

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
K.AAVFEEIDTY*ERR.S	2	3.1032	0.3207	HYPOTHETICAL PROTEIN FLJ21128.
K.AELSYRGPVSGTEPEPVY*SMEAADYR.E	3	4.716	0.1592	CTTN PROTEIN.
K.AELSYRGPVSGTEPEPVYSMEAADY*R.E	3	3.9653	0.2839	SRC SUBSTRATE CORTACTIN.
K.AISSDMY*FGR.Q	2	3.0458	0.1953	ADP-RIBOSYLATION FACTOR GTPASE-ACTIVATING PROTEIN 3.
K.AKLTDPKEDIY*DEPEGLAPVPPQGLY*DLPREP.K.D	3	3.7438	0.2639	SPLICE ISOFORM 1 OF DOCKING PROTEIN 1.
K.ALGADDSY*Y*TAR.S	2	3.6696	0.2565	TRUNCATED ZAP KINASE.
K.ALGADDSY*YTAR.S	2	3.5524	0.3073	TYROSINE-PROTEIN KINASE ZAP-70.
K.ALGADDSY*Y*TAR.S	2	3.8023	0.3091	TRUNCATED ZAP KINASE.
K.ALNGAEPNY*HSLPSAR.T	2	4.2045	0.456	FLJ20625 PROTEIN.
K.ALY*STAMESIQGEAR.R	2	4.8989	0.4332	68 KDA TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE ALPHA.
K.APEPHVEEDDDDELDSKLN*Y*KPPPQK.S	3	4.4697	0.4584	RHO GDP-DISSOCIATION INHIBITOR 2.
K.AQIWDTAGQERY*R.A	2	2.449	0.1772	RAS-RELATED PROTEIN RAB-11B.
K.ATGDETGAKVERADGY*EPPVQESV.-	2	3.0022	0.1508	RPS3A PROTEIN.
K.ATQFVY*SYGR.G	2	2.5725	0.1322	NUCLEAR TRANSCRIPTION FACTOR NFX2.
K.ATQFVYSY*GR.G	2	2.2325	0.1171	SIMILAR TO TRANSCRIPTIONAL REPRESSOR NF-X1.
K.AVTKDEDEWKELEQKEVDY*SGLR.V	3	3.3818	0.1295	HYPOTHETICAL PROTEIN.
K.AVY*TQDCPLAAK.A	2	3.1595	0.1345	ALANYL-TRNA SYNTHETASE.
K.DFNLPEY*DLNVEER.L	2	4.0318	0.2808	SPLICE ISOFORM 3 OF LAP2 PROTEIN.
K.DGTSFGGEY*GGWYK.A	2	2.7899	0.1714	SPLICE ISOFORM G OF KINESIN LIGHT CHAIN 1.
K.DKMAEAY*SEIGMK.G	2	3.4379	0.2509	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
K.DKMAEAY*SEIGMKGER.R	3	3.6903	0.336	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
K.DKVTIADDY*SDPFDKNDLK.S	3	3.8607	0.1281	SHB.
K.DSSGWSSSKDKDAY*SSFGSR.S	3	4.4413	0.3316	DEAD-BOX PROTEIN 3, X-CHROMOSOMAL.
K.DTAIY*QKDEALHVKNKAVK.Q	3	4.4518	0.3074	MICROTUBULE-ASSOCIATED PROTEIN 1A.
K.DTY*DALHMQALPPR.-	3	3.5444	0.193	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
K.EFSVNNQLQLY*QEK.C	2	3.5343	0.3123	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2.
K.EISEASENIY*SDVR.G	2	3.3786	0.2792	TRANSCRIPTION FACTOR ELYS.
K.ENPGDFDFSGAEISGNY*TK.G	2	5.016	0.4514	NUDC DOMAIN CONTAINING 2.
K.ERPPVPNPDPY*EPIR.K	2	2.7387	0.1822	T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR.
K.ERPPVPNPDPY*EPIRK.G	3	4.0906	0.2331	T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR.
K.ERWEQGGADY*MGADSFNKR.K	3	4.0965	0.1793	SPLICE ISOFORM GN-1S OF GLYCOGENIN-1.
K.ESESVSKEEKEQNY*DLTEVSESMK.A	3	3.6208	0.3906	SGT1 PROTEIN.
K.EVY*ELLDSPGK.V	2	2.4065	0.1686	MULTIFUNCTIONAL PROTEIN ADE2.

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	State	XCorr	DelCN	
K.FFDANYDGKDY*DPVAAR.Q	3	4.9704	0.3355	MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 1.
K.FVETSPGLDPNASVY*QPLKK.-	3	3.649	0.1256	HYPOTHETICAL PROTEIN FLJ10747.
K.FVKERTEIELSY*AKQLR.N	2	2.7335	0.1332	16 KDA PROTEIN.
K.FYDANYDGKEY*DPVEAR.Q	3	4.506	0.3711	SPLICE ISOFORM 2 OF MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER
K.GAAPNVVYTY*TGKR.I	2	2.5602	0.2995	CPSF6 PROTEIN.
K.GAMAATY*SALNR.N	2	3.0702	0.2676	RIBOSOMAL PROTEIN S6 KINASE ALPHA 3.
K.GFGGQY*GIQK.D	2	2.8642	0.1102	HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN.
K.GFY*DKDSSGWSSSKDKDAY*SSFSGR.S	3	4.0801	0.2268	DEAD-BOX PROTEIN 3, X-CHROMOSOMAL.
K.GFYDKDSSGWSSSKDKDAY*SSFSGR.S	3	4.582	0.3022	DEAD-BOX PROTEIN 3, X-CHROMOSOMAL.
K.GHDGLY*QGLSTATK.D	2	4.3263	0.34	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
K.GIPVETDSEEQPY*LEMDLSSPQTR.Y	2	3.9342	0.3931	SPLICE ISOFORM 3 OF CASPASE-8 PRECURSOR.
K.GLIVY*CVTSPK.K	2	2.9251	0.1993	SPLICE ISOFORM 1 OF RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 6.
K.GPNGVY*DFSQAHNAK.D	2	3.9999	0.3766	SPLICE ISOFORM 1 OF MELANOMA-ASSOCIATED ANTIGEN D1.
K.GQESEY*GNITYPPAMK.N	2	3.7778	0.3387	70 KDA SHP-1L PROTEIN.
K.GQKY*FDSGDYNMAK.A	3	4.0381	0.2684	ENDOSULFINE ALPHA.
K.GQKYFDSGDY*NMAK.A	2	3.8392	0.3261	CAMP-REGULATED PHOSPHOPROTEIN 19.
K.GY*NDDYEESYFTTR.T	2	4.0143	0.2522	EMERIN.
K.GY*SDEIYVVPDDSQNR.I	2	3.0457	0.307	RHO-GTPASE-ACTIVATING PROTEIN 5.
K.GY*YSPYSVSGSGTAGSR.T	2	3.3729	0.2779	PLECTIN 1.
K.GYNDDY*YEESYFTTR.T	2	3.8257	0.1214	EMERIN.
K.GYNDDY*EESYFTTR.T	2	4.5155	0.111	EMERIN.
K.GYNDDYEEESY*FTTR.T	2	3.1008	0.1797	EMERIN.
K.GYSDEIY*VVPDDSQNR.I	2	3.418	0.1827	RHO-GTPASE-ACTIVATING PROTEIN 5.
K.GYY*SPYSVSGSGTAGSR.T	2	3.9219	0.3598	PLECTIN 7.
K.GYYSPY*SVSGSGTAGSR.T	2	4.7761	0.2865	SPLICE ISOFORM 3 OF PLECTIN 1.
K.HFNVNTDY*QNPVR.S	2	4.5726	0.2862	TUDOR DOMAIN CONTAINING PROTEIN 3.
K.HFSGLEEAVY*R.N	2	3.1168	0.3181	T-COMPLEX PROTEIN 1, THETA SUBUNIT.
K.HGDEIY*IAPSGVQKER.I	3	3.8049	0.3192	CGI-29 PROTEIN.
K.HKENEEDY*GTCSSSVQY*TPVYK.L	3	5.8119	0.1935	HYPOTHETICAL PROTEIN FLJ20054.
K.HKENEEDY*GTCSSSVQYTPVY*K.L	3	4.6872	0.1683	HYPOTHETICAL PROTEIN FLJ20054.
K.HQDQAVVFGVDDNQDY*NRPVINEK.H	3	5.0908	0.3451	KARP-1-BINDING PROTEIN.
K.ICDPY*AWLEDPDSEQTK.A	2	2.3462	0.222	PROLYL ENDOPEPTIDASE.
K.IDSIPHLNNSLPLVDPSVY*GYGVQK.R	3	5.2739	0.111	SPLICE ISOFORM 1 OF FAR UPSTREAM ELEMENT BINDING PROTEIN 3.
K.IDSIPHLNNSLPLVDPSVYGY*GVQK.R	3	4.6886	0.1983	SPLICE ISOFORM 1 OF FAR UPSTREAM ELEMENT BINDING PROTEIN 3.
K.IEKIGEGTY*GVVYK.G	2	3.129	0.2461	HYPOTHETICAL PROTEIN DKFZP686L20222.
K.IEKIGEGTY*GVVYKGR.H	3	4.2154	0.4333	HYPOTHETICAL PROTEIN DKFZP686L20222.
K.IGEGTY*GVVYK.A	2	3.2176	0.2906	CELL DIVISION PROTEIN KINASE 2.

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	State	XCorr	DelCN	
K.IGEGTY*GVVYKGR.H	2	3.7825	0.1744	HYPOTHETICAL PROTEIN DKFZP686L20222.
K.IGEGTYGVVY*KGR.H	2	3.0381	0.1322	HYPOTHETICAL PROTEIN DKFZP686L20222.
K.IIEENITSAAPSNDQDGEY*CPEVK.L	3	4.026	0.4235	SFRS PROTEIN KINASE 2 ISOFORM A .
K.ILY*SQCGDVMR.A	2	2.9523	0.2646	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM.
K.INEELESQY*QQSMDSK.L	2	5.4014	0.4237	SMALL ACIDIC PROTEIN.
K.IRNLDNNGGFY*ISPR.I	2	4.0303	0.2606	SPLICE ISOFORM SHORT OF PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK.
K.KATQFVY*SYGR.G	2	3.2069	0.1557	NUCLEAR TRANSCRIPTION FACTOR NFX2.
K.KATQFVYSY*GR.G	2	2.7355	0.2201	SIMILAR TO TRANSCRIPTIONAL REPRESSOR NF-X1.
K.KEDALLY*QSK.G	2	2.7983	0.1459	EMERIN.
K.KELTY*QNTDLSEIKEEEQVK.S	3	5.6376	0.2785	TRANSCRIPTION REPRESSOR.
K.KFFDANYDGKDY*DPVAAR.Q	3	3.3095	0.1908	MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 1.
K.KFYDANYDGKEY*DPVEAR.Q	3	3.9742	0.2003	SPLICE ISOFORM 1 OF MICROTUBULE-ASSOCIATED PROTEIN RP/EBFAMILY MEMBER 2.
K.KITSSSAIY*DNPNIKPIPKPENQQR.I	3	4.6272	0.1414	MRNA DECAPPING ENZYME 1B.
K.KKSPATPQAKPDGVTATAADEEEDEY*SGGLC.-	3	4.805	0.4728	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN.
K.KLAEGSAY*EEVPTSMY*SENDISNSIK.N	3	4.9584	0.2806	PHOSPHOLIPASE C GAMMA 1 ISOFORM A .
K.KLAEGSAY*EEVPTSMYSENDISNSIK.N	3	5.2015	0.4128	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1.
K.KLAEGSAYEEVPTSMY*SENDISNSIK.N	3	4.957	0.3247	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1.
K.KLKEESRDEESPY*ATSLYHS.-	3	4.1226	0.1551	HYPOTHETICAL PROTEIN MGC35274.
K.KLKEESRDEESPYATSLY*HS.-	3	3.4548	0.1391	MGC35274 PROTEIN.
K.KSPATPQAKPDGVTATAADEEEDEY*SGGLC.-	3	6.4642	0.514	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN.
K.LAEGSAY*EEVPTSMYSENDISNSIK.N	3	4.892	0.456	PHOSPHOLIPASE C GAMMA 1 ISOFORM A .
K.LAEGSAYEEVPTSMY*SENDISNSIK.N	3	4.5113	0.2108	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 1.
K.LAQLQEGQDLY*SR.L	2	3.7446	0.2815	OTTHUMP00000038912.
K.LCDFGSASHVADNDITPY*LVSR.F	3	5.6939	0.2919	SERINE/THREONINE-PROTEIN KINASE PRP4 HOMOLOG.
K.LGHPEALSAGTGSPQPPSFTY*AQQR.E	3	4.8003	0.3223	ZYX PROTEIN.
K.LISDKIGSLGLGTGEDDDY*VDDFNSTSHR.S	3	5.2699	0.3939	FGFR1 ONCOGENE PARTNER (FRAGMENT).
K.LKADGLIY*CLK.E	2	3.3496	0.2827	TYROSINE-PROTEIN KINASE ZAP-70.
K.LKEESRDEESPY*ATSLYHS.-	3	4.4354	0.2456	MGC35274 PROTEIN.
K.LKEESRDEESPYATSLY*HS.-	3	4.0511	0.1157	MGC35274 PROTEIN.
K.LKHKENEEDY*GTCSSVQY*TPVYK.L	3	4.0002	0.1731	HYPOTHETICAL PROTEIN FLJ20054.
K.LKHKENEEDY*GTCSSVQYTPVY*K.L	3	3.3076	0.1416	HYPOTHETICAL PROTEIN FLJ20054.
K.LMLSTSEY*SQSPK.M	2	3.2097	0.1898	HYPOTHETICAL PROTEIN DKFZP686B146.

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	State	XCorr	DelCN	
K.LMNEDPMY*SMYAK.L	2	2.9202	0.1639	STAM.
K.LQDEANY*HLYGSR.M	2	3.8759	0.2918	RECEPTOR-INTERACTING SERINE/THREONINE-PROTEIN KINASE 2.
K.LQDEANYHLY*GSR.M	2	3.8725	0.2578	RECEPTOR-INTERACTING SERINE/THREONINE-PROTEIN KINASE 2.
K.LQLDNQY*AVLENQK.S	2	4.7966	0.321	14 KDA PROTEIN.
K.LRGPLPYSGQSSEVSTPSSLYMEY*EGGR.Y	3	4.1043	0.2364	KIAA0226 PROTEIN (FRAGMENT).
K.LRLEEEALY*AAQR.E	2	3.301	0.1395	HYPOTHETICAL PROTEIN DKFZP686P0859.
K.LSPTEPKNY*GSY*STQASAAAATAELLK.K	3	4.0603	0.184	35 KDA PROTEIN.
K.LTGIKHELQANCY*EEVKDR.C	3	4.5476	0.2549	COFILIN, NON-MUSCLE ISOFORM.
K.LTLRPPSLAAPY*APVQSWQHQPCK.L	3	4.053	0.1414	ANKYRIN REPEAT AND SAM DOMAIN-CONTAINING PROTEIN 1.
K.LVNEAPVY*SVYSK.L	2	2.8133	0.1245	SIGNAL TRANSDUCING ADAPTOR MOLECULE 2A.
K.LVNEAPVYSVY*SK.L	2	3.3461	0.2961	SIGNAL TRANSDUCING ADAPTOR MOLECULE 2A.
K.LVTEMGTY*ATQSALSSSRPTKK.E	3	3.7315	0.2135	COATOMER BETA SUBUNIT.
K.MAEAY*SEIGMK.G	2	3.7347	0.3199	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
K.MAEAY*SEIGMKGER.R	2	4.3448	0.3247	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
K.MATDEENVY*GLEENAQSR.Q	2	5.1814	0.3177	GTPASE, IMAP FAMILY MEMBER 1.
K.MENY*ELIHSSR.V	2	3.5657	0.1675	NISCHARIN.
K.MQEATPSAQATNETQMCY*ASLDHSVK.G	3	3.6927	0.199	T-CELL RECEPTOR INTERACTING MOLECULE.
K.MVVESAY*EVIK.L	2	3.1049	0.166	L-LACTATE DEHYDROGENASE B CHAIN.
K.NAEDCLY*ELPENIR.V	2	5.0106	0.3555	HSPC220.
K.NGSEADIDEGLY*SR.Q	2	4.673	0.3893	UBIQUITIN-ACTIVATING ENZYME E1 (FRAGMENT).
K.NLYPSSSPY*TR.N	2	2.7308	0.2642	SGT1B PROTEIN.
K.NPQEGLY*NELQK.D	2	2.7797	0.1049	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
K.NTDY*TELHQNTDLIY*QTGPK.S	3	5.3164	0.2999	SPLICE ISOFORM 2 OF GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 5.
K.NTDYTELHQNTDLIY*QTGPK.S	3	4.4568	0.105	SPLICE ISOFORM 1 OF GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 5.
K.NVALLSPLY*HSPAR.R	2	2.6529	0.2131	ELAV-LIKE PROTEIN 1.
K.NY*GSYSTQASAAAATAELLK.K	2	5.1813	0.4509	SCAMP3 PROTEIN (FRAGMENT).
K.NYGSY*STQASAAAATAELLK.K	2	5.6959	0.1127	SPLICE ISOFORM 2 OF SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
K.QATTNVY*QVQTGSEY*TDTSNHSSLK.R	3	3.4113	0.2325	SPLICE ISOFORM 3 OF ARF GTPASE-ACTIVATING PROTEIN GIT2.
K.QATTNVY*QVQTGSEYTDTSNHSSLK.R	3	3.3969	0.212	SPLICE ISOFORM 8 OF ARF GTPASE-ACTIVATING PROTEIN GIT2.
K.QDLAY*ERQYEQQTYQVIVEVIK.N	3	3.5576	0.1645	DJ1014D13.1 PROTEIN.
K.QDLAYERQY*EQQTYQVIVEVIK.N	3	4.092	0.1306	DJ1014D13.1 PROTEIN.
K.QKDGTSFGEY*GGWYK.A	2	2.8167	0.2685	SPLICE ISOFORM S OF KINESIN LIGHT CHAIN 1.

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	State	XCorr	DelCN	
K.QQPTQFINPETPGY*VGFANLPNQVHR.K	3	4.3798	0.2968	SEPTIN 2.
K.QTETEMLY*GSAPR.T	2	2.3932	0.1221	PROTEIN REGULATING CYTOKINESIS 1.
K.REEPEALY*AAVNK.K	2	3.3069	0.1826	INTERSECTIN 2 (SH3 DOMAIN-CONTAINING PROTEIN 1B) (SH3P18) (SH3P18-LIKE WASP ASSOCIATED PROTEIN). SPLICE ISOFORM 2.
K.RLEENDDDAY*LNSPWADNTALKR.H	3	6.0541	0.3138	PROTEIN C21ORF59.
K.RPMASEVPY*ASGMPIKK.I	3	3.6813	0.1701	68 KDA TYPE I PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE ALPHA.
K.RVGFQYEGTY*K.W	2	2.7377	0.1131	SPLICE ISOFORM LONG OF GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE.
K.SAVKNEEY*FMFPEPK.T	3	4.2116	0.118	MATERNAL EMBRYONIC LEUCINE ZIPPER KINASE.
K.SAVTTVVNPKY*EGK.-	2	3.0425	0.142	SPLICE ISOFORM BETA-1A OF INTEGRIN BETA-1 PRECURSOR.
K.SEVDETY*ALPATK.I	2	2.9224	0.1951	HOST CELL FACTOR 2.
K.SGQSLTVPESTY*TSIQGDPQR.S	2	4.6521	0.3711	HYPOTHETICAL PROTEIN FLJ20673.
K.SHY*ADVDPENQNFLESNLGK.K	3	3.7727	0.1508	PUTATIVE 40-9-1 PROTEIN.
K.SLEDPY*SQQIR.L	2	2.9663	0.2687	HYPOTHETICAL PROTEIN FLJ10736.
K.SLHPWY*GITPTSSPK.T	3	3.8916	0.1936	MOLECULE INTERACTING WITH RAB13.
K.SLSHLPLHSSKEDAY*DGVTSENMR.N	3	4.3104	0.4137	HYPOTHETICAL PROTEIN FLJ11273.
K.SLY*DEVAAQGEVVR.K	2	3.0969	0.2183	HYPOTHETICAL PROTEIN DKFZP313B047.
K.SLY*DEVAAQGEVVRK.L	2	2.6977	0.2689	HYPOTHETICAL PROTEIN DKFZP313B047.
K.SNETNGY*LDSAQAGPAAGPGAPGTAAGR.A	3	5.6972	0.3806	NEUTRAL AMINO ACID TRANSPORTER A.
K.SPGALETPSAAGSQGNTASQKKEGPY*SEPSK.R	3	4.4436	0.2937	SPLICE ISOFORM B OF A-KINASE ANCHOR PROTEIN 2.
K.SPGALETPSAAGSQGNTASQKKEGPY*SEPSKR.G	3	3.5842	0.1841	SPLICE ISOFORM B OF A-KINASE ANCHOR PROTEIN 2.
K.SQASGPEPELY*ASVCAQTR.R	3	3.4092	0.1097	SIT PROTEIN PRECURSOR.
K.SQASKPAY*GNSPYWTN.-	2	2.6164	0.1392	112 KDA PROTEIN.
K.SQASKPAYGNSPY*WTN.-	2	3.9943	0.345	112 KDA PROTEIN.
K.SQDPNPQY*SPIIK.Q	2	4.2263	0.3326	SPLICE ISOFORM 3 OF SH2 DOMAIN PROTEIN 2A.
K.SQGLSPLY*HNQSQGLLSQLQGQSK.D	3	4.7343	0.3913	EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA 2.
K.SREEDPTLTEEEISAMY*SSVNKPGQLVNK.S	3	4.7879	0.3037	HYPOTHETICAL PROTEIN FLJ20673.
K.SSSLEMPY*NTPQLSPATTPANKK.N	3	4.517	0.3677	DKFZP434C212 PROTEIN .
K.SSYHVEGTGY*DTYLR.D	2	2.8743	0.1467	HYPOTHETICAL PROTEIN DKFZP686D10123.
K.TASGDY*IDSSWELR.V	2	4.328	0.3411	SPLICE ISOFORM 2 OF UNC-112 RELATED PROTEIN 2.
K.TGAPQYGSY*GTAPVNLNIK.T	2	2.4065	0.2598	HYPOTHETICAL PROTEIN DKFZP586K0717.
K.TGVAGEDMQDNSGTY*GKIWEGSSK.C	3	4.2009	0.2658	PROTEIN KINASE C, DELTA TYPE.
K.TITY*EAAQTVK.G	2	3.158	0.1877	SPLICE ISOFORM 4 OF PROTEIN 4.1.
K.TKEVY*ELLDSPGK.V	2	2.212	0.1725	MULTIFUNCTIONAL PROTEIN ADE2.
K.TLEPVKPPTPNDY*MTSPAR.L	3	3.4526	0.1668	SPLICE ISOFORM 8 OF ABL-INTERACTOR 1.
K.TNNAQNGHLEDDY*Y*SPHGMLANGSR.G	3	3.6831	0.2334	PREDICTED: PUTATIVE ANKYRIN-REPEAT CONTAINING PROTEIN .
K.TNNAQNGHLEDDYY*SPHGMLANGSR.G	3	4.4647	0.3216	PREDICTED: PUTATIVE ANKYRIN-REPEAT CONTAINING PROTEIN .
K.TPQGPPEIY*SDTQFPSLQSTAK.H	2	3.9835	0.1972	HYPOTHETICAL PROTEIN.

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PeptideSequence	Charge			Description
	State	XCorr	DelCN	
K.TPSSNTLDDY*MSCFR.T	2	4.1383	0.329	DUAL SPECIFICITY PROTEIN KINASE TTK.
K.TTAVEIDY*DSLK.L	2	3.3317	0.1482	SPLICE ISOFORM FYB-120 OF FYN-BINDING PROTEIN.
K.TTEDEVHICHNQDGY*SYPSR.Q	3	4.4351	0.123	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR.
K.TTEDEVHICHNQDGYSY*PSR.Q	3	4.8134	0.3063	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR.
K.TTEMETIY*DLGTK.M	2	2.6429	0.2836	RUVB-LIKE 2.
K.TTGKMENY*ELIHSSR.V	3	3.7335	0.3042	NISCHARIN.
K.TTYDSSLSSY*TVPLEKDNSEEFRQR.E	3	3.8485	0.2609	SPLICE ISOFORM 3 OF ATAXIN-2-LIKE PROTEIN.
K.TYSECEDGTY*SPEISWHHR.K	3	4.2613	0.3591	PHOSPHATIDYLSERINE SYNTHASE 1.
K.VEKIGEGTY*GVVYK.A	2	3.5105	0.1721	CELL DIVISION PROTEIN KINASE 2.
K.VERADGY*EPPVQESV.-	2	3.6629	0.4163	40S RIBOSOMAL PROTEIN S3A.
K.VGINY*QPPTVVPGGDLAK.V	2	3.4819	0.1892	SPLICE ISOFORM 1 OF TUBULIN ALPHA-2 CHAIN.
K.VHQLY*ETIQR.W	2	2.7298	0.2867	45 KDA PROTEIN.
K.VLAQQGEY*SEAIPILR.A	2	3.363	0.1716	FK506-BINDING PROTEIN 8 .
K.VLEY*EMTQFDRR.G	2	2.7986	0.2127	PREDICTED: KIAA1223 PROTEIN .
K.VQENDGKPPVNY*EEDAR.S	3	4.6825	0.3408	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FER.
K.VQNATTKGPNGVY*DFSQAHNAK.D	3	4.8279	0.2619	SPLICE ISOFORM 2 OF MELANOMA-ASSOCIATED ANTIGEN D1.
K.WDTGENPIY*K.S	2	3.2313	0.2557	SPLICE ISOFORM BETA-1A OF INTEGRIN BETA-1 PRECURSOR.
K.WDTGENPIY*KSAVTTVVNPK.Y	3	4.6161	0.308	SPLICE ISOFORM BETA-1A OF INTEGRIN BETA-1 PRECURSOR.
K.WDTGENPIY*KSAVTTVVNPKY*EGK.-	3	5.3505	0.2944	SPLICE ISOFORM BETA-1A OF INTEGRIN BETA-1 PRECURSOR.
K.WIDATSGIY*NSEK.S	2	3.2776	0.2988	LIM DOMAIN ONLY 7 (FRAGMENT).
K.WPTVDASY*YGGR.G	2	3.4201	0.1002	SPLICE ISOFORM 4 OF ANTHRAX TOXIN RECEPTOR 2 PRECURSOR.
K.WPTVDASY*GGR.G	2	3.0774	0.2255	SPLICE ISOFORM 1 OF ANTHRAX TOXIN RECEPTOR 2 PRECURSOR.
K.Y*AGSALQYEDVSTAVQNLQK.A	3	4.3	0.2117	PROTEIN C6ORF55.
K.YAGSALQY*EDVSTAVQNLQK.A	2	4.9994	0.1637	PROTEIN C6ORF55.
K.YAVFKNPQNFY*LDNR.G	3	3.7325	0.2151	AMYLOID BETA (A4) PROTEIN-BINDING, FAMILY B, MEMBER 1 INTERACTING PROTEIN.
K.YDEDAKRPY*FTVDEAEAR.Q	3	4.3994	0.2937	SPLICE ISOFORM DELTA OF POLIOVIRUS RECEPTOR RELATED PROTEIN PRECURSOR.
K.YFDSDY*NMAK.A	2	3.6704	0.3598	SPLICE ISOFORM 2 OF ALPHA-ENDOSULFINE.
K.YGLFKEENPY*AR.F	2	3.3854	0.3275	PITUITARY TUMOR-TRANSFORMING GENE 1 PROTEIN-INTERACTING PROTEIN PRECURSOR.
K.YQYAIDEY*YR.M	2	2.8689	0.2363	HYPOTHETICAL PROTEIN DKFZP686J1254.
K.YQYAIDEY*YR.M	2	3.1304	0.2025	HYPOTHETICAL PROTEIN DKFZP686J1254.
K.YTISQEAY*DQRQDTR.S	2	3.2447	0.2462	TUBULIN-SPECIFIC CHAPERONE B.
L.ELILKGLNEY*LEK.K	2	3.859	0.1688	CILIARY DYNEIN HEAVY CHAIN 7.
R.AADQFDIY*SSQSK.Y	2	4.2223	0.2939	HYPOTHETICAL PROTEIN FLJ37562.
R.AAEVVMCY*TSLQLRPPQGR.I	3	4.3675	0.3162	SIT PROTEIN PRECURSOR.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge	State	XCorr	DelCN	Description
R.AASTAPSSSTSPAASSAGLIY*IDPSNLR.R		3	4.5481	0.2804	UBIQUITIN--PROTEIN LIGASE EDD.
R.ADGY*EPPVQESV.-		2	3.2218	0.1623	PREDICTED: SIMILAR TO RIBOSOMAL PROTEIN S3A.
R.ADQQY*ECVAEIGEGAYGK.V		2	5.3531	0.4192	CELL DIVISION PROTEIN KINASE 6.
R.AEIQNAEDY*NEIFQPK.N		3	4.1353	0.1338	KATANIN P80 WD40-CONTAINING SUBUNIT B1.
R.AGATASKEPPLY*YGVCPVYEDVPAR.N		3	4.6026	0.2785	KIAA0692 PROTEIN (FRAGMENT).
R.AGATASKEPPLYY*GVCPVY*EDVPARNER.I		3	4.9341	0.2134	KIAA0692 PROTEIN (FRAGMENT).
R.AGATASKEPPLYY*GVCPVYEDVPAR.N		3	4.4283	0.2762	KIAA0692 PROTEIN (FRAGMENT).
R.AGATASKEPPLYYGVCPVY*EDVPAR.N		3	4.7235	0.2928	KIAA0692 PROTEIN (FRAGMENT).
R.AGATASKEPPLYYGVCPVY*EDVPARNER.I		3	4.8187	0.3631	KIAA0692 PROTEIN (FRAGMENT).
R.APKEEADY*EDDFLEY*DQEHIR.F		3	4.8572	0.254	DICER1 .
R.APKEEADY*EDDFLEYDQEHIR.F		3	5.5407	0.3286	DICER1 .
R.AQIPEGDY*LSYR.E		2	2.3902	0.2173	SPLICE ISOFORM 6 OF LAP2 PROTEIN.
R.AQSQEDGDY*INANYIR.G		2	4.8809	0.3476	TYROSINE-PROTEIN PHOSPHATASE, NON-RECEPTOR TYPE 7.
R.AQSQEDGDYINANY*IR.G		2	3.1844	0.1116	TYROSINE-PROTEIN PHOSPHATASE, NON-RECEPTOR TYPE 7.
R.AQSYPDNHQEFSDY*DNPIFEK.F		3	3.8146	0.237	HYPOTHETICAL PROTEIN FLJ14439.
R.ARQY*TSPEEIDAQLQAEKQK.A		3	5.8236	0.1858	28 KDA HEAT- AND ACID-STABLE PHOSPHOPROTEIN.
R.ASFPDQAY*ANSQPAAS.-		2	3.1786	0.3178	SIT PROTEIN PRECURSOR.
R.ASLVSKSY*SEPVVVK.T		2	2.846	0.2381	THYMUS HIGH MOBILITY GROUP BOX PROTEIN TOX.
R.AVLY*ADY*RAPGPAR.F		2	3.2157	0.2544	KIN OF IRRE LIKE.
R.AVLY*ADYRAPGPAR.F		2	2.6506	0.1596	SPLICE ISOFORM 2 OF KIN OF IRRE-LIKE PROTEIN 1 PRECURSOR.
R.AVLYADY*RAPGPAR.F		2	3.3165	0.3272	SPLICE ISOFORM 1 OF KIN OF IRRE-LIKE PROTEIN 1 PRECURSOR.
R.AVSPQSTKPMASITY*AAVAR.H		3	3.8693	0.1389	LEUKOCYTE-ASSOCIATED IG-LIKE RECEPTOR 1 ISOFORM B PRECURSOR .
R.AVSPQSTKPMASITY*AAVARH.-		3	3.5513	0.2024	LAIR1 PROTEIN.
R.AYQHGGVTGLSQY*.-		2	2.7535	0.1431	SPLICE ISOFORM 1 OF REGULATOR OF NONSENSE TRANSCRIPTS 1.
R.CASCPY*LGMPAFKPGEK.V		3	3.4493	0.1583	SPLICE ISOFORM 3 OF ANAMORSIN.
R.DDAQY*SHLGGNWAR.N		2	2.7004	0.2743	T-CELL SURFACE GLYCOPROTEIN CD3 DELTA CHAIN PRECURSOR.
R.DGSLASNPY*SGDLTK.F		2	3.5703	0.2742	UBIQUITIN ASSOCIATED PROTEIN 2-LIKE.
R.DINSLY*DVS.R.M		2	3.0918	0.107	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2.
R.DKNSAACVVY*EDMSHSR.C		3	4.3489	0.2569	T-CELL ANTIGEN CD7 PRECURSOR.
R.DKPSVEPVEEY*DY*EDLKESNSVSNHQLSGFDQAR.L		3	4.1591	0.1628	OTTHUMP00000017253.
R.DLIHQDEDEEEEGQRFY*AGGSER.S		3	3.56	0.1864	SPLICE ISOFORM 1 OF NSFL1 COFACTOR P47.
R.DLNY*CFSGMSDHR.Y		2	3.6888	0.325	50 KDA PROTEIN.
R.DLQY*ITVSKHEELSSGDSLSPDPWKR.D		3	5.1832	0.2979	MYELOID\LYMPHOID OR MIXED-LINEAGE LEUKEMIA (FRAGMENT).
R.DLSY*CLSGMYDHR.Y		2	2.6607	0.163	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F .
R.DLY*SGLNQR.R		2	3.01	0.1536	T-CELL SURFACE GLYCOPROTEIN CD3 EPSILON CHAIN PRECURSOR.
R.DNLAQQSFNMEQANY*TIQSLKDTK.T		3	4.1087	0.3305	SNF7 DOMAIN CONTAINING PROTEIN 2.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.DRDDAQY*SHLGGNWAR.N	3	3.6367	0.2504	T-CELL SURFACE GLYCOPROTEIN CD3 DELTA CHAIN PRECURSOR.
R.DRQAFSMY*EPGSALKPFGGPPGDELTR.L	3	4.9684	0.3745	SPLICE ISOFORM 1 OF ARF GTPASE-ACTIVATING PROTEIN GIT1.
R.DSAY*QSITHYRPVSASR.S	3	3.333	0.2646	EMERIN.
R.DSQGTY*SSRDAELQDQEFQGR.D	3	3.5241	0.1386	HYPOTHETICAL PROTEIN FLJ42913.
R.DVYLSRDDGY*STKDSYSSR.D	3	3.9876	0.2531	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G.
R.DYNPNY*SDSISPFNK.S	2	2.9357	0.1309	CLIP-ASSOCIATING PROTEIN 2 .
R.EATKGFYDKDSSGWSSSKDKDAY*SSFGRS.S	3	3.342	0.1205	DEAD-BOX PROTEIN 3, X-CHROMOSOMAL.
R.EGHMMDALY*AQVK.K	2	2.5742	0.1263	SPLICE ISOFORM 7 OF PARTITIONING-DEFECTIVE 3 HOMOLOG.
R.EKQSDDEVY*APGLDISSLK.Q	3	4.3989	0.2177	SPLICING FACTOR 3A, SUBUNIT 1, 120KDA ISOFORM 2 .
R.ELFDDPSY*VNVQNLDK.A	2	4.9416	0.301	SHC TRANSFORMING PROTEIN.
R.ENDTITIY*STINHSK.E	2	2.7991	0.1732	SLAM FAMILY MEMBER 6 PRECURSOR.
R.EPPPAY*EPPAPAPLPPPSAPSLQPSR.K	3	3.5733	0.2383	SPLICE ISOFORM 1 OF SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
R.EQLY*STILSHQCQR.M	2	2.9651	0.389	G18.1B PROTEIN.
R.ERVTPEGY*EVVTVFPK.-	3	4.037	0.3496	PDZ AND LIM DOMAIN PROTEIN 1.
R.FAQPGSFEY*EYAMR.W	2	4.1101	0.1535	NONO PROTEIN.
R.FAQPGSFEY*AMR.W	2	3.4791	0.3308	NONO PROTEIN.
R.FAVPTY*AAK.Q	2	2.6127	0.1368	SPLICE ISOFORM 1 OF ADAM 9 PRECURSOR.
R.FHTSTY*DLPGPEGAGPFEASQPADSAPVATSGK.V	3	4.6241	0.179	MICROTUBULE-ASSOCIATED PROTEIN 1A.
R.FLENGSQEDLLHGNPGSTY*LASNSTSAPNWK.S	3	4.7919	0.3307	SPLICE ISOFORM 3 OF ZINC FINGER CCCH TYPE ANTIVIRAL PROTEIN 1.
R.FMTTAMY*DAR.E	2	3.1075	0.3663	HYPOTHETICAL PROTEIN FLJ43809.
R.FQDVGPQAPVGSVY*QK.T	2	5.7142	0.4204	SPLICE ISOFORM 2 OF DREBRIN-LIKE PROTEIN.
R.FQKENPGDFDGSAGISGNY*TK.G	3	5.2339	0.2837	NUDC DOMAIN CONTAINING 2.
R.FSPDSQY*IDNR.S	2	3.165	0.2983	SPLICE ISOFORM 2 OF PARTITIONING-DEFECTIVE 3 HOMOLOG.
R.FSPPEPGDTPDEPDALY*VACQGQPK.G	3	4.5385	0.2278	565 KDA PROTEIN.
R.FSTQGMGTFNPADY*SDSTSTDVCGTK.L	3	3.3869	0.3413	117 KDA PROTEIN.
R.FSTY*TSKDENKLSEASGGR.A	3	3.8025	0.1794	LEREPO4 PROTEIN.
R.FTEY*SMTSSVMR.R	2	3.2715	0.3218	C6ORF93 PROTEIN.
R.FVLDDQY*TSSTGKFPVK.W	2	4.5195	0.2944	TYROSINE-PROTEIN KINASE ITK/TSK.
R.GASQAGMTGY*GMPR.Q	2	3.7281	0.3695	TRANSGELIN 2.
R.GEPNVSY*ICSR.Y	2	3.3844	0.3036	SPLICE ISOFORM 1 OF GLYCOGEN SYNTHASE KINASE-3 BETA.
R.GFGSFRFSGNQGGAGPSQSGGGTGGSVY*TEDNDDDLG.-	3	3.797	0.1681	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE.
R.GFGSFRFSGNQGGAGPSQSGGGTGGSVYTEDNDDDLG*G.-	3	5.7553	0.3948	TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE.
R.GGHMDDGGY*SMNFMSSSR.G	3	3.5835	0.1077	PREDICTED: SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEO-PROTEIN G (HNRNP G) (RNA BINDING MOTIF PROTEIN, X CHROMOSOME) (GLYCOPROTEIN P43) .



**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.GHALY*VEPHGHGPSLSVQGLSR.A	3	3.334	0.3361	SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 3, ISOFORM A.
R.GKGHDGLY*QGLSTATK.D	2	3.3735	0.4126	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
R.GLAHPPSY*SNPPVYHGNSPK.H	3	3.3375	0.1107	PREDICTED: USP6 N-TERMINAL LIKE .
R.GLY*DGPVCEVSVTPK.T	2	4.1719	0.3625	DIHYDROPYRIMIDINASE RELATED PROTEIN-2.
R.GPQSNY*GGPYPAAPTFGSQPGPPQLPPK.R	3	3.4653	0.1258	PROTEIN TRANSPORT PROTEIN SEC24C.
R.GPVSGTEPEPVY*SMEAADYR.E	2	3.8652	0.3753	CTTN PROTEIN.
R.GQEGEY*AVPFDVAR.S	2	4.1065	0.3681	DOCKING PROTEIN 2 ISOFORM B .
R.GVGSPEPGPTAPY*LGR.S	2	2.8428	0.3791	SPLICE ISOFORM 2 OF ZINC FINGER DHHC DOMAIN CONTAINING PROTEIN 5.
R.GYFEYIEENKY*SR.A	2	2.6787	0.1844	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U, ISOFORM B.
R.HAIY*DKLDDGLIAPGVR.V	3	3.9211	0.2873	DNA-DIRECTED RNA POLYMERASE II 140 KDA POLYPEPTIDE.
R.HEVTICNY*EASANPADHR.V	3	5.7308	0.4576	AD039.
R.HFTVVGDDY*HAWNINIK.K	3	4.4869	0.3299	CATION CHANNEL, NON-LIGAND GATED FAMILY PROTEIN.
R.HHEGGTPY*AEYGGWYK.A	2	2.8724	0.1201	KINESIN-LIKE 8 ISOFORM B .
R.HHEGGTPYAEY*GGWYK.A	3	3.5989	0.1207	KINESIN-LIKE PROTEIN 8.
R.HHEGGTPYAEYGGWY*K.A	2	2.9289	0.1748	KINESIN-LIKE PROTEIN 8.
R.HIDLQFSY*APR.H	2	3.5073	0.2736	ZNF598 PROTEIN.
R.HTDDEMTGY*VATR.W	2	4.2853	0.4528	MITOGEN-ACTIVATED PROTEIN KINASE 14 ISOFORM 2 .
R.HTHLDDPIAEVEPTDSEPY*SCSK.S	3	3.9584	0.1472	SPLICE ISOFORM 1 OF RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 6.
R.HVFGQPAKADQCY*EDVR.V	3	3.8014	0.2599	CORONIN-1A.
R.IADPEHDHTGFLTEY*VATR.W	3	4.5387	0.1739	MITOGEN-ACTIVATED PROTEIN KINASE 3.
R.IAPCPSQDSLY*SDPLDSTSAQAGEGVQR.K	3	5.2441	0.4471	SPLICE ISOFORM 1 OF DOCKING PROTEIN 1.
R.IDTLNSDGY*TPEPAR.I	2	4.6043	0.3355	TYROSINE-PROTEIN KINASE ZAP-70.
R.IEEFVY*EKLDK.K	2	3.4641	0.261	SPLICE ISOFORM 2 OF SH3 DOMAIN GRB2-LIKE PROTEIN B1.
R.IIASLADRPY*EPPQKPPR.F	3	3.5548	0.1275	ANKYRIN REPEAT AND SAM DOMAIN-CONTAINING PROTEIN 1.
R.IKEEMSKDQPDY*AMY*SR.I	3	4.0412	0.2197	SPLICE ISOFORM 1 OF DEDICATOR OF CYTOKINESIS PROTEIN 2.
R.IKEEMSKDQPDY*AMYSR.I	3	4.2176	0.1296	SPLICE ISOFORM 1 OF DEDICATOR OF CYTOKINESIS PROTEIN 2.
R.IKEEMSKDQPDYAMY*SR.I	3	4.3181	0.236	SPLICE ISOFORM 1 OF DEDICATOR OF CYTOKINESIS PROTEIN 2.
R.IKSYDY*EAWAK.L	3	3.6416	0.102	HYPOTHETICAL PROTEIN FLJ21908.
R.IKSYDY*EAWAKLDVDR.I	3	3.7817	0.1289	HYPOTHETICAL PROTEIN FLJ21908.
R.IPGPGTPVKY*SEVVLDSEPK.S	3	4.0079	0.104	SIT PROTEIN PRECURSOR.
R.ISHSLY*SGIEGLDESPSR.N	2	4.007	0.3552	SPLICE ISOFORM 3 OF PARTITIONING-DEFECTIVE 3 HOMOLOG.
R.ISTY*GLPAGGIQPHPQTK.N	3	3.4895	0.2424	CD2-ASSOCIATED PROTEIN.
R.ITSPDKPRMPMDTSVY*ESPY*SDPEELK.D	3	3.7407	0.1431	TYROSINE-PROTEIN KINASE ZAP-70.
R.ITSPDKPRMPMDTSVY*ESPY*SDPEELKDK.K	3	3.5522	0.1713	TYROSINE-PROTEIN KINASE ZAP-70.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.IVQQY*HPSNNGEYQSSGPEDDFESCLR.N	3	5.6459	0.1439	HYPOTHETICAL PROTEIN DKFZP686P0859.
R.IVQQYHPSNNGEY*QSSGPEDDFESCLR.N	3	6.417	0.1202	HYPOTHETICAL PROTEIN DKFZP686P0859.
R.IYQY*IQSR.F	2	2.7565	0.1223	SPLICE ISOFORM 2 OF DUAL-SPECIFICITY TYROSINE-PHOSPHORYLATION REGULATED KINASE 1B.
R.KAPNASDFDQWEMETVY*SNSEVR.N	3	3.8815	0.1918	SPLICE ISOFORM 1 OF CENTROSOMAL PROTEIN OF 110 KDA.
R.KAQSNPY*YNGPHLNLK.A	3	5.2108	0.1516	SPLICE ISOFORM 4 OF LIM DOMAIN ONLY PROTEIN 7.
R.KAQSNPY*YNGPHLNLK.A	3	4.4879	0.2646	SPLICE ISOFORM 1 OF LIM DOMAIN ONLY PROTEIN 7.
R.KEVKY*EAPQATDGLAGALDAR.Q	3	4.3294	0.2852	TOM1 PROTEIN.
R.KFTY*LGSQDR.A	2	2.9692	0.1498	SPLICE ISOFORM 1 OF ZINC FINGER CCCH TYPE ANTIVIRAL PROTEIN 1.
R.KGPDEAEESQY*DSGIESLR.S	2	5.0815	0.4246	OTTHUMP00000016522.
R.KGTDELY*AVK.I	2	2.6558	0.1614	SPLICE ISOFORM BETA-I OF PROTEIN KINASE C, BETA TYPE.
R.KGTGLSSDY*R.I	2	2.7569	0.2207	SPLICE ISOFORM 5 OF ZINC FINGER CCCH TYPE ANTIVIRAL PROTEIN 1.
R.KIIEENITSAAPSNDDQDGEY*CPEVK.L	3	5.4923	0.3338	SFRS PROTEIN KINASE 2 ISOFORM A .
R.KKY*NDDSDSYFTSSSYFDEPVELR.S	3	4.1159	0.1138	ADP-RIBOSYLATION FACTOR GTPASE-ACTIVATING PROTEIN 3.
R.KKYNDDSDSY*FTSSSYFDEPVELR.S	3	5.0786	0.1896	ADP-RIBOSYLATION FACTOR GTPASE-ACTIVATING PROTEIN 3.
R.KKYNDDSDSYFTSSSY*FDEPVELR.S	3	3.6218	0.1195	ADP-RIBOSYLATION FACTOR GTPASE-ACTIVATING PROTEIN 3.
R.KLSPTPKNY*GSY*STQASAAAATAELLK.K	3	5.2288	0.2838	SPLICE ISOFORM 1 OF SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
R.KMATDEENVY*GLEENAQSR.Q	2	4.1074	0.3657	GTPASE, IMAP FAMILY MEMBER 1.
R.KNPQEGLY*NELQK.D	2	3.7814	0.1285	SPLICE ISOFORM CD-3-ZETA OF T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR.
R.KNPQEGLY*NELQKDK.M	3	5.1365	0.2349	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.KNPQEGLY*NELQKDKMAEAY*SEIGMK.G	3	3.974	0.1613	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.KQATTNVY*QVQTGSEY*TDTSNHSSLK.R	3	5.7513	0.3007	SPLICE ISOFORM 10 OF ARF GTPASE-ACTIVATING PROTEIN GIT2.
R.KQATTNVY*QVQTGSEYTDTSNHSSLK.R	3	6.2863	0.342	SPLICE ISOFORM 4 OF ARF GTPASE-ACTIVATING PROTEIN GIT2.
R.KQATTNVYQVQTGSEY*TDTSNHSSLK.R	3	5.1387	0.3646	SPLICE ISOFORM 8 OF ARF GTPASE-ACTIVATING PROTEIN GIT2.
R.KRYDQDLCY*TDILFTEQER.G	3	3.4342	0.1368	116 KDA U5 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPONENT.
R.KSELPQDVY*TIK.A	2	3.0068	0.1991	SPLICE ISOFORM DELTA-2 OF SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 56 KDA REGULATORY SUBUNIT, DELTA ISOFORM.
R.KSWTSSSSLSDTY*EPNY*GTVKR.R	3	3.9497	0.2763	SPLICE ISOFORM 3 OF RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 6.
R.KTAQDTLY*VLPSPSPCPSPVLVR.K	3	3.8594	0.1664	CALCIUM AND DAG-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.
R.KTEDTY*FISSAGKPTPGTQGK.I	3	5.228	0.3264	KIAA1212 .
R.KTPQGPPEIY*SDTQFPSLQSTAK.H	3	5.4463	0.2878	H41 PROTEIN.
R.KTPQGPPEIY*SNTQFPSLQSTAK.H	2	2.988	0.1916	14 KDA PROTEIN.
R.KTVTY*EDPQAVGGLASALDNR.K	3	4.2191	0.1543	51 KDA PROTEIN.
R.KTVTY*EDPQAVGGLASALDNRK.Q	3	4.796	0.3172	HYPOTHETICAL PROTEIN FLJ42340.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.LAY*INPDLALEEK.N	2	3.9246	0.2539	68 KDA PROTEIN.
R.LAY*INPDLALEEKNK.G	3	3.4748	0.2161	STRESS-INDUCED-PHOSPHOPROTEIN 1.
R.LAY*QELQIDR.K	2	3.4565	0.1386	HYPOTHETICAL PROTEIN FLJ14576.
R.LAY*VAPTIPR.R	2	2.7794	0.175	SPLICE ISOFORM 3 OF PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 12A.
R.LCNLEEGSPGSGTY*TR.H	2	4.5129	0.3063	3'-5' EXORIBONUCLEASE CSL4 HOMOLOG.
R.LFQQIY*SDGSDEVK.R	2	3.0454	0.2151	SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG.
R.LFQQIY*SDGSDEVKR.A	2	4.1459	0.248	SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG.
R.LGAAPEEESAY*VAGEKR.Q	2	4.331	0.3292	P47 PROTEIN ISOFORM C .
R.LGEY*EDVSR.V	2	2.3333	0.1673	TUBULIN-SPECIFIC CHAPERONE B.
R.LGEY*EDVSRVEK.Y	2	3.6658	0.2306	TUBULIN-SPECIFIC CHAPERONE B.
R.LGEY*EDVSRVEKY*TISQEAYDQR.Q	3	4.2561	0.4061	TUBULIN-SPECIFIC CHAPERONE B.
R.LGEY*EDVSRVEKYTISQEAYDQR.Q	3	5.0574	0.3481	TUBULIN-SPECIFIC CHAPERONE B.
R.LIEDNEY*TAR.Q	2	2.7707	0.1034	PRO3078.
R.LKGMKDDDY*DDQLC.-	2	4.0707	0.352	ARRESTIN BETA 2 ISOFORM 2 .
R.LLGSVDY*DGINDAIR.L	2	4.2649	0.405	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 3-KINASE C2 DOMAIN-CONTAINING BETA POLYPEPTIDE.
R.LLHSDY*MNMTPR.R	2	3.5602	0.3494	SPLICE ISOFORM 4 OF T-CELL-SPECIFIC SURFACE GLYCOPROTEIN CD28 PRECURSOR.
R.LQKGQKY*FDSGDY*NMAK.A	3	3.4903	0.2198	13 KDA PROTEIN.
R.LQKGQKY*FDSGDYNMAK.A	3	3.4709	0.2142	CAMP-REGULATED PHOSPHOPROTEIN 19.
R.LQNFSY*DQR.E	2	2.2603	0.1116	HYPOTHETICAL PROTEIN DKFZP667H197 (FRAGMENT).
R.LSVKEDPSY*DSVR.R	2	2.7025	0.1486	SPLICE ISOFORM 1 OF FRIEND LEUKEMIA INTEGRATION 1 TRANSCRIPTION FACTOR.
R.LVSSPCIVTSTY*GWTANMER.I	3	4.5877	0.4303	HYPOTHETICAL PROTEIN DKFZP761K0511.
R.MPWY*HSSLTR.E	2	3.1649	0.2251	TYROSINE-PROTEIN KINASE ZAP-70.
R.MQAYSNPGY*SSFPSPTGLEPCK.S	3	3.8606	0.2379	RFFL PROTEIN.
R.MRACY*Y*SLASKVEGPPGSTQKAEAAACA.-	3	3.756	0.1681	TYROSINE-PROTEIN KINASE ZAP-70.
R.MY*VDPSEINPSMPQR.T	2	3.8735	0.4313	PHOSPHOLIPASE C, GAMMA 2 (PHOSPHATIDYLINOSITOL-SPECIFIC) .
R.NEEENIY*SVPHDSTQGK.I	2	4.8828	0.3761	173 KDA PROTEIN.
R.NEEGKY*GY*VLR.S	2	2.8303	0.1249	SPLICE ISOFORM FYB-120 OF FYN-BINDING PROTEIN.
R.NFRHPEIVGY*VVPGR.N	3	3.6236	0.1942	SPLICE ISOFORM 2 OF DYNAMIN BINDING PROTEIN.
R.NGDVSQFPY*VEFTGR.D	2	3.5856	0.4371	HYPOTHETICAL PROTEIN FLJ11273.
R.NLDAQY*EMAR.S	2	2.7832	0.21	HYPOTHETICAL PROTEIN DKFZP686P16221.
R.NLDNGGFY*ISPR.I	2	3.6895	0.1498	SPLICE ISOFORM SHORT OF PROTO-ONCOGENE TYROSINE-PROTEIN KINASE LCK.
R.NLEY*VSVSPTNNTVY*ASVTHSNR.E	3	3.7071	0.1643	SLAM FAMILY MEMBER 6 PRECURSOR.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.NMGGPY*GGGNYGPGGSGGGYGGGR.S	3	3.8974	0.2468	37 KDA PROTEIN.
R.NMGGPYGGGNY*GPGGSGGGYGGGR.S	3	4.6041	0.1535	SPLICE ISOFORM A2 OF HETEROGENEOUS NUCLEAR RIBONUCLEO-PROTEINS A2/B1.
R.NPGFY*VEANPMPTFK.C	2	3.4564	0.3621	PHOSPHOLIPASE C GAMMA 1 ISOFORM A .
R.NPPQPVDWNNDY*CSSGGMQR.D	3	5.2593	0.3099	THYMUS HIGH MOBILITY GROUP BOX PROTEIN TOX.
R.NSNSY*GIPEPAHAY*AQPQTTTLPVAVSGSPGAAITPLPSTQNGPVFAK.A	3	3.9104	0.3298	CRK-LIKE PROTEIN.
R.NSNSY*GIPEPAHAYAQPQTTTLPVAVSGSPGAAITPLPSTQNGPVFAK.A	3	3.3374	0.1193	CRK-LIKE PROTEIN.
R.NSNSYGIPEPAHAY*AQPQTTTLPVAVSGSPGAAITPLPSTQNGPVFAK.A	3	3.6236	0.1498	CRK-LIKE PROTEIN.
R.NTPY*KTLEPVKPTVPNDY*MTSPAR.L	3	4.0768	0.1654	SPLICE ISOFORM 1 OF ABL-INTERACTOR 1.
R.NVPPGLDEY*NPFSDSR.T	2	2.6058	0.2055	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1.
R.QDFDVDCY*AQR.R	2	2.5077	0.1596	RAPGEF1 PROTEIN.
R.QGPGQSLSPENY*QTLPK.S	2	3.2529	0.2487	PLEKHA7 PROTEIN.
R.QHPPADSSVTMEDMNEY*SNIEEFAEGSK.I	3	3.5756	0.233	JKTBP2.
R.QLNGTY*AIAGGK.A	2	2.9083	0.312	TYROSINE-PROTEIN KINASE ZAP-70.
R.QLQEY*LAQ GK.A	2	2.4122	0.105	HYPOTHETICAL PROTEIN FLJ90068.
R.QTGGEEDGASGY*DAYWK.N	2	4.0053	0.2541	ZINC FINGER PROTEIN 330.
R.QTGGEEDGASGYDAY*WK.N	2	2.9875	0.1922	ZINC FINGER PROTEIN 330.
R.QTGSPGMIY*STR.Y	2	2.5892	0.2193	SPLICE ISOFORM 1 OF VOLTAGE-GATED POTASSIUM CHANNEL BETA-2 SUBUNIT.
R.QTVTY*EDPQAVGGLASALDNRK.Q	3	3.7425	0.1534	TARGET OF MYB1-LIKE PROTEIN 2.
R.QY*EQQTYQVIPEVIK.N	2	2.589	0.23	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 INTERACTING PROTEIN.
R.RAQIPEGDY*LSYR.E	3	4.1769	0.196	SPLICE ISOFORM 4 OF LAP2 PROTEIN.
R.RAQIPEGDYLSY*R.E	3	3.3583	0.1308	SPLICE ISOFORM 4 OF LAP2 PROTEIN.
R.RDNEVDGQDY*HFVVS.R.E	3	4.1921	0.2911	DISCS, LARGE HOMOLOG 3.
R.REEY*DVLDKR.R	3	3.9443	0.2073	HYPOTHETICAL PROTEIN FLJ46519.
R.RHEVTICNY*EASANPADHR.V	3	5.4695	0.2185	AD039.
R.RIDTLNSDGY*TPEPAR.I	2	5.7639	0.3485	TYROSINE-PROTEIN KINASE ZAP-70.
R.RISHSLY*SGIEGLDES.PSR.N	3	4.3031	0.2069	SPLICE ISOFORM 6 OF PARTITIONING-DEFECTIVE 3 HOMOLOG.
R.RKNPQEGLY*NELQK.D	3	4.5749	0.2039	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.RKNPQEGLY*NELQKDK.M	3	4.9131	0.2471	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.RNEGVVGGEDY*EEVD.R.Y	3	5.2803	0.4154	HYPOTHETICAL PROTEIN DKFZP762F135.
R.RNEGVVGGEDY*EEVD.R.Y.SR.Q	3	4.3912	0.183	HYPOTHETICAL PROTEIN DKFZP762F135.
R.RNEGVVGGEDY*EEVD.R.Y.SR.Q	3	5.0787	0.4059	ZNF598 PROTEIN.
R.RPHGDIY*GINQALGATAK.V	3	3.6484	0.1145	DIACYLGLYCEROL KINASE, ALPHA.
R.RPPSSSSSSASSY*TGRPIELDK.M	3	4.4477	0.2999	PROTEIN KINASE C, D2 TYPE.
R.RPTFVPQWY*VQQMK.R	2	2.6478	0.1905	SPLICE ISOFORM 5 OF ZINC FINGER CCCH TYPE ANTIVIRAL PROTEIN 1.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge	State	XCorr	DelCN	Description
R.RPVDSY*DIPKTEEASSGFLPGDR.N		3	3.3544	0.2183	SPLICE ISOFORM 1 OF LIM DOMAIN ONLY PROTEIN 7.
R.RQEELNNQLFLY*DTHQNL.R		3	4.291	0.1428	PHOSPHOLIPASE C, GAMMA 2 (PHOSPHATIDYLINOSITOL-SPECIFIC) .
R.RQSGLY*DSQNPPTVNNCAQDR.E		3	4.1551	0.2815	FORMIN BINDING PROTEIN 1.
R.RRDEDMLY*SPELAQR.G		3	4.0371	0.1169	SH3 DOMAIN-BINDING PROTEIN SNP70.
R.RRQEELNNQLFLY*DTHQNL.R		3	4.1737	0.3896	PHOSPHOLIPASE C, GAMMA 2 (PHOSPHATIDYLINOSITOL-SPECIFIC) .
R.RRVDGMQY*YCS.-		2	2.5127	0.1073	CHROMOSOME 14 OPEN READING FRAME 130 .
R.RSDSASSEPVGIY*QGFEEK.T		3	4.11	0.1407	PROTEIN KINASE C, DELTA.
R.RTQTCTEGGDY*CLIPR.T		2	4.2119	0.403	NOVEL PROTEIN.
R.RTQVIDDES DY*FASDSNQWLSK.L		3	4.536	0.3045	ACTIVATING SIGNAL COINTEGRATOR 1.
R.RVDGMQY*YCS.-		2	2.2142	0.2005	PROTEIN C14ORF130.
R.SADAPAY*QQGQNQLY*NELNLGR.R		3	4.6838	0.2311	HYPOTHETICAL PROTEIN FLJ46519.
R.SADAPAY*QQGQNQLY*NELNLGR.R.E		3	3.6884	0.2194	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.SADAPAY*QQGQNQLY*NELNLGR.R		2	4.8371	0.3431	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.SADAPAY*QQGQNQLY*NELNLGR.R		3	5.1805	0.3474	CD3Z ANTIGEN, ZETA POLYPEPTIDE.
R.SAEEAPLY*SKVTPR.A		2	3.5738	0.2952	PTPN18 PROTEIN.
R.SDSASSEPVGIY*QGFEEK.K		2	3.8811	0.447	PROTEIN KINASE C, DELTA.
R.SDVDLY*QVR.T		2	3.2261	0.1823	SPLICE ISOFORM P27-S OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 9.
R.SEAPNWATQDSGFY*.-		2	3.2807	0.2383	MAMMARY TUMOR INTEGRATION SITE 6.
R.SEY*DRGVNTFSPEGR.L		3	3.778	0.2382	PROTEASOME SUBUNIT ALPHA TYPE 5.
R.SGCRNPPQPVDWNNDY*CSSGGMQR.D		3	5.0583	0.3407	THYMUS HIGH MOBILITY GROUP BOX PROTEIN TOX.
R.SGESVEEVPLY*GNLHY*LQTGR.L		3	3.929	0.1527	SIT PROTEIN PRECURSOR.
R.SGESVEEVPLY*GNLHYLQTGR.L		2	4.0976	0.2932	SIT PROTEIN PRECURSOR.
R.SGPLEACY*GELGQSR.M		2	3.7071	0.3621	CONSERVED HYPOTHETICAL PROTEIN.
R.SGSY*HVREESTY*LPLTSMQPTEAMGEEPSRAE.-		3	4.6172	0.3524	INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR.
R.SGSY*SYLEER.K		2	2.7377	0.1311	SPLICE ISOFORM 3 OF PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 12A.
R.SHNVAAGSY*EAPLPPGSFHGDFAYGTYR.S		3	3.8562	0.1945	OTTHUMP00000022589.
R.SLY*ASSPGGVY*ATR.S		2	3.521	0.2647	VIMENTIN.
R.SLY*ASSPGGVYATR.S		2	3.681	0.2976	VIMENTIN.
R.SLYASSPGGVY*ATR.S		2	4.186	0.3684	VIMENTIN.
R.SNSGLATY*SPPMGPVSR.K		2	3.0594	0.1637	SPLICE ISOFORM 2 OF NEUROFIBROMIN.
R.SPSSCNDLY*ATVK.D		2	2.9582	0.4352	HYPOTHETICAL PROTEIN FLJ20673.
R.SQELSGPASNGGISQTNTY*DAQYER.A		3	4.6266	0.4025	NY-REN-25 ANTIGEN (FRAGMENT).
R.SQHFFDTSVPLMDDGDDNTLY*HR.G		3	5.5057	0.3705	35 KDA PROTEIN.
R.SQSHLPY*FTPKPPQDSAVIK.A		3	3.9889	0.2551	PLECKSTRIN HOMOLOGY DOMAIN CONTAINING, FAMILY A (PHOSPHOINOSITIDE BINDING SPECIFIC) MEMBER 1.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge	State	XCorr	DelCN	Description
R.SQY*EALKEDWR.T		2	2.9714	0.1825	TRAF3-INTERACTING JNK-ACTIVATING MODULATOR.
R.SRDY*NPYNYSISPFNK.S		3	3.9244	0.155	CLIP-ASSOCIATING PROTEIN 2 .
R.SRDYNPY*NYSISPFNK.S		3	4.4921	0.1264	CLIP-ASSOCIATING PROTEIN 2 .
R.SRPEAVSHPLNTVTEDMY*TNGSPAPGSPAQVK.G		3	4.8889	0.3284	55 KDA ERYTHROCYTE MEMBRANE PROTEIN.
R.SSAQLQTNYPSSDNSLY*TNAK.G		2	3.8741	0.2945	SPLICE ISOFORM 1 OF MAX PROTEIN.
R.SSESSCGVDGDY*EDAELNPR.F		2	5.0924	0.4108	BREAKPOINT CLUSTER REGION ISOFORM 2 .
R.SSGPYGGGGQY*FAKPR.N		2	3.2806	0.3617	PREDICTED: SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEO- PROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED) .
R.SSTQMNSYSDSGY*QEAGSFHNSQNVSK.A		3	4.2349	0.334	SPLICE ISOFORM LONG OF PLAKOPHILIN 4.
R.STLGDAEASDPPPPY*SDFHPNNQESTLSHSR.M		3	3.3897	0.2823	KIAA0157 PROTEIN.
R.STLQDSDEY*SNPAPLPLDQHSR.K		3	4.4019	0.3685	LEUPAXIN.
R.STLQDSDEY*SNPAPLPLDQHSRK.E		3	5.0178	0.4774	LEUPAXIN.
R.STSTLY*SQFQTAESNR.S		2	4.764	0.4247	SPLICE ISOFORM 3 OF SET BINDING FACTOR 1.
R.SVDGDQGLGMEGPY*EVLK.D		2	3.7459	0.2729	HYPOTHETICAL PROTEIN FLJ20673.
R.TAIY*CLTQNEW.R		2	2.6551	0.256	HYPOTHETICAL PROTEIN FLJ10704.
R.TDFY*CLVSKDDM.-		2	2.7314	0.1854	HYPOTHETICAL PROTEIN FLJ21446.
R.TEDSIRDY*EDGMEVDTTPTVAGQFEDADVDH.-		3	6.3575	0.2836	METHYLOSOME SUBUNIT PICLN.
R.TFDQNEELGLNDMKTEGY*EAGLAPQR.-		3	5.3884	0.374	ZINC-FINGER PROTEIN ZPR1.
R.TGEEDKKINEELESQY*QQSMDSK.L		3	5.1065	0.2408	SMALL ACIDIC PROTEIN.
R.TGY*ESGEYEMLGEGLVK.E		2	3.8989	0.2303	45 KDA PROTEIN.
R.TGY*ESGEYEMLGEGLVKQK.Y		3	3.3645	0.2254	DYNACTIN COMPLEX 50 KDA SUBUNIT.
R.TGYESGEY*EMLGEGLVK.E		2	5.1557	0.2438	45 KDA PROTEIN.
R.TGYESGEY*EMLGEGLVKQK.Y		3	4.5465	0.26	DYNACTIN COMPLEX 50 KDA SUBUNIT.
R.THVESCCEETY*ETLDHGSEPR.C		3	3.9026	0.1544	NOVEL PROTEIN.
R.TIKETDPDY*EDVSVALPNKR.H		3	3.3771	0.1899	YEATS DOMAIN CONTAINING 2 .
R.TKGDEEY*WNSSKFK.A		3	4.5798	0.3983	SPLICE ISOFORM 1 OF PROTEIN C14ORF133.
R.TKKPDLQIY*QPGR.L		3	3.6489	0.1657	SPLICE ISOFORM 1 OF TELOMERASE-BINDING PROTEIN EST1A.
R.TMSVDFNY*SR.T		2	3.258	0.2026	SPLICE ISOFORM 3 OF LAP2 PROTEIN.
R.TPMY*GSQTPLQDGR.T		2	4.0043	0.3818	SUPT5H PROTEIN.
R.TPYEAY*DPIGK.Y		2	3.3432	0.1473	SPLICE ISOFORM 3 OF KIN OF IRRE-LIKE PROTEIN 1 PRECURSOR.
R.TQTCTEGGDY*CLIPR.T		2	4.2642	0.3422	NOVEL PROTEIN.
R.TSAGSY*SSPPPAPYSAPQAPALSVTGPITANSEQIAR.L		3	5.2276	0.2196	TARGET OF MYB1-LIKE PROTEIN 2.
R.TSAGSYSSPPPAPY*SAPQAPALSVTGPITANSEQIAR.L		3	4.0794	0.233	TARGET OF MYB1-LIKE PROTEIN 2.
R.TSPSDGAMANY*ESTVEMGDGESAHDSR.D		3	3.9769	0.3495	VACUOLAR SORTING PROTEIN 9 DOMAIN CONTAINING PROTEIN.
R.TTPSY*VAFTDTER.L		2	2.5937	0.1823	SPLICE ISOFORM 1 OF HEAT SHOCK COGNATE 71 KDA PROTEIN.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge			Description
	State	XCorr	DelCN	
R.TTSQLY*DAVPIQSSVVLCSPPSMVR.T	3	4.2414	0.4097	PDPK1 PROTEIN.
R.TVAISDAAQLPHDY*CTTPGGTLFSTTPGGTR.I	3	4.35	0.1694	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E BINDING PROTEIN 2.
R.TYASGY*AHYEEQEN.-	2	2.5239	0.1159	ZINC FINGER PROTEIN 330.
R.TYASGYAHY*EEQEN.-	2	3.5572	0.2905	ZINC FINGER PROTEIN 330.
R.VADLTEQYNEQY*GAVR.T	2	5.6762	0.3085	HLARK.
R.VADPDHDHTGFLTEY*VATR.W	3	4.9116	0.2985	MITOGEN-ACTIVATED PROTEIN KINASE 1 .
R.VALENDRSEEEKY*TAVQR.N	3	3.3655	0.1671	SPLICE ISOFORM 1 OF ATAXIN-2.
R.VAQGIREEEVSY*QLAFNKQELR.K	3	4.8949	0.1893	SPLICE ISOFORM 2 OF EXOCYST COMPLEX COMPONENT SEC3.
R.VCEPCY*EQLNR.K	2	3.4493	0.1636	HRS PROTEIN.
R.VEEFLY*EKLDL.R	2	3.0657	0.3	SPLICE ISOFORM 1 OF SH3 DOMAIN GRB2-LIKE PROTEIN B2.
R.VEKY*TISQEAQDQR.Q	2	3.7948	0.2933	TUBULIN-SPECIFIC CHAPERONE B.
R.VFDKDGNGY*ISAAELR.H	3	4.0912	0.2578	CALMODULIN.
R.VGEEHVY*SFPNK.Q	2	3.8635	0.2762	SPLICE ISOFORM BETA OF PAXILLIN.
R.VGEEHVY*SFPNKQK.S	3	3.5137	0.157	SPLICE ISOFORM ALPHA OF PAXILLIN.
R.VGFQYEGTY*K.W	2	2.786	0.1406	SPLICE ISOFORM LONG OF GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE.
R.VIQPHGGGNSPLEGTQHLQDVPY*VMVR.E	3	4.0839	0.1955	DESMOGLEIN-2 PRECURSOR.
R.VITNQY*NNPAGLYSSENISNFNALESK.T	3	6.0617	0.2412	PDZ AND LIM DOMAIN PROTEIN 1.
R.VITNQYNNPAGLY*SSENISNFNALESK.T	3	5.8021	0.1785	PDZ AND LIM DOMAIN PROTEIN 1.
R.VKEEGY*ELPYNPATDDY*AVPPPR.S	3	3.74	0.1448	SPLICE ISOFORM 1 OF DOCKING PROTEIN 1.
R.VKEEGYELPY*NPATDDY*AVPPPR.S	3	3.5264	0.2871	SPLICE ISOFORM 1 OF DOCKING PROTEIN 1.
R.VKEEGYELPYNPATDDY*AVPPPR.S	3	3.5457	0.193	SPLICE ISOFORM 1 OF DOCKING PROTEIN 1.
R.VKEGYVPQEEVPVY*ENKY*VK.F	3	4.4934	0.1604	PYM PROTEIN.
R.VKEGYVPQEEVPVYENKY*VK.F	3	3.3857	0.1924	HYPOTHETICAL PROTEIN FLJ39603.
R.VQGGVPAGSDEY*EDECPLIALSSLNR.E	3	4.0187	0.2123	SERINE/THREONINE-PROTEIN KINASE RIO2.
R.VSLEEIY*SGCTK.R	2	3.7255	0.2995	DNAJ HOMOLOG SUBFAMILY B MEMBER 4.
R.VSLEEIY*SGCTKK.M	2	2.91	0.1519	DNAJ HOMOLOG SUBFAMILY B MEMBER 1.
R.VTPPEGY*EVVTVFPK.-	2	2.7559	0.3394	PDZ AND LIM DOMAIN PROTEIN 1.
R.VY*FQSPPGAAGEGPGGADDEGPVRR.Q	3	4.2108	0.4029	PREDICTED: PROTEIN PHOSPHATASE 1, REGULATORY (INHIBITOR) SUBUNIT 14B .
R.WEQGQADY*MGADSFNKR.K	3	4.146	0.4166	GLYCOGENIN .
R.WQPDTEEEY*EDSSGNVVKK.T	2	3.44	0.2398	SPLICING FACTOR 3A SUBUNIT 3.
R.Y*GNIIAY*DHSR.V	2	3.155	0.1992	RECEPTOR-TYPE TYROSINE-PROTEIN PHOSPHATASE MU PRECURSOR.
R.Y*TEFYHVPTSDASK.K	2	3.4541	0.2702	PDZ AND LIM DOMAIN 5 ISOFORM B .
R.Y*YDSRPGGYGYGR.S	2	3.0189	0.2329	PUTATIVE RNA-BINDING PROTEIN 3.
R.Y*YEGYAAAGPGYGGR.N	2	4.1677	0.362	LPP.
R.YALY*DATYETK.E	2	3.0937	0.1384	SPLICE ISOFORM CFL2B OF COFILIN, MUSCLE ISOFORM.
R.YALYDATY*ETK.E	2	3.0537	0.2525	COFILIN, NON-MUSCLE ISOFORM.

**SUPPLEMENTAL TABLE 1: Unique pY Peptides**

PeptideSequence	Charge	State	XCorr	DelCN	Description
R.YGDFRADDADDFGY*SR.-		3	4.3683	0.242	STAPHYLOCOCCAL NUCLEASE DOMAIN CONTAINING PROTEIN 1.
R.YGMNPHQTPAQLY*TLQPK.L		3	4.0489	0.2029	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH.
R.YGNIIAY*DHSR.V		2	3.1716	0.2089	OTTHUMP00000017184 (FRAGMENT).
R.YIEDEDY*Y*KASVTRLPIK.W		3	3.9824	0.1946	SPLICE ISOFORM 1 OF PROTEIN TYROSINE KINASE 2 BETA.
R.YLCEGTESPY*QTGQLHPAIR.V		3	3.3796	0.3082	RECEPTOR-TYPE TYROSINE-PROTEIN PHOSPHATASE KAPPA PRECURSOR.
R.YNMERDINSLY*DVS.R.M		3	3.3346	0.12	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2.
R.YTEFY*HVPTHSDASK.K		2	2.8386	0.1019	ENIGMA HOMOLOG.
R.YY*DSRPGGYGYGR.S		3	3.6044	0.3801	PUTATIVE RNA-BINDING PROTEIN 3.
R.YY*EGYYAAGPGYGGR.N		3	3.8074	0.1058	LPP.
R.YYDSRPGGY*GYGR.S		2	2.7983	0.3437	PUTATIVE RNA-BINDING PROTEIN 3.
R.YYDSRPGGYGY*GYGR.S		2	2.8528	0.2667	PUTATIVE RNA-BINDING PROTEIN 3.
R.YYDSRPGGYGYGY*GR.S		2	2.929	0.1923	PUTATIVE RNA-BINDING PROTEIN 3.
R.YYEGY*YAAGPGYGGR.N		2	2.3001	0.1283	LPP.
R.YYEGYY*AAGPGYGGR.N		2	5.0341	0.1623	LPP.
S.KTSQPEDLTDGSY*DDVLNAEQLQK.L		3	4.9669	0.3012	HYPOTHETICAL PROTEIN PSEC0198.
Y.TIQGQY*AIPQDLTK.L		2	4.2081	0.4272	POLY(RC)-BINDING PROTEIN 2 ISOFORM B .