

Datta et. al. Phosphoproteomic profiling using biopsy-scale protein amounts

Supplementary Table S1: A list of all the phosphoPSMs identified from 2Q $\mu$ g protein

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
VGSLTPPsPK	AAK1	22848	AP2-associated protein kinase 1	S8(Phospho) S9(Phospho)	S(3): 0.0; T(5): 0.0; S(8): 100.0; S(9): 100.0	S8; S9;	S623; S624		2.54	0.001	0	2	615.3	1229.5	48.75	6950
KAEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		4.49	0	1	3	854.7	2562.0	20.41	2516
AEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0	S5;	S228		1.81	0	0	2	1217.4	2433.9	25.55	3344
KAEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		1.26	0	1	2	1281.5	2562.0	20.49	2528
KAEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228	43		0	1	3	854.7	2562.0	20.41	2516
AEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0	S5;	S228	14		0	0	2	1217.4	2433.9	25.55	3344
KAEQGsEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		2.87	0.001	1	3	854.7	2562.0	20.95	2587
NMAPSQQsPVR	AB12	10152	abl interactor 2 isoform e	M2(Oxidation) S8(Phospho)	S(5): 0.0; S(8): 100.0	S8;	S165	39		0	0	2	655.8	1310.6	17.66	2083
STsQGSINSPVYSR	ABLIM1	3983	actin-binding LIM protein 1 isoform s	S3(Phospho)	S(1): 2.1; T(2): 2.1; S(3): 95.7; S(6): 0.1; S(9): 0.0; Y(12): 0.0; S(13): 0.0	S3;	S164		2.47	0	0	2	781.8	1562.7	41.23	5716
STsQGSINSPVYSR	ABLIM1	3983	actin-binding LIM protein 1 isoform s	S3(Phospho)	S(1): 2.1; T(2): 2.1; S(3): 95.7; S(6): 0.1; S(9): 0.0; Y(12): 0.0; S(13): 0.0	S3;	S164	40		0	0	2	781.8	1562.7	41.23	5716
SSSIEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 3	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S176		4.2	0	1	3	649.3	1945.8	14.4	1634
GVPAGNsDTEGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 3	S7(Phospho)	S(7): 100.0; T(9): 0.0	S7;	S798		2.4	0	0	2	789.8	1578.7	23.82	3048
GVPAGNsDTEGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 3	S7(Phospho)	S(7): 100.0; T(9): 0.0	S7;	S798	50		0	0	2	789.8	1578.7	23.82	3048
SSSIEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 3	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S176	32		0	1	3	649.3	1945.8	14.4	1634
sPGSPVGEGTGSPPK	ADD1	118	alpha-adducin isoform c	S1(Phospho)	S(1): 97.9; S(4): 2.1; T(10): 0.0; S(12): 0.0	S1;	S355		3.23	0	0	2	717.3	1433.6	28.08	3723
sPGSPVGEGTGSPPK	ADD1	118	alpha-adducin isoform c	S1(Phospho)	S(1): 97.9; S(4): 2.1; T(10): 0.0; S(12): 0.0	S1;	S355	39		0	0	2	717.3	1433.6	28.08	3723
NSYNNSQAPsPGLGSK	AFF4	27125	AF4/FMR2 family member 4	S10(Phospho)	S(2): 0.0; Y(3): 0.0; S(6): 0.0; S(10): 96.8; S(15): 3.2	S10;	S1043		2.02	0	0	2	850.9	1700.7	35.92	4844
LPSGsGAAsPTGSVAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S9(Phospho)	S(3): 2.5; S(5): 97.5; S(9): 100.0; T(11): 0.0; S(13): 0.0	S5; S9;	S212; S216		2.97	0	0	2	901.9	1802.8	63.38	9234
GGVTGsPEASISGSK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho)	T(4): 0.0; S(6): 100.0; S(10): 0.0; S(12): 0.0; S(14): 0.0	S6;	S5731		2.66	0	0	2	707.3	1413.6	36.82	4982
GGVTGsPEASISGSK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho)	T(4): 0.0; S(6): 100.0; S(10): 0.0; S(12): 0.0; S(14): 0.0	S6;	S5731	51		0	0	2	707.3	1413.6	36.82	4982
LPSGsGAAsPTGSVAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S9(Phospho)	S(3): 2.5; S(5): 97.5; S(9): 100.0; T(11): 0.0; S(13): 0.0	S5; S9;	S212; S216	43		0	0	2	901.9	1802.8	63.38	9234
CDSSPDsAEDVVR	AHSG	197	alpha-2-HS-glycoprotein preproprotein	C1(Carbamidomethyl) S7(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 100.0	S7;	S138		2.9	0	0	2	709.3	1417.5	23.86	3053
CDSSPDsAEDVRK	AHSG	197	alpha-2-HS-glycoprotein preproprotein	C1(Carbamidomethyl) S7(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 100.0	S7;	S138		2.71	0	1	2	773.3	1545.6	16.32	1915
CDSSPDsAEDVVR	AHSG	197	alpha-2-HS-glycoprotein preproprotein	C1(Carbamidomethyl) S7(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 100.0	S7;	S138	50		0	0	2	709.3	1417.5	23.86	3053
CDSSPDsAEDVRK	AHSG	197	alpha-2-HS-glycoprotein preproprotein	C1(Carbamidomethyl) S7(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 100.0	S7;	S138	33		0	1	2	773.3	1545.6	16.32	1915
SPPsPVER	AKAP12	9590	A-kinase anchor protein 12 isoform 2	S4(Phospho)	S(1): 0.0; S(4): 100.0	S4;	S1233	37		0	0	2	474.7	948.4	21.69	2702

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
NSPLDCGSAsPNK	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	C6(Carbamidomethyl) S10(Phospho)	S(2): 0.0; S(8): 0.0; S(10): 100.0	S10;	S1816		2.57	0	0	2	713.8	1426.6	29.74	3972
NSPLDCGSAsPNK	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	C6(Carbamidomethyl) S10(Phospho)	S(2): 0.0; S(8): 0.0; S(10): 100.0	S10;	S1816	45		0	0	2	713.8	1426.6	29.74	3972
SEsLSNCSIGK	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C7(Carbamidomethyl) S3(Phospho)	S(1): 2.2; S(3): 97.8; S(5): 0.1; S(8): 0.0	S3;	S647		2.74	0	0	2	631.3	1261.5	33.54	4494
SEsLSNCSIGK	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C7(Carbamidomethyl) S3(Phospho)	S(1): 2.2; S(3): 97.8; S(5): 0.1; S(8): 0.0	S3;	S647	40		0	0	2	631.3	1261.5	33.54	4494
ASEDTTSGsPPKK	API5	8539	apoptosis inhibitor 5 isoform d	S9(Phospho)	S(2): 0.0; T(5): 0.0; T(6): 0.0; S(7): 0.0; S(9): 100.0	S9;	S291		4.02	0	1	2	692.8	1384.6	12.43	1246
ASEDTTSGsPPKK	API5	8539	apoptosis inhibitor 5 isoform d	S9(Phospho)	S(2): 0.0; T(5): 0.0; T(6): 0.0; S(7): 0.0; S(9): 100.0	S9;	S291	49		0	1	2	692.8	1384.6	12.43	1246
sAGEEEDGPVLTDEQK	ARL6IP4	51329	ADP-ribosylation factor-like protein 6-interacting protein 4 isoform 7	S1(Phospho)	S(1): 100.0; T(12): 0.0	S1;	S137		2.48	0	0	2	892.4	1783.7	43.61	6114
sAGEEEDGPVLTDEQK	ARL6IP4	51329	ADP-ribosylation factor-like protein 6-interacting protein 4 isoform 7	S1(Phospho)	S(1): 100.0; T(12): 0.0	S1;	S137	20		0	0	2	892.4	1783.7	43.61	6114
YNDWsDDDDDSNESK	ARMCX3	51566	armadillo repeat-containing X-linked protein 3	S5(Phospho)	Y(1): 0.1; S(5): 99.9; S(11): 0.0; S(14): 0.0	S5;	S61		2.03	0	0	2	942.8	1884.6	36.21	4888
YNDWsDDDDDSNESK	ARMCX3	51566	armadillo repeat-containing X-linked protein 3	S5(Phospho)	Y(1): 0.1; S(5): 99.9; S(11): 0.0; S(14): 0.0	S5;	S61	10		0.003	0	2	942.8	1884.6	36.21	4888
SSGNSSSSSGSGSTSAGSSsPGAR	ASPH	444	aspartyl/asparaginyl beta-hydroxylase isoform I	S21(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(19): 0.0; S(20): 4.4; S(21): 95.6	S21;	S29		2.11	0	0	2	1091.9	2182.9	12.63	1294
SSGNSSSSSGSGSTSAGSSsPGAR	ASPH	444	aspartyl/asparaginyl beta-hydroxylase isoform I	S21(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(19): 0.0; S(20): 4.4; S(21): 95.6	S21;	S29	15		0	0	2	1091.9	2182.9	12.63	1294
LTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S4(Phospho) S8(Phospho)	T(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S1310; S1314		2.25	0	0	2	705.8	1410.5	37.17	5034
LTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S4(Phospho) S8(Phospho)	T(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S1310; S1314	29		0.003	0	2	705.8	1410.5	37.17	5034
STsTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S3(Phospho) S7(Phospho)	S(1): 2.0; T(2): 2.0; S(3): 95.9; T(4): 0.0; T(6): 2.1; S(7): 97.9	S3; S7;	S680; S684		3.11	0	0	2	624.2	1247.5	24.95	3240
STSTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S7(Phospho)	S(1): 0.0; T(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(7): 100.0	S7;	S684		2.99	0	0	2	584.3	1167.5	18.64	2234
STSTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S7(Phospho)	S(1): 0.0; T(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(7): 100.0	S7;	S684	52		0	0	2	584.3	1167.5	18.64	2234
STsTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S3(Phospho) S7(Phospho)	S(1): 2.0; T(2): 2.0; S(3): 95.9; T(4): 0.0; T(6): 2.1; S(7): 97.9	S3; S7;	S680; S684	38		0	0	2	624.2	1247.5	24.95	3240
SQsPAASDCSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl) S3(Phospho)	S(1): 2.4; S(3): 97.6; S(7): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0; S(17): 0.0; S(20): 0.0; S(21): 0.0	S3;	S173		4.72	0	0	3	760.6	2279.9	32.61	4369
SStPLHsPSPIR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho) S7(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 0.0	T3; S7;	T285; S289		2.2	0	0	2	719.8	1438.6	40.98	5671
SStPLHsPSPIR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho) S7(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 0.0	T3; S7;	T285; S289		2.19	0	0	2	719.8	1438.6	40.47	5593
SQsPAASDCSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl) S3(Phospho)	S(1): 2.4; S(3): 97.6; S(7): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0; S(17): 0.0; S(20): 0.0; S(21): 0.0	S3;	S173	56		0	0	3	760.6	2279.9	32.61	4369
SStPLHsPSPIR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho) S7(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 0.0	T3; S7;	T285; S289	39		0	0	2	719.8	1438.6	40.47	5593

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
SStPLHsPSPiR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho) S7(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 0.0	T3; S7;	T285; S289	31		0	0	2	719.8	1438.6	40.98	5671
SSVQGsSREGsPAR	BAG3	9531	BAG family molecular chaperone regulator 3	S7(Phospho) S12(Phospho)	S(1): 0.2; S(2): 0.2; S(7): 95.7; S(8): 4.1; S(12): 99.8	S7; S12;	S274; S279	18		0.006	1	2	818.3	1635.7	14.8	1700
SLsPPQSQSK	BAIAP2	10458	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 0.0; S(9): 0.0	S3;	S325		2.29	0	0	2	569.8	1138.5	24.76	3206
SLsPPQSQSK	BAIAP2	10458	brain-specific angiogenesis inhibitor 1-associated protein 2 isoform 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 0.0; S(9): 0.0	S3;	S325	36		0	0	2	569.8	1138.5	24.76	3206
TPASTPVSGTPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) S14(Phospho)	T(1): 1.6; S(4): 0.0; T(5): 0.0; S(8): 49.2; T(10): 49.2; S(14): 100.0	S14;	S261		4.9	0	0	3	701.6	2102.9	53.22	7661
TPASTPVSGTPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) S14(Phospho)	T(1): 1.6; S(4): 0.0; T(5): 0.0; S(8): 49.2; T(10): 49.2; S(14): 100.0	S14;	S261	35		0.003	0	3	701.6	2102.9	53.22	7661
LAEDGEsEPEAVGQSR	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(8): 100.0; S(16): 0.0	S8;	S1468		2.89	0	0	2	934.9	1868.8	37.01	5010
LAEDGEsEPEAVGQSR	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(8): 100.0; S(16): 0.0	S8;	S1468	57		0	0	2	934.9	1868.8	37.01	5010
EAPGsPPLsPR	BCL9L	283149	B-cell CLL/lymphoma 9-like protein	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 100.0	S5; S9;	S21; S25		3.11	0	0	2	634.3	1267.5	48.01	6839
EAPGsPPLsPR	BCL9L	283149	B-cell CLL/lymphoma 9-like protein	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 100.0	S5; S9;	S21; S25	40		0	0	2	634.3	1267.5	48.01	6839
KETQsPEQVKSEK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S5(Phospho)	T(3): 0.0; S(5): 100.0; S(11): 0.0	S5;	S494		6.39	0	2	3	533.3	1597.7	12.62	1292
FNDsEGDDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	S(4): 96.5; T(9): 3.5; T(12): 0.0; Y(15): 0.0	S4;	S395		2.63	0	0	2	1001.3	2001.7	41.98	5843
FNDsEGDDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; T(12): 0.0; Y(15): 0.0	S4; T9;	S395; T400		2.17	0	0	2	1041.3	2081.7	49.44	7061
ETQsPEQVKSEK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	T(2): 0.0; S(4): 100.0; S(10): 0.0	S4;	S494		2.08	0	1	2	735.3	1469.7	13.03	1391
KETQsPEQVKSEK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S5(Phospho)	T(3): 0.0; S(5): 100.0; S(11): 0.0	S5;	S494	51		0	2	3	533.3	1597.7	12.62	1292
ETQsPEQVKSEK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	T(2): 0.0; S(4): 100.0; S(10): 0.0	S4;	S494	44		0	1	2	735.3	1469.7	13.03	1391
FNDsEGDDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	S(4): 96.5; T(9): 3.5; T(12): 0.0; Y(15): 0.0	S4;	S395	40		0	0	2	1001.3	2001.7	41.98	5843
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175	29		0	2	3	579.6	1736.8	19	2283
FNDsEGDDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; T(12): 0.0; Y(15): 0.0	S4; T9;	S395; T400	26		0	0	2	1041.3	2081.7	49.44	7061
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175		3.68	0.001	2	3	579.6	1736.8	19	2283
KAEGEPQEEsPLK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0	S10;	S175		2.27	0.005	1	2	761.3	1521.7	22.91	2901
KAEGEPQEEsPLK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0	S10;	S175	15		0.006	1	2	761.3	1521.7	22.91	2901
NTETQPTsPQLGTK	BRD1	23774	bromodomain-containing protein 1 isoform 1	S8(Phospho)	T(2): 3.4; T(4): 0.0; T(7): 3.4; S(8): 93.3; T(13): 0.0	S8;	S906		2.24	0	0	2	791.4	1581.7	31.89	4268
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201		4.16	0	0	2	632.7	1264.4	22.26	2799
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163		3.44	0	0	2	647.7	1294.5	33.92	4547
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201		2.97	0	0	2	632.7	1264.4	21.75	2713
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201	47		0	0	2	632.7	1264.4	21.75	2713
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201	40		0	0	2	632.7	1264.4	22.26	2799
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163		3.17	0.001	0	2	647.7	1294.5	33.95	4553
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163	25		0.004	0	2	647.7	1294.5	33.92	4547
NQGIEGsPGGR	C15orf52	388115	uncharacterized protein C15orf52	S7(Phospho)	S(7): 100.0	S7;	S193		2.69	0	0	2	576.2	1151.5	19.51	2375
NQGIEGsPGGR	C15orf52	388115	uncharacterized protein C15orf52	S7(Phospho)	S(7): 100.0	S7;	S193	18		0.003	0	2	576.2	1151.5	19.51	2375

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
EVLDAVKEVGSSSDVSGK	CAMSAP1	157922	calmodulin-regulated spectrin-associated protein 1	S18(Phospho)	S(6): 0.0; S(12): 27.5; S(13): 27.5; S(14): 27.5; S(15): 27.5; S(18): 90.0	S18;	S1216		1.55	0.006	1	3	714.0	2139.9	73.82	####
EVLDAVKEVGSSSDVSGK	CAMSAP1	157922	calmodulin-regulated spectrin-associated protein 1	S18(Phospho)	S(6): 0.0; S(12): 3.6; S(13): 35.1; S(14): 35.1; S(15): 35.1; S(18): 91.0	S18;	S1216		1.19	0.006	1	3	714.0	2139.9	73.23	####
LNQSSPDNVTDTK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	S(4): 2.1; S(5): 97.9; T(10): 0.0; T(12): 0.0	S5;	S572		2.43	0	0	2	749.8	1498.6	26.95	3558
LNQSSPDNVTDTK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	S(4): 2.1; S(5): 97.9; T(10): 0.0; T(12): 0.0	S5;	S572	31		0	0	2	749.8	1498.6	26.95	3558
QKSDAEEDGGVsqEEEDR	CANX	821	calnexin precursor	T11(Phospho) S13(Phospho)	S(3): 0.1; T(11): 99.9; S(13): 100.0	T11; S13;	T562; S564		4.33	0	1	3	756.9	2268.8	26.17	3437
QKSDAEEDGGVsqEEEDR	CANX	821	calnexin precursor	T11(Phospho)	S(3): 2.7; T(11): 94.6; S(13): 2.7	T11;	T562		3.02	0	1	3	730.3	2188.9	22.8	2881
QKsDAEEDGGTVsqEEEDR	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.1; S(13): 99.9	S3; S13;	S554; S564		2.91	0	1	2	1134.9	2268.8	26.21	3446
SDAEEDGGTVsqEEEDR	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564		2.72	0	0	2	966.9	1932.7	28.23	3745
QKSDAEEDGGVsqEEEDR	CANX	821	calnexin precursor	T11(Phospho) S13(Phospho)	S(3): 0.1; T(11): 99.9; S(13): 100.0	T11; S13;	T562; S564	37		0	1	3	756.9	2268.8	26.17	3437
SDAEEDGGTVsqEEEDR	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564	36		0	0	2	966.9	1932.7	28.23	3745
QKSDAEEDGGVsqEEEDR	CANX	821	calnexin precursor	T11(Phospho)	S(3): 2.7; T(11): 94.6; S(13): 2.7	T11;	T562	28		0	1	3	730.3	2188.9	22.8	2881
QKsDAEEDGGTVsqEEEDR	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.1; S(13): 99.9	S3; S13;	S554; S564	21		0	1	2	1134.9	2268.8	26.21	3446
STVTGERQsGDGQESTEPVENK	CASC3	22794	protein CASC3	S9(Phospho)	S(1): 4.4; T(2): 4.4; T(4): 0.2; S(9): 86.4; S(15): 4.4; T(16): 0.2	S9;	S148		2.67	0	1	3	805.7	2415.0	23.32	2970
TQSSsCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S5(Phospho)	T(1): 0.1; S(3): 0.1; S(4): 2.8; S(5): 97.0; S(11): 0.0; T(12): 0.0; T(13): 0.0	S5;	S571		2.53	0	0	2	923.4	1845.8	34.82	4680
TQSSsCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S5(Phospho)	T(1): 0.1; S(3): 0.1; S(4): 2.8; S(5): 97.0; S(11): 0.0; T(12): 0.0; T(13): 0.0	S5;	S571	25		0	0	2	923.4	1845.8	34.82	4680
SLsDSESDDSKSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(12): 0.0	S3;	S95		2.83	0	1	2	732.8	1464.6	12.87	1352
SLsDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 99.9; S(5): 0.0; S(7): 0.0; S(10): 0.0	S3;	S95		2.67	0	0	2	625.2	1249.4	16.38	1924
SLsDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 99.9; S(5): 0.0; S(7): 0.0; S(10): 0.0	S3;	S95	61		0	0	2	625.2	1249.4	16.38	1924
SLsDSESDDSKSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(12): 0.0	S3;	S95	50		0	1	2	732.8	1464.6	12.87	1352
LDQPVsAPPsPR	CCDC6	8030	coiled-coil domain-containing protein 6	S6(Phospho) S10(Phospho)	S(6): 100.0; S(10): 100.0	S6; S10;	S240; S244		3.79	0	0	2	712.3	1423.6	48.62	6930
LDQPVsAPPsPR	CCDC6	8030	coiled-coil domain-containing protein 6	S6(Phospho) S10(Phospho)	S(6): 100.0; S(10): 100.0	S6; S10;	S240; S244		3.41	0	0	2	712.3	1423.6	48.11	6856
LDQPVsAPPsPR	CCDC6	8030	coiled-coil domain-containing protein 6	S6(Phospho) S10(Phospho)	S(6): 100.0; S(10): 100.0	S6; S10;	S240; S244	41		0	0	2	712.3	1423.6	48.62	6930
LDQPVsAPPsPR	CCDC6	8030	coiled-coil domain-containing protein 6	S6(Phospho) S10(Phospho)	S(6): 100.0; S(10): 100.0	S6; S10;	S240; S244	41		0	0	2	712.3	1423.6	48.11	6856
LQQGAGLeSPQGQPEPGAAsPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S9(Phospho) S20(Phospho)	S(9): 100.0; S(20): 100.0	S9; S20;	S80; S91		4.38	0	0	3	821.7	2463.1	51.7	7379
LQQGAGLeSPQGQPEPGAAsPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91		4.28	0	0	3	795.0	2383.1	45.24	6408
LQQGAGLeSPQGQPEPGAAsPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91	26		0	0	3	795.0	2383.1	45.24	6408
LQQGAGLeSPQGQPEPGAAsPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S9(Phospho) S20(Phospho)	S(9): 100.0; S(20): 100.0	S9; S20;	S80; S91	26		0	0	3	821.7	2463.1	51.7	7379
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324		3.66	0	0	2	620.8	1240.5	13.85	1555
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324		3.63	0	0	2	620.8	1240.5	13.33	1455
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324	45		0.003	0	2	620.8	1240.5	13.33	1455
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324	41		0.003	0	2	620.8	1240.5	13.85	1555
HSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 3.0; S(5): 97.0; S(16): 0.0; S(17): 0.0	S5;	S49		1.87	0	0	2	1008.8	2016.7	20.91	2581

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
HSLD5DEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 3.0; S(5): 97.0; S(16): 0.0; S(17): 0.0	S5;	S49	30		0	0	2	1008.8	2016.7	20.91	2581
KGPGQPSsPQR	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S8(Phospho)	S(7): 1.1; S(8): 98.9	S8;	S195	38		0.003	1	2	609.8	1218.6	12.52	1269
VQTI <sup>1</sup> PSKPGGDR	CDC20	991	cell division cycle protein 20 homolog	T4(Phospho)	T(3): 0.1; T(4): 99.9; S(6): 0.1	T4;	T70		1.68	0	0	2	661.8	1322.6	13.2	1425
VQTI <sup>2</sup> PSKPGGDR	CDC20	991	cell division cycle protein 20 homolog	T4(Phospho)	T(3): 0.1; T(4): 99.9; S(6): 0.1	T4;	T70	26		0	0	2	661.8	1322.6	13.2	1425
sLSSsPVKK	CDC42EP4	23580	cdc42 effector protein 4	S1(Phospho) S5(Phospho)	S(1): 97.7; S(3): 4.5; S(4): 2.3; S(5): 95.5	S1; S5;	S138; S142		2.47	0	1	2	546.7	1092.5	20.63	2548
sLSSsPVKK	CDC42EP4	23580	cdc42 effector protein 4	S1(Phospho) S5(Phospho)	S(1): 97.7; S(3): 4.5; S(4): 2.3; S(5): 95.5	S1; S5;	S138; S142	14		0	1	2	546.7	1092.5	20.63	2548
IGEGtyGVVYK	CDK1	983	cyclin-dependent kinase 1 isoform 4	T5(Phospho) Y6(Phospho)	T(5): 100.0; Y(6): 100.0; Y(10): 0.0	T5; Y6;	T14; Y15	28		0	0	2	673.3	1345.5	59.19	8584
IGEGtyGVVYK	CDK1	983	cyclin-dependent kinase 1 isoform 4	T5(Phospho) Y6(Phospho)	T(5): 100.0; Y(6): 100.0; Y(10): 0.0	T5; Y6;	T14; Y15		2.17	0.004	0	2	673.3	1345.5	59.19	8584
TQDPsPGtTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho) T9(Phospho)	T(1): 0.0; S(5): 2.8; S(6): 97.2; T(9): 97.2; T(10): 2.8	S6; T9;	S429; T432		2.62	0	0	2	850.3	1699.7	32.66	4377
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho)	T(1): 0.0; S(5): 0.1; S(6): 99.8; T(9): 0.1; T(10): 0.0	S6;	S429		2.2	0	0	2	810.4	1619.7	26.29	3460
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho)	T(1): 0.0; S(5): 0.1; S(6): 99.8; T(9): 0.1; T(10): 0.0	S6;	S429	35		0	0	2	810.4	1619.7	26.29	3460
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho) T10(Phospho)	T(1): 0.0; S(5): 2.9; S(6): 97.1; T(9): 2.9; T(10): 97.1	S6; T10;	S429; T433		1.7	0.001	0	2	850.3	1699.7	32.16	4302
TQDPsPGtTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho) T9(Phospho)	T(1): 0.0; S(5): 2.8; S(6): 97.2; T(9): 97.2; T(10): 2.8	S6; T9;	S429; T432	13		0.003	0	2	850.3	1699.7	32.66	4377
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho) T10(Phospho)	T(1): 0.0; S(5): 2.9; S(6): 97.1; T(9): 2.9; T(10): 97.1	S6; T10;	S429; T433	12		0.004	0	2	850.3	1699.7	32.16	4302
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124	26		0.003	1	3	815.3	2443.8	13.64	1518
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124		3.03	0.005	1	3	815.3	2443.8	13.64	1518
NSSNTSVGsPSNTIGR	CLASP1	23332	CLIP-associating protein 1 isoform 3	S9(Phospho)	S(2): 0.0; S(3): 0.0; T(5): 0.0; S(6): 0.0; S(9): 99.9; S(11): 0.0; T(13): 0.0	S9;	S1063		2.86	0	0	2	829.4	1657.7	32.89	4406
NSSNTSVGsPSNTIGR	CLASP1	23332	CLIP-associating protein 1 isoform 3	S9(Phospho)	S(2): 0.0; S(3): 0.0; T(5): 0.0; S(6): 0.0; S(9): 99.9; S(11): 0.0; T(13): 0.0	S9;	S1063	66		0	0	2	829.4	1657.7	32.89	4406
TASESISNLsEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S10(Phospho) S14(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S200; S204	41		0	0	2	877.4	1753.7	61.28	8888
TNSMSSSGLGsPNR	CNOT2	4848	CCR4-NOT transcription complex subunit 2	M4(Oxidation) S11(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(11): 100.0	S11;	S165		2.63	0	0	2	745.8	1490.6	19.64	2394
TNSMSSSGLGsPNR	CNOT2	4848	CCR4-NOT transcription complex subunit 2	M4(Oxidation) S11(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(11): 100.0	S11;	S165	28		0	0	2	745.8	1490.6	19.64	2394
DQTAsAPAtPLVNK	COBLL1	22837	cordon-bleu protein-like 1 isoform 4	S5(Phospho) T9(Phospho)	T(3): 3.1; S(5): 96.9; T(9): 100.0	S5; T9;	S256; T260		2.25	0.001	0	2	786.8	1572.7	50.45	7207
DQTAsAPAtPLVNK	COBLL1	22837	cordon-bleu protein-like 1 isoform 4	S5(Phospho) T9(Phospho)	T(3): 3.1; S(5): 96.9; T(9): 100.0	S5; T9;	S256; T260	20		0.006	0	2	786.8	1572.7	50.45	7207
LQsAsPSTR	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 97.8; S(7): 2.2; T(8): 0.1	S3; S5;	S148; S150		3.17	0	0	2	553.7	1106.4	20.44	2522
LQsAsPSTR	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 97.8; S(7): 2.2; T(8): 0.1	S3; S5;	S148; S150	48		0	0	2	553.7	1106.4	20.44	2522
RKGsGsEQEGEDEEGGER	CTR9	9646	RNA polymerase-associated protein CTR9 homolog	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S941; S943		6.83	0	2	3	699.3	2095.8	12.84	1343
KGsGsEQEGEDEEGGER	CTR9	9646	RNA polymerase-associated protein CTR9 homolog	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S941; S943		1.82	0	1	2	970.3	1939.7	14.11	1594
RKGsGsEQEGEDEEGGER	CTR9	9646	RNA polymerase-associated protein CTR9 homolog	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S941; S943	49		0	2	3	699.3	2095.8	12.84	1343
AKTQTTPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho)	T(3): 99.9; T(5): 0.1; S(9): 100.0; T(15): 0.0	T3; S9;	T362; S368		4.54	0	1	3	698.6	2093.9	34.33	4606
AKTQTTPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	S9(Phospho)	T(3): 50.0; T(5): 50.0; S(9): 100.0; T(15): 0.0	S9;	S368		2.15	0	1	2	1047.5	2093.9	34.36	4610

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
TQTTPVSPAPQPTTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.6; T(3): 97.4; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368		2.03	0	0	2	947.9	1894.8	45.59	6473
AKTQTPVPSPAPQPTTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho)	T(3): 99.9; T(5): 0.1; S(9): 100.0; T(15): 0.0	T3; S9;	T362; S368	32		0	1	3	698.6	2093.9	34.33	4606
TQTTPVSPAPQPTTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.6; T(3): 97.4; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368	16		0.003	0	2	947.9	1894.8	45.59	6473
MAEESSSSSSSSPTAATSQQQLK	CUL4B	8450	cullin-4B isoform 2	M1(Oxidation) T15(Phospho)	S(5): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.1; S(10): 0.1; S(11): 3.5; S(12): 3.5; S(13): 3.5; T(15): 89.2; T(18): 0.1; S(19): 0.0	T15;	T130		3.38	0	0	3	880.7	2640.1	29.48	3927
MAEESSSSSSSSPTAATSQQQLK	CUL4B	8450	cullin-4B isoform 2	M1(Oxidation) T15(Phospho)	S(5): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.1; S(10): 0.1; S(11): 3.5; S(12): 3.5; S(13): 3.5; T(15): 89.2; T(18): 0.1; S(19): 0.0	T15;	T130	32		0	0	3	880.7	2640.1	29.48	3927
YQEQGGEASQQR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0	S9;	S129		2.71	0	0	2	715.3	1429.6	16.35	1919
AMSTTSISsPQPGK	DBNL	28988	drebrin-like protein isoform d	M2(Oxidation) S9(Phospho)	S(3): 0.0; T(4): 0.0; T(5): 0.0; S(6): 0.0; S(8): 2.0; S(9): 98.0	S9;	S172		2.09	0	0	2	744.3	1487.6	25.61	3352
YQEQGGEASQQR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0	S9;	S129	39		0	0	2	715.3	1429.6	16.35	1919
AMSTTSISsPQPGK	DBNL	28988	drebrin-like protein isoform d	M2(Oxidation) S9(Phospho)	S(3): 0.0; T(4): 0.0; T(5): 0.0; S(6): 0.0; S(8): 2.0; S(9): 98.0	S9;	S172	15		0.006	0	2	744.3	1487.6	25.61	3352
KKEEPSQNDISPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89		5.21	0	2	3	527.3	1579.7	15.04	1737
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		3.06	0	0	3	597.9	1791.8	33.28	4456
KEEPSQNDISPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89		2.48	0	1	2	726.3	1451.6	18.31	2184
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		2.4	0	0	2	896.4	1791.8	33.1	4432
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		2.35	0	0	2	896.4	1791.8	33.61	4504
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	36		0	0	2	896.4	1791.8	33.1	4432
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	33		0	0	3	597.9	1791.8	33.28	4456
NEEPSSEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	25		0	0	2	896.4	1791.8	33.61	4504
KEEPSQNDISPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89	21		0.003	1	2	726.3	1451.6	18.31	2184
KAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	M9(Oxidation) S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S71		1.57	0.004	1	2	764.3	1527.6	15.13	1753
KKEEPSQNDISPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89	25		0.006	2	3	527.3	1579.7	15.04	1737
RPVLsGTGNGDTSQSRSGSGSER	DDX4	54514	probable ATP-dependent RNA helicase DDX4 isoform 4	S5(Phospho)	S(5): 99.0; T(7): 2.9; T(12): 48.8; S(13): 47.5; S(15): 47.5; S(17): 47.5; S(19): 5.9; S(21): 0.8	S5;	S57		1.63	0.005	1	4	633.8	2532.0	23.02	2920
VNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S8(Phospho)	S(8): 100.0	S8;	S83		2.5	0	0	2	788.3	1575.7	25.52	3338
VNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S8(Phospho)	S(8): 100.0	S8;	S83	16		0.004	0	2	788.3	1575.7	25.52	3338
IDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S782	11		0	1	2	830.3	1659.6	15.16	1758
IDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S782		1.78	0.001	1	2	830.3	1659.6	15.16	1758
GLsPAMsPALQR	DGCR14	8220	protein DGCR14	M6(Oxidation)S3 (Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395		2.54	0	0	2	702.3	1403.6	52.54	7536
GLsPAMsPALQR	DGCR14	8220	protein DGCR14	M6(Oxidation)S3 (Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395	38		0	0	2	702.3	1403.6	52.54	7536
LLEDsEEsSEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 97.7; S(9): 2.3; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46		2.62	0	0	2	935.4	1869.7	55.22	7978
LLEDsEEsSEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 97.2; S(9): 2.8; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46		2.34	0	0	2	935.4	1869.7	55.75	8057
LLEDsEEsSEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 97.7; S(9): 2.3; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46	38		0	0	2	935.4	1869.7	55.22	7978
LLEDsEEsSEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 97.2; S(9): 2.8; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46	36		0	0	2	935.4	1869.7	55.75	8057
DLQEQDADAGsER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	S11(Phospho)	S(11): 100.0	S11;	S127	42		0	0	2	757.3	1513.6	26.65	3517

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AGLESGAEPGDGDsDTTK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 93.7; T(16): 3.1; T(17): 3.1	S14;	S489		2.81	0	0	2	893.9	1786.7	32.96	4415
AGLESGAEPGDGDsDTTK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 93.7; T(16): 3.1; T(17): 3.1	S14;	S489	13		0	0	2	893.9	1786.7	32.96	4415
QAQAQEsEEEEESR	DNAJC17	55192	dnaJ homolog subfamily C member 17	S7(Phospho)	S(7): 100.0; S(13): 0.0	S7;	S112		2.75	0	0	2	865.3	1729.7	15.58	1818
QAQAQEsEEEEESR	DNAJC17	55192	dnaJ homolog subfamily C member 17	S7(Phospho)	S(7): 100.0; S(13): 0.0	S7;	S112	29		0	0	2	865.3	1729.7	15.58	1818
TVTPASSAKTsPAK	DPYSL2	1808	dihydropyrimidinase-related protein 2 isoform 3	S6(Phospho) S7(Phospho) S11(Phospho)	T(1): 0.0; T(3): 7.0; S(6): 96.4; S(7): 96.4; T(10): 3.9; S(11): 96.4	S6; S7; S11;	S481; S482; S486		2.33	0	1	2	793.3	1585.6	22.58	2846
sASSGAEGDVSSEREP	DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1 isoform 2	S1(Phospho)	S(1): 94.6; S(3): 2.7; S(4): 2.7; S(11): 0.0; S(12): 0.0	S1;	S194		2.15	0	1	2	822.8	1644.6	30.21	4039
sASSGAEGDVSSEREP	DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1 isoform 2	S1(Phospho)	S(1): 94.6; S(3): 2.7; S(4): 2.7; S(11): 0.0; S(12): 0.0	S1;	S194	29		0	1	2	822.8	1644.6	30.21	4039
SASSGAEGDVSSEREP	DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1 isoform 2	S12(Phospho)	S(1): 3.8; S(3): 0.2; S(4): 0.2; S(11): 3.8; S(12): 92.0	S12;	S205	27		0.004	1	2	822.8	1644.6	27.02	3568
PCSEETPAIsPSKR	DUT	1854	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2	C2(Carbamidomethyl) S10(Phospho)	S(3): 0.0; T(6): 0.0; S(10): 100.0; S(12): 0.0	S10;	S11	46		0	1	3	546.9	1638.7	27.71	3675
PCSEETPAIsPSK	DUT	1854	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2	C2(Carbamidomethyl) S10(Phospho)	S(3): 0.0; T(6): 0.0; S(10): 98.1; S(12): 1.9	S10;	S11	20		0	0	2	741.8	1482.6	34.45	4624
PCSEETPAIsPSKR	DUT	1854	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2	C2(Carbamidomethyl) S10(Phospho)	S(3): 0.0; T(6): 0.0; S(10): 98.3; S(12): 1.7	S10;	S11	20		0	1	2	819.9	1638.7	27.53	3646
KTGsPGSPGAGGVQSTAK	DYNC1L2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	S4(Phospho)	T(2): 51.3; S(4): 97.4; S(7): 51.3; S(15): 0.0; T(16): 0.0	S4;	S366		2.14	0	1	2	873.9	1746.7	20.69	2556
KTGsPGSPGAGGVQSTAK	DYNC1L2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	S4(Phospho)	T(2): 51.3; S(4): 97.4; S(7): 51.3; S(15): 0.0; T(16): 0.0	S4;	S366	11		0.003	1	2	873.9	1746.7	20.69	2556
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl) S7(Phospho)	S(1): 0.0; S(7): 100.0; S(14): 0.0	S7;	S131		3.63	0	0	2	885.4	1769.8	25.67	3361
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl) S7(Phospho)	S(1): 0.1; S(7): 99.9; S(14): 0.0	S7;	S131		2.42	0	0	2	885.4	1769.8	25.16	3279
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl) S7(Phospho)	S(1): 0.0; S(7): 100.0; S(14): 0.0	S7;	S131	43		0	0	2	885.4	1769.8	25.67	3361
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl) S7(Phospho)	S(1): 0.1; S(7): 99.9; S(14): 0.0	S7;	S131	30		0	0	2	885.4	1769.8	25.16	3279
SQSSDTEQQSPtSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	T12(Phospho)	S(1): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(10): 2.4; T(12): 95.1; S(13): 2.4	T12;	T506		3.74	0	0	2	880.9	1760.7	12.56	1277
SRTGsESSQtGTSTTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S5(Phospho) T10(Phospho)	S(1): 0.1; T(3): 2.9; S(5): 94.4; S(7): 2.9; S(8): 2.8; T(10): 94.3; T(12): 2.8; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0	S5; T10;	S422; T427		3.21	0	1	2	988.9	1976.8	12.7	1311
SQSSDTEQQSPtSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho) T12(Phospho)	S(1): 1.0; S(3): 11.0; S(4): 11.0; T(6): 11.0; S(10): 82.3; T(12): 77.6; S(13): 6.2	S10; T12;	S504; T506		1.77	0	0	2	920.8	1840.7	14.94	1722
SRTGsESSQtGTSTTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S5(Phospho) T10(Phospho)	S(1): 0.1; T(3): 2.9; S(5): 94.4; S(7): 2.9; S(8): 2.8; T(10): 94.3; T(12): 2.8; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0	S5; T10;	S422; T427	52		0	1	2	988.9	1976.8	12.7	1311
SQSSDTEQQSPtSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	T12(Phospho)	S(1): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(10): 2.4; T(12): 95.1; S(13): 2.4	T12;	T506	33		0	0	2	880.9	1760.7	12.56	1277
SQSSDTEQQSPtSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho) T12(Phospho)	S(1): 1.0; S(3): 11.0; S(4): 11.0; T(6): 11.0; S(10): 82.3; T(12): 77.6; S(13): 6.2	S10; T12;	S504; T506	13		0.003	0	2	920.8	1840.7	14.94	1722

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
NsPVTktPPR	EIF4EBP1	1978	eukaryotic translation initiation factor 4E-binding protein 1	S2(Phospho) T7(Phospho)	S(2): 100.0; T(5): 0.0; T(7): 100.0	S2; T7;	S65; T70		2.03	0	1	2	628.8	1256.5	20.08	2462
NsPVTktPPR	EIF4EBP1	1978	eukaryotic translation initiation factor 4E-binding protein 1	S2(Phospho) T7(Phospho)	S(2): 100.0; T(5): 0.0; T(7): 100.0	S2; T7;	S65; T70	32		0	1	2	628.8	1256.5	20.08	2462
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		3.21	0	0	3	705.3	2113.9	39.42	5418
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164		2.6	0	0	2	745.8	1490.5	24.37	3140
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 99.9; S(12): 0.1	S5;	S164		1.69	0	1	2	809.8	1618.6	18.47	2207
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164	34		0	0	2	745.8	1490.5	24.37	3140
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	18		0	0	3	705.3	2113.9	39.42	5418
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 99.9; S(12): 0.1	S5;	S164	15		0.003	1	2	809.8	1618.6	18.47	2207
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		1.35	0.005	0	2	1057.4	2113.9	39.46	5424
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164		1.12	0.005	1	2	809.8	1618.6	17.62	2078
YADsPGASsPEQPK	ELF1	1997	ETS-related transcription factor Elf-1 isoform b	S4(Phospho) S9(Phospho)	Y(1): 0.1; S(4): 99.9; S(8): 3.5; S(9): 96.5	S4; S9;	S139; S144		1.92	0.001	0	2	797.3	1593.6	31.43	4205
SSHSSDSGGsDVLDPDTGK	ELF3	1999	ETS-related transcription factor Elf-3	S10(Phospho)	S(1): 35.0; S(2): 35.0; S(4): 5.9; S(5): 5.9; S(7): 31.6; S(10): 86.1; T(17): 0.5	S10;	S215		1.44	0	0	2	1061.9	2122.8	39.5	5434
RLPsSPASPsPK	EPB41L1	2036	band 4.1-like protein 1 isoform d	S4(Phospho) S10(Phospho)	S(4): 97.4; S(5): 2.6; S(8): 2.6; S(10): 97.4	S4; S10;	S497; S503	21		0	1	2	692.3	1383.6	29.95	4004
RLPsSPASPsPK	EPB41L1	2036	band 4.1-like protein 1 isoform d	S4(Phospho) S10(Phospho)	S(4): 97.4; S(5): 2.6; S(8): 2.6; S(10): 97.4	S4; S10;	S497; S503		2.24	0.001	1	2	692.3	1383.6	29.95	4004
LTGsTSsLNK	EXOC1	55763	exocyst complex component 1 isoform 2	S4(Phospho) S7(Phospho)	T(2): 0.0; S(4): 97.7; T(5): 2.2; S(6): 2.3; S(7): 97.8	S4; S7;	S455; S458		2.75	0.004	0	2	584.2	1167.5	30.02	4014
LTGsTSsLNK	EXOC1	55763	exocyst complex component 1 isoform 2	S4(Phospho) S7(Phospho)	T(2): 0.0; S(4): 97.7; T(5): 2.2; S(6): 2.3; S(7): 97.8	S4; S7;	S455; S458	31		0.004	0	2	584.2	1167.5	30.02	4014
GSsGSPHSLSQK	FAM64A	54478	protein FAM64A isoform 1	S4(Phospho)	S(2): 2.1; S(4): 97.9; T(6): 0.0; S(8): 0.0; S(10): 0.0	S4;	S131		1.78	0	0	2	633.3	1265.6	14.34	1625
GSsGSPHSLSQK	FAM64A	54478	protein FAM64A isoform 1	S4(Phospho)	S(2): 2.1; S(4): 97.9; T(6): 0.0; S(8): 0.0; S(10): 0.0	S4;	S131	21		0	0	2	633.3	1265.6	14.34	1625
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 98.0; S(8): 2.0; S(10): 0.0	S3; S6;	S296; S299		2.99	0	0	2	670.3	1339.5	29.07	3871
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho)	T(1): 1.7; S(3): 98.3; S(6): 0.0; S(8): 0.0; S(10): 0.0	S3;	S296		2.85	0	0	2	630.3	1259.5	24.4	3145
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho)	T(1): 1.7; S(3): 98.3; S(6): 0.0; S(8): 0.0; S(10): 0.0	S3;	S296	67		0	0	2	630.3	1259.5	24.4	3145
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 98.0; S(8): 2.0; S(10): 0.0	S3; S6;	S296; S299	64		0	0	2	670.3	1339.5	29.07	3871
sAPAsPTHPLMSPR	FOXK1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 96.0; T(7): 3.8; S(13): 0.2	S1; S5;	S416; S420		2.27	0	0	2	841.3	1681.7	39.14	5371
sAPAsPTHPLMSPR	FOXK1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 0.0	S1; S5;	S416; S420		2.26	0	0	2	841.3	1681.7	38.64	5286
sAPAsPTHPLMSPR	FOXK1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 0.0	S1; S5;	S416; S420	34		0	0	2	841.3	1681.7	38.64	5286
sAPAsPTHPLMSPR	FOXK1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 96.0; T(7): 3.8; S(13): 0.2	S1; S5;	S416; S420	28		0	0	2	841.3	1681.7	39.14	5371
SAPAsPTHPLMSPR	FOXK1	221937	forkhead box protein K1	M12(Oxidation) T7(Phospho) S13(Phospho)	S(1): 0.0; S(5): 2.8; T(7): 97.2; S(13): 100.0	T7; S13;	T422; S428	12		0.008	0	2	841.3	1681.7	36.09	4870



Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AASSSSPGsPVASSPSR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S9(Phospho)	S(3): 25.0; S(4): 25.0; S(5): 25.0; S(6): 25.0; S(9): 100.0; S(13): 0.0; S(14): 0.0; S(16): 0.0	S9;	S1780		2.08	0	0	2	846.3	1691.7	30.22	4041
AASSSSPGsPVASSPSR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S9(Phospho)	S(3): 25.0; S(4): 25.0; S(5): 25.0; S(6): 25.0; S(9): 100.0; S(13): 0.0; S(14): 0.0; S(16): 0.0	S9;	S1780	43		0	0	2	846.3	1691.7	30.22	4041
GSEGDcSPEDKNSVTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C6(Carbamidomethyl) S7(Phospho)	S(2): 4.3; S(7): 95.7; S(13): 0.0; T(15): 0.0	S7;	S1003		1.45	0	1	2	930.9	1860.7	16.59	1948
GSEGDcSPEDKNSVTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C6(Carbamidomethyl) S7(Phospho)	S(2): 4.3; S(7): 95.7; S(13): 0.0; T(15): 0.0	S7;	S1003	13		0.004	1	2	930.9	1860.7	16.59	1948
NSsTDQGSDEEGSLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S3(Phospho)	S(2): 2.7; S(3): 97.2; T(4): 0.1; S(8): 0.0; S(13): 0.0	S3;	S1063		2.25	0	0	2	881.3	1761.7	22	2748
NSsTDQGSDEEGSLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S3(Phospho)	S(2): 2.7; S(3): 97.2; T(4): 0.1; S(8): 0.0; S(13): 0.0	S3;	S1063	47		0	0	2	881.3	1761.7	22	2748
DLDRPESQsPK	GTF3C2	2976	general transcription factor 3C polypeptide 2 isoform b	S9(Phospho)	S(7): 0.0; S(9): 100.0	S9;	S167	22		0	0	2	676.3	1351.6	20.18	2480
ARGDsEALDEES	HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 2	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S663	34		0.004	1	2	679.8	1358.5	27.95	3707
SSsDNNTNTLGR	HECTD1	25831	E3 ubiquitin-protein ligase HECTD1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; T(7): 0.0; T(9): 0.0	S3;	S1571		2.51	0	0	2	673.3	1345.5	19.69	2403
SSsDNNTNTLGR	HECTD1	25831	E3 ubiquitin-protein ligase HECTD1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; T(7): 0.0; T(9): 0.0	S3;	S1571	55		0	0	2	673.3	1345.5	19.69	2403
GEEsEEEEKGYK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 99.8; Y(12): 0.3	S4; S5;	S159; S160		1.35	0	1	2	830.8	1660.6	19.37	2350
RPPtPCsDPER	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	C6(Carbamidomethyl) T4(Phospho) S7(Phospho)	T(4): 100.0; S(7): 100.0	T4; S7;	T84; S87		2.23	0.001	0	2	736.3	1471.5	20.84	2572
AVEEsDEERQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S5(Phospho) S6(Phospho)	S(5): 100.0; S(6): 100.0	S5; S6;	S142; S143	17		0.003	1	2	797.8	1594.6	13.92	1569
GEEsEEEEKGYK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 99.8; Y(12): 0.3	S4; S5;	S159; S160	15		0.003	1	2	830.8	1660.6	19.37	2350
KQQQEPTGEPsPK	HMG2	8091	high mobility group protein HMGI-C isoform b	S11(Phospho)	T(7): 0.0; S(11): 100.0	S11;	S44		1.87	0.005	1	2	767.4	1533.7	14.07	1589
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 2.0; S(3): 98.0	S3;	S6		1.96	0	1	2	690.3	1379.6	25.83	3381
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 2.0; S(3): 98.0	S3;	S6	20		0	1	2	690.3	1379.6	25.83	3381
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 2.3; S(3): 97.7	S3;	S6	12		0.006	1	2	690.3	1379.6	25.32	3302
NDKsEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0	S4;	S220		4.18	0	1	2	817.3	1633.7	12.61	1289
NDKsEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0	S4;	S220	58		0	1	2	817.3	1633.7	12.61	1289
IDASKNEEDGHSNssPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S15(Phospho) S16(Phospho)	S(4): 0.0; S(13): 7.5; S(15): 96.2; S(16): 96.2	S15; S16;	S82; S83		3.52	0	1	3	711.3	2131.8	14.42	1639
DKEVsDDEAEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S5(Phospho)	S(5): 100.0	S5;	S231		2.13	0	1	2	737.3	1473.6	13.71	1528
DKEVsDDEAEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S5(Phospho)	S(5): 100.0	S5;	S231	24		0	1	2	737.3	1473.6	13.71	1528
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 97.7; S(12): 2.3	S6;	S207		5.84	0	2	3	649.3	1945.8	17.49	2059
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4.62	0	1	2	909.4	1817.7	22.42	2822
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4.13	0	1	3	606.6	1817.7	22.03	2752
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4.03	0	2	3	649.3	1945.8	18.01	2135

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
IEDVGsDEEDDsGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho) S12(Phospho)	S(6): 100.0; S(12): 100.0	S6; S12;	S207; S213		3.98	0	2	3	675.9	2025.8	19.14	2310
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.83	0	2	3	649.3	1945.8	16.98	1991
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 97.4; S(12): 2.6	S6;	S207		3.81	0	1	3	606.6	1817.7	22.54	2840
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.81	0	2	2	973.4	1945.8	17.55	2067
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.44	0	0	2	787.8	1574.6	28.8	3832
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.4	0	0	2	787.8	1574.6	28.29	3752
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.17	0	1	2	909.4	1817.7	21.92	2736
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.05	0	1	2	909.4	1817.7	22.93	2904
EKEIsDDEAEEEK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S5(Phospho)	S(5): 100.0	S5;	S178		1.83	0	1	2	815.8	1630.6	20.16	2474
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		1.53	0	2	2	973.4	1945.8	17.04	1998
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	83		0	1	2	909.4	1817.7	22.42	2822
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 97.7; S(12): 2.3	S6;	S207	51		0	2	3	649.3	1945.8	17.49	2059
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	45		0	2	2	973.4	1945.8	17.55	2067
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	33		0	0	2	787.8	1574.6	28.8	3832
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 97.4; S(12): 2.6	S6;	S207	32		0	1	3	606.6	1817.7	22.54	2840
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	31		0	2	3	649.3	1945.8	16.98	1991
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	31		0	2	3	649.3	1945.8	18.01	2135
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	30		0	1	3	606.6	1817.7	22.03	2752
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	25		0	0	2	787.8	1574.6	28.29	3752
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	23		0	1	2	909.4	1817.7	21.92	2736
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	21		0	1	2	909.4	1817.7	22.93	2904
IEDVGsDEEDDsGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho) S12(Phospho)	S(6): 100.0; S(12): 100.0	S6; S12;	S207; S213	20		0	1	2	949.3	1897.7	26.02	3415
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	19		0	2	2	973.4	1945.8	17.04	1998
EKEIsDDEAEEEK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S5(Phospho)	S(5): 100.0	S5;	S178	15		0	1	2	815.8	1630.6	20.16	2474
IEDVGsDEEDDsGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho) S12(Phospho)	S(6): 100.0; S(12): 100.0	S6; S12;	S207; S213	13		0.006	2	3	675.9	2025.8	19.14	2310
GSgTAsDDEFENLR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S6(Phospho)	S(2): 2.5; T(4): 0.0; S(6): 97.5	S6;	S1907		2.89	0	0	2	789.3	1577.6	53.46	7695
GSgTAsDDEFENLR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S6(Phospho)	S(2): 2.5; T(4): 0.0; S(6): 97.5	S6;	S1907	67		0	0	2	789.3	1577.6	53.46	7695
VSEEQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M16(Oxidation) M20(Oxidation) S10(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 99.3; S(17): 0.3; T(18): 0.3	S10;	S153		4.72	0	0	3	767.7	2301.0	34.58	4646
VSEEQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M16(Oxidation) M20(Oxidation) S10(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 99.3; S(17): 0.3; T(18): 0.3	S10;	S153	14		0	0	3	767.7	2301.0	34.58	4646

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
RPMEEDGEEKsPSK	ILF3	3609	interleukin enhancer-binding factor 3 isoform c	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382		5.62	0	1	3	572.2	1714.7	12.47	1255
RPMEEDGEEKsPSK	ILF3	3609	interleukin enhancer-binding factor 3 isoform c	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382	55		0	1	3	572.2	1714.7	12.47	1255
KAsPEPEGEAAGK	IRF2BP1	26145	interferon regulatory factor 2-binding protein 1	S3(Phospho)	S(3): 100.0	S3;	S384		3.25	0	1	2	675.8	1350.6	12.85	1346
KAsPEPEGEAAGK	IRF2BP1	26145	interferon regulatory factor 2-binding protein 1	S3(Phospho)	S(3): 100.0	S3;	S384	38		0	1	2	675.8	1350.6	12.85	1346
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform B	M11(Oxidation) S4(Phospho) S7(Phospho)	S(2): 2.3; S(4): 97.7; S(7): 99.9; S(9): 0.1; S(10): 0.0	S4; S7;	S441; S444		2.11	0	0	2	839.8	1678.6	21.02	2596
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform B	M11(Oxidation) S4(Phospho) S7(Phospho)	S(2): 2.3; S(4): 97.7; S(7): 99.9; S(9): 0.1; S(10): 0.0	S4; S7;	S441; S444	40		0	0	2	839.8	1678.6	21.02	2596
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform B	M11(Oxidation) S4(Phospho) S7(Phospho)	S(2): 0.1; S(4): 99.9; S(7): 99.9; S(9): 0.1; S(10): 0.0	S4; S7;	S441; S444		1.65	0.001	0	2	839.8	1678.6	20.51	2532
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform B	M11(Oxidation) S4(Phospho) S7(Phospho)	S(2): 0.1; S(4): 99.9; S(7): 99.9; S(9): 0.1; S(10): 0.0	S4; S7;	S441; S444	14		0.003	0	2	839.8	1678.6	20.51	2532
NSsSPVPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho)	S(2): 2.4; S(3): 95.1; S(4): 2.4; S(7): 0.0; S(10): 0.0	S3;	S658		2.86	0	0	2	775.4	1549.7	38.22	5213
NSSSPVPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S7(Phospho)	S(2): 1.4; S(3): 49.3; S(4): 49.3; S(7): 100.0; S(10): 0.0	S7;	S662		2.41	0	0	2	815.3	1629.7	44.58	6284
NSsSPVPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho)	S(2): 2.4; S(3): 95.1; S(4): 2.4; S(7): 0.0; S(10): 0.0	S3;	S658	59		0	0	2	775.4	1549.7	38.22	5213
NSSSPVPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S7(Phospho)	S(2): 1.4; S(3): 49.3; S(4): 49.3; S(7): 100.0; S(10): 0.0	S7;	S662	44		0	0	2	815.3	1629.7	44.58	6284
NKsEDEDEEGDATR	IRX2	153572	iroquois-class homeodomain protein IRX-2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S186		2.19	0	1	2	895.3	1789.6	13.2	1424
NKsEDEDEEGDATR	IRX2	153572	iroquois-class homeodomain protein IRX-2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S186	35		0	1	2	895.3	1789.6	13.2	1424
AAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0; S(14): 0.0	S5; S7;	S398; S400		1.97	0	1	2	905.4	1809.7	33.36	4471
AAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0; S(14): 0.0	S5; S7;	S398; S400		1.66	0	1	2	905.4	1809.7	33.87	4539
TIASDsEEEAGK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0	S4; S6;	S438; S440		1.66	0	0	2	698.7	1396.5	29.35	3905
EAEDsDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513		1.55	0	1	2	827.3	1653.6	17.83	2105
EAEDsDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513	32		0	1	2	827.3	1653.6	17.83	2105
AAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0; S(14): 0.0	S5; S7;	S398; S400	14		0	1	2	905.4	1809.7	33.87	4539
AAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0; S(14): 0.0	S5; S7;	S398; S400	14		0.003	1	2	905.4	1809.7	33.36	4471
ETPRPEGGSsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.0; S(9): 0.0; S(11): 100.0; T(15): 100.0	S11; T15;	S486; T490		3.11	0	0	3	716.3	2146.9	33.37	4472
ETPRPEGGSsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.0; S(9): 0.0; S(11): 100.0; T(15): 100.0	S11; T15;	S486; T490	16		0.003	0	3	716.3	2146.9	33.37	4472
NQsLVEENEK	KIF4A	24137	chromosome-associated kinesin KIF4A	S3(Phospho)	S(3): 100.0	S3;	S394		2.09	0	0	2	635.3	1269.5	26.42	3485
NQsLVEENEK	KIF4A	24137	chromosome-associated kinesin KIF4A	S3(Phospho)	S(3): 100.0	S3;	S394	14		0.004	0	2	635.3	1269.5	26.42	3485
LSGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0	S2;	S32		3.35	0	0	2	557.7	1114.5	32.27	4320
LSGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S9(Phospho)	S(2): 0.0; S(9): 100.0	S9;	S39		3.29	0	0	2	557.7	1114.5	30.51	4083
LSGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S9(Phospho)	S(2): 0.0; S(9): 100.0	S9;	S39	70		0	0	2	557.7	1114.5	30.51	4083

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
LsGGLGAGSCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0	S2;	S32	56		0	0	2	557.7	1114.5	32.27	4320
AFsSRsYTSGPSR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S3(Phospho) S6(Phospho)	S(3): 99.8; S(4): 0.3; S(6): 99.5; Y(7): 0.2; T(8): 0.2; S(9): 0.0; S(13): 0.0	S3; S6;	S21; S24		1.97	0	1	2	810.3	1619.6	38.22	5212
ETEsAPGsPR	LARP1	23367	la-related protein 1	S4(Phospho) S8(Phospho)	T(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S440; S444		2.92	0	0	2	595.7	1190.4	19.41	2358
ETEsAPGsPR	LARP1	23367	la-related protein 1	S4(Phospho) S8(Phospho)	T(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S440; S444	51		0	0	2	595.7	1190.4	19.41	2358
sLPTTVPESPNYR	LARP1	23367	la-related protein 1	S1(Phospho)	S(1): 97.2; T(4): 2.8; T(5): 0.0; S(9): 50.0; Y(12): 50.0	S1;	S689	23		0.004	0	2	810.8	1620.7	66.12	9721
SRPTSEGsDIESTEPQK	LARP7	51574	la-related protein 7 isoform 1	S5(Phospho) S8(Phospho)	S(1): 6.8; T(4): 6.8; S(5): 87.2; S(8): 97.1; S(12): 1.0; T(13): 1.0	S5; S8;	S258; S261		1.56	0.001	0	2	1004.4	2007.8	31.72	4244
ASVRGssEEDEDARTPDR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0; T(15): 0.0	S6; S7;	S138; S139		2.55	0	2	3	712.9	2136.8	21.73	2709
ASVRGssEEDEDAR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0	S6; S7;	S138; S139		2.17	0	1	2	834.3	1667.6	18.03	2139
ASVRGssEEDEDAR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0	S6; S7;	S138; S139	19		0.003	1	2	834.3	1667.6	18.03	2139
ENySDSEEDDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho)	Y(3): 92.0; S(4): 4.0; S(6): 4.0; S(16): 0.0; S(17): 0.0	Y3;	Y258		1.87	0	0	2	1071.4	2141.7	34.89	4692
ENySDSEEDDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho) S4(Phospho)	Y(3): 99.8; S(4): 99.8; S(6): 0.4; S(16): 0.0; S(17): 0.0	Y3; S4;	Y258; S259		1.84	0	0	2	1111.4	2221.7	41.63	5784
ENySDSEEDDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho)	Y(3): 92.0; S(4): 4.0; S(6): 4.0; S(16): 0.0; S(17): 0.0	Y3;	Y258	32		0	0	2	1071.4	2141.7	34.89	4692
ENySDSEEDDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho) S4(Phospho)	Y(3): 99.8; S(4): 99.8; S(6): 0.4; S(16): 0.0; S(17): 0.0	Y3; S4;	Y258; S259	29		0	0	2	1111.4	2221.7	41.63	5784
KLtsDEEGEPSGK	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	S4(Phospho)	T(3): 2.1; S(4): 97.9; S(11): 0.0	S4;	S570		2.46	0	1	2	728.8	1456.6	19.34	2342
KLtsDEEGEPSGK	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	S4(Phospho)	T(3): 2.1; S(4): 97.9; S(11): 0.0	S4;	S570	40		0	1	2	728.8	1456.6	19.34	2342
KLtsDEEGEPSGK	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	T3(Phospho) S4(Phospho)	T(3): 100.0; S(4): 100.0; S(11): 0.0	T3; S4;	T569; S570	26		0	1	2	768.8	1536.6	22.48	2832
VLGsEGEEDEALsPAK	LIG1	3978	DNA ligase 1 isoform 3	S4(Phospho) S14(Phospho)	S(4): 100.0; S(14): 100.0	S4; S14;	S66; S76		3.89	0	0	2	960.4	1919.8	61.36	8902
VLGsEGEEDEALsPAK	LIG1	3978	DNA ligase 1 isoform 3	S4(Phospho) S14(Phospho)	S(4): 100.0; S(14): 100.0	S4; S14;	S66; S76	32		0	0	2	960.4	1919.8	61.36	8902
ASSLSEsPPK	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S8(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 100.0	S8;	S72		2.73	0	0	2	585.3	1169.5	25.19	3283
ASSLSEsPPK	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S8(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 100.0	S8;	S72	41		0	0	2	585.3	1169.5	25.19	3283
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S3(Phospho)	S(2): 1.8; S(3): 98.2; S(5): 0.0; S(6): 0.0; T(8): 0.0; S(13): 0.0; T(15): 0.0	S3;	S404		4.49	0	0	2	799.8	1598.7	12.37	1233
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S3(Phospho) S6(Phospho)	S(2): 0.1; S(3): 97.4; S(5): 2.6; S(6): 99.9; T(8): 0.1; S(13): 0.0; T(15): 0.0	S3; S6;	S404; S407		4.37	0	0	2	839.8	1678.7	12.61	1288
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S2(Phospho)	S(2): 96.9; S(3): 49.3; S(5): 50.7; S(6): 3.1; T(8): 0.0; S(13): 0.0; T(15): 0.0	S2;	S403		3.75	0	0	3	560.2	1678.6	12.67	1303
GRASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S4(Phospho) S15(Phospho)	S(4): 97.2; S(5): 2.8; S(7): 0.0; S(8): 0.0; T(10): 2.7; S(15): 94.6; T(17): 2.7	S4; S15;	S403; S414		3.64	0	1	3	631.3	1891.8	12.43	1245
SGAQASStPLsPTR	LMNA	4000	lamin isoform C	T8(Phospho) S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.1; T(8): 99.9; S(11): 97.7; T(13): 2.3	T8; S11;	T19; S22		3.51	0	0	2	760.3	1519.6	35.53	4786
LRLsPsPTSQR	LMNA	4000	lamin isoform C	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392		3.15	0	1	2	701.3	1401.6	40.49	5597
SGAQASStPLsPTR	LMNA	4000	lamin isoform C	S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 0.0; S(11): 98.2; T(13): 1.8	S11;	S22		3.07	0	0	2	720.3	1439.7	32.33	4331

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AssHSSQTQGGGSVTKK	LMNA	4000	lamin isoform C	S2(Phospho) S3(Phospho)	S(2): 96.1; S(3): 89.3; S(5): 7.3; S(6): 7.3; T(8): 0.0; S(13): 0.0; T(15): 0.0	S2; S3;	S403; S404		2.24	0	1	3	602.9	1806.7	12.4	1240
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S3(Phospho)	S(2): 1.8; S(3): 98.2; S(5): 0.0; S(6): 0.0; T(8): 0.0; S(13): 0.0; T(15): 0.0	S3;	S404	88		0	0	2	799.8	1598.7	12.37	1233
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S3(Phospho) S6(Phospho)	S(2): 0.1; S(3): 97.4; S(5): 2.6; S(6): 99.9; T(8): 0.1; S(13): 0.0; T(15): 0.0	S3; S6;	S404; S407	63		0	0	2	839.8	1678.7	12.61	1288
SGAQASSTPLsPTR	LMNA	4000	lamin isoform C	T8(Phospho) S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.1; T(8): 99.9; S(11): 97.7; T(13): 2.3	T8; S11;	T19; S22	44		0	0	2	760.3	1519.6	35.53	4786
ASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S2(Phospho)	S(2): 96.9; S(3): 49.3; S(5): 50.7; S(6): 3.1; T(8): 0.0; S(13): 0.0; T(15): 0.0	S2;	S403	39		0	0	3	560.2	1678.6	12.67	1303
SGAQASSTPLsPTR	LMNA	4000	lamin isoform C	S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 0.0; S(11): 98.2; T(13): 1.8	S11;	S22	32		0	0	2	720.3	1439.7	32.33	4331
LRLsPsPTSQR	LMNA	4000	lamin isoform C	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392	27		0	1	2	701.3	1401.6	40.49	5597
GRASsHSSQTQGGGSVTK	LMNA	4000	lamin isoform C	S4(Phospho) S15(Phospho)	S(4): 97.2; S(5): 2.8; S(7): 0.0; S(8): 0.0; T(10): 2.7; S(15): 94.6; T(17): 2.7	S4; S15;	S403; S414	26		0.003	1	3	631.3	1891.8	12.43	1245
AGGPTtPLsPTR	LMNB1	4001	lamin-B1 isoform 1	T6(Phospho) S9(Phospho)	T(5): 0.0; T(6): 100.0; S(9): 99.9; T(11): 0.1	T6; S9;	T20; S23	30		0	0	2	657.8	1314.5	43.97	6177
LKLsPsPSSR	LMNB1	4001	lamin-B1 isoform 1   NP_116126.3	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 0.0; S(9): 0.0	S4; S6;	S391; S393    S405		2.03	0.001	1	2	616.3	1231.5	37.92	5154
ATSSsSGSLSATGR	LMNB2	84823	lamin-B2	S4(Phospho)	T(2): 0.0; S(3): 2.0; S(4): 96.0; S(5): 2.0; S(6): 0.0; S(8): 0.0; S(10): 0.0; T(12): 0.0	S4;	S420		3.1	0	0	2	674.8	1348.6	21.62	2692
ATSSsSGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho) S8(Phospho)	T(2): 3.1; S(3): 0.1; S(4): 0.1; S(5): 96.6; S(6): 0.2; S(8): 99.8; S(10): 0.1; T(12): 0.0	S5; S8;	S421; S424		2.29	0	0	2	714.8	1428.5	26.87	3547
ATSSsSGSLSATGR	LMNB2	84823	lamin-B2	S4(Phospho)	T(2): 0.0; S(3): 2.0; S(4): 96.0; S(5): 2.0; S(6): 0.0; S(8): 0.0; S(10): 0.0; T(12): 0.0	S4;	S420	83		0	0	2	674.8	1348.6	21.62	2692
AGGPATPLsPTR	LMNB2	84823	lamin-B2	T6(Phospho) S9(Phospho)	T(6): 100.0; S(9): 100.0; T(11): 0.0	T6; S9;	T34; S37	32		0	0	2	642.8	1284.5	43.39	6079
ATSSsSGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho) S8(Phospho)	T(2): 3.1; S(3): 0.1; S(4): 0.1; S(5): 96.6; S(6): 0.2; S(8): 99.8; S(10): 0.1; T(12): 0.0	S5; S8;	S421; S424	31		0	0	2	714.8	1428.5	26.87	3547
AtSSsSGSLSATGR	LMNB2	84823	lamin-B2	T2(Phospho)	T(2): 93.6; S(3): 3.1; S(4): 3.1; S(5): 0.1; S(6): 0.0; S(8): 1.6; S(10): 49.2; T(12): 49.2	T2;	T418	28		0	0	2	714.8	1428.5	27.37	3621
SHsPSASQSGSQLR	LMO7	4008	LIM domain only protein 7 isoform 1	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0	S3;	S1259		2.29	0	0	2	754.8	1508.6	15.57	1815
SHsPSASQSGSQLR	LMO7	4008	LIM domain only protein 7 isoform 1	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0	S3;	S1259	17		0	0	2	754.8	1508.6	15.57	1815
NSASATTPLsGNSSR	LRRFIP2	9209	leucine-rich repeat flightless-interacting protein 2 isoform 2	S10(Phospho)	S(2): 0.0; S(4): 0.0; T(6): 0.0; T(7): 0.0; S(10): 94.6; S(13): 2.7; S(14): 2.7	S10;	S88		2.17	0.001	0	2	765.3	1529.7	27.92	3703
NSASATTPLsGNSSR	LRRFIP2	9209	leucine-rich repeat flightless-interacting protein 2 isoform 2	S10(Phospho)	S(2): 0.0; S(4): 0.0; T(6): 0.0; T(7): 0.0; S(10): 94.6; S(13): 2.7; S(14): 2.7	S10;	S88	16		0.003	0	2	765.3	1529.7	27.92	3703
sPVSTRPLPSASQK	LSM14A	26065	protein LSM14 homolog A isoform b	S1(Phospho)	S(1): 100.0; S(4): 0.0; T(5): 0.0; S(10): 0.0; S(12): 0.0	S1;	S216		2.16	0.001	0	2	767.9	1534.8	29.78	3978
sPVSTRPLPSASQK	LSM14A	26065	protein LSM14 homolog A isoform b	S1(Phospho)	S(1): 100.0; S(4): 0.0; T(5): 0.0; S(10): 0.0; S(12): 0.0	S1;	S216	11		0.007	0	2	767.9	1534.8	29.78	3978
RsEEKEAGEI	LUC7L	55692	putative RNA-binding protein Luc7-like 1 isoform b	S2(Phospho)	S(2): 100.0	S2;	S363	24		0.007	2	2	614.3	1227.5	20.01	2448
DQsLSPSKGENK	MAGI3	260425	membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 isoform 1	S3(Phospho)	S(3): 100.0; S(5): 50.0; S(7): 50.0	S3;	S1255		1.91	0	1	2	725.3	1449.6	18.81	2255

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
DQsLSPSKGENK	MAGI3	260425	membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 isoform 1	S3(Phospho)	S(3): 100.0; S(5): 50.0; S(7): 50.0	S3;	S1255	15		0.003	1	2	725.3	1449.6	18.81	2255
SKVGSTENIK	MAP4	4134	microtubule-associated protein 4 isoform 4	S5(Phospho)	S(1): 0.0; S(5): 98.9; T(6): 1.1	S5;	S941		2.79	0	1	2	571.8	1142.5	15.72	1837
AsPSKPASAPASR	MAP4	4134	microtubule-associated protein 4 isoform 4	S2(Phospho)	S(2): 100.0; S(4): 0.0; S(8): 0.0; S(12): 0.0	S2;	S787		2.19	0	0	2	653.8	1306.6	12.94	1370
SKVGSTENIK	MAP4	4134	microtubule-associated protein 4 isoform 4	S5(Phospho)	S(1): 0.0; S(5): 98.9; T(6): 1.1	S5;	S941	26		0	1	2	571.8	1142.5	15.72	1837
AsPSKPASAPASR	MAP4	4134	microtubule-associated protein 4 isoform 4	S2(Phospho)	S(2): 100.0; S(4): 0.0; S(8): 0.0; S(12): 0.0	S2;	S787	22		0	0	2	653.8	1306.6	12.94	1370
AEDGATPSPsNETPKKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T13(Phospho)	T(6): 0.0; S(8): 0.0; S(10): 0.0; T(13): 100.0	T13;	T150		4.14	0	2	3	613.0	1836.8	13.05	1396
AEDGATPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T6(Phospho) S8(Phospho)	T(6): 100.0; S(8): 100.0; S(10): 0.0; T(13): 0.0	T6; S8;	T143; S145		2.25	0	0	2	830.8	1660.6	30.79	4121
AEDGATPSPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S10(Phospho)	T(6): 0.0; S(8): 2.4; S(10): 97.6; T(13): 0.0	S10;	S147		2.21	0	0	2	790.8	1580.6	26.3	3463
AEDGATPsNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho)	T(6): 0.1; S(8): 96.9; S(10): 2.9; T(13): 0.1	S8;	S145		1.87	0	1	2	854.9	1708.7	18.83	2261
AEDGATPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T6(Phospho) S8(Phospho)	T(6): 100.0; S(8): 100.0; S(10): 0.0; T(13): 0.0	T6; S8;	T143; S145	28		0	0	2	830.8	1660.6	30.79	4121
AEDGATPsNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho)	T(6): 0.1; S(8): 96.9; S(10): 2.9; T(13): 0.1	S8;	S145	11		0	1	2	854.9	1708.7	18.83	2261
AEDGATPSPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S10(Phospho)	T(6): 0.0; S(8): 2.4; S(10): 97.6; T(13): 0.0	S10;	S147	11		0.003	0	2	790.8	1580.6	26.3	3463
AEDGATPSPsNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T13(Phospho)	T(6): 0.0; S(8): 0.0; S(10): 2.2; T(13): 97.8	T13;	T150		1.85	0.004	1	2	854.9	1708.7	15.98	1867
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 97.5; S(11): 2.5	S3; S9;	S260; S266		4.41	0	2	3	562.2	1684.7	13.45	1481
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 2.1; S(3): 97.8; S(9): 0.0; S(11): 0.0	S3;	S260		3.88	0	2	3	535.6	1604.7	13.26	1438
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 100.0; S(11): 0.0	S3; S9;	S260; S266		2.33	0	2	2	842.8	1684.7	13.37	1463
SYsPDGKESPSDK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 2.1; Y(2): 2.1; S(3): 95.9; S(9): 0.0; S(11): 0.0	S3;	S260		2.06	0	1	2	738.8	1476.6	16.08	1886
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.1; Y(2): 0.1; S(3): 99.9; S(9): 0.0; S(11): 0.0	S3;	S260		1.8	0	2	2	802.8	1604.7	13.24	1434
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 2.1; S(3): 97.8; S(9): 0.0; S(11): 0.0	S3;	S260	18		0	2	3	535.6	1604.7	13.26	1438
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 99.9; S(11): 0.1	S3; S9;	S260; S266		2.31	0.001	2	2	842.8	1684.7	13.88	1562
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 97.5; S(11): 2.5	S3; S9;	S260; S266	18		0.003	2	3	562.2	1684.7	13.45	1481
SYsPDGKESPSDK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 2.1; Y(2): 2.1; S(3): 95.9; S(9): 0.0; S(11): 0.0	S3;	S260	15		0.003	1	2	738.8	1476.6	16.08	1886
SYsPDGKESPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 100.0; S(11): 0.0	S3; S9;	S260; S266	18		0.005	2	2	842.8	1684.7	13.37	1463
LQSVQATGPSsPGR	MCC	4163	colorectal mutant cancer protein isoform 2	S11(Phospho)	S(3): 0.0; T(7): 0.0; S(10): 2.4; S(11): 97.6	S11;	S294		2.4	0	0	2	732.8	1464.7	31.76	4248
LQSVQATGPSsPGR	MCC	4163	colorectal mutant cancer protein isoform 2	S11(Phospho)	S(3): 0.0; T(7): 0.0; S(10): 2.4; S(11): 97.6	S11;	S294	19		0.003	0	2	732.8	1464.7	31.76	4248
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S7(Phospho) S8(Phospho)	T(6): 0.0; S(7): 100.0; S(8): 100.0	S7; S8;	S26; S27		3.45	0	0	2	630.7	1260.5	43.72	6132
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 100.0	S8;	S27		3.11	0	0	2	590.8	1180.5	32.57	4364
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 100.0	S8;	S27	56		0	0	2	590.8	1180.5	32.57	4364
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S7(Phospho) S8(Phospho)	T(6): 0.0; S(7): 100.0; S(8): 100.0	S7; S8;	S26; S27	29		0	0	2	630.7	1260.5	43.72	6132
SEDEsEtEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S5(Phospho) T7(Phospho)	S(1): 5.1; S(5): 95.0; T(7): 100.0; S(14): 0.0	S5; T7;	S717; T719		2.6	0	2	3	948.7	2844.0	19.96	2441
SEDEsEtEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S5(Phospho) T7(Phospho)	S(1): 6.1; S(5): 94.2; T(7): 99.2; S(14): 0.4	S5; T7;	S717; T719		2.39	0	1	3	896.6	2687.9	21.89	2732

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
sEDESETEDEEEKSQEDQEQK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho)	S(1): 99.8; S(5): 0.2; T(7): 0.0; S(14): 0.0	S1;	S713		2.54	0.004	1	3	870.0	2608.0	23.03	2923
AETSEGSAPAVPEASsPK	MECP2	4204	methyl-CpG-binding protein 2 isoform 1	S19(Phospho)	T(3): 0.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(17): 3.5; S(19): 96.5	S19;	S80		2.43	0.005	0	2	1005.4	2009.9	39.25	5390
tLNAETPKSSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T1(Phospho)	T(1): 96.3; T(6): 3.7; S(9): 50.0; S(10): 50.0	T1;	T208		2.98	0	1	2	857.4	1713.8	39.56	5443
tLNAETPKSSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T1(Phospho)	T(1): 96.3; T(6): 3.7; S(9): 50.0; S(10): 50.0	T1;	T208	17		0	1	2	857.4	1713.8	39.56	5443
GAGATSGsPPAGRn	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 100.0	S8;	S232		2.94	0	1	2	640.3	1279.5	14.36	1629
GAGATSGsPPAGRn	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 100.0	S8;	S232	36		0	1	2	640.3	1279.5	14.36	1629
KPsPAAsPATK	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; T(10): 0.0	S3; S7;	S640; S644		3.79	0	0	2	607.8	1214.5	14.05	1585
KPsPAAsPATK	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; T(10): 0.0	S3; S7;	S640; S644		2.61	0	0	2	607.8	1214.5	13.54	1495
KPsPAAsPATK	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; T(10): 0.0	S3; S7;	S640; S644	33		0	0	2	607.8	1214.5	13.54	1495
KPsPAAsPATK	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; T(10): 0.0	S3; S7;	S640; S644	24		0	0	2	607.8	1214.5	14.05	1585
ASVsGPNSPSETR	MID1	4281	E3 ubiquitin-protein ligase Midline-1 isoform 6	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(8): 50.0; S(10): 0.0; T(12): 50.0	S4;	S92		3.03	0	0	2	724.8	1448.5	26.66	3518
ASVsGPNSPSETR	MID1	4281	E3 ubiquitin-protein ligase Midline-1 isoform 6	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(8): 50.0; S(10): 0.0; T(12): 50.0	S4;	S92	49		0	0	2	724.8	1448.5	26.66	3518
SQsLQDQPTR	MINK1	50488	misshapen-like kinase 1 isoform 1	S3(Phospho)	S(1): 0.0; S(3): 100.0; T(9): 0.0	S3;	S601		2.68	0	0	2	620.3	1239.5	21.41	2660
SQsLQDQPTR	MINK1	50488	misshapen-like kinase 1 isoform 1	S3(Phospho)	S(1): 0.0; S(3): 100.0; T(9): 0.0	S3;	S601	58		0	0	2	620.3	1239.5	21.41	2660
TPVQYSQQQNsPQK	MKI67	4288	antigen KI-67 isoform 1	S11(Phospho)	T(1): 0.0; Y(5): 0.0; S(6): 0.0; S(11): 100.0	S11;	S357		2.94	0	0	2	856.9	1712.8	25.29	3297
TPVQYSQQQNsPQK	MKI67	4288	antigen KI-67 isoform 1	S11(Phospho)	T(1): 0.0; Y(5): 0.0; S(6): 0.0; S(11): 100.0	S11;	S357	22		0	0	2	856.9	1712.8	25.29	3297
FGsTGSTPPVSPTPSER	MKL1	57591	MKL/myocardin-like protein 1 isoform 3	S3(Phospho)	S(3): 91.0; T(4): 3.0; S(6): 3.0; T(7): 3.0; S(11): 50.0; T(13): 50.0; S(15): 0.1	S3;	S446	32		0	0	2	932.4	1863.8	54.07	7796
FGsTGSTPPVSPTPSER	MKL1	57591	MKL/myocardin-like protein 1 isoform 3	S3(Phospho)	S(3): 91.0; T(4): 3.0; S(6): 3.0; T(7): 3.0; S(11): 50.0; T(13): 50.0; S(15): 0.1	S3;	S446		2.14	0.004	0	2	932.4	1863.8	54.07	7796
VLTRANSNPSPSAAK	MRGBP	55257	MRG/MORF4L-binding protein	S10(Phospho)	T(3): 0.0; S(6): 0.0; S(9): 2.6; S(10): 94.8; S(12): 2.6	S10;	S195		2.03	0	0	2	762.4	1523.7	29.47	3924
VLTRANSNPSSPsAAK	MRGBP	55257	MRG/MORF4L-binding protein	S6(Phospho) S12(Phospho)	T(3): 0.0; S(6): 99.8; S(9): 0.2; S(10): 3.8; S(12): 96.2	S6; S12;	S191; S197		1.95	0.004	0	2	802.3	1603.7	38.17	5204
VLTRANSNPSPSAAK	MRGBP	55257	MRG/MORF4L-binding protein	S10(Phospho)	T(3): 0.0; S(6): 0.0; S(9): 2.6; S(10): 94.8; S(12): 2.6	S10;	S195	16		0.006	0	2	762.4	1523.7	29.47	3924
VLTRANSNPSSPsAAK	MRGBP	55257	MRG/MORF4L-binding protein	S6(Phospho) S12(Phospho)	T(3): 0.0; S(6): 99.8; S(9): 0.2; S(10): 3.8; S(12): 96.2	S6; S12;	S191; S197	12		0.007	0	2	802.3	1603.7	38.17	5204
DPAQPMsPGEATQSGARPADR	MYBBP1A	10514	myb-binding protein 1A isoform 2	M6(Oxidation) S7(Phospho)	S(7): 100.0; T(12): 0.0; S(14): 0.0	S7;	S11		3.47	0	0	3	745.7	2235.0	27.19	3595
DPAQPMsPGEATQSGARPADR	MYBBP1A	10514	myb-binding protein 1A isoform 2	M6(Oxidation) S7(Phospho)	S(7): 100.0; T(12): 0.0; S(14): 0.0	S7;	S11	13		0.003	0	3	745.7	2235.0	27.19	3595
EIPsATQsPISK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S4(Phospho) S8(Phospho)	S(4): 100.0; T(6): 0.0; S(8): 100.0; S(11): 0.0	S4; S8;	S1159; S1163	15		0.004	0	2	709.3	1417.6	48.95	6979
EIPsATQsPISK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S4(Phospho) S8(Phospho)	S(4): 100.0; T(6): 0.0; S(8): 100.0; S(11): 0.0	S4; S8;	S1159; S1163		1.96	0.005	0	2	709.3	1417.6	48.95	6979
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		4.87	0	2	3	795.0	2383.0	22.41	2820
KGAGDGsDEEVDGK	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		4.4	0	1	2	722.3	1443.6	12.95	1371
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		4.29	0	1	3	752.3	2254.9	27.03	3570
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		3.67	0	1	3	752.3	2254.9	27.63	3663
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		3.44	0	1	3	752.3	2254.9	26.02	3413
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		2.77	0	2	3	795.0	2383.0	22.94	2906
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		1.69	0	1	2	1128.0	2254.9	27.08	3578
KGAGDGsDEEVDGK	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	60		0	1	2	722.3	1443.6	12.95	1371
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	38		0	1	3	752.3	2254.9	27.63	3663

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	26		0	1	3	752.3	2254.9	26.02	3413
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	22		0	1	3	752.3	2254.9	27.03	3570
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	20		0	2	3	795.0	2383.0	22.94	2906
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	20		0	1	2	1128.0	2254.9	27.08	3578
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	18		0	2	3	795.0	2383.0	22.41	2820
GISSDNEsVASCNSVK	NAV2	89797	neuron navigator 2 isoform 4	C12(Carbamido methyl) S8(Phospho)	S(3): 3.6; S(4): 3.6; S(8): 92.7; S(11): 0.0; S(14): 0.0	S8;	S347		1.49	0	0	2	867.4	1733.7	36.6	4942
GISSDNEsVASCNSVK	NAV2	89797	neuron navigator 2 isoform 4	C12(Carbamido methyl) S8(Phospho)	S(3): 3.6; S(4): 3.6; S(8): 92.7; S(11): 0.0; S(14): 0.0	S8;	S347	17		0	0	2	867.4	1733.7	36.6	4942
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		3.78	0	0	4	1156.4	4622.5	52.88	7597
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		3.56	0	0	3	1541.5	4622.5	52.85	7591
KEDsDEEEDDDsEEDEDEDEDEDEI EPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.12	0	1	4	1074.6	4295.4	51.93	7415
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		2.35	0	0	3	1541.5	4622.5	52.48	7525
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	36		0	0	3	1541.5	4622.5	52.85	7591
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	10		0	0	3	1541.5	4622.5	52.48	7525
AAAAAPAsEDEDEDEDEDEDDDDDEE DDsEEEAmetTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	23		0.005	0	4	1156.4	4622.5	52.88	7597
KEDsDEEEDDDsEEDEDEDEDEDEI EPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	16		0.007	1	4	1074.6	4295.4	51.93	7415
DRsPIRGsPR	NCOA5	57727	nuclear receptor coactivator 5	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S29; S34		2.26	0	2	2	650.8	1300.6	14.24	1611
DRsPIRGsPR	NCOA5	57727	nuclear receptor coactivator 5	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S29; S34	20		0.003	2	2	650.8	1300.6	14.24	1611
TASGsVsTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho)	T(1): 2.7; S(3): 2.7; S(5): 94.6; S(6): 99.8; T(8): 0.1; S(9): 0.1; T(13): 0.0	S5; S6;	S251; S252		2.58	0	0	2	749.8	1498.6	48.74	6948
tASGSSVtSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	T1(Phospho) S9(Phospho)	T(1): 90.9; S(3): 3.0; S(5): 3.0; S(6): 3.0; T(8): 3.3; S(9): 96.6; T(13): 0.1	T1; S9;	T247; S255		2.13	0	0	2	749.8	1498.6	46.66	6647
TASGsVsTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho)	T(1): 2.7; S(3): 2.7; S(5): 94.6; S(6): 99.8; T(8): 0.1; S(9): 0.1; T(13): 0.0	S5; S6;	S251; S252	54		0	0	2	749.8	1498.6	48.74	6948
tASGSSVtSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	T1(Phospho) S9(Phospho)	T(1): 90.9; S(3): 3.0; S(5): 3.0; S(6): 3.0; T(8): 3.3; S(9): 96.6; T(13): 0.1	T1; S9;	T247; S255	10		0.003	0	2	749.8	1498.6	46.66	6647
tASGSSVtSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	T1(Phospho) S9(Phospho)	T(1): 93.0; S(3): 3.4; S(5): 0.1; S(6): 3.4; T(8): 3.6; S(9): 96.4; T(13): 0.0	T1; S9;	T247; S255		1.88	0.004	0	2	749.8	1498.6	43.22	6048
SPQPVCsPAGSEGTPK	NIPBL	25836	nipped-B-like protein isoform B	C6(Carbamidomethyl) S7(Phospho)	S(1): 0.0; S(7): 100.0; S(11): 0.0; T(14): 0.0	S7;	S280		1.8	0	0	2	839.9	1678.7	30.44	4072
NNTAAEtEDDEsDGEDRGGGTSGVR	NIPBL	25836	nipped-B-like protein isoform B	T7(Phospho) S12(Phospho)	T(3): 0.0; T(7): 100.0; S(12): 100.0; T(21): 0.0; S(22): 0.0	T7; S12;	T2667; S2672	38		0	1	3	900.3	2699.0	24.71	3197
NNTAAEtEDDEsDGEDRGGGTSGSLR	NIPBL	25836	nipped-B-like protein isoform B	T7(Phospho) S12(Phospho)	T(3): 6.1; T(7): 93.9; S(12): 100.0; T(21): 0.0; S(22): 0.0; S(24): 0.0	T7; S12;	T6; S11	13		0.006	1	3	934.0	2800.0	29.49	3928



Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
GGLsPANDTGAK	NMT1	4836	glycylpeptide N-tetradecanoyltransferase 1	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S47		2.6	0	0	2	584.3	1167.5	25.77	3373
GGLsPANDTGAK	NMT1	4836	glycylpeptide N-tetradecanoyltransferase 1	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S47	64		0	0	2	584.3	1167.5	25.77	3373
EAARsPDKPGGSPASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho)	S(5): 100.0; S(12): 49.2; S(14): 49.2; S(16): 1.6	S5;	S49		4.3	0	1	3	610.6	1829.8	13.25	1436
EAARsPDKPGGSPASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho)	S(5): 100.0; S(12): 49.2; S(14): 49.2; S(16): 1.6	S5;	S49	17		0	1	3	610.6	1829.8	13.25	1436
LQTPNtFPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	T3(Phospho) T6(Phospho)	T(3): 100.0; T(6): 100.0	T3; T6;	T607; T610		2.57	0	0	2	603.3	1205.5	53.43	7690
GKGsPRPQAPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	S4(Phospho)	S(4): 100.0	S4;	S538		2.53	0	1	2	601.8	1202.6	12.52	1267
LQTPNtFPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	T3(Phospho) T6(Phospho)	T(3): 100.0; T(6): 100.0	T3; T6;	T607; T610	37		0	0	2	603.3	1205.5	53.43	7690
GKGsPRPQAPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	S4(Phospho)	S(4): 100.0	S4;	S538	28		0	1	2	601.8	1202.6	12.52	1267
GPGGSQGSQGPSPQGAR	NSMCE3	56160	melanoma-associated antigen G1	S12(Phospho)	S(5): 0.0; S(8): 0.0; S(12): 100.0	S12;	S64		2.92	0	0	2	802.8	1604.7	17.05	2001
GPGGSQGSQGPSPQGAR	NSMCE3	56160	melanoma-associated antigen G1	S12(Phospho)	S(5): 0.0; S(8): 0.0; S(12): 100.0	S12;	S64	43		0	0	2	802.8	1604.7	17.05	2001
ASAPERTPsPAPK	NSUN5	55695	probable 28S rRNA (cytosine-C(5))-methyltransferase isoform 1	T7(Phospho) S9(Phospho)	S(2): 0.0; T(7): 100.0; S(9): 100.0	T7; S9;	T442; S444		2.43	0.005	1	2	734.8	1468.6	19.53	2379
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 0.0	S6;	S58		4.9	0	1	3	602.2	1804.7	12.98	1380
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 0.0	S6;	S58		3.81	0	1	2	902.8	1804.7	12.97	1376
NSQEDsEDsEDKDVKTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 100.0; T(16): 0.0	S6; S9;	S58; S61		3.68	0	2	3	705.3	2113.8	13.26	1439
DDSHSAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S9(Phospho)	S(3): 50.0; S(5): 50.0; S(9): 100.0	S9;	S79		3	0	1	3	711.6	2132.7	12.44	1248
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.2; S(6): 99.8; S(9): 100.0	S6; S9;	S58; S61		2.48	0	1	2	942.8	1884.6	15.12	1751
ATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	T(2): 0.0; T(4): 0.0; S(6): 100.0	S6;	S181		2.26	0	1	2	582.8	1164.6	20.2	2483
ATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T4(Phospho) S6(Phospho)	T(2): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T179; S181		1.56	0	1	2	622.8	1244.6	26.41	3482
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 0.0	S6;	S58	55		0	1	2	902.8	1804.7	12.97	1376
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 0.0	S6;	S58	36		0	1	3	602.2	1804.7	12.98	1380
ATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	T(2): 0.0; T(4): 0.0; S(6): 100.0	S6;	S181	26		0	1	2	582.8	1164.6	20.2	2483
LKATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T6(Phospho) S8(Phospho)	T(4): 0.0; T(6): 100.0; S(8): 100.0	T6; S8;	T179; S181		2.2	0.001	2	2	743.4	1485.8	29.74	3973
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.2; S(6): 99.8; S(9): 100.0	S6; S9;	S58; S61	28		0.003	1	2	942.8	1884.6	15.12	1751
NSQEDsEDsEDKDVKTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 100.0; T(16): 0.0	S6; S9;	S58; S61	27		0.003	2	3	705.3	2113.8	13.26	1439
ATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T4(Phospho) S6(Phospho)	T(2): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T179; S181	26		0.003	1	2	622.8	1244.6	25.89	3391
ATVTPsPVK GK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T4(Phospho) S6(Phospho)	T(2): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T179; S181		3.14	0.004	1	2	622.8	1244.6	25.89	3391
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.2; S(6): 99.8; S(9): 100.0	S6; S9;	S58; S61		2.05	0.004	1	2	942.8	1884.6	14.61	1669
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.2; S(6): 99.8; S(9): 100.0	S6; S9;	S58; S61	12		0.004	1	2	942.8	1884.6	14.61	1669
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 0.0; S(6): 100.0; S(9): 100.0	S6; S9;	S58; S61		3.84	0.005	1	3	628.9	1884.6	14.71	1685
EKTPsPKEEDEEPESPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T3(Phospho) S5(Phospho) S15(Phospho)	T(3): 100.0; S(5): 100.0; S(15): 100.0	T3; S5; S15;	T202; S204; S214	10		0.007	2	3	808.0	2421.9	29.7	3966
GADNDGsGSESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho)	S(7): 97.9; S(9): 2.1; S(11): 0.0; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7;	S212		2.86	0	0	2	861.8	1722.7	25.97	3404

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
GADNDGsGsESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 99.8; S(11): 0.2; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7; S9;	S212; S214		2.68	0	0	2	901.8	1802.6	34.18	4585
GADNDGsGsESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 99.8; S(11): 0.2; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7; S9;	S212; S214	48		0	0	2	901.8	1802.6	34.18	4585
GADNDGsGSESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho)	S(7): 97.9; S(9): 2.1; S(11): 0.0; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7;	S212	43		0	0	2	861.8	1722.7	25.97	3404
MLAESDEsGDEESVSQTDK	OSBP	5007	oxysterol-binding protein 1	M1(Oxidation)S8(Phospho)	S(5): 51.6; S(8): 95.2; S(13): 52.0; S(15): 1.0; T(17): 0.2	S8;	S193		1.05	0.005	0	2	1116.9	2232.8	42.3	5898
SPSVPKsPTPKSPPSR	PARVA	55742	alpha-parvin	S7(Phospho) S15(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 99.9; T(9): 0.1; S(12): 0.1; S(15): 99.9	S7; S15;	S54; S62		3.36	0	2	3	603.6	1808.8	27.29	3610
SPTPKsPPSR	PARVA	55742	alpha-parvin	S6(Phospho)	S(1): 0.0; T(3): 0.0; S(6): 100.0; S(9): 0.0	S6;	S59		2.58	0	1	2	567.3	1133.5	13.78	1543
SPTPKsPPSR	PARVA	55742	alpha-parvin	S6(Phospho)	S(1): 0.0; T(3): 0.0; S(6): 100.0; S(9): 0.0	S6;	S59	20		0.003	1	2	567.3	1133.5	13.78	1543
GADsGEEKEGINR	PBDC1	51260	protein PBDC1 isoform 1	S4(Phospho)	S(4): 100.0	S4;	S197		2.59	0	1	2	785.8	1570.6	18.64	2233
GADsGEEKEGINR	PBDC1	51260	protein PBDC1 isoform 1	S4(Phospho)	S(4): 100.0	S4;	S197	23		0	1	2	785.8	1570.6	18.64	2233
DQHLLNsSSSPQR	PCM1	5108	pericentriolar material 1 protein isoform 3	S8(Phospho)	S(7): 0.0; S(8): 98.5; S(9): 0.0; S(10): 1.5	S8;	S429		4.03	0	0	2	775.3	1549.6	12.87	1351
VTNDIsPeSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 98.2; S(10): 1.8	S6; S9;	S65; S68		3.87	0	0	2	837.8	1674.7	47.88	6821
VTNDIsPeSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S10(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 0.0; S(10): 100.0	S6; S10;	S65; S69		2.85	0	0	2	837.8	1674.7	46.5	6624
VTNDIsPeSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 98.2; S(10): 1.8	S6; S9;	S65; S68	85		0	0	2	837.8	1674.7	47.88	6821
VTNDIsPeSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S10(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 0.0; S(10): 100.0	S6; S10;	S65; S69	52		0	0	2	837.8	1674.7	46.5	6624
DQHLLNsSSSPQR	PCM1	5108	pericentriolar material 1 protein isoform 3	S8(Phospho)	S(7): 0.0; S(8): 98.5; S(9): 0.0; S(10): 1.5	S8;	S429	23		0	0	2	775.3	1549.6	12.87	1351
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidylyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347		1.96	0	0	2	723.8	1446.5	44.57	6282
tsPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidylyltransferase A	C5(Carbamidomethyl)T1(Phospho) S6(Phospho)	T(1): 98.2; S(2): 1.8; S(6): 100.0; S(11): 0.0	T1; S6;	T342; S347		1.96	0	0	2	723.8	1446.5	44.06	6192
tsPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidylyltransferase A	C5(Carbamidomethyl)T1(Phospho) S6(Phospho)	T(1): 98.2; S(2): 1.8; S(6): 100.0; S(11): 0.0	T1; S6;	T342; S347	34		0	0	2	723.8	1446.5	44.06	6192
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidylyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347	23		0.003	0	2	723.8	1446.5	44.57	6282
KsLDSDeSEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S2(Phospho) S8(Phospho)	S(2): 99.9; S(5): 0.1; S(8): 100.0; Y(15): 0.0	S2; S8;	S57; S63		4.35	0	1	3	773.9	2319.8	35.04	4715
SLDsDeSEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 2.9; S(4): 97.1; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		4.23	0	1	3	783.3	2347.8	36	4856
SLDsDeSEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 8.6; S(4): 95.7; S(7): 95.7; Y(14): 0.0	S4; S7;	S60; S63		1.46	0	1	2	1174.4	2347.8	35.98	4853
SLDsDeSEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 2.9; S(4): 97.1; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	32		0	1	3	783.3	2347.8	36	4856
KsLDSDeSEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S2(Phospho) S8(Phospho)	S(2): 99.9; S(5): 0.1; S(8): 100.0; Y(15): 0.0	S2; S8;	S57; S63	20		0	1	3	773.9	2319.8	35.04	4715
SLDsDeSEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 8.6; S(4): 95.7; S(7): 95.7; Y(14): 0.0	S4; S7;	S60; S63	13		0	1	2	1174.4	2347.8	35.98	4853
SLDsDeSEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.0; S(4): 100.0; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	11		0	0	2	1096.4	2191.7	45.23	6406
SLDsDeSEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.0; S(4): 100.0; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		1.78	0.001	0	2	1096.4	2191.7	45.23	6406
KSLDsDeSEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 3.5; S(5): 96.5; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63	19		0.003	1	2	1160.4	2319.8	34.98	4708

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
KSLDSDESEDEDDYQK	PDAPI	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 3.5; S(5): 96.5; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63		1.85	0.004	1	2	1160.4	2319.8	34.98	4708
KVMDSDDEDDY	PDCD5	9141	programmed cell death protein 5	M3(Oxidation) S5(Phospho)	S(5): 100.0; Y(11): 0.0	S5;	S119	35		0	1	2	714.2	1427.5	26	3410
SSYSPTSLsPR	PDLIM2	64236	PDZ and LIM domain protein 2 isoform 3	S5(Phospho) S10(Phospho)	S(1): 0.0; S(2): 0.0; Y(3): 0.0; S(4): 0.0; S(5): 100.0; T(7): 0.0; S(8): 0.0; S(10): 100.0	S5; S10;	S124; S129	28		0.003	0	2	714.8	1428.5	48.9	6972
AAVGQEsPGGLEAGNAK	PDS5A	23244	sister chromatid cohesion protein PDS5 homolog A isoform 1	S7(Phospho)	S(7): 100.0	S7;	S1305		3.5	0	0	2	818.4	1635.7	38.16	5201
AAVGQEsPGGLEAGNAK	PDS5A	23244	sister chromatid cohesion protein PDS5 homolog A isoform 1	S7(Phospho)	S(7): 100.0	S7;	S1305	45		0	0	2	818.4	1635.7	38.16	5201
GRPSKTPsSQPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T6(Phospho) S8(Phospho)	S(4): 0.0; T(6): 100.0; S(8): 100.0; S(10): 0.0	T6; S8;	T1381; S1383		5.68	0	1	3	509.6	1526.7	12.58	1284
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(14): 97.4; S(15): 2.6	S14;	S1165		2.84	0	0	2	937.9	1874.8	28.29	3751
AEsPESSAISTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 97.3; S(6): 2.7; S(7): 0.1; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358		2.5	0	0	2	978.9	1956.8	38.42	5244
AEsPESSAISTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 97.3; S(6): 2.7; S(7): 0.1; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358	24		0	0	2	978.9	1956.8	38.42	5244
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(14): 97.4; S(15): 2.6	S14;	S1165	22		0	0	2	937.9	1874.8	28.29	3751
GRPSKTPsSQPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T6(Phospho) S8(Phospho)	S(4): 0.0; T(6): 100.0; S(8): 100.0; S(10): 0.0	T6; S8;	T1381; S1383	24		0.003	1	3	509.6	1526.7	12.58	1284
AEsPESSAISTQSTPQKGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho) T15(Phospho)	S(3): 99.3; S(6): 0.3; S(7): 0.3; S(11): 0.3; T(12): 0.3; S(14): 4.9; T(15): 94.6	S3; T15;	S1358; T1370		1.13	0.004	1	2	1125.5	2249.9	34.21	4589
GRPSKTPsSQPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T6(Phospho) S8(Phospho)	S(4): 0.0; T(6): 100.0; S(8): 97.9; S(10): 2.1	T6; S8;	T1381; S1383		2.9	0.005	1	2	763.8	1526.7	12.62	1293
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	M1(Oxidation) S1(Phospho) S14(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.1; S(9): 0.1; S(10): 0.1; S(11): 99.6; S(14): 96.9; S(15): 3.2	S11; S14;	S1162; S1165	12		0.006	0	2	985.9	1970.7	26.31	3465
GRPSKTPsSQPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T6(Phospho) S8(Phospho)	S(4): 0.0; T(6): 100.0; S(8): 97.9; S(10): 2.1	T6; S8;	T1381; S1383	16		0.007	1	2	763.8	1526.7	12.62	1293
NAIDLQNSSMSEELTK	PEX19	5824	peroxisomal biogenesis factor 19 isoform c	M10(Oxidation) T3(Phospho)	T(3): 99.7; S(8): 0.1; S(9): 0.1; S(11): 0.0; T(16): 0.0	T3;	T141		1.81	0	0	2	996.9	1992.8	43.71	6129
GDQPAAsGDSDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S7(Phospho)	S(7): 97.0; S(10): 3.0	S7;	S54		2.23	0	0	2	1058.4	2115.9	53.91	7764
GDQPAAsGDSDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S7(Phospho)	S(7): 97.0; S(10): 3.0	S7;	S54	28		0	0	2	1058.4	2115.9	53.91	7764
SSsPVQVEEPPVR	PHACTR4	65979	phosphatase and actin regulator 4 isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9	S3;	S118		2.08	0	0	2	761.8	1522.7	42.84	5982
SSsPVQVEEPPVR	PHACTR4	65979	phosphatase and actin regulator 4 isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9	S3;	S118	35		0	0	2	761.8	1522.7	42.84	5982
ISQRDPsPESNK	PHC3	80012	polyhomeotic-like protein 3 isoform 2	S7(Phospho)	S(2): 0.0; S(7): 100.0; S(10): 0.0	S7;	S263		2.12	0	1	2	719.3	1437.6	13.29	1446
RPSASsPNNNTAAK	PHF2	5253	lysine-specific demethylase PHF2	S6(Phospho)	S(3): 1.3; S(5): 1.3; S(6): 97.4; T(11): 0.0	S6;	S1059		3.09	0	0	2	747.8	1494.7	12.51	1266
RPSASsPNNNTAAK	PHF2	5253	lysine-specific demethylase PHF2	S6(Phospho)	S(3): 1.3; S(5): 1.3; S(6): 97.4; T(11): 0.0	S6;	S1059	48		0	0	2	747.8	1494.7	12.51	1266
SSGSSSSGLGTvSNsPASQR	PHF8	23133	histone lysine demethylase PHF8 isoform 4	S15(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; T(11): 0.0; S(13): 3.8; S(15): 92.5; S(18): 3.8	S15;	S751		2.04	0	0	2	966.9	1932.8	31.61	4231
SSGSSSSGLGTvSNsPASQR	PHF8	23133	histone lysine demethylase PHF8 isoform 4	S15(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; T(11): 0.0; S(13): 3.8; S(15): 92.5; S(18): 3.8	S15;	S751	15		0.006	0	2	966.9	1932.8	31.61	4231

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AEAPsPDVAPAGKEDsPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 4.6; S(6): 95.4; S(17): 99.7; S(19): 0.2; S(21): 0.0	S6; S17;	S1356; S1367		3.89	0	1	3	781.7	2343.0	35.5	4780
AEAPsPDVAPAGKEDsPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 4.6; S(6): 95.4; S(17): 99.7; S(19): 0.2; S(21): 0.0	S6; S17;	S1356; S1367	18		0	1	3	781.7	2343.0	35.5	4780
SSSEsYTSQSFQSR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S5(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 96.7; Y(6): 1.6; T(7): 1.6; S(9): 0.0; S(12): 0.0	S5;	S464		2.71	0	0	2	787.3	1573.6	41.34	5737
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.1; S(10): 99.9; S(14): 100.0	S10; S14;	S47; S51		2.35	0	0	2	924.4	1847.7	30.04	4017
SSSEsYTSQSFQSR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S5(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 96.7; Y(6): 1.6; T(7): 1.6; S(9): 0.0; S(12): 0.0	S5;	S464	38		0	0	2	787.3	1573.6	41.34	5737
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.1; S(10): 99.9; S(14): 100.0	S10; S14;	S47; S51	35		0.003	0	2	924.4	1847.7	30.04	4017
LEIsPDSsPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 100.0; S(7): 2.3; S(8): 97.7	S4; S8;	S151; S155		2.8	0	0	2	695.3	1389.5	52.84	7589
RLEIsPDSSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho)	S(5): 100.0; S(8): 50.0; S(9): 50.0	S5;	S151		2.63	0	1	2	773.3	1545.6	43.22	6047
GTAQYsSQsVEER	PKP2	5318	plakophilin-2 isoform 2a	S7(Phospho) S10(Phospho)	T(2): 0.1; Y(5): 0.1; S(6): 2.7; S(7): 97.2; S(10): 99.9	S7; S10;	S132; S135		2.23	0	1	2	865.3	1729.7	20.85	2573
LEIsPDSsPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 100.0; S(7): 2.3; S(8): 97.7	S4; S8;	S151; S155	30		0	0	2	695.3	1389.5	52.84	7589
RLEIsPDSSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho)	S(5): 100.0; S(8): 50.0; S(9): 50.0	S5;	S151	24		0	1	2	773.3	1545.6	43.22	6047
GTAQYsSQsVEER	PKP2	5318	plakophilin-2 isoform 2a	S7(Phospho) S10(Phospho)	T(2): 0.1; Y(5): 0.1; S(6): 2.7; S(7): 97.2; S(10): 99.9	S7; S10;	S132; S135	23		0	1	2	865.3	1729.7	20.85	2573
VAsPQQGVGSSSPKR	PKP4	8502	plakophilin-4 isoform e	S3(Phospho)	S(3): 96.1; S(5): 3.9; S(11): 2.0; S(12): 49.0; S(13): 49.0	S3;	S327		1.51	0.005	1	2	866.4	1731.7	20.22	2487
SDEGQLsPATR	PLEC	5339	plectin isoform 1d	S7(Phospho)	S(1): 0.0; S(7): 100.0; T(10): 0.0	S7;	S551		2.52	0	0	2	620.8	1240.5	26.61	3510
SDEGQLsPATR	PLEC	5339	plectin isoform 1d	S7(Phospho)	S(1): 0.0; S(7): 100.0; T(10): 0.0	S7;	S551	38		0	0	2	620.8	1240.5	26.61	3510
SSSVGsSSSYPIsPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S13(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(6): 97.1; S(7): 2.8; S(8): 0.1; S(9): 0.0; Y(10): 0.0; S(13): 100.0; S(17): 0.0	S6; S13;	S4220; S4227	30		0	0	2	957.9	1914.8	62	9004
SSSVGsSSSYPIsPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S13(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(6): 97.1; S(7): 2.8; S(8): 0.1; S(9): 0.0; Y(10): 0.0; S(13): 100.0; S(17): 0.0	S6; S13;	S4220; S4227		2.42	0.001	0	2	957.9	1914.8	62	9004
KVTsPLQsPTK	PLEKHA7	144100	pleckstrin homology domain-containing family A member 7	S4(Phospho) S8(Phospho)	T(3): 2.0; S(4): 98.0; S(8): 98.0; T(10): 2.0	S4; S8;	S903; S907		3.15	0	1	2	673.3	1345.6	31.84	4259
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 5	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S518; S527	20		0.002	0	2	793.8	1586.7	54.24	7826
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 5	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S518; S527		2.07	0.004	0	2	793.8	1586.7	54.24	7826
YSPTsPTYsPTsPK	POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	S5(Phospho) S12(Phospho)	Y(1): 0.0; S(2): 0.0; T(4): 0.1; S(5): 99.7; T(7): 0.1; Y(8): 0.0; S(9): 0.0; T(11): 3.2; S(12): 96.8	S5; S12;	S1913; S1920		2.81	0	0	2	836.8	1672.7	53.66	7726
YSPTsPTYsPTsPK	POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	S5(Phospho) S9(Phospho)	Y(1): 0.0; S(2): 0.0; T(4): 0.0; S(5): 100.0; T(7): 0.0; Y(8): 0.0; S(9): 97.8; T(11): 2.1; S(12): 0.0	S5; S9;	S1913; S1917		2.07	0.001	0	2	836.8	1672.7	52.42	7513
VGGsDEEASGIPSR	PPAN	56342	suppressor of SWI4 1 homolog	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(13): 0.0	S4;	S359		3.11	0	0	2	720.8	1440.6	35.87	4837
VGGsDEEASGIPSR	PPAN	56342	suppressor of SWI4 1 homolog	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(13): 0.0	S4;	S359	60		0	0	2	720.8	1440.6	35.87	4837
SSsLGNLKK	PPFIBP1	8496	liprin-beta-1 isoform 3	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0	S3;	S313		1.88	0	1	2	507.3	1013.5	20.03	2454
SSsLGNLKK	PPFIBP1	8496	liprin-beta-1 isoform 3	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0	S3;	S313	22		0.003	1	2	507.3	1013.5	20.03	2454
DTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	S3(Phospho)	T(2): 1.8; S(3): 94.6; S(5): 1.8; S(6): 1.8; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S3;	S157		2.65	0	0	2	688.8	1376.6	16.05	1880
TSRDtsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	T5(Phospho) S6(Phospho)	T(1): 4.2; S(2): 4.2; T(5): 92.1; S(6): 98.9; S(8): 0.2; S(9): 0.2; S(11): 0.2; S(14): 0.0; S(15): 0.0; S(16): 0.0	T5; S6;	T156; S157		1.63	0	1	2	900.9	1800.7	15.71	1835

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
DTSPSSGSAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	S3(Phospho)	T(2): 1.8; S(3): 94.6; S(5): 1.8; S(6): 1.8; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S3;	S157	51		0	0	2	688.8	1376.6	16.05	1880
ADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S687		1.64	0	1	2	615.8	1230.5	18.62	2229
IKQsSQDNELK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S5(Phospho)	S(4): 2.4; S(5): 97.6	S5;	S696		1.74	0.001	1	2	685.3	1369.6	15.68	1832
ADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S687	21		0.003	1	2	615.8	1230.5	18.62	2229
IQEQEsGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 95.2; S(7): 95.2; S(12): 9.7; S(15): 0.0	S6; S7;	S95; S96		2.62	0	1	3	861.0	2581.0	38.93	5334
IQEQEsGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 99.6; S(7): 99.6; S(12): 0.7; S(15): 0.0	S6; S7;	S95; S96		1.98	0	0	2	1162.4	2323.8	49.4	7057
IQEQEsGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 99.6; S(7): 99.6; S(12): 0.7; S(15): 0.0	S6; S7;	S95; S96	22		0	0	2	1162.4	2323.8	49.4	7057
IQEQEsGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 95.2; S(7): 95.2; S(12): 9.7; S(15): 0.0	S6; S7;	S95; S96	16		0.003	1	3	861.0	2581.0	38.93	5334
ARsLPSSPER	PPP1R3D	5509	protein phosphatase 1 regulatory subunit 3D	S3(Phospho)	S(3): 100.0; S(6): 50.0; S(7): 50.0	S3;	S74	23		0.003	1	2	630.3	1259.5	23.78	3038
ARsLPSSPER	PPP1R3D	5509	protein phosphatase 1 regulatory subunit 3D	S3(Phospho)	S(3): 100.0; S(6): 50.0; S(7): 50.0	S3;	S74		2.39	0.005	1	2	630.3	1259.5	23.78	3038
RVEsEEsGDEEGKK	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S24; S27		5.46	0	2	3	580.2	1738.7	12.7	1309
RVEsEEsGDEEGKK	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S24; S27		3.39	0	2	2	869.8	1738.7	12.71	1312
RVEsEEsGDEEGKK	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S24; S27	64		0	2	3	580.2	1738.7	12.7	1309
RVEsEEsGDEEGKK	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S24; S27	43		0	2	2	869.8	1738.7	12.71	1312
VEVFtDVQEDVPLVISDGGDsEQFLDEE R	PRH1	5554	salivary acidic proline-rich phosphoprotein 1/2 isoform b	T5(Phospho) S8(Phospho) S22(Phospho)	T(5): 100.0; S(8): 100.0; S(17): 0.0; S(22): 100.0	T5; S8; S22;	T34; S37; S51		4.6	0	0	3	1198.5	3593.4	114.5	####
VEVFtDVQEDVPLVISDGGDsEQFLDEE R	PRH1	5554	salivary acidic proline-rich phosphoprotein 1/2 isoform b	T5(Phospho) S8(Phospho) S22(Phospho)	T(5): 100.0; S(8): 100.0; S(17): 0.0; S(22): 100.0	T5; S8; S22;	T34; S37; S51	55		0	0	3	1198.5	3593.4	114.5	####
RRsQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(10): 0.0	S3; S5;	S527; S529		4.81	0	2	3	588.9	1764.7	14.19	1606
SQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(8): 0.0	S3;	S529		2.44	0	0	2	686.8	1372.6	18.3	2181
SQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(8): 0.0	S3;	S529	35		0	0	2	686.8	1372.6	18.3	2181
RRsQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(10): 0.0	S3; S5;	S527; S529	31		0	2	3	588.9	1764.7	14.19	1606
sRsPVDLR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S292; S294		2.21	0	1	2	545.2	1089.4	31.33	4191
sRsPVDLR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S292; S294	16		0.007	1	2	545.2	1089.4	30.83	4127
STtPTSsPFR	PRRC2C	23215	protein PRRC2C	T3(Phospho) S7(Phospho)	S(1): 0.0; T(2): 0.0; T(3): 96.7; T(5): 1.7; S(6): 1.7; S(7): 100.0	T3; S7;	T2682; S2686		2.94	0	0	2	620.7	1240.5	46.1	6563
STtPTSsPFR	PRRC2C	23215	protein PRRC2C	T3(Phospho) S7(Phospho)	S(1): 0.0; T(2): 0.0; T(3): 96.7; T(5): 1.7; S(6): 1.7; S(7): 100.0	T3; S7;	T2682; S2686	27		0	0	2	620.7	1240.5	46.1	6563
APVQPPQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S8(Phospho)	S(8): 100.0; T(16): 0.0; S(21): 0.0	S8;	S16		4.11	0	0	3	766.7	2298.1	26.72	3528
APVQPPQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S8(Phospho)	S(8): 100.0; T(16): 0.0; S(21): 0.0	S8;	S16	31		0	0	3	766.7	2298.1	26.72	3528
ELKTDsPNQAR	PTBP1	5725	polypyrimidine tract-binding protein 1 isoform c	S7(Phospho)	T(4): 0.0; S(6): 1.6; S(7): 98.4	S7;	S141		2.57	0	1	2	713.3	1425.6	14.62	1670
ELKTDsPNQAR	PTBP1	5725	polypyrimidine tract-binding protein 1 isoform c	S7(Phospho)	T(4): 0.0; S(6): 1.6; S(7): 98.4	S7;	S141	33		0	1	2	713.3	1425.6	14.62	1670
GKAsPFEEQNR	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho)	S(4): 100.0	S4;	S80		2.36	0	1	2	729.3	1457.6	22.44	2825
GKAsPFEEQNR	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho)	S(4): 100.0	S4;	S80	30		0	1	2	729.3	1457.6	22.44	2825
RGGSsGGGEEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S304		2.27	0	1	2	966.3	1931.7	23.25	2959
RGGSsGGGEEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S304	22		0.007	1	2	966.3	1931.7	23.25	2959

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
sSPGGQDEGGFMAQ GK	PXN	5829	paxillin isoform 2	M12(Oxidation) S1(Phospho)	S(1): 96.8; S(2): 3.2	S1;	S302		2.64	0	0	2	824.8	1648.6	29.45	3919
sSPGGQDEGGFMAQ GK	PXN	5829	paxillin isoform 2	M12(Oxidation) S1(Phospho)	S(1): 96.8; S(2): 3.2	S1;	S302	25		0	0	2	824.8	1648.6	29.45	3919
TSSVSNPQDSVGsPCSR	PXN	5829	paxillin isoform 2	C15(Carbamido methyl) S13(Phospho)	T(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(10): 0.0; S(13): 100.0; S(16): 0.0	S13;	S106		2.12	0.004	0	2	922.9	1844.8	31.2	4175
GGGTPDANSLAPP GK	PYGO2	90780	pygopus homolog 2	T4(Phospho)	T(4): 100.0; S(9): 0.0	T4;	T302		2.53	0	0	2	709.8	1418.6	39.75	5477
GGGTPDANSLAPP GK	PYGO2	90780	pygopus homolog 2	T4(Phospho)	T(4): 100.0; S(9): 0.0	T4;	T302	22		0	0	2	709.8	1418.6	39.75	5477
GEIKDSsPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S13(Phospho)	S(6): 0.1; S(7): 99.9; S(9): 0.0; S(10): 0.0; S(11): 0.1; S(13): 99.9	S7; S13;	S339; S345		2.46	0	1	2	831.8	1662.7	20.39	2513
GEIKDSsPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S13(Phospho)	S(6): 0.1; S(7): 99.9; S(9): 0.0; S(10): 0.0; S(11): 0.1; S(13): 99.9	S7; S13;	S339; S345	21		0	1	2	831.8	1662.7	20.39	2513
GEIKDSsPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S9(Phospho) S13(Phospho)	S(6): 0.0; S(7): 100.0; S(9): 99.8; S(10): 0.0; S(11): 0.2; S(13): 100.0	S7; S9; S13;	S339; S341; S345		1.73	0.004	1	2	871.8	1742.6	24.46	3152
ETQSTPQsAPQVR	RASAL2	9462	ras GTPase-activating protein nGAP isoform 1	S8(Phospho)	T(2): 0.0; S(4): 0.0; T(5): 0.0; S(8): 100.0	S8;	S758		2.59	0	0	2	754.8	1508.7	27.75	3681
ETQSTPQsAPQVR	RASAL2	9462	ras GTPase-activating protein nGAP isoform 1	S8(Phospho)	T(2): 0.0; S(4): 0.0; T(5): 0.0; S(8): 100.0	S8;	S758	35		0	0	2	754.8	1508.7	27.75	3681
HCAPsPDRsPELSSSR	RBM15	64783	putative RNA-binding protein 15 isoform 2	C2(Carbamidomethyl)S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 100.0; S(13): 0.0; S(14): 0.0; S(15): 0.0	S5; S9;	S670; S674		4.36	0	1	3	648.3	1942.8	25.36	3310
EVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S11(Phospho)	S(8): 0.0; S(9): 0.0; S(10): 1.7; S(11): 98.3	S11;	S188		2.47	0	0	2	741.3	1481.6	19.95	2439
EVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S11(Phospho)	S(8): 0.0; S(9): 0.0; S(10): 1.7; S(11): 98.3	S11;	S188	40		0	0	2	741.3	1481.6	19.95	2439
SALsPSKsPAK	RGPD4	285190	ranBP2-like and GRIP domain-containing protein 4	S4(Phospho) S8(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 1.9; S(8): 98.1	S4; S8;	S1301; S1305		3.42	0	1	2	616.8	1232.5	21.71	2706
SALsPSKsPAK	RGPD4	285190	ranBP2-like and GRIP domain-containing protein 4	S4(Phospho) S8(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 1.9; S(8): 98.1	S4; S8;	S1301; S1305	27		0	1	2	616.8	1232.5	21.71	2706
SQEDEIssPVN K	RIF1	55183	telomere-associated protein RIF1 isoform 2	S8(Phospho)	S(1): 0.0; S(7): 2.8; S(8): 97.2	S8;	S2196		2.02	0	0	2	706.8	1412.6	29.47	3923
GsPATsPHLGR	RIN1	9610	ras and Rab interactor 1	S2(Phospho) S6(Phospho)	S(2): 99.9; T(5): 2.5; S(6): 97.5	S2; S6;	S333; S337		2.74	0	0	2	620.2	1239.5	27.84	3694
GsPATsPHLGR	RIN1	9610	ras and Rab interactor 1	S2(Phospho) S6(Phospho)	S(2): 99.9; T(5): 2.5; S(6): 97.5	S2; S6;	S333; S337	44		0	0	2	620.2	1239.5	27.84	3694
KEEsEEsDDDMGFG LFD	RPLP1	6176	60S acidic ribosomal protein P1 isoform 2	M11(Oxidation)S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S76; S79	30		0.004	1	2	1063.4	2125.7	103.15	####
LSsLRASTSKSESSQ K	RPS6	6194	40S ribosomal protein S6	S3(Phospho)	S(2): 4.2; S(3): 95.8; S(7): 48.9; T(8): 48.9; S(9): 2.1; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3;	S236		1.15	0.004	2	2	928.4	1855.8	20.1	2466
LSsLRASTSKSESSQ K	RPS6	6194	40S ribosomal protein S6	S3(Phospho)	S(2): 6.8; S(3): 93.0; S(7): 48.8; T(8): 48.8; S(9): 2.6; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3;	S236		2.41	0.005	2	3	619.3	1855.8	20.08	2463
LSsLRASTSKSESSQ K	RPS6	6194	40S ribosomal protein S6	S3(Phospho)	S(2): 4.2; S(3): 95.8; S(7): 48.9; T(8): 48.9; S(9): 2.1; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3;	S236	10		0.006	2	2	928.4	1855.8	20.1	2466
LSsLRASTSK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S7(Phospho)	S(2): 4.0; S(3): 96.1; S(7): 92.5; T(8): 3.7; S(9): 3.7	S3; S7;	S236; S240	19		0.008	1	2	605.3	1209.5	25.35	3308
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185		5.1	0	1	3	654.3	1960.9	24.57	3164
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185		1.98	0	1	2	981.0	1960.9	24.54	3160
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185	29		0	1	3	654.3	1960.9	24.57	3164
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185	15		0	1	2	981.0	1960.9	24.54	3160
TPTSSPAssPLVAK	RRP1B	23076	ribosomal RNA processing protein 1 homolog B	S8(Phospho) S9(Phospho)	T(1): 0.2; T(3): 0.5; S(4): 4.0; S(5): 3.8; S(8): 92.3; S(9): 99.2	S8; S9;	S735; S736		2.72	0	0	2	751.8	1502.7	47.88	6820
TPTSSPAssPLVAK	RRP1B	23076	ribosomal RNA processing protein 1 homolog B	S8(Phospho) S9(Phospho)	T(1): 0.2; T(3): 0.5; S(4): 4.0; S(5): 3.8; S(8): 92.3; S(9): 99.2	S8; S9;	S735; S736	20		0	0	2	751.8	1502.7	47.88	6820

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AAESETPGKsPEKKPK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	T6(Phospho) S10(Phospho)	S(4): 0.1; T(6): 99.9; S(10): 100.0	T6; S10;	T423; S427		3.92	0	2	3	615.3	1843.8	12.48	1258
AAESETPGKsPEK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S10(Phospho)	S(4): 0.0; T(6): 0.0; S(10): 100.0	S10;	S427		3.75	0	1	2	705.8	1410.6	12.72	1316
KsPAKsPNPStPR	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S2(Phospho) S6(Phospho) T11(Phospho)	S(2): 100.0; S(6): 99.9; S(10): 2.8; T(11): 97.3	S2; S6; T11;	S392; S396; T401		3.36	0	2	2	803.8	1606.6	12.89	1357
AAESETPGKsPEK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S10(Phospho)	S(4): 0.0; T(6): 0.0; S(10): 100.0	S10;	S427	26		0	1	2	705.8	1410.6	12.72	1316
KsPAKsPNPStPR	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S2(Phospho) S6(Phospho) T11(Phospho)	S(2): 100.0; S(6): 99.9; S(10): 2.8; T(11): 97.3	S2; S6; T11;	S392; S396; T401	27	0.003	2	2	2	803.8	1606.6	12.89	1357
QRsPsPAPAPAAAAAGPPTR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(20): 0.0	S3; S5;	S498; S500		5.26	0	1	3	710.0	2128.0	41.45	5755
GPSPAPASSPKR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S3(Phospho)	S(3): 100.0; S(8): 50.0; S(9): 50.0	S3;	S719		2.98	0	1	2	656.3	1311.5	15.19	1764
sAsPPPTSSSSSSR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0	S1; S3;	S612; S614		1.98	0	0	2	783.3	1565.6	21	2593
sAsPPPTSSSSSSR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0	S1; S3;	S612; S614		1.52	0	0	2	783.3	1565.6	21.5	2677
QRsPsPAPAPAAAAAGPPTR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(20): 0.0	S3; S5;	S498; S500	44		0	1	3	710.0	2128.0	41.45	5755
EVLyDsEGLsGEER	SCAF1	58506	splicing factor, arginine/serine-rich 19	S6(Phospho) S10(Phospho)	Y(4): 0.0; S(6): 100.0; S(10): 100.0	S6; S10;	S734; S738	34		0	0	2	871.8	1742.7	67.43	9933
GPSPAPASSPKR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S3(Phospho)	S(3): 100.0; S(8): 50.0; S(9): 50.0	S3;	S719	28		0	1	2	656.3	1311.5	15.19	1764
sAsPPPTSSSSSSR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0	S1; S3;	S612; S614	18		0	0	2	783.3	1565.6	21	2593
sAsPPPTSSSSSSR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0	S1; S3;	S612; S614	13		0	0	2	783.3	1565.6	21.5	2677
YsDDTLDR	SCEL	8796	scellin isoform 3	S3(Phospho)	Y(1): 0.0; S(2): 1.8; S(3): 98.2; T(6): 0.0	S3;	S91		2.01	0	0	2	576.2	1151.4	27.57	3653
YsDDTLDR	SCEL	8796	scellin isoform 3	S3(Phospho)	Y(1): 0.0; S(2): 1.8; S(3): 98.2; T(6): 0.0	S3;	S91	32		0	0	2	576.2	1151.4	27.57	3653
EELEQQtDGDCEEEEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375		2.36	0	0	3	1012.0	3034.1	40.25	5561
EELEQQtDGDCEEEEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375	27		0	0	3	1012.0	3034.1	40.25	5561
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7		2.75	0	1	2	565.8	1130.6	15.18	1762
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7	33	0.003	1	2	2	565.8	1130.6	15.18	1762
WDQTADQTPGATPK	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T8(Phospho) T12(Phospho)	T(4): 0.1; T(8): 99.9; T(12): 100.0	T8; T12;	T207; T211		2.58	0	0	2	838.3	1675.6	42.06	5857
SrTPASANDDQQE	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	T3(Phospho)	S(1): 2.1; T(3): 97.9; S(5): 0.0; S(7): 0.0	T3;	T303	26		0.006	1	2	757.8	1514.6	13.9	1565
EAEEGPTGASESQDsPR	SH3PXD2A	9644	SH3 and PX domain-containing protein 2A	S15(Phospho)	T(7): 0.0; S(10): 0.0; S(12): 0.1; S(15): 99.9	S15;	S519	26		0	0	2	913.9	1826.7	22.72	2871
EAEEGPTGASESQDsPR	SH3PXD2A	9644	SH3 and PX domain-containing protein 2A	S15(Phospho)	T(7): 0.0; S(10): 0.0; S(12): 0.1; S(15): 99.9	S15;	S519		2.07	0.001	0	2	913.9	1826.7	22.72	2871
AQsPGsPLHAR	SHROOM2	357	protein Shroom2 isoform 1	S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0	S3; S6;	S1036; S1039		2.04	0	0	2	640.8	1280.5	27.96	3708
AQsPGsPLHAR	SHROOM2	357	protein Shroom2 isoform 1	S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0	S3; S6;	S1036; S1039	35		0	0	2	640.8	1280.5	27.96	3708
sLTNsHLEK	SLC38A1	81539	sodium-coupled neutral amino acid transporter 1 isoform 1	S1(Phospho) S5(Phospho)	S(1): 100.0; T(3): 0.0; S(5): 100.0	S1; S5;	S52; S56		2.91	0	0	2	594.7	1188.5	26.83	3540
EKQsEEEEKETR	SLC39A7	7922	zinc transporter SLC39A7 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; T(12): 0.0	S4; S5;	S150; S151		4.15	0	2	3	590.2	1768.7	12.55	1276

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
EKQsEEEEKETR	SLC39A7	7922	zinc transporter SLC39A7 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; T(12): 0.0	S4; S5;	S150; S151		2.99	0	2	2	884.8	1768.7	12.57	1280
EKQsEEEEKETR	SLC39A7	7922	zinc transporter SLC39A7 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; T(12): 0.0	S4; S5;	S150; S151	39		0	2	3	590.2	1768.7	12.55	1276
EKQsEEEEKETR	SLC39A7	7922	zinc transporter SLC39A7 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; T(12): 0.0	S4; S5;	S150; S151	35		0	2	2	884.8	1768.7	12.57	1280
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 99.9; S(5): 0.1; T(15): 0.0	S1;	S31		3.17	0	0	2	891.4	1781.8	43.26	6057
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 100.0; S(5): 0.0; T(15): 0.0	S1;	S31		3.12	0	0	2	891.4	1781.8	44.44	6259
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 99.9; S(5): 0.1; T(15): 0.0	S1;	S31	38		0	0	2	891.4	1781.8	43.26	6057
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 100.0; S(5): 0.0; T(15): 0.0	S1;	S31	38		0	0	2	891.4	1781.8	44.44	6259
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330		5.59	0	1	3	592.3	1774.8	21.18	2617
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330		5.08	0	1	3	592.3	1774.8	20.67	2553
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330		2.04	0	1	2	887.9	1774.8	20.88	2578
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330	31		0	1	3	592.3	1774.8	21.18	2617
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330	28		0	1	3	592.3	1774.8	20.67	2553
KHsPsPPPTPTESR	SMARCC1	6599	SWI/SNF complex subunit SMARCC1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0; T(12): 0.0; S(14): 0.0	S3; S5;	S328; S330	11		0.002	1	2	887.9	1774.8	20.88	2578
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; T(9): 0.0	S3; S5;	S302; S304		5.72	0	2	3	514.6	1541.7	13.36	1462
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; S(7): 0.1; T(9): 0.0	S3; S5;	S302; S304		3.48	0	2	2	771.3	1541.7	13.27	1441
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.8; S(7): 0.1; T(9): 0.1	S3; S5;	S302; S304		3.33	0	2	2	771.3	1541.7	13.59	1507
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 96.7; S(5): 96.7; S(7): 0.3; T(9): 6.3	S3; S5;	S302; S304		2.01	0	2	2	771.3	1541.7	13.77	1540
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; T(9): 0.0	S3; S5;	S302; S304	32		0	2	3	514.6	1541.7	13.36	1462
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; S(7): 0.1; T(9): 0.0	S3; S5;	S302; S304	16		0.003	2	2	771.3	1541.7	13.27	1441
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.8; S(7): 0.1; T(9): 0.1	S3; S5;	S302; S304	14		0.003	2	2	771.3	1541.7	13.59	1507
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 96.7; S(5): 96.7; S(7): 0.3; T(9): 6.3	S3; S5;	S302; S304	10		0.005	2	2	771.3	1541.7	13.77	1540
GVsRsPPK	SNIP1	79753	smad nuclear-interacting protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S74; S76		2.59	0.001	1	2	494.2	987.4	14.82	1704
GVsRsPPK	SNIP1	79753	smad nuclear-interacting protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S74; S76	25		0.006	1	2	494.2	987.4	14.82	1704
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		5.48	0	0	3	563.9	1689.7	37.12	5028
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		5.45	0	0	3	563.9	1689.7	36.62	4945
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 99.9; S(14): 0.1	S4; S12;	S224; S232		3.77	0	1	3	606.6	1817.8	28.41	3770
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 98.2; S(14): 1.8	S4; S12;	S224; S232		3.76	0	0	2	845.3	1689.7	36.93	4997
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 96.7; S(14): 3.3	S4; S12;	S224; S232		3.19	0	1	3	606.6	1817.8	27.91	3701



Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation)S4(Phospho)S12(Phospho)	S(4): 100.0; S(12): 98.2; S(14): 1.8	S4; S12;	S224; S232	30		0	0	2	845.3	1689.7	36.93	4997
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation)S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	30		0	0	3	563.9	1689.7	36.62	4945
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation)S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	26		0	0	3	563.9	1689.7	37.12	5028
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1 isoform 2	M10(Oxidation)S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	13		0.006	0	2	845.3	1689.7	36.42	4915
SVESSTPEPsK	SON	6651	protein SON isoform E	S10(Phospho)	S(1): 0.0; S(4): 0.0; T(5): 0.0; S(6): 1.6; S(10): 98.4	S10;	S287		2.69	0	0	2	614.3	1227.5	17.47	2056
SVESSTPEPsK	SON	6651	protein SON isoform E	S10(Phospho)	S(1): 0.0; S(4): 0.0; T(5): 0.0; S(6): 1.6; S(10): 98.4	S10;	S287	35		0	0	2	614.3	1227.5	17.47	2056
SVCPGGSSPGSSSGGGR	SOWAHC	65124	ankyrin repeat domain-containing protein SOWAHC	C3(Carbamidomethyl)S8(Phospho)	S(1): 0.0; S(7): 2.3; S(8): 97.7; S(11): 0.0; S(12): 0.0; S(13): 0.0	S8;	S226		2.3	0	0	2	786.8	1572.6	18.77	2250
SVCPGGSSPGSSSGGGR	SOWAHC	65124	ankyrin repeat domain-containing protein SOWAHC	C3(Carbamidomethyl)S8(Phospho)	S(1): 0.0; S(7): 2.3; S(8): 97.7; S(11): 0.0; S(12): 0.0; S(13): 0.0	S8;	S226	28		0	0	2	786.8	1572.6	18.77	2250
SQGSGNEAEPLGK	SPATS2L	26010	SPATS2-like protein isoform b	S4(Phospho)	S(1): 0.1; S(4): 99.9	S4;	S386		2.15	0	0	2	677.3	1353.6	26.29	3461
SQGSGNEAEPLGK	SPATS2L	26010	SPATS2-like protein isoform b	S4(Phospho)	S(1): 0.1; S(4): 99.9	S4;	S386	28		0	0	2	677.3	1353.6	26.29	3461
TSSKEsPIPSPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S6(Phospho)T13(Phospho)	T(1): 49.1; S(2): 49.1; S(3): 1.8; S(6): 96.5; S(7): 3.5; S(11): 0.0; T(13): 99.9; S(14): 0.1	S6; T13;	S2164; T2171		3.07	0	2	3	681.9	2043.8	28.46	3779
RPPsPEPSTK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S4(Phospho)	S(4): 100.0; S(8): 0.0; T(9): 0.0	S4;	S2102		2.81	0	0	2	588.3	1175.5	13.28	1445
TSSKEsPIPSPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S6(Phospho)S7(Phospho)	T(1): 1.1; S(2): 1.1; S(3): 10.4; S(6): 93.7; S(7): 93.7; S(11): 0.1; T(13): 0.0; S(14): 0.0	S6; S7;	S2164; S2165		1.7	0	1	2	918.4	1835.8	36.37	4907
TSsKESSIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho)S11(Phospho)	T(1): 4.6; S(2): 4.6; S(3): 89.0; S(6): 50.9; S(7): 50.9; S(11): 99.7; T(13): 0.3; S(14): 0.0	S3; S11;	S2161; S2169		1.64	0	1	2	958.4	1915.7	40.93	5665
RPPsPEPSTK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S4(Phospho)	S(4): 100.0; S(8): 0.0; T(9): 0.0	S4;	S2102	25		0	0	2	588.3	1175.5	13.28	1445
TSsKESSIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho)S11(Phospho)	T(1): 4.6; S(2): 4.6; S(3): 89.0; S(6): 50.9; S(7): 50.9; S(11): 99.7; T(13): 0.3; S(14): 0.0	S3; S11;	S2161; S2169	19		0.003	1	2	958.4	1915.7	40.93	5665
TSSKEsPIPSPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S6(Phospho)T13(Phospho)	T(1): 49.1; S(2): 49.1; S(3): 1.8; S(6): 96.5; S(7): 3.5; S(11): 0.0; T(13): 99.9; S(14): 0.1	S6; T13;	S2164; T2171	14		0.003	2	3	681.9	2043.8	28.46	3779
SRLTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho)S7(Phospho)	S(1): 2.3; T(4): 97.7; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188		4.42	0	1	3	631.9	1893.8	34.9	4694
SRLTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	S7(Phospho)	S(1): 50.0; T(4): 50.0; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	S7;	S188		1.8	0	1	2	947.4	1893.8	34.69	4661
LTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	S5(Phospho)	T(2): 0.0; S(5): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; T(11): 0.0	S5;	S188		1.64	0	0	2	785.8	1570.7	36.83	4984
SRLTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho)S7(Phospho)	S(1): 2.3; T(4): 97.7; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188	38		0	1	3	631.9	1893.8	34.9	4694
LTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	S5(Phospho)	T(2): 0.0; S(5): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; T(11): 0.0	S5;	S188	21		0	0	2	785.8	1570.7	36.83	4984
SRLTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	S7(Phospho)	S(1): 50.0; T(4): 50.0; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	S7;	S188	21		0	1	2	947.4	1893.8	34.69	4661
SRLTPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho)S7(Phospho)	S(1): 3.6; T(4): 96.4; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188	15		0.004	1	2	947.4	1893.8	35.2	4738

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
SRLtPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho) S7(Phospho)	S(1): 3.6; T(4): 96.4; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188		1.82	0.005	1	2	947.4	1893.8	35.2	4738
TVsASsTGDLPK	SRPK2	6733	SRSF protein kinase 2 isoform b precursor	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 97.6; S(5): 2.4; S(6): 97.6; T(7): 2.4	S3; S6;	S494; S497		3.51	0	0	2	661.8	1322.5	46.25	6588
TVsASsTGDLPK	SRPK2	6733	SRSF protein kinase 2 isoform b precursor	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 97.6; S(5): 2.4; S(6): 97.6; T(7): 2.4	S3; S6;	S494; S497	62		0	0	2	661.8	1322.5	46.25	6588
HRPsPPAtPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367		5.56	0	0	3	481.2	1441.6	19.16	2315
HRPsPPAtPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367		5.26	0	0	3	481.2	1441.6	19.68	2401
RRsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(9): 0.0	S3; S5;	S522; S524		4.44	0	2	3	437.5	1310.6	12.75	1322
RA sPsPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S599; S601		4.32	0	2	2	626.8	1252.6	12.34	1224
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580		4.13	0	1	2	594.7	1188.5	23.36	2975
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580		4.05	0	1	2	594.7	1188.5	22.85	2890
RA sPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S599; S601		3.53	0	1	2	548.7	1096.5	13.04	1395
KAA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 0.0	S4; S6;	S711; S713		3.53	0	1	2	644.3	1287.5	18.39	2195
HRPsPPAtPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367		3.15	0	0	2	721.3	1441.6	19.52	2377
KAA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 0.0	S4; S6;	S711; S713		3.03	0	1	2	644.3	1287.5	17.89	2115
APQTsSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	T(4): 0.1; S(5): 97.0; S(6): 5.8; S(7): 97.1	S5; S7;	S667; S669		3	0	0	2	692.3	1383.6	32.45	4350
RsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; T(8): 0.0	S2; S4;	S522; S524		2.95	0	1	2	577.7	1154.5	15.38	1790
AA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 0.0	S3; S5;	S711; S713		2.91	0	0	2	580.2	1159.5	25.9	3393
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580		2.8	0	1	2	594.7	1188.5	22.34	2812
HRPsPPAtPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367		2.79	0	0	2	721.3	1441.6	19.01	2285
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 1.4; S(3): 98.6; S(5): 100.0	S3; S5;	S578; S580		2.57	0	1	2	594.7	1188.5	23.87	3055
RRsSPPPtR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) T9(Phospho)	S(3): 100.0; S(5): 1.9; T(9): 98.1	S3; T9;	S522; T528		2.56	0	2	2	655.8	1310.6	12.79	1332
AA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 0.0	S3; S5;	S711; S713		2.41	0	0	2	580.2	1159.5	26.4	3481
HRPsPPAtPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367		2.29	0	0	2	721.3	1441.6	18.5	2212
tAsPPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T1(Phospho) S3(Phospho)	T(1): 100.0; S(3): 100.0	T1; S3;	T587; S589		2.02	0	1	2	604.3	1207.5	18.75	2246
KVELsEsEEDKGGK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S422; S424		1.35	0	2	2	847.9	1694.7	21.21	2625
AA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 0.0	S3; S5;	S711; S713	50		0	0	2	580.2	1159.5	25.9	3393
KAA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 0.0	S4; S6;	S711; S713	50		0	1	2	644.3	1287.5	17.89	2115
KAA sPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 0.0	S4; S6;	S711; S713	45		0	1	2	644.3	1287.5	18.39	2195
RA sPsPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S599; S601	38		0	2	2	626.8	1252.6	12.34	1224
APQTsSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	T(4): 0.1; S(5): 97.0; S(6): 5.8; S(7): 97.1	S5; S7;	S667; S669	38		0	0	2	692.3	1383.6	32.45	4350
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580	37		0	1	2	594.7	1188.5	23.36	2975

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
HRPsPPATPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367	36		0	0	3	481.2	1441.6	19.16	2315
AAsPsPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 0.0	S3; S5;	S711; S713	34		0	0	2	580.2	1159.5	26.4	3481
HRPsPPATPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367	30		0	0	3	481.2	1441.6	19.68	2401
RLsPsASPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S350; S352	30		0	1	2	614.3	1227.5	30.44	4071
APQTsSSPPPVV	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(4): 0.1; S(5): 99.8; S(6): 50.0; S(7): 50.0	S5;	S667	28		0	0	2	692.3	1383.6	32.97	4417
RAAsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S599; S601	28		0	1	2	548.7	1096.5	13.04	1395
APQTsSSPPPVV	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho)	T(4): 0.1; S(5): 2.1; S(6): 97.8; S(7): 0.1	S6;	S668	24		0	0	2	652.3	1303.6	26.26	3454
RLsPsASPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S350; S352	23		0	1	2	614.3	1227.5	29.94	4002
HRPsPPATPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367	21		0	0	2	721.3	1441.6	19.01	2285
HRPsPPATPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 100.0	S4; T8;	S363; T367	20		0	0	2	721.3	1441.6	19.52	2377
RsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S533; S535		3.13	0.001	1	2	611.3	1221.5	18.43	2200
RLsPsASPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S350; S352		3.13	0.001	1	2	614.3	1227.5	30.94	4145
APQTsSSPPPVV	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(4): 0.1; S(5): 99.8; S(6): 50.0; S(7): 50.0	S5;	S667		2.32	0.001	0	2	692.3	1383.6	32.97	4417
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580	13		0.002	1	2	594.7	1188.5	22.34	2812
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580	38		0.003	1	2	594.7	1188.5	22.85	2890
RLsPsASPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S350; S352	29		0.003	1	2	614.3	1227.5	30.94	4145
RRsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(9): 0.0	S3; S5;	S522; S524	26		0.003	2	3	437.5	1310.6	12.75	1322
RsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; T(8): 0.0	S2; S4;	S522; S524	21		0.003	1	2	577.7	1154.5	15.38	1790
RsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S533; S535	11		0.003	1	2	611.3	1221.5	18.43	2200
RLsPsASPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S350; S352		3.21	0.004	1	2	614.3	1227.5	30.44	4071
APQTsSSPPPVV	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho)	T(4): 0.1; S(5): 2.1; S(6): 97.8; S(7): 0.1	S6;	S668		1.92	0.004	0	2	652.3	1303.6	26.26	3454
RYsPsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	Y(2): 1.4; S(3): 98.6; S(5): 100.0	S3; S5;	S578; S580	15		0.004	1	2	594.7	1188.5	23.87	3055
RLsPsAsPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0	S3; S5; S7;	S350; S352; S354	11		0.004	1	2	654.3	1307.5	36.78	4976
RLsPsAsPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0	S3; S5; S7;	S350; S352; S354		2.19	0.005	1	2	654.3	1307.5	36.78	4976
KSRVsVsPGR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	S(2): 0.1; S(5): 99.9; S(7): 100.0	S5; S7;	S390; S392	21		0.005	2	2	616.8	1232.6	15.54	1809
tAsPPPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T1(Phospho) S3(Phospho)	T(1): 100.0; S(3): 100.0	T1; S3;	T587; S589	18		0.005	1	2	604.3	1207.5	18.75	2246
APQTsSSPPPVV	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho) S7(Phospho)	T(4): 10.8; S(5): 10.8; S(6): 89.2; S(7): 89.2	S6; S7;	S668; S669	14		0.006	0	2	692.3	1383.6	31.95	4277
RsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; T(8): 0.0	S2; S4;	S522; S524		2.37	0.008	1	2	577.7	1154.5	14.87	1711
RRPsQPpPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S8(Phospho)	S(4): 100.0; S(8): 100.0	S4; S8;	S2702; S2706		3.35	0	1	2	669.3	1337.6	12.69	1308

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
sRsPSSPELNKK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 2.3; S(6): 97.7	S1; S3; S6;	S1497; S1499; S1502		3.16	0	1	2	778.3	1555.6	26.73	3529
SRTsPAPWK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(1): 50.5; T(3): 50.5; S(4): 99.0	S4;	S1857		3.01	0	1	2	595.2	1189.5	35.52	4785
SLsGSsPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S3(Phospho) S6(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(6): 100.0	S3; S6;	S780; S783		2.91	0	0	2	590.2	1179.4	28.72	3819
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 99.9; Y(4): 0.0; S(5): 100.0	S3; S5;	S2692; S2694		2.81	0	0	2	599.2	1197.5	54.48	7863
QSHSEsPSLQSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(2): 0.0; S(4): 0.0; S(6): 96.1; S(8): 1.9; S(11): 1.9	S6;	S1083		2.75	0	0	2	697.8	1394.6	14.42	1638
SSRsPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 1.7; S(2): 1.7; S(4): 96.7; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694		2.63	0	1	2	640.3	1279.5	21.75	2712
sRsPSSPELNKK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 99.9; S(5): 50.0; S(6): 50.0	S1; S3;	S1497; S1499		2.6	0	1	2	778.3	1555.6	27.24	3603
sVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 0.0; S(10): 0.0	S1; S3;	S952; S954		2.57	0	0	2	691.2	1381.5	34.93	4699
QSHSEsPSLQSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(2): 0.0; S(4): 2.1; S(6): 95.7; S(8): 2.1; S(11): 0.1	S6;	S1083		2.52	0	0	2	697.8	1394.6	13.91	1567
sRsPLAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S2044; S2046		2.49	0	1	2	530.2	1059.5	39.52	5437
SRsVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C7(Carbamidomethyl)S3(Phospho) S5(Phospho)	S(1): 2.9; S(3): 97.1; S(5): 99.9; S(8): 0.0; S(12): 0.1	S3; S5;	S952; S954		2.45	0	1	2	812.8	1624.6	24.72	3198
AQTpPGPSLSGSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho)	T(3): 100.0; S(8): 0.0; S(10): 0.0; S(12): 0.0	T3;	T1003		2.41	0	0	2	653.8	1306.6	35.4	4766
GRsECDsPEPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S3(Phospho) S7(Phospho) S8(Phospho)	S(3): 100.0; S(7): 100.0; S(8): 100.0	S3; S7; S8;	S1478; S1482; S1483		2.41	0	1	2	794.7	1588.5	17.38	2040
SSGHsSSELsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) S10(Phospho)	S(1): 0.1; S(2): 0.1; S(5): 94.8; S(6): 2.5; S(7): 2.5; S(10): 100.0	S5; S10;	S1382; S1387		2.23	0	0	2	888.8	1776.7	37.33	5059
SGssPEVKDKPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S4(Phospho)	S(1): 2.8; S(3): 97.3; S(4): 99.9	S3; S4;	S1600; S1601		1.71	0	1	2	723.8	1446.6	12.91	1361
RSLSGssPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C9(Carbamidomethyl)S6(Phospho) S7(Phospho)	S(2): 0.3; S(4): 3.4; S(6): 96.5; S(7): 99.9	S6; S7;	S782; S783		1.67	0	1	2	668.3	1335.5	21.46	2670
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 99.9; Y(4): 0.0; S(5): 100.0	S3; S5;	S2692; S2694	42		0	0	2	599.2	1197.5	54.48	7863
SLsGSsPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S3(Phospho) S6(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(6): 100.0	S3; S6;	S780; S783	36		0	0	2	590.2	1179.4	28.72	3819
QSHSEsPSLQSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(2): 0.0; S(4): 2.1; S(6): 95.7; S(8): 2.1; S(11): 0.1	S6;	S1083	33		0	0	2	697.8	1394.6	13.91	1567
sVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 0.0; S(10): 0.0	S1; S3;	S952; S954	28		0	0	2	691.2	1381.5	34.93	4699
RPsPQPpPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S2702; S2706	27		0	0	2	591.2	1181.5	14.65	1675

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
RsLSGSsPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C9(Carbamidomethyl)S2(Phospho)S7(Phospho)	S(2): 99.9; S(4): 0.1; S(6): 0.1; S(7): 100.0	S2; S7;	S778; S783	23		0	1	2	668.3	1335.5	18.84	2262
QSHSEsPSLQSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(2): 0.0; S(4): 0.0; S(6): 96.1; S(8): 1.9; S(11): 1.9	S6;	S1083	23		0	0	2	697.8	1394.6	14.42	1638
SGssPEVKDKPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)S4(Phospho)	S(1): 2.8; S(3): 97.3; S(4): 99.9	S3; S4;	S1600; S1601	20		0	1	2	723.8	1446.6	12.91	1361
AQTpPPGSLSGSK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho)	T(3): 100.0; S(8): 0.0; S(10): 0.0; S(12): 0.0	T3;	T1003	20		0	0	2	653.8	1306.6	35.4	4766
sRsPLAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho)S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S2044; S2046	22		0.003	1	2	530.2	1059.5	39.52	5437
ARsRTpPSAPSQSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)T5(Phospho)	S(3): 100.0; T(5): 100.0; S(8): 0.0; S(11): 0.0; S(13): 0.0	S3; T5;	S2407; T2409	17		0.003	2	3	553.2	1657.7	14.39	1632
SSGHsSSELsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho)S10(Phospho)	S(1): 0.1; S(2): 0.1; S(5): 94.8; S(6): 2.5; S(7): 2.5; S(10): 100.0	S5; S10;	S1382; S1387	16		0.003	0	2	888.8	1776.7	37.33	5059
SATRPpSPER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)S8(Phospho)	S(1): 0.0; T(3): 0.0; S(6): 100.0; S(8): 100.0	S6; S8;	S351; S353	14		0.003	0	2	672.8	1344.5	16.49	1937
SATRPpSPER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)S8(Phospho)	S(1): 0.0; T(3): 0.0; S(6): 100.0; S(8): 100.0	S6; S8;	S351; S353		3.04	0.004	0	2	672.8	1344.5	16.49	1937
sRsPSSPELNKK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho)S3(Phospho)	S(1): 99.5; S(3): 99.8; S(5): 0.3; S(6): 0.3	S1; S3;	S1497; S1499		2.41	0.004	1	2	738.3	1475.6	22.64	2858
RPSQPpSPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S7(Phospho)	S(3): 0.0; S(7): 100.0	S7;	S2706	17		0.004	0	2	551.3	1101.5	13.08	1405
RPSPQPpSPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S2702; S2706		3.08	0.005	0	2	591.2	1181.5	14.65	1675
sRTsPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho)S4(Phospho)	S(1): 98.2; T(3): 3.6; S(4): 98.2; T(7): 0.0	S1; S4;	S1984; S1987		2.57	0.005	1	2	532.2	1063.4	13.28	1443
VKsSTPPRQSPsR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)S12(Phospho)	S(3): 100.0; S(4): 50.0; T(5): 50.0; S(10): 3.1; S(12): 96.9	S3; S12;	S901; S910		2.34	0.005	2	2	833.8	1666.7	12.71	1313
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)S5(Phospho)	S(1): 1.7; S(2): 1.7; S(4): 96.7; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694	19		0.007	1	2	640.3	1279.5	21.75	2712
sRTsPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho)S4(Phospho)	S(1): 98.2; T(3): 3.6; S(4): 98.2; T(7): 0.0	S1; S4;	S1984; S1987	18		0.007	1	2	532.2	1063.4	13.28	1443
VKsSTPPRQSPsR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 96.9; S(4): 50.0; T(5): 51.0; S(10): 51.0; S(12): 51.0	S3;	S901		3.57	0.009	2	3	556.2	1666.7	12.72	1314
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316		4.22	0	1	2	549.7	1098.5	15.56	1813
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316		3.9	0	1	2	549.7	1098.5	16.07	1884
ARsVsPPPKR	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316		3.17	0	2	2	627.8	1254.6	12.87	1350
SNsPLVPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(10): 0.0	S3;	S303		2.88	0	0	2	601.8	1202.6	45.88	6528
SNsPLVPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(10): 0.0	S3;	S303		2.65	0	0	2	601.8	1202.6	46.39	6607
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316		2.61	0	1	2	549.7	1098.5	15.04	1739
ARsVsPPPKR	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316	49		0	2	3	418.9	1254.6	12.65	1299
SNsPLVPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(10): 0.0	S3;	S303	40		0	0	2	601.8	1202.6	45.88	6528
ARsVsPPPKR	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316	36		0	2	2	627.8	1254.6	12.87	1350
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316	32		0	1	2	549.7	1098.5	15.56	1813
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316	25		0	1	2	549.7	1098.5	16.07	1884
SNsPLVPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(10): 0.0	S3;	S303	25		0	0	2	601.8	1202.6	46.39	6607
ARsVsPPPK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S314; S316	22		0.005	1	2	549.7	1098.5	15.04	1739

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
GSSPTPPCSPVQPsK	STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform d	C8(Carbamidomethyl)T5(Phospho) S14(Phospho)	S(2): 0.1; S(3): 0.1; T(5): 99.8; S(9): 0.0; S(14): 100.0	T5; S14;	T316; S325		1.51	0	0	2	843.3	1685.7	38.44	5249
GSSPTPPCSPVQPsK	STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform d	C8(Carbamidomethyl)T5(Phospho) S14(Phospho)	S(2): 0.1; S(3): 0.1; T(5): 99.8; S(9): 0.0; S(14): 100.0	T5; S14;	T316; S325	11		0.005	0	2	843.3	1685.7	38.44	5249
QVAEQGGDLsPAANR	STK10	6793	serine/threonine-protein kinase 10	S10(Phospho)	S(10): 100.0	S10;	S438		2.17	0	0	2	796.9	1592.7	32.42	4345
QVAEQGGDLsPAANR	STK10	6793	serine/threonine-protein kinase 10	S10(Phospho)	S(10): 100.0	S10;	S438	35		0	0	2	796.9	1592.7	32.42	4345
LSEEAECNPStPSK	STK10	6793	serine/threonine-protein kinase 10	C7(Carbamidomethyl) T12(Phospho)	S(2): 0.0; S(11): 3.8; T(12): 92.4; S(14): 3.8	T12;	T952		1.62	0.005	0	2	863.4	1725.7	30.52	4085
AKNsPPQAPSTR	STK11IP	114790	serine/threonine-protein kinase 11-interacting protein	S4(Phospho)	S(4): 100.0; S(10): 0.0; T(11): 0.0	S4;	S761		1.79	0	1	2	667.3	1333.6	15.64	1827
AKNsPPQAPSTR	STK11IP	114790	serine/threonine-protein kinase 11-interacting protein	S4(Phospho)	S(4): 100.0; S(10): 0.0; T(11): 0.0	S4;	S761	43		0	1	2	667.3	1333.6	15.64	1827
EVDQDDEENsEEDEMDSGTMVR	STK4	6789	serine/threonine-protein kinase 4	M15(Oxidation) M20(Oxidation) S10(Phospho)	S(10): 94.5; S(17): 5.2; T(19): 0.3	S10;	S320		2.02	0	0	3	891.0	2670.9	32.44	4348
EVDQDDEENsEEDEMDSGTMVR	STK4	6789	serine/threonine-protein kinase 4	M15(Oxidation) M20(Oxidation) S10(Phospho)	S(10): 94.5; S(17): 5.2; T(19): 0.3	S10;	S320	13		0.003	0	3	891.0	2670.9	32.44	4348
SSSVtSIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 50.0; T(5): 50.0; S(6): 100.0; S(11): 0.0	S6;	S749		2.38	0	1	2	728.3	1455.6	28.56	3798
SSSVtSIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	T5(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 1.5; T(5): 98.5; S(6): 100.0; S(11): 0.0	T5; S6;	T748; S749		2.37	0	1	2	728.3	1455.6	28.55	3796
SSSVtSIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	T5(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 1.5; T(5): 98.5; S(6): 100.0; S(11): 0.0	T5; S6;	T748; S749	54		0	1	2	728.3	1455.6	28.55	3796
SSSVtSIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 50.0; T(5): 50.0; S(6): 100.0; S(11): 0.0	S6;	S749	47		0	1	2	728.3	1455.6	28.56	3798
GSGDI sSDSIDHSPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 50.0; S(9): 50.0; S(13): 0.0	S6;	S141		1.97	0	0	2	866.8	1732.6	32.93	4411
GSGDI sSDSIDHSPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 50.0; S(9): 50.0; S(13): 0.0	S6;	S141	32		0	0	2	866.8	1732.6	32.93	4411
ASDPQsPPQVSR	TAOK1	57551	serine/threonine-protein kinase TAO1 isoform 2	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(11): 0.0	S6;	S421		2.16	0	0	2	674.8	1348.6	27.4	3625
ASDPQsPPQVSR	TAOK1	57551	serine/threonine-protein kinase TAO1 isoform 2	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(11): 0.0	S6;	S421	39		0	0	2	674.8	1348.6	27.4	3625
NDsPTQIPVSSDVCR	TBC1D15	64786	TBC1 domain family member 15 isoform 3	C14(Carbamidomethyl) S3(Phospho)	S(3): 100.0; T(5): 0.0; S(10): 0.0; S(11): 0.0	S3;	S658		2.95	0	0	2	877.9	1754.7	53.06	7634
NDsPTQIPVSSDVCR	TBC1D15	64786	TBC1 domain family member 15 isoform 3	C14(Carbamidomethyl) S3(Phospho)	S(3): 100.0; T(5): 0.0; S(10): 0.0; S(11): 0.0	S3;	S658	42		0	0	2	877.9	1754.7	53.06	7634
RAVSEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C7(Carbamidomethyl) S9(Phospho)	S(4): 0.0; S(9): 100.0	S9;	S460		1.9	0.004	1	2	937.9	1874.7	35.45	4772
RAVSEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C7(Carbamidomethyl) S9(Phospho)	S(4): 0.0; S(9): 100.0	S9;	S460	29		0.005	1	2	937.9	1874.7	35.45	4772
TsSTNEDEDLNPEQK	TCF12	6938	transcription factor 12 isoform e	S2(Phospho)	T(1): 3.1; S(2): 90.7; S(3): 3.1; T(4): 3.1	S2;	S322		1.09	0.001	0	2	893.9	1786.7	33.48	4488
LNASPAAREEA tSPGAK	TCF20	6942	transcription factor 20 isoform 2	T12(Phospho) S13(Phospho)	S(4): 5.5; T(12): 94.9; S(13): 99.7	T12; S13;	T582; S583		2.97	0.005	1	3	610.6	1829.8	29.6	3948
TSQVGAASAPAKesPR	TCOF1	6949	treacle protein isoform b	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S304		3.01	0	1	2	818.9	1636.8	19.52	2378
AALAPAKesPR	TCOF1	6949	treacle protein isoform b	S9(Phospho)	S(9): 100.0	S9;	S829		2.92	0	1	2	595.8	1190.6	20.24	2491
KLsGDQPAAR	TCOF1	6949	treacle protein isoform b	S3(Phospho)	S(3): 100.0	S3;	S1273		2.78	0	1	2	561.8	1122.5	13.99	1579

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
AALAPAKesPR	TCOF1	6949	treacle protein isoform b	S9(Phospho)	S(9): 100.0	S9;	S829	60		0	1	2	595.8	1190.6	20.24	2491
TSQVGAASAPAKesPR	TCOF1	6949	treacle protein isoform b	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S304	51		0	1	2	818.9	1636.8	19.52	2378
KLsGDQPAAR	TCOF1	6949	treacle protein isoform b	S3(Phospho)	S(3): 100.0	S3;	S1273	24		0	1	2	561.8	1122.5	13.99	1579
TAPsSPLTSPSDTR	TEX2	55852	testis-expressed sequence 2 protein isoform 2	S5(Phospho)	T(1): 3.7; S(4): 3.7; S(5): 92.6; T(8): 48.1; S(9): 48.1; S(11): 1.9; T(13): 1.9	S5;	S266	20		0	0	2	788.8	1576.6	45.02	6371
TAPsSPLTSPSDTR	TEX2	55852	testis-expressed sequence 2 protein isoform 2	S5(Phospho)	T(1): 3.7; S(4): 3.7; S(5): 92.6; T(8): 48.1; S(9): 48.1; S(11): 1.9; T(13): 1.9	S5;	S266		1.78	0.001	0	2	788.8	1576.6	45.02	6371
SYMNPGDQsPADSNK	TFAP2C	7022	transcription factor AP-2 gamma	M3(Oxidation) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(9): 100.0; S(13): 0.0	S9;	S434		2.44	0	0	2	853.8	1706.6	22.63	2857
SYMNPGDQsPADSNK	TFAP2C	7022	transcription factor AP-2 gamma	M3(Oxidation) S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(9): 100.0; S(13): 0.0	S9;	S434	22		0	0	2	853.8	1706.6	22.63	2857
DsPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 4 precursor	S2(Phospho)	S(2): 93.6; S(4): 3.2; S(6): 0.0; S(7): 3.2; T(12): 0.0; T(16): 0.0	S2;	S66		4.71	0	1	3	690.3	2068.9	20.24	2492
DsPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 4 precursor	S2(Phospho)	S(2): 93.6; S(4): 3.2; S(6): 0.0; S(7): 3.2; T(12): 0.0; T(16): 0.0	S2;	S66	30		0	1	3	690.3	2068.9	20.24	2492
sVASsQPAKPTK	TJP1	7082	tight junction protein ZO-1 isoform b	S1(Phospho) S5(Phospho)	S(1): 97.2; S(4): 2.9; S(5): 99.9; T(11): 0.0	S1; S5;	S175; S179		2.36	0	0	2	680.8	1360.6	17.98	2130
sVASsQPAKPTK	TJP1	7082	tight junction protein ZO-1 isoform b	S1(Phospho) S5(Phospho)	S(1): 97.2; S(4): 2.9; S(5): 99.9; T(11): 0.0	S1; S5;	S175; S179	17		0.002	0	2	680.8	1360.6	17.98	2130
sREDLSAQPVQTK	TJP1	7082	tight junction protein ZO-1 isoform b	S1(Phospho)	S(1): 100.0; S(6): 0.0; T(12): 0.0	S1;	S617	16		0.007	1	2	769.9	1538.7	27.14	3588
GRsIDQDYER	TJP2	9414	tight junction protein ZO-2 isoform 6	S3(Phospho)	S(3): 100.0; Y(8): 0.0	S3;	S244		2.94	0	1	2	659.8	1318.5	22.94	2908
GRsIDQDYER	TJP2	9414	tight junction protein ZO-2 isoform 6	S3(Phospho)	S(3): 100.0; Y(8): 0.0	S3;	S244	23		0	1	2	659.8	1318.5	22.94	2908
DAPTSPASVASSSTPSSK	TLE3	7090	transducin-like enhancer protein 3 isoform g	S5(Phospho)	T(4): 2.2; S(5): 97.8; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; T(15): 0.0; S(17): 0.0; S(18): 0.0	S5;	S230		3.22	0	0	2	922.4	1843.8	38.87	5325
ESSANNSVsPSESLR	TLE3	7090	transducin-like enhancer protein 3 isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.0; S(9): 100.0; S(11): 0.0; S(13): 0.0	S9;	S147		2.48	0	0	2	822.4	1643.7	36.15	4880
ESSANNSVsPSESLR	TLE3	7090	transducin-like enhancer protein 3 isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.1; S(9): 99.9; S(11): 0.1; S(13): 0.0	S9;	S147		2.45	0	0	2	822.4	1643.7	35.64	4809
ESSANNSVsPSESLR	TLE3	7090	transducin-like enhancer protein 3 isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.0; S(9): 100.0; S(11): 0.0; S(13): 0.0	S9;	S147	56		0	0	2	822.4	1643.7	36.15	4880
DAPTSPASVASSSTPSSK	TLE3	7090	transducin-like enhancer protein 3 isoform g	S5(Phospho)	T(4): 2.2; S(5): 97.8; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; T(15): 0.0; S(17): 0.0; S(18): 0.0	S5;	S230	51		0	0	2	922.4	1843.8	38.87	5325
ESSANNSVsPSESLR	TLE3	7090	transducin-like enhancer protein 3 isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.1; S(9): 99.9; S(11): 0.1; S(13): 0.0	S9;	S147	50		0	0	2	822.4	1643.7	35.64	4809
DAPTSVASVASSSTPSSK	TLE3	7090	transducin-like enhancer protein 3 isoform g	T15(Phospho)	T(4): 0.0; S(5): 0.0; S(8): 0.0; S(11): 1.5; S(12): 32.9; S(13): 32.9; S(14): 32.9; T(15): 95.1; S(17): 4.4; S(18): 0.2	T15;	T240	13		0.005	0	2	962.4	1923.8	44.84	6341
KVATPPNQNK	TMEM214	54867	transmembrane protein 214 isoform 2	T4(Phospho)	T(4): 100.0	T4;	T97		2.02	0.003	1	2	652.8	1304.6	12.85	1345
KVATPPNQNK	TMEM214	54867	transmembrane protein 214 isoform 2	T4(Phospho)	T(4): 100.0	T4;	T97	23		0.003	1	2	652.8	1304.6	12.85	1345
NAEREQEsEEEM	TMEM45A	55076	transmembrane protein 45A	M12(Oxidation) S8(Phospho)	S(8): 100.0	S8;	S271	25		0	1	2	788.8	1576.5	13.06	1401
SVSEINsDDELSGK	TMF1	7110	TATA element modulatory factor	S7(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 100.0; S(12): 0.0	S7;	S344		3.09	0	0	2	780.3	1559.6	43.28	6062
SVSEINsDDELSGK	TMF1	7110	TATA element modulatory factor	S7(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 100.0; S(12): 0.0	S7;	S344	46		0	0	2	780.3	1559.6	43.28	6062
SStPLPTISSSAENTR	TMPO	7112	thymopoietin isoform gamma	T3(Phospho)	S(1): 1.6; S(2): 1.6; T(3): 96.9; T(7): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; T(15): 0.0	T3;	T160		2.22	0	0	2	864.4	1727.8	51.36	7333
SStPLPTISSSAENTR	TMPO	7112	thymopoietin isoform gamma	T3(Phospho)	S(1): 1.6; S(2): 1.6; T(3): 96.9; T(7): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; T(15): 0.0	T3;	T160	29		0	0	2	864.4	1727.8	51.36	7333
VPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(14): 0.0	S3; S4;	S1620; S1621		3.67	0	0	2	923.9	1846.7	53.7	7734

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
VPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(14): 0.0	S3; S4;	S1620; S1621		3.66	0	0	2	923.9	1846.7	54.22	7821
AsPEPPGPESSSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0	S2;	S672		2.13	0	0	2	689.3	1377.6	26.05	3420
NRsAEELGELAESK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; S(12): 0.0	S3;	S1666		2.12	0	1	2	750.3	1499.6	20.67	2552
VPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(14): 0.0	S3; S4;	S1620; S1621	40		0	0	2	923.9	1846.7	53.7	7734
VPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(14): 0.0	S3; S4;	S1620; S1621	37		0	0	2	923.9	1846.7	54.22	7821
AsPEPPGPESSSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0	S2;	S672	31		0	0	2	689.3	1377.6	26.05	3420
NRsAEELGELAESK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; S(12): 0.0	S3;	S1666	11		0.003	1	2	750.3	1499.6	20.67	2552
GVGSGPHPPDTQQPSPSK	TNS3	64759	tensin-3	S15(Phospho)	S(4): 0.0; T(11): 0.0; S(15): 99.8; S(17): 0.2	S15;	S660		1.64	0	0	2	926.9	1852.8	26.2	3443
GVGSGPHPPDTQQPSPSK	TNS3	64759	tensin-3	S15(Phospho)	S(4): 0.0; T(11): 0.0; S(15): 99.8; S(17): 0.2	S15;	S660	11		0	0	2	926.9	1852.8	26.2	3443
AADsDDGAVSAPAAADGGGVSK	TOE1	114034	target of EGR1 protein 1	S4(Phospho)	S(4): 100.0; S(10): 0.0; S(15): 0.0; S(20): 0.0	S4;	S5	27		0	0	2	964.4	1927.8	37.2	5039
VPDEEENEsDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106		4.45	0	1	3	744.0	2229.9	19.74	2408
VPDEEENEsDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106	38		0	1	3	744.0	2229.9	19.74	2408
SELGNQsPSTSSR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S7(Phospho)	S(1): 0.0; S(7): 100.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(12): 0.0	S7;	S315		3.03	0	0	2	715.3	1429.6	22.17	2780
SELGNQsPSTSSR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S7(Phospho)	S(1): 0.0; S(7): 100.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(12): 0.0	S7;	S315	54		0	0	2	715.3	1429.6	22.17	2780
TSSGTsLSAMHSSGSSGK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	M10(Oxidation) S6(Phospho)	T(1): 7.2; S(2): 7.2; S(3): 49.8; T(5): 45.4; S(6): 90.0; S(8): 0.3; S(12): 0.0; S(13): 0.0; S(15): 0.0; S(16): 0.0	S6;	S1320		1.48	0	0	2	922.8	1844.7	17.37	2038
TSSGTsLSAMHSSGSSGK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	M10(Oxidation) S6(Phospho)	T(1): 7.2; S(2): 7.2; S(3): 49.8; T(5): 45.4; S(6): 90.0; S(8): 0.3; S(12): 0.0; S(13): 0.0; S(15): 0.0; S(16): 0.0	S6;	S1320	15		0	0	2	922.8	1844.7	17.37	2038
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; Y(6): 0.0; Y(7): 0.0; S(8): 0.0	S2; S4;	S158; S160		3.24	0	1	2	636.7	1272.5	25.33	3304
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; Y(6): 0.0; Y(7): 0.0; S(8): 0.0	S2; S4;	S158; S160		2.98	0	1	2	636.7	1272.5	24.82	3219
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; Y(6): 0.0; Y(7): 0.0; S(8): 0.0	S2; S4;	S158; S160	31		0	1	2	636.7	1272.5	24.82	3219
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 3	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; Y(6): 0.0; Y(7): 0.0; S(8): 0.0	S2; S4;	S158; S160	28		0	1	2	636.7	1272.5	25.33	3304
LDSQPQETsPELPR	TRAFD1	10906	TRAF-type zinc finger domain-containing protein 1	S9(Phospho)	S(3): 0.0; T(8): 1.9; S(9): 98.1	S9;	S415		2.69	0	0	2	838.9	1676.8	47.99	6836
LDSQPQETsPELPR	TRAFD1	10906	TRAF-type zinc finger domain-containing protein 1	S9(Phospho)	S(3): 0.0; T(8): 1.9; S(9): 98.1	S9;	S415	35		0	0	2	838.9	1676.8	47.99	6836
AQPGsPESSGQPK	TRERF1	55809	transcriptional-regulating factor 1 isoform 2	S5(Phospho)	S(5): 100.0; S(8): 0.0; S(9): 0.0	S5;	S491		2.18	0	0	2	675.3	1349.6	15.44	1799
AQPGsPESSGQPK	TRERF1	55809	transcriptional-regulating factor 1 isoform 2	S5(Phospho)	S(5): 100.0; S(8): 0.0; S(9): 0.0	S5;	S491	34		0	0	2	675.3	1349.6	15.44	1799
ETEEQSDsSAEQGDPAEGEK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 99.3; S(7): 0.3; S(9): 0.3	T2;	T55		1.44	0	0	2	1079.9	2158.8	21.69	2701
TSYQPsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 2.1; S(7): 97.9	S7;	S489		2.01	0.001	0	2	580.2	1159.5	21.23	2629
TSYQPsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 2.1; S(7): 97.9	S7;	S489	19		0.003	0	2	580.2	1159.5	21.23	2629
VSDQNsvPVLPK	USP24	23358	ubiquitin carboxyl-terminal hydrolase 24	S6(Phospho)	S(2): 0.0; S(6): 100.0	S6;	S2047		2.52	0	0	2	632.3	1263.6	37.59	5099
VSDQNsvPVLPK	USP24	23358	ubiquitin carboxyl-terminal hydrolase 24	S6(Phospho)	S(2): 0.0; S(6): 100.0	S6;	S2047	36		0	0	2	632.3	1263.6	37.59	5099
VQEHEDsGDsEVENEAK	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S121; S124		3.93	0	0	3	687.9	2061.7	27.35	3617
VQEHEDsGDsEVENEAK	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S121; S124		2.41	0	0	2	1031.4	2061.7	27.28	3608



Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
KTSSDDEsEEDEDDLLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S8(Phospho)	T(2): 34.9; S(3): 34.9; S(4): 34.9; S(8): 95.4	S8;	S210		1.91	0	1	2	1135.9	2270.8	51.47	7351
VQEHEDsGDsEVENeAK	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S121; S124		1.78	0	0	2	1031.4	2061.7	27.8	3688
KTSSDDEsEEDEDDLLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S8(Phospho)	T(2): 34.9; S(3): 34.9; S(4): 34.9; S(8): 95.4	S8;	S210	32		0	1	2	1135.9	2270.8	51.47	7351
VQEHEDsGDsEVENeAK	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S121; S124	17		0	0	2	1031.4	2061.7	27.28	3608
VQEHEDsGDsEVENeAK	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S121; S124	27		0.002	0	3	687.9	2061.7	27.35	3617
LQAKesPQR	WDR43	23160	WD repeat-containing protein 43	S6(Phospho)	S(6): 100.0	S6;	S77		3.13	0	1	2	568.8	1136.5	12.73	1317
LQAKesPQR	WDR43	23160	WD repeat-containing protein 43	S6(Phospho)	S(6): 100.0	S6;	S77	43		0	1	2	568.8	1136.5	12.73	1317
TTPTATGEQsPGAR	WWP2	11060	NEDD4-like E3 ubiquitin-protein ligase WWP2 isoform WWP2-N	S9(Phospho)	T(1): 0.0; T(2): 0.0; T(5): 0.0; S(9): 100.0	S9;	S211		2.55	0	0	2	676.8	1352.6	17.14	2010
TTPTATGEQsPGAR	WWP2	11060	NEDD4-like E3 ubiquitin-protein ligase WWP2 isoform WWP2-N	S9(Phospho)	T(1): 0.0; T(2): 0.0; T(5): 0.0; S(9): 100.0	S9;	S211	52		0	0	2	676.8	1352.6	17.14	2010
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		4.55	0	1	2	988.9	1976.7	28.82	3836
NsPGSQVASNPR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S2(Phospho)	S(2): 100.0; S(5): 0.0; S(9): 0.0	S2;	S448		2.92	0	0	2	647.3	1293.6	19.54	2381
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		2.21	0	1	2	988.9	1976.7	28.32	3756
AEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S499; S501		2.18	0	0	2	924.8	1848.6	38.98	5344
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		1.82	0	1	2	988.9	1976.7	29.34	3902
NsPGSQVASNPR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S2(Phospho)	S(2): 100.0; S(5): 0.0; S(9): 0.0	S2;	S448	82		0	0	2	647.3	1293.6	19.54	2381
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	51		0	1	2	988.9	1976.7	28.82	3836
AEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S499; S501	22		0	0	2	924.8	1848.6	38.98	5344
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2 isoform 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	13		0.003	1	2	988.9	1976.7	28.32	3756
NEGsESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 97.9; S(6): 2.1	S4;	S174		2.71	0	0	2	834.3	1667.7	16.73	1962
NEGsESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 99.9; S(6): 0.1	S4;	S174		2.7	0	0	2	834.3	1667.7	17.29	2029
NEGsESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 97.9; S(6): 2.1	S4;	S174	27		0	0	2	834.3	1667.7	16.73	1962
NEGsESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 99.9; S(6): 0.1	S4;	S174	19		0	0	2	834.3	1667.7	17.29	2029
GGAPDPSPGATATPGAPAQPsPDAR	ZBTB7A	51341	zinc finger and BTB domain-containing protein 7A	S22(Phospho)	S(7): 0.0; T(11): 0.0; T(13): 0.0; S(21): 0.1; S(22): 99.9	S22;	S526		4.78	0	0	3	804.0	2410.1	44.41	6253
GGAPDPSPGATATPGAPAQPsPDAR	ZBTB7A	51341	zinc finger and BTB domain-containing protein 7A	S22(Phospho)	S(7): 0.0; T(11): 0.0; T(13): 0.0; S(21): 0.1; S(22): 99.9	S22;	S526	28		0	0	3	804.0	2410.1	44.41	6253
sKGSDDISDEEAQQsK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S16(Phospho)	S(1): 99.8; S(5): 0.2; S(8): 0.0; S(16): 100.0	S1; S16;	S1010; S1025		1.68	0.001	1	2	977.9	1954.7	25.51	3336
STsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho) S10(Phospho)	S(1): 3.0; T(2): 3.0; S(3): 94.0; S(10): 99.8; S(13): 0.1; S(14): 0.1	S3; S10;	S318; S325	16		0.003	0	2	854.8	1708.7	15.07	1743
SCTPsPDQISHR	ZC3HAV1	56829	zinc finger CCCH-type antiviral protein 1 isoform 2	C2(Carbamidomethyl)T3(Phospho) S5(Phospho)	S(1): 2.0; T(3): 98.0; S(5): 100.0; S(10): 0.0	T3; S5;	T273; S275		1.81	0	0	2	772.8	1544.6	31.89	4267
SCTPsPDQISHR	ZC3HAV1	56829	zinc finger CCCH-type antiviral protein 1 isoform 2	C2(Carbamidomethyl)T3(Phospho) S5(Phospho)	S(1): 2.0; T(3): 98.0; S(5): 100.0; S(10): 0.0	T3; S5;	T273; S275	34		0	0	2	772.8	1544.6	31.89	4267
SQDATFsPGSEQAeK	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 0.0	S7;	S314		2.24	0	0	2	831.3	1661.7	35.39	4763
SQDATFsPGSEQAeK	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 0.0	S7;	S314	39		0	0	2	831.3	1661.7	35.39	4763

Phosphopeptide	Gene Symbol	Gene ID	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSite (Peptide)	PhosphoSite (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan #
QSPSGSEQLVR	ZNF185	7739	zinc finger protein 185 isoform 3	S3(Phospho)	S(2): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0	S3;	S454		3.01	0	0	2	677.8	1354.6	33.04	4426
GGQGDPAVPAQQPADPSTPER	ZNF185	7739	zinc finger protein 185 isoform 3	S17(Phospho)	S(17): 95.7; T(18): 4.3	S17;	S447		2.05	0	0	2	1078.0	2155.0	39.87	5497
QSPSGSEQLVR	ZNF185	7739	zinc finger protein 185 isoform 3	S3(Phospho)	S(2): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0	S3;	S454	52		0	0	2	677.8	1354.6	33.04	4426
RVSPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81		2.92	0	1	2	528.2	1055.4	21.03	2598
RVSPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81	29		0	1	2	528.2	1055.4	21.03	2598
RVSPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81	26		0	1	2	528.2	1055.4	21.54	2682
RVSPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81		3.07	0.001	1	2	528.2	1055.4	21.54	2682
LVEPHsPsSSK	ZNF609	23060	zinc finger protein 609	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 99.9; S(10): 0.0; S(11): 0.0	S6; S8;	S576; S578		2.96	0	0	2	712.8	1424.6	25.19	3284
GPPAsSPAPAPK	ZYX	7791	zyxin	S5(Phospho)	S(5): 98.0; S(6): 2.0	S5;	S258		2.73	0	0	2	578.8	1156.5	21.98	2744
FsPGAPGGSGSQPNQK	ZYX	7791	zyxin	S2(Phospho)	S(2): 100.0; S(9): 0.0; S(11): 0.0	S2;	S281		2.16	0	0	2	798.3	1595.7	31.15	4167
FsPGAPGGSGSQPNQK	ZYX	7791	zyxin	S2(Phospho)	S(2): 100.0; S(9): 0.0; S(11): 0.0	S2;	S281	20		0.003	0	2	798.3	1595.7	31.15	4167
GPPAsSPAPAPK	ZYX	7791	zyxin	S5(Phospho)	S(5): 98.0; S(6): 2.0	S5;	S258	13		0.005	0	2	578.8	1156.5	21.98	2744