Table S1. Phosphotyrosine sites from the nontransformed 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)										
Proto-oncogene tyrosine-protein kinase -- Src (Yes, Fyn, Hck)	Q80XU2	R.LIEDNEY@TAR.Q	Y418	N	C	1,2,3,4,5,6,8,9,10	11	11	3.47	2
		F.LEDYFTSTEPQY@QPGENL.-	Y529	N	U	11,12,13,15,16,18	7	10	4.83	2
		Y.FTSTEPQY@QPGENL.-	Y529			11,12,14	3		3.62	2
Proto-oncogene tyrosine-protein kinase -- Fyn (Yes)	P39688	R.KLDNGGYY@ITTR.A	Y213	N	U	2,3	2	2	3.31	2
		F.LEDYFTATEPQY@QPGENL.-	Y527	N	U	13,16	2	5	4.86	2
		F.TATEPQY@QPGENL.-	Y527			18	1		3.01	2
		Y.FTATEPQY@QPGENL.-	Y527			11,12	2		3.35	2
Fyn-related kinase -- Frk	Q922K9	F.C*PPEAPRSQEPERSHGQY@F.V	Y53	N*	U	11,12	2	3	3.84	3
		R.SQEPERSHGQY@FVALFDYQAR.T	Y53			3	1		3.36	3
		K.LEDYFETDC*SY@SDTNNFIN.-	Y504	N	U	9	1	10	3.31	2
		W.KLEDYFETDC*SY@SDTNNFIN.-	Y504			11,13,15,16,18	6		4.71	2
							2		3.22	3
		W.KLEDYFETDCS@Y@SDTNNFIN.-	Y504			15	1		2.80	3
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	N*	C	1,2,3,4,6,7,8,9	16	16	5.91	3
		F.GMSRQEDGGVY@SSSGL.K	Y715	N	C	11,12,13	3	3	3.26	2
Proto-oncogene tyrosine-protein kinase ABL1	P00520	M.TGDTY@TAHAGAKFPIKW.T	Y393	N	C	12,15	2	4	4.00	3
		R.LMTGDTY@TAHAGAK.F	Y393			2,3	2		3.52	2
Activated CDC42 kinase 1 -- ACK	O54967	M.RALPQNDDHY@VMQEH.R	Y284	N	U	11,12,15	3	4	3.76	3
							1		4.05	2
		W.DARPLPPPPAY@DDVAQDEDDF.E	Y650	Y	U	11,13	3	3	4.35	2
		F.ASDPKY@ATPQVIQAPGPRAGPC*.I	Y842	N	U	13	1	2	3.28	3
		K.VSSTHY@YLLPERPPYLER.Y	Y874	N	U	2,4,8,9,10	5	8	3.16	3
		R.KVSSTHY@YLLPERPPYLER.Y	Y874			4,5,7	3		3.29	3
		R.KVSS@THYY@LLPERPPYLER.Y	Y875	N	U	9	1	1	3.01	3
Activated CDC42 kinase 1 -- ACK, isoforms 2 and 3	O54967-2	H.LGRVKKPTY@DPVSEDPDPLSSDF.K	Y518	Y	U	12,15,16	3	19	4.85	3
		K.KPTY@DPVSEDPDPLSSDFKR.L	Y518			1,3,4,8	4		3.48	3
		L.GRVKKPTY@DPVSEDPDPLSSDF.K	Y518			15,16,18	3		4.76	3
		R.VKKPTY@DPVSEDPDPLSSDFK.R	Y518			3,4	2		4.67	3
		R.VKKPTY@DPVSEDPDPLSSDFKR.L	Y518			2,3,4,6,8,10	7		5.14	3
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	M.RTHAVSVSETDDY@AEIIDEEDTY.T	Y397	N	U	11,12,18	7	11	5.03	3
							1		3.81	2
		R.THAVSVSETDDY@AEIIDEEDTYTMPSTR.D	Y397			4,7	3		4.08	3
		R.Y@MEDSTY@YK.A	Y570,Y576	N*,N	U,C	6,8	2	4,73	3.17	2
		R.Y@MEDSTY@YKASK.G	Y570,Y576			1	1		2.57	2
		R.Y@MEDSTY@Y@KASK.G	Y570,Y576,Y577			8	1		2.10	2
		F.GLSRYM#EDSTY@Y.K	Y576			11,16,18	3		3.08	2
		F.GLSRYMEDSTY@Y.K	Y576			11,15,16,18	4		2.96	2
		L.GDFGLSRYM#EDSTY@Y.K	Y576			18	1		3.42	2
		L.GDFGLSRYMEDSTY@Y.K	Y576			11,13,15,16,17,18	6		3.85	2
		R.YM#EDST@YY@KASK.G	Y577	N	C	6	1	27	2.53	2
		R.YM#EDSTY@Y@K.A	Y576,Y577			8	1		2.51	2
		R.YM#EDSTY@Y@KASK.G	Y576,Y577			8,9	2		3.54	2
		R.YM#EDSTY@YK.A	Y576			1,2,3,5,6,7,8,9,10	10		3.01	2
		R.YM#EDSTY@YKASK.G	Y576			2,3,8	3		2.93	2
		R.YM#EDSTYY@K.A	Y577			4,10	2		2.54	2
		R.YMEDSTY@Y@K.A	Y576,Y577			3,6,8,9	4		2.75	2
		R.YMEDSTY@Y@KASK.G	Y576,Y577			2,5,8,9	4		3.89	2
		R.YMEDSTY@YK.A	Y576			1,2,3,4,5,6,7,8,9	17		3.16	2
							2		2.01	1
		R.YMEDSTY@YKASK.G	Y576			1,2,3,6,8,9	6		4.32	2
		R.YMEDSTYY@K.A	Y577			2,3,6,7,8,9	6		2.90	2
		Y.M#EDSTY@Y@KASKGKLPIKW.M	Y576,Y577			15,18	2		3.12	3
		Y.MEDSTY@Y@KASKGKLPIKW.M	Y576,Y577			11,13,15,16	4		3.85	3
Tyrosine-protein kinase JAK1	P52332	K.AIETDKEY@Y@TVKDDR.D	Y1033,Y1034	N,N	U,U	8	1	1,1	3.16	3
Tyrosine kinases (receptor)										
Discoidin domain receptor 2 precursor -- DDR2	Q62371	R.IFPLRPDY@QEPSR.L	Y481	N*	U	2,3,4	3	5	3.39	2
		Y.DRIFPLRPDY@QEPSRL.I	Y481			11,13	2		3.35	3
		R.NLY@SGDY@YR.I	Y735,Y739	N,N	C,C	3	1	1,1	2.73	2
Ephrin type-A receptor 2 precursor -- EphA2	Q03145	K.SEQLKPLKTY@VDPHTYEDPNQAVLK.F	Y589	N	U	7	1	6	3.13	3

		L.KTY@VDPHTYEDPNQAVL.K	Y589			12	1		3.14	2
		L.KTY@VDPHT@YEDPNQAVL.K	Y589			13	1		2.90	2
		K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	N	C	1,2,4,7,8,9,10	8	26	4.21	3
		K.TYVDPHTY@EDPNQAVLK.F	Y595			1,2,3,4,5,6,7,8,9,10	2		3.13	3
							8		3.77	2
		L.KTYVDPHTY@EDPNQAVL.K	Y595			11,13,15	3		3.68	2
		L.KTY@VDPHTY@EDPNQAVL.K	Y589,Y595			12,14,16	3		3.20	2
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	N	C	12,13,14,15,16,18	6	23	5.64	3
		L.SRVLEDDPEATY@TTSGGKIPIRW.T	Y773			11,12	2		5.33	3
		R.VLEDDPEATY@TTSGGK.I	Y773			2,3,4,6,8,10	6		5.24	2
		R.VLEDDPEATY@TTSGGKIPIR.W	Y773			1,2,3,4,6,7,8,9	9		4.03	2
Ephrin type-A receptor 3 precursor -- EphA3 (EphA4, EphA5)	P29319	R.VLEDDPEAAY@TTR.G	Y779	N	U	2,3,4	3	3	3.33	2
Ephrin type-A receptor 4 precursor -- EphA4	Q03137	Y.VDPFTY@EDPNQAVREF.A	Y602	N	U	12,15	2	2	3.85	2
Ephrin type-A receptor 5 precursor -- EphA5	Q60629	R.TY@IDPHTY@EDPNQAVHEFAK.E	Y489,Y495	N,N	U,U	2,3,4	3	3,3	3.83	3
Ephrin type-B receptor 2 precursor -- EphB2 (EphB1)	P54763	K.IY@IDPFTY@EDPNEAVR.E	Y604,Y610	N,N	U,U	3	1	1,4	2.32	2
		Y.IDPFTY@EDPNEAVREF.A	Y610			15,16,18	3		4.59	2
Ephrin type-B receptor 3 precursor -- EphB3 (EphB4)	P54754	K.VY@IDPFTY@EDPNEAVR.E	Y603,Y609	N	U	5	5	5	5.28	2
		K.VYIDPFTY@EDPNEAVR.E	Y609	N	U	2,4,6,7,8,9,10	7	12	4.61	2
		R.FLEDDPSDPTY@TSSLGGKIPIR.W	Y787	N	U	4,7	2	2	3.40	3
Eph receptor B4 -- EphB4	Q91YM0	K.HGQYLIGHGTKVY@IDPFTY@EDPNEAVR.E	Y590,Y596	N*	C	2,3,4	3	5	4.81	3
		K.HGQYLIGHGT^KVYIDPFTY@EDPNEAVR.E	Y596	N*	C	3,4	2	7	3.61	3
		Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596			11,12	2		5.85	3
		R.FLEENSS@DPTY@TSSLGGKIPIR.W	Y774	N*	U	4	1	4	2.86	3
		R.FLEENSSDPTY@TSSLGGKIPIR.W	Y774			1,3,4	3		4.11	3
Hepatocyte growth factor receptor precursor -- MET	P16056	F.GLARDMYDKEY@Y.S	Y1232	N	U	15	1	26	2.96	3
		F.GLARDMYDKEYY@.S	Y1233	N	U	12,18	2	14	2.55	2
		R.DM#YDKEY@Y@SVHNK.T	Y1232,Y1233			3,8,10	3		3.84	3
		R.DM#YDKEY@YS@VHNK.T	Y1232			6	1		2.83	3
		R.DM#YDKEY@YSVHNK.T	Y1232			8,10	2		3.85	3
		R.DMYDKEY@Y@SVHNK.T	Y1232,Y1233			1,3,8,9	3		3.51	3
							2		3.31	2
		R.DMYDKEY@Y@SVHNKTGAK.L	Y1232,Y1233			9	1		3.30	3
		R.DMYDKEY@YSVHNK.T	Y1232			1,2,3,4,5,6,7,8,9	10		4.00	3
							1		3.34	2
		R.DMYDKEY@YSVHNKT^GAK.L	Y1232			9	1		3.30	3
		R.DMYDKEY@YS^VHNK.T	Y1232			8	1		3.28	2
		R.DMYDKEYY@SVHNK.T	Y1233			3,7	1		2.71	3
							1		2.96	2
		R.DMYDKEYY@SVHNKT^GAK.L	Y1233			8	1		2.89	3
Insulin-like growth factor 1 receptor precursor -- IGF1R (InsR)	Q60751	R.DIY@ETDY@Y@RK.G	Y1163, Y1167,Y1168	N	U	8	1	2	2.45	2
		R.DIY@ETDY@YRK.G	Y1163, Y1167			8	1		2.74	2
		R.DIYETDY@YR.K	Y1167	N	U	2,3,6,8,10	5	7	2.27	2
		R.DIYETDYY@RK.G	Y1168	N	U	8	1	2	2.42	2
Proto-oncogene tyrosine-protein kinase -- MER	Q60805	K.KIY@SGDY@YR.Q	Y744,Y748	N	U	3	1	1	2.41	2
		K.KIYSGDY@YR.Q	Y748	N	U	3	1	2	2.52	2
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	F.GLSKKIYNGDY@Y.R	Y696	N*	C	11,12	2	24	3.57	2
		K.KIYNGDY@YR.Q	Y696			1,2,3,4,5,6,7,8,9,10	11		2.94	2
		K.IYNGDY@YR.Q	Y696			1,3,4,5,6,7,8,9,10	11		2.83	2
		K.IYNGDYY@R.Q	Y697	N	U	4	1	2	2.08	2
		F.GLSKKIYNGDYY@.R	Y697			13	1		3.21	2
Other protein kinases										
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IEKIGEGT@Y@GVVYK.G	Y15	N	C	1,3,4,6,8,9,10	3	132	3.31	3
							7		4.05	2
		K.IEKIGEGTY@GVVY.K	Y15			11,16	2		3.21	2
		K.IEKIGEGTY@GVVYK.G	Y15			1,2,3,4,5,7,8,9	7		4.35	3
							11		4.12	2
		K.IEKIGEGT^Y@GVVYK.G	Y15			3,5,6,7,8,9,10	3		3.96	3
							4		3.69	2
		K.IGEGT@Y@GVVYK.G	Y15			1,2,3,4,5,6,7,10	10		3.05	2
		K.IGEGTY@GVVYK.G	Y15			1,2,3,4,5,6,7,8,9,10	38		3.45	2
							1		1.85	1
		K.IGEGTY@GVVYKGR.H	Y15			1,2,3,4,5,6,8	9		3.99	2
		K.IGEGT^Y@GVVYK.G	Y15			1,2,3,4,5,6,7,8,9,10	20		3.34	2
		K.IGEGT^Y@GVVYKGR.H	Y15			2,3,4	3		2.93	2
		Y.IKIEKIGEGTY@GVVY.K	Y15			11,12,13,15,16,18	6		3.96	2
		Y.IKIEKIGEGT^Y@GVVY.K	Y15			11	1		2.76	2
		-.DYIKIEKIGEGTY@GVVY.K	Y15			11,12,13,14,15,16,18	7		4.13	2
		K.IGEGTYGVVY@K.G	Y19	N	C	9	1	1	2.76	2
Cell division protein kinase 2 -- CDK2	P97377	K.VEKIGEGTY@GVVYK.A	Y15	N	U	1,4,6	2	3	3.37	3
							1		3.39	2

Dual-specificity tyrosine-phosphorylation regulated kinase 1A -- DYRK1A (DYRK1B)	Q61214	K.VYNDGYDDDNY@DYIVK.N	Y145	N	C	3,4,6,8,9	5	29	5.48	2
		R.KVYNDGYDDDNY@DYIVK.N	Y145			1,2,3,4,6,7,8,9,10	8		5.22	3
							8		5.66	2
		R.KVYNDGYDDDNY@DYIVKNGEK.W	Y145			2,4	2		4.57	3
		Y.NDGYDDDNY@DYIVKNGEKW.M	Y145			11,13,15,16	4		4.70	3
							2		4.73	2
		R.IYQY@IQSR.F	Y321	N	C	1,2,3,4,6,7,9,10	9	11	3.24	2
		Y.QY@IQSRFY.R	Y321			12,15	2		1.98	2
Glycogen synthase kinase-3 beta -- GSK-3beta (GSK3alpha)	Q9WV60	K.QLVRGEPNVSY@IC*SRY.Y	Y216	N	C	11,12,13,15,17	5	92	4.33	3
		K.QLVRGEPNVSY@IC*SRYY.R	Y216			11,12,15,16	4		3.97	3
		L.VRGEPNVSY@IC*.S	Y216			11,16	2		2.89	2
		L.VRGEPNVSY@IC*S@RYY.R	Y216			11	1		2.92	3
		L.VRGEPNVSY@IC*SRY.Y	Y216			11,12,13,14,15,16,17,18	13		4.58	3
							13		4.57	2
		L.VRGEPNVSY@IC*SRYY.R	Y216			11,12,13,14,15,17,18	4		3.91	3
							8		4.25	2
		L.VRGEPNVSY@IC*S^RY.Y	Y216			11	1		2.74	3
		N.VSY@IC*SRY.Y	Y216			11,12,16	3		2.91	2
		N.VSY@IC*SRYY.R	Y216			11	1		2.66	2
		Q.LVRGEPNVSY@IC*SRY.Y	Y216			11,12,13,15,17,18	7		5.03	3
							1		3.46	2
		Q.LVRGEPNVSY@IC*SRYY.R	Y216			11,12,15	3		4.18	3
		R.GEPNVSY@IC*SR.Y	Y216			1,2,3,4,5,6,7,8,9,10	25		3.33	2
		R.GEPNVSY@IC*SRYY.R	Y216			13	1		2.86	2
Homeodomain-interacting protein kinase 1 -- HIPK1 (HIPK2)	O88904	H.VSKAVC*STY@LQSRY.Y	Y352	N	U	11,12,13	1	17	3.80	3
							3		4.06	2
		K.AVC*STY@LQSR.Y	Y352			1,2,3,4,5,6,8,9	10		3.17	2
		S.KAVC*STY@LQSRY.Y	Y352			11,12,13	3		3.96	2
Homeodomain-interacting protein kinase 3 -- HIPK3	Q9ERH7	H.VSKTVC*STY@L.Q	Y359	N	U	11	1	10	2.65	2
		H.VSKTVC*STY@LQSRY.Y	Y359			11,12,13	1		2.91	2
							2		4.02	3
		K.TVC*STY@LQSR.Y	Y359			1,2,3,4,6,8	6		3.13	2
Hypothetical Protein kinase-like (PK-like) structure containing protein -- SgK223	Q8CB68	K.C*VGQAAELQPASLLRDPVQPEPIY@AESAK.R	Y196	N	U	4,9	2	4	6.22	3
		K.C*VGQAAELQPASLLRDPVQPEPIY@AESAKR.K	Y196			1,3	2		4.74	3
Mitogen-activated protein kinase 3 -- ERK1	Q63844	F.GLARIADPEHDHTGFLT@EY@VATRW.Y	Y205	N	U	12	1	28	3.39	3
		F.GLARIADPEHDHTGFLTEY@VATRW.Y	Y205			11,13	3		3.67	3
		F.GLARIADPEHDHTGFLT^EY@VATRW.Y	Y205			11,12	2		4.64	3
		F.GLARIADPEHDHTGFLT^EY@VATRWY.R	Y205			11	1		2.68	3
		F.LTEY@VATRW.Y	Y205			11,12,13	3		2.61	2
		R.IADPEHDHTGFLT@EY@VATR.W	Y205			3,4,7,8,10	5		3.95	3
		R.IADPEHDHTGFLTEY@VATR.W	Y205			1,2,3,5,8,9,10	7		5.38	3
		R.IADPEHDHTGFLT^EY@VATR.W	Y205			1,2,4,7,8,10	6		4.61	3
Mitogen-activated protein kinase 1 -- ERK2	P63085	F.GLARVADPDHDHTGFLT@EY@VATRW.Y	Y185	N	U	11,12	2	63	3.68	3
		F.GLARVADPDHDHTGFLT@EY@VATRWY.R	Y185			11,14	2		3.83	3
		F.GLARVADPDHDHTGFLTEY@VATRWY.R	Y185			12,13	2		4.94	3
		F.GLARVADPDHDHTGFLT^EY@VATRW.Y	Y185			11,12	2		2.83	3
		F.GLARVADPDHDHTGFLT^EY@VATRWY.R	Y185			11,12,13	3		4.65	3
		F.GLARVADPDHDHT^GFLTEY@VATRW.Y	Y185			16	1		3.04	3
		R.VADPDHDHTGFLT@EY@VATR.W	Y185			1,2,4,5,6,7,8,9,10	12		4.31	3
		R.VADPDHDHTGFLTEY@VATR.W	Y185			1,2,3,4,5,6,7,8,9,10	15		5.44	3
							3		3.78	2
		R.VADPDHDHTGFLTEY@VATRW.Y	Y185			12,13,14	3		4.54	3
		R.VADPDHDHTGFLTEY@VAT^R.W	Y185			3,4	2		2.91	3
		R.VADPDHDHTGFLT^EY@VATR.W	Y185			1,2,4,5,7,8,9,10	11		5.85	3
							3		3.80	2
		R.VADPDHDHTGFLT^EY@VATRW.Y	Y185			13,14	2		4.86	3
Mitogen-activated protein kinase 7 -- ERK5	Q9WVS8	R.GLC*TSPAEHQYFM#TEY@VATR.W	Y221	N	U	4	1	7	3.69	3
		R.GLC*TSPAEHQYFMTEY@VATR.W	Y221			1,2,4,6,9	6		4.55	3
Mitogen-activated protein kinase 8 -- JNK1	Q91Y86	R.TAGTSFMMTPY@VVTR.Y	Y185	N	U	3	1	1	3.20	2
Mitogen-activated protein kinase 9 -- JNK2	Q9WTU6	R.TAC*TNFMMTPY@VVTR.Y	Y185	N	U	4	1	1	2.39	2
Mitogen-activated protein kinase 14 -- MAP kinase p38 alpha	P47811	F.GLARHTDDEM#TGY@VATRW.Y	Y181	N	U	11,12,13,15,16,18	6	47	4.51	3
		F.GLARHTDDEMTGY@VATRW.Y	Y181			11,12,13,14,15,18	1		2.76	2
							13		4.87	3
		F.GLARHTDDEMTGY@VATRWY.R	Y181			11,12	2		3.75	3
		L.ARHTDDEMTGY@VATRW.Y	Y181			11	1		4.56	3
		L.DFGLARHTDDEMTGY@VATRW.Y	Y181			11	1		5.57	3
		R.HTDDEM#TGY@VATR.W	Y181			1,2,6,8,10	5		3.64	2
		R.HTDDEMTGY@VATR.W	Y181			1,2,3,4,6,7,8,9	5		3.62	3
							13		4.80	2

Serine/threonine-protein kinase PAK 2	Q8CIN4	K.LRTIVSIGDPKKKYTRY@EK.I	Y252	N*	U	5	1	1	2.50	3
Serine/threonine-protein kinase -- PFTAIRE-1	O35495	K.LEKLGEGS@Y@ATVYK.G	Y146	N*	U	4	1	1	3.89	2
Serine/threonine-protein kinase -- PCTAIRE-3	Q04899	K.LDKLGEGTY@ATVFK.G	Y132	N*	U	2	1	1	2.78	3
Serine/threonine-protein kinase -- PRP4	Q61136	C.DFGS@AS@HVADNDITPY@LVSRFY.R	Y849	N	C	16	1	46	3.25	3
		F.GSASHVADNDITPY@LVSRF.Y	Y849			13,14	2		4.38	2
		F.GSASHVADNDITPY@LVSRFY.R	Y849			14	1		4.78	2
		H.VADNDITPY@LVSRF.Y	Y849			11,12,13,15,16,18	6		4.14	2
		H.VADNDITPY@LVSRFY.R	Y849			11,12,15,16,18	6		4.78	2
		K.LC*DFGSASHVADNDITPY@LVSR.F	Y849			1,2,3,4,5,6,7,8,9,10	16		6.43	3
							10		5.41	2
		K.LCDFGSAS@HVADNDITPY@LVSR.F	Y849			1	1		4.60	3
		L.C*DFGSASHVADNDITPY@LVSRF.Y	Y849			13,15	2		4.11	3
		S.HVADNDITPY@LVSRFY.R	Y849			16	1		2.85	2
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.FNSYNNAGM#PPFPIIIHDEPSY@AR.S	Y613	N*	U	10	1	1	3.40	3
		K.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638			1,2,3,4	4		4.89	3
		K.NAIKVPIVINPNAY@DNLAIYK.S	Y632	N	C	1,2,3,4	3	13	5.59	3
							3		4.64	2
		K.NAIKVPIVINPNAYDNLAIY@K.S	Y638	N	C	3	1	5	4.79	3
		K.VPIVINPNAY@DNLAIYK.S	Y632			1,3,4	3		5.03	2
Protein phosphatases										
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	N*	C	4,8,10	4	4	3.10	2
Receptor-type tyrosine-protein phosphatase alpha -- R-PTP-alpha	P18052	K.VVQEYIDAFSDY@ANFK.-	Y825	N	U	1,2,3,4,5,7,9,10	4	28	3.79	3
							12		6.22	2
		Y.IDAFSDY@ANFK.-	Y825			11	1		2.65	2
		Y.KVVQEYIDAFSDY@ANF.K	Y825			11	2		4.57	2
		Y.KVVQEYIDAFSDY@ANFK.-	Y825			11,12,13,15,16,18	5		5.88	2
							4		4.55	3
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	N	C	11,16	2	9	3.20	2
		K.IQNTGDY@YDLYGGEK.F	Y62			3,4,6,7,8,10	7		4.29	2
		R.EDSARVY@ENVGLMQQQR.S	Y584	N	U	3	1	2	3.30	3
		R.VY@ENVGLMQQQR.S	Y584			4	1		3.02	2
SIGNALING: SMALL G PROTEINS AND REGULATORS										
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	14	28	3.49	3
							14		5.15	2
		W.MPQDGFDPSDY@AEPMDAVVKPRNEEENIY.S	Y925	N	U	11	1	1	4.11	3
Breast cancer anti-estrogen resistance protein 3 -- BCAR3	Q9QZK2	F.IFRDPY@LLDPTLEY.V	Y103	Y	U	11	1	7	3.51	2
		F.IFRDPY@LLDPTLEYVKF.S	Y103			11	1		3.60	2
		Y.LLDPTLEY@VKF.S	Y111	N*	U	11	1	2	3.16	2
		R.KGENFIFRDPY@LLDPTLEY@VK.F	Y103,Y111			4	1		2.80	3
		R.KGENFIFRDPY@LLDPTLEYVK.F	Y103			2,4,5,7	4		4.09	3
		L.RLSEAY@SRVQY.Q	Y206	Y	U	11,12,13	3	3	3.27	2
ARF GTPase-activating protein -- GIT1	Q68FF6	R.SQSELDDQHDY@DS@VAS@DEDTDQEPLPSAGATR.N	Y392	Y	U	8,9	2	4	4.87	3
		R.SQSELDDQHDY@DS@VAS^DEDTDQEPLPSAGATR.N	Y392			8,9	2		5.47	3
		F.HSTELEDDAIY@SVHVPAGLY.R	Y554	N	C	11,12,13,15,16,18	6	17	5.28	2
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554			7	1		3.89	3
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554			1,2,3,4,5,7,9,10	9		6.25	3
		R.LQPFHST^ELEDDAIY@SVHVPAGLYR.I	Y554			7	1		3.60	3
ARF GTPase-activating protein -- GIT2	Q9JLQ2	K.QNSTPESDY@DNTAC*DPEPDDTGSTR.K	Y541	N	U	2,4,6	3	4	4.92	3
		K.QNSTPESDY@DNTAC*DPEPDDTGSTRK.G	Y541			3	1		3.17	3
Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	K.LQQTY@SALNSK.A	Y1510	N	C	3	1	1	2.29	2
Ras and Rab interactor 1 -- Rin1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	N	C	4,7,9	4	4	2.61	2
Rho-GTPase-activating protein 12	Q8C0D4	M.RATT@PPNQGRPDS@PVY@ANLQEL.K	Y241	N	C	15,16	2	14	3.39	3
		M.RATTPPNQGRPDS@PVY@ANLQEL.K	Y241			13	1		3.16	3
		R.AT@TPPNQGRPDS@PVY@ANLQELK.I	Y241			4	1		3.86	3
		R.AT@TPPNQGRPDS^PVY@ANLQELK.I	Y241			4	1		2.70	3
		R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241			2,3,4,6,7,8,9,10	9		4.44	3
SIGNALING: OTHER										
Abl interactor 1 -- Abi-1	Q8CBW3	K.TLEPVKPPTVPNDY@MTSPAR.L	Y212	N	U	4	1	7	2.82	3

						1		4.25	2
		R.NTPY@KTLEPVKPPTVPNDY@MTSPAR.L	Y212			4,7	2	3.70	3
		R.NTPYKT@LEPVKPPTVPNDY@MTSPAR.L	Y212			2	1	3.12	3
		Y.KTLEPVKPPTVPNDY@MTSPARL.G	Y212			12,13	2	4.57	3
Annexin A2	P07356	K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D	Y23	N	C	1,3,4	3	13	4.60	3
		K.LSLEGDHSTPPSAY@GSVKPYTNFDAERDALNIETAVK.T	Y23			4	1		4.73	3
		C.KLSLEGDHSTPPSAY@GSVKPY.T	Y23			12,13	2		3.66	3
		L.SLEGDHSTPPSAY@GSVKPY.T	Y23			11,12,13,16	2		4.45	3
							5		4.27	2
		K.RKY@GKSLYYYIQQDTK.G	Y310	N*	U	4,10	2	2	2.62	3
Ankyrin repeat and SAM domain-containing protein 1 -- ANKS1	P59672	L.AVRPRIQS@SAPQEEEEHPY@EL.L	Y471	N*	C	11	1	7	3.66	3
		L.AVRPRIQS@SAPQEEEEHPY@ELL.L	Y471			16	1		4.43	3
		L.AVRPRIQSSAPQEEEEHPY@EL.L	Y471			11,13,15	3		3.98	3
		L.AVRPRIQSSAPQEEEEHPY@ELL.L	Y471			12	1		3.69	3
		L.AVRPRIQSSAPQEEEEHPY@ELLL.T	Y471			11	1		3.16	3
Calmodulin	P62204	R.VFDKDGNGY@ISAAELR.H	Y99	N	U	2,3,4	5	6	5.06	2
		F.RVFDKDGNGY@ISAAEL.R	Y99			11	1		3.65	2
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	N	C	1,2,3,4,6,8,9	7	7	3.91	2
Caveolin-2	Q9WVC3	F.MADDAYS@HHS@GVDY@ADPEKY.V	Y27	N	U	11,12,15	3	10	4.14	3
		F.MADDAYS@HHS^GVDY@ADPEKY.V	Y27			11	1		3.23	3
		F.MADDAYSHHS@GVDY@ADPEKY.V	Y27			11,12,16	3		3.62	3
		F.MADDAYSHHSGVDY@ADPEKY.V	Y27			11	1		3.60	3
		F.MADDAYS^HHS@GVDY@ADPEKY.V	Y27			12	1		4.00	3
		Y.SHHSGVDY@ADPEKY.V	Y27			11	1		4.16	3
Proto-oncogene c-Crk	Q64010	L.IGGNQEGSHPQPLGGPEPGPY@AQPSVN.T	Y221	N	U	11,12	2	2	3.28	3
		Y.AQPSVNTPLPNLQNGPIY@ARVIQ.K	Y239	N	U	11,13,18	3	3	4.98	3
		K.RVPNAY@DKTALALEVGELVK.V	Y251	N*	C	3	1	2	3.43	3
		Q.KRVPNAY@DKTAL.A	Y251			11	1		2.56	3
Crk-like protein	P47941	Y.VRTLY@DFPGNDAEDLPF.K	Y132	N*	U	16	1	1	3.42	2
		H.GKHGNRNS@NSY@GIPEPAHAY.A	Y198	N*	U	11	1	8	3.59	3
		H.GNRNS@NSY@GIPEPAHAY.A	Y198			11,12,13	3		3.40	2
		H.GNRNSNSY@GIPEPAHAY.A	Y198			13	1		3.26	2
		R.NSNSY@GIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y198			3,4,7	3		5.00	3
		R.NSNSYGIPEPAHAY@AQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y207	N	U	1,2,5,9	5	5	5.30	3
Docking protein 1 (Dok1)	P97465	R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K	Y314	N	C	2,4,7	4	4	4.50	3
		K.KPLYWDLY@GHVQQQLLK.T	Y340	N	C	2,3,4	3	3	4.02	3
		K.LTDSKEDPIY@DEPEGLAPAPPR.G	Y361	N	C	1,2,3,4,5,6,7,8,9,10	17	54	4.06	3
							7		4.73	2
		K.TKLTDSKEDPIY@DEPEGLAPAPPR.G	Y361			1,2,3,4,5,6,7,8,9,10	18		5.71	3
		L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361			11,13,15	4		5.13	3
		L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361			11,12,13,14,15,16,17,18	8		5.23	3
		R.LKEEGYELPYNPATDDY@AVPPPR.S	Y408	N	C	1,2,3,4,6,7,8,9,10	12	12	4.42	3
		F.SSDTALY@SQVQKSGTSGAW.D	Y450	N	C	12	1	3	4.91	2
		K.GFSSDTALY@SQVQK.S	Y450			3,4	2		4.42	2
Ephrin-B2 precursor (Ephrin-B1)	P52800	R.TADSVFC*PHY@EK.V	Y307	N	U	2,3,4,8	4	4	3.57	2
		K.VSGDY@GHPVYIVQEMPPQSPANIYYKV.-	Y314	N	U	2	1	1	3.72	3
		K.VSGDYGHPVY@IVQEMPPQSPANIY@YKV.-	Y319,Y333	N	U	4	2	2	3.45	3
		K.VSGDYGHPVYIVQEM#PPQSPANIY@YKV.-	Y333	N	U	3,4,10	3	14	5.02	3
		K.VSGDYGHPVYIVQEMPPQSPANIY@YKV.-	Y333			1,2,3,4,7,9	9		5.09	3
Fibroblast growth factor receptor substrate 2 -- FRS2	Q8C180	K.LVY@ENINGLSIPSASGVR.R	Y306	N	U	3	1	1	3.94	2
		R.RPALLNY@ENLPSLPPVWEAR.K	Y349	N	U	2	1	2	3.09	3
Fish protein -- TKS5	O89032	K.VKYEEPEY@DVPAFGFDSEPEMNEEPSGDR.G	Y557	N*	U	9	1	1	4.99	3
GRB2-associated binding protein 1 -- Gab1	Q9QYY0	K.HGMNGFFQQQMMY@DC*PPSR.L	Y242	N	U	1,3	2	2	4.86	3
		K.DASSQDC*Y@DIPR.T	Y407	N	U	1,2,3,4,5,6,8,9	10	17	3.28	2
		L.RKDASSQDC*Y@DIPRTF.P	Y407			11,13	2		4.09	3
		N.KLRKDASSQDC*Y@DIPRTF.P	Y407			11	1		2.80	3
		R.KDASSQDC*Y@DIPR.T	Y407			1,2,3	2		3.66	3
							2		3.56	2
Insulin receptor substrate 2 -- IRS-2	P81122	K.SSSSNLGADDGY@MPM#TPGAALR.S	Y649	N	U	3	1	4	2.96	2
		K.SSSSNLGADDGY@MPMTPGAALR.S	Y649			2,3,8	3		5.04	2
		K.SDDY@MPMSPTSVSAPK.Q	Y671	N	U	2	1	1	3.12	2
Insulin receptor substrate-2 (IRS-2) (4PS) homolog [Fragment]	Q3U2I0	R.SYKAPC*SC*SGDDDQY@VLMSSPVGR.I	Y754	Y	U	1,2,3,4,6,7	6	6	5.28	3
Kin of IRRE-like protein 1 precursor	Q80W68	K.AIY@SSFKDDVDLK.Q	Y604	N*	U	3,4	2	3	4.07	2
		K.AIY@SSFKDDVDLKQDLR.C	Y604			3	1		3.54	3

		R.EEYEMKDPTNGY@YNVR.A	Y637	N*	C	8	1	1	3.65	3
		R.AVLY@ADY@RAPGPTR.F	Y654,Y657	N	U	3	2	2	2.76	3
		Y.NVRAHEDRPSSRAVLY@ADY.R	Y654	N	U	11	1	3	2.73	3
		R.TPY@EAYDPIGK.Y	Y753	N*	C	4	1	2	2.57	2
		Y.RLGYPQAPPSGLERTPY@EAYDPIGKY.A	Y753			11	1		4.26	3
		R.TPYEAY@DPIGK.Y	Y756	N	C	1,2,3,4,6,7,8	8	8	3.31	2
myelin protein zero-like 1 -- PZR	Q3TEW6	K.SPPSAGSHQGPVIY@AQLDHSGGHHSGK.I	Y242	N	U	3	1	1	2.84	3
		K.INKSESVVY@ADIR.K	Y264	N	U	2,3,4	1	11	3.20	3
							3		3.74	2
		K.INKSESVVY@ADIRKD.-	Y264			3	1		3.66	3
		K.SESVVY@ADIR.K	Y264			2,3	3		2.39	2
		N.KSESVVY@ADIRKD.-	Y264			11,12	2		3.13	3
		H.SGKINKSESVVY@ADIRKD.-	Y264			11	1		4.99	3
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.RKPS@VPDTASPADDSFVDPGERLY@DLNM#PAFVK.F	Y105	N	C	10	1	4	4.25	3
		K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105			9	1		4.82	3
		K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105			7,9	2		4.10	3
PDZ and LIM domain protein 5	Q8CI51	R.NTEFY@HIPTHSDASK.K	Y251	N	U	8	1	1	2.61	3
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85alpha	P26450	K.SREYDRLY@EEYTR.T	Y467	N	C	3,4,8,9	4	4	3.69	3
		R.DQY@LMWLTQK.G	Y580	N	U	4	1	1	2.14	2
		K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y607	N	C	4	1	1	5.07	3
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85beta	O08908	R.EYDQLY@EEYTR.T	Y458	N	C	7,8	2	2	3.14	2
Protein LAP2	Q80TH2	R.RTEGDY@LSYR.E	Y1097	N	U	1,2,3,4,5,6,8,9	9	13	3.28	2
		R.TEGDY@LSYR.E	Y1097			2,3,6,9	4		2.56	2
SH2 domain-containing adapter protein B -- Shb	Q6PD21	C.RLDY@C*GGGGGGDPGGGQRAF.T	Y113	N	U	11,12,15	3	11	4.74	3
		L.RAMC*RLDY@C*GGGGGGDPGGGQRAF.T	Y113			12	1		3.07	3
		M.C*RLDY@C*GGGGGGDPGGGQRAF.T	Y113			11,12,15	3		5.18	3
		R.LDY@C*GGGGGGDPGGGQR.A	Y113			5,6,8,9	4		5.16	2
		K.C*SAEETGAGQKDKVTIADDY@SDPFDAK.S	Y240	N	U	4,6,9	3	16	4.50	3
		K.DKVTIADDY@SDPFDAK.S	Y240			3,4,6,7,8	3		4.69	3
							4		4.96	2
		K.VTIADDY@SDPFDAK.S	Y240			3,4,8	3		4.12	2
		L.LNKC*SAEETGAGQKDKVTIADDY@SDPF.D	Y240			11,16,18	3		3.30	3
		F.DAKSDLKSKAGKGESAGY@M#EPY.E	Y262	N*	U	11	1	15	3.28	3
		F.DAKSDLKSKAGKGESAGY@MEPY.E	Y262			11	1		2.86	3
		K.AGKGESAGY@M#EPYEAQR.I	Y262			8,10	2		4.11	3
		K.AGKGESAGY@MEPYEAQR.I	Y262			1,2,3,4,8	1		3.89	3
							5		4.83	2
		K.GESAGY@MEPYEAQR.I	Y262			2,3,4	3		3.97	2
		K.SKAGKGESAGY@MEPYEAQR.I	Y262			3	1		2.85	3
		L.KSKAGKGESAGY@MEPY.E	Y262			11	1		3.22	2
		K.LPQDDDRPADEY@DQPWEWNR.V	Y330	N*	U	2,3,4	3	9	5.05	3
		L.RLRESKLPQDDDRPADEY@DQPW.E	Y330			11	1		3.70	3
		R.ESKLPQDDDRPADEY@DQPWEWNR.V	Y330			2,3,4,8,9	5		3.99	3
SHC transforming protein 1 -- SHC1	P98083	K.QM#LPPPPC*PGRELFDDPSY@VNIQNLDK.A	Y423	N	C	3	1	20	4.27	3
		R.ELFDDPSY@VNIQNLDK.A	Y423			1,2,3,4,5,6,7,8,9,10	15		5.46	2
		K.QMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423			1,3,9	3		5.01	3
		R.KQMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423			1	1		4.34	3
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L	Y349,Y350	N	C	1	1	1	4.64	3
		R.MAGFDGSAWDEEEEEPPDHQYY@NDFPGKEPPLGGVVDMR.L	Y350	N	C	1	1	2	3.95	3
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y987	N	C	1,2,3,4,7	8	8	5.12	3
Tyrosine-protein phosphatase non-receptor type substrate 1 -- SHPS1	P97797	Y.ASIETGKVPRPEDTLTY@ADLDMVHL.S	Y481	N	U	15	1	1	3.82	3
Signal transducer and activator of transcription 3 -- STAT3	P42227	K.YC*RPESQEHPEADPGSAAPY@LK.T	Y705	N	C	1,2,3,4,6,7,8,9	9	9	4.10	3
STAT3 splice isoform Del-701	P42227-3	K.YC*RPESQEHPEADPGAAPY@LK.T	Y704	N	U	2,3,4,6,8	5	5	3.62	3
Signal transducer and activator of transcription 5B -- STAT5B	P42232	K.AADGY@VKPQIK.Q	Y699	N	U	3	1	1	2.15	2
ADHESION: CELL/ECM										
CRK-associated substrate -- p130cas	Q61140	K.TQQGLY@QAPGPNPQFQSPPAK.Q	Y132	N	U	4,8	2	2	3.71	3
		R.VGQGYVYEAAQTEQDEY@DTPR.H	Y238	N	C	2,3,4,6,7,9	5	18	5.69	3
							5		5.31	2
		Y.VYEAAQTEQDEY@DTPRHL.L	Y238			11,12,13,15,16,18	5		4.66	3
							3		4.33	2
		R.HLLAPGPQDIY@DVPPVR.G	Y253	N	C	1,2,3,4,5,6,7,8,10	15	32	3.63	3

							16		4.73	2
		L.LAPGPQDIY@DVPPVRGLLPNQY.G	Y253			11	1		3.18	2
		R.GLLPNQYGQEVY@DTPPMAVK.G	Y271	N*	C	1,2,3,4,9	5	6	4.45	2
							1		2.76	3
		K.GPNGRDPLLDVY@DVPPSVEK.G	Y291	N*	C	1,2	2	2	4.30	3
		K.GLLSSSHHSVY@DVPPSVSK.D	Y310	N	C	1,2,3,4	7	7	4.09	3
		K.DVPDGPLLREETY@DVPPAFAKPK.P	Y331	N	U	4	1	1	4.32	3
		R.RPGPGTLY@DVPR.E	Y391	N	C	8,10	2	2	2.43	2
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	N	C	3	1	6	4.17	3
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414			1,4,7,9	5		4.75	2
		L.SRQLQKMEDVY@QTL.V	Y556	Y	C	11	1	1	2.82	2
Enhancer of filamentation 1 -- HEF1	O35177	R.TGHGYVY@EYPSR.Y	Y165	N	U	3	1	1	3.15	2
		K.ANPEERDGVY@DVPLHNPADAK.G	Y344	N*	U	4,8	2	2	4.49	3
Integrin beta-1 precursor	P09055	K.WDTGENPIY@K.S	Y783	N	U	4	1	1	2.09	2
Lipoma-preferred partner homolog - LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	N	C	11,12,13	2	14	3.69	3
							3		4.72	2
		M.AGPSSGQIY@GPGPRGY.N	Y245			11,12,13	3		3.88	2
		Y.MAGPSSGQIY@GPGPRGY.N	Y245			11,12,13,15,18	5		3.87	2
							1		4.33	3
		R.GYNNQPVPVSGQC*PPPPTC*VGTDY@AYIPPSGHPPESGYGYTSNQGR.Y	Y276	N*	U	4	1	1	4.26	3
		R.YYEPY@YAAGPSYGGR.S	Y301	N	C	2,3,4,6,7,8,9,10	8	8	4.36	2
		R.YYEPYY@AAGPSYGGR.S	Y302	N	C	1,2,3,4,6,8,9,10	8	8	4.73	2
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	N	C	11,15,16,18	4	7	3.07	2
		L.SEEPPY@SYPTGNHTY.Q	Y31			11,13	2		2.51	2
		S.KRPVFLSEEPPY@SYPTGNHTY.Q	Y31			11	1		3.41	3
		R.YAHQQPPS@PLPVY@SSSAK.N	Y88	N	U	2,3,4	4	9	3.60	2
		R.YAHQQPPSPLPVY@SSSAK.N	Y88			1,4,6	3		3.06	3
		R.YAHQQPPS^PLPVY@SSSAK.N	Y88			9,10	2		3.27	3
		R.AGEEEHVY@SFPNK.Q	Y118	N	C	1,2,3,4,5,6,7,8,9,10	11	50	4.08	3
							20		4.68	2
		R.AGEEEHVY@SFPNKQK.S	Y118			1,2,3,4,5,6,7,8,9,10	18		4.56	3
							1		3.39	2
Pleckstrin homology domain containing family C member 1	Q8CIB5	L.IMPGSGSIY@SSPGLY.S	Y179	N*	U	11	1	1	2.86	2
Syndecan-4 precursor	O35988	K.KAPTNEFY@A.-	Y197	N*	C	3	1	4	1.85	2
		Y.KKAPTNEFY@A.-	Y197			12,13,15	3		2.95	2
Talin 1	P26039	K.TM#QFEPSTMVY@DAC*R.M	Y26	N*	C	3	1	8	4.07	2
		K.TMQFEPSTMVY@DAC*R.M	Y26			1,2,3,6	4		4.88	2
		M.QFEPSTMVY@DAC*RM.I	Y26			11,12,15	3		3.24	2
		F.LSDDDPKKGIWLEAGKALDY@Y.M	Y70	N*	C	11,12,15,18	4	12	4.32	3
		K.ALDY@YM#LR.N	Y70			3,10	2		2.70	2
		K.ALDY@YMLR.N	Y70			2,3,8	3		2.83	2
		W.LEAGKALDY@Y.M	Y70			12,15,16	3		3.14	2
		R.IGITNHDEY@SLVR.E	Y127	N*	U	3	1	2	2.52	2
							1		3.22	3
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	N	C	2,3,4,6	4	4	5.20	2
Tensin	Q9DBT6	R.HAAY@GGY@STPEDR.R	Y213,Y216			10	1		3.22	2
		R.HAAY@GGYSTPEDR.R	Y213	N	U	1,6	2	3	3.04	2
		R.HAAYGGY@STPEDR.R	Y216	N	U	2,3,8,9,10	5	7	4.14	2
		R.HAAYGGY@STPEDRRPT^LSR.Q	Y216			8	1		2.72	3
Tensin 2	Q8CJ95	H.TRGPLDGSPY@AQVQ.R	Y460	N	U	11	1	11	2.77	2
		L.AHTRGPLDGSPY@AQVQ.R	Y460			11	1		3.56	2
		R.GPLDGSPY@AQVQR.V	Y460			1,2,3,4,5,6,8	9		3.57	2
		K.VGEEGHEGC*SY@AVC*SEGR.Y	Y747	N*	U	2,3	2	2	3.73	3
Tensin 3	Q5SSZ5	L.HTQGPVDGSLY@AKVR.K	Y354	N	C	12	1	1	3.65	3
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	N*	C	3,4	2	2	5.12	3
Vinculin	Q64727	R.ILLRNPGNQAAY@EHFETMK.N	Y691	N*	C	1,3,4	3	3	6.55	3
		K.SFLDSGY@R.I	Y821	N*	U	1,2,3,4,6,7,8,9,10	15	15	2.69	2

ADHESION: CELL/CELL

Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M	Y96	N	C	3,4,5,6,8,9,10	2	12	3.82	2
							10		4.57	3
		R.HYEDGYPGGSDNY@GSLSR.V	Y228	N	C	3,4,6,7,8,9,10	7	12	5.22	3
							4		4.31	2
		R.HYEDGYPGGSDNY@GS^LSR.V	Y228			2	1		3.35	2
		R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R	Y291,Y296	N,N	C,C	9	1	1,1	5.57	3
		K.SDNNY@STLNER.G	Y877	N*	U	2,5	2	2	3.07	2
Ctnnd1 protein -- p120 catenin, isoform	Q80XQ4	K.SLDNNY@STLNER.G	Y904	Y	U	1,2,3,4,6,8	6	6	3.78	2

Discs large homolog 3	P70175	R.RDNEVDGQDY@HFVVSR.E	Y705	N*	U	2,3,4	3	3	4.34	3
Fath protein [fragment]	Q497H5	K.NIY@SDIPPQVPVRPISYTPSIPSDSR.N	Y952	N*	U	2,3,4	3	3	3.77	3
Partitioning-defective 3 homolog -- PARD3	Q99NH2	R.ISHSLY@SGIEGLDESPTR.N	Y719	Y	U	3,4	1	6	4.16	3
							2		5.37	2
		R.RIS@HSLY@SGIEGLDESPTR.N	Y719			2	1		3.50	3
		R.RISHS@LY@SGIEGLDESPTR.N	Y719			4	1		4.25	3
		R.RISHSLY@SGIEGLDESPTR.N	Y719			1	1		3.02	3
		R.ERDY@AEIQDFHR.T	Y1076	N*	U	4	1	1	2.77	3
		R.EGHLMDTLY@AQVK.K	Y1123	N	U	3	1	1	3.41	2
		R.KNASSISQDSWEQNY@APGEGFQSAK.E	Y1238	N*	U	2,3,4,8	4	4	4.96	3
Plakophilin-4; Armadillo related protein	Q68FH0	R.TVHDMDQFGQQQYDIY@ER.M	Y371	N*	C	4	1	1	3.34	3
		L.RSAVSPDLHITPIY@EGRTY.Y	Y414	N	C	11	1	1	4.07	3
		R.NNY@ALNTAATY@AEPYRPVQYR.V	Y469,Y477	Y	U	2,3,4	3	3	4.49	3
		R.NNYALNTAATY@AEPYRPVQYR.V	Y477	N	U	3,5,7,8,9,10	6	11	3.50	3
		Y.ALNTAATY@AEPY.R	Y477			11,15	2		2.89	2
		R.SY@EDPYC*DDRVHFPAST@DYSTQYGLK.S	Y1137	N*	U	2	1	2	4.65	3
		R.SY@EDPYC*DDRVHFPASTDYSTQYGLK.S	Y1137			3	1		5.23	3
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	N	C	3	1	1	2.21	2
Tight junction protein ZO-1	P39447	Y.LSAPGSEY@SMY.S	Y830	N*	C	11	1	1	2.30	2
		R.HEEQPAPAY@EVHNR.Y	Y1164	N	C	1,2,3,6,8,10	6	6	4.58	3
Tight junction protein ZO-2	Q9Z0U1	R.IEIAQKHPDIY@AVPIK.A	Y1095	N	C	3,4,5	3	3	2.99	3
CYTOSKELETON: ACTIN-ASSOCIATED										
Actins and actin-related proteins; Regulators of actin assembly										
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	K.IWHHTFY@NELR.V	Y93	N	C	2,8,9	3	3	2.86	3
		M.VGMGQKDSY@VGDEAQSKRGIL.T	Y55	N	C	11	1	1	5.32	3
Cofilin-1, non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C	Y139	N	C	1,2,3,4,5,6,7,8	8	11	4.82	3
		K.LTGIKHELQANC*Y@EEVKDR.C	Y139			4	1		4.41	3
		L.TGIKHELQANC*Y@EEVKDRC*TL.A	Y139			11,13	2		3.61	3
Src substrate cortactin	Q60598	Y.TSEPVY@ETTEAPGHY.Q	Y466	N	C	11,12,13,14,15,16,17,18	1	9	3.87	3
							8		3.47	2
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R	Y39	N	C	11	1	5	3.52	2
		R.VQIY@HNPTANSFR.V	Y39			2,3,4	1		2.80	3
							3		3.96	2
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.DRETSKVIY@DFIEK.T	Y253	N	C	1,2,3	3	9	3.37	3
		K.VIY@DFIEK.T				1,2,3,4,6,7	6		3.08	2
WD-repeat protein 1; Actin interacting protein 1 -- AIP1	O88342	K.AHDGGIY@AISWSPDSTHLLSASGDK.T	Y237	N	C	9	1	1	5.53	3
Other actin-associated proteins										
Band 4.1-like protein 2	O70318	N.TLRVDGDNIY@VRHSNL.M	Y606	N	U	11,12	2	4	4.28	3
		R.VDGDNIY@VR.H	Y606			3,5	2		2.73	2
Calponin-2	Q08093	K.CASQSGMTAY@GT@RR.H	Y184	N*	U	1	1	1	2.64	3
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q	Y316	Y	C	11	1	1	2.26	2
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	N	C	11,12	2	3	3.77	3
							1		4.28	2
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	N	C	2,3,4,6	4	5	4.35	3
		K.QQPTQFINPETPGY@VGFANLPNQVHRK.S	Y17			3	1		2.82	3
Sickle tail-b (Sickle tail-a)	Q75UV8	R.NVY@YELNDVR.N	Y244	Y	U	1,2,3,4,8	5	5	3.47	2
		R.NEGFY@ADPYLYHEGR.M	Y393	Y	U	3,6,8,9	3	5	3.56	3
							2		3.29	2
CYTOSKELETON: MICROTUBULE-ASSOCIATED										
none										
CYTOSKELETON: OTHER										
Vimentin	P20152	R.FANY@IDKVR.F	Y116	N*	U	3,4,5	3	3	2.74	2

		R.SLY@SSSPGGAYVTR.S	Y52	N	C	2,3	2	2	3.68	2
TRAFFICKING/TRANSPORT										
Vesicle transport										
Double C2-like domain containing protein beta	P70169	K.TY@LKPDVDKKSK.H	Y309	Y	U	4	1	2	2.33	2
		K.TY@LKPDVDKKS^K.H	Y309			6	1		2.99	2
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	N	C	1,2,3,4,5,6,7,8,9,10	15	15	3.76	2
Low-density lipoprotein receptor precursor	P35951	F.DNPVY@QKTTEDELHIC*RSQDGY.T	Y832	N*	U	11	1	1	3.74	3
Nucleoporin-like protein RIP	Q8K2K6	K.AGLQTADKY@AALANLDNIFSAGQGGDQGSGFGTTGK.A	Y327	N*	U	4	1	1	6.08	3
Transferrin receptor protein 1 -- TfR	Q62351	F.SNLFGGEPLSY@TRF.S	Y20	N	U	12,15,16,18	4	7	3.99	2
		R.SAFSNLFGGEPLSY@TR.F	Y20			4,6,7	3		4.36	2
Nucleocytoplasmic transport										
None										
Other transport										
Gap junction alpha-1 protein -- Connexin 43	P23242	K.QASEQNWANY@SAEQNR.M	Y312	N*	U	2,3	1	2	2.94	2
							1		3.68	3
Lysosomal-associated transmembrane protein 4A	Q60961	K.IPEKEPPPPY@LPA.-	Y230	N*	U	3,4	3	3	2.56	2
Sodium bicarbonate cotransporter 2B homolog [fragment]	Q8BTY2	K.DKDSDKEDGRES@PSY@DTPSQR.V	Y92	Y	U	8	1	2	3.62	3
		K.DKDS^DKEDGRESPSY@DTPSQR.V	Y92			8	1		2.50	3
Solute carrier family 38, member 2	Q8CFE6	K.SHY@ADVDPENQNFLLESNLGK.K	Y41	N*	U	2,4	2	7	4.98	3
		K.SHY@ADVDPENQNFLLESNLGKK.K	Y41			2,3,4	3		5.04	3
		L.KSHY@ADVDPENQNF.L	Y41			11,12	2		4.14	2
METABOLIC AND BIOSYNTHETIC ENZYMES										
Glycolytic enzymes										
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G	Y24	N	C	9	1	1	3.83	2
		R.AAVPSGASTGIY@EALELR.D	Y43	N	C	1,2,3,4,9	6	6	5.24	2
Glyceraldehyde-3-phosphate dehydrogenase -- GAPDH	P16858	K.LISWYDNEY@GYSNR.V	Y315	N	C	1,2,3,4,6,9	8	8	4.40	2
Phosphoglycerate mutase 1	Q9DBJ1	R.FSGWY@DADLSPAGHEEAKR.G	Y25	N	C	4,9	2	2	3.93	3
Pyruvate kinase, isozyme M2	P52480	R.EAEAAIY@HLQLFEELRR.L	Y389	N	C	9	1	1	2.56	3
Other metabolic/biosynthetic enzymes										
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	R.VC*MVY@DLYPTLTPLAVAYAR.A	Y290	N*	C	9	1	1	4.21	3
Serine hydroxymethyltransferase, cytosolic	P50431	K.MLSQPLKDSDAEVY@SIIKK.E	Y28	N*	C	9	1	1	4.18	3
TK: Transketolase	P40142	K.NMAEQIIQEIY@SQVQSK.K	Y275	N	C	5	1	1	3.39	3
RNA SYNTHESIS AND PROCESSING										
Transcription machinery and regulation										
Polymerase I and transcript release factor	O54724	F.KVMIY@QDEVKLPAKL.S	Y158	N*	C	12,13	2	3	5.14	3
		K.VMIY@QDEVKLPAK.L	Y158			4	1		3.05	2
		F.TPDHVVY@ARSKTAVY.K	Y310	N	C	11,12	2	7	2.68	3
		K.SFTPDHVVY@AR.S	Y310			3,4,8	3		3.00	2
		R.KSFTPDHVVY@AR.S	Y310			3,5	2		2.99	3
DEAD(DEAH)-box helicases							3			
ATP-dependent RNA helicase DDX3X	Q62167	R.GRGDY@DGIGGR.G	Y103	N	C	3	1	3	3.08	2
		R.GRGDY@DGIGGRGDR.S	Y103			1,2	2		3.00	3
hnRNPs and snRNPs										
none										
Splicing factors										

none										
Other RNA binding and processing										
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232	Y	C	11	1	1	2.85	3
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S	Y124	N*	C	2,4,8	3	4	4.19	3
		Y.DSRPGGYGY@GY.G	Y124			11	1		1.98	2
		R.YDSRPGGYGYGY@GR.S	Y126	N	C	10	1	1	2.63	3
		R.YSGGNYRDNY@DN.-	Y151	N	U	5	1	1	2.54	2
RNA-binding protein 14	Q8C2Q3	R.LPDAHSDY@AR.Y	Y645	N*	U	7	1	1	2.00	2
PROTEIN SYNTHESIS AND PROCESSING										
tRNA synthetases										
None										
Translation machinery										
40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	N	C	7,9	2	2	2.96	2
60S acidic ribosomal protein P0	P14869	K.IIQLLDDY@PK.C	Y24	N	U	2,3,4,7,10	5	5	3.41	2
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.GDPQVYEELFSY@AC*PK.F	Y415	N*	C	9	1	1	4.00	2
Eukaryotic initiation factor 4A-I	P60843	R.GFKDQIY@DIFQK.L	Y197	N*	C	9	1	1	3.51	2
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	11	11	3.08	2
		R.EHALLAY@TLGVK.Q	Y141	N	C	3,4,8,9	4	4	3.34	2
Laminin receptor 1 (ribosomal protein SA)	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	N	C	1,2,4	3	3	5.52	3
G1 to phase transition 2 -- GSPT2	Q9CY91	K.Y@LIVLINK.M	Y347	Y	C	5	1	1	2.08	2
Post-translational modifiers										
Probable palmitoyltransferase ZDHHC5	Q8VDZ4	R.EPS@PVRY@DNLSR.H	Y533	Y	U	6	1	2	2.55	3
		R.LLPTGPPHREPS@PVRY@DNLSR.H	Y533			3	1		3.00	3
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	F.SPVLGPRPREPS^PVRY@DNL.S	Y538	Y	U	13	1	3	2.51	3
		R.PREPS^PVRY@DNLSR.T	Y538			5,8	2		3.18	3
		L.RSQTDSLFGDSGVY@DTPSSY.S	Y576	N*	C	12,13,15,16,18	5	5	5.17	2
Chaperones and associated proteins							4			
BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I	Y246	N	C	4	1	1	2.59	3
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I	Y336	N	C	9	1	1	2.71	3
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	N	C	3,4	2	2	2.62	2
PROTEIN DEGRADATION										
Ubiquitin conjugation regulators										
E3 ubiquitin protein ligase CBL	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L	Y672	N	C	2,5,7,9	4	4	3.55	3
E3 ubiquitin-protein ligase CBL-B	Q3TTA7	R.ASQDY@DQLPSSSDGSQAPARPPKPR.P	Y889	N	U	3,4	2	2	3.97	3
Probable E3 ubiquitin-protein ligase MGRN1	Q9D074	L.RAVSPAIPSAPLY@EEITY.S	Y389	N	U	12	1	1	4.07	2
Proteasome components										
Proteasome subunit alpha type 2 -- PSMA2	P49722	K.HIGLVY@SGMGPDYR.V	Y75	N*	C	9	1	1	4.72	2
Other proteases and endopeptidases										
ADAM 9 precursor	Q61072	K.ISSQGNLIPARPAPAPPLY@SSLT.-	Y841	N*	U	3	1	2	3.11	2
		N.LIPARPAPAPPLY@SSLT.-	Y841			11	1		3.06	2
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	N*	C	3	1	1	2.31	2

NUCLEAR PROTEINS										
Histone H2B type 1-B	Q64475	R.KESYSVY@VYK.V	Y41	N*	U	8	1	1	3.14	2
MISCELLANEOUS										
Microfibril-associated glycoprotein 3 precursor	Q922T2	R.IKERPALDAQSGIY@VINPELGR.S	Y277	N*	U	3	1	1	3.28	3
Psychosine receptor	Q61038	R.Y@LAVVYPLK.F	Y115	N*	U	2,6	2	2	2.24	2
FUNCTION UNKOWN OR UNCERTAIN										
Named proteins of unknown/uncertain function										
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213	N	C	3,4,5,7,8	6	6	5.88	3
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	Q9DBJ3	K.MIGKDY@DTLSK.Y M.IGKDY@DTLSKY.S	Y274 Y274	N*	U	2,3 11	2 1	3	3.31 3.13	2 2
Suppression of tumorigenicity 5	Q924W7	K.STLEENAYEDIVGGLPKENPY@EDVDLK.N	Y498	N*	C	3	1	1	3.90	3
Pituitary tumor-transforming gene 1 protein-interacting protein precursor	Q8R143	F.KEQNPY@EKF.- K.EQNPY@EKF.-	Y171 Y171	N*	U	11,13,14 2,3	3 2	5	2.88 2.18	2 2
WW domain binding protein 4	Q3TWW5	K.FGDY@C*K.C K.S^QPKKFGDY@C*K.C	Y15 Y15	Y	U	4,5,10 10	3 1	4	2.90 3.05	2 3
Unnamed proteins of unknown/uncertain function										
hypothetical protein --Ccdc105	Q9D4K7	K.FNQEM#Y@VTRGIIK.G	Y372	Y	U	5,7,8	2 1	3	2.66 2.61	2 3
hypothetical HAT dimerisation/BED finger/Bipartite nuclear localization signal/Zinc finger BED-type profile containing protein	Q3UMD3	W.HFFHVDPQY@TW.R	Y145	Y	U	12,15	2	2	3.42	2
hypothetical Intradiol ring-cleavage dioxygenase/WD40-like containing protein	Q3UHA3	R.YNEMTY@IFDLLHQK.H	Y2161	N	U	10	1	1	2.51	2
MKIAA1686 protein [fragment]	Q6ZPK1	K.ERPISMINEASNY@NMASDY@AVHPMSPVGR.T	Y65,Y71	Y,Y	U,U	2,3	2	2,2	3.77	3
PREDICTED: similar to Oligophrenin 1	UPI00005125B7	K.LWLEAMDGKEPIY@TLPAIISK.K R.KLWLEAM#DGKEPIY@TLPAIISK.K R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371 Y371 Y371	Y	C	2,3 4 2,4,5	2 1 3	6	4.05 4.81 4.28	3 3 3
PREDICTED: similar to zinc finger CCCH type containing 11A isoform 1	UPI00001C484B	R.IPFS@KTY@SKTEK.V	Y399	Y	U	1,2	2	2	4.02	2
Protein KIAA1914	Q5DTU0	K.VAQQPLSLVGC*DVLPDPSPDHLY@SFR.I	Y413	Y	U	1,3	2	2	3.96	3
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	Y	C	6	1	1	3.23	3

END

Table S1. Phosphotyrosine sites from the nontransformed mouse embryo fibroblast population

Protein Name(s)[a]	UniProt #[a]	Peptide[b]	pY site(s)[b]	MH[h]	dM[h]	dCn 2nd ranked peptide[i]
SIGNALING: PROTEIN KINASES AND PHOSPHATASES						
Tyrosine kinases (nonreceptor)						
Proto-oncogene tyrosine-protein kinase -- Src (Yes, Fyn, Hck)	Q80XU2	R.LIEDNEY@TAR.Q	Y418	1304.00	0.41	0.0714 R.LIEDNEYT@AR.Q
		F.LEDYFTSTEPQY@QPGENL.-	Y529	2211.47	0.52	none
		Y.FTSTEPQY@QPGENL.-	Y529	1692.24	1.50	none
Proto-oncogene tyrosine-protein kinase -- Fyn (Yes)	P39688	R.KLDNGGYY@ITTR.A	Y213	1481.13	0.40	0.0107 R.KLDNGGY@YITTR.A
		F.LEDYFTATEPQY@QPGENL.-	Y527	2196.52	1.56	none
		F.TATEPQY@QPGENL.-	Y527	1528.09	0.42	none
		Y.FTATEPQY@QPGENL.-	Y527	1676.10	1.36	none
Fyn-related kinase -- Frk	Q922K9	F.C*PPEAPRSQEPERSHGQY@F.V	Y53	2352.86	0.86	0.1624 F.C*PPEAPRSQEPERS@HGQYF.V
		R.SQEPERSHGQY@FVALFDYQAR.T	Y53	2608.70	0.50	0.1015 R.SQEPERS@HGQYFVALFDYQAR.T
		K.LEDYFETDC*SY@SDTNNFIN.-	Y504	2426.95	0.04	0.0522 K.LEDYFETDC*S@YSDTNNFIN.-
		W.KLEDYFETDC*SY@SDTNNFIN.-	Y504	2555.44	0.43	0.0306 W.KLEDYFETDC*S@YSDTNNFIN.-
				2557.37	2.35	0.0340 W.KLEDYFETDC*S@YSDTNNFIN.-
		W.KLEDYFETDCS@Y@SDTNNFIN.-	Y504	2578.11	0.10	0.0670 W.KLEDYFETDCS@YS@DTNNFIN.-
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	2366.97	1.90	none
		F.GMSRQEDGGVY@SSSGL.K	Y715	1710.37	0.65	0.1358 F.GMSRQEDGGVYS@SSGL.K
Proto-oncogene tyrosine-protein kinase ABL1	P00520	M.TGDTY@TAHAGAKFPIKW.T	Y393	1944.63	0.69	0.0372 M.TGDTYT@AHAGAKFPIKW.T
		R.LMTGDTY@TAHAGAK.F	Y393	1517.51	0.83	0.1036 R.LMTGDT@YTAHAGAK.F
Activated CDC42 kinase 1 -- ACK	O54967	M.RALPQNDDHY@VMQEH.R	Y284	1933.78	0.94	none
				1933.29	0.45	none
		W.DARPLPPPPAY@DDVAQDEDDF.E	Y650	2425.38	2.34	none
		F.ASDPKY@ATPQVIQAPGPRAGPC*.I	Y842	2362.09	0.97	0.0254 F.AS@DPKYATPQVIQAPGPRAGPC*.I
		K.VSSTHY@YLLPERPPYLER.Y	Y874	2301.01	0.87	0.0723 K.VSSTHYY@LLPERPPYLER.Y
		R.KVSSTHY@YLLPERPPYLER.Y	Y874	2429.74	1.50	0.0733 R.KVSST@HYYLLPERPPYLER.Y
		R.KVSS@THYY@LLPERPPYLER.Y	Y875	2509.73	1.49	0.0046 R.KVSSTHY@Y@LLPERPPYLER.Y
Activated CDC42 kinase 1 -- ACK, isoforms 2 and 3	O54967-2	H.LGRVKKPTY@DPVSEDPDPLSSDF.K	Y518	2642.93	0.66	0.0150 H.LGRVKKPT@YDPVSEDPDPLSSDF.K
		K.KPTY@DPVSEDPDPLSSDFKR.L	Y518	2374.59	1.49	0.0228 K.KPT@YDPVSEDPDPLSSDFKR.L
		L.GRVKKPTY@DPVSEDPDPLSSDF.K	Y518	2529.88	0.69	0.0319 L.GRVKKPT@YDPVSEDPDPLSSDF.K
		R.VKKPTY@DPVSEDPDPLSSDFK.R	Y518	2446.27	2.11	0.0007 R.VKKPT@YDPVSEDPDPLSSDFK.R
		R.VKKPTY@DPVSEDPDPLSSDFKR.L	Y518	2601.34	1.08	0.0025 R.VKKPT@YDPVSEDPDPLSSDFKR.L
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	M.RTHAVSVSETDDY@AEIIDEEDTY.T	Y397	2738.87	0.70	none
				2739.94	1.76	none
		R.THAVSVSETDDY@AEIIDEEDTYTMPSTR.D	Y397	3256.66	1.27	0.0605 R.THAVSVSET@DDYAEIIDEEDTYTMPSTR.D
		R.Y@MEDSTY@YK.A	Y570,Y576	1359.75	0.26	0.1144 R.Y@MEDST@YYK.A
		R.Y@MEDSTY@YKASK.G	Y570,Y576	1645.52	-0.14	0.0743 R.Y@MEDST@YYKASK.G
		R.Y@MEDSTY@Y@KASK.G	Y570,Y576,Y577	1725.34	-0.32	0.0530 R.Y@MEDST@YY@KASK.G
		F.GLSRYM#EDSTY@Y.K	Y576	1581.12	0.48	0.1391 F.GLSRYM#EDST@YY.K
		F.GLSRYMEDSTY@Y.K	Y576	1565.84	1.20	0.1660 F.GLSRYMEDST@YY.K
		L.GDFGLSRYM#EDSTY@Y.K	Y576	1900.27	0.52	0.0740 L.GDFGLSRYM#EDST@YY.K
		L.GDFGLSRYMEDSTY@Y.K	Y576	1883.90	0.14	0.1288 L.GDFGLSRYMEDST@YY.K
		R.YM#EDST@YY@KASK.G	Y577	1661.93	0.26	0.0032 R.YM#EDSTY@Y@KASK.G
		R.YM#EDSTY@Y@K.A	Y576,Y577	1375.66	0.17	0.0687 R.YM#EDST@YY@K.A
		R.YM#EDSTY@Y@KASK.G	Y576,Y577	1662.03	0.37	0.0785 R.YM#EDST@YY@KASK.G
		R.YM#EDSTY@YK.A	Y576	1296.10	0.61	0.0660 R.YM#EDSTYY@K.A
		R.YM#EDSTY@YKASK.G	Y576	1581.58	-0.08	0.0059 R.YM#EDST@YYKASK.G
		R.YM#EDSTYY@K.A	Y577	1296.09	0.60	0.0690 R.YM#EDSTY@YK.A
		R.YMEDSTY@Y@K.A	Y576,Y577	1359.28	-0.21	0.0628 R.YMEDST@YY@K.A
		R.YMEDSTY@Y@KASK.G	Y576,Y577	1646.24	0.58	0.1020 R.YMEDST@YY@KASK.G
		R.YMEDSTY@YK.A	Y576	1279.92	0.43	0.0734 R.YMEDSTYY@K.A
				1280.38	0.89	0.0088 R.YMEDSTYY@K.A
		R.YMEDSTY@YKASK.G	Y576	1566.08	0.42	0.0447 R.YMEDST@YYKASK.G
		R.YMEDSTYY@K.A	Y577	1279.12	-0.37	0.0949 R.YMEDSTY@YK.A
		Y.M#EDSTY@Y@KASKGKLPIKW.M	Y576,Y577	2322.87	1.77	0.0124 Y.M#EDST@YY@KASKGKLPIKW.M
		Y.MEDSTY@Y@KASKGKLPIKW.M	Y576,Y577	2305.61	0.51	0.0572 Y.MEDST@Y@YKASKGKLPIKW.M
Tyrosine-protein kinase JAK1	P52332	K.AIETDKEY@Y@TVKDDR.D	Y1033,Y1034	2006.36	0.47	0.1350 K.AIETDKEY@YT@VKDDR.D
Tyrosine kinases (receptor)						
Discoidin domain receptor 2 precursor -- DDR2	Q62371	R.IFPLRPDY@QEPSR.L	Y481	1698.03	0.19	none
		Y.DRIFPLRPDY@QEPSRL.I	Y481	2082.93	0.88	0.1556 Y.DRIFPLRPDYQEPS@RL.I
		R.NLY@SGDY@YR.I	Y735,Y739	1310.97	0.44	0.1549 R.NLY@SGDYY@R.I
Ephrin type-A receptor 2 precursor -- EphA2	Q03145	K.SEQLKPLKTY@VDPHTYEDPNQAVLK.F	Y589	2995.38	1.88	0.0360 K.SEQLKPLKT@YVDPHTYEDPNQAVLK.F

		L.KTY@VDPHTYEDPNQAVL.K	Y589	2070.37	0.40	0.0405 L.KT@YVDPHTYEDPNQAVL.K
		L.KTY@VDPHT@YEDPNQAVL.K	Y589	2150.60	0.64	0.0001 L.KTY@VDPHTY@EDPNQAVL.K
		K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	3073.16	-0.34	0.0182 K.SEQLKPLKT@YVDPHT@YEDPNQAVLK.F
		K.TYVDPHTY@EDPNQAVLK.F	Y595	2071.96	2.00	0.0577 K.TYVDPHT@YEDPNQAVLK.F
				2071.11	1.15	0.0406 K.TYVDPHT@YEDPNQAVLK.F
		L.KTYVDPHTY@EDPNQAVL.K	Y595	2070.45	0.49	0.0514 L.KTYVDPHT@YEDPNQAVL.K
		L.KTY@VDPHTY@EDPNQAVL.K	Y589,Y595	2150.41	0.45	0.0115 L.KTY@VDPHT@YEDPNQAVL.K
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	2842.81	1.39	0.1130 F.GLSRVLEDDPEAT@YTTSGGKIPIRW.T
		L.SRVLEDDPEATY@TTSGGKIPIRW.T	Y773	2672.86	1.55	0.0979 L.SRVLEDDPEAT@YTTSGGKIPIRW.T
		R.VLEDDPEATY@TTSGGK.I	Y773	1763.39	0.61	0.0487 R.VLEDDPEATYT@TSGGK.I
		R.VLEDDPEATY@TTSGGKIPIR.W	Y773	2243.67	1.57	0.0574 R.VLEDDPEAT@YTTSGGKIPIR.W
Ephrin type-A receptor 3 precursor -- EphA3 (EphA4, EphA5)	P29319	R.VLEDDPEAAY@TTR.G	Y779	1560.19	0.49	0.1136 R.VLEDDPEAAYT@TR.G
Ephrin type-A receptor 4 precursor -- EphA4	Q03137	Y.VDPFTY@EDPNQAVREF.A	Y602	2007.98	1.09	0.0647 Y.VDPFT@YEDPNQAVREF.A
Ephrin type-A receptor 5 precursor -- EphA5	Q60629	R.TY@IDPHTY@EDPNQAVHEFAK.E	Y489,Y495	2537.07	1.98	0.0004 R.T@YIDPHTY@EDPNQAVHEFAK.E
Ephrin type-B receptor 2 precursor -- EphB2 (EphB1)	P54763	K.IY@IDPFTY@EDPNEAVR.E	Y604,Y610	2102.82	0.90	0.0742 K.IY@IDPFT@YEDPNEAVR.E
		Y.IDPFTY@EDPNEAVREF.A	Y610	2023.15	1.26	0.0643 Y.IDPFT@YEDPNEAVREF.A
Ephrin type-B receptor 3 precursor -- EphB3 (EphB4)	P54754	K.VY@IDPFTY@EDPNEAVR.E	Y603,Y609	2088.96	1.05	0.0718 K.VY@IDPFT@YEDPNEAVR.E
		K.VYIDPFTY@EDPNEAVR.E	Y609	2008.83	0.91	0.0715 K.VYIDPFT@YEDPNEAVR.E
		R.FLEDDPSDPTY@TSSLGGKIPIR.W	Y787	2490.03	1.83	0.0162 R.FLEDDPSDPT@YTSSLGGKIPIR.W
Eph receptor B4 -- EphB4	Q91YM0	K.HGQYLIGHGTKVY@IDPFTY@EDPNEAVR.E	Y590,Y596	3281.88	2.36	0.0441 K.HGQYLIGHGTKVY@IDPFT@YEDPNEAVR.E
		K.HGQYLIGHGT^KVYIDPFTY@EDPNEAVR.E	Y596	3182.37	0.84	0.0078 K.HGQYLIGHGT^KVYIDPFT@YEDPNEAVR.E
		Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596	3072.78	2.35	0.0265 Y.LIGHGT@KVYIDPFTY@EDPNEAVREF.A
		R.FLEENSS@DPTY@TSSLGGKIPIR.W	Y774	2572.64	1.43	0.0545 R.FLEENS@SDPTY@TSSLGGKIPIR.W
		R.FLEENSSDPTY@TSSLGGKIPIR.W	Y774	2492.06	0.85	0.0189 R.FLEENSSDPT@YTSSLGGKIPIR.W
Hepatocyte growth factor receptor precursor -- MET	P16056	F.GLARDMYDKEY@Y.S	Y1232	1603.92	0.24	0.1510 F.GLARDMYDKEYY@.S
		F.GLARDMYDKEYY@.S	Y1233	1604.02	0.34	0.0089 F.GLARDMYDKEY@Y.S
		R.DM#YDKEY@Y@SVHNK.T	Y1232,Y1233	1869.85	2.11	0.1228 R.DM#YDKEY@YS@VHNK.T
		R.DM#YDKEY@YS@VHNK.T	Y1232	1869.06	1.32	0.0804 R.DM#YDKEY@Y@SVHNK.T
		R.DM#YDKEY@YSVHNK.T	Y1232	1789.90	2.16	0.1726 R.DM#YDKEYY@SVHNK.T
		R.DMYDKEY@Y@SVHNK.T	Y1232,Y1233	1852.08	0.34	0.1298 R.DMYDKEY@YS@VHNK.T
				1851.99	0.25	0.0430 R.DMYDKEY@YS@VHNK.T
		R.DMYDKEY@Y@SVHNKTGAK.L	Y1232,Y1233	2209.76	0.82	0.1138 R.DMYDKEY@YS@VHNKTGAK.L
		R.DMYDKEY@YSVHNK.T	Y1232	1772.51	0.77	0.1319 R.DMYDKEYY@SVHNK.T
				1772.16	0.42	0.1225 R.DMYDKEYY@SVHNK.T
		R.DMYDKEY@YSVHNKT^GAK.L	Y1232	2111.19	0.24	0.0297 R.DMYDKEYY@SVHNKT^GAK.L
		R.DMYDKEY@YS^VHNK.T	Y1232	1753.71	-0.03	none
		R.DMYDKEYY@SVHNK.T	Y1233	1772.24	0.50	0.0180 R.DMYDKEY@YSVHNK.T
				1772.72	0.98	0.0029 R.DMYDKEY@YSVHNK.T
		R.DMYDKEYY@SVHNKT^GAK.L	Y1233	2111.23	0.29	0.0008 R.DMYDKEY@YSVHNKT^GAK.L
Insulin-like growth factor 1 receptor precursor -- IGF1R (InsR)	Q60751	R.DIY@ETDY@Y@RK.G	Y1163, Y1167,Y1168	1605.90	0.27	none
		R.DIY@ETDY@YRK.G	Y1163, Y1167	1525.89	0.26	0.0862 R.DIY@ETDYY@RK.G
		R.DIYETDY@YR.K	Y1167	1318.97	1.43	0.1814 R.DIYET@DYYR.K
		R.DIYETDYY@RK.G	Y1168	1445.90	0.27	0.0426 R.DIYETDY@YRK.G
Proto-oncogene tyrosine-protein kinase -- MER	Q60805	K.KIY@SGDY@YR.Q	Y744,Y748	1324.91	0.34	0.1269 K.KIY@SGDYY@R.Q
		K.KIYSGDY@YR.Q	Y748	1245.94	1.37	0.0651 K.KIYSGDYY@R.Q
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	F.GLSKKIYNGDY@Y.R	Y696	1500.39	-0.32	0.0505 F.GLSKKIYNGDYY@.R
		K.KIYNGDY@YR.Q	Y696	1272.10	0.52	0.1473 K.KIYNGDYY@R.Q
		K.IYNGDY@YR.Q	Y696	1144.07	0.59	0.0634 K.IYNGDYY@R.Q
		K.IYNGDYY@R.Q	Y697	1144.49	1.01	0.0051 K.IYNGDY@YR.Q
		F.GLSKKIYNGDYY@.R	Y697	1501.45	0.74	0.0489 F.GLSKKIYNGDY@Y.R
Other protein kinases						
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IEKIGEGT@Y@GVVYK.G	Y15	1717.27	1.43	none
				1715.77	-0.07	none
		K.IEKIGEGTY@GVVY.K	Y15	1508.18	0.44	0.0734 K.IEKIGEGT@YGVVY.K
		K.IEKIGEGTY@GVVYK.G	Y15	1636.64	0.80	0.0541 K.IEKIGEGT@YGVVYK.G
				1635.95	0.11	0.0489 K.IEKIGEGT@YGVVYK.G
		K.IEKIGEGT^Y@GVVYK.G	Y15	1619.00	1.16	none
				1618.12	0.28	none
		K.IGEGT@Y@GVVYK.G	Y15	1346.16	0.54	none
		K.IGEGTY@GVVYK.G	Y15	1267.13	1.51	0.0888 K.IGEGT@YGVVYK.G
				1265.57	-0.05	0.1021 K.IGEGT@YGVVYK.G
		K.IGEGTY@GVVYKGR.H	Y15	1479.08	0.34	0.0572 K.IGEGT@YGVVYKGR.H
		K.IGEGT^Y@GVVYK.G	Y15	1248.01	0.39	none
		K.IGEGT^Y@GVVYKGR.H	Y15	1462.31	1.57	none
		Y.IKIEKIGEGTY@GVVY.K	Y15	1749.38	0.46	0.0942 Y.IKIEKIGEGT@YGVVY.K
		Y.IKIEKIGEGT^Y@GVVY.K	Y15	1730.66	(0,26)	none
		-.DYIKIEKIGEGTY@GVVY.K	Y15	2027.54	0.53	0.0803 -.DYIKIEKIGEGT@YGVVY.K
		K.IGEGTYGVVY@K.G	Y19	1266.15	0.53	0.1207 K.IGEGTY@GVVYK.G
Cell division protein kinase 2 -- CDK2	P97377	K.VEKIGEGTY@GVVYK.A	Y15	1622.96	1.14	0.0922 K.VEKIGEGT@YGVVYK.A
				1622.35	0.53	0.0411 K.VEKIGEGT@YGVVYK.A

Dual-specificity tyrosine-phosphorylation regulated kinase 1A -- DYRK1A (DYRK1B)	Q61214	K.VYNDGYDDDNY@DYIVK.N	Y145	2052.45	1.62	none
		R.KVYNDGYDDDNY@DYIVK.N	Y145	2180.67	1.75	0.1039 R.KVYNDGYDDDNYDY@IVK.N
				2180.63	1.71	0.1337 R.KVYNDGYDDDNYDY@IVK.N
		R.KVYNDGYDDDNY@DYIVKNGEK.W	Y145	2609.03	1.90	none
		Y.NDGYDDDNY@DYIVKNGEKW.M	Y145	2404.62	1.64	0.1351 Y.NDGY@DDDNYDYIVKNGEKW.M
				2403.40	0.42	0.1520 Y.NDGYDDDNYDY@IVKNGEKW.M
		R.IYQY@IQSR.F	Y321	1151.37	0.81	none
		Y.QY@IQSRFY.R	Y321	1186.05	1.50	none
Glycogen synthase kinase-3 beta -- GSK-3beta (GSK3alpha)	Q9WV60	K.QLVRGEPNVSY@IC*SRY.Y	Y216	2021.36	0.42	0.1148 K.QLVRGEPNVS@YIC*SRY.Y
		K.QLVRGEPNVSY@IC*SRYY.R	Y216	2184.56	0.55	0.0356 K.QLVRGEPNVS@YIC*SRYY.R
		L.VRGEPNVSY@IC*.S	Y216	1374.19	0.59	0.1286 L.VRGEPNVS@YIC*.S
		L.VRGEPNVSY@IC*S@RYY.R	Y216	2023.70	0.84	0.0640 L.VRGEPNVSY@IC*SRY@Y.R
		L.VRGEPNVSY@IC*SRY.Y	Y216	1781.23	1.43	0.1098 L.VRGEPNVS@YIC*SRY.Y
				1780.21	0.41	0.0264 L.VRGEPNVS@YIC*SRY.Y
		L.VRGEPNVSY@IC*SRYY.R	Y216	1944.89	2.03	0.1177 L.VRGEPNVS@YIC*SRYY.R
				1943.20	0.34	0.0594 L.VRGEPNVS@YIC*SRYY.R
		L.VRGEPNVSY@IC*S^RY.Y	Y216	1762.02	0.22	0.1013 L.VRGEPNVS@YIC*S^RY.Y
		N.VSY@IC*SRY.Y	Y216	1129.07	1.60	none
		N.VSY@IC*SRYY.R	Y216	1291.21	0.68	none
		Q.LVRGEPNVSY@IC*SRY.Y	Y216	1894.43	1.55	0.1234 Q.LVRGEPNVS@YIC*SRY.Y
				1893.13	0.25	0.0042 Q.LVRGEPNVS@YIC*SRY.Y
		Q.LVRGEPNVSY@IC*SRYY.R	Y216	2056.41	0.46	0.1617 Q.LVRGEPNVS@YIC*SRYY.R
		R.GEPNVSY@IC*SR.Y	Y216	1363.40	1.83	0.0889 R.GEPNVS@YIC*SR.Y
		R.GEPNVSY@IC*SRYY.R	Y216	1688.41	0.72	0.0826 R.GEPNVS@YIC*SRYY.R
Homeodomain-interacting protein kinase 1 -- HIPK1 (HIPK2)	O88904	H.VSKAVC*STY@LQSRY.Y	Y352	1742.55	0.74	0.1304 H.VSKAVC*ST@YLQSRY.Y
				1742.42	0.61	0.0391 H.VSKAVC*ST@YLQSRY.Y
		K.AVC*STY@LQSR.Y	Y352	1264.64	0.09	0.1095 K.AVC*ST@YLQSR.Y
		S.KAVC*STY@LQSRY.Y	Y352	1557.06	1.35	0.0866 S.KAVC*ST@YLQSRY.Y
Homeodomain-interacting protein kinase 3 -- HIPK3	Q9ERH7	H.VSKTVC*STY@L.Q	Y359	1237.96	0.39	0.1771 H.VSKTVC*ST@YL.Q
		H.VSKTVC*STY@LQSRY.Y	Y359	1773.71	1.89	0.0008 H.VSKTVC*STY@LQSRY.Y
				1772.23	0.41	0.1302 H.VSKTVC*ST@YLQSRY.Y
		K.TVC*STY@LQSR.Y	Y359	1294.81	0.25	0.0907 K.TVC*ST@YLQSR.Y
Hypothetical Protein kinase-like (PK-like) structure containing protein -- SgK223	Q8CB68	K.C*VGQAAELQPASLLRDPVQPEPIY@AESAK.R	Y196	3219.49	1.92	0.0171 K.C*VGQAAELQPASLLRDPVQPEPIYAES@AK.R
		K.C*VGQAAELQPASLLRDPVQPEPIY@AESAKR.K	Y196	3375.94	2.27	0.0315 K.C*VGQAAELQPASLLRDPVQPEPIYAES@AKR.K
Mitogen-activated protein kinase 3 -- ERK1	Q63844	F.GLARIADPEHDHTGFLT@EY@VATRW.Y	Y205	2916.59	1.22	0.0618 F.GLARIADPEHDHT@GFLTEY@VATRW.Y
		F.GLARIADPEHDHTGFLTEY@VATRW.Y	Y205	2836.39	1.03	0.0116 F.GLARIADPEHDHTGFLT@EYVATRW.Y
		F.GLARIADPEHDHTGFLT^EY@VATRW.Y	Y205	2818.73	1.37	0.1112 F.GLARIADPEHDHT^GFLTEY@VATRW.Y
		F.GLARIADPEHDHTGFLT^EY@VATRWY.R	Y205	2981.12	0.70	0.0131 F.GLARIADPEHDHTGFLT@EYVAT^RWY.R
		F.LTEY@VATRW.Y	Y205	1219.17	0.58	none
		R.IADPEHDHTGFLT@EY@VATR.W	Y205	2333.65	1.61	none
		R.IADPEHDHTGFLTEY@VATR.W	Y205	2253.54	1.50	0.1192 R.IADPEHDHTGFLT@EYVATR.W
		R.IADPEHDHTGFLT^EY@VATR.W	Y205	2234.94	0.90	0.1243 R.IADPEHDHTGFLT^EYVAT@R.W
Mitogen-activated protein kinase 1 -- ERK2	P63085	F.GLARVADPDHDHTGFLT@EY@VATRW.Y	Y185	2889.63	2.30	none
		F.GLARVADPDHDHTGFLT@EY@VATRWY.R	Y185	3052.12	1.73	0.0666 F.GLARVADPDHDHTGFLT@EYVAT@RWY.R
		F.GLARVADPDHDHTGFLTEY@VATRWY.R	Y185	2971.42	1.03	0.0031 F.GLARVADPDHDHTGFLT@EYVATRWY.R
		F.GLARVADPDHDHTGFLT^EY@VATRW.Y	Y185	2790.58	1.25	0.1059 F.GLARVADPDHDHTGFLTEY@VAT^RW.Y
		F.GLARVADPDHDHTGFLT^EY@VATRWY.R	Y185	2953.38	0.99	0.0290 F.GLARVADPDHDHTGFLT^EYVAT@RWY.R
		F.GLARVADPDHDHT^GFLTEY@VATRW.Y	Y185	2790.47	1.14	0.0231 F.GLARVADPDHDHT^GFLTEYVAT@RW.Y
		R.VADPDHDHTGFLT@EY@VATR.W	Y185	2304.29	0.28	none
		R.VADPDHDHTGFLTEY@VATR.W	Y185	2224.33	0.33	0.1191 R.VADPDHDHTGFLT@EYVATR.W
				2224.83	0.83	0.0759 R.VADPDHDHTGFLT@EYVATR.W
		R.VADPDHDHTGFLTEY@VATRW.Y	Y185	2410.91	0.83	0.1239 R.VADPDHDHTGFLT@EYVATRW.Y
		R.VADPDHDHTGFLTEY@VAT^R.W	Y185	2207.28	1.28	0.0626 R.VADPDHDHTGFLT^EY@VATR.W
		R.VADPDHDHTGFLT^EY@VATR.W	Y185	2207.04	1.03	0.1505 R.VADPDHDHTGFLT^EYVAT@R.W
				2207.45	1.45	0.0809 R.VADPDHDHT^GFLTEY@VATR.W
		R.VADPDHDHTGFLT^EY@VATRW.Y	Y185	2393.29	1.21	0.1412 R.VADPDHDHTGFLTEY@VAT^RW.Y
Mitogen-activated protein kinase 7 -- ERK5	Q9WVS8	R.GLC*TSPAEHQYFM#TEY@VATR.W	Y221	2457.69	0.65	0.0721 R.GLC*TSPAEHQYFM#T@EYVATR.W
		R.GLC*TSPAEHQYFMTEY@VATR.W	Y221	2442.75	1.71	0.0449 R.GLC*TSPAEHQYFMT@EYVATR.W
Mitogen-activated protein kinase 8 -- JNK1	Q91Y86	R.TAGTSFMMTPY@VVTR.Y	Y185	1743.49	1.69	0.0662 R.TAGTSFMMT@PYVVTR.Y
Mitogen-activated protein kinase 9 -- JNK2	Q9WTU6	R.TAC*TNFMMTPY@VVTR.Y	Y185	1873.63	1.83	none
Mitogen-activated protein kinase 14 -- MAP kinase p38 alpha	P47811	F.GLARHTDDEM#TGY@VATRW.Y	Y181	2175.50	0.53	0.1347 F.GLARHTDDEM#T@GYVATRW.Y
		F.GLARHTDDEMTGY@VATRW.Y	Y181	2159.40	0.43	0.0954 F.GLARHTDDEMT@GYVATRW.Y
				2160.64	1.67	0.1691 F.GLARHTDDEMT@GYVATRW.Y
		F.GLARHTDDEMTGY@VATRWY.R	Y181	2323.53	1.50	0.0947 F.GLARHTDDEMT@GYVATRWY.R
		L.ARHTDDEMTGY@VATRW.Y	Y181	1990.25	1.38	0.1864 L.ARHTDDEMT@GYVATRW.Y
		L.DFGLARHTDDEMTGY@VATRW.Y	Y181	2422.09	1.02	0.0849 L.DFGLARHTDDEMT@GYVATRW.Y
		R.HTDDEM#TGY@VATR.W	Y181	1592.19	0.54	0.0807 R.HTDDEM#T@GYVATR.W
		R.HTDDEMTGY@VATR.W	Y181	1576.90	1.25	none
				1575.91	0.26	0.0886 R.HTDDEMT@GYVATR.W

Serine/threonine-protein kinase PAK 2	Q8CIN4	K.LRTIVSIGDPKKKYTRY@EK.I	Y252	2376.11	0.79	0.0793 K.LRTIVSIGDPKKKYT@RYEK.I
Serine/threonine-protein kinase -- PFTAIRE-1	O35495	K.LEKLGEGS@Y@ATVYK.G	Y146	1718.66	0.84	0.0483 K.LEKLGEGS@YAT@VYK.G
Serine/threonine-protein kinase -- PCTAIRE-3	Q04899	K.LDKLGEGTY@ATVFK.G	Y132	1623.36	1.54	0.1410 K.LDKLGEGTYAT@VFK.G
Serine/threonine-protein kinase -- PRP4	Q61136	C.DFGS@AS@HVADNDITPY@LVSRFY.R	Y849	2716.16	2.00	0.0791 C.DFGS@AS@HVADNDITPYLVS@RFY.R
		F.GSASHVADNDITPY@LVSRF.Y	Y849	2129.80	0.80	0.1221 F.GSASHVADNDIT@PYLVSRF.Y
		F.GSASHVADNDITPY@LVSRFY.R	Y849	2294.39	2.32	0.0608 F.GSASHVADNDIT@PYLVSRFY.R
		H.VADNDITPY@LVSRF.Y	Y849	1691.52	1.70	0.1790 H.VADNDIT@PYLVSRF.Y
		H.VADNDITPY@LVSRFY.R	Y849	1853.23	0.34	0.0895 H.VADNDIT@PYLVSRFY.R
		K.LC*DFGSASHVADNDITPY@LVSR.F	Y849	2518.48	1.36	0.0690 K.LC*DFGSASHVADNDITPYLVS@R.F
				2518.24	1.12	0.0031 K.LC*DFGSASHVADNDITPYLVS@R.F
		K.LCDFGSAS@HVADNDITPY@LVSR.F	Y849	2540.29	0.17	0.0305 K.LCDFGSAS@HVADNDITPYLVS@R.F
		L.C*DFGSASHVADNDITPY@LVSRF.Y	Y849	2552.41	1.30	0.0112 L.C*DFGSASHVADNDIT@PYLVSRF.Y
		S.HVADNDITPY@LVSRFY.R	Y849	1991.45	1.50	0.1081 S.HVADNDIT@PYLVSRFY.R
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.FNSYNNAGM#PPFPIIIHDEPSY@AR.S	Y613	2847.87	1.56	0.0304 K.FNSYNNAGM#PPFPIIIHDEPS@YAR.S
		K.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638	2503.86	0.55	none
		K.NAIKVPIVINPNAY@DNLAIYK.S	Y632	2425.00	1.69	none
				2424.81	1.50	none
		K.NAIKVPIVINPNAYDNLAIY@K.S	Y638	2424.31	0.99	none
		K.VPIVINPNAY@DNLAIYK.S	Y632	1998.75	1.70	none
Protein phosphatases						
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	1483.33	0.56	none
Receptor-type tyrosine-protein phosphatase alpha -- R-PTP-alpha	P18052	K.VVQEYIDAFSDY@ANFK.-	Y825	1990.73	1.83	0.1360 K.VVQEYIDAFS@DYANFK.-
				1989.39	0.49	0.1321 K.VVQEYIDAFS@DYANFK.-
		Y.IDAFSDY@ANFK.-	Y825	1371.08	0.48	0.1983 Y.IDAFS@DYANFK.-
		Y.KVVQEYIDAFSDY@ANF.K	Y825	1990.24	1.34	0.1699 Y.KVVQEYIDAFS@DYANF.K
		Y.KVVQEYIDAFSDY@ANFK.-	Y825	2117.46	0.46	0.1423 Y.KVVQEYIDAFS@DYANFK.-
				2117.96	0.95	0.1172 Y.KVVQEYIDAFS@DYANFK.-
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	1687.55	1.77	0.0825 H.IKIQNT@GDYYDLY.G
		K.IQNTGDY@YDLYGGEK.F	Y62	1816.64	0.86	0.0608 K.IQNTGDYY@DLYGGEK.F
		R.EDSARVY@ENVGLMQQQR.S	Y584	2103.27	0.30	0.0252 R.EDS@ARVYENVGLMQQQR.S
		R.VY@ENVGLMQQQR.S	Y584	1546.68	1.95	none
SIGNALING: SMALL G PROTEINS AND REGULATORS						
Glucocorticoid receptor DNA binding factor 1 [fragment] -- p190RhoGAP	Q91YM2	R.NEEENIY@SVPHDSTQGK.I	Y943	2028.37	1.50	0.1129 R.NEEENIYS@VPHDSTQGK.I
				2027.38	0.51	0.0347 R.NEEENIYS@VPHDSTQGK.I
		W.MPQDGFDPSDY@AEPMDAVVKPRNEEENIY.S	Y925	3437.09	0.62	0.0641 W.MPQDGFDPS@DYAEPMDAVVKPRNEEENIY.S
Breast cancer anti-estrogen resistance protein 3 -- BCAR3	Q9QZK2	F.IFRDPY@LLDPTLEY.V	Y103	1836.11	1.20	none
		F.IFRDPY@LLDPTLEYVKF.S	Y103	2211.16	2.03	0.1678 F.IFRDPYLLDPT@LEYVKF.S
		Y.LLDPTLEY@VKF.S	Y111	1418.86	1.12	none
		R.KGENFIFRDPY@LLDPTLEY@VK.F	Y103,Y111	2717.86	0.53	0.0895 R.KGENFIFRDPY@LLDPT@LEYVK.F
		R.KGENFIFRDPY@LLDPTLEYVK.F	Y103	2638.73	1.40	none
		L.RLSEAY@SRVQY.Q	Y206	1451.76	0.06	0.1168 L.RLSEAYS@RVQY.Q
ARF GTPase-activating protein -- GIT1	Q68FF6	R.SQSELDDQHDY@DS@VAS@DEDTDQEPLPSAGATR.N	Y392	3719.62	1.16	0.0607 R.SQS@ELDDQHDYDS@VAS@DEDTDQEPLPSAGATR.N
		R.SQSELDDQHDY@DS@VAS^DEDTDQEPLPSAGATR.N	Y392	3621.05	0.59	0.1120 R.SQS@ELDDQHDYDS@VAS^DEDTDQEPLPSAGATR.N
		F.HSTELEDDAIY@SVHVPAGLY.R	Y554	2296.44	0.39	0.0911 F.HSTELEDDAIYS@VHVPAGLY.R
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554	3019.56	2.14	0.0239 R.LQPFHST@ELEDDAIY@SVHVPAGLYR.I
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554	2936.69	-0.74	0.1052 R.LQPFHSTELEDDAIYS@VHVPAGLYR.I
		R.LQPFHST^ELEDDAIY@SVHVPAGLYR.I	Y554	2921.29	1.87	0.0118 R.LQPFHS^TELEDDAIY@SVHVPAGLYR.I
ARF GTPase-activating protein -- GIT2	Q9JLQ2	K.QNSTPESDY@DNTAC*DPEPDDTGSTR.K	Y541	2854.17	2.11	0.0570 K.QNSTPESDYDNT@AC*DPEPDDTGSTR.K
		K.QNSTPESDY@DNTAC*DPEPDDTGSTRK.G	Y541	2982.55	2.40	0.0951 K.QNSTPESDYDNT@AC*DPEPDDTGSTRK.G
Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	K.LQQTY@SALNSK.A	Y1510	1333.04	0.38	0.0103 K.LQQTYS@ALNSK.A
Ras and Rab interactor 1 -- Rin1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	1816.51	1.69	0.1779 K.EKPST@DPLYDTPDTR.G
Rho-GTPase-activating protein 12	Q8C0D4	M.RATT@PPNQGRPDS@PVY@ANLQEL.K	Y241	2665.38	1.15	0.0400 M.RAT@TPPNQGRPDS@PVY@ANLQEL.K
		M.RATTPPNQGRPDS@PVY@ANLQEL.K	Y241	2584.73	0.50	none
		R.AT@TPPNQGRPDS@PVY@ANLQELK.I	Y241	2637.23	1.01	0.0093 R.ATT@PPNQGRPDS@PVY@ANLQELK.I
		R.AT@TPPNQGRPDS^PVY@ANLQELK.I	Y241	2539.23	1.01	0.0100 R.ATT@PPNQGRPDS^PVY@ANLQELK.I
		R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241	2637.05	0.83	0.0040 R.AT@TPPNQGRPDS@PVY@ANLQELK.I
SIGNALING: OTHER						
Abl interactor 1 -- Abi-1	Q8CBW3	K.TLEPVKPPTVPNDY@MTSPAR.L	Y212	2295.33	2.20	0.0690 K.TLEPVKPPTVPNDYMT@SPAR.L

				2293.83	0.70	0.1074 K.TLEPVKPPTVPNDYMT@SPAR.L
		R.NTPY@KTLEPVKPPTVPNDY@MTSPAR.L	Y212	2978.21	1.78	0.0601 R.NT@PYKTLEPVKPPTVPNDY@MTSPAR.L
		R.NTPYKT@LEPVKPPTVPNDY@MTSPAR.L	Y212	2977.76	1.33	0.0027 R.NTPY@KTLEPVKPPTVPNDY@MTSPAR.L
		Y.KTLEPVKPPTVPNDY@MTSPARL.G	Y212	2536.20	1.89	0.0795 Y.KTLEPVKPPTVPNDYMT@SPARL.G
Annexin A2	P07356	K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D	Y23	3019.60	1.21	0.1039 K.LSLEGDHSTPPS@AYGSVKPYTNFDAER.D
		K.LSLEGDHSTPPSAY@GSVKPYTNFDAERDALNIETAVK.T	Y23	4074.03	1.08	0.0831 K.LSLEGDHSTPPS@AYGSVKPYTNFDAERDALNIETAVK.T
		C.KLSLEGDHSTPPSAY@GSVKPY.T	Y23	2314.18	1.07	0.0405 C.KLSLEGDHSTPPS@AYGSVKPY.T
		L.SLEGDHSTPPSAY@GSVKPY.T	Y23	2072.37	0.44	none
				2072.20	0.27	0.0611 L.SLEGDHSTPPS@AYGSVKPY.T
		K.RKY@GKSLYYYIQQDTK.G	Y310	2133.59	-0.48	none
Ankyrin repeat and SAM domain-containing protein 1 -- ANKS1	P59672	L.AVRPRIQS@SAPQEEEEHPY@EL.L	Y471	2625.39	0.18	0.0703 L.AVRPRIQSS@APQEEEEHPY@EL.L
		L.AVRPRIQS@SAPQEEEEHPY@ELL.L	Y471	2739.27	0.98	0.0426 L.AVRPRIQSS@APQEEEEHPY@ELL.L
		L.AVRPRIQSSAPQEEEEHPY@EL.L	Y471	2545.60	0.39	none
		L.AVRPRIQSSAPQEEEEHPY@ELL.L	Y471	2660.04	1.75	none
		L.AVRPRIQSSAPQEEEEHPY@ELLL.T	Y471	2771.51	0.14	none
Calmodulin	P62204	R.VFDKDGNGY@ISAAELR.H	Y99	1835.70	0.83	0.1715 R.VFDKDGNGYIS@AAELR.H
		F.RVFDKDGNGY@ISAAEL.R	Y99	1835.25	0.38	0.1911 F.RVFDKDGNGYIS@AAEL.R
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	1729.56	0.73	0.1046 K.YVDSEGHLYT@VPIR.E
Caveolin-2	Q9WVC3	F.MADDAYS@HHS@GVDY@ADPEKY.V	Y27	2511.77	0.84	0.0208 F.MADDAY@SHHS@GVDY@ADPEKY.V
		F.MADDAYS@HHS^GVDY@ADPEKY.V	Y27	2413.36	0.43	0.0294 F.MADDAYS^HHS@GVDY@ADPEKY.V
		F.MADDAYSHHS@GVDY@ADPEKY.V	Y27	2431.75	0.82	0.0532 F.MADDAYS@HHSGVDY@ADPEKY.V
		F.MADDAYSHHSGVDY@ADPEKY.V	Y27	2352.07	1.14	0.1833 F.MADDAYSHHS@GVDYADPEKY.V
		F.MADDAYS^HHS@GVDY@ADPEKY.V	Y27	2413.77	0.84	0.0476 F.MADDAYS@HHS^GVDY@ADPEKY.V
		Y.SHHSGVDY@ADPEKY.V	Y27	1686.41	1.71	none
Proto-oncogene c-Crk	Q64010	L.IGGNQEGSHPQPLGGPEPGPY@AQPSVN.T	Y221	2765.21	0.94	0.1614 L.IGGNQEGSHPQPLGGPEPGPYAQPS@VN.T
		Y.AQPSVNTPLPNLQNGPIY@ARVIQ.K	Y239	2571.23	0.88	none
		K.RVPNAY@DKTALALEVGELVK.V	Y251	2267.51	1.29	0.1337 K.RVPNAYDKT@ALALEVGELVK.V
		Q.KRVPNAY@DKTAL.A	Y251	1456.62	0.85	none
Crk-like protein	P47941	Y.VRTLY@DFPGNDAEDLPF.K	Y132	2049.94	1.01	0.0171 Y.VRT@LYDFPGNDAEDLPF.K
		H.GKHGNRNS@NSY@GIPEPAHAY.A	Y198	2329.96	0.94	0.0533 H.GKHGNRNS@NS@YGIPEPAHAY.A
		H.GNRNS@NSY@GIPEPAHAY.A	Y198	2007.22	0.37	0.0145 H.GNRNS@NS@YGIPEPAHAY.A
		H.GNRNSNSY@GIPEPAHAY.A	Y198	1926.66	-0.19	0.0455 H.GNRNSNS@YGIPEPAHAY.A
		R.NSNSY@GIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y198	4954.83	1.39	0.0067 R.NSNS@YGIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A
		R.NSNSYGIPEPAHAY@AQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y207	4953.06	-0.38	0.0482 R.NSNSYGIPEPAHAYAQPQT@TTPLPTVASTPGAAINPLPSTQNGPVFAK.A
Docking protein 1 (Dok1)	P97465	R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K	Y314	2888.77	1.42	0.0507 R.IPPGPSQDS@VYSDPLGSTPAGAGEGVHSK.K
		K.KPLYWDLY@GHVQQQLLK.T	Y340	2210.90	1.75	none
		K.LTDSKEDPIY@DEPEGLAPAPPR.G	Y361	2490.85	0.67	0.0169 K.LTDS@KEDPIYDEPEGLAPAPPR.G
				2491.80	1.62	none
		K.TKLTDSKEDPIY@DEPEGLAPAPPR.G	Y361	2720.84	1.52	none
		L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	3181.70	1.12	0.1003 L.KTKLTDS@KEDPIYDEPEGLAPAPPRGLY.D
		L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	3295.51	1.84	0.0090 L.LKTKLTDS@KEDPIYDEPEGLAPAPPRGLY.D
		R.LKEEGYELPYNPATDDY@AVPPPR.S	Y408	2715.69	1.42	0.1685 R.LKEEGYELPYNPAT@DDYAVPPPR.S
		F.SSDTALY@SQVQKSGTSGAW.D	Y450	2054.41	1.49	0.0872 F.SSDTALYS@QVQKSGTSGAW.D
		K.GFSSDTALY@SQVQK.S	Y450	1611.29	0.55	0.1228 K.GFSSDTALYS@QVQK.S
Ephrin-B2 precursor (Ephrin-B1)	P52800	R.TADSVFC*PHY@EK.V	Y307	1533.58	-0.04	none
		K.VSGDY@GHPVYIVQEMPPQSPANIYYKV.-	Y314	3133.25	1.76	0.0505 K.VSGDYGHPVY@IVQEMPPQSPANIYYKV.-
		K.VSGDYGHPVY@IVQEMPPQSPANIY@YKV.-	Y319,Y333	3213.54	2.05	0.0037 K.VSGDY@GHPVYIVQEMPPQSPANIY@YKV.-
		K.VSGDYGHPVYIVQEM#PPQSPANIY@YKV.-	Y333	3148.50	1.01	0.0827 K.VSGDYGHPVYIVQEM#PPQS@PANIYYKV.-
		K.VSGDYGHPVYIVQEMPPQSPANIY@YKV.-	Y333	3132.93	1.44	none
Fibroblast growth factor receptor substrate 2 -- FRS2	Q8C180	K.LVY@ENINGLSIPSASGVR.R	Y306	1969.34	0.33	none
		R.RPALLNY@ENLPSLPPVWEAR.K	Y349	2416.51	1.25	none
Fish protein -- TKS5	O89032	K.VKYEEPEY@DVPAFGFDSEPEMNEEPSGDR.G	Y557	3443.91	1.48	0.0364 K.VKY@EEPEYDVPAFGFDSEPEMNEEPSGDR.G
GRB2-associated binding protein 1 -- Gab1	Q9QYY0	K.HGMNGFFQQQMMY@DC*PPSR.L	Y242	2412.02	1.09	none
		K.DASSQDC*Y@DIPR.T	Y407	1506.85	0.28	none
		L.RKDASSQDC*Y@DIPRTF.P	Y407	2039.52	0.64	none
		N.KLRKDASSQDC*Y@DIPRTF.P	Y407	2280.55	0.49	0.1319 N.KLRKDASSQDC*YDIPRT@F.P
		R.KDASSQDC*Y@DIPR.T	Y407	1635.93	1.27	none
				1635.28	0.62	none
Insulin receptor substrate 2 -- IRS-2	P81122	K.SSSSNLGADDGY@MPM#TPGAALR.S	Y649	2293.62	-0.38	none
		K.SSSSNLGADDGY@MPMTPGAALR.S	Y649	2279.62	1.63	none
		K.SDDY@MPMSPTSVSAPK.Q	Y671	1793.58	0.83	0.0249 K.S@DDYMPMSPTSVSAPK.Q
Insulin receptor substrate-2 (IRS-2) (4PS) homolog [Fragment]	Q3U2I0	R.SYKAPC*SC*SGDDDQY@VLMSSPVGR.I	Y754	2759.44	0.33	none
Kin of IRRE-like protein 1 precursor	Q80W68	K.AIY@SSFKDDVDLK.Q	Y604	1581.16	0.40	0.1327 K.AIYS@SFKDDVDLK.Q
		K.AIY@SSFKDDVDLKQDLR.C	Y604	2093.01	-0.02	0.1376 K.AIYS@SFKDDVDLKQDLR.C

		R.EEYEMKDPTNGY@YNVR.A	Y637	2088.84	0.95	0.0102 R.EEYEMKDPTNGYY@NVR.A
		R.AVLY@ADY@RAPGPTR.F	Y654,Y657	1710.06	0.25	none
		Y.NVRAHEDRPSSRAVLY@ADY.R	Y654	2299.69	0.59	0.1088 Y.NVRAHEDRPSS@RAVLYADY.R
		R.TPY@EAYDPIGK.Y	Y753	1334.35	0.75	0.1201 R.T@PYEAYDPIGK.Y
		Y.RLGYPQAPPSGLERTPY@EAYDPIGKY.A	Y753	3020.61	2.14	0.1308 Y.RLGYPQAPPSGLERTPYEAY@DPIGKY.A
		R.TPYEAY@DPIGK.Y	Y756	1333.93	0.33	none
myelin protein zero-like 1 -- PZR	Q3TEW6	K.SPPSAGSHQGPVIY@AQLDHSGGHHSGK.I	Y242	2788.83	0.54	none
		K.INKSESVVY@ADIR.K	Y264	1574.44	0.64	none
				1574.04	0.24	none
		K.INKSESVVY@ADIRKD.-	Y264	1817.67	0.75	none
		K.SESVVY@ADIR.K	Y264	1219.29	0.72	0.1964 K.SES@VVYADIR.K
		N.KSESVVY@ADIRKD.-	Y264	1590.69	0.90	none
		H.SGKINKSESVVY@ADIRKD.-	Y264	2090.06	0.99	none
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.RKPS@VPDTASPADDSFVDPGERLY@DLNM#PAFVK.F	Y105	3812.62	1.84	0.1535 K.RKPSVPDT@ASPADDSFVDPGERLY@DLNM#PAFVK.F
		K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3796.70	1.92	0.0441 K.RKPSVPDT@ASPADDSFVDPGERLY@DLNMPAFVK.F
		K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	3716.28	1.50	0.1820 K.RKPSVPDTASPADDS@FVDPGERLYDLNMPAFVK.F
PDZ and LIM domain protein 5	Q8CI51	R.NTEFY@HIPTHSDASK.K	Y251	1829.28	2.47	none
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85alpha	P26450	K.SREYDRLY@EEYTR.T	Y467	1860.48	0.65	none
		R.DQY@LMWLTQK.G	Y580	1407.45	1.79	none
		K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y607	3565.69	2.17	0.0197 K.LNEWLGNENTEDQYS@LVEDDEDLPHHDEK.T
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85beta	O08908	R.EYDQLY@EEYTR.T	Y458	1589.19	0.54	0.1826 R.EYDQLYEEY@TR.T
Protein LAP2	Q80TH2	R.RTEGDY@LSYR.E	Y1097	1340.40	0.80	0.0788 R.RTEGDYLS@YR.E
		R.TEGDY@LSYR.E	Y1097	1183.37	-0.13	0.1618 R.TEGDYLS@YR.E
SH2 domain-containing adapter protein B -- Shb	Q6PD21	C.RLDY@C*GGGGGGDPGGGQRAF.T	Y113	2034.85	1.01	none
		L.RAMC*RLDY@C*GGGGGGDPGGGQRAF.T	Y113	2553.43	1.40	none
		M.C*RLDY@C*GGGGGGDPGGGQRAF.T	Y113	2194.54	0.69	none
		R.LDY@C*GGGGGGDPGGGQR.A	Y113	1660.02	0.39	none
		K.C*SAEETGAGQKDKVTIADDY@SDPFDAK.S	Y240	2999.08	0.80	0.0223 K.C*SAEETGAGQKDKVTIADDYS@DPFDAK.S
		K.DKVTIADDY@SDPFDAK.S	Y240	1880.27	0.44	0.1276 K.DKVTIADDYS@DPFDAK.S
				1881.05	1.22	0.0685 K.DKVTIADDYS@DPFDAK.S
		K.VTIADDY@SDPFDAK.S	Y240	1637.43	0.72	0.0466 K.VTIADDYS@DPFDAK.S
		L.LNKC*SAEETGAGQKDKVTIADDY@SDPF.D	Y240	3039.87	0.53	0.0139 L.LNKC*SAEETGAGQKDKVTIADDYS@DPF.D
		F.DAKSDLKSKAGKGESAGY@M#EPY.E	Y262	2429.15	1.04	0.0830 F.DAKSDLKSKAGKGES@AGYM#EPY.E
		F.DAKSDLKSKAGKGESAGY@MEPY.E	Y262	2412.85	0.74	0.0262 F.DAKSDLKSKAGKGES@AGYMEPY.E
		K.AGKGESAGY@M#EPYEAQR.I	Y262	1940.45	0.62	0.0601 K.AGKGES@AGYM#EPYEAQR.I
		K.AGKGESAGY@MEPYEAQR.I	Y262	1925.54	1.71	0.0898 K.AGKGES@AGYMEPYEAQR.I
				1924.60	0.77	none
		K.GESAGY@MEPYEAQR.I	Y262	1667.98	0.31	0.1536 K.GES@AGYMEPYEAQR.I
		K.SKAGKGESAGY@MEPYEAQR.I	Y262	2139.90	0.95	none
		L.KSKAGKGESAGY@MEPY.E	Y262	1782.91	0.10	0.0766 L.KSKAGKGES@AGYMEPY.E
		K.LPQDDDRPADEY@DQPWEWNR.V	Y330	2626.86	1.76	none
		L.RLRESKLPQDDDRPADEY@DQPW.E	Y330	2810.06	0.77	none
		R.ESKLPQDDDRPADEY@DQPWEWNR.V	Y330	2969.85	0.58	none
SHC transforming protein 1 -- SHC1	P98083	K.QM#LPPPPC*PGRELFDDPSY@VNIQNLDK.A	Y423	3237.45	0.95	0.0085 K.QM#LPPPPC*PGRELFDDPS@YVNIQNLDK.A
		R.ELFDDPSY@VNIQNLDK.A	Y423	1990.62	0.70	0.0530 R.ELFDDPS@YVNIQNLDK.A
		K.QMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423	3222.94	0.40	0.0076 K.QMLPPPRCPGRELFDDPS@YVNIQNLDK.A
		R.KQMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423	3351.93	1.29	0.0313 R.KQMLPPPRCPGRELFDDPS@YVNIQNLDK.A
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L	Y349,Y350	4572.10	1.21	none
		R.MAGFDGSAWDEEEEEPPDHQYY@NDFPGKEPPLGGVVDMR.L	Y350	4493.24	2.35	0.0258 R.MAGFDGSAWDEEEEEPPDHQY@YNDFPGKEPPLGGVVDMR.L
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y987	3217.81	2.18	0.0380 K.NSFNNPAYY@VLEGVPHQLLPLEPPSLAR.A
Tyrosine-protein phosphatase non-receptor type substrate 1 -- SHPS1	P97797	Y.ASIETGKVPRPEDTLTY@ADLDMVHL.S	Y481	2852.91	1.52	0.0159 Y.ASIETGKVPRPEDTLT@YADLDMVHL.S
Signal transducer and activator of transcription 3 -- STAT3	P42227	K.YC*RPESQEHPEADPGSAAPY@LK.T	Y705	2584.06	1.95	0.0759 K.YC*RPESQEHPEADPGS@AAPYLK.T
STAT3 splice isoform Del-701	P42227-3	K.YC*RPESQEHPEADPGAAPY@LK.T	Y704	2496.75	1.67	none
Signal transducer and activator of transcription 5B -- STAT5B	P42232	K.AADGY@VKPQIK.Q	Y699	1271.08	1.43	none
ADHESION: CELL/ECM						
CRK-associated substrate -- p130cas	Q61140	K.TQQGLY@QAPGPNPQFQSPPAK.Q	Y132	2334.53	0.40	0.1231 K.T@QQGLYQAPGPNPQFQSPPAK.Q
		R.VGQGYVYEAAQTEQDEY@DTPR.H	Y238	2500.90	1.83	0.0268 R.VGQGYVYEAAQTEQDEYDT@PR.H
				2500.30	1.23	0.1051 R.VGQGYVYEAAQTEQDEYDT@PR.H
		Y.VYEAAQTEQDEY@DTPRHL.L	Y238	2245.97	0.99	0.1402 Y.VYEAAQTEQDEYDT@PRHL.L
				2246.15	1.17	none
		R.HLLAPGPQDIY@DVPPVR.G	Y253	1968.31	1.30	none

				1967.35	0.34	none
		L.LAPGPQDIY@DVPPVRGLLPNQY.G	Y253	2502.60	0.32	none
		R.GLLPNQYGQEVY@DTPPMAVK.G	Y271	2301.33	1.23	none
				2301.61	1.51	none
		K.GPNGRDPLLDVY@DVPPSVEK.G	Y291	2248.94	1.84	none
		K.GLLSSSHHSVY@DVPPSVSK.D	Y310	2076.35	0.34	none
		K.DVPDGPLLREETY@DVPPAFAKPK.P	Y331	2636.66	2.34	0.0884 K.DVPDGPLLREET@YDVPPAFAKPK.P
		R.RPGPGTLY@DVPR.E	Y391	1407.80	0.09	0.0443 R.RPGPGT@LYDVPR.E
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	2914.03	0.59	none
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	2629.75	1.46	none
		L.SRQLQKMEDVY@QTL.V	Y556	1818.84	-0.04	0.1534 L.SRQLQKMEDVYQT@L.V
Enhancer of filamentation 1 -- HEF1	O35177	R.TGHGYVY@EYPSR.Y	Y165	1510.24	1.59	none
		K.ANPEERDGVY@DVPLHNPADAK.G	Y344	2387.12	0.02	none
Integrin beta-1 precursor	P09055	K.WDTGENPIY@K.S	Y783	1303.91	1.34	none
Lipoma-preferred partner homolog - LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	1938.33	0.47	none
				1938.43	0.57	none
		M.AGPSSGQIY@GPGPRGY.N	Y245	1644.21	0.45	none
		Y.MAGPSSGQIY@GPGPRGY.N	Y245	1775.96	1.16	none
				1776.09	1.29	none
		R.GYNNQPVPVSGQC*PPPPTC*VGTDY@AYIPPSGHPPESGYGYTSNQGR.Y	Y276	5002.32	2.16	0.0858 R.GYNNQPVPVSGQC*PPPPT@C*VGTDYAYIPPSGHPPESGYGYTSNQGR.Y
		R.YYEPY@YAAGPSYGGR.S	Y301	1794.43	0.68	0.0190 R.YYEPYY@AAGPSYGGR.S
		R.YYEPYY@AAGPSYGGR.S	Y302	1794.15	0.40	0.0399 R.YYEPY@YAAGPSYGGR.S
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	1935.30	0.48	0.1599 F.LSEEPPYS@YPTGNHTY.Q
		L.SEEPPY@SYPTGNHTY.Q	Y31	1822.11	0.38	0.1081 L.SEEPPYS@YPTGNHTY.Q
		S.KRPVFLSEEPPY@SYPTGNHTY.Q	Y31	2562.44	0.24	0.0155 S.KRPVFLSEEPPYS@YPTGNHTY.Q
		R.YAHQQPPS@PLPVY@SSSAK.N	Y88	2117.57	0.59	0.0680 R.YAHQQPPS@PLPVYSS@SAK.N
		R.YAHQQPPSPLPVY@SSSAK.N	Y88	2038.11	1.13	0.0227 R.YAHQQPPSPLPVYS@SSAK.N
		R.YAHQQPPS^PLPVY@SSSAK.N	Y88	2020.40	1.42	0.0065 R.YAHQQPPS^PLPVYS@SSAK.N
		R.AGEEEHVY@SFPNK.Q	Y118	1587.51	0.82	0.1862 R.AGEEEHVYS@FPNK.Q
				1587.54	0.85	0.1021 R.AGEEEHVYS@FPNK.Q
		R.AGEEEHVY@SFPNKQK.S	Y118	1843.79	0.95	0.0905 R.AGEEEHVYS@FPNKQK.S
				1843.66	0.82	0.0656 R.AGEEEHVYS@FPNKQK.S
Pleckstrin homology domain containing family C member 1	Q8CIB5	L.IMPGSGSIY@SSPGLY.S	Y179	1610.20	1.45	0.0345 L.IMPGSGS@IYSSPGLY.S
Syndecan-4 precursor	O35988	K.KAPTNEFY@A.-	Y197	1120.70	0.19	none
		Y.KKAPTNEFY@A.-	Y197	1249.15	0.55	none
Talin 1	P26039	K.TM#QFEPSTMVY@DAC*R.M	Y26	1931.70	-0.05	none
		K.TMQFEPSTMVY@DAC*R.M	Y26	1917.52	1.77	none
		M.QFEPSTMVY@DAC*RM.I	Y26	1815.37	0.66	none
		F.LSDDDPKKGIWLEAGKALDY@Y.M	Y70	2477.47	0.27	0.0283 F.LSDDDPKKGIWLEAGKALDYY@.M
		K.ALDY@YM#LR.N	Y70	1142.35	1.83	0.1561 K.ALDYY@M#LR.N
		K.ALDY@YMLR.N	Y70	1126.77	2.25	0.1423 K.ALDYY@MLR.N
		W.LEAGKALDY@Y.M	Y70	1222.98	0.41	0.1351 W.LEAGKALDYY@.M
		R.IGITNHDEY@SLVR.E	Y127	1597.61	0.83	0.1460 R.IGITNHDEYS@LVR.E
				1597.19	0.41	0.1268 R.IGITNHDEYS@LVR.E
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	1940.75	0.79	none
Tensin	Q9DBT6	R.HAAY@GGY@STPEDR.R	Y213,Y216	1584.27	0.65	0.0415 R.HAAY@GGYS@TPEDR.R
		R.HAAY@GGYSTPEDR.R	Y213	1504.50	0.88	none
		R.HAAYGGY@STPEDR.R	Y216	1503.84	0.22	0.0381 R.HAAYGGYS@TPEDR.R
		R.HAAYGGY@STPEDRRPT^LSR.Q	Y216	2197.12	1.08	0.0284 R.HAAYGGYST@PEDRRPT^LSR.Q
Tensin 2	Q8CJ95	H.TRGPLDGSPY@AQVQ.R	Y460	1568.33	-0.41	0.0563 H.TRGPLDGS@PYAQVQ.R
		L.AHTRGPLDGSPY@AQVQ.R	Y460	1777.10	0.26	0.1306 L.AHTRGPLDGS@PYAQVQ.R
		R.GPLDGSPY@AQVQR.V	Y460	1468.33	0.63	none
		K.VGEEGHEGC*SY@AVC*SEGR.Y	Y747	2064.20	1.45	0.0532 K.VGEEGHEGC*S@YAVC*SEGR.Y
Tensin 3	Q5SSZ5	L.HTQGPVDGSLY@AKVR.K	Y354	1709.58	1.72	none
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	2647.84	1.57	0.0899 R.KPSAPTPVQAYGQS@NYSTQTWVR.Q
Vinculin	Q64727	R.ILLRNPGNQAAY@EHFETMK.N	Y691	2312.45	0.33	none
		K.SFLDSGY@R.I	Y821	1025.39	0.93	0.1505 K.SFLDS@GYR.I
ADHESION: CELL/CELL						
Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M	Y96	2054.94	-0.07	0.0532 K.LNGPQDHNHLLYS@TIPR.M
				2057.00	1.98	0.0202 K.LNGPQDHNHLLYS@TIPR.M
		R.HYEDGYPGGSDNY@GSLSR.V	Y228	2054.01	0.18	0.0958 R.HYEDGYPGGSDNYGS@LSR.V
				2054.34	0.51	0.0534 R.HYEDGYPGGSDNYGS@LSR.V
		R.HYEDGYPGGSDNY@GS^LSR.V	Y228	2036.37	0.54	0.1906 R.HYEDGYPGGS^DNYGS@LSR.V
		R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R	Y291,Y296	3893.08	1.54	0.0094 R.FHPEPYGLEDDQRS@MGYDDLDY@GMMSDYGTAR.R
		K.SDNNY@STLNER.G	Y877	1392.42	-0.16	0.1096 K.SDNNYS@TLNER.G
Ctnnd1 protein -- p120 catenin, isoform	Q80XQ4	K.SLDNNY@STLNER.G	Y904	1505.93	0.27	0.1639 K.SLDNNYS@TLNER.G

Discs large homolog 3	P70175	R.RDNEVDGQDY@HFVVSR.E	Y705	2017.09	1.20	none
Fath protein [fragment]	Q497H5	K.NIY@SDIPPQVPVRPISYTPSIPSDSR.N	Y952	2979.37	0.87	0.0523 K.NIYS@DIPPQVPVRPISYTPSIPSDSR.N
Partitioning-defective 3 homolog -- PARD3	Q99NH2	R.ISHSLY@SGIEGLDESPTR.N	Y719	2041.58	0.62	0.0075 R.ISHSLYS@GIEGLDESPTR.N
				2041.22	0.26	0.0823 R.ISHSLYS@GIEGLDESPTR.N
		R.RIS@HSLY@SGIEGLDESPTR.N	Y719	2278.02	0.96	0.0016 R.RIS@HS@LYSGIEGLDESPTR.N
		R.RISHS@LY@SGIEGLDESPTR.N	Y719	2278.89	1.83	0.0184 R.RIS@HSLY@SGIEGLDESPTR.N
		R.RISHSLY@SGIEGLDESPTR.N	Y719	2197.76	0.70	0.0938 R.RISHS@LYSGIEGLDESPTR.N
		R.ERDY@AEIQDFHR.T	Y1076	1660.64	1.91	none
		R.EGHLMDTLY@AQVK.K	Y1123	1585.31	0.56	none
		R.KNASSISQDSWEQNY@APGEGFQSAK.E	Y1238	2810.61	1.37	none
Plakophilin-4; Armadillo related protein	Q68FH0	R.TVHDMDQFGQQQYDIY@ER.M	Y371	2354.86	1.87	0.0523 R.TVHDMDQFGQQQY@DIYER.M
		L.RSAVSPDLHITPIY@EGRTY.Y	Y414	2256.00	0.88	0.1258 L.RSAVSPDLHITPIYEGRT@Y.Y
		R.NNY@ALNTAATY@AEPYRPVQYR.V	Y469,Y477	2636.51	1.30	0.0795 R.NNY@ALNTAAT@YAEPYRPVQYR.V
		R.NNYALNTAATY@AEPYRPVQYR.V	Y477	2556.47	1.26	0.0820 R.NNYALNTAAT@YAEPYRPVQYR.V
		Y.ALNTAATY@AEPY.R	Y477	1365.33	0.72	0.0377 Y.ALNTAAT@YAEPY.R
		R.SY@EDPYC*DDRVHFPAST@DYSTQYGLK.S	Y1137	3276.05	1.73	0.0055 R.S@YEDPYC*DDRVHFPAST@DYSTQYGLK.S
		R.SY@EDPYC*DDRVHFPASTDYSTQYGLK.S	Y1137	3195.28	0.96	0.0004 R.S@YEDPYC*DDRVHFPASTDYSTQYGLK.S
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	1532.14	0.43	none
Tight junction protein ZO-1	P39447	Y.LSAPGSEY@SMY.S	Y830	1284.76	0.77	0.1283 Y.LSAPGSEYS@MY.S
		R.HEEQPAPAY@EVHNR.Y	Y1164	1756.95	0.17	none
Tight junction protein ZO-2	Q9Z0U1	R.IEIAQKHPDIY@AVPIK.A	Y1095	1915.07	0.03	none
CYTOSKELETON: ACTIN-ASSOCIATED						
Actins and actin-related proteins; Regulators of actin assembly						
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	K.IWHHTFY@NELR.V	Y93	1597.18	1.43	none
		M.VGMGQKDSY@VGDEAQSKRGIL.T	Y55	2319.05	0.93	0.0078 M.VGMGQKDS@YVGDEAQSKRGIL.T
Cofilin-1, non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C	Y139	1872.14	1.35	none
		K.LTGIKHELQANC*Y@EEVKDR.C	Y139	2384.74	1.62	none
		L.TGIKHELQANC*Y@EEVKDRC*TL.A	Y139	2645.71	1.53	none
Src substrate cortactin	Q60598	Y.TSEPVY@ETTEAPGHY.Q	Y466	1762.41	1.67	0.0743 Y.T@SEPVYETTEAPGHY.Q
				1761.47	0.73	0.1176 Y.TSEPVYET@TEAPGHY.Q
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R	Y39	1714.48	0.67	none
		R.VQIY@HNPTANSFR.V	Y39	1627.93	1.15	none
				1627.16	0.38	none
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.DRETSKVIY@DFIEK.T	Y253	1825.26	2.36	none
		K.VIY@DFIEK.T		1106.98	0.43	none
WD-repeat protein 1; Actin interacting protein 1 -- AIP1	O88342	K.AHDGGIY@AISWSPDSTHLLSASGDK.T	Y237	2665.90	0.67	0.1286 K.AHDGGIYAIS@WSPDSTHLLSASGDK.T
Other actin-associated proteins						
Band 4.1-like protein 2	O70318	N.TLRVDGDNIY@VRHSNL.M	Y606	1953.32	1.35	none
		R.VDGDNIY@VR.H	Y606	1131.00	0.48	none
Calponin-2	Q08093	K.CASQSGMTAY@GT@RR.H	Y184	1647.70	-0.07	none
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q	Y316	1621.87	1.24	0.1644 Y.HGEYPDDYPREY@.Q
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	2061.91	0.95	none
				2062.13	1.17	none
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	3033.49	1.01	none
		K.QQPTQFINPETPGY@VGFANLPNQVHRK.S	Y17	3161.57	0.98	0.1711 K.QQPTQFINPET@PGYVGFANLPNQVHRK.S
Sickle tail-b (Sickle tail-a)	Q75UV8	R.NVY@YELNDVR.N	Y244	1365.69	1.07	0.1787 R.NVYY@ELNDVR.N
		R.NEGFY@ADPYLYHEGR.M	Y393	1911.53	0.72	0.1910 R.NEGFYADPY@LYHEGR.M
				1911.11	0.30	none
CYTOSKELETON: MICROTUBULE-ASSOCIATED						
none						
CYTOSKELETON: OTHER						
Vimentin	P20152	R.FANY@IDKVR.F	Y116	1205.86	0.25	none

		R.SLY@SSSPGGAYVTR.S	Y52	1525.08	0.37	0.0791 R.S@LYSSSPGGAYVTR.S
TRAFFICKING/TRANSPORT						
Vesicle transport						
Double C2-like domain containing protein beta	P70169	K.TY@LKPDVDKKSK.H	Y309	1501.15	-0.65	0.0137 K.T@YLKPDVDKKSK.H
		K.TY@LKPDVDKKS^K.H	Y309	1485.35	1.55	0.0102 K.T@YLKPDVDKKS^K.H
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	1330.16	1,51	none
Low-density lipoprotein receptor precursor	P35951	F.DNPVY@QKTTEDELHIC*RSQDGY.T	Y832	2748.60	0.42	0.1674 F.DNPVYQKT@TEDELHIC*RSQDGY.T
Nucleoporin-like protein RIP	Q8K2K6	K.AGLQTADKY@AALANLDNIFSAGQGGDQGSGFGTTGK.A	Y327	3583.60	1.91	0.0361 K.AGLQT@ADKYAALANLDNIFSAGQGGDQGSGFGTTGK.A
Transferrin receptor protein 1 -- TfR	Q62351	F.SNLFGGEPLSY@TRF.S	Y20	1668.43	0.64	0.0854 F.SNLFGGEPLSYT@RF.S
		R.SAFSNLFGGEPLSY@TR.F	Y20	1827.76	1.91	0.1348 R.SAFSNLFGGEPLS@YTR.F
Nucleocytoplasmic transport						
None						
Other transport						
Gap junction alpha-1 protein -- Connexin 43	P23242	K.QASEQNWANY@SAEQNR.M	Y312	1976.23	0.40	0.1144 K.QASEQNWANYS@AEQNR.M
				1977.21	1.38	0.0819 K.QASEQNWANYS@AEQNR.M
Lysosomal-associated transmembrane protein 4A	Q60961	K.IPEKEPPPPY@LPA.-	Y230	1528.10	0.32	none
Sodium bicarbonate cotransporter 2B homolog [fragment]	Q8BTY2	K.DKDSDKEDGRES@PSY@DTPSQR.V	Y92	2574.16	2.11	0.0283 K.DKDSDKEDGRES@PS@YDTPSQR.V
		K.DKDS^DKEDGRESPSY@DTPSQR.V	Y92	2474.89	0.84	0.0490 K.DKDS^DKEDGRESPS@YDTPSQR.V
Solute carrier family 38, member 2	Q8CFE6	K.SHY@ADVDPENQNFLLESNLGK.K	Y41	2471.70	1.57	0.0111 K.S@HYADVDPENQNFLLESNLGK.K
		K.SHY@ADVDPENQNFLLESNLGKK.K	Y41	2600.03	1.81	0.0594 K.S@HYADVDPENQNFLLESNLGKK.K
		L.KSHY@ADVDPENQNF.L	Y41	1744.38	0.65	0.0915 L.KS@HYADVDPENQNF.L
METABOLIC AND BIOSYNTHETIC ENZYMES						
Glycolytic enzymes						
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G	Y24	1486.86	0.14	0.1715 R.GNPTVEVDLYT@AK.G
		R.AAVPSGASTGIY@EALELR.D	Y43	1885.67	0.73	0.0866 R.AAVPSGAST@GIYEALELR.D
Glyceraldehyde-3-phosphate dehydrogenase -- GAPDH	P16858	K.LISWYDNEY@GYSNR.V	Y315	1861.30	1.50	0.1579 K.LISWYDNEYGY@SNR.V
Phosphoglycerate mutase 1	Q9DBJ1	R.FSGWY@DADLSPAGHEEAKR.G	Y25	2217.88	1.89	none
Pyruvate kinase, isozyme M2	P52480	R.EAEAAIY@HLQLFEELRR.L	Y389	2168.61	0.52	none
Other metabolic/biosynthetic enzymes						
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	R.VC*MVY@DLYPTLTPLAVAYAR.A	Y290	2398.26	2.10	0.0520 R.VC*MVYDLY@PTLTPLAVAYAR.A
Serine hydroxymethyltransferase, cytosolic	P50431	K.MLSQPLKDSDAEVY@SIIKK.E	Y28	2246.33	1.18	0.0277 K.MLSQPLKDSDAEVYS@IIKK.E
TK: Transketolase	P40142	K.NMAEQIIQEIY@SQVQSK.K	Y275	2091.24	2.24	0.1724 K.NMAEQIIQEIYS@QVQSK.K
RNA SYNTHESIS AND PROCESSING						
Transcription machinery and regulation						
Polymerase I and transcript release factor	O54724	F.KVMIY@QDEVKLPAKL.S	Y158	1856.39	1.38	none
		K.VMIY@QDEVKLPAK.L	Y158	1615.09	1.26	none
		F.TPDHVVY@ARSKTAVY.K	Y310	1788.15	1.26	0.0051 F.TPDHVVYARS@KTAVY.K
		K.SFTPDHVVY@AR.S	Y310	1373.76	2.12	none
		R.KSFTPDHVVY@AR.S	Y310	1500.74	1.00	none
DEAD(DEAH)-box helicases						
ATP-dependent RNA helicase DDX3X	Q62167	R.GRGDY@DGIGGR.G	Y103	1202.89	0.36	none
		R.GRGDY@DGIGGRGDR.S	Y103	1531.65	0.97	none
hnRNPs and snRNPs						
none						
Splicing factors						

none						
Other RNA binding and processing						
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232	2447.26	1.01	0.1333 Y.T@IQGQYAIPQPDLTKLHQLAM.Q
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S	Y124	1648.90	1.21	0.0356 R.YDSRPGGYGYGY@GR.S
		Y.DSRPGGYGY@GY.G	Y124	1272.00	0.49	0.1976 Y.DSRPGGY@GYGY.G
		R.YDSRPGGYGYGY@GR.S	Y126	1648.92	1.23	0.0531 R.YDSRPGGYGY@GYGR.
		R.YSGGNYRDNY@DN.-	Y151	1517.93	0.36	none
RNA-binding protein 14	Q8C2Q3	R.LPDAHSDY@AR.Y	Y645	1224.48	-0.06	none
PROTEIN SYNTHESIS AND PROCESSING						
tRNA synthetases						
None						
Translation machinery						
40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	1190.22	0.56	none
60S acidic ribosomal protein P0	P14869	K.IIQLLDDY@PK.C	Y24	1299.35	1.67	none
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.GDPQVYEELFSY@AC*PK.F	Y415	1982.78	-0.06	0.1087 K.GDPQVYEELFS@YAC*PK.F
Eukaryotic initiation factor 4A-I	P60843	R.GFKDQIY@DIFQK.L	Y197	1582.11	0.34	none
Elongation factor 1-alpha 1 -- eEF1A-1 (eEF1A-2)	P10126	K.STTTGHLIY@K.C	Y29	1201.02	0.42	none
		R.EHALLAY@TLGVK.Q	Y141	1395.43	0.69	0.0479 R.EHALLAYT@LGVK.Q
Laminin receptor 1 (ribosomal protein SA)	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	3077.58	1.12	0.0142 R.ADHQPLTEAS@YVNLPTIALC*NTDSPLR.Y
G1 to phase transition 2 -- GSPT2	Q9CY91	K.Y@LIVLINK.M	Y347	1056.15	0.53	none
Post-translational modifiers						
Probable palmitoyltransferase ZDHHC5	Q8VDZ4	R.EPS@PVRY@DNLSR.H	Y533	1593.84	1.12	none
		R.LLPTGPPHREPS@PVRY@DNLSR.H	Y533	2562.09	0.82	0.1950 R.LLPTGPPHREPSPVRY@DNLS@R.H
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	F.SPVLGPRPREPS^PVRY@DNL.S	Y538	2211.91	0.76	none
		R.PREPS^PVRY@DNLSR.T	Y538	1748.69	0.82	none
		L.RSQTDSLFGDSGVY@DTPSSY.S	Y576	2262.51	0.55	0.1555 L.RSQTDSLFGDS@GVYDTPSSY.S
Chaperones and associated proteins						
BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I	Y246	2381.14	2.05	0.1751 K.THYPAQQGEYQPQQPVY@HK.I
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I	Y336	1944.08	2.04	none
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	1240.45	-0.13	0.1861 K.SIYY@ITGESK.E
PROTEIN DEGRADATION						
Ubiquitin conjugation regulators						
E3 ubiquitin protein ligase CBL	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L	Y672	2393.32	1.04	0.0886 K.IKPSSSANAIYS@LAARPLPMPK.L
E3 ubiquitin-protein ligase CBL-B	Q3TTA7	R.ASQDY@DQLPSSSDGSQAPARPPKPR.P	Y889	2736.24	0.96	0.0634 R.AS@QDYDQLPSSSDGSQAPARPPKPR.P
Probable E3 ubiquitin-protein ligase MGRN1	Q9D074	L.RAVSPAIPSAPLY@EEITY.S	Y389	2057.51	0.47	none
Proteasome components						
Proteasome subunit alpha type 2 -- PSMA2	P49722	K.HIGLVY@SGMGPDYR.V	Y75	1645.35	0.59	0.0713 K.HIGLVYS@GMGPDYR.V
Other proteases and endopeptidases						
ADAM 9 precursor	Q61072	K.ISSQGNLIPARPAPAPPLY@SSLT.-	Y841	2430.83	0.55	0.0069 K.ISSQGNLIPARPAPAPPLYSS@LT.-
		N.LIPARPAPAPPLY@SSLT.-	Y841	1844.08	0.07	0.1111 N.LIPARPAPAPPLYS@SLT.-
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	1239.31	-0.22	0.1597 R.MTELYDY@PK.Y

NUCLEAR PROTEINS						
Histone H2B type 1-B	Q64475	R.KESYSVY@VYK.V	Y41	1346.13	0.48	0.1132 R.KESYS@VYVYK.V
MISCELLANEOUS						
Microfibril-associated glycoprotein 3 precursor	Q922T2	R.IKERPALDAQSGIY@VINPELGR.S	Y277	2520.18	0.84	0.1937 R.IKERPALDAQS@GIYVINPELGR.S
Psychosine receptor	Q61038	R.Y@LAVVYPLK.F	Y115	1145.67	0.04	none
FUNCTION UNKOWN OR UNCERTAIN						
Named proteins of unknown/uncertain function						
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213	2601.76	1.50	0.0207 R.KTPQGPPEIYS@DTQFPSLQSTAK.H
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	Q9DBJ3	K.MIGKDY@DTLSK.Y	Y274	1350.97	0.34	none
		M.IGKDY@DTLSKY.S	Y274	1383.30	0.64	none
Suppression of tumorigenicity 5	Q924W7	K.STLEENAYEDIVGGLPKENPY@EDVDLK.N	Y498	3118.71	1.26	none
Pituitary tumor-transforming gene 1 protein-interacting protein precursor	Q8R143	F.KEQNPY@EKF.-	Y171	1262.96	0.38	none
		K.EQNPY@EKF.-	Y171	1134.80	0.32	none
WW domain binding protein 4	Q3TWW5	K.FGDY@C*K.C	Y15	870.85	1.55	none
		K.S^QPKKFGDY@C*K.C	Y15	1420.64	1.00	none
Unnamed proteins of unknown/uncertain function						
hypothetical protein -- Ccdc105	Q9D4K7	K.FNQEM#Y@VTRGIIK.G	Y372	1695.48	0.63	0.0596 K.FNQEM#YVT@RGIIK.G
				1696.16	1.32	none
hypothetical HAT dimerisation/BED finger/Bipartite nuclear localization signal/Zinc finger BED-type profile containing protein	Q3UMD3	W.HFFHVDPQY@TW.R	Y145	1558.04	1.37	0.1748 W.HFFHVDPQYT@W.R
hypothetical Intradiol ring-cleavage dioxygenase/WD40-like containing protein	Q3UHA3	R.YNEMTY@IFDLLHQK.H	Y2161	1895.60	0.72	0.0984 R.YNEMT@YIFDLLHQK.H
MKIAA1686 protein [fragment]	Q6ZPK1	K.ERPISMINEASNY@NMASDY@AVHPMSPVGR.T	Y65,Y71	3397.58	1.09	0.0204 K.ERPISMINEAS@NYNMASDY@AVHPMSPVGR.T
PREDICTED: similar to Oligophrenin 1	UPI00005125B7	K.LWLEAMDGKEPIY@TLPAIISK.K	Y371	2469.33	1.04	0.0264 K.LWLEAMDGKEPIYT@LPAIISK.K
		R.KLWLEAM#DGKEPIY@TLPAIISK.K	Y371	2612.99	0.61	0.0171 R.KLWLEAM#DGKEPIYT@LPAIISK.K
		R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371	2597.30	0.92	0.0221 R.KLWLEAMDGKEPIYT@LPAIISK.K
PREDICTED: similar to zinc finger CCCH type containing 11A isoform 1	UPI00001C484B	R.IPFS@KTY@SKTEK.V	Y399	1588.48	-0.29	0.0722 R.IPFS@KTYS@KTEK.V
Protein KIAA1914	Q5DTU0	K.VAQQPLSLVGC*DVLPDPSPDHLY@SFR.I	Y413	2992.13	1.71	0.0033 K.VAQQPLSLVGC*DVLPDPSPDHLYS@FR.I
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	2910.62	-1.84	0.0491 K.EKLLLC*HGPSLS@LPALSGVRY@NAEK.K

END

Table S1. Phosphotyrosine sites from the nontransformed 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)				
Proto-oncogene tyrosine-protein kinase -- Src (Yes, Fyn, Hck)	Q80XU2	R.LIEDNEY@TAR.Q	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.
		F.LEDYFTSTEPQY@QPGENL.-	Y529	C-terminal negative regulatory site. Peptide unique to Src.
		Y.FTSTEPQY@QPGENL.-	Y529	
Proto-oncogene tyrosine-protein kinase -- Fyn (Yes)	P39688	R.KLDNGGYY@ITTR.A	Y213	Site in SH2 domain. Peptide identical in Yes (Q04736)
		F.LEDYFTATEPQY@QPGENL.-	Y527	C-terminal negative regulatory site; peptide identical in Yes (Q04736)
		F.TATEPQY@QPGENL.-	Y527	
		Y.FTATEPQY@QPGENL.-	Y527	
Fyn-related kinase -- Frk	Q922K9	F.C*PPEAPRSQEPERSHGQY@F.V	Y53	Site in SH3 domain.
		R.SQEPERSHGQY@FVALFDYQAR.T	Y53	
		K.LEDYFETDC*SY@SDTNNFIN.-	Y504	C-terminal negative regulatory site.
		W.KLEDYFETDC*SY@SDTNNFIN.-	Y504	
		W.KLEDYFETDCS@Y@SDTNNFIN.-	Y504	
Fer	P70451	K.VQENDGKEPPPVVNY@EEDAR.S	Y402	
		F.GMSRQEDGGVY@SSSGL.K	Y715	Kinase domain activation loop site.
Proto-oncogene tyrosine-protein kinase ABL1	P00520	M.TGDTY@TAHAGAKFPIKW.T	Y393	Kinase domain activation loop site.
		R.LMTGDTY@TAHAGAK.F	Y393	
Activated CDC42 kinase 1 -- ACK	O54967	M.RALPQNDDHY@VMQEH.R	Y284	Kinase domain activation loop site.
		W.DARPLPPPPAY@DDVAQDEDDF.E	Y650	The alanine residue preceding the Y-site is only found in ACK entry UPI0000D6355E
		F.ASDPKY@ATPQVIQAPGPRAGPC*.I	Y842	
		K.VSSTHY@YLLPERPPYLER.Y	Y874	
		R.KVSSTHY@YLLPERPPYLER.Y	Y874	
		R.KVSS@THYY@LLPERPPYLER.Y	Y875	
Activated CDC42 kinase 1 -- ACK, isoforms 2 and 3	O54967-2	H.LGRVKKPTY@DPVSEDPDPLSSDF.K	Y518	These peptides are unique to ACK isoforms 2 (O54967-2) and 3 (O54967-3).
		K.KPTY@DPVSEDPDPLSSDFKR.L	Y518	
		L.GRVKKPTY@DPVSEDPDPLSSDF.K	Y518	
		R.VKKPTY@DPVSEDPDPLSSDFK.R	Y518	
		R.VKKPTY@DPVSEDPDPLSSDFKR.L	Y518	
Focal adhesion kinase, isoform 3 -- FAK	P34152-3	M.RTHAVSVSETDDY@AEIIDEEDTY.T	Y397	Autophosphorylation site.
		R.THAVSVSETDDY@AEIIDEEDTYTMPSTR.D	Y397	
		R.Y@MEDSTY@YK.A	Y570,Y576	
		R.Y@MEDSTY@YKASK.G	Y570,Y576	
		R.Y@MEDSTY@Y@KASK.G	Y570,Y576,Y577	Kinase domain activation loop sites.
		F.GLSRYM#EDSTY@Y.K	Y576	
		F.GLSRYMEDSTY@Y.K	Y576	
		L.GDFGLSRYM#EDSTY@Y.K	Y576	
		L.GDFGLSRYMEDSTY@Y.K	Y576	
		R.YM#EDST@YY@KASK.G	Y577	
		R.YM#EDSTY@Y@K.A	Y576,Y577	
		R.YM#EDSTY@Y@KASK.G	Y576,Y577	
		R.YM#EDSTY@YK.A	Y576	
		R.YM#EDSTY@YKASK.G	Y576	
		R.YM#EDSTYY@K.A	Y577	
		R.YMEDSTY@Y@K.A	Y576,Y577	
		R.YMEDSTY@Y@KASK.G	Y576,Y577	
		R.YMEDSTY@YK.A	Y576	
		R.YMEDSTY@YKASK.G	Y576	
		R.YMEDSTYY@K.A	Y577	
		Y.M#EDSTY@Y@KASKGKLPIKW.M	Y576,Y577	
		Y.MEDSTY@Y@KASKGKLPIKW.M	Y576,Y577	
Tyrosine-protein kinase JAK1	P52332	K.AIETDKEY@Y@TVKDDR.D	Y1033,Y1034	Kinase domain activation loop sites.
Tyrosine kinases (receptor)				
Discoidin domain receptor 2 precursor -- DDR2	Q62371	R.IFPLRPDY@QEPSR.L	Y481	
		Y.DRIFPLRPDY@QEPSRL.I	Y481	
		R.NLY@SGDY@YR.I	Y735,Y739	Kinase domain activation loop sites.
Ephrin type-A receptor 2 precursor -- EphA2	Q03145	K.SEQLKPLKTY@VDPHTYEDPNQAVLK.F	Y589	

		L.KTY@VDPHTYEDPNQAVL.K	Y589	
		L.KTY@VDPHT@YEDPNQAVL.K	Y589	
		K.SEQLKPLKT@YVDPHTY@EDPNQAVLK.F	Y595	
		K.TYVDPHTY@EDPNQAVLK.F	Y595	
		L.KTYVDPHTY@EDPNQAVL.K	Y595	
		L.KTY@VDPHTY@EDPNQAVL.K	Y589,Y595	
		F.GLSRVLEDDPEATY@TTSGGKIPIRW.T	Y773	Kinase domain activation loop site.
		L.SRVLEDDPEATY@TTSGGKIPIRW.T	Y773	
		R.VLEDDPEATY@TTSGGK.I	Y773	
		R.VLEDDPEATY@TTSGGKIPIR.W	Y773	
Ephrin type-A receptor 3 precursor -- EphA3 (EphA4, EphA5)	P29319	R.VLEDDPEAAY@TTR.G	Y779	Kinase domain activation loop site. Peptide identical in EphA4 (Q03137) and EphA5 (Q60629).
Ephrin type-A receptor 4 precursor -- EphA4	Q03137	Y.VDPFTY@EDPNQAVREF.A	Y602	
Ephrin type-A receptor 5 precursor -- EphA5	Q60629	R.TY@IDPHTY@EDPNQAVHEFAK.E	Y489,Y495	
Ephrin type-B receptor 2 precursor -- EphB2 (EphB1)	P54763	K.IY@IDPFTY@EDPNEAVR.E	Y604,Y610	Peptide identical in EphB1.
		Y.IDPFTY@EDPNEAVREF.A	Y610	Peptide identical in EphB1-4.
Ephrin type-B receptor 3 precursor -- EphB3 (EphB4)	P54754	K.VY@IDPFTY@EDPNEAVR.E	Y603,Y609	Peptide identical in EphB4 (Q91YM0)
		K.VYIDPFTY@EDPNEAVR.E	Y609	
		R.FLEDDPSDPTY@TSSLGGKIPIR.W	Y787	Kinase domain acivation loop site.
Eph receptor B4 -- EphB4	Q91YM0	K.HGQYLIGHGTKVY@IDPFTY@EDPNEAVR.E	Y590,Y596	
		K.HGQYLIGHGT^KVYIDPFTY@EDPNEAVR.E	Y596	
		Y.LIGHGTKVY@IDPFTY@EDPNEAVREF.A	Y590,Y596	
		R.FLEENSS@DPTY@TSSLGGKIPIR.W	Y774	Kinase domain activation loop site.
		R.FLEENSSDPTY@TSSLGGKIPIR.W	Y774	
Hepatocyte growth factor receptor precursor -- MET	P16056	F.GLARDMYDKEY@Y.S	Y1232	
		F.GLARDMYDKEYY@.S	Y1233	
		R.DM#YDKEY@Y@SVHNK.T	Y1232,Y1233	Kinase domain activation loop sites.
		R.DM#YDKEY@YS@VHNK.T	Y1232	
		R.DM#YDKEY@YSVHNK.T	Y1232	
		R.DMYDKEY@Y@SVHNK.T	Y1232,Y1233	
		R.DMYDKEY@Y@SVHNKTGAK.L	Y1232,Y1233	
		R.DMYDKEY@YSVHNK.T	Y1232	
		R.DMYDKEY@YSVHNKT^GAK.L	Y1232	
		R.DMYDKEY@YS^VHNK.T	Y1232	
		R.DMYDKEYY@SVHNK.T	Y1233	
		R.DMYDKEYY@SVHNKT^GAK.L	Y1233	
Insulin-like growth factor 1 receptor precursor -- IGF1R (InsR)	Q60751	R.DIY@ETDY@Y@RK.G	Y1163, Y1167,Y1168	Kinase domain activation loop sites. Peptide identical in Insulin receptor (InsR, KinBase).
		R.DIY@ETDY@YRK.G	Y1163, Y1167	
		R.DIYETDY@YR.K	Y1167	
		R.DIYETDYY@RK.G	Y1168	
Proto-oncogene tyrosine-protein kinase -- MER	Q60805	K.KIY@SGDY@YR.Q	Y744,Y748	Kinase domain activation loop sites. Peptide identical in Tyro3 (KinBase). Axl family.
		K.KIYSGDY@YR.Q	Y748	
Tyrosine-protein kinase receptor UFO precursor -- Axl	Q00993	F.GLSKKIYNGDY@Y.R	Y696	Kinase domain activation loop sites.
		K.KIYNGDY@YR.Q	Y696	
		K.IYNGDY@YR.Q	Y696	
		K.IYNGDYY@R.Q	Y697	
		F.GLSKKIYNGDYY@.R	Y697	
Other protein kinases				
CDC2: Cell division control protein 2 homolog - CDK1 (CDK2)	P11440	K.IEKIGEGT@Y@GVVYK.G	Y15	
		K.IEKIGEGTY@GVVY.K	Y15	
		K.IEKIGEGTY@GVVYK.G	Y15	
		K.IEKIGEGT^Y@GVVYK.G	Y15	
		K.IGEGT@Y@GVVYK.G	Y15	
		K.IGEGTY@GVVYK.G	Y15	Peptide identical in CDK2.
		K.IGEGTY@GVVYKGR.H	Y15	
		K.IGEGT^Y@GVVYK.G	Y15	
		K.IGEGT^Y@GVVYKGR.H	Y15	
		Y.IKIEKIGEGTY@GVVY.K	Y15	
		Y.IKIEKIGEGT^Y@GVVY.K	Y15	
		-.DYIKIEKIGEGTY@GVVY.K	Y15	
		K.IGEGTYGVVY@K.G	Y19	Peptide identical in CDK2.
Cell division protein kinase 2 -- CDK2	P97377	K.VEKIGEGTY@GVVYK.A	Y15	

Dual-specificity tyrosine-phosphorylation regulated kinase 1A -- DYRK1A (DYRK1B)	Q61214	K.VYNDGYDDDNY@DYIVK.N R.KVYNDGYDDDNY@DYIVK.N R.KVYNDGYDDDNY@DYIVKNGEK.W Y.NDGYDDDNY@DYIVKNGEKW.M R.IYQY@IQSR.F Y.QY@IQSRFY.R	Y145 Y145 Y145 Y145 Y321 Y321	Site lies just N-terminal to the kinase domain. Kinase domain activation loop site. Identical peptide in DYRK1B (Q9Z188).
Glycogen synthase kinase-3 beta -- GSK-3beta (GSK3alpha)	Q9WV60	K.QLVRGEPNVSY@IC*SRY.Y K.QLVRGEPNVSY@IC*SRYY.R L.VRGEPNVSY@IC*.S L.VRGEPNVSY@IC*S@RYY.R L.VRGEPNVSY@IC*SRY.Y L.VRGEPNVSY@IC*SRYY.R L.VRGEPNVSY@IC*S^RY.Y N.VSY@IC*SRY.Y N.VSY@IC*SRYY.R Q.LVRGEPNVSY@IC*SRY.Y Q.LVRGEPNVSY@IC*SRYY.R R.GEPNVSY@IC*SR.Y R.GEPNVSY@IC*SRYY.R	Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216 Y216	Activation loop site. All peptides identical in GSK3alpha.
Homeodomain-interacting protein kinase 1 -- HIPK1 (HIPK2)	O88904	H.VSKAVC*STY@LQSRY.Y K.AVC*STY@LQSR.Y S.KAVC*STY@LQSRY.Y	Y352 Y352 Y352	Kinase domain activation loop site. Peptides identical in HIPK2.
Homeodomain-interacting protein kinase 3 -- HIPK3	Q9ERH7	H.VSKTVC*STY@L.Q H.VSKTVC*STY@LQSRY.Y K.TVC*STY@LQSR.Y	Y359 Y359 Y359	Kinase domain activation loop site.
Hypothetical Protein kinase-like (PK-like) structure containing protein -- SgK223	Q8CB68	K.C*VGQAAELQPASLLRDPVQPEPIY@AESAK.R K.C*VGQAAELQPASLLRDPVQPEPIY@AESAKR.K	Y196 Y196	A protein kinase of the NKF3 family.
Mitogen-activated protein kinase 3 -- ERK1	Q63844	F.GLARIADPEHDHTGFLT@EY@VATRW.Y F.GLARIADPEHDHTGFLTEY@VATRW.Y F.GLARIADPEHDHTGFLT^EY@VATRW.Y F.GLARIADPEHDHTGFLT^EY@VATRWY.R F.LTEY@VATRW.Y R.IADPEHDHTGFLT@EY@VATR.W R.IADPEHDHTGFLTEY@VATR.W R.IADPEHDHTGFLT^EY@VATR.W	Y205 Y205 Y205 Y205 Y205 Y205 Y205 Y205	Kinase domain activation loop site.
Mitogen-activated protein kinase 1 -- ERK2	P63085	F.GLARVADPDHDHTGFLT@EY@VATRW.Y F.GLARVADPDHDHTGFLT@EY@VATRWY.R F.GLARVADPDHDHTGFLTEY@VATRWY.R F.GLARVADPDHDHTGFLT^EY@VATRW.Y F.GLARVADPDHDHTGFLT^EY@VATRWY.R F.GLARVADPDHDHT^GFLTEY@VATRW.Y R.VADPDHDHTGFLT@EY@VATR.W R.VADPDHDHTGFLTEY@VATR.W R.VADPDHDHTGFLTEY@VATRW.Y R.VADPDHDHTGFLTEY@VAT^R.W R.VADPDHDHTGFLT^EY@VATR.W R.VADPDHDHTGFLT^EY@VATRW.Y	Y185 Y185 Y185 Y185 Y185 Y185 Y185 Y185 Y185 Y185 Y185 Y185	Kinase domain activation loop site.
Mitogen-activated protein kinase 7 -- ERK5	Q9WVS8	R.GLC*TSPAEHQYFM#TEY@VATR.W R.GLC*TSPAEHQYFMTEY@VATR.W	Y221 Y221	Kinase domain activation loop site.
Mitogen-activated protein kinase 8 -- JNK1	Q91Y86	R.TAGTSFMMTPY@VVTR.Y	Y185	Kinase domain activation loop site. Peptide identical in JNK3 (Q61831)
Mitogen-activated protein kinase 9 -- JNK2	Q9WTU6	R.TAC*TNFMMTPY@VVTR.Y	Y185	
Mitogen-activated protein kinase 14 -- MAP kinase p38 alpha	P47811	F.GLARHTDDEM#TGY@VATRW.Y F.GLARHTDDEMTGY@VATRW.Y F.GLARHTDDEMTGY@VATRWY.R L.ARHTDDEMTGY@VATRW.Y L.DFGLARHTDDEMTGY@VATRW.Y R.HTDDEM#TGY@VATR.W R.HTDDEMTGY@VATR.W	Y181 Y181 Y181 Y181 Y181 Y181 Y181	Kinase domain activation loop site.

Serine/threonine-protein kinase PAK 2	Q8CIN4	K.LRTIVSIGDPKKKYTRY@EK.I	Y252	PKN family.
Serine/threonine-protein kinase -- PFTAIRE-1	O35495	K.LEKLGEGS@Y@ATVYK.G	Y146	CDK family.
Serine/threonine-protein kinase -- PCTAIRE-3	Q04899	K.LDKLGEGTY@ATVFK.G	Y132	CDK family.
Serine/threonine-protein kinase -- PRP4	Q61136	C.DFGS@AS@HVADNDITPY@LVSRFY.R	Y849	DYRK family. Kinase domain activation loop site.
		F.GSASHVADNDITPY@LVSRF.Y	Y849	
		F.GSASHVADNDITPY@LVSRFY.R	Y849	
		H.VADNDITPY@LVSRF.Y	Y849	
		H.VADNDITPY@LVSRFY.R	Y849	
		K.LC*DFGSASHVADNDITPY@LVSR.F	Y849	
		K.LCDFGSAS@HVADNDITPY@LVSR.F	Y849	
		L.C*DFGSASHVADNDITPY@LVSRF.Y	Y849	
		S.HVADNDITPY@LVSRFY.R	Y849	
RIKEN CDNA C230081A13: hypothetical Protein kinase A anchoring domain containing protein -- SgK269	Q8BX56	K.FNSYNNAGM#PPFPIIIHDEPSY@AR.S	Y613	This entry contains the N terminal region of a putative protein serine/threonine kinase called 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.NAIKVPIVINPNAY@DNLAIY@K.S	Y632,Y638	
		K.NAIKVPIVINPNAY@DNLAIYK.S	Y632	
		K.NAIKVPIVINPNAYDNLAIY@K.S	Y638	
		K.VPIVINPNAY@DNLAIYK.S	Y632	
Protein phosphatases				
Protein phosphatase 2 regulatory subunit B56 delta isoform	Q99PC9	R.KSELPQDVY@T^IK.A	Y572	
Receptor-type tyrosine-protein phosphatase alpha -- R-PTP-alpha	P18052	K.VVQEYIDAFSDY@ANFK.-	Y825	
		Y.IDAFSDY@ANFK.-	Y825	
		Y.KVVQEYIDAFSDY@ANF.K	Y825	
		Y.KVVQEYIDAFSDY@ANFK.-	Y825	
Tyrosine-protein phosphatase, non-receptor type 11 -- SHP-2	P35235	H.IKIQNTGDY@YDLY.G	Y62	
		K.IQNTGDY@YDLYGGEK.F	Y62	
		R.EDSARVY@ENVGLMQQQR.S	Y584	
		R.VY@ENVGLMQQQR.S	Y584	
SIGNALING: SMALL G PROTEINS AND REGULATORS				
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. Also known as p190RhoGAP. Phosphorylation of this putative Src site positively controls GAP activity, thus inhibiting Rho.
		W.MPQDGFDPSDY@AEPMDAVVKPRNEEENIY.S	Y925	
Breast cancer anti-estrogen resistance protein 3 -- BCAR3	Q9QZK2	F.IFRDPY@LLDPTLEY.V	Y103	May act as an adapter protein and couple activated growth factor receptors to signaling molecules that regulate src kinase activity and promote cell migration. Contains 1 Ras-GEF domain and 1 SH2 domain.
		F.IFRDPY@LLDPTLEYVKF.S	Y103	
		Y.LLDPTLEY@VKF.S	Y111	
		R.KGENFIFRDPY@LLDPTLEY@VK.F	Y103,Y111	
		R.KGENFIFRDPY@LLDPTLEYVK.F	Y103	
		L.RLSEAY@SRVQY.Q	Y206	
ARF GTPase-activating protein -- GIT1	Q68FF6	R.SQSELDDQHDY@DS@VAS@DEDTDQEPLPSAGATR.N	Y392	Possesses ARF-GAP activity. Functions as part of a multi-molecular signaling complex that regulates membrane protrusions and cell migration.
		R.SQSELDDQHDY@DS@VAS^DEDTDQEPLPSAGATR.N	Y392	
		F.HSTELEDDAIY@SVHVPAGLY.R	Y554	
		R.LQPFHS@TELEDDAIY@SVHVPAGLYR.I	Y554	
		R.LQPFHSTELEDDAIY@SVHVPAGLYR.I	Y554	
		R.LQPFHST^ELEDDAIY@SVHVPAGLYR.I	Y554	
ARF GTPase-activating protein -- GIT2	Q9JLQ2	K.QNSTPESDY@DNTAC*DPEPDDTGSTR.K	Y541	Possesses ARF-GAP activity. Interacts with G protein-coupled receptor kinases, paxillin, PIX exchange factors. Important in integrin-mediated cell adhesion.
		K.QNSTPESDY@DNTAC*DPEPDDTGSTRK.G	Y541	
Ras GTPase-activating-like protein -- IQGAP1	Q9JKF1	K.LQQTY@SALNSK.A	Y1510	Binds to activated CDC42 but does not stimulate its GTPase activity. Could serve as an assembly scaffold for the organization of a multimolecular complex.
Ras and Rab interactor 1 -- Rin1	Q921Q7	K.EKPSTDPLY@DTPDTR.G	Y35	Can affect Ras signaling by competing with RAF1, by enhancing signaling from ABL1 and ABL2, and possibly by functioning as a GEF for RAB5A.
Rho-GTPase-activating protein 12	Q8C0D4	M.RATT@PPNQGRPDS@PVY@ANLQEL.K	Y241	Contains 1 PH domain, 1 Rho-GAP domain, 1 SH3 domain, 2 WW domains. GTPase activator for the Rho-type GTPase.
		M.RATTPPNQGRPDS@PVY@ANLQEL.K	Y241	
		R.AT@TPPNQGRPDS@PVY@ANLQELK.I	Y241	
		R.AT@TPPNQGRPDS^PVY@ANLQELK.I	Y241	
		R.ATT@PPNQGRPDS@PVY@ANLQELK.I	Y241	
SIGNALING: OTHER				
Abl interactor 1 -- Abi-1	Q8CBW3	K.TLEPVKPPTVPNDY@MTSPAR.L	Y212	SH3-containing adapter protein.

		R.NTPY@KTLEPVKPPTVPNDY@MTSPAR.L	Y212	
		R.NTPYKT@LEPVKPPTVPNDY@MTSPAR.L	Y212	
		Y.KTLEPVKPPTVPNDY@MTSPARL.G	Y212	
Annexin A2	P07356	K.LSLEGDHSTPPSAY@GSVKPYTNFDAER.D	Y23	
		K.LSLEGDHSTPPSAY@GSVKPYTNFDAERDALNIETAVK.T	Y23	
		C.KLSLEGDHSTPPSAY@GSVKPY.T	Y23	
		L.SLEGDHSTPPSAY@GSVKPY.T	Y23	
		K.RKY@GKSLYYYIQQDTK.G	Y310	
Ankyrin repeat and SAM domain-containing protein 1 -- ANKS1	P59672	L.AVRPRIQS@SAPQEEEEHPY@EL.L	Y471	Phosphorylated in response to EGF and PDGF. Contains seven ankyrin repeats and two sterile alpha motif domain. Alternative name is Odin.
		L.AVRPRIQS@SAPQEEEEHPY@ELL.L	Y471	
		L.AVRPRIQSSAPQEEEEHPY@EL.L	Y471	
		L.AVRPRIQSSAPQEEEEHPY@ELL.L	Y471	
		L.AVRPRIQSSAPQEEEEHPY@ELLL.T	Y471	
Calmodulin	P62204	R.VFDKDGNGY@ISAAELR.H	Y99	Mediates the control of a large number of enzymes by Ca(2+).
		F.RVFDKDGNGY@ISAAEL.R	Y99	
Caveolin-1	P49817	K.YVDSEGHLY@TVPIR.E	Y14	May act as a scaffolding protein within caveolar membranes.
Caveolin-2	Q9WVC3	F.MADDAYS@HHS@GVDY@ADPEKY.V	Y27	
		F.MADDAYS@HHS^GVDY@ADPEKY.V	Y27	
		F.MADDAYSHHS@GVDY@ADPEKY.V	Y27	
		F.MADDAYSHHSGVDY@ADPEKY.V	Y27	
		F.MADDAYS^HHS@GVDY@ADPEKY.V	Y27	
		Y.SHHSGVDY@ADPEKY.V	Y27	
Proto-oncogene c-Crk	Q64010	L.IGGNQEGSHPQPLGGPEPGPY@AQPSVN.T	Y221	Adaptor protein with SH2-SH3-SH3 domain structure.
		Y.AQPSVNTPLPNLQNGPIY@ARVIQ.K	Y239	
		K.RVPNAY@DKTALALEVGELVK.V	Y251	
		Q.KRVPNAY@DKTAL.A	Y251	
Crk-like protein	P47941	Y.VRTLY@DFPGNDAEDLPF.K	Y132	Adaptor protein with an SH2-SH3-SH3 domain structure.
		H.GKHGNRNS@NSY@GIPEPAHAY.A	Y198	
		H.GNRNS@NSY@GIPEPAHAY.A	Y198	
		H.GNRNSNSY@GIPEPAHAY.A	Y198	
		R.NSNSY@GIPEPAHAYAQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y198	
		R.NSNSYGIPEPAHAY@AQPQTTTPLPTVASTPGAAINPLPSTQNGPVFAK.A	Y207	
Docking protein 1 (Dok1)	P97465	R.IPPGPSQDSVY@SDPLGSTPAGAGEGVHSK.K	Y314	
		K.KPLYWDLY@GHVQQQLLK.T	Y340	
		K.LTDSKEDPIY@DEPEGLAPAPPR.G	Y361	
		K.TKLTDSKEDPIY@DEPEGLAPAPPR.G	Y361	
		L.KTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	
		L.LKTKLTDSKEDPIY@DEPEGLAPAPPRGLY.D	Y361	
		R.LKEEGYELPYNPATDDY@AVPPPR.S	Y408	
		F.SSDTALY@SQVQKSGTSGAW.D	Y450	
		K.GFSSDTALY@SQVQK.S	Y450	
Ephrin-B2 precursor (Ephrin-B1)	P52800	R.TADSVFC*PHY@EK.V	Y307	
		K.VSGDY@GHPVYIVQEMPPQSPANIYYKV.-	Y314	Peptide identical in Ephrin-B1 (P52795).
		K.VSGDYGHPVY@IVQEMPPQSPANIY@YKV.-	Y319,Y333	Peptide identical in Ephrin-B1 (P52795).
		K.VSGDYGHPVYIVQEM#PPQSPANIY@YKV.-	Y333	Peptide identical in Ephrin-B1 (P52795).
		K.VSGDYGHPVYIVQEMPPQSPANIY@YKV.-	Y333	Peptide identical in Ephrin-B1 (P52795).
Fibroblast growth factor receptor substrate 2 -- FRS2	Q8C180	K.LVY@ENINGLSIPSASGVR.R	Y306	Adaptor protein involved in fibroblast growth factor receptor signaling.
		R.RPALLNY@ENLPSLPPVWEAR.K	Y349	
Fish protein -- TKS5	O89032	K.VKYEEPEY@DVPAFGFDSEPEMNEEPSGDR.G	Y557	SH3 and PX domain-containing protein and Src substrate
GRB2-associated binding protein 1 -- Gab1	Q9QYY0	K.HGMNGFFQQQMMY@DC*PPSR.L	Y242	A member of the IRS-1-like multisubstrate docking protein family. Contains an N-terminal pleckstrin homology domain and several proline-rich SH3 domain-binding sequences.
		K.DASSQDC*Y@DIPR.T	Y407	
		L.RKDASSQDC*Y@DIPRTF.P	Y407	
		N.KLRKDASSQDC*Y@DIPRTF.P	Y407	
		R.KDASSQDC*Y@DIPR.T	Y407	
Insulin receptor substrate 2 -- IRS-2	P81122	K.SSSSNLGADDGY@MPM#TPGAALR.S	Y649	
		K.SSSSNLGADDGY@MPMTPGAALR.S	Y649	
		K.SDDY@MPMSPTSVSAPK.Q	Y671	
Insulin receptor substrate-2 (IRS-2) (4PS) homolog [Fragment]	Q3U2I0	R.SYKAPC*SC*SGDDDQY@VLMSSPVGR.I	Y754	The equilavent peptide in above P81122 entry is RSYKAPCSCSGDNDQYVLMSSPVGRI.
Kin of IRRE-like protein 1 precursor	Q80W68	K.AIY@SSFKDDVDLK.Q	Y604	Signaling protein that needs the presence of TEC kinases to fully trans-activate the transcription factor AP-1.
		K.AIY@SSFKDDVDLKQDLR.C	Y604	

		R.EEYEMKDPTNGY@YNVR.A	Y637	
		R.AVLY@ADY@RAPGPTR.F	Y654,Y657	
		Y.NVRAHEDRPSSRAVLY@ADY.R	Y654	
		R.TPY@EAYDPIGK.Y	Y753	
		Y.RLGYPQAPPSGLERTPY@EAYDPIGKY.A	Y753	
		R.TPYEAY@DPIGK.Y	Y756	
myelin protein zero-like 1 -- PZR	Q3TEW6	K.SPPSAGSHQGPVIY@AQLDHSGGHHSGK.I	Y242	An immunoglobulin superfamily cell surface protein. Contains two tyrosine-based inhibition motifs (ITIMs) responsible for binding of SHP-2.
		K.INKSESVVY@ADIR.K	Y264	
		K.INKSESVVY@ADIRKD.-	Y264	
		K.SESVVY@ADIR.K	Y264	
		N.KSESVVY@ADIRKD.-	Y264	
		H.SGKINKSESVVY@ADIRKD.-	Y264	
Non-catalytic region of tyrosine kinase adaptor protein 1 -- NCK1	Q99M51	K.RKPS@VPDTASPADDSFVDPGERLY@DLNM#PAFVK.F	Y105	Adapter protein containing SH2 and SH3 domains.
		K.RKPS@VPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	
		K.RKPSVPDTASPADDSFVDPGERLY@DLNMPAFVK.F	Y105	
PDZ and LIM domain protein 5	Q8CI51	R.NTEFY@HIPTHSDASK.K	Y251	
Phosphatidylinositol 3-kinase regulatory alpha subunit -- p85alpha	P26450	K.SREYDRLY@EEYTR.T	Y467	
		R.DQY@LMWLTQK.G	Y580	
		K.LNEWLGNENTEDQY@SLVEDDEDLPHHDEK.T	Y607	
Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 -- p85beta	O08908	R.EYDQLY@EEYTR.T	Y458	
Protein LAP2	Q80TH2	R.RTEGDY@LSYR.E	Y1097	Acts as an adapter for the receptor ERBB2, in epithelia. Also found to interact with ARVCF and delta catenin. Alternative Name: Erbin.
		R.TEGDY@LSYR.E	Y1097	
SH2 domain-containing adapter protein B -- Shb	Q6PD21	C.RLDY@C*GGGGGGDPGGGQRAF.T	Y113	Adapter protein which regulates several signal transduction cascades by linking activated receptors to downstream signaling components.
		L.RAMC*RLDY@C*GGGGGGDPGGGQRAF.T	Y113	
		M.C*RLDY@C*GGGGGGDPGGGQRAF.T	Y113	
		R.LDY@C*GGGGGGDPGGGQR.A	Y113	
		K.C*SAEETGAGQKDKVTIADDY@SDPFDAK.S	Y240	
		K.DKVTIADDY@SDPFDAK.S	Y240	
		K.VTIADDY@SDPFDAK.S	Y240	
		L.LNKC*SAEETGAGQKDKVTIADDY@SDPF.D	Y240	
		F.DAKSDLKSKAGKGESAGY@M#EPY.E	Y262	
		F.DAKSDLKSKAGKGESAGY@MEPY.E	Y262	
		K.AGKGESAGY@M#EPYEAQR.I	Y262	
		K.AGKGESAGY@MEPYEAQR.I	Y262	
		K.GESAGY@MEPYEAQR.I	Y262	
		K.SKAGKGESAGY@MEPYEAQR.I	Y262	
		L.KSKAGKGESAGY@MEPY.E	Y262	
		K.LPQDDDRPADEY@DQPWEWNR.V	Y330	
		L.RLRESKLPQDDDRPADEY@DQPW.E	Y330	
		R.ESKLPQDDDRPADEY@DQPWEWNR.V	Y330	
SHC transforming protein 1 -- SHC1	P98083	K.QM#LPPPPC*PGRELFDDPSY@VNIQNLDK.A	Y423	Adaptor protein containing a SH2 and PID domain. Couples activated growth factor receptors to a signaling pathways that regulate proliferation.
		R.ELFDDPSY@VNIQNLDK.A	Y423	
		K.QMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423	
		R.KQMLPPPRCPGRELFDDPSY@VNIQNLDK.A	Y423	
		R.MAGFDGSAWDEEEEEPPDHQY@Y@NDFPGKEPPLGGVVDMR.L	Y349,Y350	
		R.MAGFDGSAWDEEEEEPPDHQYY@NDFPGKEPPLGGVVDMR.L	Y350	
SH2-containing inositol 5-phosphatase 2 -- SHIP2	Q9JLL7	K.NSFNNPAY@YVLEGVPHQLLPLEPPSLAR.A	Y987	
Tyrosine-protein phosphatase non-receptor type substrate 1 -- SHPS1	P97797	Y.ASIETGKVPRPEDTLTY@ADLDMVHL.S	Y481	Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PTPN6, PTPN11 and other binding partners from the cytosol to the plasma membrane.
Signal transducer and activator of transcription 3 -- STAT3	P42227	K.YC*RPESQEHPEADPGSAAPY@LK.T	Y705	Transcription factor of the STAT family. Two alternatively spliced isoforms have been described.
STAT3 splice isoform Del-701	P42227-3	K.YC*RPESQEHPEADPGAAPY@LK.T	Y704	This peptide unique to splice isoform Del-701.
Signal transducer and activator of transcription 5B -- STAT5B	P42232	K.AADGY@VKPQIK.Q	Y699	
ADHESION: CELL/ECM				
CRK-associated substrate -- p130cas	Q61140	K.TQQGLY@QAPGPNPQFQSPPAK.Q	Y132	Substrate domain YxxP site 2.
		R.VGQGYVYEAAQTEQDEY@DTPR.H	Y238	Substrate domain YxxP site 6.
		Y.VVYEAAQTEQDEY@DTPRHL.L	Y238	
		R.HLLAPGPQDIY@DVPPVR.G	Y253	Substrate domain YxxP site 7.

		L.LAPGPQDIY@DVPPVRGLLPNQY.G	Y253	
		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.
		K.DVPDGPLLREETY@DVPPAFAKPK.P	Y331	Substrate domain YxxP site 11.
		R.RPGPGTLY@DVPR.E	Y391	Substrate domain YxxP site 14.
		R.ERVLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	Substrate domain YxxP site 15.
		R.VLPPEVADGSVVDDGVY@AVPPPAER.E	Y414	
		L.SRQLQKMEDVY@QTL.V	Y556	Site is C-terminal to the substrate domain.
Enhancer of filamentation 1 -- HEF1	O35177	R.TGHGYVY@EYPSR.Y	Y165	p130Cas - related protein. Alternative Names: CASL, NEDD9
		K.ANPEERDGVY@DVPLHNPADAK.G	Y344	
Integrin beta-1 precursor	P09055	K.WDTGENPIY@K.S	Y783	The first NPXY site in the cytoplasmic tail
Lipoma-preferred partner homolog - LPP	Q8BFW7	H.YMAGPSSGQIY@GPGPRGY.N	Y245	A LIM domain-containing that may function in focal adhesions . Interacts with alpha-actinin. J Cell Sci. 116:1359.
		M.AGPSSGQIY@GPGPRGY.N	Y245	
		Y.MAGPSSGQIY@GPGPRGY.N	Y245	
		R.GYNNQPVPVSGQC*PPPPTC*VGTDY@AYIPPSGHPPESGYGYTSNQGR.Y	Y276	
		R.YYEPY@YAAGPSYGGR.S	Y301	
		R.YYEPYY@AAGPSYGGR.S	Y302	
Paxillin	Q8VI36	F.LSEEPPY@SYPTGNHTY.Q	Y31	
		L.SEEPPY@SYPTGNHTY.Q	Y31	
		S.KRPVFLSEEPPY@SYPTGNHTY.Q	Y31	
		R.YAHQQPPS@PLPVY@SSSAK.N	Y88	
		R.YAHQQPPSPLPVY@SSSAK.N	Y88	
		R.YAHQQPPS^PLPVY@SSSAK.N	Y88	
		R.AGEEEHVY@SFPNK.Q	Y118	
		R.AGEEEHVY@SFPNKQK.S	Y118	
Pleckstrin homology domain containing family C member 1	Q8CIB5	L.IMPGSGSIY@SSPGLY.S	Y179	Participates in the connection between ECM adhesion sites and the actin cytoskeleton and also in the orchestration of actin assembly and cell shape modulation. Belongs to the kindlin family. Contains 1 FERM domain and 1 PH domain.
Syndecan-4 precursor	O35988	K.KAPTNEFY@A.-	Y197	A heparan sulfate proteoglycan type I membrane protein that promotes cell spreading in a beta(1) integrin-dependent fashion through PKC-alpha and Rho.
		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	
		F.LSDDDPKKGIWLEAGKALDY@Y.M	Y70	
		K.ALDY@YM#LR.N	Y70	
		K.ALDY@YMLR.N	Y70	
		W.LEAGKALDY@Y.M	Y70	
		R.IGITNHDEY@SLVR.E	Y127	
		K.LLGEIAQGNENY@AGIAAR.D	Y1116	
Tensin	Q9DBT6	R.HAAY@GGY@STPEDR.R	Y213,Y216	Localizes to focal adhesions. Crosslinks actin filaments and contains SH2 domain.
		R.HAAY@GGYSTPEDR.R	Y213	
		R.HAAYGGY@STPEDR.R	Y216	
		R.HAAYGGY@STPEDRRPT^LSR.Q	Y216	
Tensin 2	Q8CJ95	H.TRGPLDGSPY@AQVQ.R	Y460	
		L.AHTRGPLDGSPY@AQVQ.R	Y460	
		R.GPLDGSPY@AQVQR.V	Y460	
		K.VGEEGHEGC*SY@AVC*SEGR.Y	Y747	
Tensin 3	Q5SSZ5	L.HTQGPVDGSLY@AKVR.K	Y354	
		R.KPSAPTPVQAYGQSNY@STQTWVR.Q	Y584	
Vinculin	Q64727	R.ILLRNPGNQAAY@EHFETMK.N	Y691	
		K.SFLDSGY@R.I	Y821	
ADHESION: CELL/CELL				
Catenin delta-1 -- p120 catenin	P30999	K.LNGPQDHNHLLY@STIPR.M	Y96	
		R.HYEDGYPGGSDNY@GSLSR.V	Y228	
		R.HYEDGYPGGSDNY@GS^LSR.V	Y228	
		R.FHPEPYGLEDDQRSMGY@DDLDY@GMMSDYGTAR.R	Y291,Y296	
		K.SDNNY@STLNER.G	Y877	
Ctnnd1 protein -- p120 catenin, isoform	Q80XQ4	K.SLDNNY@STLNER.G	Y904	Peptide is unique to this isoform.

Discs large homolog 3	P70175	R.RDNEVDGQDY@HFVVSR.E	Y705	MAGUK family. Contains 1 guanylate kinase-like domain, 3 PDZ (DHR) domains and 1 SH3 domain.
Fath protein [fragment]	Q497H5	K.NIY@SDIPPQVPVRPISYTPSIPSDSR.N	Y952	Related to Fat cadherins implicated in actin dynamics at both cell-cell contacts and leading edges.
Partitioning-defective 3 homolog -- PARD3	Q99NH2	R.ISHSLY@SGIEGLDESPTR.N	Y719	Adapter protein involved in asymetrical cell division and cell polarization processes. Plays a role in the formation of epithelial tight junctions.
		R.RIS@HSLY@SGIEGLDESPTR.N	Y719	
		R.RISHS@LY@SGIEGLDESPTR.N	Y719	
		R.RISHSLY@SGIEGLDESPTR.N	Y719	
		R.ERDY@AEIQDFHR.T	Y1076	
		R.EGHLMDTLY@AQVK.K	Y1123	
		R.KNASSISQDSWEQNY@APGEGFQSAK.E	Y1238	
Plakophilin-4; Armadillo related protein	Q68FH0	R.TVHDMDQFGQQQYDIY@ER.M	Y371	Belongs to the beta-catenin family. May play a role in junctional plaques.
		L.RSAVSPDLHITPIY@EGRTY.Y	Y414	
		R.NNY@ALNTAATY@AEPYRPVQYR.V	Y469,Y477	
		R.NNYALNTAATY@AEPYRPVQYR.V	Y477	
		Y.ALNTAATY@AEPY.R	Y477	
		R.SY@EDPYC*DDRVHFPAST@DYSTQYGLK.S	Y1137	
		R.SY@EDPYC*DDRVHFPASTDYSTQYGLK.S	Y1137	
Scavenger receptor class F member 2 precursor	P59222	R.SASSVEGPSGALY@AR.V	Y615	Probable adhesion protein, which mediates homophilic and heterophilic interactions.
Tight junction protein ZO-1	P39447	Y.LSAPGSEY@SMY.S	Y830	Belongs to the MAGUK family. Contains 1 guanylate kinase-like domain, 3 PDZ (DHR) domains, 1 SH3 domain.
		R.HEEQPAPAY@EVHNR.Y	Y1164	
Tight junction protein ZO-2	Q9Z0U1	R.IEIAQKHPDIY@AVPIK.A	Y1095	
CYTOSKELETON: ACTIN-ASSOCIATED				
Actins and actin-related proteins; Regulators of actin assembly				
Actin, alpha skeletal muscle (Beta-actin) (Gamma-actin)	P68134	K.IWHHTFY@NELR.V	Y93	Peptide conserved in alpha cardiac-actin (P68033); ; Beta-actin (P70514); Gamma-actin (P63260)
		M.VGMGQKDSY@VGDEAQSKRGIL.T	Y55	Peptide conserved in alpha-cardiac actin (P68033); gamma-enteric smooth muscle actin (P63268); Beta-actin (P70514); Gamma-actin (P63260)
Cofilin-1, non-muscle isoform	P18760	K.HELQANC*Y@EEVKDR.C	Y139	This peptide only in Cofilin-1.
		K.LTGIKHELQANC*Y@EEVKDR.C	Y139	
		L.TGIKHELQANC*Y@EEVKDRC*TL.A	Y139	
Src substrate cortactin	Q60598	Y.TSEPVY@ETTEAPGHY.Q	Y466	
Vasodilator-stimulated phosphoprotein -- VASP	P70460	F.SRVQIY@HNPTANSF.R	Y39	Actin- and profilin-binding microfilament-associated protein.
		R.VQIY@HNPTANSFR.V	Y39	
N-WASP: Neural Wiskott-Aldrich syndrome protein	Q91YD9	K.DRETSKVIY@DFIEK.T	Y253	Regulates actin polymerization by stimulating the actin-nucleating activity of the Arp2/3 complex.
		K.VIY@DFIEK.T		
WD-repeat protein 1; Actin interacting protein 1 -- AIP1	O88342	K.AHDGGIY@AISWSPDSTHLLSASGDK.T	Y237	Induces disassembly of actin filaments in conjunction with ADF/cofilin family proteins. Contains 11 WD repeats.
Other actin-associated proteins				
Band 4.1-like protein 2	O70318	N.TLRVDGDNIY@VRHSNL.M	Y606	
		R.VDGDNIY@VR.H	Y606	
Calponin-2	Q08093	K.CASQSGMTAY@GT@RR.H	Y184	Thin filament-associated protein implicated in regulation of smooth muscle contraction. Capable of binding to actin, calmodulin, troponin C and tropomyosin.
Calponin-3	Q9DAW9	Y.HGEYPDDY@PREY.Q	Y316	
LIM and SH3 domain protein 1 -- LASP-1	Q61792	H.HIPTSAPVY@QQPQQQQM.T	Y173	Characterized by a LIM motif and SH3 domain. Functions as an actin-binding protein, possibly in cytoskeletal organization.
Septin-2	P42208	K.QQPTQFINPETPGY@VGFANLPNQVHR.K	Y17	Involved in cytokinesis. Alternative Name: NEDD-5.
		K.QQPTQFINPETPGY@VGFANLPNQVHRK.S	Y17	
Sickle tail-b (Sickle tail-a)	Q75UV8	R.NVY@YELNDVR.N	Y244	Both peptides identical in Sickle tail-a isoform (Q75UV9). Related to p130Cas-binding protein (p140Cap).
		R.NEGFY@ADPYLYHEGR.M	Y393	
CYTOSKELETON: MICROTUBULE-ASSOCIATED				
none				
CYTOSKELETON: OTHER				
Vimentin	P20152	R.FANY@IDKVR.F	Y116	Vimentins are class-III intermediate filaments found in various non-epithelial cells, especially mesenchymal cells.

		R.SLY@SSSPGGAYVTR.S	Y52	
TRAFFICKING/TRANSPORT				
Vesicle transport				
Double C2-like domain containing protein beta	P70169	K.TY@LKPDVDKKSK.H K.TY@LKPDVDKKS^K.H	Y309 Y309	May be involved in constitutive membrane trafficking including dynein-dependent intracellular vesicle transport. Binds calcium and phospholipids. Interacts with cytoplasmic dynein light chain.
Intersectin 2	Q9Z0R6	R.GEPEALY@AAVTK.K	Y 921	Adapter protein that may provide indirect link between the endocytic membrane traffic and the actin assembly machinery. May regulate the formation of clathrin-coated vesicles.
Low-density lipoprotein receptor precursor	P35951	F.DNPVY@QKTTEDELHIC*RSQDGY.T	Y832	Binds LDL, the major cholesterol-carrying lipoprotein of plasma, and transports it into cells by endocytosis.
Nucleoporin-like protein RIP	Q8K2K6	K.AGLQTADKY@AALANLDNIFSAGQGGDQGSGFGTTGK.A	Y327	Required for vesicle docking or fusion during acrosome biogenesis. May play a role in RNA trafficking or localization.
Transferrin receptor protein 1 -- TfR	Q62351	F.SNLFGGEPLSY@TRF.S R.SAFSNLFGGEPLSY@TR.F	Y20 Y20	Regulates the cellular uptake of iron via receptor-mediated endocytosis of ligand-occupied receptors into specialized endosomes.
Nucleocytoplasmic transport				
None				
Other transport				
Gap junction alpha-1 protein -- Connexin 43	P23242	K.QASEQNWANY@SAEQNR.M	Y312	Hexamers of connexin-43 form connexons, which aggregate together to form gap junctions, through which materials of low MW diffuse between cells.
Lysosomal-associated transmembrane protein 4A	Q60961	K.IPEKEPPPPY@LPA.-	Y230	May function in the transport of nucleosides and/or nucleoside derivatives between the cytosol and the lumen of an intracellular membrane-bound compartment.
Sodium bicarbonate cotransporter 2B homolog [fragment]	Q8BTY2	K.DKDSDKEDGRES@PSY@DTPSQR.V K.DKDS^DKEDGRESPSY@DTPSQR.V	Y92 Y92	
Solute carrier family 38, member 2	Q8CFE6	K.SHY@ADVDPENQNFLLESNLGK.K K.SHY@ADVDPENQNFLLESNLGKK.K L.KSHY@ADVDPENQNF.L	Y41 Y41 Y41	
METABOLIC AND BIOSYNTHETIC ENZYMES				
Glycolytic enzymes				
Alpha enolase (beta-enolase) (gamma enolase)	P17182	R.GNPTVEVDLY@TAK.G R.AAVPSGASTGIY@EALELR.D	Y24 Y43	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). Identical peptide in beta enolase (P21550); gamma enolase (P17183).
Glyceraldehyde-3-phosphate dehydrogenase -- GAPDH	P16858	K.LISWYDNEY@GYSNR.V	Y315	Second phase of glycolysis; first step.
Phosphoglycerate mutase 1	Q9DBJ1	R.FSGWY@DADLSPAGHEEAKR.G	Y25	Functions in second phase of glycolysis.
Pyruvate kinase, isozyme M2	P52480	R.EAEAAIY@HLQLFEELRR.L	Y389	Second phase of aerobic glycolysis; final step.
Other metabolic/biosynthetic enzymes				
Bifunctional purine biosynthesis protein PURH	Q9CWJ9	R.VC*MVY@DLYPTLTPLAVAYAR.A	Y290	Involved in de novo purine biosynthesis.
Serine hydroxymethyltransferase, cytosolic	P50431	K.MLSQPLKDSDAEVY@SIIKK.E	Y28	Interconversion of serine and glycine. Key enzyme in the biosynthesis of purines, lipids, hormones and other components.
TK: Transketolase	P40142	K.NMAEQIIQEIY@SQVQSK.K	Y275	Pentose phosphate pathway; non-oxidative stage.
RNA SYNTHESIS AND PROCESSING				
Transcription machinery and regulation				
Polymerase I and transcript release factor	O54724	F.KVMIY@QDEVKLPAKL.S K.VMIY@QDEVKLPAK.L F.TPDHVVY@ARSKTAVY.K K.SFTPDHVVY@AR.S R.KSFTPDHVVY@AR.S	Y158 Y158 Y310 Y310 Y310	Required for dissociation of the ternary transcription complex. Also found at the cell membrane and the surface of caveolae, suggesting alternative functions.
DEAD(DEAH)-box helicases				
ATP-dependent RNA helicase DDX3X	Q62167	R.GRGDY@DGIGGR.G R.GRGDY@DGIGGRGDR.S	Y103 Y103	Putative ATP-dependent RNA helicase.
hnRNPs and snRNPs				
none				
Splicing factors				

none				
Other RNA binding and processing				
Poly(rC)-binding protein 2	Q61990	Y.TIQGQY@AIPQPDLTKLHQLAM.Q	Y232	Single-stranded nucleic acid binding protein that binds preferentially to oligo dC. RNA binding protein.
Putative RNA-binding protein 3	O89086	R.YDSRPGGYGY@GYGR.S Y.DSRPGGYGY@GY.G R.YDSRPGGYGYGY@GR.S R.YSGGNYRDNY@DN.-	Y124 Y124 Y126 Y151	
RNA-binding protein 14	Q8C2Q3	R.LPDAHSDY@AR.Y	Y645	
PROTEIN SYNTHESIS AND PROCESSING				
tRNA synthetases				
None				
Translation machinery				
40S ribosomal protein S10	P63325	R.IAIY@ELLFK.E	Y12	
60S acidic ribosomal protein P0	P14869	K.IIQLLDDY@PK.C	Y24	
67 kDa polymerase-associated factor PAF67; Eukaryotic translation initiation factor 3 subunit 6-interacting protein -- Eif3s6ip	Q91YE4	K.GDPQVYEELFSY@AC*PK.F	Y415	Associated with the initiation-competent form of RNA polymerase I. The association of PAF67 with the 'core' enzyme endows Pol I with the capability to assemble into a productive transcription initiation complex at the rDNA promoter.
Eukaryotic initiation factor 4A-I	P60843	R.GFKDQIY@DIFQK.L	Y197	
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).
Laminin receptor 1 (ribosomal protein SA)	Q8BNL2	R.ADHQPLTEASY@VNLPTIALC*NTDSPLR.Y	Y139	Belongs to the ribosomal protein S2P family. GO:0005719,C:nuclear euchromatin,IDA. Protein Type: Receptor, misc., Adhesion
G1 to phase transition 2 -- GSPT2	Q9CY91	K.Y@LIVLINK.M	Y347	GSPT2 is closely related to GSPT1. GSPT1 is a positive regulator of translational accuracy and, in a binary complex with eRF1 functions as a polypeptide chain release factor.
Post-translational modifiers				
Probable palmitoyltransferase ZDHHC5	Q8VDZ4	R.EPS@PVRY@DNLSR.H R.LLPTGPPHREPS@PVRY@DNLSR.H	Y533 Y533	Peptide identical in ZDHHC8 (Q5Y5T5)
Probable palmitoyltransferase ZDHHC8	Q5Y5T5	F.SPVLGPRPREPS^PVRY@DNL.S R.PREPS^PVRY@DNLSR.T L.RSQTDSLFGDSGVY@DTPSSY.S	Y538 Y538 Y576	Putative palmitoyltransferase involved in glutamatergic transmission.
Chaperones and associated proteins				
BAG-family molecular chaperone regulator-3	Q9JLV1	K.THYPAQQGEY@QPQQPVYHK.I	Y246	Inhibits the chaperone activity of HSP70/HSC70 by promoting substrate release.
Heat shock 70 kDa protein 4	Q61316	K.LKKEDIY@AVEIVGGATR.I	Y336	
Heat shock protein HSP 90-beta	P11499	K.SIY@YITGESK.E	Y483	
PROTEIN DEGRADATION				
Ubiquitin conjugation regulators				
E3 ubiquitin protein ligase CBL	P22682	K.IKPSSSANAIY@SLAARPLPMPK.L	Y672	Acts as an E3 ubiquitin-protein ligase.
E3 ubiquitin-protein ligase CBL-B	Q3TTA7	R.ASQDY@DQLPSSSDGSQAPARPPKPR.P	Y889	
Probable E3 ubiquitin-protein ligase MGRN1	Q9D074	L.RAVSPAIPSAPLY@EEITY.S	Y389	Mahogunin ring finger protein 1
Proteasome components				
Proteasome subunit alpha type 2 -- PSMA2	P49722	K.HIGLVY@SGMGPDYR.V	Y75	Proteasome component C3. PSMA2 may have a potential regulatory effect on another component(s) of the proteasome complex through its tyrosine phosphorylation.
Other proteases and endopeptidases				
ADAM 9 precursor	Q61072	K.ISSQGNLIPARPAPAPPLY@SSLT.- N.LIPARPAPAPPLY@SSLT.-	Y841 Y841	A disintegrin and metalloproteinase domain 9
Prolyl endopeptidase	Q9QUR6	R.MTELY@DYPK.Y	Y71	Peptidase S9A family. Cleaves peptide bonds on the C-terminal side of prolyl residues within peptides that are up to ~30 amino acids long.

NUCLEAR PROTEINS				
Histone H2B type 1-B	Q64475	R.KESYSVY@VYK.V	Y41	
MISCELLANEOUS				
Microfibril-associated glycoprotein 3 precursor	Q922T2	R.IKERPALDAQSGIY@VINPELGR.S	Y277	Microfibril-associated glycoprotein 3. Protein Type: Extracellular matrix
Psychosine receptor	Q61038	R.Y@LAVVYPLK.F	Y115	Receptor for the glycosphingolipid psychosine (PSY) and several related glycosphingolipids.
FUNCTION UNKOWN OR UNCERTAIN				
Named proteins of unknown/uncertain function				
Carnitine deficiency-associated protein CDV3A (CDV3B)	Q920I4	R.KTPQGPPEIY@SDTQFPSLQSTAK.H	Y213	Peptide identical in Carnitine deficiency-associated protein CDV3B (Q920C7)
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	Q9DBJ3	K.MIGKDY@DTLSK.Y M.IGKDY@DTLSKY.S	Y274 Y274	May function as adapter protein. Contains 1 IMD (IRSp53/MIM homology) domain and 1 SH3 domain.
Suppression of tumorigenicity 5	Q924W7	K.STLEENAYEDIVGGLPKENPY@EDVDLK.N	Y498	
Pituitary tumor-transforming gene 1 protein-interacting protein precursor	Q8R143	F.KEQNPY@EKF.- K.EQNPY@EKF.-	Y171 Y171	May facilitate PTTG1 nuclear translocation.
WW domain binding protein 4	Q3TWW5	K.FGDY@C*K.C K.S^QPKKFGDY@C*K.C	Y15 Y15	
Unnamed proteins of unknown/uncertain function				
hypothetical protein -- Ccdc105	Q9D4K7	K.FNQEM#Y@VTRGIIK.G	Y372	Coiled-coil domain containing 105
hypothetical HAT dimerisation/BED finger/Bipartite nuclear localization signal/Zinc finger BED-type profile containing protein	Q3UMD3	W.HFFHVDPQY@TW.R	Y145	
hypothetical Intradiol ring-cleavage dioxygenase/WD40-like containing protein	Q3UHA3	R.YNEMTY@IFDLLHQK.H	Y2161	
MKIAA1686 protein [fragment]	Q6ZPK1	K.ERPISMINEASNY@NMASDY@AVHPMSPVGR.T	Y65,Y71	Contains 1 PH domain.
PREDICTED: similar to Oligophrenin 1	UPI00005125B7	K.LWLEAMDGKEPIY@TLPAIISK.K R.KLWLEAM#DGKEPIY@TLPAIISK.K R.KLWLEAMDGKEPIY@TLPAIISK.K	Y371 Y371 Y371	
PREDICTED: similar to zinc finger CCCH type containing 11A isoform 1	UPI00001C484B	R.IPFS@KTY@SKTEK.V	Y399	
Protein KIAA1914	Q5DTU0	K.VAQQPLSLVGC*DVLPDPSPDHLY@SFR.I	Y413	Contains 2 PH domains.
Similar to RIKEN cDNA 4930527D15 gene [fragment]	Q922B5	K.EKLLLC*HGPS@LSLPALSGVRY@NAEK.K	Y39	
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.