

**SUPPLEMENTARY MATERIALS**

**Supplementary Table 1: Complete list of identified phosphopeptides with fold change using Sequest and Mascot search algorithms.** See pages below.

Supplementary Table 1: Complete list of identified phosphopeptides with fold change using Sequest and Mascot search algorithms.

Gene Symbol	Gene Id	Description	Protein Group Accession	Sequence	Modifications	PhosphoRS Site Probabilities	Phospho Site (Protein)	Phospho Site (Peptide)	# PSMs	# Protein Groups	Phospho window	Xcorr	IonScore	MH+ [Da]	# Missed Cleavages	pY Light/Heavy
LSR	51599	lipolys-stimulated lipoprotein receptor isoform 5	386781463	SSSAG GQGSy VPLLR	Y10(Phospho); R15(Labeled:13C(6))	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(9): 2.5; Y(10): 97.5	Y264	Y10;	7	1	SAGG QGSyV PLLRD T	3.73	84	1564.74651	0	0.25
GAB1	2549	GRB2-associated-binding protein 1 isoform b	46370073	SSGSG SSVA DERV DyVV VDQQ K	Y15(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; Y(15): 100.0	Y659	Y15;	15	1	VADE RVDy VVVD QQK	5.55	42	2392.06437	1	2.29

FLNB	2317	filamin-B isoform 4	256222415	SSTET CySAI PK	C6(Carbamido methyl); Y7(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 0.1; T(5): 0.1; Y(7): 99.7; S(8): 0.1	Y2478	Y7;	4	1	RSSTE TCySA IPKAS	1.74	26	1423.58208	0	1.72
HNR NPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	4504445	SSGPY GGGG QyFAK PR	Y11(Phospho)	S(1): 0.0; S(2): 0.0; Y(5): 0.0; Y(11): 100.0	Y295	Y11;	4	1	PYGG GGQyF AKPR NQ	4.11	94	1708.74761	0	1.09
ARH GAP35	2909	rho GTPase-activating protein 35	150417981	SVSSS PWLP QDGF DPSDy AEPM DAVV KPR	Y18(Phospho)	S(1): 0.0; S(3): 0.0; S(4): 0.3; S(5): 0.0; S(16): 5.1; Y(18): 94.6	Y1087	Y18;	12	1	DGFD PSDyA EPMD AV	3.65		3257.45285	0	0.25
PRKC D	5580	protein kinase C delta type	31377782	SDSAS SEPVG IyQGF EKK	Y12(Phospho)	S(1): 0.0; S(3): 0.0; S(5): 0.0; S(6): 0.0; Y(12): 100.0	Y313	Y12;	22	1	SSEPV GlyQG FEKKT	3.75	46	2008.89055	1	4.44

PRKC D	5580	prote in kinase C delta type	31377782	SDSAS SEPVG IyQGF EKK	Y12(Ph ospho)	S(1): 0.0; S(3): 0.0; S(5): 0.0; S(6): 0.0; Y(12): 100.0	Y313	Y12;	22	1	SSEP V GlyQG FEKKT	3.75		2008. 88962	1	4.29
PRKC D	5580	prote in kinase C delta type	31377782	SDSAS SEPVG IyQGF EK	Y12(Ph ospho)	S(1): 0.0; S(3): 0.0; S(5): 0.0; S(6): 0.0; Y(12): 100.0	Y313	Y12;	12	1	SSEP V GlyQG FEKKT	4.07	53	1880. 79521	0	3.97
MPZ L1	9019	myeli n protei n zero- like protei n 1 isofo r m a precur sor	4506357	SESVV yADIR	Y6(Pho spho)	S(1): 0.0; S(3): 0.0; Y(6): 100.0	Y263	Y6;	19	1	NKSES VVyA DIRKN	2.53	57	1218. 5396	0	5.51
UMP S	7372	uridin e 5'- mono phosp hate syntha se	4507835	SGLSS PIyIDL R	Y8(Pho spho); R12(La bel:13C (6))	S(1): 0.0; S(4): 0.0; S(5): 0.0; Y(8): 100.0	Y37	Y8;	3	1	SGLSS PIyIDL RGIV	1.67	63	1406. 70452	0	0.89

VCL	7414	vinculin isoform meta-VCL	7669550	SFLDS GyR	Y7(Phospho)	S(1): 0.0; S(5): 0.1; Y(7): 99.9	Y822	Y7;	8	1	KSFLD SGyRI LGAV A	1.62	39	1024. 41301	0	0.37
C11orf52	91894	uncharacterized protein C11orf52	131889517	SPGLMSEDSNLHyADIQVCSRPHAR	Y13(Phospho); C19(Carbamidomethyl)	S(1): 0.0; S(6): 8.4; S(9): 1.0; Y(13): 82.3; S(20): 8.4	Y78	Y13;	2	1	SEDSNLHyADIQVCS	3.08		2920. 29262	0	2.12
SHB	6461	SH2 domain-containing adapter protein B	106879210	SKAGKGESAGyMEPYEARQR	K2(Label:13C(6)); K5(Label:13C(6)); Y11(Phospho); R19(Label:13C(6))	S(1): 0.0; S(8): 0.0; Y(11): 100.0; Y(15): 0.0	Y268	Y11;	11	1	GKGESAGyMEPYEAQ	4.34	79	2156. 98125	2	0.29
SHB	6461	SH2 domain-containing adapter protein B	106879210	SKAGKGESAGyMEPYEARQR	K2(Label:13C(6)); K5(Label:13C(6)); S8(Phospho); R19(Label:13C(6))	S(1): 0.0; S(8): 1.7; Y(11): 98.3; Y(15): 0.0	Y268	Y11;	11	1	GKGESAGyMEPYEAQ	4.34	46	2156. 9802	2	0.27

					bel:13C (6)											
ITGB 1	3688	integri n beta-1 isoform 1A precursor	19743823	SAVTT VVNP KyEG K	K10(La bel:13C (6)); Y11(Ph ospho); K14(La bel:13C (6))	S(1): 0.0; T(4): 0.0; T(5): 0.0; Y(11): 100.0	Y795	Y11;	3	1	TTVV NPKyE GK	3.06	40	1584. 8051	1	0.83
TGM 2	7052	protei n- gluta mine gamma - gluta myltra nsfera se 2 isoform a	39777597	SEGtY CCGP VPVR	Y5(Pho spho); C6(Car bamido methyl) ; C7(Car bamido methyl)	S(1): 0.0; T(4): 98.3; Y(5): 1.7	T368	T4;	5	1	PQEKS EGtYC CGPVP	3.26	80	1561. 61577	0	12.70

ANX A2	302	annexin A2 isoform 2	209862831	SYSPy DMLE SIR	Y5(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 0.0; Y(5): 100.0; S(10): 0.0	Y238	Y5;	4	1	RYKS YSPyD MLESI R	2.83	66	1540.63786	0	0.64
ANX A2	302	annexin A2 isoform 2	209862831	SYSPy DMLE SIRK	Y5(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 0.0; Y(5): 100.0; S(10): 0.0	Y238	Y5;	4	1	RYKS YSPyD MLESI R	2.96	43	1668.73638	1	0.63
ANX A2	302	annexin A2 isoform 2	209862831	SYSPy DMLE SIRK	Y5(Phospho); R12(Label:13C(6)); K13(Label:13C(6))	S(1): 0.0; Y(2): 0.0; S(3): 0.0; Y(5): 100.0; S(10): 0.0	Y238	Y5;	4	1	RYKS YSPyD MLESI R	2.96	43	1680.77524	1	0.61
IRS2	8660	insulin receptor substrate 2	38683860	SYKAPYTC GGDS DQyV LMSSP VGR	C8(Carbamidomethyl); Y15(Phospho)	S(1): 0.0; Y(2): 0.0; Y(6): 0.0; T(7): 0.0; S(12): 0.0; Y(15): 100.0; S(19): 0.0; S(20): 0.0	Y823	Y15;	10	1	CGGD SDQyV LMSSP V	3.60	48	2718.15946	1	9.92

ANX A2	302	annexin A2 isoform 2	209862831	SLYyY IQQDT K	Y4(Phospho); K11(Label:13C (6))	S(1): 0.0; Y(3): 0.0; Y(4): 99.9; Y(5): 0.0; T(10): 0.0	Y317	Y4;	4	1	KYGK SLYyY IQQDT K	2.61	56	1507. 67986	0	0.43
SLC3 8A2	54407	sodium-coupled neutral amino acid transporter 2	21361602	SHyAD VDPE NQNF LLESN LGKK	Y3(Phospho)	S(1): 0.0; Y(3): 100.0; S(17): 0.0	Y41	Y3;	4	1	QAAL KSHyA DVDP EN	6.35	67	2598. 18821	1	2.17
ANX A2	302	annexin A2 isoform 2	209862831	SLyYY IQQDT K	Y3(Phospho); K11(Label:13C (6))	S(1): 0.0; Y(3): 100.0; Y(4): 0.0; Y(5): 0.0; T(10): 0.0	Y316	Y3;	4	1	RKYG KSLyY YIQQD T	2.61	67	1507. 68181	0	0.36
PIK3 R2	5296	phosphatidylinositol 3-kinase regulatory subunit beta	4826908	SREY DQLyE EYTR	Y8(Phospho)	S(1): 0.0; Y(4): 0.0; Y(8): 100.0; Y(11): 0.0; T(12): 0.0	Y464	Y8;	15	1	SREY DQLyE EYTR S	4.23	56	1831. 75334	1	3.02



PIK3 R1	5295	phosphatidylinositol 3-kinase regulatory subunit alpha isoform 1	32455248	SREY DRLyE EYTR	Y8(Phospho)	S(1): 0.0; Y(4): 0.0; Y(8): 100.0; Y(11): 0.0; T(12): 0.0	Y467	Y8;	5	1	SREY DRLyE EYTR S	2.70	1859. 79526	2	2.71
PIK3 R1	5295	phosphatidylinositol 3-kinase regulatory subunit alpha isoform 1	32455248	SREY DRLyE EYTR	Y8(Phospho)	S(1): 0.0; Y(4): 0.0; Y(8): 100.0; Y(11): 0.0; T(12): 0.0	Y467	Y8;	5	1	SREY DRLyE EYTR S	2.70	1859. 79424	2	2.66
CTN ND1	1500	catenin delta-1 isoform 2A	33268822 2	SMGY DDL DyGMM SDYG TAR	Y9(Phospho)	S(1): 0.0; Y(4): 0.0; Y(9): 100.0; S(13): 0.0; Y(15): 0.0; T(17): 0.0	Y242	Y9;	15	1	MGYD DL DyGMM S DYG	4.30	96 2227. 80278	0	1.44

ICK	22858	serine/ threonine- protein kinase ICK	7662388	SKPPY TDyVS TR	Y8(Phospho)	S(1): 0.0; Y(5): 1.8; T(6): 1.8; Y(8): 94.7; S(10): 1.8; T(11): 0.0	Y159	Y8;	7	1	SKPPY TDyVS TRWY R	2.21	45	1493. 66655	0	2.27
PLEK HA6	22874	pleckstrin homology domain- containing family A member 6	37595548	SEDIy ADPA AYVM R	Y5(Phospho); R14(Label:13C (6))	S(1): 0.0; Y(5): 100.0; Y(11): 0.0	Y492	Y5;	5	1	PPRSE DIyAD PAAY V	2.75	60	1686. 7188	0	0.30
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	SNDK VyEN VTGL VK	Y6(Phospho)	S(1): 0.0; Y(6): 100.0; T(10): 0.0	Y925	Y6;	5	1	DRSN DKVy ENVT GLV	2.75	54	1645. 78105	1	1.21
NED D9	4739	enhancer of filamentation 1 isoform 3	21542237 5	SWMD DyDyV HLQG K	Y6(Phospho); Y8(Phospho)	S(1): 0.0; Y(6): 100.0; Y(8): 100.0	Y629; Y631	Y6; Y8;	3	1	ERSW MDDy DYVH LQG;S WMD DYDy VHLQ	2.14	46	1916. 69695	0	14.63

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CTN ND1	1500	catenin delta-1 isoform 2A	33268822 2	SLDN NySTP NER	Y6(Phospho); R12(Label:13C (6))	S(1): 0.0; Y(6): 98.5; S(7): 1.5; T(8): 0.0	Y844	Y6;	6	1	TKSLD NNyST PNER G	1.54	56	1495. 61528	0	0.60
PKP4	8502	plakophilin-4 isoform b	53829376	StTNY VDFY STK	Y5(Phospho); K12(Label:13C (6))	S(1): 0.1; T(2): 97.3; T(3): 0.1; Y(5): 2.5; Y(9): 0.0; S(10): 0.0; T(11): 0.0	T1122	T2;	5	1	TQYG LKStT NYVD FY	2.31		1511. 63994	0	0.53
IRS2	8660	insulin receptor substrate 2	38683860	SSSSN LGAD DGyM PMTP GAAL AGSG SGSCR	Y12(Phospho); C29(Carbamidomethyl)	S(1): 0.2; S(2): 0.2; S(3): 0.2; S(4): 0.2; Y(12): 99.0; T(16): 0.0; S(24): 0.0; S(26): 0.0; S(28): 0.0	Y653	Y12;	20	1	NLGA DDGy MPMT PGA	2.76	33	2941. 17533	0	16.99

PVRL4	81607	poliovirus receptor-related protein 4 precursor	222136611	SySTLTTVR	Y2(Phospho); R9(Label:13C(6))	S(1): 1.7; Y(2): 98.3; S(3): 0.0; T(4): 0.0; T(6): 0.0; T(7): 0.0	Y445	Y2;	7	1	EEPEGRSySTLTTVR	2.07	58	1113.52788	0	0.27
PIK3R2	5296	phosphatidylinositol 3-kinase regulatory subunit beta	4826908	sREYDQLYEYTR	Y4(Phospho)	S(1): 100.0; Y(4): 0.0; Y(8): 0.0; Y(11): 0.0; T(12): 0.0	S457	S1;	15	1	HQQYQDKsREYDQLY	4.23	44	1831.752	1	2.79
HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	4504445	SSGPyGGGGQYFAKPR	Y5(Phospho); K14(Label:13C(6)); R16(Label:13C(6))	S(1): 2.0; S(2): 2.0; Y(5): 96.0; Y(11): 0.0	Y289	Y5;	4	1	GGRSSGPyGGGGQYF	4.11	94	1720.78752	0	1.50
KRT7	3855	keratin, type II	67782365	SAyGGPVGAGIR	Y3(Phospho)	S(1): 2.0; Y(3): 98.0	Y55	Y3;	4	1	RVAVRSAYG GPVG	3.15	71	1184.54497	0	0.87

		cytoskeletal 7									AG					
HNR NPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	4504445	SSGPy GGGG QYFA KPR	Y5(Phospho)	S(1): 2.1; S(2): 2.1; Y(5): 95.8; Y(11): 0.0	Y289	Y5;	4	1	GGRSS GPyGG GGQY F	4.11	33	1708. 74479	0	1.46
PRKC D	5580	protein kinase C delta type	31377782	SDsAS SEPVG IyQGF EKK	S6(Phospho); Y12(Phospho)	S(1): 2.5; S(3): 97.5; S(5): 0.0; S(6): 0.0; Y(12): 100.0	S304; Y313	S3; Y12;	22	1	RASR RSDsA SSEPVG; SSEPVGly QGFE KKT	3.75		2088. 85654	1	13.38
PRKC D	5580	protein kinase C delta type	31377782	SDsAS SEPVG IyQGF EKK	S3(Phospho); Y12(Phospho)	S(1): 2.5; S(3): 97.5; S(5): 0.1; S(6): 0.0; Y(12): 100.0	S304; Y313	S3; Y12;	22	1	RASR RSDsA SSEPVG; SSEPVGly QGFE KKT	3.75	40	2088. 85503	1	11.69

IRS2	8660	insulin receptor substrate 2	38683860	SDDy MPMS PASVS APK	Y4(Phospho)	S(1): 2.9; Y(4): 97.1; S(8): 0.0; S(11): 0.0; S(13): 0.0	Y675	Y4;	4	1	GSCRS DDyM PMSP AS	2.61	1762. 71684	0	16.22
ARHGAP35	2909	rho GTPase-activating protein 35	150417981	SVSSS PWLP QDGF DPsDY AEPM DAVV KPR	S5(Phospho); S16(Phospho)	S(1): 47.8; S(3): 47.8; S(4): 2.2; S(5): 2.2; S(16): 95.6; Y(18): 4.4	S1085	S16;	12	1	PQDG FDPsD YAEP MD	3.65	3337. 41355	0	0.56
PRKCD	5580	protein kinase C delta type	31377782	SDSAS SEPVG IyQGF EK	S3(Phospho); Y12(Phospho)	S(1): 50.0; S(3): 50.0; S(5): 0.0; S(6): 0.0; Y(12): 100.0	Y313	Y12;	12	1	SSEPV GlyQG FEKKT	4.07	1960. 75591	0	8.75
PTPRE	5791	receptor-type tyrosine-protein phosphatase epsilon isoform 2	18860859	VVQD FIDIFS DyANF K	Y12(Phospho)	S(10): 0.0; Y(12): 100.0	Y638	Y12;	16	1	FIDIFS DyANF K	3.87	2000. 90483	0	0.31

PTPR E	5791	receptor-type tyrosine phosphatase epsilon isoform 2	18860859	VVQD FIDIFS DyANF K	Y12(Phospho); K16(Label:13C(6))	S(10): 0.0; Y(12): 100.0	Y638	Y12;	16	1	FIDIFS DyANF K_	3.87	43	2006.9282	0	0.32
GSK3 B	2932	glycogen synthase kinase-3 beta isoform 2	225903437	QLVR GEPN VSyIC SR	R4(Label:13C(6)); Y11(Phospho); C13(Carbamidomethyl); R15(Label:13C(6))	S(10): 2.7; Y(11): 97.3; S(14): 0.0	Y216	Y11;	4	1	RGEP NVSyI CSRY YR	3.26		1869.90616	1	0.51
EGFR	1956	epidermal growth factor receptor isoform	29725609	EAKP NGIFK GSTAE NAEyL R	Y18(Phospho)	S(11): 0.0; T(12): 0.0; Y(18): 100.0	Y1197	Y18;	3	1	STAEN AEyLR VAPQ S	3.15		2275.07608	1	2.64

		m a precur sor														
ARH GAP5	394	rho GTPa se- activat ing protei n 5 isoform b	71834861	VPLA HPED MDPS DNyA EPIDTI FK	Y15(Ph ospho); K24(La bel:13C (6))	S(12): 0.1; Y(15): 99.9; T(21): 0.0	Y1091	Y15;	4	1	DMDP SDNyA EPIDTI	3.38	31	2800. 25919	0	0.09
BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1 isoform 7	28239812 3	VLPPE VADG GVVD SGVyA VPPPA ER	Y17(Ph ospho); R25(La bel:13C (6))	S(14): 0.1; Y(17): 99.9	Y408	Y17;	13	1	GVVD SGVyA VPPPA E	2.31		2576. 26909	0	1.43
KRT7	3855	kerati n, type II cytosk eletal 7	67782365	LSSAR PGGL GSSSL yGLG ASRPR	Y15(Ph ospho)	S(2): 0.0; S(3): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.3; Y(15): 99.3; S(20): 0.3	Y40	Y15;	31	1	GLGSS SLyGL GASRP	3.55		2326. 16738	0	0.69



PRKC D	5580	prote in kinase C delta type	31377782	RSDSA SSEP V GlyQG FEKK	Y13(Ph ospho)	S(2): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; Y(13): 100.0	Y313	Y13;	18	1	SSEP V GlyQG FEKKT	5.12	59	2164. 98648	2	6.23
PRKC D	5580	prote in kinase C delta type	31377782	RSDSA SSEP V GlyQG FEK	Y13(Ph ospho)	S(2): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; Y(13): 100.0	Y313	Y13;	14	1	SSEP V GlyQG FEKKT	5.14	79	2036. 89739	1	4.79
PRKC D	5580	prote in kinase C delta type	31377782	RSDSA SSEP V GlyQG FEK	Y13(Ph ospho)	S(2): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; Y(13): 100.0	Y313	Y13;	14	1	SSEP V GlyQG FEKKT	5.14	43	2036. 89688	1	3.95
BAIA P2	10458	brain- specifi c angio genesi s inhibit or 1- associ ated protei n 2 isoform 3	5453565	LSDSy SNTLP VR	Y5(Pho ospho)	S(2): 0.0; S(4): 1.8; Y(5): 96.5; S(6): 1.8; T(8): 0.0	Y337	Y5;	7	1	QSKLS DSySN TLPVR	2.72	83	1431. 65032	0	1.58

PRKD	5580	protein kinase C delta type	31377782	RSDsA SSEPVG GIyQGF FEK	S4(Phospho); Y13(Phospho)	S(2): 0.0; S(4): 100.0; S(6): 0.0; S(7): 0.0; Y(13): 100.0	S304; Y313	S4; Y13;	14	1	RASR RSDsA SSEPVG; SSEPVGly QGF KKT	5.14	54	2116. 86235	1	6.24
BAIA P2	10458	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform 3	5453565	LSDsY SNTLP VRK	Y5(Phospho)	S(2): 0.0; S(4): 96.0; Y(5): 2.0; S(6): 2.0; T(8): 0.0	S336	S4;	7	1	SQSKL SDsYS NTLPV	3.51	79	1559. 74492	1	1.72
TNS3	64759	tensin-3	65288071	ESMC STPAF PVSPE TPyVK	C4(Carbamidomethyl); Y17(Phospho)	S(2): 0.0; S(5): 0.0; T(6): 0.0; S(12): 0.0; T(15): 0.1; Y(17): 99.9	Y855	Y17;	5	1	PVSPE TPyVK TALR H	2.93	47	2206. 94658	0	1.83

TNS3	64759	tensin-3	65288071	ESMC STPAF PVSPE TPyVK	M3(Oxidation); C4(Carbamido methyl); Y17(Phospho)	S(2): 0.0; S(5): 0.0; T(6): 0.0; S(12): 0.0; T(15): 2.7; Y(17): 97.3	Y855	Y17;	5	1	PVSPE TPyVK TALR H	2.93	55	2222.94048	0	1.89
EGFR	1956	epidermal growth factor receptor isoform a precursor	29725609	GSHQI SLDNP DyQQ DFFPK	Y12(Phospho)	S(2): 0.0; S(6): 0.0; Y(12): 100.0	Y1172	Y12;	9	1	ISLDN PDyQQ DFFPK	4.36	63	2315.99009	0	4.70
EGFR	1956	epidermal growth factor receptor isoform a precursor	29725609	GSHQI SLDNP DyQQ DFFPK	Y12(Phospho)	S(2): 0.0; S(6): 0.0; Y(12): 100.0	Y1172	Y12;	9	1	ISLDN PDyQQ DFFPK	4.36	91	2315.99321	0	3.64

ANX A2	302	annexin A2 isoform 2	209862831	LSLEG DHSTP PSAyG SVK	Y14(Phospho)	S(2): 0.0; S(8): 0.0; T(9): 0.0; S(12): 0.0; Y(14): 100.0; S(16): 0.0	Y24	Y14;	24	1	HSTPP SAyGS VKAY T	5.16	88	1924.8687	0	0.81
ANX A2	302	annexin A2 isoform 2	209862831	LSLEG DHSTP PSAyG SVK	Y14(Phospho); K18(Label:13C(6))	S(2): 0.0; S(8): 0.0; T(9): 0.0; S(12): 0.1; Y(14): 97.5; S(16): 2.4	Y24	Y14;	24	1	HSTPP SAyGS VKAY T	5.16	47	1930.88431	0	0.80
PTRF	284119	polymrase I and transcript release factor	42734430	KSFTP DHVV yAR	Y10(Phospho)	S(2): 0.0; T(4): 0.0; Y(10): 100.0	Y308	Y10;	2	1	FTPDH VVyA RSKT AV	4.00	39	1499.70288	1	4.83
PPP1 CA	5499	serine/threonine-protein phosphatase PP1-alpha catalyt	45827798	QSLET ICLLL AyKIK	C7(Carbamidomethyl); Y12(Phospho)	S(2): 0.0; T(5): 0.2; Y(12): 99.8	Y66	Y12;	1	1	TICLL LAyKI KYPE N	2.26		1872.9699	1	2.27

		ic subunit isoform 2														
EVPL	2125	envoplakin	156104874	ISILEP ETGK DMSPy EAYK R	Y15(Phospho)	S(2): 0.0; T(8): 0.0; S(13): 3.6; Y(15): 92.8; Y(18): 3.6	Y1700	Y15;	10	1	TGKD MSPyE AYKR GI	4.67	46	2407. 11893	2	9.95
TNS3	64759	tensin-3	65288071	LSLGQ yDND AGGQ LPFSK	Y6(Phospho); K18(Label:13C(6))	S(2): 0.0; Y(6): 100.0; S(17): 0.0	Y780	Y6;	4	1	RKLSL GQyD NDAG GQ	3.27	101	1995. 91179	0	1.66
GPRC5C	55890	G-protein coupled receptor family C group 5 member C isoform b precursor	40217833	NSQV FRNP VWD	R6(Label:13C(6)); Y9(Phospho)	S(2): 0.0; Y(9): 100.0	Y450	Y9;	2	1	SQVFR NPyV WD_	2.46	35	1610. 71184	1	0.25

KRT7	3855	keratin, type II cytoskeletal 7	67782365	LSSAR PGGL GSSSL yGLG ASRPR	S3(Phospho); Y15(Phospho)	S(2): 0.1; S(3): 1.2; S(11): 32.9; S(12): 32.9; S(13): 32.9; Y(15): 100.0; S(20): 0.0	Y40	Y15;	31	1	GLGSS SLyGL GASRP	3.55	34	2406. 13199	0	1.45
PRKD	5580	protein kinase C delta type	31377782	RSDSA SsEPV GIyQG FEKK	S4(Phospho); Y13(Phospho)	S(2): 0.1; S(4): 2.2; S(6): 2.2; S(7): 95.5; Y(13): 100.0	S307; Y313	S7; Y13;	18	1	RRSDS ASsEP VGIYQ ;SSEP VGIyQ GFEEK KT	5.12	67	2244. 95513	2	7.10
PRKD	5580	protein kinase C delta type	31377782	RSDSA SSEP VGIyQG FEKK	S4(Phospho); Y13(Phospho)	S(2): 1.0; S(4): 33.0; S(6): 33.0; S(7): 33.0; Y(13): 100.0	Y313	Y13;	18	1	SSEP VGIyQG FEKKT	5.12	42	2244. 95578	2	8.01
CTTN	2017	src substrate cortactin isoform a	20357552	LPSSP VyED AASF K	Y7(Phospho)	S(3): 0.0; S(4): 0.0; Y(7): 100.0; S(12): 0.0	Y421	Y7;	6	1	RLPSS PVyED AASF K	3.28	60	1590. 7105	0	1.90
GAB1	2549	GRB2- associated-	46370073	DASS QDCy DIPR	C7(Carbamidomethyl);	S(3): 0.0; S(4): 0.0; Y(8): 100.0	Y406	Y8;	5	1	DASS QDCy DIPRA FP	2.43	74	1506. 55742	0	1.44

		bindin g protei n 1 isoform b			Y8(Pho spho)											
SPTA N1	6709	spectri n alpha chain, non- eryth rocytic 1 isoform 3	30696613 2	ALSSE GKPyV TKEEL YQNL TR	Y9(Pho spho)	S(3): 0.0; S(4): 0.0; Y(9): 97.8; T(11): 2.1; Y(16): 0.0; T(20): 0.0	Y2403	Y9;	5	1	LSSEG KPyVT KEEL Y	2.90		2506. 21744	1	1.79
NED D9	4739	enhan cer of filame ntatio n 1 isoform 3	21542237 5	HQSL PNHPP PQLG QSVG SQND AyDVP R	Y24(Ph ospho)	S(3): 0.0; S(5): 0.0; S(16): 0.0; S(19): 0.0; Y(24): 100.0	Y317	Y24;	9	1	VGSQ NDAy DVPR GVQ	4.71	40	3105. 41762	0	12.25
NED D9	4739	enhan cer of filame ntatio n 1 isoform 3	21542237 5	HQSL PNHPP PQLG QSVG SQND AyDVP R	Y24(Ph ospho)	S(3): 0.0; S(5): 0.0; S(16): 0.0; S(19): 0.0; Y(24): 100.0	Y317	Y24;	9	1	VGSQ NDAy DVPR GVQ	4.71		3105. 41855	0	9.17

TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	110556636	DVSLGTyGSR	Y7(Phospho); R10(Label:13C(6))	S(3): 0.0; T(6): 1.9; Y(7): 96.2; S(9): 1.9	Y940	Y7;	5	1	RDVSLGTyGSRRAAEP	1.61	44	1140.50224	0	1.19
TAGLN2	8407	transgelin-2	4507357	GASQAGMTGyGMPR	Y10(Phospho); R14(Label:13C(6))	S(3): 0.0; T(8): 0.1; Y(10): 99.9	Y192	Y10;	10	1	SQAGMTGyGMPRQIL	3.32	53	1469.5999	0	0.43
TAGLN2	8407	transgelin-2	4507357	GASQAGMTGyGMPR	M7(Oxidation); Y10(Phospho); R14(Label:13C(6))	S(3): 0.0; T(8): 2.4; Y(10): 97.6	Y192	Y10;	10	1	SQAGMTGyGMPRQIL	3.32	48	1485.59563	0	0.42
CDKL5	6792	cyclin-dependent kinase-like 5	4507281	NLSEGNANYTEyVATR	Y13(Phospho)	S(3): 0.0; Y(10): 0.0; T(11): 0.0; Y(13): 100.0; T(16): 0.0	Y171	Y13;	7	1	NNANYTEyVATRWR	3.04	109	1995.84441	0	1.24
TNS3	64759	tensin-3	65288071	WDSYENLSADGEVLHTQGPVDGSLyA	Y25(Phospho)	S(3): 0.0; Y(4): 0.0; S(8): 0.0; T(16): 0.0; S(23): 0.2; Y(25): 99.8	Y354	Y25;	34	1	GPVDGSLyAKVRKKS	5.52	36	3031.33811	0	4.59



				K												
TNS3	64759	tensin-3	65288071	KLSLG QyDN DAGG QLPFS K	Y7(Phospho)	S(3): 0.0; Y(7): 100.0; S(18): 0.0	Y780	Y7;	10	1	RKLSL GQyD NDAG GQ	4.56	93	2117. 99004	1	1.80
SYK	6850	tyrosine-kinase SYK isoform 2	205277435	QESTV SFNPY EPELA PWAA DKGP QR	Y10(Phospho)	S(3): 0.2; T(4): 3.8; S(6): 3.8; Y(10): 92.2	Y300	Y10;	9	1	STVSF NPYEP ELAP W	4.64	40	2897. 31296	1	0.84
SHB	6461	SH2 domain-containing adapter protein B	106879210	GESA GyME PYEA QR	Y6(Phospho); R14(Label:13C(6))	S(3): 1.8; Y(6): 98.2; Y(10): 0.0	Y268	Y6;	5	1	GKGE SAGy MEPY EAQ	3.56	70	1673. 66069	0	0.29

TNS3	64759	tensin-3	65288071	WDsY ENLSA DGEV LHTQ GPVD GSLyA K	S3(Phospho); Y25(Phospho)	S(3): 96.2; Y(4): 3.7; S(8): 0.2; T(16): 0.0; S(23): 0.2; Y(25): 99.8	S332; Y354	S3; Y25;	34	1	DPLIR WDsY ENLSA D;GPV DGSly AKVR KKS	5.52	55	3111. 30742	0	2.99
TNS3	64759	tensin-3	65288071	WDsY ENLSA DGEV LHTQ GPVD GSLyA K	S3(Phospho); Y25(Phospho)	S(3): 99.9; Y(4): 0.1; S(8): 0.0; T(16): 0.0; S(23): 0.1; Y(25): 99.9	S332; Y354	S3; Y25;	34	1	DPLIR WDsY ENLSA D;GPV DGSly AKVR KKS	5.52	49	3111. 30686	0	2.93
PKM	5315	pyruvate kinase isozymes M1/M2 isoform a	33286418	AEGS DVAN AVLD GADCI MLSG ETAK GDyPL EAVR	C16(Carbamidomethyl); Y28(Phospho)	S(4): 0.0; S(20): 6.7; T(23): 6.7; Y(28): 86.7	Y370	Y28;	2	1	GETA KGDyP LEAV RM	4.00		3574. 61899	1	0.68
NEDD9	4739	enhancer of filamentation 1 isoform 3	215422375	RHQS LSPNH PPPQL GQSV GSQN DAyD VPR	Y25(Phospho)	S(4): 0.0; S(6): 0.0; S(17): 0.0; S(20): 0.0; Y(25): 100.0	Y317	Y25;	4	1	VGSQ NDAy DVPR GVQ	5.70	34	3261. 52114	1	10.38
RPS27	6232	40S ribosomal	4506711	LVQSP NSyFM DVK	Y8(Phospho)	S(4): 0.0; S(7): 1.4; Y(8): 98.6	Y31	Y8;	5	1	LVQSP NSyFM DVKC	2.58	72	1607. 71599	0	0.79

		protein S27									P					
NCK1	4690	cytoplasmic protein NCK1 isoform 1	5453754	RKPSV PDSAS PADD SFVDP GERLy DLNM PAYV K	Y31(Phospho)	S(4): 0.0; S(8): 0.0; S(10): 0.0; S(15): 0.0; Y(24): 95.4; Y(31): 4.6	Y105	Y24;	5	1	VDPG ERLyD LNMP AY	5.42	33	3716. 7333	2	7.10
PSMB4	5692	proteasome subunit beta type-4	22538467	VNNS TMLG ASGDy ADFQ YLK	Y13(Phospho); K20(Label:13C(6))	S(4): 0.0; T(5): 0.0; S(10): 2.6; Y(13): 97.4; Y(18): 0.0	Y102	Y13;	6	1	MLGA SGDyA DFQY LK	1.73	54	2280. 00054	0	0.50
HIPK1	204851	homeodomain-interacting protein kinase 1 isoform 2	38201638	AVCS TyLQS R	C3(Carbamidomethyl); Y6(Phospho)	S(4): 0.0; T(5): 0.0; Y(6): 100.0; S(9): 0.0	Y352	Y6;	6	1	SKAV CSTyL QSRY YR	2.67	63	1264. 53887	0	0.76

CTTN	2017	src substrate cortactin isoform a	20357552	GPVS GTEPE PVYS MEAA DyR	Y19(Phospho)	S(4): 0.0; T(6): 0.0; Y(12): 0.0; S(13): 0.0; Y(19): 100.0	Y453	Y19;	45	1	YSME AADy REASS QQ	4.20	44	2234. 93071	0	2.11
CTTN	2017	src substrate cortactin isoform a	20357552	GPVS GTEPE PVySM EAAD YR	Y12(Phospho)	S(4): 0.0; T(6): 0.0; Y(12): 98.5; S(13): 1.5; Y(19): 0.0	Y446	Y12;	45	1	GTEPE PVySM EAAD Y	4.20	79	2234. 93144	0	3.63
PKM	5315	pyruvate kinase isozymes M1/M2 isoform a	33286418	LNFSH GTHEY HAETI K	Y10(Phospho); K16(Label:13C (6))	S(4): 0.0; T(7): 0.0; Y(10): 97.5; T(14): 2.5	Y83	Y10;	5	1	FSHGT HEyH AETIK N	5.21	42	1969. 88742	0	0.73
MAP K12	6300	PREDICTED: mitogen- activated protein kinase	39713810 6	QADS EMTG yVVTR	Y9(Phospho); R13(Label:13C (6))	S(4): 0.0; T(7): 0.0; Y(9): 99.9; T(12): 0.1	Y175	Y9;	6	1	ADSE MTGy VVTR WYR	4.28	69	1542. 66069	0	2.34

		12														
MAPK12	6300	PREDICTED: mitogen-activated protein kinase 12	397138106	QADSEMTGyVVTR	M6(Oxidation); Y9(Phospho)	S(4): 0.0; T(7): 3.1; Y(9): 96.8; T(12): 0.1	Y175	Y9;	6	1	ADSEMTGyVVTRWYR	4.28	57	1552.63359	0	2.01
CTTN	2017	src substrate cortactin isoform a	20357552	AELSYRGPVSGTEPEPVySMEAADYR	Y18(Phospho)	S(4): 0.0; Y(5): 0.0; S(10): 0.0; T(12): 0.0; Y(18): 97.9; S(19): 2.1; Y(25): 0.0	Y446	Y18;	13	1	GTEPEPVySMEAADY	3.63	58	2954.28513	1	3.58
CTTN	2017	src substrate cortactin isoform a	20357552	GPVSGTEPEPVySMEAADYR	Y12(Phospho); M14(Oxidation)	S(4): 0.1; T(6): 2.4; Y(12): 95.0; S(13): 2.4; Y(19): 0.0	Y446	Y12;	45	1	GTEPEPVySMEAADY	4.20	38	2250.92754	0	3.97

NCK1	4690	cytoplasmic protein NCK1 isoform 1	5453754	RKPsV PDSAS PADD SFVDP GERLy DLNM PAYV K	S10(Phospho); S15(Phospho)	S(4): 94.5; S(8): 5.2; S(10): 0.3; S(15): 0.0; Y(24): 94.8; Y(31): 5.2	S85; Y105	S4; Y24;	5	1	GKVK RKPsV PDSAS P;VDP GERLy DLNM PAY	5.42		3796.69301	2	11.93
ENO1	2023	alpha-enolase isoform 1	4503571	AAVP SGAST GIyEA LELR	Y12(Phospho)	S(5): 0.0; S(8): 0.0; T(9): 0.0; Y(12): 100.0	Y44	Y12;	6	1	SGAST GIyEA LELRD	3.93	100	1884.9124	0	0.52
BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 7	282398123	GLPPS NHHA VYDV PPsVS K	Y11(Phospho)	S(5): 0.0; Y(11): 2.3; S(16): 97.7; S(18): 0.1	S309	S16;	10	1	AVYD VPPsV SKDV PD	3.07		2080.9852	0	2.25
NEDD9	4739	enhancer of filamentation 1 isoform 3	215422375	GPVFS VPVG EIKPQ GVyDI PPTK	Y17(Phospho)	S(5): 0.0; Y(17): 100.0; T(22): 0.0	Y214	Y17;	29	1	EIKPQ GVyDI PPTKG	3.94		2504.28696	0	9.31

BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 7	282398123	GLLPS QYGQ EVyDT PPMA VK	Y12(Phospho)	S(5): 0.0; Y(7): 0.0; Y(12): 100.0; T(14): 0.0	Y265	Y12;	12	1	SQYG QEVy DTPP MAV	2.98	63	2273.06108	0	1.93
PKP3	11187	plakophilin-3	6005830	GGVG SRADy DTLSL R	R6(Label:13C(6)); Y9(Phospho); R15(Label:13C(6))	S(5): 0.0; Y(9): 98.4; T(11): 1.6; S(13): 0.0	Y176	Y9;	6	1	GVGS RADy DTLSL RS	3.88	50	1658.7935	1	0.47
PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	89276756	LCDF GSAS HVAD NDITP yLVSR	C2(Carbamidomethyl); Y18(Phospho)	S(6): 0.0; S(8): 0.0; T(16): 0.0; Y(18): 97.5; S(21): 2.5	Y849	Y18;	74	1	ADNDI TPyLV SRFYR	5.33		2517.10965	0	1.64

CTTN	2017	src substrate cortactin isoform a	20357552	MDKN ASTFE DVTQ VSSAy QK	Y18(Phospho)	S(6): 0.0; T(7): 0.0; T(12): 0.0; S(15): 0.0; S(16): 0.0; Y(18): 100.0	Y334	Y18;	10	1	VTQV SSAyQ KTVP VE	2.89	36	2329.00467	1	2.36
CTTN	2017	src substrate cortactin isoform a	20357552	MDKN ASTFE DVTQ VSSAy QK	Y18(Phospho)	S(6): 0.0; T(7): 0.0; T(12): 0.0; S(15): 0.0; S(16): 0.1; Y(18): 99.9	Y334	Y18;	10	1	VTQV SSAyQ KTVP VE	2.89	44	2329.00786	1	2.02
GPRC 5A	9052	retinoic acid-induced protein 3	4506403	AHAW PSPYK DyEV KK	K9(Label:13C(6)); Y11(Phospho); K14(Label:13C(6)); K15(Label:13C(6))	S(6): 0.0; Y(8): 0.0; Y(11): 100.0	Y350	Y11;	60	1	WPSP YKDy EVKK EGS	4.10	51	1916.9412	2	15.72
GPRC 5A	9052	retinoic acid-induced protein 3	4506403	AHAW PSPYK DyEV KK	Y11(Phospho)	S(6): 0.0; Y(8): 0.0; Y(11): 100.0	Y350	Y11;	60	1	WPSP YKDy EVKK EGS	4.10		1898.8843	2	16.03



GPRC 5A	9052	retinoi c acid- induce d protei n 3	4506403	AHAW PSPyK DYEV KK	Y8(Pho spho)	S(6): 0.0; Y(8): 100.0; Y(11): 0.0	Y347	Y8;	60	1	AHAW PSPyK DYEV KK	4.10	37	1898. 88286	2	21.05
GPRC 5A	9052	retinoi c acid- induce d protei n 3	4506403	AHAW PSPyK DYEV K	Y8(Pho spho)	S(6): 0.0; Y(8): 100.0; Y(11): 0.0	Y347	Y8;	43	1	AHAW PSPyK DYEV KK	4.58	43	1770. 78879	1	14.23
GPRC 5A	9052	retinoi c acid- induce d protei n 3	4506403	AHAW PSPyK DYEV K	Y8(Pho spho); K9(Lab el:13C( 6)); K14(La bel:13C (6))	S(6): 0.0; Y(8): 100.0; Y(11): 0.0	Y347	Y8;	43	1	AHAW PSPyK DYEV KK	4.58	54	1782. 82732	1	14.92
GPRC 5A	9052	retinoi c acid- induce d protei n 3	4506403	AHAW PSPyK DyEV KK	Y8(Pho spho); Y11(Ph ospho)	S(6): 0.0; Y(8): 100.0; Y(11): 100.0	Y347; Y350	Y8; Y11;	60	1	AHAW PSPyK DYEV KK;WP SPYK DyEV KKEG S	4.10	51	1978. 85039	2	35.37
GPRC 5A	9052	retinoi c acid- induce d protei	4506403	AHAW PSPyK DYEV KK	Y8(Pho spho)	S(6): 0.0; Y(8): 98.3; Y(11): 1.7	Y347	Y8;	60	1	AHAW PSPyK DYEV KK	4.10		1898. 88388	2	11.64

		n 3														
DAPP 1	27071	dual adapter for phosphotyrosine and 3-phosphotyrosine and 3-phosphoserine	158631203	KVEEPSlyESVR	Y8(Phospho)	S(6): 0.0; Y(8): 98.4; S(10): 1.6	Y139	Y8;	5	1	KVEEPSlyESVRVHT	3.67	57	1515.71025	1	0.46
C6orf 132	647024	uncharacterized protein C6orf132	256574805	HKAPGSADyGFAPAAGR	Y9(Phospho)	S(6): 0.0; Y(9): 100.0	Y1142	Y9;	8	1	KAPGSADyGFAPAAG	4.79	47	1752.78458	1	11.63
C6orf 132	647024	uncharacterized protein C6orf132	256574805	HKAPGSADyGFAPAAGR	Y9(Phospho)	S(6): 0.0; Y(9): 100.0	Y1142	Y9;	8	1	KAPGSADyGFAPAAG	4.79	86	1752.78594	1	11.56

SHB	6461	SH2 domain-containing adapter protein B	106879210	AGKG ESAGy MEPY EAQR	Y9(Phospho)	S(6): 0.0; Y(9): 100.0; Y(13): 0.0	Y268	Y9;	15	1	GKGE SAGy MEPY EAQ	5.94	85	1923.79314	1	0.25
SHB	6461	SH2 domain-containing adapter protein B	106879210	AGKG ESAGy MEPY EAQR	Y9(Phospho)	S(6): 0.0; Y(9): 100.0; Y(13): 0.0	Y268	Y9;	15	1	GKGE SAGy MEPY EAQ	5.94	52	1923.79447	1	0.24
GPRC5A	9052	retinoic acid-induced protein 3	4506403	AHAW PSPyK DyEV KK	Y8(Phospho); Y11(Phospho)	S(6): 0.1; Y(8): 99.9; Y(11): 100.0	Y347; Y350	Y8; Y11;	60	1	AHAW PSPyK DyEV KK;WP SPYK DyEV KKEG S	4.10		1978.84842	2	31.79
GSK3B	2932	glycogen synthase kinase-3 beta	225903437	GEPN VSYIC SR	Y7(Phospho); C9(Carbamidomethyl)	S(6): 1.8; Y(7): 98.2; S(10): 0.0	Y216	Y7;	40	1	RGEP NVSyI CSRY YR	2.56	62	1361.55461	0	1.05

		isoform 2														
GPRC5A	9052	retinoic acid-induced protein 3	4506403	AHAWPsPYK DyEVK	S6(Phospho); Y8(Phospho)	S(6): 100.0; Y(8): 2.2; Y(11): 97.8	S345; Y350	S6; Y11;	43	1	PRAHAWPsPYKDYEV;WPSPYK DyEVKKEGS	4.58		1850.7526	1	10.43
SHB	6461	SH2 domain-containing adapter protein B	106879210	AGKGESAGyMEPYEAQR	K3(Label:13C(6)); Y9(Phospho); M10(Oxidation); R17(Label:13C(6))	S(6): 2.1; Y(9): 97.9; Y(13): 0.0	Y268	Y9;	15	1	GKGESAGyMEPYEAQ	5.94	39	1951.82938	1	0.25
SHB	6461	SH2 domain-containing adapter protein B	106879210	AGKGESAGyMEPYEAQR	K3(Label:13C(6)); Y9(Phospho); M10(Oxidation); R17(Label:13C(6))	S(6): 2.5; Y(9): 94.9; Y(13): 2.5	Y268	Y9;	15	1	GKGESAGyMEPYEAQ	5.94	31	1951.82854	1	0.23

					(6)											
PRPF 4B	8899	serine/ threon ine- protei n kinase PRP4 homol og	89276756	LCDF GsASH VADN DITPy LVSR	C2(Car bamido methyl) ; S8(Pho spho); S21(Ph ospho); R22(La bel:13C (6))	S(6): 96.6; S(8): 3.4; T(16): 0.0; Y(18): 96.6; S(21): 3.4	S837; Y849	S6; Y18;	74	1	LKLC DFGsA SHVA DN;AD NDITP yLVSR FYR	5.33	2603. 09635	0	0.69	
GPRC 5A	9052	retinoi c acid- induce d protei n 3	4506403	AHAW PsPYK DyEV KK	Y8(Pho spho); Y11(Ph ospho)	S(6): 96.9; Y(8): 3.1; Y(11): 100.0	S345; Y350	S6; Y11;	60	1	PRAH AWPsP YKDY EV;WP SPYK DyEV KKEG S	4.10	1978. 84714	2	5.60	
GPRC 5A	9052	retinoi c acid- induce d protei	4506403	AHAW PsPYK DYEV K	S6(Pho spho); Y8(Pho spho)	S(6): 99.9; Y(8): 50.0; Y(11): 50.0	S345	S6;	43	1	PRAH AWPsP YKDY EV	4.58	1850. 75517	1	6.81	

		n 3														
ELM O2	63916	engulf ment and cell motilit y protei n 2	33469947	EVCD GWSL PNPEy YTLR	C3(Car bamido methyl ; Y13(Ph ospho)	S(7): 0.0; Y(13): 95.1; Y(14): 2.4; T(15): 2.4	Y48	Y13;	11	1	WSLP NPEyY TLRY AD	1.97		2178. 92534	0	7.13
SHC1	6464	SHC- transf ormin g protei n 1 isofo r m 4	19423966 8	ELFDD PSyVN VQNL DK	Y8(Pho spho); K16(La bel:13C (6))	S(7): 2.1; Y(8): 97.9	Y317	Y8;	12	1	ELFDD PSyVN VQNL D	3.91	72	1981. 88921	0	2.52
SHC1	6464	SHC- transf ormin g protei n 1 isofo r m 4	19423966 8	ELFDD PSyVN VQNL DKAR	Y8(Pho spho)	S(7): 2.3; Y(8): 97.7	Y317	Y8;	4	1	ELFDD PSyVN VQNL D	2.79	49	2202. 99881	1	2.21
SHC1	6464	SHC- transf ormin g protei n 1	19423966 8	ELFDD PsYVN VQNL DK	S7(Pho spho)	S(7): 98.1; Y(8): 1.9	S316	S7;	12	1	RELFDD DPsYV NVQN L	3.91	34	1975. 86765	0	2.30

		isoform 4														
PXN	5829	paxillin isoform 1	170932516	FIHQQ PQSSS PVYGSsAK	S16(Phospho)	S(8): 0.0; S(9): 0.0; S(10): 0.0; Y(13): 2.2; S(15): 2.2; S(16): 95.7	S91	S16;	24	1	SSPVY GSsAK TSSVS	4.58	42	2027.9249	0	2.89
PXN	5829	paxillin isoform 1	170932516	FIHQQ PQSSs PVyGS SAK	S10(Phospho); S15(Phospho)	S(8): 0.0; S(9): 0.0; S(10): 100.0; Y(13): 96.6; S(15): 3.3; S(16): 0.1	S85; Y88	S10; Y13;	24	1	HQQP QSSsP VYGS SA;PQ SSSPV yGSSA KTS	4.58		2107.88523	0	5.82
CTN ND1	1500	catenin delta-1 isoform 2A	332688222	LNGP QDHS HLLyS TIPR	Y12(Phospho)	S(8): 0.0; Y(12): 93.0; S(13): 3.5; T(14): 3.5	Y42	Y12;	5	1	QDHS HLLyS TIPRM Q	4.03		2027.97141	0	1.05
PXN	5829	paxillin isoform 1	170932516	FIHQQ PQSSs PVyGS SAK	S10(Phospho); Y13(Phospho)	S(8): 0.1; S(9): 0.1; S(10): 99.8; Y(13): 99.9; S(15): 0.1; S(16): 0.0	S85; Y88	S10; Y13;	24	1	HQQP QSSsP VYGS SA;PQ SSSPV yGSSA KTS	4.58	40	2107.89043	0	5.43

PRKC D	5580	prote in kinase C delta type	31377782	TGVA GEDM QDNS GTyG K	Y15(Ph ospho)	T(1): 0.0; S(12): 0.0; T(14): 1.8; Y(15): 98.2	Y334	Y15;	5	1	MQDN SGTyG KIWE GS	3.85	82	1809. 69988	0	3.86
HIPK 3	10114	home odom ain- intera cting protei n kinase 3 isofo rm 2	11479663 0	TVCST yLQSR	C3(Car bamido methyl) ; Y6(Pho spho)	T(1): 0.0; S(4): 0.0; T(5): 1.1; Y(6): 98.9; S(9): 0.0	Y359	Y6;	7	1	SKTV CSTyL QSRY YR	2.84	53	1294. 55242	0	5.15
EFNB 2	1948	ephrin -B2 precur sor	4758250	TADS VFCPH yEK	C7(Car bamido methyl) ; Y10(Ph ospho); K12(La bel:13C (6))	T(1): 0.0; S(4): 0.0; Y(10): 100.0	Y304	Y10;	3	1	DSVFC PHyEK VSGD Y	3.21	69	1539. 62749	0	0.09



PTK2	5747	focal adhesion kinase 1 isoform a	24476013	THAV SVSET DDyA EIIDEE DTYT MPST R	Y12(Phospho)	T(1): 0.0; S(5): 0.0; S(7): 2.0; T(9): 0.0; Y(12): 97.9; T(21): 0.0; Y(22): 0.0; T(23): 0.0; S(26): 0.0; T(27): 0.0	Y397	Y12;	28	1	SVSET DDyA EIIDEE	4.23	83	3255. 35703	0	1.50
TLN1	7094	talin-1	223029410	TMQF EPSTM VyDA CR	M2(Oxidation); Y11(Phospho); C14(Carbamidomethyl)	T(1): 0.0; S(7): 0.0; T(8): 0.0; Y(11): 100.0	Y26	Y11;	10	1	FEPST MvYD ACRII R	4.07	46	1931. 73796	0	3.09
TLN1	7094	talin-1	223029410	TMQF EPSTM VyDA CR	Y11(Phospho); C14(Carbamidomethyl)	T(1): 0.0; S(7): 0.0; T(8): 0.0; Y(11): 100.0	Y26	Y11;	10	1	FEPST MvYD ACRII R	4.07	70	1915. 7387	0	3.54

CTTN	2017	src substrate cortactin isoform a	20357552	TQTPP VSPAP QPTEE RLPSS PVyED AASF K	Y23(Phospho)	T(1): 0.0; T(3): 0.0; S(7): 0.0; T(13): 0.2; S(19): 4.3; S(20): 4.3; Y(23): 91.3; S(28): 0.0	Y421	Y23;	8	1	RLPSS PVyED AASF K	3.83		3306.55625	1	1.54
MAPK9	5601	mitogen-activated protein kinase 9 isoform JNK2 gamma	205277412	TACT NFMM TPYV VtR	C3(Carbamidomethyl); Y11(Phospho); R15(Label:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 0.0; Y(11): 0.1; T(14): 99.9	T188	T14;	12	1	MMTP YVVtR YYRA PE	3.96	32	1877.80991	0	0.15
MAPK9	5601	mitogen-activated protein kinase 9 isoform JNK2	205277412	TACT NFMM TPyVV TR	C3(Carbamidomethyl); M7(Oxidation); Y11(Phospho); R15(Label:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 0.1; Y(11): 99.9; T(14): 0.1	Y185	Y11;	12	1	TNFM MTPy VVTR YYR	3.96	56	1893.80657	0	0.16

		gamma														
MAP K9	5601	mitogen-activated protein kinase 9 isoform JNK2 gamma	20527741 2	TACT NFMM tPyVV TR	C3(Carbamidomethyl); M7(Oxidation); T9(Phospho); Y11(Phospho); R15(Lab:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 100.0; Y(11): 100.0; T(14): 0.0	T183; Y185	T9; Y11;	12	1	ACTN FMMtP YVVT RY;TN FMMT PyVVT RYR	3.96	76	1973. 77153	0	0.12
MAP K9	5601	mitogen-activated protein kinase 9 isoform JNK2	20527741 2	TACT NFMM tPyVV TR	C3(Carbamidomethyl); T9(Phospho); Y11(Phospho); R15(Lab:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 100.0; Y(11): 100.0; T(14): 0.0	T183; Y185	T9; Y11;	12	1	ACTN FMMtP YVVT RY;TN FMMT PyVVT RYR	3.96	81	1957. 76775	0	0.12

		gamma														
MAP K9	5601	mitogen-activated protein kinase 9 isoform JNK2 gamma	20527741 2	TACT NFMM TPyVV TR	C3(Carbamido methyl); M7(Oxidation); M8(Oxidation); Y11(Phospho); R15(Label:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 2.4; Y(11): 97.5; T(14): 0.1	Y185	Y11;	12	1	TNFM MTPy VVTR YYR	3.96	51	1909. 80058	0	0.19
MAP K9	5601	mitogen-activated protein kinase 9 isoform JNK2	20527741 2	TACT NFMM TPyVV TR	C3(Carbamido methyl); M8(Oxidation); Y11(Phospho); R15(Label:13C(6))	T(1): 0.0; T(4): 0.0; T(9): 2.4; Y(11): 97.6; T(14): 0.0	Y185	Y11;	12	1	TNFM MTPy VVTR YYR	3.96	65	1893. 80657	0	0.17

		gamma														
EPHA 2	1969	ephrin type- A receptor 2 precursor	32967311	TYVD PHTyE DPNQ AVLK	Y8(Phospho); K17(Label:13C (6))	T(1): 0.0; Y(2): 0.0; T(7): 2.0; Y(8): 98.0	Y594	Y8;	14	1	TYVD PHTyE DPNQ AV	2.99	43	2075. 94101	0	0.02
NED D9	4739	enhancer of filamentation 1 isoform 3	21542237 5	TGHG YVye YPSR	Y7(Phospho)	T(1): 0.0; Y(5): 0.0; Y(7): 100.0; Y(9): 0.0; S(11): 0.0	Y166	Y7;	21	1	RTGH GYVye EYPSR YQ	4.03	56	1508. 61785	0	15.84
NED D9	4739	enhancer of filamentation 1 isoform 3	21542237 5	TGHG YVye YPSR	Y7(Phospho)	T(1): 0.0; Y(5): 0.0; Y(7): 100.0; Y(9): 0.0; S(11): 0.0	Y166	Y7;	21	1	RTGH GYVye EYPSR YQ	4.03	44	1508. 6203	0	12.77

SGK2 23	15728 5	tyrosi ne- protei n kinase SgK2 23	15790982 2	TlYLS PDSA VGVQ WPR	Y3(Pho spho); R17(La bel:13C (6))	T(1): 2.5; Y(3): 97.4; S(5): 0.1; S(6): 0.0; S(9): 0.0	Y487	Y3;	6	1	EEDH RTlYL SSPDS A	1.82	36	1961. 94353	0	0.25
EPHA 4	2043	ephrin type- A recept or 4 precur sor	4758280	TYVD PFTyE DPNQ AVR	Y2(Pho spho); Y8(Pho spho)	T(1): 50.0; Y(2): 50.0; T(7): 2.3; Y(8): 97.7	Y602	Y8;	6	1	TYVD PFTyE DPNQ AV	4.08	57	2074. 81767	0	40.00
BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1 isoform 7	28239812 3	DVPD GPLLR EEtYD VPPAF AK	R9(Lab el:13C( 6)); T12(Ph ospho); K21(La bel:13C (6))	T(12): 97.8; Y(13): 2.2	T324	T12;	4	1	GPLLR EEtYD VPPAF	3.30	50	2421. 18033	1	1.87
STAT 1	6772	signal transd ucer and activat or of transc ription	21536301	EAPEP MELD GPKG TGyIK	K12(La bel:13C (6)); Y16(Ph ospho); K18(La bel:13C (6))	T(14): 1.6; Y(16): 98.4	Y701	Y16;	6	1	DGPK GTGyI KTELI S	2.78	55	2023. 94853	1	0.27

		1-alpha/ beta isoform beta														
CFL1	1072	cofilin -1	5031635	NIILEE GKEIL VGDV GQTV DDPyA TFVK	Y23(Phospho)	T(18): 0.0; Y(23): 97.6; T(25): 2.4	Y68	Y23;	5	1	GQTV DDPyA TFVK ML	3.44	52	3142. 56296	1	0.55
MAP K14	1432	mitogen- activated protein kinase 14 isoform 3	20986514	HTDD EMTG yVATR	Y9(Phospho)	T(2): 0.0; T(7): 0.0; Y(9): 99.9; T(12): 0.1	Y182	Y9;	24	1	TDDE MTGy VATR WYR	5.29	49	1575. 61466	0	7.36
MAP K14	1432	mitogen- activated protein kinase 14 isoform 3	20986514	HTDD EMTG yVATR	Y9(Phospho); R13(Labeled:13C (6))	T(2): 0.0; T(7): 1.3; Y(9): 98.7; T(12): 0.0	Y182	Y9;	24	1	TDDE MTGy VATR WYR	5.29	92	1581. 63323	0	6.84

MAPK14	1432	mitogen-activated protein kinase 14 isoform 3	20986514	HTDD EMtGy VATR	T7(Phospho); Y9(Phospho); R13(Label:13C(6))	T(2): 0.0; T(7): 100.0; Y(9): 100.0; T(12): 0.0	T180; Y182	T7; Y9;	24	1	RHTD DEMtG YVAT RW;TD DEMT GyVA TRWY R	5.29	67	1661. 60198	0	2.52
MUC1	4582	mucin-1 isoform 15 precursor	324120968	DTYH PMSE YPTyH THGR	Y12(Phospho); R17(Label:13C(6))	T(2): 0.0; Y(3): 0.0; S(7): 0.0; Y(9): 0.0; T(11): 0.0; Y(12): 100.0; T(14): 0.0	Y198	Y12;	10	1	PMSE YPTyH THGR YV	3.50	29	2177. 88279	0	0.19
MUC1	4582	mucin-1 isoform 15 precursor	324120968	DTYH PMSEy PTyHT HGR	Y9(Phospho); Y12(Phospho); R17(Label:13C(6))	T(2): 0.0; Y(3): 0.0; S(7): 2.6; Y(9): 97.4; T(11): 2.6; Y(12): 97.4; T(14): 0.0	Y195; Y198	Y9; Y12;	10	1	TYHP MSEyP TYHT HG;PM SEYPT yHTH GRYV	3.50	29	2257. 85044	0	0.30
SHB	6461	SH2 domain-containing adapter	106879210	VTIAD DySDP FDAQ	Y7(Phospho); K14(Label:13C(6))	T(2): 0.0; Y(7): 97.9; S(8): 2.1	Y246	Y7;	5	1	KVTIA DDySD PFDA K	2.91	57	1642. 69707	0	0.22



		r protei n B														
YES1	7525	tyrosi ne- protei n kinase Yes	4885661	WTAP EAALy GR	Y9(Pho spho); R11(La bel:13C (6))	T(2): 0.0; Y(9): 100.0	Y446	Y9;	2	1	TAPEA ALyGR FTIKS	2.95	63	1320. 61443	0	1.00
EPHA 1	2041	ephrin type- A recept or 1 precur sor	22131665 0	ATDV DRED KLWL KPyVD LQAY EDPA QGAL DFTR	Y15(Ph ospho)	T(2): 0.3; Y(15): 99.7; Y(21): 0.0; T(32): 0.0	Y599	Y15;	5	1	DKLW LKPyV DLQA YE	4.14		3918. 86098	2	15.83
WAS L	8976	neural Wisko tt- Aldric h syndr ome protei n	51702526	ETSKV IyDFIE K	Y7(Pho spho)	T(2): 2.1; S(3): 2.1; Y(7): 95.8	Y256	Y7;	5	1	RETSK VIyDFI EKTG	2.60	30	1551. 7354	1	2.20
PKM	5315	pyruv ate kinase isozy mes M1/M	33286418	ITLDN AyME KCDE NILWL DYK	Y7(Pho spho); C11(Ca rbamid omethy l)	T(2): 3.1; Y(7): 96.9; Y(20): 0.0	Y148	Y7;	3	1	KITLD NAyM EKCD EN	2.53		2727. 2078	1	0.80

		2 isoform a														
PAR D3	56288	partiti oning defect ive 3 homol og isoform 7	29627819 8	DVTIG GSAPI yVK	Y11(Ph ospho); K13(La bel:13C (6))	T(3): 0.0; S(7): 0.0; Y(11): 100.0	Y445	Y11;	7	1	IGGSA PIyVK NILPR	2.27	57	1405. 70683	0	0.10
ITGB 1	3688	integri n beta-1 isoform 1A precursor	19743823	WDTG ENPIy K	Y9(Pho spho); K10(La bel:13C (6))	T(3): 0.0; Y(9): 100.0	Y783	Y9;	2	1	DTGE NPIyK SAVTT V	2.83	51	1308. 55998	0	0.67
ITGB 1	3688	integri n beta-1 isoform 1A precursor	19743823	WDTG ENPIy KSAV TTVV NPK	Y9(Pho spho)	T(3): 0.0; Y(9): 100.0; S(11): 0.0; T(14): 0.0; T(15): 0.0	Y783	Y9;	7	1	DTGE NPIyK SAVTT V	3.71	40	2299. 10063	1	0.74
SGK2 23	15728 5	tyrosi ne- protei n kinase SgK2 23	15790982 2	EATQP EPIyA ESTKR	Y9(Pho spho)	T(3): 0.0; Y(9): 100.0; S(12): 0.0; T(13): 0.0	Y411	Y9;	6	1	ATQPE PIyAE STKR K	2.57	40	1799. 82207	1	0.09

ITGB1	3688	integrin beta-1 isoform 1A precursor	19743823	WDTG ENPIy KSAV TTVV NPK	K10(La bel:13C (6)); S11(Ph ospho); K20(La bel:13C (6))	T(3): 0.0; Y(9): 98.2; S(11): 1.8; T(14): 0.0; T(15): 0.0	Y783	Y9;	7	1	DTGE NPIyK SAVTT V	3.71	53	2311. 14145	1	0.59
SGK223	157285	tyrosine-kinase SgK223	157909822	EATQP EPIyA ESTK	Y9(Pho spho); K14(La bel:13C (6))	T(3): 0.0; Y(9): 99.8; S(12): 0.1; T(13): 0.1	Y411	Y9;	7	1	ATQPE PIyAE STKR K	2.72	31	1649. 7404	0	0.11
MAPK7	5598	mitogen-activated protein kinase 7 isoform 2	20986499	GLCTS PAEH QYFM TEyVA TR	C3(Car bamido methyl) ; Y16(Ph ospho); R20(La bel:13C (6))	T(4): 0.0; S(5): 0.0; Y(11): 0.0; T(14): 1.9; Y(16): 96.1; T(19): 1.9	Y82	Y16;	10	1	HQYF MTEy VATR WYR	3.61	40	2447. 05034	0	0.21
WASL	8976	neural Wiskott-Aldrich syndrome protei	51702526	DRETS KVIyD FIEK	Y9(Pho spho)	T(4): 0.0; S(5): 0.0; Y(9): 100.0	Y256	Y9;	2	1	RETSK VIyDFI EKTG	3.56		1822. 85666	2	2.51

		n														
BCA R3	8412	breast cancer anti- estrog en resista nce protei n 3 isofo r m 1	38715790 6	HGETF TFRDP HLLDP TVEyV K	Y19(Ph ospho)	T(4): 0.0; T(6): 0.0; T(16): 0.0; Y(19): 100.0	Y117	Y19;	12	1	LLDPT VEyV KFSKE R	4.55	36	2581. 20334	1	1.91
BCA R3	8412	breast cancer anti- estrog en resista nce protei n 3 isofo r m 1	38715790 6	HGETF TFRDP HLLDP TVEyV KFSK	Y19(Ph ospho)	T(4): 0.0; T(6): 0.0; T(16): 0.0; Y(19): 96.9; S(23): 3.1	Y117	Y19;	21	1	LLDPT VEyV KFSKE R	4.09		2943. 41201	2	3.83
BCA R3	8412	breast cancer anti- estrog en resista nce protei	38715790 6	HGETF TFRDP HLLDP TVEyV KFSK	Y19(Ph ospho)	T(4): 0.0; T(6): 0.0; T(16): 2.6; Y(19): 97.4; S(23): 0.0	Y117	Y19;	21	1	LLDPT VEyV KFSKE R	4.09		2943. 4094	2	3.55

		n 3 isoform 1														
BCAR3	8412	breast cancer anti-estrogen resistance protein 3 isoform 1	387157906	HGETF TFRDP HLLDP TVEyV K	Y19(Phospho)	T(4): 0.0; T(6): 0.0; T(16): 2.7; Y(19): 97.3	Y117	Y19;	12	1	LLDPT VEyV KFSKE R	4.55	2581.20498	1	4.54	
PTPN11	5781	tyrosine-protein phosphatase non-receptor type 11 isoform 1	33356177	IQNTG DyYD LYGG EK	Y7(Phospho)	T(4): 0.0; Y(7): 98.2; Y(8): 1.8; Y(11): 0.0	Y62	Y7;	6	1	KIQNT GDyY DLYG GE	3.75	1815.74773	0	3.80	

PABP C1	26986	polyadenylation protein 1	46367787	IVATK PLyVA LAQR	K5(Label:13C(6)); Y8(Phospho); R14(Label:13C(6))	T(4): 0.0; Y(8): 100.0	Y364	Y8;	2	1	IVATK PLyVA LAQR K	3.06	56	1634. 94182	0	1.01
SHB	6461	SH2 domain-containing adapter protein B	106879210	DKVTI ADDyS DPFD AKND LK	Y9(Phospho)	T(4): 0.0; Y(9): 97.6; S(10): 2.4	Y246	Y9;	11	1	KVTIA DDySD PFDA K	4.43	36	2350. 04422	2	0.25
SHB	6461	SH2 domain-containing adapter protein B	106879210	DKVTI ADDyS DPFD AK	K2(Label:13C(6)); Y9(Phospho); K16(Label:13C(6))	T(4): 0.0; Y(9): 98.0; S(10): 1.9	Y246	Y9;	10	1	KVTIA DDySD PFDA K	4.28	53	1891. 83908	1	0.24
SHB	6461	SH2 domain-containing adapter	106879210	DKVTI ADDyS DPFD AK	Y9(Phospho)	T(4): 0.0; Y(9): 98.4; S(10): 1.6	Y246	Y9;	10	1	KVTIA DDySD PFDA K	4.28	83	1879. 8029	1	0.22

		prote in B														
IQGA P1	8826	ras GTPa se- activat ing- like protei n IQGA P1	4506787	LQQTy AALN SK	Y5(Pho spho)	T(4): 2.0; Y(5): 98.0; S(10): 0.0	Y1510	Y5;	4	1	LVKL QQTy AALN SKA	2.48	50	1316. 62273	0	3.75
CDK1	983	cyclin - depen dent kinase 1 isoform 2	16306492	IGEGT YGVV yKGR	Y10(Ph ospho)	T(5): 0.0; Y(6): 0.0; Y(10): 100.0	Y19	Y10;	15	1	EGTY GVVY KGRH KTT	3.74	46	1478. 70362	1	2.04
CDK1	983	cyclin - depen dent kinase 1 isoform 2	16306492	IGEGT YGVV yKGR	Y10(Ph ospho)	T(5): 0.0; Y(6): 0.0; Y(10): 100.0	Y19	Y10;	15	1	EGTY GVVY KGRH KTT	3.74	81	1478. 70439	1	1.82

IL18	3606	interleukin-18 isoform 1 proprotein	4504653	FIDNT LYFIA EDDE NLESD yFGKL ESK	Y20(Phospho)	T(5): 0.0; Y(7): 0.0; S(18): 2.5; Y(20): 97.5; S(26): 0.0	Y37	Y20;	7	1	DENL ESDyF GKLES K	3.90	52	3295. 46445	1	5.38
CDK5	1020	cyclin-dependent kinase 5 isoform 2	256542306	IGEGT yGTVF K	Y6(Phospho); K11(Label:13C(6))	T(5): 1.4; Y(6): 98.6; T(8): 0.0	Y15	Y6;	5	1	EKIGE GTyGT VFKA K	2.72	60	1257. 58391	0	1.33
CDK1	983	cyclin-dependent kinase 1 isoform 2	16306492	IGEGty GVVY KGR	T5(Phospho); Y6(Phospho)	T(5): 100.0; Y(6): 100.0; Y(10): 0.0	T14; Y15	T5; Y6;	15	1	IEKIG EGtYG VVYK G;EKI GEGTy GVVY KGR	3.74	70	1558. 66948	1	1.00
BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform	282398123	RPGPG TLyDV PR	Y8(Phospho)	T(6): 0.0; Y(8): 100.0	Y385	Y8;	7	1	RPGPG TLyDV PRERV	3.00	29	1407. 67618	0	1.79



		m 7														
ANP3 2A	8125	acidic leucin e-rich nuclea r phosp hoprot ein 32 family memb er A	5453880	LLPQL TYLD GyDR	Y11(Ph ospho)	T(6): 0.1; Y(7): 2.3; Y(11): 97.6	Y148	Y11;	4	1	QLTY LDGy DRDD KEA	1.98	43	1646. 78301	0	0.40
MAP K13	5603	mitog en- activat ed protei n kinase 13	4506085	HADA EMTG yVVTR	Y9(Pho spho); R13(La bel:13C (6))	T(7): 0.0; Y(9): 100.0; T(12): 0.0	Y182	Y9;	121	1	ADAE MTGy VVTR WYR	4.95	87	1535. 66411	0	4.28
MAP K13	5603	mitog en- activat ed protei n kinase 13	4506085	HADA EMTG yVVTR	M6(Oxi dation); Y9(Pho spho)	T(7): 0.1; Y(9): 99.9; T(12): 0.0	Y182	Y9;	121	1	ADAE MTGy VVTR WYR	4.95	44	1545. 63901	0	5.04

MAPK13	5603	mitogen-activated protein kinase 13	4506085	HADAE EMTGY VVTR	M6(Oxidation); Y9(Phospho); R13(Label:13C(6))	T(7): 2.0; Y(9): 96.0; T(12): 2.0	Y182	Y9;	121	1	ADAE MTGY VVTR WYR	4.95	70	1551.65996	0	4.75
ERBB2	2064	receptor tyrosine-kinase erbB-2 isoform b	54792098	LLDIDE ETeYH ADGG KVPIK	Y9(Phospho)	T(7): 2.6; Y(9): 97.4	Y847	Y9;	4	1	LDIDE TEyHA DGGK V	3.63		2193.05802	1	1.95
EPHA1	2041	ephrin type-A receptor 1 precursor	221316650	LLDDF DGTyE TQGG KIPIR	Y9(Phospho)	T(8): 0.0; Y(9): 100.0; T(11): 0.0	Y781	Y9;	15	1	LDDF DGTyE TQGG KI	4.49	60	2218.04038	1	10.75
CDK2	1017	cyclin-dependent kinase 2 isoform	166362719	VEKIGE EGTyG VVYK	Y9(Phospho)	T(8): 0.0; Y(9): 100.0; Y(13): 0.0	Y15	Y9;	15	1	EKIGE GTyG VVYK AR	4.50	65	1621.78789	1	1.25

		m 2														
BCAR3	8412	breast cancer anti-estrogen resistance protein 3 isoform 1	387157906	DPHLLDPTVEyVK	Y11(Phospho)	T(8): 0.1; Y(11): 99.9	Y117	Y11;	4	1	LLDPTVEyVKFSKER	1.85	31	1605.75945	0	4.21
C11orf52	91894	uncharacterized protein C11orf52	131889517	HVHLENATyATLR	Y10(Phospho)	T(8): 1.5; Y(10): 98.5; T(12): 0.0	Y103	Y10;	11	1	HLENATyATLRFPQ	3.45	58	1733.79949	0	2.37
CDK1	983	cyclin-dependent kinase 1 isoform 2	16306492	IEKIGEGTyGVVYK	K3(Label:13C(6)); Y9(Phospho); K14(Label:13C(6))	T(8): 1.6; Y(9): 98.4; Y(13): 0.0	Y15	Y9;	8	1	EKIGEGTyGVVYKGR	5.70	64	1647.8416	1	2.45
CDK1	983	cyclin-dependent	16306492	IEKIGEGTyGVVYK	Y9(Phospho)	T(8): 1.6; Y(9): 98.4; Y(13): 0.0	Y15	Y9;	8	1	EKIGEGTyGVVYKGR	5.70	51	1635.80252	1	2.48

		kinase 1 isoform 2														
CDK1	983	cyclin - depend ent kinase 1 isoform 2	16306492	IEKIG EGtyG VVYK	T8(Pho spho); Y9(Pho spho)	T(8): 100.0; Y(9): 100.0; Y(13): 0.0	T14; Y15	T8; Y9;	8	1	IEKIG EGtyG VVYK G;EKI GEGTy GVVY KGR	5.70	71	1715. 76995	1	1.01
CDK1	983	cyclin - depend ent kinase 1 isoform 2	16306492	IEKIG EGtyG VVYK GR	T8(Pho spho); Y9(Pho spho)	T(8): 100.0; Y(9): 100.0; Y(13): 0.0	T14; Y15	T8; Y9;	8	1	IEKIG EGtyG VVYK G;EKI GEGTy GVVY KGR	4.35	73	1928. 89372	2	0.93
CDK1	983	cyclin - depend ent kinase 1 isoform 2	16306492	IEKIG EGtyG VVYK GR	T8(Pho spho); Y9(Pho spho)	T(8): 100.0; Y(9): 100.0; Y(13): 0.0	T14; Y15	T8; Y9;	8	1	IEKIG EGtyG VVYK G;EKI GEGTy GVVY KGR	4.35	47	1928. 89267	2	0.90
CDK2	1017	cyclin - depend ent kinase	16636271 9	VEKIG EGtyG VVYK	T8(Pho spho); Y9(Pho spho)	T(8): 100.0; Y(9): 100.0; Y(13): 0.0	T14; Y15	T8; Y9;	15	1	VEKIG EGtyG VVYK A;EKI GEGTy	4.50	91	1701. 75395	1	0.42

		2 isoform 2									GVVY KAR					
CDK1	983	cyclin - depend ent kinase 1 isoform 2	16306492	IEKIG EGTyG VVYK	T8(Pho spho); Y9(Pho spho)	T(8): 100.0; Y(9): 99.9; Y(13): 0.1	T14; Y15	T8; Y9;	8	1	IEKIG EGTyG VVYK G;EKI GEGTy GVVY KGR	5.70	59	1715. 76889	1	1.00
CDK2	1017	cyclin - depend ent kinase 2 isoform 2	16636271 9	VEKIG EGTyG VVYK	Y9(Pho spho)	T(8): 2.0; Y(9): 98.0; Y(13): 0.0	Y15	Y9;	15	1	EKIGE GTyG VVYK AR	4.50	55	1621. 78562	1	1.27
SDCB P	6386	synten in-1 isoform 1	56243522	VDKVI QAQT AFSA NPAN PAILS EASAP IPHDG NLYPR	Y35(Pho spho)	T(9): 0.0; S(12): 0.0; S(22): 0.0; S(25): 0.0; Y(35): 100.0	Y46	Y35;	9	1	IPHDG NLYPR LYPEL	5.07	44	3952. 95547	1	0.53
SDCB P	6386	synten in-1 isoform 1	56243522	VDKVI QAQT AFSA NPAN PAILS EASAP	Y35(Pho spho)	T(9): 0.0; S(12): 0.0; S(22): 0.0; S(25): 0.0; Y(35): 100.0	Y46	Y35;	9	1	IPHDG NLYPR LYPEL	5.07		3952. 95957	1	0.53

				IPHDG NlyPR												
MAP K1	5594	mitog en- activat ed protei n kinase 1	66932916	VADP DHDH TGFLT EyVAT R	Y15(Ph ospho)	T(9): 0.0; T(13): 0.0; Y(15): 100.0; T(18): 0.0	Y187	Y15;	28	1	HTGFL TEyVA TRWY R	5.53	47	2223. 98746	0	1.80
MAP K1	5594	mitog en- activat ed protei n kinase 1	66932916	VADP DHDH TGFLT EyVAT R	Y15(Ph ospho)	T(9): 0.0; T(13): 0.0; Y(15): 100.0; T(18): 0.0	Y187	Y15;	28	1	HTGFL TEyVA TRWY R	5.53	64	2223. 97295	0	1.61
MAP K1	5594	mitog en- activat ed protei n kinase 1	66932916	VADP DHDH TGFLT EyVAT R	Y15(Ph ospho)	T(9): 0.0; T(13): 0.0; Y(15): 100.0; T(18): 0.0	Y187	Y15;	28	1	HTGFL TEyVA TRWY R	5.53	49	2223. 97116	0	1.54

MAP K3	5595	mitog en- activat ed protei n kinase 3 isofor m 3	15813850 7	IADPE HDHT GFLTE yVATR	Y15(Ph ospho)	T(9): 0.0; T(13): 0.0; Y(15): 99.9; T(18): 0.0	Y204	Y15;	14	1	HTGFL TEyVA TRWY R	5.36	57	2252. 00553	0	2.87
MAP K3	5595	mitog en- activat ed protei n kinase 3 isofor m 3	15813850 7	IADPE HDHT GFLTE yVATR	Y15(Ph ospho)	T(9): 0.0; T(13): 0.1; Y(15): 97.6; T(18): 2.4	Y204	Y15;	14	1	HTGFL TEyVA TRWY R	5.36	65	2252. 00762	0	3.19
MAP K1	5594	mitog en- activat ed protei n kinase 1	66932916	VADP DHDH TGFLT EyVAT R	Y15(Ph ospho)	T(9): 0.0; T(13): 0.1; Y(15): 99.9; T(18): 0.0	Y187	Y15;	28	1	HTGFL TEyVA TRWY R	5.53	58	2223. 99346	0	1.64
MAP K1	5594	mitog en- activat ed protei	66932916	VADP DHDH TGFLt EyVAT R	T13(Ph ospho); Y15(Ph ospho)	T(9): 0.0; T(13): 100.0; Y(15): 100.0;	T185; Y187	T13; Y15;	28	1	HDHT GFLtE YVAT RW;HT GFLTE	5.53	65	2303. 93755	0	4.01

		n kinase 1				T(18): 0.0					yVATR WYR					
MAP K1	5594	mitog en- activat ed protei n kinase 1	66932916	VADP DHDH TGFLt EyVAT R	T13(Ph ospho); Y15(Ph ospho)	T(9): 0.0; T(13): 100.0; Y(15): 100.0; T(18): 0.0	T185; Y187	T13; Y15;	28	1	HDHT GFLtE YVAT RW;HT GFLTE yVATR WYR	5.53	39	2303. 93955	0	3.65
MAP K3	5595	mitog en- activat ed protei n kinase 3 isofor m 3	15813850 7	IADPE HDHT GFLtE yVATR	T13(Ph ospho); Y15(Ph ospho)	T(9): 0.0; T(13): 100.0; Y(15): 100.0; T(18): 0.0	T202; Y204	T13; Y15;	14	1	HDHT GFLtE YVAT RW;HT GFLTE yVATR WYR	5.36	66	2331. 9644	0	1.66
MAP K3	5595	mitog en- activat ed protei n kinase 3 isofor m 3	15813850 7	IADPE HDHT GFLtE yVATR	T13(Ph ospho); Y15(Ph ospho)	T(9): 0.0; T(13): 100.0; Y(15): 99.9; T(18): 0.1	T202; Y204	T13; Y15;	14	1	HDHT GFLtE YVAT RW;HT GFLTE yVATR WYR	5.36	49	2331. 96183	0	1.79



CTN ND1	1500	catenin delta-1 isoform 2A	33268822 2	YRPS MEGy R	R2(Lab el:13C(6)); Y8(Phospho); R9(Lab el:13C(6))	Y(1): 0.0; S(4): 0.0; Y(8): 100.0	Y194	Y8;	3	1	YRPS MEGy RAPS R QD	2.47	30	1250. 54119	0	1.45
CAV1	857	caveolin-1 isoform alpha	15451856	YVDS EGHLY TVPIR	T10(Phospho); R14(Lab el:13C(6))	Y(1): 0.0; S(4): 0.0; Y(9): 100.0; T(10): 0.0	Y14	Y9;	11	1	VDSE GHLYT VPIR Q	4.49	94	1734. 81951	0	2.02
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyYK	M2(Oxidation); Y7(Phospho); K9(Lab el:13C(6))	Y(1): 0.0; S(5): 0.0; T(6): 0.0; Y(7): 98.2; Y(8): 1.7	Y576	Y7;	16	1	RYME DSTyY KASK GK	2.39	57	1301. 47331	0	2.34
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyyK ASK	Y7(Phospho); Y8(Phospho)	Y(1): 0.0; S(5): 0.0; T(6): 0.1; Y(7): 99.9; Y(8): 99.9; S(11): 0.1	Y576; Y577	Y7; Y8;	7	1	RYME DSTyY KASK GK;Y MEDS TYyK ASKG KL	2.85	49	1645. 58823	1	3.11

PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyYK ASK	Y7(Phospho)	Y(1): 0.0; S(5): 0.0; T(6): 1.6; Y(7): 96.7; Y(8): 1.6; S(11): 0.0	Y576	Y7;	7	1	RYME DSTyYKASK GK	2.85	48	1565.62223	1	2.73
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyYK	Y7(Phospho); K9(Label:13C(6))	Y(1): 0.0; S(5): 0.0; T(6): 1.8; Y(7): 96.4; Y(8): 1.8	Y576	Y7;	16	1	RYME DSTyYKASK GK	2.39	48	1285.47783	0	2.32
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyYK ASK	Y7(Phospho)	Y(1): 0.0; S(5): 0.0; T(6): 1.8; Y(7): 96.4; Y(8): 1.8; S(11): 0.0	Y576	Y7;	7	1	RYME DSTyYKASK GK	2.85	59	1565.62273	1	2.37
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMED STyyK	Y7(Phospho); Y8(Phospho); K9(Label:13C(6))	Y(1): 0.0; S(5): 0.0; T(6): 1.9; Y(7): 98.1; Y(8): 100.0	Y576; Y577	Y7; Y8;	16	1	RYME DSTyYKASK GK; YMEDS TyyK ASK GK KL	2.39	45	1365.44377	0	3.12

PTK2	5747	focal adhesion kinase 1 isoform a	24476013	YMEDSTyyKASK	Y7(Phospho); Y8(Phospho)	Y(1): 0.0; S(5): 2.1; T(6): 2.1; Y(7): 96.0; Y(8): 99.9; S(11): 0.0	Y576; Y577	Y7; Y8;	7	1	RYMEDSTyYKASKGK;YMEDSTYyKASKGKL	2.85	52	1645.58769	1	3.24
STAT3	6774	signal transducer and activator of transcription 3 isoform 3	47458820	YCRPE SQEHP EADP GSAA PyLK	C2(Carbamidomethyl); Y20(Phospho)	Y(1): 0.0; S(6): 0.0; S(16): 0.0; Y(20): 100.0	Y705	Y20;	4	1	DPGSAAPyLKTKFIC	4.49	38	2582.10221	0	0.76
STAT3	6774	signal transducer and activator of transcription 3 isoform 3	47458820	YCRPE SQEHP EADP GSAA PyLK	C2(Carbamidomethyl); Y20(Phospho)	Y(1): 0.0; S(6): 0.0; S(16): 2.5; Y(20): 97.5	Y705	Y20;	4	1	DPGSAAPyLKTKFIC	4.49	40	2582.10259	0	0.76

STAT3	6774	signal transducer and activator of transcription 3 isoform 2	21618338	YCRPE SQEHP EADP GAAPy LK	C2(Carbamido methyl); Y19(Phospho)	Y(1): 0.0; S(6): 0.0; Y(19): 100.0	Y704	Y19;	4	1	ADPG AAPyL KTKFI C	3.90		2495.0689	0	0.92
STAT3	6774	signal transducer and activator of transcription 3 isoform 2	21618338	YCRPE SQEHP EADP GAAPy LK	C2(Carbamido methyl); Y19(Phospho)	Y(1): 0.0; S(6): 0.0; Y(19): 100.0	Y704	Y19;	4	1	ADPG AAPyL KTKFI C	3.90	31	2495.06852	0	0.85
EEF1A1	1915	elongation factor 1-alpha 1	4503471	YEEIV KEVST yIK	K6(Label:13C(6)); Y11(Phospho); K13(Label:13C(6))	Y(1): 0.0; S(9): 0.0; T(10): 1.4; Y(11): 98.5	Y177	Y11;	5	1	IVKEV STyIK KIGYN	3.09	65	1692.85283	1	0.69

SCEL	8796	sciellin isoform 3	238908501	YIQTVySTSDR	Y6(Phospho)	Y(1): 0.0; T(4): 0.0; Y(6): 98.2; S(7): 1.7; T(8): 0.0; S(9): 0.0	Y566	Y6;	8	1	GKYYIQTVySTSDRSV	2.18	52	1412.61003	0	12.69
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-interacting protein precursor	4757886	YGLFKEENPyAR	Y10(Phospho)	Y(1): 0.0; Y(10): 100.0	Y174	Y10;	8	1	LFKEENPyARFENN	3.93	50	1566.70024	1	0.23
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-	4757886	YGLFKEENPyAR	Y10(Phospho)	Y(1): 0.0; Y(10): 100.0	Y174	Y10;	8	1	LFKEENPyARFENN	3.93	50	1566.69889	1	0.20

		interacting protein precursor														
LPP	4026	lipoma-preferred partner isoform a	5031887	YYEG YyAA GPGY GGR	Y6(Phospho)	Y(1): 0.0; Y(2): 0.0; Y(5): 2.3; Y(6): 97.7; Y(12): 0.0	Y301	Y6;	6	1	GRYY EGYy AAGP GYG	2.63	44	1723. 67766	0	2.01
CFL1	1072	cofilin-1	5031635	YALY DATyE TKESK	Y8(Phospho)	Y(1): 0.0; Y(4): 0.0; T(7): 0.0; Y(8): 98.0; T(10): 2.0; S(13): 0.0	Y89	Y8;	23	1	YALY DATyE TKESK K	3.51	37	1761. 76279	1	1.08
CFL1	1072	cofilin-1	5031635	YALY DATyE TK	Y8(Phospho)	Y(1): 0.0; Y(4): 0.0; T(7): 1.8; Y(8): 98.2; T(10): 0.0	Y89	Y8;	6	1	YALY DATyE TKESK K	3.02	50	1417. 59233	0	0.95
CFL1	1072	cofilin-1	5031635	YALY DATyE TKESK	Y8(Phospho)	Y(1): 0.0; Y(4): 0.0; T(7): 2.0; Y(8): 98.0; T(10): 0.0; S(13): 0.0	Y89	Y8;	23	1	YALY DATyE TKESK K	3.51	70	1761. 76128	1	0.82

PI4K A	5297	phosphatidylinositol 4-kinase alpha isoform 1	348041302	YAGE VyGMI R	Y6(Phospho); R10(Label:13C (6))	Y(1): 0.0; Y(6): 100.0	Y1154	Y6;	3	1	NRYA GEVy GMIRF SG	2.29	44	1244. 54643	0	0.88
PTK2 B	2185	protein-tyrosine kinase 2-beta isoform b	27886588	YIEDE DyyKA SVTRL PIK	Y7(Phospho); Y8(Phospho)	Y(1): 0.0; Y(7): 100.0; Y(8): 100.0; S(11): 0.0; T(13): 0.0	Y579; Y580	Y7; Y8;	27	1	RYIED EDyY KASV TR;YIE DEDY yKASV TRL	3.60	56	2363. 0667	2	2.85
PTK2 B	2185	protein-tyrosine kinase 2-beta isoform b	27886588	YIEDE DyyKA SVTRL PIK	Y7(Phospho); Y8(Phospho)	Y(1): 0.0; Y(7): 100.0; Y(8): 100.0; S(11): 0.0; T(13): 0.0	Y579; Y580	Y7; Y8;	27	1	RYIED EDyY KASV TR;YIE DEDY yKASV TRL	3.60	34	2363. 0643	2	2.72
PTK2 B	2185	protein-tyrosine kinase 2-beta isoform b	27886588	YIEDE DyyKA SVTR	Y7(Phospho); Y8(Phospho)	Y(1): 0.0; Y(7): 100.0; Y(8): 100.0; S(11): 0.0; T(13): 0.0	Y579; Y580	Y7; Y8;	10	1	RYIED EDyY KASV TR;YIE DEDY yKASV TRL	2.89	58	1911. 74358	1	1.97

S100 A11	6282	protein S100- A11	5032057	YAGK DGyN YTLSK	Y7(Pho spho)	Y(1): 0.0; Y(7): 100.0; Y(9): 0.0; T(10): 0.0; S(12): 0.0	Y30	Y7;	4	1	KYAG KDy NYTLS KT	3.14	38	1559. 67851	1	0.75
MYO 1B	4430	uncon ventio nal myosi n-Ib isoform 2	44889481	yFLEM K	Y1(Pho spho); M5(Oxi dation)	Y(1): 100.0	Y823	Y1;	2	1	LQRIV QKyFL EMKN K	1.25	26	926.3 8127	0	3.02
VTA1	51534	vacuol ar protei n sortin g- associ ated protei n VTA1 homol og	21361741	yAGSA LQYE DVST AVQN LQK	Y1(Pho spho)	Y(1): 100.0; S(4): 0.0; Y(8): 0.0; S(12): 0.0; T(13): 0.0	Y278	Y1;	13	1	RAQK YCKy AGSA LQY	4.69	71	2265. 0463	0	3.22
PPP1 CA	5499	serine/ threon ine- protei n phosp hatase PP1-	45827798	yGQFS GLNP GGRPI TPPR	Y1(Pho spho)	Y(1): 100.0; S(5): 0.0; T(15): 0.0	Y262	Y1;	4	1	ADKN KGKy GQFS GLN	2.36	30	1993. 97312	0	4.19



		alpha catalytic subunit isoform 2														
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	yMEDSTYYK	Y1(Phospho)	Y(1): 100.0; S(5): 0.0; T(6): 0.0; Y(7): 0.0; Y(8): 0.0	Y570	Y1;	16	1	GDFGLSRyMEDSTY Y	2.39	63	1279.4594	0	0.75
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	yMEDSTyYK	Y1(Phospho); Y7(Phospho)	Y(1): 100.0; S(5): 0.1; T(6): 2.2; Y(7): 95.6; Y(8): 2.2	Y570; Y576	Y1; Y7;	16	1	GDFGLSRyMEDSTY Y;RY MEDS TyYK ASKG K	2.39	41	1359.42473	0	2.16
PDLIM5	10611	PDZ and LIM domain protein 5 isoform g	374093210	yTEFYHVPTHSDASK	Y1(Phospho)	Y(1): 100.0; T(2): 0.0; Y(5): 0.0; T(9): 0.0; S(11): 0.0; S(14): 0.0	Y144	Y1;	19	1	RKHIV ERyTE FYHV P	4.45	30	1861.77811	0	1.84

ATIC	471	bifunctional purine biosynthesis protein PURH	20127454	yGMN PHQTP AQLY TLQPK	Y1(Phospho); K18(Label:13C(6))	Y(1): 100.0; T(8): 0.0; Y(13): 0.0; T(14): 0.0	Y208	Y1;	8	1	VSQM PLRyG MNPHT QT	4.23	45	2173.02573	0	0.59
ATIC	471	bifunctional purine biosynthesis protein PURH	20127454	yGMN PHQTP AQLY TLQPK	Y1(Phospho); K18(Label:13C(6))	Y(1): 100.0; T(8): 0.0; Y(13): 0.0; T(14): 0.0	Y208	Y1;	8	1	VSQM PLRyG MNPHT QT	4.23		2173.02593	0	0.54
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-interacting protein precursor	4757886	yGLFK EENPY AR	Y1(Phospho)	Y(1): 100.0; Y(10): 0.0	Y165	Y1;	8	1	HDEIR KKyG LFKEE N	3.93	59	1566.70061	1	0.16

PTTG 1IP	754	pituitary tumor- transforming gene 1 protein- interacting protein precursor	4757886	yGLFK EENPY AR	Y1(Phospho); K5(Label:13C(6)); R12(Label:13C(6))	Y(1): 100.0; Y(10): 0.0	Y165	Y1;	8	1	HDEIR KKyG LFKEE N	3.93	41	1578. 7399	1	0.15
DSC3	1825	desmollin-3 isoform Dsc3b prepro protein	14853984 8	YTySE WHSF TQPR	Y3(Phospho); R13(Label:13C(6))	Y(1): 2.0; T(2): 2.0; Y(3): 94.0; S(4): 2.0; S(8): 0.0; T(10): 0.0	Y818	Y3;	8	1	VDNC RYTyS EWHS FT	2.20	58	1787. 75078	0	0.23
IFNG R1	3459	interferon gamma receptor 1 precursor	4557880	yVSLI TSYQP FSLEK	Y1(Phospho)	Y(1): 97.1; S(3): 2.9; T(6): 0.0; S(7): 0.0; Y(8): 0.0; S(12): 0.0	Y304	Y1;	5	1	ETKPE SKyVS LITSY	2.18	35	1854. 8958	0	1.38

MTHFS	10588	5-formyltetrahydrofolate cyclo-ligase isoform b	315113868	yRFQSNHMDMVR	Y1(Phospho)	Y(1): 97.3; S(5): 2.7	Y26	Y1;	6	1	KICFIP RyRFQ SNHM	3.05	1663.68747	1	0.86	
DTNB	1838	dystrobrevin beta isoform 8	372626425	yVFSQMSDSNGLMIFSK	S7(Phospho); M13(Oxidation)	Y(1): 99.8; S(4): 0.0; S(7): 0.2; S(9): 0.0; S(16): 0.0	Y93	Y1;	2	1	KMLDKLRyVFSQMSD	2.11	2049.90361	0	5.19	
VTA1	51534	vacuolar protein sorting-associated protein VTA1 homolog	21361741	yAGSALQYEDVSTAVQNLQK	Y1(Phospho)	Y(1): 99.9; S(4): 0.1; Y(8): 0.0; S(12): 0.0; T(13): 0.0	Y278	Y1;	13	1	RAQKYCKyAGSALQY	4.69	77	2265.04814	0	2.93
EPHA4	2043	ephrin type-A receptor 4 precursor	4758280	VLEDPEAAytTR	Y10(Phospho)	Y(10): 1.8; T(11): 96.4; T(12): 1.8	T780	T11;	5	1	DDPEAAytTRGGKIP	3.31	45	1559.6635	0	17.70

		sor														
NED D9	4739	enhancer of filamentation 1 isoform 3	215422375	DEAG LREK DyDFP PPMR	R6(Label:13C(6)); K8(Label:13C(6)); Y10(Phospho); R17(Label:13C(6))	Y(10): 100.0	Y241	Y10;	30	1	AGLR EKDy DFPPP MR	4.29	42	2133. 98142	2	14.12
NED D9	4739	enhancer of filamentation 1 isoform 3	215422375	DEAG LREK DyDFP PPMR	Y10(Phospho)	Y(10): 100.0	Y241	Y10;	30	1	AGLR EKDy DFPPP MR	4.29	49	2115. 91948	2	22.74
NED D9	4739	enhancer of filamentation 1 isoform 3	215422375	DEAG LREK DyDFP PPMR	Y10(Phospho)	Y(10): 100.0	Y241	Y10;	30	1	AGLR EKDy DFPPP MR	4.29	31	2115. 93271	2	13.28
NED D9	4739	enhancer of filamentation 1	215422375	ANPQ ERDG VyDVP LHNPP DAK	Y10(Phospho)	Y(10): 100.0	Y345	Y10;	2	1	PQER DGVy DVPL HNP	4.45		2412. 0972	1	10.79

		isoform 3														
TNS3	64759	tensin-3	65288071	QQQM VVAH QySFA PDGE AR	Y10(Phospho)	Y(10): 100.0; S(11): 0.0	Y601	Y10;	4	1	QMVV AHQyS FAPD GE	3.79	33	2241. 97702	0	2.15
TYK2	7297	non-receptor tyrosine-kinase TYK2	187608615	LLAQ AEGEP CyIR	C10(Carbamidomethyl); Y11(Phospho); R13(Label:13C(6))	Y(11): 100.0	Y292	Y11;	4	1	QAEG EPCyI RDSG VA	3.65	56	1605. 74419	0	1.32
TJP2	9414	tight junction protein ZO-2 isoform 4	282165804	IEIAQ KHPDI yAVPI K	K6(Label:13C(6)); Y11(Phospho); K16(Label:13C(6))	Y(11): 100.0	Y1085	Y11;	4	1	AQKH PDIyA VPIKT H	4.24	43	1927. 06279	1	1.38
BCAR1	9564	breast cancer anti-estrogen resistance protein	282398123	HLLAP GPQDI yDVPP VR	Y11(Phospho)	Y(11): 100.0	Y247	Y11;	12	1	APGP QDIyD VPPVR G	3.89	83	1966. 97685	0	1.97

		n 1 isoform 7														
TJP2	9414	tight junction protein ZO-2 isoform 4	282165804	IEIAQKHPDIyAVPIK	Y11(Phospho)	Y(11): 100.0	Y1085	Y11;	4	1	AQKH PDIyA VPIKTH	4.24		1915.02005	1	1.32
TKT	7086	transketolase isoform 1	4507521	NMAEQIIQEIySQIQSK	Y11(Phospho)	Y(11): 98.3; S(12): 1.7; S(16): 0.0	Y275	Y11;	10	1	EQIIQ ElySQI QSKK	2.98	48	2102.98239	0	2.10
CTNNA1	1495	catenin alpha-1	55770844	NAGNEQDLGIQyK	Y12(Phospho); K13(Label:13C(6))	Y(12): 100.0	Y177	Y12;	2	1	EQDL GIQyK ALKPEV	3.49	41	1535.68535	0	0.82
BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 7	282398123	GPNGRDPLLEVyDVPPSV EK	Y12(Phospho)	Y(12): 100.0; S(17): 0.0	Y285	Y12;	8	1	RDPLLEVyDVPPSVE	3.33		2261.08574	1	3.83

BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1 isoform 7	28239812 3	GPNG RDPLL EVyD VPPSV EK	Y12(Ph ospho)	Y(12): 100.0; S(17): 0.0	Y285	Y12;	8	1	RDPLL EVyD VPPSV E	3.33		2261. 08646	1	0.91
VCL	7414	vincul in isoform meta- VCL	7669550	ILLRN PGNQ AAyE HFET MK	R4(Lab el:13C( 6)); Y12(Ph ospho); K19(La bel:13C (6))	Y(12): 100.0; T(17): 0.0	Y692	Y12;	4	1	NPGN QAAy EHFET MK	4.50	41	2324. 13169	1	0.69
ARH GAP4 2	14387 2	rho GTPa se- activat ing protei n 42	22130757 5	KLWL EAMD GKEPI yTLPA IISK	Y14(Ph ospho)	Y(14): 100.0; T(15): 0.0; S(21): 0.0	Y376	Y14;	5	1	MDGK EPIyTL PAIIS	4.06	36	2596. 35129	2	10.81



TME M192	20193 1	trans memb rane protei n 192	15424070 4	AKPEP DILEE EKIyA YPSNI TSETG FR	Y14(Ph ospho)	Y(14): 100.0; Y(16): 0.0; S(18): 0.0; T(21): 0.0; S(22): 0.0; T(24): 0.0	Y213	Y14;	3	1	ILEEE KIyAY PSNIT	3.19		3177. 50901	1	0.53
PEAK 1	79834	pseud opodi um- enrich ed atypic al kinase 1	14836896 2	NAIKV PIVINP NAyD NLAiy K	Y14(Ph ospho)	Y(14): 100.0; Y(20): 0.0	Y635	Y14;	8	1	IVINP NAyD NLAiy K	4.40	31	2423. 27764	1	5.67
PEAK 1	79834	pseud opodi um- enrich ed atypic al kinase 1	14836896 2	NAIKV PIVINP NAyD NLAiy K	Y14(Ph ospho)	Y(14): 100.0; Y(20): 0.0	Y635	Y14;	8	1	IVINP NAyD NLAiy K	4.40	55	2423. 26847	1	4.60
BCR	613	break point cluster region protei n isoform	82546845	KGHG QPGA DAEK PFyVN VEFH HER	Y15(Ph ospho)	Y(15): 100.0	Y177	Y15;	2	1	ADAE KPFyV NVEF HH	3.20		2829. 28774	1	0.30

		m 2														
PTK2	5747	focal adhesion kinase 1 isoform a	24476013	CIGEG QFGD VHQGI yMSPE NPAL AVAIK	C1(Carbamido methyl); Y15(Phospho)	Y(15): 99.9; S(17): 0.1	Y441	Y15;	4	1	GDVH QGIyM SPENP A	3.22	50	3081.42624	0	3.14
LYN	4067	tyrosine-protein kinase Lyn isoform A	4505055	LYAV VTREE PIyIIT EYMA K	R7(Label:13C(6)); Y12(Phospho); K20(Label:13C(6))	Y(2): 0.0; T(6): 0.1; Y(12): 99.9; T(15): 0.1; Y(17): 0.0	Y316	Y12;	9	1	VTREE PIyIIT EYMA	2.87		2494.27457	1	0.44
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-interacting protein	4757886	KYGL FKEEN PyAR	Y11(Phospho)	Y(2): 0.0; Y(11): 100.0	Y174	Y11;	4	1	LFKEE NPyAR FENN	3.66	39	1694.79399	2	0.23

		precursor														
PTTG1IP	754	pituitary tumor-transforming gene 1 protein-interacting protein precursor	4757886	KYGLFKEENPyAR	Y11(Phospho)	Y(2): 0.0; Y(11): 100.0	Y174	Y11;	4	1	LFKEENPyARFENN	3.66	37	1694.79563	2	0.20
DYRK1A	1859	dual specificity tyrosine-phosphorylation-regulated kinase 1A isoform 5	18765756	IYQyIQSR	Y4(Phospho)	Y(2): 0.0; Y(4): 100.0; S(7): 0.0	Y321	Y4;	9	1	LGQRITYQyIQSRFYR	2.28	52	1150.53105	0	1.02

ANX A5	308	annexin A5	4502107	LYDA yELK	Y5(Phospho)	Y(2): 0.0; Y(5): 100.0	Y94	Y5;	2	1	PSRLY DAyEL KHAL K	1.75	37	1094. 48003	0	0.43
ANX A5	308	annexin A5	4502107	LYDA yELKH ALK	Y5(Phospho); K8(Label:13C(6)); K12(Label:13C(6))	Y(2): 0.0; Y(5): 100.0	Y94	Y5;	3	1	PSRLY DAyEL KHAL K	2.25	48	1555. 80411	1	0.43
CTN ND1	1500	catenin delta-1 isoform 2A	33268822 2	HYED GYPG GSDNy GSLSR	Y13(Phospho); R18(Label:13C(6))	Y(2): 0.0; Y(6): 0.0; S(10): 0.0; Y(13): 100.0; S(15): 0.0; S(17): 0.0	Y174	Y13;	13	1	YPPG SDNyG SLSRV T	5.11	74	2059. 81327	0	1.05
CTN ND1	1500	catenin delta-1 isoform 2A	33268822 2	HYED GYPG GSDNy GSLSR	Y13(Phospho)	Y(2): 0.0; Y(6): 0.0; S(10): 0.0; Y(13): 99.9; S(15): 0.0; S(17): 0.0	Y174	Y13;	13	1	YPPG SDNyG SLSRV T	5.11	71	2053. 79375	0	1.07
PIK3 R1	5295	phosphatidylinositol 3-kinase regulator	32455248	EYDR LyEEY TR	Y6(Phospho)	Y(2): 0.0; Y(6): 100.0; Y(9): 0.0; T(10): 0.0	Y467	Y6;	3	1	SREY DRLyE EYTRT S	2.72		1616. 66423	1	2.60

		tyrosine phosphatase non-receptor type 11 isoform 1														
NEDD9	4739	enhancer of filamentation 1 isoform 3	215422375	LyQVP NPQA APR	Y2(Phospho)	Y(2): 100.0	Y92	Y2;	4	1	TFGQ QKLy QVPN PQA	2.92	51	1433.6939	0	39.41
PTPN11	5781	tyrosine phosphatase non-receptor type 11 isoform 1	33356177	VyEN VGLM QQQK	Y2(Phospho); K12(Label:13C(6))	Y(2): 100.0	Y580	Y2;	4	1	REDS ARVyE NVGL MQ	3.64	75	1522.70403	0	1.45
PTPN11	5781	tyrosine phosphatase non-receptor	33356177	VyEN VGLM QQQK	Y2(Phospho); M8(Oxidation)	Y(2): 100.0	Y580	Y2;	4	1	REDS ARVyE NVGL MQ	3.64	37	1532.68205	0	1.43

		or type 11 isoform 1														
ITGB 4	3691	integrin beta-4 isoform 3 precursor	54607033	DySTL TSVSS HDSR	Y2(Phospho)	Y(2): 100.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(7): 0.0; S(9): 0.0; S(10): 0.0; S(13): 0.0	Y1440	Y2;	8	1	STTLP RDyST LTSVS	3.80	72	1634. 67034	0	2.82
EPS8	2059	epidermal growth factor receptor kinase substrate 8	56682953	VySQI TVQK	Y2(Phospho); K9(Label:13C(6))	Y(2): 100.0; S(3): 0.0; T(6): 0.0	Y774	Y2;	4	1	CPEG ARVyS QITVQ K	2.98	51	1151. 58281	0	2.03
TARS	6897	threonine-- tRNA ligase, cytoplasmic isoform 1	38202255	IyGISF PDPK	Y2(Phospho)	Y(2): 100.0; S(5): 0.0	Y298	Y2;	3	1	METL QRlyG ISFPD P	2.13	48	1216. 56474	0	1.49

SDCB P	6386	synten in-1 isoform 1	56243522	LyPEL SQYM GLSLN EEEIR	Y2(Pho spho); R19(La bel:13C (6))	Y(2): 100.0; S(6): 0.0; Y(8): 0.0; S(12): 0.0	Y50	Y2;	10	1	GPLY PRLyP ELSYQ M	2.65	68	2370. 10723	0	0.63
ANX A2	302	annexin A2 isoform 2	20986283 1	AyTNF DAER	Y2(Pho spho)	Y(2): 100.0; T(3): 0.0	Y30	Y2;	4	1	AYGS VKAy TNFD AER	2.22	52	1166. 45073	0	0.59
MLL T4	4301	afadin isoform 2	90819233	EyFTF PASK	Y2(Pho spho); K9(Lab el:13C( 6))	Y(2): 100.0; T(4): 0.0; S(8): 0.0	Y1230	Y2;	4	1	TQTY TREyF TFPAS K	1.67	36	1175. 50774	0	0.47
PGA M1	5223	phospho glyc erate mutas e 1	4505753	HyGG LTGL NKAE TAAK	Y2(Pho spho)	Y(2): 100.0; T(6): 0.0; T(13): 0.0	Y92	Y2;	4	1	WRLN ERHyG GLTG LN	5.79	98	1710. 8206	1	0.59
PGA M1	5223	phospho glyc erate mutas e 1	4505753	HyGG LTGL NKAE TAAK	Y2(Pho spho)	Y(2): 100.0; T(6): 0.0; T(13): 0.0	Y92	Y2;	4	1	WRLN ERHyG GLTG LN	5.79	53	1710. 82083	1	0.53
ARH GAP5	394	rho GTPa se- activat ing protei n 5 isoform b	71834861	GYSD EIyVV PDDS QNR	Y7(Pho spho); R16(La bel:13C (6))	Y(2): 4.1; S(3): 4.1; Y(7): 91.8; S(13): 0.0	Y1109	Y7;	6	1	KGYS DEIyV VPDD SQ	2.44	35	1942. 82463	0	0.14

ANX A2	302	annexin A2 isoform 2	20986283 1	AyTNF DAER DALNI ETAIK	Y2(Phospho)	Y(2): 98.4; T(3): 1.6; T(16): 0.0	Y30	Y2;	8	1	AYGS VKAy TNFD AER	4.29	72	2235. 03374	1	0.52
ANX A2	302	annexin A2 isoform 2	20986283 1	AyTNF DAER DALNI ETAIK	Y2(Phospho)	Y(2): 99.9; T(3): 0.1; T(16): 0.0	Y30	Y2;	8	1	AYGS VKAy TNFD AER	4.29	41	2235. 02964	1	0.56
PIK3 R2	5296	phosphatidylinositol 3-kinase regulatory subunit beta	4826908	EyDQL YEEY TR	Y6(Phospho)	Y(2): 99.9; Y(6): 0.1; Y(9): 0.1; T(10): 0.0	Y460	Y2;	4	1	YQDK SREyD QLYE EY	2.48	38	1588. 62065	0	2.90
C9orf 169	37579 1	UPF0574 protein C9orf 169	25901321 1	GNQG AAPIQ NQQA WQQP GNPyS SSQR	Y21(Phospho)	Y(21): 88.2; S(22): 3.9; S(23): 3.9; S(24): 3.9	Y91	Y21;	8	1	WQQP GNPyS SSQRQ A	3.01		2892. 28177	0	1.38
GSTP 1	2950	glutathione S- transferase P	4504183	PPYTV VyFPV R	Y7(Phospho)	Y(3): 0.0; T(4): 0.0; Y(7): 100.0	Y8	Y7;	1	1	MPPY TVVyF PVRG RC	0.00	57	1417. 69255	0	2.06
INSR	3643	insulin receptor	11939573 8	DIYET DyYR	Y7(Phospho)	Y(3): 0.0; T(5): 0.0; Y(7): 98.3; Y(8): 1.7	Y1177	Y7;	5	1	RDIYE TDyYR KGGK G	2.27	41	1317. 50395	0	0.67



		isoform Short prepro protein														
INSR	3643	insulin receptor isoform Short prepro protein	119395738	DIYET DyYR K	Y7(Phospho)	Y(3): 0.0; T(5): 1.8; Y(7): 96.4; Y(8): 1.8	Y1177	Y7;	6	1	RDIYE TDyYR KGGK G	2.53	38	1445.59734	1	0.63
MET	4233	hepatocyte growth factor receptor isoform b precursor	42741655	DMYD KEyYS VHNK	K5(Label:13C(6)); Y7(Phospho); K13(Label:13C(6))	Y(3): 0.0; Y(7): 100.0; Y(8): 0.0; S(9): 0.0	Y1234	Y7;	17	1	RDMY DKEy YSVH NKT	3.93	80	1783.7459	1	0.56

MET	4233	hepato cyte growt h factor recept or isoform b precur sor	42741655	DMYD KEyYS VHNK	M2(Oxi dation); K5(Lab el:13C (6)); Y7(Pho spho); K13(La bel:13C (6))	Y(3): 0.0; Y(7): 100.0; Y(8): 0.0; S(9): 0.0	Y1234	Y7;	17	1	RDMY DKEy YSVH NKT	3.93	40	1799. 73941	1	0.82
MET	4233	hepato cyte growt h factor recept or isoform b precur sor	42741655	DMYD KEyYS VHNK	Y7(Pho spho)	Y(3): 0.0; Y(7): 100.0; Y(8): 0.0; S(9): 0.0	Y1234	Y7;	17	1	RDMY DKEy YSVH NKT	3.93	37	1771. 70542	1	0.61
WAS L	8976	neural Wisko tt- Aldric h syndr ome protei n	51702526	VIyDFI EK	Y3(Pho spho)	Y(3): 100.0	Y256	Y3;	4	1	RETSK VIyDFI EKTG	2.35	41	1106. 51628	0	2.49
ITSN 2	50618	interse ctin-2	19429452 5	LIyLV PEK	Y3(Pho spho)	Y(3): 100.0	Y553	Y3;	2	1	EYQN KLIyL	1.89	37	1054. 56084	0	1.16

		isoform 2									VPEK QL					
CTN NA1	1495	catenin alpha- 1	55770844	LVyD GIR	Y3(Pho spho)	Y(3): 100.0	Y619	Y3;	2	1	IDASR LVyD GIRD R	1.74	39	915.4 3334	0	0.79
JUP	3728	junction plako globin	12056468	LNyGI PAIVK	Y3(Pho spho); K10(La bel:13C (6))	Y(3): 100.0	Y480	Y3;	2	1	QNSV RLNyG IPAIV K	2.46	35	1173. 6375	0	0.53
DDX 3X	1654	ATP- depen dent RNA helica se DDX3 X isoform 3	30117147 5	KQyPI SLVLA PTR	Y3(Pho spho)	Y(3): 100.0; S(6): 0.0; T(12): 0.0	Y250	Y3;	4	1	RYGR RKQyP ISLVL A	3.62	77	1565. 84453	1	1.78
C9orf 169	37579 1	UPF0 574 protei n C9orf 169	25901321 1	NPyAH ISIPR	Y3(Pho spho)	Y(3): 100.0; S(7): 0.0	Y12	Y3;	5	1	EMVV KNPyA HISIPR	2.67	53	1247. 59197	0	2.69

SHB	6461	SH2 domain-containing adapter protein B	106879210	LDyCG GSGEP GGVQ R	Y3(Phospho); C4(Carbamido methyl); R15(Label:13C(6))	Y(3): 100.0; S(7): 0.0	Y114	Y3;	4	1	RAMC RLDyC GSGEP	3.11	95	1637.6751	0	0.86
PKP3	11187	plakophilin-3	6005830	GQyH TLQA GFSSR	Y3(Phospho); R13(Label:13C(6))	Y(3): 100.0; T(5): 0.0; S(11): 0.0; S(12): 0.0	Y84	Y3;	4	1	RGTSR GQyH TLQA GF	4.15	52	1537.68938	0	0.47
PKP3	11187	plakophilin-3	6005830	ADyD TLSLR	Y3(Phospho)	Y(3): 100.0; T(5): 0.0; S(7): 0.0	Y176	Y3;	4	1	GVGS RADy DTLSL RS	2.56	56	1133.48699	0	1.02
INSR	3643	insulin receptor isoform Short preproprotein	119395738	DIyET DyYR K	Y3(Phospho); Y7(Phospho); R9(Label:13C(6)); K10(Label:13C(6))	Y(3): 100.0; T(5): 2.2; Y(7): 95.5; Y(8): 2.2	Y1173; Y1177	Y3; Y7;	6	1	FGMT RDIyE TDYY RK;RD IYETD yYRK GGKG	2.53	28	1537.60564	1	0.44
PIK3R1	5295	phosphatidylinositol 3-kinase	32455248	DQyL MWLT QK	Y3(Phospho)	Y(3): 100.0; T(8): 0.0	Y580	Y3;	2	1	LRKT RDQyL MWLT QK	1.60	35	1405.62175	0	3.20

		regulatory subunit alpha isoform 1														
KIAA1217	56243	sickle tail protein homolog isoform 1	50843820	NVYVELNDVR	Y3(Phospho); R10(Label:13C(6))	Y(3): 100.0; Y(4): 0.0	Y244	Y3;	4	1	KDES RNVY YELN DVR	2.44	39	1370.60918	0	1.35
RPL15	6138	60S ribosomal protein L15 isoform 1	15431293	QGYVIYR	Y3(Phospho)	Y(3): 100.0; Y(6): 0.0	Y59	Y3;	2	1	GYKA KQGY VIYRI RV	1.75	39	978.44414	0	2.02
BAIA P2	10458	brain-specific angiogenesis inhibitor 1-associated protein 2	5453565	QRPYS VAVP AFSQ GLDD yGAR	Y18(Phospho)	Y(4): 0.0; S(5): 0.0; S(12): 0.0; Y(18): 100.0	Y505	Y18;	3	1	FSQGL DDyG ARSM SS	4.01	37	2377.09275	0	2.05

		isoform 3														
ITGB4	3691	integrin beta-4 isoform 3 precursor	54607033	VCAV GAQG EGPyS SLVSCR	C2(Carbamidomethyl); Y12(Phospho); C18(Carbamidomethyl)	Y(4): 0.0; Y(12): 98.2; S(13): 1.8; S(14): 0.0; S(17): 0.0	Y1207	Y12;	7	1	GAQG EGPyS SLVSCR	4.06	90	2140.88359	0	2.48
ITGB4	3691	integrin beta-4 isoform 3 precursor	54607033	VCAV GAQG EGPyS SLVSCR	C2(Carbamidomethyl); Y12(Phospho); C18(Carbamidomethyl)	Y(4): 0.0; Y(12): 98.4; S(13): 1.5; S(14): 0.0; S(17): 0.0	Y1207	Y12;	7	1	GAQG EGPyS SLVSCR	4.06	71	2140.88156	0	2.75
NEDD9	4739	enhancer of filamentation 1 isoform 3	215422375	DGVY DVPL HNPP DAK	Y4(Phospho)	Y(4): 100.0	Y345	Y4;	4	1	PQER DGVY DVPL HNP	3.58	35	1716.76297	0	13.95

NED D9	4739	enhancer of filamentation 1 isoform 3	215422375	DGVy DVPL HNPP DAK	Y4(Phospho)	Y(4): 100.0	Y345	Y4;	4	1	PQER DGVy DVPL HNP	3.58	70	1716.76311	0	13.86
NED D9	4739	enhancer of filamentation 1 isoform 3	215422375	EKDy DFPPP MR	Y4(Phospho)	Y(4): 100.0	Y241	Y4;	32	1	AGLR EKDy DFPPP MR	3.14	55	1474.60698	1	7.90
PAR D3	56288	partitioning defective 3 homolog isoform 7	296278198	ERDyA EIQDF HR	Y4(Phospho)	Y(4): 100.0	Y990	Y4;	4	1	RQAR ERDyA EIQDF H	3.81	66	1658.69512	1	0.71
PAR D3	56288	partitioning defective 3 homolog isoform 7	296278198	ERDyA EIQDF HR	Y4(Phospho)	Y(4): 100.0	Y990	Y4;	4	1	RQAR ERDyA EIQDF H	3.81		1658.69455	1	0.58

RPS10	6204	40S ribosomal protein S10	4506679	IAIyEL LFK	Y4(Phospho); K9(Label:13C(6))	Y(4): 100.0	Y12	Y4;	2	1	KKNRI AiyEL LFKEG	2.38	63	1195.64665	0	0.97
PTRF	284119	polymerase I and transcription release factor	42734430	VMiyQ DEVK LPAK	Y4(Phospho); K9(Label:13C(6)); K13(Label:13C(6))	Y(4): 100.0	Y156	Y4;	2	1	RNFK VMiyQ DEVK LP	1.84	51	1625.84343	1	0.87
DDX3X	1654	ATP-dependent RNA helicase DDX3X isoform 3	301171475	RKQyP ISLVL APTR	Y4(Phospho)	Y(4): 100.0; S(7): 0.0; T(13): 0.0	Y250	Y4;	3	1	RYGR RKQyP ISLVL A	3.82	32	1721.94541	2	1.91
INPP1L1	3636	phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase	222136583	ERLyE WISID KDEA GAK	Y4(Phospho)	Y(4): 100.0; S(8): 0.0	Y886	Y4;	8	1	LGTRE RLyE WISID K	3.95	55	2102.978	2	1.19



		2														
TBCB	1155	tubulin-folding cofactor B	50428925	LGEyE DVSR	Y4(Phospho); R9(Label:13C(6))	Y(4): 100.0; S(8): 0.0	Y98	Y4;	4	1	SGAR LGEyE DVSR VE	2.08	69	1153.48747	0	0.95
GPRC5C	55890	G-protein coupled receptor family C group 5 member C isoform b precursor	40217833	GVGy ETILK EQK	Y4(Phospho)	Y(4): 100.0; T(6): 0.0	Y336	Y4;	4	1	YPTR GVGy ETILK EQ	2.86	50	1444.70793	1	0.23
GPRC5C	55890	G-protein coupled receptor	40217833	GVGy ETILK	Y4(Phospho); K9(Label:13C(6))	Y(4): 100.0; T(6): 0.0	Y336	Y4;	4	1	YPTR GVGy ETILK EQ	1.53	42	1065.53313	0	0.31

		family C group 5 member C isoform b precursor														
VASP	7408	vasodilator-stimulated phosphoprotein	4507869	VQIyH NPTA NSFR	Y4(Phospho)	Y(4): 100.0; T(8): 0.0; S(11): 0.0	Y39	Y4;	5	1	AFSRV QIyHN PTANS	3.54	59	1626. 7404	0	1.05
FRK	2444	tyrosine-protein kinase FRK	4503787	HGHyF VALF DYQAR	Y4(Phospho)	Y(4): 100.0; Y(11): 0.0	Y46	Y4;	14	1	QSQR HGHyF VALF DY	3.92	44	1803. 79685	0	2.95
FRK	2444	tyrosine-protein kinase FRK	4503787	HGHyF VALF DYQAR	Y4(Phospho)	Y(4): 100.0; Y(11): 0.0	Y46	Y4;	14	1	QSQR HGHyF VALF DY	3.92	42	1803. 7974	0	2.17
FRK	2444	tyrosine-protein	4503787	HGHyF VALF DYQAR	Y4(Phospho)	Y(4): 100.0; Y(11): 0.0	Y46	Y4;	14	1	QSQR HGHyF VALF DY	3.92	55	1803. 79717	0	1.62

		kinase FRK														
FRK	2444	tyrosi- ne- protei- n kinase FRK	4503787	HGHyF VALF DYQA R	Y4(Pho- spho); R14(La- bel:13C (6))	Y(4): 100.0; Y(11): 0.0	Y46	Y4;	14	1	QSQR HGHyF VALF DY	3.92	68	1809. 81865	0	1.52
HEG1	57493	protei- n HEG homol- og 1 precur- sor	15379211 0	NGLyP AYTG LPGSR	Y4(Pho- spho); R14(La- bel:13C (6))	Y(4): 100.0; Y(7): 0.0; T(8): 0.0; S(13): 0.0	Y1347	Y4;	6	1	ELERN GLyPA YTGLP	2.67	53	1551. 72954	0	0.40
EPHB 3	2049	ephrin type- B recept- or 3 precur- sor	17975768	LQQYI APGM KVyID PFTYE DPNE AVR	Y12(Ph- ospho)	Y(4): 2.9; Y(12): 97.1; T(17): 0.0; Y(18): 0.0	Y608	Y12;	6	1	IAPGM KVyID PFTYE	2.63		3137. 47556	1	2.20
INPP L1	3636	phosp- hatidy- linosit- ol 3,4,5- trisph- osphat- e 5- phosp- hatase 2	22213658 3	ERLyE WISID KDEA GAK	Y4(Pho- spho)	Y(4): 97.8; S(8): 2.2	Y886	Y4;	8	1	LGTRE RLyE WISID K	3.95	38	2102. 97978	2	1.46

TLN1	7094	talin-1	223029410	ALDy YMLR	Y4(Phospho)	Y(4): 98.6; Y(5): 1.4	Y70	Y4;	4	1	EAGK ALDy YMLR NGD	1.75	40	1124.48479	0	1.41
PTPRA	5786	receptor-type tyrosine-protein phosphatase alpha isoform 2 precursor	18450369	VVQE YIDAF SDyAN FK	Y12(Phospho); K16(Label:13C(6))	Y(5): 0.0; S(10): 0.0; Y(12): 100.0	Y789	Y12;	13	1	YIDAF SDyAN FK	4.22	69	1994.88945	0	0.43
PTPRA	5786	receptor-type tyrosine-protein phosphatase alpha isoform 2 precursor	18450369	VVQE YIDAF SDyAN FK	Y12(Phospho); K16(Label:13C(6))	Y(5): 0.0; S(10): 0.0; Y(12): 100.0	Y789	Y12;	13	1	YIDAF SDyAN FK	4.22	60	1994.88956	0	0.42

BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 7	282398123	VGQGYVYEAAQPEQDEyDIPR	Y17(Phospho)	Y(5): 0.0; Y(7): 0.0; Y(17): 100.0	Y232	Y17;	14	1	AQPEQDEyDIPRHL	3.68	53	2507.07622	0	1.76
CTNNA1	1495	catenin alpha-1	55770844	EVKEyAQVFR	K3(Label:13C(6)); Y5(Phospho); R10(Label:13C(6))	Y(5): 100.0	Y419	Y5;	4	1	NEKEVKEyAQVFRH	2.92	47	1360.67058	1	0.37
PRKCD	5580	protein kinase C delta type	31377782	GRGEyFAIK	R2(Label:13C(6)); Y5(Phospho); K9(Label:13C(6))	Y(5): 100.0	Y374	Y5;	4	1	ELKGRGEyFAIKALK	2.76	52	1132.55901	1	0.49
TNS3	64759	tensin-3	65288071	AGVDyAPNLPPFPSPADVK	Y5(Phospho)	Y(5): 100.0; S(14): 0.0	Y802	Y5;	4	1	WGKAGVDyAPNLPPFP	2.48	38	2034.96037	0	1.37

JAK2	3717	tyrosine-protein kinase JAK2	4826776	EVGDyGQLHETE VLLK	Y5(Phospho)	Y(5): 100.0; T(11): 0.0	Y570	Y5;	7	1	VRRE VGDy GQLH ETE	3.15	30	1909. 89713	0	1.19
JAK2	3717	tyrosine-protein kinase JAK2	4826776	EVGDyGQLHETE VLLK	Y5(Phospho); K16(Label:13C(6))	Y(5): 100.0; T(11): 0.0	Y570	Y5;	7	1	VRRE VGDy GQLH ETE	3.15	66	1915. 9157	0	1.37
PLCG1	5335	1-phosphatidylinositol 4,5-bisphosphate phosphatidylinositol 3-kinase gamma-1 isoform b	33598946	NPGFy VEAN PMPTF K	Y5(Phospho)	Y(5): 100.0; T(13): 0.0	Y783	Y5;	5	1	EGRN PGFyV EANP MP	2.40	43	1791. 78032	0	2.60

ACTB	60	actin, cytoplasmic 1	4501885	EKLCy VALD FEQE MATA ASSSS LEK	K2(Label:13C(6)); C4(Carbamidomethyl); Y5(Phospho); K25(Label:13C(6))	Y(5): 100.0; T(16): 0.0; S(19): 0.0; S(20): 0.0; S(21): 0.0; S(22): 0.0	Y218	Y5;	2	1	DIKEK LCyVA LDFEQ	3.07	37	2899. 32236	1	0.85
AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	61743954	VKGE yDVT VPK	K2(Label:13C(6)); Y5(Phospho); K11(Label:13C(6))	Y(5): 100.0; T(8): 0.0	Y715	Y5;	4	1	GTKV KGEy DVTV PKL	3.02		1326. 67412	1	0.54
KIAA1217	56243	sickle tail protein homolog isoform 1	50843820	NEGFy ADPY LYHE GR	Y5(Phospho); R15(Label:13C(6))	Y(5): 100.0; Y(9): 0.0; Y(11): 0.0	Y393	Y5;	8	1	MYRN EGFyA DPYL YH	3.32	75	1916. 79399	0	0.92

BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1 isoform 7	28239812 3	VGQG YVYe AAQP EQDE YDIPR	Y7(Pho spho)	Y(5): 2.3; Y(7): 97.7; Y(17): 0.0	Y222	Y7;	14	1	RVGQ GYVy EAAQ PEQ	3.68	37	2507. 07451	0	2.79
BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1 isoform 7	28239812 3	VGQG YVYE AAQP EQDEy DIPR	Y7(Pho spho); Y17(Ph ospho)	Y(5): 50.0; Y(7): 50.0; Y(17): 100.0	Y232	Y17;	14	1	AQPE QDEy DIPRH LL	3.68	33	2587. 04166	0	2.44
AHN AK	79026	neuro blast differe ntiatio n- associ ated protei n AHN AK	61743954	MKGD yDVT VPK	K2(Lab el:13C( 6)); Y5(Pho spho); K11(La bel:13C (6))	Y(5): 97.7; T(8): 2.3	Y1469	Y5;	4	1	GPKM KGDy DVTV PKV	2.29		1344. 63188	1	0.45



		isoform 1														
ATP1A1	476	sodium/potassium-transporting ATPase subunit alpha-1 isoform a	21361181	GIVVYTGDR	Y5(Phospho); R9(Label:13C(6))	Y(5): 98.7; T(6): 1.3	Y260	Y5;	4	1	TARGIVVYTGDRVM	2.20	39	1065.50591	0	0.44
AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform	61743954	VKGEyDMTPVK	K2(Label:13C(6)); Y5(Phospho); K11(Label:13C(6))	Y(5): 99.9; T(8): 0.1	Y964	Y5;	2	1	GPKVKGEyDMTPVK	2.21		1358.6469	1	0.75

		m l														
LYN	4067	tyrosine-protein kinase Lyn isoform A	4505055	EEPIyI ITEYMAK	Y5(Phospho); K13(Label:13C(6))	Y(5): 99.9; T(8): 0.1; Y(10): 0.0	Y316	Y5;	4	1	VTREE PIyIIT EYMA	2.21	50	1685. 78276	0	0.41
G6PD	2539	glucose-6-phosphate 1-dehydrogenase isoform b	108773793	VGFQy EGTYK	Y5(Phospho); K10(Label:13C(6))	Y(5): 99.9; T(8): 0.1; Y(9): 0.0	Y503	Y5;	3	1	MKRV GFQyE GTYK WV	1.78	26	1277. 55351	0	2.41
FRK	2444	tyrosine-protein kinase FRK	4503787	WKLE DYFET DSSyS DANN FIR	K2(Label:13C(6)); Y13(Phospho); R21(Label:13C(6))	Y(6): 0.0; T(9): 0.0; S(11): 0.0; S(12): 1.5; Y(13): 97.0; S(14): 1.5	Y497	Y13;	11	1	YFETD SSySD ANNFI	4.31	78	2692. 16196	1	0.50

HNR NPA2 B1	3181	hetero geneo us nuclea r ribonu cleopr oteins A2/B1 isofo r m B1	14043072	NMGG PYGG GNyGP GGSG GSGG YGGR	Y11(Ph ospho)	Y(6): 0.1; Y(11): 99.9; S(16): 0.1; S(19): 0.0; Y(22): 0.0	Y336	Y11;	2	1	GPYG GGNy GPGG SGG	5.56	105	2269. 86846	0	1.39
CTN ND1	1500	cateni n delta- 1 isofo r m 2A	33268822 2	FHPEP yGLED DQR	Y6(Pho spho)	Y(6): 100.0	Y226	Y6;	4	1	HRFHP EPyGL EDDQ R	2.51	38	1682. 68425	0	1.47
EPB4 1L1	2036	band 4.1- like protei n 1 isofo r m d	38525140 1	IRPGE yEQFE STIGF K	Y6(Pho spho)	Y(6): 100.0; S(11): 0.0; T(12): 0.0	Y312	Y6;	3	1	IKIRP GEyEQ FESTI	2.64		1980. 91216	0	6.52
BCA R1	9564	breast cancer anti- estrog en resista nce protei n 1	28239812 3	AQQG LyQVP GPSPQ FQSP AK	Y6(Pho spho)	Y(6): 100.0; S(12): 0.0; S(17): 0.0	Y126	Y6;	14	1	SKAQ QGLy QVPG PSP	4.44	55	2305. 11197	0	1.74

		isoform 7														
BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 7	282398123	AQQG LyQVP GPSPP FQSPPAK	Y6(Phospho); K21(Label:13C(6))	Y(6): 100.0; S(12): 0.0; S(17): 0.0	Y126	Y6;	14	1	SKAQ QGLy QVPG PSP	4.44	46	2311.12895	0	1.81
PSMA2	5683	proteasome subunit alpha type-2	4506181	HIGLV ySGM GPDY R	Y6(Phospho)	Y(6): 100.0; S(7): 0.0; Y(13): 0.0	Y76	Y6;	2	1	TKHIG LVySG MGPDY	4.10	32	1644.72405	0	0.90
PGAM1	5223	phosphoglycerate mutase 1	4505753	LNER HyGG LTGL NK	R4(Label:13C(6)); Y6(Phospho); K14(Label:13C(6))	Y(6): 100.0; T(10): 0.0	Y92	Y6;	3	1	WRLN ERHyG GLTGLN	3.49	44	1663.83323	1	0.61
JAK2	3717	tyrosine-kinase JAK2	4826776	REVG DyGQ LHETE VLLK	Y6(Phospho)	Y(6): 100.0; T(12): 0.0	Y570	Y6;	2	1	VRRE VGDy GQLH ETE	3.32		2065.99674	1	1.15

ZNF185	7739	zinc finger protein 185 isoform 6	296010968	GALADyEGKDVA TR	Y6(Phospho)	Y(6): 100.0; T(13): 0.0	Y349	Y6;	4	1	PKGALADyEGKDVAT	3.85	98	1545.6939	1	1.55
EPHA1	2041	ephrin type-A receptor 1 precursor	221316650	LWLKPyVDLQAYEDPAQ GALDFTR	Y6(Phospho)	Y(6): 100.0; Y(12): 0.0; T(23): 0.0	Y599	Y6;	4	1	DKLWLKPyV DLQAYE	4.85	52	2889.39054	0	12.45
BCAR3	8412	breast cancer anti-estrogen resistance protein 3 isoform 1	387157906	CLEEHyGTSPGQAR	C1(Carbamidomethyl); Y6(Phospho)	Y(6): 97.3; T(8): 1.3; S(9): 1.3	Y266	Y6;	9	1	LRCLEEHyGTSPGQA	1.81	32	1684.67681	0	3.12
G6PD	2539	glucose-6-phosphate 1-dehydrogenase isoform	108773793	RVGFQyEGTYK	Y6(Phospho)	Y(6): 98.7; T(9): 1.3; Y(10): 0.0	Y503	Y6;	5	1	MKRVGFQyEGTYK WV	3.70	52	1427.6364	1	1.19

		m b														
YES1	7525	tyrosine- protein kinase Yes	4885661	KLDN GGYyI TTR	K1(Lab el:13C(6)); Y8(Pho spho); R12(La bel:13C(6))	Y(7): 1.8; Y(8): 98.2; T(10): 0.0; T(11): 0.0	Y223	Y8;	12	1	KLDN GGYyI TTRA QF	4.68	63	1492. 72356	1	1.25
TES	26136	testin isoform 2	23238188	EGDP AIyAE R	Y7(Pho spho)	Y(7): 100.0	Y242	Y7;	2	1	KEGD PAIyA ERAG YD	1.12	31	1200. 49199	0	2.46
ARA P2	11698 4	arf- GAP with Rho- GAP domai n, ANK repeat and PH domai n- contai ning protei n 2	21264592	MQDIP IyANV HK	Y7(Pho spho)	Y(7): 100.0	Y77	Y7;	2	1	KMQD IPIyAN VHKT K	1.81	33	1508. 69682	0	1.99

GAB1	2549	GRB2 - associ- ated- bindin g protei n 1 isoform b	46370073	GDKQ VEyLD LDLDS GK	Y7(Pho spho)	Y(7): 100.0; S(14): 0.0	Y627	Y7;	11	1	KGDK QVEyL DLDL DS	4.77	83	1874. 84233	1	2.51
GAB1	2549	GRB2 - associ- ated- bindin g protei n 1 isoform b	46370073	GDKQ VEyLD LDLDS GK	Y7(Pho spho)	Y(7): 100.0; S(14): 0.0	Y627	Y7;	11	1	KGDK QVEyL DLDL DS	4.77	49	1874. 84067	1	2.39
ANK S1A	23294	ankyri n repeat and SAM domai n- contai ning protei n 1A	14016150 0	EEDE HPyEL LLTAE TK	Y7(Pho spho)	Y(7): 100.0; T(12): 0.0; T(15): 0.0	Y455	Y7;	8	1	REEDE HPyEL LLTAE	3.08		1996. 87883	0	2.06

S100 A10	6281	protein S100- A10	4506761	FAGD KGyLT KEDL R	K5(Lab el:13C(6)); Y7(Pho spho); K10(La bel:13C(6)); R14(La bel:13C(6))	Y(7): 100.0; T(9): 0.0	Y25	Y7;	4	1	KFAG DKGy LTKE DLR	3.40	83	1710. 85991	2	0.09
CD46	4179	memb rane cofact or protei n isoform 12 precur sor	27502427	ADGG AEyAT YQTK	Y7(Pho spho)	Y(7): 100.0; T(9): 0.0; Y(10): 0.0; T(12): 0.0	Y340	Y7;	10	1	KADG GAEy ATYQ TKS	2.68	50	1454. 58293	0	0.75
YES1	7525	tyrosi ne- protei n kinase Yes	4885661	KLDN GGyYI TTR	K1(Lab el:13C(6)); Y7(Pho spho); R12(La bel:13C(6))	Y(7): 100.0; Y(8): 0.0; T(10): 0.0; T(11): 0.0	Y222	Y7;	12	1	RKLD NGGy YITTR AQ	4.68	99	1492. 72331	1	1.57
ARH GAP3 5	2909	rho GTPa se- activat	15041798 1	NEEE NIySV PHDST QGK	Y7(Pho spho); K17(La bel:13C	Y(7): 97.4; S(8): 2.6; S(13): 0.0; T(14): 0.0	Y1105	Y7;	6	1	RNEEE NIySV PHDST	4.69	33	2032. 85739	0	0.36



		ing protei n 35			(6)											
CFL1	1072	cofilin -1	5031635	HELQ ANCyE EVKDR	C7(Car bamido methyl) ; Y8(Pho spho); K12(La bel:13C (6)); R14(La bel:13C (6))	Y(8): 100.0	Y140	Y8;	2	1	HELQ ANCyE EVKDR RC	5.26	65	1882. 82187	1	0.74
RPLP 0	6175	60S acidic riboso mal protei n P0	16933546	IIQLL DDyPK	Y8(Pho spho)	Y(8): 100.0	Y24	Y8;	2	1	IIQLL DDyPK CFIVG	2.54	69	1297. 64397	0	11.27
ACT N1	87	alpha- actini n-1 isoform c	19409735 2	HRPEL IDyGK	Y8(Pho spho)	Y(8): 100.0	Y193	Y8;	2	1	HRPEL IDyGK LRKDR D	4.06	45	1307. 61298	0	1.28
LCK	3932	tyrosi ne- protei n kinase Lck	11278954 6	NLDN GGFyI SPR	Y8(Pho spho); R12(La bel:13C (6))	Y(8): 100.0; S(10): 0.0	Y192	Y8;	8	1	NLDN GGFyI SPRIT F	3.29	73	1438. 64214	0	0.08

		precur sor														
ERBB 2IP	55914	protei n LAP2 isofo r m 7	55770895	AQIPE GDyLS YR	Y8(Pho spho); R12(La bel:13C (6))	Y(8): 100.0; S(10): 0.0; Y(11): 0.0	Y1104	Y8;	5	1	AQIPE GDyLS YREF H	2.87	56	1497. 68279	0	0.52
PXN	5829	paxilli n isofo r m 1	17093251 6	VGEE EHVyS FPNK	Y8(Pho spho)	Y(8): 100.0; S(9): 0.0	Y118	Y8;	16	1	VGEE EHVyS FPNK QK	4.27	49	1614. 68401	0	2.73
PXN	5829	paxilli n isofo r m 1	17093251 6	VGEE EHVyS FPNK QK	Y8(Pho spho); K13(La bel:13C (6)); K15(La bel:13C (6))	Y(8): 100.0; S(9): 0.0	Y118	Y8;	26	1	VGEE EHVyS FPNK QK	4.68	54	1882. 87676	1	2.83
PXN	5829	paxilli n isofo r m 1	17093251 6	VGEE EHVyS FPNK	Y8(Pho spho)	Y(8): 98.3; S(9): 1.7	Y118	Y8;	16	1	VGEE EHVyS FPNK QK	4.27	40	1614. 68369	0	2.95
FAM 20B	9917	glycos amino glycan xylosy lkinas e	7662150	DHVV EGEPY AGyD R	Y12(Ph ospho); R14(La bel:13C (6))	Y(9): 1.9; Y(12): 98.1	Y141	Y12;	4	1	EGEPY AGyD RHNA EV	1.63	38	1692. 70159	0	0.58

LYN	4067	tyrosine-kinase Lymphoform A	4505055	VENC PDELY DIMK	C4(Carbamido methyl); Y9(Phospho); K13(Label:13C(6))	Y(9): 100.0	Y473	Y9;	2	1	ENCP DELYD IMKM CW	2.09	35	1711. 70342	0	0.42
HNR NPH3	3189	heterogeneous nuclear ribonucleoprotein H3 isoform b	14141159	DGMD NQGG yGSVGR	Y9(Phospho)	Y(9): 100.0; S(11): 0.0	Y281	Y9;	4	1	GMDN QGGy GSVGR RMG	2.36	60	1492. 55242	0	2.69
CAL M2	805	calmodulin	4502549	VFDK DGNG yISAA ELR	Y9(Phospho)	Y(9): 100.0; S(11): 0.0	Y100	Y9;	14	1	FDKD GNGyI SAAEL R	4.37	92	1834. 83916	1	0.44
CAL M2	805	calmodulin	4502549	VFDK DGNG yISAA ELR	Y9(Phospho)	Y(9): 100.0; S(11): 0.0	Y100	Y9;	14	1	FDKD GNGyI SAAEL R	4.37	52	1834. 83908	1	0.43

ERBB 2IP	55914	protein LAP2 isoform 7	55770895	RAQIP EGDyL SYR	R1(Lab el:13C(6)); Y9(Phospho); R13(Label:13C(6))	Y(9): 100.0; S(11): 0.0; Y(12): 0.0	Y1104	Y9;	5	1	AQIPE GDyLS YREF H	3.29	65	1659. 79302	1	0.60
CAL M2	805	calmodulin	4502549	VFDK DGNG yISAA ELR	K4(Lab el:13C(6)); Y9(Phospho); R16(Label:13C(6))	Y(9): 99.9; S(11): 0.1	Y100	Y9;	14	1	FDKD GNGyI SAAEL R	4.37	55	1846. 89079	1	0.41