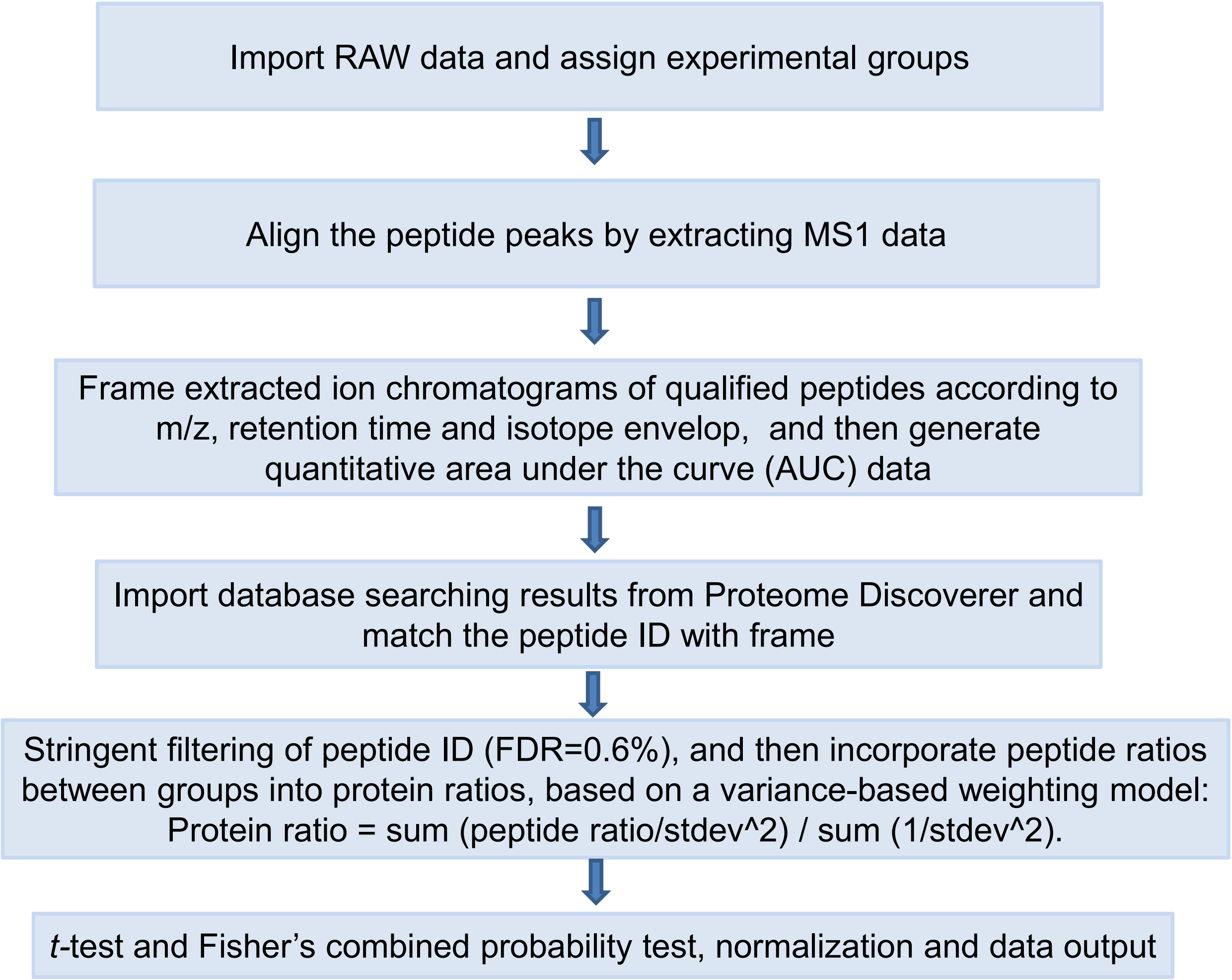
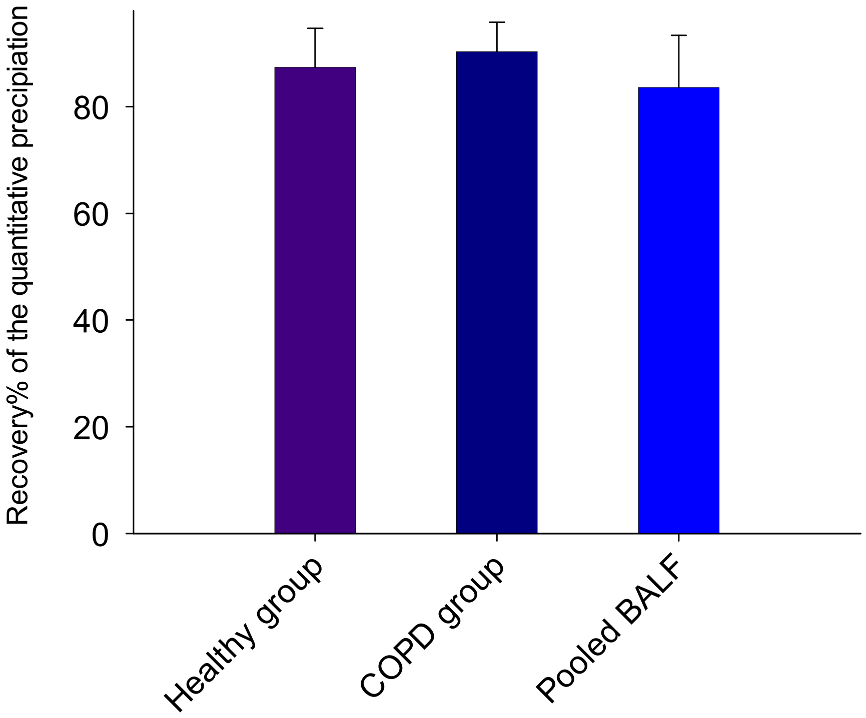
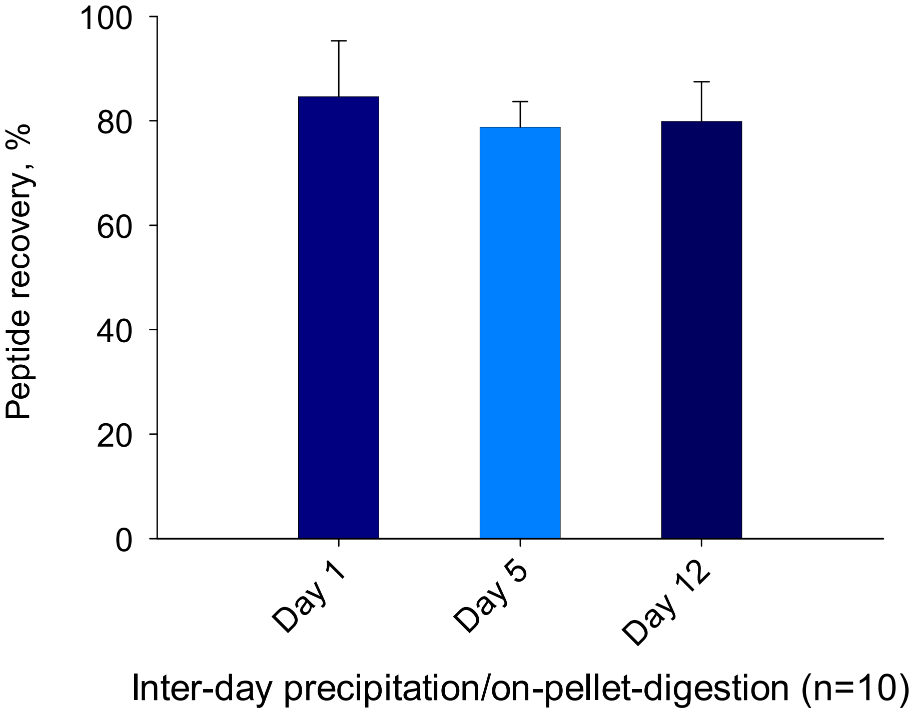


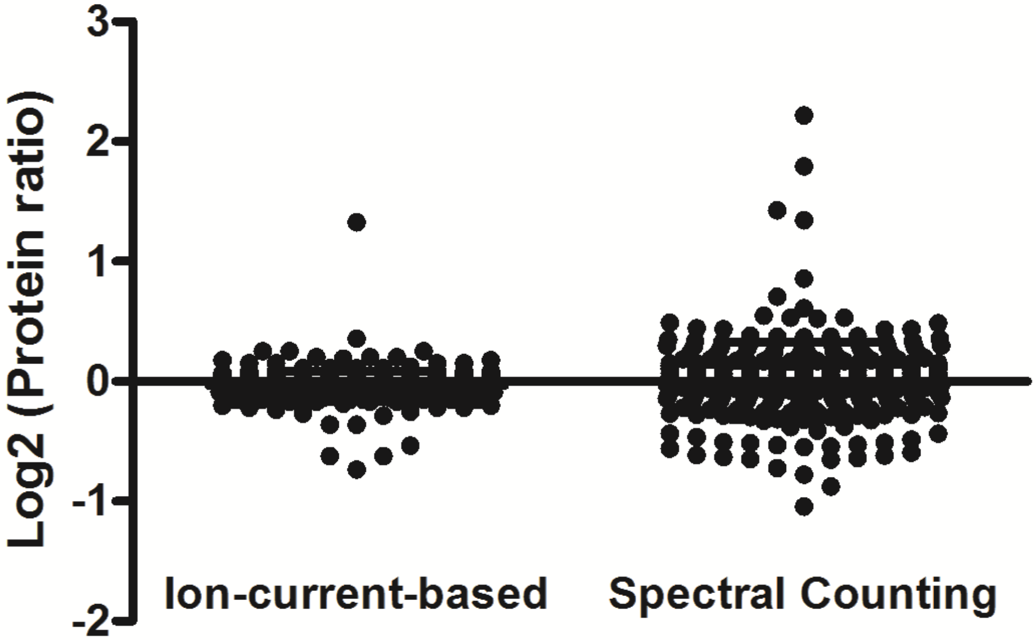
Supplemental Fig. 1. The flow chart of SIEVE analysis. The raw files generated were imported and classified into different experimental groups. The SIEVE software used the ChromAlign algorithm to perform chomatograpic alignment across multiple LC-MS/MS runs. After the alignment, The quantitative frames were generated based upon the precursor m/z and retention time. The area under the curve (AUC) values were calculated by SIEVE based on extracted ion chromograms of each precursor ion. Normalization of peak areas was achieved based on the individual toal ion current (TIC) chromatograms in each LC-MS/MS run. All raw files were searched against the human database using Proteome Discoverer software. The resulted files were imported and the protein/peptide infromation was assigned to each frame. Only peptides with unique protein assignments were considered. Through filtering and calculation of protein ratio based on the weighting formula: Protein ratio = sum (peptide ratio/stdev^2) / sum (1/stdev^2), relative quantification ratios of protein and peptide was presented by SIEVE.



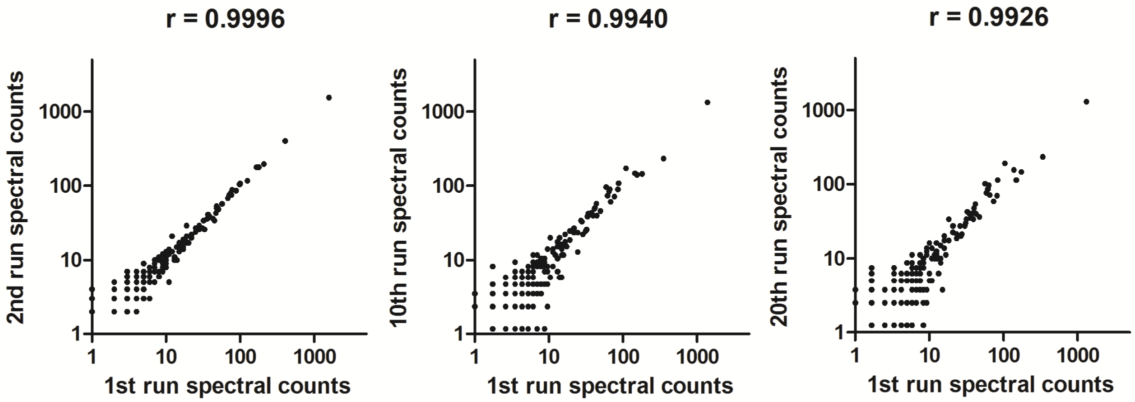
Supplemental Fig. 2. The protein recoveries (as determined by a triplicate BCA assay) of the quantitative precipitation to normalize the protein concentrations in various BALF samples (*n*=10 per group). Before normalization, the staring concentrations in all groups were highly variable (0.07-0.29 mg/mL) due to the dilution factors of the BAL procedure.



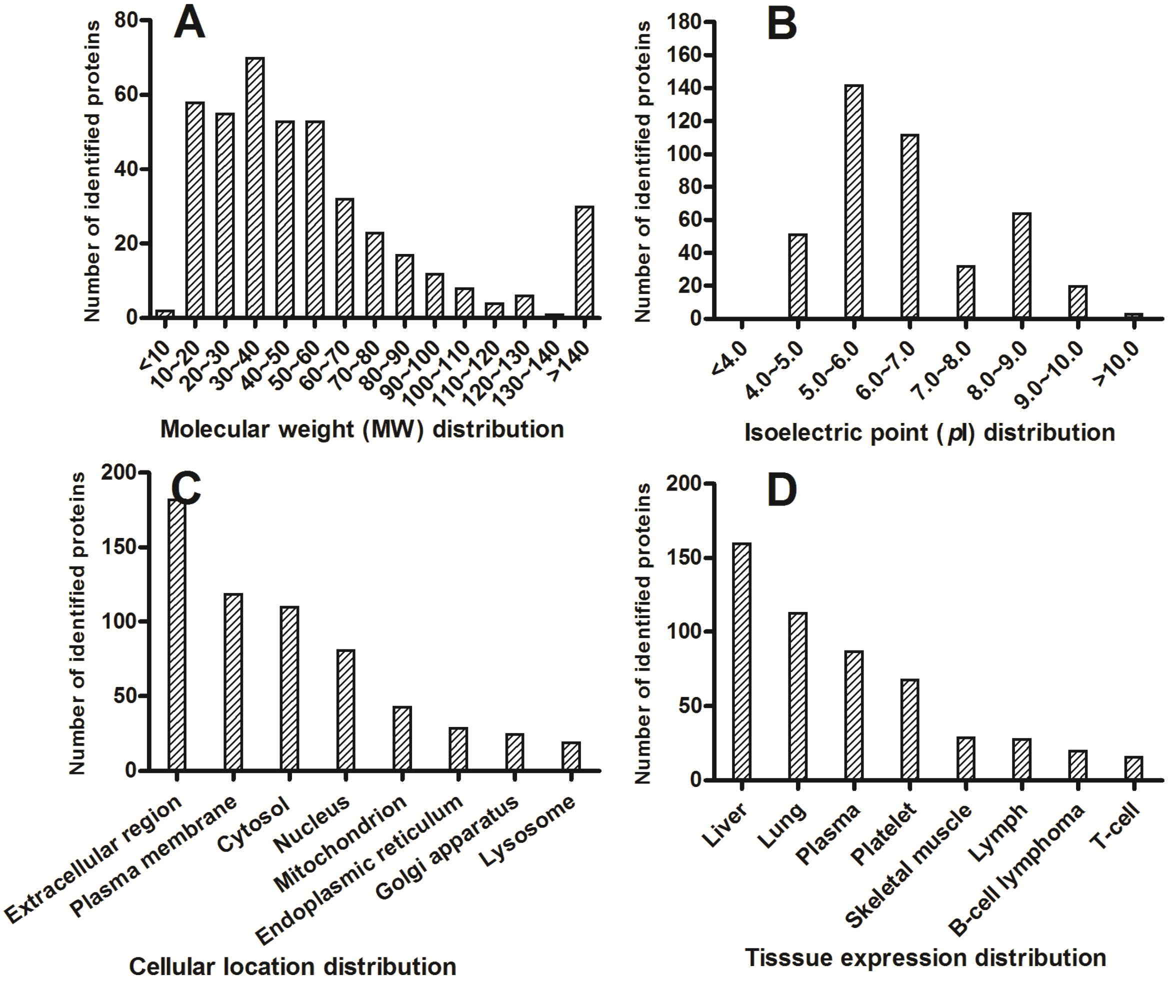
Supplemental Fig. 3. The assessment of inter-day peptide recovery and reproducibility by digesting a pooled BALF at three different days. The peptide recovery was measured with a modified BCA method.



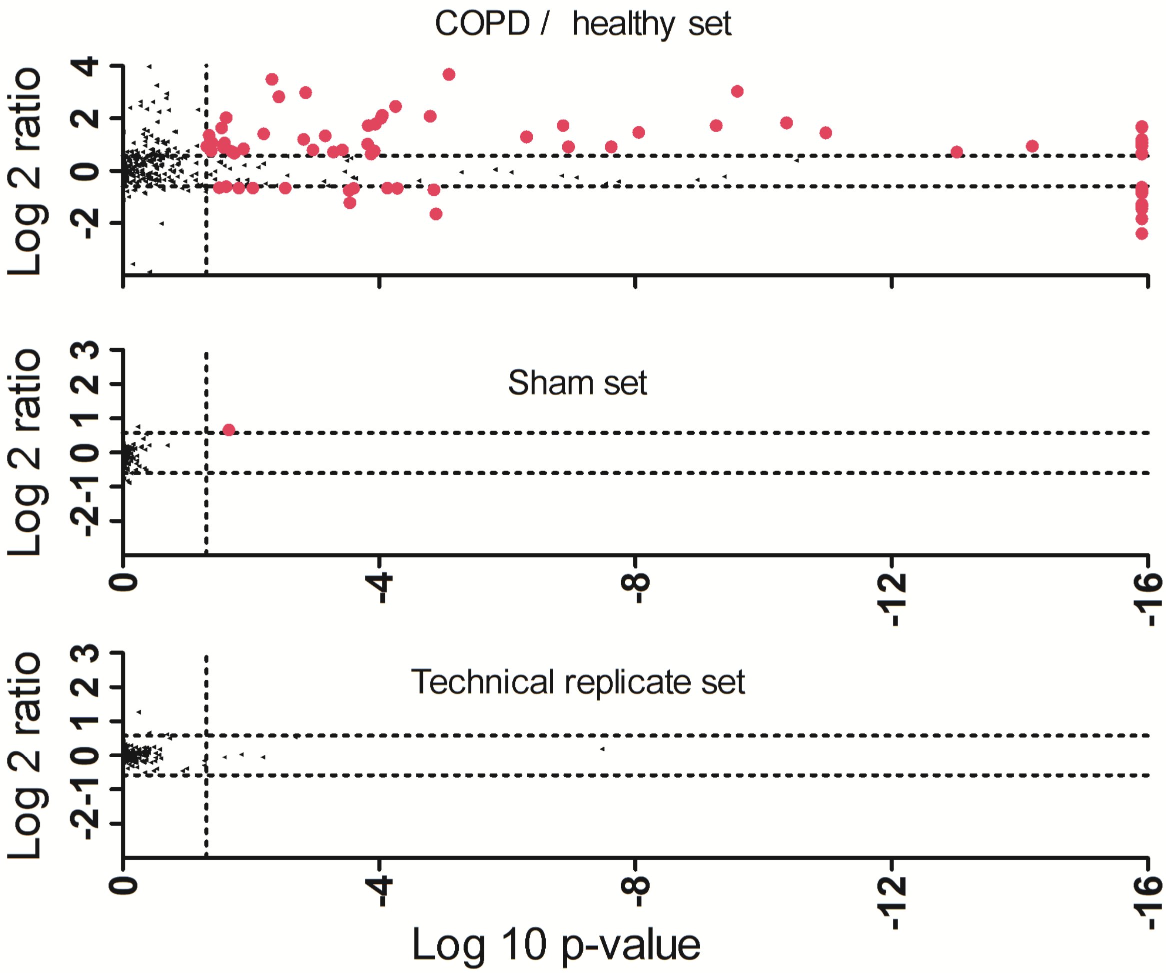
Supplemental Fig. 4. The distribution of protein ratios determined by ion-current-based approach (A) and spectral counting (B) in the technical replicate set (20 preparation and analyses of the same pooled sample, with 10 randomly assigned as the experiment group and 10 as the control group). The theoretical ratio of proteins between the experiment group and control group is 1.0 (Log2 value is 0). The ratios of proteins determined by ion-current-based approach were much tightly centered around the theoretical valued than by spectral counting, indicating better quantitative accuracy for relative protein quantification by ion-current-based approach.



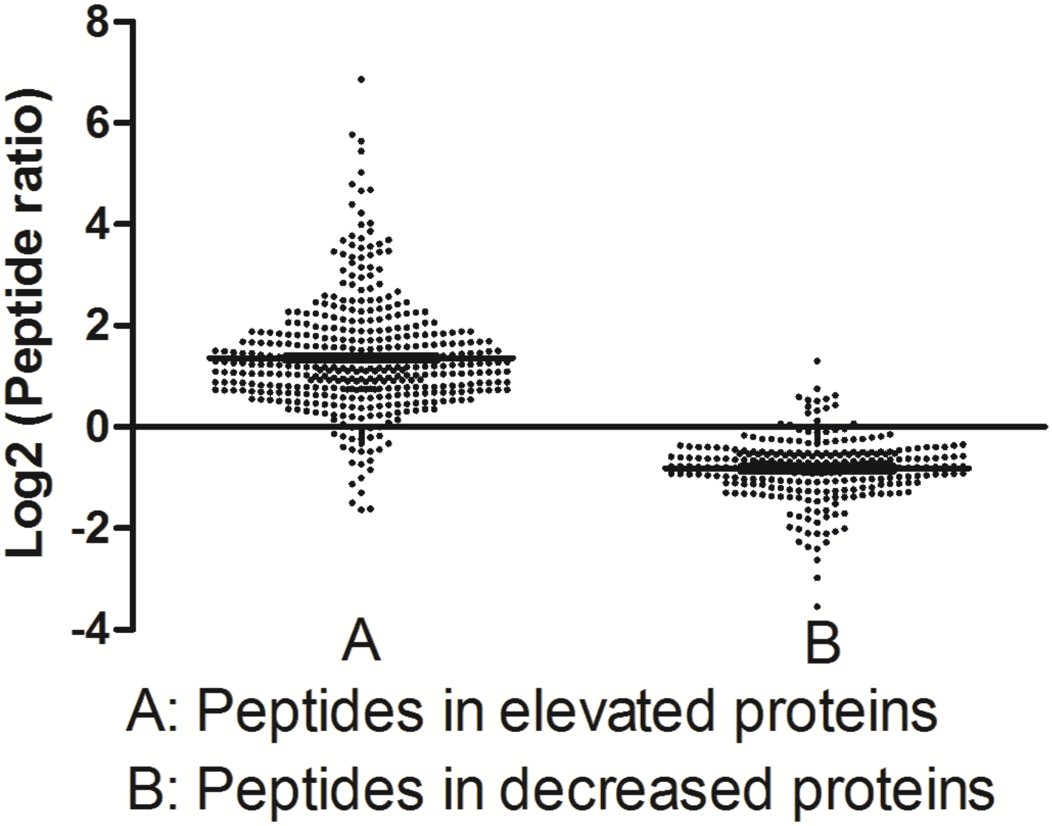
Supplemental Fig. 5. The representative plots for linear correlations of the spectral counts (a more traditional method for the determination of run-to-run reproducibility) between two analyses: the 2nd, 10th and 20th runs vs. the 1st run. Pearson correlation coefficient (*r*) is shown for each comparison.



Supplemental Fig. 6. Characteristics of the 423 identified proteins from BALF samples. (A) MW distribution. (B) *p*I distribution. (C) Cellular location distribution. (D) Tissue expression distribution.



Supplemental Fig. 7. The volcano plots of the COPD/control set, the Sham set (20 BALF samples from individual healthy subjects, with 10 randomly assigned as the experiment group and 10 as the control group) and the technical replicates set (20 preparation and analyses of the same pooled sample, with 10 randomly assigned as the experiment group and 10 as the control group). The Y axis shows the altered ratios of protein levels between two groups, while the X axis shows the *p* values for the comparison. Each dot represent a unique protein group and the dashed lines denote the optimized cutoff thresholds (p <0.05 and >1.5-fold change) that define significantly-altered proteins, which are shown as red dots.



Supplemental Fig. 8. The distribution of peptide ratios assigned to elevated proteins (A) and decreased proteins (B) observed in COPD patients versus healthy controls.

Supplemental Table I
Protein relative expression ratios in the techinical replicate dataset

Accession Number	Gene Name	Protein Name	No. of quantified peptides	Frames	Hits	Ratio	StDev	*p* value
A0M8Q6	LAC7	Ig lambda_7 chain C region	2	36	473	0.97	0.11	1.00
	Peptide				**Ratio**	**Xcorr**	**Charge**	
	AAPSVTLFPPSSEELQANK				0.99	4.6	2	
	YAASSYLSLTPEQWK				0.92	5.7	2	
A6NMY6	AXA2L	Putative annexin A2_like protein	11	21	132	0.96	0.14	1.00
	ALLYLCGGDD				1.08	1.8	1	
	AYTNFDAER				0.84	2.4	2	
	DIISDTSGDFR				1.03	3.1	2	
	GLGTDEDSLIEIICSR				0.74	3.9	2	
	LSLEGDHSTPPSAYGSVK				1.05	4.4	2	
	SALSGHLETVILGLLK				0.94	4.5	2	
	SLYYYIQQDTK				0.76	3.7	2	
	TDLEKDIISDTSGDFR				0.98	3.9	2	
	TDLEKDIISDTSGDFRK				0.96	4.5	3	
	TNQELQEINR				0.86	3.2	2	
	WISIMTER+Oxidation(4)				0.88	2.1	2	
B1AJZ9	FHAD1	Forkhead_associated domain_containing protein 1	2	2	2	0.98	0.44	0.68
	EKMAQMSSLVEKK+Oxidation(5)				1.14	2.3	2	
	KASLKMDQER				0.91	2.4	2	
O00299	CLIC1	Chloride intracellular channel protein 1	4	6	30	0.94	0.26	0.98
	FLDGNELTLADCNLLPK				0.91	3.2	2	
	GFTIPEAFR				0.90	2.4	2	
	LAALNPESNTAGLDIFAK				0.94	4.2	2	
	VLDNYLTSPLPEEVDETSAEDEGVSQR				1.08	4.6	2	
O00391	QSOX1	Sulfhydryl oxidase 1	3	7	31	0.98	0.25	1.00
	AHFSPSNIILDFPAAGSAAR				0.92	5.0	2	
	SALYSPSDPLTLLQADTVR				1.01	3.7	2	
	VLNTEANVVR				1.06	2.2	2	
O00560	SDCB1	Syntenin_1	2	3	3	0.94	0.35	0.86
	DSTGHVGFIFK				0.96	2.2	2	
	FGDQVLQINGENCAGWSSDK				0.89	4.4	2	
O00757	F16P2	Fructose_1_6_bisphosphatase isozyme 2	3	6	18	0.95	0.38	1.00
	GTGELTQLLNSMLTAIK+Oxidation(11)				0.89	2.5	2	
	IYSLNEGYAK				0.95	2.4	2	
	YVGSMVADVHR+Oxidation(4)				0.98	2.6	2	
O15050	TRNK1	TPR and ankyrin repeat_containing protein 1	2	5	27	1.01	0.25	1.00
	FDINFNLKNKEGK				0.98	2.5	2	
	YLSANKMK+Oxidation(6)				1.03	2.3	1	
O15417	TNC18	Trinucleotide repeat_containing gene 18 protein	2	2	4	0.94	0.34	0.80
	LTPSLLCSMVAK+Oxidation(8)				0.95	2.1	2	
	QDEGARLLRR				0.93	2.3	2	
O43150	ASAP2	Arf_GAP with SH3 domain_ ANK repeat and PH domain_containing protein 2	2	2	3	0.94	0.65	0.49
	EIISEVQR				0.56	2.1	2	
	MVLYKMK+Oxidation(0)				1.06	1.8	1	
O43264	ZW10	Centromere/kinetochore protein zw10 homolog	2	2	5	0.97	0.42	1.00
	ELMMMLQASLQEIGDR				0.94	2.1	2	
	YQEEVPVYVPK				0.98	2.3	2	
O43424	GRID2	Glutamate receptor delta_2 subunit	2	2	3	0.88	0.61	0.78
	ENVVDFTTR				0.86	1.8	1	
	NGQCDLYSSVDTKQK				0.90	2.2	2	
O43707	ACTN4	Alpha_actinin_4	5	7	25	1.09	0.33	0.27
	HRPELIEYDK				1.11	3.8	3	
	HTNYTMEHIR+Oxidation(5)				0.96	3.4	3	
	KHEAFESDLAAHQDR				1.43	3.3	3	
	RDHALLEEQSK				1.01	3.0	3	
	TINEVENQILTR				0.94	3.1	2	
O60282	KIF5C	Kinesin heavy chain isoform 5C	2	2	3	0.90	0.78	0.89
	EHLTRLQDAEEMKK				0.96	2.2	2	
	IEDQEREMKLEK				0.85	2.1	2	
O60524	NEMF	Nuclear export mediator factor NEMF	2	5	6	1.00	0.23	0.69

	SALANQIDWTEIGLIVK				0.95	2.1	2	
	YPLDHAR				1.03	1.9	1	
O75151	PHF2	Lysine_specific demethylase PHF2	2	2	2	0.94	0.41	0.79
	EEPPSPIEATPPQSLLEK				0.92	2.2	2	
	SDDSSDEGSLHIDTDTKPGR				0.98	2.2	2	
O75368	SH3L1	SH3 domain_binding glutamic acid_rich_like protein	3	3	31	0.95	0.34	0.98
	ENVPENSRPATGYPLPPQIFNESQYR				0.99	3.6	3	
	QQDVLGFLEANK				0.97	2.9	2	
	VYIASSSGSTAIK				0.88	3.5	2	
O75874	IDHC	Isocitrate dehydrogenase [NADP] cytoplasmic	2	2	18	0.96	0.54	0.99
	EAIICKNIPR				1.04	2.3	2	
	TVEAEAAHGTVTR				0.88	3.3	2	
O94782	UBP1	Ubiquitin carboxyl_terminal hydrolase 1	2	7	54	1.01	0.29	1.00
	LFQGQLVLR				1.00	2.9	2	
	NRLSLKFFQK				1.03	1.8	1	
O96009	NAPSA	Napsin_A	4	14	127	0.97	0.18	1.00
	FAIQYGTGR				1.03	3.1	2	
	GCAAILDTGTSLITGPTEEIR				0.97	6.6	2	
	VDGILSEDKLTIGGIK				0.95	3.2	3	
	VGPGLTLCAK				0.96	3.0	2	
P00338	LDHA	L_lactate dehydrogenase A chain	2	2	5	0.93	0.60	0.96
	LVIITAGAR				0.95	2.3	2	
	QVVESAYEVIK				0.90	2.8	2	
P00352	AL1A1	Retinal dehydrogenase 1	10	21	118	0.93	0.16	0.98
	ANNTFYGLSAGVFTK				0.98	4.9	2	
	EAGFPPGVVNIVPGYGPTAGAAISSHMDIDK				0.92	3.4	3	
	EEIFGPVQQIMK				0.94	3.2	2	
	ELGEYGFHEYTEVK				0.88	3.5	2	
	GYFVQPTVFSNVTDEMR				0.90	3.1	2	
	GYFVQPTVFSNVTDEMR+Oxidation(15)				0.99	4.5	2	
	KFPVFNPATEEELCQVEEGDKEDVDK				0.83	4.4	4	
	LYSNAYLNDLAGCIK				0.85	4.6	2	
	YILGNPLTPGVTQGPQIDK				1.09	3.9	2	
	YILGNPLTPGVTQGPQIDKEQYDK				0.84	3.5	2	
P00390	GSHR	Glutathione reductase_ mitochondrial	3	3	7	0.92	0.29	0.87
	CVMKMVCANKEEK+Oxidation(2)				0.87	2.8	2	
	CVMKMVCANKEEK+Oxidation(4)				0.87	2.7	2	
	MALLPRALSAGAGPSWR+Oxidation(0)				1.04	2.1	2	
P00450	CERU	Ceruloplasmin	23	65	445	0.96	0.09	1.00
	AEEEHLGILGPQLHADVGDK				1.04	4.4	3	
	ALYLQYTDETFR				0.90	4.2	2	
	DIASGLIGPLIICK				0.93	3.5	2	
	DIFTGLIGPMK				0.80	2.2	2	
	DLYSGLIGPLIVCR				0.97	3.3	2	
	ERGPEEEHLGILGPVIWAEVGDTIR				0.89	4.3	3	
	EVGPTNADPVCLAK				0.97	3.0	2	
	GAYPLSIEPIGVR				0.97	3.7	2	
	GPEEEHLGILGPVIWAEVGDTIR				0.85	5.2	3	
	HYYIGIIETTWDYASDHGEK				1.03	6.7	3	
	IYHSHIDAPK				0.95	3.6	3	
	KAEEEHLGILGPQLHADVGDK				0.95	6.2	3	
	KLISVDTEHSNIYLQNGPDR				1.05	5.2	3	
	LISVDTEHSNIYLQNGPDR				0.96	4.4	3	
	MFTTAPDQVDKEDEDFQESNK+Oxidation(0)				0.94	4.7	3	
	MYYSAVDPTK+Oxidation(0)				0.99	2.5	2	
	NLASRPYTFHSHGITYYK				1.09	3.8	3	
	NNEGTYYSPNYNPQSR				0.98	4.5	2	
	QSEDSTFYLGER				0.92	3.3	2	
	TTIEKPVWLGFLGPIIK				0.94	3.8	2	
	TYCSEPEKVDKDNEDFQESNR				0.86	4.4	3	
	VDKDNEDFQESNR				0.98	3.4	3	
	VNKDDEEFIESNK				0.87	4.1	2	
P00558	PGK1	Phosphoglycerate kinase 1	7	16	66	0.97	0.18	1.00
	ACANPAAGSVILLENLR				0.80	3.7	2	
	ALESPERPFLAILGGAK				0.96	4.1	3	
	GCITIIGGGDTATCCAK				0.99	4.4	2	
	ITLPVDFVTADK				0.97	2.5	2	

	ITLPVDFVTADKFDENAK				0.96	3.8	2	
	VLPGVDALSNI				0.97	2.2	2	
	YSLEPVAVELK				1.01	2.8	2	
P00568	KAD1	Adenylate kinase isoenzyme 1	2	2	6	0.95	0.41	0.96
	EVQQGEEFER				0.92	2.7	2	
	YGYTHLSTGDLLR				0.97	2.3	2	
P00734	THRB	Prothrombin	13	25	98	0.94	0.13	0.71
	DKLAACLEGNCAEGLGTNYR				0.97	4.8	2	
	ELLESYIDGR				0.85	2.8	2	
	ETAASLLQAGYK				1.03	2.8	2	
	GQPSVLQVVNLPIVERPVCK				0.96	3.4	2	
	HQDFNSAVQLVENFCR				0.80	3.0	3	
	KSPQELLCGASLISDR				1.06	3.0	2	
	LAACLEGNCAEGLGTNYR				0.85	4.4	2	
	NPDSSTTGPWCYTTDPTVR				0.78	3.4	2	
	RQECSIPVCGQDQVTVAMTPR				0.93	4.0	3	
	SEGSSVNLSPPLEQCVPDR				1.00	4.0	2	
	TATSEYQTFFNPR				0.82	3.4	2	
	TFGSGEADCGLRPLFEK				1.05	4.0	2	
	YTACETAR				0.87	2.5	2	
P00738	HPT	Haptoglobin	22	63	601	0.98	0.09	1.00
	AVGDKLPECEADDGCPKPPEIAHGYVEHSVR				1.05	6.4	4	
	AVGDKLPECEAVCGKPK				1.17	4.4	3	
	DIAPTLTLYVGK				0.48	2.7	2	
	DYAEVGR				0.83	2.2	2	
	GSFPWQAK				1.04	2.9	2	
	HYEGSTVPEK				1.05	2.8	2	
	ILGGHLDAK				0.94	3.0	2	
	LPECEADDGCPKPPEIAHGYVEHSVR				1.03	4.6	4	
	LRTEGDGVYTLNDK				0.96	4.2	2	
	LRTEGDGVYTLNDKK				1.00	4.8	2	
	LRTEGDGVYTLNNEK				1.00	4.8	2	
	SCAVAEYGVYVK				0.95	4.4	2	
	SPVGVQPILNEHTFCAGMSK				0.88	3.5	2	
	SPVGVQPILNEHTFCAGMSK+Oxidation(17)				1.00	4.0	2	
	TEGDGVYTLNDK				0.92	3.9	2	
	TEGDGVYTLNDKK				0.91	3.7	2	
	TEGDGVYTLNNEK				0.92	3.7	2	
	VGYVSGWGR				1.00	3.4	2	
	VTSIQDWVQK				1.02	3.8	2	
	VVLHPNYSQVDIGLIK				0.89	5.0	3	
	YVMLPVADQDQCIR				0.94	3.5	2	
	YVMLPVADQDQCIR+Oxidation(2)				1.01	4.9	2	
P00746	CFAD	Complement factor D	5	10	33	0.95	0.19	1.00
	DSCKGDSGGPLVCGGVLEGVVTSGSR				0.95	4.2	3	
	GDSGGPLVCGGVLEGVVTSGSR				0.98	5.2	2	
	RPDSLQHVLLPVLDR				0.94	3.3	3	
	VDRDVAPGTLCDVAGWGIVNHAGR				0.91	5.1	3	
	VQVLLGAHSLSQPEPSKR				0.97	4.1	3	
P00747	PLMN	Plasminogen	6	11	44	0.95	0.22	1.00
	FSPATHPSEGLEENYCR				1.08	4.0	2	
	HSIFTPETNPR				0.98	2.7	2	
	QLGAGSIEECAAK				1.00	3.0	2	
	TECFITGWGETQGTFGAGLLK				0.91	4.9	2	
	VILGAHQEVNLEPHVQEIEVSR				0.87	4.6	3	
	VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK				0.93	3.8	3	
P00751	CFAB	Complement factor B	15	30	192	0.97	0.13	1.00
	ALFVSEEEKK				0.91	2.6	2	
	CLVNLIEK				0.91	2.3	2	
	DAQYAPGYDK				1.11	2.3	2	
	DISEVVTPR				1.00	2.2	2	
	EKLQDEDLGFL				0.92	3.6	2	
	FIQVGVISWGVVDVCK				1.10	2.7	2	
	FLCTGGVSPYADPNTCR				1.00	4.1	2	
	LEDSVTYHCSR				1.11	3.7	2	
	LLQEGQALEYVCPSGFYPYPVQTR				0.88	4.5	3	
	LPPTTTCQQQK				0.96	2.1	2	

	VKDISEVVTPR				1.14	2.5	2	
	VSEADSSNADWVTK				0.93	4.7	2	
	WSGQTAICDNGAGYCSNPGIPIGTR				0.93	4.6	3	
	YGLVTYATYPK				0.84	4.0	2	
	YGQTIRPICLPCTEGTTR				0.96	3.9	3	
P00915	CAH1	Carbonic anhydrase 1	4	5	23	0.97	0.30	1.00
	ADGLAVIGVLMK				0.92	3.5	2	
	ADGLAVIGVLMKVGEANPK				0.98	1.9	1	
	LYPIANGNNQSPVDIK				0.92	3.5	2	
	VLDALQAIK				1.05	2.6	2	
P00918	CAH2	Carbonic anhydrase 2	2	4	26	0.92	0.30	1.00
	AVQQPDGLAVLGIFLK				0.84	3.8	2	
	YDPSLKPLSVSYDQATSLR				0.95	4.0	3	
P01008	ANT3	Antithrombin_III	12	38	232	0.96	0.13	1.00
	ADGESCSASMMYQEGK+Oxidation(10)				0.77	4.0	2	
	ADGESCSASMMYQEGK+Oxidation(9)				0.77	4.2	2	
	ADGESCSASMMYQEGK+Oxidation(9),Oxidation(10)				1.01	4.4	2	
	AFLEVNEEGSEAAASTAVVIAGR				1.03	6.8	2	
	ATEDEGSEQKIPEATNR				0.76	4.2	2	
	DDLYVSDAFHK				0.89	3.0	2	
	FATTFYQHLADSK				0.95	3.8	2	
	FRIEDGFSLK				0.88	3.8	3	
	NDNDNIFLSPLSISTAFAMTK+Oxidation(18)				0.96	3.4	3	
	SKLPGIVAEGR				1.10	2.6	2	
	TSDQIHFFFAK				0.88	3.6	2	
	VAEGTQVLELPFK				0.97	3.7	2	
P01009	A1AT	Alpha_1_antitrypsin	31	184	1878	0.95	0.05	1.00
	AVLTIDEK				1.06	2.9	2	
	DTEEEDFHVDQVTTVK				0.96	5.5	2	
	FLEDVK				0.88	2.2	2	
	FLEDVKK				0.97	2.6	2	
	FLENEDR				0.90	2.4	2	
	GKWERPFEVK				1.07	3.4	2	
	GTEAAGAMFLEAIPMSIPPEVK+Oxidation(7)				0.88	3.1	2	
	GTEAAGAMFLEAIPMSIPPEVK+Oxidation(7),Oxidation(14)				0.89	3.2	2	
	ITPNLAEFAFSLYR				0.46	3.3	2	
	KLSSWVLLMK				0.70	2.6	2	
	KLSSWVLLMK+Oxidation(8)				0.79	2.9	2	
	KLYHSEAFTVNFGDTEEAK				0.94	5.9	2	
	KLYHSEAFTVNFGDTEEAKK				0.97	5.8	3	
	KQINDYVEK				1.09	2.9	2	
	LGMFNIQHCK+Oxidation(2)				0.92	3.7	3	
	LQHLENELTHDIITK				0.94	5.2	2	
	LSITGTYDLK				0.89	3.2	2	
	LSSWVLLMK				0.28	2.7	2	
	LSSWVLLMK+Oxidation(7)				0.59	2.7	2	
	LYHSEAFTVNFGDTEEAK				0.88	4.8	2	
	LYHSEAFTVNFGDTEEAKK				0.91	6.2	2	
	QINDYVEK				0.91	2.2	2	
	RSASLHLPK				1.09	3.1	3	
	SASLHLPK				0.99	2.7	2	
	SVLGQLGITK				0.90	3.7	2	
	TDTSHHDQDHPTFNK				1.03	4.3	2	
	TLNQPDSQLQLTTGNGLFLSEGLK				0.92	6.3	3	
	VFSNGADLSGVTEEAPLK				0.98	6.2	2	
	VVNPTQK				1.04	2.4	2	
	WERPFEVK				1.15	2.6	2	
	WERPFEVKDTEEEDFHVDQVTTVK				0.83	4.2	4	
P01011	AACT	Alpha_1_antichymotrypsin	9	28	217	0.95	0.14	1.00
	ADLSGITGAR				0.87	3.5	2	
	AVLDVFEEGTEASAATAVK				0.95	6.3	2	
	DEELSCTVVELK				0.91	4.3	2	
	EIGELYLPK				1.05	2.5	2	
	ITLLSALVETR				0.94	4.6	2	
	KLINDYVK				0.97	2.4	2	
	LYGSEAFATDFQDSAAAK				0.90	5.7	2	
	NLAVSQVVHK				0.91	3.0	2	

	WRDSLEFR				1.07	2.4	2	
P01019	ANGT	Angiotensinogen	5	13	106	0.94	0.21	1.00
	ADSQAQLLLSTVVGVFTAPGLHLK				0.94	4.1	3	
	ALQDQLVLVAAK				0.86	3.9	2	
	DPTFIPAPIQAK				1.06	2.7	2	
	SLDFTELDVAAEK				0.99	3.0	2	
	VLSALQAVQGLLVAQGR				0.88	4.5	3	
P01023	A2MG	Alpha_2_macroglobulin	32	73	599	0.94	0.08	1.00
	AAQVTIQSSGTFSSK				0.91	4.9	2	
	AIGYLNTGYQR				0.95	3.1	2	
	ALLAYAFALAGNQDK				0.85	3.6	2	
	DTVIKPLLVEPEGLEK				1.03	3.9	3	
	ETTFNSLLCPSGGEVSEELSLK				0.95	4.9	2	
	FEVQVTVPK				0.93	3.1	2	
	FSGQLNSHGCFYQQVK				0.86	4.5	2	
	GHFSISIPVK				1.26	2.0	1	
	HNVYINGITYTPVSSTNEK				1.01	5.8	2	
	HYDGSYSTFGER				1.03	3.1	2	
	IAQWQSFQLEGGLK				0.90	3.7	2	
	KDTVIKPLLVEPEGLEK				0.92	3.7	3	
	KYSDASDCHGEDSQAFCEK				1.00	4.2	3	
	LHTEAQIQEEGTVVELTGR				0.97	6.4	2	
	LLIYAVLPTGDVIGDSAK				0.90	4.4	2	
	LLLQQVSLPELPGEYSMK				0.99	3.7	2	
	LLLQQVSLPELPGEYSMK+Oxidation(16)				0.81	3.4	2	
	LPPNVVEESAR				0.91	2.8	2	
	LVHVEEPHTETVR				0.97	3.3	3	
	NEDSLVFVQTDK				0.89	3.5	2	
	QFSFPLSSEPFQGSYK				0.96	4.1	2	
	QGIPFFGQVR				0.93	2.6	2	
	QQNAQGGFSSTQDTVVALHALSK				0.89	4.1	3	
	QTVSWAVTPK				0.95	2.4	2	
	TEVSSNHVLIYLDK				0.89	4.6	2	
	VSVQLEASPAFLAVPVEK				0.91	4.8	2	
	VTAAPQSVCALR				1.00	2.4	2	
	VTGEGCVYLQTSLK				0.89	3.7	2	
	VVSMDENFHPLNELIPLVYIQDPK				0.69	3.9	3	
	YDVENCLANK				0.92	2.8	2	
	YNILPEKEEFPFALGVQTLPQTCDEPK				0.86	5.3	3	
	YSDASDCHGEDSQAFCEK				0.87	4.2	3	
P01024	CO3	Complement C3	69	248	2193	0.97	0.04	1.00
	AAVYHHFISDGVR				1.05	4.0	2	
	ACEPGVDYVYK				1.05	3.6	2	
	ADIGCTPGSGK				1.01	3.3	2	
	AGDFLEANYMNLQR				0.76	3.1	2	
	AGDFLEANYMNLQR+Oxidation(9)				0.83	3.7	2	
	AYYENSPQQVFSTEFEVK				0.50	4.9	2	
	CAEENCFIQK				0.92	3.3	2	
	DAPDHQELNLDVSLQLPSR				0.98	5.1	2	
	DFDFVPPVVR				1.03	3.3	2	
	DICEEQVNSLPGSITK				0.99	4.3	2	
	DSCVGSLVVK				0.91	2.4	2	
	DTWVEHWPEEDECQDEENQK				0.85	6.5	3	
	DYAGVFSDAGLTFTSSSGQQTAQR				1.07	6.0	2	
	EDIPPADLSDQVPDTESETR				1.00	5.3	2	
	EGVQKEDIPPADLSDQVPDTESETR				0.99	5.2	3	
	ENEGFTVTAEGK				1.00	3.5	2	
	EVVADSVWVDVK				0.98	4.5	2	
	EYVLPSFEVIVEPTEK				0.54	3.5	2	
	FVTVQATFGTQVVEK				0.95	5.2	2	
	FYHPEKEDGK				0.84	2.8	2	
	FYYIYNEK				0.95	2.2	2	
	GLEVTITAR				0.96	3.2	2	
	GQGTLSVVTMYHAK				0.99	2.9	2	
	GQGTLSVVTMYHAK+Oxidation(9)				1.02	3.1	2	
	GYTQQLAFR				1.00	3.0	2	
	IHWESASLLR				0.93	3.2	3	

	ILLQGTPVAQMTEDAVDAER				0.94	5.9	2	
	ILLQGTPVAQMTEDAVDAER+Oxidation(10)				0.94	5.2	2	
	IPIEDGSGEVVLSR				0.94	3.9	2	
	IWDVVEK				1.02	2.3	2	
	KGYTQQLAFR				1.00	3.9	3	
	KQELSEAEQATR				0.96	4.0	3	
	KVEGTAFVIFGIQDGEQR				1.12	4.9	2	
	KVLLDGVQNPR				1.16	3.0	2	
	LESEETMVLEAHDAQGDVPVTVTVHDFPGK				1.00	5.2	3	
	LESEETMVLEAHDAQGDVPVTVTVHDFPGK+Oxidation(6)				0.94	4.9	4	
	LSINTHPSQKPLSITVR				0.94	4.8	3	
	NTLIIYLDK				0.92	2.8	2	
	QELSEAEQATR				0.99	3.2	2	
	RIPIEDGSGEVVLSR				0.89	4.3	2	
	RQGALELIK				0.96	2.2	2	
	SDDKVTLEER				1.07	3.7	3	
	SEETKENEGFTVTAEGK				1.00	5.2	3	
	SGIPIVTSPYQIHFTK				0.92	4.5	2	
	SGSDEVQVGQQR				1.03	4.2	2	
	SLYVSATVILHSGSDMVQAER				1.03	5.6	2	
	SLYVSATVILHSGSDMVQAER+Oxidation(15)				1.05	4.5	3	
	SNLDEDIIAEENIVSR				0.94	5.2	2	
	SSLSVPYVIVPLK				0.97	3.4	2	
	SYTVAIAGYALAQMGR				1.12	4.2	2	
	SYTVAIAGYALAQMGR+Oxidation(13)				0.98	3.0	2	
	TELRPGETLNVNFLLR				0.98	5.8	3	
	TFISPIK				0.83	2.2	2	
	TGLQEVEVK				0.92	3.3	2	
	TIYTPGSTVLYR				0.97	3.0	2	
	TKKQELSEAEQATR				0.85	3.6	3	
	TMQALPYSTVGNSNNYLHLSVLR+Oxidation(1)				0.95	3.2	3	
	TVMVNIENPEGIPVK				0.97	3.6	2	
	TVMVNIENPEGIPVK+Oxidation(2)				0.98	4.2	2	
	VELLHNPAFCSLATTK				0.95	5.1	3	
	VFLDCCNYITELR				0.96	3.7	2	
	VHQYFNVELIQPGAVK				0.90	4.5	2	
	VLLDGVQNPR				0.97	3.2	2	
	VPVAVQGEDTVQSLTQGDGVAK				1.02	6.2	2	
	VRVELLHNPAFCSLATTK				0.86	4.1	3	
	VSHSEDDCLAFK				0.87	3.6	3	
	VTIKPAPETEK				0.93	2.4	2	
	VVLVAVDK				1.04	2.5	2	
	VYAYYNLEESCTR				0.41	4.2	2	
P01031	CO5	Complement C5	5	9	29	0.94	0.21	0.93
	FQNSAILTIQPK				0.94	3.4	2	
	LHMKTLLPVSKPEIR+Oxidation(2)				1.01	2.5	2	
	LNLVATPLFLKPGIPYPIK				0.85	3.2	3	
	TDAPDLPEENQAR				0.98	2.8	2	
	VFQFLEK				0.92	2.2	2	
P01034	CYTC	Cystatin_C	2	3	23	1.13	0.39	0.46
	ALDFAVGEYNK				1.02	3.0	2	
	LVGGPMDASVEEEGVR+Oxidation(5)				1.39	2.5	2	
P01042	KNG1	Kininogen_1	10	17	133	0.98	0.20	1.00
	AATGECTATVGK				0.91	3.2	2	
	DAAKAATGECTATVGK				1.07	2.2	2	
	DIPTNSPELEETLTHTITK				0.99	4.0	2	
	ENFLFLTPDCK				0.87	3.8	2	
	ESNEELTESCETK				1.08	3.7	2	
	IASFSQNCDIYPGK				0.96	3.2	2	
	LGQSLDCNAEVYVVPWEK				0.94	4.8	2	
	SLWNGDTGECTDNAYIDIQLR				1.06	4.4	2	
	TVGSDTFYSFK				0.81	3.0	2	
	YNSQNQSNNQFVLYR				1.01	4.1	2	
P01591	IGJ	Immunoglobulin J chain	5	11	73	0.95	0.23	1.00
	CYTAVVPLVYGGETK				0.93	4.3	2	
	FVYHLSDLCK				0.92	2.8	2	
	IVLVDNK				1.03	2.0	1	

	KCDPTEVELDNQIVTATQSNICDEDSATETCYTYDR				1.00	6.5	3	
	SSEDPNEDIVER				0.95	3.3	2	
P01598	KV106	Ig kappa chain V_I region EU	3	34	306	0.93	0.11	0.80
	ASSLESGVPSR				0.86	2.2	2	
	DIQMTQSPSTLSASVGDR				0.93	5.3	2	
	DIQMTQSPSTLSASVGDR+Oxidation(3)				0.95	5.4	2	
P01611	KV119	Ig kappa chain V_I region Wes	3	17	94	0.95	0.19	0.95
	DIQMTQSPSSVSASVGDR				0.99	5.0	2	
	DIQMTQSPSSVSASVGDR+Oxidation(3)				0.96	5.0	2	
	LLIYSASSLENGVPSR				0.89	2.2	2	
P01613	KV121	Ig kappa chain V_I region Ni	3	32	323	0.95	0.12	1.00
	DIQMTQSPSSLSATVGDR				0.93	4.0	2	
	DIQMTQSPSSLSATVGDR+Oxidation(3)				0.95	4.6	2	
	LLIYDASNLETGVPSR				0.98	3.8	2	
P01767	HV306	Ig heavy chain V_III region BUT	2	12	66	0.95	0.23	0.95
	AEDTAVYYCAR				0.84	4.1	2	
	EVQLVETGGGLIQPGGSLR				1.01	3.7	2	
P01779	HV318	Ig heavy chain V_III region TUR	2	16	112	0.96	0.14	0.97
	EVQLLESGGGLVQPGGSLR				0.98	6.4	2	
	LSCAASGFTFSR				0.88	2.9	2	
P01781	HV320	Ig heavy chain V_III region GAL	2	3	29	0.91	0.42	0.95
	GLEWVANIK				0.91	3.3	2	
	VEDTALYYCAR				0.90	2.6	2	
P01833	PIGR	Polymeric immunoglobulin receptor	24	91	1105	0.96	0.07	1.00
	ADEGWYWCGVK				0.95	4.2	2	
	AFVNCDENSR				0.94	3.3	2	
	ASVDSGSSEEQGGSSR				0.87	4.7	2	
	CGLGINSR				0.85	2.1	2	
	CPLLVDSEGWVK				0.85	2.6	2	
	DAGFYWCLTNGDTLWR				0.89	4.5	2	
	DGSFSVVITGLR				0.93	4.6	2	
	GGCITLISSEGYVSSK				0.90	5.6	2	
	GSVTFHCALGPEVANVAK				0.97	5.7	2	
	GVAGGSVAVLCPYNR				1.00	3.8	2	
	IIEGEPNLK				0.95	3.0	2	
	ILLNPQDK				0.93	2.7	2	
	ILLNPQDKDGSFSVVITGLR				0.94	4.6	3	
	LSDAGQYLCQAGDDSNSNK				1.09	5.0	2	
	LSDAGQYLCQAGDDSNSNKK				1.09	5.1	2	
	LVSLTLNLVTR				0.92	3.8	2	
	NADLQVLKPEPELVYEDLR				0.92	6.5	3	
	QGHFYGETAAVYVAVEER				0.91	4.9	2	
	QSSGENCDVVVNTLGK				0.99	4.6	2	
	RAPAFEGR				1.01	2.5	2	
	SPIFGPEEVNSVEGNSVSITCYYPPTSVNR				0.96	6.5	3	
	TVTINCPFK				1.06	2.8	2	
	VYTVDLGR				1.01	2.2	2	
	WNNTGCQALPSQDEGPSK				0.99	4.8	2	
P01834	IGKC	Ig kappa chain C region	7	225	2718	0.94	0.03	0.00
	DSTYSLSSTLTLSK				0.89	4.3	2	
	HKVYACEVTHQGLSSPVTK				0.95	4.2	4	
	SGTASVVCLLNNFYPR				0.90	4.9	3	
	TVAAPSVFIFPPSDEQLK				0.95	4.9	3	
	VDNALQSGNSQESVTEQDSK				0.95	5.9	2	
	VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK				0.96	5.9	3	
	VYACEVTHQGLSSPVTK				1.06	5.7	2	
P01857	IGHG1	Ig gamma_1 chain C region	4	44	488	0.97	0.09	1.00
	FNWYVDGVEVHNAK				0.91	5.4	2	
	GPSVFPLAPSSK				1.12	2.9	2	
	THTCPPCPAPELLGGPSVFLFPPKPK				0.96	6.6	3	
	TPEVTCVVVDVSHEDPEVK				0.97	5.5	2	
P01859	IGHG2	Ig gamma_2 chain C region	3	20	163	0.96	0.16	1.00
	CCVECPPCPAPPVAGPSVFLFPPKPK				0.94	5.7	3	
	GFYPSDISVEWESNGQPENNYK				1.00	4.1	2	
	VVSVLTVVHQDWLNGK				0.96	5.1	2	
P01860	IGHG3	Ig gamma_3 chain C region	7	42	409	1.02	0.12	1.00
	CPAPELLGGPSVFLFPPKPK				0.92	5.2	3	

	EPQVYTLPPSREEMTK+Oxidation(13)				1.10	3.0	2	
	SCDTPPPCPR				1.10	2.8	2	
	STSGGTAALGCLVK				1.07	4.5	2	
	TPEVTCVVVDVSHEDPEVQFK				1.00	5.2	3	
	WQQGNIFSCSVMHEALHNR				1.10	2.9	2	
	WYVDGVEVHNAK				1.00	3.9	2	
P01861	IGHG4	Ig gamma_4 chain C region	11	53	575	0.98	0.11	1.00
	DTLMISR+Oxidation(3)				0.91	2.4	2	
	EPQVYTLPPSQEEMTK				0.97	2.5	2	
	EPQVYTLPPSQEEMTK+Oxidation(13)				1.02	2.3	2	
	GFYPSDIAVEWESNGQPENNYK				0.92	5.2	3	
	GPSVFPLAPCSR				1.23	2.2	2	
	NQVSLTCLVK				1.04	3.2	2	
	STSESTAALGCLVK				1.05	4.6	2	
	VVSVLTVLHQDWLNGK				0.93	5.0	2	
	VVSVLTVLHQDWLNGKEYK				1.00	3.6	3	
	WQEGNVFSCSVMHEALHNHYTQK				0.98	3.1	3	
	YGPPCPSCPAPEFLGGPSVFLFPPKPK				0.89	5.4	3	
P01871	IGHM	Ig mu chain C region	3	6	73	1.01	0.24	1.00
	NVPLPVIAELPPK				1.04	2.6	2	
	QVGSGVTTDQVQAEAK				0.91	4.7	2	
	YAATSQVLLPSK				1.05	3.2	2	
P01876	IGHA1	Ig alpha_1 chain C region	6	68	836	0.95	0.07	1.00
	DASGVTFTWTPSSGK				0.97	5.3	2	
	DLCGCYSVSSVLPGCAEPWNHGK				0.98	4.5	2	
	DLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESK				0.98	4.4	4	
	NFPPSQDASGDLYTTSSQLTLPATQCLAGK				0.91	6.2	3	
	TFTCTAAYPESK				0.92	3.9	2	
	TPLTATLSK				1.03	2.0	1	
P01877	IGHA2	Ig alpha_2 chain C region	12	99	940	0.99	0.06	1.00
	DASGATFTWTPSSGK				1.02	4.7	2	
	DLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELK				0.98	5.1	4	
	GDTFSCMVGHEALPLAFTQK				0.97	4.3	2	
	GDTFSCMVGHEALPLAFTQK+Oxidation(6)				0.94	4.0	3	
	HYTNPSQDVTVPCPVPPPPPCCHPR				1.06	5.6	2	
	KGDTFSCMVGHEALPLAFTQK				0.91	5.4	3	
	KGDTFSCMVGHEALPLAFTQK+Oxidation(7)				0.97	4.6	3	
	NFPPSQDASGDLYTTSSQLTLPATQCPDGK				0.98	5.2	3	
	QEPSQGTTTFAVTSILR				0.93	4.5	3	
	SAVQGPPER				1.04	2.8	2	
	WLQGSQELPR				1.05	3.7	2	
	YLTWASR				1.03	2.7	2	
P02042	HBD	Hemoglobin subunit delta	6	24	284	1.03	0.14	1.00
	GTFSQLSELHCDK				1.14	3.2	2	
	KVLGAFSDGLAHLDNLK				0.99	5.8	3	
	LHVDPENFR				1.04	2.3	2	
	VLGAFSDGLAHLDNLK				0.99	5.0	2	
	VNVDAVGGEALGR				1.08	3.9	2	
	VVAGVANALAHK				1.02	3.8	2	
P02647	APOA1	Apolipoprotein A_I	15	58	553	0.96	0.09	1.00
	AELQEGAR				1.04	2.1	2	
	AKPALEDLR				0.96	3.2	3	
	ATEHLSTLSEK				1.03	3.6	3	
	DLATVYVDVLK				0.95	3.9	2	
	DYVSQFEGSALGK				0.95	4.7	2	
	EQLGPVTQEFWDNLEK				0.40	4.0	2	
	LLDNWDSVTSTFSK				0.94	4.5	2	
	LREQLGPVTQEFWDNLEK				0.52	4.6	3	
	LSPLGEEMR+Oxidation(7)				0.86	2.4	2	
	QGLLPVLESFK				0.92	2.9	2	
	THLAPYSDELR				1.16	3.4	2	
	VKDLATVYVDVLK				0.90	3.9	2	
	VQPYLDDFQK				0.97	2.6	2	
	VSFLSALEEYTK				0.83	4.6	2	
	WQEEMELYR+Oxidation(4)				0.96	2.2	2	
P02649	APOE	Apolipoprotein E	2	3	20	0.98	0.30	1.00
	AKLEEQAQQIR				0.98	3.3	3	

	SELEEQLTPVAEETR				0.98	4.6	2	
P02652	APOA2	Apolipoprotein A_II	3	5	27	0.93	0.34	0.94
	EPCVESLVSQYFQTVTDYGK				0.77	4.5	2	
	SKEQLTPLIK				0.85	2.6	2	
	VKSPELQAEAK				1.01	3.9	3	
P02654	APOC1	Apolipoprotein C_I	2	3	7	1.11	0.77	0.87
	EWFSETFQK				1.20	2.4	1	
	LKEFGNTLEDK				0.98	2.5	2	
P02656	APOC3	Apolipoprotein C_III	2	2	25	1.02	0.36	0.95
	DALSSVQESQVAQQAR				1.10	4.2	2	
	GWVTDGFSSLK				0.95	3.0	2	
P02671	FIBA	Fibrinogen alpha chain	11	21	119	0.97	0.19	0.05
	DSHSLTTNIMEILR				0.94	3.1	2	
	ESSSHHPGIAEFPSR				1.07	3.3	3	
	EVDLKDYEDQQK				0.98	3.4	2	
	EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR				0.83	5.0	3	
	GGSTSYGTGSETESPR				1.10	3.9	2	
	GLIDEVNQDFTNR				0.86	3.3	2	
	HRHPDEAAFFDTASTGK				1.00	4.6	3	
	NPSSAGSWNSGSSGPGSTGNR				0.67	5.0	2	
	QFTSSTSYNR				0.98	2.3	2	
	RLEVDIDIK				1.09	2.4	2	
	VQHIQLLQK				1.04	2.1	2	
P02675	FIBB	Fibrinogen beta chain	14	24	172	0.98	0.13	1.00
	AHYGGFTVQNEANK				1.00	4.4	2	
	DNDGWLTSDPR				1.60	2.1	2	
	DNENVVNEYSSELEK				1.00	4.7	2	
	EEAPSLRPAPPPISGGGYR				1.02	2.2	2	
	GGETSEMYLIQPDSSVKPYR+Oxidation(6)				0.87	3.2	3	
	HGTDDGVVWMNWK+Oxidation(9)				0.88	2.5	2	
	HQLYIDETVNSNIPTNLR				0.95	4.8	2	
	LESDVSAQMEYCR				1.11	3.1	2	
	LESDVSAQMEYCR+Oxidation(8)				0.87	4.3	2	
	NYCGLPGEYWLGNDK				0.98	3.3	2	
	QGFGNVATNTDGK				0.87	3.0	2	
	REEAPSLRPAPPPISGGGYR				1.00	3.1	3	
	TPCTVSCNIPVVSGK				1.18	3.4	2	
	VYCDMNTENGGWTVIQNR				0.92	3.9	2	
P02679	FIBG	Fibrinogen gamma chain	13	27	143	0.99	0.14	1.00
	AIQLTYNPDESSKPNMIDAATLK				1.02	3.0	3	
	ASTPNGYDNGIIWATWK				0.97	3.7	2	
	CHAGHLNGVYYQGGTYSK				0.86	4.0	3	
	DNCCILDER				0.73	2.5	2	
	EGFGHLSPTGTTEFWLGNEK				0.78	3.3	3	
	IHLISTQSAIPYALR				1.02	4.0	2	
	LDGSVDFK				0.96	2.3	2	
	QSGLYFIKPLK				0.94	2.5	2	
	RLDGSVDFK				0.92	2.2	2	
	VAQLEAQCQEPCKDTVQIHDITGK				1.11	4.0	3	
	VELEDWNGR				0.98	2.6	2	
	YEASILTHDSSIR				1.09	3.9	2	
	YLQEIYNSNNQK				0.99	4.9	2	
P02743	SAMP	Serum amyloid P_component	2	4	8	0.91	0.30	0.57
	GYVIIKPLVWV				0.86	2.5	2	
	IVLGQEQDSYGGK				0.98	3.5	2	
P02746	C1QB	Complement C1q subcomponent subunit B	2	5	41	1.05	0.41	1.00
	GPMGPKGGPGAPGAPGPK				1.14	2.8	2	
	LEQGENVFLQATDK				0.92	4.0	2	
P02747	C1QC	Complement C1q subcomponent subunit C	2	3	24	0.99	0.34	0.99
	FNAVLTNPQGDYDTSTGK				1.01	5.0	2	
	FQSVFTVTR				0.95	2.3	2	
P02748	CO9	Complement component C9	5	6	50	0.97	0.21	1.00
	AEQCCEETASSISLHGK				0.97	3.2	3	
	LSPIYNLVPVK				0.87	3.0	2	
	SIEVFGQFNGK				1.00	3.3	2	
	TEHYEEQIEAFK				0.98	3.2	2	
	VVEESELAR				0.94	2.4	2	

P02749	APOH	Beta_2_glycoprotein 1	11	31	252	0.96	0.10	1.00
	ATFGCHDGYSLDGPEEIECTK				0.94	5.5	3	
	ATVVYQGER				0.96	2.9	2	
	CSYTEDAQCIDGTIEVPK				0.86	3.8	2	
	DKATFGCHDGYSLDGPEEIECTK				1.13	3.2	3	
	FICPLTGLWPINTLK				0.87	4.4	2	
	KCSYTEDAQCIDGTIEVPK				0.99	4.7	2	
	TCPKPDDLPFSTVVPLK				0.98	4.3	3	
	TDASDVKPC				0.94	2.1	2	
	TFYEPGEEITYSCKPGYVSR				0.95	4.9	2	
	VCPFAGILENGAVR				0.95	3.7	2	
	WSPELPVCAPIICPPPSIPTFATLR				0.95	3.3	2	
P02750	A2GL	Leucine_rich alpha_2_glycoprotein	5	12	78	1.01	0.18	1.00
	ALGHLDLSGNR				1.11	2.5	2	
	DGFDISGNPWICDQNLSDLYR				0.99	5.0	3	
	DLLLPQPDLR				1.07	2.7	2	
	LQELHLSSNGLESLSPEFLRPVPQLR				0.99	3.8	3	
	TLDLGENQLETLPPDLLR				0.93	4.7	2	
P02751	FINC	Fibronectin	33	72	396	0.99	0.08	1.00
	DDKESVPISDTIIPAVPPPTDLR				0.95	3.0	3	
	DLQFVEVTDVK				0.95	4.0	2	
	EESPLLIGQQSTVSDVPR				1.01	3.8	2	
	EINLAPDSSSVVVSGLMVATK				0.94	3.6	2	
	EYLGAICSCTCFGGQR				0.94	4.3	2	
	FTQVTPTSLSAQWTPPNVQLTGYR				0.93	5.2	2	
	GDSPASSKPISINYR				1.12	3.1	2	
	GEWTCIAYSQLR				0.93	2.9	2	
	GFNCESKPEAEETCFDK				1.08	3.7	2	
	GLAFTDVDVDSIK				1.03	3.0	2	
	GNLLQCICTGNGR				1.09	3.3	2	
	HTSVQTTSSGSGPFTDVR				1.05	5.1	2	
	HYQINQQWER				0.97	3.1	2	
	ITYGETGGNSPVQEFTVPGSK				0.93	3.9	2	
	LGVRPSQGGEAPR				0.97	3.9	3	
	NLQPASEYTVSLVAIK				0.65	3.0	2	
	NTFAEVTGLSPGVTYYFK				0.86	4.9	2	
	QDGHLWCSTTSNYEQDQK				1.06	2.7	2	
	SSPVVIDASTAIDAPSNLR				0.95	4.4	3	
	STATISGLKPGVDYTITVYAVTGR				0.86	3.1	3	
	SYTITGLQPGTDYK				1.01	4.2	2	
	TEIDKPSQMQVTDVQDNSISVK				1.09	3.5	2	
	TEIDKPSQMQVTDVQDNSISVK+Oxidation(8)				0.90	4.1	3	
	TETITGFQVDAVPANGQTPIQR				0.98	4.5	2	
	TYHVGEQWQK				0.99	3.9	3	
	TYLGNALVCTCYGGSR				0.97	5.0	2	
	VDVIPVNLPGEHGQR				1.35	2.3	2	
	VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK				1.02	6.4	3	
	VPGTSTSATLTGLTR				1.15	2.5	2	
	VVTPLSPPTNLHLEANPDTGVLTVSWER				0.97	4.8	3	
	WCGTTQNYDADQK				0.80	4.2	2	
	YEVSVYALK				0.90	2.3	2	
	YSFCTDHTVLVQTR				1.00	3.5	2	
P02760	AMBP	Protein AMBP	8	13	100	0.97	0.22	1.00
	CVLFPYGGCQGNGNK				0.98	3.2	2	
	EYCGVPGDGDEELLR				0.97	3.0	2	
	GECVPGEQEPEPILIPR				0.93	4.3	2	
	GVCEETSGAYEK				1.01	3.8	2	
	KGVCEETSGAYEK				0.99	3.7	2	
	TVAACNLPIVR				1.04	3.5	2	
	VVAQGVGIPEDSIFTMADR				0.93	2.9	2	
	WYNLAIGSTCPWLK				0.96	2.6	2	
P02763	A1AG1	Alpha_1_acid glycoprotein 1	5	14	163	0.95	0.21	1.00
	NWGLSVYADKPETTK				0.95	4.4	2	
	SDVVYTDWK				0.99	3.2	2	
	SDVVYTDWKK				0.88	2.7	2	
	TYMLAFDVNDEKNWGLSVYADKPETTK+Oxidation(2)				0.63	3.1	3	
	YVGGQEHFAHLLILR				0.98	4.8	2	

P02765	FETUA	Alpha_2_HS_glycoprotein	9	36	327	0.97	0.12	1.00
	AQLVPLPPSTYVEFTVSGTDCVAK				0.60	3.6	3	
	CDSSPDSAEDVR				1.12	3.8	2	
	CDSSPDSAEDVRK				0.90	3.4	3	
	EHAVEGDCDFQLLK				0.99	4.2	2	
	FSVVYAK				0.95	2.1	2	
	HTFMGVVSLGSPSGEVSHPR				0.94	3.7	3	
	HTFMGVVSLGSPSGEVSHPR+Oxidation(3)				0.90	4.8	3	
	HTLNQIDEVK				0.94	3.8	2	
	TVVQPSVGAAAGPVVPPCPGR				1.03	4.4	2	
P02766	TTHY	Transthyretin	8	30	260	0.96	0.10	1.00
	AADDTWEPFASGK				1.02	4.4	2	
	ALGISPFHEHAEVVFTANDSGPR				0.96	5.2	2	
	GSPAINVAVHVFR				1.07	4.1	2	
	RYTIAALLSPYSYSTTAVVTNPK				1.00	4.2	2	
	RYTIAALLSPYSYSTTAVVTNPKE				0.90	5.2	2	
	TSESGELHGLTTEEEFVEGIYK				0.41	4.7	2	
	YTIAALLSPYSYSTTAVVTNPK				0.94	5.1	2	
	YTIAALLSPYSYSTTAVVTNPKE				0.92	5.4	2	
P02768	ALBU	Serum albumin	66	1381	18232	0.94	0.02	0.99
	AACLLPK				0.95	2.7	2	
	AAFTECCQAADK				0.89	4.1	2	
	ADDKETCFAEEGK				0.87	4.0	3	
	ADDKETCFAEEGKK				0.96	5.3	3	
	AEFAEVSK				0.93	2.7	2	
	AEFAEVSKLVTDLTK				0.98	2.8	2	
	ALVLIAFAQYLQQCPFEDHVK				0.91	5.9	4	
	AVMDDFAAFVEK				0.48	4.1	2	
	AVMDDFAAFVEK+Oxidation(2)				0.49	4.3	2	
	CCAAADPHECYAK				0.90	4.2	2	
	CCTESLVNR				0.87	3.3	2	
	DDNPNLPR				0.93	2.7	2	
	DLGEENFK				0.99	3.1	2	
	DVFLGMFLYEYAR				0.88	4.0	2	
	DVFLGMFLYEYAR+Oxidation(5)				0.93	4.4	2	
	ECCEKPLLEK				1.05	2.8	2	
	EFNAETFTFHADICTLSEK				0.87	6.0	2	
	ETCFAEEGKK				0.90	2.4	2	
	ETYGEMADCCAK				0.83	3.4	2	
	ETYGEMADCCAK+Oxidation(5)				0.97	3.5	2	
	FKDLGEENFK				1.07	4.1	3	
	FQNALLVR				0.97	3.1	2	
	HPDYSVVLLLR				0.24	2.6	2	
	KLVAASQAALGL				0.95	3.5	2	
	KQTALVELVK				1.02	5.1	3	
	KVPQVSTPTLVEVSR				0.99	5.8	3	
	KYLYEIAR				1.09	3.3	2	
	LCTVATLR				0.94	2.4	2	
	LDELRDEGK				0.93	2.7	2	
	LDELRDEGKASSAK				1.15	3.5	3	
	LKECCEKPLLEK				0.92	4.4	2	
	LSQRFPKAEFAEVSK				1.12	4.3	3	
	LVAASQAALGL				0.87	4.4	2	
	LVNEVTEFAK				1.02	3.8	2	
	LVRPEVDVMCTAFHDNEETFLK				0.96	6.4	3	
	LVRPEVDVMCTAFHDNEETFLK+Oxidation(8)				0.89	5.9	3	
	LVRPEVDVMCTAFHDNEETFLKK				0.91	6.6	3	
	LVRPEVDVMCTAFHDNEETFLKK+Oxidation(8)				0.91	5.1	3	
	LVTDLTK				1.00	2.4	2	
	MPCAEDYLSVVLNQLCVLHEK				0.32	5.0	3	
	MPCAEDYLSVVLNQLCVLHEK+Oxidation(0)				0.30	4.9	3	
	MPCAEDYLSVVLNQLCVLHEKTPVSDR				0.91	4.4	4	
	NECFLQHKDDNPNLPR				1.10	5.3	2	
	NYAEAK				0.81	2.1	1	
	QEPERNECFLQHK				0.94	2.6	2	
	QEPERNECFLQHKDDNPNLPR				1.07	3.2	3	
	QNCELFEQLGEYK				0.88	4.4	2	

	QNCELFEQLGEYKFQNALLVR				1.13	3.9	3	
	QTALVELVK				1.04	2.4	2	
	RHPDYSVVLLLR				0.47	5.1	3	
	RMPCAEDYLSVVLNQLCVLHEK				0.96	3.6	3	
	RMPCAEDYLSVVLNQLCVLHEK+Oxidation(1)				0.47	4.7	3	
	RPCFSALEVDETYVPK				0.83	4.2	3	
	SHCIAEVENDEMPADLPSLAADFVESK				0.18	5.6	3	
	SHCIAEVENDEMPADLPSLAADFVESK+Oxidation(11)				0.51	6.3	3	
	SLHTLFGDK				1.13	2.8	1	
	SLHTLFGDKLCTVATLR				1.07	3.1	2	
	TCVADESAENCDK				0.96	4.9	2	
	TYETTLEK				0.93	2.7	2	
	VFDEFKPLVEEPQNLIK				0.94	5.5	3	
	VHTECCHGDLLECADDR				1.04	6.6	2	
	VHTECCHGDLLECADDRADLAK				1.02	5.9	3	
	VPQVSTPTLVEVSR				0.95	4.0	3	
	YICENQDSISSK				0.89	4.5	2	
	YKAAFTECCQAADK				1.10	3.5	3	
	YLYEIAR				1.02	3.3	2	
P02774	VTDB	Vitamin D_binding protein	20	87	607	0.96	0.08	1.00
	CCESASEDCMAK+Oxidation(9)				0.87	3.9	2	
	ELSSFIDKGQELCADYSENTFTEYK				0.92	5.9	3	
	EVVSLTEACCAEGADPDCYDTR				0.94	5.5	2	
	FPSGTFEQVSQLVK				0.98	4.8	2	
	GQELCADYSENTFTEYK				0.88	5.8	2	
	GQELCADYSENTFTEYKK				1.03	3.9	2	
	HLSLLTTLSNR				0.96	3.5	2	
	HQPQEFPTYVEPTNDEICEAFR				0.98	6.4	3	
	KFPSGTFEQVSQLVK				0.95	4.8	2	
	KLCMAALK+Oxidation(3)				0.97	2.2	2	
	RSDFASNCCSINSPPLYCDSEIDAELK				0.88	5.1	3	
	RTHLPEVFLSK				1.01	4.0	3	
	SCESNSPFPVHPGTAECCTK				1.19	5.1	2	
	SDFASNCCSINSPPLYCDSEIDAELK				1.01	5.2	3	
	SLGECCDVEDSTTCFNAK				0.96	5.5	2	
	SYLSMVGSCCTSASPTVCFLK				0.90	5.3	2	
	SYLSMVGSCCTSASPTVCFLK+Oxidation(4)				0.95	5.2	2	
	THLPEVFLSK				0.98	3.5	3	
	VCSQYAAYGEK				0.80	3.2	2	
	YTFELSR				0.96	2.3	1	
P02787	TRFE	Serotransferrin	54	362	3676	0.96	0.05	1.00
	ADRDQYELLCLDNTR				0.32	4.3	2	
	AIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSK				0.68	6.4	4	
	ASYLDCIR				1.06	2.9	2	
	AVANFFSGSCAPCADGTDFPQLCQLCPGCGCSTLNQYFGYSGAFK				0.94	5.6	4	
	CDEWSVNSVGK				0.99	3.9	2	
	CSTSSLLEACTFR				0.96	5.1	2	
	DCHLAQVPSHTVVAR				1.16	4.7	2	
	DDTVCLAK				0.98	2.6	2	
	DGAGDVAFVK				0.95	3.8	2	
	DLLFRDDTVCLAK				0.89	3.0	2	
	DQYELLCLDNTR				0.59	3.2	2	
	DSAHGFLK				0.93	2.3	2	
	DSGFQMNQLR				0.97	3.7	2	
	DSGFQMNQLR+Oxidation(5)				0.93	3.4	2	
	DYELLCLDGTR				0.77	3.5	2	
	EDLIWELLNQAQEHFGK				0.74	5.2	2	
	EDPQTFYYAVAVVK				0.60	4.6	2	
	EFQLFSSPHGK				1.09	3.7	2	
	EGTCPEAPTDECKPVK				0.77	3.6	2	
	EGYYGYTGAFR				0.94	3.5	2	
	FDEFFSEGCAPGSK				0.13	4.7	2	
	GDVAFVK				0.96	2.3	2	
	HQTVPQNTGGK				0.75	2.7	2	
	HSTIFENLANK				1.02	4.7	3	
	IECVSAETTEDCIAK				1.02	5.2	2	
	IMNGEADAMSLDGGFVYIAGK				0.67	5.0	2	

	IMNGEADAMSLDGGFVYIAGK+Oxidation(1)				0.89	5.6	2	
	IMNGEADAMSLDGGFVYIAGK+Oxidation(1),Oxidation(8)				1.00	5.6	2	
	IMNGEADAMSLDGGFVYIAGK+Oxidation(8)				0.89	4.2	2	
	KASYLDCIR				1.12	2.2	2	
	KCSTSSLLEACTFR				1.00	3.7	2	
	KDSGFQMNQLR				0.94	3.0	3	
	KDSGFQMNQLR+Oxidation(6)				1.09	3.6	3	
	KPVDEYKDCHLAQVPSHTVVAR				1.08	5.3	3	
	KPVEEYANCHLAR				1.36	3.9	3	
	KSASDLTWDNLK				0.94	3.3	2	
	LCMGSGLNLCEPNNK				0.98	5.0	2	
	LCMGSGLNLCEPNNK+Oxidation(2)				0.87	4.7	2	
	LKCDEWSVNSVGK				1.12	4.3	2	
	MYLGYEYVTAIR				0.35	4.2	2	
	MYLGYEYVTAIR+Oxidation(0)				0.77	4.3	2	
	NLNEKDYELLCLDGTR				0.45	4.5	2	
	QQQHLFGSNVTDCSGNFCLFR				1.25	3.9	3	
	SASDLTWDNLK				0.98	3.9	2	
	SDNCEDTPEAGYFAIAVVK				1.06	2.7	2	
	SKEFQLFSSPHGK				1.01	4.3	3	
	SMGGKEDLIWELLNQAQEHFGK				0.71	5.3	3	
	SMGGKEDLIWELLNQAQEHFGK+Oxidation(1)				0.89	5.4	3	
	SVIPSDGPSVACVK				1.07	3.3	2	
	TAGWNIPMGLLYNK				0.74	3.9	2	
	TAGWNIPMGLLYNK+Oxidation(7)				0.90	4.3	2	
	WCALSHHER				0.97	3.4	2	
	WCAVSEHEATK				1.04	4.0	2	
	YLGEEYVK				1.02	3.0	2	
P02788	TRFL	Lactotransferrin	25	54	370	0.96	0.10	1.00
	ADAVTLDGGFIYEAGLAPYK				1.02	4.4	2	
	CGLVPVLAENYK				0.95	2.8	2	
	CLAENAGDVAFVK				1.00	3.7	2	
	DSPIQCIQAIAENR				0.93	3.6	3	
	DVTVLQNTDGNNNEAWAK				1.02	5.2	2	
	ESTVFEDLSDEAERDEYELLCPDNTR				0.94	3.8	3	
	FCLFQSETK				0.86	2.6	2	
	FDEYFSQSCAPGSDPR				0.78	4.2	2	
	FFSASCVPGADK				1.11	3.1	2	
	GEADAMSLDGGYVYTAGK				0.94	4.2	2	
	GEADAMSLDGGYVYTAGK+Oxidation(5)				0.95	3.8	2	
	GGSFQLNELQGLK				0.88	3.2	2	
	IDSGLYLGSGYFTAIQNLR				0.87	5.2	2	
	KGGSFQLNELQGLK				0.89	3.1	3	
	LRPVAAEVYGTER				1.08	2.8	2	
	NLLFNDNTECLAR				0.96	4.2	2	
	RSDTSLTWNSVK				1.11	2.2	2	
	SCHLAMAPNHAVVSR+Oxidation(5)				1.22	3.4	3	
	SNLCALCIGDEQGENK				0.98	4.8	2	
	SQQSSDPDPNCVDRPVEGYLAVAVVR				0.92	5.0	3	
	SVQWCAVSQPEATK				1.02	4.3	2	
	THYYAVAVVK				0.92	3.2	3	
	VVWCAVGEQELR				0.90	3.1	2	
	YLGPQYVAGITNLK				0.93	4.3	2	
	YYGYTGAFR				0.88	2.4	2	
P02790	HEMO	Hemopexin	19	112	1007	0.95	0.07	1.00
	CSPHLVLSALTSDNHGATYAFSGTHYWR				0.88	5.3	4	
	DGWHSWPIAHQWPQGPSAVDAAFSWEEK				0.95	4.8	3	
	DYFMPCPGR				0.87	2.1	2	
	DYFMPCPGR+Oxidation(3)				0.98	2.5	2	
	EVGTPHGIILDSVDAAFICPGSSR				0.97	5.8	2	
	EWFWDLATGTMK				0.37	3.2	2	
	EWFWDLATGTMK+Oxidation(10)				0.51	3.2	2	
	GECQAEGVLFFQGDR				0.91	4.6	2	
	GGYTLVSGYPK				1.06	3.8	2	
	LLQDEFPGIPSPLDAAVECHR				0.93	5.5	2	
	LWWLDLK				0.88	2.5	2	
	NFPSPVDAAFR				0.99	2.5	2	

	RLWWLDLK				0.92	2.8	2	
	SGAQATWTELPWPHEK				0.91	4.9	3	
	SLGPNSCSANGPGLYLIHGPNLYCYSDVEK				0.94	5.1	3	
	VDGALCMEK				0.89	2.4	2	
	VDGALCMEK+Oxidation(6)				1.00	2.9	2	
	VWVYPPEK				1.01	2.5	2	
	YYCFQGNQFLR				0.95	3.6	2	
P02812	PRB2	Basic salivary proline_rich protein 2	4	20	67	1.11	0.18	0.91
	SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNK				1.35	4.7	4	
	SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGDN				1.10	5.6	6	
	SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGGS				1.11	5.5	6	
	SPPGKPQGPPQQEGNNPQGPPPPAGGNPQQPQAPPAGQPQGPPRPPQGGRPSRPPQ				0.96	4.2	5	
P03973	SLPI	Antileukoproteinase	2	5	81	1.15	0.64	0.82
	CLDPVDTPNPTR				0.99	3.0	2	
	YKKPECQSDWQCPGK				1.24	4.6	3	
P04003	C4BPA	C4b_binding protein alpha chain	2	2	17	0.96	0.34	0.31
	EDVYVVGTVLR				0.89	3.3	2	
	FSAICQGDGTWSPR				1.05	3.4	2	
P04004	VTNC	Vitronectin	5	11	87	0.97	0.26	1.00
	DVWGIEGPIDAAFTR				0.89	4.0	2	
	DWHGVPGQVDAAMAGR				1.03	2.6	2	
	FEDGVLDPDYPR				1.03	3.7	2	
	GQYCYELDEK				0.86	2.9	2	
	SIAQYWLGCPAPGHL				0.92	4.3	2	
P04075	ALDOA	Fructose_bisphosphate aldolase A	4	7	29	0.93	0.20	0.64
	GILAADESTGSIAK				1.00	3.4	2	
	GVVPLAGTNGETTTQGLDGLSER				0.93	5.4	2	
	LQSIGTENTEENR				0.79	3.2	2	
	YTPSGQAGAAASESLFVSNHAY				1.01	2.7	2	
P04080	CYTB	Cystatin_B	3	9	55	1.01	0.26	1.00
	SQVVAGTNYFIK				1.10	3.5	2	
	VFQSLPHENKPLTLSNYQTNK				1.00	4.2	3	
	VHVGDEDFVHLR				0.93	3.9	3	
P04083	ANXA1	Annexin A1	7	18	158	0.95	0.15	0.91
	AAYLQETGKPLDETLK				1.22	3.2	2	
	ALTGHLEEVVLALLK				0.71	2.8	2	
	DITSDTSGDFR				1.00	3.4	2	
	GGPGSAVSPYPTFNPSSDVAALHK				0.91	4.3	2	
	GTDVNVFNTILTTR				0.93	4.4	2	
	GVDEATIIDILTK				0.93	4.5	3	
	SEDFGVNEDLADSDAR				0.97	4.9	2	
P04114	APOB	Apolipoprotein B_100	7	10	38	0.97	0.20	0.97
	ATFQTPDFIVPLTDLR				0.96	3.0	2	
	IEGNLIFDPNNYLPK				1.04	2.4	2	
	ILGEELGFASLHDLQLLGK				0.88	3.2	3	
	TQFNNNEYSQDLDAYNTK				1.52	2.2	2	
	TSSFALNLPTLPEVK				0.92	2.4	2	
	VLLDQLGTTISFER				0.93	3.4	2	
	VNWEEEAASGLLTSLK				0.89	3.7	2	
P04196	HRG	Histidine_rich glycoprotein	5	13	82	0.95	0.18	1.00
	DGYLFQLLR				0.81	2.9	2	
	HPLKPDNQPFPQSVSESCPGK				0.99	4.0	3	
	KGEVLPLPEANFPSFPLPHHK				0.94	5.5	3	
	YKEENDDFASFR				1.01	3.6	2	
	YWNDCEPPDSR				0.60	2.5	2	
P04217	A1BG	Alpha_1B_glycoprotein	8	21	183	0.98	0.15	0.97
	ATWSGAVLAGR				0.96	4.0	2	
	CEGPIPDVTFELLR				0.52	2.7	2	
	HQFLLTGDTQGR				1.05	3.7	3	
	IFFHLNAVALGDGGHYTCR				0.94	4.2	3	
	NGVAQEPVHLDSPAIK				1.18	3.8	2	
	SGLSTGWTQLSK				1.02	3.7	2	
	SLPAPWLSMAPVSWITPGLK+Oxidation(8)				0.92	3.6	2	
	VTLTCVAPLSGVDFQLR				0.90	5.6	2	
P04220	MUCB	Ig mu heavy chain disease protein	6	14	155	0.99	0.18	1.00
	FTCTVTHTDLPSPLK				1.03	3.7	2	
	GVALHRPDVYLLPPAR				0.95	4.8	3	

	LICQATGFSPR				1.00	2.3	2	
	VSVFVPPR				0.99	2.4	2	
	YVTSAPMPEPQAPGR				0.87	2.6	2	
	YVTSAPMPEPQAPGR+Oxidation(6)				0.98	3.5	2	
P04264	K2C1	Keratin_ type II cytoskeletal 1	15	28	158	0.78	0.18	0.01
	AQYEDIAQK				0.59	2.3	2	
	EQIKSLNNQFASFIDK				0.99	2.2	2	
	FLEQQNQVLQTK				0.66	4.3	2	
	FSSCGGGGGSFGAGGGFGSR				0.66	4.2	2	
	GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR				0.52	6.9	3	
	GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR				0.52	6.1	3	
	IEISELNR				0.56	2.6	2	
	LNDLEDALQQAK				0.56	4.7	2	
	LNDLEDALQQAKEDLAR				1.02	2.1	2	
	QISNLQQSISDAEQR				0.66	4.3	2	
	SKAEAESLYQSK				0.59	3.7	2	
	SLDLDSIIAEVK				0.53	4.7	2	
	SLNNQFASFIDK				0.67	3.3	2	
	TNAENEFVTIK				0.73	3.0	2	
	WELLQQVDTSTR				0.86	3.6	2	
P04280	PRP1	Basic salivary proline_rich protein 1	4	11	28	1.05	0.24	0.92
	APPGKPQGPPQQEGNNPQGPPPPAGGNPQQPQAPPAGQPQGPPRPPQGGRPSRPPQ				0.90	6.2	5	
	SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPPQGDK				1.13	4.4	6	
	SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPQQGGNRPQGPPPPGKPQGPPPQGDK				1.16	4.1	6	
	SPQSPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNKPQGPPPPGKPQGPPAQ				1.09	4.1	6	
P04350	TBB4	Tubulin beta_4 chain	4	7	12	0.97	0.33	0.98
	ALTVPELTQQMFDAK				0.86	3.2	2	
	EIVHLQAGQCGNQIGAK				0.97	3.9	3	
	FWEVISDEHGIDPTGTYHGDSDLQLER				1.14	3.1	3	
	MAATFIGNSTAIQELFK+Oxidation(0)				0.83	4.1	2	
P04406	G3P	Glyceraldehyde_3_phosphate dehydrogenase	6	14	57	1.03	0.20	0.62
	GALQNIIPASTGAAK				1.16	3.2	2	
	GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK				1.05	4.9	4	
	IISNASCTTNCLAPLAK				1.06	4.1	2	
	LISWYDNEFGYSNR				0.95	2.9	2	
	VIHDNFGIVEGLMTTVHAITATQK				0.90	5.4	3	
	VPTANVSVVDLTCR				0.98	2.3	2	
P04746	AMYP	Pancreatic alpha_amylase	6	12	45	0.99	0.24	1.00
	AHFSISNSAEDPFIAIHAESK				1.06	4.2	3	
	ALVFVDNHDNQR				1.04	2.9	2	
	EVTINPDTTCGNDWVCEHR				1.00	3.3	2	
	IYVDAVINHMCGNAVSAGTSSTCGSYFNPGSR				0.97	3.4	3	
	TGSGDIENYNDATQVR				0.95	4.3	2	
	WVDIALECER				0.86	2.3	2	
P04792	HSPB1	Heat shock protein beta_1	3	7	24	0.97	0.26	1.00
	LATQSNEITIPVTFESR				0.98	3.7	2	
	LFDQAFGLPR				0.97	2.1	2	
	VSLDVNHFAPDELTVK				0.96	3.5	2	
P05091	ALDH2	Aldehyde dehydrogenase_ mitochondrial	7	11	49	1.00	0.16	0.97
	ANNSTYGLAAAVFTK				0.98	4.1	2	
	EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK				0.98	3.6	3	
	EEIFGPVMQILK+Oxidation(7)				1.00	3.0	2	
	ELGEYGLQAYTEVK				1.02	3.4	2	
	TEQGPQVDETQFK				0.99	3.8	2	
	VAFTGSTEIGR				0.84	2.9	2	
	VIQVAAGSSNLK				1.34	3.5	2	
P05109	S10A8	Protein S100_A8	2	4	30	1.00	0.37	1.00
	ALNSIIDVYHK				1.02	3.3	2	
	LLETECPQYIR				0.98	3.4	2	
P05155	IC1	Plasma protease C1 inhibitor	15	51	586	0.96	0.09	1.00
	DFTCVHQALK				1.04	3.2	2	
	FQPTLLTLPR				0.95	2.7	2	
	GVTSVSQIFHSPDLAIR				0.99	4.9	2	
	HRLEDMEQALSPSVFK				0.94	5.1	3	
	HRLEDMEQALSPSVFK+Oxidation(5)				0.96	3.6	3	
	KYPVAHFIDQTLK				1.02	4.0	3	
	LEDMEQALSPSVFK				0.95	4.6	2	

	LEDMEQALSPSVFK+Oxidation(3)				0.92	3.7	2	
	LLDSLPSDTR				1.00	3.3	2	
	TLYSSSPR				1.08	2.2	2	
	TNLESILSYPK				0.93	4.2	2	
	VTTSQDMLSIMEK				0.91	3.5	2	
	VTTSQDMLSIMEK+Oxidation(10)				0.94	3.1	2	
	VTTSQDMLSIMEK+Oxidation(6)				0.94	3.1	2	
	VTTSQDMLSIMEK+Oxidation(6),Oxidation(10)				0.89	2.7	2	
P05156	CFAI	Complement factor I	10	17	123	0.95	0.15	1.00
	ACDGINDCGDQSDELCCK				0.99	5.7	2	
	AQLGDLPWQVAIK				0.95	3.8	2	
	EANVACLDLGFQQGADTQR				0.95	5.9	2	
	GLETSLAECTFTK				0.98	4.2	2	
	HGNTDSEGIVEVK				0.95	3.3	2	
	TMGYQDFADVVCYTQK				0.90	4.4	2	
	VFCQPWQR				0.92	2.2	2	
	VFSLQWGEVK				0.89	3.1	2	
	VTYTSQEDLVEK				0.97	2.6	2	
	YQIWTTVVDWIHPDLK				0.87	3.9	3	
P05186	PPBT	Alkaline phosphatase_ tissue_nonspecific isozyme	3	7	34	0.86	0.33	0.73
	ANEGTVGVSAATER				0.90	3.6	2	
	HETHGGEDVAVFSK				0.98	3.9	3	
	LDGLDLVDTWK				0.37	3.8	2	
P05362	ICAM1	Intercellular adhesion molecule 1	10	18	200	0.95	0.11	1.00
	ASVSVTAEDEGTQR				0.92	4.0	2	
	DGTFPLPIGESVTVTR				0.97	3.5	2	
	DLEGTYLCR				0.80	2.4	2	
	EPAVGEPAEVTTTVLVR				0.96	3.0	2	
	GGSVLVTCSTSCDQPK				0.95	4.4	2	
	LLGIETPLPK				0.94	2.8	2	
	REPAVGEPAEVTTTVLVR				0.92	3.7	2	
	SFSCSATLEVAGQLIHK				0.94	3.7	2	
	VELAPLPSWQPVGK				0.97	3.4	2	
	VTLNGVPAQPLGPR				1.09	2.9	2	
P05452	TETN	Tetranectin	6	7	44	0.94	0.21	0.98
	GGTLGTPQTGSENDALYEYLR				0.75	2.6	2	
	LDTLAQEVALLK				0.92	4.1	2	
	NWETEITAQPDGGK				0.92	3.4	2	
	SRLDTLAQEVALLK				1.05	2.5	2	
	TENCAVLSGAANGK				0.91	4.0	2	
	TFHEASEDCISR				0.91	3.3	3	
P05543	THBG	Thyroxine_binding globulin	3	5	16	0.98	0.23	0.84
	FSISATYDLGATLLK				1.10	2.6	2	
	GTEAAAVPEVELSDQPENTFLHPIIQIDR				0.91	3.9	3	
	QEINSHVEMQTK+Oxidation(8)				1.04	2.6	2	
P05997	CO5A2	Collagen alpha-2(V) chain	3	3	4	1.02	0.33	0.56
	AGMPGTRGPPGDPGPEGK				0.94	2.2	2	
	QGPMGVIGRQGTTGAPGPPGDPGPQGDEGPDGK				0.93	3.1	3	
	TPASLQADKTVR				1.18	1.8	1	
P06310	KV206	Ig kappa chain V_II region RPMI 6410	2	11	94	1.02	0.24	1.00
	FSGSGSGTDFTLK				1.05	3.8	2	
	FSGSGSGTDFTLKISR				0.94	3.4	2	
P06314	KV404	Ig kappa chain V_IV region B17	2	4	41	0.96	0.27	0.75
	LLIYWASTR				0.79	2.9	2	
	NYLAWYQQKPGQPPK				1.01	3.7	2	
P06331	HV209	Ig heavy chain V_II region ARH_77	2	5	36	0.99	0.28	1.00
	LSSVTAADTAVYYCAR				0.89	4.5	2	
	VTISLDTSK				1.01	2.3	2	
P06396	GELS	Gelsolin	15	31	196	0.97	0.13	1.00
	AGALNSNDAFVLK				0.98	3.9	2	
	AGKEPGLQIWR				0.92	3.4	3	
	AQPVQVAEGSEPDGFWEALGGK				0.98	6.0	2	
	DPDQTDGLGLSYLSSHIANVER				0.98	5.5	3	
	DSQEEEKTEALTSAK				0.82	5.0	3	
	EVQGFESATFLGYFK				0.64	4.0	2	
	HVVPNEVVVQR				1.12	2.7	2	

	NWRDPDQTDGLGLSYLSSHIANVER				1.12	5.6	3	
	QTQVSVLPEGGETPLFK				1.06	4.0	2	
	SEDCFILDHGK				0.90	3.1	3	
	TGAQELLR				0.92	2.8	2	
	TPSAAYLWVGTGASEAEK				0.96	5.3	2	
	VSNGAGTMSVSLVADENPFAQGALK				1.02	4.6	2	
	VSNGAGTMSVSLVADENPFAQGALK+Oxidation(7)				0.91	4.2	2	
	YIETDPANR				0.91	2.3	2	
P06681	CO2	Complement C2	11	18	102	0.95	0.15	0.01
	AVISPGFDVFAK				0.93	2.6	2	
	CSSNLVLTGSSER				1.00	3.6	2	
	DFHINLFR				0.94	2.8	2	
	ECQGNGVWSGTEPICR				0.98	3.3	2	
	EVVTDQFLCSGTQEDESPCKGESGGAVFLER				0.99	5.3	3	
	GESGGAVFLER				0.76	2.8	2	
	HAFILQDTK				0.91	2.4	2	
	HAIILLTDGK				0.95	2.6	2	
	MGVEWTSCAEVVSQEK				1.00	2.7	2	
	SSGQWQTPGATR				0.84	2.2	2	
	VLMSVLNDNSR+Oxidation(2)				1.06	1.9	1	
P06702	S10A9	Protein S100_A9	5	13	116	0.99	0.21	1.00
	LGHPDTLNQGEFK				1.04	3.2	3	
	MHEGDEGPGHHHKPGLGEGTP+Oxidation(0)				1.02	3.3	3	
	NIETIINTFHQYSVK				1.00	4.7	2	
	VIEHIMEDLDTNADK				0.87	4.8	2	
	VIEHIMEDLDTNADK+Oxidation(5)				1.01	3.6	2	
P06727	APOA4	Apolipoprotein A_IV	14	25	153	0.94	0.13	0.98
	DKVNSFFSTFK				0.76	2.9	2	
	ENADSLQASLRPHADELK				0.82	2.9	2	
	IDQNVEELK				0.94	2.2	2	
	ISASAEELR				0.88	2.3	2	
	KLVPFATELHER				0.92	3.9	3	
	LGEVNTYAGDLQK				1.07	4.0	2	
	LGPHAGDVEGHLSFLEK				1.00	4.0	3	
	LKEEIGKELEELR				0.94	4.2	3	
	RVEPYGENFNK				1.16	3.2	2	
	SELTQQLNALFQDK				0.87	4.8	2	
	SLAELGGHLDQQVEEFR				0.93	4.2	3	
	SLAELGGHLDQQVEEFRR				1.00	3.4	3	
	SLAPYAQDTQEK				0.87	3.2	2	
	TQVNTQAEQLR				0.91	3.3	2	
P06733	ENOA	Alpha_enolase	7	15	97	0.99	0.15	1.00
	DATNVGDEGGFAPNILENK				1.05	4.2	2	
	FTASAGIQVVGDDLTVTNPK				0.98	4.4	2	
	HIADLAGNSEVILPVPAFNVINGGSHAGNK				0.97	4.5	3	
	IEEELGSK				0.94	2.1	2	
	IGAEVYHNLK				1.06	3.3	3	
	VNQIGSVTESLQACK				0.99	4.9	2	
	YISPDQLADLYK				0.95	3.5	2	
P06744	G6PI	Glucose_6_phosphate isomerase	3	5	31	0.96	0.30	1.00
	HFVALSTNTTK				0.97	2.3	2	
	TFTTQETITNAETAK				1.00	4.2	2	
	VWYVSNIDGTHIAK				0.91	2.7	2	
P07195	LDHB	L_lactate dehydrogenase B chain	2	4	20	1.05	0.40	0.94
	LIAPVAEEEATVPNNK				1.10	3.5	2	
	MVVESAYEVIK+Oxidation(0)				0.90	2.2	2	
P07205	PGK2	Phosphoglycerate kinase 2	3	6	24	0.90	0.21	0.50
	FHVEEEGK				1.01	2.4	2	
	LGDVYVNDAFGTAHR				0.91	3.7	2	
	VNEMIIGGGMAYTFLK+Oxidation(9)				0.87	2.2	2	
P07339	CATD	Cathepsin D	8	17	57	0.95	0.15	0.99
	AIGAVPLIQGEYMIPCEK+Oxidation(12)				0.95	3.4	2	
	AYWQVHLDQVEVASGLTLCK				0.91	3.3	3	
	DPDAQPGGELMLGGTDSK				1.09	3.2	2	
	DPDAQPGGELMLGGTDSK+Oxidation(10)				0.85	3.0	2	
	FDGILGMAYPR				0.99	3.7	2	
	FDGILGMAYPR+Oxidation(6)				0.93	2.9	2	

	VGFAEAAR				0.91	2.2	2	
	VSTLPAITLK				1.03	2.3	2	
P07355	ANXA2	Annexin A2	2	6	33	0.99	0.29	1.00
	GVDEVTIVNILTNR				0.97	4.5	2	
	QDIAFAYQR				1.01	2.7	2	
P07357	CO8A	Complement component C8 alpha chain	3	9	39	1.01	0.28	0.96
	AIDEDCSQYEPIPGSQK				1.06	3.8	2	
	FGGTICSGDIWDQASCSSSTTCVR				0.97	4.6	2	
	LGSLGAACEQTQTEGAK				0.98	3.8	2	
P07360	CO8G	Complement component C8 gamma chain	2	6	35	1.00	0.21	1.00
	SLPVSDSVLSGFEQR				1.04	4.4	2	
	VQEAHLTEDQIFYFPK				0.98	4.1	3	
P07437	TBB5	Tubulin beta chain	5	7	15	0.97	0.32	1.00
	EIVHIQAGQCGNQIGAK				0.97	3.9	3	
	GHYTEGAELVDSVLDVVR				0.98	3.6	3	
	ISEQFTAMFR				1.07	2.9	2	
	SGPFGQIFRPDNFVFGQSGAGNNWAK				0.94	5.8	3	
	YLTVAAVFR				0.92	2.5	2	
P07737	PROF1	Profilin_1	6	21	165	0.96	0.16	1.00
	DSLLQDGEFSMDLR				1.00	3.6	2	
	DSLLQDGEFSMDLR+Oxidation(10)				0.95	3.1	2	
	DSPSVWAAVPGK				1.01	3.0	2	
	SSFYVNGLTLGGQK				0.87	4.0	2	
	STGGAPTFNVTVTK				1.00	3.5	2	
	TFVNITPAEVGVLVGK				0.95	4.8	2	
P07858	CATB	Cathepsin B	3	6	31	0.98	0.26	1.00
	GQDHCGIESEVVAGIPR				1.01	4.5	2	
	HYGYNSYSVSNSEK				0.96	4.4	2	
	ICEPGYSPTYK				0.95	2.5	2	
P07900	HS90A	Heat shock protein HSP 90_alpha	4	9	68	0.97	0.23	0.96
	DQVANSAFVER				0.99	2.6	2	
	HIYYITGETK				0.98	3.2	2	
	HLEINPDHSIIETLR				0.88	3.7	3	
	NPDDITNEEYGEFYK				1.00	4.2	2	
P07951	TPM2	Tropomyosin beta chain	2	2	2	0.89	0.55	0.76
	KLVILEGELERSEER				0.91	2.4	2	
	MELQEMQLK+Oxidation(0),Oxidation(5)				0.81	2.1	1	
P07988	PSPB	Pulmonary surfactant_associated protein B	7	18	98	0.94	0.15	1.00
	EAIFQDTMR+Oxidation(7)				0.89	2.4	2	
	FLEQECNVLPLK				0.90	3.5	2	
	GALAVAVAQVCR				0.97	3.3	2	
	GWDAHTTCQALGVCGTMSSPLQCIHSPDL+Oxidation(16)				1.03	5.5	3	
	QFVEQHTPQLLTLVPR				0.95	3.4	3	
	VVPLVAGGICQCLAER				0.93	4.7	2	
	YSVILLDTLLGR				0.30	3.5	2	
P07998	RNAS1	Ribonuclease pancreatic	2	7	30	0.98	0.30	0.95
	CKPVNTFVHEPLVDVQNVCFQEK				0.88	3.6	3	
	HIIVACEGSPYVPVHFDASVEDST				1.04	4.1	3	
P08107	HSP71	Heat shock 70 kDa protein 1A/1B	6	9	41	1.02	0.21	1.00
	AQIHDLVLVGGSTR				0.97	3.1	2	
	DAGVIAGLNVLR				1.00	3.5	2	
	EIAEAYLGYPVTNAVITVPAYFNDSQR				1.17	3.6	3	
	ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK				0.93	4.5	3	
	NQVALNPQNTVFDAK				1.06	4.3	2	
	YKAEDEVQR				1.00	3.0	2	
P08185	CBG	Corticosteroid_binding globulin	5	7	37	0.99	0.39	1.00
	AVLQLNEEGVDTAGSTGVTLNLTSKPIILR				1.01	3.4	3	
	EENFYVDETTVVK				0.82	3.1	2	
	GTWTQPFDLASTR				0.96	2.3	2	
	SETEIHQGFQHLHQLFAK				1.17	4.4	3	
	WSAGLTSSQVDLYIPK				0.87	3.7	2	
P08238	HS90B	Heat shock protein HSP 90_beta	9	13	71	0.98	0.16	1.00
	ADLINNLGTIAK				1.08	3.8	2	
	EDQTEYLEER				0.75	2.9	2	
	EKEISDDEAEEEKGEK				0.97	2.3	2	
	ELISNASDALDK				1.24	2.4	2	
	EQVANSAFVER				0.96	2.1	2	

	GVVDSEDLPLNISR				0.99	4.3	2	
	HLEINPDHPIVETLR				0.97	3.6	3	
	SLTNDWEDHLAVK				0.94	3.0	2	
	YIDQEELNK				0.91	2.5	2	
P08571	CD14	Monocyte differentiation antigen CD14	3	6	33	0.97	0.26	1.00
	AFPALTSLDLSDNPGLGER				0.93	3.7	2	
	LTVGAAQVPAQLLVGALR				0.98	4.1	2	
	VLSIAQAHSPAFSCEQVR				0.97	3.9	3	
P08603	CFAH	Complement factor H	14	26	108	0.94	0.14	1.00
	AGEQVTYTCATYYK				0.94	4.3	2	
	KGEWVALNPLR				0.99	3.2	2	
	LGYVTADGETSGSITCGK				0.89	4.6	2	
	LSYTCEGGFR				0.98	2.6	2	
	NTEILTGSWSDQTYPEGTQAIYK				1.04	4.4	2	
	SITCIHGVWTQLPQCVAIDK				0.97	3.9	3	
	SPDVINGSPISQK				0.91	2.3	2	
	SPPEISHGVVAHMSDSYQYGEEVTYK				0.87	4.1	3	
	SSIDIENGFISESQYTYALK				1.03	2.6	2	
	SSNLIILEEHLK				0.88	2.7	2	
	TDCLSLPSFENAIPMGEK				0.86	2.6	2	
	TGESVEFVCK				0.91	3.0	2	
	VSVLCQENYLIQEGEEITCK				0.87	4.0	2	
	WQSIPLCVEK				0.91	2.2	2	
P08670	VIME	Vimentin	15	29	177	0.97	0.15	1.00
	DGQVINETSQHHDDLE				0.99	3.7	2	
	EEAENTLQSFR				1.05	3.1	2	
	EMEENFAVEAANYQDTIGR				1.14	4.4	2	
	EMEENFAVEAANYQDTIGR+Oxidation(1)				0.86	3.9	2	
	EYQDLLNVK				0.99	2.1	1	
	FADLSEAANR				0.93	3.1	2	
	ILLAELEQLK				0.84	3.5	2	
	ISLPLPNFSSLNLR				0.81	2.3	2	
	KVESLQEEIAFLK				0.91	4.1	3	
	LHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR				1.08	5.9	4	
	LLQDSVDFSLADAINTEFK				0.94	3.6	2	
	NLQEAEEWYK				0.87	3.3	2	
	QVQSLTCEVDALK				1.00	3.4	2	
	SLYASSPGGVYATR				1.01	3.9	2	
	VELQELNDR				0.90	2.6	2	
P08758	ANXA5	Annexin A5	9	13	83	0.99	0.15	0.99
	ALLLLCGEDD				0.95	1.9	1	
	DLLDDLKSELTGK				0.98	3.9	2	
	ETSGNLEQLLLAVVK				1.27	2.9	2	
	FITIFGTR				0.88	2.4	2	
	GLGTDEESILTLLTSR				0.78	4.1	2	
	GTVTDFPGFDER				1.01	3.3	2	
	LYDAYELK				0.94	2.6	2	
	QVYEEEYGSSLEDDVVGDTSGYYQR				1.33	5.2	2	
	VLTEIIASR				0.99	2.4	2	
P09210	GSTA2	Glutathione S_transferase A2	2	2	25	0.95	0.54	0.66
	SAEDLDKLR				0.83	2.8	2	
	SHGQDYLVGNK				1.07	3.1	2	
P09211	GSTP1	Glutathione S_transferase P	10	26	142	0.94	0.19	1.00
	AFLASPEYVNLPINGNGK				0.93	5.7	2	
	ALPGQLKPFETLLSQNQGGK				0.90	4.7	3	
	ASCLYGQLPK				1.06	3.0	2	
	DQQEAALVDMVNDGVEDLR				0.91	6.0	2	
	DQQEAALVDMVNDGVEDLR+Oxidation(9)				0.94	4.0	2	
	EEVVTVETWQEGSLK				0.90	4.3	2	
	FQDGDLTLYQSNTILR				0.70	5.3	2	
	MLLADQGQSWK+Oxidation(0)				1.00	2.9	2	
	YISLIYTNYEAGK				0.89	2.3	2	
	YISLIYTNYEAGKDDYVK				0.79	4.8	2	
P09382	LEG1	Galectin_1	2	5	22	1.01	0.33	0.94
	DSNNLCLHFNPR				1.11	2.6	2	
	FNAHGDANTIVCNSK				0.97	4.4	2	
P09467	F16P1	Fructose_1_6_bisphosphatase 1	8	12	65	0.95	0.19	0.98

	AGIAHLYGIAGSTNVTGDQVK				0.92	4.9	2	
	APVILGSPDDVLEFLK				0.70	3.3	2	
	DFDPAVTEYIQR				0.76	3.3	2	
	EAVLDVIPTDIHQR				1.09	3.1	2	
	GTGELTQLLNSLCTAVK				0.91	4.8	2	
	HAIIVEPEKR				0.80	3.2	3	
	KAGIAHLYGIAGSTNVTGDQVK				1.12	3.7	3	
	SSFATCVLVSEEDKHAIIVEPEKR				1.02	4.5	3	
P09525	ANXA4	Annexin A4	2	2	7	0.95	0.47	0.83
	DEGNYLDDALVR				1.01	3.0	2	
	VLVSLSAGGR				0.87	2.5	2	
P09668	CATH	Pro_cathepsin H	3	9	48	0.97	0.28	1.00
	GIMGEDTYPYQGK				1.03	3.0	2	
	GIMGEDTYPYQGK+Oxidation(2)				0.92	3.0	2	
	VNHAVLAVGYGEK				1.01	3.8	2	
P09960	LKHA4	Leukotriene A_4 hydrolase	11	24	124	0.94	0.12	1.00
	DGETPDPEDPSR				0.88	2.7	2	
	DLSSHQLNEFLAQTLQR				0.85	3.2	3	
	EDDLNSFNATDLK				1.11	3.7	2	
	GSPMEISLPIALSK				0.91	3.7	2	
	GSPMEISLPIALSK+Oxidation(3)				0.88	3.0	2	
	LTYTAEVSVPK				0.94	3.3	2	
	LVVDLTDIDPDVAYSSVPYEK				0.89	4.6	2	
	SLSNVIAHEISHSWTGNLVTNK				1.03	4.3	3	
	SSALQWLTPEQTSGK				0.95	3.6	2	
	TLTGTAALTVQSQEDNLR				0.91	4.5	2	
	WEDAIPLALK				0.94	2.2	2	
P09972	ALDOC	Fructose_bisphosphate aldolase C	2	4	15	1.01	0.24	0.44
	GVVPLAGTDGETTTQGLDGLSER				0.99	5.2	2	
	YASICQQNGIVPIVEPEILPDGDHDLKR				1.09	3.1	3	
P0C0L5	CO4B	Complement C4_B	35	92	748	0.96	0.07	1.00
	ADGSYAAWLSR				0.92	3.6	2	
	AEFQDALEK				1.07	2.8	2	
	CSVFYGAPSK				0.83	2.4	2	
	DFALLSLQVPLK				0.68	3.8	2	
	DHAVDLIQK				0.83	2.5	2	
	EELVYELNPLDHR				0.93	3.5	2	
	FGLLDEDGKK				0.85	3.4	3	
	GHLFLQTDQPIYNPGQR				0.97	5.7	3	
	GLCVATPVQLR				0.93	2.5	2	
	GLEEELQFSLGSK				1.03	4.8	2	
	GLQDEDGYR				0.88	2.9	2	
	GSFEFPVGDAVSK				1.01	3.3	2	
	ITQVLHFTK				1.12	2.9	2	
	KYVLPNFEVK				0.97	3.0	2	
	LELSVDGAK				1.06	2.2	2	
	LLATLCSAEVCQCAEGK				0.93	4.6	2	
	LLLFSPSVVHLGVPLSVGVQLQDVPR				0.85	5.1	3	
	LNMGITDLQGLR				0.90	3.6	2	
	LQETSNWLLSQQQADGSFQDLSPVIHR				0.97	6.0	3	
	LVNGQSHISLSK				0.95	3.3	2	
	MRPSTDTITVMVENSHGLR				0.93	4.5	3	
	MRPSTDTITVMVENSHGLR+Oxidation(0)				1.03	3.6	3	
	SCGLHQLLR				1.09	3.2	2	
	SHALQLNNR				0.96	2.8	2	
	TEQWSTLPPETK				1.11	3.7	2	
	TLEIPGNSDPNMIPDGDFNSYVR				0.89	3.3	2	
	TLEIPGNSDPNMIPDGDFNSYVR+Oxidation(11)				0.96	3.4	2	
	VDFTLSSER				0.95	3.3	2	
	VDVQAGACEGK				1.03	3.9	2	
	VEYGFQVK				1.02	2.7	2	
	VGDTLNLNLR				0.67	3.3	2	
	VLSLAQEQVGGSPEK				1.06	4.9	2	
	VTASDPLDTLGSEGALSPGGVASLLR				0.91	7.3	3	
	YIYGKPVQGVAYVR				1.02	2.9	2	
	YVLPNFEVK				1.01	2.1	1	
P0C0S5	H2AZ	Histone H2A.Z	2	2	10	1.00	0.48	1.00

	AGLQFPVGR				1.00	2.2	2	
	HLQLAIR				0.99	2.2	2	
P0CG06	LAC3	Ig lambda_3 chain C regions	2	9	57	0.94	0.28	1.00
	AGVETTTPSK				0.93	3.4	2	
	ATLVCLISDFYPGAVTVAWK				0.96	3.4	2	
P0CG39	POTEJ	POTE ankyrin domain family member J	5	13	101	0.96	0.21	1.00
	AGFAGDDAPR				0.89	3.1	2	
	IWHHTFYNELR				0.90	3.7	3	
	KDLIVMLRDTDVNK				0.85	2.4	2	
	QEYDESGPSIVHR				1.01	3.4	3	
	QMLKISSENSNPEQDLK				1.05	2.4	2	
P0CG48	UBC	Polyubiquitin_C	2	4	18	0.97	0.24	0.75
	ESTLHLVLR				1.08	2.2	2	
	TITLEVEPSDTIENVK				0.92	4.0	2	
P10253	LYAG	Lysosomal alpha_glucosidase	2	6	20	1.06	0.32	0.98
	AGYIIPLQGPGLTTTESR				1.03	3.5	2	
	VTSEGAGLQLQK				1.09	2.7	2	
P10599	THIO	Thioredoxin	3	5	25	0.92	0.22	0.71
	EKLEATINELV				0.86	2.8	2	
	LEATINELV				0.91	2.2	2	
	TAFQEALDAAGDK				0.97	3.7	2	
P10643	CO7	Complement component C7	7	13	43	0.96	0.19	1.00
	ELSHLPSLYDYSAYR				0.96	3.9	3	
	LSGNVLSYTFQVK				0.81	2.5	2	
	NVVYTCNEGYSLIGNPVAR				0.94	5.0	2	
	SCVGETTESTQCEDEELEHLR				0.95	3.3	3	
	SLVCNGDSDCDEDSADEDRCEDSER				1.56	4.3	3	
	SSGWHFVVK				0.93	2.7	2	
	YSAWAESVTNLPQVIK				0.95	3.2	2	
P10909	CLUS	Clusterin	6	15	146	0.99	0.15	1.00
	EILSVDCSTNNPSQAK				0.98	4.1	2	
	ELDESLQVAER				0.95	3.3	2	
	KTLLSNLEEAK				1.10	2.4	2	
	KTLLSNLEEAKK				0.98	3.6	3	
	LFDSDPITVTVPVEVSR				0.93	5.3	2	
	VTTVASHTSDSDVPSGVTEVVVK				1.01	5.9	2	
P11021	GRP78	78 kDa glucose_regulated protein	2	2	2	1.19	0.61	0.30
	ELEEIVQPIISK				1.08	2.7	2	
	NQLTSNPENTVFDAK				1.33	3.6	2	
P11142	HSP7C	Heat shock cognate 71 kDa protein	12	25	140	0.97	0.13	1.00
	DAGTIAGLNVLR				1.07	3.6	2	
	IINEPTAAAIAYGLDK				0.88	4.4	2	
	LLQDFFNGK				0.90	2.3	2	
	NQTAEKEEFEHQQK				1.04	3.3	3	
	NQVAMNPTNTVFDAK				0.98	3.6	2	
	NQVAMNPTNTVFDAK+Oxidation(4)				1.04	3.5	2	
	SFYPEEVSSMVLTK				0.90	3.0	2	
	SINPDEAVAYGAAVQAAILSGDK				0.93	2.7	2	
	SQIHDIVLVGGSTR				0.97	3.8	2	
	STAGDTHLGGEDFDNR				0.92	3.9	2	
	TTPSYVAFTDTER				0.99	3.0	2	
	VEIIANDQGNR				0.92	3.2	2	
P11684	UTER	Uteroglobin	3	15	211	1.00	0.26	0.97
	EAGAQLK				0.78	1.8	1	
	KLVDTLPQKPR				1.14	4.1	3	
	LVDTLPQKPR				0.91	3.1	2	
P12110	CO6A2	Collagen alpha-2(VI) chain	2	6	27	1.00	0.29	1.00
	EEGIRLFAVAPNQNLK				1.01	2.6	2	
	RGTFTDCALANMTEQIR				0.99	2.3	2	
P12277	KCRB	Creatine kinase B_type	2	3	8	0.82	0.50	0.33
	GTGGVDTAAVGGVFDVSNADR				0.87	3.2	2	
	LAVEALSSLDGDLAGR				0.79	3.1	2	
P12429	ANXA3	Annexin A3	4	6	15	0.95	0.28	0.99
	DYPDFSPSVDAEAIQK				0.91	2.6	2	
	GIGTDEFTLNR				1.03	2.5	2	
	MLISILTER+Oxidation(0)				0.92	2.4	2	
	SLGDDISSETSGDFR				0.89	3.4	2	

P12830	CADH1	Cadherin_1	2	2	3	0.95	0.33	0.65
	ETGWLKVTEPLDR				0.89	2.3	2	
	NTGVISVVTTGLDR				1.01	3.5	2	
P13489	RINI	Ribonuclease inhibitor	4	6	47	1.08	0.26	0.92
	ELCQGLGQPGSVLR				1.12	2.9	2	
	ELSLAGNELGDEGAR				1.12	3.2	2	
	ELTVSNNDINEAGVR				1.08	3.3	2	
	VNPALAELNLR				1.00	3.2	2	
P13645	K1C10	Keratin_ type I cytoskeletal 10	10	16	69	0.69	0.24	0.00
	ALEESNYELEGK				0.67	3.5	2	
	ELTTEIDNNIEQISSYK				0.72	5.2	2	
	GSLGGGFSSGGFSGGSFSR				0.58	4.1	2	
	IRLENEIQTYR				0.70	2.6	2	
	LENEIQTYR				0.75	2.7	2	
	LKYENEVALR				0.69	2.2	2	
	QSLEASLAETEGR				0.64	2.7	2	
	SLLEGEGSSGGGGR				0.73	2.4	2	
	SQYEQLAEQNR				0.71	3.4	2	
	VLDELTLTK				0.67	2.5	2	
P13671	CO6	Complement component C6	5	6	16	0.98	0.31	0.99
	DLTSLGHNENQQGSFSSQGGSSFSVPIFYSSK				0.83	3.3	3	
	GEVLDNSFTGGICK				1.03	3.1	2	
	IGESIELTCPK				1.02	2.5	2	
	TLNICEVGTIR				0.60	2.3	2	
	VPANLENVGFEVQTAEDDLKTDFYK				1.02	3.2	3	
P13796	PLSL	Plastin_2	11	23	142	0.93	0.15	1.00
	AYYHLLEQVAPK				0.93	4.2	3	
	EGICAIGGTSEQSSVGTQHSYSEEEK				0.98	3.8	3	
	FSLVGIGGQDLNEGNR				0.95	4.2	2	
	GDEEGVPAVVIDMSGLR				0.82	3.2	2	
	HVIPMNPNTNDLFNAVGDGIVLCK+Oxidation(4)				0.98	3.8	3	
	IGNFSTDIK				0.93	2.4	2	
	IKVPVDWNR				0.88	2.3	2	
	QFVTATDVVR				0.96	2.7	2	
	VNDDIIVNWVNETLR				0.91	4.7	2	
	VYALPEDLVEVNPK				0.93	3.2	2	
	YTLNILEEIGGGQK				0.89	4.1	2	
P13797	PLST	Plastin_3	5	8	49	0.95	0.22	0.84
	KLENCNYAVELGK				1.07	4.2	2	
	LENCNYAVELGK				0.91	2.6	2	
	MINLSVPDTIDER				0.83	2.2	2	
	MINLSVPDTIDER+Oxidation(0)				1.02	3.2	2	
	YAFVNWINK				0.89	2.2	2	
P13987	CD59	CD59 glycoprotein	2	4	10	0.95	0.69	0.92
	FEHCNFNDVTTR				1.16	3.4	2	
	LRENELTYYCCK				0.75	3.9	2	
P14550	AK1A1	Alcohol dehydrogenase [NADP_]	3	7	28	0.95	0.29	1.00
	GLEVTAYSPLGSSDR				0.99	3.9	2	
	GLVQALGLSNFNSR				0.89	3.4	2	
	HIDCAAIYGNEPEIGEALKEDVGPGK				0.90	3.6	3	
P14618	KPYM	Pyruvate kinase isozymes M1/M2	11	19	79	0.98	0.16	1.00
	AEGSDVANAVLDGADCIMLSGETAK				0.87	4.6	2	
	CCSGAIIVLTK				0.96	2.3	2	
	GSGTAEVELK				0.95	3.4	2	
	GSGTAEVELKK				0.89	2.5	2	
	GVNLPGAAVDLPAVSEK				1.02	4.5	2	
	KGVNLPGAAVDLPAVSEK				1.07	3.3	2	
	LAPITSDPTEATAVGAVEASFK				0.97	2.9	2	
	LDIDSPPITAR				1.01	2.5	2	
	LNFSHGTHEYHAETIK				0.95	4.0	3	
	NTGIICTIGPASR				1.07	2.9	2	
	TATESFASDPILYRPVAVALDTK				0.97	4.1	2	
P15090	FABP4	Fatty acid_binding protein_ adipocyte	3	4	50	1.01	0.27	1.00
	EDDKLVVECVMK				0.94	2.1	2	
	EVGVGFATR				0.98	2.4	2	
	STITLDGGVLVHVQK				1.05	3.6	2	
P15311	EZRI	Ezrin	3	4	42	0.93	0.32	1.00

	QLLTLSSELSQAR				0.92	3.6	2	
	RKEDEVEEWQHR				0.96	4.3	3	
	SQEQLAAELAEYTAK				0.89	5.0	2	
P15941	MUC1	Mucin_1	3	6	36	0.92	0.25	0.99
	EGTINVHDVETQFNQYK				0.93	3.6	2	
	NYGQLDIFPAR				0.93	3.2	2	
	VSAGNGGSSLSYTNPAVAATSANL				0.92	3.8	2	
P16070	CD44	CD44 antigen	3	11	68	0.96	0.17	1.00
	ALSIGFETCR				0.98	3.4	2	
	TNPEDIYPSNPTDDDVSSGSSSER				0.95	4.9	2	
	YGFIEGHVVIPR				0.94	3.9	3	
P17931	LEG3	Galectin_3	2	3	11	1.02	0.33	0.99
	GNDVAFHFNPR				1.02	2.4	2	
	IQVLVEPDHFK				1.02	3.0	3	
P18136	KV313	Ig kappa chain V_III region HIC	2	19	184	0.92	0.13	0.98
	FSGSGSGTDFTLTISR				0.93	4.8	2	
	LLIYGASSR				0.88	3.0	2	
P18669	PGAM1	Phosphoglycerate mutase 1	2	5	22	0.94	0.25	0.41
	HGESAWNLENR				1.07	3.5	2	
	YADLTEDQLPSCESLK				0.89	4.1	2	
P19652	A1AG2	Alpha_1_acid glycoprotein 2	3	7	88	0.99	0.25	0.99
	EHVAHLLFLR				1.04	3.1	3	
	TEDTIFLR				0.97	3.1	2	
	WFYIASAFR				0.97	3.6	2	
P19823	ITIH2	Inter_alpha_trypsin inhibitor heavy chain H2	6	10	32	1.01	0.22	1.00
	AEDHFSVIDFNQNIR				1.05	2.7	2	
	FLHVPDTFEGHFDGVPVISK				0.96	4.2	4	
	FYNQVSTPLLR				0.98	2.6	2	
	IQPSGGTNINEALLR				1.07	2.8	2	
	NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK				0.99	4.5	4	
	VVNNSPQPQNVVFDVQIPK				0.94	3.8	3	
P19827	ITIH1	Inter_alpha_trypsin inhibitor heavy chain H1	8	16	79	0.94	0.14	1.00
	AAISGENAGLVR				0.99	2.6	2	
	EVAFDLEIPK				0.92	2.6	2	
	FAHYVVTSQVVNTANEAR				0.84	5.5	2	
	GFSLDEATNLNGGLLR				0.95	4.5	2	
	GSLVQASEANLQAAQDFVR				0.93	4.6	2	
	LDAQASFLPK				1.00	2.8	2	
	NHMQYEIVIK+Oxidation(2)				0.94	2.1	2	
	QYYEGSEIVVAGR				0.90	3.2	2	
P19971	TYPH	Thymidine phosphorylase	2	2	2	0.93	0.57	0.72
	FGGAAVFPNQEQAR				1.02	2.2	2	
	VSLVLAPALAACGCK				0.82	2.3	2	
P20142	PEPC	Gastricsin	2	3	32	0.93	0.33	1.00
	GLLGEFLR				0.94	2.9	2	
	SYYSVYDLGNNR				0.92	3.8	2	
P20742	PZP	Pregnancy zone protein	3	5	47	0.97	0.30	1.00
	ATVLNYLPK				0.90	2.9	2	
	MVSGFIPLKPTVK+Oxidation(0)				1.02	3.3	2	
	SSGSLLNNAIK				0.97	2.8	2	
P21333	FLNA	Filamin_A	13	23	99	0.96	0.12	0.94
	AEAGVPAEFSIWTR				0.95	3.0	2	
	ALGALVDSCAPGLCPDWDSWDASKPVTNAR				0.67	4.2	3	
	DAGEGGLSLAIEGPSK				1.13	3.8	2	
	DGSCGVAYVVQEPGDYEVSVK				0.90	4.0	2	
	DKGEYTLVVK				0.85	2.2	2	
	EAGAGGLAIAVEGPSK				0.90	3.6	2	
	FNEEHIPDSPFVVPVASPSGDAR				0.99	3.3	3	
	GAGTGGLGLAVEGPSEAK				1.03	3.5	2	
	GLVEPVDVVDNADGTQTVNYVPSR				0.91	5.9	2	
	IANLQTDLSDGLR				1.21	2.3	2	
	SPFSVAVSPSLDLSK				0.89	2.2	2	
	VNQPASFAVSLNGAK				0.93	3.1	2	
	YTPVQQGPVGVNVTYGGDPIPK				0.89	4.6	2	
P21980	TGM2	Protein_glutamine gamma_glutamyltransferase 2	4	5	26	0.93	0.26	0.99
	DLYLENPEIK				0.95	2.6	2	
	NYEASVDSLTFSVVTGPAPSQEAGTK				0.88	2.8	2	

	SEGTYCCGPVPVR				0.89	3.1	2	
	TVEIPDPVEAGEEVK				0.95	2.3	2	
P22314	UBA1	Ubiquitin_like modifier_activating enzyme 1	3	5	11	1.02	0.29	1.00
	AAVATFLQSVQVPEFTPK				0.99	3.0	2	
	ALPAVQQNNLDEDLIR				1.05	3.9	2	
	SLVASLAEPDFVVTDFAK				1.05	2.6	2	
P22626	ROA2	Heterogeneous nuclear ribonucleoproteins A2/B1	2	3	19	0.92	0.35	0.93
	IDTIEIITDR				0.91	3.0	2	
	LFIGGLSFETTEESLR				0.95	2.5	2	
P22897	MRC1	Macrophage mannose receptor 1	10	14	55	0.96	0.17	0.99
	ACIGFGGNLVSIQNEK				0.92	4.0	2	
	FEGSESLWNKDPLTSVSYQINSK				0.97	3.2	3	
	FQWHEAETYCK				1.27	2.7	2	
	IYGTTDNLCSR				0.93	2.3	2	
	NWGQASLECLR				1.14	2.4	2	
	SSLSYEDADCVVIIGGASNEAGK				0.91	4.8	2	
	WENLECVQK				0.74	2.5	2	
	YFWTGLSDIQTK				0.97	3.6	2	
	YLNWLPGSPSAEPGK				0.95	2.8	2	
	YTNWAADEPK				0.80	2.3	2	
P23141	EST1	Liver carboxylesterase 1	4	7	38	1.03	0.27	0.97
	AGQLLSELFTNR				0.66	3.0	2	
	AISESGVALTSVLVK				0.99	4.0	2	
	EGYLQIGANTQAAQK				1.05	3.7	2	
	MVMKFWANFARNGNPNGEGLPHWPEYNQK+Oxidation(0),Oxidation(2)				1.22	3.1	3	
P23381	SYWC	Tryptophanyl_tRNA synthetase_ cytoplasmic	3	6	26	0.96	0.37	1.00
	DLTLDQAYSYAVENAK				0.92	4.3	2	
	GIFGFTDSDCIGK				0.97	3.5	2	
	ISFPAIQAAPSFSNSFPQIFR				1.03	2.4	2	
P23528	COF1	Cofilin_1	5	14	177	0.93	0.14	0.91
	EILVGDVGQTVDDPYATFVK				0.93	5.4	2	
	HELQANCYEEVK				0.95	3.9	2	
	HELQANCYEEVKDR				0.99	5.7	3	
	LGGSAVISLEGKPL				0.65	3.8	2	
	NIILEEGKEILVGDVGQTVDDPYATFVK				0.90	6.6	3	
P25311	ZA2G	Zinc_alpha_2_glycoprotein	2	2	21	1.01	0.42	1.00
	AYLEEECPATLR				1.07	3.3	2	
	EIPAWVPFDPAAQITK				0.97	2.5	2	
P26038	MOES	Moesin	4	5	17	0.94	0.26	0.97
	ALTSELANAR				0.92	2.2	2	
	AQMVQEDLEK+Oxidation(2)				1.08	2.3	2	
	ESEAVEWQQK				0.90	3.0	2	
	TQEQLALEMAELTAR				0.96	4.8	2	
P29401	TKT	Transketolase	6	14	33	1.01	0.18	0.93
	AVELAANTK				0.89	2.2	2	
	ILATPPQEDAPSVDIANIR				0.99	4.2	3	
	LDNLVAILDINR				1.20	2.9	2	
	SKDDQVTVIGAGVTLHEALAAAELLK				0.95	5.0	4	
	SVPTSTVFYPSDGVATEK				1.12	2.9	2	
	TSRPENAIIYNNNEDFQVGQAK				0.94	3.6	3	
P29508	SPB3	Serpin B3	5	9	48	1.06	0.24	0.03
	FKVEESYDLK				0.91	3.5	3	
	FYQTSVESVDFANAPEESR				0.98	5.1	2	
	GLVLSGVLHK				0.90	2.7	2	
	KVLHFDQVTENTTGK				1.27	3.1	3	
	VLHFDQVTENTTGK				1.26	3.8	2	
P30041	PRDX6	Peroxiredoxin_6	2	2	10	0.98	0.51	0.32
	DFTPVCTTELGR				1.11	2.5	2	
	DINAYNCEEPTEK				0.71	3.1	2	
P30044	PRDX5	Peroxiredoxin_5_ mitochondrial	8	22	208	0.94	0.12	1.00
	ALNVEPDGTGLTCSLAPNIISQL				0.89	4.5	2	
	ETDLLLDDSLVSIFGNR				0.95	4.1	2	
	FSMVVQDGIVK				1.00	3.3	2	
	GVLFGVPGAFTPGCSK				0.91	4.2	2	
	LLADPTGAFGK				1.04	2.4	2	
	THLPGFVEQAEALK				0.97	3.9	3	
	VGDAIPAVEVFEGEPGNK				0.93	5.0	2	

	VNLAELFK				0.96	2.8	2	
P30085	KCY	UMP_CMP kinase	2	2	14	1.01	0.64	0.99
	EMDQTMAANAQK+Oxidation(1),Oxidation(5)				1.26	3.2	2	
	GKSSGRSDDNR				0.92	2.2	2	
P30086	PEBP1	Phosphatidylethanolamine_binding protein 1	4	9	57	0.97	0.16	1.00
	GNDISSGTVLSDYVGSGPPK				1.01	5.3	2	
	LYTLVLTDPDAPSR				0.94	3.5	2	
	NRPTSISWDGLDSGK				0.92	3.7	2	
	WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK				0.98	5.0	4	
P30530	UFO	Tyrosine_protein kinase receptor UFO	2	2	2	0.94	0.62	0.83
	NCMLNENMSVCVADFGLSKK+Oxidation(2)				0.86	2.7	2	
	TATITVLPQQPR				1.02	2.1	2	
P30740	ILEU	Leukocyte elastase inhibitor	4	6	33	0.96	0.33	1.00
	FKLEESYTLNSDLAR				0.94	3.0	3	
	KIEEQLTLEK				1.03	2.9	2	
	LGVQDLFNSSK				0.88	3.2	2	
	TFHFNTVEEVHSR				0.95	3.4	3	
P30838	AL3A1	Aldehyde dehydrogenase_ dimeric NADP_preferring	5	9	69	1.01	0.21	1.00
	FDHILYTGSTGVGK				1.04	3.4	2	
	IQQLEALQR				1.01	2.6	2	
	LIQEQEQELVGALAADLHK				0.99	5.3	3	
	NCDLDVACR				1.03	2.5	2	
	SLEEAIQFINQR				0.97	3.2	2	
P31946	1433B	14_3_3 protein beta/alpha	2	3	8	0.99	0.38	0.45
	AVTEQGHELSNEER				1.14	4.5	2	
	YLSEVASGDNK				0.86	2.7	2	
P31949	S10AB	Protein S100_A11	2	2	4	0.86	0.45	0.48
	DGYNYTLSK				0.86	2.4	2	
	NQKDPGVLDRMMK+Oxidation(11)				0.85	2.2	2	
P32119	PRDX2	Peroxiredoxin_2	3	7	39	0.97	0.20	0.67
	ATAVVDGAFK				1.01	2.4	2	
	EGGLGPLNIPLLADVTR				0.89	3.9	2	
	QITVNDLPVGR				1.06	2.9	2	
P35241	RADI	Radixin	2	2	19	0.87	0.46	0.85
	IGFPWSEIR				0.90	2.3	2	
	RKPDTIEVQQMK+Oxidation(10)				0.81	3.8	3	
P35247	SFTPD	Pulmonary surfactant_associated protein D	8	45	490	1.02	0.10	0.89
	GESGLPDVASLR				1.09	3.2	2	
	KVELFPNGQSVGEK				1.18	4.5	2	
	NEAAFLSMTDSK				1.03	3.6	2	
	NEAAFLSMTDSK+Oxidation(7)				0.97	4.2	2	
	QQVEALQGQVQHLQAAFSQYK				1.00	4.3	3	
	SAAENAALQQLVVAK				0.99	5.2	2	
	TAGFVKPFTEAQLLCTQAGGQLASPR				0.93	5.0	2	
	VELFPNGQSVGEK				1.10	2.5	2	
P35527	K1C9	Keratin_ type I cytoskeletal 9	9	19	49	0.65	0.30	0.19
	DIENQYETQITQIEHEVSSSGQEVQSSAK				0.60	3.9	3	
	EIETYHNLLEGGQEDFESSGAGK				0.61	4.3	2	
	GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR				0.66	5.0	3	
	GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK				0.50	7.5	3	
	GGSGGSYGGGGSGGGYGGGSGSR				0.70	4.6	2	
	GGSGGSYGGGSGSGGGSGGGYGGGSGGGHSGGSGGGHSGGSGGNYGGGSGSGGG				0.51	4.2	4	
	HGVQELEIELQSQLSK				0.72	4.7	2	
	SGGGGGGGLGSGGSIR				0.88	2.4	2	
	VQALEEANNDLENK				0.66	4.4	2	
P35579	MYH9	Myosin_9	11	18	51	1.02	0.18	1.00
	DMFQETMEAMR+Oxidation(1)				1.21	2.1	2	
	IAEFTTNLTEEEEK				0.91	4.0	2	
	IAQLEEQLDNETK				1.03	3.1	2	
	LQVELDNVTGLLSQSDSK				0.97	4.3	2	
	NFINNPLAQADWAAK				1.05	4.2	2	
	QLLQANPILEAFGNAK				1.06	3.0	2	
	RGDLPFVVPR				1.06	2.1	2	
	THEAQIQEMR+Oxidation(8)				0.87	2.8	2	
	TQLEELEDELQATEDAK				0.86	4.0	2	
	VISGVLQLGNIVFK				1.07	3.9	2	

	VKLQEMEGTVK+Oxidation(5)				1.02	2.4	2	
P35749	MYH11	Myosin_11	2	3	19	1.06	0.36	0.97
	ALEEALEAK				1.09	2.5	2	
	ASRDEIFATAKENEK				1.01	2.2	2	
P35754	GLRX1	Glutaredoxin_1	2	2	8	1.01	0.52	0.98
	AQEILSQLPIK				1.07	3.1	2	
	DCIGGCSDLVSLQQSGELLTR				0.91	4.7	2	
P35908	K22E	Keratin_ type II cytoskeletal 2 epidermal	5	5	16	0.78	0.63	0.92
	GFSSGSAVVSGGSR				0.84	2.9	2	
	GGSGGGGSISGGGYGSGGGSGGR				0.72	4.1	2	
	VDLLNQEIEFLK				0.75	3.2	2	
	YEELQVTVGR				0.89	2.8	2	
	YLDGLTAER				0.69	2.5	2	
P36222	CH3L1	Chitinase_3_like protein 1	2	5	15	0.91	0.30	0.45
	GNQWVGYDDQESVK				0.84	2.7	2	
	SFTLASSETGVGAPISGPGIPGR				0.94	3.7	2	
P36871	PGM1	Phosphoglucomutase_1	3	3	20	0.97	0.38	0.56
	ADNFEYSDPVDGSISR				1.04	2.7	2	
	FNISNGGPAPEAITDK				1.12	2.8	2	
	LSGTGSAGATIR				0.88	2.9	2	
P36955	PEDF	Pigment epithelium_derived factor	9	11	72	0.98	0.21	1.00
	DTDTGALLFIGK				1.01	2.6	2	
	ELLDTVTAPQK				0.99	2.5	2	
	KTSLEDFYLDEER				1.31	2.8	2	
	LDLQEINNWVQAQMK				0.79	3.9	2	
	LDLQEINNWVQAQMKGKLAR+Oxidation(13)				1.01	3.1	3	
	LQSLFDSPDFSK				0.92	3.3	2	
	LSYEGEVTK				0.94	2.2	2	
	TVQAVLTVPK				1.05	2.8	2	
	YGLDSDLSCK				0.97	2.7	2	
P36980	FHR2	Complement factor H_related protein 2	2	3	9	0.97	0.62	0.96
	INHGILYDEEK				0.89	3.5	2	
	LQNNENNISCVER				1.08	2.7	2	
P37802	TAGL2	Transgelin_2	4	7	56	0.91	0.23	0.61
	DDGLFSGDPNWFPK				0.89	3.9	2	
	DGTVLCELINALYPEGQAPVKK				0.83	3.4	3	
	NFSDNQLQEGK				0.99	2.7	2	
	TLMNLGGLAVAR				0.91	3.6	2	
P40121	CAPG	Macrophage_capping protein	5	6	39	0.90	0.26	0.57
	ANAQAAALYK				0.80	3.1	2	
	AQVEIVTDGEEPAEMIQVLGPKPALK				0.93	3.5	3	
	EGNPEEDLTADK				0.92	2.6	2	
	VSDATGQMNLTK+Oxidation(7)				1.03	2.5	2	
	YQEGGVESAFHK				0.91	2.7	2	
P40925	MDHC	Malate dehydrogenase_ cytoplasmic	5	9	49	1.00	0.19	0.97
	DVIATDKEDVAFK				1.01	3.5	2	
	FVEGLPINDFSR				1.01	2.2	2	
	GEFVTTVQQR				0.92	3.2	2	
	NVIIWGNHSSTQYPDVNHAK				0.95	4.2	3	
	VIVVGNPANTNCLTASK				1.13	4.6	2	
P40926	MDHM	Malate dehydrogenase_ mitochondrial	2	3	6	0.99	0.50	0.86
	SQETECTYFSTPLLLGK				0.90	2.8	2	
	VAVLGASGGIGQPLSLLLK				1.18	2.7	2	
P41162	ETV3	ETS translocation variant 3	2	2	3	1.02	0.38	0.62
	EDALMPPKLRLK+Oxidation(4)				0.95	2.2	2	
	KTELSELEDGSAADWR				1.17	2.1	2	
P43366	MAGB1	Melanoma_associated antigen B1	2	4	16	1.03	0.40	0.99
	YKMREPIMK+Oxidation(2),Oxidation(7)				1.07	2.0	1	
	YLKYEQVPNSDPPR				0.98	2.2	2	
P43652	AFAM	Afamin	5	8	54	0.93	0.31	1.00
	AESPEVCFNEESPK				0.91	3.1	2	
	ESLLNHFLYEVAR				0.92	3.4	2	
	FTDSENVCQER				0.95	2.8	2	
	IAPQLSTEELVSLGEK				0.82	4.6	2	
	SDVGFLPPFPTLDPEEK				0.93	3.5	2	
P46939	UTRO	Utrophin	3	3	3	0.91	0.70	0.94
	DVMKDVMSDLQQTNSEK+Oxidation(2)				1.01	2.1	2	

	DVMKDVMSDLQQTNSEK+Oxidation(6)				0.99	2.2	2	
	NKASSSDMRTAITEK+Oxidation(7)				0.57	2.2	2	
P46940	IQGA1	Ras GTPase_activating_like protein IQGAP1	4	6	11	0.93	0.40	0.93
	ATFYGEQVDYYK				0.75	2.6	2	
	EEIQSSISGVTAAYNR				1.01	2.8	2	
	EQLSDMMMINKQK+Oxidation(5),Oxidation(6),Oxidation(7)				0.62	1.9	1	
	KNKEQLSDMMMINK				1.09	2.1	2	
P48594	SPB4	Serpin B4	2	3	15	0.97	0.45	1.00
	INSWVESQTNEK				1.00	3.4	2	
	TNSILFYGR				0.87	2.4	2	
P48741	HSP77	Putative heat shock 70 kDa protein 7	2	3	25	0.98	0.45	1.00
	ATAGDTHLGGEDFDNR				1.07	3.9	2	
	VEILANDQGNR				0.92	3.2	2	
P50395	GDIB	Rab GDP dissociation inhibitor beta	5	6	26	0.94	0.37	1.00
	DLGTESQIFISR				1.02	3.8	2	
	EIRPALELLEPIEQK				0.93	3.5	3	
	FDLGQDVIDFTGHALALYR				0.90	3.5	3	
	FVSISDLLVPK				0.95	2.5	2	
	NTNDANSCQIIIPQNQVNR				0.85	2.7	2	
P51149	RAB7A	Ras_related protein Rab_7a	3	6	12	0.95	0.29	0.76
	DPENFPFVVLGNK				0.61	3.3	2	
	EAINVEQAFQTIAR				0.95	3.6	2	
	FSNQYKATIGADFLTK				1.05	2.2	2	
P51884	LUM	Lumican	4	6	52	0.94	0.22	0.97
	FNALQYLR				0.90	2.8	2	
	ISNIPDEYFK				0.95	2.8	2	
	LKEDAVSAAFK				1.03	2.9	2	
	NIPTVNENLENYYLEVNQLEK				0.45	4.6	2	
P52209	6PGD	6_phosphogluconate dehydrogenase_ decarboxylating	4	7	40	0.97	0.21	1.00
	GILFVGSGVSGGEEGAR				1.02	4.4	2	
	LVPLLDTGDIIIDGGNSEYR				0.89	5.3	2	
	SFLEDIRK				1.06	2.1	2	
	VDDFLANEAK				0.96	2.6	2	
P53004	BIEA	Biliverdin reductase A	2	2	4	1.11	0.85	0.76
	GSLLFTAGPLEEER				0.96	2.7	2	
	SGSLENVPNVGVNK				1.27	3.5	2	
P53634	CATC	Dipeptidyl peptidase 1	3	7	23	0.91	0.20	0.83
	GTDECAIESIAVAATPIPK				0.92	4.0	2	
	KVVVYLQK				0.97	2.3	2	
	NSWGTGWGENGYFR				0.85	2.8	2	
P53804	TTC3	E3 ubiquitin_protein ligase TTC3	2	3	23	1.00	0.32	1.00
	SSQGSPSVVVAPSPKTK				0.99	2.8	2	
	VSNASEMYTQKNDGKEK+Oxidation(6)				1.02	2.6	2	
P55072	TERA	Transitional endoplasmic reticulum ATPase	2	4	23	0.96	0.39	1.00
	LIVDEAINEDNSVVSLSQPK				0.97	4.4	2	
	RSVSDNDIRK				0.92	1.9	1	
P60174	TPIS	Triosephosphate isomerase	3	4	7	0.92	0.51	0.96
	ELASQPDVDGFLVGGASLKPEFVDIINAK				0.85	3.5	3	
	SNVSDAVAQSTR				0.90	3.0	2	
	VVLAYEPVWAIGTGK				1.09	2.8	2	
P60660	MYL6	Myosin light polypeptide 6	2	2	4	0.97	0.70	0.90
	HVLVTLGEK				1.03	2.2	2	
	VLDFEHFLPMLQTVAK				0.76	3.9	3	
P61626	LYSC	Lysozyme C	6	28	295	0.97	0.14	1.00
	ATNYNAGDR				0.90	2.8	2	
	AWVAWR				0.90	2.2	2	
	GISLANWMCLAK+Oxidation(7)				1.03	2.5	2	
	QYVQGCGV				0.99	2.1	1	
	STDYGIFQINSR				0.97	4.9	2	
	TPGAVNACHLSCSALLQDNIADAVACAK				0.99	5.7	3	
P61769	B2MG	Beta_2_microglobulin	3	7	67	0.92	0.30	0.99
	SNFLNCYVSGFHPSDIEVDLLK				0.46	3.9	2	
	VEHSDLSFSK				0.95	3.4	3	
	VNHVTLSQPK				0.96	3.3	3	
P61916	NPC2	Epididymal secretory protein E1	2	3	10	0.99	0.26	0.86
	AVVHGILMGVPVPFPIPEPDGCK+Oxidation(7)				0.94	3.4	3	

	EVNVSPCPTQPCQLSK				1.21	3.3	2	
P61978	HNRPK	Heterogeneous nuclear ribonucleoprotein K	2	4	7	1.05	0.45	0.99
	GSYGDLGGPIITTQVTIPK				1.01	2.7	2	
	TDYNASVSVPDSSGPER				1.13	2.4	2	
P61981	1433G	14_3_3 protein gamma	2	3	20	1.05	0.44	1.00
	NVTELNEPLSNEER				1.05	4.1	2	
	YLAEVATGEK				1.06	2.6	2	
P62158	CALM	Calmodulin	4	8	42	0.98	0.28	0.84
	DGNGYISAAELR				1.07	2.6	2	
	EAFSLFDKDGDGTITTK				0.98	3.7	2	
	MKDTDSEEEIR+Oxidation(0)				1.08	3.7	3	
	VFDKDGNGYISAAELR				0.76	4.1	2	
P62258	1433E	14_3_3 protein epsilon	4	4	9	0.86	0.34	0.31
	EAAENSLVAYK				0.66	2.1	2	
	HLIPAANTGESK				1.07	2.5	2	
	LICCDILDVLDK				0.95	3.4	2	
	YLAEFATGNDR				0.78	2.3	2	
P62805	H4	Histone H4	6	10	96	0.97	0.21	1.00
	DAVTYTEHAK				1.07	3.1	2	
	DNIQGITKPAIR				0.96	2.5	2	
	ISGLIYEETR				0.94	3.8	2	
	TVTAMDVVYALK				0.92	3.2	2	
	TVTAMDVVYALK+Oxidation(4)				1.00	3.0	2	
	VFLENVIR				0.93	2.7	2	
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	4	9	44	0.92	0.28	0.99
	HTGPGILSMANAGPNTNGSQFFICTAK				0.99	6.5	3	
	IIPGFMCQGGDFTR				0.96	2.5	2	
	KITIADCGQLE				0.96	3.6	2	
	VSFELFADK				0.41	2.1	2	
P63104	1433Z	14_3_3 protein zeta/delta	5	10	61	0.89	0.23	1.00
	DSTLIMQLLR				0.90	2.8	2	
	DSTLIMQLLR+Oxidation(5)				0.91	3.1	2	
	GIVDQSQQAYQEAFEISK				0.63	4.8	2	
	SVTEQGAELSNEER				0.95	4.9	2	
	YLAEVAAGDDKK				0.88	3.3	2	
P63261	ACTG	Actin_ cytoplasmic 2	10	63	526	0.98	0.09	1.00
	CPEALFQPSFLGMESCGIHETTFNSIMK				0.80	5.0	3	
	CPEALFQPSFLGMESCGIHETTFNSIMK+Oxidation(12)				0.81	3.2	3	
	DLYANTVLSGGTTMYPGIADR				0.94	4.7	2	
	DLYANTVLSGGTTMYPGIADR+Oxidation(13)				0.98	5.7	2	
	GYSFTTTAER				0.99	3.4	2	
	KDLYANTVLSGGTTMYPGIADR				1.01	4.9	2	
	KDLYANTVLSGGTTMYPGIADR+Oxidation(14)				0.96	4.7	3	
	TTGIVMDSGDGVTHTVPIYEGYALPHAILR				0.96	4.6	3	
	TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)				0.98	5.1	4	
	VAPEEHPVLLTEAPLNPK				1.05	4.2	3	
P67936	TPM4	Tropomyosin alpha_4 chain	4	5	49	0.90	0.34	1.00
	IQALQQQADEAEDR				0.86	4.2	2	
	IQLVEEELDR				0.92	3.1	2	
	MEIQEMQLK+Oxidation(0),Oxidation(5)				0.81	2.1	1	
	YSEKEDKYEEEIK				0.93	3.7	3	
P68133	ACTS	Actin_ alpha skeletal muscle	9	38	244	0.93	0.13	1.00
	DLTDYLMK				1.00	2.1	1	
	DLTDYLMK+Oxidation(6)				0.93	2.6	2	
	DSYVGDEAQSK				0.99	3.4	2	
	EITALAPSTMK+Oxidation(9)				0.92	2.8	2	
	HQGVMVGMGQK+Oxidation(4)				1.00	4.3	3	
	HQGVMVGMGQK+Oxidation(4),Oxidation(7)				0.87	3.8	3	
	HQGVMVGMGQK+Oxidation(7)				0.97	3.3	3	
	YPIEHGIITNWDDMEK				0.91	3.7	3	
	YPIEHGIITNWDDMEK+Oxidation(13)				0.92	3.7	2	
P68366	TBA4A	Tubulin alpha_4A chain	2	4	16	0.95	0.31	1.00
	IHFPLATYAPVISAEK				0.99	2.6	2	
	SIQFVDWCPTGFK				0.93	3.8	2	
P68371	TBB2C	Tubulin beta_2C chain	2	3	13	0.98	0.48	0.96
	INVYYNEATGGK				1.01	3.3	2	
	MSATFIGNSTAIQELFK				0.83	4.1	2	

P68871	HBB	Hemoglobin subunit beta	6	68	1097	1.00	0.08	1.00
	EFTPPVQAAYQK				1.07	3.1	2	
	FFESFGDLSTPDAVMGNPK				0.90	5.3	2	
	FFESFGDLSTPDAVMGNPK+Oxidation(14)				0.96	5.3	2	
	GTFATLSELHCDK				1.00	4.1	2	
	SAVTALWGK				0.95	3.2	2	
	VNVDEVGGEALGR				1.05	4.7	2	
P69905	HBA	Hemoglobin subunit alpha	11	71	786	0.98	0.08	1.00
	FLASVSTVLTSK				0.96	4.0	2	
	KVADALTNAVAHVDDMPNALSALSDLHAHK				0.97	5.7	4	
	KVADALTNAVAHVDDMPNALSALSDLHAHK+Oxidation(15)				1.02	4.6	4	
	LLSHCLLVTLAAHLPAEFTPAVHASLDK				0.93	6.6	4	
	LRVDPVNFK				1.01	3.0	3	
	MFLSFPTTK				0.91	2.9	2	
	MFLSFPTTK+Oxidation(0)				0.98	2.8	2	
	TYFPHFDLSHGSAQVK				0.97	4.2	2	
	VADALTNAVAHVDDMPNALSALSDLHAHK				0.95	6.1	3	
	VADALTNAVAHVDDMPNALSALSDLHAHK+Oxidation(14)				1.01	5.7	3	
	VGAHAGEYGAEALER				1.01	5.4	3	
P78316	NOP14	Nucleolar protein 14	3	7	20	0.99	0.19	1.00
	IQKCNHPSLAEGNK				0.99	2.1	2	
	QLFNSLATQEGEWKALK				0.93	2.2	2	
	RTQTLLKEYK				1.01	2.2	2	
P78527	PRKDC	DNA_dependent protein kinase catalytic subunit	3	3	10	1.08	0.46	0.57
	FKTLSEKNNITQK				0.93	2.4	2	
	IRVVQMLGSLGGQINK+Oxidation(5)				0.90	2.1	2	
	QFINLMLPMK+Oxidation(8)				1.84	2.1	2	
P78559	MAP1A	Microtubule_associated protein 1A	2	2	2	0.98	0.38	0.94
	LDMYVLNPVKDSK				1.03	2.3	2	
	SREAFGGRELGLQGK				0.97	2.3	2	
P80188	NGAL	Neutrophil gelatinase_associated lipocalin	3	8	52	0.92	0.21	0.44
	SLGLPENHIVFPVPIDQCIDG				0.87	3.9	2	
	SYPGLTSYLVR				0.90	2.2	2	
	TFVPGCQPGEFTLGNIK				0.98	3.5	2	
P80723	BASP1	Brain acid soluble protein 1	2	3	8	0.96	0.43	0.98
	AEPPKAPEQEQAAPGPAAGGEAPK				0.93	3.0	3	
	AQGPAASAEEPKPVEAPAANSDQTVTVKE				0.97	4.7	3	
P80748	LV302	Ig lambda chain V_III region LOI	2	10	74	1.00	0.20	1.00
	FSGSNSGNTATLTISR				1.03	4.3	2	
	YVLTQPPSVSVAPGETAR				0.94	3.9	2	
P82987	ATL3	ADAMTS_like protein 3	2	2	2	1.03	0.53	0.96
	EENVIAVPLGSRSVR				1.00	2.1	2	
	SCQMPECSKIKSEMK+Oxidation(13)				1.11	2.1	2	
P98088	MUC5A	Mucin-5AC (Fragments)	3	4	21	0.96	0.41	0.88
	GQTCGLCGNFNSIQADDFR				1.07	3.3	2	
	IQCCETVNVCR				0.99	3.0	2	
	SVVGDVLEFGNSWK				0.86	2.8	2	
Q01484	ANK2	Ankyrin_2	4	11	79	1.15	0.22	0.60
	ATSPLIEETPIGSIK				1.43	2.1	1	
	ATSPLIEETPIGSIKDK				1.02	2.7	2	
	HGADQDAHTKLGYTPLIVACHYGNVK				1.32	2.1	2	
	QKEEGLQASAEK				1.30	2.2	2	
Q01518	CAP1	Adenylyl cyclase_associated protein 1	4	6	31	0.93	0.19	0.57
	ALLVTASQCQQPAENK				1.02	4.1	2	
	LSDLLAPISEQIK				0.95	3.2	2	
	NSLDCEIVSAK				0.98	2.7	2	
	VENQENVSNLVIEDTELK				0.88	4.0	2	
Q02224	CENPE	Centromere_associated protein E	2	3	4	1.08	0.49	0.76
	LNENYEEVK				1.24	1.9	1	
	QEQSLNMKEK				1.00	1.9	1	
Q04917	1433F	14_3_3 protein eta	3	3	18	0.93	0.44	1.00
	AVTELNEPLSNEDR				0.98	3.2	2	
	ELETVCNDVLSLLDK				0.89	3.6	2	
	YLAEVASGEK				0.92	2.5	2	
Q05086	UBE3A	Ubiquitin_protein ligase E3A	2	3	4	0.98	0.48	0.97
	AFRRGFHMVTNESPLK				1.00	2.3	2	
	EFVNLYSDYILNK				0.90	2.2	2	

Q06830	PRDX1	Peroxiredoxin_1	6	11	87	0.99	0.20	0.95
	ADEGISFR				0.95	2.2	2	
	HGEVCPAGWKPGSDTIKPDVQK				1.03	5.3	4	
	LNCQVIGASVDSHFCHLAWVNTPK				0.92	4.5	4	
	LVQAFQFTDK				0.86	3.3	2	
	QGGLGPMNIPLVSDPK				0.98	3.0	2	
	TIAQDYGVLK				1.07	2.9	2	
Q08380	LG3BP	Galectin_3_binding protein	11	26	285	0.93	0.12	1.00
	ASHEEVEGLVEK				0.97	3.7	3	
	AVDTWSWGER				0.82	3.2	2	
	ELSEALGQIFDSQR				0.97	4.8	2	
	IDITLSSVK				0.95	2.5	2	
	RIDITLSSVK				0.95	2.9	2	
	SDLAVPSELALLK				0.94	3.6	2	
	STHTLDLSR				0.85	3.0	3	
	STSSFPCPAGHFNGFR				0.88	3.0	2	
	TLQALEFHTVPFQLLAR				0.96	5.0	2	
	YSSDYFQAPSDYR				0.87	4.3	2	
	YYPYQSFQTPQHPSFLFQDK				1.03	3.5	2	
Q09666	AHNK	Neuroblast differentiation_associated protein AHNAK	3	3	5	1.06	0.47	0.92
	AEGPEVDVNLPK				1.02	2.2	2	
	APKVKMPDVDISVPK+Oxidation(5)				0.98	2.2	2	
	FKMPEMHFK+Oxidation(2),Oxidation(5)				1.18	1.8	1	
Q12805	FBLN3	EGF_containing fibulin_like extracellular matrix protein 1	7	9	57	0.95	0.23	1.00
	ADQVCINLR				1.03	3.4	2	
	CVNHYGGYLCLPK				0.85	3.6	3	
	DIDECDIVPDACK				0.99	3.0	2	
	FSCMCPQGYQVVR+Oxidation(3)				1.00	2.9	2	
	GSFACQCPPGYQK				0.89	4.2	2	
	IQCAAGYEQSEHNVCQDIDECTAGTHNCR				0.91	4.1	4	
	TCQDINECETTNECR				0.91	4.3	2	
Q12923	PTN13	Tyrosine_protein phosphatase non_receptor type 13	2	5	54	1.03	0.26	0.94
	CSTYQIKGSPNLTLPK				1.00	2.9	2	
	QQPQLLK				1.07	1.9	1	
Q13228	SBP1	Selenium_binding protein 1	4	6	30	0.96	0.24	1.00
	FLHNPDAAQGFVGCALSSTIQR				1.00	3.1	3	
	HEIVQTLSLK				0.90	2.4	2	
	IYVVDVGSEPR				0.96	2.6	2	
	NTGTEAPDYLATVDVDPK				0.95	3.6	2	
Q13421	MSLN	Mesothelin	3	5	38	1.05	0.30	0.26
	IQSFLGGAPTEDLK				1.14	3.8	2	
	QLLGFPCAEVSGLSTER				1.02	3.0	2	
	TDAVLPLTVAEVQK				0.99	3.2	2	
Q13439	GOGA4	Golgin subfamily A member 4	2	5	7	1.02	0.32	0.98
	IAELREELQMDQQAKK+Oxidation(9)				1.01	2.3	2	
	MKQELEAKMDEQK+Oxidation(0),Oxidation(8)				1.04	1.8	1	
Q13588	GRAP	GRB2_related adapter protein	2	4	44	0.99	0.34	0.97
	ISRQLAEEILMK				0.97	2.2	2	
	YFLWEEK				1.02	2.2	1	
Q13751	LAMB3	Laminin subunit beta_3	2	2	5	1.02	0.36	0.51
	GSQAIMLRSADLTGLEKR				0.90	2.2	2	
	QAGGGGGTGSPKLVALR				1.11	2.3	2	
Q13938	CAYP1	Calcyphosin	8	12	114	0.94	0.20	0.97
	EAVIAAAFAK				1.07	3.1	2	
	FLDNFDSSEK				0.96	2.8	2	
	GASGIQGLAR				0.85	2.2	2	
	LGLVLDQAEAEGVCR				0.93	4.5	2	
	NGSGTLDLEEFLR				0.78	3.0	2	
	SGDGVVTVDDLR				1.01	3.4	2	
	SGEWTEDEVLR				0.81	2.7	2	
	SLDADEFR				0.62	2.5	2	
Q14019	COTL1	Coactosin_like protein	3	6	26	1.00	0.27	1.00
	DDGSAVIWVTFK				1.10	4.0	2	
	KELEEDFIK				1.04	2.4	2	

	YDGSTIVPGEQGAEYQHFIQQCTDDVR				0.95	3.7	3	
Q14508	WFDC2	WAP four_disulfide core domain protein 2	2	2	16	0.98	0.54	1.00
	CCSAGCATFCSLPNDK				0.98	4.2	2	
	EGSCPQVNINFPQLGLCR				0.98	4.2	3	
Q14624	ITIH4	Inter_alpha_trypsin inhibitor heavy chain H4	6	11	51	1.03	0.22	0.99
	AEAQAQYSAAVAK				0.96	4.6	2	
	AGFSWIEVTFK				1.16	3.8	2	
	EKAEAQAQYSAAVAK				1.35	3.0	2	
	NPLVWVHASPEHVVVTR				0.98	3.5	3	
	QGPVNLLSDPEQGVEVTGQYER				0.98	4.0	2	
	SPEQQETVLDGNLIIR				0.97	3.2	2	
Q14651	PLSI	Plastin_1	2	3	19	1.00	0.52	1.00
	IENCNYAVELGK				0.91	2.6	2	
	KIENCNYAVELGK				1.07	4.2	2	
Q15019	SEPT2	Septin_2	2	2	2	1.02	1.12	0.97
	ASIPFSVVGSNQLIEAK				1.08	2.5	2	
	KVENEDMNKDQILLEK				0.96	2.2	2	
Q15154	PCM1	Pericentriolar material 1 protein	2	2	3	1.00	0.31	0.99
	QLGSILQDSLAK				1.02	2.3	2	
	YMSQMSVPEQAELEK				0.99	2.3	2	
Q15582	BGH3	Transforming growth factor_beta_induced protein ig_h3	6	10	47	0.99	0.17	0.99
	EGVYTVFAPTNEAFR				1.00	3.3	2	
	GDELADSALEIFK				0.97	3.8	2	
	LTLLAPLNSVFK				0.82	2.7	2	
	SLQGDKLEVSLK				1.11	2.5	2	
	STVISYECCPGYEK				1.00	3.7	2	
	YHIGDEILVSGGIGALVR				1.03	4.1	3	
Q16445	GBRA6	Gamma_aminobutyric acid receptor subunit alpha_6	2	3	4	0.89	0.56	0.94
	IWTPDTFFRNGKK				0.91	2.2	2	
	LEVEGNFYSENVSR				0.84	1.8	1	
Q2NKX8	ERC6L	DNA excision repair protein ERCC_6_like	2	2	2	0.90	0.80	0.63
	DDEPEEVVVKAK				0.56	2.2	2	
	NEGAWLREPVFPSSTKK				1.03	2.3	2	
Q2VYF4	LETM2	LETM1 domain_containing protein LETM2_ mitochondrial	2	3	7	0.92	0.42	0.93
	ENMVDLAPQLK				0.97	2.2	2	
	MAVKLELAKFLQETMTEMAR+Oxidation(14),Oxidation(17)				0.87	2.7	2	
Q3B7T1	EDRF1	Erythroid differentiation_related factor 1	2	2	4	0.96	0.72	0.93
	QMALFLDKMGSLQKGNYSSQSGMIPGSWQHK+Oxidation(22)				0.91	3.1	3	
	TAFARLEEKTDLK				1.03	2.3	2	
Q3V6T2	GRDN	Girdin	4	4	5	2.51	0.75	0.55
	EDLKSLYDSLIK				1.34	2.3	2	
	MVQSSPPISGEDNK				0.62	2.1	2	
	SLEQETSQLEKDKK				13.93	2.3	2	
	WERESQETTRELLK				0.61	2.2	2	
Q3ZCM7	TBB8	Tubulin beta_8 chain	3	3	3	0.98	0.76	0.97
	AVLVDLEPGTMDSVR				1.06	2.9	2	
	EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK				0.89	3.0	3	
	NMMAACDPR+Oxidation(1),Oxidation(2)				0.91	2.4	2	
Q4G0P3	HYDIN	Hydrocephalus_inducing protein homolog	2	4	9	1.00	0.46	0.78
	EQTMSEKEELNK+Oxidation(3)				1.11	2.5	2	
	FKTYELTLKDVQNILMYWDR				0.79	2.2	2	
Q4KWH8	PLCH1	1_phosphatidylinositol_4_5_bisphosphate phosphodiesterase eta_1	2	2	2	0.99	0.40	0.47
	DHLTVEELAQFLKVEQK				0.91	2.4	2	
	MNNVTTDYCLDIIK+Oxidation(0)				1.22	2.3	2	
Q4LE39	ARI4B	AT_rich interactive domain_containing protein 4B	2	3	6	0.94	0.34	0.76
	MTPTKKYNGLEEK+Oxidation(0)				0.97	2.3	2	
	NQKMYEASIK				0.92	2.1	2	
Q5M9N0	CD158	Coiled_coil domain_containing protein 158	2	2	9	1.03	0.60	0.90
	QMAAIQGKNESLEK				0.94	2.4	2	
	TEEDGRTSLGALEDRVR				1.12	2.4	2	
Q5T4S7	UBR4	E3 ubiquitin_protein ligase UBR4	2	8	36	1.03	0.26	0.89
	EEKNLQGFLEQPK				1.07	2.2	2	
	VNRQQLVK				1.01	2.1	1	

Q5TBA9	FRY	Protein furry homolog	2	2	2	1.01	0.30	0.93
	MIGMSLYYSQVRK+Oxidation(3)				1.02	2.3	2	
	QENLPKHCPTALSYAWPYAFTR				0.97	3.3	3	
Q5VST9	OBSCN	Obscurin	2	2	8	1.00	0.33	0.81
	FIEDVK				0.88	2.2	2	
	TSASLTIRPMPAHFIGR+Oxidation(9)				1.06	2.4	2	
Q5VTE0	EF1A3	Putative elongation factor 1_alpha_like 3	6	9	120	1.00	0.24	0.94
	EHALLAYTLGVK				0.97	2.6	2	
	IGGIGTVPVGR				1.05	2.9	2	
	STTTGHLIYK				1.16	2.8	2	
	THINIVVIGHVDSGK				0.87	4.2	3	
	VETGVLKPGMVVTFAPVNVTTEVK				0.91	3.7	3	
	VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)				0.98	4.5	3	
Q5VZK9	LR16A	Leucine_rich repeat_containing protein 16A	2	2	2	1.15	0.76	0.69
	FMPIPMYDASQALK				1.02	2.4	2	
	NVLLEQSGIDILNK				1.43	1.8	1	
Q5XKE5	K2C79	Keratin_ type II cytoskeletal 79	2	2	8	0.65	0.81	0.21
	FLEQQNKVLETK				0.65	3.7	2	
	NLDLDSIIAEVK				0.66	3.3	2	
Q6P1M3	L2GL2	Lethal(2) giant larvae protein homolog 2	2	2	3	0.96	0.39	0.95
	LTFSEDEQLESAGGKVK				0.97	2.4	2	
	TISSDAVLQR				0.95	2.1	2	
Q6P1M9	ARMX5	Armadillo repeat_containing X_linked protein 5	2	2	3	1.01	0.63	0.99
	AMPMSRVSTVTK+Oxidation(1),Oxidation(3)				1.09	2.1	2	
	NHANTRELISAK				0.98	2.1	2	
Q6Q759	SPG17	Sperm_associated antigen 17	2	2	3	0.96	0.45	0.97
	TMFEKGPTFIKVR+Oxidation(1)				0.94	2.2	2	
	VVIVERK				0.99	2.1	2	
Q6TFL3	CI093	Uncharacterized protein C9orf93	2	6	50	0.95	0.37	1.00
	EKAQAAQSESELQK				0.94	3.2	2	
	TNETEKAFQTSQQK				0.97	1.9	1	
Q6ZRK6	CCD73	Coiled_coil domain_containing protein 73	3	5	6	0.87	0.39	0.79
	QQIQANTEMEAELKVLK				0.85	2.3	2	
	VSEMEQKVQLHLLAK+Oxidation(3)				1.04	2.3	2	
	YSLRNSSNVMLDDK+Oxidation(9)				0.68	1.9	1	
Q70EL1	UBP54	Inactive ubiquitin carboxyl_terminal hydrolase 54	2	2	2	0.97	0.50	0.70
	NSSPSDSKPPFSQGQEK				0.90	2.2	2	
	SRTDNSWAPWSETNQHIGTR				1.10	2.3	2	
Q7RTS7	K2C74	Keratin_ type II cytoskeletal 74	2	2	4	0.60	0.99	0.39
	DLDLDSIIAEVR				0.55	2.2	2	
	FLEQQNQVLETK				0.65	3.7	2	
Q7RTV2	GSTA5	Glutathione S_transferase A5	2	2	18	0.99	0.41	0.89
	AILNYIASK				1.05	3.1	2	
	ISNLPTVK				0.91	2.2	2	
Q7RTW8	OTOAN	Otoancorin	2	2	4	0.95	0.42	0.95
	CFQMLNSLECVEILGK				0.94	2.1	2	
	DCPDLNPEQKAAVRLK				0.98	2.3	2	
Q7Z4S6	KI21A	Kinesin_like protein KIF21A	2	5	28	0.99	0.28	1.00
	LQTLKKQYEEK				0.92	2.1	1	
	VMVNQDRASQQINALR+Oxidation(1)				1.02	2.4	2	
Q7Z5N4	SDK1	Protein sidekick_1	2	2	6	0.97	0.50	0.99
	LMLPEEPPSAPPK+Oxidation(1)				0.86	2.4	2	
	YIIPSLQK				1.01	2.3	2	
Q7Z6B7	SRGP1	SLIT_ROBO Rho GTPase_activating protein 1	2	2	3	1.04	0.34	0.94
	KAEIETEYSRNLEK				1.09	2.4	2	
	SQYNTKLFNGDLETFVK				1.02	2.1	2	
Q86V48	LUZP1	Leucine zipper protein 1	2	3	5	1.03	0.45	0.96
	IEGKDEEIK				0.99	1.8	1	
	MNRDYTRNASNLER				1.10	2.1	2	
Q86VB7	C163A	Scavenger receptor cysteine_rich type 1 protein M130	2	2	21	1.00	0.90	1.00
	EAEFGQGTGPIWLNEVK				0.90	4.3	2	
	HNCDHAEDAGVICSK				1.10	4.5	3	
Q86W56	PARG	Poly(ADP-ribose) glycohydrolase	2	2	2	1.28	0.89	0.34
	DEAKPLRMFHDTIK+Oxidation(7)				1.24	2.2	2	
	FLINPELIISR				1.36	1.8	1	
Q86Z20	CC125	Coiled_coil domain_containing protein 125	3	8	33	1.00	0.25	1.00

	EEAYVMADAFRIAFEQQLMR+Oxidation(5)				1.03	2.5	2	
	NDQALQLTQMDKMHK+Oxidation(12)				0.98	2.7	2	
	YLEALAMLDIK				1.00	1.8	1	
Q8IWI9	MGAP	MAX gene_associated protein	2	2	2	0.93	0.37	0.72
	QSTISPSTSYSLKPHSVPPVSRK				0.92	2.2	2	
	RAFISKVPPGSR				0.98	1.8	1	
Q8IWJ2	GCC2	GRIP and coiled_coil domain_containing protein 2	2	5	17	0.92	0.22	0.63
	EDVILKEHITQLEK				0.94	2.1	2	
	RNTDLPLLDMHTVTR+Oxidation(9)				0.90	2.3	2	
Q8IWL2	SFTA1	Pulmonary surfactant_associated protein A1	14	205	2513	0.93	0.05	1.00
	EQCVEMYTDGQWNDR				0.86	5.1	2	
	EQCVEMYTDGQWNDR+Oxidation(5)				0.86	5.0	2	
	GALSLQGSIMTVGEK				0.90	4.9	2	
	GALSLQGSIMTVGEK+Oxidation(9)				0.96	5.2	2	
	GKEQCVEMYTDGQWNDR				0.76	5.4	2	
	GKEQCVEMYTDGQWNDR+Oxidation(7)				0.91	5.2	3	
	GPPGLPAHLDEELQATLHDFR				0.95	4.6	3	
	HQILQTR				1.02	2.4	2	
	KYNTYAYVGLTEGPSPGDFR				0.92	6.2	2	
	NCLYSR				0.99	2.4	2	
	NPEENEAIASFVK				1.03	4.4	2	
	VFSSNGQSITFDAIQEACAR				0.91	6.0	2	
	YNTYAYVGLTEGPSPGDFR				0.88	5.8	3	
	YSDGTPVNYTNWYR				0.94	3.3	2	
Q8N4F0	BPIL1	Bactericidal/permeability_increasing protein_like 1	3	5	19	0.94	0.22	0.99
	AALSYVSEIGK				0.94	2.4	2	
	AGALNLDITGQLR				0.93	3.1	2	
	ALQVTVPHFLDWSGEALQPTR				0.93	3.9	3	
Q8N8Z6	DCBD1	Discoidin_ CUB and LCCL domain_containing protein 1	2	2	3	0.95	0.73	0.98
	SFVMNFKNNNSKWK				0.95	2.2	2	
	TTGSTQSNFNFYVK				0.95	2.2	2	
Q8NB14	UBP38	Ubiquitin carboxyl_terminal hydrolase 38	3	3	4	1.00	0.31	0.84
	FLLDRLHEEEKILK				1.08	2.3	2	
	LILNQSAWTSQSNSLASCLSR				0.87	2.3	2	
	QVLSLNLNGCNSLMKK+Oxidation(13)				1.01	2.1	2	
Q8NCQ7	PRCA1	Protein PROCA1	2	2	3	0.90	0.56	0.76
	EKDKEEMDEK				0.82	2.2	2	
	SESPTGKGQGSKVIK				0.96	2.2	2	
Q8ND07	CN045	Uncharacterized protein C14orf45	2	2	2	0.94	0.34	0.64
	ELDDLKENLR				0.86	2.2	2	
	IQVERELDDLKENLR				1.00	2.2	2	
Q8NDA2	HMCN2	Hemicentin_2	2	2	2	1.14	0.51	0.37
	ELYVQGGGDCPEMSVGAIK+Oxidation(12)				1.04	2.2	2	
	GGLEMILAPEGSSSGK				1.19	2.2	2	
Q8NET4	RGAG1	Retrotransposon gag domain_containing protein 1	3	2	4	0.85	1.40	0.98
	MLSQPMSTQDPGGMSMSPMK+Oxidation(0),Oxidation(13)				0.89	2.3	2	
	MLSQPMSTQDPGGMSMSPMK+Oxidation(0),Oxidation(15)				0.89	2.2	2	
	VMSAQLTMAKTSGAMPTGSMK+Oxidation(14),Oxidation(19)				0.75	2.1	2	
Q8NEV4	MYO3A	Myosin_IIIa	2	2	3	1.19	0.83	0.72
	MSPDTCATILEKAGLDNWALGK				1.47	2.2	2	
	VYQTPKKMNNVYEEEVK				1.14	2.2	2	
Q8NF91	SYNE1	Nesprin_1	4	4	4	1.01	0.25	0.99
	EEVIELMNDTEKK+Oxidation(6)				0.99	2.1	2	
	KEIHDHMEQLK				1.07	2.1	2	
	MLHLVTLYHR+Oxidation(0)				1.02	1.9	1	
	SRLKVLTEVSSENEAQK				0.99	2.2	2	
Q8NFJ5	RAI3	Retinoic acid_induced protein 3	3	6	28	0.92	0.23	0.45
	AHAWPSPYK				0.97	2.2	2	
	AYSQEEITQGFEETGDTLYAPYSTHFQLQNQPPQK				0.95	5.0	3	
	TNVNVFSELSAPR				0.90	3.8	2	
Q8TDJ6	DMXL2	DmX_like protein 2	2	2	3	0.89	1.42	0.98
	QEVLQETFIR				0.94	1.8	1	
	QSENISAPPVLSEDIDKHRR				0.78	2.1	2	
Q8TDL5	LPLC1	Long palate_ lung and nasal epithelium carcinoma_associated protein 1	17	45	330	0.93	0.08	1.00
	ALGFEAAESSLTK				0.98	3.9	2	

	DALVLTPASLWKPSSPVSQ				0.95	4.3	2	
	EKPAGGIPVLGSLVNTVLK				0.91	4.6	3	
	GDQLILNLNNISSDR				0.91	4.1	2	
	GDTIQLYLGAK				0.79	2.8	2	
	ILTQDTPEFFIDQGHAK				0.87	3.5	2	
	IQLMNSGIGWFQPDVLK				0.96	4.8	2	
	IQLMNSGIGWFQPDVLK+Oxidation(3)				0.92	4.9	2	
	LEFDLLYPAIK				0.89	3.4	2	
	LSFLVNALAK				0.90	3.1	2	
	LVLSDCATSHGSLR				0.96	3.6	2	
	MDTSASGPTR+Oxidation(0)				0.83	2.6	2	
	NIITEIIHSILLPNQNGK				0.94	5.3	2	
	QVMNLLVPSLPNLVK				0.87	3.7	2	
	QVMNLLVPSLPNLVK+Oxidation(2)				0.89	3.4	2	
	SSIGLINEK				0.91	2.6	2	
	VITANILQLQVKPSANDQELLVK				1.02	3.6	3	
Q8TEU7	RPGF6	Rap guanine nucleotide exchange factor 6	2	2	3	1.01	0.29	0.96
	DNEDSILQREIPAR				0.99	2.3	2	
	SSLLNAKKLYEDAQMAR+Oxidation(14)				1.03	2.2	2	
Q8WUM4	PDC6I	Programmed cell death 6_interacting protein	2	2	11	0.97	0.49	1.00
	LLDEEEATDNDLR				0.91	3.2	2	
	SVIEQGGIQTVDQLIK				1.00	3.3	2	
Q8WZ42	TITIN	Titin	5	6	42	1.13	0.35	0.89
	EEGEFTDKVQIEK				1.00	2.2	2	
	EGVKITEKPSPPEK				0.95	2.6	2	
	ELEETAARMEIK+Oxidation(8)				4.93	2.2	2	
	GSPVIQVTWFKNNK				0.89	2.2	2	
	GVQWIKNGVVLESNEK				0.95	2.1	2	
Q92539	LPIN2	Phosphatidate phosphatase LPIN2	2	3	3	1.03	0.28	0.45
	ATVESWVKDKMPK				1.16	2.1	2	
	IFTVNPKGELIQER				0.95	2.1	2	
Q92576	PHF3	PHD finger protein 3	2	2	2	1.19	0.74	0.47
	TGETVVEEMIATR+Oxidation(8)				1.07	2.1	2	
	TKYIDDTVK				1.36	1.9	1	
Q92786	PROX1	Prospero homeobox protein 1	2	2	2	0.95	0.26	0.75
	EFYYIQMEKYAR				0.91	2.2	2	
	VENIIRGMSHSPSVALR				0.97	2.2	2	
Q96A65	EXOC4	Exocyst complex component 4	2	2	2	0.84	0.47	0.40
	QVPQKLEQCMASK				0.82	2.5	2	
	STVSKSKDPSGLLISVIR				0.85	2.3	2	
Q96BR6	ZN669	Zinc finger protein 669	3	2	16	0.96	0.47	1.00
	QCGKAFSRLSSLCNHR				0.93	2.4	2	
	RHMIMHSGNPAYKCTICGK+Oxidation(2)				0.99	2.6	2	
	RHMIMHSGNPAYKCTICGK+Oxidation(4)				0.99	2.6	2	
Q96DA0	ZG16B	Zymogen granule protein 16 homolog B	2	3	27	0.94	0.29	0.99
	LGALGGNTQEVTLQPGEYITK				0.96	5.3	2	
	VSVGLLLVK				0.88	2.9	2	
Q96FN5	KIF12	Kinesin_like protein KIF12	2	2	2	0.98	0.33	0.69
	MEERGSPDGDLAR+Oxidation(0)				1.07	2.1	2	
	QTAQQMPSVDPGEPPVGGK				0.94	2.2	2	
Q96G01	BICD1	Protein bicaudal D homolog 1	2	5	47	1.05	0.33	1.00
	EETLLQESASK				1.00	2.1	1	
	MKDEIREYK+Oxidation(0)				1.10	2.2	1	
Q96JB5	CK5P3	CDK5 regulatory subunit_associated protein 3	2	2	3	0.94	0.60	0.91
	LTSLQLQHLFMILASPR+Oxidation(10)				0.99	2.2	2	
	MEDHQHVPIDIQTSKLLDWLVDRR				0.91	2.1	2	
Q96KP4	CNDP2	Cytosolic non_specific dipeptidase	3	4	16	1.03	0.28	0.93
	EGGSIPVTLTFQEATGK				0.97	3.2	2	
	TVFGVEPDLTR				1.00	2.6	2	
	WVAIQSVSAWPEK				1.31	2.1	2	
Q96M86	DNHD1	Dynein heavy chain domain_containing protein 1	2	2	3	0.94	0.37	0.89
	NEQEKEQEENEEK				0.64	2.2	2	
	QILEDTIRTLNVTK				0.96	2.2	2	
Q96PD5	PGRP2	N_acetylmuramoyl_L_alanine amidase	4	8	35	0.94	0.27	0.98
	AGLLRPDYALLGHR				1.02	4.0	3	
	GCPDVQASLPDAK				1.04	2.5	2	
	GSQTQSHPDLGTEGCWDQLSAPR				0.86	4.5	3	

	TDCPGDALFDLLR				0.85	3.6	2	
Q96QR1	SG3A1	Secretoglobin family 3A member 1	2	5	8	0.90	0.33	0.43
	CVAELGPQAVGAVK				1.13	2.8	2	
	LLLSSLGIPVNHLIEGSQK				0.82	3.5	3	
Q96S96	PEBP4	Phosphatidylethanolamine_binding protein 4	5	11	45	0.93	0.23	1.00
	FHLGEPEASTQFMTQNYQDSPTLQAPR				0.93	5.4	3	
	FHLGEPEASTQFMTQNYQDSPTLQAPR+Oxidation(12)				0.85	4.1	3	
	HWLVTDIK				0.93	2.8	2	
	IQGQELSAYQAPSPPAHSGFHR				0.93	3.7	3	
	ITSWMEPIVK+Oxidation(4)				0.96	2.4	2	
Q96SN8	CK5P2	CDK5 regulatory subunit_associated protein 2	2	2	7	0.95	0.78	0.97
	FQVEHFSQEELK				1.01	2.4	2	
	KMHEGDLAMALVLDEK				0.84	2.6	2	
Q96T17	MA7D2	MAP7 domain_containing protein 2	3	4	30	1.05	0.25	0.83
	AYPQSPKTTKPPYPGSPVK				0.98	2.8	2	
	EQEEQERLEK				1.31	2.2	2	
	KEDPKVGVQPAVCVEK				1.08	2.1	2	
Q99459	CDC5L	Cell division cycle 5_like protein	2	2	2	0.95	0.89	0.95
	MKILLGGYQSRAMGLMK+Oxidation(12),Oxidation(15)				1.01	2.1	2	
	TIAPIIGRTAAQCLEHYEFLLDK				0.76	2.2	2	
Q99497	PARK7	Protein DJ_1	2	6	18	0.98	0.24	0.96
	DVVICPDASLEDAKK				1.08	2.4	2	
	EGPYDVVVLPGGNLGAQNLSESAAVK				0.95	4.0	3	
Q99715	COCA1	Collagen alpha-1(XII) chain	2	4	16	1.02	0.44	0.87
	EVEVDRSETSTSLK				0.93	2.5	2	
	MLEAYNLTEK+Oxidation(0)				1.12	2.5	2	
Q99996	AKAP9	A_kinase anchor protein 9	2	2	5	0.83	0.91	0.84
	FLDEQAIDREHER				0.83	2.1	2	
	LSKIWGQQTDGMK				0.83	1.8	1	
Q9BVJ6	UT14A	U3 small nucleolar RNA_associated protein 14 homolog A	2	2	4	0.94	0.32	0.82
	QAMQEQLSKNKELTQK				0.93	2.2	2	
	VNPAAALEELEKIEK				0.96	2.1	2	
Q9BW30	TPPP3	Tubulin polymerization_promoting protein family member 3	3	7	71	0.92	0.20	0.80
	QDILDDSGYVSAYK				0.90	4.0	2	
	SKEEAFDAICQLVAGK				0.94	4.1	3	
	SVTGTDVDIVFSK				0.98	3.4	2	
Q9BZR6	RTN4R	Reticulon_4 receptor	2	3	5	0.92	0.32	0.80
	CCQPDAADK				0.82	1.9	1	
	LAGRDLK				0.95	1.8	1	
Q9H116	GZF1	GDNF_inducible zinc finger protein 1	2	3	4	1.01	0.35	0.99
	CLDLSETCFQLK				1.00	2.3	2	
	NEGCQAGAELEELSKK				1.02	2.2	2	
Q9H299	SH3L3	SH3 domain_binding glutamic acid_rich_like protein 3	2	3	17	0.92	0.48	0.98
	IQYQLVDISQDNALR				0.95	3.7	2	
	VYSTSVTGSR				0.88	2.7	2	
Q9H2C1	LHX5	LIM/homeobox protein Lhx5	2	2	5	1.11	0.40	0.46
	CFSREGKLYCK				1.11	1.8	1	
	ETANNENEEQNSGTKR				1.10	2.3	2	
Q9H582	ZN644	Zinc finger protein 644	2	2	3	1.02	0.79	1.00
	KESSVGGEDLDSYPDFLHK				0.99	2.2	2	
	YENYRMIKK+Oxidation(5)				1.06	1.8	1	
Q9H8X2	IPPK	Inositol_pentakisphosphate 2_kinase	2	3	4	0.94	0.34	0.92
	YCMHQHLK+Oxidation(2)				0.90	1.8	1	
	YLEEFPEER				0.95	2.3	2	
Q9HC84	MUC5B	Mucin_5B	13	21	94	0.96	0.16	1.00
	AAGGAVCEQPLGLECR				1.03	4.4	2	
	ELGQVVECSLDFGLVCR				0.91	4.1	2	
	GATGGLCDLTCPPTK				1.16	3.1	2	
	GYQVCPVLADIECR				0.93	3.6	2	
	IRAAGGHLCQQPK				0.90	2.1	2	
	IVTENIPCGTTGTTCSK				0.95	3.1	2	
	LEVPCQSLEAYAELCR				0.86	2.9	2	
	LTPLQFGNLQK				1.13	2.6	2	
	NSFEDPCSLSVENENYAR				0.90	4.9	2	

	SEQLGGDVESYDK				0.88	3.5	2	
	SVVGDALEFGNSWK				0.86	2.6	2	
	TGLLVEQSGDYIK				1.00	2.8	2	
	TLLGPAFAECHALVDSTAYLAACAQDLCR				0.96	3.4	3	
Q9HCJ0	TNR6C	Trinucleotide repeat_containing gene 6C protein	2	3	6	1.06	0.38	0.91
	STWSSGPTSHTQASLSHELWK				1.11	2.1	2	
	TSSWLVLR				1.04	2.2	2	
Q9NQ79	CRAC1	Cartilage acidic protein 1	12	19	109	0.98	0.14	1.00
	DEASSVEVTWPDGK				1.30	3.3	2	
	DKPVCVNTYGSYR				1.09	2.4	2	
	DVAAEAGVSK				0.96	3.1	2	
	EHGDPLIEELNPGDALEPEGR				0.99	3.5	2	
	GDGTFVDAAASAGVDDPHQHGR				0.94	4.1	4	
	GVALADFNR				1.04	2.6	2	
	GVASLFAGR				1.01	2.5	2	
	GVSVGPILSSSASDIFCDNENGPNFLFHNR				0.89	4.1	3	
	IIDGGSGYLCEMEPVAHFGLGK				0.91	3.4	3	
	LVNIAVDER				0.88	2.2	2	
	QGNAIGVTACDIDGDGR				1.19	2.9	2	
	WEDILSDEVNVAR				0.96	4.7	2	
Q9NVP1	DDX18	ATP_dependent RNA helicase DDX18	2	2	2	1.05	0.70	0.90
	KLMVFFSSCMSVK+Oxidation(2),Oxidation(9)				0.99	2.4	2	
	QKPMNVGLSETQNGGMSQEAVGNIKVTK				1.13	2.2	2	
Q9NY65	TBA8	Tubulin alpha_8 chain	7	13	76	0.98	0.18	1.00
	AVCMLSNTTAIAEAWAR				1.00	4.2	2	
	AVMIDLEPTVVDEVR+Oxidation(2)				0.95	2.3	2	
	LISQIVSSITASLR				0.92	3.6	2	
	NLDIERPTYTNLNR				1.15	2.6	2	
	QLFHPEQLITGK				0.97	2.4	2	
	TIQFVDWCPTGFK				0.94	3.2	2	
	VGINYQPPTVVPGGDLAK				0.93	4.3	2	
Q9NYQ6	CELR1	Cadherin EGF LAG seven_pass G_type receptor 1	4	4	8	0.96	0.48	0.99
	CDNPFAEVTTLGCEVIYNGCPK				0.84	2.1	2	
	DANSVITYQLTGGNTR				1.09	2.3	2	
	LASSQPPEQRKGILK				0.93	2.4	2	
	QFVGCMRNLSVDGK				0.98	2.2	2	
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	2	5	39	1.00	0.21	0.93
	LDGEKAVLENNLGAAVLR				0.97	2.7	2	
	SANMDHWQQRFPTHVK				1.07	2.2	2	
Q9P121	NTRI	Neurotrimin	3	3	5	0.96	0.36	0.57
	EQSGDYECSASNDVAAPVVR				0.70	4.8	2	
	GTLQCEASAVPSAEFQWYK				1.03	2.4	2	
	VTVNYPPYISEAK				1.04	2.5	2	
Q9UEW3	MARCO	Macrophage receptor MARCO	3	4	7	1.02	0.53	0.85
	GTESTLWSCTK				1.25	2.6	2	
	LQVLQAQLTWVR				0.90	3.4	2	
	VGAGTGQIWLDNVQCR				0.92	3.2	2	
Q9UGL1	KDM5B	Lysine_specific demethylase 5B	2	4	17	0.95	0.23	1.00
	EFGSGFPVRDGKIK				0.93	2.5	2	
	EIEEIPAYLPNGAALK				1.00	2.2	2	
Q9UGM3	DMBT1	Deleted in malignant brain tumors 1 protein	9	20	134	0.98	0.15	1.00
	DDTYGPYSSPSLR				1.10	2.4	2	
	FGQGSGPIVLDDVR				0.98	4.3	2	
	GRVEVLYR				0.99	2.6	2	
	GSWGTVCDDSWDTNDANVVCR				0.91	5.4	2	
	GSWGTVCDDSWDTSDANVVCR				0.94	5.4	2	
	GSWGTVCDDYWDTNDANVVCR				0.91	4.8	2	
	INLGFSNLK				0.99	2.3	2	
	QLGCGWATSAPGNAR				1.01	3.3	2	
	VDVVLGPIQLQTPPR				0.97	3.5	2	
Q9UGT4	SUSD2	Sushi domain_containing protein 2	5	11	58	0.96	0.16	1.00
	DSIQTLGHVDSSGQVHCVSPLLYESGR				0.94	5.1	3	
	DVQALWTNDHALAWHLSDDFR				0.95	3.3	3	
	GHDWGAPPFR				1.06	2.5	2	
	GTGLTAVAVQEGNSDVVEVR				0.93	5.1	2	
	HDPTFEPLFPSETTLNPSLAQEAAK				0.95	5.6	3	

Q9UHK6	AMACR Alpha_methylacyl_CoA racemase	2	5	88	0.98	0.28	0.99
	GKRSLVLDLK			0.96	3.6	3	
	SDELPNQMSMDDWPEMK+Oxidation(9)			0.99	2.1	2	
Q9UIF8	BAZ2B Bromodomain adjacent to zinc finger domain protein 2B	4	5	23	0.97	0.49	0.75
	ETYMKLIVPSPDVLKAGNK+Oxidation(3)			0.73	3.2	2	
	NTSEESSLLTSELR			0.63	2.2	2	
	SIAWEKSIMK+Oxidation(8)			1.03	2.5	2	
	STSSGGGNRKCNQEQSK			1.17	2.3	2	
Q9UPV0	CE164 Centrosomal protein of 164 kDa	2	7	10	1.06	0.33	0.91
	LQDLELDLETRAKDVK			0.88	2.1	2	
	QAQQPLGIEDK			1.10	2.5	2	
Q9UQ35	SRRM2 Serine/arginine repetitive matrix protein 2	2	2	4	1.06	0.55	0.71
	QDRGEFSASPMLK+Oxidation(10)			1.11	2.3	2	
	SSTPPGESYFGVSSLQLK			0.70	2.4	2	
Q9Y2K3	MYH15 Myosin_15	2	2	3	0.92	0.48	0.84
	LQEAAEAMGVANARNASLER+Oxidation(7)			0.93	2.1	2	
	TRENMEQTITDLQK			0.92	2.2	2	
Q9Y5S2	MRCKB Serine/threonine_protein kinase MRCK beta	2	2	4	0.92	0.83	0.66
	ELLEEMEILK+Oxidation(5)			0.74	2.0	1	
	SQAKELKDAHQQR			1.16	1.8	1	
Q9Y6Q2	STON1 Stonin_1	2	2	4	1.08	0.49	0.79
	FELMRFK			1.01	2.0	1	
	WVTFDDDPAVQSSQK			1.18	2.1	2	
Q9Y6R7	FCGBP IgGFc_binding protein	3	6	32	0.95	0.27	0.88
	VNGVLTALPVSVADGR			1.07	3.9	2	
	VTLQPYNVAQLQSSVDLSGSK			0.89	4.2	2	
	VVAEVQICHGK			0.85	2.2	2	

Supplemental Table II

Relative expression ratio in the COPD patients vs. healthy controls dataset

Accession Number	Gene Name	Protein Name	No. of quantified peptides	Frames	Hits	Ratio	StDev	*p* value
A0M8Q6	LAC7	Ig lambda_7 chain C region	3	31	310	0.91	0.16	0.75
		Peptide			**Ratio**	**Xcorr**	**Charge**	
		VTHEGSTVEK			0.47	2.6	1	
		AAPSVTLFPPSSEELQANK			0.91	4.6	2	
		YAASSYLSLTPEQWK			0.94	5.8	2	
A4UGR9	XIRP2	Xin actin_binding repeat_containing protein 2	2	2	2	0.80	0.39	0.37
		GEGLEYENIK			0.17	1.9	1	
		SEQEAIHSSQVGTSRSSQEMARNEQEGSK			0.81	3.5	3	
A5A3E0	POTEF	POTE ankyrin domain family member F	2	8	93	0.93	0.35	0.31
		MVVEVDSMPAASSVK+Oxidation(7)			0.60	2.3	2	
		SYELPDGQVITIGNER			0.93	5.0	2	
A6NMY6	AXA2L	Putative annexin A2_like protein	12	19	100	0.93	0.27	0.23
		TNQELQEINR			1.17	3.6	2	
		AYTNFDAER			1.11	2.4	2	
		LSLEGDHSTPPSAYGSVK			0.83	4.5	2	
		WISIMTER+Oxidation(4)			1.21	2.5	2	
		TDLEKDIISDTSGDFRK			1.07	5.0	3	
		DIISDTSGDFR			2.18	3.1	2	
		DALNIETAIK			0.78	3.4	2	
		WISIMTER			1.74	2.5	2	
		TDLEKDIISDTSGDFR			1.10	3.1	2	
		SALSGHLETVILGLLK			0.81	4.6	2	
		SLYYYIQQDTK			1.04	2.9	2	
		TPAQYDASELK			1.26	3.4	2	
O00151	PDLI1	PDZ and LIM domain protein 1	2	2	2	1.33	0.61	0.38
		VTPPEGYEVVTVFPK			0.92	2.8	2	
		HRHPECYVCTDCGTNLK			1.56	4.8	3	
O00299	CLIC1	Chloride intracellular channel protein 1	6	11	43	1.05	0.53	0.93
		NSNPALNDNLEK			0.69	3.0	2	
		VLDNYLTSPLPEEVDETSAEDEGVSQR			1.32	5.0	3	
		LAALNPESNTAGLDIFAK			1.05	4.6	2	
		FLDGNELTLADCNLLPK			1.29	3.3	2	
		GVTFNVTTVDTK			1.73	3.7	2	
		IGNCPFSQR			0.62	2.3	2	
O00391	QSOX1	Sulfhydryl oxidase 1	5	10	34	0.87	0.37	0.70
		VLNTEANVVR			0.69	3.2	2	
		AHFSPSNIILDFPAAGSAAR			0.87	4.9	3	
		DCASHFEQMAAASMHR			0.64	4.2	3	
		NGSGAVFPVAGADVQTLR			0.56	3.2	2	
		SALYSPSDPLTLLQADTVR			0.61	3.8	2	
O00560	SDCB1	Syntenin_1	4	4	4	0.66	0.39	0.02
		DSTGHVGFIFK			0.48	2.5	2	
		FGDQVLQINGENCAGWSSDK			0.49	4.9	2	
		NGLLTEHNICEINGQNVIGLK			0.68	3.5	3	
		VIQAQTAFSANPANPAILSEASAPIPHDGNLYPR			0.65	4.1	3	

O00757	F16P2	Fructose_1_6_bisphosphatase isozyme 2	4	5	8	1.15	0.81	0.17
		YVGSMVADVHR			0.80	2.6	2	
		IYSLNEGYAK			2.71	2.7	2	
		YVGSMVADVHR+Oxidation(4)			3.81	2.6	2	
		TLVYGGIFLYPANQK			2.56	2.5	2	
O14745	NHRF1	Na(+)/H(+) exchange regulatory cofactor NHE_RF1	3	3	5	1.09	1.34	0.96
		KGPSGYGFNLHSDK			1.11	4.1	3	
		LVEVNGENVEK			0.71	2.5	2	
		LLVVDPETDEQLQK			0.75	2.6	2	
O15050	TRNK1	TPR and ankyrin repeat_containing protein 1	3	4	11	1.01	0.36	0.80
		SLMVNPEMYKLLNGELK+Oxidation(2),Oxidation(7)			1.01	2.5	2	
		FDINFNLKNKEGK			1.50	2.5	2	
		YLSANKMK+Oxidation(6)			0.98	1.9	1	
O15085	ARHGB	Rho guanine nucleotide exchange factor 11	2	2	3	1.45	2.09	0.70
		IPEMLQAEIDSR			1.45	2.4	2	
		TRNSGIWESPELDR			1.23	2.4	2	
O15143	ARC1B	Actin_related protein 2/3 complex subunit 1B	3	3	3	2.21	5.18	0.45
		NSVSQISVLSGGK			2.10	2.9	2	
		ASSEGGTAAGAGLDSLHK			2.78	3.7	2	
		EVEERPAPTPWGSK			3.36	3.3	2	
O15511	ARPC5	Actin_related protein 2/3 complex subunit 5	2	2	8	1.77	1.61	0.36
		ALAAGGVGSIVR			1.32	3.5	2	
		QGNMTAALQAALK			1.79	2.8	2	
O43707	ACTN4	Alpha_actinin_4	11	13	20	1.72	0.66	0.20
		ASIHEAWTDGK			2.65	2.4	2	
		GISQEQMQEFR			0.61	2.5	2	
		QFASQANVVGPWIQTK			1.62	3.7	2	
		ACLISLGYDVENDR			1.73	3.6	2	
		VGWEQLLTTIAR			1.00	2.4	2	
		HTNYTMEHIR			2.55	3.9	3	
		TINEVENQILTR			2.79	3.2	2	
		KHEAFESDLAAHQDR			1.65	4.4	2	
		HEAFESDLAAHQDR			5.27	4.4	3	
		FAIQDISVEETSAK			2.19	2.5	2	
		ETTDTDTADQVIASFK			1.19	4.4	2	
O75347	TBCA	Tubulin_specific chaperone A	2	3	5	1.38	1.74	0.61
		ILENEKDLEEAEEYKEAR			1.34	4.1	3	
		LEAAYLDLQR			1.59	3.2	2	
O75368	SH3L1	SH3 domain_binding glutamic acid_rich_like protein	3	3	36	1.89	1.35	0.00
		VYIASSSGSTAIK			1.94	3.2	2	
		ENVPENSRPATGYPLPPQIFNESQYR			1.86	5.0	3	
		QQDVLGFLEANK			2.05	3.2	2	
O75436	VP26A	Vacuolar protein sorting_associated protein 26A	2	2	2	0.99	1.04	0.97
		EITGIGPSTTTETETIAK			0.94	3.2	2	
		HYLFYDGESVSGK			1.00	2.4	2	
O75874	IDHC	Isocitrate dehydrogenase [NADP] cytoplasmic	4	5	13	1.88	1.03	0.04
		VEITYTPSDGTQK			2.58	3.0	2	
		ISGGSVVEMQGDEMTR			1.38	3.6	2	

		IIWELIK			2.06	2.5	2	
		TVEAEAAHGTVTR			1.67	3.2	2	
O75882	ATRN	Attractin	2	4	8	0.69	0.40	0.07
		LTGSSGFVTDGPGNYK			0.68	4.0	2	
		SCALDQNCQWEPR			0.74	3.6	2	
O75915	PRAF3	PRA1 family protein 3	2	2	4	0.60	1.64	0.69
		NKLENKMEGIGLK+Oxidation(6)			0.60	2.6	2	
		AWDDFFPGSDR			6.19	2.9	2	
O95436	NPT2B	Sodium_dependent phosphate transport protein 2B	3	6	26	0.61	0.14	0.00
		YLEGAAGQQPTAPDK			0.77	4.3	2	
		SLKPWDAVVSK			0.13	2.4	2	
		LQNWNFLPLWMR			0.31	3.5	2	
O96009	NAPSA	Napsin_A	4	8	90	0.39	0.27	0.00
		FAIQYGTGR			0.55	3.2	2	
		VGPGLTLCAK			0.53	3.1	2	
		VDGILSEDKLTIGGIK			0.62	3.2	2	
		GCAAILDTGTSLITGPTEEIR			0.38	6.6	2	
P00325	ADH1B	Alcohol dehydrogenase 1B	2	3	6	12.86	13.23	0.00
		VCLIGCGFSTGYGSAVNVAK			12.23	4.8	2	
		KFSLDALITHVLPFEK			43.69	3.7	3	
P00326	ADH1G	Alcohol dehydrogenase 1C	3	4	8	0.77	0.32	0.18
		ELGATECINPQDYK			2.17	3.7	2	
		AAVLWELK			0.15	2.4	2	
		INEGFDLLR			0.14	2.4	2	
P00338	LDHA	L_lactate dehydrogenase A chain	2	2	15	0.85	1.11	0.87
		VTLTSEEEAR			0.84	3.2	2	
		FIIPNVVK			1.59	2.3	2	
P00352	AL1A1	Retinal dehydrogenase 1	17	31	147	1.46	0.19	1.00
		VAFTGSTEVGK			1.18	2.6	2	
		SLDDVIK			0.64	2.4	2	
		ILDLIESGKK			1.74	2.8	2	
		IFINNEWHDSVSGK			0.97	3.9	2	
		ELGEYGFHEYTEVK			1.30	3.3	2	
		ANNTFYGLSAGVFTK			1.13	4.6	2	
		GYFVQPTVFSNVTDEMR+Oxidation(15)			1.19	4.5	2	
		LYSNAYLNDLAGCIK			0.83	4.5	2	
		EEIFGPVQQIMK			1.10	3.5	2	
		IGPALSCGNTVVVKPAEQTPLTALHVASLIK			1.00	5.4	3	
		GYFVQPTVFSNVTDEMR			1.40	5.2	2	
		YILGNPLTPGVTQGPQIDKEQYDK			0.89	3.7	2	
		LECGGGPWGNK			0.57	2.6	2	
		KYILGNPLTPGVTQGPQIDKEQYDK			1.08	4.2	3	
		LLLATMESMNGGK			0.53	2.6	2	
		KFPVFNPATEEELCQVEEGDKEDVDK			1.14	3.9	4	
		YILGNPLTPGVTQGPQIDK			1.30	3.7	2	
P00450	CERU	Ceruloplasmin	29	65	350	0.81	0.11	0.04
		IYHSHIDAPK			0.60	2.7	2	
		VDKDNEDFQESNR			0.35	3.1	2	
		VNKDDEEFIESNK			0.54	4.6	2	
		TYCSEPEKVDKDNEDFQESNR			0.62	4.6	3	

		EYTDASFTNR			0.83	3.3	2	
		NNEGTYYSPNYNPQSR			0.55	4.9	2	
		MFTTAPDQVDKEDEDFQESNK+Oxidation(0)			0.68	4.3	3	
		KAEEEHLGILGPQLHADVGDKVK			0.80	4.3	4	
		KAEEEHLGILGPQLHADVGDK			0.89	6.4	3	
		QSEDSTFYLGER			0.66	3.1	2	
		EVGPTNADPVCLAK			0.99	3.2	2	
		KLISVDTEHSNIYLQNGPDR			0.74	6.2	2	
		MFTTAPDQVDKEDEDFQESNK			0.55	4.0	2	
		AEEEHLGILGPQLHADVGDK			0.79	5.0	3	
		LISVDTEHSNIYLQNGPDR			0.74	4.9	2	
		ALYLQYTDETFR			0.85	4.2	2	
		GAYPLSIEPIGVR			0.95	3.7	2	
		HYYIGIIETTWDYASDHGEK			0.75	6.4	3	
		MYSVNGYTFGSLPGLSMCAEDR			0.70	4.5	2	
		DIFTGLIGPMK			0.47	2.9	1	
		DIASGLIGPLIICK			0.98	3.8	2	
		TTIEKPVWLGFLGPIIK			0.88	4.5	2	
		GPEEEHLGILGPVIWAEVGDTIR			0.53	5.2	3	
		DLYSGLIGPLIVCR			0.66	3.2	2	
		MYYSAVDPTK+Oxidation(0)			1.10	2.4	2	
		AGLQAFFQVQECNK			1.29	3.5	2	
		DIFTGLIGPMK+Oxidation(9)			0.63	2.6	2	
		ERGPEEEHLGILGPVIWAEVGDTIR			0.36	5.8	3	
		HYYIAAEEIIWNYAPSGIDIFTK			0.92	5.4	3	
P00558	PGK1	Phosphoglycerate kinase 1	10	17	59	1.49	0.60	0.00
		GCITIIGGGDTATCCAK			1.61	4.9	2	
		ALESPERPFLAILGGAK			1.50	4.4	3	
		ITLPVDFVTADKFDENAK			1.45	3.7	2	
		VLPGVDALSNI			1.68	2.3	2	
		AHSSMVGVNLPQK			2.47	3.1	2	
		TGQATVASGIPAGWMGLDCGPESSK			2.33	3.3	2	
		ACANPAAGSVILLENLR			1.26	4.8	2	
		ITLPVDFVTADK			1.23	2.3	2	
		IQLINNMLDK			1.30	2.8	2	
		YSLEPVAVELK			1.25	2.4	2	
P00568	KAD1	Adenylate kinase isoenzyme 1	3	3	11	1.11	0.67	0.01
		EVQQGEEFER			1.21	2.5	2	
		KVNAEGSVDSVFSQVCTHLDALK			2.27	5.1	3	
		YGYTHLSTGDLLR			0.98	2.6	2	
P00734	THRB	Prothrombin	16	31	101	1.27	0.25	1.00
		YTACETAR			0.87	2.5	2	
		RQECSIPVCGQDQVTVAMTPR			1.34	4.6	3	
		TATSEYQTFFNPR			1.14	3.1	2	
		SEGSSVNLSPPLEQCVPDR			1.10	3.9	2	
		KSPQELLCGASLISDR			1.11	3.6	3	
		ELLESYIDGR			1.27	3.0	2	
		LAVTTHGLPCLAWASAQAK			0.75	4.1	2	
		GQPSVLQVVNLPIVERPVCK			1.59	4.1	2	
		SGIECQLWR			1.30	2.9	2	

		DKLAACLEGNCAEGLGTNYR			1.20	5.6	2	
		ETAASLLQAGYK			0.43	2.6	2	
		TFGSGEADCGLRPLFEK			1.15	4.0	2	
		LAACLEGNCAEGLGTNYR			1.46	4.6	2	
		NPDSSTTGPWCYTTDPTVR			1.14	4.1	2	
		WYQMGIVSWGEGCDR			1.30	3.8	2	
		GDACEGDSGGPFVMK			0.48	3.1	2	
P00738	HPT	Haptoglobin	23	69	556	3.22	0.26	0.00
		HYEGSTVPEK			1.06	2.6	2	
		ILGGHLDAK			0.80	3.2	2	
		TEGDGVYTLNDKK			2.62	3.7	2	
		TEGDGVYTLNNEK			2.41	3.8	2	
		AVGDKLPECEAVCGKPK			1.41	4.7	3	
		LRTEGDGVYTLNNEK			2.27	4.7	2	
		LRTEGDGVYTLNDKK			2.31	4.7	2	
		LRTEGDGVYTLNDK			3.17	4.6	2	
		TEGDGVYTLNDK			3.37	4.1	2	
		VGYVSGWGR			1.17	3.6	2	
		LPECEADDGCPKPPEIAHGYVEHSVR			7.07	5.5	4	
		AVGDKLPECEADDGCPKPPEIAHGYVEHSVR			5.38	6.0	4	
		GSFPWQAK			1.33	2.7	2	
		SCAVAEYGVYVK			1.68	4.5	2	
		VTSIQDWVQK			1.49	3.6	2	
		YVMLPVADQDQCIR+Oxidation(2)			1.36	4.9	2	
		SPVGVQPILNEHTFCAGMSK			2.12	4.4	2	
		YVMLPVADQDQCIR			1.67	4.6	2	
		DYAEVGR			0.87	2.1	1	
		QLVEIEK			0.33	2.2	1	
		SPVGVQPILNEHTFCAGMSK+Oxidation(17)			1.52	3.7	3	
		VVLHPNYSQVDIGLIK			1.50	4.7	3	
		DIAPTLTLYVGK			1.36	2.5	2	
P00739	HPTR	Haptoglobin_related protein	2	2	5	0.63	0.34	0.00
		VGYVSGWGQSDNFK			0.62	3.9	2	
		VVLHPNYHQVDIGLIK			1.36	3.8	3	
P00746	CFAD	Complement factor D	6	11	33	1.00	0.33	0.99
		VQVLLGAHSLSQPEPSKR			0.93	3.7	3	
		GDSGGPLVCGGVLEGVVTSGSR			1.02	6.1	2	
		VDRDVAPGTLCDVAGWGIVNHAGR			0.98	5.1	3	
		DSCKGDSGGPLVCGGVLEGVVTSGSR			0.91	5.2	2	
		VQVLLGAHSLSQPEPSK			0.55	3.2	2	
		RPDSLQHVLLPVLDR			0.82	3.5	3	
P00747	PLMN	Plasminogen	13	24	94	1.18	0.37	0.14
		GNVAVTVSGHTCQHWSAQTPHTHNR			1.70	4.3	4	
		HSIFTPETNPR			1.38	3.2	2	
		CTTPPPSSGPTYQCLK			0.89	3.5	2	
		ELRPWCFTTDPNKR			1.60	4.4	3	
		VILGAHQEVNLEPHVQEIEVSR			2.03	3.7	3	
		VQSTELCAGHLAGGTDSCQGDSGGPLVCFEK			1.39	4.7	3	
		TECFITGWGETQGTFGAGLLK			1.17	5.1	2	
		FVTWIEGVMR			1.20	2.8	2	

		EQQCVIMAENR			0.73	2.7	2	
		QLGAGSIEECAAK			1.14	3.1	2	
		KLYDYCDVPQCAAPSFDCGKPQVEPK			3.72	4.5	3	
		CEEDEEFTCR			1.02	2.7	2	
		VIPACLPSPNYVVADR			1.38	3.6	2	
P00748	FA12	Coagulation factor XII	2	5	20	0.91	0.53	0.52
		GRPGPQPWCATTPNFDQDQR			1.24	4.1	3	
		TTLSGAPCQPWASEATYR			0.89	4.4	2	
P00751	CFAB	Complement factor B	17	36	175	0.86	0.16	0.00
		LEDSVTYHCSR			0.76	3.7	2	
		ALFVSEEEKK			1.20	2.8	2	
		VSEADSSNADWVTK			1.04	4.9	2	
		KCLVNLIEK			0.73	2.3	2	
		YGQTIRPICLPCTEGTTR			0.85	3.7	3	
		FLCTGGVSPYADPNTCR			0.94	4.5	2	
		WSGQTAICDNGAGYCSNPGIPIGTR			1.11	4.8	2	
		EKLQDEDLGFL			1.44	3.3	2	
		LLQEGQALEYVCPSGFYPYPVQTR			0.98	4.3	3	
		DAQYAPGYDK			0.73	2.7	2	
		DISEVVTPR			1.19	2.5	2	
		HVIILMTDGLHNMGGDPITVIDEIR			1.51	4.9	3	
		HVIILMTDGLHNMGGDPITVIDEIR+Oxidation(5)			1.08	3.5	3	
		FIQVGVISWGVVDVCK			1.27	4.0	2	
		YGLVTYATYPK			1.01	3.5	2	
		VKDISEVVTPR			1.08	3.2	2	
		EELLPAQDIK			0.68	2.1	1	
P00915	CAH1	Carbonic anhydrase 1	8	11	45	0.50	0.28	0.81
		YSAELHVAHWNSAK			0.56	4.3	2	
		HDTSLKPISVSYNPATAK			0.18	4.7	2	
		ADGLAVIGVLMKVGEANPK			0.56	2.1	1	
		LYPIANGNNQSPVDIK			0.37	4.8	2	
		VLDALQAIK			0.43	3.4	2	
		EIINVGHSFHVNFEDNDNR			0.72	4.2	2	
		ADGLAVIGVLMK			0.57	3.9	2	
		ESISVSSEQLAQFR			0.55	3.6	2	
P00918	CAH2	Carbonic anhydrase 2	4	6	11	1.68	1.66	0.21
		VVDVLDSIK			2.33	2.4	2	
		YDPSLKPLSVSYDQATSLR			3.47	3.9	3	
		AVQQPDGLAVLGIFLK			1.34	3.5	2	
		SADFTNFDPR			3.17	2.3	2	
P01008	ANT3	Antithrombin_III	17	43	328	1.14	0.11	0.96
		KATEDEGSEQKIPEATNR			0.84	4.5	3	
		ATEDEGSEQKIPEATNR			0.71	4.5	2	
		ADGESCSASMMYQEGK+Oxidation(9)			0.76	4.6	2	
		ADGESCSASMMYQEGK+Oxidation(10)			0.76	4.6	2	
		RVWELSK			1.10	2.5	2	
		ADGESCSASMMYQEGK			0.38	4.3	2	
		DDLYVSDAFHK			0.97	3.0	2	
		FATTFYQHLADSK			0.96	3.9	2	
		TSDQIHFFFAK			0.81	3.1	2	

		VAEGTQVLELPFK			1.21	3.9	2	
		DIPMNPMCIYR			0.94	2.7	1	
		AFLEVNEEGSEAAASTAVVIAGR			1.11	7.0	2	
		FRIEDGFSLK			1.36	4.3	3	
		ANRPFLVFIR			0.73	3.5	3	
		SKLPGIVAEGR			1.32	2.9	2	
		NDNDNIFLSPLSISTAFAMTK+Oxidation(18)			0.90	3.6	3	
		ADGESCSASMMYQEGK+Oxidation(9),Oxidation(10)			1.17	3.9	2	
P01009	A1AT	Alpha_1_antitrypsin	33	141	1408	1.07	0.07	0.00
		TDTSHHDQDHPTFNK			0.70	4.2	3	
		KQINDYVEK			0.72	3.1	2	
		FLEDVKK			0.69	2.6	2	
		SASLHLPK			0.90	2.8	2	
		QINDYVEK			0.68	2.0	1	
		GKWERPFEVK			0.97	3.4	2	
		LGMFNIQHCK+Oxidation(2)			0.66	3.8	3	
		AVLTIDEK			0.96	2.9	2	
		WERPFEVK			1.18	2.6	2	
		LGMFNIQHCK			0.42	3.0	2	
		LVDKFLEDVKK			1.23	3.7	3	
		KLYHSEAFTVNFGDTEEAKK			1.65	5.8	3	
		DTEEEDFHVDQVTTVK			0.93	5.5	2	
		LQHLENELTHDIITK			1.11	5.2	4	
		KLYHSEAFTVNFGDTEEAK			0.91	6.2	2	
		LYHSEAFTVNFGDTEEAKK			0.95	6.5	2	
		KLSSWVLLMK+Oxidation(8)			1.26	2.6	2	
		LSITGTYDLK			0.82	3.2	2	
		GKWERPFEVKDTEEEDFHVDQVTTVK			2.30	5.5	4	
		LYHSEAFTVNFGDTEEAK			0.84	5.7	2	
		SVLGQLGITK			1.07	3.7	2	
		VFSNGADLSGVTEEAPLK			1.00	6.1	2	
		KLSSWVLLMK			1.85	3.1	2	
		LSSWVLLMK			0.62	2.3	2	
		FNKPFVFLMIEQNTK			3.84	4.7	3	
		TLNQPDSQLQLTTGNGLFLSEGLK			1.32	6.4	3	
		GTEAAGAMFLEAIPMSIPPEVK+Oxidation(7),Oxidation(14)			1.10	2.4	2	
		GTEAAGAMFLEAIPMSIPPEVK+Oxidation(7)			1.06	4.1	2	
		GTEAAGAMFLEAIPMSIPPEVK+Oxidation(14)			1.09	2.4	2	
		WERPFEVKDTEEEDFHVDQVTTVK			2.09	5.9	3	
		LSITGTYDLKSVLGQLGITK			1.07	3.9	3	
		FLENEDR			0.82	2.5	2	
		FNKPFVFLMIEQNTK+Oxidation(8)			3.44	3.9	3	
P01011	AACT	Alpha_1_antichymotrypsin	11	24	190	0.87	0.22	1.00
		NLAVSQVVHK			0.81	3.0	2	
		ADLSGITGAR			0.94	3.6	2	
		WRDSLEFR			1.06	2.9	2	
		WEMPFDPQDTHQSR			1.18	3.1	2	
		EIGELYLPK			0.95	2.4	2	
		DEELSCTVVELK			1.08	4.5	2	
		LYGSEAFATDFQDSAAAK			1.16	5.9	2	

		AVLDVFEEGTEASAATAVK			1.04	6.4	2	
		ITLLSALVETR			1.09	3.9	2	
		MEEVEAMLLPETLK+Oxidation(0)			1.08	3.0	2	
		MEEVEAMLLPETLK			1.25	3.5	2	
P01019	ANGT	Angiotensinogen	7	10	57	0.77	0.28	0.18
		FMQAVTGWK			1.18	2.6	2	
		ALQDQLVLVAAK			0.38	4.0	2	
		DPTFIPAPIQAK			0.66	2.5	2	
		LQAILGVPWK			0.77	3.2	2	
		VLSALQAVQGLLVAQGR			0.90	4.7	3	
		VEGLTFQQNSLNWMK			0.72	3.1	2	
		SLDFTELDVAAEK			1.08	2.9	2	
P01023	A2MG	Alpha_2_macroglobulin	41	94	547	2.31	0.21	0.00
		SIYKPGQTVK			2.11	2.3	2	
		KYSDASDCHGEDSQAFCEK			1.55	5.3	3	
		YSDASDCHGEDSQAFCEK			1.56	5.7	2	
		LVHVEEPHTETVR			1.59	3.4	2	
		HYDGSYSTFGER			1.61	3.3	2	
		LPPNVVEESAR			2.15	3.3	2	
		AAQVTIQSSGTFSSK			2.35	5.2	2	
		FSGQLNSHGCFYQQVK			2.06	4.8	2	
		AIGYLNTGYQR			1.93	3.4	2	
		QTVSWAVTPK			1.74	2.4	2	
		HNVYINGITYTPVSSTNEK			1.47	6.1	2	
		GHFSISIPVK			2.15	2.9	2	
		VTGEGCVYLQTSLK			2.27	4.2	2	
		TEVSSNHVLIYLDK			1.31	4.1	2	
		LHTEAQIQEEGTVVELTGR			2.46	6.9	2	
		VDLSFSPSQSLPASHAHLR			5.11	4.6	2	
		FEVQVTVPK			1.73	3.6	2	
		KDTVIKPLLVEPEGLEK			2.52	3.7	3	
		QQNAQGGFSSTQDTVVALHALSK			3.79	4.0	2	
		QGIPFFGQVR			2.60	2.7	2	
		DTVIKPLLVEPEGLEK			1.71	4.3	3	
		QFSFPLSSEPFQGSYK			2.55	4.3	2	
		VSVQLEASPAFLAVPVEK			2.72	5.2	2	
		ALLAYAFALAGNQDK			4.18	4.4	2	
		ETTFNSLLCPSGGEVSEELSLK			3.35	5.0	2	
		LLLQQVSLPELPGEYSMK+Oxidation(16)			1.41	4.0	2	
		YNILPEKEEFPFALGVQTLPQTCDEPK			3.74	6.0	3	
		AVDQSVLLMKPDAELSASSVYNLLPEK			3.12	4.0	2	
		LLLQQVSLPELPGEYSMK			1.67	4.4	2	
		LLIYAVLPTGDVIGDSAK			1.89	4.7	2	
		SLFTDLEAENDVLHCVAFAVPK			1.76	3.6	2	
		YDVENCLANK			2.28	3.5	2	
		VTAAPQSVCALR			1.49	3.3	2	
		VGFYESDVMGR			3.92	3.5	2	
		EQAPHCICANGR			0.32	2.9	2	
		DNSVHWERPQKPK			0.98	2.7	2	
		TGTHGLLVK			2.50	2.3	2	

		VGFYESDVMGR+Oxidation(8)			2.00	2.8	2	
		MCPQLQQYEMHGPEGLR			2.23	4.3	2	
		NEDSLVFVQTDK			3.54	4.0	2	
		SPCYGYQWVSEEHEEAHHTAYLVFSPSK			1.66	4.8	4	
P01024	CO3	Complement C3	74	231	1701	0.63	0.05	0.00
		FYHPEKEDGK			0.25	2.4	2	
		TKKQELSEAEQATR			0.41	4.6	3	
		KQELSEAEQATR			0.57	4.4	3	
		SGSDEVQVGQQR			0.88	4.1	2	
		SDDKVTLEER			0.64	3.8	3	
		HQQTVTIPPK			0.49	2.4	2	
		QELSEAEQATR			0.52	3.3	2	
		SEETKENEGFTVTAEGK			0.50	5.3	3	
		VSHSEDDCLAFK			0.89	4.1	3	
		CAEENCFIQK			0.49	3.6	2	
		AAVYHHFISDGVR			0.57	4.2	2	
		KVLLDGVQNPR			0.63	3.4	2	
		KGYTQQLAFR			0.69	3.8	3	
		TGLQEVEVK			0.53	3.4	2	
		ENEGFTVTAEGK			0.71	3.1	2	
		GQGTLSVVTMYHAK+Oxidation(9)			0.59	3.1	2	
		VVLVAVDK			0.58	2.8	2	
		ACEPGVDYVYK			0.65	3.6	2	
		VLLDGVQNPR			0.50	3.3	2	
		GYTQQLAFR			0.69	2.9	2	
		DSCVGSLVVK			0.58	3.1	2	
		LSINTHPSQKPLSITVR			0.38	4.3	3	
		TFISPIK			0.66	2.4	2	
		GQGTLSVVTMYHAK			0.76	3.2	2	
		GLEVTITAR			0.70	3.2	2	
		IWDVVEK			0.58	2.5	2	
		FYYIYNEK			0.71	2.5	2	
		RIPIEDGSGEVVLSR			0.64	4.7	2	
		IHWESASLLR			0.59	2.7	1	
		EGVQKEDIPPADLSDQVPDTESETR			0.54	5.7	3	
		TIYTPGSTVLYR			0.64	2.9	2	
		DTWVEHWPEEDECQDEENQK			0.58	6.9	3	
		EDIPPADLSDQVPDTESETR			0.47	5.2	2	
		DICEEQVNSLPGSITK			0.81	4.8	2	
		TVMVNIENPEGIPVK+Oxidation(2)			0.58	4.0	2	
		VELLHNPAFCSLATTK			0.59	4.8	3	
		VPVAVQGEDTVQSLTQGDGVAK			0.72	6.1	2	
		FVTVQATFGTQVVEK			0.68	5.1	2	
		NTLIIYLDK			0.63	2.7	2	
		EVVADSVWVDVK			0.55	4.0	2	
		VHQYFNVELIQPGAVK			0.60	4.7	3	
		SLYVSATVILHSGSDMVQAER+Oxidation(15)			0.69	4.0	3	
		ILLQGTPVAQMTEDAVDAER+Oxidation(10)			0.75	5.7	2	
		LESEETMVLEAHDAQGDVPVTVTVHDFPGK+Oxidation(6)			1.55	4.4	4	
		SYTVAIAGYALAQMGR+Oxidation(13)			0.76	3.8	2	

		SGIPIVTSPYQIHFTK			0.62	4.7	2	
		AGDFLEANYMNLQR			0.71	3.7	2	
		LESEETMVLEAHDAQGDVPVTVTVHDFPGK			0.57	5.3	3	
		SNLDEDIIAEENIVSR			0.69	5.5	2	
		SLYVSATVILHSGSDMVQAER			0.67	6.0	3	
		DAPDHQELNLDVSLQLPSR			0.87	4.9	2	
		TELRPGETLNVNFLLR			0.66	5.2	3	
		DYAGVFSDAGLTFTSSSGQQTAQR			0.59	6.5	2	
		ILLQGTPVAQMTEDAVDAER			0.70	6.3	3	
		SYTVAIAGYALAQMGR			0.70	4.9	2	
		DFDFVPPVVR			0.60	3.4	2	
		SSLSVPYVIVPLK			0.79	4.2	3	
		LCRDELCR			0.32	2.6	2	
		VRVELLHNPAFCSLATTK			0.65	4.1	3	
		ADIGCTPGSGK			0.48	2.9	2	
		SGQSEDRQPVPGQQMTLK			0.60	4.3	2	
		IPIEDGSGEVVLSR			0.94	4.2	2	
		LESEETMVLEAHDAQGDVPVTVTVHDFPGKK			0.59	5.1	3	
		VYAYYNLEESCTR			0.83	4.3	2	
		TMQALPYSTVGNSNNYLHLSVLR+Oxidation(1)			0.93	3.7	3	
		VFLDCCNYITELR			0.84	3.9	2	
		EYVLPSFEVIVEPTEK			1.33	4.6	2	
		YYTYLIMNK			0.66	2.5	2	
		NTMILEICTR			0.84	2.7	2	
		QKPDGVFQEDAPVIHQEMIGGLR			0.57	4.1	3	
		TVMVNIENPEGIPVK			0.97	3.7	2	
		TMQALPYSTVGNSNNYLHLSVLR			0.83	4.0	2	
		LMNIFLK			0.40	2.5	2	
		KVEGTAFVIFGIQDGEQR			1.45	4.8	2	
P01031	CO5	Complement C5	3	3	24	0.79	0.42	0.01
		TDAPDLPEENQAR			0.72	2.8	2	
		FQNSAILTIQPK			0.78	3.6	2	
		LHMKTLLPVSKPEIR+Oxidation(2)			0.95	2.8	2	
P01033	TIMP1	Metalloproteinase inhibitor 1	3	3	4	1.69	0.76	0.29
		GFQALGDAADIR			1.49	2.7	2	
		TYTVGCEECTVFPCLSIPCK			1.85	2.7	2	
		LQSGTHCLWTDQLLQGSEK			0.88	4.5	3	
P01034	CYTC	Cystatin_C	3	4	20	1.40	1.04	0.13
		ALDFAVGEYNK			1.40	3.4	2	
		LVGGPMDASVEEEGVR			0.88	3.5	2	
		LVGGPMDASVEEEGVR+Oxidation(5)			2.28	3.5	2	
P01042	KNG1	Kininogen_1	16	34	159	1.15	0.21	0.33
		AATGECTATVGK			1.22	3.0	2	
		ESNEELTESCETK			1.11	4.0	2	
		TWQDCEYK			0.74	2.5	2	
		RPPGFSPFR			0.82	2.9	2	
		YNSQNQSNNQFVLYR			0.99	4.0	2	
		IASFSQNCDIYPGK			1.11	3.1	2	
		QVVAGLNFR			1.12	2.3	2	
		TVGSDTFYSFK			1.09	3.2	2	

		DIPTNSPELEETLTHTITK			1.00	3.7	2	
		IYPTVNCQPLGMISLMK+Oxidation(11)			2.06	4.3	2	
		LGQSLDCNAEVYVVPWEK			1.14	5.0	2	
		IYPTVNCQPLGMISLMK+Oxidation(15)			2.07	4.0	2	
		IYPTVNCQPLGMISLMK			1.20	3.8	2	
		KLGQSLDCNAEVYVVPWEK			1.94	3.9	2	
		FSVATQTCQITPAEGPVVTAQYDCLGCVHPISTQSPDLEPILR			1.24	7.0	4	
		ENFLFLTPDCK			0.59	3.6	2	
P01591	IGJ	Immunoglobulin J chain	5	12	70	1.03	0.33	0.19
		FVYHLSDLCK			0.84	3.2	2	
		CYTAVVPLVYGGETK			1.04	4.5	2	
		SSEDPNEDIVER			0.52	3.1	2	
		KCDPTEVELDNQIVTATQSNICDEDSATETCYTYDR			0.73	6.4	3	
		IVLVDNK			0.32	1.9	1	
P01613	KV121	Ig kappa chain V_I region Ni	3	26	161	0.72	0.19	0.01
		DIQMTQSPSSLSATVGDR+Oxidation(3)			0.71	4.1	2	
		DIQMTQSPSSLSATVGDR			0.72	4.3	2	
		LLIYDASNLETGVPSR			1.58	4.3	2	
P01767	HV306	Ig heavy chain V_III region BUT	3	18	75	0.91	0.29	0.04
		AEDTAVYYCAR			0.88	4.3	2	
		EVQLVETGGGLIQPGGSLR			0.96	5.8	2	
		BTVYLQMBSLR			0.62	2.5	2	
P01779	HV318	Ig heavy chain V_III region TUR	2	16	73	0.72	0.18	0.00
		LSCAASGFTFSR			0.55	2.8	2	
		EVQLLESGGGLVQPGGSLR			0.88	5.8	2	
P01781	HV320	Ig heavy chain V_III region GAL	3	4	31	0.77	0.46	0.28
		NSLYLQMNSLR			0.57	3.3	2	
		GLEWVANIK			0.86	3.3	2	
		VEDTALYYCAR			0.67	2.9	2	
P01833	PIGR	Polymeric immunoglobulin receptor	23	94	905	0.76	0.10	0.00
		ASVDSGSSEEQGGSSR			1.02	5.4	2	
		RAPAFEGR			0.69	2.4	2	
		AFVNCDENSR			0.54	3.3	2	
		IIEGEPNLK			0.59	3.1	2	
		ILLNPQDK			0.48	2.8	2	
		LSDAGQYLCQAGDDSNSNKK			0.64	5.3	2	
		WNNTGCQALPSQDEGPSK			0.50	5.5	2	
		VYTVDLGR			0.62	2.3	2	
		LSDAGQYLCQAGDDSNSNK			0.63	5.5	2	
		QSSGENCDVVVNTLGK			0.42	4.9	2	
		TVTINCPFK			0.73	2.6	2	
		GSVTFHCALGPEVANVAK			0.92	5.8	2	
		GVAGGSVAVLCPYNR			0.52	4.5	2	
		GGCITLISSEGYVSSK			0.67	5.5	2	
		QGHFYGETAAVYVAVEER			0.74	4.7	2	
		ADEGWYWCGVK			0.77	4.0	2	
		NADLQVLKPEPELVYEDLR			0.76	6.6	3	
		LVSLTLNLVTR			0.75	3.9	2	
		DGSFSVVITGLR			0.81	4.4	2	
		ILLNPQDKDGSFSVVITGLR			0.78	5.0	3	

		SPIFGPEEVNSVEGNSVSITCYYPPTSVNR			1.25	6.4	3	
		ILLNPQDKDGSFSVVITGLRK			0.96	3.8	3	
		CPLLVDSEGWVK			1.16	3.4	2	
P01834	IGKC	Ig kappa chain C region	7	185	1899	0.80	0.06	1.00
		VDNALQSGNSQESVTEQDSK			0.55	6.0	2	
		HKVYACEVTHQGLSSPVTK			0.87	5.5	3	
		VYACEVTHQGLSSPVTK			0.78	5.6	2	
		VDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK			0.89	6.0	3	
		DSTYSLSSTLTLSK			0.99	4.3	2	
		TVAAPSVFIFPPSDEQLK			0.94	4.8	2	
		SGTASVVCLLNNFYPR			0.92	4.8	3	
P01857	IGHG1	Ig gamma_1 chain C region	4	29	308	1.11	0.20	1.00
		GPSVFPLAPSSK			0.83	3.0	2	
		FNWYVDGVEVHNAK			0.85	5.3	2	
		TPEVTCVVVDVSHEDPEVK			0.92	5.5	2	
		THTCPPCPAPELLGGPSVFLFPPKPK			1.24	6.1	3	
P01859	IGHG2	Ig gamma_2 chain C region	3	11	106	0.58	0.22	0.00
		KCCVECPPCPAPPVAGPSVFLFPPKPK			0.71	4.4	4	
		VVSVLTVVHQDWLNGK			0.56	5.1	2	
		CCVECPPCPAPPVAGPSVFLFPPKPK			0.59	5.7	3	
P01860	IGHG3	Ig gamma_3 chain C region	7	38	268	0.97	0.20	0.00
		SCDTPPPCPR			1.17	3.0	2	
		WYVDGVEVHNAK			1.33	4.0	2	
		STSGGTAALGCLVK			0.86	4.6	2	
		TPEVTCVVVDVSHEDPEVQFK			1.63	5.2	3	
		CPAPELLGGPSVFLFPPKPK			1.39	5.4	3	
		WQQGNIFSCSVMHEALHNR			1.41	4.3	2	
		EPQVYTLPPSREEMTK			0.38	3.8	2	
P01861	IGHG4	Ig gamma_4 chain C region	13	50	336	0.98	0.16	0.00
		DTLMISR+Oxidation(3)			0.82	2.4	2	
		DTLMISR			0.72	2.3	2	
		STSESTAALGCLVK			0.64	4.6	2	
		EPQVYTLPPSQEEMTK+Oxidation(13)			3.11	2.3	2	
		NQVSLTCLVK			1.69	3.3	2	
		VVSVLTVLHQDWLNGKEYK			1.31	3.8	3	
		GFYPSDIAVEWESNGQPENNYK			0.74	5.4	2	
		VVSVLTVLHQDWLNGK			0.93	5.0	2	
		YGPPCPSCPAPEFLGGPSVFLFPPKPK			1.61	5.3	3	
		TYTCNVDHKPSNTK			1.37	4.0	2	
		WQEGNVFSCSVMHEALHNHYTQK+Oxidation(11)			2.38	3.6	3	
		EPQVYTLPPSQEEMTK			3.57	2.7	2	
		WQEGNVFSCSVMHEALHNHYTQK			3.66	3.8	3	
P01871	IGHM	Ig mu chain C region	6	14	83	2.12	0.95	0.30
		QVGSGVTTDQVQAEAK			1.65	4.8	2	
		YAATSQVLLPSK			1.75	3.8	2	
		NVPLPVIAELPPK			2.87	2.4	2	
		DVMQGTDEHVVCK			0.77	2.9	2	
		DVMQGTDEHVVCK+Oxidation(2)			7.03	2.9	2	
		YAATSQVLLPSKDVMQGTDEHVVCK			1.97	3.7	3	
P01876	IGHA1	Ig alpha_1 chain C region	7	65	593	0.79	0.13	0.97

		TFTCTAAYPESK			0.80	3.8	2	
		TPLTATLSK			0.53	2.3	2	
		DASGVTFTWTPSSGK			0.87	5.2	2	
		DLCGCYSVSSVLPGCAEPWNHGK			0.94	4.6	2	
		NFPPSQDASGDLYTTSSQLTLPATQCLAGK			0.78	6.2	3	
		DLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESK			0.72	4.0	4	
		LAGKPTHVNVSVVMAEVDGTCY			0.85	3.7	3	
P01877	IGHA2	Ig alpha_2 chain C region	12	75	642	0.76	0.11	0.00
		SAVQGPPER			0.60	2.5	2	
		YLTWASR			0.72	2.6	2	
		WLQGSQELPR			0.77	3.8	2	
		DASGATFTWTPSSGK			0.76	4.8	2	
		KGDTFSCMVGHEALPLAFTQK+Oxidation(7)			0.63	4.8	3	
		KGDTFSCMVGHEALPLAFTQK			0.80	5.5	3	
		GDTFSCMVGHEALPLAFTQK+Oxidation(6)			0.67	3.2	2	
		QEPSQGTTTFAVTSILR			0.78	4.6	3	
		NFPPSQDASGDLYTTSSQLTLPATQCPDGK			0.79	6.0	3	
		DLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELK			0.83	5.1	3	
		GDTFSCMVGHEALPLAFTQK			0.99	4.4	2	
		HYTNPSQDVTVPCPVPPPPPCCHPR			0.55	5.3	3	
P01880	IGHD	Ig delta chain C region	3	7	12	1.41	0.26	0.25
		DSYYMTSSQLSTPLQQWR			3.81	4.2	2	
		DAHLTWEVAGK			0.14	3.4	2	
		DSYYMTSSQLSTPLQQWR+Oxidation(4)			0.36	5.1	2	
P02042	HBD	Hemoglobin subunit delta	12	53	261	1.19	0.09	1.00
		VVAGVANALAHK			0.76	3.8	2	
		LHVDPENFR			0.57	2.5	2	
		EFTPQMQAAYQK			0.46	2.8	2	
		VNVDAVGGEALGR			0.64	4.6	2	
		TAVNALWGK			0.78	3.2	2	
		KVLGAFSDGLAHLDNLK			1.29	6.0	3	
		VLGAFSDGLAHLDNLK			1.02	5.0	2	
		FFESFGDLSSPDAVMGNPK+Oxidation(14)			0.99	4.2	2	
		FFESFGDLSSPDAVMGNPK			1.02	4.5	2	
		GTFSQLSELHCDK			0.41	3.2	2	
		LLGNVLVCVLAR			0.43	2.8	2	
		EFTPQMQAAYQK+Oxidation(5)			0.53	2.6	2	
P02545	LMNA	Prelamin_A/C	7	7	8	0.57	2.06	0.47
		AAYEAELGDAR			0.56	2.8	2	
		VAVEEVDEEGK			4.69	2.7	2	
		SLETENAGLR			2.21	2.4	2	
		AQNTWGCGNSLR			24.20	2.5	2	
		LQEKEDLQELNDR			6.06	3.9	2	
		NSNLVGAAHEELQQSR			3.81	3.7	2	
		ASASGSGAQVGGPISSGSSASSVTVTR			9.29	5.3	2	
P02647	APOA1	Apolipoprotein A_I	18	64	449	2.13	0.28	0.00
		ATEHLSTLSEK			1.29	3.6	3	
		AKPALEDLR			1.43	2.3	2	
		LSPLGEEMR+Oxidation(7)			1.77	2.5	2	
		THLAPYSDELR			1.65	3.1	2	

		WQEEMELYR+Oxidation(4)			1.28	2.6	2	
		LSPLGEEMR			0.73	2.7	2	
		VQPYLDDFQK			1.11	2.6	2	
		DSGRDYVSQFEGSALGK			3.73	4.8	2	
		VKDLATVYVDVLK			2.83	4.4	2	
		DYVSQFEGSALGK			2.34	4.7	2	
		LLDNWDSVTSTFSK			1.66	4.6	2	
		DLATVYVDVLK			2.54	3.8	2	
		QGLLPVLESFK			2.28	2.9	2	
		VSFLSALEEYTK			2.68	4.4	2	
		ETEGLRQEMSK			0.85	2.6	2	
		WQEEMELYR			1.45	2.6	2	
		LREQLGPVTQEFWDNLEK			0.72	4.7	3	
		LREQLGPVTQEFWDNLEKETEGLR			1.84	4.4	3	
P02649	APOE	Apolipoprotein E	7	13	54	0.90	0.40	1.00
		AKLEEQAQQIR			0.71	3.6	3	
		VQAAVGTSAAPVPSDNH			0.96	5.3	2	
		SELEEQLTPVAEETR			0.87	4.8	2	
		WVQTLSEQVQEELLSSQVTQELR			0.87	4.4	3	
		AATVGSLAGQPLQER			1.07	3.2	2	
		SWFEPLVEDMQR			1.36	2.5	2	
		LGADMEDVCGR			0.71	2.6	2	
P02652	APOA2	Apolipoprotein A_II	4	11	54	1.43	0.95	0.17
		VKSPELQAEAK			1.43	4.1	3	
		SPELQAEAK			3.35	3.5	2	
		SKEQLTPLIK			1.43	3.0	2	
		EPCVESLVSQYFQTVTDYGK			2.10	4.7	2	
P02654	APOC1	Apolipoprotein C_I	2	2	14	1.30	1.29	0.79
		LKEFGNTLEDK			1.30	2.7	2	
		EWFSETFQK			1.46	2.5	1	
P02656	APOC3	Apolipoprotein C_III	2	5	44	4.24	3.13	0.00
		DALSSVQESQVAQQAR			1.71	4.6	2	
		GWVTDGFSSLK			4.29	3.3	2	
P02671	FIBA	Fibrinogen alpha chain	16	32	166	2.78	0.52	0.00
		GGSTSYGTGSETESPR			1.46	4.3	2	
		NPSSAGSWNSGSSGPGSTGNR			1.74	5.6	2	
		ESSSHHPGIAEFPSR			1.57	3.5	3	
		GSESGIFTNTK			3.23	3.6	2	
		HRHPDEAAFFDTASTGK			0.88	5.1	3	
		VQHIQLLQK			1.04	2.7	2	
		EVDLKDYEDQQK			1.71	3.4	2	
		RLEVDIDIK			2.60	2.6	2	
		GLIDEVNQDFTNR			5.14	3.6	2	
		DSHSLTTNIMEILR			6.53	4.5	2	
		NSLFEYQK			2.41	2.7	2	
		HPDEAAFFDTASTGK			2.43	3.1	2	
		LEVDIDIK			4.20	2.5	2	
		DSHSLTTNIMEILR+Oxidation(9)			4.74	2.4	2	
		EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR+Oxidation(14)			3.27	5.5	3	
		EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR			4.48	4.9	3	

P02675	FIBB	Fibrinogen beta chain	21	61	309	3.17	0.40	0.00
		AHYGGFTVQNEANK			1.68	4.8	2	
		QGFGNVATNTDGK			2.12	3.1	2	
		LESDVSAQMEYCR+Oxidation(8)			1.15	4.5	2	
		LESDVSAQMEYCR			1.90	4.1	2	
		REEAPSLRPAPPPISGGGYR			2.65	3.7	3	
		TPCTVSCNIPVVSGK			2.01	3.8	2	
		GGETSEMYLIQPDSSVKPYR			2.31	4.9	2	
		DNENVVNEYSSELEK			3.07	5.4	2	
		HQLYIDETVNSNIPTNLR			3.72	5.2	2	
		VYCDMNTENGGWTVIQNR			3.95	5.2	2	
		NYCGLPGEYWLGNDK			5.96	4.2	2	
		EDGGGWWYNR			4.88	3.0	2	
		YQISVNK			2.36	1.9	1	
		EEAPSLRPAPPPISGGGYR			1.83	3.9	3	
		KGGETSEMYLIQPDSSVKPYR			2.57	5.6	3	
		HGTDDGVVWMNWK+Oxidation(9)			2.55	3.1	2	
		GGETSEMYLIQPDSSVKPYR+Oxidation(6)			3.68	3.6	3	
		VYCDMNTENGGWTVIQNR+Oxidation(4)			4.81	4.8	2	
		HGTDDGVVWMNWK			2.27	4.2	2	
		YYWGGQYTWDMAK+Oxidation(10)			3.69	2.3	2	
		DNDGWLTSDPR			0.61	2.7	2	
P02679	FIBG	Fibrinogen gamma chain	16	32	164	2.74	0.91	0.00
		CHAGHLNGVYYQGGTYSK			3.52	4.8	2	
		RLDGSVDFK			2.04	2.3	2	
		YLQEIYNSNNQK			2.24	5.3	2	
		YEASILTHDSSIR			2.14	3.9	2	
		TSTADYAMFK			2.14	3.1	2	
		VELEDWNGR			2.08	3.0	2	
		AIQLTYNPDESSKPNMIDAATLK			2.65	3.9	2	
		ASTPNGYDNGIIWATWK			3.42	4.3	2	
		QSGLYFIKPLK			7.97	2.5	2	
		IHLISTQSAIPYALR			3.27	4.5	2	
		VGPEADKYR			1.32	2.4	2	
		VAQLEAQCQEPCK			1.65	4.1	2	
		TSTADYAMFK+Oxidation(7)			3.02	2.5	2	
		LDGSVDFK			2.28	1.9	1	
		DNCCILDER			5.54	3.0	2	
		VAQLEAQCQEPCKDTVQIHDITGK			2.58	4.6	3	
P02743	SAMP	Serum amyloid P_component	3	4	23	8.23	0.95	0.00
		IVLGQEQDSYGGK			8.57	3.7	2	
		GYVIIKPLVWV			7.19	2.6	2	
		AYSLFSYNTQGR			0.99	3.4	2	
P02746	C1QB	Complement C1q subcomponent subunit B	3	4	21	0.68	0.34	0.06
		LEQGENVFLQATDK			0.26	4.4	2	
		GPMGPKGGPGAPGAPGPK			1.04	2.6	2	
		FDHVITNMNNNYEPR			0.62	3.7	2	
P02747	C1QC	Complement C1q subcomponent subunit C	3	4	25	0.32	0.25	0.00
		TNQVNSGGVLLR			0.38	3.0	2	
		FNAVLTNPQGDYDTSTGK			0.29	5.1	2	

		FQSVFTVTR			0.37	2.3	2	
P02748	CO9	Complement component C9	6	6	36	0.88	0.37	0.71
		VVEESELAR			1.67	2.5	2	
		SIEVFGQFNGK			1.10	3.2	2	
		LSPIYNLVPVK			0.88	2.9	2	
		TEHYEEQIEAFK			0.87	3.3	2	
		QCVPTEPCEDAEDDCGNDFQCSTGR			0.65	4.4	3	
		DRVVEESELAR			1.13	2.5	2	
P02749	APOH	Beta_2_glycoprotein 1	12	33	212	0.97	0.17	0.16
		ATVVYQGER			0.76	2.9	2	
		KCSYTEDAQCIDGTIEVPK			0.97	4.5	3	
		ATFGCHDGYSLDGPEEIECTK			1.08	5.2	3	
		TFYEPGEEITYSCKPGYVSR			0.85	4.8	2	
		CSYTEDAQCIDGTIEVPK			1.00	4.9	2	
		TCPKPDDLPFSTVVPLK			0.99	4.4	3	
		VCPFAGILENGAVR			1.05	4.3	2	
		FICPLTGLWPINTLK			0.81	4.7	2	
		KATVVYQGER			0.72	3.0	2	
		WSPELPVCAPIICPPPSIPTFATLR			0.94	3.5	3	
		TDASDVKPC			0.54	2.5	2	
		DKATFGCHDGYSLDGPEEIECTK			0.71	4.3	3	
P02750	A2GL	Leucine_rich alpha_2_glycoprotein	6	16	54	1.11	0.25	1.00
		ALGHLDLSGNR			1.02	2.3	2	
		DLLLPQPDLR			0.96	2.4	2	
		TLDLGENQLETLPPDLLR			1.12	4.6	2	
		DGFDISGNPWICDQNLSDLYR			1.04	5.0	3	
		LQELHLSSNGLESLSPEFLRPVPQLR			1.14	5.1	3	
		VAAGAFQGLR			1.26	2.4	2	
P02751	FINC	Fibronectin	41	91	436	0.39	0.07	0.00
		LGVRPSQGGEAPR			0.28	4.1	3	
		TYHVGEQWQK			0.42	3.9	3	
		WCGTTQNYDADQK			0.54	4.3	2	
		TFYSCTTEGR			0.40	2.8	2	
		RPGGEPSPEGTTGQSYNQYSQR			0.49	5.3	3	
		HYQINQQWER			0.47	3.8	3	
		HTSVQTTSSGSGPFTDVR			0.40	5.4	2	
		GFNCESKPEAEETCFDK			0.42	4.3	3	
		GDSPASSKPISINYR			0.39	3.7	2	
		SYTITGLQPGTDYK			0.51	4.5	2	
		YEVSVYALK			0.47	2.4	2	
		GNLLQCICTGNGR			0.46	3.3	2	
		WLPSSSPVTGYR			0.46	2.8	2	
		TYLGNALVCTCYGGSR			0.63	5.0	2	
		GEWTCIAYSQLR			0.59	3.3	2	
		EESPLLIGQQSTVSDVPR			0.53	3.9	2	
		FGFCPMAAHEEICTTNEGVMYR			0.48	3.7	3	
		TETITGFQVDAVPANGQTPIQR			0.21	4.5	2	
		DLQFVEVTDVK			0.52	3.7	2	
		GLAFTDVDVDSIK			0.58	3.5	2	
		NTFAEVTGLSPGVTYYFK			0.71	3.7	2	

		FTQVTPTSLSAQWTPPNVQLTGYR			0.54	5.5	2	
		EINLAPDSSSVVVSGLMVATK			0.63	4.3	2	
		WSRPQAPITGYR			0.49	3.8	3	
		SSPVVIDASTAIDAPSNLR			0.43	5.3	2	
		AAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLK			0.65	4.2	4	
		QDGHLWCSTTSNYEQDQK			0.38	4.8	3	
		TEIDKPSQMQVTDVQDNSISVK			0.49	5.0	3	
		EYLGAICSCTCFGGQR			0.46	4.4	2	
		ITYGETGGNSPVQEFTVPGSK			0.51	4.6	2	
		VTDATETTITISWR			0.52	3.1	2	
		VTIMWTPPESAVTGYR			0.59	3.1	2	
		VEYELSEEGDEPQYLDLPSTATSVNIPDLLPGRK			0.55	6.5	3	
		VPGTSTSATLTGLTR			0.59	3.0	2	
		YSFCTDHTVLVQTR			0.45	4.1	2	
		TKTETITGFQVDAVPANGQTPIQR			0.53	5.4	2	
		TNTNVNCPIECFMPLDVQADREDSRE			2.47	3.5	3	
		FLATTPNSLLVSWQPPR			0.85	3.2	2	
		NSITLTNLTPGTEYVVSIVALNGR			1.03	4.2	3	
		TNTNVNCPIECFMPLDVQADR			0.65	3.2	2	
		EINLAPDSSSVVVSGLMVATK+Oxidation(16)			0.96	2.8	2	
P02760	AMBP	Protein AMBP	11	13	99	0.79	0.25	0.00
		KGVCEETSGAYEK			0.62	4.0	2	
		GVCEETSGAYEK			0.72	3.8	2	
		TVAACNLPIVR			0.69	3.5	2	
		CVLFPYGGCQGNGNK			1.32	2.6	2	
		EYCGVPGDGDEELLR			0.97	3.0	2	
		VVAQGVGIPEDSIFTMADR+Oxidation(15)			1.24	2.3	2	
		VVAQGVGIPEDSIFTMADR			0.81	2.8	2	
		WYNLAIGSTCPWLK			0.90	4.1	2	
		KEDSCQLGYSAGPCMGMTSR			1.42	3.7	3	
		EDSCQLGYSAGPCMGMTSR			0.66	3.8	2	
		GECVPGEQEPEPILIPR			0.76	3.5	2	
P02763	A1AG1	Alpha_1_acid glycoprotein 1	4	10	104	0.88	0.33	0.69
		SDVVYTDWKK			0.78	2.8	2	
		SDVVYTDWK			0.77	3.4	2	
		NWGLSVYADKPETTK			0.72	4.4	2	
		YVGGQEHFAHLLILR			1.01	4.8	2	
P02765	FETUA	Alpha_2_HS_glycoprotein	9	28	230	1.01	0.27	0.00
		CDSSPDSAEDVR			0.63	3.2	2	
		HTLNQIDEVK			1.89	3.9	2	
		FSVVYAK			0.97	1.9	1	
		HTFMGVVSLGSPSGEVSHPR+Oxidation(3)			2.95	4.6	3	
		EHAVEGDCDFQLLK			0.93	4.3	2	
		HTFMGVVSLGSPSGEVSHPR			4.81	5.6	2	
		TVVQPSVGAAAGPVVPPCPGR			1.78	4.3	2	
		AQLVPLPPSTYVEFTVSGTDCVAK			0.81	4.5	3	
		CDSSPDSAEDVRK			0.67	3.0	2	
P02766	TTHY	Transthyretin	9	31	244	0.77	0.15	0.00
		GSPAINVAVHVFR			0.85	4.1	2	
		AADDTWEPFASGK			0.80	4.4	2	

		ALGISPFHEHAEVVFTANDSGPR			0.72	5.4	2	
		RYTIAALLSPYSYSTTAVVTNPK			1.01	5.0	2	
		RYTIAALLSPYSYSTTAVVTNPKE			1.20	4.6	2	
		YTIAALLSPYSYSTTAVVTNPK			0.86	5.0	2	
		YTIAALLSPYSYSTTAVVTNPKE			0.96	5.7	2	
		TSESGELHGLTTEEEFVEGIYK			0.84	4.3	2	
		KAADDTWEPFASGK			1.00	3.1	2	
P02768	ALBU	Serum albumin	68	1066	13265	0.88	0.02	0.00
		NYAEAK			0.77	2.3	1	
		ADDKETCFAEEGKK			0.91	5.3	3	
		LDELRDEGKASSAK			0.68	2.7	2	
		TCVADESAENCDK			0.82	4.8	2	
		CCAAADPHECYAK			0.75	4.8	2	
		LDELRDEGK			0.77	2.8	2	
		ETYGEMADCCAK+Oxidation(5)			0.91	3.4	2	
		ADDKETCFAEEGK			0.85	4.1	3	
		QEPERNECFLQHK			0.54	2.8	2	
		LKECCEKPLLEK			0.69	4.6	2	
		ECCEKPLLEK			0.73	2.7	2	
		AAFTECCQAADK			0.66	4.1	2	
		TYETTLEK			0.80	2.6	2	
		CCTESLVNR			0.70	3.4	2	
		AEFAEVSK			0.84	2.8	2	
		DDNPNLPR			0.86	2.7	2	
		LAKTYETTLEK			0.75	2.4	2	
		YICENQDSISSK			0.85	4.4	2	
		YKAAFTECCQAADK			1.17	4.4	2	
		ETYGEMADCCAK			0.60	3.9	2	
		VHTECCHGDLLECADDR			0.95	6.6	2	
		AACLLPK			0.90	2.7	2	
		LVTDLTK			0.79	2.4	2	
		QEPERNECFLQHKDDNPNLPR			0.92	3.7	3	
		FKDLGEENFK			1.03	4.4	3	
		DLGEENFK			0.80	3.2	2	
		NECFLQHKDDNPNLPR			0.93	4.7	2	
		LCTVATLR			0.73	2.4	2	
		KYLYEIAR			0.90	3.3	2	
		YLYEIAR			0.88	3.2	2	
		SLHTLFGDK			1.06	2.8	1	
		VHTECCHGDLLECADDRADLAK			0.87	5.7	3	
		KQTALVELVK			0.83	5.1	3	
		QTALVELVK			1.05	2.0	1	
		FQNALLVR			0.87	3.1	2	
		KVPQVSTPTLVEVSR			0.83	5.5	3	
		LVNEVTEFAK			0.90	3.8	2	
		VPQVSTPTLVEVSR			1.22	3.8	3	
		LVRPEVDVMCTAFHDNEETFLKK+Oxidation(8)			0.84	5.2	3	
		KLVAASQAALGL			0.78	3.7	2	
		RHPDYSVVLLLR			1.17	5.1	3	
		RPCFSALEVDETYVPK			1.26	4.1	3	

		LVRPEVDVMCTAFHDNEETFLK+Oxidation(8)			0.71	5.5	3	
		LVRPEVDVMCTAFHDNEETFLKK			0.89	6.7	3	
		LVRPEVDVMCTAFHDNEETFLK			0.83	6.6	3	
		QNCELFEQLGEYK			0.92	4.5	2	
		AVMDDFAAFVEK+Oxidation(2)			0.78	4.1	2	
		HPDYSVVLLLR			1.79	2.6	2	
		LVAASQAALGL			0.82	4.1	2	
		SHCIAEVENDEMPADLPSLAADFVESK+Oxidation(11)			0.88	6.0	3	
		EFNAETFTFHADICTLSEK			1.06	6.0	2	
		VFDEFKPLVEEPQNLIK			1.17	5.4	3	
		RHPYFYAPELLFFAK			1.43	4.2	3	
		SHCIAEVENDEMPADLPSLAADFVESK			0.91	5.2	3	
		AVMDDFAAFVEK			1.12	4.0	2	
		AEFAEVSKLVTDLTK			1.12	4.4	2	
		MPCAEDYLSVVLNQLCVLHEKTPVSDR+Oxidation(0)			0.61	4.3	4	
		NYAEAKDVFLGMFLYEYAR			0.97	3.1	2	
		MPCAEDYLSVVLNQLCVLHEKTPVSDR			0.89	4.5	4	
		DVFLGMFLYEYAR+Oxidation(5)			0.84	4.4	2	
		ALVLIAFAQYLQQCPFEDHVK			1.25	5.9	4	
		FKDLGEENFKALVLIAFAQYLQQCPFEDHVK			0.80	6.5	4	
		DVFLGMFLYEYAR			1.54	4.4	2	
		SLHTLFGDKLCTVATLR			1.26	3.9	4	
		QNCELFEQLGEYKFQNALLVR			1.64	3.5	3	
		MPCAEDYLSVVLNQLCVLHEK+Oxidation(0)			1.54	5.1	3	
		MPCAEDYLSVVLNQLCVLHEK			2.19	4.7	3	
		RYKAAFTECCQAADK			0.46	2.6	2	
P02774	VTDB	Vitamin D_binding protein	21	74	508	1.24	0.14	0.93
		CCESASEDCMAK+Oxidation(9)			1.11	3.8	2	
		VCSQYAAYGEK			0.86	3.4	2	
		SCESNSPFPVHPGTAECCTK			0.91	5.3	2	
		RTHLPEVFLSK			0.78	4.2	3	
		ELSSFIDK			0.71	2.3	1	
		YTFELSR			1.07	2.3	2	
		SLGECCDVEDSTTCFNAK			0.74	5.3	2	
		GQELCADYSENTFTEYKK			0.96	4.1	2	
		THLPEVFLSK			0.78	3.7	3	
		HLSLLTTLSNR			0.81	3.5	2	
		GQELCADYSENTFTEYK			0.97	5.9	2	
		EVVSLTEACCAEGADPDCYDTR			1.36	5.6	2	
		HQPQEFPTYVEPTNDEICEAFRK			1.13	3.7	3	
		KFPSGTFEQVSQLVK			1.14	5.0	2	
		RSDFASNCCSINSPPLYCDSEIDAELK			1.08	5.6	3	
		HQPQEFPTYVEPTNDEICEAFR			1.25	5.9	3	
		SYLSMVGSCCTSASPTVCFLK+Oxidation(4)			1.15	5.0	2	
		FPSGTFEQVSQLVK			1.51	4.8	2	
		SDFASNCCSINSPPLYCDSEIDAELK			1.20	5.3	3	
		ELSSFIDKGQELCADYSENTFTEYK			1.68	5.5	3	
		SYLSMVGSCCTSASPTVCFLK			1.24	5.8	2	
P02786	TFR1	Transferrin receptor protein 1	3	3	10	1.38	1.49	0.81
		LLNENSYVPR			1.31	3.0	2	

		LAVDEEENADNNTK			2.60	3.9	2	
		DSAQNSVIIVDK			1.33	2.4	2	
P02787	TRFE	Serotransferrin	48	304	3086	0.89	0.05	0.00
		HQTVPQNTGGK			0.79	2.4	2	
		WCALSHHER			0.71	3.5	2	
		KDSGFQMNQLR+Oxidation(6)			0.88	3.9	3	
		WCAVSEHEATK			0.73	4.0	2	
		EGTCPEAPTDECKPVK			0.54	3.6	2	
		KPVEEYANCHLAR			0.99	4.1	3	
		DSAHGFLK			0.84	2.4	2	
		DDTVCLAK			0.80	2.6	2	
		DSGFQMNQLR+Oxidation(5)			0.96	3.4	2	
		DCHLAQVPSHTVVAR			0.97	4.6	2	
		KDSGFQMNQLR			0.75	3.8	3	
		SKEFQLFSSPHGK			1.42	4.4	3	
		KPVDEYKDCHLAQVPSHTVVAR			1.08	5.4	3	
		LKCDEWSVNSVGK			0.90	4.5	2	
		HSTIFENLANK			0.79	4.7	2	
		CDEWSVNSVGK			0.83	3.7	2	
		IECVSAETTEDCIAK			0.95	5.3	2	
		LCMGSGLNLCEPNNK+Oxidation(2)			0.94	4.7	2	
		YLGEEYVK			0.92	3.0	2	
		DGAGDVAFVK			0.98	4.0	2	
		KSASDLTWDNLK			1.00	3.7	2	
		ASYLDCIR			0.89	3.0	2	
		KCSTSSLLEACTFR			1.20	4.4	2	
		EFQLFSSPHGK			0.87	3.7	2	
		DSGFQMNQLR			0.77	3.7	2	
		SVIPSDGPSVACVK			0.76	3.6	2	
		EGYYGYTGAFR			1.02	3.4	2	
		SASDLTWDNLK			0.90	3.8	2	
		LCMGSGLNLCEPNNK			0.57	5.1	2	
		CSTSSLLEACTFR			0.94	4.9	2	
		MYLGYEYVTAIR+Oxidation(0)			0.77	4.2	2	
		DLLFRDDTVCLAK			0.60	3.5	2	
		TAGWNIPMGLLYNK+Oxidation(7)			0.91	4.5	2	
		IMNGEADAMSLDGGFVYIAGK+Oxidation(8)			0.76	4.9	2	
		IMNGEADAMSLDGGFVYIAGK+Oxidation(1)			0.76	5.2	2	
		EDPQTFYYAVAVVK			0.91	4.1	2	
		IMNGEADAMSLDGGFVYIAGK			0.42	5.8	2	
		SMGGKEDLIWELLNQAQEHFGK+Oxidation(1)			0.57	5.5	3	
		SMGGKEDLIWELLNQAQEHFGK			0.76	6.5	3	
		AIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSK			0.97	6.0	3	
		LCMGSGLNLCEPNNKEGYYGYTGAFR			1.45	3.8	3	
		AVANFFSGSCAPCADGTDFPQLCQLCPGCGCSTLNQYFGYSGAFK			0.69	6.0	4	
		NLNEKDYELLCLDGTR			0.66	4.4	2	
		TAGWNIPMGLLYNK			0.69	4.7	2	
		EDLIWELLNQAQEHFGK			0.99	4.7	2	
		ADRDQYELLCLDNTR			0.48	4.2	3	
		MYLGYEYVTAIR			0.97	4.3	2	

		IMNGEADAMSLDGGFVYIAGK+Oxidation(1),Oxidation(8)			0.89	4.7	2	
P02788	TRFL	Lactotransferrin	32	63	234	2.82	0.39	0.99
		SCHLAMAPNHAVVSR			1.26	4.5	2	
		THYYAVAVVK			0.50	2.3	1	
		LRPVAAEVYGTER			2.32	3.5	2	
		YYGYTGAFR			1.11	2.5	2	
		SDTSLTWNSVK			3.76	3.7	2	
		FFSASCVPGADK			1.77	3.3	2	
		SNLCALCIGDEQGENK			3.13	5.0	2	
		FQLFGSPSGQK			3.86	2.5	2	
		DVTVLQNTDGNNNEAWAK			4.23	5.6	2	
		GEADAMSLDGGYVYTAGK			1.75	5.1	2	
		NLLFNDNTECLAR			6.85	3.8	2	
		SQQSSDPDPNCVDRPVEGYLAVAVVR			1.58	5.0	3	
		YLGPQYVAGITNLK			1.54	4.2	2	
		DSPIQCIQAIAENR			1.68	4.7	3	
		ADAVTLDGGFIYEAGLAPYK			1.68	5.8	2	
		IDSGLYLGSGYFTAIQNLR			0.55	4.9	3	
		SCHLAMAPNHAVVSR+Oxidation(5)			1.09	3.8	2	
		RSDTSLTWNSVK			2.26	3.5	2	
		DGAGDVAFIR			2.38	3.1	2	
		KGGSFQLNELQGLK			2.16	4.2	3	
		GGSFQLNELQGLK			1.93	3.7	2	
		SVNGKEDAIWNLLR			2.08	2.5	2	
		EDAIWNLLR			1.60	2.6	2	
		SVQWCAVSQPEATK			1.26	4.6	2	
		GEADAMSLDGGYVYTAGK+Oxidation(5)			0.45	4.2	2	
		FDEYFSQSCAPGSDPR			0.33	4.5	2	
		CLAENAGDVAFVK			2.05	4.3	2	
		VVWCAVGEQELR			1.84	3.4	2	
		CGLVPVLAENYK			2.39	3.0	2	
		CSTSPLLEACEFLR			0.96	3.6	2	
		FCLFQSETK			0.84	2.5	2	
		CAFSSQEPYFSYSGAFK			2.85	4.6	2	
P02790	HEMO	Hemopexin	21	93	830	0.83	0.08	0.99
		VDGALCMEK+Oxidation(6)			0.90	2.9	2	
		VDGALCMEK			0.77	3.0	2	
		VWVYPPEKK			0.93	2.7	2	
		DYFMPCPGR+Oxidation(3)			0.82	2.6	2	
		GGYTLVSGYPK			0.91	4.2	2	
		VWVYPPEK			0.97	2.6	2	
		DYFMPCPGR			0.91	2.8	2	
		YYCFQGNQFLR			1.02	3.7	2	
		NFPSPVDAAFR			1.00	2.6	1	
		SGAQATWTELPWPHEK			1.01	5.1	3	
		GECQAEGVLFFQGDR			1.26	4.6	2	
		CSPHLVLSALTSDNHGATYAFSGTHYWR			0.92	5.4	4	
		RLWWLDLK			1.27	2.7	2	
		SLGPNSCSANGPGLYLIHGPNLYCYSDVEK			1.00	5.1	3	
		EVGTPHGIILDSVDAAFICPGSSR			1.06	5.8	2	

		LLQDEFPGIPSPLDAAVECHR			1.09	5.1	2	
		DGWHSWPIAHQWPQGPSAVDAAFSWEEK			0.92	4.9	3	
		LWWLDLK			0.89	2.5	2	
		LYLVQGTQVYVFLTK			1.21	5.1	2	
		EWFWDLATGTMK			1.27	3.3	2	
		LHIMAGR			0.07	2.0	1	
P02812	PRB2	Basic salivary proline_rich protein 2	2	8	14	0.00	0.00	0.63
		SQGPPPPGKPQGPPPQGGSK			0.01	4.1	2	
		SPPGKPQGPPPQGGNQPQGPPPPPGKPQGPPPQGGNK			0.00	5.6	4	
P03952	KLKB1	Plasma kallikrein	3	4	19	1.14	0.66	0.85
		GVNVCQETCTK			0.89	3.3	2	
		IAYGTQGSSGYSLR			1.39	2.4	2	
		LVGITSWGEGCAR			0.85	2.4	2	
P03973	SLPI	Antileukoproteinase	4	6	70	1.08	1.00	1.00
		YKKPECQSDWQCPGK			0.94	5.1	3	
		CLDPVDTPNPTR			1.15	3.5	2	
		KPECQSDWQCPGKK			1.32	3.6	3	
		KPECQSDWQCPGK			1.79	3.6	2	
P04003	C4BPA	C4b_binding protein alpha chain	5	6	13	1.10	0.64	0.99
		YTCLPGYVR			0.81	2.8	2	
		FSAICQGDGTWSPR			0.94	3.7	2	
		EDVYVVGTVLR			0.84	2.4	2	
		WNPSPPACEPNSCINLPDIPHASWETYPRPTK			1.19	5.0	4	
		WTPYQGCEALCCPEPK			1.10	3.5	2	
P04004	VTNC	Vitronectin	6	19	101	1.39	0.19	1.00
		GQYCYELDEK			0.58	3.2	2	
		FEDGVLDPDYPR			1.42	4.0	2	
		SIAQYWLGCPAPGHL			1.10	4.4	2	
		DVWGIEGPIDAAFTR			1.44	4.3	2	
		DWHGVPGQVDAAMAGR			1.06	3.1	2	
		CQCDELCSYYQSCCTDYTAECKPQVTR			0.78	5.0	3	
P04040	CATA	Catalase	2	2	4	1.43	2.78	0.89
		FNTANDDNVTQVR			1.21	3.3	2	
		ADVLTTGAGNPVGDK			1.51	3.1	2	
P04075	ALDOA	Fructose_bisphosphate aldolase A	4	6	40	1.07	0.81	0.99
		LQSIGTENTEENR			0.87	3.4	2	
		GILAADESTGSIAK			1.49	3.9	2	
		GVVPLAGTNGETTTQGLDGLSER			0.99	5.1	2	
		RLQSIGTENTEENR			0.52	2.7	2	
P04080	CYTB	Cystatin_B	3	8	27	1.33	1.26	0.28
		VHVGDEDFVHLR			2.45	3.9	3	
		VFQSLPHENKPLTLSNYQTNK			3.80	4.9	2	
		SQVVAGTNYFIK			1.32	3.2	2	
P04083	ANXA1	Annexin A1	10	23	122	1.15	0.42	0.96
		SEIDMNDIK			1.33	2.5	2	
		GDRSEDFGVNEDLADSDAR			1.25	4.3	3	
		SEDFGVNEDLADSDAR			1.61	5.0	2	
		VLDLELK			1.26	2.5	2	
		GGPGSAVSPYPTFNPSSDVAALHK			1.40	4.1	2	
		GVDEATIIDILTK			1.27	4.5	2	

		DITSDTSGDFR			1.66	3.6	2	
		GTDVNVFNTILTTR			0.94	4.4	2	
		MYGISLCQAILDETK			1.13	3.4	2	
		AAYLQETGKPLDETLK			1.77	3.5	2	
P04114	APOB	Apolipoprotein B_100	22	28	86	3.56	0.63	0.00
		ALVEQGFTVPEIK			3.15	3.3	2	
		EFQVPTFTIPK			3.52	2.5	2	
		TSSFALNLPTLPEVK			3.56	3.2	2	
		LTISEQNIQR			1.22	2.4	2	
		ILGEELGFASLHDLQLLGK			1.55	3.8	3	
		GNVATEISTER			2.34	2.8	2	
		VLVDHFGYTK			2.17	2.3	2	
		YTYNYEAESSSGVPGTADSR			0.85	5.4	2	
		HINIDQFVR			2.35	2.8	2	
		TQFNNNEYSQDLDAYNTK			8.66	5.1	2	
		YGMVAQVTQTLK			3.65	3.3	2	
		NLQNNAEWVYQGAIR			4.36	3.6	2	
		ALYWVNGQVPDGVSK			3.09	2.9	2	
		ITENDIQIALDDAK			3.21	4.0	2	
		SVSDGIAALDLNAVANK			4.28	3.4	2	
		IVQILPWEQNEQVK			3.35	2.4	2	
		VIGNMGQTMEQLTPELK			3.00	2.4	2	
		AVSMPSFSILGSDVR			2.03	3.4	2	
		VLLDQLGTTISFER			3.47	4.0	2	
		VNWEEEAASGLLTSLK			2.83	5.3	2	
		IEGNLIFDPNNYLPK			2.38	3.5	2	
		ATFQTPDFIVPLTDLR			2.35	3.7	2	
P04196	HRG	Histidine_rich glycoprotein	5	12	58	1.17	0.26	0.01
		KYWNDCEPPDSR			0.87	3.0	2	
		YKEENDDFASFR			0.73	3.8	2	
		HPLKPDNQPFPQSVSESCPGK			0.75	4.1	3	
		KGEVLPLPEANFPSFPLPHHK			1.17	5.6	3	
		DGYLFQLLR			0.67	2.8	2	
P04217	A1BG	Alpha_1B_glycoprotein	10	24	228	0.97	0.18	0.87
		HQFLLTGDTQGR			1.02	3.7	2	
		CLAPLEGAR			0.64	2.4	2	
		LLELTGPK			0.72	2.1	1	
		ATWSGAVLAGR			0.99	3.8	2	
		SGLSTGWTQLSK			0.87	4.1	2	
		IFFHLNAVALGDGGHYTCR			0.57	3.9	3	
		TDGEGALSEPSATVTIEELAAPPPPVLMHHGESSQVLHPGNK+Oxidation(			0.93	4.3	4	
		VTLTCVAPLSGVDFQLR			0.92	5.9	3	
		SLPAPWLSMAPVSWITPGLK+Oxidation(8)			0.86	4.2	2	
		NGVAQEPVHLDSPAIK			0.63	3.7	2	
P04220	MUCB	Ig mu heavy chain disease protein	7	30	162	4.36	0.52	0.00
		YVTSAPMPEPQAPGR+Oxidation(6)			5.62	3.7	2	
		LICQATGFSPR			2.75	3.4	2	
		VSVFVPPR			2.27	3.0	2	
		FTCTVTHTDLPSPLK			1.84	3.8	2	
		GVALHRPDVYLLPPAR			2.73	4.9	3	

		DGFFGNPR			4.73	2.4	2	
		YVTSAPMPEPQAPGR			0.73	3.7	2	
P04264	K2C1	Keratin_ type II cytoskeletal 1	12	18	75	1.65	0.46	0.00
		IEISELNR			2.50	2.5	2	
		FLEQQNQVLQTK			1.46	4.5	2	
		EQIKSLNNQFASFIDK			0.71	1.9	1	
		SLDLDSIIAEVK			2.53	4.5	2	
		SKAEAESLYQSK			1.44	3.5	2	
		WELLQQVDTSTR			2.17	3.8	2	
		QISNLQQSISDAEQR			3.13	4.3	2	
		GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR			2.08	5.7	3	
		LNDLEDALQQAK			1.74	3.5	2	
		GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR			1.61	6.0	2	
		SLNNQFASFIDK			1.62	3.2	2	
		TNAENEFVTIK			1.53	2.6	2	
P04350	TBB4	Tubulin beta_4 chain	4	7	27	0.88	0.56	0.42
		FWEVISDEHGIDPTGTYHGDSDLQLER			0.86	4.5	3	
		ALTVPELTQQMFDAK			0.43	4.0	2	
		MAATFIGNSTAIQELFK+Oxidation(0)			1.55	4.6	2	
		EIVHLQAGQCGNQIGAK			0.49	4.6	2	
P04406	G3P	Glyceraldehyde_3_phosphate dehydrogenase	7	13	64	1.10	0.38	0.95
		IISNASCTTNCLAPLAK			1.28	3.9	2	
		LISWYDNEFGYSNR			0.98	4.0	2	
		VIHDNFGIVEGLMTTVHAITATQK			1.04	5.0	3	
		GALQNIIPASTGAAK			1.09	3.7	2	
		GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK			1.26	5.4	4	
		LVINGNPITIFQER			0.70	3.3	2	
		VPTANVSVVDLTCR			2.01	2.8	2	
P04632	CPNS1	Calpain small subunit 1	4	4	18	0.91	0.64	0.50
		THYSNIEANESEEVR			0.91	4.9	2	
		TDGFGIDTCR			1.25	2.5	2	
		SMVAVMDSDTTGK			0.68	2.5	2	
		ILGGVISAISEAAAQYNPEPPPPR			1.57	3.9	3	
P04745	AMY1	Alpha_amylase 1	2	3	4	1.76	0.05	0.35
		YFENGKDVNDWVGPPNDNGVTK			0.60	4.5	2	
		DVNDWVGPPNDNGVTK			1.77	4.1	2	
P04746	AMYP	Pancreatic alpha_amylase	11	20	37	1.50	0.08	0.32
		ALVFVDNHDNQR			0.21	3.1	2	
		TGSGDIENYNDATQVR			2.05	5.1	2	
		AHFSISNSAEDPFIAIHAESKL			0.33	4.8	3	
		IYVDAVINHMCGNAVSAGTSSTCGSYFNPGSR			0.18	5.5	4	
		HMWPGDIK			0.09	2.5	2	
		EVTINPDTTCGNDWVCEHR			0.07	3.9	2	
		AHFSISNSAEDPFIAIHAESK			0.26	6.5	2	
		WVDIALECER			0.06	2.7	2	
		TSIVHLFEWR			0.16	2.8	2	
		NVVDGQPFTNWYDNGSNQVAFGR			0.07	5.2	2	
		IAEYMNHLIDIGVAGFR			0.13	4.3	2	
P04792	HSPB1	Heat shock protein beta_1	4	4	14	1.09	0.93	0.98
		TKDGVVEITGK			0.94	2.5	2	

		LATQSNEITIPVTFESR			1.15	3.2	2	
		VSLDVNHFAPDELTVK			0.96	3.7	2	
		KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK			1.37	4.2	3	
P05091	ALDH2	Aldehyde dehydrogenase_ mitochondrial	12	15	32	2.11	1.40	0.04
		EEIFGPVMQILK+Oxidation(7)			1.25	3.1	2	
		GYFIQPTVFGDVQDGMTIAK			2.78	4.2	2	
		RVTLELGGK			1.58	2.7	2	
		ELGEYGLQAYTEVK			2.03	2.9	2	
		ANNSTYGLAAAVFTK			2.16	4.4	2	
		VIQVAAGSSNLKR			54.68	2.3	2	
		VIQVAAGSSNLK			116.89	4.2	2	
		TEQGPQVDETQFK			25.34	4.3	2	
		KTFPTVNPSTGEVICQVAEGDKEDVDK			3.07	5.0	3	
		EEIFGPVMQILK			10.98	3.6	2	
		VAFTGSTEIGR			7.98	3.0	2	
		EAGFPPGVVNIVPGFGPTAGAAIASHEDVDK			9.49	4.0	3	
P05109	S10A8	Protein S100_A8	5	9	33	1.06	0.24	1.00
		GNFHAVYR			0.48	2.5	2	
		GADVWFK			0.79	2.5	2	
		LLETECPQYIR			0.74	3.8	2	
		ALNSIIDVYHK			1.17	3.3	2	
		KLLETECPQYIR			1.17	2.4	2	
P05155	IC1	Plasma protease C1 inhibitor	15	49	418	0.82	0.11	0.00
		DFTCVHQALK			0.57	3.3	2	
		HRLEDMEQALSPSVFK+Oxidation(5)			0.60	4.2	3	
		LLDSLPSDTR			0.58	3.3	2	
		KYPVAHFIDQTLK			0.83	4.1	3	
		HRLEDMEQALSPSVFK			0.65	5.0	3	
		VTTSQDMLSIMEK			0.62	4.1	2	
		LEDMEQALSPSVFK+Oxidation(3)			0.68	3.8	2	
		TNLESILSYPK			0.78	4.3	2	
		GVTSVSQIFHSPDLAIR			0.78	4.9	2	
		FQPTLLTLPR			0.69	2.8	2	
		LEDMEQALSPSVFK			0.68	5.0	2	
		VTTSQDMLSIMEK+Oxidation(10)			0.48	3.2	2	
		VTTSQDMLSIMEK+Oxidation(6)			0.49	2.7	2	
		VTTSQDMLSIMEK+Oxidation(6),Oxidation(10)			0.44	2.7	2	
		LVLLNAIYLSAK			0.93	4.0	2	
P05156	CFAI	Complement factor I	11	24	135	1.15	0.21	0.03
		HGNTDSEGIVEVK			0.84	4.4	2	
		EMECAGTYDGSIDACK			0.65	4.9	2	
		GLETSLAECTFTK			0.92	4.4	2	
		EANVACLDLGFQQGADTQR			1.16	5.5	2	
		TMGYQDFADVVCYTQK+Oxidation(1)			1.03	3.3	2	
		VFSLQWGEVK			1.16	3.9	2	
		TMGYQDFADVVCYTQK			1.16	4.3	3	
		AQLGDLPWQVAIK			1.25	3.8	2	
		YQIWTTVVDWIHPDLK			0.89	4.2	3	
		ACDGINDCGDQSDELCCK			0.80	5.7	2	
		VTYTSQEDLVEK			1.21	3.0	2	

P05186	PPBT	Alkaline phosphatase_ tissue_nonspecific isozyme	5	7	44	0.87	0.27	0.00
		HETHGGEDVAVFSK			0.53	4.4	3	
		ANEGTVGVSAATER			0.49	3.3	2	
		TYNTNAQVPDSAGTATAYLCGVK			0.93	4.6	2	
		TDVEYESDEK			0.53	2.6	2	
		LDGLDLVDTWK			1.11	3.9	2	
P05362	ICAM1	Intercellular adhesion molecule 1	12	26	210	0.60	0.14	0.00
		ASVSVTAEDEGTQR			0.67	4.4	2	
		KELLLPGNNR			0.80	2.5	2	
		GGSVLVTCSTSCDQPK			0.60	4.7	2	
		DLEGTYLCR			0.54	2.6	2	
		REPAVGEPAEVTTTVLVR			0.68	4.3	3	
		VTLNGVPAQPLGPR			0.69	2.8	2	
		EPAVGEPAEVTTTVLVR			0.87	3.0	2	
		LLGIETPLPK			0.62	3.0	2	
		SFSCSATLEVAGQLIHK			0.67	4.1	2	
		VELAPLPSWQPVGK			0.78	4.1	2	
		DGTFPLPIGESVTVTR			0.77	4.1	2	
		VYELSNVQEDSQPMCYSNCPDGQSTAK			0.54	4.3	3	
P05452	TETN	Tetranectin	8	8	77	1.05	0.35	0.88
		TFHEASEDCISR			0.94	4.1	3	
		TENCAVLSGAANGK			0.95	4.4	2	
		NWETEITAQPDGGK			0.79	3.7	2	
		NWETEITAQPDGGKTENCAVLSGAANGK			1.11	4.1	3	
		SRLDTLAQEVALLK			1.18	3.5	2	
		LDTLAQEVALLK			1.21	4.6	2	
		EQQALQTVCLK			0.69	2.9	2	
		GGTLGTPQTGSENDALYEYLR			0.85	2.9	2	
P05543	THBG	Thyroxine_binding globulin	4	5	21	1.25	0.45	0.03
		FSISATYDLGATLLK			1.19	3.8	2	
		GTEAAAVPEVELSDQPENTFLHPIIQIDR			1.31	3.7	3	
		EGQMESVEAAMSSK			1.52	3.2	2	
		QEINSHVEMQTK			0.48	3.3	2	
P05546	HEP2	Heparin cofactor 2	3	3	7	0.78	0.46	0.33
		HQGTITVNEEGTQATTVTTVGFMPLSTQVR+Oxidation(22)			0.88	3.7	3	
		HQGTITVNEEGTQATTVTTVGFMPLSTQVR			0.86	3.7	3	
		GGETAQSADPQWEQLNNK			0.54	4.9	2	
P05787	K2C8	Keratin_ type II cytoskeletal 8	3	3	4	0.96	0.98	0.80
		LEGLTDEINFLR			1.18	2.5	2	
		TEMENEFVLIK			0.61	2.0	1	
		SLDMDSIIAEVK			0.80	2.9	2	
P05997	CO5A2	Collagen alpha-2(V) chain	2	3	6	0.80	0.62	0.23
		TPASLQADKTVR			0.80	2.1	1	
		IDLDNAGKLVVAK			0.46	3.1	2	
P06310	KV206	Ig kappa chain V_II region RPMI 6410	2	5	63	0.89	0.48	0.69
		FSGSGSGTDFTLK			0.90	3.7	2	
		FSGSGSGTDFTLKISR			0.82	3.5	2	
P06314	KV404	Ig kappa chain V_IV region B17	2	7	42	0.60	0.30	0.00
		NYLAWYQQKPGQPPK			1.04	4.0	2	
		LLIYWASTR			0.55	3.1	2	

P06331	HV209	Ig heavy chain V_II region ARH_77	2	3	27	0.64	0.39	0.00
		VTISLDTSK			0.64	2.3	2	
		LSSVTAADTAVYYCAR			0.66	5.0	2	
P06396	GELS	Gelsolin	14	31	198	0.95	0.16	0.79
		DSQEEEKTEALTSAK			1.00	5.5	3	
		HVVPNEVVVQR			1.00	3.6	3	
		TGAQELLR			0.78	2.7	2	
		VPFDAATLHTSTAMAAQHGMDDDGTGQK			0.92	4.1	3	
		AGALNSNDAFVLK			1.00	3.8	2	
		TPSAAYLWVGTGASEAEK			1.10	3.7	2	
		VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK			0.94	5.6	3	
		QTQVSVLPEGGETPLFK			1.44	4.3	2	
		NWRDPDQTDGLGLSYLSSHIANVER			1.13	5.3	3	
		VSNGAGTMSVSLVADENPFAQGALK+Oxidation(7)			0.90	4.7	3	
		DPDQTDGLGLSYLSSHIANVER			1.02	5.4	3	
		AQPVQVAEGSEPDGFWEALGGK			1.15	6.0	2	
		VSNGAGTMSVSLVADENPFAQGALK			0.99	5.5	3	
		YIETDPANR			0.70	2.4	2	
P06576	ATPB	ATP synthase subunit beta_ mitochondrial	4	5	6	3.67	1.18	0.30
		VALVYGQMNEPPGAR			0.49	2.3	2	
		AIAELGIYPAVDPLDSTSR			5.51	4.0	2	
		TIAMDGTEGLVR			4.61	2.7	2	
		FTQAGSEVSALLGR			9.65	2.4	2	
P06681	CO2	Complement C2	15	27	132	0.65	0.14	0.00
		HAFILQDTK			0.59	2.6	2	
		CSSNLVLTGSSER			0.75	3.9	2	
		ECQGNGVWSGTEPICR			0.53	3.5	2	
		VLMSVLNDNSR+Oxidation(2)			1.69	2.0	1	
		VLMSVLNDNSR			1.09	3.2	2	
		ALHQVFEHMLDVSK			0.76	3.6	3	
		MGVEWTSCAEVVSQEK			1.05	4.4	2	
		DFHINLFR			0.68	2.7	2	
		EVVTDQFLCSGTQEDESPCKGESGGAVFLER			0.65	6.2	3	
		AVISPGFDVFAK			0.69	2.9	2	
		LLGMETMAWQEIR			1.26	3.3	2	
		DMTEVISSLENANYK			0.56	3.3	2	
		SSGQWQTPGATR			0.40	3.0	2	
		HAIILLTDGK			0.52	3.0	2	
		GESGGAVFLER			1.29	2.7	2	
P06702	S10A9	Protein S100_A9	7	16	83	0.77	0.58	1.00
		LGHPDTLNQGEFK			0.82	3.5	3	
		VIEHIMEDLDTNADK			0.45	5.4	2	
		NIETIINTFHQYSVK			0.84	4.8	2	
		KDLQNFLK			1.05	2.8	2	
		MHEGDEGPGHHHKPGLGEGTP+Oxidation(0)			0.64	3.6	2	
		MHEGDEGPGHHHKPGLGEGTP			0.31	2.7	2	
		VIEHIMEDLDTNADK+Oxidation(5)			0.45	4.3	2	
P06727	APOA4	Apolipoprotein A_IV	18	30	191	1.04	0.40	0.00
		TQVNTQAEQLR			1.02	3.2	2	
		RVEPYGENFNK			1.28	3.6	3	

		ISASAEELR			1.20	3.3	2	
		SLAPYAQDTQEK			0.95	3.1	2	
		KLVPFATELHER			0.54	4.4	3	
		LGEVNTYAGDLQK			0.63	4.0	2	
		LKEEIGKELEELR			2.17	4.3	3	
		DKVNSFFSTFK			1.30	3.0	2	
		SLAELGGHLDQQVEEFR			1.29	5.1	3	
		SELTQQLNALFQDK			1.33	5.1	2	
		IDQNVEELK			1.36	2.9	2	
		LGPHAGDVEGHLSFLEK			2.24	4.7	2	
		LNHQLEGLTFQMK			1.31	3.8	2	
		SLAELGGHLDQQVEEFRR			1.63	4.0	3	
		LVPFATELHER			1.09	2.7	2	
		ALVQQMEQLR			0.90	2.7	2	
		AKIDQNVEELK			1.57	2.8	2	
		ENADSLQASLRPHADELK			1.01	3.6	2	
P06733	ENOA	Alpha_enolase	9	16	81	1.61	0.50	0.00
		KLNVTEQEK			1.20	2.4	2	
		IGAEVYHNLK			1.62	3.1	2	
		VNQIGSVTESLQACK			1.51	4.9	2	
		DATNVGDEGGFAPNILENK			2.07	5.2	2	
		FTASAGIQVVGDDLTVTNPK			1.68	5.2	2	
		HIADLAGNSEVILPVPAFNVINGGSHAGNK			2.25	6.2	3	
		SCNCLLLK			1.10	2.5	2	
		LMIEMDGTENK			1.13	2.6	2	
		YISPDQLADLYK			1.61	3.5	2	
P06737	PYGL	Glycogen phosphorylase_ liver form	2	3	4	1.12	0.92	0.83
		DFNVGDYIQAVLDR			1.25	2.5	1	
		LVIDQIDNGFFSPK			0.84	2.5	2	
P06744	G6PI	Glucose_6_phosphate isomerase	3	4	32	0.99	0.58	0.88
		HFVALSTNTTK			1.16	3.1	2	
		TFTTQETITNAETAK			0.97	4.8	2	
		VWYVSNIDGTHIAK			0.32	3.3	2	
P06753	TPM3	Tropomyosin alpha_3 chain	4	4	8	2.83	3.17	0.15
		YSQKEDKYEEEIK			2.24	4.0	2	
		AADAEAEVASLNR			3.80	2.6	2	
		MELQEIQLK			2.72	3.0	2	
		KLVIIEGDLER			2.89	2.4	2	
P06865	HEXA	Beta_hexosaminidase subunit alpha	2	2	2	6.20	15.12	0.35
		GSYNPVTHIYTAQDVK			6.20	2.9	2	
		IQPDTIIQVWR			6.13	2.6	2	
P07108	ACBP	Acyl_CoA_binding protein	3	3	7	1.75	1.92	0.00
		WDAWNELK			1.65	2.5	2	
		AKWDAWNELK			2.99	2.4	2	
		QATVGDINTERPGMLDFTGK			1.85	2.7	2	
P07195	LDHB	L_lactate dehydrogenase B chain	5	6	43	0.62	0.58	0.65
		IVADKDYSVTANSK			0.62	4.1	2	
		SADTLWDIQK			0.75	2.7	2	
		MVVESAYEVIK			1.10	4.3	2	
		LIAPVAEEEATVPNNK			0.47	3.1	2	

		LKDDEVAQLK			0.53	2.7	2	
P07205	PGK2	Phosphoglycerate kinase 2	2	3	24	1.41	0.91	0.17
		VSHVSTGGGASLELLEGK			0.95	5.4	2	
		LGDVYVNDAFGTAHR			1.46	4.0	2	
P07237	PDIA1	Protein disulfide_isomerase	3	3	3	0.92	1.23	0.43
		EADDIVNWLK			2.56	2.4	2	
		QFLQAAEAIDDIPFGITSNSDVFSK			0.79	3.7	3	
		VDATEESDLAQQYGVR			3.31	3.9	2	
P07339	CATD	Cathepsin D	10	32	53	2.57	0.85	0.05
		FDGILGMAYPR+Oxidation(6)			1.61	2.7	2	
		FDGILGMAYPR			4.64	3.8	2	
		AIGAVPLIQGEYMIPCEK+Oxidation(12)			1.44	3.9	2	
		DPDAQPGGELMLGGTDSK			10.16	4.9	2	
		VGFAEAAR			49.95	2.5	2	
		AYWQVHLDQVEVASGLTLCK			3.65	4.6	2	
		EGCEAIVDTGTSLMVGPVDEVR			3.58	4.2	2	
		AIGAVPLIQGEYMIPCEK			4.85	3.9	2	
		DPDAQPGGELMLGGTDSK+Oxidation(10)			8.91	5.0	2	
		EGCEAIVDTGTSLMVGPVDEVR+Oxidation(13)			4.52	5.1	2	
P07355	ANXA2	Annexin A2	2	5	30	1.33	0.75	1.00
		QDIAFAYQR			1.26	3.0	2	
		GVDEVTIVNILTNR			1.34	4.6	2	
P07357	CO8A	Complement component C8 alpha chain	6	10	51	0.77	0.29	0.00
		INVGGGLSGDHCK			0.85	3.0	2	
		LGSLGAACEQTQTEGAK			0.64	3.9	2	
		AIDEDCSQYEPIPGSQK			0.63	4.0	2	
		FGGTICSGDIWDQASCSSSTTCVR			0.77	4.5	2	
		HLVCNGDQDCLDGSDEDDCEDVR			0.45	6.7	3	
		CGPCFNNGVPILEGTSCR			0.88	3.5	2	
P07358	CO8B	Complement component C8 beta chain	3	3	13	0.68	0.50	0.00
		CEGFVCAQTGR			0.68	3.3	2	
		RLLCNGDNDCGDQSDEANCR			0.45	4.2	3	
		CDCICPVGSQGLACEVSYR			0.73	4.4	2	
P07360	CO8G	Complement component C8 gamma chain	3	7	37	1.07	0.31	0.95
		QLYGDTGVLGR			0.83	2.8	2	
		VQEAHLTEDQIFYFPK			1.07	4.2	2	
		SLPVSDSVLSGFEQR			1.06	4.5	2	
P07437	TBB5	Tubulin beta chain	9	11	36	1.24	0.46	0.14
		ISVYYNEATGGK			1.21	2.6	2	
		ISEQFTAMFR			0.65	3.4	2	
		YLTVAAVFR			0.81	2.5	2	
		AILVDLEPGTMDSVR			1.46	3.9	2	
		ALTVPELTQQVFDAK			1.58	2.9	2	
		EIVHIQAGQCGNQIGAK			0.49	4.6	2	
		EVDEQMLNVQNK			0.34	3.8	2	
		IMNTFSVVPSPK			0.64	3.6	2	
		SGPFGQIFRPDNFVFGQSGAGNNWAK			0.53	6.7	3	
P07602	SAP	Proactivator polypeptide	2	2	2	1.04	1.05	0.62
		LVGYLDR			4.76	2.3	2	
		GCSFLPDPYQK			1.03	2.3	2	

P07686	HEXB	Beta_hexosaminidase subunit beta	2	2	2	1.56	1.66	0.27
		GSIVWQEVFDDK			1.56	3.4	2	
		GIAAQPLYAGYCNHENM			1.52	2.4	2	
P07737	PROF1	Profilin_1	6	13	109	1.32	0.50	0.00
		STGGAPTFNVTVTK			1.80	3.6	2	
		DSPSVWAAVPGK			1.83	2.7	2	
		DSLLQDGEFSMDLR+Oxidation(10)			1.39	3.3	2	
		DSLLQDGEFSMDLR			1.30	4.8	2	
		TFVNITPAEVGVLVGK			1.71	4.7	2	
		SSFYVNGLTLGGQK			1.43	4.3	2	
P07858	CATB	Cathepsin B	4	5	16	6.86	12.65	0.22
		HYGYNSYSVSNSEK			16.23	4.7	2	
		SGVYQHVTGEMMGGHAIR			10.43	4.4	3	
		GQDHCGIESEVVAGIPR			17.08	5.1	2	
		ICEPGYSPTYK			5.59	3.2	2	
P07900	HS90A	Heat shock protein HSP 90_alpha	9	16	49	1.24	0.48	1.00
		HIYYITGETK			1.27	3.4	2	
		DQVANSAFVER			1.25	2.9	2	
		YYTSASGDEMVSLK			1.19	3.2	2	
		NPDDITNEEYGEFYK			0.96	4.5	2	
		TLTIVDTGIGMTK			1.31	3.8	2	
		HLEINPDHSIIETLR			1.17	3.8	2	
		YYTSASGDEMVSLK+Oxidation(9)			0.98	3.3	2	
		ELHINLIPNKQDR			0.89	2.9	2	
		RAPFDLFENR			0.61	2.6	2	
P07988	PSPB	Pulmonary surfactant_associated protein B	8	14	60	0.89	0.27	0.00
		GALAVAVAQVCR			0.63	3.6	2	
		VVPLVAGGICQCLAER			0.55	4.7	2	
		QFVEQHTPQLLTLVPR			0.70	3.9	3	
		GWDAHTTCQALGVCGTMSSPLQCIHSPDL+Oxidation(16)			1.00	5.7	3	
		GWDAHTTCQALGVCGTMSSPLQCIHSPDL			0.83	5.9	3	
		FLEQECNVLPLK			0.96	3.9	2	
		YSVILLDTLLGR			0.25	3.1	2	
		KFLEQECNVLPLK			1.09	3.1	2	
P07998	RNAS1	Ribonuclease pancreatic	5	11	27	0.63	0.19	0.00
		HIIVACEGSPYVPVHFDASVEDST			0.68	3.9	3	
		QHMDSDSSPSSSSTYCNQMMR+Oxidation(19)			0.23	4.3	3	
		QHMDSDSSPSSSSTYCNQMMR+Oxidation(18)			0.23	4.2	3	
		QHMDSDSSPSSSSTYCNQMMR			0.19	4.6	3	
		CKPVNTFVHEPLVDVQNVCFQEK			0.54	4.4	4	
P08107	HSP71	Heat shock 70 kDa protein 1A/1B	7	11	43	1.13	0.44	0.67
		YKAEDEVQR			1.24	3.7	3	
		LVNHFVEEFK			1.03	2.5	2	
		AQIHDLVLVGGSTR			1.16	3.7	2	
		LLQDFFNGR			1.13	2.6	2	
		ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK			1.76	5.0	3	
		NQVALNPQNTVFDAK			1.10	4.5	2	
		DAGVIAGLNVLR			1.17	3.6	2	
P08185	CBG	Corticosteroid_binding globulin	6	9	38	0.81	0.37	1.00
		HLVALSPK			1.01	2.3	2	

		SETEIHQGFQHLHQLFAK			1.05	4.0	3	
		EENFYVDETTVVK			0.80	3.1	2	
		GTWTQPFDLASTR			0.98	3.0	2	
		WSAGLTSSQVDLYIPK			0.70	3.3	2	
		MNTVIAALSR			1.24	2.5	2	
P08238	HS90B	Heat shock protein HSP 90_beta	11	20	68	1.31	0.35	0.98
		EDQTEYLEER			0.77	3.0	2	
		EQVANSAFVER			1.29	2.7	2	
		HFSVEGQLEFR			1.44	2.8	2	
		ADLINNLGTIAK			1.39	3.6	2	
		TLTLVDTGIGMTK			1.31	3.8	2	
		GVVDSEDLPLNISR			1.09	4.1	2	
		YIDQEELNK			0.72	2.6	1	
		HLEINPDHPIVETLR			1.68	3.9	3	
		SLTNDWEDHLAVK			1.23	3.3	2	
		HNDDEQYAWESSAGGSFTVR			0.73	5.7	2	
		NPDDITQEEYGEFYK			0.70	4.2	2	
P08571	CD14	Monocyte differentiation antigen CD14	3	4	18	0.97	0.55	0.98
		LTVGAAQVPAQLLVGALR			0.92	4.4	2	
		ITGTMPPLPLEATGLALSSLR+Oxidation(4)			1.23	2.5	2	
		ITGTMPPLPLEATGLALSSLR			1.03	2.6	2	
P08603	CFAH	Complement factor H	15	26	129	0.97	0.23	0.99
		TGESVEFVCK			0.96	2.8	2	
		LSYTCEGGFR			1.04	2.6	2	
		AGEQVTYTCATYYK			0.99	4.8	2	
		IVSSAMEPDREYHFGQAVR			0.71	3.7	3	
		LGYVTADGETSGSITCGK			1.13	4.6	2	
		SPPEISHGVVAHMSDSYQYGEEVTYK			1.26	5.0	3	
		SSNLIILEEHLK			1.12	3.5	2	
		NTEILTGSWSDQTYPEGTQAIYK			1.04	4.6	2	
		TDCLSLPSFENAIPMGEK			1.10	3.2	2	
		SITCIHGVWTQLPQCVAIDK			1.29	4.1	3	
		WSSPPQCEGLPCK			0.88	2.8	2	
		KGEWVALNPLR			0.96	3.2	2	
		AVYTCNEGYQLLGEINYR			1.99	2.6	2	
		SSIDIENGFISESQYTYALK			1.24	4.1	2	
		SPDVINGSPISQK			1.12	3.2	2	
P08637	FCG3A	Low affinity immunoglobulin gamma Fc region receptor III_A	2	2	19	0.77	0.42	0.11
		YFHHNSDFYIPK			0.71	3.7	3	
		AVVFLEPQWYR			0.86	3.3	2	
P08670	VIME	Vimentin	26	40	123	3.12	0.55	0.03
		DGQVINETSQHHDDLE			2.10	3.4	2	
		FADLSEAANR			12.98	3.1	2	
		VELQELNDR			3.13	2.9	2	
		SLYASSPGGVYATR			3.69	4.3	2	
		QVQSLTCEVDALK			11.87	4.1	2	
		LHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR			4.96	5.8	4	
		ISLPLPNFSSLNLR			0.41	2.5	2	
		EEAENTLQSFR			8.91	3.1	2	
		LGDLYEEEMR			7.75	3.6	2	

		NLQEAEEWYK			25.68	3.2	2	
		DNLAEDIMR			12.82	2.9	2	
		KVESLQEEIAFLK			2.43	3.9	2	
		EKLQEEMLQR			21.06	2.7	2	
		TNEKVELQELNDR			6.37	3.0	2	
		LQDEIQNMKEEMAR			13.26	3.3	2	
		EYQDLLNVK			15.95	2.3	1	
		KVESLQEEIAFLKK			5.53	3.7	3	
		ETNLDSLPLVDTHSK			10.24	3.9	2	
		MALDIEIATYR			2.08	3.8	2	
		LLQDSVDFSLADAINTEFK			1.37	2.6	2	
		KLLEGEESR			11.57	2.5	2	
		LQEEMLQR+Oxidation(4)			18.73	2.6	2	
		LQEEMLQR			14.59	2.5	2	
		DNLAEDIMR+Oxidation(7)			10.64	2.4	2	
		KLHEEEIQELQAQIQEQHVQIDVDVSKPDLTAALR			4.94	4.6	4	
P08697	A2AP	Alpha_2_antiplasmin	2	2	4	0.81	0.71	0.49
		LGNQEPGGQTALK			0.58	2.4	2	
		LCQDLGPGAFR			0.81	2.3	2	
P08727	K1C19	Keratin_ type I cytoskeletal 19	2	2	2	1.15	2.85	0.99
		IVLQIDNAR			1.02	2.5	2	
		TKFETEQALR			1.15	2.5	2	
P08758	ANXA5	Annexin A5	7	12	56	2.10	0.63	0.00
		LYDAYELK			1.35	2.4	2	
		VLTEIIASR			2.27	2.6	2	
		GTVTDFPGFDER			2.01	3.3	2	
		FITIFGTR			1.68	2.4	2	
		SEIDLFNIR			2.92	2.4	2	
		DLLDDLKSELTGK			2.10	4.0	2	
		YMTISGFQIEETIDR			1.43	3.5	2	
P09104	ENOG	Gamma_enolase	2	3	17	1.70	1.36	0.00
		IEEELGDEAR			1.64	2.6	2	
		FGANAILGVSLAVCK			2.15	4.2	2	
P09210	GSTA2	Glutathione S_transferase A2	5	6	32	0.87	0.57	0.90
		SHGQDYLVGNK			0.47	3.6	2	
		SAEDLDKLR			0.38	2.7	2	
		NDGYLMFQQVPMVEIDGMK+Oxidation(17)			0.89	3.6	2	
		NDGYLMFQQVPMVEIDGMK+Oxidation(11)			0.92	3.4	2	
		NDGYLMFQQVPMVEIDGMK			1.83	4.4	2	
P09211	GSTP1	Glutathione S_transferase P	9	19	113	1.32	0.45	0.00
		ASCLYGQLPK			1.18	3.1	2	
		ALPGQLKPFETLLSQNQGGK			1.28	4.3	3	
		AFLASPEYVNLPINGNGK			1.20	5.1	2	
		DQQEAALVDMVNDGVEDLR			1.73	6.4	2	
		MLLADQGQSWK+Oxidation(0)			1.37	2.9	2	
		MLLADQGQSWK			1.38	3.5	2	
		EEVVTVETWQEGSLK			1.24	4.5	2	
		YISLIYTNYEAGKDDYVK			0.73	4.9	2	
		FQDGDLTLYQSNTILR			2.84	4.7	2	
P09228	CYTT	Cystatin_SA	3	3	4	0.07	0.12	0.39

		ATEDEYYR			0.06	2.6	2	
		SQPNLDTCAFHEQPELQK			0.03	4.8	2	
		IIEGGIYDADLNDER			0.19	4.7	2	
P09382	LEG1	Galectin_1	2	3	23	1.97	2.04	0.46
		FNAHGDANTIVCNSK			2.57	4.3	2	
		DSNNLCLHFNPR			1.46	3.2	2	
P09467	F16P1	Fructose_1_6_bisphosphatase 1	8	14	58	1.60	0.99	0.02
		AGIAHLYGIAGSTNVTGDQVK			1.47	5.4	2	
		DFDPAVTEYIQR			2.20	3.1	2	
		LLYECNPMAYVMEK			2.35	3.6	2	
		GTGELTQLLNSLCTAVK			2.23	4.4	2	
		KAGIAHLYGIAGSTNVTGDQVK			1.87	4.8	2	
		EAVLDVIPTDIHQR			3.29	4.4	2	
		STDEPSEKDALQPGR			2.68	2.7	2	
		TLVYGGIFLYPANKK			2.56	2.5	2	
P09525	ANXA4	Annexin A4	4	5	8	1.36	0.91	0.81
		VLVSLSAGGRDEGNYLDDALVR			1.62	3.9	3	
		VLVSLSAGGR			1.19	2.6	2	
		AASGFNAMEDAQTLR			1.32	3.7	2	
		DEGNYLDDALVR			1.04	3.0	2	
P09668	CATH	Pro_cathepsin H	6	13	47	1.17	0.59	1.00
		VNHAVLAVGYGEK			1.28	3.8	3	
		TPDKVNHAVLAVGYGEK			1.28	3.8	3	
		GIMGEDTYPYQGK			1.13	3.7	2	
		GIMGEDTYPYQGK+Oxidation(2)			0.94	3.1	2	
		NMCGLAACASYPIPLV+Oxidation(1)			1.25	2.3	2	
		NMCGLAACASYPIPLV			1.09	2.7	2	
P09960	LKHA4	Leukotriene A_4 hydrolase	14	30	125	1.02	0.20	0.16
		DGETPDPEDPSR			1.09	2.5	2	
		LTYTAEVSVPK			1.57	3.1	2	
		EDDLNSFNATDLK			1.37	4.1	2	
		TLTGTAALTVQSQEDNLR			0.90	5.6	2	
		SAYEFSETESMLK			1.09	3.3	2	
		HFNALGGWGELQNSVK			0.97	4.0	2	
		SSALQWLTPEQTSGK			1.76	4.6	2	
		SLSNVIAHEISHSWTGNLVTNK			1.25	4.1	3	
		WEDAIPLALK			1.31	2.8	2	
		GSPMEISLPIALSK			1.90	3.8	2	
		LVVDLTDIDPDVAYSSVPYEK			1.13	4.3	2	
		DLSSHQLNEFLAQTLQR			0.94	3.6	3	
		EHPYLFSQCQAIHCR			2.20	3.5	2	
		GSPMEISLPIALSK+Oxidation(3)			2.42	3.3	2	
P09972	ALDOC	Fructose_bisphosphate aldolase C	3	4	8	1.91	1.31	0.05
		GVVPLAGTDGETTTQGLDGLSER			2.06	5.3	2	
		YASICQQNGIVPIVEPEILPDGDHDLKR			1.85	4.5	3	
		YASICQQNGIVPIVEPEILPDGDHDLK			1.61	4.4	3	
P0C0L5	CO4B	Complement C4_B	47	112	708	0.65	0.08	0.00
		SHALQLNNR			0.61	3.0	2	
		VDVQAGACEGK			0.62	3.8	2	
		LGQYASPTAK			0.46	2.5	2	

		LVNGQSHISLSK			0.47	3.7	2	
		SCGLHQLLR			0.70	3.5	2	
		CSVFYGAPSK			0.69	3.0	2	
		ITQVLHFTK			0.68	2.9	2	
		AEFQDALEK			0.53	3.0	2	
		EMSGSPASGIPVK			1.43	2.6	2	
		LELSVDGAK			0.61	2.0	1	
		VEYGFQVK			0.72	3.0	2	
		VLSLAQEQVGGSPEK			0.53	5.3	2	
		TEQWSTLPPETK			0.47	3.7	2	
		VDFTLSSER			0.70	3.2	2	
		MRPSTDTITVMVENSHGLR+Oxidation(0)			0.70	5.0	3	
		MRPSTDTITVMVENSHGLR+Oxidation(10)			0.70	3.6	3	
		KYVLPNFEVK			0.59	3.9	3	
		VGDTLNLNLR			0.30	3.2	2	
		MRPSTDTITVMVENSHGLR			0.73	5.9	3	
		LLATLCSAEVCQCAEGK			0.68	5.2	3	
		GHLFLQTDQPIYNPGQR			0.49	5.6	2	
		ADGSYAAWLSR			0.73	3.6	2	
		GLCVATPVQLR			0.74	2.6	2	
		EGAIHREELVYELNPLDHR			0.64	5.4	3	
		AEMADQASAWLTR			1.51	2.8	2	
		GSFEFPVGDAVSK			0.58	3.6	2	
		EELVYELNPLDHR			0.76	3.4	2	
		LNMGITDLQGLR			0.57	3.9	2	
		GLEEELQFSLGSK			0.80	4.7	2	
		LQETSNWLLSQQQADGSFQDLSPVIHR			0.85	6.4	3	
		TLEIPGNSDPNMIPDGDFNSYVR			0.85	3.8	2	
		DFALLSLQVPLKDAK			0.98	3.6	2	
		DFALLSLQVPLK			0.51	4.4	2	
		VTASDPLDTLGSEGALSPGGVASLLR			0.83	6.7	3	
		GLQDEDGYR			0.37	3.0	2	
		DHAVDLIQK			0.44	2.8	2	
		LLLFSPSVVHLGVPLSVGVQLQDVPR			0.32	6.0	3	
		TYNVLDMK			0.42	3.3	2	
		YVLPNFEVK			0.72	2.1	1	
		YIYGKPVQGVAYVR			0.84	4.0	2	
		VGLSGMAIADVTLLSGFHALR			0.48	4.4	3	
		YLDKTEQWSTLPPETK			0.41	3.8	2	
		LNMGITDLQGLR+Oxidation(2)			1.47	2.8	2	
		TLEIPGNSDPNMIPDGDFNSYVR+Oxidation(11)			0.61	3.4	2	
		ITPGKPYILTVPGHLDEMQLDIQAR			0.54	4.1	3	
		RCSVFYGAPSK			1.21	2.6	2	
		TTNIQGINLLFSSR			0.30	2.6	2	
P0C0S5	H2AZ	Histone H2A.Z	2	2	3	2.91	6.53	0.42
		AGLQFPVGR			3.22	2.6	2	
		HLQLAIR			2.51	2.4	2	
P0CG39	POTEJ	POTE ankyrin domain family member J	6	11	56	1.10	0.40	0.30
		RGILTLK			1.90	2.4	2	
		QEYDESGPSIVHR			1.76	3.7	3	

		IWHHTFYNELR			1.03	3.7	3	
		KDLIVMLRDTDVNK			1.42	2.4	2	
		QMLKISSENSNPEQDLK			2.16	2.7	2	
		AGFAGDDAPR			1.18	3.2	2	
P10253	LYAG	Lysosomal alpha_glucosidase	3	3	3	1.39	2.58	0.54
		VTSEGAGLQLQK			14.40	3.6	2	
		AGYIIPLQGPGLTTTESR			11.40	4.4	2	
		NHNSLLSLPQEPYSFSEPAQQAMR			1.28	5.4	3	
P10599	THIO	Thioredoxin	2	3	31	1.49	1.05	0.17
		EKLEATINELV			1.50	3.4	2	
		TAFQEALDAAGDK			1.19	3.9	2	
P10643	CO7	Complement component C7	9	10	39	0.86	0.44	0.97
		EQTMSECEAGALR			0.63	3.5	2	
		SSGWHFVVK			0.87	2.5	2	
		SCVGETTESTQCEDEELEHLR			0.79	4.1	3	
		NVVYTCNEGYSLIGNPVAR			1.11	4.8	2	
		LSGNVLSYTFQVK			0.85	3.1	2	
		LIDQYGTHYLQSGSLGGEYR			1.17	5.0	2	
		YSAWAESVTNLPQVIK			1.19	3.2	2	
		SLVCNGDSDCDEDSADEDRCEDSER			0.37	4.1	3	
		DGFVQDEGTMFPVGK			0.66	2.8	2	
P10809	CH60	60 kDa heat shock protein_ mitochondrial	2	2	3	9.56	19.56	0.30
		VGGTSDVEVNEK			11.70	2.5	2	
		TVIIEQSWGSPK			7.46	2.8	2	
P10909	CLUS	Clusterin	6	15	105	0.92	0.35	0.93
		KYNELLK			0.74	2.5	2	
		KTLLSNLEEAKK			1.63	4.8	3	
		EILSVDCSTNNPSQAK			0.98	4.0	2	
		ELDESLQVAER			0.84	3.4	2	
		VTTVASHTSDSDVPSGVTEVVVK			0.74	6.1	2	
		LFDSDPITVTVPVEVSR			1.04	5.3	2	
P11021	GRP78	78 kDa glucose_regulated protein	6	6	8	2.65	2.46	0.49
		TWNDPSVQQDIK			2.05	3.2	2	
		TKPYIQVDIGGGQTK			1.35	4.1	2	
		NQLTSNPENTVFDAK			1.92	2.9	2	
		SQIFSTASDNQPTVTIK			3.64	3.9	2	
		DAGTIAGLNVMR			2.63	3.6	2	
		ELEEIVQPIISK			4.94	2.8	2	
P11142	HSP7C	Heat shock cognate 71 kDa protein	13	22	144	1.37	0.33	0.97
		VEIIANDQGNR			1.40	3.4	2	
		SQIHDIVLVGGSTR			1.06	4.1	2	
		TTPSYVAFTDTER			1.54	3.4	2	
		TVTNAVVTVPAYFNDSQR			1.43	2.6	2	
		DAGTIAGLNVLR			1.73	3.7	2	
		IINEPTAAAIAYGLDK			1.41	4.4	2	
		FEELNADLFR			1.29	3.1	2	
		SFYPEEVSSMVLTK			1.05	2.7	2	
		SINPDEAVAYGAAVQAAILSGDK			1.08	6.1	2	
		STAGDTHLGGEDFDNR			1.38	3.5	2	
		NQVAMNPTNTVFDAK+Oxidation(4)			1.40	3.3	2	

		NQVAMNPTNTVFDAK			0.99	3.8	2	
		QTQTFTTYSDNQPGVLIQVYEGER			1.17	4.1	3	
P11182	ODB2	Lipoamide acyltransferase component of branched_chain alpha_keto acid dehydrogenase complex_ mitochondrial	2	2	4	1.78	1.21	0.37
		SYLENPAFMLLDLK+Oxidation(8)			0.31	2.2	1	
		DMTVPILVSKPPVFTGK+Oxidation(1)			1.88	2.4	2	
P11684	UTER	Uteroglobin	3	9	133	1.25	0.91	0.99
		KLVDTLPQKPR			1.25	4.0	3	
		LVDTLPQKPR			1.00	3.2	2	
		IAQSSLCN			0.65	1.9	1	
P11686	PSPC	Pulmonary surfactant_associated protein C	3	3	4	0.83	0.36	0.37
		EVLMESPPDYSAAPR+Oxidation(3)			1.06	2.6	2	
		EVLMESPPDYSAAPR			0.86	2.6	2	
		IAPESIPSLEALNR			0.12	2.5	2	
P12273	PIP	Prolactin_inducible protein	2	3	17	1.12	2.44	1.00
		TVQIAAVVDVIR			1.15	4.2	2	
		ELGICPDDAAVIPIK			0.98	3.3	2	
P12277	KCRB	Creatine kinase B_type	4	5	16	0.97	0.49	0.93
		LAVEALSSLDGDLAGR			1.07	4.3	2	
		FCTGLTQIETLFK			0.56	2.5	2	
		GTGGVDTAAVGGVFDVSNADR			0.79	4.4	2	
		DLFDPIIEDR			0.12	2.5	2	
P12429	ANXA3	Annexin A3	7	12	36	3.34	0.46	0.00
		GIGTDEFTLNR			3.51	2.9	2	
		SEIDLLDIR			4.15	2.6	2	
		SLGDDISSETSGDFRK			3.79	2.4	2	
		ALLTLADGR			3.20	2.4	2	
		DYPDFSPSVDAEAIQK			2.13	3.8	2	
		SLGDDISSETSGDFR			0.76	3.5	2	
		MLISILTER			5.42	2.5	2	
P12814	ACTN1	Alpha_actinin_1	2	2	2	2.30	1.54	0.29
		ETADTDTADQVMASFK			1.22	3.2	2	
		ICDQWDNLGALTQK			3.98	3.8	2	
P12830	CADH1	Cadherin_1	2	4	5	0.81	0.48	0.31
		DTANWLEINPDTGAISTR			0.81	3.6	2	
		NTGVISVVTTGLDR			0.65	2.4	2	
P13489	RINI	Ribonuclease inhibitor	7	8	28	0.77	0.68	0.96
		ELTVSNNDINEAGVR			1.75	3.2	2	
		ELSLAGNELGDEGAR			1.37	4.1	2	
		VNPALAELNLR			0.76	3.3	2	
		ELCQGLGQPGSVLR			1.53	3.3	2	
		LESCGVTSDNCR			0.92	2.9	2	
		LDDCGLTEAR			1.40	2.4	2	
		SCSFTAACCSHFSSVLAQNR			1.31	3.7	3	
P13639	EF2	Elongation factor 2	6	7	8	0.93	0.43	0.07
		IKPVLMMNKMDR+Oxidation(9)			0.33	1.9	1	
		ETVSEESNVLCLSK			1.08	3.4	2	
		AYLPVNESFGFTADLR			1.24	2.8	2	
		TFCQLILDPIFK			0.77	2.8	2	
		IWCFGPDGTGPNILTDITK			1.23	4.2	2	

		DSVVAGFQWATK			4.22	3.4	2	
P13645	K1C10	Keratin_ type I cytoskeletal 10	12	19	47	2.47	0.46	0.00
		LENEIQTYR			1.66	2.4	2	
		LKYENEVALR			3.14	3.1	2	
		ELTTEIDNNIEQISSYK			1.84	4.7	2	
		ALEESNYELEGK			2.93	3.5	2	
		VLDELTLTK			2.83	2.3	2	
		GSLGGGFSSGGFSGGSFSR			0.46	4.1	2	
		QSLEASLAETEGR			3.30	2.8	2	
		SLLEGEGSSGGGGR			4.85	2.8	2	
		SQYEQLAEQNR			2.13	3.5	2	
		NQILNLTTDNANILLQIDNAR			1.65	5.8	3	
		IRLENEIQTYR			2.98	3.0	2	
		SQYEQLAEQNRK			1.87	2.9	2	
P13667	PDIA4	Protein disulfide_isomerase A4	2	2	2	2.55	3.58	0.37
		IDATSASVLASR			5.10	3.8	2	
		VEGFPTIYFAPSGDK			1.93	4.0	2	
P13671	CO6	Complement component C6	5	7	10	1.05	0.56	0.96
		VPANLENVGFEVQTAEDDLKTDFYK			1.05	3.7	3	
		TLNICEVGTIR			0.98	2.6	2	
		IGESIELTCPK			1.06	2.4	2	
		SVLRPSQFGGQPCTAPLVAFQPCIPSK			1.78	4.1	3	
		GEVLDNSFTGGICK			1.07	2.9	2	
P13796	PLSL	Plastin_2	17	26	116	1.23	0.34	0.48
		EGICAIGGTSEQSSVGTQHSYSEEEK			2.06	4.6	3	
		IGNFSTDIK			1.62	2.7	2	
		QFVTATDVVR			1.93	2.7	2	
		AYYHLLEQVAPK			1.60	4.2	3	
		YPALHKPENQDIDWGALEGETR			1.70	4.6	3	
		NWMNSLGVNPR			1.37	2.6	2	
		FSLVGIGGQDLNEGNR			1.46	4.6	2	
		HVIPMNPNTNDLFNAVGDGIVLCK+Oxidation(4)			1.03	4.2	3	
		GDEEGVPAVVIDMSGLR			1.54	4.5	2	
		VNDDIIVNWVNETLR			1.25	4.8	2	
		VYALPEDLVEVNPK			1.45	3.2	2	
		AECMLQQAER			0.86	2.9	2	
		HVIPMNPNTNDLFNAVGDGIVLCK			1.31	3.5	3	
		YTLNILEEIGGGQK			1.51	3.6	2	
		TENLNDDEKLNNAK			0.77	4.0	2	
		WANYHLENAGCNK			3.32	3.9	2	
		GDEEGVPAVVIDMSGLR+Oxidation(12)			0.94	3.2	2	
P13797	PLST	Plastin_3	6	9	40	1.03	0.41	0.70
		KLENCNYAVELGK			1.82	3.9	2	
		YAFVNWINK			1.70	2.7	2	
		MINLSVPDTIDER			1.03	3.0	2	
		ANDDIIVNWVNR			0.77	3.2	2	
		MINLSVPDTIDER+Oxidation(0)			1.05	3.3	2	
		LENCNYAVELGK			1.22	2.9	2	
P13987	CD59	CD59 glycoprotein	2	4	27	0.68	0.53	0.07
		FEHCNFNDVTTR			0.87	4.0	2	

		LRENELTYYCCK			0.51	4.0	2	
P14550	AK1A1	Alcohol dehydrogenase [NADP_]	4	7	11	1.29	0.45	0.79
		GLEVTAYSPLGSSDR			1.26	4.1	2	
		VFDFTFSPEEMK			1.31	3.3	2	
		GLVQALGLSNFNSR			1.59	3.6	2	
		NADGTICYDSTHYK			0.89	3.5	2	
P14618	KPYM	Pyruvate kinase isozymes M1/M2	15	23	100	0.97	0.35	1.00
		GSGTAEVELKK			1.36	2.7	2	
		GSGTAEVELK			1.60	3.2	2	
		LNFSHGTHEYHAETIK			0.93	4.0	2	
		CCSGAIIVLTK			1.16	2.5	2	
		LDIDSPPITAR			0.94	3.2	2	
		KGVNLPGAAVDLPAVSEK			1.27	3.8	2	
		GVNLPGAAVDLPAVSEK			1.87	4.5	2	
		GADFLVTEVENGGSLGSK			1.53	4.9	2	
		RFDEILEASDGIMVAR			1.10	3.5	3	
		TATESFASDPILYRPVAVALDTK			1.05	3.5	3	
		LAPITSDPTEATAVGAVEASFK			1.07	3.9	2	
		AEGSDVANAVLDGADCIMLSGETAK			1.21	5.4	2	
		FDEILEASDGIMVAR			1.38	3.7	2	
		VNFAMNVGK			0.83	2.5	2	
		NTGIICTIGPASR			1.37	3.8	2	
P15090	FABP4	Fatty acid_binding protein_ adipocyte	3	7	28	1.61	1.14	0.21
		EVGVGFATR			1.75	2.8	2	
		STITLDGGVLVHVQK			1.35	4.0	2	
		EDDKLVVECVMK			2.15	2.5	2	
P15311	EZRI	Ezrin	5	7	47	0.98	0.54	1.00
		RKEDEVEEWQHR			1.16	4.6	3	
		ALQLEEER			0.68	2.4	2	
		QLLTLSSELSQAR			0.97	4.0	2	
		SQEQLAAELAEYTAK			0.91	4.8	2	
		THNDIIHNENMR+Oxidation(10)			0.75	3.4	2	
P15559	NQO1	NAD(P)H dehydrogenase [quinone] 1	3	4	7	0.84	1.61	0.98
		IQILEGWK			1.43	2.6	2	
		EGHLSPDIVAEQK			0.77	3.2	2	
		LKDPANFQYPAESVLAYK			0.83	4.0	3	
P15941	MUC1	Mucin_1	3	4	17	0.64	0.44	0.00
		NYGQLDIFPAR			0.70	3.1	2	
		EGTINVHDVETQFNQYK			0.93	3.6	2	
		VSAGNGGSSLSYTNPAVAATSANL			0.47	4.1	2	
P16070	CD44	CD44 antigen	5	10	38	0.56	0.22	0.00
		TEAADLCK			0.56	2.3	2	
		LVINSGNGAVEDR			0.71	2.8	2	
		ALSIGFETCR			0.55	3.3	2	
		YGFIEGHVVIPR			0.53	3.8	3	
		TNPEDIYPSNPTDDDVSSGSSSER			0.90	4.6	2	
P16152	CBR1	Carbonyl reductase [NADPH] 1	2	3	5	2.46	2.80	0.05
		LFSGDVVLTAR			2.34	2.5	2	
		EYGGLDVLVNNAGIAFK			2.50	3.9	2	
P17931	LEG3	Galectin_3	3	3	9	2.52	2.22	0.00

		GNDVAFHFNPR			1.69	2.4	2	
		IQVLVEPDHFK			2.74	2.6	2	
		QSVFPFESGKPFK			2.40	2.5	2	
P18065	IBP2	Insulin_like growth factor_binding protein 2	4	4	8	0.59	0.54	0.10
		HGLYNLK			0.77	2.4	2	
		LEGEACGVYTPR			0.59	2.6	2	
		GECWCVNPNTGK			0.47	2.5	2	
		LAACGPPPVAPPAAVAAVAGGAR			0.54	3.4	2	
P18136	KV313	Ig kappa chain V_III region HIC	3	19	158	0.97	0.19	0.00
		LLIYGASSR			0.79	3.3	2	
		ASQSVSSSYLAWYQQKPGQAPR			4.84	5.0	2	
		FSGSGSGTDFTLTISR			1.00	4.7	2	
P18669	PGAM1	Phosphoglycerate mutase 1	3	5	13	1.94	0.77	0.07
		HGESAWNLENR			1.94	3.4	2	
		YADLTEDQLPSCESLK			1.48	4.8	2	
		FSGWYDADLSPAGHEEAK			1.30	3.1	2	
P19652	A1AG2	Alpha_1_acid glycoprotein 2	3	6	74	0.79	0.40	0.32
		EHVAHLLFLR			0.57	2.9	2	
		TEDTIFLR			0.73	3.0	2	
		WFYIASAFR			0.92	3.7	2	
P19823	ITIH2	Inter_alpha_trypsin inhibitor heavy chain H2	10	14	36	1.52	0.40	0.98
		IQPSGGTNINEALLR			0.92	2.9	2	
		FLHVPDTFEGHFDGVPVISK			1.56	4.2	4	
		VQFELHYQEVK			0.99	2.8	2	
		AEDHFSVIDFNQNIR			1.23	3.8	3	
		NVQFNYPHTSVTDVTQNNFHNYFGGSEIVVAGK			1.55	4.9	4	
		AHVSFKPTVAQQR			0.83	2.7	2	
		MLADAPPQDPSCCSGALYYGSK			0.80	3.2	2	
		VVNNSPQPQNVVFDVQIPK			1.61	4.0	2	
		IYGNQDTSSQLK			1.16	3.4	2	
		FYNQVSTPLLR			1.08	2.3	2	
P19827	ITIH1	Inter_alpha_trypsin inhibitor heavy chain H1	8	15	79	1.02	0.35	0.13
		AAISGENAGLVR			1.08	3.1	2	
		FAHYVVTSQVVNTANEAR			0.98	4.3	3	
		QYYEGSEIVVAGR			0.99	3.6	2	
		GFSLDEATNLNGGLLR			1.77	4.7	2	
		GSLVQASEANLQAAQDFVR			1.20	5.9	2	
		NHMQYEIVIK			1.35	2.4	2	
		LDAQASFLPK			1.07	2.4	2	
		QAVDTAVDGVFIR			1.72	2.5	2	
P19971	TYPH	Thymidine phosphorylase	4	5	6	1.71	2.20	0.63
		FGGAAVFPNQEQAR			1.70	2.9	2	
		TLVGVGASLGLR			1.84	2.5	2	
		VSLVLAPALAACGCK			2.70	2.8	2	
		ALPLALVLHELGAGR			1.51	4.4	2	
P20061	TCO1	Transcobalamin_1	2	2	3	2.11	2.57	0.69
		GTSAVNVVLSLK			2.23	2.7	2	
		LVGIQIQTLMQK			0.78	2.7	2	
P20142	PEPC	Gastricsin	2	3	29	0.19	0.16	0.00
		SYYSVYDLGNNR			0.16	4.4	2	

		GLLGEFLR			0.21	2.5	2	
P20742	PZP	Pregnancy zone protein	6	8	38	1.64	0.82	0.14
		YGAATFTR			1.04	2.4	2	
		SSGSLLNNAIK			1.39	3.3	2	
		ATVLNYLPK			2.83	3.0	2	
		AGAFCLSEDAGLGISSTASLR			1.34	5.6	2	
		MVSGFIPLKPTVK			2.32	2.8	2	
		MVSGFIPLKPTVK+Oxidation(0)			1.09	3.0	2	
P20810	ICAL	Calpastatin	2	2	3	0.86	1.07	0.59
		DTMSDQALEALSASLGTR+Oxidation(2)			0.59	2.4	2	
		GTVPDDAVEALADSLGK			1.23	3.5	2	
P21333	FLNA	Filamin_A	25	33	65	7.12	0.47	0.00
		YGGPYHIGGSPFK			2.89	3.3	2	
		YTPVQQGPVGVNVTYGGDPIPK			2.81	4.8	2	
		DGSCGVAYVVQEPGDYEVSVK			1.18	3.4	2	
		AEAGVPAEFSIWTR			2.59	3.2	2	
		ALGALVDSCAPGLCPDWDSWDASKPVTNAR			2.41	4.2	3	
		AFGPGLQGGSAGSPAR			13.68	2.4	2	
		EAGAGGLAIAVEGPSK			4.75	4.1	2	
		VNQPASFAVSLNGAK			3.03	2.9	2	
		VQVQDNEGCPVEALVK			3.47	4.3	2	
		IANLQTDLSDGLR			2.98	3.2	2	
		GLVEPVDVVDNADGTQTVNYVPSR			0.91	5.7	2	
		SPFSVAVSPSLDLSK			3.88	3.2	2	
		AWGPGLEGGVVGK			3.19	2.5	2	
		VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR			1.57	5.3	3	
		VTAQGPGLEPSGNIANK			12.07	4.0	2	
		GAGTGGLGLAVEGPSEAK			4.37	3.4	2	
		DAGEGGLSLAIEGPSK			3.21	3.8	2	
		VDVGKDQEFTVK			5.69	2.8	2	
		TGVELGKPTHFTVNAK			1.69	2.8	2	
		YNEQHVPGSPFTAR			10.49	2.8	2	
		DVDIIDHHDNTYTVK			16.33	3.3	2	
		AYGPGIEPTGNMVK			5.73	2.7	2	
		LDVQFSGLTK			3.59	2.3	2	
		FNEEHIPDSPFVVPVASPSGDAR			4.11	3.7	2	
		IPEISIQDMTAQVTSPSGK			1.87	4.2	2	
P21695	GPDA	Glycerol_3_phosphate dehydrogenase [NAD_]_ cytoplasmic	2	2	2	1.20	1.08	0.25
		IVGGNAAQLAQFDPR			1.16	2.6	2	
		NVVAVGAGFCDGLGFGDNTK			1.46	2.7	2	
P21796	VDAC1	Voltage_dependent anion_selective channel protein 1	4	4	4	3.00	7.46	0.47
		SENGLEFTSSGSANTETTK			10.72	4.8	2	
		YQIDPDACFSAK			4.72	2.4	2	
		VNNSSLIGLGYTQTLKPGIK			2.38	2.5	2	
		WNTDNTLGTEITVEDQLAR			4.68	3.8	2	
P21980	TGM2	Protein_glutamine gamma_glutamyltransferase 2	7	10	34	5.02	4.96	0.19
		SEGTYCCGPVPVR			6.57	3.4	2	
		TVSYNGILGPECGTK			4.27	3.4	2	
		TVEIPDPVEAGEEVK			5.48	3.3	2	

		DLYLENPEIK			4.76	2.9	1	
		NYEASVDSLTFSVVTGPAPSQEAGTK			2.53	4.6	3	
		CDLELETNGR			5.43	2.9	2	
		YRDCLTESNLIK			11.92	3.0	2	
P22314	UBA1	Ubiquitin_like modifier_activating enzyme 1	6	7	17	1.06	0.49	0.02
		AENYDIPSADR			0.91	2.7	2	
		LQTSSVLVSGLR			0.68	2.9	2	
		AAVATFLQSVQVPEFTPK			1.63	2.5	2	
		ALPAVQQNNLDEDLIR			1.33	4.6	2	
		NEEDAAELVALAQAVNAR			0.80	4.1	2	
		DNPGVVTCLDEAR			1.35	2.9	2	
P22897	MRC1	Macrophage mannose receptor 1	17	28	106	1.26	0.24	0.63
		IYGTTDNLCSR			1.01	2.5	2	
		FQWHEAETYCK			1.15	3.4	2	
		ALGGDLASINNKEEQQTIWR			1.20	3.7	3	
		ACIGFGGNLVSIQNEK			1.06	4.5	2	
		SSLSYEDADCVVIIGGASNEAGK			1.09	5.0	2	
		GCEWPLGYICK			1.42	3.1	2	
		FEGSESLWNKDPLTSVSYQINSK			1.14	3.8	2	
		YFWTGLSDIQTK			1.42	3.5	2	
		TGIAGGLWDVLK			1.22	4.0	2	
		YTNWAADEPK			0.94	3.1	2	
		SQGPEIVEVEK			0.91	2.4	2	
		YLNWLPGSPSAEPGK			1.10	2.6	2	
		DYQYYFSK			2.10	2.2	1	
		NFGDLVSIQSESEKK			0.85	2.8	2	
		SALTWHQAR			0.70	2.5	2	
		NFGDLVSIQSESEK			0.45	3.0	2	
		WVSESQIMSVAFK			1.48	2.5	2	
P23141	EST1	Liver carboxylesterase 1	3	6	21	5.63	5.52	0.54
		EGYLQIGANTQAAQK			9.76	4.1	2	
		AISESGVALTSVLVK			7.29	4.7	2	
		KGDVKPLAEQIAITAGCK			2.38	5.0	3	
P23142	FBLN1	Fibulin_1	5	6	13	1.44	1.21	0.44
		TGYYFDGISR			1.67	3.0	2	
		MCVDVNECQR			1.43	3.3	2	
		CVDVDECAPPAEPCGK			0.80	4.2	2	
		SQETGDLDVGGLQETDK			1.46	3.8	2	
		SQETGDLDVGGLQETDKIIEVEEEQEDPYLNDR			4.54	4.9	3	
P23381	SYWC	Tryptophanyl_tRNA synthetase_ cytoplasmic	5	5	7	1.17	0.95	0.62
		AGNASKDEIDSAVK			0.54	3.4	2	
		MSASDPNSSIFLTDTAK			1.17	3.7	2	
		ISFPAIQAAPSFSNSFPQIFR			1.19	2.5	2	
		GIFGFTDSDCIGK			1.85	3.9	2	
		DLTLDQAYSYAVENAK			1.53	4.1	2	
P23528	COF1	Cofilin_1	5	17	132	1.56	0.48	0.00
		HELQANCYEEVKDR			1.90	6.2	3	
		HELQANCYEEVK			3.01	4.3	2	
		LGGSAVISLEGKPL			1.22	4.3	2	
		EILVGDVGQTVDDPYATFVK			0.63	5.5	2	

		NIILEEGKEILVGDVGQTVDDPYATFVK			1.89	7.4	3	
P25311	ZA2G	Zinc_alpha_2_glycoprotein	2	3	11	0.83	0.55	0.88
		EIPAWVPFDPAAQITK			0.84	3.2	2	
		AYLEEECPATLR			0.79	3.1	2	
P25705	ATPA	ATP synthase subunit alpha_ mitochondrial	7	7	8	5.14	2.43	0.43
		VVDALGNAIDGK			17.96	2.5	2	
		HALIIYDDLSK			8.37	2.3	2	
		TGTAEMSSILEER			2.70	3.0	2	
		ILGADTSVDLEETGR			1.16	3.1	2	
		TSIAIDTIINQK			17.03	2.7	2	
		TGAIVDVPVGEELLGR			4.09	3.1	2	
		GMSLNLEPDNVGVVVFGNDK			4.89	4.3	2	
P26038	MOES	Moesin	6	9	43	1.18	0.51	1.00
		ESEAVEWQQK			1.18	3.1	2	
		ALTSELANAR			1.33	2.6	2	
		TQEQLALEMAELTAR			1.20	4.8	2	
		TAMSTPHVAEPAENEQDEQDENGAEASADLR			0.82	5.5	3	
		IQVWHEEHR			1.20	2.4	2	
		KTQEQLALEMAELTAR			1.02	4.0	2	
P27487	DPP4	Dipeptidyl peptidase 4	2	2	4	0.43	0.38	0.00
		LGTFEVEDQIEAAR			0.49	3.4	2	
		VLEDNSALDK			0.40	2.4	2	
P27797	CALR	Calreticulin	3	4	5	1.02	0.78	0.51
		FYALSASFEPFSNK			1.02	3.7	2	
		HEQNIDCGGGYVK			3.24	3.4	2	
		IKDPDASKPEDWDER			11.15	3.9	2	
P27824	CALX	Calnexin	2	2	3	0.82	1.55	0.41
		EEEEEKEEEKDK			0.64	2.4	2	
		IVDDWANDGWGLK			2.88	2.5	2	
P28325	CYTD	Cystatin_D	2	4	4	0.08	0.07	0.71
		TLAGGIHATDLNDK			0.00	4.3	2	
		SQPNLDNCPFNDQPK			0.08	3.6	2	
P28838	AMPL	Cytosol aminopeptidase	3	3	9	1.04	1.15	1.00
		TIQVDNTDAEGR			0.93	2.9	2	
		LYGSGDQEAWQK			1.15	2.7	2	
		GVLFASGQNLAR			1.05	3.2	2	
P29401	TKT	Transketolase	6	8	17	0.88	0.51	0.73
		AVELAANTK			0.62	2.4	2	
		SKDDQVTVIGAGVTLHEALAAAELLK			1.25	4.9	4	
		ILATPPQEDAPSVDIANIR			0.94	4.2	2	
		TSRPENAIIYNNNEDFQVGQAK			1.00	4.8	3	
		SVPTSTVFYPSDGVATEK			0.98	3.1	2	
		LDNLVAILDINR			0.61	2.9	2	
P29508	SPB3	Serpin B3	4	7	36	0.95	0.68	1.00
		FKVEESYDLK			0.74	2.7	2	
		VLHFDQVTENTTGK			0.78	3.9	2	
		GLVLSGVLHK			1.16	2.9	2	
		FYQTSVESVDFANAPEESR			0.83	4.8	2	
P30040	ERP29	Endoplasmic reticulum resident protein 29	2	2	2	1.15	1.00	0.59
		FDTQYPYGEK			0.99	2.3	2	

		DGDFENPVPYTGAVK			8.06	3.5	2	
P30041	PRDX6	Peroxiredoxin_6	3	4	27	1.79	1.09	0.01
		DINAYNCEEPTEK			1.80	3.8	2	
		VVISLQLTAEK			1.74	3.0	2	
		LSILYPATTGR			0.89	2.3	2	
P30043	BLVRB	Flavin reductase	4	4	7	1.70	0.55	0.10
		TVAGQDAVIVLLGTR			0.66	3.0	2	
		NDLSPTTVMSEGAR			1.07	2.3	2	
		YVAVMPPHIGDQPLTGAYTVTLDGR+Oxidation(4)			1.38	3.8	3	
		YVAVMPPHIGDQPLTGAYTVTLDGR			1.90	3.6	3	
P30044	PRDX5	Peroxiredoxin_5_ mitochondrial	9	24	144	0.85	0.26	0.00
		LLADPTGAFGK			0.62	2.7	2	
		THLPGFVEQAEALK			1.18	3.8	3	
		FSMVVQDGIVK			0.78	3.6	2	
		VNLAELFK			1.17	2.9	2	
		VGDAIPAVEVFEGEPGNK			0.75	5.0	2	
		GVLFGVPGAFTPGCSK			1.41	4.4	2	
		ETDLLLDDSLVSIFGNR			1.03	4.4	2	
		ALNVEPDGTGLTCSLAPNIISQL			1.05	4.3	2	
		FSMVVQDGIVK+Oxidation(2)			0.93	3.7	2	
P30048	PRDX3	Thioredoxin_dependent peroxide reductase_ mitochondrial	2	4	14	0.25	0.57	0.25
		DLSLDDFK			0.25	2.2	1	
		DYGVLLEGSGLALR			19.77	3.6	2	
P30050	RL12	60S ribosomal protein L12	2	2	2	0.86	1.04	0.14
		EILGTAQSVGCNVDGR			0.83	3.0	2	
		CTGGEVGATSALAPK			2.47	2.3	2	
P30086	PEBP1	Phosphatidylethanolamine_binding protein 1	4	7	45	1.90	0.95	0.00
		NRPTSISWDGLDSGK			2.07	4.1	2	
		GNDISSGTVLSDYVGSGPPK			1.90	5.2	2	
		WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK			2.25	4.9	4	
		LYTLVLTDPDAPSR			1.42	3.3	2	
P30740	ILEU	Leukocyte elastase inhibitor	6	8	42	1.09	0.53	1.00
		KIEEQLTLEK			1.19	3.5	2	
		LGVQDLFNSSK			1.13	3.1	2	
		HNSSGSILFLGR			1.07	2.6	2	
		TYGADLASVDFQHASEDAR			0.92	4.3	2	
		IEEQLTLEK			0.97	2.7	2	
		LEESYTLNSDLAR			0.81	2.9	2	
P30838	AL3A1	Aldehyde dehydrogenase family 3 member A1	9	13	58	3.33	0.89	0.00
		LIQEQEQELVGALAADLHK			5.27	5.8	3	
		SLEEAIQFINQR			5.06	3.6	3	
		IQQLEALQR			3.72	3.3	2	
		NCDLDVACR			3.30	2.6	2	
		VMGLIEGQK			4.16	2.7	2	
		FDHILYTGSTGVGK			5.68	3.3	2	
		SCLVRPLMNDEGLK			0.35	3.1	2	
		LPEWAADEPVEK			3.53	3.4	2	
		FMNSGQTCVAPDYILCDPSIQNQIVEK			2.98	3.5	3	
P31146	COR1A	Coronin_1A	2	2	4	1.51	1.90	0.75

		AAPEASGTPSSDAVSR			0.40	3.9	2	
		KLQATVQELQK			1.88	2.5	2	
P31946	1433B	14_3_3 protein beta/alpha	3	4	29	1.36	1.27	1.00
		AVTEQGHELSNEER			0.97	4.5	2	
		YLSEVASGDNK			1.23	2.7	2	
		YLIPNATQPESK			1.37	2.6	2	
P32119	PRDX2	Peroxiredoxin_2	3	7	31	1.53	0.86	1.00
		QITVNDLPVGR			1.53	2.7	2	
		KEGGLGPLNIPLLADVTR			0.93	4.8	2	
		EGGLGPLNIPLLADVTR			0.89	3.8	2	
P32455	GBP1	Interferon_induced guanylate_binding protein 1	2	2	4	2.17	3.53	0.20
		IMKNEIQDLQTK+Oxidation(1)			2.06	2.8	2	
		TLSGGIQVNGPR			3.31	2.4	2	
P33241	LSP1	Lymphocyte_specific protein 1	2	2	4	1.14	0.70	0.26
		QQHEGAQGALDSGEPPQCR			1.06	3.9	3	
		WETGEVQAQSAAK			6.67	2.5	2	
P35237	SPB6	Serpin B6	3	4	12	1.15	0.94	1.00
		IAELLSPGSVDPLTR			1.16	3.2	2	
		ADFSGMSQTDLSLSK			0.92	3.2	2	
		GNTAAQMAQILSFNK			1.00	2.8	2	
P35241	RADI	Radixin	3	5	18	0.98	0.45	1.00
		RKPDTIEVQQMK+Oxidation(10)			0.99	3.7	3	
		RKPDTIEVQQMK			0.98	3.7	2	
		IGFPWSEIR			0.98	3.2	2	
P35247	SFTPD	Pulmonary surfactant_associated protein D	8	32	330	0.41	0.11	0.00
		NEAAFLSMTDSK+Oxidation(7)			0.46	4.3	2	
		KVELFPNGQSVGEK			0.44	4.4	2	
		VELFPNGQSVGEK			0.35	2.9	2	
		NEAAFLSMTDSK			0.44	4.5	2	
		GESGLPDVASLR			0.39	3.3	2	
		SAAENAALQQLVVAK			0.41	5.6	3	
		QQVEALQGQVQHLQAAFSQYK			0.74	4.5	3	
		TAGFVKPFTEAQLLCTQAGGQLASPR			0.57	5.1	2	
P35527	K1C9	Keratin_ type I cytoskeletal 9	4	5	10	1.71	1.13	0.04
		GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK			1.39	7.8	3	
		DIENQYETQITQIEHEVSSSGQEVQSSAK			1.84	3.8	3	
		GGSGGSYGGGGSGGGYGGGSGSR			1.35	3.6	2	
		VQALEEANNDLENK			1.96	3.7	2	
P35579	MYH9	Myosin_9	19	30	69	1.82	0.29	0.16
		IAEFTTNLTEEEEK			1.21	3.8	2	
		QEEEMMAKEEELVK			0.96	2.4	2	
		EQADFAIEALAK			1.26	3.0	2	
		LQVELDNVTGLLSQSDSK			1.14	5.1	2	
		QLLQANPILEAFGNAK			1.86	3.7	2	
		VISGVLQLGNIVFK			1.26	3.9	2	
		IIGLDQVAGMSETALPGAFK			1.74	3.7	2	
		NFINNPLAQADWAAK			1.36	4.5	2	
		ELEDATETADAMNR			0.87	3.4	2	
		THEAQIQEMR+Oxidation(8)			0.80	2.5	2	
		RQLEEAEEEAQR			3.28	3.2	2	

		IAQLEEQLDNETK			1.90	3.6	2	
		TQLEELEDELQATEDAK			1.18	4.6	2	
		IIGLDQVAGMSETALPGAFK+Oxidation(9)			2.21	2.9	2	
		DLEAHIDSANK			8.39	2.5	2	
		ELEDATETADAMNR+Oxidation(11)			9.53	3.8	2	
		EDQSILCTGESGAGK			2.46	3.3	2	
		DELADEIANSSGK			2.39	2.6	2	
		TDLLLEPYNK			1.83	2.7	2	
P35749	MYH11	Myosin_11	2	2	10	4.01	4.03	0.00
		ALEEALEAK			4.26	2.7	2	
		ASRDEIFATAKENEK			2.62	2.5	2	
P35754	GLRX1	Glutaredoxin_1	2	4	13	1.61	1.49	0.36
		AQEILSQLPIK			1.87	3.1	2	
		DCIGGCSDLVSLQQSGELLTR			1.58	5.2	3	
P35858	ALS	Insulin_like growth factor_binding protein complex acid labile subunit	2	2	6	1.05	0.80	1.00
		NLIAAVAPGAFLGLK			1.05	2.4	2	
		LEALPNSLLAPLGR			1.15	2.8	2	
P35908	K22E	Keratin_ type II cytoskeletal 2 epidermal	6	6	14	1.27	0.96	0.03
		GFSSGSAVVSGGSR			6.72	3.6	2	
		GGGFGGGSSFGGGSGFSGGGFGGGGFGGGR			1.21	2.7	2	
		YEELQVTVGR			4.80	3.1	2	
		GGSGGGGSISGGGYGSGGGSGGR			4.06	4.8	2	
		VDLLNQEIEFLK			2.56	3.2	2	
		YLDGLTAER			2.94	2.6	2	
P36222	CH3L1	Chitinase_3_like protein 1	2	4	11	0.61	0.52	0.24
		GNQWVGYDDQESVK			0.53	2.7	2	
		SFTLASSETGVGAPISGPGIPGR			0.98	3.9	2	
P36871	PGM1	Phosphoglucomutase_1	3	5	21	0.55	0.56	0.45
		LSGTGSAGATIR			0.92	3.2	2	
		YDYEEVEAEGANK			0.48	3.3	2	
		FNISNGGPAPEAITDK			1.32	3.1	2	
P36955	PEDF	Pigment epithelium_derived factor	6	14	64	1.08	0.29	0.99
		YGLDSDLSCK			0.99	3.2	2	
		LQSLFDSPDFSK			1.08	3.4	2	
		DTDTGALLFIGK			0.82	3.0	2	
		LDLQEINNWVQAQMK			1.00	4.7	2	
		TVQAVLTVPK			0.93	2.8	2	
		ELLDTVTAPQK			1.03	3.4	2	
P36980	FHR2	Complement factor H_related protein 2	2	3	21	1.32	0.81	0.49
		LQNNENNISCVER			1.44	3.8	2	
		ITCAEEGWSPTPK			1.29	3.4	2	
P37802	TAGL2	Transgelin_2	7	9	68	1.74	0.97	0.00
		NFSDNQLQEGK			0.99	3.5	2	
		TLMNLGGLAVAR			2.12	3.8	2	
		DDGLFSGDPNWFPK			1.77	4.2	2	
		NVIGLQMGTNR			2.85	2.9	2	
		QMEQISQFLQAAER			1.34	3.8	2	
		TLMNLGGLAVAR+Oxidation(2)			1.72	3.0	2	
		QMEQISQFLQAAER+Oxidation(1)			1.87	3.3	2	
P37837	TALDO	Transaldolase	3	4	17	2.09	0.51	0.03

		SYEPLEDPGVK			0.50	2.6	2	
		LLGELLQDNAK			1.78	3.4	2	
		ALAGCDFLTISPK			2.18	3.0	2	
P38646	GRP75	Stress_70 protein_ mitochondrial	7	7	7	59.62	5.30	0.30
		EQQIVIQSSGGLSK			62.40	3.5	2	
		SQVFSTAADGQTQVEIK			13.52	2.9	2	
		TTPSVVAFTADGER			11.55	3.1	2	
		DAGQISGLNVLR			13.11	3.1	2	
		VINEPTAAALAYGLDK			16.89	3.7	2	
		GAVVGIDLGTTNSCVAVMEGK			2.49	4.6	2	
		STNGDTFLGGEDFDQALLR			3.91	4.3	2	
P40121	CAPG	Macrophage_capping protein	8	10	33	0.98	1.07	0.12
		YQEGGVESAFHK			0.90	3.4	2	
		VSDATGQMNLTK			3.73	4.0	2	
		EGNPEEDLTADK			2.74	2.8	2	
		MQYAPNTQVEILPQGHESPIFK			1.84	3.8	3	
		AQVEIVTDGEEPAEMIQVLGPKPALK			3.17	3.9	3	
		ANAQAAALYK			4.12	3.0	2	
		QAALQVAEGFISR			1.64	3.1	2	
		VSDATGQMNLTK+Oxidation(7)			4.07	2.9	2	
P40394	ADH7	Alcohol dehydrogenase class 4 mu/sigma chain	4	5	13	0.96	1.40	0.62
		AMAVGATECISPK			2.39	2.7	2	
		VCLIGCGFSTGYGAAVK			0.69	3.8	2	
		ISEGFELLNSGQSIR			1.57	3.8	2	
		FPVIVGHEATGIVESIGEGVTTVKPGDK			2.45	4.8	4	
P40925	MDHC	Malate dehydrogenase_ cytoplasmic	7	11	48	1.68	0.69	0.02
		GEFVTTVQQR			1.85	3.1	2	
		DVIATDKEDVAFK			1.74	3.8	2	
		VIVVGNPANTNCLTASK			1.55	4.8	2	
		FVEGLPINDFSR			1.89	2.8	2	
		EVGVYEALKDDSWLK			1.24	2.9	2	
		NVIIWGNHSSTQYPDVNHAK			1.73	3.9	3	
		LGVTANDVK			0.56	2.3	2	
P40926	MDHM	Malate dehydrogenase_ mitochondrial	4	5	5	1.21	0.97	0.54
		VDFPQDQLTALTGR			1.16	2.9	2	
		AGAGSATLSMAYAGAR			2.96	3.0	2	
		GYLGPEQLPDCLK			3.91	2.6	2	
		SQETECTYFSTPLLLGK			1.75	4.1	2	
P40939	ECHA	Trifunctional enzyme subunit alpha_ mitochondrial	2	2	2	15.84	8.02	0.39
		TGIEQGSDAGYLCESQK			18.32	4.0	2	
		SEVSSDEDIQFR			2.65	3.4	2	
P41218	MNDA	Myeloid cell nuclear differentiation antigen	2	2	2	7.70	0.21	0.18
		SLLAYDLGLTTK			7.69	3.4	2	
		INQEEVGLAAPAPTAR			10.00	3.3	2	
P41222	PTGDS	Prostaglandin_H2 D_isomerase	2	3	10	2.03	1.46	0.00
		AQGFTEDTIVFLPQTDK			1.63	3.5	2	
		TMLLQPAGSLGSYSYR			2.09	3.6	2	
P41250	SYG	Glycyl_tRNA synthetase	2	3	3	1.17	0.71	0.52
		GEFTIETEGK			1.17	2.0	1	

		EDKAPQVDVDKAVAELK			1.11	2.6	2	
P42330	AK1C3	Aldo_keto reductase family 1 member C3	2	4	8	4.11	1.55	0.02
		HIDSAHLYNNEEQVGLAIR			1.97	5.3	3	
		TPALIALR			32.57	2.4	2	
P43251	BTD	Biotinidase	2	2	15	0.72	0.61	0.01
		SHLIIAQVAK			0.77	3.6	3	
		LSSGLVTAALYGR			0.70	3.5	2	
P43353	AL3B1	Aldehyde dehydrogenase family 3 member B1	2	4	7	0.74	0.73	0.94
		FYGDDPQSSPNLGR			0.73	3.9	2	
		NLATQLDSAFIR			1.23	3.3	2	
P43652	AFAM	Afamin	6	6	45	0.71	0.37	0.02
		SDVGFLPPFPTLDPEEK			0.89	3.4	2	
		FTDSENVCQER			0.66	3.4	2	
		ESLLNHFLYEVAR			0.65	3.5	2	
		IAPQLSTEELVSLGEK			0.75	4.6	2	
		ICAMEGLPQK			0.68	2.5	2	
		AESPEVCFNEESPK			0.46	3.7	2	
P46439	GSTM5	Glutathione S_transferase Mu 5	2	3	4	11.26	14.64	0.00
		LGLDFPNLPYLIDGAHK			11.04	4.2	3	
		HNLCGETEEEK			27.68	2.8	2	
P46940	IQGA1	Ras GTPase_activating_like protein IQGAP1	5	6	6	1.18	0.55	0.31
		LEGVLAEVAQHYQDTLIR			2.05	3.6	3	
		EQLSDMMMINKQK+Oxidation(5),Oxidation(6),Oxidation(7)			0.23	2.1	1	
		EEIQSSISGVTAAYNR			1.17	4.1	2	
		TLQALQIPAAK			2.58	3.1	2	
		TLINAEDPPMVVVR			1.21	3.1	2	
P47755	CAZA2	F_actin_capping protein subunit alpha_2	3	3	7	1.39	1.35	0.33
		LLLNNDNLLR			2.58	2.5	2	
		FTITPSTTQVVGILK			1.35	3.4	2	
		DIQDSLTVSNEVQTAK			0.53	2.6	2	
P47756	CAPZB	F_actin_capping protein subunit beta	4	5	5	0.77	0.64	0.88
		LEVEANNAFDQYR			0.77	2.5	2	
		SGSGTMNLGGSLTR			0.99	2.4	2	
		KLEVEANNAFDQYR			1.22	4.0	2	
		GCWDSIHVVEVQEK			1.19	3.6	2	
P48448	AL3B2	Aldehyde dehydrogenase family 3 member B2	2	2	6	0.58	1.02	0.05
		LLPALQSTITR			0.51	2.4	2	
		HLTPVTLELGGK			20.96	2.9	1	
P48594	SPB4	Serpin B4	4	4	24	1.04	0.80	0.97
		INSWVESQTNEK			0.97	4.2	2	
		TNSILFYGR			1.09	2.3	2	
		LMEWTSLQNMR			0.73	3.2	2	
		LMEWTSLQNMR+Oxidation(1)			0.74	2.9	2	
P48741	HSP77	Putative heat shock 70 kDa protein 7	3	4	34	1.42	1.23	0.11
		VEILANDQGNR			1.40	3.4	2	
		ATAGDTHLGGEDFDNR			1.42	4.3	2	
		FEELCSDLFR			1.97	3.6	2	
P48960	CD97	CD97 antigen	2	2	10	0.65	0.67	0.03
		GGHWATEGCQVLGSK			0.65	4.2	2	

		VCTDVNECTSGQNPCHSSTHCLNNVGSYQCR			0.51	4.0	4	
P50395	GDIB	Rab GDP dissociation inhibitor beta	7	8	19	1.53	0.77	0.21
		DLGTESQIFISR			1.16	3.4	2	
		EIRPALELLEPIEQK			1.78	3.5	3	
		FVSISDLLVPK			1.68	2.5	2	
		TYDATTHFETTCDDIK			1.74	4.0	2	
		NPYYGGESASITPLEDLYK			1.93	4.8	2	
		NTNDANSCQIIIPQNQVNR			2.35	4.0	2	
		TDDYLDQPCYETINR			1.53	4.3	2	
P50552	VASP	Vasodilator_stimulated phosphoprotein	2	2	2	2.21	3.86	0.24
		VKQELLEEVKK			1.74	3.7	3	
		SSSSVTTSETQPCTPSSSDYSDLQR			4.43	4.4	2	
P50995	ANX11	Annexin A11	2	2	3	1.50	1.01	0.72
		GFGTDEQAIIDCLGSR			1.16	3.1	2	
		GTITDAPGFDPLR			1.62	2.7	2	
P51149	RAB7A	Ras_related protein Rab_7a	2	4	6	1.42	1.32	0.25
		EAINVEQAFQTIAR			1.35	3.9	2	
		DPENFPFVVLGNK			2.05	2.8	2	
P51659	DHB4	Peroxisomal multifunctional enzyme type 2	2	2	2	1.77	5.62	0.88
		AVANYDSVEEGEK			1.67	2.5	2	
		ATSTATSGFAGAIGQK			10.00	3.2	2	
P51884	LUM	Lumican	5	5	47	1.93	1.01	0.00
		ISNIPDEYFK			1.96	3.1	2	
		FNALQYLR			1.93	2.8	2	
		RFNALQYLR			1.90	3.2	2	
		LKEDAVSAAFK			1.94	3.2	2	
		ISETSLPPDMYECLR			2.28	2.7	2	
P52209	6PGD	6_phosphogluconate dehydrogenase_ decarboxylating	7	7	28	1.64	0.79	0.73
		VDDFLANEAK			1.33	2.5	2	
		LVPLLDTGDIIIDGGNSEYR			1.20	5.7	2	
		SAVENCQDSWR			2.61	2.9	2	
		VGTGEPCCDWVGDEGAGHFVK			2.13	2.5	2	
		GILFVGSGVSGGEEGAR			1.98	4.7	2	
		AGQAVDDFIEK			1.22	2.6	2	
		HEMLPASLIQAQR			1.38	2.9	2	
P52565	GDIR1	Rho GDP_dissociation inhibitor 1	2	2	3	1.29	0.79	0.36
		AEEYEFLTPVEEAPK			1.30	3.0	2	
		TDYMVGSYGPR			0.94	2.7	2	
P52566	GDIR2	Rho GDP_dissociation inhibitor 2	3	9	18	0.97	0.69	0.52
		APEPHVEEDDDDELDSK			0.73	6.0	2	
		TLLGDGPVVTDPK			2.63	3.4	2	
		ELQEMDKDDESLIK			1.73	3.6	2	
P52790	HXK3	Hexokinase_3	3	3	3	2.10	2.73	0.24
		FDASVDQASINPGK			2.09	2.4	2	
		LLEETLAPFR			2.99	2.8	2	
		FLSEIESDSLALR			2.05	2.8	2	
P52907	CAZA1	F_actin_capping protein subunit alpha_1	2	2	3	1.36	2.64	0.65
		EASDPQPEEADGGLK			1.31	2.6	2	
		DVQDSLTVSNEAQTAK			1.95	3.5	2	
P53004	BIEA	Biliverdin reductase A	2	2	3	2.66	3.48	0.01

		FGFPAFSGISR			3.00	2.5	2	
		SGSLENVPNVGVNK			1.60	2.9	2	
P53634	CATC	Dipeptidyl peptidase 1	3	5	14	1.40	1.11	0.46
		YYSSEYHYVGGFYGGCNEALMK			1.33	4.5	3	
		NSWGTGWGENGYFR			1.71	3.1	2	
		GTDECAIESIAVAATPIPK			1.88	4.0	2	
P53804	TTC3	E3 ubiquitin_protein ligase TTC3	2	2	6	0.82	0.65	0.00
		SSQGSPSVVVAPSPKTK			0.58	2.8	2	
		VSNASEMYTQKNDGKEK+Oxidation(6)			8.47	2.6	2	
P55008	AIF1	Allograft inflammatory factor 1	2	2	3	0.70	0.75	0.06
		YSSDEDLPSKLEGFK			0.64	2.9	2	
		LIGEVSSGSGETFSYPDFLR			1.76	3.9	2	
P55072	TERA	Transitional endoplasmic reticulum ATPase	3	5	9	1.41	0.76	0.67
		RSVSDNDIRK			0.97	1.9	1	
		AIANECQANFISIK			0.61	3.0	2	
		LIVDEAINEDNSVVSLSQPK			1.63	4.4	2	
P57721	PCBP3	Poly(rC)_binding protein 3	2	4	8	1.15	1.81	0.97
		INISEGNCPER			1.15	3.0	2	
		ESTGAQVQVAGDMLPNSTER			1.40	4.2	2	
P60174	TPIS	Triosephosphate isomerase	4	5	25	1.05	0.71	0.92
		IAVAAQNCYK			0.91	2.6	2	
		IIYGGSVTGATCK			1.12	2.7	2	
		SNVSDAVAQSTR			1.08	3.7	2	
		HVFGESDELIGQK			1.85	3.2	2	
P60660	MYL6	Myosin light polypeptide 6	5	6	17	1.47	1.40	0.21
		HVLVTLGEK			1.69	2.5	2	
		VLDFEHFLPMLQTVAK			1.74	4.6	3	
		ALGQNPTNAEVLK			2.38	3.0	2	
		ILYSQCGDVMR			1.08	2.5	2	
		NKDQGTYEDYVEGLR			2.00	3.8	2	
P60709	ACTB	Actin_ cytoplasmic 1	9	67	399	1.56	0.20	0.00
		GYSFTTTAER			1.28	3.3	2	
		VAPEEHPVLLTEAPLNPK			1.25	4.5	3	
		KDLYANTVLSGGTTMYPGIADR+Oxidation(14)			1.27	4.9	2	
		KDLYANTVLSGGTTMYPGIADR			1.72	5.8	2	
		DLYANTVLSGGTTMYPGIADR+Oxidation(13)			1.39	5.7	2	
		TTGIVMDSGDGVTHTVPIYEGYALPHAILR+Oxidation(5)			1.17	5.1	3	
		TTGIVMDSGDGVTHTVPIYEGYALPHAILR			1.17	5.5	3	
		DLYANTVLSGGTTMYPGIADR			1.69	6.1	2	
		CPEALFQPSFLGMESCGIHETTFNSIMK			1.18	4.4	3	
P61088	UBE2N	Ubiquitin_conjugating enzyme E2 N	2	3	8	1.65	0.85	0.00
		YFHVVIAGPQDSPFEGGTFK			1.65	4.1	3	
		LELFLPEEYPMAAPK			1.00	3.0	2	
P61626	LYSC	Lysozyme C	8	27	195	1.11	0.25	1.00
		RLGMDGYR			0.84	2.4	2	
		QYVQGCGV			1.19	2.3	1	
		AWVAWR			1.04	2.3	2	
		STDYGIFQINSR			1.12	4.9	2	
		TPGAVNACHLSCSALLQDNIADAVACAK			1.08	5.8	3	
		GISLANWMCLAK+Oxidation(7)			1.15	2.8	2	

		ATNYNAGDR			1.04	2.4	2	
		GISLANWMCLAK			0.44	2.4	2	
P61769	B2MG	Beta_2_microglobulin	3	7	77	0.88	0.32	0.00
		VNHVTLSQPK			0.56	2.9	2	
		VEHSDLSFSK			0.71	3.2	2	
		IEKVEHSDLSFSK			0.98	4.3	2	
P61916	NPC2	Epididymal secretory protein E1	2	2	6	0.73	1.01	0.79
		EVNVSPCPTQPCQLSK			0.93	3.0	2	
		LVVEWQLQDDK			0.73	2.8	2	
P61978	HNRPK	Heterogeneous nuclear ribonucleoprotein K	2	3	6	1.31	1.06	0.99
		IDEPLEGSEDR			1.03	2.6	2	
		GSYGDLGGPIITTQVTIPK			1.56	3.5	2	
P62158	CALM	Calmodulin	4	7	41	1.28	0.55	0.38
		MKDTDSEEEIR+Oxidation(0)			0.73	2.8	2	
		VFDKDGNGYISAAELR			1.30	4.3	3	
		DGNGYISAAELR			1.09	2.7	2	
		EAFSLFDKDGDGTITTK			0.87	2.7	2	
P62258	1433E	14_3_3 protein epsilon	4	4	17	0.90	0.91	1.00
		HLIPAANTGESK			0.69	2.9	2	
		YLAEFATGNDR			0.97	2.5	2	
		LICCDILDVLDK			0.60	3.7	2	
		YLAEFATGNDRK			0.99	2.4	2	
P62805	H4	Histone H4	6	10	50	1.19	0.95	0.77
		DAVTYTEHAK			4.14	2.9	2	
		ISGLIYEETR			2.60	3.8	2	
		VFLENVIR			1.38	2.7	2	
		TVTAMDVVYALK			1.27	3.1	2	
		DNIQGITKPAIR			6.62	2.9	2	
		TVTAMDVVYALK+Oxidation(4)			0.87	2.8	2	
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	3	8	61	1.92	1.34	0.00
		KITIADCGQLE			1.91	3.6	2	
		IIPGFMCQGGDFTR			2.07	3.0	2	
		HTGPGILSMANAGPNTNGSQFFICTAK			3.13	5.5	3	
P63104	1433Z	14_3_3 protein zeta/delta	5	10	90	1.16	0.45	0.80
		YLAEVAAGDDKK			1.45	3.5	2	
		SVTEQGAELSNEER			0.35	4.8	2	
		DSTLIMQLLR			2.06	3.6	2	
		YLAEVAAGDDK			1.22	2.4	2	
		DSTLIMQLLR+Oxidation(5)			1.02	3.1	2	
P63208	SKP1	S_phase kinase_associated protein 1	2	2	4	1.13	0.75	0.90
		TVANMIKGKTPEEIR+Oxidation(4)			1.14	2.6	2	
		NDFTEEEEAQVR			0.91	3.1	2	
P67809	YBOX1	Nuclease_sensitive element_binding protein 1	2	2	4	1.61	5.44	0.60
		EDGNEEDKENQGDETQGQQPPQR			1.60	4.6	3	
		GAEAANVTGPGGVPVQGSK			4.96	4.3	2	
P67936	TPM4	Tropomyosin alpha_4 chain	6	10	45	1.78	1.41	0.20
		YSEKEDKYEEEIK			1.80	4.2	2	
		IQALQQQADEAEDR			2.86	4.5	2	
		IQLVEEELDR			2.51	3.2	2	
		LVILEGELER			71.48	2.7	2	

		MEIQEMQLK+Oxidation(0),Oxidation(5)			1.39	2.3	1	
		KIQALQQQADEAEDR			1.61	4.5	2	
P68133	ACTS	Actin_ alpha skeletal muscle	10	39	289	1.24	0.42	0.07
		HQGVMVGMGQK+Oxidation(4),Oxidation(7)			1.25	3.8	3	
		HQGVMVGMGQK+Oxidation(7)			1.39	3.7	3	
		HQGVMVGMGQK+Oxidation(4)			1.99	3.8	3	
		DSYVGDEAQSK			2.25	3.4	2	
		HQGVMVGMGQK			1.33	2.9	2	
		EITALAPSTMK+Oxidation(9)			1.53	2.7	2	
		EITALAPSTMK			1.32	2.8	1	
		YPIEHGIITNWDDMEK+Oxidation(13)			1.24	3.9	2	
		YPIEHGIITNWDDMEK			2.42	4.0	3	
		DLTDYLMK			1.23	2.9	2	
P68366	TBA4A	Tubulin alpha_4A chain	4	6	27	1.29	0.66	1.00
		AYHEQLSVAEITNACFEPANQMVK			0.78	4.3	3	
		IHFPLATYAPVISAEK			0.93	3.2	2	
		SIQFVDWCPTGFK			1.33	3.7	2	
		AYHEQLSVAEITNACFEPANQMVK+Oxidation(21)			0.89	3.7	3	
P68371	TBB2C	Tubulin beta_2C chain	3	7	17	0.80	0.61	0.27
		MSATFIGNSTAIQELFK			1.55	4.5	2	
		INVYYNEATGGK			0.54	3.0	2	
		MSATFIGNSTAIQELFK+Oxidation(0)			0.79	2.7	2	
P68871	HBB	Hemoglobin subunit beta	7	92	858	0.94	0.17	0.99
		GTFATLSELHCDK			1.30	4.1	2	
		VNVDEVGGEALGR			0.99	4.6	2	
		EFTPPVQAAYQK			0.82	3.1	2	
		SAVTALWGK			1.03	3.1	2	
		FFESFGDLSTPDAVMGNPK+Oxidation(14)			0.94	5.1	2	
		LLGNVLVCVLAHHFGK			1.10	4.2	4	
		FFESFGDLSTPDAVMGNPK			0.97	5.4	2	
P69892	HBG2	Hemoglobin subunit gamma_2	3	12	81	0.70	0.50	0.31
		LLVVYPWTQR			0.70	3.1	2	
		FFDSFGNLSSASAIMGNPK			1.67	3.3	2	
		VNVEDAGGETLGR			2.02	2.8	2	
P69905	HBA	Hemoglobin subunit alpha	11	104	663	0.67	0.12	0.97
		VGAHAGEYGAEALER			0.67	5.1	3	
		LRVDPVNFK			0.67	2.7	2	
		TYFPHFDLSHGSAQVK			0.75	4.4	2	
		MFLSFPTTK+Oxidation(0)			0.88	2.7	2	
		FLASVSTVLTSK			0.69	4.3	2	
		MFLSFPTTK			1.04	3.0	2	
		KVADALTNAVAHVDDMPNALSALSDLHAHK+Oxidation(15)			0.97	5.2	4	
		VADALTNAVAHVDDMPNALSALSDLHAHK+Oxidation(14)			0.92	6.1	3	
		KVADALTNAVAHVDDMPNALSALSDLHAHK			0.69	5.9	4	
		VADALTNAVAHVDDMPNALSALSDLHAHK			0.97	7.0	3	
		LLSHCLLVTLAAHLPAEFTPAVHASLDK			0.35	6.4	4	
P78316	NOP14	Nucleolar protein 14	2	3	4	0.93	0.41	0.80
		RTQTLLKEYK			0.93	2.0	1	
		QLFNSLATQEGEWKALK			1.11	2.4	2	
P78417	GSTO1	Glutathione S_transferase omega_1	2	2	2	1.29	1.26	0.39

		HEVININLK			1.93	2.7	2	
		SQNKEDYAGLKEEFR			1.26	3.5	3	
P80188	NGAL	Neutrophil gelatinase_associated lipocalin	7	8	43	1.44	0.72	0.84
		MYATIYELK			1.22	2.5	2	
		TFVPGCQPGEFTLGNIK			1.41	3.3	2	
		SLGLPENHIVFPVPIDQCIDG			1.44	4.1	2	
		SYPGLTSYLVR			0.80	2.7	2	
		WYVVGLAGNAILR			1.20	3.6	2	
		VPLQQNFQDNQFQGK			1.81	3.9	2	
		VVSTNYNQHAMVFFK			1.38	3.8	2	
P80723	BASP1	Brain acid soluble protein 1	2	3	3	0.81	1.28	0.88
		AQGPAASAEEPKPVEAPAANSDQTVTVKE			0.95	4.4	3	
		AQGPAASAEEPKPVEAPAANSDQTVTVK			0.64	4.6	3	
P80748	LV302	Ig lambda chain V_III region LOI	2	11	66	0.47	0.50	1.00
		FSGSNSGNTATLTISR			0.46	4.4	2	
		YVLTQPPSVSVAPGETAR			1.04	3.7	2	
P98088	MUC5A	Mucin-5AC (Fragments)	13	14	24	1.23	0.40	0.63
		FHPGDVIYHTTDGTGGCISAR			1.00	2.3	2	
		VLVDNYFCGAEDGLSCPR			0.90	2.3	2	
		GQTCGLCGNFNSIQADDFR			1.06	4.3	2	
		NQLPPICYNYEIR			1.46	2.4	2	
		HQDGLVVVTTK			2.34	2.9	2	
		AEACVCTYNGQR			5.08	3.2	2	
		EQASGLCYNYQIR			1.22	2.9	2	
		SHPEVSIEHLGQVVQCSR			2.31	3.7	3	
		SVVGDVLEFGNSWK			2.00	3.5	2	
		MCLNYEVR			1.39	2.3	2	
		VVTENVPCGTTGTTCSK			1.04	3.6	2	
		SLIIQQQGCSSSEPVR			1.98	4.0	2	
		NSFEDPCSLSVENEK			2.72	4.1	2	
Q01105	SET	Protein SET	2	2	2	0.76	0.85	0.44
		LNEQASEEILK			0.42	2.4	2	
		VEVTEFEDIK			1.19	2.5	2	
Q01469	FABP5	Fatty acid_binding protein_ epidermal	3	4	9	1.06	0.96	0.99
		TTQFSCTLGEK			1.36	2.7	2	
		KMGAMAKPDCIITCDGKNLTIK+Oxidation(4)			1.05	2.5	2	
		LVVECVMNNVTCTR			1.51	4.1	2	
Q01518	CAP1	Adenylyl cyclase_associated protein 1	5	7	25	1.38	1.22	0.14
		LSDLLAPISEQIK			1.97	3.8	2	
		VENQENVSNLVIEDTELK			1.08	4.1	2	
		NSLDCEIVSAK			2.69	3.0	2	
		LEAVSHTSDMHR+Oxidation(9)			0.67	2.7	2	
		ALLVTASQCQQPAENK			1.43	3.6	2	
Q03591	FHR1	Complement factor H_related protein 1	2	2	17	1.28	1.19	0.03
		TGESAEFVCK			1.51	3.2	2	
		EIMENYNIALR			1.23	2.7	2	
Q04760	LGUL	Lactoylglutathione lyase	2	2	4	1.59	2.23	0.36
		DFLLQQTMLR			1.50	3.0	2	
		RFEELGVK			1.79	2.4	2	
Q04917	1433F	14_3_3 protein eta	3	7	33	1.43	0.50	0.83

		YLAEVASGEK			1.37	2.6	2	
		AVTELNEPLSNEDR			1.82	4.2	2	
		ELETVCNDVLSLLDK			1.44	3.8	2	
Q06830	PRDX1	Peroxiredoxin_1	5	11	77	1.21	0.55	0.01
		HGEVCPAGWKPGSDTIKPDVQK			2.41	5.8	3	
		TIAQDYGVLK			2.30	2.8	2	
		LVQAFQFTDK			0.80	3.2	2	
		QGGLGPMNIPLVSDPK			1.71	3.4	2	
		KQGGLGPMNIPLVSDPK			2.26	2.8	2	
Q08380	LG3BP	Galectin_3_binding protein	10	30	267	0.57	0.10	0.00
		ASHEEVEGLVEK			0.57	3.9	3	
		RIDITLSSVK			0.42	3.0	2	
		YSSDYFQAPSDYR			0.64	4.3	2	
		AVDTWSWGER			0.46	3.3	2	
		IDITLSSVK			0.39	2.8	2	
		YYPYQSFQTPQHPSFLFQDK			0.52	4.0	2	
		ELSEALGQIFDSQR			0.65	4.8	2	
		SDLAVPSELALLK			0.61	3.5	2	
		TLQALEFHTVPFQLLAR			0.52	4.6	2	
		STSSFPCPAGHFNGFR			0.40	3.4	2	
Q09666	AHNK	Neuroblast differentiation_associated protein AHNAK	6	6	8	1.30	1.21	0.80
		AEGPEVDVNLPK			1.51	2.8	2	
		VKGDVDVSVPK			2.57	2.5	2	
		VDVEGPDVNIEGPEGK			1.20	3.3	2	
		GEGPDVDVNLPK			2.80	2.6	2	
		VDVEVPDVSLEGPEGK			1.53	2.7	2	
		VDINAPDVEVQGK			0.71	2.3	2	
Q12805	FBLN3	EGF_containing fibulin_like extracellular matrix protein 1	10	24	121	0.91	0.21	0.39
		TCQDINECETTNECR			0.79	4.9	2	
		LNCEDIDECR			0.82	3.4	2	
		GSFACQCPPGYQK			0.78	4.5	2	
		ADQVCINLR			0.93	3.3	2	
		IQCAAGYEQSEHNVCQDIDECTAGTHNCR			0.86	6.3	3	
		FSCMCPQGYQVVR			0.93	3.6	2	
		DIDECDIVPDACK			0.54	3.2	2	
		FSCMCPQGYQVVR+Oxidation(3)			0.68	3.2	2	
		CVNHYGGYLCLPK			0.81	5.1	3	
		TCQDINECETTNECREDEMCWNYHGGFR+Oxidation(18)			1.79	4.0	4	
Q12860	CNTN1	Contactin_1	2	2	11	0.86	0.89	0.19
		VQVTSQEYSAR			0.85	2.8	2	
		ELTITWAPLSR			1.54	2.4	2	
Q13228	SBP1	Selenium_binding protein 1	6	8	32	1.40	0.38	0.00
		HEIVQTLSLK			1.01	2.5	2	
		IYVVDVGSEPR			0.99	3.4	2	
		NTGTEAPDYLATVDVDPK			0.99	3.4	2	
		GGPVQVLEDEELKSQPEPLVVK			2.64	4.4	3	
		LTGQLFLGGSIVK			1.46	2.9	2	
		EEIVYLPCIYR			1.65	2.6	2	
Q13421	MSLN	Mesothelin	7	10	46	1.88	1.43	0.03

		IQSFLGGAPTEDLK			1.81	4.7	2	
		QLLGFPCAEVSGLSTER			6.03	3.9	2	
		GLLPVLGQPIIR			1.27	2.4	2	
		GSLLSEADVR			2.51	2.6	2	
		TDAVLPLTVAEVQK			2.74	3.1	2	
		EIDESLIFYK			1.40	2.7	1	
		ALGGLACDLPGR			2.31	3.1	2	
Q13439	GOGA4	Golgin subfamily A member 4	2	3	4	1.00	0.46	0.04
		EEGVKQDTTLNELQEQLK			1.02	2.4	2	
		MKQELEAKMDEQK+Oxidation(0),Oxidation(8)			0.94	2.4	2	
Q13642	FHL1	Four and a half LIM domains protein 1	2	2	4	5.53	6.49	0.00
		FCANTCVECR			5.97	2.3	2	
		AIVAGDQNVEYK			4.86	2.8	2	
Q13938	CAYP1	Calcyphosin	9	14	81	1.03	0.37	1.00
		GASGIQGLAR			0.39	2.6	2	
		SLDADEFR			0.78	2.4	2	
		SGDGVVTVDDLR			1.18	3.4	2	
		FLDNFDSSEK			0.69	2.9	2	
		SGEWTEDEVLR			0.51	2.4	2	
		EAVIAAAFAK			1.10	3.1	2	
		LGLVLDQAEAEGVCR			0.79	4.4	2	
		NGSGTLDLEEFLR			0.73	2.5	2	
		ALRPPMSQAR			0.13	2.4	2	
Q14103	HNRPD	Heterogeneous nuclear ribonucleoprotein D0	2	2	3	1.04	2.56	0.91
		IFVGGLSPDTPEEK			0.96	3.4	2	
		FGEVVDCTLK			1.37	2.4	2	
Q14118	DAG1	Dystroglycan	2	3	7	0.90	0.84	0.97
		VTIPTDLIASSGDIIK			0.90	3.6	2	
		VVENGALLSWK			0.95	2.4	2	
Q14508	WFDC2	WAP four_disulfide core domain protein 2	4	7	26	1.69	1.10	0.76
		DQCQVDSQCPGQMK			0.47	4.5	2	
		CCSAGCATFCSLPNDK			1.65	4.5	2	
		EGSCPQVNINFPQLGLCR			1.93	3.8	3	
		DQCQVDSQCPGQMK+Oxidation(12)			1.74	4.5	2	
Q14624	ITIH4	Inter_alpha_trypsin inhibitor heavy chain H4	10	18	73	1.26	0.42	0.50
		AEAQAQYSAAVAK			1.50	4.8	2	
		NPLVWVHASPEHVVVTR			1.05	3.9	3	
		ANTVQEATFQMELPK			1.50	3.9	2	
		QGPVNLLSDPEQGVEVTGQYER			1.55	4.2	2	
		AGFSWIEVTFK			1.82	3.5	2	
		EKAEAQAQYSAAVAK			1.02	3.8	2	
		AISGGSIQIENGYFVHYFAPEGLTTMPK			1.59	3.5	3	
		NMEQFQVSVSVAPNAK+Oxidation(1)			1.15	3.2	2	
		SPEQQETVLDGNLIIR			2.11	4.2	2	
		MNFRPGVLSSR			0.90	2.7	2	
Q14651	PLSI	Plastin_1	2	3	21	1.41	1.00	0.64
		KIENCNYAVELGK			1.82	3.9	2	
		IENCNYAVELGK			1.22	2.9	2	
Q15019	SEPT2	Septin_2	2	2	3	2.85	1.60	0.16
		KVENEDMNKDQILLEK			0.89	2.4	2	

		ASIPFSVVGSNQLIEAK			3.68	3.1	2	
Q15084	PDIA6	Protein disulfide_isomerase A6	2	2	2	2.44	5.80	0.45
		NLEPEWAAAASEVK			2.08	3.1	2	
		TGEAIVDAALSALR			3.98	2.7	2	
Q15149	PLEC	Plectin	6	6	7	2.31	0.34	0.00
		FRELAEEAAR			0.60	2.5	2	
		GGELVYTDSEAR			4.00	2.6	2	
		QVQVALETAQR			2.18	2.4	2	
		AYSDPSTGEPATYGELQQR			5.64	3.5	2	
		AQVEQELTTLR			3.88	2.8	2	
		DDGTGQLLLPLSDAR			1.76	2.5	2	
Q15365	PCBP1	Poly(rC)_binding protein 1	2	2	2	1.02	0.74	0.95
		IITLTGPTNAIFK			1.03	2.5	2	
		AITIAGVPQSVTECVK			0.93	2.5	2	
Q15582	BGH3	Transforming growth factor_beta_induced protein ig_h3	7	11	53	0.58	0.18	0.00
		STVISYECCPGYEK			0.76	3.7	2	
		EGVYTVFAPTNEAFR			0.60	3.4	2	
		GDELADSALEIFK			0.53	3.5	2	
		LTLLAPLNSVFK			0.59	3.0	2	
		YHIGDEILVSGGIGALVR			0.76	3.7	3	
		FSMLVAAIQSAGLTETLNR			0.71	3.6	3	
		SLQGDKLEVSLK			0.47	2.8	2	
Q15828	CYTM	Cystatin_M	2	2	3	0.75	1.01	0.77
		VTGDHVDLTTCPLAAGAQQEK			0.82	3.8	3	
		AQSQLVAGIK			0.75	2.4	2	
Q16555	DPYL2	Dihydropyrimidinase_related protein 2	2	3	7	0.88	0.88	0.89
		SSAEVIAQAR			0.79	2.4	2	
		AITIANQTNCPLYITK			1.15	3.8	2	
Q30154	DRB5	HLA class II histocompatibility antigen_ DR beta 5 chain	4	5	8	0.59	0.88	0.87
		FDSDVGEYR			0.79	2.7	2	
		HNYGVGESFTVQR			0.57	2.9	2	
		SGEVYTCQVEHPSVTSPLTVEWR			0.54	4.6	2	
		AVTELGRPDAEYWNSQK			1.38	3.7	2	
Q32MZ4	LRRF1	Leucine_rich repeat flightless_interacting protein 1	2	2	4	6.26	7.35	0.54
		SAVEAQNEVTENPK			1.95	4.1	2	
		IAAESSENVDCPENPK			6.69	4.1	2	
Q3ZCM7	TBB8	Tubulin beta_8 chain	3	4	10	0.93	0.48	0.33
		AVLVDLEPGTMDSVR			0.49	4.0	2	
		EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK			0.94	5.1	3	
		AVLVDLEPGTMDSVR+Oxidation(10)			0.65	3.5	2	
Q562R1	ACTBL	Beta_actin_like protein 2	2	3	23	1.26	1.35	0.36
		VAPDEHPILLTEAPLNPK			1.25	4.2	3	
		DLYANTVLSGGSTMYPGIADR+Oxidation(13)			2.31	3.6	2	
Q5T9S5	CCD18	Coiled_coil domain_containing protein 18	2	3	11	0.78	0.56	0.70
		QLKEENNNGKEK			0.77	2.6	2	
		LEAQLEKKDQQFK			0.90	2.3	2	
Q5VTE0	EF1A3	Putative elongation factor 1_alpha_like 3	7	14	91	1.32	0.45	0.82
		STTTGHLIYK			1.11	2.7	2	
		THINIVVIGHVDSGK			1.36	4.8	3	

		EHALLAYTLGVK			1.12	3.0	2	
		VETGVLKPGMVVTFAPVNVTTEVK+Oxidation(9)			1.24	5.4	3	
		VETGVLKPGMVVTFAPVNVTTEVK			1.38	4.5	3	
		IGGIGTVPVGR			1.33	3.2	2	
		YYVTIIDAPGHR			1.51	2.7	2	
Q5XKE5	K2C79	Keratin_ type II cytoskeletal 79	2	3	18	3.43	2.88	0.00
		FLEQQNKVLETK			2.06	4.0	2	
		NLDLDSIIAEVK			4.62	4.2	2	
Q6GPH6	IPIL1	Inositol 1_4_5_triphosphate receptor_interacting protein_like 1	2	2	2	0.77	1.03	0.57
		LLEMEFEER			0.77	2.0	1	
		MSEEMRLLEMEFEERK+Oxidation(4),Oxidation(9)			0.68	2.4	2	
Q6IBS0	TWF2	Twinfilin_2	2	2	2	1.65	3.04	0.49
		HQTLQGLAFPLQPEAQR			1.58	3.2	2	
		HLSSCAAPAPLTSAER			2.05	3.5	2	
Q6NUK1	SCMC1	Calcium_binding mitochondrial carrier protein SCaMC_1	2	2	2	3.33	6.76	0.00
		TGQYSGIYDCAK			2.57	2.4	2	
		NLGIPLGQDAEEK			3.69	2.3	2	
Q6P5S2	CF058	UPF0762 protein C6orf58	3	5	11	1.16	0.85	0.46
		FCYDVSSCR			1.08	2.5	2	
		SFEDRYDYYSK			1.81	2.5	2	
		YLWAAHTSTLADNIK			1.04	4.4	2	
Q6PEY2	TBA3E	Tubulin alpha_3E chain	2	3	18	1.31	0.81	0.40
		DVNAAIATIK			0.75	2.9	2	
		LIGQIVSSITASLR			1.31	3.9	2	
Q7Z7M9	GALT5	Polypeptide N_acetylgalactosaminyltransferase 5	2	2	6	0.64	0.57	0.01
		WYLENVFPDLR			0.64	3.3	2	
		EGNFNVYLSDLIPVDR			0.67	2.3	2	
Q86UX7	URP2	Fermitin family homolog 3	2	2	3	5.03	4.20	0.07
		VVLAGGVAPALFR			2.44	3.6	2	
		VFVGEEDPEAESVTLR			10.56	3.7	2	
Q86VB7	C163A	Scavenger receptor cysteine_rich type 1 protein M130	5	6	44	1.13	0.61	1.00
		HNCDHAEDAGVICSK			1.05	5.1	3	
		LVDGVTECSGR			0.81	2.8	2	
		HYCNHNEDAGVTCSDGSDLELR			1.24	6.2	3	
		LEVFYNGAWGTVGK			1.17	3.2	2	
		EAEFGQGTGPIWLNEVK			1.03	4.4	2	
Q86Z20	CC125	Coiled_coil domain_containing protein 125	2	3	4	0.87	0.55	0.99
		EEAYVMADAFRIAFEQQLMR+Oxidation(5)			0.86	2.6	2	
		NDQALQLTQMDKMHK+Oxidation(12)			1.03	2.3	2	
Q8IUD2	RB6I2	ELKS/Rab6_interacting/CAST family member 1	2	2	2	0.73	1.45	0.61
		TNSTGGSSGSSVGGGSGK			0.56	2.4	2	
		GQLQDELEKGER			1.27	2.0	1	
Q8IWL2	SFTA1	Pulmonary surfactant_associated protein A1	13	224	2283	0.28	0.03	0.00
		HQILQTR			0.38	2.7	2	
		GKEQCVEMYTDGQWNDR+Oxidation(7)			0.36	5.2	2	
		GKEQCVEMYTDGQWNDR			0.09	5.5	2	
		GALSLQGSIMTVGEK			0.27	5.2	3	
		EQCVEMYTDGQWNDR+Oxidation(5)			0.25	5.3	2	

		EQCVEMYTDGQWNDR			0.23	5.3	2	
		GALSLQGSIMTVGEK+Oxidation(9)			0.40	5.3	2	
		NPEENEAIASFVK			0.19	4.6	2	
		YSDGTPVNYTNWYR			0.24	4.0	2	
		KYNTYAYVGLTEGPSPGDFR			0.50	6.2	2	
		VFSSNGQSITFDAIQEACAR			0.40	6.1	2	
		YNTYAYVGLTEGPSPGDFR			0.31	5.6	3	
		GPPGLPAHLDEELQATLHDFR			0.29	5.0	3	
Q8IZP2	ST134	Putative protein FAM10A4	2	3	5	1.17	1.46	1.00
		AIEINPDSAQPYK			1.13	2.5	2	
		VAAIEALNDGELQK			1.26	4.2	2	
Q8N4F0	BPIL1	Bactericidal/permeability_increasing protein_like 1	2	4	10	0.92	1.61	1.00
		AGALNLDITGQLR			0.66	3.5	2	
		ALQVTVPHFLDWSGEALQPTR			1.04	5.1	2	
Q8NFJ5	RAI3	Retinoic acid_induced protein 3	3	4	7	0.64	0.44	0.02
		AHAWPSPYK			0.41	2.4	2	
		TNVNVFSELSAPR			0.64	3.6	2	
		AYSQEEITQGFEETGDTLYAPYSTHFQLQNQPPQK			0.42	4.6	3	
Q8TDL5	LPLC1	Long palate_ lung and nasal epithelium carcinoma_associated protein 1	20	42	251	1.06	0.29	0.30
		LVLSDCATSHGSLR			1.40	3.2	2	
		SSIGLINEK			1.17	3.1	2	
		HIIWLK			1.01	2.5	2	
		TIVEFHMTTEAQATIR			1.54	2.7	2	
		ALGFEAAESSLTK			1.33	3.9	2	
		GDQLILNLNNISSDR			1.25	4.0	2	
		LSFLVNALAK			0.80	3.4	2	
		IQLMNSGIGWFQPDVLK+Oxidation(3)			1.04	5.0	2	
		LEFDLLYPAIK			1.02	3.7	2	
		EKPAGGIPVLGSLVNTVLK			1.62	4.6	3	
		IQLMNSGIGWFQPDVLK			0.85	5.7	2	
		NIITEIIHSILLPNQNGK			1.13	5.1	2	
		DALVLTPASLWKPSSPVSQ			1.01	4.7	2	
		GDTIQLYLGAK			0.96	3.0	2	
		ILTQDTPEFFIDQGHAK			1.16	3.9	2	
		VITANILQLQVKPSANDQELLVK			0.65	3.6	3	
		IPLDMVAGFNTPLVK+Oxidation(4)			1.93	3.2	2	
		QVMNLLVPSLPNLVK			1.52	3.9	2	
		QVMNLLVPSLPNLVK+Oxidation(2)			1.21	3.9	2	
		IPLDMVAGFNTPLVK			1.85	3.6	2	
Q8WUM4	PDC6I	Programmed cell death 6_interacting protein	3	4	21	1.04	0.60	0.99
		SVIEQGGIQTVDQLIK			0.97	3.8	2	
		LLDEEEATDNDLR			1.06	3.6	2	
		NIQVSHQEFSK			1.01	2.6	2	
Q8WWI1	LMO7	LIM domain only protein 7	2	2	8	0.78	1.45	0.30
		QLRYEEMQKIK+Oxidation(6)			0.74	2.8	2	
		EEREEIEKQALEK			3.57	2.6	2	
Q8WWY3	PRP31	U4/U6 small nuclear ribonucleoprotein Prp31	2	2	2	0.79	0.42	0.02
		TVKELGNSLDKCK			0.33	1.9	1	
		MFAEIMMKIEEYISK+Oxidation(0),Oxidation(5),Oxidation(6)			0.84	2.5	2	

Q96C19	EFHD2	EF_hand domain_containing protein D2	3	3	7	2.04	3.57	0.22
		FEEEIKAEQEER			2.46	3.1	2	
		LSEIDVSSEGVK			1.73	3.6	2	
		ADLNQGIGEPQSPSR			10.45	3.6	2	
Q96CX2	KCD12	BTB/POZ domain_containing protein KCTD12	3	4	9	1.00	0.58	1.00
		LGAPQQPGPGPPPSR			1.00	2.7	2	
		MFTQQQPQELAR			1.01	3.2	2	
		DLQLVLPDYFPER			0.94	2.9	2	
Q96DA0	ZG16B	Zymogen granule protein 16 homolog B	4	8	15	0.63	0.25	0.12
		YFSTTEDYDHEITGLR			0.70	4.7	2	
		VSVGLLLVK			0.63	3.0	2	
		LGALGGNTQEVTLQPGEYITK			0.70	4.9	2	
		LGDSWDVK			0.49	2.7	2	
Q96KP4	CNDP2	Cytosolic non_specific dipeptidase	4	5	16	1.07	0.65	0.72
		EGGSIPVTLTFQEATGK			1.06	2.7	2	
		WVAIQSVSAWPEK			1.97	3.1	2	
		TVFGVEPDLTR			1.11	2.7	2	
		MMEVAAADVK			0.24	2.3	2	
Q96NY7	CLIC6	Chloride intracellular channel protein 6	3	3	3	1.19	0.44	0.25
		VGDGPQQEPGEDEER			0.16	3.3	2	
		GAAEPEAQLSNHLAEEGPAEGSGEAAR			0.32	4.6	3	
		FLDGDELTLADCNLLPK			1.46	2.5	2	
Q96PD5	PGRP2	N_acetylmuramoyl_L_alanine amidase	6	11	51	0.68	0.29	0.00
		AGLLRPDYALLGHR			0.83	4.1	3	
		TDCPGDALFDLLR			0.96	4.0	2	
		GCPDVQASLPDAK			0.71	2.5	2	
		GSQTQSHPDLGTEGCWDQLSAPR			0.68	4.7	3	
		DGSPDVTTADIGANTPDATK			0.40	4.6	2	
		EFTEAFLGCPAIHPR			0.81	2.9	2	
Q96S96	PEBP4	Phosphatidylethanolamine_binding protein 4	6	14	73	0.88	0.31	0.09
		IQGQELSAYQAPSPPAHSGFHR			1.40	4.7	2	
		HWLVTDIK			0.71	3.0	2	
		FHLGEPEASTQFMTQNYQDSPTLQAPR+Oxidation(12)			0.68	5.0	3	
		ITSWMEPIVK			0.74	2.8	2	
		FHLGEPEASTQFMTQNYQDSPTLQAPR			0.93	5.9	3	
		HKNQAEIAAC			0.92	2.9	2	
Q96T17	MA7D2	MAP7 domain_containing protein 2	2	3	8	0.93	0.44	0.72
		EQEEQERLEK			0.92	2.5	2	
		AYPQSPKTTKPPYPGSPVK			0.98	2.5	2	
Q96TA2	YMEL1	ATP_dependent zinc metalloprotease YME1L1	2	3	5	0.89	1.04	0.28
		MVTKFGMSEK+Oxidation(0)			0.50	2.0	1	
		GSDVESLDKLMKTK+Oxidation(10)			1.52	2.5	2	
Q99497	PARK7	Protein DJ_1	4	6	22	1.48	0.76	0.03
		GAEEMETVIPVDVMR			1.59	3.2	2	
		EGPYDVVVLPGGNLGAQNLSESAAVK			1.43	4.3	2	
		GAEEMETVIPVDVMR+Oxidation(4)			32.18	2.3	2	
		DVVICPDASLEDAKK			0.49	3.1	2	
Q99536	VAT1	Synaptic vesicle membrane protein VAT_1 homolog	4	7	9	1.36	1.07	0.34
		LPPLPVTPGMEGAGVVIAVGEGVSDR			1.36	4.9	3	

		VVTYGMANLLTGPK			3.87	2.9	2	
		EVAEAATGEDASSPPPK			5.14	4.4	2	
		TVENVTVFGTASASK			3.29	4.0	2	
Q9BW30	TPPP3	Tubulin polymerization_promoting protein family member 3	4	9	61	1.29	0.53	1.00
		QDILDDSGYVSAYK			1.33	4.0	2	
		SVTGTDVDIVFSK			1.06	3.5	2	
		SKEEAFDAICQLVAGK			0.94	4.6	3	
		VINYEEFKK			0.73	2.7	2	
Q9H299	SH3L3	SH3 domain_binding glutamic acid_rich_like protein 3	2	2	16	1.05	1.18	0.97
		VYSTSVTGSR			1.05	3.0	2	
		IQYQLVDISQDNALR			1.16	3.6	2	
Q9H2A7	CXL16	C_X_C motif chemokine 16	2	2	15	0.82	0.75	0.49
		ISSDSPPSVQFMNR			0.83	3.7	2	
		ECGHAYSGIVAHQK			0.60	2.4	2	
Q9H4G4	GAPR1	Golgi_associated plant pathogenesis_related protein 1	2	3	3	0.91	0.94	0.76
		ASASDGSSFVVAR			0.93	3.2	2	
		GQCGENLAWASYDQTGK			0.90	4.0	2	
Q9H6S3	ES8L2	Epidermal growth factor receptor kinase substrate 8_like protein 2	2	3	4	0.78	0.36	0.07
		IVENLGILTGPQLFSLNK			0.83	2.8	2	
		SQPVSQPLTYESGPDEVR			0.35	3.8	2	
Q9HC84	MUC5B	Mucin_5B	36	47	94	0.79	0.06	0.92
		VYKPCGPIQPATCNSR			0.21	3.7	2	
		SEQLGGDVESYDK			0.24	4.2	2	
		VCSTWGDFHYK			0.45	2.6	2	
		AAGGAVCEQPLGLECR			0.26	4.4	2	
		MCFNYEIR			0.14	2.8	2	
		TGLLVEQSGDYIK			0.26	3.8	2	
		SEDCLCAALSSYVHACAAK			0.56	4.7	2	
		GYQVCPVLADIECR			0.39	4.5	2	
		LEVPCQSLEAYAELCR			0.40	3.4	2	
		TLLGPAFAECHALVDSTAYLAACAQDLCR			0.89	4.0	3	
		LSPSCPDALAPK			0.35	2.5	2	
		LTPLQFGNLQK			0.17	2.8	2	
		YSAEAQAMQHQCTCCQER			0.09	4.5	3	
		TGCCYSCEEDSCQVR			0.10	4.7	2	
		TCPLNMQHQECGSPCTDTCSNPQR+Oxidation(5)			0.30	4.2	3	
		AQAQPGVPLR			0.02	2.8	2	
		AGCHFYAVCNQHCDIDR			0.25	4.2	3	
		CGLTDNENCLK			0.27	2.8	2	
		TCPLNMQHQECGSPCTDTCSNPQR			0.32	4.6	3	
		LSCLGASLQK			0.45	2.9	2	
		CVAQCGCYDKDGNYYDVGAR			0.31	3.9	3	
		IVTENIPCGTTGTTCSK			0.11	4.4	2	
		VHCDVHFGLVCR			0.19	3.4	2	
		QCSILHGPTFAACR			1.24	2.6	2	
		CPPSQPFFNEDQMK+Oxidation(12)			0.11	2.4	2	
		GATGGLCDLTCPPTK			0.20	4.4	2	
		LYDLHGDCSYVLSK			0.94	4.0	2	

		CPPSQPFFNEDQMK			0.49	3.3	2	
		WVSNCQSCVCDEGSVSVQCKPLPCDAQGQPPPCNRPGFVTVTRPR			0.41	4.0	5	
		NSFEDPCSLSVENENYAR			0.15	5.7	2	
		NPSGHCLVDLPGLEGCYPK			0.54	4.9	2	
		AAQLPDMPLEELGQQVDCDR+Oxidation(6)			0.44	4.5	2	
		SVVGDALEFGNSWK			0.64	3.8	2	
		AAQLPDMPLEELGQQVDCDR			0.27	4.9	2	
		ELGQVVECSLDFGLVCR			0.21	4.6	2	
		AENYPEVSIDQVGQVLTCSLETGLTCK			0.73	5.0	3	
Q9NP55	PLUNC	Protein Plunc	2	2	12	1.56	2.19	0.32
		LQVNTPLVGASLLR			1.56	3.2	2	
		VTSVIPGLNNIIDIK			1.55	3.3	2	
Q9NQ79	CRAC1	Cartilage acidic protein 1	16	25	116	0.67	0.20	0.00
		DVAAEAGVSK			0.86	2.8	2	
		LVNIAVDER			0.53	2.9	2	
		GVASLFAGR			0.63	3.2	2	
		GNQGFNNNWLR			0.76	2.5	2	
		WEDILSDEVNVAR			0.73	4.7	2	
		EHGDPLIEELNPGDALEPEGR			0.89	4.4	2	
		IIDGGSGYLCEMEPVAHFGLGK			0.80	3.8	2	
		GVSVGPILSSSASDIFCDNENGPNFLFHNR			0.84	4.0	3	
		DKPVCVNTYGSYR			0.54	2.7	2	
		VDIVYGNWNGPHR			0.70	2.5	2	
		GVALADFNR			0.64	3.2	2	
		GDGTFVDAAASAGVDDPHQHGR			0.69	5.2	2	
		DEASSVEVTWPDGK			0.90	3.4	2	
		LYLQMSTHGK			0.48	2.4	2	
		QGNAIGVTACDIDGDGR			0.74	3.3	2	
		NVASGEMNSVLEILYPR			0.95	3.6	3	
Q9NQC3	RTN4	Reticulon_4	2	2	2	4.76	9.58	0.28
		HQAQIDHYLGLANK			7.07	3.7	2	
		YSNSALGHVNCTIK			3.06	3.6	2	
Q9NUQ9	FA49B	Protein FAM49B	2	3	3	0.96	0.77	0.38
		DQPPNSVEGLLNALR			0.96	3.1	2	
		INNVPAEGENEVNNELANR			2.61	2.7	2	
Q9NY65	TBA8	Tubulin alpha_8 chain	8	14	61	1.01	0.41	1.00
		NLDIERPTYTNLNR			0.53	2.7	2	
		VGINYQPPTVVPGGDLAK			0.61	4.6	2	
		AFVHWYVGEGMEEGEFSEAR			1.27	4.8	3	
		AVCMLSNTTAIAEAWAR			1.05	4.3	2	
		AVMIDLEPTVVDEVR+Oxidation(2)			0.97	2.4	2	
		LISQIVSSITASLR			1.11	4.1	2	
		AFVHWYVGEGMEEGEFSEAR+Oxidation(10)			0.75	4.1	3	
		TIQFVDWCPTGFK			0.98	3.8	2	
Q9P121	NTRI	Neurotrimin	3	6	24	1.04	0.95	1.00
		EQSGDYECSASNDVAAPVVR			0.68	5.6	2	
		VTVNYPPYISEAK			1.16	2.9	2	
		GTLQCEASAVPSAEFQWYK			1.25	4.7	2	
Q9UBR2	CATZ	Cathepsin Z	4	5	5	7.92	6.90	0.00
		NVDGVNYASITR			3.87	3.3	2	

		YNLAIEEHCTFGDPIV			7.02	2.5	2	
		VGDYGSLSGR			6.65	2.9	2	
		DQECDKFNQCGTCNEFK			11.12	4.6	2	
Q9UEW3	MARCO	Macrophage receptor MARCO	3	3	18	0.36	0.22	0.00
		LQVLQAQLTWVR			0.42	3.9	2	
		VSHEHLLQR			0.25	2.9	2	
		GTESTLWSCTK			0.62	2.9	2	
Q9UGM3	DMBT1	Deleted in malignant brain tumors 1 protein	11	17	73	0.74	0.12	0.17
		GRVEVLYR			1.27	2.8	2	
		QLGCGWATSAPGNAR			0.70	3.4	2	
		FGQGSGPIVLDDVR			1.12	4.3	2	
		GSWGTVCDDSWDTNDANVVCR			0.44	5.4	2	
		GWFSHNCNHR			1.75	2.7	2	
		DDTYGPYSSPSLR			0.52	2.5	2	
		QLGCGWAMSAPGNAR			0.79	2.6	2	
		GSFTSSSNFMSIR			0.90	2.8	2	
		GSWGTVCDDSWDTSDANVVCR			0.09	5.6	2	
		VDVVLGPIQLQTPPR			0.74	4.0	2	
		GSWGTVCDDYWDTNDANVVCR			0.48	4.9	2	
Q9UGT4	SUSD2	Sushi domain_containing protein 2	7	11	49	0.85	0.25	0.00
		AGTWLAVHPNK			0.57	2.5	2	
		FFTDYGCDMEQGSVCTYHPGAVHCVR			0.74	4.7	4	
		GTGLTAVAVQEGNSDVVEVR			0.58	5.2	2	
		HDPTFEPLFPSETTLNPSLAQEAAK			0.85	5.6	3	
		GHDWGAPPFR			0.61	2.3	2	
		DVQALWTNDHALAWHLSDDFR			0.84	3.9	2	
		DSIQTLGHVDSSGQVHCVSPLLYESGR			0.53	4.2	3	
Q9UIF8	BAZ2B	Bromodomain adjacent to zinc finger domain protein 2B	2	2	4	1.14	0.99	0.56
		SIAWEKSIMK+Oxidation(8)			9.86	2.5	2	
		ETYMKLIVPSPDVLKAGNK			1.10	2.3	2	
Q9UIF9	BAZ2A	Bromodomain adjacent to zinc finger domain protein 2A	2	3	4	1.35	1.68	0.27
		QFPEVIK			3.68	2.3	2	
		QQMILEEMK+Oxidation(2),Oxidation(7)			1.29	2.1	1	
Q9ULV4	COR1C	Coronin_1C	2	3	4	1.52	1.40	0.31
		AIFLADGNVFTTGFSR			1.52	3.3	2	
		SIKDTICNQDER			18.05	2.3	2	
Q9ULZ3	ASC	Apoptosis_associated speck_like protein containing a CARD	3	4	10	2.33	1.81	0.30
		VLTDEQYQAVR			2.28	3.0	2	
		DLLLQALR			2.64	2.8	2	
		GALLSMDALDLTDK			1.30	3.0	2	
Q9UQ52	CNTN6	Contactin_6	4	4	8	0.72	0.60	0.38
		SDAGSYTCIATNQFGTAK			0.78	3.6	2	
		VVAGNSIGIGEPSEPSELLR			0.63	2.7	2	
		TVSDGGDGSSSEEIR			1.18	2.8	2	
		FVSQETGNLYIAK			0.51	3.0	2	
Q9Y279	VSIG4	V_set and immunoglobulin domain_containing protein 4	2	4	16	0.97	0.51	1.00
		GDVNLPCTYDPLQGYTQVLVK			0.97	4.5	2	
		SHYTCEVTWQTPDGNQVVR			0.94	5.0	2	

Q9Y3Z3	SAMH1	SAM domain and HD domain_containing protein 1	2	2	2	5.33	19.55	0.78
		YVGETQPTGQIK			0.00	2.5	2	
		EWNDSTSVQNPTR			5.33	3.5	2	
Q9Y490	TLN1	Talin_1	3	3	6	1.56	1.39	0.35
		AAAFEEQENETVVVK			1.29	3.6	2	
		AVSSAIAQLLGEVAQGNENYAGIAAR			1.60	4.1	3	
		AVAEQIPLLVQGVR			2.95	2.7	2	
Q9Y624	JAM1	Junctional adhesion molecule A	2	2	11	0.65	0.82	0.24
		ITASYEDR			0.65	2.3	2	
		VTFLPTGITFK			0.65	2.7	2	
Q9Y6R7	FCGBP	IgGFc_binding protein	9	12	32	1.48	0.82	0.18
		VVAEVQICHGK			1.92	2.7	2	
		TCQGSCAALSGLTGCTTR			1.43	4.2	2	
		ASQHGSDVVIETDFGLR			2.30	4.3	2	
		VNGVLTALPVSVADGR			1.46	4.1	2	
		AGCVAESTAVCR			0.97	3.0	2	
		AIGYATAADCGR			1.70	3.2	2	
		VTLQPYNVAQLQSSVDLSGSK			1.51	4.4	2	
		VAVIVSNDHAGK			1.65	3.1	2	
		VPAAYAGSLCGLCGNYNQDPADDLK			1.92	4.5	3	

Supplemental Table III

Key biological processes in altered proteins using Gene Ontology analysis

Accession Number	Gene Name	Protein Name	No. of quantified peptides	Frames	Hits	Ratio	StDev	*p* value
Alcohol metabolic process								
P00325	ADH1B	Alcohol dehydrogenase 1B	2	3	6	12.86	13.23	< 0.01
P02647	APOA1	Apolipoprotein A_I	18	64	449	2.13	0.28	< 0.01
P02656	APOC3	Apolipoprotein C_III	2	5	44	4.24	3.13	< 0.01
P04114	APOB	Apolipoprotein B_100	22	28	86	3.56	0.63	< 0.01
P05091	ALDH2	Aldehyde dehydrogenase_ mitochondrial	12	15	32	2.11	1.40	0.04
P06733	ENOA	Alpha_enolase	9	16	81	1.61	0.50	< 0.01
P09104	ENOG	Gamma_enolase	2	3	17	1.70	1.36	< 0.01
P09467	F16P1	Fructose_1_6_bisphosphatase 1	8	14	58	1.60	0.99	0.02
P09972	ALDOC	Fructose_bisphosphate aldolase C	3	4	8	1.91	1.31	0.05
P30838	AL3A1	Aldehyde dehydrogenase family 3 member A1	9	13	58	3.33	0.89	< 0.01
P37837	TALDO	Transaldolase	3	4	17	2.09	0.51	0.03
P40925	MDHC	Malate dehydrogenase_ cytoplasmic	7	11	48	1.68	0.69	0.02
Cell migration								
O00560	SDCB1	Syntenin_1	4	4	4	0.66	0.39	0.02
P02647	APOA1	Apolipoprotein A_I	18	64	449	2.13	0.28	< 0.01
P02751	FINC	Fibronectin	41	91	436	0.39	0.07	< 0.01
P04114	APOB	Apolipoprotein B_100	22	28	86	3.56	0.63	< 0.01
P05362	ICAM1	Intercellular adhesion molecule 1	12	26	210	0.60	0.14	< 0.01
P12429	ANXA3	Annexin A3	7	12	36	3.34	0.46	< 0.01
P16070	CD44	CD44 antigen	5	10	38	0.56	0.22	< 0.01
P23528	COF1	Cofilin_1	5	17	132	1.56	0.48	< 0.01
P27487	DPP4	Dipeptidyl peptidase 4	2	2	4	0.43	0.38	< 0.01
P35247	SFTPD	Pulmonary surfactant_associated protein D	8	32	330	0.41	0.11	< 0.01
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	3	8	61	1.92	1.34	< 0.01
Wound healing								
P01023	A2MG	Alpha_2_macroglobulin	41	94	547	2.31	0.21	< 0.01
P02647	APOA1	Apolipoprotein A_I	18	64	449	2.13	0.28	< 0.01
P02671	FIBA	Fibrinogen alpha chain	16	32	166	2.78	0.52	< 0.01
P02675	FIBB	Fibrinogen beta chain	21	61	309	3.17	0.40	< 0.01
P02679	FIBG	Fibrinogen gamma chain	16	32	164	2.74	0.91	< 0.01
P02751	FINC	Fibronectin	41	91	436	0.39	0.07	< 0.01
P04114	APOB	Apolipoprotein B_100	22	28	86	3.56	0.63	< 0.01
P04264	K2C1	Keratin_ type II cytoskeletal 1	12	18	75	1.65	0.46	< 0.01
P08758	ANXA5	Annexin A5	7	12	56	2.10	0.63	< 0.01
P16070	CD44	CD44 antigen	5	10	38	0.56	0.22	< 0.01
P21333	FLNA	Filamin_A	25	33	65	7.12	0.47	< 0.01
P23528	COF1	Cofilin_1	5	17	132	1.56	0.48	< 0.01
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	3	8	61	1.92	1.34	< 0.01
Proteolysis								
O96009	NAPSA	Napsin_A	4	8	90	0.39	0.27	< 0.01
P00738	HPT	Haptoglobin	23	69	556	3.22	0.26	< 0.01
P00739	HPTR	Haptoglobin_related protein	2	2	5	0.63	0.34	< 0.01
P01024	CO3	Complement C3	74	231	1701	0.63	0.05	< 0.01

P06681	CO2	Complement C2	15	27	132	0.65	0.14	< 0.01
P07339	CATD	Cathepsin D	10	32	53	2.57	0.85	0.05
P20142	PEPC	Gastricsin	2	3	29	0.19	0.16	< 0.01
P27487	DPP4	Dipeptidyl peptidase 4	2	2	4	0.43	0.38	< 0.01
P61088	UBE2N	Ubiquitin_conjugating enzyme E2 N	2	3	8	1.65	0.85	< 0.01
Q9UBR2	CATZ	Cathepsin Z	4	5	5	7.92	6.90	< 0.01
Oxidation reduction process								
O75874	IDHC	Isocitrate dehydrogenase [NADP] cytoplasmic	4	5	13	1.88	1.03	0.04
P00325	ADH1B	Alcohol dehydrogenase 1B	2	3	6	12.86	13.23	< 0.01
P05091	ALDH2	Aldehyde dehydrogenase_ mitochondrial	12	15	32	2.11	1.40	0.04
P30041	PRDX6	Peroxiredoxin_6	3	4	27	1.79	1.09	0.01
P30838	AL3A1	Aldehyde dehydrogenase family 3 member A1	9	13	58	3.33	0.89	< 0.01
P37837	TALDO	Transaldolase	3	4	17	2.09	0.51	0.03
P40925	MDHC	Malate dehydrogenase_ cytoplasmic	7	11	48	1.68	0.69	0.02
P42330	AK1C3	Aldo_keto reductase family 1 member C3	2	4	8	4.11	1.55	0.02
P53004	BIEA	Biliverdin reductase A	2	2	3	2.66	3.48	0.01
Gluconeogenesis/Glycolysis								
P06733	ENOA	Alpha_enolase	9	16	81	1.61	0.50	< 0.01
P09104	ENOG	Gamma_enolase	2	3	17	1.70	1.36	< 0.01
P09467	F16P1	Fructose_1_6_bisphosphatase 1	8	14	58	1.60	0.99	0.02
P09972	ALDOC	Fructose_bisphosphate aldolase C	3	4	8	1.91	1.31	0.05
P40925	MDHC	Malate dehydrogenase_ cytoplasmic	7	11	48	1.68	0.69	0.02
Platelet activation								
P01023	A2MG	Alpha_2_macroglobulin	41	94	547	2.31	0.21	< 0.01
P02647	APOA1	Apolipoprotein A_I	18	64	449	2.13	0.28	< 0.01
P02671	FIBA	Fibrinogen alpha chain	16	32	166	2.78	0.52	< 0.01
P02675	FIBB	Fibrinogen beta chain	21	61	309	3.17	0.40	< 0.01
P02679	FIBG	Fibrinogen gamma chain	16	32	164	2.74	0.91	< 0.01
P02751	FINC	Fibronectin	41	91	436	0.39	0.07	< 0.01
P04114	APOB	Apolipoprotein B_100	22	28	86	3.56	0.63	< 0.01
P21333	FLNA	Filamin_A	25	33	65	7.12	0.47	< 0.01
P23528	COF1	Cofilin_1	5	17	132	1.56	0.48	< 0.01
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	3	8	61	1.92	1.34	< 0.01
Inflammatory response								
P01023	A2MG	Alpha_2_macroglobulin	41	94	547	2.31	0.21	< 0.01
P01024	CO3	Complement C3	74	231	1701	0.63	0.05	< 0.01
P02671	FIBA	Fibrinogen alpha chain	16	32	166	2.78	0.52	< 0.01
P02675	FIBB	Fibrinogen beta chain	21	61	309	3.17	0.40	< 0.01
P02679	FIBG	Fibrinogen gamma chain	16	32	164	2.74	0.91	< 0.01
P02743	SAMP	Serum amyloid P_component	3	4	23	8.23	0.95	< 0.01
P02747	C1QC	Complement C1q subcomponent subunit C	3	4	25	0.32	0.25	< 0.01
P02751	FINC	Fibronectin	41	91	436	0.39	0.07	< 0.01
P06681	CO2	Complement C2	15	27	132	0.65	0.14	< 0.01
P0C0L5	CO4B	Complement C4_B	47	112	708	0.65	0.08	< 0.01
P16070	CD44	CD44 antigen	5	10	38	0.56	0.22	< 0.01
P17931	LEG3	Galectin_3	3	3	9	2.52	2.22	< 0.01
P48960	CD97	CD97 antigen	2	2	10	0.65	0.67	0.03

Supplemental Table IV

The 76 significantly altered proteins in BALF of COPD patients (n=10) versus healthy controls (n=10) by the well-controlled ion-current-based approach.

Accession Number	Gene Name	Protein name	No. quantified peptides	Ratio (COPD / Normal)	Standard Deviation	*p* -value	GO Annotation: Cellular Location	Previously reported in COPD	References	Protein abundance
P60709	ACTB	Actin_ cytoplasmic 1	9	1.56	0.2	< 0.01	Cytoplasm			High
P07108	DBI	Acyl_CoA_binding protein	3	1.75	1.92	< 0.01	Cytoplasm			Moderate
P00325	ADH1B	Alcohol dehydrogenase 1B	2	12.86	13.23	< 0.01	Cytoplasm			Low
P30838	ALDH3A1	Aldehyde dehydrogenase family 3 member A1	9	3.33	0.89	< 0.01	Cytoplasm			Moderate
P05091	ALDH2	Aldehyde dehydrogenase_ mitochondrial	12	2.11	1.4	0.04	Cytoplasm	Increased in quadriceps muscles of COPD patients	*International Journal of COPD* 2008, 3: 637–658.	Moderate
P42330	AKR1C3	Aldo_keto reductase family 1 member C3	2	4.11	1.55	0.02	Cytoplasm			Moderate
P01023	A2M	Alpha_2_macroglobulin	41	2.31	0.21	< 0.01	Extracellular	Increased in serum of COPD patients	Am J Respir Crit Care Med. 2011, 183: 1633-1643.	High
P06733	ENO1	Alpha_enolase	9	1.61	0.5	< 0.01	Plasma membrane			High
P12429	ANXA3	Annexin A3	7	3.34	0.46	< 0.01	Plasma membrane			Moderate
P08758	ANXA5	Annexin A5	7	2.1	0.63	< 0.01	Cytoplasm			Moderate
P02647	APOA1	Apolipoprotein A_I	18	2.13	0.28	< 0.01	Extracellular; Plasma membrane	Decreased in induced sputum of COPD patients	*Am J Respir Crit Care Med* . 2010, 181: 1049-60.	High
P04114	APOB	Apolipoprotein B_100	22	3.56	0.63	< 0.01	Extracellular; Plasma membrane			High
P02656	APOC3	Apolipoprotein C_III	2	4.24	3.13	< 0.01	Extracellular			Moderate
P53004	BLVRA	Biliverdin reductase A	2	2.66	3.48	0.01	Cytoplasm	Increased in COPD patients	*Pharmacol Rev.* 2004, 56: 515-548.	Low
Q6NUK1	SLC25A24	Calcium_binding mitochondrial carrier protein SCaMC_1	2	3.33	6.76	< 0.01	Cytoplasm			Low
P07339	CTSD	Cathepsin D	10	2.57	0.85	0.05	Extracellular	Increased in pulmonary macrophages of cigarette smoke-exposed mice	*Int Arch Allergy Immunol* 2005, 138: 169–179.	Moderate
Q9UBR2	CTSZ	Cathepsin Z	4	7.92	6.9	< 0.01	Extracellular			Low
P16070	CD44	CD44 antigen	5	0.56	0.22	< 0.01	Plasma membrane	Decreased in pulmonary macrophage of COPD patients	Respir Res. 2012, 13: 101.	Moderate
P48960	CD97	CD97 antigen	2	0.65	0.67	0.03	Extracellular; Plasma membrane			Moderate
P23528	CFL1	Cofilin_1	5	1.56	0.48	< 0.01	Cytoplasm	Increased in epithelial lining fluid of COPD patients	*Electrophoresis* . 2013 May 28. [Epub ahead of print].	High
P02747	C1QC	Complement C1q subcomponent subunit C	3	0.32	0.25	< 0.01	Extracellular			Moderate
P06681	C2	Complement C2	15	0.65	0.14	< 0.01	Extracellular			High
P01024	C3	Complement C3	74	0.63	0.05	< 0.01	Extracellular	Decreased in serum of COPD patients	*Indian J Med Res* . 1990, 92: 241-245.	High
P0C0L5	C4B	Complement C4_B	47	0.65	0.08	< 0.01	Extracellular	Decreased in serum of COPD patients	*Indian J Med Res* . 1990, 92: 241-245.	High
P27487	DPP4	Dipeptidyl peptidase 4	2	0.43	0.38	< 0.01	Extracellular; Plasma membrane	Decreased in serum of COPD patients	*Clin Biochem* . 2012, 45: 1245-1250.	Low
P02671	FGA	Fibrinogen alpha chain	16	2.78	0.52	< 0.01	Extracellular; Plasma membrane	Increased in serum of COPD patients	Thorax. 2013, 68: 670-676.	High
P02675	FGB	Fibrinogen beta chain	21	3.17	0.4	< 0.01	Extracellular; Plasma membrane	Increased in serum of COPD patients	Thorax. 2013, 68: 670-676.	High

P02679	FGG	Fibrinogen gamma chain	16	2.74	0.91	< 0.01	Extracellular; Plasma membrane	Increased in serum of COPD patients	Thorax. 2013, 68: 670-676.	High
P02751	FN1	Fibronectin	41	0.39	0.07	< 0.01	Extracellular	Decreased in serum of severe COPD and increased in lung tissue of COPD	*Eur Respir J* . 2008, 32: 1451-1457.	High
P21333	FLNA	Filamin_A	25	7.12	0.47	< 0.01	Extracellular; Plasma membrane			High
Q13642	FHL1	Four and a half LIM domains protein 1	2	5.53	6.49	< 0.01	Plasma membrane			Low
P09467	FBP1	Fructose_1_6_bisphosphatase 1	8	1.6	0.99	0.02	Cytoplasm			Moderate
P09972	ALDOC	Fructose_bisphosphate aldolase C	3	1.91	1.31	0.05	Cytoplasm			Moderate
P17931	LGALS3	Galectin_3	3	2.52	2.22	< 0.01	Extracellular; Plasma membrane	Increased in small airway of severe COPD	*Eur Respir J* . 2007, 29: 914-922.	Moderate
Q08380	LGALS3BP	Galectin_3_binding protein	10	0.57	0.1	< 0.01	Extracellular			High
P09104	ENO2	Gamma_enolase	2	1.7	1.36	< 0.01	Plasma membrane			Moderate
P20142	PGC	Gastricsin	2	0.19	0.16	< 0.01	Extracellular			Moderate
P46439	GSTM5	Glutathione S_transferase Mu 5	2	11.26	14.64	< 0.01	Cytoplasm			Low
P00738	HP	Haptoglobin	23	3.22	0.26	< 0.01	Extracellular	Increased in serum of COPD patients	*Am J Respir Crit Care Med. 2011,* 183: 1633-1643.	High
P00739	HPR	Haptoglobin_related protein	2	0.63	0.34	< 0.01	Extracellular			Low
P01859	IGHG2	Ig gamma_2 chain C region	3	0.58	0.22	< 0.01	Extracellular			High
P06331	HV209	Ig heavy chain V_II region ARH_77	2	0.64	0.39	< 0.01	Extracellular			Moderate
P06314	KV404	Ig kappa chain V_IV region B17	2	0.6	0.3	< 0.01	Extracellular			Moderate
P04220	MUCB	Ig mu heavy chain disease protein	7	4.36	0.52	< 0.01	Membrane fraction			High
P05362	ICAM1	Intercellular adhesion molecule 1	12	0.6	0.14	< 0.01	Extracellular; Plasma membrane	Increased in serum of COPD patients	*Biomark Med.* 2012, 6: 805-811.	High
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	4	1.88	1.03	0.04	Cytoplasm			Moderate
P13645	KRT10	Keratin_ type I cytoskeletal 10	12	2.47	0.46	< 0.01	Cytoskeleton			Moderate
P35527	KRT9	Keratin_ type I cytoskeletal 9	4	1.71	1.13	0.04	Cytoplasm			Moderate
P04264	KRT1	Keratin_ type II cytoskeletal 1	12	1.65	0.46	< 0.01	Plasma membrane; Cytoplasm			High
Q5XKE5	KRT79	Keratin_ type II cytoskeletal 79	2	3.43	2.88	< 0.01	Cytoskeleton			Moderate
P51884	LUM	Lumican	5	1.93	1.01	< 0.01	Extracellular	Increased in lung tissue of severe emphysema	*Am J Respir Cell Mol Biol* . 2004, 31 :601-610.	Moderate
Q9UEW3	MARCO	Macrophage receptor MARCO	3	0.36	0.22	< 0.01	Plasma membrane			Moderate
P40925	MDH1	Malate dehydrogenase_ cytoplasmic	7	1.68	0.69	0.02	Cytoplasm			Moderate
Q13421	MSLN	Mesothelin	7	1.88	1.43	0.03	Extracellular; Plasma membrane	Increased in the serum of COPD patients	*Clin Cancer Res* . 2007, 13: 5076-5081.	Moderate
P15941	MUC1	Mucin_1	3	0.64	0.44	< 0.01	Extracellular; Plasma membrane			Moderate
P35749	MYH11	Myosin_11	2	4.01	4.03	< 0.01	Cytoplasm			Moderate
O96009	NAPSA	Napsin_A	4	0.39	0.27	< 0.01	Extracellular			High
P62937	PPIA	Peptidyl_prolyl cis_trans isomerase A	3	1.92	1.34	< 0.01	Extracellular			Moderate
P30041	PRDX6	Peroxiredoxin_6	3	1.79	1.09	0.01	Cytoplasm			Moderate
P30086	PEBP1	Phosphatidylethanolamine_binding protein 1	4	1.9	0.95	< 0.01	Extracellular			Moderate
Q15149	PLEC	Plectin	6	2.31	0.34	< 0.01	Plasma membrane			Moderate

Q7Z7M9	GALNT5	Polypeptide N_acetylgalactosaminyltransferase 5	2	0.64	0.57	0.01	Cytoplasm			Low
P41222	PTGDS	Prostaglandin_H2 D_isomerase	2	2.03	1.46	< 0.01	Extracellular			Moderate
Q8IWL2	SFTPA1	Pulmonary surfactant_associated protein A1	13	0.28	0.03	< 0.01	Extracellular	Decreased in lung tissue of COPD patients	*Chest* . 2010, 137: 37-45.	High
P35247	SFTPD	Pulmonary surfactant_associated protein D	8	0.41	0.11	< 0.01	Extracellular	Decreased in BALF and increased in serum of COPD patients	*Respir Res.* 2011, 12: 29.	High
Q8NFJ5	GPRC5A	Retinoic acid_induced protein 3	3	0.64	0.44	0.02	Plasma membrane			Moderate
P07998	RNASE1	Ribonuclease pancreatic	5	0.63	0.19	< 0.01	Extracellular			Moderate
P02743	APCS	Serum amyloid P_component	3	8.23	0.95	< 0.01	Extracellular			Moderate
O75368	SH3BGRL	SH3 domain_binding glutamic acid_rich_like protein	3	1.89	1.35	< 0.01	Cytoplasm			Moderate
O95436	SLC34A2	Sodium_dependent phosphate transport protein 2B	3	0.61	0.14	< 0.01	Plasma membrane			Moderate
O00560	SDCBP	Syntenin_1	4	0.66	0.39	0.02	Plasma membrane			Low
P37837	TALDO1	Transaldolase	3	2.09	0.51	0.03	Cytoplasm			Moderate
Q15582	TGFBI	Transforming growth factor_beta_induced protein ig_h3	7	0.58	0.18	< 0.01	Extracellular			Moderate
P37802	TAGLN2	Transgelin_2	7	1.74	0.97	< 0.01	Plasma membrane	Increased in lung tissue of smoking-induced emphysema	*Chest.* 2011, 140: 569A.	High
P61088	UBE2N	Ubiquitin_conjugating enzyme E2 N	2	1.65	0.85	< 0.01	Cytoplasm			Moderate
P08670	VIM	Vimentin	26	3.12	0.55	0.03	Plasma membrane; Cytoplasm	Increased in quadriceps muscles of COPD patients	*International Journal of COPD* 2008, 3: 637–658	High

The abundance of proteins observed in BALF was indicated by total spectral counts or peptide hits gained in the COPD patients vs. healthy controls dataset. The first quartile (top 25%) of proteins ranked by spectral count (high to low) were designated as high-abundance proteins; the 25-75th percentiles were designated as moderate-abundance proteins; and the last quartile of proteins were designated as low-abundance proteins. BALF: bronchoalveolar lavage fluid; COPD: chronic obstructive pulmonary disease; GO: gene ontology.