Table S2. Phosphotyrosine sites from the Src-transformed mouse embryo fibroblast population

Protein Name(s)[a]	UniProt #[a]	Peptide[b]	pY site(s)[b]	Novel[c] Yes/No	Com or Uncom[d]	Rounds found[e]	Total IDs[f]	Site count[f]	XCorr[g]	z[g]
SIGNALING: PROTEIN KINASES AND PHOSPHATASES										
Tyrosine kinases (nonreceptor)										
Rous sarcoma oncogene, isoform 2 -- Src (Yes) (Fyn)	Q80XU2	F.VALY@DYESRTETDL.S	Y92	Y	U	11,12,13,14,16,17,18	8	37	4.12	2
		F.VALY@DYESRTETDLSF.K	Y92			11	11		4.23	2
		R.AGPLAGGVTTFVALY@DYESR.T	Y92			1,3,4,5,8,9	18		5.88	2
		R.TQFNSLQQLVAY@YSK.H	Y231	Y	U	1,7	2	2	4.37	2
		L.IEDNEY@TARQGAKFPIKW.T	Y418	N	C	11,12,14,15,16,17,18	7	27	4.68	3
		R.LIEDNEY@TAR.Q	Y418			1,2,3,4,5,6,7,8,9,10	20		3.58	2
		K.FPIKWTAPEAALY@GR.F	Y438	Y	U	1,2,3,9	4	21	4.43	3
							3		4.19	2
		K.WTAPEAALY@GR.F	Y438			1,2,3,4,5,6,7,9,10	9		2.72	2
		W.TAPEAALY@GRF.T	Y438			11,12,14,16	5		3.01	2
Proto-oncogene tyrosine-protein kinase LCK	P06240	F.GLARLIEDNEY@TAREGAKFPIKW.T	Y393	N	U	12	1	4	2.79	3
		F.GLARLIEDNEY@TAREGAKF.P	Y393			14	1		3.36	3
		R.LIEDNEY@TAREGAKFPIKW.T	Y393			11,17	2		4.15	3
Tyrosine-protein kinase CSK	P41241	L.IKPKVMEGTVAAQDEFY@RSGW.A	Y184	N	U	12	1	1	4.02	3
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	N*	C	2	1	1	4.58	3
		F.GMSRQEDGGVY@SSSGL.K	Y715	N	C	11	1	1	3.44	2
Proto-oncogene tyrosine-protein kinase ABL1	P00520	R.LMTGDTY@TAHAGAK.F	Y393	N	C	1,2,3	3	3	3.56	2
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	R.YM#EDSTY@YK.A	Y576	N	C	3,8	2	17	3.02	2
		R.YMEDSTY@YK.A	Y576			2,5,6,7,8,9,10	9		3.11	2
		R.YMEDSTY@YKASK.G	Y576			2,3	2		3.96	2
		R.YMEDSTY@Y@K.A	Y576,Y577	N	C	9,10	2	4	2.79	2
		R.YMEDSTY@Y@KASK.G	Y576,Y577			9,10	2		3.72	2
Tyrosine kinases (receptor)										
Discoidin domain receptor 2 precursor -- DDR2	Q62371	F.GMSRNLY@SGDY@Y.R	Y735,Y739	N	C	11,12	2	4	3.65	2
		R.NLY@S@GDYYR.I	Y735	N	C	2	1	5	1.85	2
		R.NLY@SGDY@YR.I	Y735,Y739			4,9	2		2.30	2
Ephrin type-A receptor 2 precursor	Q03145	K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	N	C	1	1	1	3.36	3
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	N	C	12	1	1	3.31	3
Eph receptor B4	Q91YM0	Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596	N,N	C,C	12	1	1,1	4.75	3
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	K.IYNGDY@YR.Q	Y696	N*	C	9	1	3	2.43	2
		K.KIYNGDY@YR.Q	Y696			2,3	2		2.73	2
Other protein kinases										
Akt1: RAC-alpha serine/threonine-protein kinase (Akt-2) (Akt-3)	P31750	K.TFC*GTPEYLAPEVLEDNDY@GR.A	Y326	N	U	6	1	1	4.24	3
Akt-3: RAC-gamma serine/threonine-protein kinase	Q9WUA6	K.Y@Y@AM#KILKKEVIIAK.D	Y173,Y174	N*,N*	U,U	7	1	1,1	2.99	2
Calcium/calmodulin-dependent protein kinase type 1 --CaM kinase I	Q91YS8	R.DLKPENLLYY@SLDEDSK.I	Y150	Y	U	2	1	2	4.19	3
							1		3.69	2
Casein kinase I isoform alpha	Q8BK63	R.TLNHQYDY@TFDWTMLK.Q	Y294	N*	U	1,9	1	2	3.71	2
							1		4.35	3
Casein kinase II, alpha chain	Q60737	K.VLGTEDLY@DYIDKYNIELDPR.F	Y255	N	U	8	1	1	3.60	3
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IGEGTY@GVVYK.G	Y15	N	C	1,2,3,4,7,8,9,10	8	9	3.15	2
		K.IGEGT^Y@GVVYK.G	Y15			7	1		2.33	2
		K.IGEGTYGVVY@K.G	Y19	N	C	4	1	2	2.39	2
		K.IGEGTYGVVY@KGR.H	Y19			2	1		2.28	2
Dual-specificity tyrosine-phosphorylation regulated kinase 1A --DYRK1A (DYRK1B)	Q61214	K.HINEVY@YAK.K	Y111	N*	U	1,2,3	3	3	2.58	2
		K.VYNDGYDDDNY@DYIVK.N	Y145	N	C	7	1	7	4.47	2
		R.KVYNDGYDDDNY@DYIVK.N	Y145			6,7,8,10	4		5.48	2

		Y.NDGYDDDNY@DYIVKNGEKW.M	Y145			15,16	2		4.49	3
		R.IYQY@IQSR.F	Y321	N	C	1	1	1	2.17	2
Glycogen synthase kinase-3 beta -- GSK-3 beta (GSK-3 alpha)	Q9WV60	L.VRGEPNVSY@IC*SRY.Y	Y216	N	C	17	1	5	3.56	3
		L.VRGEPNVSY@IC*SRYY.R	Y216			11,12	1		3.53	3
							1		3.96	2
		R.GEPNVSY@IC*SR.Y	Y216			3,8	2		3.32	2
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638	N	C	1,2,3,4,5,7,8	7	13	5.43	3
							1		4.67	2
		K.VPIVINPNAY@DNLAIY@K.S	Y632,Y638			2,5	2		2.76	2
		K.VPIVINPNAYDNLAIY@K.S	Y638	N	C	2	1	14	1.97	2
		N.AIKVPIVINPNAY@DNLAIY@KSF.L	Y632,Y638			11,14,17	3		5.35	3
Serine/threonine-protein kinase Nek9	Q8K1R7	R.NKEVYSWGC*GEY@GR.L	Y509	Y	U	2,4	1	3	3.43	2
							2		5.16	3
Serine/threonine-protein kinase PRP4 homolog	Q61136	K.LC*DFGSASHVADNDITPY@LVSR.F	Y849	N	C	1,2,3,6,9	5	6	5.91	3
		H.VADNDITPY@LVSRF.Y	Y849			14	1		3.10	2
Protein phosphatases										
Low molecular weight phosphotyrosine protein phosphatase	Q9D358	K.QLIIEDPY@YGNDSDFEVVYQQC*LR.C	Y131	N	U	4,5	3	5	4.80	3
		L.GSYDPQKQLIIEDPY@YGNDSDF.E	Y131			15,18	2		4.50	2
		K.QLIIEDPYY@GNDSDFEVVYQQC*LR.C	Y132	N	U	4,5	2	3	3.89	3
							1		2.37	2
14 kDa phosphohistidine phosphatase -- Phosphohistidine phosphatase 1	Q9DAK9	R.KIHVYGY@SM#GYGR.A	Y92	N*	U	2,5	2	2	4.26	3
Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	R.TYDETY@TR.Y	Y764	N	U	1,10	2	7	2.27	2
		Y.SRTYDETY@TRY.R	Y764			11,15,16,17,18	5		3.47	2
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	N*	C	1,3	2	2	3.23	2
Serine/threonine protein phosphatase 2A, catalytic subunit, alpha isoform -- PP2A alpha (PP2A beta)	P63330	R.QITQVY@GFYDEC*LR.K	Y127	Y	U	1,2,3,7,9	5	5	3.60	2
		R.C*GNQAAIMELDDTLKY@SFLQFDPAPR.R	Y284	N*	U	3	1	1	3.10	3
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	N	C	11,12,13,14,15,16,17,18	8	16	3.55	2
		K.IQNTGDY@YDLYGGEK.F	Y62			1,2,3,4,5,7	8		4.69	2
Tyrosine-protein phosphatase, non-receptor type 14	Q62130	R.NLNIINTHAYNQPEELVY@SQPEMR.E	Y485	Y	U	1,3,5,6,7,9	6	6	5.64	3
SIGNALING: SMALL G PROTEINS AND REGULATORS										
ARF GTPase-activating protein GIT1	Q68FF6	F.HSTELEDDAIY@SVHVPAGLY.R	Y554	N	C	11,12,13,14,15,16,17,18	8	40	5.00	2
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554			2,7	2		4.57	3
		R.LQPFHST@ELEDDAIY@SVHVPAGLYR.I	Y554			8	1		4.68	3
		R.LQPFHSTELEDDAIY@SVHVPAGLY@R.I	Y554,Y563	N	U	1,2,3,4,5,6,7,8,9,10	10	10	5.61	3
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554			1,2,3,4,5,6,8,9,10	16		6.32	3
		R.LQPFHS^TELEDDAIY@SVHVPAGLYR.I	Y554			2,8,9	3		4.06	3
Engulfment and cell motility protein 2 -- ELMO2	Q8BHL5	K.EVC*DGWSLPNPEY@YTLR.Y	Y48	N	U	2	1	1	3.09	2
Glucocorticoid receptor DNA binding factor 1 [fragment] -- p190RhoGAP	Q91YM2	R.NEEENIY@SVPHDSTQGK.I	Y943	N	C	1,2,3,4,5,6,7,8,9,10	10	20	3.38	3
							10		5.09	2
Myosin phosphatase Rho-interacting protein -- MRIP	P97434	K.VRVESGY@FSLEK.A	Y268	N*	U	1,2,4,5	5	6	3.59	2
							1		4.04	3
		K.YASDKYKDIY@TELSIAK.A	Y944	N*	U	4,5	2	2	4.01	3
Rab GDP dissociation inhibitor alpha -- Rab GDI alpha (Rab GDI beta)	P50396	K.VLHMDRNPY@YGGESSSITPLEELYK.R	Y38	N*	U	3,9	2	2	5.00	3
		K.SPYLYPLY@GLGELPQGFAR.L	Y229	N*	U	10	1	1	3.60	2
Rab GDP dissociation inhibitor beta -- Rab GDI beta	Q61598	K.KVLHMDQNPY@YGGESASITPLEDLYK.R	Y38	Y	U	1,3,5,6,7,9	6	31	5.77	3
		K.KVLHMDQNPY@YGGESASITPLEDLYKR.F	Y38			1,2,3,4,5	5		6.08	3
		K.VLHM#DQNPY@YGGESASITPLEDLYKR.F	Y38			2,6,8	3		5.39	3
		K.VLHMDQNPY@YGGESASITPLEDLYK.R	Y38			1,4,7,8,9,10	6		4.99	3
		K.VLHMDQNPY@YGGESASITPLEDLYKR.F	Y38			1,2,3,4,5,6,7,9,10	10		6.58	3
		L.HMDQNPY@YGGESASITPLEDLY.K	Y38			11	1		4.62	2
		K.KVLHMDQNPYY@GGESASITPLEDLYKR.F	Y39	Y	U	7	1	5	5.63	3
		K.VLHM#DQNPYY@GGESASITPLEDLYKR.F	Y39			3	1		5.54	3
		K.VLHMDQNPYY@GGESASITPLEDLYK.R	Y39			3,5,6	3		4.22	3

Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	L.RSPDVGLY@GVIPEC*GETY.Q	Y654	N*	U	11,14	2	4	4.09	2
		L.SALRSPDVGLY@GVIPEC*GETY.Q	Y654			11,16	2		4.84	2
		L.VKLQQTY@SAL.N	Y1510	N	C	12	1	1	2.36	2
Ras and Rab interactor 1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	N	C	1,2,3,10	3	4	2.61	2
							1		2.84	3
Rho-GTPase-activating protein 12	Q8C0D4	R.AT@TPPNQGRPDS@PVY@ANLQELK.I	Y241	N	C	9	1	3	2.78	3
		R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241			2,4	2		3.82	3
Rho/rac guanine nucleotide exchange factor (GEF) 2 -- ARHGEF2	Q923E0	R.RRS@LPAGDALY@LSFNPPQPSR.G	Y893	N*	U	2	1	3	3.75	3
		R.SLPAGDALY@LSFNPPQPSR.G	Y893			2,4	2		3.09	2
TBC1 domain family member 15	Q9CXF4	K.SLSQSFENLLDEPAY@GLIQK.I	Y215	N	U	8	1	1	4.90	2
SIGNALING: OTHER										
53BP2: Apoptosis stimulating of p53 protein 2 [fragment]	Q8CG79	R.KPQTVAASSIY@SMYTQQQAPGK.N	Y569	N*	U	2,9	2	2	4.37	3
Ankyrin repeat and SAM domain containing protein 1 -- ANKS1	P59672	L.ILHFDTHADEEGPY@EALY.N	Y377	Y	U	16,17	2	2	3.06	2
		L.AVRPRIQSSAPQEEEEHPY@EL.L	Y471	N*	C	12,15,18	3	7	3.75	3
		L.AVRPRIQSSAPQEEEEHPY@ELL.L	Y471			15	1		3.96	3
		R.IQSSAPQEEEEHPY@ELLLTAETK.K	Y471			2	1		3.41	3
		R.IQSSAPQEEEEHPY@ELLLTAETKK.L	Y471			2,3	2		3.92	3
Annexin A1	P10107	R.ALY@EAGER.R	Y206	N*	U	1	1	2	2.23	2
		R.ALY@EAGERR.K	Y206			4	1		2.22	2
Annexin A2	P07356	C.KLSLEGDHSTPPSAY@GSVKPY.T	Y23	N	C	12	1	17	3.56	3
		K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D	Y23			1,2,4,5,8,9	6		5.43	3
		L.SLEGDHSTPPSAY@GSVKPY.T	Y23			11,12,13,14,16,18	4		3.87	3
							6		4.45	2
		K.SYSPY@DMLESIK.K	Y237	N	U	10	1	10	2.60	2
		K.SYSPY@DMLESIKK.E	Y237			1,2,4,5,7,8,9,10	9		3.71	2
		F.ADRLY@DSM.K	Y274	N*	U	11	1	14	1.94	2
		L.YFADRLY@DSM#.K	Y274			11,17,18	4		3.16	2
		L.YFADRLY@DSM.K	Y274			11,12,15,16,17,18	6		3.00	2
		Y.FADRLY@DSM.K	Y274			11,16,18	3		2.27	2
		K.SLY@YYIQQDTK.G	Y315	N*	U	6,7,9,10	4	6	3.70	2
		K.SLYY@YIQQDTK.G	Y316	N*	U	2,4,7,9,10	5	7	4.05	2
		K.SLY@Y@YIQQDTK.G	Y315,Y316			1,2	2		3.46	2
Annexin A5	P48036	R.SIPAYLAETLY@YAMK.G	Y254	N*	U	8	1	1	2.72	2
		K.NFATSLY@SMIK.G	Y295	N*	U	7	1	1	2.53	2
Annexin A6	P14824	R.GSVHDFPEFDANQDAEALY@TAM#K.G	Y29	N*	U	9	1	21	4.38	3
		R.GSVHDFPEFDANQDAEALY@TAMK.G	Y29			1,2,6,7,8,9,10	8		5.59	3
							3		5.47	2
		Y.RGSVHDFPEFDANQDAEALY@TAM#.K	Y29			15,17	2		4.32	3
		Y.RGSVHDFPEFDANQDAEALY@TAM.K	Y29			11,12,15,16,17	2		3.81	2
							5		3.99	3
Annexin A11	P97384	K.TPVLFDVY@EIKEAIK.G	Y277	N*	U	1,2,6,7,8	5	6	4.29	3
							1		3.49	2
Cell division cycle and apoptosis regulator protein 1 -- CARP1	Q8CH18	R.VLVEATY@NPNMPFK.W	Y189	N	U	2,3,4,5	4	5	4.23	2
		R.VLVEATY@NPNMPFKWNAQR.I	Y189			5	1		3.16	3
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	N	C	1,2,3,4,5,6	6	6	3.75	2
Proto-oncogene c-Crk	Q64010	Q.KRVPNAY@DKTAL.A	Y251	N*	C	11	1	1	2.60	3
Cyclin-dependent kinases regulatory subunit 2	P56390	Y.SDKYFDEHY@EY.R	Y17	Y	U	11,12,17,18	4	5	3.30	2
		Y.YSDKYFDEHY@EY.R	Y17			17	1		2.67	2
Docking protein 1 --Dok1	P97465	K.TVPPPVPQDPLGSPPALY@AEPLDSLR.I	Y295	N	U	2	1	1	2.60	3
		R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K	Y314	N	C	1,2,4,5,6,7,8,9,10	9	9	4.62	3
		K.KPLY@WDLY@GHVQQQLLK.T	Y336,Y340	N	U	3,4	2	2	3.06	3
		K.KPLYWDLY@GHVQQQLLK.T	Y340	N	C	1,2,3,5,8,10	8	10	5.06	3
		K.LTDSKEDPIY@DEPEGLAPAPPR.G	Y361	N	C	1,2,3,4,5,6,7,8	8	34	3.94	3
							3		4.36	2
		K.TKLTDSKEDPIY@DEPEGLAPAPPR.G	Y361			1,2,3,4,5,6,8,9,10	14		5.25	3
		K.TKLTDS^KEDPIY@DEPEGLAPAPPRGLYDLPQEPR.D	Y361			3	1		3.41	3
		L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361			12,18	2		3.79	3
		L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361			11	1		5.15	3
		K.LTDSKEDPIY@DEPEGLAPAPPRGLY@DLPQEPR.D	Y361,Y376			1,2,3,4,5	5		4.46	3
		K.LTDS^KEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D	Y376	N	U	5	1	6	3.33	3
		R.LKEEGY@ELPY@NPATDDYAVPPPR.S	Y397,Y401	N	U	4	1	3	2.88	3

		R.LKEEGYELPY@NPAT@DDYAVPPPR.S	Y401	N	U	1,2	2	13	3.30	3
		R.LKEEGYELPY@NPATDDYAVPPPR.S	Y401			6	1		2.68	3
		R.LKEEGYELPYNPATDDY@AVPPPR.S	Y408	N	C	2	1	12	2.92	3
		R.LKEEGY@ELPYNPATDDY@AVPPPR.S	Y397,Y408			4,7	2		3.21	3
		R.LKEEGYELPY@NPATDDY@AVPPPR.S	Y401,Y408			3,4,5,6,7,9,10	8		3.59	3
		R.LKEEGYELPY@NPATDDY@AVPPPRS@PK.P	Y401,Y408			2	1		3.66	3
		F.SSDTALY@SQVQKSGTSGAW.D	Y450	N	C	11,12	2	7	5.11	2
		K.GFSSDTALY@SQVQK.S	Y450			1,2,3,4,5	5		4.89	2
Epidermal growth factor receptor kinase substrate 8 -- EPS8	Q08509	R.LSTEHSNVSDY@PPADGYAYSSSMYHR.G	Y484	N	U	2,7,9,10	4	4	3.92	3
Hepatocyte growth factor-regulated tyrosine kinase substrate -- HGS/ Hrs	Q99LI8	R.VC*EPC*Y@EQLNK.K	Y216	N	U	1,2,3,7,10	5	5	3.55	2
Insulin receptor substrate 1 -- IRS-1	P35569	R.AASEAGGPARLEY@YENEKK.W	Y46	N	U	2	1	1	3.34	3
Insulin receptor substrate 2 -- IRS-2	P81122	K.VAYNPYPEDY@GDIEIGSHK.S	Y628	N*	U	2,4	2	2	2.58	3
Kin of IRRE-like protein 1 precursor -- KIRREL	Q80W68	R.C*DTIDTREEY@EMKDPTNGY@YNVR.A	Y628,Y637	N*	U	1	1	1	3.51	3
		R.C*DTIDT@REEYEMKDPTNGY@YNVR.A	Y637	N*	C	2	1	4	4.29	3
		R.EEYEMKDPTNGY@YNVR.A	Y637			1,2	2		3.07	3
		Y.RLGYPQAPPSGLERTPY@EAY@DPIGKY.A	Y753,Y756	N*,N	C,C	11,16	2	2,2	3.95	3
Latrophilin-2	Q8JZZ7	R.SENEDIY@YK.S	Y838	N*	U	2	1	1	2.05	2
		R.GNSDGY@IIPINK.E	Y865	N*	U	1	1	1	2.06	2
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.PSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	N	C	2,10	2	9	3.65	3
		K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105			5,10	2		4.81	3
		K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105			4	1		4.70	3
		R.KPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105			1,3,4,5	4		4.88	3
Notchless homolog 1	Q8VEJ4	K.LATDLPGHADEVY@AVDWSPDGQR.V	Y459	Y	U	1,3,4	3	3	4.36	3
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85 alpha	P26450	K.SREYDRLY@EEYTR.T	Y467	N	C	2,3,6,8,9,10	6	6	4.07	3
		K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y607	N	C	1,2,4,9	4	4	5.67	3
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85 beta	O08908	R.EYDQLY@EEYTR.T	Y458	N	C	1,10	2	2	2.82	2
Phospholipase C, gamma 1	Q6P1G1	K.IGTAEPDY@GALY@EGRNPGFYVEANPMPTFK.C	Y771,Y775	N	U	9	1	1	3.70	3
		K.IGTAEPDYGALY@EGRNPGFY@VEANPMPTFK.C	Y775,Y783	N	U	2,10	3	3	5.26	3
		K.IGTAEPDYGALY@EGRNPGFYVEANPMPTFK.C	Y775	N	U	1,2,10	3	7	5.18	3
Protein Wnt-2b precursor	O70283	K.GTDGC*EIMCCGRGY@DTTR.V	Y342	N*	U	3	1	1	2.85	2
Guanine nucleotide-binding protein beta subunit 2-like 1 -- RACK1	P68040	K.HLY@TLDGGDIINALC*FSPNR.Y	Y227	N	U	7,8,10	2	7	3.88	3
							1		5.57	2
		L.WDLNEGKHLY@TLDGGDIINAL.C	Y227			11	1		3.29	2
		W.DLNEGKHLY@TLDGGDIINAL.C	Y227			11,12	2		4.41	2
		W.DLNEGKHLY@TLDGGDIINALC*F.S	Y227			17	1		3.14	3
Retinoic acid-induced protein 3	Q8BHL4	F.SIPRAQAPASPY@NDY@EGRKGDS.-	Y346,Y349	N	U	11,12	2	2	4.84	3
		F.SIPRAQAPASPY@NDYEGRKGDS^.-	Y346	N	U	11	1	3	2.84	3
SH2 domain-containing adapter protein B -- SHB	Q6PD21	R.DFEDPY@NGPGSSLR.K	Y95	Y	U	2,4	3	3	3.52	2
SHC transforming protein 1 -- SHC1	P98083	R.ELFDDPSY@VNIQNLDK.A	Y423	N	C	1,2,3,4,6,7,9,10	8	8	5.21	2
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM#R.L	Y349,Y350	N	C	8	1	9	3.98	3
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L	Y349,Y350	N	C	1,3,8,9,10	7	9	4.82	3
		F.DGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM.R	Y349,Y350			16	1		4.98	3
SHC SH2 domain-binding protein 1	Q9Z179	R.SWDEEEEDEY@DYFVR.C	Y217	N*	U	6,7,9,10	4	4	5.15	2
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	R.FSEEEISFPPTY@RYER.G	Y662	N*	U	6,8	2	2	2.88	3
		K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y987	N	C	3,4,5,7,8,9,10	9	9	5.83	3
Sorbin and SH3 domain-containing protein 1 -- SORBS1	Q62417	K.TPVDYIDLPY@SSSPSR.S	Y1198	N	U	2,4,7,8	4	4	4.82	2
Signal transducing adapter molecule 2 -- STAM-2	O88811	K.LVNEAPVY@SVYS@K.L	Y371	N	U	2	1	6	2.89	2
		K.LVNEAPVY@SVYSK.L	Y371			1,2,4,7	4		3.25	2
		Y.NKLVNEAPVY@SVY.S	Y371			15	1		2.45	2
Signal transducer and activator of transcription 3 - STAT3	P42227	R.QFLAPWIESQDWAY@AASK.E	Y45	N*	U	1	1	1	3.81	2
		K.YC*RPESQEHPEADPGSAAPY@LK.T	Y705	N	C	7	1	1	2.97	3

STRAP: serine/threonine kinase receptor associated protein	Q8BP89	K.IGFPETAEEELEEIASENSDSIY@SSTPEVK.A	Y342	Y	U	4,8	2	4	4.01	3
		K.IGFPETAEEELEEIASENSDSIY@SSTPEVKA.-	Y342			8,10	2		4.58	3
Striatin	O55106	K.STSLDVEPIY@TFR.A	Y510	Y	U	3,7,8,9	4	5	3.80	2
		W.NLQKTAPAKKSTSLDVEPIY@TF.R	Y510			15	1		2.91	3
Striatin-3	Q9ERG2	K.SASLDVEPIY@TFR.A	Y526	N*	U	1,2,4,5,6,7,8,9,10	10	10	3.72	2
hypothetical SH3/Phox-like/Src homology 3 (SH3) domain profile/Proline-rich region profile/PX domain profile containing protein -- TKS4	Q3TB89	R.VTWSSGATEAIY@R.R	Y42	Y	U	2,4	2	2	2.77	2
		K.TEPAQSEDHVDIY@NLR.S	Y661	N	U	1,2,3,7,8,9,10	7	7	4.82	2
ADHESION: CELL/ECM										
Bystin	O54825	R.GREVEEEEEY@VGPR.L	Y48	Y	U	2,7	2	3	4.15	2
CRK-associated substrate -- p130cas	Q61140	-.MTVPNVLAKALY@DNVAESPDELSFR.K	Y12	Y	U	1	1	3	3.33	3
		K.ALY@DNVAESPDELSFR.K	Y12			1,10	2		5.05	2
		Y.VYEAAQTEQDEY@DTPRHL.L	Y238	N	C	17	1	1	3.87	3
		R.HLLAPGPQDIY@DVPPVR.G	Y253	N	C	1,2,3,4,5,7	5	10	3.43	3
							5		4.37	2
		R.GLLPNQYGQEVY@DTPPMAVK.G	Y271	N*	C	2,4,7,8	2	6	3.34	3
							4		4.07	2
		K.GPNGRDPLLDVY@DVPPSVEK.G	Y291	N*	C	2,5	2	2	4.38	3
		K.GLLSSSHHSVY@DVPPSVSK.D	Y310	N	C	2	1	1	3.76	3
		R.RPGPGTLY@DVPR.E	Y391	N	C	2	1	2	2.05	2
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	N	C	1,2,3,4,6,7,8,9,10	18	19	4.98	2
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414			9	1		3.32	3
		L.SRQLQKMEDVY@QTL.V	Y556	Y	C	11,12	2	2	3.06	2
Lipoma-preferred partner homolog -- LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	N	C	11,12,13	4	10	4.67	2
		Y.MAGPSSGQIY@GPGPRGY.N	Y245			11,12,14	3		3.93	2
							1		4.47	3
		M.AGPSSGQIY@GPGPRGY.N	Y245			11,12	2		3.39	2
		R.YYEPY@YAAGPSYGGR.S	Y301	N	C	1,2,3,4,5,6,7,8,9,10	1	16	3.14	3
							13		4.44	2
		Y.TSNQGRYYEPY@YAAGPSY.G	Y301			11	1		5.02	2
		R.YYEPY@Y@AAGPSYGGR.S	Y301,Y302			7	1		3.35	2
		R.YYEPYY@AAGPSYGGR.S	Y302	N	C	1,2,3,4,5,6,7,8,9,10	2	15	3.80	3
							12		4.83	2
		K.KMLY@DMENPPADDYFGR.C	Y403	Y	U	1,2,4	1	6	3.33	3
							2		5.85	2
		K.MLY@DMENPPADDYFGR.C	Y403			1,2,4	3		5.63	2
		K.KMLYDMENPPADDY@FGR.C	Y413	Y	U	1,2,4	3	8	3.73	3
							1		4.01	2
		K.MLYDMENPPADDY@FGR.C	Y413			1,2,4,9	4		5.51	2
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	N	C	11,14	2	2	3.82	2
		R.AGEEEHVY@SFPNK.Q	Y118	N	C	1,2,7,8,10	2	18	3.65	3
							5		4.40	2
		R.AGEEEHVY@SFPNKQK.S	Y118			1,2,3,4,5,6,9,10	11		4.44	3
Syndecan-4 precursor	O35988	Y.KKAPTNEFY@A.-	Y197	N*	C	11	1	1	2.04	2
Talin 1	P26039	K.TM#QFEPSTMVY@DAC*R.M	Y26	N*	C	3,5	2	11	5.10	2
		K.TMQFEPSTMVY@DAC*R.M	Y26			1,2,3,4,5,9,10	1		2.64	3
							7		5.00	2
		M.QFEPSTMVY@DAC*RM.I	Y26			12	1		2.79	2
		K.ALDY@YM#LR.N	Y70	N	C	3,5,6	3	9	2.34	2
		K.ALDY@YMLR.N	Y70			2,3,4,6,7	6		2.81	2
		K.ALDYY@MLR.N	Y71	N*	U	1	1	1	1.93	2
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	N	C	1,2,3	3	3	4.83	2
		K.TLAESALQLLY@TAK.E	Y1777	N*	U	1,2,3,7,8,10	6	6	4.32	2
Tensin 2	Q8CJ95	R.YGHSGYPALVTY@GYGGAVPSYC*PAYGR.A	Y766	Y	U	2,6,8,9,10	5	5	4.10	3
Tensin 3	Q5SSZ5	K.LYQAMQPVYTSGIY@NVGSENPSR.I	Y216	Y	U	2,3,4	3	4	5.70	3
							1		4.55	2
		L.HTQGPVDGSLY@AKVR.K	Y354	N	C	11,12	2	2	4.93	3
		R.KPSAPTPVQAY@GQSNY@STQTWVR.Q	Y579,Y584	N*	U	1,4,8	3	3	3.91	3
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	N*	C	2,3	2	5	5.61	3
Vinculin	Q64727	K.LVQAAQMLQSDPY@SVPAR.D	Y99	N	U	1,2	1	12	3.52	3
							2		3.82	2
		K.LVQAAQMLQSDPY@SVPARDYLIDGSR.G	Y99			2,3,5,6,7,10	6		5.28	3
		L.QSDPY@SVPARDY.L	Y99			11	1		1.98	2
		Q.MLQSDPY@SVPARDY.L	Y99			11,12	2		3.99	2
		R.ILLRNPGNQAAY@EHFETMK.N	Y691	N*	C	3	1	1	6.07	3
ADHESION: CELL/CELL										

Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M	Y96	N	C	1,2,3,4,5,7,8,9,10	12	15	4.05	3
							3		4.13	2
		R.HYEDGYPGGSDNY@GSLSR.V	Y228	N	C	3,8,9,10	4	4	4.31	3
		R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R	Y291,Y296	N	C	10	1	1	5.27	3
		R.FHPEPYGLEDDQRS@MGYDDLDY@GMMS@DYGTAR.R	Y296	N	C	10	1	5	5.48	3
		R.FHPEPYGLEDDQRS^MGYDDLDY@GMMS@DYGTAR.R	Y296			10	1		4.99	3
		R.FHPEPYGLEDDQRS^MGYDDLDY@GMMSDYGTAR.R	Y296			10	1		4.72	3
		R.SMGYDDLDY@GMMSDYGTAR.R	Y296			10	1		5.25	2
		R.SMGYDDLDYGMMSDY@GTAR.R	Y302	N	U	10	1	1	5.24	2
		R.SYEDMIGEEVPPDQY@YWAPLAQHER.G	Y334	N	U	1,2	2	2	4.04	3
		R.SYEDMIGEEVPPDQYY@WAPLAQHER.G	Y335	N*	U	9,10	2	2	3.84	3
Plakophilin-4	Q68FH0	R.TVHDMDQFGQQQY@DIY@ER.M	Y368,Y371	N*	U	3,4,5	3	3	3.90	3
		R.TVHDMDQFGQQQYDIY@ER.M	Y371	N*	C	3	1	4	2.52	3
		L.RSAVSPDLHITPIY@EGRT@YY.S	Y414	N	C	17	1	10	4.56	3
		R.SAVSPDLHITPIY@EGRT@YYSPVYR.S	Y414			3,4,5,6,7,8,9,10	8		5.37	3
		R.SAVS^PDLHITPIY@EGRTYYSPVYR.S	Y414			9	1		2.67	3
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	N	C	1	1	1	2.44	2
Tight junction protein ZO-1	P39447	R.LSYLSAPGSEY@SMYSTDSR.H	Y830	N*	C	2	1	1	4.27	2
		R.HEEQPAPAY@EVHNR.Y	Y1164	N	C	1,2,3,4,5,6,7,9,10	9	10	4.49	3
		L.RHEEQPAPAY@EVHNRY.R	Y1164			11	1		3.74	3
		R.YRPEAQPY@SSTGPK.S	Y1177	N	U	1,2,3,4,5,10	6	7	3.18	2
		Y.RPEAQPY@SSTGPKSSEPKQY.F	Y1177			14	1		3.15	3
		R.SNHY@DPEEDEEYYRK.Q	Y1345	Y	U	1,2,3,4,7	5	5	4.98	3
		R.SNHYDPEEDEEY@YR.K	Y1353	N*	U	7	1	8	2.98	3
		R.SNHYDPEEDEEY@YRK.Q	Y1353			2,4,6,7,8,9,10	7		5.01	3
Tight junction protein ZO-2	Q9Z0U1	R.SYHEAY@EPDY@GGGYSPSYDRR.A	Y230, Y234			6,7	2		4.09	3
		R.SYHEAY@EPDYGGGY@SPSYDRR.A	Y230, Y238	N*	U	10	1	1	4.05	3
		R.SYHEAY@EPDYGGGYSPSYDRR.A	Y230	Y	U	2,9	2	5	4.47	3
		R.SYHEAYEPDY@GGGYSPSYDRR.A	Y234	N*	U	3,8,10	3	5	4.57	3
		R.VFLRPSPEDEAIY@GPNTK.M	Y486	N*	U	2	1	2	3.93	2
		F.LRPSPEDEAIY@GPNTKMVRF.K	Y486			11	1		4.30	3
		R.GLVREDAVLY@LLEIPKGETVTILAQSR.A	Y554	N	U	5	1	1	4.67	3
		R.IEIAQKHPDIY@AVPIK.A	Y1095	N	C	2	1	1	3.32	3

CYTOSKELETON: ACTIN-ASSOCIATED

Actins and actin-related proteins; Regulators of actin assembly

Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	M.VGMGQKDSY@VGDEAQSKRGIL.T	Y55	N	C	12	1	1	4.38	3
		K.IWHHTFY@NELR.V	Y93	N	C	1,2,3,4,6,8,9,10	11	12	3.35	3
							1		2.91	2
		K.EKLC*Y@VALDFENEM#ATAASSSSLEK.S	Y220	N	U	1,4,8,10	4	4	4.88	3
Actin, cytoplasmic 1 (Beta-actin)	P70514	K.EKLC*Y@VALDFEQEMATAASSSSLEK.S	Y218	N	U	2	1	1	4.08	3
Beta-centractin	Q8R5C5	R.TTGVVLDSGDGVTHAVPIY@EGFAMPHSIMR.V	Y171	Y	U	1,2,3	3	3	5.73	3
Actin-like protein 2 -- Arp2	P61161	K.HLWDY@TFGPEK.L	Y91	N*	U	2,3,5,6,7,8,9,10	8	13	3.37	2
		K.HLWDY@TFGPEKLNIDTR.N	Y91			1,2,7,9,10	5		3.97	3
Actin-like protein 3 - Arp3	Q99JY9	L.RAEPEDHY@F.L	Y108	N*	U	11	1	1	1.87	2
Actin-related protein 2/3 complex subunit 3 -- p21-ARC	Q9JM76	F.KGPAPRETKDTDIVDEAIY@Y.F	Y46	Y	U	17	1	13	3.26	3
		F.KGPAPRETKDTDIVDEAIY@YF.K	Y46			11,13,15,16,18	5		3.75	3
		K.DTDIVDEAIY@YFK.A	Y46			1,5,7,8,9,10	6		4.59	2
		Q.FKGPAPRETKDTDIVDEAIY@Y.F	Y46			17	1		3.47	3
Adenylyl cyclase-associated protein 1 -- CAP1	P40124	R.LEAVSHTSDMHC*GY@GDSPSK.G	Y30	N	U	1,2,3	3	3	4.00	3
Cofilin-1 non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C	Y139	N	C	1,2,3,4,5,7,8,9,10	9	10	5.21	3
		K.LTGIKHELQANC*Y@EEVKDR.C	Y139			2	1		4.74	3
Src substrate cortactin	Q60598	F.KAEPSYRGSEPEPEY@SIEAAGIPEAGSQQGL.T	Y442	N	U	11,12,16,17,18	6	6	3.86	3
		L.TYTSEPVY@ETTEAPGHY.Q	Y466	N	C	11,12,15,16,17,18	1	16	3.15	3
							6		4.86	2
		Y.TSEPVY@ETTEAPGHY.Q	Y466			11,12,13,14,15,16,17,18	1		3.97	3
							8		3.51	2
Cytoplasmic FMR1 interacting protein 1	Q7TMB8	K.C*NEQPNRVEIY@EK.T	Y108	N*	U	1,2	2	2	3.16	3
Coronin-1C	Q9WUM4	R.YFEITDESPY@VHYLNTFSSKEPQR.G	Y301	N*	U	10	1	1	5.75	3
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.VIY@DFIEK.T	Y253	N	C	2	1	1	2.40	2

Twinfilin-1	Q91YR1	R.KIEIDNGDELTADFLY@DEVHPK.Q	Y309	N	U	1,2,5,8	4	4	6.27	3
Twinfilin-2	Q9Z0P5	K.KIEIGDGAELTAEFLY@DEVHPK.Q	Y309	N	U	2,3,8	3	3	5.85	3
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R R.VQIY@HNPTANSFR.V	Y39 Y39	N	C	11,12 2,3,4,7	2 3 2	7	4.02 3.28 4.30	2 3 2
WD-repeat protein 1 -- Actin interacting protein 1, AIP1	O88342	F.IYDGKTGEKVC*ALGESKAHDGGIY@AISW.S K.AHDGGIY@AISWSPDSTHLLSASGDK.T K.AHDGGIY@AISWSPDSTHLLSASGDKTSK.I	Y237 Y237 Y237	N	C	11 1,2,3,4,5,6,7,8,9,10 1,2,4,5,7,9,10	1 10 7	18	3.26 6.03 5.84	3 3 3
Other actin-associated proteins										
Alpha-actinin 1	Q7TPR4	R.HRPELIDY@GK.L K.AIM#TYVSSFY@HAFSGAQK.A K.AIMTYVSSFY@HAFSGAQK.A	Y193 Y246 Y246	N* N*	U U	2 6,7,10 1,2,3,4,5,6,7,8,9,10	1 2 2 2 12	1 18	3.60 2.87 4.47 3.10 4.96	3 3 2 3 2
Anillin	Q8K298	R.AESADSLGSEDRDLLY@SIDAYR.S	Y666	N	U	1,2,3,4,5,6,7,8,9,10	10	10	5.45	3
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q Y.HGEYPDDYPREY@QYGDDQGIDY.-	Y316 Y320	Y Y	C U	11,12 11,15,17,18	2 4	2 4	3.52 4.51	2 3
Filamin-B	Q80X90	K.GFLDGVY@SFEYYPSTPGK.Y K.QKGFLDGVY@SFEYYPSTPGK.Y M.KSRMDGTY@AC*SY.T R.MDGTY@AC*SYTPLK.A	Y511 Y511 Y704 Y704	Y N*	U U	1,2,3,5,6,7,8,9,10 1,3,5,6,9,10 11 1,2,4	11 6 1 3	17 4	5.07 4.29 2.78 3.63	2 3 2 2
Girdin	Q5SNZ0	K.TEDAY@TISSAGKPTPSTQGK.I L.RTGPQKTEDAY@TISSAGKPTPSTQ.G	Y1739 Y1739	N	U	2 11	1 1	2	3.41 4.91	3 3
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	N	C	11	1	1	4.60	2
Moesin	P26041	K.EGILNDDIY@C*PPETAVLLASYAVQSK.Y	Y115	N*	U	5	1	1	3.53	3
Myosin-9	Q8VDD5	R.HEMPPHIY@AITDTAYR.S	Y150	N*	U	1	1	1	3.61	3
Myosin-10	Q61879	R.AVIY@NPATQADWTAK.K Y.LFVDRAVIY@NPATQADW.T	Y22 Y22	N*	U	2,4 11	2 1	3	4.11 2.41	2 2
PDZ and LIM domain protein 1	O70400	R.VITNQYNSPTGLY@SSENISNFNNAVESK.T	Y148	N	U	2	1	1	4.00	3
Profilin-1	P10924	K.C*Y@EMASHLR.R	Y128	N	U	1,2,3	3	3	2.96	3
Profilin-2	Q9JJV2	K.SQGGEPTY@NVAVGR.A	Y98	N*	U	2	1	1	3.75	2
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	N	C	2,4,5,6,7,8,10	8	8	5.24	3
Septin-7	O55131	K.NLEGY@VGFANLPNQVYR.K R.KLAAVTY@NGVDNNK.N R.KLAAVTY@NGVDNNKNK.G	Y29 Y318 Y318	N* N	U U	2 4 1	1 1 1	1 2	4.77 2.56 3.73	2 2 3
Synaptopodin	Q8CC35	R.TPPASLY@HGYLPENGVLRPEPTK.Q	Y775	Y	U	2,3	3	3	4.07	3
CYTOSKELETON: MICROTUBULE-ASSOCIATED										
Tubulin alpha-1 chain	P68369	F.MVDNEAIY@DIC*RR.N F.MVDNEAIY@DIC*.R F.MVDNEAIY@DIC*RRNLDIERPTY.T	Y210 Y210 Y210	N*	U	11 14 11,13,16	1 1 3	5	3.34 2.34 3.38	2 2 3
Tubulin beta-3 chain	Q9ERD7	Y.C*IDNEALY@DIC*F.R K.NSSY@FVEWIPNNVK.V	Y208 Y340	Y Y	U U	11,16,17,18 1,2	5 2	5 2	3.10 3.32	2 2
CLIP-associating protein 2 -- CLASP2	Q8BRT1	R.DYNPY@NYSDSISPFNK.S	Y1014	N*	U	1,2,3,4,5,6,7,8,9,10	11	11	4.62	2
Dynein heavy chain, cytosolic	Q9JHU4	R.YQVGVHY@ELTEEEKFYR.N	Y1008	N*	U	2,3	2	2	4.70	3
Kinesin light chain 1	O88447	K.DGSAFGEY@GGWYK.A K.QKDGSAFGEY@GGWYK.A	Y444 Y444	Y	U	1,2,3,7,10 1	5 1	6	3.48 3.20	2 3
Kinesin light chain 2	Q91YS4	R.DSAPYGEY@GSWYK.A	Y434	N*	U	9	1	1	2.92	2
Kinesin-associated protein 3 -- KAP3	P70188	R.PATAYGFRPDEPY@YYSFGSR.- R.PATAYGFRPDEPYY@YSFGSR.- R.PATAYGFRPDEPYYY@SFGSR.-	Y786 Y787 Y788	Y Y Y	U U U	2,4 2,3,5,6,7,8 1,9,10	2 6 3	2 6 3	4.19 4.61 5.10	3 3 3

Kinesin family member 11	Q6P9P6	R.SPNEVY@TWEEDPLAGIIPR.T	Y124	Y	U	1,2	2	2	5.01	2
Microtubule-associated protein 1B -- MAP 1B	P14873	K.VLSPLRS@PPLLGSESPY@EDFLSADSK.V	Y1405	N*	U	2,7,8	3	4	4.92	3
		R.SPPLLGSESPY@EDFLSADSK.V	Y1405			9	1		4.85	2
Microtubule-associated protein 1B -- isoform	UPI0000021C8B	R.THDVGGYY@YEKTER.T	Y1901	N*	U	1,2	2	2	3.18	3
Microtubule-associated protein 4 -- MAP 4	P27546	F.TERDNPSEDSY@GMLPC*DSF.A	Y176	Y	U	11,12,15	3	3	4.26	2
Nuclear distribution protein nudE homolog 1 -- NudE	Q9CZA6	R.NFMY@DQSPSR.T	Y279	N	U	3	1	1	2.20	2
PREDICTED: similar to centrosome spindle pole associated protein	UPI0000D65977	R.TPYDDAY@YFYGAR.N	Y468	Y	U	4,6,8,10	4	4	3.78	2
Platelet-activating factor acetylhydrolase IB alpha subunit	P63005	R.SNGYEEAY@SVFKK.E	Y27	N*	U	1,2	2	2	3.04	2
RCC2 protein	Q8BK67	R.VFSWGFGGY@GR.L	Y357	N*	U	2,9,10	3	3	2.97	2
CYTOSKELETON: OTHER										
Plectin 1	Q6S394	Y.VSSLY@DAMPRVPGAQDGVRANEL.Q	Y288	N*	U	11,14	2	2	2.63	3
		K.AVTGYRDPY@SGQSVSLFQALK.K	Y3134	Y	U	9	1	9	3.78	3
		K.AVTGYRDPY@SGQSVSLFQALKK.G	Y3134			2,3,5,6,7,8,9,10	8		5.83	3
		R.ARQEEVY@SELQAR.E	Y3250	Y	U	1,2,3,4,5,7,8,9,10	6	17	4.73	3
							11		4.37	2
		R.LTAEDLY@EAR.I	Y3678	Y	U	1,3	2	2	2.66	2
		R.QQNLASY@DYVR.R	Y3665	N*	U	2,5	2	2	2.10	2
		R.AVTGYKDPY@SGK.L	Y4043	N*	U	9,10	2	2	3.50	2
		R.LLEAAAQSSKGY@YSPYSVSGSGSTAGSR.T	Y4499	N	U	2	1	1	5.12	3
		K.GYYSPY@S@VSGSGSTAGSR.T	Y4503	N	U	7	1	10	2.85	2
		K.GYYSPY@SVSGSGSTAGSR.T	Y4503			1,3,4,5,6,7,8,9,10	9		4.99	2
Protein 4.1	P48193	K.VSLLDDTVY@EC*VVEK.H	Y223	N*	U	8	1	1	3.57	2
Spectrin beta chain, brain 1	Q62261	L.KIVSSNDVGHDEY@STQ.S	Y777	N*	U	11	1	1	3.86	2
Vimentin	P20152	R.TY@SLGSALRPSTSR.S	Y37	N*	U	2	1	1	2.73	3
		L.RPSTSRSLY@SSSPGGAY.V	Y52	N	C	11	1	17	3.14	2
		R.SLY@SSS@PGGAYVTR.S	Y52			10	1		3.24	2
		R.SLY@SSSPGGAYVTR.S	Y52			1,2,3,4,5,6,7,8,9,10	11		4.32	2
		S.RSLY@SSSPGGAY.V	Y52			11	1		2.66	2
		S.TSRSLY@SSSPGGAY.V	Y52			11,12,17	3		3.50	2
TRAFFICKING/TRANSPORT										
Vesicle transport										
Adapter-related protein complex 3 mu 1 subunit	Q9JKC8	K.SVVSQSVC*DY@FFEAQEK.A	Y31	N*	U	2,3,4	3	3	4.63	2
Clathrin heavy chain	Q68FD5	R.ALEHFTDLY@DIKR.A	Y634	N*	U	1,2,3,4,5,7	6	6	5.13	3
		R.FLRENPY@YDSR.V	Y899	N	U	1,2,3,4,8	5	5	3.20	3
Coatomer protein complex subunit alpha	Q8BTF0	R.VKGNNVY@C*LDR.E	Y 579	N*	U	1,3	2	2	2.33	2
Coatomer beta subunit	Q9JIF7	K.LVTEMGTY@ATQSALSSSRPTKK.E	Y521	N*	U	1,2	2	2	3.12	3
Coatomer beta' subunit	O55029	K.GVNC*IDYY@SGGDKPYLISGADDR.L	Y194	Y	U	3,5	2	2	4.15	3
HECT domain and RCC1-like domain-containing protein 2 -- Herc2	Q4U2R1	R.SRTPLDKDLINTGIY@ESSGK.Q	Y999	Y	U	2,8,9	3	4	4.43	3
		R.TPLDKDLINTGIY@ESSGK.Q	Y999			10	1		4.02	3
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	N	C	1,2,3,4	9	9	3.16	2
Lysosomal trafficking regulator	P97412	R.AVWYDPIY@YPTSWQLDPTEGPNR.E	Y 2929	Y	U	1	1	2	3.56	3
							1		3.96	2
SEC24 related gene family, member B	Q80ZX0	K.MTSLPLDSQC*DSY@YSRPYTVPTQNSGTPSSANQPGAQQMYGR.G	Y79	Y	U	4,10	2	2	5.30	3
		R.LDDRVY@AMC*QMK.S	Y1083	N*	U	2	1	1	3.34	3
SH3-containing GRB2-like protein 1	Q62419	K.ALY@DFEPENDGELGFR.E	Y315	N	U	2	1	1	4.61	2
Sorting nexin-9	Q91VH2	K.IAIIVGDY@GPMWVYPTSTFDC*VVADPR.K	Y239	N	U	5	1	16	3.29	3
		L.AKPKEKIAIIVGDY@GPM#.W	Y239			11,16,17,18	4		3.96	3
		L.AKPKEKIAIIVGDY@GPM.W	Y239			11,12,13,14,15,16,17,18	7		3.29	3
							4		4.18	2

Sorting nexin 17	Q8R0N8	R.KSYWDSAY@DDDVMENR.V	Y210	Y	U	1,2,3	3	6	4.37	3
							3		5.32	2
Transitional endoplasmic reticulum ATPase -- TER ATPase	Q01853	K.VVETDPSPY@C*IVAPDTVIHC*EGEPIKR.E	Y172	N*	U	1,3	2	2	3.41	3
		R.GILLY@GPPGTGK.T	Y243	N*	U	2	1	1	2.72	2
Nucleocytoplasmic transport										
GTP-binding nuclear protein Ran	P62827	K.NLQY@YDISAK.S	Y145	N*	U	2,3,4,6,7,10	6	8	2.94	2
		R.KKNLQY@YDISAK.S	Y145			1,3	2		2.92	3
		K.NLQYY@DISAK.S	Y146	N	U	2,3,4,5,9	6	6	3.13	2
		K.SNY@NFEKPFLWLAR.K	Y154	N*	U	7	1	1	2.64	3
Importin-9	Q91YE6	R.VKGEEIY@SMDEGIR.T	Y888	Y	U	1,2,3,4,5,6,7,10	4	11	4.13	3
							7		4.03	2
RAE1 RNA export 1 homolog	Q8C570	R.SNGTNTSAPQDIY@AVNGIAFHPVHGTLATVGSDGR.F	Y274	N*	U	1,3,5,8	4	4	4.76	3
Ran-binding protein 2	Q9ERU9	R.GDDY@FNYNVQQTSTNPPLPEPGYFTKPPLVAHASR.S	Y960	N*	U	2,3	2	2	5.10	3
		K.EGPY@WNC*NSC*SFK.N	Y1349	N*	U	7	1	1	2.65	2
Other transport										
none										
METABOLIC AND BIOSYNTHETIC ENZYMES										
Glycolytic enzymes										
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G	Y24	N	C	1,2,3,4,5,7,8,9,10	73	100	4.12	2
		F.DSRGNPTVEVDLY@TAKGLF.R	Y24			11,12,13,14,16,17,18	24		5.57	2
		F.DSRGNPTVEVDLY@TAKGLFR.A	Y24			11,12,13	3		5.81	3
		F.RAAVPSGASTGIY@EAL.E	Y43	N	C	11,12,14,16,18	6	81	3.66	2
		F.RAAVPSGASTGIY@EALEL.R	Y43			11,12,13,14,16,17,18	16		3.64	2
		R.AAVPSGASTGIY@EALELR.D	Y43			1,2,3,4,5,6,7,8,9,10	11		3.99	3
							40		5.59	2
		F.RAAVPSGASTGIY@EALELRDNDKTRF.M	Y43			11,12,13,15,16	7		4.46	3
		R.AAVPSGASTGIY@EALELRDNDK.T	Y43			3	1		4.87	2
		R.IGAEVY@HNLK.N	Y188	N*	U	2	1	1	2.09	2
GAPDH: Glyceraldehyde-3-phosphate dehydrogenase	P16858	F.VKLISWYDNEY@GY.S	Y315	N	C	11,16,17,18	4	41	3.99	2
		K.LISWYDNEY@GYSNR.V	Y315			1,2,3,4,5,6,7,8,9,10	5		4.50	3
							29		4.77	2
		L.ISWYDNEY@GY.S	Y315			17	1		3.12	2
		L.ISWYDNEY@GYSNRVVDL.M	Y315			11,18	2		4.01	2
L-lactate dehydrogenase A chain	P06151	W.KEVHKQVVDSAY@EVIKL.K	Y238	N	U	11,12,14	3	3	3.85	3
6-phosphofructokinase, liver type	P12382	K.C*HEHYTTEFLY@NLYSSEGR.G	Y639	N*	U	1,6,7,8,9,10	6	6	4.55	3
Phosphoglycerate mutase 1	Q9DBJ1	F.SGWY@DADLSPAGHEEAKRGGQAL.R	Y25	N	C	12	1	23	4.24	3
		F.SGWY@DADLSPAGHEEAKRGGQ.A	Y25			14	1		4.08	3
		R.FSGWY@DADLSPAGHEEAK.R	Y25			1,2,3,4,5,6,9,10	5		4.50	3
							5		5.33	2
		R.FSGWY@DADLSPAGHEEAKR.G	Y25			1,2,3,4,5,6,7,9,10	10		4.39	3
							1		3.07	2
Pyruvate kinase, isozyme M2	P52480	R.EATESFASDPILY@RPVAVALDTK.G	Y104	N	U	1,3,4,5,7,8	6	9	4.63	3
		R.EATESFASDPILY@RPVAVALDTKGPEIR.T	Y104			1,3	2		4.28	3
		Y.HAETIKNVREATESFASDPILY@RPVAVAL.D	Y104			11	1		5.13	3
		K.ITLDNAY@MEKC*DENILWLDYK.N	Y147	N*	U	2,4,8	3	3	4.85	3
		L.IAREAEAAIY@HLQL.F	Y389	N	C	11	1	17	3.48	2
		L.IAREAEAAIY@HL.Q	Y389			14	1		2.29	2
		L.IAREAEAAIY@HLQLF.E	Y389			11,14	2		3.63	2
		L.IAREAEAAIY@HLQLFEEL.R	Y389			11,13,14	3		4.68	2
		M.QHLIAREAEAAIY@HLQLFEEL.R	Y389			13	1		3.31	3
		R.EAEAAIY@HLQLFEELR.R	Y389			7,8,10	3		3.25	3
		R.EAEAAIY@HLQLFEELRR.L	Y389			1,4,7,9,10	6		3.10	3
Other metabolic/biosynthetic enzymes										
ADP/ATP translocase 2	P51881	R.AAYFGIY@DTAK.G	Y194	N*	U	1	1	1	2.76	2
ATP citrate lyase	Q91V92	R.TTDGVY@EGVAIGGDRYPGSTFMDHVLR.Y	Y 672	N	U	1,2,3,4,5,8,10	8	9	4.21	3
		R.TTDGVY@EGVAIGGDRYPGSTFM#DHVLR.Y	Y 672			2	1		3.87	3
Aldo-keto reductase family 1 member C18	Q8K023	K.IELNDGHSIPVLGFGTY@ATEEHLK.K	Y24	N*	U	4,6,7	3	3	6.16	3
Aldo-keto reductase family 1, member B3	Q5U415	R.HIDC*AQVY@QNEK.E	Y49	N*	U	1	1	5	3.57	2
		R.HIDC*AQVY@QNEKEVGVALQEK.L				1,2,3,5	4		5.25	3

Aldose reductase-related protein 2	P45377	R.AC*LLPETVNMEEYPYDAEY@.-	Y315	N*	U	7,9,10	3	4	3.86	2
		W.RAC*LLPETVNMEEYPYDAEY@.-	Y315			16	1		4.63	2
Adenylosuccinate synthetase, non-muscle isozyme	P46664	K.DGVY@FLYEALHGPPK.K	Y236	N*	U	7,8,9	3	11	3.88	2
		K.DGVY@FLYEALHGPPKK.I	Y236			1,3,4,5,6,7,9,10	8		4.32	3
		K.DGVYFLY@EALHGPPKK.I	Y239	N*	U	1	1	1	2.79	3
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	L.SEDEARVC*MVY@DLYPTLTPL.A	Y290	N*	C	11	1	31	3.14	2
		R.VC*M#VY@DLYPTLTPLAVAYAR.A	Y290			3,4,5,6,7,8,9	6		5.05	3
							8		5.51	2
		R.VC*MVY@DLYPTLTPLAVAYAR.A	Y290			1,2,3,4,5,6,7,8,9,10	6		4.92	3
							10		4.98	2
		R.VC*MVYDLY@PTLTPLAVAYAR.A	Y293	N*	U	1	1	1	4.85	3
CTP synthase	P70698	Y.INIDAGTFSPY@EHGEVF.V	Y53	N*	U	11,12,17	3	3	4.86	2
Glycerol-3-phosphate dehydrogenase 2	Q8VDT0	R.FLYY@EMGYK.S	Y601	Y	U	1,2	2	2	2.10	2
Glucose-6-phosphate 1-dehydrogenase X	Q00612	R.NSYVAGQY@DDAASYK.H	Y111	N*	U	1,2,3,4,5,7	6	6	4.75	2
		R.VQPNEAVY@TK.M	Y400	N	U	3,4	2	14	2.23	2
		L.VIRVQPNEAVY@TKM#.M	Y400			15	1		4.31	3
		L.VIRVQPNEAVY@TKM.M	Y400			11,12,13,15,18	4		5.21	3
							3		4.35	2
		L.VIRVQPNEAVY@TKMM.T	Y400			11,12	2		4.41	3
							2		3.60	2
		K.KPGMFFNPEESELDLTY@GNRYK.N	Y423	N*	U	9,10	2	2	6.48	3
		K.RVGFQYEGTY@K.W	Y506	N	U	6,7,8,9,10	2	13	3.02	3
							5		3.66	2
		R.VGFQYEGTY@K.W	Y506			2,6,7,9,10	6		3.08	2
Inosine-5'-monophosphate dehydrogenase 2	P24547	L.AATTEAPGEY@FFSDGIRL.K	Y400	N	U	11,12,13,15,16	5	5	4.32	2
Phosphoglucomutase 2	Q5RJV4	K.IALY@ETPTGWK.F	Y353	N*	U	2	1	1	1.96	2
Ribonucleoside-diphosphate reductase large subunit	P07742	K.KVFSDVMEDLY@NYINPHNGR.H	Y102	N*	U	1,2,3,4,5,9,10	7	8	6.31	3
		K.KVFSDVM#EDLY@NYINPHNGR.H	Y102			7	1		3.62	3
Serine hydroxymethyltransferase, cytosolic	P50431	K.M#LSQPLKDSDAEVY@SIIKK.E	Y28	N*	C	2,3,4,5,6,7	6	16	4.89	3
		K.MLSQPLKDSDAEVY@SIIKK.E	Y28			1,2,3,5,6,7,8,9,10	10		5.78	3
S-adenosylhomocysteine hydrolase	Q5M9P0	K.SKFDNLY@GC*R.E	Y193	N*	U	2,5,8	3	3	3.05	2
Thioredoxin reductase 1, cytoplasmic	Q9JMH6	K.KVVYENAY@GR.F	Y131	N	U	1,2,3,4,5	3	15	3.69	3
							6		3.55	2
		K.VVYENAY@GR.F	Y131			1,2,3,4,5	6		2.63	2
Thioredoxin reductase 1 [fragment]	Q3UEB7	K.EVVYENAY@GR.F	Y131	Y	U	1,4	2	2	3.55	3
TK: Transketolase	P40142	K.NM#AEQIIQEIY@SQVQSK.K	Y275	N	C	8	1	10	4.06	3
		K.NMAEQIIQEIY@SQVQSK.K	Y275			1,2,3,4,5,8,9	3		6.04	3
							6		4.76	2
UDP-glucose 6-dehydrogenase	O70475	R.INAWNSPTLPIY@EPGLK.E	Y53	N*	U	2	1	2	3.45	2
		R.INAWNSPTLPIY@EPGLKEVVESC*R.G	Y53			2	1		4.18	3
RNA SYNTHESIS AND PROCESSING										
Transcription machinery and regulation										
CCR4-NOT transcription complex subunit 2	Q8C5L3	F.VEGVDSDYHDENM#Y@Y.S	Y43	N*	U	17	1	18	4.02	2
		F.VEGVDSDYHDENMY@Y.S	Y43			17,18	2		3.83	2
		K.FVEGVDSDYHDENM#Y@YSQSSMFPHR.S	Y43			3	1		4.75	3
		K.FVEGVDSDYHDENMY@YSQSSM#FPHR.S	Y43			3,5,6,7	4		5.11	3
		K.FVEGVDSDYHDENMY@YSQSSMFPHR.S	Y43			1,2,3,5,6,7,9,10	10		6.55	3
DNA-directed RNA polymerase I 40 kDa polypeptide -- RPA40	P52432	R.NVHTTDFPGNY@AGYDDAWDQNRFEK.N	Y33	N	U	2	1	1	4.78	3
LIM domains containing protein 1 -- LIMD1	Q9QXD8	K.VFC*EEDFLY@SGFQQSADR.C	Y519	Y	U	1,2,4,6,8,9,10	4	10	5.92	3
							6		5.89	2
NF-kappa-B DNA binding subunit p105	P25799	F.TRRLEPVVSDAIY@DSKAPNASNL.K	Y238	N*	U	11,12	2	7	4.74	3
		R.RLEPVVSDAIY@DSKAPNASNLK.I	Y238			1,2,3,5,7	5		5.03	3
Polymerase I and transcript release factor -- PTRF	O54724	F.KVMIY@QDEVKLPAKL.S	Y158	N*	C	12	1	2	4.97	3
		K.VMIY@QDEVKLPAK.L	Y158			2	1		3.47	2
		R.KSFTPDHVVY@AR.S	Y310	N	C	3,7	2	3	3.48	3
		K.SFTPDHVVY@AR.S	Y310			7	1		2.34	2
Staphylococcal nuclease domain-containing protein 1	Q78PY7	R.ADDADEFGY@SR.-	Y908	N	U	8	1	5	3.35	2

		R.YGDFRADDADEFGY@SR.-	Y908			6,7,9,10	4		4.20	3
Transcription initiation factor IIE alpha subunit	Q9D0D5	R.FNEQIEPIY@ALLR.E	Y188	Y	U	6,7	2	2	4.09	2
Transcription elongation factor SPT6	Q62383	K.AAEDDELEEEADWIY@R.N	Y321	Y	U	9,10	2	2	5.00	2
Tripartite motif protein 25	Q61510	K.FDTIY@QVLVK.K	Y277	N	U	2,7	2	9	3.32	2
		R.VYGKFDTIY@QVLVK.K	Y277			1,2,3,4,5,8	1		2.52	3
							6		4.10	2
DEAD(DEAH)-box helicases										
ATP-dependent RNA helicase DDX3X (DDX3Y) (PL10)	Q62167	K.GFY@DKDSSGWSS@SKDKDAYSSFGSR.G	Y52	N*	U	2	1	1	3.20	3
		K.DKDAY@SSFGSR.D	Y68	N	U	1,2,3,4,5,6,8,9,10	9	14	3.58	2
		W.SSSKDKDAY@SSF.G	Y68			11,12,13,15,17	5		3.10	2
		R.FDDRGRGDY@DGIGGR.G	Y103	N	C	2	1	24	2.62	3
		R.GDY@DGIGGR.G	Y103			1,2,4,8,10	5		2.80	2
		R.GDY@DGIGGRGDR.S	Y103			1	1		2.00	2
		R.GRGDY@DGIGGR.G	Y103			1,2,3,4,5,6,8,10	10		3.44	2
							1		2.56	3
		R.GRGDY@DGIGGRGDR.S	Y103			1,2,4,5,6,10	6		4.16	3
		K.TAAFLLPILSQIY@ADGPGEALR.A	Y242	N*	U	3,5	1	2	5.29	3
							1		5.59	2
		L.VLAPTRELAVQIY@EEARKF.S	Y282	Y	U	11,12,15,18	4	4	5.72	3
		R.VRPC*VVY@GGAEIGQQIR.D	Y300	N*	U	1,3,4,5	4	4	4.36	3
		F.VETKKGADSLEDFLY@HEGY.A	Y461	N*	U	11,12,13,14,16,17,18	6	40	5.63	3
							5		3.53	2
		K.GADSLEDFLY@HEGYAC*TSIHGDR.S	Y461			1,3,4,5,6,7,8,9,10	9		6.05	3
		K.KGADSLEDFLY@HEGYAC*TSIHGDR.S	Y461			2,3,4,5,7,8,9,10	13		6.28	3
		L.VFVETKKGADSLEDFLY@HEGY.A	Y461			11,12,13,15,16,17	6		5.35	3
							1		3.90	2
Putative ATP-dependent RNA helicase DHX30	Q99PU8	R.ENYLEENLLY@APSLR.F	Y991	N*	U	7	1	1	2.83	2
Probable ATP-dependent RNA helicase DDX6	P54823	K.GVTQY@YAYVTER.Q	Y312	N*	U	7	1	1	2.37	2
Putative pre-mRNA splicing factor ATP-dependent RNA helicase DHX15	O35286	K.QNHESVQWC*Y@DNFINYR.S	Y645	Y	U	4,7	2	2	3.68	3
Probable ATP-dependent RNA helicase DDX17 (DDX5)	Q501J6	K.STC*IY@GGAPK.G	Y200	Y	U	3	1	3	2.41	2
		R.LKSTC*IY@GGAPK.G	Y200			1,3	2		2.27	2
Probable ATP-dependent RNA helicase DDX20 -- DEAD-box protein 20	Q9JJY4	R.VQSEPQEESWY@DC*HR.E	Y757	N*	U	1,2,3,4,9,10	6	6	3.98	2
		R.AWQEY@YAAASHSYYWNAQR.H	Y788	Y	U	3,5,6,7	4	4	4.22	3
Probable ATP-dependent helicase DDX48	Q91VC3	K.GFKEQIY@DVYR.Y	Y202	N*	U	1,2,3,4,5,7,9,10	6	14	3.59	3
							8		3.02	2
hnRNPs and snRNPs										
Heterogeneous nuclear ribonucleoprotein A1	P49312	F.GGRSSGPY@GGGGQYF.A	Y288	N*	U	11,17	2	2	3.45	2
		R.SSGPYGGGGQY@FAKPR.N	Y294	N	U	2	1	1	3.60	2
Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Y.GGGYGSGGGSGGY@GSRRF.-	Y374	N*	U	12	1	1	2.56	3
Heterogeneous nuclear ribonucleoprotein A/B	Q3TMZ8	Y.GPGYGGYDYSPY@GYY.G	Y291	Y	U	16,17	2	2	2.67	2
		Y.GYQQGYGPGYGGYDY@SPYGYY.G	Y288	Y	U	15,16,17	3	3	3.76	2
Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	K.ATENDIY@NFFSPLNPVR.V	Y306	Y	U	1,3,4,5,6,7,8,9,10	2	11	3.69	3
							9		5.04	2
		R.DLSYC*LSGMY@DHR.Y	Y272	Y	U	1,2,4,9	4	4	3.68	2
Heterogeneous nuclear ribonucleoprotein H1	Q811L7	R.GAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D	Y243	N*	U	2,3,4,9,10	5	5	5.03	3
		R.GAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246	N	U	1,6,7,8	4	8	4.30	3
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDR.F	Y246			6,7,8	3		5.94	3
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246			6	1		4.18	3
		R.GAYGGGYGGYDDYNGY@NDGYGFGSDRFGR.D	Y249	N*	U	5	1	1	3.68	3
Heterogeneous nuclear ribonucleoprotein H'	P70333	R.GAYGGGYGGY@DDYGGYNDGYGFGSDRFGR.D	Y243	N*	U	9	1	1	2.81	3
		R.GAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246	Y	U	1,5,6,7,8,9,10	8	14	4.73	3
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDR.F	Y246			2,8,9	3		5.75	3
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246			10	1		3.73	3
		Y.GGGYGGYDDY@GGYNDGYGF.G	Y246			11	1		2.99	2
		Y.GGGYGGYDDY@GGYNDGYGFGSDRF.G	Y246			16	1		4.66	2
		R.ATENDIY@NFFSPLNPMR.V	Y306	Y	U	1,2,7,10	4	5	4.91	2
		Y.RATENDIY@NFF.S	Y306			15	1		2.24	2
Heterogeneous nuclear ribonucleoprotein L	Q8R081	M.VKMAAAGGGGGGGRY@Y.G	Y16	N*	U	12	1	1	2.62	3

Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	N.RFEPY@SNPTKRY.R	Y62	N*	U	11	1	1	3.34	3
Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Q.RQAAKNQMYDDYY@YY.G	Y432	Y	U	15,18	2	2	4.30	2
		R.GGYEDPY@YGYEDFQVGAR.G	Y485	Y	U	8	1	85	4.46	2
		Y.RGGYEDPY@YGY@EDFQVGAR.G	Y485,Y488	Y	U	15	1	3	3.61	3
		Y.RGGYEDPY@YGY@EDF.Q	Y485,Y488			14	2		3.71	2
		Y.RGGYEDPY@YGYEDF.Q	Y485			11,12,13,14,15,16,17,18	80		4.40	2
		Y.RGGYEDPY@YGYEDFQ.V	Y485			11	1		3.18	2
Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Y.RGGYEDPY@YGYDDGY.A	Y489	Y	U	11,12,13,14,15,16,17,18	8	8	4.29	2
Heterogeneous nuclear ribonucleoprotein U	O88568	K.NQSQGYNQWQQGQFWGQKPWSQHYHQGY@Y.-	Y797	Y	U	1,3,5,6,10	5	5	5.26	3
Polypirimidine tract binding protein	Q8R509	Y.TSVAPVLRGQPNY@IQF.S	Y126	Y	U	15,16	2	2	4.23	2
Polypyrimidine tract-binding protein 1 -- hnRNP	P17225	R.GQPIY@IQFSNHK.E	Y126	N	U	2,6	2	4	2.23	2
		Y.TSVAPVLRGQPIY@IQF.S	Y126			17,18	2		3.21	2
U1 small nuclear ribonucleoprotein 70 kDa	Q62376	K.HHNQPY@C*GIAPYIR.E	Y38	Y	U	1,2,3,4,5,6,7,8,9,10	11	11	5.25	3
U1 small nuclear ribonucleoprotein C	Q62241	K.FYC*DYC*DTY@LTHDSPSVR.K	Y12	N	U	1,2,6	3	3	3.31	3
Splicing factors										
Apoptosis-related RNA binding protein	Q9Z0H4	K.ELFEPYGAVY@QINVLR.D	Y67	N*	U	7,8	2	2	4.33	2
Crooked neck-like protein 1	P63154	R.KVQADDGSDAGWEEY@Y@DYIFPEDAANQPNLK.L	Y640,Y641			10	1		5.79	3
		R.KVQADDGSDAGWEEY@YDYIFPEDAANQPNLK.L	Y640	Y	U	2	1	2	5.72	3
		R.KVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L	Y641	Y	U	1,5,6,8,9,10	6	10	5.88	3
		R.RKVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L	Y641			1,7,10	3		6.20	3
RNA binding motif, single-stranded interacting protein 1	Q91W59	K.QQMYPQY@ATYYYPQYLQAK.Q	Y13	Y	U	1,4,6,7,8,9,10	4	14	4.39	3
							6		4.31	2
		W.KQQMYPQY@ATY.Y	Y13			11,12,15	3		2.90	2
		K.QQMYPQY@ATY@YYPQYLQAK.Q	Y13,Y16			4	1		4.81	3
		K.QQM#YPQYATY@YYPQYLQAK.Q	Y16	Y	U	3,4,6	1	17	3.74	2
							3		4.64	3
		K.QQMYPQYATY@YYPQYLQAK.Q	Y16			1,2,3,4,6,9,10	2		4.49	3
							10		4.64	2
		L.HNGFYPSPY@SIATN.R	Y272	Y	U	11,18	2	2	3.20	2
Splicing factor, arginine/serine-rich 1	Q6PDM2	F.VRKEDMTY@AVR.K	Y169	N*	U	11	1	1	2.69	3
Splicing factor, arginine/serine-rich 3	P84104	R.AFGY@YGPLR.S	Y32	N*	U	1,2,3,4,5,6,7,8	8	8	3.06	2
Splicing factor 3b, subunit 4	Q8QZY9	F.IGNLDPEIDEKLLY@DTF.S	Y117	Y	U	11,12,13,14,15,16,17	7	7	4.29	2
Splicing factor, arginine/serine-rich 5	O35326	F.GFVEFEDPRDADDAVY@ELDGKEL.C	Y55	Y	U	11,12,16,17	2	8	4.62	3
							3		4.60	2
		R.GFGFVEFEDPRDADDAVY@ELDGK.E	Y55			8	1		2.79	3
		R.GFGFVEFEDPRDADDAVY@ELDGKELC*SER.V	Y55			1,8	2		5.18	3
Arginine/serine-rich splicing factor 6	Q921K3	K.NGYGFVEFEDSRDADDAVY@ELNSK.E	Y53	Y	U	1,3,4,5,7,8,9,10	8	9	6.58	3
		Y.GFVEFEDSRDADDAVY@ELNSKEL.C	Y53			17	1		4.10	3
Splicing factor, arginine/serine-rich 9	Q9D0B0	R.DAEDAIY@GR.N	Y71	N*	U	1,2,3	3	3	3.36	2
Splicing factor, proline- and glutamine-rich	Q8VIJ6	R.FAQHGTFEY@EYSQR.W	Y480	N*	U	8	1	1	3.50	2
Other RNA binding and processing										
DAZ-associated protein 1	Q9JII5	L.AFPPPPSQAAPDMSKPPTAQPDFPY@GQY.G	Y346	Y	U	11,12,15,17	4	4	3.72	3
Double-stranded RNA-binding protein Staufen homolog	Q9Z108	R.ELLY@GGTSPTAETILK.S	Y371	Y	U	1,3,5,7	4	4	3.42	2
		R.TRPSEQLY@YLSR.A	Y404	Y	U	1,2,3,4,5,6,7,8,9,10	3	18	3.93	3
							15		3.88	2
ELAV-like protein 1	P70372	K.NMALLSQLY@HSPAR.R	Y200	N*	U	2,4,5,9	3	4	3.52	2
							1		2.61	3
ELAV-like protein 2	Q60899	K.TNQAILSQLY@QSPNR.R	Y219	Y	U	2,3,7	3	3	4.34	2
Fragile X mental retardation syndrome related protein 1 homolog	Q61584	K.EISEGDEVEVY@SR.A	Y68	N*	U	9	1	5	2.41	2
		K.KEISEGDEVEVY@SR.A	Y68			1,2,8,9	2		3.02	3
							2		4.35	2
		L.KDPDSNPY@SLL.D	Y506	N	U	12	1	1	3.16	2

Fragile X mental retardation syndrome related protein 2 homolog	Q9WVR4	R.LPPPADYNKEITEGDEVEVY@SR.A	Y78	Y	U	1,2	2	2	3.92	3
		L.KDPDSNPY@SLLDTSEPEPPVDSEPGEPPPASAR.R	Y520	N	U	11	1	1	4.18	3
Insulin-like growth factor 2 mRNA-binding protein 2	Q5SF07	K.SGY@AFVDYPDQNWAIR.A	Y40	N*	U	2,3,6,8,9,10	6	6	5.17	2
Insulin-like growth factor 2, binding protein 1	Q80US9	K.SGY@AFVDC*PDEHWAMK.A	Y39	N*	U	2,10	2	2	3.49	3
Interleukin enhancer-binding factor 3	Q9Z1X4	R.VLEC*LASGIVMPDGSGIY@DPC*EKEATDAIGHLDR.Q	Y292	Y	U	3,4,5	3	3	5.29	3
Matrin-3	Q8K310	R.SATREPPY@RVPR.D	Y171	N*	U	1	1	1	2.55	3
		R.SQESGYY@DRMDYEDDRLR.D	Y214	N*	U	2,8,9,10	4	4	3.65	3
Polyadenylate-binding protein 1 -- PABP1 (PABC4)	P29341	Y.VGDLHPDVTEAM#LY@EKF.S	Y28	Y	U	17	1	5	4.08	3
		Y.VGDLHPDVTEAMLY@EKF.S	Y28			11,16,17,18	4		3.82	2
		K.ALY@DTFSAFGNILSC*K.V	Y116	N*	U	8	1	1	4.27	2
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKL.H	Y232	Y	C	11,12,14,16	4	10	3.90	2
		Y.TIQGQY@AIPQPDLTKLHQLAM#.Q	Y232			11,12	2		4.64	3
		Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232			11,13,17	3		3.47	3
							1		3.76	2
Poly(rC)-binding protein 3	P57722	K.PASTPVIFAGGQAYTIQGQY@AIPHPDLTK.L	Y201	Y	U	1,2	2	2	3.97	3
Protein SMG7	Q5RJH6	K.VPEFYWDSSY@SMADNR.A	Y826	Y	U	9,10	2	2	4.78	2
Pumilio homolog 1	Q80U78	R.SQDDAMVDY@FFQR.Q	Y83	N*	U	2,7,9	3	3	4.55	2
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S	Y124	N*	C	7,8	2	2	3.64	3
		R.YDSRPGGYGYGY@GR.S	Y126	N	C	6,10	2	2	3.19	3
Ras-GTPase-activating protein binding protein 1 -- G3bp1	P97855	K.NSSYAHGGLDSNGKPADAVY@GQK.E	Y56	N	U	2,8	2	2	3.83	3
Ras-GTPase-activating protein SH3-domain binding protein	UPI0000D62F64	K.NSSYAHGGLDSNGKPADAVY@GKK.E	Y56	Y	U	1,7,9,10	4	4	4.06	3
Ras-GTPase-activating protein binding protein 2	P97379	R.NSSYVHGGVDASGKPQEAVY@GQNDIHHK.V	Y56	N*	U	2	1	2	3.91	3
		Y.VHGGVDASGKPQEAVY@GQNDIHHKVL.S	Y56			11	1		5.24	3
Regulator of differentiation 1 -- Rod1	Q8BHD7	R.SQPVY@IQYSNHR.E	Y98	N*	U	1,7	2	2	2.51	2
Regulator of nonsense transcripts 1 -- RENT1	Q9EPU0	L.AELNFEEDEEDTY@YTKDLPVHAC*SY.C	Y108	Y	U	16,18	2	4	4.78	3
		L.AELNFEEDEEDTY@YTKDLPVHAC*.S	Y108			14	1		4.18	3
		L.LAELNFEEDEEDTY@YTKDLPVHAC*.S	Y108			14	1		4.94	3
		K.RFTAQGLPDLNHSQVY@AVK.T	Y472	N*	U	1,3,4,5,7	5	5	4.77	3
		R.FM#TTAMY@DAR.E	Y930	N*	U	3	1	7	2.56	2
		R.FMTTAMY@DAR.E	Y930			1,2,3,4,5,9	6		3.48	2
		R.AYQHGGVTGLSQY@.-	Y1113	N*	U	2	1	1	2.37	2
PROTEIN SYNTHESIS AND PROCESSING										
tRNA synthetases										
Alanyl-tRNA synthetase	Q8BGQ7	K.DNFWEMGDTGPC*GPC*SEIHY@DR.I	Y192	N*	U	1,3,4,6,7,10	6	6	4.55	3
Arginyl-tRNA synthetase	Q9D0I9	K.SDGGYTY@DTSDLAAIK.Q	Y384	N*	U	2,8,9,10	4	4	4.92	2
Bifunctional aminoacyl-tRNA synthetase	Q8CGC7	R.GFFIC*DQPYEPVSPY@SC*R.E	Y690	N	U	1,2,3,4,5,6,7,8,9,10	2	28	3.56	3
							16		4.53	2
		R.RGFFIC*DQPYEPVSPY@SC*R.E	Y690			1,2,5,6,7,8,10	7		4.83	3
							3		4.13	2
Cysteinyl-tRNA synthetase	Q9ER72	K.VTWYC*C*GPTVY@DASHMGHAR.S	Y143	N*	U	1,3	2	2	2.78	3
Histidyl-tRNA synthetase	Q61035	K.LIY@DLKDQGGELLSLR.Y	Y115	Y	U	1,2,3,4,5,6,7,9,10	9	21	5.12	3
							7		5.95	2
		K.YGEDSKLIY@DLKDQGGELLSLR.Y	Y115			2,6,7,8	4		5.02	3
		L.TGKYGEDSKLIY@DLKDQGGELL.S	Y115			14	1		3.46	3
Isoleucine-tRNA synthetase	Q6NXK4	K.NNDLC*Y@WVPEFVR.E	Y434	N*	U	1,2,3,4,5,6,7,8,9,10	10	10	4.45	2
lysyl-tRNA synthetase	Q8C292	K.ITYHPDGPEGQAY@EVDFTPPFR.R	Y381	Y	U	1,3,8,9	4	5	4.19	3
		K.ITYHPDGPEGQAY@EVDFTPPFRR.I	Y381			7	1		4.27	3
Valyl-tRNA synthetase	Q9Z1Q9	R.LHEEGVIY@R.S	Y468	N*	U	1,2,3,10	4	4	2.77	2
Translation machinery										

40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	N	C	1,4,6,7,8,9,10	7	7	3.24	2
60S ribosomal protein L3	P27659	K.NNASTDY@DLSDK.S	Y306	N	U	1,2,4,8,10	5	5	3.47	2
60S ribosomal protein L4	Q9D8E6	R.KLDELY@GTWR.K	Y264	N*	U	1,4,5,9	4	4	2.95	2
mitochondrial ribosomal protein S27	UPI00001C5303	F.VDNIASREDLDSAEY@YLY.K	Y90	Y	U	16,17,18	3	6	3.36	2
		R.FVDNIASREDLDSAEY@YLYK.F	Y90			2,3	2		4.12	3
		R.EDLDSAEY@YLYK.F	Y90		U	7	1		3.79	2
Eukaryotic translation initiation factor 2A	Q640P8	L.VIASTEVDKTGASY@YGEQTLH.Y	Y250	N*	U	11	1	4	3.10	3
		L.VIASTEVDKTGASY@YGEQTLHY.I	Y250			11,16,17	3		5.43	3
		K.LISKPVASDSTY@FAWC*PDGEHILTATC*APR.L	Y362	Y	U	2,3,4,5,10	8	13	5.67	3
		K.PVASDSTY@FAWC*PDGEHILTATC*APR.L	Y362			3	1		3.43	3
		L.ISKPVASDSTY@F.A	Y362			11,12	2		3.25	2
		Y.KLISKPVASDSTY@F.A	Y362			11,18	2		4.10	2
Eukaryotic translation initiation factor 3 subunit 1	Q66JS6	L.KATM#KDDLADY@GGYEGGYVQDYEDFM#.-	Y248	Y	U	17	1	5	5.69	3
		L.KATMKDDLADY@GGYEGGYVQDYEDFM#.-	Y248			17	1		3.96	3
		L.KATMKDDLADY@GGYEGGYVQDYEDFM.-	Y248			16,17,18	3		5.00	3
Eukaryotic translation initiation factor 3, subunit 7	O70194	R.NLAMEATY@INHNFSQQC*LR.M	Y317	Y	U	1,3,4,5,6,7,8,10	8	8	4.21	3
Eukaryotic translation initiation factor 3, subunit 8	Q8R1B4	F.DHKQGTY@GGY.F	Y879	N*	U	11	1	14	2.31	2
		F.DHKQGTY@GGYF.R	Y879			11,12,13,14,15,18	6		3.77	2
		L.GSLVENNERVFDHKQGTY@GGY.F	Y879			11,13,15,16,17,18	6		4.29	3
		R.VFDHKQGTY@GGYFR.D	Y879			3	1		2.52	3
Eukaryotic translation initiation factor 3, subunit 9	Q8JZQ9	R.MTLDTLSIY@ETPSMGLLDKK.S	Y 438	N*	U	1,2,3,4,5	5	5	3.86	3
Eukaryotic translation initiation factor 3 subunit 10	P23116	K.KQPALDVLY@DVMK.S	Y32	N*	U	1,2,3,5,6,7,9,10	10	11	4.47	2
		F.LEVGKKQPALDVLY@DVM.K	Y32			14	1		3.04	2
Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Y.SASQGAY@YIPGQGRSTY.V	Y110	Y	U	11,12	2	2	3.57	2
Eukaryotic translation initiation factor 4B	Q8BGD9	F.LGNLPY@DVTEDSIKDFF.R	Y105	N*	U	11,12,13,14	4	6	4.96	2
		K.SPPYTAFLGNLPY@DVTEDSIKDFFR.G	Y105			4,5	2		6.60	3
Eukaryotic initiation factor 4A-I	P60843	K.VVMALGDY@MGASC*HAC*IGGTNVR.A	Y126	Y	U	2	1	2	3.36	3
		M.ALGDY@MGASC*H.A	Y126			11	1		2.16	2
		R.GFKDQIY@DIFQK.L	Y197	N*	C	1,2,3,4,5,6,7,8,9,10	8	21	3.80	3
							13		4.00	2
Eukaryotic translation initiation factor 4H	Q9WUK2	R.AY@SSFGGGR.G	Y11	N	U	8,9,10	3	3	2.52	2
		H.GSRSQKELPTEPPY@TAY.V	Y41	N*	U	11	1	5	3.29	2
		Q.KELPTEPPY@TAY.V	Y41			11,12,17,18	4		3.49	2
		R.SQKELPTEPPYTAY@VGNLPFNTVQGDIDAIFK.D	Y44	N	U	8	1	1	4.86	3
Elongation factor 1-alpha 1 -- eEF1A-1 (eEF1A-2)	P10126	K.STTTGHLIY@K.C	Y29	N	C	1,2,3,4,5,6,7,8,9,10	18	18	3.09	2
		R.EHALLAY@TLGVK.Q	Y141	N	C	1,3,4,7	4	4	3.17	2
G1 to phase transition 2 (GSPT2)	Q9CY91	K.TAGVKY@LIVLINK.M	Y347	Y	C	8	1	1	2.99	2
Laminin receptor 1 -- ribosomal protein SA	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	N	C	1,2,3,5,7	5	5	6.27	3
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.TVSDLIDQKVY@ELQASR.V	Y72	N*	U	1,2,3,4,5,6,7,8,9,10	12	27	5.06	3
							11		5.02	2
		K.VY@ELQASR.V	Y72			8	1		2.24	2
		Y.FHKTVSDLIDQKVY@EL.Q	Y72			11,12,14	3		3.87	2
		R.VSSDVIDQKVY@EIQDIYENSWTK.L	Y89	N*	U	5	1	1	4.49	3
		R.QLEVY@TSGGDPESVAGEYGR.H	Y247	Y	U	2,10	2	2	4.72	2
		K.GDPQVYEELFSY@AC*PK.F	Y415	N*	C	1,2,3,5,6,7,8,9,10	10	11	4.88	2
		R.MQKGDPQVYEELFSY@AC*PK.F	Y415			2	1		2.64	2
Post-translational modifiers										
N-terminal acetyltransferase complex ARD1 subunit homolog A	Q9QY36	F.QISEVEPKY@YADGEDAY.A	Y137	N*	U	11,12	2	9	3.31	2
		L.NFQISEVEPKY@YADGEDAY.A	Y137			11,12,13,14,15,16,17	7		4.92	2
		K.YYADGEDAY@AMKR.D	Y145	N*	U	2,7,8,9	4	4	3.21	2
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	L.RSQTDSLFGDSGVY@DTPSSY.S	Y576	N*	C	17	1	1	4.42	2
Glutathione S-transferase P 1	P19157	K.YVTLIY@TNYENGK.N	Y108	Y	U	7	1	2	3.38	2
		K.YVTLIY@TNYENGKNDYVK.A	Y108			7	1		4.04	2
Chaperones and associated proteins										

BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I	Y246	N	C	1,2,7	3	4	4.24	3
		K.THYPAQQGEYQPQQPVY@HK.I	Y253	N	U	1,2,4,5,6,8,9,10	8	9	4.98	3
		K.THYPAQQGEY@QPQQPVY@HK.I	Y246,Y253			2	1		3.92	3
DnaJ homolog subfamily B member 4	Q9D832	K.VSLEEIY@SGC*TK.R	Y172	N	U	2,3,4	3	3	3.20	2
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I	Y336	N	C	1,2,3,4,5,8,9,10	10	14	3.70	3
							4		5.24	2
		K.NAVEEYVY@EMRDKLSGEYEK.F	Y627	Y	U	6,7,8,9,10	5	5	4.31	3
Heat shock cognate 71 kDa protein	P63017	R.MVQEAEKY@KAEDEKQR.D	Y525	N*	U	1	1	1	3.66	3
Heat shock protein 75 kDa, mitochondrial precursor	Q9CQN1	R.NIY@YLC*APNR.H	Y500	N*	U	2,4,5,6,7,9,10	7	7	3.43	2
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	N	C	1,2,3,5,6,7,8,9,10	11	11	3.26	2
Heat-shock protein 105 kDa	Q61699	K.NAVEEC*VY@EFR.D	Y644	N*	U	4	1	4	2.70	2
		K.NAVEEC*VY@EFRDK.L	Y644			1,2,7	3		3.85	2
T-complex protein 1, beta subunit	P80314	F.INRQLIY@NYPEQLF.G	Y296	N*	U	11,12,13,14,16,17,18	8	11	3.84	2
		R.QLIY@NYPEQLFGAAGVMAIEHADFAGVER.L	Y296			3,4,5	3		4.22	3
T-complex protein 1, theta subunit	P42932	K.HFSGLEEAVY@R.N	Y29	N	U	1,2,6,7,8,9,10	7	7	3.53	2
PROTEIN DEGRADATION										
Ubiquitin conjugation regulators										
Anaphase promoting complex subunit 2	Q8BZQ7	K.VRDQQLIY@SAGVYR.L	Y825	N*	U	2,3,4	1	30	2.58	3
							2		4.44	2
		K.VRDQQLIY@SAGVYRLPK.N	Y825			1,2,3,5,6,7,8,9,10	9		6.13	3
		R.DQQLIY@SAGVYR.L	Y825			1,2,3,4,6,7,8,10	8		4.35	2
		R.DQQLIY@SAGVYRLPK.N	Y825			1,2,5,7,8,9,10	3		3.45	3
							7		4.40	2
CBL E3 ubiquitin protein ligase	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L	Y672	N	C	1	1	4	2.71	3
		K.PSSSANAIY@SLAARPLPMPK.L	Y672			1,3,7	3		4.45	3
F-box-like/WD-repeat protein TBL1X	Q9QXE7	K.HQEPVY@SVAFSPDGK.Y	Y459	N*	U	1,4,5,6,7,9,10	7	7	4.17	2
F-box-like/WD-repeat protein TBLR1	Q8BHJ5	K.HQEPVY@SVAFSPDGR.Y	Y446	N*	U	1,2,3,4	4	4	4.21	2
HECT, UBA and WWE domain-containing protein 1	Q7TMY8	R.EMFNPMY@ALFR.T	Y4081	N*	U	9	1	1	2.84	2
Ubiquitin conjugating enzyme 7 interacting protein 3	Q9WUB0	R.NSQEAEVAC*PFIDSTY@SC*PGK.L	Y318	N	U	1,2,3,4,6,7,8,9,10	3	12	5.35	3
							9		5.61	2
Ubiquitin-conjugating enzyme	O88738	K.VIFVDDY@AVGC*R.K	Y107	Y	U	4	1	2	2.34	2
		K.VIFVDDY@AVGC*RK.D	Y107			2	1		3.18	2
Ubiquitin-conjugating enzyme E2O	Q6PCR9	K.LRPSGDDVELIGEEEDVSVY@DIADHPDFR.F	Y412	Y	U	8,10	2	2	5.39	3
Ubiquitin-protein ligase E3 Mdm2	P23804	S.DEDDEVY@RVTVY@QTGESDTDSFEGDPEISLADY.W	Y279	N*	U	15	1	1	2.66	3
Proteasome components										
26S protease regulatory subunit S10B	P62334	K.GC*LLY@GPPGTGK.T	Y173	N*	U	1,3,4	3	3	3.44	2
26S protease regulatory subunit 8	P62196	K.GVLLY@GPPGTGK.T	Y189	N*	U	2	1	1	2.47	2
26S protease regulatory subunit 6B	P54775	L.SFLGPEPEDLEDLY@SRY.K	Y41	N*	U	11	1	1	3.11	2
26S proteasome non-ATPase regulatory subunit 7	P26516	W.FLDHDYLENM#Y@GM#F.K	Y79	Y	U	15,18	2	9	3.49	2
		W.FLDHDYLENMY@GM#F.K	Y79			16,17,18	3		3.55	2
		W.FLDHDYLENMY@GMF.K	Y79			11,12,16,18	4		3.81	2
Proteasome subunit alpha type 2 -- PSMA2	P49722	L.ATEKKQKSILY@DERSVH.K	Y56	N*	U	11	1	1	3.37	3
		H.IGLVY@SGM#GPDYRVL.V	Y75	N*	C	11,15	2	72	3.74	2
		H.IGLVY@SGMGPDYRVL.V	Y75			11,12,13,14,15,16,17,18	9		4.40	2
		H.KVEPITKHIGLVY@SGM#GPDYRVL.V	Y75			11,17	2		4.37	3
		H.KVEPITKHIGLVY@SGMGPDYRVL.V	Y75			11,12,13,15,16,17,18	8		6.11	3
		K.HIGLVY@SGM#GPDYR.V	Y75			1,2,3,4,5,6,7,8,10	9		4.21	3
							9		4.56	2
		K.HIGLVY@SGM#GPDYRVL.V	Y75			12	1		2.17	2
		K.HIGLVY@SGMGPDYR.V	Y75			1,2,3,4,5,6,7,8,9,10	10		3.86	3
							14		5.16	2
		K.HIGLVY@SGMGPDYRVL.V	Y75			11,12,13,15,16,17	4		3.42	3
							3		4.35	2

		L.VY@SGMGPDYRVL.V	Y75			18	1		2.75	2
		K.LAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100	N	U	5,6,7	3	10	4.75	3
		K.LAQQYYLVY@QEPIPTAQLVQR.V	Y100	N*	U	1,2,3,4,5,6,7,8,10	9	45	5.16	3
							8		5.18	2
		R.KLAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100			1,2,4,5,6,7,8	7		5.64	3
		R.KLAQQYYLVY@QEPIPTAQLVQR.V	Y100			1,2,3,4,5,6,7,8,9,10	13		5.74	3
							3		4.38	2
		Y.YLVY@QEPIPTAQL.V	Y100			12,14	2		2.96	2
Proteasome subunit alpha type 6	Q9QUM9	Y.KC*DPAGYY@C*GF.K	Y160	N*	U	11	1	1	2.85	2
Proteasome subunit beta type 1	O09061	K.GAVY@SFDPVGSYQR.D	Y149	N*	U	1,2,3,4,5,7,8,10	8	8	4.44	2
		K.DVFISAAERDVY@TGDALR.I	Y215	Y	U	1,3	2	2	4.58	3
Proteasome subunit beta type 4 precursor	P99026	M.RVNDSTMLGASGDY@ADF.Q	Y102	N	U	17,18	2	7	4.81	2
		R.VNDSTMLGASGDY@ADFQYLK.Q	Y102			3,4,7,8,10	5		4.81	2
Proteasome subunit beta type 5 precursor	O55234	K.RGPGLY@YVDSEGNR.I	Y116	Y	U	1,2,4	3	11	3.86	2
							1		2.98	3
		R.GPGLY@YVDSEGNR.I	Y116			2,3,4,5,7	6		3.54	2
		W.DKRGPGLY@YVDSEGNRISGTAF.S	Y116			11	1		3.07	3
		R.AIY@QATYR.D	Y165	N*	U	1,3,4,6,8,9,10	7	7	2.71	2
		R.DAYSGGAVNLY@HVR.E	Y181	Y	U	2	1	6	3.54	2
		R.DAYSGGAVNLY@HVREDGWIR.V	Y181			1,2,3,5,10	5		3.03	3
Proteasome subunit beta type 7 precursor	P70195	L.VLGGVDVTGPHLY@SIYPHGSTDKLPY.V	Y154	N	U	11,12,18	3	3	4.40	3
Other proteolytic regulators										
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	K.VISSVSY@YTHR.H	Y367	Y	U	3,7,9,10	4	4	2.88	2
		F.NDY@FEFPRELDMEPY.T	Y1815	Y	U	12,14	2	9	3.69	2
		K.FNDY@FEFPR.E	Y1815			1,2,7,9,10	5		3.12	2
		K.FNDY@FEFPRELDMEPYTVAGVAK.L	Y1815			1,8	2		5.97	3
		R.PY@T@GNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2431,Y2439	Y	U	7,9	2	2	4.10	3
		R.RPYTGNPQY@TYNNWSPPVQSNETSNGYFLER.S	Y2437	Y	U	2,3	2	2	5.48	3
		R.RPYTGNPQYT@Y@NNWSPPVQSNETSNGYFLER.S	Y2439	N*	U	2,7,9,10	4	20	4.31	3
		R.RPYTGNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2439			1,2,3,4,5,6,7,8,9,10	12		7.26	3
		R.RPYTGNPQYT^Y@NNWSPPVQSNETSNGYFLER.S	Y2439			2,10	2		4.85	3
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	N*	C	2,4,5,6,7,8,9	7	14	3.00	2
		R.MTELY@DYPKYSC*HFK.K	Y71			10	1		3.15	3
		Y.KERM#TELY@DYPKY.S	Y71			11,17	2		2.93	3
		Y.KERMTELY@DYPKY.S	Y71			11,12,13,15	1		4.15	3
							3		2.95	2
NUCLEAR PROTEINS										
Histone H2B type 1-B	Q64475	R.KESYSVYVY@K.V	Y43	Y	U	5,6,7,8,9,10	6	6	3.92	2
Histone H4	P62806	K.RISGLIY@EETRGVL.K	Y51	N	U	11	1	12	3.72	2
		R.ISGLIY@EETR.G	Y51			1,2,3,4,5,7,8,9,10	11		3.51	2
Nucleolar protein 10	Q5RJG1	K.MGIY@YIPVLGPAPR.W	Y339	N*	U	1	1	1	3.28	2
Nucleolin	P09405	R.SVSLY@YTGEK.G	Y464	N*	U	1,3	2	2	2.47	2
PREDICTED: scaffold attachment factor B	UPI00001E3C2C	R.RDDAY@WPEAK.R	Y723	N*	U	2	1	1	2.19	2
SET protein	Q9EQU5	F.YFDENPY@FENKVL.S	Y145	N*	U	11	1	20	2.38	2
		R.IDFYFDENPY@FENK.V	Y145			1,2,3,4,5,7,8,9,10	13		4.74	2
		R.IDFYFDENPY@FENKVLSK.E	Y145			3,4,5	2		3.07	3
							1		4.91	2
		Y.RIDFYFDENPY@FENKVL.S	Y145			11,12	2		5.43	2
		Y.FDENPY@FENKVL.S	Y145			14	1		2.80	2
Structural maintenance of chromosome 3	Q9CW03	Y.IEERLHTLEEEKEELAQY@QKW.D	Y213	N*	U	11	1	1	3.38	3
Telomerase-binding protein EST1A	P61406	K.FQNSDNPY@YYPR.T	Y507	N*	U	1,2,3,4,5,6,7,8	8	8	4.27	2
Translin	Q62348	K.KVEEVVY@DLSIR.G	Y210	N*	U	5	1	1	2.21	2
MISCELLANEOUS										
Catalase	P24270	K.GAGAFGY@FEVTHDITR.Y	Y83	N*	U	2	1	1	3.36	2
		K.LVNADGEAVY@C*K.F	Y230	N	U	2	1	1	3.68	2
DNA dC->dU editing enzyme APOBEC-3	Q99J72	K.HLC*Y@YHR.M	Y255	Y	U	1,2,3,4,5,6,8,9,10	1	22	2.70	3
							12		2.44	2

		R.VKHLC*Y@YHR.M	Y255			1,2,3,4,5,9,10	7		3.54	3
		Y.NQRVKHLC*Y@Y.H	Y255			11,17	2		3.01	2
		K.HLC*YY@HR.M	Y256	Y	U	5	1	4	2.10	2
		Y.NQRVKHLC*YY@.H	Y256			12,15,18	3		2.97	2
Pol polyprotein [Moloney murine leukemia virus (MoMLV); Mus musculus]	P03355	L.AAAY@QEQLDRPVVPHPY.R	Y1105	Y	U	11,12,14,17	4	11	4.22	3
		H.PY@RVGDTVW.V	Y1118	Y	U	11,12,14,15,16	9	20	2.73	2
		L.AAAY@QEQLDRPVVPHPY@RVGDTVW.V	Y1105,Y1118			11,12,14,15,16,17,18	7		4.38	3
		L.AAAYQEQLDRPVVPHPY@RVGDTVW.V	Y1118			12,16,17	3		4.66	3
		Y.QEQLDRPVVPHPY@RVGDTVW.V	Y1118			18	1		2.71	3
		K.NLEPRWKGPY@TVL.L	Y1142	Y	U	11,13,16	3	14	2.24	2
		R.WKGPY@TVLLTTPTALK.V	Y1142			1,2,3,4,5,6,7,8,9,10	11		4.62	2
Serpin B6	Q60854	K.FKLEENYNMNDALY@KLGMTDAFGGR.A	Y289	Y	U	2	1	3	5.18	3
		Y.NMNDALY@KLGMTDAF.G	Y289			12,14	2		4.10	2
Voltage-dependent anion-selective channel protein 1	Q60932	K.YRWTEY@GLTFTEK.W	Y80	N*	U	10	1	1	2.83	2
FUNCTION UNKOWN OR UNCERTAIN										
Named proteins of unknown/uncertain function										
Ankyrin repeat domain-containing protein 25	Q8BX02	L.HVPAPFPGTPGQASPAAFPSKEPDPPY@S@VETPYGY.R	Y32	Y	U	15,17	2	3	4.26	3
		L.HVPAPFPGTPGQASPAAFPSKEPDPPY@SVETPYGY.R	Y32			18	1		4.63	3
Anthrax toxin receptor 1 precursor	Q9CZ52	K.WPTVDASY@YGGR.G	Y380	N*	U	4,7	2	2	2.30	2
ApoA-I binding protein	Q8K4Z3	K.KYQLNLPSYPDTEC*VY@RLQ.-	Y279	Y	U	1,2,3,4,6,7,8,10	8	10	4.48	3
		K.YQLNLPS@YPDT@ECVY@RLQ.-	Y279			4	1		3.01	3
		K.YQLNLPSYPDTEC*VY@RLQ.-	Y279			7	1		3.42	2
Ataxin-2	O70305	K.GLPQPTISFDGIY@ANVR.M	Y233	Y	U	2,3,8	3	3	4.42	2
		R.VALENDDRSEEEKY@TAVQR.N	Y440	Y	U	1,3,4,5,8,9,10	7	8	4.14	3
		R.VALENDDRS^EEEKY@TAVQR.N				7	1		3.23	3
Ataxin-2-like protein	Q7TQH0	K.GPPQSPVFEGVY@NNSR.M	Y116	N*	U	2,7,8	3	3	4.24	2
BAT2-ISO homolog [fragment] (Bat2d)	Q8BMJ4	R.M#MWGSDPY@HAEPQQAATPK.S	Y788	Y	U	3,5	2	10	3.75	3
		R.MM#WGSDPY@HAEPQQAATPK.S	Y788			3	1		3.16	3
		R.MMWGSDPY@HAEPQQAATPK.S	Y788			1,2,3,4,5	4		3.65	3
							3		4.77	2
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	L.TTTRKTPQGPPEIY@SDTQFPSLQ.S	Y213	N	C	11,12	2	14	2.95	3
		R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213			1,2,3,4,5,6,7,8,9,10	11		5.88	3
							1		2.71	2
Centrosomal protein 170	UPI0000D62DCC	K.HVEGQSAAASEEALFPFC*REPSY@FEIPTK.E	Y240	Y	U	1,2	2	2	5.12	3
DENN/MADD domain containing 2C	Q6P9P8	K.SLENIY@YEPEGQEC*GPSINPLPKPR.R	Y185	Y	U	1,2	2	2	5.06	3
Dihydropyrimidinase-related protein 2	O08553	K.THNSALEY@NIFEGMEC*R.G	Y431	N*	U	1,6,9,10	3	4	3.69	3
							1		5.25	2
Discoidin, CUB and LCCL domain containing protein 2 precursor -- DCBLD2	Q91ZV3	K.SAATPEELVY@QVPQSTQELSGAGR.D	Y744	N	U	4	1	1	3.96	3
Discs, large homolog 5	Q3UGX5	Y.KEERDAVY@SEY.K	Y429	Y	U	15,18	2	2	2.56	2
Far upstream element binding protein 3 (FUSE binding protein 3) homolog	Q3TIX6	K.IDSIPHLNNSTPLVDPS@VY@GYGVQKR.A	Y51	N*	U	8,9	2	2	3.27	3
GPI-anchored protein p137 -- p137GPI	Q60865	F.TAPRDY@SGY.Q	Y609	Y	U	11,12,15,16,17,18	6	6	2.80	2
Grb10 interacting GYF protein 2	Q6Y7W8	F.LKEVESPY@EVHDY.T	Y1174	Y	U	11,12,15,16,17	4	11	3.91	2
							1		4.01	3
		F.LKEVESPY@EVHDYTRAY.L	Y1174			11,13,15,16,17,18	1		4.23	2
							5		4.72	3
High glucose-regulated protein 8	Q8K325	K.DGLNDDDFEPY@LSPQAR.P	Y37	N	U	1,2,3,4,6,7,8,9,10	9	9	4.63	2
Large proline-rich protein BAT2	Q7TSC1	K.KYSSLNLFDTY@KGK.S	Y26	Y	U	2	1	7	3.13	3
		K.YSSLNLFDTY@KGK.S	Y26			1,2,3,4,5	1		2.75	3
							5		3.77	2
		K.APPSTY@SGVFR.T	Y2098	Y	U	1,2,3	4	8	2.89	2
		R.LKAPPSTY@SGVFR.T	Y2098			1,2,4	3		3.65	3
							1		2.72	2
		R.IDLY@QQASPPDALR.W	Y2110	N*	U	4	1	1	2.72	2
Leucine rich repeat (in FLII) interacting protein 2 (Lrrfip2) [fragment]	Q8C062	R.DIY@DLKDQIHDVEGR.Y	Y5	N*	U	1,2,3,4,7	5	5	4.88	3

Mage-d2	Q99PB4	R.VPNSNPPEY@EFFWGLR.S	Y439	N*	U	1	1	1	3.86	2
Nsun2 protein	Q91YX9	R.LAQEGIY@TLYPFINSR.I	Y372	N*	U	6	1	1	4.21	2
OTU domain containing 4 protein -- Otud4; PREDICTED: HIV-1 induced protein HIN-1 isoform 1;	UPI0000218B34	K.DSSAMC*QSLLY@ELLYEK.V	Y169	Y	U	4,9,10	3	3	4.26	2
		R.ESY@YFGLSPEER.R	Y436	Y	U	1,2,3,4,5,6,7,8,9,10	10	10	3.30	2
		R.ESYY@FGLSPEER.R	Y437	Y	U	1,2,4	3	3	3.25	2
		R.LLY@EIQNR.D	Y458	Y	U	1,2,3,4,5,6,7,8,9,10	10	16	3.28	2
		R.LLY@EIQNRDEQAFPALSSSSVSQSPSQNSNAC*VPR.K	Y458			2,3,5,7,9,10	6		6.61	3
Pericentriolar material gene 1 protein [fragment]	Q91Y51	K.SNRPVS^ADGNY@RPLAK.T	Y961	N*	U	1	1	1	3.72	3
Periodic tryptophan protein 1 homolog -- Pwp1	Q9D6T6	R.VTWNHFSPC*HFLASTDDGFVY@NLDAR.S	Y367	Y	U	1,5,8	3	3	5.70	3
Pleckstrin homology-like domain, family B, member 2 -- PHLDB2	Q8K1N2	K.ADLDHY@TGRDSER.S	Y130	N	U	1,3,4,10	4	4	3.53	3
		K.SHDSVY@FLGGLEGR.K	Y161	N*	U	4	1	2	1.90	2
		R.NKSHDSVY@FLGGLEGR.K	Y161			2	1		3.63	3
Protein FAM51A1	Q8BHE1	R.LNDY@VNADHGLY@FNHR.R	Y167,Y175	Y	U	2,3,7	3	8	2.93	3
		R.LNDY@VNADHGLY@FNHRR.S	Y167,Y175			1,2,3,4,5	5		3.77	3
		R.LNDYVNADHGLY@FNHR.R	Y175	Y	U	1,2	2	10	3.52	3
PYM protein	Q8CHP5	R.VKEGYVPQEEVPVYENKY@VK.F	Y49	N*	U	7	1	1	3.13	3
Suppression of tumorigenicity 5	Q924W7	K.STLEENAY@EDIVGGLPKENPY@EDVDLK.N	Y485,Y498	N*,N*	U,C	2,8,9	3	3,3	4.37	3
SR-related CTD associated factor 6	Q8CGZ0	R.NSEGWEQNGLY@EFFR.A	Y723	N*	U	1,2,3,4,5,6,7,8,9,10	10	10	4.52	2
Tanc2 protein [fragment]	Q5EBP6	K.TNNAQNGHLLEDDY@YSPHGMLANGSR.G	Y1349	N*	U	1	1	1	5.38	3
Testis derived transcript	Q921W7	K.HTM#NEGEPAIY@AER.A	Y249	Y	U	3	1	9	1.96	2
		K.HTMNEGEPAIY@AER.A	Y249			1,2,3,4	4		3.76	3
							4		4.54	2
Trinucleotide repeat containing 6b	Q6NVE4	K.DLGTTDSGPY@FEK.G	Y1128	N*	U	1,4	2	4	2.80	2
		K.DLGTTDSGPY@FEKGGSHGLFGNSTAQSR.G	Y1128			1,3	2		4.44	3
		K.GIQNIDPESDPY@VTPGSVLGGTTTSPIVDTDHQLLR.D	Y1440	N*	U	2	1	1	3.19	3
Tripartite motif protein 16	Q99PP9	F.DC*KFSEPVY@AAF.W	Y523	Y	U	11	1	2	1.92	2
		K.FSEPVY@AAFWLSK.K	Y523			1	1		3.06	2
Tudor domain-containing protein 3	Q91W18	L.SNIKPVQTEAWEEEGTY@DHTIEF.R	Y618	Y	U	14,15,17	3	3	5.00	3
Ubiquitin-associated protein 2 -- UBAP2	Q91VX2	R.LPMDY@YGIPFAAPTALASR.D	Y853	N	U	1,2,4,5,6,7,8,9,10	9	12	5.84	2
							2		4.23	3
		R.LPM#DY@YGIPFAAPTALASR.D	Y853			7	1		3.85	2
		R.LPMDYY@GIPFAAPTALASR.D	Y854	N	U	7,8,9,10	4	4	5.57	2
		F.AAPTALASRDGNLANNPY@SGDVTKF.G	Y876	N	U	11,12,13,16,18	5	18	5.85	3
		L.ASRDGNLANNPY@SGDVTKF.G	Y876			11,12,15	2		6.06	2
							1		4.39	3
		N.NPY@SGDVTKF.G	Y876			12	1		2.95	2
		R.DGNLANNPY@SGDVTK.F	Y876			1,2,3,4,7,8,9,10	9		4.67	2
		K.SQASKPTY@GSAPYWTN.-	Y1124	N*	U	2,9,10	4	4	3.73	2
Ubiquitin associated protein 2-like -- UBAP2L	Q80X50	Y.TSQNNAQGPLY@EQRSTQ.T	Y612	Y	U	11,12,13,14,15,16,17,18	4	13	3.89	3
							9		4.53	2
		R.FPLDY@YSIPFPTPTTPLTGR.D	Y854	N	U	9	1	1	3.99	2
		R.DGSLASNPY@SGDLTK.F	Y878	Y	U	1,2,3,4,5,7,8,9,10	9	16	4.27	2
		L.TGRDGSLASNPY@SGDLTKF.G	Y878			11,12,13,14,16,17,18	7		5.79	2
Yippee-like 5	Q65Z92	N.S@KLGWIY@EFATEDSQRY.K	Y84	Y	U	11,13	2	2	3.20	2
YTH domain protein 3 -- Ythdf3	Q6NXJ8	K.SVVDYNAY@AGVWSQDKWK.G	Y488	Y	U	1,2,3,4,5	5	5	5.20	2
Novel ZZ type zinc finger domain containing protein	Q5SSH7	K.WKDFELPGDTLY@YR.F	Y2706	Y	U	1,2,3,4,5,6,9,10	7	18	4.42	3
							7		4.89	2
		W.KDFELPGDTLY@Y.R	Y2706			15,16,17,18	4		2.92	2
Unnamed proteins of unknown/uncertain function										
BC003940 protein [fragment]	Q8QZS4	R.FIY@EAWQGVER.D	Y70	Y	U	1,2,3,6,7,8,9,10	8	8	4.44	2
BC053440 protein [fragment]	Q8R2W2	K.INDTMY@FAPSMK.D	Y19	Y	U	4,5	2	2	3.62	2
Hypothetical ATP/GTP-binding site motif A homolog	Q3UHH1	L.HKTKEAAPAVGEEDDDYQAY@Y.L	Y729	Y	U	11,12,15,16,17,18	6	8	4.68	3

hypothetical ATP/GTP-binding site motif A (P-loop)/Zinc finger C-x8-C-x5-C-x3-H type containing protein	Q9DBS7	K.EAVY@SGVQSLR.S	Y508	N	U	2,9,10	3	3	2.28	2
hypothetical Domain of unknown function DUF71 containing protein	Q9CQ28	R.VYTQC*EGDEVEDLY@ELLK.L	Y97	N	U	7,8,9,10	4	4	5.08	2
hypothetical G-protein beta WD-40 repeat/Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats circular profile/Serine-rich region profile/WD40-like containing protein -- WDR70	Q3TWF6	K.AAEDNPY@WVSPAYSK.T	Y621	N*	U	2	1	1	3.53	2
hypothetical 5'3'-Exonuclease N- and I-domains containing protein	Q8BMI4	R.LQENC*GANTSLPY@SFSDK.A	Y747	Y	U	1,2,3	3	3	4.13	2
DNA segment, Chr 5, ERATO Doi 585, expressed -- D5Ertd585e	Q6P1H6	R.IREYLM#GHY@YVPLLR.A	Y483	Y	U	6,7	2	8	3.36	3
		R.IREYLMGHY@YVPLLR.A	Y483			1,2,3,5,6,7	6		4.63	3
hypothetical protein: E230015L20Rik protein	Q8C304	R.TNEIY@YLDPDAPLSRPSTQDNQYQK.S	Y416	Y	U	1,2,4,5,10	5	5	4.33	3
hypothetical protein LOC106840	Q8C4B4	K.PEDNVY@SIDFTR.F	Y92	Y	U	5,6	2	7	3.80	2
		R.VTENYLC*KPEDNVY@SIDFTR.F	Y92			1,2,5,6,8	5		5.27	3
PREDICTED: zinc finger protein 650	UPI0000D65C57	K.KLPIAEEEQIY@PWDTC*AAVHDVR.L	Y335	Y	U	1,3	2	2	4.09	3
PREDICTED: similar to Oligophrenin 1	UPI0000D668EB	K.LWLEAMDGKEPIY@TLPAIISK.K	Y371	Y	C	1,2,8	3	6	4.16	3
		R.KLWLEAM#DGKEPIY@TLPAIISK.K	Y371			6	1		3.72	3
		R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371			1,10	2		4.65	3
PREDICTED: similar to ring finger and KH domain containing 2	UPI000042893E	R.LSEQGGDFGY@SGYLFPGYGVGK.Q	Y188	Y	U	2,3,5,6,7,9,10	7	7	5.48	2
hypothetical protein 1500002O20Rik	Q9DB90	K.EGQRPTQPVY@QIQNR.G	Y147	N	U	2	1	1	2.69	3
MKIAA0183 protein [fragment]	Q6A0A9	K.PAVPQVPSPGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457	Y	U	1,2,4,6,7	5	7	4.65	3
		K.PAVPQVPS@PGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457			7	1		4.00	3
		K.PAVPQVPSPGGT@PGQAPYPY@SLSEPALTLDTSGK.N	Y457			1	1		4.33	3
		F.GGHY@GETVATGPY@RAF.R	Y968	Y	U	11	1	2	3.02	2
		F.GGHYGETVATGPY@RAF.R	Y968			11	1		3.62	2
Protein FAM125A	Q78HU3	R.RTDSIY@EASS@LYGISAMDGVPFTLHPR.F	Y202	N	U	2	1	1	4.42	3
PREDICTED: similar to la related protein isoform 1	UPI0000D66C58	R.THFDYQFGY@R.K	Y412	N*	U	1,2,5,6,8,9,10	7	7	3.15	2
Similar to leucine-rich neuronal protein homolog	Q3U222	L.GFGSC*HEELY@SGRPY.G	Y203	Y	U	11,17	2	3	3.22	3
							1		3.45	2
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	Y	C	1,2,3	3	3	3.69	3

END

Table S2. Phosphotyrosine sites from the Src-transformed mouse embryo fibroblast population

Protein Name(s)[a]	UniProt #[a]	Peptide[b]	pY site(s)[b]	MH[h]	dM[h]	ΔCn 2nd ranked peptide[i]
SIGNALING: PROTEIN KINASES AND PHOSPHATASES						
Tyrosine kinases (nonreceptor)						
Rous sarcoma oncogene, isoform 2 -- Src (Yes) (Fyn)	Q80XU2	F.VALY@DYESRTETDL.S	Y92	1756.24	1.45	0.1686 F.VALYDY@ESRTETDL.S
		F.VALY@DYESRTETDLSF.K	Y92	1990.08	1.19	0.1415 F.VALYDY@ESRTETDLSF.K
		R.AGPLAGGVTTFVALY@DYESR.T	Y92	2168.38	1.34	0.1428 R.AGPLAGGVTTFVALYDY@ESR.T
		R.TQFNSLQQLVAY@YSK.H	Y231	1871.54	1.63	0.1431 R.TQFNSLQQLVAYY@SK.H
		L.IEDNEY@TARQGAKFPIKW.T	Y418	2247.74	1.64	0.0272 L.IEDNEYT@ARQGAKFPIKW.T
		R.LIEDNEY@TAR.Q	Y418	1304.34	0.75	0.0960 R.LIEDNEYT@AR.Q
		K.FPIKWTAPEAALY@GR.F	Y438	1801.66	1.74	none
				1800.72	0.80	none
		K.WTAPEAALY@GR.F	Y438	1315.29	0.67	none
		W.TAPEAALY@GRF.T	Y438	1277.18	1.57	none
Proto-oncogene tyrosine-protein kinase LCK	P06240	F.GLARLIEDNEY@TAREGAKFPIKW.T	Y393	2758.06	0.65	0.0692 F.GLARIIEDNEYT@AREGAKFPIKW.T
		F.GLARLIEDNEY@TAREGAKF.P	Y393	2233.42	0.32	none
		R.LIEDNEY@TAREGAKFPIKW.T	Y393	2361.29	1.12	0.0060 R.IIEDNEYT@AREGAKFPIKW.T
Tyrosine-protein kinase CSK	P41241	L.IKPKVMEGTVAAQDEFY@RSGW.A	Y184	2494.10	1.90	0.0801 L.IKPKVMEGTVAAQDEFYRS@GW.A
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	2365.75	0.68	none
		F.GMSRQEDGGVY@SSSGL.K	Y715	1710.81	1.09	0.1669 F.GMSRQEDGGVYS@SSGL.K
Proto-oncogene tyrosine-protein kinase ABL1	P00520	R.LMTGDTY@TAHAGAK.F	Y393	1517.37	0.69	0.0155 R.LMTGDTYT@AHAGAK.F
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	R.YM#EDSTY@YK.A	Y576	1296.63	1.14	0.0381 R.YM#EDS@TYYK.A
		R.YMEDSTY@YK.A	Y576	1279.91	0.42	0.0710 R.YMEDSTYY@K.A
		R.YMEDSTY@YKASK.G	Y576	1566.33	0.67	0.0349 R.YMEDST@YYKASK.G
		R.YMEDSTY@Y@K.A	Y576,Y577	1359.57	0.08	0.0699 R.YMEDST@YY@K.A
		R.YMEDSTY@Y@KASK.G	Y576,Y577	1646.05	0.39	0.0632 R.YMEDST@YY@KASK.G
Tyrosine kinases (receptor)						
Discoidin domain receptor 2 precursor -- DDR2	Q62371	F.GMSRNLY@SGDY@Y.R	Y735,Y739	1585.96	0.35	0.0552 F.GMSRNLY@SGDYY@.R
		R.NLY@S@GDYYR.I	Y735	1310.19	-0.33	0.1053 R.NLY@SGDY@YR.I
		R.NLY@SGDY@YR.I	Y735,Y739	1310.63	0.11	none
Ephrin type-A receptor 2 precursor	Q03145	K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	3074.95	1.45	0.0100 K.SEQLKPLKTY@VDPHTY@EDPNQAVLK.F
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	2842.29	0.87	0.1282 F.GLSRVLEDDPEAT@YTTSGGKIPIRW.T
Eph receptor B4	Q91YM0	Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596	3072.25	1.82	0.0665 Y.LIGHGTKVY@IDPFT@YEDPNEAVREF.A
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	K.IYNGDY@YR.Q	Y696	1143.81	0.33	0.0650 K.IYNGDYY@R.Q
		K.KIYNGDY@YR.Q	Y696	1272.39	0.81	0.1291 K.KIYNGDYY@R.Q
Other protein kinases						
Akt1: RAC-alpha serine/threonine-protein kinase (Akt-2) (Akt-3)	P31750	K.TFC*GTPEYLAPEVLEDNDY@GR.A	Y326	2527.51	1.44	none
Akt-3: RAC-gamma serine/threonine-protein kinase	Q9WUA6	K.Y@Y@AM#KILKKEVIIAK.D	Y173,Y174	1987.81	0.72	none
Calcium/calmodulin-dependent protein kinase type 1 --CaM kinase I	Q91YS8	R.DLKPENLLYY@SLDEDSK.I	Y150	2123.24	1.24	0.0970 R.DLKPENLLY@YSLDEDSK.I
				2122.80	0.80	0.0165 R.DLKPENLLY@YSLDEDS
Casein kinase I isoform alpha	Q8BK63	R.TLNHQYDY@TFDWTMLK.Q	Y294	2156.75	0.80	0.1528 R.TLNHQY@DYTFDWTMLK.Q
				2156.72	0.77	0.0489 R.TLNHQYDYT@FDWTMLK.Q
Casein kinase II, alpha chain	Q60737	K.VLGTEDLY@DYIDKYNIELDPR.F	Y255	2624.82	0.57	0.1599 K.VLGTEDLYDY@IDKYNIELDPR.F
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IGEGTY@GVVYK.G	Y15	1265.90	0.28	0.0999 K.IGEGT@YGVVYK.G
		K.IGEGT^Y@GVVYK.G	Y15	1248.05	0.43	none
		K.IGEGTYGVVY@K.G	Y19	1266.15	0.53	0.1347 K.IGEGTY@GVVYK.G
		K.IGEGTYGVVY@KGR.H	Y19	1479.30	0.56	0.0432 K.IGEGTY@GVVYKGR.H
Dual-specificity tyrosine-phosphorylation regulated kinase 1A --DYRK1A (DYRK1B)	Q61214	K.HINEVY@YAK.K	Y111	1218.25	1.68	0.1105 K.HINEVYY@AK.K
		K.VYNDGYDDDNY@DYIVK.N	Y145	2051.96	1.13	0.1993 K.VYNDGYDDDNYDY@IVK.N
		R.KVYNDGYDDDNY@DYIVK.N	Y145	2179.65	0.73	0.1330 R.KVYNDGYDDDNYDY@IVK.N

		Y.NDGYDDDNY@DYIVKNGEKW.M	Y145	2404.54	1.56	none
		R.IYQY@IQSR.F	Y321	1151.46	0.90	none
Glycogen synthase kinase-3 beta -- GSK-3 beta (GSK-3 alpha)	Q9WV60	L.VRGEPNVSY@IC*SRY.Y	Y216	1781.45	1.65	0.0666 L.VRGEPNVS@YIC*SRY.Y
		L.VRGEPNVSY@IC*SRYY.R	Y216	1944.85	1.99	0.1050 L.VRGEPNVS@YIC*SRYY.R
				1943.83	0.97	0.0427 L.VRGEPNVS@YIC*SRYY.R
		R.GEPNVSY@IC*SR.Y	Y216	1363.60	2.03	0.0862 R.GEPNVS@YIC*SR.Y
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638	2505.74	2.43	none
				2504.28	0.97	none
		K.VPIVINPNAY@DNLAIY@K.S	Y632,Y638	2076.41	-0.64	none
		K.VPIVINPNAYDNLAIY@K.S	Y638	1997.93	0.88	none
		N.AIKVPIVINPNAY@DNLAIY@KSF.L	Y632,Y638	2625.19	1.83	0.1125 N.AIKVPIVINPNAY@DNLAIYKS@F.L
Serine/threonine-protein kinase Nek9	Q8K1R7	R.NKEVYSWGC*GEY@GR.L	Y509	1785.16	0.44	none
				1785.91	1.18	none
Serine/threonine-protein kinase PRP4 homolog	Q61136	K.LC*DFGSASHVADNDITPY@LVSR.F	Y849	2519.30	2.18	0.0397 K.LC*DFGSASHVADNDITPYLVS@R.F
		H.VADNDITPY@LVSRF.Y	Y849	1690.14	0.32	0.1385 H.VADNDIT@PYLVSRF.Y
Protein phosphatases						
Low molecular weight phosphotyrosine protein phosphatase	Q9D358	K.QLIIEDPY@YGNDSDFEVVYQQC*LR.C	Y131	3046.44	2.09	0.0635 K.QLIIEDPYY@GNDSDFEVVYQQC*LR.C
		L.GSYDPQKQLIIEDPY@YGNDSDF.E	Y131	2646.00	1.85	0.1046 L.GSYDPQKQLIIEDPYY@GNDSDF.E
		K.QLIIEDPYY@GNDSDFEVVYQQC*LR.C	Y132	3045.49	1.14	0.0208 K.QLIIEDPY@YGNDSDFEVVYQQC*LR.C
				3045.81	1.46	0.0086 K.QLIIEDPY@YGNDSDFEVVYQQC*LR.C
14 kDa phosphohistidine phosphatase -- Phosphohistidine phosphatase 1	Q9DAK9	R.KIHVYGY@SM#GYGR.A	Y92	1628.10	1.35	0.1921 R.KIHVY@GYSM#GYGR.A
Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	R.TYDETY@TR.Y	Y764	1129.04	0.58	0.0450 R.TYDETYT@R.Y
		Y.SRTYDETY@TRY.R	Y764	1536.20	1.55	0.0398 Y.SRTYDET@YTRY.R
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	1484.24	1.47	none
Serine/threonine protein phosphatase 2A, catalytic subunit, alpha isoform -- PP2A alpha (PP2A beta)	P63330	R.QITQVY@GFYDEC*LR.K	Y127	1872.93	1.11	none
		R.C*GNQAAIMELDDTLKY@SFLQFDPAPR.R	Y284	3081.11	0.71	0.0390 R.C*GNQAAIMELDDT@LKYSFLQFDPAPR.R
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	1686.36	0.58	0.0791 H.IKIQNT@GDYYDLY.G
		K.IQNTGDY@YDLYGGEK.F	Y62	1815.88	0.10	0.0776 K.IQNTGDYY@DLYGGEK.F
Tyrosine-protein phosphatase, non-receptor type 14	Q62130	R.NLNIINTHAYNQPEELVY@SQPEMR.E	Y485	2954.15	0.76	0.0789 R.NLNIINTHAYNQPEELVYS@QPEMR.E
SIGNALING: SMALL G PROTEINS AND REGULATORS						
ARF GTPase-activating protein GIT1	Q68FF6	F.HSTELEDDAIY@SVHVPAGLY.R	Y554	2296.34	0.29	0.1029 F.HSTELEDDAIYS@VHVPAGLY.R
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554	3018.84	1.42	0.0484 R.LQPFHST@ELEDDAIY@SVHVPAGLYR.I
		R.LQPFHST@ELEDDAIY@SVHVPAGLYR.I	Y554	3018.69	1.27	0.0263 R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I
		R.LQPFHSTELEDDAIY@SVHVPAGLY@R.I	Y554,Y563	3018.72	1.30	0.1026 R.LQPFHSTELEDDAIYS@VHVPAGLY@R.I
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554	2939.39	1.97	0.0863 R.LQPFHSTELEDDAIYS@VHVPAGLYR.I
		R.LQPFHS^TELEDDAIY@SVHVPAGLYR.I	Y554	2920.86	1.44	0.0425 R.LQPFHST^ELEDDAIY@SVHVPAGLYR.I
Engulfment and cell motility protein 2 -- ELMO2	Q8BHL5	K.EVC*DGWSLPNPEY@YTLR.Y	Y48	2179.80	0.87	0.1206 K.EVC*DGWSLPNPEYYT@LR.Y
Glucocorticoid receptor DNA binding factor 1 [fragment] -- p190RhoGAP	Q91YM2	R.NEEENIY@SVPHDSTQGK.I	Y943	2027.34	0.47	0.1491 R.NEEENIYS@VPHDSTQGK.I
				2027.18	0.31	0.0454 R.NEEENIYS@VPHDSTQGK.I
Myosin phosphatase Rho-interacting protein -- MRIP	P97434	K.VRVESGY@FSLEK.A	Y268	1493.84	0.10	0.0161 K.VRVES@GYFSLEK.A
				1495.26	1.52	none
		K.YASDKYKDIY@TELSIAK.A	Y944	2090.07	2.04	
Rab GDP dissociation inhibitor alpha -- Rab GDI alpha (Rab GDI beta)	P50396	K.VLHMDRNPY@YGGESSSITPLEELYK.R	Y38	2979.22	0.82	0.0689 K.VLHMDRNPYY@GGESSSITPLEELYK.R
		K.SPYLYPLY@GLGELPQGFAR.L	Y229	2221.76	0.65	0.0852 K.SPYLY@PLYGLGELPQGFAR.L
Rab GDP dissociation inhibitor beta -- Rab GDI beta	Q61598	K.KVLHMDQNPY@YGGESASITPLEDLYK.R	Y38	3049.21	0.77	0.1151 K.KVLHMDQNPYY@GGESASITPLEDLYK.R
		K.KVLHMDQNPY@YGGESASITPLEDLYKR.F	Y38	3204.96	0.42	0.0675 K.KVLHMDQNPYY@GGESASITPLEDLYKR.F
		K.VLHM#DQNPY@YGGESASITPLEDLYKR.F	Y38	3094.14	1.69	0.0109 K.VLHM#DQNPYY@GGESASITPLEDLYKR.F
		K.VLHMDQNPY@YGGESASITPLEDLYK.R	Y38	2920.90	0.56	0.0025 K.VLHMDQNPYY@GGESASITPLEDLYK.R
		K.VLHMDQNPY@YGGESASITPLEDLYKR.F	Y38	3077.28	0.83	0.0702 K.VLHMDQNPYY@GGESASITPLEDLYKR.F
		L.HMDQNPY@YGGESASITPLEDLY.K	Y38	2581.36	1.26	0.0309 L.HMDQNPYY@GGESASITPLEDLY.K
		K.KVLHMDQNPYY@GGESASITPLEDLYKR.F	Y39	3206.67	2.13	0.0014 K.KVLHMDQNPY@YGGESASITPLEDLYKR.F
		K.VLHM#DQNPYY@GGESASITPLEDLYKR.F	Y39	3093.25	0.80	0.0075 K.VLHM#DQNPY@YGGESASITPLEDLYKR.F
		K.VLHMDQNPYY@GGESASITPLEDLYK.R	Y39	2921.24	0.90	0.0066 K.VLHMDQNPY@YGGESASITPLEDLYK.R

Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	L.RSPDVGLY@GVIPEC*GETY.Q	Y654	2092.39	0.47	none
		L.SALRSPDVGLY@GVIPEC*GETY.Q	Y654	2363.51	0.44	none
		L.VKLQQTY@SAL.N	Y1510	1230.96	0.31	0.1154 L.VKLQQT@YSAL.N
Ras and Rab interactor 1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	1815.44	0.62	0.1892 K.EKPST@DPLYDTPDTR.G
				1815.30	0.48	0.0035 K.EKPST@DPLYDTPDTR.G
Rho-GTPase-activating protein 12	Q8C0D4	R.AT@TPPNQGRPDS@PVY@ANLQELK.I	Y241	2636.11	-0.11	0.0159 R.ATT@PPNQGRPDS@PVY@ANLQELK.I
		R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241	2637.43	1.21	0.0075 R.AT@TPPNQGRPDS@PVY@ANLQELK.I
Rho/rac guanine nucleotide exchange factor (GEF) 2 -- ARHGEF2	Q923E0	R.RRS@LPAGDALY@LSFNPPQPSR.G	Y893	2504.02	1.78	none
		R.SLPAGDALY@LSFNPPQPSR.G	Y893	2110.51	0.48	0.1470 R.SLPAGDALYLS@FNPPQPSR.G
TBC1 domain family member 15	Q9CXF4	K.SLSQSFENLLDEPAY@GLIQK.I	Y215	2332.54	0.40	none
SIGNALING: OTHER						
53BP2: Apoptosis stimulating of p53 protein 2 [fragment]	Q8CG79	R.KPQTVAASSIY@SMYTQQQAPGK.N	Y569	2465.08	0.88	0.0767 R.KPQTVAAS@SIYSMYTQQQAPGK.N
Ankyrin repeat and SAM domain containing protein 1 -- ANKS1	P59672	L.ILHFDTHADEEGPY@EALY.N	Y377	2201.56	1.61	0.1259 L.ILHFDTHADEEGPYEALY@.N
		L.AVRPRIQSSAPQEEEEHPY@EL.L	Y471	2546.21	1.00	none
		L.AVRPRIQSSAPQEEEEHPY@ELL.L	Y471	2659.39	1.10	none
		R.IQSSAPQEEEEHPY@ELLLTAETK.K	Y471	2724.54	2.26	0.0675 R.IQSSAPQEEEEHPYELLLT@AETK.K
		R.IQSSAPQEEEEHPY@ELLLTAETKK.L	Y471	2851.79	1.41	0.1325 R.IQSSAPQEEEEHPYELLLT@AETKK.L
Annexin A1	P10107	R.ALY@EAGER.R	Y206	989.01	0.56	none
		R.ALY@EAGERR.K	Y206	1144.76	0.21	none
Annexin A2	P07356	C.KLSLEGDHSTPPSAY@GSVKPY.T	Y23	2315.40	2.29	0.0081 C.KLSLEGDHSTPPS@AYGSVKPY.T
		K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D	Y23	3019.97	1.58	0.1079 K.LSLEGDHSTPPS@AYGSVKPYTNFDAER.D
		L.SLEGDHSTPPSAY@GSVKPY.T	Y23	2072.75	0.82	none
				2072.63	0.70	0.0719 L.SLEGDHSTPPS@AYGSVKPY.T
		K.SYSPY@DMLESIK.K	Y237	1512.22	-0.45	none
		K.SYSPY@DMLESIKK.E	Y237	1641.52	0.76	none
		F.ADRLY@DSM.K	Y274	1050.94	0.51	none
		L.YFADRLY@DSM#.K	Y274	1377.36	0.80	none
		L.YFADRLY@DSM.K	Y274	1360.37	-0.19	none
		Y.FADRLY@DSM.K	Y274	1197.54	0.04	none
		K.SLY@YYIQQDTK.G	Y315	1502.65	0.96	0.1004 K.S@LYYYIQQDTK.G
		K.SLYY@YIQQDTK.G	Y316	1502.70	1.01	0.0625 K.SLY@YYIQQDTK.G
		K.SLY@Y@YIQQDTK.G	Y315,Y316	1582.68	0.99	0.1193 K.S@LYY@YIQQDTK.G
Annexin A5	P48036	R.SIPAYLAETLY@YAMK.G	Y254	1814.41	0.53	0.1242 R.SIPAYLAET@LYYAMK.G
		K.NFATSLY@SMIK.G	Y295	1354.94	0.30	0.0812 K.NFATSLYS@MIK.G
Annexin A6	P14824	R.GSVHDFPEFDANQDAEALY@TAM#K.G	Y29	2653.34	1.21	0.0530 R.GSVHDFPEFDANQDAEALYT@AM#K.G
		R.GSVHDFPEFDANQDAEALY@TAMK.G	Y29	2638.45	2.32	0.0949 R.GSVHDFPEFDANQDAEALYT@AMK.G
				2636.43	0.30	0.0199 R.GSVHDFPEFDANQDAEALYT@AMK.G
		Y.RGSVHDFPEFDANQDAEALY@TAM#.K	Y29	2681.46	1.32	0.0616 Y.RGSVHDFPEFDANQDAEALYT@AM#.K
		Y.RGSVHDFPEFDANQDAEALY@TAM.K	Y29	2664.53	0.39	0.0017 Y.RGSVHDFPEFDANQDAEALYT@AM.K
				2665.58	1.44	0.0634 Y.RGSVHDFPEFDANQDAEALYT@AM.K
Annexin A11	P97384	K.TPVLFDVY@EIKEAIK.G	Y277	1846.58	1.60	none
				1846.26	1.28	none
Cell division cycle and apoptosis regulator protein 1 -- CARP1	Q8CH18	R.VLVEATY@NPNMPFK.W	Y189	1703.62	0.80	0.1452 R.VLVEAT@YNPNMPFK.W
		R.VLVEATY@NPNMPFKWNAQR.I	Y189	2359.02	0.88	0.0875 R.VLVEAT@YNPNMPFKWNAQR.I
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	1729.23	0.40	0.0850 K.YVDSEGHLYT@VPIR.E
Proto-oncogene c-Crk	Q64010	Q.KRVPNAY@DKTAL.A	Y251	1456.89	1.12	0.1533 Q.KRVPNAYDKT@AL.A
Cyclin-dependent kinases regulatory subunit 2	P56390	Y.SDKYFDEHY@EY.R	Y17	1575.53	-0.07	none
		Y.YSDKYFDEHY@EY.R	Y17	1739.37	0.71	none
Docking protein 1 --Dok1	P97465	K.TVPPPVPQDPLGSPPALY@AEPLDSLR.I	Y295	2807.66	1.22	0.1222 K.TVPPPVPQDPLGSPPALYAEPLDS@LR.I
		R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K	Y314	2888.60	1.25	0.0146 R.IPPGPSQDSVYS@DPLGSTPAGAGEGVHSK.K
		K.KPLY@WDLY@GHVQQQLLK.T	Y336,Y340	2290.89	1.74	none
		K.KPLYWDLY@GHVQQQLLK.T	Y340	2211.58	2.43	0.1680 K.KPLY@WDLYGHVQQQLLK.T
		K.LTDSKEDPIY@DEPEGLAPAPPR.G	Y361	2491.80	1.62	0.0650 K.LTDS@KEDPIYDEPEGLAPAPPR.G
				2490.92	0.74	none
		K.TKLTDSKEDPIY@DEPEGLAPAPPR.G	Y361	2721.28	1.96	none
		K.TKLTDS^KEDPIY@DEPEGLAPAPPRGLYDLPQEPR.D	Y361	3872.22	2.31	0.0003 K.TKLTDS^KEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D
		L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	3181.82	1.24	0.0228 L.KTKLTDS@KEDPIYDEPEGLAPAPPRGLY.D
		L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	3295.91	2.24	0.0358 L.LKTKLTDS@KEDPIYDEPEGLAPAPPRGLY.D
		K.LTDSKEDPIY@DEPEGLAPAPPRGLY@DLPQEPR.D	Y361,Y376	3740.92	2.15	0.1147 K.LT@DSKEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D
		K.LTDS^KEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D	Y376	3642.13	1.37	0.0005 K.LT^DSKEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D
		R.LKEEGY@ELPY@NPATDDYAVPPPR.S	Y397,Y401	2795.76	1.49	none

		R.LKEEGYELPY@NPAT@DDYAVPPPR.S	Y401	2796.49	1.57	0.0063 R.LKEEGYELPY@NPATDDY@AVPPPR.S
		R.LKEEGYELPY@NPATDDYAVPPPR.S	Y401	2715.12	0.85	0.1652 R.LKEEGYELPYNPAT@DDYAVPPPR.S
		R.LKEEGYELPYNPATDDY@AVPPPR.S	Y408	2715.12	0.85	0.0058 R.LKEEGYELPYNPAT@DDYAVPPPR.S
		R.LKEEGY@ELPYNPATDDY@AVPPPR.S	Y397,Y408	2795.73	1.46	0.0636 R.LKEEGYELPY@NPATDDY@AVPPPR.S
		R.LKEEGYELPY@NPATDDY@AVPPPR.S	Y401,Y408	2795.23	0.96	0.1159 R.LKEEGY@ELPYNPATDDY@AVPPPR.S
		R.LKEEGYELPY@NPATDDY@AVPPPRS@PK.P	Y401,Y408	3187.64	1.19	0.0628 R.LKEEGY@ELPYNPATDDY@AVPPPRS@PK.P
		F.SSDTALY@SQVQKSGTSGAW.D	Y450	2054.11	1.19	0.0846 F.SSDTALYS@QVQKSGTSGAW.D
		K.GFSSDTALY@SQVQK.S	Y450	1611.59	0.85	0.1118 K.GFSSDTALYS@QVQK.S
Epidermal growth factor receptor kinase substrate 8 -- EPS8	Q08509	R.LSTEHSNVSDY@PPADGYAYSSSMYHR.G	Y484	3015.46	1.20	0.1683 R.LSTEHSNVS@DYPPADGYAYSSSMYHR.G
Hepatocyte growth factor-regulated tyrosine kinase substrate -- HGS/ Hrs	Q99LI8	R.VC*EPC*Y@EQLNK.K	Y216	1519.93	0.34	none
Insulin receptor substrate 1 -- IRS-1	P35569	R.AASEAGGPARLEY@YENEKK.W	Y46	2163.48	0.47	0.1355 R.AASEAGGPARLEYY@ENEKK.W
Insulin receptor substrate 2 -- IRS-2	P81122	K.VAYNPYPEDY@GDIEIGSHK.S	Y628	2247.94	0.94	none
Kin of IRRE-like protein 1 precursor -- KIRREL	Q80W68	R.C*DTIDTREEY@EMKDPTNGY@YNVR.A	Y628,Y637	3030.00	0.78	0.0581 R.C*DTIDT@REEYEMKDPTNGY@YNVR.A
		R.C*DTIDT@REEYEMKDPTNGY@YNVR.A	Y637	3029.81	0.59	0.0176 R.C*DTIDTREEY@EMKDPTNGY@YNVR.A
		R.EEYEMKDPTNGY@YNVR.A	Y637	2089.23	1.35	0.0316 R.EEYEMKDPTNGYY@NVR.A
		Y.RLGYPQAPPSGLERTPY@EAY@DPIGKY.A	Y753,Y756	3099.26	0.79	0.1675 Y.RLGYPQAPPSGLERT@PYEAY@DPIGKY.A
Latrophilin-2	Q8JZZ7	R.SENEDIY@YK.S	Y838	1241.21	0.70	0.1688 R.SENEDIYY@K.S
		R.GNSDGY@IIPINK.E	Y865	1370.74	0.07	0.0837 R.GNS@DGYIIPINK.E
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.PSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3432.55	1.96	none
		K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3796.48	1.70	0.0168 K.RKPSVPDT@ASPADDSFVDPGERLY@DLNMPAFVK.F
		K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3716.18	1.40	0.1164 K.RKPSVPDTASPADDS@FVDPGERLYDLNMPAFVK.F
		R.KPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3560.94	2.26	none
Notchless homolog 1	Q8VEJ4	K.LATDLPGHADEVY@AVDWSPDGQR.V	Y459	2593.81	1.63	none
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85 alpha	P26450	K.SREYDRLY@EEYTR.T	Y467	1861.24	1.41	0.1544 K.SREYDRLYEEY@TR.T
		K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y607	3565.40	1.89	0.0421 K.LNEWLGNENTEDQYS@LVEDDEDLPHHDEK.T
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85 beta	O08908	R.EYDQLY@EEYTR.T	Y458	1590.44	1.79	0.1065 R.EYDQLYEEY@TR.T
Phospholipase C, gamma 1	Q6P1G1	K.IGTAEPDY@GALY@EGRNPGFYVEANPMPTFK.C	Y771,Y775	3465.23	0.67	0.1939 K.IGT@AEPDY@GALYEGRNPGFYVEANPMPTFK.C
		K.IGTAEPDYGALY@EGRNPGFY@VEANPMPTFK.C	Y775,Y783	3465.49	0.93	none
		K.IGTAEPDYGALY@EGRNPGFYVEANPMPTFK.C	Y775	3385.80	1.24	0.0283 K.IGTAEPDY@GALYEGRNPGFYVEANPMPTFK.C
Protein Wnt-2b precursor	O70283	K.GTDGC*EIMCCGRGY@DTTR.V	Y342	2074.12	-0.64	none
Guanine nucleotide-binding protein beta subunit 2-like 1 -- RACK1	P68040	K.HLY@TLDGGDIINALC*FSPNR.Y	Y227	2357.31	1.22	0.0189 K.HLYT@LDGGDIINALC*FSPNR.Y
				2356.97	0.88	0.0595 K.HLYT@LDGGDIINALC*FSPNR.Y
		L.WDLNEGKHLY@TLDGGDIINAL.C	Y227	2438.42	1.24	0.0921 L.WDLNEGKHLYT@LDGGDIINAL.C
		W.DLNEGKHLY@TLDGGDIINAL.C	Y227	2252.20	1.10	0.0263 W.DLNEGKHLYT@LDGGDIINAL.C
		W.DLNEGKHLY@TLDGGDIINALC*F.S	Y227	2559.76	1.58	0.0307 W.DLNEGKHLYT@LDGGDIINALC*F.S
Retinoic acid-induced protein 3	Q8BHL4	F.SIPRAQAPASPY@NDY@EGRKGDS.-	Y346,Y349	2539.79	0.66	0.0655 F.SIPRAQAPASPY@NDYEGRKGDS@.-
		F.SIPRAQAPASPY@NDYEGRKGDS^.-	Y346	2442.48	1.35	0.1095 F.SIPRAQAPASPYNDY@EGRKGDS^.-
SH2 domain-containing adapter protein B -- SHB	Q6PD21	R.DFEDPY@NGPGSSLR.K	Y95	1635.59	1.90	none
SHC transforming protein 1 -- SHC1	P98083	R.ELFDDPSY@VNIQNLDK.A	Y423	1991.42	1.50	0.0433 R.ELFDDPS@YVNIQNLDK.A
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM#R.L	Y349,Y350	4589.22	2.33	none
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L	Y349,Y350	4569.94	-0.95	none
		F.DGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM.R	Y349,Y350	4009.78	1.16	none
SHC SH2 domain-binding protein 1	Q9Z179	R.SWDEEEEDEY@DYFVR.C	Y217	2091.18	0.39	0.1524 R.SWDEEEEDEYDY@FVR.C
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	R.FSEEEISFPPTY@RYER.G	Y662	2131.40	1.44	0.0177 R.FSEEEISFPPT@YRYER.G
		K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y987	3217.18	1.55	0.0566 K.NSFNNPAYY@VLEGVPHQLLPLEPPSLAR.A
Sorbin and SH3 domain-containing protein 1 -- SORBS1	Q62417	K.TPVDYIDLPY@SSSPSR.S	Y1198	1877.89	1.02	0.0418 K.TPVDYIDLPYS@SSPSR.S
Signal transducing adapter molecule 2 -- STAM-2	O88811	K.LVNEAPVY@SVYS@K.L	Y371	1629.25	0.48	0.0074 K.LVNEAPVY@SVY@SK.L
		K.LVNEAPVY@SVYSK.L	Y371	1548.90	0.13	0.0201 K.LVNEAPVYS@VYSK.L
		Y.NKLVNEAPVY@SVY.S	Y371	1575.69	-0.09	0.1266 Y.NKLVNEAPVYS@VY.S
Signal transducer and activator of transcription 3 - STAT3	P42227	R.QFLAPWIESQDWAY@AASK.E	Y45	2191.74	0.72	none
		K.YC*RPESQEHPEADPGSAAPY@LK.T	Y705	2581.97	-0.14	none

STRAP: serine/threonine kinase receptor associated protein	Q8BP89	K.IGFPETAEEELEEIASENSDSIY@SSTPEVK.A	Y342	3382.35	1.82	0.0660 K.IGFPETAEEELEEIASENS@DSIYSSTPEVK.A
		K.IGFPETAEEELEEIASENSDSIY@SSTPEVKA.-	Y342	3453.36	1.81	0.0893 K.IGFPETAEEELEEIASENSDS@IYSSTPEVKA.-
Striatin	O55106	K.STSLDVEPIY@TFR.A	Y510	1608.98	1.21	0.0636 K.STSLDVEPIYT@FR.A
		W.NLQKTAPAKKSTSLDVEPIY@TF.R	Y510	2532.43	1.12	none
Striatin-3	Q9ERG2	K.SASLDVEPIY@TFR.A	Y526	1577.81	0.05	0.1014 K.SASLDVEPIYT@FR.A
hypothetical SH3/Phox-like/Src homology 3 (SH3) domain profile/Proline-rich region profile/PX domain profile containing protein -- TKS4	Q3TB89	R.VTWSSGATEAIY@R.R	Y42	1521.35	0.64	none
		K.TEPAQSEDHVDIY@NLR.S	Y661	1966.82	-0.07	none
ADHESION: CELL/ECM						
Bystin	O54825	R.GREVEEEEEY@VGPR.L	Y48	1758.55	0.78	none
CRK-associated substrate -- p130cas	Q61140	-.MTVPNVLAKALY@DNVAESPDELSFR.K	Y12	2859.30	-0.10	none
		K.ALY@DNVAESPDELSFR.K	Y12	1906.53	0.67	none
		Y.VYEAAQTEQDEY@DTPRHL.L	Y238	2245.17	0.19	0.1373 Y.VYEAAQT@EQDEYDTPRHL.L
		R.HLLAPGPQDIY@DVPPVR.G	Y253	1969.23	2.22	none
				1968.74	1.73	none
		R.GLLPNQYGQEVY@DTPPMAVK.G	Y271	2301.22	1.12	0.0092 R.GLLPNQYGQEVYDT@PPMAVK.G
				2300.89	0.79	none
		K.GPNGRDPLLDVY@DVPPSVEK.G	Y291	2249.57	2.47	none
		K.GLLSSSHHSVY@DVPPSVSK.D	Y310	2077.88	1.86	0.1877 K.GLLSSSHHS@VYDVPPSVSK.D
		R.RPGPGTLY@DVPR.E	Y391	1408.33	0.62	0.0259 R.RPGPGT@LYDVPR.E
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	2629.52	1.23	none
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	2914.26	0.82	none
		L.SRQLQKMEDVY@QTL.V	Y556	1820.99	2.11	0.1930 L.SRQLQKMEDVYQT@L.V
Lipoma-preferred partner homolog -- LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	1938.23	0.37	none
		Y.MAGPSSGQIY@GPGPRGY.N	Y245	1774.53	-0.27	none
				1776.10	1.30	none
		M.AGPSSGQIY@GPGPRGY.N	Y245	1644.25	0.49	none
		R.YYEPY@YAAGPSYGGR.S	Y301	1795.86	2.11	0.0018 R.YYEPYY@AAGPSYGGR.S
				1794.36	0.61	0.0716 R.YYEPYY@AAGPSYGGR.S
		Y.TSNQGRYYEPY@YAAGPSY.G	Y301	2168.03	1.12	none
		R.YYEPY@Y@AAGPSYGGR.S	Y301,Y302	1874.90	1.15	none
		R.YYEPYY@AAGPSYGGR.S	Y302	1795.16	1.41	0.0295 R.YYEPY@YAAGPSYGGR.S
				1795.27	1.52	0.0274 R.YYEPY@YAAGPSYGGR.S
		K.KMLY@DMENPPADDYFGR.C	Y403	2143.53	1.63	none
				2142.71	0.81	none
		K.MLY@DMENPPADDYFGR.C	Y403	2014.68	0.87	none
		K.KMLYDMENPPADDY@FGR.C	Y413	2143.01	1.11	none
				2142.60	0.70	none
		K.MLYDMENPPADDY@FGR.C	Y413	2015.55	1.74	none
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	1936.20	1.38	0.1327 F.LSEEPPYS@YPTGNHTY.Q
		R.AGEEEHVY@SFPNK.Q	Y118	1588.38	1.69	0.1758 R.AGEEEHVYS@FPNK.Q
				1587.41	0.71	0.0646 R.AGEEEHVYS@FPNK.Q
		R.AGEEEHVY@SFPNKQK.S	Y118	1843.41	0.57	0.1332 R.AGEEEHVYS@FPNKQK.S
Syndecan-4 precursor	O35988	Y.KKAPTNEFY@A.-	Y197	1250.02	1.42	none
Talin 1	P26039	K.TM#QFEPSTMVY@DAC*R.M	Y26	1932.47	0.71	none
		K.TMQFEPSTMVY@DAC*R.M	Y26	1916.98	1.23	none
				1916.68	0.92	none
		M.QFEPSTMVY@DAC*RM.I	Y26	1816.12	1.41	0.1893 M.QFEPST@MVYDAC*RM.I
		K.ALDY@YM#LR.N	Y70	1141.46	0.94	0.0609 K.ALDYY@M#LR.N
		K.ALDY@YMLR.N	Y70	1125.17	0.65	0.1407 K.ALDYY@MLR.N
		K.ALDYY@MLR.N	Y71	1124.25	-0.27	0.0243 K.ALDY@YMLR.N
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	1940.75	0.79	none
		K.TLAESALQLLY@TAK.E	Y1777	1602.54	0.69	0.1472 K.TLAESALQLLYT@AK.E
Tensin 2	Q8CJ95	R.YGHSGYPALVTY@GYGGAVPSYC*PAYGR.A	Y766	2965.54	2.24	0.0122 R.YGHSGYPALVT@YGYGGAVPSYC*PAYGR.A
Tensin 3	Q5SSZ5	K.LYQAMQPVYTSGIY@NVGSENPSR.I	Y216	2655.44	1.21	0.1558 K.LYQAMQPVYTS@GIYNVGSENPSR.I
				2654.76	0.53	0.1760 K.LYQAMQPVYTS@GIYNVGSENPSR.I
		L.HTQGPVDGSLY@AKVR.K	Y354	1708.54	0.68	none
		R.KPSAPTPVQAY@GQSNY@STQTWVR.Q	Y579,Y584	2727.80	1.53	0.1132 R.KPSAPTPVQAY@GQS@NYSTQTWVR.Q
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	2647.86	1.59	0.0762 R.KPSAPTPVQAYGQS@NYSTQTWVR.Q
Vinculin	Q64727	K.LVQAAQMLQSDPY@SVPAR.D	Y99	2055.41	1.40	0.0072 K.LVQAAQMLQSDPYS@VPAR.D
				2054.67	0.66	0.1258 K.LVQAAQMLQSDPYS@VPAR.D
		K.LVQAAQMLQSDPY@SVPARDYLIDGSR.G	Y99	2975.19	1.74	0.0276 K.LVQAAQMLQSDPYS@VPARDYLIDGSR.G
		L.QSDPY@SVPARDY.L	Y99	1478.01	0.38	0.0290 L.QSDPYS@VPARDY.L
		Q.MLQSDPY@SVPARDY.L	Y99	1721.78	0.02	0.0557 Q.MLQSDPYS@VPARDY.L
		R.ILLRNPGNQAAY@EHFETMK.N	Y691	2313.73	1.61	none
ADHESION: CELL/CELL						

Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M	Y96	2055.83	0.82	0.0441 K.LNGPQDHNHLLYS@TIPR.M
				2055.72	0.71	0.0819 K.LNGPQDHNHLLYS@TIPR.M
		R.HYEDGYPGGSDNY@GSLSR.V	Y228	2054.75	0.92	0.0694 R.HYEDGYPGGSDNYGS@LSR.V
		R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R	Y291,Y296	3892.72	1.18	0.0179 R.FHPEPYGLEDDQRS@MGYDDLDY@GMMSDYGTAR
		R.FHPEPYGLEDDQRS@MGYDDLDY@GMMS@DYGTAR.R	Y296	3973.02	1.48	0.0095 R.FHPEPYGLEDDQRSMGY@DDLDY@GMMS@DYGTAR.R
		R.FHPEPYGLEDDQRS^MGYDDLDY@GMMS@DYGTAR.R	Y296	3874.69	1.15	none
		R.FHPEPYGLEDDQRS^MGYDDLDY@GMMSDYGTAR.R	Y296	3794.55	1.01	0.1799 R.FHPEPYGLEDDQRS^MGYDDLDYGMMS@DYGTAR.R
		R.SMGYDDLDY@GMMSDYGTAR.R	Y296	2228.06	0.22	none
		R.SMGYDDLDYGMMSDY@GTAR.R	Y302	2229.31	1.47	0.1514 R.SMGYDDLDYGMMS@DYGTAR.R
		R.SYEDMIGEEVPPDQY@YWAPLAQHER.G	Y334	3105.19	1.84	0.0150 R.SYEDMIGEEVPPDQYY@WAPLAQHER.G
		R.SYEDMIGEEVPPDQYY@WAPLAQHER.G	Y335	3105.15	1.80	0.0309 R.SYEDMIGEEVPPDQY@YWAPLAQHER.G
Plakophilin-4	Q68FH0	R.TVHDMDQFGQQQY@DIY@ER.M	Y368,Y371	2433.03	0.04	none
		R.TVHDMDQFGQQQYDIY@ER.M	Y371	2354.91	1.92	0.0699 R.TVHDMDQFGQQQY@DIYER.M
		L.RSAVSPDLHITPIY@EGRT@YY.S	Y414	2500.67	2.49	none
		R.SAVSPDLHITPIY@EGRT@YYSPVYR.S	Y414	2944.88	0.48	0.1987 R.SAVSPDLHIT@PIYEGRT@YYSPVYR.S
		R.SAVS^PDLHITPIY@EGRTYYSPVYR.S	Y414	2847.06	0.66	0.0934 R.SAVSPDLHIT^PIY@EGRTYYSPVYR.S
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	1532.93	1.22	none
Tight junction protein ZO-1	P39447	R.LSYLSAPGSEY@SMYSTDSR.H	Y830	2194.55	0.61	0.1378 R.LSYLSAPGS@EYSMYSTDSR.H
		R.HEEQPAPAY@EVHNR.Y	Y1164	1756.19	-0.59	none
		L.RHEEQPAPAY@EVHNRY.R	Y1164	2077.52	1.59	0.1767 L.RHEEQPAPAYEVHNRY@.R
		R.YRPEAQPY@SSTGPK.S	Y1177	1661.11	0.34	0.0739 R.YRPEAQPYS@STGPK.S
		Y.RPEAQPY@SSTGPKSSEPKQY.F	Y1177	2318.46	1.38	0.0051 Y.RPEAQPYS@STGPKSSEPKQY.F
		R.SNHY@DPEEDEEYYRK.Q	Y1345	2054.34	0.53	0.1312 R.S@NHYDPEEDEEYYRK.Q
		R.SNHYDPEEDEEY@YR.K	Y1353	1926.92	1.20	0.0304 R.SNHYDPEEDEEYY@R.K
		R.SNHYDPEEDEEY@YRK.Q	Y1353	2055.03	1.22	0.0759 R.SNHYDPEEDEEYY@RK.Q
Tight junction protein ZO-2	Q9Z0U1	R.SYHEAY@EPDY@GGGYSPSYDRR.A	Y230, Y234	2630.83	1.79	0.1574 R.SYHEAY@EPDYGGGY@SPSYDRR.A
		R.SYHEAY@EPDYGGGY@SPSYDRR.A	Y230, Y238	2629.61	0.57	0.0614 R.SYHEAY@EPDY@GGGYSPSYDRR.A
		R.SYHEAY@EPDYGGGYSPSYDRR.A	Y230	2550.44	1.40	0.0760 R.SYHEAYEPDY@GGGYSPSYDRR.A
		R.SYHEAYEPDY@GGGYSPSYDRR.A	Y234	2549.10	0.05	0.1245 R.SYHEAY@EPDYGGGYSPSYDRR.A
		R.VFLRPSPEDEAIY@GPNTK.M	Y486	2113.78	0.75	0.0464 R.VFLRPSPEDEAIYGPNT@K.M
		F.LRPSPEDEAIY@GPNTKMVRF.K	Y486	2402.29	2.11	none
		R.GLVREDAVLY@LLEIPKGETVTILAQSR.A	Y554	3064.68	1.00	none
		R.IEIAQKHPDIY@AVPIK.A	Y1095	1916.29	1.25	none
CYTOSKELETON: ACTIN-ASSOCIATED						
Actins and actin-related proteins; Regulators of actin assembly						
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	M.VGMGQKDSY@VGDEAQSKRGIL.T	Y55	2319.16	1.04	0.0262 M.VGMGQKDS@YVGDEAQSKRGIL.T
		K.IWHHTFY@NELR.V	Y93	1597.41	1.66	none
				1596.60	0.85	0.1687 K.IWHHT@FYNELR.V
		K.EKLC*Y@VALDFENEM#ATAASSSSLEK.S	Y220	2889.26	-0.01	none
Actin, cytoplasmic 1 (Beta-actin)	P70514	K.EKLC*Y@VALDFEQEMATAASSSSLEK.S	Y218	2888.34	1.05	none
Beta-centractin	Q8R5C5	R.TTGVVLDSGDGVTHAVPIY@EGFAMPHSIMR.V	Y171	3239.76	2.22	none
Actin-like protein 2 -- Arp2	P61161	K.HLWDY@TFGPEK.L	Y91	1472.82	0.16	0.0095 K.HLWDYT@FGPEK.L
		K.HLWDY@TFGPEKLNIDTR.N	Y91	2186.70	1.65	0.0416 K.HLWDYT@FGPEKLNIDTR.N
Actin-like protein 3 - Arp3	Q99JY9	L.RAEPEDHY@F.L	Y108	1243.06	-0.45	none
Actin-related protein 2/3 complex subunit 3 -- p21-ARC	Q9JM76	F.KGPAPRETKDTDIVDEAIY@Y.F	Y46	2360.92	-0.21	0.0307 F.KGPAPRETKDTDIVDEAIYY@.F
		F.KGPAPRETKDTDIVDEAIY@YF.K	Y46	2509.45	1.25	0.1436 F.KGPAPRETKDTDIVDEAIYY@F.K
		K.DTDIVDEAIY@YFK.A	Y46	1672.80	1.05	0.1190 K.DTDIVDEAIYY@FK.A
		Q.FKGPAPRETKDTDIVDEAIY@Y.F	Y46	2508.91	0.71	0.0014 Q.FKGPAPRETKDTDIVDEAIYY@.F
Adenylyl cyclase-associated protein 1 -- CAP1	P40124	R.LEAVSHTSDMHC*GY@GDSPSK.G	Y30	2259.00	1.10	0.1411 R.LEAVSHTSDMHC*GYGDS@PSK.G
Cofilin-1 non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C	Y139	1872.43	1.63	none
		K.LTGIKHELQANC*Y@EEVKDR.C	Y139	2383.98	0.86	none
Src substrate cortactin	Q60598	F.KAEPSYRGSEPEPEY@SIEAAGIPEAGSQQGL.T	Y442	3329.23	1.69	0.0268 F.KAEPSYRGSEPEPEYS@IEAAGIPEAGSQQGL.T
		L.TYTSEPVY@ETTEAPGHY.Q	Y466	2025.91	1.06	0.0481 L.TYT@SEPVYETTEAPGHY.Q
				2025.19	0.34	none
		Y.TSEPVY@ETTEAPGHY.Q	Y466	1762.84	2.10	0.0775 Y.T@SEPVYETTEAPGHY.Q
				1761.05	0.31	0.1074 Y.TSEPVYET@TEAPGHY.Q
Cytoplasmic FMR1 interacting protein 1	Q7TMB8	K.C*NEQPNRVEIY@EK.T	Y108	1759.93	1.17	none
Coronin-1C	Q9WUM4	R.YFEITDESPY@VHYLNTFSSKEPQR.G	Y301	3031.52	1.13	0.0542 R.YFEITDES@PYVHYLNTFSSKEPQR.G
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.VIY@DFIEK.T	Y253	1107.47	0.92	none

Twinfilin-1	Q91YR1	R.KIEIDNGDELTADFLY@DEVHPK.Q	Y309	2642.78	1.54	none
Twinfilin-2	Q9Z0P5	K.KIEIGDGAELTAEFLY@DEVHPK.Q	Y309	2555.74	1.50	none
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R	Y39	1715.31	1.50	none
		R.VQIY@HNPTANSFR.V	Y39	1628.13	1.35	none
				1628.22	1.44	none
WD-repeat protein 1 -- Actin interacting protein 1, AIP1	O88342	F.IYDGKTGEKVC*ALGESKAHDGGIY@AISW.S	Y237	3106.90	1.45	none
		K.AHDGGIY@AISWSPDSTHLLSASGDK.T	Y237	2667.52	2.29	0.1793 K.AHDGGIYAIS@WSPDSTHLLSASGDK.T
		K.AHDGGIY@AISWSPDSTHLLSASGDKTSK.I	Y237	2983.39	1.99	0.0600 K.AHDGGIYAIS@WSPDSTHLLSASGDKTSK.I
Other actin-associated proteins						
Alpha-actinin 1	Q7TPR4	R.HRPELIDY@GK.L	Y193	1308.32	0.67	none
		K.AIM#TYVSSFY@HAFSGAQK.A	Y246	2105.98	2.02	0.1464 K.AIM#TYVSS@FYHAFSGAQK.A
				2105.69	1.73	0.0812 K.AIM#TYVSS@FYHAFSGAQK.A
		K.AIMTYVSSFY@HAFSGAQK.A	Y246	2090.46	2.50	none
				2088.72	0.76	0.1050 K.AIMTYVSS@FYHAFSGAQK.A
Anillin	Q8K298	R.AESADSLGSEDRDLLY@SIDAYR.S	Y666	2527.33	1.19	0.1358 R.AESADSLGSEDRDLLYS@IDAYR.S
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q	Y316	1622.10	1.47	0.1785 Y.HGEYPDDYPREY@.Q
		Y.HGEYPDDYPREY@QYGDDQGIDY.-	Y320	2775.84	0.75	0.1461 Y.HGEYPDDYPREYQY@GDDQGIDY.-
Filamin-B	Q80X90	K.GFLDGVY@SFEYYPSTPGK.Y	Y511	2108.30	1.36	0.0622 K.GFLDGVYS@FEYYPSTPGK.Y
		K.QKGFLDGVY@SFEYYPSTPGK.Y	Y511	2363.77	0.67	0.0795 K.QKGFLDGVYS@FEYYPSTPGK.Y
		M.KSRMDGTY@AC*SY.T	Y704	1518.67	0.08	0.0280 M.KSRMDGT@YAC*SY.T
		R.MDGTY@AC*SYTPLK.A	Y704	1587.73	1.08	0.0802 R.MDGT@YAC*SYTPLK.A
Girdin	Q5SNZ0	K.TEDAY@TISSAGKPTPSTQGK.I	Y1739	2120.28	1.29	0.1079 K.TEDAYT@ISSAGKPTPSTQGK.I
		L.RTGPQKTEDAY@TISSAGKPTPSTQ.G	Y1739	2601.97	0.72	0.1136 L.RTGPQKT@EDAYTISSAGKPTPSTQ.G
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	2060.61	-0.35	none
Moesin	P26041	K.EGILNDDIY@C*PPETAVLLASYAVQSK.Y	Y115	2947.46	1.06	0.1893 K.EGILNDDIYC*PPET@AVLLASYAVQSK.Y
Myosin-9	Q8VDD5	R.HEMPPHIY@AITDTAYR.S	Y150	1996.03	1.11	0.1968 R.HEMPPHIYAIT@DTAYR.S
Myosin-10	Q61879	R.AVIY@NPATQADWTAK.K	Y22	1729.74	0.91	none
		Y.LFVDRAVIY@NPATQADW.T	Y22	2059.21	0.21	none
PDZ and LIM domain protein 1	O70400	R.VITNQYNSPTGLY@SSENISNFNNAVESK.T	Y148	3172.07	1.60	0.0349 R.VITNQYNSPT@GLYSSENISNFNNAVESK.T
Profilin-1	P10924	K.C*Y@EMASHLR.R	Y128	1247.39	0.90	none
Profilin-2	Q9JJV2	K.SQGGEPTY@NVAVGR.A	Y98	1515.34	0.64	0.0172 K.SQGGEPT@YNVAVGR.A
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	3033.18	0.70	0.1368 K.QQPTQFINPET@PGYVGFANLPNQVHR.K
Septin-7	O55131	K.NLEGY@VGFANLPNQVYR.K	Y29	2034.72	0.74	none
		R.KLAAVTY@NGVDNNK.N	Y318	1587.31	0.52	0.0620 R.KLAAVT@YNGVDNNK.N
		R.KLAAVTY@NGVDNNKNK.G	Y318	1827.66	-1.27	0.0113 R.KLAAVT@YNGVDNNKNK.G
Synaptopodin	Q8CC35	R.TPPASLY@HGYLPENGVLRPEPTK.Q	Y775	2618.09	1.77	0.0762 R.TPPAS@LYHGYLPENGVLRPEPTK.Q
CYTOSKELETON: MICROTUBULE-ASSOCIATED						
Tubulin alpha-1 chain	P68369	F.MVDNEAIY@DIC*RR.N	Y210	1736.18	1.43	none
		F.MVDNEAIY@DIC*.R	Y210	1424.03	1.49	none
		F.MVDNEAIY@DIC*RRNLDIERPTY.T	Y210	2837.23	0.93	none
Tubulin beta-3 chain	Q9ERD7	Y.C*IDNEALY@DIC*F.R	Y208	1613.52	0.92	none
		K.NSSY@FVEWIPNNVK.V	Y340	1777.38	0.55	0.0804 K.NS@SYFVEWIPNNVK.V
CLIP-associating protein 2 -- CLASP2	Q8BRT1	R.DYNPY@NYSDSISPFNK.S	Y1014	2005.52	1.68	0.1369 R.DY@NPYNYSDSISPFNK.S
Dynein heavy chain, cytosolic	Q9JHU4	R.YQVGVHY@ELTEEEKFYR.N	Y1008	2271.25	1.20	none
Kinesin light chain 1	O88447	K.DGSAFGEY@GGWYK.A	Y444	1516.59	-0.02	none
		K.QKDGSAFGEY@GGWYK.A	Y444	1774.01	1.24	0.1585 K.QKDGSAFGEYGGWY@K.A
Kinesin light chain 2	Q91YS4	R.DSAPYGEY@GSWYK.A	Y434	1602.38	-0.27	0.0823 R.DSAPYGEYGS@WYK.A
Kinesin-associated protein 3 -- KAP3	P70188	R.PATAYGFRPDEPY@YYSFGSR.-	Y786	2426.06	1.99	0.0252 R.PATAYGFRPDEPYYY@SFGSR.-
		R.PATAYGFRPDEPYY@YSFGSR.-	Y787	2425.97	1.90	0.0538 R.PATAYGFRPDEPY@YYSFGSR.-
		R.PATAYGFRPDEPYYY@SFGSR.-	Y788	2424.91	0.84	0.0346 R.PATAYGFRPDEPY@YYSFGSR.-

Kinesin family member 11	Q6P9P6	R.SPNEVY@TWEEDPLAGIIPR.T	Y124	2266.86	0.78	0.0874 R.SPNEVYT@WEEDPLAGIIPR.T
Microtubule-associated protein 1B -- MAP 1B	P14873	K.VLSPLRS@PPLLGSESPY@EDFLSADSK.V	Y1405	2966.93	2.49	0.0892 K.VLS@PLRSPPLLGSESPY@EDFLSADSK.V
		R.SPPLLGSESPY@EDFLSADSK.V	Y1405	2221.32	2.31	0.1381 R.SPPLLGSES@PYEDFLSADSK.V
Microtubule-associated protein 1B -- isoform	UPI0000021C8B	R.THDVGGYY@YEKTER.T	Y1901	1798.86	1.08	0.1121 R.THDVGGY@YYEKTER.T
Microtubule-associated protein 4 -- MAP 4	P27546	F.TERDNPSEDSY@GMLPC*DSF.A	Y176	2300.12	0.26	0.0760 F.TERDNPSEDS@YGMLPC*DSF.A
Nuclear distribution protein nudE homolog 1 -- NudE	Q9CZA6	R.NFMY@DQSPSR.T	Y279	1325.61	1.07	none
PREDICTED: similar to centrosome spindle pole associated protein	UPI0000D65977	R.TPYDDAY@YFYGAR.N	Y468	1683.35	1.66	0.1372 R.TPYDDAYY@FYGAR.N
Platelet-activating factor acetylhydrolase IB alpha subunit	P63005	R.SNGYEEAY@SVFKK.E	Y27	1602.23	0.51	0.1109 R.SNGYEEAYS@VFKK.E
RCC2 protein	Q8BK67	R.VFSWGFGGY@GR.L	Y357	1313.16	0.58	none
CYTOSKELETON: OTHER						
Plectin 1	Q6S394	Y.VSSLY@DAMPRVPGAQDGVRANEL.Q	Y288	2525.96	0.74	none
		K.AVTGYRDPY@SGQSVSLFQALK.K	Y3134	2369.33	2.16	0.0091 K.AVTGY@RDPYSGQSVSLFQALK.K
		K.AVTGYRDPY@SGQSVSLFQALKK.G	Y3134	2496.52	1.25	0.0489 K.AVTGYRDPYS@GQSVSLFQALKK.G
		R.ARQEEVY@SELQAR.E	Y3250	1660.12	1.33	0.1558 R.ARQEEVYS@ELQAR.E
				1658.80	0.01	0.0940 R.ARQEEVYS@ELQAR.E
		R.LTAEDLY@EAR.I	Y3678	1260.95	0.37	none
		R.QQNLASY@DYVR.R	Y3665	1437.36	0.71	0.0656 R.QQNLAS@YDYVR.R
		R.AVTGYKDPY@SGK.L	Y4043	1366.36	0.72	0.1227 R.AVTGYKDPYS@GK.L
		R.LLEAAAQSSKGY@YSPYSVSGSGSTAGSR.T	Y4499	2862.50	1.17	0.0213 R.LLEAAAQSSKGYY@SPYSVSGSGSTAGSR.T
		K.GYYSPY@S@VSGSGSTAGSR.T	Y4503	1943.55	0.76	none
		K.GYYSPY@SVSGSGSTAGSR.T	Y4503	1863.40	0.61	0.0626 K.GYYSPYS@VSGSGSTAGSR.T
Protein 4.1	P48193	K.VSLLDDTVY@EC*VVEK.H	Y223	1849.85	1.00	0.1719 K.VSLLDDT@VYEC*VVEK.H
Spectrin beta chain, brain 1	Q62261	L.KIVSSNDVGHDEY@STQ.S	Y777	1859.55	0.73	0.0106 L.KIVSSNDVGHDEYS@TQ.S
Vimentin	P20152	R.TY@SLGSALRPSTSR.S	Y37	1576.54	0.75	0.0470 R.T@YSLGSALRPSTSR.S
		L.RPSTSRSLY@SSSPGGAY.V	Y52	1853.19	0.33	0.0421 L.RPSTSRS@LYSSSPGGAY.V
		R.SLY@SSS@PGGAYVTR.S	Y52	1604.85	0.14	0.0825 R.S@LYSSS@PGGAYVTR.S
		R.SLY@SSSPGGAYVTR.S	Y52	1525.10	0.39	0.0869 R.S@LYSSSPGGAYVTR.S
		S.RSLY@SSSPGGAY.V	Y52	1324.93	0.34	0.0926 S.RSLYS@SSPGGAY.V
		S.TSRSLY@SSSPGGAY.V	Y52	1513.29	0.62	0.1063 S.TSRSLYS@SSPGGAY.V
TRAFFICKING/TRANSPORT						
Vesicle transport						
Adapter-related protein complex 3 mu 1 subunit	Q9JKC8	K.SVVSQSVC*DY@FFEAQEK.A	Y31	2104.36	1.47	none
Clathrin heavy chain	Q68FD5	R.ALEHFTDLY@DIKR.A	Y634	1702.03	1.19	none
		R.FLRENPY@YDSR.V	Y899	1540.32	0.62	0.1987 R.FLRENPYY@DSR.V
Coatomer protein complex subunit alpha	Q8BTF0	R.VKGNNVY@C*LDR.E	Y 579	1418.38	0.73	0.0197 K.MERS@SHPLHQGSSIKPEK.K
Coatomer beta subunit	Q9JIF7	K.LVTEMGTY@ATQSALSSSRPTKK.E	Y521	2438.20	1.98	0.0183 K.LVTEMGT@YATQSALSSSRPTKK.E
Coatomer beta' subunit	O55029	K.GVNC*IDYY@SGGDKPYLISGADDR.L	Y194	2615.95	0.83	0.0193 K.GVNC*IDYYS@GGDKPYLISGADDR.L
HECT domain and RCC1-like domain-containing protein 2 -- Herc2	Q4U2R1	R.SRTPLDKDLINTGIY@ESSGK.Q	Y999	2275.28	1.14	0.0535 R.SRTPLDKDLINT@GIYESSGK.Q
		R.TPLDKDLINTGIY@ESSGK.Q	Y999	2031.84	0.84	0.0734 R.TPLDKDLINTGIYESS@GK.Q
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	1328.72	0.06	none
Lysosomal trafficking regulator	P97412	R.AVWYDPIY@YPTSWQLDPTEGPNR.E	Y 2929	2848.69	0.39	0.0161 R.AVWYDPIYY@PTSWQLDPTEGPNR.E
				2850.18	1.88	0.0527 R.AVWY@DPIYYPTSWQLDPTEGPNR.E
SEC24 related gene family, member B	Q80ZX0	K.MTSLPLDSQC*DSY@YSRPYTVPTQNSGTPSSANQPGAQQMYGR.G	Y79	4722.60	1.55	none
		R.LDDRVY@AMC*QMK.S	Y1083	1610.79	1.12	none
SH3-containing GRB2-like protein 1	Q62419	K.ALY@DFEPENDGELGFR.E	Y315	1954.22	2.28	none
Sorting nexin-9	Q91VH2	K.IAIIVGDY@GPMWVYPTSTFDC*VVADPR.K	Y239	3124.76	2.31	none
		L.AKPKEKIAIIVGDY@GPM#.W	Y239	1927.77	1.75	none
		L.AKPKEKIAIIVGDY@GPM.W	Y239	1910.61	0.59	none
				1910.30	0.28	none

Sorting nexin 17	Q8R0N8	R.KSYWDSAY@DDDVMENR.V	Y210	2076.21	2.39	0.0794 R.KSYWDS@AYDDDVMENR.V
				2075.41	1.59	0.0915 R.KSYWDS@AYDDDVMENR.V
Transitional endoplasmic reticulum ATPase -- TER ATPase	Q01853	K.VVETDPSPY@C*IVAPDTVIHC*EGEPIKR.E	Y172	3161.60	0.14	0.1175 K.VVETDPS@PYC*IVAPDTVIHC*EGEPIKR.E
		R.GILLY@GPPGTGK.T	Y243	1253.07	0.40	none
Nucleocytoplasmic transport						
GTP-binding nuclear protein Ran	P62827	K.NLQY@YDISAK.S	Y145	1296.40	1.79	0.0204 K.NLQYY@DISAK.S
		R.KKNLQY@YDISAK.S	Y145	1552.09	1.29	0.1394 R.KKNLQYY@DISAK.S
		K.NLQYY@DISAK.S	Y146	1294.80	0.19	0.0155 K.NLQY@YDISAK.S
		K.SNY@NFEKPFLWLAR.K	Y154	1865.38	0.47	none
Importin-9	Q91YE6	R.VKGEEIY@SMDEGIR.T	Y888	1708.23	2.44	0.1530 R.VKGEEIYS@MDEGIR.T
				1705.73	-0.06	0.0703 R.VKGEEIYS@MDEGIR.T
RAE1 RNA export 1 homolog	Q8C570	R.SNGTNTSAPQDIY@AVNGIAFHPVHGTLATVGSDGR.F	Y274	3606.69	1.97	0.1796 R.SNGTNTS@APQDIYAVNGIAFHPVHGTLATVGSDGR.F
Ran-binding protein 2	Q9ERU9	R.GDDY@FNYNVQQTSTNPPLPEPGYFTKPPLVAHASR.S	Y960	4003.16	2.27	0.0485 R.GDDYFNY@NVQQTSTNPPLPEPGYFTKPPLVAHASR.S
		K.EGPY@WNC*NSC*SFK.N	Y1349	1729.49	0.88	none
Other transport						
none						
METABOLIC AND BIOSYNTHETIC ENZYMES						
Glycolytic enzymes						
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G	Y24	1487.27	0.55	0.0992 R.GNPTVEVDLYT@AK.G
		F.DSRGNPTVEVDLY@TAKGLF.R	Y24	2162.49	0.44	0.0913 F.DSRGNPTVEVDLYT@AKGLF.R
		F.DSRGNPTVEVDLY@TAKGLFR.A	Y24	2319.34	1.19	0.0881 F.DSRGNPTVEVDLYT@AKGLFR.A
		F.RAAVPSGASTGIY@EAL.E	Y43	1644.40	1.58	none
		F.RAAVPSGASTGIY@EALEL.R	Y43	1885.73	0.79	0.1412 F.RAAVPSGAS@TGIYEALEL.R
		R.AAVPSGASTGIY@EALELR.D	Y43	1885.92	0.97	none
				1886.66	1.71	0.1261 R.AAVPSGAST@GIYEALELR.D
		F.RAAVPSGASTGIY@EALELRDNDKTRF.M	Y43	2918.54	1.09	0.0612 F.RAAVPSGAST@GIYEALELRDNDKTRF.M
		R.AAVPSGASTGIY@EALELRDNDK.T	Y43	2357.70	0.56	0.1774 R.AAVPSGAST@GIYEALELRDNDK.T
		R.IGAEVY@HNLK.N	Y188	1223.84	0.22	none
GAPDH: Glyceraldehyde-3-phosphate dehydrogenase	P16858	F.VKLISWYDNEY@GY.S	Y315	1731.19	1.41	0.0992 F.VKLISWYDNEYGY@.S
		K.LISWYDNEY@GYSNR.V	Y315	1860.51	0.71	none
				1861.29	1.49	0.1354 K.LISWYDNEYGY@SNR.V
		L.ISWYDNEY@GY.S	Y315	1390.09	0.55	none
		L.ISWYDNEY@GYSNRVVDL.M	Y315	2173.71	0.75	none
L-lactate dehydrogenase A chain	P06151	W.KEVHKQVVDSAY@EVIKL.K	Y238	2065.71	0.60	0.0596 W.KEVHKQVVDS@AYEVIKL.K
6-phosphofructokinase, liver type	P12382	K.C*HEHYTTEFLY@NLYSSEGR.G	Y639	2487.79	1.77	none
Phosphoglycerate mutase 1	Q9DBJ1	F.SGWY@DADLSPAGHEEAKRGGQAL.R	Y25	2497.02	1.89	0.0093 F.S@GWYDADLSPAGHEEAKRGGQAL.R
		F.SGWY@DADLSPAGHEEAKRGGQ.A	Y25	2312.53	1.52	0.1254 F.S@GWYDADLSPAGHEEAKRGGQ.A
		R.FSGWY@DADLSPAGHEEAK.R	Y25	2060.43	0.55	0.1895 R.FS@GWYDADLSPAGHEEAK.R
				2061.53	1.65	0.0797 R.FS@GWYDADLSPAGHEEAK.R
		R.FSGWY@DADLSPAGHEEAKR.G	Y25	2215.86	-0.12	none
				2216.83	0.84	0.0203 R.FS@GWYDADLSPAGHEEAKR.G
Pyruvate kinase, isozyme M2	P52480	R.EATESFASDPILY@RPVAVALDTK.G	Y104	2575.27	1.98	none
		R.EATESFASDPILY@RPVAVALDTKGPEIR.T	Y104	3127.25	1.66	0.1336 R.EATESFAS@DPILYRPVAVALDTKGPEIR.T
		Y.HAETIKNVREATESFASDPILY@RPVAVAL.D	Y104	3278.92	1.22	0.1694 Y.HAETIKNVREATESFAS@DPILYRPVAVAL.D
		K.ITLDNAY@MEKC*DENILWLDYK.N	Y147	2728.04	0.82	0.1779 K.IT@LDNAYMEKC*DENILWLDYK.N
		L.IAREAEAAIY@HLQL.F	Y389	1678.08	0.21	none
		L.IAREAEAAIY@HL.Q	Y389	1437.13	0.40	none
		L.IAREAEAAIY@HLQLF.E	Y389	1827.32	2.38	none
		L.IAREAEAAIY@HLQLFEEL.R	Y389	2196.18	0.07	none
		M.QHLIAREAEAAIY@HLQLFEEL.R	Y389	2576.78	2.47	none
		R.EAEAAIY@HLQLFEELR.R	Y389	2013.22	1.23	none
		R.EAEAAIY@HLQLFEELRR.L	Y389	2169.17	1.08	none
Other metabolic/biosynthetic enzymes						
ADP/ATP translocase 2	P51881	R.AAYFGIY@DTAK.G	Y194	1300.18	0.58	0.0091 R.AAYFGIYDT@AK.G
ATP citrate lyase	Q91V92	R.TTDGVY@EGVAIGGDRYPGSTFMDHVLR.Y	Y 672	2995.35	1.97	0.1688 R.TT@DGVYEGVAIGGDRYPGSTFMDHVLR.Y
		R.TTDGVY@EGVAIGGDRYPGSTFM#DHVLR.Y	Y 672	3011.67	2.28	0.1310 R.T@TDGVYEGVAIGGDRYPGSTFM#DHVLR.Y
Aldo-keto reductase family 1 member C18	Q8K023	K.IELNDGHSIPVLGFGTY@ATEEHLK.K	Y24	2721.66	1.33	0.0445 K.IELNDGHSIPVLGFGT@YATEEHLK.K
Aldo-keto reductase family 1, member B3	Q5U415	R.HIDC*AQVY@QNEK.E	Y49	1585.25	0.59	none
		R.HIDC*AQVY@QNEKEVGVALQEK.L		2538.86	0.68	none

Aldose reductase-related protein 2	P45377	R.AC*LLPETVNMEEYPYDAEY@.-	Y315	2389.42	2.46	0.0421 R.AC*LLPETVNMEEYPY@DAEY.-
		W.RAC*LLPETVNMEEYPYDAEY@.-	Y315	2543.25	0.19	0.0880 W.RAC*LLPETVNMEEYPY@DAEY.-
Adenylosuccinate synthetase, non-muscle isozyme	P46664	K.DGVY@FLYEALHGPPK.K	Y236	1786.69	0.83	0.1974 K.DGVYFLY@EALHGPPK.K
		K.DGVY@FLYEALHGPPKK.I	Y236	1915.78	1.83	none
		K.DGVYFLY@EALHGPPKK.I	Y239	1915.42	1.47	none
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	L.SEDEARVC*MVY@DLYPTLTPL.A	Y290	2452.49	0.40	none
		R.VC*M#VY@DLYPTLTPLAVAYAR.A	Y290	2412.86	0.70	0.1387 R.VC*M#VYDLY@PTLTPLAVAYAR.A
				2413.65	1.49	none
		R.VC*MVY@DLYPTLTPLAVAYAR.A	Y290	2397.51	1.35	0.0339 R.VC*MVYDLY@PTLTPLAVAYAR.A
				2396.96	0.80	0.1803 R.VC*MVYDLY@PTLTPLAVAYAR.A
		R.VC*MVYDLY@PTLTPLAVAYAR.A	Y293	2398.64	2.48	0.0159 R.VC*MVY@DLYPTLTPLAVAYAR.A
CTP synthase	P70698	Y.INIDAGTFSPY@EHGEVF.V	Y53	1977.27	1.39	0.0857 Y.INIDAGTFS@PYEHGEVF.V
Glycerol-3-phosphate dehydrogenase 2	Q8VDT0	R.FLYY@EMGYK.S	Y601	1293.78	0.22	0.1060 R.FLY@YEMGYK.S
Glucose-6-phosphate 1-dehydrogenase X	Q00612	R.NSYVAGQY@DDAASYK.H	Y111	1732.46	0.74	none
		R.VQPNEAVY@TK.M	Y400	1229.40	0.81	0.0551 R.VQPNEAVYT@K.M
		L.VIRVQPNEAVY@TKM#.M	Y400	1745.04	1.15	0.0798 L.VIRVQPNEAVYT@KM#.M
		L.VIRVQPNEAVY@TKM.M	Y400	1728.63	0.73	0.0690 L.VIRVQPNEAVYT@KM.M
				1728.53	0.64	0.0903 L.VIRVQPNEAVYT@KM.M
		L.VIRVQPNEAVY@TKMM.T	Y400	1860.52	0.59	0.0481 L.VIRVQPNEAVYT@KMM.T
				1859.37	0.44	0.1131 L.VIRVQPNEAVYT@KMM.T
		K.KPGMFFNPEESELDLTY@GNRYK.N	Y423	2716.37	1.11	0.0442 K.KPGMFFNPEESELDLT@YGNRYK.N
		K.RVGFQYEGTY@K.W	Y506	1428.28	0.61	0.0364 K.RVGFQYEGT@YK.W
				1428.11	0.44	0.1714 K.RVGFQYEGT@YK.W
		R.VGFQYEGTY@K.W	Y506	1273.00	1.43	0.0784 R.VGFQYEGT@YK.W
Inosine-5'-monophosphate dehydrogenase 2	P24547	L.AATTEAPGEY@FFSDGIRL.K	Y400	2025.93	0.99	none
Phosphoglucomutase 2	Q5RJV4	K.IALY@ETPTGWK.F	Y353	1359.54	0.87	none
Ribonucleoside-diphosphate reductase large subunit	P07742	K.KVFSDVMEDLY@NYINPHNGR.H	Y102	2492.68	1.54	0.1362 K.KVFSDVMEDLYNY@INPHNGR.H
		K.KVFSDVM#EDLY@NYINPHNGR.H	Y102	2508.75	1.61	0.0611 K.KVFSDVM#EDLYNY@INPHNGR.H
Serine hydroxymethyltransferase, cytosolic	P50431	K.M#LSQPLKDSDAEVY@SIIKK.E	Y28	2261.90	0.75	0.0858 K.M#LSQPLKDSDAEVYS@IIKK.E
		K.MLSQPLKDSDAEVY@SIIKK.E	Y28	2246.63	1.48	0.0409 K.MLSQPLKDSDAEVYS@IIKK.E
S-adenosylhomocysteine hydrolase	Q5M9P0	K.SKFDNLY@GC*R.E	Y193	1340.32	0.76	none
Thioredoxin reductase 1, cytoplasmic	Q9JMH6	K.KVVYENAY@GR.F	Y131	1279.76	1.14	none
				1279.41	0.79	none
		K.VVYENAY@GR.F	Y131	1150.68	0.15	none
Thioredoxin reductase 1 [fragment]	Q3UEB7	K.EVVYENAY@GR.F	Y131	1280.86	1.29	none
TK: Transketolase	P40142	K.NM#AEQIIQEIY@SQVQSK.K	Y275	2106.94	1.94	0.1420 K.NM#AEQIIQEIYS@QVQSK.K
		K.NMAEQIIQEIY@SQVQSK.K	Y275	2091.27	2.27	0.1295 K.NMAEQIIQEIYS@QVQSK.K
				2090.21	1.21	0.1119 K.NMAEQIIQEIYS@QVQSK.K
UDP-glucose 6-dehydrogenase	O70475	R.INAWNSPTLPIY@EPGLK.E	Y53	1993.78	0.76	0.1794 R.INAWNSPT@LPIYEPGLK.E
		R.INAWNSPTLPIY@EPGLKEVVESC*R.G	Y53	2853.36	0.98	0.1570 R.INAWNSPT@LPIYEPGLKEVVESC*R.G

RNA SYNTHESIS AND PROCESSING

Transcription machinery and regulation

CCR4-NOT transcription complex subunit 2	Q8C5L3	F.VEGVDSDYHDENM#Y@Y.S	Y43	1932.21	0.50	0.0044 F.VEGVDSDYHDENM#YY@.S
		F.VEGVDSDYHDENMY@Y.S	Y43	1916.61	0.90	0.0073 F.VEGVDSDYHDENMYY@.S
		K.FVEGVDSDYHDENM#Y@YSQSSMFPHR.S	Y43	3137.60	1.35	0.1041 K.FVEGVDSDYHDENM#YY@SQSSMFPHR.S
		K.FVEGVDSDYHDENMY@YSQSSM#FPHR.S	Y43	3137.55	1.30	0.1199 K.FVEGVDSDYHDENMYY@SQSSM#FPHR.S
		K.FVEGVDSDYHDENMY@YSQSSMFPHR.S	Y43	3120.79	0.54	0.0836 K.FVEGVDSDYHDENMYY@SQSSMFPHR.S
DNA-directed RNA polymerase I 40 kDa polypeptide -- RPA40	P52432	R.NVHTTDFPGNY@AGYDDAWDQNRFEK.N	Y33	3041.75	1.46	0.1220 R.NVHTTDFPGNYAGY@DDAWDQNRFEK.N
LIM domains containing protein 1 -- LIMD1	Q9QXD8	K.VFC*EEDFLY@SGFQQSADR.C	Y519	2278.51	0.58	0.1106 K.VFC*EEDFLYS@GFQQSADR.C
				2278.78	0.85	0.0923 K.VFC*EEDFLYS@GFQQSADR.C
NF-kappa-B DNA binding subunit p105	P25799	F.TRRLEPVVSDAIY@DSKAPNASNL.K	Y238	2597.89	1.58	0.1017 F.TRRLEPVVSDAIYDS@KAPNASNL.K
		R.RLEPVVSDAIY@DSKAPNASNLK.I	Y238	2468.36	1.10	0.1473 R.RLEPVVSDAIYDS@KAPNASNLK.I
Polymerase I and transcript release factor -- PTRF	O54724	F.KVMIY@QDEVKLPAKL.S	Y158	1856.46	1.45	none
		K.VMIY@QDEVKLPAK.L	Y158	1614.53	0.70	none
		R.KSFTPDHVVY@AR.S	Y310	1501.01	1.27	none
		K.SFTPDHVVY@AR.S	Y310	1371.90	0.25	none
Staphylococcal nuclease domain-containing protein 1	Q78PY7	R.ADDADEFGY@SR.-	Y908	1326.82	1.32	0.1384 R.ADDADEFGYS@R.-

		R.YGDFRADDADEFGY@SR.-	Y908	1965.34	1.56	0.0838 R.YGDFRADDADEFGYS@R.-
Transcription initiation factor IIE alpha subunit	Q9D0D5	R.FNEQIEPIY@ALLR.E	Y188	1686.85	0.99	none
Transcription elongation factor SPT6	Q62383	K.AAEDDELEEEADWIY@R.N	Y321	2033.99	0.15	none
Tripartite motif protein 25	Q61510	K.FDTIY@QVLVK.K	Y277	1306.61	0.93	none
		R.VYGKFDTIY@QVLVK.K	Y277	1755.35	2.42	none
				1753.14	0.21	0.1319 R.VYGKFDT@IYQVLVK.K
DEAD(DEAH)-box helicases						
ATP-dependent RNA helicase DDX3X (DDX3Y) (PL10)	Q62167	K.GFY@DKDSSGWSS@SKDKDAYSSFGSR.G	Y52	2925.64	1.43	0.1009 K.GFY@DKDSSGWS@SSKDKDAYSSFGSR.G
		K.DKDAY@SSFGSR.D	Y68	1313.01	0.46	0.0944 K.DKDAYS@SFGSR.D
		W.SSSKDKDAY@SSF.G	Y68	1402.42	0.83	0.1348 W.SSSKDKDAYS@SF.G
		R.FDDRGRGDY@DGIGGR.G	Y103	1738.12	2.37	none
		R.GDY@DGIGGR.G	Y103	989.61	0.20	none
		R.GDY@DGIGGRGDR.S	Y103	1318.29	0.73	none
		R.GRGDY@DGIGGR.G	Y103	1203.18	0.65	none
				1203.80	1.27	none
		R.GRGDY@DGIGGRGDR.S	Y103	1531.84	1.16	none
		K.TAAFLLPILSQIY@ADGPGEALR.A	Y242	2397.50	1.24	none
				2398.00	1.74	none
		L.VLAPTRELAVQIY@EEARKF.S	Y282	2315.54	2.31	none
		R.VRPC*VVY@GGAEIGQQIR.D	Y300	1983.25	1.27	none
		F.VETKKGADSLEDFLY@HEGY.A	Y461	2282.58	1.54	none
				2281.83	0.79	0.1563 F.VETKKGADSLEDFLYHEGY@.A
		K.GADSLEDFLY@HEGYAC*TSIHGDR.S	Y461	2694.29	1.18	none
		K.KGADSLEDFLY@HEGYAC*TSIHGDR.S	Y461	2823.23	2.03	0.1667 K.KGADSLEDFLYHEGY@AC*TSIHGDR.S
		L.VFVETKKGADSLEDFLY@HEGY.A	Y461	2528.99	1.81	0.1241 L.VFVETKKGADSLEDFLYHEGY@.A
				2528.63	1.45	0.0826 L.VFVETKKGADSLEDFLYHEGY@.A
Putative ATP-dependent RNA helicase DHX30	Q99PU8	R.ENYLEENLLY@APSLR.F	Y991	1904.76	0.84	none
Probable ATP-dependent RNA helicase DDX6	P54823	K.GVTQY@YAYVTER.Q	Y312	1531.35	1.65	0.1139 K.GVT@QYYAYVTER.Q
Putative pre-mRNA splicing factor ATP-dependent RNA helicase DHX15	O35286	K.QNHESVQWC*Y@DNFINYR.S	Y645	2354.91	1.95	none
Probable ATP-dependent RNA helicase DDX17 (DDX5)	Q501J6	K.STC*IY@GGAPK.G	Y200	1133.66	0.18	none
		R.LKSTC*IY@GGAPK.G	Y200	1376.84	2.18	0.0842 R.LKST@C*IYGGAPK.G
Probable ATP-dependent RNA helicase DDX20 -- DEAD-box protein 20	Q9JJY4	R.VQSEPQEESWY@DC*HR.E	Y757	2030.07	0.28	0.0515 R.VQSEPQEES@WYDC*HR.E
		R.AWQEY@YAAASHSYYWNAQR.H	Y788	2445.45	0.41	0.0745 R.AWQEYY@AAASHSYYWNAQR.H
Probable ATP-dependent helicase DDX48	Q91VC3	K.GFKEQIY@DVYR.Y	Y202	1499.04	1.33	none
				1498.44	0.73	none
hnRNPs and snRNPs						
Heterogeneous nuclear ribonucleoprotein A1	P49312	F.GGRSSGPY@GGGGQYF.A	Y288	1526.42	-0.22	none
		R.SSGPYGGGGQY@FAKPR.N	Y294	1708.75	-0.03	none
Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Y.GGGYGSGGGSGGY@GSRRF.-	Y374	1718.16	2.43	0.0301 Y.GGGYGSGGGSGGYGS@RRF.-
Heterogeneous nuclear ribonucleoprotein A/B	Q3TMZ8	Y.GPGYGGYDYSPY@GYY.G	Y291	1759.36	0.69	none
		Y.GYQQGYGPGYGGYDY@SPYGYY.G	Y288	2456.33	1.36	none
Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	K.ATENDIY@NFFSPLNPVR.V	Y306	2077.60	0.61	0.1897 K.AT@ENDIYNFFSPLNPVR.V
				2077.75	0.76	0.1895 K.AT@ENDIYNFFSPLNPVR.V
		R.DLSYC*LSGMY@DHR.Y	Y272	1698.59	1.93	0.1833 R.DLSYC*LS@GMYDHR.Y
Heterogeneous nuclear ribonucleoprotein H1	Q811L7	R.GAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D	Y243	3157.52	0.28	0.0374 R.GAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D
		R.GAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246	3159.41	2.17	0.0285 R.GAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDR.F	Y246	2954.06	0.91	0.0365 R.RGAYGGGYGGY@DDYNGYNDGYGFGSDR.F
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246	3314.92	1.89	0.0274 R.RGAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D
		R.GAYGGGYGGYDDYNGY@NDGYGFGSDRFGR.D	Y249	3157.92	0.68	0.0333 R.GAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D
Heterogeneous nuclear ribonucleoprotein H'	P70333	R.GAYGGGYGGY@DDYGGYNDGYGFGSDRFGR.D	Y243	3100.80	0.59	0.0469 R.GAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D
		R.GAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246	3101.06	0.85	0.1258 R.GAYGGGYGGYDDYGGY@NDGYGFGSDRFGR.D
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDR.F	Y246	2896.60	0.48	0.1462 R.RGAYGGGYGGY@DDYGGYNDGYGFGSDR.F
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246	3256.76	1.14	0.1400 R.RGAYGGGYGGYDDYGGY@NDGYGFGSDRFGR.D
		Y.GGGYGGYDDY@GGYNDGYGF.G	Y246	2034.33	0.61	0.1927 Y.GGGYGGY@DDYGGYNDGYGF.G
		Y.GGGYGGYDDY@GGYNDGYGFGSDRF.G	Y246	2596.25	0.28	0.1144 Y.GGGYGGYDDYGGY@NDGYGFGSDRF.G
		R.ATENDIY@NFFSPLNPMR.V	Y306	2109.47	0.52	0.1990 R.AT@ENDIYNFFSPLNPMR.V
		Y.RATENDIY@NFF.S	Y306	1470.32	0.68	none
Heterogeneous nuclear ribonucleoprotein L	Q8R081	M.VKMAAAGGGGGGGRY@Y.G	Y16	1553.17	1.46	0.0236 M.VKMAAAGGGGGGGRYY@.G

Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	N.RFEPY@SNPTKRY.R	Y62	1638.31	0.53	0.0622 N.RFEPYS@NPTKRY.R
Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Q.RQAAKNQMYDDYY@YY.G	Y432	2072.98	1.12	0.0285 Q.RQAAKNQMYDDYYY@Y.G
		R.GGYEDPY@YGYEDFQVGAR.G	Y485	2166.94	1.06	0.0889 R.GGYEDPYY@GYEDFQVGAR.G
		Y.RGGYEDPY@YGY@EDFQVGAR.G	Y485,Y488	2401.92	-0.07	0.1253 Y.RGGYEDPYY@GY@EDFQVGAR.G
		Y.RGGYEDPY@YGY@EDF.Q	Y485,Y488	1892.33	1.63	0.0998 Y.RGGYEDPY@Y@GYEDF.Q
		Y.RGGYEDPY@YGYEDF.Q	Y485	1812.07	1.37	0.0700 Y.RGGYEDPYY@GYEDF.Q
		Y.RGGYEDPY@YGYEDFQ.V	Y485	1939.52	0.76	0.0449 Y.RGGYEDPYY@GYEDFQ.V
Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Y.RGGYEDPY@YGYDDGY.A	Y489	1870.15	0.45	0.1472 Y.RGGYEDPYY@GYDDGY.A
Heterogeneous nuclear ribonucleoprotein U	O88568	K.NQSQGYNQWQQGQFWGQKPWSQHYHQGY@Y.-	Y797	3740.91	2.30	none
Polypirimidine tract binding protein	Q8R509	Y.TSVAPVLRGQPNY@IQF.S	Y126	1871.74	1.78	none
Polypyrimidine tract-binding protein 1 -- hnRNP	P17225	R.GQPIY@IQFSNHK.E	Y126	1511.57	-0.17	none
		Y.TSVAPVLRGQPIY@IQF.S	Y126	1870.66	1.66	none
U1 small nuclear ribonucleoprotein 70 kDa	Q62376	K.HHNQPY@C*GIAPYIR.E	Y38	1806.75	0.94	none
U1 small nuclear ribonucleoprotein C	Q62241	K.FYC*DYC*DTY@LTHDSPSVR.K	Y12	2380.07	1.17	0.0584 K.FYC*DYC*DT@YLTHDSPSVR.K
Splicing factors						
Apoptosis-related RNA binding protein	Q9Z0H4	K.ELFEPYGAVY@QINVLR.D	Y67	1991.96	0.96	none
Crooked neck-like protein 1	P63154	R.KVQADDGSDAGWEEY@Y@DYIFPEDAANQPNLK.L	Y640,Y641	3709.15	0.57	0.0753 R.KVQADDGSDAGWEEY@YDY@IFPEDAANQPNLK.L
		R.KVQADDGSDAGWEEY@YDYIFPEDAANQPNLK.L	Y640	3630.34	1.76	0.0014 R.KVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L
		R.KVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L	Y641	3629.24	0.66	0.0544 R.KVQADDGSDAGWEEY@YDYIFPEDAANQPNLK.L
		R.RKVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L	Y641	3785.88	1.20	0.0535 R.RKVQADDGSDAGWEEY@YDYIFPEDAANQPNLK.L
RNA binding motif, single-stranded interacting protein 1	Q91W59	K.QQMYPQY@ATYYYPQYLQAK.Q	Y13	2528.18	1.04	0.0658 K.QQMYPQYAT@YYYPQYLQAK.Q
				2527.81	0.67	0.1028 K.QQMYPQYAT@YYYPQYLQAK.Q
		W.KQQMYPQY@ATY.Y	Y13	1501.93	1.27	0.1365 W.KQQMY@PQYATY.Y
		K.QQMYPQY@ATY@YYPQYLQAK.Q	Y13,Y16	2608.71	1.57	0.0433 K.QQMYPQY@AT@YYYPQYLQAK.Q
		K.QQM#YPQYATY@YYPQYLQAK.Q	Y16	2544.16	1.02	0.0094 K.QQM#YPQYATYY@YPQYLQAK.Q
				2545.02	1.88	0.0237 K.QQM#YPQYAT@YYYPQYLQAK.Q
		K.QQMYPQYATY@YYPQYLQAK.Q	Y16	2529.11	1.97	0.0147 K.QQMYPQYAT@YYYPQYLQAK.Q
				2528.00	0.86	0.0157 K.QQMYPQYAT@YYYPQYLQAK.Q
		L.HNGFYPSPY@SIATN.R	Y272	1648.43	0.71	0.1024 L.HNGFYPSPYS@IATN.R
Splicing factor, arginine/serine-rich 1	Q6PDM2	F.VRKEDMTY@AVR.K	Y169	1448.14	0.43	0.1135 F.VRKEDMT@YAVR.K
Splicing factor, arginine/serine-rich 3	P84104	R.AFGY@YGPLR.S	Y32	1124.17	0.64	0.1722 R.AFGYY@GPLR.S
Splicing factor 3b, subunit 4	Q8QZY9	F.IGNLDPEIDEKLLY@DTF.S	Y117	2075.45	0.45	0.1569 F.IGNLDPEIDEKLLYDT@F.S
Splicing factor, arginine/serine-rich 5	O35326	F.GFVEFEDPRDADDAVY@ELDGKEL.C	Y55	2711.02	1.83	none
				2710.83	1.64	none
		R.GFGFVEFEDPRDADDAVY@ELDGK.E	Y55	2673.41	2.25	none
		R.GFGFVEFEDPRDADDAVY@ELDGKELC*SER.V	Y55	3447.57	2.10	none
Arginine/serine-rich splicing factor 6	Q921K3	K.NGYGFVEFEDSRDADDAVY@ELNSK.E	Y53	2821.59	1.39	0.1583 K.NGYGFVEFEDSRDADDAVYELNS@K.E
		Y.GFVEFEDSRDADDAVY@ELNSKEL.C	Y53	2730.50	2.30	none
Splicing factor, arginine/serine-rich 9	Q9D0B0	R.DAEDAIY@GR.N	Y71	1090.19	0.73	none
Splicing factor, proline- and glutamine-rich	Q8VIJ6	R.FAQHGTFEY@EYSQR.W	Y480	1842.64	-0.14	none
Other RNA binding and processing						
DAZ-associated protein 1	Q9JII5	L.AFPPPPSQAAPDMSKPPTAQPDFPY@GQY.G	Y346	3084.01	1.61	0.1810 L.AFPPPPSQAAPDMSKPPTAQPDFPYGQY@.G
Double-stranded RNA-binding protein Staufen homolog	Q9Z108	R.ELLY@GGTSPTAETILK.S	Y371	1772.86	-0.05	none
		R.TRPSEQLY@YLSR.A	Y404	1593.68	0.90	0.1324 R.TRPSEQLYY@LSR.A
				1593.49	0.70	0.0605 R.TRPSEQLYY@LSR.A
ELAV-like protein 1	P70372	K.NMALLSQLY@HSPAR.R	Y200	1681.12	0.29	0.0766 K.NMALLSQLYHS@PAR.R
				1681.83	1.00	0.0995 K.NMALLSQLYHS@PAR.R
ELAV-like protein 2	Q60899	K.TNQAILSQLY@QSPNR.R	Y219	1814.48	1.58	none
Fragile X mental retardation syndrome related protein 1 homolog	Q61584	K.EISEGDEVEVY@SR.A	Y68	1594.00	2.31	none
		K.KEISEGDEVEVY@SR.A	Y68	1720.41	0.63	0.0952 K.KEISEGDEVEVYS@R.A
				1720.51	0.73	0.0539 K.KEISEGDEVEVYS@R.A
		L.KDPDSNPY@SLL.D	Y506	1329.29	0.68	0.1248 L.KDPDSNPYS@LL.D

Fragile X mental retardation syndrome related protein 2 homolog	Q9WVR4	R.LPPPADYNKEITEGDEVEVY@SR.A	Y78	2602.73	1.52	0.0431 R.LPPPADYNKEITEGDEVEVYS@R.A
		L.KDPDSNPY@SLLDTSEPEPPVDSEPGEPPPASAR.R	Y520	3570.84	0.23	0.0459 L.KDPDSNPYS@LLDTSEPEPPVDSEPGEPPPASAR.R
Insulin-like growth factor 2 mRNA-binding protein 2	Q5SF07	K.SGY@AFVDYPDQNWAIR.A	Y40	1983.39	1.51	0.0062 K.S@GYAFVDYPDQNWAIR.A
Insulin-like growth factor 2, binding protein 1	Q80US9	K.SGY@AFVDC*PDEHWAMK.A	Y39	1994.13	1.35	0.0899 K.S@GYAFVDC*PDEHWAMK.A
Interleukin enhancer-binding factor 3	Q9Z1X4	R.VLEC*LASGIVMPDGSGIY@DPC*EKEATDAIGHLDR.Q	Y292	3770.36	1.67	0.0452 R.VLEC*LASGIVMPDGS@GIYDPC*EKEATDAIGHLDR.Q
Matrin-3	Q8K310	R.SATREPPY@RVPR.D	Y171	1509.57	0.80	none
		R.SQESGYY@DRMDYEDDRLR.D	Y214	2379.59	1.62	0.0267 R.SQESGY@YDRMDYEDDRLR.D
Polyadenylate-binding protein 1 -- PABP1 (PABC4)	P29341	Y.VGDLHPDVTEAM#LY@EKF.S	Y28	2061.61	1.66	none
		Y.VGDLHPDVTEAMLY@EKF.S	Y28	2044.23	0.28	none
		K.ALY@DTFSAFGNILSC*K.V	Y116	1887.61	0.76	0.1746 K.ALYDT@FSAFGNILSC*K.V
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKL.H	Y232	1867.27	1.30	none
		Y.TIQGQY@AIPQPDLTKLHQLAM#.Q	Y232	2464.22	1.97	none
		Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232	2447.42	1.17	none
				2446.44	0.19	0.1033 Y.T@IQGQYAIPQPDLTKLHQLAM.Q
Poly(rC)-binding protein 3	P57722	K.PASTPVIFAGGQAYTIQGQY@AIPHPDLTK.L	Y201	3123.08	1.51	none
Protein SMG7	Q5RJH6	K.VPEFYWDSSY@SMADNR.A	Y826	2047.17	0.34	0.0240 K.VPEFYWDS@SYSMADNR.A
Pumilio homolog 1	Q80U78	R.SQDDAMVDY@FFQR.Q	Y83	1702.58	0.88	none
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S	Y124	1649.29	1.60	0.0718 R.YDSRPGGYGYGY@GR.S
		R.YDSRPGGYGYGY@GR.S	Y126	1648.32	0.64	0.1379 R.YDSRPGGYGY@GYGR.S
Ras-GTPase-activating protein binding protein 1 -- G3bp1	P97855	K.NSSYAHGGLDSNGKPADAVY@GQK.E	Y56	2417.01	0.92	none
Ras-GTPase-activating protein SH3-domain binding protein	UPI0000D62F64	K.NSSYAHGGLDSNGKPADAVY@GKK.E	Y56	2418.61	2.48	none
Ras-GTPase-activating protein binding protein 2	P97379	R.NSSYVHGGVDASGKPQEAVY@GQNDIHHK.V	Y56	3075.79	1.38	0.1362 R.NSSYVHGGVDAS@GKPQEAVYGQNDIHHK.V
		Y.VHGGVDASGKPQEAVY@GQNDIHHKVL.S	Y56	2836.92	1.53	none
Regulator of differentiation 1 -- Rod1	Q8BHD7	R.SQPVY@IQYSNHR.E	Y98	1572.85	1.12	0.1990 R.S@QPVYIQYSNHR.E
Regulator of nonsense transcripts 1 -- RENT1	Q9EPU0	L.AELNFEEDEEDTY@YTKDLPVHAC*SY.C	Y108	3120.26	1.99	0.0028 L.AELNFEEDEEDT@YYTKDLPVHAC*SY.C
		L.AELNFEEDEEDTY@YTKDLPVHAC*.S	Y108	2870.34	2.17	0.0424 L.AELNFEEDEEDT@YYTKDLPVHAC*.S
		L.LAELNFEEDEEDTY@YTKDLPVHAC*.S	Y108	2981.81	0.55	0.0528 L.LAELNFEEDEEDT@YYTKDLPVHAC*.S
		K.RFTAQGLPDLNHSQVY@AVK.T	Y472	2224.55	0.43	0.1566 K.RFTAQGLPDLNHS@QVYAVK.T
		R.FM#TTAMY@DAR.E	Y930	1303.56	1.03	none
		R.FMTTAMY@DAR.E	Y930	1288.28	1.75	none
		R.AYQHGGVTGLSQY@.-	Y1113	1461.38	0.73	0.1952 R.AYQHGGVTGLS@QY.-
PROTEIN SYNTHESIS AND PROCESSING						
tRNA synthetases						
Alanyl-tRNA synthetase	Q8BGQ7	K.DNFWEMGDTGPC*GPC*SEIHY@DR.I	Y192	2724.93	1.94	0.1390 K.DNFWEMGDTGPC*GPC*S@EIHYDR.I
Arginyl-tRNA synthetase	Q9D0I9	K.SDGGYTY@DTSDLAAIK.Q	Y384	1757.13	0.37	0.0596 K.SDGGYT@YDTSDLAAIK.Q
Bifunctional aminoacyl-tRNA synthetase	Q8CGC7	R.GFFIC*DQPYEPVSPY@SC*R.E	Y690	2303.26	1.33	0.0087 R.GFFIC*DQPYEPVSPYS@C*R.E
				2302.41	0.48	0.0973 R.GFFIC*DQPYEPVSPYS@C*R.E
		R.RGFFIC*DQPYEPVSPY@SC*R.E	Y690	2459.14	1.11	0.0328 R.RGFFIC*DQPYEPVSPYS@C*R.E
				2459.31	1.27	0.0657 R.RGFFIC*DQPYEPVSPYS@C*R.E
Cysteinyl-tRNA synthetase	Q9ER72	K.VTWYC*C*GPTVY@DASHMGHAR.S	Y143	2449.20	1.24	0.0731 K.VTWYC*C*GPTVYDAS@HMGHAR.S
Histidyl-tRNA synthetase	Q61035	K.LIY@DLKDQGGELLSLR.Y	Y115	1914.13	1.12	none
				1914.11	1.10	none
		K.YGEDSKLIY@DLKDQGGELLSLR.Y	Y115	2593.99	1.70	none
		L.TGKYGEDSKLIY@DLKDQGGELL.S	Y115	2523.44	1.20	none
Isoleucine-tRNA synthetase	Q6NXK4	K.NNDLC*Y@WVPEFVR.E	Y434	1792.18	0.41	none
lysyl-tRNA synthetase	Q8C292	K.ITYHPDGPEGQAY@EVDFTPPFR.R	Y381	2618.27	2.09	none
		K.ITYHPDGPEGQAY@EVDFTPPFRR.I	Y381	2773.74	1.48	none
Valyl-tRNA synthetase	Q9Z1Q9	R.LHEEGVIY@R.S	Y468	1196.22	0.64	none
Translation machinery						

40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	1191.28	1.62	none
60S ribosomal protein L3	P27659	K.NNASTDY@DLSDK.S	Y306	1422.85	0.27	0.1716 K.NNAST@DYDLSDK.S
60S ribosomal protein L4	Q9D8E6	R.KLDELY@GTWR.K	Y264	1361.44	0.78	none
mitochondrial ribosomal protein S27	UPI00001C5 303	F.VDNIASREDLDSAEY@YLY.K	Y90	2216.95	0.97	0.1226 F.VDNIASREDLDSAEYY@LY.K
		R.FVDNIASREDLDSAEY@YLYK.F	Y90	2492.48	1.34	0.0509 R.FVDNIASREDLDSAEYY@LYK.F
		R.EDLDSAEY@YLYK.F	Y90	1590.13	1.45	0.1150 R.EDLDSAEYY@LYK.F
Eukaryotic translation initiation factor 2A	Q640P8	L.VIASTEVDKTGASY@YGEQTLH.Y	Y250	2349.94	0.84	0.1589 L.VIASTEVDKTGAS@YYGEQTLH.Y
		L.VIASTEVDKTGASY@YGEQTLHY.I	Y250	2513.63	1.47	0.0953 L.VIASTEVDKTGAS@YYGEQTLHY.I
		K.LISKPVASDSTY@FAWC*PDGEHILTATC*APR.L	Y362	3445.11	1.54	0.0135 K.LISKPVASDST@YFAWC*PDGEHILTATC*APR.L
		K.PVASDSTY@FAWC*PDGEHILTATC*APR.L	Y362	3003.18	0.89	0.0212 K.PVASDST@YFAWC*PDGEHILTATC*APR.L
		L.ISKPVASDSTY@F.A	Y362	1395.07	0.41	0.1554 L.ISKPVASDST@YF.A
		Y.KLISKPVASDSTY@F.A	Y362	1636.09	0.25	0.0186 Y.KLISKPVASDST@YF.A
Eukaryotic translation initiation factor 3 subunit 1	Q66JS6	L.KATM#KDDLADY@GGYEGGYVQDYEDFM#.-	Y248	3094.72	1.47	0.1430 L.KAT@M#KDDLADYGGYEGGYVQDYEDFM#.-
		L.KATMKDDLADY@GGYEGGYVQDYEDFM#.-	Y248	3078.11	0.86	0.1523 L.KATMKDDLADYGGY@EGGYVQDYEDFM#.-
		L.KATMKDDLADY@GGYEGGYVQDYEDFM.-	Y248	3061.03	-0.22	none
Eukaryotic translation initiation factor 3, subunit 7	O70194	R.NLAMEATY@INHNFSQQC*LR.M	Y317	2391.75	1.69	0.0479 R.NLAMEAT@YINHNFSQQC*LR.M
Eukaryotic translation initiation factor 3, subunit 8	Q8R1B4	F.DHKQGTY@GGY.F	Y879	1205.78	0.28	0.1391 F.DHKQGT@YGGY.F
		F.DHKQGTY@GGYF.R	Y879	1353.00	0.44	0.0580 F.DHKQGT@YGGYF.R
		L.GSLVENNERVFDHKQGTY@GGY.F	Y879	2451.21	1.09	0.0391 L.GSLVENNERVFDHKQGT@YGGY.F
		R.VFDHKQGTY@GGYFR.D	Y879	1754.36	-0.44	0.0405 R.VFDHKQGT@YGGYFR.D
Eukaryotic translation initiation factor 3, subunit 9	Q8JZQ9	R.MTLDTLSIY@ETPSMGLLDKK.S	Y 438	2338.47	2.32	none
Eukaryotic translation initiation factor 3 subunit 10	P23116	K.KQPALDVLY@DVMK.S	Y32	1600.72	0.89	none
		F.LEVGKKQPALDVLY@DVM.K	Y32	1998.68	0.64	none
Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Y.SASQGAY@YIPGQGRSTY.V	Y110	1886.33	0.48	0.0767 Y.SASQGAYY@IPGQGRSTY.V
Eukaryotic translation initiation factor 4B	Q8BGD9	F.LGNLPY@DVTEDSIKDFF.R	Y105	2054.21	1.26	none
		K.SPPYTAFLGNLPY@DVTEDSIKDFFR.G	Y105	2973.64	1.23	0.1623 K.SPPYTAFLGNLPYDVT@EDSIKDFFR.G
Eukaryotic initiation factor 4A-I	P60843	K.VVMALGDY@MGASC*HAC*IGGTNVR.A	Y126	2520.57	1.51	none
		M.ALGDY@MGASC*H.A	Y126	1263.36	1.91	none
		R.GFKDQIY@DIFQK.L	Y197	1582.47	0.70	none
				1583.90	2.13	none
Eukaryotic translation initiation factor 4H	Q9WUK2	R.AY@SSFGGGR.G	Y11	981.64	0.22	none
		H.GSRSQKELPTEPPY@TAY.V	Y41	2003.78	-0.16	0.0030 H.GSRSQKELPTEPPYT@AY.V
		Q.KELPTEPPY@TAY.V	Y41	1490.20	1.50	0.0841 Q.KELPTEPPYT@AY.V
		R.SQKELPTEPPYTAY@VGNLPFNTVQGDIDAIFK.D	Y44	3633.62	0.83	0.0019 R.SQKELPTEPPYT@AYVGNLPFNTVQGDIDAIFK.D
Elongation factor 1-alpha 1 -- eEF1A-1 (eEF1A-2)	P10126	K.STTTGHLIY@K.C	Y29	1201.30	0.70	none
		R.EHALLAY@TLGVK.Q	Y141	1394.83	0.09	0.0802 R.EHALLAYT@LGVK.Q
G1 to phase transition 2 (GSPT2)	Q9CY91	K.TAGVKY@LIVLINK.M	Y347	1512.19	0.29	0.1153 K.T@AGVKYLIVLINK.M
Laminin receptor 1 -- ribosomal protein SA	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	3077.63	1.17	0.0029 R.ADHQPLTEAS@YVNLPTIALC*NTDSPLR.Y
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.TVSDLIDQKVY@ELQASR.V	Y72	2046.87	1.84	none
				2045.46	0.43	none
		K.VY@ELQASR.V	Y72	1045.98	0.47	none
		Y.FHKTVSDLIDQKVY@EL.Q	Y72	2015.25	0.23	none
		R.VSSDVIDQKVY@EIQDIYENSWTK.L	Y89	2840.70	1.36	0.1171 R.VS@SDVIDQKVYEIQDIYENSWTK.L
		R.QLEVY@TSGGDPESVAGEYGR.H	Y247	2194.26	0.29	0.0943 R.QLEVYT@SGGDPESVAGEYGR.H
		K.GDPQVYEELFSY@AC*PK.F	Y415	1983.38	0.54	0.0843 K.GDPQVYEELFS@YAC*PK.F
		R.MQKGDPQVYEELFSY@AC*PK.F	Y415	2369.50	-0.53	0.0788 R.MQKGDPQVYEELFS@YAC*PK.F
Post-translational modifiers						
N-terminal acetyltransferase complex ARD1 subunit homolog A	Q9QY36	F.QISEVEPKY@YADGEDAY.A	Y137	2057.32	0.44	0.0849 F.QISEVEPKYY@ADGEDAY.A
		L.NFQISEVEPKY@YADGEDAY.A	Y137	2319.18	1.19	0.0569 L.NFQISEVEPKYY@ADGEDAY.A
		K.YYADGEDAY@AMKR.D	Y145	1632.95	0.28	none
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	L.RSQTDSLFGDSGVY@DTPSSY.S	Y576	2263.61	1.64	0.1236 L.RSQTDSLFGDS@GVYDTPSSY.S
Glutathione S-transferase P 1	P19157	K.YVTLIY@TNYENGK.N	Y108	1657.98	0.20	0.0215 K.YVTLIYT@NYENGK.N
		K.YVTLIY@TNYENGKNDYVK.A	Y108	2277.74	0.66	0.0671 K.YVTLIYT@NYENGKNDYVK.A
Chaperones and associated proteins						

BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I	Y246	2380.34	1.25	none
		K.THYPAQQGEYQPQQPVY@HK.I	Y253	2379.97	0.88	none
		K.THYPAQQGEY@QPQQPVY@HK.I	Y246,Y253	2461.40	2.31	none
DnaJ homolog subfamily B member 4	Q9D832	K.VSLEEIY@SGC*TK.R	Y172	1465.88	0.24	0.1309 K.VSLEEIYS@GC*TK.R
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I	Y336	1942.45	0.41	none
				1942.76	0.72	none
		K.NAVEEYVY@EMRDKLSGEYEK.F	Y627	2533.35	1.22	0.1692 K.NAVEEY@VYEMRDKLSGEYEK.F
Heat shock cognate 71 kDa protein	P63017	R.MVQEAEKY@KAEDEKQR.D	Y525	2063.01	1.05	none
Heat shock protein 75 kDa, mitochondrial precursor	Q9CQN1	R.NIY@YLC*APNR.H	Y500	1364.14	0.54	0.1345 R.NIYY@LC*APNR.H
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	1240.75	0.16	0.1627 K.SIYY@ITGESK.E
Heat-shock protein 105 kDa	Q61699	K.NAVEEC*VY@EFR.D	Y644	1496.16	0.56	none
		K.NAVEEC*VY@EFRDK.L	Y644	1739.54	0.81	none
T-complex protein 1, beta subunit	P80314	F.INRQLIY@NYPEQLF.G	Y296	1891.42	0.47	0.1811 F.INRQLIYNY@PEQLF.G
		R.QLIY@NYPEQLFGAAGVMAIEHADFAGVER.L	Y296	3291.35	1.78	0.1012 R.QLIYNY@PEQLFGAAGVMAIEHADFAGVER.L
T-complex protein 1, theta subunit	P42932	K.HFSGLEEAVY@R.N	Y29	1387.92	0.28	none
PROTEIN DEGRADATION						
Ubiquitin conjugation regulators						
Anaphase promoting complex subunit 2	Q8BZQ7	K.VRDQQLIY@SAGVYR.L	Y825	1749.42	1.53	0.1396 K.VRDQQLIYS@AGVYR.L
				1748.60	0.71	0.0724 K.VRDQQLIYS@AGVYR.L
		K.VRDQQLIY@SAGVYRLPK.N	Y825	2087.01	0.89	0.1056 K.VRDQQLIYS@AGVYRLPK.N
		R.DQQLIY@SAGVYR.L	Y825	1493.37	0.64	0.0776 R.DQQLIYS@AGVYR.L
		R.DQQLIY@SAGVYRLPK.N	Y825	1832.50	1.55	0.1299 R.DQQLIYS@AGVYRLPK.N
				1832.49	1.54	0.0863 R.DQQLIYS@AGVYRLPK.N
CBL E3 ubiquitin protein ligase	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L	Y672	2393.89	1.61	0.1037 K.IKPSSSANAIYS@LAARPLPMPK.L
		K.PSSSANAIY@SLAARPLPMPK.L	Y672	2153.32	2.22	0.0627 K.PSSSANAIYS@LAARPLPMPK.L
F-box-like/WD-repeat protein TBL1X	Q9QXE7	K.HQEPVY@SVAFSPDGK.Y	Y459	1740.71	-0.09	0.0867 K.HQEPVYS@VAFSPDGK.Y
F-box-like/WD-repeat protein TBLR1	Q8BHJ5	K.HQEPVY@SVAFSPDGR.Y	Y446	1769.34	0.54	0.0964 K.HQEPVYS@VAFSPDGR.Y
HECT, UBA and WWE domain-containing protein 1	Q7TMY8	R.EMFNPMY@ALFR.T	Y4081	1499.36	0.70	none
Ubiquitin conjugating enzyme 7 interacting protein 3	Q9WUB0	R.NSQEAEVAC*PFIDSTY@SC*PGK.L	Y318	2441.62	1.65	0.0063 R.NSQEAEVAC*PFIDST@YSC*PGK.L
				2441.54	1.57	0.0243 R.NSQEAEVAC*PFIDS@TYSC*PGK.L
Ubiquitin-conjugating enzyme	O88738	K.VIFVDDY@AVGC*R.K	Y107	1495.89	2.22	none
		K.VIFVDDY@AVGC*RK.D	Y107	1622.64	0.88	none
Ubiquitin-conjugating enzyme E2O	Q6PCR9	K.LRPSGDDVELIGEEEDVSVY@DIADHPDFR.F	Y412	3368.77	1.24	0.0670 K.LRPSGDDVELIGEEEDVS@VYDIADHPDFR.F
Ubiquitin-protein ligase E3 Mdm2	P23804	S.DEDDEVY@RVTVY@QTGESDTDSFEGDPEISLADY.W	Y279	3920.96	1.38	0.0850 S.DEDDEVYRVT@VY@QTGESDTDSFEGDPEISLADY.W
Proteasome components						
26S protease regulatory subunit S10B	P62334	K.GC*LLY@GPPGTGK.T	Y173	1300.04	0.45	none
26S protease regulatory subunit 8	P62196	K.GVLLY@GPPGTGK.T	Y189	1239.42	0.76	none
26S protease regulatory subunit 6B	P54775	L.SFLGPEPEDLEDLY@SRY.K	Y41	2109.33	-0.61	0.0766 L.SFLGPEPEDLEDLYS@RY.K
26S proteasome non-ATPase regulatory subunit 7	P26516	W.FLDHDYLENM#Y@GM#F.K	Y79	1907.22	0.47	none
		W.FLDHDYLENMY@GM#F.K	Y79	1891.65	0.89	0.1940 W.FLDHDYLENM#Y@GMF.K
		W.FLDHDYLENMY@GMF.K	Y79	1875.11	0.36	none
Proteasome subunit alpha type 2 -- PSMA2	P49722	L.ATEKKQKSILY@DERSVH.K	Y56	2113.38	1.30	0.1652 L.ATEKKQKS@ILYDERSVH.K
		H.IGLVY@SGM#GPDYRVL.V	Y75	1737.18	1.33	0.1353 H.IGLVYS@GM#GPDYRVL.V
		H.IGLVY@SGMGPDYRVL.V	Y75	1721.70	1.85	0.1064 H.IGLVYS@GMGPDYRVL.V
		H.KVEPITKHIGLVY@SGM#GPDYRVL.V	Y75	2670.18	1.78	0.0645 H.KVEPITKHIGLVYS@GM#GPDYRVL.V
		H.KVEPITKHIGLVY@SGMGPDYRVL.V	Y75	2653.34	0.94	0.0319 H.KVEPITKHIGLVYS@GMGPDYRVL.V
		K.HIGLVY@SGM#GPDYR.V	Y75	1661.63	0.87	0.1234 K.HIGLVYS@GM#GPDYR.V
				1661.23	0.47	0.0712 K.HIGLVYS@GM#GPDYR.V
		K.HIGLVY@SGM#GPDYRVL.V	Y75	1875.20	2.29	0.0032 K.HIGLVYS@GM#GPDYRVL.V
		K.HIGLVY@SGMGPDYR.V	Y75	1646.90	2.14	0.0951 K.HIGLVYS@GMGPDYR.V
				1645.00	0.24	0.0910 K.HIGLVYS@GMGPDYR.V
		K.HIGLVY@SGMGPDYRVL.V	Y75	1858.22	1.31	0.0068 K.HIGLVYS@GMGPDYRVL.V
				1858.28	1.37	0.0189 K.HIGLVYS@GMGPDYRVL.V

		L.VY@SGMGPDYRVL.V	Y75	1436.84	0.17	none
		K.LAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100	2682.78	1.44	0.0610 K.LAQQY@YLVY@QEPIPTAQLVQR.V
		K.LAQQYYLVY@QEPIPTAQLVQR.V	Y100	2602.59	1.25	0.0997 K.LAQQY@YLVYQEPIPTAQLVQR.V
				2603.19	1.85	none
		R.KLAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100	2810.10	0.66	0.0294 R.KLAQQY@YLVY@QEPIPTAQLVQR.V
		R.KLAQQYYLVY@QEPIPTAQLVQR.V	Y100	2730.53	1.09	0.1299 R.KLAQQYY@LVYQEPIPTAQLVQR.V
				2730.10	0.66	none
		Y.YLVY@QEPIPTAQL.V	Y100	1616.07	1.25	none
Proteasome subunit alpha type 6	Q9QUM9	Y.KC*DPAGYY@C*GF.K	Y160	1417.90	0.41	0.1672 Y.KC*DPAGY@YC*GF.K
Proteasome subunit beta type 1	O09061	K.GAVY@SFDPVGSYQR.D	Y149	1627.36	1.63	0.1511 K.GAVYS@FDPVGSYQR.D
		K.DVFISAAERDVY@TGDALR.I	Y215	2079.40	1.41	0.0521 K.DVFISAAERDVYT@GDALR.I
Proteasome subunit beta type 4 precursor	P99026	M.RVNDSTMLGASGDY@ADF.Q	Y102	1900.31	1.51	0.1851 M.RVNDSTMLGAS@GDYADF.Q
		R.VNDSTMLGASGDY@ADFQYLK.Q	Y102	2275.68	0.68	0.1357 R.VNDSTMLGAS@GDYADFQYLK.Q
Proteasome subunit beta type 5 precursor	O55234	K.RGPGLY@YVDSEGNR.I	Y116	1663.18	0.42	0.0144 K.RGPGLYY@VDSEGNR.I
				1663.57	0.81	0.0477 K.RGPGLYY@VDSEGNR.I
		R.GPGLY@YVDSEGNR.I	Y116	1508.50	1.84	0.1311 R.GPGLYY@VDSEGNR.I
		W.DKRGPGLY@YVDSEGNRISGTAF.S	Y116	2483.69	1.52	0.0600 W.DKRGPGLYY@VDSEGNRISGTAF.S
		R.AIY@QATYR.D	Y165	1066.45	0.94	none
		R.DAYSGGAVNLY@HVR.E	Y181	1602.50	0.76	none
		R.DAYSGGAVNLY@HVREDGWIR.V	Y181	2359.17	1.07	none
Proteasome subunit beta type 7 precursor	P70195	L.VLGGVDVTGPHLY@SIYPHGSTDKLPY.V	Y154	2865.24	-0.18	0.0434 L.VLGGVDVTGPHLYS@IYPHGSTDKLPY.V
Other proteolytic regulators						
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	K.VISSVSY@YTHR.H	Y367	1392.42	0.75	0.0543 K.VISSVSYY@THR.H
		F.NDY@FEFPRELDMEPY.T	Y1815	2046.17	1.33	none
		K.FNDY@FEFPR.E	Y1815	1315.06	0.51	none
		K.FNDY@FEFPRELDMEPYTVAGVAK.L	Y1815	2820.20	1.92	none
		R.PY@T@GNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2431,Y2439	3764.50	0.92	0.0504 R.PY@TGNPQYT@Y@NNWSPPVQSNETSNGYFLER.S
		R.RPYTGNPQY@TYNNWSPPVQSNETSNGYFLER.S	Y2437	3761.81	2.31	0.0009 R.RPYTGNPQYT@YNNWSPPVQSNETSNGYFLER.S
		R.RPYTGNPQYT@Y@NNWSPPVQSNETSNGYFLER.S	Y2439	3841.66	1.98	0.0594 R.RPYTGNPQY@T@YNNWSPPVQSNETSNGYFLER.S
		R.RPYTGNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2439	3761.57	1.89	0.0486 R.RPYTGNPQYT@YNNWSPPVQSNETSNGYFLER.S
		R.RPYTGNPQYT^Y@NNWSPPVQSNETSNGYFLER.S	Y2439	3743.74	2.06	0.0699 R.RPYTGNPQY@T^YNNWSPPVQSNETSNGYFLER.S
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	1239.80	0.27	none
		R.MTELY@DYPKYSC*HFK.K	Y71	2062.76	0.89	none
		Y.KERM#TELY@DYPKY.S	Y71	1832.87	1.03	0.1508 Y.KERM#TELYDY@PKY.S
		Y.KERMTELY@DYPKY.S	Y71	1816.91	1.07	none
				1816.31	0.47	0.0945 Y.KERMTELYDY@PKY.S
NUCLEAR PROTEINS						
Histone H2B type 1-B	Q64475	R.KESYSVYVY@K.V	Y43	1347.62	1.98	none
Histone H4	P62806	K.RISGLIY@EETRGVL.K	Y51	1686.95	1.05	0.1814 K.RISGLIYEET@RGVL.K
		R.ISGLIY@EETR.G	Y51	1260.96	0.34	0.1364 R.ISGLIYEET@R.G
Nucleolar protein 10	Q5RJG1	K.MGIY@YIPVLGPAPR.W	Y339	1628.06	1.21	0.1064 K.MGIYY@IPVLGPAPR.W
Nucleolin	P09405	R.SVSLY@YTGEK.G	Y464	1227.60	1.03	0.1078 R.SVSLYY@TGEK.G
PREDICTED: scaffold attachment factor B	UPI00001E3C2C	R.RDDAY@WPEAK.R	Y723	1330.75	0.17	none
SET protein	Q9EQU5	F.YFDENPY@FENKVL.S	Y145	1758.75	0.96	none
		R.IDFYFDENPY@FENK.V	Y145	1922.53	1.72	none
		R.IDFYFDENPY@FENKVLSK.E	Y145	2349.38	1.29	none
				2349.83	1.74	none
		Y.RIDFYFDENPY@FENKVL.S	Y145	2290.25	1.19	none
		Y.FDENPY@FENKVL.S	Y145	1595.23	0.51	none
Structural maintenance of chromosome 3	Q9CW03	Y.IEERLHTLEEEKEELAQY@QKW.D	Y213	2783.13	1.78	none
Telomerase-binding protein EST1A	P61406	K.FQNSDNPY@YYPR.T	Y507	1643.62	-0.07	0.0945 K.FQNSDNPYY@YPR.T
Translin	Q62348	K.KVEEVVY@DLSIR.G	Y210	1531.43	1.64	none
MISCELLANEOUS						
Catalase	P24270	K.GAGAFGY@FEVTHDITR.Y	Y83	1820.92	0.09	none
		K.LVNADGEAVY@C*K.F	Y230	1420.50	1.89	none
DNA dC->dU editing enzyme APOBEC-3	Q99J72	K.HLC*Y@YHR.M	Y255	1129.50	1.04	0.1538 K.HLC*YY@HR.M
				1128.85	0.38	0.0263 K.HLC*YY@HR.M

		R.VKHLC*Y@YHR.M	Y255	1355.71	0.09	0.0793 R.VKHLC*YY@HR.M
		Y.NQRVKHLC*Y@Y.H	Y255	1460.94	0.28	0.0052 Y.NQRVKHLC*YY@.H
		K.HLC*YY@HR.M	Y256	1128.46	0.00	0.0533 K.HLC*Y@YHR.M
		Y.NQRVKHLC*YY@.H	Y256	1461.15	0.49	0.0150 Y.NQRVKHLC*Y@Y.H
Pol polyprotein [Moloney murine leukemia virus (MoMLV); Mus musculus]	P03355	L.AAAY@QEQLDRPVVPHPY.R	Y1105	2035.27	1.29	none
		H.PY@RVGDTVW.V	Y1118	1173.01	0.46	none
		L.AAAY@QEQLDRPVVPHPY@RVGDTVW.V	Y1105,Y1118	2929.14	1.74	0.1031 L.AAAY@QEQLDRPVVPHPYRVGDT@VW.V
		L.AAAYQEQLDRPVVPHPY@RVGDTVW.V	Y1118	2849.22	1.82	0.0174 L.AAAYQEQLDRPVVPHPYRVGDT@VW.V
		Y.QEQLDRPVVPHPY@RVGDTVW.V	Y1118	2472.33	1.11	0.0221 Y.QEQLDRPVVPHPYRVGDT@VW.V
		K.NLEPRWKGPY@TVL.L	Y1142	1654.71	1.86	0.0318 K.NLEPRWKGPYT@VL.L
		R.WKGPY@TVLLTTPTALK.V	Y1142	1869.70	0.67	0.0359 R.WKGPYT@VLLTTPTALK.V
Serpin B6	Q60854	K.FKLEENYNMNDALY@KLGMTDAFGGR.A	Y289	2978.72	1.36	none
		Y.NMNDALY@KLGMTDAF.G	Y289	1784.37	0.59	none
Voltage-dependent anion-selective channel protein 1	Q60932	K.YRWTEY@GLTFTEK.W	Y80	1774.62	0.80	0.1047 K.YRWTEYGLT@FTEK.W

FUNCTION UNKOWN OR UNCERTAIN

Named proteins of unknown/uncertain function

Ankyrin repeat domain-containing protein 25	Q8BX02	L.HVPAPFPGTPGQASPAAFPSKEPDPPY@S@VETPYGY.R	Y32	3816.76	1.02	none
		L.HVPAPFPGTPGQASPAAFPSKEPDPPY@SVETPYGY.R	Y32	3737.52	1.78	0.0051 L.HVPAPFPGTPGQASPAAFPSKEPDPPYS@VETPYGY.R
Anthrax toxin receptor 1 precursor	Q9CZ52	K.WPTVDASY@YGGR.G	Y380	1452.54	0.91	0.0029 K.WPTVDAS@YYGGR.G
ApoA-I binding protein	Q8K4Z3	K.KYQLNLPSYPDTEC*VY@RLQ.-	Y279	2468.40	1.25	none
		K.YQLNLPS@YPDT@ECVY@RLQ.-	Y279	2440.99	-1.06	0.0228 K.YQLNLPS@Y@PDTECVY@RLQ.-
		K.YQLNLPSYPDTEC*VY@RLQ.-	Y279	2340.41	1.36	0.1552 K.YQLNLPSYPDT@EC*VYRLQ.-
Ataxin-2	O70305	K.GLPQPTISFDGIY@ANVR.M	Y233	1928.96	0.99	none
		R.VALENDDRSEEEKY@TAVQR.N	Y440	2332.70	0.62	0.0531 R.VALENDDRSEEEKYT@AVQR.N
		R.VALENDDRS^EEEKY@TAVQR.N		2314.87	0.79	0.0880 R.VALENDDRS^EEEKYT@AVQR.N
Ataxin-2-like protein	Q7TQH0	K.GPPQSPVFEGVY@NNSR.M	Y116	1828.51	0.67	0.1438 K.GPPQSPVFEGVYNNS@R.M
BAT2-ISO homolog [fragment] (Bat2d)	Q8BMJ4	R.M#MWGSDPY@HAEPQQAATPK.S	Y788	2243.09	2.14	0.0067 R.MM#WGSDPY@HAEPQQAATPK.S
		R.MM#WGSDPY@HAEPQQAATPK.S	Y788	2242.48	1.53	0.0045 R.M#MWGSDPY@HAEPQQAATPK.S
		R.MMWGSDPY@HAEPQQAATPK.S	Y788	2226.21	1.26	none
				2225.37	0.42	none
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	L.TTTRKTPQGPPEIY@SDTQFPSLQ.S	Y213	2673.75	1.46	none
		R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213	2600.06	-0.20	0.1233 R.KT@PQGPPEIYSDTQFPSLQSTAK.H
				2600.92	0.66	0.0557 R.KTPQGPPEIYS@DTQFPSLQSTAK.H
Centrosomal protein 170	UPI0000D62DCC	K.HVEGQSAAASEEALFPFC*REPSY@FEIPTK.E	Y240	3379.69	2.16	0.0296 K.HVEGQSAAASEEALFPFC*REPS@YFEIPTK.E
DENN/MADD domain containing 2C	Q6P9P8	K.SLENIY@YEPEGQEC*GPSINPLPKPR.R	Y185	2968.93	1.56	0.0868 K.SLENIYY@EPEGQEC*GPSINPLPKPR.R
Dihydropyrimidinase-related protein 2	O08553	K.THNSALEY@NIFEGMEC*R.G	Y431	2150.87	-0.01	0.1756 K.THNS@ALEYNIFEGMEC*R.G
				2153.15	2.27	none
Discoidin, CUB and LCCL domain containing protein 2 precursor -- DCBLD2	Q91ZV3	K.SAATPEELVY@QVPQSTQELSGAGR.D	Y744	2599.59	1.35	none
Discs, large homolog 5	Q3UGX5	Y.KEERDAVY@SEY.K	Y429	1468.63	0.00	0.1192 Y.KEERDAVYS@EY.K
Far upstream element binding protein 3 (FUSE binding protein 3) homolog	Q3TIX6	K.IDSIPHLNNSTPLVDPS@VY@GYGVQKR.A	Y51	3030.94	1.46	none
GPI-anchored protein p137 -- p137GPI	Q60865	F.TAPRDY@SGY.Q	Y609	1109.61	0.15	none
Grb10 interacting GYF protein 2	Q6Y7W8	F.LKEVESPY@EVHDY.T	Y1174	1688.15	0.39	0.1125 F.LKEVES@PYEVHDY.T
				1689.98	2.22	none
		F.LKEVESPY@EVHDYTRAY.L	Y1174	2179.15	0.14	0.1011 F.LKEVES@PYEVHDYTRAY.L
				2181.01	2.00	0.1537 F.LKEVES@PYEVHDYTRAY.L
High glucose-regulated protein 8	Q8K325	K.DGLNDDDFEPY@LSPQAR.P	Y37	2033.48	1.61	none
Large proline-rich protein BAT2	Q7TSC1	K.KYSSLNLFDTY@KGK.S	Y26	1744.45	0.58	0.0621 K.KYSSLNLFDT@YKGK.S
		K.YSSLNLFDTY@KGK.S	Y26	1617.31	1.54	0.0231 K.YSSLNLFDT@YKGK.S
				1616.78	1.01	0.0479 K.YSSLNLFDT@YKGK.S
		K.APPSTY@SGVFR.T	Y2098	1262.17	0.58	0.0488 K.APPSTYS@GVFR.T
		R.LKAPPSTY@SGVFR.T	Y2098	1504.09	1.32	0.1292 R.LKAPPST@YSGVFR.T
				1503.70	0.93	0.0750 R.LKAPPSTYS@GVFR.T
		R.IDLY@QQASPPDALR.W	Y2110	1667.40	0.58	none
Leucine rich repeat (in FLII) interacting protein 2 (Lrrfip2) [fragment]	Q8C062	R.DIY@DLKDQIHDVEGR.Y	Y5	1897.75	1.86	none

Mage-d2	Q99PB4	R.VPNSNPPEY@EFFWGLR.S	Y439	2032.59	0.66	none
Nsun2 protein	Q91YX9	R.LAQEGIY@TLYPFINSR.I	Y372	1965.41	0.42	0.0789 R.LAQEGIYT@LYPFINSR.I
OTU domain containing 4 protein -- Otud4; PREDICTED: HIV-1 induced protein HIN-1 isoform 1;	UPI0000218B34	K.DSSAMC*QSLLY@ELLYEK.V	Y169	2130.03	0.10	none
		R.ESY@YFGLSPEER.R	Y436	1557.08	0.42	0.0644 R.ES@YYFGLSPEER.R
		R.ESYY@FGLSPEER.R	Y437	1557.39	0.73	0.1265 R.ESY@YFGLSPEER.R
		R.LLY@EIQNR.D	Y458	1129.15	0.57	none
		R.LLY@EIQNRDEQAFPALSSSSVSQSPSQNSNAC*VPR.K	Y458	3962.24	2.40	none
Pericentriolar material gene 1 protein [fragment]	Q91Y51	K.SNRPVS^ADGNY@RPLAK.T	Y961	1807.99	1.08	0.1885 K.S^NRPVSADGNY@RPLAK.T
Periodic tryptophan protein 1 homolog -- Pwp1	Q9D6T6	R.VTWNHFSPC*HFLASTDDGFVY@NLDAR.S	Y367	3150.86	1.49	none
Pleckstrin homology-like domain, family B, member 2 -- PHLDB2	Q8K1N2	K.ADLDHY@TGRDSER.S	Y130	1616.13	1.44	0.1046 K.ADLDHYT@GRDSER.S
		K.SHDSVY@FLGGLEGR.K	Y161	1617.10	0.36	0.1491 K.SHDS@VYFLGGLEGR.K
		R.NKSHDSVY@FLGGLEGR.K	Y161	1860.31	1.43	0.0984 R.NKS@HDSVYFLGGLEGR.K
Protein FAM51A1	Q8BHE1	R.LNDY@VNADHGLY@FNHR.R	Y167,Y175	2109.77	1.86	none
		R.LNDY@VNADHGLY@FNHRR.S	Y167,Y175	2266.17	2.16	none
		R.LNDYVNADHGLY@FNHR.R	Y175	2028.80	0.89	none
PYM protein	Q8CHP5	R.VKEGYVPQEEVPVYENKY@VK.F	Y49	2479.14	1.91	0.0534 R.VKEGYVPQEEVPVY@ENKYVK.F
Suppression of tumorigenicity 5	Q924W7	K.STLEENAY@EDIVGGLPKENPY@EDVDLK.N	Y485,Y498	3199.32	1.87	none
SR-related CTD associated factor 6	Q8CGZ0	R.NSEGWEQNGLY@EFFR.A	Y723	1956.63	0.80	none
Tanc2 protein [fragment]	Q5EBP6	K.TNNAQNGHLLEDDY@YSPHGMLANGSR.G	Y1349	2955.55	1.26	0.0660 K.TNNAQNGHLLEDDYY@SPHGMLANGSR.G
Testis derived transcript	Q921W7	K.HTM#NEGEPAIY@AER.A	Y249	1713.53	-0.20	none
		K.HTMNEGEPAIY@AER.A	Y249	1698.74	1.01	none
				1698.44	0.71	none
Trinucleotide repeat containing 6b	Q6NVE4	K.DLGTTDSGPY@FEK.G	Y1128	1510.29	0.64	0.1792 K.DLGTTDS@GPYFEK.G
		K.DLGTTDSGPY@FEKGGSHGLFGNSTAQSR.G	Y1128	2967.49	1.16	0.1242 K.DLGTTDS@GPYFEKGGSHGLFGNSTAQSR.G
		K.GIQNIDPESDPY@VTPGSVLGGTTTSPIVDTDHQLLR.D	Y1440	3874.35	1.46	0.1664 K.GIQNIDPESDPYVT@PGSVLGGTTTSPIVDTDHQLLR.D
Tripartite motif protein 16	Q99PP9	F.DC*KFSEPVY@AAF.W	Y523	1514.01	0.39	none
		K.FSEPVY@AAFWLSK.K	Y523	1625.77	0.99	none
Tudor domain-containing protein 3	Q91W18	L.SNIKPVQTEAWEEEGTY@DHTIEF.R	Y618	2804.47	1.22	0.0786 L.SNIKPVQTEAWEEEGT@YDHTIEF.R
Ubiquitin-associated protein 2 -- UBAP2	Q91VX2	R.LPMDY@YGIPFAAPTALASR.D	Y853	2135.76	1.72	0.0560 R.LPMDYY@GIPFAAPTALASR.D
				2135.80	1.76	0.0580 R.LPMDYY@GIPFAAPTALASR.D
		R.LPM#DY@YGIPFAAPTALASR.D	Y853	2150.88	0.84	0.0345 R.LPM#DYY@GIPFAAPTALASR.D
		R.LPMDYY@GIPFAAPTALASR.D	Y854	2134.39	0.35	0.0292 R.LPMDY@YGIPFAAPTALASR.D
		F.AAPTALASRDGNLANNPY@SGDVTKF.G	Y876	2631.57	1.31	0.0472 F.AAPTALASRDGNLANNPYS@GDVTKF.G
		L.ASRDGNLANNPY@SGDVTKF.G	Y876	2107.29	1.33	0.0376 L.ASRDGNLANNPYS@GDVTKF.G
				2106.87	0.91	0.0288 L.ASRDGNLANNPYS@GDVTKF.G
		N.NPY@SGDVTKF.G	Y876	1207.92	0.38	0.1018 N.NPYS@GDVTKF.G
		R.DGNLANNPY@SGDVTK.F	Y876	1645.46	0.74	0.0869 R.DGNLANNPYS@GDVTK.F
		K.SQASKPTY@GSAPYWTN.-	Y1124	1838.21	0.40	0.0221 K.SQASKPTYGS@APYWTN.-
Ubiquitin associated protein 2-like -- UBAP2L	Q80X50	Y.TSQNNAQGPLY@EQRSTQ.T	Y612	2003.09	1.19	none
				2002.45	0.55	none
		R.FPLDY@YSIPFPTPTTPLTGR.D	Y854	2364.17	1.00	0.0827 R.FPLDYY@SIPFPTPTTPLTGR.D
		R.DGSLASNPY@SGDLTK.F	Y878	1605.11	0.39	0.0496 R.DGSLASNPYS@GDLTK.F
		L.TGRDGSLASNPY@SGDLTKF.G	Y878	2067.39	1.43	0.0571 L.TGRDGSLASNPYS@GDLTKF.G
Yippee-like 5	Q65Z92	N.S@KLGWIY@EFATEDSQRY.K	Y84	2252.51	-0.49	none
YTH domain protein 3 -- Ythdf3	Q6NXJ8	K.SVVDYNAY@AGVWSQDKWK.G	Y488	2196.81	0.80	none
Novel ZZ type zinc finger domain containing protein	Q5SSH7	K.WKDFELPGDTLY@YR.F	Y2706	1883.40	0.53	0.1001 K.WKDFELPGDTLYY@R.F
				1884.26	1.39	0.0697 K.WKDFELPGDTLYY@R.F
		W.KDFELPGDTLY@Y.R	Y2706	1541.44	0.75	0.1259 W.KDFELPGDTLYY@.R
Unnamed proteins of unknown/uncertain function						
BC003940 protein [fragment]	Q8QZS4	R.FIY@EAWQGVER.D	Y70	1479.96	2.28	none
BC053440 protein [fragment]	Q8R2W2	K.INDTMY@FAPSMK.D	Y19	1498.68	1.03	none
Hypothetical ATP/GTP-binding site motif A homolog	Q3UHH1	L.HKTKEAAPAVGEEDDDYQAY@Y.L	Y729	2481.38	1.32	0.0117 L.HKTKEAAPAVGEEDDDYQAYY@.L

hypothetical ATP/GTP-binding site motif A (P-loop)/Zinc finger C-x8-C-x5-C-x3-H type containing protein	Q9DBS7	K.EAVY@SGVQSLR.S	Y508	1289.24	0.61	0.1217 K.EAVYS@GVQSLR.S
hypothetical Domain of unknown function DUF71 containing protein	Q9CQ28	R.VYTQC*EGDEVEDLY@ELLK.L	Y97	2282.98	-0.01	none
hypothetical G-protein beta WD-40 repeat/Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats circular profile/Serine-rich region profile/WD40-like containing protein -- WDR70	Q3TWF6	K.AAEDNPY@WVSPAYSK.T	Y621	1778.50	0.72	none
hypothetical 5'3'-Exonuclease N- and I-domains containing protein	Q8BMI4	R.LQENC*GANTSLPY@SFSDK.A	Y747	2110.82	-0.07	0.0624 R.LQENC*GANTSLPYS@FSDK.A
DNA segment, Chr 5, ERATO Doi 585, expressed -- D5Ertd585e	Q6P1H6	R.IREYLM#GHY@YVPLLR.A	Y483	2021.02	1.99	0.0536 R.IREYLM#GHYY@VPLLR.A
		R.IREYLMGHY@YVPLLR.A	Y483	2004.32	1.29	0.1334 R.IREYLMGHYY@VPLLR.A
hypothetical protein: E230015L20Rik protein	Q8C304	R.TNEIY@YLDPDAPLSRPSTQDNQYQK.S	Y416	3036.73	0.33	0.0924 R.TNEIYY@LDPDAPLSRPSTQDNQYQK.S
hypothetical protein LOC106840	Q8C4B4	K.PEDNVY@SIDFTR.F	Y92	1535.89	0.21	0.0459 K.PEDNVYS@IDFTR.F
		R.VTENYLC*KPEDNVY@SIDFTR.F	Y92	2544.95	1.82	0.0678 R.VTENYLC*KPEDNVYS@IDFTR.F
PREDICTED: zinc finger protein 650	UPI0000D65C57	K.KLPIAEEEQIY@PWDTC*AAVHDVR.L	Y335	2822.45	2.13	none
PREDICTED: similar to Oligophrenin 1	UPI0000D668EB	K.LWLEAMDGKEPIY@TLPAIISK.K	Y371	2468.94	0.65	0.0652 K.LWLEAMDGKEPIYT@LPAIISK.K
		R.KLWLEAM#DGKEPIY@TLPAIISK.K	Y371	2612.62	0.24	0.0042 R.KLWLEAM#DGKEPIYT@LPAIISK.K
		R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371	2598.34	1.96	0.0228 R.KLWLEAMDGKEPIYT@LPAIISK.K
PREDICTED: similar to ring finger and KH domain containing 2	UPI000042893E	R.LSEQGGDFGY@SGYLFPGYGVGK.Q	Y188	2379.95	1.88	0.1423 R.LSEQGGDFGYS@GYLFPGYGVGK.Q
hypothetical protein 1500002O20Rik	Q9DB90	K.EGQRPTQPVY@QIQNR.G	Y147	1895.06	1.13	none
MKIAA0183 protein [fragment]	Q6A0A9	K.PAVPQVPSPGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457	3461.89	2.18	0.0207 K.PAVPQVPSPGGTPGQAPYPYS@LSEPALTLDTSGK.N
		K.PAVPQVPS@PGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457	3541.89	2.18	0.0895 K.PAVPQVPSPGGTPGQAPY@PY@SLSEPALTLDTSGK.N
		K.PAVPQVPSPGGT@PGQAPYPY@SLSEPALTLDTSGK.N	Y457	3541.83	2.11	0.0049 K.PAVPQVPS@PGGTPGQAPYPY@SLSEPALTLDTSGK.N
		F.GGHY@GETVATGPY@RAF.R	Y968	1843.31	0.52	0.0645 F.GGHY@GETVAT@GPYRAF.R
		F.GGHYGETVATGPY@RAF.R	Y968	1763.46	0.67	0.1678 F.GGHYGETVAT@GPYRAF.R
Protein FAM125A	Q78HU3	R.RTDSIY@EASS@LYGISAMDGVPFTLHPR.F	Y202	3144.64	1.18	0.0215 R.RTDSIY@EAS@SLYGISAMDGVPFTLHPR.F
PREDICTED: similar to la related protein isoform 1	UPI0000D66C58	R.THFDYQFGY@R.K	Y412	1414.59	0.99	none
Similar to leucine-rich neuronal protein homolog	Q3U222	L.GFGSC*HEELY@SGRPY.G	Y203	1839.35	0.62	0.0896 L.GFGSC*HEELYS@GRPY.G
				1839.10	0.37	0.1651 L.GFGSC*HEELYS@GRPY.G
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	2910.62	-0.84	0.0717 K.EKLLLC*HGPSLS@LPALSGVRY@NAEK.K

END

Table S2. Phosphotyrosine sites from the Src-transformed mouse embryo fibroblast population

Protein Name(s)[a]	UniProt #[a]	Peptide[b]	pY site(s)[b]	Comments[j]
SIGNALING: PROTEIN KINASES AND PHOSPHATASES				
Tyrosine kinases (nonreceptor)				
Rous sarcoma oncogene, isoform 2 -- Src (Yes) (Fyn)	Q80XU2	F.VALY@DYESRTETDL.S	Y92	SH3 domain site
		F.VALY@DYESRTETDLSF.K	Y92	
		R.AGPLAGGVTTFVALY@DYESR.T	Y92	
		R.TQFNSLQQLVAY@YSK.H	Y231	SH2 domain site
		L.IEDNEY@TARQGAKFPIKW.T	Y418	Kinase domain activation loop site; peptide identical in Fyn (P39688) and Yes (Q04736). Equivalent Hck (P08103) peptide (IIEDNEY@TAR) also not distinguishable by MS.
		R.LIEDNEY@TAR.Q	Y418	
		K.FPIKWTAPEAALY@GR.F	Y438	Kinase domain site; peptide identical in Fyn (P39688) and Yes (Q04736)
		K.WTAPEAALY@GR.F	Y438	Kinase domain site; peptide identical in Fyn (P39688) and Yes (Q04736)
		W.TAPEAALY@GRF.T	Y438	Kinase domain site; peptide identical in Fyn (P39688) and Yes (Q04736)
Proto-oncogene tyrosine-protein kinase LCK	P06240	F.GLARLIEDNEY@TAREGAKFPIKW.T	Y393	Kinase domain activation loop site
		F.GLARLIEDNEY@TAREGAKF.P	Y393	
		R.LIEDNEY@TAREGAKFPIKW.T	Y393	
Tyrosine-protein kinase CSK	P41241	L.IKPKVMEGTVAAQDEFY@RSGW.A	Y184	A tyrosine kinase that phosphorylates and inhibits Src family kinases. Site lies between SH2 and kinase domains.
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	Site N-terminal to SH2 domain
		F.GMSRQEDGGVY@SSSGL.K	Y715	Kinase domain activation loop site
Proto-oncogene tyrosine-protein kinase ABL1	P00520	R.LMTGDTY@TAHAGAK.F	Y393	Kinase domain activation loop site
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	R.YM#EDSTY@YK.A	Y576	
		R.YMEDSTY@YK.A	Y576	
		R.YMEDSTY@YKASK.G	Y576	
		R.YMEDSTY@Y@K.A	Y576,Y577	Kinase domain activation loop sites
		R.YMEDSTY@Y@KASK.G	Y576,Y577	
Tyrosine kinases (receptor)				
Discoidin domain receptor 2 precursor -- DDR2	Q62371	F.GMSRNLY@SGDY@Y.R	Y735,Y739	Kinase domain activation loop sites
		R.NLY@S@GDYYR.I	Y735	
		R.NLY@SGDY@YR.I	Y735,Y739	
Ephrin type-A receptor 2 precursor	Q03145	K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	Site is N-terminal to kiniase domain
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	Kinase domain activation loop site
Eph receptor B4	Q91YM0	Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596	Sites are N-terminal to kinase domain
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	K.IYNGDY@YR.Q	Y696	Kinase domain activation loop site
		K.KIYNGDY@YR.Q	Y696	
Other protein kinases				
Akt1: RAC-alpha serine/threonine-protein kinase (Akt-2) (Akt-3)	P31750	K.TFC*GTPEYLAPEVLEDNDY@GR.A	Y326	Kinase domain site. Peptide identical in Akt-2 (Q60823) and Akt-3 (Q9WUA6)
Akt-3: RAC-gamma serine/threonine-protein kinase	Q9WUA6	K.Y@Y@AM#KILKKEVIIAK.D	Y173,Y174	Site in kinase domain near conserved lysine
Calcium/calmodulin-dependent protein kinase type 1 --CaM kinase I	Q91YS8	R.DLKPENLLYY@SLDEDSK.I	Y150	Kinase domain site
Casein kinase I isoform alpha	Q8BK63	R.TLNHQYDY@TFDWTMLK.Q	Y294	Site in C-terminal inhibitory domain
Casein kinase II, alpha chain	Q60737	K.VLGTEDLY@DYIDKYNIELDPR.F	Y255	Site in kinase domain near C-terminus
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IGEGTY@GVVYK.G	Y15	Site in kinase domain ATP-binding region. Peptide also in CDK2 (P97377)
		K.IGEGT^Y@GVVYK.G	Y15	Site in kinase domain ATP-binding region. Peptide also in CDK2 (P97377)
		K.IGEGTYGVVY@K.G	Y19	
		K.IGEGTYGVVY@KGR.H	Y19	Peptide unique to Cdc2
Dual-specificity tyrosine-phosphorylation regulated kinase 1A --DYRK1A (DYRK1B)	Q61214	K.HINEVY@YAK.K	Y111	Site N-terminal to kinase domain. Peptide identical to DYRK1B (Q9Z188)
		K.VYNDGYDDDNY@DYIVK.N	Y145	Site N-erminal to kinase domain.
		R.KVYNDGYDDDNY@DYIVK.N	Y145	

		Y.NDGYDDDNY@DYIVKNGEKW.M	Y145	
		R.IYQY@IQSR.F	Y321	Kinase domain activation loop site. Peptide identical to DYRK1B (Q9Z188).
Glycogen synthase kinase-3 beta -- GSK-3 beta (GSK-3 alpha)	Q9WV60	L.VRGEPNVSY@IC*SRY.Y	Y216	Kinase domain activation loop site. All peptides identical to GSK-3 alpha (UPI00001C3B75).
		L.VRGEPNVSY@IC*SRYY.R	Y216	
		R.GEPNVSY@IC*SR.Y	Y216	
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638	This entry contains the N terminal region of putative protein serine/threonine kinase SgK269 (NKF3 family) in the KinBase resource. MKIAA2002 protein [fragment] (Q69Z38) contains the SgK269 kinase domain. There is no overlap between Q8BX56 and Q69Z38. Possible alternative splicing.
		K.VPIVINPNAY@DNLAIY@K.S	Y632,Y638	
		K.VPIVINPNAYDNLAIY@K.S	Y638	
		N.AIKVPIVINPNAY@DNLAIY@KSF.L	Y632,Y638	
Serine/threonine-protein kinase Nek9	Q8K1R7	R.NKEVYSWGC*GEY@GR.L	Y509	Site is C-terminal to kinase domain. Not conserved in NEK family.
Serine/threonine-protein kinase PRP4 homolog	Q61136	K.LC*DFGSASHVADNDITPY@LVSR.F	Y849	DYRK family. Kinase domain activation loop site.
		H.VADNDITPY@LVSRF.Y	Y849	
Protein phosphatases				
Low molecular weight phosphotyrosine protein phosphatase	Q9D358	K.QLIIEDPY@YGNDSDFEVVYQQC*LR.C	Y131	Alternative Names: ACP1, Protein-tyrosine-phosphatase, acid phosphatase 1
		L.GSYDPQKQLIIEDPY@YGNDSDF.E	Y131	
		K.QLIIEDPYY@GNDSDFEVVYQQC*LR.C	Y132	
14 kDa phosphohistidine phosphatase -- Phosphohistidine phosphatase 1	Q9DAK9	R.KIHVYGY@SM#GYGR.A	Y92	
Protein phosphatase 1 regulatory subunit 12A	Q9DBR7	R.TYDETY@TR.Y	Y764	
		Y.SRTYDETY@TRY.R	Y764	
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	
Serine/threonine protein phosphatase 2A, catalytic subunit, alpha isoform -- PP2A alpha (PP2A beta)	P63330	R.QITQVY@GFYDEC*LR.K	Y127	Ubiquitous cytosolic Ser/Thr protein phosphatase, catalytic subunit. Both peptides conserved in PP2A beta isoform (P62715)
		R.C*GNQAAIMELDDTLKY@SFLQFDPAPR.R	Y284	
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	Site lies in the N-terminal SH2 domain.
		K.IQNTGDY@YDLYGGEK.F	Y62	
Tyrosine-protein phosphatase, non-receptor type 14	Q62130	R.NLNIINTHAYNQPEELVY@SQPEMR.E	Y485	Site lies between FERM and PTPase domains.
SIGNALING: SMALL G PROTEINS AND REGULATORS				
ARF GTPase-activating protein GIT1	Q68FF6	F.HSTELEDDAIY@SVHVPAGLY.R	Y554	ARF GTPase-activating protein (GAP) activity.
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554	
		R.LQPFHST@ELEDDAIY@SVHVPAGLYR.I	Y554	
		R.LQPFHSTELEDDAIY@SVHVPAGLY@R.I	Y554,Y563	
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554	
		R.LQPFHS^TELEDDAIY@SVHVPAGLYR.I	Y554	
Engulfment and cell motility protein 2 -- ELMO2	Q8BHL5	K.EVC*DGWSLPNPEY@YTLR.Y	Y48	Proposed to be required in complex with DOCK1 to activate Rac. Enhances the GEF activity of DOCK1.
Glucocorticoid receptor DNA binding factor 1 [fragment] -- p190RhoGAP	Q91YM2	R.NEEENIY@SVPHDSTQGK.I	Y943	Represses transcription of the glucocorticoid receptor by binding to a cis-acting regulatory sequence. Better known as p190RhoGAP. Phosphorylation of this putative Src site (equivalent to Y1105 in the human protein) positively controls GAP activity, thus inhibiting Rho.
Myosin phosphatase Rho-interacting protein -- MRIP	P97434	K.VRVESGY@FSLEK.A	Y268	Required for regulation of actin cytoskeleton by RhoA and ROCK1. Alternate name: Rho-interacting protein 3, RIP3.
		K.YASDKYKDIY@TELSIAK.A	Y944	
Rab GDP dissociation inhibitor alpha -- Rab GDI alpha (Rab GDI beta)	P50396	K.VLHMDRNPY@YGGESSSITPLEELYK.R	Y38	Regulates the GDP/GTP exchange reaction of Rab proteins.
		K.SPYLYPLY@GLGELPQGFAR.L	Y229	This peptide identical in Rab GDP dissociation inhibitor beta (Q61598).
Rab GDP dissociation inhibitor beta -- Rab GDI beta	Q61598	K.KVLHMDQNPY@YGGESASITPLEDLYK.R	Y38	Regulates the GDP/GTP exchange reaction of Rab proteins.
		K.KVLHMDQNPY@YGGESASITPLEDLYKR.F	Y38	
		K.VLHM#DQNPY@YGGESASITPLEDLYKR.F	Y38	
		K.VLHMDQNPY@YGGESASITPLEDLYK.R	Y38	
		K.VLHMDQNPY@YGGESASITPLEDLYKR.F	Y38	
		L.HMDQNPY@YGGESASITPLEDLY.K	Y38	
		K.KVLHMDQNPYY@GGESASITPLEDLYKR.F	Y39	
		K.VLHM#DQNPYY@GGESASITPLEDLYKR.F	Y39	
		K.VLHMDQNPYY@GGESASITPLEDLYK.R	Y39	

Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	L.RSPDVGLY@GVIPEC*GETY.Q L.SALRSPDVGLY@GVIPEC*GETY.Q L.VKLQQTY@SAL.N	Y654 Y654 Y1510	Binds to activated CDC42 but does not stimulate its GTPase activity. Associates with calmodulin. Could serve as an assembly scaffold.
Ras and Rab interactor 1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	Alternative Name: Ras interaction/interference protein 1. Can affect Ras signaling at different levels.
Rho-GTPase-activating protein 12	Q8C0D4	R.AT@TPPNQGRPDS@PVY@ANLQELK.I R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241 Y241	A Rho/Rac/Cdc42-like GTPase activating (RhoGAP) protein.
Rho/rac guanine nucleotide exchange factor (GEF) 2 -- ARHGEF2	Q923E0	R.RRS@LPAGDALY@LSFNPPQPSR.G R.SLPAGDALY@LSFNPPQPSR.G	Y893 Y893	Guanine nucleotide exchange factor, Rac/Rho.
TBC1 domain family member 15	Q9CXF4	K.SLSQSFENLLDEPAY@GLIQK.I	Y215	May act as a GTPase activating protein for Rab family protein(s). Contains 1 Rab-GAP TBC domain.
SIGNALING: OTHER				
53BP2: Apoptosis stimulating of p53 protein 2 [fragment]	Q8CG79	R.KPQTVAASSIY@SMYTQQQAPGK.N	Y569	
Ankyrin repeat and SAM domain containing protein 1 -- ANKS1	P59672	L.ILHFDTHADEEGPY@EALY.N L.AVRPRIQSSAPQEEEEHPY@EL.L L.AVRPRIQSSAPQEEEEHPY@ELL.L R.IQSSAPQEEEEHPY@ELLLTAETK.K R.IQSSAPQEEEEHPY@ELLLTAETKK.L	Y377 Y471 Y471 Y471 Y471	Phosphorylated in response to EGF and PDGF. Contains seven ankyrin repeats and two sterile alpha motif domains. Alternative name is Odin.
Annexin A1	P10107	R.ALY@EAGER.R R.ALY@EAGERR.K	Y206 Y206	Alternative Names: Calpactin II, Lipocortin I.
Annexin A2	P07356	C.KLSLEGDHSTPPSAY@GSVKPY.T K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D L.SLEGDHSTPPSAY@GSVKPY.T K.SYSPY@DMLESIK.K K.SYSPY@DMLESIKK.E F.ADRLY@DSM.K L.YFADRLY@DSM#.K L.YFADRLY@DSM.K Y.FADRLY@DSM.K K.SLY@YYIQQDTK.G K.SLYY@YIQQDTK.G K.SLY@Y@YIQQDTK.G	Y23 Y23 Y23 Y237 Y237 Y274 Y274 Y274 Y274 Y315 Y316 Y315,Y316	Alternative Names: Calpactin I, Lipocortin II.
Annexin A5	P48036	R.SIPAYLAETLY@YAMK.G K.NFATSLY@SMIK.G	Y254 Y295	
Annexin A6	P14824	R.GSVHDFPEFDANQDAEALY@TAM#K.G R.GSVHDFPEFDANQDAEALY@TAMK.G Y.RGSVHDFPEFDANQDAEALY@TAM#.K Y.RGSVHDFPEFDANQDAEALY@TAM.K	Y29 Y29 Y29 Y29	
Annexin A11	P97384	K.TPVLFDVY@EIKEAIK.G	Y277	
Cell division cycle and apoptosis regulator protein 1 -- CARP1	Q8CH18	R.VLVEATY@NPNMPFK.W R.VLVEATY@NPNMPFKWNAQR.I	Y189 Y189	CARP-1 promotes apoptosis by activating p38 MAPK and caspase-9. Rishi AK, et al. J Biol Chem 2006 Mar 16
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	
Proto-oncogene c-Crk	Q64010	Q.KRVPNAY@DKTAL.A	Y251	Site lies between the two SH3 domains
Cyclin-dependent kinases regulatory subunit 2	P56390	Y.SDKYFDEHY@EY.R Y.YSDKYFDEHY@EY.R	Y17 Y17	Binds to the catalytic subunit of the cyclin dependent kinases and is essential for their biological function.
Docking protein 1 --Dok1	P97465	K.TVPPPVPQDPLGSPPALY@AEPLDSLR.I R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K K.KPLY@WDLY@GHVQQQLLK.T K.KPLYWDLY@GHVQQQLLK.T K.LTDSKEDPIY@DEPEGLAPAPPR.G K.TKLTDSKEDPIY@DEPEGLAPAPPR.G K.TKLTDS^KEDPIY@DEPEGLAPAPPRGLYDLPQEPR.D L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D K.LTDSKEDPIY@DEPEGLAPAPPRGLY@DLPQEPR.D K.LTDS^KEDPIYDEPEGLAPAPPRGLY@DLPQEPR.D R.LKEEGY@ELPY@NPATDDYAVPPPR.S	Y295 Y314 Y336,Y340 Y340 Y361 Y361 Y361 Y361 Y361 Y361,Y376 Y376 Y397,Y401	

		R.LKEEGYELPY@NPAT@DDYAVPPPR.S R.LKEEGYELPY@NPATDDYAVPPPR.S R.LKEEGYELPYNPATDDY@AVPPPR.S R.LKEEGY@ELPYNPATDDY@AVPPPR.S R.LKEEGYELPY@NPATDDY@AVPPPR.S R.LKEEGYELPY@NPATDDY@AVPPPRS@PK.P F.SSDTALY@SQVQKSGTSGAW.D K.GFSSDTALY@SQVQK.S	Y401 Y401 Y408 Y397,Y408 Y401,Y408 Y401,Y408 Y450 Y450	
Epidermal growth factor receptor kinase substrate 8 -- EPS8	Q08509	R.LSTEHSNVSDY@PPADGYAYSSSMYHR.G	Y484	Contains 1 PH domain. 1 SH3 domain. Phosphorylated by several receptor tyrosine kinases.
Hepatocyte growth factor-regulated tyrosine kinase substrate -- HGS/ Hrs	Q99LI8	R.VC*EPC*Y@EQLNK.K	Y216	
Insulin receptor substrate 1 -- IRS-1	P35569	R.AASEAGGPARLEY@YENEKK.W	Y46	Major substrate of the insulin receptor kinase. Contains multiple tyrosine phosphorylation motifs that serve as docking sites for SH2-containing proteins .
Insulin receptor substrate 2 -- IRS-2	P81122	K.VAYNPYPEDY@GDIEIGSHK.S	Y628	
Kin of IRRE-like protein 1 precursor -- KIRREL	Q80W68	R.C*DTIDTREEY@EMKDPTNGY@YNVR.A R.C*DTIDT@REEYEMKDPTNGY@YNVR.A R.EEYEMKDPTNGY@YNVR.A Y.RLGYPQAPPSGLERTPY@EAY@DPIGKY.A	Y628,Y637 Y637 Y637 Y753,Y756	Signaling protein that needs the presence of TEC kinases to fully trans-activate the transcription factor AP-1. Alternative Name: Nephrin-like protein 1.
Latrophilin-2	Q8JZZ7	R.SENEDIY@YK.S R.GNSDGY@IIPINK.E	Y838 Y865	Latrophilins are members of the secretin family of G protein-coupled receptors. Sites are in a predicted cytoplasmic region.
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.PSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F R.KPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105 Y105 Y105 Y105	Site falls between first two SH3 domains.
Notchless homolog 1	Q8VEJ4	K.LATDLPGHADEVY@AVDWSPDGQR.V	Y459	Site near the C-terminus in the last WD repeat. Dros. homolog binds Notch and acts as a neg. regulator of notch signaling.
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85 alpha	P26450	K.SREYDRLY@EEYTR.T K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y467 Y607	Acts as an adaptor. Binds to activated protein-Tyr kinases, through its SH2 domain, and mediates association of the p110 catalytic unit.
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85 beta	O08908	R.EYDQLY@EEYTR.T	Y458	
Phospholipase C, gamma 1	Q6P1G1	K.IGTAEPDY@GALY@EGRNPGFYVEANPMPTFK.C K.IGTAEPDYGALY@EGRNPGFY@VEANPMPTFK.C K.IGTAEPDYGALY@EGRNPGFYVEANPMPTFK.C	Y771,Y775 Y775,Y783 Y775	
Protein Wnt-2b precursor	O70283	K.GTDGC*EIMCCGRGY@DTTR.V	Y342	Ligand for members of the frizzled family of seven transmembrane receptors.
Guanine nucleotide-binding protein beta subunit 2-like 1 -- RACK1	P68040	K.HLY@TLDGGDIINALC*FSPNR.Y L.WDLNEGKHLY@TLDGGDIINAL.C W.DLNEGKHLY@TLDGGDIINAL.C W.DLNEGKHLY@TLDGGDIINALC*F.S	Y227 Y227 Y227 Y227	Receptor of activated protein kinase C 1. Acts to anchor activated PKC to the cytoskeleton. Contains 7 WD domains.
Retinoic acid-induced protein 3	Q8BHL4	F.SIPRAQAPASPY@NDY@EGRKGDS.- F.SIPRAQAPASPY@NDYEGRKGDS^.-	Y346,Y349 Y346	Retinoic acid-inducible GPCR. Site near C-terminus.
SH2 domain-containing adapter protein B -- SHB	Q6PD21	R.DFEDPY@NGPGSSLR.K	Y95	Adapter protein which links activated receptors to downstream signaling components.
SHC transforming protein 1 -- SHC1	P98083	R.ELFDDPSY@VNIQNLDK.A R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM#R.L R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L F.DGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDM.R	Y423 Y349,Y350 Y349,Y350 Y349,Y350	
SHC SH2 domain-binding protein 1	Q9Z179	R.SWDEEEEDEY@DYFVR.C	Y217	Interacts directly with isoform p52shc of SHC1 via its SH2 domain.
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	R.FSEEEISFPPTY@RYER.G K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y662 Y987	SH2-containing inositol phosphatase. Recruited to activated receptor complexes .
Sorbin and SH3 domain-containing protein 1 -- SORBS1	Q62417	K.TPVDYIDLPY@SSSPSR.S	Y1198	Contains 3 SH3 domains. Site lies between last two SH3 domains. Links CBL to the insulin receptor.
Signal transducing adapter molecule 2 -- STAM-2	O88811	K.LVNEAPVY@SVYS@K.L K.LVNEAPVY@SVYSK.L Y.NKLVNEAPVY@SVY.S	Y371 Y371 Y371	Adaptor protein involved in the downstream signaling of cytokine receptors. Contain a SH3 domain and ITAM motif. Alternative Names: HRS binding protein.
Signal transducer and activator of transcription 3 -STAT3	P42227	R.QFLAPWIESQDWAY@AASK.E K.YC*RPESQEHPEADPGSAAPY@LK.T	Y45 Y705	

STRAP: serine/threonine kinase receptor associated protein	Q8BP89	K.IGFPETAEEELEEIASENSDSIY@SSTPEVK.A	Y342	This protein is largely composed of 6 WD repeats. The site is near the C-terminus, beyond the WDs.
		K.IGFPETAEEELEEIASENSDSIY@SSTPEVKA.-	Y342	
Striatin	O55106	K.STSLDVEPIY@TFR.A	Y510	Binds calmodulin in a calcium dependent manner. May function as scaffolding or signaling protein. Belongs to the WD-repeat striatin family.
		W.NLQKTAPAKKSTSLDVEPIY@TF.R	Y510	
Striatin-3	Q9ERG2	K.SASLDVEPIY@TFR.A	Y526	Belongs to the WD-repeat striatin family.
hypothetical SH3/Phox-like/Src homology 3 (SH3) domain profile/Proline-rich region profile/PX domain profile containing protein -- TKS4	Q3TB89	R.VTWSSGATEAIY@R.R	Y42	Related to mouse TKS5 FISH protein. Y42 is in the N-terminal PX (phox) domain.
		K.TEPAQSEDHVDIY@NLR.S	Y661	
ADHESION: CELL/ECM				
Bystin	O54825	R.GREVEEEEEY@VGPR.L	Y48	Could be involved in a cell adhesion molecule complex that mediates an initial attachment of the blastocyst to uterine epithelial cells.
CRK-associated substrate -- p130cas	Q61140	-.MTVPNVLAKALY@DNVAESPDELSFR.K	Y12	Site is in the SH3 domain.
		K.ALY@DNVAESPDELSFR.K	Y12	
		Y.VVYEAAQTEQDEY@DTPRHL.L	Y238	Substrate domain YxxP site 6.
		R.HLLAPGPQDIY@DVPPVR.G	Y253	Substrate domain YxxP site 7.
		R.GLLPNQYGQEVY@DTPPMAVK.G	Y271	Substrate domain YxxP site 8.
		K.GPNGRDPLLDVY@DVPPSVEK.G	Y291	Substrate domain YxxP site 9.
		K.GLLSSSHHSVY@DVPPSVSK.D	Y310	Substrate domain YxxP site 10.
		R.RPGPGTLY@DVPR.E	Y391	Substrate domain YxxP site 14.
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	Substrate domain YxxP site 15.
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	
		L.SRQLQKMEDVY@QTL.V	Y556	Site is C-terminal to the substrate domain.
Lipoma-preferred partner homolog -- LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	
		Y.MAGPSSGQIY@GPGPRGY.N	Y245	
		M.AGPSSGQIY@GPGPRGY.N	Y245	
		R.YYEPY@YAAGPSYGGR.S	Y301	
		Y.TSNQGRYYEPY@YAAGPSY.G	Y301	
		R.YYEPY@Y@AAGPSYGGR.S	Y301,Y302	
		R.YYEPYY@AAGPSYGGR.S	Y302	
		K.KMLY@DMENPPADDYFGR.C	Y403	
		K.MLY@DMENPPADDYFGR.C	Y403	
		K.KMLYDMENPPADDY@FGR.C	Y413	
		K.MLYDMENPPADDY@FGR.C	Y413	
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	
		R.AGEEEHVY@SFPNK.Q	Y118	
		R.AGEEEHVY@SFPNKQK.S	Y118	
Syndecan-4 precursor	O35988	Y.KKAPTNEFY@A.-	Y197	
Talin 1	P26039	K.TM#QFEPSTMVY@DAC*R.M	Y26	
		K.TMQFEPSTMVY@DAC*R.M	Y26	
		M.QFEPSTMVY@DAC*RM.I	Y26	
		K.ALDY@YM#LR.N	Y70	
		K.ALDY@YMLR.N	Y70	
		K.ALDYY@MLR.N	Y71	
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	
		K.TLAESALQLLY@TAK.E	Y1777	
Tensin 2	Q8CJ95	R.YGHSGYPALVTY@GYGGAVPSYC*PAYGR.A	Y766	
Tensin 3	Q5SSZ5	K.LYQAMQPVYTSGIY@NVGSENPSR.I	Y216	
		L.HTQGPVDGSLY@AKVR.K	Y354	
		R.KPSAPTPVQAY@GQSNY@STQTWVR.Q	Y579,Y584	
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	
Vinculin	Q64727	K.LVQAAQMLQSDPY@SVPAR.D	Y99	
		K.LVQAAQMLQSDPY@SVPARDYLIDGSR.G	Y99	
		L.QSDPY@SVPARDY.L	Y99	
		Q.MLQSDPY@SVPARDY.L	Y99	
		R.ILLRNPGNQAAY@EHFETMK.N	Y691	
ADHESION: CELL/CELL				

Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M R.HYEDGYPGGSDNY@GSLSR.V R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R R.FHPEPYGLEDDQRS@MGYDDLDY@GMMS@DYGTAR.R R.FHPEPYGLEDDQRS^MGYDDLDY@GMMS@DYGTAR.R R.FHPEPYGLEDDQRS^MGYDDLDY@GMMSDYGTAR.R R.SMGYDDLDY@GMMSDYGTAR.R R.SMGYDDLDYGMMSDY@GTAR.R R.SYEDMIGEEVPPDQY@YWAPLAQHER.G R.SYEDMIGEEVPPDQYY@WAPLAQHER.G	Y96 Y228 Y291,Y296 Y296 Y296 Y296 Y296 Y302 Y334 Y335	
Plakophilin-4	Q68FH0	R.TVHDMDQFGQQQY@DIY@ER.M R.TVHDMDQFGQQQYDIY@ER.M L.RSAVSPDLHITPIY@EGRT@YY.S R.SAVSPDLHITPIY@EGRT@YYSPVYR.S R.SAVS^PDLHITPIY@EGRTYYSPVYR.S	Y368,Y371 Y371 Y414 Y414 Y414	Belongs to the beta-catenin family.
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	
Tight junction protein ZO-1	P39447	R.LSYLSAPGSEY@SMYSTDSR.H R.HEEQPAPAY@EVHNR.Y L.RHEEQPAPAY@EVHNRY.R R.YRPEAQPY@SSTGPK.S Y.RPEAQPY@SSTGPKSSEPKQY.F R.SNHY@DPEEDEEYYRK.Q R.SNHYDPEEDEEY@YR.K R.SNHYDPEEDEEY@YRK.Q	Y830 Y1164 Y1164 Y1177 Y1177 Y1345 Y1353 Y1353	MAGUK family. Contains 1 guanylate kinase-like domain, 3 PDZ (DHR) domains, 1 SH3 domain.
Tight junction protein ZO-2	Q9Z0U1	R.SYHEAY@EPDY@GGGYSPSYDRR.A R.SYHEAY@EPDYGGGY@SPSYDRR.A R.SYHEAY@EPDYGGGYSPSYDRR.A R.SYHEAYEPDY@GGGYSPSYDRR.A R.VFLRPSPEDEAIY@GPNTK.M F.LRPSPEDEAIY@GPNTKMVRF.K R.GLVREDAVLY@LLEIPKGETVTILAQSR.A R.IEIAQKHPDIY@AVPIK.A	Y230, Y234 Y230, Y238 Y230 Y234 Y486 Y486 Y554 Y1095	
CYTOSKELETON: ACTIN-ASSOCIATED				
Actins and actin-related proteins; Regulators of actin assembly				
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	M.VGMGQKDSY@VGDEAQSKRGIL.T K.IWHHTFY@NELR.V K.EKLC*Y@VALDFENEM#ATAASSSSLEK.S	Y55 Y93 Y220	Peptide conserved in alpha-cardiac actin (P68033); gamma-enteric smooth muscle actin (P63268); Beta-actin (P70514); Gamma-actin (P63260) Peptide conserved in alpha cardiac-actin (P68033); ; Beta-actin (P70514); Gamma-actin (P63260)
Actin, cytoplasmic 1 (Beta-actin)	P70514	K.EKLC*Y@VALDFEQEMATAASSSSLEK.S	Y218	
Beta-centractin	Q8R5C5	R.TTGVVLDSGDGVTHAVPIY@EGFAMPHSIMR.V	Y171	Part of a complex involved in microtubule based vesicle motility. Associated with the centrosome. Belongs to the actin family, ARP1 subfamily.
Actin-like protein 2 -- Arp2	P61161	K.HLWDY@TFGPEK.L K.HLWDY@TFGPEKLNIDTR.N	Y91 Y91	Actin-related protein. Part of a complex implicated in the control of actin polymerization in cells.
Actin-like protein 3 - Arp3	Q99JY9	L.RAEPEDHY@F.L	Y108	
Actin-related protein 2/3 complex subunit 3 -- p21-ARC	Q9JM76	F.KGPAPRETKDTDIVDEAIY@Y.F F.KGPAPRETKDTDIVDEAIY@YF.K K.DTDIVDEAIY@YFK.A Q.FKGPAPRETKDTDIVDEAIY@Y.F	Y46 Y46 Y46 Y46	Part of a complex implicated in the control of actin polymerization in cells.
Adenylyl cyclase-associated protein 1 -- CAP1	P40124	R.LEAVSHTSDMHC*GY@GDSPSK.G	Y30	Actin monomer binding protein. Promotes rapid actin dynamics in conjunction with ADF/cofilin.
Cofilin-1 non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C K.LTGIKHELQANC*Y@EEVKDR.C	Y139 Y139	
Src substrate cortactin	Q60598	F.KAEPSYRGSEPEPEY@SIEAAGIPEAGSQQGL.T L.TYTSEPVY@ETTEAPGHY.Q Y.TSEPVY@ETTEAPGHY.Q	Y442 Y466 Y466	
Cytoplasmic FMR1 interacting protein 1	Q7TMB8	K.C*NEQPNRVEIY@EK.T	Y108	Alternative name: Specifically Rac-associated protein (Sra-1). Essential component of a WAVE2- and Abi-1-containing complex linking Rac to site-directed actin assembly. Peptide also in Cytoplasmic FMR1 interacting protein 2 (Q5SQX6).
Coronin-1C	Q9WUM4	R.YFEITDESPY@VHYLNTFSSKEPQR.G	Y301	Contains 4 WD repeats. Site in fourth repeat.
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.VIY@DFIEK.T	Y253	Regulates actin polymerization by stimulating the actin-nucleating activity of the Arp2/3 complex.

Twinfilin-1	Q91YR1	R.KIEIDNGDELTADFLY@DEVHPK.Q	Y309	Twinfilins are composed of two ADF/cofilin-like repeats (ADF-H domains).
Twinfilin-2	Q9Z0P5	K.KIEIGDGAELTAEFLY@DEVHPK.Q	Y309	
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R R.VQIY@HNPTANSFR.V	Y39 Y39	Actin- and profilin-binding microfilament-associated protein.
WD-repeat protein 1 -- Actin interacting protein 1, AIP1	O88342	F.IYDGKTGEKVC*ALGESKAHDGGIY@AISW.S K.AHDGGIY@AISWSPDSTHLLSASGDK.T K.AHDGGIY@AISWSPDSTHLLSASGDKTSK.I	Y237 Y237 Y237	Induces disassembly of actin filaments in conjunction with ADF/cofilin family proteins. Contains 11 WD repeats.

Other actin-associated proteins

Alpha-actinin 1	Q7TPR4	R.HRPELIDY@GK.L K.AIM#TYVSSFY@HAFSGAQK.A K.AIMTYVSSFY@HAFSGAQK.A	Y193 Y246 Y246	
Anillin	Q8K298	R.AESADSLGSEDRDLLY@SIDAYR.S	Y666	A substrate of anaphase-promoting complex/cyclosome that controls spatial contractility of myosin during late cytokinesis.
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q Y.HGEYPDDYPREY@QYGDDQGIDY.-	Y316 Y320	Thin filament-associated protein implicated in the regulation and modulation of smooth muscle contraction. Capable of binding to actin, calmodulin, troponin C and tropomyosin.
Filamin-B	Q80X90	K.GFLDGVY@SFEYYPSTPGK.Y K.QKGFLDGVY@SFEYYPSTPGK.Y M.KSRMDGTY@AC*SY.T R.MDGTY@AC*SYTPLK.A	Y511 Y511 Y704 Y704	
Girdin	Q5SNZ0	K.TEDAY@TISSAGKPTPSTQGK.I L.RTGPQKTEDAY@TISSAGKPTPSTQ.G	Y1739 Y1739	Actin binding protein. Akt/PKB regulates actin organization and cell motility via Girdin/APE. 2005, Dev. Cell, 9, 389-402.
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	LIM protein subfamily, characterized by a LIM motif and SH3 domain. An actin-binding protein, may play a role in cytoskeletal organization.
Moesin	P26041	K.EGILNDDIY@C*PPETAVLLASYAVQSK.Y	Y115	"Membrane-organizing extension spike protein". Site is in the FERM domain. Actin-binding protein. Plays a role in the formation of microvilli-like structures.
Myosin-9	Q8VDD5	R.HEMPPHIY@AITDTAYR.S	Y150	
Myosin-10	Q61879	R.AVIY@NPATQADWTAK.K Y.LFVDRAVIY@NPATQADW.T	Y22 Y22	
PDZ and LIM domain protein 1	O70400	R.VITNQYNSPTGLY@SSENISNFNNAVESK.T	Y148	Associates with the actin stress fibers. May act as an adapter that brings other proteins (like kinases) to the cytoskeleton.
Profilin-1	P10924	K.C*Y@EMASHLR.R	Y128	
Profilin-2	Q9JJV2	K.SQGGEPTY@NVAVGR.A	Y98	Binds to actin and affects the structure of the cytoskeleton.
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	Involved in cytokinesis. Alternative Name: NEDD-5.
Septin-7	O55131	K.NLEGY@VGFANLPNQVYR.K R.KLAAVTY@NGVDNNK.N R.KLAAVTY@NGVDNNKNK.G	Y29 Y318 Y318	
Synaptopodin	Q8CC35	R.TPPASLY@HGYLPENGVLRPEPTK.Q	Y775	Actin-associated protein that may play a role in modulating actin-based shape and motility of dendritic spines and renal podocyte foot processes.

CYTOSKELETON: MICROTUBULE-ASSOCIATED

Tubulin alpha-1 chain	P68369	F.MVDNEAIY@DIC*RR.N F.MVDNEAIY@DIC*.R F.MVDNEAIY@DIC*RRNLDIERPTY.T	Y210 Y210 Y210	All peptides identical in alpha tubulins 2 (P05213), 3 (Q5FW91), 4 (P68368), 6 (P68373), 7 (P05214), and 8 (Q9JJZ2).
Tubulin beta-3 chain	Q9ERD7	Y.C*IDNEALY@DIC*F.R K.NSSY@FVEWIPNNVK.V	Y208 Y340	Peptide identical in beta tubulins 2 (Q3TG26), 2C (P68372), 4 (Q9D6F9), 5 (P99024), and 6 (Q922F4) Peptide identical in Q9D6F9 P99024 Q922F4
CLIP-associating protein 2 -- CLASP2	Q8BRT1	R.DYNPY@NYSDSISPFNK.S	Y1014	Clasps are CLIP-115 and -170 associating proteins involved in the regional regulation of microtubule dynamics in motile fibroblasts.
Dynein heavy chain, cytosolic	Q9JHU4	R.YQVGVHY@ELTEEEKFYR.N	Y1008	Acts as a motor for the intracellular retrograde motility of vesicles and organelles along microtubules.
Kinesin light chain 1	O88447	K.DGSAFGEY@GGWYK.A K.QKDGSAFGEY@GGWYK.A	Y444 Y444	Microtubule-associated force-producing protein that plays a role in organelle transport. Peptide identical in several Kinesin light chain 1 isoforms (Q7M703, Q7M701, Q7M700, Q7M6Z9, Q7M6Z8, Q7M6Z7, Q7M6Z6, Q7TNF4)
Kinesin light chain 2	Q91YS4	R.DSAPYGEY@GSWYK.A	Y434	
Kinesin-associated protein 3 -- KAP3	P70188	R.PATAYGFRPDEPY@YYSFGSR.- R.PATAYGFRPDEPYY@YSFGSR.- R.PATAYGFRPDEPYYY@SFGSR.-	Y786 Y787 Y788	Component of KIF3 motor involved in microtubule plus-end-directed translocatoion of membrane organelles. KAP3 may regulate the association of KIF3 (kinesin family protein 3) motor with its cargos. Phosphorylation by Src reduces binding affinity for RAP1GDS1.

Kinesin family member 11	Q6P9P6	R.SPNEVY@TWEEDPLAGIIPR.T	Y124	Alternative name: Kinesin-related mitotic motor protein (Q9Z1J0).
Microtubule-associated protein 1B -- MAP 1B	P14873	K.VLSPLRS@PPLLGSESPY@EDFLSADSK.V R.SPPLLGSESPY@EDFLSADSK.V	Y1405 Y1405	
Microtubule-associated protein 1B -- isoform	UPI0000021C8B	R.THDVGGYY@YEKTER.T	Y1901	Cannot be combined with P14873. In P14873, is HDVVRY. Two entries only have 7 different aa.
Microtubule-associated protein 4 -- MAP 4	P27546	F.TERDNPSEDSY@GMLPC*DSF.A	Y176	May play a role in microtubule stabilization as well as promoting microtubule assembly.
Nuclear distribution protein nudE homolog 1 -- NudE	Q9CZA6	R.NFMY@DQSPSR.T	Y279	Localizes to the interphase centrosome and to the mitotic spindle. Required for centrosome duplication and formation and function of the mitotic spindle. Concentrates at the plus ends of microtubules coincident with kinetochores in metaphase and anaphase.
PREDICTED: similar to centrosome spindle pole associated protein	UPI0000D65977	R.TPYDDAY@YFYGAR.N	Y468	
Platelet-activating factor acetylhydrolase IB alpha subunit	P63005	R.SNGYEEAY@SVFKK.E	Y27	May participate in targeting cytoplasmic dynein to microtubule plus ends, thereby playing an essential role in dynein-mediated microtubule sliding. Non-catalytic subunit of a acetylhydrolase complex.
RCC2 protein	Q8BK67	R.VFSWGFGGY@GR.L	Y357	Contains 7 RCC1 repeats. Interacts with microtubules. Required for completion of mitosis and cytokinesis. May function as a guanine nucleotide exchange factor for RAC1.
CYTOSKELETON: OTHER				
Plectin 1	Q6S394	Y.VSSLY@DAMPRVPGAQDGVRANEL.Q K.AVTGYRDPY@SGQSVSLFQALK.K K.AVTGYRDPY@SGQSVSLFQALKK.G R.ARQEEVY@SELQAR.E R.LTAEDLY@EAR.I R.QQNLASY@DYVR.R R.AVTGYKDPY@SGK.L R.LLEAAAQSSKGY@YSPYSVSGSGSTAGSR.T K.GYYSPY@S@VSGSGSTAGSR.T K.GYYSPY@SVSGSGSTAGSR.T	Y288 Y3134 Y3134 Y3250 Y3678 Y3665 Y4043 Y4499 Y4503 Y4503	Plectins are long filamentous molecules (500 kDa) that cross-link microtubules to intermediate filaments and to actin microfilaments. All peptides identical in plectin isoforms 2, 3, 5, 6, 7, 8, 10, 11 (Respective UniProt refs.: Q6S393, Q6S392, Q6S390, Q6S389, Q6S388, Q6S387, Q6S385, and Q6S384.
Protein 4.1	P48193	K.VSLLDDTVY@EC*VVEK.H	Y223	Major structural element of the erythrocyte membrane skeleton. Stabilizes spectrin-actin interaction.
Spectrin beta chain, brain 1	Q62261	L.KIVSSNDVGHDEY@STQ.S	Y777	Alternative Name: Fodrin beta chain.
Vimentin	P20152	R.TY@SLGSALRPSTSR.S L.RPSTSRSLY@SSSPGGAY.V R.SLY@SSS@PGGAYVTR.S R.SLY@SSSPGGAYVTR.S S.RSLY@SSSPGGAY.V S.TSRSLY@SSSPGGAY.V	Y37 Y52 Y52 Y52 Y52 Y52	Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells.
TRAFFICKING/TRANSPORT				
Vesicle transport				
Adapter-related protein complex 3 mu 1 subunit	Q9JKC8	K.SVVSQSVC*DY@FFEAQEK.A	Y31	Part of the AP-3 adaptor-related complex which is not clathrin-associated. Facilitates budding of vesicles from the Golgi membrane and may be involved in trafficking to lysosomes.
Clathrin heavy chain	Q68FD5	R.ALEHFTDLY@DIKR.A R.FLRENPY@YDSR.V	Y634 Y899	Major component of the cytoplasmic face of coated vesicles and coated pits.
Coatomer protein complex subunit alpha	Q8BTF0	R.VKGNNVY@C*LDR.E	Y 579	The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-clathrin-coated vesicles, which further mediate biosynthetic protein transport from the ER, via the Golgi up to the trans Golgi network.
Coatomer beta subunit	Q9JIF7	K.LVTEMGTY@ATQSALSSSRPTKK.E	Y521	
Coatomer beta' subunit	O55029	K.GVNC*IDYY@SGGDKPYLISGADDR.L	Y194	
HECT domain and RCC1-like domain-containing protein 2 -- Herc2	Q4U2R1	R.SRTPLDKDLINTGIY@ESSGK.Q R.TPLDKDLINTGIY@ESSGK.Q	Y999 Y999	A very large protein implicated in protein trafficking. Contains 1 HECT (E6AP-type E3 ubiquitin-protein ligase) domain.
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	Adapter protein involved in the formation of clathrin-coated vesicles.
Lysosomal trafficking regulator	P97412	R.AVWYDPIY@YPTSWQLDPTEGPNR.E	Y 2929	May be required for sorting endosomal resident proteins into late multivesicular endosomes by a mechanism involving microtubules.
SEC24 related gene family, member B	Q80ZX0	K.MTSLPLDSQC*DSY@YSRPYTVPTQNSGTPSSANQPGAQQMYGR.G R.LDDRVY@AMC*QMK.S	Y79 Y1083	Component of the copii coat, that covers ER-derived vesicles involved in transport from the endoplasmic reticulum to the golgi apparatus.
SH3-containing GRB2-like protein 1	Q62419	K.ALY@DFEPENDGELGFR.E	Y315	Belongs to the endophilin family. May play a regulatory role in synaptic vesicle recycling.
Sorting nexin-9	Q91VH2	K.IAIIVGDY@GPMWVYPTSTFDC*VVADPR.K L.AKPKEKIAIIVGDY@GPM#.W L.AKPKEKIAIIVGDY@GPM.W	Y239 Y239 Y239	Sorting nexins are characterized by a phox-homology domain, which mediates their association with phosphoinositides. Involved in membrane trafficking and sorting by binding to target proteins

Sorting nexin 17	Q8R0N8	R.KSYWDSAY@DDDVMENR.V	Y210	SNX17 enhances the endocytosis rate of the LDL receptor.
Transitional endoplasmic reticulum ATPase -- TER ATPase	Q01853	K.VVETDPSPY@C*IVAPDTVIHC*EGEPIKR.E	Y172	Alternative name: valosin-containing protein (VCP). Member of a family that includes putative ATP-binding proteins involved in vesicle transport and fusion, 26S proteasome function, and assembly of peroxisomes.
		R.GILLY@GPPGTGK.T	Y243	
Nucleocytoplasmic transport				
GTP-binding nuclear protein Ran	P62827	K.NLQY@YDISAK.S	Y145	Small GTP binding protein belonging to the RAS superfamily that is essential for the translocation of RNA and proteins through the nuclear pore complex.
		R.KKNLQY@YDISAK.S	Y145	
		K.NLQYY@DISAK.S	Y146	
		K.SNY@NFEKPFLWLAR.K	Y154	
Importin-9	Q91YE6	R.VKGEEIY@SMDEGIR.T	Y888	Functions in nuclear protein import as nuclear transport receptor. Serves as receptor for nuclear localization signals (NLS) in cargo substrates.
RAE1 RNA export 1 homolog	Q8C570	R.SNGTNTSAPQDIY@AVNGIAFHPVHGTLATVGSDGR.F	Y274	Thought to be involved in nucleocytoplasmic transport, and in directly or indirectly attaching cytoplasmic mRNPs to the cytoskeleton.
Ran-binding protein 2	Q9ERU9	R.GDDY@FNYNVQQTSTNPPLPEPGYFTKPPLVAHASR.S	Y960	Large RAN-binding nucleoporin located on the cytoplasmic side of the nuclear pore complex which plays a role in nuclear protein import.
		K.EGPY@WNC*NSC*SFK.N	Y1349	
Other transport				
none				
METABOLIC AND BIOSYNTHETIC ENZYMES				
Glycolytic enzymes				
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G	Y24	Catalyzes the first common step of glycolysis and gluconeogenesis. Mammalian enolase is composed of 3 isozyme subunits, alpha, beta and gamma, which can form homodimers or heterodimers. This peptide also identical in gamma enolase (P17183).
		F.DSRGNPTVEVDLY@TAKGLF.R	Y24	Identical peptide in gamma enolase (P17183).
		F.DSRGNPTVEVDLY@TAKGLFR.A	Y24	Identical peptide in gamma enolase (P17183).
		F.RAAVPSGASTGIY@EAL.E	Y43	Identical peptide in beta enolase (P21550); gamma enolase (P17183).
		F.RAAVPSGASTGIY@EALEL.R	Y43	Identical peptide in beta enolase (P21550); gamma enolase (P17183).
		R.AAVPSGASTGIY@EALELR.D	Y43	Identical peptide in beta enolase (P21550); gamma enolase (P17183).
		F.RAAVPSGASTGIY@EALELRDNDKTRF.M	Y43	alpha enolase only.
		R.AAVPSGASTGIY@EALELRDNDK.T	Y43	alpha enolase only.
		R.IGAEVY@HNLK.N	Y188	Identical peptide in beta enolase (P21550);
GAPDH: Glyceraldehyde-3-phosphate dehydrogenase	P16858	F.VKLISWYDNEY@GY.S	Y315	Second phase of glycolysis; first step.
		K.LISWYDNEY@GYSNR.V	Y315	
		L.ISWYDNEY@GY.S	Y315	
		L.ISWYDNEY@GYSNRVVDL.M	Y315	
L-lactate dehydrogenase A chain	P06151	W.KEVHKQVVDSAY@EVIKL.K	Y238	Anaerobic glycolysis; final step.
6-phosphofructokinase, liver type	P12382	K.C*HEHYTTEFLY@NLYSSEGR.G	Y639	The rate-limiting enzyme of glycolysis.
Phosphoglycerate mutase 1	Q9DBJ1	F.SGWY@DADLSPAGHEEAKRGGQAL.R	Y25	Functions in second phase of glycolysis.
		F.SGWY@DADLSPAGHEEAKRGGQ.A	Y25	
		R.FSGWY@DADLSPAGHEEAK.R	Y25	
		R.FSGWY@DADLSPAGHEEAKR.G	Y25	
Pyruvate kinase, isozyme M2	P52480	R.EATESFASDPILY@RPVAVALDTK.G	Y104	Second phase of aerobic glycolysis; final step.
		R.EATESFASDPILY@RPVAVALDTKGPEIR.T	Y104	
		Y.HAETIKNVREATESFASDPILY@RPVAVAL.D	Y104	
		K.ITLDNAY@MEKC*DENILWLDYK.N	Y147	
		L.IAREAEAAIY@HLQL.F	Y389	
		L.IAREAEAAIY@HL.Q	Y389	
		L.IAREAEAAIY@HLQLF.E	Y389	
		L.IAREAEAAIY@HLQLFEEL.R	Y389	
		M.QHLIAREAEAAIY@HLQLFEEL.R	Y389	
		R.EAEAAIY@HLQLFEELR.R	Y389	
		R.EAEAAIY@HLQLFEELRR.L	Y389	
Other metabolic/biosynthetic enzymes				
ADP/ATP translocase 2	P51881	R.AAYFGIY@DTAK.G	Y194	Belongs to the mitochondrial carrier family. Catalyzes the exchange of ADP and ATP across the mitochondrial inner membrane.
ATP citrate lyase	Q91V92	R.TTDGVY@EGVAIGGDRYPGSTFMDHVLR.Y	Y 672	The primary enzyme responsible for the synthesis of cytosolic acetyl-CoA and oxaloacetate, a key step for the biosynthesis of fatty acids, cholestrol, acetylcholine, as well as for glucogenesis.
		R.TTDGVY@EGVAIGGDRYPGSTFM#DHVLR.Y	Y 672	
Aldo-keto reductase family 1 member C18	Q8K023	K.IELNDGHSIPVLGFGTY@ATEEHLK.K	Y24	Catalyzes the conversion of aldehydes and ketones to their corresponding alcohols by utilizing NADH and/or NADPH as cofactors.
Aldo-keto reductase family 1, member B3	Q5U415	R.HIDC*AQVY@QNEK.E	Y49	
		R.HIDC*AQVY@QNEKEVGVALQEK.L		

Aldose reductase-related protein 2	P45377	R.AC*LLPETVNMEEYPYDAEY@.- W.RAC*LLPETVNMEEYPYDAEY@.-	Y315 Y315	
Adenylosuccinate synthetase, non-muscle isozyme	P46664	K.DGVY@FLYEALHGPPK.K K.DGVY@FLYEALHGPPKK.I K.DGVYFLY@EALHGPPKK.I	Y236 Y236 Y239	Plays an important role in the de novo pathway of purine nucleotide biosynthesis.
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	L.SEDEARVC*MVY@DLYPTLTPL.A R.VC*M#VY@DLYPTLTPLAVAYAR.A R.VC*MVY@DLYPTLTPLAVAYAR.A R.VC*MVYDLY@PTLTPLAVAYAR.A	Y290 Y290 Y290 Y293	Involved in de novo purine biosynthesis.
CTP synthase	P70698	Y.INIDAGTFSPY@EHGEVF.V	Y53	Catalyzes the ATP-dependent amination of UTP to CTP.
Glycerol-3-phosphate dehydrogenase 2	Q8VDT0	R.FLYY@EMGYK.S	Y601	Functions in glycerol metabolism.
Glucose-6-phosphate 1-dehydrogenase X	Q00612	R.NSYVAGQY@DDAASYK.H R.VQPNEAVY@TK.M L.VIRVQPNEAVY@TKM#.M L.VIRVQPNEAVY@TKM.M L.VIRVQPNEAVY@TKMM.T K.KPGMFFNPEESELDLTY@GNRYK.N K.RVGFQYEGTY@K.W R.VGFQYEGTY@K.W	Y111 Y400 Y400 Y400 Y400 Y423 Y506 Y506	Pentose phosphate pathway; oxidative stage. A cytosolic enzyme whose main function is to produce NADPH.
Inosine-5'-monophosphate dehydrogenase 2	P24547	L.AATTEAPGEY@FFSDGIRL.K	Y400	Rate limiting enzyme in the de novo synthesis of guanine nucleotides.
Phosphoglucomutase 2	Q5RJV4	K.IALY@ETPTGWK.F	Y353	Glycogen metabolism.
Ribonucleoside-diphosphate reductase large subunit	P07742	K.KVFSDVMEDLY@NYINPHNGR.H K.KVFSDVM#EDLY@NYINPHNGR.H	Y102 Y102	Catalyzes the biosynthesis of deoxyribonucleotides from the corresponding ribonucleotides.
Serine hydroxymethyltransferase, cytosolic	P50431	K.M#LSQPLKDSDAEVY@SIIKK.E K.MLSQPLKDSDAEVY@SIIKK.E	Y28 Y28	Interconversion of serine and glycine. Key enzyme in the biosynthesis of purines, lipids, hormones and other components.
S-adenosylhomocysteine hydrolase	Q5M9P0	K.SKFDNLY@GC*R.E	Y193	Enzyme in the Activated Methyl Cycle, where the methyl group of methionine is activated by the formation of S-adenosylmethionine.
Thioredoxin reductase 1, cytoplasmic	Q9JMH6	K.KVVYENAY@GR.F K.VVYENAY@GR.F	Y131 Y131	This protein reduces thioredoxins as well as other substrates, and plays a role in selenium metabolism and protection against oxidative stress.
Thioredoxin reductase 1 [fragment]	Q3UEB7	K.EVVYENAY@GR.F	Y131	A distinct peptide from Thioredoxin reductase 1, cytoplasmic (Q9JMH6).
TK: Transketolase	P40142	K.NM#AEQIIQEIY@SQVQSK.K K.NMAEQIIQEIY@SQVQSK.K	Y275 Y275	Pentose phosphate pathway; non-oxidative stage.
UDP-glucose 6-dehydrogenase	O70475	R.INAWNSPTLPIY@EPGLK.E R.INAWNSPTLPIY@EPGLKEVVESC*R.G	Y53 Y53	Involved in biosynthesis of glycosaminoglycans; hyaluronan, chondroitin sulfate, and heparan sulfate.
RNA SYNTHESIS AND PROCESSING				
Transcription machinery and regulation				
CCR4-NOT transcription complex subunit 2	Q8C5L3	F.VEGVDSDYHDENM#Y@Y.S F.VEGVDSDYHDENMY@Y.S K.FVEGVDSDYHDENM#Y@YSQSSMFPHR.S K.FVEGVDSDYHDENMY@YSQSSM#FPHR.S K.FVEGVDSDYHDENMY@YSQSSMFPHR.S	Y43 Y43 Y43 Y43 Y43	The CCR4-NOT complex functions as general transcription regulation complex.
DNA-directed RNA polymerase I 40 kDa polypeptide -- RPA40	P52432	R.NVHTTDFPGNY@AGYDDAWDQNRFEK.N	Y33	Catalyzes the transcription of DNA into RNA.
LIM domains containing protein 1 -- LIMD1	Q9QXD8	K.VFC*EEDFLY@SGFQQSADR.C	Y519	Has 3 Ct LIM domains. Site is in the first LIM domain. Interacts with pRB, inhibits E2F-mediated transcription, and suppresses the expression of the majority of genes with E2F1-responsive elements.
NF-kappa-B DNA binding subunit p105	P25799	F.TRRLEPVVSDAIY@DSKAPNASNL.K R.RLEPVVSDAIY@DSKAPNASNLK.I	Y238 Y238	Transcription regulator that is activated by various intra- and extra-cellular stimuli. Site in the Rel homology domain (RHD)
Polymerase I and transcript release factor -- PTRF	O54724	F.KVMIY@QDEVKLPAKL.S K.VMIY@QDEVKLPAK.L R.KSFTPDHVVY@AR.S K.SFTPDHVVY@AR.S	Y158 Y158 Y310 Y310	Required for dissociation of the ternary transcription complex.
Staphylococcal nuclease domain-containing protein 1	Q78PY7	R.ADDADEFGY@SR.-	Y908	Transcriptional coactivator for STAT5 and STAT6. May function as a bridging factor between STAT6 and the basal transcription machinery.

		R.YGDFRADDADEFGY@SR.-	Y908	
Transcription initiation factor IIE alpha subunit	Q9D0D5	R.FNEQIEPIY@ALLR.E	Y188	Recruits TFIIH to the initiation complex and stimulates the RNA polymerase II C-terminal domain kinase and DNA-dependent ATPase activities of TFIIH.
Transcription elongation factor SPT6	Q62383	K.AAEDDELEEEADWIY@R.N	Y321	Acts to stimulate transcriptional elongation by RNA polymerase II.
Tripartite motif protein 25	Q61510	K.FDTIY@QVLVK.K	Y277	Transcription factor. Mediates estrogen action in various target organs. Contains one RING-type zinc finger and one SPRY domain.
		R.VYGKFDTIY@QVLVK.K	Y277	
DEAD(DEAH)-box helicases				
ATP-dependent RNA helicase DDX3X (DDX3Y) (PL10)	Q62167	K.GFY@DKDSSGWSS@SKDKDAYSSFGSR.G	Y52	The DEAD(DEAH) box helicases are involved in various aspects of RNA metabolism, including nuclear transcription, pre mRNA splicing, ribosome biogenesis, nucleocytoplasmic transport, translation, RNA decay and organellar gene expression.
		K.DKDAY@SSFGSR.D	Y68	Peptide in DDX3Y (Q62095) and putative ATP-dependent RNA helicase PL10 (P16381).
		W.SSSKDKDAY@SSF.G	Y68	
		R.FDDRGRGDY@DGIGGR.G	Y103	
		R.GDY@DGIGGR.G	Y103	
		R.GDY@DGIGGRGDR.S	Y103	
		R.GRGDY@DGIGGR.G	Y103	
		R.GRGDY@DGIGGRGDR.S	Y103	
		K.TAAFLLPILSQIY@ADGPGEALR.A	Y242	
		L.VLAPTRELAVQIY@EEARKF.S	Y282	Peptide in DDX3Y (Q62095) and putative ATP-dependent RNA helicase PL10 (P16381).
		R.VRPC*VVY@GGAEIGQQIR.D	Y300	
		F.VETKKGADSLEDFLY@HEGY.A	Y461	Peptide in putative ATP-dependent RNA helicase PL10 (P16381).
		K.GADSLEDFLY@HEGYAC*TSIHGDR.S	Y461	Peptide in putative ATP-dependent RNA helicase PL10 (P16381).
		K.KGADSLEDFLY@HEGYAC*TSIHGDR.S	Y461	Peptide in putative ATP-dependent RNA helicase PL10 (P16381).
		L.VFVETKKGADSLEDFLY@HEGY.A	Y461	Peptide in putative ATP-dependent RNA helicase PL10 (P16381).
Putative ATP-dependent RNA helicase DHX30	Q99PU8	R.ENYLEENLLY@APSLR.F	Y991	
Probable ATP-dependent RNA helicase DDX6	P54823	K.GVTQY@YAYVTER.Q	Y312	
Putative pre-mRNA splicing factor ATP-dependent RNA helicase DHX15	O35286	K.QNHESVQWC*Y@DNFINYR.S	Y645	
Probable ATP-dependent RNA helicase DDX17 (DDX5)	Q501J6	K.STC*IY@GGAPK.G	Y200	Peptide also in probable ATP-dependent RNA helicase DDX5 (Q61656).
		R.LKSTC*IY@GGAPK.G	Y200	Peptide also in probable ATP-dependent RNA helicase DDX5 (Q61656).
Probable ATP-dependent RNA helicase DDX20 -- DEAD-box protein 20	Q9JJY4	R.VQSEPQEESWY@DC*HR.E	Y757	
		R.AWQEY@YAAASHSYYWNAQR.H	Y788	
Probable ATP-dependent helicase DDX48	Q91VC3	K.GFKEQIY@DVYR.Y	Y202	
hnRNPs and snRNPs				
Heterogeneous nuclear ribonucleoprotein A1	P49312	F.GGRSSGPY@GGGGQYF.A	Y288	
		R.SSGPYGGGGQY@FAKPR.N	Y294	
Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Y.GGGYGSGGGSGGY@GSRRF.-	Y374	
Heterogeneous nuclear ribonucleoprotein A/B	Q3TMZ8	Y.GPGYGGYDYSPY@GYY.G	Y291	
		Y.GYQQGYGPGYGGYDY@SPYGYY.G	Y288	
Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	K.ATENDIY@NFFSPLNPVR.V	Y306	
		R.DLSYC*LSGMY@DHR.Y	Y272	
Heterogeneous nuclear ribonucleoprotein H1	Q811L7	R.GAYGGGYGGY@DDYNGYNDGYGFGSDRFGR.D	Y243	
		R.GAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246	
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDR.F	Y246	
		R.RGAYGGGYGGYDDY@NGYNDGYGFGSDRFGR.D	Y246	
		R.GAYGGGYGGYDDYNGY@NDGYGFGSDRFGR.D	Y249	
Heterogeneous nuclear ribonucleoprotein H'	P70333	R.GAYGGGYGGY@DDYGGYNDGYGFGSDRFGR.D	Y243	
		R.GAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246	
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDR.F	Y246	
		R.RGAYGGGYGGYDDY@GGYNDGYGFGSDRFGR.D	Y246	
		Y.GGGYGGYDDY@GGYNDGYGF.G	Y246	
		Y.GGGYGGYDDY@GGYNDGYGFGSDRF.G	Y246	
		R.ATENDIY@NFFSPLNPMR.V	Y306	
		Y.RATENDIY@NFF.S	Y306	
Heterogeneous nuclear ribonucleoprotein L	Q8R081	M.VKMAAAGGGGGGGRY@Y.G	Y16	

Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	N.RFEPY@SNPTKRY.R	Y62	
Heterogeneous nuclear ribonucleoprotein Q	Q7TMK9	Q.RQAAKNQMYDDYY@YY.G R.GGYEDPY@YGYEDFQVGAR.G Y.RGGYEDPY@YGY@EDFQVGAR.G Y.RGGYEDPY@YGY@EDF.Q Y.RGGYEDPY@YGYEDF.Q Y.RGGYEDPY@YGYEDFQ.V	Y432 Y485 Y485,Y488 Y485,Y488 Y485 Y485	
Heterogeneous nuclear ribonucleoprotein R	Q8VHM5	Y.RGGYEDPY@YGYDDGY.A	Y489	
Heterogeneous nuclear ribonucleoprotein U	O88568	K.NQSQGYNQWQQGQFWGQKPWSQHYHQGY@Y.-	Y797	
Polypirimidine tract binding protein	Q8R509	Y.TSVAPVLRGQPNY@IQF.S	Y126	Sequence is similar with Polypyrimidine tract-binding protein 1, score 90%.
Polypyrimidine tract-binding protein 1 -- hnRNP	P17225	R.GQPIY@IQFSNHK.E Y.TSVAPVLRGQPIY@IQF.S	Y126 Y126	Alternative Name: Heterogeneous nuclear ribonucleoprotein I, hnRNP I
U1 small nuclear ribonucleoprotein 70 kDa	Q62376	K.HHNQPY@C*GIAPYIR.E	Y38	
U1 small nuclear ribonucleoprotein C	Q62241	K.FYC*DYC*DTY@LTHDSPSVR.K	Y12	
Splicing factors				
Apoptosis-related RNA binding protein	Q9Z0H4	K.ELFEPYGAVY@QINVLR.D	Y67	
Crooked neck-like protein 1	P63154	R.KVQADDGSDAGWEEY@Y@DYIFPEDAANQPNLK.L R.KVQADDGSDAGWEEY@YDYIFPEDAANQPNLK.L R.KVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L R.RKVQADDGSDAGWEEYY@DYIFPEDAANQPNLK.L	Y640,Y641 Y640 Y641 Y641	Contains 16 HAT repeats. Sites in the 15th HAT domain. Involved in pre-mRNA splicing.
RNA binding motif, single-stranded interacting protein 1	Q91W59	K.QQMYPQY@ATYYYPQYLQAK.Q W.KQQMYPQY@ATY.Y K.QQMYPQY@ATY@YYPQYLQAK.Q K.QQM#YPQYATY@YYPQYLQAK.Q K.QQMYPQYATY@YYPQYLQAK.Q L.HNGFYPSPY@SIATN.R	Y13 Y13 Y13,Y16 Y16 Y16 Y272	
Splicing factor, arginine/serine-rich 1	Q6PDM2	F.VRKEDMTY@AVR.K	Y169	
Splicing factor, arginine/serine-rich 3	P84104	R.AFGY@YGPLR.S	Y32	
Splicing factor 3b, subunit 4	Q8QZY9	F.IGNLDPEIDEKLLY@DTF.S	Y117	
Splicing factor, arginine/serine-rich 5	O35326	F.GFVEFEDPRDADDAVY@ELDGKEL.C R.GFGFVEFEDPRDADDAVY@ELDGK.E R.GFGFVEFEDPRDADDAVY@ELDGKELC*SER.V	Y55 Y55 Y55	
Arginine/serine-rich splicing factor 6	Q921K3	K.NGYGFVEFEDSRDADDAVY@ELNSK.E Y.GFVEFEDSRDADDAVY@ELNSKEL.C	Y53 Y53	
Splicing factor, arginine/serine-rich 9	Q9D0B0	R.DAEDAIY@GR.N	Y71	
Splicing factor, proline- and glutamine-rich	Q8VIJ6	R.FAQHGTFEY@EYSQR.W	Y480	Essential pre-mRNA splicing factor required early in spliceosome formation. Seems to also bind DNA.
Other RNA binding and processing				
DAZ-associated protein 1	Q9JII5	L.AFPPPPSQAAPDMSKPPTAQPDFPY@GQY.G	Y346	RNA-binding protein, which may be required during spermatogenesis.
Double-stranded RNA-binding protein Staufen homolog	Q9Z108	R.ELLY@GGTSPTAETILK.S R.TRPSEQLY@YLSR.A	Y371 Y404	May play a role in specific positioning of mRNAs at given sites in the cell by crosslinking cytoskeletal and RNA components, and in stimulating their translation at the site.
ELAV-like protein 1	P70372	K.NMALLSQLY@HSPAR.R	Y200	ELAV family proteins are Implicated in mRNA stability and translatability, control of cytoplasmic mRNA stability mediated by AU-rich elements in 3'-UNT.
ELAV-like protein 2	Q60899	K.TNQAILSQLY@QSPNR.R	Y219	Peptide identical in ELAV-like neuronal protein-3 (Q91XI9).
Fragile X mental retardation syndrome related protein 1 homolog	Q61584	K.EISEGDEVEVY@SR.A K.KEISEGDEVEVY@SR.A L.KDPDSNPY@SLL.D	Y68 Y68 Y506	Human fragile X mental-retardation protein (FMRP) and the fragile X-related proteins 1 and 2 (FXR1P and FXR2P) form a gene family with functional similarities, such as RNA binding, polyribosomal association and nucleocytoplasmic shuttling.

Fragile X mental retardation syndrome related protein 2 homolog	Q9WVR4	R.LPPPADYNKEITEGDEVEVY@SR.A L.KDPDSNPY@SLLDTSEPEPPVDSEPGEPPPASAR.R	Y78 Y520	
Insulin-like growth factor 2 mRNA-binding protein 2	Q5SF07	K.SGY@AFVDYPDQNWAIR.A	Y40	Binds to the 5' untranslated region of IGF2 mRNAs. Binding is isoform-specific. May regulate translation of target mRNAs.
Insulin-like growth factor 2, binding protein 1	Q80US9	K.SGY@AFVDC*PDEHWAMK.A	Y39	
Interleukin enhancer-binding factor 3	Q9Z1X4	R.VLEC*LASGIVMPDGSGIY@DPC*EKEATDAIGHLDR.Q	Y292	May facilitate double-stranded RNA-regulated gene expression at the level of post-transcription. Can act as a translation inhibitory protein.
Matrin-3	Q8K310	R.SATREPPY@RVPR.D R.SQESGYY@DRMDYEDDRLR.D	Y171 Y214	Contains 1 matrin-type zinc finger, 2 RRM (RNA recognition motif) domains. May play a role in nuclear retention of defective RNAs.
Polyadenylate-binding protein 1 -- PABP1 (PABC4)	P29341	Y.VGDLHPDVTEAM#LY@EKF.S Y.VGDLHPDVTEAMLY@EKF.S K.ALY@DTFSAFGNILSC*K.V	Y28 Y28 Y116	May be involved in cytoplasmic regulatory processes of mRNA metabolism. May be involved in translationally coupled mRNA turnover. Identical peptide in poly A binding protein, cytoplasmic 4 (Q3UX16).
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKL.H Y.TIQGQY@AIPQPDLTKLHQLAM#.Q Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232 Y232 Y232	Single-stranded nucleic acid binding protein that binds preferentially to oligo dC. RNA binding protein.
Poly(rC)-binding protein 3	P57722	K.PASTPVIFAGGQAYTIQGQY@AIPHPDLTK.L	Y201	
Protein SMG7	Q5RJH6	K.VPEFYWDSSY@SMADNR.A	Y826	Plays a role in nonsense-mediated mRNA decay. Recruits RENT1 (see below) to cytoplasmic mRNA decay bodies.
Pumilio homolog 1	Q80U78	R.SQDDAMVDY@FFQR.Q	Y83	Sequence-specific RNA-binding protein that regulates translation and mRNA stability by binding the 3' untranslated regions (UTRs) of mRNA targets.
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S R.YDSRPGGYGYGY@GR.S	Y124 Y126	
Ras-GTPase-activating protein binding protein 1 -- G3bp1	P97855	K.NSSYAHGGLDSNGKPADAVY@GQK.E	Y56	hnRNA-binding protein and an element of the Ras signal transduction pathway. These proteins have endoribonuclease activity and mediate RNA decay in response to growh factors.
Ras-GTPase-activating protein SH3-domain binding protein	UPI0000D62F64	K.NSSYAHGGLDSNGKPADAVY@GKK.E	Y56	
Ras-GTPase-activating protein binding protein 2	P97379	R.NSSYVHGGVDASGKPQEAVY@GQNDIHHK.V Y.VHGGVDASGKPQEAVY@GQNDIHHKVL.S	Y56 Y56	
Regulator of differentiation 1 -- Rod1	Q8BHD7	R.SQPVY@IQYSNHR.E	Y98	Contains 4 RRM (RNA recognition motif) domains. May play a role in regulation of differentiation. In vitro, binds RNA, preferentially to both poly(G) and poly(U).
Regulator of nonsense transcripts 1 -- RENT1	Q9EPU0	L.AELNFEEDEEDTY@YTKDLPVHAC*SY.C L.AELNFEEDEEDTY@YTKDLPVHAC*.S L.LAELNFEEDEEDTY@YTKDLPVHAC*.S K.RFTAQGLPDLNHSQVY@AVK.T R.FM#TTAMY@DAR.E R.FMTTAMY@DAR.E R.AYQHGGVTGLSQY@.-	Y108 Y108 Y108 Y472 Y930 Y930 Y1113	Part of a post-splicing multiprotein complex involved in nonsense-mediated decay (NMD) of mRNAs containing premature stop codons.
PROTEIN SYNTHESIS AND PROCESSING				
tRNA synthetases				
Alanyl-tRNA synthetase	Q8BGQ7	K.DNFWEMGDTGPC*GPC*SEIHY@DR.I	Y192	
Arginyl-tRNA synthetase	Q9D0I9	K.SDGGYTY@DTSDLAAIK.Q	Y384	
Bifunctional aminoacyl-tRNA synthetase	Q8CGC7	R.GFFIC*DQPYEPVSPY@SC*R.E R.RGFFIC*DQPYEPVSPY@SC*R.E	Y690 Y690	
Cysteinyl-tRNA synthetase	Q9ER72	K.VTWYC*C*GPTVY@DASHMGHAR.S	Y143	
Histidyl-tRNA synthetase	Q61035	K.LIY@DLKDQGGELLSLR.Y K.YGEDSKLIY@DLKDQGGELLSLR.Y L.TGKYGEDSKLIY@DLKDQGGELL.S	Y115 Y115 Y115	
Isoleucine-tRNA synthetase	Q6NXK4	K.NNDLC*Y@WVPEFVR.E	Y434	
lysyl-tRNA synthetase	Q8C292	K.ITYHPDGPEGQAY@EVDFTPPFR.R K.ITYHPDGPEGQAY@EVDFTPPFRR.I	Y381 Y381	
Valyl-tRNA synthetase	Q9Z1Q9	R.LHEEGVIY@R.S	Y468	
Translation machinery				

40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	
60S ribosomal protein L3	P27659	K.NNASTDY@DLSDK.S	Y306	
60S ribosomal protein L4	Q9D8E6	R.KLDELY@GTWR.K	Y264	
mitochondrial ribosomal protein S27	UPI00001C5303	F.VDNIASREDLDSAEY@YLY.K R.FVDNIASREDLDSAEY@YLYK.F R.EDLDSAEY@YLYK.F	Y90 Y90 Y90	
Eukaryotic translation initiation factor 2A	Q640P8	L.VIASTEVDKTGASY@YGEQTLH.Y L.VIASTEVDKTGASY@YGEQTLHY.I K.LISKPVASDSTY@FAWC*PDGEHILTATC*APR.L K.PVASDSTY@FAWC*PDGEHILTATC*APR.L L.ISKPVASDSTY@F.A Y.KLISKPVASDSTY@F.A	Y250 Y250 Y362 Y362 Y362 Y362	
Eukaryotic translation initiation factor 3 subunit 1	Q66JS6	L.KATM#KDDLADY@GGYEGGYVQDYEDFM#.- L.KATMKDDLADY@GGYEGGYVQDYEDFM#.- L.KATMKDDLADY@GGYEGGYVQDYEDFM.-	Y248 Y248 Y248	Eukaryotic translation initiation factor-3 (eIF3) is a multisubunit complex (~10 subunits) that binds to the 40S ribosomal subunit and promotes the binding of methionyl-tRNAi and mRNA.
Eukaryotic translation initiation factor 3, subunit 7	O70194	R.NLAMEATY@INHNFSQQC*LR.M	Y317	
Eukaryotic translation initiation factor 3, subunit 8	Q8R1B4	F.DHKQGTY@GGY.F F.DHKQGTY@GGYF.R L.GSLVENNERVFDHKQGTY@GGY.F R.VFDHKQGTY@GGYFR.D	Y879 Y879 Y879 Y879	
Eukaryotic translation initiation factor 3, subunit 9	Q8JZQ9	R.MTLDTLSIY@ETPSMGLLDKK.S	Y 438	
Eukaryotic translation initiation factor 3 subunit 10	P23116	K.KQPALDVLY@DVMK.S F.LEVGKKQPALDVLY@DVM.K	Y32 Y32	
Eukaryotic translation initiation factor 4 gamma 1	Q6NZJ6	Y.SASQGAY@YIPGQGRSTY.V	Y110	
Eukaryotic translation initiation factor 4B	Q8BGD9	F.LGNLPY@DVTEDSIKDFF.R K.SPPYTAFLGNLPY@DVTEDSIKDFFR.G	Y105 Y105	
Eukaryotic initiation factor 4A-I	P60843	K.VVMALGDY@MGASC*HAC*IGGTNVR.A M.ALGDY@MGASC*H.A R.GFKDQIY@DIFQK.L	Y126 Y126 Y197	
Eukaryotic translation initiation factor 4H	Q9WUK2	R.AY@SSFGGGR.G H.GSRSQKELPTEPPY@TAY.V Q.KELPTEPPY@TAY.V R.SQKELPTEPPYTAY@VGNLPFNTVQGDIDAIFK.D	Y11 Y41 Y41 Y44	
Elongation factor 1-alpha 1 -- eEF1A-1 (eEF1A-2)	P10126	K.STTTGHLIY@K.C R.EHALLAY@TLGVK.Q	Y29 Y141	Promotes the GTP-dependent binding of aminoacyl-tRNA to the A-site of ribosomes during protein biosynthesis. Both peptides identical in eEF1A-2 (P62631; P27706).
G1 to phase transition 2 (GSPT2)	Q9CY91	K.TAGVKY@LIVLINK.M	Y347	GSPT2 is closely related to GSPT1. GSPT1 is a positive regulator of translational accuracy and, in a binary complex with eRF1functions as a polypeptide chain release factor.
Laminin receptor 1 -- ribosomal protein SA	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.TVSDLIDQKVY@ELQASR.V K.VY@ELQASR.V Y.FHKTVSDLIDQKVY@EL.Q R.VSSDVIDQKVY@EIQDIYENSWTK.L R.QLEVY@TSGGDPESVAGEYGR.H K.GDPQVYEELFSY@AC*PK.F R.MQKGDPQVYEELFSY@AC*PK.F	Y72 Y72 Y72 Y89 Y247 Y415 Y415	
Post-translational modifiers				
N-terminal acetyltransferase complex ARD1 subunit homolog A	Q9QY36	F.QISEVEPKY@YADGEDAY.A L.NFQISEVEPKY@YADGEDAY.A K.YYADGEDAY@AMKR.D	Y137 Y137 Y145	In complex with NARG1, displays alpha (N-terminal) acetyltransferase activity. Without NARG1, displays epsilon (internal) acetyltransferase activity towards HIF1A, thereby promoting its degradation.
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	L.RSQTDSLFGDSGVY@DTPSSY.S	Y576	Putative palmitoyltransferase involved in glutamatergic transmission.
Glutathione S-transferase P 1	P19157	K.YVTLIY@TNYENGK.N K.YVTLIY@TNYENGKNDYVK.A	Y108 Y108	Conjugates reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles.
Chaperones and associated proteins				

BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I K.THYPAQQGEYQPQQPVY@HK.I K.THYPAQQGEY@QPQQPVY@HK.I	Y246 Y253 Y246,Y253	Inhibits the chaperone activity of HSP70/HSC70 by promoting substrate release.
DnaJ homolog subfamily B member 4	Q9D832	K.VSLEEIY@SGC*TK.R	Y172	
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I K.NAVEEYVY@EMRDKLSGEYEK.F	Y336 Y627	
Heat shock cognate 71 kDa protein	P63017	R.MVQEAEKY@KAEDEKQR.D	Y525	
Heat shock protein 75 kDa, mitochondrial precursor	Q9CQN1	R.NIY@YLC*APNR.H	Y500	
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	
Heat-shock protein 105 kDa	Q61699	K.NAVEEC*VY@EFR.D K.NAVEEC*VY@EFRDK.L	Y644 Y644	
T-complex protein 1, beta subunit	P80314	F.INRQLIY@NYPEQLF.G R.QLIY@NYPEQLFGAAGVMAIEHADFAGVER.L	Y296 Y296	Belongs to the TCP-1 chaperonin family.
T-complex protein 1, theta subunit	P42932	K.HFSGLEEAVY@R.N	Y29	Belongs to the TCP-1 chaperonin family.
PROTEIN DEGRADATION				
Ubiquitin conjugation regulators				
Anaphase promoting complex subunit 2	Q8BZQ7	K.VRDQQLIY@SAGVYR.L K.VRDQQLIY@SAGVYRLPK.N R.DQQLIY@SAGVYR.L R.DQQLIY@SAGVYRLPK.N	Y825 Y825 Y825 Y825	Belongs to the cullin family. Component of the anaphase promoting complex/cyclosome (APC/C), a cell cycle-regulated ubiquitin ligase that controls progression through mitosis and the G1 phase of the cell cycle.
CBL E3 ubiquitin protein ligase	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L K.PSSSANAIY@SLAARPLPMPK.L	Y672 Y672	Acts as an E3 ubiquitin-protein ligase.
F-box-like/WD-repeat protein TBL1X	Q9QXE7	K.HQEPVY@SVAFSPDGK.Y	Y459	F-box-like protein involved in the recruitment of the ubiquitin/19S proteasome complex to nuclear receptor-regulated transcription units.
F-box-like/WD-repeat protein TBLR1	Q8BHJ5	K.HQEPVY@SVAFSPDGR.Y	Y446	
HECT, UBA and WWE domain-containing protein 1	Q7TMY8	R.EMFNPMY@ALFR.T	Y4081	Alternative Name: E3 ubiquitin protein ligase URE-B1. Regulates apoptosis by catalyzing the polyubiquitination and degradation of MCL1. Also ubiquitinates the p53 tumor suppressor and core histones including H1, H2A, H2B, H3 and H4.
Ubiquitin conjugating enzyme 7 interacting protein 3	Q9WUB0	R.NSQEAEVAC*PFIDSTY@SC*PGK.L	Y318	Contains 1 ubiquitin-like domain, 1 RING-type zinc finger, 1 RanBP2-type zinc finger, 1 B box-type zinc finger. Might act as an E3 ubiquitin-protein ligase, or as part of the E3 complex.
Ubiquitin-conjugating enzyme	O88738	K.VIFVDDY@AVGC*R.K K.VIFVDDY@AVGC*RK.D	Y107 Y107	GENE NAME Birc6
Ubiquitin-conjugating enzyme E2O	Q6PCR9	K.LRPSGDDVELIGEEEDVSVY@DIADHPDFR.F	Y412	
Ubiquitin-protein ligase E3 Mdm2	P23804	S.DEDDEVY@RVTVY@QTGESDTDSFEGDPEISLADY.W	Y279	Only the first Y in the peptide (Y274) is in Psite
Proteasome components				
26S protease regulatory subunit S10B	P62334	K.GC*LLY@GPPGTGK.T	Y173	The 26S protease is involved in the ATP-dependent degradation of ubiquitinated proteins. Proteasome subunit p42; Proteasome 26S subunit ATPase 6. GENE NAME Psmc6.
26S protease regulatory subunit 8	P62196	K.GVLLY@GPPGTGK.T	Y189	Proteasome subunit p45, p45/SUG, Proteasome 26S subunit ATPase 5, mSUG1. GENE NAME Name: Psmc5
26S protease regulatory subunit 6B	P54775	L.SFLGPEPEDLEDLY@SRY.K	Y41	
26S proteasome non-ATPase regulatory subunit 7	P26516	W.FLDHDYLENM#Y@GM#F.K W.FLDHDYLENMY@GM#F.K W.FLDHDYLENMY@GMF.K	Y79 Y79 Y79	
Proteasome subunit alpha type 2 -- PSMA2	P49722	L.ATEKKQKSILY@DERSVH.K H.IGLVY@SGM#GPDYRVL.V H.IGLVY@SGMGPDYRVL.V H.KVEPITKHIGLVY@SGM#GPDYRVL.V H.KVEPITKHIGLVY@SGMGPDYRVL.V K.HIGLVY@SGM#GPDYR.V K.HIGLVY@SGM#GPDYRVL.V K.HIGLVY@SGMGPDYR.V K.HIGLVY@SGMGPDYRVL.V	Y56 Y75 Y75 Y75 Y75 Y75 Y75 Y75 Y75	Proteasome component C3. PSMA2 may have a potential regulatory effect on another component(s) of the proteasome complex through its tyrosine phosphorylation.

		L.VY@SGMGPDYRVL.V	Y75	
		K.LAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100	
		K.LAQQYYLVY@QEPIPTAQLVQR.V	Y100	
		R.KLAQQYY@LVY@QEPIPTAQLVQR.V	Y97,Y100	
		R.KLAQQYYLVY@QEPIPTAQLVQR.V	Y100	
		Y.YLVY@QEPIPTAQL.V	Y100	
Proteasome subunit alpha type 6	Q9QUM9	Y.KC*DPAGYY@C*GF.K	Y160	
Proteasome subunit beta type 1	O09061	K.GAVY@SFDPVGSYQR.D	Y149	
		K.DVFISAAERDVY@TGDALR.I	Y215	
Proteasome subunit beta type 4 precursor	P99026	M.RVNDSTMLGASGDY@ADF.Q	Y102	Proteasomal protein of the T1B peptidase family.
		R.VNDSTMLGASGDY@ADFQYLK.Q	Y102	
Proteasome subunit beta type 5 precursor	O55234	K.RGPGLY@YVDSEGNR.I	Y116	Belongs to the peptidase T1B family.
		R.GPGLY@YVDSEGNR.I	Y116	
		W.DKRGPGLY@YVDSEGNRISGTAF.S	Y116	
		R.AIY@QATYR.D	Y165	
		R.DAYSGGAVNLY@HVR.E	Y181	
		R.DAYSGGAVNLY@HVREDGWIR.V	Y181	
Proteasome subunit beta type 7 precursor	P70195	L.VLGGVDVTGPHLY@SIYPHGSTDKLPY.V	Y154	
Other proteolytic regulators				
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	K.VISSVSY@YTHR.H	Y367	Belongs to the peptidase C19 family. May function as a ubiquitin-protein or polyubiquitin hydrolase involved both in the processing of ubiquitin precursors and of ubiquitinated proteins.
		F.NDY@FEFPRELDMEPY.T	Y1815	
		K.FNDY@FEFPR.E	Y1815	
		K.FNDY@FEFPRELDMEPYTVAGVAK.L	Y1815	
		R.PY@T@GNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2431,Y2439	
		R.RPYTGNPQY@TYNNWSPPVQSNETSNGYFLER.S	Y2437	
		R.RPYTGNPQYT@Y@NNWSPPVQSNETSNGYFLER.S	Y2439	
		R.RPYTGNPQYTY@NNWSPPVQSNETSNGYFLER.S	Y2439	
		R.RPYTGNPQYT^Y@NNWSPPVQSNETSNGYFLER.S	Y2439	
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	Belongs to the peptidase S9A family. Cleaves peptide bonds on the C-terminal side of prolyl residues within peptides that are up to ~30 amino acids long.
		R.MTELY@DYPKYSC*HFK.K	Y71	
		Y.KERM#TELY@DYPKY.S	Y71	
		Y.KERMTELY@DYPKY.S	Y71	
NUCLEAR PROTEINS				
Histone H2B type 1-B	Q64475	R.KESYSVYVY@K.V	Y43	
Histone H4	P62806	K.RISGLIY@EETRGVL.K	Y51	
		R.ISGLIY@EETR.G	Y51	
Nucleolar protein 10	Q5RJG1	K.MGIY@YIPVLGPAPR.W	Y339	Contains 5 WD repeats. Site in 5th WD repeat.
Nucleolin	P09405	R.SVSLY@YTGEK.G	Y464	Associated with intranucleolar chromatin and preribosomal particles. Induces chromatin decondensation by binding to histone H1.
PREDICTED: scaffold attachment factor B	UPI00001E3C2C	R.RDDAY@WPEAK.R	Y723	DNA binding protein
SET protein	Q9EQU5	F.YFDENPY@FENKVL.S	Y145	Multitasking protein, involved in apoptosis, transcription, nucleosome assembly and histone binding.
		R.IDFYFDENPY@FENK.V	Y145	
		R.IDFYFDENPY@FENKVLSK.E	Y145	
		Y.RIDFYFDENPY@FENKVL.S	Y145	
		Y.FDENPY@FENKVL.S	Y145	
Structural maintenance of chromosome 3	Q9CW03	Y.IEERLHTLEEEKEELAQY@QKW.D	Y213	Central component of cohesin complex required for the cohesion of sister chromatids after DNA replication.
Telomerase-binding protein EST1A	P61406	K.FQNSDNPY@YYPR.T	Y507	Component of the telomerase ribonucleoprotein (RNP) complex that is essential for the replication of chromosome termini.
Translin	Q62348	K.KVEEVVY@DLSIR.G	Y210	DNA-binding protein that specifically recognizes consensus sequences at the breakpoint junctions in chromosomal translocations, mostly involving immunoglobulin (Ig)/T-cell receptor gene segments.
MISCELLANEOUS				
Catalase	P24270	K.GAGAFGY@FEVTHDITR.Y	Y83	Occurs in almost all aerobically respiring organisms and serves to protect cells from the toxic effects of hydrogen peroxide. Peroxisomal.
		K.LVNADGEAVY@C*K.F	Y230	
DNA dC->dU editing enzyme APOBEC-3	Q99J72	K.HLC*Y@YHR.M	Y255	Belongs to the cytidine and deoxycytidylate deaminase family. Mediates G-to-A hypermutation in newly synthetized HIV-1 viral DNA and is thus able to prevent HIV-1 infectivity in vitro.

		R.VKHLC*Y@YHR.M Y.NQRVKHLC*Y@Y.H K.HLC*YY@HR.M Y.NQRVKHLC*YY@.H	Y255 Y255 Y256 Y256	
Pol polyprotein [Moloney murine leukemia virus (MoMLV); Mus musculus]	P03355	L.AAAY@QEQLDRPVVPHPY.R H.PY@RVGDTVW.V L.AAAY@QEQLDRPVVPHPY@RVGDTVW.V L.AAAYQEQLDRPVVPHPY@RVGDTVW.V Y.QEQLDRPVVPHPY@RVGDTVW.V K.NLEPRWKGPY@TVL.L R.WKGPY@TVLLTTPTALK.V	Y1105 Y1118 Y1105,Y1118 Y1118 Y1118 Y1142 Y1142	
Serpin B6	Q60854	K.FKLEENYNMNDALY@KLGMTDAFGGR.A Y.NMNDALY@KLGMTDAF.G	Y289 Y289	Placental thrombin inhibitor. Serine-type endopeptidase inhibitor activity.
Voltage-dependent anion-selective channel protein 1	Q60932	K.YRWTEY@GLTFTEK.W	Y80	Forms a voltage-dependent anion channel through the mitochondrial outer membrane and also the plasma membrane.

FUNCTION UNKOWN OR UNCERTAIN

Named proteins of unknown/uncertain function

Ankyrin repeat domain-containing protein 25	Q8BX02	L.HVPAPFPGTPGQASPAAFPSKEPDPPY@S@VETPYGY.R L.HVPAPFPGTPGQASPAAFPSKEPDPPY@SVETPYGY.R	Y32 Y32	Contains 5 ANK repeats.
Anthrax toxin receptor 1 precursor	Q9CZ52	K.WPTVDASY@YGGR.G	Y380	
ApoA-I binding protein	Q8K4Z3	K.KYQLNLPSYPDTEC*VY@RLQ.- K.YQLNLPS@YPDT@ECVY@RLQ.- K.YQLNLPSYPDTEC*VY@RLQ.-	Y279 Y279 Y279	
Ataxin-2	O70305	K.GLPQPTISFDGIY@ANVR.M R.VALENDDRSEEEKY@TAVQR.N R.VALENDDRS^EEEKY@TAVQR.N	Y233 Y440	Spinocerebellar ataxia type 2 protein homolog
Ataxin-2-like protein	Q7TQH0	K.GPPQSPVFEGVY@NNSR.M	Y116	
BAT2-ISO homolog [fragment] (Bat2d)	Q8BMJ4	R.M#MWGSDPY@HAEPQQAATPK.S R.MM#WGSDPY@HAEPQQAATPK.S R.MMWGSDPY@HAEPQQAATPK.S	Y788 Y788 Y788	Unknown function. UPI0000511F95 is full length, 2718 aa. Q8BMJ4 is fragment, N terminal 1105 aa. Q3TLH4: 893 aa.
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	L.TTTRKTPQGPPEIY@SDTQFPSLQ.S R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213 Y213	Both peptides identical in Carnitine deficiency-associated protein CDV3B (Q920C7)
Centrosomal protein 170	UPI0000D62DCC	K.HVEGQSAAASEEALFPFC*REPSY@FEIPTK.E	Y240	
DENN/MADD domain containing 2C	Q6P9P8	K.SLENIY@YEPEGQEC*GPSINPLPKPR.R	Y185	
Dihydropyrimidinase-related protein 2	O08553	K.THNSALEY@NIFEGMEC*R.G	Y431	CRMP-2 (mouse) an enzyme with dihydropyrimidinase activity. Plays a role in RhoA-dependent signaling, through interaction with and regulation of Rho kinase.
Discoidin, CUB and LCCL domain containing protein 2 precursor -- DCBLD2	Q91ZV3	K.SAATPEELVY@QVPQSTQELSGAGR.D	Y744	
Discs, large homolog 5	Q3UGX5	Y.KEERDAVY@SEY.K	Y429	
Far upstream element binding protein 3 (FUSE binding protein 3) homolog	Q3TIX6	K.IDSIPHLNNSTPLVDPS@VY@GYGVQKR.A	Y51	May interact with single-stranded DNA from the far-upstream element (FUSE). May activate gene expression.
GPI-anchored protein p137 -- p137GPI	Q60865	F.TAPRDY@SGY.Q	Y609	Attached to the membrane by a GPI-anchor (Probable). May play a role in transporting nutrient from the gut lumen across the gutlining epithelial cell layer (By similarity).
Grb10 interacting GYF protein 2	Q6Y7W8	F.LKEVESPY@EVHDY.T F.LKEVESPY@EVHDYTRAY.L	Y1174 Y1174	Gene Name: Tnrc15; trinucleotide repeat containing 15
High glucose-regulated protein 8	Q8K325	K.DGLNDDDFEPY@LSPQAR.P	Y37	Similar to YTH domain protein 3 (below)
Large proline-rich protein BAT2	Q7TSC1	K.KYSSLNLFDTY@KGK.S K.YSSLNLFDTY@KGK.S K.APPSTY@SGVFR.T R.LKAPPSTY@SGVFR.T R.IDLY@QQASPPDALR.W	Y26 Y26 Y2098 Y2098 Y2110	May play a role in the regulation of pre-mRNA splicing. Unknown function.
Leucine rich repeat (in FLII) interacting protein 2 (Lrrfip2) [fragment]	Q8C062	R.DIY@DLKDQIHDVEGR.Y	Y5	Full length: 504aa gi:51765208, no Uniprot number.

Mage-d2	Q99PB4	R.VPNSNPPEY@EFFWGLR.S	Y439	
Nsun2 protein	Q91YX9	R.LAQEGIY@TLYPFINSR.I	Y372	Myc-induced SUN domain containing protein. Sun domain found in tRNA and rRNA cytosine-C5-methylases
OTU domain containing 4 protein -- Otud4; PREDICTED: HIV-1 induced protein HIN-1 isoform 1;	UPI0000218B34	K.DSSAMC*QSLLY@ELLYEK.V R.ESY@YFGLSPEER.R R.ESYY@FGLSPEER.R R.LLY@EIQNR.D R.LLY@EIQNRDEQAFPALSSSSVSQSPSQNSNAC*VPR.K	Y169 Y436 Y437 Y458 Y458	MKIAA1046 protein [fragment] (Q80TL3) represents part of the same protein. Contains OTU domain near N-terminus. Possible cysteine protease activity.
Pericentriolar material gene 1 protein [fragment]	Q91Y51	K.SNRPVS^ADGNY@RPLAK.T	Y961	Unknown function
Periodic tryptophan protein 1 homolog -- Pwp1	Q9D6T6	R.VTWNHFSPC*HFLASTDDGFVY@NLDAR.S	Y367	Belongs to the WD-repeat PWP1 family. Contains 5 WD40 repeats.
Pleckstrin homology-like domain, family B, member 2 -- PHLDB2	Q8K1N2	K.ADLDHY@TGRDSER.S K.SHDSVY@FLGGLEGR.K R.NKSHDSVY@FLGGLEGR.K	Y130 Y161 Y161	Contains 1 PH domain.
Protein FAM51A1	Q8BHE1	R.LNDY@VNADHGLY@FNHR.R R.LNDY@VNADHGLY@FNHRR.S R.LNDYVNADHGLY@FNHR.R	Y167,Y175 Y167,Y175 Y175	
PYM protein	Q8CHP5	R.VKEGYVPQEEVPVYENKY@VK.F	Y49	
Suppression of tumorigenicity 5	Q924W7	K.STLEENAY@EDIVGGLPKENPY@EDVDLK.N	Y485,Y498	
SR-related CTD associated factor 6	Q8CGZ0	R.NSEGWEQNGLY@EFFR.A	Y723	Calcium Homeostasis Endoplasmic Reticulum Protein (CHERP).
Tanc2 protein [fragment]	Q5EBP6	K.TNNAQNGHLLEDDY@YSPHGMLANGSR.G	Y1349	TPR domain, ankyrin-repeat and coiled-coil-containing
Testis derived transcript	Q921W7	K.HTM#NEGEPAIY@AER.A K.HTMNEGEPAIY@AER.A	Y249 Y249	Function unkown. Contains 3 Ct LIM domains. Caution - other proteins are also called “testin”.
Trinucleotide repeat containing 6b	Q6NVE4	K.DLGTTDSGPY@FEK.G K.DLGTTDSGPY@FEKGGSHGLFGNSTAQSR.G K.GIQNIDPESDPY@VTPGSVLGGTTTSPIVDTDHQLLR.D	Y1128 Y1128 Y1440	
Tripartite motif protein 16	Q99PP9	F.DC*KFSEPVY@AAF.W K.FSEPVY@AAFWLSK.K	Y523 Y523	Unknown function. Alternative Name: Ebbp, estrogen-responsive B box protein.
Tudor domain-containing protein 3	Q91W18	L.SNIKPVQTEAWEEEGTY@DHTIEF.R	Y618	Unkown function.
Ubiquitin-associated protein 2 -- UBAP2	Q91VX2	R.LPMDY@YGIPFAAPTALASR.D R.LPM#DY@YGIPFAAPTALASR.D R.LPMDYY@GIPFAAPTALASR.D F.AAPTALASRDGNLANNPY@SGDVTKF.G L.ASRDGNLANNPY@SGDVTKF.G N.NPY@SGDVTKF.G R.DGNLANNPY@SGDVTK.F K.SQASKPTY@GSAPYWTN.-	Y853 Y853 Y854 Y876 Y876 Y876 Y876 Y1124	Has an ubiquitin associated (UBA) domain, a common motif in some members of the ubiquitination pathway, UV excision repair proteins, and certain protein kinases. Unknown function.
Ubiquitin associated protein 2-like -- UBAP2L	Q80X50	Y.TSQNNAQGPLY@EQRSTQ.T R.FPLDY@YSIPFPTPTTPLTGR.D R.DGSLASNPY@SGDLTK.F L.TGRDGSLASNPY@SGDLTKF.G	Y612 Y854 Y878 Y878	Alternative names: Nice-4 protein homolog, isoform 2 (Q8CIG7), Lingerer protein-2a (Q812D5); Lingerer protein-2b (Q812D4). Unknown function.
Yippee-like 5	Q65Z92	N.S@KLGWIY@EFATEDSQRY.K	Y84	
YTH domain protein 3 -- Ythdf3	Q6NXJ8	K.SVVDYNAY@AGVWSQDKWK.G	Y488	Similar to high-glucose-regulated protein 8 (above).
Novel ZZ type zinc finger domain containing protein	Q5SSH7	K.WKDFELPGDTLY@YR.F W.KDFELPGDTLY@Y.R	Y2706 Y2706	BLAST results: Mouse protein Zzef appears to represent a shorter variant of the same protein - identity starting from residue 2227. Similarity to cullen-7 near N-terminus; regions of similarity to Herc2; a region similar to anaphase promoting complex subunit 10
Unnamed proteins of unknown/uncertain function				
BC003940 protein [fragment]	Q8QZS4	R.FIY@EAWQGVER.D	Y70	No full length form found. Unkown function.
BC053440 protein [fragment]	Q8R2W2	K.INDTMY@FAPSMK.D	Y19	hypothetical NAF1/Proline-rich region profile/Serine-rich region profile containing protein
Hypothetical ATP/GTP-binding site motif A homolog	Q3UHH1	L.HKTKEAAPAVGEEDDDYQAY@Y.L	Y729	No functional information.

hypothetical ATP/GTP-binding site motif A (P-loop)/Zinc finger C-x8-C-x5-C-x3-H type containing protein	Q9DBS7	K.EAVY@SGVQSLR.S	Y508	
hypothetical Domain of unknown function DUF71 containing protein	Q9CQ28	R.VYTQC*EGDEVEDLY@ELLK.L	Y97	
hypothetical G-protein beta WD-40 repeat/Trp-Asp (WD) repeats profile/Trp-Asp (WD) repeats circular profile/Serine-rich region profile/WD40-like containing protein -- WDR70	Q3TWF6	K.AAEDNPY@WVSPAYSK.T	Y621	
hypothetical 5'3'-Exonuclease N- and I-domains containing protein	Q8BMI4	R.LQENC*GANTSLPY@SFSDK.A	Y747	
DNA segment, Chr 5, ERATO Doi 585, expressed -- D5Ertd585e	Q6P1H6	R.IREYLM#GHY@YVPLLR.A	Y483	
		R.IREYLMGHY@YVPLLR.A	Y483	
hypothetical protein: E230015L20Rik protein	Q8C304	R.TNEIY@YLDPDAPLSRPSTQDNQYQK.S	Y416	Gene name: Ccdc66, coiled-coil domain containing 66
hypothetical protein LOC106840	Q8C4B4	K.PEDNVY@SIDFTR.F	Y92	Related to Unc-119 protein homolog. Peptide also in hypothetical protein (Q8BRC4). N terminal 120 aa are identical.
		R.VTENYLC*KPEDNVY@SIDFTR.F	Y92	
PREDICTED: zinc finger protein 650	UPI0000D65C57	K.KLPIAEEEQIY@PWDTC*AAVHDVR.L	Y335	
PREDICTED: similar to Oligophrenin 1	UPI0000D668EB	K.LWLEAMDGKEPIY@TLPAIISK.K	Y371	
		R.KLWLEAM#DGKEPIY@TLPAIISK.K	Y371	
		R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371	
PREDICTED: similar to ring finger and KH domain containing 2	UPI000042893E	R.LSEQGGDFGY@SGYLFPGYGVGK.Q	Y188	
hypothetical protein 1500002O20Rik	Q9DB90	K.EGQRPTQPVY@QIQNR.G	Y147	
MKIAA0183 protein [fragment]	Q6A0A9	K.PAVPQVPSPGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457	
		K.PAVPQVPS@PGGTPGQAPYPY@SLSEPALTLDTSGK.N	Y457	
		K.PAVPQVPSPGGT@PGQAPYPY@SLSEPALTLDTSGK.N	Y457	
		F.GGHY@GETVATGPY@RAF.R	Y968	Upstream site Y959 found only once.
		F.GGHYGETVATGPY@RAF.R	Y968	
Protein FAM125A	Q78HU3	R.RTDSIY@EASS@LYGISAMDGVPFTLHPR.F	Y202	
PREDICTED: similar to la related protein isoform 1	UPI0000D66C58	R.THFDYQFGY@R.K	Y412	Contains LA ribonucleoprotein domain
Similar to leucine-rich neuronal protein homolog	Q3U222	L.GFGSC*HEELY@SGRPY.G	Y203	
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	DUF572 domain

END

Footnotes:

a The protein name is typically taken from the UniProt entry. Additional proteins (in parentheses) indicates ambiguity due to peptides being found in multiple related proteins. If a peptide is not unambiguously identified, additional relevant information is given in the Comments column. The UniProt ID #, indicates the UniProt Knowledgebase ID number representing the latest annotation update for the protein at the time of analyis.

b Peptides are shown in single letter amino acid code, with periods indicating cleavage sites. Y@, phosphotyrosine; S@, phosphoserine; T@, phosphothreonine; S^ and T^, phosphoserine and phosphothreomine detected thrugh neutral loss of phosphoric acid; C*, carboxyimidomethylated cysteine; M#, oxidated methionine. In the pY site column, the position of the phosphotyrosine site is based on the sequence of the given UniProt entry.

c The Novel column indicates whether or not the phosphotyrosine site has been previously recognized in either UniProt or PhosphoSite entries. N with an asterisk indicates that the site is represented in PhosphoSite as an unpublished site.

d The Com/Uncom column indicates whether the site was also found in the other cell population analyzed in this study.

e The "Rounds found" column indicates which of the 18 independent rounds of analysis the peptide was identified. Rounds 1-5, trypsin cleavage with affinity purification using antibody pY100. 6-10, trypsin cleavage with affinity purification using antibody 4G10. 11-14, chymotrypsin cleavage with affinity purification using pY100. 15-18, chymotrypsin cleavage with affinity purification using 4G10.

f "Total IDs" indicates number of independent spectra (combined from the indicated rounds) for which the indicated peptide was top-scoring. "Site count" indicates total number of times the indicated site was identified from all peptides.

g Cross-correlation score (xcorr) and charge (z) of the peptide. For peptides identified multiple times, the highest xcorr value is listed.

h Experimental mass of a singly charged peptide (MH) and the difference of the experimental from the calculated mass (dM), for the peptide with the highest xcorr value.

i If the delta correlation (dCn) score for the second-ranking peptide is < 0.2, these are shown.

j Short notes of interest.