Table: PTMScan® Results, Phospho-PKA Substrate Motif (RRXS*/T*), label-free quantitation

Study design: rat cell line PC-12; Trypsin digest; Antibody: Phospho-PKA Substrate Motif (RRXS*/T*), PTMScan® Kit #1984, #5565

Treatments: Untreated, forskolin treated

Index	Fold-Change (Forskolin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (Untreated)
3	**Adaptor/scaffold**								
4	**10.4**	AHNAK	159	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 1	RVtAYTVDVTGR	XP_574618	581	2	8.69E+05
5	**11.2**	AHNAK	161	PREDICTED: similar to AHNAK nucleoprotein isoform 1 isoform 1	RVTAyTVDVTGREGVKDIDISSPE	XP_574618	581	1	6.14E+04
6	2.8	AKAP1	101	A-kinase anchor protein 1	RRsESSGNLPSIVDTR	O88884	92	1	2.49E+06
7	2.2	AKAP2	850	A kinase (PRKA) anchor protein 2	RKsALALRWE	Q5U301	96	1	5.57E+05
8	**6.7**	AP3D1	754, 758, 760	adaptor-related protein complex 3, delta 1 subunit	RHsSLPtEsDEDIAPAQRVDIITE	XP_234908	136	1	5.47E+04
9	3.2	AP3D1	754, 760	adaptor-related protein complex 3, delta 1 subunit	RHsSLPTEsDEDIAPAQRVDIITE	XP_234908	136	1	3.61E+05
10	**-6.2**	CTNND1	320	catenin (cadherin associated protein), delta 1	LRsYEDM#IGEEVPPDQYYWAPLAQHE	XP_001064294	105	1	5.76E+05
11	3.8	DOCK1	1756	dedicator of cyto-kinesis 1	RFsVSPASPCSQPTPPPVTPR	NP_001137330	215	1	1.01E+06
12	1.7	FNBP1L	488	formin binding protein 1-like	RHsSDINHLVTQGRESPE	Q2HWF0	70	1	3.98E+05
13	-1.2	FRS2	132, 135, 138	fibroblast growth factor receptor substrate 2	LEVPRtPRtPTtPGLGAQSLPNGYPR	EDM16633	57	2	2.59E+05
14	2.2	FRS2	428	fibroblast growth factor receptor substrate 2	DCTPTVFNFDIRRPsLE	EDM16633	57	1	8.14E+05
15	3.2	IRS-2	557	PREDICTED: similar to Insulin receptor substrate 2 (IRS-2) (4PS)	RVsGDGAQDLDR	O70360	137	1	1.75E+05
16	2.4	MPDZ	1802	multiple PDZ domain protein	IKAAPFHSERRPsQSSQVSE	O55164	219	1	2.14E+06
17	1.4	MPDZ	1802, 1804, 1808	multiple PDZ domain protein	IKAAPFHSERRPsQsSQVsE	O55164	219	1	5.29E+05
18	2.3	MPDZ	1804, 1805	multiple PDZ domain protein	AAPFHSERRPSQssQVSE	O55164	219	1	5.37E+05
19	4.5	MTSS1	307	metastasis suppressor 1	KSsVCSSLNSVNSSDSR	NP_001124035	86	1	2.74E+05
20	**9.5**	Nck1	21	NCK adaptor protein 1	RKPsVPDTASPADDSFVDPGER	XP_217246	36	3	2.51E+05
21	2.1	PARD3	715	partitioning-defective protein 3 homolog	RIsHSLYSGIE	Q9Z340	149	1	3.76E+05
22	2.2	LIM	228	PDZ and LIM domain 5	RGsQGDIKQQNGPPR	Q62920	63	4	2.01E+06
23	3.4	tensin 3	648	PREDICTED: similar to tensin-like SH2 domain containing 1	KPsAPTPTQAYGQSNYSTQTWVR	XP_341257	117	1	1.16E+05
26	**23.6**	14-3-3 zeta	58	tyr 3-monooxygenase/tryp 5-monooxygenase activation prot, zeta polypep	RSsWRVVSSIEQKTE	P63102	28	2	2.02E+05
27	**Adhesion or extracellular matrix protein**								
28	2.5	CTNNB1	552	beta-catenin	RTsMGGTQQQFVE	Q9WU82	85	2	2.91E+06
29	1.1	desmoplakin	174	PREDICTED: similar to desmoplakin isoform II isoform 1	RAsSKGGYTCQSGSGWDE	Q4QQR7	332	2	5.62E+06
30	-2.6	desmoplakin	174, 175	PREDICTED: similar to desmoplakin isoform II isoform 1	RAssKGGYTCQSGSGWDE	Q4QQR7	332	1	2.60E+05
31	1.2	desmoplakin	175	PREDICTED: similar to desmoplakin isoform II isoform 1	VRRASsKGGYTCQSGSGWDE	Q4QQR7	332	1	4.87E+06
32	1.8	desmoplakin	56	PREDICTED: similar to desmoplakin isoform II isoform 1	RCtVNDQNSDGYCQTGTM#SR	Q4QQR7	332	1	1.18E+05
33	-2.3	LAD1	62	ladinin	SVERLPsVEEAE	NP_001101412	57	1	1.17E+06
34	-1.4	Nogo iso2; Nogo	107; 107	Reticulon-4	GPLPAAPPAAPERQPsWE	Q9JK11-2; Q9JK11	39; 126	2	1.92E+07
35	**10.7**	plakophilin 3	159	plakophilin 3	RLsSAHNGGSAFGAVGYGGAQPTPPM#PTRPVSFHE	NP_001099785	90	4	6.07E+05
36	1.2	plakophilin 3	159, 188	plakophilin 3	RLsSAHNGGSAFGAVGYGGAQPTPPM#PTRPVsFHE	NP_001099785	90	1	5.02E+05
37	**Apoptosis**								
38	**9.9**	EI24	46	etoposide induced 2.4 mRNA	RAsSLLAQR	Q4KM77	39	1	1.31E+05
39	1.3	PAR-4	155	PRKC, apoptosis, WT1, regulator	RStGVVNIPAAECLDEYEDDE	Q62627	36	1	6.74E+05
40	-2.7	PEA-15	116	phosphoprotein enriched in astrocytes 15A	YKDIIRQPsEEE	Q5U318	15	1	1.54E+06
41	**Cell cycle regulation**								
42	3.7	AFAP1L2	341	PREDICTED: similar to Protein KIAA1914	KKsTSLEPPDRSLE	XP_217643	92	1	4.05E+05
43	3.4	CLASP1	600	rCG37592	SRsDIDVNAAASAK	EDL87905	167	2	1.02E+06
44	**6.0**	CLASP1	658	rCG37593	TRRQsSGSTTNVASTSSDSR	EDL87905	167	5	2.93E+05
45	**6.0**	CLASP1	658, 661	rCG37594	RQsSGsTTNVASTSSDSR	EDL87905	167	1	8.97E+04
46	2.4	CLASP1	690	rCG37595	sSSPGKLLGSGYGGLAGGSSRGPPVTPSSE	EDL87905	167	1	9.95E+05
47	3.9	CLASP1	692	rCG37596	SSsPGKLLGSGYGGLAGGSSR	EDL87905	167	1	2.38E+05
48	**7.7**	B99	501	G-2 and S-phase expressed 1	RLsGLTPQGLPSSM#R	XP_217016	80	2	1.78E+05
49	1.6	KAB1	968	rCG20491, isoform CRA_b	IRQPsIDLTDDDQTSSVPHSAISDIMSSDQE	EDL94780	170	1	2.35E+05
50	-1.1	NuMA-1	337	PREDICTED: similar to nuclear mitotic apparatus protein 1 isoform 1	RRtTQIINITMTK	Q4G051	71	1	4.21E+05
51	**5.0**	NUSAP1	113	nucleolar and spindle associated protein 1	RRDsTTFQNQE	NP_001101232	43	3	9.67E+05
52	2.5	NUSAP1	115	nucleolar and spindle associated protein 1	M#KRRDSTtFQNQE	NP_001101232	43	1	4.79E+04
53	2.4	MCC	354	PREDICTED: mutated in colorectal cancers	KKsSCSLSVAE	XP_225962	112	1	4.00E+05
54	2.6	MCC	354, 355	PREDICTED: mutated in colorectal cancers	KKssCSLSVAE	XP_225962	112	1	6.54E+05
55	3.9	SPECC1L	833	SPECC1-like	RSsTSSEPTPTVK	Q2KN99	124	3	3.30E+06
56	**14.1**	SPECC1L	833, 836	SPECC1-like	RSsTSsEPTPTVK	Q2KN99	124	1	4.98E+04

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

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Treatments: Untreated, forskolin treated

Index	Fold-Change (Forskolin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (Untreated)
57	**Chaperone**								
58	**12.1**	HSP20	16	heat shock protein, alpha-crystallin-related, B6	RAsAPLPGFSTPGR	P97541	18	1	3.86E+05
59	**Chromatin, DNA-binding, DNA repair or DNA replication protein**								
60	1.9	capicua	1394, 1405	capicua homolog	KNsTDLDSAPEDPtSPKRK	NP_001100960	164	2	1.06E+06
61	**45.7**	H1C	36	histone cluster 1, H1d	KAsGPPVSE	P15865	22	9	1.08E+05
62	-1.7	LBR	101	lamin B receptor	SVsASYQADAKEKE	O08984	71	1	2.70E+05
63	2.9	polybromo 1	39	PREDICTED: similar to polybromo 1 isoform 2 isoform 1	RLsSLPTVDPIAVCHE	XP_001059112	181	1	9.24E+05
64	4.0	TERF2IP	43	telomeric repeat binding factor 2, interacting protein	RLsTLILHGGGILCR	Q5EAN7	43	1	4.59E+05
65	**5.8**	TTF1	103	PREDICTED: similar to transcription termination factor 1	RREsQTPAQENLE	XP_001079280	96	1	8.21E+04
66	**Cytoskeletal protein**								
67	**51.5**	cordon-bleu	1042	cordon-bleu homolog	KVsSLASEE	NP_001100706	122	1	5.88E+04
68	-1.6	cordon-bleu	219	cordon-bleu homolog	KSsLGNDETDKE	NP_001100706	122	2	1.02E+04
69	3.3	cordon-bleu	648	cordon-bleu homolog	RNsMEKYLNGPAE	NP_001100706	122	1	4.21E+05
70	**7.9**	DAL-1	423	erythrocyte protein band 4.1-like 3	RAsALIDRPAPYFE	Q9JMB3	122	1	2.41E+05
71	1.9	EPPK1	2290, 2709, 3224	PREDICTED: similar to Epiplakin	AQAATGFIIDPVHNRRLsVEE	XP_001059215	370	1	6.03E+05
72	**6.4**	FLNB	2107	filamin, beta	TSRAPsVATVGSICD	XP_224561	278	1	2.27E+05
73	1.5	FNBP1	496	formin binding protein 1	RQsGLYDGQTHQTVTNCAQDRE	Q8R511	71	2	1.65E+05
74	3.7	KIF23	903	kinesin family member 23	RsSTLAPAQPDGTESE	NP_001101625	109	1	3.07E+05
75	1.1	KIF23	903, 904	kinesin family member 23	KRRssTLAPAQPDGTESE	NP_001101625	109	1	4.28E+05
76	4.7	KIF23	904	kinesin family member 23	RSsTLAPAQPDGTESEWTDVE	NP_001101625	109	2	3.80E+05
77	**5.7**	KIF23	905	kinesin family member 23	RSStLAPAQPDGTE	NP_001101625	109	2	1.32E+06
78	**-7.6**	K14	40	keratin 14	M#SSVLAGGSCRAPsTYGGM#SR	Q6IFV1	53	2	1.03E+06
79	-2.8	K14	42	keratin 14	M#SSVLAGGSCRAPSTyGGMSR	Q6IFV1	53	1	7.33E+05
80	-1.9	eplin	225	PREDICTED: similar to Epithelial protein lost in neoplasm (mEPLIN)	RLsENSCSLDDLE	Q6J4T4	84	2	1.83E+06
81	-1.1	nestin; nestin iso2	1166; 1078	nestin	RKsIDTQEPLWSTE	P21263; P21263-2	209; 199	1	9.61E+06
82	-1.6	plectin 1	4641, 4645	plectin 1	AGsRRGsFDATGSGFSM#TFSSSSYSSSGYGR	P30427	534	1	3.22E+05
83	-3.0	plectin 1	4645	plectin 1	RGsFDATGSGFSM#TFSSSSYSSSGYGR	P30427	534	2	2.12E+06
84	1.3	RIL	119	reversion induced LIM	RSsISGISLE	P36202	36	1	2.02E+07
85	**71.4**	KIF13B	1718, 1719	kinesin 13B	RRssGLQPQGAPE	Q70AM4	197	1	9.17E+04
86	**Enzyme, misc.**								
87	3.7	CPOX	117	coproporphyrinogen oxidase	RCsTFM#SSPVTE	Q3B7D0	49	1	1.25E+05
88	2.9	GYS1	709	glycogen synthase 1 (muscle)	sNSVDTGPSSSLSTPTEPLSPTSSLGEERN	A2RRU1	84	1	3.79E+05
89	2.4	HELZ	1785	helicase with zinc finger domain	RIsSGAAQPCVEE	NP_001099318	220	1	4.35E+06
90	3.4	HMGCS1	471	hydroxymethylglutaryl-CoA synthase 1	TYARRPsTNDHSLDE	P17425	57	2	3.55E+06
91	3.5	UQCRC1	214	ubiquinol-cytochrome c reductase core protein I	RLSRtDLTDYLSR	Q68FY0	53	1	1.45E+06
92	**G protein or regulator**								
93	-1.0	ARF GAP1	360	ADP-ribosylation factor GTPase activating protein 1	RSsDSWDIWGSGSASNNKNSNSDGWE	Q62848	45	1	6.01E+05
94	**7.4**	ARHGAP17	710	nadrin	RCsSSLPPIQAPNHPPPQPPTQPR	Q99N37	94	1	6.31E+05
95	4.7	ARHGAP17	712	nadrin	RCSSsLPPIQAPNHPPPQPPTQPR	Q99N37	94	1	7.61E+05
96	4.0	ARHGAP23	790	PREDICTED: similar to Rho GTPase activating protein 21	HYsQDCSSIKAGR	XP_220918	177	1	1.13E+05
97	-1.1	ARHGEF5	1079	PREDICTED: similar to rho guanine nucleotide exchange factor 5 isoform 1	RCsKLINSSQLLYQE	XP_342677	177	1	5.87E+05
98	**6.4**	ARPP-19	104	cyclic AMP phosphoprotein	VTGDHIPTPQDLPQRKPsLVASKLAG	Q712U5	12	10	8.48E+06
99	**8.5**	DOCK6	41	dedicator of cytokinesis 6	RSSsSLGVPLTE	NP_001102467	202	1	8.55E+05
100	1.1	RalGAPA1	753	PREDICTED: similar to GTPase activating RANGAP domain-like 1 isoform 3	SIVRQKtVDIDDSQILPR	O55007	234	1	2.95E+05
101	-1.4	RalGAPA1	772	PREDICTED: similar to GTPase activating RANGAP domain-like 1 isoform 3	VRHFsQSEDTGNE	O55007	234	1	1.78E+05
102	-1.4	GIT2	614	G protein-coupled receptor kinase interacting ArfGAP 2	QRsM#LWQGDGPLPDTAEPHAVPSPALPSTE	Q66H91	85	1	1.31E+06
103	1.7	PLEKHG3	743	PREDICTED: sim to pleckstrin homol domain containing, family G, member 3	RSsLAAEDGKCSGLGTPR	XP_234320	149	1	6.18E+05
104	-1.6	RALBP1	29	RalA binding protein 1	HGSGLTRTPsSEE	Q62796	75	1	2.52E+05
105	1.7	Rap1GAP	589	PREDICTED: similar to Rap1 GTPase-activating protein 1 (Rap1GAP)	RSsAIGIENIQE	Q5EB70	83	1	1.26E+06
106	1.7	SGSM3	405	small G protein signaling modulator 3	RKsGITSLLFGEDDLE	Q6P6R7	85	1	2.52E+05
107	1.0	TBC1D10B	139	TBC1 domain family member 10B	ASPVPGPGTPTRtPSRTASGALTAKPPLAPKPGTTVASGVTAR	NP_001102391	87	1	8.90E+04

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Index	Fold-Change (Forskolin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (Untreated)
108	-4.0	TBC1D10B	661, 670	TBC1 domain family member 10B	AVGGAPsPPPPVRRAsAGPVPGAVVIAE	NP_001102391	87	2	5.67E+06
109	3.6	TBC1D10B	670	TBC1 domain family member 10B	RAsAGPVPGAVVIAE	NP_001102391	87	2	9.04E+06
110	-2.2	Tiam1	318	PREDICTED: similar to T-lymphoma invasion and metastasis-inducing prot	RAKtTQDVNTGEGSEFADSGIE	XP_001072877	177	1	4.96E+05
111	**Kinase (non-protein)**								
112	4.9	PANK2	42	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	RRAsSAAPSESGPAE	EDL80236	49	1	1.31E+05
113	4.1	PANK2	42, 43	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	RRAssAAPSESGPAE	EDL80236	49	1	5.01E+04
114	4.4	PANK2	43	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	RASsAAPSESGPAE	EDL80236	49	1	4.41E+05
115	**-6.9**	PIK4CA	172	phosphatidylinositol 4-kinase a	RRsFNDFRSILPSNLLTVCQE	O08662	231	1	5.77E+05
116	1.3	PIK4CA	198	phosphatidylinositol 4-kinase a	RKTsSVSSISQVSPE	O08662	231	1	3.34E+05
117	**Motor or contractile protein**								
118	**8.9**	DNCH1	1228	cytoplasmic dynein 1 heavy chain 1	RKDsAIQQQVANLQMK	Q6LCG3	532	1	8.84E+04
119	-3.7	MRLC2	19, 20	myosin light chain, regulatory B	KRPQRAtsNVFAM#FDQSQIQE	P13832	20	1	2.15E+06
120	-1.0	MYH9	1940, 1944	myosin, heavy chain 9, non-muscle	KGtGDCsDEEVDGKADGADAK	Q62812	226	2	4.06E+05
121	**Phosphatase**								
122	**7.9**	CTDSPL2	9	CTD (carboxy-term domain, RNA polymerase II, polypepA)	KAsQQSSPIQTQR	Q5XIK8	53	1	1.36E+04
123	-1.3	PHACTR4	636	PREDICTED: similar to phosphatase and actin regulator 4	KLsQRPTVAE	XP_001063709	93	1	6.20E+06
124	**24.9**	MTMR3	666	myotubularin-related protein 3	RPsRLLGGAE	Q5PQT2	134	1	2.45E+04
125	3.1	PFKFB2	469	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 isoform b	RNsFTPLSSSNTIR	Q9JJH5	64	1	6.80E+05
126	2.8	PFKFB2	471	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 isoform b	RNSFtPLSSSNTIR	Q9JJH5	64	1	8.00E+05
127	2.2	PFKFB2	486	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 isoform b	NYsVGSRPLKPLSPLR	Q9JJH5	64	1	1.05E+06
128	1.3	PFKFB2	486, 496	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 isoform b	NYsVGSRPLKPLsPLRALDM#QE	Q9JJH5	64	1	2.93E+05
129	**5.2**	PFKFB3	490	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	RNsVTPLASPEPTKKPR	O35552	64	1	1.62E+05
130	**7.0**	MYPT1; PPP1R12B	669; 616	protein phosphatase 1, regulatory (inhibitor) subunit 12A	RRsYLTPVRDEE	Q10728; NP_001100648	115; 111	1	1.02E+06
131	-1.5	MYPT1	855	protein phosphatase 1, regulatory (inhibitor) subunit 12A	RStGVSFWTQDSDENE	Q10728	115	2	1.02E+06
132	-1.9	MYPT1	855, 864	protein phosphatase 1, regulatory (inhibitor) subunit 12A	RStGVSFWTQDsDENEQE	Q10728	115	1	3.09E+05
133	2.2	PPP2R5D	593	PREDICTED: similar to reg subunit B56, prot phosphatase 2A isoform 1	RKsELPQDVYTIKALE	Q499R1	72	4	7.97E+06
134	4.6	PTPN14	335	protein tyrosine phosphatase, non-receptor type 14	RNtLREQGPSEE	NP_001100670	95	1	2.57E+05
135	-1.1	SYNJ1; SYNJ1 iso4; SYNJ1 iso5	1073; 1073; 1073	synaptojanin 1	YSAPSLPIRPSRAPsRTPGPLSSQGAPVDTQPAAQKE	Q62910; Q62910-4; Q62910-5	173; 171; 143	1	2.82E+05
136	3.5	SYNJ2	1307	synaptojanin 2 isoform 1	RPsGGKPEPDDAPPVTGAVE	O55207	165	1	1.32E+05
137	**Protease**								
138	1.2	Casp8	188	caspase 8	RM#sTEGGEELPVSVLDE	Q9JHX4	55	1	1.09E+06
139	**Protein kinase, Ser/Thr (non-receptor)**								
140	1.3	B-Raf	484	PREDICTED: similar to v-raf murine sarcoma viral oncogene homolog B1	TLGRRDSsDDWEIPDGQITVGQR	XP_231692	89	1	3.22E+05
141	2.2	MRCKa	1545	CDC42-binding protein kinase alpha	RYsFRVPEEE	O54874	197	1	1.82E+06
142	1.6	QSK	384	PREDICTED: similar to KIAA0999 protein	RHtVGVADPRTE	XP_001068984	143	7	2.34E+07
143	-1.1	QSK	466	PREDICTED: similar to KIAA0999 protein	RAsDGGANIQLHAQQLLK	XP_001068984	143	4	9.29E+06
144	-1.3	HGK; TNIK; MINK	132; 187; 187	mitogen-activated protein kinase kinase kinase kinase 4	RNtFIGTPYWM#APE	NP_001100374; XP_215530; XP_001079459	135; 150; 146	1	2.05E+06
145	**8.0**	HGK	839	mitogen-activated protein kinase kinase kinase kinase 4	KGsVVNVNPTNTRPQSDTPE	NP_001100374	135	3	5.76E+05
146	3.0	KHS1	415	PREDICTED: similar to MAPK/ERK kinase kinase kinase 5 (MEKK 5)	RQSsPSCVPIAE	XP_001076790	93	1	7.09E+06
147	4.8	MARK4	511	PREDICTED: similar to MAP/microtubule affinity-regulating kinase 4	RNtYVCTERPGSE	XP_001057742	83	1	4.86E+05
148	-1.7	PCTAIRE3	109	PCTAIRE protein kinase 3	RAsLSDIGFGKLE	O35832	52	1	2.66E+06
149	-3.5	PKN1; PKN2	776; 815	protein kinase N1	GM#GYGDRtSTFCGTPE	Q63433; O08874	104; 112	1	2.28E+06
150	-1.9	PKN1; PKN2	778; 817	protein kinase N1	GMGYGDRTStFCGTPE	Q63433; O08874	104; 112	1	1.37E+06
151	**-5.7**	PLK1	210	polo-like kinase 1	KKtLCGTPNYIAPE	Q62673	68	1	1.24E+06
152	-3.2	PKCD	505	protein kinase C, delta	NRAStFCGTPDYIAPE	P09215	78	1	6.50E+05
153	2.2	PKD2	197	protein kinase D2	RLsSTSLASGHSVR	Q5XIS9	96	3	4.10E+06
154	1.9	PKD2	397	protein kinase D2	KSsTTLRE	Q5XIS9	96	2	5.72E+05
155	1.4	PKD3	109	protein kinase D3	RLsNVSLPGPGLSVPRPLQPE	Q568X9	34	2	2.46E+06
156	4.8	Raf1	43	v-raf-leukemia viral oncogene 1	RAsDDGKLTDSSKTSNTIR	P11345	73	1	1.18E+05

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Study design: rat cell line PC-12; Trypsin digest; Antibody: Phospho-PKA Substrate Motif (RRXS*/T*), PTMScan® Kit #1984, #5565

Treatments: Untreated, forskolin treated

Index	Fold-Change (Forskolin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (Untreated)
157	**6.5**	RIPK2	411	PREDICTED: similar to receptor (TNFRSF)-interacting ser-thr kinase 2	RAsSCSLTVIRPLLVE	XP_001056736	61	1	1.00E+06
158	2.2	ROCK2	1352	Rho-associated coiled-coil containing protein kinase 2	KPPAPDPFARsSPR	Q62868	159	1	8.76E+05
159	**13.4**	ROCK2	1370	Rho-associated coiled-coil containing protein kinase 2	RPsRQLAPNKPS	Q62868	159	2	9.71E+05
160	-2.9	SLK	181, 189	serine/threonine kinase 2	LADFGVSAKNtRTIQRRDsFIGTPYWM#APE	O08815	138	1	3.42E+05
161	-1.2	SLK	183, 189	serine/threonine kinase 2	NTRtIQRRDsFIGTPYWM#APE	O08815	138	3	6.21E+06
162	1.1	SLK; LOK	189; 191	serine/threonine kinase 2	RDsFIGTPYWM#APE	O08815; Q62830	138; 113	4	2.41E+07
163	**6.4**	WNK1	58	WNK lysine deficient protein kinase 1	RHtMDKDSR	Q9JIH7	225	1	3.12E+05
164	**Protein kinase, Tyr (receptor)**								
165	**-7.5**	Axl	503	Axl receptor tyrosine kinase isoform 2	RTtEATLNSLGISEE	Q8VIA0	98	1	6.99E+06
166	**Protein kinase, atypical**								
167	**10.3**	ChaK1	1501	PREDICTED: similar to Long transient receptor potential channel 7 (LTrpC7)	RAsTEDSPDVDSR	Q925B3	212	1	4.94E+04
168	**Protein kinase, dual-specificity**								
169	-1.8	CLK3	9	CDC-like kinase 3	YRsPEPDPYLSYR	Q63117	58	2	2.70E+06
170	**Protein kinase, regulatory subunit**								
171	-1.2	Kidins220	1671	kinase D-interacting substrate 220	AYNLNRtPSTVTLNNNTAPTNR	Q9EQG6	196	1	4.83E+06
172	-1.1	Kidins220	1673	kinase D-interacting substrate 220	AYNLNRTPsTVTLNNNTAPTNR	Q9EQG6	196	1	3.80E+05
173	-3.3	Kidins220	1674	kinase D-interacting substrate 220	AYNLNRTPStVTLNNNTAPTNRANQNFDE	Q9EQG6	196	1	9.62E+05
174	1.5	PKAR2B	112	protein kinase, cAMP dependent regulatory, type II beta	RAsVCAE	P12369	46	1	1.41E+06
175	1.3	STK11IP	388	serine/threonine kinase 11 interacting protein	RAsISEPSDTDPE	NP_001100392	118	2	7.96E+05
176	**RNA processing**								
177	2.1	FXR1	540	fragile X mental retardation gene 1, autosomal	RRtDEDAVLM#DGM#TE	Q5XI81	64	1	1.55E+05
178	-1.9	RBM15	256, 258	PREDICTED: similar to Putative RNA-binding protein 15 (122 protein)	RRsRsPLDKDTYAPSSSVVGSSVGSHR	XP_001068152	106	2	2.32E+06
179	-1.2	RBM15	293	PREDICTED: similar to Putative RNA-binding protein 15 (122 protein)	SLsPGGAALGYR	XP_001068152	106	1	1.92E+06
180	-2.1	LARP	1084	PREDICTED: similar to la related protein isoform 2	CPsQSSSRPATGISQPPTTPTGQATRE	XP_220446	127	1	8.57E+05
181	-2.1	LRRFIP1	88	leucine rich repeat (in FLII) interacting protein 1	RGsGDTSISMDTE	Q66HF9	80	5	8.04E+06
182	2.7	matrin 3	188	matrin 3	RDsFDDRGPSLNPVLDYDHGSRSQE	P43244	94	4	7.18E+06
183	**7.3**	NCBP1	22	nuclear cap binding protein subunit 1, 80kDa	RKTsDANETEDHLE	Q56A27	92	2	4.52E+05
184	**17.0**	NCBP1	7	nuclear cap binding protein subunit 1, 80kDa	RHsYENDGGQPHK	Q56A27	92	2	3.99E+03
185	1.7	RBM34	20	RNA binding motif protein 34	RQSsEDDVGNAATDYLVGQVADSLR	Q5M9F1	48	2	1.29E+06
186	-4.5	SAMD4	609	sterile alpha motif domain containing 4A	HALGDGVDRTStI	B5DF21	67	1	1.17E+06
187	1.4	SRm160	567, 569	serine/arginine repetitive matrix 1	RRsPsPAPPPPPPPPPRR	XP_001069368	104	1	2.09E+05
188	-1.1	SRm160	610	serine/arginine repetitive matrix 1	RYsPPIQR	XP_001069368	104	1	9.56E+05
189	1.0	SRm300	1340	PREDICTED: similar to serine/arginine repetitive matrix 2	RsSSELSPEIVE	XP_220207	296	1	5.64E+06
190	1.2	SRm300	1342	PREDICTED: similar to serine/arginine repetitive matrix 2	SSRRSSsELSPE	XP_220207	296	2	8.81E+05
191	3.0	SRm300	1575, 1577, 1579, 1580	PREDICTED: similar to serine/arginine repetitive matrix 2	AQsGtDssPEHKIPAPR	XP_220207	296	1	3.34E+05
192	3.1	SRm300	1931, 1943, 1955, 1967	PREDICTED: similar to serine/arginine repetitive matrix 2	SRTsPVTR	XP_220207	296	1	4.42E+04
194	**Receptor, channel, transporter or cell surface protein**								
195	1.9	IP3R3	934	inositol 1,4,5-triphosphate receptor, type 3	KQsVFGASSLPTGVGVPE	Q63269	304	1	4.75E+05
196	2.1	NUP133	259	PREDICTED: similar to Nuclear pore complex protein Nup133	RVsSLFGILSPTSD	XP_001053507	128	1	1.74E+05
197	**15.4**	NUP133	37	PREDICTED: similar to Nuclear pore complex protein Nup134	GLsLGSAVSSPVLFSPVGR	XP_001053507	128	2	2.35E+05
198	1.3	SUN2	193, 196	PREDICTED: similar to unc-84 homolog B	RRGtGGsESSKANGLTM#E	XP_001076724	89	1	1.57E+05
199	1.3	SUN2	193, 196, 199	PREDICTED: similar to unc-84 homolog B	RGtGGsESsKANGLTM#E	XP_001076724	89	1	1.79E+05
200	**Secreted protein**								
201	-3.1	PDAP1	18	PDGFA associated protein 1	VRQYtSPEEIDAQLQAE	Q62785	21	1	9.83E+05
202	**Transcriptional regulator**								
203	3.3	CBX5	93	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	KSsFSNSADDIKSK	NP_001100267	22	1	1.02E+05
204	4.6	DDX17	138	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	GVKDGGRRDsTSYR	Q568Z8	29	1	1.75E+04
205	**10.8**	FLII	436	flightless I homolog	RKDsAQDVQAK	Q5RKI5	145	1	6.90E+04
206	2.5	FLNA	2152	filamin, alpha	RAPsVANVGSHCDLSLKIPE	XP_238167	281	15	6.51E+07
207	**12.0**	FLNA	2336	filamin, alpha	RLtVSSLQE	XP_238167	281	1	3.28E+06
208	2.9	FosB	224	FBJ osteosarcoma oncogene B	RSsSSGDQSSDSLNSPTLLAL	Q62738	26	1	2.87E+06
209	1.3	FosB	224, 236	FBJ osteosarcoma oncogene B	RSsSSGDQSSDSLNsPTLLAL	Q62738	26	1	8.08E+05
212	-1.2	TFIIIC-alpha	547	general transcription factor III C 1	SRRSsACRDGLDTSSSSE	Q63505	242	2	2.75E+05

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213	2.8	HBP1	378	HMG-box transcription factor 1	RAsLSCGGPGTGQE	Q62661	57	1	1.47E+05
214	**18.6**	HMBOX1	170	PREDICTED: similar to F54A5.1	RDsSVIKEE	XP_224289	47	1	3.59E+04
216	2.9	NCoA6	2013	PREDICTED: similar to Nuclear receptor coactivator 6 (ASC-2)	RNsRTEEPTMASE	Q9JLI4	218	1	1.04E+05
217	**6.9**	N-CoR1; SMRT	71; 67	PREDICTED: similar to nuclear receptor co-repressor 1	RRPsLLSE	Q498D3; NP_001101804	273; 270	1	2.76E+06
218	1.3	NFAT4	262, 266, 270	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NWLSPRPAsGPSsRPTsPCGK	NP_001101917	115	1	7.44E+05
219	1.3	NFAT4	266, 270	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	NWLSPRPASGPSsRPTsPCGK	NP_001101917	115	1	6.86E+05
220	-1.0	NFAT3	264	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	DSWLLLSAPGPIPASPRPAsPCGKR	NP_001100734	96	1	7.09E+05
221	**6.3**	NFAT3	334	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	RTsSEQAVALPR	NP_001100734	96	1	7.72E+04
222	1.5	SQSTM1	24	sequestosome 1 isoform 1	RFsFCFSPEPEAE	O08623	48	1	8.12E+05
223	1.5	YAP1; YAP1 iso3	112; 112	yes-associated protein	AHsSPASLQLGAGTLTASGVVSGPAATPAAQHLR	Q2EJA0; Q3LRU4	51; 39	4	1.25E+07
224	1.7	YAP1; YAP1 iso3	88, 94; 88, 94	yes-associated protein	sHSRQAsTDAGTAGALTPQHVR	Q2EJA0; Q3LRU4	51; 39	1	5.02E+05
225	1.9	YAP1; YAP1 iso3	88, 95; 88, 95	yes-associated protein	sHSRQAStDAGTAGALTPQHVR	Q2EJA0; Q3LRU4	51; 39	1	5.75E+06
226	2.3	YAP1; YAP1 iso3	90, 95; 90, 95	yes-associated protein	SHsRQAStDAGTAGALTPQHVR	Q2EJA0; Q3LRU4	51; 39	1	7.36E+06
227	2.2	YAP1; YAP1 iso3	94; 94	yes-associated protein	QAsTDAGTAGALTPQHVR	Q2EJA0; Q3LRU4	51; 39	2	1.40E+07
228	1.0	YAP1; YAP1 iso3	94, 95, 104; 94, 95, 104	yes-associated protein	SHSRQAstDAGTAGALtPQHVR	Q2EJA0; Q3LRU4	51; 39	1	1.93E+05
229	2.3	YAP1; YAP1 iso3	95; 95	yes-associated protein	SHSRQAStDAGTAGALTPQHVR	Q2EJA0; Q3LRU4	51; 39	1	1.60E+06
230	**Translation**								
231	-1.7	eIF4B	406	eukaryotic translation initiation factor 4B	ERHPsWRSEE	Q5RKG9	69	1	9.87E+06
234	**13.0**	eIF4B	422	eukaryotic translation initiation factor 4B	SRTGsESSQTGTSATSGR	Q5RKG9	69	2	2.37E+04
236	1.4	S6	235, 236, 240, 244	ribosomal protein S6	RLssLRAsTSKsE	P62755	29	3	1.03E+07
237	**Tumor suppressor**								
238	**16.0**	LIMD1	303	LIM domains containing 1	RDsSLGYEAPGR	XP_236734	71	2	4.81E+05
239	**Ubiquitin conjugating system**								
240	-1.3	NICE-4	624, 628	Atpase, class I, type 8B, member 2	RYPsSISsSPQKD	NP_001019969	117	1	2.97E+05
242	2.2	HECTD1	1763	PREDICTED: similar to E3 ubiquitin-protein ligase HECTD1 (EULIR)	RRtWDDDYVLKR	XP_343061	289	1	3.94E+05
243	**11.2**	MARCH7	153	membrane-associated ring finger (C3HC4) 7	RRRDsSISSLMDYSHR	Q5XI50	76	1	4.37E+04
244	1.6	C14ORF4	644, 646	polyglutamine-containing protein	RNsSsPVSPASVPGQR	Q5EIC4	81	1	2.73E+05
245	1.1	C14ORF4	644, 646, 649	polyglutamine-containing protein	RNsSsPVsPASVPGQRR	Q5EIC4	81	2	5.72E+05
246	-1.2	UBE1	13	ubiquitin-activating enzyme E1	RVsGPDPKPGSNCSSAQSVLSE	Q5U300	118	1	3.93E+07
247	**Unknown function**								
248	**10.9**	ANKRD15	70	ankyrin repeat domain 15	RKPsGPCAE	NP_001032274	148	1	6.92E+04
249	-1.1	ANKRD34A	290	ankyrin repeat domain 34A	RHsTEGPEDPPPWAE	Q5BJT1	52	1	4.08E+05
250	3.2	ARL6IP2	26	ADP-ribosylation factor-like 6 interacting protein 2	RRQTSDsSVGVNHVSSTTSLGEDYE	NP_001094141	66	1	2.58E+05
251	**6.8**	ASPSCR1	23	PREDICTED: similar to alveolar soft part sarcoma chromosome region	RHtVKVTPSTVLLQVLE	XP_001076577	58	1	5.88E+04
252	**14.9**	BCAS3	14	PREDICTED: similar to Breast carcinoma amplified seq 3 homolog (K20D4)	RPsRCTGGVVVRPQAVTE	XP_001081081	101	1	6.40E+05
253	4.2	CCDC120	277	PREDICTED: hypothetical protein	RNsVASPTSPTR	XP_001063966	68	1	8.26E+04
254	**9.4**	Ccdc52	823	coiled-coil domain containing 52	RSsGAISNSCSPLNATSGSGKFTPVNPR	NP_001008286	96	1	6.47E+04
255	**76.6**	Clec16a	844	PREDICTED: similar to CG12753-PA, isoform A	RGsSDPTVQR	XP_213209	116	2	3.34E+03
256	1.1	CUEDC1	9	CUE domain containing 1	RSsSGSGGGGATGARGAGTGTGDGSAAPQE	Q5PQP8	43	1	2.15E+05
257	**6.7**	Cux1	1480	PREDICTED: similar to CCAAT displacement protein isoform a	SSALPSTSAPANAPARRPsSLQSLFGLPE	XP_001070482	167	1	2.58E+05
258	2.6	DENND1A	487	PREDICTED: similar to CG18659-PA, isoform A isoform 1	GRRtSISSPEQPQPYR	XP_001054659	108	1	9.94E+05
259	1.7	FAM122A	36	hypothetical protein LOC309420	RSNsAPLIHGLSDSSPVFQAEAPSAR	Q6AYT4	30	1	8.58E+05
260	**5.9**	FAM122A	63	hypothetical protein LOC309420	RNSTtFPSRHGLLLPASPVR	Q6AYT4	30	1	1.67E+05
261	-1.6	FAM83H	959	family with sequence similarity 83, member H	RGsPVPPVPER	XP_343266	131	1	4.16E+05
262	-2.5	FAM83H	959, 970	family with sequence similarity 83, member H	RGsPVPPVPERRGsLTFAGE	XP_343266	131	1	1.63E+06
263	3.6	Heatr3	342	PREDICTED: similar to CG10286-PA	RKtFISDLLPSTDKE	XP_001067127	75	1	2.09E+05
264	2.0	ZNHIT4	9	PAP-1 binding protein	RGsTSGAM#EPPEPGETLE	Q0D2L4	39	1	2.45E+05
266	2.4	C9orf140	218	hypothetical protein LOC680531	RHtITNGVDCSLLK	NP_001102888	42	3	2.46E+06
267	**69.6**	LOC682138	6	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 43	REsAANASSSGVASR	XP_001060057	72	2	2.27E+04
268	**16.0**	C14orf156	49	SRA stem-loop-interacting RNA-binding protein	RCtVPFDKE	NP_001102977	13	1	2.62E+05
269	-1.3	LDLRAP1	199	low density lipoprotein receptor adaptor protein 1	GGDVPGTRRDStPSLKTSVATGNLLDLEE	NP_001102741	34	2	2.96E+06

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270	1.0	Lmod2	332, 339	leiomodin 2 (cardiac)	ENtTLLRLGy	NP_001094434	62	1	6.13E+06
271	1.9	LRBA	1550	LPS-responsive vesicle trafficking, beach and anchor containing	RRDsGLGEE	NP_001102025	307	2	8.39E+05
272	-2.8	LRRFIP2	133	leucine rich repeat (in FLII) interacting protein 2	RGsGDTSSLIDPDTSLSE	Q4V7E8	50	1	2.96E+06
273	**15.5**	BPY2-IP1	659	microtubule-associated protein 1S	RSTsPHDVDLCLVSPCE	P0C5W1	103	1	2.86E+04
274	**7.7**	MDM1	565	Mdm1 nuclear protein homolog	RRPsSQDGLE	Q5PQN4	81	1	1.62E+04
275	2.9	Mki67	193	PREDICTED: similar to Antigen KI-67	RNsVNLDESE	XP_225460	346	1	5.79E+05
276	1.3	NHSL1	207	rCG57359, isoform CRA_b	RKtISGIPDIIQKE	EDL93774	155	1	4.48E+05
277	**15.3**	Nck1	66	NCK adaptor protein 1	KAsIVKNLKDTLGIGKVK	NP_001100321	43	1	1.91E+05
278	-1.0	Nfx1	28	PREDICTED: similar to nuclear transcription factor, X-box binding 1	KNsGLNCGTQR	XP_001064398	129	1	1.08E+05
279	3.4	PAN3	305	PREDICTED: similar to PABP-dependent poly(A) nuclease 3	RRSHtPNPASFMVPPSASTPANNPVPQTPSSGQVIQKE	XP_001068449	90	2	1.03E+05
280	**13.1**	PCNXL3	127	PREDICTED: similar to pecanex-like 3	KVsSTPPVR	XP_001074181	179	1	8.46E+04
281	4.2	PCNXL3	135	PREDICTED: similar to pecanex-like 3	CsSQHSVFGFNQVSE	XP_001074181	179	1	1.27E+05
282	**5.6**	PHLDB1	148	PREDICTED: similar to pleckstrin homology-like domain, family B, member 1	RPsRGLAGAIVVSGR	Q63312	94	2	8.73E+05
283	**15.8**	PHLDB1	27, 33	PREDICTED: similar to pleckstrin homology-like domain, family B, member 1	KGsFSGRLsPAYSLGSLTGASPR	Q63312	94	1	2.69E+05
284	-1.8	PHLDB1	29, 33, 45, 49	PREDICTED: similar to pleckstrin homology-like domain, family B, member 1	KGSFsGRLsPAYSLGSLTGAsPRQsPHAQR	Q63312	94	1	1.30E+06
285	2.0	PHLDB1	72, 77	PREDICTED: similar to pleckstrin homology-like domain, family B, member 1	KNsITEIsDNEDDLLE	Q63312	94	1	9.29E+05
286	3.9	Pla2r1	105	PREDICTED: similar to phospholipase A2, group IB, pancreas, receptor	LKRPLsLYE	XP_001069062	170	1	3.36E+06
287	**7.9**	Prr14; LOC687819	358; 358	PREDICTED: hypothetical protein	RHtVGCGE	XP_001080025; XP_001080247	80; 51	1	3.19E+04
288	**13.1**	Qars	70	glutaminyl-tRNA synthetase	RLsFLVGYIANK	NP_001007625	88	1	1.08E+05
289	**8.7**	rubicon	445	PREDICTED: similar to Protein KIAA0226	RPsEGQSLISYLSE	XP_221382	106	1	1.13E+05
290	**5.5**	Smchd1	2028	PREDICTED: similar to SMC hinge domain containing 1	RCsDSLCLSPKIE	XP_001056555	233	1	9.79E+05
291	2.0	RGD1307882	946, 948	PREDICTED: similar to U2-associated SR140 protein isoform 2	VKsPsPKSE	XP_001065014	118	1	7.72E+04
292	1.0	RGD1308350	833	PREDICTED: similar to formin 3 CG33556-PA	RsSWYVDASDFLAPEDILNTQPSE	XP_001072750	111	1	7.70E+05
293	-1.6	RGD1308350	834	PREDICTED: similar to formin 3 CG33556-PA	RSsWYVDASDFLAPE	XP_001072750	111	3	3.10E+06
294	-1.1	C18orf25	66	hypothetical protein LOC307249	LRRDsSESQLASTE	NP_001100844	43	1	5.20E+06
295	1.8	LOC196752	604	PREDICTED: similar to CG32542-PA	RLsSEDSSLEPDLAE	XP_001057186	197	1	7.77E+05
296	**17.6**	SECISBP2L	251	PREDICTED: similar to Protein KIAA0256	RAsHPAAE	XP_001077702	120	1	2.49E+04
297	-1.3	WWC3	1124	PREDICTED: similar to plectin 1	SQtFSPGAR	XP_228858	147	1	4.79E+05
298	-1.8	WWC3	1142	PREDICTED: similar to plectin 1	LYRSDsDSSTLPR	XP_228858	147	1	3.40E+05
299	-1.4	KIAA1522	171	hypothetical protein LOC500552	RRsTVLGLPQHVQKE	XP_575914	107	1	1.01E+06
300	2.5	KIAA1522	172	hypothetical protein LOC500552	RStVLGLPQHVQKE	XP_575914	107	2	1.34E+06
301	**11.2**	KIAA1522	968	hypothetical protein LOC500552	KPsVGVPLSPSLPRAE	XP_575914	107	3	3.46E+05
302	-1.6	CNST	154	PREDICTED: hypothetical protein	VTRLPsVSDENE	XP_001060344	88	2	1.10E+06
303	**15.0**	Rgl2	738	ral guanine nucleotide dissociation stimulator-like 2	RRPsAATSGSHSGPSASGTPPSEGGGGSFPR	NP_997712	84	1	2.81E+04
304	4.1	Sav1	91	salvador homolog 1	REsNRLSAPSSYLVR	NP_001091050	45	1	1.31E+05
305	-2.4	Sfrs6	97	splicing factor, arginine/serine-rich 6	RTsGRDKYGPPVRTE	NP_001014207	39	1	4.76E+05
306	1.7	SGOL2	480	PREDICTED: similar to tripin	RRQtYTTDEQEE	XP_001068385	131	1	4.37E+04
307	-1.7	Sgpp1	201	PREDICTED: similar to Sphingosine-1-phosphate phosphatase 1 (Spp1)	RNsLTGEEGE	XP_001080791	58	1	1.19E+05
308	2.5	SH2D5	12	PREDICTED: hypothetical protein	RAsDCGPAPYRPR	XP_001070433	47	1	6.75E+05
309	**6.7**	SIP1	70	survival of motor neuron protein interacting protein 1	RKQsVNVSLSGCHPAPE	Q9QZP1	30	2	1.62E+05
310	1.8	SLAIN2	87	SLAIN motif family, member 2	RTsSEDLRDATSLLAAGE	NP_001100684	65	1	3.74E+05
311	-2.5	Slc22a17	497	solute carrier family 22, member 17	LCRRPsLLRQPPPNRCDHVPLLATPNPAL	NP_803156	56	1	6.54E+05
312	**5.2**	Spag5	64	sperm associated antigen 5	RNSsSPVNFVNAE	NP_001037689	132	1	6.10E+05
313	2.8	TMCC1	63, 64	PREDICTED: similar to Transmembrane and coiled-coil domains protein 1	RRssVSPHDVQQIQADAEPEVDLDSQNTCAE	XP_001054467	77	1	1.25E+05
314	-2.9	TMCC1	64	PREDICTED: similar to Transmembrane and coiled-coil domains protein 1	RRSsVSPHDVQQIQADAEPEVDLDSQNTCAE	XP_001054467	77	1	1.43E+05
315	**-38.9**	TMEM40	390	PREDICTED: similar to transmembrane protein 40	RRGsGSAEGEVE	XP_001059205	62	1	2.11E+05
317	**17.4**	TRAK2	729	trafficking protein, kinesin binding 1	RDsTITFSSTR	Q8R2H7	102	1	4.95E+04
318	-1.2	TUSC2	50	tumor suppressor candidate 2	RGsM#FYDEDGDLAHE	NP_001102767	12	2	9.79E+05
319	3.1	Txlna	218	taxilin alpha	KQsQLVQE	NP_001121105	63	1	1.93E+05
321	-2.6	Utx	924, 927, 939, 943	PREDICTED: similar to ubiquitously transcribed tetratricopeptide repeat gene	PPsSPyPPLPKDKLNPPtPSIyLENK	XP_001055391	154	1	4.55E+05
322	1.0	WDR20	401	PREDICTED: similar to WD repeat domain 20 isoform 1	ARTHtNVM#NATSPPAGSNGNSVTTPGDSGPPPLPR	Q5BJW6	65	1	2.27E+05
323	2.4	WDR20	432	PREDICTED: similar to WD repeat domain 20 isoform 1	sNSLPHSAVSNAGSK	Q5BJW6	65	1	1.66E+05

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Phospho-PKA Substrate Motif (RRXS*/T*), label-free quantitation

Study design: rat cell line PC-12; Trypsin digest; Antibody: Phospho-PKA Substrate Motif (RRXS*/T*), PTMScan® Kit #1984, #5565

Treatments: Untreated, forskolin treated

Index	Fold-Change (Forskolin/Untreated)	Protein Name	Phosphorylation Site	Description	Peptide	Accession	kD	Count in Study	Intensity (Untreated)
324	**Vesicle protein**								
325	1.9	EHBP1L1	462	EH domain binding protein 1-like 1 isoform 1	ARSStSPVVPTEGLVNGVGAPASVSGVR	Q5PQM3	84	1	5.23E+05
326	1.7	EHBP1L1	463	EH domain binding protein 1-like 1 isoform 1	SSTsPVVPTEGLVNGVGAPASVSGVR	Q5PQM3	84	2	7.25E+05
327	-1.2	GOLGA3	345	golgi autoantigen, golgin subfamily a, 3	RDsICSSVSM#E	NP_001101317	163	3	1.15E+06
328	-1.1	NDRG1	330, 333, 336	N-myc downstream regulated gene 1	SRTAsGSsVTsLEGTR	Q6JE36	43	1	5.16E+05
329	1.1	NDRG1	330, 333, 336, 342	N-myc downstream regulated gene 1	SRTAsGSsVTsLEGTRsR	Q6JE36	43	1	2.78E+05
330	**8.2**	NDRG1	346	N-myc downstream regulated gene 1	SHtSEGPR	Q6JE36	43	8	5.80E+05
331	2.2	NDRG1	366	N-myc downstream regulated gene 1	SHtSEDARLNITPSSGATGNNAGPK	Q6JE36	43	2	6.84E+05
332	3.0	NSFL1C	176	NSFL1 (p97) cofactor (p47)	RHsGQDVHVVLK	O35987	41	3	7.22E+05
333	1.1	REPS1	272	RalBP1 associated Eps domain containing 1	IRRQsSSYDDPWKITDE	NP_001099734	67	2	7.64E+06
334	**Inhibitor**								
335	**11.6**	ENSA	109	endosulfine alpha isoform 1	KSsLVTSKLAG	P60841	13	1	2.08E+05
336	**Lipid binding**								
337	**29.6**	OSBPL11	185	oxysterol binding protein-like 11	SFsLASSGNSPISQR	NP_001100560	84	1	1.68E+05
338	**6.2**	OSBPL11	200	oxysterol binding protein-like 11	RPsQNAISFFNVGHSK	NP_001100560	84	3	2.12E+06

LEGEND: * = phosphorylation; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted