

## Inferred proteins based on identification of peptides from the human platelet membrane/cytoskeletal sub-proteome

Group	Acc Num <sup>A</sup>	Gene Name <sup>B</sup>	Protein Description <sup>C</sup>	PScore <sup>D</sup>	%C <sup>E</sup>	Ion Score <sup>F</sup>	HScore <sup>G</sup>	Evalue <sup>H</sup>	Precursor m/z <sup>I</sup>	Charge State <sup>J</sup>	Calculated Peptide Mass <sup>K</sup>	Delta Mass <sup>L</sup>	Sequence <sup>M</sup>	Study Overlap <sup>N</sup>	Previous Platelet ID <sup>O</sup>
1	P31946	YWHA B	14-3-3 protein beta/alpha (Protein kinase C inhibitor protein-1)	58.6	17	58.6	36.0	4.31E-03	591.63	2	1181.56	-0.31	(R)YLSEVASGDNK(Q)	B	WP / M / MP
						49.8	51.4	3.77E-02	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						32.9	37.5	1.80E+00	907.58	1	906.52	0.06	(R)NLLSVAYK(N)		
2	P62258	YWHA E	14-3-3 protein epsilon (14-3-3E).	66.0	22	64.0	38.6	1.22E-03	619.38	2	1236.65	0.10	(K)HLIPAANTGESK(V)	B	WP / M / MP
						49.8	51.4	3.77E-02	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						44.1	54.5	1.72E-01	459.43	2	916.52	0.34	(R)IISSIEQK(E)		
						40.5	38.5	3.88E-01	459.43	2	916.52	0.34	(R)IISSIEQK(E)		
						32.9	37.5	1.80E+00	907.58	1	906.52	0.06	(R)NLLSVAYK(N)		
3	Q04917	YWHA H	14-3-3 protein eta (Protein AS1).	55.6	25	54.8	21.4	7.71E-03	1238.57	2	2474.27	0.86	(K)AVTELNEPLSNEDNLLSVAYK(N)	B	WP / M / MP
						49.8	51.4	3.77E-02	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						45.0	44.2	1.12E-01	579.03	2	1155.60	0.45	(-)SGDREQLLQR(A)		
						32.9	37.5	1.80E+00	907.58	1	906.52	0.06	(R)NLLSVAYK(N)		
4	P61981	YWHA G	14-3-3 protein gamma (Protein kinase C inhibitor protein-1) (KCIP-1).	62.8	17	62.5	35.4	1.77E-03	619.10	2	1235.65	0.55	(R)YLAEVATGEKR(A)	B	MP
						49.8	51.4	3.77E-02	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						40.4	40.6	3.26E-01	578.91	2	1155.62	0.20	(-)SVDREQLVQK(A)		
						32.9	37.5	1.80E+00	907.58	1	906.52	0.06	(R)NLLSVAYK(N)		
						29.5	29.2	3.32E+00	923.35	2	1843.81	0.88	(R)LAQAERYDDmAAmK(N)		
5	P63104	YWHA Z	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein-1)	371.3	53	112.0	35.4	1.72E-08	1021.37	2	2039.98	0.75	(K)GIVDQSQQAQAEFEISK(K)	B	WP / M / MP
						109.6	38.5	2.92E-08	1066.79	2	2130.98	0.60	(K)TAFDEAIAELDTLSEESYK(D)		
						85.7	41.1	8.66E-06	774.81	2	1547.71	-0.10	(K)SVTEQGAELSNEER(N)		
						85.2	28.3	7.82E-06	1085.33	2	2168.07	0.59	(K)GIVDQSQQAQAEFEISK(E)		
						83.1	53.2	1.57E-05	640.29	2	1278.65	-0.08	(R)YLAEVAAGDDKK(G)		
						69.6	31.6	3.60E-04	753.02	2	1503.78	0.25	(R)VVSIEQKTEGAEK(K)		
						51.6	41.6	2.45E-02	652.77	2	1303.68	-0.15	(K)FLIPNASQAESK(V)		
						49.8	51.4	3.77E-02	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						45.4	36.6	9.52E-02	710.54	2	1417.71	1.37	(R)DICNDVLSLLEK(F)		
						33.3	33.2	1.77E+00	603.41	2	1204.65	0.16	(K)DSTLImQLLR(D)		
						32.9	37.5	1.80E+00	907.58	1	906.52	0.06	(R)NLLSVAYK(N)		
6	P10809	HSPD 1	60 kDa heat shock protein, mitochondrial precursor (Hsp60)	208.8	15	148.1	37.2	3.62E-12	1241.90	2	2481.39	0.41	(R)TALDAAGVASLLTAEVVTIPK(E)	B	WP / M / MP
						71.9	41.2	2.69E-04	480.97	2	959.50	0.44	(R)VTDALNATR(A)		
						63.8	33.8	1.52E-03	617.28	2	1232.59	-0.04	(K)VGGTSDVEVNEK(K)		
						15.7	36.3	7.12E+01	1062.87	2	2123.77	-0.81	(K)EEKDPGmGAmGGmGGmGGmGmF(-)		
						15.6	36.3	7.27E+01	1062.87	2	2123.77	-0.81	(K)EEKDPGmGAmGGmGGmGGmGmF(-)		

Supplementary Table 1

7	P11021	HSPA 5	78 kDa glucose- regulated protein precursor (GRP 78)	149.0	14	95.2	36.2	9.87E-07	794.86	2	1587.85	-0.14	(K)KSDIDEIVLVGGSTR(I)	B	WP / M / MP
						61.3	31.7	2.30E-03	778.66	2	1554.79	0.52	(K)NGRVEIANDQGNR(I)		
						56.7	32.6	6.73E-03	606.01	2	1209.58	0.43	(K)EFFNGKEPSR(G)		
8	P68032	ACTC	Actin, alpha cardiac (Alpha-cardiac actin).	41.8	59	42.8	60.4	1.44E-01	978.52	2	1955.04	1.30	(R)VAPEEHPTLLTEAPLNPK(A)	B	
						41.8	30.5	1.88E-01	989.33	2	1975.90	0.75	(K)YPIEHGIITNWDmEK(I)		
						39.6	47.0	3.74E-01	599.78	2	1197.51	0.05	(K)DSYVGDEAQS(KR)		
9	P60709	ACTB	Actin, cytoplasmic 1 (Beta-actin).	972.2	86	110.8	75.8	1.83E-08	1284.43	2	2565.16	1.70	(K)LCYVALDFEQEmATAASSSSLEK(S)	B	M / MP
						104.3	71.9	9.05E-08	1172.49	2	2342.16	0.81	(R)KDLANTVLSGGTmYPGIADR(M)		
						95.5	43.7	8.64E-07	896.22	2	1789.88	0.56	(K)SYELPDGQVITIGNER(F)		
						94.3	25.4	8.13E-07	1309.98	2	2617.32	0.64	(K)YSVWIGGSILASLSTFQmWISK(Q)		
						93.0	52.8	8.74E-07	1643.57	2	3284.59	0.55	(K)mTQImFETFNTPAmYVAIAVLSLYASGR(T)		
						90.5	28.8	2.20E-06	1172.49	2	2342.16	0.81	(R)KDLANTVLSGGTmYPGIADR(M)		
						89.4	28.1	2.95E-06	1116.16	2	2230.06	0.25	(K)DLANTVLSGGTmYPGIADR(M)		
						78.6	46.1	3.72E-05	977.82	2	1953.06	0.57	(R)VAPEEHPVLLTEAPLNPK(A)		
						74.3	46.3	6.44E-05	1643.57	2	3284.59	0.55	(K)mTQImFETFNTPAmYVAIAVLSLYASGR(T)		
						72.5	47.9	2.27E-04	488.88	2	975.44	0.32	(K)AGFAGDDAPR(A)		
						71.5	27.3	1.75E-04	795.32	3	2382.06	0.91	(R)HQGVmVGmGQKDSYVGDEAQS(KR)		
						69.9	33.8	3.69E-04	600.20	2	1197.70	0.69	(R)AVFPSIVGRPR(H)		
						68.6	30.4	4.65E-04	758.63	2	1515.70	-0.45	(K)QEYDESGPSIVHR(K)		
						66.0	30.3	4.40E-04	1067.60	3	3198.60	1.21	(R)TTGIVmDSGDGVTHTVPIYEGYALPHAILR(L)		
						63.6	52.8	7.56E-04	1643.57	2	3284.59	0.55	(K)MTQImFETFNTPAmYVAIAVLSLYASGR(T)		
						63.5	52.8	7.75E-04	1643.57	2	3284.59	0.55	(K)mTQIMFETFNTPAmYVAIAVLSLYASGR(T)		
						60.7	35.7	2.70E-03	823.18	2	1643.79	0.56	(K)QEYDESGPSIVHR(C)		
						60.6	30.3	2.65E-03	791.02	2	1579.79	0.25	(R)mQKEITALAPSTmK(I)		
						59.9	25.7	2.37E-03	627.89	4	2506.17	1.40	(R)HQGVmVGmGQKDSYVGDEAQS(KR)		
						57.7	29.5	6.45E-03	566.89	2	1131.52	0.25	(R)GYSFTTTAER(E)		
						56.9	34.5	7.42E-03	589.48	2	1176.61	0.34	(K)EITALAPSTmK(I)		
						54.0	28.9	1.25E-02	814.21	2	1625.83	0.59	(R)DLTDYmKILTER(G)		
						51.5	35.6	1.25E-02	1067.60	3	3198.60	1.21	(R)TTGIVmDSGDGVTHTVPIYEGYALPHAILR(L)		
						51.2	50.7	2.55E-02	1515.77	1	1514.74	0.03	(K)IWHHTFYNELR(V)		
						50.4	27.8	1.91E-02	1398.50	2	2794.22	0.77	(M)\$DDIAALVVDNGSGmCKAGFAGDDAPR(A)		
						47.8	21.6	4.09E-02	795.32	3	2382.06	0.91	(R)HQGVmVGmGQKDSYVGDEAQS(KR)		
						40.9	25.4	1.67E-01	1413.02	2	2822.30	1.73	(K)EKLCYVALDFEQEmATAASSSSLEK(S)		
						39.6	47.0	3.74E-01	599.78	2	1197.51	0.05	(K)DSYVGDEAQS(KR)		
						37.2	36.3	3.93E-01	1413.02	2	2822.30	1.73	(K)EKLCYVALDFEQEmATAASSSSLEK(S)		
						36.8	29.3	6.88E-01	815.77	2	1628.82	0.71	(R)GYSFTTTAEREIVR(D)		
						35.9	21.6	6.28E-01	795.32	3	2382.06	0.91	(R)HQGVmVGmGQKDSYVGDEAQS(KR)		
						34.6	25.2	7.84E-01	627.89	4	2506.17	1.40	(R)HQGVmVGmGQKDSYVGDEAQS(KR)		

Supplementary Table 1

						32.5	31.9	1.81E+00	519.02	2	1035.64	0.40	(K)IKIIPAPER(K)		
						31.0	25.2	1.82E+00	627.89	4	2506.17	1.40	(R)HQGVMMVmGQKDSYVGDEAQSKR(G)		
10	P61158	ACTR 3	Actin-like protein 3 (Actin-related protein 3).	133.8	15	82.5	36.8	1.35E-05	1222.98	2	2443.18	0.77	(K)GVDDLDFFIGDEAIKPTYATK(W)	B	WP / MP
						75.8	49.7	8.37E-05	705.58	2	1408.77	0.39	(R)DITYFIQQLLR(D)		
						59.2	37.3	3.95E-03	611.84	2	1221.67	0.01	(K)QYTGINAISK(E)		
						50.6	47.3	3.56E-02	529.41	2	1056.53	0.29	(R)FmEQVIFK(Y)		
11	O15144	ARPC 2	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kDa)	42.8	11	42.8	19.5	9.68E-02	1545.22	2	3087.54	0.90	(R)VYGSFLVNPESGYNVSLLYDENLPASK(D)	B	WP / MP
						21.0	30.5	2.73E+01	457.68	3	1369.71	0.33	(K)DSIVHQAGmLKR(N)		
12	O15145	ARPC 3	Actin-related protein 2/3 complex subunit 3	63.8	18	63.8	34.4	7.80E-03	739.42	2	1476.66	0.17	(-)PAYHSSLmDPDTK(L)	B	WP
						43.0	53.9	1.97E-01	446.37	2	890.50	0.23	(R)AYLQQLR(Q)		
						42.2	41.9	2.00E-01	739.42	2	1476.66	0.17	(-)PAYHSSLmDPDTK(L)		
13	P59998	ARPC 4	Actin-related protein 2/3 complex subunit 4	77.8	25	64.5	43.2	1.34E-03	594.01	2	1185.67	0.35	(K)VLIEGSINSVR(V)	B	MP
						42.8	29.6	1.82E-01	695.67	2	1388.78	0.55	(-)STATLRPYLSAVR(A)		
						39.4	44.6	3.82E-01	635.13	2	1267.75	0.50	(K)ELLQPVTISR(N)		
14	O15511	ARPC 5	Actin-related protein 2/3 complex subunit 5	117.5	36	67.4	39.2	5.87E-04	824.16	2	1645.87	0.45	(K)AVQSLDKNGVDLLmK(Y)	B	WP / MP
						65.9	36.6	8.95E-04	667.04	2	1331.69	0.38	(R)QGNmTAALQAALK(N)		
						49.7	29.0	2.82E-02	699.76	3	2096.10	0.18	(R)QGNmTAALQAALKNPPINTK(S)		
15	Q10567	AP1B1	Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1)	67.5	3	67.5	25.6	4.40E-04	1147.00	2	2292.31	-0.32	(K)LAPPLVTLISAEPQLQYVALR(N)	2	M / MP
16	Q5T0S2	CAP1	Adenylyl cyclase- associated protein (CAP).	75.2	28	75.2	27.7	7.50E-05	1140.91	2	2279.18	0.64	(K)GAAPYVQAFDSLLAGPVAEYLK(I)	B	WP / M / MP
						23.8	38.6	1.37E+01	606.68	2	1211.68	-0.33	(K)KEPAVLELGK(K)		
17	Q01518	CAP1	Adenylyl cyclase- associated protein 1 (CAP 1).	402.9	32	124.3	41.2	1.06E-09	965.79	2	1929.08	0.50	(K)JLGLVFDDVVGIVEIISK(D)	B	WP / M / MP
						115.2	31.8	8.09E-09	1030.08	2	2057.18	0.97	(K)KLGLVFDDVVGIVEIISK(D)		
						100.3	29.8	2.25E-07	1175.87	2	2350.22	-0.48	(K)JAGAAPYVQAFDSLLAGPVAEYLK(I)		
						88.9	37.6	3.34E-06	1086.99	2	2171.22	0.75	(K)JLSDLLAPISEIQIKEVIFR(E)		
						85.8	39.5	7.40E-06	964.81	2	1927.02	0.59	(R)SALFAQINQGESITHALK(H)		
						43.4	31.7	1.50E-01	1426.87	1	1425.81	0.06	(K)JLSDLLAPISEIQI(E)		
						43.2	28.0	1.37E-01	613.66	3	1836.97	1.01	(R)SGPKPFSAPKPQTSPSPK(R)		
18	P05141	SLC25 A5	ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)	106.0	16	106.0	28.2	6.61E-08	1076.91	2	2151.12	0.70	(-)STDAVSFAKDFLAGGVAIAISK(T)	B	SEN
19	P12236	SLC25 A6	ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)	119.9	14	100.3	32.3	2.36E-07	1126.44	2	2250.19	0.68	(-)STEQAISFAKDFLAGGIAAISK(T)	B	M / MP
						43.9	24.3	7.46E-02	1030.50	3	3087.66	0.85	(-)STEQAISFAKDFLAGGIAAISKTAVAPIER(V)		
20	P61204	ARF3	ADP-ribosylation factor 3.	144.0	44	67.4	34.8	7.32E-04	545.47	2	1088.62	0.32	(R)DAVLLVFANK(Q)	B	WP / MP
						62.3	41.0	1.61E-03	1031.96	2	2062.08	-0.17	(R)mLAEDLRDAVLLVFANK(Q)		
						55.8	45.9	1.04E-02	552.49	2	1102.61	0.36	(R)lImVGLDAAGK(T)		
						48.2	19.0	3.14E-02	1359.69	2	2716.37	1.01	(R)DAVLLVFANKQDLNAmNAEITDK(L)		
						46.3	30.1	5.70E-02	1162.19	2	2322.24	0.13	(K)JLGEIVTTIPTIGFNVETVEYK(N)		

Supplementary Table 1

21	P06733	ENO1	Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)	118.2	24	66.2	45.4	7.79E-04	713.65	2	1424.72	0.57	(R)YISPDQLADLYK(S)	B	WP / M / MP
						49.9	32.5	2.94E-02	609.52	3	1825.85	-0.28	(R)SGKYDLDFKSPDDPSR(Y)		
						48.5	42.4	5.68E-02	572.56	2	1142.61	0.50	(R)IGAEVYHNLK(N)		
						47.0	48.7	8.58E-02	480.47	2	958.53	0.41	(R)NFRNPLAK(-)		
						45.0	36.1	1.32E-01	536.98	2	1071.52	0.44	(R)SGKYDLDFK(S)		
						44.5	25.0	6.87E-02	1506.84	2	3010.56	1.12	(R)HIADLAGNSEVILPVPFNVINGGSHAGNK(L)		
22	P12814	ACTN 1	Alpha-actinin 1 (Alpha-actinin cytoskeletal isoform)	958.8	48	44.5	51.5	1.22E-01	514.50	2	1026.64	0.36	(K)TIAPALVSKK(L)	B	WP / M / MP
						100.9	37.8	2.21E-07	1012.75	2	2022.95	0.55	(K)AlmTYVSSFYHAFSGAQK(A)		
						97.0	38.7	5.62E-07	934.76	2	1867.01	0.50	(K)LLETIDQLYLEYAKR(A)		
						96.6	30.3	6.40E-07	946.41	2	1889.94	0.87	(R)KDDPLTNLNTAFDVAEK(Y)		
						84.5	33.5	1.09E-05	888.76	2	1774.84	0.68	(K)mLDAEDIVGTARPDEK(A)		
						83.9	40.5	1.40E-05	694.11	2	1385.77	0.44	(R)VGWEQLLTTIAR(T)		
						82.9	35.9	1.55E-05	872.95	2	1744.75	-0.86	(R)ETADTDTADQVmAASF(K)(I)		
						82.2	35.1	1.90E-05	740.76	2	1478.80	0.71	(K)mTLGmWTILR(F)		
						76.0	34.7	6.12E-05	1170.35	2	2338.18	0.51	(K)IDQLEGDHQLIQEALIFDNK(H)		
						74.6	32.4	3.47E-05	1465.96	3	4393.03	1.86	(R)AAPFNNWmEGAmEDLQDTFIVHTIEEIQLTTAHEQFK(A)		
						73.4	32.0	9.74E-05	874.39	3	2619.34	0.84	(R)KDDPLTNLNTAFDVAEKYLDIPK(M)		
						72.5	38.4	1.99E-04	695.19	2	1387.77	0.61	(K)LmLLLEVISGER(L)		
						72.3	31.6	1.88E-04	772.15	2	1541.83	0.46	(K)LVSIGAEIIVDGNV(K)(M)		
						72.2	32.4	1.76E-04	943.69	2	1885.02	0.36	(R)KQFGAQANVIGPWQTK(M)		
						70.9	36.2	2.49E-04	769.61	2	1536.77	0.44	(R)FAIQDISVEETSAK(E)		
						67.7	20.7	3.46E-04	1454.15	2	2905.43	0.86	(K)IVQTYHVNmAGTNPYTTITPQINGK(W)		
						63.6	38.5	1.52E-03	715.63	2	1428.76	0.49	(R)TINEVENQILTR(D)		
						62.4	31.1	1.69E-03	884.71	2	1766.89	0.52	(K)ILAGDKNYITmDELR(R)		
						60.7	50.4	3.11E-03	410.15	3	1226.64	0.82	(R)HRPELIDYGK(L)		
						60.7	34.8	2.72E-03	647.65	2	1292.75	0.54	(R)LAILGIHNEVSK(I)		
						60.5	28.6	2.39E-03	998.35	2	1993.99	0.70	(R)ISIEmHGTLEDQLSHLR(Q)		
						53.6	32.6	1.32E-02	879.64	2	1756.93	0.34	(K)QFGAQANVIGPWQTK(M)		
						51.3	34.1	2.81E-02	564.94	2	1127.61	0.26	(R)LDHLAEKFR(Q)		
						49.1	31.7	3.91E-02	678.06	2	1353.60	0.51	(K)GISQEQmNEFR(A)		
						47.9	28.0	5.06E-02	763.65	2	1524.77	0.52	(R)QKDYETATLSEIK(A)		
						46.1	33.1	9.03E-02	405.46	3	1213.57	-0.18	(K)ASIHEAWTDGK(E)		
						42.3	37.5	2.43E-01	530.72	2	1059.54	-0.11	(R)ImSIVDPNR(L)		
						40.3	34.5	3.24E-01	432.89	2	863.48	0.29	(K)ALDFIASK(G)		
23	O43707	ACTN 4	Alpha-actinin 4 (Non-muscle alpha-actinin 4)	71.1	20	57.7	33.8	5.47E-03	517.03	3	1547.76	0.34	(K)HRDYETATLSDIK(A)	1	MP
						45.6	26.2	8.81E-02	684.66	2	1367.61	-0.29	(K)GISQEQmQEFR(A)		
						41.2	42.0	2.38E-01	484.12	3	1448.71	0.66	(R)LSNRPAFmPSEGG(M)		
24	P37840	SNCA	Alpha-synuclein	78.5	23	57.6	30.5	5.31E-03	648.58	2	1294.69	0.46	(K)EGVVHG VATVAEK(T)	B	MP

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			(Non-A beta component of AD amyloid)			43.0	31.1	1.55E-01	509.23	3	1523.83	0.87	(K)TKEGVVHG VATVAEK(T)		
						40.7	31.7	2.77E-01	590.81	2	1179.65	-0.04	(K)TKEGVLYV GSK(T)		
25	P55145	ARME T	ARME T protein precursor (Arginine-rich protein).	52.8	10	52.8	47.1	1.62E-02	838.83	2	1675.87	-0.22	(R)DVTFSPATIE NELIK(F)	2	WP / MP
26	P24539	ATP5F 1	ATP synthase B chain, mitochondrial precursor (EC 3.6.3.14)	21.0	8	21.0	16.9	2.15E+01	1012.07	2	2022.14	-1.18	(K)TGVTPGYVLGTGLIYALSK(E)	2	M
27	P06576	ATP5B	ATP synthase beta chain, mitochondrial precursor (EC 3.6.3.14)	45.7	16	41.9	25.8	8.61E-02	1282.19	3	3841.97	1.60	(K)KGSITSVQAIYVPADLTD PAPATTF AHL DATT VLSR(A)	1	WP / M
						25.6	21.7	6.81E+00	1149.78	2	2297.07	0.48	(R)IPSAVG YQPTLATmGtM QER(I)		
28	O75947	ATP5 H	ATP synthase D chain, mitochondrial (EC 3.6.3.14) (My032 protein).	54.9	13	54.9	25.6	7.54E-03	1241.49	2	2480.18	0.79	(K)NLIPFDQmTIEDLNEAF PETK(L)	1	WP / M / MP
29	P56134	ATP5J 2	ATP synthase f chain, mitochondrial (EC 3.6.3.14).	56.7	14	56.7	29.3	7.08E-03	715.08	2	1427.68	0.48	(R)DFSPSGIFGAFQR(G)	2	
30	P48047	ATP5 O	ATP synthase oligomycin sensitivity conferral protein, mitochondrial	60.3	31	43.3	41.7	1.46E-01	513.22	2	1024.63	-0.20	(R)VAQILKEPK(V)	B	WP / M / MP
						40.3	23.3	2.30E-01	1160.05	2	2317.14	0.95	(R)GEVPCTVTSASPLEEATLSELK(T)		
						27.0	29.7	6.21E+00	513.18	3	1535.94	-0.70	(K)ELLRVAQILKEPK(V)		
31	P61769	B2M	Beta-2-microglobulin precursor	36.5	18	36.5	24.8	5.04E-01	1278.35	2	2553.22	1.48	(K)SNFLNCYVSGFHPSDIEVDLLK(N)	1	WP / M
32	Q9HBI1	PARV B	Beta-parvin (Affixin).	107.6	10	72.9	45.0	1.63E-04	685.00	2	1367.74	0.26	(K)JARPEDVNVLDLK(S)	B	M / MP
						72.0	37.3	1.92E-04	856.68	2	1711.91	-0.55	(K)VLLDWINDVLVEER(I)		
						24.8	33.7	1.03E+01	551.58	3	1651.81	-0.06	(R)TmIDPTSKEDPKFK(E)		
33	Q05682	CALD 1	Caldesmon (CDM)	33.4	4	33.4	27.9	1.60E+00	645.18	2	1287.70	0.66	(K)QSVDKVTSPTKV(-)	2	WP / MP
34	P62158	CALM 1	Calmodulin (CaM).	200.9	31	102.5	41.4	1.70E-07	878.36	2	1753.86	0.86	(R)VFDKDGNGYISAAELR(H)	B	WP
						82.9	29.9	8.55E-06	1130.59	3	3388.62	0.16	(-)SADQLTEEQIAEFKEAFSLFDKGDGTITTK(E)		
						82.3	37.1	1.76E-05	923.26	2	1843.88	0.64	(K)EAFSLFDKGDGTITTK(E)		
35	P04632	CAPN S1	Calpain small subunit 1 (CSS1) (Calcium-dependent protease small subunit 1)	122.1	34	94.4	30.9	5.32E-07	1799.92	2	3596.65	1.18	(K)GGGGGGGGGGGLGGGLGNVLGGLISGAGGGGGGGGGGGGGGGGGGGGGTAmR(I)	B	WP / MP
						45.6	17.8	6.33E-02	1278.45	2	2554.23	0.66	(R)LFQAQLAGDDmEVSATELmNILNK(V)		
36	P07384	CAPN 1	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calpain-1 large subunit)	66.4	8	51.9	33.2	1.76E-02	1007.84	2	2013.06	0.62	(K)RPTTELLSNPQFIVDGATR(T)	B	M / MP
						51.9	37.5	2.29E-02	694.89	2	1387.81	-0.04	(R)KAPSDLYQILK(A)		
						29.2	30.3	3.81E+00	437.52	3	1308.66	-0.19	(R)SDFFLANASRAR(S)		
37	Q99439	CNN2	Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin).	89.2	13	89.2	40.7	3.31E-06	971.78	2	1940.95	0.60	(-)SSTQFNKGPSYGLSAEVK(N)	1	WP / MP
						28.2	29.3	4.78E+00	676.69	2	1350.60	0.78	(K)CASQVGmTAPGTR(R)		
38	P27797	CALR	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (grp60).	81.0	15	63.9	22.5	7.14E-04	1635.43	2	3267.49	1.36	(K)SGTIFDNFLITNDEAYAEF FGNETWGVTK(A)	B	WP / M
						45.1	28.0	8.00E-02	696.53	3	2085.96	0.64	(K)FYGDEEKDKGLQTSQDAR(F)		
						36.2	46.4	8.75E-01	1147.61	1	1146.65	-0.04	(K)KVHVIFNYK(G)		
39	P00918	CA2	Carbonic anhydrase II (EC 4.2.1.1) (Carbonate dehydratase II) (CA-II)	90.9	15	68.6	29.3	4.24E-04	835.20	2	1667.96	0.44	(K)AVQQPDGLAVLGIFLK(V)	2	WP / MP
						51.8	29.6	1.71E-02	1070.84	2	2139.08	0.60	(K)YDPSLKPLSVSYDQATSLR(I)		
40	P21926	CD9	CD9 antigen (p24)	85.8	10	68.8	67.2	4.13E-04	782.74	2	1562.73	0.74	(K)EVGEFYKDTYNK(L)	B	M / MP /

Supplementary Table 1

			(Leukocyte antigen MIC3) (Motility-related protein)			56.5	39.5	7.32E-03	590.57	2	1178.65	0.49	(K)KDVLETFTVK(S)		SEN
41	P60953	CDC4 2	Cell division control protein 42 homolog (G25K GTP-binding protein)	29.9	11	29.9	27.7	2.57E+00	1179.21	2	2357.25	-0.84	(K)TPFLLVGTQIDLRDDPSTIEK(L)	1	WP / M / MP
42	O00299	CLIC1	Chloride intracellular channel protein 1 (Nuclear chloride ion channel 1)	162.1	41	91.3	22.9	1.41E-06	1497.19	2	2991.38	1.00	(K)VLDNYLTSPLPEEVEDTSAEDEVVSQR(K)	B	WP / MP
						71.8	32.5	1.97E-04	923.21	2	1843.97	0.44	(K)LAALNPESNTAGLDIFAK(F)		
						59.4	28.0	3.90E-03	1328.56	1	1327.64	-0.08	(K)NSNPALNDNLEK(G)		
43	Q9Y696	CLIC4	Chloride intracellular channel protein 4	34.3	3	34.3	32.9	1.58E+00	494.18	2	986.48	-0.12	(R)YLTNAYS(RD)	2	MP
44	Q00610	CLTC	Clathrin heavy chain 1 (CLH-17).	125.9	5	72.1	61.3	1.94E-04	677.38	2	1352.84	-0.09	(R)NLQNLILTAK(A)	B	M / MP
						50.6	23.6	2.12E-02	790.17	3	2367.25	0.26	(R)KFDVNTSAVQVLIHIGNLDR(A)		
						48.1	26.5	2.71E-02	1594.37	2	3186.67	0.07	(R)FQSVPAQPGQTSPLLQYFILLDQGLNK(Y)		
						46.5	41.4	7.77E-02	667.98	2	1333.63	0.32	(K)IYIDSNNNPER(F)		
45	P10909	CLU	Clusterin precursor (Complement-associated protein SP-40,40)	67.2	5	67.2	28.5	4.85E-04	1158.10	2	2313.17	1.02	(R)JVTVASHTSDSDVPSGVTEVVVK(L)	B	WP / MP
46	Q14019	COTL 1	Coactosin-like protein.	50.6	18	49.4	33.2	4.49E-02	467.91	2	933.49	0.33	(K)EVVQNFAK(E)	B	WP / MP
						41.5	40.3	2.73E-01	403.70	2	805.44	-0.04	(R)AAYNLVR(D)		
						30.9	42.9	2.79E+00	497.47	2	992.53	0.40	(K)EFVISDRK(E)		
47	P00488	F13A1	Coagulation factor XIII A chain precursor (EC 2.3.2.13)	278.4	22	90.1	28.7	2.70E-06	973.26	2	1944.05	0.46	(R)GVNLQEFNLVNTSVHLFK(E)	B	WP / M / MP
						84.6	35.0	7.79E-06	1302.04	2	2601.30	0.78	(R)AVPPNNSNAEDDLPTVELQGVVPR(G)		
						68.8	32.8	4.41E-04	729.23	2	1455.75	0.70	(R)HVVYGEILDVQIQR(R)		
						64.8	53.0	1.03E-03	648.92	2	1295.68	0.15	(R)JLALETALmYGAK(K)		
						55.0	32.3	9.61E-03	564.96	3	1690.83	1.06	(K)DGTHVVENV DATHIGK(L)		
						52.9	33.1	1.11E-02	1308.28	2	2613.30	1.25	(K)EREEYVLNDIGVIFYGEVNDIK(T)		
						51.1	29.0	2.38E-02	662.51	2	1322.69	0.32	(R)KLIASmSSDSL(R)(H)		
						50.0	43.6	3.29E-02	664.19	2	1325.82	0.55	(K)STVLTIPEIIK(V)		
						49.1	40.9	3.87E-02	456.00	4	1818.92	1.09	(K)KDGTHVVENV DATHIGK(L)		
						44.4	44.0	1.50E-01	516.10	2	1029.53	0.66	(R)CGPASVQA(K)(H)		
						43.0	31.9	1.55E-01	598.48	2	1194.59	0.37	(K)LIASmSSDSL(R)(H)		
						32.5	34.7	1.89E+00	662.51	2	1322.69	0.32	(R)KLIASmSSDSL(R)(H)		
48	P23528	CFL1	Cofilin, non-muscle isoform (Cofilin-1) (18 kDa phosphoprotein) (p18)	423.9	67	138.9	39.6	3.32E-11	1083.74	2	2165.09	0.38	(K)EILVGDVGTVDPPYATFVK(M)	B	WP / M / MP
						96.9	36.1	6.53E-07	670.95	2	1339.77	0.13	(K)LGGSAVISLEGKPL(-)		
						87.0	35.7	4.83E-06	1167.98	2	2333.23	0.73	(K)ESKKEDLVFIFWAPESAPLK(S)		
						74.0	34.5	1.11E-04	995.75	2	1989.06	0.44	(K)KEDLVFIFWAPESAPLK(S)		
						67.4	43.7	7.07E-04	572.75	2	1143.61	-0.11	(-)SASGVAVSDGV(K)(V)		
						60.2	30.3	2.75E-03	948.32	2	1893.95	0.69	(-)SASGVAVSDGV(K)(V)FNDmK(V)		
						59.8	37.7	3.15E-03	931.73	2	1860.97	0.48	(K)EDLVFIFWAPESAPLK(S)		
						59.5	31.9	3.50E-03	669.59	2	1336.62	0.55	(R)YALYDATYETK(E)		

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						54.0	24.1	7.30E-03	1532.10	2	3061.59	0.80	(K)NIILEEGKEILVGDVGQTVDDPYATFVK(M)		
						31.5	35.4	3.08E+00	915.53	1	914.51	0.02	(K)NIILEEGK(E)		
49	P31146	CORO 1A	Coronin-1A (Coronin-like protein p57) (Coronin-like protein A)	31.6	4	31.6	21.7	1.68E+00	1207.20	2	2412.13	0.27	(R)YFEITSEAPFLHYLSmFSSK(E)	1	WP / MP
50	P21291	CSRP 1	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1)	70.2	13	69.9	32.4	3.42E-04	717.61	2	1432.67	0.55	(K)GFGGQAGALVHSE(-)	B	WP / MP
						36.2	36.7	8.53E-01	564.26	2	1125.51	1.01	(R)CSQAVYAAEK(V)		
						36.1	35.8	8.83E-01	564.26	2	1125.51	1.01	(R)CSQAVYAAEK(V)		
51	Q8TB65	COX5 A	Cytochrome c oxidase subunit Va, (COX5A protein).	52.3	7	52.3	33.5	2.11E-02	589.57	2	1177.62	-0.49	(R)RLNDFASTVR(I)	1	WP
52	P99999	CYCS	Cytochrome c.	71.4	13	71.4	31.8	2.40E-04	714.85	2	1427.67	0.02	(K)TGOAPGYSYTAANK(N)	B	MP
53	Q99497	PARK 7	DJ-1 protein (Oncogene DJ1).	59.3	34	59.3	25.9	2.67E-03	1293.06	2	2583.32	0.79	(K)EGPYDVVLPGGNLGAQNLSESAVK(E)	B	WP / MP
54	Q9UJU6	DBNL	Drebrin-like protein (SH3 domain-containing protein 7) (Drebrin F)	31.0	5	31.0	27.3	2.57E+00	704.47	2	1406.67	0.27	(R)AmSTTSSSQPGK(L)	1	WP
55	O00429	DNM1 L	Dynamin 1-like protein (EC 3.6.5.5) (Dynamin-like protein) (Dnm1p/Vps)	102.4	3	102.4	33.8	1.50E-07	1106.44	2	2210.22	0.65	(R)TLESVDPLGLNTIDILTAIR(N)	2	MP
						35.7	50.0	1.06E+00	551.29	2	1100.58	0.92	(R)\$SQLDINNKK(S)		
56	P63167	DNCL 1	Dynein light chain 1, cytoplasmic (8 kDa dynein light chain) (DLC8)	44.2	12	44.2	38.3	1.18E-01	642.01	2	1281.60	0.41	(R)NFGSYVTHETK(H)	B	MP
57	Q9H4M9	EHD1	EH-domain containing protein 1 (Testlin) (hPAST1).	74.5	8	74.5	28.9	7.03E-05	1466.96	2	2930.48	1.43	(R)FmCAQLPNPVLDSISIIDTPGILSGEK(Q)	B	M / MP
58	Q9NZN3	EHD3	EH-domain containing protein 3.	53.7	9	53.7	25.4	8.62E-03	1443.18	2	2882.51	1.84	(R)FVCAQLPNPVLESISVIDTPGILSGEK(Q)	1	WP / M / MP
59	P14625	TRA1	Endoplasmic precursor (94 kDa glucose-regulated protein) (GRP94)	171.2	9	60.6	32.7	2.57E-03	491.92	2	981.48	0.35	(K)SGTSEFLNK(M)	B	WP / M / MP
						56.2	27.1	6.11E-03	1130.88	2	2259.06	0.69	(R)FQSSHPTDITSLDQYVER(M)		
						55.6	25.8	5.69E-03	1366.83	2	2732.45	-0.80	(R)IJEDEDDKTVLDAVLVFETATLR(S)		
60	P27105	STOM	Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b)	68.2	29	67.8	33.3	4.41E-04	1072.35	2	2142.18	0.51	(K)NSTIVFPLPIDmLQGIIIGAK(H)	B	M / MP / SEN
						49.0	49.9	5.53E-02	458.25	2	914.55	-0.05	(R)LLAQTTLR(N)		
						46.5	46.1	9.79E-02	458.25	2	914.55	-0.05	(R)LLAQTTLR(N)		
						33.8	35.8	1.33E+00	598.66	2	1194.71	0.60	(K)DVKLPLVQLQR(A)		
61	P10768	ESD	Esterase D (EC 3.1.1.1)	40.2	3	40.2	32.7	4.20E-01	509.02	2	1016.53	-0.50	(K)AYDATHLVK(S)	2	WP / MP
62	P63241	EIF5A	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D)	42.9	13	42.9	31.4	1.73E-01	1298.58	1	1297.74	-0.16	(K)VHLVGIDIFTGK(K)	2	WP
63	P47755	CAPZ A2	F-actin capping protein alpha-2 subunit (CapZ alpha-2)	45.9	4	45.9	36.1	1.05E-01	438.96	2	875.47	0.45	(R)TSVETALR(A)	B	WP / MP
64	P47756	CAPZ B	F-actin capping protein beta subunit (CapZ beta).	99.0	10	99.0	39.2	3.93E-07	677.59	2	1352.64	0.53	(K)SGSGTmNLGGSLTR(Q)	B	WP / MP
65	P02671	FGA	Fibrinogen alpha/alpha-E chain precursor [Contains:	233.0	26	92.1	26.5	1.82E-06	944.32	2	1885.87	0.77	(R)HRHPDEAAFFDFASTGK(T)	B	WP / MP
						76.4	40.6	7.38E-05	570.82	2	1139.55	0.08	(R)GSESGIFTNTK(E)		

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			Fibrinopeptide A]			69.7	53.0	3.31E-04	755.70	2	1508.70	0.69	(R)EVDLKDIEDYEQQK(Q)		
						60.5	27.3	2.20E-03	1141.24	2	2280.04	0.44	(K)TFPGFFSPmLGEFVSETESR(G)		
						54.2	51.0	1.46E-02	464.97	2	927.54	0.39	(K)QLEQVIK(D)		
						52.7	30.3	1.45E-02	1021.77	2	2040.90	0.64	(K)QTSSTSYNRGDSFESK(S)		
						52.2	34.3	2.06E-02	729.76	2	1456.77	0.75	(K)mKPVPLVPGNFK(S)		
						48.6	36.8	4.83E-02	1106.52	1	1105.66	-0.14	(K)VQHIQLLQK(N)		
						45.4	56.5	1.18E-01	551.09	2	1099.62	0.56	(K)RLEVDIDIK(I)		
						39.5	41.0	3.78E-01	506.51	3	1516.73	-0.19	(R)mELERPGGNEIR(G)		
						24.1	29.9	9.67E+00	1141.24	2	2280.04	0.44	(K)TFPGFFSPMLGEFVSETESR(G)		
66	P02675	FGB	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].	419.5	44	106.8	28.1	5.07E-08	1185.00	2	2367.16	0.84	(K)AHYGGFTVQNEANKYQISVVK(Y)	B	WP / M / MP
						91.9	33.2	1.68E-06	1064.40	2	2126.08	0.71	(K)HQLYIDETVNSNIPTNLR(V)		
						80.7	35.9	2.52E-05	862.19	2	1722.78	-0.40	(R)mGPTELLIEmEDWK(G)		
						74.1	22.5	6.89E-05	1592.69	2	3182.47	0.91	(R)NSVDELNNVEAVSQSSSFQYmYLLK(D)		
						72.0	26.7	2.02E-04	655.04	2	1307.61	0.47	(K)QGFGNVATNTDGK(N)		
						71.2	44.9	2.33E-04	490.86	2	979.44	0.27	(R)QDGSVDFGR(K)		
						64.8	34.4	7.93E-04	801.41	3	2400.16	1.08	(R)KGGETSEmYLIQPDSSVKPYR(V)		
						60.3	26.5	1.25E-03	1293.05	3	3875.84	0.31	(K)DNENVVNEYSSELEKHQLYIDETVNSNIPTNLR(V)		
						42.0	20.2	2.04E-01	780.84	2	1559.68	0.00	(K)HGTDDGVVWmNWK(G)		
						38.6	45.2	4.28E-01	851.52	1	850.45	0.07	(K)YQISVVK(Y)		
67	P02679	FGG	Fibrinogen gamma chain precursor.	341.4	53	87.8	35.0	4.24E-06	1104.41	2	2206.03	0.79	(K)EGFGHLSPTGTTEFWLGNEK(I)	B	WP / M / MP
						86.4	33.3	7.58E-06	772.99	2	1544.81	-0.84	(R)LTIGEGQQHHLGGAK(Q)		
						75.4	36.5	8.61E-05	842.23	2	1681.95	0.51	(K)IHLISTQSAIPYALR(V)		
						74.8	25.7	6.85E-05	1418.09	2	2833.17	1.00	(R)LTAYFAGGDAGDAFDGDFGDDPSDK(F)		
						58.8	21.6	2.97E-03	632.72	4	2525.25	1.64	(R)KmLEEImKYEASILTHDSSIR(Y)		
						57.6	30.7	5.75E-03	647.64	2	1292.75	0.52	(K)QSGLYFIKPLK(A)		
						52.7	40.3	1.74E-02	746.69	2	1490.74	0.63	(K)YEASILTHDSSIR(Y)		
						46.4	51.9	7.43E-02	504.96	2	1007.53	0.38	(R)LDGSVDFKK(N)		
						45.7	38.1	8.91E-02	504.96	2	1007.53	0.38	(R)LDGSVDFKK(N)		
						44.3	42.3	1.25E-01	518.95	2	1035.53	0.37	(K)RLDGSVDFK(K)		
						43.6	28.8	6.50E-02	1212.48	3	3633.55	1.11	(R)\$DNCCILDERFGSYCPTTCGIADFLSTYQTK(V)		
						39.9	28.1	3.48E-01	575.87	2	1149.50	0.24	(R)TSTADYAmFK(V)		
68	Q86W11	PKHD 1L1	Fibrocystin L.	65.7	1	65.7	26.6	5.93E-04	1342.48	2	2682.38	0.58	(K)DLSQSmTPFTYAVSLTPLTAVSPK(R)	1	
69	P21333	FLNA	Filamin A (Alpha-filamin) (Filamin 1)	1994.4	45	108.2	29.7	4.11E-08	980.21	2	1957.95	0.46	(K)HTAmVSWGGSIPNSPFR(V)	B	WP / M
						105.5	36.4	6.65E-08	1272.93	2	2543.25	0.60	(K)GLVEPVDVVDNADGTQTQVNYVPSR(E)		
						99.8	30.8	3.17E-07	882.66	2	1762.85	0.46	(R)VANPSGNLTETYVQDR(G)		
						94.8	24.8	6.76E-07	1447.55	2	2892.54	0.56	(K)VGSAADIPINISSETDLSLLTATVPPSGR(E)		
						93.8	25.1	1.03E-06	1171.95	2	2341.22	0.67	(K)ASGPGLNTTGPASLPVEFTIDAK(D)		
						91.6	47.6	2.42E-06	708.64	2	1414.74	0.54	(R)IANLQTDLSDDLRL(L)		



91.5	68.1	2.32E-06	613.85	2	1225.76	-0.06	(R)LIALLEVLSQK(K)
91.0	32.8	2.07E-06	1100.90	2	2199.12	0.67	(R)LVSNHSLHETSSVFVDSLTK(A)
86.7	36.7	6.27E-06	908.26	2	1813.95	0.57	(K)VAQPTITDNKDGTVTVR(Y)
85.2	36.4	8.31E-06	969.76	2	1937.01	0.51	(K)DAGEGLLAVQITDEGKPK(K)
83.6	29.6	1.49E-05	751.99	2	1501.79	0.18	(K)VNQPASFVSLNGAK(G)
83.4	29.6	1.14E-05	1156.85	2	2311.15	0.55	(R)GAGSYTImVLFADQATPTSPIR(V)
83.2	27.8	1.12E-05	1225.02	2	2447.24	0.79	(K)NGQHVASSPIPVVISQSEIGDASR(V)
80.7	37.0	2.92E-05	722.15	2	1441.69	0.61	(R)AGQSAAGAAPGGGVDR(D)
80.5	35.4	2.69E-05	879.07	2	1755.83	0.31	(K)SPFEVYVDKSGDASK(V)
77.5	19.6	4.49E-05	1157.42	2	2312.09	0.75	(R)SAGQGEVLVYVEDPAGHQEEAK(V)
76.9	24.6	3.99E-05	1473.74	2	2944.48	1.00	(R)FGGEHVPNSPFQVTALAGDQPSVQPPLR(S)
76.3	35.7	5.57E-05	1252.07	2	2501.28	0.85	(R)EAGAGGLAIEGSPKAEISFDRK(D)
76.0	32.9	8.54E-05	715.70	2	1428.71	0.69	(K)AFGPGLQGGSGAGSPAR(F)
75.8	46.4	8.46E-05	690.59	2	1378.67	0.50	(K)YGGPYHIGGSPFK(A)
73.1	32.8	1.57E-04	613.39	2	1224.56	0.22	(R)EATTEFSVDAR(A)
71.5	31.1	2.27E-04	683.09	2	1363.70	0.47	(K)VDVGKDQEFTVK(S)
71.1	45.0	2.38E-04	850.33	2	1697.91	0.74	(R)TGVELGKPTHFTVNAK(A)
70.5	22.2	2.26E-04	1143.93	2	2285.17	0.68	(K)YTPVQQGPVGVNVTYGGDPIPK(S)
70.2	31.3	3.17E-04	718.14	2	1433.72	0.55	(R)ANLPQSFOVDTSK(A)
69.1	31.9	4.01E-04	1570.71	1	1569.80	-0.09	(R)GAGTGGGLLAVEGPPSEAK(M)
67.0	28.0	6.19E-04	827.25	2	1651.85	0.65	(K)VTAQGGPLEPSGNIANK(T)
66.9	32.8	6.73E-04	647.13	2	1291.71	0.55	(K)GKLDVQFSGLT(K)
66.0	34.9	8.28E-04	613.95	2	1225.65	0.24	(R)AWGPGLEGGVVGK(S)
65.6	30.6	8.90E-04	824.15	2	1645.87	0.42	(K)TGVAVNKPAEFTVDAK(H)
65.2	23.6	7.06E-04	1221.03	2	2439.18	0.88	(R)VSGQGLHEGHTFEPAEFIIDTR(D)
64.0	32.1	1.32E-03	760.01	2	1517.75	0.27	(R)FVPAEmGHTVSVK(Y)
63.8	23.9	9.77E-04	1234.56	2	2466.18	0.94	(K)FNEEHIPDSPFVVPVASPSGDAR(R)
63.3	36.2	1.52E-03	1533.73	1	1532.81	-0.08	(K)SPFSVAVSPSLDSL(I)
63.3	39.8	1.58E-03	758.74	2	1514.75	0.73	(K)FADQHVPGSPFSVK(V)
60.1	42.6	3.08E-03	802.29	2	1601.76	0.81	(K)YNEQHVPGPSFTAR(V)
60.0	31.4	3.23E-03	677.71	2	1353.86	-0.45	(R)LIALLEVLSQKK(M)
55.7	34.5	8.68E-03	642.60	2	1282.74	0.45	(K)VTVLFAGQHIAK(S)
54.5	29.8	1.21E-02	646.01	2	1289.64	0.37	(K)YGGQPVNPFPSK(L)
54.1	34.3	1.38E-02	651.47	2	1300.66	0.27	(K)FNGTHIPGSPFK(I)
53.7	25.9	9.50E-03	1294.12	2	2586.25	-0.02	(K)KTHIQDNHDGTYTVAYVPDVTGR(Y)
52.6	54.2	1.90E-02	700.94	2	1399.64	0.24	(K)YGGDEIPFSPYR(V)
52.5	37.6	1.76E-02	484.40	3	1449.75	0.46	(K)AGNNmLLVGVHGPRT(T)
51.7	31.0	1.71E-02	1120.07	2	2237.27	0.86	(R)LLGWIQNKLPQLPITNFSR(D)

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						50.6	39.2	3.01E-02	700.94	2	1399.64	0.24	(K)YGGDEIPFSPYR(V)		
						50.0	37.5	3.24E-02	542.54	2	1082.53	0.54	(K)SPFEVYVDK(S)		
						49.3	38.0	4.18E-02	643.60	2	1284.72	0.47	(K)LPQLPITNFSR(D)		
						48.6	37.4	4.51E-02	576.48	2	1150.62	0.34	(K)DKGEYTLVVK(W)		
						48.3	37.9	4.76E-02	713.16	2	1423.68	0.64	(R)DAPQDFHPDRVK(A)		
						48.2	27.3	4.60E-02	879.21	2	1755.91	0.51	(R)VTYTPmAPGSYLISIK(Y)		
						47.2	35.1	5.30E-02	441.73	2	881.53	-0.07	(K)AGVAPLQVK(V)		
						46.8	29.0	6.71E-02	803.05	2	1603.73	0.36	(R)YAPSEAGLHEmDIR(Y)		
						45.7	39.2	1.01E-01	550.48	2	1098.57	0.38	(K)GTVEPQLEAR(G)		
						44.8	26.5	8.23E-02	1175.00	2	2348.20	-0.20	(R)QMQLENVSVALEFLDRESIK(L)		
						43.3	37.9	1.86E-01	543.79	2	1085.57	0.01	(K)VAQPTITDNK(D)		
						42.1	27.6	1.93E-01	527.28	2	1052.48	0.07	(R)NDNDTFTVK(Y)		
						41.2	43.3	2.51E-01	533.43	2	1064.53	0.33	(R)LSPFmADIR(D)		
						40.6	29.9	2.15E-01	1175.00	2	2348.20	-0.20	(R)QmQLENVSVALEFLDRESIK(L)		
						40.1	30.6	2.68E-01	679.41	3	2034.06	1.17	(K)VSGLGEKVDVGKDQFTVK(S)		
						38.1	29.4	4.68E-01	896.25	2	1788.82	1.68	(K)ATCAPQHGAPGPGPADASK(V)		
						35.2	21.5	4.70E-01	1173.23	3	3516.88	-0.18	(K)VLPTHDASKVKASGPLNTTGVPASLPVEFTIDAK(D)		
						33.9	38.2	1.33E+00	599.25	2	1196.52	-0.02	(R)DAPQDFHPDR(V)		
						31.8	27.8	1.99E+00	584.54	3	1749.87	0.76	(R)TFSWVYVPEVTGTHK(V)		
						31.2	32.7	3.39E+00	415.31	2	828.47	0.15	(K)AIVDGNLK(L)		
						30.2	28.6	3.09E+00	1154.68	1	1153.62	0.06	(R)NGHVGISFVPK(E)		
70	Q14315	FLNC	Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc)	56.3	2	56.3	34.4	7.46E-03	793.08	2	1583.82	0.33	(R)GAGTGLGLAIEGPSEAK(M)	B	MP
71	P04075	ALDO A	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)	84.3	12	64.5	22.2	9.12E-04	1114.56	2	2227.02	0.09	(K)YTPSGQAGAAASESLFVSNHAY(-)	B	WP / M / MP
						46.2	38.2	9.08E-02	486.47	2	970.58	0.36	(K)GGVVGKVDK(G)		
						43.0	31.2	8.45E-02	1114.73	3	3340.58	-0.08	(R)ALANSLACQGYTPSGQAGAAASESLFVSNHAY(-)		
72	Q96A87	G6B	G6b protein precursor (Chromosome 6 open reading frame 25)	36.4	4	36.4	33.9	6.97E-01	505.29	2	1008.57	0.11	(R)TVLHVLGDR(T)	1	M / SEN
73	P06396	GSN	Gelsolin precursor (Actin-depolymerizing factor) (ADF)	587.5	35	89.1	39.7	3.80E-06	833.52	2	1664.77	0.27	(K)DSQEEKTEALTSK(R)	1	WP / M / MP
						89.1	23.9	3.15E-06	1136.80	2	2271.08	0.52	(R)AQPVQVAEGSEPDGFWEALGGK(A)		
						87.1	32.4	6.70E-06	660.50	2	1318.69	0.30	(K)AGALNSNDAFLK(T)		
						80.3	23.7	2.20E-05	1241.00	2	2478.21	1.78	(K)VSNGAGTmSVSLVADENPFQAQALK(S)		
						75.5	25.2	6.02E-05	1386.59	2	2770.33	0.84	(K)VPVPATYQGFGGDSYIILYNRY(H)		
						72.3	23.1	1.28E-04	1354.23	2	2705.37	1.08	(K)TPSAAYLWVG TGASEAEKTAQELLR(V)		
						66.8	28.1	7.44E-04	638.59	2	1274.71	0.46	(K)HVPVNEVVQR(L)		
						63.0	60.8	2.35E-03	444.82	2	886.49	1.14	(K)TGAQELLR(V)		
						62.8	21.4	1.16E-03	1353.52	2	2703.38	1.66	(K)FDLVPVPTNLYGDDFTGDAYVILK(T)		
						62.4	33.0	1.65E-03	1838.08	1	1836.89	0.19	(K)TPSAAYLWVG TGASEAEK(T)		

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						53.1	32.9	1.52E-02	608.16	3	1820.88	-0.04	(K)DSQEEKEALTSKR(Y)		
						52.5	35.5	1.98E-02	539.61	2	1077.51	-0.30	(R)YIETDPANR(D)		
						51.3	25.2	1.21E-02	1700.93	2	3398.65	1.20	(R)IEGSNKVPDPATYGGFYGGDSYIILYNYR(H)		
						50.0	21.5	1.91E-02	1531.26	2	3059.59	0.92	(R)VEKFDLVPVPTNLYGDFFTGDAYVILK(T)		
						46.7	36.8	6.05E-02	441.89	2	881.45	0.32	(K)TASDFITK(M)		
						41.3	32.0	2.39E-01	549.24	2	1096.59	-0.11	(M)VVEHPEFLK(A)		
74	P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD)	45.3	4	45.3	37.6	8.93E-02	593.34	3	1777.86	-0.84	(R)LNSHmNALHLSQANR(L)	1	WP / MP
75	P06744	GPI	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)	48.4	3	48.4	29.2	5.26E-02	1218.60	1	1217.64	-0.04	(K)HFVALSTNTTK(V)	B	MP
76	P07203	GPX1	Glutathione peroxidase 1 (EC 1.11.1.9) (GSHPx-1)	37.6	13	37.6	34.3	5.98E-01	657.51	2	1312.57	0.45	(R)DYTQmNELQR(R)	2	MP
77	P09211	GSTP1	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1).	227.6	34	92.2	34.6	1.75E-06	942.75	2	1882.94	0.56	(K)FQDGLTLYQSNTILR(H)	B	WP / M / MP
						78.1	25.0	4.08E-05	1063.90	2	2125.15	0.65	(K)ALPGQLKPFETLLSQNGGK(T)		
						69.7	23.5	2.84E-04	1078.50	2	2154.05	0.95	(K)YISLIYNTYEAGKDDYVK(A)		
						67.2	31.1	5.83E-04	669.62	2	1336.72	0.51	(-)PPYTVVYFPVR(G)		
78	P78417	GSTO1	Glutathione transferase omega 1 (EC 2.5.1.18) (GSTO 1-1).	95.1	24	64.5	27.1	9.39E-04	1026.95	2	2051.15	0.74	(K)mILELFSKVPSLVGSFIR(S)	B	WP
						50.9	34.5	2.67E-02	540.45	2	1078.61	0.29	(R)HEVININLK(N)		
						44.6	41.5	1.41E-01	538.00	2	1073.62	0.38	(K)VPSLVGSFIR(S)		
						43.7	32.7	1.42E-01	661.06	2	1319.68	0.44	(K)GSAPPGVPPEGSIR(I)		
79	P04406	GAPD	Glyceraldehyde-3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)	152.3	31	112.7	115.6	1.32E-08	1147.29	2	2292.03	0.54	(K)WGDAGAEYVVESTGVFTTmEK(A)	B	WP / M / MP
						77.3	79.2	4.14E-05	871.46	3	2610.35	1.04	(K)VIHDFNGIVEGLMTTVHAITATQK(T)		
						74.4	81.3	7.83E-05	871.46	3	2610.35	1.04	(K)VIHDFNGIVEGLmTTVHAITATQK(T)		
						73.7	64.3	9.25E-05	871.46	3	2610.35	1.04	(K)VIHDFNGIVEGLmTTVHAITATQK(T)		
						65.2	35.5	9.63E-04	1411.68	1	1410.78	-0.10	(R)GALQNIIPASTGAAG(A)		
						49.6	59.9	4.61E-02	403.27	2	804.42	0.12	(K)JGVNGFGR(I)		
						46.1	45.6	1.02E-01	403.27	2	804.42	0.12	(K)JGVNGFGR(I)		
80	Q9NR31	SARA1	GTP-binding protein SAR1a (COPII-associated small GTPase).	116.9	28	94.8	28.0	7.63E-07	1257.40	2	2512.35	0.44	(K)VELNALmTDEISNPILGNK(I)	B	WP / MP
						44.0	34.1	1.52E-01	1146.71	1	1145.64	0.07	(K)LVFLGLDNAGK(T)		
						38.8	26.7	4.50E-01	1313.63	1	1312.67	-0.04	(R)EIFGLYQTTGK(G)		
81	P11142	HSPA8	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8).	211.5	25	95.3	81.8	8.61E-07	919.64	2	1837.01	0.26	(K)LDKSIHDIIVLGGSTR(I)	B	WP / M / MP
						91.3	95.4	2.25E-06	894.96	2	1786.98	0.94	(R)IINEPTAAAIAYGLDKK(V)		
						74.8	47.7	1.00E-04	596.87	3	1786.98	0.64	(R)IINEPTAAAIAYGLDKK(V)		
						61.4	27.6	2.24E-03	846.69	2	1690.72	0.65	(K)STAGDTHLGGEDFDNR(M)		
						60.1	56.4	3.13E-03	634.74	2	1267.65	-0.18	(K)mKEIAEAYLGK(T)		
						58.2	33.5	4.63E-03	741.10	2	1479.75	0.44	(R)ARFEELNADLFR(G)		
						52.4	42.9	2.15E-02	615.14	2	1227.62	0.66	(K)VEIANDQGNR(T)		
						43.7	41.3	1.31E-01	626.55	2	1250.61	0.49	(R)mVNHFIAEFK(R)		

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						38.3	23.3	3.00E-01	1387.93	2	2773.32	0.53	(K)QTQTFTTYSNQPGVLQVYEGER(A)		
82	P04792	HSPB1	Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein)	83.1	18	65.1	43.0	1.21E-03	538.56	2	1074.57	0.54	(R)QLSSGVSEIR(H)	B	WP / M / MP
						61.4	43.1	2.53E-03	582.65	2	1162.61	0.69	(R)LFDAQFGLPR(L)		
83	P69905	HBA1	Hemoglobin alpha chain.	78.6	25	65.2	58.7	1.00E-03	765.57	2	1528.73	0.40	(K)VGAHAGEYGAELER(M)	B	MP
						29.9	24.5	3.16E+00	612.18	3	1832.88	0.66	(K)TYFPHFDLSHGSAQVK(G)		
84	P68871	HBB	Hemoglobin beta chain.	68.3	25	56.8	26.5	6.68E-03	725.62	2	1448.79	0.44	(K)VVAGVANALAHKYH(-)	1	MP
						51.0	39.5	2.76E-02	658.09	2	1313.66	0.51	(K)VNVDEVGGEALGR(L)		
85	P19367	HK1	Hexokinase, type I (EC 2.7.1.1) (HK I) (Brain form hexokinase).	75.8	3	75.8	29.7	6.28E-05	1210.00	2	2417.22	0.77	(-)\$mIAAQLLAYFTLEKDDQVK(K)	B	M / MP
86	Q9P005	HSPC176	HSPC159.	56.5	19	56.5	42.8	9.26E-03	501.43	2	1000.56	0.29	(K)INGDLQITK(L)	2	MP
						48.2	55.4	5.66E-02	602.12	2	1201.69	0.55	(R)IQTLSAIDTIK(I)		
87	P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT)	59.8	5	59.8	56.9	3.88E-03	622.87	2	1243.65	0.08	(K)FFADLLDYIK(A)	2	WP / MP
88	P23229	ITGA6	Integrin alpha-6 precursor (VLA-6) (CD49f)	48.6	2	48.6	39.0	5.81E-02	478.31	2	954.52	0.10	(R)LPNAGTQVR(V)	B	M / WP / MP / SEN
89	P08514	ITGA2B	Integrin alpha-IIb precursor (Platelet membrane glycoprotein IIb)	532.8	28	146.7	40.6	5.67E-12	1077.98	2	2153.22	0.73	(R)RVLLGSQQAGTTLNLDLGGK(H)	B	WP / M / MP / SEN
						97.3	35.6	6.07E-07	752.19	2	1501.83	0.54	(R)GQVLVFLGQSEGLR(S)		
						86.1	37.2	5.09E-06	1413.48	2	2824.37	0.58	(R)GAVDIDDNGYPDILVGAYGANQVAVYR(A)		
						80.8	28.4	2.28E-05	1011.84	2	2021.11	0.56	(R)GPHALGAPSLLTGTQLYGR(F)		
						66.7	31.7	5.21E-04	1177.52	2	2352.19	0.84	(R)SRPSQVLDSPPFTGSAFGSLR(G)		
						63.1	38.7	1.76E-03	518.44	2	1034.59	0.29	(R)VYLFLQPR(G)		
						61.6	42.0	2.41E-03	651.03	2	1299.69	0.37	(R)GEAQVWTQLLR(A)		
						59.6	29.9	1.99E-03	1547.11	2	3091.50	0.71	(R)FGSAIAPLDLDRDGYNDIAVAAPYGGPSGR(G)		
						56.8	35.1	6.84E-03	809.10	2	1615.80	0.40	(R)HDLVLGAPLYmESR(A)		
						56.0	50.9	1.11E-02	458.41	2	914.48	0.34	(R)AEAQVELR(G)		
						55.5	29.3	9.24E-03	765.04	2	1527.63	0.45	(R)NRPPLEEDDEEGE(-)		
						53.3	30.9	1.55E-02	611.89	2	1221.64	0.13	(R)NVGSQTLQTFK(A)		
						52.1	35.7	2.17E-02	561.48	2	1120.55	0.41	(R)ALSNVEGFER(L)		
						43.7	28.2	1.21E-01	960.86	2	1919.12	0.59	(K)IVLLDVPVRAEAQVELR(G)		
						36.6	43.1	7.61E-01	1331.70	1	1330.69	0.01	(R)FGSAIAPLDLDR(D)		
28.2	20.9	2.89E+00	1488.19	2	2973.41	0.96	(R)GNSFPASLVAAEEGEREQNSLDSWGPK(V)								
90	P05556	ITGB1	Integrin beta-1 precursor (Fibronectin receptor beta subunit)	79.5	3	79.5	32.1	2.69E-05	1236.05	2	2469.24	0.86	(K)LSENNIQTIFAVTEEFQPVYK(E)	1	M / MP / SEN
91	P05106	ITGB3	Integrin beta-3 precursor (Platelet membrane glycoprotein IIIa)	164.7	12	84.6	39.1	1.11E-05	766.55	2	1530.77	0.32	(R)NDASHLLVFTTDAK(T)	B	M / MP / SEN
						55.2	28.1	1.02E-02	702.60	2	1402.67	0.53	(K)EATSTFTNITYR(G)		
						55.0	32.4	9.83E-03	642.11	2	1281.70	0.52	(K)HVLTLTDQVTR(F)		
						50.2	20.8	2.09E-02	1343.55	2	2684.34	0.75	(R)VLEDRLPSDKSGSDSQVTQVSPQR(I)		

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						44.7	43.7	1.08E-01	1223.53	1	1222.51	0.02	(R)FQYYEDSSGK(S)		
92	Q13418	ILK	Integrin-linked protein kinase 1 (EC 2.7.1.37) (ILK-1)	99.3	17	66.6	36.2	6.89E-04	792.69	2	1582.76	0.61	(R)GDDTPLHLAASHGHR(D)	B	WP / M / MP
						56.2	31.0	8.00E-03	650.13	2	1298.55	-0.30	(R)SVmIDeDmTAR(I)		
						46.6	39.1	7.27E-02	664.13	2	1325.64	0.61	(K)LNENHSGELWK(G)		
93	P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial precursor	34.4	11	34.4	31.9	1.10E+00	570.41	3	1707.78	0.46	(K)VAKPVVEmDGDEmTR(I)	B	M / WP / MP
94	Q13584	kr-znf3	Isocitrate dehydrogenase.	98.6	9	79.8	39.8	3.43E-05	678.59	2	1354.68	0.50	(K)TIEAAAHGTVTR(H)	B	
						73.6	54.8	1.27E-04	938.31	2	1873.98	0.63	(K)GRPTSTNPISAFWTR(G)		
95	Q9Y624	F11R	Junctional adhesion molecule A precursor (JAM-A)	34.8	9	34.8	28.3	1.10E+00	692.34	2	1382.62	0.06	(R)NGYGTmTNAVR(M)	2	M / MP / SEN
96	Q14766	LTBP1	Latent transforming growth factor beta binding protein, isoform 1L	64.3	1	64.3	28.7	1.18E-03	528.95	3	1583.82	0.04	(K)HPPEASVQIHQVSR(I)	1	MP
97	P30740	SERPINB1	Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor)	36.6	3	36.6	29.5	8.28E-01	503.80	2	1005.49	0.10	(K)EATTNAPFR(L)	1	WP / MP
98	P50851	LRBA	Lipopolysaccharide-responsive and beige-like anchor protein	38.2	1	38.2	31.7	4.84E-01	720.78	2	1439.74	-0.18	(R)EIFVDFAPFLSR(T)	B	
99	P00338	LDHA	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A)	153.0	27	69.2	38.2	3.91E-04	788.33	2	1573.91	0.74	(-)S\$ATLKDQLIYNLLK(E)	B	WP / MP
						68.9	37.8	3.98E-04	748.66	2	1494.77	0.54	(K)IVSGKDYNVTANSK(L)		
						63.6	29.2	1.00E-03	1265.59	2	2528.35	0.82	(-)S\$ATLKDQLIYNLLKEEQTPQNK(I)		
						53.4	44.5	1.55E-02	457.46	2	912.58	0.33	(K)LVIITAGAR(Q)		
						52.1	42.8	2.25E-02	567.90	2	1133.56	0.23	(K)VTLTSEEAR(L)		
100	P07195	LDHB	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B)	198.1	36	103.0	38.4	1.47E-07	936.29	2	1870.03	0.54	(K)SLADELALVDVLEDKLG(G)	B	WP / MP
						77.1	29.9	6.04E-05	756.22	2	1509.77	0.66	(K)IVADKDYVTANSK(I)		
						55.5	44.6	1.09E-02	580.10	2	1157.63	0.56	(K)LKDDEVAQLK(K)		
						53.8	42.4	1.35E-02	1283.61	1	1282.65	-0.04	(K)mVVESAYEVIK(L)		
						52.1	46.7	2.08E-02	457.45	2	912.58	0.31	(K)IVVVTAGVR(Q)		
						48.6	41.8	4.94E-02	429.80	3	1285.72	0.68	(K)LKDDEVAQLKK(S)		
						37.5	24.0	2.47E-01	1273.12	3	3814.94	1.43	(K)SLADELALVDVLEDKLGEmmDLQHGSLFLQTPK(I)		
101	P14174	MIF	Macrophage migration inhibitory factor (MIF)	65.0	9	65.0	33.2	1.14E-03	652.34	2	1302.68	-0.47	(-)PmFIVNTNVPR(A)	2	
102	P40926	MDH2	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37).	51.7	14	47.7	35.8	5.22E-02	896.95	2	1792.08	-0.18	(K)JAVLGGASGGIGPLSLLLK(N)	2	MP
						38.4	34.4	5.49E-01	574.54	2	1146.65	0.43	(R)JNVNPVIGGHAG(T)		
						35.8	48.1	1.12E+00	537.37	2	1072.58	0.15	(R)IQEAGTEVVK(A)		
						23.1	35.2	1.56E+01	706.99	2	1411.77	0.83	(K)\$TIIPISQCTPK(V)		
103	P26038	MSN	Moesin (Membrane-organizing extension spike protein).	194.9	22	129.7	34.3	2.67E-10	1141.47	2	2280.13	0.80	(R)AKFYPEDVSEELIQDITQR(L)	B	WP / M / MP
						58.4	42.8	5.81E-03	481.37	2	960.56	0.18	(R)KESPLLFK(F)		
						58.4	36.4	4.92E-03	709.70	2	1416.77	0.63	(K)SGYLAGDKLLPQR(V)		

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						50.8	36.6	3.22E-02	553.01	2	1103.58	0.43	(K)IGFPWSEIR(N)		
						47.1	45.5	5.38E-02	651.59	3	1950.99	0.79	(R)VLEQHKLNKDQWEER(I)		
						42.3	57.5	2.72E-01	887.49	1	886.49	0.00	(K)EALLQASR(D)		
						37.2	25.4	3.87E-01	1434.55	2	2865.41	1.69	(K)EGILNDDIYCPPETAVLLASAVQSK(Y)		
104	Q99685	MGLL	Monoglyceride lipase (EC 3.1.1.23) (HU-K5) (Lysophospholipase homolog)	53.3	7	53.3	31.3	1.22E-02	1103.80	2	2205.27	0.33	(K)VNLNLPNLSLGPIDSSVLSR(N)	2	WP / MP
105	Q13201	MMRN 1	Multimerin 1 precursor (Endothelial cell multimerin 1) (EMILIN-4)	105.9	8	64.0	32.2	1.04E-03	1071.94	2	2141.18	0.70	(K)FVLVQENRPTLTDIVELR(N)	B	WP / M / MP
						53.0	42.5	1.69E-02	646.72	2	1290.73	0.70	(K)HSLPDIQLLQK(G)		
						47.0	28.0	6.21E-02	545.93	3	1633.78	1.02	(K)QTHLEGALEQHSR(S)		
						39.3	27.0	3.00E-01	577.32	4	2304.12	1.17	(R)AQEQQLIHTNQAESHTAVGR(G)		
106	P35579	MYH9	Myosin heavy chain, nonmuscle type A	1074.8	32	115.7	51.9	7.75E-09	973.80	2	1945.00	0.59	(K)LQVELDNVTGLLSQSDSK(S)	B	M / MP
						110.5	43.8	2.55E-08	935.26	2	1867.91	0.60	(R)IAEFTTNLTETEEKSK(S)		
						108.8	108.4	3.70E-08	975.83	2	1948.99	0.66	(R)LQQLDLDLVDLDHQR(Q)		
						91.6	76.8	1.70E-06	1193.10	2	2384.23	-0.04	(R)INFVDVNGYIVGANIETYLEK(S)		
						89.0	44.5	3.34E-06	999.01	2	1995.03	0.98	(R)TFHIFYLLSGAGEHLK(T)		
						87.5	34.0	4.85E-06	1017.93	2	2033.05	0.80	(R)IIGLDQVAGmSETALPGAFAK(T)		
						87.1	29.7	4.45E-06	1247.46	2	2492.17	0.74	(K)DFSALSQLQDTQELLQEENR(Q)		
						82.9	38.8	1.38E-05	666.47	3	1995.00	1.42	(K)HSQAVEELAEQLEQTKR(V)		
						82.4	43.1	1.76E-05	864.18	2	1725.94	0.42	(R)QLLQANPILEAFGNAK(T)		
						81.2	44.7	2.06E-05	999.96	2	1997.05	0.87	(K)KANLQIDQINTDLNLR(S)		
						77.8	84.4	3.16E-05	1509.72	2	3016.47	0.97	(R)DLGEELEALKTEEDTLDSTAAQQLR(S)		
						77.5	32.6	5.74E-05	808.38	2	1613.99	0.76	(R)VISGVLQGNIVFKK(E)		
						77.4	44.8	4.57E-05	736.75	3	2206.13	1.12	(K)TRLQQELDLDLVDLDHQR(Q)		
						76.2	35.8	8.14E-05	744.07	2	1485.89	0.25	(R)VISGVLQGNIVFK(K)		
						74.7	35.9	1.12E-04	786.76	2	1570.85	0.66	(K)VSHLLGINVDFTR(G)		
						69.0	40.3	4.14E-04	607.05	2	1211.58	0.51	(K)DLEAHIDSANK(N)		
						68.0	61.2	4.24E-04	1045.29	2	2087.97	0.61	(R)QAAQERDELADEIANSSGK(G)		
						67.2	53.8	6.63E-04	666.53	2	1330.60	0.45	(R)QLEEAEEEAQR(A)		
						65.5	32.6	8.17E-04	615.33	3	1841.93	1.07	(K)LKNKHEAmITDLEER(L)		
						63.5	41.7	1.45E-03	788.27	2	1573.89	0.65	(K)AGKLDPHLVLDQLR(C)		
						62.2	47.5	2.08E-03	578.57	2	1154.66	0.47	(R)RGDLPFVVP(R)		
						62.1	28.1	2.03E-03	721.53	2	1440.74	0.31	(K)QIATLHAQVADmK(K)		
						62.1	31.7	2.05E-03	597.46	2	1192.61	0.30	(K)ALELDSNLYR(I)		
						58.1	61.0	5.75E-03	608.61	2	1214.66	0.56	(R)ASREEILAQAQ(E)		
						57.0	41.9	8.78E-03	452.35	2	902.51	0.18	(K)ASITALEAK(I)		
						56.7	22.2	4.10E-03	1509.72	2	3016.47	0.97	(R)DLGEELEALKTEEDTLDSTAAQQLR(S)		
						56.2	48.3	8.59E-03	611.06	2	1219.64	0.48	(K)KFDQLLAEEK(T)		

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						54.5	40.3	1.18E-02	689.64	2	1376.77	0.50	(R)TVGQLYKEQLAK(L)		
						53.9	27.6	1.33E-02	739.73	2	1477.79	-0.33	(K)VIQYLAYVASSHK(S)		
						53.8	23.4	7.21E-03	1070.59	3	3207.60	1.18	(M)\$AQQAADKYLVDKNFINNPLAQADWAAK(K)		
						49.7	31.9	3.39E-02	598.07	2	1193.67	0.46	(K)YKASITALEAK(I)		
						48.6	30.5	4.29E-02	859.06	2	1715.72	0.40	(R)TEmEDLmSSKDDVGK(S)		
						48.5	33.1	4.49E-02	534.87	3	1600.75	0.87	(K)NKHEAmITDLEER(L)		
						47.8	21.2	3.93E-02	1242.58	2	2482.20	0.95	(K)JLQQLFNHTmFILEQEEYQR(E)		
						47.4	39.7	7.56E-02	551.08	2	1099.62	0.54	(R)EQEVNLIK(K)(T)		
						46.7	45.7	1.02E-01	415.75	2	829.45	0.05	(K)GALALEEK(R)		
						46.0	37.0	7.65E-02	865.83	2	1728.86	0.80	(K)QTLENERGELANEVK(V)		
						44.4	27.4	1.14E-01	536.52	3	1605.89	0.68	(K)KVIQYLAYVASSHK(S)		
						42.4	39.7	1.90E-01	780.10	2	1557.85	0.35	(R)QRYEILTPNSIPK(G)		
						41.6	26.6	1.86E-01	687.15	3	2057.97	0.49	(K)TLEEEAKTHEAQIQEmR(Q)		
						40.8	40.4	2.58E-01	514.51	3	1539.90	0.64	(R)KKVEAQLQELQVK(F)		
						40.6	41.5	3.52E-01	536.30	2	1070.61	-0.01	(K)KLWVVP SDK(S)		
						39.2	44.3	3.49E-01	462.90	2	923.49	0.30	(R)VVFQEFR(Q)		
						36.9	33.5	5.91E-01	644.48	3	1929.90	0.54	(R)HEmPPHIAITDTAYR(S)		
						33.1	42.8	1.46E+00	520.52	2	1038.65	0.39	(K)VKPLLQVSR(Q)		
107	P60660	MYL6	Myosin light polypeptide 6 (Myosin light chain alkali 3)	268.6	71	104.4	32.8	1.10E-07	894.15	2	1785.82	0.47	(K)NKDQGT YEDVVEGLR(V)	B	WP / M / MP
						75.5	32.3	8.29E-05	870.12	2	1737.84	0.39	(R)VFDKEGNGTVmGAEIR(H)		
						63.5	35.2	1.43E-03	678.13	2	1353.73	0.52	(R)ALGQNPTNAEVLK(V)		
						61.7	35.4	2.04E-03	498.44	2	994.58	0.30	(R)HVLVTLGEK(M)		
						58.0	29.4	4.57E-03	952.77	2	1902.99	0.55	(K)VLD FEHFLPmLQTVAK(N)		
						50.1	32.9	3.19E-02	742.69	2	1482.71	0.66	(K)EAFQLFDR TGDGK(I)		
						48.4	42.7	4.48E-02	513.37	2	1024.50	0.23	(K)EAFQLFDR(T)		
108	P19105	MLCB	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC).	183.1	53	43.3	28.5	1.62E-01	625.30	2	1248.58	0.01	(K)EGNGTVmGAEIR(H)	B	WP / M / MP
						97.0	32.6	5.30E-07	1054.33	2	2105.97	0.69	(R)ATSNVFAmFDQSQIQEFK(E)		
						75.2	39.1	8.53E-05	1010.94	2	2018.96	0.92	(R)DGFIDKEDLHDmLASLGK(N)		
						71.6	58.2	2.49E-04	630.92	2	1259.59	0.25	(K)GNFNIEFTR(I)		
						57.5	37.9	6.38E-03	615.05	2	1227.61	0.48	(K)LNGTDPEDVIR(N)		
						53.8	37.0	1.30E-02	627.53	2	1252.55	0.51	(K)EAFNmIDQNR(D)		
						33.4	35.2	1.46E+00	526.46	2	1050.50	0.42	(R)ELLTmGDR(F)		
109	P24844	MYL9	Myosin regulatory light chain 2, smooth muscle isoform (Myosin RLC)	57.6	46	32.8	32.6	1.66E+00	526.46	2	1050.50	0.42	(R)ELLTmGDR(F)	B	WP / MP
						57.6	33.6	6.34E-03	623.78	2	1245.58	-0.03	(K)GNFNIEFTR(I)		
110	P58546	MTPN	Myotrophin (V-1 protein).	164.2	28	33.4	35.2	1.46E+00	526.46	2	1050.50	0.42	(R)ELLTmGDR(F)	B	WP / MP
						87.1	31.6	5.98E-06	874.63	2	1746.84	0.42	(K)GPDGLTA FEATDNQAIK(A)		
						76.3	28.1	6.29E-05	1038.86	2	2075.05	0.67	(K)TVKGP DGLTA FEATDNQAIK(A)		
						60.3	31.4	2.97E-03	733.53	2	1464.71	0.34	(K)NGDLDEVKDYVAK(G)		

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111	P34059	GALN S	N-acetylglactosamine-6-sulfatase precursor (EC 3.1.6.4)	40.2	2	40.2	37.8	4.11E-01	400.82	2	799.46	-0.17	(M)SAAVVAATR(W)	2	
112	P07514	CYB5 R3	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (Diaphorase 1).	59.8	10	58.7	26.6	3.14E-03	1258.24	2	2514.37	0.11	(R)FALPSPEHILGLPVGHILYSAR(I)	B	M / MP
						36.4	35.2	7.27E-01	748.88	2	1494.84	0.92	(K)DILLRPELEELR(N)		
113	P15531	NME1	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A)	46.1	22	45.9	30.4	7.60E-02	901.75	2	1800.90	0.60	(R)VmLGETNPADSKPGTIR(G)	1	WP / MP
						29.8	29.7	3.59E+00	673.92	2	1343.76	2.07	(R)TFIAIKPDGVQR(G)		
114	P22392	NME2	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B) (NDP kinase B)	76.2	22	56.9	30.4	6.14E-03	901.75	2	1800.90	0.60	(R)VmLGETNPADSKPGTIR(G)	2	WP
						48.3	29.7	5.15E-02	673.92	2	1343.76	2.07	(R)TFIAIKPDGVQR(G)		
						39.3	40.0	4.28E-01	588.49	2	1174.65	0.32	(K)DRPFFPGLVK(Y)		
						33.1	32.5	1.78E+00	588.49	2	1174.65	0.32	(K)DRPFFPGLVK(Y)		
115	O00151	PDLIM 1	PDZ and LIM domain protein 1 (LIM domain protein CLP-36)	135.3	18	83.5	26.9	8.51E-06	1551.29	2	3100.47	0.11	(R)VITNQYNNPAGLYSSENISFNNALESK(T)	B	WP / MP
						62.1	37.2	1.97E-03	782.14	2	1560.83	1.44	(R)IKGCTDNLTLTVAR(S)		
						53.5	26.6	1.42E-02	800.07	2	1597.74	0.40	(R)SAmPFTASPASSTTAR(V)		
116	P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase)	153.2	42	71.4	54.7	2.68E-04	629.62	2	1256.64	0.59	(R)ALSTGEKGFYK(G)	B	M / WP / MP
						68.4	36.6	4.28E-04	916.79	2	1830.90	0.68	(K)SIYGEKFEDENFILK(H)		
						64.4	37.1	1.15E-03	690.68	2	1378.75	0.60	(R)VSFELFADKVPK(T)		
						59.0	51.0	3.93E-03	769.74	2	1536.73	0.74	(K)VKEGmNIVEAmER(F)		
						55.5	48.0	9.24E-03	577.94	2	1153.57	0.30	(K)FEDENFILK(H)		
						49.1	41.8	3.87E-02	656.04	2	1309.56	0.52	(K)EGmNIVEAmER(F)		
117	P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIase)	88.4	23	71.5	26.3	2.22E-04	822.20	2	1641.82	0.57	(R)VIKDFmIQGGDFTR(G)	B	WP / MP
						56.3	39.5	9.14E-03	524.51	2	1046.54	0.48	(K)VLEGmEVVR(K)		
						42.3	51.8	1.91E-01	801.34	2	1600.75	-0.07	(K)SIYGERFPDENFK(L)		
118	P30405	PPIF	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (EC 5.2.1.8) (PPIase)	54.0	19	50.6	24.0	1.77E-02	945.37	3	2832.35	0.77	(K)GSGDPSSSSSGNPLVLYDNDANGKPLGR(V)	1	WP / MP
						41.9	38.5	1.95E-01	556.06	2	1109.54	0.57	(R)FPDENFTLK(H)		
119	P32119	PRDX 2	Peroxioredoxin 2 (EC 1.11.1.15) (Thioredoxin peroxidase 1)	61.4	8	61.4	37.3	2.42E-03	606.60	2	1210.67	0.52	(R)QITVNDLPVGR(S)	2	WP / MP
120	P30044	PRDX 5	Peroxioredoxin 5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)	57.9	21	39.1	35.2	3.29E-01	1032.44	2	2062.07	0.80	(K)ETDLLLDDSLVSIFGNRR(L)	1	WP / MP
						36.8	18.0	4.41E-01	1372.18	2	2741.43	0.92	(K)JVGDAIPAVEVEFEGEPGNKNLAEFLK(G)		
121	P30041	PRDX 6	Peroxioredoxin 6 (EC 1.11.1.15) (Antioxidant protein 2)	101.9	40	78.0	30.3	4.18E-05	1049.87	2	2097.09	0.64	(-)PGGLLLGDVAPNFEANTTVGR(I)	B	WP / MP
						51.9	36.7	1.72E-02	678.01	3	2029.98	1.06	(R)FHDFLGDSWGILFSHPR(D)		
						51.5	44.7	2.67E-02	543.52	2	1084.59	0.45	(K)LPFHIDDR(N)		
						41.8	40.0	2.29E-01	568.41	2	1134.64	0.18	(R)VVFVFGPKDK(L)		
						35.6	40.5	1.04E+00	453.54	2	905.46	-0.38	(R)NFDEILR(V)		
122	Q00325	SLC25 A3	Phosphate carrier protein, mitochondrial precursor (PTP)	41.6	4	41.6	32.0	2.31E-01	681.65	2	1360.71	0.58	(R)IQTPGYANTLR(D)	2	
123	P36871	PGM1	Phosphoglucomutase (EC 5.4.2.2) (Glucose)	131.8	9	92.2	34.4	1.26E-06	1400.42	2	2798.39	0.44	(K)VFGSSANYAENFIQSIISTVEPAQR(Q)	B	MP
						88.8	49.2	5.00E-06	546.06	2	1089.58	0.53	(R)LSGTGSAGATIR(L)		



Supplementary Table 1

			phosphomutase) (PGM).												
124	P00558	PGK1	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2)	58.2	10	58.2	38.7	4.65E-03	545.58	3	1633.78	-0.04	(K)JLGDVYVNDAFGTAHR(A)	2	WP / MP
125	P18669	PGAM 1	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13)	33.0	4	33.0	25.8	1.68E+00	1150.62	1	1149.66	-0.04	(R)VLIAAHGNSLR(G)	1	WP / MP
126	P48059	LIMS1	PINCH protein (Particularly interesting new Cys- His protein)	59.3	6	59.3	36.4	4.28E-03	622.53	2	1242.68	0.38	(R)VIEGDVVSALNK(A)	2	WP / M / MP
127	P02775	PPBP	Platelet basic protein precursor (PBP) (Small inducible cytokine B7)	156.1	37	135.5	36.0	8.33E-11	863.10	2	1723.83	0.36	(K)GKEESLSDLYAELR(C)	B	MP
						51.5	36.4	2.83E-02	550.95	2	1099.62	0.28	(K)NIQSLEIVIGK(G)		
						31.7	26.2	1.92E+00	950.28	2	1896.95	1.60	(K)GTHCNQVEVIATLKDGR(K)		
128	P02776	PF4	Platelet factor 4 precursor (PF-4) (CXCL4) (Oncostatin A) (Iroplact).	50.5	29	50.5	32.5	2.73E-02	1041.55	1	1038.61	1.94	(R)HITSLEVIK(A)	B	WP / MP
						35.5	44.4	9.81E-01	668.08	2	1332.71	1.45	(K)ICLDLQAPLYK(K)		
						34.4	34.6	1.18E+00	732.24	2	1460.81	1.66	(R)KICLDLQAPLYK(K)		
129	P07359	GP1B A	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ibalpha)	95.1	19	66.8	29.2	4.16E-04	1465.53	2	2928.49	0.57	(K)DTTILHSENLLYTFSLATLmPYTR(L)	B	M / MP / SEN
						59.7	48.5	3.38E-03	591.71	2	1181.62	-0.21	(R)GVLQGHLESSR(N)		
						48.6	31.5	5.19E-02	594.90	2	1187.65	0.15	(R)GQDLLSTVSIR(Y)		
						28.4	40.5	6.09E+00	918.74	1	917.55	0.19	(R)AWLLFLR(G)		
130	P13224	GP1B B	Platelet glycoprotein Ib beta chain precursor (GP-Ib beta) (GPIbB)	125.0	21	68.9	37.3	4.23E-04	773.33	2	1543.84	0.81	(R)GRLLPYLADELRA(A)	B	WP / M / MP / SEN
						65.2	39.4	1.06E-03	607.38	2	1212.67	0.09	(R)LSLTDPLVAER(A)		
						65.0	43.6	1.12E-03	666.53	2	1330.71	0.35	(R)LLPYLADELRA(A)		
						40.1	31.2	3.22E-01	562.08	2	1121.57	0.59	(R)TAHLGANPWR(C)		
						32.3	43.7	1.96E+00	528.52	2	1054.57	0.46	(R)AWLAGRPER(A)		
131	P14770	GP9	Platelet glycoprotein IX precursor (GPIX) (CD42A).	160.5	24	71.2	33.1	2.74E-04	637.63	2	1272.73	0.52	(R)GHGLTALPALPAR(T)	B	WP / M / MP / SEN
						67.5	29.6	5.11E-04	920.34	2	1838.01	0.66	(R)JLWLEDRTPEALLQVR(C)		
						65.3	30.6	9.33E-04	698.04	2	1392.69	1.39	(R)CASPSLAAHGPLGR(L)		
						54.1	37.5	1.22E-02	514.01	2	1025.59	0.42	(R)TPEALLQVR(C)		
132	P40197	GP5	Platelet glycoprotein V precursor (GPV) (CD42D).	228.7	26	110.8	32.5	2.07E-08	1192.58	2	2382.29	0.87	(R)JLVSLDSGLLSNLSGALTELOFHR(N)	B	M / MP / SEN
						84.6	26.9	5.33E-06	1157.84	3	3468.91	1.62	(R)JSALPQGAQGLGELQVLALHSNGLTALPDGLLR(G)		
						68.6	28.2	2.37E-04	1657.45	2	3311.78	1.11	(K)LVNLQELALNQNLDFLPASLFTNLENLK(L)		
						45.8	26.1	7.10E-02	1058.42	2	2114.15	0.68	(R)SIAPGAFDRLPNLSLTLNR(N)		
133	P08567	PLEK	Pleckstrin (Platelet p47 protein).	128.9	15	79.4	27.4	2.14E-05	1008.52	3	3021.50	1.07	(R)KSEENLFEITADEVHYFLQAATPK(E)	B	WP / M / MP
						75.4	25.8	5.87E-05	1448.17	2	2893.40	0.94	(K)SEENLFEITADEVHYFLQAATPK(E)		
134	P07737	PFN1	Profilin-1 (Profilin I).	403.4	70	92.6	36.9	1.86E-06	736.21	2	1469.75	0.67	(R)SSFYVNGTLGGQK(C)	B	WP / M / MP
						90.7	43.8	2.65E-06	821.55	2	1640.74	0.35	(R)JDSLQDGEFSmDLR(T)		
						83.7	33.2	1.25E-05	862.81	2	1722.88	0.73	(K)STGGAPTFTNVTTKTDK(T)		
						81.1	28.0	2.23E-05	958.45	2	1914.06	0.83	(K)TFVNITPAEVLGVGKDR(S)		
						80.1	32.0	3.07E-05	822.78	2	1642.93	0.62	(K)TFVNITPAEVLGVGK(D)		

						72.3	33.8	1.92E-04	690.26	2	1378.71	-0.20	(K)STGGAPTfNVTVK(T)		
						65.8	34.2	9.07E-04	618.14	2	1233.70	0.57	(K)TDKTLVLLmGK(E)		
						52.0	34.8	2.64E-02	445.70	2	889.53	-0.13	(K)TLVLLmGK(E)		
						46.9	33.3	5.66E-02	651.62	3	1952.02	-0.15	(R)TKSTGGAPTfNVTVKTDK(T)		
						45.2	33.7	1.05E-01	607.37	2	1212.61	0.13	(K)DSPSVWAAVPGK(T)		
135	P40306	PSMB10	Proteasome subunit beta type 10 precursor (EC 3.4.25.1)	76.5	11	72.3	80.3	1.57E-04	1022.79	2	2043.06	0.52	(R)LPFTALGSGQDAALAVLEDR(F)	2	WP
						70.7	66.5	2.30E-04	1022.79	2	2043.06	0.52	(R)LPFTALGSGQDAALAVLEDR(F)		
136	Q9P1F3	C6orf115	Protein C6orf115.	67.2	40	55.3	35.5	8.66E-03	897.78	2	1792.90	0.66	(R)DDKCANLFEALVGLK(A)	B	
						46.8	38.9	5.95E-02	669.25	3	2003.97	0.78	(-)SmNVHEVNLLVEEHR(L)		
						40.5	36.5	2.91E-01	718.50	2	1434.75	0.25	(K)CANLFEALVGLK(A)		
137	P30101	PDIA3	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1)	140.4	20	65.5	40.3	9.36E-04	599.55	2	1196.71	0.39	(K)LSKDPNIVIAK(M)	B	WP / M / MP
						56.4	21.0	4.99E-03	1352.77	2	2702.39	1.15	(R)KTFSHELSDFGLESTAGEIPVVAIR(T)		
						50.8	31.2	2.96E-02	596.36	2	1190.59	0.13	(R)LAPEYEAATR(L)		
						48.3	29.5	2.93E-02	980.27	3	2937.37	0.45	(K)FISDKDASIVGFFDDSFSEAHSEFLK(A)		
						43.7	54.9	1.22E-01	599.64	3	1795.01	-0.41	(K)SELGEKLSKDPNIVIAK(M)		
						34.6	39.2	1.15E+00	758.55	2	1514.75	0.35	(R)FLQDYFDGNLKR(Y)		
						33.3	35.2	1.76E+00	594.90	2	1187.53	0.26	(K)FVmQEEFSR(D)		
						30.1	29.0	3.26E+00	758.55	2	1514.75	0.35	(R)FLQDYFDGNLKR(Y)		
138	Q15084	PDIA6	Protein disulfide-isomerase A6 precursor (EC 5.3.4.1)	72.5	12	50.1	37.5	4.32E-02	508.53	2	1014.61	0.44	(K)AATALKDVVK(V)	1	WP / M / MP
						47.2	24.8	4.14E-02	1319.04	2	2636.36	-0.29	(R)ALDLFSDNAPPELLEINEDIAK(R)		
139	P07237	P4HB	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PDI)	160.1	21	123.6	58.3	8.46E-10	1468.80	2	2934.49	1.10	(R)TGPAATTLPDGAAASLVESSEVAVIGFFK(D)	B	WP / M / MP
						52.1	25.6	8.67E-03	1256.45	3	3765.85	0.51	(R)TGPAATTLPDGAAASLVESSEVAVIGFKDVEDSAK(Q)		
						36.8	26.5	7.38E-01	429.28	3	1285.68	-0.83	(R)KSNFAEALAAHK(Y)		
140	Q96A00	PPP1R14A	Protein phosphatase 1 regulatory subunit 14A	44.7	11	44.7	33.4	1.04E-01	918.07	2	1832.93	1.21	(K)SCGKPVDFIQELLAK(L)	1	
141	P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77)	55.5	5	55.5	41.9	1.06E-02	595.00	2	1187.61	0.39	(R)KDDPTLLSSGR(V)	B	WP
142	P00491	NP	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase)	79.1	12	79.1	30.3	2.76E-05	1301.07	2	2600.39	-0.26	(K)QAAQKLEQFVSILmASIPLPKAS(-)	B	WP / MP
143	Q9NTK5	PTD004	GTP-binding protein PTD004 (isoform 1 or 3).	82.2	4	82.2	41.8	1.90E-05	785.10	2	1567.93	0.27	(K)IPAFLNVVDIAGLVK(G)	B	WP
144	P14618	PKM2	Pyruvate kinase, isozymes M1/M2 (EC 2.7.1.40) (Pyruvate kinase muscle)	405.4	46	138.6	32.5	3.62E-11	1088.33	2	2174.11	0.55	(R)LAPITSDPTEATAVGAVEASF(K)	B	WP / M / MP
						104.7	33.1	1.00E-07	938.80	2	1874.89	0.70	(K)FGVEQDVMVFASFIR(K)		
						76.7	60.5	8.94E-05	495.50	2	989.50	-0.50	(K)GSGTAEVELK(K)		
						76.4	41.4	7.48E-05	731.68	2	1461.81	-0.46	(K)IYVDDGLISLQVK(Q)		
						64.2	26.4	8.86E-04	826.73	3	2476.35	0.84	(K)KGVNLPGAADVLPVSEKDIQDLK(F)		

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						57.6	35.2	5.05E-03	629.03	3	1882.90	1.20	(R)LNFSHGTHEYHAETIK(N)		
						57.0	27.6	5.25E-03	1044.92	2	2087.08	0.75	(R)EAEAAIYHLQLFEELRR(L)		
						52.7	48.8	1.72E-02	465.60	3	1393.77	0.04	(K)IISKIENHEGVR(R)		
						51.4	32.7	2.09E-02	919.72	2	1836.90	0.54	(R)RFDEILEASDGIImVAR(G)		
						47.1	23.0	4.52E-02	1233.52	2	2464.28	0.76	(R)TATESFASDPILYRPVAVALDTK(G)		
						45.7	38.0	7.88E-02	420.76	2	839.52	0.00	(R)APIIAVTR(N)		
145	P50395	GDI2	Rab GDP dissociation inhibitor beta (Rab GDI beta) (GDI-2).	125.9	9	87.1	32.8	5.15E-06	1070.91	2	2140.10	-0.29	(K)SPYLYPLYGLGELPQGFAR(L)	B	WP / MP
						72.7	33.9	1.35E-04	760.65	3	2278.17	0.78	(K)KFDLGQDVIDFTGHALALYR(T)		
146	Q15404	RSU1	Ras suppressor protein 1 (Rsu-1) (RSP-1).	189.0	38	92.7	33.9	1.30E-06	1181.96	2	2361.25	0.66	(R)ALYLSNDNDFELPPDIGLTK(L)	B	WP / M / MP
						78.5	38.4	4.33E-05	904.80	2	1807.01	0.58	(R)LTVLPELGNLDTGQK(Q)		
						69.6	32.6	2.28E-04	1410.19	2	2817.45	0.93	(K)NLEVLNFFNNQIEELPTQISSLQK(L)		
						61.1	43.5	2.23E-03	919.89	2	1837.07	0.70	(K)LQILSLRDNLDISLPK(E)		
						22.1	20.5	1.16E+01	1516.06	2	3029.50	0.62	(K)AENNPWVTPIADQFQLGVSHVFEYIR(S)		
147	P15153	RAC2	Ras-related C3 botulinum toxin substrate 2 (p21-Rac2)	36.4	17	36.4	28.8	7.61E-01	728.72	2	1454.85	0.58	(K)LPITYPQGLALAK(E)	B	MP
						26.2	40.4	8.06E+00	731.02	2	1459.75	0.29	(K)LDLRDDKDTIEK(L)		
148	P61026	RAB10	Ras-related protein Rab-10.	57.6	19	57.6	47.0	6.21E-03	631.63	2	1260.71	0.54	(K)AFLTLAEDILR(K)	2	M / MP
149	Q15907	RAB11 B	Ras-related protein Rab-11B (GTP-binding protein YPT3).	58.0	23	58.0	40.6	5.71E-03	658.81	2	1315.62	-0.21	(K)\$AQIWDTAGQER(Y)	B	M / MP
						45.3	61.4	1.18E-01	1043.63	1	1042.60	0.03	(K)VVLIGDSGVGK(S)		
						39.2	39.9	5.21E-01	472.71	2	943.48	-0.07	(R)AITSAYYR(G)		
						35.2	38.7	1.05E+00	1289.81	1	1288.74	0.07	(R)GAVGALLVYDIK(H)		
150	P62820	RAB1 A	Ras-related protein Rab-1A (YPT1-related protein).	68.3	26	68.3	24.5	3.25E-04	1302.04	2	2601.32	0.76	(K)VVDYTTAKEFADSLGIPFLETSK(N)	1	M / MP
151	Q9H0U4	RAB1 B	Ras-related protein Rab-1B.	174.3	43	72.4	24.5	1.30E-04	1277.34	2	2552.30	0.38	(K)VVDNTTAKAFADSLGIPFLETSK(N)	B	M
						69.7	29.8	2.29E-04	1341.74	2	2680.40	1.07	(K)KVDNTTAKAFADSLGIPFLETSK(N)		
						61.2	58.9	3.06E-03	536.49	2	1070.63	0.35	(K)LLIGDSGVGK(S)		
						58.8	23.2	3.28E-03	1139.82	2	2277.13	0.50	(R)GAHGIIVYDVTDQESYANVK(Q)		
						58.0	40.6	5.71E-03	658.70	2	1315.65	-0.25	(K)LQIWDTAGQER(F)		
						45.7	38.9	1.05E-01	495.81	2	989.48	0.14	(R)TITSSYYR(G)		
152	O00194	RAB27 B	Ras-related protein Rab-27B (C25KG).	73.0	38	59.2	24.2	2.71E-03	1266.40	2	2530.22	0.58	(R)ELADKYGIPYFETSAATGQNVEK(A)	B	WP / M / MP
						52.2	41.6	2.07E-02	473.40	3	1416.80	0.41	(K)AVETLLDLImKR(M)		
						34.7	31.4	1.39E+00	1029.69	1	1028.59	0.10	(K)LLALGDSGVGK(T)		
153	Q9NRW 1	RAB6 B	Ras-related protein Rab-6B.	58.5	18	58.5	34.9	5.14E-03	631.08	2	1259.63	0.52	(M)\$SAGDFGNPLRK(F)	2	MP
154	P51149	RAB7	Ras-related protein Rab-7.	58.9	18	58.9	30.2	4.29E-03	738.76	2	1474.75	0.76	(R)DPENFPFVVLGNK(I)	2	M / MP
155	P61224	RAP1 B	Ras-related protein Rap-1b (GTP-binding protein smg p21B).	200.4	54	99.2	36.6	3.52E-07	855.67	2	1708.91	0.43	(K)SKINVNEIFYDLVR(Q)	B	WP / M / MP
						81.9	32.9	2.05E-05	830.77	2	1658.85	0.69	(R)VKDTRDDVPmILVGNK(C)		
						76.2	48.5	7.52E-05	747.77	2	1493.79	-0.26	(K)INVNEIFYDLVR(Q)		
						52.8	39.0	1.99E-02	493.37	2	984.60	0.13	(K)LLVLGSGGVGK(S)		

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						45.5	36.3	1.05E-01	630.01	2	1257.55	0.47	(K)YDPTIEDSYR(K)		
						40.1	38.6	3.30E-01	694.06	2	1385.65	0.46	(K)YDPTIEDSYR(Q)		
156	Q9NQC3	RTN4	Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foccen)	54.5	1	54.5	35.4	1.11E-02	536.98	3	1606.82	1.13	(R)HQAQIDHYLGLANK(N)	B	M / MP / SEN
157	P52566	ARHG DIB	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI).	77.8	31	62.8	34.0	1.68E-03	656.57	2	1310.71	0.42	(K)TLLGDGPVVTDPK(A)	B	WP / MP
						43.6	28.5	1.58E-01	429.18	2	854.50	1.85	(K)APNVVTR(L)		
158	O14983	ATP2A 1	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (EC 3.6.3.8)	103.3	5	68.2	26.1	3.58E-04	1221.00	2	2440.14	-0.14	(K)TASEmVLADNFSTIVAAVEEGR(A)	B	
						65.2	30.1	7.89E-04	1089.51	2	2176.17	0.85	(R)DIVPGDIVEVAVGDKVPADLR(L)		
159	P16615	ATP2A 2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (EC 3.6.3.8)	123.4	5	81.3	30.0	1.88E-05	1095.88	2	2190.19	-0.44	(K)DIVPGDIVEIAGDKVPADIR(L)	B	M / MP / SEN
						68.2	26.1	3.58E-04	1221.00	2	2440.14	-0.14	(K)TASEmVLADNFSTIVAAVEEGR(A)		
160	Q93084	ATP2A 3	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 (EC 3.6.3.8)	145.5	6	82.7	34.6	1.55E-05	943.46	2	1883.95	0.96	(R)HFSVTAEGGLSPAQVTGAR(E)	1	M / SEN
						65.2	30.1	7.89E-04	1089.51	2	2176.17	0.85	(R)DIVPGDIVEVAVGDKVPADLR(L)		
						53.1	25.5	1.50E-02	783.20	2	1563.81	0.58	(-)SmEAAHLLPAADVLR(H)		
161	Q16181	SEPT7	Septin 7 (CDC10 protein homolog).	91.7	8	77.3	24.6	4.13E-05	1304.61	2	2606.30	0.92	(K)STLINSFLTLDYSPEYGPSPHR(I)	B	WP
						49.7	35.3	3.32E-02	762.61	2	1522.68	0.53	(K)DVTNNVHYENYR(S)		
162	P02768	ALB	Serum albumin precursor (UNQ696/PRO1341).	163.1	32	71.1	34.5	2.11E-04	1023.40	2	2044.09	0.70	(K)VFDEFKPLVEEPQNLK(Q)	B	WP / M / MP
						67.5	32.9	5.36E-04	820.55	2	1638.93	0.16	(K)KVPQVSTPTLVEVSR(N)		
						57.8	37.4	4.75E-03	950.40	2	1897.99	0.80	(R)RHPYFYAPELLFFAK(R)		
						55.3	41.7	9.26E-03	490.02	3	1466.84	0.23	(R)RHPDYSVVLLR(L)		
						48.3	43.7	6.24E-02	480.92	2	959.56	0.27	(K)FQNALLVR(Y)		
						47.6	38.6	5.75E-02	613.87	2	1225.60	0.13	(R)FKDLGEENFK(A)		
						47.0	37.1	5.91E-02	470.93	2	939.44	0.42	(K)DDNPNLPR(L)		
163	O95810	SDPR	Serum deprivation response (Hypothetical protein SDPR).	160.7	15	88.3	28.8	2.44E-06	1122.95	3	3364.73	1.13	(R)DNSQVNAVTVTLTLDKLVNmLDAVQENQHK(M)	B	WP / M / MP
						78.7	31.3	4.16E-05	865.25	2	1728.93	-0.44	(R)DNSQVNAVTVTLTLDK(L)		
						60.6	35.6	2.45E-03	981.30	2	1961.05	-0.45	(K)VLIFQEENEIPASVFVK(Q)		
						37.0	43.6	9.41E-01	444.96	2	887.47	0.45	(K)GIQNDLTK(L)		
164	O75368	SH3B GRL	SH3 domain-binding glutamic acid-rich-like protein	39.5	11	39.5	37.5	3.65E-01	642.50	2	1282.68	0.31	(R)VYIASSSGSTAIK(K)	1	WP / MP
165	Q9UJC5	SH3B GRL2	SH3 domain-binding glutamic acid-rich-like protein 2 (Fovea-associate	68.4	25	68.4	28.9	4.45E-04	798.35	2	1593.85	0.85	(K)ESNTVFSFLGLKPR(L)	B	
166	Q16836	HADH SC	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor	76.6	20	76.6	22.8	5.32E-05	1187.46	2	2372.16	0.76	(K)LGAGYPmGPFELLDYVGLDTTK(F)	2	MP
167	P11169	SLC2A 3	Solute carrier family 2, facilitated glucose transporter, member 3	53.8	4	53.8	41.1	1.62E-02	552.84	2	1103.63	0.05	(K)QVTVLELFR(V)	B	M / MP / SEN
						32.9	36.0	1.48E+00	441.37	2	880.43	0.30	(R)TFEDITR(A)		
						30.6	48.4	3.96E+00	452.50	2	902.57	0.42	(R)FLLINRK(E)		
						20.1	34.5	3.13E+01	535.45	3	1602.87	0.49	(R)FLLINRKEENAK(Q)		

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168	P04179	SOD2	Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1).	109.2	27	77.1	36.5	5.73E-05	870.15	2	1737.84	0.46	(K)HHAAYVNNLNVTEEK(Y)	B	WP / MP
						58.8	46.1	4.99E-03	514.98	2	1027.60	0.36	(K)GELLEAIKR(D)		
						51.9	38.6	2.29E-02	674.57	2	1346.65	0.49	(R)DFGSFDKFKEK(L)		
						36.2	29.9	9.43E-01	1089.90	1	1089.51	-0.61	(R)DFGSFDKFK(E)		
169	Q96AX7	SACM1L	Suppressor of actin 1	41.4	4	41.4	28.5	2.43E-01	654.03	2	1305.67	0.39	(R)HFDSQVIYKG(Q)	B	M
170	O00161	SNAP23	Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane fusion)	70.5	11	58.0	47.2	6.37E-03	522.29	2	1042.55	0.03	(R)DRIDIANAR(A)	1	WP / M / MP
						40.7	28.2	2.71E-01	548.52	3	1641.81	0.76	(R)AHQITDESLESTR(I)		
171	Q9UPX3	TLN1	Talin-1	1711.7	38	137.0	29.8	5.33E-11	1045.83	2	2090.15	-0.50	(R)GVGAAATAVTQALNELLQHV(K)	B	WP / M / MP
						136.8	30.1	5.01E-11	1235.39	2	2468.30	0.48	(R)GVAALTSDBAVQAIVLDTASDVLDK(A)		
						104.3	29.4	8.37E-08	1287.56	2	2572.32	0.80	(K)AVSSAIAQLLGEVAQGNENYAGIAAR(D)		
						103.0	27.8	1.26E-07	1156.02	2	2309.18	0.85	(K)VGAIPANALDDGQWSQGLISAAR(M)		
						102.4	33.9	1.99E-07	709.10	2	1415.77	0.43	(K)LAQAAQSSVATITR(L)		
						101.9	27.1	1.32E-07	1367.51	2	2732.20	0.82	(R)FGQDFSTFLEAGVEmAGQAPSQEDR(A)		
						91.7	36.3	1.77E-06	1098.45	2	2194.18	0.72	(K)LGAASLGAEDPETQVVLINAVK(D)		
						90.5	26.5	1.72E-06	1499.12	2	2995.34	0.90	(R)YDQATDTILTVTENIFSSmGDAGEmVR(Q)		
						86.5	26.9	4.69E-06	1378.11	2	2753.40	0.81	(R)GSQAQPDSPSAQLALIAASQSLQPGGK(M)		
						86.1	36.8	8.36E-06	729.13	2	1455.83	0.42	(R)ILAQATSDLVNAIK(A)		
						85.1	25.7	8.39E-06	998.41	2	1994.02	0.79	(K)QAAASATQTIAAAQHAATPK(A)		
						84.9	31.5	1.07E-05	717.84	2	1433.72	-0.05	(K)VLGEAmTGISQNAK(N)		
						79.2	31.3	4.35E-05	622.60	2	1242.66	0.53	(K)VLVQNAAGSQEK(L)		
						78.7	32.9	2.55E-05	1526.38	2	3050.51	0.24	(K)GTEWVDPEDPTVIAENELGAAAAIEAAK(K)		
						78.4	24.2	3.68E-05	1143.47	2	2284.09	0.84	(R)IPEAPAGPPSDFGLFLSDDDPK(K)		
						78.0	27.0	5.09E-05	761.71	2	1520.84	0.58	(K)TLAESALQLLYTAK(E)		
						77.5	52.6	5.72E-05	682.71	2	1362.75	0.67	(K)AGFLDLKDFLPK(E)		
						76.7	33.8	7.02E-05	732.09	2	1462.74	-0.56	(K)TmLESAGGLIQTAR(A)		
						76.6	28.4	5.80E-05	1061.98	2	2121.18	0.77	(K)LLAALLEDEGGSGRPLQAAG(K)		
						73.7	25.1	6.51E-05	1176.12	3	3524.88	0.49	(R)GVAALTSDBAVQAIVLDTASDVLDKASSLIEEAKK(A)		
						73.7	23.6	1.10E-04	1100.49	2	2197.11	1.86	(K)VSQmAQYFEPLTLAAVGAASK(T)		
						73.1	24.9	9.41E-05	1499.12	2	2995.34	0.90	(R)YDQATDTILTVTENIFSSmGDAGEmVR(Q)		
						72.3	25.1	9.10E-05	1736.45	2	3469.74	1.15	(R)AATAPLLEAVDNLAFASNPEFSSIPAQISPEGR(A)		
						70.6	34.2	3.04E-04	542.81	2	1083.67	-0.06	(K)AVASAAAALVLK(A)		
						65.5	42.4	9.61E-04	571.08	2	1139.59	0.57	(R)ALEATTEHIR(Q)		
						64.3	52.9	1.58E-03	501.54	2	1000.57	0.51	(K)KGIWLEAGK(A)		
						63.8	26.4	6.95E-04	1130.04	3	3385.73	1.40	(R)EGISQEALHTQmLTAVQEISHLIEPLANAAR(A)		
						62.8	23.9	1.32E-03	1125.26	2	2248.06	0.46	(K)SNTSPEELGPLANQLTSDYGR(L)		
						62.2	38.9	2.08E-03	611.07	2	1219.68	0.46	(K)VmVTNVTSLK(T)		
						61.4	30.3	2.45E-03	759.22	2	1515.77	0.66	(R)GITHNDEYSLVR(E)		

						59.0	31.0	4.01E-03	746.80	2	1491.88	-0.29	(K)JAVAEQIPLLVQGV(R)		
						57.3	34.0	7.86E-03	494.88	2	987.56	0.19	(K)ALGDLISAT(K)		
						53.5	47.3	1.41E-02	619.20	2	1235.63	0.76	(K)STVLQQYNR(V)		
						46.3	42.7	9.62E-02	516.40	2	1030.60	0.20	(K)SIAAATSALVK(A)		
						44.3	29.9	1.44E-01	573.54	2	1144.61	0.46	(K)EVANSTANLVK(T)		
						42.3	24.3	1.01E-01	1130.04	3	3385.73	1.40	(R)EGISQEAHTQMLTAVQEISHLIEPLANAAR(A)		
						41.4	34.8	2.40E-01	1197.60	1	1196.64	-0.04	(K)ALSTDPAAPNLK(S)		
						40.4	37.6	3.41E-01	420.63	3	1257.66	1.23	(K)LKPLPGETmEK(C)		
						36.5	24.6	3.39E-01	1193.51	3	3576.88	0.66	(R)ALHYGRECANGYLELLDHVLLTLQKPSPELK(Q)		
						33.1	24.9	9.38E-01	1499.12	2	2995.34	0.90	(R)YDQATDTILTVTENIFFSmGDAGEMVR(Q)		
172	Q9Y4A1	DMXL 1	Talin-related protein (Fragment).	156.8	9	63.3	27.0	1.50E-03	761.72	2	1519.90	1.53	(K)TLAKSALQLLYTAK(E)	B	WP / M / MP
						44.9	27.0	1.03E-01	761.52	2	1520.84	-0.31	(K)STLASSALQLLYTAK(E)		
						42.9	27.0	1.64E-01	761.57	2	1519.86	1.28	(K)TLAQSAQLLYTAK(E)		
						35.8	27.2	8.37E-01	761.57	2	1522.84	-1.70	(K)TLAMSALQLLYTAK(E)		
173	P30048	PRDX 3	Thioredoxin- dependent peroxide reductase, mitochondrial precursor	94.9	14	73.0	43.3	1.63E-04	731.83	2	1461.78	-0.12	(R)DYGVLLEGSGLALR(G)	2	WP / MP
						46.6	24.7	7.65E-02	603.73	2	1205.65	-0.19	(K)HLSVNDLPVGR(S)		
174	P07996	THBS 1	Thrombospondin-1 precursor.	674.3	32	150.4	31.5	2.33E-12	1098.35	2	2194.05	0.65	(R)IPESGGDNVSFDIFELTGAAR(K)	B	WP / M / MP
						85.8	51.5	8.24E-06	837.32	2	1671.88	0.75	(R)KVTEENKELANELR(R)		
						80.5	36.5	2.87E-05	809.05	2	1615.81	0.28	(K)GGVNDNFQGVQLQNR(F)		
						79.3	26.5	3.99E-05	731.14	2	1459.71	0.56	(K)DHSGQVFSVVSNGK(A)		
						77.9	32.5	4.95E-05	798.74	2	1594.74	0.73	(K)QVTQSYWDTNPT(R)		
						77.1	33.4	5.74E-05	938.76	2	1874.89	0.63	(R)FTGSQPFQGVVEHATANK(Q)		
						71.6	31.2	1.54E-04	1290.67	2	2578.33	1.00	(R)IEDANLIPPVDDKFQDLVDVAVR(T)		
						67.6	30.9	4.73E-04	654.04	3	1957.96	1.17	(K)KImADSGPIYDKTYAGGR(L)		
						66.6	34.5	7.58E-04	652.05	2	1301.72	0.37	(K)AGTDLDSLTVQGGK(Q)		
						63.9	50.9	1.70E-03	495.38	2	988.61	0.14	(K)GFLLLASLR(Q)		
						63.5	33.5	1.62E-03	624.06	2	1245.69	0.43	(R)TIVTTLQDSIR(K)		
						60.8	38.8	2.56E-03	677.63	2	1352.66	0.60	(K)KImADSGPIYDK(T)		
						53.0	45.7	2.06E-02	515.90	2	1029.49	0.30	(K)GPDPSAPFR(I)		
						52.8	36.6	1.68E-02	530.53	3	1587.80	0.80	(R)KDHSQGVFSVVSNGK(A)		
						51.4	38.2	2.92E-02	565.59	2	1128.66	0.52	(K)TRGTLLALER(K)		
						50.0	47.8	3.43E-02	686.98	2	1371.65	0.31	(K)GTSQNDPNWVVR(H)		
						49.9	30.7	3.37E-02	775.75	2	1549.77	-0.27	(R)NALWHTGNTPGQVR(T)		
						49.8	36.7	4.03E-02	553.08	2	1103.57	0.58	(R)FQmIPLDPK(G)		
						47.8	46.6	7.35E-02	436.85	2	871.51	0.19	(R)GTLLALER(K)		
						46.9	47.0	8.51E-02	494.95	2	987.49	0.40	(R)FYVvWK(Q)		
						42.8	33.5	1.80E-01	1207.75	1	1206.62	0.13	(K)SITLFVQEDR(A)		

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						41.4	31.0	2.32E-01	787.83	2	1572.66	1.00	(R)DNCQYVYNVDQR(D)		
						41.2	32.3	2.43E-01	1395.06	1	1393.72	0.34	(R)FVFGTTPEDILR(N)		
						39.3	27.6	3.48E-01	611.07	3	1829.86	0.36	(K)ImADSGPIYDKTYAGGR(L)		
						38.9	41.5	4.39E-01	457.77	3	1369.74	0.58	(R)LVKGPDSPSAPFR(I)		
						38.5	28.1	4.44E-01	465.48	3	1392.69	0.75	(R)HIGWKDFTAYR(W)		
						37.9	31.7	5.04E-01	505.35	2	1008.52	0.18	(R)AQGYSLSVK(V)		
						34.2	43.4	1.58E+00	501.21	2	999.61	0.80	(R)GTLALERK(D)		
						29.4	33.1	3.27E+00	455.88	2	909.49	0.27	(R)LVLPNDQK(D)		
						27.1	34.8	5.68E+00	462.85	2	923.46	0.24	(R)TLWHDPH(H)		
175	P24557	TBXA S1	Thromboxane-A synthase (EC 5.3.99.5) (TXA synthase) (TXS).	50.0	5	50.0	48.7	3.30E-02	611.82	2	1222.60	-0.96	(R)DFLQmVLDAR(H)	2	M / MP
						39.4	42.6	3.72E-01	449.81	2	897.43	0.18	(R)mASGLEFK(S)		
176	P19971	ECGF 1	Thymidine phosphorylase precursor (EC 2.4.2.4) (TdRPase) (TP)	64.6	6	64.6	35.9	7.77E-04	1283.20	2	2563.35	1.05	(R)DLVTTLGALLWLSGHAGTQAQGAAR(V)	2	WP / MP
177	Q8TCG3	TPM3	Tropomyosin skeletal muscle-3	101.3	48	101.3	31.4	2.31E-07	886.30	2	1769.89	0.71	(R)KIQVLQQADDAEER(A)	B	MP
178	Q86SZ2	TRAP PC6B	Trafficking protein particle complex subunit 6B (isoform not determined).	66.7	15	66.7	28.5	5.59E-04	1104.34	2	2206.10	0.57	(M)\$ADEALFLLHNEmVSGVYK(S)	1	
179	P61586	RHOA	Transforming protein RhoA (H12).	55.2	4	55.2	42.6	1.02E-02	499.74	2	997.45	0.03	(R)EVFEmATR(A)	B	MP
180	P37802	TAGL N2	Transgelin-2 (SM22-alpha homolog).	398.0	66	141.3	34.4	1.99E-11	1050.81	2	2099.02	0.60	(R)YGINTTDIFQTVDLWEGK(N)	B	WP / M / MP
						86.4	40.4	6.96E-06	848.12	2	1693.81	0.42	(K)QmEQISQFLQAAER(Y)		
						77.7	32.2	5.24E-05	798.09	2	1593.71	0.46	(R)DDGLFSGDPNWFPK(K)		
						67.3	31.9	4.49E-04	1208.90	2	2414.25	1.55	(K)DGTVLCELINALYPEGQAPVK(I)		
						64.1	39.5	1.46E-03	616.55	2	1230.68	0.41	(R)TlMNLGGLAVAR(D)		
						61.3	48.6	2.35E-03	640.52	2	1278.58	0.46	(R)NFSDNQLQEGK(N)		
						58.4	33.1	5.31E-03	610.04	2	1217.62	0.45	(K)NVIGLQmGTNR(G)		
						56.1	36.7	6.23E-03	1145.32	2	2286.16	2.47	(K)DGTVLCELINALYPEGQAPVK(K)		
						53.0	33.2	1.83E-02	602.46	2	1202.62	0.29	(-)SANRGPAYGLSR(E)		
						48.7	53.0	4.39E-02	506.72	2	1011.51	-0.08	(K)QASTmAFK(Q)		
						47.3	22.8	4.02E-02	1344.95	2	2687.30	0.60	(K)QASTmAFKQmEQISQFLQAAER(Y)		
						43.6	40.0	1.40E-01	506.72	2	1011.51	-0.08	(K)QASTmAFK(Q)		
						30.6	32.4	2.38E+00	681.23	3	2040.03	0.67	(K)DVGRPQPGRENFQNLK(D)		
181	P13693	TPT1	Translationally controlled tumor protein (TCTP) (p23)	47.6	10	47.6	33.3	5.54E-02	718.74	2	1434.75	0.73	(R)VKPFmTGAAEQIK(H)	B	WP / MP
						36.1	36.4	8.98E-01	421.89	2	841.48	0.30	(K)HILANFK(N)		
182	P02766	TTR	Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR).	57.8	16	57.8	28.0	3.81E-03	1259.08	2	2515.33	0.83	(R)RYTIAALLSPYSYSTAVVTNPK(E)	1	
183	P60174	TP11	Triosephosphate	112.8	35	71.3	33.0	2.59E-04	618.08	2	1233.59	0.57	(K)SNVSDAVAQSTR(I)	B	WP / MP

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184	P06753-2	TPM3	isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate isomer)	185.9	53	53.8	29.1	1.44E-02	708.14	2	1413.78	0.50	(K)QSLGELIGLTNAAK(V)	B	MP
						50.2	33.4	3.48E-02	638.31	2	1273.67	0.94	(K)VIADNVKDWSK(V)		
						101.3	31.4	2.31E-07	886.30	2	1769.89	0.71	(R)KIQVLQQQADDAEER(A)		
						83.5	43.9	1.48E-05	772.81	2	1542.77	0.85	(R)AREQAEAEVASLNR(R)		
						65.5	47.1	7.98E-04	981.42	2	1960.02	0.81	(R)ALKDEEKmELQEILK(E)		
						60.7	40.7	3.16E-03	600.61	2	1199.69	-0.48	(-)SAGITTIEAVKR(K)		
						49.2	42.4	3.69E-02	567.53	3	1698.88	0.72	(R)AREQAEAEVASLNR(I)		
						40.1	48.6	4.65E-01	415.87	2	829.53	0.20	(K)ILTDKLK(E)		
185	P67936	TPM4	Tropomyosin alpha 4 chain (Tropomyosin 4) (TM30p1).	373.9	82	94.1	37.6	1.14E-06	872.15	2	1741.86	0.43	(R)KIQALQQQADEADR(A)	B	WP / MP
						85.8	53.0	8.94E-06	737.80	2	1472.77	0.83	(K)TIDDLKLAQAK(E)		
						77.1	37.2	6.55E-05	722.72	2	1442.80	0.63	(R)LATALQKLEAEK(A)		
						74.8	45.1	1.04E-04	845.64	2	1688.78	0.49	(K)YSEKEDYEEIK(L)		
						73.9	36.7	1.48E-04	636.87	2	1271.65	0.08	(R)EKAEGDVAALNR(R)		
						66.9	35.1	4.94E-04	799.73	3	2395.22	0.98	(R)KIQALQQQADEADRAQGLQR(E)		
						58.1	40.7	5.73E-03	600.58	2	1198.67	0.48	(-)SAGLSLEAVKR(K)		
						55.4	27.3	7.67E-03	735.06	3	2201.12	1.07	(R)LATALQKLEAEKADESER(G)		
						53.9	41.7	1.38E-02	702.17	2	1401.78	0.56	(K)LLSDKLKEATR(A)		
						53.9	39.8	1.58E-02	481.86	2	961.46	0.25	(K)TIDDLK(L)		
						48.7	33.5	4.15E-02	864.67	2	1726.88	0.46	(R)IQLVEEELDRAQER(L)		
						48.3	38.2	4.47E-02	908.85	2	1814.89	0.81	(K)HIAEADRKYEEVAR(K)		
						45.7	44.2	7.95E-02	595.57	3	1782.98	0.73	(R)KLVILEGELERAER(A)		
						44.5	41.8	1.03E-01	628.98	3	1882.99	0.96	(R)RIQLVEEELDRAQER(L)		
						42.1	46.8	1.94E-01	590.98	2	1180.55	-0.60	(K)mEIQEmQLK(E)		
						40.7	33.8	2.58E-01	604.00	3	1807.83	1.18	(K)LEEAEEKADESERGMK(V)		
186	Q9BQE3	TUBA 6	Tubulin alpha-6 chain (Alpha-tubulin 6)	297.2	44	94.3	32.3	8.92E-07	1205.37	2	2408.20	0.54	(R)FDGALNVDLTFQTNLVPYPR(I)	2	M / MP
						94.0	51.9	1.32E-06	744.68	2	1486.87	0.49	(R)LISQIVSSITASLR(F)		
						86.6	27.9	5.74E-06	1004.87	2	2006.89	0.84	(K)TIGGGDDSFNTFFSETGAGK(H)		
						75.8	30.2	7.75E-05	913.25	2	1823.98	0.51	(K)VGINYQPPTVVPGGDLAK(V)		
						68.5	35.9	4.26E-04	879.32	2	1755.96	0.67	(R)IHFLATYAPVISAER(A)		
						53.8	39.2	1.29E-02	860.22	2	1717.87	0.57	(R)NLDIERPTYTNLNR(L)		
						50.6	41.4	2.77E-02	706.13	2	1409.77	0.48	(R)QLFHPEQLITGK(E)		
						102.1	32.3	1.49E-07	1205.37	2	2408.20	0.54	(R)FDGALNVDLTFQTNLVPYPR(I)		
187	P68363	ALTBE	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous)	318.8	46	94.0	51.9	1.32E-06	744.68	2	1486.87	0.49	(R)LISQIVSSITASLR(F)	1	WP
						86.6	27.9	5.74E-06	1004.87	2	2006.89	0.84	(K)TIGGGDDSFNTFFSETGAGK(H)		
						79.5	30.2	3.38E-05	879.32	2	1755.96	0.67	(R)IHFLATYAPVISAER(A)		
						75.8	35.9	7.75E-05	913.25	2	1823.98	0.51	(K)VGINYQPPTVVPGGDLAK(V)		
						56.7	39.2	6.65E-03	860.22	2	1717.87	0.57	(R)NLDIERPTYTNLNR(L)		
						50.6	41.4	2.77E-02	706.13	2	1409.77	0.48	(R)QLFHPEQLITGK(E)		
						102.1	32.3	1.49E-07	1205.37	2	2408.20	0.54	(R)FDGALNVDLTFQTNLVPYPR(I)		



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188	Q9H4B7	TUBB 1	Tubulin beta-1 chain.	423.0	40	123.0	32.1	1.27E-09	1142.91	2	2283.13	0.69	(R)GLSmAATFIGNNTAIQEIFNR(V)	B	WP / M
						118.1	40.5	4.10E-09	1014.91	2	2027.03	0.79	(K)GHYTEGAELIENVLEVVR(H)		
						87.4	20.7	3.97E-06	1346.64	2	2690.39	0.89	(K)LTPTYGDLNHLVSLTMSGITSLR(F)		
						73.7	47.5	1.38E-04	685.61	2	1368.64	0.58	(R)ImNSFSVmPSPK(V)		
						59.5	19.3	2.80E-03	1156.64	2	2311.12	0.16	(R)LHFFmPGFAPLTAQGSQQYR(A)		
						56.7	60.4	9.23E-03	472.94	2	943.51	0.36	(R)GASALQLER(I)		
						56.3	41.6	9.27E-03	566.01	2	1129.59	0.42	(R)FPGQLNADLR(K)		
						56.3	20.5	5.04E-03	1346.64	2	2690.39	0.89	(K)LTPTYGDLNHLVSLTmSGITSLR(F)		
						54.9	46.3	1.41E-02	472.94	2	943.51	0.36	(R)GASALQLER(I)		
						43.0	36.8	1.20E-01	1194.50	2	2386.15	0.84	(K)LGALFQPDSPFVHGNAGNNWAK(G)		
						41.1	25.9	2.77E-01	644.66	2	1286.72	0.59	(R)KLAVNmVPFPR(L)		
						37.7	28.8	5.51E-01	732.20	2	1461.73	0.66	(R)ISVYYNEAYGRK(Y)		
189	P07437	TUBB 2	Tubulin beta-2 chain.	245.8	39	93.8	36.0	1.15E-06	980.31	2	1957.97	0.65	(K)GHYTEGAELVDSVLDVVR(K)	B	WP / M / MP
						75.8	35.7	9.27E-05	651.50	2	1300.63	0.36	(R)ISVYYNEATGGK(Y)		
						75.8	80.9	7.22E-05	1021.84	2	2041.07	0.60	(K)mAVTFIGNSTAIQELFKR(I)		
						65.9	36.7	6.68E-04	696.57	3	2086.07	0.65	(K)GHYTEGAELVDSVLDVVR(E)		
						65.1	26.6	6.41E-04	1400.12	2	2797.34	0.89	(R)SGPFGQIFRPDNFVFGQSGAGNNWAK(G)		
						62.3	49.0	1.98E-03	731.65	2	1461.68	-0.39	(K)EVDEQmLNVQNK(N)		
						51.2	29.0	2.32E-02	819.30	2	1635.82	0.78	(R)LHFFmPGFAPLTSR(G)		
						39.6	30.9	2.97E-01	1021.84	2	2041.07	0.60	(K)mAVTFIGNSTAIQELFKR(I)		
190	Q9NRH3	TUBG 2	Tubulin gamma-2 chain (Gamma-2 tubulin)	33.6	5	33.6	25.7	1.06E+00	1167.67	2	2333.21	0.12	(R)YPGYmNNDLIGLIASLIPTPR(L)	1	
191	Q06187	BTK	Tyrosine-protein kinase BTK (EC 2.7.1.112) (Bruton's tyrosine kinase)	78.6	2	78.6	39.7	4.82E-05	701.99	2	1400.84	1.13	(M)\$AAVILESIFLKR(S)	B	M / MP
192	P62988	RPS27 A	Ubiquitin	42.6	16	42.6	31.5	1.70E-01	541.18	2	1080.55	-0.20	(R)TLDYNIQK(E)	1	
193	P68036	UBE2L 3	Ubiquitin-conjugating enzyme E2 L3 (EC 6.3.2.19) (Ubiquitin-protein l	116.5	27	95.7	44.1	6.25E-07	1242.44	2	2482.32	0.55	(K)TDQVIQSLIALVNDPQPEHPLR(A)	1	WP
						49.6	28.8	3.31E-02	895.82	2	1788.94	0.70	(R)IEINFPAEYFPKPPK(I)		
						34.2	38.3	1.45E+00	564.98	2	1127.56	0.40	(K)YHPNIDEK(G)		
194	Q86UX7	URP2	Unc-112 related protein 2 (Kindlin-3) (MIG2-like).	488.2	42	104.5	34.7	8.45E-08	1224.70	2	2446.20	1.20	(R)TmADSSYTSEVQAI AFLSLQR(T)	B	M / MP
						89.0	35.4	3.40E-06	1052.97	2	2103.14	0.80	(R)ILEAHQNVQSLAEALQR(F)		
						86.2	27.9	6.35E-06	1050.32	2	2098.10	0.54	(K)LEGSAPTDVLDSLTTPELK(D)		
						82.7	27.1	1.01E-05	1513.63	2	3024.48	0.77	(K)LSQSSEVGEPA GTDPLGDDLDVALSNLEV(K)		
						80.7	35.6	2.62E-05	655.66	2	1308.74	0.57	(R)VTGESHIGGVLLK(I)		
						77.3	33.5	5.70E-05	889.30	2	1775.86	0.73	(R)VFVGEEDPEAESVTLR(V)		
						71.3	30.5	1.52E-04	1392.03	2	2781.32	0.74	(R)TGSGGPGNHPHGPDSAEGLNPYGLVAPR(F)		
						63.7	35.1	1.31E-03	860.66	2	1718.89	0.43	(K)LLVSPSEGmSEIYLR(C)		
						59.0	36.7	4.43E-03	635.64	2	1268.76	0.51	(K)VVLAGGVAPALFR(G)		
						53.3	40.5	1.63E-02	561.52	2	1120.59	0.44	(R)LTQLYEQAR(W)		

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						50.1	47.3	3.48E-02	621.87	2	1241.67	0.07	(R)KDEILGIANNR(L)		
						50.1	36.3	3.13E-02	647.81	2	1293.59	0.03	(K)YYSFDDLDPK(T)		
						43.9	38.6	1.53E-01	514.88	2	1027.59	0.17	(R)IDLAVGDVVK(T)		
						42.6	41.5	2.10E-01	550.07	2	1098.60	-0.46	(R)LRPSSLSDK(T)		
						38.9	48.2	3.90E-01	456.44	4	1820.99	0.75	(R)LRPSSLSDKTQLHSR(W)		
						30.1	34.0	3.05E+00	559.39	3	1674.98	0.20	(R)LLSIRHPEELSLLR(A)		
						27.5	33.7	3.50E+00	954.04	3	2858.51	0.62	(K)EKEPEEELYDLKVVLAGGVAPALFR(G)		
						26.5	30.4	6.96E+00	790.85	2	1578.91	0.79	(R)LFFGPQHRPVILR(L)		
195	Q70J99	UNC13D	Unc-13 homolog D (Munc13-4).	51.6	2	51.6	28.9	1.79E-02	1089.78	2	2176.19	1.36	(R)LPITYPAPNGDPILQLEGR(K)	1	M / MP
196	P50552	VASP	Vasodilator-stimulated phosphoprotein (VASP)	38.2	7	38.2	31.6	4.85E-01	516.50	3	1545.77	0.74	(R)VQIYHNPTANSFR(V)	2	WP / M / MP
197	P18206	VCL	Vinculin (Metavinculin).	807.3	43	123.5	33.7	1.17E-09	1082.90	2	2163.14	0.66	(R)GILSGTSDLLLTDFDEAEVR(K)	B	WP / M / MP
						114.6	34.5	8.49E-09	1195.83	2	2389.07	0.58	(R)mQEAmTQEVSDVSDTTPIK(L)		
						101.8	27.9	1.77E-07	1038.67	2	2075.17	0.17	(K)AIPDLTAPVAQAAVSNLVR(V)		
						98.8	24.7	2.91E-07	1317.22	2	2631.32	1.12	(K)GILEYLTVAEVETmEDLVITYTK(N)		
						95.6	48.8	9.41E-07	729.77	2	1456.79	0.74	(K)AQQVSQGLDVLTA(K)		
						93.8	37.8	1.12E-06	1018.75	2	2035.05	0.44	(R)GILSGTSDLLLTDFDEAEVR(K)		
						77.6	30.7	5.46E-05	755.71	2	1508.70	0.71	(K)mLGmTDQVADLR(A)		
						77.4	60.1	6.40E-05	658.05	2	1313.73	0.36	(K)QVATALQNLTQK(T)		
						73.1	37.6	1.46E-04	615.97	3	1844.00	0.92	(R)VGKETVQTTEQILKR(D)		
						65.0	38.2	1.12E-03	652.47	2	1302.70	0.24	(K)SLDASEEA(K)		
						62.5	32.6	2.00E-03	624.61	2	1246.64	0.57	(R)EAVKAASDELSK(T)		
						61.7	37.8	2.58E-03	553.34	2	1104.60	0.08	(R)SLGEISALTSK(L)		
						60.3	47.1	4.16E-03	436.86	2	871.48	0.23	(K)GNDIAAAK(R)		
						57.5	32.4	6.42E-03	585.86	2	1169.64	0.07	(R)ELTPQVVSAR(I)		
						54.3	39.1	1.21E-02	765.53	2	1528.85	-0.58	(R)ALASQLQDSLKDL(K)		
						53.8	33.6	1.37E-02	517.50	3	1548.84	0.67	(K)AAVHLEGKIEQAQR(W)		
						53.0	50.1	1.43E-02	441.24	2	879.45	1.02	(R)TDAGFTLR(W)		
						52.3	34.1	1.61E-02	992.42	2	1981.96	0.88	(K)GWLDRPSASPGDAGEQAIR(Q)		
						52.2	36.1	2.04E-02	635.41	2	1268.67	0.15	(K)AVAGNISDPGLQK(S)		
						51.3	34.3	2.32E-02	784.16	2	1565.70	0.61	(K)AGEVINQPMmmAAR(Q)		
						50.2	30.5	3.65E-02	1173.66	1	1172.64	0.02	(R)ALASQLQDSL(K)		
						48.1	34.7	5.10E-02	592.42	2	1182.55	0.29	(R)LANVmmGPYR(Q)		
						47.3	45.4	5.93E-02	634.50	2	1266.63	0.37	(R)VmLVNSmNTVK(E)		
						44.8	37.4	1.17E-01	652.62	2	1302.68	0.55	(K)ETVREAEAAIK(I)		
						43.3	43.8	1.59E-01	575.66	2	1148.63	0.68	(K)IRTDAGFTLR(W)		
						42.9	42.9	1.92E-01	515.01	2	1027.58	0.43	(K)GNDIAAAKR(M)		
						40.7	43.7	2.40E-01	406.92	2	811.56	0.28	(R)ILLVAKR(E)		

						40.4	37.8	3.66E-01	500.94	2	999.60	0.27	(R)IPTISTQLK(I)		
						36.7	40.5	6.77E-01	562.97	2	1123.53	0.40	(K)TISPMVmDAK(A)		
198	P21796	VDAC 1	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1)	41.4	9	41.4	28.0	1.92E-01	1052.50	2	2102.17	0.83	(K)VNNSSLIGLYGTQLRPGIK(L)	2	WP / M / MP
199	P45880	VDAC 2	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)	112.3	9	112.3	42.6	1.56E-08	1052.25	2	2102.15	0.34	(K)VNNSSLIGVGYTQLRPGVK(L)	2	WP / M / MP
200	Q9Y277	VDAC 3	Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3)	97.7	11	97.7	57.4	4.46E-07	1051.46	2	2100.17	0.74	(K)VNNASLIGLYGTQLRPGVK(L)	B	M / MP
201	P04275	VWF	Von Willebrand factor precursor (VWF) [Contains: Von Willebrand antigen]	72.7	2	72.7	28.2	1.44E-04	1040.84	2	2079.12	0.55	(R)IGWPNAPILIQDFETLPR(E)	1	MP
202	O75083	WDR1	WD-repeat protein 1 (Actin interacting protein 1) (AIP1) (NORI-1).	181.2	22	77.1	28.8	6.05E-05	769.62	2	1536.84	0.39	(R)LYSILGTTLKDEGK(L)	B	WP / M / MP
						67.2	27.5	4.54E-04	1210.00	2	2417.23	0.77	(R)NIDNPALADIYTEHAHQVVAK(Y)		
						66.4	22.4	5.23E-04	1270.95	2	2539.21	0.69	(K)VVTVFSVADGYSENNVFYGHAK(I)		
						51.6	33.6	2.36E-02	731.07	2	1460.76	-0.62	(K)IKDIAWTEDSKR(I)		
						40.2	37.8	4.11E-01	800.57	1	799.46	0.11	(R)IAVVGEGR(E)		
203	Q15942	ZYG	Zyxin (Zyxin 2).	143.5	12	83.2	50.4	1.59E-05	758.49	2	1514.71	0.27	(K)FSPGAPGGSGSQPNQK(L)	B	WP / MP
						61.3	21.6	1.61E-03	1299.36	2	2596.27	0.44	(K)ILGHPEALSAGTGSPPPSFTYAQR(E)		
						60.0	39.4	3.10E-03	519.52	2	1036.59	0.45	(R)SPGAPGLTLK(E)		

A Protein accession numbers were from the Uniprot database, <http://www.ebi.uniprot.org/index.shtml>.

B Gene Name were from GOSlim, <http://geneontology.org>.

C Proteins listed alphabetically according to their description, derived from GOSlim.

D Protein Score, calculated according to Equation 2 (*Experimental Procedures*).

E Sequence Coverage, the sequence coverage expressed as a percentage of the intact protein.

F Mascot™ peptide Ions score (The reported score is  $-10\log(P)$ , <http://www.matrixscience.com/>).

G Mascot™ Homology score (<http://www.matrixscience.com/>).

H Mascot™ expectation score (a value of 1 indicates that 1 other protein could correspond to the same score based on random matching) (<http://www.matrixscience.com/>).

I The observed precursor mass to charge.

J The observed peptide charge state.

K The calculated molecular mass of each peptide.

L Delta peptide mass (difference between calculated and observed peptide mass).

M Identified peptides for each inferred protein. Note: an acetylated N-terminus is indicated by (\$), and *m* indicates methionine-sulfoxide.

N Indicates whether proteins identified in either platelet preparation 1, 2 or in both (B) (*Experimental Procedures*).

O Comparison of proteins described previously in either the whole-platelet (O'Neill *et al.*, 2002, Garcia *et al.*, 2004) (WP), the platelet membrane proteome (Moebius *et al.*, 2005) (M), the transmembrane platelet study (Senis *et al.*, 2007) (SEN), or the platelet microparticle proteome (Garcia *et al.*, 2005) (MP). References included in main text.

Proteins validated based solely on manual verification are shaded.