

Supplementary Table S1b- MS2 significant phosphopeptides (sheet = 'rTg4510 sig LIB vs sham')

PG.Genes	PG.ProteinGroups	PG.ProteinDescriptions	EG.PrecursorId	Phos site	Expression Ratio	LOG2FC	pvalue	(-) Log10 p value
Tdbk1	Q6PCN3	Tau-tubulin kinase 1	_RVNS[Phospho (STY)]PESER_2	#N/A	0.0698	-3.8405	0.0000	6.3618
Hepacam	Q640R3	Hepatocyte cell adhesion molecule	_SEADTPRS[Phospho (STY)]GEQER_2	#N/A	2.3820	1.2522	0.0000	4.3240
Vdac3	Q60931	Voltage-dependent anion-selective channel protein 3	_WNTDNTLGTEISWENK_1	#N/A	0.4164	-1.2640	0.0001	3.8572
Tubb4b	P68172	Tubulin beta-4b chain	_TAVC[Carbamidomethyl (C)]DPPR_2	#N/A	0.6352	-0.6547	0.0002	3.6608
Hnrnpcc	Q9I204	Heterogeneous nuclear ribonucleoproteins C1/C2	_QADLSPSS[Phospho (STY)]PVVM[Oxidation (M)]IK_2	#N/A	0.2549	-1.9720	0.0003	3.5822
Smarrc2	Q6PDG5	SWI/SNF complex subunit SMARCC2	_TLTDEVNS[Phospho (STY)]PDS[Phospho (STY)]DRBDK_3	#N/A	0.7359	-0.4424	0.0003	3.5386
Gria2	P23819	Glutamate receptor 2	_YTSALTYDANQVM[Oxidation (M)]TEAFR_2	#N/A	1.8506	0.8880	0.0003	3.4836
Adgrl3	Q80753	Adhesion G protein-coupled receptor L3	_GSSDGFVPPNKGAS[Phospho (STY)]PEGTSK_3	#N/A	0.2666	-1.9074	0.0004	3.3682
Ank3	G5E8K5	Ankyrin-3	_TEEPVS[Phospho (STY)]PLTAYCK_2	G5E8K5_S1883_M1_Ank3	8.1876	3.0334	0.0006	3.2461
Epb413	Q9WV92	Band 4.1-like protein 3	_SSSKLS[Phospho (STY)]RS[Phospho (STY)]PIUK_2	#N/A	1.3275	0.4087	0.0006	3.2144
Cntn2	Q61330	Contactin-2	_TTGPGGGDPAEVHVR_3	#N/A	0.4419	-1.1782	0.0007	3.1712
Zc3h13	E9Q784	Zinc finger CCH domain-containing protein 13	_SKLS[Phospho (STY)]PS[Phospho (STY)]PSLRK_2	#N/A	0.2158	-2.2124	0.0008	3.1110
Paip1	Q99JF8	PC4 and SFRS1-interacting protein	_FSSQQASTK_2	#N/A	0.3788	-1.4006	0.0011	2.9717
Cnp	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	_M[Oxidation (M)]VSADAYK_2	#N/A	0.6769	-0.5630	0.0014	2.8475
Cct7	P80313	T-complex protein 1 subunit eta	_ATISNDGATLK_2	#N/A	1.7170	0.7799	0.0015	2.8162
Fyb1	O35601	PNV-binding protein 1	_VAGQSS[Phospho (STY)]PSGIQR_2	O35601_S28_M1_Fyb1	0.2375	-2.0738	0.0017	2.7805
Cyb5a	P56395	Cytochrome b5	_Acetyl (Protein N-term)[AGQS[Phospho (STY)]DKDVK_2	P56395_S5_M1_Cyb5a	0.6005	-0.7358	0.0020	2.7067
Hsp90aa1	P07901	Heat shock protein HSP 90-alpha	_HGLEVYM[Oxidation (M)]EPIDEY[Carbamidomethyl (C)]VQQLK_3	#N/A	0.4754	-1.0727	0.0021	2.6736
Rabep1	O35551	Rab GTPase-binding effector protein 1	_RAQS[Phospho (STY)]TDS[Phospho (STY)]LGTSSLSQSK_2	#N/A	1.7132	0.7767	0.0022	2.6502
Hsp90b1	P08113	Endoglin	_LSLTDENALAGNELTVK_2	#N/A	1.9566	0.9684	0.0024	2.6266
Eno2	P17183	Gamma-enolase	_NYPVSVSEDPDQDDWAWSK_3	#N/A	2.1240	1.0868	0.0024	2.6176
Scn1a	A2APX8	Sodium channel protein type 1 subunit alpha	_QAS[Phospho (STY)]FTYNYK_2	A2APX8_S1939_M1_Scn1a	4.5433	2.1837	0.0029	2.5432
Pnt2	E9PUL5	Proline-rich transmembrane protein 2	_AELAPETTETPVETPVQATDLSNPEEGSK_3	#N/A	0.4005	-1.3200	0.0029	2.5427
Pdhx1	P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	_AAASTDYVVR_2	#N/A	0.6736	-0.5701	0.0029	2.5423
Pdo	Q9QYK7	Protein piccolo	_LPAQCGPQPTAAK_2	#N/A	0.2916	-1.7777	0.0030	2.5263
Gtf2f2	Q8R0A0	General transcription factor IIF subunit 2	_HYQTEEKS[Phospho (STY)]D_2	Q8R0A0_S248_M1_Gtf2f2	0.3302	-1.5987	0.0031	2.5139
Shank2	Q80Z38	SH3 and multiple ankyrin repeat domains protein 2	_QSNVEDS[Phospho (STY)]PEK_2	#N/A	4.9765	2.3151	0.0031	2.5041
Ubpap2l	Q80X50	Ubiquitin-associated protein 2-like	_YPSISSS[Phospho (STY)]PQKDLTQAK_2	#N/A	2.9965	1.5833	0.0032	2.4957
Ndufs1	Q91V09	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	_HSFC[Carbamidomethyl (C)]EVLK_2	#N/A	1.4834	0.5689	0.0034	2.4624
Samn50	Q8BGH2	Sorting and assembly machinery component 50 homolog	_LELNYC[Carbamidomethyl (C)]IPM[Oxidation (M)]GVGGDGR_2	#N/A	0.4366	-1.1958	0.0035	2.4613
Srsf3	P84104	Serine/arginine-rich splicing factor 3	_VYVGNLGNNGNK_2	#N/A	0.2509	-1.9949	0.0035	2.4580
Dennd4b	Q3U1Y4	DENN domain-containing protein 4B	_S[Phospho (STY)]APSS[Phospho (STY)]PAPR_2	Q3U1Y4_S232_M2_Dennd4b	3.9846	1.9944	0.0036	2.4496
Sgpl1	Q8VD37	SH3-containing GRB2-like protein 3-interacting protein 1	_KVAEQTFKDDYLETSS[Phospho (STY)]PK_3	#N/A	1.6840	0.7519	0.0036	2.4392
Kpnb1	P70168	Importin subunit beta-1	_Acetyl (Protein N-term)[M[Oxidation (M)]ELITILEK_2	#N/A	0.6113	-0.7102	0.0037	2.4303
Srrm1	Q52K18	Serine/arginine repetitive matrix protein 1	_RWQSS[Phospho (STY)]PVTK_2	#N/A	0.1629	-2.6177	0.0038	2.4198
Pde1b	Q01065	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B	_QLDTEDELREL_3	#N/A	1.9354	0.9527	0.0038	2.4179
Paflah1b1	P63005	Platelet-activating factor acetylhydrolase 1B subunit beta	_FLSC[Carbamidomethyl (C)]ADKK_2	#N/A	0.7444	-0.4259	0.0040	2.4031
Rab14	Q91V41	Ras-related protein Rab-14	_QFAEENGLFEASAK_2	#N/A	1.6222	0.6979	0.0040	2.4013
Sugt1	Q9C0X4	Protein SGT1 homolog	_ALEONPODAQYVC[Carbamidomethyl (C)]QR_2	#N/A	0.5925	-0.7552	0.0040	2.3966
Ppia	P17742	Peptidyl-prolyl cis-trans isomerase A	_VKEGM[Oxidation (M)]NVEAM[Oxidation (M)]ER_3	#N/A	0.6390	-0.6461	0.0041	2.3873
Hdgf12	Q3UMU9	Hepatoma-derived growth factor-related protein 2	_AQEGDGS[Phospho (STY)]EDGPR_2	Q3UMU9_S620_M1_Hdgf12	0.3336	-1.5839	0.0042	2.3796
Tjp2	Q9D2U1	Tight junction protein ZO-2	_GRS[Phospho (STY)]IRDYDR_3	#N/A	1.5091	0.5937	0.0043	2.3674
Eci1	P42125	Enoyl-CoA delta isomerase 1, mitochondrial	_EADQNFTFSK_2	#N/A	1.5592	0.6408	0.0044	2.3596
Srrm2	Q8BT18	Serine/arginine repetitive matrix protein 2	_SGSQELDGKPSAS[Phospho (STY)]PQER_2	Q8BT18_S1508_M1_Srrm2	0.0123	-6.3438	0.0044	2.3587
Syncrip	Q77MK9	Heterogeneous nuclear ribonucleoprotein Q	_TGYTLDTTGGR_2	#N/A	0.2688	-1.8951	0.0045	2.3444
Pmp	P04925	Major prion protein	_PM[Oxidation (M)]HFGNDWEDR_3	#N/A	0.5764	-0.7950	0.0047	2.3322
Tpm3	P21107	Tropomyosin alpha-3 chain	_TEERAELAEK_2	#N/A	1.6208	0.6967	0.0048	2.3208
Atg2b	Q80XK6	Autophagy-related protein 2 homolog B	_S[Phospho (STY)]SPVC[Carbamidomethyl (C)]STAPVETEPK_2	Q80XK6_S239_M1_Atg2b	1.7650	0.8197	0.0048	2.3188
Ssr3	Q9D0F9	Translocon-associated protein subunit gamma	_QGS[Phospho (STY)]EEDLLQDFSR_2	Q9D0F9_S11_M1_Ssr3	0.1160	-3.1083	0.0049	2.3088
Flt1	P35969	Vascular endothelial growth factor receptor 1	_DGFADPFHSGS[Phospho (STY)]SDVVR_3	P35969_S1207_M1_Flt1	1.7968	0.8454	0.0051	2.2954
Vipax39	Q8BGQ1	Spermatogenesis-defective protein 39 homolog	_ETAGS[Phospho (STY)]SGSTPEGR_2	Q8BGQ1_S77_M1_Vipax39	1.7973	0.8458	0.0051	2.2907
Mtmr7	Q9Z2C9	Myotubularin-related protein 7	_S[Phospho (STY)]PSGGHAPSEDSGKDR_3	#N/A	1.7981	0.8465	0.0052	2.2816
Chchd6	Q91VN4	MICOS complex subunit Mic25	_KXAS[Phospho (STY)]LTSPDQGSAR_2	#N/A	0.4718	-1.0836	0.0053	2.2797
Gatad2b	Q8VHR5	Transcriptional repressor p66-beta	_S[Phospho (STY)]LDPADEKDDVAK_2	#N/A	1.7984	0.8467	0.0053	2.2785
Ctin	Q60598	Src substrate cortactin	_YQIDKDKK_2	#N/A	1.7076	0.7720	0.0053	2.2774
Aq3b2	Q9IMES	AP-3 complex subunit beta-2	_QLVPSFEGGALSRL_2	#N/A	0.6730	-0.5714	0.0053	2.2733
Ndufb8	Q9Q6I5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit B, mitochondrial	_DPWYQWDSLELA_2	#N/A	2.1523	1.1059	0.0054	2.2642
Ef4g1	Q6NZ16	Eukaryotic translation initiation factor 4 gamma 1	_AAS[Phospho (STY)]LTEDR_2	#N/A	1.8378	0.8780	0.0056	2.2547
Arcp2	Q9CVB6	Actin-related protein 2/3 complex subunit 2	_YFQJQEEKEGENR_2	#N/A	1.6471	0.7199	0.0056	2.2503
Sptbn1	Q62261	Spectrin beta chain, non-erythrocytic 1	_RRPPSS[Phospho (STY)]PDNPNTK_2	#N/A	0.0401	-4.6386	0.0057	2.2440
ApoE	P08226	Apolipoprotein E	_DAEDLQKR_2	#N/A	1.8015	0.8492	0.0057	2.2412
Ank2	Q8CBR3	Ankyrin-2	_HTPVSPSS[Phospho (STY)]KNEKLS[Phospho (STY)]PVS[Phospho (STY)]PSAK_3	Q8CBR3_S1810_M3_Ank2	1.5821	0.6619	0.0058	2.2353
Scp2	P32020	Sterol carrier protein 2	_GSVLPNSDKK_2	#N/A	0.3998	-1.3228	0.0059	2.2319
Snn1	P97801	Survival motor neuron protein	_RGTT[Phospho (STY)]GGSDSDSDWDDTALK_3	P97801_T22_M1_Snn1	1.6162	0.6926	0.0059	2.2288
Oxr1	Q4KMM3	Oxidation resistance protein 1	_DQDQGLKRD[Phospho (STY)]ETEVEELR_3	#N/A	1.7574	0.8134	0.0059	2.2270
MAPT	P10636	Microtubule-associated protein tau	_SKGSS[Phospho (STY)]TENLK_2	#N/A	2.5561	1.3540	0.0059	2.2267
Sern1	Q9CZC8	Secernin-1	_DEVQEVEVYFVAVDHAESK_3	#N/A	1.9367	0.9536	0.0060	2.2193
Tlpl11	Q9ERA6	Tuftelin-interacting protein 11	_TTQSQDQFVADS[Phospho (STY)]EEEEEEEFQK_3in	Q9ERA6_S211_M1_Tlpl11	0.6578	-0.6042	0.0062	2.2107
Sklc16a7	O70451	Monocarboxylate transporter 2	_VGS[Phospho (STY)]RHDS[Phospho (STY)]TLKK_2	#N/A	2.3437	1.2288	0.0063	2.1993
Ubqln1	Q8R317	Ubiquilin-1	_FQOOLEQLSAM[Oxidation (M)]GLFLNR_2	#N/A	0.6109	-0.7109	0.0065	2.1897
Map1b	P14873	Microtubule-associated protein 1B	_TLVVSFSPQS[Phospho (STY)]VQSPDTEK_3	#N/A	1.8478	0.8858	0.0065	2.1851
Fam171a2	A2A699	Protein FAM171A2	_RDS[Phospho (STY)]LTPDELGAEVGEAGDK_3	#N/A	1.8060	0.8528	0.0066	2.1811
Agap2	Q3UH09	Arl-GAP with GTPase, ANK repeat and PH domain-containing protein 2	_SCNS[Phospho (STY)]LNKEWK_2	Q3UH09_S684_M1_Agap2	0.3512	-1.5095	0.0067	2.1745
Ncan	P55066	Neurocan core protein	_HLQAFFEDFGDNC[Carbamidomethyl (C)]DAGWLSDR_3	#N/A	0.4223	-1.2437	0.0069	2.1619

Nsf	P46460	Vesicle-fusing ATPase	_VEVDMEK_2	#N/A	1.8074	0.8539	0.0069	2.1608
Hscw1	Q8K4P8	E3 ubiquitin-protein ligase HECW1	_C[Carbamidomethyl (C)]SPC[Carbamidomethyl (C)]SS[Phospho (STY)]PQNSPGLQR_2	Q8K4P8_S1203_M1_Hscw1	1.6771	0.7459	0.0070	2.1565
Vcp	Q01853	Transitional endoplasmic reticulum ATPase	_AAINEC[Carbamidomethyl (C)]QANFSGIK_2	#N/A	1.6139	0.6905	0.0071	2.1496
Rpl34	Q9D189	60S ribosomal protein L34	_SAC[Carbamidomethyl (C)]GVC[Carbamidomethyl (C)]PGR_2	#N/A	0.5361	-0.8994	0.0073	2.1377
Smc3	Q9CWO3	Structural maintenance of chromosomes protein 3	_GOVEGSGS[Phospho (STY)]QDEGGGSESR_2	#N/A	1.8711	0.9039	0.0073	2.1364
Linc7	Q80TE7	Leucine-rich repeat-containing protein 7	_S[Phospho (STY)]REQQPVGGNNK_2	#N/A	1.5699	0.6507	0.0074	2.1316
Sec16a	E9QAT4	Protein transport protein Sec16A	_RSS[Phospho (STY)]LS[Phospho (STY)]SHSQSQIYR_3	E9QAT4_S1384_M2_Sec16a	1.8094	0.8555	0.0074	2.1315
Sorbs1	Q62417	Sorbin and SH3 domain-containing protein 1	_DS[Phospho (STY)]PEEDLDKEPYYK_2	#N/A	1.5570	0.6387	0.0075	2.1267
Mia3	Q8BI84	Transport and Golgi organization protein 1 homolog	_EEAKPAS[Phospho (STY)]PSSVQDR_2	#N/A	1.7087	0.7729	0.0075	2.1248
Srrm1	Q52KJ8	Serine/arginine repetitive matrix protein 1	_LS[Phospho (STY)]PSAS[Phospho (STY)]PPR_2	#N/A	1.8103	0.8562	0.0076	2.1169
Ctnna2	Q61301	Catenin alpha-2	_SKLDAEVAK_2	#N/A	0.4258	-1.2317	0.0077	2.1143
Ndufa3	Q9IKL4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	_VTGAALIPPPGTTALASLGQASE_2	#N/A	0.5718	-0.8064	0.0077	2.1132
Naca	P70670;Q60817	olypeptide-associated complex subunit alpha, muscle-specific form;Nascent polypeptide-associated complex sub	_DIEIVMSQANVSR_2	#N/A	1.8107	0.8566	0.0078	2.1104
Map1a	Q9QYR6	Microtubule-associated protein 1A	_AKPAS[Phospho (STY)]PAR_2	#N/A	1.4377	0.5237	0.0079	2.1020
Kcnh7	Q9ER47	Potassium voltage-gated channel subfamily H member 7	_SFS[Phospho (STY)]PSSQC[Carbamidomethyl (C)]PEFLDLK_2	Q9ER47_S1103_M1_Kcnh7	1.7094	0.7735	0.0079	2.0999
Itsn1	Q920R4	Intersectin-1	_SGS[Phospho (STY)]GM[Oxidation (M)]SVSSSSVDQR_2	#N/A	2.4167	1.2731	0.0080	2.0992
Parva	Q9EPC1	Alpha-parvin	_Acetyl (Protein N-term))ATS[Phospho (STY)]PKQSPLPVK_2	Q9EPC1_S4_M1_Parva	2.3086	1.2070	0.0080	2.0957
Alcam	Q61490	CD156 antigen	_VLQPVGEVAILFK_2	#N/A	0.6376	-0.6492	0.0081	2.0900
Cars1	Q9ER72	Cysteine-18NA ligase, cytoplasmic	_ALQEGGDLSS[Phospho (STY)]ADR_2	Q9ER72_S390_M1_Cars1	1.6624	0.7333	0.0081	2.0892
C2cd4c	Q5H022	C2 calcium-dependent domain-containing protein 4C	_BAT[Phospho (STY)]PEKPGESGQAPR_3	Q5H022_T282_M1_C2cd4c	1.7413	0.8002	0.0082	2.0869
Gpr371f	Q99JG2	G-protein coupled receptor 37-like 1	_PRES[Phospho (STY)]PPLLPLGTFC[Carbamidomethyl (C)]_2	#N/A	0.1230	-0.3049	0.0082	2.0865
Cep170b	Q8OU49	Centrosomal protein of 170 kDa protein B	_AGS[Phospho (STY)]TGTGPGSETAPAR_2	Q8OU49_S1166_M1_Cep170b	1.4096	0.4953	0.0082	2.0850
Ube2m	P61082	NEDD8-conjugating enzyme Ubc12	_TC[Carbamidomethyl (C)]DSFSDDPLLNNFK_2	#N/A	0.6743	-0.5684	0.0082	2.0844
Pcdo	Q9QYX7	Protein piccolo	_TTLVPDEEPLEEM[Oxidation (M)]ESLTS[Phospho (STY)]PEDR_3	#N/A	1.8126	0.8580	0.0083	2.0814
Gnao1	P18872	Guanine nucleotide-binding protein G(o) subunit alpha	_PVVYSNTIGSLAAVR_2	#N/A	1.8129	0.8583	0.0084	2.0763
Psap	Q61207	Prosaposin	_TVTVEAGNLK_2	#N/A	1.3519	0.4350	0.0085	2.0691
Cap2	Q9CYT6	Adenylyl cyclase-associated protein 2	_SSEM[Oxidation (M)]NVLVPQDDDDREFPIPEQFK_3	#N/A	0.6899	-0.5355	0.0087	2.0627
Cops4	Q88544	COP9 signalosome complex subunit 4	_ISQTAPETWTAQAM[Oxidation (M)]EAQM[Oxidation (M)]AQ_2	#N/A	0.3856	-1.3748	0.0087	2.0587
Add2	Q9QYB8	Beta-adducin	_SAGQSQQLASVIAEKS[Phospho (STY)]R_3	#N/A	1.7048	0.7696	0.0089	2.0500
Acat1	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	_AAFAADAADVDDIPLAPAYAVPK_3	#N/A	1.5684	0.6493	0.0090	2.0462
Pcdo	Q9QYX7	Protein piccolo	_SPVPSQQAAS[Phospho (STY)]PKK_2	#N/A	1.3806	0.4653	0.0090	2.0446
Sgpl1	Q8VD37	SH3-containing GRB2-like protein 3-interacting protein 1	_RS[Phospho (STY)]PGAIIK_2	#N/A	1.5616	0.6430	0.0091	2.0420
Akt1s1	Q9D1F4	Proline-rich AKT1 substrate 1	_AATATRPPGPPAPQPS[Phospho (STY)]PAIPS[Phospho (STY)]PPRRPALAR_4	Q9D1F4_S88_M2_Akt1s1	1.7110	0.7748	0.0092	2.0351
Syn1	Q88935	Synapsin-1	_QAS[Phospho (STY)]QAGGPRR_2	#N/A	1.7123	0.7759	0.0093	2.0338
Arfgap1	Q9EPI9	ADP-ribosylation factor GTPase-activating protein 1	_TLQFTAHR_2	#N/A	0.7422	-0.4302	0.0094	2.0273
Waf1	Q8RSJ6	Wiskott-Aldrich syndrome protein family member 1	_STSIQDQQLFORK_2	#N/A	1.5445	0.6272	0.0096	2.0194
Fad1	Q77PM6	Fibronectin type II and SPRY domain-containing protein 1	_LQGSTSHQNR_2	#N/A	0.5850	-0.7734	0.0096	2.0183
Cpne1	Q8C166	Copine-1	_APPT[Phospho (STY)]PGKGPAQAPQA_2	Q8C166_T525_M1_Cpne1	3.3994	1.7653	0.0096	2.0179
Myo18a	Q9IMH9	Unconventional myosin-XVIIIa	_SSPSTSHWPLAPDPS[Phospho (STY)]DDSDHPVDGSRPR_5	Q9IMH9_S2016_M1_Myo18a	1.7114	0.7752	0.0096	2.0168
Taldo1	Q93092	Transaldolase	_M[Oxidation (M)]ESALDQIK_2	#N/A	0.6455	-0.6314	0.0097	2.0134
Chap	Q86144	Voltage-dependent calcium channel beta subunit-associated regulatory protein	_ASS[Phospho (STY)]LDRGGS[Phospho (STY)]PK_2	#N/A	1.3877	0.4727	0.0097	2.0113
Rbm1	Q91VM5	RNA binding motif protein, X-linked-like-1	_SDLVSSGR_2	#N/A	1.7404	0.7994	0.0098	2.0107
Tjp2	Q9ZDU1	Tight junction protein ZO-2	_ERPS[Phospho (STY)]SRRETSGR_3	Q9ZDU1_S420_M1_Tjp2	0.7426	-0.4294	0.0100	1.9983
Kif2a	P28740	Kinesin-like protein KIF2A	_DFRGS[Phospho (STY)]LDVRLPTAOPIDEHR_4	P28740_S206_M1_Kif2a	1.6443	0.7175	0.0101	1.9970
Stx1a	Q35526	Syntaxin-1A	_LKS[Phospho (STY)]IEGSEIEEGLNR_3	Q35526_S95_M1_Stx1a	1.3214	0.4021	0.0101	1.9949
Syngap1	F65E14	Ras/Rap GTPase-activating protein SyngAP	_GKS[Phospho (STY)]QLTIVSAAQK_2	#N/A	2.0961	1.0677	0.0102	1.9920
Smg6	P61406	Telomerase-binding protein EST1A	_NWS[Phospho (STY)]GC[Carbamidomethyl (C)]JGEGEQK_2	P61406_S331_M1_Smg6	2.1935	1.1332	0.0103	1.9878
Speg	Q62407	Striated muscle-specific serine/threonine-protein kinase	_AAS[Phospho (STY)]VELPQR_2	#N/A	1.3612	0.4449	0.0103	1.9865
Rad23b	P54728	UV excision repair protein RAD23 homolog B	_QIIQQNPSSLPAQLQGR_3	#N/A	1.5698	0.6505	0.0104	1.9847
Vapb	Q9QY76	Vesicle-associated membrane protein-associated protein B	_LTS[Phospho (STY)]PLDDTEVK_2	#N/A	1.7122	0.7759	0.0104	1.9842
Acat13	Q9CQ84	Acyl-coenzyme A thioesterase 13	_TLAFASVDLTNK_2	#N/A	1.4059	0.4915	0.0105	1.9790
Actr3b	Q641P0	Actin-related protein 3B	_LSQELSGGR_2	#N/A	1.5251	0.6090	0.0106	1.9756
Ina	P46660	Alpha-internein	_VSSAGLSK_2	#N/A	0.6252	-0.6777	0.0106	1.9740
Creg2	Q8BG69	Protein CREG2	_RES[Phospho (STY)]GS[Phospho (STY)]SEASGPRR_2	Q8BG69_S109_M2_Creg2	1.7339	0.7940	0.0106	1.9738
Chd2	E9P2M4	Chromodomain-helicase-DNA-binding protein 2	_SPLDHRS[Phospho (STY)]PIER_2	E9P2M4_S1806_M1_Chd2	0.6214	-0.6864	0.0107	1.9721
Ptpn3	A2AJK8	Tyrosine-protein phosphatase non-receptor type 3	_SSSSVSPSNAPGS[Phospho (STY)]C[Carbamidomethyl (C)]SPQGVQQR_2	A2AJK8_S467_M1_Ptpn3	1.5032	0.5880	0.0107	1.9694
Ndufs1	Q91V09	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	_VAGM[Oxidation (M)]LQNFEGNAXAAAGGVDAEALVAK_3	#N/A	2.0957	1.0674	0.0108	1.9686
Atp6v1c1	Q921G3	V-type proton ATPase subunit C 1	_LDAFVEGVVK_2	#N/A	0.6214	-0.6863	0.0108	1.9669
Cit	P49025	Citron Rho-interacting kinase	_DKMNS[Phospho (STY)]PGLQSK_2	#N/A	0.7433	-0.4279	0.0109	1.9630
Cend1	Q9IKC6	Cell cycle exit and neuronal differentiation protein 1	_SASS[Phospho (STY)]PKPOTK_2	#N/A	1.6325	0.7071	0.0110	1.9585
Mett126	Q9DCS2	Methyltransferase-like 26	_DTVLEELGQASGLVLR_2	#N/A	1.3730	0.4573	0.0110	1.9574
Dctn2	Q99KJ8	Dynactin subunit 2	_TGYES[Phospho (STY)]GDYEM[Oxidation (M)]LEGLGVK_2	Q99KJ8_S83_M1_Dctn2	1.6940	0.7605	0.0110	1.9571
Cbx3	P23198	Chromobox protein homolog 3	_LSLS[Phospho (STY)]DSESDSSKSK_2	#N/A	1.6549	0.7268	0.0112	1.9527
Kans13	A2R5Y1	KAT8 regulatory NSL complex subunit 3	_GSRPAS[Phospho (STY)]PAAR_2	A2R5Y1_S515_M1_Kans13	0.6216	-0.6860	0.0112	1.9522
Ndufa4	Q9CX21	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	_NNMGSGVNNTKK_2	#N/A	1.8131	0.8585	0.0113	1.9470
Tpm1	P58771	Tropomyosin alpha-1 chain	_C[Carbamidomethyl (C)]AELEELKTVNNLK_3	#N/A	1.6359	0.7101	0.0113	1.9459
Borcs5	Q80920	BLOC-1-related complex subunit 5	_GLSSGQTS[Phospho (STY)]PTNAKLEK_2	#N/A	3.9173	1.9698	0.0114	1.9420
Glo4a	Q9CPV4	Glyoxalase domain-containing protein 4	_LELGQIGGAVDHAAAFGR_3	#N/A	1.3219	0.4026	0.0114	1.9416
Gigyl1	Q99MR1	GRB10-interacting GYF protein 1	_GLEEEEEEEESS[Phospho (STY)]GVDEERPEAGGK_3	Q99MR1_S343_M1_Gigyl1	0.6217	-0.6857	0.0115	1.9390
Sic38a3	Q80CP2	Sodium-coupled neutral amino acid transporter 3	_AYELQGYR_2	#N/A	0.5446	-0.8768	0.0116	1.9339
Acat2	Q8CAV6	Acetyl-CoA acetyltransferase, cytosolic	_VAVLSQNR_2	#N/A	0.6467	-0.6289	0.0117	1.9331
Seg2	Q03517	Secretogranin-2	_VPSPVSSDDLDQEEQLQAKHEHLGPS[Phospho (STY)]SQEM[Oxidation (M)]ER_4	#N/A	1.6883	0.7556	0.0117	1.9327
Srrm2	Q8BT18	Serine/arginine repetitive matrix protein 2	_VSS[Phospho (STY)]PALETYVQQR[Phospho (STY)]PSR_3	Q8BT18_S1360_M2_Srrm2	1.7343	0.7944	0.0117	1.9316
Exoc1	Q8R356	Exocyst complex component 1	_LTGSTSS[Phospho (STY)]LNK_2	Q8R356_S473_M1_Exoc1	2.0928	1.0655	0.0117	1.9304
Rab3c	P62823	Ras-related protein Rab-3C	_TYSWDNAQZVLGNK_2	#N/A	1.3144	0.3944	0.0118	1.9293
Cob11	Q3UMF0	Cordon-bleu protein-like 1	_GSS[Phospho (STY)]LTGSSDPEHVR_2	#N/A	0.6218	-0.6855	0.0118	1.9292
Stub1	Q9WU01	STIP1 homology and U box-containing protein 1	_WNS[Phospho (STY)]IEER_2	Q9WU01_S150_M1_Stub1	0.5447	-0.8764	0.0119	1.9239
Tubb4b	P68372	Tubulin beta-4B chain	_TLKLTTPYTGDLNLVSA[Oxidation (M)]SGVTTCC[Carbamidomethyl (C)]LR_3	#N/A	0.4443	-1.1704	0.0122	1.9132
Rpl20	P60867	40S ribosomal protein S20	_TPVEEVAIHR_3	#N/A	2.4748	1.3073	0.0123	1.9116

Cs	Q9CZU6	Citrate synthase, mitochondrial	_EVGKDVSEKLR_3	#N/A	0.6311	-0.6642	0.0123	1.9093
PsmD9	Q9CR00	26S proteasome non-ATPase regulatory subunit 9	_ADVDVQVVR_2	#N/A	0.6112	-0.7102	0.0127	1.8976
Actr1b	Q8R5C5	Beta-centractin	_AC[Carbamidomethyl (C)]VLSINPKQDALETEK_3	#N/A	0.4483	-1.1573	0.0127	1.8964
Clsap2	Q8BR71	CLIP-associating protein 2	_IPRPVS[Phospho (STY)]QG[C]Carbamidomethyl (C)]S[Phospho (STY)]R_2	Q8BR71_S531_M2_Clsap2	0.2229	-2.1656	0.0127	1.8963
Dist	Q8Q262	hydrolypolylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondr	_TINELGEK_2	#N/A	0.3698	-1.4354	0.0127	1.8961
Nsmf	Q299F2	NMDA receptor synaptotransmembrane protein 1	_ERS[Phospho (STY)]FS[Phospho (STY)]RS[Phospho (STY)]WSOPTPMK_2	#N/A	1.6295	0.7044	0.0128	1.8930
Ywhaz	P63101	14-3-3 protein zeta/delta	_KGVVQSQQYQEAFFSK_3	#N/A	1.5444	0.6271	0.0128	1.8929
Map4k4	P97820	Mitogen-activated protein kinase kinase kinase kinase 4	_DSPLOGGGGQNSQAQGR_2	#N/A	0.5563	-0.8462	0.0128	1.8918
Ptprz1	B9EKR1	Receptor-type tyrosine-protein phosphatase zeta	_QSPINDEIDLTQVNVNLK_2	#N/A	1.4799	0.5655	0.0129	1.8892
Lmnb1	P14733	Lamin-B1	_LSPS[Phospho (STY)]PSSR_2	P14733_S394_M1_Lmnb1	0.2765	-1.8545	0.0129	1.8891
Lxn	P70202	Latexin	_AASVAENC[Carbamidomethyl (C)]INVQGTGPHK_2	#N/A	1.5616	0.6430	0.0130	1.8861
Faf1	P54731	FAS-associated factor 1	_TPS[Phospho (STY)]GELERL_2	P54731_S581_M1_Faf1	0.6222	-0.6845	0.0130	1.8859
Uba1	Q02053	Ubiquitin-like modifier-activating enzyme 1	_YDODFFQNLGQVANAALNDIAR_3	#N/A	0.6047	-0.7258	0.0131	1.8812
Znf385a	QBVD12	Zinc finger protein 385A	_QPQ[S]Phospho (STY)]SPSPSPESQGVTK_2	QBVD12_S160_M1_Znf385a	1.7148	0.7780	0.0132	1.8790
Chtop	Q9CY57	Chromatin target of PRMT1 protein	_GHLDALDAYM[Oxidation (M)]AQDTPETND_2	#N/A	0.5249	-0.9299	0.0133	1.8777
Hivep3	A2A884	Transcription factor HIVEP3	_RSS[Phospho (STY)]VESPK_2	A2A884_S489_M1_Hivep3	0.6554	-0.6096	0.0133	1.8776
Tufm	Q8BRF5	Elongation factor Tu, mitochondrial	_DKPHVNVGTGHVDHGK_4	#N/A	0.6223	-0.6843	0.0133	1.8774
Icam5	Q60625	Intercellular adhesion molecule 5	_SFGEPFR_2	#N/A	0.4611	-1.1168	0.0134	1.8726
Gls	D3Z7P3	Glutaminase kidney isoform, mitochondrial	_ILQEVQVQYTPQGSQSDGK_2	#N/A	0.6224	-0.6842	0.0135	1.8693
Epb41l1	Q9Z2H5	Band 4.1-like protein 1	_LPSPASPS[Phospho (STY)]PKGT[Phospho (STY)]PEKASER_3	#N/A	12.9846	3.6987	0.0136	1.8674
Ogdh	Q60597	2-oxoglutarate dehydrogenase, mitochondrial	_ELEQIFC[Carbamidomethyl (C)]QDFSK_2	#N/A	1.7738	0.8268	0.0137	1.8624
Nefh	P19246	Neurofilament heavy polypeptide	_VKS[Phospho (STY)]EEMKRVAK_3	#N/A	0.6224	-0.6840	0.0138	1.8609
Slc25a11	Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein	_M[Oxidation (M)]DGGPEYK_2	#N/A	0.6230	-0.6828	0.0138	1.8605
Znf609	Q8B247	Zinc finger protein 609	_AEADKHYFTDNAP[Phospho (STY)]PSGGSRR_3	Q8B247_S803_M1_Znf609	1.7153	0.7785	0.0139	1.8569
Camk2g	Q9Z3T9	Calcium/calmodulin-dependent protein kinase type II subunit gamma	_QET[Phospho (STY)]VE[C]Carbamidomethyl (C)]LR_2	Q9Z3T9_T287_M1_Camk2g	1.6788	0.7474	0.0139	1.8560
Cd99i2	Q8BIF0	CD99 antigen-like protein 2	_QETQS[Phospho (STY)]AEPFPPFPR_2	Q8BIF0_S226_M1_Cd99i2	0.6225	-0.6839	0.0140	1.8546
Ctcf	Q68F05	Clathrin heavy chain 1	_LEKHLEFRR_3	#N/A	0.6765	-0.5638	0.0140	1.8538
Champ1	Q8K327	Chromosome alignment-maintaining phosphoprotein 1	_LKQDS[Phospho (STY)]QENS[Phospho (STY)]DAELSSSEYR_3	Q8K327_S613_M2_Camp1	0.6225	-0.6838	0.0141	1.8502
Champ1	Q8K327	Chromosome alignment-maintaining phosphoprotein 1	_GQES[Phospho (STY)]SS[Phospho (STY)]DQEQVDESIDFSK_2	Q8K327_S641_M2_Camp1	0.6225	-0.6838	0.0141	1.8501
Map1a	Q9QYR6	Microtubule-associated protein 1A	_AKPAS[Phospho (STY)]PARR_2	#N/A	1.7492	0.8067	0.0141	1.8496
Camk2g	Q9Z3T9	Calcium/calmodulin-dependent protein kinase type II subunit gamma	_KTS[Phospho (STY)]QEVYAK_2	Q9Z3T9_S36_M1_Camk2g	1.8131	0.8585	0.0142	1.8480
Ncoa7	Q6DFV7	Nuclear receptor coactivator 7	_YYS[Phospho (STY)]VDDNQMK_2	Q6DFV7_S92_M1_Ncoa7	4.9702	2.3133	0.0142	1.8467
Srrm4	Q8BKA3	Serine/arginine repetitive matrix protein 4	_SRGQEKGS[Phospho (STY)]PGDLSK_3	#N/A	1.6169	0.6932	0.0144	1.8420
Eci2	Q9WUR2	Enoyl-CoA delta isomerase 2	_ASQQDFENALNQVK_2	#N/A	1.8638	0.8983	0.0144	1.8405
Ina	P46660	Alpha-intensin	_EEIHEVRR_2	#N/A	0.6958	-0.5232	0.0144	1.8402
Sptbn1	Q6Z261	Spectrin beta chain, non-erythrocytic 1	_HDTASQDS[Phospho (STY)]T[Phospho (STY)]PASSR_2	Q6Z261_T319_M2_Sptbn1	1.4420	0.5281	0.0147	1.8326
Obi1	Q8K2V0	ORC ubiquitin ligase 1	_LKAEDVNR[Phospho (STY)]PKK_2	#N/A	2.3606	1.2392	0.0148	1.8293
Cadm2	Q8B1Q9	Cell adhesion molecule 2	_GAEDAPDADTAINAEGS[Phospho (STY)]QVNAEEKK_3	#N/A	1.9006	0.9264	0.0149	1.8275
Tbr1	Q64336	T-box brain protein 1	_RIS[Phospho (STY)]PADTPVSESSPLK_3	Q64336_S640_M1_Tbr1	1.6720	0.7415	0.0150	1.8238
Hmnpa2b1	Q8B569	Heterogeneous nuclear ribonucleoproteins A2/B1	_GFGDGTNYGGGGGNGFGGS[Phospho (STY)]PGVGGGR_3	Q8B569_S259_M1_Hmnpa2b1	1.6189	0.6950	0.0150	1.8235
Srrm2	Q8B718	Serine/arginine repetitive matrix protein 2	_S[Phospho (STY)]RS[Phospho (STY)]KTS[Phospho (STY)]PVTR_2	Q8B718_S1927_M3_Srrm2	2.8693	1.5207	0.0150	1.8234
Dclk1	Q9JLM8	Serine/threonine-protein kinase DCLK1	_TLQTLSEK_2	#N/A	0.5473	-0.8695	0.0150	1.8227
Glu1	P15105	Glutamine synthetase	_Y[Phospho (STY)]NKRKPAETLR_3	#N/A	0.7417	-0.4311	0.0153	1.8155
Tanc2	A2A690	Protein TANC2	_SQS[Phospho (STY)]ASYPVC[Carbamidomethyl (C)]HSK_2	A2A690_S1726_M1_Tanc2	1.7237	0.7855	0.0153	1.8142
Trappc2	Q9CQP2	Trafficking protein particle complex subunit 2	_FAMNPFYEPNS[Phospho (STY)]PIR_2	Q9CQP2_S119_M1_Trappc2	2.0438	1.0313	0.0153	1.8141
Glu4d	Q9CPV4	Glyoxalase domain-containing protein 4	_FRLQDRS[Phospho (STY)]PSGDSPLVK_3	#N/A	0.6282	-0.6707	0.0156	1.8074
Cct8	P42932	T-complex protein 1 subunit theta	_KDWDDQND_2	#N/A	0.7146	-0.4847	0.0156	1.8064
Wwc2	Q6NXX0	Protein WWC2	_UNRSOS[Phospho (STY)]DSSTLAK_2	#N/A	1.6421	0.7155	0.0157	1.8048
Nrgn	P60761	Neurogranin	_KGPFGPGPGGAGGAR_2	#N/A	1.3255	0.4065	0.0157	1.8046
Stl13	Q99L47	Hsc70-interacting protein	_QDPVLUHTEEMR_3	#N/A	1.9226	0.9430	0.0158	1.8020
Nefh	P19246	Neurofilament heavy polypeptide	_SAQEETVRR_3	#N/A	1.6477	0.7205	0.0161	1.7942
Wars1	P32921	Tryptophan-tRNA ligase, cytoplasmic	_DLTEOAYSIVYENAK_2	#N/A	1.6085	0.6857	0.0161	1.7924
Arpp21	Q9DCB4	cAMP-regulated phosphoprotein 21	_AWSS[Phospho (STY)]TDSQSNR_2	Q9DCB4_S362_M1_Arpp21	1.4188	0.5047	0.0162	1.7910
Sh3glb2	Q8R3V5	Endophilin-B2	_RLDLAC[Carbamidomethyl (C)]K_2	#N/A	0.3692	-1.4376	0.0163	1.7883
Pkce	P16054	Protein kinase C epsilon type	_SKS[Phospho (STY)]APTS[Phospho (STY)]PC[Carbamidomethyl (C)]DQLKLENNIR_3	#N/A	1.7232	0.7851	0.0163	1.7883
Zswim8	Q3UHH1	Zinc finger SWIM domain-containing protein 8	_KQS[Phospho (STY)]AGPNS[Phospho (STY)]PTGGGGGGSGGTR_2	#N/A	0.6791	-0.5584	0.0164	1.7856
Ap2a2	P17427	AP-2 complex subunit alpha-2	_LSTVASTDLATLEEM[Oxidation (M)]PPFPER_3	#N/A	1.5152	0.5995	0.0164	1.7849
Igfb1	Q8R366	Immunoglobulin superfamily member 8	_AVLAHVQVTLSSQLAVTVGQER_3	#N/A	0.6725	-0.5723	0.0164	1.7848
Retreg2	Q6N582	Reticulophagy regulator 2	_SAPPAAGDEPLATES[Phospho (STY)]ESEALAGFSPVVDVK_3	Q6N582_S276_M1_Retreg2	1.5366	0.6197	0.0165	1.7817
Mapk4	Q6P5G0	Mitogen-activated protein kinase 4	_AGSTT[Phospho (STY)]PLAEDVQVQDR_2	Q6P5G0_T383_M1_Mapk4	0.4488	-1.1560	0.0168	1.7756
Ganab	Q8BHN3	Neutral alpha-glucosidase AB	_DAVHYGGWEHR_3	#N/A	1.6410	0.7146	0.0168	1.7734
Uhrf1bp1	A2R514	UHRF1-binding protein 1-like	_SS[Phospho (STY)]PEISLR_2	A2R514_S1250_M1_Uhrf1bp1	0.4664	-1.1003	0.0171	1.7658
Rims2	Q9EQZ7	Regulating synaptic membrane exocytosis protein 2	_RAD[S]Phospho (STY)]LRK_2	Q9EQZ7_S493_M1_Rims2	2.6427	1.4020	0.0173	1.7630
Ap3b2	Q9JME5	AP-3 complex subunit beta-2	_TLTVAGSVAM[Oxidation (M)]AFEEVC[Carbamidomethyl (C)]PER_2	#N/A	1.8898	0.9183	0.0173	1.7622
Fmnl1	Q9JL26	Formin-like protein 1	_SKPLDQSVDEL[S]Phospho (STY)]K_2	Q9JL26_S189_M1_Fmnl1	1.8435	0.8825	0.0174	1.7595
Ogfr1	QBVE52	Opioid growth factor receptor-like protein 1	_DSAADQSOS[Phospho (STY)]PPEK_2	QBVE52_S406_M1_Ogfr1	0.6412	-0.6411	0.0179	1.7463
Ranbp2	Q9ERU9	E3 SUMO-protein ligase RanBP2	_NRPGVYS[Phospho (STY)]EEEEDEDEYEM[Oxidation (M)]AVK_3	Q9ERU9_S2505_M1_Ranbp2	0.7280	-0.4579	0.0181	1.7424
Cacna1d	Q99246	Voltage-dependent L-type calcium channel subunit alpha-1D	_QT[Phospho (STY)]VLSWQDAIDAAR_2	Q99246_T49_M1_Cacna1d	1.7185	0.7811	0.0185	1.7329
Abi1	P00520	Tyrosine-protein kinase Abi1	_SC[Carbamidomethyl (C)]S[Phospho (STY)]ASC[Carbamidomethyl (C)]M[Oxidation (M)]PHGAR_2	#N/A	1.6739	0.7433	0.0186	1.7310
Arhgap23	Q69Z9H	Rho GTPase-activating protein 23	_ARS[Phospho (STY)]DDVLR_2	Q69Z9H_S351_M1_Arhgap23	1.4220	0.5080	0.0186	1.7307
Atrx	Q61687	Transcriptional regulator ATRX	_VC[Carbamidomethyl (C)]DQTSKS[Phospho (STY)]PK_2	Q61687_S315_M1_Atrx	0.4474	-1.1604	0.0187	1.7277
Dctn4	Q8CBY8	Dynactin subunit 4	_LIEYQGLACK_2	#N/A	1.8039	0.8511	0.0187	1.7274
Hmnpk	P61979	Heterogeneous nuclear ribonucleoprotein K	_GGOLM[Oxidation (M)]AYDRR_2	#N/A	0.4608	-1.1179	0.0190	1.7215
Agap1	Q8BXX8	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	_VQDVAQK_2	#N/A	1.5428	0.6256	0.0191	1.7183
Safb	D3YXK2	Scaffold attachment factor B1	_SVVS[Phospho (STY)]FKVK_2	D3YXK2_S626_M1_Safb	1.9536	0.9661	0.0192	1.7173
Iqsec1	Q8R0S2	IQ motif and SEC7 domain-containing protein 1	_VLUNFNAPNQDR_2	#N/A	0.4979	-1.0059	0.0193	1.7155
Spat18	Q0P557	Mitochondria-eating protein	_SKS[Phospho (STY)]PC[Carbamidomethyl (C)]TTVAK_2	Q0P557_S273_M1_Spat18	0.4072	-1.2963	0.0193	1.7148
Limd2	Q8BGB5	LIM domain-containing protein 2	_SKS[Phospho (STY)]FSLR_2	Q8BGB5_S30_M1_Limd2	1.3230	0.4038	0.0193	1.7145
Ptdss2	Q9Z1X2	Phosphatidylserine synthase 2	_RVAGSGSGES[Phospho (STY)]PLK_2	#N/A	1.6511	0.7234	0.0194	1.7127

Rala	P63321	Ras-related protein Raf-A	_VIM[Oxidation (M)]VSGGSGVK_2	#N/A	0.7477	-0.4195	0.0194	1.7124
Caskin1	Q6P9K8	Caskin-1	_RRAS[Phospho (STY)]DIAGSVDTGSAGVK_3	#N/A	0.4954	-1.0132	0.0194	1.7111
Dck	P43346	Deoxytydine kinase	_FC[Carbamidomethyl (C)]PS[Phospho (STY)]PSTSEGETR_2	P43346_S31_M1_Dck	6.0431	2.5953	0.0195	1.7109
Camk2b	P28652	Calcium/calmodulin-dependent protein kinase type II subunit beta	_QET[Phospho (STY)]VEC[Carbamidomethyl (C)]LKK_2	#N/A	2.0944	1.0665	0.0197	1.7065
Mctp1	E9PV66	Multiple C2 and transmembrane domain-containing protein 1	_AAS[Phospho (STY)]PSFOAR_2	E9PV66_S16_M1_Mctp1	6.1820	2.6281	0.0200	1.7000
Igfb8	Q8R366	Immunoglobulin superfamily member 8	_HAAYSVGWEM[Oxidation (M)]APAGAPGGR_3	#N/A	0.4406	-1.1825	0.0200	1.6995
Tp1	P17751	Triosephosphate isomerase	_ELASQPDVDFVLGGASLKPFVDINAK_3	#N/A	0.5057	-0.9837	0.0200	1.6991
Rnf14	Q3I90	E3 ubiquitin-protein ligase RNF14	_LTYHGLS[Phospho (STY)]PC[Carbamidomethyl (C)]KVTAEK_3	#N/A	1.8895	0.9180	0.0200	1.6991
Adam22	Q9R1V6	Disintegrin and metalloproteinase domain-containing protein 22	_KLAS[Phospho (STY)]GEC[Carbamidomethyl (C)]K_2	Q9R1V6_S387_M1_Adam22	0.6322	-0.6616	0.0200	1.6987
Spatn1	P16546	Spectrin alpha chain, non-erythrocytic 1	_TKGDENVAAAWQR_3	#N/A	0.4252	-1.2338	0.0200	1.6980
Mars1	Q68FL6	Methionine-tRNA ligase, cytoplasmic	_NNSLELNNGAFINR_2	#N/A	0.5976	-0.7428	0.0200	1.6980
Pde7b	Q9QXQ1	cAMP-specific 3',5'-cyclic phosphodiesterase 7B	_GSGQDLAGAPETLEQTGAT[Phospho (STY)]P_2	Q9QXQ1_T445_M1_Pde7b	0.2454	-2.0265	0.0202	1.6951
Ptprz1	B9EKR1	Receptor-type tyrosine-protein phosphatase zeta	_QSPINDEDLTQVNVNLKK_3	#N/A	1.3356	0.4175	0.0202	1.6949
Tbr1	Q64336	T-box brain protein 1	_SKLS[Phospho (STY)]PVLGVSP[Phospho (STY)]ELRHSGDGSAAOR_4	Q64336_S84_M2_Tbr1	0.6582	-0.6035	0.0204	1.6902
Arfgap2	Q99X28	ADP-ribosylation factor GTPase-activating protein 2	_LAYQLQIR_2	#N/A	0.6976	-0.5195	0.0205	1.6875
Fasn	P19096	Fatty acid synthase	_TLEAVQDLLEQGR_2	#N/A	0.6449	-0.6328	0.0208	1.6816
Atp1a3	Q6PIC5	Sodium/potassium-transporting ATPase subunit alpha-3	_KADIGVAM[Oxidation (M)]GIAGSDVSK_2	#N/A	0.5528	-0.8552	0.0209	1.6807
Dnajc5	P60904	DnaJ homolog subfamily C member 5	_QRS[Phospho (STY)]LS[Phospho (STY)]TSGESLYHHGLDK_3	P60904_S10_M2_Dnajc5	0.6826	-0.5509	0.0209	1.6791
Rassf5	Q5EBH1	Ras association domain-containing protein 5	_S[Phospho (STY)]PESTLPTLNQNV[Carbamidomethyl (C)]K_2	Q5EBH1_S177_M1_Rassf5	2.2680	1.1814	0.0210	1.6769
Hernpua1	Q8VDM6	Heterogeneous nuclear ribonucleoprotein L-like protein 1	_NLYLDQTNVYGS[Phospho (STY)]AQR_2	Q8VDM6_S513_M1_Hernpua1	2.0621	1.0441	0.0211	1.6763
Srm2	Q8BTI8	Serine/arginine repetitive matrix protein 2	_VSSPVLTVQQR[Phospho (STY)]PS[Phospho (STY)]RR_3	Q8BTI8_S1372_M2_Srm2	0.3080	-1.6990	0.0211	1.6754
Gap43	P06837	Neuromodulin	_QDEKEKPEADQEHA_2	#N/A	0.4773	-1.0669	0.0211	1.6751
Atn1	O35126	Atrophin-1	_TAS[Phospho (STY)]PPGPQVSK_2	O35126_S617_M1_Atn1	0.4190	-1.2550	0.0214	1.6705
Pdk	Q8K183	Pyridoxal kinase	_KPDGSGTVQR_2	#N/A	1.9500	0.9634	0.0214	1.6688
Srm1	O52X18	Serine/arginine repetitive matrix protein 1	_VSHS[Phospho (STY)]PPPK_2	O52X18_S657_M1_Srm1	5.6731	2.5041	0.0214	1.6686
Actn1	Q7TPR4	Alpha-actinin-1	_LLETIDQLYLEYAK_2	#N/A	1.5177	0.6019	0.0219	1.6605
Camk2a	P11798	Calcium/calmodulin-dependent protein kinase type II subunit alpha	_QET[Phospho (STY)]VD[Carbamidomethyl (C)]LK_2	#N/A	4.8904	2.2900	0.0219	1.6602
Anxa11	P97384	Annexin A11	_SDTSGHFOR_2	#N/A	0.6064	-0.7216	0.0219	1.6594
Rab1A	P62821	Ras-related protein Rab-1A	_KQST[Phospho (STY)]PVK_2	P62821_T195_M1_Rab1A	2.4522	1.2941	0.0220	1.6572
Cep170b	Q8OU49	Centrosomal protein of 170 kDa protein B	_SCSQ[Phospho (STY)]FHTPPADPK_2	Q8OU49_S421_M1_Cep170b	6.3521	2.6672	0.0223	1.6524
Gdap11	Q8VE33	Ganglioside-induced differentiation-associated protein 1-like 1	_LDHEEPQLESEPLSK_3	#N/A	0.6313	-0.6636	0.0224	1.6502
Atg6v1b2	P62814	V-type proton ATPase subunit B, brain isoform	_TVETLDIGWQLLR_2	#N/A	1.6051	0.6827	0.0225	1.6481
Zeb2	Q9R0G7	Zinc finger E-box-binding homeobox 2	_S[Phospho (STY)]DHEEDNMEDGME_2	#N/A	1.4700	0.5559	0.0225	1.6476
Wdr7	Q920I9	WD repeat-containing protein 7	_RQS[Phospho (STY)]REDSDPYR_3	Q920I9_S772_M1_Wdr7	0.6561	-0.6081	0.0225	1.6475
Sorbs1	Q62417	Sorbin and SH3 domain-containing protein 1	_SKS[Phospho (STY)]EM[Oxidation (M)]NVEGEK_2	#N/A	0.4718	-1.0838	0.0225	1.6469
Pgam1	Q9DBU1	Phosphoglycerate mutase 1	_FSGWYDADSPAGHEAK_2	#N/A	1.3307	0.4122	0.0226	1.6461
Rab11fip5	Q8R361	Rab11 family-interacting protein 5	_RTYS[Phospho (STY)]DEASQLR_2	#N/A	2.7503	1.4596	0.0226	1.6452
Vars1	Q92109	Valine-tRNA ligase	_DINLDVNR_2	#N/A	0.5654	-0.8225	0.0227	1.6447
Kif2a	P28740	Kinesin-like protein KIF2A	_LDIGNSC[Carbamidomethyl (C)]R_2	#N/A	0.4390	-1.1877	0.0227	1.6436
H1-2	P15864	Histone H1.2	_ASGPPVSELTK_2	#N/A	0.5293	-0.9177	0.0229	1.6411
Ndr3	Q62433	Protein NDRG1	_SKT[Phospho (STY)]AS[Phospho (STY)]GSSVTEGTR_2	#N/A	0.5406	-0.8874	0.0230	1.6375
Ptpra	P18052	Receptor-type tyrosine-protein phosphatase alpha	_QAGSHNS[Phospho (STY)]FR_2	P18052_S180_M1_Ptpra	0.7617	-0.3927	0.0230	1.6374
Peak1	Q69238	Inactive tyrosine-protein kinase PEAK1	_SLFTSQSSGEGEAHQTTES[Phospho (STY)]PT[Phospho (STY)]AK_3	Q69238_S836_M2_Peak1	0.6371	-0.6504	0.0231	1.6366
Caskin1	Q6P9K8	Caskin-1	_SLPQS[Phospho (STY)]PTHR_2	Q6P9K8_S828_M1_Caskin1	6.0388	2.5943	0.0231	1.6362
Wdr33	Q8K4P0	pre-mRNA 3' end processing protein WDR33	_Acetyl (Protein N-term)[ATEQS[Phospho (STY)]PPR_2	Q8K4P0_S7_M1_Wdr33	0.1211	-3.0456	0.0233	1.6319
Tomm34	Q9CYG7	Mitochondrial import receptor subunit TOM34	_SSLSDISSLLQIEPR_2	#N/A	1.6687	0.7387	0.0234	1.6303
Ppp3cb	P48453	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform	_VDEIALR_2	#N/A	1.6547	0.7266	0.0237	1.6260
Gpd11	Q3ULJ0	Glycerol 3-phosphate dehydrogenase 1-like protein	_VC[Carbamidomethyl (C)]VSGNGWGSAAVK_2	#N/A	2.0334	1.0239	0.0238	1.6234
Setd2	E9Q5F9	Histone-lysine N-methyltransferase SETD2	_TGS[Phospho (STY)]PTPSNOLDSPFTK_2	E9Q5F9_S614_M1_Setd2	1.7755	0.8282	0.0238	1.6230
Usp11	Q99K46	Ubiquitin carboxyl-terminal hydrolase 11	_QSQTSSSDTPAS[Phospho (STY)]PVSSSTPNSD[M[Oxidation (M)]DIN_3	#N/A	1.7624	0.8175	0.0239	1.6213
Add2	Q9QYB8	Beta-adducin	_SPAVS[Phospho (STY)]PSK_2	#N/A	2.5515	1.3513	0.0240	1.6190
Nefh	P19246	Neurofilament heavy polypeptide	_JPSSTHK_2	#N/A	1.4062	0.4918	0.0241	1.6176
Synj1	Q8CHC4	Synaptojanin-1	_FIEAPKS[Phospho (STY)]PGTAR_2	#N/A	1.8558	0.8920	0.0241	1.6172
Naa15	Q80UM3	N-alpha-acetyltransferase 15, NATA auxiliary subunit	_ITVNGDS[Phospho (STY)]SAETEEALNEL_2	Q80UM3_S854_M1_Naa15	1.3866	0.4715	0.0242	1.6166
Setd7	Q8VHL1	Histone-lysine N-methyltransferase SETD7	_JAYVYPOQR_2	#N/A	1.8549	0.8914	0.0242	1.6163
Pold3	Q9EQ28	DNA polymerase delta subunit 3	_VDLS[Phospho (STY)]DEAEKETELHK_3	Q9EQ28_S306_M1_Pold3	0.4019	-1.3152	0.0243	1.6143
Pkp4	Q68FHD	Plakophilin-4	_S[Phospho (STY)]YEDPYC[Carbamidomethyl (C)]DDR_2	Q68FHD_S1136_M1_Pkp4	2.0300	1.0215	0.0245	1.6103
Dmn	Q9WV69	Dematin	_TSVGGS[Phospho (STY)]PCSK_2	#N/A	1.3356	0.4175	0.0248	1.6057
Pum3	P14685	26S proteasome non-ATPase regulatory subunit 3	_LQLDS[Phospho (STY)]PEDAEFAVK_2	P14685_S426_M1_Pum3	0.6708	-0.5761	0.0249	1.6046
Amph	Q7TQ77	Amphiphysin	_LYEVM[Oxidation (M)]TK_2	#N/A	1.6585	0.7299	0.0249	1.6042
Fry	E9Q8I9	Protein furry homolog	_LLPGSSPS[Phospho (STY)]S[Phospho (STY)]PEDEVKDR_2	E9Q8I9_S1382_M2_Fry	1.5102	0.5947	0.0249	1.6034
Scn3b	Q8BHK2	Sodium channel subunit beta-3	_AEEAAQENASDY[Phospho (STY)]LAIPSENK_2	Q8BHK2_Y198_M1_Scn3b	0.2607	-1.9395	0.0249	1.6030
Ubqln1	Q8R317	Ubiquitin-1	_ALNLESIPGGYNALR_2	#N/A	1.5529	0.6350	0.0250	1.6021
Ernn	Q5EBI4	Ermin	_YNTISYR_2	#N/A	0.7287	-0.4566	0.0250	1.6021
Nefh	P19246	Neurofilament heavy polypeptide	_S[Phospho (STY)]LEGEAAALR_2	P19246_S122_M1_Nefh	0.4641	-1.1075	0.0250	1.6014
Stxbp5l	Q5DQ84	Syntaxin-binding protein 5-like	_EIKQESLTSYFYQIC[Carbamidomethyl (C)]K_2	#N/A	1.7936	0.8428	0.0253	1.5970
Ndufs2	Q91WDS	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	_TSM[Oxidation (M)]JLSUHHFK_3	#N/A	1.7298	0.7906	0.0256	1.5913
Arpp21	Q9DCB4	cAMP-regulated phosphoprotein 21	_TGS[Phospho (STY)]JESSSSAGSSLSLR_2	Q9DCB4_S408_M1_Arpp21	1.5286	0.6122	0.0256	1.5910
Wac	Q924H7	WW domain-containing adaptor protein with coiled-coil	_S[Phospho (STY)]NS[Phospho (STY)]PENKYSDDSTGHNK_2	Q924H7_S62_M2_Wac	1.4886	0.5740	0.0257	1.5903
Dpyl5	Q9EQF6	Dihydropyrimidine-related protein 5	_THC[Carbamidomethyl (C)]PIVLNVSSISAGDVAANK_3	#N/A	1.7715	0.8250	0.0257	1.5900
Glu	P15105	Glutamine synthetase	_QM[Oxidation (M)]YM[Oxidation (M)]JSLPOGEG_2	#N/A	0.5559	-0.8472	0.0258	1.5886
Rhoa	Q9QU0D	Transforming protein RhoA	_M[Oxidation (M)]KQEPVKEEGR_3	#N/A	0.5696	-0.8120	0.0258	1.5878
Trim2	Q9ESN6	Tripartite motif-containing protein 2	_ASVODHSTFDLQK_3	#N/A	0.5149	-0.9575	0.0259	1.5872
Sptbn1	Q62261	Spectrin beta chain, non-erythrocytic 1	_EAK[Carbamidomethyl (C)]EVALDYKK_3	#N/A	1.5375	0.6206	0.0259	1.5869
Tnr	Q8BYI9	Tenascin-R	_DGOEAVFAYDKFAVEDSR_3	#N/A	0.6938	-0.5274	0.0261	1.5835
Kcnq5	Q9IK45	Potassium voltage-gated channel subfamily KQT member 5	_RSPSTDTTAEGS[Phospho (STY)]PTK_2	#N/A	3.3339	1.7372	0.0262	1.5825
Hpc4	P84075	Neuron-specific calcium-binding protein hippocalin	_TFDTNSDGTIDR_2	#N/A	0.4253	-1.2333	0.0264	1.5791
Sptbn1	Q62261	Spectrin beta chain, non-erythrocytic 1	_DLVIAEK_2	#N/A	0.4819	-1.0532	0.0265	1.5773
CH1	P70232	Neural cell adhesion molecule L1-like protein	_DETGEYS[Phospho (STY)]DSDEKPLKGS[Phospho (STY)]R_3	P70232_S1148_M2_CH1	1.3802	0.4649	0.0266	1.5754

Lingo1	Q9D1T0	Leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 1	_S[Phospho (STY)]DAGISSADAPR_2	#N/A	1.3044	0.3834	0.0266	1.5748
Nos1	Q9Z0I4	Nitric oxide synthase, brain	_KSS[Phospho (STY)]GQDPDLR_2	Q9Z0I4_S858_M1_Nos1	2.4359	1.2844	0.0267	1.5732
Ociad2	Q9D8W7	OIA domain-containing protein 2	_FHSFEQLR_2	#N/A	1.6955	0.7617	0.0269	1.5702
Dpp6	Q9Z2I8	Dipeptidyl aminopeptidase-like protein 6	_HLYSANTVDVFNLR_2	#N/A	0.6098	-0.7136	0.0270	1.5681
Dlgap3	Q6PFD5	Disks large-associated protein 3	_WRPSGVHGVETIS[Phospho (STY)]SDTENR_3	Q6PFD5_S641_M1_Dlgap3	0.5168	-0.9523	0.0271	1.5674
Dcx	Q88809	Neuronal migration protein doublecortin	_GNPSAAGPKAS[Phospho (STY)]PTPKK_2	Q88809_S287_M1_Dcx	0.6862	-0.5433	0.0271	1.5673
Eepd1	Q3TGW2	Endonuclease/exonuclease/phosphatase family domain-containing protein 1	_GNSAQHS[Phospho (STY)]PSSLRR_3	#N/A	0.2958	-1.7574	0.0271	1.5668
Ndg3	Q9CYF9	Protein NDRG3	_S[Phospho (STY)]RT[Phospho (STY)]HSTSSGSGSGSPSR_3	Q9CYF9_T329_M2_Ndg3	0.6244	-0.6795	0.0272	1.5662
Vps26b	Q8CDE2	Vacuolar protein sorting-associated protein 26B	_ETTGTPGVNYHENDIAK_3	#N/A	1.6108	0.6878	0.0273	1.5631
Ncbp3	Q88Z89	Nuclear cap-binding protein subunit 3	_AEAPAGPAGLGLPS[Phospho (STY)]PEVESGLER_2	Q88Z89_S25_M1_Ncbp3	0.7255	-0.4630	0.0274	1.5629
Phyhlpl	Q8BGT8	Phytanoyl-CoA hydroxylase-interacting protein-like	_ISWDMDSK_2	#N/A	1.6052	0.6827	0.0275	1.5610
Ernm	Q5EBI4	Ermin	_SRPVDLHS[Phospho (STY)]K_3	Q5EBI4_S166_M1_Ermn	0.6883	-0.5389	0.0275	1.5603
Bsn	Q88737	Protein bassoon	_YSS[Phospho (STY)]VSNYSDHR_2	Q88737_S2068_M1_Bsn	1.8226	0.8660	0.0276	1.5598
Pccb	Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	_IM[Oxidation (M)]DQAITVGAPVGLNDSGGAR_2	#N/A	0.7151	-0.4838	0.0277	1.5572
Pitpnm1	Q35954	Membrane-associated phosphatidylinositol transfer protein 1	_C[Carbamidomethyl (C)]NTGSEGGEAQ[Phospho (STY)]PGK_2	Q35954_T270_M1_Pitpnm1	1.6797	0.7482	0.0278	1.5557
Smpd3	Q9IYF3	Spingomyelin phosphodiesterase 3	_TAS[Phospho (STY)]VEYKGDDGR_2	Q9IYF3_S208_M1_Smpd3	2.2849	1.1922	0.0280	1.5535
Cpe	Q0Q493	Carboxypeptidase E	_YIGNM[Oxidation (M)]HGNEAVGR_3	#N/A	0.5597	-0.8372	0.0280	1.5525
Nefm	P08553	Neurofilament medium polypeptide	_KAES[Phospho (STY)]PVKEK_2	#N/A	1.3942	0.4794	0.0281	1.5509
Dnm3	Q88Z98	Dynamin-3	_LQGQLLSIEVEAFK_3	#N/A	1.6896	0.7566	0.0281	1.5507
Prkacb	P68181	cAMP-dependent protein kinase catalytic subunit beta	_ATEQYAMK_2	#N/A	0.6905	-0.5343	0.0284	1.5463
Vcplp1	Q8CDG3	Deubiquitinating protein VCP1P1	_S[Phospho (STY)]RESS[Phospho (STY)]PSHGLXK_2	Q8CDG3_S993_M2_Vcplp1	0.7131	-0.4879	0.0286	1.5441
Pcdc4	Q61823	Programmed cell death protein 4	_SGVAVPTS[Phospho (STY)]PKGR_2	#N/A	0.3430	-1.5435	0.0286	1.5440
AK1	Q9R0Y5	Adenylate kinase isoenzyme 1	_AEVSSGSR_2	#N/A	0.4986	-1.0039	0.0287	1.5421
Znf318	Q99P92	Zinc finger protein 318	_RAS[Phospho (STY)]PS[Phospho (STY)]PPRGR_3	#N/A	1.7009	0.7663	0.0287	1.5416
Mast1	Q9R1L5	Microtubule-associated serine/threonine-protein kinase 1	_HFGS[Phospho (STY)]TESTDEDDGR_2	#N/A	0.6187	-0.6926	0.0288	1.5413
Tra2b	P6Z996	Transformer-2 protein homolog beta	_S[Phospho (STY)]RS[Phospho (STY)]YS[Phospho (STY)]ROYR_2	P6Z996_S87_M3_Tra2b	0.3582	-1.4810	0.0289	1.5398
Gda	Q9R111	Guanine deaminase	_AVM[Oxidation (M)]VSNVLLINK_2	#N/A	0.3728	-1.4236	0.0289	1.5388
Arhgef7	Q9E528	Rho guanine nucleotide exchange factor 7	_LETFDANDLVGGQFNKK_2	#N/A	1.5517	0.6338	0.0290	1.5381
Ctifa	P80317	T-complex protein 1 subunit zeta	_VLAQNSGFLQELVK_2	#N/A	1.9146	0.9370	0.0290	1.5370
Mtx2	Q88441	Metaxin-2	_Acetyl (Protein N-term)[SLVAAFPVQAATPEWPNATLVQQLR_3	#N/A	0.6805	-0.5553	0.0292	1.5354
Lin7c	Q88952	Protein lin-7 homolog C	_VLSGFC[Carbamidomethyl (C)]NAVR_2	#N/A	1.3246	0.4056	0.0292	1.5347
Atat1	Q8K341	Alpha-tubulin N-acetyltransferase 1	_SS[Phospho (STY)]LGNSPDR_2	Q8K341_S272_M1_Atata1	4.3407	2.1179	0.0292	1.5345
Ppp4r3a	Q6PZK6	Serine/threonine-protein phosphatase 4 regulatory subunit 3A	_TNSGKRS[Phospho (STY)]PSFK_2	Q6PZK6_S248_M1_Ppp4r3a	2.1568	1.1089	0.0292	1.5341
Kcnab2	P6Z482	Voltage-gated potassium channel subunit beta-2	_LQLEYDVVAVNRDPNPTM[Oxidation (M)]EETVR_3	#N/A	0.6977	-0.5194	0.0294	1.5317
Pgrmc1	O55022	Membrane-associated progesterone receptor component 1	_GDQPGASGNDODEPPPLR_2	#N/A	0.7449	-0.4248	0.0296	1.5288
Aco2	Q99K00	Aconitate hydratase, mitochondrial	_HPNGTQETILLNHTNETQIEWFR_4	#N/A	0.6534	-0.6140	0.0297	1.5273
Fibp15	Q6P9Q6	FK506-binding protein 15	_VTS[Phospho (STY)]LEELIDR_2	Q6P9Q6_S722_M1_Fibp15	0.6534	-0.6139	0.0297	1.5265
Pkc5	P56812	Programmed cell death protein 5	_KVM[Oxidation (M)]DS[Phospho (STY)]DEDDADY_2	#N/A	1.7967	0.8454	0.0298	1.5252
Sgta	Q88I00	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	_APORT[Phospho (STY)]PPSEDSAEAR_3	#N/A	1.8975	0.9241	0.0299	1.5245
Pcm1	Q9R0L6	Pericentriolar material 1 protein	_HIS[Phospho (STY)]ESDR_2	Q9R0L6_S1432_M1_Pcm1	0.6535	-0.6137	0.0300	1.5229
Cc	Q9Z4A2	Protein capicua homolog	_SS[Phospho (STY)]PPPLPAEERPTK_2	Q9Z4A2_S2148_M1_Cc	5.4391	2.4434	0.0301	1.5207
Stambpl1	Q76N33	AMSH-like protease	_SGGSNFANY[Phospho (STY)]PPVNR_2	Q76N33_S242_M1_Stambpl1	1.7472	0.8050	0.0302	1.5194
Napb	P28663	Beta-soluble NSF attachment protein	_LLEAHEEQNEAYTEAVK_3	#N/A	1.6082	0.6855	0.0303	1.5187
Actn1	Q77P84	Alpha-actinin-1	_AIM[Oxidation (M)]TVYSSYHAFSGAQK_2	#N/A	1.4152	0.5010	0.0303	1.5186
Znf608	Q56A10	Zinc finger protein 608	_DRHS[Phospho (STY)]PFSQR_3	Q56A10_S1452_M1_Znf608	0.5875	-0.7673	0.0304	1.5170
Bcar1	Q61140	Breast cancer anti-estrogen resistance protein 1	_GS[Phospho (STY)]GGTFREDLR_2	Q61140_S572_M1_Bcar1	0.6477	-0.6266	0.0306	1.5148
Esd	Q9R0P3	S-formylglutathione hydrolase	_AVDATC[Carbamidomethyl (C)]LVK_2	#N/A	0.4377	-1.1920	0.0306	1.5140
Vps35	Q9EQH3	Vacuolar protein sorting-associated protein 35	_LFDISQQVATVQSR_2	#N/A	0.6458	-0.6308	0.0306	1.5139
Pdia6	Q9Z2R8	Protein disulfide-isomerase A6	_LAADVATVNVQLASR_2	#N/A	1.8643	0.8986	0.0307	1.5134
Rad23b	P54728	UV excision repair protein RAD23 homolog B	_NENLAANFLQQNFED_2	#N/A	0.5387	-0.8925	0.0307	1.5132
Elfn1	Q8C877	Protein ELFN1	_AVAAAAGS[Phospho (STY)]LKK_2	Q8C877_S460_M1_Elfn1	1.3730	0.4573	0.0307	1.5125
Add2	Q9QYB8	Beta-adducin	_EQDHFLSPK_2	#N/A	1.4609	0.5469	0.0307	1.5124
Prkaca	P05132	cAMP-dependent protein kinase catalytic subunit alpha	_WETPSQNTAQDLQDFDR_2	#N/A	2.7659	1.4678	0.0309	1.5104
Top2b	Q64511	DNA topoisomerase 2-beta	_NETINGS[Phospho (STY)]DSEFGPK_2	#N/A	1.3269	0.4080	0.0310	1.5080
Speg	Q6Z407	Striated muscle-specific serine/threonine-protein kinase	_SR[Phospho (STY)]VQDLR_2	Q6Z407_S2396_M1_Speg	9.2145	3.2039	0.0311	1.5073
Usp34	Q6ZQ93	Ubiquitin carboxyl-terminal hydrolase 34	_DSSGPGTEQDLP[Phospho (STY)]PENSDVK_2	Q6ZQ93_S3443_M1_Usp34	2.7453	1.4570	0.0314	1.5030
Setd2	E9Q5F9	Histone-lysine N-methyltransferase SETD2	_RRGS[Phospho (STY)][S[Phospho (STY)]PPSSAYER_3	#N/A	0.7034	-0.5077	0.0317	1.4991
Dpyl4	Q35098	Dihydropyrimidinase-related protein 4	_C[Carbamidomethyl (C)]Q[C[Carbamidomethyl (C)]TDGQVIFSLIR_2	#N/A	0.5737	-0.8018	0.0317	1.4991
Ppp1r1b	Q60829	Protein phosphatase 1 regulatory subunit 1B	_ELGYQEDEDEDEDEEEDSGAEVLK_3	#N/A	0.7143	-0.4855	0.0318	1.4976
Epb41i2	O70318	Band 4.1-like protein 2	_VTGRTREEQECC[Carbamidomethyl (C)]DEEEEPGGQAK_3	#N/A	0.6879	-0.5397	0.0318	1.4970
Ap1b1	Q35643	AP-1 complex subunit beta-1	_C[Carbamidomethyl (C)]KDEDPVVRK_3	#N/A	0.6069	-0.7206	0.0320	1.4954
Dpyl5	Q9EQF6	Dihydropyrimidinase-related protein 5	_TPLGDVANVHPGK_3	#N/A	0.6837	-0.5486	0.0321	1.4940
Otud7a	Q88554	OTU domain-containing protein 7A	_AS[Phospho (STY)]PGPTAAOPTQLVLK_2	Q88554_S711_M1_Otud7a	1.6305	0.7053	0.0322	1.4921
Npm1	Q61937	Nucleophosmin	_C[Carbamidomethyl (C)]GSGPVHSGQLHVAVEEDAES[Phospho (STY)]EDEDEEDVKLLGM[Oxidation (M)]SGK_5	Q61937_S125_M1_Npm1	1.6162	0.6926	0.0323	1.4914
Ppfia2	Q88559	Liprin-alpha-2	_S[Phospho (STY)]LGDHEWNR_2	#N/A	1.6080	0.6853	0.0323	1.4914
Tmem38a	Q37MP8	Trimeric intracellular cation channel type A	_AKEELGEGS[Phospho (STY)]RK_3	#N/A	1.6150	0.6916	0.0323	1.4912
Ripor2	Q8OU16	Rho family-interacting cell polarization regulator 2	_SQS[Phospho (STY)]FAGSGLQER_2	Q8OU16_S46_M1_Ripor2	0.3428	-1.5444	0.0323	1.4903
Pkp4	Q68FH0	Plakophilin-4	_GLVPGSKSPYI[Phospho (STY)]ISSY[Phospho (STY)]SPAR_3	Q68FH0_S1098_M2_Pkp4	0.3631	-1.4614	0.0323	1.4902
Ltst3	A2AHG0	Leucine zipper putative tumor suppressor 3	_LFRIES[Phospho (STY)]TEL_2	A2AHG0_S687_M1_Ltst3	0.6544	-0.6118	0.0324	1.4894
Sh3glb2	Q8R3V5	Endophilin-B2	_SQTTYAQ[C[Carbamidomethyl (C)]VLR_2	#N/A	0.4659	-1.1020	0.0324	1.4892
Gnl1	P36916	Guanine nucleotide-binding protein-like 1	_GLQDGLRS[Phospho (STY)]SS[Phospho (STY)]NSR_2	P36916_S32_M2_Gnl1	0.7185	-0.4769	0.0326	1.4869
Ywhaz	P63101	14-3-3 protein zeta/delta	_TAFQEAUHLDTLSEESYKOSTUMLQLLR_3	#N/A	0.6843	-0.5473	0.0326	1.4865
Otu4	B2RKE7	OTU domain-containing protein 4	_LQRPKRES[Phospho (STY)][S[Phospho (STY)]EDENSVNLR_3	#N/A	0.7220	-0.4699	0.0327	1.4850
Mical3	Q8C119	[F-actin]-monooxygenase MICAL3	_SVPS[Phospho (STY)]GVKK_2	Q8C119_S1736_M1_Mical3	2.2348	1.1601	0.0327	1.4850
Cmpk1	Q9D8P5	UMP-CMP kinase	_KNPDSQYGELEK_3	#N/A	1.5908	0.6698	0.0328	1.4839
Ubpap2l	Q8QX50	Ubiquitin-associated protein 2-like	_NQDEQ[Carbamidomethyl (C)]VALHDC[Carbamidomethyl (C)]NGDVNR_3	#N/A	1.3056	0.3847	0.0328	1.4835
Pnn	Q35691	Pinin	_RFGS[Phospho (STY)]DSGGGPAK_2	#N/A	1.5898	0.6688	0.0329	1.4834
Anxa5	P48036	Annexin A5	_DLVDDLKSLTGK_2	#N/A	0.7347	-0.4449	0.0329	1.4829
Dst	Q91ZU6	Dystonin	_QLS[Phospho (STY)]LLDSR_2	Q91ZU6_S5407_M1_Dst	1.5876	0.6668	0.0329	1.4823

Arpp21	Q9DCB4	cAMP-regulated phosphoprotein 21	_TAS[Phospho (STY)]GGGTVLTR_2	Q9DCB4_S381_M1_Arpp21	0.2600	-1.9436	0.0329	1.4823
Rpl35a	O55142	60S ribosomal protein L35a	_JEGVYR_2	#N/A	0.5410	-0.8864	0.0330	1.4816
Lcp1	Q61233	Plastin-2	_GS[Phospho (STY)]VSDDEEMELR_2	Q61233_S5_M1_Lcp1	1.5855	0.6649	0.0330	1.4812
Pitpnm1	Q35954	Membrane-associated phosphatidylinositol transfer protein 1	_SSVSSQGQGV[Phospho (STY)]PQGS[Phospho (STY)]LSEWR_3	Q35954_S326_M2_Pitpnm1	0.6546	-0.6113	0.0331	1.4807
Camk2	Q8C078	Calcium/calmodulin-dependent protein kinase kinase 2	_KMS[Phospho (STY)]LQEPSSQGGPASSSSLSMDMGR_3	Q8C078_S99_M1_Camk2	0.7145	-0.4850	0.0331	1.4804
Gnl1	P36916	Guanine nucleotide-binding protein-like 1	_ERREEQTDT[Phospho (STY)]S[Phospho (STY)]DGGSEVTHHR_4	#N/A	0.1827	-2.4522	0.0331	1.4800
Septin7	O55131	Septin-7	_NLEAQHKEEEK_2	#N/A	0.5994	-0.7385	0.0333	1.4772
Ish3a	O20682	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	_EVAENC[Carbamidomethyl (C)]KDKI_2	#N/A	0.7358	-0.4427	0.0334	1.4758
Gatd3a	Q90172	Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	_YNKVER_2	#N/A	0.6094	-0.7146	0.0335	1.4755
Npr2	Q6VWV5	Atrial natriuretic peptide receptor 2	_GSS[Phospho (STY)]VGLSM[Oxidation (M)]TTHGK_2	Q6VWV5_S523_M1_Npr2	0.2390	-2.0648	0.0338	1.4714
Map1b	P14873	Microtubule-associated protein 1B	_ESVVS[Phospho (STY)]QDDR_2	#N/A	0.3075	-1.7014	0.0338	1.4712
Tjp2	Q820U1	Tight junction protein ZO-2	_HSHDMLSHS[Phospho (STY)]WEGNR_3	#N/A	1.7357	0.7955	0.0338	1.4712
Ak3	Q9WTP7	GTP-AMP phosphotransferase AK3, mitochondrial	_GVLETFSGTETNK_2	#N/A	2.3584	1.2378	0.0339	1.4698
Rpl18a	P62717	60S ribosomal protein L18a	_DLTTAGAVTQC[Carbamidomethyl (C)]YR_2	#N/A	1.5426	0.6254	0.0339	1.4694
Ckmt1	P30275	Creatine kinase U-type, mitochondrial	_GLSUPPAC[Carbamidomethyl (C)]TR_2	#N/A	4.6285	2.2105	0.0339	1.4692
Rcn2	Q8BP92	Reticulocalbin-2	_HYAMQEAQ_2	#N/A	1.5681	0.6491	0.0339	1.4692
Nav1	Q8CH77	Neuron navigator 1	_SLAESGUNWFS[Phospho (STY)]ES[Phospho (STY)]EETKPK_3	Q8CH77_S477_M2_Nav1	1.5435	0.6262	0.0340	1.4691
Aars1	Q8BGQ7	Alanine-tRNA ligase, cytoplasmic	_M[Oxidation (M)]ALELLETFQGPVER_2	#N/A	0.4140	-1.2724	0.0340	1.4688
Ssh1	Q76779	Protein phosphatase Slingshot homolog 1	_SDS[Phospho (STY)]PQVEELK_2	Q76779_S585_M1_Ssh1	3.9035	1.9648	0.0340	1.4682
Celsr2	Q980M0	Cadherin EGF LAG seven-pass G-type receptor 2	_SLTSSYN[C[Carbamidomethyl (C)]PS[Phospho (STY)]PYADGR_2	Q980M0_S2648_M1_Celsr2	0.5829	-0.7787	0.0340	1.4680
Hecw1	Q8K4P8	E3 ubiquitin-protein ligase HECW1	_SYS[Phospho (STY)]AGEASEVSR_2	Q8K4P8_S1073_M1_Hecw1	1.4312	0.5172	0.0340	1.4680
Bin1	O08539	Myc box-dependent-interacting protein 1	_MANNDDLWM[Oxidation (M)]DYHOK_3	#N/A	1.3680	0.4521	0.0341	1.4679
Atxn2	O70305	Ataxin-2	_MSSEGPPRM[Oxidation (M)]S[Phospho (STY)]PK_2	O70305_S593_M1_Atnx2	1.8187	0.8629	0.0341	1.4679
Rpl34	O20189	60S ribosomal protein L34	_LSYNTASK_2	#N/A	0.6549	-0.6107	0.0341	1.4678
Pma6	Q9QUM9	Proteasome subunit alpha type-6	_HTIFSPGR_2	#N/A	0.4349	-1.2014	0.0342	1.4665
Cplx1	P63040	Complexin-1	_EAEAQAA[M[Oxidation (M)]EANKSEGS[Phospho (STY)]LTRPK_2	#N/A	2.0642	1.0456	0.0342	1.4662
Gnb5	P62881	Guanine nucleotide-binding protein subunit beta-5	_VSPDGTAF[C[Carbamidomethyl (C)]SGSWDHTLR_2	#N/A	0.5351	-0.9021	0.0343	1.4651
Tmem63c	Q8CBX0	Calcium permeable stress-gated cation channel 1	_LALUHNDS[Phospho (STY)]LTSLYGEQEK_3	Q8CBX0_S75_M1_Tmem63c	1.5456	0.6282	0.0343	1.4647
Rps3a	P97351	40S ribosomal protein S3a	_EVQTDLKEVKNK_3	#N/A	1.5459	0.6284	0.0344	1.4638
Arhgap21	Q6DfV3	Rho GTPase-activating protein 21	_KISS[Phospho (STY)]SEVSDAAR_2	Q6DfV3_S917_M1_Arhgap21	0.5256	-0.9280	0.0345	1.4622
Rpl18	P35980	60S ribosomal protein L18	_ILTFDQLALESK_2	#N/A	0.6130	-0.7061	0.0345	1.4618
Atp8a1	P70704	Phospholipid-transporting ATPase 1A	_SESLQOQLLHGAYFGQDGVSGVSEVR_3	#N/A	0.7107	-0.4927	0.0345	1.4617
Gigyf2	Q6Y7W8	GRB10-interacting GYF protein 2	_ALSSGGSTIS[Phospho (STY)]PLSPALPK_2	Q6Y7W8_S236_M1_Gigyf2	0.7020	-0.5106	0.0345	1.4617
Atxn7i3	A2AWT3	Ataxin-7-like protein 3	_LQWDGSSDLS[Phospho (STY)]PSDSSGSK_2	A2AWT3_S281_M1_Atnx7i3	0.3810	-1.3923	0.0346	1.4615
Dmx2	Q8BPX8	Dmx-like protein 2	_LDHELSLDES[Phospho (STY)]EAGTGSSEHDEGEREGS[Phospho (STY)]PR_4	Q8BPX8_S456_M2_Dmx2	1.5465	0.6290	0.0346	1.4612
Cryab	P23927	Alpha-crystallin B chain	_HEERQDEHGFSR_4	#N/A	1.5589	0.6405	0.0346	1.4607
Map1a	Q9QYR6	Microtubule-associated protein 1A	_DEAS[Phospho (STY)]EEKEQVLQK_2	#N/A	0.6550	-0.6103	0.0347	1.4601
Thrap3	Q56926	Thyroid hormone receptor-associated protein 3	_S[Phospho (STY)]YS[Phospho (STY)]PAHNR_2	Q56926_S55_M2_Thrap3	0.3039	-1.7183	0.0347	1.4601
Cser2	Q3UHD0	Serine-rich coiled-coil domain-containing protein 2	_HTSSNNLS[Phospho (STY)]POTDYR_2	#N/A	0.2614	-1.9359	0.0349	1.4567
Palm	Q9Z0P4	Paralemnin-1	_PQSA[Phospho (STY)]PAKEEQK_2	#N/A	1.4287	0.5147	0.0350	1.4560
Pbx2	O35984	Pre-B-cell leukemia transcription factor 2	_TAVSVAQGGHS[Phospho (STY)]JR_2	O35984_S330_M1_Pbx2	1.9897	0.9925	0.0350	1.4553
Cpne6	Q92140	Copine-6	_YSVLLVLTDGVVSDM[Oxidation (M)]AETR_2	#N/A	0.6806	-0.5552	0.0351	1.4548
Apc	Q61315	Adenomatous polyposis coli protein	_T[Phospho (STY)]GSSSSLSASSESEK_2	Q61315_T2567_M1_Apc	1.5377	0.6207	0.0351	1.4548
Syl3	Q35681	Synaptotagmin-3	_KLHFS[Phospho (STY)]VYDFR_3	#N/A	0.1973	-2.3413	0.0351	1.4546
Dhx30	Q99PU8	ATP-dependent RNA helicase DHX30	_GGS[Phospho (STY)]FEM[Oxidation (M)]TODDSAIR_2	#N/A	1.7296	0.7905	0.0351	1.4543
Ak1	Q9R0Y5	Adenylate kinase isoenzyme 1	_LETYNATEPVSFYDKR_3	#N/A	1.4484	0.5345	0.0352	1.4535
Atp5pb	Q9CQQ7	ATP synthase F(0) complex subunit B1, mitochondrial	_LDYHVSQNM[Oxidation (M)]M[Oxidation (M)]R_3	#N/A	1.5503	0.6326	0.0354	1.4514
Klc1	O88447	Kinesin light chain 1	_RS[Phospho (STY)]RES[Phospho (STY)]LNMDVWK_3	#N/A	0.6553	-0.6099	0.0354	1.4507
Pic2	Q8K394	Inactive phospholipase C-like protein 2	_TPS[Phospho (STY)]PAAGVPVR_2	Q8K394_S87_M1_Pic2	0.6764	-0.5640	0.0354	1.4506
Sptbn1	Q62261	Spectrin beta chain, non-erythrocytic 1	_DVSVELLM[Oxidation (M)]NNHQGK_2	#N/A	0.7367	-0.4409	0.0356	1.4489
Wdr7	Q92019	WD repeat-containing protein 7	_LPASC[Carbamidomethyl (C)]LPASDSFR_2	#N/A	0.3916	-1.3527	0.0356	1.4487
Kcnab2	P62482	Voltage-gated potassium channel subunit beta-2	_QTGS[Phospho (STY)]PGM[Oxidation (M)]YSTR_2	#N/A	1.8859	0.9152	0.0356	1.4485
Eef2	PS8252	Elongation factor 2	_YDFPANGK_2	#N/A	0.3992	-1.3249	0.0357	1.4479
Apeh	Q8R146	Acylamino-acid-releasing enzyme	_ALDVSAS[Phospho (STY)]DEEM[Oxidation (M)]ARPK_2	#N/A	0.6691	-0.5796	0.0357	1.4470
Arhgef17	Q8OU35	Rho guanine nucleotide exchange factor 17	_SLS[Phospho (STY)]DRPQR_2	Q8OU35_S728_M1_Arhgef17	0.2295	-2.1235	0.0358	1.4462
Agap1	Q88XK8	Arl-GAP with GTPase, ANK repeat and PH domain-containing protein 1	_ATSAC[Carbamidomethyl (C)]APSS[Phospho (STY)]PK_2	Q88XK8_S422_M1_Agap1	4.0272	2.0098	0.0359	1.4450
Cnnm3	Q32N94	Metal transporter CNNM3	_PVYEEER_2	#N/A	0.5194	-0.9452	0.0359	1.4449
Mphosph8	Q3TYA6	M-phase phosphoprotein 8	_GTVAVGDS[Phospho (STY)]EEDGEDVEFER_2	Q3TYA6_S51_M1_Mphosph8	0.7365	-0.4412	0.0360	1.4440
Rnh1	Q91V17	Ribonuclease inhibitor	_ELSLASNELKDEGAR_3	#N/A	0.5148	-0.9580	0.0360	1.4436
Dbn1	Q62418	Drebrin-like protein	_VAGTGGEGGEEVEELNSGK_2	#N/A	0.7087	-0.4967	0.0362	1.4412
Pdhb	Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	_EAINOGM[Oxidation (M)]DEELERDEK_3	#N/A	0.7507	-0.4137	0.0363	1.4405
Cpne1	Q8C166	Copine-1	_FAAQAAQQR_2	#N/A	4.8839	2.2880	0.0363	1.4398
Ndufa5	Q9CP96	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	_LEALLQGGVEEVILQAEK_2	#N/A	0.7147	-0.4845	0.0363	1.4395
Elav2	Q60899	ELAV-like protein 2	_FANNPSOK_2	#N/A	1.5692	0.6500	0.0364	1.4387
Rbx1	P62878	E3 ubiquitin-protein ligase RBX1	_QVC[Carbamidomethyl (C)]PLDNR_2	#N/A	0.5454	-0.8746	0.0364	1.4386
Rbbp6	P97868	E3 ubiquitin-protein ligase RBBP6	_PSANREDFS[Phospho (STY)]PER_2	#N/A	0.4450	-1.1681	0.0365	1.4383
Pacs1	Q8K212	Phosphofurin acidic cluster sorting protein 1	_S[Phospho (STY)]TLPEKR_2	Q8K212_S508_M1_Pacs1	0.7237	-0.4666	0.0365	1.4382
Samm50	Q8BGH2	Sorting and assembly machinery component S0 homolog	_SSLSHAM[Oxidation (M)]VIDSR_2	#N/A	1.5581	0.6398	0.0365	1.4377
Cct3	P80318	T-complex protein 1 subunit gamma	_NLQDAM[Oxidation (M)]QVC[Carbamidomethyl (C)]R_2	#N/A	0.3339	-1.5824	0.0365	1.4377
Ank3	G5E8K5	Ankyrin-3	_NEDLAELLNGM[Oxidation (M)]DEELDS[Phospho (STY)]PEELGTGR_3	#N/A	1.5559	0.6378	0.0365	1.4373
Akap5	D3YVFO	A kinase anchor protein 5	_QUSM[Oxidation (M)]NEQVQVFNSSDFEGR_3	#N/A	1.6526	0.7248	0.0367	1.4353
Armcx3	Q8BH56	Armado-like repeat-containing X-linked protein 3	_RAS[Phospho (STY)]PNSDQVLSQLELK_3	Q8BH56_S110_M1_Armcx3	1.6042	0.6819	0.0368	1.4338
Tcf20	Q9EPQ8	Transcription factor 20	_LSTS[Phospho (STY)]PATRDEAAS[Phospho (STY)]PGAK_3	Q9EPQ8_S603_M2_Tcf20	1.5420	0.6248	0.0369	1.4335
Myh9	Q8VD05	Myosin-9	_ELETQSELEDELESEK_2	#N/A	1.5410	0.6239	0.0369	1.4331
Abat	P61922	4-aminobutyrate aminotransferase, mitochondrial	_TLTGLDLQAQYPPQPSR_2	#N/A	0.7233	-0.4673	0.0369	1.4328
Gfap	Q93995	Glial fibrillary acidic protein	_GTNES[Phospho (STY)]LER_2	P03995_S302_M1_Gfap	1.5510	0.6332	0.0369	1.4326
Cit	P49025	Citron Rho-interacting kinase	_S[Phospho (STY)]PENQPSAMSLAPPSR_3	P49025_S1348_M1_Cit	1.5352	0.6184	0.0370	1.4316
Pde4a	Q80984	cAMP-specific 3',5'-cyclic phosphodiesterase 4A	_QSG[Phospho (STY)]PSPITLLEEQVSDPALPDK_2	Q80984_S672_M1_Pde4a	1.5350	0.6182	0.0370	1.4313
Pkm	PS2480	Pyruvate kinase PKM	_LNFSGHTHEYHETIK_3	#N/A	1.8210	0.8647	0.0371	1.4312

Tox4	Q8BU11	TOX high mobility group box family member 4	_LSTTSP[Phospho (STY)]PT[Phospho (STY)]NSLHEDGVDFRR_3	Q8BU11_5178_M2_Tox4	0.7252	-0.4636	0.0371	1.4308
Sowaha	Q8BL57	Ankyrin repeat domain-containing protein SOWAHA	_QRS[Phospho (STY)]EESPFR_2	Q8BL57_5242_M1_Sowaha	1.7502	0.8075	0.0372	1.4296
Bca3	Q8CCN5	Breast carcinoma-amplified sequence 3 homolog	_VKS[Phospho (STY)]PQSPSK_2	Q8CCN5_5565_M1_Bca3	13.4173	3.7460	0.0372	1.4296
Samn50	Q8BGH2	Sorting and assembly machinery component 50 homolog	_DVVVQHVFHFDGLGR_3	#N/A	1.5314	0.6149	0.0372	1.4293
H1-2	P15864	Histone H1.2	_ALAAAGVGVKVNNSR_2	#N/A	1.3597	0.4433	0.0374	1.4276
Znf148	Q61624	Zinc finger protein 148	_AGMTSS[Phospho (STY)]PDATGGTG_2	Q61624_5784_M1_Znf148	1.3800	0.4646	0.0375	1.4261
Dock7	Q8RI44	Dedicator of cytokinesis protein 7	_KGS[Phospho (STY)]WSER_2	Q8RI44_5432_M1_Dock7	2.2021	1.1388	0.0375	1.4258
Slc25a3	Q8VEM8	Phosphate carrier protein, mitochondrial	_YYALC[Carbamidomethyl (C)]GGGVLS[Carbamidomethyl (C)]GLTHTAVVPLDLVK_3	#N/A	0.7404	-0.4336	0.0375	1.4255
Rem2	Q8VEL9	GTP-binding protein REM 2	_GS[Phospho (STY)]MPVPVK_2	#N/A	0.7405	-0.4334	0.0375	1.4255
Fam171a2	A2A699	Protein FAM171A2	_TGLC[Carbamidomethyl (C)]SPEDNS[Phospho (STY)]LTPLLDEVVAPEGR_3	A2A699_5744_M1_Fam171a2	0.5758	-0.7964	0.0376	1.4253
Rbm8a	Q9CW23	RNA-binding protein 8A	_J[Acetyl (Protein N-term)]ADVLDLHEAGGEFAM[Oxidation (M)]DEGDGES[Phospho (STY)]JHK_3	Q9CW23_524_M1_Rbm8a	0.7396	-0.4352	0.0376	1.4249
Grin2b	Q01097	Glutamate receptor ionotropic, NMDA 2B	_AGNLVDS[Phospho (STY)]EDNSLQELDQAPAAVAVSSNASTTK_3	Q01097_51255_M1_Grin2b	0.7412	-0.4321	0.0376	1.4248
Ernn	Q5EBI4	Ermin	_EDSLGS[Phospho (STY)]PGSQGTGPDEQPVFGK_3	#N/A	0.6056	-0.7236	0.0376	1.4245
Pich2	A2AP18	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2	_IRDC[Carbamidomethyl (C)]EDPNDFSVSTLS[Phospho (STY)]PSGK_3	A2AP18_5619_M1_Pich2	0.7414	-0.4318	0.0376	1.4244
Rims1	Q99NE5	Regulating synaptic membrane exocytosis protein 1	_S[Phospho (STY)]RSVS[Phospho (STY)]PHR_2	Q99NE5_5786_M2_Rims1	0.7130	-0.4880	0.0378	1.4228
Cand1	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	_ITSEALLVTQQLVK_2	#N/A	1.3919	0.4770	0.0378	1.4224
Agap1	Q88XK8	Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 1	_LDPPPS[Phospho (STY)]PHANR_2	Q88XK8_5521_M1_Agap1	1.3501	0.4331	0.0378	1.4222
Dnajc19	Q9CQV7	Mitochondrial import inner membrane translocase subunit TIM14	_EAAULGV[S[Phospho (STY)]ITPANK_2	Q9CQV7_570_M1_Dnajc19	0.7384	-0.4376	0.0379	1.4215
Ehd3	Q9QXY6	EH domain-containing protein 3	_IGPEPTTDSFAVM[Oxidation (M)]QGQVEIGIIGNALVDPK_3	#N/A	0.7423	-0.4299	0.0379	1.4212
Snn	P61807	Stannin	_LM[Oxidation (M)]TANS[Phospho (STY)]PEVHG_2	#N/A	1.3911	0.4762	0.0381	1.4190
Tnn2	Q8CG86	Tennin-2	_APHSC[Carbamidomethyl (C)]GS[Phospho (STY)]PSEGR_2	Q8CG86_5811_M1_Tnn2	1.5163	0.6006	0.0381	1.4189
Map1a	Q9QYR6	Microtubule-associated protein 1A	_WLAESPVLGPPEEDKLTR_3	#N/A	0.4958	-1.0121	0.0381	1.4188
Tp532l2	Q9CYZ2	Tumor protein D54	_S[Phospho (STY)]FEDRVGTIK_2	#N/A	1.7244	0.7861	0.0382	1.4181
Map1a	Q9QYR6	Microtubule-associated protein 1A	_EQXDEAS[Phospho (STY)]EEKEQVLEQK_3	#N/A	0.7430	-0.4286	0.0382	1.4180
Ctic	Q68F05	Clathrin heavy chain 1	_NNRPSEGQLTR_2	#N/A	0.5811	-0.7833	0.0382	1.4180
Dmxl2	Q88P88	Dmx-like protein 2	_ALLT[Phospho (STY)]PQDEEC[Carbamidomethyl (C)]ADGGTEVDVIAEQIK_3	Q88P88_T2017_M1_Dmxl2	1.5137	0.5981	0.0383	1.4168
Hmrnp1h	Q35737	Heterogeneous nuclear ribonucleoprotein H	_EGRPSEGAFFVELES[Phospho (STY)]DEEVK_3	Q35737_563_M1_Hmrnp1h	1.5732	0.6537	0.0384	1.4158
Sash3	Q8K352	SAM and SH3 domain-containing protein 3	_SSS[Phospho (STY)]KFQFAK_2	Q8K352_527_M1_Sash3	0.7200	-0.4740	0.0384	1.4158
Akap1	O08715	A-kinase anchor protein 1, mitochondrial	_S[Phospho (STY)]ESSGNLPSVADTR_2	#N/A	1.5247	0.6085	0.0385	1.4151
Slc12a5	Q91V14	Solute carrier family 12 member 5	_FTVAQM[Oxidation (M)]DDNSQM[Oxidation (M)]K_2	#N/A	0.7436	-0.4274	0.0386	1.4137
	Q3UE31	Uncharacterized protein KIAA0930 homolog	_SHS[Phospho (STY)]ANDSEFFREDDSGADLNHNATNLK_4	Q3UE31_5324_M1_	0.7368	-0.4407	0.0387	1.4127
Srsf5	O35326	Serine/arginine-rich splicing factor 5	_VS[Phospho (STY)]WQDLK_2	Q35326_5120_M1_Srsf5	1.6947	0.7610	0.0387	1.4123
Etfb	Q9DCW4	Electron transfer flavoprotein subunit beta	_EIIAVSC[Carbamidomethyl (C)]GPSQC[Carbamidomethyl (C)]QIETR_2	#N/A	0.7041	-0.5061	0.0387	1.4119
Srx6	Q6P8X1	Sorting nexin-6	_J[Acetyl (Protein N-term)]M[Oxidation (M)]EGLDGGDFLS[Phospho (STY)]IEEDR_2	Q6P8X1_513_M1_Srx6	0.7439	-0.4268	0.0388	1.4116
Daam1	Q88PM0	Dishevelled-associated activator of morphogenesis 1	_ESS[Phospho (STY)]EESGEFDLVSAIR_2	Q88PM0_51026_M1_Daam1	0.7442	-0.4263	0.0389	1.4096
Hint1	P70349	Histidine triad nucleotide-binding protein 1	_C[Carbamidomethyl (C)]AADGLK_2	#N/A	0.6989	-0.5168	0.0390	1.4090
Alpl	P09242	Alkaline phosphatase, tissue-nonspecific isoenzyme	_TYNTNAQVPS[Phospho (STY)]AGTATAYLC[Carbamidomethyl (C)]GVK_3	P09242_5110_M1_Alpl	0.6693	-0.5793	0.0390	1.4088
Mef2c	Q8CFN5	Myocyte-specific enhancer factor 2C	_PSPDERES[Phospho (STY)]PSVKR_3	Q8CFN5_5460_M1_Mef2c	0.6591	-0.6015	0.0390	1.4087
Scamp3	O35609	Secretory carrier-associated membrane protein 3	_TAANAAGAAAGNAFR_2	#N/A	0.4524	-1.1444	0.0390	1.4086
ildr2	B5TVM2	Immunoglobulin-like domain-containing receptor 2	_GWTYS[Phospho (STY)]PAPAR_2	B5TVM2_5511_M1_ildr2	23.9086	4.5795	0.0390	1.4084
Ddost	O54734	Dolichyl-diphosphoglycerate-4-epimerase	_TLVLNDLNVK_2	#N/A	0.5735	-0.8022	0.0391	1.4084
Mag3	Q9EQI9	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3	_QPEDESHQAFQSONGS[Phospho (STY)]PR_3	#N/A	1.4821	0.5676	0.0391	1.4078
Stoml2	Q99JB2	Stomatin-like protein 2, mitochondrial	_APVPGAGNSQSR_2	#N/A	0.6407	-0.6422	0.0391	1.4076
Thop1	Q8C1A5	Thimet oligopeptidase	_YDQVLHTQTADDAPEAYR_3	#N/A	1.9496	0.9632	0.0392	1.4072
Adcy	Q91V92	ATP-citrate synthase	_SINNPDNR_2	#N/A	0.6905	-0.5343	0.0392	1.4065
Prdx1	P35700	Peroxisomal protein 1	_IGVPAPNFK_2	#N/A	0.7354	-0.4435	0.0392	1.4063
Prrc2b	Q77PM1	Protein PRRC2B	_LKFS[Phospho (STY)]DDDEEDVVK_2	#N/A	0.6532	-0.6145	0.0393	1.4054
Srrm2	Q88T18	Serine/arginine repetitive matrix protein 2	_DTPQT[Phospho (STY)]PSR_2	Q88T18_T1428_M1_Srrm2	0.7358	-0.4426	0.0393	1.4051
Ndrg3	Q9QY99	Protein NDRC3	_LHQAQDINQENQLFLGSGYNGR_3	#N/A	1.5077	0.5923	0.0394	1.4051
Lrp1	Q912X7	Prolow-density lipoprotein receptor-related protein 1	_FFSDHFGNIQIQNDQSGSR_3	#N/A	0.7358	-0.4427	0.0394	1.4046
Gnb4	P29387	Guanine nucleotide-binding protein subunit beta-4	_SGVLAGHNR_2	#N/A	0.0347	-4.8492	0.0395	1.4038
Skt	A2AQ25	Sickle tail protein	_VSS[Phospho (STY)]EDGPTPTQTR_2	A2AQ25_51087_M1_Skt	1.4878	0.5732	0.0395	1.4033
Aagab	Q8R283	Alpha- and gamma-adaptin-binding protein p34	_AFWM[Oxidation (M)]AIGGDRDEIGLGS[Phospho (STY)]DDEH_3	Q8R283_5312_M1_Aagab	1.5541	0.6361	0.0396	1.4023
Pczb	Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	_EFFNLFPLSSQDPAPIR_2	#N/A	1.4030	0.4885	0.0396	1.4022
Msl1	Q61474	RNA-binding protein Musashi homolog 1	_J[Acetyl (Protein N-term)]M[Oxidation (M)]ETDAPOQGLAS[Phospho (STY)]POSHPDPC[Carbamidomethyl (C)]K_2	#N/A	1.3802	0.4649	0.0397	1.4014
Hrh1	P70174	Histamine H1 receptor	_RIS[Phospho (STY)]ETSEDTQLVDR_2	P70174_5344_M1_Hrh1	1.4964	0.5815	0.0397	1.4013
Slc32a1	O35633	Vesicular inhibitory amino acid transporter	_LTHVATSVSNK_2	#N/A	0.6010	-0.7345	0.0399	1.3990
Omg	Q63912	Oligodendrocyte-myelin glycoprotein	_AHVIGTPC[Carbamidomethyl (C)]JSK_2	#N/A	1.3104	0.3900	0.0399	1.3990
Pgm2l1	Q8CAA7	Glucose 1,6-bisphosphate synthase	_DITTOYDSSQPNKK_2	#N/A	0.6248	-0.6785	0.0399	1.3985
Pipa	P58389	Serine/threonine-protein phosphatase 2A activator	_FGSLPHPVTS_2	#N/A	0.6839	-0.5482	0.0402	1.3959
Sptbn1	Q6Z261	Spectrin beta chain, non-erythrocytic 1	_IQEKVDSIDOR_3	#N/A	0.7131	-0.4878	0.0402	1.3955
Hspd1	P63038	60 kDa heat shock protein, mitochondrial	_DM[Oxidation (M)]AAITGAAGVAGEGGLNLELDVQAHDGLK_3	#N/A	1.5137	0.5981	0.0402	1.3954
Atg6v1a	P50516	V-type proton ATPase catalytic subunit A	_EASVYGTILSEYR_2	#N/A	0.7015	-0.5115	0.0403	1.3947
Gad1	P48318	Glutamate decarboxylase 1	_ERQS[Phospho (STY)]SKNLLSC[Carbamidomethyl (C)]ENSDQGAR_3	#N/A	1.4910	0.5763	0.0403	1.3943
Cavin2	Q63918	Caveolin-associated protein 2	_S[Phospho (STY)]SPFKVS[Phospho (STY)]PLSGR_2	Q63918_5287_M2_Cavin2	0.6559	-0.6085	0.0404	1.3936
Ap2a1	P17426	AP-2 complex subunit alpha-1	_AVEYLTSSVASTDLATVLEEM[Oxidation (M)]PPFFER_3	#N/A	0.7037	-0.5069	0.0405	1.3928
Nfia	Q02780	Nuclear factor 1 A-type	_S[Phospho (STY)]PGSGSQSGSWHEVGLPSPSTLK_3	Q02780_5323_M1_Nfia	0.7455	-0.4238	0.0407	1.3906
Sars1	P26638	Serine-tRNA ligase, cytoplasmic	_EIGNLHPSPVPSNDEADNKVER_4	#N/A	1.4900	0.5753	0.0407	1.3904
Arhgef2	Q60875	Rho guanine nucleotide exchange factor 2	_LES[Phospho (STY)]FESLRGER_2	#N/A	7.7845	2.9606	0.0408	1.3898
Sphkap	Q6NSW3	A-kinase anchor protein SPHKAP	_RAS[Phospho (STY)]ITDLGK_2	Q6NSW3_5841_M1_Sphkap	0.7045	-0.5053	0.0408	1.3898
Hgs	Q99JL8	Hepatocyte growth factor-regulated tyrosine kinase substrate	_ASSTELPEVLYTSPISQSQS[Phospho (STY)]QLPPK_3	Q99JL8_5246_M1_Hgs	0.7461	-0.4226	0.0408	1.3896
Wdr44	Q6NVE8	WD repeat-containing protein 44	_S[Phospho (STY)]NSGRELDEILASVNNK_3	Q6NVE8_5344_M1_Wdr44	0.7341	-0.4459	0.0409	1.3882
Rims3	Q8OU57	Regulating synaptic membrane exocytosis protein 3	_QGSRESTDGSGTNS[Phospho (STY)]NSSEGTFFIPTTR_3	Q8OU57_5114_M1_Rims3	0.7341	-0.4459	0.0409	1.3881
Akap12	Q9WTC5	A-kinase anchor protein 12	_RPS[Phospho (STY)]ES[Phospho (STY)]DKEELDLK_2	Q9WTC5_5613_M2_Akap12	1.4886	0.5740	0.0410	1.3872
Chp1	P61022	Calcineurin B homologous protein 1	_ETGFSHSQTR_3	#N/A	0.7463	-0.4222	0.0410	1.3870
Pcm1	Q9R0L6	Pericentriolar material 1 protein	_ILEGDHGS[Phospho (STY)]PAGEIDDEOKKDETETVK_4	Q9R0L6_51729_M1_Pcm1	0.7464	-0.4219	0.0412	1.3854
Pgp5c	Q60676	Serine/threonine-protein phosphatase 5	_GNHETDNMMQYGFGEVVK_3	#N/A	1.4879	0.5733	0.0412	1.3854
Marcks	P26645	Myristoylated alanine-rich C-kinase substrate	_AEDGAAPS[Phospho (STY)]PSEST[Phospho (STY)]PKKK_2	#N/A	0.4393	-1.1867	0.0412	1.3853
Actn1	Q77P84	Alpha-actinin-1	_IDQLECC[Carbamidomethyl (C)]DHQLQALFQNK_3	#N/A	0.6468	-0.6286	0.0412	1.3853

Ranbp2	Q9ERU9	E3 SUMO-protein ligase RanBP2	_SALS[Phospho (STY)]PSKSPAK_2	Q9ERU9_S2113_M1_Ranbp2	2.3066	1.2058	0.0413	1.3837
Scn4b	Q7M729	Sodium channel subunit beta-4	_EC[Carbamidomethyl (C)]LVSSGNDNTENGLPGSK_2	#N/A	1.6856	0.7532	0.0414	1.3832
Cnksr2	Q80YA9	Connector enhancer of kinase suppressor of ras 2	_GSES[Phospho (STY)]PNSFIDQERYK_2	#N/A	2.9093	1.5407	0.0414	1.3825
Sybu	Q8BH58	Syntabulin	_SGSS[Phospho (STY)]PPSP[Phospho (STY)]PIR_2	Q8BH58_S199_M2_Sybu	0.7064	-0.5014	0.0415	1.3823
Bcl11b	Q99PV8	B-cell lymphoma/leukemia 11B	_SPFLST[Phospho (STY)]PPLPMPAGT[Phospho (STY)]PPPOPPAK_3	Q99PV8_T406_M2_Bcl11b	0.7467	-0.4215	0.0415	1.3822
Gria2	P23B19	Glutamate receptor 2	_ADIAAPLTLTVR_2	#N/A	1.3381	0.4202	0.0415	1.3819
Tmcc2	Q80W04	Transmembrane and coiled-coil domains protein 2	_GS[Phospho (STY)]PHLLR_2	Q80W04_S189_M1_Tmcc2	1.5659	0.6470	0.0416	1.3811
Ugp2	Q91ZJ5	UTP-glucose-1-phosphate uridylyltransferase	_NENTFLDLTVQQEHLNK_3	#N/A	0.7335	-0.4472	0.0417	1.3800
Lmtk3	Q5XV66	Serine/threonine-protein kinase LMTK3	_AQRPPEGM[Oxidation (M)]SS[Phospho (STY)]PELPPR_3	#N/A	0.5929	-0.7541	0.0417	1.3796
Rtn4	Q99P72	Reticulon-4	_ESAEFVSLEYSEM[Oxidation (M)]GSSSNGS[Phospho (STY)]PK_3	Q99P72_S291_M1_Rtn4	1.7369	0.7965	0.0417	1.3796
Ndufb5	Q9CQH3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	_NFDYGPKEK_2	#N/A	0.6788	-0.5590	0.0418	1.3793
Giccl1	Q8K3I9	Glucocorticoid-induced transcript 1 protein	_TSS[Phospho (STY)]LDTTGTGVLTGQWPR_2	Q8K3I9_S163_M1_Giccl1	0.7470	-0.4209	0.0419	1.3780
Atp6v1c1	Q9Z1G3	V-type proton ATPase subunit C 1	_SRAS[Phospho (STY)]AVNNLK_2	Q9Z1G3_S141_M1_Atp6v1c1	1.5251	0.6089	0.0420	1.3767
Syngap1	F65EU4	Ras/Rap GTPase-activating protein Syngap	_TVS[Phospho (STY)]VPVEGRPHGEHYHLGR_4	#N/A	0.6885	-0.5385	0.0421	1.3755
Ppid	Q9CR16	Peptidyl-prolyl cis-trans isomerase D	_I[Acetyl (Protein N-term)]SHASPAAKPSNSK_3	#N/A	0.7147	-0.4846	0.0422	1.3746
Pdelc	Q64338	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1C	_I[Acetyl (Protein N-term)]MES[Phospho (STY)]PTKEIEEFSSNSLK_3	Q64338_S3_M1_Pdelc	0.7330	-0.4482	0.0423	1.3740
Cttn	Q60598	Src substrate cortactin	_HC[Carbamidomethyl (C)]S[Phospho (STY)]QVDSVR_2	Q60598_S113_M1_Cttn	0.6403	-0.6432	0.0424	1.3730
Prickle2	Q80Y24	Prickle-like protein 2	_S[Phospho (STY)]FQESLGGQGR_2	#N/A	1.4499	0.5360	0.0424	1.3721
Arhgef2	Q60875	Rho guanine nucleotide exchange factor 2	_EAQELGSS[Phospho (STY)]PEDR_2	#N/A	1.4136	0.4993	0.0425	1.3720
Stim2	P83093	Stromal interaction molecule 2	_S[Phospho (STY)]MIFSPASK_2	P83093_S661_M1_Stim2	0.6670	-0.5843	0.0425	1.3718
Tecr	Q9CY27	Very-long-chain enoyl-CoA reductase	_S[Phospho (STY)]LKHDEVLQK_2	Q9CY27_S58_M1_Tecr	1.6419	0.7153	0.0425	1.3717
Chgb	P16014	Secretogranin-1	_ADEFPDPY[Phospho (STY)]DS[Phospho (STY)]EEQM[Oxidation (M)]GPHQEANDEK_3	P16014_S626_M2_Chgb	1.4831	0.5686	0.0426	1.3710
BclA1	Q9D859	BclA-like protein 1	_FEGAM[Oxidation (M)]S[Phospho (STY)]PLQR_2	#N/A	1.8563	0.8925	0.0426	1.3707
Vars1	Q9Z1Q9	Valine-tRNA ligase	_LSATVTEAFVR_2	#N/A	0.7588	-0.3982	0.0426	1.3706
Sbtp1	O08599	Syntaxin-binding protein 1	_LDAKYADDPMTGEGGPK_3	#N/A	1.5093	0.5939	0.0427	1.3700
Camk4	P08414	Calcium/calmodulin-dependent protein kinase type IV	_DSTDLGKK_2	#N/A	1.3319	0.4135	0.0427	1.3694
Pgm2	Q775V4	Phosphoglucomutase-2	_I[Acetyl (Protein N-term)]AAAT[Phospho (STY)]PTETPAPEGSGGLMDAR_2	Q775V4_TS_M1_Pgm2	0.7476	-0.4197	0.0428	1.3688
Oxblp6	Q8BX89	Oxysterol-binding protein-related protein 6	_TAS[Phospho (STY)]SSTEPSVR_2	Q8BX89_S44_M1_Oxblp6	1.4089	0.4946	0.0428	1.3681
Tuba1b	P05213	Tubulin alpha-1B chain	_RAFVHWYVVGEGMEEGESEAR_3	#N/A	0.7478	-0.4194	0.0430	1.3665
Cacnb2	Q8CZ27	Voltage-dependent L-type calcium channel subunit beta-2	_SGGNSSS[Phospho (STY)]SLGDVPPSR_2	Q8CZ27_S202_M1_Cacnb2	0.0951	-3.3940	0.0430	1.3663
Dync1h1	Q91HU4	Cytoplasmic dynein 1 heavy chain 1	_LALESXC[Carbamidomethyl (C)]LLGESTDWDK_2	#N/A	0.7087	-0.4967	0.0430	1.3660
Son	Q9QX47	Protein SON	_RFS[Phospho (STY)]RS[Phospho (STY)]PIR_2	#N/A	2.0965	1.0680	0.0431	1.3659
Calcoo1	Q8CGU1	Calcium-binding and coiled-coil domain-containing protein 1	_LPSYGLC[Carbamidomethyl (C)]ESGNTSSS[Phospho (STY)]PPGP_R2	Q8CGU1_S563_M1_Calcoo1	4.8836	2.2879	0.0431	1.3657
Kcnq2	Q9Z351	Potassium voltage-gated channel subfamily KQT member 2	_VQYQT[Phospho (STY)]WNGR_2	Q9Z351_T287_M1_Kcnq2	0.6934	-0.5282	0.0431	1.3655
Gab2	Q9Z158	GRB2-associated-binding protein 2	_ASS[Phospho (STY)]C[Carbamidomethyl (C)]JETEYPAAR_2	Q9Z158_S402_M1_Gab2	1.7624	0.8175	0.0431	1.3653
Kiaa1109	A2AAE1	Transmembrane protein KIAA1109	_SLQDQS[Phospho (STY)]PSRK_2	A2AAE1_S3835_M1_Kiaa1109	0.6702	-0.5772	0.0432	1.3648
Hspa12a	Q8K0U4	Heat shock 70 kDa protein 12A	_WSS[Phospho (STY)]QGGM_R2	Q8K0U4_S437_M1_Hspa12a	1.4813	0.5669	0.0432	1.3648
Abi2	Q4IIM5	Tyrosine-protein kinase Abi2	_STQASSGS[Phospho (STY)]PALPR_2	Q4IIM5_S621_M1_Abi2	1.3522	0.4353	0.0432	1.3647
Rbm26	Q6N2N0	RNA-binding protein 26	_RLNHS[Phospho (STY)]PPSSSR_3	#N/A	0.4862	-1.0404	0.0432	1.3646
Atp2a2	O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	_TASEM[Oxidation (M)]VLADONFSTVAAVEGR_3	#N/A	1.4117	0.4975	0.0432	1.3645
Tnrc6b	Q8BK12	Trinucleotide repeat-containing gene 6B protein	_SSSS[Phospho (STY)]AGSEVGGSQSGSNHK_2	Q8BK12_S601_M1_Tnrc6b	0.7479	-0.4191	0.0432	1.3643
Hspa2	P17156	Heat shock-related 70 kDa protein 2	_QTQTFTTYSNQGSSVQVVEGR_3	#N/A	0.7322	-0.4496	0.0433	1.3640
Cadps	Q80T11	Calcium-dependent secretion activator 1	_SLTSNLPNVLPMVNLPK_2	#N/A	0.6048	-0.7255	0.0433	1.3637
Zfyve26	Q5DUJ7	Zinc finger FYVE domain-containing protein 26	_GPLGLARS[Phospho (STY)]PSES[Phospho (STY)]PQHAATER_3	Q5DUJ7_S605_M2_Zfyve26	0.7480	-0.4189	0.0433	1.3630
Top2b	Q64511	DNA topoisomerase 2-beta	_KTSFQDS[Phospho (STY)]DVIDFSDTSEPPPALPR_3	Q64511_S1568_M1_Top2b	0.7098	-0.4946	0.0434	1.3624
Codc8a	Q55P85	Coiled-coil domain-containing protein 85A	_STS[Phospho (STY)]PEHLHKPR_2	#N/A	2.4914	1.3169	0.0434	1.3624
Hecw1	Q8K4P8	E3 ubiquitin-protein ligase HECW1	_APS[Phospho (STY)]PYRR_2	Q8K4P8_S1219_M1_Hecw1	0.7080	-0.4982	0.0435	1.3617
Bclaf1	Q8K0I9	Bcl-2-associated transcription factor 1	_LRC[Carbamidomethyl (C)]DS[Phospho (STY)]ADLR_2	Q8K0I9_S688_M1_Bclaf1	0.7076	-0.4989	0.0435	1.3614
Nagk	Q9QZ08	N-acetyl-D-glucosamine kinase	_I[Acetyl (Protein N-term)]AALYGGVGGGTR_2	#N/A	0.5210	-0.9406	0.0435	1.3610
Ndrp2	Q9QYG0	Protein NDRP2	_LTGLTSSPDM[Oxidation (M)]LGLHLSFQSELSGNSLQIK_3	#N/A	0.7495	-0.4161	0.0436	1.3602
Calb2	Q08331	Calretinin	_EM[Oxidation (M)]NIQQLTVRR_2	#N/A	0.7508	-0.4134	0.0437	1.3597
Srcin1	Q9QW16	SRC kinase signaling inhibitor 1	_LGGAPTGGGVSPPSAILER_2	#N/A	2.0920	1.0649	0.0437	1.3595
Atp6v0d1	P51863	V-type proton ATPase subunit d 1	_AGVLSQADYLVNLVQC[Carbamidomethyl (C)]TELEDK_3	#N/A	0.7140	-0.4860	0.0438	1.3590
Csbr2	Q3UH0D	Serine-rich coiled-coil domain-containing protein 2	_SSS[Phospho (STY)]GESLAQSPONAK_2	Q3UH0D_S198_M1_Csbr2	1.5341	0.6174	0.0438	1.3585
Tmem230	Q8CB86	Transmembrane protein 230	_LAS[Phospho (STY)]TDDGVLDQPK_2	Q8CB86_S24_M1_Tmem230	0.7498	-0.4155	0.0439	1.3577
Kmt2d	Q6PDK2	Histone-lysine N-methyltransferase 2D	_LC[Carbamidomethyl (C)]PQFEIPVLS[Phospho (STY)]PQPEPR_2	Q6PDK2_S727_M1_Kmt2d	0.2509	-1.9949	0.0439	1.3575
Cox6	Q8B6D8	Cytochrome c oxidase assembly factor 6 homolog	_KXFAGGFGSSGSTENS_2	#N/A	2.5558	1.3537	0.0440	1.3568
Iso2a	P85094	Isochorismatase domain-containing protein 2A	_QSGAFPLATSESLQLVR_2	#N/A	0.7107	-0.4927	0.0440	1.3565
Six17	Q9D004	Syntaxin-17	_LTS[Phospho (STY)]C[Carbamidomethyl (C)]POLPSQSDK_2	Q9D004_S288_M1_Six17	5.6961	2.5100	0.0442	1.3548
Prip3	Q9Z2U1	U4/U6 small nuclear ribonucleoprotein Prip3	_WDEQTSNTKGDDDEES[Phospho (STY)]DEEAVKK_3	#N/A	1.7365	0.7962	0.0442	1.3541
Prr13	Q6PE13	Proline-rich transmembrane protein	_S[Phospho (STY)]DAALFR_2	Q6PE13_S806_M1_Prr13	0.7163	-0.4813	0.0443	1.3539
Iqsec2	Q5DU25	IQ motif and SEC7 domain-containing protein 2	_AAHLPLLTIEPPSDSS[Phospho (STY)]VDSLR_3	Q5DU25_S593_M1_Iqsec2	0.5409	-0.8865	0.0443	1.3538
Arhgef2	A2ASR2	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	_HLDVLDLRQS[Phospho (STY)]LSSIDR_3	A2ASR2_S1518_M1_Arhgef2	0.7315	-0.4510	0.0443	1.3537
Atxn1	P54254	Ataxin-1	_EAS[Phospho (STY)]PSTLNDK_2	P54254_S382_M1_Atxn1	0.4111	-1.2823	0.0443	1.3535
Calr	P14211	Calreticulin	_VHVIFVNYK_2	#N/A	0.6589	-0.6019	0.0443	1.3534
Ugp2	Q91ZJ5	UTP-glucose-1-phosphate uridylyltransferase	_AM[Oxidation (M)]S[Phospho (STY)]QDGASQFQEVILQELSLVK_3	Q91ZJ5_S13_M1_Ugp2	0.7486	-0.4177	0.0444	1.3528
Cdk14	Q35495	Cyclin-dependent kinase 14	_TIS[Phospho (STY)]ESFSR_2	Q35495_S24_M1_Cdk14	0.7314	-0.4513	0.0445	1.3515
Washc2	Q6PGL7	WASH complex subunit 2	_EGLLPASDQEGAGGSPDSIFSSS[Phospho (STY)]PLDK_3	Q6PGL7_S783_M1_Washc2	1.4927	0.5780	0.0446	1.3506
Nipsnap1	O55125	Protein Nipsnap homolog 1	_JQFHNVPK[C[Carbamidomethyl (C)]DAYSNLTEAVLPK_4	#N/A	0.7487	-0.4175	0.0446	1.3505
Cadm2	Q8BLQ9	Cell adhesion molecule 2	_GAEDPADTADTAINEAGS[Phospho (STY)]QVNAEEK_3	#N/A	1.6072	0.6845	0.0447	1.3501
Gapdh	P16858	Glyceraldehyde-3-phosphate dehydrogenase	_LEKPAKYDOK_3	#N/A	0.5219	-0.9383	0.0448	1.3490
Map7f1	A3AJ0	MAP7 domain-containing protein 1	_LSTGELS[Phospho (STY)]PK_2	A3AJ0_S460_M1_Map7f1	0.7489	-0.4172	0.0448	1.3483
Ppp1r14c	Q8R450	Protein phosphatase 1 regulatory subunit 14C	_KLS[Phospho (STY)]PPQKK_2	Q8R450_S157_M1_Ppp1r14c	0.6741	-0.5689	0.0449	1.3480
Septin2	P4Z208	Septin-2	_STLNSLFLTDLPPER_2	#N/A	0.5468	-0.8708	0.0449	1.3476
Ipo5	Q8BKCS	Importin-5	_HIVENAVOK_2	#N/A	1.4337	0.5197	0.0449	1.3474
Hspa8	P63017	Heat shock cognate 71 kDa protein	_GLRS[Phospho (STY)]KEDIER_3	P63017_S511_M1_Hspa8	1.3371	0.4191	0.0449	1.3473
Sh3bgr3	Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3	_VYSTSVTSGR_2	#N/A	0.3942	-1.3430	0.0451	1.3463
Itsn1	Q9Z0R4	Intersectin-1	_AQSS[Phospho (STY)]FDVASAPAAEAWAPQSSR_2	Q9Z0R4_S203_M1_Itsn1	0.7310	-0.4520	0.0451	1.3458
Dic1	Q9R0Z9	Rho GTPase-activating protein 7	_KRSEDS[Phospho (STY)]DEDEPC[Carbamidomethyl (C)]AISGK_3	#N/A	1.4344	0.5204	0.0452	1.3449

Napb	P28663	Beta-soluble NSF attachment protein	_AIAHYEQSADYYK_3	#N/A	1.4903	0.5756	0.0452	1.3448
Trim28	Q62318	Transcription intermediary factor 1-beta	_VS[Phospho (STY)]LERLDLDTSSQPPVKF_3	Q62318_S489_M1_Trim28	0.7524	-0.4105	0.0452	1.3445
Ranbp2	Q9ERU9	E3 SUMO-protein ligase RanBP2	_LNVNNSAS[Phospho (STY)]PHR_2	Q9ERU9_S837_M1_Ranbp2	0.6159	-0.6993	0.0455	1.3422
Tmod2	Q9IKK7	Tropomodulin-2	_DREDVPPTGEK_2	#N/A	0.7407	-0.4331	0.0456	1.3414
Atg5f1c	Q91VR2	ATP synthase subunit gamma, mitochondrial	_EUEIGSAAAID_2	#N/A	1.4053	0.4909	0.0456	1.3411
Plkm	P47857	ATP-dependent 6-phosphofructokinase, muscle type	_SSYLVNVLGSLGNDIC[Carbamidomethyl (C)]CTDM[Oxidation (M)]TGTD5ALHR_3	#N/A	1.5369	0.6200	0.0458	1.3396
Adgrl1	Q80TR1	Adhesion G protein-coupled receptor L1	_TOTLTYASWEDYVAAR_2	#N/A	0.7520	-0.4112	0.0458	1.3388
Tbc1d5	Q80XQ2	TBC1 domain family member 5	_FTGS[Phospho (STY)]PPPSATKK_2	Q80XQ2_S578_M1_Tbc1d5	9.8818	3.3048	0.0459	1.3382
Hecw1	Q8K4P8	E3 ubiquitin-protein ligase HECW1	_SGS[Phospho (STY)]VHQMEQLNR_2	Q8K4P8_S871_M1_Hecw1	1.6693	0.7393	0.0459	1.3379
Rbm1	Q91VM5	RNA binding motif protein, X-linked-like-1	_DRDYSDHPSGGSYR_3	#N/A	0.5660	-0.8212	0.0460	1.3370
Ppp3r1	Q63810	Calcineurin subunit B type 1	_KLDDNSGSLSEEFM[Oxidation (M)]SLPELQONPLVQR_3	#N/A	0.7495	-0.4159	0.0461	1.3359
Snap25	P60879	Synaptosomal-associated protein 25	_HM[Oxidation (M)]ALDM[Oxidation (M)]GNEIDTQNR_3	#N/A	0.6708	-0.5759	0.0462	1.3357
Rem2	Q8VEL9	GTP-binding protein REM 2	_BRGS[Phospho (STY)]M[Oxidation (M)]PVPYK_3	#N/A	0.7213	-0.4713	0.0463	1.3347
Eps15l1	Q60902	Epidermal growth factor receptor substrate 15-like 1	_GIDPPQVLS[Phospho (STY)]PDM[Oxidation (M)]VPPSR_2	Q60902_S353_M1_Eps15l1	0.4538	-1.1399	0.0463	1.3341
Relch	Q148V7	RAB11-binding protein RELCH	_AGGSTLSGLDFARY[Phospho (STY)]SDGNNRETDER_3	Q148V7_Y192_M1_Relch	0.6089	-0.7158	0.0464	1.3337
Phactr1	Q2M3X8	Phosphatase and actin regulator 1	_RLS[Phospho (STY)]QRPTAELEQR_3	Q2M3X8_S467_M1_Phactr1	1.4837	0.5692	0.0465	1.3327
Atg4c	Q811C2	Cysteine protease ATG4C	_DFOFTSTAAS[Phospho (STY)]EEDLFSDEDERK_3	Q811C2_S434_M1_At4c	1.4736	0.5594	0.0465	1.3322
Arf6ip5	Q8RSJ9	PRA1 family protein 3	_TPMGILDALEQQEDNNK_2	#N/A	0.6803	-0.5557	0.0465	1.3321
Icam5	Q60625	Intercellular adhesion molecule 5	_LDDLDC[Carbamidomethyl (C)]PR_2	#N/A	0.7621	-0.3920	0.0466	1.3319
Plig	A2AR02	Peptidyl-prolyl cis-trans isomerase G	_FGS[Phospho (STY)]PVSK_2	#N/A	0.6154	-0.7005	0.0466	1.3318
Necab2	Q912P9	N-terminal EF-hand calcium-binding protein 2	_TIS[Phospho (STY)]FDLQQR_2	Q912P9_S711_M1_Necab2	0.1253	-2.9969	0.0466	1.3314
Rap2b	P61226	Ras-related protein Rap-2b	_SALTQVYTGSGRIK_2	#N/A	0.6061	-0.7223	0.0467	1.3311
Pnpo	Q913FO	Pyridoxine-5'-phosphate oxidase	_GLATGDS[Phospho (STY)]LPGPM[Oxidation (M)]THHGDEWVYR_4	#N/A	1.3566	0.4400	0.0467	1.3303
Kcnma1	Q08460	Calcium-activated potassium channel subunit alpha-1	_LEDEQPPTLS[Phospho (STY)]PK_2	#N/A	0.4716	-1.0844	0.0468	1.3301
Ctic	Q68F05	Clathrin heavy chain 1	_YQAAAC[Carbamidomethyl (C)]K_2	#N/A	0.5737	-0.8017	0.0468	1.3294
Rab3b	Q9CZT8	Ras-related protein Rab-3b	_LLAELGFGDFEFASAK_2	#N/A	1.4783	0.5639	0.0469	1.3291
Hmrnpa1	P49312	Heterogeneous nuclear ribonucleoprotein A1	_GFAVTFDDHDSVDK_2	#N/A	1.5706	0.6513	0.0469	1.3286
Cep170b	Q80U49	Centrosomal protein of 170 kDa protein B	_ESPLS[Phospho (STY)]PPTVPDRGGATPGSAR_2	Q80U49_S981_M1_Cep170b	0.4673	-1.0975	0.0470	1.3282
Homer1	Q9Z2Y3	Homer protein homolog 1	_TELNQTVQLELETK_2	#N/A	1.5600	0.6416	0.0470	1.3282
Ctnna2	Q61301	Catenin alpha-2	_LVYDQVR_2	#N/A	0.5860	-0.7710	0.0471	1.3273
Vat1l	Q80T88	Synaptic vesicle membrane protein VAT-1 homolog-like	_DSVTHLFR_2	#N/A	0.6083	-0.7173	0.0471	1.3268
Myh9	Q8VDD5	Myosin-9	_GTGDC[Carbamidomethyl (C)]S[Phospho (STY)]DEEDVGK_2	#N/A	0.7432	-0.4282	0.0472	1.3265
Hk1	P17710	Hexokinase-1	_GAAM[Oxidation (M)]TAVAYR_2	#N/A	1.3871	0.4720	0.0473	1.3252
Prkcb	P68404	Protein kinase C beta type	_QPVELT[Phospho (STY)]PTDK_2	P68404_T642_M1_Prkcb	0.0697	-3.8436	0.0473	1.3251
Wdr1	O88342	WD repeat-containing protein 1	_LATGSDONC[Carbamidomethyl (C)]AAFFEGPPFK_2	#N/A	0.5275	-0.9227	0.0473	1.3247
Sgpl1	Q8V037	SH3-containing GRB2-like protein 3-interacting protein 1	_RNLS[Phospho (STY)]SEEVAPR_3	#N/A	4.0908	2.0324	0.0474	1.3238
Rims2	Q9EQZ7	Regulating synaptic membrane exocytosis protein 2	_TSHNS[Phospho (STY)]PPTPR_2	Q9EQZ7_S472_M1_Rims2	2.4144	1.2717	0.0475	1.3234
Brsk2	Q69298	Serine/threonine-protein kinase BRK2	_S[Phospho (STY)]SGASSGLSTS[Phospho (STY)]PLSPSR_2	Q69298_S413_M2_Brsk2	0.2633	-1.9254	0.0475	1.3232
Skabp4	Q9WV89	Syntaxin-binding protein 4	_SSS[Phospho (STY)]PLDRAPR_2	Q9WV89_S12_M1_Skabp4	0.7502	-0.4146	0.0475	1.3229
Snip1	Q88026	Smad nuclear-interacting protein 1	_HRS[Phospho (STY)]GDALTYVVK_3	#N/A	1.7784	0.8305	0.0476	1.3228
Grm5	Q3UVX5	Metabotropic glutamate receptor 5	_GS[Phospho (STY)]SGETUR_2	#N/A	0.7436	-0.4274	0.0476	1.3224
Cow6c	Q9CPQ1	Cytochrome c oxidase subunit 6C	_NYDSMKDFEEMR_3	#N/A	0.7503	-0.4145	0.0477	1.3217
Nsf	P46460	Vesicle-fusing ATPase	_KNIDSNPPTDK_2	#N/A	0.4841	-1.0466	0.0477	1.3215
Prkce	P16054	Protein kinase C epsilon type	_SAPTS[Phospho (STY)]PC[Carbamidomethyl (C)]DQELKELENRRK_3	#N/A	0.1857	-2.4292	0.0477	1.3209
Aldh1b1	Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	_TFVEESYR_2	#N/A	0.7349	-0.4443	0.0478	1.3204
Mast1	Q9R1L5	Microtubule-associated serine/threonine-protein kinase 1	_S[Phospho (STY)]PITQR_2	Q9R1L5_S968_M1_Mast1	0.7541	-0.4072	0.0478	1.3202
Fei1	Q8K0X8	Fasciculation and elongation protein zeta-1	_GLS[Phospho (STY)]LGSNR_2	Q8K0X8_S298_M1_Fei1	0.1641	-2.6075	0.0479	1.3200
Dclk1	Q9ILM8	Serine/threonine-protein kinase DCLK1	_Acetyl (Protein N-term)[S[Phospho (STY)]JGRDMLEHFDER_3	#N/A	0.7156	-0.4828	0.0479	1.3197
Pikb1	Q9Z1B3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1	_LQVTPGR_2	#N/A	0.6744	-0.5682	0.0479	1.3196
Pomb5	O55234	Proteasome subunit beta type-5	_DAYSGAVNLVHVR_2	#N/A	1.7145	0.7778	0.0479	1.3194
Kiaa1107	Q80TK0	AP2-interacting clathrin-endocytosis protein	_SSVSSROS[Phospho (STY)]DENYR_2	Q80TK0_S353_M1_Kiaa1107	0.7195	-0.4749	0.0480	1.3188
Aldh6a1	Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	_DMDLVSYR_2	#N/A	1.5003	0.5853	0.0481	1.3178
Znrf2	Q71F05	E3 ubiquitin-protein ligase ZNRF2	_AYS[Phospho (STY)]CSDLPSGTGSGGGADGAR_2	Q71F05_S18_M1_Znrf2	17.9883	4.1690	0.0482	1.3173
Fabp3	P11404	Fatty acid-binding protein, heart	_NGOTTIK_2	#N/A	1.4472	0.5332	0.0482	1.3170
Plec	Q9QXS1	Plectin	_EEELQQTLQEQNMILDR_2	#N/A	1.4793	0.5649	0.0482	1.3169
Myo5a	Q99104	Unconventional myosin Va	_QLELDNDR_2	#N/A	0.6442	-0.6344	0.0482	1.3168
Dcx	O88809	Neuronal migration protein doublecortin	_SKGS[Phospho (STY)]PSTPTS[Phospho (STY)]PGSLRK_3	O88809_S332_M2_Dcx	0.7416	-0.4313	0.0482	1.3166
Oxc11	Q9D0K2	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	_GM[Oxidation (M)]GGAM[Oxidation (M)]DLVSSK_2	#N/A	0.5701	-0.8108	0.0484	1.3154
Iso2a	P85094	Isochorismatase domain-containing protein 2A	_DASHPQFK_2	#N/A	0.6907	-0.5338	0.0484	1.3151
Rhob	P62746	Rho-related GTP-binding protein Rhob	_IQAYDYLEC[Carbamidomethyl (C)]SAK_2	#N/A	1.4961	0.5812	0.0484	1.3149
Kif2a	P28740	Kinesin-like protein KIF2A	_AVFQESIR_2	#N/A	0.6980	-0.5188	0.0486	1.3137
Vps50	Q8C71	Syndetin	_KKS[Phospho (STY)]DYSLNK_2	Q8C71_S595_M1_Vps50	0.3998	-1.3225	0.0487	1.3126
Cc2d1a	Q8K1A6	Coiled-coil and C2 domain-containing protein 1A	_LANHDEGS[Phospho (STY)]DEEETPKK_3	#N/A	0.7688	-0.3794	0.0487	1.3124
Ahcy2	Q68FL4	Putative adenosylhomocysteinease 3	_QVWC[Carbamidomethyl (C)]GVGEVGK_2	#N/A	0.7508	-0.4134	0.0489	1.3106
Qdpr	Q88V4	Dihydropyrimidine reductase	_VDAILC[Carbamidomethyl (C)]VAGGWAGGNAK_2	#N/A	1.9116	0.9347	0.0491	1.3092
Emi1	Q058C3	Echinoderm microtubule-associated protein-like 1	_TSSS[Phospho (STY)]ERVS[Phospho (STY)]PGGR_2	Q058C3_S135_M2_Emi1	1.5377	0.6207	0.0492	1.3078
Sir2	Q8VDQ8	NAD-dependent protein deacetylase siruin-2	_FFSC[Carbamidomethyl (C)]M[Oxidation (M)]QSDPSK_2	#N/A	1.7318	0.7923	0.0493	1.3070
Ptpn12	P35831	Tyrosine-protein phosphatase non-receptor type 12	_DQITKS[Phospho (STY)]PAEVDIGFGNR_3	#N/A	0.6725	-0.5723	0.0494	1.3066
Atf1	Q88H66	Atlastin-1	_VAVLLM[Oxidation (M)]DTGGTFDSQSTUR_2	#N/A	1.9197	0.9409	0.0494	1.3064
Tiam3	Q60610	T-lymphoma invasion and metastasis-inducing protein 1	_RSNATNSSYS[Phospho (STY)]PPTGR_2	#N/A	0.0581	-4.1060	0.0494	1.3060
Nduf62	Q91W05	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	_APGFAGLAGDK_2	#N/A	1.3006	0.3792	0.0494	1.3059
Dlg4	Q62108	Disks large homolog 4	_EQLMNSSGSGT[Phospho (STY)]ASLRS[Phospho (STY)]NPKR_3	Q62108_S425_M2_Dlg4	1.5384	0.6214	0.0496	1.3046
Taldo1	Q93092	Transaldolase	_WUHNEDQM[Oxidation (M)]AVEK_3	#N/A	0.5845	-0.7748	0.0496	1.3042
Napb	P28663	Beta-soluble NSF attachment protein	_ASHS[Phospho (STY)]RLR_2	P28663_S28_M1_Napb	0.7512	-0.4128	0.0497	1.3037
Spatan1	P16546	Spectrin alpha chain, non-erythrocytic 1	_ASAFNSWFENAAEDLTPVR_2	#N/A	1.4414	0.5274	0.0497	1.3034
Arvcf	P98203	Armadillo repeat protein deleted in velo-cardio-facial syndrome homolog	_NFDT[Phospho (STY)]LDLPK_2	P98203_T643_M1_Arvcf	1.4823	0.5678	0.0498	1.3032
Tkt	P40142	Transketolase	_GSDLOGHVPVK_3	#N/A	1.5197	0.6038	0.0498	1.3024
Wdr47	Q8CGF6	WD repeat-containing protein 47	_YQHLQEK_2	#N/A	1.4800	0.5656	0.0499	1.3022
Ncor1	Q60974	Nuclear receptor corepressor 1	_YS[Phospho (STY)]PESGSGTVLHPR_2	Q60974_S2116_M1_Ncor1	1.4827	0.5682	0.0499	1.3020