



Protein Name	Phosphorylation Site	Peptide Sequence	GI	xcorr max	mass error	0 sec SIC Peak Area	10 sec SIC Peak Area	30 sec SIC Peak Area	1 min SIC Peak Area	1.5 min SIC Peak Area	2 min SIC Peak Area	3 min SIC Peak Area	5 min SIC Peak Area	10 min SIC Peak Area
Fc IgE receptor,gamma	Y76	R.SQETY*ETLKHEKPPQ.-	6753830	2.98	0.6	2.81E+04	6.28E+04	8.71E+04	1.63E+05	1.62E+05	1.50E+05	2.02E+05	2.44E+05	1.08E+05
Fc IgE receptor,gamma	Y76T78	R.SQETY*ET*LKHEKPPQ.-	6753830	2.987	0.5	6.32E+03	1.31E+04	2.43E+04	4.67E+04	4.09E+04	5.71E+04	5.85E+04	5.23E+04	3.39E+04
FER tyrosine kinase	Y402	K.VQENDGKEPPPVVNY*EEDAR.S	1673620	4.876	0.1	5.58E+04	4.69E+04	1.14E+05	2.24E+05	1.33E+05	1.14E+05	5.74E+04	1.63E+05	1.08E+05
FPS/FES tyrosine kinase	Y711	R.EEADGIY*AASAGLR.Q	23452674	4.002	0.9	2.73E+04	3.62E+04	5.18E+04	8.72E+04	7.11E+04	9.64E+04	5.24E+04	1.13E+05	1.21E+05
FXR1	Y68	K.EISEGDEVEVY*SR.A	1122422	2.966	0.4	3.57E+04	3.01E+04	4.88E+04	4.48E+04	3.59E+04	2.07E+04	2.15E+04	2.62E+04	
FYB/SLAP130	Y559*PS561	K.TTAVEIDY*DS*LKR.K	2232152	4.08	0.1	6.00E+04	7.02E+04	7.44E+04	1.89E+05	1.06E+05	1.41E+05	1.22E+05	3.72E+05	2.64E+05
Fyn	Y417*	R.LIEDNEY*TAR.Q	309241	3.709	0.1	1.69E+05	1.30E+05	1.85E+05	2.04E+05	1.80E+05	1.96E+05	2.79E+05	3.39E+05	2.36E+05
GAB2	S261Y263*	R.HNTEFKDS*TY*DLPR.S	4589377	4.554	0.1	5.63E+04	8.52E+04	2.11E+05	4.51E+05	3.73E+05	6.16E+05	1.04E+06	2.40E+06	9.44E+04
GAB2	T262Y263*	R.HNTEFKDST*Y*DLPR.S	4589377	4.758	0.2	5.46E+04	1.15E+05	2.04E+05	4.31E+05	3.74E+05	6.16E+05	1.05E+06	2.12E+05	5.27E+04
GAB2	Y263*	R.HNTEFKDSTY*DLPR.S	4589377	4.398	0.2	1.94E+04	6.03E+04	1.22E+05	2.61E+05	1.94E+05	2.45E+05	3.40E+05	5.73E+05	3.19E+05
GAB2	Y290*	K.SSLTGSSETDNEDVY*TFK.M	4589377	5.464	0.1	3.12E+04	1.38E+05	4.50E+05	1.50E+06	8.26E+05	1.17E+06	1.23E+06	1.24E+06	5.11E+05
GAPDH	Y316*P	K.LISWYDNEY*GYSNR.V	6679937	5.38	0.1	2.43E+06	3.40E+06	3.08E+06	5.48E+06	2.79E+06	3.40E+06	4.28E+06	6.70E+06	5.23E+06
GAPDH	Y318	K.LISWYDNEYGY*SNR.V	6679937	4.486	3.4	2.43E+06	3.40E+06	3.08E+06	5.48E+06	2.79E+06	3.40E+06	4.28E+06	6.70E+06	5.23E+06
Glycyl tRNA synthetase	Y443	K.TSY*GWIEIVGCADR.S	30725863	5.207	3.8	9.38E+04	9.62E+04	5.88E+04	1.04E+05	4.37E+04	2.59E+04	3.21E+04	8.45E+04	1.18E+05
GSK3 beta	Y216*	R.GEPNVSY*ICSR.Y	7025915	3.186	6.0	8.17E+07	6.00E+07	6.44E+07	8.91E+07	6.77E+07	5.63E+07	7.52E+07	1.52E+08	8.66E+07
GSK3 beta	Y216*S219	R.GEPNVSY*ICS*R.Y	7025915	3.535	5.2	1.49E+06	1.14E+06	9.89E+05	1.18E+06	9.59E+05	9.92E+05	8.53E+05	1.50E+06	1.15E+06
H4 Histone A	Y52*P	R.ISGLIY*EETR.G	51309	3.787	1.2	3.48E+05	2.48E+05	2.98E+05	3.91E+05	2.57E+05	2.04E+05	2.98E+05	5.78E+05	4.89E+05
HCV NS5A transactivated protein 7	Y210*P	R.YSYYDESQGEIY*R.S	17046305	3.966	1.0	6.07E+04	5.24E+04	6.25E+04	7.81E+04	5.72E+04	4.87E+04	6.79E+04	1.32E+05	9.96E+04
Heat shock 70kDa protein 4	Y336*P	K.LKKEDIY*AVEIVGGATR.I	31982275	3.601	0.6	9.35E+05	6.99E+05	5.30E+05	7.25E+05	3.80E+05	3.70E+05	4.35E+05	7.56E+05	6.88E+05
Heat shock 70kDa protein 4	Y661	K.LEDTENWLY*EDGEDQPK.Q	31982275	5.758	0.7	5.23E+04	2.33E+04	3.79E+04	6.28E+04	7.04E+04	1.90E+04	4.67E+04	1.19E+05	3.47E+04
Heat shock 90 KD protein 1 alpha	Y493	K.HIY*FITGETK.D	6754254	3.129	1.7	3.86E+04	3.75E+04	3.41E+04	5.12E+04	3.31E+04	2.04E+04	2.82E+04	4.66E+04	4.65E+04
Heat shock 90 KD protein 1 beta	Y484	K.SIY*YITGESK.E	6680305	4.103	1.2	5.97E+05	3.47E+05	3.64E+05	3.83E+05	3.04E+05	2.50E+05	2.50E+05	4.52E+05	3.42E+05
hypothetical protein XP_150108	Y278	R.ESYY*FGLSPEER.R	28972590	2.78	2.0	6.39E+04	8.95E+04	2.86E+05	5.18E+04	8.02E+04	1.07E+05	1.54E+05	2.86E+05	1.89E+05
Hypothetical protein, LOC134492	Y145	K.ENPGDFDFSGAEISGNY*TK.G	13542906	3.574	0.1		4.34E+03	1.87E+04	2.02E+04	2.46E+04	2.01E+04	3.17E+04	2.84E+04	2.49E+04
IL3 receptor, beta	S752Y765*	R.VPS*GSPALGPPGFEDY*VELPPSVSQAAS.S	110595	4.737	0.8	4.17E+05	5.19E+05	7.78E+05	9.90E+05	6.06E+05	4.22E+05	5.88E+05	8.97E+05	6.31E+05
IL3 receptor, beta	Y765*	R.VPSGSPALGPPGFEDY*VELPPSVSQAAS.S	110595	4.862	0.4	2.64E+05	4.23E+05	5.84E+05	7.81E+05	5.63E+05	4.34E+05	5.11E+05	7.87E+05	7.40E+05
insulin receptor/IGF-1 receptor	Y1179*	R.DIYETDY*YRK.G	6754360	2.541	1.4	1.04E+05	7.84E+04	6.95E+04	9.27E+04	8.00E+04	8.61E+04	1.14E+05	2.52E+05	1.60E+05
integrin beta 1 subunit	Y783*	K.WDTGENPIY*K.S	90972	3.185	0.9	6.14E+04	7.03E+04	9.39E+04	1.05E+05	8.08E+04	5.47E+04	7.37E+04	1.55E+05	7.65E+04
Intersectin 2	Y553*P	K.LIY*LVPEK.Q	6755502	2.836	0.5	1.35E+04	1.03E+04	1.33E+04	2.17E+04	1.91E+04	2.06E+04	4.46E+04	1.70E+05	1.48E+05
Intersectin 2	Y921*P	R.GEPEALY*AAVTK.K	6755502	3.853	0.7	5.75E+04	8.59E+04	2.06E+05	3.45E+05	4.14E+05	5.96E+05	9.91E+05	1.59E+06	9.69E+05
Kinesin 2	Y444	K.DGSFAFGEY*GGWYK.A	13878546	3.694	1.8	1.29E+04	1.78E+04	4.36E+04	6.72E+04	5.14E+04	3.74E+04	3.67E+04	5.37E+04	1.42E+04
Lactate dehydrogenase A	Y239*P	K.QVVDASAY*EVIK.L	1200099	3.11	1.1	8.36E+04	6.95E+04	8.30E+04	8.01E+04	7.21E+04	5.60E+04	6.82E+04	1.50E+05	9.61E+04
Lyn	Y194	R.SLDNGGY*ISPR.I	307144	3.228	0.1	3.12E+04	3.60E+04	4.72E+04	7.63E+04	5.14E+04	4.52E+04	5.09E+04	1.35E+05	9.08E+04
Lysosomal-associated protein 5	Y258	K.VALPSYEEALSPLPKTPEGDPAPPY*SEV.-	1255242	3.648	1.9	2.35E+05	5.25E+05	1.46E+06	3.36E+06	1.68E+06	1.37E+06	1.78E+06	1.82E+06	2.05E+06
MAWD/STRAP	Y342	K.IGFPETAEEEEIEIASSENSDSIY*SSTPEVK.A	26344646	4.228	3.7	7.83E+04	5.43E+04	7.63E+04	1.29E+05	9.25E+04	2.74E+04	4.74E+04	4.89E+04	1.50E+04
MIST/Clnk	Y69	K.CNSNNDY*EDPEFQLLK.A	6492366	4.911	4.0	2.86E+04	6.29E+04	3.22E+05	8.71E+05	6.76E+05	1.18E+06	1.58E+06	2.07E+06	1.22E+06
Monocyte Activated Protein, MAPA	Y289	R.SVDQDSQPVY*CNLESLSGR.-	23346481	4.566	2.0	3.42E+04	1.02E+05	1.83E+05	1.83E+05	7.78E+04	8.22E+04	5.45E+04	4.87E+04	7.48E+04
Myosin heavy chain 9	Y754	K.ALELDSNLY*R.I	20137006	3.027	0.5	7.82E+04	6.22E+04	7.86E+04	7.02E+04	5.99E+04	4.49E+04	6.02E+04	1.04E+05	6.16E+04
Myotubularin related protein 6	Y108	K.YEDLY*AFSYNPK.Q	18043664	4.47	1.2	1.22E+05	6.07E+04	7.70E+04	1.12E+05	7.00E+04	5.90E+04	5.56E+04	6.14E+04	7.19E+04
NCK2/Grb4 SH2/SH3 adaptor	Y110*P	R.DASPTPSTDAEYPANGSGADRIY*DLNIPAFVK.F	20532395	3.959	1.1		1.40E+04	6.93E+04	9.89E+04	7.57E+04	1.27E+05	2.82E+05	3.93E+05	5.33E+05
p38	T180Y182*	R.HTDDEMT*GY*VATR.-	15126598	4.806	0.2	5.25E+04	4.80E+04	7.15E+04	4.62E+04	6.07E+04	6.84E+04	4.27E+04	1.00E+05	5.39E+04
p38	Y182*	R.HTDDEMTGY*VATR.-	15126598	4.826	0.0	1.28E+05	1.16E+05	1.52E+05	1.95E+05	1.77E+05	2.70E+05	3.71E+05	4.59E+05	1.65E+05
PCTAIRE protein kinase 1	Y176	K.LGEGTY*ATVYK.G	53611	2.912	0.2	7.53E+05	5.60E+05	5.06E+05	8.69E+05	8.43E+05	8.47E+05	1.24E+06	3.47E+06	2.16E+06
Phosphofructokinase 1	Y650*P	R.NESCSVNYTTDFIY*QLYSEEGK.G	6634465	4.437	2.7	2.02E+04	2.82E+04	4.07E+04	4.07E+04	2.78E+04	1.59E+04	3.00E+04	3.51E+04	4.08E+04
Phosphoglucosmutase 1	Y353	K.IALY*ETPTGWK.F	31980726	3.499	1.1	2.38E+05	1.52E+05	1.55E+05	1.58E+05	1.41E+05	1.36E+05	1.29E+05	3.25E+05	1.74E+05
Phosphoglycerate mutase 1	Y26*P	R.FSGWY*DADLSPAGHEEAK.R	10179944	4.674	0.1	1.11E+05	7.67E+04	1.76E+05	1.08E+05	1.70E+05	1.19E+05	1.26E+05	2.10E+05	1.43E+05
PI 3 kinase regulatory p85, alpha	Y467	K.SREYDRLY*EEYTR.T	20897586	4.517	0.2	3.32E+05	1.93E+05	1.71E+05	2.25E+05	1.42E+05	1.61E+05	1.34E+05	2.97E+05	2.05E+05
PI 3 kinase regulatory p85, beta	Y458*P	K.SREYDQLY*EEYTR.T	2181945	4.097	0.9	9.35E+04	7.28E+04	8.93E+04	4.06E+04	2.92E+04	3.31E+04	5.58E+04	1.92E+05	
PKC delta	Y311*	R.KLDTTTSVGIY*QGFEK.K	8778120	6.403	0.2	6.93E+04	3.13E+04	7.35E+05	1.32E+06	1.27E+06	1.76E+06	2.62E+06	4.64E+06	2.66E+06
PLC, gamma 1	Y771*	K.IGTAEPDY*GALYEGR.N	40675439	3.858	1.6		3.14E+04	7.85E+04	1.41E+05	1.14E+05	9.97E+04	1.09E+05	2.11E+05	1.15E+05
PLC, gamma 1	Y775*	K.IGTAEPDYGALY*EGR.N	40675439	3.41	0.8		3.14E+04	7.85E+04	1.41E+05	1.14E+05	1.01E+05	1.18E+05	2.11E+05	1.15E+05
PLC, gamma 2	Y1217*	R.RQEELNNQLFLY*DTHQNL.R.G	23271777	7.012	2.3	9.57E+03	4.19E+04	9.39E+04	2.10E+05	1.48E+05	2.25E+05	2.84E+05	6.46E+05	5.35E+05
PLC, gamma 2	Y1245*P	K.EFNVNENQLQLY*QEK.C	23271777	4.277	0.2		9.57E+03	3.23E+04	5.56E+04	4.11E+04	6.83E+04	9.10E+04	6.90E+04	1.42E+05
PLC, gamma 2	Y753*	R.DINSLY*DVS.R.M	23271777	3.936	0.6	1.24E+04	1.58E+05	1.46E+05	4.10E+05	3.33E+05	3.61E+05	6.72E+05	1.45E+06	8.25E+05
Plectin 1	Y26	R.TSSEDNLY*LAVLR.A	41322941	2.732	0.9		7.35E+03	1.17E+04	1.84E+04	2.12E+04	1.16E+04	1.20E+04	2.73E+04	2.14E+03
Plectin 1	Y3649	R.LTAEDLY*EAR.I	41322941	3.151	1.8	3.39E+04	3.27E+04	3.88E+04	4.57E+04	3.58E+04	2.19E+04	2.80E+04	3.75E+04	
Poly(A) binding protein	Y116	K.ALY*DTFSAFGNILSCK.V	53754	5.251	5.1	1.11E+05	1.13E+05	9.36E+04	1.45E+05	9.61E+04	5.39E+04	9.15E+04	1.96E+05	1.54E+05
PRP4 kinase	Y849*P	K.LCDFGSASHVADNDITPY*LVSR.F	20330556	6.054	1.2	5.26E+05	5.45E+05	6.23E+05	1.06E+06	6.06E+05	5.44E+05	4.79E+05	1.10E+06	5.30E+05
PTP receptor type alpha	Y825*	K.VVQEYIDAFSDY*ANFK.-	6679557	6.541	2.3	2.93E+05	1.50E+05	2.40E+05	5.79E+05	4.54E+05	5.35E+05	6.55E+05	1.29E+06	9.31E+05
PTP receptor type epsilon	Y695*	K.VVQDFIDIFSDY*ANFK.-	7110707	5.552	2.2	4.03E+04	1.05E+05	3.02E+						

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RasGAP3	Y66	K.SLCPFYGEDFY*CEIPR.S	972944	3.089	15.2	1.23E+05	8.23E+04	6.52E+04	1.04E+05	7.68E+04	4.72E+04	7.01E+04	1.73E+05	9.44E+04
Rho GAP p190A	Y943*	R.NEEENIY*SVPHDSTQGK.I	55977867	3.808	0.3	5.05E+05	5.28E+05	1.05E+06	1.23E+06	7.88E+05	1.30E+06	1.64E+06	1.26E+06	1.49E+06
RhoGAP 12	S238*PY241*P	R.ATTPPNQGRPDS*PVY*ANLQELK.I	26986539	3.325	2.1	4.90E+04	8.23E+04	1.15E+05	2.47E+05	1.76E+05	1.76E+05	3.23E+05	9.67E+05	6.09E+05
RhoGAP1/CDC42GAP	Y65	K.WDDPYY*DIAR.H	31981892	2.559	3.0	1.54E+05	8.61E+04	1.23E+05	2.08E+05	9.74E+04	1.39E+05	6.01E+04	6.49E+04	3.79E+04
Ribosomal protein L10a	Y11	R.DTLY*EAVR.E	54035460	2.811	3.6	3.52E+04	2.32E+04	2.87E+04	5.16E+04	3.53E+04	1.21E+04	2.61E+04	2.83E+04	6.18E+04
Ribosomal protein S10	Y12*P	R.IAIY*ELLFK.E	56541262	3.251	0.7	8.22E+05	6.35E+05	7.38E+05	8.15E+05	5.64E+05	2.52E+05	6.55E+05	1.06E+06	1.18E+06
Ribosomal protein S3a	Y256*P	R.ADGY*EPPVQESV.-	1841932	2.803	0.3			2.32E+04	3.61E+04	2.11E+04	3.76E+04	6.39E+04	9.45E+04	8.72E+04
Ribosomal protein, large, P0	Y24*P	K.IIQLDDY*PK.C	71139	3.299	1.0	6.05E+04	5.01E+04	7.60E+04	8.89E+04	6.50E+04	3.81E+04	2.70E+04	8.88E+04	
RIKEN cDNA 2610016F04	Y81	K.VVDDEIY*YFR.K	27229015	3.235	0.4	3.49E+04	4.30E+04	4.27E+04	5.75E+04	3.50E+04	3.81E+04	3.98E+04	7.12E+04	5.09E+04
RIKEN cDNA 2810441C07	Y152	R.GLVY*EDVHR.A	27369543	2.769	0.1	2.08E+04	2.04E+04	2.80E+04	1.16E+05	9.05E+04	8.39E+04	1.15E+05	1.80E+05	1.67E+05
RIKEN cDNA 9130009D18	Y508*P	K.EAVY*SGVQSLR.S	12836199	2.788	2.4	3.12E+05	2.91E+05	2.38E+05	3.64E+05	2.55E+05	3.73E+05	3.93E+05	1.00E+06	6.17E+05
RIKEN cDNA 9930117H01	Y160	R.NADY*ECLPTLKEEKPNSPSPDNES.-	28893325	5.654	3.7	1.58E+05	3.03E+05	5.35E+05	7.07E+05	3.82E+05	4.20E+05	4.63E+05	4.11E+05	2.01E+05
SAM domain protein SAMSN1	Y152	R.DSFRLDDDDSPY*SGPFCGR.A	10800126	4.497	5.3	7.87E+04	1.65E+05	3.69E+05	5.56E+05	3.99E+05	3.07E+05	2.40E+05	2.85E+05	1.73E+05
Scinderin	Y599	R.GDY*QTSPLLETR.A	7441455	3.171	1.8	8.37E+04	8.09E+04	1.13E+05	7.78E+04	8.54E+04	9.24E+04	1.57E+05	2.84E+05	1.52E+05
SET	Y145	R.IDFYFDENPY*FENK.V	13591862	5.005	3.5	1.64E+06	1.28E+06	1.28E+06	1.82E+06	8.38E+05	8.53E+05	8.15E+05	1.55E+06	1.16E+06
SHC	Y423*	R.ELFDDPSY*VNIQNLDK.A	14211984	6.017	1.7	9.18E+04	2.11E+05	1.20E+06	3.54E+06	3.14E+06	1.73E+06	1.27E+06	2.43E+06	2.43E+06
SHIP	S934Y944	K.STLS*PDQQLTAWSY*DQLPK.D	1209068	5.978	1.9	2.81E+04	1.35E+05	4.53E+05	8.05E+05	7.76E+05	3.90E+05	2.45E+05	1.12E+06	4.84E+05
SHIP	Y867*P	K.LY*DFVK.T	1209068	2.727	0.5	1.04E+04	3.30E+04	6.91E+04	1.50E+05	1.52E+05	1.10E+05	1.36E+05	1.74E+05	9.45E+04
SHIP	Y944	K.STLSPDQQLTAWSY*DQLPK.D	1209068	4.794	2.8		1.69E+04	8.40E+04	1.75E+05	1.34E+05	1.04E+05	1.37E+05	9.67E+04	3.90E+04
SHP1	Y377	R.VYGLY*SVTNSR.E	4097669	2.924	1.9	2.81E+04	1.82E+04	2.78E+04	3.88E+04	3.55E+04	2.12E+04	2.36E+04	4.76E+04	
SHP2	Y62*P	K.IQNTGDY*YDLYGGEK.F	1304169	4.339	0.0	1.68E+05	1.45E+05	2.23E+05	2.50E+05	1.94E+05	1.40E+05	1.87E+05	2.80E+05	2.63E+05
SKAP55R	Y151	K.TVIFY*YGSDKDK.Q	4091780	3.799	1.3	1.72E+05	1.37E+05	1.32E+05	1.36E+05	1.43E+05	1.24E+05	1.44E+05	2.87E+05	1.79E+05
SKAP55R	Y260*P	R.SQPIDDEIY*EELPEEEEDTASVK.M	4091780	5.516	0.1	7.17E+05	1.08E+06	1.89E+06	2.99E+06	1.96E+06	1.77E+06	2.25E+06	4.76E+06	2.62E+06
SKAP55R	Y75*P	K.SVYLQEFQDKGDAEDGDEY*DDPFAGPADTISLASER.Y	4091780	7.383	4.8	2.49E+04	3.06E+04	3.89E+04	8.12E+04	5.82E+04	3.82E+04	4.70E+04	9.08E+04	5.22E+04
SLP76	Y23	R.SEVLAWNSDNLADY*FR.K	1083554	4.537	1.5		1.68E+04	1.97E+04	1.80E+04	2.57E+04	1.99E+04	1.44E+04	6.46E+04	4.91E+04
Small fragment nuclease	Y152	R.WYPEDY*EFAPK.K	13097411	2.391	2.8	1.50E+05	1.57E+05	1.80E+05	2.52E+05	1.47E+05	1.73E+05	2.12E+05	4.69E+05	2.90E+05
STE20 like kinase MST1	Y433	K.IPQDGDY*EFLK.S	8489867	2.59	2.6	7.02E+04	3.16E+04	5.88E+04	1.06E+05	1.08E+05	8.28E+04	1.08E+05	2.18E+05	1.24E+05
SYK	Y342*Y346*	R.EALPMDTEVY*ESPY*ADPEEIRPK.E	818861	3.298	1.0	3.93E+04	1.04E+05	1.63E+05	3.51E+05	3.42E+05	2.59E+05	3.76E+05	6.07E+05	3.50E+05
SYK	Y540	K.WYAPECINY*YK.F	818861	2.533	14.5	5.30E+04	4.79E+04	4.52E+04	6.26E+04	5.05E+04	3.00E+04	5.15E+04	1.24E+05	1.37E+05
T-cell activation protein, MAPRE2	Y166*P	K.FYDANYDGKEY*DPVEAR.Q	19387961	4.169	2.9	5.02E+04	6.07E+04	1.12E+05	1.24E+05	1.21E+05	6.56E+04	7.34E+04	8.78E+04	5.61E+04
TEC tyrosine kinase	Y415	R.YVLDDQY*TSSSGAK.F	110868	4.111	0.6		1.32E+04	3.24E+04	7.35E+04	5.61E+04	8.76E+04	1.30E+05	2.91E+05	1.93E+05
TIAM1	Y1323*P	R.LSIY*EEWDPFR.F	6678351	3.725	2.4	1.19E+05	1.87E+05	3.58E+05	5.03E+05	4.10E+05	2.96E+05	4.35E+05	6.60E+05	6.01E+05
Tight junction protein 1; ZO-1	Y1353	R.SNHYPDEEDEEY*YRK.Q	303710	4.689	0.5		2.69E+04	4.42E+04	7.74E+04	8.65E+04	1.02E+05	1.76E+05	3.14E+05	1.11E+05
Transferrin receptor	Y20*P	R.SAFSNLFGGEPLSY*TR.F	54915	5.541	1.6	1.50E+05	2.53E+05	2.74E+05	3.09E+05	2.37E+05	2.48E+05	2.80E+05	5.27E+05	4.41E+05
TRIP4	Y289*P	R.TQVIDDES DY*FASDSNQWLSK.V	18204665	4.527	0.3	2.06E+04	3.79E+04	7.59E+04	9.16E+04	5.74E+04	3.61E+04	4.69E+04	7.84E+04	6.82E+04
Tubulin, beta	Y340	K.NSSY*FVEWIPNNVK.T	91857	3.665	4.8	4.39E+04	1.61E+04	2.47E+04	4.02E+04	2.31E+04	2.76E+04	5.03E+04	1.27E+05	8.73E+04
TXK tyrosine kinase	Y420*	R.YVLDDDEY*ISSSGAK.F	7305601	3.572	0.0	3.24E+04	3.61E+04	4.01E+04	5.73E+04	3.71E+04	3.46E+04	3.98E+04	9.45E+04	5.92E+04
TYK2 tyrosine kinase	Y600	R.TNVY*EGLLR.V	5733095	2.645	1.4	1.83E+04	1.71E+04	1.84E+04	2.37E+04	1.88E+04	1.51E+04	9.85E+03	1.98E+04	
UBCH6	Y77	K.GDNIY*EWR.S	6678479	2.97	0.6	4.23E+04	4.82E+04	4.54E+04	8.26E+04	6.74E+04	4.69E+04	5.40E+04	1.06E+05	6.56E+04
Ubiquitin activating enzyme E1	Y55*P	K.NGSEADIDESLY*SR.Q	111228	4.471	1.6	1.63E+04	3.34E+04	8.17E+04	1.57E+05	8.29E+04	6.76E+04	6.01E+04	1.36E+05	1.01E+05
ubiquitin specific protease 24	Y484	R.YVITIEDFY*SVPR.T	51709370	4.015	3.5	7.07E+04	4.48E+04	4.77E+04	5.95E+04	4.22E+04	3.29E+04	5.51E+04	1.09E+05	1.17E+05
Ubiquitin-specific protease 9. FAF-X	Y1815	K.FNDY*FEFPR.E	1527199	2.793	4.1	3.56E+04	3.51E+04	4.44E+04	5.08E+04	4.09E+04	2.68E+04	2.94E+04	4.26E+04	5.85E+04
VAV	Y844*P	R.IGWFPSNYVEEDYSEY*C.-	6755955	5.476	2.7	2.76E+06	5.11E+05	7.41E+05	2.20E+06	1.41E+06	1.77E+06	3.61E+06	6.91E+06	5.52E+06
Vimentin	Y53*P	R.SLY*SSSPGGAYVTR.S	55408	3.73	2.6	8.12E+03	1.31E+04	1.33E+04	3.09E+04	4.43E+04	6.75E+04	1.23E+05	3.65E+05	1.58E+05
VPS35	Y791	R.ESPESEGPYI*EGLIL.-	11875394	3.324	1.9	3.70E+04	4.79E+04	7.41E+04	9.85E+04	7.76E+04	2.66E+04	3.58E+04	6.30E+04	6.51E+04
WASP	Y293*	K.LIY*DFIEDQGGLEAVR.Q	4096355	6.724	0.7		1.44E+05	3.87E+05	6.14E+05	3.51E+05	2.59E+05	3.45E+05	8.62E+05	3.76E+05

B) BMMC data set											
Protein Name	Phosphorylation Site	Peptide Sequence	GI	xcorr max	mass error	0 sec SIC Peak Area	1 min SIC Peak Area	5 min SIC Peak Area			
Advillin	Y748	K.NATLY*LNPSDGEPK.Y	6857753	4.609	0.6	4.67E+05	1.76E+06	5.03E+05			
Advillin	Y748Y758	K.NATLY*LNPSDGEPKY*YPVEVLLK.G	6857753	3.169	1.0		9.46E+05	1.06E+05			
Advillin	Y85	K.DSSQDEQSCAAIYTTQLDDY*LGGSPVQHR.E	6857753	4.966	0.5	2.81E+04	1.49E+05	1.04E+05			
AHNAK nucleoprotein isoform 1	S116Y126	R.SSEVVLS*GDDEDYQRIY*TTK.I	61743961	3.686	1.9	1.35E+05	2.09E+06	3.68E+05			
AHNAK nucleoprotein isoform 1	Y122	R.SSEVVLSGDDEDY*QR.I	61743961	5.941	0.0	8.56E+05	1.28E+07	4.98E+06			
AHNAK nucleoprotein isoform 1	Y122Y126	R.SSEVVLSGDDEDY*QRIY*TTK.I	61743961	4.327	1.2		2.09E+06	5.05E+04			
AHNAK nucleoprotein isoform 1	Y716	K.VKGEY*EVTPPKLEGELK.G	61743961	3.04	0.5		2.99E+05	1.06E+05			
AHNAK nucleoprotein isoform 1	S116Y122	R.SSEVVLS*GDDEDY*QRIYTTK.I	61743961	5.282	0.8	1.23E+05	2.10E+06	3.68E+05			
aldo-keto reductase AKR1C12	Y323	R.YLPAEFLADHPEYPFSEEY*.-	6407382	4.657	0.1	7.04E+04	1.47E+06	1.10E+05			
Aminopeptidase N	Y852	R.YLSYTLNPDY*IR.K	1674501	2.953	1.2	1.44E+04	3.69E+04	1.51E+04			
AMP deaminase 2	Y64	R.SAPY*EFPEESPIEQLEER.R	21311925	4.012	2.7	1.18E+04	2.64E+05	1.07E+05			
ARAP3	Y1404*	K.SPQGSVVEEQDELEEPVYEEPVY*EEVGAFPELTK.D	18700709	5.345	0.2	2.35E+05	1.13E+06				
ATP receptor P2X4 subunit	Y378	K.YKYVEDY*EQGLSGETDQ.-	4019304	4.854	0.4	6.57E+04	6.07E+05	3.63E+05			
BC003940 protein	Y56	R.FIY*EAWQGVVER.D	12805435	3.768	4.1	9.00E+03	4.86E+04	2.01E+04			
BCR	S26Y36*	R.GRSS*ESSCGLDGDY*EDAELNPR.F	37994655	5.164	6.9		4.32E+05	2.75E+05			
BCR	Y36*	R.SSESSCGLDGDY*EDAELNPR.F	37994655	4.311	6.0	5.96E+04	3.73E+05				
BCR downstream signaling 1/STAP1	Y170	K.EKEPVQDY*ADVLNPLPECFYAVSR.K	9910568	5.311	5.6		4.05E+05	9.38E+04			
BCSC1	Y622	R.FY*SSFSGGFK.G	37596282	3.229	0.4	4.92E+04	3.34E+05	1.56E+05			
Bruton's tyrosine kinase	Y551*	R.YVLDDEY*TSSVGSK.F	1666703	5.428	0.2	1.60E+05	3.19E+06	4.96E+05			
C1qR/CD93	Y636	R.AESQAPENQY*SPTPGTDC.-	5714405	4.084	11.3	3.75E+04	1.44E+05	6.73E+04			
C9orf78	Y147*P	K.NAEDCLY*ELPENIR.V	13542853	3.093	5.4	1.29E+05	2.85E+05	1.63E+05			
Catenin, delta 1	Y904	K.SLDNNY*STLNER.G	32451614	2.731	0.3	8.73E+03	3.00E+04				
CBP/PAG	Y224*P	K.ADFAEY*ASVDR.N	12005671	3.782	0.2	1.09E+05	4.52E+05	1.65E+05			
CD244	Y396	R.ELENFVY*S.-	9651827	2.217	0.1		3.89E+05	1.08E+05			
CD31	Y702*	R.ATETVY*SEIR.K	6679273	3.138	0.2	2.29E+04	8.80E+04	2.32E+04			
CD34	Y326*P	R.LGEDPY*YTENGGGQYSSGPGASPETQGK.A	13879274	5.778	0.5	4.20E+04		8.62E+04			
CDC2	Y15*	K.IGEGTY*GVVYK.G	50360	3.471	0.2	2.77E+05	1.26E+05	3.00E+05			
Chromosome 20 open reading frame 18	Y318*P	R.NSQEAEVACPFIDSTY*SCPGK.L	9790279	4.712	18.0		1.02E+06	7.67E+05			
Cofilin 1	Y140*P	K.HELQANCY*EEVKDR.C	109675	4.706	15.2		1.60E+05	5.66E+04			
Cofilin 1	Y68*P	K.NIILEEGKEILVGDVGTVDVDPY*TTFVK.M	109675	7.046	2.1	2.00E+05	5.47E+05	2.17E+05			
Cofilin 1	Y89*P	R.YALYDATY*ETK.E	109675	3.674	1.0	5.27E+05	2.66E+06				
Cytoskeleton associated protein 1	Y98*P	R.LGEY*EDVSKVEK.Y	60390860	4.111	1.4	1.34E+04	8.52E+04	2.27E+04			
DAP12	Y92*	K.QHIAETESPY*QELQGQRPEVYSDLNTQR.Q	2906002	2.967	0.5	1.02E+05	2.35E+05	6.15E+04			
DAP12	Y92*Y103*	K.QHIAETESPY*QELQGQRPEVY*SDLNTQR.Q	2906002	3.868	2.2	1.01E+05	6.00E+05	1.15E+05			
DAPP1	Y139*	R.EVEEPCY*ESVR.V	5733602	3.716	9.5	3.73E+06	4.81E+07	2.30E+07			
Diaphanous homolog 1	Y1104	K.ELGDY*FVFDPK.K	6681183	2.907	2.0	1.97E+04	9.43E+04	4.90E+04			
DOK1; p62dok	Y361*	K.TKLTDSKEDIPIY*DEPEGLAPAPPR.G	4007990	5.707	0.0	2.05E+05	1.89E+06	1.94E+05			
DOK1; p62dok	Y408*	R.LKEEGYELPYNPATDDY*AVPPPR.S	4007990	4.01	0.7	2.95E+04	5.40E+05	5.89E+04			
DOK1; p62dok	Y450*P	K.GFSSDTALY*SQVQK.S	4007990	5.265	2.0	5.75E+04	2.41E+06	2.64E+05			
DOK3; p62dok-like	S314Y325*P	R.KLPLTDPGPQSLPLLLS*PTQEGPASGLY*ASVCK.Q	7305003	5.061	3.2		1.30E+06	2.20E+05			
Elongation factor 1 alpha 1	Y141*P	R.EHALLAY*TLGVK.Q	50797	3.257	0.8	3.23E+04	1.57E+05				
Enolase	Y25*P	R.GNPTVEVDLY*TAK.G	182116	4.369	0.6	4.04E+05	1.57E+06	4.44E+05			
Enolase	Y44*P	R.AAVPSGASTGIY*EALELR.D	50847	4.62	0.4	1.24E+05	4.12E+05	1.44E+05			
Erbin	Y1122*P	R.RTEGDY*LSYR.E	28972678	3.155	0.3	2.61E+04	2.18E+05	5.53E+04			
ERK1	T203*Y205*	R.IADPEHDHTGFLT*EY*VATR.-	21489933	5.138	0.2	4.24E+04	1.01E+07	3.04E+06			
ERK2	T183*Y185*	R.VADPDHDHTGFLT*EY*VATR.W	53002	5.622	0.5		5.74E+06	1.14E+06			
Ezrin	Y270	K.APDFVY*APR.L	50881	3.92	0.8	1.04E+05	2.96E+05	1.42E+05			
FBP17	S113Y116	R.RQS*GLY*DGQTHQVTNCAQDR.E	1255033	3.442	7.2		2.73E+04	1.99E+04			
Fc IgE receptor, beta	Y216	R.LYEELNVY*SPIYSELEDKGETSSPVDS.-	110554	3.895	0.5	4.14E+05	2.86E+06	2.03E+06			
Fc IgE receptor, beta	Y220	R.LYEELNVYSPIY*SELEDKGETSSPVDS.-	110554	4.732	0.0	4.14E+05	2.86E+06	2.03E+06			
Fc IgE receptor, beta	Y210*	K.KVPDDRLY*EELNVYSPIYSELEDKGETSSPVDS.-	110554	7.114	0.8	1.13E+05	7.70E+05	1.80E+05			
Fc IgE receptor, beta	Y210*S217	K.KVPDDRLY*EELNVYS*PIYSELEDKGETSSPVDS.-	110554	6.805	0.3		1.05E+06	5.60E+05			
Fc IgE receptor, beta	Y210*Y216Y220	K.KVPDDRLY*EELNVY*SPIY*SELEDKGETSSPVDS.-	110554	5.01	1.6		4.00E+05	1.89E+05			
Fc IgE receptor, beta	Y210*Y220	K.KVPDDRLY*EELNVYSPIY*SELEDKGETSSPVDS.-	110554	7.13	3.9	7.55E+04		5.61E+05			
Fc IgE receptor, gamma	Y65	K.ADAVY*TGLNTR.S	6753830	4.604	0.0	3.13E+05	4.72E+06	1.36E+06			
FER tyrosine kinase	Y402	K.VQENDGKEPPPVVNY*EEDAR.S	1673620	5.768	0.2	2.53E+05	2.01E+06	4.63E+05			
FOP	Y317	K.IGSLGLGTGEDEDY*ADDFNASASHR.S	47777353	3.25	2.5		2.12E+05	8.40E+04			
Fps/Fes tyrosine kinase	Y711	R.EEADGIY*AAASAGLR.Q	23452674	4.863	0.6	2.58E+03	4.31E+05	2.25E+05			
FYB/SLAP130	Y277	K.SSFFSAPQY*FED.-	19547899	3.715	0.2		3.52E+05	8.93E+04			

Protein Name	Phosphorylation Site	Peptide Sequence	GI	xcorr max	mass error	0 sec SIC Peak Area	1 min SIC Peak Area	5 min SIC Peak Area
FYB/SLAP130	Y559*P	K.TTAVEIDY*DSLKR.K	2232152	4.063	0.5	1.14E+05	8.52E+04	8.96E+04
FYB/SLAP130	Y559*PS561	K.TTAVEIDY*DS*LKR.K	2232152	5.233	0.7	7.03E+05	1.23E+06	4.14E+05
GAB2	S261Y263*	R.HNTEFKDS*TY*DLPR.S	4589377	3.585	0.1		6.06E+05	1.89E+05
GAB2	Y263*	R.HNTEFKDSTY*DLPR.S	4589377	4.042	0.7		9.06E+05	1.95E+05
GAB2	Y290*	K.SSLTGSETDNEDVY*TFK.M	4589377	5.034	0.5	2.60E+04	1.89E+06	2.08E+05
GAPDH	Y316*P	K.LISWYDNEY*GYSNR.V	6679937	4.292	5.1	1.82E+05	1.68E+06	
Glucose-6-phosphate dehydrogenase	Y507*P	R.VGFQYEGTY*K.W	51114	2.708	1.7	5.08E+03	1.88E+05	1.31E+05
Grb4	Y110*P	R.DASPTPSTDAEYPANGSGADRIY*DLNIPAFVK.F	20532395	4.61	2.1	1.03E+05	4.87E+05	4.25E+05
GSK3 beta	Y216*	R.GEPNVSY*ICSR.Y	7025915	3.169	16.0	2.20E+06	1.07E+07	1.56E+06
Heat shock 70kDa protein 4	Y661	K.LEDTENWLY*EDGEDQPK.Q	31982275	4.804	4.3	9.40E+03	1.03E+05	5.64E+04
Hematopoietic cell specific LYN substrate 1	Y140	K.SAVGFDY*KGEVEK.H	13938627	3.824	1.0		1.36E+05	4.63E+04
Heterogeneous nuclear ribonucleoprotein U	Y240	R.GYFEYIEENKY*SR.A	3329496	3.794	3.1	1.52E+04		5.40E+04
Hrs	Y308*P	K.AEPTPLASSAPPAGSLY*SSPVNSSAPLAEDIDPELAR.Y	1089781	4.463	2.7	3.29E+04	2.15E+05	
Hypothetical protein H41	Y213*P	R.KTPQGPPEIY*SDTQFPSLQSTAK.H	18147007	4.257	1.7	3.60E+04		2.70E+05
hypothetical protein MGC36956	Y132	K.NTGVTPEPLY*R.S	21595104	2.736	0.4	1.26E+04	4.25E+04	2.34E+04
Ig heavy chain V region	S84Y93T96	K.SQVFFKMNS*LQADDTAIY*YCT*K.E	110132	3.27	0.8		3.98E+06	1.53E+06
Ig heavy chain V region	Y62T64S65	R.NKANGYTTTEY*NT*S*LK.G	110220	2.918	8.6	9.25E+05	3.34E+06	8.49E+05
IL 3 receptor, beta	S752Y765*	R.VPS*GSPALGPPGFEDY*VELPPSVSQAAS.S	110595	4.463	2.0	1.51E+05		1.67E+05
IL 3 receptor, beta	S754Y765*	R.VPSGS*PALGPPGFEDY*VELPPSVSQAAS.S	110595	3.459	0.1	1.51E+05	3.55E+05	1.67E+05
IL 3 receptor, beta	Y765*	R.VPSGSPALGPPGFEDY*VELPPSVSQAAS.S	110595	5.148	0.3	2.61E+05	1.78E+06	4.07E+05
Interleukin 2 receptor, gamma	Y325	K.GLTESLQPDY*SER.F	15928484	2.908	0.9	6.14E+04	1.08E+05	4.47E+04
Intersectin 2	Y921*P	R.GEPEALY*AAVTK.K	6755502	4.144	0.9	1.77E+05	1.24E+06	5.09E+05
Jak2	Y570*	R.REVGDY*GQLHETEVLLK.V	2499669	3.616	0.6	2.47E+04	1.07E+05	
KIT	Y567*	K.VVEEINGNNY*VYIDPTQLPYDHK.W	28512901	4.291	2.0	1.90E+05	1.56E+06	
KIT	Y567*Y569*	K.VVEEINGNNY*VY*IDPTQLPYDHK.W	28512901	4.79	1.4	7.55E+04	3.67E+05	1.76E+05
KIT	Y569*	K.VVEEINGNNY*VY*IDPTQLPYDHK.W	28512901	5.283	0.2	1.90E+05	1.56E+06	5.58E+05
KIT	Y702*	R.DSFIFSKQEEQAEALY*K.N	28512901	4.562	0.5	1.24E+05	2.76E+05	8.03E+04
KIT	Y934*	K.HIY*SNLANCNPENPVVVDHSVR.V	28512901	5.48	6.7	1.79E+05	4.12E+05	1.48E+05
Leupaxin	Y22*P	R.CTFQDSEEY*SNPVSCHLDQQSTEESK.I	22035901	4.035	12.7	6.56E+04		1.62E+05
Leupaxin	Y62	K.VQLVY*ATNIQEPNVYSEVQEPK.E	22035901	5.956	1.4	1.31E+04	1.77E+05	9.11E+03
Leupaxin	Y62Y72	K.VQLVY*ATNIQEPNVY*SEVQEPK.E	22035901	4.73	2.0	2.84E+04	5.37E+05	1.16E+05
Leupaxin	Y72	K.VQLVYATNIQEPNVY*SEVQEPK.E	22035901	5.603	0.8	1.82E+05	1.51E+06	3.27E+05
Lpp	Y302*P	R.YYEPYY*AAGPSYGGGR.S	55154563	4.154	0.9	2.80E+04	8.43E+04	6.15E+04
Lyn	Y193*P	R.SLDNGGY*YISPR.I	307144	3.273	0.2	1.17E+05	3.84E+05	9.78E+04
Lysosomal-associated protein 5	Y258	K.VALPSYEEALSLPPKTPGDPAPPPY*SEV.-	1255242	3.04	1.8	3.50E+05	7.68E+05	
mast cell protease 6	Y98	R.EQYLY*GDQLLSLNR.I	6857814	3.384	4.2	3.41E+04		2.51E+04
MAWD/STRAP	Y342	K.IGFPETAEELIEIASENSISY*SSTPEVKA.-	26344646	3.974	4.7		1.87E+05	6.36E+04
Metastasis suppressor 1	Y544	R.AGPVSDY*DYFSVSGDQEAQQEFDKSSSTIPR.N	37359942	3.571	1.0	1.20E+04	7.50E+04	
MIST/Clnk	Y69	K.CNSNDY*EDPEFQLLK.A	6492366	4.997	6.6	4.55E+05	2.59E+06	8.23E+05
mKIAA1522 protein	Y108	K.GGWDHGDTSIQSSQTGPDEDTISIY*SQK.S	25021466	5.546	1.2	2.69E+04	1.64E+05	
Moesin	Y116	K.EGILNDDIY*CPPETAVLLASYAVQSK.Y	28703650	4.183	4.7	1.02E+04	8.97E+04	3.86E+04
NSFL1C cofactor p47	Y167	R.LGAAPPEESAY*VAGER.R	41017503	3.283	0.1	5.72E+04	2.15E+05	
NTAL	Y59	R.NRQENASAAAQTY*SLAR.Q	8470890	4.725	1.0	1.76E+04	6.29E+05	1.79E+05
NTAL	Y59S60	R.NRQENASAAAQTY*S*LAR.Q	8470890	4.731	0.7		3.74E+05	7.34E+04
p38	Y182*	R.HTDDEMTGY*VATR.-	15126598	4.401	1.3		2.48E+05	4.51E+04
Phosphofructokinase 1	Y650*P	R.NESCSVNYTTDFIY*QLYSEEGK.G	6634465	2.869	8.2		3.15E+04	1.98E+04
Phosphoglycerate mutase 1	Y26*P	R.FSGWY*DADLSPAGHEEAK.R	10179944	3.144	3.4	3.07E+04	5.99E+04	
PKC delta	Y311*	R.KLDTTESVGIY*QGFEK.K	8778120	6.633	0.2	3.99E+05	1.67E+07	4.38E+06
PLC, gamma 1	Y771*	K.IGTAEPDY*GALYEGR.N	40675439	3.897	0.3	2.53E+04	5.96E+05	1.27E+05
PLC, gamma 2	Y1217*	R.RQEELNNQLFLY*DTHQNL.R.G	23271777	7.077	0.3	3.35E+04	9.36E+05	1.47E+05
PLC, gamma 2	Y1245*P	K.EFNVNENQLQLY*QEK.C	23271777	4.205	0.7	2.05E+04	6.35E+05	1.40E+05
PLC, gamma 2	Y753*	R.DINSLY*DVS.R.M	23271777	3.613	0.6	8.02E+04		6.21E+05
Plectin 1	Y3364	R.ARQEEVY*SELQAR.E	41322931	3.146	0.2	4.61E+03	3.63E+04	1.54E+04
Plectin 1	Y2783	R.DAPDGPVSEAEPEY*TFEGLR.Q	41322931	3.013	2.0	4.35E+04		8.76E+04
Plectin 1	Y3035	K.GGELVY*TDTEAR.D	41322931	3.125	0.7		4.20E+04	2.47E+04
Plectin 1	Y4617*P	K.GYYSPY*SVSGSGSTAGSR.T	41322931	4.277	0.7		4.00E+04	5.38E+04
protein tyrosine phosphatase 18	Y381*P	R.APTSTDTPY*SQVAPR.A	2584837	4.558	0.2	7.56E+04	1.17E+05	3.61E+05
protein tyrosine phosphatase 18	Y419	R.RVPADQNSSGPDAY*EEVTDGAQTGGLGFNLR.I	2584837	5.621	0.0		2.77E+05	9.48E+04
PRP4 kinase	Y849*P	K.LCDFGSASHVADNDITPY*LVSR.F	20330556	5.02	7.0	4.86E+05	1.46E+06	4.04E+05
PSTPIP2	Y323	K.RIPDDPDY*SVVEDYSLLYQ.-	3947712	4.638	1.8	3.51E+04	8.89E+05	2.30E+05

Protein Name	Phosphorylation Site	Peptide Sequence	GI	xcorr max	mass error	0 sec SIC Peak Area	1 min SIC Peak Area	5 min SIC Peak Area
PSTPIP2	Y329	K.RIPDDPDYSVVEDY*SLLYQ.-	3947712	4.611	0.7		6.19E+05	2.12E+05
PTP receptor type alpha	Y825*	K.VVQEYIDAFSDY*ANFK.-	6679557	6.073	0.1	3.71E+05	1.16E+06	2.49E+05
PTP receptor type epsilon	Y695*	K.VVQDFIDIFSDY*ANFK.-	7110707	4.308	3.2	5.95E+03		1.66E+04
PYK2	Y402*	R.SHLSSECSIESDIY*AEIPDETLR.R	988305	4.008	6.9	1.02E+05		4.39E+04
PYK2	Y579*	R.YIEDEDY*YKASVTR.L	988305	3.232	2.3	6.65E+03	2.19E+05	5.27E+04
PYK2	Y579*Y580*	R.YIEDEDY**Y*KASVTR.L	988305	2.648	2.4		5.21E+04	2.60E+04
Rho GAP p190A	Y943*	R.NEEENIY*SVPHDSTQGK.I	55977867	4.544	0.7	3.11E+05	1.43E+06	9.14E+05
Ribosomal protein S10	Y12*P	R.IAIY*ELLFK.E	56541262	2.757	2.2	1.17E+04	1.03E+05	3.75E+04
Ribosomal protein S3a	Y256*P	R.ADGY*EPPVQESV.-	1841932	3.144	1.3	3.73E+04	4.20E+05	2.58E+05
RIKEN cDNA 2310011J03	Y63*P	R.AEDSEIQEQEY*QQSR.A	21313500	3.677	0.6	1.30E+04	6.33E+04	2.24E+04
RIKEN cDNA 2810407E01	Y81	R.IGIVGGCQEY*TGAPYFAGISALK.V	18043481	4.08	7.7	3.03E+04		5.32E+04
RIKEN cDNA 2810441C07	Y131*P	R.FTFPALEEDVIY*DDVPCESPDHAHQPGAER.G	27369543	4.658	1.4	1.14E+05	4.79E+05	
RIKEN cDNA 9130009D18	Y508*P	K.EAVY*SGVQSLR.S	12836199	2.371	0.7	9.05E+03	3.34E+04	
RIKEN cDNA 9930117H01	Y160	R.NADY*ECLPTLKKEEKPNSPSPDNES.-	28893325	6.555	0.6	1.32E+06	6.32E+06	1.24E+06
RIKEN cDNA 9930117H01	Y160S177	R.NADY*ECLPTLKKEEKPNSPSPS*DNES.-	28893325	5.237	6.7	1.47E+05	8.47E+05	2.56E+05
RIKEN cDNA F630103L12	Y13	R.TEGLDY*DTFPEVPATPGER.E	27369954	4.219	1.7	1.26E+05	1.69E+05	2.22E+05
Scinderin	Y102	R.ELQGY*ESTDFVGYFK.G	7441455	4.036	1.3	1.42E+04	9.56E+04	
Scinderin	Y599	R.GDY*QTSPLLETR.A	7441455	3.886	0.0	5.09E+05	1.62E+06	5.06E+05
Serpin	Y166	R.LVLVNAIY*FK.G	15029834	3.38	2.4	1.12E+04		2.09E+04
SET	Y145	R.IDFYFDENPY*FENK.V	13591862	4.237	1.2	1.28E+04	7.86E+05	1.47E+04
SHC	Y423*	R.ELFDDPSY*VNIQNLDK.A	21264509	5.864	0.5	1.90E+05	2.76E+06	1.66E+06
SHIP	S934Y944	K.STLS*PDQQLTAWSY*DQLPK.D	1209068	6.187	0.0	2.16E+05	2.78E+06	1.57E+06
SHIP	Y867*P	K.LY*DFVK.T	1209068	2.677	0.1	1.24E+05	6.81E+05	1.87E+05
SHIP	Y944	K.STLSPDQQLTAWSY*DQLPK.D	1209068	4.626	1.8	5.67E+04	5.77E+05	
SHIP1	Y536*	K.GQESEY*GNITYPPAVR.S	4097669	4.103	1.1	4.31E+05	4.90E+06	
SHIP2	Y62*P	K.IQNTGDY*YDLYGGEK.F	1304169	4.371	0.3		1.20E+06	2.73E+05
Similar to hypothetical protein FLJ32731	Y217	R.ADPLSADY*QPETR.R	23272280	3.228	0.5	2.99E+04	8.66E+04	4.28E+04
SKAP55R	Y142	R.GLFLY*YANEK.S	4091780	3.668	0.1	4.98E+05	1.68E+06	7.53E+05
SKAP55R	Y151	K.TVFY*YGSDDKDK.Q	4091780	3.53	0.4	2.99E+04	1.35E+05	5.30E+04
SKAP55R	Y260*P	R.SQPIDDEIY*EELPEEEEDTASVK.M	4091780	6.038	0.0	3.12E+06	9.69E+06	5.30E+06
SKAP55R	Y75*P	K.SVYLQEFQDKGDAEDGDEY*DDPFAGPADTISLASER.Y	4091780	6.9	3.4	5.94E+04	7.03E+05	2.39E+05
SLP76	Y23	R.SEVLAWNSDNLADY*FR.K	1083554	4.244	0.3	9.14E+03	1.15E+05	3.08E+04
STE20 like kinase MST1	Y433	K.IPQDGDY*EFLK.S	8489867	3.022	1.3	6.94E+04	5.27E+05	1.69E+05
SYK	S310S313Y317*	K.KPAPPQGSRPES*TVS*FNPY*EPTGGPWGPDR.G	818861	7.101	0.4		9.30E+05	1.00E+06
SYK	S310Y317*	K.KPAPPQGSRPES*TVSFNPY*EPTGGPWGPDR.G	818861	4.828	0.0		8.63E+05	1.09E+05
SYK	Y317*	K.KPAPPQGSRPES*TVSFNPY*EPTGGPWGPDR.G	818861	4.165	3.7	1.71E+05	9.98E+05	1.57E+05
SYK	Y519*Y520*	R.ADENY*Y*KAQTHGKWPVK.W	479013	3.387	1.1		1.05E+06	1.90E+05
SYK	Y623	R.LRNY*YDVVN.-	818861	2.567	0.1		3.33E+07	1.56E+07
SYK	Y624	R.LRNY*YDVVN.-	818861	2.978	0.2		3.33E+07	1.56E+07
Tec tyrosine kinase	Y415	R.YVLDDQY*TSSSGAK.F	38566061	4.195	0.2	3.59E+04	3.16E+05	9.49E+04
Thyroid hormone receptor interactor 4	Y289*P	R.TQVIDDES DY*FASDSNQWLSK.V	18204665	5.038	0.7		1.08E+05	6.63E+04
TIAM1	Y1323*P	R.LSIY*EEWDPPFR.F	6678351	3.693	1.1	6.09E+05	2.97E+06	1.09E+06
Tight junction protein 1; ZO-1	Y1139	R.FEEPAPLSY*DSR.T	303710	3.056	0.6		1.66E+05	1.19E+05
TXK tyrosine kinase	Y420*	R.YVLDDDEY*ISSSGAK.F	7305601	4.859	1.4	7.40E+04	2.35E+05	7.11E+04
TXK tyrosine kinase	Y91*	K.ALY*DFLPR.E	2117815	3.06	1.0	1.53E+05	4.36E+05	2.53E+05
Ubiquitin activating enzyme E1	Y55*P	K.NGSEADIDESLY*SR.Q	111228	4.77	0.3	8.23E+04	1.92E+05	1.71E+05
Ubiquitin-specific protease 9. FAF-X	Y2540*P	R.AQENY*EGGEEVSPQTK.D	1527199	3.478	2.0		7.10E+04	1.42E+04
VAV	Y844*P	R.IGWFPNSYVEEDYSEY*C.-	6755955	5.701	4.9	3.32E+05	3.06E+06	1.20E+06
Vimentin	Y53*P	R.SLY*SSSPGGAYVTR.S	55291	4.412	0.2	7.41E+04	1.71E+05	1.99E+05
Vimentin	Y53*PY61*P	R.SLY*SSSPGGAY*VTR.S	55291	2.902	0.6		2.70E+05	4.95E+04
VPS35	Y791	R.ESPESEGPY*EGLIL.-	7656643	4.024	0.9	6.38E+04	7.52E+05	2.05E+05
WASP	Y293*	K.LIY*DFIEDQGGLEAVR.Q	695151	6.333	0.5	2.80E+05	1.25E+06	4.97E+05