Supplemental Figures 1a-k. MALDI-O-TOF mass spectra of peptides resulted from in gel trypsin-digested protein spots excised from preparative pick gel. Mass spectra were acquired on a prOTOF 2000 ^{TM} MALDI O-TOF mass spectrometer (PerkinElmer) in the positive ion mode using TOFworks ™, an integrated workflow-based software platform. The peptide ion mass (M + H) were accurate to within 30 ppm after external calibration. The labeled peptide ions (M+H) were used to generate statistically-significant matches to the proteins as indicated in Supplemental Table 1.

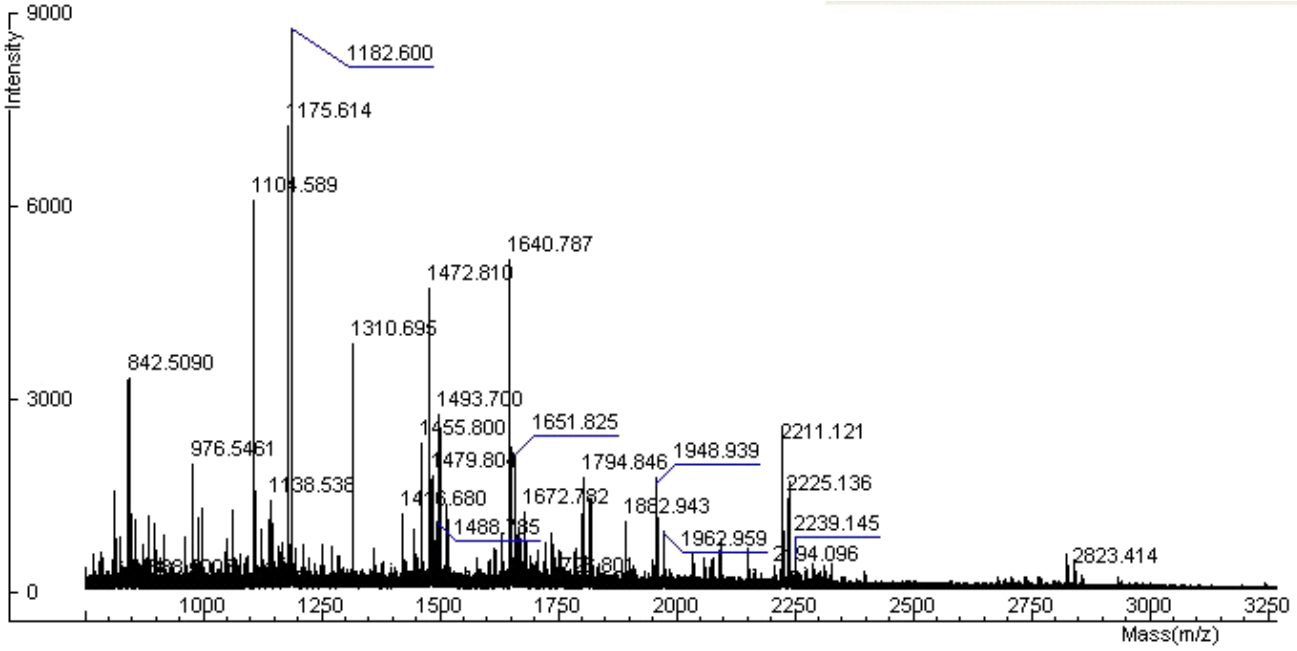

Figure 1a, spot no 13 (*Vil2*)

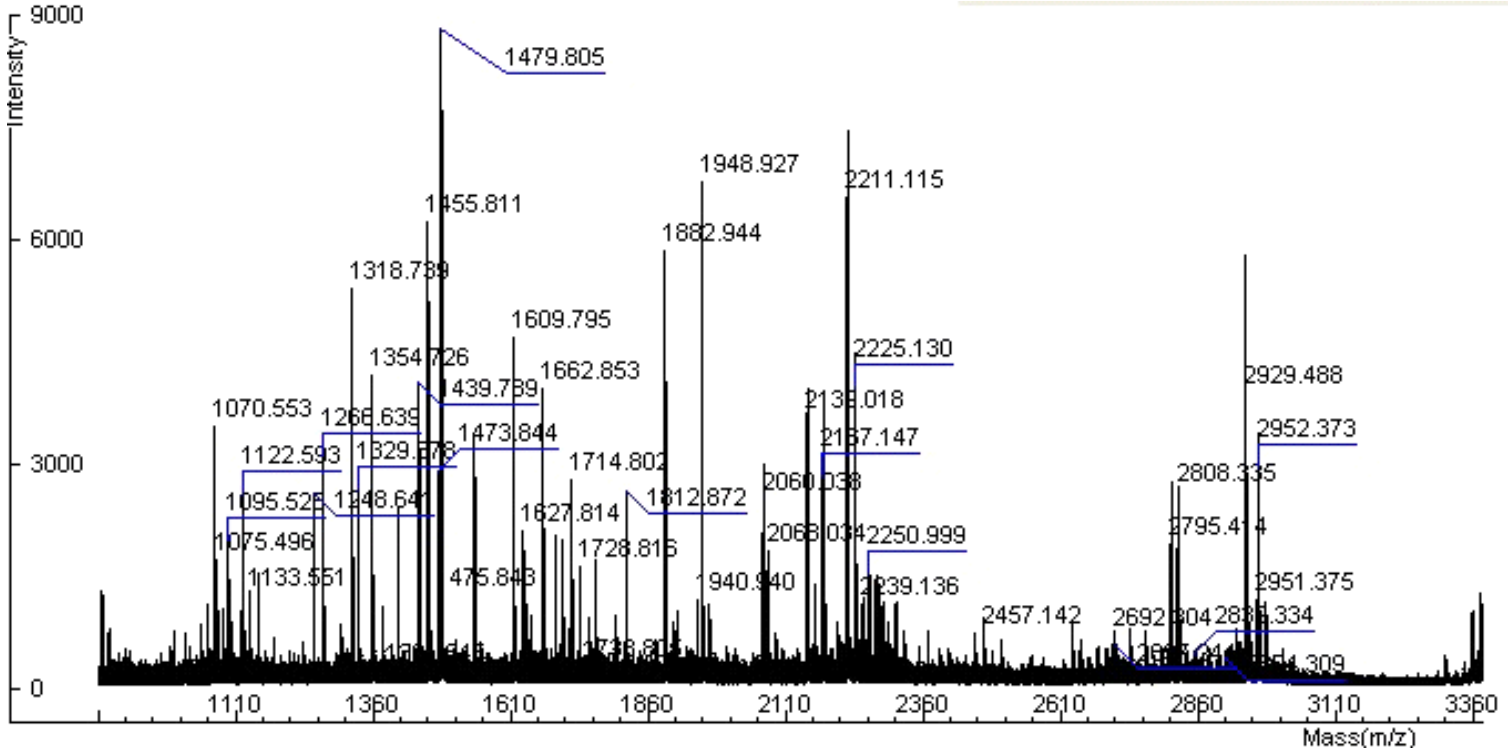

Figure 1b, spot no 16 (*Sdha*)

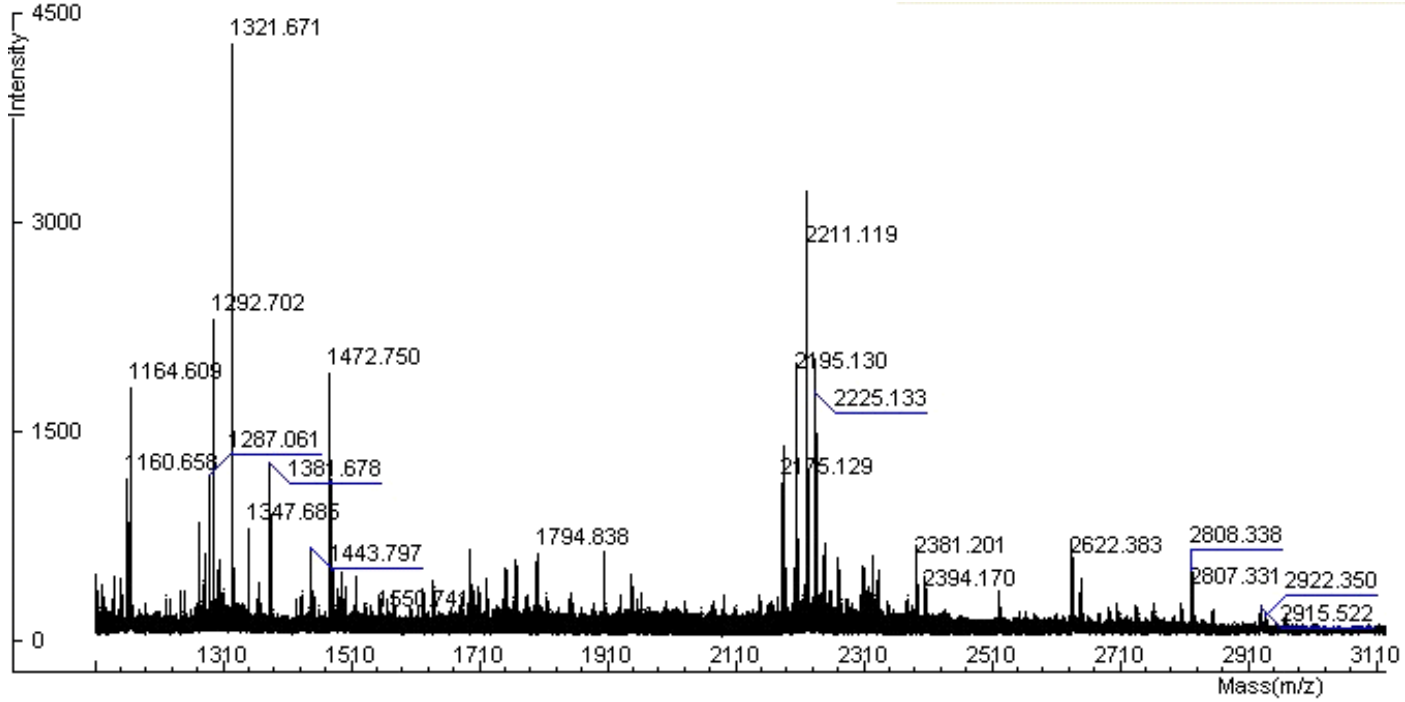

Figure 1c, spot no 17 (*Spin2b*)

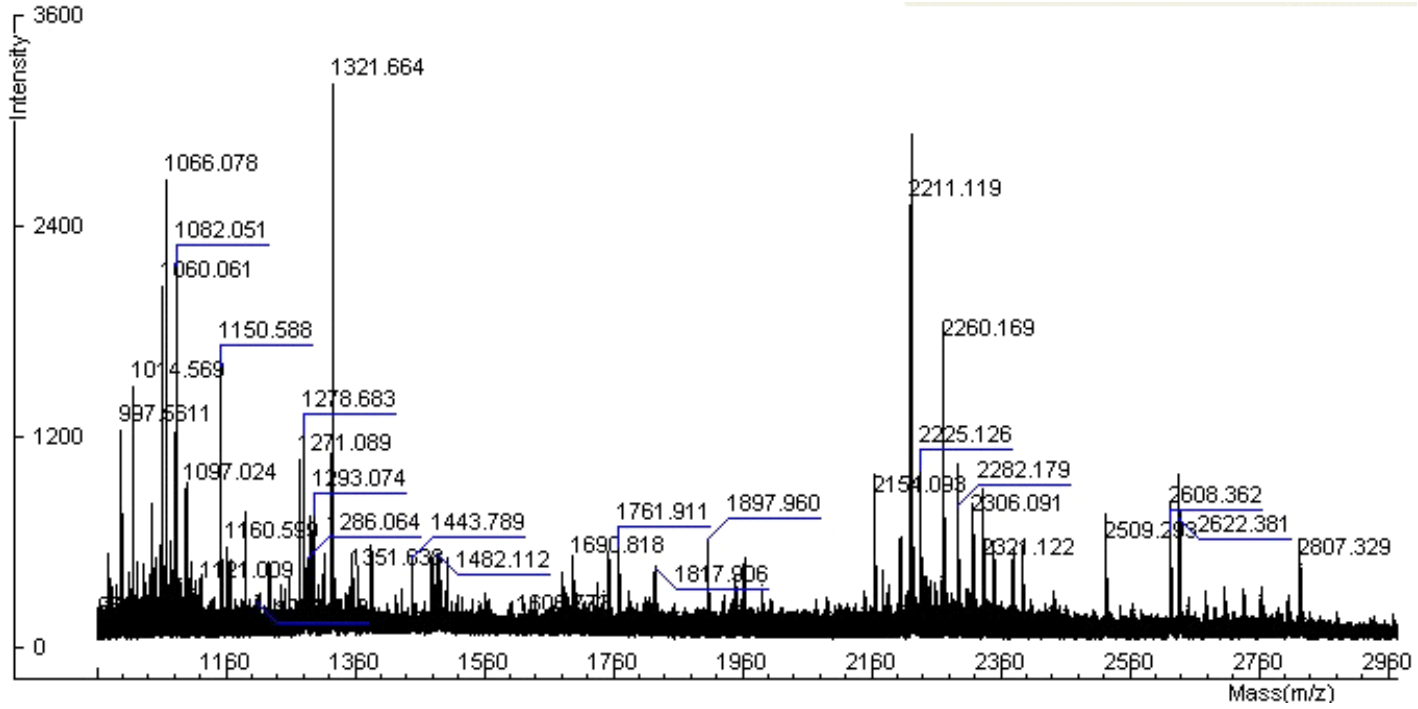

Figure 1d, spot no 18 (*Spin2a*)

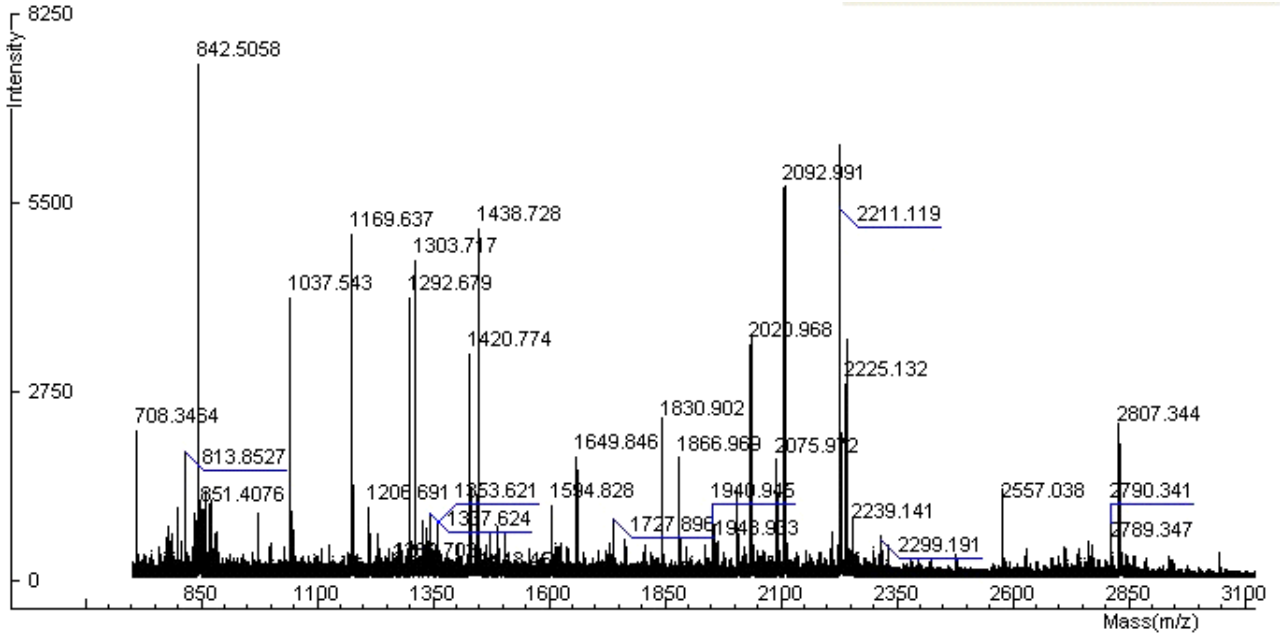

Figure 1e, spot no 21 (*Ehd2*)

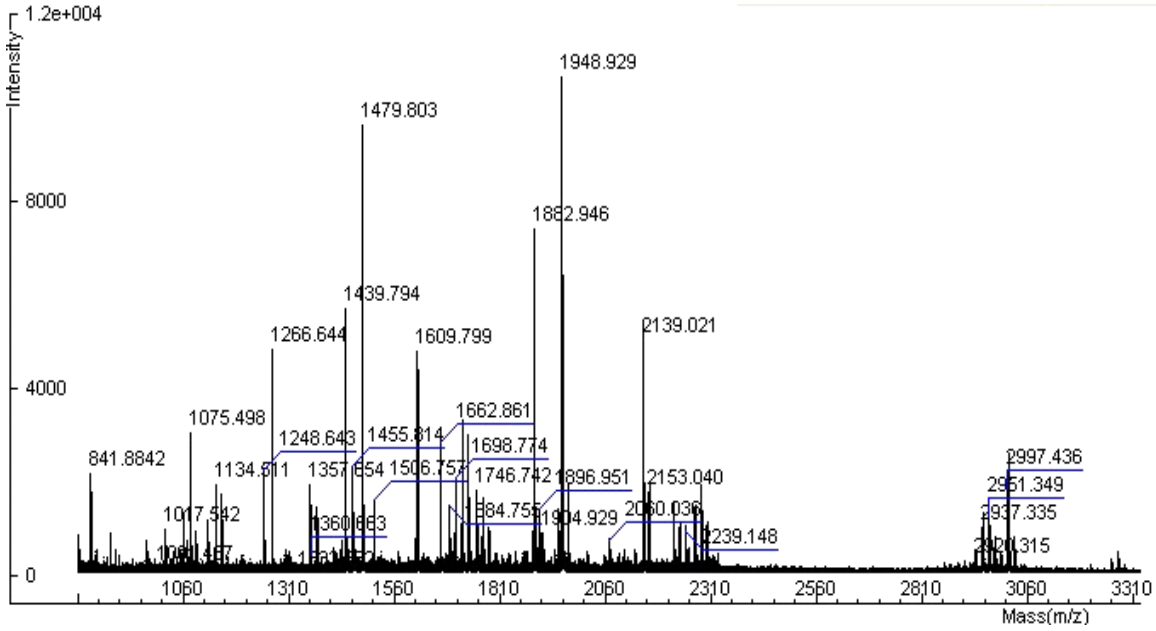

Figure 1f, spot no 25 (*Alb*)

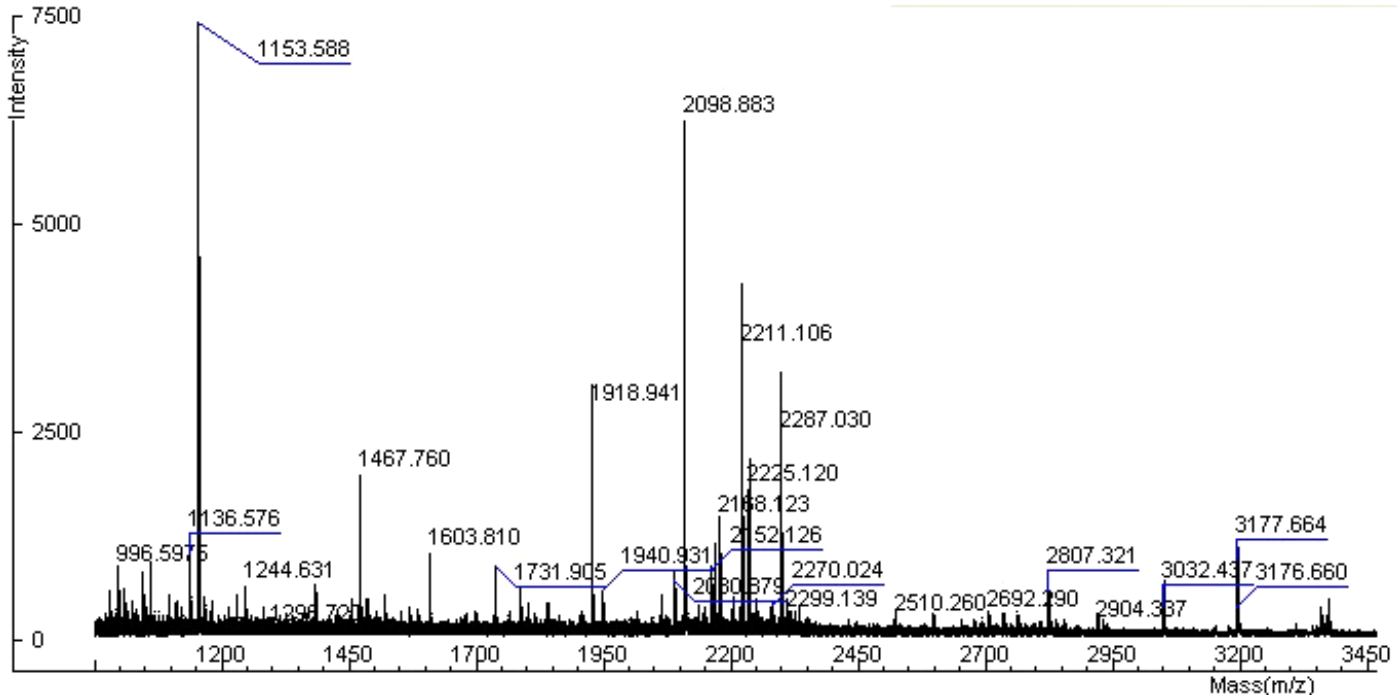

Figure 1g, spot no 30 (*Serpina1*)

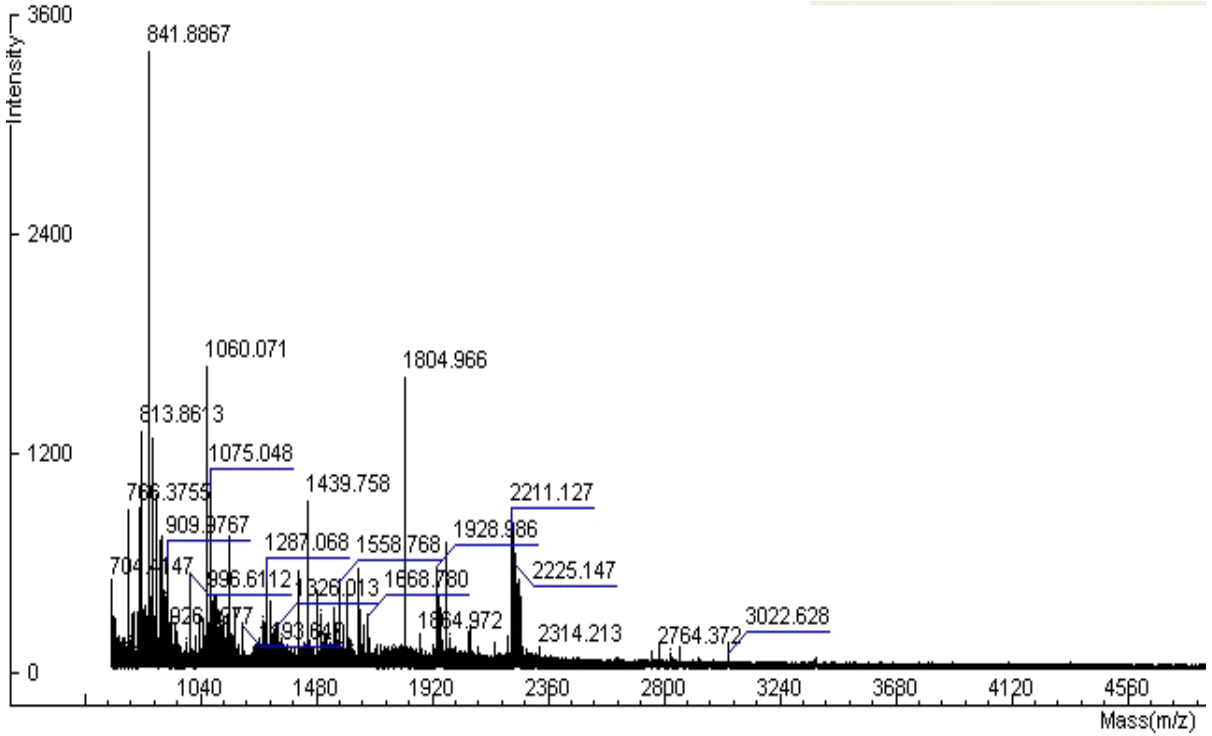

Figure 1h, spot no 34 (*Eno1*)

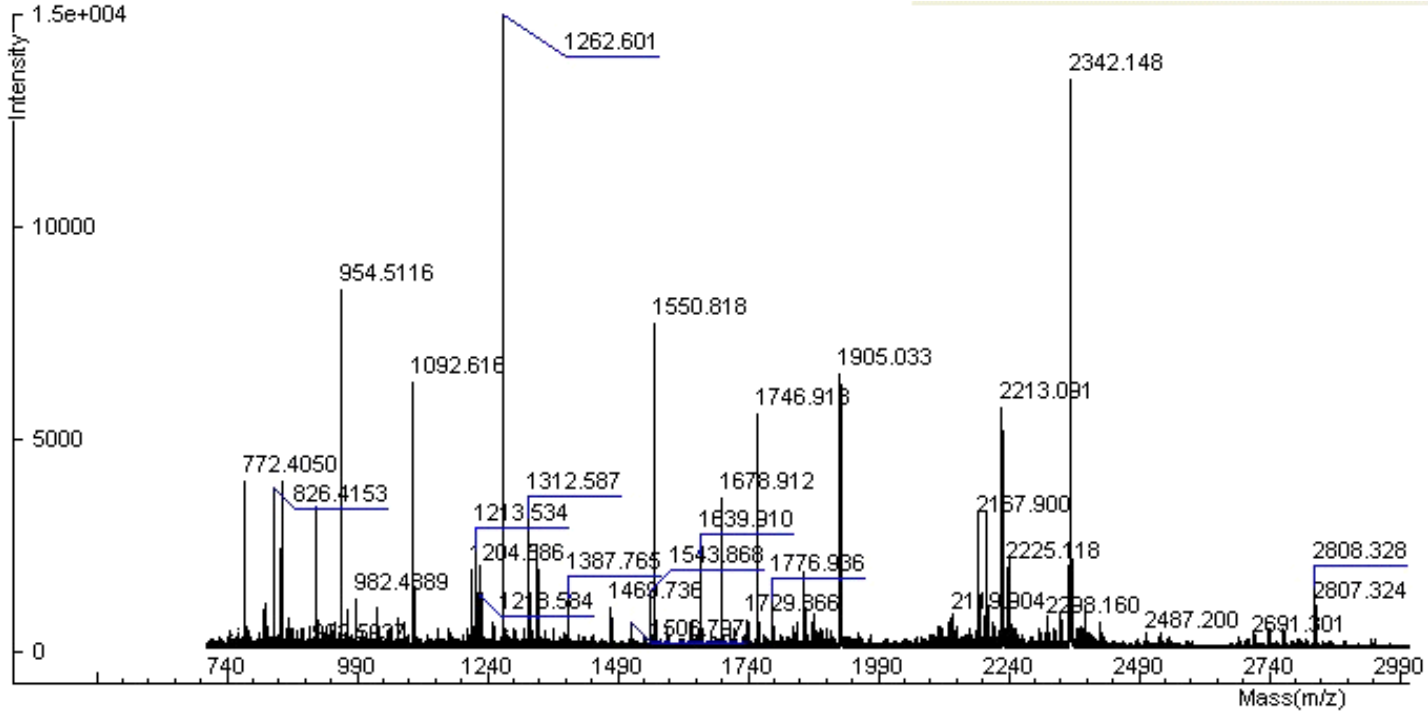

Figure 1i, spot no 41 (*Anxa1*)

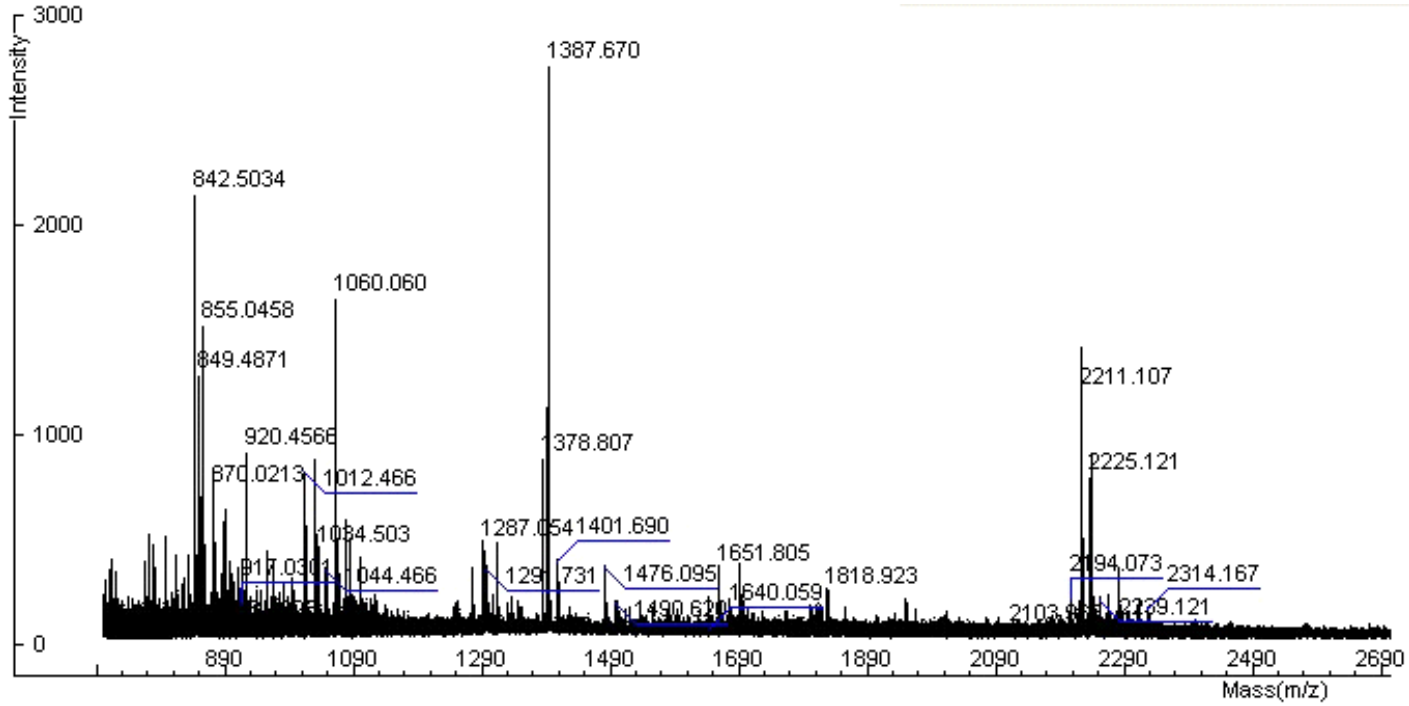

Figure 1j, spot no 43 (*Hp*)

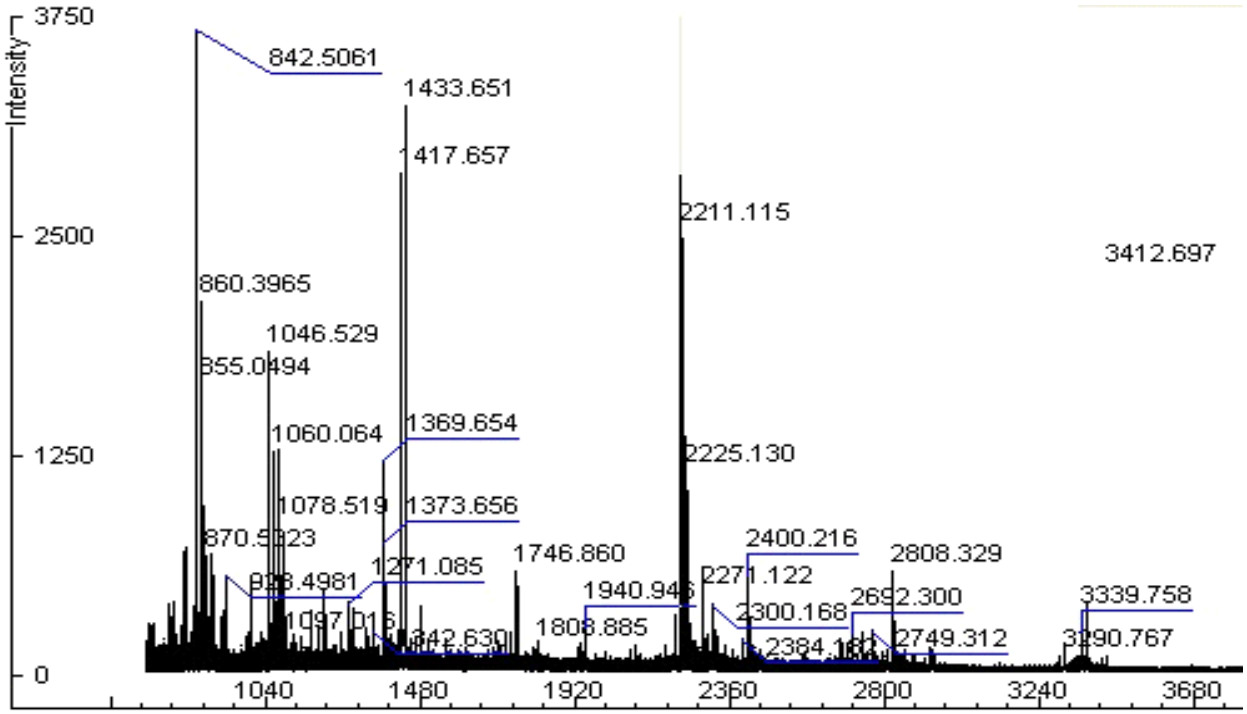

Figure 1k, spot no 51 (*Cnn1*)

Supplemental Table 1. STZ-induced diabetes and duration mediated protein profiles.

Gene name	Pos.	Protein identities	Accession number	MW (KDa), pI[1]	Log_{10}(Average ratio)[2]				One way ANOVA[3] p-value	Two way ANOVA p-value [4]		
					2/1	4/3	3/1	4/2		Treatment	Time	Interact
Alb	25	Albumin	P02770	68.73, 6.09	-1.22	**-1.84**	1.85	1.22	0.011	1.20E-02	0.014	1.70E-01
Anxa1	41	Annexin 1	P07150	38.8, 6.97	1.41	**2.4**	**1.96**	**3.33**	7.80E-06	0.00012	1.30E-05	0.015
Anxa8	45	Annexin A8	Q4FZU6	36.7, 5.55	-1.1	**1.84**	1.5	**3.04**	0.00059	0.038	0.00066	0.0077
Apoa1	52	Apolipoprotein A-I	P04639	30.0, 5.52	1.36	**1.73**	**1.71**	**2.16**	0.00014	2.40E-03	8.00E-05	2.60E-01
Apoa4	38	Apolipoprotein A-IV	P02651	44.5, 5.12	1.35	**1.79**	1.22	**1.62**	0.00017	0.00015	0.0021	0.09
Argbp2	26	Arg/Abl-interacting protein ArgBP2	O35413	134.1, 8.70	**1.55**	1.09	1.17	**-1.81**	0.00083	0.0087	0.00043	0.073
Arhgdib	49	RHO, GDP dissociation inhibitor (GDI) beta	Q5M860	22.9, 4.98	-1.12	**1.87**	**1.67**	**3.08**	0.0001	0.045	4.80E-05	0.0075
Blmh	35	Bleomycin hydrolase	P70645	52.3, 6.04	1.15	**1.52**	1.13	**1.37**	0.004	0.0027	0.047	0.071
Capg	39	Capping protein (actin filament),	Q6AYC4	38.8, 6.11	1.09	**1.54**	1.24	**1.55**	0.0068	0.015	0.017	0.063
Ces3	32	Carboxylesterase 3	P16303	62.2, 6.21	**-1.95**	-1.25	1.1	**1.7**	0.0032	0.0036	0.043	0.028
Ckap4	22	Cytoskeleton-associated protein 4	gi|34862422|	63.5, 5.44	-1.45	**-2.10**	1.36	-1.07	0.015	0.0037	0.84	0.12
Cnn1	51	Calponin	Q08290	33.3, 8.6	**-2.43**	1.88	**-4.29**	1.06	0.021	0.79	0.022	0.015
Col1a1	9	Procollagen type 1, alpha 1	P02454	137.8, 5.77	**-2.13**	**-2.69**	-2.61	**-2.1**	0.0001	0.00011	0.00076	0.29
Col1a2	10	Procollagen type 1, alpha 2	P02466	129.7, 9.39	**-2.03**	**-2.76**	-1.84	-2.5	0.018	0.017	0.11	0.23
Col6a1	6	Procollagen, type VI, alpha 1	gi|109509939|	108.8, 5.21	-1.48	**-4.29**	1.44	**-2.01**	2.40E-05	5.70E-06	0.15	0.0006
Csde1	11	Unr protein, cold shock protein domain	P18395	88.9, 5.97	1.13	-1.46	-1.35	**-2.24**	0.0014	0.14	0.00071	0.021
Dmn	5	Desmuslin	Q810D0	140.7, 5.06	-1.35	**-4.14**	**1.76**	-1.74	7.10E-06	1.90E-06	0.92	9.90E-05
Ehd2	21	EH-domain containing 2	Q4V8H8	61.2, 6.12	-1.05	**-1.54**	-1.09	**-1.45**	0.0023	0.0049	0.02	0.019
Eno1	34	Alpha-enolase (2-phospho-D-glycerate hydro-lyase	P04764	47.1, 6.16	1.04	**1.55**	1.09	**1.43**	0.017	0.016	0.17	0.038
Etfa	47	Alpha ETF	P13803	34.9, 8.62	-1.3	**-1.88**	1.1	-1.05	0.018	0.0041	0.49	0.18
Fbln5	29	Fibulin 5	Q9WVH8	50.1, 4.51	1.53	**2.46**	**2.28**	**3.66**	2.20E-05	0.0016	7.70E-06	0.3
Flna	1	Alpha-Filamin	gi|109462323|	281.2, 5.69	-1.45	**-2.19**[a]	**-2.32**	**-3.49**	0.0011	0.0063	0.0013	0.093
Flnc	4	Filamin C, gamma	gi|109473205|	281.7, 5.54	-1.21	**-1.51**	-1.14	-1.32	0.0098	0.0055	0.079	0.2
Gnb1	46	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	P54311	37.4, 5.40	-1.26	**-2.13**	1.05	**-1.6**	0.0056	0.0019	0.1	0.049
Gsta3	50	glutathione-S-transferase, alpha type3	P04904	25.5, 8.89	-1.3	**-1.65**	-1.18	**-1.48**	8.60E-05	6.90E-05	0.0014	0.1
Hnrnpk	28	Heterogeneous nuclear ribonucleoprotein K	P61980	50.97, 5.39	1.05	**1.58**	**1.29**	**1.72**	0.002	0.012	0.0038	0.033

Supplemental Table 1 continued

Gene name	Pos.	Protein identities	Accession number	MW (KDa), pI[1]	Log_{10}(Average ratio)[2]				One way ANOVA[3] p-value	Two way ANOVA p-value [4]		
					2/1	4/3	3/1	4/2		Treatment	Time	Interact
Hnrpa2b1	48	Heterogeneous nuclear ribonucleoprotein A2/B1	gi|109473494|	37.4, 8.97	1.11	**1.58**	1	1.27	0.034	1.20E-02	0.66	9.70E-02
Hp	43	Haptoglobin	P06866	38.6, 6.10	**-1.79**	1.18	1.87	**3.96**	0.00037	0.08	7.00E-05	0.096
Hspa8	15	Hsc70-ps1	P63018	70.9, 5.43	-1.33	**-1.81**	**1.8**	1.33	0.0023	0.0038	0.0069	0.15
Hspb1	53	Heat shock protein 27	P42930	22.8, 6.12	**1.47**	**2.13**	**1.49**	**2.15**	0.00021	0.00024	0.00021	0.05
Kng1	20	Major acute phase alpha 1	P01048	47.0, 5.99	-2.17	**-1.89**	-1.14	1.01	0.019	0.003	0.61	0.9
Krt1-12	36	Keratin complex 1 gene 12	Q6IFW5	48.8, 4.71	-1.02	**1.6**	**2.5**	**4.08**	0.001	0.086	0.0003	0.09
Lamc1	3	Laminin gamma-1	gi|109498845|	177.4, 5.09	1.06	**-1.84**	-1.03	**-2.1**	0.00097	0.02	0.002	0.0081
Lmna	14	Lamin A	P48679	71.6, 6.20	-2.02	**-1.62**	1.3	**1.62**	0.00018	7.50E-05	0.0024	4.30E-01
Lum	27	Lumican	P51886	38.3, 6.00	-1.27	**-1.97**	**1.7**	1.09	0.0037	0.0025	0.022	0.059
Mrlcb	54a	Myosin regulatory light chain 2-B, smooth muscle isoform	P18666	19.8, 4.78	**1.88**	1.05	1.02	**-2.20**	5.20E-07	4.80E-05	1.10E-06	0.00014
Mrlcb	54b	Myosin regulatory light chain 2-B, smooth muscle isoform	P18666	19.8, 4.78	**1.80**	1.03	1.02	**-1.69**	0.00013	0.00072	0.0027	0.0018
Myh11	2	Myosin heavy polypeptide smooth muscle	gi|109489759|	227.3, 5.41	-1.2	**-1.8**	1.09	-1.31	0.037	0.02	0.35	0.14
Nefl	19	Neurofilament light polypeptide	P19527	61.4, 4.63	-1.31	**-2.13**	1.36	-1.2	0.026	0.0074	0.85	0.12
Nid1	8	Nidogen 1	gi|109505096|	137.0, 5.24	-1.09	**-1.73**	**-1.29**	**-2.04**	0.0002	0.0021	0.00064	0.0096
P4hb	33	Prolyl 4-hydroxylase, beta polypeptide	P04785	56.9, 4.82	1.26	**1.62**	**1.62**	**1.84**	0.001	0.006	0.0009	0.18
Ppp2r1a	23	Protein phosphatase 2	Q5XI34	65.3, 5.00	-1.07	**-1.54**	1.38	-1.01	0.013	0.012	0.12	4.60E-02
Prkcsh	12	protein kinase C substrate 80K-H	gi|109484382|	59.2, 4.44	-1.38	**-1.64**	1.07	-1.11	0.0077	0.0014	0.6	0.18
S100a9	56	S100 calcium binding protein A9 (calgranulin B)	P50116	13.1, 7.05	-1.05	**3.12**	4.37	**14.35**	1.20E-06	0.034	1.780E-07	0.022
Sdha	16	Succinate dehydrogenase complex subunit A	Q0QF18	61.1, 6.04	-1.3	**-1.79**	1.42	1.03	0.043	0.013	0.16	0.57
Serpina1	30	Alpha-1-proteinase inhibitor	P17475	46.1, 5.70	**1.72**	**2.38**	**2.29**	**3.16**	1.30E-06	2.80E-05	1.30E-06	0.082
Serpinb1a	37	Serine or cysteine protease inhibitor, clade B member 1a	Q4G075	42.7, 5.92	-1.08	**1.91**	1.44	**2.96**	0.002	0.047	0.0024	0.019
Sgta	44	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	O70593	34.2, 5.05	-1.6	1.17	**2.29**	**4.28**	0.00016	0.26	2.60E-05	0.067
Spin2a	18	Serine protease inhibitor 2a	P05544	68.2, 5.31	-1.45	**-1.83**	1.6	1.26	0.014	0.005	0.12	0.23
Spin2b	17	Serine protease inhibitor	P05545	46.6, 5.31	-1.33	**-1.8**	1.7	1.26	0.011	0.0064	0.059	0.18

Supplemental Table 1 continued

Gene name	Pos.	Protein identities	Accession number	MW (KDa), pI[1]	Log_{10}(Average ratio)[2]				One way ANOVA[3] p-value	Two way ANOVA p-value [4]		
					2/1	4/3	3/1	4/2		Treatment	Time	Interact
Tagln	55	Transgelin	P31232	22.6, 8.87	-1.61	1.37	**-2.68**	-1.21	0.0091	0.95	0.0045	0.029
Taldo1	42	Transaldolase 1	Q9EQS0	37.5, 6.57	-1.03	**1.88**	**1.73**	**2.81**	0.0015	0.047	0.00098	0.031
Tuba1	31	Tubulin alpha 1	P68370	50.1, 4.94	**1.43**	**1.58**	**1.82**	**2.01**	2.90E-06	0.00011	1.70E-06	0.35
Ublcp1	40	Ubiquitin –like domain containing CTD phosphatase 1	Q5FWT7	36.9, 6.07	-1.08	**2.19**	1.32	**3.13**	0.0003	0.019	0.00033	0.0066
Vcl	7	Vinculin	gi|109502103|	123.6, 5.54	1	**-1.52**	-1.11	**-1.49**	0.0098	0.031	0.036	0.026
Vil2	13	Villin 2	P31977	69.4, 5.83	1.14	**1.62**	**1.56**	**1.95**	0.0029	0.02	0.0024	0.11
Vim	24	Vimentin	P31000	53.7, 5.06	-1.25	**-1.76**	1.07	-1.29	0.0013	0.00036	0.35	0.039

[1]The theoretical molecular weight (MW) and isoelectric point (pI) were calculated using ExPASY compute pI/Mw tool from the data base entries.

[2,3,4] The difference in the standardized abundance for the proteins between the groups are expressed as average ratio that are calculated by taking the means of standardized volume values, from four independent biological replicates per group, for the protein spot in the corresponding groups (Group 1 = one week control, Group 2 = one week STZ-induced diabetic, Group 3 = two months control, Group 4 = two months STZ-induced diabetic), Values are displayed in the range of -∞ to -1 for decreases in expression and +1 to + ∞ for increases in expression. One-way and two-way analysis of variances (ANOVA) p-values calculated using DeCyder software version 6.5, using mixed sample internal standard methods as described in the material and methods.

[a] Boldface for ratios indicating significant fold changes ($p \leq 0.05$)

Supplemental Table 2. Database Search Results of spectra acquired on the prOTOF MALDI O-TOF Mass Spectrometry using TOFworks ™, an integrated workflow-based software platform. Monoisotopic peptide peak lists were generated in the mass range *m*/*z* 500–5000, with a signal to noise ratio threshold of 3.0, and peak resolution threshold of 10,000 using peak picking algorithm of the TOFworks software version 1.0.1.797. Trypsin autolysis fragment peaks and peaks from the matrix were not excluded unless and otherwise stated. The resulting peptide mass lists were used to search the sequences present in an indexed rat subset database (36,274 sequences), created from NCBInr 3,893,302 sequences (release 07/04/06) and stored locally, by running ProFound^{TM} search engine V 2003.6.2.1 (Genomic Solutions, Ann Arbor, MI). The searching criteria used were (1) Protein molecular weight search window of 10 to 300 KDa; (2) protein expectation P<0.001; (3) minimum sequence coverage of 10%; (4) peptide mass tolerance limits of 30 parts per million (ppm); (5) complete cysteine modification by iodoacetamide (57 Da) and partial methionine oxidation (M)(16 Da). A positive identification was accepted when a minimum of 6 peptide masses matched a particular protein with a mass error tolerance of ≤ 30 ppm, and sequence coverage ≥ 25%, and low expectation value (P < 0.001).

Pos.	Gene name	MALDI-TOF MS								
		Accession number	Expect.	% seq. cove.	No. matched peak	No. unmatched peak	Measured mass (M + H)	Match error (ppm)	Peptide Sequence	Modification
13	*Vil2*	P31977	3.09E-04	34	18	24	976.538	0	QLFDQVVK	
							1104.582	5	IGFPWSEIR	
							1175.606	6	IQVWHAEHR	
							1182.592	4	APDFVFYAPR	
							1310.688	5	KAPDFVFYAPR	
							1416.673	7	AQEEAERLEADR	
							1472.802	14	RKPDTIEVQQMK	
							1472.802	19	ITEAEKNERVQR	
							1488.777	1	RKPDTIEVQQMK	1 Oxidation (M)
							1493.692	6	THNDIIHNENMR	
							1509.688	7	THNDIIHNENMR	1 Oxidation (M)
							1640.780	6	RKEDEVEEWQHR	
							1651.817	5	SQEQLAAELAEYTAK	
							1809.850	8	ILQLCMGNHELYMR	1 Oxidation (M)
							1962.951	4	IAQDLEMYGINYFEIK	1 Oxidation (M)
							2023.993	7	FYPEDVADELIQDITQK	
							2082.014	8	VTTMDAELEFAIQPNTTGK	1 Oxidation (M)
							2823.406	1	EGILSDEIYCPPETAVLLGSYAVQAK	
16	*Sdha*	Q0QF18	3.29E-04	54	25	53	1070.545	0	KPFAEHWR	
							1095.518	0	WHFYDTVK	
							1122.585	3	NTIIATGGYGR	
							1133.543	-1	SMQSHAAVFR	

							1149.570	27	SMQSHAAVFR	1 Oxidation (M)
							1318.731	1	VTLDYRPVIDK	
							1329.670	2	GEGGILINSQGER	
							1354.718	2	TGHSLLHTLYGR	
							1400.747	1	VSQLYGDLQHLK	
							1473.836	1	LGANSLLDLVVFGR	
							1539.790	2	GVIALCIEDGSIHR	
							1662.845	25	ANAGEESVMNLDKLR	1 Oxidation (M)
							1757.851	4	AAFGLSEAGFNTACLTK	
							1812.864	4	IDEYDYSKPIEGQQK	
							1940.932	-24	FADGSVRTSELRLSMQK	1 Oxidation (M)
							2068.026	0	VRIDEYDYSKPIEGQQK	
							2167.139	3	DHVYLQLHHLPPEQLATR	
							2249.991	11	TYFSCTSAHTSTGDGTAMVTR	
							2265.991	8	TYFSCTSAHTSTGDGTAMVTR	1 Oxidation (M)
							2274.990	-22	CCCVADRTGHSLLHTLYGR	
							2457.134	9	SHTVAAQGGINAALGNMEEDNWR	1 Oxidation (M)
							2794.406	4	GCGPEKDHVYLQLHHLPPEQLATR	
							2864.340	-18	IDEYDYSKPIEGQQKKPFAEHWR	
							2929.480	7	VSDAISTQYPVVDHEFDAVVVGAGG AGLR	
							2950.367	4	HVNGQDQIVPGLYACGEAACASVH GANR	
17	*Spin2b*	P05545	5.32E-04	31	12	28	1160.650	-28	SVKVPMMKIK	
							1164.601	7	IFSQQADLSR	
							1292.694	5	KIFSQQADLSR	
							1321.6634	5	IAELFSELDER	
							1347.677	4	EQPILSEFQEK	
							1443.742	3	TSMVLVNYLLFK	1 Oxidation (M)
							1472.742	5	ALYQAEAFVADFK	
							2195.122	3	FSISTDYNLEEVLPELGIR	
							2381.193	5	DLTTPYIRDEELSCSVLELK	
							2622.375	5	IKDLTTPYIRDEELSCSVLELK	
							2915.515	-12	IAELFSELDERTSMVLVNYLLFKGK	
							3504.761	9	LSQPEDQAEINTGSALFIDKEQPILSE FQEK	
18	*Spin2a*	P05544	9.51E-05	50	17	38	1014.561	-4	WKDSLIPR	
							1150.580	3	VFSQQADLSR	
							1160.591	13	FSISTDYSLK	
							1187.633	-1	DLYVSQVVHK	

							1278.675	2	KVFSQQADLSR	
							1321.656	0	IAELFSDLEER	
							1351.630	2	DTLSHEDHGKGR	
							1443.781	-2	TSMVLVNYLLFK	1 Oxidation (M)
							1486.753	2	ALYQAEAFIADFK	
							1761.903	3	MQQVESSLQPETLKK	1 Oxidation (M)
							2154.085	3	ALYQAEAFIADFKQPNEAK	
							2260.161	1	AVLDVDETGTEATAATGVATVIR	
							2282.171	-1	ALYQAEAFIADFKQPNEAKK	
							2337.237	-26	QLHSLTLASSNTDFALSLYKK	
							2367.171	2	EVTTPYVRDEELSCSVLELK	
							2608.354	3	IKEVTTPYVRDEELSCSVLELK	
							3532.783	6	LSQPEDQVEINTGSALFIDKEQPILSE FQEK	
21	*Ehd2*	Q4V8H8	7.60E-05	48	23	33	708.339	0	WFAER	
							851.400	0	MGPFVER	1 Oxidation (M)
							855.490	-8	LPNSVLGR	
							1037.535	1	GYDFPAVLR	
							1037.535	-2	AKTWMVGTK	1 Oxidation (M)
							1169.630	6	LLPLEEHYR	
							1206.683	2	VHAYIISYLK	
							1292.671	3	LNPFGNTFLNR	
							1337.616	4	ADMVETQQLMR	1 Oxidation (M)
							1353.613	5	ADMVETQQLMR	2 Oxidation (M)
							1420.766	3	KLNPFGNTFLNR	
							1438.720	5	LFELEEQDLFR	
							1495.703	13	MQELLMAHDFTK	2 Oxidation (M)
							1594.820	4	RLFELEEQDLFR	
							1649.838	5	LEISDEFSEAIGALR	
							1830.894	6	SKYDEIFYNLAPADGK	
							1866.961	5	TSFIQYLLEQEVPGSR	
							1991.040	5	VYIGSFWSQPLLVPDNR	
							2020.960	7	IQLEHHISPGDFPDCQK	
							2092.984	7	QEELESVEAGVQGGAFEGTR	
							2789.339	6	LSDVDRDGMLDDEEFALASHLIEAK	
							2805.337	7	LSDVDRDGMLDDEEFALASHLIEAK	1 Oxidation (M)
							3171.522	7	FGSFHSPALEDADFDGKPMVLVAGQ YSTGK	
25	*Alb*	P02770	1.85E-04	54	24	52	1017.534	5	SIHTLFGDK	

							1067.460	7	CCSGSLVER	
							1075.490	-1	NECFLQHK	
							1075.490	9	CPYEEHIK	
							1134.503	7	CCTLPEAQR	
							1149.590	-15	LVQEVTDFAK	
							1248.635	5	FKDLGEQHFK	
							1266.636	5	FPNAEFAEITK	
							1357.647	7	TVMGDFAQFVDK	
							1373.644	8	TVMGDFAQFVDK	1 Oxidation (M)
							1439.786	6	APQVSTPTLVEAAR	
							1455.807	6	RHPDYSVSLLLR	
							1459.739	6	LQACCDKPVLQK	
							1609.792	6	DVFLGTFLYEYSR	
							1662.853	5	LPCVEDYLSAILNR	
							1683.747	8	LRDNYGELADCCAK	
							1713.798	6	QEPERNECFLQHK	
							1745.734	6	YNEVLTQCCTESDK	
							1748.692	22	ECCHGDLLECADDR	
							1882.938	5	RPCFSALTVDETYVPK	
							2060.028	4	RHPYFYAPELLYYAEK	
							2138.013	7	AETFTFHSDICTLPDKEK	
							2261.972	10	ECCHGDLLECADDRAELAK	
							2937.327	9	CCAEGDPPACYGTVLAEFQPLVEEPK	
30	*Serpina1*	P17475	4.30E-05	36	15	28	938.521	-6	SAILYFPK	
							1060.623	-5	TLLSSLGITR	
							1153.580	2	RPFNPEHTR	
							1244.623	1	MQHLEQTLTK	1 Oxidation (M)
							1467.752	-1	WKRPFNPEHTR	
							1603.802	-1	ISSNLADFAFSLYR	
							1731.897	-1	KISSNLADFAFSLYR	
							1918.933	1	VFNNDADLSGITEDAPLK	
							2152.118	-2	GTEAAGATVVEAVPMSLPPQVK	
							2158.929	3	NNYHSEAFSVNFADSEEAK	
							2168.115	-1	GTEAAGATVVEAVPMSLPPQVK	1 Oxidation (M)
							2287.022	2	NNYHSEAFSVNFADSEEAKK	
							2904.329	2	FLEEVKNNYHSEAFSVNFADSEEAK	
							3032.429	3	FLEEVKNNYHSEAFSVNFADSEEAKK	
							3176.652	0	AFHHLLQTLNRPDSELQLNTGNGLF	

									VNK	
34	*Eno1*	P04764	5.87E-04	37	11	29	704.407	9	GVPLYR	
							766.368	4	EIFDSR	
							1143.622	12	IGAEVYHNLK	
							1406.727	14	GNPTVEVDLYTAK	
							1439.750	11	YITPDQLADLYK	
							1633.833	12	VNQIGSVTESLQACK	
							1668.772	21	IDQLMIEMDGTENK	2 Oxidation (M)
							1804.944	12	AAVPSGASTGIYEALELR	
							1928.979	13	LAMQEFMILPVGASSFR	2 Oxidation (M)
							1960.941	13	DATNVGDEGGFAPNILENK	
							3022.620	18	HIADLAGNPEVILPVPAFNVINGGSH AGNK	
41	*Anxa1*	P07150	3.78E-05	60	19	33	772.397	-6	SYPHLR	
							826.407	-7	VFQNYR	
							908.434	-6	ALYEAGER	
							954.504	-4	KVFQNYR	
							954.504	-4	VFQNYRK	
							1092.608	0	VYREELKR	
							1213.526	1	DITSDTSGDFR	
							1221.602	-1	QEQEYVQAVK	
							1262.593	0	TPAQFDADELR	
							1328.605	-1	CATSTPAFFAEK	
							1387.757	-2	GVDEATIIDILTK	
							1543.860	-1	GVDEATIIDILTKR	
							1550.810	1	GTDVNVFNTILTTR	
							1639.902	1	ALTGHLEEVVLAMLK	1 Oxidation (M)
							1678.904	0	KGTDVNVFNTILTTR	
							1746.905	1	GLGTDEDTLIEILTTR	
							1776.928	-1	AAYLQETGKPLDETLK	
							1835.005	0	RKGTDVNVFNTILTTR	
							1905.024	1	AAYLQETGKPLDETLKK	
43	*Hp*	P06866	4.84E-04	25	11	27	849.479	-8	VVLHPER	
							920.449	-7	GSFPWQAK	
							1012.458	-1	MGYVSGWGR	
							1028.452	-2	MGYVSGWGR	1 Oxidation (M)
							1033.495	-6	HTFCAGLTK	
							1308.642	0	YVMLPVADQEK	1 Oxidation (M)
							1378.799	1	GAVSPVGVQPILNK	
							1651.797	3	ATDLKDWVQETMAK	1 Oxidation (M)

							1818.915	-1	VMPICLPSKDYVAPGR	1 Oxidation (M)
							2251.073	4	YVMLPVADQEKCELHYEK	
							2267.067	3	YVMLPVADQEKCELHYEK	1 Oxidation (M)
51	*Cnn1*	Q08290	2.62E-04	37	14	30	928.490	-2	RHLYDPK	
							1046.521	2	EWIEGVTGR	
							1074.599	1	RFEPEKLR	
							1091.564	-1	GPAYGLSAEVK	
							1188.630	-2	NIIGLQMGTNK	
							1204.631	3	NIIGLQMGTNK	1 Oxidation (M)
							1321.679	4	DGIILCEFINK	
							1373.648	0	YDHQREQELR	
							1417.649	3	FASQQGMTAYGTR	
							1433.643	2	FASQQGMTAYGTR	1 Oxidation (M)
							2271.114	3	VNESTQNWHQLENIGNFIK	
							2384.174	-7	IGSNFMDGLKDGIILCEFINK	
							2399.202	0	KVNESTQNWHQLENIGNFIK	
							2400.209	10	IGSNFMDGLKDGIILCEFINK	1 Oxidation (M)

Supplemental Table 3. Database Search Results of spectra acquired on the LC-LTQ Mass Spectrometry. The tandem mass spectra were annotated and generated peak list files (.DTA), by running SEQUEST extract_msn algorithm in Bioworks version 3.2 (Thermo Electron, Bremen, Germany). The resulting peptide mass lists were then used to interrogated sequences present in an indexed rat subset database (36,274 sequences), that was created from NCBInr 3,893,302 sequences (release 07/04/06) and stored locally, by running SEQUEST SEARCH algorithm of Bioworks software version 3.2. SEQUEST searching were performed with maximum peptide and fragment ion mass tolerance of 2.5 and 1.0 Da respectively, and with partial methionine oxidation (M)and complete carbamidomethylation of cysteine (C), and 2 missed cleavage sites were also allowed in the search parameter. For each protein identification, a minimum of two peptides with a significant peptide expectation (P<0.001), peptide Xcorr 1.9, 2.7, and 3.5 for the charge states and +1, +2, and +3 respectively, minimum Delta CN (Delta correlation) of 0.1.

		LC-MS/MS							
Pos.	Gene name	Accession number	P (Pro.) P (pep.)	% seq. cove.	Score Xc, z	ΔCn	Measured mass (M + H)	ΔM	Peptide Sequence	Modification
1	*Flna*	gi|109462323|	9.62E-09	11.07	220.23					
			8.72E-04		2.71, 2	0.24	988.54218	0.40026	K.KGEITGEVR.M	
			6.22E-05		2.79, 2	0.34	1108.6109	0.89922	R.ALTQTGGPHVK.A	
			6.06E-05		3.04, 2	0.40	1108.5745	1.39665	K.RAEFTVETR.S	
			3.39E-05		3.46, 2	0.54	1460.5849	0.78568	K.M#DC*QEC*PEGYR.V	Oxidation (M), Carbamidomethylation (C)
			1.05E-04		2.83, 2	0.34	1502.7193	-0.20015	R.SGQSAAGASPAGGIDTR.D	
			3.44E-04		2.75, 2	0.28	1185.6601	1.39800	K.IVSPSGAAVPC*K.V	Carbamidomethylation (C)
			6.95E-05		2.71, 2	0.18	1053.4847	0.96623	K.NDNDTFTVK.Y	
			4.30E-05		2.76, 2	0.41	1230.6241	0.34713	K.AHVVPC*FDASK.V	Carbamidomethylation (C)
			5.14E-06		2.73, 2	0.28	1151.6306	0.99614	K.DKGEYTLVVK.W	
			9.62E-09		4.02, 2	0.52	1652.8602	1.17180	K.VTAQGPGLEPSGNIANK.T	
			2.66E-05		2.84, 2	0.29	1225.5695	0.39629	R.EATTEFSVDAR.A	
			8.50E-04		2.83, 2	0.34	1660.8905	-0.67146	K.TGVAINKPAEFTVDAK.H	
			3.18E-04		2.86, 2	0.25	1589.6954	1.00481	K.DNGNGTYSC*SYVPR.K	Carbamidomethylation (C)
			3.86E-07		4.29, 2	0.61	1570.8071	0.38420	R.GAGTGGLGLAVEGPSEAK.M	
			6.12E-06		2.73, 2	0.40	1083.5356	0.98393	K.SPFEVYVDK.S	
			5.15E-04		2.97, 2	0.31	1077.5938	0.93767	K.LDVQFSGLAK.G	
			2.46E-08		4.61, 2	0.42	1938.0178	1.05742	K.DAGEGLLAVQITDPEGKPK.K	

			3.39E-04		3.17, 2	0.38	1500.7540	0.09245	K.DAGEGGLSLAIEGPSK.A	
			8.98E-07		2.93, 2	0.19	1400.6480	0.70683	K.YGGDEIPFSPYR.V	
			1.78E-07		4.59, 2	0.50	1913.9127	0.55315	R.EGSYSISVLYGEEEVPR.S	
			2.66E-07		3.88, 2	0.48	2544.2575	0.89531	K.GLVEPVDVVDNADGTQTVNYVPSR.E	
			3.29E-07		2.79, 2	0.31	1226.7718	0.86235	R.LIALLEVLSQK.R	
2	*Myh11*	gi|109489759|	1.11E-13	23.95	378.32					
			1.24E-08		4.16, 2	0.52	1607.6965	-0.10058	R.NTDQASM#PDNTAAQK.V	Oxidation (M)
			4.80E-05		3.86, 3	0.17	1214.5582	0.35917	R.SHEAQVQEMR.Q	
			8.40E-04		3.48, 2	0.33	1269.5449	0.89408	R.ALETQM#EEM#R.T	Oxidation (M)
			1.11E-04		3.34, 2	0.43	1209.6221	-0.06355	K.LRGPPPQETSQ	
			9.66E-04		2.70, 2	0.31	1153.5405	-0.09149	K.M#TESSLPSASK.T	Oxidation (M)
			2.09E-06		3.67, 2	0.36	1347.6022	0.65630	R.QLEEAEEESQR.I	
			8.81E-04		3.50, 3	0.16	1347.6022	1.20868	R.QLEEAEEESQR.I	
			5.13E-05		3.03, 2	0.36	1224.6219	0.78508	R.ASRDEIFATSK.E	
			6.34E-05		2.56, 2	0.45	889.49890	0.71691	K.STVAALEAK.I	
			1.08E-04		3.21, 2	0.38	1187.6630	0.80876	R.SKLQEVEGAVK.A	
			8.52E-05		3.56, 2	0.30	1456.6260	1.17528	K.EM#EGLGQQYEEK.A	Oxidation (M)
			4.62E-04		3.22, 2	0.42	1257.6796	0.26799	K.KEEELQAALAR.V	
			8.40E-06		3.85, 3	0.21	1400.7744	1.29316	K.KLEGQLQELQSK.C	
			5.06E-07		4.39, 2	0.49	1400.7744	0.80254	K.KLEGQLQELQSK.C	
			3.94E-05		3.35, 2	0.29	1331.6801	0.71367	K.AESELKELEQR.H	
			5.73E-05		3.38, 3	0.39	1441.7645	1.36600	R.HVSTLNIQLSDSK.K	
			8.22E-05		3.17, 2	0.33	1220.6521	0.57048	K.KFDQLLAEEK.G	
			3.08E-06		3.37, 2	0.39	1253.6484	0.68474	R.TGVLAHLEEER.D	
			1.51E-06		3.29, 2	0.46	1440.6311	0.71831	K.EMEGLGQQYEEK.A	
			1.06E-04		2.77, 2	0.27	1551.7260	0.80658	R.EDQSILC*TGESGAGK.T	Carbamidomethylation (C)
			1.10E-07		2.87, 2	0.39	1690.7554	0.89885	R.QLHEYETELEDER.K	
			1.49E-11		4.43, 2	0.58	1776.8861	0.58562	R.VSDLTTNLAEEEEKAK.N	
			1.20E-05		2.85, 2	0.34	1092.5571	0.82353	K.FDQLLAEEK.G	
			3.48E-08		4.40, 2	0.48	1665.7272	0.86232	R.NSLQDQLDEEM#EAK.Q	Oxidation (M)
			6.71E-06		3.86, 3	0.30	1470.8162	1.46912	K.LKEVLLQVEDER.K	
			2.04E-08		4.14, 2	0.48	1470.8162	1.21343	K.LKEVLLQVEDER.K	
			2.04E-08		4.67, 2	0.46	1629.8330	0.65386	R.ALEEALEAKEELER.T	
			1.87E-10		3.50, 3	0.39	1629.8330	1.00699	R.ALEEALEAKEELER.T	
			3.79E-05		2.71, 2	0.24	1229.6372	1.12908	K.EVLLQVEDER.K	
			2.41E-06		3.33, 2	0.42	1202.6779	0.70757	R.YEILAANAIPK.G	
			1.27E-07		4.97, 3	0.35	1972.0596	1.12583	K.KLEGDLKDLELQADSAVK.G	

			4.37E-07		3.44, 2	0.44	1584.8227	0.37212	K.IVQLEEQIEQEAR.E	
			4.72E-08		3.86, 3	0.47	1963.9277	1.06532	K.LQNEVESVTGM#LNEAEGK.A	Oxidation (M)
			7.59E-07		3.11, 2	0.37	1630.8675	0.87300	K.VC*HLVGINVTDFTR.A	Carbamidomethylation (C)
			1.01E-08		5.46, 2	0.56	1949.9298	0.69719	K.TELEDTLDSTATQQELR.A	
			9.42E-06		2.60, 2	0.36	1203.6368	0.23967	K.ALELDPNLYR.I	
			7.38E-06		2.59, 2	0.54	1305.6684	0.06352	K.EQADFAIEALAK.A	
			2.96E-12		5.52, 2	0.55	2063.9549	0.44205	K.NM#DPLNDNVTSLLNASSDK.F	Oxidation (M)
			1.63E-05		3.53, 3	0.29	2175.0776	1.26468	K.QADLEKEELAEELASSLSGR.N	
			1.65E-09		4.02, 2	0.40	1662.8254	0.72026	K.LQDLASTIEVMEEGK.K	
			3.31E-10		5.43, 2	0.68	1961.9185	0.65154	R.TQLEELEDELQATEDAK.L	
			1.11E-13		6.41, 2	0.11	2374.1733	0.73003	K.EVASLGSQLQDTQELLQEETR.Q	
3	*Lamc1*	gi|109498845|	9.00E-10	7.80	90.22					
			3.06E-09		4.37, 3	0.43	2017.9189	1.24769	R.TGQC*EC*QPGITGQHC*ER.C	Carbamidomethylation (C)
			1.94E-04		2.76, 2	0.24	860.44720	0.98308	K.TAAEEALR.R	
			1.44E-04		2.86, 2	0.34	1031.5116	1.08745	K.VSNLENEAR.K	
			9.00E-10		3.73, 2	0.55	1923.8658	0.74410	R.ATAESANQC*LPC*DC*NGR.S	Carbamidomethylation (C)
			3.36E-05		3.26, 2	0.49	1438.6080	0.80950	R.DGSEASLEWSSDR.Q	
			7.85E-05		3.92, 2	0.50	1539.6965	0.61218	K.C*IYNTAGFYC*DR.C	Carbamidomethylation (C)
			4.19E-08		3.62, 2	0.49	1495.7063	0.32842	R.LNTFGDEVFNDPK.V	
			1.61E-06		3.70, 2	0.54	1573.7645	0.25041	K.EGFFGNPLAPNPADK.C	
			8.21E-07		3.07, 2	0.39	1442.7849	0.25932	R.LSAEDLVLEGAGLR.V	
4	*Flnc*	gi|109473205|	9.14E-10	5.7	120.19					
			1.85E-04		2.79, 2	0.26	929.48395	0.63896	K.HVTNSPFK.I	
			2.31E-04		2.15, 2	0.31	1078.5527	0.33953	K.AEIAFEDRK.D	
			5.27E-05		3.63, 3	0.23	1871.9934	1.46720	K.TARPNITDNKDGTITVR.Y	
			1.41E-04		2.80, 2	0.38	1124.5597	0.89938	K.TPC*EEVYVK.H	Carbamidomethylation (C)
			1.61E-09		3.50, 2	0.41	1386.7164	0.51067	K.YGGPQHIVGSPFK.A	
			9.14E-10		2.60, 2	0.43	1565.7682	0.69693	R.VPQTFTVDC*SQAGR.A	Carbamidomethylation (C)
			6.38E-06		3.78, 2	0.46	1188.6372	0.72344	R.GPGLSQAFVGQK.N	
			1.01E-04		2.91, 2	0.39	1549.8067	-0.08235	R.TSQLNVGTSTDVSLK.I	
			1.15E-04		2.08, 2	0.17	1442.7485	1.12529	R.EAGAGGLSIAVEGPSK.A	
			7.74E-04		2.02, 2	0.30	1289.7310	0.02263	R.LTVTSLQETGLK.V	

			6.80E-05		2.29, 2	0.35	1788.9465	0.87087	R.QAPSIATIGSTC*DLNLK.I	Carbamidomethylation (C)
			6.49E-07		2.54, 2	0.25	1503.8012	-0.10811	K.ITEGDLSQLTASIR.A	
5	*Dmn*	Q810D0	1.78E-14	13.86	170.29					
			1.78E-14		5.70, 2	0.63	2003.8648	0.86345	R.DEQSASTSSQASAGDAHQAR.G	
			2.89E-04		3.63, 3	0.12	1560.6416	1.17799	R.M#REEYGM#QAEER.Q	Oxidation (M)
			5.09E-04		2.75, 2	0.30	934.51050	0.97740	R.ATGPAAPPPR.L	
			1.85E-05		3.60, 3	0.42	2003.8648	0.97409	R.DEQSASTSSQASAGDAHQAR.G	
			9.44E-04		2.72, 2	0.39	952.43707	0.32054	K.GTEQAGFDK.T	
			7.61E-11		5.85, 2	0.60	1896.8907	1.07683	R.GHQGNVAAGAVNSTQSNER.T	
			1.01E-06		3.79, 3	0.30	1544.6467	-0.22946	R.MREEYGM#QAEER.Q	Oxidation (M)
			9.82E-05		3.69, 3	0.28	1544.6467	0.73624	R.M#REEYGMQAEER.Q	Oxidation (M)
			3.65E-08		3.88, 3	0.37	1947.8692	1.21408	R.DTGSEVEAHSVSHHGGWR.V	
			1.08E-05		3.69, 2	0.42	1528.6518	0.97197	R.MREEYGMQAEER.Q	
			3.72E-04		2.72, 2	0.24	981.5000	0.64903	R.YTDSVLQR.K	
			7.54E-08		2.70, 2	0.30	1416.6965	-0.06038	R.QSQGEPGSVSVDVK.K	
			5.19E-04		3.05, 2	0.29	1177.6245	0.90288	R.MKEELSALTR.Q	
			9.48E-05		2.90, 2	0.47	1414.6154	0.92242	R.ESM#QLYEDEVR.E	Oxidation (M)
			2.77E-05		2.76, 2	0.39	1398.6206	0.30058	R.ESMQLYEDEVR.E	
			2.09E-04		3.81, 2	0.34	1213.6535	0.93218	R.NQALELEQLR.A	
			1.69E-08		3.81, 2	0.49	1921.9575	0.73684	K.VVNVEIVEEPM#SYVGGGK.V	Oxidation (M)
			1.32E-05		3.63, 2	0.47	1620.8512	0.77669	K.STETVIGEM#INLGLK.G	Oxidation (M)
6	*Col6a1*	gi|109509939|	3.33E-14	21.76	160.29					
			4.50E-07		3.48, 2	0.43	1340.5825	0.70574	R.GDPGEAGPQGDQGR.E	
			1.64E-09		4.60, 2	0.36	1929.7692	0.71782	K.GDEGEAGDPGEDNNDVSPR.G	
			7.83E-10		3.79, 2	0.53	1701.8667	0.21868	R.VAVVQYSGQGQQQPGR.A	
			6.73E-04		3.20, 2	0.43	1022.5629	0.96764	R.GVLYQTVSR.K	
			8.26E-05		2.33, 2	0.26	1180.5593	0.02410	R.GDEGPPGPEGLR.G	
			1.72E-07		3.31, 2	0.48	1289.6848	0.30449	R.LSIIATDHTYR.R	
			3.72E-04		3.21, 2	0.46	1488.6940	0.90172	K.EPC*GGLEDAVNEAK.H	Carbamidomethylation (C)
			1.71E-04		1.89, 1	0.40	1257.5745	0.04968	K.TAEYDVAFGER.H	
			4.85E-06		2.86, 2	0.37	957.57275	0.96855	R.IALVITDGR.S	
			2.90E-10		5.11, 2	0.56	1985.9178	0.54484	K.NNVEQVC*C*TFEC*QAAR.G	Carbamidomethylation (C)
			9.26E-11		5.09, 3	0.53	1985.9178	0.42893	K.NNVEQVC*C*TFEC*QAAR.G	Carbamidomethylation (C)
			9.49E-04		3.84, 3	0.33	1493.8686	1.41498	K.KGLEELLIGGSHLK.E	
			2.37E-07		4.84, 2	0.46	1493.8686	0.71233	K.KGLEELLIGGSHLK.E	

			3.93E-05		2.23, 2	0.34	1073.6102	0.48711	R.VPNYQALLR.G	
			4.26E-08		2.93, 2	0.53	1257.5745	1.01763	K.TAEYDVAFGER.H	
			7.38E-06		3.56, 2	0.45	1580.8431	0.63579	K.VFSVAITPDHLEPR.L	
			2.36E-07		4.31, 2	0.48	1703.9002	-0.11824	K.YLIVVTDGHPLEGYK.E	
			6.80E-04		3.96, 3	0.16	1949.9814	0.75809	R.VLLFSDGNSQGATAEAIEK.A	
			2.54E-12		5.26, 2	0.56	1949.9814	0.60332	R.VLLFSDGNSQGATAEAIEK.A	
			3.33E-14		5.76, 2	0.61	2188.1835	1.37417	R.DTTPLSVLC*GSDIQVVSVGIK.D	Carbamidomethylation (C)
7	*Vcl*	gi|109502103|	4.16E-09	10.49	100.24					
			6.86E-04		2.47, 2	0.36	872.48358	0.21233	K.GNDIIAAAK.R	
			3.74E-05		3.08, 2	0.25	1183.5598	0.45929	R.LANVM#M#GPYR.Q	Oxidation (M)
			7.42E-07		3.53, 2	0.45	1497.6928	0.74468	R.DPNASPGDAGEQAIR.Q	
			1.37E-07		3.33, 2	0.53	1269.6796	0.48271	K.AVAGNISDPGLQK.S	
			1.34E-05		3.28, 2	0.41	1191.6037	1.06289	K.M#SAEINEIIR.V	Oxidation (M)
			5.48E-05		3.12, 2	0.42	1303.7103	0.93352	K.SLLDASEEAIKK.D	
			4.16E-09		4.82, 2	0.53	1457.7957	1.02043	K.AQQVSQGLDVLTAK.V	
			2.08E-08		4.08, 2	0.60	1292.6402	0.87541	K.MTGLVDEAIDTK.S	
			4.41E-05		3.09, 2	0.55	1089.6149	0.61492	R.SLGEIAALTSK.L	
			1.97E-08		4.20, 2	0.47	1477.7137	0.67107	K.MLGQMTDQVADLR.A	
8	*Nid1*	gi|109505096|	2.33E-11	20.71	220.23					
			3.31E-08		3.09, 2	0.55	1260.5637	0.76299	K.IETSHMDGTNR.R	
			1.51E-04		2.73, 2	0.30	1131.5516	0.74452	R.QC*VAEGSPQR.V	Carbamidomethylation (C)
			1.65E-07		3.84, 2	0.45	1572.7292	1.02809	R.C*QC*KPGYQGDGFR.C	
			2.11E-05		2.96, 2	0.42	1242.6200	0.22066	R.AEC*LNPAQPSR.R	Carbamidomethylation (C)
			3.71E-08		3.10, 2	0.44	1351.7327	0.71636	R.ASLHGGEPTTIIR.Q	
			2.52E-08		3.74, 2	0.42	1517.7957	0.10881	K.KDENQVPAVVGFSK.G	
			2.82E-04		2.85, 2	0.48	1149.5062	0.72352	R.DYATGFC*C*R.C	Carbamidomethylation (C)
			3.40E-05		2.70, 2	0.19	1590.6380	-0.35898	R.C*EC*MEGYHFSDR.G	Carbamidomethylation (C)
			7.01E-09		3.61, 3	0.37	2736.2111	1.18777	R.DGSPDALQNPC*YIGTHGC*DSNAAC*R.P	Carbamidomethylation (C)
			1.78E-09		3.69, 2	0.58	1364.7089	0.53619	K.TNSVIAM#DLAVSK.E	Oxidation (M)
			2.76E-08		3.92, 3	0.25	2745.2539	1.02304	R.EYTVTEPDQDSAVPSHTHVYQWR.Q	
			6.40E-10		3.57, 2	0.46	1386.7851	1.12676	R.RVLFDTGLVNPR.G	

			2.76E-07		2.67, 2	0.44	1390.6750	0.70317	R.TIFWTDSHLDR.I	
			1.18E-07		3.13, 2	0.45	1389.7009	0.78227	K.DENQVPAVVGFSK.G	
			2.78E-06		3.54, 2	0.45	1348.7141	0.83452	K.TNSVIAMDLAVSK.E	
			5.00E-06		2.74, 2	0.31	1341.6181	1.10307	K.SNGAYNIFANDR.E	
			4.01E-06		2.95, 2	0.45	1230.6840	0.09575	R.VLFDTGLVNPR.G	
			7.73E-05		3.22, 2	0.56	1324.6069	0.74419	R.GNLYWTDWNR.E	
			1.08E-09		3.73, 2	0.51	1621.8220	-0.08784	K.VVYWTDISEPSIGR.A	
			1.94E-06		2.77, 2	0.45	1349.7438	0.69049	K.VIIGLAFDC*VDK.V	Carbamidomethylation (C)
			2.33E-11		4.69, 2	0.58	1771.9265	0.87798	K.VLEGLQYPFAVTSYGK.N	
			3.38E-10		4.52, 2	0.63	2025.9949	0.66985	R.EDLSPFIIQM#AAEYVQR.G	Oxidation (M)
9	*Col1a1*	P02454	7.63E-12	6.06	60.20					
			6.81E-04		2.72, 2	0.26	945.43848	0.19475	K.QGPSGASGER.G	
			2.63E-05		2.83, 2	0.21	836.43732	0.46739	R.GPAGPQGPR.G	
			6.29E-08		3.29, 2	0.53	1311.6287	0.86370	K.GETGPSGPAGPTGAR.G	
			7.63E-12		4.09, 2	0.49	1532.7816	0.69866	R.GETGPAGPAGPIGPAGAR.G	
			1.76E-07		2.78, 2	0.41	1452.7263	0.37383	K.SAGVSVPGPMGPSGPR.G	
			8.59E-04		4.00, 2	0.50	1800.8697	1.24970	R.GPPGPM#GPPGLAGPPGESGR.E	Oxidation (M)
10	*Col1a2*	P02466	9.17E-12	6.63	88.21					
			1.66E-08		2.70, 2	0.41	1187.6279	0.90154	R.SGHPGPVGPAGVR.G	
			4.58E-05		1.81, 1	0.21	868.46356	-0.04376	R.GPSGPQGIR.G	
			1.43E-07		4.27, 2	0.46	1251.6076	0.41924	R.GEAGAAGPSGPAGPR.G	
			1.82E-04		1.98, 1	0.37	937.51013	0.05017	R.GPAGPSGPIGK.D	
			1.30E-06		2.94, 2	0.48	937.51013	0.71337	R.GPAGPSGPIGK.D	
			3.62E-05		2.19, 2	0.35	918.51556	0.52184	R.PGPIGPAGPR.G	
			1.14E-09		4.17, 2	0.21	1399.6820	0.26636	K.GVSAGPGPM#GLMGPR.G	Oxidation (M)
			9.50E-06		3.28, 2	0.54	1399.6820	0.26636	K.GVSAGPGPMGLM#GPR.G	Oxidation (M)
			9.17E-12		3.66, 2	0.48	1560.8128	0.88078	R.GEPGPAGSVGPVGAVGPR.G	
			1.04E-09		3.06, 2	0.51	1383.6871	0.80168	K.GVSAGPGPMGLMGPR.G	
11	*Csde1*	P18395	6.65E-12	22.93	150.25					
			1.36E-04		2.53, 2	0.39	1247.6743	0.67644	K.IKPEIHPEER.M	
			3.88E-05		2.79, 2	0.43	1129.6087	0.64724	R.PGQQIATC*VR.L	Carbamidomethylation (C)
			7.98E-06		2.70, 2	0.39	1253.5215	0.96804	R.GPDNSM#GFGAER.K	Oxidation
			7.69E-12		4.02, 2	0.54	1763.8322	0.93439	K.SPAAPGQSPTGSVC*YER.N	Carbamidomethylation (C)
			2.62E-04		3.44, 3	0.33	1413.7696	1.41193	R.LKNITLDDASAPR.L	
			1.43E-07		3.58, 2	0.40	1237.5266	0.31108	R.GPDNSMGFGAER.K	
			3.05E-04		2.70, 2	0.18	1609.7452	0.71086	K.VGDDVEFEVSSDRR.T	
			2.92E-05		3.84, 3	0.39	2017.9825	0.90171	K.THSVNGITEEANPTIYSGK.V	

			2.90E-11		4.94, 2	0.58	1897.8789	0.70363	K.DKEAEDGIIAYDDC*GVK.L	Carbamidomethylation (C)
			5.41E-11		4.35, 2	0.63	1453.6441	0.34685	K.VGDDVEFEVSSDR.R	
			2.79E-08		3.80, 2	0.18	1507.6811	0.78606	K.DNFGFIETANHDK.E	
			1.51E-04		2.74, 2	0.22	1058.6608	0.44780	R.IKVDFVIPK.E	
			6.65E-12		4.81, 2	0.60	2238.0771	0.76689	K.DVEGSTSPQIGDKVEFSISDK.Q	
			5.07E-06		2.71, 2	0.48	1573.7984	-0.22710	K.LLTSYGFIQC*SER.Q	Carbamidomethylation (C)
			1.39E-07		4.04, 2	0.53	1746.8333	0.61186	K.DQFGFINYEVGDSKK.L	
12	*Prkcsh*	gi|109484382|	1.99E-07	12.76	60.22					
			1.35E-06		3.73, 2	0.43	1301.6848	0.83806	R.KLWEEQQAAAK.A	
			2.48E-07		2.79, 2	0.36	1306.6485	0.85503	K.ETVVTSTTEPSR.C	
			4.08E-04		2.86, 2	0.54	1552.6902	0.65925	K.YEQGTGC*WQGPNR.S	Carbamidomethylation (C)
			1.99E-07		4.43, 2	0.49	1530.8122	0.73418	K.EKESLQQLAEVTR.E	
			3.39E-04		2.84, 2	0.24	1058.6245	0.73821	K.KILIEEWK.T	
			1.82E-05		2.93, 2	0.43	1189.6059	0.78996	K.SLEDQVETLR.T	
14	*Lmna*	P48679	2.18E-13	36.70	220.28					
			2.65E-05		3.75, 2	0.55	1502.7233	0.87419	R.AQHEDQVEQYKK.E	
			1.05E-04		2.97, 2	0.22	1102.5738	-0.02217	R.KLLEGEEER.L	
			3.48E-05		3.12, 2	0.29	1029.5938	0.55046	K.LEAALGEAKK.Q	
			5.37E-05		2.65, 2	0.36	1406.7013	0.08924	R.TVLC*GTC*GQPADK.A	Carbamidomethylation (C)
			7.29E-04		2.52, 2	0.25	1171.6429	0.06743	K.KEGDLLAAQAR.L	
			2.05E-10		4.23, 2	0.65	1736.7598	0.91564	R.GSHC*SSSGDPAEYNLR.S	Carbamidomethylation (C)
			7.56E-06		2.75, 2	0.41	1148.5793	0.70024	R.ITESEEVVSR.E	
			2.64E-06		2.97, 2	0.51	1293.6433	0.78008	K.AAYEAELGDARK.T	
			1.77E-08		3.31, 2	0.53	1203.5739	0.55205	R.VAVEEVDEEGK.F	
			9.41E-04		2.64, 2	0.44	1089.5534	0.26567	R.SLETENAGLR.L	
			1.23E-05		3.70, 3	0.25	1629.8078	0.93491	R.LQEKEDLQELNDR.L	
			5.21E-08		4.53, 2	0.46	1629.8078	0.68291	R.LQEKEDLQELNDR.L	
			3.35E-04		2.33, 2	0.42	1043.5479	1.29570	K.EGDLLAAQAR.L	
			3.28E-06		3.18, 2	0.48	1165.5483	0.51225	K.AAYEAELGDAR.K	
			4.54E-05		3.06, 2	0.30	1187.6378	0.45720	K.LRDLEDSLAR.E	
			3.27E-05		4.34, 3	0.63	2268.1062	0.92191	K.AASGSGAQVGGSISSGSSASSVTVTR.S	
			2.18E-13		5.55, 2	0.66	2268.1062	0.60210	K.AASGSGAQVGGSISSGSSASSVTVTR.S	

			2.24E-13		4.84, 2	0.58	1752.8623	0.83037	R.NSNLVGAAHEELQQSR.I	
			8.32E-11		4.48, 2	0.46	1605.8118	0.89690	R.VAVEEVDEEGKFVR.L	
			1.71E-08		4.33, 2	0.61	1491.7471	0.55856	R.TALINATGEEVAM#R.K	Oxidation (M)
			1.22E-04		2.65, 2	0.38	1182.6113	0.87822	R.TLEGELHDLR.G	
			2.28E-10		3.13, 2	0.44	1566.7507	0.51152	R.SVGGSGGGSFGDNLVTR.S	
			1.97E-06		4.02, 2	0.36	1491.8053	0.91863	R.LQTLKEELDFQK.N	
			6.84E-07		3.54, 2	0.50	1475.7522	0.48039	R.TALINATGEEVAMR.K	
15	*Hspa8*	P63018	4.01E-10	14.71	90.3					
			2.34E-06		3.62, 3	0.37	1745.8089	1.36545	K.NQTAEKEEFEHQQK.E	
			5.46E-09		4.17, 2	0.57	1691.7255	0.82451	K.STAGDTHLGGEDFDNR.M	
			1.54E-05		3.14, 2	0.37	1270.5619	0.57393	R.FDDAVVQSDM#K.H	Oxidation (M)
			1.33E-04		3.35, 2	0.46	1410.6682	0.64946	R.RFDDAVVQSDMK.H	
			7.13E-09		4.35, 2	0.63	1481.8071	0.75859	K.SQIHDIVLVGGSTR.I	
			1.15E-06		2.85, 2	0.45	1254.5671	0.57256	R.FDDAVVQSDMK.H	
			4.00E-05		3.09, 2	0.44	1319.5936	0.58905	K.NSLESYAFNM#K.A	Oxidation (M)
			1.12E-05		3.41, 2	0.42	1480.7542	0.29534	R.ARFEELNADLFR.G	
			4.01E-10		5.23, 2	0.57	1659.8952	0.61333	R.IINEPTAAAIAYGLDK.K	
19	*Nefl*	P19527	1.65E-12	29.70	170					
			4.58E-04		2.92, 2	0.20	1074.5789	0.72124	R.KLLEGEETR.L	
			5.46E-05		2.15, 1	0.54	1061.5109	-0.03625	R.LAAEDATNEK.Q	
			5.74E-06		3.18, 2	0.50	1061.5109	0.71196	R.LAAEDATNEK.Q	
			2.33E-05		3.00, 2	0.27	1001.5374	1.11864	R.KGADEAALAR.A	
			2.22E-04		2.72, 2	0.33	946.48400	0.19060	K.LLEGEETR.L	
			2.55E-04		2.72, 2	0.30	1021.5313	0.54668	R.ALYEQEIR.D	
			2.65E-04		3.32, 2	0.39	1728.8874	0.78911	K.QALQGEREGLEETLR.N	
			2.09E-09		4.57, 2	0.44	1548.7322	0.93950	K.QNADISAMQDTINK.L	
			9.54E-10		4.73, 2	0.58	1723.7955	0.66638	R.SAYSGLQSSSYLM#SAR.A	Oxidation (M)
			2.88E-09		4.86, 2	0.53	1747.8497	0.81218	R.SAYSSYSAPVSSSLSVR.R	
			3.96E-06		2.37, 1	0.24	1121.5837	0.16235	K.EYQDLLNVK.M	
			1.07E-06		4.78, 2	0.39	1525.8260	1.40520	R.YLKEYQDLLNVK.M	
			1.65E-12		5.03, 2	0.56	1707.8006	0.97637	R.SAYSGLQSSSYLMSAR.A	
			3.24E-06		4.01, 2	0.44	1538.8134	0.57208	R.IDSLM#DEIAFLKK.V	Oxidation (M)
			2.74E-06		3.91, 3	0.31	1678.9196	1.17386	K.RIDSLMDEIAFLKK.V	
			9.20E-06		2.33, 1	0.33	1154.7143	0.04309	K.VLEAELLVLR.Q	
			6.20E-07		2.82, 2	0.59	1154.7143	0.30547	K.VLEAELLVLR.Q	
			1.63E-08		3.98, 2	0.46	1522.8184	0.06951	R.IDSLMDEIAFLKK.V	
			1.18E-08		3.69, 2	0.45	1394.7236	1.08281	R.IDSLMDEIAFLK.K	
20	*Kng1*	P01048	5.81E-08	20.00	70.21					
			4.85E-05		3.41, 2	0.31	1407.6685	1.25756	K.SAHSQVVAGM#NYK.I	Oxidation (M)
			3.79E-07		3.91, 2	0.42	1391.6735	0.52446	K.SAHSQVVAGMNYK.I	

			3.47E-04		3.50, 3	0.28	1783.9060	0.25965	K.EGTTRLLNSC*EYKGR.L	Carbamidomethylation (C)
			8.02E-04		2.67, 2	0.39	1026.5229	0.42017	R.LLNSC*EYK.G	Carbamidomethylation (C)
			5.81E-08		4.18, 2	0.58	1873.9542	0.65203	R.VTEGTKKDGAETLYSFK.Y	
			7.21E-04		3.65, 3	0.39	2142.0234	1.44616	R.C*QALDM#M#ISRPPGFSPFR.L	Carbamidomethylation (C) and Oxidation (M)
			7.28E-05		2.93, 2	0.43	1802.8708	0.02825	K.YNAELESGNQFVLYR.V	
22	*Ckap4*	gi|34862422|	1.48E-10	12.70	60.2					
			2.89E-04		2.55, 2	0.15	973.53131	0.61827	R.ERDIEALK.S	
			1.48E-10		3.46, 2	0.57	1357.6859	0.80095	K.VGAHGSEEAVVFR.D	
			3.77E-04		2.74, 2	0.27	1178.5899	-0.07881	K.SSVSQVESDLK.M	
			1.13E-07		4.77, 2	0.58	1760.8007	0.68687	K.SSLQTM#ESDVYTEVR.E	Oxidation (M)
			1.49E-04		3.69, 2	0.42	1439.6649	0.57659	R.DFTSLENTVEER.L	
			3.27E-10		3.95, 2	0.53	1577.8170	-0.28218	K.SINDNIAIFTDVQK.R	
23	*Ppp2r1a*	Q5XI34	3.30E-07	10.53	70.16					
			9.24E-06		2.88, 2	0.24	1239.6328	0.91741	K.ELVSDANQHVK.S	
			7.70E-05		2.74, 2	0.36	1160.5793	0.70830	K.LTQDQDVDVK.Y	
			8.61E-05		2.97, 2	0.46	1323.5972	0.65667	R.NLC*SDDTPM#VR.R	Oxidation (M), Carbamidomethylation (C)
			8.52E-05		2.85, 2	0.40	1307.6023	0.11959	R.NLC*SDDTPMVR.R	Carbamidomethylation (C)
			2.98E-04		2.77, 2	0.30	929.53021	0.66606	K.VLELDNVK.S	
			3.30E-07		3.25, 2	0.51	1109.5374	0.72673	R.LAGGDWFTSR.T	
			5.15E-04		2.75, 2	0.23	1392.7191	0.81093	K.TDLVPAFQNLM#K.D	Oxidation (M)
24	*Vim*	P31000	1.93E-06	9.87	40					
			8.70E-05		3.47, 2	0.51	1216.6280	0.17107	R.RQVDQLTNDK.A	
			1.55E-05		2.73, 2	0.32	1115.5690	1.04314	K.VELQELNDR.F	
			1.92E-06		2.77, 2	0.37	1444.7066	0.89433	R.SLYSSSPGGAYVTR.S	
			3.59E-06		3.59, 2	0.60	1490.7824	0.80377	R.QVQSLTC*EVDALK.G	
26	*Argbp2*	O35413	1.51E-13	11.87	124.30					
			7.39E-05		2.74, 2	0.15	1258.4735	0.85300	K.SHS@DNGTDAFK.E	
			7.91E-06		2.49, 2	0.25	1212.5313	0.50798	R.PSSSASMAGDFR.K	
			2.25E-05		2.42, 2	0.30	1064.6098	0.82134	K.KGDTVYILR.K	
			1.21E-07		3.06, 2	0.41	1250.6375	0.73564	R.PVSVYQSSIDR.S	
			5.05E-13		4.96, 3	0.46	2201.1308	1.33493	K.SSILQHERPVSVYQSSIDR.S	
			2.78E-05		2.85, 2	0.48	2018.8726	0.57146	K.GSEDYPDPPLPHSYSSDR.I	

			6.91E-05		2.74, 2	0.47	1199.5902	-0.70796	R.SYSSTLTDLGR.S	
			1.93E-07		3.87, 2	0.46	1299.5728	0.92713	K.C*DDGWFVGTSR.R	Carbamidomethylation (C)
			1.51E-13		5.92, 2	0.56	2403.1311	0.59648	R.ADLPGSSSTFTTSFISSSPSSPSR.A	
			2.37E-06		2.36, 2	0.27	1251.6983	0.35185	R.VGIFPISYVEK.L	
27	*Lum*	P51886	9.18E-07	10.4	30.19					
			2.13E-06		3.64, 2	0.41	1225.5808	0.92327	R.NNQIDHIDEK.A	
			2.64E-05		3.36, 2	0.46	1243.6640	0.42986	K.SLQDLQLANNK.I	
			9.18E-07		3.87, 2	0.59	1690.7992	0.13219	K.SLEYLDLSFNQM#SK.L	Oxidation (M)
28	*Hnrnpk*	P61980	1.22E-14	34.34	110					
			1.57E-06		3.22, 2	0.42	1154.4895	1.00810	R.RDYDDMSPR.R	
			5.77E-05		2.79, 2	0.39	1053.6414	0.87175	R.VVLIGGKPDR.V	
			7.07E-11		4.50, 3	0.44	1735.8067	1.28476	K.RPAEDMEEEQAFKR.S	
			7.02E-06		3.18, 2	0.28	1349.6478	0.89763	R.SRNTDEMVELR.I	
			5.72E-07		2.92, 2	0.45	1259.5749	0.68303	K.IDEPLEGSEDR.I	
			4.25E-07		4.57, 3	0.58	2068.9782	0.99350	R.HESGASIKIDEPLEGSEDR.I	
			6.32E-04		2.89, 2	0.36	1098.4825	0.61316	K.GSDFDC*ELR.L	Carbamidomethylation (C)
			1.22E-14		5.25, 2	0.62	2121.0207	0.92339	K.ALRTDYNASVSVPDSSGPER.I	
			4.23E-05		3.11, 2	0.26	1194.6993	0.68999	R.NLPLPPPPPR.G	
			4.88E-11		3.32, 2	0.49	1553.9261	0.80486	K.IILDLISESPIKGR.A	
			1.26E-04		3.37, 2	0.51	1340.8035	0.72478	K.IILDLISESPIK.G	
29	*Fbln5*	Q9WVH8	1.11E-09	13.39	60.2					
			4.90E-07		2.56, 3	0.33	1447.6299	1.28075	R.SC*QDINEC*EHR.N	Carbamidomethylation (C)
			6.91E-06		2.81, 2	0.53	1355.5875	0.73381	R.C*MC*PAENTGC*R.D	Carbamidomethylation (C)
			1.16E-05		2.77, 2	0.54	1374.7409	1.25737	R.QTGPISATLVMTR.P	
			1.11E-09		3.21, 2	0.64	1580.7737	-0.02268	R.SVPADIFQM#QATTR.Y	Oxidation (M)
			1.96E-08		4.61, 2	0.61	1564.7788	1.49272	R.SVPADIFQMQATTR.Y	
			1.40E-06		3.23, 2	0.32	1362.7092	1.06157	R.YPGAYYIFQIK.S	
31	*Tuba1*	P68370	1.64E-10	22.62	110.27					
			3.85E-05		2.75, 3	0.15	1396.6929	0.87931	R.LDHKFDLM#YAK.R	Oxidation (M)
			2.47E-05		2.74, 2	0.44	1380.6980	0.60039	R.LDHKFDLMYAK.R	
			2.47E-05		2.74, 2	0.50	1265.6086	0.31857	K.YM#AC*C*LLYR.G	Oxidation (M), Carbamidomethylation (C)
			1.48E-04		1.81, 1	0.26	887.43317	0.05798	K.FDLMYAK.R	
			3.35E-05		2.70, 2	0.37	1249.6137	0.72033	K.YMAC*C*LLYR.G	Carbamidomethylation (C)

			4.47E-08		5.02, 3	0.40	2346.0131	1.39471	R.AFVHWYVGEGM#EEGEFSEAR.E	Oxidation (M)
			2.43E-07		3.36, 2	0.60	1756.9632	0.69670	R.IHFPLATYAPVISAEK.A	
			7.73E-08		4.63, 2	0.47	1880.9298	0.52698	R.AVC*M#LSNTTAIAEAWAR.L	Carbamidomethylation (C)
			1.01E-05		3.52, 3	0.37	1756.9632	0.85123	R.IHFPLATYAPVISAEK.A	
			1.29E-08		3.75, 3	0.31	2330.0183	0.25986	R.AFVHWYVGEGMEEGEFSEAR.E	
			1.64E-10		5.36, 2	0.64	2007.8930	0.72368	K.TIGGGDDSFNTFFSETGAGK.H	
			2.32E-04		2.22, 1	0.34	1085.6201	0.25415	K.EIIDLVLDR.I	
			3.97E-04		2.71, 2	0.34	1085.6201	0.41313	K.EIIDLVLDR.I	
32	*Ces3*	P16303	1.56E-08	17.35	90.21					
			6.62E-06		4.25, 2	0.43	1382.6699	0.99004	R.AKEAAEEPSHWK.H	
			6.46E-05		3.50, 3	0.26	1382.6699	1.10880	R.AKEAAEEPSHWK.H	
			5.84E-06		2.70, 2	0.42	1183.5378	0.22124	K.EAAEEPSHWK.H	
			6.00E-06		3.52, 2	0.34	1002.5326	1.33025	K.IGASTQAAQR.L	
			4.89E-07		3.51, 2	0.48	1391.7075	0.30011	K.TTTSAVM#VHC*LR.Q	Oxidation (M), Carbamidomethylation (C)
			4.43E-07		3.99, 2	0.39	1279.5648	0.73223	K.DGASEEETNLSK.M	
			7.99E-05		3.09, 2	0.40	1375.7126	0.63583	K.TTTSAVMVHC*LR.Q	Carbamidomethylation (C)
			8.72E-06		2.72, 2	0.40	1029.5462	0.25786	K.TPEEILAEK.S	
			4.54E-05		3.91, 3	0.36	1620.8743	1.15549	R.LKDKEVAFWSELR.A	
			1.56E-08		3.71, 2	0.46	1451.7893	1.41228	K.SFNTVPYIVGINK.Q	
33	*P4hb*	P04785	1.94E-07	13.56	60.20					
			3.16E-07		2.50, 2	0.38	1409.6794	0.08525	K.YKPESDELTAEK.I	
			3.35E-07		3.51, 3	0.48	1729.9118	1.45377	K.LGETYKDHENIVIAK.M	
			8.33E-06		4.03, 2	0.31	1355.6478	1.47771	K.NFEEVAFDEKK.N	
			2.64E-05		3.12, 2	0.41	1222.6235	0.57026	R.LITLEEEM#TK.Y	Oxidation (M)
			1.21E-05		3.51, 3	0.34	1424.7784	1.45942	K.YQLDKDGVVLFK.K	
			2.42E-06		3.32, 2	0.29	1424.7784	0.83000	K.YQLDKDGVVLFK.K	
			1.94E-07		2.65, 2	0.29	1081.6768	0.71233	K.THILLFLPK.S	
35	*Blmh*	P70645	1.13E-07	14.32	50.21					
			4.59E-05		3.63, 3	0.40	1563.7525	1.11565	K.KC*FPESHTTEATR.R	Carbamidomethylation (C)
			2.11E-07		4.24, 2	0.59	1875.8098	0.60228	K.GEISSTQDAM#M#EEIFR.V	Oxidation (M)
			2.37E-06		2.75, 2	0.35	1262.7143	0.88103	K.VGPITPLQFYK.E	
			2.19E-04		3.20, 2	0.40	1465.7685	0.47368	K.TLYNNQPIDFLK.K	
			1.13E-07		3.31, 2	0.54	1439.6565	0.61012	R.DGEAVWFGC*DVGK.H	Carbamidomethylation (C)
36	*Krt1-12*	Q6IFW5	3.22E-06	4.6	20.0					

			7.73E-06		2.81, 2	0.33	1007.5156	0.90282	K.YENELALR.Q	
			3.22E-06		3.44, 2	0.41	1029.5938	0.28703	R.VLDELTLAR.A	
37	*Serpinb1a*	Q4G075	7.11E-14	42.70	178.24					
			5.70E-04		1.93, 1	0.43	980.44659	0.32184	K.ADLSGMSGSR.D	
			6.85E-07		2.92, 2	0.48	980.44659	0.11504	K.ADLSGMSGSR.D	
			1.97E-05		2.86, 2	0.31	1278.6800	0.71831	R.FQSLNAEVSKR.G	
			2.16E-06		3.24, 2	0.49	1472.6838	0.91193	K.FM#KQDTTDAPFR.L	Oxidation (M)
			3.50E-07		4.55, 3	0.34	1465.7757	0.45783	K.RENLENIDVHVK.L	
			3.26E-06		3.16, 2	0.38	1465.7757	0.60979	K.RENLENIDVHVK.L	
			4.93E-07		2.74, 1	0.32	1230.6939	-0.01331	K.KIEEQITLEK.L	
			3.34E-05		2.85, 1	0.25	1122.5789	-0.11536	R.FQSLNAEVSK.R	
			1.47E-06		2.78, 2	0.39	1122.5789	0.55120	R.FQSLNAEVSK.R	
			1.69E-04		2.97, 2	0.38	1230.6939	0.65117	K.KIEEQITLEK.L	
			2.04E-09		4.02, 2	0.55	1575.7186	0.85600	K.TFHFDSVEDVHSR.F	
			1.20E-07		4.07, 3	0.49	1575.7186	1.47440	K.TFHFDSVEDVHSR.F	
			1.17E-06		3.11, 2	0.46	1309.6746	0.68157	R.ENLENIDVHVK.L	
			2.10E-07		3.62, 3	0.34	2237.0291	1.36963	K.M#YGADLAPVDFQHASEDARK.E	Oxidation (M)
			7.35E-09		3.78, 2	0.60	1338.7276	0.44719	R.HNPTANVLFLGR.V	
			8.19E-08		4.77, 2	0.59	2108.9341	0.54853	K.M#YGADLAPVDFQHASEDAR.K	Oxidation (M)
			7.11E-14		4.48, 2	0.57	2092.9392	0.83086	K.MYGADLAPVDFQHASEDAR.K	
			1.66E-09		4.46, 2	0.49	1782.9384	0.91875	K.FKIEESYILNSNLGR.L	
			8.63E-06		4.13, 2	0.46	1364.7248	0.85381	K.KFFFGYISDLK.C	
			4.79E-09		4.52, 2	0.49	1587.8662	0.20269	K.IPELLAVGVVDSM#TK.L	Oxidation (M)
			3.99E-06		4.08, 2	0.48	1179.7136	1.06706	R.LVLVNAIYFK.G	
			3.71E-04		2.75, 1	0.33	1221.6473	1.00232	R.LGLQDLFNSSK.A	
			2.57E-07		3.50, 2	0.40	1221.6473	0.21611	R.LGLQDLFNSSK.A	
			3.86E-07		2.91, 2	0.38	1236.6298	0.20513	K.FFFGYISDLK.C	
			3.19E-05		2.92, 2	0.14	2108.9341	1.41711	K.M#YGADLAPVDFQHASEDAR.K	Oxidation (M)
38	Apoa4	P02651	2.15E-07	16.37	40.2					
			1.27E-05		2.94, 2	0.29	984.54724	1.12663	R.RAVEPLGDK.F	
			5.04E-06		3.55, 2	0.42	1268.5939	0.76645	K.VSQM#FGDNVQK.L	Oxidation (M)
			2.15E-07		3.36, 2	0.62	1312.7106	0.89287	K.NLAPLVEDVQSK.L	
			1.90E-04		2.71, 2	0.26	1287.6539	0.79216	K.ATIDQNLEDLR.S	
39	*Capg*	Q6AYC4	1.02E-11	37.82	160.31					
			1.45E-04		2.84, 2	0.47	1203.6691	0.39263	K.TTSGTTPAAIRK.L	
			9.07E-05		1.93, 1	0.42	1280.6150	0.04276	K.VSDATGQM#NLTK.V	Oxidation (M)
			1.22E-04		3.77, 3	0.32	1379.6702	1.02073	K.YREGGVESAFHK.T	
			2.49E-07		3.53, 2	0.46	1280.6150	0.14608	K.VSDATGQM#NLTK.V	Oxidation (M)
			3.67E-04		2.82, 2	0.43	1075.5742	0.07817	K.TTSGTTPAAIR.K	
			7.23E-04		2.84, 2	0.39	1379.6702	1.39006	K.YREGGVESAFHK.T	

			1.18E-09		2.95, 1	0.28	1264.6201	0.06995	K.VSDATGQMNLTK.V	
			2.43E-06		4.05, 3	0.31	2117.0622	1.30429	R.EGGVESAFHKTTSGTTPAAIR.K	
			1.07E-07		3.06, 2	0.51	1264.6201	0.13713	K.VSDATGQMNLTK.V	
			5.97E-04		2.71, 2	0.17	1904.9646	1.00069	R.M#RYSPNTQVEILPQGR.E	Oxidation (M)
			1.58E-08		3.11, 2	0.54	1601.8282	-0.06978	R.YSPNTQVEILPQGR.E	
			1.02E-11		5.79, 2	0.63	2349.0839	0.84355	K.EGNPEEDITADQTNAQAAALYK.V	
			1.64E-08		4.57, 3	0.59	2349.0839	1.27042	K.EGNPEEDITADQTNAQAAALYK.V	
			2.95E-04		3.74, 3	0.27	2792.4750	1.49542	K.AQVEIITDGEEPAEM#IQVLGPKPALK.E	Oxidation (M)
			2.25E-06		4.08, 2	0.45	2383.2061	0.64502	K.AQVEIITDGEEPAEM#IQVLGPK.P	Oxidation (M)
			7.97E-06		3.52, 3	0.36	2776.4802	0.71994	K.AQVEIITDGEEPAEMIQVLGPKPALK.E	
			2.93E-09		5.36, 2	0.56	2205.0168	0.75542	R.EVQGNESDLFM#SYFPQGLK.Y	Oxidation (M)
			4.61E-06		3.28, 2	0.45	2367.2111	0.92974	K.AQVEIITDGEEPAEMIQVLGPK.P	
			7.20E-07		3.27, 2	0.42	1375.7327	0.84856	R.QAALQVADGFISR.M	
			2.14E-05		3.76, 2	0.51	2189.0219	0.90264	R.EVQGNESDLFMSYFPQGLK.Y	
40	*Ublcp1*	Q5FWT7	8.33E-05	22.33	60.20					
			9.27E-06		3.83, 2	0.26	1470.7256	0.96320	K.M#KELGVSTNANYK.I	Oxidation (M)
			8.35E-05		2.78, 2	0.27	1343.7318	0.89836	K.EYKVEVLNPPR.E	
			6.73E-04		2.67, 2	0.50	1252.5965	0.39860	R.SC*AETGVELMR.P	Carbamidomethylation (C)
			1.24E-04		3.81, 2	0.36	1309.6568	0.92009	K.KNTIMFDDIGR.N	
			4.79E-07		2.78, 2	0.31	1243.6317	0.58940	K.LDDFLELNHK.Y	
			8.33E-05		4.01, 3	0.38	1847.0061	1.25150	K.KLLVLDVDYTLFDHR.S	
42	*Taldo1*	Q9EQS0	3.87E-08	29.08	100.19					
			1.00E-05		2.98, 2	0.19	1098.5789	0.33782	K.LGGPQEEQIK.N	
			5.45E-04		3.47, 3	0.28	1515.6896	0.99133	R.WLHNEDQM#AVEK.L	Oxidation (M)
			2.35E-06		2.72, 2	0.45	1248.5742	0.69585	K.SYEPQEDPGVK.S	
			2.18E-05		3.03, 2	0.49	1268.6303	0.76779	R.LSFDKDAM#VAR.A	Oxidation (M)
			1.37E-04		2.83, 2	0.21	997.51351	0.67526	K.TIVM#GASFR.N	Oxidation (M)
			7.22E-04		2.90, 2	0.24	1050.5135	0.87905	R.M#ESALDQLK.Q	Oxidation (M)
			3.87E-08		3.19, 2	0.38	1252.6353	0.46221	R.LSFDKDAMVAR.A	
			5.43E-07		2.86, 2	0.32	1311.6691	0.04521	R.ILDWHVANTDK.K	
			1.28E-05		3.71, 2	0.50	1276.6532	0.93730	K.LSSTWEGIQAGK.E	
			7.55E-07		3.71, 2	0.53	1392.7497	0.92491	K.ALAGC*DFLTISPK.L	Carbamidomethylation (C)
44	*Sgta*	O70593	8.41E-11	13.56	40.2					
			1.7E-05		2.79, 2	0.52	1051.5207	1.10100	K.HAEAVAYYK.K	
			8.41E-11		3.33, 2	0.60	1417.6077	0.70110	R.TPPSEEDSAEAER.L	
			1.07E-05		3.72, 2	0.56	1480.7154	1.48114	K.LGNYVGAVQDC*ER.A	Carbamidomethyla

									tion (C)
			1.87E-08		2.75, 2	0.46	1393.6481	0.68181	K.ALELDPDNDTYK.S
45	*Anxa8*	Q4FZU6	2.78E-11	46.79	150.24				
			8.88E-04		2.91, 2	0.18	1052.5371	0.98332	K.SELSGKFER.L
			4.74E-04		2.70, 2	0.50	922.45499	0.48200	K.ILGTDEM#K.F Oxidation (M)
			6.35E-04		2.90, 2	0.28	943.44073	1.03166	R.VFEEYEK.I
			2.78E-11		3.62, 2	0.54	1746.8578	0.59962	K.SETHGSLEEAM#LTVVK.C Oxidation (M)
			8.84E-06		3.11, 2	0.33	1231.6317	0.95073	K.AWVEQEGVSVK.G
			5.55E-04		2.74, 2	0.32	1073.5949	0.37993	K.GAGTLDGTLIR.N
			3.36E-06		2.73, 2	0.32	1669.7447	0.92849	K.TLSSM#IMGDTSGYYK.T
			3.80E-04		2.91, 2	0.37	1023.5961	0.78456	K.FITILC*TR.S Carbamidomethylation (C)
			1.61E-05		3.55, 2	0.45	1231.7260	0.35238	R.ILVC*LLQGC*R.D Carbamidomethylation (C)
			2.94E-09		3.89, 2	0.60	1730.8629	0.49407	K.SETHGSLEEAMLTVVK.C
			5.31E-09		3.68, 2	0.59	1420.7529	0.94902	K.DLTETLKSELSGK.F
			9.73E-08		3.58, 2	0.55	1351.7442	1.06489	R.LIVALM#YPPYR.Y Oxidation (M)
			2.73E-05		2.84, 2	0.30	1653.7498	0.74663	K.TLSSMIMGDTSGYYK.T
			6.23E-09		4.56, 2	0.40	2568.2211	0.86333	R.DDVSGFVDPGLALQDAQDLHAAGEK.I
			3.23E-04		4.72, 2	0.51	1571.8638	1.24187	K.GIGTNEQAIIDVLTK.R
46	*Gnb1*	P54311	9.06E-11	19.12	50.22				
			5.17E-06		2.85, 2	0.47	1017.5575	0.81847	R.LLVSASQDGK.L
			5.64E-07		3.25, 2	0.55	1523.7340	0.79580	R.ELAGHTGYLSC*C*R.F Carbamidomethylation (C)
			1.83E-07		3.08, 2	0.28	1352.6051	0.95273	K.IYAM#HWGTDSR.L Oxidation (M)
			1.74E-07		3.74, 2	0.43	1225.6186	0.71510	R.LFVSGAC*DASAK.L Carbamidomethylation (C)
			9.06E-11		4.41, 2	0.57	2016.0120	1.38671	K.AC*ADATLSQITNNIDPVGR.I Carbamidomethylation (C)
47	*Etfa*	P13803	2.68E-07	10.51	30.16				
			5.52E-07		2.77, 2	0.31	1143.6157	0.96636	K.VLVAQHDAYK.G
			2.68E-07		3.11, 2	0.39	1310.7078	0.63474	R.TIYAGNALC*TVK.C Carbamidomethylation (C)
			3.94E-04		3.04, 2	0.45	1290.7027	0.04693	R.LGGEVSC*LVAGTK.C Carbamidomethylation (C)
48	*Hnrpa2b1*	gi|109473494|	1.33E-14	21.53	70.34				
			7.09E-04		2.62, 2	0.40	993.51613	0.56021	K.LTDC*VVMR.D Carbamidomethylation (C)

			1.40E-06		6.75, 3	0.63	2205.9002	1.48394	R.NM#GGPYGGGNYGPGGSGGSGGYGGR.S	Oxidation (M)
			1.33E-14		6.35, 2	0.58	2205.9002	0.79852	R.NM#GGPYGGGNYGPGGSGGSGGYGGR.S	Oxidation (M)
			2.21E-04		3.32, 2	0.35	1377.6293	0.78569	R.GGGGNFGPGPGSNFR.G	
			3.89E-04		2.96, 2	0.25	1013.4435	0.85381	R.GGNFGFGDSR.G	
			1.78E-14		5.75, 2	0.64	2189.9052	0.80425	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S	
			9.78E-05		2.00, 1	0.29	1050.4415	0.23254	R.DYFEEYGK.I	
			3.22E-06		3.65, 2	0.34	1188.6470	0.88640	K.IDTIEIITDR.Q	
49	*Arhgdib*	Q5M860	1.314E-12	36.00	70.23					
			6.29E-04		2.81, 2	0.30	1084.6149	0.44670	K.LNYKPPPQK.S	
			6.26E-04		2.24, 2	0.33	957.47888	0.47002	K.YVQQTYR.N	
			3.73E-07		3.93, 2	0.55	1696.7581	0.27166	K.ELQEM#DKDDESLTK.Y	Oxidation (M)
			9.83E-09		4.53, 2	0.50	1680.7633	0.88445	K.ELQEMDKDDESLTK.Y	Oxidation (M)
			1.31E-12		3.48, 2	0.41	2219.1239	-0.26083	R.LSLVC*DSAPGPITM#DLTGDLK.A	Oxidation (M), Carbamidomethylation (C)
			1.54E-09		4.27, 2	0.54	2163.2019	1.19390	K.TLLGDVPVVADPTVPNVTVTR.L	
			1.73E-11		3.92, 2	0.43	2203.1290	0.80462	R.LSLVC*DSAPGPITMDLTGDLK.A	Carbamidomethylation (C)
			3.07E-05		3.64, 3	0.49	2203.1290	0.96586	R.LSLVC*DSAPGPITMDLTGDLK.A	Carbamidomethylation (C)
50	*Gsta3*	P04904	3.89E-11	29.41	78.22					
			1.41E-05		2.48, 2	0.21	985.60406	0.04125	R.VSNLPTVKK.F	
			2.25E-05		2.50, 1	0.30	1245.5970	0.15869	K.SHGQDYLVGNR.L	
			9.34E-05		3.78, 3	0.43	1585.8444	1.25235	K.VLKSHGQDYLVGNR.L	
			1.03E-06		3.55, 2	0.40	1245.5970	0.80937	K.SHGQDYLVGNR.L	
			6.31E-07		3.20, 2	0.43	1631.8614	0.14423	R.KPLEDEKC*VESAVK.I	Carbamidomethylation (C)
			3.40E-07		3.53, 3	0.21	1631.8614	1.41497	R.KPLEDEKC*VESAVK.I	Carbamidomethylation (C)
			1.05E-05		2.69, 2	0.53	1006.5931	0.02696	K.AILNYIATK.Y	
			5.65E-09		4.00, 2	0.54	2186.9766	0.70020	R.NDGSLM#FQQVPM#VEIDGM#K.L	Oxidation (M)
			3.89E-11		4.50, 2	0.39	2170.9817	0.85672	R.NDGSLM#FQQVPM#VEIDGMK.L	Oxidation (M)
			3.47E-05		2.74, 2	0.50	2170.9817	0.85672	R.NDGSLM#FQQVPMVEIDGM#K.L	Oxidation (M)
52	*Apoa1*	P04639	1.16E-09	28.57	90.21					
			6.56E-04		2.87, 2	0.28	1197.5853	0.93204	K.IM#SM#IDEAKK.K	Oxidation (M)
			1.35E-04		3.16, 2	0.34	1349.6365	0.77415	R.NEM#NKDLENVK.Q	Oxidation (M)
			2.32E-04		2.76, 2	0.28	1069.4903	0.43679	K.IM#SM#IDEAK.K	Oxidation (M)

			6.11E-04		3.89, 2	0.32	1333.6416	0.99346	R.NEMNKDLENVK.Q	
			5.56E-04		2.80, 2	0.42	849.44647	0.27110	K.VVAEEFR.D	
			6.86E-06		3.54, 2	0.36	1417.6416	0.39284	K.M#QPHLDEFQEK.W	Oxidation (M)
			4.44E-05		2.86, 2	0.36	1195.5378	0.21660	K.WNEEVEAYR.Q	
			1.16E-09		4.26, 2	0.48	1454.7889	0.99675	R.VKDFATVYVDAVK.D	
			3.83E-07		3.14, 2	0.47	1460.6903	0.21697	R.DYVSQFESSTLGK.Q	
53	*Hspb1*	P42930	3.37E-08	12.14	20.0					
			2.08E-05		3.44, 2	0.36	987.60980	0.65434	R.RVPFSLLR.S	
			3.37E-08		3.54, 2	0.54	1832.9752	0.65178	K.AVTQSAEITIPVTFEAR.A	
54	*Mrlcb*	P18666	1.52E-09	47.09	78.23					
			6.32E-05		2.18, 2	0.25	1253.5579	0.75746	K.EAFNM#IDQNR.D	Oxidation (M)
			1.51E-04		2.48, 2	0.34	1035.5139	1.19951	R.ELLTTMGDR.F	
			5.08E-05		2.55, 2	0.30	1228.6168	0.30547	K.LNGTDPEDVIR.N	
			6.46E-05		2.62, 2	0.42	1344.6463	0.19608	K.EDLHDM#LASLGK.N	Oxidation (M)
			1.03E-08		3.65, 2	0.44	1415.6325	1.00627	R.FTDEEVDELYR.E	
			9.70E-05		3.08, 2	0.50	1260.6007	1.38494	K.GNFNYIEFTR.I	
			1.52E-09		4.59, 2	0.59	2106.9800	1.07198	R.ATSNVFAM#FDQSQIQEFK.E	Oxidation (M)
			5.44E-07		3.30, 2	0.46	2186.9464	1.04608	R.ATSNVFAM#FDQSQIQEFK.E	Phosphorylation (T), Oxidation (M)
55	*Tagln*	P31232	5.44E-08	42.79	120.21					
			4.22E-07		2.76, 2	0.41	953.45746	0.31035	K.AAEDYGVTK.T	
			1.96E-04		2.08, 1	0.44	953.45746	0.02875	K.AAEDYGVTK.T	
			4.08E-06		3.14, 2	0.36	1210.5585	1.10332	K.KYDEELEER.L	
			1.24E-06		3.04, 2	0.32	1530.8526	0.70769	K.LVNSLYPEGSKPVK.V	
			4.65E-04		2.92, 2	0.34	1082.4636	0.80474	K.YDEELEER.L	
			1.25E-04		2.73, 2	0.27	1260.6292	0.89531	K.VPENPPSM#VFK.Q	Oxidation (M)
			8.26E-04		2.71, 2	0.23	1237.6245	0.37565	K.QM#EQVAQFLK.A	Oxidation (M)
			8.50E-04		2.82, 2	0.33	1010.4400	0.82932	R.GDPNWFM#K.K	Oxidation (M)
			1.53E-05		2.96, 2	0.37	1244.6344	0.98650	K.VPENPPSMVFK.Q	
			2.81E-05		3.08, 2	0.37	1206.6762	1.06479	R.TVM#ALGSLAVTK.N	Oxidation (M)
			3.61E-05		4.18, 2	0.42	1190.6812	1.09734	R.TVMALGSLAVTK.N	
			5.44E-08		4.06, 2	0.51	1546.7093	0.89114	K.TDM#FQTVDLFEGK.D	Oxidation (M)
			7.00E-08		4.20, 2	0.53	1530.7144	0.97283	K.TDMFQTVDLFEGK.D	
56	*S100a9*	P50116	8.29E-08	21.24	20.19					
			6.36E-04		2.71, 2	0.24	1172.6058	1.05522	R.KYGHPDTLNK.A	
			8.29E-08		3.89, 2	0.51	1664.8754	0.96245	R.SISTIINVFHQYSR.K	

P (pro): The protein probability is the highest peptide probability that was found

P (pep): The protein probability that the search could have produced a better match using a random sequence.

Coverage: The percentage of identified peptides

Score: This is the original Eng-Yates-Scoring, in which a primary match receives 10 points, a secondary match receives 8 points, a tertiary match gets 6 points, 4 points, 2 points, etc. The points for all the peptides are summed together. This was the original way of sorting a consensus report.

Xc: The cross correlation of the primary match. Xc (Cross Correlation) is a measure of the "goodness of fit" of a theoretical spectra created from the sequences b + y ions, along with water and amine losses compared to the actual MS/MS spectra acquired by the instrument.

ΔCn: The delta correlation of the primary match being compared to the secondary match.

ΔM: The delta mass is the difference between the mass theoretical mass of the peptide identified and the actual mass measurement of the instrument.