHPEPASGLAALTK+Oxidation(2)	1.308608775	2	3.26107
P12785	TGGTYGEDLGADYNLSQVCDGK	1.237393938	2	4.99308
P12785	TMEAVQGLLEQGR	1.085505967	2	3.77631
P12785	TMEAVQGLLEQGR+Oxidation(1)	0.955835705	2	3.41256
P12785	VGDPQELNGITR	1.234989333	2	3.44143
P12785	VHLTGIDINPNALFPPVEFPVPR	1.135434248	2	4.63587
P12785	VLEALLPLK	1.178293132	2	2.82442
P12785	VLESDLVMNVYR	0.978936486	2	2.99136
P12785	VSVHIIEGDHR	1.149431484	2	2.79637

P12785	VTAIYIDPATHLQK	1.150818076	2	3.41565
P12785	VYATILNAGTNTDGCK	1.010626937	2	4.13514
P12785	VYQWEDPDSK	1.142238324	2	2.94497
P12791	**CP2BA Cytochrome P450 2B10**	**0.863881355**	**0.0011**	**2**
P12791	IQEEAQCLVEELR	0.961391759	2	4.39904
P12791	IQEEAQCLVEELRK	0.786449854	2	3.63835
P12847	**MYH3 Myosin_3**	**1.142658639**	**0.8503**	**4**
P12847	GTLEDQIISANPLLEAFGNAK	1.17026145	2	2.98504
P12847	MKGTLEDQIISANPLLEAFGNAK	1.183965685	3	6.32139
P12847	MKGTLEDQIISANPLLEAFGNAK+Oxidation(0)	1.082792353	3	4.84786
P12847	NLTEELAGLDETIAK	0.828427802	2	2.35153
P12928	**KPYR Pyruvate kinase isozymes R/L**	**1.272981718**	**1E-19**	**18**
P12928	AAVIAVTR	1.800284544	2	2.55618
P12928	AETSDVANAVLDGADCIMLSGETAK	1.359354078	2	5.58516
P12928	CCAAAIIVLTK	0.932080509	2	2.54685
P12928	CNLAGKPVVCATQMLESMITK	1.203696297	3	4.97367
P12928	EATESFATSPLSYRPVAIALDTK	1.53830567	2	4.36712
P12928	EPPEAIWADDVDRR	1.425436456	2	2.45048
P12928	GDLGIEIPAEK	1.27604471	2	2.78384
P12928	GSQVLVTVDPK	1.558073445	2	3.14199
P12928	GVNLPNTEVDLPGLSEQDLLDLR	1.512217081	2	5.02403
P12928	IGPEGLVTEVEHGGILGSR	1.451644347	2	5.25555
P12928	IYIDDGLISLVVQK	1.562346358	2	4.39408
P12928	KGVNLPNTEVDLPGLSEQDLLDLR	1.539768796	3	4.63622
P12928	RVQFGIESGK	0.858578276	2	2.40448
P12928	STSIIATIGPASR	1.286446873	2	3.7229
P12928	TGVLQGGPESEVEIVK	1.622809864	2	4.75941
P12928	TVWVDYHNITR	1.409507227	2	2.41708
P12928	VGDLVIVVTGWRPGSGYTNIMR	1.357656846	3	3.59263
P12928	VQFGIESGK	1.347665807	1	1.99521
P12938	**CP2D3 Cytochrome P450 2D3**	**0.84484625**	**3E-12**	**4**
P12938	DLTDAFLAEIEK	0.767267661	2	4.41802
P12938	FDYGDPDFIK	0.847091102	2	2.5738
P12938	GNPESSFNDANLR	0.820102702	2	4.39534
P12938	RFDYGDPDFIK	0.799575203	2	2.88214
P12939	**CP2DA Cytochrome P450 2D10**	**1.170368233**	**0.2976**	**8**
P12939	ALCNVIASLIFAR	1.11560512	2	2.39347
P12939	AVQEVLVTHGEDTADRPPVPIFK	1.082416172	3	5.43044
P12939	FEYEDPYLIR	1.394946295	2	3.15457
P12939	FGDIAPLNLPR	1.343907632	2	3.28706
P12939	ITSCDIEVQDFVIPK	1.218521091	2	4.1894
P12939	NLTDAFLAEVEK	1.15947007	2	4.17721
P12939	RFEYEDPYLIR	1.151082836	3	3.65449
P12939	TTWDPAQPPR	1.15357385	2	2.76574
P13084	**NPM Nucleophosmin**	**1.128929066**	**0.6431**	**2**
P13084	MTDQEAIQDLWQWR	1.136921073	2	2.97916
P13084	VDNDENEHQLSLR	1.071481312	2	3.98822
P13086	**SUCA Succinyl_CoA ligase [ADP/GDP_forming] subunit alpha_ mitochondrial**	**0.997782559**	**0.9872**	**3**
P13086	LIGPNCPGIINPGECK	1.07660874	2	4.14703
P13086	MGHAGAIIAGGK	0.836128118	2	2.80029
P13086	QGTFHSQQALEYGTK	0.930956591	2	2.82405
P13107	**CP2B3 Cytochrome P450 2B3**	**0.980033231**	**0.9066**	**7**
P13107	DFIDTFLLHMEK	1.092072489	2	3.22798
P13107	EIDQVIGSQR	0.899592035	2	2.34813
P13107	EVLDYIDHSVENHR	0.913939967	2	3.74617
P13107	FSDVSPMGLPCR+Oxidation(6)	0.995016219	2	2.50464

P13107	GIIAVLQPIMQEYGVSFVNEER	1.30747132	3	6.51599
P13107	QSVEDQIKEEAK	1.111358068	2	2.68427
P13107	SFIQLQEK	1.000811791	2	2.55245
P13221	**AATC Aspartate aminotransferase_ cytoplasmic**	**2.224996412**	**1E-19**	**6**
P13221	ITWSNPPAQGAR	1.540651146	2	3.56399
P13221	IVATTLSNPELFK	1.883086194	2	3.42102
P13221	NLDYVATSINEAVTK	1.909912659	2	4.61579
P13221	SCASQLVLGDNSPALR	2.232766661	2	4.44989
P13221	TDDSQPWVLPVVR	2.228367356	2	3.43986
P13221	VGGVQSLGGTGALR	2.871758871	2	2.60102
P13255	**GNMT Glycine N_methyltransferase**	**1.077697045**	**0.1597**	**7**
P13255	AHMVTLDYTVQVPGAGR	0.986393354	2	4.60463
P13255	AWLLGLLR	2.195127794	2	2.62566
P13255	DITTSVLTVNNK	1.023994396	2	3.78676
P13255	NIASMVRPGGLLVIDHR+Oxidation(4)	1.21475091	3	3.85525
P13255	NYDYILSTGCAPPGK	0.990193035	2	4.50686
P13255	SDLTKDITTSVLTVNNK	0.878797303	2	2.98036
P13255	SLGVAAEGIPDQYADGEAAR	1.091916761	2	5.39579
P13383	**NUCL Nucleolin**	**0.893038663**	**0.0004**	**4**
P13383	GFGFVDFNSEEDAK	1.166964499	2	3.38593
P13383	GLSEDTTEETLK	0.919678122	2	2.89546
P13383	IEGSEPTTPFNLFIGNLNPNK	0.681216657	2	2.73831
P13383	SEADAEKNLEEK	0.859575072	2	3.01915
P13437	**THIM 3_ketoacyl_CoA thiolase_ mitochondrial**	**0.820014916**	**1E-19**	**21**
P13437	AANEAGYFNEEMAPIEVK	0.836213049	2	5.32065
P13437	AANEAGYFNEEMAPIEVK+Oxidation(11)	0.778712593	2	5.1164
P13437	DAEVVLCGGTESMSQSPYSVR	0.779916089	2	5.06921
P13437	DAEVVLCGGTESMSQSPYSVR+Oxidation(12)	1.242608646	2	3.18735
P13437	DFTATDLTEFAAR	0.730824141	2	4.03871
P13437	DMDLIDVNEAFAPQFLAVQK	0.784898157	3	6.02509
P13437	DMDLIDVNEAFAPQFLAVQK+Oxidation(1)	0.801962697	2	4.5104
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVK	0.764940863	2	5.59789
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK	0.676998421	3	4.51279
P13437	EGTVTAGNASGMSDGAGVVIIASEDAVKK+Oxidation(11)	0.673837277	3	3.53606
P13437	FGLDLK	0.866480616	2	2.34252
P13437	GVFIVAAK	0.907895703	2	2.46682
P13437	ITAHLVHELR	1.291168867	2	2.97402
P13437	LCGSGFQSIVSGCQEICSK	1.010037376	2	5.14019
P13437	LEDTLWAGLTDQHVK	0.791726983	2	5.06184
P13437	RTPFGAYGGLLK	0.781842149	2	2.53273
P13437	SLDLDPSK	0.737754807	2	2.89667
P13437	TNVSGGAIALGHPLGGSGSR	0.748136639	2	6.08917
P13437	VGVPTETGALTLNR	0.792470723	2	3.7811
P13437	VPPETIDSVIVGNVMQSSSDAAYLAR	0.748389063	2	6.12936
P13437	VVGYFVSGCDPAIMGIGPVPAITGALK	1.031772878	3	4.8471
P13444	**METK1 S_adenosylmethionine synthase isoform type_1**	**1.210347327**	**1E-19**	**8**
P13444	FVIGGPQGDAGVTGR	1.205679079	2	4.81984
P13444	HIGYDDSAK	1.441676729	2	2.78495
P13444	ICDQISDAVLDAHLK	1.288413114	3	5.10603
P13444	NEEDVGAGDQGLMFGYATDETEECMPLTIVLAHK	1.06818823	3	6.60046
P13444	SEFPWEVPK	1.232504013	2	2.45008
P13444	SGVLPWLRPDSK	0.928171716	2	2.91682
P13444	TCNVLVALEQQSPDIAQCVHLDR	1.403286367	3	5.00903
P13444	TQVTVQYVQDNGAVIPVR	1.355039901	2	4.75377
P13471	**RS14 40S ribosomal protein S14**	**0.991290102**	**0.0876**	**4**
P13471	ADRDESSPYAAMLAAQDVAQR	1.074659924	2	5.67141
P13471	DESSPYAAMLAAQDVAQR	1.233794675	2	3.34797

P13471	ELGITALHIK	1.366475038	2	2.46862
P13471	IEDVTPIPSDSTR	0.987536236	2	3.74114
P13601	**AL1A7 Aldehyde dehydrogenase_ cytosolic 1**	**0.373902981**	**1E-19**	**15**
P13601	EEIFGPVQQIMK	0.360558035	2	3.42742
P13601	EMGEQGVYEYTELK	0.267176045	2	3.30121
P13601	FPVINPATEEVICHVEEGDKADVDK	0.433421868	4	5.15345
P13601	IAKEEIFGPVQQIMK	0.514991325	2	3.1116
P13601	IHGQTIPSDGDVFTYTR	0.545296759	2	3.81836
P13601	ILDLIESGK	0.38101494	2	3.25449
P13601	ILDLIESGKK	0.32363887	3	3.54331
P13601	KFPVINPATEEVICHVEEGDKADVDK	0.519150375	3	3.63965
P13601	KYVLGNPLDSGISQGPQIDKEQHAK	0.076522818	3	4.51551
P13601	LFVEESIYDEFVR	0.36209133	2	3.72501
P13601	VLLATMESMNAGK	0.838827598	2	2.86151
P13601	VSFTGSTEVGK	0.324192195	2	2.35532
P13601	YFAGWADK	0.649942361	1	2.09162
P13601	YVLGNPLDSGISQGPQIDK	0.333300575	2	4.85262
P13601	YVLGNPLDSGISQGPQIDKEQHAK	0.220155982	2	4.20875
P13697	**MAOX NADP_dependent malic enzyme**	**0.701659652**	**8E-07**	**5**
P13697	AECSAEECYK	0.684132866	2	3.03468
P13697	AIFASGSPFDPVTLPDGR	0.756099905	2	4.28198
P13697	GHIASVLNAWPEDVVK	0.899639022	2	2.84262
P13697	HINDSVFLTTAEVISQQVSDK	0.681229115	3	4.09601
P13697	ILGLGDLGCNGMGIPVGK	0.706703527	2	2.38563
P13803	**ETFA Electron transfer flavoprotein subunit alpha_ mitochondrial**	**0.986249649**	**0.0015**	**13**
P13803	AAVDAGFVPNDMQVGQTGK	0.919266902	2	4.38862
P13803	AAVDAGFVPNDMQVGQTGK+Oxidation(11)	1.031695265	2	3.84849
P13803	GLLPEELTPLILETQK	0.97378028	2	4.51459
P13803	GTSFEAAAASGGSASSEK	0.991565749	2	5.1656
P13803	LGGEVSCLVAGTK	0.953627792	2	4.51105
P13803	LLYDLADQLHAAVGASR	1.075616703	2	5.12332
P13803	LNVAPVSDIIEIK	1.134614421	3	4.64965
P13803	QFSYTHICAGASAFGK	0.986211189	2	2.8531
P13803	SDRPELTGAK	0.960876272	3	3.40216
P13803	TIVAINKDPEAPIFQVADYGIVADLFK	0.921075554	3	7.17158
P13803	TIYAGNALCTVK	0.986373726	2	3.51976
P13803	VLVAQHDAYK	0.917078672	2	3.3737
P13803	VVQDLCK	1.032959097	2	2.61792
P13832	**MRLCA Myosin regulatory light chain RLC_A**	**1.09746804**	**0.4819**	**3**
P13832	ATSNVFAMFDQSQIQEFK	1.081362851	2	4.96734
P13832	FTDEEVDELYR	1.165498112	2	3.42814
P13832	GNFNYIEFTR	1.090943542	2	2.52402
P14046	**A1I3 Alpha_1_inhibitor 3**	**1.06637279**	**0.7735**	**7**
P14046	FSIDTNGISDYSLNIK	1.369124656	2	2.31945
P14046	GDPIPNEQVLIK	1.02875018	2	2.48965
P14046	GMYESLPVVAVK	0.984389527	2	3.09285
P14046	GMYESLPVVAVK+Oxidation(1)	0.894292049	2	2.80014
P14046	ISLCHGNPTFSSETK	1.097931909	2	3.18366
P14046	QQNSYGGFSSTQDTVVALDALSK	1.159475091	2	4.10768
P14046	QSPGPCGSEVATVPETGR	1.042391157	2	3.60634
P14141	**CAH3 Carbonic anhydrase 3**	**0.978870106**	**3E-10**	**17**
P14141	EAPFNHFDPSCLFPACR	0.891225015	2	4.10022
P14141	EKGEFQILLDALDK	0.917613382	2	4.34433
P14141	EPMTVSSDQMAK	1.49933544	2	2.64079
P14141	EWGYASHNGPEHWHELYPIAK	0.929093849	3	4.7989
P14141	GDNQSPIELHTK	0.968090999	2	3.51034
P14141	GEFQILLDALDK	0.938831218	2	4.75077

P14141	GEFQILLDALDKIK	0.897072142	2	3.00972
P14141	GGPLSGPYR	1.02056662	2	2.97935
P14141	GKEAPFNHFDPSCLFPACR	0.902636201	2	3.88513
P14141	HDPSLQPWSVSYDPGSAK	0.990235211	3	5.33305
P14141	QFHLHWGSSDDHGSEHTVDGVK	0.843537402	2	4.54561
P14141	QPDGIAVVGIFLK	1.222991367	2	2.69548
P14141	SLFASAENEPPVPLVGNWRPPQPIK	0.932164988	3	5.7628
P14141	VVFDDTFDR	0.947246179	2	3.2788
P14141	YAAELHLVHWNPK	1.480068423	2	4.10161
P14141	YNTFGEALK	1.008518711	2	2.52015
P14141	YNTFGEALKQPDGIAVVGIFLK	0.979533887	3	5.95166
P14173	**DDC Aromatic_L_amino_acid decarboxylase**	**1.01914091**	**0.2403**	**7**
P14173	AGEGGGVIQGSASEATLVALLAAR	1.177536231	2	5.2869
P14173	ALIPTTAPQEPETYEDIIR	1.038339565	2	3.48248
P14173	GSNQLNETLLQR	1.004807633	2	2.88497
P14173	HSHQDSGLITDYR	0.940385525	3	3.68244
P14173	MLELPEAFLAGR	1.110353977	2	2.63082
P14173	QLQAASPELTQAALMEK	1.016867107	2	3.70303
P14173	TDLTEAFNMDPVYLR	0.972192679	2	3.54349
P14408	**FUMH Fumarate hydratase_ mitochondrial**	**0.963445504**	**4E-06**	**11**
P14408	AAAEVNQEYGLDPK	1.081679188	2	4.28679
P14408	AIEMLGGELGSK	0.879212788	2	3.94295
P14408	IEYDTFGELKVPTDK	1.001133083	2	3.03899
P14408	IYELAAGGTAVGTGLNTR	0.956114467	2	5.51948
P14408	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	0.988391256	3	5.99212
P14408	SGLGELILPENEPGSSIMPGK	0.920566658	2	4.60818
P14408	SGLGELILPENEPGSSIMPGK+Oxidation(17)	0.903814189	2	3.06904
P14408	SQSSNDTFPTAMHIAAALEVHQVLLPGLQK	0.856159758	3	4.38157
P14408	TAIELGYLTAEQFDEWVKPK	0.929701628	2	4.93693
P14408	THTQDAVPLTLGQEFSGYVQQVQYAMER	1.024671372	3	6.25283
P14408	YYGAQTVR	0.763614392	2	2.50347
P14480	**FIBB Fibrinogen beta chain**	**0.768288957**	**0.0003**	**6**
P14480	AHYGGFTVQTEANK	0.749367049	2	2.36867
P14480	GFGNIATNEDTKK	0.738100325	2	2.92216
P14480	LESDISAQTEYCHTPCTVNCNIPVVSGK	0.815859248	3	4.75645
P14480	LYIDETVNDNIPLNLR	0.894533894	2	2.54741
P14480	TENGGWTVIQNR	0.712085139	2	3.48412
P14480	YCGLPGEYWLGNDK	0.689076451	2	3.2445
P14604	**ECHM Enoyl_CoA hydratase_ mitochondrial**	**0.985048322**	**1**	**7**
P14604	AFAAGADIK	1.014695137	2	3.13213
P14604	AQFGQPEILLGTIPGAGGTQR	0.981647025	2	5.72905
P14604	FLSHWDHITR	0.942479845	2	3.0123
P14604	IFPVETLVEEAIQCAEK	0.885514228	2	5.63218
P14604	NSSVGLIQLNRPK	1.028898314	2	3.51359
P14668	**ANXA5 Annexin A5**	**0.837007161**	**0.1371**	**5**
P14668	EFRKNFATSLYSMIK	1.049933813	2	2.39026
P14668	ETSGNLENLLLAVVK	0.83698039	2	3.33549
P14668	GAGTDDHTLIR	0.809001077	2	2.7146
P14668	GLGTDEDSILNLLTAR	0.905558007	2	3.95647
P14668	GTVTDFSGFDGR	0.879317032	2	2.56835
P14669	**ANXA3 Annexin A3**	**0.793693672**	**0.0008**	**6**
P14669	GMGTDEDTLIEILTTR	0.772731798	2	3.12885
P14669	GTINNYPGFNPSVDAEAIR	0.793550786	2	4.62311
P14669	KDAQTLYDAGEKK	0.689990727	3	3.76387
P14669	QYQEAYEQALK	0.848531531	2	2.78182
P14669	SEIDLLDIR	1.063022765	2	2.99695
P14669	WGTDEDKFTEILCLR	0.869886564	3	3.48555

P14685	**PSMD3 26S proteasome non_ATPase regulatory subunit 3**	**1.10909052**	**2E-06**	**2**
P14685	LQLDSPEDAEFIVAK	1.094838752	2	4.04152
P14685	SVFPEQANNNEWAR	1.147015789	2	3.14449
P14740	**DPP4 Dipeptidyl peptidase 4**	**0.896354853**	**3E-06**	**3**
P14740	FRPAEPHFTSDGSSFYK	0.948377879	2	2.72321
P14740	LGTLEVEDQIEAAR	0.846363633	2	3.55022
P14740	VLEDNSALDK	0.826008362	2	2.68994
P14882	**PCCA Propionyl_CoA carboxylase alpha chain_ mitochondrial**	**0.971036502**	**0.0012**	**11**
P14882	EIGYPVMIKASAGGGGK+Oxidation(6)	0.976730355	2	2.40752
P14882	FLSDVYPDGFK	0.939166603	2	2.9276
P14882	FSSQEAASSFGDDR	1.089757738	2	2.91851
P14882	HGNALWLNER	1.27839689	2	2.9325
P14882	HKQEDIPISGWAVECR	0.995753955	3	3.52011
P14882	MADEAVCVGPAPTSK	0.945228582	2	3.96764
P14882	MEDALDSYVIR	0.92542238	2	3.03372
P14882	SYLNMDAIMEAIK	0.775253184	2	2.33653
P14882	TGAQAVHPGYGFLSENK	0.989464829	2	4.03558
P14882	TVAIHSDVDASSVHVK	1.075889118	3	3.44137
P14882	VVEEAPSIFLDPETR	0.934861268	2	3.53563
P14942	**GSTA4 Glutathione S_transferase alpha_4**	**0.831332103**	**0.0061**	**2**
P14942	KPPPDGHYVDVVR	0.832051308	2	2.70752
P14942	YFPVFEK	0.806117578	1	1.91788
P15083	**PIGR Polymeric immunoglobulin receptor**	**1.041590086**	**0.9759**	**3**
P15083	EIQNAGDQAQENR	1.043760159	2	3.98802
P15083	GVTGGSVAIVCPYNPK	1.051932323	2	3.7448
P15083	NNADLQVLEPEPELLYK	0.834709275	2	3.0054
P15149	**CP2A2 Cytochrome P450 2A2**	**0.767289192**	**1E-19**	**10**
P15149	DVQECILEEAGYLIK	0.687033549	3	5.15156
P15149	DVYSSITQLSER	0.845541141	2	3.06834
P15149	FSNLAPLGIPR	0.869186806	2	3.20062
P15149	GELPTFNILFK	0.690823352	2	2.70464
P15149	GTDVFPIIGSLMTEPK	0.682233579	3	3.72354
P15149	GYGFSLSNVEQAK	0.78341775	2	3.43775
P15149	NFIDSFLIR	0.765538271	2	2.45658
P15149	QNHSTLDPNSPR	0.953560497	2	2.96759
P15149	TLQGTCGAPIDPSIYLSK	0.76602681	2	4.72555
P15149	TVSNVINSIVFGNR	0.835559817	2	3.46598
P15178	**SYDC Aspartyl_tRNA synthetase_ cytoplasmic**	**1.06983947**	**0.8479**	**2**
P15178	GEEILSGAQR	1.05487397	2	2.73186
P15178	QMVKFAANINK+Oxidation(1)	1.08246136	2	2.35481
P15429	**ENOB Beta_enolase**	**1.074700144**	**1**	**5**
P15429	DATNVGDEGGFAPNILENNEALELLK	1.157211684	2	4.98473
P15429	HIADLAGNPDLVLPVPAFNVINGGSHAGNK	0.970036281	3	5.20497
P15429	IEEALGDK	1.13530916	1	2.11577
P15429	TAIQAAGYPDK	1.333834169	2	2.74873
P15429	VNQIGSVTESIQACK	1.071418899	2	5.13829
P15650	**ACADL Long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.959644727**	**1E-14**	**21**
P15650	AFVDSCLQLHETK	1.029697697	2	4.12089
P15650	AQDTAELFFEDVR	1.171475794	2	4.8683
P15650	AQDTAELFFEDVRLPASALLGEENK	1.005313966	3	4.4008
P15650	CIGAIAMTEPGAGSDLQGVR	0.917950217	2	6.15964
P15650	CIGAIAMTEPGAGSDLQGVR+Oxidation(6)	0.92920317	2	5.63947
P15650	EQIEQFIPQMTAGK	0.791626483	2	5.02133
P15650	FFQEEVIPYHEEWEK	1.38108102	2	4.74433
P15650	GFYYLMQELPQER	1.040011833	2	2.97616
P15650	GFYYLMQELPQER+Oxidation(5)	1.15680216	2	2.65493

P15650	IFSSEHDIFR	1.067340298	2	2.84125
P15650	KFFQEEVIPYHEEWEK	1.133728956	2	4.77187
P15650	LDSASASMAK	0.850410992	2	2.41946
P15650	LDSASASMAK+Oxidation(7)	1.010904942	2	2.44125
P15650	LPASALLGEENK	0.968376101	2	3.33571
P15650	LPASALLGEENKGFYYLMQELPQER	1.657911835	3	3.96827
P15650	QGLLGINIAEK	0.935741848	2	3.28251
P15650	RLDSASASMAK	0.810374518	2	2.9681
P15650	RLDSASASMAK+Oxidation(8)	1.072550589	2	2.79229
P15650	SGSDWILNGSK	1.110438642	2	2.97819
P15650	VQPIYGGTNEIMK	1.003914472	2	3.55062
P15650	VQPIYGGTNEIMK+Oxidation(11)	0.99818557	2	3.06033
P15651	**ACADS Short_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.9262205**	**0.0001**	**7**
P15651	ASSTANLIFEDCR	1.101744842	2	3.42759
P15651	EEGDSWVLNGTK	0.789269013	2	2.71993
P15651	ELVPIAAQLDKEHLFPTSQVK	0.61144417	2	4.54529
P15651	IGCFALSEPGNGSDAGAASTTAR	1.079664431	2	5.90469
P15651	IGIASQALGIAQASLDCAVK	1.17727388	2	4.64005
P15651	ITEIYEGTSEIQR	0.924850626	2	4.28648
P15651	LAASEAATAISHQAIQILGGMGYVTEMPAER	1.077985435	4	4.80843
P15684	**AMPN Aminopeptidase N**	**0.765986821**	**0.1369**	**3**
P15684	ALGDTPAPNIDTTELVER	0.893190205	2	3.73857
P15684	AQIIHDSFNLASAGK	0.746183746	2	3.4102
P15684	VVATTQMQAADAR	0.989388963	2	3.26723
P15709	**ST2A1 Bile salt sulfotransferase**	**0.513886477**	**0.0001**	**2**
P15709	GNVLYGSWFEHIR	0.716120674	2	2.9798
P15709	NHFTVSQAEAFDK	0.511476869	2	3.6919
P15999	**ATPA ATP synthase subunit alpha_ mitochondrial**	**1.025218397**	**7E-13**	**23**
P15999	AVDSLVPIGR	0.987199998	2	3.48319
P15999	EVAAFAQFGSDLDAATQQLLSR	1.070605819	2	6.42532
P15999	FESAFLSHVVSQHQSLLGNIR	1.154881076	3	5.9234
P15999	GIRPAINVGLSVSR	1.559996675	2	3.02806
P15999	GMSLNLEPDNVGVVVFGNDK	1.141754313	2	4.95854
P15999	GMSLNLEPDNVGVVVFGNDK+Oxidation(1)	1.030463219	2	3.55332
P15999	GYLDKLEPSK	0.876552534	2	2.44305
P15999	HALIIYDDLSK	1.397988942	2	2.46942
P15999	ILGADTSVDLEETGR	1.1107306	2	5.07682
P15999	LELAQYR	1.07304988	2	2.74124
P15999	LKEIVTNFLAGFEP	1.055554686	2	2.36143
P15999	LYCIYVAIGQK	1.046394216	2	2.49529
P15999	NVQAEEMVEFSSGLK	1.360038514	2	4.41445
P15999	QGQYSPMAIEEQVAVIYAGVR	1.017336464	3	4.95107
P15999	RLTDADAMK	0.854390702	2	2.33588
P15999	RTGAIVDVPVGDELLGR	1.152425433	2	3.09704
P15999	STVAQLVK	1.021596966	2	2.32218
P15999	TGAIVDVPVGDELLGR	0.988276586	2	4.58103
P15999	TGTAEMSSILEER	1.043408428	2	4.26712
P15999	TGTAEMSSILEER+Oxidation(5)	0.99704226	2	3.36895
P15999	TSIAIDTIINQK	0.968143182	2	4.34086
P15999	VLSIGDGIAR	1.093892606	2	3.24282
P15999	VVDALGNAIDGK	0.983543045	2	4.31178
P16036	**MPCP Phosphate carrier protein_ mitochondrial**	**1.072103426**	**0.0024**	**8**
P16036	ALYSNILGEENTYLWR	0.900589717	2	2.72008
P16036	EEGLNAFYK	1.114748112	1	2.08078
P16036	EKGSTASQVLQR	0.957699315	2	3.08668
P16036	FGFYEVFK	1.050870589	1	1.99456

P16036	GIFNGFSITLK	1.218243279	2	2.69391
P16036	GSTASQVLQR	1.036400217	2	3.04368
P16036	IQTQPGYANTLR	1.121106305	2	3.26257
P16036	MYKEEGLNAFYK+Oxidation(0)	0.924642632	2	2.6755
P16086	**SPTA2 Spectrin alpha chain_ brain**	**0.976142934**	**0.8543**	**28**
P16086	ALINADELANDVAGAEALLDR	0.960285468	3	4.29678
P16086	ALSSEGKPYVTK	0.910869606	2	3.24581
P16086	CNSLEEIKALREAHDAFR	1.537040245	2	2.58024
P16086	DVTGAEALLER	1.11638454	2	2.52613
P16086	GVIDMGNSLIER	0.91933702	2	2.94299
P16086	HQALQAEIAGHEPR	0.959705598	3	3.43094
P16086	KFEEFQTDLAAHEER	1.045128661	2	4.444
P16086	LFGAAEVQR	0.972103273	2	2.35294
P16086	LGDSHDLQR	0.926839518	2	3.01277
P16086	LGESQTLQQFSR	0.903443333	2	3.24827
P16086	LIQEQHPEEELIK	0.891197529	2	2.85121
P16086	LQQSHPLSANQIQVK	1.091937027	2	3.67016
P16086	LQTASDESYKDPTNIQSK	1.081790965	2	5.07851
P16086	LQVASDENYKDPTNLQGK	0.907586138	2	4.90293
P16086	LSDDNTIGQEEIQQR	0.858479456	2	4.33598
P16086	MQHNLEQQIQAR+Oxidation(0)	0.963890723	2	2.62275
P16086	NQALNTDNYGHDLASVQALQR	0.999238259	2	5.815
P16086	NTTGVTEEALK	0.930976511	2	2.41464
P16086	QFQDAGHFDAENIKK	1.02499093	2	2.5176
P16086	SADESGQALLAAGHYASDEVR	1.015567344	2	5.21896
P16086	SLQQLAEER	1.000249044	2	2.61294
P16086	SQLLGSAHEVQR	0.959714307	2	3.25905
P16086	SSLSSAQADFNQLAELDR	1.045147193	2	5.19909
P16086	TATDEAYKDPSNLQGK	0.904208745	2	3.8134
P16086	TKQEEVNAAWQR	0.974648381	2	3.06743
P16086	VLETAEDIQER	0.896084511	2	2.83283
P16086	VNDVCTNGQDLIK	0.947610173	2	2.66141
P16086	VNSLGETAQR	1.04356073	2	2.59214
P16232	**DHI1 Corticosteroid 11_beta_dehydrogenase isozyme 1**	**0.674771133**	**3E-11**	**6**
P16232	EECALEIIK	0.650033645	1	2.28021
P16232	ETSGIILSQAAPK	0.623951842	2	3.55305
P16232	FALDGFFSTIR	0.968243158	2	2.72643
P16232	KDEVYYDK	0.644525839	1	2.55453
P16232	MTQPLIASYSASK	0.855917561	2	2.55557
P16232	SSWTPLLLGNPGR	0.682217748	2	3.50762
P16290	**PGAM2 Phosphoglycerate mutase 2**	**1.064642122**	**0.9846**	**4**
P16290	AMEAVAAQGK	1.110174241	2	2.50142
P16290	AMEAVAAQGK+Oxidation(1)	0.542148016	2	3.03278
P16290	HYGGLTGLNK	1.071825909	1	2.83401
P16290	VLIAAHGNSLR	1.008782579	2	2.50912
P16303	**CES3 Carboxylesterase 3**	**0.734320701**	**1E-19**	**13**
P16303	AKEAAEEPSHWK	0.858975052	2	3.94873
P16303	DGASEEETNLSK	0.676448604	2	4.30071
P16303	ESYPFLPTVIDGVVLPK	0.583030995	2	4.29574
P16303	LDLLGNPK	0.79406456	2	2.39438
P16303	MIPVVAEK	0.603114399	1	1.94573
P16303	QEFGWIIPTLMGYPLSEGK	0.958868093	2	3.86512
P16303	QKTEDELLETSLK	0.647727349	2	3.44549
P16303	SFNTVPYIVGINK	0.849078028	2	2.59327
P16303	TEDELLETSLK	0.706276161	2	3.62898
P16303	TPEEILAEK	0.978711337	2	2.33163
P16303	TTTSAVMVHCLR	0.762365149	2	2.49585

P16303	TVIGDHGDELFSVFGSPFLK	0.791370567	2	5.55486
P16303	YFGGTDDPAK	0.625474591	2	3.07163
P16332	**MUTA Methylmalonyl_CoA mutase_ mitochondrial**	**1.233501981**	**0.0007**	**4**
P16332	AHCQTSGWSLTEQDPYNNIVR	1.138579202	3	4.28628
P16332	IDSGSEVIVGVNK	1.233505784	2	3.52451
P16332	NTQIIIQEESGIPK	1.209873736	2	3.88251
P16332	TGLQAGLTIDEFAPR	1.102306067	2	3.04656
P16409	**MYL3 Myosin light chain 3**	**1.300529651**	**0.9693**	**6**
P16409	AAPAPAAAPAAAPEPERPK	1.24202742	2	4.31258
P16409	ALGQNPTQAEVLR	1.785029413	2	3.85524
P16409	DTGTYEDFVEGLR	1.291589121	2	3.06671
P16409	IEFTPEQIEEFK	1.285600272	2	2.46709
P16409	NKDTGTYEDFVEGLR	1.421143566	2	3.40117
P16409	VFDKEGNGTVMGAELR	1.235262295	2	3.81775
P16617	**PGK1 Phosphoglycerate kinase 1**	**1.167414476**	**0.0056**	**19**
P16617	AHSSMVGVNLPQK	1.083117802	2	3.50766
P16617	AHSSMVGVNLPQK+Oxidation(4)	0.82286463	2	2.81574
P16617	ALESPERPFLAILGGAK	0.9986512	3	4.45404
P16617	DCVGSEVENACANPAAGTVILLENLR	1.006299874	3	5.92439
P16617	FCLDNGAK	0.888897707	1	2.02842
P16617	GCITIIGGGDTATCCAK	0.994623733	2	5.30764
P16617	IQLINNMLDK	1.037098712	2	2.3349
P16617	IQLINNMLDK+Oxidation(6)	1.415735628	2	2.45683
P16617	ITLPVDFVTADK	1.071031858	2	2.33842
P16617	ITLPVDFVTADKFDENAK	1.305953314	2	4.6603
P16617	QIVWNGPVGVFEWEAFAR	1.204321523	2	3.04603
P16617	SVVLMSHLGRPDGVPMPDKYSLEPVAAELK	1.205146744	4	4.70571
P16617	TGQATVASGIPAGWMGLDCGTESSK	1.088467107	2	4.72055
P16617	TGQATVASGIPAGWMGLDCGTESSKK	0.993553596	3	4.14253
P16617	VLNNMEIGTSLYDEEGAK	1.135095169	2	4.84194
P16617	VLNNMEIGTSLYDEEGAK+Oxidation(4)	0.967564631	2	2.67029
P16617	VLPGVDALSNV	1.171486237	2	2.40267
P16617	WNTEDKVSHVSTGGGASLELLEGK	1.009547666	3	4.5441
P16617	YSLEPVAAELK	1.010214944	2	2.97467
P16638	**ACLY ATP_citrate synthase**	**1.170632222**	**3E-07**	**20**
P16638	AFDSGIIPMEFVNK	0.91665319	2	3.47556
P16638	AFDSGIIPMEFVNK+Oxidation(8)	0.852738663	2	3.19852
P16638	DEPSVAAMVYPFTGDHK	1.005748088	2	3.52614
P16638	DGVYILDLAAK	0.897534882	2	2.3298
P16638	DLVSSLTSGLLTIGDR	0.846856221	2	3.74462
P16638	EAYPEEAYIADLDAK	1.017970436	2	3.24635
P16638	FGGALDAAAK	1.018222708	2	2.72558
P16638	GAIVPAQEVPPPTVPMDYSWAR	1.002014627	2	4.0506
P16638	GGPNYQEGLR	1.121208058	2	2.95501
P16638	GVTIIGPATVGGIKPGCFK	1.083512259	2	3.40001
P16638	IGNTGGMLDNILASK	1.104933343	2	3.59441
P16638	LGLVGVNLSLDGVK	1.333444888	2	2.49912
P16638	LLVGVDEK	1.118090692	2	2.31624
P16638	RGGPNYQEGLR	1.156768263	2	3.29658
P16638	SGGMSNELNNIISR	1.13266165	2	3.33239
P16638	TIAIIAEGIPEALTR	1.008986343	2	4.54741
P16638	TTDGVYEGVAIGGDR	1.230581252	2	2.81797
P16638	TTDGVYEGVAIGGDRYPGSTFMDHVLR	0.922155777	3	3.6497
P16638	WGDIEFPPPFGR	0.788908265	2	3.9985
P16638	YICTTSAIQNR	1.125134585	2	2.99804
P16970	**ABCD3 ATP_binding cassette sub_family D member 3**	**0.753501819**	**1E-13**	**7**
P16970	EGGWDSVQDWMDVLSGGEK	0.916877987	2	3.99481

P16970	FDHVPLATPNGDILIQDLSFEVR	0.984685752	3	4.00784
P16970	GIEGAQASPLIPGAGEIINADNIIK	0.691135408	3	4.55975
P16970	GYLDNVQLGHILER	0.783260051	2	3.37217
P16970	HLHSTHSELLEDYYQSGR	0.815425819	3	4.73919
P16970	IANPDQLLTQDVEK	0.937580061	2	3.17072
P16970	SGANVLICGPNGCGK	0.827607212	2	3.45422
P17077	**RL9 60S ribosomal protein L9**	**1.133013538**	**0.9392**	**7**
P17077	FLDGIYVSEK	0.954945353	2	3.36401
P17077	GTVQQPDE	1.180791465	1	2.05099
P17077	KFLDGIYVSEK	1.08424726	2	2.4775
P17077	SVYAHFPINVVIQENGSLVEIR	1.058573016	3	3.38509
P17077	TGVACSVSQAQK	1.176146978	2	3.08648
P17077	TICSHVQNMIK	0.832290847	2	2.91288
P17077	TILSNQTVDIPENVDITLK	0.961114875	2	3.92861
P17078	**RL35 60S ribosomal protein L35**	**1.000485261**	**0.9667**	**2**
P17078	QLDDLKVELSQLR	0.93064247	2	2.41582
P17078	VLTVINQTQK	1.028716223	2	2.97669
P17178	**CP27A Sterol 26_hydroxylase_ mitochondrial**	**0.992750097**	**0.4645**	**3**
P17178	MLKPAEAALYTDALNEVISDFIAR	1.223664692	3	3.71891
P17178	VGCLEPSIPEDTATFIR	1.116184094	2	3.06342
P17178	YEVVLSPGMGEVK	0.955209167	2	3.23402
P17425	**HMCS1 Hydroxymethylglutaryl_CoA synthase_ cytoplasmic**	**0.282571466**	**1E-19**	**10**
P17425	ASAELFNQK	0.314308337	2	3.01004
P17425	GTHMQHAYDFYKPDMLSEYPVVDGK+Oxidation(3)	0.263553172	3	4.79415
P17425	LEDTYFDRDVEK	0.235846862	2	2.82849
P17425	MFLNDFLNDQNR	0.401300518	2	2.61977
P17425	MFLNDFLNDQNR+Oxidation(0)	0.301759413	2	3.40863
P17425	NSLSYDCIGR	0.243441323	2	2.67405
P17425	RPSTNDHSLDEGVGLVHSNTATEHIPSPAK	0.474642392	4	4.6524
P17425	TCVAPDVFAENMK	0.287340398	2	2.46807
P17425	VTQDATPGSALDK	0.322564737	2	3.92519
P17425	YTIGLGQAR	0.295620208	2	2.61365
P17426	**AP2A1 AP_2 complex subunit alpha_1**	**1.025332354**	**0.0941**	**3**
P17426	FVCKNSGVLFENQLLQIGVK	3.091223262	2	2.30254
P17426	NADVELQQR	0.957336094	2	2.64329
P17426	VGGYILGEFGNLIAGDPR	0.989716841	2	3.42639
P17475	**A1AT Alpha_1_antiproteinase**	**1.032911572**	**0.1662**	**6**
P17475	IVDLMK+Oxidation(4)	1.142344049	1	2.05017
P17475	MQHLEQTLTK	0.751270439	2	2.31718
P17475	NNYHSEAFSVNFADSEEAKK	1.162605537	3	4.3516
P17475	TLLSSLGITR	1.048299115	2	2.9887
P17475	VFNNDADLSGITEDAPLK	0.952049644	2	5.46066
P17475	VINDYVEK	0.825845383	1	2.1906
P17712	**HXK4 Glucokinase**	**1.138729333**	**0.3754**	**4**
P17712	ASGAEGNNIVGLLR	1.148080793	2	2.90532
P17712	LETHEEASVK	1.276780955	2	2.51661
P17712	STPEGSEVGDFLSLDLGGTNFR	1.14318969	2	4.22112
P17712	VGEGEAGQWSVK	1.110788096	2	3.03338
P17764	**THIL Acetyl_CoA acetyltransferase_ mitochondrial**	**1.056566739**	**1E-19**	**16**
P17764	EEQDKYAIGSYTR	0.887480344	2	3.54635
P17764	ENGTVTAANASTLNDGAAAVVLMTAEAAQR	0.935968614	3	3.38944
P17764	EVYMGNVIQGGEGQAPTR	1.068228333	2	4.75122
P17764	FANEITPITISVK	1.20537248	2	3.71886
P17764	GKPDVVVKEDEEYK	0.80890842	2	3.23836
P17764	GKPDVVVKEDEEYKR	0.92699493	2	4.57542
P17764	IAAFADAAVDPIDFPLAPAYAVPK	1.282282419	2	3.88792
P17764	IHMGNCAENTAK	1.026503143	2	3.19775

P17764	IHMGNCAENTAK+Oxidation(2)	1.350956397	2	3.02954
P17764	LEDLIVK	0.869237823	1	2.18632
P17764	LGTIAIQGAIEK	1.317088547	2	2.88635
P17764	QATLGAGLPIATPCTTVNK	0.97866362	2	4.6391
P17764	QGEFGLASICNGGGGASAVLIEK	1.064998878	2	4.76139
P17764	TPIGSFLGSLASQPATK	1.590897341	2	3.99727
P17764	VNVHGGAVSLGHPIGMSGAR	0.751591309	3	3.64917
P17764	VNVHGGAVSLGHPIGMSGAR+Oxidation(15)	0.964939963	3	3.31125
P17879	**HS71B Heat shock 70 kDa protein 1B**	**1.116851879**	**0.0194**	**3**
P17879	QTQTFTTYSDNQPGVLIQVYEGER	1.093899134	3	4.6592
P17879	TTPSYVAFTDTER	1.274121076	2	3.6979
P17879	VEIIANDQGNR	1.084045742	2	3.8048
P17988	**ST1A1 Sulfotransferase 1A1**	**1.361139378**	**1E-19**	**4**
P17988	CPGVPSGLETLEETPAPR	1.676560565	2	4.92401
P17988	NTFTVAQNER	1.42245412	2	3.46223
P17988	SLPEETVDSIVHHTSFK	1.479716208	2	4.3453
P17988	THLPLSLLPQSLLDQK	1.695819877	2	4.72451
P18163	**ACSL1 Long_chain_fatty_acid__CoA ligase 1**	**1.024042676**	**0.1711**	**23**
P18163	AELSVIFADKPEK	0.96251852	2	3.35586
P18163	ALKPPCDLSMQSVEVTGTTEGVR	0.934037424	2	4.49232
P18163	ALKPPCDLSMQSVEVTGTTEGVR+Oxidation(9)	1.003152849	3	3.65705
P18163	CGVEIIGLK	0.857110165	2	3.07871
P18163	DGWLHTGDIGK	0.915769159	2	2.87043
P18163	GAMVTHQNIMNDCSGFIK+Oxidation(2)	1.349301677	3	3.73793
P18163	GFQGSFEELCR	1.073209198	2	3.2005
P18163	GIAVHPELFSIDNGLLTPTLK	1.539627685	2	5.66803
P18163	GIQVSNDGPCLGSR	0.976010804	2	4.57707
P18163	IENIYLR	1.021187214	2	2.84489
P18163	IFGQANTSVK	1.003553856	2	2.4036
P18163	IIVIMDSYDNDLVER	1.042915325	2	4.29589
P18163	LLLEGVENK	0.955298915	2	3.22922
P18163	LVDVEDMNYQAAK	1.048438261	2	4.5051
P18163	LVDVEDMNYQAAK+Oxidation(6)	1.003666735	2	3.40841
P18163	NAGLKPFEQVK	0.988707834	2	3.57308
P18163	NNSLWDK	0.93708175	2	2.6721
P18163	QVAEMAECIGSALIQK	1.026434604	2	5.34555
P18163	SQIDELYSTIK	0.931338233	2	3.57992
P18163	SQIDELYSTIKI	1.015931863	2	3.95376
P18163	TAEALDKDGWLHTGDIGK	1.012206307	2	5.24855
P18163	VLQPTIFPVVPR	0.98184834	2	3.63525
P18163	WLLDFASK	1.12393097	2	2.3317
P18297	**SPRE Sepiapterin reductase**	**0.951640453**	**0.0219**	**4**
P18297	ALAPQLAGLLSPGSVLLLSAR	0.880816618	3	4.80423
P18297	LNSEGELVDCGTSAQK	0.931614582	2	4.74238
P18297	TVVNISSLCALQPFK	1.163517228	2	2.69967
P18297	VLSYAPGPLDTNMQQLAR	0.966551454	2	2.48966
P18298	**METK2 S_adenosylmethionine synthase isoform type_2**	**1.320131029**	**3E-10**	**2**
P18298	IIVDTYGGWGAHGGGAFSGK	0.988511237	2	5.27725
P18298	YLDEDTIYHLQPSGR	1.749557335	2	4.52686
P18418	**CALR Calreticulin**	**1.0150793**	**8E-10**	**19**
P18418	AKIDDPTDSKPEDWDKPEHIPDPDAK	0.921964105	3	5.90937
P18418	CKDDEFTHLYTLIVRPDNTYEVK	1.339918021	4	4.89991
P18418	DMHGDSEYNIMFGPDICGPGTK	1.110809217	2	5.8518
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(1)	1.102946042	3	3.70668
P18418	DMHGDSEYNIMFGPDICGPGTK+Oxidation(10)	1.102946042	3	3.4793
P18418	EQFLDGDAWTNR	0.860422337	2	3.08592
P18418	FYGDQEK	1.117626561	1	1.9565

P18418	FYGDQEKDK	1.107943889	1	2.91121
P18418	GQTLVVQFTVK	1.112585766	2	3.3287
P18418	HEQNIDCGGGYVK	1.031761536	2	4.50742
P18418	IDDPTDSKPEDWDKPEHIPDPDAK	1.224570783	3	4.04155
P18418	IDNSQVESGSLEDDWDFLPPK	1.256378495	2	5.15647
P18418	IDNSQVESGSLEDDWDFLPPKK	1.357627636	2	4.71347
P18418	IKDPDAAKPEDWDER	1.055106354	2	4.24478
P18418	KPEDWDEEMDGEWEPPVIQNPEYK	0.989281672	3	4.97388
P18418	LFPGGLDQK	1.090942139	1	2.18857
P18418	QIDNPDYK	1.021448752	1	2.17454
P18418	SGTIFDNFLITNDEAYAEEFGNETWGVTK	1.105503725	3	5.72654
P18418	VHVIFNYK	1.311790853	1	2.32342
P18420	**PSA1 Proteasome subunit alpha type_1**	**0.994963161**	**0.7771**	**3**
P18420	AQPSQAADEPAEK	1.110239173	2	3.73488
P18420	ETLPAEQDLTTK	0.85409441	2	2.42912
P18420	NQYDNDVTVWSPQGR	0.988370857	2	3.65085
P18421	**PSB1 Proteasome subunit beta type_1**	**1.087687154**	**0.0528**	**2**
P18421	AGGSASAMLQPLLDNQVGFK	1.020222613	3	4.45752
P18421	GAVYSFDPVGSYQR	1.506795959	2	3.66226
P18445	**RL27A 60S ribosomal protein L27a**	**0.908814047**	**0.1369**	**2**
P18445	NGVAPIIDVVR	0.926847674	2	2.64837
P18445	NQSFCPTVNLDK	1.071711191	2	2.97949
P18484	**AP2A2 AP_2 complex subunit alpha_2**	**0.944357427**	**0.4199**	**5**
P18484	FVNLFPEVK	0.887624754	2	2.75243
P18484	KGPSTVTDLEETKR	1.021228312	3	3.39886
P18484	NNGVLFENQLLQIGLK	1.280604759	2	3.26417
P18484	QLSNPQQEVQNIFK	1.141412648	2	3.38691
P18484	THIETVINALK	1.07784023	2	2.31337
P18596	**AT2A3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 3**	**1.077521059**	**1**	**3**
P18596	DIVPGDIVEVAVGDKVPADLR	1.0637976	2	3.05682
P18596	SLPSVETLGCTSVICSDK	1.082264273	2	4.12725
P18596	VGEATETALTCLVEK	1.04927942	2	4.18403
P18757	**CGL Cystathionine gamma_lyase**	**0.962343887**	**0.0458**	**16**
P18757	AGDEVICMDEVYGGTNR	0.885873396	2	5.11028
P18757	AGDEVICMDEVYGGTNR+Oxidation(7)	1.030920874	2	3.87536
P18757	ATLGISDTLIR	0.967020037	2	3.61405
P18757	AVAALDGAK	1.05562096	2	2.35464
P18757	AVVLPISLATTFK	0.962006009	3	4.00649
P18757	FLQNSLGAVPSPFDCYLCCR	1.171915277	2	3.3921
P18757	GTLQHAQVFLK	0.940950612	2	2.75793
P18757	LFALAESLGGYESLAELPAIMTHASVPEK	1.383974249	3	4.27541
P18757	LFALAESLGGYESLAELPAIMTHASVPEKDR	1.067167803	4	4.96069
P18757	LLEAAITPQTK	0.904797237	2	3.87627
P18757	LSVGLEDEKDLLEDLGQALK	0.950017344	3	6.23347
P18757	LVWIETPTNPTLK	0.929728347	2	3.67406
P18757	QCTGCPGMVSFYIK	0.942851244	2	3.75661
P18757	QDSPGQSSGFVYSR	1.09555618	2	3.90645
P18757	RVASEFGLK	0.904785997	2	2.62401
P18757	VIYPGLPSHPQHELAK	0.825110506	2	3.89286
P18886	**CPT2 Carnitine O_palmitoyltransferase 2_ mitochondrial**	**1.000870368**	**0.9781**	**11**
P18886	ATNLTVSAVR	1.025923438	2	3.17474
P18886	ELHAHLLAQDK	0.823684503	2	2.86276
P18886	LIFDGNEETLK	0.94348512	2	2.68689
P18886	QKLIFDGNEETLKK	1.04533505	2	2.40026
P18886	QYGQTVATYESCSTAAFK	0.899928908	2	4.11356
P18886	SEYNDQLTR	1.023656481	2	2.84606
P18886	TETIRPASIFTK	0.932560747	2	2.45677

P18886	TLQAGLLEPEVFHLNPSK	3.280646257	2	3.46711
P18886	TLSIDSIQFQR	0.937988276	2	3.16756
P18886	YILSDSSPVPEFPVAYLTSENR	0.898562471	2	5.20472
P18886	YLNAQKPLLDDSQFR	0.985431562	2	3.83311
P19112	**F16P1 Fructose_1_6_bisphosphatase 1**	**1.092790499**	**2E-12**	**18**
P19112	AGGLATTGNEDILDIVPTEIHQK	1.042826002	3	6.20588
P19112	AGGTGEMTQLLNSLCTAIK	1.093876443	2	5.32427
P19112	AGGTGEMTQLLNSLCTAIK+Oxidation(6)	1.238946023	2	3.36578
P19112	APVIMGSTEDVQEFLEIYNK	1.266161069	2	5.0439
P19112	APVIMGSTEDVQEFLEIYNKDK	0.958228959	3	3.67353
P19112	DFDPAINEYIQR	0.862187926	2	3.82698
P19112	FPPDNSAPYGAR	1.148552424	2	2.59981
P19112	GNIYSINEGYAK	1.135678566	2	4.13688
P19112	KGNIYSINEGYAK	1.140153195	2	4.00568
P19112	KLDILSNDLVINMLK	1.06727895	2	5.29614
P19112	KTSANEPSEKDALQPGR	0.886504813	3	4.05417
P19112	LDILSNDLVINMLK	1.056578586	2	4.91645
P19112	LLYECNPIAYVMEK	1.20843647	2	4.13245
P19112	QAGIAQLYGIAGSTNVTGDQVK	1.111542187	3	5.94876
P19112	SRPSLPLPQSR	0.964200663	2	3.41265
P19112	SSYATCVLVSEEDTHAIIIEPEKR	1.099192526	3	5.30585
P19112	TLVYGGIFLYPANK	0.996103913	2	3.763
P19112	TSANEPSEKDALQPGR	0.988914813	2	3.70776
P19225	**CP270 Cytochrome P450 2C70**	**0.810472944**	**0.0012**	**9**
P19225	ACIGEGLAR	0.828372549	2	2.60974
P19225	ASLNLSNPQDFIDYFLIK	1.142912623	2	3.83638
P19225	EALIDRGEEFSDK	0.924642632	2	3.02281
P19225	IQEEVVYLLEALR	0.988606348	2	2.78222
P19225	KLPPGPTPLPIFGNILQVGVK	1.123699304	3	3.49089
P19225	KTTQDVEFR	0.830024128	2	2.32936
P19225	LPPGPTPLPIFGNILQVGVK	0.828039586	2	4.95572
P19225	SDYFMAFSAGRR+Oxidation(4)	1.058157676	1	1.96065
P19225	YIDFVPIPLPR	0.804512782	2	3.09975
P19234	**NDUV2 NADH dehydrogenase [ubiquinone] flavoprotein 2_ mitochondrial**	**0.99998977**	**0.1509**	**4**
P19234	DIEEIIDELR	0.939354309	2	3.41742
P19234	DTPENNPDTPFDFTPENYER	1.376706121	2	4.25552
P19234	FCCEPAGGLTSLTEPPK	1.208277386	2	2.85983
P19234	YHIQVCTTTPCMLR	1.048006262	2	2.47098
P19468	**GSH1 Glutamate__cysteine ligase catalytic subunit**	**0.960578711**	**0.7847**	**6**
P19468	CNQIANELCECPELLGSGFR	1.023277426	2	5.12767
P19468	EATSVLGEHQALCTITSFPR	0.822425667	2	3.72695
P19468	LDFLIPLSKVDENMK	0.86193835	2	2.46578
P19468	NTPSPFVETFPEDEEASK	1.119222649	2	4.42126
P19468	SLFFPDEAINK	0.942086223	2	2.62129
P19468	VQLLLNGGDVLETLQEK	0.985650407	2	4.81689
P19488	**UDB37 UDP_glucuronosyltransferase 2B37**	**0.930472473**	**1E-19**	**7**
P19488	ANAIAWALAQIPQK	1.292970314	3	6.17779
P19488	EVINNPFYK	1.102538343	1	2.29306
P19488	FETFPTSVSKDELEK	0.885222622	2	3.87159
P19488	GHEVTVLKPSAYYVLDPK	1.405132337	3	4.39868
P19488	NWDPFYTEILGRPTTLAETMGK	1.442711705	2	4.81902
P19488	SDLFNALK	0.715463612	2	2.79247
P19488	TILDELVQR	1.079120658	2	3.15476
P19511	**AT5F1 ATP synthase subunit b_ mitochondrial**	**0.904642832**	**0.1324**	**8**
P19511	HVIQSISAQQEK	0.995592281	2	3.88344
P19511	HVIQSISAQQEKETIAK	0.98194472	3	4.0154

P19511	HYLFDVQR	0.923906478	2	2.44848
P19511	LDYHISVQDMMR	1.067991347	3	3.99332
P19511	LNEEKIAQLEEIK	0.927668594	2	2.6918
P19511	RKEGEHMINWVEK	0.747973946	2	2.52264
P19511	YGASIGEFIDK	0.987507866	2	2.91781
P19511	YGASIGEFIDKLNEEK	1.006795659	2	3.60312
P19643	**AOFB Amine oxidase [flavin_containing] B**	**1.021815999**	**0.9691**	**11**
P19643	FIGGSGQVSER	1.073042168	2	3.21318
P19643	IISTTNGGQER	1.227201034	2	2.82676
P19643	IPEDEIWQPEPESVDVPARPITNTFLER	1.380462415	3	5.00739
P19643	KFIGGSGQVSER	1.182311704	2	2.95702
P19643	LERPVIHIDQTGENVVVK	1.132572375	3	5.09073
P19643	TLNHEIYEAK	1.011464809	2	2.99146
P19643	TMDEMGQEIPSDAPWK	1.145514849	2	3.21928
P19643	VLNSQEALQPVHYEEK	1.05020348	2	4.56713
P19643	YVDLGGSYVGPTQNR	0.985843302	2	4.19194
P19643	YVISAIPPVLGMK	0.963076113	2	3.15493
P19643	YVISAIPPVLGMK+Oxidation(11)	0.882448024	2	2.44538
P19686	**GCYA3 Guanylate cyclase soluble subunit alpha_3**	**0.86288225**	**0.0144**	**2**
P19686	DLAILQLGNGIR	0.866132384	2	2.70777
P19686	MMELSNEVMSPHGEPIK+Oxidation(8)	0.810238421	2	2.72507
P19804	**NDKB Nucleoside diphosphate kinase B**	**0.989165522**	**0.0033**	**8**
P19804	DRPFFPGLVK	0.688994455	2	2.42531
P19804	EIGLWFKPEELIDYK	0.908389029	2	3.92629
P19804	GDFCIQVGR	1.020913457	2	3.35049
P19804	NIIHGSDSVESAEK	0.975620284	1	3.90311
P19804	TFIAIKPDGVQR	0.998419215	2	2.88821
P19804	VMLGETNPADSKPGTIR	1.136749514	2	4.02131
P19804	VMLGETNPADSKPGTIR+Oxidation(1)	0.998058671	2	4.23787
P19804	YMNSGPVVAMVWEGLNVVK	1.226153573	2	4.93064
P19944	**RLA1 60S acidic ribosomal protein P1**	**1.07190233**	**1E-09**	**2**
P19944	AAGVNVEPFWPGLFAK	1.874330211	2	2.75832
P19944	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSAAAAPAEEK	1.0708035	4	6.73869
P19945	**RLA0 60S acidic ribosomal protein P0**	**1.080814239**	**3E-13**	**9**
P19945	AFLADPSAFAAAAPVAAATTAAPAAAAAPAK	0.977245027	2	5.7766
P19945	AGAIAPCEVTVPAQNTGLGPEK	0.974031774	3	4.38966
P19945	CFIVGADNVGSK	1.088331482	2	3.24024
P19945	GHLENNPALEK	0.956521147	2	3.54428
P19945	GNVGFVFTK	1.082317312	2	2.71427
P19945	GTIEILSDVQLIK	1.088975828	2	3.06176
P19945	IIQLLDDYPK	0.582979865	2	3.82948
P19945	TSFFQALGITTK	1.203144409	2	3.99835
P19945	VLALSVETDYTFPLAEK	1.328521166	2	2.45887
P20059	**HEMO Hemopexin**	**0.873503183**	**0.9703**	**6**
P20059	ELGSPPGISLDTIDAAFSCPGSSK	0.896696988	2	4.4177
P20059	FNPVTGEVPPR	0.909252939	2	2.45819
P20059	GECQSEGVLFFQGNR	0.870000943	2	3.78654
P20059	GGNNLVSGYPK	0.923728421	2	2.37534
P20059	LFQEEFPGIPYPPDAAVECHR	0.939277337	3	3.6533
P20059	SGAQATWAELSWPHEK	0.802994956	3	3.48147
P20069	**MPPA Mitochondrial_processing peptidase subunit alpha**	**1.123898205**	**0.9184**	**2**
P20069	HGGICDCQTSR	1.125831525	2	2.80956
P20069	LTDEEIEMTR	1.079614808	2	2.94816
P20070	**NB5R3 NADH_cytochrome b5 reductase 3**	**1.007952499**	**0.541**	**8**
P20070	DILLRPELEELR	0.903975521	2	2.55524
P20070	IDGNLVIRPYTPVSSDDDKGFVDLVVK	1.056481774	3	5.77773
P20070	LIDKEIISHDTR	0.993727966	3	3.51053

P20070	MSQYLENMNIGDTIEFR	1.476870306	2	3.92273
P20070	SSPAITLENPDIK	0.99584961	2	4.06346
P20070	SSPAITLENPDIKYPLR	0.913517007	2	3.40195
P20070	SVGMIAGGTGITPMLQVIR	0.895643089	2	4.37545
P20070	SVGMIAGGTGITPMLQVIR+Oxidation(3)	1.008108941	2	2.44581
P20280	**RL21 60S ribosomal protein L21**	**0.941770299**	**0.0026**	**3**
P20280	KGDIVDIK	0.948381909	1	1.90231
P20280	TNGKEPELLEPIPYEFMA	0.533368814	2	2.94176
P20280	VYNVTQHAVGIIVNK	1.029796507	2	4.29937
P20673	**ARLY Argininosuccinate lyase**	**1.045577706**	**1E-09**	**15**
P20673	AEAECEVLFPGYTHLQR	0.99792882	2	4.25052
P20673	AEMQQILQGLDK	0.968245612	2	3.79675
P20673	AEMQQILQGLDK+Oxidation(2)	0.917419086	2	3.15258
P20673	EFNFVQLSDAYSTGSSLMPQK	1.032183389	2	5.649
P20673	FNSSIAYDR	1.104894159	2	2.59438
P20673	HLWNVDLQGSK	1.024920728	1	3.21947
P20673	INVLPLGSGAIAGNPLGVDR	1.132903052	2	4.91881
P20673	KNPDSLELIR	1.079499426	2	2.43733
P20673	LKELIGEAAGK	1.011852033	2	2.81665
P20673	LYPNDEDIHTANER	1.051795985	2	3.83043
P20673	MAEDLILYGTK	0.933563213	2	3.49914
P20673	MAEDLILYGTK+Oxidation(0)	1.021579283	2	2.46255
P20673	NDQVVTDLR	1.013666983	2	3.43802
P20673	SRNDQVVTDLR	0.647606722	2	2.77456
P20673	VAEEWAQGIFK	1.37807099	2	3.29224
P20788	**UCRI Cytochrome b_c1 complex subunit Rieske_ mitochondrial**	**1.086624323**	**0.4796**	**3**
P20788	EIDQEAAVEVSQLR	1.096820346	2	4.34408
P20788	GVAGALRPLLQSAVPATSEPPVLDVK	1.095283331	3	4.56071
P20788	SGPFAPVLSATSR	1.107808303	2	2.95112
P20801	**TNNC2 Troponin C_ skeletal muscle**	**1.088256695**	**0.8667**	**3**
P20801	GKSEEELAECFR	1.149912835	2	3.04579
P20801	NADGYIDAEELAEIFR	1.08228099	2	4.4879
P20801	SEEELAECFR	1.551890323	2	2.83499
P20814	**CP2CD Cytochrome P450 2C13_ male_specific**	**1.153788809**	**0.8576**	**3**
P20814	FDYEDKDFLNLIEK	1.043998281	3	3.6812
P20814	GTAVLTSLTSVLHDSK	1.042383597	2	3.31265
P20814	IKEHEESLDVSNPR	1.15855067	3	3.85185
P20817	**CP4AE Cytochrome P450 4A14**	**0.785813208**	**2E-13**	**6**
P20817	ACQIAHEHTDGVIK	0.401017968	2	3.81262
P20817	AQLQNEEELQK	0.424818275	2	3.39083
P20817	AVEDLNNLTFFR	0.576334542	2	3.26148
P20817	EFQQVLTWVEK	0.539859001	2	2.70812
P20817	MRKAQLQNEEELQK+Oxidation(0)	0.879399995	2	2.91101
P20817	VLLYDPDYVK	0.364771421	2	2.83023
P20852	**CP2A5 Cytochrome P450 2A5**	**0.82543569**	**0.0101**	**2**
P20852	DFIDSFLIR	0.857624202	2	2.50323
P20852	EALVDQAEEFSGR	0.824583997	2	3.40568
P21213	**HUTH Histidine ammonia_lyase**	**0.882602169**	**0.4988**	**10**
P21213	DIITTELNSATDNPMVFASR	1.074482295	2	2.98424
P21213	GETISGGNFHGEYPAK	0.870113446	2	3.87225
P21213	LQELQVNLVR	0.880287907	2	3.0479
P21213	NKPDNGGFTSVDEVR	0.83826106	2	3.41548
P21213	SHSSGVGKPLSPER	1.350981981	2	4.09309
P21213	SLLDSDHHPSEIAESHR	0.791022962	3	4.53264
P21213	TVVYGITTGFGK	1.061591013	2	2.90026
P21213	VQDAYTLR	0.885196265	2	2.3822
P21213	VWEVAAPYIEK	0.898260544	2	2.36307

P21213	YIALDGDSLSTEDLVNLGK	0.774870453	2	4.67255
P21396	**AOFA Amine oxidase [flavin_containing] A**	**1.019546767**	**0.7834**	**6**
P21396	DVPAIEITHTFLER	0.950489538	2	3.17589
P21396	INVLVLEAR	1.162193303	2	3.14378
P21396	KDIWVEEPESK	0.910956377	2	3.25748
P21396	VLGSQEALYPVHYEEK	0.985619973	2	3.90242
P21396	WVDVGGAYVGPTQNR	0.950465824	2	4.23585
P21396	YVISAIPPILTAK	1.252939832	2	2.53902
P21531	**RL3 60S ribosomal protein L3**	**1.106301504**	**0.4939**	**6**
P21531	AHLMEIQVNGGTVAEK	1.076765004	2	3.86823
P21531	ERLEQQVPVNQVFGQDEMIDVIGVTK	0.987868743	3	5.46125
P21531	HGSLGFLPR	1.031246341	2	2.69091
P21531	LEQQVPVNQVFGQDEMIDVIGVTK	1.297187668	2	4.05551
P21531	NNASTDYDLSDK	1.049897002	2	3.30835
P21531	TVFAEHISDECK	1.06471977	2	3.12186
P21533	**RL6 60S ribosomal protein L6**	**1.204541254**	**1E-19**	**6**
P21533	HQEGEIFDTEK	1.21518382	2	3.2541
P21533	HQEGEIFDTEKEK	1.03290539	2	3.92587
P21533	HQEGEIFDTEKEKYEITEQR	1.089533878	3	3.79087
P21533	QLGSGLLLVTGPLALNR	1.341609291	2	4.89407
P21533	SSITPGTVLIILTGR	1.094548958	2	4.06855
P21533	YYPTEDVPR	1.060144844	1	2.09765
P21571	**ATP5J ATP synthase_coupling factor 6_ mitochondrial**	**1.10563733**	**6E-12**	**6**
P21571	FEVLDKPQS	1.073573277	2	3.11043
P21571	GEMDKFPTFNFEDPK	1.084507104	3	3.707
P21571	GEMDKFPTFNFEDPKFEVLDKPQS	0.981951649	3	3.4255
P21571	LASGGPVDTGPEYQQEVDR	1.416483837	2	5.13274
P21571	LASGGPVDTGPEYQQEVDRELFK	1.112960282	2	2.48142
P21571	RLASGGPVDTGPEYQQEVDR	1.020322952	3	4.11158
P21643	**T23O Tryptophan 2_3_dioxygenase**	**1.101649771**	**0.1965**	**2**
P21775	**THIKA 3_ketoacyl_CoA thiolase A_ peroxisomal**	**0.803694301**	**8E-14**	**2**
P21775	LKPECLGDISVGNVLEPGAGAVMAR	0.794488065	3	5.87609
P21775	LKPECLGDISVGNVLEPGAGAVMAR+Oxidation(22)	0.857657114	3	4.06459
P21913	**DHSB Succinate dehydrogenase [ubiquinone] iron_sulfur subunit_ mitochondrial**	**1.025332716**	**0.056**	**7**
P21913	CGPMVLDALIKIK	0.916349932	2	2.42095
P21913	CHTIMNCTQTCPK	0.875394664	2	4.29317
P21913	CHTIMNCTQTCPK+Oxidation(4)	1.317821248	2	3.79977
P21913	IKNEIDSTLTFR	1.17627892	2	2.44128
P21913	LQDPFSLYR	1.311676271	2	2.60086
P21913	NEIDSTLTFR	1.052171322	2	2.35649
P21913	RIDTDLGK	1.003804259	2	2.54245
P21981	**TGM2 Protein_glutamine gamma_glutamyltransferase 2**	**1.062633494**	**0.9449**	**4**
P21981	CDLEIQANGR	1.046947219	2	3.26577
P21981	DLYLENPEIK	1.00077791	2	2.6983
P21981	SEGTYCCGPVSVR	1.062747696	2	3.55967
P21981	YSGCLTESNLIK	1.140419209	2	3.05601
P22734	**COMT Catechol O_methyltransferase**	**1.298999256**	**1E-19**	**12**
P22734	AIYQGPSSPDKS	1.261281582	2	2.97669
P22734	EWAMNVGDAK	1.263440047	1	2.62291
P22734	GQIMDAVIR	1.312947481	2	2.33831
P22734	GQIMDAVIR+Oxidation(3)	1.355172307	2	2.54982
P22734	GTVLLADNVIVPGTPDFLAYVR	1.716651892	3	4.70601
P22734	KGTVLLADNVIVPGTPDFLAYVR	1.809305658	2	4.687
P22734	KYDVDTLDMVFLDHWK	1.529901335	3	4.873
P22734	VTILNGASQDLIPQLK	1.222314148	2	4.35623
P22734	VVDGLEK	1.430292658	2	2.43901

P22734	YDVDTLDMVFLDHWK	1.36669213	3	4.28956
P22734	YLPDTLLLEK	1.301136818	1	2.67115
P22734	YVQQNAKPGDPQSVLEAIDTYCTQK	1.461578612	3	5.96864
P22789	**ST2A2 Alcohol sulfotransferase A**	**1.088660245**	**9E-06**	**4**
P22789	EEDLILLTYPK	1.181104628	2	2.32095
P22789	ETLQNVCNK	0.387291169	1	2.27839
P22789	KLEPDELDLVLK	0.471673278	3	3.90803
P22789	NHFTVAQAEAFDK	1.039156909	2	3.71498
P22791	**HMCS2 Hydroxymethylglutaryl_CoA synthase_ mitochondrial**	**0.963151736**	**7E-13**	**19**
P22791	ASLDMFNK	1.057400026	2	2.90056
P22791	ASLDMFNKK	0.88547807	2	2.51672
P22791	GLKLEETYTNK	1.068618013	2	2.99163
P22791	GTHMENAYDFYKPNLASEYPLVDGK	1.086008626	3	6.62505
P22791	GTHMENAYDFYKPNLASEYPLVDGK+Oxidation(3)	1.04080698	3	5.79219
P22791	IGAFSYGSGLAASFFSFR	1.15282661	2	3.0814
P22791	LEETYTNK	1.075204706	2	2.87661
P22791	LEETYTNKDVDK	0.986646314	2	4.3151
P22791	LEVGTETIIDK	0.980905745	2	3.73095
P22791	LMFNDFLSSSSDK	1.379524622	2	4.13389
P22791	LMFNDFLSSSSDK+Oxidation(1)	1.381912067	2	4.02719
P22791	LVSSVSDLPK	1.103103904	2	3.61719
P22791	MGFCSVQEDINSLCLTVVQR	1.180690095	2	3.11578
P22791	MSPEEFTEIMNQR	0.985163262	2	4.83076
P22791	MSPEEFTEIMNQR+Oxidation(0)	1.017105871	2	4.04699
P22791	MSPEEFTEIMNQR+Oxidation(9)	1.019084845	2	3.32034
P22791	TKLPWDAVGR	0.96903264	3	4.0271
P22791	VNFSPPGDTSNLFPGTWYLER	1.263484667	2	5.05121
P22791	YTVGLGQTR	1.012483592	2	3.29762
P22985	**XDH Xanthine dehydrogenase/oxidase**	**1.053935868**	**0.9988**	**8**
P22985	DEVTCVGHIIGAVVADTPEHAQR	1.010092272	3	3.67183
P22985	ITSIDTSEAK	1.140092641	1	1.90107
P22985	LDPTFASATLLFQK	1.157433208	2	3.83405
P22985	NQPEPTVEEIENAFQGNLCR	1.027688392	2	4.90342
P22985	QLFQLDSPATPEK	1.082957515	2	3.00266
P22985	SVASIGGNIITASPISDLNPVFMASGAK	1.074714184	3	5.62266
P22985	TGTVVALEVAHFSNGGNTEDLSR	0.972135092	3	4.89942
P22985	TNLPSNTAFR	0.939938023	1	2.07468
P23358	**RL12 60S ribosomal protein L12**	**0.974684481**	**8E-12**	**5**
P23358	CTGGEVGATSALAPK	1.035469157	2	3.82629
P23358	EILGTAQSVGCNVDGR	0.858490883	2	4.81103
P23358	HNGNITFDEIVNIAR	1.091570694	2	4.09509
P23358	HPHDIIDDINSGAVECPAS	0.990496026	2	4.10481
P23358	QAQIEVVPSASALIIK	1.331504899	2	3.92014
P23457	**DIDH 3_alpha_hydroxysteroid dehydrogenase**	**1.219566661**	**1E-19**	**8**
P23457	ALDGLNR	1.081941505	2	2.43837
P23457	ELTQVFEFQLASEDMK	1.08049898	2	3.49398
P23457	HFDSAYLYEVEEEVGQAIR	1.218903106	2	5.92174
P23457	MLDYCK	0.885573267	1	1.91229
P23457	SIGVSNFNCR	1.081995336	2	3.46889
P23457	SPVLLDDPVLCAIAK	1.780159272	2	4.0377
P23457	VALNDGNFIPVLGFGTTVPEK	1.573233712	2	4.85325
P23457	YFDDHPNHPFTDE	1.362532227	2	4.19453
P23514	**COPB Coatomer subunit beta**	**1.016245017**	**0.0306**	**5**
P23514	EAGELKPEEEITVGPVQK	0.994481045	2	4.5155
P23514	NFENLIPDAPELIHDFLVNEK	0.958099231	3	4.45395
P23514	TNNVSEHEDTDKYR	1.640714006	2	4.32995
P23514	VLQDLVMDILR	0.996235382	2	3.00051

P23514	YEAAGTLVTLSSAPTAIK	1.181824913	2	4.79541
P23591	**FCL GDP_L_fucose synthase**	**1.011972388**	**0.8774**	**2**
P23591	DADLTDAAQTQALFQK	1.083554231	2	3.37049
P23591	VVADGAGLPGEEWVFVSSK	0.954951317	2	3.73895
P23965	**ECI1 Enoyl_CoA delta isomerase 1_ mitochondrial**	**0.659173612**	**1E-19**	**7**
P23965	ALQLGTLFPPAEALK	0.596316112	2	4.76797
P23965	DNYVNTIGHR	0.53796173	2	2.76127
P23965	GVILTSERPGIFSAGLDLMEMYGR	0.795742508	3	5.55288
P23965	QREADIQNFTSFISR	0.960762876	2	2.66451
P23965	SLHVYLEK	0.587566585	2	2.3176
P23965	VGLVDEVVPEDQVHSK	0.626686804	2	4.53712
P23965	WFTIPDHSR	1.025976814	2	3.17508
P24049	**RL17 60S ribosomal protein L17**	**0.984681167**	**1E-16**	**3**
P24049	EQIVPKPEEEVAQK	0.986074282	2	3.65681
P24049	GLDVDSLVIEHIQVNK	1.016675912	2	4.55785
P24049	YSLDPENPTK	0.785284592	1	2.73131
P24090	**FETUA Alpha_2_HS_glycoprotein**	**0.899946665**	**0.8324**	**6**
P24090	ELACDDPETEHVALIAVDYLNK	1.036538672	2	4.73212
P24090	HAFSPVASVESASGEVLHSPK	0.954527278	3	5.55562
P24090	LGGEEVSVACK	0.852002852	2	3.37913
P24090	QQAEHAVEGDCDFHILK	1.091614863	3	3.35075
P24090	VGQPGDAGAAGPVAPLCPGR	0.812716325	2	4.78992
P24090	VLHAQCHSTPDSAEDVRK	0.829714421	3	3.46941
P24268	**CATD Cathepsin D**	**1.177241522**	**0.0073**	**3**
P24268	AIGAVPLIQGEYMIPCEK	0.975006408	2	3.12601
P24268	DPTGQPGGELMLGGTDSR	1.104575135	2	3.82147
P24268	LGGQNYELHPEK	1.303103753	2	2.99286
P24329	**THTR Thiosulfate sulfurtransferase**	**0.883955316**	**1E-19**	**12**
P24329	EGHPVTSEPSRPEPAVFK	0.816049189	2	4.90278
P24329	FQLVDSR	0.92531874	2	2.61509
P24329	GSVNVPFMNFLTEDGFEK	1.158984259	2	3.52668
P24329	HVPGASFFDIEECR	1.261019996	2	3.43571
P24329	KVDLSQPLIATCR	1.125381206	2	4.1364
P24329	RFQLVDSR	0.999838689	2	2.3782
P24329	TVSVLNGGFR	0.912899019	2	3.16413
P24329	TYEQVLENLQSK	0.88413763	2	5.03022
P24329	VDLSQPLIATCR	1.114652139	2	3.83573
P24329	VLDASWYSPGTR	0.925623628	2	3.72661
P24329	WLAESIR	0.82617343	2	2.3667
P24329	YLGTQPEPDAVGLDSGHIR	0.992789263	3	4.78427
P24368	**PPIB Peptidyl_prolyl cis_trans isomerase B**	**0.933215041**	**0.9634**	**8**
P24368	DKPLKDVIIVDCGK	0.942710571	2	3.77821
P24368	DTNGSQFFITTVK	0.904334002	2	4.035
P24368	HYGPGWVSMANAGK	1.020631036	2	3.27285
P24368	IEVEKPFAIAK	0.944118448	2	3.18201
P24368	IEVEKPFAIAKE	0.759901462	2	3.05273
P24368	TVDNFVALATGEK	0.994264369	2	3.54878
P24368	VLEGMDVVR	1.02268285	2	2.67682
P24368	VYFDFQIGDEPVGR	0.965153172	2	3.80976
P24457	**CP2DB Cytochrome P450 2D11**	**1.414207591**	**0.0104**	**2**
P24457	RFSVSTLR	1.423669679	2	2.82721
P24457	SLEEWVTK	1.293923936	2	2.65561
P24470	**CP2CN Cytochrome P450 2C23**	**0.817759883**	**1E-19**	**7**
P24470	ACVGESLAR	0.871842575	2	2.46286
P24470	DLDIKPITTGIINLPPPYK	0.741858921	3	3.78334
P24470	EALLQQGDEFLGR	0.630949972	2	2.5545
P24470	GYGLIFSNGER	0.804680139	2	3.6168

P24470	IEEEKDNLK	1.019130998	1	2.92438
P24470	TFLNLMDLLNK	0.876717791	2	3.60569
P24470	YITLLPSSLPHAVVQDTK	0.693332544	2	3.16862
P24473	**GSTK1 Glutathione S_transferase kappa 1**	**0.963240486**	**0.1514**	**7**
P24473	AGMATAQAQHLLNK	0.949063174	2	3.88455
P24473	DEDITESQNILSAAEK	1.123954751	2	5.43109
P24473	DSGNQPPAMVPHK	0.905150191	2	2.32207
P24473	FLTAVSMEQPEMLEK	0.925732653	2	3.98601
P24473	IWSRDEDITESQNILSAAEK	0.904816846	3	3.43273
P24473	MELLAYLLGEK	1.201205713	2	3.94634
P24473	YGAFGLPTTVAHVDGK	0.952930439	2	3.8203
P25093	**FAAA Fumarylacetoacetase**	**0.95884728**	**1E-12**	**14**
P25093	AIDVGQGQTR	1.017344357	2	3.54454
P25093	ASLQNLLSASQAQLR	1.139872187	2	4.66278
P25093	ASLQNLLSASQAQLRDDK	1.084365964	2	3.00562
P25093	ASSVVVSGTPIR	1.066343704	2	3.4442
P25093	DIQQWEYVPLGPFLGK	0.867804028	2	4.64119
P25093	FGEPIPISK	1.04013807	2	2.8973
P25093	GEGMSQAATICR	0.882924706	2	3.61084
P25093	GEGMSQAATICR+Oxidation(3)	0.951010669	2	2.90214
P25093	GKENALLPNWLHLPVGYHGR	2.422512134	3	3.33274
P25093	HLFTGPVLSK	0.918854344	1	2.47116
P25093	HQHVFDETTLNSFMGLGQAAWK	1.106541129	2	5.51093
P25093	IGVAIGDQILDLSVIK	1.250790669	2	5.53254
P25093	TFLLDGDEVIITGHCQGDGYR	0.88854425	2	5.01644
P25093	VGFGQCAGK	0.998667746	1	1.93865
P25113	**PGAM1 Phosphoglycerate mutase 1**	**1.118823071**	**0.1065**	**6**
P25113	ALPFWNEEIVPQIK	1.133298773	2	3.88551
P25113	FSGWYDADLSPAGHEEAK	1.074376512	2	4.73097
P25113	HGESAWNLENR	1.04244922	2	3.78752
P25113	SYDVPPPPMEPDHPFYSNISK	1.159097165	2	4.29675
P25113	YADLTEDQLPSCESLK	1.050644318	2	5.34707
P25113	YADLTEDQLPSCESLKDTIAR	1.023308553	2	5.01171
P25235	**RPN2 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit 2**	**1.00744185**	**1E-19**	**13**
P25235	EDQVIQLMNTIFSK	1.129700586	2	3.26069
P25235	EETVLATVQALHTASHLSQQADLR	1.084118861	3	5.23806
P25235	FELDTSER	0.990840135	1	2.00651
P25235	FPEEEAPSTVLSQNLFTPK	0.732073313	2	3.90851
P25235	ISTEVGITNVDLSTVDKDQSIAPK	1.096642986	2	4.62573
P25235	LQVSSVLSQPLAQAAVK	1.256165549	2	4.86108
P25235	LSKEETVLATVQALHTASHLSQQADLR	1.024412764	3	5.42841
P25235	NFESLSEAFSVASAAAALSQNR	1.059020623	3	4.31454
P25235	NIVEEIEDLVAR	0.896183352	3	4.72779
P25235	NPILWNVADVVIK	1.324977832	2	2.37568
P25235	TGQEVVFVAEPDNK	1.008243987	2	3.87823
P25235	YHVPVVVVPEGSASDTQEQAILR	1.253786377	3	5.42244
P25235	YIANTVELR	1.014187203	2	2.66046
P25318	**chain**	**0.734022028**	**0.005**	**2**
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.721457147	2	2.65632
P25318	GQYLEMPLPMLPMDLKGEPGPPGKPGPR+Oxidation(5)	0.721457147	2	2.5496
P25409	**ALAT1 Alanine aminotransferase 1**	**3.179640749**	**1E-19**	**3**
P25409	AWALDIAELR	3.729669316	2	2.56619
P25409	LTEQVFNEAPGIR	2.703796764	2	3.57794
P25409	VLCVINPGNPTGQVQTR	11.62432022	2	4.27352
P26039	**TLN1 Talin_1**	**0.869162888**	**0.0111**	**14**
P26039	AGALQCSPSDVYTK	0.818499852	2	2.63114

P26039	AQEACGPLEMDSALSVVQNLEK	1.073270993	2	3.79139
P26039	ASAGPQPLLVQSCK	0.954117057	2	2.53924
P26039	AVAEQIPLLVQGVR	0.884811439	2	3.405
P26039	EAAEGLRMATNAAAQNAIKK	0.955919449	2	2.80724
P26039	GVGAAATAVTQALNELLQHVK	0.865124576	3	4.44852
P26039	LGAASLGAEDPETQVVLINAVK	1.183038814	2	3.58318
P26039	LLGEIAQGNENYAGIAAR	1.049127225	2	3.79113
P26039	LNEAAAGLNQAATELVQASR	0.987958104	2	5.26423
P26039	SNTSPEELGPLANQLTSDYGR	0.943157394	2	3.9661
P26039	VGAIPANALDDGQWSQGLISAAR	0.891137262	2	4.50898
P26039	VGDDPAVWQLK	0.879435433	2	3.13115
P26039	VLVQNAAGSQEK	0.9571052	2	2.83711
P26039	VVAPTISSPVCQEQLVEAGR	0.873668329	2	4.75194
P26043	**RADI Radixin**	**0.981679072**	**0.9788**	**10**
P26043	AFAAQEDLEK	1.011719245	2	2.36415
P26043	ALELEQER	0.938531362	1	1.95868
P26043	FFPEDVSEELIQEITQR	0.96334808	3	4.11106
P26043	KKEEEATEWQHK	0.55563302	3	4.27476
P26043	KTQNDVLHAENVK	0.987855087	2	4.92621
P26043	NQEQLAAELAEFTAK	0.946825058	2	4.91598
P26043	QLQALSSELAQAR	0.978262523	2	3.36235
P26043	RKPDTIEVQQMK	0.876718582	2	3.70748
P26043	RKPDTIEVQQMK+Oxidation(10)	1.08680357	2	2.48106
P26043	TQNDVLHAENVK	1.023086553	2	3.58634
P26231	**CTNA1 Catenin alpha_1**	**1.017930686**	**0.6497**	**7**
P26231	AVMDHVSDSFLETNVPLLVLIEAAK	0.888209998	3	3.64538
P26231	IAEQVASFQEEK	1.161361643	2	2.65031
P26231	LIEVANLACSISNNEEGVK	0.963718538	2	3.85995
P26231	LLEPLVTQVTTLVNTNSK	0.983628607	2	3.72508
P26231	QIIVDPLSFSEER	1.005418192	2	2.48735
P26231	SAAGEFADDPCSSVK	1.017264561	2	4.0184
P26231	TIADHCPDSACK	0.18152912	2	3.07811
P26284	**ODPA Pyruvate dehydrogenase E1 component subunit alpha_ somatic form_ mitochondrial**	**0.867571378**	**0.0627**	**7**
P26284	AILAELTGR	0.855733363	2	2.62506
P26284	EEIQEVRSK	0.998201554	1	1.96172
P26284	GFCHLCDGQEACCVGLEAGINPTDHLITAYR	0.968233947	3	6.47797
P26284	LEEGPPVTTVLTR	0.875184665	2	3.60521
P26284	RGDFIPGLR	1.047031653	2	2.70311
P26284	TREEIQEVR	1.038916823	2	2.8873
P26284	VDGMDILCVR	0.945390776	2	3.25842
P26453	**BASI Basigin**	**1.13055712**	**2E-06**	**6**
P26453	GNINVEGPPR	1.15485978	2	3.34943
P26453	RKPDQTLDEDDPGAAPLK	1.181251808	3	3.75508
P26453	SEASHPPVDEWVWFK	1.102044885	3	3.8958
P26453	SEHASEGEFVK	1.326698545	2	3.00601
P26453	SGEYSCIFLPEPVGR	1.119473898	2	3.15877
P26453	VLQEDTLPDLQMK	0.986232575	2	4.10628
P26772	**CH10 10 kDa heat shock protein_ mitochondrial**	**1.124915661**	**0.0084**	**6**
P26772	GGEIQPVSVK	0.97267288	2	3.37843
P26772	GGIMLPEK+Oxidation(3)	0.983658604	2	2.4629
P26772	GKGGEIQPVSVK	0.964978952	2	3.08695
P26772	VLLPEYGGTK	0.845235922	1	2.10664
P26772	VLQATVVAVGSGGK	0.929482959	2	5.08633
P26772	VVLDDKDYFLFR	1.101652272	3	3.62946
P27139	**CAH2 Carbonic anhydrase 2**	**0.704050819**	**0.1074**	**2**
P27139	AVQHPDGLAVLGIFLK	0.702506614	2	3.22529

P27139	IGPASQGLQK	0.618446888	2	3.13077
P27321	**ICAL Calpastatin**	**0.88598605**	**0.0074**	**3**
P27321	KGSDEVTASSAATGTSPR	0.890303313	2	5.0186
P27321	LSAAVSETVSQVPAPSNHTAAPPPGTER	1.178957086	3	4.31722
P27321	SQSSEPPVIHEK	0.919308913	2	3.1737
P27364	**3BHS5 3 beta_hydroxysteroid dehydrogenase type 5**	**0.891872427**	**0.0949**	**5**
P27364	AVLAANGSILK	0.863358104	2	2.7384
P27364	ETILNDREEEHR	0.886519947	2	2.73543
P27364	GDIVDAQFLR	0.859380008	2	3.12632
P27364	NGGTFHTCALR	1.131299936	2	2.57344
P27364	QTILDVNVK	0.814622191	1	2.17894
P27605	**HPRT Hypoxanthine_guanine phosphoribosyltransferase**	**0.812261764**	**1E-05**	**6**
P27605	DLNHVCVISESGK	0.771108536	2	3.50849
P27605	FFADLLDYIK	0.875632108	2	3.4555
P27605	NVLIVEDIIDTGK	0.893807213	2	3.79786
P27605	SVGYRPDFVGFEIPDK	0.885385349	3	3.57219
P27605	SYCNDQSTGDIK	0.897306269	2	3.95982
P27605	VIGGDDLSTLTGK	1.228872877	2	3.18914
P27653	**C1TC C_1_tetrahydrofolate synthase_ cytoplasmic**	**0.934833531**	**1E-11**	**17**
P27653	ASQAPSSFQLLYDLK	1.450921545	2	4.30461
P27653	AYTEEDLDLVEK	1.161362482	2	2.5063
P27653	GEWIKPGAVVIDCGINYVPDDTKPNGR	1.060187506	3	3.77893
P27653	IFHELTQTDK	0.981277886	2	2.84866
P27653	ITIGQAPTEK	1.155807867	2	2.47841
P27653	IYGADDIELLPEAQNK	1.379678367	2	5.25658
P27653	KITIGQAPTEK	1.055870599	2	3.18077
P27653	KVVGDVAYDEAK	0.992674117	2	3.81902
P27653	LDIDPETITWQR	1.071561295	2	3.63466
P27653	MHGGGPTVTAGLPLPK+Oxidation(0)	0.942874783	2	3.6224
P27653	QGFGNLPICMAK	0.89824001	2	3.27286
P27653	TADLDKEVNKGDILVVATGQPEMVK	0.981851084	3	4.16299
P27653	TDPAALTDDEINR	0.895070853	2	4.33579
P27653	THLSLSHNPEQK	1.190846138	2	3.81897
P27653	VVGDVAYDEAK	1.072869043	2	3.35609
P27653	YSGLQPHVVVLVATVR	1.201428943	3	3.30683
P27653	YVVVTGITPTPLGEGK	1.081260556	2	4.21329
P27657	**LIPP Pancreatic triacylglycerol lipase**	**0.718000673**	**0.1431**	**2**
P27657	ATYTQATQNVR	0.266646871	2	2.49848
P27657	ITGLDAAEPYFQGTPEEVR	0.770130596	2	2.51092
P27661	**H2AX Histone H2A.x**	**0.998379486**	**0.566**	**3**
P27661	AGLQFPVGR	0.965891755	2	3.23277
P27661	HLQLAIR	1.061367903	2	2.60604
P27661	LLGGVTIAQGGVLPNIQAVLLPK	0.949241228	3	4.10022
P27867	**DHSO Sorbitol dehydrogenase**	**0.945204824**	**1E-08**	**13**
P27867	AMGASQVVVIDLSASR	1.000538142	2	4.11757
P27867	AVEAFETAK	0.880664517	2	3.01735
P27867	EVGADFTIQVAK	0.909660606	2	2.64929
P27867	GENLSLVVHGPGDIR	0.942571411	3	3.80431
P27867	HSADFCYK	1.006281749	2	2.85
P27867	IGDFVVK	1.019074948	2	2.54351
P27867	LENYPIPELGPNDVLLK	0.946579977	2	4.85463
P27867	LPDSVTFEEGALIEPLSVGIYACR	1.285182887	2	4.72599
P27867	MHSVGICGSDVHYWEHGR+Oxidation(0)	1.088206537	3	3.88586
P27867	TLNVKPLVTHR	0.969792431	2	3.17169
P27867	VAIEPGVPR	1.233520378	2	2.40722
P27867	VAIEPGVPREIDEFCKIGR	0.84858655	2	2.34694
P27867	VLVCGAGPIGIVTLLVAK	1.308924702	2	5.42327

P27952	**RS2 40S ribosomal protein S2**	**1.07034887**	**0.4232**	**5**
P27952	AEDKEWIPVTK	1.072606047	3	3.35124
P27952	AFVAIGDYNGHVGLGVK	1.270840062	2	4.06886
P27952	GCTATLGNFAK	1.051068484	2	2.80629
P27952	GTGIVSAPVPK	1.080941163	2	2.77703
P27952	TYSYLTPDLWK	1.093192208	2	2.593
P28037	**AL1L1 Cytosolic 10_formyltetrahydrofolate dehydrogenase**	**0.961029482**	**9E-06**	**25**
P28037	ADPLGLEAEK	1.122320196	2	2.53789
P28037	ANATEFGLASGVFTR	1.109831595	2	4.16629
P28037	AVQMGMSSVFFNK	1.037503571	2	2.86603
P28037	CPQSEEGATYEGIQK	2.253800182	2	4.59369
P28037	DLGEAALNEYLR	0.795746396	2	3.65357
P28037	ECEVLPDDTVSTLYNR	1.156192917	2	3.88477
P28037	EGHEVVGVFTIPDKDGK	0.951651825	2	4.85121
P28037	GNDKVPGAWTEACGQK	0.904455116	2	3.55453
P28037	GQALPEVVAK	0.963738798	2	2.52297
P28037	GSASSDLELTEAELATAEAVR	1.022317367	2	6.49627
P28037	GVVNILPGSGSLVGQR	0.939827967	2	4.84727
P28037	IGFTGSTEVGK	1.025580653	2	3.00185
P28037	ILPNVPEVEDSTDFFK	1.067851902	2	3.8518
P28037	INWDQPAEAIHNWIR	0.955385004	2	3.83085
P28037	IQGATIPINQARPNR	0.980139662	2	2.33813
P28037	KEGHEVVGVFTIPDKDGK	0.800693644	3	3.37735
P28037	KIGFTGSTEVGK	0.941405853	2	2.82224
P28037	KLVEYCQR	1.229166104	2	2.42457
P28037	LFVEESIHNQFVQK	0.897531201	2	4.41216
P28037	LIAEGTAPR	0.959290984	2	2.4941
P28037	LSDHPDVR	0.807809755	1	2.12673
P28037	NIQLEDGK	0.936104647	1	2.32416
P28037	TAACLAAGNTVVIKPAQVTPLTALK	1.08421701	3	4.18165
P28037	TDVAAPFGGFK	0.903519742	2	3.01462
P28037	TYNTINPTDGSVICQVSLAQVSDVDK	1.015365195	2	5.16575
P28064	**PSB8 Proteasome subunit beta type_8**	**1.041372274**	**0.6087**	**3**
P28064	ASAGSYIATIR	0.920265009	2	2.87183
P28064	QDLSPEEAYDLAR	1.04228139	2	2.90783
P28064	VESTDVSDLLHK	1.282593448	2	2.39108
P28480	**TCPA T_complex protein 1 subunit alpha**	**0.948964785**	**0.0375**	**8**
P28480	AFHNEAQVNPER	0.919800287	2	3.47714
P28480	FATEAAITILR	1.044450183	2	2.72551
P28480	HGGYENAVHSGALDD	1.246251099	2	3.71735
P28480	ICDDELILIK	1.096831983	2	2.55301
P28480	LLEVEHPAAK	0.942249018	2	2.46742
P28480	SLLVIPNTLAVNAAQDSTDLVAK	1.035698217	2	4.15325
P28480	SQNVMAAASIANIVK	1.136200114	2	3.53311
P28480	YINENLIINTDELGR	1.07639334	2	4.68646
P28492	**GLSL Glutaminase liver isoform_ mitochondrial**	**1.066688107**	**0.4526**	**3**
P28492	ATGLQTSDPR	0.988015122	2	2.44686
P28492	LSLNEEGIPHNPMVNAGAIVVSSLIK	1.092302015	3	4.75565
P28492	SNPDLWGVSLCTVDGQR	1.13204751	2	2.58539
P29147	**BDH D_beta_hydroxybutyrate dehydrogenase_ mitochondrial**	**0.97066651**	**1E-19**	**16**
P29147	AVLVTGCDSGFGFSLAK	0.93802623	2	5.55481
P29147	FGVEAFSDCLR	1.011031842	2	3.361
P29147	GFLVFAGCLLK	1.047731074	2	3.2531
P29147	KMWDELPEVVR	1.240464725	2	2.48633
P29147	MANPARSPYCITK+Oxidation(0)	0.839449252	2	2.41989
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR	1.247666293	3	4.85652
P29147	METYCNSGSTDTSSVINAVTHALTAATPYTR+Oxidation(0)	1.081545472	3	4.83018

P29147	MQVMTHFPGAISDK	1.155970065	2	3.57599
P29147	MQVMTHFPGAISDK+Oxidation(0)	1.002265944	2	2.78998
P29147	MQVMTHFPGAISDK+Oxidation(3)	1.002265944	2	2.96961
P29147	MWDELPEVVR	0.791444206	2	2.46938
P29147	MWDELPEVVR+Oxidation(0)	0.83022116	2	3.22726
P29147	TIQLNVCNSEEVEK	0.944770145	2	4.42579
P29147	VSVVEPGNFIAATSLYSPER	0.864866908	2	6.25877
P29147	VVNISSMLGR	0.865773045	2	3.75515
P29147	YEMHPLGVK	0.77866848	2	2.54178
P29266	**3HIDH 3_hydroxyisobutyrate dehydrogenase_ mitochondrial**	**0.829641549**	**1E-19**	**8**
P29266	DLGLAQDSATSTK	0.782899317	2	3.85325
P29266	EAGEQVASSPADVAEK	0.843279169	2	4.75589
P29266	GSLLIDSSTIDPSVSK	0.950018662	2	4.46235
P29266	HGYPLILYDVFPDVCK	1.056620089	2	5.17433
P29266	KGSLLIDSSTIDPSVSK	1.008215142	2	4.36925
P29266	MGAVFMDAPVSGGVGAAR	0.938512647	2	4.60188
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(0)	0.833723032	2	4.19421
P29266	MGAVFMDAPVSGGVGAAR+Oxidation(5)	0.833723032	2	3.24167
P29314	**RS9 40S ribosomal protein S9**	**1.143813414**	**0.0006**	**5**
P29314	IEDFLER	1.033805006	2	2.36702
P29314	KGQGGAGAGDDEEED	1.215263915	2	3.59923
P29314	LDYILGLK	1.151739702	2	2.65572
P29314	LFEGNALLR	1.177048182	2	2.96702
P29314	SRLDQELK	0.997615538	2	2.36779
P29315	**RINI Ribonuclease inhibitor**	**1.045396777**	**0.3995**	**5**
P29315	ASLQELDLGSNK	1.020885736	2	2.48623
P29315	LDDCGLTEVR	1.026638952	2	3.14782
P29315	LENCGITSANCK	1.010680961	2	3.02173
P29315	SAIQANPALTELSLR	1.180131446	2	4.20273
P29315	TNELGDAGVGLVLQGLQNPTCK	1.046815746	2	5.24535
P29410	**KAD2 Adenylate kinase 2_ mitochondrial**	**1.013285092**	**0.8015**	**10**
P29410	AMVASGSELGK	0.968065203	2	2.62889
P29410	AMVASGSELGKK	0.777316587	2	2.6265
P29410	AVLLGPPGAGK	0.885100812	2	2.46397
P29410	EAMKDDITGEPLIR	1.046870798	2	2.4345
P29410	GIHCAIDASQTPDVVFASILAAFSK	1.139809998	3	4.30324
P29410	LEAYHTQTTPLVEYYR	1.085727619	2	4.8241
P29410	LVSDEMVVELIEK	1.052333349	2	4.34415
P29410	NGFLLDGFPR	0.995817853	2	2.98944
P29410	NLETPSCK	1.004555304	1	2.01153
P29410	SYHEEFNPPK	1.001783537	3	3.31996
P29411	**KAD3 GTP:AMP phosphotransferase_ mitochondrial**	**1.177652271**	**0.8862**	**4**
P29411	AYEAQTEPVLQYYQK	0.971153429	2	5.00317
P29411	EDDKPETVIK	0.866605355	2	2.60277
P29411	TVGIDDLTGEPLIQR	1.011882598	2	3.52663
P29411	VYNIEFNPPK	1.179206489	2	2.67018
P29419	**ATP5I ATP synthase subunit e_ mitochondrial**	**0.910389907**	**0.0011**	**2**
P29419	ELAEAEDVSIFK	0.911479226	1	3.32243
P29419	YSALILGMAYGAK	1.514918968	2	3.44123
P30009	**MARCS Myristoylated alanine_rich C_kinase substrate**	**1.122904515**	**0.0011**	**2**
P30009	AEDGAAPSPSSETPK	0.955296378	2	3.61428
P30009	GEAAAERPGEAAVASSPSK	1.236927835	2	4.37953
P30276	**CCNB2 G2/mitotic_specific cyclin_B2**	**0.853756168**	**0.2569**	**2**
P30276	AVLEEIGNK	0.924265197	1	2.06732
P30276	FELGRPLPLHFLRR	0.827775735	2	2.47323
P30349	**LKHA4 Leukotriene A_4 hydrolase**	**0.963729283**	**0.8785**	**2**
P30349	SLSNVIAHEISHSWTGNLVTNK	1.064802067	3	4.4457

P30349	SSALQWLTPEQTSGK	1.021360716	2	3.21243
P30427	**PLEC Plectin**	**1.014395126**	**0.1654**	**6**
P30427	AQVEQELTTLR	0.854256992	2	2.67106
P30427	LLDPEDVDVPQPDEK	0.797147016	2	3.32022
P30427	MSAAQALKKGWLYYEAGQR+Oxidation(0)	0.905419521	2	2.3988
P30427	SDQLTGLSLLPLSEK	1.051727314	2	2.84238
P30427	SQVEEELFSVR	1.304813013	2	2.34276
P30427	YLYGTGSVAGVYLPGSR	1.363376954	2	2.5481
P30713	**GSTT2 Glutathione S_transferase theta_2**	**0.827114542**	**1E-19**	**5**
P30713	AQVHEYLGWHADNIR	0.792897458	2	4.52083
P30713	GQHLSEQFSQVNCLK	0.824571281	2	4.76745
P30713	VEAFLGAELCQEAHNPIMSVLGQAAK	0.827243343	3	3.41161
P30713	VLGPLIGVQVPEEK	0.860808235	2	3.93285
P30713	YQVADHWYPADLQAR	0.757255842	2	4.56313
P30839	**AL3A2 Fatty aldehyde dehydrogenase**	**0.866686776**	**1E-19**	**9**
P30839	DILAAIAADLSK	0.763519796	2	2.67238
P30839	EKDILAAIAADLSK	0.737108896	2	3.69608
P30839	FDHILYTGNTAVGK	0.894460876	2	3.50277
P30839	HLTPVTLELGGK	0.905945851	2	2.92693
P30839	NVEEAINFINDR	1.094860013	2	3.95834
P30839	QRFDHILYTGNTAVGK	1.219399131	2	3.03698
P30839	VMQEEIFGPILPIVSVK	0.745436381	3	4.32109
P30839	VMQEEIFGPILPIVSVK+Oxidation(1)	0.826590048	2	4.66052
P30839	YIAPTILTDVDPNSK	0.841251424	2	4.32633
P30904	**MIF Macrophage migration inhibitory factor**	**1.123019906**	**0.3784**	**2**
P30904	LHISPDR	0.931844132	1	2.04431
P30904	LLCGLLSDR	1.51211749	2	2.54545
P31000	**VIME Vimentin**	**0.814366415**	**2E-08**	**14**
P31000	DGQVINETSQHHDDLE	0.937778484	2	3.24235
P31000	ETNLESLPLVDTHSK	0.919338811	2	2.62891
P31000	FADLSEAANR	0.896196241	2	2.73474
P31000	KLLEGEESR	0.893263485	2	2.66326
P31000	KVESLQEEIAFLK	0.718459232	2	3.76883
P31000	LGDLYEEEMR	0.862686784	2	2.36507
P31000	LLEGEESR	0.87131758	2	2.65074
P31000	NLQEAEEWYK	0.859025369	2	2.78847
P31000	QDVDNASLAR	0.724073491	2	2.53648
P31000	QVQSLTCEVDALK	0.955671761	2	3.32225
P31000	RQVDQLTNDK	0.827683221	2	2.66143
P31000	SLYSSSPGGAYVTR	0.957089283	2	2.37995
P31000	TNEKVELQELNDR	0.792095173	2	2.44468
P31000	VELQELNDR	0.806185511	2	2.71593
P31044	**PEBP1 Phosphatidylethanolamine_binding protein 1**	**0.998757401**	**0.0183**	**6**
P31044	GNDISSGTVLSEYVGSGPPK	1.005433646	2	6.04556
P31044	LYTLVLTDPDAPSR	1.256119984	2	4.43865
P31044	VDYGGVTVDELGK	0.920741525	2	4.49212
P31044	VLTPTQVMNRPSSISWDGLDPGK	0.967902047	3	4.84973
P31044	YHLGAPVAGTCFQAEWDDSVPK	0.936147381	2	5.33946
P31044	YVWLVYEQEQPLNCDEPILSNK	1.005048588	2	5.23354
P31210	**AK1D1 3_oxo_5_beta_steroid 4_dehydrogenase**	**0.866939636**	**0.9824**	**17**
P31210	DELLTSLGK	0.708812877	2	2.58049
P31210	DIEALNK	0.645063981	1	2.47355
P31210	EEMKDIEALNK	0.793188617	2	3.36921
P31210	ENFQIFDFSLTK	0.89678947	2	3.1913
P31210	HIDGAYVYR	0.827912951	2	3.21222
P31210	IKENFQIFDFSLTK	1.039338885	2	3.90028
P31210	NEHEVGEAIR	0.819943805	2	3.0926

P31210	NPLWVNVSSPPLLK	0.971045959	2	4.30871
P31210	NPLWVNVSSPPLLKDELLTSLGK	0.812790731	3	4.68551
P31210	QLEVILNKPGLK	0.764721632	2	3.32212
P31210	REEIFYCGK	0.808851372	2	2.96265
P31210	SLGVSNFNR	1.038906801	2	2.58314
P31210	SNLCATWEALEACK	0.883446399	2	4.38785
P31210	SNLCATWEALEACKDAGLVK	0.53217759	2	4.71038
P31210	TAIDEGYR	0.917992805	2	2.61565
P31210	TQAQIVLR	0.882538554	2	3.08622
P31210	YKPVTNQVECHPYFTQTK	0.956855094	2	5.0516
P31399	**ATP5H ATP synthase subunit d_ mitochondrial**	**1.003429542**	**0.0826**	**8**
P31399	ANVDKPGLVDDFK	0.994467504	2	3.52002
P31399	NCAQFVTGSQAR	1.023101814	2	4.75305
P31399	NMIPFDQMTIDDLNEVFPETK	1.039933542	2	4.98344
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(1)	0.964544357	2	4.06988
P31399	NMIPFDQMTIDDLNEVFPETK+Oxidation(7)	0.905834431	2	3.93758
P31399	SWNETFHTR	1.003508606	2	2.60636
P31399	TIDWVSFVEIMPQNQK	1.246284244	3	3.51429
P31399	YTALVDAEEKEDVK	1.167722293	2	3.4593
P32089	**TXTP Tricarboxylate transport protein_ mitochondrial**	**1.028300679**	**0.957**	**5**
P32089	FIHDQTSSNPK	1.257057934	1	3.60147
P32089	GLSSLLYGSIPK	1.044342016	2	3.06509
P32089	GTYQGLTATVLK	0.907913818	2	2.43997
P32089	SHGVLGLYR	0.890127578	1	2.09772
P32089	TQLQLDER	1.063230527	2	2.61708
P32198	**CPT1A Carnitine O_palmitoyltransferase 1_ liver isoform**	**1.001269393**	**0.6419**	**4**
P32198	ELEQQMQQILDDPSEPQPGEAK	0.995374129	2	4.37218
P32198	GDTNPNIPKPTR	0.898070939	2	2.4931
P32198	MTALAQDFAVNLGPK	0.975187624	2	3.25762
P32198	MTALAQDFAVNLGPK+Oxidation(0)	0.654114934	2	3.76634
P32232	**CBS Cystathionine beta_synthase**	**1.229687198**	**1E-19**	**8**
P32232	AGTLKPGDTIIEPTSGNTGIGLALAAAVK	1.563451975	3	5.92462
P32232	FDSPESHVGVAWR	1.142332977	2	3.46856
P32232	LKNEIPNSHILDQYR	1.258261746	3	3.4666
P32232	NASNPLAHYDDTAEEILQQCDGK	1.713601851	2	5.38436
P32232	SNDDDSFAFAR	1.739469608	2	3.36945
P32232	VDMLVASAGTGGTITGIAR	1.329489438	2	4.32904
P32232	VQELSLSAPLTVLPTVTCEHTIAILR	1.772165637	3	4.1958
P32232	VRPSDEVCK	2.044418134	2	2.50546
P32551	**QCR2 Cytochrome b_c1 complex subunit 2_ mitochondrial**	**1.124233484**	**0.038**	**10**
P32551	AVAFQNPQTR	1.121823022	2	2.79525
P32551	AVAQGNLSSADVQAAK	1.023509949	2	4.78252
P32551	GNNTTSLLSQSVAK	1.06916504	2	4.21587
P32551	IIENLHDVAYK	1.040477143	2	3.69603
P32551	LPNGLVIASLENYAPLSR	1.321410917	3	3.42979
P32551	RGNNTTSLLSQSVAK	0.58958681	2	2.96213
P32551	SMTASGNLGHTPFLDEL	1.102098832	2	3.16481
P32551	SMTASGNLGHTPFLDEL+Oxidation(1)	1.088068917	2	3.37443
P32551	TSAPGGVPLQPQELEFTK	0.986397569	2	3.57565
P32551	YENYNYLGTSHLLR	1.284686503	2	4.00042
P32755	**HPPD 4_hydroxyphenylpyruvate dioxygenase**	**1.411757355**	**1E-19**	**16**
P32755	AFEEEQALR	1.326055842	2	3.36486
P32755	DIAFEVEDCEHIVQK	1.232974781	2	3.29479
P32755	FAVLQTYGDTTHTLVEK	1.382906351	2	5.07312
P32755	FLPGFEAPTYK	1.23283973	2	2.51381
P32755	FWSVDDTQVHTEYSSLR	1.377012183	2	5.5479
P32755	GMEFLAVPSSYYR	1.435870464	2	3.04553

P32755	GNLTDLETNGVR	1.177186743	2	3.61468
P32755	HNHQGFGAGNFNSLFK	1.489953761	3	4.99724
P32755	ILVDYDEK	1.28684757	2	2.87203
P32755	IVFVLCSALNPWNK	1.327778569	2	3.05992
P32755	IVREPWVEEDKFGK	1.259025876	3	4.24686
P32755	LPSCNLEIIDHIVGNQPDQEMESASEWYLK	1.293789574	3	7.49554
P32755	MGFEPLAYK	1.696995058	2	2.34365
P32755	SIVVANYEESIK	1.284193169	2	4.15149
P32755	SQIQEYVDYNGGAGVQHIALR	1.397866557	2	5.48854
P32755	TEDIITTIR	1.301408189	2	3.40263
P33124	**ACSL6 Long_chain_fatty_acid__CoA ligase 6**	**1.006676989**	**1**	**2**
P33124	ALRPTIFPVVPR	0.983731104	2	3.07722
P33124	IENIYIR	1.021187214	2	2.84489
P33273	**CP255 Cytochrome P450 2C55**	**0.726414075**	**1E-06**	**2**
P33273	ELRHFSLMTLR	0.898827378	2	2.31736
P33273	FDYKDENFLNLMEK	0.722302554	3	3.54445
P34058	**HS90B Heat shock protein HSP 90_beta**	**1.014563596**	**1E-19**	**24**
P34058	ADLINNLGTIAK	1.026769523	2	4.10553
P34058	EDQTEYLEER	1.157144812	2	3.34114
P34058	EGLELPEDEEEKKK	1.024216468	2	3.1422
P34058	ELISNASDALDK	0.858863322	2	3.63725
P34058	ELISNASDALDKIR	0.26595971	2	2.98653
P34058	GVVDSEDLPLNISR	1.040937654	2	4.74997
P34058	HLEINPDHPIVETLR	1.063168947	2	4.41815
P34058	HSQFIGYPITLYLEK	1.819680567	2	3.80158
P34058	IDIIPNPQER	1.025325599	2	2.96713
P34058	KHLEINPDHPIVETLR	0.956412421	2	3.26683
P34058	LGIHEDSTNR	1.012872834	2	3.29688
P34058	NPDDITQEEYGEFYK	1.353565938	2	4.88495
P34058	RAPFDLFENK	1.069349986	2	2.91025
P34058	RAPFDLFENKK	0.760877838	2	2.33402
P34058	SIYYITGESK	1.194748112	2	3.0952
P34058	SLTNDWEDHLAVK	1.063774252	2	3.89272
P34058	TLTLVDTGIGMTK	1.007382287	2	3.86571
P34058	TLTLVDTGIGMTK+Oxidation(10)	0.994355936	2	3.91848
P34058	VFIMDSCDELIPEYLNFIR	1.236207203	2	2.85972
P34058	VILHLKEDQTEYLEER	0.943621059	3	4.21972
P34058	YESLTDPSK	1.074674212	2	2.84651
P34058	YESLTDPSKLDSGK	0.947415993	2	3.66766
P34058	YHTSQSGDEMTSLSEYVSR	1.147716119	2	5.42996
P34058	YIDQEELNK	1.077571496	2	3.63116
P34067	**PSB4 Proteasome subunit beta type_4**	**0.915200711**	**0.7642**	**3**
P34067	GVEIEGPLSAQTNWDIAHMISGFE	0.910636389	2	3.44295
P34067	TQNPMVTGTSVLGVK	0.917383283	2	2.54274
P34067	VNDSTMLGASGDYADFQYLK	0.931582571	2	4.18301
P35171	**CX7A2 Cytochrome c oxidase subunit 7A2_ mitochondrial**	**1.095015593**	**0.3798**	**3**
P35171	GGTSDALLYR	1.078145449	2	3.28033
P35171	LFQEDNGMPVHLK	1.091948174	2	3.8312
P35171	LFQEDNGMPVHLK+Oxidation(7)	0.933960717	2	2.69428
P35213	**1433B 14_3_3 protein beta/alpha**	**1.05724524**	**0.4941**	**5**
P35213	AVTEQGHELSNEER	1.340701177	2	4.56786
P35213	EKIEAELQDICSDVLELLDK	1.088045244	3	4.37551
P35213	QTTVSNSQQAYQEAFEISK	1.000985625	2	5.24787
P35213	TAFDEAIAELDTLNEESYK	1.065881197	2	5.3102
P35213	YLSEVASGDNK	1.042584087	1	3.12953
P35233	**PTN2 Tyrosine_protein phosphatase non_receptor type 2**	**0.904246003**	**0.3218**	**2**
P35233	CAQYWPTDDREMVFK+Oxidation(11)	1.736001287	2	2.36275

P35233	KRWLYWQPILTK	0.904159748	1	2.09969
P35278	**RAB5C Ras_related protein Rab_5C**	**0.900946538**	**0.6526**	**2**
P35278	FEIWDTAGQER	0.892003719	2	2.66588
P35278	GVDLQESNPASR	1.00930532	2	2.90358
P35427	**RL13A 60S ribosomal protein L13a**	**1.123533407**	**0.8985**	**2**
P35427	CEGINISGNFYR	1.128385178	2	2.71695
P35427	YQAVTATLEEK	1.002867986	2	2.98451
P35434	**ATPD ATP synthase subunit delta_ mitochondrial**	**1.011050166**	**1**	**2**
P35434	AQSELSGAADEAAR	1.023038495	2	4.63804
P35434	IEANEALVK	1.012498414	2	3.30401
P35435	**ATPG ATP synthase subunit gamma_ mitochondrial**	**1.030637571**	**0.0005**	**6**
P35435	GLCGAIHSSVAK	1.029093009	2	3.69751
P35435	HLIIGVSSDR	0.993094961	2	2.91291
P35435	NASDMIDK	1.007660308	1	2.10388
P35435	NDMAALTAAGK	1.022812302	2	3.34334
P35435	THSDQFLVSFK	1.204850639	2	3.12993
P35435	VYGTGSLALYEK	1.454718161	2	2.87493
P35565	**CALX Calnexin**	**1.033981654**	**0.6769**	**8**
P35565	AEEDEILNR	1.150422202	2	2.59397
P35565	GSLSGWILSK	1.152588002	2	2.31165
P35565	KIPNPDFFEDLEPFR	0.992503036	3	4.4728
P35565	NKGDEEEEEEKLEEK	1.079888289	2	4.7012
P35565	TDAPQPDVKDEEGKEEEK	0.984584642	3	3.75537
P35565	TSELNLDQFHDK	1.026877252	2	3.64798
P35565	VVDDWANDGWGLK	1.030347319	2	3.88499
P35565	VVDDWANDGWGLKK	0.848519959	2	3.45435
P35704	**PRDX2 Peroxiredoxin_2**	**0.932558874**	**0.1403**	**5**
P35704	EGGLGPLNIPLLADVTK	0.816050163	2	2.89706
P35704	KEGGLGPLNIPLLADVTK	0.860868672	2	4.29223
P35704	NDEGIAYR	0.92359259	1	2.07535
P35704	QITVNDLPVGR	0.964535914	2	2.8042
P35704	SLSQNYGVLK	0.860069731	2	2.41341
P35738	**ODBB 2_oxoisovalerate dehydrogenase subunit beta_ mitochondrial**	**0.929488809**	**0.6648**	**2**
P35738	AAVEQVPVEPYK	0.930101511	2	2.31245
P35738	GLLLSCIEDKNPCIFFEPK	0.858387856	2	2.81734
P36201	**CRIP2 Cysteine_rich protein 2**	**1.062858843**	**0.9993**	**3**
P36201	GVNIGGAGSYIYEKPPTEAPQVTGPIEVPVVR	1.062352721	3	6.76126
P36201	GVNTGAVGSYIYDKDPEGTVQP	1.050932339	2	4.43165
P36201	VYFAEKVTSLGK	1.017614904	2	2.46953
P36365	**FMO1 Dimethylaniline monooxygenase [N_oxide_forming] 1**	**1.066759272**	**0.0007**	**9**
P36365	ALQSDYITYIDDLLTSINAKPDLR	0.947524288	3	3.73404
P36365	ASLYNSVVSNSSK	1.09501683	2	2.97712
P36365	ENSVVFNNTPK	1.110091524	2	2.45723
P36365	FTEHVEEGR	0.867339989	2	2.88866
P36365	NLLPTPVVSWLISK	0.894061377	2	2.30393
P36365	SCDLGGLWR	0.84115803	2	2.82858
P36365	TQLREPVLNDELPGR	0.350691524	2	2.94378
P36365	VEDGQASLYK	0.938146424	2	3.30455
P36365	VLVVGMGNSGTDIAVEASHLAK	0.811948254	2	2.48082
P36511	**UDB15 UDP_glucuronosyltransferase 2B15**	**1.213645965**	**7E-07**	**6**
P36511	ANIIAWALAQIPQK	0.758345033	3	4.37607
P36511	FVNVWTYELPR	0.84073465	2	2.78159
P36511	FVTFPTSFSSHDLENFFTR	1.324759488	2	3.88148
P36511	GHEVTVLRPSAFVFLDPK	0.397518742	2	2.96172
P36511	IILEELVQK	0.847887053	2	3.40104
P36511	TLGRPTTLAEIMGK	0.832007992	2	2.58266

P36972	**APT Adenine phosphoribosyltransferase**	**1.071543386**	**0.0122**	**3**
P36972	GFLFGPSLAQELGVGCVLIR	1.434306254	2	2.78198
P36972	IDYIAGLDSR	1.118675828	1	2.29404
P36972	SFPDFPIPGVLFR	0.939757958	2	3.14498
P38650	**DYHC1 Cytoplasmic dynein 1 heavy chain 1**	**1.155964112**	**0.5536**	**7**
P38650	EALELTDTGLLSGSEER	0.883296594	2	2.40881
P38650	FGNPLLVQDVESYDPVLNPVLNR	1.111988632	3	3.39261
P38650	ILDDDTIITTLENLK	1.163670761	2	2.3526
P38650	QLQNISQAAAAGGAK	1.000625364	2	2.80931
P38650	SSLQSQCLNEVLK	1.034829696	2	3.11208
P38650	VQGLTVEQAEAVAR	0.905648264	2	3.09291
P38650	VQVALEELQDLK	0.990578895	2	2.64115
P38652	**PGM1 Phosphoglucomutase_1**	**0.935936581**	**2E-05**	**16**
P38652	ADNFEYSDPVDGSISK	0.958556303	2	4.86348
P38652	AIGGIILTASHNPGGPNGDFGIK	1.038219507	2	5.27492
P38652	FNISNGGPAPEAITDK	1.140892416	2	4.24181
P38652	IDAMHGVVGPYVK	0.460171438	2	3.11898
P38652	INQDPQVMLAPLISIALK	1.051428015	2	4.72899
P38652	KQRVEDILK	1.058518641	1	2.05302
P38652	LSGTGSAGATIR	1.544724814	2	2.67467
P38652	LSLCGEESFGTGSDHIR	1.763461232	2	3.24331
P38652	LVIGQNGILSTPAVSCIIR	1.100583098	2	3.55415
P38652	NIFDFNALK	1.036344021	1	2.10787
P38652	QEATLVVGGDGR	1.037470923	2	3.02026
P38652	SFVGKQFSANDK	1.033638732	1	2.06125
P38652	SGEHDFGAAFDGDGDR	0.931366606	2	4.39383
P38652	TIEEYAICPDLK	0.88706252	2	2.92078
P38652	TQAYPDQKPGTSGLR	0.830106384	2	3.70698
P38652	YDYEEVEAEGANK	1.089374404	2	4.93605
P38656	**LA Lupus La protein homolog**	**1.184481929**	**0.1451**	**3**
P38656	GSIFAVFDSIQSAK	1.182407251	2	2.35563
P38656	ITDDQQESLNK	1.184460835	2	3.98058
P38656	LDEGWVPLETMIK	1.767019299	2	2.94786
P38659	**PDIA4 Protein disulfide_isomerase A4**	**1.205274238**	**1E-16**	**18**
P38659	DLGLSESGEDVNAAILDESGKK	1.234380735	2	4.99685
P38659	EVSQPDWTPPPEVTLTLTK	1.033856853	2	3.43654
P38659	FDVSGYPTIK	1.058199952	2	3.29415
P38659	FDVSGYPTLK	1.058199952	2	3.29415
P38659	FIDEHATK	1.289775915	2	2.47149
P38659	FIDEHATKR	1.367710332	2	2.57292
P38659	GQAVDYDGSR	0.775206112	2	2.42531
P38659	GRPFDYNGPR	1.142733742	2	2.92812
P38659	IDATSASMLASK	1.200771155	2	3.49741
P38659	IDATSASMLASK+Oxidation(7)	1.169784651	2	3.21176
P38659	KGQAVDYDGSR	1.564655234	2	2.43213
P38659	MDATANDITNDR	1.231023921	2	3.83002
P38659	QLEPVYTSLGK	1.078806242	2	2.46622
P38659	RFDVSGYPTLK	1.179467186	2	3.06469
P38659	RSPPIPLAK	1.27561496	2	2.48976
P38659	VDATEQTDLAK	1.128076746	2	3.95297
P38659	VEGFPTIYFAPSGDK	0.787794578	2	3.2346
P38659	YGIVDYMVEQSGPPSK	1.388755282	2	4.40117
P38918	**ARK73 Aflatoxin B1 aldehyde reductase member 3**	**0.912663448**	**0.0039**	**4**
P38918	FYAFNPLAGGLLTGR	1.047595673	2	4.32189
P38918	MDVTSSSASVR	0.786063994	2	3.49402
P38918	RMDVTSSSASVR	0.710242858	2	2.92389
P38918	TTYGPTAPSMISAAVR	0.918334806	2	3.53978

P38983	**RSSA 40S ribosomal protein SA**	**1.126975426**	**4E-11**	**6**
P38983	ADHQPLTEASYVNLPTIALCNTDSPLR	1.117081755	3	5.73563
P38983	AIVAIENPADVSVISSR	1.071020921	2	5.55578
P38983	FTPGTFTNQIQAAFR	1.243410055	2	4.70143
P38983	KSDGIYIINLK	2.544416725	2	2.86672
P38983	SDGIYIINLK	0.971589979	2	2.92307
P38983	YVDIAIPCNNK	1.212198907	2	3.33045
P40307	**PSB2 Proteasome subunit beta type_2**	**1.100553484**	**0.0071**	**2**
P40307	FILNLPTFSVR	1.37369857	2	2.63939
P40307	NGYELSPTAAANFTR	1.094225655	2	3.28974
P40329	**SYRC Arginyl_tRNA synthetase_ cytoplasmic**	**1.009331936**	**0.9653**	**2**
P40329	EENLKLK	1.076846691	1	1.94561
P40329	SDGGYTYDTSDLAAIK	0.997694581	2	3.69103
P41034	**TTPA Alpha_tocopherol transfer protein**	**1.170823002**	**1E-05**	**6**
P41034	AECPELSADLHPR	0.928157846	2	2.48415
P41034	AIFDLEGWQISHAFQITPSVAK	1.040508847	2	4.57545
P41034	AQEEGVPETPQPLTDAFLLR	1.31906432	2	3.38788
P41034	QLNEQPDHSPLVQPGLAELR	1.116787268	3	3.39409
P41034	SEDYLSSISETIQ	1.335062376	2	2.32095
P41034	VSLITSELIVQEVETQR	1.27250238	2	3.53946
P41123	**RL13 60S ribosomal protein L13**	**1.097821066**	**0.0647**	**3**
P41123	LATQLTGPVMPIR	1.302345585	2	2.46074
P41123	STESLQANVQR	1.013094964	2	3.925
P41123	VDTWFNQPAR	1.123377097	2	3.55145
P41498	**PPAC Low molecular weight phosphotyrosine protein phosphatase**	**1.013521087**	**0.9191**	**3**
P41498	IDSAATSTYEVGNPPDYR	1.074804566	2	4.77351
P41498	IELLGSYDPQK	0.924197788	2	3.73886
P41498	LVTDENVSDNWR	0.949691302	2	3.45028
P41542	**USO1 General vesicular transport factor p115**	**1.13783064**	**0.927**	**13**
P41542	AWFEVGDENPGWSAQK	1.140478986	2	4.0297
P41542	CQNEQLQTAVTQQASQIQQHK	1.036234473	3	4.86563
P41542	EQDDLLVLLADQDQK	1.042033071	2	2.68509
P41542	LQTENSELQQR	1.039287784	2	2.8181
P41542	LREEIEELR	0.967641928	2	2.41329
P41542	NDGVLLLQALTR	1.086461879	2	3.84166
P41542	NNNSNQNFFK	0.997240229	2	2.5191
P41542	QLDSSNSTIAILQTEK	1.132966814	2	3.4837
P41542	QSEDLGSQFTEIFIK	0.926362894	2	3.19642
P41542	SQLCSQSLEITR	1.144931282	2	3.1228
P41542	SVPVEGESELVTAAK	1.073323822	2	3.75491
P41542	TLEQHDNIVTHYK	1.030027435	2	3.23454
P41542	VLVSPTNPPGATSSCQK	1.077069215	2	3.26783
P41562	**IDHC Isocitrate dehydrogenase [NADP] cytoplasmic**	**0.924609018**	**9E-12**	**16**
P41562	ATDFVVPGPGK	0.971399488	2	3.37105
P41562	CATITPDEK	1.110343633	2	2.58677
P41562	DIFQEIYDK	0.774653759	1	2.46158
P41562	FKDIFQEIYDK	0.902250257	3	4.43045
P41562	GQETSTNPIASIFAWSR	1.079573344	2	5.1142
P41562	IIWELIK	1.066494093	2	2.56511
P41562	LIDDMVAQAMK	0.920654611	2	3.52528
P41562	LIDDMVAQAMK+Oxidation(9)	1.025598971	2	2.3334
P41562	LILPYVELDLHSYDLGIENR	1.292723581	3	3.66364
P41562	LVTGWVKPIIIGR	1.185384158	3	4.0294
P41562	SDYLNTFEFMDK	0.923433134	2	4.08199
P41562	SDYLNTFEFMDK+Oxidation(9)	0.969412562	2	2.98484
P41562	SEGGFIWACK	0.926895628	2	3.31787

P41562	SIEDFAHSSFQMALSK	1.005545316	2	4.40045
P41562	TVEAEAAHGTVTR	0.902352628	2	3.54924
P41562	VEITYTPK	1.013556995	2	2.53725
P42123	**LDHB L_lactate dehydrogenase B chain**	**1.042599256**	**0.9935**	**4**
P42123	DYSVTANSK	1.024677499	2	2.65798
P42123	LIAPVADDETAVPNNK	0.97574171	2	3.36886
P42123	SLADELALVDVLEDK	1.20590416	2	3.42354
P42123	VIGSGCNLDSAR	1.078650347	2	3.75145
P42676	**NEUL Neurolysin_ mitochondrial**	**0.929352962**	**0.4592**	**2**
P42676	AELGALPDDFIDSLEK	1.071642648	2	2.4118
P42676	TRTEQLIAQTK	0.851348998	2	3.17631
P42932	**TCPQ T_complex protein 1 subunit theta**	**0.952144672**	**0.0961**	**6**
P42932	AIAGTGANVIVTGGK	1.111572499	2	4.0802
P42932	AVDDGVNTFK	1.243868511	2	2.82986
P42932	ELEVQHPAAK	0.922744768	2	2.79269
P42932	GEENLMDAQVK	1.029168292	2	3.01129
P42932	NVGLDIEAEVPAVK	1.062390517	2	3.98783
P42932	QITSYGETCPGLEQYAIK	0.954943082	2	4.78094
P43244	**MATR3 Matrin_3**	**0.905592451**	**0.061**	**3**
P43244	GNLGAGNGNLQGPR	0.782398223	2	2.36443
P43244	ITPENLPQILLQLK	1.150719112	2	3.46125
P43244	TEEGPTLSYGR	1.006203541	2	2.4744
P43274	**H14 Histone H1.4**	**0.907644865**	**1E-19**	**3**
P43274	ALAAAGYDVEK	0.877527244	2	3.52905
P43274	SGVSLAALK	0.939461222	2	3.14896
P43274	SGVSLAALKK	0.876306944	2	2.66596
P43276	**H15 Histone H1.5**	**1.020231069**	**0.7926**	**2**
P43276	ALAAGGYDVEK	1.056619402	2	2.35007
P43276	ATGPPVSELITK	0.879232488	2	2.34949
P43278	**H10 Histone H1.0**	**0.878404336**	**0.1398**	**2**
P43278	VGENADSQIK	0.898956966	2	3.52504
P43278	YSDMIVAAIQAEK	0.965878803	2	3.5231
P45591	**COF2 Cofilin_2**	**0.942094652**	**0.957**	**2**
P45591	HEWQVNGLDDIKDR	1.064313	3	4.24089
P45591	QILVGDIGDTVEDPYTSFVK	0.942901951	2	4.52944
P45592	**COF1 Cofilin_1**	**0.968413506**	**0.9998**	**3**
P45592	EILVGDVGQTVDDPYTTFVK	1.018148274	2	4.65155
P45592	HELQANCYEEVKDR	0.944810338	3	4.69718
P45592	NIILEEGKEILVGDVGQTVDDPYTTFVK	0.982606014	3	3.66372
P45878	**FKBP2 Peptidyl_prolyl cis_trans isomerase FKBP2**	**1.12110271**	**0.106**	**4**
P45878	GWDQGLLGMCEGEK	1.124227046	2	3.93231
P45878	KLVIPSELGYGER	0.994638798	2	2.56855
P45878	LEDGTEFDSSLPQNQPFVFSLGTGQVIK	1.187009559	3	4.28806
P45878	LVIPSELGYGER	1.176471502	2	2.5386
P45953	**ACADV Very long_chain specific acyl_CoA dehydrogenase_ mitochondrial**	**1.077060775**	**1E-19**	**17**
P45953	AMVENGGLVTSNPLR	1.027408151	2	2.64419
P45953	AMVENGGLVTSNPLRV	1.259925718	2	3.19195
P45953	ASNTSEVYFDGVK	1.541567521	2	4.16431
P45953	ELGAFGLQVPSELGGLGLSNTQYAR	0.999072698	2	4.90607
P45953	ENMASLQSNPQQQELFR	0.937025008	2	4.45201
P45953	FFEEVNDPAK	1.122633228	2	2.42576
P45953	FFEEVNDPAKNDSLEKVEEDTLQGLK	0.984279061	3	6.28358
P45953	GIVNEQFLLQR	1.184458074	2	2.98357
P45953	IFEGTNDILR	1.032630864	2	2.80414
P45953	NDSLEKVEEDTLQGLK	1.116942767	2	3.59756
P45953	NPLGNVGLLIGEASK	1.637633842	2	3.5549

P45953	SFGGVTHGLPEK	1.090459469	2	2.89819
P45953	SFGGVTHGLPEKK	1.595282823	2	2.80309
P45953	SGELAVQALEQFATVVEAK	1.13739099	3	5.00038
P45953	SLSEGYPTAQHEK	1.057148837	2	3.24165
P45953	TGIGSGLSLSGIVHPELSR	1.054546184	3	4.58204
P45953	VEEDTLQGLK	1.180474625	2	2.62239
P46418	**GSTA5 Glutathione S_transferase alpha_5**	**0.571470652**	**7E-08**	**3**
P46418	AILNYIATK	0.782952719	2	3.08858
P46418	SHGQDYLVGNK	0.401768273	2	3.00017
P46418	VSNLPTVK	0.892757766	2	2.60299
P46425	**GSTP2 Glutathione S_transferase P 2**	**0.789510825**	**0.0285**	**2**
P46425	ALPGHLKPFETLLSQNQGGK	0.86021505	3	3.98809
P46425	FEDGDLTLYQSNAILR	0.670412079	2	4.07114
P46462	**TERA Transitional endoplasmic reticulum ATPase**	**0.967226974**	**0.081**	**23**
P46462	AIANECQANFISIK	0.899996016	2	3.10789
P46462	ELQELVQYPVEHPDK	0.909448379	2	4.37007
P46462	ETVVEVPQVTWEDIGGLEDVK	0.962396083	2	3.18303
P46462	ETVVEVPQVTWEDIGGLEDVKR	0.856484738	2	4.28812
P46462	EVDIGIPDATGR	0.777999391	2	2.6448
P46462	GDDLSTAILK	1.047742627	2	3.02562
P46462	GGNIGDGGGAADR	1.188308907	2	3.32362
P46462	GILLYGPPGTGK	0.957542191	2	3.17706
P46462	LADDVDLEQVANETHGHVGADLAALCSEAALQAIR	1.183782834	3	6.83826
P46462	LAGESESNLRKAFEEAEK	0.737186094	2	2.34734
P46462	LDQLIYIPLPDEK	0.918924956	2	4.26556
P46462	LEILQIHTK	0.902100132	1	2.3388
P46462	LGDVISIQPCPDVK	0.916523399	2	4.10316
P46462	LIVDEAINEDNSVVSLSQPK	1.033630825	2	5.61971
P46462	MDELQLFR	0.866006292	2	2.48809
P46462	MTNGFSGADLTEICQR+Oxidation(0)	0.985491042	2	3.87168
P46462	NAPAIIFIDELDAIAPK	0.946463711	2	4.68887
P46462	QAAPCVLFFDELDSIAK	1.27371473	2	3.46075
P46462	QTNPSAMEVEEDDPVPEIR	0.958804934	2	4.40537
P46462	RSVSDNDIR	0.47166987	2	2.92965
P46462	VINQILTEMDGMSTK	1.030568863	2	3.54364
P46462	VINQILTEMDGMSTK+Oxidation(8)	0.398226779	2	2.37183
P46462	WALSQSNPSALR	1.221040127	2	3.00092
P46664	**PURA2 Adenylosuccinate synthetase isozyme 2**	**0.956708427**	**0.2371**	**4**
P46664	FIEDELQIPVK	0.94457372	2	3.07449
P46664	LDILDMFTEIK	0.854606403	2	3.70676
P46664	VGIGAFPTEQDNEIGELLQTR	1.51326979	2	4.04445
P46664	VVDLLAQDADIVCR	1.05958482	2	3.7339
P46720	**SO1A1 Solute carrier organic anion transporter family member 1A1**	**1.100700773**	**0.1705**	**3**
P46720	ESEHTDVHGSPQVENDGELK	1.12807755	3	3.44242
P46720	GIGETPIVPLGISYIEDFAK	1.11647497	2	3.36015
P46720	SENSPLYIGILEMGK	0.882966455	2	2.91782
P46953	**3HAO 3_hydroxyanthranilate 3_4_dioxygenase**	**0.991086643**	**0.5364**	**6**
P46953	AQGSVALSVTQDPACK	0.307409996	2	4.2429
P46953	DLGTQLAPIIQEFFHSEQYR	1.052353896	2	3.98507
P46953	QDVDVWLWQLEGSSK	0.869755163	2	3.47318
P46953	QGEIFLLPAR	1.005995209	2	3.03658
P46953	TGKPNPDQLLK	0.934272631	3	3.79759
P46953	YYVGDTEDVLFEK	1.019832537	2	3.57261
P46978	**STT3A Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit STT3A**	**1.38094155**	**0.0002**	**6**
P46978	FESVIHEFDPYFNYR	1.064390684	3	3.82331

P46978	FGQVYTEAK	1.173315607	2	2.41714
P46978	FYSLLDPSYAK	1.147203431	2	3.28769
P46978	NLDISRPDKK	1.060683238	2	2.54968
P46978	VGQAMASTEEK	1.381548504	2	3.24323
P46978	VGQAMASTEEK+Oxidation(4)	1.535875309	2	3.25699
P47198	**RL22 60S ribosomal protein L22**	**1.026785317**	**0.1908**	**2**
P47198	AGNLGGGVVTIER	1.002360646	2	2.97492
P47198	FTLDCTHPVEDGIMDAANFEQFLQER	1.250068531	3	5.09232
P47875	**CSRP1 Cysteine and glycine_rich protein 1**	**1.139090439**	**0.241**	**3**
P47875	GFGFGQGAGALVHSE	1.060229207	2	3.15471
P47875	GLESTTLADKDGEIYCK	1.175008968	2	4.74863
P47875	NLDSTTVAVHGEEIYCK	0.920697136	2	4.80259
P47942	**DPYL2 Dihydropyrimidinase_related protein 2**	**0.840655388**	**2E-07**	**2**
P47942	GLYDGPVCEVSVTPK	0.851308067	2	3.09319
P47942	SITIANQTNCPLYVTK	0.812398145	2	3.28508
P48004	**PSA7 Proteasome subunit alpha type_7**	**0.943678608**	**0.0007**	**3**
P48004	GRDIVVLGVEK	0.876126215	2	2.65837
P48004	NYTDDAIETDDLTIK	1.077858025	2	3.89874
P48004	YVAEIEKEKEENEK	0.539206527	2	4.99171
P48024	**EIF1 Eukaryotic translation initiation factor 1**	**1.153584623**	**0.0505**	**2**
P48024	FACNGTVIEHPEYGEVIQLQGDQR	1.159560594	3	4.82772
P48024	TLTTVQGIADDYDK	1.149956278	2	3.23139
P48037	**ANXA6 Annexin A6**	**0.854729006**	**3E-08**	**15**
P48037	AANDFNPDADAK	0.97853024	2	3.01725
P48037	AINEAYKEDYHK	0.87106052	2	3.12415
P48037	DAFVAIVQSVK	0.892311489	2	2.89361
P48037	DLESDIIGDTSGHFQK	0.83683456	2	4.10617
P48037	ENDDVVSEDLVQQDVQDLYEAGELK	1.051065459	2	4.67014
P48037	GELSGDFEK	0.916022878	1	2.06645
P48037	GFGSDKESILELITSR	0.933420071	2	3.96482
P48037	GIGTDEATIIDIITQR	0.742760606	2	4.32599
P48037	QRQEICQSYK	0.675857245	2	2.95098
P48037	SEIDLLNIR	1.079816861	2	3.12238
P48037	SEISGDLAR	0.937886821	2	2.35896
P48037	SLEDALSSDTSGHFK	0.968470536	2	3.81991
P48037	TNEQIHQLVAAYK	0.8776303	2	4.02107
P48037	TNYDIEHVIK	0.874189139	2	3.29197
P48037	TTGKPIEASIR	0.890712684	2	2.62764
P48500	**TPIS Triosephosphate isomerase**	**1.052852894**	**1E-19**	**12**
P48500	CNVSEGVAQCTR	1.009365351	2	3.61883
P48500	DLGATWVVLGHSER	0.914542949	2	3.13717
P48500	ELASQPDVDGFLVGGASLKPEFVDIINAK	0.974871679	4	6.58527
P48500	HIFGESDELIGQK	1.185791614	2	4.07179
P48500	IIYGGSVTGATCK	1.188175959	2	3.88552
P48500	LPADTEVVCAPPTAYIDFAR	2.099859437	2	5.21575
P48500	RHIFGESDELIGQK	1.056748649	2	3.30636
P48500	TATPQQAQEVHEK	1.400594064	2	3.74413
P48500	VNHALSEGLGVIACIGEK	1.044724704	2	5.46101
P48500	VTNGAFTGEISPGMIK	1.00292697	2	4.79841
P48500	VTNGAFTGEISPGMIK+Oxidation(13)	0.909445772	2	3.60527
P48500	VVLAYEPVWAIGTGK	1.066999455	2	3.81503
P48508	**GSH0 Glutamate__cysteine ligase regulatory subunit**	**0.918842029**	**0.0355**	**5**
P48508	ASTLHLQTGNLLNWGR	1.444226793	3	4.03284
P48508	EFPDVLECTMSHAVEK	0.877019511	2	3.14434
P48508	INPDEREEMK+Oxidation(8)	1.095190543	2	2.32567
P48508	QFDIQLLTHNDPK	0.966280473	2	3.05097
P48508	TLNEWSSQISPDLVR	0.873094709	2	5.12403

P48675	**DESM Desmin**	**1.154748344**	**0.9283**	**2**
P48675	TSGGAGGLGSLR	1.160853857	2	2.41495
P48675	VSDLTQAANK	1.110615693	2	2.9215
P48679	**LMNA Prelamin_A/C**	**0.943043814**	**0.3652**	**16**
P48679	AASGSGAQVGGSISSGSSASSVTVTR	0.925621844	2	3.67184
P48679	AAYEAELGDAR	1.084785089	2	2.62455
P48679	AQHEDQVEQYKK	1.20017656	2	3.91219
P48679	GSHCSSSGDPAEYNLR	0.919417705	2	4.05365
P48679	IDSLSAQLSQLQK	0.896118057	2	3.08751
P48679	ITESEEVVSR	0.932842167	2	3.15237
P48679	LKDLEALLNSK	0.988366429	2	2.79663
P48679	LQEKEDLQELNDR	0.822104654	2	4.15137
P48679	MQQQLDEYQELLDIK	1.03389044	2	4.5597
P48679	MQQQLDEYQELLDIK+Oxidation(0)	1.036322318	2	4.32563
P48679	NSNLVGAAHEELQQSR	1.016337867	2	3.7401
P48679	SGAQASSTPLSPTR	0.851010605	2	3.02487
P48679	SVGGSGGGSFGDNLVTR	1.119625582	2	3.54155
P48679	TALINATGEEVAMR	0.965954582	2	3.1932
P48679	TLEGELHDLR	0.936982746	2	2.54717
P48679	TVLCGTCGQPADK	0.944846639	2	3.27734
P48721	**GRP75 Stress_70 protein_ mitochondrial**	**0.996933009**	**0.0037**	**26**
P48721	AQFEGIVTDLIK	0.995204855	2	3.77469
P48721	ASNGDAWVEAHGK	1.09528302	2	3.85942
P48721	DAGQISGLNVLR	1.036050067	2	3.70301
P48721	EQQIVIQSSGGLSK	1.044696643	2	4.04772
P48721	ERVEAVNMAEGIIHDTETK	0.929812154	3	4.91217
P48721	ETAENYLGHTAK	0.959942473	2	3.36357
P48721	GAVVGIDLGTTNSCVAVMEGK	1.074799941	2	4.48086
P48721	LLGQFTLIGIPPAPR	1.291574061	2	3.15183
P48721	MEEFKDQLPADECNK	0.986941751	2	4.16089
P48721	MEEFKDQLPADECNK+Oxidation(0)	1.041632395	2	3.61134
P48721	MKETAENYLGHTAK	1.030741116	3	3.63569
P48721	MKETAENYLGHTAK+Oxidation(0)	1.278885408	2	3.81875
P48721	NAVITVPAYFNDSQR	1.018827999	2	3.47406
P48721	QAASSLQQASLK	2.329012042	2	2.44278
P48721	QAVTNPNNTFYATK	1.367926999	2	3.57466
P48721	RYDDPEVQK	1.086959011	2	2.51901
P48721	RYDDPEVQKDTK	1.398632116	2	3.7613
P48721	SDIGEVILVGGMTR	0.996581717	2	3.92496
P48721	SQVFSTAADGQTQVEIK	1.366515025	2	4.80987
P48721	STNGDTFLGGEDFDQALLR	0.947513008	2	5.63714
P48721	TTPSVVAFTPDGER	1.032841568	2	3.7806
P48721	VEAVNMAEGIIHDTETK	1.007712051	2	4.53974
P48721	VINEPTAAALAYGLDK	1.257546725	2	3.39653
P48721	VLENAEGAR	1.04559559	2	3.0295
P48721	VQQTVQDLFGR	1.04458295	2	3.85575
P48721	YDDPEVQKDTK	0.935371205	2	2.82338
P49134	**ITB1 Integrin beta_1**	**1.023886096**	**0.7571**	**4**
P49134	CNCQSHGIPASPK	1.02391009	2	3.54162
P49134	GEFFNELVGQQR	0.927470603	2	2.87632
P49134	RITSDFRIGFGSFVEK	1.113436118	2	2.43621
P49134	SAVTTVVNPK	1.038094694	2	2.53363
P49242	**RS3A 40S ribosomal protein S3a**	**0.947967662**	**1E-05**	**8**
P49242	ACQSIYPLHDVFVR	1.229859234	2	3.64877
P49242	ADGYEPPVQESV	1.435145929	1	1.92742
P49242	LITEDVQGK	1.02575519	2	2.71349
P49242	LMELHGEGGSSGK	1.044897573	2	3.47221

P49242	LMELHGEGGSSGK+Oxidation(1)	1.363055782	2	3.34476
P49242	NCLTNFHGMDLTR	0.895956651	2	3.24013
P49242	TTDGYLLR	1.051830699	2	2.67832
P49242	VFEVSLADLQNDEVAFR	1.000452148	2	4.10222
P49432	**ODPB Pyruvate dehydrogenase E1 component subunit beta_ mitochondrial**	**0.968610265**	**0.6193**	**5**
P49432	ILEDNSIPQVK	1.003472289	2	3.54815
P49432	IMEGPAFNFLDAPAVR	0.948198383	2	4.30943
P49432	IMEGPAFNFLDAPAVR+Oxidation(1)	0.977138393	2	3.15926
P49432	TIRPMDIEAIEASVMK	0.87755205	3	4.08455
P49432	VFLLGEEVAQYDGAYK	1.261751023	2	3.58158
P49889	**ST1E3 Estrogen sulfotransferase_ isoform 3**	**0.913507776**	**1**	**12**
P49889	CKEDALFNR	1.036245883	2	2.67502
P49889	FEEHYQQQMK	1.162897357	2	2.64004
P49889	FMEGQVPYGSWYDHVK	1.009822568	2	3.46074
P49889	IIQHTSFQEMK	0.989388963	2	2.77055
P49889	LIEFLER	1.199640562	2	2.50028
P49889	LIEFLERDPSAELVDR	0.978778423	3	5.06749
P49889	NEDLINGIK	0.964483735	2	3.06086
P49889	NNPCTNYSMLPETMIDLK	0.991830562	2	5.6164
P49889	NNPCTNYSMLPETMIDLK+Oxidation(13)	0.952231131	2	3.53226
P49889	NNPCTNYSMLPETMIDLK+Oxidation(8)	0.953035027	2	4.64175
P49889	SFSEFVEK	1.032676888	2	2.34377
P49889	SGSTWISEIVDMIYK	0.982135384	3	4.73795
P50137	**TKT Transketolase**	**0.962923743**	**1E-19**	**20**
P50137	AVELAANTK	0.931257093	1	1.99058
P50137	GHAAPILYAVWAEAGFLPEAELLNLR	0.953590527	3	3.38643
P50137	GITGIEDK	0.855535576	1	2.50284
P50137	IIALDGDTK	0.946543918	2	2.74987
P50137	ILATPPQEDAPSVDIANIR	1.031231971	2	4.65536
P50137	ISSDLDGHPVPK	0.846149114	2	3.20853
P50137	KISSDLDGHPVPK	0.917793659	2	4.5077
P50137	LAVSQVPRSGKPAELLK	2.125081464	2	2.6875
P50137	LDNLVAIFDINR	0.876276193	2	3.64367
P50137	LGQSDPAPLQHQVDVYQK	1.015656665	2	4.0932
P50137	MFGIDKDAIVQAVK	0.937837849	2	3.79272
P50137	MFGIDKDAIVQAVK+Oxidation(0)	0.867525172	2	4.54005
P50137	NMAEQIIQEIYSQVQSK	0.907731724	3	6.01915
P50137	NMAEQIIQEIYSQVQSK+Oxidation(1)	1.324185447	3	3.80804
P50137	SKDDQVTVIGAGVTLHEALAAAEMLK	0.84964807	4	5.04938
P50137	SVPMSTVFYPSDGVATEK	0.963166182	2	4.5178
P50137	SVPMSTVFYPSDGVATEK+Oxidation(3)	0.882259121	2	3.4201
P50137	TSRPENAIIYSNNEDFQVGQAK	1.057806517	3	5.64093
P50137	VLDPFTIKPLDK	0.915483404	2	3.2029
P50137	VLDPFTIKPLDKK	0.895791237	2	2.84944
P50169	**RDH3 Retinol dehydrogenase 3**	**0.907609452**	**4E-07**	**9**
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR	0.869377322	3	5.58879
P50169	AMESLVNTCSGDLSLVTDCMEHALTSCHPR+Oxidation(1)	0.996979623	4	5.06103
P50169	FQDSYMK	0.936363589	1	1.94389
P50169	KLWDQTTEEVK	0.931323316	2	3.06398
P50169	KLWDQTTEEVKEIYGEK	0.872052322	3	4.00357
P50169	LWDQTTEEVK	0.987955531	2	3.16059
P50169	LWDQTTEEVKEIYGEK	0.882870077	2	4.88275
P50169	MSLVGGGYCISK	0.78107559	2	3.43716
P50169	MSLVGGGYCISK+Oxidation(0)	0.982595303	2	2.63029
P50237	**ST1C1 Sulfotransferase 1C1**	**0.900667064**	**7E-08**	**6**
P50237	AGTTWTQEIVDMIQNDGDVQK	0.882884842	2	5.31967

P50237	DISEEVLNK	0.829153017	1	2.49385
P50237	DLHLGEQDLQPETR	0.917369061	2	4.45397
P50237	MLPDPGTLGEYIEQFK	0.86692893	3	4.95733
P50237	MLPDPGTLGEYIEQFK+Oxidation(0)	0.927086473	2	3.01235
P50237	VLWGSWYDHVK	0.815139157	2	2.68481
P50398	**GDIA Rab GDP dissociation inhibitor alpha**	**1.065361798**	**0.0007**	**7**
P50398	FDLGQDVIDFTGHALALYR	1.16991482	3	4.63797
P50398	FQLLEGPPESMGR	1.044235422	2	3.09211
P50398	KQNDVFGEADQ	1.059956966	2	2.66786
P50398	NPYYGGESSSITPLEELYK	1.205864276	2	5.31777
P50398	QLICDPSYIPDR	0.976239998	2	3.11675
P50398	TDDYLDQPCLETINR	1.114642921	2	4.47608
P50398	TFEGVDPQTTSMR	1.073561372	2	2.46836
P50399	**GDIB Rab GDP dissociation inhibitor beta**	**1.154783141**	**7E-07**	**6**
P50399	AYDATTHFETTCDDIKDIYK	1.160762531	3	5.26483
P50399	EIRPALELLEPIEQK	1.128692234	3	3.68457
P50399	FDLGQDVIDFTGHSLALYR	1.143115053	3	4.21286
P50399	FVSISDLFVPK	1.159851868	2	3.5785
P50399	NTNDANSCQIIIPQNQVNR	1.165820209	2	4.14893
P50399	TDDYLDQPCCETINR	1.188822465	2	4.82915
P50431	**GLYC Serine hydroxymethyltransferase_ cytosolic**	**1.175408387**	**5E-12**	**5**
P50431	ALSDALTELGYK	1.119414824	2	3.72758
P50431	AVLEALGSCLNNK	1.236011223	2	3.9784
P50431	GLLEEDFQK	1.092139275	1	2.02447
P50431	NLDYAR	1.473282003	1	1.91591
P50431	VLEACSIACNK	1.097082027	2	3.22227
P50475	**SYAC Alanyl_tRNA synthetase_ cytoplasmic**	**0.98859584**	**2E-05**	**14**
P50475	ASEWVQQVSGLMDGK	0.963147556	2	4.02502
P50475	AVFDETYPDPVR	1.004561498	2	3.44916
P50475	DIINEEEVQFLK	0.913854494	2	3.23143
P50475	ESDGVLKPLPK	0.749759796	2	2.49095
P50475	GLEATDDSPK	0.907737566	1	2.02287
P50475	ITCLCQVPQNAANR	1.141980628	2	4.36458
P50475	IVAVTGAEAQK	1.028875054	2	2.5993
P50475	NVGCLQEALQLATSFAQLR	0.927466616	2	3.89468
P50475	RIVAVTGAEAQK	0.858928962	2	3.12074
P50475	SVLGDADQK	0.756860317	1	2.14714
P50475	TEEIVNGMIEAAKPVYTLDCPLAAAK	0.988789458	3	3.50432
P50475	TITVALADGGRPDNTGR	0.930828648	2	2.9626
P50475	VDDSSEDKTEFTVK	1.354445251	2	3.31742
P50475	VGAEDTDGIDMAYR	1.058491093	2	3.36262
P50503	**F10A1 Hsc70_interacting protein**	**1.499837982**	**1E-19**	**4**
P50503	AIDLFTDAIK	1.239878792	1	2.15544
P50503	AIEINPDSAQPYK	1.538712904	2	2.80614
P50503	GAAIDALNDGELQK	1.43601219	2	3.75628
P50503	KGAAIDALNDGELQK	1.386576106	2	4.47207
P50554	**GABT 4_aminobutyrate aminotransferase_ mitochondrial**	**1.10398192**	**9E-05**	**9**
P50554	GNYLVDVDGNR	1.075804871	1	2.12301
P50554	GTFCSFDTPDEAIR	1.010308879	2	3.42426
P50554	HGCAFLVDEVQTGGGCTGK	1.477785541	2	4.5514
P50554	IDIPSFDWPIAPFPR	1.037108686	2	3.73551
P50554	NLLLAEVINIIK	1.115213061	3	4.54306
P50554	REDLLNNVAHAGK	1.026624544	2	2.45902
P50554	TLLTGLLDLQAQYPQFVSR	1.192509297	3	4.10356
P50554	TVAGIIVEPIQSEGGDNHASDDFFR	1.107110924	2	3.76339
P50554	VDFEFDYDGPLMK	0.183108528	2	2.47293
P50580	**PA2G4 Proliferation_associated protein 2G4**	**1.097235293**	**0.568**	**2**

P50580	HELLQPFNVLYEK	1.191663393	2	2.70909
P50580	TIIQNPTDQQK	1.094963145	2	3.0938
P50878	**RL4 60S ribosomal protein L4**	**1.069867235**	**0.0008**	**7**
P50878	KLDELYGTWR	1.028585911	2	2.624
P50878	KLEAAAAALAAK	1.102442929	2	3.14033
P50878	LDELYGTWR	1.074337531	2	2.63756
P50878	LEAAAAALAAK	1.205260916	2	3.05621
P50878	NIPGITLLNVSK	1.241483559	1	2.55968
P50878	RGPCIIYNEDNGIIK	1.038362377	2	3.17715
P50878	SGQGAFGNMCR	0.972039765	2	2.8714
P51635	**AK1A1 Alcohol dehydrogenase [NADP_]**	**0.73372062**	**6E-13**	**7**
P51635	ALEALVAK	0.964276648	2	2.5996
P51635	GLEVTAYSPLGSSDR	0.890561324	2	3.99151
P51635	HHPEDVEPAVR	0.887980154	3	3.74727
P51635	HIDCASVYGNETEIGEALK	0.997438721	2	5.98395
P51635	HIDCASVYGNETEIGEALKESVGAGK	0.676941031	3	5.31116
P51635	HPDEPVLLEEPVVLALAEK	1.241502944	3	5.81331
P51635	YIVPMITVDGK	0.835227496	2	2.3039
P51647	**AL1A1 Retinal dehydrogenase 1**	**0.61584068**	**1E-19**	**14**
P51647	ANNTTYGLAAGVFTK	0.457682114	2	4.58405
P51647	EAGFPPGVVNIVPGYGPTAGAAISSHMDVDK	0.616564179	3	3.97622
P51647	ELGEHGLYEYTELK	0.408005559	2	3.46419
P51647	FPVLNPATEEVICHVEEGDKADVDK	0.433421868	4	5.15345
P51647	IFINNEWHDSVSGK	0.518615812	2	4.25935
P51647	IFVEESVYDEFVR	0.539930334	2	4.1608
P51647	IGPALSCGNTVVVKPAEQTPLTALHMASLIK	0.514523419	3	4.8077
P51647	IHGQTIPSDGDIFTFTR	0.591203963	2	3.83275
P51647	KFPVLNPATEEVICHVEEGDKADVDK	0.519150375	3	3.63965
P51647	LLLATIEAINGGK	1.540429872	2	3.32114
P51647	VFANAYLSDLGGSIK	0.459836032	2	4.13326
P51647	YCAGWADK	0.44425712	1	1.95946
P51647	YVLGNPLTQGINQGPQIDK	0.54498596	2	4.88056
P51647	YVLGNPLTQGINQGPQIDKEQHDK	0.460429061	2	3.72434
P51650	**SSDH Succinate_semialdehyde dehydrogenase_ mitochondrial**	**1.014357794**	**0.5853**	**9**
P51650	EVGEVLCTDPLVSK	0.896637704	2	3.82619
P51650	GIHDSFVTK	0.796420006	1	1.9289
P51650	HQSGGNFFEPTLLSNVTR	1.060120132	2	3.62814
P51650	IITAESGKPLK	1.09072385	2	2.45695
P51650	LGTVADCGVPEAR	1.044136432	2	3.29468
P51650	VGNGFEEGTTQGPLINEK	0.938129974	2	4.7433
P51650	VYGDIIYTSAK	0.98049386	2	2.54581
P51650	WLPTPATFPVYDPASGAK	0.902956214	2	2.78812
P51650	YGIDEYLEVK	0.930367824	2	2.94467
P51869	**CP4F4 Cytochrome P450 4F4**	**1.191449401**	**7E-07**	**4**
P51869	ALPSQHEDDILK	1.237601675	2	2.65231
P51869	NISLMTLDSLQK	1.059978215	2	2.90265
P51869	TLDFIDVLLLTK	1.559635332	2	2.87039
P51869	WQDLASGGSAR	1.191297472	2	2.55183
P51886	**LUM Lumican**	**0.923889989**	**0.789**	**2**
P51886	NNQIDHIDEK	1.132762052	2	3.32161
P51886	SLQDLQLANNK	0.82418493	2	3.09091
P52296	**IMB1 Importin subunit beta_1**	**1.018349077**	**0.2001**	**4**
P52296	AAVENLPTFLVELSR	0.88164679	2	2.59822
P52296	SNEILTAIIQGMR	0.888126038	2	2.72962
P52296	TVSPDRLELEAAQK	0.919391614	2	2.52815
P52296	VLANPGNSQVAR	1.087403256	2	3.18862
P52303	**AP1B1 AP_1 complex subunit beta_1**	**0.973264008**	**0.0081**	**3**

P52303	NINLIVQK	0.913001628	1	2.21432
P52303	NSFGLAPAAPLQVHAPLSPNQTVEISLPLNTVGSVMK	1.068993987	3	4.00899
P52303	YNDPIYVK	1.243695557	2	2.48967
P52555	**ERP29 Endoplasmic reticulum resident protein 29**	**1.167660959**	**0.0829**	**3**
P52555	ILDQGEDFPASELAR	1.126445186	2	4.53079
P52555	QGQDGLSGVK	1.313186697	2	2.46315
P52555	SLNLILTAFR	1.167534109	2	2.76702
P52759	**UK114 Ribonuclease UK114**	**1.105046039**	**0.0028**	**7**
P52759	AAGCDFTNVVK	1.502961234	2	2.8162
P52759	APAAIGAYSQAVLVDR	1.286967489	2	3.94013
P52759	IEIEAIAVQGPFTTAGL	1.132760381	1	3.48095
P52759	NLGEILK	0.904583168	1	2.2241
P52759	TIYVSGQIGMDPSSGQLVPGGVAEEAK	1.0638508	2	3.92437
P52759	TTVLLADINDFGTVNEIYK	1.063304409	2	5.19122
P52759	TYFQGNLPAR	0.979897887	2	2.97519
P52845	**ST1E2 Estrogen sulfotransferase_ isoform 2**	**0.911244068**	**0.9971**	**2**
P52845	CKEDAIFNR	1.036245883	2	2.67502
P52845	SGSTWIGEIVDMIYK	0.909648013	2	4.48599
P52847	**ST1B1 Sulfotransferase family cytosolic 1B member 1**	**1.188613292**	**9E-09**	**6**
P52847	DNPLVNYTHLPTEIMDHSK	1.192533864	2	4.16266
P52847	FLAGNVAYGSWFDHVK	1.293080977	2	2.59062
P52847	IEEFQSRPCDIVIPTYPK	1.048537537	3	4.40213
P52847	NYFTMTQSEK	1.05960318	1	2.68298
P52847	THLPIDLLPK	1.099574461	3	3.40365
P52847	TLDEHTLER	1.178352506	2	2.97859
P52873	**PYC Pyruvate carboxylase_ mitochondrial**	**1.019477197**	**1E-19**	**32**
P52873	ADEAYLIGR	1.164947304	2	2.84
P52873	ADFAQACQDAGVR	1.052431499	2	4.14713
P52873	AEAEAQAEELSFPR	1.134310325	2	4.38919
P52873	AGTHILCIK	1.589057368	2	2.66686
P52873	ALAVSDLNR	1.032737458	2	2.74746
P52873	AYSEALAAFGNGALFVEK	1.090177897	2	4.01858
P52873	AYVEANQMLGDLIK	1.062022099	2	4.58683
P52873	DAHQSLLATR	0.945082337	1	3.14014
P52873	DFTATFGPLDSLNTR	0.82373272	2	4.26398
P52873	DMAGLLKPAACTMLVSSLR	1.115928785	2	2.96559
P52873	ELIPNIPFQMLLR	1.406782006	2	2.34254
P52873	ENGVDAVHPGYGFLSER	1.222578122	2	2.86456
P52873	FLYECPWR	1.148629988	1	2.14017
P52873	GANAVGYTNYPDNVVFK	1.469930305	2	4.37819
P52873	GTPLDTEVPLER	1.029309165	2	3.59878
P52873	HGEEVTPEDVLSAAMYPDVFAQFK	1.133608204	2	5.65172
P52873	HIEVQILGDQYGNILHLYER	1.200031443	3	5.40582
P52873	HYFIEVNSR	1.151860301	2	2.72182
P52873	IAEEFEVELER	1.005653392	2	3.24918
P52873	IEGRPGASLPPLNLK	0.921014583	2	3.60173
P52873	INGCAIQCR	1.225503407	2	2.43643
P52873	IVGDLAQFMVQNGLSR	1.201069887	2	4.01246
P52873	LDNASAFQGAVISPHYDSLLVK	1.126124548	3	5.6108
P52873	LQVEHTVTEEITDVDLVHAQIHVSEGR	1.089382925	4	4.61287
P52873	QVGYENAGTVEFLVDK	1.211403346	2	3.76786
P52873	SVVEFLQGYIGIPHGGFPEPFR	1.328229973	2	4.17808
P52873	TVAVYSEQDTGQMHR	1.186285188	2	4.05088
P52873	VFDYSEYWEGAR	1.105256335	2	4.57888
P52873	VSPSPVDPIVPVVPIGPPPAGFR	1.019505374	2	4.32831
P52873	VVEIAPATHLDPQLR	1.024617983	2	4.87125
P52873	VVHSYEELEENYTR	1.103960342	2	5.10714

P52873	YSLEYYMGLAEELVR	1.24796054	3	4.43642
P52944	**PDLI1 PDZ and LIM domain protein 1**	**0.92199904**	**0.1202**	**4**
P52944	GHFFVGDQIYCEK	0.949991098	2	3.48473
P52944	QSTSFLVLQEILESDGK	0.939569244	2	2.35759
P52944	TSASGEEANSRPSAQPHPSGGLIIDK	0.841396416	3	4.28578
P52944	VTPPEGYDVVTVFPK	0.820633804	2	2.73218
P53395	**ODB2 Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial**	**0.91633629**	**0.5294**	**3**
P53395	LSDIGEGIR	1.044596912	2	2.35938
P53395	LSEVVGSGK	1.223214035	1	2.03584
P53395	SYLENPAFMLLDLK	1.155835601	2	4.02904
P53987	**MOT1 Monocarboxylate transporter 1**	**1.172386746**	**2E-14**	**4**
P53987	DGKEDETSTDVDEKPK	1.557731135	3	5.22769
P53987	DGKEDETSTDVDEKPKK	1.038601779	3	3.69507
P53987	ETQSPAPLQNSSGDPAEEESPV	1.163874219	2	4.73893
P53987	SDANTDLIGGSPK	1.1656626	2	3.75559
P54319	**PLAP Phospholipase A_2_activating protein**	**1.015361586**	**0.995**	**4**
P54319	GQTLGLGNTSFSDPFTGGGR	0.936027865	2	3.28922
P54319	IGDVVGSSGANQQTSGK	1.017400242	2	4.17649
P54319	TGDLGDINAEQLPGR	0.784832016	2	3.79812
P54319	YVPGTSGPSNTVQTADPFTGAGR	1.071443388	2	3.30035
P54921	**SNAA Alpha_soluble NSF attachment protein**	**0.981382803**	**0.0398**	**5**
P54921	AIAHYEQSADYYKGEESNSSANK	0.975407923	3	3.7382
P54921	AIDIYEQVGTSAMDSPLLK	1.142470358	2	3.40204
P54921	HDAATCFVDAGNAFK	0.881537233	2	2.51986
P54921	NSQSFFSGLFGGSSK	0.988034822	2	3.24861
P54921	YEELFPAFSDSR	0.994024021	2	2.61775
P55006	**RDH7 Retinol dehydrogenase 7**	**1.053464591**	**1E-09**	**11**
P55006	LETVILDVTK	0.993455421	2	2.95732
P55006	TESIVAATQWVK	0.894988465	2	3.96016
P55006	TNVTNMER	1.095468688	2	2.30728
P55006	TNVTNMER+Oxidation(5)	1.277443981	2	2.45132
P55006	TSDRLETVILDVTK	1.025326248	3	4.42367
P55006	VAIIEPGGFK	1.35456187	2	2.34095
P55006	VLAACLTEK	1.212598285	2	2.79519
P55006	VVNIASTMGR	0.954603952	2	3.49625
P55006	VVNIASTMGR+Oxidation(7)	0.940235065	2	2.67002
P55006	YGVEAFSDSLR	1.173840397	2	3.48712
P55006	YVFITGCDSGFGNLLAR	1.306778972	2	3.77707
P55051	**FABP7 Fatty acid_binding protein_ brain**	**0.984189175**	**0.2702**	**2**
P55051	LTDSQNFDEYMK	0.835298526	2	4.02945
P55051	QVGNVTKPTVIISQEGGK	0.992741743	3	3.86626
P55053	**FABP5 Fatty acid_binding protein_ epidermal**	**0.769210097**	**4E-09**	**4**
P55053	KTETVCTFTDGALVQHQK	0.725373112	3	4.39169
P55053	LVESHGFEDYMK	0.869992569	2	2.83176
P55053	MGAMAKPDCIITLDGNNLTVK	1.106746324	3	3.33938
P55053	TETVCTFTDGALVQHQK	0.734259477	2	4.51512
P55159	**PON1 Serum paraoxonase/arylesterase 1**	**0.8417403**	**4E-07**	**6**
P55159	GIEAGAEDLEILPNGLTFFSTGLK	1.271051369	3	5.33763
P55159	IFFYDSENPPGSEVLR	0.832336719	2	5.41295
P55159	IQSILSEDPK	0.903906508	2	3.12762
P55159	TITHELLPSINDIAAVGPESFYATNDHYFADPYLR	0.950511202	3	4.07429
P55159	VVADGFDFANGIGISLDGK	0.841710409	2	4.61414
P55159	YVYIAELLAHK	0.992679916	2	2.9503
P55260	**ANXA4 Annexin A4**	**0.962632281**	**0.6894**	**6**
P55260	AEIDMLDIPANFK	1.24431045	1	2.1351
P55260	GAGTDEGCLIEILASR	0.983109086	2	3.60862

P55260	GLGTDDSTLIR	0.972125546	2	2.89776
P55260	GLGTDEDAIIGVLACR	0.980759225	2	3.2461
P55260	KAMKGLGTDEDAIIGVLACR+Oxidation(2)	0.732073313	2	2.44394
P55260	SETSGSFEDALLAIVK	1.023866365	2	2.77143
P55770	**NH2L1 NHP2_like protein 1**	**0.919256743**	**0.3476**	**2**
P55770	LLDLVQQSCNYK	1.063975664	2	3.00273
P55770	QQIQSIQQSIER	0.915078381	2	2.7288
P56399	**UBP5 Ubiquitin carboxyl_terminal hydrolase 5**	**1.096468405**	**0.4454**	**3**
P56399	GTGLQPGEEELPDIAPPLVTPDEPK	0.996414668	2	4.51432
P56399	IFQNAPTDPTQDFSTQVAK	1.092244101	2	3.6315
P56399	IGEWELIQESGVPLKPLFGPGYTGIR	1.255259212	3	4.09165
P56522	**ADRO NADPH:adrenodoxin oxidoreductase_ mitochondrial**	**0.888596537**	**0.0778**	**4**
P56522	AVPTGDVEDLPCGLLLSSVGYK	0.915123156	2	4.13537
P56522	NVINTFTQTAR	0.93510356	2	2.52749
P56522	TATEKPGVEEAAR	0.893908081	2	3.12471
P56522	TDITEVALGVLR	0.872682028	2	3.46133
P56574	**IDHP Isocitrate dehydrogenase [NADP]_ mitochondrial**	**1.04605336**	**0.0006**	**10**
P56574	ATDFVVDR	1.304546227	2	2.57967
P56574	CATITPDEAR	1.19100918	2	2.33323
P56574	DQTNDQVTIDSALATQK	1.037157558	2	5.50417
P56574	GKLDGNQDLIR	1.054528201	2	3.108
P56574	LDGNQDLIR	1.003843483	2	2.35427
P56574	LIDDMVAQVLK	1.026605666	2	4.07631
P56574	LNEHFLNTTDFLDTIK	1.179060882	3	3.49321
P56574	NILGGTVFR	0.884592877	2	2.50328
P56574	SSGGFVWACK	1.126319613	2	2.525
P56574	TIEAEAAHGTVTR	1.31986198	2	3.85152
P56593	**CP2AC Cytochrome P450 2A12**	**1.189261058**	**0.1621**	**3**
P56593	MLQGTCGAPIDPTIYLSK	0.777291123	2	3.9414
P56593	MLQGTCGAPIDPTIYLSK+Oxidation(0)	1.242683368	2	3.07027
P56593	NRQPQYEDHMK	0.908198334	3	3.4141
P56656	**CP239 Cytochrome P450 2C39**	**0.810215578**	**1E-19**	**5**
P56656	EHQESLDVTNPR	0.536441254	2	3.37415
P56656	IKEHQESLDVTNPR	0.63604717	2	5.08095
P56656	NYLIPK	1.119909252	1	1.98419
P56656	VCAGEGLAR	1.768459767	2	2.39504
P56656	VQEEIDHVIGR	0.88137951	2	2.70477
P57093	**PAHX Phytanoyl_CoA dioxygenase_ peroxisomal**	**0.93287066**	**6E-07**	**3**
P57093	AISCHYGSSDCK	0.979629775	2	3.07568
P57093	IQDFQQNEELFR	1.076229676	2	4.03726
P57093	NLVSDDDIQR	0.685947222	1	2.50934
P57113	**MAAI Maleylacetoacetate isomerase**	**0.900648093**	**0.8335**	**12**
P57113	AITSGFNALEK	0.853701237	2	3.32191
P57113	ALLALEAFQVSHPCR	1.121173073	2	4.43866
P57113	DGGQQFSEEFQTLNPMK	0.934994088	2	4.8539
P57113	DGGQQFSEEFQTLNPMK+Oxidation(15)	0.942324842	2	2.3882
P57113	FKVDLSPYPTISHINK	0.983762355	3	4.89407
P57113	GIDYEIVPINLIK	0.960028644	2	4.25431
P57113	IDGITIGQSLAILEYLEETRPIPR	1.003220104	3	3.83377
P57113	MISDLIASGIQPLQNLSVLK	1.093069675	2	4.55273
P57113	MISDLIASGIQPLQNLSVLK+Oxidation(0)	1.113890013	2	5.44221
P57113	QVGQENQMPWAQK	0.952341502	2	3.62146
P57113	VDLSPYPTISHINK	1.052112926	2	3.7296
P57113	YCVGDEVSMADVCLAPQVANAER	1.007432934	2	5.95365
P57722	**PCBP3 Poly(rC)_binding protein 3**	**0.937967073**	**0.1117**	**2**
P57722	ESTGAQVQVAGDMLPNSTER	0.887568922	2	4.82714
P57722	INISEGNCPER	1.070808967	2	3.35926

P58321	**UCHL4 Ubiquitin carboxyl_terminal hydrolase isozyme L4**	**0.968830737**	**1**	**2**
P58321	VTHETSAHEGQTEAPSIDEK	0.958303516	2	4.40929
P58321	WLPLEANPEVTNQFLK	0.968830737	2	3.53485
P58751	**RELN Reelin**	**0.992259655**	**0.5325**	**2**
P58775	**TPM2 Tropomyosin beta chain**	**1.843633236**	**0.9998**	**10**
P58775	AISEELDNALNDITSL	1.781782106	2	4.33054
P58775	ATDAEADVASLNR	1.436102864	2	3.80096
P58775	CGDLEEELK	1.278350696	2	2.82984
P58775	KATDAEADVASLNR	1.449743931	2	4.32546
P58775	LDKENAIDR	1.666157898	1	2.07886
P58775	LKGTEDEVEK	1.468130369	3	3.54806
P58775	MELQEMQLK	0.80188551	2	2.62533
P58775	QLEEEQQALQK	1.31891501	2	3.97325
P58775	SLEAQADKYSTK	1.10452639	2	3.14157
P58775	TIDDLEDEVYAQK	1.698356855	2	3.71379
P59279	**RAB2B Ras_related protein Rab_2B**	**1.071613872**	**0.8842**	**2**
P59279	LQIWDTAGQESFR	1.028691047	2	3.15208
P59279	SYYRGAAGALLVYDITR	1.184835142	2	2.79916
P60335	**PCBP1 Poly(rC)_binding protein 1**	**1.085059795**	**0.4014**	**2**
P60335	AITIAGVPQSVTECVK	1.077771315	2	3.13124
P60335	LVVPATQCGSLIGK	1.188747285	2	3.07523
P60843	**IF4A1 Eukaryotic initiation factor 4A_I**	**1.016450605**	**0.9992**	**4**
P60843	ATQALVLAPTR	0.972844364	1	2.28062
P60843	GFKDQIYDIFQK	1.019204185	2	3.33683
P60843	KGVAINMVTEEDKR	1.023180997	3	3.47956
P60843	LQMEAPHIIVGTPGR	1.104703796	3	3.39221
P60868	**RS20 40S ribosomal protein S20**	**0.807350637**	**0.0003**	**2**
P60868	DTGKTPVEPEVAIHR	0.72661741	3	4.15312
P60868	LIDLHSPSEIVK	1.094102856	2	3.01281
P60901	**PSA6 Proteasome subunit alpha type_6**	**1.285423408**	**0.0065**	**2**
P60901	AINQGGLTSVAVR	1.284681299	2	3.5068
P60901	LLDSSTVTHLFK	1.46762413	2	2.56895
P61087	**UBE2K Ubiquitin_conjugating enzyme E2 K**	**1.104289992**	**0.1231**	**2**
P61087	GEIAGPPDTPYEGGR	1.102215457	2	3.52621
P61087	VDLVDENFTELR	1.165823832	2	2.60081
P61107	**RAB14 Ras_related protein Rab_14**	**0.950867833**	**0.718**	**3**
P61107	NLTNPNTVIILIGNK	0.932631691	2	3.90158
P61107	SCLLHQFTEK	0.976261273	2	2.93796
P61107	STYNHLSSWLTDAR	0.850763326	2	2.54797
P61222	**ABCE1 ATP_binding cassette sub_family E member 1**	**0.957695267**	**0.6847**	**2**
P61222	NTVANSPQTLLAGMNK	0.930162945	2	2.88966
P61222	NVEDLSGGELQR	0.986467903	2	2.93536
P61314	**RL15 60S ribosomal protein L15**	**1.042546518**	**0.3004**	**5**
P61314	FFEVILIDPFHK	0.970493281	3	3.83222
P61314	GATYGKPVHHGVNQLK	1.496641213	2	4.2882
P61314	SLQSVAEER	1.038025579	2	2.90032
P61314	VLNSYWVGEDSTYK	1.05954561	2	3.17686
P61314	YIQELWR	1.094338774	2	2.3221
P61459	**PHS Pterin_4_alpha_carbinolamine dehydratase**	**1.061417523**	**0.4022**	**3**
P61459	AVGWNELEGR	1.047437476	2	2.81039
P61459	LDHHPEWFNVYNK	1.022642999	3	4.89418
P61459	LSAEERDQLLPNLR	1.073795327	3	4.08985
P61589	**RHOA Transforming protein RhoA**	**1.066213648**	**0.9668**	**2**
P61589	MKQEPVKPEEGR	1.04399826	3	3.57017
P61589	MKQEPVKPEEGR+Oxidation(0)	1.094607731	2	2.96881
P61751	**ARF4 ADP_ribosylation factor 4**	**1.144760922**	**0.4428**	**3**
P61751	IQEGAAVLQK	1.07066413	2	2.48765

P61751	LGEIVTTIPTIGFNVETVEYK	1.071771281	3	4.82535
P61751	NICFTVWDVGGQDK	1.256406311	2	3.55078
P61805	**DAD1 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase subunit DAD1**	**1.1212356**	**0.2144**	**2**
P61805	ADFQGISPER	0.996205387	2	2.65911
P61805	FLEEYLSSTPQR	1.108981967	2	3.69794
P61924	**COPZ1 Coatomer subunit zeta_1**	**1.16716573**	**4E-06**	**2**
P61924	GEDVPLTEQTVSQVLQSAK	1.173736435	2	3.79322
P61924	YYDDTYPSVK	1.091327295	2	2.77864
P61980	**HNRPK Heterogeneous nuclear ribonucleoprotein K**	**0.967151836**	**1E-12**	**7**
P61980	GSDFDCELR	0.948775475	2	2.63631
P61980	GSYGDLGGPIITTQVTIPK	0.886287082	2	4.77486
P61980	IDEPLEGSEDR	0.928947428	2	3.35345
P61980	IILDLISESPIK	0.937662524	2	4.13629
P61980	IITITGTQDQIQNAQYLLQNSVK	0.959341939	3	5.27998
P61980	LFQECCPHSTDR	0.984408678	2	3.45565
P61980	TDYNASVSVPDSSGPER	0.945085416	2	4.40746
P61983	**1433G 14_3_3 protein gamma**	**1.041458508**	**1**	**4**
P61983	AYSEAHEISK	1.005137314	2	3.42011
P61983	NVTELNEPLSNEER	0.973897676	2	4.89528
P61983	TAFDDAIAELDTLNEDSYK	1.023752109	2	4.36381
P61983	YLAEVATGEK	1.137732432	2	2.81219
P62076	**TIM13 Mitochondrial import inner membrane translocase subunit Tim13**	**0.878577898**	**1E-08**	**4**
P62076	CIGKPGGSLDNSEQK	0.842020522	2	3.9513
P62076	KCIGKPGGSLDNSEQK	1.087577437	3	3.96031
P62076	LDPGAIMEQVK	0.88478567	2	2.8421
P62076	VQIAVANAQELLQR	0.948061621	2	4.20429
P62083	**RS7 40S ribosomal protein S7**	**1.083901004**	**0.302**	**3**
P62083	AIIIFVPVPQLK	1.096532728	2	3.73099
P62083	KAIIIFVPVPQLK	1.086072488	2	3.73043
P62083	TLTAVHDAILEDLVFPSEIVGK	1.042666533	2	5.25204
P62161	**CALM Calmodulin**	**1.123617103**	**0.0009**	**3**
P62161	EADIDGDGQVNYEEFVQMMTAK	1.504564367	2	4.76689
P62161	EAFSLFDKDGDGTITTK	1.177634866	2	4.05378
P62161	VFDKDGNGYISAAELR	1.096823788	2	4.87202
P62198	**PRS8 26S protease regulatory subunit 8**	**1.062592431**	**0.0002**	**3**
P62198	IEELQLIVNDK	1.088303708	2	2.74543
P62198	LEGGSGGDSEVQR	1.070911352	2	3.44481
P62198	TMLELLNQLDGFEATK	1.254091288	2	3.12486
P62243	**RS8 40S ribosomal protein S8**	**1.248360112**	**4E-12**	**9**
P62243	ADGYVLEGK	1.117720548	2	2.82564
P62243	IIDVVYNASNNELVR	1.063024259	2	3.63052
P62243	ISSLLEEQFQQGK	1.359539649	2	3.62546
P62243	KYELGRPAANTK	1.028463681	2	3.51506
P62243	LDVGNFSWGSECCTR	1.120672644	2	3.43152
P62243	LTPEEEEILNK	1.009717063	2	3.14226
P62243	NCIVLIDSTPYR	1.136123443	2	3.13019
P62243	QWYESHYALPLGR	0.998541302	2	2.33818
P62243	YELGRPAANTK	0.894310768	2	2.77112
P62246	**RS15A 40S ribosomal protein S15a**	**1.128160374**	**4E-05**	**3**
P62246	HGYIGEFEIIDDHR	1.083441755	3	4.61457
P62246	IVVNLTGR	1.160329448	2	2.46352
P62246	WQNNLLPSR	1.069398932	2	2.58888
P62250	**RS16 40S ribosomal protein S16**	**1.31949107**	**7E-05**	**4**
P62250	ALVAYYQK	1.030158924	1	2.00934
P62250	GGGHVAQIYAIR	1.424034351	2	3.04808

P62250	LLEPVLLLGK	1.110541484	2	2.75476
P62250	TLLVADPR	1.034355597	2	2.46284
P62260	**1433E 14_3_3 protein epsilon**	**0.961061631**	**7E-07**	**4**
P62260	AAFDDAIAELDTLSEESYK	1.068128529	2	5.83026
P62260	HLIPAANTGESK	0.978947623	2	2.34773
P62260	LICCDILDVLDK	1.339603307	2	3.57556
P62260	YLAEFATGNDRK	0.960749174	2	2.65621
P62271	**RS18 40S ribosomal protein S18**	**1.024742935**	**0.9781**	**5**
P62271	AGELTEDEVER	1.076592345	2	3.22494
P62271	LREDLER	0.949389748	1	2.00734
P62271	RAGELTEDEVER	0.71440908	2	3.31675
P62271	VLNTNIDGR	1.025414912	2	2.82521
P62271	YSQVLANGLDNK	1.02844937	1	3.5095
P62278	**RS13 40S ribosomal protein S13**	**1.029111349**	**0.3698**	**4**
P62278	GLAPDLPEDLYHLIK	0.996083986	2	2.91285
P62278	GLSQSALPYR	1.303080815	1	2.03685
P62278	GLTPSQIGVILR	1.082986412	2	2.54795
P62278	KGLTPSQIGVILR	1.005048177	2	2.66401
P62332	**ARF6 ADP_ribosylation factor 6**	**1.174625018**	**0.7856**	**2**
P62332	FNVWDVGGQDK	1.176873605	2	3.05842
P62332	LGQSVTTIPTVGFNVETVTYK	1.081471071	2	2.50828
P62334	**PRS10 26S protease regulatory subunit 10B**	**0.988958295**	**0.0488**	**4**
P62334	ALQSVGQIVGEVLK	1.133316481	2	3.43536
P62334	EVIELPLTNPELFQR	0.864411156	2	3.3984
P62334	HGEIDYEAIVK	0.722915087	2	2.52707
P62334	IHIDLPNEQAR	0.995385221	2	2.43277
P62425	**RL7A 60S ribosomal protein L7a**	**1.030506811**	**0.2558**	**9**
P62425	AGVNTVTTLVENK	1.030214492	2	4.15003
P62425	AGVNTVTTLVENKK	0.987721482	2	2.91987
P62425	NFGIGQDIQPK	1.041365815	2	3.54022
P62425	TCTTVAFTQVNSEDK	1.06888589	2	3.85201
P62425	TCTTVAFTQVNSEDKGALAK	1.492270532	2	4.34496
P62425	TNYNDRYDEIR	0.832406873	2	2.31982
P62425	VAPAPAVVK	1.104070006	1	1.95917
P62425	VPPAINQFTQALDR	1.167331607	2	3.79195
P62425	VVNPLFEK	1.334835363	1	1.90689
P62630	**EF1A1 Elongation factor 1_alpha 1**	**1.059909236**	**1E-19**	**13**
P62630	DGSASGTTLLEALDCILPPTRPTDKPLR	1.041952665	3	4.87193
P62630	KDGSASGTTLLEALDCILPPTRPTDKPLR	1.14177424	4	5.13988
P62630	MDSTEPPYSQK	0.906463616	2	3.81272
P62630	MDSTEPPYSQK+Oxidation(0)	1.059827974	2	3.03707
P62630	NDPPMEAAGFTAQVIILNHPGQISAGYAPVLDCHTAHIACK	1.204898637	5	6.6669
P62630	RYEEIVK	0.985542791	2	2.37998
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR	1.11705532	3	5.26733
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(14)	1.161686786	3	4.48349
P62630	SGDAAIVDMVPGKPMCVESFSDYPPLGR+Oxidation(8)	1.17878409	3	4.08079
P62630	VETGVLKPGMVVTFAPVNVTTEVK	1.042402267	2	5.37011
P62630	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)	1.059621923	3	5.04586
P62630	YEEIVK	1.009683184	1	2.17746
P62630	YYVTIIDAPGHR	1.01975701	3	3.61709
P62632	**EF1A2 Elongation factor 1_alpha 2**	**1.097792063**	**2E-16**	**8**
P62632	EHALLAYTLGVK	1.130766098	1	3.54115
P62632	IGGIGTVPVGR	1.255479704	2	3.50874
P62632	NMITGTSQADCAVLIVAAGVGEFEAGISK	1.027203109	3	5.18758
P62632	QLIVGVNK	0.957808643	1	2.77082
P62632	QTVAVGVIK	0.955245683	1	2.06439
P62632	STTTGHLIYK	1.117050173	2	2.89936

P62632	THINIVVIGHVDSGK	1.07806307	2	4.84455
P62632	VETGILRPGMVVTFAPVNITTEVK	1.286823146	3	3.6685
P62703	**RS4X 40S ribosomal protein S4_ X isoform**	**1.134617155**	**0.8603**	**6**
P62703	FDTGNLCMVTGGANLGR	0.992151252	2	4.62941
P62703	FDTGNLCMVTGGANLGR+Oxidation(7)	0.678814487	2	4.25834
P62703	GIPHLVTHDAR	0.996326896	2	2.48957
P62703	LSNIFVIGK	0.90486318	2	2.46587
P62703	TDITYPAGFMDVISIDK	0.975328617	2	3.8332
P62703	VNDTIQIDLETGK	1.083075697	2	3.77194
P62718	**RL18A 60S ribosomal protein L18a**	**0.926375652**	**0.3925**	**2**
P62718	DLTTAGAVTQCYR	0.925050993	2	3.01477
P62718	SSGEIVYCGQVFEKSPLR	0.947355275	2	2.46834
P62752	**RL23A 60S ribosomal protein L23a**	**1.025467205**	**0.1626**	**5**
P62752	LAPDYDALDVANK	0.993955677	2	3.85355
P62752	LDHYAIIK	1.042029415	2	2.64419
P62752	NKLDHYAIIK	1.247849256	2	2.79978
P62752	VNTLIRPDGEK	1.075646461	2	2.81972
P62752	VNTLIRPDGEKK	1.074083527	2	2.86813
P62755	**RS6 40S ribosomal protein S6**	**1.000045671**	**0.7049**	**5**
P62755	DIPGLTDTTVPR	0.809323465	2	2.63617
P62755	LIEVDDER	1.029522716	2	2.73585
P62755	LNISFPATGCQK	0.870447032	2	2.99794
P62755	MATEVAADALGEEWK	1.071319359	2	3.75005
P62755	MATEVAADALGEEWK+Oxidation(0)	1.024274109	2	4.35912
P62804	**H4 Histone H4**	**0.885245728**	**1E-19**	**7**
P62804	DAVTYTEHAK	0.69954547	2	3.03361
P62804	DNIQGITKPAIR	0.742738469	2	3.42249
P62804	ISGLIYEETR	1.346450139	2	3.32766
P62804	RISGLIYEETR	0.896496717	2	2.41841
P62804	TVTAMDVVYALK	0.993291487	2	3.98923
P62804	TVTAMDVVYALK+Oxidation(4)	0.98406101	2	3.22767
P62804	VFLENVIR	0.882682507	2	3.25071
P62815	**VATB2 V_type proton ATPase subunit B_ brain isoform**	**0.892260565**	**0.0095**	**2**
P62815	AVVQVFEGTSGIDAK	0.498767152	2	3.22027
P62815	QIYPPINVLPSLSR	1.101803157	2	2.38589
P62853	**RS25 40S ribosomal protein S25**	**1.33123926**	**2E-05**	**2**
P62853	GGDAPAAGEDA	1.062441151	1	2.02221
P62853	LNNLVLFDK	1.427351381	2	2.80851
P62856	**RS26 40S ribosomal protein S26**	**0.935830319**	**0.7208**	**2**
P62856	DISEASVFDAYVLPK	0.9391135	2	3.40282
P62856	NIVEAAAVR	0.956164935	2	2.8791
P62890	**RL30 60S ribosomal protein L30**	**1.054687123**	**0.617**	**2**
P62890	TGVHHYSGNNIELGTACGK	1.027704071	2	5.55729
P62890	VCTLAIIDPGDSDIIR	1.120863464	2	3.71755
P62898	**CYC Cytochrome c_ somatic**	**1.105059087**	**0.2196**	**6**
P62898	ADLIAYLK	1.022612239	2	2.77708
P62898	GITWGEDTLMEYLENPK	1.092787993	2	4.88249
P62898	GITWGEDTLMEYLENPKK	0.991674253	2	4.3341
P62898	KTGQAAGFSYTDANK	1.130703457	2	4.89112
P62898	TGPNLHGLFGR	0.986562745	2	3.25397
P62898	TGQAAGFSYTDANK	1.128070699	2	4.15838
P62902	**RL31 60S ribosomal protein L31**	**1.155031538**	**0.0004**	**2**
P62902	NLQTVNVDEN	1.433285254	1	2.29141
P62902	SAINEVVTR	1.141036917	2	3.11726
P62907	**RL10A 60S ribosomal protein L10a**	**1.008423184**	**0.8262**	**5**
P62907	AVDIPHMDIEALK	0.990317763	2	2.32868
P62907	AVDIPHMDIEALKK	0.851218374	2	2.63058

P62907	FSVCVLGDQQHCDEAK	1.021952823	2	3.92255
P62907	KYDAFLASESLIK	0.980717086	2	3.71356
P62907	YDAFLASESLIK	1.202750383	2	3.74726
P62909	**RS3 40S ribosomal protein S3**	**0.941385531**	**3E-13**	**10**
P62909	AELNEFLTR	1.064994454	2	2.86139
P62909	DEILPTTPISEQK	0.899228226	2	3.75529
P62909	ELAEDGYSGVEVR	0.919259226	2	3.42427
P62909	ELTAVVQK	0.898565997	2	2.31501
P62909	FGFPEGSVELYAEK	1.743909618	2	3.34449
P62909	FVDGLMIHSGDPVNYYVDTAVR	1.039586695	3	4.01566
P62909	GCEVVVSGK	1.105457086	2	2.49661
P62909	GGKPEPPAMPQPVPTA	1.346666568	2	3.73576
P62909	GLCAIAQAESLR	1.082656963	2	3.16031
P62909	TEIIILATR	1.119386595	2	2.79602
P62912	**RL32 60S ribosomal protein L32**	**1.134839248**	**0.2777**	**2**
P62912	ELEVLLMCNK	1.147305412	2	2.53029
P62912	SYCAEIAHNVSSK	1.132004205	2	4.36585
P62914	**RL11 60S ribosomal protein L11**	**1.016979606**	**0.9993**	**2**
P62914	VLEQLTGQTPVFSK	1.010264385	2	4.05051
P62914	YDGIILPGK	1.039342106	2	2.92345
P62919	**RL8 60S ribosomal protein L8**	**1.065561682**	**0.1944**	**3**
P62919	ASGNYATVISHNPETK	1.090106143	2	4.45845
P62919	AVVGVVAGGGR	1.020650645	2	3.55993
P62919	KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR	1.045325686	3	4.88739
P62959	**HINT1 Histidine triad nucleotide_binding protein 1**	**0.993184127**	**0.8591**	**3**
P62959	AQVAQPGGDTIFGK	0.972581125	2	4.58619
P62959	CLAFHDISPQAPTHFLVIPK	1.062574396	3	4.56672
P62959	KHISQISVADDDDESLLGHLMIVGK	0.861604348	3	4.15185
P62961	**YBOX1 Nuclease_sensitive element_binding protein 1**	**1.06882323**	**4E-08**	**4**
P62961	EDGNEEDKENQGDETQGQQPPQR	1.019409159	3	5.16661
P62961	GAEAANVTGPGGVPVQGSK	1.078069391	2	5.04964
P62961	NEGSESAPEGQAQQR	1.5739721	2	4.98983
P62961	NYQQNYQNSESGEKNEGSESAPEGQAQQR	1.488380245	3	5.49586
P62963	**PROF1 Profilin_1**	**1.137771875**	**0.0111**	**4**
P62963	DSPSVWAAVPGK	1.096347964	1	2.20515
P62963	SSFFVNGLTLGGQK	1.158172783	2	4.52821
P62963	STGGAPTFNVTVTMTAK	0.944335888	2	2.63065
P62963	TFVSITPAEVGVLVGK	0.841259823	2	4.50028
P63018	**HSP7C Heat shock cognate 71 kDa protein**	**0.950101877**	**1E-19**	**22**
P63018	ARFEELNADLFR	1.073298597	3	3.62338
P63018	CNEIISWLDK	1.305816786	2	3.1373
P63018	DAGTIAGLNVLR	0.97935224	2	3.59799
P63018	FDDAVVQSDMK	1.202434691	2	3.70682
P63018	FEELNADLFR	1.045279605	2	3.10022
P63018	FELTGIPPAPR	1.048010974	2	3.1347
P63018	IINEPTAAAIAYGLDK	1.326054744	2	4.7496
P63018	IINEPTAAAIAYGLDKK	1.05641981	2	4.55417
P63018	LLQDFFNGK	1.261473276	2	2.67693
P63018	NQTAEKEEFEHQQK	1.357608815	2	5.24712
P63018	NQVAMNPTNTVFDAK	1.142025661	2	4.50646
P63018	NQVAMNPTNTVFDAK+Oxidation(4)	1.128188288	2	4.27117
P63018	NSLESYAFNMK	1.422370488	2	3.24587
P63018	QATKDAGTIAGLNVLR	0.839823086	2	2.44163
P63018	RFDDAVVQSDMK	1.008003994	2	2.74919
P63018	SFYPEEVSSMVLTK	1.090670762	2	4.13757
P63018	SFYPEEVSSMVLTK+Oxidation(9)	1.035447877	2	2.89805
P63018	SINPDEAVAYGAAVQAAILSGDK	1.168924981	2	6.27647

P63018	SQIHDIVLVGGSTR	1.062256522	2	4.9614
P63018	STAGDTHLGGEDFDNR	1.076022704	2	4.42649
P63018	TVTNAVVTVPAYFNDSQR	1.066914359	2	4.08492
P63018	VCNPIITK	1.189164901	2	2.40217
P63029	**TCTP Translationally_controlled tumor protein**	**0.968938024**	**1**	**2**
P63029	DLISHDELFSDIYK	0.968374164	2	3.55469
P63029	EIADGLCLEVEGK	0.988189646	2	3.25748
P63036	**DNJA1 DnaJ homolog subfamily A member 1**	**1.007110477**	**0.0995**	**6**
P63036	HYNGEAYEDDEHHPR	1.428140238	3	4.90377
P63036	ITFHGEGDQEPGLEPGDIIIVLDQK	1.094183316	3	3.76342
P63036	NVVHQLSVTLEDLYNGATR	0.99065332	2	5.87586
P63036	QISQAYEVLADSK	1.012584298	2	3.60797
P63036	TIVITSHPGQIVK	1.07930988	2	2.92738
P63036	VNFPENGFLSPDK	1.096906714	2	2.93688
P63039	**CH60 60 kDa heat shock protein_ mitochondrial**	**0.922163544**	**1E-19**	**28**
P63039	AAVEEGIVLGGGCALLR	0.982656684	3	5.97951
P63039	ALMLQGVDLLADAVAVTMGPK+Oxidation(17)	1.041641631	3	3.31645
P63039	CEFQDAYVLLSEK	1.330161956	2	4.69298
P63039	CIPALDSLKPANEDQK	0.832682521	2	3.31315
P63039	DDAMLLKGKGDK+Oxidation(3)	1.193220166	2	2.40922
P63039	DIGNIISDAMK	0.994347954	2	3.61682
P63039	GVMLAVDAVIAELKK	0.831744549	2	4.30389
P63039	GYISPYFINTSK	0.954835562	2	3.63694
P63039	ILQSSSEVGYDAMLGDFVNMVEK	1.113948362	2	4.96898
P63039	IQEITEQLDITTSEYEK	1.024746006	2	5.60253
P63039	IQEITEQLDITTSEYEKEK	0.64725913	2	5.16319
P63039	ISSVQSIVPALEIANAHR	1.176371215	2	4.0915
P63039	KISSVQSIVPALEIANAHR	1.433446276	3	3.30923
P63039	KPLVIIAEDVDGEALSTLVLNR	1.169345708	2	5.91552
P63039	LSDGVAVLK	1.063344134	2	2.69831
P63039	LVQDVANNTNEEAGDGTTTATVLAR	1.010072111	2	6.63829
P63039	NAGVEGSLIVEK	1.001211937	2	3.4665
P63039	QSKPVTTPEEIAQVATISANGDK	1.013580826	2	3.82041
P63039	QSKPVTTPEEIAQVATISANGDKDIGNIISDAMK	0.812000335	3	5.26728
P63039	RGVMLAVDAVIAELKK	1.13448362	3	4.54621
P63039	TLNDELEIIEGMK	0.903885229	2	4.58435
P63039	TLNDELEIIEGMK+Oxidation(11)	0.973489057	2	3.49444
P63039	TVIIEQSWGSPK	0.906540324	2	4.45821
P63039	VGEVIVTK	0.918368017	2	2.98112
P63039	VGGTSDVEVNEK	0.931000165	2	3.84081
P63039	VGGTSDVEVNEKK	0.912893132	2	3.07049
P63039	VGLQVVAVK	0.98539465	2	3.453
P63039	VTDALNATR	0.96063389	2	3.47774
P63088	**PP1G Serine/threonine_protein phosphatase PP1_gamma catalytic subunit**	**1.056294251**	**0.6424**	**2**
P63088	EIFLSQPILLELEAPLK	1.266202104	2	3.06916
P63088	TFTDCFNCLPIAAIVDEK	1.021375491	2	3.3464
P63095	**subunit alpha isoforms short**	**1.109947825**	**0.3355**	**2**
P63095	AFEPFYDEIKSKGALVK	1.061666627	2	2.79722
P63095	YTTPEDATPEPGEDPR	1.121456058	2	2.93099
P63102	**1433Z 14_3_3 protein zeta/delta**	**0.982573649**	**1**	**7**
P63102	DICNDVLSLLEK	0.916730559	3	3.90997
P63102	FLIPNASQPESK	1.012339639	2	3.0245
P63102	GIVDQSQQAYQEAFEISK	0.981734054	2	5.71689
P63102	KGIVDQSQQAYQEAFEISK	0.946595457	2	5.32462
P63102	SVTEQGAELSNEER	1.095137194	2	4.96664
P63102	TAFDEAIAELDTLSEESYK	1.068087167	2	5.78041

P63102	YLAEVAAGDDKK	1.00539402	2	2.92751
P63159	**HMGB1 High mobility group protein B1**	**1.010773973**	**0.9681**	**3**
P63159	GEHPGLSIGDVAK	0.916929675	2	3.05594
P63159	IKGEHPGLSIGDVAK	1.09893544	3	3.71582
P63159	KHPDASVNFSEFSK	0.945410474	2	3.87865
P63174	**RL38 60S ribosomal protein L38**	**1.018811071**	**0.6905**	**2**
P63174	KIEEIKDFLLTAR	1.023806048	3	3.97775
P63174	YLYTLVITDKEK	1.125873284	2	2.3242
P63245	**GBLP Guanine nucleotide_binding protein subunit beta_2_like 1**	**1.008941626**	**3E-07**	**8**
P63245	DGQAMLWDLNEGK	1.058651265	2	2.42034
P63245	FSPNSSNPIIVSCGWDK	1.11127701	2	4.53951
P63245	HLYTLDGGDIINALCFSPNR	1.115278916	2	5.68484
P63245	IIVDELKQEVISTSSK	0.955653778	2	4.00242
P63245	LWDLTTGTTTR	1.170981464	1	2.155
P63245	TNHIGHTGYLNTVTVSPDGSLCASGGK	1.125953805	3	5.23219
P63245	VWQVTIGTR	1.203524782	2	2.74027
P63245	YTVQDESHSEWVSCVR	1.160312962	2	4.20818
P63259	**ACTG Actin_ cytoplasmic 2**	**0.992924251**	**0.1568**	**8**
P63259	CPEALFQPSFLGMESCGIHETTFNSIMK	1.529885342	3	4.29657
P63259	DLYANTVLSGGTTMYPGIADR	0.930575098	2	5.75515
P63259	DLYANTVLSGGTTMYPGIADR+Oxidation(13)	0.852841773	2	4.15426
P63259	GYSFTTTAER	0.975004435	2	3.22664
P63259	KDLYANTVLSGGTTMYPGIADR	1.019801802	2	5.74754
P63259	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)	0.998403571	3	4.13513
P63259	QEYDESGPSIVHR	0.964632582	3	3.51557
P63259	VAPEEHPVLLTEAPLNPK	1.021141352	2	4.48851
P63324	**RS12 40S ribosomal protein S12**	**1.040347597**	**0.646**	**3**
P63324	KVVGCSCVVVK	1.038343899	2	2.72043
P63324	LGEWVGLCK	1.154286478	1	2.25158
P63324	VVGCSCVVVK	1.103375323	2	2.35862
P67779	**PHB Prohibitin**	**0.794633017**	**1E-19**	**9**
P67779	AAELIANSLATAGDGLIELR	0.888566596	3	5.03152
P67779	AAIISAEGDSK	1.13290949	2	2.45583
P67779	DLQNVNITLR	0.798490932	2	3.26906
P67779	FDAGELITQR	0.839677667	2	3.83395
P67779	GVQDIVVGEGTHFLIPWVQKPIIFDCR	1.10138794	3	4.14826
P67779	IYTSIGEDYDER	1.23917202	2	3.07873
P67779	KLEAAEDIAYQLSR	0.863934881	2	4.40247
P67779	NVPVITGSK	0.770554765	1	2.20591
P67779	VLPSITTEILK	0.878850199	2	2.34398
P68037	**UB2L3 Ubiquitin_conjugating enzyme E2 L3**	**1.06521682**	**0.0011**	**3**
P68037	ADLAEEYSK	1.173353565	2	2.56233
P68037	GQVCLPVISAENWKPATK	1.163935922	2	3.00738
P68037	TDQVIQSLIALVNDPQPEHPLR	1.107272046	2	4.95021
P68101	**IF2A Eukaryotic translation initiation factor 2 subunit 1**	**1.024832184**	**0.9588**	**3**
P68101	HAVSDPSILDSLDLNEDEREVLINNINR	0.846562071	3	3.44658
P68101	TEGLSVLNQAMAVIK	1.066211198	2	3.86983
P68101	VVTDTDETELAR	1.022206638	2	2.38498
P68136	**ACTS Actin_ alpha skeletal muscle**	**0.942265243**	**0.0556**	**15**
P68136	AGFAGDDAPR	1.376202975	2	3.2151
P68136	AVFPSIVGRPR	0.966187005	2	2.53418
P68136	DLYANNVMSGGTTMYPGIADR	1.203380273	2	4.44604
P68136	DSYVGDEAQSK	0.876307657	2	3.6203
P68136	EITALAPSTMK	0.92142577	2	3.00928
P68136	EITALAPSTMK+Oxidation(9)	0.929919168	2	2.85863
P68136	GYSFVTTAER	1.0573835	2	3.37831
P68136	KDLYANNVMSGGTTMYPGIADR	1.258047229	2	5.46115

P68136	KDLYANNVMSGGTTMYPGIADR+Oxidation(14)	1.193381778	3	3.68418
P68136	QEYDEAGPSIVHR	1.440923604	2	2.95769
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR	1.515669004	3	6.36245
P68136	TTGIVLDSGDGVTHNVPIYEGYALPHAIMR+Oxidation(28)	1.672831594	3	4.60274
P68136	VAPEEHPTLLTEAPLNPK	1.197924197	2	4.436
P68136	YPIEHGIITNWDDMEK	1.38233825	2	4.56606
P68136	YPIEHGIITNWDDMEK+Oxidation(13)	0.930000753	2	3.45926
P68255	**1433T 14_3_3 protein theta**	**0.920581295**	**0.9904**	**4**
P68255	AVTEQGAELSNEER	0.941407541	2	4.71373
P68255	SICTTVLELLDK	1.150454196	2	3.25298
P68255	TAFDEAIAELDTLNEDSYK	0.979170876	2	4.26542
P68255	VISSIEQK	1.038211756	2	2.326
P68511	**1433F 14_3_3 protein eta**	**1.107538451**	**0.3947**	**3**
P68511	AVTELNEPLSNEDR	1.000549163	2	4.50381
P68511	ELETVCNDVLALLDK	1.138083089	2	3.27648
P68511	NSVVEASEAAYK	1.106412149	2	2.63407
P69735		**1.032227774**	**0.1443**	**6**
P69735	AKMEENPPVK+Oxidation(2)	1.10200396	1	1.94467
P69735	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	0.890673514	3	3.74464
P69735	EDEVQLLVEK	0.813345439	1	1.91127
P69735	GEPKLPAMDKPGGK+Oxidation(7)	0.945947383	2	2.31241
P69735	LIDDYGVEEEPAELPEGTSLTVDNKR	0.88203466	3	4.68484
P69735	QFDKMQAQLK	1.072345288	2	2.56431
P69897	**TBB5 Tubulin beta_5 chain**	**1.024039682**	**0.9279**	**3**
P69897	ALTVPELTQQVFDAK	1.007433177	2	2.3053
P69897	ISVYYNEATGGK	1.145364778	2	2.89591
P69897	LTTPTYGDLNHLVSATMSGVTTCLR	1.283634447	2	4.92111
P70372	**ELAV1 ELAV_like protein 1**	**0.871587534**	**0.1496**	**3**
P70372	SLFSSIGEVESAK	0.442130086	2	3.54891
P70372	TNLIVNYLPQNMTQEELR	0.841176927	2	2.98183
P70372	VLVDQTTGLSR	0.871672769	2	2.81549
P70470	**LYPA1 Acyl_protein thioesterase 1**	**1.189993608**	**0.044**	**2**
P70470	ASFSQGPINSANR	2.39995249	2	2.80932
P70470	DISVLQCHGDCDPLVPLMFGSLTVER	1.135461167	3	3.53478
P70473	**AMACR Alpha_methylacyl_CoA racemase**	**0.807164997**	**1E-19**	**12**
P70473	ADVLLEPFR	0.836847617	2	3.40322
P70473	AEWCQIFDGTDACVTPVLTLEEALHHQHNR	0.825144873	5	5.02812
P70473	DYGFSQEEIHQLHSDR	0.731193046	2	4.88701
P70473	GLGLESEELPSQMSIEDWPEMK	0.787428262	3	4.70272
P70473	GQNLLDGGAPFYTTYK	0.852577137	2	4.89444
P70473	LGSVNHPSHLAR	1.296382076	2	2.85048
P70473	LQLGPETLR	0.841866813	2	2.30093
P70473	LSGFGQSGIFSK	1.094529355	2	2.41753
P70473	RDPSVGEHTVEVLK	0.810562986	3	4.29321
P70473	RDPSVGEHTVEVLKDYGFSQEEIHQLHSDR	0.797876305	5	4.78818
P70473	TADGEFMAVGAIEPQFYTLLLK	1.232563006	3	3.9656
P70473	TQAMGLWAQPR	0.833762082	2	2.81047
P70552	**GFRP GTP cyclohydrolase 1 feedback regulatory protein**	**1.246349603**	**0.0117**	**2**
P70552	MEVGPTMVGDEHSDPELMQQLGASK	1.116589202	3	3.70346
P70552	VLGNNFYEYYVNDPPR	1.338052629	2	3.88821
P70580	**PGRC1 Membrane_associated progesterone receptor component 1**	**1.051739904**	**0.3378**	**7**
P70580	EGEEPTVYSDDEEPKDEAAR	0.778104872	2	4.24125
P70580	FYGPEGPYGVFAGR	0.973619607	2	3.58662
P70580	GDQPGASGDNDDDEPPPLPR	0.972729996	2	4.95271
P70580	IVRGDQPGASGDNDDDEPPPLPR	0.670323676	3	4.23778
P70580	KFYGPEGPYGVFAGR	0.962515261	2	3.74459

P70580	RYDGVQDPR	0.744570746	1	2.32899
P70580	YDGVQDPR	0.929596702	2	2.54432
P70584	**ACDSB Short/branched chain specific acyl_CoA dehydrogenase_ mitochondrial**	**0.709946189**	**1E-19**	**8**
P70584	ASSTCQLTFENVK	0.715451727	2	3.12806
P70584	FAQEQIAPLVSTMDENSK	0.737186094	2	4.06228
P70584	IFDFQGLQHQVAHVATQLEAAR	0.679609188	3	6.08649
P70584	IGTIYEGTSNIQLNTIAK	0.790056619	2	4.33642
P70584	KFAQEQIAPLVSTMDENSK	0.616449105	2	5.47095
P70584	SGNYYVINGSK	0.669050465	2	3.12127
P70584	VDASVALLCDIQNTVINK	1.268277944	2	4.67323
P70584	YYASEVAGLTTSK	0.761260893	2	3.57634
P70615	**LMNB1 Lamin_B1**	**0.916281479**	**0.3251**	**3**
P70615	ALYETELADAR	0.94382307	2	3.11318
P70615	LSSEMNTSTVNSAR	0.763708588	2	2.70259
P70615	MLSDKEREMAEIR+Oxidation(0)	1.019082934	2	2.38043
P70694	**DHB5 Estradiol 17 beta_dehydrogenase 5**	**1.048731483**	**0.9988**	**2**
P70694	REDIFYTSK	1.065704117	2	2.97953
P70694	SIGVSNFNR	1.038906801	2	2.58314
P70712	**KYNU Kynureninase**	**1.260926446**	**1E-05**	**8**
P70712	IATELNCDPTDER	1.349240477	2	3.82167
P70712	IGAYGHEVGK	1.336117448	2	2.4907
P70712	LDEEDKLKR	1.25841111	2	2.51528
P70712	LLTAILDSTERN	1.253944193	2	3.29521
P70712	TYLEEELDK	1.315989743	1	2.0387
P70712	TYLEEELDKWAK	1.157914969	2	2.40375
P70712	VAPVPLYNSFHDVYK	1.543939664	2	3.10541
P70712	YLNSGAGGLAGAFIHEK	1.295403192	2	4.07879
P80067	**CATC Dipeptidyl peptidase 1**	**1.15012501**	**0.0879**	**4**
P80067	GTDECAIESIAMAAIPIPK	1.108530481	3	4.95378
P80067	NSWGSQWGESGYFR	1.165233635	2	3.49413
P80067	RGTDECAIESIAMAAIPIPK	0.933164967	2	3.65765
P80067	YAQDFGVVEENCFPYTATDAPCKPK	1.24884162	3	4.70029
P80254	**DOPD D_dopachrome decarboxylase**	**0.64925075**	**2E-07**	**4**
P80254	FFPLEPWQIGK	0.642766304	2	2.51926
P80254	FLTEELSLDQDR	0.774349314	2	3.54553
P80254	LCAATATILDKPEDR	0.907964632	2	4.56479
P80254	STEPCAHLLISSIGVVGTAEQNR	0.748923631	2	5.31799
P80299	**HYES Epoxide hydrolase 2**	**0.93033258**	**0.3171**	**2**
P80299	GHIEDCGHWTQIEKPAEVNQILIK	0.952642508	3	4.83779
P80299	TEIQNPSVTSK	0.902561429	2	2.91395
P80313	**TCPH T_complex protein 1 subunit eta**	**1.042610095**	**0.9569**	**6**
P80313	ATISNDGATILK	1.03032521	2	2.5459
P80313	EGTDSSQGIPQLVSNISACQVIAEAVR	0.863101018	3	3.72948
P80313	GGAEQFMEETER	1.074001874	2	2.90607
P80313	LLDVVHPAAK	1.064368091	2	2.32272
P80313	QLCDNAGFDATNILNK	1.051442272	2	3.91719
P80313	SQDAEVGDGTTSVTLLAAEFLK	1.073601241	2	5.25033
P80317	**TCPZ T_complex protein 1 subunit zeta**	**1.140176935**	**0.1022**	**8**
P80317	ALQFLEQVK	1.096823497	2	2.73788
P80317	DGNVLLHEMQIQHPTASLIAK	1.029263371	3	4.1148
P80317	GIDPFSLDALAK	1.175634175	2	2.43048
P80317	HKSETDTSLIR	1.202095956	2	2.30049
P80317	NAIDDGCVVPGAGAVEVALAEALIK	0.936155027	3	5.68314
P80317	TEVNSGFFYK	1.293531319	2	2.48864
P80317	VATAQDDITGDGTTSNVLIIGELLK	1.027483853	2	4.92921
P80317	VLAQNSGFDLQETLVK	1.073786018	2	3.8775

P81155	**VDAC2 Voltage_dependent anion_selective channel protein 2**	**1.016108922**	**0.9936**	**4**
P81155	LTFDTTFSPNTGK	0.980501631	2	3.17595
P81155	TGDFQLHTNVNNGTEFGGSIYQK	1.084098852	3	3.54564
P81155	VNNSSLIGVGYTQTLRPGVK	1.135051275	2	3.62247
P81155	YQLDPTASISAK	0.98648521	1	3.00689
P82995	**HS90A Heat shock protein HSP 90_alpha**	**0.920022215**	**1E-07**	**13**
P82995	ELHINLIPNKQDR	0.983169514	2	3.03204
P82995	ELISNSSDALDK	0.942062179	2	2.83532
P82995	HIYFITGETK	1.085358034	2	2.40486
P82995	HLEINPDHSIIETLR	1.09629726	2	4.0038
P82995	HSQFIGYPITLFVEK	2.471680792	2	2.90459
P82995	LGIHEDSQNR	0.226788794	3	3.47087
P82995	NPDDITNEEYGEFYK	1.308219299	2	4.72333
P82995	RAPFDLFENR	1.05039437	2	2.92167
P82995	SLTNDWEEHLAVK	1.17587261	2	4.10598
P82995	TLTIVDTGIGMTK	1.007382287	2	3.86571
P82995	TLTIVDTGIGMTK+Oxidation(10)	0.994355936	2	3.91848
P82995	VFIMDNCEELIPEYLNFIR	1.642697141	3	3.48798
P82995	YYTSASGDEMVSLK	1.293496017	2	3.29257
P83868	**TEBP Prostaglandin E synthase 3**	**1.249717817**	**0.0031**	**2**
P83868	HLNEIDLFHCIDPNDSK	1.643729355	3	3.52715
P83868	LTFSCLGGSDNFK	1.192574906	2	2.5286
P83883	**RL36A 60S ribosomal protein L36a**	**1.033139535**	**0.8303**	**2**
P83883	HFELGGDK	1.022663681	1	2.02057
P83883	LECVEPNCR	1.117296589	2	2.52882
P84082	**ARF2 ADP_ribosylation factor 2**	**0.936764872**	**0.9805**	**2**
P84082	NISFTVWDVGGQDK	1.094404017	2	3.98987
P84082	QDLPNAMNAAEITDK	0.935533747	2	4.20974
P84083	**ARF5 ADP_ribosylation factor 5**	**1.066964726**	**0.2432**	**3**
P84083	DAVLLVFANK	1.281797819	2	3.05868
P84083	QDMPNAMPVSELTDK+Oxidation(2)	0.799338683	2	2.7171
P84083	VQESADELQK	1.038719261	2	2.59998
P84100	**RL19 60S ribosomal protein L19**	**1.03576273**	**0.6703**	**2**
P84100	LLADQAEAR	1.079786721	2	3.33508
P84100	VWLDPNETNEIANANSR	1.012796971	2	5.16201
P84245	**H33 Histone H3.3**	**0.786730454**	**0.0258**	**4**
P84245	DIQLAR	0.705139101	1	1.97694
P84245	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	0.900563415	3	6.78579
P84245	RVTIMPKDIQLAR+Oxidation(4)	0.869618817	1	1.91577
P84245	STELLIR	0.970708316	2	2.45772
P84817	**FIS1 Mitochondrial fission 1 protein**	**1.046295659**	**0.0619**	**4**
P84817	FQSEQAAGSVSK	1.011549827	2	2.54949
P84817	GIVLLEELLPK	1.032996967	2	2.65863
P84817	GLLQTEPQNNQAK	1.106423438	2	3.53933
P84817	KFQSEQAAGSVSK	1.448666167	2	3.49916
P85834	**EFTU Elongation factor Tu_ mitochondrial**	**0.978464256**	**0.9093**	**14**
P85834	AEAGDNLGALVR	1.040148807	2	3.41324
P85834	DKPHVNVGTIGHVDHGK	0.85800585	2	3.49496
P85834	DLEKPFLLPVESVYSIPGR	1.037244084	2	4.12934
P85834	GDECELLGHNK	1.022008633	2	2.57568
P85834	GEETPVIVGSALCALEQR	1.012335511	2	4.28836
P85834	GITINAAHVEYSTAAR	0.907964632	2	4.01904
P85834	GTVVTGTLER	1.015092534	2	2.64555
P85834	HYAHTDCPGHADYVK	0.978453702	2	4.1168
P85834	KGDECELLGHNK	0.959600405	3	3.86336
P85834	KYEEIDNAPEER	0.902780118	2	3.66724
P85834	LLDAVDTYIPVPTR	0.90361558	2	3.22709

P85834	TIGTGLVTDVPAMTEEDK	0.979378868	2	3.40355
P85834	TIGTGLVTDVPAMTEEDKNIK	0.866719392	2	4.00458
P85834	YEEIDNAPEER	0.980320455	2	3.33106
P85968	**6PGD 6_phosphogluconate dehydrogenase_ decarboxylating**	**1.052913769**	**0.0003**	**8**
P85968	AGQAVDDFIEK	1.08456102	2	3.10356
P85968	CLSSLKEER	1.076941739	2	2.42336
P85968	FQDTDGKELLPK	0.886042175	2	3.03017
P85968	GILFVGSGVSGGEEGAR	1.025802397	2	4.72588
P85968	LVPLLDTGDIIIDGGNSEYR	1.030450951	2	5.26126
P85968	NPELQNLLLDDFFK	1.27911826	2	4.66022
P85968	SAVDDCQDSWR	1.104509168	2	2.50686
P85968	VGTGEPCCDWVGDEGAGHFVK	1.076377689	3	4.65039
P85971	**6PGL 6_phosphogluconolactonase**	**0.993560289**	**0.0015**	**5**
P85971	DLPAATAPAGPASFAR	0.958491161	2	2.54599
P85971	ILEDQESALPAAMVQPR	1.14566123	2	4.2331
P85971	LPIPDSQVLTIDPALPVEDAADEYAR	0.938202266	2	4.75659
P85971	TGALCWFLDEAAAR	1.222604037	2	3.85347
P85971	WTLGFCDER	1.188201566	2	2.49302
P85972	**VINC Vinculin**	**0.946348658**	**0.0416**	**6**
P85972	ALASQLQDSLK	0.883457974	2	2.32211
P85972	AQQVSQGLDVLTAK	1.01765016	2	4.20348
P85972	AVAGNISDPGLQK	0.900016668	2	3.26817
P85972	KIDAAQNWLADPNGGPEGEEQIR	0.819120958	3	5.29389
P85972	QVATALQNLQTK	1.000042195	2	3.1181
P85972	WIDNPTVDDR	0.945512768	2	2.72919
P85973	**PNPH Purine nucleoside phosphorylase**	**0.973043226**	**0.0002**	**10**
P85973	ASHQEVLEAGK	1.080125163	2	3.80538
P85973	DHINLPGFCGQNPLR	0.822765339	2	3.52973
P85973	ELQEGTYIMSAGPTFETVAESCLLR	0.986657556	2	5.17002
P85973	HRPQVAVICGSGLGGLTAK	0.954616247	3	5.79437
P85973	LTQPQAFDYNEIPNFPQSTVQGHAGR	1.255232439	3	4.30745
P85973	MLGADAVGMSTVPEVIVAR	0.888419318	2	4.22285
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(0)	0.934609585	2	5.2815
P85973	MLGADAVGMSTVPEVIVAR+Oxidation(8)	0.934609585	2	3.41608
P85973	VFGFSLITNK	1.004646616	2	2.47214
P85973	VFHLLGVDTLVVTNAAGGLNPK	0.963818506	2	4.92463
P86048	**RL10L 60S ribosomal protein L10_like**	**1.08524451**	**0.9852**	**2**
P86048	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1.004989307	3	6.14916
P86048	VDEFPLCGHMVSDEYEQLSSEALEAAR	1.117428667	3	4.87255
P97313	**PRKDC DNA_dependent protein kinase catalytic subunit**	**0.95274043**	**0.5347**	**2**
P97313	FHGVMKTLCLEVVLCR+Oxidation(4)	0.833766032	2	2.30776
P97313	LCHDAFTENMVGESQLLEK	1.443804424	2	2.55094
P97384	**ANX11 Annexin A11**	**0.932463066**	**0.0734**	**2**
P97384	GFGTDEQAIIDCLGSR	0.922944019	2	3.61506
P97384	SELDLLDIR	1.063022765	2	2.99695
P97519	**HMGCL Hydroxymethylglutaryl_CoA lyase_ mitochondrial**	**0.975929385**	**2E-06**	**7**
P97519	EVSIFGAASELFTR	1.025071753	2	2.97662
P97519	GFEEAVAAGAK	0.989037688	2	3.45354
P97519	GYVSCALGCPYEGK	0.958571077	2	4.11287
P97519	KNVNCSIEESFQR	0.949942668	2	3.45766
P97519	LLEAGDFICQALNR	1.189966354	2	4.46894
P97519	NVNCSIEESFQR	0.975378884	2	3.62254
P97519	WVPQMADHSDVLK	1.025749853	2	2.31539
P97521	**MCAT Mitochondrial carnitine/acylcarnitine carrier protein**	**0.912337663**	**0.2803**	**4**
P97521	CLLQIQASSGK	0.848080136	2	3.04065
P97521	LQTQPPSLPGQPPMYSGTIDCFR	0.923326401	2	3.70087
P97521	SVHDLSVPR	0.872003086	2	2.35477

P97521	YSGTLDCAK	1.017935939	2	2.45393
P97524	**S27A2 Very long_chain acyl_CoA synthetase**	**0.996457568**	**0.9626**	**11**
P97524	GEVGLLICK	1.02834812	2	2.34005
P97524	IQDTIEITGTFK	1.13996301	2	2.81144
P97524	TILHVFLEQAR	0.914688488	2	2.9432
P97524	TSNTNGVDTVLDK	0.962654348	2	2.70655
P97524	TSNTNGVDTVLDKVDGVSADPIPESWR	0.909454768	3	4.73825
P97524	TYVPMTEDIYNAIIDK	0.960652419	2	2.78521
P97524	VLLASPELHEAVEEVLPTLK	0.918415501	3	4.21283
P97524	VTLMEEGFNPSVIK	1.073420244	2	3.9528
P97524	YDVEKDEPVR	0.963036082	2	2.74465
P97524	YLCNTPQKPNDR	1.137400252	2	2.82635
P97524	YNATVIQYIGELLR	1.22736354	2	3.5824
P97532	**THTM 3_mercaptopyruvate sulfurtransferase**	**1.020629661**	**0.0016**	**9**
P97532	AFGHHSVSLLDGGFR	1.020999617	2	3.22254
P97532	ALVSAQWVAEALK	1.191641735	2	3.22225
P97532	AQPEHVISQGR	0.948094226	1	2.67728
P97532	DGIEPGHIPGSVNIPFTEFLTSEGLEK	0.968075121	3	6.65042
P97532	FQGTQPEPR	0.921359011	2	3.33701
P97532	LLDASWYLPK	1.293361208	2	3.35326
P97532	SPSEPAEFCAQLDPSFIK	0.415031506	2	2.84577
P97532	THEDILENLDAR	0.916347141	2	3.67338
P97532	YWLSQNLPISSGK	0.959504634	2	3.39403
P97536	**CAND1 Cullin_associated NEDD8_dissociated protein 1**	**1.074507697**	**0.0462**	**5**
P97536	AADIDQEVK	1.340985455	2	2.44515
P97536	AVAALLTIPEAEK	1.008811037	2	2.98288
P97536	EGPAVVGQFIQDVK	1.013517967	2	2.41236
P97536	ITSEALLVTQQLVK	1.075166289	2	2.63474
P97536	SVILEAFSSPSEEVK	1.023540096	2	2.4738
P97562	**ACOX2 Peroxisomal acyl_coenzyme A oxidase 2**	**1.196769679**	**1E-19**	**17**
P97562	ATFADFCAQGAEICR	1.169496198	2	4.85067
P97562	CSAQTAADFR	1.488244679	2	3.0859
P97562	DFSLLPELHALSTGMK	0.96463293	2	2.34036
P97562	EAFLDLLPLIR	1.077973223	2	2.7272
P97562	FAEVLPDGTYQR	1.51318693	2	2.4534
P97562	HSPSFSVER	1.115991952	2	2.4285
P97562	ILEYQTQQQK	1.144102795	2	3.83991
P97562	KVESIIQSDPVFNLK	1.163721133	2	4.78679
P97562	LDKEPEIQR	1.011025144	2	3.24491
P97562	LGTPQSNYLGMLVTR	1.200044099	2	2.53585
P97562	LTNILDGGLPNTVLR	1.302568091	2	4.59799
P97562	MGLEHIDNGFLQLNHVR	1.174063905	3	4.82818
P97562	MGLEHIDNGFLQLNHVR+Oxidation(0)	0.927849401	3	3.61944
P97562	SGVDQHDAWNQTTVIHLQAAK	1.275492632	3	6.05918
P97562	SLEDHTPLPGITVGDIGPK	1.065652999	3	4.70285
P97562	SLGSDEQIAK	1.115220298	2	3.04997
P97562	VESIIQSDPVFNLK	1.182617186	2	4.59149
P97576	**GRPE1 GrpE protein homolog 1_ mitochondrial**	**0.910625968**	**0.0055**	**2**
P97576	ATQSVPKEEVSNNNPHLK	0.925839653	3	3.40799
P97576	DLLEVADILEK	0.869534712	2	3.05581
P97584	**PTGR1 Prostaglandin reductase 1**	**0.855115416**	**1E-19**	**5**
P97584	ALTDLMNWVSEGK	0.754464882	2	4.1307
P97584	GGETVLVNAAAGAVGSVVGQIAK	0.886722431	2	5.00809
P97584	HFEGFPTDSNFELR	0.779862611	2	3.69526
P97584	TGPCPPGPSPEVIIYQQLR	0.968011548	2	4.30028
P97584	YHEYITEGFEK	0.762963457	2	2.85119
P97608	**OPLA 5_oxoprolinase**	**1.047030099**	**0.0794**	**7**

P97608	AGDFGAAFVER	1.204641837	2	3.00888
P97608	GSILDPSPEAAVVGGNVLTSQR	0.886308831	2	4.88557
P97608	ISVGAEGPSMADTR	1.008310195	2	2.71408
P97608	ISVGAEGPSMADTR+Oxidation(9)	1.22945588	2	2.46619
P97608	LEEQCVDALQVQGFPR	0.917633459	2	3.04927
P97608	LLSEDPANYADAPTEGIR	1.003565528	2	2.83912
P97608	TGDLLEIQQPVDLEALR	0.946468303	2	4.8292
P97612	**FAAH1 Fatty_acid amide hydrolase 1**	**1.180687408**	**0.0342**	**4**
P97612	GHDSTLGLSLNEGMPSESDCVVVQVLK	1.279795375	3	3.5913
P97612	GTNCVTSYLTDCETQLSQAPR	1.119076818	2	4.87985
P97612	NSVGLPVAVQCVALPWQEELCLR	1.284030237	2	4.06335
P97612	SPGGSSGGEGALIGSGGSPLGLGTDIGGSIR	1.324761126	2	4.87486
P97700	**M2OM Mitochondrial 2_oxoglutarate/malate carrier protein**	**0.955879061**	**1E-10**	**3**
P97700	AVVVNAAQLASYSQSK	0.814943786	2	4.31182
P97700	GIYTGLSAGLLR	0.99230568	2	2.62217
P97700	LTGADGTPPGFLLK	0.953158172	2	3.42235
P97840	**LEG9 Galectin_9**	**1.1894621**	**2E-07**	**3**
P97840	FEEGGYVVCNTK	1.113211434	2	3.23733
P97840	NTQINNSWGPEER	1.700491653	2	2.72305
P97840	SINISGVVLPDAK	1.515848251	2	3.43342
P97852	**DHB4 Peroxisomal multifunctional enzyme type 2**	**0.923609173**	**1E-12**	**18**
P97852	AVANYDSVEAGEK	0.926887516	2	3.92973
P97852	AYALAFAER	1.056542371	2	3.26389
P97852	DTTSLNQAALYR	0.808087037	2	3.22986
P97852	FVYEGSADFSCLPTFGVIVAQK	0.974187011	2	2.94755
P97852	GALVVVNDLGGDFK	1.176421261	2	4.20091
P97852	GSSAADKVVEEIR	0.761231132	2	2.39747
P97852	HVLQQFADNDVSR	0.868014246	2	4.40733
P97852	ICDFSNASKPK	0.866593287	2	3.2545
P97852	IDSEGISQNHTGQVASADASGFAGVVGHK	0.89239	3	5.58683
P97852	IDVVVNNAGILR	0.876700197	2	3.94408
P97852	ISDEDWDIIQR	0.829110203	2	4.12311
P97852	KNNIHCNTIAPNAGSR	1.018088276	2	4.65894
P97852	NGSGEVYQGPAK	1.002609271	2	3.57651
P97852	NNIHCNTIAPNAGSR	0.858489552	2	4.35841
P97852	SIQESTGGIIEVLHK	0.927317644	2	4.30546
P97852	SLMSGGLAEVPGLSINFAK	0.838054018	2	3.5113
P97852	VLHGEQYLELYKPLPR	0.842780776	2	3.99406
P97852	VVLVTGAGGGLGR	0.973128515	2	3.59703
Q00438	**PTBP1 Polypyrimidine tract_binding protein 1**	**1.014971899**	**0.5022**	**3**
Q00438	KLPSDVTEGEVISLGLPFGK	1.01923788	2	4.22799
Q00438	LSLDGQNIYNACCTLR	1.197950108	2	3.75361
Q00438	NNQFQALLQYADPVSAQHAK	1.064984065	2	5.37589
Q00PI9	**HNRL2 Heterogeneous nuclear ribonucleoprotein U_like protein 2**	**0.96013045**	**6E-07**	**2**
Q00PI9	AVEEQGDDQDSEK	0.543516804	2	3.89722
Q00PI9	EEAQPIVTKYK	1.949530295	1	1.98446
Q01177	**PLMN Plasminogen**	**0.956967793**	**0.8892**	**3**
Q01177	CTTPPPPPGPTYQCLK	0.952610829	2	2.53773
Q01177	ILGSDVQQIAVTK	1.000008373	2	3.47818
Q01177	LVLEPNDADIALLK	1.128203338	2	2.8149
Q01205	**ODO2 Dihydrolipoyllysine_residue succinyltransferase component of 2_oxoglutarate dehydrogenase complex_ mitochondrial**	**1.056582781**	**1E-06**	**4**
Q01205	ASAFALQEQPVVNAVIDDATK	0.905183718	2	6.29209
Q01205	NDVITVQTPAFAESVTEGDVR	1.088770942	2	5.23766
Q01205	NVETMNYADIER	0.990962325	2	3.53902

Q01205	VEGGTPLFTLR	0.997368655	2	3.12645
Q01279	**EGFR Epidermal growth factor receptor**	**1.143380092**	**0.3663**	**2**
Q01279	NLQEILIGAVR	1.143487019	2	3.52345
Q01279	NYVVTDHGSCVR	0.751863873	2	2.72102
Q01405	**SC23A Protein transport protein Sec23A**	**1.079968003**	**1E-19**	**4**
Q01405	AETEEGPDVLR	0.300500164	2	3.10498
Q01405	AVLNPLCQVDYR	1.078677247	2	2.91763
Q01405	HLLQAPVDDAQEILHSR	1.266596629	3	5.48907
Q01405	YIDTEHGGSQAR	2.084678536	2	3.12801
Q02253	**MMSA Methylmalonate_semialdehyde dehydrogenase [acylating]_ mitochondrial**	**0.898872192**	**1E-19**	**29**
Q02253	AEMEAAVAACK	0.976690145	2	3.75611
Q02253	AEMEAAVAACK+Oxidation(2)	0.891848382	2	2.36936
Q02253	AEMEAAVAACKR	0.973152402	2	2.44191
Q02253	AFPAWADTSILSR	1.066567905	2	4.04344
Q02253	AISFVGSNQAGEYIFER	1.018992113	2	5.21023
Q02253	CMALSTAVLVGEAK	1.145587756	2	4.28448
Q02253	CMALSTAVLVGEAK+Oxidation(1)	0.959407963	2	3.39011
Q02253	EEDATLSSPAVVMPTMGR	0.876491604	2	4.36403
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(12)	0.871120595	2	2.65885
Q02253	EEDATLSSPAVVMPTMGR+Oxidation(15)	0.871120595	2	2.99436
Q02253	EGASILLDGR	0.749419992	2	2.5253
Q02253	ENTLNQLVGAAFGAAGQR	0.849525733	2	5.26509
Q02253	GLQVVEHACSVTSLMLGETMPSITK	0.9280922	2	3.12899
Q02253	IVNDNPYGNGTAIFTTNGAIAR	1.00255563	2	5.46838
Q02253	LFIDGK	0.892730088	1	1.98009
Q02253	LITLEQGK	0.969783809	2	2.54244
Q02253	LLQDSGAPDGTLNIIHGQHEAVNFICDHPDIK	1.410770075	3	4.53488
Q02253	NHGVVMPDANK	0.827757078	1	3.37557
Q02253	NHGVVMPDANK+Oxidation(5)	1.212923817	2	3.13333
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR	0.852367986	3	5.583
Q02253	NHGVVMPDANKENTLNQLVGAAFGAAGQR+Oxidation(5)	0.793011429	3	4.53694
Q02253	QGIQFYTQLK	1.277265748	2	2.63347
Q02253	SDKWIDIHNPATNEVVGR	0.932562047	2	5.00344
Q02253	TITSQWKEEDATLSSPAVVMPTMGR	0.887295241	2	5.22912
Q02253	TLADAEGDVFR	0.928037044	2	3.55727
Q02253	VCNLIDSGAK	0.985183612	2	3.41987
Q02253	VNAGDQPGADLGPLITPQAK	0.924111707	2	5.87265
Q02253	WIDIHNPATNEVVGR	0.967300202	2	4.80653
Q02253	WLPELVER	0.794984633	1	2.04743
Q02769	**FDFT Squalene synthase**	**0.853563943**	**0.0348**	**3**
Q02769	KLEDFVKPENVDVAVK	1.068268651	2	4.00819
Q02769	TQSLPNCQLISR	0.276870803	2	2.3738
Q02769	VVLEDFPTISLEFR	0.709335385	2	3.19125
Q02874	**H2AY Core histone macro_H2A.1**	**0.964538552**	**0.9903**	**2**
Q02874	AASADSTTEGAPTDGFTVLSTK	0.975798437	2	3.90074
Q02874	GVTIASGGVLPNIHPELLAK	0.931133341	2	3.7257
Q02974	**KHK Ketohexokinase**	**0.96865887**	**0.9867**	**7**
Q02974	CGLQGFDGIV	0.966374537	1	1.9318
Q02974	GATLICAWAEEGADALGPDGQLLHSDAFPPPR	1.004791982	3	5.78986
Q02974	GGNASNSCTVLSLLGAR	1.062275328	2	4.76952
Q02974	GNSMQEALR	0.915486613	2	2.79644
Q02974	GVDVSQVAWQSQGDTPCSCCIVNNSNGSR	0.917404741	3	5.77613
Q02974	IEQYNATQPLQQK	0.99242866	2	4.82333
Q02974	TIILYDTNLPDVSAK	0.923280155	2	4.1603
Q03070	**CHIO Beta_chimaerin**	**0.956514355**	**0.5651**	**2**
Q03248	**BUP1 Beta_ureidopropionase**	**0.980218397**	**1E-19**	**12**

Q03248	AHHDLGYFYGSSYVAAPDGSR	1.061071328	2	6.31155
Q03248	EDLVLAPSSG	0.874597389	1	2.16939
Q03248	EKLPWTEFAESAEDGLTTR	0.905880211	3	5.42065
Q03248	ELAEAVKPNYSPNIVK	0.76410967	2	3.99963
Q03248	ELAEAVKPNYSPNIVKEDLVLAPSSG	0.934393411	3	3.45047
Q03248	HNMVVISPILER+Oxidation(2)	1.078877901	3	3.32312
Q03248	IPLPTSAPVAEQVSALHK	1.379918213	3	4.73686
Q03248	KHNMVVISPILER+Oxidation(3)	0.915623113	2	2.8544
Q03248	NAAIANHCFTCALNR	1.07490362	2	4.61519
Q03248	VGDFNESTYYMEGNLGHPVFQTQFGR	1.375828185	3	4.76682
Q03248	VGQEHYPNEFTSGDGK	1.233013758	2	4.20286
Q03248	VGQEHYPNEFTSGDGKK	1.006607733	3	4.39057
Q03336	**RGN Regucalcin**	**1.013994577**	**2E-09**	**16**
Q03336	CGESPVWEEASK	0.975605054	2	4.63456
Q03336	CLLFVDIPSK	1.093186138	2	3.58707
Q03336	DEQIPDGMCIDVEGK	1.161530222	2	3.84422
Q03336	DYSEMYVTCAR	0.834955403	2	3.53396
Q03336	FNDGKVDPAGR	1.068232978	2	3.09441
Q03336	HQGSLYSLFPDHSVK	1.368426658	2	4.67337
Q03336	KYFDQVDISNGLDWSLDHK	1.028307072	3	5.10245
Q03336	LWVACYNGGR	1.122633228	2	2.36953
Q03336	MEKDEQIPDGMCIDVEGK	1.05633456	2	4.94173
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(0)	1.076663663	2	4.42183
Q03336	MEKDEQIPDGMCIDVEGK+Oxidation(10)	1.082887858	2	2.58264
Q03336	QSGGYVATIGTK	1.075317358	2	2.83251
Q03336	VGVDAPVSSVALR	1.07285946	2	3.73256
Q03336	YFAGTMAEETAPAVLER	1.076036577	2	5.61584
Q03336	YFAGTMAEETAPAVLER+Oxidation(5)	1.025788598	2	5.25827
Q03336	YFDQVDISNGLDWSLDHK	1.048890453	3	4.20341
Q03626	**MUG1 Murinoglobulin_1**	**0.993760112**	**0.0269**	**7**
Q03626	EESSCIHSSCTAER	1.120974402	2	4.0157
Q03626	FQVDNSNR	0.792477022	1	2.28701
Q03626	GGEFEMMPLGVNK	0.785235888	2	2.40922
Q03626	LTAQPAPSPEDLALSMGTIK	1.001203433	2	3.48027
Q03626	NLHPLNELFPLAYIEDPK	1.395367234	3	4.3533
Q03626	VQTVPLTCNNPK	0.920686707	2	3.02871
Q03626	VYHKEESSCIHSSCTAER	1.136609647	3	4.32211
Q04462	**SYVC Valyl_tRNA synthetase**	**0.874822728**	**0.0869**	**2**
Q04462	ALNPLEEWLR	0.995668716	2	2.6182
Q04462	SVTQQPGSEITAPQK	0.897100724	2	3.72762
Q05144	**RAC2 Ras_related C3 botulinum toxin substrate 2**	**0.999431585**	**0.511**	**2**
Q05144	MQAIKCVVVGDGAVGK+Oxidation(0)	0.897843193	2	2.59498
Q05144	YLECSALTQR	1.043042915	2	2.62865
Q06647	**ATPO ATP synthase subunit O_ mitochondrial**	**1.010577487**	**0.4365**	**5**
Q06647	FSPLTANLMNLLAENGR	1.197638616	3	3.96317
Q06647	GEVPCTVTTAFPLDEAVLSELK	1.012646862	3	5.99183
Q06647	GQILNLEVK	1.097140616	2	2.61595
Q06647	LGNTQGVISAFSTIMSVHR	1.120849048	3	3.54184
Q06647	TDPSIMGGMIVR	1.006858433	2	2.30175
Q07071	**GCKR Glucokinase regulatory protein**	**1.354868586**	**7E-12**	**8**
Q07071	AAPISCHVQVAHEK	1.212832427	2	4.98641
Q07071	LLGQCDAEIFQEEGQIVPTYQR	2.429135584	2	2.985
Q07071	QEAFVLNPAIGPEGLSGSSR	1.199349889	2	4.1022
Q07071	STQALEDPPACGTLN	1.175722996	2	2.64691
Q07071	TVDQGVVSSQR	1.172438148	2	3.20456
Q07071	VIPTALLSLLLR	1.600860519	2	2.58984
Q07071	VQEVLKEPDGGLVVLSGGGTSGR	0.961748065	2	5.32051

Q07071	YQHVIETPEPGEWELSGYEAAVPITEK	1.285571304	3	5.38837
Q07116	**SUOX Sulfite oxidase_ mitochondrial**	**0.9010566**	**0.2147**	**6**
Q07116	AVDDSYNVQPDTVAPIWNLR	0.91327096	2	4.81601
Q07116	FVDLHPGGQSK	0.79461232	2	2.82156
Q07116	IGELNPEDR	0.966804346	2	2.32568
Q07116	LHVVGAPGGQSLSLSLDDLHK	1.098599729	3	3.88607
Q07116	NHLPVPNLDPDTYR	0.900291057	2	2.47862
Q07116	VSVESEESYSHWQR	0.913460458	2	3.83073
Q07523	**HAOX2 Hydroxyacid oxidase 2**	**0.961715985**	**0.0116**	**11**
Q07523	ALKEEKPTQSVPVSFPK	0.877712875	2	4.13306
Q07523	ALVITIDTPVLGNR	0.98785661	2	4.48049
Q07523	ASFCWNDLSLLQSITR	1.081352167	2	4.3169
Q07523	EEKPTQSVPVSFPK	1.02495873	2	3.17334
Q07523	EVLDILTAELHR	0.913484332	2	3.35861
Q07523	GEDGVKEVLDILTAELHR	0.81160679	3	5.20111
Q07523	HNVQGIVVSNHGGR	0.947944264	3	5.9516
Q07523	NQLNLEANILLK	0.985368891	2	3.47047
Q07523	QLDEVSASIDALR	0.98335361	2	3.48437
Q07523	TSWDFIEGEADDGITYSENIAAFK	1.008189236	3	3.5434
Q07523	TTIQGQEISAPICISPTAFHSIAWPDGEK	1.059617074	3	3.98979
Q07936	**ANXA2 Annexin A2**	**0.757397374**	**0.001**	**2**
Q07936	GLGTDEDSLIEIICSR	0.947006906	2	2.93208
Q07936	GVDEVTIVNILTNR	0.741857254	2	3.44998
Q07984	**SSRD Translocon_associated protein subunit delta**	**1.004647868**	**0.8495**	**2**
Q07984	FFDEESYSLLR	1.173061128	2	3.22459
Q07984	NNEDVSIIPPLFTVSVDHR	1.015636999	3	3.84233
Q08163	**CAP1 Adenylyl cyclase_associated protein 1**	**1.094540151**	**0.2241**	**5**
Q08163	ALLVTASQCQQPAGNK	0.699610958	2	4.61304
Q08163	LEAVSHTSDMHCGYGDSPSK	0.963926287	3	4.2197
Q08163	SALFAQINQGESITHALK	1.039651407	2	4.03799
Q08163	SSEMNVLIPTEGGDFNEFPVPEQFK	1.043274262	2	3.93078
Q08163	VENQENVSNLVIDDTELK	0.960118649	2	4.95315
Q08415	**KAT1 Kynurenine__oxoglutarate transaminase 1_ mitochondrial**	**1.005318328**	**0.2128**	**3**
Q08415	EQQHFGQPSSYFLQLPQAMELNR	0.993454021	3	4.52657
Q08415	ILVLNTPNNPLGK	1.212052757	2	2.83256
Q08415	LGASNDWQLDPAELASK	0.493848017	2	3.29377
Q09073	**ADT2 ADP/ATP translocase 2**	**1.424371467**	**0.1316**	**7**
Q09073	AAYFGIYDTAK	1.304455473	2	2.48069
Q09073	DFLAGGVAAAISK	0.948022041	2	4.6752
Q09073	GLGDCLVK	1.089421297	2	2.62315
Q09073	GTDIMYTGTLDCWR	1.217537368	2	3.47945
Q09073	LLLQVQHASK	1.424439263	2	2.47651
Q09073	QIFLGGVDK	0.981661175	2	2.50334
Q09073	QIFLGGVDKR	0.982171161	2	2.57101
Q09199	**B4GN2 Beta_1_4 N_acetylgalactosaminyltransferase 2**	**0.988046401**	**0.7411**	**2**
Q09199	MKYKFQDAYNQK+Oxidation(0)	0.982256142	2	3.00798
Q09199	QQTVPKLYDPGPER	1.052170284	2	2.30905
Q0D2L3	**SPEB Agmatinase_ mitochondrial**	**0.928714026**	**3E-15**	**5**
Q0D2L3	EHGPVGLVHVGAHSNTSDKPLEDK	1.051073963	3	3.74122
Q0D2L3	IREESLMLGTVNPSTGALPFQSLR	1.064056935	3	3.91361
Q0D2L3	SVDEGLLDSK	0.902966384	1	1.90349
Q0D2L3	SVDEGLLDSKR	0.836277574	2	2.74898
Q0D2L3	VADLGNVNVNLYNLQDSCR	1.299377304	2	5.48389
Q0VGK3	**GLCTK Glycerate kinase**	**0.969685312**	**0.1408**	**4**
Q0VGK3	AVLGMAAAADELLGQHLVQGVISVPK	0.809463858	3	5.45504
Q0VGK3	GATIQELNTIR	0.935422366	2	3.50195
Q0VGK3	QLFDSAVGAVQPGPMLQR	0.934491601	2	2.39961

Q0VGK3	VAAACLTSSTAERPLEEEAK	1.162937488	3	3.37933
Q0ZHH6	**ATLA3 Atlastin_3**	**1.046711597**	**0.9999**	**4**
Q0ZHH6	EHGHSNWLGDPEEPLTGFSWR	0.935450266	3	4.16363
Q0ZHH6	EQLQTLIPYVLNPSK	1.046515507	2	2.87554
Q0ZHH6	GGSDPETTGIQIWSEVFTVK	1.055498625	2	4.5745
Q0ZHH6	YQQELEEEITELYENFCK	1.068537428	2	5.47397
Q10758	**K2C8 Keratin_ type II cytoskeletal 8**	**0.788376125**	**1E-19**	**23**
Q10758	AEAETMYQIK	0.922424219	2	3.21711
Q10758	AQYEEIANR	0.836270398	2	3.31733
Q10758	ATLEAAIADAEQR	0.834334788	2	4.67324
Q10758	ELQSQISDTSVVLSMDNSR	0.8774367	2	6.02147
Q10758	GSLGGFGGAGVGGITAVTVNQSLLNPLK	1.020971555	2	4.4565
Q10758	LEGLTDEINFLR	0.844656614	2	4.17265
Q10758	LESGMQNMSIHTK	0.749872888	2	3.79113
Q10758	LEVDPNIQAVR	0.880578672	2	3.75479
Q10758	LEVELGNMQGLVEDFK	0.821895727	2	4.83817
Q10758	LKLEVELGNMQGLVEDFK	1.010763328	3	3.92451
Q10758	LQAEIDALK	0.884985734	2	2.71283
Q10758	LVSESSDIMSK	0.916063374	2	3.27688
Q10758	QIHEEEIR	0.820222081	1	2.26044
Q10758	RQLEALGQEK	0.742143381	2	2.34214
Q10758	SKTEISEMNR	0.763401685	3	3.43588
Q10758	SKTEISEMNR+Oxidation(7)	0.834742988	3	3.31696
Q10758	SLDMDSIIAEVR	0.832418174	2	4.38511
Q10758	SNMDNMFESYINNLR	0.967060165	2	3.931
Q10758	SRAEAETMYQIK	0.829718135	2	3.41921
Q10758	TEMENEFVLIK	0.834625896	2	3.70411
Q10758	TEMENEFVLIK+Oxidation(2)	0.795697556	2	2.60711
Q10758	WSLLQQQK	0.811828567	2	2.62178
Q10758	YEELQTLAGK	0.848174048	2	3.53382
Q14DH7	**ACSS3 Acyl_CoA synthetase short_chain family member 3_ mitochondrial**	**0.827866715**	**7E-12**	**4**
Q14DH7	STLSALVNGKPYK	0.806522041	2	2.8071
Q14DH7	THFAASVADPER	0.809319713	2	3.36301
Q14DH7	VDDVINVAGHR	0.685753402	2	3.01359
Q14DH7	VTPTIEDPSIFGHIEEVLK	0.913425863	2	3.44813
Q1HCL7	**NAKD1 NAD kinase domain_containing protein 1**	**0.838691355**	**9E-06**	**10**
Q1HCL7	ALNEVFIGESLSSR	0.736839648	2	2.59747
Q1HCL7	ASYYEISVDDGPWEK	0.937247347	2	3.46948
Q1HCL7	LKPVIGVNTDPER	0.853615833	2	2.84285
Q1HCL7	LYLEGTGINPSPVDLHEQQLSLNQHSR	1.013003361	3	3.94495
Q1HCL7	NVEHIIDSLRDEGIEVR	0.88192993	2	2.6372
Q1HCL7	QGNLTLPLNK	0.790292368	2	2.57634
Q1HCL7	SEASGPQLLPVR	0.929777522	2	3.09542
Q1HCL7	SEGHLCLPVR	0.790140607	2	2.40608
Q1HCL7	SSGLNLCTGTGSK	0.837030431	2	3.35412
Q1HCL7	VTNEYNESLLYSPEEPK	0.965236992	2	4.72075
Q1JU68	**EIF3A Eukaryotic translation initiation factor 3 subunit A**	**1.007620247**	**0.9707**	**5**
Q1JU68	EEEEQRRAEEQMLK	0.970455988	2	2.59425
Q1JU68	EQPEKEPELQQYVPQLQNNTILR	0.94164232	3	3.70921
Q1JU68	FNVLQYVVPEVK	1.040933795	2	3.46859
Q1JU68	ILQEHEQIK	1.20577431	2	2.48497
Q1JU68	MPAYFQRPENALK	1.080188695	2	2.50114
Q29RW1	**MYH4 Myosin_4**	**0.919986078**	**0.9882**	**5**
Q29RW1	LQDAEEHVEAVNSK	0.894175735	2	4.55867
Q29RW1	NAYEESLDQLETLK	0.902091657	2	4.67246
Q29RW1	NAYEESLDQLETLKR	1.185221371	2	3.78842

Q29RW1	TLEDQLSEVK	1.188796218	1	1.93845
Q29RW1	VKNLTEEMAGLDENIVKLTK+Oxidation(7)	0.935509179	2	2.48752
Q2V057	**PROD2 Probable proline dehydrogenase 2**	**1.083170528**	**0.3016**	**5**
Q2V057	EDCTQPDYEATSR	0.920814867	2	3.19085
Q2V057	GCVQQLQAIGLQPLLAVPTEEEPDSAAK	1.124456299	3	3.58326
Q2V057	NLQLSCLSTEQNQHLQASLSR	1.116423231	2	5.54773
Q2V057	REQALLSQELWR	1.095176552	2	3.06729
Q2V057	SIPYGCLEEVIPYLIR	1.445542744	2	2.36529
Q3B7D0	**HEM6 Coproporphyrinogen_III oxidase_ mitochondrial**	**0.876619821**	**0.4813**	**3**
Q3B7D0	AGVNISVVHGNLSEEAANQMR	0.864155903	3	3.80679
Q3B7D0	HCDDSYTPQDK	1.298626071	2	2.98564
Q3B7D0	LEEDGDELAR	0.975615146	2	2.45005
Q3B7U9	**FKBP8 Peptidyl_prolyl cis_trans isomerase FKBP8**	**0.937265195**	**0.6331**	**4**
Q3B7U9	SCSQVLEHQPDNIK	0.88142215	2	3.92912
Q3B7U9	TAEDGPDLEMLSGQER	0.948821694	2	3.19839
Q3B7U9	VDMTCEEEEELLQLK	1.015346898	2	3.34904
Q3B7U9	VLAQQGEYSEAIPILR	0.88966895	2	3.62744
Q3KRD8	**IF6 Eukaryotic translation initiation factor 6**	**0.998334051**	**0.3789**	**2**
Q3KRD8	HGLLVPNNTTDQELQHIR	1.01102417	3	4.52834
Q3KRD8	TSIEDQDELSSLLQVPLVAGTVNR	1.038653606	3	4.26425
Q3KRE0	**ATAD3 ATPase family AAA domain_containing protein 3**	**1.074123104**	**0.4303**	**2**
Q3KRE0	GEGTGPPLPLPPAQPGAESGGDR	1.101406894	2	3.39096
Q3KRE0	QEESVQKQEAIRR	1.068696413	2	2.44646
Q3KRE8	**TBB2B Tubulin beta_2B chain**	**1.199411259**	**0.1283**	**2**
Q3KRE8	ALTVPELTQQMFDSK	1.120791178	2	3.12692
Q3KRE8	ESESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.196768782	3	4.44284
Q3MIE0	**ECHD3 Enoyl_CoA hydratase domain_containing protein 3_ mitochondrial**	**0.938912404**	**0.0022**	**5**
Q3MIE0	DGQEGIEAFIQK	0.982135705	2	3.31548
Q3MIE0	SDILHEAESEDLK	0.920747296	2	3.21786
Q3MIE0	SSFATPGVNVGLFCSTPAVALGR	1.005048723	2	4.29326
Q3MIE0	VIIISAEGPVFSSGHDLK	0.910465522	2	4.24602
Q3MIE0	VVPEEQLEEEATR	0.874478553	2	3.8628
Q3MIF4	**XYLB Xylulose kinase**	**1.023707025**	**0.9936**	**6**
Q3MIF4	DLPEFGTQGGVHVHK	0.961517394	2	2.58044
Q3MIF4	FNADNMEVSAFPGDVEIR	0.98542102	2	3.54328
Q3MIF4	IRDESASCSWNK	0.983238582	2	4.03811
Q3MIF4	VVAFTGDNPASLAGMR	1.097985199	2	3.41045
Q3MIF4	VWSQACLDACAPHLK	1.068709254	2	3.48241
Q3MIF4	YSPIDYSDGSGMNLLQIQEK	1.070367434	2	5.23297
Q3T1J1	**IF5A1 Eukaryotic translation initiation factor 5A_1**	**0.998099211**	**0.5119**	**4**
Q3T1J1	EDLRLPEGDLGK	1.017614904	2	2.93007
Q3T1J1	EDLRLPEGDLGKEIEQK	0.988288422	2	3.86186
Q3T1J1	NDFQLIGIQDGYLSLLQDSGEVR	1.17492055	3	5.47226
Q3T1J1	RNDFQLIGIQDGYLSLLQDSGEVR	1.143024598	3	3.90233
Q3T1K5	**CAZA2 F_actin_capping protein subunit alpha_2**	**1.049548176**	**0.8787**	**2**
Q3T1K5	FIIHAPPGEFNEVFNDVR	1.04486089	3	3.79289
Q3T1K5	FTVTPSTTQVVGILK	1.047047416	2	3.44804
Q3U2P1	**SC24A Protein transport protein Sec24A**	**1.04881475**	**0.5215**	**2**
Q3U2P1	SVTASLSDAR	1.096858651	2	2.60314
Q3U2P1	TLETQSALGPALQAAFK	0.985356742	2	3.10147
Q3UHR0	**BAHC1 BAH and coiled_coil domain_containing protein 1**	**1.008912254**	**0.9331**	**2**
Q3UHR0	MQILQRKDTWAPK+Oxidation(0)	0.946282238	2	2.32107
Q3UHR0	NLEEPGLLSR	1.011025144	2	2.32372
Q3ULJ0	**GPD1L Glycerol_3_phosphate dehydrogenase 1_like protein**	**1.004782375**	**0.4228**	**2**
Q3ULJ0	GIDEGPDGLK	1.015671932	2	2.67981
Q3ULJ0	LGLMEMIAFAK	1.207694636	2	3.30973

Q3UQ44	**IQGA2 Ras GTPase_activating_like protein IQGAP2**	**1.107071733**	**1E-06**	**13**
Q3UQ44	ALVGSENPPLTVIR	1.111598073	2	3.41862
Q3UQ44	AWVNQLETQTGEASK	1.073158863	2	5.00814
Q3UQ44	GVLLGIDDLQTNQFK	1.130366939	2	4.80286
Q3UQ44	HTDNTVQWLR	0.949597088	2	2.32222
Q3UQ44	LFEGENEHLSSMNNYLSETYQEFR	1.462060612	3	4.13605
Q3UQ44	LGIAPQIQDLLGK	1.429122758	2	2.56322
Q3UQ44	LPYDVTTEQALTYPEVK	1.132358771	2	4.8749
Q3UQ44	LSAEEMDER	1.231111235	2	2.67249
Q3UQ44	NPNAVLTCVDDSLSQEYQK	1.043038994	2	4.9455
Q3UQ44	TALEEEIK	0.915861465	1	1.90905
Q3UQ44	TLDTLLLPTANIR	1.033491129	2	2.73328
Q3UQ44	VDQVQDIVTGNPTVIK	1.152350257	2	5.28731
Q3UQ44	YQDILNEIAK	1.13893033	2	2.58773
Q3UU35	**OVOS Ovostatin homolog**	**0.37143081**	**0.0672**	**2**
Q3UU35	EQQAKSLLSILDK	0.319933087	2	2.37259
Q3UU35	FSGPNNTPLVDK	1.05100737	2	2.36487
Q3V0K9	**PLSI Plastin_1**	**0.935924825**	**2E-11**	**3**
Q3V0K9	AYFHLLNQIAPK	0.935955887	2	2.66322
Q3V0K9	KIENCNYAVELGK	0.724565035	2	3.58923
Q3V0K9	QFVTPADVVSGNPK	0.846991638	2	3.49965
Q3V132	**ADT4 ADP/ATP translocase 4**	**1.178499671**	**0.0743**	**2**
Q3V132	GNLANVIR	1.040358866	2	2.64625
Q3V132	YFPTQALNFAFK	1.683240053	2	2.50243
Q497B0	**NIT2 Omega_amidase NIT2**	**1.224180406**	**7E-05**	**14**
Q497B0	ADLYSVESK	1.075087422	2	3.00803
Q497B0	AGTEETILYSDIDLK	1.071159011	2	3.69965
Q497B0	ASYVAWGHSTVVDPWGQVLTK	1.100920044	2	4.76271
Q497B0	AVDNQVYVATASPAR	0.952912809	2	4.74165
Q497B0	AVDNQVYVATASPARDEK	0.766703217	2	3.29263
Q497B0	ENSIYLIGGSIPEEDDGK	0.912481095	2	2.58646
Q497B0	ENSIYLIGGSIPEEDDGKLYNTCAVFGPDGNLLVK	0.924618151	3	4.02408
Q497B0	FAELAQIYAR	1.283067928	2	3.68881
Q497B0	IHLFDIDVPGK	1.124091598	2	2.80904
Q497B0	KIHLFDIDVPGK	1.014427369	3	4.67906
Q497B0	LALIQLQVSSIK	1.225702487	2	3.06025
Q497B0	LYNTCAVFGPDGNLLVK	1.1444818	2	4.11781
Q497B0	QGANIVSLPECFNSPYGTNYFPEYAEK	0.955013782	2	4.25036
Q497B0	TLSPGDSFSTFDTPYCR	1.13220831	2	4.69905
Q499N5	**ACSF2 Acyl_CoA synthetase family member 2_ mitochondrial**	**1.094928813**	**0.2356**	**7**
Q499N5	GATLSHHNIVNNSNLIGQR	0.971752552	2	4.68265
Q499N5	GGENIYPAELEDFFHK	1.049942147	2	2.7422
Q499N5	GGVIAGSLAPPELIR	0.959062537	2	2.78532
Q499N5	SGETTTEEEIK	1.093616728	2	3.2943
Q499N5	TGDIASMDEQGFCR	1.126611217	2	3.37253
Q499N5	TVGECLDATAQR	1.087409067	2	2.63107
Q499N5	YIVFVEGYPLTVSGK	1.156879511	2	4.14755
Q4AEF8	**COPG Coatomer subunit gamma**	**1.214185006**	**5E-09**	**4**
Q4AEF8	FGAQNEEMLPSILVLLK	1.271075881	2	4.00944
Q4AEF8	QEIFQEQLAAVPEFQGLGPLFK	1.145132736	2	3.80168
Q4AEF8	SSPEPVALTESETEYVIR	1.280266246	2	3.88168
Q4AEF8	TLEEAVGNIVK	1.098144862	2	2.43452
Q4FZT0	**STML2 Stomatin_like protein 2**	**1.217275677**	**0.0052**	**7**
Q4FZT0	AEQINQAAGEASAVLAK	1.000274848	2	5.2182
Q4FZT0	ASYGVEDPEYAVTQLAQTTMR	0.935489017	2	4.07367
Q4FZT0	ATVLESEGTR	0.623757898	2	2.57217
Q4FZT0	DVQTTDTSIEELGR	2.395689612	2	2.91735

Q4FZT0	ESLNANIVDAINQAADCWGIR	0.758529398	2	3.01485
Q4FZT0	ILEPGLNVLIPVLDR	0.885595531	2	2.651
Q4FZT0	NTVILFVPQQEAWVVER	0.950955036	2	3.3097
Q4FZT9	**PSMD2 26S proteasome non_ATPase regulatory subunit 2**	**1.056782563**	**0.8933**	**5**
Q4FZT9	DKTPVQSQQPSATAPSGADEK	0.87083778	3	4.87964
Q4FZT9	FGGSGSQVDSAR	1.058004415	2	3.54568
Q4FZT9	SGALLACGIVNSGVR	0.98691535	2	3.5387
Q4FZT9	TPVQSQQPSATAPSGADEK	1.029230423	2	4.18017
Q4FZT9	VGQAVDVVGQAGKPK	1.287528133	2	2.71734
Q4FZX7	**SRPRB Signal recognition particle receptor subunit beta**	**1.275343602**	**1E-19**	**4**
Q4FZX7	GDAGSADVQDLEK	1.246572105	2	3.07603
Q4FZX7	GNSLTLIDLPGHESLR	1.051606225	2	3.20831
Q4FZX7	SAAPSTLDSSSTAPAQLGK	1.573055755	2	4.37316
Q4FZX7	VGDGAGGAFQPYLDSLR	1.243692156	2	3.32009
Q4G061	**EIF3B Eukaryotic translation initiation factor 3 subunit B**	**1.050217649**	**0.7667**	**3**
Q4G061	AEEEGGSDGSAAEAEPR	0.86283299	2	4.59944
Q4G061	AKPAAQSEEETAASPAASPTPQSAQEPSAPGK	0.272688663	3	5.27545
Q4G061	GTQGVVTNFEIFR	1.035228469	2	3.06553
Q4KLP0	**DHTK1 Probable 2_oxoglutarate dehydrogenase E1 component DHKTD1_ mitochondrial**	**1.14777944**	**1E-19**	**9**
Q4KLP0	KSIPDTYAEHLIASGLMTQEEVSDIK	1.222621131	3	4.8656
Q4KLP0	LEELCPFPLDSLQQEMGK	1.193999591	2	4.99239
Q4KLP0	LLLESQEFDHFLATK	1.15164996	2	3.3713
Q4KLP0	LVTVYCEHGHK	1.502614508	2	2.36755
Q4KLP0	SIPDTYAEHLIASGLMTQEEVSDIK	1.185687987	3	5.0542
Q4KLP0	SSLYSSDIGK	1.228679396	1	2.06288
Q4KLP0	SVEVPEELQLHSHLLK	1.253689745	2	3.52528
Q4KLP0	YGGEGAESMMGFFHELLK	1.284595026	3	4.72278
Q4KLP0	YPVAVSTLEEMAPGTAFKPVIGDSSVDPK	1.087193381	3	4.71288
Q4KLZ6		**0.920235565**	**1E-07**	**12**
Q4KLZ6	AAPTEPAEAPEATAAGGVASK	1.036052778	2	5.05164
Q4KLZ6	AILEVLQTK	1.169984663	2	3.14129
Q4KLZ6	ANTDLPAWSAAMDAGLK	1.150201525	2	3.14783
Q4KLZ6	ASYISSAQLDQPDPGAVAAAAIFR	0.927510466	2	5.35219
Q4KLZ6	AVAQAGTAGTLLIVK	1.244636674	2	3.99246
Q4KLZ6	EGPTPASPAQVLSK	1.113740164	1	3.08632
Q4KLZ6	ISTTLIGLEEHLNALDR	2.148427085	2	3.04408
Q4KLZ6	LIDAETNAK	1.134049251	2	2.53858
Q4KLZ6	LNFGLAMEQAK	0.84677681	2	2.75687
Q4KLZ6	LSVLLLEK	1.68263089	2	2.38109
Q4KLZ6	MVNSVEGCAGDALAGFVACNPDLQLLQGYR	1.103345066	3	5.41391
Q4KLZ6	VAGALAEEGMGLEEITK	1.407012668	2	4.00246
Q4KM49	**SYYC Tyrosyl_tRNA synthetase_ cytoplasmic**	**1.196811728**	**2E-08**	**6**
Q4KM49	AFCEPGNVENNGVLSFVK	1.242683368	2	3.16033
Q4KM49	IDVGEAEPR	1.061867508	2	2.33178
Q4KM49	QVEHPLLSGLLYPGLQALDEEYLK	0.848536633	3	3.43755
Q4KM49	QVEPLDPPAGSAPGER	0.994426506	2	2.73163
Q4KM49	TVVSGLVQFVPK	1.114933201	2	2.93474
Q4KM49	VDAQFGGIDQR	1.299485398	2	3.16366
Q4KM73	**KCY UMP_CMP kinase**	**1.028268635**	**0.9467**	**6**
Q4KM73	EMDQTMAANAQK+Oxidation(1)	0.693866931	2	2.5465
Q4KM73	IQTYLESTKPIIDLYEEMGK	1.084648966	2	4.26574
Q4KM73	KNPDSQYGELIEK	1.052169237	2	4.05924
Q4KM73	NQDNLQGWNK	1.069898053	2	3.00312
Q4KM73	SVDEVFGDVMK	1.051693597	1	2.38003
Q4KM73	YGYTHLSAGELLR	1.076653624	3	4.36374
Q4KM74	**SC22B Vesicle_trafficking protein SEC22b**	**1.186797266**	**0.0009**	**3**

Q4KM74	DLQQYQSQAK	1.184683078	2	3.04468
Q4KM74	GEALSALDSK	1.224701416	2	2.94312
Q4KM74	NLGSINTELQDVQR	1.167089932	2	4.12268
Q4KMA2	**RD23B UV excision repair protein RAD23 homolog B**	**1.074739993**	**0.2573**	**2**
Q4KMA2	IDIDPEETVK	1.10200396	1	2.55256
Q4KMA2	QIIQQNPSLLPALLQQIGR	1.094672675	2	4.85145
Q4LDD4	**ARAP1 Arf_GAP with Rho_GAP domain_ ANK repeat and PH domain_containing protein 1**	**1.062510056**	**0.6786**	**2**
Q4LDD4	LLDSLRQDAR	1.03529965	2	2.35372
Q4LDD4	LSSASVLGVRGSEQPDR	1.120863464	2	2.46986
Q4QQV3	**F162A Protein FAM162A**	**0.966279046**	**0.646**	**2**
Q4QQV3	EEEIPETISFEMLDAAK	0.870243374	2	3.69103
Q4QQV3	RHESLTSLNLER	0.970849258	3	3.91306
Q4QQW3	**HOT Hydroxyacid_oxoacid transhydrogenase_ mitochondrial**	**0.960636005**	**0.8644**	**3**
Q4QQW3	HLETAEILGANIR	0.974863447	2	2.34029
Q4QQW3	NLSQLPPVQIVMDSLSK	0.941552421	2	2.71356
Q4QQW3	VEPTDGSFMDAIEFAK	0.960426147	2	3.16251
Q4QRB4	**TBB3 Tubulin beta_3 chain**	**1.072230043**	**0.0003**	**4**
Q4QRB4	AILVDLEPGTMDSVR	1.014351381	2	3.54907
Q4QRB4	AILVDLEPGTMDSVR+Oxidation(10)	0.912866535	2	3.75968
Q4QRB4	EIVHIQAGQCGNQIGAK	0.93027656	2	5.06257
Q4QRB4	ISEQFTAMFR	1.265675172	2	3.34963
Q4V7C7	**ARP3 Actin_related protein 3**	**0.964178002**	**0.1918**	**4**
Q4V7C7	KDYEEIGPSICR	0.940650701	2	3.17963
Q4V7C7	LGYAGNTEPQFIIPSCIAIK	1.280205976	2	2.61928
Q4V7C7	LSEELSGGR	0.914011999	2	2.44701
Q4V7C7	YSYVCPDLVK	1.24507065	2	2.42144
Q4V8K1	**STEA4 Metalloreductase STEAP4**	**0.980785981**	**0.6542**	**3**
Q4V8K1	MNQYPESNAEYLAQLVPGAHVVK+Oxidation(0)	1.201501186	3	3.37502
Q4V8K1	SDVIVLAVHR	1.145911225	2	2.301
Q4V8K1	TCADEFPLTVDSSEK	0.980026327	2	4.5081
Q505J8	**SYFA Phenylalanyl_tRNA synthetase alpha chain**	**0.987836882**	**0.9883**	**2**
Q505J8	LQQVQAGQAEK	1.147838111	2	2.70053
Q505J8	SLQALGEVIEAELR	0.983152859	2	3.16297
Q561R9	**LACB2 Beta_lactamase_like protein 2**	**0.783341793**	**0.0005**	**3**
Q561R9	ANIIYPGHGPVIHNAEAK	0.787888626	2	4.07384
Q561R9	ILIDTGEPSVPEYISCLK	0.783446586	2	3.59189
Q561R9	NISNDATYCIK	0.779677178	2	2.50869
Q561S0	**NDUAA NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10_ mitochondrial**	**1.243018015**	**0.0004**	**3**
Q561S0	VITVDGNICSGK	1.251746091	2	3.29776
Q561S0	VVEDIEYLNYNK	1.217129779	2	3.91076
Q561S0	YGLLASILGDK	1.207648035	2	3.63839
Q562C4	**MET7B Methyltransferase_like protein 7B**	**0.750175182**	**0.6509**	**4**
Q562C4	AQFSEVQLEWQPPPFK	0.726902761	2	4.92883
Q562C4	HIGDGCHLTR	0.747256328	3	3.3981
Q562C4	VLQEVQR	0.58423486	1	1.9042
Q562C4	VTCVDPNPNFEK	0.910088164	2	3.53056
Q562C9	**MTND 1_2_dihydroxy_3_keto_5_methylthiopentene dioxygenase**	**1.063238018**	**0.9484**	**2**
Q562C9	LDADKYENDPELEQIR	1.070676972	2	3.77164
Q562C9	LDADKYENDPELEQIRK	0.965684436	3	3.79158
Q58FK9	**KAT3 Kynurenine__oxoglutarate transaminase 3**	**1.434763925**	**0.0018**	**8**
Q58FK9	AIILNTPHNPIGK	1.290122819	2	3.31121
Q58FK9	ALSCLYGK	1.331789832	1	2.00117
Q58FK9	DSTLDAAEEIFR	1.08676158	2	3.07597
Q58FK9	IEGLDQNVWVEFTK	1.097538739	2	4.02499

Q58FK9	LAADPSVVNLGQGFPDITLPSYVQEELSK	1.435743738	3	5.25334
Q58FK9	MDDPECYFNSLPK	1.255096647	2	3.72679
Q58FK9	RIEGLDQNVWVEFTK	1.2686234	2	4.38706
Q58FK9	WTSSDWTFNPQELESK	1.297725409	2	5.09691
Q5BJQ0	**ADCK3 Chaperone activity of bc1 complex_like_ mitochondrial**	**1.128575289**	**0.2348**	**3**
Q5BJQ0	AVLDSSPFLSEANAER	1.127313393	2	4.84283
Q5BJQ0	MGGSFLICSKLK+Oxidation(0)	1.202750383	2	2.32613
Q5BJQ0	TLNNDLGPHWR	1.125676698	2	2.41275
Q5BJY9	**K1C18 Keratin_ type I cytoskeletal 18**	**0.842262471**	**1E-19**	**21**
Q5BJY9	AQIFANSVDNAR	0.81883124	2	3.21205
Q5BJY9	AQYEQLAQK	0.83593251	2	3.08697
Q5BJY9	DAETTLLELR	0.641876768	2	3.57211
Q5BJY9	KVVDDTNITR	0.820582521	2	3.02396
Q5BJY9	LEAEIATYR	0.841546931	2	2.95828
Q5BJY9	LLEDGDDFSLNDALDSSNSMQTVQR	0.693555753	2	3.58432
Q5BJY9	LQLETEIEALK	0.894766006	2	2.33407
Q5BJY9	LQLETEIEALKEELLFMK	1.01722619	2	4.95938
Q5BJY9	NHEEEVQGLEAQIASSGLTVEVDAPK	0.884649544	2	5.93171
Q5BJY9	NQNINLENNLGEVEAR	0.876154243	2	5.396
Q5BJY9	NREELDKYWSQQIEESTTVVTTK	0.898337351	3	4.904
Q5BJY9	QSVESDIHGLR	0.820360286	2	2.75445
Q5BJY9	QTQEYEALLNIK	0.870464323	2	3.81838
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK	0.793550786	2	6.06866
Q5BJY9	SVWGGSVGSAGLAGMGGVQTEK+Oxidation(14)	1.000533904	2	4.62451
Q5BJY9	TLQTLEIDLDSMK	0.804358555	2	4.18777
Q5BJY9	VKLEAEIATYR	0.866482464	2	2.89355
Q5BJY9	VQMEQLNGVLLHLESELAQTR	0.872700926	2	5.02855
Q5BJY9	VRPASSAASVYAGAGGSGSR	0.689155016	2	4.95988
Q5BJY9	VVDDTNITR	0.871090111	2	3.51254
Q5BJY9	YWSQQIEESTTVVTTK	0.945011648	2	4.2408
Q5BK63	**NDUA9 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9_ mitochondrial**	**1.071436545**	**0.0754**	**3**
Q5BK63	IHISDVMATDLPGLEDLGVQPTPLELK	1.339574625	3	4.82217
Q5BK63	NFDFEDVFVNIPR	1.026644114	2	4.03915
Q5BK63	WLSSEIEETKPAK	1.050723421	2	2.54913
Q5BK81	**PTGR2 Prostaglandin reductase 2**	**0.944209528**	**0.9704**	**2**
Q5BK81	VEEVSLPDTINEGQVR	0.938271815	2	4.29747
Q5EB77	**RAB18 Ras_related protein Rab_18**	**1.109391747**	**0.2617**	**2**
Q5EB77	LDNWLNELETYCTR	0.884522034	2	3.12767
Q5EB77	NDIVNMLVGNK	1.103331853	2	3.27066
Q5FVM6	**MTMRC Myotubularin_related protein 12**	**0.955372893**	**0.0056**	**3**
Q5FVM6	IVSGIIHHTQSPK	0.759564416	2	2.57723
Q5FVM6	LLEMMEEVQSLQEK+Oxidation(3)	2.192190791	2	2.73012
Q5FVM6	LLEMMEEVQSLQEK+Oxidation(4)	2.192190791	2	2.67655
Q5FVN1	**STBD1 Starch_binding domain_containing protein 1**	**0.93990284**	**0.5317**	**3**
Q5FVN1	DGGAEPLKDAPPGEAAAPGGGPGGGGSGGLSPEPSDR	0.981241189	3	5.40767
Q5FVN1	DLGNLTEAQR	0.90747938	2	2.49159
Q5FVN1	NSLVGGGWEVDGK	1.520464015	2	2.39608
Q5FVQ4	**MLEC Malectin**	**0.986278256**	**1**	**2**
Q5FVQ4	KEEEEEEEEYDEGSNLKR	0.994261796	3	5.36425
Q5FVQ4	STPEDQILYQTER	0.982256142	2	2.93495
Q5FVR2	**TYPH Thymidine phosphorylase**	**0.95163655**	**0.998**	**2**
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(10)	0.957205727	2	2.66791
Q5FVR2	AQDTQIGAMLMAIR+Oxidation(8)	0.951995299	2	2.40685
Q5FVR5	**ACNT2 Acyl_coenzyme A amino acid N_acyltransferase 2**	**1.916962691**	**0.0084**	**3**
Q5FVR5	DEKENLFQSK	1.544979803	2	2.50989
Q5FVR5	ILFIVGENDQCLASK	1.195561972	2	3.51952

Q5FVR5	IQQPGIGVISVSK	2.100087169	2	2.7653
Q5FW57	**GLYAL Glycine N_acyltransferase_like protein**	**0.915938465**	**0.9194**	**2**
Q5FW57	AIDQEMFK	0.906868712	2	2.45172
Q5FW57	SSQMLQMLESSLR	1.029802074	2	3.60312
Q5HZV9	**PP1R7 Protein phosphatase 1 regulatory subunit 7**	**1.05513877**	**0.9337**	**2**
Q5HZV9	AIENIDTLTNLESLFLGK	0.934740891	2	2.58709
Q5HZV9	ELDLYDNQIKK	1.198523525	2	2.51766
Q5HZY0	**UBXN4 UBX domain_containing protein 4**	**0.963691841**	**0.9366**	**2**
Q5HZY0	LPDGSSFTNQFPSDAPLEEAR	1.002941219	2	4.45228
Q5HZY0	NTELCETPTTSDPK	0.963611946	2	3.90686
Q5I0C3	**MCCA Methylcrotonoyl_CoA carboxylase subunit alpha_ mitochondrial**	**0.991684356**	**0.0006**	**4**
Q5I0C3	HAPLVEFEEEV	0.993578014	2	2.60123
Q5I0C3	IIEEAPAPGIDPEVR	0.890360063	2	3.8031
Q5I0C3	SEKEFQEQLESAR	0.836331398	2	3.13714
Q5I0C3	YLSPVSAEGTQGGTIAPMTGTIEK	0.937017173	2	5.25078
Q5I0D1	**GLOD4 Glyoxalase domain_containing protein 4**	**0.840688929**	**0.0137**	**2**
Q5I0D1	ESQSILTPLVSLDTPGK	0.838324653	2	3.62535
Q5I0D1	HEEFEEGCK	0.997485478	2	2.58027
Q5I0E7	**TMED9 Transmembrane emp24 domain_containing protein 9**	**0.911984207**	**0.4893**	**2**
Q5I0E7	QLVEQVEQIQK	0.958068263	2	3.77522
Q5I0E7	QREEYQPATPGLGMFVEVKDPEDK	0.815319889	3	3.45501
Q5I0H9	**PDIA5 Protein disulfide_isomerase A5**	**1.098602602**	**0.0013**	**7**
Q5I0H9	DKNQDLCQQESVK	0.908025244	2	4.36469
Q5I0H9	DVVHIDSEKDFR	0.932562951	2	2.4113
Q5I0H9	GPPLWEEDPGAK	1.023451877	2	2.99178
Q5I0H9	GQGTICWVDCGDAESR	1.034694807	2	3.93327
Q5I0H9	NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK	1.222705335	3	3.49596
Q5I0H9	NQDLCQQESVK	1.227719864	2	3.27369
Q5I0H9	TELGFTSFIR	1.213638478	2	2.81583
Q5I0J9	**ASPD Putative L_aspartate dehydrogenase**	**1.014159131**	**0.6462**	**6**
Q5I0J9	HANLLVGSPSALADQTTER	1.060348744	2	5.25548
Q5I0J9	LDAAGGLQSLR	1.07119935	2	3.73436
Q5I0J9	LEGPLAAAHSSGPR	0.904594473	2	3.40162
Q5I0J9	MAGSVPPALQLEDLTTLEER	1.12382685	2	3.6543
Q5I0J9	NSNTMAAAALAAPSLGFDR	0.903031745	2	4.0275
Q5I0J9	NSNTMAAAALAAPSLGFDR+Oxidation(4)	0.927433074	2	2.83042
Q5I0M2	**NADC Nicotinate_nucleotide pyrophosphorylase [carboxylating]**	**1.041628878**	**0.9982**	**3**
Q5I0M2	DNHVVAAGSMEK	0.953041392	2	2.52527
Q5I0M2	EALQAAEAGADLVMLDNFKPEELHPTAATLK	1.033688154	3	4.90322
Q5I0M2	LYAEGDIPVPHAR	1.043676229	2	3.49706
Q5I0P2	**GCSH Glycine cleavage system H protein_ mitochondrial**	**0.984719325**	**0.2136**	**2**
Q5I0P2	MTLSDPSELDELMSEEAYEK	0.734812261	2	4.96954
Q5I0P2	SCYEDGWLIK	1.039926043	2	2.60166
Q5M7U6	**ARP2 Actin_related protein 2**	**0.931521712**	**0.246**	**3**
Q5M7U6	GYAFNHSADFETVR	0.94871576	2	3.55326
Q5M7U6	HLWDYTFGPEK	0.951982587	2	3.08675
Q5M7U6	KVVVCDNGTGFVK	0.744399221	2	2.48113
Q5M7W5	**MAP4 Microtubule_associated protein 4**	**0.811147288**	**4E-11**	**7**
Q5M7W5	AAVGLTGNDIATPPNK	0.820725538	2	3.34035
Q5M7W5	ATSPSTLVSTGSSSR	0.806479485	2	3.85022
Q5M7W5	NTAPPTEEETVPGK	0.913196485	2	2.46544
Q5M7W5	NTTPTGATPPAGMASTR	0.755035179	2	2.77565
Q5M7W5	STLPVDEGSPLEK	0.935264403	2	2.50582
Q5M7W5	VGSLDNVGHLPAGGTVK	0.803108668	2	3.65
Q5M7W5	VTEFNNVTPLSEEVASIK	0.892018099	2	3.57993
Q5M875	**DHB13 17_beta_hydroxysteroid dehydrogenase 13**	**1.493772872**	**8E-08**	**6**

Q5M875	ALTAELDTLGK	1.248349139	1	2.00957
Q5M875	IQNIQFEAIVGHR	1.396088245	3	3.42727
Q5M875	LWPVLEPDEVAR	1.215610281	2	2.75059
Q5M875	NSGHIVTVASVCGHR	0.986490352	2	2.89139
Q5M875	SVAGQTVLITGAGHGIGR	1.254384376	2	4.07124
Q5M875	TSCLCPVFVNTGFTK	2.036236307	2	3.54883
Q5M9G3	**CAPR1 Caprin_1**	**1.073839705**	**0.982**	**2**
Q5M9G3	LNQDQLDAVSK	1.021310128	2	3.38426
Q5M9G3	YQEVTNNLEFAK	0.956774329	2	2.47077
Q5PPL3	**NSDHL Sterol_4_alpha_carboxylate 3_dehydrogenase_ decarboxylating**	**0.814497685**	**1E-19**	**8**
Q5PPL3	AVLDANDPKK	0.599883519	2	2.31806
Q5PPL3	CTVIGGSGFLGQHMVEQLLSR	0.704174065	2	4.76149
Q5PPL3	GQVTGTDLINEVSK	0.599492653	2	3.78243
Q5PPL3	GVSTVFHCASPPSNSNNK	0.520008871	2	3.94223
Q5PPL3	GYAVNVFDVR	0.704429165	2	3.43059
Q5PPL3	ILTGLNYEAPK	0.547821068	2	2.7866
Q5PPL3	KGQVTGTDLINEVSK	0.589854673	2	4.61658
Q5PPL3	VQFFIGDLCNQQDLYPALK	0.635376816	2	5.28494
Q5PQT3	**GLYAT Glycine N_acyltransferase**	**0.931868459**	**2E-13**	**4**
Q5PQT3	AIQNLASIHSLQVK	1.008746416	2	3.01343
Q5PQT3	DPENCQEFLGSSEVINWK	0.839737455	2	4.73794
Q5PQT3	LSSLDVTHAALVNK	1.532084902	2	3.05235
Q5PQT3	QHLQIQSSQSHLNK	0.687514667	2	3.55053
Q5RJR2	**TWF1 Twinfilin_1**	**1.065009193**	**0.0831**	**2**
Q5RJR2	HQTLQGVAFPISR	1.0684154	2	2.34311
Q5RJR2	YLLSQSSPAPLTAAEEELR	1.189632199	2	3.58955
Q5RJR8	**LRC59 Leucine_rich repeat_containing protein 59**	**1.027587084**	**0.4603**	**5**
Q5RJR8	ATVLDLSCNK	0.960906589	2	2.69356
Q5RJR8	DKLDGNELDLSLSDLNEVPVK	0.951094916	2	5.99664
Q5RJR8	LDGNELDLSLSDLNEVPVK	1.111081244	2	3.12499
Q5RJR8	LQQLPADFGR	1.206720463	2	2.63103
Q5RJR8	LSTLPSDFCGLTHLVK	1.396400478	2	2.3977
Q5RKI0	**WDR1 WD repeat_containing protein 1**	**1.0240516**	**0.9738**	**3**
Q5RKI0	AHDGGIYAISWSPDSTHLLSASGDK	1.10235427	3	4.83996
Q5RKI0	CFSIDNPGYEPEVVAVHPGGDTVAVGGSDGNVR	1.018654109	3	4.40759
Q5RKI0	YAPSGFYIASGDISGK	1.019849662	2	4.4148
Q5RKI1	**IF4A2 Eukaryotic initiation factor 4A_II**	**1.096348901**	**0.2597**	**4**
Q5RKI1	ELAQQIQK	0.965822325	1	2.1123
Q5RKI1	GIDVQQVSLVINYDLPTNR	1.145835122	2	4.48256
Q5RKI1	GYDVIAQAQSGTGK	1.075128228	2	5.12246
Q5RKI1	MFVLDEADEMLSR	0.985212326	2	3.71357
Q5SGE0	**LPPRC Leucine_rich PPR motif_containing protein_ mitochondrial**	**0.914826084**	**0.0315**	**11**
Q5SGE0	AALDLEQVPSELAVTR	0.887030477	2	3.78792
Q5SGE0	CIANNQVETLEK	0.867715402	2	2.86599
Q5SGE0	GLDAIELSR	0.973514772	2	2.4475
Q5SGE0	HCVTMDTPAEK	0.51880452	2	3.0397
Q5SGE0	HDNAEDALNLK	0.920735698	2	3.427
Q5SGE0	MEGANIQPNR	0.897662024	2	2.65386
Q5SGE0	SCGSLLPELSLAER	0.953182206	2	2.49183
Q5SGE0	SGSPGSNQALLLLR	0.977982769	2	2.80307
Q5SGE0	SSLSSSSPSAGDTVTEK	0.835473048	2	4.04511
Q5SGE0	SYVADKDVASAK	0.811582425	2	2.45732
Q5SGE0	TLLELIPELR	0.824651269	2	2.73224
Q5SNZ0	**GRDN Girdin**	**1.100829067**	**0.7568**	**2**
Q5SNZ0	KVEILENEIIQEK	1.102473227	2	2.5229

Q5SNZ0	LEMENQSLTKTVEELR	1.074445285	2	2.36422
Q5SX40	**MYH1 Myosin_1**	**1.050054903**	**1**	**69**
Q5SX40	AAYLQNLNSADLLK	0.318384202	2	4.36819
Q5SX40	ADIAESQVNK	1.247741413	2	3.50964
Q5SX40	AEDEEEINAELTAK	1.409909077	2	4.01398
Q5SX40	AGLLGLLEEMR	1.269013539	2	3.42772
Q5SX40	AGLLGLLEEMRDDK	1.006442228	2	3.17781
Q5SX40	ALQEAHQQTLDDLQAEEDKVNTLTK	1.289789216	3	6.30463
Q5SX40	ANLLQAEIEELR	0.830800322	2	3.87706
Q5SX40	ANSEVAQWR	1.105668696	2	3.15769
Q5SX40	DLEEATLQHEATAATLR	1.453113816	2	4.85521
Q5SX40	DTQLHLDDALR	1.329081956	2	3.19818
Q5SX40	EEQAEPDGTEVADK	1.348568094	2	3.29626
Q5SX40	ELEEISER	1.299778758	1	2.06178
Q5SX40	ELEGEVENEQK	1.587620367	2	2.54884
Q5SX40	ELEGEVENEQKR	1.297865073	2	3.28148
Q5SX40	ELTYQTEEDRK	1.49228984	2	3.07815
Q5SX40	ENQSILITGESGAGK	1.379650843	2	4.18193
Q5SX40	EQYEEEQEAK	1.222441045	1	3.34458
Q5SX40	GQEDLKEQLAMVER	1.249831507	2	4.11823
Q5SX40	GSSFQTVSALFR	1.808983439	2	3.08222
Q5SX40	HADSVAELGEQIDNLQR	1.333190042	2	5.58638
Q5SX40	IAEQELLDASER	1.628116377	2	3.24455
Q5SX40	IEDEQALGMQLQK	1.390928887	2	4.09116
Q5SX40	IEELEEEIEAER	1.149533863	2	3.77815
Q5SX40	IKLEQQVDDLEGSLEQEK	1.218605495	2	5.02405
Q5SX40	IQHELEEAEER	1.465968865	2	3.57284
Q5SX40	IQLELNQVK	1.188765147	2	2.88145
Q5SX40	KALQEAHQQTLDDLQAEEDKVNTLTK	1.21574441	3	6.36394
Q5SX40	KIAEQELLDASER	1.139019404	2	3.76416
Q5SX40	KIQHELEEAEER	1.27576202	3	4.04226
Q5SX40	KKLETDISQIQGEMEDIVQEAR	1.074533072	3	4.50565
Q5SX40	KLEDECSELK	1.102240257	2	2.7194
Q5SX40	KLEDECSELKK	1.070767541	3	4.91678
Q5SX40	KLETDISQIQGEMEDIVQEAR	0.958764844	2	5.62567
Q5SX40	LAQESTMDVENDKQQLDEK	1.443804424	2	4.90519
Q5SX40	LDEAEQLALK	1.264316219	2	3.59203
Q5SX40	LEEAGGATSAQIEMNK	1.084257212	2	3.56629
Q5SX40	LEQQVDDLEGSLEQEK	1.516157015	2	5.02346
Q5SX40	LEQQVDDLEGSLEQEKK	1.166117404	2	3.91195
Q5SX40	LETDISQIQGEMEDIVQEAR	1.108787455	2	5.3709
Q5SX40	LINELTAQR	1.437878377	2	3.1303
Q5SX40	LQDAEEHVEAVNAK	1.349550015	2	4.68479
Q5SX40	LQDLVDK	1.333529857	1	2.01056
Q5SX40	LQNEVEDLMIDVER	1.22753884	2	3.96971
Q5SX40	LQTESGEYSR	1.33330701	2	2.35999
Q5SX40	MEIDDLASNMEVISK	1.201424301	2	4.62605
Q5SX40	MEIDDLASNMEVISKSKGNLEK	1.430280173	2	2.31264
Q5SX40	MQGTLEDQIISANPLLEAFGNAK	1.186474441	3	6.0546
Q5SX40	MQGTLEDQIISANPLLEAFGNAK+Oxidation(0)	1.082792353	3	4.77429
Q5SX40	NDLQLQVQSEADSLADAEER	1.277640953	2	6.22834
Q5SX40	NKDPLNETVVGLYQK	1.386901789	2	4.19736
Q5SX40	NLQQEISDLTEQIAEGGK	1.157534931	2	5.72428
Q5SX40	NLQQEISDLTEQIAEGGKR	1.015774012	2	4.70023
Q5SX40	NLTEEMAGLDETIAK	1.413434976	2	4.40276
Q5SX40	QAEEAEEQSNVNLAK	1.191968498	2	4.41463
Q5SX40	QKYEETHAELEASQK	1.366719884	2	4.12408

Q5SX40	QLDEKDSLVSQLSR	1.022174623	2	3.12892
Q5SX40	QREEQAEPDGTEVADK	1.297940249	2	3.99264
Q5SX40	SELQAALEEAEASLEHEEGK	1.202775018	2	5.3967
Q5SX40	SSVFVVDAK	1.170462533	2	2.6903
Q5SX40	TKYETDAIQR	1.166585252	3	3.58655
Q5SX40	TLEDQVSELK	1.209188247	2	2.86684
Q5SX40	TNAACAALDK	1.479645951	2	2.90554
Q5SX40	TNAACAALDKK	1.026030777	2	2.96631
Q5SX40	VLNASAIPEGQFIDSK	1.356341164	2	3.6488
Q5SX40	VQLLHTQNTSLINTK	1.373549058	2	4.96899
Q5SX40	VRELEGEVENEQK	0.965043381	2	2.58607
Q5SX40	VRELEGEVENEQKR	1.258075064	3	3.51247
Q5SX40	VVESMQSTLDAEIR	1.063124967	2	3.97063
Q5SX40	YETDAIQR	1.154011251	2	2.30081
Q5U206	**CALL3 Calmodulin_like protein 3**	**1.051858124**	**0.0002**	**3**
Q5U206	DTDSEEEIR	1.065697457	2	2.85672
Q5U206	MKDTDSEEEIR	1.071684877	3	3.90192
Q5U206	MKDTDSEEEIR+Oxidation(0)	1.571908103	2	3.65695
Q5U211	**SNX3 Sorting nexin_3**	**0.855122816**	**0.1089**	**2**
Q5U211	CLHMFLQDEIIDK	0.822521985	2	2.51261
Q5U211	GDDGIFDDNFIEER	1.192708022	2	2.74731
Q5U2Q7	**ERF1 Eukaryotic peptide chain release factor subunit 1**	**1.166544206**	**1E-19**	**3**
Q5U2Q7	GFGGIGGILR	1.105301795	2	2.72618
Q5U2Q7	YFDEISQDTGK	1.061145403	2	3.00252
Q5U2Q7	YVLHCQGTEEEK	1.30119427	2	3.45781
Q5U2Z3	**NP1L4 Nucleosome assembly protein 1_like 4**	**1.026713914**	**0.1825**	**2**
Q5U2Z3	LDNVSHTPSSYIETLPK	1.011247693	3	3.51845
Q5U2Z3	TYKMKSEPDK	1.465439739	1	2.3071
Q5U300	**UBA1 Ubiquitin_like modifier_activating enzyme 1**	**1.11680252**	**0.5694**	**10**
Q5U300	AAVASLLQSVQVPEFTPK	0.925534995	3	3.66384
Q5U300	AENYDISPADR	0.988726167	2	3.15248
Q5U300	DNPGVVTCLDEAR	0.96681277	2	3.13419
Q5U300	IYDDDFFQNLDGVANALDNVDAR	0.986440253	3	4.48319
Q5U300	LDQPMTEIVSR	1.263722775	2	2.74506
Q5U300	NEEDATELVTLAQAVNAR	1.100374134	2	4.58514
Q5U300	NFPNAIEHTLQWAR	1.140012993	2	2.32908
Q5U300	SLPASLAEPDFVMTDFAK	0.936990312	2	3.86816
Q5U300	SPPAVQQDNVDEDLIR	0.991937218	2	4.67607
Q5U300	VVQGHQQLDSYK	1.141965012	2	3.24777
Q5U312	**RAI14 Ankycorbin**	**1.133150248**	**0.1515**	**2**
Q5U312	ISQDADLKTPTK	0.654055419	2	2.35152
Q5U312	MHLLYAVQGQMDEDVQKVLK	1.166138467	2	2.52444
Q5U315	**RNA polymerase GLD2**	**0.989151736**	**0.6456**	**3**
Q5U315	KLDSAQQQCTEFLELIQQSLKDK	1.059744551	3	3.89171
Q5U315	QANNINMLKDGMK	1.24431045	1	2.10137
Q5U315	WEMDDPRPIAKAER	0.930828648	2	2.41845
Q5XFW8	**SEC13 Protein SEC13 homolog**	**0.961436131**	**0.9993**	**2**
Q5XFW8	DVAWAPSIGLPTSTIASCSQDGR	0.989409602	2	3.58338
Q5XFW8	NGGQILIADLR	1.023465451	2	2.93064
Q5XFX0	**TAGL2 Transgelin_2**	**0.886722319**	**2E-12**	**3**
Q5XFX0	DDGLFSGDPNWFPK	0.796222679	2	3.69449
Q5XFX0	NFSDNQLQEGK	0.910355941	2	2.93938
Q5XFX0	YGINTTDIFQTVDLWEGK	0.915343303	2	4.764
Q5XHY5	**SYTC Threonyl_tRNA synthetase_ cytoplasmic**	**1.132046462**	**0.0968**	**7**
Q5XHY5	AEHDSILAEK	1.127735128	2	2.75744
Q5XHY5	FLGDIEIWNQAEK	1.04833846	2	3.65248
Q5XHY5	GFQEVVTPNIFNSR	1.539021391	2	3.17693

Q5XHY5	QLENSLNEFGEK	1.148321559	2	3.05734
Q5XHY5	TTPYQIACGISQGLADNTVVAK	1.110643401	2	4.13682
Q5XHY5	VVWDLDRPLETDCTLELLK	1.244403239	2	3.95537
Q5XHY5	WELNPGDGAFYGPK	1.180318469	2	3.82698
Q5XHZ0	**TRAP1 Heat shock protein 75 kDa_ mitochondrial**	**1.037185201**	**1**	**11**
Q5XHZ0	AFLEALQHQAETSSR	0.994782928	2	4.42413
Q5XHZ0	AQLLQPTLEINPR	0.900711569	2	3.76916
Q5XHZ0	EELVSNLGTIAR	0.986266658	2	2.38036
Q5XHZ0	FEDTSPAGER	1.00817785	2	2.82867
Q5XHZ0	GTITIQDTGIGMTK	0.93738331	2	3.35475
Q5XHZ0	GVVDSEDIPLNLSR	1.040937654	2	4.74997
Q5XHZ0	HLAEHSPYYEAMK	1.11775829	2	2.33802
Q5XHZ0	LDTHPAMVTVLEMGAAR	0.977801188	3	3.74412
Q5XHZ0	SDCKDFANESR	1.026048909	2	2.91195
Q5XHZ0	YESSALPAGQLTSLSDYASR	1.076461195	2	4.79422
Q5XHZ0	YIAQAYDKPR	0.96087984	2	2.60285
Q5XI22	**THIC Acetyl_CoA acetyltransferase_ cytosolic**	**0.70315415**	**4E-05**	**5**
Q5XI22	AGHFDKEIVPVHVSSR	0.827498004	2	3.86483
Q5XI22	LKPYFLTDGTGTVTPANASGMNDGAAAVVLMK	0.677782665	3	4.46889
Q5XI22	TAIGSFNGALSTVPVHNLGTTVIK	0.675386832	2	5.00217
Q5XI22	VAPEEVSEVIFGHVLTAGCGQNPTR	0.567129413	3	4.57248
Q5XI22	VNIDGGAIALGHPLGASGCR	0.620566687	2	5.47193
Q5XI32	**CAPZB F_actin_capping protein subunit beta**	**0.879589911**	**0.1134**	**4**
Q5XI32	GCWDSIHVVEVQEK	1.020565394	2	3.06121
Q5XI32	KLEVEANNAFDQYR	0.841436109	2	4.07821
Q5XI32	LEVEANNAFDQYR	0.912854344	2	3.36615
Q5XI32	STLNEIYFGK	0.985608104	2	2.40468
Q5XI60	**REEP6 Receptor expression_enhancing protein 6**	**1.061905952**	**0.5189**	**3**
Q5XI60	ALDIAAGITR	0.921739557	2	3.05507
Q5XI60	HHVALDSAASQLSGR	1.244821703	2	3.62374
Q5XI60	NVATDALGALEAR	0.955238524	2	4.19022
Q5XI73	**GDIR1 Rho GDP_dissociation inhibitor 1**	**1.027713835**	**0.0496**	**3**
Q5XI73	AEEYEFLTPMEEAPK	1.018586517	2	4.38174
Q5XI73	SIQEIQELDKDDESLR	1.233281562	2	4.68881
Q5XI73	VAVSADPNVPNVIVTR	1.083725006	2	4.14052
Q5XI78	**ODO1 2_oxoglutarate dehydrogenase_ mitochondrial**	**1.025933765**	**4E-12**	**11**
Q5XI78	FGLEGCEVLIPALK	0.921953717	2	3.33971
Q5XI78	FLDTAFDLDAFKK	0.67518664	2	2.81303
Q5XI78	GHHVAQLDPLGILDADLDSSVPADIISSTDK	0.838259138	3	4.39293
Q5XI78	ICEEAFTR	0.994218489	2	2.63135
Q5XI78	IEQLSPFPFDLLLK	0.996716183	2	3.81311
Q5XI78	LEAADEGSGDMK	0.965087518	2	3.32373
Q5XI78	LNVLANVIR	0.723244166	2	2.32263
Q5XI78	NITLSLVANPSHLEAADPVVMGK	1.189383522	3	4.67448
Q5XI78	NTNAGAPPGTAYQSPLSLSR	0.97851571	2	4.11785
Q5XI78	VIPEDGPAAQNPDK	0.901346443	2	3.18819
Q5XI78	YAELLVSQGVVNQPEYEEEISK	1.063447726	2	4.32488
Q5XI95	**ADH6 Alcohol dehydrogenase 6**	**1.011965546**	**0.0568**	**4**
Q5XI95	ATVLWKPGAPLAIEEIEVAPPK	0.721305512	2	3.9448
Q5XI95	IIAVDINK	1.149481118	2	2.78274
Q5XI95	NNICTEIR	0.769682754	2	2.31509
Q5XI95	TVGATDCVDPR	0.704122496	2	2.72137
Q5XIC0	**ECI2 Enoyl_CoA delta isomerase 2_ mitochondrial**	**0.938301427**	**0.3586**	**5**
Q5XIC0	ATQQDFENAMNQVK	0.936972768	2	4.65977
Q5XIC0	GILVTSEGGITK	0.914423722	2	3.94582
Q5XIC0	LHAVNEEECTTLR	0.947633832	2	3.72783
Q5XIC0	QNYVDLVSSLSSSSEASSQGK	0.966981198	2	4.54003

Q5XIC0	WDAWNALGSLPK	0.85297122	2	3.72013
Q5XIC1	**GMPPA Mannose_1_phosphate guanyltransferase alpha**	**1.036727601**	**0.9485**	**2**
Q5XIC1	NQQDGQLEESPGSWPGAGTIR	1.053881687	2	4.4455
Q5XIC1	VEGTPNDPNPNDPR	1.036723023	2	3.21192
Q5XIE6	**HIBCH 3_hydroxyisobutyryl_CoA hydrolase_ mitochondrial**	**0.983785332**	**0.7772**	**4**
Q5XIE6	AGIATHFVDSEK	1.006107616	2	3.3862
Q5XIE6	AGQTLSQDLFR	1.000814317	2	2.64133
Q5XIE6	AVLIDKDQTPK	0.848175601	2	2.39078
Q5XIE6	INSCFSANTVEQILENLR	0.916154452	2	4.05447
Q5XIF3	**NDUS4 NADH dehydrogenase [ubiquinone] iron_sulfur protein 4_ mitochondrial**	**1.136727007**	**0.0222**	**2**
Q5XIF3	HGWSYDVEGR	1.09236609	2	2.73058
Q5XIF3	LDVTPLTGVPEEHIK	1.152015304	2	3.47746
Q5XIF6	**TBA4A Tubulin alpha_4A chain**	**0.990499874**	**0.0288**	**5**
Q5XIF6	AVFVDLEPTVIDEIR	0.910723748	2	3.90375
Q5XIF6	AYHEQLSVAEITNACFEPANQMVK	1.064353987	3	4.69404
Q5XIF6	DVNAAIAAIK	1.049560228	2	2.87089
Q5XIF6	SIQFVDWCPTGFK	0.82569217	2	3.77968
Q5XIF6	TIGGGDDSFTTFFCETGAGK	1.264595325	2	3.97955
Q5XIG4	**OCAD1 OCIA domain_containing protein 1**	**1.016979871**	**0.9869**	**3**
Q5XIG4	SVPLAATSMLITQGLISK	0.937469842	2	3.56214
Q5XIG4	YDSNVSGQSSFGTSPAADNIEK	1.08315947	2	5.29973
Q5XIG4	YDSNVSGQSSFGTSPAADNIEKETLPR	0.999615548	3	3.84246
Q5XIH7	**PHB2 Prohibitin_2**	**0.917576123**	**1E-16**	**7**
Q5XIH7	DLQMVNISLR	1.514594634	2	2.91434
Q5XIH7	FNASQLITQR	0.870744159	2	3.94119
Q5XIH7	IGGVQQDTILAEGLHFR	1.259604825	3	4.6695
Q5XIH7	IVQAEGEAEAAK	0.919926725	2	4.23622
Q5XIH7	IYLTADNLVLNLQDESFTR	1.327359882	2	3.98079
Q5XIH7	LGLDYEER	0.957188632	1	2.50945
Q5XIH7	VLPSIVNEVLK	0.89645793	2	2.62547
Q5XIM9	**TCPB T_complex protein 1 subunit beta**	**1.081076001**	**6E-16**	**6**
Q5XIM9	EALLSSAVDHGSDEVK	0.983101825	2	4.03453
Q5XIM9	GATQQILDEAER	1.164085891	2	3.9354
Q5XIM9	GSGNLEAIHVIK	1.068236632	2	2.64783
Q5XIM9	NIGVDNPAAK	1.071742153	1	2.01951
Q5XIM9	SLHDALCVLAQTVK	0.457203985	2	3.24651
Q5XIM9	VQDDEVGDGTTSVTVLAAELLR	1.060241519	2	4.55136
Q5XIN6	**LETM1 LETM1 and EF_hand domain_containing protein 1_ mitochondrial**	**1.026619593**	**0.1858**	**8**
Q5XIN6	AAEVEGEQVDNK	1.080104543	2	3.73909
Q5XIN6	DIQPEVAEATVPGRPGAELQPK	0.829089038	2	4.53597
Q5XIN6	FLQDTIEEMALK	0.99205265	2	2.94561
Q5XIN6	LDPAAASSPTGESVISVDELISAMK	0.870489782	2	5.34761
Q5XIN6	LEEGGPVYSPPAQVVVK	0.805832198	2	2.75055
Q5XIN6	LFEDELTLDNLTRPQLVALCK	1.004592053	3	4.06422
Q5XIN6	LLELQSIGTNNFLR	0.525052689	2	2.46313
Q5XIN6	STLQTLPEIVAK	0.966721465	2	2.31867
Q5XIT9	**MCCB Methylcrotonoyl_CoA carboxylase beta chain_ mitochondrial**	**0.896873539**	**4E-13**	**8**
Q5XIT9	AATGEEVSAEDLGGADLHCR	0.878937701	2	4.72403
Q5XIT9	ALYGDTLVTGFAR	0.961215854	2	3.4031
Q5XIT9	AQEIALQNR	0.91269089	2	2.85476
Q5XIT9	DRIDNLIDPGSPFLEFSQFAGYK	0.966283079	3	4.57605
Q5XIT9	KLDVTVEPSEEPLFPADELYGIVGANLK	1.027434943	3	4.91976
Q5XIT9	LGTQPDSGSSTYQENYEQMK	1.066690725	2	5.12345
Q5XIT9	LWDDGIIDPVDTR	1.0923334	2	3.26987

Q5XIT9	LYGEEEVPAGGIITGIGR	0.910716379	2	4.30929
Q5XIU9	**PGRC2 Membrane_associated progesterone receptor component 2**	**0.917101696**	**0.8345**	**2**
Q5XIU9	GLATFCLDK	1.175907723	2	2.73602
Q5XIU9	GLCSGPGAGEESPAATLPR	0.917238043	2	4.02121
Q60587	**ECHB Trifunctional enzyme subunit beta_ mitochondrial**	**0.901808125**	**3E-15**	**6**
Q60587	AQDEGHLSDIVPFK	0.969697396	2	3.18987
Q60587	DFIYVSQDPK	0.920706892	2	2.94157
Q60587	DGGQYALVAACAAGGQGHAMIVEAYPK	0.954948704	3	4.11985
Q60587	DNGIRPSSLEQMAK	0.930197341	2	2.79037
Q60587	DQLLLGPTYATPK	0.733934767	2	3.4083
Q60587	NIVVVEGVR	0.814645268	2	2.83845
Q60759	**GCDH Glutaryl_CoA dehydrogenase_ mitochondrial**	**0.917400846**	**0.0038**	**4**
Q60759	DILGGNGISDEYHVIR	0.855930113	2	4.07044
Q60759	DIVYEMGELGVLGPTIK	1.025349443	2	3.51354
Q60759	GYGCAGVSSVAYGLLTR	1.224177847	2	3.35245
Q60759	HAMNLEAVNTYEGTHDIHALILGR	1.284221509	4	5.06404
Q61029	**LAP2B Lamina_associated polypeptide 2_ isoforms beta/delta/epsilon/gamma**	**0.935782475**	**0.0277**	**2**
Q61029	SELVANNVTLPAGEQR	0.967023656	2	4.07399
Q61029	SSTPLPTVSSSAENTR	0.872859899	2	2.93379
Q61035	**SYHC Histidyl_tRNA synthetase_ cytoplasmic**	**1.038369383**	**0.9584**	**2**
Q61035	ASAEQIEEEVTK	1.038365818	2	3.25026
Q61035	REDLVEEIR	1.039670723	2	2.35553
Q61092	**LAMC2 Laminin subunit gamma_2**	**1.062069022**	**0.3395**	**3**
Q61092	DRRQTSDQLLSR	1.307671669	2	2.41435
Q61092	LDDLKMTAER+Oxidation(5)	0.909504152	2	2.5347
Q61092	TKSLSQQLSLEGTQADIEADR	1.099901789	2	2.47665
Q61301	**CTNA2 Catenin alpha_2**	**1.035856781**	**0.7474**	**3**
Q61301	LLEPLVTQVTTLVNTSNK	0.983628607	2	3.57184
Q61301	TSVQTEDDQLIAGQSAR	1.129837002	2	4.74149
Q61301	WDDSGNDIIVLAK	1.046735397	2	3.10773
Q61335	**BAP31 B_cell receptor_associated protein 31**	**1.02010266**	**0.6582**	**4**
Q61335	AENEALAMQK	1.005964447	2	3.47405
Q61335	AENEALAMQK+Oxidation(7)	1.066147949	2	2.30297
Q61335	KYMEENDQLKK+Oxidation(2)	0.365923763	3	3.77462
Q61335	YMEENDQLKK+Oxidation(1)	1.362669425	2	2.45354
Q61550	**RAD21 Double_strand_break repair protein rad21 homolog**	**1.17085646**	**0.522**	**2**
Q61550	KLMMWKETGGVEK	1.174536772	2	2.33304
Q61550	TTIEESAMPPPPPQGVK+Oxidation(7)	0.94976621	2	2.38721
Q61595	**KTN1 Kinectin**	**0.921905463**	**0.7499**	**2**
Q61595	TAEHEAAQQDLQSK	1.023293382	2	3.30937
Q61595	VEPVLVTK	0.821264287	2	2.39416
Q61941	**transhydrogenase_ mitochondrial**	**0.939544177**	**0.1366**	**9**
Q61941	AISPDKDNFHFEVK	0.973639484	2	3.53288
Q61941	EANSIVITPGYGLCAAK	0.857726669	2	3.64774
Q61941	FGIHPVAGR	1.082885914	2	2.30262
Q61941	GITHIGYTDLPSR	0.940800714	2	3.65284
Q61941	KTTVLAMDQVPR	0.982691614	2	2.47119
Q61941	QGFNVVVESGAGEASK	1.031659358	2	4.35052
Q61941	SLGAEPLEVDLK	1.007025657	2	2.61531
Q61941	TTVLAMDQVPR	1.007558036	2	2.8229
Q61941	VTIAQGYDALSSMANISGYK	1.029942412	2	5.43501
Q62095	**DDX3Y ATP_dependent RNA helicase DDX3Y**	**1.037162261**	**0.6822**	**3**
Q62095	SFLLDLLNATGK	1.019890254	2	4.17336
Q62095	VGNLGLATSFFNER	1.314137845	2	2.34604
Q62095	VGSTSENITQK	1.262443615	2	3.03079

Q62261	**SPTB2 Spectrin beta chain_ brain 1**	**0.918350816**	**0.0006**	**8**
Q62261	ALVADSHPESER	0.955983535	2	3.09841
Q62261	EAEKLESEHPDQAQAILSR	0.91279162	3	3.45419
Q62261	HLLGVEDLLQK	1.518331015	2	2.72689
Q62261	HQILEQAVEDYAETVHQLSK	1.186215257	3	4.1181
Q62261	LVSDGNINSDR	1.074422962	2	3.20324
Q62261	SQNIITDSSSLNAEAIR	0.887824773	2	5.2605
Q62261	TLETPAAQMEGFLNR	1.554051101	2	3.54291
Q62261	VIESTQDLGNDLAGVMALQR	0.919871538	2	3.33983
Q62425	**NDUA4 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4**	**1.217456113**	**0.0013**	**2**
Q62425	FYSVNVDYSK	1.218095161	1	2.77669
Q62425	LGPNEQYK	1.155339817	2	2.37314
Q62452	**UD19 UDP_glucuronosyltransferase 1_9**	**1.069022463**	**1E-19**	**5**
Q62452	AMEIAEALGR	0.71669378	2	3.27057
Q62452	GAGVTLNVLEMTADDLENALK	0.629874316	3	6.27366
Q62452	GAGVTLNVLEMTADDLENALK+Oxidation(10)	0.929419868	2	4.25056
Q62452	WLPQNDLLGHPK	0.943121983	2	2.96823
Q62452	YTGTRPSNLAK	0.689757131	2	2.79702
Q62465	**VAT1 Synaptic vesicle membrane protein VAT_1 homolog**	**0.904877323**	**0.6681**	**6**
Q62465	ACGLNFADLMGR	1.10072569	2	2.84327
Q62465	CLVLTGFGGYDK	0.903237254	2	2.58057
Q62465	ENGVTHPIDYHTTDYVDEIKK	1.183339762	3	3.47864
Q62465	GVDIVMDPLGGSDTAK	0.901189895	2	4.32106
Q62465	TVENVTVFGTASASK	1.046063057	2	3.25373
Q62465	VLLVPGPEKET	0.951568844	2	2.51432
Q62468	**VILI Villin_1**	**1.344388477**	**6E-06**	**2**
Q62468	HEDCYILDQGGLKIFVWK	1.176524162	2	2.44237
Q62468	SGAMSQALNFIKAK	1.344003594	2	2.82686
Q62636	**RAP1B Ras_related protein Rap_1b**	**0.81377813**	**0.0005**	**2**
Q62636	INVNEIFYDLVR	1.425767014	2	4.08528
Q62636	VVGKEQGQNLAR	0.762384752	2	2.48075
Q62638	**GSLG1 Golgi apparatus protein 1**	**1.081819928**	**0.6416**	**2**
Q62638	LNDRIEMWSYAAK	1.08926084	2	2.35153
Q62638	NSELMDPKCKQMITK+Oxidation(4)	0.855762246	2	2.34578
Q62651	**ECH1 Delta(3_5)_Delta(2_4)_dienoyl_CoA isomerase_ mitochondrial**	**0.554192652**	**1E-19**	**5**
Q62651	EVDVGLAADVGTLQR	0.397968444	2	3.48631
Q62651	HVLHVQLNRPEK	0.537157058	2	2.99119
Q62651	IPEEVSDHNYESIQVTSAQK	0.750087266	3	4.51687
Q62651	RIPEEVSDHNYESIQVTSAQK	0.558518826	3	4.8227
Q62651	SLVNELTFTAR	0.542952793	2	3.26219
Q62730	**DHB2 Estradiol 17_beta_dehydrogenase 2**	**0.784951544**	**0.1125**	**5**
Q62730	AVLVTGADSGFGHALAK	0.6744629	2	4.34663
Q62730	EIQENYGQEYVHTQK	0.844307487	2	4.25664
Q62730	LSVLQMDVTKPEQIK	0.584445646	2	2.85363
Q62730	LSVLQMDVTKPEQIKDVHSEVAEK	0.806468066	3	5.20745
Q62730	VVTIHPGGFQTNIVGSQDSWDK	0.730236611	2	5.41076
Q62736	**CALD1 Non_muscle caldesmon**	**1.09418729**	**0.9977**	**10**
Q62736	ASGDKEAEGAPQVEAGKR	0.966332831	3	4.0665
Q62736	EFDPTITDGSLSVPSR	1.029060059	2	3.4269
Q62736	GETESEEFEK	1.352612313	2	2.36579
Q62736	GGNLGENQIKDEK	0.944308311	2	3.27289
Q62736	LEQYTNAIEGTK	1.101219459	2	3.26561
Q62736	MQNNSAENETAEGEEKGESR	0.992412404	3	4.6323
Q62736	MQNNSAENETAEGEEKGESR+Oxidation(0)	1.074347798	3	4.78866
Q62736	NDDDEEEAAR	1.647150443	2	3.40921

Q62736	RGETESEEFEK	1.108608069	2	3.12807
Q62736	VLEEEEQR	1.012130505	1	1.95714
Q62745	**CD81 CD81 antigen**	**0.883108085**	**0.2593**	**2**
Q62745	NSLCPSSSNSFTQLLK	0.806152649	2	2.83213
Q62745	QFYDQALQQAVMDDDANNAK	0.937412869	2	4.5501
Q62769	**UN13B Protein unc_13 homolog B**	**0.825600463**	**0.0008**	**2**
Q62769	DHMVREETRNLTPK	0.770656443	2	2.48372
Q62769	SNDEVAREFVK	0.982809593	1	1.99004
Q62785	**HAP28 28 kDa heat_ and acid_stable phosphoprotein**	**0.950199423**	**0.9537**	**3**
Q62785	ANEEDEQEEGGDGASGDPK	1.138971452	2	4.12502
Q62785	GVEGLIDIENPNR	0.940595515	2	2.96677
Q62785	QYTSPEEIDAQLQAEK	0.95128552	2	3.37712
Q62789	**UD2B7 UDP_glucuronosyltransferase 2B7**	**0.992385051**	**1E-19**	**2**
Q62789	IILDELVQR	1.795683973	2	3.50917
Q62789	WIPQNDLLGHPK	0.943121983	2	2.96823
Q62812	**MYH9 Myosin_9**	**0.981148027**	**0.0809**	**57**
Q62812	ALEEAMEQK	0.893564417	2	2.96158
Q62812	ALELDSNLYR	0.920817211	2	3.40032
Q62812	ALEQQVEEMK	0.992681154	2	2.93722
Q62812	ANLQIDQINTDLNLER	0.992941904	2	5.01623
Q62812	ASIAALEAK	1.051139664	2	2.60282
Q62812	ASREEILAQAK	0.996676299	2	2.70698
Q62812	CQYLQAEK	1.047034038	2	2.52924
Q62812	DFSALESQLQDTQELLQEENR	0.937947613	3	5.97507
Q62812	DLEAHIDTANK	0.935282843	2	3.41565
Q62812	DLQGRDEQSEEK	1.047961901	2	2.56895
Q62812	EEILAQAK	0.979157907	1	2.19908
Q62812	ELEDATETADAMNR	0.908958245	2	3.69872
Q62812	ELETQISELQEDLESER	0.867874797	2	3.89905
Q62812	HEDELLAK	0.974607808	2	3.10068
Q62812	HSQAVEELAEQLEQTK	1.010818588	2	4.96254
Q62812	HSQAVEELAEQLEQTKR	0.935077111	3	5.54691
Q62812	IAQLEEQLDNETK	1.00258736	2	4.01623
Q62812	IIGLDQVAGMSETALPGAFK	0.910665825	2	3.78374
Q62812	IRELETQISELQEDLESER	1.077684844	3	3.83592
Q62812	KEEELQAALAR	0.920598494	2	3.10038
Q62812	KKVEAQLQELQVK	0.928380991	2	4.66188
Q62812	KLEEDQIIMEDQNCK	0.807597991	2	5.65819
Q62812	KLEGDSTDLSDQIAELQAQIAELK	0.891067532	2	6.29156
Q62812	KQELEEICHDLEAR	1.011299443	2	4.28188
Q62812	KVEAQLQELQVK	1.029266372	2	4.21173
Q62812	LEEDQIIMEDQNCK	1.125535376	2	3.81416
Q62812	LEGDSTDLSDQIAELQAQIAELK	0.898118504	2	4.91829
Q62812	LQQELDDLLVDLDHQR	0.860131898	2	4.85152
Q62812	LQVELDSVTGLLNQSDSK	0.966180077	2	5.96439
Q62812	LTEMETMQSQLMAEK	1.426216559	2	3.32464
Q62812	MQQNIQELEEQLEEEESAR	1.107234473	2	6.00335
Q62812	MQQNIQELEEQLEEEESAR+Oxidation(0)	1.111326928	2	4.65277
Q62812	NAEQFKDQADK	0.942543753	2	3.68965
Q62812	NLPIYSEEIVDMYK	1.105663119	2	3.77623
Q62812	NMDPLNDNIATLLHQSSDK	1.039314673	2	4.42769
Q62812	NTDQASMPDNTAAQK	0.992406104	2	5.27744
Q62812	NTDQASMPDNTAAQK+Oxidation(6)	1.10196097	2	5.07344
Q62812	QAQQERDELADEIANSSGK	1.012084536	3	4.12031
Q62812	QIATLHAQVTDMK	1.105341378	2	2.6809
Q62812	QLEEAEEEAQR	0.967762838	2	3.27016
Q62812	QNKELK	1.370402107	1	2.19138

Q62812	QSVSNLEK	1.102771849	2	2.58709
Q62812	QTLENERGELANEVK	1.095421854	2	3.29656
Q62812	RGDMPFVVTR	0.991920686	2	2.33096
Q62812	RKLEGDSTDLSDQIAELQAQIAELK	1.041082455	3	5.60279
Q62812	RQLEEAEEEAQR	0.990057654	2	4.41887
Q62812	SMEAEMIQLQEELAAAER	0.914403479	2	4.25543
Q62812	SMEAEMIQLQEELAAAERAKR+Oxidation(1)	0.999898822	2	2.30145
Q62812	TDLLLEPYNK	1.016423254	2	3.19375
Q62812	TELEDTLDSTAAQQELR	1.074445285	2	4.91138
Q62812	THEAQIQEMR	0.848636195	2	3.15137
Q62812	THEAQIQEMR+Oxidation(8)	1.290174034	2	3.4003
Q62812	TQLEELEDELQATEDAK	0.958684683	2	6.10976
Q62812	VEAQLQELQVK	0.791181897	2	3.24004
Q62812	VEDMAELTCLNEASVLHNLK	1.130757613	2	4.39552
Q62812	VSHLLGINVTDFTR	1.271750619	2	3.70919
Q62812	YEILTPNSIPK	0.871025194	2	2.80418
Q62826	**HNRPM Heterogeneous nuclear ribonucleoprotein M**	**0.980725472**	**1**	**4**
Q62826	ADILEDKDGK	0.978193042	2	2.3082
Q62826	AFITNIPFDVK	0.971403922	2	3.19885
Q62826	GNFGGSFAGSFGGAGGHAPGVAR	0.891172708	2	3.86221
Q62826	MGPVMDRMATGLER+Oxidation(0)	0.990357243	2	2.46011
Q62868	**ROCK2 Rho_associated protein kinase 2**	**0.652226388**	**0.0563**	**2**
Q62868	EENEEKTKLCK	0.412056031	2	2.36738
Q62868	LAEIMNRK+Oxidation(4)	0.726641784	1	2.05368
Q62871	**DC1I2 Cytoplasmic dynein 1 intermediate chain 2**	**1.120317406**	**0.8064**	**2**
Q62871	ADAEEEAATR	1.133071321	2	3.27852
Q62871	SVSTPSEAGSQDSGDGAVGSR	1.046190334	2	4.73295
Q62902	**LMAN1 Protein ERGIC_53**	**1.191234093**	**2E-16**	**6**
Q62902	GAGTPGQPGQVSQQELDTVVR	1.199997663	2	4.22636
Q62902	GHPDLQGQPADDIFESIGDR	1.140492673	2	4.89019
Q62902	NNPAIVVVGNNGQINYDHQNDGATQALASCQR	1.190184636	3	5.00546
Q62902	RGAGTPGQPGQVSQQELDTVVR	1.083664655	3	5.04385
Q62902	YQEEFEHFQQELDK	1.044656662	2	5.1436
Q62902	YVSSLTEEISR	1.012107137	2	3.40039
Q63041	**A1M Alpha_1_macroglobulin**	**0.73429342**	**1E-19**	**8**
Q63041	AEDITHNGIVYTPK	0.682890635	2	3.52898
Q63041	AEQGAYLGPLPYK	0.809033663	2	3.3371
Q63041	DTVVKPVIVEPEGIEK	0.722690295	2	3.12329
Q63041	GSIFNSGSHVLPLEQGK	0.689426322	2	3.69715
Q63041	LQDQSNIQR	0.774893455	2	3.06841
Q63041	QDLNDNDAYSVFQSIGLK	0.727979474	2	3.23403
Q63041	YNILPEAEGEAPFTLK	0.805310248	2	3.9193
Q63041	YVVLVPSELYAGVPEK	0.855250837	2	3.31287
Q63060	**GLPK Glycerol kinase**	**1.524245296**	**1E-19**	**10**
Q63060	AVLGPLVGAVDQGTSSTR	1.40776511	2	5.32653
Q63060	DCGIPLSHLQVDGGMTSNK	1.503279683	2	3.26533
Q63060	EILQSVYECIEK	1.267279913	2	3.87281
Q63060	FEPQINAEESEIR	1.230843608	2	3.48312
Q63060	KAVLGPLVGAVDQGTSSTR	0.891679216	3	3.50119
Q63060	KVQEAVEENR	1.356937511	2	3.32033
Q63060	LGQLNIDISNIK	1.528057518	2	3.02982
Q63060	NTYGTGCFLLCNTGHK	1.206840134	2	3.91685
Q63060	TAELLSHHQVEIK	1.454139934	2	3.17095
Q63060	VQEAVEENR	1.244467535	2	3.06073
Q63081	**PDIA6 Protein disulfide_isomerase A6**	**1.051824731**	**0.8502**	**9**
Q63081	GESPVDYDGGR	1.057357249	2	2.94421
Q63081	GSFSEQGINEFLR	1.052136657	2	3.62426

Q63081	GSTAPVGGGSFPNITPR	1.018704913	2	4.28021
Q63081	HQSLGGQYGVQGFPTIK	1.053074165	2	5.04369
Q63081	KTCEEHQLCVVAVLPHILDTGATGR	1.077636094	3	4.08478
Q63081	NLEPEWAAAATEVK	1.055932808	2	3.90702
Q63081	NSYLEVLLK	1.028739498	2	2.91281
Q63081	TCEEHQLCVVAVLPHILDTGATGR	1.182348925	3	4.69039
Q63081	TGEAIVDAALSALR	1.042090738	3	4.68916
Q63108	**EST3 Liver carboxylesterase 3**	**0.824707855**	**4E-16**	**5**
Q63108	DFNTVPYIVGINK	0.976160218	2	2.6296
Q63108	GGTSKEEINLSK	0.862221548	2	3.49264
Q63108	LDPMTATSLLK	1.004471773	2	3.05915
Q63108	QKTEEELLETTLK	0.907176243	2	3.58062
Q63108	SSFLLNLPEEAIPVAVEK	0.759015297	2	4.65714
Q63120	**MRP2 Canalicular multispecific organic anion transporter 1**	**1.265490749**	**0.2541**	**2**
Q63120	ACALLPDLEILPGGDMAEIGEK	1.133141324	2	2.96548
Q63120	YFAWEPSFQEQVQGIR	1.088990589	2	3.74345
Q63150	**DPYS Dihydropyrimidinase**	**0.848255717**	**1E-19**	**10**
Q63150	ALGKDDFTK	0.944615678	2	2.62096
Q63150	DQTCTPIPVK	0.710945717	1	2.12038
Q63150	DQTCTPIPVKR	0.826417849	2	2.63375
Q63150	EIGAIAQVHAENGDLIAEGAK	0.898634664	2	5.48412
Q63150	FVAVTSTNAAK	0.879054557	2	3.1109
Q63150	GEVITLKPR	0.799619657	2	2.31463
Q63150	GSSLIEAFETWR	0.866111612	2	2.99476
Q63150	VVNDDFSQVADVLVEDGVVR	0.810869489	2	5.24056
Q63150	VVYEAGVFDVTAGHGK	0.939464676	2	3.86045
Q63150	VVYGEPIAAGLGTDGTQYWNK	0.898810572	2	5.62722
Q63270	**ACOC Cytoplasmic aconitate hydratase**	**1.050335913**	**4E-06**	**16**
Q63270	AVEAGLNVKPYVK	0.942212581	2	3.14445
Q63270	AVLAESYER	0.951720725	2	2.86139
Q63270	FVEFFGPGVAQLSIADR	1.124032607	2	4.41195
Q63270	GFQVAPDHHNDHK	1.409966904	2	3.03708
Q63270	IDFEKEPLGVNAQGQQVFLK	0.933468675	3	4.60964
Q63270	KNDIENILNWSIMQHK	0.933053249	3	3.82754
Q63270	NDIENILNWSIMQHK	0.942409704	2	2.45794
Q63270	NQDLEFER	0.810489987	2	2.3738
Q63270	QAPQTVHLPSGETLDVFDAAER	0.997941669	3	3.9533
Q63270	SIEVPFKPAR	0.915959983	2	2.42862
Q63270	SIVDAYVLLNLGDSVTTDHISPAGNIAR	1.092746615	3	4.80059
Q63270	SPPFFESLTLDLQPPK	0.965541631	2	2.68145
Q63270	SWNALAAPSEK	0.870917892	1	2.60438
Q63270	TSLSPGSGVVTYYLR	1.161585899	2	2.9123
Q63270	VILQDFTGVPAVVDFAAMR	0.842650791	3	4.06327
Q63270	YQQAGLPLIVLAGK	1.051750184	2	3.21348
Q63276	**BAAT Bile acid_CoA:amino acid N_acyltransferase**	**1.093647891**	**0.1268**	**13**
Q63276	AHGHFLFVVGEDDKNLNSK	1.19261652	2	5.96721
Q63276	ASEVGEVDLER	1.063644094	2	3.97332
Q63276	DDKGNLFNSQAFYR	1.079700153	3	3.42137
Q63276	GNLFNSQAFYR	1.316738063	2	2.76085
Q63276	LTAVPLSALVDEPVHIR	1.832308897	3	3.43337
Q63276	QHLNPGFNSQL	1.30578584	2	3.5194
Q63276	QITATVLINGPNFVSSNPHVYR	1.064545634	3	4.94574
Q63276	TFEETADKDSK	0.887263503	2	3.79294
Q63276	VFQPTPCSEEFVTTNALGLVEFYR	1.145430123	2	5.23463
Q63276	VISSSLDSLILER	0.84476254	2	3.94121
Q63276	VTGLTPFQVVCLQASLK	1.153190526	3	3.64786
Q63276	WYVAPGVTR	0.656532212	2	2.74042

Q63276	YCFPIEK	1.016958222	2	2.54156
Q63279	**K1C19 Keratin_ type I cytoskeletal 19**	**1.011347955**	**0.9965**	**2**
Q63279	IVLQIDNAR	1.009206316	2	2.96024
Q63279	TIEDLRDKILGATIENSK	1.014956083	2	2.32248
Q63342	**M2GD Dimethylglycine dehydrogenase_ mitochondrial**	**1.177596549**	**1E-19**	**20**
Q63342	ADIINIVNGPITYSPDILPMVGPHQGVR	1.224181996	3	5.46054
Q63342	AWGSEMNCDTNPLEAGLDYFIK	1.283936767	2	4.50589
Q63342	EGQESPPSPPEWK	0.813020074	2	2.66461
Q63342	GQDSTQLLDHLCANVIPK	1.145436034	2	4.08773
Q63342	IMNAGQEEGIDNFGTYALNALR	0.838820519	2	4.73565
Q63342	ISDIPVTAIR	1.167220766	2	3.03494
Q63342	KADIINIVNGPITYSPDILPMVGPHQGVR	1.100276376	3	6.02937
Q63342	LEEETGQVVGFHQPGSIR	1.100469146	2	4.58648
Q63342	LNKPADFTGK	1.588091213	1	2.53007
Q63342	LTSEDLSDDVFK	1.135612808	2	3.30914
Q63342	NITDELGVLGVAGPYAR	1.143120547	2	4.23884
Q63342	NYPATIIQEPLVLTEPTR	1.278686358	3	4.33988
Q63342	REDSAALYER	0.566446655	2	2.96674
Q63342	TNWHATEQYIIEPEK	1.240692298	2	4.07105
Q63342	VGVIDLSPFGK	1.216939566	2	3.63084
Q63342	VIGNTTSGSYSYSIQK	1.139707056	2	4.26892
Q63342	VYAELTVSHQSPGEFLLITGSGSELHDLR	1.275659034	3	4.25547
Q63342	WIEEAAVR	1.105647408	2	2.70467
Q63342	WTTTQYTEAK	1.182720726	2	2.307
Q63342	YLSDWILHGEPPFDLIELDPNR	1.316615574	3	4.06442
Q63347	**PRS7 26S protease regulatory subunit 7**	**0.921676978**	**0.0611**	**6**
Q63347	ALDEGDIALLK	0.920656544	2	2.81046
Q63347	FDDGAGGDNEVQR	0.94062045	2	3.57591
Q63347	IINADSEDPK	1.026579689	2	2.53634
Q63347	QTLQSEQPLQVAR	1.092944236	2	4.10368
Q63347	QVEDDIQQLLK	1.022016594	2	2.61795
Q63347	TMLELINQLDGFDPR	0.934022396	2	2.67088
Q63362	**NDUA5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5**	**1.043423231**	**0.0107**	**3**
Q63362	KLENLLQGGEVEEVILQAEK	1.046920323	2	4.67545
Q63362	TTGLVGLAVCDTPHER	1.026358802	2	4.07293
Q63362	YTEQITSEK	1.346123714	2	2.43544
Q63429	**UBC Polyubiquitin_C**	**0.991356191**	**0.925**	**3**
Q63429	ESTLHLVLR	0.967419295	2	2.34047
Q63429	TITLEVEPSDTIENVK	1.006302936	2	4.72344
Q63429	TLSDYNIQK	1.057590441	2	2.49632
Q63448	**ACOX3 Peroxisomal acyl_coenzyme A oxidase 3**	**1.012238206**	**1**	**9**
Q63448	ADWLDSEAPLAAYR	1.012607171	2	4.53859
Q63448	EIHALASAGKPLASWTAQR	0.996847113	2	4.21823
Q63448	GGYISGEQTGK	1.038188415	1	2.3837
Q63448	NLWAAVLQQSGVLER	1.016397075	2	4.0974
Q63448	QFGPTDKEEIPVLEYPLQQWR	0.906598623	3	5.08842
Q63448	TIFLDLIELQR	1.048804232	2	3.46772
Q63448	TIFSTLENDPLFARPFGADLPLEK	0.916864474	3	4.33692
Q63448	TTAHYDPATQEFILHSPDFEAAK	1.017481174	3	4.35303
Q63448	TVNFLEAYPGILGQK	1.08307759	2	4.9494
Q63493	**CD1D Antigen_presenting glycoprotein CD1d**	**1.191638734**	**0.0239**	**2**
Q63493	DIKEIVKMMSPK+Oxidation(7)	1.191638734	2	2.62599
Q63493	DIKEIVKMMSPK+Oxidation(8)	1.191638734	2	2.47016
Q63505	**TF3C1 General transcription factor 3C polypeptide 1**	**1.164400498**	**0.0196**	**2**
Q63505	NPNLEIPDTLQELFAKYR	1.169666459	2	2.54708
Q63505	YEEIDLETGILESRR	0.561324189	2	2.74006

Q63524	**TMED2 Transmembrane emp24 domain_containing protein 2**	**1.08093675**	**0.9931**	**2**
Q63524	GQDMETEAHQNKLEEMINELAVAMTAVK	1.011839234	3	5.03396
Q63524	HEQEYMEVR	1.080984748	2	2.81175
Q63525	**NUDC Nuclear migration protein nudC**	**1.069950137**	**0.9635**	**3**
Q63525	GQAPVIDGELYNEVK	1.053946359	2	3.08018
Q63525	LSDLDSETR	1.181890456	2	2.50884
Q63525	VEESSWLIEDGK	1.135561993	2	2.80843
Q63569	**PRS6A 26S protease regulatory subunit 6A**	**0.968606408**	**0.428**	**7**
Q63569	AMEVDERPTEQYSDIGGLDK	1.120933044	3	3.90371
Q63569	CTDDFNGAQCK	0.927674116	2	2.73155
Q63569	DSYLILETLPTEYDSR	0.910066459	2	3.40302
Q63569	MNVSPDVNYEELAR	0.969549503	2	3.03285
Q63569	QTYFLPVIGLVDAEK	1.111219722	2	2.69761
Q63569	TMLELLNQLDGFQPNTQVK	0.742138134	2	2.54887
Q63569	VDILDPALLR	0.969493389	2	2.39299
Q63584	**TMEDA Transmembrane emp24 domain_containing protein 10**	**1.071422401**	**0.4602**	**4**
Q63584	ITDSAGHILYAK	1.168367723	2	3.57769
Q63584	LEDLSESIVNDFAYMK	1.042010535	2	3.55448
Q63584	NYEEIAK	1.004007923	1	2.23362
Q63584	RLEDLSESIVNDFAYMK	0.768178111	2	4.04176
Q63598	**PLST Plastin_3**	**0.901592976**	**5E-07**	**8**
Q63598	AESMLQQADK	0.973347816	2	2.73197
Q63598	ATDDIIVNWVNGTLSEAGK	0.845283918	2	4.55638
Q63598	IDINMSGFNETDDLKR	0.867274169	2	3.48928
Q63598	KLENCNYAVELGK	0.724565035	2	3.58923
Q63598	VDLNSNGFICDYELHELFK	1.000877196	2	4.03626
Q63598	VYALPEDLVEVKPK	0.893200149	2	3.18946
Q63598	YPALTKPENQDIDWTLLEGETR	0.85008841	3	5.64059
Q63598	YTLNVMEDLGEGQK	0.897220669	2	3.3985
Q63610	**TPM3 Tropomyosin alpha_3 chain**	**1.230366655**	**6E-11**	**8**
Q63610	EQAEAEVASLNR	1.079054502	2	2.92513
Q63610	IQVLQQQADDAEER	1.262001161	2	4.82078
Q63610	KIQVLQQQADDAEER	1.175645474	2	5.40084
Q63610	KLVIIEGDLER	1.078549234	2	2.30448
Q63610	LVIIEGDLER	1.09334508	2	2.69653
Q63610	MELQEIQLK	1.104689359	2	3.09523
Q63610	TIDDLEDKLK	1.043682216	2	2.67984
Q63610	YSQKEDKYEEEIK	1.076746016	2	4.47917
Q63617	**HYOU1 Hypoxia up_regulated protein 1**	**1.138014815**	**2E-06**	**13**
Q63617	AANSLEAFIFETQDK	1.30734392	2	3.98516
Q63617	DAVITVPAFFNQAER	0.997559455	2	2.46626
Q63617	EGETPDEKESGDKSEAQKPNEK	1.22647598	3	3.86946
Q63617	FLGDSAAGMAIK	1.052699904	2	2.3732
Q63617	GQAGPEGVPPAPEEEKK	0.910719344	2	3.22551
Q63617	LGNTISSLFGGGTSSDAK	1.177876811	2	3.25162
Q63617	LYQPEYQEVSTEEQR	1.35096848	2	4.60917
Q63617	NINADEAAAMGAVYQAAALSK	1.108019944	2	4.64856
Q63617	SLAEDFAEQPIK	1.10657279	2	2.75734
Q63617	SLAEDFAEQPIKDAVITVPAFFNQAER	1.100849763	3	3.80923
Q63617	VEFEELCADLFDR	0.966416925	2	3.39113
Q63617	VESVFETLVEDSPEEESTLTK	0.931961996	3	4.17932
Q63617	VLQLINDNTATALSYGVFR	1.099544937	2	4.00108
Q63692	**CDC37 Hsp90 co_chaperone Cdc37**	**1.156283993**	**0.0006**	**2**
Q63692	EGEEAGPGDPLLEAVPK	0.822522938	2	3.82494
Q63692	LGPGGLDPVEVYESLPEELQK	1.165244085	2	2.77542
Q63716	**PRDX1 Peroxiredoxin_1**	**0.911522112**	**0.0009**	**15**
Q63716	ADEGISFR	0.977282172	2	3.13706

Q63716	ATAVMPDGQFK	0.932677003	2	2.77505
Q63716	ATAVMPDGQFK+Oxidation(4)	1.089191033	2	2.33678
Q63716	DISLSDYK	0.800746966	1	2.04732
Q63716	HGEVCPAGWKPGSDTIKPDVNK	0.930576553	3	6.00501
Q63716	IGHPAPSFK	2.549752018	1	2.04062
Q63716	KQGGLGPMNIPLVSDPK	0.85919344	2	3.26397
Q63716	KQGGLGPMNIPLVSDPK+Oxidation(7)	1.078474338	2	2.54693
Q63716	LVQAFQFTDK	1.541631571	2	2.89571
Q63716	QGGLGPMNIPLVSDPK	1.006224186	2	3.83508
Q63716	QGGLGPMNIPLVSDPK+Oxidation(6)	0.983237446	2	3.25654
Q63716	QITINDLPVGR	0.931279745	2	3.08592
Q63716	RTIAQDYGVLK	1.077082994	2	2.57225
Q63716	SVDEILR	0.931225743	2	2.37259
Q63716	TIAQDYGVLK	0.966406519	2	3.39276
Q63787	**P85A Phosphatidylinositol 3_kinase regulatory subunit alpha**	**0.812162042**	**0.3131**	**2**
Q63787	MHGDYTLTLRKGGNNK+Oxidation(0)	0.813891933	2	2.30273
Q63787	SRISEIIDSR	0.768483728	1	2.03854
Q63797	**PSME1 Proteasome activator complex subunit 1**	**0.991622024**	**0.2485**	**8**
Q63797	ISELDAFLKEPALNEANLSNLK	0.986257683	2	5.31646
Q63797	KGDEDDKGPPCGPVNCNEK	1.038888469	3	4.31563
Q63797	KISELDAFLKEPALNEANLSNLK	0.964446979	3	4.83323
Q63797	LEGFQTQISK	1.002222875	2	2.7417
Q63797	NAYAVLYDIILK	1.272206945	2	4.11996
Q63797	QLVHELDEAEYQEIR	0.882920222	2	4.09165
Q63797	TENLLGSYFPK	1.026392497	2	3.42015
Q63797	VDVFREDLCSK	0.920390977	2	2.64134
Q63798	**PSME2 Proteasome activator complex subunit 2**	**0.968004125**	**0.962**	**4**
Q63798	AFYAELHHIISSNLEK	0.964703178	3	3.5007
Q63798	IEDGNDFGVAIQEK	0.960243973	2	4.38716
Q63798	TKVEAFQTAISK	0.947348132	2	3.18013
Q63798	VEAFQTAISK	0.880937605	2	2.30816
Q63836	**SBP2 Selenium_binding protein 2**	**1.037591981**	**0.0021**	**4**
Q63836	GGSVQVLEDQELTCQPEPLVVK	1.068356025	3	5.65349
Q63836	IYVVDVGSEPR	0.804173819	2	3.22778
Q63836	LNPNFLVDFGK	1.197783663	2	2.41039
Q63836	LNPNFLVDFGKEPLGPALAHELR	0.912549909	3	4.40079
Q63965	**SFXN1 Sideroflexin_1**	**1.110861407**	**0.009**	**6**
Q63965	MSGEVPPNINIK+Oxidation(0)	0.959229637	1	1.92955
Q63965	NILLTNEQLENAR	1.090574969	2	4.62913
Q63965	QAITQVVISR	1.326622061	2	2.61143
Q63965	QGIVPAGLTENELWR	1.071297076	2	2.90478
Q63965	WDQSTFIGR	1.024702108	2	2.57481
Q63965	YAYDSAFHPDTGEK	1.155855569	2	4.02994
Q64057	**AL7A1 Alpha_aminoadipic semialdehyde dehydrogenase**	**0.979638255**	**0.0008**	**16**
Q64057	AWNIWADIPAPK	0.957401346	2	3.65717
Q64057	EDNEGVFNGSWGGR	0.88732358	2	3.54155
Q64057	FKNEEEVFEWNNEVK	0.950173261	2	5.35176
Q64057	GAPTTSLVSIAVTK	0.878527703	2	4.53102
Q64057	GEVITTYCPANNEPIAR	0.977630037	2	5.23091
Q64057	GSDCGIVNVNIPTSGAEIGGAFGGEK	0.993813836	2	5.73102
Q64057	LFLHESIHDEVVDR	0.972387622	2	2.8614
Q64057	NEEEVFEWNNEVK	1.088547853	2	4.3744
Q64057	QAVSMFVQAVEEAK	1.074810377	2	2.92136
Q64057	QGLSSSIFTK	1.067455899	2	2.56712
Q64057	QVALMVQER	0.835854798	2	2.46026
Q64057	STCTINYSTALPLAQGIK	0.966052423	2	3.98954
Q64057	VGNPWDPNILYGPLHTK	1.360600641	3	3.64423

Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK	1.092337154	3	5.5145
Q64057	VMDHPGNYVEPTIVTGLVHDAPIVHK+Oxidation(1)	0.944123138	3	5.97842
Q64057	VNLLSFTGSTQVGK	1.464724334	2	4.53876
Q64060	**DDX4 Probable ATP_dependent RNA helicase DDX4**	**0.898914957**	**0.4008**	**2**
Q64060	MLDMGFGPEMKK+Oxidation(0)	0.898914957	2	2.4291
Q64060	MLDMGFGPEMKK+Oxidation(3)	0.898914957	2	2.32356
Q64119	**MYL6 Myosin light polypeptide 6**	**1.104517465**	**0.0786**	**5**
Q64119	DQGTYEDYVEGLR	0.878761969	2	3.35391
Q64119	HVLVTLGEK	0.992638067	2	2.39061
Q64119	NKDQGTYEDYVEGLR	1.044684244	2	4.31594
Q64119	VFDKEGNGTVMGAEIR	1.235262295	2	3.81775
Q64119	VLDFEHFLPMLQTVAK	1.003205262	3	4.49315
Q64122	**MYL9 Myosin regulatory light polypeptide 9**	**0.881993509**	**9E-08**	**2**
Q64122	DGFIDKEDLHDMLASLGK	0.746349078	2	4.82231
Q64122	LNGTDPEDVIR	0.922378222	2	2.6019
Q64176	**EST22 Liver carboxylesterase 22**	**0.740476315**	**1E-19**	**4**
Q64176	AISESGVALTAGLVK	0.763708146	2	4.2377
Q64176	EGYLQIGATTQQAQK	0.710925682	2	4.31814
Q64176	LDQMTAMSLLK+Oxidation(3)	0.57205584	2	2.51784
Q64176	NFNTVPYIVGINK	1.145424966	2	2.69482
Q641K1	**CBPC1 Cytosolic carboxypeptidase 1**	**1.505632271**	**0.0606**	**2**
Q641K1	GTLEYLMSNSPTAQSLR	1.505170167	2	2.3375
Q641K1	KDFGLPLTVLSCTK	1.505819822	2	2.37878
Q641Y0	**OST48 Dolichyl_diphosphooligosaccharide__protein glycosyltransferase 48 kDa subunit**	**1.220289851**	**4E-10**	**8**
Q641Y0	ELGSECGIEFDEEK	1.710084548	2	2.3807
Q641Y0	GFELTFK	1.00645711	2	2.5462
Q641Y0	NTLLIAGLQAR	1.140796086	2	3.61323
Q641Y0	SSLNPILFR	1.379669179	2	2.56217
Q641Y0	TAVIDHHNYDVSDLGQHTLIVADTENLLK	1.272874265	3	6.58361
Q641Y0	TLVLLDNLNVR	1.16340338	2	3.46115
Q641Y0	WVPFDGDDIQLEFVR	0.978445944	2	3.25475
Q641Y0	YSQTGNYELAVALSR	1.11424325	2	3.22133
Q641Y2	**NDUS2 NADH dehydrogenase [ubiquinone] iron_sulfur protein 2_ mitochondrial**	**1.234556203**	**0.0275**	**3**
Q641Y2	IDEVEEMLTNNR	1.092861354	2	3.38024
Q641Y2	IIEQCLNK	1.186440632	2	2.36141
Q641Y2	TQPYDVYDQVEFDVPIGSR	1.230685434	2	4.09984
Q641Y8	**DDX1 ATP_dependent RNA helicase DDX1**	**1.097865421**	**0.9783**	**2**
Q641Y8	GHVDILAPTVQELAALEK	0.992089463	3	3.46178
Q641Y8	GSAFAIGSDGLCCQSR	1.113823303	2	3.20167
Q641Z6	**EHD1 EH domain_containing protein 1**	**1.070653297**	**0.5228**	**2**
Q641Z6	KEMPNVFGKESK+Oxidation(2)	1.101828584	2	2.31129
Q641Z6	LLDTVDDMLANDIAR	1.064545528	2	2.6704
Q64232	**TECR Trans_2_3_enoyl_CoA reductase**	**0.916319685**	**0.5943**	**3**
Q64232	LCFLDKVEPQATISEIK	0.938456609	2	4.08523
Q64232	SLKDEDVLQK	0.905577261	2	2.90039
Q64232	THPQWYPAR	0.870427926	2	2.52925
Q64240	**AMBP Protein AMBP**	**0.869752229**	**5E-05**	**3**
Q64240	AFAELWAFDAAQGK	1.01075201	2	3.82506
Q64240	AVLPQENEGSGSEPLITGTLK	0.796093709	2	4.34526
Q64240	TIAACNLPIVQGPCR	0.521302066	2	3.54196
Q64380	**SARDH Sarcosine dehydrogenase_ mitochondrial**	**0.823074359**	**5E-15**	**19**
Q64380	AIDSLSIEK	1.039119113	2	2.57966
Q64380	AYGIESHVLSPAETK	0.83586336	2	4.65886
Q64380	DGTMDPAGTCTTLTR	0.746315384	2	3.78573
Q64380	DILQDVLDADLSNEAFPFSTHQLVR	0.966703363	3	5.71569

Q64380	DLYPLMNVDDLYGTLYVPR	0.797710144	2	2.61801
Q64380	EEAQGASVVPQGPSQPLPSTANVVVIGGGSLGCQTLYHLAK	0.988362152	3	4.30358
Q64380	FHHSLTDHPR	0.837041197	2	2.35478
Q64380	FYLLGADAR	0.979049235	2	2.84094
Q64380	GAQVIENCAVTGIR	1.102564535	2	4.32882
Q64380	HGLVNAGYR	1.104949171	2	2.51591
Q64380	IEGIQNMPNVR	0.852574052	2	2.80898
Q64380	LQGDALSVGGYEANPIFWDEVSDK	0.719000759	2	4.57527
Q64380	NYSVVFPHDEPLAGR	0.839772914	2	4.44087
Q64380	QVVSHDLEEETGLHTGWIQNGGLFIASNQQR	0.898359338	3	4.74978
Q64380	RDPLHEELLGQGCVFQER	0.929841382	3	5.38756
Q64380	SDDSPLEAGLAFTCK	0.984012052	2	4.04966
Q64380	STVCGPESFTPDHKPLMGEAPELR	1.069723166	3	4.08844
Q64380	STVCGPESFTPDHKPLMGEAPELR+Oxidation(16)	0.893938681	3	3.93777
Q64380	VTAVETQHGSIQTPCVVNCAGVWASSVGR	0.968395558	3	4.93879
Q64428	**ECHA Trifunctional enzyme subunit alpha_ mitochondrial**	**0.906855968**	**1E-19**	**26**
Q64428	ADMVIEAVFEDLAVK	0.736254928	3	4.25756
Q64428	ADMVIEAVFEDLAVK+Oxidation(2)	0.762951734	2	2.66073
Q64428	ALMGLYNGQVLCK	0.930376788	2	2.64749
Q64428	DSIFSNLIGQLDYK	0.778766706	2	2.781
Q64428	DTTASAVAVGLK	0.749727883	2	3.3925
Q64428	DTTVTGLGR	0.802802302	2	2.92376
Q64428	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK	0.913417799	3	5.4017
Q64428	EVQSEFVEVMNEIWANDQIR	0.771461966	3	5.76725
Q64428	FGELALTK	0.925331955	2	2.76605
Q64428	FGGGSVELLK	0.881072825	2	2.95207
Q64428	FVDLYGAQK	0.898243421	2	2.90537
Q64428	GFYIYQSGSK	0.815240518	1	2.11367
Q64428	ILQEGVDPK	0.842012629	2	2.65965
Q64428	KTVLGVPEVLLGILPGAGGTQR	0.803772805	2	3.76652
Q64428	LPAKPEVSSDEDIQYR	1.445750038	2	4.45614
Q64428	MGLVDQLVDPLGPGIK	0.74622709	2	4.5254
Q64428	MGLVDQLVDPLGPGIK+Oxidation(0)	0.806413519	2	4.19966
Q64428	MQLLEIITTDK	0.838887891	2	3.89846
Q64428	MQLLEIITTDK+Oxidation(0)	0.812015321	2	2.9167
Q64428	MVGVPAAFDMMLTGR	0.961571454	2	2.8855
Q64428	NLNSEIDNILVNLR	0.832430818	2	4.5758
Q64428	SAVLISSKPGCFVAGADINMLASCTTPQEAAR	0.932261504	3	3.8613
Q64428	TGLEQGNDAGYLAESEK	0.987168638	2	5.07455
Q64428	TIEYLEEVAVNFAK	0.835520992	2	3.43744
Q64428	TVLGVPEVLLGILPGAGGTQR	0.868882724	3	4.91002
Q64428	TVQQLAILGAGLMGAGIAQVSVDK	0.881206429	3	5.37674
Q64458	**CP2CT Cytochrome P450 2C29**	**1.949317754**	**1E-19**	**5**
Q64458	EHKESLDVTNPR	0.536441254	2	3.37415
Q64458	IKEHKESLDVTNPR	0.642448483	3	5.17661
Q64458	LPPGPTPLPIIGNFLQIDVK	1.86937826	3	4.46102
Q64458	VQEEAQCLVEELR	2.103786734	2	4.22867
Q64458	VQEEAQCLVEELRK	2.023433933	2	3.69962
Q64464	**CP3AD Cytochrome P450 3A13**	**0.727204135**	**0.1334**	**2**
Q64464	ALLSPTFTSGR	1.06069056	2	2.70603
Q64464	LQDEIDAALPNK	0.684699938	2	2.53917
Q64550	**UD11 UDP_glucuronosyltransferase 1_1**	**1.136708863**	**6E-16**	**4**
Q64550	GHEVVVIAPEASIHIK	0.546329794	2	4.54839
Q64550	NMIIALTENFLCR	0.824186954	2	3.99684
Q64550	SVFDQDPFLLR	0.737370198	2	3.46312
Q64550	VVYSPYGSLATEILQK	0.657908028	3	4.38318
Q64560	**TPP2 Tripeptidyl_peptidase 2**	**0.882319627**	**0.0232**	**4**

Q64560	ACVDSNENGDLGK	0.716336323	2	2.66859
Q64560	DPVQVAAPSDHGVGIEPVFPENTENSEK	1.487647412	3	4.16925
Q64560	GTLIEAFPVLGGK	0.882302286	2	3.03531
Q64560	HEQISDLDR	1.251162522	2	2.36494
Q64563	**ADH4 Alcohol dehydrogenase 4**	**0.531624092**	**1E-19**	**13**
Q64563	AAVDCTVVGWGSCTVVGAK	0.398998426	2	2.83725
Q64563	ALFPVVLGHECAGIVESVGPGVTNFKPGDK	0.687001945	3	4.20972
Q64563	ALGATDCLNPR	0.504696492	2	3.32316
Q64563	DLDKPVQDVITELTGGGVDFSLDCAGTAQTLK	0.59496912	3	3.96249
Q64563	FDLDLLVTHALPFDK	0.88360911	2	3.9491
Q64563	INDAIDLMNQGK	0.675901744	2	3.80934
Q64563	KFDLDLLVTHALPFDK	0.423538549	3	5.11897
Q64563	SVDSVPNLVTDYK	0.422951719	2	3.699
Q64563	TDSPLCIEEIEVSPPK	0.548651626	2	4.00042
Q64563	VCLIGCGFTSGYGAAINTAK	0.648778838	2	4.41473
Q64563	VDDEANLER	0.534685639	2	2.61144
Q64563	VDEMNISTVDMILGR	0.594432371	2	3.65356
Q64563	VIATCVCPTDINATNPK	0.488706453	2	4.61527
Q64565	**AGT2 Alanine__glyoxylate aminotransferase 2_ mitochondrial**	**0.96174522**	**0.9988**	**11**
Q64565	AYSNHTDIISFR	0.993541202	2	2.88498
Q64565	GGVCIADEVQTGFGR	0.91392334	2	4.10384
Q64565	GIGNGFPMAAVVTTPEIASSLAK	0.921685089	2	4.28113
Q64565	HNMPPCDFSPEK	0.975063732	2	2.35069
Q64565	LRDEFDIVGDVR	1.08330028	2	2.44488
Q64565	LSALLPEPLK	1.194148096	2	3.19558
Q64565	SALTQHMER	1.018896907	2	2.66144
Q64565	SALTQHMER+Oxidation(6)	0.682420533	2	2.69212
Q64565	TEVNQIHEDCK	1.04458758	2	2.92372
Q64565	TEVNQIHEDCKDMGLLVGR	0.904677165	2	5.30421
Q64565	YIEQFK	0.934393546	1	2.03067
Q64578	**AT2A1 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1**	**1.026389971**	**0.9934**	**4**
Q64578	DIVPGDIVEVAVGDKVPADIR	1.0637976	2	3.05682
Q64578	IGIFSENEEVADR	1.133421891	2	2.79268
Q64578	VGEATETALTTLVEK	0.914198349	2	4.40429
Q64578	YGPNELPAEEGK	1.350362227	2	2.78259
Q64591	**DECR 2_4_dienoyl_CoA reductase_ mitochondrial**	**0.692036795**	**1E-19**	**8**
Q64591	ATAEEITSK	0.909729941	2	2.85052
Q64591	CDVRDPDMVHNTVLELIK	0.633784862	4	4.58439
Q64591	EEWDVIEGLIR	0.552674717	2	3.90097
Q64591	FNIIQPGPIK	0.733990058	2	2.75594
Q64591	NIDVLK	0.560405556	1	1.98223
Q64591	SLAAEWGR	0.683042213	2	2.64881
Q64591	VAGHPDVVINNAAGNFISPSER	0.887312189	2	6.15307
Q64591	VTKEEWDVIEGLIR	0.698710817	3	4.5253
Q64602	**AADAT Kynurenine/alpha_aminoadipate aminotransferase_ mitochondrial**	**0.969421753**	**0.9797**	**7**
Q64602	ASFSQVTPAQMDLVFQR	0.997056407	2	4.61395
Q64602	DIISLAPGSPNPK	1.025965282	2	3.0493
Q64602	EILLVPGNSFFVDNSAPSSFFR	0.888952754	3	3.50378
Q64602	FLYTIPNGNNPTGNSLTGDR	0.990733219	2	4.06963
Q64602	LHNPPTVNYSPNEGQMDLCITSGCQDGLCK	1.061567644	3	5.65472
Q64602	SAVFTVENGSTIR	0.938894046	2	3.25726
Q64602	VLSQWKPEDSKDPTKR	0.401769683	3	4.20015
Q64604	**PTPRF Receptor_type tyrosine_protein phosphatase F**	**0.759757694**	**0.0019**	**2**
Q64604	DHPPIPITDLADNIERLK	0.738302566	2	2.31108
Q64604	RADEARPNTIDFGK	0.765174709	2	2.36615
Q64611	**CSAD Cysteine sulfinic acid decarboxylase**	**1.077141779**	**1**	**11**

Q64611	AQGGQGLEWR	0.984196054	2	2.95097
Q64611	CHGSQASYLFQQDK	0.952985677	2	4.93477
Q64611	DVFGIVVDEAIR	1.041367082	2	3.26128
Q64611	FFNQLFSGLDPHALAGR	1.396791712	3	3.9409
Q64611	FYNVALDTGDK	0.928913674	2	2.87234
Q64611	GAAFLGLGTDSVR	1.091365632	2	3.10568
Q64611	IDQAFALTR	1.039877703	2	3.17386
Q64611	QLLDLELQSQGESR	0.916680851	2	4.21569
Q64611	TLDGDPVAVEALLR	1.022514035	2	4.51316
Q64611	VCEWKEPEELK	1.007813013	3	3.4601
Q64611	YLVEEIK	0.884524981	1	2.29215
Q64640	**ADK Adenosine kinase**	**1.052332721**	**1E-19**	**10**
Q64640	AADAHVDAHYYEQNEQPTGTCAACITGGNR	1.304739377	3	7.07768
Q64640	AATFFGCIGIDK	0.824970901	2	2.95619
Q64640	AGHYAASVIIR	1.209353238	2	2.87764
Q64640	FGEILK	1.192782271	2	2.33908
Q64640	HKELFDELVK	1.259692109	3	3.54821
Q64640	HLDLENNWMLVEK	1.144606565	2	3.32582
Q64640	SLVANLAAANCYK	1.197725084	2	4.68054
Q64640	VEYHAGGSTQNSMK	0.017292931	2	3.78348
Q64640	VEYHAGGSTQNSMK+Oxidation(12)	1.521613054	2	4.03429
Q64640	YSLKPNDQILAEDK	1.177473234	3	4.24766
Q64654	**CP51A Lanosterol 14_alpha demethylase**	**0.276186692**	**1E-19**	**5**
Q64654	EPAEDILQTLLDSTYK	0.511100237	2	3.14244
Q64654	GVAYDVPNAVFLEQK	0.457323711	2	3.27983
Q64654	NEDLNAEEVYGR	0.437245214	2	4.03508
Q64654	TVCGEDLPPLTYEQLK	0.26910774	2	4.14721
Q64654	YLQDNPASGEK	0.285945379	2	2.44868
Q64725	**KSYK Tyrosine_protein kinase SYK**	**0.916368177**	**0.6325**	**2**
Q64725	GMKGSEVTAMLEKGER+Oxidation(1)	0.916368177	2	2.41366
Q64725	GMKGSEVTAMLEKGER+Oxidation(9)	0.916368177	2	2.44539
Q65Z40	**WAPL Wings apart_like protein homolog**	**1.002111072**	**1**	**2**
Q65Z40	EKSISRIPEDNANK	1.002039763	2	2.47202
Q65Z40	LGQKRPNFKPDIQEIPK	1.007372121	2	2.84779
Q66H12	**NAGAB Alpha_N_acetylgalactosaminidase**	**0.86656948**	**0.3749**	**2**
Q66H12	INQDPLGIQGR	0.866317203	2	3.38079
Q66H12	TISPQNIDILQNPLLIK	0.869580527	2	2.46993
Q66H80	**COPD Coatomer subunit delta**	**0.972016823**	**0.9976**	**5**
Q66H80	GVQLQTHPNVDKK	0.911170913	2	3.54685
Q66H80	IEGLLAAFPK	1.083106446	2	2.42501
Q66H80	NSNILEDLETLR	0.997927326	2	3.34523
Q66H80	NTLEWCLPVIDAK	0.954616518	2	2.98865
Q66H80	VTQVDGNSPVR	1.203317477	2	2.90752
Q66HA8	**HS105 Heat shock protein 105 kDa**	**1.142125374**	**8E-06**	**6**
Q66HA8	AGGIETIANEFSDR	1.178047303	2	3.4842
Q66HA8	NQQITHANNTVSSFK	1.129734168	2	4.55478
Q66HA8	SVLDAAQIVGLNCLR	1.243553194	2	2.95345
Q66HA8	TEEVSAIEIVGGATR	0.801488957	2	2.91511
Q66HA8	VLGTAFDPFLGGK	1.025250309	2	3.07786
Q66HA8	YNHIDESEMKKVEK	1.00578274	2	2.32349
Q66HD0	**ENPL Endoplasmin**	**1.051310548**	**1E-19**	**22**
Q66HD0	DISTNYYASQK	0.845061279	2	3.08035
Q66HD0	EATEKEFEPLLNWMK	1.010529037	2	3.68222
Q66HD0	EEASDYLELDTIK	1.044782985	2	4.12642
Q66HD0	EEEAIQLDGLNASQIR	1.131235918	2	4.33877
Q66HD0	EVEEDEYK	0.915629999	1	2.54878
Q66HD0	FQSSHHSTDITSLDQYVER	1.112004795	2	5.87734

Q66HD0	GVVDSDDLPLNVSR	1.105828116	2	4.4227
Q66HD0	GYEVIYLTEPVDEYCIQALPEFDGKR	1.383107302	3	3.71086
Q66HD0	KEAESSPFVER	1.125183846	2	3.02475
Q66HD0	LGVIEDHSNR	1.127648283	2	2.86495
Q66HD0	LISLTDENALAGNEELTVK	1.404324854	2	4.98911
Q66HD0	LTESPCALVASQYGWSGNMER	1.133778514	2	5.47744
Q66HD0	NLLHVTDTGVGMTR	1.131506341	2	3.45042
Q66HD0	NLLHVTDTGVGMTR+Oxidation(11)	0.934617603	2	3.22203
Q66HD0	SGTSEFLNK	1.135665043	2	3.14956
Q66HD0	SGYLLPDTK	1.065531351	2	3.22208
Q66HD0	SILFVPTSAPR	1.042531872	2	3.48098
Q66HD0	TDDEVVQR	1.30383285	2	3.2864
Q66HD0	TDDEVVQREEEAIQLDGLNASQIR	0.995550588	3	4.96581
Q66HD0	TVWDWELMNDIKPIWQRPSK	1.208661136	3	3.44037
Q66HD0	VFITDDFHDMMPK	1.000470503	2	2.75423
Q66HD0	YNDTFWK	0.994850386	1	2.13521
Q66HF1	**NDUS1 NADH_ubiquinone oxidoreductase 75 kDa subunit_ mitochondrial**	**1.010767001**	**0.0004**	**10**
Q66HF1	ALSEIAGITLPYDTLDQVR	1.004588939	2	4.92581
Q66HF1	DDGAAILAAVSSIAQK	1.006281693	2	4.88352
Q66HF1	FASEIAGVDDLGTTGR	1.237815482	2	4.18272
Q66HF1	GLLTYTSWEDALSR	1.059113546	2	3.8635
Q66HF1	ILQDIASGNHEFSK	1.172165423	2	3.80436
Q66HF1	LGEVSPNLVR	1.243956189	2	2.58907
Q66HF1	LVDQEFLADPLVPPQLTIK	1.072079674	3	3.58954
Q66HF1	SATYVNTEGR	1.044917623	2	2.34487
Q66HF1	VDSDTLCTEEIFPNEGAGTDLR	1.208717337	2	4.0963
Q66HF1	YDHLGDSPK	1.127980371	2	2.33414
Q66HF8	**AL1B1 Aldehyde dehydrogenase X_ mitochondrial**	**1.535793479**	**1E-19**	**10**
Q66HF8	EAGFPPGVVNIITGYGPTAGAAIAQHMDVDK	1.630302325	3	3.30618
Q66HF8	EEIFGPVQPLFK	0.860384097	2	2.98464
Q66HF8	KTFPTVNPTTGEVIGHVAEGDR	1.856382001	3	4.18721
Q66HF8	KVGNPFELDTQQGPQVDKEQFEK	1.540473377	3	3.37276
Q66HF8	TFPTVNPTTGEVIGHVAEGDR	1.900118958	2	4.38989
Q66HF8	TFVEESIYHEFLER	1.547860379	2	3.87797
Q66HF8	VAEQTPLSALYLASLIK	2.315330795	2	3.06982
Q66HF8	VAFTGSTEVGHLIQK	2.378179337	2	3.01021
Q66HF8	VGNPFELDTQQGPQVDKEQFEK	1.356006838	2	4.423
Q66HF8	YGLAAAVFTR	1.099768702	2	2.67892
Q66HG4	**GALM Aldose 1_epimerase**	**0.716840137**	**1E-19**	**3**
Q66HG4	ASDVVLGFAELEGYLQK	0.723914148	2	3.56574
Q66HG4	TVFGELPSGGGAVEK	0.745590368	2	3.63367
Q66HG4	VSPDGEEGYPGELK	0.706491	2	3.71394
Q66HG9	**MAVS Mitochondrial antiviral_signaling protein**	**1.043898031**	**0.5127**	**2**
Q66HG9	ICELPGLAEQVTR	1.01880118	2	2.6565
Q66HG9	STAATPSTVPTNIAPSK	1.090313791	2	2.38438
Q66X93	**SND1 Staphylococcal nuclease domain_containing protein 1**	**1.089659499**	**9E-09**	**18**
Q66X93	ALLLPDHYLVTVMLSGIK	1.019900935	3	3.84643
Q66X93	DIQNTQCLLNVEHLSASCPHVTLQFADSK	1.063421339	3	5.45938
Q66X93	DTNGENIAESLVAEGLASR	1.017121706	2	5.08052
Q66X93	DVQIILESCHNQNILGTILHPNGNITELLLK	1.100550014	3	6.25671
Q66X93	ETDGSETPEPFAAEAK	1.209092677	2	3.47693
Q66X93	GDVGLGLVK	1.096140112	2	2.47306
Q66X93	LEGDNIQDK	1.114310378	2	2.60373
Q66X93	NLPGLVQEGEPFSEEATLFTK	1.50217067	2	5.63891
Q66X93	SAYYKPLLSAEEAAK	1.059584317	2	3.11932
Q66X93	SDISSHPPVEGAYAPR	1.072599346	3	4.06537

Q66X93	SEAVVEYVFSGSR	1.12952522	2	2.61583
Q66X93	SSHYDELLAAEAR	1.05369727	2	3.61264
Q66X93	TCATVTIGGINIAEALVSK	0.990778404	2	3.91251
Q66X93	TDAVDSVVR	1.072809073	2	2.51206
Q66X93	VADISGDTQK	1.055069547	2	2.4124
Q66X93	VITEYLNAQESAK	1.345016476	2	4.20499
Q66X93	VSVTVDYIRPASPATETVPAFSER	1.112537053	3	4.6836
Q66X93	VWAHYEEQPVEEVMPVLEEK	0.983740082	3	3.82219
Q68FP2	**PON3 Serum paraoxonase/lactonase 3**	**0.825072991**	**7E-16**	**8**
Q68FP2	EIKPTEPQNCHLIEGLENGSEDIDILPSGLAFISTGLK	1.237759535	3	4.45309
Q68FP2	HELFESVNDIVVLGPEQFYATR	1.095160076	3	3.34134
Q68FP2	HNNWDLTPVK	0.824691154	2	3.00581
Q68FP2	IFLMDLNEPYPK	1.017032612	2	2.82245
Q68FP2	IQDPLSDNPR	0.91532356	2	2.8887
Q68FP2	LLIYNPEDPPGSEVLR	1.097292583	2	3.91172
Q68FP2	VVAQGFSSANGITVSLDQK	0.627538836	2	3.56188
Q68FP2	YVYVADVTAK	0.837539864	1	2.96802
Q68FQ0	**TCPE T_complex protein 1 subunit epsilon**	**0.994571556**	**1**	**3**
Q68FQ0	HKLDVTSVEDYK	0.992615122	2	3.56082
Q68FQ0	ISDNVLVDINNPEPLIQTAK	1.032176033	2	5.37216
Q68FQ0	WVGGPEIELIAIATGGR	1.029740616	2	3.52353
Q68FR6	**EF1G Elongation factor 1_gamma**	**0.95177634**	**4E-09**	**6**
Q68FR6	AAAPAPEEEMDECEQALAAEPK	1.095141908	2	5.32889
Q68FR6	ALIAAQYSGAQIR	1.198437277	2	3.82993
Q68FR6	GQDLAFPLSPDWQVDYESYTWR	1.628139309	2	3.98325
Q68FR6	KAAAPAPEEEMDECEQALAAEPK	1.015370828	3	3.74121
Q68FR6	KLDPGSEETQTLVR	0.91753571	2	4.24968
Q68FR6	LDPGSEETQTLVR	1.305154147	2	3.32643
Q68FR9	**EF1D Elongation factor 1_delta**	**1.065160002**	**0.9983**	**6**
Q68FR9	ATAPQTQHVSPMR	0.90518227	2	3.25445
Q68FR9	FYEQMNGPVTAGSR	1.018212436	2	4.04438
Q68FR9	GVVQDLQQAISK	1.033700587	2	3.94137
Q68FR9	SIQLDGLVWGASK	1.033459845	2	3.06955
Q68FR9	SLAGSSGPGASSGPGGDHSDLIVR	1.006359657	2	5.43173
Q68FR9	VGTDLLEEEITK	1.169584165	2	3.06004
Q68FS2	**CSN4 COP9 signalosome complex subunit 4**	**0.961966678**	**0.9985**	**2**
Q68FS2	NAAQVLVGIPLETGQK	1.10039673	2	3.09318
Q68FS2	QDLAQLMNSSGSHK	0.958268866	2	2.85077
Q68FS4	**AMPL Cytosol aminopeptidase**	**1.074689969**	**0.014**	**19**
Q68FS4	ADMGGAATICSAIVSAAK	1.056177183	2	4.93695
Q68FS4	ADMGGAATICSAIVSAAK+Oxidation(2)	0.985122812	2	4.23116
Q68FS4	DKDDDVPQFTSAGENFNK	1.081678986	2	4.221
Q68FS4	GITFDSGGISIK	0.991202666	2	2.78281
Q68FS4	GLVLGIYSK	1.017223476	1	2.07524
Q68FS4	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	1.164978393	3	6.03729
Q68FS4	GVLFASGQNLAR	1.078324553	2	3.06796
Q68FS4	LFEASVETGDR	1.09273186	2	2.7428
Q68FS4	LHGSGDLEAWEK	1.074381579	2	2.80802
Q68FS4	LNLPINIIGLAPLCENMPSGK	1.375399193	2	4.5735
Q68FS4	QLMESPANEMTPTR	0.995948384	2	3.88785
Q68FS4	QVIDCQLADVNNLGK	0.992269993	2	4.65348
Q68FS4	SAGACTAAAFLR	1.146261608	2	3.38734
Q68FS4	SAGVDDQENWHEGK	1.104464959	2	3.81368
Q68FS4	SAGVDDQENWHEGKENIR	1.019529805	3	3.41094
Q68FS4	SWIEEQEMGSFLSVAK	1.059474234	2	5.25653
Q68FS4	TFYGLHQDFPSVVVVGLGK	1.146845458	2	4.16792
Q68FS4	TIQVDNTDAEGR	1.023275315	2	3.8174

Q68FS4	TLIEFLLR	1.268057625	2	2.63057
Q68FT1	**COQ9 Ubiquinone biosynthesis protein COQ9_ mitochondrial**	**0.948246437**	**0.9198**	**3**
Q68FT1	LNHVLEEEQK	0.935654902	2	3.19416
Q68FT1	STGEALVQGLMGAAVTLK	0.9715715	2	3.25109
Q68FT1	YTDQSGEEEEDYESEEQIQHR	0.94888476	3	4.99451
Q68FT3	**PYRD2 Pyridine nucleotide_disulfide oxidoreductase domain_containing protein 2**	**0.830450443**	**0.002**	**6**
Q68FT3	ISQLDTQSPVTK	0.654055419	2	3.36576
Q68FT3	SLLLGTDVAENQK	0.685603539	2	3.49195
Q68FT3	TLGAQLPQYYEVLTAPISK	0.574004254	2	3.9835
Q68FT3	VFDCIEAYAPGFK	0.870088827	2	2.46249
Q68FT3	VLDQWFESEPLK	0.862928953	2	3.10449
Q68FT3	VQGVVLQGGEEVR	0.576009952	2	3.37119
Q68FT5	**BHMT2 Betaine__homocysteine S_methyltransferase 2**	**1.390386411**	**1E-19**	**10**
Q68FT5	AGANIIGVNCR	1.260039986	2	3.7503
Q68FT5	AGLWTPEAVVEYPSAVR	1.32995216	2	4.48058
Q68FT5	AIAEELAPER	1.613030998	2	3.70167
Q68FT5	DAGLQAHLMVQCLGFHTPDCGK	1.184589567	3	4.23602
Q68FT5	EVGAPVAVTMCIGPEGDMHGVTPGECAVR	1.166729409	3	3.51477
Q68FT5	FGPWTSLQTMK	1.194465354	2	2.38989
Q68FT5	GFLPPASEK	2.067699105	1	1.90661
Q68FT5	GGFVDLPEYPFGLEPR	1.237751378	2	4.27889
Q68FT5	LDSGEVVVGDGGFLFTLEK	1.20460441	2	2.94522
Q68FT5	YIGGCCGFEPYHIR	3.209213219	2	4.42087
Q68FT9	**SCLY Selenocysteine lyase**	**0.715945658**	**1E-19**	**4**
Q68FT9	AEVDLIVQDLK	0.714809228	2	3.6156
Q68FT9	CFHEQQTLQGR	0.785541702	2	2.59543
Q68FT9	RVDVEDLGVDFLTIVGHK	0.950710398	3	5.67652
Q68FT9	VLVHTDAAQALGK	0.806197043	2	2.85484
Q68FU3	**ETFB Electron transfer flavoprotein subunit beta**	**0.9412602**	**3E-09**	**8**
Q68FU3	AGDLGVDLTSK	0.9447635	2	3.81668
Q68FU3	EIIAVSCGPPQCQETIR	0.896281764	2	4.80398
Q68FU3	GIHVEVPGAEAENLGPLQVAR	1.078830323	2	5.86638
Q68FU3	HSMNPFCEIAVEEAVR	1.13501555	2	4.73933
Q68FU3	HSMNPFCEIAVEEAVR+Oxidation(2)	0.939749875	2	4.38278
Q68FU3	VDLLFLGK	1.007295285	2	2.80374
Q68FU3	VETTEDLVAK	0.84024181	2	3.27835
Q68FU3	VSVISVEEPPQR	0.962805026	2	3.44097
Q68FY0	**QCR1 Cytochrome b_c1 complex subunit 1_ mitochondrial**	**1.000573616**	**0.0001**	**11**
Q68FY0	EMQENDASMQNVVFDYLHATAFQGTPLAQAVEGPSENVR	1.323149616	3	4.4138
Q68FY0	EVESIGAHLNAYSTR	0.971732256	2	3.12697
Q68FY0	HQQLLDLAQDHFSSVSQVYEEDAVPSITPCR	1.078451746	3	5.21156
Q68FY0	IEEVDAQMVR	0.999519197	2	3.66264
Q68FY0	LCTSATESEVTR	1.293906858	2	2.98398
Q68FY0	NALISHLDGTTPVCEDIGR	0.98753382	2	4.193
Q68FY0	NNGAGYFLEHLAFK	1.173907031	2	3.48745
Q68FY0	RIPLAEWESR	1.102610897	2	2.59403
Q68FY0	TDLTDYLSR	0.985378858	2	2.65771
Q68FY0	VVELLADIVQNISLEDSQIEK	0.992575868	3	5.97771
Q68FY0	YFYDQCPAVAGYGPIEQLSDYNR	1.085805176	3	5.09761
Q68G31	**PBLD Phenazine biosynthesis_like domain_containing protein**	**0.904235994**	**0.0363**	**7**
Q68G31	AAIGDTTVQDIQYSPDTR	0.80265949	2	4.44032
Q68G31	AEDGIVLDFPLYPTFPQDFHEVK	0.906380481	3	3.64173
Q68G31	GESGGQTTPYDFYSR	1.115706497	2	3.9154
Q68G31	LQPTDSFSQSSCFGLR	1.007646264	2	3.26736
Q68G31	NVNSTLTFVTLSGELK	0.909290468	2	3.97203
Q68G31	RAEDGIVLDFPLYPTFPQDFHEVK	0.925130905	3	4.92885

Q68G31	VNTEPLPGIEK	0.920085233	2	2.95572
Q69Z66	**MYSM1 Histone H2A deubiquitinase MYSM1**	**0.91086155**	**0.9739**	**3**
Q69Z66	KYTNSLQK	0.849454725	1	1.98369
Q69Z66	NSAELNEK	1.030479643	1	1.95088
Q69Z66	QTKTPERYLK	1.077082994	2	2.30858
Q6A000	**K0753 Uncharacterized protein KIAA0753**	**1.027567632**	**0.5046**	**2**
Q6A000	EIQEELDKLSPQK	0.927668594	2	2.35546
Q6A000	ILGSETSARLGDSK	1.044051987	2	2.55159
Q6A0A9	**F120A Constitutive coactivator of PPAR_gamma_like protein 1**	**1.024628043**	**0.232**	**2**
Q6A0A9	SQGGVQPIPSQGGK	1.245683918	2	2.66582
Q6A0A9	VEGSSTASSGSQLAEGK	1.016132031	2	4.21785
Q6AXM8	**PON2 Serum paraoxonase/arylesterase 2**	**0.835523221**	**0.4083**	**2**
Q6AXM8	FQEEENSLLHLK	1.037668291	2	2.57851
Q6AXM8	LFVYDPNHPPSSEVLR	0.835307774	2	2.30048
Q6AXS5	**PAIRB Plasminogen activator inhibitor 1 RNA_binding protein**	**0.856181659**	**0.0021**	**2**
Q6AXS5	FDQLFDDESDPFEVLK	0.834864488	2	4.72208
Q6AXS5	SAAQAAAQTNSNAAGK	1.273885387	2	4.59404
Q6AXY0	**GSTA6 Glutathione S_transferase A6**	**0.728486566**	**5E-07**	**2**
Q6AXY0	FLQPGSQR	0.879194614	2	2.45229
Q6AXY0	YFPAFEK	0.712287346	1	1.99458
Q6AY09	**HNRH2 Heterogeneous nuclear ribonucleoprotein H2**	**0.965338834**	**0.5268**	**3**
Q6AY09	ATENDIYNFFSPLNPMR	0.982765841	2	2.52228
Q6AY09	HTGPNSPDTANDGFVR	0.983069701	2	4.61125
Q6AY09	STGEAFVQFASQEIAEK	0.787408243	2	3.94314
Q6AY30	**SCPDH Probable saccharopine dehydrogenase**	**0.886561712**	**0.0089**	**4**
Q6AY30	ACIENGTSCIDICGEPQFLELMHVK	0.983854809	3	3.82857
Q6AY30	GVYIIGSSGFDSIPADLGVLYTR	1.225037681	2	3.90887
Q6AY30	LQQVLEK	0.831434056	1	1.9821
Q6AY30	SVSNLKPVPVIGSK	0.866506848	2	3.21064
Q6AY56	**TBA8 Tubulin alpha_8 chain**	**1.049963249**	**0.0195**	**7**
Q6AY56	AVCMLSNTTAIAEAWAR	0.969165818	2	4.09488
Q6AY56	FDGALNVDLTEFQTNLVPYPR	1.012089496	2	5.40133
Q6AY56	LISQIVSSITASLR	1.111321161	2	3.31975
Q6AY56	NLDIERPTYTNLNR	1.034903704	2	3.09734
Q6AY56	QLFHPEQLITGK	1.041950635	2	2.35307
Q6AY56	TIQFVDWCPTGFK	1.085011782	2	3.72154
Q6AY56	VGINYQPPTVVPGGDLAK	0.972557605	2	4.90402
Q6AY80	**NQO2 Ribosyldihydronicotinamide dehydrogenase [quinone]**	**1.18090495**	**0.5686**	**2**
Q6AY80	NDVTGALSNPEVFK	0.997513935	2	3.46657
Q6AY80	VLAPQISFGPEVSSEEQR	1.387073181	2	3.7164
Q6AYG5	**ECHD1 Enoyl_CoA hydratase domain_containing protein 1**	**0.679000676**	**2E-05**	**2**
Q6AYG5	DVLETLWGGPANLEAIAK	0.710431237	2	3.74149
Q6AYG5	ILEQFPGGSIDLQK	0.686153696	2	3.06805
Q6AYQ8	**FAHD1 Acylpyruvase FAHD1_ mitochondrial**	**0.90605421**	**0.0334**	**3**
Q6AYQ8	IITLEEGDLILTGTPK	0.896490019	2	3.71954
Q6AYQ8	NLHHEVELGVLLGR	0.930707634	3	4.70335
Q6AYQ8	SFTSSCPVSAFVPK	0.915957363	2	3.87519
Q6AYS8	**DHB11 Estradiol 17_beta_dehydrogenase 11**	**0.989880049**	**0.1301**	**3**
Q6AYS8	ALTDELAALGCTGVR	0.920990298	2	3.5769
Q6AYS8	FDAVVGYK	0.603640101	1	2.09792
Q6AYS8	SVAGEIVLITGAGHGIGR	1.081267844	2	3.34668
Q6AYT9	**ACSM5 Acyl_coenzyme A synthetase ACSM5_ mitochondrial**	**0.715046736**	**0.5538**	**2**
Q6AYT9	ASPPYDVQIVDEEGNVLPPGK	0.753578562	2	3.12929
Q6AYT9	NDDVINSSSYR	0.680967143	2	3.37767
Q6AYZ1	**TBA1C Tubulin alpha_1C chain**	**1.111498845**	**1E-19**	**5**
Q6AYZ1	AVFVDLEPTVIDEVR	1.066856139	2	5.31807
Q6AYZ1	DVNAAIATIK	1.036164501	2	3.21186

Q6AYZ1	IHFPLATYAPVISAEK	1.032995721	2	3.04958
Q6AYZ1	TIGGGDDSFNTFFSETGAGK	1.250464547	2	5.43011
Q6AYZ1	VGINYQPPTVVPGGDLAR	1.206930248	2	4.59305
Q6DGG1	**ABHEB Abhydrolase domain_containing protein 14B**	**0.913868552**	**1E-09**	**7**
Q6DGG1	AVAIDLPGLGR	0.896767525	2	3.33265
Q6DGG1	FSSETWQNLGTLHR	0.962342458	2	3.52961
Q6DGG1	FSVLLLHGIR	1.075711718	2	2.80667
Q6DGG1	GYVPVAPICTDK	0.87533744	2	3.0102
Q6DGG1	INAADYAR	0.96518196	2	2.37239
Q6DGG1	TPTLIVYGDQDPMGSSSFQHLK	1.182561165	3	5.22736
Q6DGG1	VLVMEGAGHPCYLDKPDEWHTGLLDFLQELA	1.237128835	3	3.58092
Q6EDY6	**LR16A Leucine_rich repeat_containing protein 16A**	**1.048702696**	**0.3106**	**3**
Q6EDY6	ELMESIK+Oxidation(2)	1.068443924	1	1.95034
Q6EDY6	IENYLLR	1.020521477	2	2.57294
Q6EDY6	SSDAHELGEGDEKKK	0.829332938	2	2.43231
Q6GQP4	**RAB31 Ras_related protein Rab_31**	**1.063550261**	**0.7629**	**2**
Q6GQP4	CDLSDIREVPLK	1.074854224	2	2.54403
Q6GQP4	CDLSDIREVPLKDAK	0.901194189	2	2.63013
Q6IE52	**MUG2 Murinoglobulin_2**	**0.976063815**	**0.983**	**15**
Q6IE52	AHFSVMGDILSSAIK	1.014703754	2	3.28282
Q6IE52	GDPIPNEQVFIK	0.657917696	2	2.43829
Q6IE52	HGIPFFVK	1.302510553	2	2.54525
Q6IE52	HTSSWLVTPK	1.041344225	2	2.58389
Q6IE52	LPSSEEEESLDINIEGAK	1.12471078	2	4.96468
Q6IE52	MLIYTILPDGEVIADSVK	0.960673386	2	4.17554
Q6IE52	MLIYTILPDGEVIADSVK+Oxidation(0)	0.945855046	2	3.31502
Q6IE52	MLSGFIPLKPTVK+Oxidation(0)	0.879529541	2	2.5876
Q6IE52	NLYPLKELVQDPK	0.869618817	1	1.91046
Q6IE52	QLSFSLSAEPIQGPYK	1.022327464	2	4.06407
Q6IE52	VKTVPLTCNNPK	0.931346865	2	3.02871
Q6IE52	VLIVEPEGIKK	0.880094814	2	2.40573
Q6IE52	VTASPQSLCGLR	1.228468149	2	2.57167
Q6IE52	YMVLVPSQLYTETPEK	1.082040061	2	3.81036
Q6IE52	YMVLVPSQLYTETPEK+Oxidation(1)	0.997268102	2	3.26145
Q6IMF3	**K2C1 Keratin_ type II cytoskeletal 1**	**0.766709815**	**1E-14**	**3**
Q6IMF3	TNAENEFVTIK	1.102756208	2	2.50218
Q6IMF3	WELLQQVDTSTR	0.792532394	2	3.49627
Q6IMF3	YEELQITAGK	0.853448934	2	3.32366
Q6IRK9	**PGCP Plasma glutamate carboxypeptidase**	**0.866734079**	**0.0637**	**2**
Q6IRK9	AIQIMYQNLQQDGLENVHLEQVR	0.893806116	3	5.17048
Q6IRK9	TYPDTDSFNTVAEITGSK	0.865498826	2	4.38045
Q6MGB5	**DHB8 Estradiol 17_beta_dehydrogenase 8**	**0.908649901**	**0.0216**	**3**
Q6MGB5	AGVIGLTQTAAR	0.883044257	2	3.4823
Q6MGB5	GSIINISSIVGK	0.954452075	2	2.47966
Q6MGB5	SALALVTGAGSGIGR	0.834087455	2	2.6422
Q6NYB7	**RAB1A Ras_related protein Rab_1A**	**1.044447848**	**0.6709**	**4**
Q6NYB7	EFADSLGIPFLETSAK	0.966676778	2	3.45207
Q6NYB7	MGPGATAGGAEK+Oxidation(0)	0.872946849	2	2.38115
Q6NYB7	NATNVEQSFMTMAAEIK	1.027397157	2	4.22324
Q6NYB7	RMGPGATAGGAEKSNVK	1.200136812	2	2.50414
Q6NZJ6	**IF4G1 Eukaryotic translation initiation factor 4 gamma 1**	**1.195681987**	**0.0043**	**7**
Q6NZJ6	GLPLVDDGGWNTVPISK	1.112939336	2	2.76246
Q6NZJ6	GSSGGSGAKPSDTASEATRPATLNR	1.074304856	3	3.36027
Q6NZJ6	IHNAENIQPGEQK	1.005000991	2	4.33098
Q6NZJ6	ITKPGSIDSNNQLFAPGGR	1.265338695	3	3.56328
Q6NZJ6	LKEELEEAR	1.247418953	2	2.53077
Q6NZJ6	QVTQLAIDTEER	1.055520278	2	3.24107

Q6NZJ6	TASTPTPPQTGGSLEPQPNGESPQVAVIIRPDDR	0.982212357	3	4.13048
Q6P502	**TCPG T_complex protein 1 subunit gamma**	**1.181691758**	**3E-15**	**6**
Q6P502	AVAQALEVIPR	1.01332864	2	2.51775
Q6P502	KGESQTDIEITR	1.166949918	2	2.41945
Q6P502	NLQDAMQVCR	1.188119332	2	2.9822
Q6P502	TAVETAVLLLR	1.237741493	2	3.39825
Q6P502	TLIQNCGASTIR	1.090727227	2	2.8703
Q6P502	WSSLACNIALDAVK	1.197952386	2	3.49202
Q6P6R2	**DLDH Dihydrolipoyl dehydrogenase_ mitochondrial**	**0.958924979**	**9E-13**	**9**
Q6P6R2	IDVSVEAASGGK	0.856510301	2	3.5843
Q6P6R2	ILGAHILGPGAGEMVNEAALALEYGASCEDVAR	1.490133402	3	3.38248
Q6P6R2	NETLGGTCLNVGCIPSK	0.883296594	2	5.13078
Q6P6R2	NQVTATTADGSTQVIGTK	0.897318515	2	5.75596
Q6P6R2	RPFTQNLGLEELGIELDPK	1.234090619	3	4.76678
Q6P6R2	SEEQLKEEGVEFK	0.849406458	3	3.82415
Q6P6R2	TNADTDGMVK	0.901201769	2	2.60184
Q6P6R2	TNADTDGMVK+Oxidation(7)	1.109779645	2	2.79798
Q6P6R2	VCHAHPTLSEAFR	0.956009766	3	3.43788
Q6P6S9	**ENTP5 Ectonucleoside triphosphate diphosphohydrolase 5**	**0.857308266**	**0.0966**	**6**
Q6P6S9	AAETHLIDYEK	1.057366809	2	2.33201
Q6P6S9	AQTLLLEVEEIFK	0.79438067	2	3.06565
Q6P6S9	GQETVGTLDLGGASTQITFLPQLEK	0.76923148	2	4.31555
Q6P6S9	QGAETVQELLEVAK	0.868931688	2	3.17528
Q6P6S9	TSGQLPFLEGEIFDSVKPGLSAFVDQPK	0.849496848	3	3.49878
Q6P6S9	WLEAEWIFGGVK	0.745543848	2	2.481
Q6P6V0	**G6PI Glucose_6_phosphate isomerase**	**1.073549412**	**3E-07**	**7**
Q6P6V0	DVMPEVNKVLDK+Oxidation(2)	0.905819394	2	2.71557
Q6P6V0	HFVALSTNTDK	1.236434563	2	2.64157
Q6P6V0	KIEPELDGSSAVTSHDSSTNGLIGFIK	1.062160637	3	5.27914
Q6P6V0	TFTTQETITNAETAK	1.194656377	2	4.74233
Q6P6V0	TLANLNPESSLFIIASK	1.140140126	3	4.63954
Q6P6V0	VFEGNRPTNSIVFTK	1.04348943	2	2.97378
Q6P6V0	VWFVSNIDGTHIAK	1.043971063	2	3.65567
Q6P7Q4	**LGUL Lactoylglutathione lyase**	**1.064310214**	**0.8811**	**3**
Q6P7Q4	DFLLQQTMLR	1.282086748	2	3.11342
Q6P7Q4	GLAFVQDPDGYWIEILNPNK	1.046650611	2	5.51717
Q6P7Q4	RFEELGVK	1.096725482	2	2.49651
Q6P7R8	**DHB12 Estradiol 17_beta_dehydrogenase 12**	**1.127253635**	**0.3099**	**2**
Q6P7R8	GIFVQSVLPFFVATK	1.423423623	2	2.79988
Q6P7R8	LGEWAVVTGGTDGIGK	1.130357747	2	3.53235
Q6P9T8	**TBB2C Tubulin beta_2C chain**	**1.070789001**	**5E-08**	**11**
Q6P9T8	AVLVDLEPGTMDSVR	1.080148853	2	3.05749
Q6P9T8	AVLVDLEPGTMDSVR+Oxidation(10)	1.063020873	2	3.90781
Q6P9T8	EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.079724375	3	5.46732
Q6P9T8	EIVHLQAGQCGNQIGAK	0.93027656	2	5.06257
Q6P9T8	EVDEQMLNVQNK	0.989607278	2	4.34698
Q6P9T8	FWEVISDEHGIDPTGTYHGDSDLQLER	1.226804524	3	4.32235
Q6P9T8	INVYYNEATGGK	1.209048948	2	3.07058
Q6P9T8	KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK	1.108361852	3	6.14839
Q6P9T8	MSATFIGNSTAIQELFK	1.196071666	2	4.05878
Q6P9T8	TAVCDIPPR	1.123322239	2	2.59536
Q6P9T8	YLTVAAVFR	1.283989667	2	2.39762
Q6P9U8	**EIF3H Eukaryotic translation initiation factor 3 subunit H**	**0.831439373**	**5E-07**	**2**
Q6P9U8	ANITFEHMFEEVPIVIK	0.986153699	3	3.43386
Q6P9U8	EGTGSTATSSSSTGGAVGK	0.829619124	2	4.24961
Q6PA06	**ATLA2 Atlastin_2**	**1.135315035**	**0.1827**	**2**
Q6PA06	NLVPLLLAPENLVEK	1.130988549	2	3.07585

Q6PA06	QNQHEELQNVR	1.144197826	2	2.74013
Q6PEC1	**TBCA Tubulin_specific chaperone A**	**1.5100007**	**0.0771**	**3**
Q6PEC1	LEAAYTDLR	1.08847523	2	2.86263
Q6PEC1	QAEILQESR	1.255559387	2	2.84812
Q6PEC1	RLEAAYTDLR	1.092512652	2	2.36175
Q6PEC4	**SKP1 S_phase kinase_associated protein 1**	**0.91884852**	**0.8941**	**4**
Q6PEC4	NDFTEEEEAQVR	1.028383675	2	3.24999
Q6PEC4	RTDDIPVWDQEFLK	0.876880078	2	2.37591
Q6PEC4	TDDIPVWDQEFLK	1.027209922	2	2.53283
Q6PEC4	TVANMIKGKTPEEIR+Oxidation(4)	1.086325903	2	2.32726
Q6Q0N1	**CNDP2 Cytosolic non_specific dipeptidase**	**1.087829614**	**0.013**	**4**
Q6Q0N1	EGGSIPVTLTFQEATGK	1.158729243	2	2.67347
Q6Q0N1	LGGSVELVDIGK	0.808052074	2	2.94109
Q6Q0N1	MTEAAAADVQR	1.095746216	2	2.57604
Q6Q0N1	TVFGVEPDLTR	1.00077791	2	2.46437
Q6TUG0	**DJB11 DnaJ homolog subfamily B member 11**	**1.275378916**	**2E-15**	**4**
Q6TUG0	FQDLGAAYEVLSDSEK	1.241215482	2	4.79879
Q6TUG0	FQMTQEVVCDECPNVK	1.438453427	2	4.66228
Q6TUG0	KGEGLPNFDNNNIK	1.217925183	2	2.88369
Q6TUG0	TLEVEIEPGVR	1.153397658	2	2.3814
Q6UPE1	**ETFD Electron transfer flavoprotein_ubiquinone oxidoreductase_ mitochondrial**	**0.925417448**	**7E-16**	**13**
Q6UPE1	AAQIGAHTLSGACLDPAAFK	1.244000481	2	4.28078
Q6UPE1	ALNEGGLQSIPK	0.974124986	2	3.16741
Q6UPE1	ASCDAQTYGIGLK	1.010408062	2	3.47742
Q6UPE1	FCPAGVYEFVPLEQGDGFR	0.867184679	2	4.81853
Q6UPE1	GAPLNTPVTEDR	0.947610209	2	3.38125
Q6UPE1	GIATNDVGIQK	0.904241536	2	3.19397
Q6UPE1	LQINAQNCVHCK	0.996610377	2	3.18893
Q6UPE1	NLSIYDGPEQR	0.917741009	2	3.0424
Q6UPE1	QLTSENLQSK	0.934934392	2	2.59144
Q6UPE1	SGSLAAEAIFK	0.898502837	2	3.3202
Q6UPE1	TAGLHVTEYEDNLK	0.765174709	2	3.14144
Q6UPE1	TCDIKDPSQNINWVVPEGGGGPAYNGM	0.916278085	2	3.76191
Q6UPE1	VTIFAEGCHGHLAK	0.757414815	2	3.18493
Q6URK4	**ROA3 Heterogeneous nuclear ribonucleoprotein A3**	**0.936833423**	**6E-11**	**7**
Q6URK4	EDSVKPGAHLTVK	0.716967206	2	3.45955
Q6URK4	GFAFVTFDDHDTVDK	1.001141281	2	3.8424
Q6URK4	IETIEVMEDR	0.9391752	2	3.40297
Q6URK4	IFVGGIKEDTEEYNLR	1.242104664	3	3.36361
Q6URK4	SSGSPYGGGYGSGGGSGGYGSR	1.044665217	2	5.10676
Q6URK4	WGTLTDCVVMR	0.866153448	2	2.9328
Q6URK4	YHTINGHNCEVK	1.476049648	2	3.54013
Q6URW6	**MYH14 Myosin_14**	**0.972661175**	**0.9843**	**4**
Q6URW6	EDQSILCTGESGAGK	0.960146475	2	3.94093
Q6URW6	FDQLLAEEK	0.964677832	2	2.51015
Q6URW6	KFDQLLAEEK	1.038092639	2	2.8865
Q6URW6	QLLQANPILEAFGNAK	0.959228439	2	4.355
Q6VGS5	**DAPLE Protein Daple**	**1.119437591**	**0.4748**	**2**
Q6VGS5	ELKTSLNNSQLELSR	1.138083089	2	2.30233
Q6VGS5	YGELEKENQQLSKK	1.023467252	2	2.32462
Q6XQN1	**PNCB Nicotinate phosphoribosyltransferase**	**0.813702023**	**0.992**	**4**
Q6XQN1	GSEVNVIGIGTNVVTCPK	0.778890154	2	4.09035
Q6XQN1	LDSGDLLQQAK	0.922965811	2	2.7833
Q6XQN1	LYLQQGQPYEPLPSLEESR	0.844631229	2	4.5337
Q6XQN1	QLQNPAVYQVALSEK	0.823298591	2	3.48442
Q6ZPF3	**TIAM2 T_lymphoma invasion and metastasis_inducing protein 2**	**1.103353584**	**0.3074**	**2**

Q6ZPF3	KMAELQLSVVSDPK+Oxidation(1)	1.255640666	2	2.30212
Q6ZPF3	STELEKDAQEGLAEFPDGLIK	1.100963905	2	2.40852
Q6ZPJ3	**UBE2O Ubiquitin_conjugating enzyme E2 O**	**1.086124544**	**0.7381**	**3**
Q6ZPJ3	FLDDIKKLQENLK	1.029897179	2	2.38437
Q6ZPJ3	FRTTDIVIR	0.95792019	2	2.3268
Q6ZPJ3	NCAQGEGSMAKKVK	1.110137745	2	2.48007
Q70FJ1	**AKAP9 A_kinase anchor protein 9**	**1.032720159**	**0.9357**	**2**
Q70FJ1	LMKEKLEVQCQAEK+Oxidation(1)	1.03273458	2	2.50939
Q70FJ1	QRNTFAFAEK	0.985582782	1	1.95215
Q711G3	**IAH1 Isoamyl acetate_hydrolyzing esterase 1 homolog**	**1.018225797**	**0.1056**	**4**
Q711G3	DCGTDVLDLWTLMQK	1.152204885	2	3.88
Q711G3	DVEETKPELSLLGDGDH	1.047650209	2	3.43247
Q711G3	QHVPLDEYSANLR	0.840822262	2	2.58597
Q711G3	VILITPPPLCEAAWEK	0.936743803	2	2.63391
Q71LX4	**TLN2 Talin_2**	**0.997542993**	**0.8389**	**2**
Q71LX4	QEDVIATANLSR	1.109767104	2	2.95065
Q71LX4	QVAASTAQLLVACK	0.997471267	2	3.02824
Q75N33	**SC16B Protein transport protein Sec16B**	**1.272660673**	**0.0398**	**2**
Q75N33	EALEWAMK	2.349134844	1	1.94777
Q75N33	NLLTGEIPLNVDTPAQIVEK	0.942233742	2	4.31105
Q75Q39	**TOM70 Mitochondrial import receptor subunit TOM70**	**1.029806354**	**0.1282**	**2**
Q75Q39	NADLSTFYQNR	1.052141027	2	2.57928
Q75Q39	SDEDKDKEGEALEVK	0.790628869	2	3.68577
Q75WE7	**VWA5A von Willebrand factor A domain_containing protein 5A**	**1.182850251**	**0.0172**	**2**
Q75WE7	LDADLGGTEILTPLR	1.296878786	2	2.44487
Q75WE7	YVQELPLESDGALR	0.565240467	2	2.8958
Q76MZ3	**2AAA Serine/threonine_protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform**	**1.202183397**	**4E-06**	**8**
Q76MZ3	AISHEHSPSDLEAHFVPLVK	0.990733746	3	4.43382
Q76MZ3	DNTIEHLLPLFLAQLK	1.090472353	3	3.6036
Q76MZ3	DNTIEHLLPLFLAQLKDECPEVR	0.972382604	3	3.86212
Q76MZ3	IGPILDNSTLQSEVKPILEK	1.009249051	2	4.53703
Q76MZ3	LTQDQDVDVK	0.623077141	2	2.6221
Q76MZ3	QLSQSLLPAIVELAEDAK	0.876487983	2	3.68184
Q76MZ3	SALASVIMGLSPILGK	0.936903578	2	3.25298
Q76MZ3	SEIIPMFSNLASDEQDSVR	0.574040507	2	3.54472
Q791V5	**MTCH2 Mitochondrial carrier homolog 2**	**0.978533779**	**0.0002**	**5**
Q791V5	EEGIVGFFAGLIPR	1.491002242	2	3.86593
Q791V5	GLFTGLTPR	0.930355586	2	2.36367
Q791V5	SAATLITHPFHVITLR	1.14336661	3	3.53502
Q791V5	VLIQVGYEPLPPTIGR	0.987486482	2	4.15637
Q791V5	YCGLCDSIVTIYR	1.167285576	2	3.03486
Q794E4	**HNRPF Heterogeneous nuclear ribonucleoprotein F**	**0.917229968**	**0.604**	**3**
Q794E4	ATENDIYNFFSPLNPVR	1.046004847	3	4.33331
Q794E4	HSGPNSADSANDGFVR	0.913284499	2	3.96095
Q794E4	VHIEIGPDGR	0.911040026	2	3.11919
Q7TMA5	**APOB Apolipoprotein B_100**	**0.743416269**	**0.0006**	**6**
Q7TMA5	GFEPTLEALFGK	0.822192211	2	2.87498
Q7TMA5	IEGNLVFDPSSYLPK	0.746265968	2	3.16996
Q7TMA5	IEIDIPLPLGGK	0.733685422	2	2.92328
Q7TMA5	ITDNDVLIALDSAK	1.03742751	2	3.13813
Q7TMA5	KGTVATEMSTER	0.392438662	2	2.70431
Q7TMA5	TILFDTFVNDVAPVEK	0.937236081	2	3.30712
Q7TNG8	**LDHD Probable D_lactate dehydrogenase_ mitochondrial**	**1.089113307**	**0.8344**	**3**
Q7TNG8	AVVGSPHVSTASAVR	1.092462384	2	2.95506
Q7TNG8	AYSTDVCVPISR	1.080229741	2	3.09192
Q7TNG8	GSQGGLSQDFVEALK	0.982949295	2	3.50235

Q7TP47	**HNRPQ Heterogeneous nuclear ribonucleoprotein Q**	**1.020441645**	**0.3238**	**2**
Q7TP47	DLFEDELVPLFEK	1.223309577	2	3.20802
Q7TP47	NLANTVTEEILEK	1.017673267	2	3.66182
Q7TP48	**APMAP Adipocyte plasma membrane_associated protein**	**0.998463206**	**0.0142**	**4**
Q7TP48	GLFEVNPQK	0.945857487	1	2.12339
Q7TP48	LENGEIETIAR	0.943144085	2	3.02794
Q7TP48	LLEYDTVTK	1.009022522	2	2.41379
Q7TP48	LLLSSETPIEGK	1.284914917	2	2.85483
Q7TP52	**CMBL Carboxymethylenebutenolidase homolog**	**0.921533884**	**0.0239**	**7**
Q7TP52	AGVSVYGIIR	0.843406607	2	2.59197
Q7TP52	EDCSPADKPYIEEAR	0.901628092	2	3.28361
Q7TP52	KREDCSPADKPYIEEAR	0.859223903	3	4.44815
Q7TP52	LDYGGMGQEVQVEHIK	0.969992855	2	4.53714
Q7TP52	LKEHCIVNYQVK	1.239147016	2	3.53243
Q7TP52	NLIEWLNK	0.894165075	1	2.51928
Q7TP52	TFSGQTHGFVHR	0.929956412	2	3.38756
Q7TPB1	**TCPD T_complex protein 1 subunit delta**	**1.039313188**	**0.9515**	**6**
Q7TPB1	AFADAMEVIPSTLAENAGLNPISTVTELR	1.018128382	3	3.38423
Q7TPB1	ALIAGGGAPEIELALR	1.152101364	2	3.54671
Q7TPB1	ETLLNSATTSLNSK	1.095407393	2	3.43297
Q7TPB1	GDVTITNDGATILK	1.04544578	2	3.44556
Q7TPB1	GIHPTIISESFQK	0.974493129	2	2.38466
Q7TPB1	VIDPATATSVDLR	1.010302056	2	3.34163
Q7TPJ0	**SSRA Translocon_associated protein subunit alpha**	**1.051033399**	**3E-10**	**2**
Q7TPJ0	GEDFPANNIVK	1.193509768	2	2.73709
Q7TPJ0	GTEDFIVESLDASFR	1.02480153	2	4.33216
Q7TQM4	**SOAT2 Sterol O_acyltransferase 2**	**0.939456057**	**0.7765**	**3**
Q7TQM4	AIWEAVQAYPK	0.892953167	2	2.33615
Q7TQM4	QDRPLPSTASDSTR	0.945211972	2	3.14916
Q7TQM4	TQCLEQAQR	0.576141876	2	2.62961
Q7TSI0	**ZNF12 Zinc finger protein 12**	**0.398838936**	**0.2984**	**2**
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(1)	0.398838936	3	3.57211
Q7TSI0	HMSRLMEEDQGGEENQSSSAVFSYR+Oxidation(5)	0.398838936	3	3.56228
Q80W21	**GSTM7 Glutathione S_transferase Mu 7**	**0.985703973**	**0.0419**	**10**
Q80W21	CLDAFPNLK	0.977641925	2	3.14887
Q80W21	CLDAFPNLKDFIAR	1.045493747	2	3.2526
Q80W21	FKLGLDFPNLPYLIDGSHK	0.993864969	3	3.79427
Q80W21	HNLCGETEEER	1.190068089	2	3.99777
Q80W21	ITQSNAILR	1.118232937	2	3.11647
Q80W21	KHNLCGETEEER	0.821657185	3	4.13091
Q80W21	LFLEYTDSSYEEK	1.055298352	2	3.74244
Q80W21	LGLDFPNLPYLIDGSHK	1.098522385	3	4.35242
Q80W21	LYSEFLGK	0.997027649	1	2.4295
Q80W21	VDILENQLMDNR	0.96434596	2	3.50387
Q80W93	**HYDIN Hydrocephalus_inducing protein**	**2.082735038**	**0.0003**	**2**
Q80W93	FIVPVKAR	1.063185912	2	2.42765
Q80W93	LAKEMQEK	2.349134844	1	2.03376
Q80WE4	**KI20B Kinesin_like protein KIF20B**	**0.980863713**	**0.939**	**2**
Q80WE4	ELLDLIEK	0.933339111	1	2.11198
Q80WE4	LNTGTMDDLDVLTR+Oxidation(5)	0.982256142	2	2.60278
Q80WP8	**GADL1 Glutamate decarboxylase_like protein 1**	**1.026579934**	**0.0301**	**3**
Q80WP8	ADSVAWNPHK	1.029240156	2	2.70277
Q80WP8	MLMAGIQCSALLVK+Oxidation(0)	0.878252259	2	2.42859
Q80WP8	MMKKGSLMLGYQPHR	1.379790451	2	2.49322
Q80X90	**FLNB Filamin_B**	**0.993093232**	**0.9935**	**6**
Q80X90	GAGIGGLGITVEGPSESK	1.101465449	2	3.66237
Q80X90	GEAGIPAEFSIWTR	0.994342	2	2.58823

Q80X90	IGNLQTDLSDGLR	1.031491563	2	3.2046
Q80X90	VDIQTEDLEDGTCK	1.101115569	2	3.5142
Q80X90	VGEPGILCVDCSEAGPGTLGLEAVSDSGAK	1.042216703	2	4.96507
Q80X90	VTASGPGLSAYGVPASLPVEFAIDAR	0.965982776	2	4.23913
Q80Y84	**KDM5B Lysine_specific demethylase 5B**	**0.926501378**	**0.1831**	**2**
Q80Y84	CDIGLLGLK	0.870465998	2	2.56829
Q80Y84	YRYTLDDLYPMMNALK+Oxidation(10)	1.107896957	2	2.30415
Q80Z25	**OFD1 Oral_facial_digital syndrome 1 protein homolog**	**1.129003014**	**0.3451**	**2**
Q80Z25	MIEESLK+Oxidation(0)	1.08589837	2	2.36906
Q80Z25	RMIEESLK+Oxidation(1)	1.131891301	2	2.31251
Q80Z29	**NAMPT Nicotinamide phosphoribosyltransferase**	**0.988340078**	**0.7333**	**4**
Q80Z29	STEAPLIIRPDSGNPLDTVLK	1.071709323	2	3.69175
Q80Z29	TPAGTFVTLEEGKGDLEEYGHDLLHTVFK	1.395976854	5	4.81294
Q80Z29	VIQGDGVDINTLQEIVEGMK	0.990422713	2	4.50637
Q80Z29	YLLETSGNLDGLEYK	1.112773159	2	3.90361
Q811X6	**CRYL1 Lambda_crystallin homolog**	**1.083666504**	**0.1384**	**2**
Q811X6	LYDIEQQQITNALESIR	0.977155465	2	3.16924
Q811X6	TFGPVPEFSGDTVEK	1.165392687	2	3.10729
Q8BFZ3	**ACTBL Beta_actin_like protein 2**	**1.016418897**	**0.0044**	**9**
Q8BFZ3	CDVDIR	0.997736835	2	2.38123
Q8BFZ3	HQGVMVGMGQK	0.860657205	2	3.21497
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	0.975435533	3	3.49903
Q8BFZ3	HQGVMVGMGQK+Oxidation(4)	1.115299383	3	3.93826
Q8BFZ3	HQGVMVGMGQK+Oxidation(7)	0.961193906	3	3.31415
Q8BFZ3	SYELPDGQVITIGNER	1.032277715	2	5.05147
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR	1.124003961	3	6.45518
Q8BFZ3	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)	1.121803125	3	5.97459
Q8BFZ3	VAPDEHPILLTEAPLNPK	1.023945632	3	4.2765
Q8BG32	**PSD11 26S proteasome non_ATPase regulatory subunit 11**	**0.926208782**	**0.2777**	**3**
Q8BG32	LYDNLLEQNLIR	0.925906798	2	3.63311
Q8BG32	TTANAIYCPPK	0.989347659	2	3.1405
Q8BG32	VQIEHISSLIK	0.765747881	2	2.79455
Q8BGT6	**MILK1 MICAL_like protein 1**	**0.946352666**	**0.8084**	**2**
Q8BGT6	EEEEDKMLETMIKK	0.946174828	2	2.33937
Q8BGT6	KDPPWITLVQTEPKK	0.950963616	2	2.34766
Q8BGY2	**IF5A2 Eukaryotic translation initiation factor 5A_2**	**1.066282581**	**0.1601**	**5**
Q8BGY2	IVEMSTSK+Oxidation(3)	0.536014942	2	2.31006
Q8BGY2	KYEDICPSTHNMDVPNIK	1.131924773	3	4.16038
Q8BGY2	KYEDICPSTHNMDVPNIK+Oxidation(11)	1.103504131	3	3.41157
Q8BGY2	VHLVGIDIFTGK	1.096659082	2	3.40269
Q8BGY2	YEDICPSTHNMDVPNIK	1.033216917	2	3.76037
Q8BH00	**AL8A1 Aldehyde dehydrogenase family 8 member A1**	**1.045750726**	**1E-19**	**10**
Q8BH00	DSYDFFTEIK	0.64024285	2	2.33492
Q8BH00	ELLMLENFIGGK	0.826930009	2	3.53648
Q8BH00	ELNLPFGGMK	0.862364166	1	2.29164
Q8BH00	FLPCNSYIDSYDPSTGEVYCK	1.101945808	2	5.06076
Q8BH00	ILCGEGVDQLSLPLR	1.180992476	3	4.14802
Q8BH00	ITQLSAPHCK	1.314617325	2	2.81505
Q8BH00	KLSLELGGK	0.936707801	2	2.3087
Q8BH00	NPAIIFEDANLEECIPATVR	1.054795049	3	4.40374
Q8BH00	NQAGYFMLPTVITDIK	1.374739478	2	3.43048
Q8BH00	SSFANQGEICLCTSR	2.672094351	2	3.86517
Q8BHN3	**GANAB Neutral alpha_glucosidase AB**	**1.106621436**	**0.8843**	**8**
Q8BHN3	AEKDEPGAWEETFK	1.009017374	2	2.91662
Q8BHN3	DDNSVELTVAEGPYK	1.073647496	2	3.22897
Q8BHN3	MLDYLQGSGETPQTDIR	1.064332065	2	4.77361
Q8BHN3	MLDYLQGSGETPQTDIR+Oxidation(0)	1.025600713	2	5.25516

Q8BHN3	REPWLLASQYQDAIR	1.043878224	3	3.60171
Q8BHN3	SGGIERPFVLSR	1.106648988	2	2.35822
Q8BHN3	SIRPGLSPYR	0.795639839	2	2.37334
Q8BHN3	THSDSKPYGPTSVGLDFSLPGMEHVYGIPEHADSLR	1.043879234	5	4.58978
Q8BIJ6	**SYIM Isoleucyl_tRNA synthetase_ mitochondrial**	**0.924739934**	**0.6876**	**2**
Q8BIJ6	DTVLLPQTSFPMK	1.24431045	1	2.17718
Q8BIJ6	SCQTALAEILDVLVR	0.912635043	2	3.90387
Q8BJ64	**CHDH Choline dehydrogenase_ mitochondrial**	**1.001459137**	**0.7095**	**7**
Q8BJ64	ADSAYHPSCTCK	2.047669343	2	3.33855
Q8BJ64	AEVQTLVSR	1.016008471	2	2.46131
Q8BJ64	ELQPGSHVQSDKEIDAFVR	0.954107663	2	4.10009
Q8BJ64	GGDGPLHVSR	1.011661645	2	2.43899
Q8BJ64	SRPGVPHPDIQFHFLPSQVIDHGR	0.94445171	5	4.99109
Q8BJ64	TNHPLHQAFLQAAR	1.1336676	3	4.02171
Q8BJ64	VLLLEAGPK	0.959155769	2	2.64987
Q8BK64	**AHSA1 Activator of 90 kDa heat shock protein ATPase homolog 1**	**1.278544415**	**0.126**	**2**
Q8BK64	ADATNVNNWHWTER	1.046821504	2	2.87722
Q8BK64	LDGEASINNR	1.308160715	2	2.63895
Q8BL97	**SRSF7 Serine/arginine_rich splicing factor 7**	**1.134609532**	**0.0552**	**2**
Q8BL97	NPPGFAFVEFEDPR	1.065514111	2	2.49188
Q8BL97	VYVGNLGTGAGK	1.135206768	2	2.8021
Q8BMJ2	**SYLC Leucyl_tRNA synthetase_ cytoplasmic**	**0.908433501**	**0.665**	**2**
Q8BMJ2	SFITTDVNPYYDSFVR	0.924416046	2	3.41427
Q8BMJ2	STGNFLTLSQAVDK	0.769170838	2	2.60738
Q8BP47	**SYNC Asparaginyl_tRNA synthetase_ cytoplasmic**	**0.836182436**	**0.0003**	**2**
Q8BP47	KEDGTFYEFGDDIPEAPER	1.617650211	2	4.32333
Q8BP47	LTESVDVLMPNVGEIVGGSMR	0.756358486	2	2.62214
Q8BQ33	**TICRR Treslin**	**0.975943732**	**0.9897**	**2**
Q8BQ33	MNTMSRSLK+Oxidation(0)	1.020908932	1	2.23968
Q8BQ33	QKMNTMSRSLK+Oxidation(2)	0.975525173	2	2.51505
Q8BTM8	**FLNA Filamin_A**	**0.99003048**	**0.9756**	**3**
Q8BTM8	AFGPGLQGGNAGSPAR	0.954426883	2	3.85674
Q8BTM8	GAGTGGLGLAVEGPSEAK	1.015662856	2	3.70338
Q8BTM8	GLVEPVDVVDNADGTQTVNYVPSR	0.857074962	2	5.16387
Q8BTZ7	**GMPPB Mannose_1_phosphate guanyltransferase beta**	**1.145354083**	**0.1274**	**2**
Q8BTZ7	HHGQEGSILVTK	1.131684498	3	3.35131
Q8BTZ7	YGVVVCEADTGR	1.145355782	2	2.77291
Q8BU14	**SEC62 Translocation protein SEC62**	**1.227860449**	**0.0003**	**2**
Q8BU14	AVECLLDSKWAK	1.169340175	2	2.48978
Q8BU14	IQEVGEPSKEEK	1.230638812	2	3.41826
Q8BU33	**ILVBL Acetolactate synthase_like protein**	**0.967379938**	**0.9999**	**2**
Q8BU33	LPNSLMGR+Oxidation(5)	1.007140593	2	2.63353
Q8BU33	NAQVAQSPVLLLGGAASTLLQK	0.974819221	2	5.11265
Q8BV79	**TRNK1 TPR and ankyrin repeat_containing protein 1**	**0.668308926**	**0.0031**	**2**
Q8BV79	LQLMSMDWPGQVPKRLLK+Oxidation(3)	0.668308926	2	2.45698
Q8BV79	LQLMSMDWPGQVPKRLLK+Oxidation(5)	0.668308926	2	2.39415
Q8BVE3	**VATH V_type proton ATPase subunit H**	**0.985588899**	**0.9333**	**2**
Q8BVE3	GAVDAAVPTNIIAAK	1.048473427	2	2.55597
Q8BVE3	QLQSEQPQTAAAR	0.978980348	2	2.41242
Q8C147	**DOCK8 Dedicator of cytokinesis protein 8**	**0.948368287**	**0.094**	**2**
Q8C147	LNFASKLASAR	0.893102858	2	2.46652
Q8C147	RFMYTTPFTLEGRPR+Oxidation(2)	1.024222209	2	2.52717
Q8C8R3	**ANK2 Ankyrin_2**	**0.878368818**	**0.57**	**2**
Q8C8R3	STSSSGRPGTSPTRESR	0.975581594	2	2.54064
Q8C8R3	TSTDFSEVIKQELEDNDK	0.890710463	2	2.98302
Q8CC88	**K0564 Uncharacterized protein KIAA0564 homolog**	**1.007162808**	**0.9995**	**3**
Q8CC88	HQATGELDDAK	1.076345737	2	3.35348

Q8CC88	NLADQGIINYPYSTR	0.965407421	2	2.99264
Q8CC88	VSSDQLSSENLTSAVGQK	1.006724737	2	3.60243
Q8CFN2	**CDC42 Cell division control protein 42 homolog**	**1.01328433**	**0.9492**	**3**
Q8CFN2	DDPSTIEK	1.028449561	1	1.96874
Q8CFN2	NVFDEAILAALEPPEPK	1.013873829	3	5.0909
Q8CFN2	YVECSALTQK	0.994970229	2	2.89281
Q8CG45	**ARK72 Aflatoxin B1 aldehyde reductase member 2**	**1.071684911**	**0.153**	**9**
Q8CG45	AVSGAPLRPGTVLGTMEMGR	0.73117463	2	2.64077
Q8CG45	EHHFEAIALVEK	0.890015254	2	2.68847
Q8CG45	FFGNSWSETYR	0.944727077	2	2.76071
Q8CG45	FYAYNPLAGGLLTGK	1.194110467	2	4.21113
Q8CG45	MDASASAATVR	0.976964478	2	3.72497
Q8CG45	QVETELLPCLR	0.976954389	2	2.67958
Q8CG45	RMDASASAATVR	1.198921422	2	2.49078
Q8CG45	TTYGTSAPSMTSAALR	1.102325205	2	4.25633
Q8CG45	VDLFYLHAPDHGTPIVETLQACQQLHQEGK	1.294902523	3	4.24458
Q8CGC7	**SYEP Bifunctional aminoacyl_tRNA synthetase**	**0.958600854**	**0.982**	**10**
Q8CGC7	AIQGATSHHLGQNFSK	1.128113224	2	4.10818
Q8CGC7	DQDVEPGAPSMGAK	0.971347377	2	3.08286
Q8CGC7	DQVDSAVQELLQLK	1.012419942	2	4.0168
Q8CGC7	GDVSISVEEGKENLLR	0.970427659	2	3.31641
Q8CGC7	GSQFGQSCCLR	1.02983447	2	2.3653
Q8CGC7	KEENLAEWYSQVITK	0.88820829	2	4.08489
Q8CGC7	SLCIPFNPLCELQPGAMCVCGK	1.116206273	2	4.21992
Q8CGC7	SQGSGLSSGGAGEGQGPK	1.013400801	2	4.89804
Q8CGC7	TELAEPIAIRPTSETVMYPAYAK	0.84506083	2	2.9215
Q8CGC7	VYEELLAIPVVR	0.938902733	2	2.78672
Q8CGN4	**BCOR BCL_6 corepressor**	**0.981780244**	**0.9268**	**2**
Q8CGN4	FLTDYLNDLQGR	0.888938484	1	2.00373
Q8CGN4	NWLLLSDVLK	0.985768007	2	2.49696
Q8CHB8	**TTLL5 Tubulin polyglutamylase TTLL5**	**0.953722547**	**0.8313**	**2**
Q8CHB8	ASSNLQHSLRMVLPSR+Oxidation(10)	0.960762876	2	2.50587
Q8CHB8	DSGGQTLSPSWAAK	0.946787799	1	2.00453
Q8CHM7	**HACL1 2_hydroxyacyl_CoA lyase 1**	**1.133609434**	**0.0144**	**8**
Q8CHM7	DTSKPCLINIMIEPQSTR	1.06061298	2	3.4783
Q8CHM7	DTSKPCLINIMIEPQSTRK	0.928279412	2	2.32057
Q8CHM7	GAAYSHAEDSIR	1.311797589	2	3.29516
Q8CHM7	GVVPDNHPNCVGAAR	0.841453022	2	3.3696
Q8CHM7	GYFVQTPEELQDSLR	1.17285203	2	4.16779
Q8CHM7	LVELCNLPFLPTPMGK	1.269876901	2	4.13165
Q8CHM7	NCFIVSEGANTMDIGR	0.973943954	2	4.7332
Q8CHM7	NQEAMGAFQEFPQVEACR	1.037555481	2	4.90859
Q8CIB5	**FERM2 Fermitin family homolog 2**	**0.930014208**	**0.196**	**2**
Q8CIB5	GCEVTPDVNISGQK	0.929051072	2	3.29999
Q8CIB5	TSTILGDITSIPELADYIK	0.869335568	2	3.07929
Q8CIE6	**COPA Coatomer subunit alpha**	**1.08561134**	**0.0004**	**6**
Q8CIE6	ASNLENSTYDLYTIPK	1.359963961	2	4.0084
Q8CIE6	DADSQNPDAPEGK	0.84704567	2	3.41779
Q8CIE6	GITGVDLFGTTDAVVK	1.123600519	2	2.70298
Q8CIE6	LLELGPKPEVAQQTR	1.127170237	2	2.59502
Q8CIE6	SILLSVPLLVVDNK	1.077301282	2	3.18921
Q8CIE6	TLDLPIYVTR	1.085607986	2	2.62364
Q8JZN5	**ACAD9 Acyl_CoA dehydrogenase family member 9_ mitochondrial**	**0.955015387**	**0.9357**	**2**
Q8JZN5	GSNTCEVHFENTR	1.053483504	2	4.25574
Q8JZN5	NLSEFGLIQEK	0.94320869	2	3.13609
Q8K009	**AL1L2 Mitochondrial 10_formyltetrahydrofolate dehydrogenase**	**0.938516069**	**0.2352**	**16**

Q8K009	ADPLALAAEK	1.172402959	2	2.6036
Q8K009	AGFSVFWADDGLDTGPILLQR	1.141705017	2	2.35005
Q8K009	AMVEAVQLIADGK	0.986074439	2	3.67798
Q8K009	ANNTEYGLASGVFTR	0.417699217	2	4.7427
Q8K009	DLGEEALNEYLK	1.006195176	2	3.68613
Q8K009	FLFPEGIK	0.977046957	2	2.31152
Q8K009	FQNGDIDGVLQR	1.075492207	2	2.99038
Q8K009	GVINIIPGSGGVAGQR	0.944743282	2	2.77907
Q8K009	HGSIIYHPSLLPR	0.897395463	2	3.76479
Q8K009	NLQFEDGK	0.973140773	1	2.18711
Q8K009	SAACLAAGNTLVLKPAQVTPLTALK	1.302632883	3	3.44593
Q8K009	SCDVKPNDTVDSLYNR	1.042971842	2	4.63426
Q8K009	SPLIIFSDCDLEK	1.533490271	2	2.43467
Q8K009	TPQPEEGATYEGIQK	1.811783168	2	2.98095
Q8K009	VSYASLADVDR	1.2448116	2	3.61373
Q8K009	VVGVFTVPDKDGK	0.989337058	2	2.95327
Q8K2F0	**BRD3 Bromodomain_containing protein 3**	**1.031024876**	**0.2242**	**2**
Q8K2F0	KMDSREYPDAQGFAADIR	1.403747628	2	2.31435
Q8K2F0	QLSLDINRLPGEK	0.89531239	2	2.39281
Q8K442	**ABC8A ATP_binding cassette sub_family A member 8_A**	**0.836621841**	**0.1518**	**4**
Q8K442	GQITAILGHSGAGK	0.748051511	2	3.35449
Q8K442	IDDFIHSLEQQNIALEVDAFGTR	0.820532681	3	3.61572
Q8K442	NTQNILVQNLSGGQK	0.689831904	2	2.64868
Q8K442	STLLNVLSGLCVPTK	0.892019529	2	3.20381
Q8K4C0	**FMO5 Dimethylaniline monooxygenase [N_oxide_forming] 5**	**0.703471682**	**1E-19**	**9**
Q8K4C0	CCLEEGLEPVCFER	0.721894333	2	4.08128
Q8K4C0	EYKNPVEFTGK	0.593264329	2	2.32707
Q8K4C0	GYPIDILLSSR	0.807770399	2	3.55792
Q8K4C0	HSALGQHPTINDDLPNR	0.689340128	2	4.98257
Q8K4C0	IAVIGSGASGLTCIK	0.920750866	2	3.2945
Q8K4C0	KLPSQSEMMAEINK	0.691431368	2	3.64247
Q8K4C0	KQPDFSTSGQWQVVTEHEGK	0.743014926	3	4.32213
Q8K4C0	KTILTTEDR	0.75747056	2	2.42411
Q8K4C0	SDDIGGLWR	0.697238096	2	2.91392
Q8K4Q0	**RPTOR Regulatory_associated protein of mTOR**	**0.993421629**	**0.0096**	**2**
Q8K4Q0	MPESVNVMQIVK+Oxidation(0)	0.749371914	2	2.33729
Q8K4Q0	QAQQVIQKGITR	1.254264254	1	2.1206
Q8K4Z3	**AIBP Apolipoprotein A_I_binding protein**	**1.029520121**	**3E-09**	**2**
Q8K4Z3	GNPSGIQPDLLISLTAPK	0.832358891	2	4.11803
Q8K4Z3	SPPTVLVICGPGNNGGDGLVCAR	1.01162411	2	5.58946
Q8K586	**RANT GTP_binding nuclear protein Ran_ testis_specific isoform**	**0.983870922**	**0.9618**	**3**
Q8K586	FNVWDTAGQEK	1.023461907	2	3.00587
Q8K586	NLQYYDISAK	1.093953901	1	2.33346
Q8K586	VCENIPIVLCGNK	0.924715447	2	3.39396
Q8QZY1	**EIF3L Eukaryotic translation initiation factor 3 subunit L**	**0.946386228**	**0.9766**	**3**
Q8QZY1	QYEQQTYQVIPEVIK	1.04043008	2	2.67363
Q8QZY1	VFSDEVQQQAQLSTIR	0.942073971	2	4.06817
Q8QZY1	VYEIQDIYENSWTK	0.987450927	2	2.50332
Q8R081	**HNRPL Heterogeneous nuclear ribonucleoprotein L**	**0.929408177**	**0.2543**	**4**
Q8R081	ASLNGADIYSGCCTLK	1.215337397	2	3.50728
Q8R081	NDQDTWDYTNPNLSGQGDPGSNPNKR	0.997752515	3	4.91136
Q8R081	SDALETLGFLNHYQMK	0.942741856	2	2.99527
Q8R081	TENAGDQHGGGGGGGSGAAGGGGGENYDDPHK	0.806611226	3	7.47052
Q8R0F9	**S14L4 SEC14_like protein 4**	**0.827779868**	**0.0002**	**2**
Q8R0F9	FDNTYSLLHTK	0.827795083	2	2.90302
Q8R0F9	GSSHQVENEILFPGCVLR	0.670316243	2	5.48631
Q8R0K2	**TRI31 E3 ubiquitin_protein ligase TRIM31**	**1.061488351**	**0.8559**	**2**

Q8R0K2	AQVDLEKLKIHEEFK	1.061276349	2	2.46533
Q8R0K2	QRLDEEESFLLSR	1.092349696	2	2.41237
Q8R146	**APEH Acylamino_acid_releasing enzyme**	**0.924397891**	**0.9011**	**2**
Q8R146	GSTGFGQDSILSLPGNVGHQDVK	1.061888745	2	3.55629
Q8R146	QVLLSEPQEAAALYR	0.922385946	2	3.61127
Q8R164	**BPHL Valacyclovir hydrolase**	**0.868424679**	**2E-05**	**2**
Q8R164	QVSLLGWSDGGITALIAAAK	1.078013296	2	3.75606
Q8R164	TDFAPQLQSLNK	0.822135425	2	3.24938
Q8R1V4	**TMED4 Transmembrane emp24 domain_containing protein 4**	**0.957929295**	**0.9392**	**2**
Q8R1V4	CFIEEIPDETMVIGNYR	0.946274642	2	3.69245
Q8R1V4	QLLDQVEQIQK	0.958068263	2	3.23942
Q8R491	**EHD3 EH domain_containing protein 3**	**1.02224544**	**0.8479**	**3**
Q8R491	LDISDEFSEVIK	1.060967299	2	3.3748
Q8R491	LFEAEEQDLFK	1.022802936	2	3.1238
Q8R491	MQDQLQAQDFSK	0.875683524	2	3.12121
Q8VBU2	**NDRG2 Protein NDRG2**	**1.015744601**	**0.089**	**6**
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK	0.94739929	3	4.6379
Q8VBU2	CPVMLVVGDQAPHEDAVVECNSK+Oxidation(3)	1.095870311	3	4.70909
Q8VBU2	LDPTQTSFLK	0.897099448	2	2.39448
Q8VBU2	MADSGGQPQLTQPGK	0.549176463	2	3.08305
Q8VBU2	TASLTSAASIDGSR	1.486564015	2	3.38155
Q8VBU2	YALNHPDTVEGLVLINIDPNAK	1.427178991	2	3.55328
Q8VC12	**HUTU Urocanate hydratase**	**1.046868816**	**2E-09**	**6**
Q8VC12	HQLVVGSQAR	1.172565188	2	2.87839
Q8VC12	LLALEFAQELR	1.410657902	2	3.63897
Q8VC12	LVITNGMVIPNYSSR	1.176449904	2	2.74392
Q8VC12	VAIAVAINQAIASGK	1.525206449	2	2.99113
Q8VC12	VFVTSGLGGMSGAQAK	0.961841478	2	4.37381
Q8VC12	VFVTSGLGGMSGAQAK+Oxidation(9)	1.236900411	2	2.72628
Q8VCD5	**MED17 Mediator of RNA polymerase II transcription subunit 17**	**0.904499141**	**0.5149**	**2**
Q8VCD5	EIFAQLSREAVQIK	0.904159748	1	2.10893
Q8VCD5	MELLMSALSPCLL+Oxidation(0)	1.18567409	2	2.32529
Q8VED5	**K2C79 Keratin_ type II cytoskeletal 79**	**0.780625628**	**0.0023**	**4**
Q8VED5	NKYEDEINK	0.851496291	2	2.55467
Q8VED5	NKYEDEINKR	0.735392772	2	2.5352
Q8VED5	NLDLDSIIAEVK	0.621306059	2	2.76017
Q8VED5	YEDEINK	1.024489416	1	2.05325
Q8VEK3	**HNRPU Heterogeneous nuclear ribonucleoprotein U**	**1.020327718**	**0.9972**	**9**
Q8VEK3	EKPYFPIPEDCTFIQNVPLEDR	0.970799474	3	4.28999
Q8VEK3	GYFEYIEENK	0.837643191	2	3.31653
Q8VEK3	LLEQYKEESK	0.992945185	2	2.92343
Q8VEK3	LLEQYKEESKK	1.014718549	2	3.18978
Q8VEK3	LQAALDNEAGGRPAMEPGNGSLDLGGDAAGR	1.051486942	3	4.98696
Q8VEK3	NFILDQTNVSAAAQR	0.896705014	2	4.66294
Q8VEK3	TCNCETEDYGEK	1.047594721	2	3.4796
Q8VEK3	VSELKEELKK	0.992934855	2	3.03126
Q8VEK3	YNILGTNTIMDK	0.925005112	2	3.62491
Q8VHE9	**RETST All_trans_retinol 13_14_reductase**	**0.620754922**	**1E-19**	**4**
Q8VHE9	ATVQSVLLDSAGR	0.679580521	2	3.82277
Q8VHE9	GATYGADHDLAR	0.68510145	2	3.00801
Q8VHE9	NLYSDLQALGSK	0.633367126	2	3.07243
Q8VHE9	RPPEPLVTDK	0.614543365	2	2.97071
Q8VHF5	**CISY Citrate synthase_ mitochondrial**	**0.90459752**	**0.0003**	**3**
Q8VHF5	DILSNLIPK	0.765027111	2	2.42043
Q8VHF5	EGSSIGAIDSK	0.79064731	1	2.13931
Q8VHF5	GLVYETSVLDPDEGIR	0.916133306	2	4.02319
Q8VHT6	**AS3MT Arsenite methyltransferase**	**1.077290457**	**1E-19**	**3**

Q8VHT6	ILDLGSGSGR	0.985231544	2	2.96238
Q8VHT6	SLQNVHEEVISR	1.693808796	2	2.93766
Q8VHT6	TSADLQTNACVTPAK	1.470844037	2	3.49723
Q8VID1	**DHRS4 Dehydrogenase/reductase SDR family member 4**	**0.872910146**	**0.0009**	**4**
Q8VID1	AVATLQGEGLSVTGVVCHVGK	0.935555884	2	4.48799
Q8VID1	LAEDGAHVVISSR	1.214167056	2	3.25577
Q8VID1	NFAAELAPK	0.812967052	2	2.59451
Q8VID1	VALVTASTDGIGLAIAR	1.18412371	2	2.98933
Q8VID6	**PDE11 Dual 3__5__cyclic_AMP and _GMP phosphodiesterase 11A**	**0.690773558**	**0.0013**	**2**
Q8VID6	MFMELGMVQKFK+Oxidation(0)	0.690773558	1	1.91772
Q8VID6	MFMELGMVQKFK+Oxidation(2)	0.690773558	1	1.90643
Q8VIF7	**SBP1 Selenium_binding protein 1**	**0.901061041**	**0.0787**	**8**
Q8VIF7	CGPGYATPLEAMK	0.875307359	2	3.23483
Q8VIF7	FLHDPDATQGFVGCALSSNIQR	0.899627663	2	4.39094
Q8VIF7	GGFVLLDGETFEVK	0.904574053	2	3.94081
Q8VIF7	GTWEKPGGEAPMGYDFWYQPR	0.894968348	3	4.05698
Q8VIF7	NEGGTWSVEK	0.873475964	2	2.33168
Q8VIF7	NTGIEAPDYLATVDVDPK	0.847835288	2	5.02269
Q8VIF7	QYDISNPK	0.751245054	1	2.10013
Q8VIF7	VIEPNEIHAK	0.805787524	2	2.49132
Q8VIJ6	**SFPQ Splicing factor_ proline_ and glutamine_rich**	**1.071437027**	**0.8783**	**2**
Q8VIJ6	NLSPYVSNELLEEAFSQFGPIER	0.966489974	3	3.43464
Q8VIJ6	YGEPGEVFINK	1.077561189	2	2.69571
Q91VA0	**ACSM1 Acyl_coenzyme A synthetase ACSM1_ mitochondrial**	**0.771793306**	**9E-08**	**5**
Q91VA0	AFIVLNPEFLSHDQEQLIK	0.771432143	2	5.30659
Q91VA0	AILPFDLQIIDEK	0.813934519	2	4.14646
Q91VA0	GNILPPNTEGYIGIR	0.80648854	2	2.92295
Q91VA0	HNQGLAFR	0.615382319	2	2.3806
Q91VA0	KVEFVSELPK	0.857645772	2	2.63062
Q91VA6	**PDIP2 Polymerase delta_interacting protein 2**	**1.231156911**	**0.6069**	**2**
Q91VA6	NHPWLELSDVHR	1.048320051	3	3.70734
Q91VA6	VLETVGVFEVPK	1.234489125	2	2.37326
Q91VH2	**SNX9 Sorting nexin_9**	**1.176143241**	**7E-07**	**2**
Q91VH2	GEQGLVPTDYVEILPNDGK	0.941508337	2	2.38426
Q91VH2	ITPQDKQTMVK+Oxidation(8)	1.991618516	1	2.10074
Q91VM9	**IPYR2 Inorganic pyrophosphatase 2_ mitochondrial**	**0.930433051**	**0.0034**	**2**
Q91VM9	IIAINVNDPEAEK	0.629428785	2	3.19357
Q91VM9	MEIATEEPLNPIK	0.996791651	2	3.63225
Q91W43	**GCSP Glycine dehydrogenase [decarboxylating]_ mitochondrial**	**0.911991698**	**0.4515**	**3**
Q91W43	IDDIYGDQHLVCTCPPMEVYESPFSEQK	1.102381728	3	3.69771
Q91W43	NLLENSGWVTQYTPYQPEVSQGR	0.860333133	2	4.24506
Q91W43	VSFQPNSGAQGEYAGLATIR	0.992661058	2	4.52631
Q91X77	**CY250 Cytochrome P450 2C50**	**0.687559604**	**1E-15**	**3**
Q91X77	IKEHEESLDVTIPR	0.629352706	3	3.91903
Q91X77	NFLLEK	0.703559694	1	1.96525
Q91X77	YALLLLLK	1.220496735	2	2.59787
Q91X78	**ERLN1 Erlin_1**	**0.95963327**	**0.984**	**2**
Q91X78	ISEIEDAAFLAR	0.987433583	2	3.67408
Q91X78	SVQTTLQTDEVK	0.952859885	2	3.41667
Q91Y81	**SEPT2 Septin_2**	**1.118049721**	**0.2948**	**2**
Q91Y81	ASIPFSVVGSNQLIEAK	1.327336473	2	2.70076
Q91Y81	LTVVDTPGYGDAINSR	1.072715633	2	3.79749
Q91YT0	**NDUV1 NADH dehydrogenase [ubiquinone] flavoprotein 1_ mitochondrial**	**1.178389952**	**7E-06**	**8**
Q91YT0	GAGAYICGEETALIESIEGK	1.125374018	2	3.47646
Q91YT0	GDARPAEIDSLWEISK	0.969584569	2	3.0918

Q91YT0	GGAGFPTGLK	1.117861304	2	2.30261
Q91YT0	KTSFGSLKDEDR	1.210332591	2	3.03097
Q91YT0	LKPPFPADVGVFGCPTTVANVETVAVSPTICR	1.411612902	3	4.96474
Q91YT0	LVEGCLVGGR	0.87079331	2	2.44372
Q91YT0	TSFGSLKDEDR	1.276404654	2	2.55183
Q91YT0	YLVVNADEGEPGTCK	1.208087488	2	5.29796
Q91Z53	**GRHPR Glyoxylate reductase/hydroxypyruvate reductase**	**0.990793626**	**0.0134**	**7**
Q91Z53	GDVVNQEDLYQALASGQIAAAGLDVTTPEPLPPSHPLLTLK	0.976950364	3	6.32099
Q91Z53	LLDAAGANLR	0.961236446	2	3.22163
Q91Z53	NCVILPHIGSATYK	1.053433089	2	3.31537
Q91Z53	NTMSLLAANNLLAGLR	0.961795557	2	3.66477
Q91Z53	NTMSLLAANNLLAGLR+Oxidation(2)	0.952971385	2	3.65781
Q91Z53	RLPEAIEEVK	0.824118568	2	2.64402
Q91Z53	VISTLSVGVDHLALDEIK	1.140487445	2	3.91288
Q91ZJ5	**UGPA UTP__glucose_1_phosphate uridylyltransferase**	**0.820162917**	**1E-19**	**12**
Q91ZJ5	AMSQDGASQFQEVILQELELSVK	0.87114346	3	4.74835
Q91ZJ5	GGTLTQYEGK	0.816106209	2	2.493
Q91ZJ5	GLPDNISSVLNK	0.824179447	2	3.2697
Q91ZJ5	GTVIIIANHGDR	0.888737068	2	3.20004
Q91ZJ5	IDIPPGAVLENK	0.798492434	2	2.74069
Q91ZJ5	IQRPPEDSIQPYEK	0.825963886	2	3.90405
Q91ZJ5	LQEQNAIDMEIIVNPK	1.931858903	2	3.34486
Q91ZJ5	LVEIAQVPK	0.796257766	2	3.37806
Q91ZJ5	NENTFLDLTVQQIEHLNK	0.704766083	2	5.33607
Q91ZJ5	SFENSLGINVPR	0.783274122	2	3.39287
Q91ZJ5	TLDGGLNVIQLETAVGAAIK	0.773241685	2	4.7902
Q91ZJ5	TYNTDVPLVLMNSFNTDEDTKK	0.937553305	2	4.56544
Q91ZX7	**LRP1 Prolow_density lipoprotein receptor_related protein 1**	**1.056805821**	**0.7723**	**3**
Q91ZX7	AVTDEEPFLIFANR	1.086518564	2	2.61346
Q91ZX7	GCHVNECLSR	1.182347567	2	2.63022
Q91ZX7	MYDAQQQQVGTNK	0.960383908	2	4.1467
Q920A6	**RISC Retinoid_inducible serine carboxypeptidase**	**0.753547691**	**0.0837**	**2**
Q920A6	DLDTVASDMMVLLK	0.803163085	2	2.69524
Q920A6	GLAEVSDIAEQVLNAVNK	0.779482696	3	5.02439
Q920D2	**DYR Dihydrofolate reductase**	**1.089944132**	**0.8016**	**3**
Q920D2	LIEQPELASK	0.916264813	2	2.84925
Q920D2	LLPEYPGVLSEIQEEK	1.115118849	2	3.4571
Q920D2	NGDLPWPLLR	1.195406893	2	3.04326
Q920F5	**DCMC Malonyl_CoA decarboxylase_ mitochondrial**	**0.957567789**	**0.5764**	**3**
Q920F5	EIAEVTGDPVHESLK	0.762072501	2	3.26842
Q920F5	ISECEAVHPVK	0.966445109	2	3.4044
Q920F5	WLLGLLNVQGK	1.140531029	2	3.26145
Q920J4	**TXNL1 Thioredoxin_like protein 1**	**1.054270544**	**0.0594**	**2**
Q920J4	AGCECLNESDEHGFDNCLR	1.159887677	3	3.57145
Q920J4	IDQYQGADAVGLEEK	1.035057502	2	3.96545
Q920L2	**DHSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit_ mitochondrial**	**0.914769237**	**0.0002**	**20**
Q920L2	AAFGLSEAGFNTACLTK	0.862479036	2	2.37338
Q920L2	ACALSIAESCRPGDK	1.050969708	2	2.87348
Q920L2	AGLPCQDLEFVQFHPTGIYGAGCLITEGCR	1.106909743	3	4.80377
Q920L2	ANAGEESVMNLDK	1.029108394	2	3.51816
Q920L2	DVVSRSMTLEIR+Oxidation(6)	1.091156235	2	2.3657
Q920L2	GEGGILINSQGER	0.956041821	2	3.95603
Q920L2	GVIALCIEDGSIHR	1.146849466	2	3.21592
Q920L2	HTLSYVDTK	1.162465361	2	2.30996
Q920L2	HVNGQDQIVPGLYACGEAACASVHGANR	1.021483142	3	6.71219
Q920L2	IDEYDYSKPIEGQQK	0.906768551	2	4.47247

Q920L2	KHTLSYVDTK	0.122153673	2	2.60817
Q920L2	NTIIATGGYGR	0.943256864	2	3.00048
Q920L2	SMQSHAAVFR+Oxidation(1)	0.968417884	2	2.4176
Q920L2	TGHSLLHTLYGR	0.871641708	2	2.58104
Q920L2	TLNEADCATVPPAIR	1.057499916	2	3.63917
Q920L2	TYFSCTSAHTSTGDGTAMVTR	1.056343177	2	5.37804
Q920L2	VGSVLQEGCEK	1.079293319	2	3.6919
Q920L2	VSDAISTQYPVVDHEFDAVVVGAGGAGLR	0.912585549	3	4.45153
Q920L2	VSQLYGDLQHLK	1.000493706	2	2.90264
Q920L2	VTLDYRPVIDK	0.969645781	2	2.95304
Q920P0	**DCXR L_xylulose reductase**	**0.933428278**	**0.0008**	**4**
Q920P0	AVVQVSQIVAR	0.946898337	2	3.10054
Q920P0	GVPGAIVNVSSQASQR	0.910720831	2	5.66815
Q920P0	STVLALQAAGAQVVAVSR	1.177533591	2	3.83354
Q920P0	TREDLDSLVR	0.870879236	2	2.79953
Q921F2	**TADBP TAR DNA_binding protein 43**	**0.964248258**	**0.9831**	**3**
Q921F2	FGGNPGGFGNQGGFGNSR	0.939030165	2	4.21349
Q921F2	KDLKTGHSK	0.971212508	2	2.48049
Q921F2	TSDLIVLGLPWK	0.991601679	2	3.12083
Q922F4	**TBB6 Tubulin beta_6 chain**	**1.024008199**	**0.1255**	**5**
Q922F4	ALTVPELTQQMFDAK	1.08291942	2	4.03344
Q922F4	GHYTEGAELVDSVLDVVR	1.021389939	2	6.55341
Q922F4	IREEYPDR	1.02734604	2	2.63664
Q922F4	MASTFIGNSTAIQELFK	1.196071666	2	3.98106
Q922F4	NSSYFVEWIPNNVK	1.075766906	2	4.49696
Q922J3	**CLIP1 CAP_Gly domain_containing linker protein 1**	**0.975609633**	**0.7782**	**3**
Q922J3	EMETMQAKLMK+Oxidation(4)	0.975525173	2	2.55292
Q922J3	LQNELDTLKENNLK	1.014926556	2	2.31623
Q922J3	TASESISNLSEAGSVK	0.547134884	2	2.38444
Q923D2		**0.933749211**	**0.5058**	**3**
Q923D2	LQDVTDDHIR	0.895511307	2	3.23294
Q923D2	TGLTTLAQAVQAGYEVTVLVR	0.990050199	3	4.75114
Q923D2	YVAVMPPHIGDQPLTGAYTVTLDGR	0.96120168	3	4.61981
Q923M1	**MSRA Mitochondrial peptide methionine sulfoxide reductase**	**1.021873225**	**0.1596**	**2**
Q923M1	SAVYPTSAVQMEAALK	1.931231041	2	3.19339
Q923M1	VISAEEALPGR	0.941505627	2	2.42951
Q923V8	**SEP15 15 kDa selenoprotein**	**1.029483151**	**0.401**	**3**
Q923V8	GCCQEEAQFETK	0.976533512	2	3.87992
Q923V8	LLDDNGNIAEELSILK	1.027918425	2	3.2275
Q923V8	WNTDSVEEFLSEK	1.306080417	2	3.2608
Q924C3	**ENPP1 Ectonucleotide pyrophosphatase/phosphodiesterase family member 1**	**1.141402825**	**4E-09**	**2**
Q924C3	AEYLHTWGGLLPVISK	1.148293423	3	3.91513
Q924C3	SGTYFWPGSDVEIDGILPDIYK	1.030093197	2	4.20803
Q924S5	**LONM Lon protease homolog_ mitochondrial**	**0.99711816**	**0.6336**	**8**
Q924S5	AQLSATVLTLLIK	1.268971075	2	2.64341
Q924S5	EHQEALAVER	0.810011601	2	2.49351
Q924S5	ELGLEKDDKDAIEEK	0.963351766	2	3.40094
Q924S5	HVMDVVDEELSK	1.067928441	2	2.44928
Q924S5	IVSGEAQTVHVTPENLQDFVGKPVFTVER	1.096900122	3	5.97532
Q924S5	QLEVEPEGLEPEAENK	1.129579884	2	4.35844
Q924S5	QSDENLDLAR	0.927117739	2	2.49252
Q924S5	TENPLVLIDEVDK	0.978676818	2	3.30673
Q99020	**ROAA Heterogeneous nuclear ribonucleoprotein A/B**	**0.932881706**	**0.0005**	**2**
Q99020	FGEVVDCTIK	0.771620826	2	2.91991
Q99020	IFVGGLNPEATEEK	1.108624659	2	3.60464
Q99JI4	**PSMD6 26S proteasome non_ATPase regulatory subunit 6**	**1.003378899**	**0.9414**	**2**

Q99JI4	RLDEELEDAEK	0.987319592	2	2.95322
Q99JI4	VNEIVETNRPDSK	1.082461361	2	3.47608
Q99L04	**DHRS1 Dehydrogenase/reductase SDR family member 1**	**0.948290174**	**0.8639**	**2**
Q99L04	ATAQEAQSLGGR	0.950787477	2	3.30614
Q99L04	CVPVVCDSSQESEVK	0.913460458	2	3.27059
Q99LF4	**RTCB tRNA_splicing ligase RtcB homolog**	**1.115613421**	**0.9304**	**4**
Q99LF4	NLDFQDVLDK	1.069676848	2	2.73157
Q99LF4	NVTDVVNTCHDAGISK	1.058705596	2	4.2084
Q99LF4	NYNDELQFLDK	1.090175037	2	3.0581
Q99LF4	TNLDESDVQPVK	1.128853569	2	3.4685
Q99ML5	**PCYOX Prenylcysteine oxidase**	**1.016285859**	**0.004**	**2**
Q99ML5	LLNQTLRENLK	1.074601626	2	2.40102
Q99ML5	NFDPPIEEFNDPYQQLVTTLIK	0.791371073	3	3.43225
Q99MR9	**PPR3A Protein phosphatase 1 regulatory subunit 3A**	**1.174106021**	**0.0071**	**2**
Q99MR9	DDLGANHPNVDDINK	1.175008825	2	2.44357
Q99MR9	SRSKEEPLLAPEENK	1.166822193	2	2.45781
Q99MS0	**S14L2 SEC14_like protein 2**	**0.981692101**	**0.0938**	**2**
Q99MS0	AGEMTEVLPNQR	0.76295295	2	3.11169
Q99MS0	HISPDQLPVEYGGTMTDPDGNPK	1.044230934	3	4.44467
Q99MZ8	**LASP1 LIM and SH3 domain protein 1**	**0.911453853**	**0.8834**	**5**
Q99MZ8	GFSVVADTPELQR	0.894119033	2	3.58835
Q99MZ8	TGDTGMLPANYVEAI	1.079180234	1	2.07862
Q99MZ8	TQDQISNIK	1.072641568	2	2.46016
Q99MZ8	YHEEFEK	0.910456323	1	2.48047
Q99MZ8	YKEEFEK	1.049181608	1	2.22995
Q99NA5	**IDH3A Isocitrate dehydrogenase [NAD] subunit alpha_ mitochondrial**	**0.976106692**	**0.7431**	**2**
Q99NA5	ENTEGEYSGIEHVIVDGVVQSIK	0.835786565	2	4.05043
Q99NA5	NVTAIQGPGGK	0.976355653	2	2.58935
Q99PF5	**FUBP2 Far upstream element_binding protein 2**	**0.913042984**	**0.4441**	**5**
Q99PF5	GGGGPGGGGPGGGGASGGPSQPPGGGGPGIR	0.922389166	2	5.75508
Q99PF5	IGGDAATTVNNNTPDFGFGGQK	0.92284829	2	4.31157
Q99PF5	IGQQPQQPGAPPQQDYTK	0.813788656	2	2.53465
Q99PF5	SVSLTGAPESVQK	0.967856842	2	3.3042
Q99PF5	VGGGIDVPVPR	1.057392134	2	2.39725
Q99PL5	**RRBP1 Ribosome_binding protein 1**	**0.9717565**	**0.0059**	**20**
Q99PL5	AMEALALAER	1.080084733	2	2.39402
Q99PL5	DALNQATSQVESK	0.941471268	2	3.54741
Q99PL5	EAEETQNSLQAECDQYR	0.984199359	2	5.19342
Q99PL5	EHTSHLEAELEK	0.904462157	2	3.49253
Q99PL5	ELESQVSCLEK	0.997332783	2	2.5808
Q99PL5	GELESSDQVR	1.07840816	2	2.8394
Q99PL5	HMAAASAECQNYAK	0.788337811	2	4.17748
Q99PL5	HMAAASAECQNYAK+Oxidation(1)	1.216084624	2	4.40717
Q99PL5	LKELESQVSCLEK	0.88593371	2	3.50325
Q99PL5	LLATEQEDAAVAK	0.947879683	2	3.72832
Q99PL5	LQQENSILR	1.11599356	2	2.66032
Q99PL5	LQSSEVEVK	1.05037854	2	2.30502
Q99PL5	LREAEETQNSLQAECDQYR	0.947815877	3	4.0468
Q99PL5	QLHLAEAQTK	1.199210168	2	2.5839
Q99PL5	QLLLESQSQLDEAK	0.960691949	2	2.59909
Q99PL5	TILAETEGMLK	0.958397402	2	2.42795
Q99PL5	TILAETEGMLK+Oxidation(8)	1.25311143	2	2.31481
Q99PL5	TLQEQLENGPNTQLAR	0.960762876	2	5.44788
Q99PL5	TLVSTVGSMVFSEGEAQR	1.162909989	2	4.56144
Q99PL5	VEPAVSSIVNSIQVLASK	1.017265994	3	3.97112
Q99PV0	**PRP8 Pre_mRNA_processing_splicing factor 8**	**0.963412926**	**0.9718**	**3**

Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.969992855	2	2.43589
Q99PV0	AAVMHDILDMMPEGIK+Oxidation(3)	0.969992855	2	2.50849
Q99PV0	KGMLDPLEVHLLDFPNIVIK	0.935248053	2	2.33469
Q9CPQ1	**COX6C Cytochrome c oxidase subunit 6C**	**1.010258139**	**0.696**	**2**
Q9CPQ1	FGVAEPR	1.155506969	2	2.34045
Q9CPQ1	NYDSMKDFEEMR	1.006544026	2	3.29581
Q9CQZ5	**NDUA6 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6**	**1.250912719**	**0.2533**	**2**
Q9CQZ5	FFHETETPRPK	1.112209166	2	2.85928
Q9CQZ5	VVDLLVIK	1.347843462	2	2.48711
Q9CRB9	**CHCH3 Coiled_coil_helix_coiled_coil_helix domain_containing protein 3_ mitochondrial**	**1.007947145**	**1**	**2**
Q9CRB9	VAEELALEQAK	0.993828502	2	3.47003
Q9CRB9	YEYHPVCADLQTK	1.008050921	2	3.45689
Q9CW42	**MOSC1 MOSC domain_containing protein 1_ mitochondrial**	**0.796534879**	**7E-05**	**2**
Q9CW42	DLLLPITPPATNPLLQCR	0.748288331	2	4.03178
Q9CW42	GLSVSEAECTAMGLR	0.964065601	2	3.79409
Q9CWH6	**PSA7L Proteasome subunit alpha type_7_like**	**1.098708722**	**0.7796**	**4**
Q9CWH6	AITVFSPDGHLFQVEYAQEAVK	1.042767109	2	4.29511
Q9CWH6	ALLEVVQSGGK	1.101419778	2	3.0262
Q9CWH6	LTVEDPVTVEYITR	1.08550948	2	4.00338
Q9CWH6	LYQTDPSGTYHAWK	1.303190483	2	2.34727
Q9CWK8	**SNX2 Sorting nexin_2**	**1.146297181**	**0.5728**	**4**
Q9CWK8	AVNTQALSGAGILR	1.039797468	2	3.1607
Q9CWK8	QQQFENLDQQLR	1.167234091	2	2.69077
Q9CWK8	WEDAQITLLK	1.091139353	2	2.64058
Q9CWK8	YWEAFLPEAK	1.149636045	2	2.60906
Q9CXS4	**CENPV Centromere protein V**	**0.906987168**	**0.0023**	**2**
Q9CXS4	LLLDTFEYQGLVK	0.899018833	2	3.67604
Q9CXS4	SVVTEEFNGSDWER	0.907794001	2	3.54666
Q9CYN2	**SPCS2 Signal peptidase complex subunit 2**	**0.9132239**	**0.6635**	**2**
Q9CYN2	LHDSLATER	0.940933293	2	2.65284
Q9CYN2	YVENFGLIDGR	0.859395743	2	2.82993
Q9CZY3	**UB2V1 Ubiquitin_conjugating enzyme E2 variant 1**	**0.970716232**	**0.9878**	**2**
Q9CZY3	LLEELEEGQK	0.9672078	2	2.42698
Q9CZY3	VNMSGVSSSNGVVDPR	0.991158613	2	2.91094
Q9D0M3	**CY1 Cytochrome c1_ heme protein_ mitochondrial**	**1.035789662**	**0.0557**	**5**
Q9D0M3	ALAEEVEVQDGPNDDGEMFMRPGK	1.005724683	3	3.55996
Q9D0M3	GLLSSLDHTSIR	1.020237957	2	2.88851
Q9D0M3	HGGEDYVFSLLTGYCEPPTGVSLR	1.303991758	3	5.57031
Q9D0M3	HLVGVCYTEEEAK	1.041146097	2	3.58469
Q9D0M3	LSDYFPKPYPNPEAAR	1.069181113	3	3.49944
Q9D0S9	**HINT2 Histidine triad nucleotide_binding protein 2_ mitochondrial**	**1.006573331**	**0.8887**	**2**
Q9D0S9	ISQAEEDDQQLLGHLLLVAK	1.075122418	2	4.95961
Q9D0S9	SLPADILYEDQQCLVFR	0.969932067	2	3.44505
Q9D172	**ES1 ES1 protein homolog_ mitochondrial**	**1.044589389**	**0.8016**	**4**
Q9D172	GVEVTVGHEQEEGGK	0.988717354	2	3.64731
Q9D172	ITSLAQLNAANHDAAIFPGGFGAAK	1.170215524	3	4.529
Q9D172	NLSTFAVDGK	1.01954653	1	2.44497
Q9D172	NVLAESAR	1.077709543	1	1.94351
Q9D1Q6	**ERP44 Endoplasmic reticulum resident protein 44**	**1.079832139**	**3E-16**	**4**
Q9D1Q6	MNPAVFLSLADLR+Oxidation(0)	6.683869625	2	2.69559
Q9D1Q6	NIIGYFEQK	1.055742802	1	2.29655
Q9D1Q6	SNPVHEIQSLDEVTNLDR	1.03651792	2	4.96729
Q9D1Q6	VDCDQHSDIAQR	1.132601431	2	3.82175
Q9D2U9	**H2B3A Histone H2B type 3_A**	**0.940690882**	**0.2829**	**5**

Q9D2U9	AMGIMNSFVNDIFER	0.930071449	2	4.80314
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.955860381	2	4.48539
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(1)	0.846931637	2	2.96093
Q9D2U9	AMGIMNSFVNDIFER+Oxidation(4)	0.951607651	2	3.66554
Q9D2U9	LLLPGELAK	1.025224716	2	2.53921
Q9D552	**SPT17 Spermatogenesis_associated protein 17**	**1.103314793**	**0.2305**	**3**
Q9D552	DINEVLEQR	1.17850813	2	2.54153
Q9D552	FENDAAVMIQSWFR	1.205510895	2	2.53936
Q9D552	MNLYNEMAVRIQR+Oxidation(0)	1.058177856	2	2.40668
Q9D6M3	**GHC1 Mitochondrial glutamate carrier 1**	**1.3281011**	**4E-14**	**2**
Q9D6M3	GAAVNLTLVTPEK	1.439582482	2	3.44339
Q9D6M3	GVNEDTYSGFLDCAR	1.27911452	2	4.47436
Q9D6Y9	**GLGB 1_4_alpha_glucan_branching enzyme**	**1.0580988**	**0.7752**	**9**
Q9D6Y9	CSDGGIYCK	1.273917425	1	2.14786
Q9D6Y9	CVAYAESHDQALVGDK	0.984833289	2	4.35537
Q9D6Y9	EFKDEDWNMGNIVYTLTNR	1.56462446	3	3.48271
Q9D6Y9	GTHDLWDSR	0.971017251	2	2.52799
Q9D6Y9	IVLDSDAAEYGGHQR	1.008546574	2	4.09841
Q9D6Y9	IYESHVGISSHEGK	0.949668479	2	3.06856
Q9D6Y9	NSEDGLNMFDGTDSCYFHSGPR	1.273316845	3	3.91893
Q9D6Y9	QFNLTDDDLLR	1.022004741	2	2.55812
Q9D6Y9	WELYIPPK	1.097380893	2	2.45851
Q9D7B6	**ACAD8 Isobutyryl_CoA dehydrogenase_ mitochondrial**	**1.097777211**	**0.9034**	**3**
Q9D7B6	AVIFEDCAVPVANR	0.93281698	2	3.64251
Q9D7B6	FASYCLTEPGSGSDAASLLTSAK	1.057356441	2	4.33649
Q9D7B6	VHQILEGSNEVMR	1.086415454	2	2.43571
Q9D819	**IPYR Inorganic pyrophosphatase**	**0.974109695**	**9E-12**	**4**
Q9D819	GISCMNTTVSESPFK	1.161644277	2	4.20554
Q9D819	GISCMNTTVSESPFK+Oxidation(4)	0.977832736	2	4.20847
Q9D819	VLGILAMIDEGETDWK	1.185687716	2	2.59918
Q9D819	YVANLFPYK	1.005321278	1	2.02722
Q9D880	**TIM50 Mitochondrial import inner membrane translocase subunit TIM50**	**1.170553814**	**0.5327**	**2**
Q9D880	TIALNQVEDVR	1.105920044	2	2.56946
Q9D880	TVLEHYALEDDPLEAFK	1.181103516	2	3.42939
Q9D8V0	**HM13 Minor histocompatibility antigen H13**	**1.042163711**	**0.7539**	**2**
Q9D8V0	EESTEASASKRLEK	1.080188695	2	2.73452
Q9D8V0	SSSDMPETITSR	1.038120595	2	2.80614
Q9DC70	**NDUS7 NADH dehydrogenase [ubiquinone] iron_sulfur protein 7_ mitochondrial**	**1.173680408**	**0.0006**	**2**
Q9DC70	LDDLINWAR	1.175343377	2	3.61363
Q9DC70	QADVMIVAGTLTNK	1.222115067	2	2.74404
Q9DCM0	**ETHE1 Protein ETHE1_ mitochondrial**	**1.112484643**	**0.1081**	**3**
Q9DCM0	IFTLPGNCLIYPAHDYHGLTVSTVEEER	1.176298495	3	3.31575
Q9DCM0	SLLPGCQSVISR	1.104244535	2	3.33936
Q9DCM0	TDFQQGCAK	1.297501876	2	2.91063
Q9DCS9	**NDUBA NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10**	**1.268260861**	**3E-09**	**2**
Q9DCS9	AYDLVVDWPVTLVR	1.261020848	2	4.54356
Q9DCS9	TPAPSPQTSLPNPITYLTK	2.284632625	2	2.38401
Q9DCT2	**NDUS3 NADH dehydrogenase [ubiquinone] iron_sulfur protein 3_ mitochondrial**	**1.16793421**	**9E-07**	**4**
Q9DCT2	FDLNSPWEAFPAYR	1.173564088	2	2.98088
Q9DCT2	KFDLNSPWEAFPAYR	0.942867464	2	3.49393
Q9DCT2	SLADLTAVDVPTR	1.211257689	2	3.67081
Q9DCT2	VVAEPVELAQEFR	0.701277359	2	3.31772

Q9DCU9	**HOGA1 Probable 4_hydroxy_2_oxoglutarate aldolase_ mitochondrial**	**0.987427591**	**0.5981**	**3**
Q9DCU9	GFVVQGSTGEFPFLTSLER	0.997540542	2	5.2033
Q9DCU9	LIEPNTAVTR	0.982026957	2	3.05442
Q9DCU9	TMDWFGYYGGPCR	1.269671575	2	3.06446
Q9EP75	**CP4FE Leukotriene_B4 omega_hydroxylase 3**	**1.008504101**	**0.0036**	**2**
Q9EP75	DEDGKELSDEDIR	1.649452687	2	3.15584
Q9EP75	IFNDSTNIMHAK	0.924886575	2	3.00365
Q9EP89	**LACTB Serine beta_lactamase_like protein LACTB_ mitochondrial**	**0.9941122**	**0.2648**	**7**
Q9EP89	EVWSEGLGYADVENR	0.893488018	2	3.55372
Q9EP89	FENSIESLR	0.918528779	2	2.49425
Q9EP89	IKDEVGAPGIVVGVSVDGK	0.846846549	2	4.80436
Q9EP89	KNDFEQGELYLK	1.041265756	2	2.3477
Q9EP89	LDLDLPVQHYVPEFPEKEYEGEK	1.05974173	3	3.77404
Q9EP89	LVNTPYVDNSYK	1.132213014	2	3.07392
Q9EP89	WAGGGFLSTVGDLLK	1.203045681	2	4.58895
Q9EPE9	**AT131 Probable cation_transporting ATPase 13A1**	**0.949513936**	**0.1092**	**2**
Q9EPE9	MAVVGNAVPCGARPGGAR+Oxidation(0)	0.941000214	2	2.82417
Q9EPE9	VLALGYK	1.330833639	2	2.33111
Q9EPH2	**MRP MARCKS_related protein**	**0.983931834**	**0.0281**	**2**
Q9EPH2	AAATPESQEPQAK	0.99040396	2	2.42341
Q9EPH2	GDVTAEEAAGASPAK	0.736305933	2	2.69591
Q9EPH8	**PABP1 Polyadenylate_binding protein 1**	**1.090364154**	**0.1507**	**5**
Q9EPH8	ALDTMNFDVIK	1.16408017	2	3.221
Q9EPH8	EFSPFGTITSAK	1.06214763	2	2.52382
Q9EPH8	GFGFVSFER	1.17809696	2	2.55918
Q9EPH8	KEFSPFGTITSAK	0.83288197	2	2.58329
Q9EPH8	SKVDEAVAVLQAHQAK	1.003409117	2	5.0934
Q9EQ76	**FMO3 Dimethylaniline monooxygenase [N_oxide_forming] 3**	**1.721466471**	**1E-19**	**12**
Q9EQ76	ASIYQSVFTNSSK	1.967488342	2	2.76411
Q9EQ76	GTCILPSVNDMMDDIDEK	1.615965861	2	4.04344
Q9EQ76	KEPVFNDELPAR	1.712176419	3	3.71688
Q9EQ76	LQEYITSFATEK	1.833354634	2	3.19928
Q9EQ76	NNEVTLYK	2.024878362	2	2.40115
Q9EQ76	NNLPTAISDWWYMK	1.520988752	2	2.86003
Q9EQ76	SCLEEGLEPTCFER	1.460533822	2	4.42511
Q9EQ76	SDDVGGLWK	2.089635992	2	2.71212
Q9EQ76	VAVIGAGVSGLAAIR	1.182877931	2	2.83871
Q9EQ76	VLVIGLGNSGCDIAAELSHVAQQVIISSR	2.039832947	3	3.86818
Q9EQ76	VWNDGYPWDMVVITR	1.295258637	2	3.95411
Q9EQ76	YIQFETLVTR	2.082739851	2	3.15389
Q9EQH3	**VPS35 Vacuolar protein sorting_associated protein 35**	**1.167732575**	**0.645**	**4**
Q9EQH3	IREDLPNLESSEETEQINK	1.086879632	2	5.47707
Q9EQH3	LNLEHIATSSAVSK	1.07870909	2	3.46595
Q9EQH3	LSQLEGVNVER	0.965123076	2	2.77935
Q9EQH3	VLETTVEIFNK	1.212175356	2	2.55935
Q9EQS0	**TALDO Transaldolase**	**1.081216803**	**0.0193**	**6**
Q9EQS0	ALAGCDFLTISPK	1.048633589	2	3.39146
Q9EQS0	ILDWHVANTDKK	0.744855271	2	3.08359
Q9EQS0	LGGPQEEQIK	1.176054361	2	2.81071
Q9EQS0	SYEPQEDPGVK	0.814561067	2	2.88496
Q9EQS0	VSTEVDAR	1.293270048	1	1.92669
Q9EQS0	WLHNEDQMAVEK	0.95787411	2	2.49516
Q9EQX9	**UBE2N Ubiquitin_conjugating enzyme E2 N**	**1.064066789**	**0.5096**	**3**
Q9EQX9	LELFLPEEYPMAAPK	1.028095271	2	4.24261
Q9EQX9	SNEAQAIETAR	1.085186192	2	3.38814
Q9EQX9	YFHVVIAGPQDSPFEGGTFK	1.164619409	3	4.3043

Q9ER34	**ACON Aconitate hydratase_ mitochondrial**	**1.068747873**	**0.004**	**18**
Q9ER34	ADIANLAEEFK	1.033547652	2	3.0169
Q9ER34	CTTDHISAAGPWLK	0.947797848	2	3.91597
Q9ER34	DINQEVYNFLATAGAK	0.998970992	2	4.35485
Q9ER34	DLEDLQILIK	1.008654172	2	2.44353
Q9ER34	FKLEAPDADELPR	1.04999188	3	3.96993
Q9ER34	FNPETDFLTGK	1.112960282	1	2.27027
Q9ER34	GHLDNISNNLLIGAINIENGK	1.101250968	2	5.65551
Q9ER34	IVYGHLDDPANQEIER	1.459713696	2	4.65566
Q9ER34	LEAPDADELPR	1.245109128	2	2.51305
Q9ER34	LTGTLSGWTSPK	1.241261237	2	2.86316
Q9ER34	NAVTQEFGPVPDTAR	1.018519657	2	4.35867
Q9ER34	NDANPETHAFVTSPEIVTALAIAGTLK	1.105191975	3	4.07107
Q9ER34	QGLLPLTFADPSDYNK	1.099303411	2	3.34785
Q9ER34	SDFDPGQDTYQHPPK	1.024350874	2	2.66801
Q9ER34	SQFTITPGSEQIR	1.054164099	2	3.22964
Q9ER34	VDVSPTSQR	1.035634896	2	2.45164
Q9ER34	VGLIGSCTNSSYEDMGR	1.272551846	2	4.1295
Q9ER34	WVVIGDENYGEGSSR	1.112546559	2	4.31266
Q9ES21	**SAC1 Phosphatidylinositide phosphatase SAC1**	**0.93157238**	**0.8136**	**4**
Q9ES21	GSEKPLEQTFAK	0.968148957	2	2.57621
Q9ES21	LEEQDEFEK	0.892455448	2	2.50447
Q9ES21	TQLGLVMDGFNSLLR	1.055857599	2	3.15657
Q9ES21	VVTNQEGVFR	1.071312423	2	2.47277
Q9ES38	**S27A5 Bile acyl_CoA synthetase**	**0.866885644**	**0.1183**	**11**
Q9ES38	ACQAAWALK	1.191263779	2	2.36709
Q9ES38	ADVWENFQQR	0.862935114	2	3.14468
Q9ES38	EGFDVGVIADPLYILDNK	0.865067158	2	5.33677
Q9ES38	GATAILVLPSK	0.759249688	1	2.09269
Q9ES38	IQDSLEITNTYK	0.915893837	2	3.54167
Q9ES38	LKEATIQEDK	0.842086564	2	2.51468
Q9ES38	QGFCIPVETGKPGLLLTK	0.983498149	3	3.4396
Q9ES38	SISALSVFLGLAK	0.837418844	2	3.09557
Q9ES38	SLMPDVYQAVCEGTWK	1.009171995	2	3.85262
Q9ES38	YLCNVPGQPEDK	0.957777728	2	2.88206
Q9ES38	YLCNVPGQPEDKK	0.602048707	2	3.07558
Q9ES40	**PRAF3 PRA1 family protein 3**	**1.105634288**	**0.3451**	**2**
Q9ES40	AWDDFFPGSDR	1.075872102	2	2.7625
Q9ES40	LENKMEGIGLK	1.132985832	2	2.3248
Q9EST6	**AN32B Acidic leucine_rich nuclear phosphoprotein 32 family member B**	**0.971556156**	**0.1438**	**3**
Q9EST6	LAEELPSLTHLNLSGNNLK	0.903752218	2	4.14976
Q9EST6	SLDLFGCEVTNR	0.97953135	2	2.68416
Q9EST6	TPAAVQELVLDNCK	1.275103176	2	3.61139
Q9ESW0	**DDB1 DNA damage_binding protein 1**	**1.040729878**	**0.8156**	**3**
Q9ESW0	IEVQDTSGGTTALRPSASTQALSSSVSSSK	1.095261844	3	5.8052
Q9ESW0	KTEPATGFIDGDLIESFLDISRPK	1.087082274	3	4.38001
Q9ESW0	QGQGQLVTCSGAFK	0.986918918	2	2.79321
Q9HB97	**PARVA Alpha_parvin**	**1.051970524**	**0.9704**	**2**
Q9HB97	LNVAEVTQSEIAQK	1.052917995	2	4.27197
Q9HB97	QIQEEITGNTEALSGR	1.047035117	2	2.47727
Q9JHL4	**DBNL Drebrin_like protein**	**1.093120276**	**0.0805**	**2**
Q9JHL4	AMSTTSVSSSQPGK	1.042328762	2	2.35558
Q9JHL4	TGELEQEVVSR	1.110788096	2	3.02602
Q9JI85	**NUCB2 Nucleobindin_2**	**1.230626724**	**1E-19**	**6**
Q9JI85	FQQGIAPSGPAGELK	1.339548474	2	2.92359
Q9JI85	LSQELDLVSHK	0.99340574	2	2.3217

Q9JI85	QEYQQAVQQLEQK	1.234904643	2	4.02301
Q9JI85	QVIEVLETDPHFR	0.951642136	2	2.43191
Q9JI85	TRLDELK	1.123314101	1	1.90317
Q9JI85	VHNVEPVESAR	1.414926162	2	2.67674
Q9JI91	**ACTN2 Alpha_actinin_2**	**0.856302404**	**0.7036**	**6**
Q9JI91	ETADTDTAEQVIASFR	1.292197117	2	3.00439
Q9JI91	GYEEWLLNEIR	0.856229585	2	3.77578
Q9JI91	HTNYTMEHIR	1.042986786	3	3.54253
Q9JI91	KHEAFESDLAAHQDR	0.852000006	2	5.40143
Q9JI91	QSILAIQNEVEK	1.087754753	2	2.8084
Q9JI91	TINEVETQILTR	1.216335985	2	2.67362
Q9JIL8	**RAD50 DNA repair protein RAD50**	**0.975740985**	**0.9171**	**2**
Q9JIL8	KEEQLSSYEDK	0.975525173	2	2.30628
Q9JIL8	MIELKTEILTK+Oxidation(0)	0.982377876	2	2.33845
Q9JJ19	**NHRF1 Na(_)/H(_) exchange regulatory cofactor NHE_RF1**	**1.018792999**	**0.9724**	**3**
Q9JJ19	AVDPDSPAEASGLR	1.018734556	2	3.15912
Q9JJ19	LVEVNGENVEK	0.681159294	2	2.42654
Q9JJ19	SEHTEPPAAADTK	1.114870224	2	3.02143
Q9JJ46	**EBP 3_beta_hydroxysteroid_Delta(8)_Delta(7)_isomerase**	**1.052240571**	**0.0003**	**2**
Q9JJ46	HLTNAQSMLDNK	1.222416458	2	3.14961
Q9JJ46	HLTNAQSMLDNK+Oxidation(7)	0.845995673	2	2.91994
Q9JJ54	**HNRPD Heterogeneous nuclear ribonucleoprotein D0**	**0.85303401**	**0.0003**	**2**
Q9JJ54	FGDVVDCTLK	0.839009084	2	2.68361
Q9JJ54	IFVGGLSPDTPEEK	1.042191838	2	4.00692
Q9JJ79	**DYHC2 Cytoplasmic dynein 2 heavy chain 1**	**1.098471628**	**0.1447**	**5**
Q9JJ79	DQIEVMKGNVKSR	1.337175436	2	2.31349
Q9JJ79	LVQSVHQSLAALSKVIR	1.061758811	2	2.62911
Q9JJ79	NCLEEWTKAAGLEK	1.067180182	2	2.56091
Q9JJ79	TVLRGSGNLLR	1.237741493	2	2.58366
Q9JJ79	YVVQIGDK	0.944643311	1	2.29421
Q9JJU8	**SH3L1 SH3 domain_binding glutamic acid_rich_like protein**	**1.030860742**	**0.8652**	**2**
Q9JJU8	GDYDAFFEAR	1.022674838	2	2.83613
Q9JJU8	QQDVLCFLEANK	1.316520618	2	3.31448
Q9JK38	**GNA1 Glucosamine 6_phosphate N_acetyltransferase**	**1.066961337**	**0.0031**	**4**
Q9JK38	GRVEDVVVSDECR	0.940416545	2	3.03268
Q9JK38	ITLECLPQNVGFYK	1.635597939	2	3.01209
Q9JK38	VEDVVVSDECR	1.085212737	2	3.15315
Q9JK38	VLGQLTETGVVSPEQFMK	1.042714232	2	2.46703
Q9JLA3	**UGGG1 UDP_glucose:glycoprotein glucosyltransferase 1**	**1.000277006**	**0.6864**	**5**
Q9JLA3	GQYQGLSQDPNSLSNLDQDLPNNMIHQVPIK	1.012248739	3	5.82075
Q9JLA3	IVPEWQDYDQEIK	0.907713665	2	3.44055
Q9JLA3	LGIEGLSLHNILK	1.406918321	3	3.37365
Q9JLA3	LNIQPSETDYAVDIR	1.080721002	2	2.62119
Q9JLA3	VWQLQDLSFQTAAR	1.094104112	2	4.56084
Q9JLJ3	**AL9A1 4_trimethylaminobutyraldehyde dehydrogenase**	**1.076291952**	**1E-19**	**17**
Q9JLJ3	AGAPNGLFNVVQGGAATGQFLCQHR	1.367442302	2	3.89628
Q9JLJ3	ANDTTFGLAAGVFTR	1.260719633	2	4.7528
Q9JLJ3	CQVLLEAAR	1.041148723	2	3.12383
Q9JLJ3	EQGATVLCGGEPYAPEDPK	1.055211084	2	4.83193
Q9JLJ3	EQGATVLCGGEPYAPEDPKLK	0.976833373	3	3.4038
Q9JLJ3	EVNLAVENAK	0.886462698	1	2.86323
Q9JLJ3	GALLANFLTQGQVCCNGTR	1.172854419	3	4.66162
Q9JLJ3	GIKPITLELGGK	1.182823134	3	4.02842
Q9JLJ3	IGDPLLEDTR	1.119498983	2	3.91392
Q9JLJ3	MGPLINAPHLER	1.155603045	2	3.08443
Q9JLJ3	MGPLINAPHLER+Oxidation(0)	1.084382506	2	2.82389
Q9JLJ3	RDEIAIMETINNGK	1.118099728	2	5.14414

Q9JLJ3	SAPALACGNAMIFKPSPFTPVSALLLAEIYTK	1.520511685	3	3.97744
Q9JLJ3	VEPVDASGTEK	1.083736286	2	2.31258
Q9JLJ3	VSFTGSVPTGMK	1.084080734	2	3.47068
Q9JLJ3	VSFTGSVPTGMK+Oxidation(10)	1.095525085	2	2.65625
Q9JLJ3	VTIEYYSQLK	1.476657117	2	2.91103
Q9JLZ3	**AUHM Methylglutaconyl_CoA hydratase_ mitochondrial**	**0.878806511**	**0.0339**	**4**
Q9JLZ3	AVGLISHVLEQNQEGDAAYR	0.85723251	2	4.93263
Q9JLZ3	AVGLISHVLEQNQEGDAAYRK	0.809419763	3	3.94479
Q9JLZ3	GIVVLGINR	1.113437086	2	2.87364
Q9JLZ3	SEVPGIFCAGADLK	0.879317054	2	2.60328
Q9JM53	**AIFM1 Apoptosis_inducing factor 1_ mitochondrial**	**0.945602027**	**3E-08**	**14**
Q9JM53	AIASAAEGGSVPPIR	0.98416367	2	2.58557
Q9JM53	CLIATGGTPR	0.99967185	2	2.72794
Q9JM53	DGEQHEDLNEVAK	0.848509557	2	3.59124
Q9JM53	KSQASGIEVIQLFPEK	0.761194809	2	3.51522
Q9JM53	KVETDHIVTAVGLEPNVELAK	0.865209996	2	6.35309
Q9JM53	LNDGSQITFEK	0.958577381	2	3.3771
Q9JM53	SATEQSGTGIR	1.053067825	2	2.34741
Q9JM53	SITVIGGGFLGSELACALGR	1.019281543	2	3.04191
Q9JM53	SQASGIEVIQLFPEK	1.033127586	2	4.25788
Q9JM53	TGGLEIDSDFGGFR	0.941585098	2	3.85795
Q9JM53	VETDHIVTAVGLEPNVELAK	1.120168472	2	4.65845
Q9JM53	VLIVSEDPELPYMRPPLSK	0.940183289	2	2.6951
Q9JM53	VMPNAIVQSVGVSGGK	1.067205114	2	2.8594
Q9JM53	VMPNAIVQSVGVSGGK+Oxidation(1)	0.897625036	2	3.20344
Q9JMD3	**PCTL PCTP_like protein**	**1.044262616**	**0.1951**	**5**
Q9JMD3	AVSIQTGYLIQSTGPK	1.04533505	2	4.74025
Q9JMD3	ESVQVPDDQDFR	1.028436333	2	2.59228
Q9JMD3	MECCDVPAETLYDVLHDIEYR	1.151880795	2	4.2919
Q9JMD3	MECCDVPAETLYDVLHDIEYR+Oxidation(0)	1.17093836	3	3.76826
Q9JMD3	WDSNVIETFDIAR	1.049448746	2	4.04863
Q9QVC8	**FKBP4 Peptidyl_prolyl cis_trans isomerase FKBP4**	**0.88156416**	**6E-05**	**5**
Q9QVC8	GEPNNVAGNQAQVK	0.862877136	2	3.73493
Q9QVC8	RGEAHLAVNDFDLAR	1.137103289	3	3.3679
Q9QVC8	TQLAVCQQR	0.905487811	2	2.46733
Q9QVC8	VAENGAQSAPLPLEGVDISPK	0.79057343	2	4.04462
Q9QVC8	VGEVCHITCKPEYAYGSAGSPPK	0.82384606	3	5.93432
Q9QX79	**FETUB Fetuin_B**	**0.805654204**	**0.1015**	**2**
Q9QX79	GSIQHLPEQEEPEDSKGK	0.780696813	3	3.89259
Q9QX79	NTAPTSSPSITAPR	0.813761385	2	2.8806
Q9QXG4	**ACSA Acetyl_coenzyme A synthetase_ cytoplasmic**	**0.747354154**	**0.1612**	**2**
Q9QXG4	AELGMNDSPSQSPPVK	0.760565287	2	3.48687
Q9QXG4	IGPIATPDYIQNAPGLPK	0.707891344	2	2.84736
Q9QXQ0	**ACTN4 Alpha_actinin_4**	**1.22383035**	**4E-09**	**25**
Q9QXQ0	ACLISLGYDVENDR	1.088782955	2	3.16139
Q9QXQ0	AGTQIENIDEDFR	1.223875606	2	3.37348
Q9QXQ0	AGTQIENIDEDFRDGLK	0.937419306	2	4.40953
Q9QXQ0	ASFNHFDKDHGGALGPEEFK	1.062659199	3	3.55192
Q9QXQ0	DDPVTNLNNAFEVAEK	0.840762228	2	2.90691
Q9QXQ0	ETTDTDTADQVIASFK	1.167467239	2	4.74458
Q9QXQ0	GISQEQMQEFR	1.086352773	2	3.00024
Q9QXQ0	HRDYETATLSDIK	1.210479296	2	3.74364
Q9QXQ0	HRPELIEYDK	1.026277096	3	3.96307
Q9QXQ0	HTNYTMEHLR	1.042986786	3	3.54253
Q9QXQ0	ICDQWDNLGSLTHSR	0.943986591	3	4.23142
Q9QXQ0	KDDPVTNLNNAFEVAEK	0.907925588	3	4.84177
Q9QXQ0	LSGSNPYTSVTPQIINSK	1.204490248	2	4.53451

Q9QXQ0	LVSIGAEEIVDGNAK	1.115343069	2	3.25497
Q9QXQ0	MAPYQGPDAAPGALDYK	1.037608092	2	4.42265
Q9QXQ0	MAPYQGPDAAPGALDYK+Oxidation(0)	1.048006262	2	4.27477
Q9QXQ0	MLDAEDIVNTARPDEK	1.012175132	2	3.09719
Q9QXQ0	MLDAEDIVNTARPDEK+Oxidation(0)	1.23561778	2	2.60371
Q9QXQ0	QFASQANMVGPWIQTK	1.052153055	2	3.23254
Q9QXQ0	RDHALLEEQSK	1.278599788	2	4.05208
Q9QXQ0	SIVDYKPNLDLLEQQHQLIQEALIFDNK	1.200364333	3	4.50077
Q9QXQ0	TINEVENQILTR	0.837060905	2	3.61686
Q9QXQ0	VGWEQLLTTIAR	1.225311583	2	4.08855
Q9QXQ0	VLAGDKNFITAEELR	1.888409463	2	2.49605
Q9QXQ0	VLAVNQENEHLMEDYER	1.210938761	2	4.56155
Q9QXT0	**CNPY2 Protein canopy homolog 2**	**1.097884192**	**0.4916**	**4**
Q9QXT0	ALVDELEWEIAR	1.056182154	2	4.07868
Q9QXT0	IDSDISGTLK	0.983580628	2	2.52143
Q9QXT0	INPDGSQSVVEVPYAR	1.148634639	2	3.94291
Q9QXT0	TDLCDHALHR	1.00520233	2	2.33388
Q9QXX4	**CMC2 Calcium_binding mitochondrial carrier protein Aralar2**	**1.098184143**	**5E-05**	**15**
Q9QXX4	ASGDAARPFLLQLAESAYR	1.090197722	3	4.4418
Q9QXX4	DVEVTKEEFALAAQK	0.884235676	2	4.44064
Q9QXX4	FGLGSIAGAVGATAVYPIDLVK	1.031069248	2	5.22129
Q9QXX4	GLLPQLLGVAPEK	1.07512456	2	3.04968
Q9QXX4	IAPLEEGMLPFNLAEAQR	1.072841889	2	4.31109
Q9QXX4	ITLPAPNPDHVGGYK	1.505819822	2	2.35006
Q9QXX4	KDVEVTKEEFALAAQK	0.99054038	2	4.54294
Q9QXX4	LQVAGEITTGPR	1.15209845	2	3.46494
Q9QXX4	LTVNDFVR	1.310635748	2	2.59244
Q9QXX4	NGEFFMSPHDFVTR	1.024447211	2	3.6141
Q9QXX4	SSPQFGVTLLTYELLQR	1.204879069	2	4.17905
Q9QXX4	STGSFVGELMYK	0.949629681	2	2.77306
Q9QXX4	TVELLSGVVDQTK	1.030652864	2	4.10021
Q9QXX4	YEGFFGLYR	1.076043931	1	2.2286
Q9QXX4	YLNIFGESQPNPK	0.957109162	2	4.5528
Q9QY44	**ABCD2 ATP_binding cassette sub_family D member 2**	**1.503084676**	**0.0027**	**2**
Q9QY44	EGGWDAVMDWKDVLSGGEK+Oxidation(7)	1.093109831	2	2.74204
Q9QY44	VLKACSPKFGTLVAEEAHR	1.593969524	2	2.4426
Q9QYU4	**CRYM Thiomorpholine_carboxylate dehydrogenase**	**0.947108516**	**0.8456**	**2**
Q9QYU4	GFLGVMPAYSAAEDALTTK	0.946920802	2	2.5388
Q9QYU4	SSSLLIPPLEAALANFSK	0.955972555	2	2.40248
Q9QZ09	**PHTF1 Putative homeodomain transcription factor 1**	**0.86929387**	**0.0095**	**2**
Q9QZ09	KMDMSVLEISGIIMSR+Oxidation(1)	0.862242553	2	2.78661
Q9QZ09	MGHIKPDLIDVDLIRGSTFAK+Oxidation(0)	1.172189193	2	2.43317
Q9QZ76	**MYG Myoglobin**	**1.244549438**	**0.9982**	**4**
Q9QZ76	GQHAAEIQPLAQSHATK	1.077996837	2	5.10497
Q9QZ76	HGCTVLTALGTILK	1.415692689	2	3.08959
Q9QZ76	KGQHAAEIQPLAQSHATK	1.381586228	4	5.42427
Q9QZ76	VEGDLAGHGQEVLISLFK	1.193086575	3	5.31498
Q9QZA2	**PDC6I Programmed cell death 6_interacting protein**	**1.032575418**	**0.4689**	**7**
Q9QZA2	ATLVKPTPVNVPISQK	1.032716938	2	3.44932
Q9QZA2	DTIALLCKPEPELNAAIPSANPAK	1.509782217	2	3.21168
Q9QZA2	FYNELTEILVR	1.113316042	2	2.9606
Q9QZA2	LLDEEEATDNDLR	1.086607796	2	3.59775
Q9QZA2	NIQVSHQEFSK	1.100691004	2	3.02424
Q9QZA2	NLATAYDNFVELVANLK	1.061193712	3	3.5896
Q9QZA2	STAVVEQGGIQTVDQLIK	0.999801153	2	3.87014
Q9QZD8	**DIC Mitochondrial dicarboxylate carrier**	**1.005778923**	**0.9984**	**4**
Q9QZD8	GALVTVGQLSCYDQAK	0.965093577	2	3.82447

Q9QZD8	NYSHALDGLYR	1.059793352	2	2.72563
Q9QZD8	VHLQTQQEVK	1.013878519	1	2.76056
Q9QZD8	VLLGGISGLTGGFVGTPADLVNVR	1.037551842	2	5.71202
Q9QZH8	**AAAD Arylacetamide deacetylase**	**1.122317465**	**0.2802**	**2**
Q9QZH8	LDAVVVSTDYGLAPK	1.203926367	2	3.97266
Q9QZH8	WFLQEDILEK	1.114884868	2	3.35009
Q9QZU7	**BODG Gamma_butyrobetaine dioxygenase**	**1.215639373**	**0.2634**	**5**
Q9QZU7	DNCQCSDCYLHSAK	0.8983261	2	2.90905
Q9QZU7	IDANNVAYTTGK	1.26800536	2	3.26272
Q9QZU7	IIELDDKGQVVR	0.937046041	2	2.42509
Q9QZU7	MNPGDVITFDNWR	0.865718788	2	2.57743
Q9QZU7	QTVTGGDSEIVDGFNVCQK	1.01815149	2	4.42389
Q9QZX8	**SO1B2 Solute carrier organic anion transporter family member 1B2**	**1.246393841**	**3E-05**	**2**
Q9QZX8	GIGETPIVPLGISYLDDFAK	1.384186637	2	3.73714
Q9QZX8	QFTDEGNPDSVNK	1.217824062	2	3.41076
Q9R063	**PRDX5 Peroxiredoxin_5_ mitochondrial**	**0.863730401**	**1E-19**	**9**
Q9R063	ALNVEPDGTGLTCSLAPNILSQL	1.178800827	2	3.7077
Q9R063	ETDLLLDDSLVSLFGNR	0.908513948	2	4.40707
Q9R063	GVLFGVPGAFTPGCSK	0.869517667	2	4.17797
Q9R063	KGVLFGVPGAFTPGCSK	0.908616539	2	3.10607
Q9R063	THLPGFVEQAGALK	0.857878676	3	3.97799
Q9R063	VGDTIPSVEVFEGEPGK	0.909990295	2	4.23533
Q9R063	VGDTIPSVEVFEGEPGKK	0.8115824	2	3.68879
Q9R063	VNLAELFK	0.946940561	2	2.82648
Q9R063	VQLLADPTGAFGK	0.952411325	2	4.03533
Q9R0N0	**GALK1 Galactokinase**	**0.855528437**	**0.0136**	**5**
Q9R0N0	AEHSFAGVPCGIMDQLIALLGQK	0.871745345	3	4.34018
Q9R0N0	RQCEEVAQALGK	0.846720191	2	2.81854
Q9R0N0	SLETSLVPLSDPK	0.858026687	2	2.6946
Q9R0N0	TDGLVSLLTTSK	0.808864589	2	3.59816
Q9R0N0	VEELLAEAR	0.985623898	2	2.65661
Q9R0T3	**DNJC3 DnaJ homolog subfamily C member 3**	**1.112240465**	**0.0153**	**5**
Q9R0T3	AEPSVAEYTVR	1.121713999	2	3.02172
Q9R0T3	FDDGEDPLDAETQQGGGSNPFHR	1.257947853	3	3.57937
Q9R0T3	ICSEVLQLEPDNVNALK	1.08067762	2	4.95538
Q9R0T3	KFDDGEDPLDAETQQGGGSNPFHR	1.08159589	3	5.36797
Q9R0T3	SNPSENEEKEAQSQLVK	0.868029168	2	4.64681
Q9R112	**SQRD Sulfide:quinone oxidoreductase_ mitochondrial**	**1.009961305**	**0.8914**	**4**
Q9R112	EGNALFTFPNTPVK	0.984945137	2	2.56796
Q9R112	STLSVIPSGVQWIQDR	1.271044669	2	2.39154
Q9R112	TAAAVAAQSGILDR	1.031555557	2	2.33543
Q9R112	VGAENVAIVEPSER	0.943543567	2	2.3249
Q9R1T3	**CATZ Cathepsin Z**	**0.906853703**	**0.3153**	**2**
Q9R1T3	HGIPDETCNNYQAK	0.906891757	2	3.90078
Q9R1T3	VGDYGSLSGR	0.855086366	2	2.55213
Q9R1Z0	**VDAC3 Voltage_dependent anion_selective channel protein 3**	**1.028463611**	**0.0393**	**3**
Q9R1Z0	LTLSALVDGK	1.463087382	2	2.63151
Q9R1Z0	LTVDTIFVPNTGK	1.028796035	2	3.086
Q9R1Z0	VNNASLIGLGYTQSLRPGVK	0.97642593	2	3.91722
Q9R257	**HEBP1 Heme_binding protein 1**	**1.121261364**	**0.282**	**2**
Q9R257	FATVEVTDKPVDEALR	1.080705815	2	2.70688
Q9R257	NSLFGSVETWPWQVLSTGGK	1.170385696	2	3.74353
Q9WTR8	**PHLP1 PH domain leucine_rich repeat protein phosphatase 1**	**1.047189211**	**0.9637**	**2**
Q9WTR8	LEELEEIDISGNK	1.230758927	2	2.71612
Q9WTR8	LEELEEIDISGNKLK	1.028295085	2	2.31674
Q9WTT6	**GUAD Guanine deaminase**	**1.18697585**	**0.0057**	**7**

Q9WTT6	EIGNFEVGKDFDALLINPR	0.944492114	2	3.53715
Q9WTT6	ETTEESVKETER	1.055774908	2	3.23958
Q9WTT6	FQSTDVAEEVYTR	1.186978842	2	3.58575
Q9WTT6	IVFLEESSQQEK	1.406465138	2	3.75731
Q9WTT6	NIEEVYVGGK	1.269369136	1	1.93236
Q9WTT6	NYTDVYDKNNLLTNK	0.92759179	2	4.3723
Q9WTT6	VCMDLNNTVPEYK	1.083495651	2	3.7372
Q9WTV5	**PSMD9 26S proteasome non_ATPase regulatory subunit 9**	**1.062481136**	**0.9873**	**2**
Q9WTV5	ADVDLYQVR	1.064369014	2	2.62052
Q9WTV5	RKEEIEAQIK	1.040367911	3	3.32969
Q9WU19	**HAOX1 Hydroxyacid oxidase 1**	**0.891366204**	**0.2669**	**7**
Q9WU19	AVFVGRPIIWGLAFQGEK	1.382304989	3	3.38986
Q9WU19	GVQDVLEILK	0.966005599	1	2.00785
Q9WU19	GVQDVLEILKEEFR	0.850071765	2	4.04979
Q9WU19	HGVDGILVSNHGAR	1.020302726	3	5.17638
Q9WU19	NFETNDLAFSPK	0.996736353	2	2.94799
Q9WU19	NVADIDLSTSVLGQR	1.004897325	2	4.9746
Q9WU19	VEVFLDGGVR	1.054216877	2	2.90611
Q9WU82	**CTNB1 Catenin beta_1**	**0.950805019**	**0.8826**	**4**
Q9WU82	AGDREDITEPAICALR	1.189871637	2	2.37607
Q9WU82	HQEAEMAQNAVR	0.909874188	2	3.24012
Q9WU82	LLNDEDQVVVNK	0.975215734	2	3.15532
Q9WU82	TMQNTNDVETAR	0.941186992	2	3.08916
Q9WUC4	**ATOX1 Copper transport protein ATOX1**	**0.973350295**	**1E-19**	**4**
Q9WUC4	LGGVEFNIDLPNK	1.16317515	2	2.83904
Q9WUC4	LGGVEFNIDLPNKK	1.252420718	3	3.33666
Q9WUC4	VCIESEHSSDILLATLNK	1.396201713	2	5.47917
Q9WUC4	VLNKLGGVEFNIDLPNK	0.949390697	2	2.31441
Q9WUJ8	**ORC6 Origin recognition complex subunit 6**	**1.076746016**	**0.9648**	**2**
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(6)	1.076746016	2	2.31794
Q9WUJ8	LSGLNKMMYQSCLK+Oxidation(7)	1.076746016	2	2.37582
Q9WUS0	**KAD4 Adenylate kinase isoenzyme 4_ mitochondrial**	**0.831486333**	**0.0055**	**4**
Q9WUS0	AVILGPPGSGK	0.796137332	2	2.3928
Q9WUS0	GVLHQFSGTETNR	0.851050603	2	3.17975
Q9WUS0	TLVQAEALDR	0.844332594	2	2.75131
Q9WUS0	VYNLDFNPPQVLGVDDITGEPLVQQEDDKPEALAAR	1.099247534	3	5.10717
Q9WVC0	**SEPT7 Septin_7**	**0.929619485**	**0.7221**	**2**
Q9WVC0	NLEGYVGFANLPNQVYR	0.86721628	2	3.74011
Q9WVC0	STLINSLFLTDLYSPEYPGPSHR	0.983780995	3	3.37594
Q9WVF7	**DPOE1 DNA polymerase epsilon catalytic subunit A**	**0.78755696**	**0.0971**	**2**
Q9WVF7	AANMPDSELFELISENR	0.773328984	2	2.30188
Q9WVF7	MAWQWRGEFMPASR+Oxidation(0)	1.314364843	2	2.44538
Q9WVK3	**PECR Peroxisomal trans_2_enoyl_CoA reductase**	**0.908611283**	**1E-19**	**11**
Q9WVK3	AGVYNLTK	0.985575448	2	2.53997
Q9WVK3	ASQPPSSSTQVTAIQCNIR	0.873584919	2	5.49192
Q9WVK3	DHGGSIVNIIVLLNNGFPTAAHSGAAR	0.960872414	3	5.98571
Q9WVK3	ELLHLGCNVVIASR	0.73000491	2	3.9054
Q9WVK3	INFLVNNAGGQFMAPAEDITAK	0.924939905	2	5.52429
Q9WVK3	KEEEVNNLVK	0.835239459	3	3.98836
Q9WVK3	LTAAVDELR	1.08837107	2	3.07218
Q9WVK3	NFTIPDHDNWPVGAGDSSFIK	0.788941974	2	5.14316
Q9WVK3	SGQSYLAAGLLQNQVAVVTGGATGIGK	0.910013208	2	6.00371
Q9WVK3	TMALTWASSGVR	0.914851806	2	3.38855
Q9WVK3	TMALTWASSGVR+Oxidation(1)	0.856066849	2	2.93812
Q9WVK7	**HCDH Hydroxyacyl_coenzyme A dehydrogenase_ mitochondrial**	**0.831931001**	**1E-19**	**12**
Q9WVK7	AADEFVEK	0.946398486	2	3.17468
Q9WVK7	DTPGFIVNR	0.741233039	2	2.32094

Q9WVK7	EDIDTAMK	0.725592719	1	2.16189
Q9WVK7	FAAEHTIFASNTSSLQITNIANATTR	1.081945453	3	4.21055
Q9WVK7	FILDGWHEMDPENPLFQPSPSMNNLVAQK	0.854686068	3	5.34133
Q9WVK7	GDASKEDIDTAMK	0.729609171	2	3.47116
Q9WVK7	GDASKEDIDTAMK+Oxidation(11)	0.969319283	2	3.24662
Q9WVK7	HVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAK	0.829588483	4	5.13642
Q9WVK7	KGIEESLKR	0.875845611	2	2.78606
Q9WVK7	LKNELFQR	0.898749365	2	2.63105
Q9WVK7	LLVPYLIEAIR	1.169042678	2	2.44785
Q9WVK7	TFESLVDFCK	0.880588132	2	3.39419
Q9Z0N2	**IF2H Eukaryotic translation initiation factor 2 subunit 3_ Y_linked**	**0.981421378**	**0.9582**	**3**
Q9Z0N2	IVLTNPVCTEVGEK	1.077633658	2	3.24015
Q9Z0N2	SFDVNKPGCEVDDLK	0.956345668	2	3.05022
Q9Z0N2	VGQEIEVRPGIVSK	0.959966209	2	3.05574
Q9Z0U5	**ADO Aldehyde oxidase**	**1.0211829**	**0.9996**	**8**
Q9Z0U5	CTGYRPIIDACK	0.82650306	2	2.66535
Q9Z0U5	DLEPLILTIEEAIQHK	1.080101575	2	2.78969
Q9Z0U5	ELSILYGGVGPTTIGAK	0.808060033	2	3.79964
Q9Z0U5	GTSTETVPNTNASGGSVVADLNGLAVK	0.939709119	2	4.60314
Q9Z0U5	KLECGNVDEAFK	0.810653523	2	3.42765
Q9Z0U5	LVLDEVTLAGSAPGGK	0.854524396	2	3.2858
Q9Z0U5	MTWISPVTLEELVEAK	1.022955757	2	3.20056
Q9Z0U5	VVENNVDPEMMLLPYLR	0.913987335	2	2.53118
Q9Z0V5	**PRDX4 Peroxiredoxin_4**	**0.951690439**	**0.2331**	**4**
Q9Z0V5	ENECHFYAGGQVYPGEVSR	0.947097107	3	4.57093
Q9Z0V5	GLFIIDDK	1.021118734	2	3.1181
Q9Z0V5	QITLNDLPVGR	0.931279745	2	3.08592
Q9Z0V5	TRENECHFYAGGQVYPGEVSR	0.847279926	3	5.8101
Q9Z0V6	**PRDX3 Thioredoxin_dependent peroxide reductase_ mitochondrial**	**0.972348765**	**0.1336**	**4**
Q9Z0V6	AFQFVETHGEVCPANWTPESPTIKPSPTASK	0.944798913	3	6.444
Q9Z0V6	GLFIIDPNGVIK	0.93631304	2	3.12625
Q9Z0V6	GTAVVNGEFK	0.95710048	2	2.40765
Q9Z0V6	HLSVNDLPVGR	0.921432641	2	2.80017
Q9Z122	**FADS2 Fatty acid desaturase 2**	**0.545195605**	**0.0069**	**2**
Q9Z122	AFHLDLDFVGK	0.651137423	3	3.60596
Q9Z122	HGIEYQEKPLLR	0.54460551	3	3.63334
Q9Z1A6	**VIGLN Vigilin**	**0.998410254**	**0.8176**	**17**
Q9Z1A6	ASVITQVFHVPLEER	1.241504289	2	2.95726
Q9Z1A6	DKFPEVIINFPDPAQK	0.901235143	3	3.47754
Q9Z1A6	DLANIAEVEVSIPAK	1.018948041	2	2.3364
Q9Z1A6	EALEALVPVTIEVEVPFDLHR	1.050258445	2	3.17429
Q9Z1A6	GNSLQEILER	1.030924046	2	2.83425
Q9Z1A6	IDLPAENSNSETIVITGK	0.996221754	2	5.20564
Q9Z1A6	IEGDPQGVQQAK	1.093958675	2	3.60026
Q9Z1A6	IQIPRPDDPSNQIK	0.914947222	2	2.85397
Q9Z1A6	ITLEGPTEDVNVAQEQIEGMVK	1.25954239	2	2.72399
Q9Z1A6	IVGELEQMVSEDVPLDHR	0.94839866	2	3.99379
Q9Z1A6	LQDLELK	0.967195612	1	2.36292
Q9Z1A6	LQTQASATVPIPK	1.059939458	2	3.50546
Q9Z1A6	LVGEIMQETGTR	1.085860247	2	3.48363
Q9Z1A6	RCDIIVISGR	1.039788835	2	2.76133
Q9Z1A6	TGAHLELSLAK	1.201538332	3	3.41978
Q9Z1A6	TGVSVEIPPSDSISETVILR	1.058569043	2	2.63476
Q9Z1A6	VKELQAEQEDR	1.109130389	3	3.41165
Q9Z1J8	**S14L3 SEC14_like protein 3**	**0.90394261**	**0.985**	**3**
Q9Z1J8	ENVQDVLPALPNPDDYFLLR	0.955090134	2	3.2049

Q9Z1J8	FRENVQDVLPALPNPDDYFLLR	0.907838304	2	4.4139
Q9Z1J8	GSSHQVEYEILFPGCVLR	0.984155292	2	4.31054
Q9Z1M9	**SMC1A Structural maintenance of chromosomes protein 1A**	**0.946135066**	**0.4255**	**2**
Q9Z1M9	EIKEKDSELNQK	0.873939891	2	2.31844
Q9Z1M9	MDKVEDELKEK	1.00337728	2	2.36524
Q9Z1W6	**LYRIC Protein LYRIC**	**0.980067837**	**0.9989**	**3**
Q9Z1W6	KREEVTPPTPAPEDPAQLK	1.017056841	3	3.47372
Q9Z1W6	SWQDELAQQAEEGSAR	0.974637064	2	5.5947
Q9Z1W6	TELGLDLGLEPK	0.986285864	2	3.01344
Q9Z269	**VAPB Vesicle_associated membrane protein_associated protein B**	**1.020997748**	**0.9997**	**2**
Q9Z269	TEAPVAAKPLTSPLDDAEVKK	0.994327203	3	3.45576
Q9Z269	VEQVLSLEPQHELK	1.02216846	2	3.78472
Q9Z277	**BAZ1B Tyrosine_protein kinase BAZ1B**	**0.9631552**	**0.0004**	**2**
Q9Z277	IHPLEKVDEEAVEK	0.710060803	2	2.45171
Q9Z277	LQKGGLGYMEGTSEFEARVISLEK	1.160744208	2	2.39933
Q9Z2I8	**SUCB2 Succinyl_CoA ligase [GDP_forming] subunit beta_ mitochondrial**	**0.977701036**	**1E-12**	**8**
Q9Z2I8	DIFAMDDKSENEPIENEAAR	1.075260988	3	4.11281
Q9Z2I8	IDATQVEVNPFGETPEGQVVCFDAK	0.90132146	2	4.60788
Q9Z2I8	INFDDNAEFR	0.889637105	2	3.19536
Q9Z2I8	LEGTNVQEAQNILK	0.927668594	2	5.07144
Q9Z2I8	SENEPIENEAAR	0.957804742	2	3.75394
Q9Z2I8	SHNGPVIVGSPQGGVDIEEVAASSPELIFK	0.800927079	2	5.94784
Q9Z2I8	SSGLPITSAVDLEDAAK	0.926722487	2	4.56245
Q9Z2I8	SSGLPITSAVDLEDAAKK	0.696443987	2	3.5442
Q9Z2I9	**SUCB1 Succinyl_CoA ligase [ADP_forming] subunit beta_ mitochondrial**	**1.001596981**	**0.6349**	**6**
Q9Z2I9	ALIADSGLK	0.876894421	1	1.98628
Q9Z2I9	ILACDDLDEAAK	0.979812262	2	2.90932
Q9Z2I9	INFDSNSAYR	1.057387354	2	2.67281
Q9Z2I9	LSEIVTLAK	1.115414487	2	2.41355
Q9Z2I9	MGFPSNIVDSAAENMIK	0.474279494	2	2.77517
Q9Z2I9	SSDEAYAIAK	1.048830289	2	3.56995
Q9Z2L0	**VDAC1 Voltage_dependent anion_selective channel protein 1**	**1.043564827**	**1**	**11**
Q9Z2L0	KLETAVNLAWTAGNSNTR	1.037667178	2	4.8327
Q9Z2L0	LTFDSSFSPNTGK	1.088576539	2	3.71987
Q9Z2L0	LTFDSSFSPNTGKK	0.905304772	2	2.84859
Q9Z2L0	SENGLEFTSSGSANTETTK	1.042482648	2	4.25682
Q9Z2L0	TDEFQLHTNVNDGTEFGGSIYQK	1.038839336	3	5.04215
Q9Z2L0	TKSENGLEFTSSGSANTETTK	0.728824635	3	3.51891
Q9Z2L0	VNNSSLIGLGYTQTLKPGIK	1.073653057	2	4.44197
Q9Z2L0	VTQSNFAVGYK	1.022877038	2	2.80404
Q9Z2L0	WNTDNTLGTEITVEDQLAR	1.039289125	2	4.44851
Q9Z2L0	WTEYGLTFTEK	0.967181591	2	2.79451
Q9Z2L0	YQVDPDACFSAK	1.027356188	2	3.79237
Q9Z2M4	**DECR2 Peroxisomal 2_4_dienoyl_CoA reductase**	**0.997759663**	**0.0002**	**3**
Q9Z2M4	GQVLQLHAGAAK	1.004155595	2	2.94973
Q9Z2M4	HLAVEWGPQNIR	0.727182296	2	3.11372
Q9Z2M4	VNSLAPGAISGTEGLR	0.82455822	2	4.3013
Q9Z2M7	**PMM2 Phosphomannomutase 2**	**1.07155276**	**0.3396**	**3**
Q9Z2M7	LQEQLGNDVVEK	0.848233251	2	3.5974
Q9Z2M7	TVGYTVTAPEDTR	1.071552788	2	2.68926
Q9Z2M7	YDYVFPENGLVAYK	1.016695322	2	3.18683
Q9Z2Q1	**SC31A Protein transport protein Sec31A**	**1.042555077**	**0.9075**	**12**
Q9Z2Q1	AQDGSNPLSLQDLIEK	1.115092083	2	4.14739
Q9Z2Q1	AVQLTQALDTNTVGALLAEK	1.098076239	2	5.07723

Q9Z2Q1	CLSSATDPQTK	1.282867529	2	3.008
Q9Z2Q1	DQTLSPTIISGLHSIAR	0.976503377	2	2.56569
Q9Z2Q1	GGPGPLAGHPQVSR	0.870635684	2	3.0431
Q9Z2Q1	KIDASQTDFEK	1.009257868	2	2.65866
Q9Z2Q1	LVTFENVTGQPQQGAEQPR	1.166866472	2	3.63777
Q9Z2Q1	QVQHILASASPSGR	1.036955558	2	2.73276
Q9Z2Q1	SSYEGQPLPK	1.000302919	2	2.43834
Q9Z2Q1	TQPPEDISCIAWNR	0.986465437	2	3.07142
Q9Z2Q1	TTFEDLIQR	1.036592666	2	2.89606
Q9Z2Q1	VNFEEDSR	0.946063171	2	2.32576
Q9Z2U2	**ZN292 Zinc finger protein 292**	**0.99126158**	**0.7282**	**2**
Q9Z2U2	KLEVLSNNPDRTVLK	1.154882887	2	2.37697
Q9Z2U2	LINEDSTNAENQGNTTLK	0.963804957	2	2.69927
Q9Z2Z8	**DHCR7 7_dehydrocholesterol reductase**	**0.749325202**	**9E-06**	**4**
Q9Z2Z8	AIECSYTSADGLK	0.655646069	2	3.86921
Q9Z2Z8	ASLADIWAK	0.685095103	2	2.30635
Q9Z2Z8	FLPGYVGGVQEGAITPAGIVNK	0.680257401	2	4.8964
Q9Z2Z8	GYLFPTSAEDCK	0.678517826	2	2.37011
Q9Z339	**GSTO1 Glutathione S_transferase omega_1**	**0.920050177**	**4E-07**	**2**
Q9Z339	GSAPPGPVPEGQIR	0.838812418	2	2.9094
Q9Z339	LEALELNECIDHTPK	0.937530297	2	4.10039