

Supplementary Table S2: A list of all the phosphoPSMs identified from 100 µg 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#
IYHLPDAEsDEDEDFKEQTR	SEPT2	4735	septin-2 isoform a	S9(Phospho)	Y(2): 0.0; S(9): 100.0; T(19): 0.0	S9;	S218	20		0	1	3	839.7	2517	53.28	10423
IYHLPDAEsDEDEDFKEQTR	SEPT2	4735	septin-2 isoform a	S9(Phospho)	Y(2): 0.0; S(9): 100.0; T(19): 0.0	S9;	S218		4.05	0	1	3	839.7	2517	53.28	10423
sFEVEEVETPNSTPPR	SEPT9	10801	septin-9 isoform g	S1(Phospho)	S(1): 100.0; T(9): 0.0; S(12): 0.0; T(13): 0.0	S1;	S11	35		0	0	2	949.4	1898	61.8	12258
SFEVEEVETPNSTPPR	SEPT9	10801	septin-9 isoform g	T9(Phospho) T13(Phospho)	S(1): 0.0; T(9): 96.3; S(12): 7.4; T(13): 96.3	T9; T13;	T19; T23	23		0	0	2	989.4	1978	67.28	13569
sFEVEEVETPNSTPPR	SEPT9	10801	septin-9 isoform g	S1(Phospho)	S(1): 100.0; T(9): 0.0; S(12): 0.0; T(13): 0.0	S1;	S11		3.6	0	0	2	949.4	1898	61.8	12258
SFEVEEVETPNSTPPR	SEPT9	10801	septin-9 isoform g	T9(Phospho) T13(Phospho)	S(1): 0.0; T(9): 96.3; S(12): 7.4; T(13): 96.3	T9; T13;	T19; T23		2.76	0	0	2	989.4	1978	67.28	13569
HVDSLQRsPK	SEPT9	10801	septin-9 isoform g	S9(Phospho)	S(4): 0.0; S(6): 0.0; S(9): 100.0	S9;	S66		4.57	0.003	1	3	445.2	1334	14.22	2106
HVDSLQRsPK	SEPT9	10801	septin-9 isoform g	S9(Phospho)	S(4): 0.0; S(6): 0.0; S(9): 100.0	S9;	S66	19		0.004	1	3	445.2	1334	14.22	2106
sFEVEEVETPNSTPPR	SEPT9	10801	septin-9 isoform g	S1(Phospho) T9(Phospho) T13(Phospho)	S(1): 100.0; T(9): 100.0; S(12): 5.1; T(13): 94.9	S1; T9; T13;	S11; T19; T23		2.04	0.005	0	2	1029	2058	86.49	17322
TTCMSSQGsDDEQIKR	SEPT10	151011	septin-10 isoform 1	C3(Carbamidomethyl) S9(Phospho)	T(1): 0.0; T(2): 0.0; S(5): 0.0; S(6): 0.0; S(9): 100.0	S9;	S28	34		0	1	3	641.6	1923	23.44	4063
TTCMSSQGsDDEQIKR	SEPT10	151011	septin-10 isoform 1	C3(Carbamidomethyl) S9(Phospho)	T(1): 0.0; T(2): 0.0; S(5): 0.0; S(6): 0.0; S(9): 100.0	S9;	S28		4.04	0	1	3	641.6	1923	23.44	4063
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		3.41	0	0	2	615.3	1230	48.4	9369
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	18		0.005	0	2	615.3	1230	48.4	9369
VGSLtPPSSPK	AAK1	22848	AP2-associated protein kinase 1	T5(Phospho)	S(3): 3.5; T(5): 96.5; S(8): 50.0; S(9): 50.0	T5;	T620		2.35	0.008	0	2	615.3	1230	47.86	9255
YLVDGtKPNAGsEEIssEDELVEEK	AATF	26574	protein AATF	S12(Phospho) S16(Phospho) S17(Phospho)	Y(1): 1.5; T(6): 15.4; S(12): 91.9; S(16): 91.9; S(17): 99.2	S12; S16; S17;	S316; S320; S321	15		0	0	3	1032	3093	76.16	15368
YLVDGtKPNAGsEEIssEDELVEEK	AATF	26574	protein AATF	T6(Phospho) S12(Phospho) S17(Phospho)	Y(1): 7.4; T(6): 93.2; S(12): 98.9; S(16): 7.4; S(17): 93.2	T6; S12; S17;	T310; S316; S321	13		0	0	3	1032	3093	75.65	15283
YLVDGtKPNAGsEEIssEDELVEEK	AATF	26574	protein AATF	S12(Phospho) S16(Phospho) S17(Phospho)	Y(1): 1.5; T(6): 15.4; S(12): 91.9; S(16): 91.9; S(17): 99.2	S12; S16; S17;	S316; S320; S321		2.51	0	0	3	1032	3093	76.16	15368
YLVDGtKPNAGsEEIssEDELVEEK	AATF	26574	protein AATF	T6(Phospho) S12(Phospho) S17(Phospho)	Y(1): 7.4; T(6): 93.2; S(12): 98.9; S(16): 7.4; S(17): 93.2	T6; S12; S17;	T310; S316; S321		2.03	0	0	3	1032	3093	75.65	15283
yLVDGtKPNAGSEEEIssEDELVEEK	AATF	26574	protein AATF	Y1(Phospho) S16(Phospho) S17(Phospho)	Y(1): 98.8; T(6): 20.6; S(12): 8.5; S(16): 86.1; S(17): 86.1	Y1; S16; S17;	Y305; S320; S321		2.76	0.004	1	3	1074	3221	63.23	12616
DNEESEQPPVPGtPTLR	ABCC4	10257	multidrug resistance-associated protein 4 isoform 4	T13(Phospho)	S(5): 0.0; T(13): 99.9; T(15): 0.1	T13;	T571		2.51	0.001	0	2	973.4	1946	58.76	11629
DNEESEQPPVPGtPTLR	ABCC4	10257	multidrug resistance-associated protein 4 isoform 4	T13(Phospho)	S(5): 0.0; T(13): 99.9; T(15): 0.1	T13;	T571	25		0.006	0	2	973.4	1946	58.76	11629
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	50		0	1	3	854.7	2562	20.21	3382
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	47		0	0	2	1217	2434	25.43	4484
KLSVPtsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho) S7(Phospho)	S(3): 0.0; T(6): 100.0; S(7): 100.0	T6; S7;	T108; S109	46		0	1	3	752	2254	49.74	9648

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#
KAEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228	45		0	1	2	1281	2562	20.26	3391
KAEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228	45		0	1	3	854.7	2562	20.86	3519
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109	41		0	1	3	778.7	2334	55.1	10820
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) S7(Phospho)	S(3): 99.8; T(6): 4.2; S(7): 95.9	S3; S7;	S105; S109	32		0	1	3	752	2254	50.28	9764
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109	32		0	0	2	1063	2126	57.66	11378
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109	31		0	0	3	709.3	2126	57.62	11369
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109	30		0	1	3	778.7	2334	54.57	10711
KAEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228	28		0	1	2	1281	2562	20.38	3417
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109	28		0	1	2	1167	2334	54.79	10758
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.1; T(5): 99.9; S(6): 100.0	T5; S6;	T108; S109	28		0	0	3	709.3	2126	57.12	11265
AEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0	S5;	S228	27		0	0	3	812	2434	25.53	4505
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(2): 0.0; T(5): 0.1; S(6): 99.9	S6;	S109	27		0	0	3	682.7	2046	51.3	9978
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109	27		0	0	2	1063	2126	57.14	11271
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho)	S(3): 0.0; T(6): 97.6; S(7): 2.4	T6;	T108	25		0	1	3	725.4	2174	45.33	8724
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho) S7(Phospho)	S(3): 0.0; T(6): 100.0; S(7): 100.0	T6; S7;	T108; S109	24		0	1	3	752	2254	49.22	9540
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(2): 0.0; T(5): 0.1; S(6): 99.9	S6;	S109	21		0	0	2	1023	2046	51.44	10007
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109	16		0	1	3	778.7	2334	55.63	10932
QQPPEPEWIGDGESTsPSDKVVK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S16(Phospho)	S(14): 3.2; T(15): 3.2; S(16): 93.6; S(18): 0.0	S16;	S22	14		0	1	3	864.1	2590	58.33	11515
KAEQGsEEEEGESEEEEEGGESKADDPY AHLK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0; Y(28): 0.0; S(32): 0.0	S6;	S228	13		0	2	4	915.6	3659	37.76	7099
KAEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		6.92	0	1	3	854.7	2562	20.21	3382
KAEQGsEEEEGESEEEEEGGESKADDPY AHLK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0; Y(28): 0.0; S(32): 0.0	S6;	S228		6.15	0	2	4	915.6	3659	37.76	7099
KAEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		4.75	0	1	3	854.7	2562	20.86	3519
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho) S7(Phospho)	S(3): 0.0; T(6): 100.0; S(7): 100.0	T6; S7;	T108; S109		4.64	0	1	3	752	2254	49.74	9648
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109		4.61	0	1	3	778.7	2334	55.1	10820
AEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0	S5;	S228		4.4	0	0	3	812	2434	25.53	4505
AEQGsEEEEGESEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0	S5;	S228		4.08	0	0	2	1217	2434	25.43	4484
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho) S7(Phospho)	S(3): 0.0; T(6): 100.0; S(7): 100.0	T6; S7;	T108; S109		4.07	0	1	3	752	2254	49.22	9540

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#
KAEQGSEEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		4.05	0	1	2	1281	2562	20.26	3391
KAEQGSEEEEEGEEEEEGGESK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(6): 100.0; S(22): 0.0	S6;	S228		3.91	0	1	2	1281	2562	20.38	3417
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109		3.74	0	1	3	778.7	2334	54.57	10711
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) S7(Phospho)	S(3): 99.8; T(6): 4.2; S(7): 95.9	S3; S7;	S105; S109		3.74	0	1	3	752	2254	50.28	9764
QQPPEWIGDGESTsPSDKVVK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S16(Phospho)	S(14): 3.2; T(15): 3.2; S(16): 93.6; S(18): 0.0	S16;	S22		3.46	0	1	3	864.1	2590	58.33	11515
LSVPtsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109		3.27	0	0	3	709.3	2126	57.62	11369
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(2): 0.0; T(5): 0.1; S(6): 99.9	S6;	S109		2.99	0	0	3	682.7	2046	51.3	9978
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.1; T(5): 99.9; S(6): 100.0	T5; S6;	T108; S109		2.89	0	0	3	709.3	2126	57.12	11265
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T6(Phospho)	S(3): 0.0; T(6): 97.6; S(7): 2.4	T6;	T108		2.8	0	1	3	725.4	2174	45.33	8724
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109		2.68	0	1	3	778.7	2334	55.63	10932
AEQGSEEEEEGEEEEEGGESKADDPYAHL SK	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S5(Phospho)	S(5): 100.0; S(21): 0.0; Y(27): 0.0; S(31): 0.0	S5;	S228		2.4	0	1	3	1178	3531	41.28	7842
KLsVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S3(Phospho) T6(Phospho) S7(Phospho)	S(3): 100.0; T(6): 100.0; S(7): 100.0	S3; T6; S7;	S105; T108; S109		2.38	0	1	2	1167	2334	54.79	10758
LSVPTsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	S6(Phospho)	S(2): 0.0; T(5): 0.1; S(6): 99.9	S6;	S109		2.3	0	0	2	1023	2046	51.44	10007
LSVPtsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109		2.27	0	0	2	1063	2126	57.66	11378
LSVPtsDEEDEVPAKPR	ABCF1	23	ATP-binding cassette sub-family F member 1 isoform a	T5(Phospho) S6(Phospho)	S(2): 0.0; T(5): 100.0; S(6): 100.0	T5; S6;	T108; S109		2.15	0	0	2	1063	2126	57.14	11271
NMAPSQSsPVR	ABI2	10152	abl interactor 2 isoform e	S8(Phospho)	S(5): 0.0; S(8): 100.0	S8;	S165	42		0	0	2	647.8	1295	25.64	4528
NMAPSQSsPVR	ABI2	10152	abl interactor 2 isoform e	S8(Phospho)	S(5): 0.0; S(8): 100.0	S8;	S165		3.23	0	0	2	647.8	1295	25.64	4528
TLsPTPsAEGYQDVR	ABLIM1	3983	actin-binding LIM protein 1 isoform s	S7(Phospho)	T(1): 0.1; S(3): 50.0; T(5): 50.0; S(7): 99.9; Y(11): 0.1	S7;	S147	38		0	0	2	890.9	1781	59.49	11783
TLsPTPsAEGYQDVR	ABLIM1	3983	actin-binding LIM protein 1 isoform s	S7(Phospho)	T(1): 0.1; S(3): 50.0; T(5): 50.0; S(7): 99.9; Y(11): 0.1	S7;	S147		2.76	0	0	2	890.9	1781	59.49	11783
KsSPSTGSLDSGNESK	ACAP2	23527	arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	S3(Phospho)	S(2): 2.6; S(3): 97.4; S(5): 0.0; T(6): 0.0; S(8): 0.0; S(11): 0.0; S(15): 0.0	S3;	S379	35		0	1	2	830.9	1661	15.96	2474
KsSPSTGSLDSGNESK	ACAP2	23527	arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2	S3(Phospho)	S(2): 2.6; S(3): 97.4; S(5): 0.0; T(6): 0.0; S(8): 0.0; S(11): 0.0; S(15): 0.0	S3;	S379		3.74	0	1	2	830.9	1661	15.96	2474
AEsSDSGAEsEEEEAEQEVK	ACBD5	91452	acyl-CoA-binding domain-containing protein 5 isoform 4	S3(Phospho) S10(Phospho)	S(3): 95.6; S(4): 4.2; S(6): 0.2; S(10): 100.0	S3; S10;	S75; S82	28		0	0	2	1150	2300	48.34	9357
AEsSDSGAEsEEEEAEQEVK	ACBD5	91452	acyl-CoA-binding domain-containing protein 5 isoform 4	S3(Phospho) S10(Phospho)	S(3): 95.6; S(4): 4.2; S(6): 0.2; S(10): 100.0	S3; S10;	S75; S82		2.74	0	0	2	1150	2300	48.34	9357
AEsSDSGAEsEEEEAEQEVKGAEQSDNDK	ACBD5	91452	acyl-CoA-binding domain-containing protein 5 isoform 4	S3(Phospho)	S(3): 95.7; S(4): 50.0; S(6): 50.0; S(10): 4.3; S(25): 0.0	S3;	S75		2.9	0.001	2	3	1125	3372	49.41	9581
TPSSPLQSQSTPSLsPR	ACD	65057	adrenocortical dysplasia protein homolog isoform 3	C9(Carbamidomethyl)S14(Phospho)	T(1): 0.1; S(3): 32.2; S(4): 32.2; S(8): 1.6; T(10): 32.2; S(12): 1.9; S(14): 99.7	S14;	S432	21		0.002	0	2	937.9	1875	64.39	12912
GVPAGNsDTGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S7(Phospho)	S(7): 98.3; T(9): 1.7	S7;	S837	75		0	0	2	789.8	1579	23.46	4068

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#
GVPAGNsDTGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S7(Phospho)	S(7): 100.0; T(9): 0.0	S7;	S837	72		0	0	2	789.8	1579	23.99	4179
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216	57		0	1	2	973.4	1946	14.33	2128
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216	55		0	1	3	649.3	1946	14.79	2226
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216	49		0	1	3	649.3	1946	14.29	2119
KSSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S12(Phospho)	S(2): 0.0; S(3): 0.0; S(4): 0.0; S(6): 0.0; S(12): 100.0	S12;	S216	45		0	2	3	692	2074	13.13	1876
AAKLsEGSQPAEEEEQETPSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S5(Phospho)	S(5): 99.9; S(8): 0.1; T(19): 0.0; S(21): 0.0	S5;	S240	45		0	1	3	823.4	2468	31.82	5840
KSSsISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S4(Phospho) S12(Phospho)	S(2): 2.8; S(3): 2.8; S(4): 91.5; S(6): 2.8; S(12): 100.0	S4; S12;	S208; S216	43		0	2	3	718.6	2154	13.48	1951
AAKLsEGSQPAEEEEQETPSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 100.0; T(19): 0.0; S(21): 0.0	S5; S8;	S240; S243	40		0	1	3	850	2548	36.11	6752
KsLsPGVSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(8): 0.0	S2; S4;	S655; S657	35		0	1	2	545.7	1090	23.99	4178
SSsISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S3(Phospho) S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; S(5): 0.1; S(11): 100.0	S3; S11;	S208; S216	31		0	1	3	675.9	2026	16.32	2553
KSSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S12(Phospho)	S(2): 0.0; S(3): 0.0; S(4): 0.0; S(6): 0.0; S(12): 100.0	S12;	S216		7.13	0	2	3	692	2074	13.13	1876
AAKLsEGSQPAEEEEQETPSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 100.0; T(19): 0.0; S(21): 0.0	S5; S8;	S240; S243		5.77	0	1	3	850	2548	36.11	6752
KSSsISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S4(Phospho) S12(Phospho)	S(2): 2.8; S(3): 2.8; S(4): 91.5; S(6): 2.8; S(12): 100.0	S4; S12;	S208; S216		5.73	0	2	3	718.6	2154	13.48	1951
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216		5.14	0	1	3	649.3	1946	14.29	2119
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216		4.88	0	1	3	649.3	1946	14.79	2226
AAKLsEGSQPAEEEEQETPSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S5(Phospho)	S(5): 99.9; S(8): 0.1; T(19): 0.0; S(21): 0.0	S5;	S240		4.58	0	1	3	823.4	2468	31.82	5840
SSSISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 100.0	S11;	S216		3.74	0	1	2	973.4	1946	14.33	2128
GVPAGNsDTGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S7(Phospho)	S(7): 98.3; T(9): 1.7	S7;	S837		3.65	0	0	2	789.8	1579	23.46	4068
KsLsPGVSR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(8): 0.0	S2; S4;	S655; S657		3.34	0	1	2	545.7	1090	23.99	4178

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#
GVPAGNsDTEGGQPGR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S7(Phospho)	S(7): 100.0; T(9): 0.0	S7;	S837		2.86	0	0	2	789.8	1579	23.99	4179
SKsPSPRLIEDR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S3(Phospho) T10(Phospho)	S(1): 3.0; S(3): 97.0; S(5): 3.0; T(10): 97.0	S3; T10;	S386; T393	11		0.001	2	3	543.9	1630	29.32	5322
SKsPSPRLIEDR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S3(Phospho) T10(Phospho)	S(1): 3.0; S(3): 97.0; S(5): 3.0; T(10): 97.0	S3; T10;	S386; T393		3.46	0.001	2	3	543.9	1630	29.32	5322
SSsISEEKGDsDDEKPR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S3(Phospho) S11(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; S(5): 0.1; S(11): 100.0	S3; S11;	S208; S216		3.36	0.003	1	3	675.9	2026	16.32	2553
SKsPSPRLIEDR	ACIN1	22985	apoptotic chromatin condensation inducer in the nucleus isoform 2	S3(Phospho) T10(Phospho)	S(1): 3.1; S(3): 96.9; S(5): 0.1; T(10): 99.9	S3; T10;	S386; T393		2.93	0.004	2	3	543.9	1630	28.78	5209
SWsPPPEVSR	ACSS2	55902	acetyl-coenzyme A synthetase, cytoplasmic isoform 1	S3(Phospho)	S(1): 0.1; S(3): 99.9; S(9): 0.0	S3;	S30	24		0	0	2	611.3	1222	52.83	10320
SWsPPPEVSR	ACSS2	55902	acetyl-coenzyme A synthetase, cytoplasmic isoform 1	S3(Phospho)	S(1): 0.1; S(3): 99.9; S(9): 0.0	S3;	S30		1.67	0	0	2	611.3	1222	52.83	10320
HVsPVtPPR	ADAM9	8754	disintegrin and metalloproteinase domain-containing protein 9 precursor	S3(Phospho) T6(Phospho)	S(3): 100.0; T(6): 100.0	S3; T6;	S758; T761	26		0	0	2	575.2	1149	29.9	5442
HVsPVtPPR	ADAM9	8754	disintegrin and metalloproteinase domain-containing protein 9 precursor	S3(Phospho) T6(Phospho)	S(3): 100.0; T(6): 100.0	S3; T6;	S758; T761		2.62	0.001	0	2	575.2	1149	29.9	5442
SPGsPVGEGTGSPPK	ADD1	118	alpha-adducin isoform c	S4(Phospho)	S(1): 0.0; S(4): 100.0; T(10): 0.0; S(12): 0.0	S4;	S358	76		0	0	2	717.3	1434	27.53	4944
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S4(Phospho)	S(4): 100.0	S4;	S586	55		0	1	2	728.3	1456	17.37	2785
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S5(Phospho)	S(5): 100.0	S5;	S586	54		0	2	2	792.4	1584	13.87	2034
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S5(Phospho)	S(5): 100.0	S5;	S586	45		0	2	3	528.6	1584	13.82	2022
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S5(Phospho)	S(5): 100.0	S5;	S586		5	0	2	3	528.6	1584	13.82	2022
SPGsPVGEGTGSPPK	ADD1	118	alpha-adducin isoform c	S4(Phospho)	S(1): 0.0; S(4): 100.0; T(10): 0.0; S(12): 0.0	S4;	S358		4.26	0	0	2	717.3	1434	27.53	4944
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S5(Phospho)	S(5): 100.0	S5;	S586		3.67	0	2	2	792.4	1584	13.87	2034
KQKGsEENLDEAR	ADD1	118	alpha-adducin isoform c	S4(Phospho)	S(4): 100.0	S4;	S586		3.39	0	1	2	728.3	1456	17.37	2785
LMHNA _s DsEVDQDDVVEWK	ADNP	23394	activity-dependent neuroprotector homeobox protein	M2(Oxidation) S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S953; S955	40		0	0	3	798.3	2393	62.19	12346
LMHNA _s DsEVDQDDVVEWK	ADNP	23394	activity-dependent neuroprotector homeobox protein	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S953; S955	32		0	0	3	793	2377	67.05	13520
NVHsEDFENR	ADNP	23394	activity-dependent neuroprotector homeobox protein	S4(Phospho)	S(4): 100.0	S4;	S98	28		0	0	2	663.8	1327	21.83	3721
LMHNA _s DsEVDQDDVVEWK	ADNP	23394	activity-dependent neuroprotector homeobox protein	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S953; S955		4.36	0	0	3	793	2377	67.05	13520
LMHNA _s DsEVDQDDVVEWK	ADNP	23394	activity-dependent neuroprotector homeobox protein	M2(Oxidation) S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S953; S955		4.04	0	0	3	798.3	2393	62.19	12346
NVHsEDFENR	ADNP	23394	activity-dependent neuroprotector homeobox protein	S4(Phospho)	S(4): 100.0	S4;	S98		3.18	0	0	2	663.8	1327	21.83	3721
SGTsSPQsPVFR	AFAP1	60312	actin filament-associated protein 1 isoform B	S5(Phospho) S8(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 2.0; S(5): 98.0; S(8): 100.0	S5; S8;	S665; S668	37		0	0	2	705.3	1410	52.48	10242
SGTsSPQsPVFR	AFAP1	60312	actin filament-associated protein 1 isoform B	S5(Phospho) S8(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 2.0; S(5): 98.0; S(8): 100.0	S5; S8;	S665; S668		2.33	0	0	2	705.3	1410	52.48	10242
NSYNN _s QAPsPGLGSK	AFF4	27125	AF4/FMR2 family member 4	S10(Phospho)	S(2): 0.0; Y(3): 0.0; S(6): 0.0; S(10): 95.8; S(15): 4.2	S10;	S1043		3	0	0	2	850.9	1701	35.26	6574

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#
LIsPLAsPADGVK	AHCTF1	25909	protein ELYS	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S2231; S2235	35		0	0	2	714.3	1428	78.69	15862
LIsPLAsPADGVK	AHCTF1	25909	protein ELYS	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S2231; S2235		2.81	0	0	2	714.3	1428	78.69	15862
GKGGVTGsPEASISGSK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho)	T(6): 0.0; S(8): 100.0; S(12): 0.0; S(14): 0.0; S(16): 0.0	S8;	S5731	83		0	1	2	799.9	1599	26.42	4698
LPsGSGAAsPTGSAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S9(Phospho)	S(3): 0.1; S(5): 99.9; S(9): 100.0; T(11): 0.0; S(13): 0.0	S5; S9;	S212; S216	70		0	0	2	901.9	1803	63.01	12560
LPsGSGAAsPTGSAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 97.3; T(11): 2.7; S(13): 0.1	S9;	S216	62		0	0	2	861.9	1723	51.21	9959
ssKASLGsLEGEAEAEASSPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S1(Phospho) S2(Phospho)	S(1): 99.8; S(2): 99.8; S(5): 0.1; S(8): 0.4; S(18): 0.0; S(19): 0.0	S1; S2;	S5745; S5746	58		0	1	3	732.3	2195	65.16	13084
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	1414	36.12	6753
SSKASLGsLEGEAEAEASSPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho)	S(1): 50.0; S(2): 3.2; S(5): 48.4; S(8): 98.4; S(18): 0.0; S(19): 0.0	S8;	S5752	49		0	1	2	1098	2195	65.08	13071
LKsEDGVEGDLGETQSR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho)	S(3): 100.0; T(14): 0.0; S(16): 0.0	S3;	S135	45		0	1	3	633.9	1900	37.65	7076
KGDRsPEPGQTWTR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho)	S(5): 100.0; T(11): 0.0; T(13): 0.0	S5;	S93	45		0	2	3	565.6	1695	24.64	4314
GKGGVTGsPEASISGSKGDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho) S16(Phospho)	T(6): 0.0; S(8): 100.0; S(12): 3.0; S(14): 3.0; S(16): 94.1	S8; S16;	S5731; S5739	44		0	2	3	698	2092	35.51	6625
LPsGSGAAsPTGSAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho) S9(Phospho)	S(3): 96.1; S(5): 4.1; S(9): 99.7; T(11): 0.2; S(13): 0.0	S3; S9;	S210; S216	43		0	0	2	901.9	1803	63.53	12692
LPsGSGAAsPTGsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho) S13(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 100.0; T(11): 0.1; S(13): 99.9	S9; S13;	S216; S220	42		0	0	2	901.9	1803	59.43	11771
LKsEDGVEGDLGETQSR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho)	S(3): 100.0; T(14): 0.0; S(16): 0.0	S3;	S135	38		0	1	2	950.4	1900	37.74	7093
GGVTGsPEASISGSKGDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho) S14(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 0.1; S(12): 0.1; S(14): 99.8	S6; S14;	S5731; S5739	38		0	1	2	953.9	1907	45.04	8662
LPsGSGAAsPTGSAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho)	S(3): 50.0; S(5): 50.0; S(9): 100.0; T(11): 0.0; S(13): 0.0	S9;	S216	38		0	0	2	901.9	1803	63.17	12602
GGVTGsPEASISGSKGDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho) S14(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 0.0; S(12): 3.2; S(14): 96.8	S6; S14;	S5731; S5739	33		0	1	3	636.3	1907	45.11	8676
AsLGsLEGEAEAEASSPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(15): 0.0; S(16): 0.0	S2; S5;	S5749; S5752	30		0	0	2	946.9	1893	83.11	16708
SKGHYEVTGsDDETGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 97.6; T(14): 2.4	S10;	S5841	29		0	1	2	895.4	1790	18.11	2943
SSKAsLGsLEGEAEAEASsPKGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.6; S(2): 0.6; S(5): 99.4; S(8): 99.4; S(18): 4.1; S(19): 95.9	S5; S8; S19;	S5749; S5752; S5763	29		0	2	3	820.7	2460	60.37	11954

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#
SSKAsLGsLEGEAEAEASsPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.2; S(2): 0.2; S(5): 99.6; S(8): 100.0; S(18): 4.1; S(19): 95.9	S5; S8; S19;	S5749; S5752; S5763	28		0	1	3	759	2275	70.44	14248
SKGHYEVTGsDDETGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 99.9; T(14): 0.1	S10;	S5841	26		0	1	3	597.2	1790	18.4	3002
DDGVFVQEVQTNsPAAR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S13(Phospho)	T(10): 0.0; S(13): 100.0	S13;	S41	23		0	0	2	956.9	1913	65.53	13168
SKGHYEVTGsDDETGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 99.9; T(14): 0.1	S10;	S5841	18		0	1	3	597.2	1790	17.85	2889
GKGGVTGsPEASISGsKDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho) S16(Phospho)	T(6): 0.0; S(8): 100.0; S(12): 3.0; S(14): 3.0; S(16): 94.1	S8; S16;	S5731; S5739		5.91	0	2	3	698	2092	35.51	6625
SSKAsLGsLEGEAEAEASsPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.2; S(2): 0.2; S(5): 99.6; S(8): 100.0; S(18): 4.1; S(19): 95.9	S5; S8; S19;	S5749; S5752; S5763		5.8	0	1	3	759	2275	70.44	14248
SSKAsLGsLEGEAEAEASsPKGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.6; S(2): 0.6; S(5): 99.4; S(8): 99.4; S(18): 4.1; S(19): 95.9	S5; S8; S19;	S5749; S5752; S5763		5.66	0	2	3	820.7	2460	60.37	11954
ssKASLGsLEGEAEAEASsPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S1(Phospho) S2(Phospho)	S(1): 99.8; S(2): 99.8; S(5): 0.1; S(8): 0.4; S(18): 0.0; S(19): 0.0	S1; S2;	S5745; S5746		5.13	0	1	3	732.3	2195	65.16	13084
SKGHYEVTGsDDETGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 99.9; T(14): 0.1	S10;	S5841		4.9	0	1	3	597.2	1790	18.4	3002
GKGGVTGsPEASISGSK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho)	T(6): 0.0; S(8): 100.0; S(12): 0.0; S(14): 0.0; S(16): 0.0	S8;	S5731		4.88	0	1	2	799.9	1599	26.42	4698
LPSGsGAAsPTGSsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S9(Phospho)	S(3): 0.1; S(5): 99.9; S(9): 100.0; T(11): 0.0; S(13): 0.0	S5; S9;	S212; S216		4.76	0	0	2	901.9	1803	63.01	12560
LKsEDGVEGLGETQSR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho)	S(3): 100.0; T(14): 0.0; S(16): 0.0	S3;	S135		4.68	0	1	3	633.9	1900	37.65	7076
KGDRsPEPGQTWTR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho)	S(5): 100.0; T(11): 0.0; T(13): 0.0	S5;	S93		4.57	0	2	3	565.6	1695	24.64	4314
SSKAsLGsLEGEAEAEASsPKGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.6; S(2): 0.6; S(5): 99.4; S(8): 99.4; S(18): 0.2; S(19): 99.8	S5; S8; S19;	S5749; S5752; S5763		4.5	0	2	3	820.7	2460	59.84	11847
LPSGsGAAsPTGSsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho)	S(3): 50.0; S(5): 50.0; S(9): 100.0; T(11): 0.0; S(13): 0.0	S9;	S216		4.3	0	0	2	901.9	1803	63.17	12602
LKsEDGVEGLGETQSR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho)	S(3): 100.0; T(14): 0.0; S(16): 0.0	S3;	S135		4.15	0	1	2	950.4	1900	37.74	7093
LPSGsGAAsPTGSsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 97.3; T(11): 2.7; S(13): 0.1	S9;	S216		4.08	0	0	2	861.9	1723	51.21	9959
SKGHYEVTGsDDETGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 99.9; T(14): 0.1	S10;	S5841		3.86	0	1	3	597.2	1790	17.85	2889
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		3.79	0	0	2	707.3	1414	36.12	6753

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#
SSKASLGSLEGEAEAEASSPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S8(Phospho)	S(1): 50.0; S(2): 3.2; S(5): 48.4; S(8): 98.4; S(18): 0.0; S(19): 0.0	S8;	S5752		3.66	0	1	2	1098	2195	65.08	13071
AsLGSLEGEAEAEASSPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(15): 0.0; S(16): 0.0	S2; S5;	S5749; S5752		3.56	0	0	2	946.9	1893	83.11	16708
LPSGSGAAsPTGsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S9(Phospho) S13(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 100.0; T(11): 0.1; S(13): 99.9	S9; S13;	S216; S220		3.5	0	0	2	901.9	1803	59.43	11771
AsLGSLEGEAEAEASsPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S2(Phospho) S16(Phospho)	S(2): 99.5; S(5): 0.3; S(15): 4.9; S(16): 95.3	S2; S16;	S5749; S5763		3.14	0	0	2	946.9	1893	78.62	15841
SKGHYEVTGsDDETgK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S10(Phospho)	S(1): 0.0; Y(5): 0.0; T(8): 0.0; S(10): 97.6; T(14): 2.4	S10;	S5841		2.96	0	1	2	895.4	1790	18.11	2943
LPsGSGAAsPTGSsAVDIR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S3(Phospho) S9(Phospho)	S(3): 96.1; S(5): 4.1; S(9): 99.7; T(11): 0.2; S(13): 0.0	S3; S9;	S210; S216		2.94	0	0	2	901.9	1803	63.53	12692
DDGVFVQEVtQNsPAAR	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S13(Phospho)	T(10): 0.0; S(13): 100.0	S13;	S41		2.75	0	0	2	956.9	1913	65.53	13168
AsLGSLEGEAEAEASsPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S2(Phospho) S16(Phospho)	S(2): 100.0; S(5): 0.0; S(15): 4.9; S(16): 95.1	S2; S16;	S5749; S5763		2.57	0	0	2	946.9	1893	78.12	15747
SSKAsLGSLEGEAEAEAssPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S18(Phospho) S19(Phospho)	S(1): 4.0; S(2): 4.0; S(5): 92.1; S(8): 0.0; S(18): 100.0; S(19): 100.0	S5; S18; S19;	S5749; S5762; S5763		3.19	0.001	1	2	1138	2275	70.49	14258
SSKAsLGSLEGEAEAEAssPKGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S8(Phospho) S19(Phospho)	S(1): 0.6; S(2): 0.6; S(5): 99.4; S(8): 99.4; S(18): 0.2; S(19): 99.8	S5; S8; S19;	S5749; S5752; S5763	23		0.003	2	3	820.7	2460	59.84	11847
AsLGSLEGEAEAEAssPKGK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S2(Phospho) S16(Phospho)	S(2): 95.1; S(5): 4.9; S(15): 4.9; S(16): 95.1	S2; S16;	S5749; S5763		2.35	0.003	1	2	1039	2078	65.26	13109
GGVTGsPEASISGsKGDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho) S14(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 0.0; S(12): 3.2; S(14): 96.8	S6; S14;	S5731; S5739		4.21	0.005	1	3	636.3	1907	45.11	8676
GGVTGsPEASISGsKGDLK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S6(Phospho) S14(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 0.1; S(12): 0.1; S(14): 99.8	S6; S14;	S5731; S5739		3.58	0.005	1	2	953.9	1907	45.04	8662
SSKAsLGSLEGEAEAEAssPK	AHNAK	79026	neuroblast differentiation-associated protein AHNAK isoform 1	S5(Phospho) S18(Phospho) S19(Phospho)	S(1): 4.0; S(2): 4.0; S(5): 92.1; S(8): 0.0; S(18): 100.0; S(19): 100.0	S5; S18; S19;	S5749; S5762; S5763	23		0.007	1	2	1138	2275	70.49	14258
CDSSPDsAEDVR	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	70		0	0	2	709.3	1417	23.51	4078
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	64		0	1	2	773.3	1546	16.63	2623
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	47		0	1	2	773.3	1546	16.11	2505
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	41		0	1	3	515.9	1546	16.12	2507
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		3.94	0	1	3	515.9	1546	16.12	2507

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#
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		3.72	0	1	2	773.3	1546	16.11	2505
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		3.64	0	1	2	773.3	1546	16.63	2623
CDSSPDsAEDVR	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		3.35	0	0	2	709.3	1417	23.51	4078
AALDGGVASAAsPESKPSPGtK	AIM1	202	absent in melanoma 1 protein	S12(Phospho)T21(Phospho)	S(9): 0.0; S(12): 100.0; S(15): 0.0; S(18): 2.6; T(21): 97.4	S12; T21;	S75; T84	27		0	0	3	720	2158	42.21	8034
AALDGGVASAAsPESKPSPGtK	AIM1	202	absent in melanoma 1 protein	S12(Phospho)	S(9): 0.0; S(12): 99.9; S(15): 0.1; S(18): 0.0; T(21): 0.0	S12;	S75	25		0	0	3	693.3	2078	36.05	6739
AALDGGVASAAsPESKPSPGtK	AIM1	202	absent in melanoma 1 protein	S12(Phospho)T21(Phospho)	S(9): 0.0; S(12): 100.0; S(15): 0.0; S(18): 2.6; T(21): 97.4	S12; T21;	S75; T84		6.95	0	0	3	720	2158	42.21	8034
AALDGGVASAAsPESKPSPGtK	AIM1	202	absent in melanoma 1 protein	S12(Phospho)	S(9): 0.0; S(12): 99.9; S(15): 0.1; S(18): 0.0; T(21): 0.0	S12;	S75		4.34	0	0	3	693.3	2078	36.05	6739
AALDGGVAsAAsPESKPSPGtK	AIM1	202	absent in melanoma 1 protein	S9(Phospho)T21(Phospho)	S(9): 100.0; S(12): 0.0; S(15): 0.0; S(18): 0.2; T(21): 99.8	S9; T21;	S72; T84		2.61	0.005	0	2	1079	2158	42.26	8047
MVPPVVVGsPPGSPSR	AIM1L	55057	absent in melanoma 1-like protein	S9(Phospho)	S(9): 100.0; S(13): 50.0; S(15): 50.0	S9;	S224	30		0	0	2	861.9	1723	77.83	15701
MVPPVVVGsPPGSPSR	AIM1L	55057	absent in melanoma 1-like protein	S9(Phospho)	S(9): 100.0; S(13): 50.0; S(15): 50.0	S9;	S224		2.59	0.004	0	2	861.9	1723	77.83	15701
KPEsPYGNLCDAPDsPRPVK	AKAP11	11215	A-kinase anchor protein 11	C10(Carbamidomethyl)S4(Phospho)S15(Phospho)	S(4): 94.9; Y(6): 5.1; S(15): 100.0	S4; S15;	S422; S433		3.9	0.005	0	3	796.3	2387	44.56	8543
sAESPTsPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S1(Phospho)S7(Phospho)	S(1): 99.9; S(4): 0.1; T(6): 0.1; S(7): 99.9; T(10): 0.0; S(11): 0.0; T(13): 0.0; S(15): 0.0; T(16): 0.0	S1; S7;	S280; S286	58		0	0	2	986.9	1973	62.3	12374
SPPsPVER	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S4(Phospho)	S(1): 0.0; S(4): 100.0	S4;	S1331	44		0	0	2	474.7	948.4	21.28	3609
EVsSLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamidomethyl)C20(Carbamidomethyl)S3(Phospho)	S(3): 97.0; S(4): 3.0; S(8): 0.0; T(21): 0.0	S3;	S1390	40		0	0	3	818.7	2454	62.41	12400
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 2.7; S(17): 97.3	S17;	S598	38		0	0	3	734	2200	42.35	8064
SAESPTsPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S7(Phospho)	S(1): 2.7; S(4): 2.7; T(6): 2.7; S(7): 89.1; T(10): 2.7; S(11): 0.1; T(13): 0.0; S(15): 0.0; T(16): 0.0	S7;	S286	34		0	0	2	946.9	1893	50.12	9729
sAESPTsPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S1(Phospho)	S(1): 97.9; S(4): 2.0; T(6): 0.0; S(7): 0.0; T(10): 0.0; S(11): 0.0; T(13): 0.0; S(15): 0.0; T(16): 0.0	S1;	S280	34		0	0	2	946.9	1893	51.09	9933
GLAEVQQDGEAEEGATsDGEKKR	AKAP12	9590	A-kinase anchor protein 12 isoform 1	T16(Phospho)	T(16): 97.0; S(17): 3.0	T16;	T597	32		0	2	3	828.7	2484	31.4	5753
LKETCVSGEDPTQGADLsPDEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C5(Carbamidomethyl)S18(Phospho)	T(4): 0.0; S(7): 0.0; T(12): 0.0; S(18): 100.0	S18;	S483	32		0	1	3	819.4	2456	43.41	8289

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#
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 0.2; S(17): 99.8	S17;	S598	28		0	0	2	1100	2200	42.12	8016
GLAEVQQDGEAEEGATsDGEKKR	AKAP12	9590	A-kinase anchor protein 12 isoform 1	T16(Phospho)	T(16): 96.5; S(17): 3.5	T16;	T597	26		0	2	3	828.7	2484	31.93	5862
EVssLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamido methyl) C20(Carbamido methyl)S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(8): 0.0; T(21): 0.0	S3; S4;	S1390; S1391	26		0	0	3	845.3	2534	70.81	14323
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629	23		0	2	3	645.6	1935	27.36	4907
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629	22		0	2	3	645.6	1935	26.83	4784
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629	22		0	2	3	645.6	1935	28.47	5143
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 0.2; S(17): 99.8	S17;	S598	21		0	0	2	1100	2200	42.64	8126
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629	15		0	2	2	967.9	1935	26.97	4815
EVssLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamido methyl) C20(Carbamido methyl)S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(8): 0.0; T(21): 0.0	S3; S4;	S1390; S1391	10		0	0	2	1268	2534	70.73	14309
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 2.7; S(17): 97.3	S17;	S598		6.14	0	0	3	734	2200	42.35	8064
GLAEVQQDGEAEEGATsDGEKKR	AKAP12	9590	A-kinase anchor protein 12 isoform 1	T16(Phospho)	T(16): 97.0; S(17): 3.0	T16;	T597		5.81	0	2	3	828.7	2484	31.4	5753
EVssLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamido methyl) C20(Carbamido methyl)S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(8): 0.0; T(21): 0.0	S3; S4;	S1390; S1391		5.8	0	0	3	845.3	2534	70.81	14323
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629		5.65	0	2	3	645.6	1935	27.36	4907
GLAEVQQDGEAEEGATsDGEKKR	AKAP12	9590	A-kinase anchor protein 12 isoform 1	T16(Phospho)	T(16): 96.5; S(17): 3.5	T16;	T597		5.53	0	2	3	828.7	2484	31.93	5862
EVssLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamido methyl) C20(Carbamido methyl)S3(Phospho)	S(3): 97.0; S(4): 3.0; S(8): 0.0; T(21): 0.0	S3;	S1390		5.05	0	0	3	818.7	2454	62.41	12400
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629		4.93	0	2	3	645.6	1935	27.88	5018
LKETCVSGEDPTQGADLSPEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C5(Carbamidomethyl) S18(Phospho)	T(4): 0.0; S(7): 0.0; T(12): 0.0; S(18): 100.0	S18;	S483		4.56	0	1	3	819.4	2456	43.41	8289
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629		4.54	0	2	3	645.6	1935	26.83	4784
RPseSDKEDELdkvk	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629		4.24	0	2	3	645.6	1935	28.47	5143
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 0.2; S(17): 99.8	S17;	S598		4.15	0	0	2	1100	2200	42.12	8016

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#
sAESPTSPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S1(Phospho) S7(Phospho)	S(1): 99.9; S(4): 0.1; T(6): 0.1; S(7): 99.9; T(10): 0.0; S(11): 0.0; T(13): 0.0; S(15): 0.0; T(16): 0.0	S1; S7;	S280; S286		3.47	0	0	2	986.9	1973	62.3	12374
sAESPTSPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S1(Phospho)	S(1): 97.9; S(4): 2.0; T(6): 0.0; S(7): 0.0; T(10): 0.0; S(11): 0.0; T(13): 0.0; S(15): 0.0; T(16): 0.0	S1;	S280		3.34	0	0	2	946.9	1893	51.09	9933
SAESPTSPVTSETGSTFK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S7(Phospho)	S(1): 2.7; S(4): 2.7; T(6): 2.7; S(7): 89.1; T(10): 2.7; S(11): 0.1; T(13): 0.0; S(15): 0.0; T(16): 0.0	S7;	S286		2.92	0	0	2	946.9	1893	50.12	9729
RPSEsDKEDELDKVK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629		2.8	0	2	2	967.9	1935	26.97	4815
GLAEVQQDGEAEEGATsDGEK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S17(Phospho)	T(16): 0.2; S(17): 99.8	S17;	S598		3.36	0.001	0	2	1100	2200	42.64	8126
EVssLEGSPPPCLGQEEAVCTK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	C12(Carbamidomethyl) C20(Carbamidomethyl) S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; S(8): 0.0; T(21): 0.0	S3; S4;	S1390; S1391		2.4	0.001	0	2	1268	2534	70.73	14309
SPPsPVER	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S4(Phospho)	S(1): 0.0; S(4): 100.0	S4;	S1331		2.15	0.001	0	2	474.7	948.4	21.28	3609
RPSEsDKEDELDKVK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S627; S629	16		0.002	2	3	645.6	1935	27.88	5018
sATLSSTESTAsEMQEEMK	AKAP12	9590	A-kinase anchor protein 12 isoform 1	S1(Phospho) S12(Phospho)	S(1): 82.5; T(3): 5.8; S(5): 0.5; S(6): 0.5; T(7): 0.5; S(9): 6.1; T(10): 6.1; S(12): 98.0	S1; S12;	S640; S651		1.91	0.002	0	2	1104	2207	66.72	13442
DMAECSTPLPEDCsPTHsPR	AKAP13	11214	A-kinase anchor protein 13 isoform 2	C5(Carbamidomethyl) C13(Carbamidomethyl) S14(Phospho) S18(Phospho)	S(6): 0.0; T(7): 0.0; S(14): 99.9; T(16): 0.1; S(18): 100.0	S14; S18;	S2398; S2402		4.13	0	0	3	816.3	2447	54.01	10587
DMAECSTPLPEDCsPTHsPR	AKAP13	11214	A-kinase anchor protein 13 isoform 2	M2(Oxidation) C5(Carbamidomethyl) C13(Carbamidomethyl) S18(Phospho)	S(6): 0.0; T(7): 0.0; S(14): 50.0; T(16): 50.0; S(18): 100.0	S18;	S2402		3.44	0	0	3	821.6	2463	47.36	9153
LsSSEETESTQCCPGSPVAQTESPCDLSI VEEENTDR	AKAP13	11214	A-kinase anchor protein 13 isoform 2	C12(Carbamidomethyl) C13(Carbamidomethyl) C25(Carbamidomethyl) S2(Phospho)	S(2): 81.2; S(3): 8.4; S(4): 8.4; T(7): 1.0; S(9): 0.1; T(10): 0.1; S(16): 0.1; T(21): 0.1; S(23): 0.1; S(28): 0.1; S(29): 0.1; T(36): 0.0	S2;	S331		2.89	0.007	0	4	1075	4296	75.26	15209
GQKsPGALETPSAAGSQGNTASQGK	AKAP2	11217	A-kinase anchor protein 2 isoform 2	S4(Phospho)	S(4): 100.0; T(10): 0.0; S(12): 0.0; S(16): 0.0; T(20): 0.0; S(22): 0.0	S4;	S393	48		0	1	3	803.7	2409	28.53	5156
GQKsPGALETPSAAGSQGNTASQGK	AKAP2	11217	A-kinase anchor protein 2 isoform 2	S4(Phospho)	S(4): 100.0; T(10): 0.0; S(12): 0.0; S(16): 0.0; T(20): 0.0; S(22): 0.0	S4;	S393		5.8	0	1	3	803.7	2409	28.53	5156
VDsEGDFsENDDAAGDFR	AKAP8	10270	A-kinase anchor protein 8	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S323; S328	65		0	0	2	1053	2106	69.03	13958
VDsEGDFsENDDAAGDFR	AKAP8	10270	A-kinase anchor protein 8	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S323; S328		3.4	0	0	2	1053	2106	69.03	13958

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#
TEARSSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S15(Phospho)	T(1): 0.1; S(5): 50.0; S(6): 50.0; S(14): 0.1; S(15): 99.9	S15;	S212	32		0	1	3	773.6	2319	36.45	6825
tEARsSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	T1(Phospho) S5(Phospho) S15(Phospho)	T(1): 100.0; S(5): 95.9; S(6): 4.1; S(14): 0.0; S(15): 100.0	T1; S5; S15;	T198; S202; S212	22		0	1	3	800.3	2399	45.58	8778
RTEARssDEENGPPSSPDLDLR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S6(Phospho) S7(Phospho)	T(2): 0.0; S(6): 100.0; S(7): 100.0; S(15): 50.0; S(16): 50.0	S6; S7;	S202; S203	21		0	2	3	852.3	2555	35.51	6626
SSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(10): 2.2; S(11): 97.8	S11;	S212	21		0	0	2	891.4	1782	37.28	6999
LNTSDFQK	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	T3(Phospho)	T(3): 98.5; S(4): 1.5	T3;	T246	21		0	0	2	516.7	1032	29.77	5415
SSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S11(Phospho)	S(1): 50.0; S(2): 50.0; S(10): 4.0; S(11): 96.0	S11;	S212	20		0	0	2	931.3	1862	47.74	9229
RTEARssDEENGPPSSPDLDLR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S6(Phospho) S7(Phospho)	T(2): 0.0; S(6): 100.0; S(7): 100.0; S(15): 50.0; S(16): 50.0	S6; S7;	S202; S203		6.19	0	2	3	852.3	2555	35.51	6626
TEARSSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S15(Phospho)	T(1): 0.1; S(5): 50.0; S(6): 50.0; S(14): 0.1; S(15): 99.9	S15;	S212		5.14	0	1	3	773.6	2319	36.45	6825
tEARsSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	T1(Phospho) S5(Phospho) S15(Phospho)	T(1): 100.0; S(5): 95.9; S(6): 4.1; S(14): 0.0; S(15): 100.0	T1; S5; S15;	T198; S202; S212		4.42	0	1	3	800.3	2399	45.58	8778
SSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(10): 2.2; S(11): 97.8	S11;	S212		3.17	0	0	2	891.4	1782	37.28	6999
LNTSDFQK	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	T3(Phospho)	T(3): 98.5; S(4): 1.5	T3;	T246		2.1	0	0	2	516.7	1032	29.77	5415
SSDEENGPPSPDLDR	AKT1S1	84335	proline-rich AKT1 substrate 1 isoform b	S11(Phospho)	S(1): 50.0; S(2): 50.0; S(10): 4.0; S(11): 96.0	S11;	S212		2.86	0.001	0	2	931.3	1862	47.74	9229
SGsAAQAEGLCK	ALG3	10195	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase isoform a	C11(Carbamido methyl) S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S13	51		0	0	2	629.8	1259	25.84	4569
SGsAAQAEGLCK	ALG3	10195	dol-P-Man:Man(5)GlcNAc(2)-PP-Dol alpha-1,3-mannosyltransferase isoform a	C11(Carbamido methyl) S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S13		3.61	0	0	2	629.8	1259	25.84	4569
YQEDsDPERsDYEEQLQKEEFAR	ALKBH5	54890	RNA demethylase ALKBH5	S5(Phospho) S10(Phospho)	Y(1): 0.0; S(5): 100.0; S(10): 94.8; Y(12): 5.2	S5; S10;	S64; S69	22		0	2	3	1054	3161	47.1	9096
YQEDsDPERSDYEEQLQKEEFAR	ALKBH5	54890	RNA demethylase ALKBH5	S5(Phospho)	Y(1): 48.4; S(5): 92.9; S(10): 51.6; Y(12): 7.1	S5;	S64	11		0	2	4	791.1	3161	47.11	9099
YQEDsDPERSDYEEQLQKEEFAR	ALKBH5	54890	RNA demethylase ALKBH5	S5(Phospho)	Y(1): 48.4; S(5): 92.9; S(10): 51.6; Y(12): 7.1	S5;	S64		4.69	0	2	4	791.1	3161	47.11	9099
YQEDsDPERsDYEEQLQKEEFAR	ALKBH5	54890	RNA demethylase ALKBH5	S5(Phospho) S10(Phospho)	Y(1): 0.0; S(5): 100.0; S(10): 94.8; Y(12): 5.2	S5; S10;	S64; S69		4.21	0	2	3	1054	3161	47.1	9096
GHNSSNsPSLQAGGAEGAGDR	ANKHD1-EIF4EB	404734	ANKHD1-EIF4EBP3 protein	S7(Phospho)	S(4): 2.6; S(5): 2.6; S(7): 94.7; S(9): 0.0	S7;	S2598	43		0	0	3	683.6	2049	23.22	4020
GHNSSNsPSLQAGGAEGAGDR	ANKHD1-EIF4EB	404734	ANKHD1-EIF4EBP3 protein	S7(Phospho)	S(4): 2.6; S(5): 2.6; S(7): 94.7; S(9): 0.0	S7;	S2598		4.45	0	0	3	683.6	2049	23.22	4020
EHYPVsSPSSPPAPGPGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S6(Phospho) S12(Phospho)	Y(3): 0.0; S(6): 96.4; S(7): 3.5; S(9): 0.1; S(10): 0.0; S(12): 100.0; S(21): 0.0	S6; S12;	S1790; S1796	40		0	0	3	794	2380	48.1	9306
APsPAPSSVPLGSEKPSNVSQDR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(8): 0.0; S(13): 0.0; S(17): 0.0; S(20): 0.0	S3;	S2150	39		0	0	3	796.4	2387	44.21	8459
EHYPVsSPSSPPAPGPGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	Y3(Phospho) S6(Phospho)	Y(3): 100.0; S(6): 99.7; S(7): 0.3; S(9): 0.0; S(10): 0.0; S(12): 0.0; S(21): 0.0	Y3; S6;	Y1787; S1790	27		0	0	3	794	2380	48.8	9452

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#
EHPVVsPSSSPsPPAQPGGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S7(Phospho) S12(Phospho)	Y(3): 0.0; S(6): 3.5; S(7): 92.9; S(9): 3.5; S(10): 3.7; S(12): 96.3; S(21): 0.0	S7; S12;	S1791; S1796	27		0	0	3	794	2380	47.57	9195
APsPAPSSVPLGSEKPSNVSQDR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(8): 0.0; S(13): 0.0; S(17): 0.0; S(20): 0.0	S3;	S2150		5.22	0	0	3	796.4	2387	44.21	8459
EHPVVsSPSSSPsPPAQPGGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S6(Phospho) S12(Phospho)	Y(3): 0.0; S(6): 96.4; S(7): 3.5; S(9): 0.1; S(10): 0.0; S(12): 100.0; S(21): 0.0	S6; S12;	S1790; S1796		5.08	0	0	3	794	2380	48.1	9306
EHPVVsPSSSPsPPAQPGGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	S7(Phospho) S12(Phospho)	Y(3): 0.0; S(6): 3.5; S(7): 92.9; S(9): 3.5; S(10): 3.7; S(12): 96.3; S(21): 0.0	S7; S12;	S1791; S1796		3.37	0	0	3	794	2380	47.57	9195
EHYPVsSPSSSPsPPAQPGGVSR	ANKRD17	26057	ankyrin repeat domain-containing protein 17 isoform b	Y3(Phospho) S6(Phospho)	Y(3): 100.0; S(6): 99.7; S(7): 0.3; S(9): 0.0; S(10): 0.0; S(12): 0.0; S(21): 0.0	Y3; S6;	Y1787; S1790		3.27	0	0	3	794	2380	48.8	9452
SEsLSNCSIGK	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C7(Carbamidomethyl) S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(8): 0.0	S3;	S647	67		0	0	2	631.3	1262	32.92	6068
sLSKSDSLLTCSPTEDATMGSR	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C12(Carbamidomethyl) S1(Phospho)	S(1): 90.8; S(3): 3.1; S(5): 3.1; S(7): 3.1; T(11): 0.0; S(13): 0.0; T(15): 0.0; T(19): 0.0; S(22): 0.0	S1;	S622	26		0	1	3	846.7	2538	58.93	11668
SEsLSNCSIGK	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C7(Carbamidomethyl) S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(8): 0.0	S3;	S647		3.62	0	0	2	631.3	1262	32.92	6068
sLSKSDSLLTCSPTEDATMGSR	ANKS1A	23294	ankyrin repeat and SAM domain-containing protein 1A	C12(Carbamidomethyl) S1(Phospho)	S(1): 90.8; S(3): 3.1; S(5): 3.1; S(7): 3.1; T(11): 0.0; S(13): 0.0; T(15): 0.0; T(19): 0.0; S(22): 0.0	S1;	S622		3.54	0	1	3	846.7	2538	58.93	11668
AA sPPRP LLSNASAtPVGR	ANLN	54443	actin-binding protein anillin isoform 3	S3(Phospho) T15(Phospho)	S(3): 100.0; S(10): 0.0; S(13): 0.1; T(15): 99.9	S3; T15;	S182; T194	33		0	0	3	674.7	2022	56.57	11133
SCEGQNPELLPKtPi sPLK	ANLN	54443	actin-binding protein anillin isoform 3	C2(Carbamidomethyl)T13(Phospho) S16(Phospho)	S(1): 0.0; T(13): 100.0; S(16): 100.0	T13; S16;	T320; S323	12		0.002	1	3	756.7	2268	70.82	14326
AA sPPRP LLSNASAtPVGR	ANLN	54443	actin-binding protein anillin isoform 3	S3(Phospho) T15(Phospho)	S(3): 100.0; S(10): 0.0; S(13): 0.1; T(15): 99.9	S3; T15;	S182; T194		2.36	0.002	0	3	674.7	2022	56.57	11133
SCEGQNPELLPKtPi sPLK	ANLN	54443	actin-binding protein anillin isoform 3	C2(Carbamidomethyl)T13(Phospho) S16(Phospho)	S(1): 0.0; T(13): 100.0; S(16): 100.0	T13; S16;	T320; S323		3.27	0.003	1	3	756.7	2268	70.82	14326
TEAQGEEDDAEGQDQDKKsPKPK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S19(Phospho)	T(1): 0.0; S(19): 100.0	S19;	S931	21		0	2	3	870.7	2610	13.78	2014
NTETSKsPEKDVP MVEK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S7(Phospho)	T(2): 0.0; T(4): 0.1; S(5): 2.3; S(7): 97.6	S7;	S829	19		0	2	3	667	1999	32.45	5972
NTETSKsPEKDVP MVEK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S7(Phospho)	T(2): 0.0; T(4): 0.0; S(5): 0.0; S(7): 100.0	S7;	S829	16		0	2	3	667	1999	31.92	5861
TEAQGEEDDAEGQDQDKKsPKPK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S19(Phospho)	T(1): 0.0; S(19): 100.0	S19;	S931	12		0	2	4	653.3	2610	13.92	2043
TEAQGEEDDAEGQDQDKKsPKPK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S19(Phospho)	T(1): 0.0; S(19): 100.0	S19;	S931		5.14	0	2	4	653.3	2610	13.92	2043
NTETSKsPEKDVP MVEK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S7(Phospho)	T(2): 0.0; T(4): 0.0; S(5): 0.0; S(7): 100.0	S7;	S829		4.47	0	2	3	667	1999	31.92	5861
TEAQGEEDDAEGQDQDKKsPKPK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S19(Phospho)	T(1): 0.0; S(19): 100.0	S19;	S931		4.43	0	2	3	870.7	2610	13.78	2014
NTETSKsPEKDVP MVEK	AP3D1	8943	AP-3 complex subunit delta-1 isoform 3	S7(Phospho)	T(2): 0.0; T(4): 0.1; S(5): 2.3; S(7): 97.6	S7;	S829		4.27	0	2	3	667	1999	32.45	5972
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	46		0	1	2	692.8	1385	12.4	1703

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#
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		4.03	0	1	2	692.8	1385	12.4	1703
GGSDGtPRGsPSPASVSSGR	ARAF	369	serine/threonine-protein kinase A-Raf isoform 1	T6(Phospho) S10(Phospho)	S(3): 0.2; T(6): 99.8; S(10): 99.8; S(12): 0.2; S(15): 0.0; S(17): 0.0; S(18): 0.0	T6; S10;	T253; S257	20		0	1	2	988.4	1976	27.28	4887
GGSDGtPRGsPSPASVSSGR	ARAF	369	serine/threonine-protein kinase A-Raf isoform 1	T6(Phospho) S10(Phospho)	S(3): 0.2; T(6): 99.8; S(10): 99.8; S(12): 0.2; S(15): 0.0; S(17): 0.0; S(18): 0.0	T6; S10;	T253; S257		1.89	0.003	1	2	988.4	1976	27.28	4887
ELEKPIQSKPQsPVIQAAAVsPK	ARFGEF2	10564	brefeldin A-inhibited guanine nucleotide-exchange protein 2	S12(Phospho) S21(Phospho)	S(8): 0.1; S(12): 99.9; S(21): 100.0	S12; S21;	S218; S227	16		0	0	3	869.1	2605	51.12	9941
ELEKPIQSKPQsPVIQAAAVsPK	ARFGEF2	10564	brefeldin A-inhibited guanine nucleotide-exchange protein 2	S12(Phospho) S21(Phospho)	S(8): 0.1; S(12): 99.9; S(21): 100.0	S12; S21;	S218; S227		5.75	0	0	3	869.1	2605	51.12	9941
SDDSKsSPELVTHLK	ARHGAP1	392	rho GTPase-activating protein 1	S6(Phospho)	S(1): 0.2; S(4): 3.9; S(6): 94.1; S(7): 50.9; S(8): 50.9; T(13): 0.0	S6;	S49	14		0	1	3	630.6	1890	42.95	8192
SDDSKsSPELVTHLK	ARHGAP1	392	rho GTPase-activating protein 1	S6(Phospho)	S(1): 0.2; S(4): 3.9; S(6): 94.1; S(7): 50.9; S(8): 50.9; T(13): 0.0	S6;	S49		2.78	0	1	3	630.6	1890	42.95	8192
IHQDSEsGDELSSTSEQIR	ARHGAP12	94134	rho GTPase-activating protein 12 isoform 5	S7(Phospho)	S(5): 0.0; S(7): 100.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0; T(16): 0.0	S7;	S215	53		0	0	3	762.3	2285	36.67	6872
TSFSQEQSCDsAGEGSR	ARHGAP12	94134	rho GTPase-activating protein 12 isoform 5	C9(Carbamidomethyl) S11(Phospho)	T(1): 2.7; S(2): 2.7; S(4): 0.0; S(8): 0.0; S(11): 94.6; S(16): 0.0	S11;	S201	44		0	0	2	1021	2042	28.87	5227
IHQDSEsGDELSSTSEQIR	ARHGAP12	94134	rho GTPase-activating protein 12 isoform 5	S7(Phospho)	S(5): 0.0; S(7): 100.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0; T(16): 0.0	S7;	S215		5.63	0	0	3	762.3	2285	36.67	6872
ATTPNQGRPDsPVYANLQELK	ARHGAP12	94134	rho GTPase-activating protein 12 isoform 5	S12(Phospho)	T(2): 51.5; T(3): 51.5; S(12): 97.0; Y(15): 0.0	S12;	S240		3.44	0	0	3	852.7	2556	66.45	13381
TSFSQEQSCDsAGEGSR	ARHGAP12	94134	rho GTPase-activating protein 12 isoform 5	C9(Carbamidomethyl) S11(Phospho)	T(1): 2.7; S(2): 2.7; S(4): 0.0; S(8): 0.0; S(11): 94.6; S(16): 0.0	S11;	S201		2.73	0	0	2	1021	2042	28.87	5227
sPSPPTQHTGQPPGQPSAPLSAPR	ARHGAP17	55114	rho GTPase-activating protein 17 isoform 1	S1(Phospho)	S(1): 90.2; S(3): 3.3; T(6): 3.3; T(9): 3.3; S(17): 0.0; S(20): 0.0; S(23): 0.0	S1;	S674	21		0	0	3	896.4	2687	44.05	8425
sPSPPTQHTGQPPGQPSAPLSAPR	ARHGAP17	55114	rho GTPase-activating protein 17 isoform 1	S1(Phospho)	S(1): 90.2; S(3): 3.3; T(6): 3.3; T(9): 3.3; S(17): 0.0; S(20): 0.0; S(23): 0.0	S1;	S674		4.64	0	0	3	896.4	2687	44.05	8425
AESSSGGGTVPSSAGILEQGSPSGDGsPKPK	ARHGAP17	55114	rho GTPase-activating protein 17 isoform 1	S27(Phospho)	S(3): 0.0; S(4): 0.0; S(5): 0.0; T(9): 0.0; S(12): 0.0; S(13): 0.0; S(22): 0.0; S(27): 100.0	S27;	S575		3.47	0	0	3	1006	3015	53.92	10568
sAEALPGALVsPR	ARHGAP23	57636	rho GTPase-activating protein 23	S1(Phospho) S12(Phospho)	S(1): 100.0; S(12): 100.0	S1; S12;	S361; S372	52		0	0	2	742.8	1485	76.37	15404
sAEALPGALVsPR	ARHGAP23	57636	rho GTPase-activating protein 23	S1(Phospho) S12(Phospho)	S(1): 100.0; S(12): 100.0	S1; S12;	S361; S372		4.12	0	0	2	742.8	1485	76.37	15404
RTHSDAsDDEAFTTSK	ARHGAP5	394	rho GTPase-activating protein 5 isoform b	S7(Phospho)	T(2): 50.0; S(4): 50.0; S(7): 100.0; T(13): 0.0; T(14): 0.0; S(15): 0.0	S7;	S1176	53		0	1	3	643.2	1928	23.72	4122
THSDAsDDEAFTTSK	ARHGAP5	394	rho GTPase-activating protein 5 isoform b	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 100.0; T(12): 0.0; T(13): 0.0; S(14): 0.0	S3; S6;	S1173; S1176	44		0	0	2	886.3	1772	31.64	5803
RTHSDAsDDEAFTTSK	ARHGAP5	394	rho GTPase-activating protein 5 isoform b	S7(Phospho)	T(2): 50.0; S(4): 50.0; S(7): 100.0; T(13): 0.0; T(14): 0.0; S(15): 0.0	S7;	S1176		6.85	0	1	3	643.2	1928	23.72	4122

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#
THsDAsDDEAFTTSK	ARHGAP5	394	rho GTPase-activating protein 5 isoform b	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 100.0; T(12): 0.0; T(13): 0.0; S(14): 0.0	S3; S6;	S1173; S1176		3.96	0	0	2	886.3	1772	31.64	5803
YDTNNNEEEGEQDFDfDsGDEIPEADR	ARHGEF10	9639	rho guanine nucleotide exchange factor 10 isoform 2	S18(Phospho)	Y(1): 5.5; T(3): 5.5; S(18): 89.0	S18;	S35	26		0	0	3	1082	3244	73.12	14793
YDTNNNEEEGEQDFDfDsGDEIPEADR	ARHGEF10	9639	rho guanine nucleotide exchange factor 10 isoform 2	S18(Phospho)	Y(1): 5.5; T(3): 5.5; S(18): 89.0	S18;	S35		2.52	0	0	3	1082	3244	73.12	14793
sLGGEssGGTfPVGSFHTEAAR	ARHGEF11	9826	rho guanine nucleotide exchange factor 11 isoform 1	S1(Phospho) T11(Phospho)	S(1): 93.7; S(6): 5.6; S(7): 0.4; T(10): 6.0; T(11): 94.3; S(15): 0.0; T(18): 0.0	S1; T11;	S1452; T1462		3.09	0	0	3	755.6	2265	53.29	10425
GLNtsQESDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	S5(Phospho)	T(4): 4.1; S(5): 91.8; S(8): 4.1; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S5;	S227	45		0	0	2	1317	2632	58.3	11511
GLNtsQEsDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	S8(Phospho)	T(4): 3.4; S(5): 3.4; S(8): 93.1; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S8;	S230	39		0	0	3	878	2632	58.24	11496
GLNtsQESDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	T4(Phospho) S5(Phospho)	T(4): 99.5; S(5): 99.5; S(8): 1.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	T4; S5;	T226; S227	20		0	0	3	904.7	2712	69.73	14117
GLNtsQEsDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	S8(Phospho)	T(4): 3.4; S(5): 3.4; S(8): 93.1; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S8;	S230		4.21	0	0	3	878	2632	58.24	11496
GLNtsQESDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	S5(Phospho)	T(4): 4.1; S(5): 91.8; S(8): 4.1; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S5;	S227		3.19	0	0	2	1317	2632	58.3	11511
GLNtsQESDDdILDEssSPEGTQK	ARHGEF16	27237	rho guanine nucleotide exchange factor 16	T4(Phospho) S5(Phospho)	T(4): 99.5; S(5): 99.5; S(8): 1.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	T4; S5;	T226; S227		2.77	0	0	3	904.7	2712	69.73	14117
LQDSSDPDTGSEEEGSSRLSPPHsPR	ARHGEF2	9181	rho guanine nucleotide exchange factor 2 isoform 3	S24(Phospho)	S(4): 0.0; S(5): 0.0; T(9): 1.6; S(11): 32.3; S(16): 1.6; S(17): 32.3; S(20): 32.3; S(24): 100.0	S24;	S932		3.52	0.007	1	3	976.4	2927	39.13	7386
GPSPSPVGsPASVAQSR	ARID1A	8289	AT-rich interactive domain-containing protein 1A isoform b	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.0; S(9): 100.0; S(12): 0.0; S(16): 0.0	S3; S9;	S696; S702	43		0	0	2	870.9	1741	54.14	10615
GPSPSPVGsPASVAQSR	ARID1A	8289	AT-rich interactive domain-containing protein 1A isoform b	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.0; S(9): 100.0; S(12): 0.0; S(16): 0.0	S3; S9;	S696; S702		3.32	0	0	2	870.9	1741	54.14	10615
AAAAGLGHpAsPGGsEDGPPGSEEEDAAR	ARID3A	1820	AT-rich interactive domain-containing protein 3A	S11(Phospho) S15(Phospho) S22(Phospho)	S(11): 100.0; S(15): 100.0; S(22): 100.0	S11; S15; S22;	S77; S81; S88	21		0	0	3	967.4	2900	53.59	10489
AAAAGLGHpAsPGGsEDGPPGSEEEDAAR	ARID3A	1820	AT-rich interactive domain-containing protein 3A	S11(Phospho) S15(Phospho) S22(Phospho)	S(11): 100.0; S(15): 100.0; S(22): 100.0	S11; S15; S22;	S77; S81; S88		4.48	0	0	3	967.4	2900	53.59	10489
KDIEVLSedTDYEEDEVTK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S7(Phospho) T10(Phospho)	S(7): 100.0; T(10): 99.9; Y(12): 0.1; T(18): 0.0	S7; T10;	S790; T793	45		0	1	3	806.3	2417	64.19	12857
DIEVLSedTDYEEDEVTKK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S6(Phospho)	S(6): 100.0; T(9): 50.0; Y(11): 0.1; T(17): 50.0	S6;	S790	34		0	1	3	806.3	2417	66.79	13461
GtNSSDSEELSAGESITK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	T2(Phospho)	T(2): 99.7; S(4): 0.1; S(5): 0.1; S(7): 0.1; S(11): 0.0; S(15): 0.0; T(17): 0.0	T2;	T1150	29		0	0	2	946.4	1892	46.88	9051
DIEVLSedTDYEEDEVTK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S6(Phospho) T9(Phospho)	S(6): 96.0; T(9): 96.0; Y(11): 7.9; T(17): 0.0	S6; T9;	S790; T793	21		0	0	2	1145	2289	83.5	16774
KDIEVLSedTDYEEDEVTKK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S7(Phospho) T10(Phospho)	S(7): 100.0; T(10): 99.8; Y(12): 0.3; T(18): 0.0	S7; T10;	S790; T793	18		0	2	3	849	2545	54.61	10719
KDIEVLSedTDYEEDEVTK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S7(Phospho) T10(Phospho)	S(7): 100.0; T(10): 99.9; Y(12): 0.1; T(18): 0.0	S7; T10;	S790; T793		4.46	0	1	3	806.3	2417	64.19	12857

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#
DIEVLsEDtDYEEDEVTKK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S6(Phospho)	S(6): 100.0; T(9): 50.0; Y(11): 0.1; T(17): 50.0	S6;	S790		4.39	0	1	3	806.3	2417	66.79	13461
KDIEVLsEDtDYEEDEVTKK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S7(Phospho) T10(Phospho)	S(7): 100.0; T(10): 99.8; Y(12): 0.3; T(18): 0.0	S7; T10;	S790; T793		3.58	0	2	3	849	2545	54.61	10719
GtNSSDSEELSAGESITK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	T2(Phospho)	T(2): 99.7; S(4): 0.1; S(5): 0.1; S(7): 0.1; S(11): 0.0; S(15): 0.0; T(17): 0.0	T2;	T1150		2.92	0	0	2	946.4	1892	46.88	9051
DIEVLsEDtDYEEDEVTK	ARID4B	51742	AT-rich interactive domain-containing protein 4B isoform 1	S6(Phospho) T9(Phospho)	S(6): 96.0; T(9): 96.0; Y(11): 7.9; T(17): 0.0	S6; T9;	S790; T793		2.07	0	0	2	1145	2289	83.5	16774
AEFsAGAWsEPR	ARL6IP6	151188	ADP-ribosylation factor-like protein 6-interacting protein 6	S4(Phospho) S9(Phospho)	S(4): 100.0; S(9): 100.0	S4; S9;	S60; S65	29		0	0	2	734.3	1468	72.83	14732
YNDWsDDDDSNESK	ARMCX3	51566	armadillo repeat-containing X-linked protein 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0; S(11): 0.0; S(14): 0.0	S5;	S61	51		0	0	2	942.8	1885	35.69	6664
YNDWsDDDDSNESK	ARMCX3	51566	armadillo repeat-containing X-linked protein 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0; S(11): 0.0; S(14): 0.0	S5;	S61		3.49	0	0	2	942.8	1885	35.69	6664
YFDsGDYNMAK	ARPP19	10776	cAMP-regulated phosphoprotein 19 isoform 2	S4(Phospho)	Y(1): 1.9; S(4): 98.1; Y(7): 0.0	S4;	S62	38		0	0	2	695.8	1391	55.57	10920
YFDsGDYNMAK	ARPP19	10776	cAMP-regulated phosphoprotein 19 isoform 2	S4(Phospho)	Y(1): 1.9; S(4): 98.1; Y(7): 0.0	S4;	S62		1.84	0	0	2	695.8	1391	55.57	10920
SSGNSSSSGSGSGTSAGSSsPGAR	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): 3.2; S(21): 96.8	S21;	S29	33		0	0	2	1092	2183	12.56	1746
SSGNSSSSGSGSGTSAGSSsPGAR	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): 3.2; S(21): 96.8	S21;	S29		3.74	0	0	2	1092	2183	12.56	1746
LSsAGPRsPYCK	ATAD2	29028	ATPase family AAA domain-containing protein 2	C11(Carbamido methyl)S3(Phospho) S8(Phospho)	S(2): 0.0; S(3): 100.0; S(8): 100.0; Y(10): 0.0	S3; S8;	S337; S342	24		0	1	2	741.8	1483	26.45	4703
NNsNTCNIENELEDSRK	ATAD2	29028	ATPase family AAA domain-containing protein 2	C6(Carbamidomethyl)S3(Phospho)	S(3): 99.9; T(5): 0.1; S(15): 0.0	S3;	S1243	19		0	1	3	706.3	2117	48.55	9400
LSsAGPRsPYCK	ATAD2	29028	ATPase family AAA domain-containing protein 2	C11(Carbamido methyl)S3(Phospho) S8(Phospho)	S(2): 0.0; S(3): 100.0; S(8): 100.0; Y(10): 0.0	S3; S8;	S337; S342		3.4	0	1	2	741.8	1483	26.45	4703
NNsNTCNIENELEDSRK	ATAD2	29028	ATPase family AAA domain-containing protein 2	C6(Carbamidomethyl)S3(Phospho)	S(3): 99.9; T(5): 0.1; S(15): 0.0	S3;	S1243		3.17	0	1	3	706.3	2117	48.55	9400
TQSEESRPQSLQQPATSTTETPAsPAHTT PQTQSTSGR	ATF2	1386	cyclic AMP-dependent transcription factor ATF-2 isoform 4	S24(Phospho)	T(1): 0.0; S(3): 0.0; S(6): 0.0; S(10): 0.0; T(16): 0.0; S(17): 0.0; T(18): 0.0; T(19): 0.0; T(21): 0.0; S(24): 88.7; T(28): 5.6; T(29): 5.6; T(32): 0.0; S(34): 0.0; T(35): 0.0; S(36): 0.0	S24;	S270	13		0	0	4	1023	4091	35.23	6568

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TQSESRPQSLQQPATSTTETPAshPTT PQTQSTSGR	ATF2	1386	cyclic AMP-dependent transcription factor ATF-2 isoform 4	S24(Phospho)	T(1): 0.0; S(3): 0.0; S(6): 0.0; S(10): 0.0; T(16): 0.0; S(17): 0.0; T(18): 0.0; T(19): 0.0; T(21): 0.0; S(24): 88.7; T(28): 5.6; T(29): 5.6; T(32): 0.0; S(34): 0.0; T(35): 0.0; S(36): 0.0	S24;	S270		5.44	0	0	4	1023	4091	35.23	6568
SKsEDMDNVQSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S3(Phospho)	S(1): 1.4; S(3): 98.6; S(11): 0.0	S3;	S558	44		0	1	2	724.3	1448	14.88	2245
MESSFGsPSKQESSES LPK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S7(Phospho)	S(3): 0.0; S(4): 2.3; S(7): 95.3; S(9): 2.3; S(13): 0.0; S(14): 0.0; S(16): 0.0	S7;	S477	37		0	1	3	708	2122	43.04	8209
NKQDDDLNCEPLsPHNITPEPVSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	C9(Carbamidomethyl)S13(Phospho)	S(13): 100.0; T(18): 0.0; S(23): 0.0	S13;	S113	25		0	1	3	943.1	2827	51.83	10088
MESsFGsPSKQESSES LPK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S4(Phospho)S7(Phospho)	S(3): 4.1; S(4): 95.9; S(7): 95.9; S(9): 4.1; S(13): 0.0; S(14): 0.0; S(16): 0.0	S4; S7;	S474; S477	12		0	1	3	734.6	2202	49.36	9570
SKsEDMDNVQSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S3(Phospho)	S(1): 1.4; S(3): 98.6; S(11): 0.0	S3;	S558		4.66	0	1	2	724.3	1448	14.88	2245
NKQDDDLNCEPLsPHNITPEPVSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	C9(Carbamidomethyl)S13(Phospho)	S(13): 100.0; T(18): 0.0; S(23): 0.0	S13;	S113		3.85	0	1	3	943.1	2827	51.83	10088
MESSFGsPSKQESSES LPK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S7(Phospho)	S(3): 0.0; S(4): 2.3; S(7): 95.3; S(9): 2.3; S(13): 0.0; S(14): 0.0; S(16): 0.0	S7;	S477		3.79	0	1	3	708	2122	43.04	8209
MESsFGsPSKQESSES LPK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	S4(Phospho)S7(Phospho)	S(3): 4.1; S(4): 95.9; S(7): 95.9; S(9): 4.1; S(13): 0.0; S(14): 0.0; S(16): 0.0	S4; S7;	S474; S477		2.83	0	1	3	734.6	2202	49.36	9570
NKQDDDLNCEPLsPHNITPEPVSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	C9(Carbamidomethyl)S13(Phospho)T18(Phospho)	S(13): 100.0; T(18): 99.7; S(23): 0.3	S13; T18;	S113; T118	14		0.001	1	3	969.7	2907	53.77	10530
NKQDDDLNCEPLsPHNITPEPVSK	ATF7IP	55729	activating transcription factor 7-interacting protein 1 isoform 4	C9(Carbamidomethyl)S13(Phospho)T18(Phospho)	S(13): 100.0; T(18): 99.7; S(23): 0.3	S13; T18;	S113; T118		3.14	0.008	1	3	969.7	2907	53.77	10530
DRNsWGGFSEK	ATL1	51062	atlastin-1 isoform b	S4(Phospho)	S(4): 100.0; S(9): 0.0	S4;	S10	27		0	1	2	681.8	1363	43.54	8314
DRNsWGGFSEK	ATL1	51062	atlastin-1 isoform b	S4(Phospho)	S(4): 100.0; S(9): 0.0	S4;	S10		3.32	0	1	2	681.8	1363	43.54	8314
TYEWsEEEEPVKK	ATL1	51062	atlastin-1 isoform b	S5(Phospho)S6(Phospho)	T(1): 0.0; Y(2): 0.0; S(5): 100.0; S(6): 100.0	S5; S6;	S22; S23		1.52	0.003	1	2	950.9	1901	50.75	9864
SEEsEsESEETNAPK	ATN1	1822	atrophin-1	S5(Phospho)S7(Phospho)	S(1): 0.2; S(5): 99.9; S(7): 99.8; S(9): 0.1; T(12): 0.0	S5; S7;	S77; S79	51		0	0	2	963.4	1926	38.28	7206
SEEsEsESEETNAPK	ATN1	1822	atrophin-1	S5(Phospho)S7(Phospho)	S(1): 0.2; S(5): 99.9; S(7): 99.8; S(9): 0.1; T(12): 0.0	S5; S7;	S77; S79		3.3	0	0	2	963.4	1926	38.28	7206
DsPTLSNSGIR	ATP13A1	57130	manganese-transporting ATPase 13A1	S2(Phospho)	S(2): 99.9; T(4): 0.1; S(6): 0.0; S(8): 0.0	S2;	S899	37		0	0	2	613.8	1227	41.07	7796
DsPTLSNSGIR	ATP13A1	57130	manganese-transporting ATPase 13A1	S2(Phospho)	S(2): 99.9; T(4): 0.1; S(6): 0.0; S(8): 0.0	S2;	S899		2.39	0	0	2	613.8	1227	41.07	7796
RPTETNPVTSNsDEECNETVK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamidomethyl)S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 0.0; S(12): 100.0; T(19): 0.0	S12;	S639	67		0	0	3	829.7	2487	30.84	5636
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	54		0	0	2	705.8	1411	36.92	6923
RPTETNPVTSNsDEECNETVKEK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamidomethyl)S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 3.0; S(12): 96.9; T(19): 0.1	S12;	S639	41		0	1	3	915.4	2744	26.83	4786

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#
HKLTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S6(Phospho) S10(Phospho)	T(4): 0.0; S(6): 100.0; S(10): 100.0	S6; S10;	S1310; S1314	40		0	1	2	838.3	1676	22.91	3955
RPTETNPVTsNsDEECNETVKEK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S10(Phospho) S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 100.0; S(12): 100.0; T(19): 0.0	S10; S12;	S637; S639	39		0	1	3	942.1	2824	29.73	5407
RPTETNPVTsNsDEECNETVK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S10(Phospho) S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.3; S(10): 99.7; S(12): 100.0; T(19): 0.0	S10; S12;	S637; S639	28		0	0	3	856.3	2567	36.17	6766
LTVsDGEsGEEKK	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	28		0	1	2	769.8	1539	25.69	4538
RPTETNPVTsNsDEECNETVK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 0.0; S(12): 100.0; T(19): 0.0	S12;	S639		6.2	0	0	3	829.7	2487	30.84	5636
RPTETNPVTsNsDEECNETVKEK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 3.0; S(12): 96.9; T(19): 0.1	S12;	S639		5.16	0	1	3	915.4	2744	26.83	4786
HKLTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S6(Phospho) S10(Phospho)	T(4): 0.0; S(6): 100.0; S(10): 100.0	S6; S10;	S1310; S1314		3.92	0	1	2	838.3	1676	22.91	3955
RPTETNPVTsNsDEECNETVK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S10(Phospho) S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.3; S(10): 99.7; S(12): 100.0; T(19): 0.0	S10; S12;	S637; S639		3.31	0	0	3	856.3	2567	36.17	6766
RPTETNPVTsNsDEECNETVKEK	ATRX	546	transcriptional regulator ATRX isoform 2	C16(Carbamido methyl)S10(Phospho) S12(Phospho)	T(3): 0.0; T(5): 0.0; T(9): 0.0; S(10): 100.0; S(12): 100.0; T(19): 0.0	S10; S12;	S637; S639		3.1	0	1	3	942.1	2824	29.73	5407
HKLTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S6(Phospho) S10(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 100.0	S6; S10;	S1310; S1314	17		0.001	1	3	559.2	1676	22.95	3963
LTVsDGEsGEEKK	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		3.25	0.001	1	2	769.8	1539	25.69	4538
yVESDDEKPLDDETVNEDASNENSENDITMQSLPK	ATRX	546	transcriptional regulator ATRX isoform 2	Y1(Phospho)	Y(1): 92.4; S(4): 7.6; T(14): 0.0; S(20): 0.0; S(24): 0.0; T(29): 0.0; S(32): 0.0	Y1;	Y89		2.27	0.001	0	3	1351	4051	66.89	13484
HKLTVsDGEsGEEK	ATRX	546	transcriptional regulator ATRX isoform 2	S6(Phospho) S10(Phospho)	T(4): 0.1; S(6): 99.9; S(10): 100.0	S6; S10;	S1310; S1314		3.9	0.002	1	3	559.2	1676	22.95	3963
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		3.15	0.003	0	2	705.8	1411	36.92	6923
QNSPAGNKENIKPNETSPsFSK	ATXN2	6311	ataxin-2 isoform 3	S19(Phospho)	S(3): 0.0; T(16): 51.0; S(17): 51.0; S(19): 97.8; S(21): 0.3	S19;	S485		5.06	0	1	3	845.4	2534	33.02	6090
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	46		0	0	2	584.3	1168	18.37	2996
STsTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S3(Phospho) S7(Phospho)	S(1): 2.3; T(2): 2.3; S(3): 95.4; T(4): 0.1; T(6): 2.3; S(7): 97.7	S3; S7;	S680; S684	38		0	0	2	624.2	1247	24.99	4390
QSGSGREsPSLASR	ATXN2L	11273	ataxin-2-like protein isoform D	S7(Phospho)	S(3): 2.8; S(7): 97.1; S(9): 0.1; S(12): 0.0	S7;	S339	29		0	1	2	706.3	1412	17.8	2877
TESVSDKEDKPLAPSGGTGTEPQPPPCPSQTGsPPVGLIK	ATXN2L	11273	ataxin-2-like protein isoform D	C29(Carbamido methyl)S35(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(16): 0.0; T(19): 0.0; S(31): 6.3; T(33): 6.3; S(35): 87.3	S35;	S634		4.43	0	1	4	1087	4345	62.29	12373
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		3.27	0	0	2	584.3	1168	18.37	2996

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#
STsTPTsPGPR	ATXN2L	11273	ataxin-2-like protein isoform D	S3(Phospho) S7(Phospho)	S(1): 2.3; T(2): 2.3; S(3): 95.4; T(4): 0.1; T(6): 2.3; S(7): 97.7	S3; S7;	S680; S684		3.15	0	0	2	624.2	1247	24.99	4390
QSGSGREsPSLASR	ATXN2L	11273	ataxin-2-like protein isoform D	S7(Phospho)	S(3): 2.8; S(7): 97.1; S(9): 0.1; S(12): 0.0	S7;	S339		2.87	0	1	2	706.3	1412	17.8	2877
LQWDGSSDLsPSDSGSSK	ATXN7L3	56970	ataxin-7-like protein 3 isoform b	S10(Phospho)	S(6): 0.0; S(7): 0.0; S(10): 96.8; S(12): 3.0; S(14): 0.0; S(16): 0.1; S(17): 0.1	S10;	S281	35		0	0	2	966.9	1933	57.76	11399
LQWDGSSDLsPSDSGSSK	ATXN7L3	56970	ataxin-7-like protein 3 isoform b	S10(Phospho)	S(6): 0.0; S(7): 0.0; S(10): 96.8; S(12): 3.0; S(14): 0.0; S(16): 0.1; S(17): 0.1	S10;	S281		2.31	0	0	2	966.9	1933	57.76	11399
REPGGWGAGASAPVEDDSDAEYGEEN DEQGNYSK	AVEN	57099	cell death regulator Aven	T22(Phospho)	S(11): 0.0; S(18): 4.4; T(22): 91.3; Y(23): 4.4; Y(33): 0.0; S(34): 0.0	T22;	T98	57		0	1	3	1257	3768	55.46	10896
REPGGWGAGASAPVEDDSDAEYGEEN DEQGNYSK	AVEN	57099	cell death regulator Aven	T22(Phospho)	S(11): 0.0; S(18): 4.4; T(22): 91.3; Y(23): 4.4; Y(33): 0.0; S(34): 0.0	T22;	T98		5	0	1	3	1257	3768	55.46	10896
SEGEGEAASADDGSLNtSGAGPK	BABAM1	29086	BRISC and BRCA1-A complex member 1 isoform 2	T17(Phospho)	S(1): 0.0; S(9): 0.0; S(14): 0.0; T(17): 96.0; S(18): 4.0	T17;	T65	23		0	0	2	1094	2187	36.5	6836
SEGEGEAASADDGSLNtSGAGPK	BABAM1	29086	BRISC and BRCA1-A complex member 1 isoform 2	T17(Phospho)	S(1): 0.0; S(9): 0.0; S(14): 0.0; T(17): 96.0; S(18): 4.0	T17;	T65		4.12	0	0	2	1094	2187	36.5	6836
SQsPAASDCSSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl) S3(Phospho)	S(1): 3.1; S(3): 96.9; 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	59		0	0	2	1140	2280	32.1	5898
SQsPAASDCSSSSSSASLPSSGR	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	55		0	0	3	760.6	2280	32.11	5900
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): 98.4; S(9): 1.6	T3; S7;	T285; S289	49		0	0	2	719.8	1439	40.75	7730
sQSPAASDCSSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl) S1(Phospho)	S(1): 96.7; S(3): 3.3; 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	S1;	S171	47		0	0	2	1140	2280	32.67	6017
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	44		0	0	2	719.8	1439	39.69	7507
SSVQGASSREGsPAR	BAG3	9531	BAG family molecular chaperone regulator 3	S12(Phospho)	S(1): 0.0; S(2): 0.0; S(7): 50.0; S(8): 50.0; S(12): 100.0	S12;	S279	35		0	1	2	818.3	1636	14.97	2263
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	35		0	0	2	719.8	1439	40.22	7620
SStPLHsPsPIR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho) S7(Phospho) S9(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 100.0	T3; S7; S9;	T285; S289; S291	35		0	0	2	759.8	1519	46.97	9069
VPPAPVPCPPPsPGPSAVPsPK	BAG3	9531	BAG family molecular chaperone regulator 3	C8(Carbamidomethyl) S12(Phospho) S21(Phospho)	S(12): 99.8; S(16): 0.2; S(20): 4.3; S(21): 95.7	S12; S21;	S377; S386	29		0	0	3	793.7	2379	72.52	14659
SSVQGAsSREGSPAR	BAG3	9531	BAG family molecular chaperone regulator 3	S7(Phospho)	S(1): 0.0; S(2): 0.0; S(7): 97.9; S(8): 2.1; S(12): 0.0	S7;	S274	19		0	1	2	778.3	1556	13.87	2032

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#
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		4.93	0	0	3	760.6	2280	32.11	5900
VPPAPVPCPPSPGPSAVPSsPK	BAG3	9531	BAG family molecular chaperone regulator 3	C8(Carbamidomethyl)S12(Phospho)S21(Phospho)	S(12): 99.8; S(16): 0.2; S(20): 4.3; S(21): 95.7	S12; S21;	S377; S386		4.92	0	0	3	793.7	2379	72.52	14659
SQsPAASDCSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl)S3(Phospho)	S(1): 3.1; S(3): 96.9; 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		4.11	0	0	2	1140	2280	32.1	5898
SStPLHsPPIR	BAG3	9531	BAG family molecular chaperone regulator 3	T3(Phospho)S7(Phospho)S9(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 100.0; S(7): 100.0; S(9): 100.0	T3; S7; S9;	T285; S289; S291		3.84	0	0	2	759.8	1519	46.97	9069
SStPLHsPPIR	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): 98.4; S(9): 1.6	T3; S7;	T285; S289		3.46	0	0	2	719.8	1439	40.75	7730
sQSPAASDCSSSSSASLPSSGR	BAG3	9531	BAG family molecular chaperone regulator 3	C9(Carbamidomethyl)S1(Phospho)	S(1): 96.7; S(3): 3.3; 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	S1;	S171		2.87	0	0	2	1140	2280	32.67	6017
SStPLHsPPIR	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		2.84	0	0	2	719.8	1439	39.69	7507
SStPLHsPPIR	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		2.79	0	0	2	719.8	1439	40.22	7620
SSGNSPtPVSR	BAG4	9530	BAG family molecular chaperone regulator 4 isoform 2	T7(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; T(7): 100.0; S(10): 0.0	T7;	T145	65		0	0	2	584.8	1168	17.26	2762
SSGNSPtPVSR	BAG4	9530	BAG family molecular chaperone regulator 4 isoform 2	T7(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; T(7): 100.0; S(10): 0.0	T7;	T145		3.29	0	0	2	584.8	1168	17.26	2762
LQEDPNYsPQR	BAG6	7917	large proline-rich protein BAG6 isoform d	S8(Phospho)	Y(7): 0.0; S(8): 100.0	S8;	S1062	45		0	0	2	713.8	1427	32.34	5948
AsPEPQRENAsPAPGTTAEAMSR	BAG6	7917	large proline-rich protein BAG6 isoform d	S2(Phospho)S11(Phospho)	S(2): 100.0; S(11): 99.9; T(16): 0.1; T(17): 0.0; S(23): 0.0	S2; S11;	S958; S967	40		0	1	3	882	2644	45.2	8696
AsPEPQRENAsPAPGTTAEAMSR	BAG6	7917	large proline-rich protein BAG6 isoform d	M22(Oxidation)S2(Phospho)S11(Phospho)	S(2): 100.0; S(11): 100.0; T(16): 0.0; T(17): 0.0; S(23): 0.0	S2; S11;	S958; S967	17		0	1	3	887.4	2660	32.88	6061
APPQTHLPsGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 99.8; T(30): 0.2	S26;	S113	16		0	0	4	717.1	2865	30.84	5638
APPQTHLPsGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 100.0; T(30): 0.0	S26;	S113	13		0	0	4	717.1	2865	30.23	5512

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#
APPQTHLPSGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 99.8; T(30): 0.2	S26;	S113		7.8	0	0	4	717.1	2865	30.84	5638
APPQTHLPSGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 100.0; T(30): 0.0	S26;	S113		5.9	0	0	4	717.1	2865	30.23	5512
AsPEPQRENAsPAPGTTAEAMSR	BAG6	7917	large proline-rich protein BAG6 isoform d	S2(Phospho) S11(Phospho)	S(2): 100.0; S(11): 99.9; T(16): 0.1; T(17): 0.0; S(23): 0.0	S2; S11;	S958; S967		5.28	0	1	3	882	2644	45.2	8696
AsPEPQRENAsPAPGTTAEAMSR	BAG6	7917	large proline-rich protein BAG6 isoform d	M22(Oxidation) S2(Phospho) S11(Phospho)	S(2): 100.0; S(11): 100.0; T(16): 0.0; T(17): 0.0; S(23): 0.0	S2; S11;	S958; S967		4.39	0	1	3	887.4	2660	32.88	6061
APPQTHLPSGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 100.0; T(30): 0.0	S26;	S113		3.82	0	0	3	955.8	2865	31.1	5692
APPQTHLPSGASSGTGSASATHGGGsPPGTR	BAG6	7917	large proline-rich protein BAG6 isoform d	S26(Phospho)	T(5): 0.0; S(9): 0.0; S(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.0; S(19): 0.0; T(21): 0.0; S(26): 99.7; T(30): 0.3	S26;	S113		3.11	0.001	0	3	955.8	2865	30.24	5514
LQEDPNYsPQR	BAG6	7917	large proline-rich protein BAG6 isoform d	S8(Phospho)	Y(7): 0.0; S(8): 100.0	S8;	S1062		2.71	0.001	0	2	713.8	1427	32.34	5948
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	1139	24.34	4252
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		2.34	0	0	2	569.8	1139	24.34	4252
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 0.0; T(10): 100.0; S(14): 100.0	T10; S14;	T257; S261	47		0	0	2	1044	2087	60.82	12050
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) T10(Phospho) S14(Phospho)	T(1): 0.1; S(4): 0.0; T(5): 0.0; S(8): 0.1; T(10): 99.8; S(14): 100.0	T10; S14;	T257; S261	39		0	0	3	701.6	2103	52.87	10330
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 0.0; T(10): 100.0; S(14): 100.0	T10; S14;	T257; S261	38		0	0	3	696.3	2087	60.85	12058
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 3.1; T(10): 96.9; S(14): 100.0	T10; S14;	T257; S261	22		0	0	2	1052	2103	52.86	10327
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) T10(Phospho) S14(Phospho)	T(1): 0.1; S(4): 0.0; T(5): 0.0; S(8): 0.1; T(10): 99.8; S(14): 100.0	T10; S14;	T257; S261		6.13	0	0	3	701.6	2103	52.87	10330
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 0.0; T(10): 100.0; S(14): 100.0	T10; S14;	T257; S261		5.89	0	0	3	696.3	2087	60.85	12058
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 0.0; T(10): 100.0; S(14): 100.0	T10; S14;	T257; S261		4	0	0	2	1044	2087	60.82	12050

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#
TPASTPVSGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	M16(Oxidation) T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.0; T(5): 0.0; S(8): 3.1; T(10): 96.9; S(14): 100.0	T10; S14;	T257; S261		2.91	0	0	2	1052	2103	52.86	10327
TPASTPVsGtPQAsPMIER	BAIAP2L1	55971	brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	S8(Phospho) T10(Phospho) S14(Phospho)	T(1): 0.0; S(4): 0.3; T(5): 5.3; S(8): 94.7; T(10): 99.7; S(14): 100.0	S8; T10; S14;	S255; T257; S261		2.51	0.003	0	2	1084	2167	71.55	14468
APAASEGNHTDGAEEAAGSCAQAPSHs PPNKPK	BAP1	8314	ubiquitin carboxyl-terminal hydrolase BAP1	C20(Carbamido methyl) S27(Phospho)	S(5): 0.0; T(10): 0.0; S(19): 0.0; S(25): 0.3; S(27): 99.7	S27;	S327		5.99	0	0	4	831.1	3321	25.93	4592
KAEGAAtEEEGtPKESEPQAAAEPAEAK	BASP1	10409	brain acid soluble protein 1	T7(Phospho) T12(Phospho)	T(7): 100.0; T(12): 94.6; S(16): 5.4	T7; T12;	T31; T36	33		0	2	3	996.1	2986	30.38	5543
KtEAPAAPAAQETKSDGAPASDSKPGSS EAAPSSK	BASP1	10409	brain acid soluble protein 1	T2(Phospho)	T(2): 93.7; T(13): 5.9; S(15): 0.4; S(21): 0.0; S(23): 0.0; S(27): 0.0; S(28): 0.0; S(33): 0.0; S(34): 0.0	T2;	T151	29		0	2	4	852.4	3407	24.64	4315
KtEAPAAPAAQETKSDGAPASDSKPGSS EAAPSSK	BASP1	10409	brain acid soluble protein 1	T2(Phospho)	T(2): 99.9; T(13): 0.0; S(15): 0.0; S(21): 0.0; S(23): 0.0; S(27): 0.0; S(28): 0.0; S(33): 0.0; S(34): 0.0	T2;	T151	6.98	0	2	4	852.4	3407	25.18	4430	
KtEAPAAPAAQETKSDGAPASDSKPGSS EAAPSSK	BASP1	10409	brain acid soluble protein 1	T2(Phospho)	T(2): 93.7; T(13): 5.9; S(15): 0.4; S(21): 0.0; S(23): 0.0; S(27): 0.0; S(28): 0.0; S(33): 0.0; S(34): 0.0	T2;	T151	6.75	0	2	4	852.4	3407	24.64	4315	
KAEGAAtEEEGtPKESEPQAAAEPAEAK	BASP1	10409	brain acid soluble protein 1	T7(Phospho) T12(Phospho)	T(7): 100.0; T(12): 94.6; S(16): 5.4	T7; T12;	T31; T36		4.72	0	2	3	996.1	2986	30.38	5543
LAEDGEGsEPEAVGQSR	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(8): 100.0; S(16): 0.0	S8;	S1468	86		0	0	2	934.9	1869	36.49	6832
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho)	S(2): 0.1; S(8): 99.7; S(10): 0.1; S(11): 0.0; S(16): 0.0; S(17): 0.0	S8;	S158	40		0	2	3	933.7	2799	16.68	2634
SDGACDSPsSDKENsSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C5(Carbamidomethyl) S9(Phospho) S15(Phospho)	S(1): 0.0; S(7): 4.4; S(9): 91.8; S(10): 8.0; S(15): 91.6; S(16): 4.2	S9; S15;	S160; S166	28		0	1	3	917.7	2751	21.36	3623
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho) S11(Phospho)	S(2): 0.3; S(8): 94.7; S(10): 9.9; S(11): 94.7; S(16): 0.3; S(17): 0.0	S8; S11;	S158; S161	25		0	2	3	960.4	2879	17.8	2878
RSDVQEEsEGSDTDDNKDSAAFEDNEV QDEFLEK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(2): 0.0; S(8): 99.3; S(11): 4.5; T(13): 48.1; S(19): 48.1	S8;	S705	19		0	2	4	1010	4038	67.57	13634
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho)	S(2): 0.0; S(8): 99.7; S(10): 0.5; S(11): 2.7; S(16): 48.6; S(17): 48.6	S8;	S158	18		0	2	4	720.5	2879	17.76	2870
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho)	S(2): 0.2; S(8): 84.0; S(10): 3.9; S(11): 3.9; S(16): 3.9; S(17): 3.9	S8;	S158	11		0	2	4	700.5	2799	16.5	2591
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho)	S(2): 0.1; S(8): 99.7; S(10): 0.1; S(11): 0.0; S(16): 0.0; S(17): 0.0	S8;	S158	5.99	0	2	3	933.7	2799	16.68	2634	
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl) S8(Phospho) S11(Phospho)	S(2): 0.3; S(8): 94.7; S(10): 9.9; S(11): 94.7; S(16): 0.3; S(17): 0.0	S8; S11;	S158; S161		5.21	0	2	3	960.4	2879	17.8	2878

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#
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl)S8(Phospho)	S(2): 0.2; S(8): 84.0; S(10): 3.9; S(11): 3.9; S(16): 3.9; S(17): 3.9	S8;	S158		4.16	0	2	4	700.5	2799	16.5	2591
RSDVQEEsEGSDTDDNKDSAAFEDNEVQDEFLEK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(2): 0.0; S(8): 99.3; S(11): 4.5; T(13): 48.1; S(19): 48.1	S8;	S705		4.14	0	2	4	1010	4038	67.57	13634
SDGACDSPsSDKENsSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C5(Carbamidomethyl)S9(Phospho)S15(Phospho)	S(1): 0.0; S(7): 4.4; S(9): 91.8; S(10): 8.0; S(15): 91.6; S(16): 4.2	S9; S15;	S160; S166		4.06	0	1	3	917.7	2751	21.36	3623
LADEGDsEPEAVGQSR	BAZ1B	9031	tyrosine-protein kinase BAZ1B	S8(Phospho)	S(8): 100.0; S(16): 0.0	S8;	S1468		3.75	0	0	2	934.9	1869	36.49	6832
KSDGACDsPSSDKENSSQIAQDHQK	BAZ1B	9031	tyrosine-protein kinase BAZ1B	C6(Carbamidomethyl)S8(Phospho)	S(2): 0.0; S(8): 99.7; S(10): 0.5; S(11): 2.7; S(16): 48.6; S(17): 48.6	S8;	S158		3.96	0.003	2	4	720.5	2879	17.76	2870
RLsASStGSTR	BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 9	S3(Phospho)T7(Phospho)	S(3): 100.0; S(5): 0.1; S(6): 0.1; T(7): 97.7; S(9): 2.2; T(10): 0.1	S3; T7;	S218; T222	32		0	1	2	641.8	1283	15.78	2436
RLsASStGSTR	BCAR1	9564	breast cancer anti-estrogen resistance protein 1 isoform 9	S3(Phospho)T7(Phospho)	S(3): 100.0; S(5): 0.1; S(6): 0.1; T(7): 97.7; S(9): 2.2; T(10): 0.1	S3; T7;	S218; T222		3.36	0	1	2	641.8	1283	15.78	2436
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S16(Phospho)S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.3; S(10): 5.4; S(14): 0.6; S(16): 94.0; S(18): 99.7; T(22): 0.0; S(23): 0.0	S16; S18;	S120; S122	24		0	0	3	970.1	2908	50.42	9793
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S10(Phospho)S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.0; S(10): 100.0; S(14): 51.4; S(16): 51.4; S(18): 97.2; T(22): 0.0; S(23): 0.0	S10; S18;	S114; S122	18		0	0	3	996.7	2988	59.15	11715
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.0; S(10): 0.2; S(14): 4.0; S(16): 4.0; S(18): 91.8; T(22): 0.0; S(23): 0.0	S18;	S122	16		0	0	3	943.4	2828	44.98	8649
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S16(Phospho)S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.3; S(10): 5.4; S(14): 0.6; S(16): 94.0; S(18): 99.7; T(22): 0.0; S(23): 0.0	S16; S18;	S120; S122		4.21	0	0	3	970.1	2908	50.42	9793
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.0; S(10): 0.2; S(14): 4.0; S(16): 4.0; S(18): 91.8; T(22): 0.0; S(23): 0.0	S18;	S122		4.05	0	0	3	943.4	2828	44.98	8649
VDSSTNSSPSPQQSEsLsPAHTSDFR	BCL7B	9275	B-cell CLL/lymphoma 7 protein family member B isoform 1	S10(Phospho)S18(Phospho)	S(3): 0.0; S(4): 0.0; T(5): 0.0; S(7): 0.0; S(8): 0.0; S(10): 100.0; S(14): 51.4; S(16): 51.4; S(18): 97.2; T(22): 0.0; S(23): 0.0	S10; S18;	S114; S122		3.96	0	0	3	996.7	2988	59.15	11715
GtEPsPGGtPQPSRPVSPAGPPEGVPVEEAQPPR	BCL7C	9274	B-cell CLL/lymphoma 7 protein family member C isoform 2	T2(Phospho)S5(Phospho)T9(Phospho)	T(2): 99.9; S(5): 99.2; T(9): 91.9; S(13): 8.2; S(17): 0.8	T2; S5; T9;	T111; S114; T118	26		0	0	4	875.6	3500	65.06	13065
GtEPsPGGTPQPSRPVSPAGPPEGVPVEEAQPPR	BCL7C	9274	B-cell CLL/lymphoma 7 protein family member C isoform 2	T2(Phospho)S5(Phospho)	T(2): 97.6; S(5): 90.1; T(9): 8.7; S(13): 1.8; S(17): 1.8	T2; S5;	T111; S114	24		0	0	4	855.6	3420	58	11446
GtEPsPGGTPQPSRPVSPAGPPEGVPVEEAQPPR	BCL7C	9274	B-cell CLL/lymphoma 7 protein family member C isoform 2	T2(Phospho)S5(Phospho)	T(2): 97.6; S(5): 90.1; T(9): 8.7; S(13): 1.8; S(17): 1.8	T2; S5;	T111; S114		3.62	0	0	4	855.6	3420	58	11446

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#
GTEPSPGGTQPQSRPVSAPGPEGVPEE AQPPR	BCL7C	9274	B-cell CLL/lymphoma 7 protein family member C isoform 2	T2(Phospho) S5(Phospho) T9(Phospho)	T(2): 99.9; S(5): 99.2; T(9): 91.9; S(13): 8.2; S(17): 0.8	T2; S5; T9;	T111; S114; T118		3.02	0	0	4	875.6	3500	65.06	13065
GTEPSPGGTQPQSRPVSPAGPPEGVPEE AQPPR	BCL7C	9274	B-cell CLL/lymphoma 7 protein family member C isoform 2	S17(Phospho)	T(2): 7.0; S(5): 0.7; T(9): 7.0; S(13): 7.0; S(17): 78.4	S17;	S126		2.99	0.001	0	3	1114	3340	52.18	10179
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	43		0	0	2	634.3	1268	47.68	9217
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		3.54	0	0	2	634.3	1268	47.94	9271
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		3.36	0	0	2	634.3	1268	47.68	9217
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	31		0.002	0	2	634.3	1268	47.94	9271
FNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; T(12): 0.0; Y(15): 0.0	S4;	S395	72		0	0	2	1001	2002	41.44	7873
FNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 99.9; T(12): 0.1; Y(15): 0.0	S4; T9;	S395; T400	72		0	0	2	1041	2082	49.01	9498
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	58		0	2	2	799.4	1598	12.53	1739
KAEGEPQEEsPLK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0	S10;	S175	56		0	1	2	761.3	1522	22.48	3861
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395	53		0	1	2	1129	2258	34	6293
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395	51		0	1	3	753.3	2258	33.84	6259
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395	48		0	1	3	753.3	2258	34.39	6375
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	47		0	2	3	533.3	1598	12.49	1727
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	47		0	1	2	735.3	1470	12.97	1843
ySPSQNsPIHHIPSR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	Y1(Phospho) S7(Phospho)	Y(1): 97.2; S(2): 2.8; S(4): 0.0; S(7): 100.0; S(14): 0.0	Y1; S7;	Y282; S288	46		0	0	3	627.3	1880	37.96	7138
NTPSQHSHSIQHsPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	S13;	S266	45		0	0	3	641.3	1922	12.92	1833
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 98.5; S(14): 1.5	S10;	S175	42		0	2	2	868.9	1737	18.22	2964
NtPSQHSHSIQHsPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	T2(Phospho) S13(Phospho)	T(2): 100.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	T2; S13;	T255; S266	38		0	0	3	667.9	2002	13.05	1859
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175	37		0	2	3	579.6	1737	18.61	3045
NTPSQHSHSIQHsPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	S13;	S266	32		0	0	2	961.4	1922	13.1	1871
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175	32		0	2	3	579.6	1737	18.09	2937
NTPSQHSHSIQHsPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S9(Phospho) S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S262; S266	29		0	0	3	667.9	2002	13.59	1974
ySPSQNsPIHHIPSR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	Y1(Phospho) S7(Phospho)	Y(1): 97.7; S(2): 2.3; S(4): 0.1; S(7): 99.9; S(14): 0.0	Y1; S7;	Y282; S288	26		0	0	3	627.3	1880	38.49	7249
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175	23		0	2	2	868.9	1737	18.77	3078
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		7.31	0	2	3	533.3	1598	12.49	1727
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175		7.06	0	2	3	579.6	1737	18.61	3045
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175		6.4	0	2	3	579.6	1737	18.09	2937

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#
NTPSQSHSIQHSPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	T2(Phospho) S13(Phospho)	T(2): 100.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	T2; S13;	T255; S266		5.79	0	0	3	667.9	2002	13.05	1859
NTPSQSHSIQHSPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	S13;	S266		5.21	0	0	3	641.3	1922	12.92	1833
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395		4.97	0	1	3	753.3	2258	33.84	6259
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		4.72	0	2	2	799.4	1598	12.53	1739
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395		4.7	0	1	3	753.3	2258	34.39	6375
QKFNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S6(Phospho)	S(6): 100.0; T(11): 0.0; T(14): 0.0; Y(17): 0.0	S6;	S395		4.53	0	1	2	1129	2258	34	6293
KAEGEPQEEsPLK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0	S10;	S175		4.5	0	1	2	761.3	1522	22.48	3861
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 98.5; S(14): 1.5	S10;	S175		4.47	0	2	2	868.9	1737	18.22	2964
ySPSQNsPIHHIPSR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	Y1(Phospho) S7(Phospho)	Y(1): 97.2; S(2): 2.8; S(4): 0.0; S(7): 100.0; S(14): 0.0	Y1; S7;	Y282; S288		4.17	0	0	3	627.3	1880	37.96	7138
FNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 99.9; T(12): 0.1; Y(15): 0.0	S4; T9;	S395; T400		3.73	0	0	2	1041	2082	49.01	9498
FNDSEGGDTEETEDYR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; T(12): 0.0; Y(15): 0.0	S4;	S395		3.57	0	0	2	1001	2002	41.44	7873
ySPSQNsPIHHIPSR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	Y1(Phospho) S7(Phospho)	Y(1): 97.7; S(2): 2.3; S(4): 0.1; S(7): 99.9; S(14): 0.0	Y1; S7;	Y282; S288		3.21	0	0	3	627.3	1880	38.49	7249
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		3.09	0	1	2	735.3	1470	12.97	1843
YSPSQNSPIHHIPsR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S14(Phospho)	Y(1): 49.1; S(2): 49.1; S(4): 1.8; S(7): 0.2; S(14): 99.9	S14;	S295	24		0.001	0	2	940.4	1880	37.98	7144
NTPSQSHSIQHSPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S9(Phospho) S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S262; S266		4.72	0.001	0	3	667.9	2002	13.59	1974
AEGEWEDQEALDYfSKESGK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S15(Phospho)	Y(13): 4.5; S(15): 95.3; S(19): 0.2	S15;	S383		3.24	0.001	1	3	838.3	2513	68.24	13798
KAEGEPQEEsPLKSK	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S10(Phospho)	S(10): 100.0; S(14): 0.0	S10;	S175		3.03	0.001	2	2	868.9	1737	18.77	3078
YSPSQNSPIHHIPsR	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S14(Phospho)	Y(1): 49.1; S(2): 49.1; S(4): 1.8; S(7): 0.2; S(14): 99.9	S14;	S295		2.04	0.001	0	2	940.4	1880	37.98	7144
NTPSQSHSIQHSPER	BCLAF1	9774	bcl-2-associated transcription factor 1 isoform 2	S13(Phospho)	T(2): 0.0; S(4): 0.0; S(7): 0.0; S(9): 0.0; S(13): 100.0	S13;	S266		2.71	0.007	0	2	961.4	1922	13.1	1871
ASASRPQPAPADGADPPPAEEPEARPD GEGsPGK	BCR	613	breakpoint cluster region protein isoform 2	S31(Phospho)	S(2): 0.0; S(4): 0.0; S(31): 100.0	S31;	S122	21		0	0	4	847.9	3389	33.67	6224
ASASRPQPAPADGADPPPAEEPEARPD GEGsPGK	BCR	613	breakpoint cluster region protein isoform 2	S31(Phospho)	S(2): 0.0; S(4): 0.0; S(31): 100.0	S31;	S122		7.1	0	0	4	847.9	3389	33.67	6224
ASASRPQPAPADGADPPPAEEPEARPD GEGsPGK	BCR	613	breakpoint cluster region protein isoform 2	S31(Phospho)	S(2): 0.0; S(4): 0.0; S(31): 100.0	S31;	S122		4.97	0	0	3	1130	3389	33.88	6268
TSPGGRTSPEAR	BICD2	23299	protein bicaudal D homolog 2 isoform 2	T7(Phospho)	T(1): 50.0; S(2): 50.0; T(7): 97.1; S(8): 2.9	T7;	T573		2.55	0	1	2	688.3	1376	13.08	1866
VAGEAAEtDsEPEPEPEPTAAPR	BLOC1S3	388552	biogenesis of lysosome-related organelles complex 1 subunit 3	T8(Phospho) S10(Phospho)	T(8): 100.0; S(10): 100.0; T(19): 0.0	T8; S10;	T63; S65	66		0	0	2	1256	2510	53.46	10463
VAGEAAEtDsEPEPEPEPTAAPR	BLOC1S3	388552	biogenesis of lysosome-related organelles complex 1 subunit 3	T8(Phospho) S10(Phospho)	T(8): 100.0; S(10): 100.0; T(19): 0.0	T8; S10;	T63; S65	17		0	0	3	837.3	2510	53.27	10422
VAGEAAEtDsEPEPEPEPTAAPR	BLOC1S3	388552	biogenesis of lysosome-related organelles complex 1 subunit 3	T8(Phospho) S10(Phospho)	T(8): 100.0; S(10): 100.0; T(19): 0.0	T8; S10;	T63; S65		4.31	0	0	3	837.3	2510	53.27	10422
VAGEAAEtDsEPEPEPEPTAAPR	BLOC1S3	388552	biogenesis of lysosome-related organelles complex 1 subunit 3	T8(Phospho) S10(Phospho)	T(8): 100.0; S(10): 100.0; T(19): 0.0	T8; S10;	T63; S65		3.18	0	0	2	1256	2510	53.46	10463

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#
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 0.3; Y(2): 0.3; S(3): 99.6; S(5): 99.9; T(10): 0.0	S3; S5;	S482; S484	69		0	0	2	940.3	1880	64.44	12923
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 3.3; Y(2): 3.3; S(3): 93.4; S(5): 99.9; T(10): 0.0	S3; S5;	S482; S484	55		0	0	2	940.3	1880	64.96	13043
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 0.4; Y(2): 0.4; S(3): 99.6; S(5): 99.6; T(10): 0.0	S3; S5;	S482; S484	38		0	0	2	940.3	1880	64.39	12911
sVSDPVEDKKEQESDEEEEEDEPSGA TTR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S1(Phospho)	S(1): 94.6; S(3): 0.3; S(14): 5.1; S(27): 0.0; T(30): 0.0; T(31): 0.0	S1;	S2973	28		0	2	3	1240	3718	37.7	7085
TDTGIVTVQSPSSK	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S13(Phospho)	T(1): 0.0; T(3): 0.0; T(7): 0.0; S(11): 2.7; S(13): 91.9; S(14): 2.7; S(15): 2.7	S13;	S2907	23		0	0	2	858.4	1716	45.16	8686
sVSDPVEDKKEQESDEEEEEDEPSGA TTR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S14(Phospho)	S(1): 94.6; S(3): 0.3; S(14): 5.1; S(27): 0.0; T(30): 0.0; T(31): 0.0	S1;	S2973		3.51	0	2	3	1240	3718	37.7	7085
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 0.3; Y(2): 0.3; S(3): 99.6; S(5): 99.9; T(10): 0.0	S3; S5;	S482; S484		3.18	0	0	2	940.3	1880	64.44	12923
TDTGIVTVQSPSSK	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S13(Phospho)	T(1): 0.0; T(3): 0.0; T(7): 0.0; S(11): 2.7; S(13): 91.9; S(14): 2.7; S(15): 2.7	S13;	S2907		3.04	0	0	2	858.4	1716	45.16	8686
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 3.3; Y(2): 3.3; S(3): 93.4; S(5): 99.9; T(10): 0.0	S3; S5;	S482; S484		2.83	0	0	2	940.3	1880	64.96	13043
YYsDsDDELTVQR	BOD1L1	259282	biorientation of chromosomes in cell division protein 1-like 1	S3(Phospho) S5(Phospho)	Y(1): 0.4; Y(2): 0.4; S(3): 99.6; S(5): 99.6; T(10): 0.0	S3; S5;	S482; S484		2.67	0	0	2	940.3	1880	64.39	12911
IGDEYAEDssDEEDIR	BOP1	23246	ribosome biogenesis protein BOP1	S9(Phospho) S10(Phospho)	Y(5): 0.0; S(9): 100.0; S(10): 100.0	S9; S10;	S126; S127	62		0	0	2	1002	2003	58.7	11613
IGDEYAEDssDEEDIR	BOP1	23246	ribosome biogenesis protein BOP1	S9(Phospho) S10(Phospho)	Y(5): 0.0; S(9): 100.0; S(10): 100.0	S9; S10;	S126; S127	44		0	0	2	1002	2003	58.17	11481
IGDEYAEDssDEEDIR	BOP1	23246	ribosome biogenesis protein BOP1	S9(Phospho) S10(Phospho)	Y(5): 0.0; S(9): 100.0; S(10): 100.0	S9; S10;	S126; S127	3.09		0	0	2	1002	2003	58.7	11613
IGDEYAEDssDEEDIR	BOP1	23246	ribosome biogenesis protein BOP1	S9(Phospho) S10(Phospho)	Y(5): 0.0; S(9): 100.0; S(10): 100.0	S9; S10;	S126; S127	2.72		0	0	2	1002	2003	58.17	11481
TTVEERksSEAsPTAQR	BRAP	8315	BRCA1-associated protein	S8(Phospho) S12(Phospho)	T(1): 0.0; T(2): 0.0; S(8): 97.6; S(9): 2.4; S(12): 97.6; T(14): 2.4	S8; S12;	S93; S97	38		0	2	3	679.6	2037	15.57	2391
TTVEERksSEAsPTAQR	BRAP	8315	BRCA1-associated protein	S8(Phospho) S12(Phospho)	T(1): 0.0; T(2): 0.0; S(8): 97.6; S(9): 2.4; S(12): 97.6; T(14): 2.4	S8; S12;	S93; S97	4.68		0	2	3	679.6	2037	15.57	2391
SDELLGsDDsHDGESESNAK	BRCA1	672	breast cancer type 1 susceptibility protein isoform 3	S7(Phospho) S10(Phospho)	S(1): 0.0; S(7): 100.0; S(10): 100.0; S(15): 0.0; S(17): 0.0	S7; S10;	S348; S351	20		0	0	2	1126	2252	42.39	8072
SDELLGsDDsHDGESESNAK	BRCA1	672	breast cancer type 1 susceptibility protein isoform 3	S7(Phospho) S10(Phospho)	S(1): 0.0; S(7): 100.0; S(10): 100.0; S(15): 0.0; S(17): 0.0	S7; S10;	S348; S351	2.44		0	0	2	1126	2252	42.39	8072
SRsTCGDSEVEEESPGKR	BRD1	23774	bromodomain-containing protein 1 isoform 1	C5(Carbamidomethyl) S3(Phospho)	S(1): 1.7; S(3): 96.6; T(4): 1.7; S(8): 0.0; S(14): 0.0	S3;	S934	58		0	2	3	697.3	2090	19.18	3165
SRsTCGDSEVEEESPGKR	BRD1	23774	bromodomain-containing protein 1 isoform 1	C5(Carbamidomethyl) S3(Phospho)	S(1): 1.7; S(3): 96.6; T(4): 1.7; S(8): 0.0; S(14): 0.0	S3;	S934	5.36		0	2	3	697.3	2090	19.18	3165
NTETQTPsPQLGTK	BRD1	23774	bromodomain-containing protein 1 isoform 1	S8(Phospho)	T(2): 0.1; T(4): 0.0; T(7): 0.1; S(8): 99.8; T(13): 0.0	S8;	S906		2.9	0	0	2	791.4	1582	31.2	5711
KADTTTTPTTAILAPGsPAsPPGSLEPK	BRD2	6046	bromodomain-containing protein 2 isoform 4	S17(Phospho) S20(Phospho)	T(4): 0.0; T(5): 0.0; T(6): 0.0; T(8): 0.0; T(10): 0.0; S(17): 100.0; S(20): 100.0; S(24): 0.0	S17; S20;	S178; S181		4.44	0	1	3	954.8	2862	78.32	15782
RSPsPYSLK	BRPF3	27154	bromodomain and PHD finger-containing protein 3	S4(Phospho)	S(2): 49.4; S(4): 99.9; Y(6): 49.5; S(7): 1.2	S4;	S19	19		0	1	2	597.8	1194	33.58	6205

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#
RSPsPYSLK	BRPF3	27154	bromodomain and PHD finger-containing protein 3	S4(Phospho)	S(2): 49.4; S(4): 99.9; Y(6): 49.5; S(7): 1.2	S4;	S19		3.29	0	1	2	597.8	1194	33.58	6205
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201	43		0	0	2	632.7	1264	21.83	3720
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201	43		0	0	2	632.7	1264	21.32	3616
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201		3.91	0	0	2	632.7	1264	21.32	3616
HDsPDPsPPR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201		3.86	0	0	2	632.7	1264	21.83	3720
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163		3.49	0	0	2	647.7	1294	33.75	6239
ARHDTpDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T5(Phospho) S9(Phospho)	T(5): 100.0; S(9): 100.0	T5; S9;	T159; S163		3.19	0	1	2	761.3	1522	24.51	4288
ARHDTpDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T5(Phospho) S9(Phospho)	T(5): 100.0; S(9): 100.0	T5; S9;	T159; S163	26		0.001	1	2	761.3	1522	24.51	4288
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163	18		0.001	0	2	647.7	1294	33.75	6239
IRHDsSDTsPPR	BUD13	84811	BUD13 homolog isoform 1	S5(Phospho) S6(Phospho) S9(Phospho)	S(5): 96.9; S(6): 96.9; T(8): 9.4; S(9): 96.9	S5; S6; S9;	S184; S185; S188	25		0.002	1	2	804.3	1608	16.37	2562
HDsPDPsPPRR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201	12		0.003	1	2	710.8	1421	15.61	2400
HDsPDPsPPRR	BUD13	84811	BUD13 homolog isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S197; S201		3.05	0.003	1	2	710.8	1421	15.61	2400
IRHDsSDTsPPR	BUD13	84811	BUD13 homolog isoform 1	S5(Phospho) S6(Phospho) S9(Phospho)	S(5): 96.9; S(6): 96.9; T(8): 9.4; S(9): 96.9	S5; S6; S9;	S184; S185; S188		2.62	0.005	1	2	804.3	1608	16.37	2562
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163		2.92	0.007	0	2	647.8	1294	33.22	6131
HDtPDPsPLR	BUD13	84811	BUD13 homolog isoform 1	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T159; S163	25		0.009	0	2	647.8	1294	33.22	6131
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	M1(Oxidation) S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98	30		0	0	2	1109	2217	65.85	13243
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98	24		0	0	2	1101	2201	70.4	14239
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98	17		0	0	2	1101	2201	69.89	14146
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98		2.93	0	0	2	1101	2201	69.89	14146
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98		2.92	0	0	2	1101	2201	70.4	14239
MPQDGsDDEDEEWPTLEK	BYSL	705	bystin	M1(Oxidation) S6(Phospho)	S(6): 100.0; T(15): 0.0	S6;	S98		2.89	0	0	2	1109	2217	65.85	13243
NAEEEsEAEEGD	BZW1	9689	basic leucine zipper and W2 domain-containing protein 1 isoform 4	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S345; S347		3.2	0.005	0	2	842.7	1684	35.21	6563
RSAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S4(Phospho)	S(2): 2.9; S(4): 97.1; S(11): 0.0; S(12): 0.0	S4;	S17	50		0	1	3	891	2671	60.51	11982
sAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S1(Phospho)	S(1): 99.9; S(3): 0.1; S(10): 0.0; S(11): 0.0	S1;	S15	40		0	0	2	1258	2515	70.33	14227
sAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(10): 0.0; S(11): 0.0	S1; S3;	S15; S17	30		0	0	3	865.7	2595	84.58	16961
RsAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(11): 0.0; S(12): 0.0	S2; S4;	S15; S17	25		0	1	3	917.7	2751	68.84	13924
SAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S3(Phospho)	S(1): 4.1; S(3): 95.7; S(10): 0.2; S(11): 0.0	S3;	S17	24		0	0	3	839	2515	70.92	14347
SAsPDDDLGSSNWEAADLGNEERK	C11orf58	10944	small acidic protein	S3(Phospho)	S(1): 3.7; S(3): 96.3; S(10): 0.0; S(11): 0.0	S3;	S17	20		0	1	3	881.7	2643	60.26	11932
RSAsPDDDLGSSNWEAADLGNEER	C11orf58	10944	small acidic protein	S4(Phospho)	S(2): 2.9; S(4): 97.1; S(11): 0.0; S(12): 0.0	S4;	S17		4.9	0	1	3	891	2671	60.51	11982
SAsPDDDLGSSNWEAADLGNEERK	C11orf58	10944	small acidic protein	S3(Phospho)	S(1): 3.7; S(3): 96.3; S(10): 0.0; S(11): 0.0	S3;	S17		4.59	0	1	3	881.7	2643	60.26	11932

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#
SApDDDLGSSNWEADLGNEER	C11orf58	10944	small acidic protein	S3(Phospho)	S(1): 4.1; S(3): 95.7; S(10): 0.2; S(11): 0.0	S3;	S17		4.36	0	0	3	839	2515	70.92	14347
sASPDDDLGSSNWEADLGNEER	C11orf58	10944	small acidic protein	S1(Phospho)	S(1): 99.9; S(3): 0.1; S(10): 0.0; S(11): 0.0	S1;	S15		3.79	0	0	2	1258	2515	70.33	14227
sApDDDLGSSNWEADLGNEER	C11orf58	10944	small acidic protein	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(10): 0.0; S(11): 0.0	S1; S3;	S15; S17		3.6	0	0	3	865.7	2595	84.58	16961
RsApDDDLGSSNWEADLGNEER	C11orf58	10944	small acidic protein	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(11): 0.0; S(12): 0.0	S2; S4;	S15; S17		3.28	0	1	3	917.7	2751	68.84	13924
sASPDDDLGSSNWEADLGNEER	C11orf58	10944	small acidic protein	S1(Phospho)	S(1): 94.5; S(3): 4.9; S(10): 0.3; S(11): 0.3	S1;	S15		1.47	0.005	0	2	1258	2515	71.51	14460
AEsPSPAPPPGLR	C11orf84	144097	uncharacterized protein C11orf84	S3(Phospho)	S(3): 100.0; S(5): 0.0	S3;	S308	40		0	0	2	678.3	1356	45.11	8677
AEQPsPPNsDSGQDAHPDPDANPDAA R	C11orf84	144097	uncharacterized protein C11orf84	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 94.1; S(11): 5.9	S5; S9;	S148; S152	23		0	0	3	972.7	2916	36.87	6913
AEQPsPPNsDSGQDAHPDPDANPDAA R	C11orf84	144097	uncharacterized protein C11orf84	S5(Phospho)	S(5): 100.0; S(9): 0.0; S(11): 0.0	S5;	S148	14		0	0	3	946.1	2836	33.29	6146
AEQPsPPNsDSGQDAHPDPDANPDAA R	C11orf84	144097	uncharacterized protein C11orf84	S5(Phospho)	S(5): 100.0; S(9): 0.0; S(11): 0.0	S5;	S148		4.26	0	0	3	946.1	2836	33.29	6146
AEQPsPPNsDSGQDAHPDPDANPDAA R	C11orf84	144097	uncharacterized protein C11orf84	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 94.1; S(11): 5.9	S5; S9;	S148; S152		4.12	0	0	3	972.7	2916	36.87	6913
AEsPSPAPPPGLR	C11orf84	144097	uncharacterized protein C11orf84	S3(Phospho)	S(3): 100.0; S(5): 0.0	S3;	S308		2.69	0	0	2	678.3	1356	45.11	8677
NQGIEGsPGGR	C15orf52	388115	uncharacterized protein C15orf52	S7(Phospho)	S(7): 100.0	S7;	S193	30		0	0	2	576.2	1151	19.23	3175
NQGIEGsPGGR	C15orf52	388115	uncharacterized protein C15orf52	S7(Phospho)	S(7): 100.0	S7;	S193		2.91	0	0	2	576.2	1151	19.23	3175
RDsSESQLASTESDKPTTGR	C18orf25	147339	uncharacterized protein C18orf25 isoform b	S3(Phospho)	S(3): 100.0; S(4): 0.0; S(6): 0.0; S(10): 0.0; T(11): 0.0; S(13): 0.0; T(17): 0.0; T(18): 0.0	S3;	S66	55		0	1	3	744.7	2232	24.72	4331
RDsSESQLASTESDKPTTGR	C18orf25	147339	uncharacterized protein C18orf25 isoform b	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 0.1; S(6): 100.0; S(10): 0.0; T(11): 0.0; S(13): 0.0; T(17): 0.0; T(18): 0.0	S3; S6;	S66; S69	48		0	1	3	771.3	2312	28.12	5070
RDsSESQLASTESDKPTTGR	C18orf25	147339	uncharacterized protein C18orf25 isoform b	S3(Phospho)	S(3): 100.0; S(4): 0.0; S(6): 0.0; S(10): 0.0; T(11): 0.0; S(13): 0.0; T(17): 0.0; T(18): 0.0	S3;	S66		6.84	0	1	3	744.7	2232	24.72	4331
RDsSESQLASTESDKPTTGR	C18orf25	147339	uncharacterized protein C18orf25 isoform b	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 0.1; S(6): 100.0; S(10): 0.0; T(11): 0.0; S(13): 0.0; T(17): 0.0; T(18): 0.0	S3; S6;	S66; S69		6.45	0	1	3	771.3	2312	28.12	5070
TSAPAtPEIQGR	C1orf106	55765	uncharacterized protein C1orf106 isoform 2	T6(Phospho)	T(1): 50.0; S(2): 50.0; T(6): 100.0	T6;	T306	49		0	0	2	694.3	1388	41.66	7920
TSAPAtPEIQGR	C1orf106	55765	uncharacterized protein C1orf106 isoform 2	T6(Phospho)	T(1): 50.0; S(2): 50.0; T(6): 100.0	T6;	T306		2.71	0	0	2	694.3	1388	41.66	7920
RPAAEtSSPTsPERPR	C1orf35	79169	multiple myeloma tumor-associated protein 2	T6(Phospho) S11(Phospho)	T(6): 99.9; S(7): 0.1; S(8): 0.1; T(10): 0.0; S(11): 100.0	T6; S11;	T215; S220	31		0	0	3	633.6	1899	18.44	3009
RPAAEtSSPTsPERPR	C1orf35	79169	multiple myeloma tumor-associated protein 2	T6(Phospho) S11(Phospho)	T(6): 99.8; S(7): 0.1; S(8): 0.1; T(10): 0.0; S(11): 100.0	T6; S11;	T215; S220	19		0	0	3	633.6	1899	18.97	3119
RPAAEtSSPTsPERPR	C1orf35	79169	multiple myeloma tumor-associated protein 2	T6(Phospho) S11(Phospho)	T(6): 99.9; S(7): 0.1; S(8): 0.1; T(10): 0.0; S(11): 100.0	T6; S11;	T215; S220		4.75	0	0	3	633.6	1899	18.44	3009
RPAAEtSPTsPERPR	C1orf35	79169	multiple myeloma tumor-associated protein 2	S7(Phospho) S11(Phospho)	T(6): 0.1; S(7): 96.8; S(8): 3.1; T(10): 3.1; S(11): 96.9	S7; S11;	S216; S220		3.19	0	0	2	949.9	1899	18.54	3032
RPAAEtSPTsPERPR	C1orf35	79169	multiple myeloma tumor-associated protein 2	S7(Phospho) S11(Phospho)	T(6): 0.1; S(7): 96.8; S(8): 3.1; T(10): 3.1; S(11): 96.9	S7; S11;	S216; S220	12		0.002	0	2	949.9	1899	18.54	3032

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#
SQsESSDEVTELDLSHGK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S3(Phospho) S5(Phospho)	S(1): 4.5; S(3): 95.5; S(5): 95.5; S(6): 4.5; T(10): 0.0; S(15): 0.0	S3; S5;	S659; S661	49		0	0	2	1054	2108	55.91	10991
NQTYSFsPSK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S7(Phospho)	T(3): 0.0; Y(4): 0.0; S(5): 0.0; S(7): 100.0; S(9): 0.0	S7;	S295	38		0	0	2	619.8	1239	40.2	7616
SQsESSDEVTELDLSHGK	C2CD5	9847	C2 domain-containing protein 5 isoform e	T10(Phospho)	S(1): 49.8; S(3): 49.8; S(5): 5.4; S(6): 5.4; T(10): 89.5; S(15): 0.0	T10;	T666	23		0	0	3	703.3	2108	55.84	10975
SQsESSDEVTELDLSHGKK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S3(Phospho)	S(1): 4.6; S(3): 95.4; S(5): 48.8; S(6): 48.8; T(10): 2.4; S(15): 0.0	S3;	S659	16		0	1	3	746	2236	44.49	8529
SQsESSDEVTELDLSHGKK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S3(Phospho)	S(1): 4.6; S(3): 95.4; S(5): 48.8; S(6): 48.8; T(10): 2.4; S(15): 0.0	S3;	S659		4.05	0	1	3	746	2236	44.49	8529
NQTYSFsPSK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S7(Phospho)	T(3): 0.0; Y(4): 0.0; S(5): 0.0; S(7): 100.0; S(9): 0.0	S7;	S295		2.86	0	0	2	619.8	1239	40.2	7616
SQsESSDEVTELDLSHGK	C2CD5	9847	C2 domain-containing protein 5 isoform e	S3(Phospho) S5(Phospho)	S(1): 4.5; S(3): 95.5; S(5): 95.5; S(6): 4.5; T(10): 0.0; S(15): 0.0	S3; S5;	S659; S661		2.76	0	0	2	1054	2108	55.91	10991
SQsESSDEVTELDLSHGK	C2CD5	9847	C2 domain-containing protein 5 isoform e	T10(Phospho)	S(1): 49.8; S(3): 49.8; S(5): 5.4; S(6): 5.4; T(10): 89.5; S(15): 0.0	T10;	T666		2.65	0	0	3	703.3	2108	55.84	10975
KSPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S9(Phospho) S13(Phospho)	S(2): 0.0; S(4): 0.0; S(9): 100.0; S(13): 97.2; T(17): 2.8; T(18): 0.1	S9; S13;	S147; S151	32		0	2	3	740.7	2220	48.02	9289
KsPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S2(Phospho) S9(Phospho) S13(Phospho)	S(2): 100.0; S(4): 0.0; S(9): 100.0; S(13): 100.0; T(17): 0.0; T(18): 0.0	S2; S9; S13;	S140; S147; S151	31		0	2	3	767.4	2300	55.11	10821
KSPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S9(Phospho) S13(Phospho)	S(2): 0.0; S(4): 0.0; S(9): 100.0; S(13): 97.2; T(17): 2.8; T(18): 0.1	S9; S13;	S147; S151		6.75	0	2	3	740.7	2220	48.02	9289
KsPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S2(Phospho) S9(Phospho) S13(Phospho)	S(2): 100.0; S(4): 0.0; S(9): 100.0; S(13): 100.0; T(17): 0.0; T(18): 0.0	S2; S9; S13;	S140; S147; S151		5.74	0	2	3	767.4	2300	55.11	10821
KSPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S9(Phospho) S13(Phospho) T18(Phospho)	S(2): 0.0; S(4): 0.0; S(9): 100.0; S(13): 100.0; T(17): 3.8; T(18): 96.2	S9; S13; T18;	S147; S151; T156		4.39	0	2	3	767.4	2300	52.53	10253
KsPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S2(Phospho) S9(Phospho)	S(2): 99.6; S(4): 0.4; S(9): 100.0; S(13): 0.0; T(17): 0.0; T(18): 0.0	S2; S9;	S140; S147		3.49	0	2	3	740.7	2220	50.87	9889
KsPSGPVKsPPLsPVGttTPVK	C2orf49	79074	ashwin isoform 2	S2(Phospho) S9(Phospho) T17(Phospho) T18(Phospho)	S(2): 100.0; S(4): 0.0; S(9): 95.1; S(13): 5.2; T(17): 99.7; T(18): 100.0	S2; S9; T17; T18;	S140; S147; T155; T156	19		0.001	2	3	794	2380	61.14	12121
KsPSGPVKsPPLsPVGttTPVK	C2orf49	79074	ashwin isoform 2	S2(Phospho) T17(Phospho) T18(Phospho)	S(2): 100.0; S(4): 0.0; S(9): 0.2; S(13): 0.2; T(17): 99.6; T(18): 100.0	S2; T17; T18;	S140; T155; T156	15		0.002	2	3	767.4	2300	56.23	11058
KSPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S9(Phospho) S13(Phospho) T18(Phospho)	S(2): 0.0; S(4): 0.0; S(9): 100.0; S(13): 100.0; T(17): 3.8; T(18): 96.2	S9; S13; T18;	S147; S151; T156	12		0.002	2	3	767.4	2300	52.53	10253
KSPSGPVKsPPLsPVGTTTPVK	C2orf49	79074	ashwin isoform 2	S13(Phospho) T18(Phospho)	S(2): 0.0; S(4): 0.0; S(9): 0.2; S(13): 99.7; T(17): 4.4; T(18): 95.6	S13; T18;	S151; T156		3.78	0.003	2	3	740.7	2220	48.58	9407
VDEEDsDEESHHDemSEEEEELEDDPT VVK	C6orf203	51250	uncharacterized protein C6orf203 isoform a	S16(Phospho)	S(6): 52.4; S(10): 52.4; S(16): 95.1; T(27): 0.0	S16;	S116		1.99	0	0	3	1231	3690	59.16	11718
VDEEDsDEESHHDemSEEEEELEDDPT VVK	C6orf203	51250	uncharacterized protein C6orf203 isoform a	S6(Phospho)	S(6): 94.8; S(10): 52.6; S(16): 52.6; T(27): 0.0	S6;	S106		1.91	0	0	4	923.3	3690	59.19	11722
VDEEDsDEESHHDemSEEEEELEDDPT VVK	C6orf203	51250	uncharacterized protein C6orf203 isoform a	S6(Phospho)	S(6): 94.8; S(10): 52.6; S(16): 52.6; T(27): 0.0	S6;	S106	11		0.002	0	4	923.3	3690	59.19	11722

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#
SQsFSHQQPSR	C7orf43	55262	uncharacterized protein C7orf43 isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(10): 0.0	S3;	S248	58		0	0	2	684.8	1369	16	2482
SQsFSHQQPSR	C7orf43	55262	uncharacterized protein C7orf43 isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(10): 0.0	S3;	S248		3.06	0	0	2	684.8	1369	16	2482
RGDsEsEEDEQDSEEV	C9orf78	51759	uncharacterized protein C9orf78	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(13): 0.0	S4; S6;	S15; S17	34		0	1	2	1078	2156	24.48	4281
VGDTEKPEPERsPPNR	C9orf78	51759	uncharacterized protein C9orf78	S12(Phospho)	T(4): 0.0; S(12): 100.0	S12;	S261	17		0	1	3	630	1888	18.49	3020
VGDTEKPEPERsPPNR	C9orf78	51759	uncharacterized protein C9orf78	S12(Phospho)	T(4): 0.0; S(12): 100.0	S12;	S261		5.11	0	1	3	630	1888	18.49	3020
RGDsEsEEDEQDSEEV	C9orf78	51759	uncharacterized protein C9orf78	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(13): 0.0	S4; S6;	S15; S17		3.03	0	1	2	1078	2156	24.48	4281
RRGDsEsEEDEQDSEEV	C9orf78	51759	uncharacterized protein C9orf78	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 99.7; S(14): 0.3	S5; S7;	S15; S17		1.95	0.004	2	2	1156	2312	20.05	3348
GNVFSsPTAAGtPNKETAGLK	CALD1	800	caldesmon isoform 5	S6(Phospho) T12(Phospho)	S(5): 3.8; S(6): 96.2; T(8): 0.0; T(12): 100.0; T(17): 0.0	S6; T12;	S463; T469	18		0	1	3	736.3	2207	55.54	10914
GNVFSsPTAAGtPNKETAGLK	CALD1	800	caldesmon isoform 5	S6(Phospho) T12(Phospho)	S(5): 3.8; S(6): 96.2; T(8): 0.0; T(12): 100.0; T(17): 0.0	S6; T12;	S463; T469		4.09	0	1	3	736.3	2207	55.54	10914
GNVFSsPTAAGtPNKETAGLK	CALD1	800	caldesmon isoform 5	S6(Phospho) T12(Phospho)	S(5): 5.6; S(6): 88.9; T(8): 6.0; T(12): 99.1; T(17): 0.4	S6; T12;	S463; T469		2.08	0.001	1	2	1104	2207	55.67	10942
SEsVEGFLsPSR	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S3(Phospho) S9(Phospho)	S(1): 1.8; S(3): 98.2; S(9): 98.2; S(11): 1.8	S3; S9;	S1286; S1292	38		0	0	2	727.8	1455	75.88	15324
YDGESDKEQFDDDDQK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0	S5;	S1121	28		0	1	2	949.9	1899	28.48	5146
YDGESDKEQFDDDDQK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0	S5;	S1121	19		0	1	3	633.6	1899	28.48	5147
YDGESDKEQFDDDDQK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0	S5;	S1121		3.78	0	1	3	633.6	1899	28.48	5147
SEsVEGFLsPSR	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S3(Phospho) S9(Phospho)	S(1): 1.8; S(3): 98.2; S(9): 98.2; S(11): 1.8	S3; S9;	S1286; S1292		2.98	0	0	2	727.8	1455	75.88	15324
YDGESDKEQFDDDDQK	CAMSAP2	23271	calmodulin-regulated spectrin-associated protein 2 isoform 3	S5(Phospho)	Y(1): 0.0; S(5): 100.0	S5;	S1121		2.41	0	1	2	949.9	1899	28.48	5146
APsPSGLMsPSR	CAMSAP3	57662	calmodulin-regulated spectrin-associated protein 3 isoform 2	S3(Phospho) S9(Phospho)	S(3): 99.9; S(5): 0.2; S(9): 97.4; S(11): 2.6	S3; S9;	S1074; S1080	37		0	0	2	673.8	1347	58.43	11541
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 96.7; T(11): 3.3; S(13): 100.0	S3; S13;	S554; S564	87		0	1	3	756.9	2269	25.99	4604
SDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.0; S(11): 100.0	S11;	S564	56		0	0	2	966.9	1933	27.74	4989
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 97.3; T(11): 2.6; S(13): 0.1	S3;	S554	55		0	1	3	730.3	2189	22.81	3933
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554	50		0	1	2	1095	2189	22.65	3897
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	48		0	1	2	1135	2269	25.95	4595
LEEKQKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S7(Phospho) S17(Phospho)	S(7): 100.0; T(15): 0.0; S(17): 100.0	S7; S17;	S554; S564	44		0	2	3	923.4	2768	26.34	4681
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564	41		0	1	3	762.7	2286	22.14	3789
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554	41		0	1	3	730.3	2189	22.31	3825
AEDEILNRsPR	CANX	821	calnexin precursor	S10(Phospho)	S(10): 100.0	S10;	S583	40		0	1	2	754.8	1509	35.59	6643
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.1; S(13): 99.9	S13;	S564	37		0	1	2	1095	2189	22.07	3775
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554	36		0	2	4	636.3	2542	20.37	3414
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 3.6; S(11): 96.4	S11;	S564	29		0	1	2	1143	2286	21.89	3735

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#
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554	29		0	2	4	636.3	2542	19.81	3297
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 100.0	S3; S13;	S554; S564	27		0	2	4	656.3	2622	21.05	3558
AEDEILNRsPR	CANX	821	calnexin precursor	S10(Phospho)	S(10): 100.0	S10;	S583	27		0	1	3	503.6	1509	35.52	6628
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.3; S(13): 99.7	S3; S13;	S554; S564	26		0	2	3	874.7	2622	21.48	3648
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.0; S(13): 100.0	S13;	S564	26		0	2	3	848	2542	19.55	3243
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 100.0	S3; S13;	S554; S564	25		0	2	3	874.7	2622	20.96	3540
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564	25		0	1	3	762.7	2286	21.62	3678
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.0; S(13): 100.0	S13;	S564	24		0	2	4	636.3	2542	19.31	3192
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.2; S(13): 99.8	S3; S13;	S554; S564	23		0	2	3	874.7	2622	20.04	3346
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554	20		0	2	3	848	2542	20.2	3378
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554		7.84	0	2	4	636.3	2542	19.81	3297
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 100.0	S3; S13;	S554; S564		7.45	0	2	3	874.7	2622	20.96	3540
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 96.7; T(11): 3.3; S(13): 100.0	S3; S13;	S554; S564		7.06	0	1	3	756.9	2269	25.99	4604
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 100.0	S3; S13;	S554; S564		6.87	0	2	4	656.3	2622	21.05	3558
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554		6.72	0	2	3	848	2542	20.2	3378
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554		6.33	0	2	4	636.3	2542	20.37	3414
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.3; S(13): 99.7	S3; S13;	S554; S564		5.97	0	2	3	874.7	2622	21.48	3648
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.0; S(13): 100.0	S13;	S564		5.85	0	2	4	636.3	2542	19.31	3192
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.0; S(13): 100.0	S13;	S564		5.57	0	2	3	848	2542	19.55	3243
QKsDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S3(Phospho) S13(Phospho)	S(3): 100.0; T(11): 0.2; S(13): 99.8	S3; S13;	S554; S564		5.48	0	2	3	874.7	2622	20.04	3346
LEEKQKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S7(Phospho) S17(Phospho)	S(7): 100.0; T(15): 0.0; S(17): 100.0	S7; S17;	S554; S564		5.43	0	2	3	923.4	2768	26.34	4681
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554		4.98	0	1	3	730.3	2189	22.31	3825
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		4.36	0	1	2	1135	2269	25.95	4595
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564		4.12	0	1	3	762.7	2286	22.14	3789
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 97.3; T(11): 2.6; S(13): 0.1	S3;	S554		4.08	0	1	3	730.3	2189	22.81	3933
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.1; S(11): 99.9	S11;	S564		4.04	0	1	3	762.7	2286	21.62	3678
QKsDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 0.0; S(13): 0.0	S3;	S554		3.95	0	1	2	1095	2189	22.65	3897
SDAEEDGGTVsQEEEDR	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 0.0; S(11): 100.0	S11;	S564		3.65	0	0	2	966.9	1933	27.74	4989
AEDEILNRsPR	CANX	821	calnexin precursor	S10(Phospho)	S(10): 100.0	S10;	S583		3.08	0	1	2	754.8	1509	35.59	6643
SDAEEDGGTVsQEEEDRKPK	CANX	821	calnexin precursor	S11(Phospho)	S(1): 0.0; T(9): 3.6; S(11): 96.4	S11;	S564		2.88	0	1	2	1143	2286	21.89	3735
AEDEILNRsPR	CANX	821	calnexin precursor	S10(Phospho)	S(10): 100.0	S10;	S583		3.57	0.001	1	3	503.6	1509	35.52	6628

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#
QKSDAEEDGGTVSQQEEDR	CANX	821	calnexin precursor	S13(Phospho)	S(3): 0.0; T(11): 0.1; S(13): 99.9	S13;	S564		3.38	0.002	1	2	1095	2189	22.07	3775
QKsDAEEDGGTVSQQEEDRKPK	CANX	821	calnexin precursor	S3(Phospho)	S(3): 100.0; T(11): 50.0; S(13): 50.0	S3;	S554		2.1	0.007	2	2	1312	2622	20.84	3514
SGPKPFSAPKPQTSPsPK	CAP1	10487	adenylyl cyclase-associated protein 1	S16(Phospho)	S(1): 0.0; S(7): 0.0; T(13): 0.0; S(14): 0.1; S(16): 99.9	S16;	S310	11		0	0	3	640	1918	31.34	5741
SGPKPFSAPKPQTSPsPK	CAP1	10487	adenylyl cyclase-associated protein 1	S16(Phospho)	S(1): 0.0; S(7): 0.0; T(13): 0.0; S(14): 0.1; S(16): 99.9	S16;	S310		3.68	0.001	0	3	640	1918	31.34	5741
SGPKPFSAPKPQTSPsPK	CAP1	10487	adenylyl cyclase-associated protein 1	S14(Phospho) S16(Phospho)	S(1): 0.0; S(7): 0.0; T(13): 3.8; S(14): 96.2; S(16): 100.0	S14; S16;	S308; S310	13		0.002	0	3	666.6	1998	35.04	6529
SGPKPFSAPKPQTSPsPK	CAP1	10487	adenylyl cyclase-associated protein 1	S14(Phospho) S16(Phospho)	S(1): 0.0; S(7): 0.0; T(13): 3.8; S(14): 96.2; S(16): 100.0	S14; S16;	S308; S310		3.22	0.003	0	3	666.6	1998	35.04	6529
SGPKPFSAPKPQTSPsPK	CAP1	10487	adenylyl cyclase-associated protein 1	S16(Phospho)	S(1): 0.0; S(7): 0.0; T(13): 0.0; S(14): 0.1; S(16): 99.9	S16;	S310		3.56	0.004	0	3	640	1918	30.77	5624
AEAGEAEFEAGAGsGsEAEDALWER	CARD10	29775	caspace recruitment domain-containing protein 10	S14(Phospho) S16(Phospho)	S(14): 100.0; S(16): 100.0	S14; S16;	S18; S20	32		0	0	3	937.4	2810	78.09	15743
AEAGEAEFEAGAGsGsEAEDALWER	CARD10	29775	caspace recruitment domain-containing protein 10	S14(Phospho) S16(Phospho)	S(14): 100.0; S(16): 100.0	S14; S16;	S18; S20		3.42	0	0	3	937.4	2810	78.09	15743
ERsPsPLRGNVVPSPLpR	CARHSP1	23589	calcium-regulated heat stable protein 1	S3(Phospho) S5(Phospho) T18(Phospho)	S(3): 100.0; S(5): 100.0; S(14): 0.0; T(18): 100.0	S3; S5; T18;	S30; S32; T45	13		0	2	3	767	2299	63.71	12739
ERsPsPLRGNVVPSPLpR	CARHSP1	23589	calcium-regulated heat stable protein 1	S3(Phospho) S5(Phospho) T18(Phospho)	S(3): 100.0; S(5): 100.0; S(14): 0.0; T(18): 100.0	S3; S5; T18;	S30; S32; T45		4.49	0	2	3	767	2299	63.71	12739
STVTGERQsGDGQESTEPVENK	CASC3	22794	protein CASC3	S9(Phospho)	S(1): 0.0; T(2): 0.0; T(4): 0.0; S(9): 100.0; S(15): 0.0; T(16): 0.0	S9;	S148	27		0	1	3	805.7	2415	22.9	3953
STVTGERQsGDGQESTEPVENK	CASC3	22794	protein CASC3	S9(Phospho)	S(1): 0.0; T(2): 0.0; T(4): 0.0; S(9): 100.0; S(15): 0.0; T(16): 0.0	S9;	S148		4.54	0	1	3	805.7	2415	22.9	3953
TQsSSCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S3(Phospho)	T(1): 2.3; S(3): 93.1; S(4): 2.3; S(5): 2.3; S(11): 0.0; T(12): 0.0; T(13): 0.0	S3;	S569	35		0	0	2	923.4	1846	34.19	6334
TQsSSCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S3(Phospho)	T(1): 50.0; S(3): 98.4; S(4): 50.0; S(5): 1.6; S(11): 0.0; T(12): 0.0; T(13): 0.0	S3;	S569	31		0	0	2	963.4	1926	44.33	8492
TQsSSCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S3(Phospho)	T(1): 2.3; S(3): 93.1; S(4): 2.3; S(5): 2.3; S(11): 0.0; T(12): 0.0; T(13): 0.0	S3;	S569		3.25	0	0	2	923.4	1846	34.19	6334
TQsSSCEDLPSTTQPK	CASK	8573	peripheral plasma membrane protein CASK isoform 3	C6(Carbamidomethyl) S3(Phospho)	T(1): 50.0; S(3): 98.4; S(4): 50.0; S(5): 1.6; S(11): 0.0; T(12): 0.0; T(13): 0.0	S3;	S569		2.78	0.001	0	2	963.4	1926	44.33	8492
GSQHSQEQPAPQPSGGDPsPPQER	CASKIN2	57513	casin-2 isoform b	S19(Phospho)	S(2): 0.0; S(5): 0.0; S(14): 0.0; S(19): 100.0	S19;	S643	22		0	0	3	836.4	2507	26.46	4706
GSQHSQEQPAPQPSGGDPsPPQER	CASKIN2	57513	casin-2 isoform b	S19(Phospho)	S(2): 0.0; S(5): 0.0; S(14): 0.0; S(19): 100.0	S19;	S643		3.91	0	0	3	836.4	2507	26.46	4706
MDDDSYSHHSGLYADPEK	CAV2	858	caveolin-2 isoform b	M1(Oxidation) S10(Phospho)	S(5): 33.4; Y(6): 33.4; S(7): 33.4; S(10): 99.8; Y(14): 0.0	S10;	S10	14		0	0	3	791.3	2372	42.17	8028
MDDDSYSHHSGLYADPEK	CAV2	858	caveolin-2 isoform b	M1(Oxidation) S10(Phospho)	S(5): 33.4; Y(6): 33.4; S(7): 33.4; S(10): 99.8; Y(14): 0.0	S10;	S10		3.13	0	0	3	791.3	2372	42.17	8028
RQQDPsPGSNLGGGDDLK	CBFB	865	core-binding factor subunit beta isoform 1	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S173	61		0	1	3	641	1921	34.06	6306

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#
RQQDPsPGSNLGGGDDLK	CBFB	865	core-binding factor subunit beta isoform 1	S6(Phospho)	S(6): 99.9; S(9): 0.1	S6;	S173	59		0	1	2	960.9	1921	33.98	6290
RQQDPsPGSNLGGGDDLK	CBFB	865	core-binding factor subunit beta isoform 1	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S173		5.32	0	1	3	641	1921	34.06	6306
RQQDPsPGSNLGGGDDLK	CBFB	865	core-binding factor subunit beta isoform 1	S6(Phospho)	S(6): 99.9; S(9): 0.1	S6;	S173		2.91	0	1	2	960.9	1921	33.98	6290
KADsDSEDKGEESKPK	CBX1	10951	chromobox protein homolog 1	S4(Phospho)	S(4): 100.0; S(6): 0.0; S(13): 0.0	S4;	S89	43		0	2	3	610.6	1830	12.27	1665
KADsDSEDKGEESKPK	CBX1	10951	chromobox protein homolog 1	S4(Phospho)	S(4): 100.0; S(6): 0.0; S(13): 0.0	S4;	S89		7.43	0	2	3	610.6	1830	12.27	1665
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(3): 100.0; S(5): 0.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3;	S93	80		0	2	2	767.3	1534	12.48	1725
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3; S5;	S93; S95	66		0	2	2	807.3	1614	12.55	1745
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3; S5;	S93; S95	65		0	2	3	538.5	1614	12.63	1765
SLsDSESDDSKSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(12): 0.0	S3;	S95	59		0	1	2	732.8	1465	12.78	1803
SLsDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(10): 0.0	S3;	S95	53		0	0	2	625.2	1249	16.31	2550
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3; S5;	S93; S95		6.87	0	2	3	538.5	1614	12.63	1765
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3; S5;	S93; S95		5.73	0	2	2	807.3	1614	12.55	1745
RKsLSDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(3): 100.0; S(5): 0.0; S(7): 0.0; S(9): 0.0; S(12): 0.0	S3;	S93		5.7	0	2	2	767.3	1534	12.48	1725
SLsDSESDDSKSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(12): 0.0	S3;	S95		4.14	0	1	2	732.8	1465	12.78	1803
SLsDSESDDSK	CBX3	11335	chromobox protein homolog 3	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; S(7): 0.0; S(10): 0.0	S3;	S95		3.87	0	0	2	625.2	1249	16.31	2550
KQNspVAPTAQPK	CC2D1A	54862	coiled-coil and C2 domain-containing protein 1A	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S455	30		0	1	2	723.4	1446	17.05	2716
KQNspVAPTAQPK	CC2D1A	54862	coiled-coil and C2 domain-containing protein 1A	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S455		3.95	0	1	2	723.4	1446	17.05	2716
sVAsNQSEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	S1(Phospho) S4(Phospho)	S(1): 100.0; S(4): 100.0; S(7): 0.0; S(12): 0.0; S(13): 0.0	S1; S4;	S675; S678	42		0	0	2	1138	2275	87.94	17592
SVASNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M9(Oxidation) S7(Phospho)	S(1): 51.3; S(4): 51.3; S(7): 97.1; S(12): 0.3; S(13): 0.0	S7;	S681	37		0	0	2	1146	2291	79.34	15991
SVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M17(Oxidation) S4(Phospho) S7(Phospho)	S(1): 4.7; S(4): 95.3; S(7): 95.0; S(12): 4.7; S(13): 0.3	S4; S7;	S678; S681	30		0	0	2	1146	2291	74.16	14989
LEDSEVRsVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M24(Oxidation) S11(Phospho) S14(Phospho)	S(4): 50.0; S(8): 50.0; S(11): 100.0; S(14): 100.0; S(19): 0.0; S(20): 0.0	S11; S14;	S678; S681	23		0	1	3	1067	3199	76.89	15513

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#
LEDSEVRSVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M16(Oxidation) M24(Oxidation) S11(Phospho) S14(Phospho)	S(4): 50.2; S(8): 50.2; S(11): 99.9; S(14): 99.5; S(19): 0.2; S(20): 0.1	S11; S14;	S678; S681	22		0	1	3	1072	3215	69.07	13966
LEDSEVRSVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M16(Oxidation) S8(Phospho) S11(Phospho) S14(Phospho)	S(4): 6.3; S(8): 93.7; S(11): 93.7; S(14): 88.0; S(19): 6.3; S(20): 12.0	S8; S11; S14;	S675; S678; S681	16		0	1	3	1067	3199	81.84	16473
sVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	S1(Phospho) S4(Phospho)	S(1): 100.0; S(4): 100.0; S(7): 0.0; S(12): 0.0; S(13): 0.0	S1; S4;	S675; S678		3.18	0	0	2	1138	2275	87.94	17592
SVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M17(Oxidation) S4(Phospho) S7(Phospho)	S(1): 4.7; S(4): 95.3; S(7): 95.0; S(12): 4.7; S(13): 0.3	S4; S7;	S678; S681		2.92	0	0	2	1146	2291	74.16	14989
SVASNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M9(Oxidation) S7(Phospho)	S(1): 51.3; S(4): 51.3; S(7): 97.1; S(12): 0.3; S(13): 0.0	S7;	S681		2.84	0	0	2	1146	2291	79.34	15991
LEDSEVRSVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M24(Oxidation) S11(Phospho) S14(Phospho)	S(4): 50.0; S(8): 50.0; S(11): 100.0; S(14): 100.0; S(19): 0.0; S(20): 0.0	S11; S14;	S678; S681		2.58	0	1	3	1067	3199	76.89	15513
LEDSEVRSVAsNQsEMEFSSLQDMPK	CCAR2	57805	cell cycle and apoptosis regulator protein 2	M16(Oxidation) S8(Phospho) S11(Phospho) S14(Phospho)	S(4): 6.3; S(8): 93.7; S(11): 93.7; S(14): 88.0; S(19): 6.3; S(20): 12.0	S8; S11; S14;	S675; S678; S681		2.44	0	1	3	1067	3199	81.84	16473
SNsSEALLVDR	CCDC120	90060	coiled-coil domain-containing protein 120 isoform 4	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(4): 0.0	S3;	S348	54		0	0	2	635.8	1271	51	9915
SNsSEALLVDR	CCDC120	90060	coiled-coil domain-containing protein 120 isoform 4	S3(Phospho)	S(1): 1.6; S(3): 98.4; S(4): 0.0	S3;	S348		2.67	0	0	2	635.8	1271	51	9915
SAYQEYDsDVPPEELKR	CCDC132	55610	coiled-coil domain-containing protein 132 isoform X1	S8(Phospho) S10(Phospho)	S(1): 0.0; Y(3): 0.0; Y(6): 0.1; S(8): 99.9; S(10): 100.0	S8; S10;	S370; S372	24		0	1	3	764.3	2291	58.37	11526
SAYQEYDsDVPPEELKR	CCDC132	55610	coiled-coil domain-containing protein 132 isoform X1	S8(Phospho) S10(Phospho)	S(1): 0.0; Y(3): 0.0; Y(6): 0.1; S(8): 99.9; S(10): 100.0	S8; S10;	S370; S372		2.41	0	1	3	764.3	2291	58.37	11526
VENMSSNQDGNdsDEFM	CCDC25	55246	coiled-coil domain-containing protein 25 isoform 4	M17(Oxidation) S13(Phospho)	S(5): 0.0; S(6): 0.0; S(13): 100.0	S13;	S136	23		0.003	0	2	1008	2015	52.92	10342
VENMSSNQDGNdsDEFM	CCDC25	55246	coiled-coil domain-containing protein 25 isoform 4	M17(Oxidation) S13(Phospho)	S(5): 0.0; S(6): 0.0; S(13): 100.0	S13;	S136		2.8	0.003	0	2	1008	2015	52.92	10342
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	66		0	0	2	712.3	1424	48.31	9351
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	57		0	0	2	712.3	1424	48.83	9459
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	49		0	0	2	712.3	1424	47.77	9237
SNsPDKFK	CCDC6	8030	coiled-coil domain-containing protein 6	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S419	31		0	1	2	501.7	1002	14.39	2141
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		4.23	0	0	2	712.3	1424	48.31	9351
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		3.93	0	0	2	712.3	1424	47.77	9237
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		3.77	0	0	2	712.3	1424	48.83	9459
SNsPDKFK	CCDC6	8030	coiled-coil domain-containing protein 6	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S419		2.61	0	1	2	501.7	1002	14.39	2141

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#
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91	39		0	0	3	795	2383	44.63	8562
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91	36		0	0	2	1192	2383	44.83	8613
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.0; S(16): 0.0; S(19): 100.0	S8; S19;	S102; S113	34		0	1	4	671	2681	47.5	9181
LQQGAGLEsPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S9(Phospho) S20(Phospho)	S(9): 100.0; S(20): 100.0	S9; S20;	S80; S91	34		0	0	3	821.7	2463	51.37	9992
LQQGAGLEsPQGQPEPGAA sPQR	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	2	1232	2463	51.42	10003
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S16(Phospho)	S(8): 100.0; Y(15): 0.1; S(16): 99.7; S(19): 0.1	S8; S16;	S102; S110	24		0	1	3	894.4	2681	47.22	9123
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.0; S(16): 0.0; S(19): 100.0	S8; S19;	S102; S113	21		0	1	3	894.4	2681	47.81	9244
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91	14		0	0	2	1192	2383	44.62	8558
AGLGsPERPPKtSPGsPR	CCDC86	79080	coiled-coil domain-containing protein 86	S5(Phospho) T12(Phospho) S16(Phospho)	S(5): 100.0; T(12): 96.3; S(13): 3.7; S(16): 100.0	S5; T12; S16;	S58; T65; S69		6.83	0	1	3	677.6	2031	36.7	6877
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91		5.77	0	0	3	795	2383	44.63	8562
LQQGAGLEsPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S9(Phospho) S20(Phospho)	S(9): 100.0; S(20): 100.0	S9; S20;	S80; S91		5.45	0	0	3	821.7	2463	51.37	9992
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.0; S(16): 0.0; S(19): 100.0	S8; S19;	S102; S113		5.03	0	1	3	894.4	2681	47.81	9244
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91		4.48	0	0	2	1192	2383	44.83	8613
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S16(Phospho)	S(8): 100.0; Y(15): 0.1; S(16): 99.7; S(19): 0.1	S8; S16;	S102; S110		4.4	0	1	3	894.4	2681	47.22	9123
LQQGAGLEsPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S9(Phospho) S20(Phospho)	S(9): 100.0; S(20): 100.0	S9; S20;	S80; S91		3.17	0	0	2	1232	2463	51.42	10003
LQQGAGLESPQGQPEPGAA sPQR	CCDC86	79080	coiled-coil domain-containing protein 86	S20(Phospho)	S(9): 0.0; S(20): 100.0	S20;	S91		2.56	0.001	0	2	1192	2383	44.62	8558
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S16(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.3; S(16): 99.7; S(19): 100.0	S8; S16; S19;	S102; S110; S113	19		0.003	1	3	921	2761	52.28	10200
AGLGsPERPPKtSPGsPR	CCDC86	79080	coiled-coil domain-containing protein 86	S5(Phospho) S16(Phospho)	S(5): 100.0; T(12): 50.0; S(13): 50.0; S(16): 100.0	S5; S16;	S58; S69	14		0.003	1	2	1016	2031	36.66	6869
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.0; S(16): 0.0; S(19): 100.0	S8; S19;	S102; S113		4.37	0.003	1	4	671	2681	47.5	9181
QDDLHLEsPQRQPEYsPESPR	CCDC86	79080	coiled-coil domain-containing protein 86	S8(Phospho) S16(Phospho) S19(Phospho)	S(8): 100.0; Y(15): 0.3; S(16): 99.7; S(19): 100.0	S8; S16; S19;	S102; S110; S113		3.8	0.003	1	3	921	2761	52.28	10200
AGLGsPERPPKtSPGsPR	CCDC86	79080	coiled-coil domain-containing protein 86	S5(Phospho) S16(Phospho)	S(5): 100.0; T(12): 50.0; S(13): 50.0; S(16): 100.0	S5; S16;	S58; S69		3.1	0.008	1	2	1016	2031	36.66	6869
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 97.5; S(7): 0.1; S(8): 2.4	S3;	S324	29		0	0	2	580.8	1161	12.42	1707
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324		4.32	0.001	0	2	620.8	1241	13.38	1929
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324	32		0.002	0	2	620.8	1241	13.38	1929
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324		4.12	0.002	0	2	620.8	1241	14.02	2064
KPsPQPSSPR	CCNK	8812	cyclin-K	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(8): 50.0	S3;	S324	42		0.007	0	2	620.8	1241	14.02	2064
LPsPEPSMSPK	CCP110	9738	centriolar coiled-coil protein of 110 kDa isoform 2	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(9): 50.0	S3;	S366		1.97	0.001	0	2	665.3	1330	56.52	11120
LPsPEPSMSPK	CCP110	9738	centriolar coiled-coil protein of 110 kDa isoform 2	S3(Phospho)	S(3): 100.0; S(7): 50.0; S(9): 50.0	S3;	S366	13		0.004	0	2	665.3	1330	56.52	11120

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#
HSDsKEDDGQEIA	CD276	80381	CD276 antigen isoform b precursor	S4(Phospho)	S(2): 0.0; S(4): 100.0	S4;	S307	57		0	1	2	755.8	1511	17.88	2894
HSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 1.9; S(5): 98.1; S(16): 0.0; S(17): 0.0	S5;	S49	60		0	0	2	1009	2017	21.14	3577
HSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 2.1; S(5): 97.9; S(16): 0.0; S(17): 0.0	S5;	S49	55		0	0	2	1009	2017	20.59	3461
KGPGQPSSPQR	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S8(Phospho)	S(7): 1.0; S(8): 99.0	S8;	S195	41		0	1	2	609.8	1219	12.45	1718
GKHSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S7(Phospho)	S(4): 0.1; S(7): 99.9; S(18): 0.0; S(19): 0.0	S7;	S49	27		0	1	3	734.6	2202	16.16	2517
GKHSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S7(Phospho)	S(4): 0.1; S(7): 99.9; S(18): 0.0; S(19): 0.0	S7;	S49		4.15	0	1	3	734.6	2202	16.16	2517
HSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 1.9; S(5): 98.1; S(16): 0.0; S(17): 0.0	S5;	S49		3.65	0	0	2	1009	2017	21.14	3577
HSLDsDEEEDDDGGSSK	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S5(Phospho)	S(2): 2.1; S(5): 97.9; S(16): 0.0; S(17): 0.0	S5;	S49		3.59	0	0	2	1009	2017	20.59	3461
KGPGQPSSPQR	CD2BP2	10421	CD2 antigen cytoplasmic tail-binding protein 2	S8(Phospho)	S(7): 1.0; S(8): 99.0	S8;	S195		4.03	0.002	1	2	609.8	1219	12.45	1718
TNPEDIYPSNPTDDVSSGSsSER	CD44	960	CD44 antigen isoform 1 precursor	S21(Phospho)	T(1): 0.0; Y(7): 0.0; S(9): 0.0; T(12): 0.0; S(17): 0.0; S(18): 0.0; S(20): 3.5; S(21): 93.1; S(22): 3.5	S21;	S183	24		0	0	3	883.7	2649	55.99	11007
TNPEDIYPSNPTDDVSSGSsSER	CD44	960	CD44 antigen isoform 1 precursor	S21(Phospho)	T(1): 0.0; Y(7): 0.0; S(9): 0.0; T(12): 0.0; S(17): 0.0; S(18): 0.0; S(20): 3.5; S(21): 93.1; S(22): 3.5	S21;	S183		4.64	0	0	3	883.7	2649	55.99	11007
NHLHtTQMAGTSSNTISAGWEPNEEN EDER	CD44	960	CD44 antigen isoform 1 precursor	T5(Phospho)	T(5): 92.5; T(6): 6.9; T(7): 0.6; T(12): 0.0; S(13): 0.0; S(14): 0.0; T(16): 0.0; S(18): 0.0	T5;	T260		3.77	0.008	0	3	1179	3536	100.2	20037
VQTtPSKPGGDR	CDC20	991	cell division cycle protein 20 homolog	T4(Phospho)	T(3): 0.1; T(4): 97.7; S(6): 2.2	T4;	T70	62		0	0	2	661.8	1323	13.15	1881
VQTtPSKPGGDR	CDC20	991	cell division cycle protein 20 homolog	T4(Phospho)	T(3): 0.1; T(4): 97.7; S(6): 2.2	T4;	T70		2.41	0	0	2	661.8	1323	13.15	1881
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 100.0; S(18): 0.0	S15;	S1690	48		0	0	3	741	2221	17.41	2793
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho) S18(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 100.0; S(18): 100.0	S15; S18;	S1690; S1693	41		0	0	3	767.6	2301	18.57	3037
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 99.9; S(18): 0.1	S15;	S1690	22		0	0	3	741	2221	16.88	2680
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 100.0; S(18): 0.0	S15;	S1690		6.72	0	0	3	741	2221	17.41	2793
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho) S18(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 100.0; S(18): 100.0	S15; S18;	S1690; S1693		6.39	0	0	3	767.6	2301	18.57	3037
HSTPSNSSNPSGPPsPNSPHR	CDC42BPB	9578	serine/threonine-protein kinase MRCK beta	S15(Phospho)	S(2): 0.0; T(3): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(11): 0.0; S(15): 99.9; S(18): 0.1	S15;	S1690		5.33	0	0	3	741	2221	16.88	2680

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#
AGEPDGEsLDEQPSSSSSK	CDC42EP4	23580	cdc42 effector protein 4	S8(Phospho)	S(8): 100.0; S(14): 0.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S8;	S64	35		0	0	2	993.9	1987	32.2	5918
AGEPDGEsLDEQPSSSSSK	CDC42EP4	23580	cdc42 effector protein 4	S8(Phospho)	S(8): 100.0; S(14): 0.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S8;	S64		3.24	0	0	2	993.9	1987	32.2	5918
sLSSsPVKK	CDC42EP4	23580	cdc42 effector protein 4	S1(Phospho) S5(Phospho)	S(1): 100.0; S(3): 2.3; S(4): 2.3; S(5): 95.4	S1; S5;	S138; S142		3.15	0	1	2	546.7	1092	20.41	3423
LPKsLSSSPVKK	CDC42EP4	23580	cdc42 effector protein 4	S4(Phospho)	S(4): 100.0; S(6): 49.4; S(7): 49.4; S(8): 1.1	S4;	S138		3.75	0.001	2	2	715.9	1431	29.51	5360
THsVPAiPTSTPVPNPPEAESSK	CDC45	113130	sororin	S3(Phospho) T7(Phospho)	T(1): 4.1; S(3): 95.9; T(7): 99.8; T(9): 0.0; S(10): 0.0; T(11): 0.2; S(20): 0.0; S(21): 0.0; S(22): 0.0	S3; T7;	S107; T111	23		0	0	3	827.7	2481	49.28	9555
THsVPAiPTSTPVPNPPEAESSK	CDC45	113130	sororin	S3(Phospho) T7(Phospho)	T(1): 4.1; S(3): 95.9; T(7): 99.8; T(9): 0.0; S(10): 0.0; T(11): 0.2; S(20): 0.0; S(21): 0.0; S(22): 0.0	S3; T7;	S107; T111		4.48	0	0	3	827.7	2481	49.28	9555
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	42		0	0	2	673.3	1346	58.82	11644
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	38		0	0	2	673.3	1346	59.32	11749
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		2.36	0	0	2	673.3	1346	58.82	11644
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		2.05	0	0	2	673.3	1346	59.32	11749
KETTSGTSTEPVKNSsPAPPQPAPGK	CDK12	51755	cyclin-dependent kinase 12 isoform 2	S16(Phospho)	T(3): 0.0; T(4): 0.0; S(5): 0.0; T(7): 0.0; S(8): 0.0; T(9): 0.0; S(15): 3.6; S(16): 96.4	S16;	S1083	46		0	2	3	891.8	2673	24.29	4242
KETTSGTSTEPVKNSsPAPPQPAPGK	CDK12	51755	cyclin-dependent kinase 12 isoform 2	S16(Phospho)	T(3): 0.0; T(4): 0.0; S(5): 0.0; T(7): 0.0; S(8): 0.0; T(9): 0.0; S(15): 3.6; S(16): 96.4	S16;	S1083		5.83	0	2	3	891.8	2673	24.29	4242
SLsRsPLPSR	CDK12	51755	cyclin-dependent kinase 12 isoform 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 99.9; S(9): 0.1	S3; S5;	S343; S345		2.52	0.001	1	2	630.3	1260	36.62	6861
RRsSSPFLSK	CDK12	51755	cyclin-dependent kinase 12 isoform 2	S3(Phospho)	S(3): 98.4; S(4): 50.8; S(5): 50.8; S(9): 0.1	S3;	S332		2.17	0.007	2	2	662.8	1325	25.07	4407
sLsRsPLPSR	CDK12	51755	cyclin-dependent kinase 12 isoform 2	S1(Phospho) S3(Phospho) S5(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 100.0; S(9): 0.0	S1; S3; S5;	S341; S343; S345		1.96	0.007	1	2	670.3	1340	45.75	8813
HSsIsPSTLTlk	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S3(Phospho) S5(Phospho)	S(2): 2.7; S(3): 97.3; S(5): 100.0; S(7): 0.0; T(8): 0.0; T(10): 0.0	S3; S5;	S437; S439	41		0	0	2	715.8	1431	57.63	11370
SRKsPsPAGGGSSPYSR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S4(Phospho) S6(Phospho)	S(1): 0.5; S(4): 99.8; S(6): 99.8; S(12): 25.0; S(13): 25.0; Y(15): 25.0; S(16): 25.0	S4; S6;	S340; S342	32		0	2	3	639.9	1918	18.19	2958
SRKsPsPAGGGSSPYSR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S4(Phospho) S6(Phospho)	S(1): 0.2; S(4): 99.8; S(6): 100.0; S(12): 0.1; S(13): 0.1; Y(15): 49.9; S(16): 49.9	S4; S6;	S340; S342	16		0	2	2	959.4	1918	18.36	2992
QtDPSTPQQESSKPLGGIQSSQTIQPK	CDK13	8621	cyclin-dependent kinase 13 isoform 2	T2(Phospho)	T(2): 100.0; S(5): 0.0; T(6): 0.0; S(11): 0.0; S(12): 0.0; S(21): 0.0; S(22): 0.0; T(24): 0.0	T2;	T1083	12		0	0	3	1015	3044	48.96	9486

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#
SRKsPsPAGGGSSPYSR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S4(Phospho) S6(Phospho)	S(1): 0.5; S(4): 99.8; S(6): 99.8; S(12): 25.0; S(13): 25.0; Y(15): 25.0; S(16): 25.0	S4; S6;	S340; S342		6.21	0	2	3	639.9	1918	18.19	2958
QtdPSTPQQESSKPLGGIQPSSQTIQPK	CDK13	8621	cyclin-dependent kinase 13 isoform 2	T2(Phospho)	T(2): 100.0; S(5): 0.0; T(6): 0.0; S(11): 0.0; S(12): 0.0; S(21): 0.0; S(22): 0.0; T(24): 0.0	T2;	T1083		4.3	0	0	3	1015	3044	48.96	9486
SRKsPsPAGGGSSPYSR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S4(Phospho) S6(Phospho)	S(1): 0.2; S(4): 99.8; S(6): 100.0; S(12): 0.1; S(13): 0.1; Y(15): 49.9; S(16): 49.9	S4; S6;	S340; S342		3.43	0	2	2	959.4	1918	18.36	2992
HSsIsPSTLTlk	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S3(Phospho) S5(Phospho)	S(2): 2.7; S(3): 97.3; S(5): 100.0; S(7): 0.0; T(8): 0.0; T(10): 0.0	S3; S5;	S437; S439		3.39	0	0	2	715.8	1431	57.63	11370
sRsPYsPVLR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; Y(5): 2.0; S(6): 98.0	S1; S3; S6;	S395; S397; S400		2.94	0	1	2	701.3	1402	61.42	12178
sRsPYsPVLR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; Y(5): 2.0; S(6): 98.0	S1; S3; S6;	S395; S397; S400	18		0.001	1	2	701.3	1402	61.42	12178
LPRsPsPYSR	CDK13	8621	cyclin-dependent kinase 13 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; Y(8): 0.0; S(9): 0.0	S4; S6;	S358; S360		2.79	0.001	1	2	660.3	1320	29.86	5433
EGEAAGGDHtESTSDKETIDDDR	CDS1	1040	phosphatidate cytidylyltransferase 1	T11(Phospho)	T(11): 92.9; S(13): 3.5; T(14): 3.5; S(15): 0.0; T(19): 0.0	T11;	T33	19		0	1	3	882	2644	23.87	4153
EGEAAGGDHtESTSDKETIDDDR	CDS1	1040	phosphatidate cytidylyltransferase 1	T11(Phospho)	T(11): 92.9; S(13): 3.5; T(14): 3.5; S(15): 0.0; T(19): 0.0	T11;	T33		3.12	0	1	3	882	2644	23.87	4153
VAHEPVAPPEDKESEAKVDGETAsDs ESR	CDS2	8760	phosphatidate cytidylyltransferase 2	S26(Phospho)	S(14): 0.6; S(16): 0.1; T(24): 7.3; S(26): 91.4; S(28): 0.6; S(30): 0.1	S26;	S33		4.52	0.007	2	4	841.4	3362	34.43	6385
AYLGyQAVPSGSSGSLSTSSSSPPGtPSP ADaK	CEBPB	1051	CCAAT/enhancer-binding protein beta isoform c	T27(Phospho)	Y(2): 0.0; Y(5): 0.0; S(10): 0.4; S(12): 0.4; S(13): 0.4; S(15): 0.4; S(17): 0.4; T(18): 0.4; S(19): 0.4; S(20): 0.4; S(21): 0.4; S(22): 48.3; S(23): 48.3; T(27): 99.2; S(29): 0.8	T27;	T37		2.68	0.005	0	3	1120	3358	74.23	15007
SQLDDHPeSDDEENFIDANDDDEMEK	CEBPZ	10153	CCAAT/enhancer-binding protein zeta	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S629	30		0	0	3	1045	3132	61.1	12112
SQLDDHPeSDDEENFIDANDDDEMEK	CEBPZ	10153	CCAAT/enhancer-binding protein zeta	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S629		5.48	0	0	3	1045	3132	61.1	12112
RRsPsPTPTPGPSR	CENPA	1058	histone H3-like centromeric protein A isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 0.0; T(9): 0.0; S(13): 0.0	S3; S5;	S17; S19	31		0	2	3	551.6	1653	16.95	2694
RRsPsPTPTPGPSR	CENPA	1058	histone H3-like centromeric protein A isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 0.0; T(9): 0.0; S(13): 0.0	S3; S5;	S17; S19	28		0	2	3	551.6	1653	17.5	2814
RRsPsPTPTPGPSR	CENPA	1058	histone H3-like centromeric protein A isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 0.0; T(9): 0.0; S(13): 0.0	S3; S5;	S17; S19		6.37	0	2	3	551.6	1653	17.5	2814
RRsPsPTPTPGPSR	CENPA	1058	histone H3-like centromeric protein A isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 0.0; T(9): 0.0; S(13): 0.0	S3; S5;	S17; S19		6.14	0	2	3	551.6	1653	16.95	2694
RRSPSPTPTPGPsR	CENPA	1058	histone H3-like centromeric protein A isoform b	S13(Phospho)	S(3): 49.0; S(5): 49.0; T(7): 2.1; T(9): 2.1; S(13): 97.7	S13;	S27		2.65	0.005	2	2	826.9	1653	16.95	2695

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#
VAASPKSPTAALNEsLVECPK	CEP55	55165	centrosomal protein of 55 kDa	C19(Carbamido methyl)S15(Phospho)	S(4): 66.7; S(7): 66.7; T(9): 66.7; S(15): 100.0	S15;	S436	17		0	1	3	803.7	2409	72	14552
VAASPKSPTAALNEsLVECPK	CEP55	55165	centrosomal protein of 55 kDa	C19(Carbamido methyl)S15(Phospho)	S(4): 66.7; S(7): 66.7; T(9): 66.7; S(15): 100.0	S15;	S436		3.73	0	1	3	803.7	2409	72	14552
TPPPRSsPNPSPERPR	CEP89	84902	centrosomal protein of 89 kDa	S6(Phospho) S10(Phospho)	T(1): 0.0; S(6): 100.0; S(10): 100.0	S6; S10;	S40; S44		4.57	0.001	1	3	615.6	1845	19.52	3237
LVEDERsDREEtEssEGEEAAAGGGAK	CERS2	29956	ceramide synthase 2	S7(Phospho) T12(Phospho) S14(Phospho) S15(Phospho)	S(7): 100.0; T(12): 100.0; S(14): 100.0; S(15): 100.0	S7; T12; S14; S15;	S341; T346; S348; S349	46		0	2	3	1043	3128	37.26	6994
LVEDERsDREEtEssEGEEAAAGGGAK	CERS2	29956	ceramide synthase 2	S7(Phospho) T12(Phospho) S14(Phospho) S15(Phospho)	S(7): 100.0; T(12): 100.0; S(14): 100.0; S(15): 100.0	S7; T12; S14; S15;	S341; T346; S348; S349	32		0	2	3	1043	3128	37.79	7103
LVEDERsDREEtEssEGEEAAAGGGAK	CERS2	29956	ceramide synthase 2	S7(Phospho) T12(Phospho) S14(Phospho) S15(Phospho)	S(7): 100.0; T(12): 100.0; S(14): 100.0; S(15): 100.0	S7; T12; S14; S15;	S341; T346; S348; S349	23		0	2	3	1043	3128	36.71	6880
ELAsGLQMTAMVEYHPDK	CFAP47	286464	cilia- and flagella-associated protein 47 isoform 2	M8(Oxidation) M11(Oxidation) S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 99.2; Y(14): 0.8	S4; T9;	S97; T102		5.04	0.006	0	3	738	2212	27.15	4859
SHsQASLAGPGVPDPSNR	CGN	57530	cingulin	S3(Phospho)	S(1): 1.9; S(3): 98.0; S(6): 0.0; S(16): 0.0	S3;	S137	41		0	0	3	619.6	1857	37.1	6962
SHsQASLAGPGVPDPSNR	CGN	57530	cingulin	S3(Phospho)	S(1): 1.9; S(3): 98.0; S(6): 0.0; S(16): 0.0	S3;	S137		4.34	0	0	3	619.6	1857	37.1	6962
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho)	T(1): 0.0; S(5): 0.1; S(6): 97.7; T(9): 2.2; T(10): 0.1	S6;	S429	50		0	0	2	810.3	1620	25.89	4582
TQDPsPGTTPPQAR	CHAF1B	8208	chromatin assembly factor 1 subunit B	S6(Phospho)	T(1): 0.0; S(5): 0.1; S(6): 97.7; T(9): 2.2; T(10): 0.1	S6;	S429		3.53	0	0	2	810.3	1620	25.89	4582
LAPVPsPEPQKPAPVsPESVK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S6(Phospho) S16(Phospho)	S(6): 100.0; S(16): 97.8; S(19): 2.2	S6; S16;	S204; S214	42		0	0	3	772	2314	58.72	11620
SSSVsPSSWKsPPAsPESWK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S5(Phospho) S11(Phospho) S15(Phospho)	S(1): 0.2; S(2): 0.2; S(3): 3.6; S(5): 88.9; S(7): 3.6; S(8): 3.6; S(11): 100.0; S(15): 99.8; S(18): 0.2	S5; S11; S15;	S376; S382; S386	21		0	1	3	786.6	2358	73.26	14816
LAPVPsPEPQKPAPVsPESVK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S6(Phospho) S16(Phospho)	S(6): 100.0; S(16): 100.0; S(19): 0.0	S6; S16;	S204; S214	16		0	0	3	772	2314	59.25	11733
KPGPLsPEIRsPAGsPELR	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S7(Phospho) S12(Phospho) S16(Phospho)	S(7): 100.0; S(12): 100.0; S(16): 100.0	S7; S12; S16;	S427; S432; S436	15		0	1	3	775.7	2325	60.48	11975
LAPVPsPEPQKPAPVsPESVK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S6(Phospho) S16(Phospho)	S(6): 100.0; S(16): 97.8; S(19): 2.2	S6; S16;	S204; S214		5.74	0	0	3	772	2314	58.72	11620
KPGPLsPEIRsPAGsPELR	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S7(Phospho) S12(Phospho) S16(Phospho)	S(7): 100.0; S(12): 100.0; S(16): 100.0	S7; S12; S16;	S427; S432; S436		5.19	0	1	3	775.7	2325	60.48	11975
KPSPsEPsEPWKPFAVsPEPR	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S7(Phospho) S18(Phospho)	S(3): 50.0; S(5): 50.0; S(7): 100.0; S(18): 100.0	S7; S18;	S286; S297		4.06	0	0	3	896.1	2686	76.83	15500
LAPVPsPEPQKPAPVsPESVK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S6(Phospho) S16(Phospho)	S(6): 100.0; S(16): 100.0; S(19): 0.0	S6; S16;	S204; S214		3.98	0	0	3	772	2314	59.25	11733
SSSVsPSSWKsPPAsPESWK	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S5(Phospho) S11(Phospho) S15(Phospho)	S(1): 0.2; S(2): 0.2; S(3): 3.6; S(5): 88.9; S(7): 3.6; S(8): 3.6; S(11): 100.0; S(15): 99.8; S(18): 0.2	S5; S11; S15;	S376; S382; S386		3.53	0	1	3	786.6	2358	73.26	14816
KPSPsEPsEPWKPFAVsPEPR	CHAMP1	283489	chromosome alignment-maintaining phosphoprotein 1	S7(Phospho) S18(Phospho)	S(3): 50.0; S(5): 50.0; S(7): 100.0; S(18): 100.0	S7; S18;	S286; S297	14		0.001	0	3	896.1	2686	76.83	15500

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#
QIDssEEDDDDEEDYDNDKR	CHD1	1105	chromodomain-helicase-DNA-binding protein 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; Y(14): 0.0	S4; S5;	S215; S216	43		0	1	3	826.3	2477	36.07	6743
RQIDssEEDDDDEEDYDNDKR	CHD1	1105	chromodomain-helicase-DNA-binding protein 1	S5(Phospho) S6(Phospho)	S(5): 100.0; S(6): 100.0; Y(15): 0.0	S5; S6;	S215; S216	18		0	2	3	878.3	2633	29.73	5406
RQIDssEEDDDDEEDYDNDKR	CHD1	1105	chromodomain-helicase-DNA-binding protein 1	S5(Phospho) S6(Phospho)	S(5): 100.0; S(6): 100.0; Y(15): 0.0	S5; S6;	S215; S216		4.35	0	2	3	878.3	2633	29.73	5406
QIDssEEDDDDEEDYDNDKR	CHD1	1105	chromodomain-helicase-DNA-binding protein 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; Y(14): 0.0	S4; S5;	S215; S216		4.22	0	1	3	826.3	2477	36.07	6743
KQDssDEDDDDDEAPKR	CHD2	1106	chromodomain-helicase-DNA-binding protein 2 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S207; S208	65		0	2	3	708.9	2125	13.23	1898
KQDssDEDDDDDEAPKR	CHD2	1106	chromodomain-helicase-DNA-binding protein 2 isoform 2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S207; S208		5.71	0	2	3	708.9	2125	13.23	1898
METEADAPsPAPsLGER	CHD3	1107	chromodomain-helicase-DNA-binding protein 3 isoform 2	M1(Oxidation) S9(Phospho) S13(Phospho)	T(3): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S1601; S1605	34		0	0	2	967.4	1934	51.77	10074
METEADAPsPAPsLGER	CHD3	1107	chromodomain-helicase-DNA-binding protein 3 isoform 2	S9(Phospho) S13(Phospho)	T(3): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S1601; S1605	25		0	0	2	959.4	1918	56.67	11154
METEADAPsPAPsLGER	CHD3	1107	chromodomain-helicase-DNA-binding protein 3 isoform 2	S9(Phospho) S13(Phospho)	T(3): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S1601; S1605		3.63	0	0	2	959.4	1918	56.67	11154
METEADAPsPAPsLGER	CHD3	1107	chromodomain-helicase-DNA-binding protein 3 isoform 2	M1(Oxidation) S9(Phospho) S13(Phospho)	T(3): 0.0; S(9): 100.0; S(13): 100.0	S9; S13;	S1601; S1605		2.63	0	0	2	967.4	1934	51.77	10074
tsPTTPEASATNSPCTSKPATPAPSEK	CHD3	1107	chromodomain-helicase-DNA-binding protein 3 isoform 2	C15(Carbamido methyl) T1(Phospho) S2(Phospho)	T(1): 99.9; S(2): 99.9; T(4): 0.1; T(5): 0.0; S(9): 0.0; T(11): 0.0; S(13): 0.0; T(16): 0.0; S(17): 0.0; T(21): 0.0; S(25): 0.0	T1; S2;	T1537; S1538		2.63	0.001	0	3	959.1	2875	36.46	6827
KMsQPGsPSPK	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 98.7; S(9): 1.3	S3; S7;	S1524; S1528	45		0	1	2	652.3	1304	17.67	2851
MSQPGsPSPK	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(8): 0.0	S6;	S1528	35		0	0	2	548.2	1095	18.66	3055
SSsEDDDLVDSEDFDDASINSYSVSDGSTSR	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S3(Phospho)	S(1): 52.0; S(2): 52.0; S(3): 96.0; S(12): 0.1; S(18): 0.0; S(21): 0.0; Y(22): 0.0; S(23): 0.0; S(25): 0.0; S(28): 0.0; T(29): 0.0; S(30): 0.0	S3;	S303	21		0	0	3	1154	3461	95.81	19151
KMsQPGsPSPK	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 98.7; S(9): 1.3	S3; S7;	S1524; S1528		4.89	0	1	2	652.3	1304	17.67	2851
SSsEDDDLVDSEDFDDASINSYSVSDGSTSR	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S3(Phospho)	S(1): 52.0; S(2): 52.0; S(3): 96.0; S(12): 0.1; S(18): 0.0; S(21): 0.0; Y(22): 0.0; S(23): 0.0; S(25): 0.0; S(28): 0.0; T(29): 0.0; S(30): 0.0	S3;	S303		3.57	0	0	3	1154	3461	95.81	19151
MSQPGsPSPK	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	S6(Phospho)	S(2): 0.0; S(6): 100.0; S(8): 0.0	S6;	S1528		3.3	0	0	2	548.2	1095	18.66	3055
TPTPSTPGDQTNPNTAPVPVPAEDGIK	CHD4	1108	chromodomain-helicase-DNA-binding protein 4 isoform 2	T10(Phospho)	T(1): 47.5; T(3): 47.5; S(5): 2.5; T(6): 2.5; T(10): 99.7; T(14): 0.3	T10;	T1542		2.99	0.003	0	3	915.7	2745	65.63	13191
NIPsPGQLDPDTR	CHD7	55636	chromodomain-helicase-DNA-binding protein 7 isoform 1	S4(Phospho)	S(4): 100.0; T(12): 0.0	S4;	S2559	52		0	0	2	745.3	1490	60.64	12011
NIPsPGQLDPDTR	CHD7	55636	chromodomain-helicase-DNA-binding protein 7 isoform 1	S4(Phospho)	S(4): 100.0; T(12): 0.0	S4;	S2559		2.3	0	0	2	745.3	1490	60.64	12011
NTSSDSDVEMPAQsPREDEESSIQK	CHD8	57680	chromodomain-helicase-DNA-binding protein 8 isoform 2	S16(Phospho)	T(2): 64.4; S(3): 64.4; S(4): 64.4; S(7): 6.9; S(16): 99.9; S(23): 0.1; S(24): 0.0	S16;	S283		3.06	0	1	3	1074	3219	61.27	12147

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#
NTSSDNsDVEVMPAQsPREDEESSIQK	CHD8	57680	chromodomain-helicase-DNA-binding protein 8 isoform 2	M12(Oxidation) S7(Phospho) S16(Phospho)	T(2): 33.6; S(3): 33.6; S(4): 33.6; S(7): 99.2; S(16): 100.0; S(23): 0.0; S(24): 0.0	S7; S16;	S274; S283		2.83	0	1	3	1079	3235	51.47	10014
SENKEEPQssEEESMSSVETR	CHD9	80205	chromodomain-helicase-DNA-binding protein 9 isoform 2	S10(Phospho) S11(Phospho)	S(1): 0.0; S(10): 99.9; S(11): 99.9; S(15): 0.2; S(17): 0.0; S(18): 0.0; T(21): 0.0	S10; S11;	S2058; S2059	59		0	1	3	891.4	2672	47.01	9078
SENKEEPQssEEESMSSVETR	CHD9	80205	chromodomain-helicase-DNA-binding protein 9 isoform 2	S10(Phospho) S11(Phospho)	S(1): 0.0; S(10): 99.9; S(11): 99.9; S(15): 0.2; S(17): 0.0; S(18): 0.0; T(21): 0.0	S10; S11;	S2058; S2059		4.35	0	1	3	891.4	2672	47.01	9078
KNEssDEIsDAEQMPQHTLK	CHD9	80205	chromodomain-helicase-DNA-binding protein 9 isoform 2	S4(Phospho) S5(Phospho) S9(Phospho)	S(4): 100.0; S(5): 100.0; S(9): 100.0; T(18): 0.0	S4; S5; S9;	S611; S612; S616		3.3	0	1	3	843	2527	54.58	10714
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124	66		0	1	3	815.3	2444	13.43	1939
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124		4.49	0	1	3	815.3	2444	13.43	1939
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124	23		0.002	1	2	1222	2444	13.47	1949
REEDEENDNDNEsDHDEADS	CHRA1	54108	chromatin accessibility complex protein 1	S13(Phospho)	S(13): 100.0; S(20): 0.0	S13;	S124		2.69	0.004	1	2	1222	2444	13.47	1949
NPSPTTRPVsR	CIZ1	25792	cip1-interacting zinc finger protein isoform 6	S10(Phospho)	S(3): 0.1; T(5): 2.1; T(6): 0.1; S(10): 97.8	S10;	S744	20		0.001	0	2	646.3	1292	17.33	2775
NPSPTTRPVsR	CIZ1	25792	cip1-interacting zinc finger protein isoform 6	S10(Phospho)	S(3): 0.1; T(5): 2.1; T(6): 0.1; S(10): 97.8	S10;	S744		2.32	0.005	0	2	646.3	1292	17.33	2775
RQsSGSATNVASTPDNR	CLASP1	23332	CLIP-associating protein 1 isoform 3	S3(Phospho)	S(3): 97.6; S(4): 2.4; S(6): 0.0; T(8): 0.0; S(12): 0.0; T(13): 0.0	S3;	S646	39		0	1	2	914.4	1828	18.19	2959
RQsSGSATNVASTPDNR	CLASP1	23332	CLIP-associating protein 1 isoform 3	S3(Phospho)	S(3): 97.6; S(4): 2.4; S(6): 0.0; T(8): 0.0; S(12): 0.0; T(13): 0.0	S3;	S646		2.89	0	1	2	914.4	1828	18.19	2959
ESSTESSQSAKPVSGQDTSNGTEGSPAAEK	CLCC1	23155	chloride channel CLIC-like protein 1 isoform 4 precursor	S25(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; S(6): 0.0; S(7): 0.0; S(9): 0.0; S(14): 0.0; T(18): 0.0; S(19): 0.0; T(22): 0.0; S(25): 100.0	S25;	S324	22		0	0	3	1012	3033	21.09	3568
ESSTESSQSAKPVSGQDTSNGTEGSPAAEK	CLCC1	23155	chloride channel CLIC-like protein 1 isoform 4 precursor	S25(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; S(6): 0.0; S(7): 0.0; S(9): 0.0; S(14): 0.0; T(18): 0.0; S(19): 0.0; T(22): 0.0; S(25): 100.0	S25;	S324		5.25	0	0	3	1012	3033	21.09	3568
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	50		0	0	2	877.4	1754	60.85	12059
TASESISNLSEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S3(Phospho) S14(Phospho)	T(1): 2.2; S(3): 95.7; S(5): 2.2; S(7): 0.0; S(10): 0.0; S(14): 100.0	S3; S14;	S193; S204	44		0	0	2	877.4	1754	63.19	12608
TASESISNLsEAGsIKKGER	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S5(Phospho) S10(Phospho) S14(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 100.0; S(7): 0.0; S(10): 100.0; S(14): 100.0	S5; S10; S14;	S195; S200; S204	35		0	2	3	768.6	2304	44.27	8476
TASESISNLsEAGsIKKGER	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	35		0	2	3	742	2224	39.89	7548
TASESISNLsEAGSIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S5(Phospho) S10(Phospho)	T(1): 0.1; S(3): 0.1; S(5): 99.8; S(7): 0.0; S(10): 100.0; S(14): 0.0	S5; S10;	S195; S200	34		0	0	2	877.4	1754	62.41	12401

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#
AsSTPSSETQEEFVDDFR	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S2(Phospho)	S(2): 99.6; S(3): 0.2; T(4): 0.2; S(6): 1.8; S(7): 49.1; T(9): 49.1	S2;	S43	33		0	0	2	1096	2192	85.75	17180
TASESISNLSEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S14(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(14): 100.0	S14;	S204	30		0	0	2	837.4	1674	54.01	10588
TASESISNLsEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S10(Phospho) S14(Phospho)	T(1): 49.2; S(3): 49.2; S(5): 1.7; S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S200; S204	29		0	0	2	917.4	1834	73.64	14890
TASESISNLsEAGsIKK	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	27		0	1	2	941.4	1882	46.2	8908
TASESISNLsEAGsIKKGER	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S5(Phospho) S10(Phospho) S14(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 100.0; S(7): 0.0; S(10): 100.0; S(14): 100.0	S5; S10; S14;	S195; S200; S204		5.69	0	2	3	768.6	2304	44.27	8476
TASESISNLsEAGsIKKGER	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		5.09	0	2	3	742	2224	39.89	7548
TASESISNLsEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S10(Phospho) S14(Phospho)	T(1): 49.2; S(3): 49.2; S(5): 1.7; S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S200; S204		4.05	0	0	2	917.4	1834	73.64	14890
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		3.92	0	0	2	877.4	1754	60.85	12059
TAsESISNLSEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S3(Phospho) S14(Phospho)	T(1): 2.2; S(3): 95.7; S(5): 2.2; S(7): 0.0; S(10): 0.0; S(14): 100.0	S3; S14;	S193; S204		3.85	0	0	2	877.4	1754	63.19	12608
AsSTPSSETQEEFVDDFR	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S2(Phospho)	S(2): 99.6; S(3): 0.2; T(4): 0.2; S(6): 1.8; S(7): 49.1; T(9): 49.1	S2;	S43		2.14	0	0	2	1096	2192	85.75	17180
TASESISNLSEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S14(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(10): 0.0; S(14): 100.0	S14;	S204		3.21	0.001	0	2	837.4	1674	54.01	10588
TASESISNLsEAGsIKK	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		3.01	0.002	1	2	941.4	1882	46.2	8908
TASESISNLsEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S10(Phospho) S14(Phospho)	T(1): 49.2; S(3): 49.2; S(5): 1.7; S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S200; S204	30		0.004	0	2	917.3	1834	74.15	14987
TASESISNLsEAGsIK	CLIP1	6249	CAP-Gly domain-containing linker protein 1 isoform b	S5(Phospho) S10(Phospho)	T(1): 0.1; S(3): 0.1; S(5): 99.8; S(7): 0.0; S(10): 100.0; S(14): 0.0	S5; S10;	S195; S200		2.9	0.005	0	2	877.4	1754	62.41	12401
RfSdSEGEETVPEPR	CLN3	1201	battenin isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0	S3; S5;	S12; S14	31		0	1	2	947.9	1895	46.63	9000
RfSdSEGEETVPEPR	CLN3	1201	battenin isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(10): 0.0	S3; S5;	S12; S14		3.74	0	1	2	947.9	1895	46.63	9000
KSEPLDEsDNDF	CLUAP1	23059	clusterin-associated protein 1 isoform 2	S8(Phospho)	S(2): 2.8; S(8): 97.2	S8;	S243	24		0.003	1	2	738.3	1476	52.48	10241
SEDPGQEQAGsEEEGSSASGLAK	CLUH	23277	clustered mitochondria protein homolog	S11(Phospho)	S(1): 0.0; S(11): 96.3; S(16): 3.5; S(17): 0.1; S(19): 0.0	S11;	S664	34		0	0	2	1150	2299	37.63	7071
SEDPGQEQAGsEEEGSSASGLAK	CLUH	23277	clustered mitochondria protein homolog	S11(Phospho)	S(1): 0.0; S(11): 96.3; S(16): 3.5; S(17): 0.1; S(19): 0.0	S11;	S664		2.98	0	0	2	1150	2299	37.63	7071
TNSMSSSLGSPNR	CNOT2	4848	CCR4-NOT transcription complex subunit 2	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	84		0	0	2	737.8	1475	29.94	5451

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#
TNSMSSSGLGsPNR	CNOT2	4848	CCR4-NOT transcription complex subunit 2	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		4.02	0	0	2	737.8	1475	29.94	5451
DQTAsAPAtPLVnk	COBL1	22837	cordons-bleu protein-like 1 isoform 4	S5(Phospho) T9(Phospho)	T(3): 0.0; S(5): 100.0; T(9): 100.0	S5; T9;	S256; T260	38		0	0	2	786.8	1573	50.32	9772
DQTAsAPAtPLVnk	COBL1	22837	cordons-bleu protein-like 1 isoform 4	S5(Phospho) T9(Phospho)	T(3): 0.0; S(5): 100.0; T(9): 100.0	S5; T9;	S256; T260		3.37	0	0	2	786.8	1573	50.32	9772
HAYEGSSSGNsPEYPR	COL17A1	1308	collagen alpha-1(XVII) chain	S12(Phospho)	Y(3): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(11): 2.2; S(12): 97.8; Y(15): 0.0	S12;	S118	40		0	0	2	952.9	1905	26.17	4644
LQsAsPSTR	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 98.2; S(7): 1.8; T(8): 0.0	S3; S5;	S148; S150	39		0	0	2	553.7	1106	20.25	3388
AHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S11(Phospho)	S(3): 100.0; S(6): 0.0; T(7): 0.0; S(11): 100.0; S(14): 0.0; T(15): 0.0	S3; S11;	S85; S93	34		0	0	3	672.6	2016	53.16	10397
RAHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S4(Phospho) S12(Phospho)	S(4): 100.0; S(7): 0.0; T(8): 0.0; S(12): 100.0; S(15): 0.0; T(16): 0.0	S4; S12;	S85; S93	30		0	1	3	724.6	2172	44.79	8602
HAYEGSSSGNsPEYPR	COL17A1	1308	collagen alpha-1(XVII) chain	S12(Phospho) Y15(Phospho)	Y(3): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(11): 5.9; S(12): 97.1; Y(15): 97.1	S12; Y15;	S118; Y121	29		0	0	2	992.9	1985	32.55	5993
AHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S11(Phospho)	S(3): 100.0; S(6): 0.0; T(7): 0.0; S(11): 100.0; S(14): 0.0; T(15): 0.0	S3; S11;	S85; S93	18		0	0	2	1008	2016	53.2	10408
RAHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S4(Phospho) S12(Phospho)	S(4): 100.0; S(7): 0.0; T(8): 0.0; S(12): 100.0; S(15): 0.0; T(16): 0.0	S4; S12;	S85; S93		4.92	0	1	3	724.6	2172	44.79	8602
AHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S11(Phospho)	S(3): 100.0; S(6): 0.0; T(7): 0.0; S(11): 100.0; S(14): 0.0; T(15): 0.0	S3; S11;	S85; S93		4.46	0	0	3	672.6	2016	53.16	10397
LQsAsPSTR	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 98.2; S(7): 1.8; T(8): 0.0	S3; S5;	S148; S150		3.17	0	0	2	553.7	1106	20.25	3388
AHsPASTLPNsPGSTFER	COL17A1	1308	collagen alpha-1(XVII) chain	S3(Phospho) S11(Phospho)	S(3): 100.0; S(6): 0.0; T(7): 0.0; S(11): 100.0; S(14): 0.0; T(15): 0.0	S3; S11;	S85; S93		3.15	0	0	2	1008	2016	53.2	10408
HAYEGSSSGNsPEYPR	COL17A1	1308	collagen alpha-1(XVII) chain	S12(Phospho) Y15(Phospho)	Y(3): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(11): 5.9; S(12): 97.1; Y(15): 97.1	S12; Y15;	S118; Y121		2.98	0	0	2	992.9	1985	32.55	5993
HAYEGSSSGNsPEYPR	COL17A1	1308	collagen alpha-1(XVII) chain	S12(Phospho)	Y(3): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(11): 2.2; S(12): 97.8; Y(15): 0.0	S12;	S118		2.64	0	0	2	952.9	1905	26.17	4644
NLSPGAVESDVR	COPA	1314	coatamer subunit alpha isoform 2	S3(Phospho)	S(3): 100.0; S(9): 0.0	S3;	S173	70		0	0	2	662.3	1324	54.87	10774
NLSPGAVESDVR	COPA	1314	coatamer subunit alpha isoform 2	S3(Phospho)	S(3): 100.0; S(9): 0.0	S3;	S173		2.41	0	0	2	662.3	1324	54.87	10774
STAQQELDGKPaSTPTVIVASHTANKEE K	COPB2	9276	coatamer subunit beta'	S13(Phospho)	S(1): 3.9; T(2): 3.9; S(13): 92.0; T(15): 0.2; S(21): 0.0; T(23): 0.0	S13;	S859	19		0	1	4	779.1	3114	42.94	8189
STAQQELDGKPaSTPTVIVASHTANKEE K	COPB2	9276	coatamer subunit beta'	S13(Phospho)	S(1): 0.0; T(2): 0.0; S(13): 96.9; T(15): 3.1; S(21): 0.0; T(23): 0.0	S13;	S859	13		0	1	4	779.1	3114	42.14	8022
STAQQELDGKPaSTPTVIVASHTANKEE K	COPB2	9276	coatamer subunit beta'	S13(Phospho)	S(1): 3.9; T(2): 3.9; S(13): 92.0; T(15): 0.2; S(21): 0.0; T(23): 0.0	S13;	S859		8.52	0	1	4	779.1	3114	42.94	8189
STAQQELDGKPaSTPTVIVASHTANKEE K	COPB2	9276	coatamer subunit beta'	S13(Phospho)	S(1): 0.0; T(2): 0.0; S(13): 96.9; T(15): 3.1; S(21): 0.0; T(23): 0.0	S13;	S859		6.82	0	1	4	779.1	3114	42.14	8022

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#
SLLSHEFQDEtDIEETLYSSK	CPD	1362	carboxypeptidase D isoform 2	T11(Phospho) T13(Phospho)	S(1): 0.0; S(4): 0.0; T(11): 100.0; T(13): 100.0; T(17): 0.0; Y(19): 0.0; S(20): 0.0; S(21): 0.0	T11; T13;	T1121; T1123		2.7	0	0	3	916.7	2748	74.87	15142
SLLSHEFQDEtDIEETLYSSK	CPD	1362	carboxypeptidase D isoform 2	T11(Phospho) T13(Phospho)	S(1): 0.0; S(4): 0.0; T(11): 100.0; T(13): 100.0; T(17): 0.0; Y(19): 0.0; S(20): 0.0; S(21): 0.0	T11; T13;	T1121; T1123	15	0.002	0	3	916.7	2748	74.87	15142	
NCSsPEFSK	CPNE1	8904	copine-1 isoform c	C2(Carbamidomethyl) S4(Phospho)	S(3): 0.0; S(4): 100.0; S(8): 0.0	S4;	S55	26	0	0	2	568.2	1135	23.35	4046	
NCSsPEFSK	CPNE1	8904	copine-1 isoform c	C2(Carbamidomethyl) S4(Phospho)	S(3): 0.0; S(4): 100.0; S(8): 0.0	S4;	S55		2.4	0	0	2	568.2	1135	23.35	4046
EADIDssDEsDIEEDIDQPSAHK	CPSF2	53981	cleavage and polyadenylation specificity factor subunit 2	S6(Phospho) S7(Phospho) S10(Phospho)	S(6): 100.0; S(7): 100.0; S(10): 100.0; S(20): 0.0	S6; S7; S10;	S419; S420; S423		2.77	0	0	3	929	2785	71.8	14519
EADIDssDEsDIEEDIDQPSAHK	CPSF2	53981	cleavage and polyadenylation specificity factor subunit 2	S6(Phospho) S7(Phospho) S10(Phospho)	S(6): 100.0; S(7): 100.0; S(10): 100.0; S(20): 0.0	S6; S7; S10;	S419; S420; S423	16	0.002	0	3	929	2785	71.29	14416	
EADIDssDEsDIEEDIDQPSAHK	CPSF2	53981	cleavage and polyadenylation specificity factor subunit 2	S6(Phospho) S7(Phospho) S10(Phospho)	S(6): 100.0; S(7): 100.0; S(10): 100.0; S(20): 0.0	S6; S7; S10;	S419; S420; S423		1.53	0.005	0	3	929	2785	71.29	14416
DSSDSADGRAtPSENLVPSSAR	CPSF7	79869	cleavage and polyadenylation specificity factor subunit 7 isoform 3	T11(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; T(11): 100.0; S(13): 0.0; S(19): 0.0; S(20): 0.0	T11;	T194	34	0	1	3	767	2299	44.22	8462	
DSSDSADGRAtPSENLVPSSAR	CPSF7	79869	cleavage and polyadenylation specificity factor subunit 7 isoform 3	T11(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; T(11): 100.0; S(13): 0.0; S(19): 0.0; S(20): 0.0	T11;	T194		5.33	0	1	3	767	2299	44.22	8462
ASQCNVsLKK	CTDSPL	10217	CTD small phosphatase-like protein isoform 2	C4(Carbamidomethyl) S7(Phospho)	S(2): 0.0; S(7): 100.0	S7;	S33	22	0.001	1	2	607.8	1215	17.77	2871	
SRTSVQtEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T7(Phospho)	S(1): 33.4; T(3): 33.4; S(4): 33.4; T(7): 99.9; S(17): 0.0	T7;	T288	59	0	1	3	741.3	2222	47.06	9088	
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0; S(19): 100.0	S8; S19;	S271; S282	50	0	1	3	854.7	2562	74.46	15062	
TPEELDDsDFETEDFDVR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0	S8;	S271	48	0	0	2	1120	2239	78.85	15893	
SRTSVQtEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T7(Phospho)	S(1): 1.5; T(3): 49.3; S(4): 49.3; T(7): 99.9; S(17): 0.0	T7;	T288	46	0	1	2	1111	2222	47.05	9087	
tsVQTEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T1(Phospho) S2(Phospho)	T(1): 100.0; S(2): 100.0; T(5): 0.0; S(15): 0.0	T1; S2;	T284; S285	42	0	0	2	989.9	1979	62.87	12524	
TPEELDDsDFetEDFDVR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) T12(Phospho)	T(1): 3.2; S(8): 96.8; T(12): 100.0	S8; T12;	S271; T275	41	0	0	2	1160	2319	87.95	17595	
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0; S(19): 100.0	S8; S19;	S271; S282	36	0	1	3	854.7	2562	74.98	15159	
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 99.9; T(12): 0.1; S(19): 100.0	S8; S19;	S271; S282	24	0	1	2	1281	2562	74.58	15088	
sRTSVQTEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	S1(Phospho)	S(1): 95.2; T(3): 2.4; S(4): 2.4; T(7): 0.0; S(17): 0.0	S1;	S282	23	0	1	2	1071	2142	41.24	7834	
SRTSVQtEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T7(Phospho)	S(1): 33.4; T(3): 33.4; S(4): 33.4; T(7): 99.9; S(17): 0.0	T7;	T288		6.59	0	1	3	741.3	2222	47.06	9088
TPEELDDsDFETEDFDVR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0	S8;	S271		3.86	0	0	2	1120	2239	78.85	15893
SRTSVQtEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T7(Phospho)	S(1): 1.5; T(3): 49.3; S(4): 49.3; T(7): 99.9; S(17): 0.0	T7;	T288		3.78	0	1	2	1111	2222	47.05	9087

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#
sRTSVQTEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	S1(Phospho)	S(1): 95.2; T(3): 2.4; S(4): 2.4; T(7): 0.0; S(17): 0.0	S1;	S282		3.56	0	1	2	1071	2142	41.24	7834
TPEELDDsDFETEDFDVR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) T12(Phospho)	T(1): 3.2; S(8): 96.8; T(12): 100.0	S8; T12;	S271; T275		2.96	0	0	2	1160	2319	87.95	17595
tsVQTEDDQLIAGQSAR	CTNNA1	1495	catenin alpha-1 isoform 5	T1(Phospho) S2(Phospho)	T(1): 100.0; S(2): 100.0; T(5): 0.0; S(15): 0.0	T1; S2;	T284; S285		2.58	0	0	2	989.9	1979	62.87	12524
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0; S(19): 100.0	S8; S19;	S271; S282		4.78	0.002	1	3	854.7	2562	74.46	15062
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 99.9; T(12): 0.1; S(19): 100.0	S8; S19;	S271; S282		2.83	0.003	1	2	1281	2562	74.58	15088
TPEELDDsDFETEDFDVRsR	CTNNA1	1495	catenin alpha-1 isoform 5	S8(Phospho) S19(Phospho)	T(1): 0.0; S(8): 100.0; T(12): 0.0; S(19): 100.0	S8; S19;	S271; S282		3.7	0.005	1	3	854.7	2562	74.98	15159
VGGssVDLHR	CTNND1	1500	catenin delta-1 isoform 3A	S4(Phospho)	S(4): 98.9; S(5): 1.1	S4;	S167	78		0	0	2	553.7	1106	26.22	4654
VGGssVDLHR	CTNND1	1500	catenin delta-1 isoform 3A	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S167; S168	74		0	0	2	593.7	1186	29.99	5460
HYEDGYPGGSDNYGSLsR	CTNND1	1500	catenin delta-1 isoform 3A	S17(Phospho)	Y(2): 0.0; Y(6): 0.0; S(10): 0.0; Y(13): 0.0; S(15): 1.6; S(17): 98.4	S17;	S131	55		0	0	3	685.3	2054	44.85	8618
GsLAsLDSLr	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(8): 0.0	S2; S5;	S245; S248	34		0	0	2	589.7	1178	78.03	15733
GsLAsLDSLrK	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(8): 0.0	S2; S5;	S245; S248	33		0	1	2	653.8	1307	57.23	11289
SLDNNYSrPNER	CTNND1	1500	catenin delta-1 isoform 3A	T8(Phospho)	S(1): 0.0; Y(6): 0.0; S(7): 1.7; T(8): 98.3	T8;	T799	30		0	0	2	745.3	1490	29.55	5369
GSLAsLsLrK	CTNND1	1500	catenin delta-1 isoform 3A	S5(Phospho) S8(Phospho)	S(2): 0.0; S(5): 100.0; S(8): 100.0	S5; S8;	S248; S251	27		0	1	2	653.8	1307	57.74	11394
HYEDGYPGGSDNYGSLsR	CTNND1	1500	catenin delta-1 isoform 3A	S17(Phospho)	Y(2): 0.0; Y(6): 0.0; S(10): 0.0; Y(13): 0.0; S(15): 1.6; S(17): 98.4	S17;	S131		5.75	0	0	3	685.3	2054	44.85	8618
VGGssVDLHR	CTNND1	1500	catenin delta-1 isoform 3A	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S167; S168		3.47	0	0	2	593.7	1186	29.99	5460
VGGssVDLHR	CTNND1	1500	catenin delta-1 isoform 3A	S4(Phospho)	S(4): 98.9; S(5): 1.1	S4;	S167		3.26	0	0	2	553.7	1106	26.22	4654
SLDNNYSrPNER	CTNND1	1500	catenin delta-1 isoform 3A	T8(Phospho)	S(1): 0.0; Y(6): 0.0; S(7): 1.7; T(8): 98.3	T8;	T799		3.18	0	0	2	745.3	1490	29.55	5369
GSLAsLsLrK	CTNND1	1500	catenin delta-1 isoform 3A	S5(Phospho) S8(Phospho)	S(2): 0.0; S(5): 100.0; S(8): 100.0	S5; S8;	S248; S251		2.64	0	1	2	653.8	1307	57.74	11394
GsLAsLDSLr	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(8): 0.0	S2; S5;	S245; S248		2.12	0	0	2	589.7	1178	78.03	15733
GsLAsLDSLrK	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S5(Phospho)	S(2): 100.0; S(5): 100.0; S(8): 0.0	S2; S5;	S245; S248		2.06	0	1	2	653.8	1307	57.23	11289
GsLAsLsLrK	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S5(Phospho) S8(Phospho)	S(2): 100.0; S(5): 100.0; S(8): 100.0	S2; S5; S8;	S245; S248; S251	16		0.004	1	2	693.8	1387	65.19	13092
GsLASLsLrK	CTNND1	1500	catenin delta-1 isoform 3A	S2(Phospho) S8(Phospho)	S(2): 100.0; S(5): 0.0; S(8): 100.0	S2; S8;	S245; S251	13		0.004	1	2	653.8	1307	53.46	10462
SGSsPDSEITELK	CTPS1	1503	CTP synthase 1 isoform b	S4(Phospho) S5(Phospho)	S(1): 0.0; S(3): 0.1; S(4): 99.9; S(5): 100.0; S(8): 0.0; T(11): 0.0	S4; S5;	S418; S419	52		0	0	2	798.8	1597	65.59	13182
DTYSrSGsSPDSEITELK	CTPS1	1503	CTP synthase 1 isoform b	S7(Phospho) S9(Phospho)	T(2): 14.3; Y(3): 14.3; S(4): 14.3; S(7): 78.5; S(9): 78.5; S(10): 0.0; S(11): 0.0; S(14): 0.0; T(17): 0.0	S7; S9;	S415; S417	23		0	1	3	778.6	2334	60.28	11935
DtysDRSGSSPDSEITELK	CTPS1	1503	CTP synthase 1 isoform b	T2(Phospho) Y3(Phospho) S4(Phospho)	T(2): 81.6; Y(3): 81.6; S(4): 81.6; S(7): 24.1; S(9): 24.1; S(10): 3.6; S(11): 3.6; S(14): 0.0; T(17): 0.0	T2; Y3; S4;	T410; Y411; S412	18		0	1	3	805.3	2414	73.06	14781

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#
DTYSDRsGSSSPDSEITLK	CTPS1	1503	CTP synthase 1 isoform b	S7(Phospho)	T(2): 0.2; Y(3): 0.2; S(4): 0.2; S(7): 99.4; S(9): 2.0; S(10): 48.9; S(11): 48.9; S(14): 0.1; T(17): 0.0	S7;	S415	12		0	1	2	1167	2334	60.25	11929
DTYSDRsGsSSPDSEITLK	CTPS1	1503	CTP synthase 1 isoform b	S7(Phospho) S9(Phospho)	T(2): 14.3; Y(3): 14.3; S(4): 14.3; S(7): 78.5; S(9): 78.5; S(10): 0.0; S(11): 0.0; S(14): 0.0; T(17): 0.0	S7; S9;	S415; S417		4.6	0	1	3	778.6	2334	60.28	11935
DtysDRsGSSSPDSEITLK	CTPS1	1503	CTP synthase 1 isoform b	T2(Phospho) Y3(Phospho) S4(Phospho)	T(2): 81.6; Y(3): 81.6; S(4): 81.6; S(7): 24.1; S(9): 24.1; S(10): 3.6; S(11): 3.6; S(14): 0.0; T(17): 0.0	T2; Y3; S4;	T410; Y411; S412		2.69	0	1	3	805.3	2414	73.06	14781
SGSsPDSEITLK	CTPS1	1503	CTP synthase 1 isoform b	S4(Phospho) S5(Phospho)	S(1): 0.0; S(3): 0.1; S(4): 99.9; S(5): 100.0; S(8): 0.0; T(11): 0.0	S4; S5;	S418; S419		2.51	0	0	2	798.8	1597	65.59	13182
DTYSDRsGSSSPDSEITLK	CTPS1	1503	CTP synthase 1 isoform b	S7(Phospho)	T(2): 0.2; Y(3): 0.2; S(4): 0.2; S(7): 99.4; S(9): 2.0; S(10): 48.9; S(11): 48.9; S(14): 0.1; T(17): 0.0	S7;	S415		2.46	0	1	2	1167	2334	60.25	11929
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S11(Phospho) S14(Phospho)	S(2): 0.0; S(3): 0.1; S(4): 2.4; Y(7): 48.7; S(8): 48.7; S(11): 100.0; S(14): 99.7; S(16): 0.3	S11; S14;	S571; S574	31		0	1	3	787.6	2361	53.4	10449
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S8(Phospho) S11(Phospho) S14(Phospho)	S(2): 4.3; S(3): 4.3; S(4): 0.0; Y(7): 4.3; S(8): 87.2; S(11): 100.0; S(14): 99.7; S(16): 0.3	S8; S11; S14;	S568; S571; S574	24		0	1	2	1181	2361	53.42	10454
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S8(Phospho) S11(Phospho)	S(2): 0.0; S(3): 0.0; S(4): 0.0; Y(7): 5.3; S(8): 94.7; S(11): 99.6; S(14): 0.3; S(16): 0.0	S8; S11;	S568; S571	18		0	1	2	1141	2281	47.31	9142
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S11(Phospho) S14(Phospho)	S(2): 0.0; S(3): 0.1; S(4): 2.4; Y(7): 48.7; S(8): 48.7; S(11): 100.0; S(14): 99.7; S(16): 0.3	S11; S14;	S571; S574		4.14	0	1	3	787.6	2361	53.4	10449
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S8(Phospho) S11(Phospho) S14(Phospho)	S(2): 4.3; S(3): 4.3; S(4): 0.0; Y(7): 4.3; S(8): 87.2; S(11): 100.0; S(14): 99.7; S(16): 0.3	S8; S11; S14;	S568; S571; S574		2.91	0	1	2	1181	2361	53.42	10454
LSSSDRYSDAsDDsFSEPR	CTPS2	56474	CTP synthase 2	S8(Phospho) S11(Phospho)	S(2): 0.0; S(3): 0.0; S(4): 0.0; Y(7): 5.3; S(8): 94.7; S(11): 99.6; S(14): 0.3; S(16): 0.0	S8; S11;	S568; S571		2.32	0	1	2	1141	2281	47.31	9142
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	61		0	2	3	699.3	2096	12.71	1786
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	58		0	2	2	1048	2096	12.71	1785
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	35		0	1	2	970.3	1940	14	2061
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		7.37	0	2	3	699.3	2096	12.71	1786
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		4.69	0	2	2	1048	2096	12.71	1785
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		3.02	0	1	2	970.3	1940	14	2061
TQtPPVSPAPQPTTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho)	T(1): 0.0; T(3): 100.0; S(7): 0.0; T(13): 0.0	T3;	T364	60		0	0	2	907.9	1815	41.18	7820

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#
TQtPPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.2; T(3): 97.8; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368	52		0	0	2	947.9	1895	45.28	8711
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	36		0	1	3	698.6	2094	34.18	6330
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	34		0	1	3	698.6	2094	33.67	6225
AKtQTTPVSPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho)	T(3): 96.7; T(5): 3.3; S(9): 50.0; T(15): 50.0	T3;	T362	32		0	1	2	1047	2094	33.76	6242
TQtPPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.3; T(3): 97.7; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368	31		0	0	2	947.9	1895	45.81	8826
AKtQTTPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho) T15(Phospho)	T(3): 99.5; T(5): 7.3; S(9): 93.2; T(15): 98.9; S(21): 0.6; S(22): 0.6; Y(25): 0.0; S(30): 0.0	T3; S9; T15;	T362; S368; T374	18		0	2	4	917.2	3666	70.23	14209
AKtQtPPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) T5(Phospho) T15(Phospho)	T(3): 100.0; T(5): 93.5; S(9): 6.5; T(15): 99.0; S(21): 0.5; S(22): 0.5; Y(25): 0.0; S(30): 0.0	T3; T5; T15;	T362; T364; T374	15		0	2	3	1223	3666	70.28	14217
AKtQTTPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho)	T(3): 99.5; T(5): 0.5; S(9): 100.0; T(15): 0.0; S(21): 0.0; S(22): 0.0; Y(25): 0.0; S(30): 0.0	T3; S9;	T362; S368	13		0	2	4	897.2	3586	65.5	13161
AKtQTTPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho) T15(Phospho)	T(3): 99.5; T(5): 7.3; S(9): 93.2; T(15): 98.9; S(21): 0.6; S(22): 0.6; Y(25): 0.0; S(30): 0.0	T3; S9; T15;	T362; S368; T374		4.68	0	2	4	917.2	3666	70.23	14209
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		4.45	0	1	3	698.6	2094	33.67	6225
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		4.32	0	1	3	698.6	2094	34.18	6330
AKtQTTPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S9(Phospho)	T(3): 99.5; T(5): 0.5; S(9): 100.0; T(15): 0.0; S(21): 0.0; S(22): 0.0; Y(25): 0.0; S(30): 0.0	T3; S9;	T362; S368		4.21	0	2	4	897.2	3586	65.5	13161
AKtQTTPVSPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho)	T(3): 96.7; T(5): 3.3; S(9): 50.0; T(15): 50.0	T3;	T362		4.09	0	1	2	1047	2094	33.76	6242
TQtPPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.2; T(3): 97.8; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368		3.32	0	0	2	947.9	1895	45.28	8711
AKtQtPPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) T5(Phospho) T15(Phospho)	T(3): 100.0; T(5): 93.5; S(9): 6.5; T(15): 99.0; S(21): 0.5; S(22): 0.5; Y(25): 0.0; S(30): 0.0	T3; T5; T15;	T362; T364; T374		3.31	0	2	3	1223	3666	70.28	14217
TQtPPVSPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho)	T(1): 0.0; T(3): 100.0; S(7): 0.0; T(13): 0.0	T3;	T364		3.28	0	0	2	907.9	1815	41.18	7820
TQtPPVsPAPQPTEER	CTTN	2017	src substrate cortactin isoform b	T3(Phospho) S7(Phospho)	T(1): 2.3; T(3): 97.7; S(7): 100.0; T(13): 0.0	T3; S7;	T364; S368		2.55	0	0	2	947.9	1895	45.81	8826
TQTTPVsPAPQPTEERLPSSPVYEDAA SFK	CTTN	2017	src substrate cortactin isoform b	S7(Phospho)	T(1): 50.0; T(3): 50.0; S(7): 79.3; T(13): 6.7; S(19): 6.7; S(20): 6.7; Y(23): 0.6; S(28): 0.0	S7;	S368		2.49	0	1	3	1130	3387	75.14	15186
SATDGNSTtPPTSAK	CUL4B	8450	cullin-4B isoform 2	T10(Phospho)	S(1): 0.0; T(3): 0.0; T(7): 0.0; S(8): 0.0; T(9): 2.6; T(10): 97.3; T(13): 0.1; S(14): 0.0	T10;	T31	30		0	0	2	808.3	1616	21.03	3555

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#
MAEESSSSSSSPTAATSQQQLK	CUL4B	8450	cullin-4B isoform 2	S13(Phospho)	S(5): 0.2; S(6): 3.5; S(7): 0.2; S(8): 0.2; S(9): 3.5; S(10): 0.2; S(11): 3.5; S(12): 3.5; S(13): 81.7; T(15): 3.5; T(18): 0.0; S(19): 0.0	S13;	S128	24		0	0	3	875.4	2624	32.92	6069
MAEESSSSSSSPTAATSQQQLK	CUL4B	8450	cullin-4B isoform 2	S13(Phospho)	S(5): 0.2; S(6): 3.5; S(7): 0.2; S(8): 0.2; S(9): 3.5; S(10): 0.2; S(11): 3.5; S(12): 3.5; S(13): 81.7; T(15): 3.5; T(18): 0.0; S(19): 0.0	S13;	S128		4.21	0	0	3	875.4	2624	32.92	6069
SATDGNTStPPTSAK	CUL4B	8450	cullin-4B isoform 2	T10(Phospho)	S(1): 0.0; T(3): 0.0; T(7): 0.0; S(8): 0.0; T(9): 2.6; T(10): 97.3; T(13): 0.1; S(14): 0.0	T10;	T31		2.85	0	0	2	808.3	1616	21.03	3555
SATDGNTSTTPtSAK	CUL4B	8450	cullin-4B isoform 2	T13(Phospho) S14(Phospho)	S(1): 0.0; T(3): 0.0; T(7): 0.0; S(8): 0.0; T(9): 0.0; T(10): 0.4; T(13): 99.8; S(14): 99.8	T13; S14;	T34; S35		2.9	0.007	0	2	848.3	1696	26.24	4659
RNsFSENEK	CWC22	57703	pre-mRNA-splicing factor CWC22 homolog	S3(Phospho)	S(3): 100.0; S(5): 0.0	S3;	S829	33		0.001	1	2	595.7	1190	13.35	1922
RNsFSENEK	CWC22	57703	pre-mRNA-splicing factor CWC22 homolog	S3(Phospho)	S(3): 100.0; S(5): 0.0	S3;	S829		3.39	0.005	1	2	595.7	1190	13.35	1922
YQEQGGEAsPQR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0	S9;	S129	58		0	0	2	715.3	1430	16.16	2516
YQEQGGEAsPQSR	DBNL	28988	drebrin-like protein isoform e	S9(Phospho)	Y(1): 0.0; S(9): 98.4; S(12): 1.6	S9;	S137	53		0	0	2	758.8	1517	16.52	2595
YQEQGGEAsPQRTWEQQQEVVSR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0; T(13): 0.0; S(22): 0.0	S9;	S129	22		0	1	3	934.1	2800	49.26	9549
YQEQGGEAsPQRTWEQQQEVVSR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0; T(13): 0.0; S(22): 0.0	S9;	S129		3.55	0	1	3	934.1	2800	49.26	9549
YQEQGGEAsPQR	DBNL	28988	drebrin-like protein isoform d	S9(Phospho)	Y(1): 0.0; S(9): 100.0	S9;	S129		3.48	0	0	2	715.3	1430	16.16	2516
YQEQGGEAsPQSR	DBNL	28988	drebrin-like protein isoform e	S9(Phospho)	Y(1): 0.0; S(9): 98.4; S(12): 1.6	S9;	S137		3.42	0	0	2	758.8	1517	16.52	2595
AMSTTSISsPQPGK	DBNL DBNL	28988 289	drebrin-like protein isoform d drebrin-like protein isoform e	S9(Phospho)	S(3): 0.0; T(4): 0.0; T(5): 0.0; S(6): 0.0; S(8): 0.0; S(9): 100.0	S9;	S172 S181	33		0	0	2	736.3	1472	34.57	6415
AMSTTSISsPQPGK	DBNL DBNL	28988 289	drebrin-like protein isoform d drebrin-like protein isoform e	S9(Phospho)	S(3): 0.0; T(4): 0.0; T(5): 0.0; S(6): 0.0; S(8): 0.0; S(9): 100.0	S9;	S172 S181		3.27	0	0	2	736.3	1472	34.57	6415
SSGsPEPSPAIAK	DCAF15	90379	DDB1- and CUL4-associated factor 15	S4(Phospho)	S(1): 0.1; S(2): 0.1; S(4): 99.8; S(8): 0.0	S4;	S310	12		0	0	2	654.3	1308	32.24	5927
SSGsPEPSPAIAK	DCAF15	90379	DDB1- and CUL4-associated factor 15	S4(Phospho)	S(1): 0.1; S(2): 0.1; S(4): 99.8; S(8): 0.0	S4;	S310		2.09	0	0	2	654.3	1308	32.24	5927
VHDRsEEEEEEEEEEQPR	DCAF8	50717	DDB1- and CUL4-associated factor 8	S5(Phospho)	S(5): 100.0	S5;	S99	34		0	1	3	918	2752	30.68	5605
VHDRsEEEEEEEEEEQPR	DCAF8	50717	DDB1- and CUL4-associated factor 8	S5(Phospho)	S(5): 100.0	S5;	S99		6.01	0	1	3	918	2752	30.68	5605
tDSCSsAAQAQYDTPK	DCBLD2	131566	discoidin, CUB and LCCL domain-containing protein 2 precursor	C4(Carbamidomethyl)T1(Phospho) S6(Phospho)	T(1): 97.4; S(3): 2.5; S(5): 0.1; S(6): 100.0; Y(11): 0.0; T(13): 0.0	T1; S6;	T722; S727	62		0	0	2	909.8	1819	36.41	6817
tDSCSsAAQAQYDTPK	DCBLD2	131566	discoidin, CUB and LCCL domain-containing protein 2 precursor	C4(Carbamidomethyl)T1(Phospho) S6(Phospho)	T(1): 97.4; S(3): 2.5; S(5): 0.1; S(6): 100.0; Y(11): 0.0; T(13): 0.0	T1; S6;	T722; S727		3.4	0	0	2	909.8	1819	36.41	6817
SPsPSPTsPGSLR	DCLK1	9201	serine/threonine-protein kinase DCLK1 isoform 4	S3(Phospho) S8(Phospho)	S(1): 2.0; S(3): 97.9; S(5): 0.0; T(7): 0.0; S(8): 97.9; S(11): 2.0	S3; S8;	S25; S30	34		0	0	2	715.3	1430	48.36	9362

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#
SPsPSPTsPGSLR	DCLK1	9201	serine/threonine-protein kinase DCLK1 isoform 4	S3(Phospho) S8(Phospho)	S(1): 2.0; S(3): 97.9; S(5): 0.0; T(7): 0.0; S(8): 97.9; S(11): 2.0	S3; S8;	S25; S30		2.39	0	0	2	715.3	1430	48.36	9362
KASPSPLTIGTPESQR	DCP1A	55802	mRNA-decapping enzyme 1A isoform e	S3(Phospho)	S(3): 98.3; S(4): 50.9; S(6): 50.9; T(9): 0.0; T(12): 0.0; S(15): 0.0	S3;	S363	22		0	1	2	958.4	1916	49.72	9645
KASPSPLTIGTPESQR	DCP1A	55802	mRNA-decapping enzyme 1A isoform e	S3(Phospho)	S(3): 98.3; S(4): 50.9; S(6): 50.9; T(9): 0.0; T(12): 0.0; S(15): 0.0	S3;	S363		3.3	0	1	2	958.4	1916	49.72	9645
TDsPDMHEDT	DDA1	79016	DET1- and DDB1-associated protein 1	S3(Phospho)	T(1): 0.0; S(3): 100.0; T(10): 0.0	S3;	S95	23		0	0	2	614.2	1227	22.95	3964
TDsPDMHEDT	DDA1	79016	DET1- and DDB1-associated protein 1	S3(Phospho)	T(1): 0.0; S(3): 100.0; T(10): 0.0	S3;	S95		3.15	0	0	2	614.2	1227	22.95	3964
SRsPLELEPEAK	DDB2	1643	DNA damage-binding protein 2 isoform D1	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S26	29		0	1	2	718.3	1436	39.69	7505
sRsPLELEPEAK	DDB2	1643	DNA damage-binding protein 2 isoform D1	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S24; S26	13		0	1	2	758.3	1516	50.2	9746
SRsPLELEPEAK	DDB2	1643	DNA damage-binding protein 2 isoform D1	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S26		4.21	0	1	2	718.3	1436	39.69	7505
sRsPLELEPEAK	DDB2	1643	DNA damage-binding protein 2 isoform D1	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S24; S26		3.48	0	1	2	758.3	1516	50.2	9746
SYLEGssDNQLKDSESTPVDDR	DDX20	11218	probable ATP-dependent RNA helicase DDX20	S6(Phospho) S7(Phospho)	S(1): 8.1; Y(2): 8.1; S(6): 95.7; S(7): 88.1; S(14): 0.0; S(16): 0.0; T(17): 0.0	S6; S7;	S677; S678	38		0	1	3	868	2602	56.91	11216
SYLEGssDNQLKDSESTPVDDR	DDX20	11218	probable ATP-dependent RNA helicase DDX20	S7(Phospho)	S(1): 0.0; Y(2): 0.0; S(6): 3.4; S(7): 96.6; S(14): 0.0; S(16): 0.0; T(17): 0.0	S7;	S678	28		0	1	3	841.4	2522	48.62	9415
SYLEGssDNQLKDSESTPVDDR	DDX20	11218	probable ATP-dependent RNA helicase DDX20	S7(Phospho)	S(1): 0.0; Y(2): 0.0; S(6): 3.4; S(7): 96.6; S(14): 0.0; S(16): 0.0; T(17): 0.0	S7;	S678		3.99	0	1	3	841.4	2522	48.62	9415
SYLEGssDNQLKDSESTPVDDR	DDX20	11218	probable ATP-dependent RNA helicase DDX20	S6(Phospho) S7(Phospho)	S(1): 8.1; Y(2): 8.1; S(6): 95.7; S(7): 88.1; S(14): 0.0; S(16): 0.0; T(17): 0.0	S6; S7;	S677; S678		3.26	0	1	3	868	2602	56.91	11216
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89	80		0	2	2	790.4	1580	15.26	2325
KEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89	57		0	1	2	726.3	1452	17.81	2879
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89	56		0	2	2	790.4	1580	14.75	2217
NEEPsEEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	51		0	0	2	896.4	1792	32.78	6041
KAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S71	50		0	1	2	756.3	1512	24.37	4257
NEEPsEEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	41		0	0	3	597.9	1792	32.83	6050
KEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89	39		0	1	2	726.3	1452	18.33	2988
KAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	M9(Oxidation) S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S71	36		0	1	2	764.3	1528	15.19	2311
NEEPsEEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	36		0	0	2	896.4	1792	32.28	5935
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89	34		0	2	3	527.3	1580	15.17	2307
NEEPsEEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121	33		0	0	3	597.9	1792	32.32	5945
KKAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S12(Phospho)	S(6): 0.0; S(12): 100.0	S12;	S71	26		0	2	2	820.4	1640	20.14	3366
VTKNEEPsEEEIDAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S8(Phospho)	T(2): 0.0; S(8): 100.0	S8;	S121	25		0	1	3	707.3	2120	27.79	4998

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#
KKAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S12(Phospho)	S(6): 0.0; S(12): 100.0	S12;	S71	23		0	2	3	547.3	1640	20.05	3347
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89		6.55	0	2	3	527.3	1580	15.17	2307
KKAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S12(Phospho)	S(6): 0.0; S(12): 100.0	S12;	S71		5.06	0	2	3	547.3	1640	20.05	3347
KAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S71		4.88	0	1	2	756.3	1512	24.37	4257
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89		4.69	0	2	2	790.4	1580	15.26	2325
KKEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S11(Phospho)	S(6): 0.0; S(11): 100.0	S11;	S89		4.48	0	2	2	790.4	1580	14.75	2217
KEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89		4.47	0	1	2	726.3	1452	17.81	2879
KEEPSQNDIsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S10(Phospho)	S(5): 0.0; S(10): 100.0	S10;	S89		4	0	1	2	726.3	1452	18.33	2988
NEEPsEEIIdAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		3.95	0	0	3	597.9	1792	32.83	6050
KAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	M9(Oxidation) S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S71		3.84	0	1	2	764.3	1528	15.19	2311
VTKNEEPsEEIIdAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S8(Phospho)	T(2): 0.0; S(8): 100.0	S8;	S121		3.78	0	1	3	707.3	2120	27.79	4998
KKAEPSEVDMNsPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S12(Phospho)	S(6): 0.0; S(12): 100.0	S12;	S71		3.48	0	2	2	820.4	1640	20.14	3366
NEEPsEEIIdAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		3.43	0	0	2	896.4	1792	32.78	6041
NEEPsEEIIdAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		3.13	0	0	3	597.9	1792	32.32	5945
NEEPsEEIIdAPKPK	DDX21	9188	nucleolar RNA helicase 2 isoform 1	S5(Phospho)	S(5): 100.0	S5;	S121		2.85	0	0	2	896.4	1792	32.28	5935
RSsLsPGR	DDX23	9416	probable ATP-dependent RNA helicase DDX23	S3(Phospho) S5(Phospho)	S(2): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S107; S109		3.72	0.001	1	2	510.2	1019	15.33	2340
KAQAVsEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S6(Phospho)	S(6): 100.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S6;	S82	56		0	2	3	753.3	2258	20.77	3500
AQAVsEEEEEEGK	DDX24	57062	ATP-dependent RNA helicase DDX24	S5(Phospho)	S(5): 100.0	S5;	S82	35		0	0	2	822.3	1644	26.66	4750
AQAVsEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S5(Phospho)	S(5): 100.0; S(15): 48.9; S(16): 48.9; S(17): 2.1	S5;	S82	15		0	1	2	1105	2210	27.05	4834
KAQAVsEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S6(Phospho)	S(6): 100.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S6;	S82		6.06	0	2	3	753.3	2258	20.77	3500
AQAVsEEEEEEGK	DDX24	57062	ATP-dependent RNA helicase DDX24	S5(Phospho)	S(5): 100.0	S5;	S82		3.46	0	0	2	822.3	1644	26.66	4750
AQAVsEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S5(Phospho)	S(5): 100.0; S(15): 48.9; S(16): 48.9; S(17): 2.1	S5;	S82		3.41	0	1	2	1105	2210	27.05	4834
AQAVSEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S16(Phospho)	S(5): 0.0; S(15): 2.8; S(16): 94.4; S(17): 2.8	S16;	S93	14		0.002	1	2	1065	2130	21.58	3670
AQAVSEEEEEEGKSSSPK	DDX24	57062	ATP-dependent RNA helicase DDX24	S16(Phospho)	S(5): 0.0; S(15): 2.8; S(16): 94.4; S(17): 2.8	S16;	S93		2.6	0.003	1	2	1065	2130	21.58	3670
TDEVPAAGsRsEAEDDEDVYPVPLR	DDX41	51428	probable ATP-dependent RNA helicase DDX41	S9(Phospho) S11(Phospho)	T(1): 0.1; S(9): 100.0; S(11): 100.0; Y(21): 0.0; Y(24): 0.0	S9; S11;	S21; S23	31		0	1	3	1091	3270	84.13	16875
TDEVPAAGsRsEAEDDEDVYPVPLR	DDX41	51428	probable ATP-dependent RNA helicase DDX41	S9(Phospho) S11(Phospho)	T(1): 0.1; S(9): 100.0; S(11): 100.0; Y(21): 0.0; Y(24): 0.0	S9; S11;	S21; S23		2.74	0	1	3	1091	3270	84.13	16875
KADGEDAGAESNEEAPGEPsAGSSEAP GEPsAGSSEAPGER	DDX51	317781	ATP-dependent RNA helicase DDX51	S20(Phospho)	S(11): 5.5; S(20): 83.6; S(23): 5.5; S(24): 5.5; S(32): 0.0; S(35): 0.0; S(36): 0.0	S20;	S112	36		0	1	4	1053	4209	42.01	7995

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#
RVNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S9(Phospho)	S(9): 100.0	S9;	S83	34		0	1	2	866.4	1732	21.02	3553
KADGEDAGAESNEEAPGEPsAGSSEEP GEPsAGSSEEPGER	DDX51	317781	ATP-dependent RNA helicase DDX51	S20(Phospho)	S(11): 5.5; S(20): 83.6; S(23): 5.5; S(24): 5.5; S(32): 0.0; S(35): 0.0; S(36): 0.0	S20;	S112		5.13	0	1	4	1053	4209	42.01	7995
RVNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S9(Phospho)	S(9): 100.0	S9;	S83		3.54	0	1	2	866.4	1732	21.02	3553
VNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S8(Phospho)	S(8): 100.0	S8;	S83		3.31	0	0	2	788.3	1576	25.22	4440
VNDAEPGsPEAPQGK	DDX51	317781	ATP-dependent RNA helicase DDX51	S8(Phospho)	S(8): 100.0	S8;	S83	28		0.001	0	2	788.3	1576	25.22	4440
GsDsEDGEFEIQAEDDAR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S39; S41	60		0	0	2	1065	2130	71.89	14531
QKIDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S8(Phospho)	S(8): 100.0; S(14): 0.0	S8;	S782	44		0	2	3	639.3	1916	14.72	2211
IDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S782	32		0	1	3	553.9	1660	15.41	2357
IDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S782		5.18	0	1	3	553.9	1660	15.41	2357
QKIDDRDsDEEGASDR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S8(Phospho)	S(8): 100.0; S(14): 0.0	S8;	S782		4.78	0	2	3	639.3	1916	14.72	2211
GsDsEDGEFEIQAEDDAR	DDX54	79039	ATP-dependent RNA helicase DDX54 isoform 2	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S39; S41		3.68	0	0	2	1065	2130	71.89	14531
EEsEEEEDEDDDEEEEEKEK	DEK	7913	protein DEK isoform 1	S3(Phospho)	S(3): 100.0	S3;	S32	17		0	1	3	908.3	2723	27.28	4888
EEsEEEEDEDDDEEEEEKEK	DEK	7913	protein DEK isoform 1	S3(Phospho)	S(3): 100.0	S3;	S32		4.25	0	1	3	908.3	2723	27.28	4888
KESEsEDssDDEPLIKK	DEK	7913	protein DEK isoform 1	S5(Phospho) S8(Phospho) S9(Phospho)	S(3): 0.2; S(5): 99.8; S(8): 100.0; S(9): 100.0	S5; S8; S9;	S303; S306; S307		3.56	0	2	3	725.9	2176	40.02	7576
KESEsEDssDDEPLIKK	DEK	7913	protein DEK isoform 1	S5(Phospho) S8(Phospho) S9(Phospho)	S(3): 0.2; S(5): 99.8; S(8): 100.0; S(9): 100.0	S5; S8; S9;	S303; S306; S307	16		0.001	2	3	725.9	2176	40.02	7576
KEsESEdssDDEPLIK	DEK	7913	protein DEK isoform 1	S3(Phospho) S8(Phospho) S9(Phospho)	S(3): 99.7; S(5): 0.6; S(8): 99.7; S(9): 100.0	S3; S8; S9;	S301; S306; S307	12		0.002	1	2	1024	2048	58.25	11499
KEsESEdssDDEPLIK	DEK	7913	protein DEK isoform 1	S3(Phospho) S8(Phospho) S9(Phospho)	S(3): 99.7; S(5): 0.6; S(8): 99.7; S(9): 100.0	S3; S8; S9;	S301; S306; S307		2.18	0.003	1	2	1024	2048	58.25	11499
HsQSPSEPHSPTEPPAWGSSIVK	DENND4C	55667	DENN domain-containing protein 4C	S2(Phospho)	S(2): 93.4; S(5): 6.6; S(10): 50.0; T(12): 50.0; S(19): 0.0; S(20): 0.0	S2;	S965		3.25	0.003	0	3	871.4	2612	56.73	11168
LtVENS PKQEAGISEGQGTAGEEEK	DENR	8562	density-regulated protein	T2(Phospho)	T(2): 100.0; S(6): 0.0; S(14): 0.0; T(19): 0.0	T2;	T69	31		0	1	3	933.1	2797	39.41	7445
LtVENS PKQEAGISEGQGTAGEEEK	DENR	8562	density-regulated protein	T2(Phospho)	T(2): 100.0; S(6): 0.0; S(14): 0.0; T(19): 0.0	T2;	T69	13		0	1	3	933.1	2797	39.93	7558
LtVENS PKQEAGISEGQGTAGEEEK	DENR	8562	density-regulated protein	T2(Phospho)	T(2): 100.0; S(6): 0.0; S(14): 0.0; T(19): 0.0	T2;	T69		3.96	0	1	3	933.1	2797	39.41	7445
LtVENS PKQEAGISEGQGTAGEEEK	DENR	8562	density-regulated protein	T2(Phospho)	T(2): 100.0; S(6): 0.0; S(14): 0.0; T(19): 0.0	T2;	T69		3.45	0	1	3	933.1	2797	39.93	7558
AsPPGDLQNPk	DFFA	1676	DNA fragmentation factor subunit alpha isoform 1	S2(Phospho)	S(2): 100.0	S2;	S315	46		0	0	2	602.3	1204	31.03	5676
AsPPGDLQNPk	DFFA	1676	DNA fragmentation factor subunit alpha isoform 1	S2(Phospho)	S(2): 100.0	S2;	S315		2.5	0	0	2	602.3	1204	31.03	5676
GLsPAMsPALQR	DGCR14	8220	protein DGCR14	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395	38		0	0	2	694.3	1388	66.98	13505
GLsPAMsPALQR	DGCR14	8220	protein DGCR14	M6(Oxidation) S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395	35		0	0	2	702.3	1404	52.27	10198

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#
GLSPAMsPALQR	DGCR14	8220	protein DGCR14	M6(Oxidation)S3(Phospho)S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395		2.64	0	0	2	702.3	1404	52.27	10198
GLSPAMsPALQR	DGCR14	8220	protein DGCR14	S3(Phospho)S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S391; S395		2.15	0.003	0	2	694.3	1388	66.98	13505
YGGDsDHPsDGETSVQPMMTK	DGCR8	54487	microprocessor complex subunit DGCR8 isoform 2	S5(Phospho)S9(Phospho)	Y(1): 0.0; S(5): 99.9; S(9): 94.4; T(13): 5.6; S(14): 0.0; T(20): 0.0	S5; S9;	S271; S275	17		0	0	3	800.3	2399	52.39	10223
YGGDsDHPsDGETSVQPMMTK	DGCR8	54487	microprocessor complex subunit DGCR8 isoform 2	M19(Oxidation)S5(Phospho)T13(Phospho)	Y(1): 5.0; S(5): 95.0; S(9): 4.8; T(13): 90.5; S(14): 4.8; T(20): 0.0	S5; T13;	S271; T279	15		0	0	3	805.6	2415	43.33	8271
YGGDsDHPsDGETSVQPMMTK	DGCR8	54487	microprocessor complex subunit DGCR8 isoform 2	S5(Phospho)S9(Phospho)	Y(1): 0.0; S(5): 99.9; S(9): 94.4; T(13): 5.6; S(14): 0.0; T(20): 0.0	S5; S9;	S271; S275		3.43	0	0	3	800.3	2399	52.39	10223
YGGDsDHPsDGETSVQPMMTK	DGCR8	54487	microprocessor complex subunit DGCR8 isoform 2	M19(Oxidation)S5(Phospho)T13(Phospho)	Y(1): 5.0; S(5): 95.0; S(9): 4.8; T(13): 90.5; S(14): 4.8; T(20): 0.0	S5; T13;	S271; T279		2.69	0	0	3	805.6	2415	43.33	8271
LLEDsEESsEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho)S9(Phospho)	S(5): 100.0; S(8): 1.9; S(9): 98.1; T(12): 0.0; S(14): 0.0	S5; S9;	S43; S47	92		0	0	2	935.4	1870	55.53	10910
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): 97.8; S(9): 2.2; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46	48		0	0	2	935.4	1870	55.02	10802
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): 97.9; S(9): 2.1; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46	45		0	0	2	935.4	1870	56.03	11017
QQTEKPEsEDEWER	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S8(Phospho)	T(3): 0.0; S(8): 100.0	S8;	S100	19		0	0	2	935.9	1871	29.82	5426
LLEDsEESsEETVSR	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S5(Phospho)S9(Phospho)	S(5): 100.0; S(8): 1.9; S(9): 98.1; T(12): 0.0; S(14): 0.0	S5; S9;	S43; S47		4.17	0	0	2	935.4	1870	55.53	10910
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): 97.8; S(9): 2.2; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46		2.91	0	0	2	935.4	1870	55.02	10802
QQTEKPEsEDEWER	DHX16	8449	putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16 isoform 2	S8(Phospho)	T(3): 0.0; S(8): 100.0	S8;	S100		2.67	0	0	2	935.9	1871	29.82	5426
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): 97.9; S(9): 2.1; T(12): 0.0; S(14): 0.0	S5; S8;	S43; S46		2.66	0	0	2	935.4	1870	56.03	11017
LQEEQDGGssDEDragPAPPGASDGVDIQDVK	DHX34	9704	probable ATP-dependent RNA helicase DHX34	S9(Phospho)S10(Phospho)	S(9): 100.0; S(10): 100.0; S(23): 0.0	S9; S10;	S749; S750		2.68	0.003	1	3	1134	3399	61.84	12268
GLSGEEEDDEPDCCNDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C13(Carbamido methyl)C14(Carbamido methyl)S3(Phospho)	S(3): 100.0	S3;	S132	35		0	0	2	1103	2206	37.55	7054
DLQEQDADAGsERGLsGEEEDDEPDCCNDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C26(Carbamido methyl)C27(Carbamido methyl)S11(Phospho)S16(Phospho)	S(11): 100.0; S(16): 100.0	S11; S16;	S127; S132	22		0	1	3	1234	3700	50.7	9852

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#
DLQEQQADAGsERGLsGEEEDDEPDC NDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C26(Carbamido methyl) C27(Carbamido methyl)S11(Phospho) S16(Phospho)	S(11): 100.0; S(16): 100.0	S11; S16;	S127; S132	21		0	1	4	925.8	3700	50.84	9882
GLsGEEEDDEPDCNDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C13(Carbamido methyl) C14(Carbamido methyl) S3(Phospho)	S(3): 100.0	S3;	S132		4.17	0	0	2	1103	2206	37.55	7054
DLQEQQADAGsERGLsGEEEDDEPDC NDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C26(Carbamido methyl) C27(Carbamido methyl)S11(Phospho) S16(Phospho)	S(11): 100.0; S(16): 100.0	S11; S16;	S127; S132		2.88	0	1	3	1234	3700	50.7	9852
DLQEQQADAGsERGLsGEEEDDEPDC NDER	DHX57	90957	putative ATP-dependent RNA helicase DHX57	C26(Carbamido methyl) C27(Carbamido methyl)S11(Phospho) S16(Phospho)	S(11): 100.0; S(16): 100.0	S11; S16;	S127; S132		2.56	0.001	1	4	925.8	3700	50.84	9882
QEAIPLDEsPPVsDSEEQQESAR	DIDO1	11083	death-inducer obliterator 1 isoform c	S10(Phospho) S14(Phospho)	S(10): 100.0; S(14): 100.0; S(16): 0.0; S(22): 0.0	S10; S14;	S805; S809	33		0	0	3	939.4	2816	74.42	15053
VKGGDDHDDtsDsDSDGLTLK	DIDO1	11083	death-inducer obliterator 1 isoform c	T10(Phospho) S11(Phospho) S13(Phospho)	T(10): 100.0; S(11): 100.0; S(13): 99.8; S(15): 0.2; T(19): 0.0	T10; S11; S13;	T151; S152; S154	26		0	1	3	806.3	2417	46.38	8948
VKGGDDHDDtsDsDSDGLTLK	DIDO1	11083	death-inducer obliterator 1 isoform c	T10(Phospho) S11(Phospho) S13(Phospho)	T(10): 100.0; S(11): 100.0; S(13): 99.7; S(15): 0.3; T(19): 0.0	T10; S11; S13;	T151; S152; S154	15		0	1	3	806.3	2417	45.86	8836
VKGGDDHDDtsDsDGLTLK	DIDO1	11083	death-inducer obliterator 1 isoform c	S11(Phospho) S13(Phospho) S15(Phospho)	T(10): 5.4; S(11): 94.9; S(13): 100.0; S(15): 99.7; T(19): 0.0	S11; S13; S15;	S152; S154; S156	15		0	1	3	806.3	2417	46.98	9072
QEAIPLDEsPPVsDSEEQQESAR	DIDO1	11083	death-inducer obliterator 1 isoform c	S10(Phospho) S14(Phospho)	S(10): 100.0; S(14): 95.0; S(16): 5.0; S(22): 0.0	S10; S14;	S805; S809	13		0	0	2	1409	2816	74.54	15078
QEAIPLDEsPPVsDSEEQQESAR	DIDO1	11083	death-inducer obliterator 1 isoform c	S10(Phospho) S14(Phospho)	S(10): 100.0; S(14): 100.0; S(16): 0.0; S(22): 0.0	S10; S14;	S805; S809		5.58	0	0	3	939.4	2816	74.42	15053
QEAIPLDEsPPVsDSEEQQESAR	DIDO1	11083	death-inducer obliterator 1 isoform c	S10(Phospho) S14(Phospho)	S(10): 100.0; S(14): 95.0; S(16): 5.0; S(22): 0.0	S10; S14;	S805; S809		1.83	0.001	0	2	1409	2816	74.54	15078
SSSPAGETEGDREPQARPGEGtAPLPP GQK	DIDO1	11083	death-inducer obliterator 1 isoform c	T22(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; T(8): 0.5; T(22): 99.3	T22;	T1733		3.89	0.003	1	4	795.9	3180	37.4	7023
VKGGDDHDDtsDsDSDGLTLK	DIDO1	11083	death-inducer obliterator 1 isoform c	T10(Phospho) S11(Phospho) S13(Phospho)	T(10): 100.0; S(11): 100.0; S(13): 99.8; S(15): 0.2; T(19): 0.0	T10; S11; S13;	T151; S152; S154		2.85	0.003	1	3	806.3	2417	46.38	8948
VKGGDDHDDtsDsDSDGLTLK	DIDO1	11083	death-inducer obliterator 1 isoform c	T10(Phospho) S11(Phospho) S13(Phospho)	T(10): 100.0; S(11): 100.0; S(13): 99.7; S(15): 0.3; T(19): 0.0	T10; S11; S13;	T151; S152; S154		2.6	0.003	1	3	806.3	2417	45.86	8836
KREsEsDETPPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450	44		0	2	3	818	2452	56.64	11148
KREsEsDETPPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 0.0; T(11): 0.0	S4; S6;	S446; S448	40		0	2	2	1187	2372	49.02	9499
KREsEsDETPPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 0.0; T(11): 0.0	S4; S6;	S446; S448	34		0	2	3	791.4	2372	49.39	9576
KREsEsDETPPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 99.9; S(6): 97.2; S(8): 2.8; T(11): 0.0	S4; S6;	S446; S448	31		0	2	3	791.4	2372	48.85	9463
KREsEsDETPPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 99.9; S(8): 0.1; T(11): 0.0	S4; S6;	S446; S448	30		0	2	3	791.4	2372	49.92	9687

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#
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450	25		0	2	3	818	2452	57.17	11277
AGLESGAEPGDGDsDTTKK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 97.6; T(16): 2.3; T(17): 0.1	S14;	S489	21		0	1	3	638.9	1915	24.21	4227
AGLESGAEPGDGDsDTTK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 99.8; T(16): 0.1; T(17): 0.1	S14;	S489	21		0	0	2	893.9	1787	32.42	5965
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450	15		0	2	3	818	2452	58.14	11476
AGLESGAEPGDGDsDTTKK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 99.9; T(16): 0.1; T(17): 0.0	S14;	S489	14		0	2	3	681.6	2043	19.13	3154
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 0.0; T(11): 0.0	S4; S6;	S446; S448		6.32	0	2	3	791.4	2372	49.39	9576
AGLESGAEPGDGDsDTTKK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 99.9; T(16): 0.1; T(17): 0.0	S14;	S489		5.3	0	2	3	681.6	2043	19.13	3154
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 99.9; S(6): 97.2; S(8): 2.8; T(11): 0.0	S4; S6;	S446; S448		5.17	0	2	3	791.4	2372	48.85	9463
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450		5.02	0	2	3	818	2452	56.64	11148
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450		4.99	0	2	3	818	2452	57.17	11277
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 99.9; S(8): 0.1; T(11): 0.0	S4; S6;	S446; S448		4.74	0	2	3	791.4	2372	49.92	9687
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho) S8(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 100.0; T(11): 0.0	S4; S6; S8;	S446; S448; S450		3.84	0	2	3	818	2452	58.14	11476
KREsEsDETTPAAPQLIK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; S(8): 0.0; T(11): 0.0	S4; S6;	S446; S448		3.16	0	2	2	1187	2372	49.02	9499
AGLESGAEPGDGDsDTTKK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 97.6; T(16): 2.3; T(17): 0.1	S14;	S489		4.61	0.001	1	3	638.9	1915	24.21	4227
AGLESGAEPGDGDsDTTK	DKC1	1736	H/ACA ribonucleoprotein complex subunit 4 isoform 2	S14(Phospho)	S(5): 0.0; S(14): 99.8; T(16): 0.1; T(17): 0.1	S14;	S489		3.3	0.001	0	2	893.9	1787	32.42	5965
NKDQSEQETSDADQHVTSNAsDSESSYR	DLG1	1739	disks large homolog 1 isoform 3	S21(Phospho)	S(5): 0.0; T(9): 0.0; S(10): 0.0; T(17): 0.0; S(18): 0.0; S(21): 99.9; S(23): 0.1; S(25): 0.0; S(26): 0.0; Y(27): 0.0	S21;	S675	48		0	1	3	1066	3195	27.13	4852
DQSEQETSDADQHVTSNAsDSESSYR	DLG1	1739	disks large homolog 1 isoform 3	S21(Phospho)	S(3): 0.0; T(7): 0.0; S(8): 0.0; T(15): 0.0; S(16): 0.0; S(19): 5.8; S(21): 92.9; S(23): 0.4; S(24): 0.4; Y(25): 0.4	S21;	S677	18		0	0	3	985	2953	32.59	6002
NKDQSEQETSDADQHVTSNAsDSESSYR	DLG1	1739	disks large homolog 1 isoform 3	S21(Phospho)	S(5): 0.0; T(9): 0.0; S(10): 0.0; T(17): 0.0; S(18): 0.0; S(21): 99.9; S(23): 0.1; S(25): 0.0; S(26): 0.0; Y(27): 0.0	S21;	S675		6.7	0	1	3	1066	3195	27.13	4852
DQSEQETSDADQHVTSNAsDSESSYR	DLG1	1739	disks large homolog 1 isoform 3	S21(Phospho)	S(3): 0.0; T(7): 0.0; S(8): 0.0; T(15): 0.0; S(16): 0.0; S(19): 5.8; S(21): 92.9; S(23): 0.4; S(24): 0.4; Y(25): 0.4	S21;	S677		3.47	0.001	0	3	985	2953	32.59	6002
EDAEGVAAEEEEQEGDsGEQETGATDAR PR	DNAJC1	64215	dnaJ homolog subfamily C member 1 precursor	S16(Phospho)	S(16): 100.0; T(21): 0.0; T(24): 0.0	S16;	S430	18		0	0	3	1038	3113	39.81	7532
EDAEGVAAEEEEQEGDsGEQETGATDAR PR	DNAJC1	64215	dnaJ homolog subfamily C member 1 precursor	S16(Phospho)	S(16): 100.0; T(21): 0.0; T(24): 0.0	S16;	S430		3.88	0	0	3	1038	3113	39.81	7532

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#
QAAQAEsEEEEESR	DNAJC17	55192	dnaJ homolog subfamily C member 17	S7(Phospho)	S(7): 100.0; S(13): 0.0	S7;	S112	42		0	0	2	865.3	1730	15.78	2434
QAAQAEsEEEEESR	DNAJC17	55192	dnaJ homolog subfamily C member 17	S7(Phospho)	S(7): 100.0; S(13): 0.0	S7;	S112		3.77	0	0	2	865.3	1730	15.78	2434
RsPTSsPTPQR	DNM1	1759	dynamain-1 isoform 2	S2(Phospho) S6(Phospho)	S(2): 100.0; T(4): 0.0; S(5): 0.0; S(6): 98.4; T(8): 1.6	S2; S6;	S774; S778	26		0	1	2	687.3	1374	13.81	2019
RsPTSsPTPQR	DNM1	1759	dynamain-1 isoform 2	S2(Phospho) S6(Phospho)	S(2): 100.0; T(4): 0.0; S(5): 0.0; S(6): 98.4; T(8): 1.6	S2; S6;	S774; S778		3.91	0.001	1	2	687.3	1374	13.81	2019
EADDDEEVDDNIPEMPsPKK	DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform b	S17(Phospho)	S(17): 100.0	S17;	S714	12		0	1	3	785	2353	54.19	10627
EADDDEEVDDNIPEMPsPK	DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform b	S17(Phospho)	S(17): 100.0	S17;	S714	11		0	0	2	1113	2225	66.28	13339
EADDDEEVDDNIPEMPsPKK	DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform b	M15(Oxidation) S17(Phospho)	S(17): 100.0	S17;	S714		3.43	0	1	3	790.3	2369	40.68	7715
EADDDEEVDDNIPEMPsPKK	DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform b	S17(Phospho)	S(17): 100.0	S17;	S714		3.36	0	1	3	785	2353	54.19	10627
EADDDEEVDDNIPEMPsPK	DNMT1	1786	DNA (cytosine-5)-methyltransferase 1 isoform b	S17(Phospho)	S(17): 100.0	S17;	S714		2.46	0	0	2	1113	2225	66.28	13339
SEPQPEEGsPAGGQK	DNMT3A	1788	DNA (cytosine-5)-methyltransferase 3A isoform c	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S105	35		0	0	2	789.3	1578	19.01	3128
SEPQPEEGsPAGGQK	DNMT3A	1788	DNA (cytosine-5)-methyltransferase 3A isoform c	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S105		2.8	0	0	2	789.3	1578	19.01	3128
ASLASLDsNPSTNEK	DOCK10	55619	dedicator of cytokinesis protein 10 DOCK10.2	S5(Phospho) S8(Phospho)	S(2): 0.1; S(5): 99.9; S(8): 100.0; S(11): 0.0; T(12): 0.0	S5; S8;	S1286; S1289	43		0	0	2	847.3	1694	59.23	11730
ASLASLDsNPSTNEK	DOCK10	55619	dedicator of cytokinesis protein 10 DOCK10.2	S5(Phospho) S8(Phospho)	S(2): 0.1; S(5): 99.9; S(8): 100.0; S(11): 0.0; T(12): 0.0	S5; S8;	S1286; S1289		2.28	0	0	2	847.3	1694	59.23	11730
SPSGSAFGsQENLR	DOCK7	85440	dedicator of cytokinesis protein 7 isoform 4	S9(Phospho)	S(1): 0.0; S(3): 0.0; S(5): 2.4; S(9): 97.6	S9;	S1398	39		0	0	2	758.8	1517	43.13	8229
SPSGSAFGsQENLR	DOCK7	85440	dedicator of cytokinesis protein 7 isoform 4	S9(Phospho)	S(1): 0.0; S(3): 0.0; S(5): 2.4; S(9): 97.6	S9;	S1398		3.22	0	0	2	758.8	1517	43.13	8229
sLSNSNPDISGTPTsPDDEVr	DOCK7	85440	dedicator of cytokinesis protein 7 isoform 4	S1(Phospho) S15(Phospho)	S(1): 92.8; S(3): 3.6; S(5): 3.6; S(10): 0.0; T(12): 0.0; T(14): 3.8; S(15): 96.2	S1; S15;	S896; S910		2.77	0	0	2	1174	2348	60.78	12040
sLSNSNPDISGTPTsPDDEVr	DOCK7	85440	dedicator of cytokinesis protein 7 isoform 4	S1(Phospho) S15(Phospho)	S(1): 92.8; S(3): 3.6; S(5): 3.6; S(10): 0.0; T(12): 0.0; T(14): 3.8; S(15): 96.2	S1; S15;	S896; S910	11		0.001	0	2	1174	2348	60.78	12040
DHsPPSQGSPGNsAAR	DOK7	285489	protein Dok-7 isoform 3	S3(Phospho)	S(3): 100.0; S(6): 0.0; S(9): 0.0; S(13): 0.0	S3;	S109	44		0	0	2	822.8	1645	14.9	2248
DHsPPSQGSPGNsAAR	DOK7	285489	protein Dok-7 isoform 3	S3(Phospho)	S(3): 100.0; S(6): 0.0; S(9): 0.0; S(13): 0.0	S3;	S109		3.31	0	0	2	822.8	1645	14.9	2248
ARSTsPVLQPR	DOT1L	84444	histone-lysine N-methyltransferase, H3 lysine-79 specific	T4(Phospho) S6(Phospho)	S(3): 2.0; T(4): 98.0; S(6): 100.0	T4; S6;	T900; S902	26		0	1	2	734.8	1469	35.91	6709
ARSTsPVLQPR	DOT1L	84444	histone-lysine N-methyltransferase, H3 lysine-79 specific	T4(Phospho) S6(Phospho)	S(3): 2.0; T(4): 98.0; S(6): 100.0	T4; S6;	T900; S902		2.58	0	1	2	734.8	1469	35.91	6709
tVTPASsAKTSPAKQQAPPVR	DPYSL2	1808	dihydropyrimidinase-related protein 2 isoform 3	T1(Phospho) S7(Phospho)	T(1): 99.8; T(3): 0.2; S(6): 4.2; S(7): 93.8; T(10): 51.0; S(11): 51.0	T1; S7;	T476; S482	18		0	2	3	788	2362	32.36	5952
tVTPASsAKTSPAKQQAPPVR	DPYSL2	1808	dihydropyrimidinase-related protein 2 isoform 3	T1(Phospho) S7(Phospho)	T(1): 99.8; T(3): 0.2; S(6): 4.2; S(7): 93.8; T(10): 51.0; S(11): 51.0	T1; S7;	T476; S482		4.73	0	2	3	788	2362	32.36	5952
AAsYTEEDENHTAK	DSG2	1829	desmoglein-2 preproprotein	S3(Phospho)	S(3): 98.2; Y(4): 1.8; T(5): 0.0; T(12): 0.0	S3;	S782	30		0	0	2	823.3	1646	16.52	2596

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#
AAsYTEEDENHTAK	DSG2	1829	desmoglein-2 preproprotein	S3(Phospho)	S(3): 98.2; Y(4): 1.8; T(5): 0.0; T(12): 0.0	S3;	S782		3.25	0	0	2	823.3	1646	16.52	2596
GsHTMLCTEDPCSR	DSG3	1830	desmoglein-3 preproprotein	C7(Carbamidomethyl) C12(Carbamidomethyl) S2(Phospho)	S(2): 97.6; T(4): 2.4; T(8): 0.0; S(13): 0.0	S2;	S985	22		0	0	2	865.8	1731	34.45	6388
GsHTMLCTEDPCSR	DSG3	1830	desmoglein-3 preproprotein	C7(Carbamidomethyl) C12(Carbamidomethyl) S2(Phospho)	S(2): 97.6; T(4): 2.4; T(8): 0.0; S(13): 0.0	S2;	S985		3	0	0	2	865.8	1731	34.45	6388
GLPSPYNMSSAPGsR	DSP	1832	desmoplakin isoform II	S14(Phospho)	S(4): 0.0; Y(6): 0.0; S(9): 0.0; S(10): 0.0; S(14): 100.0	S14;	S2226	58		0	0	2	800.8	1601	58.95	11671
GLPsPYNMSSAPGsR	DSP	1832	desmoplakin isoform II	S4(Phospho) S14(Phospho)	S(4): 100.0; Y(6): 0.0; S(9): 0.0; S(10): 0.0; S(14): 100.0	S4; S14;	S2216; S2226	51		0	0	2	840.8	1681	68.78	13910
RAssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C12(Carbamidomethyl) S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; Y(10): 0.0; T(11): 0.0; S(14): 0.0; S(16): 0.0; T(22): 0.0	S3; S4;	S165; S166	33		0	2	3	861.7	2583	52.73	10296
AEsGPDLR	DSP	1832	desmoplakin isoform II	S3(Phospho)	S(3): 100.0	S3;	S22	32		0	0	2	462.7	924.4	25.57	4514
RAssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C12(Carbamidomethyl) S3(Phospho) S4(Phospho) Y10(Phospho)	S(3): 100.0; S(4): 99.9; Y(10): 89.4; T(11): 5.4; S(14): 5.4; S(16): 0.0; T(22): 0.0	S3; S4; Y10;	S165; S166; Y172	22		0	2	3	888.3	2663	61.11	12113
AssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C11(Carbamidomethyl) S2(Phospho) S3(Phospho)	S(2): 99.3; S(3): 99.3; Y(9): 0.5; T(10): 0.4; S(13): 0.4; S(15): 0.0; T(21): 0.0	S2; S3;	S165; S166	22		0	1	3	809.6	2427	61.63	12222
RAssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C12(Carbamidomethyl) S3(Phospho) S4(Phospho) Y10(Phospho)	S(3): 100.0; S(4): 99.9; Y(10): 89.4; T(11): 5.4; S(14): 5.4; S(16): 0.0; T(22): 0.0	S3; S4; Y10;	S165; S166; Y172		5.36	0	2	3	888.3	2663	61.11	12113
RAssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C12(Carbamidomethyl) S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0; Y(10): 0.0; T(11): 0.0; S(14): 0.0; S(16): 0.0; T(22): 0.0	S3; S4;	S165; S166		4.41	0	2	3	861.7	2583	52.73	10296
AssKGGGGYTCQSGSGWDEFTK	DSP	1832	desmoplakin isoform II	C11(Carbamidomethyl) S2(Phospho) S3(Phospho)	S(2): 99.3; S(3): 99.3; Y(9): 0.5; T(10): 0.4; S(13): 0.4; S(15): 0.0; T(21): 0.0	S2; S3;	S165; S166		3.54	0	1	3	809.6	2427	61.63	12222
AEsGPDLR	DSP	1832	desmoplakin isoform II	S3(Phospho)	S(3): 100.0	S3;	S22		2.25	0	0	2	462.7	924.4	25.57	4514
GLPSPYNMSSAPGsR	DSP	1832	desmoplakin isoform II	S14(Phospho)	S(4): 0.0; Y(6): 0.0; S(9): 0.0; S(10): 0.0; S(14): 100.0	S14;	S2226		2.67	0.003	0	2	800.8	1601	58.95	11671
GLPSPYNMSsAPGsR	DSP	1832	desmoplakin isoform II	M8(Oxidation) S10(Phospho) S14(Phospho)	S(4): 0.0; Y(6): 0.0; S(9): 2.3; S(10): 97.7; S(14): 100.0	S10; S14;	S2222; S2226	23		0.004	0	2	848.8	1697	58.55	11575
sASSGAEGDVSSEREP	DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1	S1(Phospho)	S(1): 100.0; S(3): 0.0; S(4): 0.0; S(11): 0.0; S(12): 0.0	S1;	S194	50		0	1	2	822.8	1645	29.54	5367
sASSGAEGDVSSEREP	DTD1	92675	D-tyrosyl-tRNA(Tyr) deacylase 1	S1(Phospho)	S(1): 100.0; S(3): 0.0; S(4): 0.0; S(11): 0.0; S(12): 0.0	S1;	S194		3.47	0	1	2	822.8	1645	29.54	5367

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#
DSCISPEPETK	DTX3L	151636	E3 ubiquitin-protein ligase DTX3L	C3(Carbamidomethyl)S5(Phospho)	S(2): 0.0; S(5): 99.9; S(7): 0.0; T(11): 0.0	S5;	S221	38		0	0	2	715.3	1430	32.03	5883
DSCISPEPETK	DTX3L	151636	E3 ubiquitin-protein ligase DTX3L	C3(Carbamidomethyl)S5(Phospho)	S(2): 0.0; S(5): 99.9; S(7): 0.0; T(11): 0.0	S5;	S221		3.32	0	0	2	715.3	1430	32.03	5883
QENCGAQQVPAGPGtSTPPSSPVR	DUS3L	56931	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like isoform 1	C4(Carbamidomethyl)T15(Phospho)	T(15): 99.6; S(16): 0.2; T(17): 0.2; S(20): 50.0; S(21): 50.0	T15;	T271		5.17	0	0	3	861.4	2582	50.87	9888
QENCGAQQVPAGPGtSTPPSSPVR	DUS3L	56931	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]-like isoform 1	C4(Carbamidomethyl)T15(Phospho)	T(15): 99.6; S(16): 0.2; T(17): 0.2; S(20): 50.0; S(21): 50.0	T15;	T271	20		0.002	0	3	861.4	2582	50.87	9888
PCSEETPAIsPSK	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	59		0	0	2	741.8	1483	33.83	6257
PCSEETPAIsPSKR	DUT	1854	deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial isoform 2	C2(Carbamidomethyl)S10(Phospho)	S(3): 0.0; T(6): 0.0; S(10): 98.7; S(12): 1.3	S10;	S11	57		0	1	3	546.9	1639	26.65	4748
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	38		0	1	2	819.9	1639	26.62	4743
DFQDYMEPEGCQGSPQR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	M6(Oxidation)C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117	30		0	0	2	1135	2269	50.67	9846
DFQDYMEPEGCQGSPQR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117	25		0	0	2	1127	2253	66.27	13337
DFQDYMEPEGCQGSPQR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117		3.36	0	0	2	1127	2253	66.27	13337
DFQDYMEPEGCQGSPQR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	M6(Oxidation)C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117		3.31	0.001	0	2	1135	2269	50.67	9846
DFQDYMEPEGCQGSPQRR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117	14		0.003	1	3	803.6	2409	55.7	10947
ASEsPARGPSGsPR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	S4(Phospho)S12(Phospho)	S(2): 0.1; S(4): 99.9; S(10): 0.0; S(12): 100.0	S4; S12;	S306; S314	21		0.008	1	2	758.3	1516	15.57	2392
DFQDYMEPEGCQGSPQRR	DYNC1LI2	1783	cytoplasmic dynein 1 light intermediate chain 2 isoform 2	C12(Carbamidomethyl)S15(Phospho)	Y(5): 0.0; S(15): 100.0	S15;	S117		3.59	0.008	1	3	803.6	2409	55.7	10947
TSPLKDNPsPEPQLDDIKR	EAF1	85403	ELL-associated factor 1	S9(Phospho)	T(1): 50.0; S(2): 50.0; S(9): 100.0	S9;	S165	31		0	2	3	770.7	2310	49.06	9509
TSPLKDNPsPEPQLDDIKR	EAF1	85403	ELL-associated factor 1	S9(Phospho)	T(1): 50.0; S(2): 50.0; S(9): 100.0	S9;	S165		3.63	0	2	3	770.7	2310	49.06	9509
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl)S7(Phospho)	S(1): 0.0; S(7): 97.7; S(14): 2.3	S7;	S131	49		0	0	2	885.4	1770	24.92	4374
SQDVAVsPQQQQCSKsYVDR	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl)S7(Phospho)S16(Phospho)	S(1): 0.0; S(7): 100.0; S(14): 2.4; S(16): 95.1; Y(17): 2.4	S7; S16;	S131; S140	34		0	1	3	824	2470	38.09	7165
SQDVAVsPQQQQCSKsYVDR	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamidomethyl)S7(Phospho)S16(Phospho)	S(1): 0.0; S(7): 100.0; S(14): 2.4; S(16): 95.1; Y(17): 2.4	S7; S16;	S131; S140		4.67	0	1	3	824	2470	38.09	7165

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#
SQDVAVsPQQQQCSK	EDC3	80153	enhancer of mRNA-decapping protein 3	C13(Carbamido methyl) S7(Phospho)	S(1): 0.0; S(7): 97.7; S(14): 2.3	S7;	S131		4.26	0	0	2	885.4	1770	24.92	4374
DsQDAAEQSDHDDEVASLASGGFG TK	EDC4	23644	enhancer of mRNA-decapping protein 4	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(10): 0.0; S(18): 0.0; S(21): 0.0; S(23): 0.0; T(28): 0.0	S2;	S871	45		0	0	3	988.1	2962	64.21	12860
DsQDAAEQSDHDDEVASLASGGFG TK	EDC4	23644	enhancer of mRNA-decapping protein 4	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(10): 0.0; S(18): 0.0; S(21): 0.0; S(23): 0.0; T(28): 0.0	S2;	S871		4.94	0	0	3	988.1	2962	64.21	12860
LsSDENSNPDLSGDENDDAVSIESGTNT ERPDTPTNTNPAGR	EED	8726	polycomb protein EED isoform a	S2(Phospho) T33(Phospho)	S(2): 83.6; S(3): 8.2; S(7): 8.2; S(12): 0.0; S(21): 0.0; S(24): 0.0; T(26): 0.1; T(28): 1.0; T(33): 97.9; T(35): 1.0; T(37): 0.0	S2; T33;	S24; T55		3.65	0	0	4	1162	4646	60.99	12089
YGPADVEDTTGSGATDSKDDDDIDLFGs DDEEESEAKR	EEF1B2	1933	elongation factor 1-beta	S28(Phospho)	Y(1): 0.0; T(9): 0.0; T(10): 0.0; S(12): 0.0; T(15): 0.0; S(17): 0.0; S(28): 100.0; S(34): 0.0	S28;	S106	15		0	2	4	1066	4261	66.21	13324
YGPADVEDTTGSGATDSKDDDDIDLFGs DDEEESEAKR	EEF1B2	1933	elongation factor 1-beta	S28(Phospho)	Y(1): 0.0; T(9): 0.0; T(10): 0.0; S(12): 0.0; T(15): 0.0; S(17): 0.0; S(28): 100.0; S(34): 0.0	S28;	S106		3.8	0	2	4	1066	4261	66.21	13324
YGPADVEDTTGSGATDSKDDDDIDLFGs DDEEESEAK	EEF1B2	1933	elongation factor 1-beta	T9(Phospho)	Y(1): 6.3; T(9): 79.5; T(10): 6.3; S(12): 6.3; T(15): 0.5; S(17): 0.5; S(28): 0.5; S(34): 0.0	T9;	T87		2.47	0	1	3	1369	4105	73.55	14872
KYEsDEDsLGSSGR	EEF2K	29904	eukaryotic elongation factor 2 kinase	S4(Phospho) S8(Phospho)	Y(2): 0.1; S(4): 99.9; S(8): 100.0; S(11): 0.0; S(12): 0.0	S4; S8;	S470; S474	67		0	1	2	845.3	1690	27.25	4881
YSSsGsPANSFHK	EEF2K	29904	eukaryotic elongation factor 2 kinase	S4(Phospho) S6(Phospho)	Y(1): 0.1; S(2): 0.1; S(3): 3.0; S(4): 96.8; S(6): 100.0; S(10): 0.0	S4; S6;	S72; S74	28		0	0	2	838.3	1676	54.66	10730
KYEsDEDsLGSSGR	EEF2K	29904	eukaryotic elongation factor 2 kinase	S4(Phospho) S8(Phospho)	Y(2): 0.1; S(4): 99.9; S(8): 100.0; S(11): 0.0; S(12): 0.0	S4; S8;	S470; S474		4.7	0	1	2	845.3	1690	27.25	4881
YSSsGsPANSFHK	EEF2K	29904	eukaryotic elongation factor 2 kinase	S4(Phospho) S6(Phospho)	Y(1): 0.1; S(2): 0.1; S(3): 3.0; S(4): 96.8; S(6): 100.0; S(10): 0.0	S4; S6;	S72; S74		2.38	0	0	2	838.3	1676	54.66	10730
ADLNQGIGEPQSPsR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.6; S(14): 98.4	S14;	S76	42		0	0	2	824.9	1649	42.03	7998
ADLNQGIGEPQSPsRR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.8; S(14): 98.2	S14;	S76	31		0	1	3	602.3	1805	33.26	6140
RADLNQGIGEPQsPSRR	EFHD2	79180	EF-hand domain-containing protein D2	S13(Phospho)	S(13): 98.0; S(15): 2.0	S13;	S74	26		0	2	3	654.3	1961	28.18	5082
ADLNQGIGEPQSPsRR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.8; S(14): 98.2	S14;	S76		5.22	0	1	3	602.3	1805	33.26	6140
ADLNQGIGEPQSPsR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.6; S(14): 98.4	S14;	S76		4.86	0	0	2	824.9	1649	42.03	7998
RADLNQGIGEPQsPSRR	EFHD2	79180	EF-hand domain-containing protein D2	S13(Phospho)	S(13): 98.0; S(15): 2.0	S13;	S74		4.58	0	2	3	654.3	1961	28.18	5082
ADLNQGIGEPQSPsRR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.9; S(14): 98.1	S14;	S76	25		0.002	1	2	902.9	1805	33.19	6126
ADLNQGIGEPQSPsRR	EFHD2	79180	EF-hand domain-containing protein D2	S14(Phospho)	S(12): 1.9; S(14): 98.1	S14;	S76		2.81	0.005	1	2	902.9	1805	33.19	6126
DLSTSPKPsPIPsPVLGR	EHBP1	23301	EH domain-binding protein 1 isoform 3	S9(Phospho) S13(Phospho)	S(3): 33.4; T(4): 33.4; S(5): 33.3; S(9): 100.0; S(13): 100.0	S9; S13;	S397; S401	19		0	0	3	696.6	2088	85.04	17049

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#
DLSTSPKpPIpPVLGR	EHBP1	23301	EH domain-binding protein 1 isoform 3	S9(Phospho) S13(Phospho)	S(3): 33.4; T(4): 33.4; S(5): 33.3; S(9): 100.0; S(13): 100.0	S9; S13;	S397; S401		4.17	0	0	3	696.6	2088	85.04	17049
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	42		0	0	3	859	2575	70.73	14308
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	41		0	0	3	859	2575	70.61	14282
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	32		0	0	2	1288	2575	70.57	14274
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	M6(Oxidation) S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	30		0	0	2	1296	2591	64.6	12964
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	4.7	0	0	3	859	2575	70.73	14308	
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	4.47	0	0	3	859	2575	70.61	14282	
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	3.59	0	0	2	1288	2575	70.57	14274	
GPDEAMEDGEEGsDDEAEWVVTk	EHD2	30846	EH domain-containing protein 2	M6(Oxidation) S13(Phospho)	S(13): 100.0; T(22): 0.0	S13;	S438	3.36	0	0	2	1296	2591	64.6	12964	
FPsPHpPAK	EI24	9538	etoposide-induced protein 2.4 homolog isoform 3	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S312; S316		3.27	0.002	0	2	612.7	1224	34.65	6435
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68	43		0	0	5	908.4	4538	61.06	12102
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68	20		0	0	4	1135	4538	61.46	12186
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68	12		0	0	4	1135	4538	60.95	12080
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68		5.63	0	0	4	1135	4538	60.95	12080
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68		5.4	0	0	4	1135	4538	61.46	12186
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68		4.97	0	0	5	908.4	4538	61.06	12102
tEPAAEEAASGPSESPPPAAEELPGSH AEPVPVPAQGEAPGEQAR	EIF3B	8662	eukaryotic translation initiation factor 3 subunit B	T1(Phospho)	T(1): 100.0; S(11): 0.0; S(14): 0.0; S(16): 0.0; S(18): 0.0; S(28): 0.0	T1;	T68		4.01	0	0	3	1513	4538	61.04	12099
TCFsPNR	EIF3F	8665	eukaryotic translation initiation factor 3 subunit F	C2(Carbamidomethyl) S4(Phospho)	T(1): 0.0; S(4): 100.0	S4;	S258	36		0	0	2	481.2	961.4	25.61	4523
TCFsPNR	EIF3F	8665	eukaryotic translation initiation factor 3 subunit F	C2(Carbamidomethyl) S4(Phospho)	T(1): 0.0; S(4): 100.0	S4;	S258		2.39	0	0	2	481.2	961.4	25.61	4523
SQSSDTEQQsPTSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho)	S(1): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(10): 98.1; T(12): 1.8; S(13): 0.0	S10;	S504	78		0	0	2	880.8	1761	12.5	1731
SRTGsEsSQTGTSTTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S5(Phospho) S7(Phospho)	S(1): 2.6; T(3): 2.6; S(5): 94.9; S(7): 97.2; S(8): 2.6; T(10): 0.0; T(12): 0.0; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0	S5; S7;	S422; S424	63		0	1	2	988.9	1977	12.67	1777
TGsEsSQTGTSTTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S3(Phospho) S6(Phospho)	T(1): 2.5; S(3): 97.4; S(5): 0.1; S(6): 99.9; T(8): 0.1; T(10): 0.0; S(11): 0.0; T(12): 0.0; T(13): 0.0; S(14): 0.0; S(15): 0.0	S3; S6;	S422; S425	48		0	0	2	867.3	1734	16.28	2544
SQSSDTEQQsPTSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho)	S(1): 0.1; S(3): 1.9; S(4): 49.0; T(6): 49.0; S(10): 99.8; T(12): 0.2; S(13): 0.0	S10;	S504	35		0	0	2	920.8	1841	15.06	2283

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#
SQSSDTEQQsPTSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho)	S(1): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(10): 98.1; T(12): 1.8; S(13): 0.0	S10;	S504		5.01	0	0	2	880.8	1761	12.5	1731
SRTGsEsSQTGTSTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S5(Phospho) S7(Phospho)	S(1): 2.6; T(3): 2.6; S(5): 94.9; S(7): 97.2; S(8): 2.6; T(10): 0.0; T(12): 0.0; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0	S5; S7;	S422; S424		3.8	0	1	2	988.9	1977	12.67	1777
TGsEsSQTGTSTSSR	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S3(Phospho) S6(Phospho)	T(1): 2.5; S(3): 97.4; S(5): 0.1; S(6): 99.9; T(8): 0.1; T(10): 0.0; S(11): 0.0; T(12): 0.0; T(13): 0.0; S(14): 0.0; S(15): 0.0	S3; S6;	S422; S425		3.33	0	0	2	867.3	1734	16.28	2544
SQSSDTEQQsPTSGGGK	EIF4B	1975	eukaryotic translation initiation factor 4B isoform 2	S10(Phospho)	S(1): 0.1; S(3): 1.9; S(4): 49.0; T(6): 49.0; S(10): 99.8; T(12): 0.2; S(13): 0.0	S10;	S504		2.75	0	0	2	920.8	1841	15.06	2283
SFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S992	62		0	1	2	595.8	1191	30.77	5623
SFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S992	48		0	1	2	595.8	1191	31.28	5729
sFSKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S1(Phospho)	S(1): 100.0; S(3): 0.0	S1;	S990	44		0	1	2	595.8	1191	26.65	4747
SFsKEVEERsR	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S3(Phospho) S10(Phospho)	S(1): 0.0; S(3): 100.0; S(10): 100.0	S3; S10;	S992; S999	42		0	2	3	505.2	1514	28.64	5179
RsFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S990; S992	40		0	2	2	713.8	1427	28.06	5057
RsFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0	S2; S4;	S990; S992		3.1	0	2	2	713.8	1427	28.06	5057
sFSKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S1(Phospho)	S(1): 100.0; S(3): 0.0	S1;	S990		2.97	0	1	2	595.8	1191	26.65	4747
SFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S992		2.87	0	1	2	595.8	1191	30.77	5623
SFsKEVEER	EIF4G1	1981	eukaryotic translation initiation factor 4 gamma 1 isoform 4	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S992		2.32	0	1	2	595.8	1191	31.28	5729
FSAsSGGGGSr	EIF4G2	1982	eukaryotic translation initiation factor 4 gamma 2 isoform 2	S5(Phospho)	S(2): 0.0; S(4): 0.0; S(5): 100.0; S(10): 0.0	S5;	S17	53		0	0	2	525.2	1049	16.25	2538
FSAsSGGGGSr	EIF4G2	1982	eukaryotic translation initiation factor 4 gamma 2 isoform 2	S5(Phospho)	S(2): 0.0; S(4): 0.0; S(5): 100.0; S(10): 0.0	S5;	S17		2.8	0	0	2	525.2	1049	16.25	2538
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390	43		0	0	3	954.7	2862	72.57	14669
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390	35		0	0	2	1432	2862	72.78	14722
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390	29		0	0	3	954.7	2862	73.1	14788
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390	19		0	0	3	954.7	2862	72.07	14567
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390	16		0	0	2	1432	2862	72.28	14605
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390		4.91	0	0	3	954.7	2862	72.57	14669
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390		3.74	0	0	3	954.7	2862	73.1	14788
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390		3.15	0	0	2	1432	2862	72.78	14722
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390		2.91	0	0	3	954.7	2862	72.07	14567
EAAEEssGGEEDEDENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; Y(22): 0.0; S(23): 0.0	S6; S7;	S389; S390		2.2	0	0	2	1432	2862	72.28	14605

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#
EAEESsGGEEDEENIEVVYSK	EIF5	1983	eukaryotic translation initiation factor 5	S6(Phospho) S7(Phospho)	S(6): 99.8; S(7): 99.8; Y(22): 0.2; S(23): 0.2	S6; S7;	S389; S390		2.3	0.003	0	3	954.7	2862	73.88	14933
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164	79		0	1	2	809.8	1619	18.05	2930
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164	62		0	1	2	809.8	1619	18.59	3041
WDGsEEDEDNSKK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164	58		0	1	2	809.8	1619	17.3	2771
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	57		0	0	3	705.3	2114	38.94	7345
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation) S5(Phospho) S7(Phospho)	Y(4): 2.4; S(5): 97.6; S(7): 100.0	S5; S7;	S135; S137	54		0	1	3	750.9	2251	58.5	11561
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164	52		0	0	2	745.8	1490	24.13	4209
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	47		0	0	3	705.3	2114	38.39	7229
QsFDDNDSEELDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S2(Phospho)	S(2): 97.5; S(8): 2.5; S(16): 0.0	S2;	S107	46		0	1	2	1041	2081	34.38	6374
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation) S5(Phospho) S7(Phospho)	Y(4): 2.4; S(5): 97.6; S(7): 99.9	S5; S7;	S135; S137	45		0	1	3	750.9	2251	59.04	11693
KWDGsEEDEDNSKK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164	45		0	2	3	582.9	1747	14.25	2112
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	45		0	0	2	1057	2114	38.95	7346
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	41		0	0	2	1057	2114	38.43	7237
QSFDDNDsEELEDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S8(Phospho)	S(2): 0.0; S(8): 100.0; S(16): 0.0	S8;	S113	38		0	1	3	694.3	2081	34.31	6357
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho) S7(Phospho)	Y(4): 2.9; S(5): 97.1; S(7): 100.0	S5; S7;	S135; S137	36		0	1	3	745.6	2235	66.46	13383
KQSFDDNDsEELEDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(3): 0.0; S(9): 100.0; S(17): 0.0	S9;	S113	33		0	2	2	1105	2209	27.34	4903
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214	25		0	0	3	705.3	2114	39.46	7454
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho) S7(Phospho)	Y(4): 0.4; S(5): 99.8; S(7): 99.8	S5; S7;	S135; S137	23		0	1	2	1118	2235	66.43	13378
VEMYsGsDDDDDFNK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho) S7(Phospho)	Y(4): 0.1; S(5): 99.9; S(7): 99.9	S5; S7;	S135; S137	23		0	0	2	948.8	1897	61.29	12153
VEMYsGSDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation) S5(Phospho)	Y(4): 50.9; S(5): 98.2; S(7): 50.9	S5;	S135	21		0	1	2	1126	2251	59	11684
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S7(Phospho)	Y(4): 50.1; S(5): 50.1; S(7): 99.9	S7;	S137	12		0	1	2	1118	2235	66.97	13502
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		6.18	0	0	3	705.3	2114	38.94	7345
QSFDDNDsEELEDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S8(Phospho)	S(2): 0.0; S(8): 100.0; S(16): 0.0	S8;	S113		5.92	0	1	3	694.3	2081	34.31	6357
KWDGsEEDEDNSKK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164		5.84	0	2	3	582.9	1747	14.25	2112
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation) S5(Phospho) S7(Phospho)	Y(4): 2.4; S(5): 97.6; S(7): 99.9	S5; S7;	S135; S137		5.17	0	1	3	750.9	2251	59.04	11693
NKPGPNIESGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		4.67	0	0	3	705.3	2114	38.39	7229
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164		4.58	0	1	2	809.8	1619	18.05	2930

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#
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation)S5(Phospho)S7(Phospho)	Y(4): 2.4; S(5): 97.6; S(7): 100.0	S5; S7;	S135; S137		4.42	0	1	3	750.9	2251	58.5	11561
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		4.13	0	0	3	705.3	2114	39.46	7454
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)S7(Phospho)	Y(4): 2.9; S(5): 97.1; S(7): 100.0	S5; S7;	S135; S137		3.85	0	1	3	745.6	2235	66.46	13383
QsFDDNDSEELDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S2(Phospho)	S(2): 97.5; S(8): 2.5; S(16): 0.0	S2;	S107		3.77	0	1	2	1041	2081	34.38	6374
KQSFDDNDsEELEDKDSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(3): 0.0; S(9): 100.0; S(17): 0.0	S9;	S113		3.64	0	2	2	1105	2209	27.34	4903
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164		3.56	0	0	2	745.8	1490	24.13	4209
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		3.53	0	0	2	1057	2114	38.95	7346
KWDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)	S(5): 100.0; S(12): 0.0	S5;	S164		3.36	0	1	2	809.8	1619	18.59	3041
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)S7(Phospho)	Y(4): 0.4; S(5): 99.8; S(7): 99.8	S5; S7;	S135; S137		3.07	0	1	2	1118	2235	66.43	13378
NKPGPNIEsGNEDDDASFK	EIF5B	9669	eukaryotic translation initiation factor 5B	S9(Phospho)	S(9): 100.0; S(17): 0.0	S9;	S214		3.01	0	0	2	1057	2114	38.43	7237
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	M3(Oxidation)S5(Phospho)	Y(4): 50.9; S(5): 98.2; S(7): 50.9	S5;	S135		2.98	0	1	2	1126	2251	59	11684
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S5(Phospho)S7(Phospho)	Y(4): 0.1; S(5): 99.9; S(7): 99.9	S5; S7;	S135; S137		2.26	0	0	2	948.8	1897	61.29	12153
WDGsEEDEDNSK	EIF5B	9669	eukaryotic translation initiation factor 5B	S4(Phospho)	S(4): 100.0; S(11): 0.0	S4;	S164		3.13	0.001	1	2	809.8	1619	17.3	2771
VEMYsGsDDDDDFNKLKPK	EIF5B	9669	eukaryotic translation initiation factor 5B	S7(Phospho)	Y(4): 50.1; S(5): 50.1; S(7): 99.9	S7;	S137		2.13	0.001	1	2	1118	2235	66.97	13502
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): 2.8; S(9): 97.2	S4; S9;	S139; S144	34		0	0	2	797.3	1594	31.15	5700
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): 2.8; S(9): 97.2	S4; S9;	S139; S144	3.15	0	0	0	2	797.3	1594	31.15	5700
SSHSSDsGGsDVLDPDPTDGK	ELF3	1999	ETS-related transcription factor Elf-3	S7(Phospho)S10(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 0.1; S(5): 0.1; S(7): 99.7; S(10): 100.0; T(17): 0.0	S7; S10;	S212; S215	45		0	0	2	1062	2123	38.92	7342
SSHSSDsGGsDVLDPDPTDGK	ELF3	1999	ETS-related transcription factor Elf-3	S7(Phospho)S10(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 0.1; S(5): 0.1; S(7): 99.7; S(10): 100.0; T(17): 0.0	S7; S10;	S212; S215	3.32	0	0	0	2	1062	2123	38.92	7342
APVSSTESVIQSNTPtPPPpQPLNETAEEESR	EML4	27436	echinoderm microtubule-associated protein-like 4 isoform b	T16(Phospho)S20(Phospho)	S(4): 0.9; S(5): 0.9; T(6): 0.9; S(8): 0.6; S(12): 6.6; T(14): 6.6; T(16): 86.3; S(20): 97.3; T(26): 0.0; S(31): 0.0	T16; S20;	T841; S845	15		0	0	4	885.6	3540	68.92	13942
APVSSTESVIQSNTPtPPPpQPLNETAEEESR	EML4	27436	echinoderm microtubule-associated protein-like 4 isoform b	T16(Phospho)S20(Phospho)	S(4): 0.9; S(5): 0.9; T(6): 0.9; S(8): 0.6; S(12): 6.6; T(14): 6.6; T(16): 86.3; S(20): 97.3; T(26): 0.0; S(31): 0.0	T16; S20;	T841; S845	4.02	0	0	0	4	885.6	3540	68.92	13942
TNssSSSPVVLK	EMSY	56946	protein EMSY isoform 4	S3(Phospho)	T(1): 0.0; S(3): 99.9; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0	S3;	S209	26		0	0	2	643.3	1286	40.44	7667
TNssSSSPVVLK	EMSY	56946	protein EMSY isoform 4	S3(Phospho)	T(1): 0.0; S(3): 99.9; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0	S3;	S209	2.82	0	0	0	2	643.3	1286	40.44	7667
TEIKEEDQPSTSATQsPAPGQSK	EP300	2033	histone acetyltransferase p300	S18(Phospho)	T(1): 0.0; S(11): 0.0; T(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.2; S(18): 95.3; S(24): 4.5	S18;	S1038	17		0	1	3	904.7	2712	27.59	4956

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#
TEIKEEDQPSTSATQSSPAPGQSK	EP300	2033	histone acetyltransferase p300	S18(Phospho)	T(1): 0.0; S(11): 0.0; T(12): 0.0; S(13): 0.0; T(15): 0.0; S(17): 0.2; S(18): 95.3; S(24): 4.5	S18;	S1038		3.8	0	1	3	904.7	2712	27.59	4956
RLPSSPASPSPK	EPB41L1	2036	band 4.1-like protein 1 isoform b	S8(Phospho) S10(Phospho)	S(4): 0.1; S(5): 0.1; S(8): 99.9; S(10): 100.0	S8; S10;	S470; S472	22		0	1	2	692.3	1384	31.16	5703
APESDtGDEDDQDERDVTFLK	EPB41L1	2036	band 4.1-like protein 1 isoform b	S4(Phospho) T6(Phospho)	S(4): 100.0; T(6): 100.0; T(17): 0.0	S4; T6;	S504; T506		4.49	0	1	3	852.3	2555	60.81	12048
RLPSSPASPSPK	EPB41L1	2036	band 4.1-like protein 1 isoform b	S8(Phospho) S10(Phospho)	S(4): 0.1; S(5): 0.1; S(8): 99.9; S(10): 100.0	S8; S10;	S470; S472		3.5	0	1	2	692.3	1384	31.16	5703
RLSTSPVR	EPB41L3	23136	band 4.1-like protein 3 isoform 4	S5(Phospho)	S(3): 50.0; T(4): 50.0; S(5): 100.0	S5;	S472	16		0.003	1	2	538.2	1075	23.21	4019
RLSTSPVR	EPB41L3	23136	band 4.1-like protein 3 isoform 4	S5(Phospho)	S(3): 50.0; T(4): 50.0; S(5): 100.0	S5;	S472		2.73	0.005	1	2	538.2	1075	23.21	4019
GSSQPNLSTSHSEQYQK	EPN2	22905	epsin-2 isoform a	S3(Phospho)	S(2): 3.2; S(3): 96.5; S(8): 0.1; T(9): 0.1; S(10): 0.0; S(12): 0.0; Y(16): 0.0	S3;	S173	16		0	0	2	1008	2016	27.76	4993
GSSQPNLSTSHSEQYQK	EPN2	22905	epsin-2 isoform a	S3(Phospho)	S(2): 3.2; S(3): 96.5; S(8): 0.1; T(9): 0.1; S(10): 0.0; S(12): 0.0; Y(16): 0.0	S3;	S173		2.16	0	0	2	1008	2016	27.76	4993
EYIPGQPPLSQSSDSsPTR	EPRS	2058	bifunctional glutamate/proline--tRNA ligase	S16(Phospho)	Y(2): 0.0; S(10): 0.0; S(12): 0.0; S(13): 0.0; S(15): 2.1; S(16): 95.8; T(18): 2.1	S16;	S886	26		0	0	2	1063	2126	58.61	11590
EYIPGQPPLSQSSDSsPTR	EPRS	2058	bifunctional glutamate/proline--tRNA ligase	S16(Phospho)	Y(2): 0.0; S(10): 0.0; S(12): 0.0; S(13): 0.0; S(15): 2.1; S(16): 95.8; T(18): 2.1	S16;	S886		3.47	0	0	2	1063	2126	58.61	11590
IsAAASDSGVEsFDEGSSH	EPS8	2059	epidermal growth factor receptor kinase substrate 8	S2(Phospho) S12(Phospho)	S(2): 100.0; S(6): 0.0; S(8): 0.0; S(12): 91.9; S(17): 4.1; S(18): 4.1	S2; S12;	S805; S815	21		0	0	2	1007	2013	59.52	11790
IsAAASDSGVEsFDEGSSH	EPS8	2059	epidermal growth factor receptor kinase substrate 8	S2(Phospho) S12(Phospho)	S(2): 100.0; S(6): 0.0; S(8): 0.0; S(12): 91.9; S(17): 4.1; S(18): 4.1	S2; S12;	S805; S815		2.06	0.003	0	2	1007	2013	59.52	11790
NsQKHSPTSEPTPPGDALPPVsPHTHR	EPS8L2	64787	epidermal growth factor receptor kinase substrate 8-like protein 2	S2(Phospho) S23(Phospho)	S(2): 99.0; S(6): 0.5; T(8): 0.0; S(9): 0.0; T(12): 0.5; S(22): 6.1; S(23): 93.5; T(26): 0.4	S2; S23;	S459; S480	10		0	1	4	780.4	3118	37.49	7042
NsQKHSPTSEPTPPGDALPPVsPHTHR	EPS8L2	64787	epidermal growth factor receptor kinase substrate 8-like protein 2	S2(Phospho) S23(Phospho)	S(2): 99.0; S(6): 0.5; T(8): 0.0; S(9): 0.0; T(12): 0.5; S(22): 6.1; S(23): 93.5; T(26): 0.4	S2; S23;	S459; S480		7.1	0	1	4	780.4	3118	37.49	7042
NsQKHSPTSEPTPPGDALPPVsPHTHR	EPS8L2	64787	epidermal growth factor receptor kinase substrate 8-like protein 2	S2(Phospho) S23(Phospho)	S(2): 99.4; S(6): 0.3; T(8): 0.0; S(9): 0.0; T(12): 0.3; S(22): 4.9; S(23): 94.9; T(26): 0.3	S2; S23;	S459; S480		4.99	0	1	4	780.4	3118	36.97	6933
TEPHDCsVDLGISkSTEDLSPQK	ERBB2IP	55914	protein LAP2 isoform 7	C8(Carbamidomethyl)S6(Phospho) S9(Phospho) S17(Phospho)	T(1): 5.6; S(6): 94.7; S(9): 99.7; S(15): 0.0; S(17): 99.6; T(18): 0.3; S(22): 0.0	S6; S9; S17;	S841; S844; S852	16		0	1	3	995.7	2985	60.94	12077
TEPHDCsVDLGISkSTEDLSPQK	ERBB2IP	55914	protein LAP2 isoform 7	C8(Carbamidomethyl)S6(Phospho) S9(Phospho) S17(Phospho)	T(1): 5.6; S(6): 94.7; S(9): 99.7; S(15): 0.0; S(17): 99.6; T(18): 0.3; S(22): 0.0	S6; S9; S17;	S841; S844; S852		3.47	0	1	3	995.7	2985	60.94	12077
VEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S7(Phospho) S11(Phospho)	S(4): 0.0; S(5): 0.0; S(7): 100.0; S(11): 100.0	S7; S11;	S17; S21	28		0	1	2	772.3	1544	15.86	2453

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#
SVGKVEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S11(Phospho) S15(Phospho)	S(1): 0.0; S(8): 0.0; S(9): 0.1; S(11): 99.9; S(15): 100.0	S11; S15;	S17; S21		5.55	0	2	3	639	1915	19.52	3236
VEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S7(Phospho) S11(Phospho)	S(4): 0.0; S(5): 0.0; S(7): 100.0; S(11): 100.0	S7; S11;	S17; S21		3.78	0	1	2	772.3	1544	15.86	2453
SVGKVEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S11(Phospho) S15(Phospho)	S(1): 0.0; S(8): 0.0; S(9): 0.1; S(11): 99.9; S(15): 100.0	S11; S15;	S17; S21	24		0.001	2	3	639	1915	19.52	3236
sVGKVEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S1(Phospho) S11(Phospho) S15(Phospho)	S(1): 100.0; S(8): 4.0; S(9): 0.2; S(11): 95.8; S(15): 100.0	S1; S11; S15;	S7; S17; S21	16		0.001	2	3	665.6	1995	25.6	4519
sVGKVEPSSQsPGRsPR	ERC1	23085	ELKS/Rab6-interacting/CAST family member 1 isoform zeta	S1(Phospho) S11(Phospho) S15(Phospho)	S(1): 100.0; S(8): 4.0; S(9): 0.2; S(11): 95.8; S(15): 100.0	S1; S11; S15;	S7; S17; S21	3.9	0.007	2	3	3	665.6	1995	25.6	4519
FDSSLLsDDETK	ERCC5	2073	DNA repair protein complementing XP-G cells	S7(Phospho) S8(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 99.9; S(8): 97.2; T(12): 2.9	S7; S8;	S562; S563	28		0	0	2	802.3	1604	70.44	14247
FDSSLLsDDETK	ERCC5	2073	DNA repair protein complementing XP-G cells	S7(Phospho) S8(Phospho)	S(3): 0.0; S(4): 0.0; S(7): 99.9; S(8): 97.2; T(12): 2.9	S7; S8;	S562; S563	2.41	0.005	0	2	2	802.3	1604	70.44	14247
AEPAsPDsPKGSSETETETPPVALAPGPAPTR	ESRRA	2101	steroid hormone receptor ERR1 isoform 2	S5(Phospho) S8(Phospho)	S(5): 91.3; S(8): 91.3; S(12): 17.3; S(13): 33.4; T(15): 33.4; T(17): 33.4; T(30): 0.0	S5; S8;	S19; S22	21		0	1	3	1095	3283	77.98	15726
AEPAsPDsPKGSSETETETPPVALAPGPAPTR	ESRRA	2101	steroid hormone receptor ERR1 isoform 2	S5(Phospho)	S(5): 87.3; S(8): 8.2; S(12): 8.2; S(13): 32.1; T(15): 32.1; T(17): 32.1; T(30): 0.0	S5;	S19	18		0	1	3	1068	3203	65.05	13062
AEPAsPDsPKGSSETETETPPVALAPGPAPTR	ESRRA	2101	steroid hormone receptor ERR1 isoform 2	S5(Phospho) S8(Phospho)	S(5): 91.3; S(8): 91.3; S(12): 17.3; S(13): 33.4; T(15): 33.4; T(17): 33.4; T(30): 0.0	S5; S8;	S19; S22	3.39	0	1	3	3	1095	3283	77.98	15726
AEPAsPDsPKGSSETETETPPVALAPGPAPTR	ESRRA	2101	steroid hormone receptor ERR1 isoform 2	S5(Phospho)	S(5): 87.3; S(8): 8.2; S(12): 8.2; S(13): 32.1; T(15): 32.1; T(17): 32.1; T(30): 0.0	S5;	S19	2.98	0	1	3	3	1068	3203	65.05	13062
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	T18(Phospho)	S(1): 0.0; S(4): 0.0; S(6): 0.0; S(12): 49.9; T(14): 49.9; S(17): 6.3; T(18): 93.9; S(24): 0.0	T18;	T677	30		0	0	3	1072	3213	44.4	8509
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	M3(Oxidation)S 17(Phospho) T18(Phospho)	S(1): 0.1; S(4): 0.1; S(6): 0.1; S(12): 0.0; T(14): 6.9; S(17): 92.8; T(18): 99.8; S(24): 0.0	S17; T18;	S676; T677	12		0	0	3	1077	3229	41.11	7806
SHMsGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	S4(Phospho) T14(Phospho) T18(Phospho)	S(1): 0.4; S(4): 93.8; S(6): 5.8; S(12): 0.4; T(14): 99.6; S(17): 5.9; T(18): 94.1; S(24): 0.0	S4; T14; T18;	S663; T673; T677	10		0	0	4	824.1	3293	49.36	9569
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	M3(Oxidation)T 14(Phospho) T18(Phospho)	S(1): 0.0; S(4): 0.0; S(6): 0.0; S(12): 0.4; T(14): 99.6; S(17): 5.5; T(18): 94.6; S(24): 0.0	T14; T18;	T673; T677	10		0	0	4	808.1	3229	41.06	7794
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	T18(Phospho)	S(1): 0.0; S(4): 0.0; S(6): 0.0; S(12): 49.9; T(14): 49.9; S(17): 6.3; T(18): 93.9; S(24): 0.0	T18;	T677	6		0	0	3	1072	3213	44.4	8509
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	M3(Oxidation)T 14(Phospho) T18(Phospho)	S(1): 0.0; S(4): 0.0; S(6): 0.0; S(12): 0.4; T(14): 99.6; S(17): 5.5; T(18): 94.6; S(24): 0.0	T14; T18;	T673; T677	5.86	0	0	4	4	808.1	3229	41.06	7794

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#
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	S4(Phospho) T14(Phospho) T18(Phospho)	S(1): 0.4; S(4): 93.8; S(6): 5.8; S(12): 0.4; T(14): 99.6; S(17): 5.9; T(18): 94.1; S(24): 0.0	S4; T14; T18;	S663; T673; T677		5.05	0	0	4	824.1	3293	49.36	9569
SHMSGSPGPGGSNTAPStPVIGGSDKPG MEEK	ESYT2	57488	extended synaptotagmin-2	M3(Oxidation) S17(Phospho) T18(Phospho)	S(1): 0.1; S(4): 0.1; S(6): 0.1; S(12): 0.0; T(14): 6.9; S(17): 92.8; T(18): 99.8; S(24): 0.0	S17; T18;	S676; T677		4.04	0	0	3	1077	3229	41.11	7806
LTGSTsSLNK	EXOC1	55763	exocyst complex component 1 isoform 2	T5(Phospho) S7(Phospho)	T(2): 0.0; S(4): 2.1; T(5): 95.9; S(6): 4.1; S(7): 97.9	T5; S7;	T456; S458	16		0	0	2	584.2	1167	29.76	5411
LTGSTsSLNK	EXOC1	55763	exocyst complex component 1 isoform 2	T5(Phospho) S7(Phospho)	T(2): 0.0; S(4): 2.1; T(5): 95.9; S(6): 4.1; S(7): 97.9	T5; S7;	T456; S458		2.66	0.003	0	2	584.2	1167	29.76	5411
LSSGDPSTSPSLQTTPSKDTDDQSR	EYA3	2140	eyes absent homolog 3 isoform d	T16(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.0; T(8): 0.0; S(9): 0.0; S(11): 0.0; S(13): 4.4; T(15): 4.4; T(16): 90.8; S(18): 0.2; T(21): 0.0; S(25): 0.0	T16;	T216	17		0	1	3	925.4	2774	36.21	6773
LSSGDPSTSPSLQTTPSKDTDDQSR	EYA3	2140	eyes absent homolog 3 isoform d	T16(Phospho)	S(2): 0.0; S(3): 0.0; S(7): 0.0; T(8): 0.0; S(9): 0.0; S(11): 0.0; S(13): 4.4; T(15): 4.4; T(16): 90.8; S(18): 0.2; T(21): 0.0; S(25): 0.0	T16;	T216		3.96	0	1	3	925.4	2774	36.21	6773
RIDFTVPsPAPsPTR	FAM122B	159090	protein FAM122B isoform 5	S8(Phospho) S12(Phospho)	T(5): 2.7; S(8): 97.3; S(12): 99.9; T(14): 0.1	S8; S12;	S81; S85	20		0	1	2	900.9	1801	63.61	12714
RIDFTVPsPAPsPTR	FAM122B	159090	protein FAM122B isoform 5	S8(Phospho) S12(Phospho)	T(5): 2.7; S(8): 97.3; S(12): 99.9; T(14): 0.1	S8; S12;	S81; S85		3.43	0	1	2	900.9	1801	63.61	12714
IDFTVPsPAPsPTR	FAM122B	159090	protein FAM122B isoform 5	S7(Phospho) S11(Phospho)	T(4): 0.0; S(7): 100.0; S(11): 97.8; T(13): 2.2	S7; S11;	S81; S85	11		0.009	0	2	822.9	1645	77.12	15572
IDFTVPsPAPsPTR	FAM122B	159090	protein FAM122B isoform 5	S7(Phospho) S11(Phospho)	T(4): 0.0; S(7): 100.0; S(11): 97.8; T(13): 2.2	S7; S11;	S81; S85		2.26	0.009	0	2	822.9	1645	77.12	15572
AAPEASsPPAsPLQHLLPGK	FAM129B	64855	niban-like protein 1 isoform 2	S7(Phospho) S11(Phospho)	S(6): 4.3; S(7): 95.7; S(11): 100.0	S7; S11;	S679; S683	13		0	0	3	710	2128	77.3	15610
AAPEASsPPAsPLQHLLPGK	FAM129B	64855	niban-like protein 1 isoform 2	S7(Phospho) S11(Phospho)	S(6): 4.3; S(7): 95.7; S(11): 100.0	S7; S11;	S679; S683		3.23	0	0	3	710	2128	77.3	15610
AAPEASsPPAsPLQHLLPGK	FAM129B	64855	niban-like protein 1 isoform 2	S6(Phospho) S11(Phospho)	S(6): 95.1; S(7): 5.2; S(11): 99.7	S6; S11;	S678; S683		1.82	0	0	2	1065	2128	77.41	15625
QALDsEEEEEDVAAK	FAM134A	79137	protein FAM134A	S5(Phospho)	S(5): 100.0	S5;	S385	36		0	0	2	871.9	1743	41.58	7904
QALDsEEEEEDVAAK	FAM134A	79137	protein FAM134A	S5(Phospho)	S(5): 100.0	S5;	S385		3.01	0	0	2	871.9	1743	41.58	7904
GQTPLtEGsEDLDGHsDPEESFAR	FAM134C	162427	protein FAM134C	T6(Phospho) S9(Phospho) S16(Phospho)	T(3): 6.4; T(6): 93.6; S(9): 100.0; S(16): 99.5; S(21): 0.5	T6; S9; S16;	T310; S313; S320	22		0	0	3	938.7	2814	75.52	15255
AMDNHsDsEEELAAFCPLQDDSTVAR	FAM134C	162427	protein FAM134C	M2(Oxidation) C16(Carbamido methyl) S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(22): 0.0; T(23): 0.0	S6; S8;	S258; S260	17		0	0	3	1029	3084	80.08	16135
GQTPLtEGsEDLDGHsDPEESFAR	FAM134C	162427	protein FAM134C	S9(Phospho) S16(Phospho)	T(3): 0.3; T(6): 5.1; S(9): 94.6; S(16): 100.0; S(21): 0.0	S9; S16;	S313; S320	12		0	0	3	912	2734	64.76	13000
AMDNHsDsEEELAAFCPLQDDSTVAR	FAM134C	162427	protein FAM134C	C16(Carbamido methyl) S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(22): 0.0; T(23): 0.0	S6; S8;	S258; S260	11		0	0	3	1023	3068	82.82	16653

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#
AMDNHsDsEEELAAFCPLDDSTVAR	FAM134C	162427	protein FAM134C	M2(Oxidation) C16(Carbamido methyl)S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(22): 0.0; T(23): 0.0	S6; S8;	S258; S260		4.26	0	0	3	1029	3084	80.08	16135
AMDNHsDsEEELAAFCPLDDSTVAR	FAM134C	162427	protein FAM134C	C16(Carbamido methyl)S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(22): 0.0; T(23): 0.0	S6; S8;	S258; S260		3.88	0	0	3	1023	3068	82.82	16653
GQTPLEGSEDLDGHSDPESFAR	FAM134C	162427	protein FAM134C	S9(Phospho) S16(Phospho)	T(3): 0.3; T(6): 5.1; S(9): 94.6; S(16): 100.0; S(21): 0.0	S9; S16;	S313; S320		3.46	0	0	3	912	2734	64.76	13000
GQTPLEGSEDLDGHSDPESFAR	FAM134C	162427	protein FAM134C	T6(Phospho) S9(Phospho) S16(Phospho)	T(3): 6.4; T(6): 93.6; S(9): 100.0; S(16): 99.5; S(21): 0.5	T6; S9; S16;	T310; S313; S320		4.12	0.003	0	3	938.7	2814	75.52	15255
LESTARPSessEEFLEEEPEQR	FAM169A	26049	soluble lamin-associated protein of 75 kDa	S10(Phospho) S11(Phospho)	S(3): 11.0; T(4): 11.0; S(8): 7.6; S(10): 85.2; S(11): 85.2	S10; S11;	S378; S379	29		0	0	3	913.7	2739	58.28	11505
LESTARPSessEEFLEEEPEQR	FAM169A	26049	soluble lamin-associated protein of 75 kDa	S10(Phospho) S11(Phospho)	S(3): 11.0; T(4): 11.0; S(8): 7.6; S(10): 85.2; S(11): 85.2	S10; S11;	S378; S379		3.61	0	0	3	913.7	2739	58.28	11505
ASKMssPetDEEIEK	FAM175A	84142	BRCA1-A complex subunit Abraxas	S5(Phospho) S6(Phospho) T9(Phospho)	S(2): 0.0; S(5): 100.0; S(6): 100.0; T(9): 100.0	S5; S6; T9;	S386; S387; T390		2.42	0.001	1	2	960.8	1921	39.29	7420
ASKMssPetDEEIEK	FAM175A	84142	BRCA1-A complex subunit Abraxas	S5(Phospho) S6(Phospho) T9(Phospho)	S(2): 0.0; S(5): 100.0; S(6): 100.0; T(9): 100.0	S5; S6; T9;	S386; S387; T390	12		0.006	1	2	960.8	1921	39.29	7420
GGNLPPVsPND SGAK	FAM208A	23272	protein TASOR isoform b	S8(Phospho)	S(8): 100.0; S(12): 0.0	S8;	S666	41		0	0	2	745.3	1490	39.43	7448
GGNLPPVsPND SGAK	FAM208A	23272	protein TASOR isoform b	S8(Phospho)	S(8): 100.0; S(12): 0.0	S8;	S666		2.86	0	0	2	745.3	1490	39.43	7448
RTPsDDEEDNLFAPPK	FAM21C	253725	WASH complex subunit FAM21C isoform 2	S4(Phospho)	T(2): 0.1; S(4): 99.9	S4;	S333	30		0	1	2	955.9	1911	54.75	10750
sRPTsFADELAAR	FAM21C	253725	WASH complex subunit FAM21C isoform 2	S1(Phospho) S5(Phospho)	S(1): 97.0; T(4): 6.1; S(5): 97.0	S1; S5;	S284; S288	18		0	0	2	790.8	1581	62.31	12376
ERRTPsDDEEDNLFAPPK	FAM21C	253725	WASH complex subunit FAM21C isoform 2	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T331; S333	18		0	2	3	759.3	2276	53.78	10532
ERRTPsDDEEDNLFAPPK	FAM21C	253725	WASH complex subunit FAM21C isoform 2	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T331; S333		5.9	0	2	3	759.3	2276	53.78	10532
RTPsDDEEDNLFAPPK	FAM21C	253725	WASH complex subunit FAM21C isoform 2	S4(Phospho)	T(2): 0.1; S(4): 99.9	S4;	S333		2.68	0	1	2	955.9	1911	54.75	10750
sRPTsFADELAAR	FAM21C	253725	WASH complex subunit FAM21C isoform 2	S1(Phospho) S5(Phospho)	S(1): 97.0; T(4): 6.1; S(5): 97.0	S1; S5;	S284; S288		2.12	0.001	0	2	790.8	1581	62.31	12376
KsQENLGNPSKNEDNVK	FAM234A	83986	protein ITFG3	S2(Phospho)	S(2): 100.0; S(10): 0.0	S2;	S21	29		0	2	3	661	1981	17.83	2884
KsQENLGNPSKNEDNVK	FAM234A	83986	protein ITFG3	S2(Phospho)	S(2): 100.0; S(10): 0.0	S2;	S21		5.23	0	2	3	661	1981	17.83	2884
GSgSPTHSLSQK	FAM64A	54478	protein FAM64A isoform 1	S4(Phospho)	S(2): 0.0; S(4): 100.0; T(6): 0.0; S(8): 0.0; S(10): 0.0	S4;	S131	44		0	0	2	633.3	1266	14.41	2145
GSgSPTHSLSQK	FAM64A	54478	protein FAM64A isoform 1	S4(Phospho)	S(2): 0.0; S(4): 100.0; T(6): 0.0; S(8): 0.0; S(10): 0.0	S4;	S131		4.19	0	0	2	633.3	1266	14.41	2145
FSTYSQsPPDTPSLR	FAM65A	79567	protein FAM65A isoform 1	S7(Phospho) T11(Phospho)	S(2): 0.1; T(3): 0.0; Y(4): 0.0; S(5): 0.1; S(7): 99.8; T(11): 96.8; S(13): 3.2	S7; T11;	S347; T351	22		0	0	2	921.9	1843	64.01	12811
FSTYSQsPPDTPSLR	FAM65A	79567	protein FAM65A isoform 1	S7(Phospho) T11(Phospho)	S(2): 0.1; T(3): 0.0; Y(4): 0.0; S(5): 0.1; S(7): 99.8; T(11): 96.8; S(13): 3.2	S7; T11;	S347; T351		2.48	0	0	2	921.9	1843	64.01	12811
ISNLsPEEEQGLWK	FAM76B	143684	protein FAM76B	S5(Phospho)	S(2): 0.0; S(5): 100.0	S5;	S193	41		0	0	2	855.4	1710	68.8	13914
ISNLsPEEEQGLWK	FAM76B	143684	protein FAM76B	S5(Phospho)	S(2): 0.0; S(5): 100.0	S5;	S193		2.88	0	0	2	855.4	1710	68.8	13914

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#
LCSSSDTLVsEGEENQKPK	FAM83B	222584	protein FAM83B	C2(Carbamidomethyl)S5(Phospho)S10(Phospho)	S(3): 0.2; S(4): 3.8; S(5): 92.3; T(7): 3.8; S(10): 100.0	S5; S10;	S804; S809	27		0	0	3	756.6	2268	41.62	7913
TPSPGPVESK	FAM83B	222584	protein FAM83B	S3(Phospho)	T(1): 0.0; S(3): 98.1; S(9): 1.9	S3;	S869	16		0	0	2	539.7	1078	23.78	4136
LCSSSDTLVsEGEENQKPK	FAM83B	222584	protein FAM83B	C2(Carbamidomethyl)S5(Phospho)S10(Phospho)	S(3): 0.2; S(4): 3.8; S(5): 92.3; T(7): 3.8; S(10): 100.0	S5; S10;	S804; S809		3.58	0	0	3	756.6	2268	41.62	7913
TPSPGPVESK	FAM83B	222584	protein FAM83B	S3(Phospho)	T(1): 0.0; S(3): 98.1; S(9): 1.9	S3;	S869		2.41	0	0	2	539.7	1078	23.78	4136
VPVPGPGSGGNGPER	FAM83H	286077	protein FAM83H	S8(Phospho)	S(8): 100.0	S8;	S647	39		0	0	2	728.8	1457	38.49	7248
RGSPtGFIEQKGsPTSAYPER	FAM83H	286077	protein FAM83H	T6(Phospho)S14(Phospho)	S(3): 4.2; T(5): 0.2; T(6): 95.6; S(14): 99.8; T(16): 0.2; S(17): 0.0; Y(19): 0.0	T6; S14;	T895; S903	27		0	2	3	842.7	2526	48.04	9294
RGSPtGFIEQKGsPTSAYPER	FAM83H	286077	protein FAM83H	T6(Phospho)S14(Phospho)	S(3): 4.2; T(5): 0.2; T(6): 95.6; S(14): 99.8; T(16): 0.2; S(17): 0.0; Y(19): 0.0	T6; S14;	T895; S903		5.1	0	2	3	842.7	2526	48.04	9294
VPVPGPGSGGNGPER	FAM83H	286077	protein FAM83H	S8(Phospho)	S(8): 100.0	S8;	S647		3.12	0	0	2	728.8	1457	38.49	7248
RsQSSSQGDNPLAPGYLPPHYK	FAM83H	286077	protein FAM83H	S2(Phospho)	S(2): 97.2; S(4): 67.6; S(5): 67.6; S(6): 67.6; Y(16): 0.1; Y(21): 0.0	S2;	S5		2.12	0.003	1	3	880.4	2639	68.65	13884
RMDEGGFPVPQENGQPEsPR	FAM83H	286077	protein FAM83H	M2(Oxidation)S19(Phospho)	S(19): 100.0	S19;	S998		2.74	0.007	1	3	818	2452	50.3	9769
TTPPPGRPPAPsSEEDGEAVAH	FAM84B	157638	protein FAM84B	S13(Phospho)	T(1): 50.0; T(2): 50.0; S(12): 5.5; S(13): 94.6	S13;	S300		3.21	0.004	0	3	830	2488	45.37	8733
DsSSSLTDPPQVSyVksPAAER	FARP2	9855	FERM, RhoGEF and pleckstrin domain-containing protein 2 isoform c	S2(Phospho)S16(Phospho)	S(2): 90.4; S(3): 3.2; S(4): 3.2; S(5): 3.2; T(7): 0.0; S(12): 0.0; Y(13): 0.0; S(16): 100.0	S2; S16;	S425; S439	13		0	1	3	795.3	2384	57.24	11292
DsSSSLTDPPQVSyVksPAAER	FARP2	9855	FERM, RhoGEF and pleckstrin domain-containing protein 2 isoform c	S2(Phospho)S16(Phospho)	S(2): 90.4; S(3): 3.2; S(4): 3.2; S(5): 3.2; T(7): 0.0; S(12): 0.0; Y(13): 0.0; S(16): 100.0	S2; S16;	S425; S439		2.72	0	1	3	795.3	2384	57.24	11292
DMPAAGsLGsSSR	FAT1	2195	protocadherin Fat 1 precursor	S7(Phospho)S10(Phospho)	S(7): 100.0; S(10): 100.0; S(11): 0.0; S(12): 0.0	S7; S10;	S4473; S4476	47		0	0	2	698.3	1396	52.51	10248
DMPAAGsLGsSSR	FAT1	2195	protocadherin Fat 1 precursor	S7(Phospho)S10(Phospho)	S(7): 100.0; S(10): 100.0; S(11): 0.0; S(12): 0.0	S7; S10;	S4473; S4476		3.34	0	0	2	698.3	1396	52.51	10248
HsPVQMNR	FCHO2	115548	F-BAR domain only protein 2 isoform b	S2(Phospho)	S(2): 100.0	S2;	S361	27		0	0	2	524.7	1048	14.37	2137
NLSNEELTK	FCHO2	115548	F-BAR domain only protein 2 isoform b	S3(Phospho)	S(3): 100.0; T(8): 0.0	S3;	S370	25		0	0	2	564.3	1127	35.27	6576
HsPVQMNR	FCHO2	115548	F-BAR domain only protein 2 isoform b	S2(Phospho)	S(2): 100.0	S2;	S361		2.9	0	0	2	524.7	1048	14.37	2137
NLSNEELTK	FCHO2	115548	F-BAR domain only protein 2 isoform b	S3(Phospho)	S(3): 100.0; T(8): 0.0	S3;	S370		2.48	0	0	2	564.3	1127	35.27	6576
VTPQEEADsDVGEEPDSENTPQKADK	FGD3	89846	FYVE, RhoGEF and PH domain-containing protein 3 isoform b	S9(Phospho)	T(2): 4.8; S(9): 95.2; S(17): 0.0; T(20): 0.0	S9;	S128	12		0	1	3	965.7	2895	34.57	6414
VTPQEEADsDVGEEPDSENTPQKADK	FGD3	89846	FYVE, RhoGEF and PH domain-containing protein 3 isoform b	S9(Phospho)	T(2): 4.8; S(9): 95.2; S(17): 0.0; T(20): 0.0	S9;	S128		3.96	0	1	3	965.7	2895	34.57	6414
EKGPTTGEGALDLSVHsPPKsPEGK	FGFR1OP	11116	FGFR1 oncogene partner isoform b	S18(Phospho)S22(Phospho)	T(5): 0.0; T(6): 0.0; S(14): 0.0; S(18): 100.0; S(22): 100.0	S18; S22;	S156; S160	15		0	2	3	931.8	2793	45.95	8856
EKGPTTGEGALDLSVHsPPKsPEGK	FGFR1OP	11116	FGFR1 oncogene partner isoform b	S18(Phospho)S22(Phospho)	T(5): 0.0; T(6): 0.0; S(14): 0.0; S(18): 100.0; S(22): 100.0	S18; S22;	S156; S160	11		0	2	4	699.1	2793	45.94	8854

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#
EKGPTTGEGALDLSDVHsPPKsPEGK	FGFR1OP	11116	FGFR1 oncogene partner isoform b	S18(Phospho) S22(Phospho)	T(5): 0.0; T(6): 0.0; S(14): 0.0; S(18): 100.0; S(22): 100.0	S18; S22;	S156; S160		7.43	0	2	4	699.1	2793	45.94	8854
EKGPTTGEGALDLSDVHsPPKsPEGK	FGFR1OP	11116	FGFR1 oncogene partner isoform b	S18(Phospho) S22(Phospho)	T(5): 0.0; T(6): 0.0; S(14): 0.0; S(18): 100.0; S(22): 100.0	S18; S22;	S156; S160		4.39	0	2	3	931.8	2793	45.95	8856
GPTTGEGALDLSDVHsPPKsPEGK	FGFR1OP	11116	FGFR1 oncogene partner isoform b	S16(Phospho) S20(Phospho)	T(3): 0.0; T(4): 0.0; S(12): 0.5; S(16): 99.5; S(20): 100.0	S16; S20;	S156; S160		2.8	0.009	1	3	846	2536	51.01	9917
DHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(7): 0.0; S(11): 0.0	S3;	S418	47		0	0	2	898.9	1797	43.24	8251
ERDHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S5(Phospho) S13(Phospho)	S(5): 97.8; T(7): 2.2; S(9): 0.0; S(13): 100.0	S5; S13;	S418; S426	32		0	1	3	721.3	2162	39.21	7402
DHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S3(Phospho) S11(Phospho)	S(3): 100.0; T(5): 0.0; S(7): 0.0; S(11): 100.0	S3; S11;	S418; S426	31		0	0	2	938.8	1877	50.41	9791
ERDHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S5(Phospho)	S(5): 99.9; T(7): 0.1; S(9): 0.0; S(13): 0.0	S5;	S418	30		0	1	3	694.6	2082	35.14	6550
ERDHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S5(Phospho) S13(Phospho)	S(5): 97.8; T(7): 2.2; S(9): 0.0; S(13): 100.0	S5; S13;	S418; S426		5.13	0	1	3	721.3	2162	39.21	7402
ERDHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S5(Phospho)	S(5): 99.9; T(7): 0.1; S(9): 0.0; S(13): 0.0	S5;	S418		4.71	0	1	3	694.6	2082	35.14	6550
DHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(7): 0.0; S(11): 0.0	S3;	S418		3.43	0	0	2	898.9	1797	43.24	8251
DHsPTPSVFNsDEER	FIP1L1	81608	pre-mRNA 3'-end-processing factor FIP1 isoform 3	S3(Phospho) S11(Phospho)	S(3): 100.0; T(5): 0.0; S(7): 0.0; S(11): 100.0	S3; S11;	S418; S426		2.52	0.005	0	2	938.8	1877	50.41	9791
RPsQEQSASASSGQPQAPLNR	FKBP15	23307	FK506-binding protein 15	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(12): 0.0	S3;	S956	72		0	0	3	759.4	2276	27.33	4901
SLsGDEEDELfK	FKBP15	23307	FK506-binding protein 15	S2(Phospho) S4(Phospho)	S(1): 5.0; S(2): 97.5; S(4): 97.5	S2; S4;	S1162; S1164	60		0	0	2	808.3	1616	82.1	16515
RPsQEQSASASSGQPQAPLNR	FKBP15	23307	FK506-binding protein 15	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(12): 0.0	S3;	S956		6.18	0	0	3	759.4	2276	27.33	4901
SLsGDEEDELfK	FKBP15	23307	FK506-binding protein 15	S2(Phospho) S4(Phospho)	S(1): 5.0; S(2): 97.5; S(4): 97.5	S2; S4;	S1162; S1164		3.85	0	0	2	808.3	1616	82.1	16515
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 98.6; S(8): 1.4; S(10): 0.0	S3; S6;	S296; S299	89		0	0	2	670.3	1339	28.94	5241
TVsDNsLSNSRGEGKPDfK	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 99.8; S(8): 0.2; S(10): 0.0	S3; S6;	S296; S299	31		0	1	3	722	2164	30.7	5609
TVsDNsLSNSRGEGKPDfK	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 99.8; S(8): 0.2; S(10): 0.0	S3; S6;	S296; S299		5.85	0	1	3	722	2164	30.7	5609
TVsDNsLSNSR	FNBP1	23048	formin-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 98.6; S(8): 1.4; S(10): 0.0	S3; S6;	S296; S299		4.24	0	0	2	670.3	1339	28.94	5241
IDENsDKEMEVEEsPEKfK	FNBP4	23360	formin-binding protein 4	S5(Phospho) S14(Phospho)	S(5): 100.0; S(14): 100.0	S5; S14;	S499; S508	12		0	2	3	803.7	2409	43.32	8269
IDENsDKEMEVEEsPEKfK	FNBP4	23360	formin-binding protein 4	S5(Phospho) S14(Phospho)	S(5): 100.0; S(14): 100.0	S5; S14;	S499; S508		3.67	0	2	3	803.7	2409	43.32	8269
NESSDSALGDsESEDtGHDMTR	FNIP1	96459	folliculin-interacting protein 1 isoform 2	S11(Phospho)	S(3): 0.0; S(4): 0.0; S(6): 0.0; S(11): 96.8; S(13): 3.2; T(16): 0.0; T(21): 0.0	S11;	S918	24		0	0	3	807.3	2420	33.53	6195
NESSDSALGDsESEDtGHDMTR	FNIP1	96459	folliculin-interacting protein 1 isoform 2	S11(Phospho)	S(3): 0.0; S(4): 0.0; S(6): 0.0; S(11): 96.8; S(13): 3.2; T(16): 0.0; T(21): 0.0	S11;	S918		3.79	0	0	3	807.3	2420	33.53	6195

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#
HSTENDSPTNVQQ	FNTA	2339	protein farnesyltransferase/geranylgeranyl transferase type-1 subunit alpha	S7(Phospho)	S(2): 0.1; T(3): 2.2; S(7): 97.7; T(9): 0.0	S7;	S373	40		0.002	0	2	768.8	1537	17.71	2857
GSSGSAPAHAESYSSGGGGQK	FOSL2	2355	fos-related antigen 2	S5(Phospho)	S(2): 0.1; S(3): 2.5; S(5): 97.5; S(11): 0.0; Y(12): 0.0; S(13): 0.0; S(14): 0.0	S5;	S19	46		0	0	2	1008	2016	15.5	2376
QEPLEEDSPSSSSAGLDK	FOSL2	2355	fos-related antigen 2	S8(Phospho)	S(8): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S8;	S230	33		0	0	2	978.4	1956	45.61	8784
GSSGSAPAHAESYSSGGGGQK	FOSL2	2355	fos-related antigen 2	S5(Phospho)	S(2): 0.1; S(3): 2.5; S(5): 97.5; S(11): 0.0; Y(12): 0.0; S(13): 0.0; S(14): 0.0	S5;	S19		4.08	0	0	2	1008	2016	15.5	2376
QEPLEEDSPSSSSAGLDK	FOSL2	2355	fos-related antigen 2	S8(Phospho)	S(8): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S8;	S230		3.27	0	0	2	978.4	1956	45.61	8784
KDPSGASNPSADsPLHR	FOXA1	3169	hepatocyte nuclear factor 3-alpha	S13(Phospho)	S(4): 0.0; S(7): 0.0; S(10): 0.0; S(13): 100.0	S13;	S307	58		0	1	3	605.9	1816	21.4	3632
KDPSGASNPSADsPLHR	FOXA1	3169	hepatocyte nuclear factor 3-alpha	S13(Phospho)	S(4): 0.0; S(7): 0.0; S(10): 0.0; S(13): 100.0	S13;	S307		5.65	0	1	3	605.9	1816	21.4	3632
sAPAsPTHPLMSPR	FOXX1	221937	forkhead box protein K1	S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 0.0	S1; S5;	S416; S420	70		0	0	2	833.3	1666	47.98	9280
sAPAsPTHPLMSPR	FOXX1	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	53		0	0	2	841.3	1682	38.06	7160
sAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 100.0	S1; S5; S13;	S416; S420; S428	47		0	0	2	873.3	1746	58.82	11646
SAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	S5(Phospho) S13(Phospho)	S(1): 2.7; S(5): 97.3; T(7): 0.0; S(13): 100.0	S5; S13;	S420; S428	22		0	0	2	833.3	1666	46.8	9034
sAPAsPTHPLMSPR	FOXX1	221937	forkhead box protein K1	S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 0.0	S1; S5;	S416; S420		3.67	0	0	2	833.3	1666	47.98	9280
sAPAsPTHPLMSPR	FOXX1	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		3.49	0	0	2	841.3	1682	38.06	7160
SGGLQ ^t PECLsREGsPIPHDPEFGSK	FOXX1	221937	forkhead box protein K1	C9(Carbamidomethyl)T6(Phospho) S11(Phospho) S15(Phospho)	S(1): 19.4; T(6): 93.5; S(11): 93.5; S(15): 93.5; S(25): 0.0	T6; S11; S15;	T436; S441; S445		2.97	0	1	4	756.3	3022	66.3	13345
SGGLQ ^t PECLsREGsPIPHDPEFGSK	FOXX1	221937	forkhead box protein K1	C9(Carbamidomethyl)T6(Phospho) S11(Phospho) S15(Phospho)	S(1): 0.8; T(6): 99.2; S(11): 99.9; S(15): 99.8; S(25): 0.2	T6; S11; S15;	T436; S441; S445		2.49	0	1	3	1008	3022	66.04	13287
sAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 100.0	S1; S5; S13;	S416; S420; S428	18		0.002	0	2	881.3	1762	45.78	8819
sAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	M12(Oxidation) S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 100.0	S1; S5; S13;	S416; S420; S428		3.05	0.002	0	2	881.3	1762	45.78	8819
SAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	M12(Oxidation) S5(Phospho) S13(Phospho)	S(1): 0.1; S(5): 97.6; T(7): 2.4; S(13): 100.0	S5; S13;	S420; S428		2.7	0.004	0	2	841.3	1682	35.7	6666
sAPAsPTHPLMsPR	FOXX1	221937	forkhead box protein K1	S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 100.0; T(7): 0.0; S(13): 100.0	S1; S5; S13;	S416; S420; S428		3.06	0.005	0	2	873.3	1746	58.82	11646

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#
GQsTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C12(Carbamido methyl)S3(Phospho) S6(Phospho)	S(3): 96.9; T(4): 3.1; S(6): 100.0; T(10): 0.0	S3; S6;	S164; S167	71		0	0	2	811.8	1623	58.38	11529
GQSTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C12(Carbamido methyl) S6(Phospho)	S(3): 0.1; T(4): 0.1; S(6): 99.9; T(10): 0.0	S6;	S167	57		0	0	2	771.8	1543	46.73	9021
EIGSSTSSsSETVVK	FRMD6	122786	FERM domain-containing protein 6 isoform 3	S8(Phospho) S9(Phospho)	S(4): 0.0; S(5): 0.0; T(6): 0.0; S(7): 0.0; S(8): 100.0; S(9): 100.0; S(10): 0.0; T(12): 0.0	S8; S9;	S152; S153	39		0	0	2	829.3	1658	47.15	9109
LRGQsTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C14(Carbamido methyl)S5(Phospho) S8(Phospho)	S(5): 97.4; T(6): 5.2; S(8): 97.4; T(12): 0.0	S5; S8;	S164; S167	38		0	1	2	946.4	1892	49.54	9608
EIGSSTSSsSETVVK	FRMD6	122786	FERM domain-containing protein 6 isoform 3	S8(Phospho) S9(Phospho)	S(4): 0.0; S(5): 0.0; T(6): 0.0; S(7): 0.0; S(8): 100.0; S(9): 100.0; S(10): 0.0; T(12): 0.0	S8; S9;	S152; S153		2.84	0	0	2	829.3	1658	47.15	9109
GQSTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C12(Carbamido methyl) S6(Phospho)	S(3): 0.1; T(4): 0.1; S(6): 99.9; T(10): 0.0	S6;	S167		2.48	0	0	2	771.8	1543	46.73	9021
GQsTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C12(Carbamido methyl)S3(Phospho) S6(Phospho)	S(3): 96.9; T(4): 3.1; S(6): 100.0; T(10): 0.0	S3; S6;	S164; S167		2.42	0	0	2	811.8	1623	58.38	11529
LRGQsTDsLPQTICR	FRMD6	122786	FERM domain-containing protein 6 isoform 3	C14(Carbamido methyl)S5(Phospho) S8(Phospho)	S(5): 97.4; T(6): 5.2; S(8): 97.4; T(12): 0.0	S5; S8;	S164; S167		2.39	0	1	2	946.4	1892	49.54	9608
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.8; S(7): 4.5; S(8): 95.7; S(19): 0.0; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336	41		0	0	3	906	2716	76.96	15532
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 95.1; S(7): 9.7; S(8): 94.8; S(19): 0.3; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336	32		0	0	3	906	2716	76.43	15416
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.7; S(7): 5.3; S(8): 94.6; S(19): 0.3; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336	29		0	0	2	1359	2716	76.96	15531
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.6; S(7): 6.4; S(8): 93.6; S(19): 0.4; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336	25		0	0	2	1359	2716	76.43	15417
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.8; S(7): 4.5; S(8): 95.7; S(19): 0.0; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336		4.33	0	0	3	906	2716	76.96	15532
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 95.1; S(7): 9.7; S(8): 94.8; S(19): 0.3; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336		3.35	0	0	3	906	2716	76.43	15416
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.7; S(7): 5.3; S(8): 94.6; S(19): 0.3; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336		2.96	0	0	2	1359	2716	76.96	15531
ALDI sLSsGEEDEGDEEDSTAGTTK	FTSJ3	117246	pre-rRNA processing protein FTSJ3	S5(Phospho) S8(Phospho)	S(5): 99.6; S(7): 6.4; S(8): 93.6; S(19): 0.4; T(20): 0.0; T(23): 0.0; T(24): 0.0	S5; S8;	S333; S336		2.2	0	0	2	1359	2716	76.43	15417
GLPPEAWQEECPsDsEEDEGRGER	FURIN	5045	furin preproprotein	C11(Carbamido methyl)S13(Phospho) S15(Phospho)	S(13): 100.0; S(15): 100.0	S13; S15;	S773; S775	24		0	1	3	973.7	2919	60.41	11961

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#
GLPPEAWQEECPsDsEEDEGRGER	FURIN	5045	furin preproprotein	C11(Carbamido methyl)S13(Phospho) S15(Phospho)	S(13): 100.0; S(15): 100.0	S13; S15;	S773; S775		3.14	0	1	3	973.7	2919	60.41	11961
GLPPEAWQEECPsDsEEDEGRGER	FURIN	5045	furin preproprotein	C11(Carbamido methyl)S13(Phospho) S15(Phospho)	S(13): 100.0; S(15): 100.0	S13; S15;	S773; S775		2.28	0.003	1	3	973.7	2919	60.93	12075
RGPNYTSGYGTNSELSPsETESER	FXR1	8087	fragile X mental retardation syndrome-related protein 1 isoform c	S19(Phospho)	Y(5): 0.0; T(6): 0.0; S(7): 0.0; Y(9): 0.0; T(11): 0.0; S(13): 0.0; S(16): 0.0; S(19): 97.6; T(21): 2.4; S(23): 0.0	S19;	S324	53		0	1	3	938.1	2812	44.01	8416
KDELSDWSLAGEDDRDsR	FXR1	8087	fragile X mental retardation syndrome-related protein 1 isoform c	S5(Phospho) S17(Phospho)	S(5): 99.9; S(8): 3.7; S(17): 96.5	S5; S17;	S335; S347	30		0	2	3	752	2254	59.47	11780
RGPNYTSGYGTNSELSPsETESER	FXR1	8087	fragile X mental retardation syndrome-related protein 1 isoform c	S19(Phospho)	Y(5): 0.0; T(6): 0.0; S(7): 0.0; Y(9): 0.0; T(11): 0.0; S(13): 0.0; S(16): 0.0; S(19): 97.6; T(21): 2.4; S(23): 0.0	S19;	S324		5.06	0	1	3	938.1	2812	44.01	8416
KDELSDWSLAGEDDRDsR	FXR1	8087	fragile X mental retardation syndrome-related protein 1 isoform c	S5(Phospho) S17(Phospho)	S(5): 99.9; S(8): 3.7; S(17): 96.5	S5; S17;	S335; S347		3.98	0	2	3	752	2254	59.47	11780
TDGSLsGDRQPVTVADYISR	FXR2	9513	fragile X mental retardation syndrome-related protein 2	S4(Phospho) S6(Phospho)	T(1): 7.2; S(4): 96.4; S(6): 96.4; T(13): 0.0; Y(17): 0.0; S(19): 0.0	S4; S6;	S601; S603	23		0	1	3	766.3	2297	70.2	14205
TDGSLsGDRQPVTVADYISR	FXR2	9513	fragile X mental retardation syndrome-related protein 2	S4(Phospho) S6(Phospho)	T(1): 7.2; S(4): 96.4; S(6): 96.4; T(13): 0.0; Y(17): 0.0; S(19): 0.0	S4; S6;	S601; S603		3.21	0	1	3	766.3	2297	70.2	14205
SPVNEDNQDGVTHSDGAGNLDEEQDs EGETYEDIEASK	FYB	2533	FYN-binding protein isoform 2	S26(Phospho)	S(1): 0.0; T(12): 0.0; S(14): 0.0; S(26): 94.4; T(30): 5.3; Y(31): 0.3; S(37): 0.0	S26;	S457	35		0	0	4	1041	4161	55.64	10934
SPVNEDNQDGVTHSDGAGNLDEEQDs EGETYEDIEASK	FYB	2533	FYN-binding protein isoform 2	S26(Phospho)	S(1): 0.0; T(12): 0.0; S(14): 0.0; S(26): 94.4; T(30): 5.3; Y(31): 0.3; S(37): 0.0	S26;	S457		3.89	0	0	4	1041	4161	55.64	10934
SSsPAPADIAQTVQEDLR	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S3(Phospho)	S(1): 2.9; S(2): 2.9; S(3): 94.2; T(12): 0.0	S3;	S232	39		0	0	2	983	1965	81.01	16308
YQDEVFGGFVTEPQEEsEEEEVEEPEER	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S17(Phospho)	Y(1): 0.0; T(11): 0.2; S(17): 99.8	S17;	S149	34		0	0	3	1099	3296	84.84	17010
SSsPAPADIAQTVQEDLR	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S3(Phospho)	S(1): 0.1; S(2): 0.1; S(3): 99.9; T(12): 0.0	S3;	S232	33		0	0	2	983	1965	80.47	16208
SSsPAPADIAQTVQEDLR	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S3(Phospho)	S(1): 0.1; S(2): 0.1; S(3): 99.9; T(12): 0.0	S3;	S232		3.4	0	0	2	983	1965	80.47	16208
YQDEVFGGFVTEPQEEsEEEEVEEPEER	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S17(Phospho)	Y(1): 0.0; T(11): 0.2; S(17): 99.8	S17;	S149		3.27	0	0	3	1099	3296	84.84	17010
SSsPAPADIAQTVQEDLR	G3BP1	10146	ras GTPase-activating protein-binding protein 1	S3(Phospho)	S(1): 2.9; S(2): 2.9; S(3): 94.2; T(12): 0.0	S3;	S232		3.19	0	0	2	983	1965	81.01	16308
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 100.0; S(17): 0.0; S(18): 0.0	S4; S11;	S100; S107	55		0	0	3	784	2350	62.67	12470
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S17(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.0; S(17): 100.0; S(18): 100.0	S4; S17; S18;	S100; S113; S114	43		0	0	3	810.7	2430	73.87	14931
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.0; S(17): 2.7; S(18): 97.3	S4; S18;	S100; S114	35		0	0	3	784	2350	65.57	13178

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#
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S17(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.5; S(17): 99.8; S(18): 99.8	S4; S17; S18;	S100; S113; S114	29		0	0	3	810.7	2430	73.7	14902
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 98.2; S(17): 50.9; S(18): 50.9	S4; S11;	S100; S107	29		0	0	3	810.7	2430	73.37	14836
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S17(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.0; S(17): 100.0; S(18): 100.0	S4; S17; S18;	S100; S113; S114	5.59	0	0	0	3	810.7	2430	73.87	14931
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 100.0; S(17): 0.0; S(18): 0.0	S4; S11;	S100; S107	5.35	0	0	0	3	784	2350	62.67	12470
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S17(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.5; S(17): 99.8; S(18): 99.8	S4; S17; S18;	S100; S113; S114	5.09	0	0	0	3	810.7	2430	73.7	14902
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 98.2; S(17): 50.9; S(18): 50.9	S4; S11;	S100; S107	3.99	0	0	0	3	810.7	2430	73.37	14836
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S18(Phospho)	S(4): 100.0; S(11): 0.0; S(17): 2.7; S(18): 97.3	S4; S18;	S100; S114	3.77	0	0	0	3	784	2350	65.57	13178
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 100.0; S(17): 50.0; S(18): 50.0	S4; S11;	S100; S107	2.93	0.001	0	0	2	1216	2430	73.52	14865
RPPsPDVIVLSDNEQPSSPR	GATAD2A	54815	transcriptional repressor p66-alpha isoform 2	S4(Phospho) S11(Phospho)	S(4): 100.0; S(11): 100.0; S(17): 50.0; S(18): 50.0	S4; S11;	S100; S107	19	0.002	0	0	2	1216	2430	73.52	14865
GRLLPsPDIIVLSDNEASSPR	GATAD2B	57459	transcriptional repressor p66-beta	T4(Phospho) S6(Phospho) S13(Phospho)	T(4): 100.0; S(6): 100.0; S(13): 100.0; S(18): 0.0; S(19): 0.0	T4; S6; S13;	T120; S122; S129	57		0	1	3	822	2464	86.23	17273
GRLLPSPDIIVLSDNEASSPR	GATAD2B	57459	transcriptional repressor p66-beta	T4(Phospho) S13(Phospho) S19(Phospho)	T(4): 100.0; S(6): 0.0; S(13): 96.6; S(18): 6.8; S(19): 96.6	T4; S13; S19;	T120; S129; S135	50		0	1	3	822	2464	89.4	17887
GRLLPSPDIIVLSDNEASSPR	GATAD2B	57459	transcriptional repressor p66-beta	T4(Phospho) S13(Phospho) S19(Phospho)	T(4): 100.0; S(6): 0.0; S(13): 96.6; S(18): 6.8; S(19): 96.6	T4; S13; S19;	T120; S129; S135	4.23	0	1	1	3	822	2464	89.4	17887
AASSSsPGsPVASSPSR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S6(Phospho) S9(Phospho)	S(3): 2.8; S(4): 2.8; S(5): 2.8; S(6): 91.5; S(9): 100.0; S(13): 0.0; S(14): 0.0; S(16): 0.0	S6; S9;	S1777; S1780	68		0	0	2	846.3	1692	30.02	5468
ADAPDAGAQsDSELPsyHQNDVSLDR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S10(Phospho)	S(10): 99.8; S(12): 0.2; S(16): 0.0; Y(17): 0.0; S(23): 0.0	S10;	S1298	29		0	0	3	946.7	2838	54.68	10735
GYTsDSEVYTDHGRPGK	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S4(Phospho)	Y(2): 0.1; T(3): 2.3; S(4): 95.3; S(6): 2.3; Y(9): 0.0; T(10): 0.0	S4;	S1318	16		0	0	3	650.3	1949	31.68	5810
ADAPDAGAQsDSELPsyHQNDVSLDR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S10(Phospho)	S(10): 99.8; S(12): 0.2; S(16): 0.0; Y(17): 0.0; S(23): 0.0	S10;	S1298	5.26	0	0	0	3	946.7	2838	54.68	10735
GYTsDSEVYTDHGRPGK	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S4(Phospho)	Y(2): 0.1; T(3): 2.3; S(4): 95.3; S(6): 2.3; Y(9): 0.0; T(10): 0.0	S4;	S1318	3.47	0	0	0	3	650.3	1949	31.68	5810
AASSSsPGsPVASSPSR	GBF1	8729	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 isoform 3	S6(Phospho) S9(Phospho)	S(3): 2.8; S(4): 2.8; S(5): 2.8; S(6): 91.5; S(9): 100.0; S(13): 0.0; S(14): 0.0; S(16): 0.0	S6; S9;	S1777; S1780	3.17	0	0	0	2	846.3	1692	30.02	5468
REsEDDPesEPDDHEKR	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180	22		0	2	3	743.9	2230	14.51	2167
REsEDDPesEPDDHEK	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180	20		0	1	3	691.9	2074	16.32	2551
REsEDDPesEPDDHEK	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180	4.96	0	1	1	3	691.9	2074	16.32	2551
REsEDDPesEPDDHEKR	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180	4.25	0	2	2	3	743.9	2230	14.51	2167

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#
REsEDDPeEPDDHEK	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180	12		0.003	1	2	1037	2074	16.3	2547
REsEDDPeEPDDHEK	GCFC2	6936	GC-rich sequence DNA-binding factor 2 isoform 3	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0	S3; S9;	S174; S180		2.84	0.003	1	2	1037	2074	16.3	2547
VDsTTCLFPVVEEK	GFPT1	2673	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform 2	C6(Carbamidomethyl) S3(Phospho)	S(3): 97.9; T(4): 2.1; T(5): 0.1	S3;	S243	34		0	0	2	802.8	1605	71.39	14438
VDsTTCLFPVVEEK	GFPT1	2673	glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 isoform 2	C6(Carbamidomethyl) S3(Phospho)	S(3): 97.9; T(4): 2.1; T(5): 0.1	S3;	S243		2.33	0	0	2	802.8	1605	71.39	14438
ALsSGGSITSPPLsPALPK	GIGYF2	26058	PERQ amino acid-rich with GYF domain-containing protein 2 isoform c	S3(Phospho) S14(Phospho)	S(3): 93.4; S(4): 3.3; S(7): 3.3; T(9): 0.0; S(10): 0.0; S(14): 100.0	S3; S14;	S19; S30	12		0.007	0	2	970.5	1940	85.3	17100
ALsSGGSITSPPLsPALPK	GIGYF2	26058	PERQ amino acid-rich with GYF domain-containing protein 2 isoform c	S3(Phospho) S14(Phospho)	S(3): 93.4; S(4): 3.3; S(7): 3.3; T(9): 0.0; S(10): 0.0; S(14): 100.0	S3; S14;	S19; S30		1.9	0.007	0	2	970.5	1940	85.3	17100
SQsDLDDQHdYDSVAsDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S3(Phospho) S16(Phospho)	S(1): 5.6; S(3): 94.4; Y(11): 0.4; S(13): 0.4; S(16): 98.9; T(20): 0.4	S3; S16;	S375; S388	43		0	0	3	1047	3140	57.93	11431
SQsDLDDQHdYDSVAsDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S16(Phospho)	S(1): 0.0; S(3): 0.0; Y(11): 0.2; S(13): 0.2; S(16): 99.5; T(20): 0.0	S16;	S388	40		0	0	3	1021	3060	53.04	10372
HGsGADsDYENTQSGDPLLGLEK	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; Y(9): 0.0; T(12): 0.0; S(14): 0.0	S3; S7;	S592; S596	37		0	0	3	869.7	2607	75.11	15182
HGsGADsDYENTQSGDPLLGLEK	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; Y(9): 0.0; T(12): 0.0; S(14): 0.0	S3; S7;	S592; S596		4.19	0	0	3	869.7	2607	75.11	15182
SQsDLDDQHdYDSVAsDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S16(Phospho)	S(1): 0.0; S(3): 0.0; Y(11): 0.2; S(13): 0.2; S(16): 99.5; T(20): 0.0	S16;	S388		3.25	0	0	3	1021	3060	53.04	10372
SQsDLDDQHdYDSVAsDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S3(Phospho) S16(Phospho)	S(1): 5.6; S(3): 94.4; Y(11): 0.4; S(13): 0.4; S(16): 98.9; T(20): 0.4	S3; S16;	S375; S388		3.14	0	0	3	1047	3140	57.93	11431
sQsDLDDQHdYDSVASDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S1(Phospho)	S(1): 92.2; S(3): 9.4; Y(11): 31.9; S(13): 31.9; S(16): 31.9; T(20): 2.6	S1;	S373		1.94	0.001	0	3	1047	3140	58.46	11550
sQsDLDDQHdYDSVASDEDTDQEPLR	GIT1	28964	ARF GTPase-activating protein GIT1 isoform 2	S1(Phospho)	S(1): 92.2; S(3): 9.4; Y(11): 31.9; S(13): 31.9; S(16): 31.9; T(20): 2.6	S1;	S373	20		0.003	0	3	1047	3140	58.46	11550
TINNQHsVesQDNDQPDYDSVASDEDT DLETTASK	GIT2	9815	ARF GTPase-activating protein GIT2 isoform 4	S10(Phospho)	T(1): 44.6; S(7): 44.6; S(10): 76.0; Y(18): 6.3; S(20): 6.3; S(23): 19.7; T(27): 2.4; T(31): 0.0; T(32): 0.0; S(34): 0.0	S10;	S384		3.21	0	0	3	1344	4029	57.31	11307
SAsWGSADQLK	GLCC1	113263	glucocorticoid-induced transcript 1 protein	S3(Phospho)	S(1): 2.6; S(3): 97.3; S(6): 0.1	S3;	S223	13		0	0	2	615.3	1230	48.92	9479
SAsWGSADQLK	GLCC1	113263	glucocorticoid-induced transcript 1 protein	S3(Phospho)	S(1): 2.6; S(3): 97.3; S(6): 0.1	S3;	S223		1.68	0	0	2	615.3	1230	48.92	9479
SVsKESVAsMGADsGDDFASDGSSSR	GOLGA1	2800	golgin subfamily A member 1	S14(Phospho)	S(1): 48.7; S(3): 48.7; S(6): 2.7; S(9): 0.3; S(14): 99.7; S(20): 0.0; S(23): 0.0; S(24): 0.0; S(25): 0.0	S14;	S41	24		0	1	3	899.3	2696	54.36	10664
SVsKESVAsMGADsGDDFASDGSSSR	GOLGA1	2800	golgin subfamily A member 1	S14(Phospho)	S(1): 48.7; S(3): 48.7; S(6): 2.7; S(9): 0.3; S(14): 99.7; S(20): 0.0; S(23): 0.0; S(24): 0.0; S(25): 0.0	S14;	S41		2.94	0	1	3	899.3	2696	54.36	10664
SSsKESLVR	GOLGA4	2803	golgin subfamily A member 4 isoform 2	S3(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(6): 100.0	S3; S6;	S89; S92	24		0.001	1	2	576.7	1152	22.56	3879

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#
SSsKEsLVR	GOLGA4	2803	golgin subfamily A member 4 isoform 2	S3(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(6): 100.0	S3; S6;	S89; S92		2.19	0.005	1	2	576.7	1152	22.56	3879
DLESCsDDDNQGSK	GPATCH4	54865	G patch domain-containing protein 4 isoform 2	C5(Carbamidomethyl) S6(Phospho)	S(4): 0.0; S(6): 100.0; S(13): 0.0	S6;	S130	50		0	0	2	825.3	1650	21.02	3552
DLESCsDDDNQGSK	GPATCH4	54865	G patch domain-containing protein 4 isoform 2	C5(Carbamidomethyl) S6(Phospho)	S(4): 0.0; S(6): 100.0; S(13): 0.0	S6;	S130		2.97	0	0	2	825.3	1650	21.02	3552
MATLTSGGGEKPNKDLESCsDDDNQGSK	GPATCH4	54865	G patch domain-containing protein 4 isoform 2	C18(Carbamidomethyl)S19(Phospho)	T(3): 48.1; T(5): 48.1; S(6): 10.9; S(17): 7.7; S(19): 85.1; S(26): 0.1	S19;	S130		2.74	0.004	1	3	1015	3044	37.29	7000
KPsVSEEVQATPNK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	S3(Phospho)	S(3): 98.6; S(5): 1.4; T(11): 0.0	S3;	S1029	54		0	0	2	797.4	1594	27.01	4825
GPKEPPGsGsPAPPR	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	S9(Phospho) S11(Phospho)	S(9): 100.0; S(11): 100.0	S9; S11;	S660; S662	29		0	0	2	844.4	1688	29.99	5461
ATGPPSQNSNIGTGRGSEGCsPEDKNS VTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C21(Carbamidomethyl)T2(Phospho) S22(Phospho)	T(2): 99.1; S(6): 0.8; S(9): 0.8; T(13): 0.7; S(17): 0.1; S(22): 98.5; S(28): 0.0; T(30): 0.0	T2; S22;	T983; S1003	12		0	2	4	845.4	3378	31.45	5764
ATGPPSQNSNIGTGRGSEGCsPEDKNS VTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C21(Carbamidomethyl)T2(Phospho) S9(Phospho)	T(2): 100.0; S(6): 0.4; S(9): 93.9; T(13): 5.7; S(17): 0.0; S(22): 0.0; S(28): 0.0; T(30): 0.0	T2; S9;	T983; S990	11		0	2	3	1127	3378	31.51	5777
ATGPPSQNSNIGTGRGSEGCsPEDKNS VTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C21(Carbamidomethyl)T2(Phospho) S22(Phospho)	T(2): 99.1; S(6): 0.8; S(9): 0.8; T(13): 0.7; S(17): 0.1; S(22): 98.5; S(28): 0.0; T(30): 0.0	T2; S22;	T983; S1003		6.97	0	2	4	845.4	3378	31.45	5764
KPsVSEEVQATPNK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	S3(Phospho)	S(3): 98.6; S(5): 1.4; T(11): 0.0	S3;	S1029		4.97	0	0	2	797.4	1594	27.01	4825
ATGPPSQNSNIGTGRGSEGCsPEDKNS VTAK	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	C21(Carbamidomethyl)T2(Phospho) S9(Phospho)	T(2): 100.0; S(6): 0.4; S(9): 93.9; T(13): 5.7; S(17): 0.0; S(22): 0.0; S(28): 0.0; T(30): 0.0	T2; S9;	T983; S990		3.57	0	2	3	1127	3378	31.51	5777
GPKEPPGsGsPAPPR	GPATCH8	23131	G patch domain-containing protein 8 isoform 3	S9(Phospho) S11(Phospho)	S(9): 100.0; S(11): 100.0	S9; S11;	S660; S662		3.46	0	0	2	844.4	1688	29.99	5461
GTLDEEDEADSDtDDIDHR	GPN1	11321	GPN-loop GTPase 1 isoform d	T14(Phospho)	T(2): 0.0; S(12): 0.0; T(14): 100.0	T14;	T245	57		0	0	3	786.3	2357	41.18	7819
GTLDEEDEADSDtDDIDHR	GPN1	11321	GPN-loop GTPase 1 isoform d	T14(Phospho)	T(2): 0.0; S(12): 0.0; T(14): 100.0	T14;	T245		4.66	0	0	3	786.3	2357	41.18	7819
DDQRStPDSTYSSEFKDAATEK	GRHL2	79977	grainyhead-like protein 2 homolog	T6(Phospho)	S(5): 4.1; T(6): 95.9; S(9): 0.0; T(10): 0.0; Y(11): 0.0; S(12): 0.0; S(14): 0.0; T(20): 0.0	T6;	T211	11		0	2	3	853.4	2558	43.38	8282
DDQRStPDSTYSSEFKDAATEK	GRHL2	79977	grainyhead-like protein 2 homolog	T6(Phospho)	S(5): 4.1; T(6): 95.9; S(9): 0.0; T(10): 0.0; Y(11): 0.0; S(12): 0.0; S(14): 0.0; T(20): 0.0	T6;	T211		2.51	0	2	3	853.4	2558	43.38	8282
ERsPsPTTIQSK	GSE1	23199	genetic suppressor element 1 isoform 2	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; T(8): 0.1; S(11): 0.0	S3; S5;	S722; S724	27		0	1	2	743.8	1487	29.59	5378
ERsPsPTTIQSK	GSE1	23199	genetic suppressor element 1 isoform 2	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(8): 0.0; S(11): 0.0	S3; S5;	S722; S724	27		0	1	2	743.8	1487	30.1	5484
ERsPsPTTIQSK	GSE1	23199	genetic suppressor element 1 isoform 2	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(8): 0.0; S(11): 0.0	S3; S5;	S722; S724		3.89	0	1	2	743.8	1487	30.1	5484
ERsPsPTTIQSK	GSE1	23199	genetic suppressor element 1 isoform 2	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; T(8): 0.1; S(11): 0.0	S3; S5;	S722; S724		3.24	0	1	2	743.8	1487	29.59	5378
TSsFAEPGGGGGGGGPGGSASGPG GTGGGK	GSK3A	2931	glycogen synthase kinase-3 alpha	S3(Phospho)	T(1): 4.2; S(2): 4.2; S(3): 91.6; S(21): 0.0; S(23): 0.0; T(28): 0.0	S3;	S21	35		0	0	3	838.4	2513	37.63	7072

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#
TSsFAEPGGGGGGGGPGGSASGPG GTGGGK	GSK3A	2931	glycogen synthase kinase-3 alpha	S3(Phospho)	T(1): 4.2; S(2): 4.2; S(3): 91.6; S(21): 0.0; S(23): 0.0; T(28): 0.0	S3;	S21		5.72	0	0	3	838.4	2513	37.63	7072
GNsRPGtPSAEGGSTSSTLR	GTF2F1	2962	general transcription factor IIF subunit 1	S3(Phospho) T7(Phospho)	S(3): 100.0; T(7): 100.0; S(9): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0; T(18): 0.0	S3; T7;	S385; T389	48		0	0	3	693.6	2079	30.41	5549
GNsRPGtPSAEGGSTSSTLR	GTF2F1	2962	general transcription factor IIF subunit 1	S3(Phospho) T7(Phospho)	S(3): 100.0; T(7): 100.0; S(9): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0; T(18): 0.0	S3; T7;	S385; T389	34		0	0	2	1040	2079	30.51	5570
STPQPSPGKttPNSGDVQVTEDAVR	GTF2F1	2962	general transcription factor IIF subunit 1	T10(Phospho) T11(Phospho)	S(1): 0.3; T(2): 0.3; S(7): 9.9; T(10): 89.8; T(11): 89.8; S(14): 9.9; T(20): 0.0	T10; T11;	T445; T446	31		0	1	3	910.1	2728	50.4	9788
GNsRPGtPSAEGGSTSSTLR	GTF2F1	2962	general transcription factor IIF subunit 1	S3(Phospho) T7(Phospho)	S(3): 100.0; T(7): 100.0; S(9): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0; T(18): 0.0	S3; T7;	S385; T389		4.45	0	0	3	693.6	2079	30.41	5549
STPQPSPGKttPNSGDVQVTEDAVR	GTF2F1	2962	general transcription factor IIF subunit 1	T10(Phospho) T11(Phospho)	S(1): 0.3; T(2): 0.3; S(7): 9.9; T(10): 89.8; T(11): 89.8; S(14): 9.9; T(20): 0.0	T10; T11;	T445; T446		3.83	0	1	3	910.1	2728	50.4	9788
GNsRPGtPSAEGGSTSSTLR	GTF2F1	2962	general transcription factor IIF subunit 1	S3(Phospho) T7(Phospho)	S(3): 100.0; T(7): 100.0; S(9): 0.0; S(14): 0.0; T(15): 0.0; S(16): 0.0; S(17): 0.0; T(18): 0.0	S3; T7;	S385; T389		1.93	0	0	2	1040	2079	30.51	5570
LDTGPQSLsGKStPQPSPGK	GTF2F1	2962	general transcription factor IIF subunit 1	S9(Phospho) T13(Phospho)	T(3): 0.0; S(7): 0.1; S(9): 99.9; S(12): 3.5; T(13): 96.5; S(18): 0.0	S9; T13;	S433; T437		3.57	0.001	1	3	714.7	2142	40.4	7660
TNtPVKEDWNVR	GTF2I	2969	general transcription factor II-I isoform 4	T3(Phospho)	T(1): 1.8; T(3): 98.2	T3;	T517	37		0	1	2	769.9	1539	40.11	7596
TNtPVKEDWNVR	GTF2I	2969	general transcription factor II-I isoform 4	T3(Phospho)	T(1): 1.8; T(3): 98.2	T3;	T517		2.71	0	1	2	769.9	1539	40.11	7596
NSSTDQGsDEEGSLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S8(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; S(8): 100.0; S(13): 0.0	S8;	S1068	76		0	0	2	881.3	1762	21.8	3715
KNSSTDQGsDEEGSLQKEQESAMDK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	T5(Phospho) S9(Phospho)	S(3): 3.5; S(4): 3.5; T(5): 92.9; S(9): 99.8; S(14): 0.2; S(21): 0.0	T5; S9;	T1064; S1068	39		0	2	3	963.4	2888	37.97	7142
KNSSTDQGSDEEGsLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	T5(Phospho) S14(Phospho)	S(3): 2.2; S(4): 2.2; T(5): 95.6; S(9): 0.0; S(14): 100.0	T5; S14;	T1064; S1073	33		0	1	2	985.4	1970	20.43	3429
EDPQARPLEGSSSEDSPPPEGQAPPSHsP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.0; S(27): 100.0	S27;	S1856	31		0	0	3	1041	3121	34.05	6303
NSSTDQGsDEEGSLQKEQESAMDK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S8(Phospho)	S(2): 3.2; S(3): 0.1; T(4): 0.0; S(8): 96.7; S(13): 0.0; S(20): 0.0	S8;	S1068	29		0	1	3	894	2680	38.74	7301
EDPQARPLEGSSSEDSPPPEGQAPPSHsP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.2; S(27): 99.8	S27;	S1856	24		0	0	4	781.1	3121	33.89	6270
EDPQARPLEGSSSEDSPPPEGQAPPSHsP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.1; S(27): 99.9	S27;	S1856	21		0	0	4	781.1	3121	34.44	6386
TSQPPVPQGEAEEDsQGKEGPSGSGDS QLSASSR	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S15(Phospho)	T(1): 0.0; S(2): 0.0; S(15): 100.0; S(22): 0.0; S(24): 0.0; S(27): 0.0; S(30): 0.0; S(32): 0.0; S(33): 0.0	S15;	S739	16		0	1	3	1156	3466	39.89	7550
EDPQARPLEGSSSEDSPPPEGQAPPSHsP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.2; S(27): 99.8	S27;	S1856		7.81	0	0	4	781.1	3121	33.89	6270

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#
EDPQARPLEGSSSEDSPPPEGQAPPShSP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.0; S(27): 100.0	S27;	S1856		6.29	0	0	3	1041	3121	34.05	6303
EDPQARPLEGSSSEDSPPPEGQAPPShSP R	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S27(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 0.0; S(16): 0.0; S(25): 0.1; S(27): 99.9	S27;	S1856		5.71	0	0	4	781.1	3121	34.44	6386
KNSSTDQGsDEEGSLQKEQESAMDK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	T5(Phospho) S9(Phospho)	S(3): 3.5; S(4): 3.5; T(5): 92.9; S(9): 99.8; S(14): 0.2; S(21): 0.0	T5; S9;	T1064; S1068		5.38	0	2	3	963.4	2888	37.97	7142
NSSTDQGsDEEGSLQKEQESAMDK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S8(Phospho)	S(2): 3.2; S(3): 0.1; T(4): 0.0; S(8): 96.7; S(13): 0.0; S(20): 0.0	S8;	S1068		4.93	0	1	3	894	2680	38.74	7301
TSQPPVPQGEAEEDsQGKEGPSGSGDS QLSASSR	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S15(Phospho)	T(1): 0.0; S(2): 0.0; S(15): 100.0; S(22): 0.0; S(24): 0.0; S(27): 0.0; S(30): 0.0; S(32): 0.0; S(33): 0.0	S15;	S739		3.24	0	1	3	1156	3466	39.89	7550
KNSSTDQGsDEEGsLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	T5(Phospho) S14(Phospho)	S(3): 2.2; S(4): 2.2; T(5): 95.6; S(9): 0.0; S(14): 100.0	T5; S14;	T1064; S1073		3.24	0	1	2	985.4	1970	20.43	3429
NSSTDQGsDEEGSLQK	GTF3C1	2975	general transcription factor 3C polypeptide 1 isoform 2	S8(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; S(8): 100.0; S(13): 0.0	S8;	S1068		2.59	0	0	2	881.3	1762	21.8	3715
DLDRPESQsPK	GTF3C2	2976	general transcription factor 3C polypeptide 2	S9(Phospho)	S(7): 0.0; S(9): 100.0	S9;	S167	25		0	0	2	676.3	1352	19.73	3281
DLDRPESQsPK	GTF3C2	2976	general transcription factor 3C polypeptide 2	S9(Phospho)	S(7): 0.0; S(9): 100.0	S9;	S167		3.35	0.003	0	2	676.3	1352	19.73	3281
GKLSAEENPDDSEVPSSSGINSTK	GTF3C3	9330	general transcription factor 3C polypeptide 3 isoform 2	S4(Phospho)	S(4): 100.0; S(12): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; S(22): 0.0; T(23): 0.0	S4;	S43	30		0	1	3	843.4	2528	41.35	7855
GKLSAEENPDDSEVPSSSGINSTK	GTF3C3	9330	general transcription factor 3C polypeptide 3 isoform 2	S4(Phospho)	S(4): 100.0; S(12): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; S(22): 0.0; T(23): 0.0	S4;	S43		6.85	0	1	3	843.4	2528	41.35	7855
ILLVDsPGMGNADDEQQEEGTSSK	GTF3C4	9329	general transcription factor 3C polypeptide 4	S6(Phospho)	S(6): 100.0; T(21): 0.0; S(22): 0.0; S(23): 0.0	S6;	S611	27		0	0	3	867.4	2600	68.69	13893
ILLVDsPGMGNADDEQQEEGTSSK	GTF3C4	9329	general transcription factor 3C polypeptide 4	S6(Phospho)	S(6): 100.0; T(21): 0.0; S(22): 0.0; S(23): 0.0	S6;	S611		3.91	0	0	3	867.4	2600	68.69	13893
LHGGFDsDCsEDGEALNGEPELDLTSK	GTPBP1	9567	GTP-binding protein 1	C9(Carbamidomethyl)S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0; T(25): 0.0; S(26): 0.0	S7; S10;	S44; S47	19		0	0	3	1018	3052	78.42	15800
LHGGFDsDCsEDGEALNGEPELDLTSK	GTPBP1	9567	GTP-binding protein 1	C9(Carbamidomethyl)S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0; T(25): 0.0; S(26): 0.0	S7; S10;	S44; S47		3.98	0	0	3	1018	3052	78.42	15800
FSIGDsPDSSTPK	GTSE1	51512	G2 and S phase-expressed protein 1	S6(Phospho)	S(2): 0.0; S(6): 99.9; S(9): 49.0; S(10): 49.0; T(11): 2.0	S6;	S480		1.73	0.003	0	2	749.3	1498	60.64	12012
AAsADsTTEGTPADGFTVLSTK	H2AFY	9555	core histone macro-H2A.1 isoform 1	S3(Phospho) S6(Phospho)	S(3): 99.8; S(6): 96.3; T(7): 3.7; T(8): 0.2; T(11): 0.0; T(17): 0.0; S(20): 0.0; T(21): 0.0	S3; S6;	S170; S173	22		0	0	2	1144	2287	86.64	17353
AAsADsTTEGTPADGFTVLSTK	H2AFY	9555	core histone macro-H2A.1 isoform 1	S3(Phospho) S6(Phospho)	S(3): 99.8; S(6): 96.3; T(7): 3.7; T(8): 0.2; T(11): 0.0; T(17): 0.0; S(20): 0.0; T(21): 0.0	S3; S6;	S170; S173		2.56	0	0	2	1144	2287	86.64	17353

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#
AAaADSTTEGTPADGFTVLSTK	H2AFY	9555	core histone macro-H2A.1 isoform 1	S3(Phospho)	S(3): 96.6; S(6): 48.6; T(7): 48.6; T(8): 3.0; T(11): 3.0; T(17): 0.0; S(20): 0.0; T(21): 0.0	S3;	S170		2.42	0.003	0	2	1144	2287	86.6	17344
SLPAPVAQRPDsPGGGLQAPGQK	HABP4	22927	intracellular hyaluronan-binding protein 4	S12(Phospho)	S(1): 0.0; S(12): 100.0	S12;	S108		3.52	0	0	3	770.1	2308	50.91	9897
MTGEPDNNRstSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	S10(Phospho) T11(Phospho)	T(2): 0.0; S(10): 95.9; T(11): 95.9; S(12): 7.6; T(16): 0.5	S10; T11;	S326; T327	23		0	1	3	808	2422	43.74	8358
MTGEPDNNRstSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	M1(Oxidation) S10(Phospho) T11(Phospho)	T(2): 0.0; S(10): 99.8; T(11): 95.7; S(12): 4.5; T(16): 0.0	S10; T11;	S326; T327	20		0	1	3	813.3	2438	38.82	7320
KMtGEPDNNRSTSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	M2(Oxidation) T3(Phospho)	T(3): 99.8; S(11): 48.8; T(12): 48.8; S(13): 2.5; T(17): 0.1	T3;	T318		5.65	0	2	3	856	2566	30.45	5557
MTGEPDNNRstSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	S10(Phospho) T11(Phospho)	T(2): 0.0; S(10): 95.9; T(11): 95.9; S(12): 7.6; T(16): 0.5	S10; T11;	S326; T327		4.38	0	1	3	808	2422	43.74	8358
MTGEPDNNRstSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	M1(Oxidation) S10(Phospho) T11(Phospho)	T(2): 0.0; S(10): 99.8; T(11): 95.7; S(12): 4.5; T(16): 0.0	S10; T11;	S326; T327		3.97	0	1	3	813.3	2438	38.82	7320
KMtGEPDNNRSTSVELTGDPNK	HCAR2	338442	hydroxycarboxylic acid receptor 2	M2(Oxidation) T3(Phospho)	T(3): 99.8; S(11): 48.8; T(12): 48.8; S(13): 2.5; T(17): 0.1	T3;	T318	12		0.002	2	3	856	2566	30.45	5557
ITGEPDNNRSTSVELTGDPNK	HCAR3	8843	hydroxycarboxylic acid receptor 3	T16(Phospho)	T(2): 0.0; S(10): 34.5; T(11): 34.5; S(12): 32.9; T(16): 98.2	T16;	T332	17		0	1	3	802	2404	45	8652
ITGEPDNNRSTSVELTGDPNK	HCAR3	8843	hydroxycarboxylic acid receptor 3	T16(Phospho)	T(2): 0.0; S(10): 34.5; T(11): 34.5; S(12): 32.9; T(16): 98.2	T16;	T332		5.2	0	1	3	802	2404	45	8652
IACEEEFsDsEEEEGEGGR	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423	76		0	0	2	1095	2190	50.91	9896
IACEEEFsDsEEEEGEGGR	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423	49		0	0	2	1095	2190	50.41	9790
IACEEEFsDsEEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423	38		0	1	3	773.3	2318	39.2	7399
IACEEEFsDsEEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423	28		0	1	2	1159	2318	39.11	7381
IACEEEFsDsEEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		6.2	0	1	3	773.3	2318	39.2	7399
IACEEEFsDsEEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		4.83	0	1	3	773.3	2318	39.77	7522
IACEEEFsDsEEEEGEGGR	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl) S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		4.42	0	0	2	1095	2190	50.91	9896

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#
IACEEEFsDsEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		4.08	0	1	3	773.3	2318	40.32	7642
IACEEEFsDsEEEGEGGR	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		3.95	0	0	2	1095	2190	50.41	9790
IACEEEFsDsEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		3.84	0	1	2	1159	2318	39.11	7381
IACEEEFsDsEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423		2.54	0.001	1	2	1159	2318	39.64	7496
IACEEEFsDsEEEGEGGRK	HDAC1	3065	histone deacetylase 1	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S421; S423	14		0.002	1	3	773.3	2318	39.77	7522
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424	49		0	1	3	773.3	2318	38.65	7282
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424	40		0	0	2	1081	2162	49.49	9598
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424	25		0	1	3	773.3	2318	40.32	7642
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424	19		0	1	2	1159	2318	38.61	7274
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424		5.64	0	1	3	773.3	2318	38.65	7282
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424		3.52	0	0	2	1081	2162	49.49	9598
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424		2.61	0.001	1	2	1159	2318	38.61	7274
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424		3.79	0.005	1	3	773.3	2318	40.93	7769
IACDEEFsDsEDEGEGR	HDAC2	3066	histone deacetylase 2	C3(Carbamidomethyl)S8(Phospho)S10(Phospho)	S(8): 100.0; S(10): 100.0	S8; S10;	S422; S424	14		0.008	1	3	773.3	2318	40.93	7769
GESAEDEKHEEGRDSEEGPR	HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 2	S15(Phospho)	S(3): 0.0; S(15): 100.0	S15;	S625	20		0	2	4	581.5	2323	13.79	2016

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#
GEAERGSGGssGDELREDDEPVK	HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 2	S7(Phospho) S10(Phospho) S11(Phospho)	S(7): 100.0; S(10): 100.0; S(11): 100.0	S7; S10; S11;	S366; S369; S370	14		0	2	3	872.7	2616	38.36	7223
GESAEDKEHEEGRDSEEGPR	HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 2	S15(Phospho)	S(3): 0.0; S(15): 100.0	S15;	S625		6.81	0	2	4	581.5	2323	13.79	2016
GEAERGSGGssGDELREDDEPVK	HDGFRP2	84717	hepatoma-derived growth factor-related protein 2 isoform 2	S7(Phospho) S10(Phospho) S11(Phospho)	S(7): 100.0; S(10): 100.0; S(11): 100.0	S7; S10; S11;	S366; S369; S370		3.61	0	2	3	872.7	2616	38.36	7223
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	84		0	0	2	673.3	1346	19.47	3226
VsTLAGPSSDDENEESKPEKEDEPQEDAK	HECTD1	25831	E3 ubiquitin-protein ligase HECTD1	S2(Phospho)	S(2): 95.0; T(3): 5.0; S(8): 0.0; S(9): 0.0; S(17): 0.0	S2;	S625		4.66	0	1	4	843.1	3369	33.31	6149
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		3.15	0	0	2	673.3	1346	19.47	3226
VsTLAGPSSDDENEESKPEKEDEPQEDAK	HECTD1	25831	E3 ubiquitin-protein ligase HECTD1	S2(Phospho)	S(2): 94.2; T(3): 5.8; S(8): 0.0; S(9): 0.0; S(17): 0.0	S2;	S625		2.86	0	1	3	1124	3369	33.32	6154
SRSESDLSQPEsDEEGYALSGR	HERC1	8925	probable E3 ubiquitin-protein ligase HERC1	S12(Phospho)	S(1): 50.0; S(3): 50.0; S(5): 0.0; S(8): 0.1; S(12): 99.9; Y(17): 0.0; S(20): 0.0	S12;	S1521	36		0	1	3	853.7	2559	54.28	10646
SRSESDLSQPEsDEEGYALSGR	HERC1	8925	probable E3 ubiquitin-protein ligase HERC1	S12(Phospho)	S(1): 50.0; S(3): 50.0; S(5): 0.0; S(8): 0.1; S(12): 99.9; Y(17): 0.0; S(20): 0.0	S12;	S1521		3.83	0	1	3	853.7	2559	54.28	10646
LAELPAAAPsAEDSDTEDDSEAEQTER	HERC2	8924	E3 ubiquitin-protein ligase HERC2	S11(Phospho)	S(11): 93.3; S(15): 35.6; T(17): 35.6; S(21): 35.6; T(26): 0.0	S11;	S1938	27		0	0	3	1046	3135	69.17	13987
LAELPAAAPsAEDSDTEDDSEAEQTER	HERC2	8924	E3 ubiquitin-protein ligase HERC2	S11(Phospho)	S(11): 93.3; S(15): 35.6; T(17): 35.6; S(21): 35.6; T(26): 0.0	S11;	S1938		2.47	0	0	3	1046	3135	69.17	13987
TQsPGGCSAEAVLAR	HEXIM2	124790	protein HEXIM2 isoform 1	C7(Carbamidomethyl) S3(Phospho)	T(1): 1.9; S(3): 98.1; S(8): 0.0	S3;	S76	64		0	0	2	792.3	1584	48.67	9426
TQsPGGCSAEAVLAR	HEXIM2	124790	protein HEXIM2 isoform 1	C7(Carbamidomethyl) S3(Phospho) S8(Phospho)	T(1): 0.1; S(3): 99.9; S(8): 100.0	S3; S8;	S76; S81	62		0	0	2	832.3	1664	58.77	11631
TQsPGGCSAEAVLAR	HEXIM2	124790	protein HEXIM2 isoform 1	C7(Carbamidomethyl) S3(Phospho)	T(1): 1.9; S(3): 98.1; S(8): 0.0	S3;	S76		3.12	0	0	2	792.3	1584	48.67	9426
TQsPGGCSAEAVLAR	HEXIM2	124790	protein HEXIM2 isoform 1	C7(Carbamidomethyl) S3(Phospho) S8(Phospho)	T(1): 0.1; S(3): 99.9; S(8): 100.0	S3; S8;	S76; S81		2.9	0	0	2	832.3	1664	58.77	11631
AVEssDEERQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S5(Phospho) S6(Phospho)	S(5): 100.0; S(6): 100.0	S5; S6;	S142; S143	47		0	1	2	797.8	1595	13.72	2001
KQAREEsEESEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S196	44		0	2	3	694.6	2082	18.76	3076
GEEsEEEEKGYK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; Y(12): 0.0	S4; S5;	S159; S160	40		0	1	2	830.8	1661	19.1	3148
KQAREEsEESEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	39		0	2	3	721.3	2162	20.12	3361
RLsGsEDEEDSGKGEPTAK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S3(Phospho) S5(Phospho) S6(Phospho)	S(3): 100.0; S(5): 100.0; S(6): 100.0; S(12): 0.0; T(18): 0.0	S3; S5; S6;	S330; S332; S333	36		0	2	3	773.6	2319	23.16	4007
SLKESEQEsEEIILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S9(Phospho)	S(1): 50.0; S(5): 50.0; S(9): 100.0	S9;	S227	27		0	1	3	713	2137	50.7	9851
SLKESEQEsEEIILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S9(Phospho)	S(1): 50.0; S(5): 50.0; S(9): 99.9	S9;	S227	25		0	1	2	1069	2137	50.75	9863

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#
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	21		0	2	2	1081	2162	20.18	3374
SLKEsEQEsEEEILAQKK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S5(Phospho) S9(Phospho)	S(1): 0.0; S(5): 100.0; S(9): 100.0	S5; S9;	S223; S227	18		0	2	3	755.7	2265	40.8	7741
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	17		0	2	3	721.3	2162	20.73	3492
sLKEsEQEsEEEILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S1(Phospho) S9(Phospho)	S(1): 95.0; S(5): 5.3; S(9): 99.7	S1; S9;	S219; S227	17		0	1	3	713	2137	51.23	9963
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	6.4	0	0	2	3	721.3	2162	20.12	3361
RLsGssEDEEDSGKGPE TAK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S3(Phospho) S5(Phospho) S6(Phospho)	S(3): 100.0; S(5): 100.0; S(6): 100.0; S(12): 0.0; T(18): 0.0	S3; S5; S6;	S330; S332; S333	5.62	0	0	2	3	773.6	2319	23.16	4007
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S196	4.65	0	0	2	3	694.6	2082	18.76	3076
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	4.15	0	0	2	3	721.3	2162	20.73	3492
SLKEsEQEsEEEILAQKK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S5(Phospho) S9(Phospho)	S(1): 0.0; S(5): 100.0; S(9): 100.0	S5; S9;	S223; S227	4	0	0	2	3	755.7	2265	40.8	7741
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	3.7	0	0	0	2	736.3	1472	20.47	3436
SLKEsEQEsEEEILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S9(Phospho)	S(1): 50.0; S(5): 50.0; S(9): 100.0	S9;	S227	3.47	0	0	1	3	713	2137	50.7	9851
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	3.4	0	0	0	2	736.3	1472	21.05	3560
DLP AQGEssEEEEKG YK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S10(Phospho) S11(Phospho)	S(10): 100.0; S(11): 100.0; Y(18): 0.1	S10; S11;	S159; S160	3.07	0	0	2	3	781	2341	29.97	5457
SLKEsEQEsEEEILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S9(Phospho)	S(1): 50.0; S(5): 50.0; S(9): 99.9	S9;	S227	2.97	0	0	1	2	1069	2137	50.75	9863
sLKEsEQEsEEEILAQK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S1(Phospho) S9(Phospho)	S(1): 95.0; S(5): 5.3; S(9): 99.7	S1; S9;	S219; S227	2.93	0	0	1	3	713	2137	51.23	9963
GEEsEEEEKG YK	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; Y(12): 0.0	S4; S5;	S159; S160	2.78	0	0	1	2	830.8	1661	19.1	3148
KQAREEEsEAEPVQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S196; S199	2.67	0	0	2	2	1081	2162	20.18	3374
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	16		0.002	0	2	736.3	1472	20.47	3436
AVEssDEERQR	HIRIP3	8479	HIRA-interacting protein 3 isoform 1	S5(Phospho) S6(Phospho)	S(5): 100.0; S(6): 100.0	S5; S6;	S142; S143	2.9	0.003	0.003	1	2	797.8	1595	13.72	2001
SETAPAETATPAPVEKsPAK	HIST1H1B	3009	histone H1.5	S17(Phospho)	S(1): 0.0; T(3): 0.0; T(8): 0.0; T(10): 0.0; S(17): 100.0	S17;	S18	31		0	1	2	1031	2062	31.45	5763
SETAPAETATPAPVEKsPAK	HIST1H1B	3009	histone H1.5	S17(Phospho)	S(1): 0.0; T(3): 0.0; T(8): 0.0; T(10): 0.0; S(17): 100.0	S17;	S18	27		0	1	3	688	2062	31.44	5762
SETAPAETATPAPVEKsPAKK	HIST1H1B	3009	histone H1.5	S17(Phospho)	S(1): 0.0; T(3): 0.0; T(8): 0.0; T(10): 0.0; S(17): 100.0	S17;	S18	22		0	2	3	730.7	2190	25.21	4437
SETAPAETATPAPVEKsPAKK	HIST1H1B	3009	histone H1.5	T8(Phospho) S17(Phospho)	S(1): 3.4; T(3): 3.4; T(8): 93.0; T(10): 0.1; S(17): 100.0	T8; S17;	T9; S18	17		0	2	4	568.3	2270	34.9	6499

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#
SETAPAETATPAPVEKsPAK	HIST1H1B	3009	histone H1.5	T10(Phospho) S17(Phospho)	S(1): 0.0; T(3): 0.0; T(8): 0.0; T(10): 100.0; S(17): 100.0	T10; S17;	T11; S18	15		0	1	3	714.7	2142	34.18	6331
SETAPAETATPAPVEKsPAK	HIST1H1B	3009	histone H1.5	S17(Phospho)	S(1): 0.0; T(3): 0.0; T(8): 50.0; T(10): 50.0; S(17): 100.0	S17;	S18	14		0	1	2	1071	2142	34.23	6341
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	66		0	2	3	799.6	2397	37.27	6995
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	53		0	2	3	826.3	2477	42.9	8179
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	50		0	2	3	799.6	2397	34.7	6448
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho)	S(11): 98.4; S(14): 50.8; S(15): 50.8	S11;	S99	49		0	2	3	799.6	2397	33.09	6105
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	47		0	2	3	799.7	2397	35.29	6580
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	47		0	2	3	799.7	2397	34.18	6329
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	44		0	2	3	799.6	2397	36.74	6886
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	43		0	2	3	826.3	2477	42.38	8070
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	42		0	2	2	1239	2477	40.83	7747
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	42		0	2	2	1199	2397	35.33	6589
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	41		0	2	3	826.3	2477	39.03	7363
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	40		0	2	2	1239	2477	39.24	7408
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	37		0	2	2	1239	2477	39.76	7521
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	36		0	2	3	826.3	2477	41.33	7852
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	35		0	2	3	826.3	2477	43.41	8287
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.0; S(14): 97.0; S(15): 100.0	S14; S15;	S102; S103	34		0	2	3	799.6	2397	35.98	6725
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.3; S(14): 96.8; S(15): 99.9	S14; S15;	S102; S103	34		0	2	3	799.6	2397	38.4	7231
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	32		0	2	2	1199	2397	34.82	6479
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	29		0	2	2	1199	2397	34.26	6347
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.4; S(14): 96.7; S(15): 99.9	S14; S15;	S102; S103	26		0	2	3	799.6	2397	39.17	7394
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S15(Phospho)	S(11): 0.0; S(14): 3.0; S(15): 97.0	S15;	S103	21		0	2	3	773	2317	30.58	5584
KQPPVSPGTLVGSQKPESEVPtPK	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S6(Phospho) T23(Phospho)	S(6): 100.0; T(9): 0.0; S(14): 0.0; S(19): 0.0; T(23): 100.0	S6; T23;	S36; T53	11		0	2	3	906.8	2718	53.1	10386

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#
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		6.59	0	2	3	799.7	2397	34.18	6329
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		6.45	0	2	3	799.7	2397	35.29	6580
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		5.3	0	2	3	799.6	2397	37.27	6995
KQPPVsPGTALVGSQKEPSEVPtPK	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S6(Phospho) T23(Phospho)	S(6): 100.0; T(9): 0.0; S(14): 0.0; S(19): 0.0; T(23): 100.0	S6; T23;	S36; T53		5.13	0	2	3	906.8	2718	53.1	10386
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S15(Phospho)	S(11): 0.0; S(14): 3.0; S(15): 97.0	S15;	S103		4.32	0	2	3	773	2317	30.58	5584
KQPPVsPGTALVGSQKEPSEVPtPK	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S6(Phospho) T23(Phospho)	S(6): 100.0; T(9): 0.0; S(14): 0.0; S(19): 0.0; T(23): 100.0	S6; T23;	S36; T53		3.85	0	2	3	906.8	2718	53.62	10494
KQPPVsPGTALVGSQKEPSEVPtPK	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S6(Phospho) T23(Phospho)	S(6): 100.0; T(9): 0.0; S(14): 0.0; S(19): 0.0; T(23): 100.0	S6; T23;	S36; T53		3.08	0	2	3	906.8	2718	54.15	10617
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S15(Phospho)	S(11): 96.5; S(14): 3.6; S(15): 99.9	S11; S15;	S99; S103	36		0.001	2	3	799.6	2397	33.66	6223
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		6.54	0.001	2	3	799.6	2397	34.7	6448
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		6.14	0.001	2	3	826.3	2477	39.03	7363
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho)	S(11): 98.4; S(14): 50.8; S(15): 50.8	S11;	S99		5.52	0.001	2	3	799.6	2397	33.09	6105
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		5.27	0.001	2	3	799.6	2397	36.74	6886
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.3; S(14): 96.8; S(15): 99.9	S14; S15;	S102; S103		4.43	0.001	2	3	799.6	2397	38.4	7231
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		4.22	0.001	2	2	1199	2397	35.33	6589
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		4.06	0.001	2	2	1239	2477	40.83	7747
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	34		0.002	2	3	826.3	2477	41.86	7963
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103	27		0.002	2	2	1199	2397	36.36	6806
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.6; S(14): 96.5; S(15): 99.9	S14; S15;	S102; S103	24		0.002	2	2	1199	2397	35.85	6698
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		5.07	0.002	2	3	826.3	2477	42.9	8179
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	42		0.003	2	3	826.3	2477	39.61	7488
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103	36		0.003	2	2	1239	2477	40.3	7638
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S15(Phospho)	S(11): 0.0; S(14): 2.8; S(15): 97.2	S15;	S103	19		0.003	2	2	1159	2317	29.59	5376
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		5.71	0.003	2	3	826.3	2477	41.86	7963
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		5.66	0.003	2	3	826.3	2477	41.33	7852

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#
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		5	0.003	2	2	1199	2397	34.26	6347
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		4.59	0.003	2	3	826.3	2477	43.41	8287
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		4.53	0.003	2	2	1199	2397	34.82	6479
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.4; S(14): 96.7; S(15): 99.9	S14; S15;	S102; S103		3.65	0.003	2	3	799.6	2397	39.17	7394
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.6; S(14): 96.5; S(15): 99.9	S14; S15;	S102; S103		3.47	0.003	2	2	1199	2397	35.85	6698
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S15(Phospho)	S(11): 99.9; S(14): 3.7; S(15): 96.4	S11; S15;	S99; S103	26		0.004	2	2	1199	2397	33.19	6125
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S15(Phospho)	S(11): 99.9; S(14): 3.7; S(15): 96.4	S11; S15;	S99; S103		3.52	0.004	2	2	1199	2397	33.19	6125
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		6.5	0.005	2	3	826.3	2477	39.61	7488
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S15(Phospho)	S(11): 96.5; S(14): 3.6; S(15): 99.9	S11; S15;	S99; S103		4.75	0.005	2	3	799.6	2397	33.66	6223
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		4.37	0.005	2	3	826.3	2477	38.5	7252
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		4.28	0.005	2	2	1239	2477	39.76	7521
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		3.99	0.005	2	2	1239	2477	39.24	7408
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		3.98	0.005	2	2	1239	2477	40.3	7638
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.0; S(14): 100.0; S(15): 100.0	S14; S15;	S102; S103		3.5	0.005	2	2	1199	2397	36.36	6806
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S15(Phospho)	S(11): 0.0; S(14): 2.8; S(15): 97.2	S15;	S103		3.17	0.006	2	2	1159	2317	29.59	5376
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S15(Phospho)	S(11): 95.3; S(14): 4.9; S(15): 99.8	S11; S15;	S99; S103	12		0.007	2	2	1199	2397	33.72	6234
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		4.89	0.007	2	3	826.3	2477	42.38	8070
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 3.4; S(14): 96.7; S(15): 99.9	S14; S15;	S102; S103		3.86	0.007	2	3	799.6	2397	37.88	7122
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S11(Phospho) S14(Phospho) S15(Phospho)	S(11): 100.0; S(14): 100.0; S(15): 100.0	S11; S14; S15;	S99; S102; S103		3.07	0.007	2	2	1239	2477	41.36	7858
KLEKEEEEGISQEsEEEEQ	HMGA1	3159	high mobility group protein HMG-I/HMG-Y isoform a	S14(Phospho) S15(Phospho)	S(11): 0.2; S(14): 99.8; S(15): 100.0	S14; S15;	S102; S103	16		0.009	2	2	1199	2397	36.88	6916
KQQQEPTGEPsPK	HMGA2	8091	high mobility group protein HMGI-C isoform b	S11(Phospho)	T(7): 0.0; S(11): 100.0	S11;	S44	36		0	1	2	767.4	1534	13.83	2025
KQQQEPTGEPsPK	HMGA2	8091	high mobility group protein HMGI-C isoform b	S11(Phospho)	T(7): 0.0; S(11): 100.0	S11;	S44		4.37	0	1	2	767.4	1534	13.83	2025
TEESPASDEAGEKEAKsD	HMGN1	3150	non-histone chromosomal protein HMG-14	S17(Phospho)	T(1): 0.0; S(4): 0.0; S(7): 0.0; S(17): 100.0	S17;	S99	32		0	2	2	980.4	1960	16.37	2563
TEEsPAsDEAGEKEAK	HMGN1	3150	non-histone chromosomal protein HMG-14	S4(Phospho) S7(Phospho)	T(1): 0.0; S(4): 100.0; S(7): 100.0	S4; S7;	S86; S89	26		0	1	2	919.3	1838	17.97	2912
TEESPASDEAGEKEAKsD	HMGN1	3150	non-histone chromosomal protein HMG-14	S17(Phospho)	T(1): 0.0; S(4): 0.0; S(7): 0.0; S(17): 100.0	S17;	S99		4.57	0	2	3	653.9	1960	16.29	2546

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#
TEESPASDEAGEKEAKsD	HMGN1	3150	non-histone chromosomal protein HMG-14	S17(Phospho)	T(1): 0.0; S(4): 0.0; S(7): 0.0; S(17): 100.0	S17;	S99		4.45	0	2	2	980.4	1960	16.37	2563
TEESpAsDEAGEKEAK	HMGN1	3150	non-histone chromosomal protein HMG-14	S4(Phospho) S7(Phospho)	T(1): 0.0; S(4): 100.0; S(7): 100.0	S4; S7;	S86; S89		3.1	0	1	2	919.3	1838	17.97	2912
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 1.4; S(3): 98.6	S3;	S6	55		0	1	3	460.5	1380	25.1	4415
NQGGYGGSSSSSYGSGR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S9(Phospho)	Y(5): 0.1; S(8): 2.8; S(9): 94.2; S(10): 2.8; S(11): 0.0; S(12): 0.0; S(13): 0.0; Y(14): 0.0; S(16): 0.0	S9;	S309	46		0	0	2	887.8	1775	23.65	4107
sESPKEPEQLRK	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S1(Phospho)	S(1): 98.5; S(3): 1.5	S1;	S4	39		0	2	3	503.2	1508	19.51	3234
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S6	38		0	1	2	690.3	1380	24.77	4340
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S6	35		0	1	2	690.3	1380	25.29	4455
NQGGYGGSSSSSYGSGR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S11(Phospho)	Y(5): 0.0; S(8): 0.0; S(9): 0.1; S(10): 3.0; S(11): 93.8; S(12): 3.0; S(13): 0.1; Y(14): 0.0; S(16): 0.0	S11;	S311	34		0	0	2	887.8	1775	23.11	3997
SEsPKEPEQLRK	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 2.0; S(3): 98.0	S3;	S6	16		0	2	2	754.4	1508	19.56	3245
sESPKEPEQLRK	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S1(Phospho)	S(1): 98.5; S(3): 1.5	S1;	S4		5.2	0	2	3	503.2	1508	19.51	3234
NQGGYGGSSSSSYGSGR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S9(Phospho)	Y(5): 0.1; S(8): 2.8; S(9): 94.2; S(10): 2.8; S(11): 0.0; S(12): 0.0; S(13): 0.0; Y(14): 0.0; S(16): 0.0	S9;	S309		3.55	0	0	2	887.8	1775	23.65	4107
NQGGYGGSSSSSYGSGR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S11(Phospho)	Y(5): 0.0; S(8): 0.0; S(9): 0.1; S(10): 3.0; S(11): 93.8; S(12): 3.0; S(13): 0.1; Y(14): 0.0; S(16): 0.0	S11;	S311		3.44	0	0	2	887.8	1775	23.11	3997
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 1.4; S(3): 98.6	S3;	S6		3.25	0	1	3	460.5	1380	25.1	4415
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S6		2.42	0	1	2	690.3	1380	24.77	4340
SEsPKEPEQLR	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S6		2.23	0	1	2	690.3	1380	25.29	4455
SEsPKEPEQLRK	HNRNPA1	3178	heterogeneous nuclear ribonucleoprotein A1 isoform a	S3(Phospho)	S(1): 2.0; S(3): 98.0	S3;	S6		2.12	0	2	2	754.4	1508	19.56	3245
SSGsPYGGGYSGGGSGGYGSR	HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3	S4(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 97.9; Y(6): 2.0; Y(10): 0.0; S(12): 0.0; S(16): 0.0; Y(19): 0.0; S(21): 0.0	S4;	S358	89		0	0	2	995.9	1991	36.08	6745
SSGsPYGGGYSGGGSGGYGSR	HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3	S4(Phospho)	S(1): 1.9; S(2): 1.9; S(4): 94.4; Y(6): 1.9; Y(10): 0.0; S(12): 0.0; S(16): 0.0; Y(19): 0.0; S(21): 0.0	S4;	S358	83		0	0	2	995.9	1991	36.62	6860
SSGsPYGGGYSGGGSGGYGSR	HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3	S4(Phospho)	S(1): 1.9; S(2): 1.9; S(4): 94.4; Y(6): 1.9; Y(10): 0.0; S(12): 0.0; S(16): 0.0; Y(19): 0.0; S(21): 0.0	S4;	S358		5.16	0	0	2	995.9	1991	36.62	6860
SSGsPYGGGYSGGGSGGYGSR	HNRNPA3	220988	heterogeneous nuclear ribonucleoprotein A3	S4(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 97.9; Y(6): 2.0; Y(10): 0.0; S(12): 0.0; S(16): 0.0; Y(19): 0.0; S(21): 0.0	S4;	S358		4.33	0	0	2	995.9	1991	36.08	6745
NDKsEEEQSSSVK	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	65		0	1	2	817.3	1634	12.49	1729

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#
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	3	545.2	1634	12.54	1742
QAVEMKNDKSEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S10;	S220	38		0	2	3	774	2320	22.28	3818
QAVEMKNDKSEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S10;	S220	23		0	2	3	774	2320	20.22	3384
MESEGGADDsAEEGDLLDDDDNEDR	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(3): 0.3; S(10): 99.7	S10;	S247	18		0	0	3	927	2779	59.77	11834
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		5.66	0	1	3	545.2	1634	12.54	1742
QAVEMKNDKSEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S10;	S220		5.05	0	2	3	774	2320	20.22	3384
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		4.7	0	1	2	817.3	1634	12.49	1729
MESEGGADDsAEEGDLLDDDDNEDR	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(3): 0.3; S(10): 99.7	S10;	S247		3.28	0	0	3	927	2779	59.77	11834
QAVEMKNDKSEEEQSSSSVK	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	S10(Phospho)	S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S10;	S220		4.62	0.003	2	3	774	2320	22.28	3818
MeSEGGADDsAEEGDLLDDDDNEDR	HNRNPC	3183	heterogeneous nuclear ribonucleoproteins C1/C2 isoform b	M1(Oxidation) S3(Phospho)	S(3): 93.1; S(10): 6.9	S3;	S240		1.9	0.005	0	3	932.3	2795	56.99	11233
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.1; S(15): 2.6; S(16): 97.3	S16;	S83	60		0	1	2	1026	2052	13.21	1893
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.0; S(15): 1.9; S(16): 98.1	S16;	S83	41		0	1	3	684.6	2052	13.17	1884
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho) S16(Phospho)	S(4): 0.0; S(13): 97.0; S(15): 6.0; S(16): 97.0	S13; S16;	S80; S83	28		0	1	2	1066	2132	14.43	2150
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.1; S(15): 2.9; S(16): 97.0	S16;	S83	25		0	1	2	1026	2052	13.3	1911
IDASKNEEDEGHsNSSPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho)	S(4): 0.0; S(13): 98.1; S(15): 50.9; S(16): 50.9	S13;	S80	19		0	1	3	711.3	2132	14.29	2120
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.0; S(15): 1.9; S(16): 98.1	S16;	S83		8.5	0	1	3	684.6	2052	13.17	1884
IDASKNEEDEGHsNSSPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho)	S(4): 0.0; S(13): 98.1; S(15): 50.9; S(16): 50.9	S13;	S80		7.18	0	1	3	711.3	2132	14.29	2120
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho) S16(Phospho)	S(4): 0.0; S(13): 97.1; S(15): 5.8; S(16): 97.1	S13; S16;	S80; S83		5.1	0	1	3	711.3	2132	14.81	2229
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.1; S(15): 2.6; S(16): 97.3	S16;	S83		4.89	0	1	2	1026	2052	13.21	1893
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S16(Phospho)	S(4): 0.0; S(13): 0.1; S(15): 2.9; S(16): 97.0	S16;	S83		4.34	0	1	2	1026	2052	13.3	1911
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho) S16(Phospho)	S(4): 0.0; S(13): 97.1; S(15): 5.8; S(16): 97.1	S13; S16;	S80; S83	18		0.003	1	3	711.3	2132	14.81	2229
IDASKNEEDEGHsNsPR	HNRNPD	3184	heterogeneous nuclear ribonucleoprotein D0 isoform c	S13(Phospho) S16(Phospho)	S(4): 0.0; S(13): 97.0; S(15): 6.0; S(16): 97.0	S13; S16;	S80; S83		2.69	0.004	1	2	1066	2132	14.43	2150
HTGPNsPDTANDGFVR	HNRNPH1	3187	heterogeneous nuclear ribonucleoprotein H	S6(Phospho)	T(2): 0.0; S(6): 98.1; T(9): 1.9	S6;	S104	44		0	0	2	882.9	1765	33.36	6160
HTGPNsPDTANDGFVR	HNRNPH1	3187	heterogeneous nuclear ribonucleoprotein H	S6(Phospho)	T(2): 0.0; S(6): 98.1; T(9): 1.9	S6;	S104		3.23	0	0	2	882.9	1765	33.36	6160

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#
AAEEQGDDQDsEKSKPAGSDGER	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S11(Phospho)	S(11): 100.0; S(14): 0.0; S(19): 0.0	S11;	S185	46		0	1	3	829.3	2486	12.7	1783
REEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S10(Phospho)	S(10): 100.0; T(14): 0.0; S(17): 0.0	S10;	S161	35		0	2	3	875.4	2624	28.5	5150
REEDEPEERsGDEtPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S10(Phospho) T14(Phospho)	S(10): 100.0; T(14): 100.0; S(17): 0.0	S10; T14;	S161; T165	27		0	2	3	902	2704	30.94	5658
EEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S9(Phospho)	S(9): 100.0; T(13): 0.0; S(16): 0.0	S9;	S161	20		0	1	3	823.3	2468	32.53	5987
SGDETPGsEVPGDKAAEEQGDDQDSEK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S8(Phospho)	S(1): 50.0; T(5): 50.0; S(8): 100.0; S(25): 0.0	S8;	S168	19		0	1	3	979.7	2937	38.84	7324
AAEEQGDDQDsEKsKPAGSDGER	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 100.0; S(19): 0.0	S11; S14;	S185; S188	16		0	1	3	856	2566	13.15	1880
EEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S9(Phospho)	S(9): 99.8; T(13): 0.2; S(16): 0.0	S9;	S161	13		0	1	2	1234	2468	32.67	6018
AAEEQGDDQDsEKSKPAGSDGER	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S11(Phospho)	S(11): 100.0; S(14): 0.0; S(19): 0.0	S11;	S185		6.82	0	1	3	829.3	2486	12.7	1783
REEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S10(Phospho)	S(10): 100.0; T(14): 0.0; S(17): 0.0	S10;	S161		5.61	0	2	3	875.4	2624	28.5	5150
REEDEPEERsGDEtPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S10(Phospho) T14(Phospho)	S(10): 100.0; T(14): 100.0; S(17): 0.0	S10; T14;	S161; T165		4.59	0	2	3	902	2704	30.94	5658
AAEEQGDDQDsEKsKPAGSDGER	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 100.0; S(19): 0.0	S11; S14;	S185; S188		4.25	0	1	3	856	2566	13.15	1880
sGDETPGSEVPGDKAAEEQGDDQDSEK SKPAGSDGER	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S1(Phospho)	S(1): 99.1; T(5): 0.4; S(8): 0.0; S(25): 0.4; S(28): 0.0; S(33): 0.0	S1;	S161		4.01	0	2	4	961.2	3842	27.63	4965
SGDETPGsEVPGDKAAEEQGDDQDSEK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S8(Phospho)	S(1): 50.0; T(5): 50.0; S(8): 100.0; S(25): 0.0	S8;	S168		3.4	0	1	3	979.7	2937	38.84	7324
EEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S9(Phospho)	S(9): 100.0; T(13): 0.0; S(16): 0.0	S9;	S161		3.04	0	1	3	823.3	2468	32.53	5987
EEDEPEERsGDETPGSEVPGDK	HNRNPUL2	221092	heterogeneous nuclear ribonucleoprotein U-like protein 2	S9(Phospho)	S(9): 99.8; T(13): 0.2; S(16): 0.0	S9;	S161		1.59	0	1	2	1234	2468	32.67	6018
GHTDTEGRPPSPPTStPEK	HSF1	3297	heat shock factor protein 1	T17(Phospho)	T(3): 0.0; T(5): 0.0; S(11): 2.2; T(15): 50.0; S(16): 50.0; T(17): 97.8	T17;	T369		5.85	0	0	3	750	2248	25.68	4536
VKEEPPsPPQsPR	HSF1	3297	heat shock factor protein 1	S7(Phospho) S11(Phospho)	S(7): 100.0; S(11): 100.0	S7; S11;	S303; S307		3.75	0	1	2	804.3	1608	30.72	5614
GHTDTEGRPPsPPPTSTPEK	HSF1	3297	heat shock factor protein 1	S11(Phospho)	T(3): 0.0; T(5): 3.5; S(11): 96.5; T(15): 0.0; S(16): 0.0; T(17): 0.0	S11;	S363		3.6	0	0	3	723.3	2168	24.59	4303
VKEEPPsPPQsPR	HSF1	3297	heat shock factor protein 1	S7(Phospho) S11(Phospho)	S(7): 100.0; S(11): 100.0	S7; S11;	S303; S307	25		0.003	1	2	804.3	1608	30.72	5614
GHTDTEGRPPSPPTStPEK	HSF1	3297	heat shock factor protein 1	T17(Phospho)	T(3): 0.0; T(5): 0.0; S(11): 0.0; T(15): 51.3; S(16): 51.3; T(17): 97.5	T17;	T369		3.31	0.007	0	3	750	2248	25.15	4425

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#
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	48		0	2	4	704.8	2816	30.01	5465
DKEVsDDEAEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S5(Phospho)	S(5): 100.0	S5;	S231	40		0	1	2	737.3	1474	13.77	2012
ESEDKPEIEDVGsDEEEKK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	36		0	1	3	801	2401	32.1	5897
ESEDKPEIEDVGsDEEEKK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	35		0	1	3	801	2401	31.6	5794
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	30		0	2	4	704.8	2816	30.57	5582
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	29		0	2	4	704.8	2816	29.36	5331
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263	25		0	2	3	939.4	2816	29.93	5447
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 4.4; S(13): 95.6	S13;	S263	23		0	2	3	939.4	2816	29.42	5341
ESEDKPEIEDVGsDEEEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 3.7; S(13): 96.3	S13;	S263	23		0	0	3	758.3	2273	38.57	7266
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		6.82	0	2	4	704.8	2816	30.01	5465
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		6.58	0	2	4	704.8	2816	30.57	5582
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		5.86	0	2	3	939.4	2816	29.93	5447
ESEDKPEIEDVGsDEEEKK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		5.48	0	1	3	801	2401	32.1	5897
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		5.16	0	2	4	704.8	2816	29.36	5331
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		4.74	0	2	3	939.4	2816	30.44	5555
ESEDKPEIEDVGsDEEEKK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 0.0; S(13): 100.0	S13;	S263		4.63	0	1	3	801	2401	31.6	5794
ESEDKPEIEDVGsDEEEKKDGDK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 4.4; S(13): 95.6	S13;	S263		4.44	0	2	3	939.4	2816	29.42	5341
ESEDKPEIEDVGsDEEEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S13(Phospho)	S(2): 3.7; S(13): 96.3	S13;	S263		4.36	0	0	3	758.3	2273	38.57	7266
DKEVsDDEAEK	HSP90AA1	3320	heat shock protein HSP 90-alpha isoform 2	S5(Phospho)	S(5): 100.0	S5;	S231		4.06	0	1	2	737.3	1474	13.77	2012
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	91		0	0	2	787.8	1575	27.88	5017
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	75		0	1	2	909.4	1818	22.21	3804
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	66		0	2	2	973.4	1946	17.49	2811
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	57		0	2	2	973.4	1946	16.97	2699
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	48		0	2	2	973.4	1946	18.03	2925
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	48		0	1	2	909.4	1818	21.67	3688
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 98.0; S(12): 2.0	S6;	S207	47		0	2	3	649.3	1946	16.28	2542
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 99.9; S(12): 0.1	S6;	S207	46		0	2	3	649.3	1946	17.45	2802
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	45		0	1	2	909.4	1818	22.73	3915
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	43		0	1	3	606.6	1818	22.24	3812

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#
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	42		0	1	2	949.3	1898	25.7	4541
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	40		0	0	2	787.8	1575	28.43	5134
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	40		0	1	3	606.6	1818	21.71	3695
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	39		0	2	2	1013	2026	18.81	3086
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	38		0	2	2	973.4	1946	16.38	2565
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	34		0	2	3	675.9	2026	18.74	3072
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207	32		0	2	3	649.3	1946	18.35	2991
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 96.6; S(12): 3.4	S6;	S207	21		0	2	3	649.3	1946	22.12	3784
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 99.9; S(12): 0.1	S6;	S207		6.25	0	2	3	649.3	1946	17.45	2802
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 98.0; S(12): 2.0	S6;	S207		5.82	0	2	3	649.3	1946	16.28	2542
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		5.8	0	2	3	675.9	2026	18.74	3072
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		5.28	0	1	3	606.6	1818	22.24	3812
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		5.06	0	2	3	649.3	1946	18.35	2991
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		5.01	0	1	2	909.4	1818	22.21	3804
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4.71	0	1	3	606.6	1818	21.71	3695
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4.47	0	2	2	973.4	1946	16.97	2699
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		4	0	0	2	787.8	1575	27.88	5017
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.99	0	1	2	909.4	1818	21.67	3688
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 96.6; S(12): 3.4	S6;	S207		3.97	0	2	3	649.3	1946	22.12	3784
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		3.82	0	2	2	1013	2026	18.81	3086
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		3.75	0	1	2	949.3	1898	25.7	4541
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.49	0	2	2	973.4	1946	17.49	2811
IEDVGsDEEDDSGKDK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.31	0	1	2	909.4	1818	22.73	3915
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.14	0	2	2	973.4	1946	16.38	2565
IEDVGsDEEDDSGK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.77	0	0	2	787.8	1575	28.43	5134
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		2.5	0	2	2	973.4	1946	18.03	2925
IEDVGsDEEDDSGKDKK	HSP90AB1	3326	heat shock protein HSP 90-beta isoform b	S6(Phospho)	S(6): 100.0; S(12): 0.0	S6;	S207		3.69	0.001	2	3	649.3	1946	20.22	3383
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		4.1	0.004	1	3	633.2	1898	25.74	4549
QLSGVSEIR	HSPB1	3315	heat shock protein beta-1	S3(Phospho)	S(3): 100.0; S(4): 0.0; S(7): 0.0	S3;	S82	54		0	0	2	578.3	1156	44.37	8501

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#
QLSGVSEIR	HSPB1	3315	heat shock protein beta-1	S3(Phospho)	S(3): 100.0; S(4): 0.0; S(7): 0.0	S3;	S82		3.22	0	0	2	578.3	1156	44.37	8501
IESPKLER	HSPH1	10808	heat shock protein 105 kDa isoform 4	S3(Phospho)	S(3): 100.0	S3;	S733	50		0	1	2	526.3	1052	25.93	4591
IESPKLER	HSPH1	10808	heat shock protein 105 kDa isoform 4	S3(Phospho)	S(3): 100.0	S3;	S733		2.66	0	1	2	526.3	1052	25.93	4591
EsSPEKEAEEGCPEKESEEGCPK	HTATSF1	27336	HIV Tat-specific factor 1	C12(Carbamido methyl) C21(Carbamido methyl) S2(Phospho)	S(2): 96.9; S(3): 3.1; S(17): 0.0	S2;	S452	29		0	2	3	901.4	2702	26.73	4765
VLDEEGsEREFDsDEKEEEDTYEK	HTATSF1	27336	HIV Tat-specific factor 1	S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0; T(24): 0.0; Y(25): 0.0	S7; S15;	S616; S624	22		0	2	3	1147	3440	50.53	9815
VLDEEGsEREFDsDEKEEEDTYEK	HTATSF1	27336	HIV Tat-specific factor 1	S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0; T(24): 0.0; Y(25): 0.0	S7; S15;	S616; S624	18		0	2	4	860.8	3440	50.57	9825
EsSPEKEAEEGCPEKESEEGCPK	HTATSF1	27336	HIV Tat-specific factor 1	C12(Carbamido methyl) C21(Carbamido methyl) S2(Phospho)	S(2): 96.9; S(3): 3.1; S(17): 0.0	S2;	S452		5.37	0	2	3	901.4	2702	26.73	4765
VLDEEGsEREFDsDEKEEEDTYEK	HTATSF1	27336	HIV Tat-specific factor 1	S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0; T(24): 0.0; Y(25): 0.0	S7; S15;	S616; S624		5.18	0	2	4	860.8	3440	50.57	9825
VLDEEGsEREFDsDEKEEEDTYEK	HTATSF1	27336	HIV Tat-specific factor 1	S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0; T(24): 0.0; Y(25): 0.0	S7; S15;	S616; S624		4.24	0	2	3	1147	3440	50.53	9815
GSgTAsDDEFENLR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S6(Phospho)	S(2): 2.2; T(4): 0.1; S(6): 97.8	S6;	S1907	71		0	0	2	789.3	1578	52.77	10304
DGGsGNsTIIVSR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 97.3; T(8): 2.7; S(12): 0.0	S4; S7;	S2362; S2365	61		0	0	2	711.8	1423	57.76	11398
REESPMVDQPsPSAQDTQSIASDGTG QGEK	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S12(Phospho)	S(4): 0.0; S(12): 94.9; S(14): 5.1; T(18): 0.0; S(20): 0.0; S(23): 0.0; T(26): 0.0	S12;	S3816	36		0	1	3	1123	3367	50.93	9901
sDGGSESAQPPEDSPPASSESSSTR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S1(Phospho)	S(1): 99.8; S(4): 0.2; S(7): 0.0; S(14): 0.0; S(15): 0.0; S(19): 0.0; S(20): 0.0; S(22): 0.0; S(23): 0.0; S(24): 0.0; T(25): 0.0	S1;	S2904	12		0	0	2	1309	2616	29.47	5353
REESPMVDQPsPSAQDTQSIASDGTG QGEK	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S12(Phospho)	S(4): 0.0; S(12): 94.9; S(14): 5.1; T(18): 0.0; S(20): 0.0; S(23): 0.0; T(26): 0.0	S12;	S3816		5.14	0	1	3	1123	3367	50.93	9901
GSgTAsDDEFENLR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S6(Phospho)	S(2): 2.2; T(4): 0.1; S(6): 97.8	S6;	S1907		3.21	0	0	2	789.3	1578	52.77	10304
DGGsGNsTIIVSR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 97.3; T(8): 2.7; S(12): 0.0	S4; S7;	S2362; S2365		2.95	0	0	2	711.8	1423	57.76	11398
sDGGSESAQPPEDSPPASSESSSTR	HUWE1	10075	E3 ubiquitin-protein ligase HUWE1	S14(Phospho)	S(1): 99.8; S(4): 0.2; S(7): 0.0; S(14): 0.0; S(15): 0.0; S(19): 0.0; S(20): 0.0; S(22): 0.0; S(23): 0.0; S(24): 0.0; T(25): 0.0	S1;	S2904		2.84	0	0	2	1309	2616	29.47	5353
RAsPPDPSPsPSAASASER	ICE1	23379	little elongation complex subunit 1	S3(Phospho) S10(Phospho)	S(3): 99.9; S(8): 0.1; S(10): 99.9; S(12): 0.1; S(15): 0.0; S(17): 0.0	S3; S10;	S1692; S1699	44		0	1	3	676.3	2027	33.54	6198
RAsPPDPSPsPSAASASER	ICE1	23379	little elongation complex subunit 1	S3(Phospho) S10(Phospho)	S(3): 99.9; S(8): 0.1; S(10): 99.9; S(12): 0.1; S(15): 0.0; S(17): 0.0	S3; S10;	S1692; S1699		4.51	0	1	3	676.3	2027	33.54	6198
VSEEQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	S10(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 100.0; S(17): 0.0; T(18): 0.0	S10;	S153	42		0	0	2	1135	2269	53.07	10378

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#
VSEEQQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M16(Oxidation) S10(Phospho)	S(2): 0.2; T(6): 0.2; S(10): 99.7; S(17): 0.0; T(18): 0.0	S10;	S153	31		0	0	2	1143	2285	41.83	7955
VSEEQQTQPPsPAGAGMsTAMGRSPsPK	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	S10(Phospho) S17(Phospho) S25(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 100.0; S(17): 88.9; T(18): 5.6; S(23): 5.9; S(25): 99.6	S10; S17; S25;	S153; S160; S168		6.36	0	1	3	975.7	2925	58.77	11633
VSEEQQTQPPsPAGAGMStAMGRsPsPK	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M16(Oxidation) T18(Phospho) S23(Phospho) S25(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 0.0; S(17): 6.2; T(18): 93.7; S(23): 100.0; S(25): 100.0	T18; S23; S25;	T161; S166; S168		5.73	0	1	3	981.1	2941	49.7	9640
VSEEQQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	S10(Phospho)	S(2): 0.0; T(6): 0.0; S(10): 100.0; S(17): 0.0; T(18): 0.0	S10;	S153		4.5	0	0	2	1135	2269	53.07	10378
VSEEQQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M16(Oxidation) S10(Phospho)	S(2): 0.2; T(6): 0.2; S(10): 99.7; S(17): 0.0; T(18): 0.0	S10;	S153		3.64	0	0	2	1143	2285	41.83	7955
VSEEQQTQPPsPAGAGMSTAMGR	IFI16	3428	gamma-interferon-inducible protein 16 isoform 2	M20(Oxidation) S10(Phospho)	S(2): 0.0; T(6): 6.2; S(10): 92.8; S(17): 0.5; T(18): 0.5	S10;	S153		2.4	0	0	2	1143	2285	43.77	8364
SSsDEQGLSYSSLK	IL1RAP	3556	interleukin-1 receptor accessory protein isoform 1 precursor	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; S(9): 0.0; Y(10): 0.0; S(11): 0.0; S(12): 0.0	S3;	S557	31		0	0	2	784.3	1568	50.62	9836
SSsDEQGLSYSSLK	IL1RAP	3556	interleukin-1 receptor accessory protein isoform 1 precursor	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9; S(9): 0.0; Y(10): 0.0; S(11): 0.0; S(12): 0.0	S3;	S557		2.63	0	0	2	784.3	1568	50.62	9836
DSSKGEDSAEEtEAKPAVVAPAPVVEAV STPSAAFPsDATAEQGPILTK	ILF3	3609	interleukin enhancer-binding factor 3 isoform c	T12(Phospho)	S(2): 0.9; S(3): 0.1; S(8): 8.8; T(12): 90.1; S(29): 0.0; T(30): 0.0; S(32): 0.0; S(37): 0.0; T(40): 0.0; T(48): 0.0	T12;	T486		3.98	0	1	4	1234	4932	83.3	16738
DSSKGEDSAEEtEAKPAVVAPAPVVEAV STPSAAFPsDATAENVK	ILF3	3609	interleukin enhancer-binding factor 3 isoform e	T12(Phospho)	S(2): 7.9; S(3): 7.9; S(8): 7.9; T(12): 76.1; S(29): 0.1; T(30): 0.1; S(32): 0.1; S(37): 0.0; T(40): 0.0	T12;	T486		3.95	0	1	4	1135	4536	76.4	15411
RPMEEDGEEKsPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382	57		0	1	3	566.9	1699	13.01	1852
RPMEEDGEEKsPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382	56		0	1	3	572.2	1715	12.38	1696
RPMEEDGEEKsPSKK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 98.3; S(13): 1.7	S11;	S382 S382	40		0	2	3	609.6	1827	12.57	1750
RPMEEDGEEKsPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382	38		0	1	2	849.9	1699	13.06	1862
RPMEEDGEEKsPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382		7.03	0	1	3	566.9	1699	13.01	1852
RPMEEDGEEKsPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382		6.75	0	1	3	572.2	1715	12.38	1696

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#
RPMEEDGEEKSPSKK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 98.3; S(13): 1.7	S11;	S382 S382		6.53	0	2	3	609.6	1827	12.57	1750
RPMEEDGEEKSPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382		4.19	0	1	2	849.9	1699	13.06	1862
RPMEEDGEEKSPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382		3.19	0.001	1	2	857.8	1715	12.41	1706
RPMEEDGEEKSPSK	ILF3 ILF3	3609 3609	interleukin enhancer-binding factor 3 isoform c interleukin enhancer-binding factor 3 isoform e	M3(Oxidation) S11(Phospho)	S(11): 100.0; S(13): 0.0	S11;	S382 S382	15		0.003	1	2	857.8	1715	12.41	1706
AlTDDSDENEEEDAFTDQK	INADL	10207	inaD-like protein	T3(Phospho) S6(Phospho)	T(3): 100.0; S(6): 100.0; T(16): 0.0	T3; S6;	T1209; S1212	36		0	0	2	1166	2332	65.49	13157
AlTDDSDENEEEDAFTDQK	INADL	10207	inaD-like protein	T3(Phospho)	T(3): 100.0; S(6): 0.0; T(16): 0.0	T3;	T1209	31		0	0	2	1126	2252	55.91	10990
AlTDDSDENEEEDAFTDQK	INADL	10207	inaD-like protein	T3(Phospho) S6(Phospho)	T(3): 100.0; S(6): 100.0; T(16): 0.0	T3; S6;	T1209; S1212		3.42	0	0	2	1166	2332	65.49	13157
AlTDDSDENEEEDAFTDQK	INADL	10207	inaD-like protein	T3(Phospho)	T(3): 100.0; S(6): 0.0; T(16): 0.0	T3;	T1209		2.73	0	0	2	1126	2252	55.91	10990
INPDNYGMDLNsDDStDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828	45		0	0	3	944.3	2831	70.97	14356
INPDNYGMDLNsDDStDDEAHPR	INCENP	3619	inner centromere protein isoform 2	M8(Oxidation) S12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 5.2; S(12): 94.8; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828	44		0	0	3	949.7	2847	57.05	11249
INPDNYGMDLNsDDStDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 99.7; T(16): 0.3	S12; S15;	S824; S827	20		0	0	3	917.7	2751	61.4	12174
INPDNYGMDLNsDDStDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828	18		0	0	3	944.3	2831	71.57	14473
TDSQSVRHsPIAPsPSPQVLAQK	INCENP	3619	inner centromere protein isoform 2	S9(Phospho) S15(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(9): 100.0; S(14): 0.2; S(15): 96.0; S(17): 3.9	S9; S15;	S306; S312	12		0	1	3	893.1	2677	46.16	8900
TLSPTPASATAPTSQGIPtsDEESTPKK	INCENP	3619	inner centromere protein isoform 2	T25(Phospho)	T(1): 49.9; S(3): 49.9; T(5): 0.2; S(8): 0.0; T(10): 0.0; T(13): 0.0; S(14): 0.0; T(19): 0.0; S(20): 0.4; S(24): 5.7; T(25): 93.9	T25;	T219		4.79	0	1	3	987.1	2959	55.15	10831
TDSQSVRHsPIAPsPSPQVLAQK	INCENP	3619	inner centromere protein isoform 2	S9(Phospho) S15(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 0.0; S(9): 100.0; S(14): 0.2; S(15): 96.0; S(17): 3.9	S9; S15;	S306; S312		4.65	0	1	3	893.1	2677	46.16	8900
TLSPTPASATAPTSQGIPtsDEESTPKK	INCENP	3619	inner centromere protein isoform 2	S20(Phospho) T25(Phospho)	T(1): 0.0; S(3): 0.0; T(5): 0.0; S(8): 0.0; T(10): 0.0; T(13): 0.0; S(14): 0.0; T(19): 6.1; S(20): 93.4; S(24): 6.5; T(25): 93.9	S20; T25;	S214; T219		4.52	0	1	3	987.1	2959	53.85	10551
TLSPTPASATAPTSQGIPtsDEESTPKK	INCENP	3619	inner centromere protein isoform 2	S20(Phospho)	T(1): 48.6; S(3): 48.6; T(5): 2.9; S(8): 0.0; T(10): 0.0; T(13): 0.0; S(14): 0.0; T(19): 0.4; S(20): 99.6; S(24): 0.0; T(25): 0.0	S20;	S214		3.96	0	1	3	987.1	2959	54.4	10673
INPDNYGMDLNsDDStDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 99.7; T(16): 0.3	S12; S15;	S824; S827		2.93	0	0	3	917.7	2751	61.4	12174

Phosphopeptide	Gene Symbol	Gene Id	Protein Name	Modifications	phosphoRS Site Probabilities	PhosphoSIt (Peptide)	PhosphoSIt (Protein)	IonScore (Mascot)	Xcorr (Sequest)	q-Value	# Missed Cleavages	Charge	m/z [Da]	MH+ [Da]	RT [min]	Scan#
INPDNYGMDLNsDDstDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828		2.84	0	0	3	944.3	2831	70.97	14356
INPDNYGMDLNsDDstDDEAHPR	INCENP	3619	inner centromere protein isoform 2	S12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 0.0; S(12): 100.0; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828		2.77	0	0	3	944.3	2831	71.57	14473
INPDNYGMDLNsDDstDDEAHPR	INCENP	3619	inner centromere protein isoform 2	M8(Oxidation)S 12(Phospho) S15(Phospho) T16(Phospho)	Y(6): 5.2; S(12): 94.8; S(15): 100.0; T(16): 100.0	S12; S15; T16;	S824; S827; T828		2.76	0	0	3	949.7	2847	57.05	11249
TDSQSVRHsPIAPsPsPQVLAQK	INCENP	3619	inner centromere protein isoform 2	S9(Phospho) S15(Phospho) S17(Phospho)	T(1): 4.6; S(3): 4.6; S(5): 4.6; S(9): 86.3; S(14): 5.1; S(15): 95.0; S(17): 100.0	S9; S15; S17;	S306; S312; S314	10		0.001	1	3	919.7	2757	50.55	9821
TDSQSVRHsPIAPsPsPQVLAQK	INCENP	3619	inner centromere protein isoform 2	S9(Phospho) S15(Phospho) S17(Phospho)	T(1): 4.6; S(3): 4.6; S(5): 4.6; S(9): 86.3; S(14): 5.1; S(15): 95.0; S(17): 100.0	S9; S15; S17;	S306; S312; S314		4.22	0.001	1	3	919.7	2757	50.55	9821
KAsPEPEGEAAGK	IRF2BP1	26145	interferon regulatory factor 2-binding protein 1	S3(Phospho)	S(3): 100.0	S3;	S384	61		0	1	2	675.8	1351	12.8	1807
KAsPEPEGEAAGK	IRF2BP1	26145	interferon regulatory factor 2-binding protein 1	S3(Phospho)	S(3): 100.0	S3;	S384		5.26	0	1	2	675.8	1351	12.8	1807
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S4(Phospho) S7(Phospho)	S(2): 0.0; S(4): 100.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S4; S7;	S457; S460	43		0	0	2	831.8	1663	36.15	6760
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S7(Phospho)	S(2): 50.0; S(4): 50.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S7;	S460	42		0	0	2	831.8	1663	35.64	6654
KPsPEPEGEVGPPK	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S3(Phospho)	S(3): 100.0	S3;	S360	40		0	0	2	764.4	1528	28.6	5170
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S7(Phospho)	S(2): 0.0; S(4): 0.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S7;	S460	39		0	0	2	791.8	1583	28.26	5100
RNSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S5(Phospho) S8(Phospho)	S(3): 2.3; S(5): 97.7; S(8): 100.0; S(10): 0.0; S(11): 0.0	S5; S8;	S457; S460	25		0	1	2	909.9	1819	27.61	4961
RKPsPEPEGEVGPPK	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S4(Phospho)	S(4): 100.0	S4;	S360	25		0	1	3	561.9	1684	23.57	4090
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	M11(Oxidation) S7(Phospho)	S(2): 0.0; S(4): 0.0; S(7): 99.9; S(9): 0.0; S(10): 0.0	S7;	S460	24		0	0	2	799.8	1599	16.03	2489
LEEPPELNQRsPNPR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S11(Phospho)	S(11): 100.0	S11;	S175	21		0	1	3	619.3	1856	40.4	7658
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	M11(Oxidation) S7(Phospho)	S(2): 50.0; S(4): 50.0; S(7): 99.9; S(9): 0.1; S(10): 0.0	S7;	S460	21		0	0	2	839.8	1679	20.65	3474
RKPsPEPEGEVGPPK	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S4(Phospho)	S(4): 100.0	S4;	S360		4.61	0	1	3	561.9	1684	23.57	4090
KPsPEPEGEVGPPK	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S3(Phospho)	S(3): 100.0	S3;	S360		4.23	0	0	2	764.4	1528	28.6	5170
NSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S4(Phospho) S7(Phospho)	S(2): 0.0; S(4): 100.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S4; S7;	S457; S460		3.46	0	0	2	831.8	1663	36.15	6760
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S7(Phospho)	S(2): 50.0; S(4): 50.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S7;	S460		3.11	0	0	2	831.8	1663	35.64	6654
RNSNsPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S5(Phospho) S8(Phospho)	S(3): 2.3; S(5): 97.7; S(8): 100.0; S(10): 0.0; S(11): 0.0	S5; S8;	S457; S460		3.04	0	1	2	909.9	1819	27.61	4961
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S7(Phospho)	S(2): 0.0; S(4): 0.0; S(7): 100.0; S(9): 0.0; S(10): 0.0	S7;	S460		2.88	0	0	2	791.8	1583	28.26	5100

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#
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	M11(Oxidation) S7(Phospho)	S(2): 0.0; S(4): 0.0; S(7): 99.9; S(9): 0.0; S(10): 0.0	S7;	S460		2.42	0	0	2	799.8	1599	16.03	2489
NSNSPPsPSSMNQR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	M11(Oxidation) S7(Phospho)	S(2): 50.0; S(4): 50.0; S(7): 99.9; S(9): 0.1; S(10): 0.0	S7;	S460		2.21	0	0	2	839.8	1679	20.65	3474
LEEPPELNQRqSPNPR	IRF2BP2	359948	interferon regulatory factor 2-binding protein 2 isoform A	S11(Phospho)	S(11): 100.0	S11;	S175		3.64	0.001	1	3	619.3	1856	40.4	7658
NSSsPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S4(Phospho) S7(Phospho)	S(2): 2.7; S(3): 2.7; S(4): 94.5; S(7): 97.2; S(10): 2.8	S4; S7;	S659; S662	48		0	0	2	815.3	1630	44.36	8499
RPGsVsSTDQER	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 96.0; S(7): 2.0; T(8): 2.0	S4; S6;	S334; S336	48		0	0	2	739.8	1479	15.67	2412
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S4(Phospho)	S(3): 99.8; S(4): 96.1; S(5): 4.0; S(8): 0.0; S(11): 0.0	S3; S4;	S657; S658	22		0	1	2	893.4	1786	35.94	6717
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S8(Phospho)	S(3): 94.7; S(4): 2.7; S(5): 2.7; S(8): 99.9; S(11): 0.1	S3; S8;	S657; S662	22		0	1	2	893.4	1786	33.85	6261
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 96.9; S(4): 6.3; S(5): 96.9; S(8): 100.0; S(11): 0.0	S3; S5; S8;	S657; S659; S662	20		0	1	2	933.4	1866	42.19	8031
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S4(Phospho)	S(3): 99.8; S(4): 96.1; S(5): 4.0; S(8): 0.0; S(11): 0.0	S3; S4;	S657; S658		3.6	0	1	2	893.4	1786	35.94	6717
RPGsVsSTDQER	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 96.0; S(7): 2.0; T(8): 2.0	S4; S6;	S334; S336		3.58	0	0	2	739.8	1479	15.67	2412
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 96.9; S(4): 6.3; S(5): 96.9; S(8): 100.0; S(11): 0.0	S3; S5; S8;	S657; S659; S662		3.52	0	1	2	933.4	1866	42.19	8031
NSSsPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S4(Phospho) S7(Phospho)	S(2): 2.7; S(3): 2.7; S(4): 94.5; S(7): 97.2; S(10): 2.8	S4; S7;	S659; S662		3.16	0	0	2	815.3	1630	44.36	8499
RNsSPVsPASVPGQR	IRF2BPL	64207	interferon regulatory factor 2-binding protein-like	S3(Phospho) S8(Phospho)	S(3): 94.7; S(4): 2.7; S(5): 2.7; S(8): 99.9; S(11): 0.1	S3; S8;	S657; S662		2.94	0.002	1	2	893.4	1786	33.85	6261
ASSDGEgTMSRPASVDGSPVsPSTNR	IRS1	3667	insulin receptor substrate 1	S21(Phospho)	S(2): 0.0; S(3): 0.0; T(8): 0.0; S(10): 50.0; S(14): 50.0; S(18): 0.0; S(21): 99.8; S(23): 0.2; T(24): 0.0	S21;	S348		3.62	0.001	0	3	903.7	2709	46.11	8891
NKsEDEDEDEGDATR	IRX2	153572	iroquois-class homeodomain protein IRX-2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S186	88		0	1	2	895.3	1790	13.04	1858
NKsEDEDEDEGDATR	IRX2	153572	iroquois-class homeodomain protein IRX-2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S186		4.27	0	1	2	895.3	1790	13.04	1858
DYSTLTsVsHDSR	ITGB4	3691	integrin beta-4 isoform 3 precursor	S10(Phospho)	Y(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(7): 0.0; S(9): 0.0; S(10): 100.0; S(13): 0.0	S10;	S1448	31		0	0	2	817.8	1635	39.69	7506
DYSTLTsVsHDSR	ITGB4	3691	integrin beta-4 isoform 3 precursor	S10(Phospho)	Y(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(7): 0.0; S(9): 0.0; S(10): 100.0; S(13): 0.0	S10;	S1448		2.96	0.001	0	2	817.8	1635	39.69	7506
VLsTSSTLTR	ITGB4	3691	integrin beta-4 isoform 3 precursor	S3(Phospho)	S(3): 95.3; T(4): 4.6; S(5): 49.2; S(6): 49.2; T(7): 1.7; T(9): 0.1	S3;	S1413	14		0.002	0	2	612.8	1225	59.85	11851
TVSPGSVsPIHGQGVVENLK	ITSN2	50618	intersectin-2 isoform 2	S8(Phospho)	T(1): 50.0; S(3): 50.0; S(6): 4.0; S(8): 96.0	S8;	S889	23		0	0	3	765	2293	62.19	12345
TVSPGSVsPIHGQGVVENLK	ITSN2	50618	intersectin-2 isoform 2	S8(Phospho)	T(1): 50.0; S(3): 50.0; S(6): 4.0; S(8): 96.0	S8;	S889		3.07	0	0	3	765	2293	62.19	12345
GPAsDsETEDASR	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(12): 0.0	S4; S6;	S313; S315	79		0	0	2	741.2	1481	23.9	4160
VVsDADDsDSDAVSDK	IWS1	55677	protein IWS1 homolog	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0; S(10): 0.0; S(14): 0.0	S3; S8;	S415; S420	68		0	0	2	892.8	1785	36.71	6881

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#
EAEDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513	65		0	1	2	827.3	1654	17.57	2829
KAAVLsDsEDEEK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S398; S400	61		0	1	2	790.8	1581	29.84	5429
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	60		0	1	2	905.4	1810	32.88	6060
KAAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(15): 0.0	S6; S8;	S398; S400	52		0	2	3	646.6	1938	25.97	4600
EAEDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513	50		0	1	2	827.3	1654	18.11	2942
KAAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(15): 0.0	S6; S8;	S398; S400	48		0	2	2	969.4	1938	26.01	4609
EKTiAsDsEEEAGK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	T(3): 2.5; S(6): 97.5; S(8): 100.0	S6; S8;	S438; S440	47		0	1	2	827.3	1654	22.84	3939
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	44		0	1	3	603.9	1810	32.9	6065
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	40		0	0	2	698.7	1396	29.19	5296
AAVLsDsEDEEK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S398; S400	38		0	0	2	726.8	1453	41.55	7897
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	36		0	1	2	905.4	1810	33.5	6189
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	M1(Oxidation) S3(Phospho)	S(3): 100.0	S3;	S377	27		0	1	2	883.3	1766	12.89	1826
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	S3(Phospho)	S(3): 100.0	S3;	S377	27		0	1	2	875.3	1750	14.35	2133
TIAsDsEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440	26		0	1	2	984.9	1969	43.07	8215
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 4.4; S(4): 95.6; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440	25		0	2	3	699.6	2097	35.47	6617
TIAsDSEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S15(Phospho)	T(1): 0.0; S(4): 99.9; S(6): 3.7; S(15): 96.5	S4; S15;	S438; S449	24		0	1	3	656.9	1969	43.4	8286
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440	23		0	2	2	1049	2097	35.09	6539
AAVLsDsEDEEKASAKK	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	23		0	2	3	646.6	1938	25.34	4464
TIAsDsEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440	22		0	1	2	984.9	1969	43.57	8322
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	22		0	1	2	905.4	1810	33.05	6095
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.3; S(4): 99.3; S(6): 99.7; S(15): 0.7	S4; S6;	S438; S440	21		0	2	3	699.6	2097	34.95	6510
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	S3(Phospho)	S(3): 100.0	S3;	S377	18		0	1	3	583.9	1750	14.59	2184
KAAVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(15): 0.0	S6; S8;	S398; S400		5.97	0	2	3	646.6	1938	25.97	4600
KAAVLsDsEDEEK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S398; S400		4.97	0	1	2	790.8	1581	29.84	5429
AAVLsDsEDEEKASAKK	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		4.83	0	2	3	646.6	1938	25.34	4464
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		4.63	0	1	3	603.9	1810	32.9	6065
TIAsDSEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S15(Phospho)	T(1): 0.0; S(4): 99.9; S(6): 3.7; S(15): 96.5	S4; S15;	S438; S449		4.32	0	1	3	656.9	1969	43.4	8286
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		4.11	0	1	2	905.4	1810	32.88	6060
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 4.4; S(4): 95.6; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440		4.08	0	2	3	699.6	2097	35.47	6617
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	S3(Phospho)	S(3): 100.0	S3;	S377		4.01	0	1	3	583.9	1750	14.59	2184
GPAsDsETEDASR	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(12): 0.0	S4; S6;	S313; S315		3.96	0	0	2	741.2	1481	23.9	4160

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#
VVsDADDSDSDAVSDK	IWS1	55677	protein IWS1 homolog	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0; S(10): 0.0; S(14): 0.0	S3; S8;	S415; S420		3.96	0	0	2	892.8	1785	36.71	6881
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		3.8	0	1	2	905.4	1810	33.05	6095
KA AVLsDsEDEEKASAK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(15): 0.0	S6; S8;	S398; S400		3.7	0	2	2	969.4	1938	26.01	4609
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		3.3	0	0	2	698.7	1396	29.19	5296
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.3; S(4): 99.3; S(6): 99.7; S(15): 0.7	S4; S6;	S438; S440		3.26	0	2	3	699.6	2097	34.95	6510
TIAsDsEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440		3.23	0	1	2	984.9	1969	43.57	8322
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	S3(Phospho)	S(3): 100.0	S3;	S377		3.18	0	1	2	875.3	1750	14.35	2133
TIAsDsEEEAGKELSDK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440		3.09	0	1	2	984.9	1969	43.07	8215
MDsDEDEKEGEEEEK	IWS1	55677	protein IWS1 homolog	M1(Oxidation) S3(Phospho)	S(3): 100.0	S3;	S377		3.03	0	1	2	883.3	1766	12.89	1826
EAEDsDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513		2.92	0	1	2	827.3	1654	17.57	2829
AAVLsDsEDEEK	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S398; S400		2.9	0	0	2	726.8	1453	41.55	7897
EAEDsDsDDNIKR	IWS1	55677	protein IWS1 homolog	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S511; S513		2.83	0	1	2	827.3	1654	18.11	2942
TIAsDsEEEAGKELSDKK	IWS1	55677	protein IWS1 homolog	S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 100.0; S(15): 0.0	S4; S6;	S438; S440		2.26	0	2	2	1049	2097	35.09	6539
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		2.14	0	1	2	905.4	1810	33.5	6189
EKTIAsDsEEEAGK	IWS1	55677	protein IWS1 homolog	S6(Phospho) S8(Phospho)	T(3): 2.5; S(6): 97.5; S(8): 100.0	S6; S8;	S438; S440		2.84	0.001	1	2	827.3	1654	22.84	3939
NSSTETDQQPHsPDSSSSSVHSIR	JADE3	9767	protein Jade-3	S12(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(12): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; S(21): 0.0	S12;	S566	24		0	0	3	855	2563	23.61	4100
NSSTETDQQPHsPDSSSSSVHSIR	JADE3	9767	protein Jade-3	S12(Phospho)	S(2): 0.0; S(3): 0.0; T(4): 0.0; T(6): 0.0; S(12): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; S(21): 0.0	S12;	S566		5.17	0	0	3	855	2563	23.61	4100
EtPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	T2(Phospho) T15(Phospho)	T(2): 100.0; S(9): 0.0; S(11): 0.0; T(15): 100.0	T2; T15;	T477; T490	34		0	0	3	716.3	2147	33.62	6215
ETPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.1; S(9): 0.1; S(11): 99.8; T(15): 100.0	S11; T15;	S486; T490	24		0	0	3	716.3	2147	33.01	6087
ETPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.2; S(9): 0.0; S(11): 99.8; T(15): 100.0	S11; T15;	S486; T490	21		0	0	3	716.3	2147	32.5	5981
EtPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	T2(Phospho) T15(Phospho)	T(2): 100.0; S(9): 0.0; S(11): 0.0; T(15): 100.0	T2; T15;	T477; T490		4.31	0	0	3	716.3	2147	33.62	6215
ETPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.2; S(9): 0.0; S(11): 99.8; T(15): 100.0	S11; T15;	S486; T490		3.96	0	0	3	716.3	2147	32.5	5981
ETPRPEGGSPsPAGtPPQPK	JPH2	57158	junctophilin-2 isoform 1	S11(Phospho) T15(Phospho)	T(2): 0.1; S(9): 0.1; S(11): 99.8; T(15): 100.0	S11; T15;	S486; T490		3.92	0	0	3	716.3	2147	33.01	6087
SRDATPPVsPINMEDQER	JUNB	3726	transcription factor jun-B	T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	48		0	1	3	734.6	2202	53.23	10413
SRDATPPVsPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	47		0	1	3	740	2218	41.78	7945
sRDATPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 0.0	S1; T5;	S251; T255	44		0	1	3	740	2218	47.48	9176

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#
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 0.0	S1; T5;	S251; T255	39		0	1	3	734.6	2202	59.43	11770
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	37		0	1	3	766.6	2298	51.06	9928
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	33		0	1	3	761.3	2282	63.37	12653
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	29		0	1	3	766.6	2298	50.53	9817
SRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	29		0	1	2	1101	2202	53.15	10396
DAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T255; S259	22		0	0	2	979.9	1959	69.99	14162
DAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M11(Oxidation) T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T255; S259	19		0	0	2	987.9	1975	56.49	11114
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	6.93	0	0	1	3	766.6	2298	51.06	9928
SRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	6.25	0	0	1	3	734.6	2202	53.23	10413
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	5.57	0	0	1	3	761.3	2282	63.37	12653
SRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	5.52	0	0	1	3	740	2218	41.78	7945
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho) S9(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 100.0	S1; T5; S9;	S251; T255; S259	5.43	0	0	1	3	766.6	2298	50.53	9817
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M13(Oxidation) S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 0.0	S1; T5;	S251; T255	3.71	0	0	1	3	740	2218	47.48	9176
SRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	T5(Phospho) S9(Phospho)	S(1): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T255; S259	3.3	0	0	1	2	1101	2202	53.15	10396
sRDAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0; S(9): 0.0	S1; T5;	S251; T255	3.09	0	0	1	3	734.6	2202	59.43	11770
DAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T255; S259	2.61	0	0	0	2	979.9	1959	69.99	14162
DAtPPVSPINMEDQER	JUNB	3726	transcription factor jun-B	M11(Oxidation) T3(Phospho) S7(Phospho)	T(3): 100.0; S(7): 100.0	T3; S7;	T255; S259	1.9	0	0	0	2	987.9	1975	56.49	11114
KSNCLGTDEdSdQsSDGIPsAPR	KAT5	10524	histone acetyltransferase KAT5 isoform 3	C4(Carbamidomethyl)S11(Phospho) S14(Phospho)	S(2): 0.0; T(7): 0.0; S(11): 96.5; S(14): 96.5; S(15): 7.0; S(20): 0.0	S11; S14;	S147; S150	39		0	1	3	866	2596	51.26	9969
KSNCLGTDEdSdQsSDGIPsAPR	KAT5	10524	histone acetyltransferase KAT5 isoform 3	C4(Carbamidomethyl)S11(Phospho) S14(Phospho)	S(2): 0.0; T(7): 0.0; S(11): 96.5; S(14): 96.5; S(15): 7.0; S(20): 0.0	S11; S14;	S147; S150	3.39	0	0	1	3	866	2596	51.26	9969
SSGsETEQQVDFSDR	KAT7	11143	histone acetyltransferase KAT7 isoform 4	S4(Phospho)	S(1): 0.1; S(2): 0.1; S(4): 97.2; T(6): 2.6; S(13): 0.0	S4;	S102	55		0	0	2	861.8	1723	56.96	11226

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#
LSQSSQDSsPVR	KAT7	11143	histone acetyltransferase KAT7 isoform 4	S9(Phospho)	S(2): 0.0; S(4): 0.0; S(5): 0.0; S(8): 1.4; S(9): 98.6	S9;	S57	48		0	0	2	685.8	1371	18.53	3028
LSQSSQDSsPVR	KAT7	11143	histone acetyltransferase KAT7 isoform 4	S9(Phospho)	S(2): 0.0; S(4): 0.0; S(5): 0.0; S(8): 1.4; S(9): 98.6	S9;	S57		3.8	0	0	2	685.8	1371	18.53	3028
SSGsETEQVVDFSDR	KAT7	11143	histone acetyltransferase KAT7 isoform 4	S4(Phospho)	S(1): 0.1; S(2): 0.1; S(4): 97.2; T(6): 2.6; S(13): 0.0	S4;	S102		3	0	0	2	861.8	1723	56.96	11226
LFCVFyGLFGVPLCLtWIsALGK	KCNK5	8645	potassium channel subfamily K member 5	C3(Carbamidomethyl) C14(Carbamidomethyl)Y6(Phospho) T16(Phospho) S19(Phospho)	Y(6): 100.0; T(16): 100.0; S(19): 100.0	Y6; T16; S19;	Y118; T128; S131		6.85	0.001	0	4	726.1	2901	24.84	4356
LFCVFyGLFGVPLCLtWIsALGK	KCNK5	8645	potassium channel subfamily K member 5	C3(Carbamidomethyl) C14(Carbamidomethyl)Y6(Phospho) T16(Phospho) S19(Phospho)	Y(6): 100.0; T(16): 100.0; S(19): 100.0	Y6; T16; S19;	Y118; T128; S131		5.83	0.005	0	4	726.1	2901	26.5	4714
sPSGGAAGPLLTPSQSLDGSR	KCTD12	115207	BTB/POZ domain-containing protein KCTD12	S1(Phospho)	S(1): 97.6; S(3): 2.4; T(12): 0.0; S(14): 0.0; S(16): 0.0; S(20): 0.0	S1;	S185	41		0	0	2	1018	2035	67.34	13583
sPSGGAAGPLLTPSQSLDGSR	KCTD12	115207	BTB/POZ domain-containing protein KCTD12	S1(Phospho)	S(1): 97.6; S(3): 2.4; T(12): 0.0; S(14): 0.0; S(16): 0.0; S(20): 0.0	S1;	S185		3.47	0	0	2	1018	2035	67.34	13583
EMDESLANLsEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S10(Phospho) S16(Phospho)	S(5): 0.2; S(10): 99.8; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S10; S16;	S131; S137	42		0	0	3	866.6	2598	80.88	16280
EMDESLANLsEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	M2(Oxidation)S 10(Phospho) S16(Phospho)	S(5): 4.1; S(10): 95.9; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S10; S16;	S131; S137	31		0	0	3	872	2614	74.47	15063
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166	25		0	1	4	902.4	3607	59.74	11829
EMDES LANLSEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	M2(Oxidation)S 5(Phospho) S16(Phospho)	S(5): 99.7; S(10): 0.2; Y(14): 0.0; Y(15): 0.2; S(16): 99.7	S5; S16;	S126; S137	19		0	0	2	1307	2614	74.46	15061
EMDES LANLSEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S5(Phospho) S16(Phospho)	S(5): 100.0; S(10): 0.0; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S5; S16;	S126; S137	19		0	0	2	1299	2598	80.82	16268
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166	19		0	1	3	1203	3607	59.94	11869
EMDES LANLSEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S5(Phospho) S16(Phospho)	S(5): 99.7; S(10): 0.3; Y(14): 0.0; Y(15): 0.3; S(16): 99.7	S5; S16;	S126; S137	17		0	0	2	1299	2598	81.32	16374
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166	17		0	1	3	1203	3607	60.61	12002
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166		3.59	0	1	4	902.4	3607	59.74	11829
EMDES LANLsEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	M2(Oxidation)S 10(Phospho) S16(Phospho)	S(5): 4.1; S(10): 95.9; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S10; S16;	S131; S137		3.44	0	0	3	872	2614	74.47	15063
EMDES LANLsEDEYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S10(Phospho) S16(Phospho)	S(5): 0.2; S(10): 99.8; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S10; S16;	S131; S137		3.32	0	0	3	866.6	2598	80.88	16280
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166		3.27	0	1	3	1203	3607	59.94	11869
KLPPPPQAPPEEENsEPEEPsGVEGA AFQSR	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S17(Phospho)	S(17): 100.0; S(23): 0.0; S(32): 0.0	S17;	S166		2.65	0	1	3	1203	3607	60.61	12002

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#
EMDEsLANLSEDEYYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	M2(Oxidation)S5(Phospho)S16(Phospho)	S(5): 99.7; S(10): 0.2; Y(14): 0.0; Y(15): 0.2; S(16): 99.7	S5; S16;	S126; S137		2.62	0.001	0	2	1307	2614	74.46	15061
EMDEsLANLSEDEYYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S5(Phospho)S16(Phospho)	S(5): 100.0; S(10): 0.0; Y(14): 0.0; Y(15): 0.2; S(16): 99.8	S5; S16;	S126; S137		2.47	0.001	0	2	1299	2598	80.82	16268
EMDEsLANLSEDEYYsEEER	KDM1A	23028	lysine-specific histone demethylase 1A isoform b	S5(Phospho)S16(Phospho)	S(5): 99.7; S(10): 0.3; Y(14): 0.0; Y(15): 0.3; S(16): 99.7	S5; S16;	S126; S137		2.21	0.001	0	2	1299	2598	81.32	16374
TPQRGDEEGLGGEIEEEEEEDDsAE EGGAAR	KDM2A	22992	lysine-specific demethylase 2A isoform b	S26(Phospho)	T(1): 0.0; S(26): 100.0	S26;	S430	57		0	1	3	1258	3773	44.8	8604
TPQRGDEEGLGGEIEEEEEEDDsAE EGGAAR	KDM2A	22992	lysine-specific demethylase 2A isoform b	S26(Phospho)	T(1): 0.0; S(26): 100.0	S26;	S430		6.32	0	1	3	1258	3773	44.8	8604
TENSLANENQQPIKsEPsEGEePK	KDM2B	84678	lysine-specific demethylase 2B isoform b	S15(Phospho)S19(Phospho)	T(1): 0.0; S(4): 0.0; S(15): 100.0; S(19): 100.0	S15; S19;	S906; S910	19		0	1	3	982.1	2944	41.84	7959
TENSLANENQQPIKsEPsEGEePK	KDM2B	84678	lysine-specific demethylase 2B isoform b	S15(Phospho)S19(Phospho)	T(1): 0.0; S(4): 0.0; S(15): 100.0; S(19): 100.0	S15; S19;	S906; S910		4.8	0	1	3	982.1	2944	41.84	7959
DsISSDSETPSLSCR	KDM4A	9682	lysine-specific demethylase 4A	C15(Carbamidomethyl)S2(Phospho)	S(2): 99.9; S(4): 0.1; S(5): 0.0; S(7): 0.0; T(9): 0.0; S(10): 0.0; S(14): 0.0	S2;	S520	69		0	0	2	925.4	1850	48.33	9354
DsISSDSETPSLSCR	KDM4A	9682	lysine-specific demethylase 4A	C15(Carbamidomethyl)S2(Phospho)	S(2): 99.9; S(4): 0.1; S(5): 0.0; S(7): 0.0; T(9): 0.0; S(10): 0.0; S(14): 0.0	S2;	S520		3.19	0	0	2	925.4	1850	48.33	9354
EKVEPEVLSTDTQTSPePGtr	KDM5A	5927	lysine-specific demethylase 5A	T20(Phospho)	S(9): 0.0; T(10): 0.0; T(12): 0.0; T(14): 0.0; S(15): 3.4; T(20): 96.6	T20;	T209	22		0	1	3	794	2380	47.03	9083
EKVEPEVLSTDTQTSPePGtr	KDM5A	5927	lysine-specific demethylase 5A	T20(Phospho)	S(9): 0.0; T(10): 0.0; T(12): 0.0; T(14): 0.0; S(15): 3.4; T(20): 96.6	T20;	T209		3.39	0	1	3	794	2380	47.03	9083
SGsMDPSGAHPsVR	KHDRBS1	10657	KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 0.0; S(12): 0.0	S3;	S20	43		0	0	2	732.8	1465	25.65	4529
SGsMDPSGAHPsVR	KHDRBS1	10657	KH domain-containing, RNA-binding, signal transduction-associated protein 1 isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 0.0; S(12): 0.0	S3;	S20		3.52	0	0	2	732.8	1465	25.65	4529
VQIsPDSGGLPER	KHSRP	8570	far upstream element-binding protein 2	S4(Phospho)	S(4): 99.9; S(7): 0.1	S4;	S181	52		0	0	2	717.8	1435	50.68	9848
VQIsPDSGGLPER	KHSRP	8570	far upstream element-binding protein 2	S4(Phospho)	S(4): 99.9; S(7): 0.1	S4;	S181		2.66	0	0	2	717.8	1435	50.68	9848
VTSFsTPPtPER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	S5(Phospho)T9(Phospho)	T(2): 0.0; S(3): 0.0; S(5): 100.0; T(6): 0.0; T(9): 100.0	S5; T9;	S289; T293	52		0	0	2	739.8	1479	54	10585
VsTGDTPSPCGTEEDSSPAsPMHER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	C9(Carbamidomethyl)S2(Phospho)S19(Phospho)	S(2): 96.5; T(3): 3.2; T(6): 0.1; S(7): 0.1; T(11): 0.0; S(15): 0.0; S(16): 0.0; S(19): 100.0	S2; S19;	S262; S279	20		0	0	3	898.7	2694	39.34	7429
VsTGDTPSPCGTEEDSSPAsPMHER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	C9(Carbamidomethyl)S2(Phospho)	S(2): 99.6; T(3): 0.1; T(6): 0.1; S(7): 0.1; T(11): 0.0; S(15): 0.0; S(16): 0.0; S(19): 0.0	S2;	S262	19		0	0	3	872	2614	35.57	6639
VsTGDTPSPCGTEEDSSPAsPMHER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	C9(Carbamidomethyl)S2(Phospho)	S(2): 99.6; T(3): 0.1; T(6): 0.1; S(7): 0.1; T(11): 0.0; S(15): 0.0; S(16): 0.0; S(19): 0.0	S2;	S262		4.16	0	0	3	872	2614	35.57	6639
VsTGDTPSPCGTEEDSSPAsPMHER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	C9(Carbamidomethyl)S2(Phospho)	S(2): 96.5; T(3): 3.2; T(6): 0.1; S(7): 0.1; T(11): 0.0; S(15): 0.0; S(16): 0.0; S(19): 100.0	S2; S19;	S262; S279		3.73	0	0	3	898.7	2694	39.34	7429

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#
VTSFsTPPtPER	KIAA0930	23313	uncharacterized protein KIAA0930 isoform b	S5(Phospho) T9(Phospho)	T(2): 0.0; S(3): 0.0; S(5): 100.0; T(6): 0.0; T(9): 100.0	S5; T9;	S289; T293		3.14	0	0	2	739.8	1479	54	10585
NADsQEDAEEK	KIAA1462	57608	junctional protein associated with coronary artery disease	S4(Phospho)	S(4): 100.0	S4;	S1281		1.97	0.005	0	2	714.8	1429	28.63	5177
GsPSGGSTAEASDTLSIR	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S2(Phospho)	S(2): 100.0; S(4): 0.0; S(7): 0.0; T(8): 0.0; S(12): 0.0; T(14): 0.0; S(16): 0.0	S2;	S404	35		0	0	2	886.9	1773	50.66	9844
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673	32		0	0	3	760.7	2280	47.81	9243
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673	30		0	0	3	760.7	2280	48.32	9352
GsPsGGSTAEASDTLSIR	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S2(Phospho) S4(Phospho)	S(2): 99.8; S(4): 96.3; S(7): 3.9; T(8): 0.0; S(12): 0.0; T(14): 0.0; S(16): 0.0	S2; S4;	S404; S406	24		0	0	2	926.9	1853	63.1	12583
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673		5.44	0	0	3	760.7	2280	48.32	9352
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673		5.12	0	0	3	760.7	2280	47.81	9243
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673		3.94	0	0	3	760.7	2280	47.3	9139
GsPSGGSTAEASDTLSIR	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S2(Phospho)	S(2): 100.0; S(4): 0.0; S(7): 0.0; T(8): 0.0; S(12): 0.0; T(14): 0.0; S(16): 0.0	S2;	S404		3.81	0	0	2	886.9	1773	50.66	9844
DQsPPPsPPPSYHPPPPPTK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 99.6; S(11): 0.4; Y(12): 0.0; T(19): 0.0	S3; S7;	S669; S673		3.5	0	0	3	760.7	2280	47.2	9118
GsPsGGSTAEASDTLSIR	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S2(Phospho) S4(Phospho)	S(2): 99.8; S(4): 96.3; S(7): 3.9; T(8): 0.0; S(12): 0.0; T(14): 0.0; S(16): 0.0	S2; S4;	S404; S406		3.43	0	0	2	926.9	1853	63.1	12583
TLsPSSGYSSQSGTPlPPK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) T16(Phospho)	T(1): 4.8; S(3): 75.4; S(5): 4.8; S(6): 4.8; Y(8): 0.7; S(9): 5.1; S(10): 5.1; S(12): 0.8; T(14): 6.0; T(16): 92.4	S3; T16;	S520; T533	12		0.003	0	2	1076	2152	64.27	12879
TLsPSSGYSSQSGTPlPPK	KIAA1522	57648	uncharacterized protein KIAA1522 isoform 2	S3(Phospho) T16(Phospho)	T(1): 4.8; S(3): 75.4; S(5): 4.8; S(6): 4.8; Y(8): 0.7; S(9): 5.1; S(10): 5.1; S(12): 0.8; T(14): 6.0; T(16): 92.4	S3; T16;	S520; T533		1.69	0.003	0	2	1076	2152	64.27	12879
YQKLPSDEDESGTEESDNTPLLK	KIDINS220	57498	kinase D-interacting substrate of 220 kDa	S6(Phospho)	Y(1): 0.0; S(6): 97.2; S(11): 51.3; T(13): 51.3; S(16): 0.2; T(19): 0.0	S6;	S1521	18		0	1	3	919	2755	59.8	11840
YQKLPSDEDESGTEESDNTPLLK	KIDINS220	57498	kinase D-interacting substrate of 220 kDa	S6(Phospho)	Y(1): 0.0; S(6): 97.2; S(11): 51.3; T(13): 51.3; S(16): 0.2; T(19): 0.0	S6;	S1521		3.22	0	1	3	919	2755	59.8	11840
SDKNQQGFsPK	KIF15	56992	kinesin-like protein KIF15	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S568	44		0	1	2	658.3	1316	16.12	2509
SDKNQQGFsPK	KIF15	56992	kinesin-like protein KIF15	S9(Phospho)	S(1): 0.0; S(9): 100.0	S9;	S568		3.61	0	1	2	658.3	1316	16.12	2509
LDADsDsGDDSDKR	KIF1B	23095	kinesin-like protein KIF1B isoform alpha	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 99.9; S(11): 0.1	S5; S7;	S663; S665	56		0	1	2	828.3	1656	15.23	2321
LDADsDsGDDSDKR	KIF1B	23095	kinesin-like protein KIF1B isoform alpha	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 99.9; S(11): 0.1	S5; S7;	S663; S665		2.93	0	1	2	828.3	1656	15.23	2321
LYADsDsGDDSDKR	KIF1C	10749	kinesin-like protein KIF1C	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0; S(11): 0.0	S5; S7;	S674; S676	58		0	1	2	852.3	1704	24.03	4188

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#
LYADsDsGDDSDKR	KIF1C	10749	kinesin-like protein KIF1C	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0; S(11): 0.0	S5; S7;	S674; S676	54		0	1	2	852.3	1704	23.52	4080
LYADsDsGDDSDKR	KIF1C	10749	kinesin-like protein KIF1C	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0; S(11): 0.0	S5; S7;	S674; S676		3.12	0	1	2	852.3	1704	23.52	4080
LYADsDsGDDSDKR	KIF1C	10749	kinesin-like protein KIF1C	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0; S(11): 0.0	S5; S7;	S674; S676		2.6	0	1	2	852.3	1704	24.03	4188
SStVAPAQPDGAESEWTDVETR	KIF23	9493	kinesin-like protein KIF23 isoform 3	T3(Phospho)	S(1): 2.6; S(2): 2.6; T(3): 94.9; S(14): 0.0; T(17): 0.0; T(21): 0.0	T3;	T719	18		0	0	2	1207	2413	65.27	13111
SStVAPAQPDGAESEWTDVETR	KIF23	9493	kinesin-like protein KIF23 isoform 3	T3(Phospho)	S(1): 2.6; S(2): 2.6; T(3): 94.9; S(14): 0.0; T(17): 0.0; T(21): 0.0	T3;	T719		2.26	0	0	2	1207	2413	65.27	13111
NQsLVEENEK	KIF4A	24137	chromosome-associated kinesin KIF4A	S3(Phospho)	S(3): 100.0	S3;	S394		2.5	0	0	2	635.3	1270	25.96	4599
NQsLVEENEK	KIF4A	24137	chromosome-associated kinesin KIF4A	S3(Phospho)	S(3): 100.0	S3;	S394	12		0.002	0	2	635.3	1270	25.96	4599
sSPPSAGNSPSSLK	KLF3	51274	Krueppel-like factor 3	S1(Phospho)	S(1): 98.0; S(2): 2.0; S(5): 0.0; S(9): 0.0; S(11): 0.0; S(12): 0.0	S1;	S70	36		0	0	2	698.3	1396	28.78	5207
sSPPSAGNSPSSLK	KLF3	51274	Krueppel-like factor 3	S1(Phospho)	S(1): 98.0; S(2): 2.0; S(5): 0.0; S(9): 0.0; S(11): 0.0; S(12): 0.0	S1;	S70		2.59	0	0	2	698.3	1396	28.78	5207
QVLTAPGSAGQPRSEDEDSLEEAGSPAPGPCR	KLHDC4	54758	kelch domain-containing protein 4 isoform 3	C31(Carbamidomethyl)T4(Phospho)	T(4): 89.8; S(8): 7.1; S(14): 51.6; S(19): 51.6; S(25): 0.0	T4;	T346	18		0	1	4	881.4	3522	60.05	11892
QVLTAPGSAGQPRSEDEDSLEEAGSPAPGPCR	KLHDC4	54758	kelch domain-containing protein 4 isoform 3	C31(Carbamidomethyl)T4(Phospho)	T(4): 99.1; S(8): 4.2; S(14): 48.3; S(19): 48.3; S(25): 0.0	T4;	T346	18		0	1	3	1175	3522	59.97	11874
QVLTAPGSAGQPRSEDEDSLEEAGSPAPGPCR	KLHDC4	54758	kelch domain-containing protein 4 isoform 3	C31(Carbamidomethyl)T4(Phospho)	T(4): 89.8; S(8): 7.1; S(14): 51.6; S(19): 51.6; S(25): 0.0	T4;	T346		3.95	0	1	4	881.4	3522	60.05	11892
QVLTAPGSAGQPRSEDEDSLEEAGSPAPGPCR	KLHDC4	54758	kelch domain-containing protein 4 isoform 3	C31(Carbamidomethyl)T4(Phospho)	T(4): 99.1; S(8): 4.2; S(14): 48.3; S(19): 48.3; S(25): 0.0	T4;	T346		3	0	1	3	1175	3522	59.97	11874
ALSSAVQASPTsPGGSPsPSSGQR	KMT2A	4297	histone-lysine N-methyltransferase 2A isoform 2 precursor	S12(Phospho) S19(Phospho)	S(3): 0.0; S(4): 0.0; S(9): 0.2; T(11): 4.3; S(12): 95.3; S(16): 0.2; S(18): 0.2; S(19): 99.8; S(21): 0.0; S(22): 0.0	S12; S19;	S3511; S3518	21		0	0	3	820.7	2460	50.33	9774
ALSSAVQASPTsPGGSPsPSSGQR	KMT2A	4297	histone-lysine N-methyltransferase 2A isoform 2 precursor	S12(Phospho) S19(Phospho)	S(3): 0.0; S(4): 0.0; S(9): 0.2; T(11): 4.3; S(12): 95.3; S(16): 0.2; S(18): 0.2; S(19): 99.8; S(21): 0.0; S(22): 0.0	S12; S19;	S3511; S3518		4.83	0	0	3	820.7	2460	50.33	9774
GPGEPTsPTLHPPTpPILSTDR	KMT2A	4297	histone-lysine N-methyltransferase 2A isoform 2 precursor	S7(Phospho) T15(Phospho)	S(7): 96.2; T(9): 3.8; T(15): 99.7; S(20): 0.2; T(21): 0.2	S7; T15;	S1837; T1845		3.54	0	0	3	846.7	2538	81.29	16369
NVPQEESLEDSDVDADFK	KPNA3	3839	importin subunit alpha-4	S11(Phospho)	S(7): 0.0; S(11): 100.0	S11;	S60	42		0	0	2	1059	2117	63.5	12685
NVPQEESLEDSDVDADFK	KPNA3	3839	importin subunit alpha-4	S11(Phospho)	S(7): 0.0; S(11): 100.0	S11;	S60		2.52	0	0	2	1059	2117	63.5	12685
NVPHEDECEDsDIDGDYR	KPNA4	3840	importin subunit alpha-3	C8(Carbamidomethyl) S11(Phospho)	S(11): 100.0; Y(17): 0.0	S11;	S60	40		0	0	3	743.6	2229	48.23	9334
NVPHEDECEDsDIDGDYR	KPNA4	3840	importin subunit alpha-3	C8(Carbamidomethyl) S11(Phospho)	S(11): 100.0; Y(17): 0.0	S11;	S60		3.26	0	0	3	743.6	2229	48.23	9334
YVDEENsDGETSNGHR	KRI1	65095	protein KRI1 homolog	S7(Phospho)	Y(1): 0.0; S(7): 100.0; T(11): 0.0; S(12): 0.0	S7;	S142	66		0	0	2	916.3	1832	16.04	2492
AFVEDsEDEGDGAGEGGSSLLQK	KRI1	65095	protein KRI1 homolog	S6(Phospho)	S(6): 100.0; S(17): 0.0; S(18): 0.0	S6;	S177	29		0	0	2	1160	2320	63.85	12774

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#
AFVEdsEDEDGAGEGGSSLLQK	KRI1	65095	protein KRI1 homolog	S6(Phospho)	S(6): 100.0; S(17): 0.0; S(18): 0.0	S6;	S177	24		0	0	3	774	2320	63.84	12771
AFVEdsEDEDGAGEGGSSLLQK	KRI1	65095	protein KRI1 homolog	S6(Phospho)	S(6): 100.0; S(17): 0.0; S(18): 0.0	S6;	S177		3.76	0	0	3	774	2320	63.84	12771
AFVEdsEDEDGAGEGGSSLLQK	KRI1	65095	protein KRI1 homolog	S6(Phospho)	S(6): 100.0; S(17): 0.0; S(18): 0.0	S6;	S177		3.39	0	0	2	1160	2320	63.85	12774
YVDEENsDGETSNHR	KRI1	65095	protein KRI1 homolog	S7(Phospho)	Y(1): 0.0; S(7): 100.0; T(11): 0.0; S(12): 0.0	S7;	S142		3.15	0	0	2	916.3	1832	16.04	2492
LsGGLGAGSCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0	S2;	S32	65		0	0	2	557.7	1114	31.59	5792
LsGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl)S2(Phospho) S9(Phospho)	S(2): 100.0; S(9): 100.0	S2; S9;	S32; S39	58		0	0	2	597.7	1194	42.27	8048
LSGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S9(Phospho)	S(2): 0.0; S(9): 100.0	S9;	S39	56		0	0	2	557.7	1114	29.72	5405
QFtSsSSIKGSSGLGGSSR	KRT17	3872	keratin, type I cytoskeletal 17	T3(Phospho) S5(Phospho)	T(3): 99.9; S(4): 3.4; S(5): 90.2; S(6): 3.3; S(7): 3.3; S(11): 0.0; S(12): 0.0; S(18): 0.0; S(19): 0.0	T3; S5;	T9; S11	34		0	1	3	683	2047	42.87	8175
QFtSSSSIKGSSGLGGSSR	KRT17	3872	keratin, type I cytoskeletal 17	T3(Phospho)	T(3): 97.7; S(4): 49.9; S(5): 49.9; S(6): 0.2; S(7): 2.3; S(11): 0.0; S(12): 0.0; S(18): 0.0; S(19): 0.0	T3;	T9	31		0	1	2	1024	2047	42.91	8184
TSCRLsGGLGAGSCR	KRT17	3872	keratin, type I cytoskeletal 17	C3(Carbamidomethyl) C14(Carbamido methyl)S6(Phospho)	T(1): 50.8; S(2): 50.8; S(6): 98.3; S(13): 0.0	S6;	S32	27		0	1	2	849.8	1699	39.05	7368
LSGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S9(Phospho)	S(2): 0.0; S(9): 100.0	S9;	S39		3.49	0	0	2	557.7	1114	29.72	5405
QFtSsSSIKGSSGLGGSSR	KRT17	3872	keratin, type I cytoskeletal 17	T3(Phospho) S5(Phospho)	T(3): 99.9; S(4): 3.4; S(5): 90.2; S(6): 3.3; S(7): 3.3; S(11): 0.0; S(12): 0.0; S(18): 0.0; S(19): 0.0	T3; S5;	T9; S11		3.46	0	1	3	683	2047	42.87	8175
LsGGLGAGSCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0	S2;	S32		3.41	0	0	2	557.7	1114	31.59	5792
LsGGLGAGsCR	KRT17	3872	keratin, type I cytoskeletal 17	C10(Carbamido methyl)S2(Phospho) S9(Phospho)	S(2): 100.0; S(9): 100.0	S2; S9;	S32; S39		3.23	0	0	2	597.7	1194	42.27	8048
QFtSSSSIKGSSGLGGSSR	KRT17	3872	keratin, type I cytoskeletal 17	T3(Phospho)	T(3): 97.7; S(4): 49.9; S(5): 49.9; S(6): 0.2; S(7): 2.3; S(11): 0.0; S(12): 0.0; S(18): 0.0; S(19): 0.0	T3;	T9		2.74	0	1	2	1024	2047	42.91	8184
TSCRLsGGLGAGSCR	KRT17	3872	keratin, type I cytoskeletal 17	C3(Carbamidomethyl) C14(Carbamido methyl)S6(Phospho)	T(1): 50.8; S(2): 50.8; S(6): 98.3; S(13): 0.0	S6;	S32		2.67	0	1	2	849.8	1699	39.05	7368
APsiHGGSGGR	KRT19	3880	keratin, type I cytoskeletal 19	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S35	28		0	0	2	538.2	1075	13.67	1992
APsiHGGSGGR	KRT19	3880	keratin, type I cytoskeletal 19	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S35		3.05	0	0	2	538.2	1075	13.67	1992
sLYNLGGSK	KRT5	3852	keratin, type II cytoskeletal 5	S1(Phospho)	S(1): 100.0; Y(3): 0.0; S(8): 0.0	S1;	S64	50		0	0	2	509.7	1018	47.86	9256

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#
sLYNLGGSK	KRT5	3852	keratin, type II cytoskeletal 5	S1(Phospho)	S(1): 100.0; Y(3): 0.0; S(8): 0.0	S1;	S64		3.22	0	0	2	509.7	1018	47.86	9256
GLGVGFGSGGGsSSsVK	KRT5	3852	keratin, type II cytoskeletal 5	S12(Phospho) S15(Phospho)	S(8): 0.0; S(12): 99.9; S(13): 0.1; S(14): 3.3; S(15): 96.7	S12; S15;	S571; S574	11		0.001	0	2	800.3	1600	70.06	14178
GLGVGFGSGGGsSSsVK	KRT5	3852	keratin, type II cytoskeletal 5	S12(Phospho) S15(Phospho)	S(8): 0.0; S(12): 99.9; S(13): 0.1; S(14): 3.3; S(15): 96.7	S12; S15;	S571; S574		3.19	0.005	0	2	800.3	1600	70.06	14178
AFsSRsYTSGPGR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 0.2; S(6): 99.7; Y(7): 0.1; T(8): 0.1; S(9): 0.0; S(13): 0.0	S3; S6;	S21; S24	15		0	1	2	810.3	1620	38.06	7159
AFsSRsYTSGPGR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 3.1; S(6): 93.9; Y(7): 3.0; T(8): 0.1; S(9): 0.0; S(13): 0.0	S3; S6;	S21; S24	11		0.001	1	2	810.3	1620	37.53	7050
AFsSRsYTSGPGR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 0.2; S(6): 99.7; Y(7): 0.1; T(8): 0.1; S(9): 0.0; S(13): 0.0	S3; S6;	S21; S24		2.19	0.001	1	2	810.3	1620	38.06	7159
IsSSsFSR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S2(Phospho) S5(Phospho)	S(2): 95.3; S(3): 2.5; S(4): 4.7; S(5): 97.5; S(7): 0.1	S2; S5;	S34; S37	20		0.003	0	2	515.7	1030	44.49	8528
AFsSRsYTSGPGR	KRT8	3856	keratin, type II cytoskeletal 8 isoform 2	S3(Phospho) S6(Phospho)	S(3): 99.9; S(4): 3.1; S(6): 93.9; Y(7): 3.0; T(8): 0.1; S(9): 0.0; S(13): 0.0	S3; S6;	S21; S24		2.6	0.003	1	2	810.3	1620	37.53	7050
IPSEEEADMSsPTQR	LAD1	3898	ladinin-1	S12(Phospho)	S(3): 0.0; S(11): 0.0; S(12): 99.9; T(14): 0.0	S12;	S356	40		0	1	3	628.9	1885	27.38	4911
IPSEEEADMSsPTQR	LAD1	3898	ladinin-1	S12(Phospho)	S(3): 0.0; S(11): 0.0; S(12): 99.9; T(14): 0.0	S12;	S356		4.43	0	1	3	628.9	1885	27.38	4911
LEAEGRNsLsPVQATQKPLVSK	LAD1	3898	ladinin-1	S9(Phospho) S11(Phospho)	S(9): 100.0; S(11): 100.0; T(16): 0.0; S(22): 0.0	S9; S11;	S121; S123		3.86	0	1	3	881.1	2641	48.93	9481
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	41		0	0	2	595.7	1190	19.27	3184
sLPTTVPEsPNYR	LARP1	23367	la-related protein 1	S1(Phospho)	S(1): 99.9; T(4): 0.1; T(5): 0.0; S(9): 50.0; Y(12): 50.0	S1;	S689	30		0	0	2	810.8	1621	65.81	13234
sLPTTVPEsPNYR	LARP1	23367	la-related protein 1	S1(Phospho)	S(1): 99.9; T(4): 0.1; T(5): 0.0; S(9): 50.0; Y(12): 50.0	S1;	S689	29		0	0	2	810.8	1621	66.34	13355
NTFTAWsDEEsDYEIDDRDVNK	LARP1	23367	la-related protein 1	S7(Phospho) S11(Phospho)	T(2): 0.0; T(4): 0.0; S(7): 94.4; S(11): 94.4; Y(13): 11.2	S7; S11;	S550; S554		3.42	0	1	3	937	2809	73.78	14917
sLPTTVPEsPNYR	LARP1	23367	la-related protein 1	S1(Phospho)	S(1): 99.9; T(4): 0.1; T(5): 0.0; S(9): 50.0; Y(12): 50.0	S1;	S689		3.08	0	0	2	810.8	1621	65.81	13234
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		2.69	0	0	2	595.7	1190	19.27	3184
sLPTTVPEsPNYR	LARP1	23367	la-related protein 1	S1(Phospho)	S(1): 99.9; T(4): 0.1; T(5): 0.0; S(9): 50.0; Y(12): 50.0	S1;	S689		2.68	0	0	2	810.8	1621	66.34	13355
tPRTPRtPQLK	LARP1	23367	la-related protein 1	T1(Phospho) T7(Phospho)	T(1): 100.0; T(4): 0.0; T(7): 100.0	T1; T7;	T705; T711		4.19	0.001	2	3	485.6	1455	22.67	3903
SLPTTVPeSPNYR	LARP1	23367	la-related protein 1	S9(Phospho)	S(1): 0.0; T(4): 0.0; T(5): 0.0; S(9): 99.9; Y(12): 0.1	S9;	S697	17		0.002	0	2	770.9	1541	53.88	10560
tPRTPRtPQLK	LARP1	23367	la-related protein 1	T1(Phospho) T7(Phospho)	T(1): 100.0; T(4): 0.0; T(7): 100.0	T1; T7;	T705; T711		3.92	0.003	2	3	485.6	1455	23.19	4014
NTFTAWsDEEsDYEIDDRDVNK	LARP1	23367	la-related protein 1	T4(Phospho)	T(2): 8.3; T(4): 91.2; S(7): 33.5; S(11): 33.5; Y(13): 33.5	T4;	T547		1.73	0.005	1	2	1405	2809	73.97	14950
NTFTAWsDEEsDYEIDDRDVNK	LARP1	23367	la-related protein 1	S7(Phospho)	T(2): 0.5; T(4): 0.5; S(7): 98.9; S(11): 50.0; Y(13): 50.0	S7;	S550		2.54	0.006	1	3	937	2809	74.31	15028
SPsPAHLpDDPK	LARP4B	23185	la-related protein 4B	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S601	26		0	0	2	670.8	1341	31.8	5835
SPsPAHLpDDPK	LARP4B	23185	la-related protein 4B	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S601		3.48	0	0	2	670.8	1341	31.8	5835

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#
YLSPGWGsAsEEEPSR	LARP6	55323	la-related protein 6 isoform 2	S8(Phospho) S10(Phospho)	Y(1): 0.0; S(3): 0.0; S(8): 100.0; S(10): 99.9; S(15): 0.1	S8; S10;	S56; S58	32		0	0	2	956.4	1912	73.54	14868
YLSPGWGsAsEEEPSR	LARP6	55323	la-related protein 6 isoform 2	S8(Phospho) S10(Phospho)	Y(1): 0.0; S(3): 0.0; S(8): 100.0; S(10): 99.9; S(15): 0.1	S8; S10;	S56; S58		2.26	0.001	0	2	956.4	1912	73.54	14868
SSsEDAESLAPR	LARP7	51574	la-related protein 7 isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(8): 0.0	S3;	S300	78		0	0	2	664.8	1329	38.32	7216
sRPTSEGsDIESTEPQK	LARP7	51574	la-related protein 7 isoform 1	S1(Phospho) S8(Phospho)	S(1): 93.8; T(4): 3.1; S(5): 3.1; S(8): 100.0; S(12): 0.0; T(13): 0.0	S1; S8;	S254; S261	28		0	0	2	1004	2008	31.14	5699
DIEIstEEEKDTGDLK	LARP7	51574	la-related protein 7 isoform 1	S5(Phospho) T6(Phospho)	S(5): 100.0; T(6): 100.0; T(12): 0.0	S5; T6;	S337; T338	19		0	1	2	991.4	1982	57.79	11403
sRPTSEGsDIESTEPQK	LARP7	51574	la-related protein 7 isoform 1	S1(Phospho) S8(Phospho)	S(1): 93.8; T(4): 3.1; S(5): 3.1; S(8): 100.0; S(12): 0.0; T(13): 0.0	S1; S8;	S254; S261		3.35	0	0	2	1004	2008	31.14	5699
SSsEDAESLAPR	LARP7	51574	la-related protein 7 isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(8): 0.0	S3;	S300		3.03	0	0	2	664.8	1329	38.32	7216
DIEIstEEEEKDTGDLK	LARP7	51574	la-related protein 7 isoform 1	S5(Phospho) T6(Phospho)	S(5): 100.0; T(6): 100.0; T(12): 0.0	S5; T6;	S337; T338		2.05	0	1	2	991.4	1982	57.79	11403
DIEIstEEEEKDTGDLKDSSLLK	LARP7	51574	la-related protein 7 isoform 1	S5(Phospho) T6(Phospho)	S(5): 100.0; T(6): 99.5; T(12): 0.6; S(18): 0.0; S(19): 0.0	S5; T6;	S337; T338		1.61	0.005	2	3	875.7	2625	68.58	13870
SSVQGLPAGPNSDTSIDAKVLGsk	LATS2	26524	serine/threonine-protein kinase LATS2	S23(Phospho)	S(1): 0.0; S(2): 0.0; S(12): 0.0; T(14): 0.0; S(15): 0.0; S(23): 99.9	S23;	S54		4.8	0.003	1	3	803.4	2408	84.83	17007
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	38		0	1	2	834.3	1668	17.79	2875
WTKPsFsDSER	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S8(Phospho)	T(2): 0.0; S(5): 0.0; S(6): 100.0; S(8): 100.0; S(10): 0.0	S6; S8;	S497; S499	24		0	0	2	793.8	1587	43.36	8278
ASVRGssEEDEDARTPDR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 99.8; S(7): 95.7; T(15): 4.6	S6; S7;	S138; S139	14		0	2	3	712.9	2137	21.18	3587
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		4.01	0	1	2	834.3	1668	17.79	2875
GSsEEDEDARTPDR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S3(Phospho)	S(2): 2.3; S(3): 97.7; T(11): 0.0	S3;	S139	26		0.001	1	2	822.3	1644	15.88	2457
ASVRGssEEDEDARTPDR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 99.8; S(7): 95.7; T(15): 4.6	S6; S7;	S138; S139		3.93	0.003	2	3	712.9	2137	21.18	3587
ASVRGssEEDEDARTPDR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S7(Phospho)	S(2): 0.3; S(6): 99.5; S(7): 95.2; T(15): 5.1	S6; S7;	S138; S139		3.79	0.003	2	3	712.9	2137	21.79	3711
RASVRGssEEDEDAR	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S3(Phospho) S7(Phospho) S8(Phospho)	S(3): 100.0; S(7): 100.0; S(8): 100.0	S3; S7; S8;	S134; S138; S139		2.43	0.005	2	2	952.3	1904	16.97	2700
WTKPsFsDSER	LEMD2	221496	LEM domain-containing protein 2 isoform 1	S6(Phospho) S8(Phospho)	T(2): 0.0; S(5): 0.0; S(6): 100.0; S(8): 100.0; S(10): 0.0	S6; S8;	S497; S499		2.18	0.009	0	2	793.8	1587	43.36	8278
ENySDSEEEEEDDVVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	S4(Phospho)	Y(3): 50.8; S(4): 98.5; S(6): 50.8; S(16): 0.0; S(17): 0.0	S4;	S259	75		0	0	2	1111	2222	41.27	7838
ENySDSEEEEEDDVVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho)	Y(3): 93.9; S(4): 3.1; S(6): 3.1; S(16): 0.0; S(17): 0.0	Y3;	Y258	61		0	0	2	1071	2142	34.48	6395
ENySDSEEEEEDDVVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho) S4(Phospho)	Y(3): 99.8; S(4): 100.0; S(6): 0.2; S(16): 0.0; S(17): 0.0	Y3; S4;	Y258; S259	54		0	0	2	1111	2222	41.8	7950
LVPySCRENySDSEEEEEDDVVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	C6(Carbamidomethyl)Y4(Phospho) S5(Phospho)	Y(4): 97.8; S(5): 97.8; Y(10): 1.4; S(11): 1.4; S(13): 1.4; S(23): 0.0; S(24): 0.0	Y4; S5;	Y252; S253	32		0	1	3	1033	3097	53.5	10470

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#
ENySDSEEDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho)	Y(3): 93.9; S(4): 3.1; S(6): 3.1; S(16): 0.0; S(17): 0.0	Y3;	Y258		3.47	0	0	2	1071	2142	34.48	6395
ENySDSEEDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	S4(Phospho)	Y(3): 50.8; S(4): 98.5; S(6): 50.8; S(16): 0.0; S(17): 0.0	S4;	S259		3.2	0	0	2	1111	2222	41.27	7838
ENySDSEEDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	Y3(Phospho) S4(Phospho)	Y(3): 99.8; S(4): 100.0; S(6): 0.2; S(16): 0.0; S(17): 0.0	Y3; S4;	Y258; S259		2.89	0	0	2	1111	2222	41.8	7950
LVPySCRENySDSEEDDDVASSR	LEMD3	23592	inner nuclear membrane protein Man1 isoform 2	C6(Carbamidomethyl)Y4(Phospho) S5(Phospho)	Y(4): 97.8; S(5): 97.8; Y(10): 1.4; S(11): 1.4; S(13): 1.4; S(23): 0.0; S(24): 0.0	Y4; S5;	Y252; S253		2.8	0	1	3	1033	3097	53.5	10470
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	65		0	1	2	768.8	1537	22.19	3799
KLtsDEEGEPSGK	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	S4(Phospho)	T(3): 1.7; S(4): 98.3; S(11): 0.0	S4;	S570	60		0	1	2	728.8	1457	18.88	3100
KLtsDEEGEPSGKR	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	35		0	2	3	564.9	1693	18.01	2921
KLtsDEEGEPSGK	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	S4(Phospho)	T(3): 1.7; S(4): 98.3; S(11): 0.0	S4;	S570		4.43	0	1	2	728.8	1457	18.88	3100
KLtsDEEGEPSGKR	LEO1	123169	RNA polymerase-associated protein LEO1 isoform 2	S4(Phospho)	T(3): 2.6; S(4): 97.4; S(11): 0.0	S4;	S570		2.88	0.004	2	3	538.2	1613	16.41	2572
VLGsEGEEDEALSPAK	LIG1	3978	DNA ligase 1 isoform 3	S4(Phospho) S14(Phospho)	S(4): 100.0; S(14): 100.0	S4; S14;	S66; S76	65		0	0	2	960.4	1920	61.14	12120
VLGsEGEEDEALSPAK	LIG1	3978	DNA ligase 1 isoform 3	S4(Phospho) S14(Phospho)	S(4): 100.0; S(14): 100.0	S4; S14;	S66; S76		4.93	0	0	2	960.4	1920	61.14	12120
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	63		0	0	2	585.3	1170	24.94	4378
SEVQQPVHPKPLsPDSR	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S13(Phospho)	S(1): 0.0; S(13): 100.0; S(16): 0.0	S13;	S60	25		0	0	3	661	1981	32.05	5888
SEVQQPVHPKPLsPDSR	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S13(Phospho)	S(1): 0.0; S(13): 100.0; S(16): 0.0	S13;	S60	25		0	0	3	661	1981	31.55	5784
SEVQQPVHPKPLsPDSR	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S13(Phospho)	S(1): 0.0; S(13): 100.0; S(16): 0.0	S13;	S60		5.02	0	0	3	661	1981	32.05	5888
SEVQQPVHPKPLsPDSR	LIMA1	51474	LIM domain and actin-binding protein 1 isoform 4	S13(Phospho)	S(1): 0.0; S(13): 100.0; S(16): 0.0	S13;	S60		3.99	0	0	3	661	1981	31.55	5784
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		3.55	0	0	2	585.3	1170	24.94	4378
ASVLDTSMSAGSGsPSK	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S14(Phospho)	S(2): 0.0; T(6): 0.0; S(7): 0.0; S(9): 0.0; S(12): 0.0; S(14): 100.0; S(16): 0.0	S14;	S357	72		0	0	2	831.4	1662	49.24	9545
GSSDGRGsDSESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S8(Phospho)	S(2): 0.1; S(3): 3.6; S(8): 96.3; S(10): 0.0; S(12): 0.0	S8;	S77	45		0	1	3	613.6	1839	19.11	3150
SRQTPsPDVVLR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	T4(Phospho) S6(Phospho)	S(1): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T61; S63	33		0	1	2	757.8	1515	48.97	9489
GSSDGRGsDsESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S8(Phospho) S10(Phospho)	S(2): 0.0; S(3): 0.0; S(8): 100.0; S(10): 96.6; S(12): 3.4	S8; S10;	S77; S79	23		0	1	2	959.9	1919	21.72	3698
GSSDGRGsDSESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S3(Phospho) S8(Phospho)	S(2): 0.1; S(3): 99.9; S(8): 99.7; S(10): 0.1; S(12): 0.1	S3; S8;	S72; S77	19		0	1	3	640.2	1919	23.11	3996
GSSDGRGsDSESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S8(Phospho)	S(2): 0.1; S(3): 3.6; S(8): 96.3; S(10): 0.0; S(12): 0.0	S8;	S77		4.84	0	1	3	613.6	1839	19.11	3150
ASVLDTSMSAGSGsPSK	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S14(Phospho)	S(2): 0.0; T(6): 0.0; S(7): 0.0; S(9): 0.0; S(12): 0.0; S(14): 100.0; S(16): 0.0	S14;	S357		4.62	0	0	2	831.4	1662	49.24	9545

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#
GSsDGRGsDSESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S3(Phospho) S8(Phospho)	S(2): 0.1; S(3): 99.9; S(8): 99.7; S(10): 0.1; S(12): 0.1	S3; S8;	S72; S77		3.25	0	1	3	640.2	1919	23.11	3996
SRQTpSPDVVLR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	T4(Phospho) S6(Phospho)	S(1): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T61; S63		3	0	1	2	757.8	1515	48.97	9489
GSSDGRGsDsESDLPHR	LIMCH1	22998	LIM and calponin homology domains-containing protein 1 isoform e	S8(Phospho) S10(Phospho)	S(2): 0.0; S(3): 0.0; S(8): 100.0; S(10): 96.6; S(12): 3.4	S8; S10;	S77; S79		2.1	0	1	2	959.9	1919	21.72	3698
SCsIDRSPGAGSLGSPASQR	LIMK1	3984	LIM domain kinase 1 isoform 2	C2(Carbamidomethyl)S3(Phospho)	S(1): 4.2; S(3): 91.7; S(7): 4.3; S(12): 49.9; S(15): 49.9; S(18): 0.0	S3;	S264	12		0.004	1	3	717.3	2150	41.84	7960
SCsIDRSPGAGSLGSPASQR	LIMK1	3984	LIM domain kinase 1 isoform 2	C2(Carbamidomethyl)S3(Phospho)	S(1): 4.2; S(3): 91.7; S(7): 4.3; S(12): 49.9; S(15): 49.9; S(18): 0.0	S3;	S264		3.15	0.007	1	3	717.3	2150	41.84	7960
ERECsPSPPLPPEDEEGSEVTNSK	LIN37	55957	protein lin-37 homolog	C4(Carbamidomethyl)S5(Phospho) S7(Phospho)	S(5): 95.2; S(7): 95.2; S(8): 9.7; S(20): 0.0; T(23): 0.0; S(25): 0.0	S5; S7;	S135; S137	20		0	1	3	1011	3030	62.63	12460
ERECsPSPPLPPEDEEGSEVTNSK	LIN37	55957	protein lin-37 homolog	C4(Carbamidomethyl)S5(Phospho) S7(Phospho)	S(5): 95.2; S(7): 95.2; S(8): 9.7; S(20): 0.0; T(23): 0.0; S(25): 0.0	S5; S7;	S135; S137		3.95	0	1	3	1011	3030	62.63	12460
IAIsPLKsPNK	LIN54	132660	protein lin-54 homolog isoform b	S4(Phospho) S8(Phospho)	S(4): 100.0; S(8): 100.0	S4; S8;	S89; S93		2.52	0.005	1	2	664.3	1328	50.67	9847
ARNsGtQSDGEEKQPGLVMER	LLGL2	3993	lethal(2) giant larvae protein homolog 2 isoform a	S4(Phospho) T6(Phospho)	S(4): 100.0; T(6): 96.1; S(8): 3.9	S4; T6;	S961; T963	33		0	2	3	817	2449	37.89	7125
ARNsGtQSDGEEKQPGLVMER	LLGL2	3993	lethal(2) giant larvae protein homolog 2 isoform a	M19(Oxidation) S4(Phospho) T6(Phospho)	S(4): 99.8; T(6): 99.8; S(8): 0.4	S4; T6;	S961; T963	30		0	2	3	822.3	2465	28.22	5092
ARNsGtQSDGEEKQPGLVMER	LLGL2	3993	lethal(2) giant larvae protein homolog 2 isoform a	S4(Phospho) T6(Phospho)	S(4): 100.0; T(6): 96.1; S(8): 3.9	S4; T6;	S961; T963		4.24	0	2	3	817	2449	37.89	7125
ARNsGtQSDGEEKQPGLVMER	LLGL2	3993	lethal(2) giant larvae protein homolog 2 isoform a	M19(Oxidation) S4(Phospho) T6(Phospho)	S(4): 99.8; T(6): 99.8; S(8): 0.4	S4; T6;	S961; T963		3.47	0	2	3	822.3	2465	28.22	5092
ASsHSsQTQGGGSVTK	LMNA	4000	lamin isoform A-delta10	S3(Phospho) S6(Phospho)	S(2): 0.1; S(3): 99.8; S(5): 0.2; S(6): 97.1; T(8): 2.8; S(13): 0.0; T(15): 0.0	S3; S6;	S404; S407	57		0	0	2	839.8	1679	12.55	1744
sVGGSGGGSGFDNLVTR	LMNA	4000	lamin isoform A-delta10	S1(Phospho)	S(1): 99.9; S(5): 0.1; S(9): 0.0; T(16): 0.0	S1;	S598	52		0	0	2	823.9	1647	58.42	11539
SGAQASSTPLsPTR	LMNA	4000	lamin isoform A-delta10	S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 0.0; S(11): 98.6; T(13): 1.4	S11;	S22	49		0	0	2	720.3	1440	31.62	5799
SGAQASSTPLsPTR	LMNA	4000	lamin isoform A-delta10	T8(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 100.0; S(11): 50.0; T(13): 50.0	T8;	T19	36		0	0	2	760.3	1520	35.18	6557
LRLsPSPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392	32		0	1	2	701.3	1402	40.18	7611
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458	27		0	1	2	929.9	1859	46.71	9017
LRLsPSPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392	25		0	1	2	701.3	1402	39.64	7495
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	M9(Oxidation) S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458	25		0	1	3	625.6	1875	33.92	6277
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	M9(Oxidation) S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458	24		0	1	2	937.9	1875	33.89	6271
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458	22		0	1	3	620.3	1859	46.89	9053
LRLsPSPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392	20		0	1	2	701.3	1402	40.7	7720

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#
ASsHSsQTQGGGSVTK	LMNA	4000	lamin isoform A-delta10	S3(Phospho) S6(Phospho)	S(2): 0.1; S(3): 99.8; S(5): 0.2; S(6): 97.1; T(8): 2.8; S(13): 0.0; T(15): 0.0	S3; S6;	S404; S407		4.76	0	0	2	839.8	1679	12.55	1744
SGAQASStPLSPTR	LMNA	4000	lamin isoform A-delta10	T8(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 100.0; S(11): 50.0; T(13): 50.0	T8;	T19		4.3	0	0	2	760.3	1520	35.18	6557
SGAQASStPLSPTR	LMNA	4000	lamin isoform A-delta10	S11(Phospho)	S(1): 0.0; S(6): 0.0; S(7): 0.0; T(8): 0.0; S(11): 98.6; T(13): 1.4	S11;	S22		4.25	0	0	2	720.3	1440	31.62	5799
LRLsPsPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392		3.5	0	1	2	701.3	1402	39.64	7495
sVGGSGGGSGFDNLVTR	LMNA	4000	lamin isoform A-delta10	S1(Phospho)	S(1): 99.9; S(5): 0.1; S(9): 0.0; T(16): 0.0	S1;	S598		3.23	0	0	2	823.9	1647	58.42	11539
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458		3.23	0	1	3	620.3	1859	46.89	9053
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	M9(Oxidation) S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458		3.14	0	1	3	625.6	1875	33.92	6277
LRLsPsPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392		3.1	0	1	2	701.3	1402	40.7	7720
LRLsPsPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392		3.08	0	1	2	701.3	1402	40.18	7611
LRLsPsPTSQR	LMNA	4000	lamin isoform A-delta10	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(8): 0.0; S(9): 0.0	S4; S6;	S390; S392		2.54	0	1	2	701.3	1402	41.23	7829
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458		1.99	0	1	2	929.9	1859	46.71	9017
sNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	S1(Phospho)	S(1): 96.4; S(6): 3.6	S1;	S458		1.94	0	0	2	808.8	1617	56.83	11195
NKsNEDQSMGNWQIK	LMNA	4000	lamin isoform A-delta10	M9(Oxidation) S3(Phospho)	S(3): 100.0; S(8): 0.0	S3;	S458		2.11	0.005	1	2	937.9	1875	33.89	6271
LSPsPTSQRSR	LMNA	4000	lamin isoform A-delta10	S4(Phospho)	S(2): 0.0; S(4): 99.9; T(6): 0.1; S(7): 50.0; S(10): 50.0	S4;	S392	16		0.007	1	2	688.3	1376	19.36	3203
AGGPtTtPLSPTR	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	25		0	0	2	657.8	1315	43.66	8340
LKLsPsPSSR	LMNB1 LMNB2	4001 84823	lamin-B1 isoform 1 lamin-B2	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	18		0	1	2	616.3	1232	37.52	7048
LKLsPsPSSR	LMNB1 LMNB2	4001 84823	lamin-B1 isoform 1 lamin-B2	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	3.52		0	1	2	616.3	1232	37.52	7048
ATSSsGSLSATGR	LMNB2	84823	lamin-B2	S6(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; S(5): 0.0; S(6): 99.9; S(8): 0.0; S(10): 0.0; T(12): 0.0	S6;	S422	84		0	0	2	674.8	1349	20.63	3471
ATSSsGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 1.9; S(5): 96.2; S(6): 1.9; S(8): 0.0; S(10): 0.0; T(12): 0.0	S5;	S421	74		0	0	2	674.8	1349	21.2	3591
ATSSsGSLsATGR	LMNB2	84823	lamin-B2	S10(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(8): 0.0; S(10): 100.0; T(12): 0.0	S10;	S426	70		0	0	2	674.8	1349	20.04	3345
AGGPAtPLSPTR	LMNB2	84823	lamin-B2	T6(Phospho) S9(Phospho)	T(6): 100.0; S(9): 98.2; T(11): 1.8	T6; S9;	T34; S37	30		0	0	2	642.8	1285	43.02	8206
ATSSsGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho)	T(2): 3.8; S(3): 0.2; S(4): 3.8; S(5): 88.6; S(6): 3.8; S(8): 49.0; S(10): 49.0; T(12): 2.1	S5;	S421	14		0	0	2	714.8	1429	27.28	4889
ATSSsGSLsATGR	LMNB2	84823	lamin-B2	S10(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; S(5): 0.0; S(6): 0.0; S(8): 0.0; S(10): 100.0; T(12): 0.0	S10;	S426	3.56		0	0	2	674.8	1349	20.04	3345

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#
ATSSSsGSLSATGR	LMNB2	84823	lamin-B2	S6(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; S(5): 0.0; S(6): 99.9; S(8): 0.0; S(10): 0.0; T(12): 0.0	S6;	S422		3.38	0	0	2	674.8	1349	20.63	3471
AGGPATPLsPTR	LMNB2	84823	lamin-B2	T6(Phospho) S9(Phospho)	T(6): 100.0; S(9): 98.2; T(11): 1.8	T6; S9;	T34; S37		3.35	0	0	2	642.8	1285	43.02	8206
ATSSSsGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 1.9; S(5): 96.2; S(6): 1.9; S(8): 0.0; S(10): 0.0; T(12): 0.0	S5;	S421		2.9	0	0	2	674.8	1349	21.2	3591
ATSSsSGSLSATGR	LMNB2	84823	lamin-B2	S5(Phospho)	T(2): 3.8; S(3): 0.2; S(4): 3.8; S(5): 88.6; S(6): 3.8; S(8): 49.0; S(10): 49.0; T(12): 2.1	S5;	S421		2.33	0.003	0	2	714.8	1429	27.28	4889
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	56		0	0	2	754.8	1509	15.6	2397
SRsTTELDYSTNK	LMO7	4008	LIM domain only protein 7 isoform 1	S3(Phospho)	S(1): 0.9; S(3): 98.1; T(4): 0.9; T(5): 0.0; Y(10): 0.0; S(11): 0.0; T(12): 0.0	S3;	S1089	50		0	1	2	848.9	1697	29.54	5366
SRsTTELDYSTNK	LMO7	4008	LIM domain only protein 7 isoform 1	S3(Phospho)	S(1): 0.9; S(3): 98.1; T(4): 0.9; T(5): 0.0; Y(10): 0.0; S(11): 0.0; T(12): 0.0	S3;	S1089		4.64	0	1	2	848.9	1697	29.54	5366
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		4.04	0	0	2	754.8	1509	15.6	2397
AEELsPAALsPSLEPIR	LOC102725117	102725117	rho guanine nucleotide exchange factor 5-like isoform X1	S5(Phospho) S10(Phospho)	S(5): 100.0; S(10): 99.9; S(12): 0.1	S5; S10;	S418; S423	28		0	0	2	970.4	1940	92.33	18448
YYsPCEEHPAETNQNEGSESGTIR	LOC102725117	102725117	rho guanine nucleotide exchange factor 5-like isoform X1	C5(Carbamidomethyl) S3(Phospho)	Y(1): 3.9; Y(2): 3.9; S(3): 92.3; T(12): 0.0; S(18): 0.0; S(20): 0.0; T(22): 0.0	S3;	S157	16		0	0	3	945.7	2835	38.4	7232
YYsPCEEHPAETNQNEGSESGTIR	LOC102725117	102725117	rho guanine nucleotide exchange factor 5-like isoform X1	C5(Carbamidomethyl) S3(Phospho)	Y(1): 3.9; Y(2): 3.9; S(3): 92.3; T(12): 0.0; S(18): 0.0; S(20): 0.0; T(22): 0.0	S3;	S157		4.22	0	0	3	945.7	2835	38.4	7232
AEELsPAALsPSLEPIR	LOC102725117	102725117	rho guanine nucleotide exchange factor 5-like isoform X1	S5(Phospho) S10(Phospho)	S(5): 100.0; S(10): 99.9; S(12): 0.1	S5; S10;	S418; S423		2.73	0	0	2	970.4	1940	92.33	18448
QPSQSPQPRPPAsQER	LOC105377639	105377639	adhesive plaque matrix protein-like	S13(Phospho)	S(3): 50.0; S(6): 50.0; S(13): 100.0	S13;	S294		3.62	0.005	0	3	650.6	1950	15.86	2452
TASRPDDIPDPSsPK	LRRRC16A	55604	leucine-rich repeat-containing protein 16A isoform 2	S14(Phospho)	T(1): 0.0; S(3): 0.0; S(11): 50.0; S(13): 50.0; S(14): 100.0	S14;	S1285	29		0	0	2	915.4	1830	35.35	6594
TASRPDDIPDPSsPK	LRRRC16A	55604	leucine-rich repeat-containing protein 16A isoform 2	S14(Phospho)	T(1): 0.0; S(3): 0.0; S(11): 50.0; S(13): 50.0; S(14): 100.0	S14;	S1285		3.79	0	0	2	915.4	1830	35.35	6594
sWGQQAQEQYEQEK	LRRRC16A	55604	leucine-rich repeat-containing protein 16A isoform 2	S1(Phospho)	S(1): 99.8; Y(9): 0.2	S1;	S1325		2.03	0.007	0	2	845.3	1690	44.25	8470
IDGATQsPAEPK	LRRFIP1	9208	leucine-rich repeat flightless-interacting protein 1 isoform 5	S8(Phospho)	T(5): 0.0; S(7): 2.2; S(8): 97.8	S8;	S658	23		0	0	2	690.8	1381	23.38	4052
IDGATQsPAEPK	LRRFIP1	9208	leucine-rich repeat flightless-interacting protein 1 isoform 5	S8(Phospho)	T(5): 0.0; S(7): 2.2; S(8): 97.8	S8;	S658		3.65	0	0	2	690.8	1381	23.38	4052
NSASATTLsGNSSR	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): 100.0; S(13): 0.0; S(14): 0.0	S10;	S88	65		0	0	2	765.3	1530	27.44	4925

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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): 100.0; S(13): 0.0; S(14): 0.0	S10;	S88		3.89	0	0	2	765.3	1530	27.44	4925
SAGAGsPARPPsPR	LSM11	134353	U7 snRNA-associated Sm-like protein Lsm11	S6(Phospho) S12(Phospho)	S(1): 0.0; S(6): 100.0; S(12): 100.0	S6; S12;	S15; S21	21		0	0	2	734.3	1468	23.44	4064
SAGAGsPARPPsPR	LSM11	134353	U7 snRNA-associated Sm-like protein Lsm11	S6(Phospho) S12(Phospho)	S(1): 0.0; S(6): 100.0; S(12): 100.0	S6; S12;	S15; S21		2.67	0	0	2	734.3	1468	23.44	4064
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	23		0	0	2	767.9	1535	28.64	5178
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		3	0.001	0	2	767.9	1535	28.64	5178
ARsVDALDDLtPPSTAESGSR	LSR	51599	lipolysis-stimulated lipoprotein receptor isoform 5	S3(Phospho) T11(Phospho)	S(3): 100.0; T(11): 100.0; S(14): 0.0; T(15): 0.0; S(18): 0.0; S(20): 0.0	S3; T11;	S385; T393	22		0	1	3	769	2305	61.57	12210
ARsVDALDDLtPPSTAESGSR	LSR	51599	lipolysis-stimulated lipoprotein receptor isoform 5	S3(Phospho) T11(Phospho)	S(3): 100.0; T(11): 100.0; S(14): 0.0; T(15): 0.0; S(18): 0.0; S(20): 0.0	S3; T11;	S385; T393		3.23	0.002	1	3	769	2305	61.57	12210
RsEEKEAGEI	LUC7L	55692	putative RNA-binding protein Luc7-like 1 isoform b	S2(Phospho)	S(2): 100.0	S2;	S363	52		0	2	2	614.3	1228	19.56	3244
RsEEKEAGEI	LUC7L	55692	putative RNA-binding protein Luc7-like 1 isoform b	S2(Phospho)	S(2): 100.0	S2;	S363		3.58	0.007	2	2	614.3	1228	19.56	3244
ESDTKNEVNGTSEDIKSEGDTQsN	LUC7L3	51747	luc7-like protein 3	S23(Phospho)	S(2): 6.2; T(4): 6.2; T(11): 0.0; S(12): 0.0; S(17): 0.1; T(21): 6.2; S(23): 81.4	S23;	S431		3.45	0.007	2	3	888.7	2664	28.65	5182
LSKsQGGEEEGPLSDK	MAF1	84232	repressor of RNA polymerase III transcription MAF1 homolog	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(14): 0.0	S4;	S75	54		0	1	2	870.9	1741	28.21	5088
LSKsQGGEEEGPLSDK	MAF1	84232	repressor of RNA polymerase III transcription MAF1 homolog	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(14): 0.0	S4;	S75		3.8	0	1	2	870.9	1741	28.21	5088
DQsLsPSKGENK	MAGI3	260425	membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 97.6; S(7): 2.4	S3; S5;	S1255; S1257	26		0	1	2	725.3	1450	18.5	3023
DQsLsPSKGENK	MAGI3	260425	membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 97.6; S(7): 2.4	S3; S5;	S1255; S1257		3.27	0	1	2	725.3	1450	18.5	3023
ALEQQEAesDSSDTEEKDDDDDEEDV GKR	MAK16	84549	protein MAK16 homolog	S9(Phospho)	S(9): 97.7; S(11): 51.1; S(12): 51.1; T(14): 0.1	S9;	S197	46		0	2	4	890.6	3559	32.96	6077
ALEQQEAesDSSDTEEKDDDDDEEDV GKR	MAK16	84549	protein MAK16 homolog	S9(Phospho)	S(9): 97.7; S(11): 51.1; S(12): 51.1; T(14): 0.1	S9;	S197		7.07	0	2	4	890.6	3559	32.96	6077
GLDsGAetEEEKDTWEEK	MAP1A	4130	microtubule-associated protein 1A	S4(Phospho) T8(Phospho)	S(4): 100.0; T(8): 99.8; T(14): 0.2	S4; T8;	S612; T616		3.02	0.003	1	3	738.3	2213	52.26	10196
SLMsSPEDLTK	MAP1B	4131	microtubule-associated protein 1B	S4(Phospho)	S(1): 0.2; S(4): 98.0; S(5): 50.9; T(10): 50.9	S4;	S831	23		0	0	2	684.3	1368	81.4	16391
ESsPLYSPTFSDSTSAVK	MAP1B	4131	microtubule-associated protein 1B	S3(Phospho)	S(2): 35.1; S(3): 97.2; Y(6): 33.7; S(7): 33.7; T(9): 0.1; S(11): 0.1; S(13): 0.0; T(14): 0.0; S(15): 0.0	S3;	S1793	15		0	0	2	1032	2063	73.17	14801
ASVSPMDEPVPDEsPIEK	MAP1B	4131	microtubule-associated protein 1B	S15(Phospho)	S(2): 50.0; S(4): 50.0; S(13): 0.0; S(15): 100.0	S15;	S1389	13		0	0	2	1087	2174	69.2	13991
DVMSDETNNETEsPSQEFVNITK	MAP1B	4131	microtubule-associated protein 1B	S14(Phospho)	S(4): 0.0; T(7): 4.4; T(12): 4.4; S(14): 86.7; S(16): 4.4; T(23): 0.0	S14;	S1154		2.83	0	0	3	941.7	2823	79.13	15951

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#
ESsPLYSTPTFSDSTSAVK	MAP1B	4131	microtubule-associated protein 1B	S3(Phospho)	S(2): 35.1; S(3): 97.2; Y(6): 33.7; S(7): 33.7; T(9): 0.1; S(11): 0.1; S(13): 0.0; T(14): 0.0; S(15): 0.0	S3;	S1793		2.31	0	0	2	1032	2063	73.17	14801
SLMsSPEDLTK	MAP1B	4131	microtubule-associated protein 1B	S4(Phospho)	S(1): 0.2; S(4): 98.0; S(5): 50.9; T(10): 50.9	S4;	S831		2.28	0	0	2	684.3	1368	81.4	16391
HMDPPPAPVQDRsPsPR	MAP1B	4131	microtubule-associated protein 1B	S13(Phospho) S15(Phospho)	S(13): 100.0; S(15): 100.0	S13; S15;	S2209; S2211		4.16	0.003	1	3	682	2044	34.92	6503
VSPSKSPsLSPSPsPLEK	MAP1B	4131	microtubule-associated protein 1B	S8(Phospho) S15(Phospho)	S(2): 0.1; S(4): 50.0; S(6): 50.0; S(8): 99.7; S(10): 0.2; S(12): 0.0; S(15): 100.0	S8; S15;	S1258; S1265	16		0.007	1	3	721	2161	62.83	12513
ASVSPMDEPVPDESIEK	MAP1B	4131	microtubule-associated protein 1B	S15(Phospho)	S(2): 50.0; S(4): 50.0; S(13): 0.0; S(15): 100.0	S15;	S1389		2.21	0.007	0	2	1087	2174	69.2	13991
VSPSKSPsLSPSPsPLEK	MAP1B	4131	microtubule-associated protein 1B	S8(Phospho) S15(Phospho)	S(2): 0.1; S(4): 50.0; S(6): 50.0; S(8): 99.7; S(10): 0.2; S(12): 0.0; S(15): 100.0	S8; S15;	S1258; S1265		2.82	0.008	1	3	721	2161	62.83	12513
AVPMAPAPAsPGSSNDSSAR	MAP1S	55201	microtubule-associated protein 1S isoform 2	S10(Phospho)	S(10): 100.0; S(13): 0.0; S(14): 0.0; S(17): 0.0; S(18): 0.0	S10;	S733	43		0	0	2	975.4	1950	45.61	8783
AVPMAPAPAsPGSSNDSSAR	MAP1S	55201	microtubule-associated protein 1S isoform 2	S10(Phospho)	S(10): 100.0; S(13): 0.0; S(14): 0.0; S(17): 0.0; S(18): 0.0	S10;	S733		2.09	0	0	2	975.4	1950	45.61	8783
sIQDLTVTGTEPGQVSsR	MAP3K7	6885	mitogen-activated protein kinase kinase kinase 7 isoform D	S1(Phospho) S17(Phospho)	S(1): 100.0; T(6): 0.0; T(8): 0.0; T(10): 0.0; S(16): 3.7; S(17): 96.3	S1; S17;	S412; S428	23		0.006	0	2	1018	2035	73.01	14766
SKVGsTENIK	MAP4	4134	microtubule-associated protein 4 isoform 4	S5(Phospho)	S(1): 0.0; S(5): 99.0; T(6): 1.0	S5;	S941	40		0	1	2	571.8	1143	15.53	2383
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	36		0	0	2	653.8	1307	12.96	1841
SKVGsTENIK	MAP4	4134	microtubule-associated protein 4 isoform 4	S5(Phospho)	S(1): 0.0; S(5): 99.0; T(6): 1.0	S5;	S941		3.11	0	1	2	571.8	1143	15.53	2383
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		2.34	0	0	2	653.8	1307	12.96	1841
TTsRsPVLSR	MAP4K4	9448	mitogen-activated protein kinase kinase kinase 4 isoform 1	S3(Phospho) S5(Phospho)	T(1): 0.2; T(2): 0.2; S(3): 99.9; S(5): 99.7; S(9): 0.0	S3; S5;	S544; S546	16		0	1	2	632.3	1264	24.74	4335
TTsRsPVLSR	MAP4K4	9448	mitogen-activated protein kinase kinase kinase 4 isoform 1	S3(Phospho) S5(Phospho)	T(1): 0.2; T(2): 0.2; S(3): 99.9; S(5): 99.7; S(9): 0.0	S3; S5;	S544; S546		3.09	0.001	1	2	632.3	1264	24.74	4335
ASNEKESAAPAsPAPsPAPsPTPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S12(Phospho) S16(Phospho) S20(Phospho)	S(2): 0.3; S(7): 0.0; S(12): 99.7; S(16): 100.0; S(20): 94.6; T(22): 5.4	S12; S16; S20;	S507; S511; S515	23		0	1	3	974.8	2922	43.76	8362
ASNEKESAAPAsPAPsPAPsPTPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S12(Phospho)	S(2): 3.9; S(7): 0.0; S(12): 96.1; S(16): 0.0; S(20): 0.0; T(22): 0.0	S12;	S507	20		0	1	3	921.4	2762	36.58	6854
sRGPIPPAMGPR	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0	S1; T5;	S93; T97	19		0	1	2	692.3	1384	37.24	6990
SSQPsPTAVPASDsPPTKQEVK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S5(Phospho) S14(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 97.1; T(7): 2.9; S(12): 0.0; S(14): 100.0; T(17): 0.0	S5; S14;	S116; S125	16		0	1	3	800	2398	41.53	7892
ESAAPAsPAPsPAPsPTPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S7(Phospho) S11(Phospho) S15(Phospho)	S(2): 4.7; S(7): 95.3; S(11): 100.0; S(15): 99.7; T(17): 0.3	S7; S11; S15;	S507; S511; S515	12		0	0	3	798.3	2393	57.79	11405
ASNEKESAAPAsPAPsPAPsPTPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S12(Phospho) S16(Phospho) S20(Phospho)	S(2): 0.3; S(7): 0.0; S(12): 99.7; S(16): 100.0; S(20): 94.6; T(22): 5.4	S12; S16; S20;	S507; S511; S515		5.78	0	1	3	974.8	2922	43.76	8362

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#
SSQPSPTAVPASDsPPTKQEVK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S5(Phospho) S14(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 97.1; T(7): 2.9; S(12): 0.0; S(14): 100.0; T(17): 0.0	S5; S14;	S116; S125		4.39	0	1	3	800	2398	41.53	7892
ASNEKESAAPsPAPSPAPSPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S12(Phospho)	S(2): 3.9; S(7): 0.0; S(12): 96.1; S(16): 0.0; S(20): 0.0; T(22): 0.0	S12;	S507		4.16	0	1	3	921.4	2762	36.58	6854
ESAAPAsPAPsPAPsPTPAPPQK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S7(Phospho) S11(Phospho) S15(Phospho)	S(2): 4.7; S(7): 95.3; S(11): 100.0; S(15): 99.7; T(17): 0.3	S7; S11; S15;	S507; S511; S515		4.02	0	0	3	798.3	2393	57.79	11405
SSQPSPTAVPASDsPPTKQEVK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S14(Phospho)	S(1): 32.9; S(2): 32.9; S(5): 32.9; T(7): 1.4; S(12): 0.0; S(14): 100.0; T(17): 0.0	S14;	S125		3.5	0	1	3	800	2398	41.01	7784
SSQPSPTAVPASDsPPTKQEVK	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S5(Phospho) S14(Phospho)	S(1): 50.0; S(2): 50.0; S(5): 100.0; T(7): 0.0; S(12): 0.0; S(14): 100.0; T(17): 0.0	S5; S14;	S116; S125		2.88	0	1	3	826.7	2478	49.66	9632
RQsLPAsPR	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S405; S409	24		0.001	1	2	586.3	1172	24.42	4269
RQsLPAsPR	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0	S3; S7;	S405; S409		3.1	0.003	1	2	586.3	1172	24.42	4269
sRGPTPPAMGPR	MAP7D1	55700	MAP7 domain-containing protein 1 isoform 2	S1(Phospho) T5(Phospho)	S(1): 100.0; T(5): 100.0	S1; T5;	S93; T97		2.64	0.004	1	2	692.3	1384	37.24	6990
EAPAEGEAAEPGSPTAAEGEAASAsST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S13(Phospho)	S(13): 96.7; T(15): 3.3; S(23): 0.0; S(26): 0.0; S(27): 0.0; T(28): 0.0; S(29): 0.0; S(30): 0.0	S13;	S118	41		0	0	3	999.1	2995	52.59	10266
EAPAEGEAAEPGSPTAAEGEAASAsST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S27(Phospho)	S(13): 0.0; T(15): 0.0; S(23): 0.0; S(26): 3.7; S(27): 92.5; T(28): 3.7; S(29): 0.2; S(30): 0.0	S27;	S132	39		0	0	3	999.1	2995	48.07	9300
AEDGATPsPSNETPK	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	36		0	0	2	830.8	1661	30.58	5585
GEPAASAAPEAGAsPVEK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S14(Phospho)	S(14): 100.0	S14;	S101	33		0	0	2	851.9	1703	37.79	7105
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	26		0	2	3	613	1837	12.8	1806
GEAAAEERPGEAAVASsPSK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S16(Phospho)	S(15): 0.0; S(16): 97.9; S(18): 2.0	S16;	S27	26		0	0	2	932.9	1865	24.08	4198
AEDGATPSPSNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S10(Phospho)	T(6): 0.0; S(8): 2.9; S(10): 94.2; T(13): 2.9	S10;	S147	25		0	0	2	790.8	1581	25.9	4583
AEDGATPSPSNETPKK	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	24		0	1	2	854.9	1709	15.82	2443
AEDGATPsPSNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho)	T(6): 0.0; S(8): 99.9; S(10): 0.1; T(13): 0.0	S8;	S145	23		0	1	2	854.9	1709	18.38	2997
AEDGATPSPSNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T13(Phospho)	T(6): 0.0; S(8): 0.0; S(10): 2.5; T(13): 97.5	T13;	T150	22		0	0	2	790.8	1581	22.62	3892
EAPAEGEAAEPGSPTAAEGEAAsAsST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S23(Phospho) S26(Phospho) S27(Phospho)	S(13): 0.6; T(15): 0.6; S(23): 98.8; S(26): 98.4; S(27): 86.2; T(28): 7.4; S(29): 7.4; S(30): 0.6	S23; S26; S27;	S128; S131; S132	22		0	0	3	1052	3155	60.63	12008
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	18		0	2	2	918.9	1837	12.8	1808
AEDGATPsPSNETPKKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho) T13(Phospho)	T(6): 0.0; S(8): 97.3; S(10): 2.7; T(13): 100.0	S8; T13;	S145; T150	13		0	2	3	639.6	1917	13.6	1978

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#
EAPAEGEAAEPGsPTAAEGEAAASST SSPKAEDGATPSPSNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S13(Phospho) T15(Phospho)	S(13): 83.0; T(15): 83.0; S(23): 18.5; S(26): 4.6; S(27): 4.6; T(28): 4.6; S(29): 0.8; S(30): 0.8; T(38): 0.1; S(40): 0.0; S(42): 0.0; T(45): 0.0	S13; T15;	S118; T120	11		0	1	4	1140	4557	55.41	10885
AEDGATPSPSNETPKK	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		7.03	0	2	3	613	1837	12.8	1806
EAPAEGEAAEPGSPTAAEGEAAASST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S27(Phospho)	S(13): 0.0; T(15): 0.0; S(23): 0.0; S(26): 3.7; S(27): 92.5; T(28): 3.7; S(29): 0.2; S(30): 0.0	S27;	S132		6.35	0	0	3	999.1	2995	48.07	9300
EAPAEGEAAEPGsPTAAEGEAAASST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S13(Phospho)	S(13): 96.7; T(15): 3.3; S(23): 0.0; S(26): 0.0; S(27): 0.0; T(28): 0.0; S(29): 0.0; S(30): 0.0	S13;	S118		5.99	0	0	3	999.1	2995	52.59	10266
EAPAEGEAAEPGsPTAAEGEAAASST SSPKAEDGATPSPSNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S13(Phospho) T15(Phospho)	S(13): 83.0; T(15): 83.0; S(23): 18.5; S(26): 4.6; S(27): 4.6; T(28): 4.6; S(29): 0.8; S(30): 0.8; T(38): 0.1; S(40): 0.0; S(42): 0.0; T(45): 0.0	S13; T15;	S118; T120		5.25	0	1	4	1140	4557	55.41	10885
AEDGATPSPSNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	T13(Phospho)	T(6): 0.0; S(8): 0.0; S(10): 2.5; T(13): 97.5	T13;	T150		4.31	0	0	2	790.8	1581	22.62	3892
AEDGATPsNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho) T13(Phospho)	T(6): 0.0; S(8): 97.3; S(10): 2.7; T(13): 100.0	S8; T13;	S145; T150		4.26	0	2	3	639.6	1917	13.6	1978
GEPA AAAAPEAGAsPVEK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S14(Phospho)	S(14): 100.0	S14;	S101		4.11	0	0	2	851.9	1703	37.79	7105
EAPAEGEAAEPGSPTAAEGEAAAsST SSPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S23(Phospho) S26(Phospho) S27(Phospho)	S(13): 0.6; T(15): 0.6; S(23): 98.8; S(26): 98.4; S(27): 86.2; T(28): 7.4; S(29): 7.4; S(30): 0.6	S23; S26; S27;	S128; S131; S132		3.91	0	0	3	1052	3155	60.63	12008
AEDGATPSPSNETPKK	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		3.6	0	1	2	854.9	1709	15.82	2443
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		3.32	0	0	2	830.8	1661	30.58	5585
AEDGATPsNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho)	T(6): 0.0; S(8): 99.9; S(10): 0.1; T(13): 0.0	S8;	S145		3.25	0	1	2	854.9	1709	18.38	2997
GEAAAERPGEAAVAsPSK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S16(Phospho)	S(15): 0.0; S(16): 97.9; S(18): 2.0	S16;	S27		3.22	0	0	2	932.9	1865	24.08	4198
AEDGATPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho) S10(Phospho)	T(6): 0.0; S(8): 100.0; S(10): 99.9; T(13): 0.1	S8; S10;	S145; S147		3.11	0	0	2	830.8	1661	28.81	5213
AEDGATPSPSNETPKK	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		3.29	0.001	2	2	918.9	1837	12.8	1808
AEDGATPSPsNETPK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S10(Phospho)	T(6): 0.0; S(8): 2.9; S(10): 94.2; T(13): 2.9	S10;	S147		3.16	0.001	0	2	790.8	1581	25.9	4583
AEDGATPSPSNETPKK	MARCKS	4082	myristoylated alanine-rich C-kinase substrate	S8(Phospho) T13(Phospho)	T(6): 0.0; S(8): 99.9; S(10): 0.1; T(13): 100.0	S8; T13;	S145; T150		3.49	0.005	1	2	894.9	1789	19.15	3159
AAATPeSQEPQAK	MARCKSL1	65108	MARCKS-related protein	T4(Phospho) S7(Phospho)	T(4): 100.0; S(7): 100.0	T4; S7;	T148; S151	21		0	0	2	744.3	1488	21.72	3697
GAEASAAEEEEAGPQATEPSTPSGPESG PTPASAEQNE	MARCKSL1	65108	MARCKS-related protein	S27(Phospho)	S(5): 1.1; S(8): 0.0; T(17): 1.1; S(20): 1.1; T(21): 1.1; S(23): 1.1; S(27): 92.3; T(30): 1.1; S(33): 1.1	S27;	S184		5.52	0	0	3	1236	3706	57.19	11280
AAATPeSQEPQAK	MARCKSL1	65108	MARCKS-related protein	T4(Phospho) S7(Phospho)	T(4): 100.0; S(7): 100.0	T4; S7;	T148; S151		3.12	0	0	2	744.3	1488	21.72	3697
SYSPDGKESPSDK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 0.0; S(11): 0.0	S3;	S260	50		0	1	2	738.8	1477	15.99	2481

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#
SYsPDGKEsPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 0.0; S(11): 0.0	S3;	S260	36		0	2	2	802.8	1605	12.92	1832
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	33		0	2	2	842.8	1685	13.32	1916
SYsPDGKEsPSDK	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	27		0	1	2	778.8	1557	18.92	3110
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	27		0	2	2	842.8	1685	13.86	2029
SYsPDGKEsPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 1.7; S(3): 98.2; S(9): 0.0; S(11): 0.0	S3;	S260	25		0	2	3	535.6	1605	12.96	1840
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): 97.3; S(11): 2.7	S3; S9;	S260; S266	20		0	2	3	562.2	1685	13.35	1924
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): 97.3; S(11): 2.7	S3; S9;	S260; S266		5.53	0	2	3	562.2	1685	13.35	1924
SYsPDGKEsPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 1.7; S(3): 98.2; S(9): 0.0; S(11): 0.0	S3;	S260		5.04	0	2	3	535.6	1605	12.96	1840
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		4.06	0	2	2	842.8	1685	13.32	1916
SYsPDGKEsPSDKK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 0.0; S(11): 0.0	S3;	S260		3.81	0	2	2	802.8	1605	12.92	1832
SYsPDGKEsPSDK	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		3.68	0	1	2	778.8	1557	18.92	3110
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		3.41	0	2	2	842.8	1685	13.86	2029
SYsPDGKEsPSDK	MATR3	9782	matrin-3 isoform c	S3(Phospho)	S(1): 0.0; Y(2): 0.0; S(3): 100.0; S(9): 0.0; S(11): 0.0	S3;	S260		3.35	0	1	2	738.8	1477	15.99	2481
LQSVQATGPsPGR	MCC	4163	colorectal mutant cancer protein isoform 2	S11(Phospho)	S(3): 0.0; T(7): 0.0; S(10): 0.0; S(11): 100.0	S11;	S294	60		0	0	2	732.8	1465	31.11	5693
LQSVQATGPsPGR	MCC	4163	colorectal mutant cancer protein isoform 2	S11(Phospho)	S(3): 0.0; T(7): 0.0; S(10): 0.0; S(11): 100.0	S11;	S294		4	0	0	2	732.8	1465	31.11	5693
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 100.0	S8;	S27	52		0	0	2	590.8	1181	32.4	5960
GLLYDsDEEDEERPAR	MCM2	4171	DNA replication licensing factor MCM2	S6(Phospho)	Y(4): 1.9; S(6): 98.1	S6;	S139	50		0	0	3	658.6	1974	49.46	9590
GLLYDsDEEDEERPAR	MCM2	4171	DNA replication licensing factor MCM2	S6(Phospho)	Y(4): 2.2; S(6): 97.8	S6;	S139	31		0	0	2	987.4	1974	49.58	9614
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 1.8; S(8): 98.2	S8;	S27	28		0	0	2	590.8	1181	31.86	5848
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	24		0	0	2	630.7	1260	43.36	8277
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 100.0	S8;	S27		4.05	0	0	2	590.8	1181	32.4	5960
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		3.82	0	0	2	630.7	1260	43.36	8277
GLLYDsDEEDEERPAR	MCM2	4171	DNA replication licensing factor MCM2	S6(Phospho)	Y(4): 1.9; S(6): 98.1	S6;	S139		3.17	0	0	3	658.6	1974	49.46	9590
GNDPLTsPGR	MCM2	4171	DNA replication licensing factor MCM2	S8(Phospho)	T(6): 0.0; S(7): 1.8; S(8): 98.2	S8;	S27		3.21	0.003	0	2	590.8	1181	31.86	5848
GLLYDsDEEDEERPAR	MCM2	4171	DNA replication licensing factor MCM2	S6(Phospho)	Y(4): 2.2; S(6): 97.8	S6;	S139		1.52	0.005	0	2	987.4	1974	49.58	9614

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#
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) T7(Phospho)	S(1): 99.9; S(5): 0.1; T(7): 100.0; S(14): 0.0	S1; T7;	S713; T719	38		0	2	3	948.7	2844	19.69	3271
RSEDEsEtEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S6(Phospho) T8(Phospho)	S(2): 0.0; S(6): 100.0; T(8): 100.0; S(15): 0.0	S6; T8;	S717; T719	37		0	2	3	948.7	2844	18.31	2982
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S5(Phospho)	S(1): 2.6; S(5): 97.3; T(7): 0.1; S(14): 0.0	S5;	S717	30		0	2	3	922	2764	21.75	3703
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	T7(Phospho)	S(1): 50.0; S(5): 50.0; T(7): 100.0; S(14): 0.0	T7;	T719	28		0	2	3	948.7	2844	20.21	3380
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	T7(Phospho)	S(1): 50.1; S(5): 50.1; T(7): 99.8; S(14): 0.0	T7;	T719	26		0	1	3	896.6	2688	22	3757
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) T7(Phospho) S14(Phospho)	S(1): 95.0; S(5): 5.3; T(7): 99.7; S(14): 100.0	S1; T7; S14;	S713; T719; S726	24		0	2	3	975.3	2924	21.45	3643
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) T7(Phospho)	S(1): 99.9; S(5): 0.1; T(7): 100.0; S(14): 0.0	S1; T7;	S713; T719		5.54	0	2	3	948.7	2844	19.69	3271
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S5(Phospho)	S(1): 2.6; S(5): 97.3; T(7): 0.1; S(14): 0.0	S5;	S717		5.32	0	2	3	922	2764	21.75	3703
DGDSYDPYDFSDTEEMPQVHtPK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	T22(Phospho)	S(4): 0.0; Y(5): 0.0; Y(8): 0.1; S(11): 49.9; T(13): 49.9; T(22): 100.0	T22;	T767		4.96		0	3	988	2962	80.57	16225
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	T7(Phospho)	S(1): 50.0; S(5): 50.0; T(7): 100.0; S(14): 0.0	T7;	T719		4.93	0	2	3	948.7	2844	20.21	3380
SEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	T7(Phospho)	S(1): 50.1; S(5): 50.1; T(7): 99.8; S(14): 0.0	T7;	T719		4.75	0	1	3	896.6	2688	22	3757
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) T7(Phospho) S14(Phospho)	S(1): 95.0; S(5): 5.3; T(7): 99.7; S(14): 100.0	S1; T7; S14;	S713; T719; S726		4.3	0	2	3	975.3	2924	21.45	3643
DGDSYDPYDFSDTEEMPQVHtPK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	M17(Oxidation) T22(Phospho)	S(4): 0.0; Y(5): 0.1; Y(8): 33.3; S(11): 33.3; T(13): 33.3; T(22): 100.0	T22;	T767		3.58	0	0	3	993.4	2978	70.31	14222
DGDSYDPYDFsDtEEEMPQVHtPK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	M17(Oxidation) S11(Phospho) T13(Phospho) T22(Phospho)	S(4): 1.7; Y(5): 1.7; Y(8): 1.0; S(11): 96.7; T(13): 98.8; T(22): 100.0	S11; T13; T22;	S756; T758; T767		2.82	0	0	3	1020	3058	79.05	15935
DGDSYDPYDFsDtEEEMPQVHtPK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S11(Phospho) T13(Phospho) T22(Phospho)	S(4): 0.1; Y(5): 0.1; Y(8): 13.7; S(11): 93.1; T(13): 93.1; T(22): 100.0	S11; T13; T22;	S756; T758; T767		2.74	0	0	3	1015	3042	88.29	17660
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) S14(Phospho)	S(1): 93.6; S(5): 6.0; T(7): 0.9; S(14): 99.5	S1; S14;	S713; S726		2.7	0	2	3	948.7	2844	21.59	3671
DGDsYDPyDFSDTEEMPQVHTPK	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S4(Phospho) Y8(Phospho)	S(4): 79.3; Y(5): 10.8; Y(8): 79.3; S(11): 15.3; T(13): 15.3; T(22): 0.0	S4; Y8;	S749; Y753		2.34	0	0	3	988	2962	77.88	15710
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) S5(Phospho)	S(1): 94.9; S(5): 94.9; T(7): 10.2; S(14): 0.0	S1; S5;	S713; S717	11		0.001	1	2	1344	2688	21.76	3705
RSEDEsEtEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S6(Phospho) T8(Phospho)	S(2): 0.0; S(6): 100.0; T(8): 100.0; S(15): 0.0	S6; T8;	S717; T719		4.07	0.001	2	3	948.7	2844	18.31	2982
sEDESETEDEEEKSQEDQEQR	MCM3	4172	DNA replication licensing factor MCM3 isoform 1	S1(Phospho) S5(Phospho)	S(1): 94.9; S(5): 94.9; T(7): 10.2; S(14): 0.0	S1; S5;	S713; S717		1.88	0.003	1	2	1344	2688	21.76	3705
VsPSTSYTPSR	MCMBP	79892	mini-chromosome maintenance complex-binding protein isoform 2	S2(Phospho)	S(2): 99.9; S(4): 0.1; T(5): 0.0; S(6): 0.0; Y(7): 0.0; T(8): 0.0; S(10): 0.0	S2;	S154	43		0	0	2	631.3	1262	32.12	5903
VsPSTSYTPSR	MCMBP	79892	mini-chromosome maintenance complex-binding protein isoform 2	S2(Phospho)	S(2): 99.9; S(4): 0.1; T(5): 0.0; S(6): 0.0; Y(7): 0.0; T(8): 0.0; S(10): 0.0	S2;	S154		2.5	0	0	2	631.3	1262	32.12	5903
SQTTTERDsDtDVEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.2; T(3): 0.2; T(4): 0.2; T(5): 4.7; S(9): 94.9; T(11): 99.7	S9; T11;	S453; T455	40		0	1	3	947	2839	53.66	10503

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#
SQTTERDsDtDVEEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.0; T(3): 0.0; T(4): 0.0; T(5): 0.0; S(9): 100.0; T(11): 100.0	S9; T11;	S453; T455	33		0	1	3	947	2839	53.04	10373
SQTTERDsDtDVEEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.4; T(3): 0.4; T(4): 0.4; T(5): 5.7; S(9): 93.6; T(11): 99.5	S9; T11;	S453; T455	12		0	1	2	1420	2839	53.25	10418
SQTTERDsDtDVEEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.2; T(3): 0.2; T(4): 0.2; T(5): 4.7; S(9): 94.9; T(11): 99.7	S9; T11;	S453; T455		4.17	0	1	3	947	2839	53.66	10503
SQTTERDsDtDVEEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.0; T(3): 0.0; T(4): 0.0; T(5): 0.0; S(9): 100.0; T(11): 100.0	S9; T11;	S453; T455		3.85	0	1	3	947	2839	53.04	10373
SQTTERDsDtDVEEEELPVENR	MDC1	9656	mediator of DNA damage checkpoint protein 1	S9(Phospho) T11(Phospho)	S(1): 0.4; T(3): 0.4; T(4): 0.4; T(5): 5.7; S(9): 93.6; T(11): 99.5	S9; T11;	S453; T455		1.44	0	1	2	1420	2839	53.25	10418
REPGSGTESDTSDFHNQENEPSQEDPELDGSGVQGVKPKQK	MEAF6	64769	chromatin modification-related protein MEAF6 isoform 2	S5(Phospho)	S(5): 86.8; T(7): 9.7; S(9): 9.7; T(11): 46.7; S(12): 46.7; S(23): 0.3; S(33): 0.0	S5;	S118	19		0	1	4	1157	4627	51.01	9919
REPGSGTESDTSDFHNQENEPSQEDPELDGSGVQGVKPKQK	MEAF6	64769	chromatin modification-related protein MEAF6 isoform 2	S5(Phospho)	S(5): 86.8; T(7): 9.7; S(9): 9.7; T(11): 46.7; S(12): 46.7; S(23): 0.3; S(33): 0.0	S5;	S118		4.12	0	1	4	1157	4627	51.01	9919
AETSEGSAPSAPVPEASAsPK	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): 0.1; S(19): 99.9	S19;	S80	36		0	0	2	1005	2010	38.57	7267
AETSEGSAPSAPVPEASAsPK	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): 0.1; S(19): 99.9	S19;	S80		4.67	0	0	2	1005	2010	38.57	7267
NSSQSGGKPGSsPITK	MED1	5469	mediator of RNA polymerase II transcription subunit 1	S12(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 2.3; S(12): 97.7; T(15): 0.1	S12;	S1156	37		0	0	2	806.4	1612	13.94	2047
NSSQSGGKPGSsPITK	MED1	5469	mediator of RNA polymerase II transcription subunit 1	S12(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; S(11): 2.3; S(12): 97.7; T(15): 0.1	S12;	S1156		4.55	0	0	2	806.4	1612	13.94	2047
SYQNSPssDDGIRLPLEYSTEK	MED1	5469	mediator of RNA polymerase II transcription subunit 1	S7(Phospho) S8(Phospho)	S(1): 0.3; Y(2): 0.3; S(5): 5.5; S(7): 94.4; S(8): 99.3; Y(18): 0.0; S(19): 0.0; T(20): 0.0	S7; S8;	S1481; S1482		3.23	0.001	0	3	877.4	2630	61.39	12170
sNNWSLEDVTASDK	MELK	9833	maternal embryonic leucine zipper kinase isoform 9	S1(Phospho)	S(1): 97.4; S(5): 2.6; T(10): 0.0; S(12): 0.0	S1;	S158	68		0	0	2	823.3	1646	63.99	12808
sNNWSLEDVTASDK	MELK	9833	maternal embryonic leucine zipper kinase isoform 9	S1(Phospho)	S(1): 97.4; S(5): 2.6; T(10): 0.0; S(12): 0.0	S1;	S158		3.24	0	0	2	823.3	1646	63.99	12808
TLNAETPKsSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T6(Phospho) S9(Phospho)	T(1): 0.0; T(6): 99.9; S(9): 99.9; S(10): 0.1	T6; S9;	T213; S216	29		0	1	3	571.9	1714	38.96	7348
TLNAETPKsSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T6(Phospho) S9(Phospho)	T(1): 0.0; T(6): 100.0; S(9): 99.9; S(10): 0.1	T6; S9;	T213; S216	27		0	1	2	857.4	1714	38.82	7318
TLNAETPKsSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T6(Phospho) S9(Phospho)	T(1): 0.0; T(6): 99.9; S(9): 99.9; S(10): 0.1	T6; S9;	T213; S216		4.68	0	1	3	571.9	1714	38.96	7348
TLNAETPKsSPLPAK	MEPCE	56257	7SK snRNA methylphosphate capping enzyme isoform A	T6(Phospho) S9(Phospho)	T(1): 0.0; T(6): 100.0; S(9): 99.9; S(10): 0.1	T6; S9;	T213; S216		3.78	0	1	2	857.4	1714	38.82	7318
SVSPPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	M8(Oxidation)S10(Phospho) S13(Phospho)	S(1): 0.0; S(3): 0.0; T(5): 2.7; T(6): 0.1; S(10): 97.2; S(13): 100.0; Y(16): 0.0	S10; S13;	S997; S1000	48		0	0	2	1039	2077	52.78	10307
SVSPPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	S10(Phospho) S13(Phospho)	S(1): 0.0; S(3): 0.0; T(5): 0.0; T(6): 0.0; S(10): 100.0; S(13): 99.9; Y(16): 0.1	S10; S13;	S997; S1000	35		0	0	2	1031	2061	63.18	12604

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#
SVSPtTEMVsNESVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	T5(Phospho) S10(Phospho)	S(1): 2.9; S(3): 2.9; T(5): 91.2; T(6): 2.9; S(10): 100.0; S(13): 0.0; Y(16): 0.0	T5; S10;	T992; S997	28		0	0	2	1031	2061	65.09	13072
SVsPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	S3(Phospho) S10(Phospho) S13(Phospho)	S(1): 0.2; S(3): 99.5; T(5): 0.2; T(6): 0.2; S(10): 100.0; S(13): 100.0; Y(16): 0.0	S3; S10; S13;	S990; S997; S1000	28		0	0	2	1071	2141	77.61	15658
SVsPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	M8(Oxidation) S3(Phospho) S10(Phospho) S13(Phospho)	S(1): 0.1; S(3): 99.9; T(5): 0.0; T(6): 0.0; S(10): 100.0; S(13): 99.9; Y(16): 0.1	S3; S10; S13;	S990; S997; S1000	25		0	0	2	1079	2157	65.18	13089
SVsPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	M8(Oxidation) S3(Phospho) S10(Phospho) S13(Phospho)	S(1): 0.1; S(3): 99.9; T(5): 0.0; T(6): 0.0; S(10): 100.0; S(13): 99.9; Y(16): 0.1	S3; S10; S13;	S990; S997; S1000	2.76	0	0	0	2	1079	2157	65.18	13089
SVSPtTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	M8(Oxidation) S10(Phospho) S13(Phospho)	S(1): 0.0; S(3): 0.0; T(5): 2.7; T(6): 0.1; S(10): 97.2; S(13): 100.0; Y(16): 0.0	S10; S13;	S997; S1000	2.65	0	0	0	2	1039	2077	52.78	10307
SVSPtTEMVsNESVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	T5(Phospho) S10(Phospho)	S(1): 2.9; S(3): 2.9; T(5): 91.2; T(6): 2.9; S(10): 100.0; S(13): 0.0; Y(16): 0.0	T5; S10;	T992; S997		2.63	0	0	2	1031	2061	65.09	13072
SVSPtTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	S10(Phospho) S13(Phospho)	S(1): 0.0; S(3): 0.0; T(5): 0.0; T(6): 0.0; S(10): 100.0; S(13): 99.9; Y(16): 0.1	S10; S13;	S997; S1000	2.98	0.001	0	0	2	1031	2061	63.18	12604
SVsPTTEMVsNEsVDYR	MET	4233	hepatocyte growth factor receptor isoform b precursor	S3(Phospho) S10(Phospho) S13(Phospho)	S(1): 0.2; S(3): 99.5; T(5): 0.2; T(6): 0.2; S(10): 100.0; S(13): 100.0; Y(16): 0.0	S3; S10; S13;	S990; S997; S1000	2.75	0.001	0	0	2	1071	2141	77.61	15658
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	61		0	1	3	929.7	2787	54.48	10690
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	60		0	1	3	929.7	2787	53.9	10563
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	M1(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	59		0	1	3	935	2803	52.49	10245
KIVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S116; S118	49		0	1	3	830.7	2490	72.24	14598
IVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S10(Phospho) S12(Phospho)	S(10): 100.0; S(12): 100.0	S10; S12;	S116; S118	46		0	0	3	788	2362	86.92	17411
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	M1(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	34		0	1	3	935	2803	51.95	10117
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	23		0	1	2	1394	2787	53.97	10579
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	5.43	0	0	1	3	929.7	2787	53.9	10563
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	M1(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	5.37	0	0	1	3	935	2803	52.49	10245
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	5.03	0	0	1	3	929.7	2787	54.48	10690
MEREDssEEEEEEIDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	M1(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133	4.61	0	0	1	3	935	2803	51.95	10117
IVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S10(Phospho) S12(Phospho)	S(10): 100.0; S(12): 100.0	S10; S12;	S116; S118	4.38	0	0	0	3	788	2362	86.92	17411

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#
KIVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S116; S118		4.05	0	1	3	830.7	2490	72.24	14598
MEREDssEEEEIEDDEEIER	MFAP1	4236	microfibrillar-associated protein 1	M1(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133		3.14	0	2	3	987	2959	45.7	8802
MEREDssEEEEIEDDEIER	MFAP1	4236	microfibrillar-associated protein 1	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0	S6; S7;	S132; S133		2.74	0	1	2	1394	2787	53.97	10579
KIVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S116; S118		2.44	0	1	2	1246	2490	72.38	14625
KIVEPEVVGESDsEVEGDAWR	MFAP1	4236	microfibrillar-associated protein 1	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S116; S118	12		0.001	1	2	1246	2490	72.38	14625
GAGATSGsPPAGR	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 100.0	S8;	S232	57		0	0	2	583.3	1165	15.27	2328
GAGATSGsPPAGR	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 99.9	S8;	S232	44		0	1	2	640.3	1280	14.33	2129
GAGATSGsPPAGR	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 100.0	S8;	S232		4.18	0	0	2	583.3	1165	15.27	2328
GAGATSGsPPAGR	MGMT	4255	methylated-DNA--protein-cysteine methyltransferase	S8(Phospho)	T(5): 0.0; S(6): 0.0; S(8): 99.9	S8;	S232		3.81	0	1	2	640.3	1280	14.33	2129
DTMDLssSSEEEKEDDDALVPDSK	MIA3	375056	melanoma inhibitory activity protein 3 isoform 1 precursor	S7(Phospho) S8(Phospho)	T(2): 9.3; S(7): 82.0; S(8): 82.0; S(9): 13.4; S(10): 13.4; S(25): 0.0	S7; S8;	S405; S406	26		0	1	3	1016	3046	70.13	14192
DTMDLssSSEEEKEDDDALVPDSK	MIA3	375056	melanoma inhibitory activity protein 3 isoform 1 precursor	S7(Phospho) S8(Phospho)	T(2): 9.3; S(7): 82.0; S(8): 82.0; S(9): 13.4; S(10): 13.4; S(25): 0.0	S7; S8;	S405; S406		2.58	0	1	3	1016	3046	70.13	14192
DEPPPSQSTSQDCSQALKQsP	MIA3	375056	melanoma inhibitory activity protein 3 isoform 1 precursor	C14(Carbamido methyl) S21(Phospho)	S(7): 0.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(15): 0.0; S(21): 100.0	S21;	S1906		3.87	0.003	1	3	813.3	2438	41.07	7798
APsAsPLALHASR	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(12): 0.0	S3; S5;	S484; S486	68		0	0	2	719.3	1438	48.16	9318
APsAsPLALHASR	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(12): 0.0	S3; S5;	S484; S486	65		0	0	2	719.3	1438	48.67	9425
KPsPAAAsPATK	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	41		0	0	2	607.8	1215	13.81	2020
SPVPSPGSSsPQLQVK	MICALL1	85377	MICAL-like protein 1	S10(Phospho)	S(1): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 100.0	S10;	S621	34		0	0	2	837.9	1675	51.64	10047
KPsPAAAsPATK	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		4.75	0	0	2	607.8	1215	13.81	2020
SPVPSPGSSsPQLQVK	MICALL1	85377	MICAL-like protein 1	S10(Phospho)	S(1): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 100.0	S10;	S621		4.06	0	0	2	837.9	1675	51.64	10047
APsAsPLALHASR	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(12): 0.0	S3; S5;	S484; S486		3.28	0	0	2	719.3	1438	48.16	9318
APsAsPLALHASR	MICALL1	85377	MICAL-like protein 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(12): 0.0	S3; S5;	S484; S486		3.21	0	0	2	719.3	1438	48.67	9425
TPRPASPGPSLPARsPPR	MICALL2	79778	MICAL-like protein 2	S15(Phospho) S17(Phospho)	T(1): 50.0; S(6): 50.0; S(10): 0.0; S(15): 100.0; S(17): 100.0	S15; S17;	S658; S660		4.41	0.004	1	3	755.7	2265	45.36	8730
ASVsGPNsPSETRR	MID1	4281	E3 ubiquitin-protein ligase Midline-1 isoform 6	S4(Phospho) S8(Phospho)	S(2): 0.1; S(4): 99.9; S(8): 99.9; S(10): 0.1; T(12): 0.0	S4; S8;	S92; S96	24		0.001	1	2	802.8	1605	19.53	3240
AlSAPTSPTR	MIEF1	54471	mitochondrial dynamics protein MID51 isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; T(6): 0.0; S(7): 99.9; T(9): 0.0	S3; S7;	S55; S59	23		0	0	2	580.7	1160	39.13	7385
AlSAPTSPTR	MIEF1	54471	mitochondrial dynamics protein MID51 isoform 1	S3(Phospho) S7(Phospho)	S(3): 100.0; T(6): 0.0; S(7): 99.9; T(9): 0.0	S3; S7;	S55; S59		3.23	0	0	2	580.7	1160	39.13	7385
GTPKPPGPPAQPPGPPNAsSNPDLR	MINK1	50488	misshapen-like kinase 1 isoform 4	S19(Phospho)	T(2): 0.0; S(19): 96.4; S(20): 3.6	S19;	S712		3.57	0	0	3	842.7	2526	48.54	9397
ALsSDSILsPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S3(Phospho)	S(3): 98.3; S(4): 1.7; S(6): 0.0; S(9): 0.0	S3;	S394	59		0	0	2	790.4	1580	66.38	13365
ALsSDSILsPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S4(Phospho) S9(Phospho)	S(3): 1.9; S(4): 98.1; S(6): 0.0; S(9): 100.0	S4; S9;	S395; S400	56		0	0	2	830.4	1660	76.34	15398

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#
ALSSDsILSPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S6(Phospho)	S(3): 50.6; S(4): 50.6; S(6): 98.8; S(9): 0.0	S6;	S397	48		0	0	2	830.4	1660	77.67	15670
SQsSLLER	MISP	126353	mitotic interactor and substrate of PLK1	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(4): 0.0	S3;	S543	39		0	0	2	557.7	1114	39.01	7360
ALSSDsILSPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S3(Phospho)	S(3): 98.3; S(4): 1.7; S(6): 0.0; S(9): 0.0	S3;	S394		3.59	0	0	2	790.4	1580	66.38	13365
ALSSDsILSPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S6(Phospho)	S(3): 50.6; S(4): 50.6; S(6): 98.8; S(9): 0.0	S6;	S397		3.29	0	0	2	830.4	1660	77.67	15670
ALSSDsILSPAPDAR	MISP	126353	mitotic interactor and substrate of PLK1	S4(Phospho) S9(Phospho)	S(3): 1.9; S(4): 98.1; S(6): 0.0; S(9): 100.0	S4; S9;	S395; S400		2.71	0	0	2	830.4	1660	76.34	15398
SQsSLLER	MISP	126353	mitotic interactor and substrate of PLK1	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(4): 0.0	S3;	S543		2.44	0	0	2	557.7	1114	39.01	7360
SGGSGHAVAEPAsPEQELDQNK	MKI67	4288	antigen KI-67 isoform 1	S13(Phospho)	S(1): 0.0; S(4): 0.0; S(13): 100.0	S13;	S308	52		0	0	3	763.3	2288	38.54	7259
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	42		0	0	2	856.9	1713	24.94	4380
MPCESsPPESADTPSTSTR	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S6(Phospho)	S(5): 2.3; S(6): 97.7; S(10): 0.0; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S6;	S1376	37		0	0	2	1015	2030	38.37	7225
IACKsPQPDVPDTPASTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 100.0; T(13): 0.0; S(16): 0.0; T(17): 0.0	S5;	S2344	31		0	1	3	664.6	1992	31.97	5872
AQSLVIsPPAPsPR	MKI67	4288	antigen KI-67 isoform 1	S7(Phospho) S12(Phospho)	S(3): 0.0; S(7): 100.0; S(12): 100.0	S7; S12;	S579; S584	30		0	0	2	790.4	1580	72.96	14758
IACKsPPPEsVSDTPSTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 100.0; S(10): 0.0; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S5;	S1131	28		0	1	3	665.6	1995	30.15	5495
ILCKsPQSDPADtPTNTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho) T13(Phospho)	S(5): 99.9; S(8): 0.1; T(13): 96.5; T(15): 3.4; T(17): 0.1	S5; T13;	S1861; T1869	25		0	1	3	711.6	2133	33.1	6106
AQSLVIsPPAPsPRKtPVASDQR	MKI67	4288	antigen KI-67 isoform 1	S7(Phospho) S12(Phospho) T16(Phospho)	S(3): 0.3; S(7): 99.7; S(12): 100.0; T(16): 100.0; S(20): 0.0	S7; S12; T16;	S579; S584; T588	14		0	2	3	881.4	2642	58.73	11622
SGGSGHAVAEPAsPEQELDQNK	MKI67	4288	antigen KI-67 isoform 1	S13(Phospho)	S(1): 0.3; S(4): 0.0; S(13): 99.6	S13;	S308	13		0	0	2	1145	2288	38.88	7333
IPCDsPQSDVPDTPSTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 99.9; S(8): 0.1; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S5;	S1253	13		0	0	2	1013	2025	44.7	8579
SGGSGHAVAEPAsPEQELDQNK	MKI67	4288	antigen KI-67 isoform 1	S13(Phospho)	S(1): 0.0; S(4): 0.0; S(13): 100.0	S13;	S308		5.57	0	0	3	763.3	2288	38.54	7259
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		4.94	0	0	2	856.9	1713	24.94	4380
IACKsPQPDVPDTPASTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 100.0; T(13): 0.0; S(16): 0.0; T(17): 0.0	S5;	S2344		4.54	0	1	3	664.6	1992	31.97	5872
ILCKsPQSDPADtPTNTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho) T13(Phospho)	S(5): 99.9; S(8): 0.1; T(13): 96.5; T(15): 3.4; T(17): 0.1	S5; T13;	S1861; T1869		4.38	0	1	3	711.6	2133	33.1	6106
AQSLVIsPPAPsPRKtPVASDQR	MKI67	4288	antigen KI-67 isoform 1	S7(Phospho) S12(Phospho) T16(Phospho)	S(3): 0.3; S(7): 99.7; S(12): 100.0; T(16): 100.0; S(20): 0.0	S7; S12; T16;	S579; S584; T588		4.22	0	2	3	881.4	2642	58.73	11622
AQSLVIsPPAPsPR	MKI67	4288	antigen KI-67 isoform 1	S7(Phospho) S12(Phospho)	S(3): 0.0; S(7): 100.0; S(12): 100.0	S7; S12;	S579; S584		3.86	0	0	2	790.4	1580	72.96	14758
IACKsPPPEsVSDTPSTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 100.0; S(10): 0.0; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S5;	S1131		3.81	0	1	3	665.6	1995	30.15	5495

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#
MPCESPPESADTPTSTR	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S6(Phospho)	S(5): 2.3; S(6): 97.7; S(10): 0.0; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S6;	S1376		3.34	0	0	2	1015	2030	38.37	7225
IPCDsPQSDPVDTPSTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho)	S(5): 99.9; S(8): 0.1; T(13): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0	S5;	S1253		1.99	0	0	2	1013	2025	44.7	8579
IPCDsPQSDPVDTPSTK	MKI67	4288	antigen KI-67 isoform 1	C3(Carbamidomethyl) S5(Phospho) T13(Phospho)	S(5): 100.0; S(8): 0.0; T(13): 97.1; T(15): 2.8; S(16): 0.0; T(17): 0.1	S5; T13;	S1253; T1261	14		0.001	0	2	1053	2105	50.21	9748
SGGSGHAVAEPAsPEQLDQNK	MKI67	4288	antigen KI-67 isoform 1	S13(Phospho)	S(1): 0.3; S(4): 0.0; S(13): 99.6	S13;	S308		2.58	0.003	0	2	1145	2288	38.88	7333
FGSTGStPPVSPTPSER	MKL1	57591	MKL/myocardin-like protein 1 isoform 3	T7(Phospho)	S(3): 3.2; T(4): 0.1; S(6): 3.2; T(7): 93.4; S(11): 50.0; T(13): 50.0; S(15): 0.0	T7;	T450	36		0	0	2	932.4	1864	53.71	10514
FGSTGStPPVSPTPSER	MKL1	57591	MKL/myocardin-like protein 1 isoform 3	T7(Phospho)	S(3): 3.2; T(4): 0.1; S(6): 3.2; T(7): 93.4; S(11): 50.0; T(13): 50.0; S(15): 0.0	T7;	T450		2.95	0	0	2	932.4	1864	53.71	10514
ADHRSSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S15(Phospho)	S(5): 50.0; S(6): 50.0; S(15): 100.0	S15;	S1165	35		0	1	3	692.6	2076	22.18	3798
SSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(11): 100.0	S11;	S1165	31		0	0	2	758.8	1517	26.78	4775
sQDADSPGsSGAPENLTFK	MLLT4	4301	afadin isoform 1	S1(Phospho) S9(Phospho)	S(1): 95.0; S(6): 5.0; S(9): 95.0; S(10): 5.0; T(17): 0.0	S1; S9;	S1693; S1701	21		0	0	2	1034	2068	68.83	13920
SQDADsPGSSGAPENLTFK	MLLT4	4301	afadin isoform 1	S6(Phospho)	S(1): 3.4; S(6): 93.1; S(9): 3.4; S(10): 0.0; T(17): 0.0	S6;	S1698	16		0	0	2	994.4	1988	56.3	11073
ADHRSSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S15(Phospho)	S(5): 50.0; S(6): 50.0; S(15): 100.0	S15;	S1165	13		0	1	3	692.6	2076	21.24	3600
ADHRSSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S15(Phospho)	S(5): 50.0; S(6): 50.0; S(15): 100.0	S15;	S1165		7.17	0	1	3	692.6	2076	22.18	3798
ADHRSSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S15(Phospho)	S(5): 50.0; S(6): 50.0; S(15): 100.0	S15;	S1165		6.28	0	1	3	692.6	2076	21.24	3600
SSPNVANQPPsPGGK	MLLT4	4301	afadin isoform 1	S11(Phospho)	S(1): 0.0; S(2): 0.0; S(11): 100.0	S11;	S1165		4.08	0	0	2	758.8	1517	26.78	4775
SQDADsPGSSGAPENLTFK	MLLT4	4301	afadin isoform 1	S6(Phospho)	S(1): 3.4; S(6): 93.1; S(9): 3.4; S(10): 0.0; T(17): 0.0	S6;	S1698		2.73	0	0	2	994.4	1988	56.3	11073
sQDADSPGsSGAPENLTFK	MLLT4	4301	afadin isoform 1	S1(Phospho) S9(Phospho)	S(1): 95.0; S(6): 5.0; S(9): 95.0; S(10): 5.0; T(17): 0.0	S1; S9;	S1693; S1701		2.31	0.001	0	2	1034	2068	68.83	13920
DKDQPPSPsPPPQSEALSSTSR	MON1B	22879	vacuolar fusion protein MON1 homolog B isoform 1	S9(Phospho)	S(7): 2.6; S(9): 97.4; S(14): 0.0; S(18): 0.0; S(19): 0.0; T(20): 0.0; S(21): 0.0	S9;	S61	30		0	1	3	796.7	2388	43.3	8265
DKDQPPSPsPPPQSEALSSTSR	MON1B	22879	vacuolar fusion protein MON1 homolog B isoform 1	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 100.0; S(14): 0.0; S(18): 0.0; S(19): 0.0; T(20): 0.0; S(21): 0.0	S7; S9;	S59; S61	16		0	1	3	823.4	2468	46.99	9074
DKDQPPSPsPPPQSEALSSTSR	MON1B	22879	vacuolar fusion protein MON1 homolog B isoform 1	S9(Phospho)	S(7): 2.6; S(9): 97.4; S(14): 0.0; S(18): 0.0; S(19): 0.0; T(20): 0.0; S(21): 0.0	S9;	S61		4.48	0	1	3	796.7	2388	43.3	8265
DKDQPPSPsPPPQSEALSSTSR	MON1B	22879	vacuolar fusion protein MON1 homolog B isoform 1	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 100.0; S(14): 0.0; S(18): 0.0; S(19): 0.0; T(20): 0.0; S(21): 0.0	S7; S9;	S59; S61		4.25	0	1	3	823.4	2468	46.99	9074
KDSNELsDsAGEEDSADLKR	MORC2	22880	MORC family CW-type zinc finger protein 2 isoform 3	S7(Phospho) S9(Phospho)	S(3): 0.0; S(7): 100.0; S(9): 100.0; S(15): 0.0	S7; S9;	S715; S717	57		0	2	3	776	2326	33.23	6133

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#
KTESPIKLSPatPSR	MORC2	22880	MORC family CW-type zinc finger protein 2 isoform 3	S9(Phospho) T12(Phospho)	T(2): 50.0; S(4): 50.0; S(9): 100.0; T(12): 97.0; S(14): 3.0	S9; T12;	S668; T671	25		0	2	3	617.9	1852	44.46	8521
KDSNELSDsAGEEDSADLKR	MORC2	22880	MORC family CW-type zinc finger protein 2 isoform 3	S7(Phospho) S9(Phospho)	S(3): 9.1; S(7): 95.4; S(9): 95.4; S(15): 0.0	S7; S9;	S715; S717	14		0	2	3	776	2326	33.97	6288
KDSNELSDsAGEEDSADLKR	MORC2	22880	MORC family CW-type zinc finger protein 2 isoform 3	S7(Phospho) S9(Phospho)	S(3): 0.0; S(7): 100.0; S(9): 100.0; S(15): 0.0	S7; S9;	S715; S717		7.96	0	2	3	776	2326	33.23	6133
KDSNELSDsAGEEDSADLKR	MORC2	22880	MORC family CW-type zinc finger protein 2 isoform 3	S7(Phospho) S9(Phospho)	S(3): 9.1; S(7): 95.4; S(9): 95.4; S(15): 0.0	S7; S9;	S715; S717		4.1	0	2	3	776	2326	33.97	6288
GAEAFGDSSEEDGEDVFEVEK	MPHOSPH8	54737	M-phase phosphoprotein 8	S8(Phospho)	S(8): 100.0	S8;	S51	16		0	0	2	1120	2239	74.71	15111
GAEAFGDSSEEDGEDVFEVEK	MPHOSPH8	54737	M-phase phosphoprotein 8	S8(Phospho)	S(8): 100.0	S8;	S51		2.47	0.001	0	2	1120	2239	74.71	15111
TKDQPDGSSLSPAQsPSQSQPPAASSLR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S15(Phospho)	T(1): 0.0; S(8): 0.0; S(9): 0.0; S(11): 100.0; S(15): 99.8; S(17): 0.2; S(19): 0.0; S(25): 0.0; S(26): 0.0	S11; S15;	S220; S224	37		0	1	3	995.4	2984	49.04	9504
SKsNPDFLK	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S993	26		0	1	2	558.3	1116	30.97	5665
DQPDGSSLSPAQSPsQSQPPAASSLR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S15(Phospho)	S(6): 2.9; S(7): 48.5; S(9): 48.5; S(13): 5.5; S(15): 89.3; S(17): 5.3; S(23): 0.0; S(24): 0.0	S15;	S226	23		0	0	3	919.1	2755	63.39	12659
AEEQQLPPPLsPPsPSTPNHR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 97.0; S(16): 2.9; T(17): 0.1	S11; S14;	S289; S292	23		0	0	3	813.7	2439	62.29	12372
AEEQQLPPPLsPPsPSTPNHR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 96.7; S(16): 3.2; T(17): 0.1	S11; S14;	S289; S292	11		0	0	3	813.7	2439	61.76	12249
TKDQPDGSSLSPAQsPSQSQPPAASSLR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S15(Phospho)	T(1): 0.0; S(8): 0.0; S(9): 0.0; S(11): 100.0; S(15): 99.8; S(17): 0.2; S(19): 0.0; S(25): 0.0; S(26): 0.0	S11; S15;	S220; S224		6	0	1	3	995.4	2984	49.04	9504
AEEQQLPPPLsPPsPSTPNHR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 97.0; S(16): 2.9; T(17): 0.1	S11; S14;	S289; S292		5.36	0	0	3	813.7	2439	62.29	12372
AEEQQLPPPLsPPsPSTPNHR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S11(Phospho) S14(Phospho)	S(11): 100.0; S(14): 96.7; S(16): 3.2; T(17): 0.1	S11; S14;	S289; S292		4.46	0	0	3	813.7	2439	61.76	12249
DQPDGSSLSPAQSPsQSQPPAASSLR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S15(Phospho)	S(6): 2.9; S(7): 48.5; S(9): 48.5; S(13): 5.5; S(15): 89.3; S(17): 5.3; S(23): 0.0; S(24): 0.0	S15;	S226		2.88	0	0	3	919.1	2755	63.39	12659
SKsNPDFLK	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S3(Phospho)	S(1): 0.0; S(3): 100.0	S3;	S993		2.85	0	1	2	558.3	1116	30.97	5665
AEEQQLPPPLsPPsPSTPNHR	MPRIP	23164	myosin phosphatase Rho-interacting protein isoform 2	S14(Phospho)	S(11): 0.0; S(14): 97.0; S(16): 2.9; T(17): 0.1	S14;	S292		2.8	0.001	0	3	787	2359	57.16	11276
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661	40		0	0	2	1319	2638	101.6	20329
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	M16(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661	28		0	0	3	885.3	2654	91.3	18247
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	M16(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661	24		0	0	2	1327	2654	91.28	18242
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661		2.79	0	0	2	1319	2638	101.6	20329
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	M16(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661		2.71	0	0	3	885.3	2654	91.3	18247
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	M16(Oxidation) S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(18): 0.0; S(19): 0.0; S(20): 0.0	S6; S7;	S660; S661		2.06	0	0	2	1327	2654	91.28	18242

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#
GVDFEssEDDDDDPFMNTSSLR	MRE11A	4361	double-strand break repair protein MRE11A isoform 2	M16(Oxidation) S6(Phospho) S7(Phospho)	S(6): 98.7; S(7): 98.7; T(18): 2.0; S(19): 0.3; S(20): 0.3	S6; S7;	S660; S661		1.41	0.004	0	2	1327	2654	91.98	18376
VLTA _{NS} NP _S PSAAK	MRGBP	55257	MRG/MORF4L-binding protein	S6(Phospho) S10(Phospho)	T(3): 2.9; S(6): 94.2; S(9): 3.0; S(10): 99.8; S(12): 0.1	S6; S10;	S191; S195	33		0	0	2	802.3	1604	37.88	7123
VLTA _{NS} NP _S PSAAK	MRGBP	55257	MRG/MORF4L-binding protein	S6(Phospho) S10(Phospho)	T(3): 2.9; S(6): 94.2; S(9): 3.0; S(10): 99.8; S(12): 0.1	S6; S10;	S191; S195		3.45	0	0	2	802.3	1604	37.88	7123
SQEPI _{DD} QKV _S DDDK _{KEK}	MTDH	92140	protein LYRIC	S12(Phospho)	S(1): 0.0; S(12): 100.0	S12;	S426		5.21	0	2	3	718.3	2153	25.56	4511
SQEPI _{DD} QKV _S DDDK _{KEK}	MTDH	92140	protein LYRIC	S12(Phospho)	S(1): 0.0; S(12): 100.0	S12;	S426	11		0.001	2	3	718.3	2153	25.56	4511
RCsDPSLNEK	MTMR3	8897	myotubularin-related protein 3 isoform b	C2(Carbamidomethyl) S3(Phospho)	S(3): 100.0; S(6): 0.0	S3;	S633	37		0	1	2	643.3	1286	15.95	2471
RCsDPSLNEK	MTMR3	8897	myotubularin-related protein 3 isoform b	C2(Carbamidomethyl) S3(Phospho)	S(3): 100.0; S(6): 0.0	S3;	S633		4	0	1	2	643.3	1286	15.95	2471
NQKPSQVNGAPGsPTEPAGQK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S13(Phospho)	S(5): 0.0; S(13): 99.9; T(15): 0.1	S13;	S1267	35		0	0	3	724.7	2172	23	3974
EIPsATQsPISK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S8(Phospho)	S(4): 0.0; T(6): 0.0; S(8): 98.8; S(11): 1.2	S8;	S1163	33		0	0	2	669.3	1338	38.97	7351
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	31		0	0	3	745.7	2235	26.63	4744
DPAQPMsPGEATQSGARPADR	MYBBP1A	10514	myb-binding protein 1A isoform 2	S7(Phospho)	S(7): 100.0; T(12): 0.0; S(14): 0.0	S7;	S11	15		0	0	3	740.3	2219	36.53	6842
NQKPSQVNGAPGsPTEPAGQK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S13(Phospho)	S(5): 0.0; S(13): 99.9; T(15): 0.1	S13;	S1267		5.49	0	0	3	724.7	2172	23	3974
SPAPGAPTRSPstPAKsPK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S12(Phospho) T13(Phospho) S17(Phospho)	S(1): 0.0; T(8): 0.4; S(10): 5.6; S(12): 94.4; T(13): 99.6; S(17): 100.0	S12; T13; S17;	S1243; T1244; S1248		5.12	0	2	3	692	2074	23.85	4149
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		4.16	0	0	3	745.7	2235	26.63	4744
DPAQPMsPGEATQSGARPADR	MYBBP1A	10514	myb-binding protein 1A isoform 2	S7(Phospho)	S(7): 100.0; T(12): 0.0; S(14): 0.0	S7;	S11		4.04	0	0	3	740.3	2219	36.53	6842
EIPsATQsPISK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S8(Phospho)	S(4): 0.0; T(6): 0.0; S(8): 98.8; S(11): 1.2	S8;	S1163		3.51	0	0	2	669.3	1338	38.97	7351
EIPsATQSPISK	MYBBP1A	10514	myb-binding protein 1A isoform 2	S4(Phospho)	S(4): 100.0; T(6): 0.0; S(8): 50.0; S(11): 50.0	S4;	S1159	23		0.007	0	2	709.3	1418	48.53	9396
ALLssPEGEEK	MYCBP2	23077	E3 ubiquitin-protein ligase MYCBP2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S3931; S3932	23		0	0	2	660.3	1320	57	11236
SSsPHDKNLPQK	MYCBP2	23077	E3 ubiquitin-protein ligase MYCBP2	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9	S3;	S2844	20		0	1	2	709.3	1418	12.66	1774
SSsPHDKNLPQK	MYCBP2	23077	E3 ubiquitin-protein ligase MYCBP2	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 99.9	S3;	S2844		2.55	0	1	2	709.3	1418	12.66	1774
ALLssPEGEEK	MYCBP2	23077	E3 ubiquitin-protein ligase MYCBP2	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0	S4; S5;	S3931; S3932		1.46	0.005	0	2	660.3	1320	57	11236
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho)	S(7): 100.0; S(18): 0.0; S(21): 0.0; S(27): 0.0	S7;	S1969	40		0	0	3	1131	3391	53.53	10476
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S27(Phospho)	S(7): 93.9; S(18): 0.0; S(21): 6.1; S(27): 100.0	S7; S27;	S1969; S1989	19		0	0	4	868.6	3471	61.55	12205
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S27(Phospho)	S(7): 99.5; S(18): 0.0; S(21): 0.5; S(27): 100.0	S7; S27;	S1969; S1989	18		0	0	3	1158	3471	61.43	12179
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S21(Phospho)	S(7): 100.0; S(18): 7.0; S(21): 93.0; S(27): 0.0	S7; S21;	S1969; S1983	17		0	0	3	1158	3471	59.73	11826
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S21(Phospho) S27(Phospho)	S(7): 100.0; S(18): 0.6; S(21): 99.4; S(27): 100.0	S7; S21; S27;	S1969; S1983; S1989	15		0	0	4	888.6	3551	72.3	14611
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho)	S(7): 100.0; S(18): 0.0; S(21): 0.0; S(27): 0.0	S7;	S1969		4.99	0	0	3	1131	3391	53.53	10476
LEEGVAsDEEAEEAQP _{SGSP} PEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S27(Phospho)	S(7): 99.5; S(18): 0.0; S(21): 0.5; S(27): 100.0	S7; S27;	S1969; S1989		4.44	0	0	3	1158	3471	61.43	12179

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#
LEEGVAsDEEAEEAQPGSGSPPEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S27(Phospho)	S(7): 93.9; S(18): 0.0; S(21): 6.1; S(27): 100.0	S7; S27;	S1969; S1989		4.21	0	0	4	868.6	3471	61.55	12205
LEEGVAsDEEAEEAQPGSGSPPEPEGSP PAHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S21(Phospho)	S(7): 100.0; S(18): 7.0; S(21): 93.0; S(27): 0.0	S7; S21;	S1969; S1983		3.75	0	0	3	1158	3471	59.73	11826
LEEGVAsDEEAEEAQPGSGSPPEPEGSP AHPQ	MYH14	79784	myosin-14 isoform 2	S7(Phospho) S21(Phospho) S27(Phospho)	S(7): 100.0; S(18): 0.7; S(21): 99.3; S(27): 100.0	S7; S21; S27;	S1969; S1983; S1989		3.44	0	0	3	1184	3551	72.65	14689
KGAGDGsDEEVDGK	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	89		0	1	2	722.3	1444	12.79	1805
GAGDGsDEEVDGK	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	83		0	0	2	658.2	1315	16.51	2594
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	71		0	2	3	795	2383	24.03	4187
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	68		0	2	3	795	2383	22.98	3969
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	60		0	2	2	1192	2383	21.91	3738
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	58		0	2	3	795	2383	21.66	3685
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	57		0	2	3	795	2383	24.54	4294
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	55		0	2	3	795	2383	22.44	3852
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	50		0	2	3	795	2383	20.62	3468
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	50		0	2	3	795	2383	23.51	4077
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	41		0	1	3	752.3	2255	25.57	4513
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	38		0	1	3	752.3	2255	26.41	4694
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	36		0	1	3	752.3	2255	27.21	4870
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	33		0	1	2	1128	2255	26.46	4705
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	28		0	2	3	795	2383	21.15	3580
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	26		0	2	2	1192	2383	22.78	3927
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943	12		0	1	2	1128	2255	27.24	4878
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		9.58	0	2	3	795	2383	22.98	3969
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		9.39	0	2	3	795	2383	22.44	3852
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		9.02	0	2	3	795	2383	20.62	3468
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		8.45	0	2	3	795	2383	23.51	4077
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		8.01	0	2	3	795	2383	24.03	4187
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		7.49	0	2	3	795	2383	21.66	3685
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		7.28	0	2	3	795	2383	24.54	4294
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		6.41	0	1	3	752.3	2255	26.41	4694
KGAGDGsDEEVDGK	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		6.32	0	1	2	722.3	1444	12.79	1805
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		6.23	0	1	3	752.3	2255	27.21	4870
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		5.5	0	1	3	752.3	2255	25.57	4513
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		5.14	0	2	2	1192	2383	21.91	3738
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		4.76	0	2	3	795	2383	21.15	3580
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		4.37	0	1	2	1128	2255	26.46	4705
GAGDGsDEEVDGK	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		4.15	0	0	2	658.2	1315	16.51	2594
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		4.03	0	2	2	1192	2383	22.15	3790
GAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S6(Phospho)	S(6): 100.0	S6;	S1943		2.6	0	1	2	1128	2255	27.24	4878
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943		2.58	0	2	2	1192	2383	22.78	3927
KGAGDGsDEEVDGKADGAEAKPAE	MYH9	4627	myosin-9	S7(Phospho)	S(7): 100.0	S7;	S1943	17		0.001	2	2	1192	2383	22.15	3790
YSHSYLsDsDTEAK	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S7(Phospho) S9(Phospho)	Y(1): 0.0; S(2): 0.0; S(4): 0.0; Y(5): 0.0; S(7): 100.0; S(9): 100.0; T(11): 0.0	S7; S9;	S2026; S2028	32		0	0	2	881.8	1763	39.58	7480
YSHSYLsDsDTEAK	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S7(Phospho) S9(Phospho)	Y(1): 0.0; S(2): 0.0; S(4): 0.0; Y(5): 0.0; S(7): 100.0; S(9): 100.0; T(11): 0.0	S7; S9;	S2026; S2028		4.03	0	0	2	881.8	1763	39.58	7480
AAaDDGsLKSSSPTSYYWK	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 99.7; S(10): 48.5; S(11): 2.8; S(12): 48.7; T(14): 0.2; S(15): 0.2; Y(16): 0.0	S3; S7;	S1983; S1987		2.94	0	1	3	709.6	2127	69.17	13986
AAaDDGsLKSSSPTSYYWK	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(10): 0.0; S(11): 0.2; S(12): 0.2; T(14): 48.5; S(15): 48.5; Y(16): 2.7	S3; S7;	S1983; S1987		2.61	0	1	2	1064	2127	68.96	13948

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#
AA sDDGsLKSSSPSYWK	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(10): 0.0; S(11): 0.2; S(12): 0.2; T(14): 48.5; S(15): 48.5; Y(16): 2.7	S3; S7;	S1983; S1987	10		0.001	1	2	1064	2127	68.96	13948
sRDEASSETSTPSEHSAAPSPQVEVR	MYO18A	399687	unconventional myosin-XVIIIa isoform b	S1(Phospho)	S(1): 94.9; S(5): 4.6; S(7): 0.2; T(9): 0.0; S(10): 0.0; T(11): 0.0; S(13): 0.2; S(16): 0.0; S(20): 0.0	S1;	S145		3.03	0.001	1	3	941.1	2821	34.15	6326
VQEKPDsPGGSTQIQR	MYO9B	4650	unconventional myosin-IXb isoform 2	S7(Phospho)	S(7): 100.0; S(11): 0.0; T(12): 0.0	S7;	S1290	67		0	0	3	603	1807	23.29	4033
VQEKPDsPGGSTQIQR	MYO9B	4650	unconventional myosin-IXb isoform 2	S7(Phospho)	S(7): 100.0; S(11): 0.0; T(12): 0.0	S7;	S1290	20		0	0	2	903.9	1807	23.25	4026
SPLEHSSPEKEAPsPEK	MYO9B	4650	unconventional myosin-IXb isoform 2	S14(Phospho)	S(1): 1.4; S(6): 49.3; S(7): 49.3; S(14): 100.0	S14;	S1122	13		0	1	3	670.3	2009	27.3	4893
VQEKPDsPGGSTQIQR	MYO9B	4650	unconventional myosin-IXb isoform 2	S7(Phospho)	S(7): 100.0; S(11): 0.0; T(12): 0.0	S7;	S1290		5.99	0	0	3	603	1807	23.29	4033
SPLEHSSPEKEAPsPEK	MYO9B	4650	unconventional myosin-IXb isoform 2	S14(Phospho)	S(1): 1.4; S(6): 49.3; S(7): 49.3; S(14): 100.0	S14;	S1122		5.42	0	1	3	670.3	2009	27.3	4893
VQEKPDsPGGSTQIQR	MYO9B	4650	unconventional myosin-IXb isoform 2	S7(Phospho)	S(7): 100.0; S(11): 0.0; T(12): 0.0	S7;	S1290		2.97	0	0	2	903.9	1807	23.25	4026
VSPAPAGsAPeTPEDK	MYO9B	4650	unconventional myosin-IXb isoform 2	S8(Phospho) T12(Phospho)	S(2): 0.0; S(8): 100.0; T(12): 100.0	S8; T12;	S1267; T1271	28		0.006	0	2	869.8	1739	44.24	8467
sPLEHSSPEKEAPsPEK	MYO9B	4650	unconventional myosin-IXb isoform 2	S1(Phospho) S14(Phospho)	S(1): 98.5; S(6): 0.8; S(7): 0.8; S(14): 99.9	S1; S14;	S1109; S1122		2.21	0.008	1	2	1005	2009	27.23	4876
TPVDEsDDEIQHDEIPTGK	MYPN	84665	myopalladin isoform b	S6(Phospho)	T(1): 0.2; S(6): 99.8; T(17): 0.0	S6;	S634		2.42	0	0	3	735.6	2205	46.94	9064
GNsPPSSGEACREEK	NAA10	8260	N-alpha-acetyltransferase 10 isoform 2	C11(Carbamido methyl) S3(Phospho)	S(3): 99.9; S(6): 0.1; S(7): 0.0	S3;	S171	17		0	1	2	842.8	1685	14.42	2149
GNsPPSSGEACREEK	NAA10	8260	N-alpha-acetyltransferase 10 isoform 2	C11(Carbamido methyl) S3(Phospho)	S(3): 99.9; S(6): 0.1; S(7): 0.0	S3;	S171		1.88	0	1	2	842.8	1685	14.42	2149
APsPTAEQPPGGGDSAR	NAB2	4665	NGFI-A-binding protein 2	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(15): 0.0	S3;	S6	56		0	0	2	837.9	1675	28.74	5201
APsPTAEQPPGGGDSAR	NAB2	4665	NGFI-A-binding protein 2	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(15): 0.0	S3;	S6		4.2	0	0	2	837.9	1675	28.74	5201
VQGEAVSNIQENTQTPTVQEEsEEEEVD ETGVEVK	NACA	4666	nascent polypeptide-associated complex subunit alpha isoform b	S22(Phospho)	S(7): 0.0; T(13): 5.4; T(15): 5.4; T(17): 5.4; S(22): 83.9; T(30): 0.0	S22;	S166	22		0	0	4	985.9	3941	65.46	13151
VQGEAVSNIQENTQTPTVQEEsEEEEVD ETGVEVK	NACA	4666	nascent polypeptide-associated complex subunit alpha isoform b	S22(Phospho)	S(7): 0.0; T(13): 0.5; T(15): 0.5; T(17): 6.3; S(22): 92.7; T(30): 0.0	S22;	S166	17		0	0	3	1314	3941	65.91	13257
VQGEAVSNIQENTQTPTVQEEsEEEEVD ETGVEVK	NACA	4666	nascent polypeptide-associated complex subunit alpha isoform b	S22(Phospho)	S(7): 0.0; T(13): 5.4; T(15): 5.4; T(17): 5.4; S(22): 83.9; T(30): 0.0	S22;	S166		4.08	0	0	4	985.9	3941	65.46	13151
VQGEAVSNIQENTQTPTVQEEsEEEEVD ETGVEVK	NACA	4666	nascent polypeptide-associated complex subunit alpha isoform b	S22(Phospho)	S(7): 0.0; T(13): 0.5; T(15): 0.5; T(17): 6.3; S(22): 92.7; T(30): 0.0	S22;	S166		3.47	0	0	3	1314	3941	65.91	13257
VQGEAVSNIQENTQTPTVQEEsEEEEVD ETGVEVK	NACA	4666	nascent polypeptide-associated complex subunit alpha isoform b	S22(Phospho)	S(7): 0.0; T(13): 6.6; T(15): 6.6; T(17): 6.6; S(22): 80.1; T(30): 0.0	S22;	S166		2.54	0	0	3	1314	3941	66.42	13375
NDQEPPPEALDFsDDEKEKEAK	NAF1	92345	H/ACA ribonucleoprotein complex non-core subunit NAF1 isoform b	S13(Phospho)	S(13): 100.0	S13;	S315		4.79	0	2	3	871	2611	45.74	8810
NDQEPPPEALDFsDDEKEK	NAF1	92345	H/ACA ribonucleoprotein complex non-core subunit NAF1 isoform b	S13(Phospho)	S(13): 100.0	S13;	S315		4.7	0	1	3	761.7	2283	53.02	10369

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#
GGAAPGPNNAEVTSGKPEQVDPDAEE EKSVSGTDVQEECR	NASP	4678	nuclear autoantigenic sperm protein isoform 4	C40(Carbamidomethyl) S30(Phospho)	T(14): 0.0; S(15): 0.0; S(30): 99.1; S(32): 0.8; T(34): 0.1	S30;	S180	24		0	1	4	1095	4379	48.55	9401
GGAAPGPNNAEVTSGKPEQVDPDAEE EKSVSGTDVQEECR	NASP	4678	nuclear autoantigenic sperm protein isoform 4	C40(Carbamidomethyl) S30(Phospho)	T(14): 0.0; S(15): 0.0; S(30): 99.1; S(32): 0.8; T(34): 0.1	S30;	S180		6.2	0	1	4	1095	4379	48.55	9401
SPsDAGRSSGDESKPLPSSSR	NAV2	89797	neuron navigator 2 isoform 4	S3(Phospho)	S(1): 4.8; S(3): 95.1; S(8): 50.1; S(9): 50.1; S(13): 0.0; S(19): 0.0; S(20): 0.0; S(21): 0.0	S3;	S178		2.39	0.003	2	3	798	2392	17.38	2788
TLHCEGTEINsDDEQESK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 99.9; S(17): 0.1	S11;	S674	46		0	0	3	724.6	2172	26.97	4816
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.1; S(11): 99.8; S(17): 0.1; T(23): 0.0; T(25): 0.0	S11;	S674	46		0	1	4	783.3	3130	46.69	9012
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 100.0; S(17): 0.0; T(23): 0.0; T(25): 0.0	S11;	S674	44		0	1	3	1044	3130	46.59	8993
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 99.9; S(17): 0.1; T(23): 0.0; T(25): 0.0	S11;	S674	41		0	1	3	1044	3130	47.15	9108
RCQTAEADsEsDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C2(Carbamidomethyl) S9(Phospho) S11(Phospho)	T(4): 0.0; S(9): 100.0; S(11): 100.0; S(20): 0.0	S9; S11;	S973; S975	24		0	1	3	941	2821	38.43	7238
RCQTAEADsEsDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C2(Carbamidomethyl) M22(Oxidation) S9(Phospho) S11(Phospho)	T(4): 0.5; S(9): 100.0; S(11): 99.6; S(20): 0.0	S9; S11;	S973; S975	11		0	1	3	946.3	2837	29.63	5386
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 99.9; S(17): 0.1; T(23): 0.0; T(25): 0.0	S11;	S674		6.56	0	1	3	1044	3130	47.15	9108
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.1; S(11): 99.8; S(17): 0.1; T(23): 0.0; T(25): 0.0	S11;	S674		6.25	0	1	4	783.3	3130	46.69	9012
TLHCEGTEINsDDEQESKEVEETATAK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 100.0; S(17): 0.0; T(23): 0.0; T(25): 0.0	S11;	S674		5.42	0	1	3	1044	3130	46.59	8993
TLHCEGTEINsDDEQESK	NCAPG	64151	condensin complex subunit 3	C4(Carbamidomethyl) S11(Phospho)	T(1): 0.0; T(7): 0.0; S(11): 99.9; S(17): 0.1	S11;	S674		5.02	0	0	3	724.6	2172	26.97	4816
RCQTAEADsEsDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C2(Carbamidomethyl) S9(Phospho) S11(Phospho)	T(4): 0.0; S(9): 100.0; S(11): 100.0; S(20): 0.0	S9; S11;	S973; S975		4.74	0	1	3	941	2821	38.43	7238
RCQTAEADsEsDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C2(Carbamidomethyl) M22(Oxidation) S9(Phospho) S11(Phospho)	T(4): 0.5; S(9): 100.0; S(11): 99.6; S(20): 0.0	S9; S11;	S973; S975		4.69	0	1	3	946.3	2837	29.63	5386
CQTAEADsESDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C1(Carbamidomethyl) S8(Phospho)	T(3): 0.0; S(8): 96.6; S(10): 51.7; S(19): 51.7	S8;	S973		2.94	0	0	3	889	2665	46.45	8963
CQTAEADsESDHEVPEPESEM	NCAPG	64151	condensin complex subunit 3	C1(Carbamidomethyl) S8(Phospho) S10(Phospho)	T(3): 13.2; S(8): 93.4; S(10): 93.4; S(19): 0.1	S8; S10;	S973; S975		3.45	0.001	0	3	889	2665	45.91	8848

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#
CQTAADSEsDHEVPEPESEMK	NCAPG	64151	condensin complex subunit 3	C1(Carbamidomethyl) M21(Oxidation) S10(Phospho)	T(3): 50.3; S(8): 50.3; S(10): 99.3; S(19): 0.2	S10;	S975		2.37	0.005	0	3	894.3	2681	36.04	6738
MISTPsPKK	NCBP3	55421	uncharacterized protein C17orf85	T4(Phospho) S6(Phospho)	S(3): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T413; S415	17		0	1	2	574.7	1148	21.36	3624
MISTPsPKK	NCBP3	55421	uncharacterized protein C17orf85	T4(Phospho) S6(Phospho)	S(3): 0.0; T(4): 100.0; S(6): 100.0	T4; S6;	T413; S415		2.8	0.001	1	2	574.7	1148	21.36	3624
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	58		0	0	3	1536	4606	63.16	12599
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	46		0	1	3	1427	4279	62.99	12555
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	44		0	1	3	1427	4279	63.51	12688
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	41		0	0	3	1536	4606	64.19	12855
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	40		0	1	3	1427	4279	62.42	12404
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	39		0	1	3	1427	4279	62.43	12407
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho)	S(4): 100.0; S(12): 0.0	S4;	S145	38		0	1	3	1400	4199	55.62	10930
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	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	33		0	0	4	1156	4623	53.15	10395
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	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	32		0	0	4	1156	4623	52.57	10261
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 93.8; S(30): 6.2; T(37): 0.0; T(38): 0.0	S8;	S184	31		0	0	3	1510	4527	56	11011
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	30		0	1	3	1432	4295	51.7	10061
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 99.9; T(37): 0.1; T(38): 0.1	S8; S30;	S184; S206	30		0	0	3	1542	4623	52.53	10254
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 99.5; S(30): 0.5; T(37): 0.0; T(38): 0.0	S8;	S184	29		0	0	4	1132	4527	54.42	10677
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	29		0	1	3	1427	4279	64.04	12820
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho)	S(8): 99.6; S(30): 0.4; T(37): 0.0; T(38): 0.0	S8;	S184	27		0	0	3	1515	4543	45.34	8726
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	26		0	0	3	1536	4606	63.49	12683
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	25		0	1	4	1075	4295	51.78	10077
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 100.0; S(30): 0.0; T(37): 0.0; T(38): 0.0	S8;	S184	25		0	0	3	1510	4527	54.88	10776
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	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	0	3	1536	4606	63.7	12735
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	23		0	1	3	1427	4279	64.56	12955
KEDsDEEEDDDsEEDEEDEDDEDE IEPAAMK	NCL	4691	nucleolin	S12(Phospho)	S(4): 0.0; S(12): 100.0	S12;	S153	22		0	1	3	1400	4199	55.08	10817
AAAAAPAsEDEDEDDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206	22		0	0	3	1536	4606	62.94	12541

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#
AAAAAPAsEDEDEDDEDDEDDDDDEEDS DSEEEAMETTPAK	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	22		0	0	3	1542	4623	53.34	10437
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	20		0	1	3	1432	4295	61.72	12242
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S12(Phospho)	S(4): 0.0; S(12): 100.0	S12;	S153	20		0	1	3	1406	4215	45.57	8775
MAPPPKVEEDsEDEEMsEDEEDSSG EEVIPQKK	NCL	4691	nucleolin	M17(Oxidation) S12(Phospho) S18(Phospho)	S(12): 99.9; S(18): 94.7; S(25): 52.7; S(26): 52.7	S12; S18;	S28; S34	20		0	2	4	1080	4319	58.6	11587
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	20		0	1	4	1075	4295	52.31	10207
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	19		0	1	3	1427	4279	59.18	11721
AAAAAPAsEDEDEDDEDDEDDDDDEEDS DSEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho)	S(8): 99.5; S(30): 0.5; T(37): 0.0; T(38): 0.0	S8;	S184	19		0	0	4	1136	4543	45.42	8744
VVVsPTKK	NCL	4691	nucleolin	S4(Phospho)	S(4): 100.0; T(6): 0.0	S4;	S67	19		0	1	2	469.3	937.5	15.27	2327
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	19		0	1	3	1427	4279	62.94	12542
AAAAAPAsEDEDEDDEDDEDDDDDEEDS DSEEEAMETTPAK	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	16		0	0	3	1541	4622	52.79	10311
MAPPPKVEEDsEDEEMsEDEEDSSG EEVIPQKK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho)	S(12): 99.4; S(18): 94.7; S(25): 53.0; S(26): 53.0	S12; S18;	S28; S34	15		0	2	4	1076	4303	61.68	12233
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	14		0	1	3	1432	4295	60.73	12029
MAPPPKVEEDSEDEEMSEDEEDSSG EEVIPQK	NCL	4691	nucleolin	S25(Phospho) S26(Phospho)	S(12): 50.8; S(18): 50.8; S(25): 99.2; S(26): 99.2	S25; S26;	S41; S42	12		0	1	4	1044	4175	73.34	14830
AAAAAPAsEDEDEDDEDDEDDDDDEEDS DSEEEAMETTPAK	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	11		0	0	3	1542	4623	60.57	11994
NAKKEDsDEEEDDDsEEDEEDDEDEDED EDEIEPAAMK	NCL	4691	nucleolin	M37(Oxidation) S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0	S7; S15;	S145; S153	10		0	2	4	1153	4609	43.46	8299
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.9	0	1	3	1427	4279	62.99	12555
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.89	0	1	3	1427	4279	62.43	12407
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.86	0	1	4	1075	4295	51.78	10077
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.59	0	1	3	1427	4279	63.51	12688
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.54	0	1	3	1432	4295	51.7	10061
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.48	0	1	4	1075	4295	52.31	10207
AAAAAPAsEDEDEDDEDDEDDDDDEEDS DSEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		5.39	0	0	3	1536	4606	63.16	12599
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		5.25	0	1	3	1427	4279	62.94	12542

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#
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho)	S(4): 100.0; S(12): 0.0	S4;	S145		4.84	0	1	3	1400	4199	55.62	10930
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		4.74	0	1	3	1427	4279	62.42	12404
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	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		4.67	0	0	4	1156	4623	52.57	10261
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		4.6	0	0	3	1536	4606	62.94	12541
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 99.5; S(30): 0.5; T(37): 0.0; T(38): 0.0	S8;	S184		4.44	0	0	4	1132	4527	54.42	10677
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		4.27	0	1	3	1427	4279	64.04	12820
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	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		4.14	0	0	4	1156	4623	53.15	10395
MAPPKVEEDsEDEEMsEDEEDSSGEEVVIQKK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho)	S(12): 99.4; S(18): 94.7; S(25): 53.0; S(26): 53.0	S12; S18;	S28; S34		4.07	0	2	4	1076	4303	61.68	12233
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		4	0	0	3	1536	4606	64.19	12855
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		3.97	0	0	3	1536	4606	63.49	12683
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho)	S(8): 99.5; S(30): 0.5; T(37): 0.0; T(38): 0.0	S8;	S184		3.95	0	0	4	1136	4543	45.42	8744
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.93	0	1	3	1432	4295	61.72	12242
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 99.9; T(37): 0.1; T(38): 0.1	S8; S30;	S184; S206		3.77	0	0	3	1542	4623	52.53	10254
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	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		3.76	0	0	3	1541	4622	52.79	10311
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho)	S(8): 99.6; S(30): 0.4; T(37): 0.0; T(38): 0.0	S8;	S184		3.7	0	0	3	1515	4543	45.34	8726
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.6	0	1	3	1432	4295	60.73	12029
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	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	1542	4623	53.34	10437
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.55	0	1	3	1427	4279	64.56	12955
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S12(Phospho)	S(4): 0.0; S(12): 100.0	S12;	S153		3.48	0	1	3	1400	4199	55.08	10817
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		3.41	0	0	3	1536	4606	63.7	12735
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.36	0	1	4	1071	4279	64.29	12884
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 93.8; S(30): 6.2; T(37): 0.0; T(38): 0.0	S8;	S184		3.28	0	0	3	1510	4527	56	11011
KEDsDEEEDDDsEEDEEDEDDEDEDEIEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S12(Phospho)	S(4): 0.0; S(12): 100.0	S12;	S153		3.17	0	1	3	1406	4215	45.57	8775
AAAAAPAsEDEDEDDEDEDDDDDDEEDDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho)	S(8): 100.0; S(30): 0.0; T(37): 0.0; T(38): 0.0	S8;	S184		3.01	0	0	3	1510	4527	54.88	10776

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#
MAPPPKEVEEDSEDEEMSEDEEDSSGEEVVIPQK	NCL	4691	nucleolin	S25(Phospho) S26(Phospho)	S(12): 50.8; S(18): 50.8; S(25): 99.2; S(26): 99.2	S25; S26;	S41; S42		2.87	0	1	4	1044	4175	73.34	14830
KEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		2.81	0	1	3	1427	4279	59.18	11721
EDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	S3(Phospho) S11(Phospho)	S(3): 100.0; S(11): 100.0	S3; S11;	S145; S153		2.73	0	0	3	1384	4151	78.13	15749
NAKKEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0	S7; S15;	S145; S153		2.73	0	2	4	1149	4593	52.56	10260
EVEEDsEDEEMsEEDEEDSSGEEVVIPQK	NCL	4691	nucleolin	M11(Oxidation) S6(Phospho) S12(Phospho) S19(Phospho) S20(Phospho)	S(6): 75.0; S(12): 75.0; S(19): 75.0; S(20): 75.0	S6; S12; S19; S20;	S28; S34; S41; S42		2.7	0	1	3	1233	3697	63.8	12761
KEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		2.68	0	1	3	1432	4295	59.68	11817
MAPPPKEVEEDsEDEEMsEEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	M1(Oxidation) S12(Phospho) S18(Phospho) S25(Phospho)	S(12): 90.8; S(18): 90.8; S(25): 90.8; S(26): 27.6	S12; S18; S25;	S28; S34; S41		2.65	0	2	4	1080	4319	57.93	11433
AAAAAPAsEDEDEDEDEDEDDDDDEEDSEEEEAMETTPAK	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		2.6	0	0	3	1542	4623	60.57	11994
KEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		2.51	0	1	3	1432	4295	59.14	11712
MAPPPKEVEEDSEDEEMsEEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 16.1; S(18): 87.8; S(25): 98.1; S(26): 98.1	S18; S25; S26;	S34; S41; S42		2.38	0	2	3	1435	4303	61.24	12142
VVVSPTKK	NCL	4691	nucleolin	S4(Phospho)	S(4): 100.0; T(6): 0.0	S4;	S67		2.3	0	1	2	469.3	937.5	15.27	2327
KEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		2.24	0	1	3	1427	4279	60.6	12001
EVEEDsEDEEMsEEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	S6(Phospho) S12(Phospho)	S(6): 95.0; S(12): 95.0; S(19): 55.0; S(20): 55.0	S6; S12;	S28; S34		2.11	0	1	3	1228	3681	68.25	13802
MAPPPKEVEEDSEDEEMSEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	M17(Oxidation) S25(Phospho) S26(Phospho)	S(12): 50.9; S(18): 50.9; S(25): 99.1; S(26): 99.1	S25; S26;	S41; S42		2.08	0	2	3	1440	4319	58.44	11545
AAAAAPAsEDEDEDEDEDEDDDDDEEDSEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho) T38(Phospho)	S(8): 99.8; S(30): 98.8; T(37): 11.4; T(38): 90.0	S8; S30; T38;	S184; S206; T214		1.99	0	0	3	1563	4686	76.37	15405
KEDsDEEEDDDsEEDEEDDEDEDEDEIEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		1.89	0	1	3	1427	4279	65.13	13079
MAPPPKEVEEDsEDEEMsEEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	M17(Oxidation) S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42		1.88	0	2	3	1440	4319	57.44	11335
MAPPPKEVEEDsEDEEMsEEDEEDSSGEEVVIPQK	NCL	4691	nucleolin	M1(Oxidation) S12(Phospho) S18(Phospho)	S(12): 94.5; S(18): 94.5; S(25): 55.5; S(26): 55.5	S12; S18;	S28; S34		1.83	0	1	3	1398	4191	69.04	13961
MAPPPKEVEEDsEDEEMsEEDEEDSSGEEVVIPQKK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42		1.83	0	2	3	1435	4303	61.76	12251

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#
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42		1.69	0	1	3	1392	4175	73.81	14921
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153	19		0.001	1	4	1071	4279	64.29	12884
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQKK	NCL	4691	nucleolin	M1(Oxidation) S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 90.8; S(18): 90.8; S(25): 90.8; S(26): 27.6	S12; S18; S25; S28; S34; S41		12		0.001	2	4	1080	4319	57.93	11433
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQKK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42	11		0.001	2	3	1435	4303	61.76	12251
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42	11		0.001	1	4	1044	4175	73.85	14928
MAPPPKEVEEDsEDEEMsEDEEDSSG EEVIPQKK	NCL	4691	nucleolin	M17(Oxidation) S12(Phospho) S18(Phospho)	S(12): 99.9; S(18): 94.7; S(25): 52.7; S(26): 52.7	S12; S18;	S28; S34		3.62	0.001	2	4	1080	4319	58.6	11587
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.24	0.001	1	4	1071	4279	62.2	12349
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		3.04	0.001	1	3	1432	4295	62.26	12365
MAPPPKEVEEDsEDEEMSEDEEDSSGE EVVIPQKK	NCL	4691	nucleolin	M1(Oxidation) S12(Phospho) S25(Phospho) S26(Phospho)	S(12): 90.7; S(18): 27.9; S(25): 90.7; S(26): 90.7	S12; S25; S26;	S28; S41; S42		2.99	0.001	2	4	1080	4319	57.38	11321
MAPPPKEVEEDsEDEEMSEDEEDSSG EEVIPQKK	NCL	4691	nucleolin	S25(Phospho) S26(Phospho)	S(12): 55.8; S(18): 55.8; S(25): 94.2; S(26): 94.2	S25; S26;	S41; S42		2.55	0.001	2	4	1076	4303	61.16	12126
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	S12(Phospho) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 75.0; S(18): 75.0; S(25): 75.0; S(26): 75.0	S12; S18; S25; S26;	S28; S34; S41; S42		2.4	0.001	1	4	1044	4175	73.85	14928
KEDsDEEEDDDsEEDEEDDEDEDEDE IEPAAMK	NCL	4691	nucleolin	M34(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S145; S153		2.11	0.001	1	3	1432	4295	51.02	9920
NAKKEDsDEEEDDDsEEDEEDDEDEDE EDEIEPAAMK	NCL	4691	nucleolin	M37(Oxidation) S7(Phospho) S15(Phospho)	S(7): 100.0; S(15): 100.0	S7; S15;	S145; S153		2.02	0.001	2	4	1153	4609	43.46	8299
MAPPPKEVEEDsEDEEMsEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	M17(Oxidation) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 12.4; S(18): 88.2; S(25): 99.7; S(26): 99.7	S18; S25; S26;	S34; S41; S42		1.84	0.001	1	3	1398	4191	70.71	14304
MAPPPKEVEEDsEDEEMsEDEEDSSG EEVIPQKK	NCL	4691	nucleolin	M1(Oxidation) M17(Oxidation) S12(Phospho) S18(Phospho)	S(12): 99.0; S(18): 99.0; S(25): 51.0; S(26): 51.0	S12; S18;	S28; S34	13		0.002	2	4	1084	4335	54.02	10589
LELQPRGS PNAR	NCL	4691	nucleolin	S9(Phospho)	S(9): 100.0	S9;	S563	12		0.002	1	2	737.9	1475	32.55	5992
EVEEDsEDEEMsEDEEDSSGEEVIPQ KK	NCL	4691	nucleolin	S6(Phospho) S12(Phospho)	S(6): 95.0; S(12): 95.0; S(19): 55.0; S(20): 55.0	S6; S12;	S28; S34	11		0.002	1	3	1228	3681	68.25	13802

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#
MAPPPKEVEEDsEDEEMSEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	M17(Oxidation) S12(Phospho) S25(Phospho) S26(Phospho)	S(12): 90.5; S(18): 9.6; S(25): 99.9; S(26): 100.0	S12; S25; S26;	S28; S41; S42	11		0.002	1	4	1048	4191	70.69	14301
AAAAAPAsEDEDEDEDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	M35(Oxidation) S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 99.7; T(37): 0.3; T(38): 0.0	S8; S30;	S184; S206		3.29	0.003	0	5	925.3	4623	52.65	10279
AAAAAPAsEDEDEDEDEDDDDDEE DDsEEEEAMETTPAK	NCL	4691	nucleolin	S8(Phospho) S30(Phospho)	S(8): 100.0; S(30): 100.0; T(37): 0.0; T(38): 0.0	S8; S30;	S184; S206		2.49	0.004	0	4	1152	4606	64.39	12910
MAPPPKEVEEDSEDEEMsEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	M1(Oxidation) S18(Phospho) S25(Phospho) S26(Phospho)	S(12): 10.3; S(18): 90.8; S(25): 99.0; S(26): 99.9	S18; S25; S26;	S34; S41; S42		2.47	0.005	1	4	1048	4191	69.08	13967
LELQGPRGsPNAR	NCL	4691	nucleolin	S9(Phospho)	S(9): 100.0	S9;	S563		1.65	0.005	1	2	737.9	1475	32.55	5992
MAPPPKEVEEDsEDEEMSEDEEDSSGE EVVIPQK	NCL	4691	nucleolin	M1(Oxidation) S12(Phospho) S25(Phospho) S26(Phospho)	S(12): 91.2; S(18): 8.9; S(25): 99.9; S(26): 100.0	S12; S25; S26;	S28; S41; S42		2.68	0.007	1	4	1048	4191	70.69	14301
DTSSITSCGDGNVVKQEQLSPK	NCOA3	8202	nuclear receptor coactivator 3 isoform d	C8(Carbamidomethyl) S20(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(7): 0.0; S(20): 100.0	S20;	S738		4.71	0	1	3	810.7	2430	46.8	9036
DTSSITSCGDGNVVKQEQLSPK	NCOA3	8202	nuclear receptor coactivator 3 isoform d	C8(Carbamidomethyl) S20(Phospho)	T(2): 0.0; S(3): 0.0; S(4): 0.0; T(6): 0.0; S(7): 0.0; S(20): 100.0	S20;	S738	18		0.001	1	3	810.7	2430	46.8	9036
DRsPIRGsPR	NCOA5	57727	nuclear receptor coactivator 5	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S29; S34	27		0	2	2	650.8	1301	13.85	2028
DRsPIRGsPR	NCOA5	57727	nuclear receptor coactivator 5	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S29; S34		2.89	0	2	2	650.8	1301	13.85	2028
HEAPSSPISGQPCGDDQNAsPSK	NCOR1	9611	nuclear receptor corepressor 1 isoform 3	C13(Carbamidomethyl) S20(Phospho)	S(5): 50.0; S(6): 50.0; S(9): 0.0; S(20): 100.0; S(22): 0.0	S20;	S172	30		0	0	3	842.7	2526	32.41	5963
YETPSDAIEVisPASSPAPPQEK	NCOR1	9611	nuclear receptor corepressor 1 isoform 3	S12(Phospho) S16(Phospho)	Y(1): 0.0; T(3): 0.2; S(5): 0.2; S(12): 99.3; S(15): 0.4; S(16): 99.8	S12; S16;	S1874; S1878	19		0	0	3	858.4	2573	77.88	15711
HEAPSSPISGQPCGDDQNAsPSK	NCOR1	9611	nuclear receptor corepressor 1 isoform 3	C13(Carbamidomethyl) S20(Phospho)	S(5): 50.0; S(6): 50.0; S(9): 0.0; S(20): 100.0; S(22): 0.0	S20;	S172		4.89	0	0	3	842.7	2526	32.41	5963
YETPSDAIEVisPASSPAPPQEK	NCOR1	9611	nuclear receptor corepressor 1 isoform 3	S12(Phospho) S16(Phospho)	Y(1): 0.0; T(3): 0.2; S(5): 0.2; S(12): 99.3; S(15): 0.4; S(16): 99.8	S12; S16;	S1874; S1878		3.32	0	0	3	858.4	2573	77.88	15711
TDDTsGEDNDEKEAVASK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	T4(Phospho) S5(Phospho)	T(1): 0.0; T(4): 100.0; S(5): 100.0; S(17): 0.0	T4; S5;	T553; S554	42		0	1	2	1036	2071	25.78	4557
EKTDDTSGEDNDEKEAVASK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	T3(Phospho)	T(3): 99.9; T(6): 50.0; S(7): 50.0; S(19): 0.0	T3;	T550	33		0	2	3	776.6	2328	20.64	3473
sSGAPQDSDSSATCSADEVDEAEGGDK NR	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	C14(Carbamidomethyl) S1(Phospho)	S(1): 89.0; S(2): 3.5; S(8): 0.1; S(10): 0.1; S(11): 0.1; T(13): 3.5; S(15): 3.5	S1;	S908	25		0	1	3	1008	3022	30.36	5539
GECSGPA TVNNSSDTsIPsPHTAAK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	C3(Carbamidomethyl) T15(Phospho) S17(Phospho) S20(Phospho)	S(4): 2.6; T(8): 25.6; S(12): 8.9; S(13): 8.9; T(15): 77.1; S(17): 77.1; S(20): 99.1; T(23): 0.9	T15; S17; S20;	T748; S750; S753		4.38	0	0	3	995	2983	51.72	10065
sSGAPQDSDSSATCSADEVDEAEGGDK NR	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	C14(Carbamidomethyl) S1(Phospho)	S(1): 89.0; S(2): 3.5; S(8): 0.1; S(10): 0.1; S(11): 0.1; T(13): 3.5; S(15): 3.5	S1;	S908		4.09	0	1	3	1008	3022	30.36	5539
EKTDDTSGEDNDEKEAVASK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	T3(Phospho)	T(3): 99.9; T(6): 50.0; S(7): 50.0; S(19): 0.0	T3;	T550		4.06	0	2	3	776.6	2328	20.64	3473

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#
SLGYHGSSYSPEGVEPVsPVsSPSLTHDK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	S10(Phospho) S18(Phospho) S21(Phospho)	S(1): 0.0; Y(4): 0.0; S(7): 0.0; S(8): 0.4; Y(9): 5.8; S(10): 93.8; S(18): 100.0; S(21): 94.1; S(22): 5.9; S(24): 0.0; T(26): 0.0	S10; S18; S21;	S2046; S2054; S2057		3.84	0	0	3	1081	3240	66.06	13291
TDDTsGEDNDEKEAVASK	NCOR2	9612	nuclear receptor corepressor 2 isoform 1	T4(Phospho) S5(Phospho)	T(1): 0.0; T(4): 100.0; S(5): 100.0; S(17): 0.0	T4; S5;	T553; S554		3.32	0	1	2	1036	2071	25.78	4557
tDTAVQATGSGVPStPIAHR	NDE1	54820	nuclear distribution protein nudE homolog 1	T1(Phospho) T14(Phospho)	T(1): 93.0; T(3): 3.4; T(8): 0.1; S(10): 3.4; S(13): 0.1; T(14): 99.9	T1; T14;	T202; T215	33		0	0	3	690.3	2069	46.86	9048
tDTAVQATGSGVPStPIAHR	NDE1	54820	nuclear distribution protein nudE homolog 1	T1(Phospho) T14(Phospho)	T(1): 93.0; T(3): 3.4; T(8): 0.1; S(10): 3.4; S(13): 0.1; T(14): 99.9	T1; T14;	T202; T215		3.7	0	0	3	690.3	2069	46.86	9048
TAsGSSVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S3(Phospho)	T(1): 0.0; S(3): 99.9; S(5): 0.0; S(6): 0.0; T(8): 0.0; S(9): 0.0; T(13): 0.0	S3;	S249	92		0	0	2	709.8	1419	38.41	7233
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho)	T(1): 0.1; S(3): 3.3; S(5): 96.6; S(6): 96.6; T(8): 3.3; S(9): 0.1; T(13): 0.0	S5; S6;	S251; S252	66		0	0	2	749.8	1499	48.45	9378
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 100.0; S(6): 100.0; T(8): 0.1; S(9): 99.9; T(13): 0.0	S5; S6; S9;	S251; S252; S255	42		0	0	2	789.8	1579	58.5	11560
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 0.1; S(3): 0.1; S(5): 99.8; S(6): 100.0; T(8): 0.1; S(9): 99.9; T(13): 0.0	S5; S6; S9;	S251; S252; S255	39		0	0	2	789.8	1579	58.55	11573
SRtAsGSSVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	T3(Phospho) S5(Phospho)	S(1): 0.1; T(3): 99.9; S(5): 100.0; S(7): 0.0; S(8): 0.0; T(10): 0.0; S(11): 0.0; T(15): 0.0	T3; S5;	T247; S249	34		0	1	2	871.4	1742	36.47	6829
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 3.4; S(3): 0.1; S(5): 96.5; S(6): 100.0; T(8): 3.4; S(9): 96.6; T(13): 0.0	S5; S6; S9;	S251; S252; S255	30		0	0	2	789.8	1579	59.08	11702
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 3.4; S(3): 0.1; S(5): 96.5; S(6): 100.0; T(8): 3.4; S(9): 96.6; T(13): 0.0	S5; S6; S9;	S251; S252; S255		3.67	0	0	2	789.8	1579	59.08	11702
TAsGSSVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S3(Phospho)	T(1): 0.0; S(3): 99.9; S(5): 0.0; S(6): 0.0; T(8): 0.0; S(9): 0.0; T(13): 0.0	S3;	S249		3.57	0	0	2	709.8	1419	38.41	7233
SRtAsGSSVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	T3(Phospho) S5(Phospho)	S(1): 0.1; T(3): 99.9; S(5): 100.0; S(7): 0.0; S(8): 0.0; T(10): 0.0; S(11): 0.0; T(15): 0.0	T3; S5;	T247; S249		3.34	0	1	2	871.4	1742	36.47	6829
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho)	T(1): 0.1; S(3): 3.3; S(5): 96.6; S(6): 96.6; T(8): 3.3; S(9): 0.1; T(13): 0.0	S5; S6;	S251; S252		3.17	0	0	2	749.8	1499	48.45	9378
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 0.0; S(3): 0.0; S(5): 100.0; S(6): 100.0; T(8): 0.1; S(9): 99.9; T(13): 0.0	S5; S6; S9;	S251; S252; S255		2.87	0	0	2	789.8	1579	58.5	11560
TASGssVTSLDGTR	NDRG1	10397	protein NDRG1 isoform 3	S5(Phospho) S6(Phospho) S9(Phospho)	T(1): 0.1; S(3): 0.1; S(5): 99.8; S(6): 100.0; T(8): 0.1; S(9): 99.9; T(13): 0.0	S5; S6; S9;	S251; S252; S255		2.9	0.003	0	2	789.8	1579	58.55	11573
SRtLSQSSSEGLTSSGPPGHTMEVSC	NDRG2	57447	protein NDRG2 isoform f	C26(Carbamido methyl)T3(Phospho) S5(Phospho)	S(1): 5.8; T(3): 94.2; S(5): 100.0; S(7): 44.5; S(8): 44.5; S(10): 2.7; T(12): 2.7; S(14): 2.7; S(15): 2.7; T(21): 0.0; S(25): 0.0	T3; S5;	T288; S290	12		0.002	1	3	973.7	2919	65.05	13063

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#
SRTLsQSSSESGTLSSGPPGHTMEVSC	NDRG2	57447	protein NDRG2 isoform f	C26(Carbamido methyl)T3(Phospho)S5(Phospho)	S(1): 5.8; T(3): 94.2; S(5): 100.0; S(7): 44.5; S(8): 44.5; S(10): 2.7; T(12): 2.7; S(14): 2.7; S(15): 2.7; T(21): 0.0; S(25): 0.0	T3; S5;	T288; S290		2.3	0.007	1	3	973.7	2919	65.05	13063
SVTSNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S16(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 0.0; S(7): 0.0; T(10): 0.0; S(13): 0.0; S(16): 100.0	S16;	S349	62		0	0	3	831	2491	46.4	8952
sVTSNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S1(Phospho)	S(1): 97.2; T(3): 0.1; S(4): 0.1; S(7): 2.6; T(10): 0.1; S(13): 0.0; S(16): 0.0	S1;	S334	51		0	0	2	1246	2491	49.8	9662
SVTsNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S4(Phospho)	S(1): 2.9; T(3): 2.9; S(4): 91.3; S(7): 2.9; T(10): 0.1; S(13): 0.0; S(16): 0.0	S4;	S337	46		0	0	3	831	2491	49.76	9653
tHsTSsSLSGESPFsR	NDRG3	57446	protein NDRG3 isoform b	T1(Phospho)S3(Phospho)S6(Phospho)	T(1): 93.7; S(3): 93.7; T(4): 11.7; S(5): 6.6; S(6): 88.6; S(7): 5.7; S(10): 0.0; S(13): 0.0; S(16): 0.0	T1; S3; S6;	T317; S319; S322	24		0	0	2	982.4	1964	60.17	11913
SVTsNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S4(Phospho)	S(1): 2.9; T(3): 2.9; S(4): 91.3; S(7): 2.9; T(10): 0.1; S(13): 0.0; S(16): 0.0	S4;	S337	3.53		0	0	3	831	2491	49.76	9653
SVTSNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S16(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 0.0; S(7): 0.0; T(10): 0.0; S(13): 0.0; S(16): 100.0	S16;	S349	3.52		0	0	3	831	2491	46.4	8952
sVTSNQSDGTQESCEsPDVLDR	NDRG3	57446	protein NDRG3 isoform b	C14(Carbamido methyl)S1(Phospho)	S(1): 97.2; T(3): 0.1; S(4): 0.1; S(7): 2.6; T(10): 0.1; S(13): 0.0; S(16): 0.0	S1;	S334	2.71		0	0	2	1246	2491	49.8	9662
tHsTSsSLSGESPFsR	NDRG3	57446	protein NDRG3 isoform b	T1(Phospho)S3(Phospho)S6(Phospho)	T(1): 93.7; S(3): 93.7; T(4): 11.7; S(5): 6.6; S(6): 88.6; S(7): 5.7; S(10): 0.0; S(13): 0.0; S(16): 0.0	T1; S3; S6;	T317; S319; S322	2.32		0	0	2	982.4	1964	60.17	11913
KVTSPSSSSSSSSsDSESDEADVSEVTPR	NDUFV3	4731	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a precursor	S14(Phospho)	T(3): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.1; S(9): 0.3; S(10): 3.1; S(11): 35.0; S(12): 33.6; S(13): 33.6; S(14): 85.5; S(16): 4.4; S(18): 4.4; S(25): 0.0; T(28): 0.0	S14;	S160	52		0	1	3	1069	3206	46.89	9054
KVTSPSSSSSSSSsDSESDEADVSEVTPR	NDUFV3	4731	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a precursor	S13(Phospho)S14(Phospho)	T(3): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.6; S(12): 7.7; S(13): 84.9; S(14): 84.9; S(16): 11.0; S(18): 11.0; S(25): 0.0; T(28): 0.0	S13; S14;	S159; S160	49		0	1	3	1069	3206	47.44	9167
KVTSPSSSSSSSSsDSESDEADVSEVTPR	NDUFV3	4731	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a precursor	S13(Phospho)S14(Phospho)	T(3): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.6; S(12): 7.7; S(13): 84.9; S(14): 84.9; S(16): 11.0; S(18): 11.0; S(25): 0.0; T(28): 0.0	S13; S14;	S159; S160	4.25		0	1	3	1069	3206	47.44	9167
KVTSPSSSSSSSSsDSESDEADVSEVTPR	NDUFV3	4731	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial isoform a precursor	S14(Phospho)	T(3): 0.0; S(4): 0.0; S(6): 0.0; S(7): 0.0; S(8): 0.1; S(9): 0.3; S(10): 3.1; S(11): 35.0; S(12): 33.6; S(13): 33.6; S(14): 85.5; S(16): 4.4; S(18): 4.4; S(25): 0.0; T(28): 0.0	S14;	S160	3.83		0	1	3	1069	3206	46.89	9054

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#
DTLSNPQsPQPSPYNsPKPQHK	NEDD4L	23327	E3 ubiquitin-protein ligase NEDD4-like isoform 6	S8(Phospho) S12(Phospho) S16(Phospho)	T(2): 0.0; S(4): 0.0; S(8): 100.0; S(12): 99.8; Y(14): 0.4; S(16): 99.8	S8; S12; S16;	S338; S342; S346		6.4	0	0	3	896.4	2687	37.5	7044
sISADDDLQESSR	NELFE	7936	negative elongation factor E	S1(Phospho)	S(1): 98.3; S(3): 1.7; S(11): 0.0; S(12): 0.0	S1;	S113	55		0	0	2	751.8	1503	38.69	7292
sISADDDLQESSR	NELFE	7936	negative elongation factor E	S1(Phospho)	S(1): 98.3; S(3): 1.7; S(11): 0.0; S(12): 0.0	S1;	S113		3.74	0	0	2	751.8	1503	38.69	7292
TEMDKsPFNSPSPQDsPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S16(Phospho)	T(1): 0.1; S(6): 99.9; S(10): 0.0; S(12): 0.0; S(16): 100.0	S6; S16;	S333; S343	41		0	1	3	727.3	2180	45.74	8811
TEMDKsPFNSPSPQDsPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S12(Phospho)	T(1): 2.5; S(6): 97.5; S(10): 0.0; S(12): 100.0; S(16): 0.0	S6; S12;	S333; S339	40		0	1	3	727.3	2180	46.28	8925
TEMDKsPFNSPSPQDsPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S12(Phospho)	T(1): 0.1; S(6): 99.9; S(10): 0.0; S(12): 100.0; S(16): 0.0	S6; S12;	S333; S339	34		0	1	2	1090	2180	46.09	8886
SGSMEEDVDTSPPGDyYTSPSPSTSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	Y16(Phospho) S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 0.2; S(11): 0.2; Y(16): 95.5; Y(17): 4.0; T(18): 0.2; S(19): 0.0; S(21): 0.0; S(22): 95.8; T(24): 4.0; S(25): 0.2; S(26): 0.0; S(27): 0.0	Y16; S22;	Y299; S305	25		0	0	3	1015	3043	63.32	12640
SGSMEEDVDTSPPGDYYTSPSPSTSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 0.0; S(11): 0.0; Y(16): 0.0; Y(17): 0.0; T(18): 0.0; S(19): 0.0; S(21): 0.2; S(22): 95.8; T(24): 3.9; S(25): 0.2; S(26): 0.0; S(27): 0.0	S22;	S305	19		0	0	3	988.4	2963	56.12	11036
SGSMEEDVDTSPPGDYYTSPSPSTSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	M4(Oxidation) S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 1.6; S(11): 1.6; Y(16): 31.8; Y(17): 31.8; T(18): 31.8; S(19): 1.6; S(21): 0.0; S(22): 99.7; T(24): 0.3; S(25): 0.0; S(26): 0.0; S(27): 0.0	S22;	S305	17		0	0	3	1020	3059	57.02	11241
SGSMEEDVDTSPPGDyYTSPSPSTSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	Y16(Phospho) S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 0.2; S(11): 0.2; Y(16): 95.5; Y(17): 4.0; T(18): 0.2; S(19): 0.0; S(21): 0.0; S(22): 95.8; T(24): 4.0; S(25): 0.2; S(26): 0.0; S(27): 0.0	Y16; S22;	Y299; S305		4.37	0	0	3	1015	3043	63.32	12640
TEMDKsPFNSPSPQDsPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S12(Phospho)	T(1): 2.5; S(6): 97.5; S(10): 0.0; S(12): 100.0; S(16): 0.0	S6; S12;	S333; S339		4.23	0	1	3	727.3	2180	46.28	8925
TEMDKsPFNSPSPQDsPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S16(Phospho)	T(1): 0.1; S(6): 99.9; S(10): 0.0; S(12): 0.0; S(16): 100.0	S6; S16;	S333; S343		3.39	0	1	3	727.3	2180	45.74	8811
SGSMEEDVDTSPPGDYYTSPSPSTSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 0.0; S(11): 0.0; Y(16): 0.0; Y(17): 0.0; T(18): 0.0; S(19): 0.0; S(21): 0.2; S(22): 95.8; T(24): 3.9; S(25): 0.2; S(26): 0.0; S(27): 0.0	S22;	S305		3.26	0	0	3	988.4	2963	56.12	11036

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#
TEMDKsPFNSPsPQDSPR	NFIC	4782	nuclear factor 1 C-type isoform 5	S6(Phospho) S12(Phospho)	T(1): 0.1; S(6): 99.9; S(10): 0.0; S(12): 100.0; S(16): 0.0	S6; S12;	S333; S339		3.03	0	1	2	1090	2180	46.09	8886
SGSMEEDVDTSPGGDYTSPSPSSSR	NFIC	4782	nuclear factor 1 C-type isoform 5	M4(Oxidation) S22(Phospho)	S(1): 0.0; S(3): 0.0; T(10): 1.6; S(11): 1.6; Y(16): 31.8; Y(17): 31.8; T(18): 31.8; S(19): 1.6; S(21): 0.0; S(22): 99.7; T(24): 0.3; S(25): 0.0; S(26): 0.0; S(27): 0.0	S22;	S305		2.73	0.003	0	3	1020	3059	57.02	11241
RVQQEIDsDEsPVAR	NHS	4810	Nance-Horan syndrome protein isoform 4	S8(Phospho) S11(Phospho)	S(8): 100.0; S(11): 100.0	S8; S11;	S217; S220	29		0	1	2	944.9	1889	34.84	6484
RVQQEIDsDEsPVAR	NHS	4810	Nance-Horan syndrome protein isoform 4	S8(Phospho) S11(Phospho)	S(8): 100.0; S(11): 100.0	S8; S11;	S217; S220		2.47	0.002	1	2	944.9	1889	34.84	6484
SEPSDPAPESPSSCSPsK	NHSL1	57224	NHS-like protein 1 isoform 2	C14(Carbamidomethyl) S17(Phospho)	S(1): 0.0; S(4): 0.0; S(10): 0.0; S(12): 0.0; S(13): 0.0; S(15): 0.1; S(17): 99.9	S17;	S1470	28		0	0	2	963.4	1926	30.2	5505
SEPSDPAPESPSSCSPsK	NHSL1	57224	NHS-like protein 1 isoform 2	C14(Carbamidomethyl) S17(Phospho)	S(1): 0.0; S(4): 0.0; S(10): 0.0; S(12): 0.0; S(13): 0.0; S(15): 0.1; S(17): 99.9	S17;	S1470		3.06	0	0	2	963.4	1926	30.2	5505
SPGAPSAGEAEARPSPSTPLPDSSPsR	NHSL1	57224	NHS-like protein 1 isoform 2	S15(Phospho) S27(Phospho)	S(1): 0.3; S(6): 4.7; S(15): 80.7; S(17): 4.7; T(18): 4.7; T(19): 4.7; S(24): 0.3; S(25): 5.6; S(27): 94.1	S15; S27;	S1177; S1189		3.26	0.001	0	3	956.1	2866	51.05	9926
TVDSQGPtPVCtPTFLER	NIFK	84365	MKI67 FHA domain-interacting nucleolar phosphoprotein	C11(Carbamidomethyl) T8(Phospho) T12(Phospho)	T(1): 0.0; S(4): 0.3; T(8): 99.7; T(12): 94.9; T(14): 5.1	T8; T12;	T234; T238		2.31	0.005	0	2	1083	2165	79.71	16059
NNTAAETDEsDGEDRGGGTSGVR	NIPBL	25836	nipped-B-like protein isoform B	S12(Phospho)	T(3): 0.0; T(7): 0.0; S(12): 100.0; T(21): 0.0; S(22): 0.0	S12;	S2672	51		0	1	3	873.7	2619	22.66	3901
NNTAAETDEsDGEDRGGGTSGSLR	NIPBL	25836	nipped-B-like protein isoform A	S12(Phospho)	T(3): 0.0; T(7): 0.0; S(12): 100.0; T(21): 0.0; S(22): 0.0; S(24): 0.0	S12;	S2672	50		0	1	3	907.4	2720	26.43	4699
NNTAAETDEsDGEDRGGGTSGSLR	NIPBL	25836	nipped-B-like protein isoform A	T7(Phospho) S12(Phospho)	T(3): 0.3; T(7): 99.7; S(12): 100.0; T(21): 0.0; S(22): 0.0; S(24): 0.0	T7; S12;	T2667; S2672	48		0	1	3	934	2800	29.09	5273
NNTAAETDEsDGEDRGGGTSGVR	NIPBL	25836	nipped-B-like protein isoform B	T7(Phospho) S12(Phospho)	T(3): 0.5; T(7): 99.5; S(12): 99.5; T(21): 0.0; S(22): 0.5	T7; S12;	T2667; S2672	41		0	1	3	900.3	2699	24.38	4261
NNTAAETDEsDGEDRGGGTSGVR	NIPBL	25836	nipped-B-like protein isoform B	S12(Phospho)	T(3): 0.0; T(7): 0.0; S(12): 100.0; T(21): 0.0; S(22): 0.0	S12;	S2672		4.92	0	1	3	873.7	2619	22.66	3901
NNTAAETDEsDGEDRGGGTSGSLR	NIPBL	25836	nipped-B-like protein isoform A	S12(Phospho)	T(3): 0.0; T(7): 0.0; S(12): 100.0; T(21): 0.0; S(22): 0.0; S(24): 0.0	S12;	S2672		4.47	0	1	3	907.4	2720	26.43	4699
NNTAAETDEsDGEDRGGGTSGVR	NIPBL	25836	nipped-B-like protein isoform B	T7(Phospho) S12(Phospho)	T(3): 0.5; T(7): 99.5; S(12): 99.5; T(21): 0.0; S(22): 0.5	T7; S12;	T2667; S2672		3.59	0.001	1	3	900.3	2699	24.38	4261
NNTAAETDEsDGEDRGGGTSGSLR	NIPBL	25836	nipped-B-like protein isoform A	T7(Phospho) S12(Phospho)	T(3): 0.3; T(7): 99.7; S(12): 100.0; T(21): 0.0; S(22): 0.0; S(24): 0.0	T7; S12;	T2667; S2672		3.2	0.007	1	3	934	2800	29.09	5273
SPQPVCsPAGSEGTpK	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	C6(Carbamidomethyl) S7(Phospho) T14(Phospho)	S(1): 0.0; S(7): 100.0; S(11): 2.0; T(14): 98.0	S7; T14;	S280; T287 S280	46		0	0	2	879.8	1759	37.19	6979
SPQPVCsPAGSEGTpK	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	C6(Carbamidomethyl) S7(Phospho)	S(1): 0.1; S(7): 99.8; S(11): 0.1; T(14): 0.1	S7;	S280 S280	43		0	0	2	839.9	1679	29.67	5394

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#
NRsPSDSMDMedysPPPSLSEVAR	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	S3(Phospho) Y12(Phospho) S13(Phospho)	S(3): 99.7; S(5): 0.4; S(7): 10.2; Y(12): 94.9; S(13): 94.9; S(17): 0.0; S(19): 0.0	S3; Y12; S13;	S1150; Y1159; S1160 S1150	15		0	1	3	926	2776	77.82	15700
SPQPVCsPAGSEGTpk	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	C6(Carbamidomethyl)S7(Phospho) T14(Phospho)	S(1): 0.0; S(7): 100.0; S(11): 2.0; T(14): 98.0	S7; T14;	S280; T287 S280		3.66	0	0	2	879.8	1759	37.19	6979
SPQPVCsPAGSEGTpk	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	C6(Carbamidomethyl)S7(Phospho)	S(1): 0.1; S(7): 99.8; S(11): 0.1; T(14): 0.1	S7;	S280 S280		3.54	0	0	2	839.9	1679	29.67	5394
NRsPSDSMDMedysPPPSLSEVAR	NIPBL NIPBL	25836 25836	nipped-B-like protein isoform A nipped-B-like protein isoform B	S3(Phospho) Y12(Phospho) S13(Phospho)	S(3): 99.7; S(5): 0.4; S(7): 10.2; Y(12): 94.9; S(13): 94.9; S(17): 0.0; S(19): 0.0	S3; Y12; S13;	S1150; Y1159; S1160 S1150		3.11	0	1	3	926	2776	77.82	15700
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470	51		0	0	2	967.3	1934	62.14	12332
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470	44		0	0	2	967.4	1934	61.5	12195
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470	14		0	0	2	967.3	1934	62.65	12464
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470		2.99	0	0	2	967.3	1934	62.14	12332
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470		2.96	0	0	2	967.4	1934	61.5	12195
DSaIPVesDtDDEGAPR	NMD3	51068	60S ribosomal export protein NMD3	S8(Phospho) T10(Phospho)	S(2): 0.0; S(8): 100.0; T(10): 100.0	S8; T10;	S468; T470		1.47	0.001	0	2	967.3	1934	62.65	12464
NIHGsDSVESAEK	NME1	4830	nucleoside diphosphate kinase A isoform b	S6(Phospho)	S(6): 97.5; S(8): 2.5; S(11): 0.0	S6;	S120	11		0	0	2	783.3	1566	32.71	6027
NIHGsDSVESAEK	NME1	4830	nucleoside diphosphate kinase A isoform b	S6(Phospho)	S(6): 97.5; S(8): 2.5; S(11): 0.0	S6;	S120		1.58	0.005	0	2	783.3	1566	32.71	6027
GGLsPANDTGAK	NMT1	4836	glycylpeptide N-tetradecanoyltransferase 1	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S47	72		0	0	2	584.3	1168	25.38	4473
GGLsPANDTGAK	NMT1	4836	glycylpeptide N-tetradecanoyltransferase 1	S4(Phospho)	S(4): 100.0; T(9): 0.0	S4;	S47		3.23	0	0	2	584.3	1168	25.38	4473
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho) S12(Phospho)	S(5): 100.0; S(12): 99.6; S(14): 0.2; S(16): 0.2	S5; S12;	S49; S56	42		0	1	2	915.4	1830	13.3	1912
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho)	S(5): 100.0; S(12): 0.0; S(14): 0.0; S(16): 0.0	S5;	S49	34		0	1	3	583.9	1750	12.85	1817
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho) S12(Phospho)	S(5): 100.0; S(12): 100.0; S(14): 0.0; S(16): 0.0	S5; S12;	S49; S56	29		0	1	3	610.6	1830	13.17	1885
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho) S12(Phospho)	S(5): 100.0; S(12): 100.0; S(14): 0.0; S(16): 0.0	S5; S12;	S49; S56		5.21	0	1	3	610.6	1830	13.17	1885
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho)	S(5): 100.0; S(12): 0.0; S(14): 0.0; S(16): 0.0	S5;	S49		5.19	0	1	3	583.9	1750	12.85	1817
EAARsPDKPGGsPSASR	NOC2L	26155	nucleolar complex protein 2 homolog	S5(Phospho) S12(Phospho)	S(5): 100.0; S(12): 99.6; S(14): 0.2; S(16): 0.2	S5; S12;	S49; S56		3.63	0.001	1	2	915.4	1830	13.3	1912
FLEtDsEEEEQEEVNEK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822	28		0	0	2	1058	2115	59.73	11824
FLEtDsEEEEQEEVNEK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822	28		0	0	2	1058	2115	60.24	11927
TCDSITPSKsPVPVSDTQK	NOL8	55035	nucleolar protein 8 isoform b	C2(Carbamidomethyl)S11(Phospho)	T(1): 0.0; S(4): 0.0; T(6): 0.1; S(8): 50.0; S(10): 50.0; S(11): 99.9; S(16): 0.0; T(18): 0.0	S11;	S200	23		0	1	3	765.3	2294	42.35	8066
FLEtDsEEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822	20		0	1	2	1122	2243	46.36	8943
NDREYDsGdIDEIAMK	NOL8	55035	nucleolar protein 8 isoform b	S7(Phospho) T10(Phospho)	Y(5): 0.1; S(7): 99.9; T(10): 100.0	S7; T10;	S310; T313	19		0	1	3	711.3	2132	61.95	12290
NDREYDsGdIDEIAMK	NOL8	55035	nucleolar protein 8 isoform b	S7(Phospho) T10(Phospho)	Y(5): 0.1; S(7): 99.9; T(10): 100.0	S7; T10;	S310; T313	19		0	1	2	1066	2132	61.87	12273

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#
FLETdSEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822	15		0	1	3	748.3	2243	46.75	9025
NDREYDsGDTdEIIAMK	NOL8	55035	nucleolar protein 8 isoform b	S7(Phospho) T10(Phospho)	Y(5): 0.1; S(7): 99.9; T(10): 100.0	S7; T10;	S310; T313		3.35	0	1	3	711.3	2132	61.95	12290
FLETdSEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822		3.29	0	1	2	1122	2243	46.36	8943
FLETdSEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822		3.24	0	1	3	748.3	2243	46.12	8892
TCDSITPSKSsPVPVSDTQK	NOL8	55035	nucleolar protein 8 isoform b	C2(Carbamidomethyl)S11(Phospho)	T(1): 0.0; S(4): 0.0; T(6): 0.1; S(8): 50.0; S(10): 50.0; S(11): 99.9; S(16): 0.0; T(18): 0.0	S11;	S200		3.24	0	1	3	765.3	2294	42.35	8066
FLETdSEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822		3.18	0	1	3	748.3	2243	46.75	9025
FLETdSEEEQEEVNEK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822		2.73	0	0	2	1058	2115	60.24	11927
FLETdSEEEQEEVNEK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822		2.67	0	0	2	1058	2115	59.73	11824
NDREYDsGDTdEIIAMK	NOL8	55035	nucleolar protein 8 isoform b	S7(Phospho) T10(Phospho)	Y(5): 0.1; S(7): 99.9; T(10): 100.0	S7; T10;	S310; T313		2.49	0	1	2	1066	2132	61.87	12273
FLETdSEEEQEEVNEKK	NOL8	55035	nucleolar protein 8 isoform b	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T820; S822	13		0.002	1	3	748.3	2243	46.12	8892
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	40		0	0	2	603.3	1206	53.03	10371
GKGsPRPQAPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	S4(Phospho)	S(4): 100.0	S4;	S538	37		0	1	2	601.8	1203	12.41	1704
GKGsPRPQAPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	S4(Phospho)	S(4): 100.0	S4;	S538		3.58	0	1	2	601.8	1203	12.41	1704
IKLQTPNtFPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	T5(Phospho) T8(Phospho)	T(5): 100.0; T(8): 100.0	T5; T8;	T607; T610		2.73	0	1	2	723.8	1447	54.67	10733
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		1.99	0.001	0	2	603.3	1206	53.03	10371
IKLQTPNtFPK	NOLC1	9221	nucleolar and coiled-body phosphoprotein 1 isoform 2	T5(Phospho) T8(Phospho)	T(5): 100.0; T(8): 100.0	T5; T8;	T607; T610	14		0.002	1	2	723.8	1447	54.67	10733
FAEDEEKsENssEDGDITDK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) S11(Phospho) S12(Phospho)	S(8): 100.0; S(11): 100.0; S(12): 100.0; T(18): 0.0	S8; S11; S12;	S317; S320; S321	38		0	1	3	828.9	2485	46.62	8997
AQEAEAQsEDDDdTEEEQGEEKEK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) T15(Phospho)	S(8): 100.0; T(15): 100.0	S8; T15;	S280; T287	16		0	1	3	1010	3028	24.42	4268
KAQEAEAQsEDDDdTEEEQGEEKEK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S9(Phospho) T16(Phospho)	S(9): 100.0; T(16): 100.0	S9; T16;	S280; T287	13		0	2	3	1053	3156	20.39	3419
FAEDEEKsENssEDGDITDK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) S11(Phospho) S12(Phospho)	S(8): 100.0; S(11): 100.0; S(12): 100.0; T(18): 0.0	S8; S11; S12;	S317; S320; S321	12		0	1	2	1243	2485	46.47	8967
KAQEAEAQsEDDDdTEEEQGEEKEK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S9(Phospho) T16(Phospho)	S(9): 100.0; T(16): 100.0	S9; T16;	S280; T287		4.67	0	2	3	1053	3156	20.39	3419
FAEDEEKsENssEDGDITDK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) S11(Phospho) S12(Phospho)	S(8): 100.0; S(11): 100.0; S(12): 100.0; T(18): 0.0	S8; S11; S12;	S317; S320; S321		3.58	0	1	3	828.9	2485	46.62	8997
AQEAEAQsEDDDdTEEEQGEEKEK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) T15(Phospho)	S(8): 100.0; T(15): 100.0	S8; T15;	S280; T287		3.33	0	1	3	1010	3028	24.42	4268
FAEDEEKsENssEDGDITDK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) S11(Phospho) S12(Phospho)	S(8): 100.0; S(11): 99.9; S(12): 99.9; T(18): 0.2	S8; S11; S12;	S317; S320; S321		2.64	0	1	3	828.9	2485	45.95	8855
FAEDEEKsENssEDGDITDK	NOM1	64434	nucleolar MIF4G domain-containing protein 1	S8(Phospho) S11(Phospho) S12(Phospho)	S(8): 100.0; S(11): 100.0; S(12): 100.0; T(18): 0.0	S8; S11; S12;	S317; S320; S321		2.31	0	1	2	1243	2485	46.47	8967

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#
GPQPPTVsPIR	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S8(Phospho)	T(6): 1.1; S(8): 98.9	S8;	S782	46		0	0	2	614.8	1229	47.13	9104
TNKsPEAKPLPGK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S4(Phospho)	T(1): 0.0; S(4): 100.0	S4;	S67	45		0	1	3	482.9	1447	14.51	2166
GTDQTTPAVLsPSK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S11(Phospho)	T(2): 0.0; T(4): 0.0; T(6): 0.0; S(11): 98.3; S(13): 1.7	S11;	S728	27		0	0	2	741.3	1482	42.73	8145
AAAAGIQWsEEEEtEDEEEKEVTPESGPPK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S9(Phospho) T13(Phospho)	S(9): 100.0; T(13): 100.0; T(23): 0.0; S(26): 0.0	S9; T13;	S177; T181	16		0	1	3	1164	3490	65.92	13260
TNKsPEAKPLPGK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S4(Phospho)	T(1): 0.0; S(4): 100.0	S4;	S67		4.35	0	1	3	482.9	1447	14.51	2166
GTDQTTPAVLsPSK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S11(Phospho)	T(2): 0.0; T(4): 0.0; T(6): 0.0; S(11): 98.3; S(13): 1.7	S11;	S728		3.74	0	0	2	741.3	1482	42.73	8145
AAAAGIQWsEEEEtEDEEEKEVTPESGPPK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S9(Phospho) T13(Phospho)	S(9): 100.0; T(13): 100.0; T(23): 0.0; S(26): 0.0	S9; T13;	S177; T181		3.24	0	1	3	1164	3490	66.42	13374
AAAAGIQWsEEEEtEDEEEKEVTPESGPPK	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S9(Phospho) T13(Phospho)	S(9): 100.0; T(13): 100.0; T(23): 0.0; S(26): 0.0	S9; T13;	S177; T181		2.59	0	1	3	1164	3490	65.92	13260
GPQPPTVsPIR	NOP2	4839	probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase isoform 1	S8(Phospho)	T(6): 1.1; S(8): 98.9	S8;	S782		2.65	0.001	0	2	614.8	1229	47.13	9104
HIKEEPLsEEEEPCTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho) S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514	48		0	2	3	957.4	2870	44.48	8525
HIKEEPLsEEEEPCTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho) S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514	48		0	1	3	914.7	2742	50.44	9797
HIKEEPLsEEEEPCTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho) S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514	47		0	1	3	914.7	2742	49.91	9685
HIKEEPLsEEEEPCTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 0.0	S8;	S502	38		0	1	3	888.1	2662	47.85	9252
HIKEEPLsEEEEPCTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho) S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514	37		0	2	4	718.3	2870	44.4	8507
HIKEEPLsEEEEPCTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho) S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514	35		0	2	3	957.4	2870	43.96	8405
HIKEEPLsEEEEPCTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 0.0	S8;	S502	30		0	1	3	888.1	2662	47.31	9141
EEPLsEEEEPCTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C10(Carbamido methyl)S5(Phospho) S17(Phospho)	S(5): 100.0; T(11): 0.0; S(12): 0.0; T(13): 0.0; S(17): 100.0	S5; S17;	S502; S514	26		0	1	3	831.3	2492	54.43	10680

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#
EEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C10(Carbamido methyl)S5(Phospho)S17(Phospho)	S(5): 100.0; T(11): 0.0; S(12): 0.0; T(13): 0.0; S(17): 100.0	S5; S17;	S502; S514	13		0	1	2	1247	2492	54.37	10668
HIKEEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514		6.98	0	2	3	957.4	2870	44.48	8525
HIKEEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514		6.76	0	2	4	718.3	2870	44.4	8507
HIKEEPLSEEEPTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514		6.45	0	1	3	914.7	2742	49.91	9685
HIKEEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514		5.97	0	2	3	957.4	2870	43.96	8405
HIKEEPLSEEEPTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)S20(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 100.0	S8; S20;	S502; S514		5.72	0	1	3	914.7	2742	50.44	9797
EEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C10(Carbamido methyl)S5(Phospho)S17(Phospho)	S(5): 100.0; T(11): 0.0; S(12): 0.0; T(13): 0.0; S(17): 100.0	S5; S17;	S502; S514		5.5	0	1	3	831.3	2492	54.43	10680
HIKEEPLSEEEPTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 0.0	S8;	S502		5.46	0	1	3	888.1	2662	47.85	9252
HIKEEPLSEEEPTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S8(Phospho)	S(8): 100.0; T(14): 0.0; S(15): 0.0; T(16): 0.0; S(20): 0.0	S8;	S502		5	0	1	3	888.1	2662	47.31	9141
EEPLSEEEPTSTAIAsPEKK	NOP58	51602	nucleolar protein 58	C10(Carbamido methyl)S5(Phospho)S17(Phospho)	S(5): 100.0; T(11): 0.0; S(12): 0.0; T(13): 0.0; S(17): 100.0	S5; S17;	S502; S514		2.87	0	1	2	1247	2492	54.37	10668
HIKEEPLSEEEPTSTAIAsPEK	NOP58	51602	nucleolar protein 58	C13(Carbamido methyl)S20(Phospho)	S(8): 25.0; T(14): 25.0; S(15): 25.0; T(16): 25.0; S(20): 100.0	S20;	S514		1.9	0.003	1	2	1372	2742	50.17	9739
AAEDDSAsPPGAAsDAEPGDEERPGDQVDCVCGDK	NR2F6	2063	nuclear receptor subfamily 2 group F member 6	C30(Carbamido methyl)C33(Carbamido methyl)S8(Phospho)S14(Phospho)	S(6): 3.2; S(8): 98.4; S(14): 98.4	S8; S14;	S34; S40		2.44	0.001	0	3	1278	3832	66.89	13483
LyKAAGEDAR	NRAP	4892	nebulin-related-anchoring protein isoform 1	Y2(Phospho)	Y(2): 100.0	Y2;	Y1202	14		0	1	2	587.3	1174	17.12	2732
LyKAAGEDAR	NRAP	4892	nebulin-related-anchoring protein isoform 1	Y2(Phospho)	Y(2): 100.0	Y2;	Y1202		1.3	0.003	1	2	587.3	1174	17.12	2732
VEENPDADsDFDAKSSADDEIEETR	NSRP1	84081	nuclear speckle splicing regulatory protein 1 isoform 2	S9(Phospho)	S(9): 100.0; S(15): 50.0; S(16): 50.0; T(24): 0.0	S9;	S194	43		0	1	3	982	2944	56.04	11018
VEENPDADsDFDAKSSADDEIEETR	NSRP1	84081	nuclear speckle splicing regulatory protein 1 isoform 2	S9(Phospho)S15(Phospho)S16(Phospho)	S(9): 100.0; S(15): 100.0; S(16): 100.0; T(24): 0.0	S9; S15; S16;	S194; S200; S201	11		0	1	3	1009	3024	62.39	12395
VEENPDADsDFDAKSSADDEIEETR	NSRP1	84081	nuclear speckle splicing regulatory protein 1 isoform 2	S9(Phospho)	S(9): 100.0; S(15): 50.0; S(16): 50.0; T(24): 0.0	S9;	S194		3.35	0	1	3	982	2944	56.04	11018

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#
VEENPDADsDFDAKsADDEIEETR	NSRP1	84081	nuclear speckle splicing regulatory protein 1 isoform 2	S9(Phospho) S15(Phospho) S16(Phospho)	S(9): 100.0; S(15): 100.0; S(16): 100.0; T(24): 0.0	S9; S15; S16;	S194; S200; S201		2.63	0	1	3	1009	3024	62.39	12395
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716	48		0	0	4	794.3	3174	54.05	10596
NNsGEEFDCAFR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C9(Carbamidomethyl) S3(Phospho)	S(3): 100.0	S3;	S558	46		0	0	2	763.3	1526	58.02	11450
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716	42		0	0	3	1059	3174	53.77	10529
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl) S6(Phospho)	S(6): 100.0; S(14): 0.0; T(18): 0.0	S6;	S708	36		0	0	3	1032	3094	49.44	9585
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716	28		0	0	3	1059	3174	55.02	10803
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.1	S6; S14;	S708; S716	25		0	0	3	1059	3174	54.49	10695
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl) S14(Phospho)	S(6): 0.1; S(14): 99.8; T(18): 0.0	S14;	S716	16		0	0	3	1032	3094	48.51	9391
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716		5.78	0	0	4	794.3	3174	54.05	10596
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl) S6(Phospho)	S(6): 100.0; S(14): 0.0; T(18): 0.0	S6;	S708		5.33	0	0	3	1032	3094	49.44	9585
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716		5.21	0	0	3	1059	3174	53.77	10529
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.1	S6; S14;	S708; S716		3.58	0	0	3	1059	3174	54.49	10695
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl)S6(Phospho) S14(Phospho)	S(6): 100.0; S(14): 100.0; T(18): 0.0	S6; S14;	S708; S716		3.42	0	0	3	1059	3174	55.02	10803
AGEPNsPDAEEANsPDVTAGCDPAGVH PPR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C21(Carbamido methyl) S14(Phospho)	S(6): 0.1; S(14): 99.8; T(18): 0.0	S14;	S716		3.1	0	0	3	1032	3094	48.51	9391
NNsGEEFDCAFR	NSUN2	54888	tRNA (cytosine(34)-C(5))-methyltransferase isoform 2	C9(Carbamidomethyl) S3(Phospho)	S(3): 100.0	S3;	S558		2.36	0	0	2	763.3	1526	58.02	11450
ASAPERTsPAPK	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		3.65	0	1	2	734.8	1469	19.26	3182
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 98.0; S(9): 2.0	S6;	S58	83		0	1	2	902.8	1805	12.83	1813

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#
NSQEDsEDsEDKDKVK	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	62		0	1	2	942.8	1885	15.34	2343
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19	61		0	1	3	816	2446	52.64	10275
NSQEDsEDsEDKDKVK	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	56		0	1	2	942.8	1885	14.84	2235
VVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S10(Phospho)	Y(4): 0.1; S(5): 0.0; S(10): 99.9; Y(17): 0.0	S10;	S19	55		0	0	3	773.3	2318	59.93	11866
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19	52		0	1	3	816	2446	52.12	10162
VVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S10(Phospho)	Y(4): 0.1; S(5): 0.0; S(10): 99.9; Y(17): 0.0	S10;	S19	50		0	0	2	1159	2318	59.8	11838
NSQEDsESEDKDKVK	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	45		0	1	3	602.2	1805	12.87	1822
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	43		0	2	2	743.4	1486	28.77	5205
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19	41		0	1	3	816	2446	51.95	10118
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	36		0	2	3	495.9	1486	28.83	5219
KVVDYSQFQEsDDADEDYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.1; S(11): 99.9; Y(18): 0.0; S(22): 0.0; T(26): 0.0	S11;	S19	32		0	2	4	782.8	3128	48.68	9428
KVVDYSQFQEsDDADEDYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.1; S(11): 99.9; Y(18): 0.0; S(22): 0.0; T(26): 0.0	S11;	S19	31		0	2	3	1043	3128	48.68	9427
ATVtPsPVK	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	29		0	0	2	530.2	1059	35.73	6671
KDDSHsAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S10(Phospho)	S(4): 0.1; S(6): 99.9; S(10): 100.0	S6; S10;	S75; S79	28		0	2	3	754.3	2261	12.27	1663
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	27		0	1	2	582.8	1165	19.82	3300
VVDySQFQEsDDADEDYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	Y4(Phospho)	Y(4): 93.7; S(5): 3.1; S(10): 3.1; Y(17): 0.0; S(21): 0.0; T(25): 0.0	Y4;	Y13	26		0	1	3	1001	3000	53.41	10453
DSGSDEFLMEDDDsDYGSSK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S16(Phospho)	S(2): 0.0; S(4): 0.0; S(16): 96.2; Y(18): 3.5; S(20): 0.1; S(21): 0.1	S16;	S144	26		0	0	2	1255	2509	74.92	15149
NSQEDsEDsEDKDKVK	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	24		0	1	3	628.9	1885	15.09	2289
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.1; S(6): 2.9; S(11): 97.0; Y(18): 0.0	S11;	S19	21		0	1	2	1223	2446	52.08	10151

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#
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214	19		0	2	2	1067	2133	20.39	3420
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214	19		0	2	3	711.7	2133	20.79	3504
EKTPSPKEEDEEPsPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S15(Phospho)	T(3): 0.0; S(5): 0.0; S(15): 100.0	S15;	S214	19		0	2	3	754.7	2262	24.02	4186
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	19		0	1	2	622.8	1245	25.55	4509
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214	17		0	2	3	711.6	2133	20.07	3352
TPsPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S3(Phospho) S13(Phospho)	T(1): 2.9; S(3): 97.1; S(13): 100.0	S3; S13;	S204; S214	17		0	2	3	738.3	2213	24.07	4196
SGKNsQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S5(Phospho) S9(Phospho) S12(Phospho)	S(1): 0.2; S(5): 99.8; S(9): 100.0; S(12): 100.0	S5; S9; S12;	S54; S58; S61	17		0	2	3	746.3	2237	13.48	1952
EKtPsPKEEDEEPsPPEK	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	15		0	2	3	808	2422	29.5	5358
EKtPSPKEEDEEPsPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	T3(Phospho)	T(3): 99.8; S(5): 50.1; S(15): 50.1	T3;	T202	14		0	2	3	781.3	2342	25.49	4497
LKATVtPsPVK	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	14		0	1	2	650.8	1301	38.19	7187
EKTPSPKEEDEEPsPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S15(Phospho)	T(3): 0.0; S(5): 0.0; S(15): 100.0	S15;	S214	14		0	2	3	754.7	2262	23.49	4074
EKtPsPKEEDEEPsPPEK	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	14		0	2	3	808	2422	28.9	5233
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214	14		0	2	3	711.6	2133	19.47	3225
KDDSHsAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S10(Phospho)	S(4): 0.1; S(6): 99.9; S(10): 100.0	S6; S10;	S75; S79		9.23	0	2	3	754.3	2261	12.27	1663
KDDSHsAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S10(Phospho)	S(4): 4.2; S(6): 95.8; S(10): 100.0	S6; S10;	S75; S79		8.62	0	2	4	566	2261	12.31	1675
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		7.49	0	1	3	711.6	2133	12.33	1680
KDDsHsAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S4(Phospho) S6(Phospho) S10(Phospho)	S(4): 100.0; S(6): 100.0; S(10): 100.0	S4; S6; S10;	S73; S75; S79		6.83	0	2	3	780.9	2341	12.28	1667
SGKNsQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S5(Phospho) S9(Phospho) S12(Phospho)	S(1): 0.2; S(5): 99.8; S(9): 100.0; S(12): 100.0	S5; S9; S12;	S54; S58; S61		6.52	0	2	3	746.3	2237	13.48	1952
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214		6.24	0	2	3	711.7	2133	20.79	3504

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#
KVVDYSQFQEsDDADEYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.1; S(11): 99.9; Y(18): 0.0; S(22): 0.0; T(26): 0.0	S11;	S19		5.93	0	2	3	1043	3128	48.68	9427
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		5.74	0	1	3	602.2	1805	12.87	1822
TPsPKEEDEEPesPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S3(Phospho) S13(Phospho)	T(1): 2.9; S(3): 97.1; S(13): 100.0	S3; S13;	S204; S214		5.58	0	2	3	738.3	2213	24.07	4196
TPSPKEEDEEPesPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214		5.52	0	2	3	711.6	2133	19.47	3225
TPSPKEEDEEPesPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214		5.36	0	2	3	711.6	2133	20.07	3352
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		5.3	0	1	2	942.8	1885	14.84	2235
EKTSPSPKEEDEEPesPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S15(Phospho)	T(3): 0.0; S(5): 0.0; S(15): 100.0	S15;	S214		5.16	0	2	3	754.7	2262	24.02	4186
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		5.16	0	1	3	628.9	1885	15.09	2289
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19		5.11	0	1	3	816	2446	52.64	10275
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		5.05	0	1	2	942.8	1885	15.34	2343
KVVDYSQFQEsDDADEYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.1; S(11): 99.9; Y(18): 0.0; S(22): 0.0; T(26): 0.0	S11;	S19		5.05	0	2	4	782.8	3128	48.68	9428
NSQEDsEDSEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho)	S(2): 0.0; S(6): 98.0; S(9): 2.0	S6;	S58		4.9	0	1	2	902.8	1805	12.83	1813
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19		4.8	0	1	3	816	2446	52.12	10162
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		4.73	0	2	3	495.9	1486	28.83	5219
EKTSPSPKEEDEEPesPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S15(Phospho)	T(3): 0.0; S(5): 0.0; S(15): 100.0	S15;	S214		4.35	0	2	3	754.7	2262	23.49	4074
VVDySQFQEsDDADEYGRDSGPPTK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	Y4(Phospho)	Y(4): 93.7; S(5): 3.1; S(10): 3.1; Y(17): 0.0; S(21): 0.0; T(25): 0.0	Y4;	Y13		4.26	0	1	3	1001	3000	53.41	10453
TPSPKEEDEEPesPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214		4.21	0	1	3	669	2005	25.52	4504
EKTsPSPKEEDEEPesPPEK	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		4.19	0	2	3	808	2422	28.9	5233
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		4.18	0	2	2	743.4	1486	28.77	5205

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#
VVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S10(Phospho)	Y(4): 0.1; S(5): 0.0; S(10): 99.9; Y(17): 0.0	S10;	S19		4	0	0	3	773.3	2318	59.93	11866
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.0; S(6): 0.0; S(11): 100.0; Y(18): 0.0	S11;	S19		3.99	0	1	3	816	2446	51.95	10118
VVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S10(Phospho)	Y(4): 0.1; S(5): 0.0; S(10): 99.9; Y(17): 0.0	S10;	S19		3.66	0	0	2	1159	2318	59.8	11838
LKATVtPsPVK	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		3.48	0	1	2	650.8	1301	38.19	7187
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 4.5; S(6): 95.5; S(9): 100.0	S6; S9;	S58; S61		3.29	0	1	2	942.8	1885	15.15	2303
ATVtPsPVKGK	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		3.25	0	1	2	622.8	1245	25.02	4396
DSGSDEFLMEDDDsDYGSSK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S16(Phospho)	S(2): 0.0; S(4): 0.0; S(16): 96.2; Y(18): 3.5; S(20): 0.1; S(21): 0.1	S16;	S144		3.11	0	0	2	1255	2509	74.92	15149
ATVTPsPVKGK	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		3.08	0	1	2	582.8	1165	19.82	3300
ATVtPsPVKGK	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		3.03	0	1	2	622.8	1245	25.55	4509
TPSPKEEDEEPsPPEKK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214		2.58	0	2	2	1067	2133	20.39	3420
KVVDYSQFQEsDDADEDYGR	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S11(Phospho)	Y(5): 0.1; S(6): 2.9; S(11): 97.0; Y(18): 0.0	S11;	S19		2.54	0	1	2	1223	2446	52.08	10151
ATVtPsPVKGK	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	22		0.001	1	2	622.8	1245	25.02	4396
TPSPKEEDEEPsPPEK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S13(Phospho)	T(1): 0.0; S(3): 0.0; S(13): 100.0	S13;	S214	14		0.001	1	3	669	2005	25.52	4504
EKTpSPKEEDEEPsPPEK	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		3.92	0.001	2	3	808	2422	29.5	5358
ATVtPsPVK	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		2.19	0.001	0	2	530.2	1059	35.73	6671
KDDsHSAEDsEDEKEDHK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S4(Phospho) S10(Phospho)	S(4): 99.9; S(6): 0.1; S(10): 100.0	S4; S10;	S73; S79	14		0.002	2	2	1131	2261	12.32	1676
NSQEDsEDsEDKDVK	NUCKS1	64710	nuclear ubiquitous casein and cyclin-dependent kinase substrate 1	S6(Phospho) S9(Phospho)	S(2): 4.5; S(6): 95.5; S(9): 100.0	S6; S9;	S58; S61	11		0.003	1	2	942.8	1885	15.15	2303
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		2.55	0.003	1	2	1067	2133	12.34	1682
EKTpSPKEEDEEPsPPEK	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		1.96	0.006	2	2	1211	2422	29.29	5316

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)	S(7): 100.0; S(9): 0.0; S(11): 0.0; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7;	S212	87		0	0	2	861.8	1723	25.61	4522
GADNDGsGSESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) S9(Phospho)	S(7): 99.9; S(9): 97.8; S(11): 2.2; Y(13): 0.1; T(14): 0.0; T(15): 0.0	S7; S9;	S212; S214	80		0	0	2	901.8	1803	34.05	6302
NLSDEATNPISR	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S3(Phospho)	S(3): 100.0; S(4): 0.0; T(8): 0.0; S(12): 0.0	S3;	S112	59		0	0	2	742.3	1484	45.7	8803
NDsWGSFDLR	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S3(Phospho)	S(3): 100.0; S(6): 0.0	S3;	S652	46		0	0	2	638.8	1277	75.3	15215
GADNDGsGSESGYTtPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) T15(Phospho)	S(7): 99.7; S(9): 0.2; S(11): 0.2; Y(13): 0.0; T(14): 0.2; T(15): 99.8	S7; T15;	S212; T220	18		0	0	2	901.8	1803	29.27	5313
GADNDGsGSESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) S9(Phospho)	S(7): 99.9; S(9): 97.8; S(11): 2.2; Y(13): 0.1; T(14): 0.0; T(15): 0.0	S7; S9;	S212; S214		3.88	0	0	2	901.8	1803	34.05	6302
GADNDGsGSESGYTTPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho)	S(7): 100.0; S(9): 0.0; S(11): 0.0; Y(13): 0.0; T(14): 0.0; T(15): 0.0	S7;	S212		3.82	0	0	2	861.8	1723	25.61	4522
NLSDEATNPISR	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S3(Phospho)	S(3): 100.0; S(4): 0.0; T(8): 0.0; S(12): 0.0	S3;	S112		3.35	0	0	2	742.3	1484	45.7	8803
NDsWGSFDLR	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S3(Phospho)	S(3): 100.0; S(6): 0.0	S3;	S652		1.97	0	0	2	638.8	1277	75.3	15215
GADNDGsGSESGYTtPK	NUFIP2	57532	nuclear fragile X mental retardation-interacting protein 2	S7(Phospho) T15(Phospho)	S(7): 99.7; S(9): 0.2; S(11): 0.2; Y(13): 0.0; T(14): 0.2; T(15): 99.8	S7; T15;	S212; T220		2.52	0.006	0	2	901.8	1803	29.27	5313
TQPDGTSVPGEPA ^s PISQR	NUMA1	4926	nuclear mitotic apparatus protein 1 isoform 2	S14(Phospho)	T(1): 0.0; T(6): 0.0; S(7): 0.0; S(14): 99.9; S(17): 0.1	S14;	S1743	38		0	0	2	1002	2004	47.68	9216
RVsLEPHQGPGtPESK	NUMA1	4926	nuclear mitotic apparatus protein 1 isoform 2	S3(Phospho) T12(Phospho)	S(3): 100.0; T(12): 97.1; S(15): 2.9	S3; T12;	S1977; T1986	35		0	1	3	626.9	1879	29.68	5395
TQPDGTSVPGEPA ^s PISQR	NUMA1	4926	nuclear mitotic apparatus protein 1 isoform 2	S14(Phospho)	T(1): 0.0; T(6): 0.0; S(7): 0.0; S(14): 99.9; S(17): 0.1	S14;	S1743		2.78	0	0	2	1002	2004	47.68	9216
RVsLEPHQGPGtPESK	NUMA1	4926	nuclear mitotic apparatus protein 1 isoform 2	S3(Phospho) T12(Phospho)	S(3): 100.0; T(12): 97.1; S(15): 2.9	S3; T12;	S1977; T1986		4.32	0.003	1	3	626.9	1879	29.68	5395
NTSLPPLWsPEAER	NUP153	9972	nuclear pore complex protein Nup153 isoform 3	S9(Phospho)	T(2): 50.0; S(3): 50.0; S(9): 100.0	S9;	S209		2.21	0.001	0	2	878.9	1757	93.19	18615
NTSLPPLWsPEAER	NUP153	9972	nuclear pore complex protein Nup153 isoform 3	S9(Phospho)	T(2): 50.0; S(3): 50.0; S(9): 100.0	S9;	S209	15		0.002	0	2	878.9	1757	93.19	18615
VQMTsPSSTG ^s PMFK	NUP153	9972	nuclear pore complex protein Nup153 isoform 3	S5(Phospho) S11(Phospho)	T(4): 0.2; S(5): 99.6; S(7): 0.2; S(8): 0.0; T(9): 0.2; S(11): 99.8	S5; S11;	S516; S522	14		0.002	0	2	872.8	1745	68.59	13871
VQMTsPSSTG ^s PMFK	NUP153	9972	nuclear pore complex protein Nup153 isoform 3	S5(Phospho) S11(Phospho)	T(4): 0.2; S(5): 99.7; S(7): 0.2; S(8): 0.0; T(9): 0.2; S(11): 99.8	S5; S11;	S516; S522	11		0.005	0	2	872.8	1745	68.64	13881
VQMTsPSSTG ^s PMFK	NUP153	9972	nuclear pore complex protein Nup153 isoform 3	S5(Phospho) S11(Phospho)	T(4): 0.2; S(5): 99.6; S(7): 0.2; S(8): 0.0; T(9): 0.2; S(11): 99.8	S5; S11;	S516; S522		2.07	0.005	0	2	872.8	1745	68.59	13871
NQsPTEAEKPASSSLPSSPPQLLTR	NUP88	4927	nuclear pore complex protein Nup88	S3(Phospho)	S(3): 99.8; T(5): 0.2; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(17): 0.0; S(18): 0.0; T(25): 0.0	S3;	S35	15		0	0	3	933.8	2799	59.81	11842
NQsPTEAEKPASSSLPSSPPQLLTR	NUP88	4927	nuclear pore complex protein Nup88	S3(Phospho)	S(3): 99.8; T(5): 0.2; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(17): 0.0; S(18): 0.0; T(25): 0.0	S3;	S35		4.13	0	0	3	933.8	2799	59.81	11842

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#
NQSPTEAEKPASSSLPSPPPQLLTR	NUP88	4927	nuclear pore complex protein Nup88	S18(Phospho)	S(3): 0.4; T(5): 0.0; S(12): 0.4; S(13): 0.4; S(14): 0.4; S(17): 5.9; S(18): 92.4; T(25): 0.0	S18;	S50		2.93	0	0	3	933.8	2799	58.21	11491
DSENLASPEYPENGER	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	S7(Phospho)	S(2): 2.1; S(7): 97.9; S(9): 0.0; Y(11): 0.0	S7;	S606	56		0	0	2	987.4	1974	48.66	9424
ADTsQEICSPR	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	C8(Carbamidomethyl) S4(Phospho)	T(3): 2.3; S(4): 95.3; S(9): 2.3	S4;	S1006	54		0	0	2	672.3	1344	29.12	5280
YGLQSDSEEEEEHPsK	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	S15(Phospho)	Y(1): 0.0; S(6): 0.1; S(15): 99.9	S15;	S880	39		0	0	2	986.4	1972	31.89	5855
DSENLASPEYPENGER	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	S7(Phospho)	S(2): 2.1; S(7): 97.9; S(9): 0.0; Y(11): 0.0	S7;	S606		4.16	0	0	2	987.4	1974	48.66	9424
YGLQSDSEEEEEHPsK	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	S15(Phospho)	Y(1): 0.0; S(6): 0.1; S(15): 99.9	S15;	S880		3.2	0	0	2	986.4	1972	31.89	5855
ADTsQEICSPR	NUP98	4928	nuclear pore complex protein Nup98-Nup96 isoform 4	C8(Carbamidomethyl) S4(Phospho)	T(3): 2.3; S(4): 95.3; S(9): 2.3	S4;	S1006		2.66	0	0	2	672.3	1344	29.12	5280
VPsPPDEHQEAENAVSSG NR	NUSAP1	51203	nucleolar and spindle-associated protein 1 isoform 6	S3(Phospho)	S(3): 100.0; S(16): 0.0; S(17): 0.0	S3;	S112	29		0	0	3	734	2200	37.66	7077
VPsPPDEHQEAENAVSSG NR	NUSAP1	51203	nucleolar and spindle-associated protein 1 isoform 6	S3(Phospho)	S(3): 100.0; S(16): 0.0; S(17): 0.0	S3;	S112		3.59	0	0	3	734	2200	37.66	7077
KVEEEGsPGDPDHEASTQGR	OGFR	11054	opioid growth factor receptor	S7(Phospho)	S(7): 100.0; S(16): 0.0; T(17): 0.0	S7;	S315	51		0	1	3	735.6	2205	18.8	3083
KVEEEGsPGDPDHEASTQGR	OGFR	11054	opioid growth factor receptor	S7(Phospho)	S(7): 100.0; S(16): 0.0; T(17): 0.0	S7;	S315	25		0	1	2	1103	2205	18.94	3113
SQGDEAGGHGDRPEPLsPK	OGFR	11054	opioid growth factor receptor	S18(Phospho)	S(1): 0.0; S(18): 100.0	S18;	S378	14		0	0	3	715	2143	25.47	4493
KVEEEGsPGDPDHEASTQGR	OGFR	11054	opioid growth factor receptor	S7(Phospho)	S(7): 100.0; S(16): 0.0; T(17): 0.0	S7;	S315		6.78	0	1	3	735.6	2205	18.8	3083
SQGDEAGGHGDRPEPLsPK	OGFR	11054	opioid growth factor receptor	S18(Phospho)	S(1): 0.0; S(18): 100.0	S18;	S378		5.33	0	0	3	715	2143	25.47	4493
KVEEEGsPGDPDHEASTQGR	OGFR	11054	opioid growth factor receptor	S7(Phospho)	S(7): 100.0; S(16): 0.0; T(17): 0.0	S7;	S315		2.91	0	1	2	1103	2205	18.94	3113
SQGDEAGGHGDRPEPLsPK	OGFR	11054	opioid growth factor receptor	S18(Phospho)	S(1): 0.0; S(18): 100.0	S18;	S378		5.23	0.001	0	3	715	2143	24.92	4375
SQGDEAGGHGDRPEPLsPK	OGFR	11054	opioid growth factor receptor	S18(Phospho)	S(1): 0.0; S(18): 100.0	S18;	S378	19		0.002	0	3	715	2143	24.92	4375
QQAEAsQESENELK	OLR1	4973	oxidized low-density lipoprotein receptor 1 isoform 2	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S95	33		0	0	2	900.4	1800	27.45	4927
QQAEAsQESENELK	OLR1	4973	oxidized low-density lipoprotein receptor 1 isoform 2	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S95		3.24	0	0	2	900.4	1800	27.45	4927
MLAEsDEsGDEESVSQDKTELQNTLR	OSBP	5007	oxysterol-binding protein 1	M1(Oxidation) S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 99.8; S(13): 0.2; S(15): 0.0; T(17): 0.0; T(20): 0.0; T(25): 0.0	S5; S8;	S190; S193	39		0	1	3	1063	3188	62.47	12416
MLAEsDEsGDEESVSQTDK	OSBP	5007	oxysterol-binding protein 1	M1(Oxidation) S5(Phospho) S8(Phospho)	S(5): 99.7; S(8): 99.7; S(13): 0.5; S(15): 0.0; T(17): 0.0	S5; S8;	S190; S193	30		0	0	2	1117	2233	42.05	8003
MLAEsDEsGDEESVSQTDK	OSBP	5007	oxysterol-binding protein 1	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 99.7; S(13): 0.3; S(15): 0.0; T(17): 0.0	S5; S8;	S190; S193	28		0	0	2	1109	2217	51.43	10004
MLAEsDEsGDEESVSQDKTELQNTLR	OSBP	5007	oxysterol-binding protein 1	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 100.0; S(13): 0.0; S(15): 0.0; T(17): 0.0; T(20): 0.0; T(25): 0.0	S5; S8;	S190; S193	25		0	1	3	1058	3172	66.99	13508
MLAEsDEsGDEESVSQDKTELQNTLR	OSBP	5007	oxysterol-binding protein 1	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 100.0; S(13): 0.0; S(15): 0.0; T(17): 0.0; T(20): 0.0; T(25): 0.0	S5; S8;	S190; S193		4.68	0	1	3	1058	3172	66.99	13508

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#
MLAEsDEsGDEESVSQTDKTELQNTLR	OSBP	5007	oxysterol-binding protein 1	M1(Oxidation)S S(Phospho) S8(Phospho)	S(5): 100.0; S(8): 99.8; S(13): 0.2; S(15): 0.0; T(17): 0.0; T(20): 0.0; T(25): 0.0	S5; S8;	S190; S193		3.8	0	1	3	1063	3188	62.47	12416
MLAEsDEsGDEESVSQTDK	OSBP	5007	oxysterol-binding protein 1	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 99.7; S(13): 0.3; S(15): 0.0; T(17): 0.0	S5; S8;	S190; S193		2.94	0	0	2	1109	2217	51.43	10004
MLAEsDEsGDEESVSQTDK	OSBP	5007	oxysterol-binding protein 1	M1(Oxidation)S S(Phospho) S8(Phospho)	S(5): 99.7; S(8): 99.7; S(13): 0.5; S(15): 0.0; T(17): 0.0	S5; S8;	S190; S193		2.47	0	0	2	1117	2233	42.05	8003
SFSLAsSSNsPISQR	OSBPL11	114885	oxysterol-binding protein-related protein 11	S6(Phospho) S10(Phospho)	S(1): 3.1; S(3): 0.1; S(6): 96.7; S(7): 0.1; S(8): 0.1; S(10): 99.9; S(13): 0.0	S6; S10;	S177; S181		1.67	0.001	0	2	864.4	1728	67.97	13737
SFSLAsSSNsPISQR	OSBPL11	114885	oxysterol-binding protein-related protein 11	S6(Phospho) S10(Phospho)	S(1): 3.1; S(3): 0.1; S(6): 96.7; S(7): 0.1; S(8): 0.1; S(10): 99.9; S(13): 0.0	S6; S10;	S177; S181	12		0.002	0	2	864.4	1728	67.97	13737
GYSSPEPDIQDSSGSEAQSVKPstr	OSBPL8	114882	oxysterol-binding protein-related protein 8 isoform b	S23(Phospho) T24(Phospho)	Y(2): 0.1; S(3): 0.1; S(4): 0.0; S(12): 49.6; S(13): 49.6; S(15): 0.8; S(19): 2.6; S(23): 98.6; T(24): 98.6	S23; T24;	S776; T777		2.59	0	0	3	950.4	2849	54.52	10700
GYSSPEPDIQDssGsEAQSVKPSTR	OSBPL8	114882	oxysterol-binding protein-related protein 8 isoform b	S12(Phospho) S13(Phospho) S15(Phospho)	Y(2): 0.3; S(3): 0.3; S(4): 0.3; S(12): 99.6; S(13): 99.6; S(15): 99.9; S(19): 0.0; S(23): 0.0; T(24): 0.0	S12; S13; S15;	S765; S766; S768	14		0.001	0	3	950.4	2849	55.08	10815
GYSSPEPDIQDssGsEAQSVKPSTR	OSBPL8	114882	oxysterol-binding protein-related protein 8 isoform b	S12(Phospho) S13(Phospho) S15(Phospho)	Y(2): 0.3; S(3): 0.3; S(4): 0.3; S(12): 99.6; S(13): 99.6; S(15): 99.9; S(19): 0.0; S(23): 0.0; T(24): 0.0	S12; S13; S15;	S765; S766; S768		2.88	0.001	0	3	950.4	2849	55.08	10815
TLsNAEDYLDDEDsD	OSTF1	26578	osteoclast-stimulating factor 1	S3(Phospho) S14(Phospho)	T(1): 2.8; S(3): 97.2; Y(8): 0.0; S(14): 100.0	S3; S14;	S202; S213	21		0.003	0	2	931.3	1862	108.7	21827
TLsNAEDYLDDEDsD	OSTF1	26578	osteoclast-stimulating factor 1	S14(Phospho)	T(1): 50.0; S(3): 50.0; Y(8): 0.0; S(14): 100.0	S14;	S213	20		0.006	0	2	931.3	1862	108.2	21721
VQRPKEEsEDENEVSNI LR	OTUD4	54726	OTU domain-containing protein 4 isoform 3	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0; S(16): 0.0	S8; S9;	S958; S959	31		0	1	3	840	2518	54.56	10709
VQRPKEEsEDENEVSNI LR	OTUD4	54726	OTU domain-containing protein 4 isoform 3	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0; S(16): 0.0	S8; S9;	S958; S959		4.27	0	1	3	840	2518	54.56	10709
QAPGVGAVGGGSPEREVEVGAGYNsEDE YEA AAAAR	OTUD5	55593	OTU domain-containing protein 5 isoform b	S24(Phospho)	S(12): 51.8; Y(22): 51.8; S(24): 95.7; Y(28): 0.6	S24;	S177	16		0	1	3	1171	3510	61.24	12141
QAPGVGAVGGGSPEREVEVGAGYNsEDE YEA AAAAR	OTUD5	55593	OTU domain-containing protein 5 isoform b	S24(Phospho)	S(12): 51.8; Y(22): 51.8; S(24): 95.7; Y(28): 0.6	S24;	S177		3.75	0	1	3	1171	3510	61.24	12141
STPESGDSKESVGSSTsNEGGR	OTUD7B	56957	OTU domain-containing protein 7B	S12(Phospho)	S(1): 3.0; T(2): 3.0; S(5): 3.0; S(8): 3.0; S(12): 84.7; S(15): 3.0; S(16): 0.1; S(17): 0.0; T(18): 0.0; S(19): 0.0	S12;	S471	24		0	1	3	813	2437	18.63	3050
STPESGDSKESVGSSTsNEGGR	OTUD7B	56957	OTU domain-containing protein 7B	S12(Phospho)	S(1): 3.0; T(2): 3.0; S(5): 3.0; S(8): 3.0; S(12): 84.7; S(15): 3.0; S(16): 0.1; S(17): 0.0; T(18): 0.0; S(19): 0.0	S12;	S471		3.01	0	1	3	813	2437	18.63	3050
tEDGGWEWSDFDEESEEGK	OXR1	9943	serine/threonine-protein kinase OSR1	T1(Phospho)	T(1): 95.7; S(9): 4.3; S(17): 0.0	T1;	T331	17		0	0	2	1278	2556	79.61	16039
tEDGGWEWSDFDEESEEGK	OXR1	9943	serine/threonine-protein kinase OSR1	T1(Phospho)	T(1): 95.7; S(9): 4.3; S(17): 0.0	T1;	T331		2.65	0	0	2	1278	2556	79.61	16039
APPGAGPGPGSGAPGsQEEEEEPGLVE GDPGDGAIEDPELEAIK	PABPN1	8106	polyadenylate-binding protein 2	S17(Phospho)	S(12): 0.7; S(17): 99.3	S17;	S95		3.59	0	0	4	1097	4386	85.51	17136

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DGTAPPPQSPGSPGTGGQDEEWsDEESPRK	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.8; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 99.1; S(26): 0.1	S22;	S354	22		0	1	3	1040	3118	44.85	8616
DGTAPPPQSPGSPGTGGQDEEWsDEESPR	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 100.0; S(26): 0.0	S22;	S354	20		0	0	3	997.4	2990	54.1	10606
DGTAPPPQSPGSPGTGGQDEEWsDEESPR	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 100.0; S(26): 0.0	S22;	S354	12		0	0	3	997.4	2990	54.63	10723
DGTAPPPQSPGSPGTGGQDEEWsDEESPR	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 100.0; S(26): 0.0	S22;	S354		4.12	0	0	3	997.4	2990	54.1	10606
DGTAPPPQSPGSPGTGGQDEEWsDEESPR	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 100.0; S(26): 0.0	S22;	S354		2.75	0	0	3	997.4	2990	54.63	10723
DGTAPPPQSPGSPGTGGQDEEWsDEESPRK	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 99.9; S(26): 0.0	S22;	S354	12		0.002	1	3	1040	3118	44.34	8495
DGTAPPPQSPGSPGTGGQDEEWsDEESPRK	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.8; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 99.1; S(26): 0.1	S22;	S354		3.87	0.004	1	3	1040	3118	44.85	8616
DGTAPPPQSPGSPGTGGQDEEWsDEESPRK	PACIN3	29763	protein kinase C and casein kinase substrate in neurons protein 3	S22(Phospho)	T(3): 0.0; S(9): 0.0; S(12): 0.0; T(15): 0.0; S(22): 99.9; S(26): 0.0	S22;	S354		3.57	0.007	1	3	1040	3118	44.34	8495
DKRPLsGPDVGTGPAGLASGAK	PAK4	10298	serine/threonine-protein kinase PAK 4 isoform 1	S6(Phospho)	S(6): 100.0; T(12): 0.0; S(20): 0.0	S6;	S181	27		0	1	3	767.1	2299	48.76	9444
DKRPLsGPDVGTGPAGLASGAK	PAK4	10298	serine/threonine-protein kinase PAK 4 isoform 1	S6(Phospho)	S(6): 100.0; T(12): 0.0; S(20): 0.0	S6;	S181		4.21	0	1	3	767.1	2299	48.76	9444
TAPATGQLPGRSSPAGsPR	PAK6	56924	serine/threonine-protein kinase PAK 6 isoform 2	S17(Phospho)	T(1): 0.0; T(5): 1.6; S(12): 49.2; S(13): 49.2; S(17): 100.0	S17;	S351		2.98	0.007	1	2	984.4	1968	35.52	6629
IAsDEEIQGTK	PALLD	23022	palladin isoform 4	S3(Phospho)	S(3): 100.0; T(10): 0.0	S3;	S182	55		0	0	2	635.8	1271	33.01	6088
sRsRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 100.0	S1; S3; S6;	S405; S407; S410	37		0	2	3	705.6	2115	26.6	4738
SRSRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S6(Phospho)	S(1): 50.0; S(3): 50.0; S(6): 100.0	S6;	S410	26		0	2	3	678.9	2035	20.18	3375
sRsRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 100.0	S1; S3; S6;	S405; S407; S410	6.8	0	2	3	705.6	2115	26.6	4738	
SRSRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S6(Phospho)	S(1): 50.0; S(3): 50.0; S(6): 100.0	S6;	S410	4.92	0	2	3	678.9	2035	20.18	3375	
sRsRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 100.0	S1; S3; S6;	S405; S407; S410	4.47	0	2	3	705.6	2115	26.08	4624	
IAsDEEIQGTK	PALLD	23022	palladin isoform 4	S3(Phospho)	S(3): 100.0; T(10): 0.0	S3;	S182		3.73	0	0	2	635.8	1271	33.01	6088
sRsRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 100.0	S1; S3; S6;	S405; S407; S410	2.94	0	2	2	1058	2115	26.7	4758	
sRsRDsGDENEPIQER	PALLD	23022	palladin isoform 4	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(6): 100.0	S1; S3; S6;	S405; S407; S410	2.29	0.007	2	2	1058	2115	26.17	4643	
NSCQDsEADEETSPGFDEQEDGSSSQTANKPSR	PARG	8505	poly(ADP-ribose) glycohydrolase isoform c	C3(Carbamidomethyl) S6(Phospho)	S(2): 4.0; S(6): 96.0; T(12): 0.0; S(13): 0.0; S(23): 0.0; S(24): 0.0; S(25): 0.0; T(27): 0.0; S(32): 0.0	S6;	S208	40		0	0	3	1224	3669	36.08	6746

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#
NSCQDsEADEETSPGFDEQEDGSSSQTA NKPSR	PARG	8505	poly(ADP-ribose) glycohydrolase isoform c	C3(Carbamidomethyl) S6(Phospho)	S(2): 4.0; S(6): 96.0; T(12): 0.0; S(13): 0.0; S(23): 0.0; S(24): 0.0; S(25): 0.0; T(27): 0.0; S(32): 0.0	S6;	S208		4.98	0	0	3	1224	3669	36.08	6746
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	35		0	1	2	567.3	1134	13.86	2031
SPSVPKsPTPKsPPSR	PARVA	55742	alpha-parvin	S7(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 99.9; T(9): 0.1; S(12): 50.0; S(15): 50.0	S7;	S54	26		0	2	3	603.6	1809	26.45	4704
SPSVPKsPTPKsPPSR	PARVA	55742	alpha-parvin	S7(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 99.9; T(9): 0.1; S(12): 50.0; S(15): 50.0	S7;	S54		6.66	0	2	3	603.6	1809	26.45	4704
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		3.14	0	1	2	567.3	1134	13.86	2031
SPSVPKsPTPKsPPSR	PARVA	55742	alpha-parvin	S7(Phospho) S12(Phospho)	S(1): 0.0; S(3): 0.0; S(7): 100.0; T(9): 0.1; S(12): 96.8; S(15): 3.1	S7; S12;	S54; S59		2.18	0.004	2	2	904.9	1809	26.71	4762
RSTsPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S4(Phospho) S9(Phospho)	S(2): 2.3; T(3): 2.3; S(4): 95.4; S(9): 100.0	S4; S9;	S179; S184	23		0	1	2	763.9	1527	51.04	9923
RstSPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S2(Phospho) T3(Phospho)	S(2): 100.0; T(3): 99.9; S(4): 0.1; S(9): 0.0	S2; T3;	S177; T178	13		0	1	2	763.9	1527	51.57	10034
RstSPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S2(Phospho) T3(Phospho)	S(2): 100.0; T(3): 99.9; S(4): 0.1; S(9): 0.0	S2; T3;	S177; T178		2.48	0	1	2	763.9	1527	51.57	10034
RstSPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S2(Phospho) T3(Phospho) S9(Phospho)	S(2): 100.0; T(3): 99.9; S(4): 0.1; S(9): 100.0	S2; T3; S9;	S177; T178; S184	21		0.002	1	2	803.8	1607	63.16	12598
RstSPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S2(Phospho) T3(Phospho) S9(Phospho)	S(2): 100.0; T(3): 99.9; S(4): 0.1; S(9): 100.0	S2; T3; S9;	S177; T178; S184		2.87	0.003	1	2	803.8	1607	63.16	12598
RSTsPIIGsPPVR	PATL1	219988	protein PAT1 homolog 1	S4(Phospho) S9(Phospho)	S(2): 2.3; T(3): 2.3; S(4): 95.4; S(9): 100.0	S4; S9;	S179; S184		2.69	0.005	1	2	763.9	1527	51.04	9923
GADsGEEKEEGINR	PBDC1	51260	protein PBDC1 isoform 1	S4(Phospho)	S(4): 100.0	S4;	S197	36		0	1	2	785.8	1571	18.24	2969
GADsGEEKEEGINR	PBDC1	51260	protein PBDC1 isoform 1	S4(Phospho)	S(4): 100.0	S4;	S197		2.88	0	1	2	785.8	1571	18.24	2969
ATSPSSsVSGDFDDGHHSVSTPGPSR	PBRM1	55193	protein polybromo-1	S7(Phospho)	T(2): 25.1; S(3): 25.1; S(5): 25.0; S(6): 25.1; S(7): 99.7; S(9): 0.0; S(18): 0.0; S(20): 0.0; T(21): 0.0; S(25): 0.0	S7;	S14	22		0	0	3	911	2731	42.9	8180
ATSPSSsVSGDFDDGHHSVSTPGPSR	PBRM1	55193	protein polybromo-1	S7(Phospho)	T(2): 25.1; S(3): 25.1; S(5): 25.0; S(6): 25.1; S(7): 99.7; S(9): 0.0; S(18): 0.0; S(20): 0.0; T(21): 0.0; S(25): 0.0	S7;	S14		4.3	0	0	3	911	2731	42.9	8180
GEADDEDDDEDGQDNQGTVTEGSsPA YLK	PBRM1	55193	protein polybromo-1	S24(Phospho)	T(18): 0.0; T(20): 0.0; S(23): 4.4; S(24): 95.3; Y(27): 0.2	S24;	S178		3.41	0	0	3	1046	3137	54.27	10644
sNSPLPSQLQPQSPSASK	PCDH1	5097	protocadherin-1 isoform 4	S1(Phospho)	S(1): 90.4; S(3): 6.9; S(7): 0.1; S(14): 32.8; S(16): 34.9; S(18): 34.9	S1;	S592		1.75	0.006	0	2	1063	2126	78.86	15896
SRSPIIHsPK	PCF11	51585	pre-mRNA cleavage complex 2 protein Pcf11	S8(Phospho)	S(1): 50.0; S(3): 50.0; S(8): 100.0	S8;	S494	20		0.002	1	2	641.3	1282	20.84	3515
SRSPIIHsPK	PCF11	51585	pre-mRNA cleavage complex 2 protein Pcf11	S8(Phospho)	S(1): 50.0; S(3): 50.0; S(8): 100.0	S8;	S494		2.77	0.005	1	2	641.3	1282	20.84	3515
VTNDIsPeSSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 98.5; S(10): 1.5	S6; S9;	S65; S68	91		0	0	2	837.8	1675	47.64	9208
VTNDIsPeSSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 50.0; S(10): 50.0	S6;	S65	50		0	0	2	837.8	1675	46.29	8929

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#
VTNDISPEssPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho) S10(Phospho)	T(2): 0.1; S(6): 99.9; S(9): 100.0; S(10): 100.0	S6; S9; S10;	S65; S68; S69	36		0	0	2	877.8	1755	56.22	11057
KDEETEESEYDsEHENSEPVTNIR	PCM1	5108	pericentriolar material 1 protein isoform 3	T5(Phospho) S12(Phospho)	T(5): 100.0; S(8): 50.1; Y(10): 50.1; S(12): 99.8; S(17): 0.0; T(21): 0.0	T5; S12;	T530; S537	33		0	1	3	1036	3106	47.19	9115
sDISDQEEDEEsEGCPVSINLSK	PCM1	5108	pericentriolar material 1 protein isoform 3	C15(Carbamidomethyl)S1(Phospho) S12(Phospho)	S(1): 95.4; S(4): 4.6; S(12): 100.0; S(18): 0.0; S(22): 0.0	S1; S12;	S1711; S1722	27		0	0	3	909.7	2727	77.43	15628
VTNDISPEsPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 98.5; S(10): 1.5	S6; S9;	S65; S68		4.98	0	0	2	837.8	1675	47.64	9208
VTNDISPESSPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho)	T(2): 0.0; S(6): 100.0; S(9): 50.0; S(10): 50.0	S6;	S65		4.6	0	0	2	837.8	1675	46.29	8929
VTNDISPEssPGVGR	PCM1	5108	pericentriolar material 1 protein isoform 3	S6(Phospho) S9(Phospho) S10(Phospho)	T(2): 0.1; S(6): 99.9; S(9): 100.0; S(10): 100.0	S6; S9; S10;	S65; S68; S69		3.19	0	0	2	877.8	1755	56.22	11057
sDISDQEEDEEsEGCPVSINLSK	PCM1	5108	pericentriolar material 1 protein isoform 3	C15(Carbamidomethyl)S1(Phospho) S12(Phospho)	S(1): 95.4; S(4): 4.6; S(12): 100.0; S(18): 0.0; S(22): 0.0	S1; S12;	S1711; S1722		3.16	0	0	3	909.7	2727	77.43	15628
KDEETEESEYDsEHENSEPVTNIR	PCM1	5108	pericentriolar material 1 protein isoform 3	T5(Phospho) S12(Phospho)	T(5): 100.0; S(8): 50.1; Y(10): 50.1; S(12): 99.8; S(17): 0.0; T(21): 0.0	T5; S12;	T530; S537		3.08	0	1	3	1036	3106	47.19	9115
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347	28		0	0	2	723.8	1447	43.7	8349
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347	25		0	0	2	723.8	1447	44.16	8448
MLQAIsPKQsPSSsPTR	PCYT1A	5130	choline-phosphate cytidyltransferase A	S6(Phospho) S10(Phospho) S14(Phospho)	S(6): 99.8; S(10): 99.8; S(12): 0.4; S(13): 4.1; S(14): 91.9; T(16): 4.0	S6; S10; S14;	S315; S319; S323	23		0	1	2	1028	2055	54.5	10696
ERsPsPSFR	PCYT1A	5130	choline-phosphate cytidyltransferase A	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S329; S331	19		0	1	2	611.7	1222	26.16	4642
ERsPsPSFR	PCYT1A	5130	choline-phosphate cytidyltransferase A	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 0.0	S3; S5;	S329; S331		2.96	0	1	2	611.7	1222	26.16	4642
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347		2.46	0	0	2	723.8	1447	44.16	8448
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 96.9; S(11): 3.1	S6;	S347		2.32	0	0	2	723.8	1447	44.2	8457
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 100.0; S(11): 0.0	S6;	S347		2.21	0	0	2	723.8	1447	43.7	8349
TSPPCsPANLSR	PCYT1A	5130	choline-phosphate cytidyltransferase A	C5(Carbamidomethyl)S6(Phospho)	T(1): 50.0; S(2): 50.0; S(6): 96.9; S(11): 3.1	S6;	S347	26		0.002	0	2	723.8	1447	44.2	8457
MLQAIsPKQsPSSsPTR	PCYT1A	5130	choline-phosphate cytidyltransferase A	S6(Phospho) S10(Phospho) S14(Phospho)	S(6): 99.8; S(10): 99.8; S(12): 0.4; S(13): 4.1; S(14): 91.9; T(16): 4.0	S6; S10; S14;	S315; S319; S323		2.51	0.006	1	2	1028	2055	54.5	10696
SLDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	72		0	0	2	1096	2192	45.77	8817
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 2.7; S(4): 97.3; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	55		0	1	3	783.3	2348	35.98	6724
KSLLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 0.1; S(5): 99.9; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63	39		0	2	3	826	2476	28.77	5206

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#
SLDsDEsEDEDDYQQKR	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	37		0	1	2	1174	2348	35.49	6622
KSLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S8(Phospho)	S(2): 50.0; S(5): 50.0; S(8): 100.0; Y(15): 0.0	S8;	S63	36		0	1	2	1160	2320	35.08	6537
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	35		0	1	3	783.3	2348	35.43	6610
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho)	S(1): 0.1; S(4): 97.7; S(7): 2.3; Y(14): 0.0	S4;	S60	34		0	1	3	756.6	2268	32.08	5894
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63	33		0	1	2	1174	2348	36.02	6733
KSLSDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 0.0; S(5): 100.0; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63	32		0	2	2	1238	2476	28.87	5226
KSLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 2.5; S(5): 97.5; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63	32		0	1	2	1160	2320	34.53	6407
SLDSDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S7(Phospho)	S(1): 50.0; S(4): 50.0; S(7): 99.9; Y(14): 0.0	S7;	S63	31		0	0	2	1096	2192	45.23	8702
SLDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho)	S(1): 0.1; S(4): 97.4; S(7): 2.6; Y(14): 0.0	S4;	S60	31		0	0	2	1056	2112	38.09	7166
KsLSDsDEsEDEDDYQQK	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	27		0	1	3	773.9	2320	34.6	6423
KSLSDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 0.1; S(5): 99.9; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63		6.93	0	2	3	826	2476	28.77	5206
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 2.7; S(4): 97.3; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		6.44	0	1	3	783.3	2348	35.98	6724
KsLSDsDEsEDEDDYQQK	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		6.22	0	1	3	773.9	2320	34.6	6423
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		4.57	0	1	3	783.3	2348	35.43	6610
KSLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S8(Phospho)	S(2): 50.0; S(5): 50.0; S(8): 100.0; Y(15): 0.0	S8;	S63		4.34	0	1	2	1160	2320	35.08	6537
SLDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		4.31	0	0	2	1096	2192	45.77	8817
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho)	S(1): 0.1; S(4): 97.7; S(7): 2.3; Y(14): 0.0	S4;	S60		4.27	0	1	3	756.6	2268	32.08	5894
SLDSDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S7(Phospho)	S(1): 50.0; S(4): 50.0; S(7): 99.9; Y(14): 0.0	S7;	S63		4.22	0	0	2	1096	2192	45.23	8702
KSLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 2.5; S(5): 97.5; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63		4.12	0	1	2	1160	2320	34.53	6407
SLDsDEsEDEDDYQQKR	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		3.82	0	1	2	1174	2348	35.49	6622
SLDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho) S7(Phospho)	S(1): 0.1; S(4): 99.9; S(7): 100.0; Y(14): 0.0	S4; S7;	S60; S63		3.57	0	1	2	1174	2348	36.02	6733
SLDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S4(Phospho)	S(1): 0.1; S(4): 97.4; S(7): 2.6; Y(14): 0.0	S4;	S60		3.26	0	0	2	1056	2112	38.09	7166
KSLSDsDEsEDEDDYQQKR	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S5(Phospho) S8(Phospho)	S(2): 0.0; S(5): 100.0; S(8): 100.0; Y(15): 0.0	S5; S8;	S60; S63		3.17	0	2	2	1238	2476	28.87	5226
sLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S1(Phospho) S7(Phospho)	S(1): 96.6; S(4): 3.4; S(7): 100.0; Y(14): 0.0	S1; S7;	S57; S63		2.83	0	0	2	1096	2192	46.33	8936
sLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S1(Phospho) S7(Phospho)	S(1): 96.6; S(4): 3.4; S(7): 100.0; Y(14): 0.0	S1; S7;	S57; S63	11		0.001	0	2	1096	2192	46.33	8936
sLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S1(Phospho) S7(Phospho)	S(1): 96.8; S(4): 3.3; S(7): 99.9; Y(14): 0.0	S1; S7;	S57; S63		1.59	0.003	0	2	1096	2192	44.73	8586
sLSDsDEsEDEDDYQQK	PDAP1	11333	28 kDa heat- and acid-stable phosphoprotein	S1(Phospho) S7(Phospho)	S(1): 96.8; S(4): 3.3; S(7): 99.9; Y(14): 0.0	S1; S7;	S57; S63	12		0.004	0	2	1096	2192	44.73	8586
DSGRGDsVSDSGSDALR	PDCC4	27250	programmed cell death protein 4 isoform 3	S7(Phospho)	S(2): 0.0; S(7): 99.9; S(9): 0.1; S(11): 0.0; S(13): 0.0	S7;	S62	31		0	1	2	880.9	1761	27.51	4939
DSGRGDsVSDSGSDALR	PDCC4	27250	programmed cell death protein 4 isoform 3	S7(Phospho)	S(2): 0.0; S(7): 99.9; S(9): 0.1; S(11): 0.0; S(13): 0.0	S7;	S62		3.17	0	1	2	880.9	1761	27.51	4939

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#
KVMDsDEDDDY	PDCD5	9141	programmed cell death protein 5	S5(Phospho)	S(5): 100.0; Y(11): 0.0	S5;	S119	43		0	1	2	706.2	1411	36.54	6843
KVMDsDEDDDY	PDCD5	9141	programmed cell death protein 5	S5(Phospho)	S(5): 100.0; Y(11): 0.0	S5;	S119		4	0.005	1	2	706.2	1411	36.54	6843
SSYSPTSLSsPR	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	30		0	0	2	714.8	1429	48.49	9388
SSYSPTSLSsPR	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		2.84	0.004	0	2	714.8	1429	48.49	9388
AAVGQEsPGGLEAGNAK	PDS5A	23244	sister chromatid cohesion protein PDS5 homolog A isoform 1	S7(Phospho)	S(7): 100.0	S7;	S1305	54		0	0	2	818.4	1636	37.53	7051
AAVGQEsPGGLEAGNAK	PDS5A	23244	sister chromatid cohesion protein PDS5 homolog A isoform 1	S7(Phospho)	S(7): 100.0	S7;	S1305		3.72	0	0	2	818.4	1636	37.53	7051
AEsPESSAIESTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 100.0; S(6): 0.0; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358	59		0	0	2	978.9	1957	37.41	7026
METVSNASSSSNPSsPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S15(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): 1.6; S(15): 98.4	S15;	S1166	55		0	0	2	937.9	1875	27.54	4947
METVSNASSSSNPSsPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	M1(Oxidation) S15(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): 0.0; S(15): 100.0	S15;	S1166	47		0	0	2	945.9	1891	21.49	3650
AEsPESSAIESTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 99.9; S(6): 0.1; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358	47		0	0	2	978.9	1957	37.93	7134
METVSNASSSSNPSsPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	M1(Oxidation) S11(Phospho) S15(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.1; S(11): 99.9; S(14): 2.8; S(15): 97.2	S11; S15;	S1162; S1166	39		0	0	2	985.9	1971	26.2	4651
METVSNASSSSNPSsPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S11(Phospho) S15(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.1; S(11): 99.9; S(14): 0.1; S(15): 99.9	S11; S15;	S1162; S1166	36		0	0	2	977.9	1955	34.19	6333
GHTASESDEQQWPPEEK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T3(Phospho)	T(3): 98.3; S(5): 1.7; S(7): 0.0	T3;	T1255	33		0	0	3	646.6	1938	31.11	5694
LKEDILENEDEQNsPPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283	30		0	1	2	1039	2078	46.25	8921
GRPSKtPsPSQPK	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	28		0	1	2	763.8	1527	12.53	1738
LKEDILENEDEQNsPPKK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283	26		0	2	3	736	2206	37.01	6942
AEsPESSAIESTQStPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho) T15(Phospho)	S(3): 100.0; S(6): 0.0; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 2.6; T(15): 97.4	S3; T15;	S1358; T1370	23		0	0	2	1019	2037	42.93	8187
LKEDILENEDEQNsPPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283	20		0	1	3	693.3	2078	46.11	8890
GHTASESDEQQWPPEEK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T3(Phospho)	T(3): 100.0; S(5): 0.0; S(7): 0.0	T3;	T1255	18		0	1	3	698.6	2094	26.67	4753
GHTASESDEQQWPPEEK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T3(Phospho)	T(3): 98.3; S(5): 1.7; S(7): 0.0	T3;	T1255		4.84	0	0	3	646.6	1938	31.11	5694

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#
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S15(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): 1.6; S(15): 98.4	S15;	S1166		4.81	0	0	2	937.9	1875	27.54	4947
LKEDILENEDEQNPPKK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283		4.54	0	2	3	736	2206	37.01	6942
AEsPESSAIESTQStPQKGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho) T15(Phospho)	S(3): 100.0; S(6): 0.0; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 3.6; T(15): 96.4	S3; T15;	S1358; T1370		4.47	0	1	3	750.7	2250	33.61	6212
AEsPESSAIESTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 100.0; S(6): 0.0; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358		4.46	0	0	2	978.9	1957	37.41	7026
GHTASESDEQWPPEEK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	T3(Phospho)	T(3): 100.0; S(5): 0.0; S(7): 0.0	T3;	T1255		4.32	0	1	3	698.6	2094	26.67	4753
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	M1(Oxidation) S15(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): 0.0; S(15): 100.0	S15;	S1166		4.17	0	0	2	945.9	1891	21.49	3650
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S11(Phospho) S15(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.1; S(11): 99.9; S(14): 0.1; S(15): 99.9	S11; S15;	S1162; S1166		3.82	0	0	2	977.9	1955	34.19	6333
LKEDILENEDEQNPPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283		3.81	0	1	3	693.3	2078	46.11	8890
AEsPESSAIESTQSTPQK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho)	S(3): 99.9; S(6): 0.1; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 0.0; T(15): 0.0	S3;	S1358		3.61	0	0	2	978.9	1957	37.93	7134
LKEDILENEDEQNPPK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S14(Phospho)	S(14): 100.0	S14;	S1283		3.19	0	1	2	1039	2078	46.25	8921
GRPSKTPsPSQPK	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		4.67	0.001	1	2	763.8	1527	12.53	1738
METVSNASSSSNPSPGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	M1(Oxidation) S11(Phospho) S15(Phospho)	T(3): 0.0; S(5): 0.0; S(8): 0.0; S(9): 0.0; S(10): 0.1; S(11): 99.9; S(14): 2.8; S(15): 97.2	S11; S15;	S1162; S1166		3.38	0.001	0	2	985.9	1971	26.2	4651
AEsPESSAIESTQStPQKGR	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S3(Phospho) T15(Phospho)	S(3): 100.0; S(6): 0.0; S(7): 0.0; S(11): 0.0; T(12): 0.0; S(14): 3.6; T(15): 96.4	S3; T15;	S1358; T1370	19		0.003	1	3	750.7	2250	33.61	6212
GRPSKTPsPSQPK	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		5.9	0.003	1	3	509.6	1527	12.54	1740
GRPSKTPsPSQPK	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	22		0.004	1	3	509.6	1527	12.54	1740
LDSSEMDHSENEGYTMSPLPGK	PDS5B	23047	sister chromatid cohesion protein PDS5 homolog B	S18(Phospho)	S(3): 0.0; S(4): 0.0; S(9): 0.0; Y(14): 49.9; T(15): 49.9; S(17): 0.4; S(18): 99.8	S18;	S1191		2.03	0.005	0	3	910.3	2729	60.34	11946
GsDALSETSSVSHIEDLEK	PDXDC1	23042	pyridoxal-dependent decarboxylase domain-containing protein 1 isoform 5	S2(Phospho) S12(Phospho)	S(2): 99.5; S(6): 0.7; T(8): 35.4; S(9): 35.5; S(10): 35.5; S(12): 93.4	S2; S12;	S623; S633	11		0	0	2	1122	2244	75.2	15197
GsDALSETSSVSHIEDLEK	PDXDC1	23042	pyridoxal-dependent decarboxylase domain-containing protein 1 isoform 5	S2(Phospho) S12(Phospho)	S(2): 99.5; S(6): 0.7; T(8): 35.4; S(9): 35.5; S(10): 35.5; S(12): 93.4	S2; S12;	S623; S633		1.93	0.001	0	2	1122	2244	75.2	15197
LRsPRGsPDGSLQTGKPSAPK	PELP1	27043	proline-, glutamic acid- and leucine-rich protein 1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; T(14): 0.0; S(18): 0.0	S3; S7;	S330; S334	18		0	2	3	766	2296	26.8	4779

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#
LRsPRGsPDGSLQTGKPSAPK	PELP1	27043	proline-, glutamic acid- and leucine-rich protein 1 isoform 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 100.0; S(11): 0.0; T(14): 0.0; S(18): 0.0	S3; S7;	S330; S334		6.3	0	2	3	766	2296	26.8	4779
NATDLQNSSMSEELTK	PEX19	5824	peroxisomal biogenesis factor 19 isoform c	T3(Phospho)	T(3): 97.6; S(8): 0.1; S(9): 2.3; S(11): 0.0; T(16): 0.0	T3;	T141	42		0	0	2	988.9	1977	51.51	10020
NATDLQNSSMSEELTK	PEX19	5824	peroxisomal biogenesis factor 19 isoform c	T3(Phospho)	T(3): 97.6; S(8): 0.1; S(9): 2.3; S(11): 0.0; T(16): 0.0	T3;	T141		3.37	0	0	2	988.9	1977	51.51	10020
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57	85		0	0	2	1058	2116	53.36	10440
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57	71		0	0	2	1058	2116	52.85	10325
IVRGDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S13(Phospho)	S(10): 0.0; S(13): 100.0	S13;	S57	55		0	1	3	828.7	2484	47.73	9227
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57	34		0	0	3	706	2116	53	10362
IVRGDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S13(Phospho)	S(10): 0.0; S(13): 100.0	S13;	S57		4.21	0	1	3	828.7	2484	47.73	9227
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57		4.04	0	0	2	1058	2116	53.36	10440
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57		3.99	0	0	2	1058	2116	52.85	10325
GDQPAASGDsDDDEPPPLPR	PGRMC1	10857	membrane-associated progesterone receptor component 1 isoform 2	S10(Phospho)	S(7): 0.1; S(10): 99.9	S10;	S57		3.8	0	0	3	706	2116	53	10362
LLKPGEEPSEYtDEEDTKDHNKQD	PGRMC2	10424	membrane-associated progesterone receptor component 2	T12(Phospho)	S(9): 0.0; Y(11): 4.4; T(12): 95.4; T(17): 0.2	T12;	T235	26		0	2	4	725.1	2897	34.22	6338
LLKPGEEPSEYtDEEDTKDHNKQD	PGRMC2	10424	membrane-associated progesterone receptor component 2	T12(Phospho)	S(9): 0.0; Y(11): 4.4; T(12): 95.4; T(17): 0.2	T12;	T235		7.34	0	2	4	725.1	2897	34.22	6338
LLKPGEEPSEYtDEEDTKDHNKQD	PGRMC2	10424	membrane-associated progesterone receptor component 2	T12(Phospho)	S(9): 0.2; Y(11): 4.3; T(12): 95.4; T(17): 0.0	T12;	T235		4.34	0.001	2	4	725.1	2897	34.88	6495
LLKPGEEPSEYtDEEDTKDHNKQD	PGRMC2	10424	membrane-associated progesterone receptor component 2	S9(Phospho)	S(9): 95.3; Y(11): 50.0; T(12): 50.0; T(17): 4.7	S9;	S232		2.6	0.003	2	3	993.1	2977	36.59	6856
LLKPGEEPSEYtDEEDTKDHNKQD	PGRMC2	10424	membrane-associated progesterone receptor component 2	S9(Phospho)	S(9): 99.4; Y(11): 33.7; T(12): 33.5; T(17): 33.5	S9;	S232		3.49	0.005	2	4	745.1	2977	36.57	6851
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	47		0	0	2	761.8	1523	42.09	8012
RPLsSSHEASEGQAK	PHACTR4	65979	phosphatase and actin regulator 4 isoform 1	S4(Phospho)	S(4): 98.5; S(5): 1.4; S(6): 0.0; S(10): 0.0	S4;	S176	31		0	0	3	555.3	1664	14.05	2070
RPLsSSHEASEGQAK	PHACTR4	65979	phosphatase and actin regulator 4 isoform 1	S4(Phospho)	S(4): 98.5; S(5): 1.4; S(6): 0.0; S(10): 0.0	S4;	S176		5.1	0	0	3	555.3	1664	14.05	2070
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		2.5	0	0	2	761.8	1523	42.09	8012
ISQRDPsPESNK	PHC3	80012	polyhomeotic-like protein 3 isoform 2	S7(Phospho)	S(2): 0.0; S(7): 97.8; S(10): 2.2	S7;	S263	20		0	1	2	719.3	1438	13.19	1890
ISQRDPsPESNK	PHC3	80012	polyhomeotic-like protein 3 isoform 2	S7(Phospho)	S(2): 0.0; S(7): 97.8; S(10): 2.2	S7;	S263		3.1	0	1	2	719.3	1438	13.19	1890

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#
GTSDSSSGNVsEGESPPDsQEDSFQGR	PHF10	55274	PHD finger protein 10 isoform b	S11(Phospho)	T(2): 0.2; S(3): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(11): 95.2; S(15): 4.5; S(19): 0.0; S(23): 0.0	S11;	S325	55		0	0	3	941.7	2823	43.13	8228
NKGTSDSSSGNVSEGESPPDsQEDSFQGR	PHF10	55274	PHD finger protein 10 isoform b	S21(Phospho)	T(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.0; S(13): 4.0; S(17): 4.0; S(21): 91.9; S(25): 0.2	S21;	S333	33		0	1	3	1022	3065	35.4	6604
GTSDSSSGNVsEGESPPDsQEDSFQGR	PHF10	55274	PHD finger protein 10 isoform b	S11(Phospho)	T(2): 0.2; S(3): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(11): 95.2; S(15): 4.5; S(19): 0.0; S(23): 0.0	S11;	S325		4.79	0	0	3	941.7	2823	43.13	8228
NKGTSDSSSGNVSEGESPPDsQEDSFQGR	PHF10	55274	PHD finger protein 10 isoform b	S21(Phospho)	T(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.0; S(13): 4.0; S(17): 4.0; S(21): 91.9; S(25): 0.2	S21;	S333		3.95	0	1	3	1022	3065	35.4	6604
TTsPSsDTLLDR	PHF12	57649	PHD finger protein 12 isoform 2	S3(Phospho) S6(Phospho)	T(1): 0.0; T(2): 0.0; S(3): 97.1; S(5): 3.0; S(6): 99.8; T(8): 0.1	S3; S6;	S131; S134	33		0	0	2	784.3	1568	64.31	12888
TTsPSsDTLLDR	PHF12	57649	PHD finger protein 12 isoform 2	S3(Phospho) S6(Phospho)	T(1): 0.0; T(2): 0.0; S(3): 97.1; S(5): 3.0; S(6): 99.8; T(8): 0.1	S3; S6;	S131; S134		2.17	0	0	2	784.3	1568	64.31	12888
tAHNSEADLEESFNEHELEPsSPK	PHF6	84295	PHD finger protein 6 isoform 1	T1(Phospho) S22(Phospho)	T(1): 99.9; S(5): 0.1; S(12): 0.0; S(21): 7.2; S(22): 92.8	T1; S22;	T134; S155		2.62	0.003	0	3	953	2857	59.28	11740
TAHNSEADLEESFNEHELEPsSPK	PHF6	84295	PHD finger protein 6 isoform 1	S21(Phospho) S22(Phospho)	T(1): 0.0; S(5): 0.0; S(12): 0.7; S(21): 99.4; S(22): 99.9	S21; S22;	S154; S155		3.21	0.005	0	3	953	2857	55.54	10912
DAEYIYPSLeDDDDPALK	PHF8	23133	histone lysine demethylase PHF8 isoform 4	S11(Phospho)	Y(4): 0.0; Y(6): 50.1; S(8): 50.1; S(11): 99.9	S11;	S804		2.26	0.001	0	2	1158	2316	95.64	19116
VLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0	S3; S5;	S1281; S1283	53		0	1	2	1155	2310	49.59	9618
VLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0	S3; S5;	S1281; S1283	45		0	1	3	770.6	2310	49.59	9617
KVLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(18): 0.0; S(19): 0.0; T(20): 0.0	S4; S6;	S1281; S1283	43		0	2	3	813.3	2438	40.1	7594
KVLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(18): 0.0; S(19): 0.0; T(20): 0.0	S4; S6;	S1281; S1283	37		0	2	2	1220	2438	40.28	7633
KVLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(18): 0.0; S(19): 0.0; T(20): 0.0	S4; S6;	S1281; S1283		5.57	0	2	3	813.3	2438	40.1	7594
VLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0	S3; S5;	S1281; S1283		5.4	0	1	3	770.6	2310	49.59	9617
VLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0	S3; S5;	S1281; S1283		4.12	0	1	2	1155	2310	49.59	9618
KVLsDsEDEEKDADVPGTSTR	PHIP	55023	PH-interacting protein	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0; T(18): 0.0; S(19): 0.0; T(20): 0.0	S4; S6;	S1281; S1283		3.28	0	2	2	1220	2438	40.28	7633
TRsPSPTLGESLAPHK	PHLDB1	23187	pleckstrin homology-like domain family B member 1 isoform b	S3(Phospho) S5(Phospho)	T(1): 2.8; S(3): 97.2; S(5): 99.9; T(7): 0.1; S(11): 0.0	S3; S5;	S518; S520	22		0	1	3	613.3	1838	42.86	8173

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#
TRsPPTLGESLAPHK	PHLDB1	23187	pleckstrin homology-like domain family 8 member 1 isoform b	S3(Phospho) S5(Phospho)	T(1): 2.8; S(3): 97.2; S(5): 99.9; T(7): 0.1; S(11): 0.0	S3; S5;	S518; S520		3.38	0	1	3	613.3	1838	42.86	8173
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho)	S(5): 2.8; S(6): 97.2; S(17): 0.0; S(19): 0.0; S(21): 0.0	S6;	S1356	52		0	1	3	755	2263	30.76	5621
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 0.1; S(6): 99.9; S(17): 99.9; S(19): 0.1; S(21): 0.0	S6; S17;	S1356; S1367	36		0	1	3	781.7	2343	34.94	6508
GRECPTSsLER	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	C4(Carbamidomethyl)S5(Phospho) S9(Phospho)	S(5): 99.9; T(7): 0.1; S(8): 2.2; S(9): 97.8	S5; S9;	S1120; S1124	35		0	1	2	769.8	1539	25.02	4397
AEAPSSPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S17(Phospho)	S(5): 0.0; S(6): 0.0; S(17): 99.9; S(19): 0.1; S(21): 0.0	S17;	S1367	21		0	1	3	755	2263	31.33	5739
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S5(Phospho) S6(Phospho) S17(Phospho)	S(5): 100.0; S(6): 100.0; S(17): 94.8; S(19): 5.2; S(21): 0.0	S5; S6; S17;	S1355; S1356; S1367	20		0	1	3	808.3	2423	42.39	8074
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 0.4; S(6): 99.6; S(17): 99.6; S(19): 0.4; S(21): 0.0	S6; S17;	S1356; S1367	20		0	1	2	1172	2343	34.99	6519
GRECPTSSLER	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	C4(Carbamidomethyl) S5(Phospho)	S(5): 99.9; T(7): 0.0; S(8): 0.0; S(9): 0.0	S5;	S1120	19		0	1	2	729.8	1459	23.98	4177
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 0.1; S(6): 99.9; S(17): 99.9; S(19): 0.1; S(21): 0.0	S6; S17;	S1356; S1367		8.56	0	1	3	781.7	2343	34.94	6508
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S5(Phospho) S6(Phospho) S17(Phospho)	S(5): 100.0; S(6): 100.0; S(17): 94.8; S(19): 5.2; S(21): 0.0	S5; S6; S17;	S1355; S1356; S1367		5.82	0	1	3	808.3	2423	42.39	8074
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho)	S(5): 2.8; S(6): 97.2; S(17): 0.0; S(19): 0.0; S(21): 0.0	S6;	S1356		5.68	0	1	3	755	2263	30.76	5621
AEAPSSPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S17(Phospho)	S(5): 0.0; S(6): 0.0; S(17): 99.9; S(19): 0.1; S(21): 0.0	S17;	S1367		5.37	0	1	3	755	2263	31.33	5739
GRECPTSSLER	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	C4(Carbamidomethyl) S5(Phospho)	S(5): 99.9; T(7): 0.0; S(8): 0.0; S(9): 0.0	S5;	S1120		2.92	0	1	2	729.8	1459	23.98	4177
AEAPsPDVAPAGKEDSPSASGR	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	S6(Phospho) S17(Phospho)	S(5): 0.4; S(6): 99.6; S(17): 99.6; S(19): 0.4; S(21): 0.0	S6; S17;	S1356; S1367		2.58	0	1	2	1172	2343	34.99	6519
GRECPTSsLER	PHRF1	57661	PHD and RING finger domain-containing protein 1 isoform 4	C4(Carbamidomethyl)S5(Phospho) S9(Phospho)	S(5): 99.9; T(7): 0.1; S(8): 2.2; S(9): 97.8	S5; S9;	S1120; S1124		2.29	0.006	1	2	769.8	1539	25.02	4397
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51	50		0	0	3	616.6	1848	29.37	5333
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51	49		0	1	3	711.6	2133	24.67	4320
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51	42		0	1	3	711.6	2133	25.21	4438
SSSEsYTQSFQSR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S5(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 96.6; Y(6): 1.7; T(7): 1.7; S(9): 0.0; S(12): 0.0	S5;	S464	42		0	0	2	787.3	1574	40.51	7681
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S14(Phospho)	S(7): 0.0; S(10): 0.0; S(14): 100.0	S14;	S51	26		0	1	3	685	2053	22.7	3910
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51	19		0	1	3	711.6	2133	24.15	4212

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#
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51		8.23	0	1	3	711.6	2133	24.67	4320
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51		6.49	0	1	3	711.6	2133	25.21	4438
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51		6.38	0	0	3	616.6	1848	29.37	5333
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 0.0; S(10): 100.0; S(14): 100.0	S10; S14;	S47; S51		5.59	0	1	3	711.6	2133	24.15	4212
VAAAAGSGPsPPGsPGHDRER	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S14(Phospho)	S(7): 0.0; S(10): 0.0; S(14): 100.0	S14;	S51		4.35	0	1	3	685	2053	22.7	3910
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 4.1; S(10): 95.9; S(14): 100.0	S10; S14;	S47; S51		3.71	0	0	2	924.4	1848	29.33	5324
SSSEsYTSQFSR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S5(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 0.0; S(5): 96.6; Y(6): 1.7; T(7): 1.7; S(9): 0.0; S(12): 0.0	S5;	S464		3	0	0	2	787.3	1574	40.51	7681
VAAAAGSGPsPPGsPGHDR	PI4K2A	55361	phosphatidylinositol 4-kinase type 2-alpha	S10(Phospho) S14(Phospho)	S(7): 4.1; S(10): 95.9; S(14): 100.0	S10; S14;	S47; S51	10		0.002	0	2	924.4	1848	29.33	5324
sVENLPECGITHEQR	PI4KB	5298	phosphatidylinositol 4-kinase beta isoform 3	C8(Carbamidomethyl) S1(Phospho)	S(1): 100.0; T(11): 0.0	S1;	S96	60		0	0	2	924.9	1849	43.2	8243
sVENLPECGITHEQR	PI4KB	5298	phosphatidylinositol 4-kinase beta isoform 3	C8(Carbamidomethyl) S1(Phospho)	S(1): 100.0; T(11): 0.0	S1;	S96		3.33	0	0	2	924.9	1849	43.2	8243
TCPsLsPTSPLNNK	PIAS1	8554	E3 SUMO-protein ligase PIAS1	C2(Carbamidomethyl) S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 99.9; T(8): 0.1; S(9): 0.0	S4; S6;	S483; S485	11		0.003	0	2	838.3	1676	63.64	12722
TCPsLsPTSPLNNK	PIAS1	8554	E3 SUMO-protein ligase PIAS1	C2(Carbamidomethyl) S4(Phospho) S6(Phospho)	T(1): 0.0; S(4): 100.0; S(6): 99.9; T(8): 0.1; S(9): 0.0	S4; S6;	S483; S485		1.35	0.005	0	2	838.3	1676	63.64	12722
DPGLEPGDPsPGGSSPPR	PIEZO1	9780	piezo-type mechanosensitive ion channel component 1	S10(Phospho)	S(10): 98.1; S(14): 51.0; S(15): 51.0	S10;	S1391		1.84	0.003	0	2	939.9	1879	58.98	11679
GtAGKSPDLSSQK	PIKFYVE	200576	1-phosphatidylinositol 3-phosphate 5-kinase isoform 2	T2(Phospho)	T(2): 97.7; S(6): 2.3; S(10): 0.0; S(11): 0.0	T2;	T1750	15		0	1	2	678.3	1356	14.3	2123
GtAGKSPDLSSQK	PIKFYVE	200576	1-phosphatidylinositol 3-phosphate 5-kinase isoform 2	T2(Phospho)	T(2): 97.7; S(6): 2.3; S(10): 0.0; S(11): 0.0	T2;	T1750		3.09	0	1	2	678.3	1356	14.3	2123
SLDDsEEDDEDGSHSSR	PKD2	5311	polycystin-2	S5(Phospho)	S(1): 0.0; S(5): 100.0; S(13): 0.0; S(16): 0.0; S(17): 0.0	S5;	S812	66		0	0	3	692.2	2075	19.02	3132
SLDDsEEDDEDGSHSSR	PKD2	5311	polycystin-2	S5(Phospho)	S(1): 0.0; S(5): 100.0; S(13): 0.0; S(16): 0.0; S(17): 0.0	S5;	S812		4.53	0	0	3	692.2	2075	19.02	3132
LNLGTDSDsPQK	PKN1	5585	serine/threonine-protein kinase N1 isoform 2	S10(Phospho)	T(5): 0.0; S(7): 0.0; S(9): 0.0; S(10): 100.0	S10;	S562	38		0	0	2	721.3	1442	37.37	7017
LNLGTDSDsPQK	PKN1	5585	serine/threonine-protein kinase N1 isoform 2	S10(Phospho)	T(5): 0.0; S(7): 0.0; S(9): 0.0; S(10): 100.0	S10;	S562		3.71	0	0	2	721.3	1442	37.37	7017
RLEIsPDSSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho)	S(5): 100.0; S(8): 50.0; S(9): 50.0	S5;	S151	42		0	1	2	773.3	1546	42.47	8089
RLEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 98.2; S(9): 1.8	S5; S8;	S151; S154	41		0	1	2	773.3	1546	42.98	8196
GTAQYsSQKsVEER	PKP2	5318	plakophilin-2 isoform 2a	S7(Phospho) S10(Phospho)	T(2): 2.7; Y(5): 0.1; S(6): 0.1; S(7): 97.2; S(10): 100.0	S7; S10;	S132; S135	32		0	1	2	865.4	1730	20.58	3460
LEIsPDSSPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 98.1; S(7): 3.8; S(8): 98.1	S4; S8;	S151; S155	32		0	0	2	695.3	1390	52.47	10240
LEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 100.0; S(7): 2.1; S(8): 97.9	S4; S8;	S151; S155	31		0	0	2	695.3	1390	53.02	10368

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#
RLEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 98.0; S(9): 2.0	S5; S8;	S151; S154	25		0	1	2	773.3	1546	43.5	8306
RLEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 98.2; S(9): 1.8	S5; S8;	S151; S154		4.09	0	1	2	773.3	1546	42.98	8196
RLEIsPDSSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho)	S(5): 100.0; S(8): 50.0; S(9): 50.0	S5;	S151		3.92	0	1	2	773.3	1546	42.47	8089
LEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 100.0; S(7): 2.1; S(8): 97.9	S4; S8;	S151; S155		3.16	0	0	2	695.3	1390	53.02	10368
LEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S4(Phospho) S8(Phospho)	S(4): 98.1; S(7): 3.8; S(8): 98.1	S4; S8;	S151; S155		3.03	0	0	2	695.3	1390	52.47	10240
RLEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho) S8(Phospho)	S(5): 100.0; S(8): 98.0; S(9): 2.0	S5; S8;	S151; S154		3.05	0.001	1	2	773.3	1546	43.5	8306
GtAQYSSQKsVEER	PKP2	5318	plakophilin-2 isoform 2a	T2(Phospho) S10(Phospho)	T(2): 97.0; Y(5): 0.0; S(6): 0.0; S(7): 3.0; S(10): 100.0	T2; S10;	T127; S135	15		0.002	1	3	577.2	1730	20.55	3453
RLEIsPDsSPER	PKP2	5318	plakophilin-2 isoform 2a	S5(Phospho) S8(Phospho) S9(Phospho)	S(5): 100.0; S(8): 100.0; S(9): 100.0	S5; S8; S9;	S151; S154; S155	26		0.003	1	2	813.3	1626	51.96	10120
GtAQYSSQKsVEER	PKP2	5318	plakophilin-2 isoform 2a	T2(Phospho) S10(Phospho)	T(2): 97.0; Y(5): 0.0; S(6): 0.0; S(7): 3.0; S(10): 100.0	T2; S10;	T127; S135		3.1	0.003	1	3	577.2	1730	20.55	3453
GTAQYSSQKsVEER	PKP2	5318	plakophilin-2 isoform 2a	S7(Phospho) S10(Phospho)	T(2): 2.7; Y(5): 0.1; S(6): 0.1; S(7): 97.2; S(10): 100.0	S7; S10;	S132; S135		2.88	0.005	1	2	865.4	1730	20.58	3460
VAsPSQGQVGSSsPKR	PKP4	8502	plakophilin-4 isoform e	S3(Phospho) S13(Phospho)	S(3): 100.0; S(5): 0.0; S(11): 0.0; S(12): 0.1; S(13): 99.9	S3; S13;	S327; S337	21		0	1	2	866.4	1732	20.03	3343
VASPSQGQVGSSsPK	PKP4	8502	plakophilin-4 isoform e	S13(Phospho)	S(3): 0.0; S(5): 0.0; S(11): 0.0; S(12): 0.0; S(13): 100.0	S13;	S337	14		0	0	2	748.3	1496	21.8	3714
AAsPYSQRPAsPTAIR	PKP4	8502	plakophilin-4 isoform e	S3(Phospho) S11(Phospho)	S(3): 100.0; Y(5): 0.0; S(6): 0.0; S(11): 96.4; T(13): 3.5	S3; S11;	S273; S281	11		0	0	3	611.6	1833	41.71	7930
VASPSQGQVGSSsPK	PKP4	8502	plakophilin-4 isoform e	S13(Phospho)	S(3): 0.0; S(5): 0.0; S(11): 0.0; S(12): 0.0; S(13): 100.0	S13;	S337		2.58	0	0	2	748.3	1496	21.8	3714
VAsPSQGQVGSSsPKR	PKP4	8502	plakophilin-4 isoform e	S3(Phospho) S13(Phospho)	S(3): 100.0; S(5): 0.0; S(11): 0.0; S(12): 0.1; S(13): 99.9	S3; S13;	S327; S337		2.78	0.002	1	2	866.4	1732	20.03	3343
AAsPYSQRPAsPTAIR	PKP4	8502	plakophilin-4 isoform e	S3(Phospho) S11(Phospho)	S(3): 100.0; Y(5): 0.0; S(6): 0.0; S(11): 96.4; T(13): 3.5	S3; S11;	S273; S281		2.37	0.003	0	3	611.6	1833	41.71	7930
sPAPPKPR	PLA2G3	50487	group 3 secretory phospholipase A2 precursor	S1(Phospho)	S(1): 100.0	S1;	S296		1.34	0.008	0	2	465.2	929.5	15.1	2293
HIVSNDSSDsDDESHEPK	PLA2G4A	5321	cytosolic phospholipase A2 isoform 2	S10(Phospho)	S(4): 0.0; S(7): 0.0; S(8): 0.0; S(10): 100.0; S(14): 0.0	S10;	S377	27		0	0	3	693.3	2078	17.47	2806
HIVSNDSSDsDDESHEPK	PLA2G4A	5321	cytosolic phospholipase A2 isoform 2	S10(Phospho)	S(4): 0.0; S(7): 0.0; S(8): 0.0; S(10): 100.0; S(14): 0.0	S10;	S377		3.9	0.001	0	3	693.3	2078	17.47	2806
GYSPYSVSGSGstAGSR	PLEC	5339	plectin isoform 1d	S13(Phospho) T14(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 100.0; T(14): 97.7; S(17): 2.3	S13; T14;	S4453; T4454	65		0	0	2	971.9	1943	62.27	12367
GYSPYSVSGSGStAGsR	PLEC	5339	plectin isoform 1d	S17(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 1.7; T(14): 0.0; S(17): 98.3	S17;	S4457	59		0	0	2	931.9	1863	50.86	9887

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#
ssSVGSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S1(Phospho) S2(Phospho)	S(1): 93.1; S(2): 93.1; S(3): 6.6; S(6): 3.5; S(7): 3.4; S(8): 0.3; S(9): 0.0; Y(10): 0.0; S(13): 0.0; S(17): 0.0	S1; S2;	S4215; S4216	55		0	0	2	957.9	1915	67.38	13593
SSSVGssSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S7(Phospho)	S(1): 0.3; S(2): 0.3; S(3): 0.5; S(6): 95.5; S(7): 95.5; S(8): 6.9; S(9): 0.5; Y(10): 0.5; S(13): 0.0; S(17): 0.0	S6; S7;	S4220; S4221	51		0	0	2	957.9	1915	66.86	13477
GYySPYSVSGSGsTAGSR	PLEC	5339	plectin isoform 1d	Y3(Phospho) S13(Phospho)	Y(2): 2.6; Y(3): 94.9; S(4): 2.6; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 97.4; T(14): 2.6; S(17): 0.0	Y3; S13;	Y4443; S4453	46		0	0	2	971.9	1943	61.11	12114
GYYPYSVsGSGTAGSR	PLEC	5339	plectin isoform 1d	S9(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 2.3; S(7): 2.3; S(9): 93.0; S(11): 2.3; S(13): 0.1; T(14): 0.1; S(17): 0.1	S9;	S4449	38		0	0	2	931.9	1863	50.36	9780
AQLEPVA _s PAK	PLEC	5339	plectin isoform 1d	S8(Phospho)	S(8): 100.0	S8;	S1266	35		0	0	2	595.8	1191	37.19	6978
GYySPYSVsGSGTAGSR	PLEC	5339	plectin isoform 1d	S4(Phospho) S9(Phospho)	Y(2): 0.0; Y(3): 0.1; S(4): 99.8; Y(6): 0.1; S(7): 0.0; S(9): 100.0; S(11): 0.0; S(13): 0.0; T(14): 0.0; S(17): 0.0	S4; S9;	S4444; S4449	32		0	0	2	971.9	1943	59.98	11878
GYYPYSVSGSGTAGsRtGSR	PLEC	5339	plectin isoform 1d	S17(Phospho) T19(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.1; S(13): 0.1; T(14): 0.1; S(17): 99.5; T(19): 99.8; S(21): 0.3	S17; T19;	S4457; T4459	21		0	1	3	782	2344	48.85	9464
SSSVGSSSSYPisPAVSR	PLEC	5339	plectin isoform 1d	S13(Phospho)	S(1): 16.7; S(2): 16.7; S(3): 16.7; S(6): 16.7; S(7): 16.7; S(8): 16.7; S(9): 0.0; Y(10): 0.0; S(13): 100.0; S(17): 0.0	S13;	S4227	19		0	0	2	957.9	1915	61.67	12231
GYySPYSVsGSGsTAGSR	PLEC	5339	plectin isoform 1d	S4(Phospho) S9(Phospho) T14(Phospho)	Y(2): 0.0; Y(3): 3.9; S(4): 96.1; Y(6): 0.0; S(7): 0.0; S(9): 96.1; S(11): 3.9; S(13): 3.9; T(14): 95.9; S(17): 0.2	S4; S9; T14;	S4444; S4449; T4454	16		0	0	2	1012	2023	77.54	15645
GYYPYSVSGSGTAGsR	PLEC	5339	plectin isoform 1d	S17(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 1.7; T(14): 0.0; S(17): 98.3	S17;	S4457		4.21	0	0	2	931.9	1863	50.86	9887
GYySPYSVSGSGsTAGSR	PLEC	5339	plectin isoform 1d	Y3(Phospho) S13(Phospho)	Y(2): 2.6; Y(3): 94.9; S(4): 2.6; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 97.4; T(14): 2.6; S(17): 0.0	Y3; S13;	Y4443; S4453		3.75	0	0	2	971.9	1943	61.11	12114
SSSVGssSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S7(Phospho)	S(1): 0.3; S(2): 0.3; S(3): 0.5; S(6): 95.5; S(7): 95.5; S(8): 6.9; S(9): 0.5; Y(10): 0.5; S(13): 0.0; S(17): 0.0	S6; S7;	S4220; S4221		3.56	0	0	2	957.9	1915	66.86	13477

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#
ssSVGSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S1(Phospho) S2(Phospho)	S(1): 93.1; S(2): 93.1; S(3): 6.6; S(6): 3.5; S(7): 3.4; S(8): 0.3; S(9): 0.0; Y(10): 0.0; S(13): 0.0; S(17): 0.0	S1; S2;	S4215; S4216		3.48	0	0	2	957.9	1915	67.38	13593
AQLEPVA\$PAK	PLEC	5339	plectin isoform 1d	S8(Phospho)	S(8): 100.0	S8;	S1266		3.26	0	0	2	595.8	1191	37.19	6978
GYYPYSVsGSGSTAGSR	PLEC	5339	plectin isoform 1d	S9(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 2.3; S(7): 2.3; S(9): 93.0; S(11): 2.3; S(13): 0.1; T(14): 0.1; S(17): 0.1	S9;	S4449		3.15	0	0	2	931.9	1863	50.36	9780
GYYPYSVsGSGSTAGSR	PLEC	5339	plectin isoform 1d	S4(Phospho) S9(Phospho)	Y(2): 0.0; Y(3): 0.1; S(4): 99.8; Y(6): 0.1; S(7): 0.0; S(9): 100.0; S(11): 0.0; S(13): 0.0; T(14): 0.0; S(17): 0.0	S4; S9;	S4444; S4449		2.39	0	0	2	971.9	1943	59.98	11878
GYySPYSVSGSG\$TAGsR	PLEC	5339	plectin isoform 1d	Y3(Phospho) S13(Phospho) S17(Phospho)	Y(2): 3.2; Y(3): 93.5; S(4): 3.2; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.1; S(13): 96.5; T(14): 3.3; S(17): 100.0	Y3; S13; S17;	Y4443; S4453; S4457	21		0.001	0	2	1012	2023	79.21	15966
GYYPYSVsGSGSTAGsR	PLEC	5339	plectin isoform 1d	S9(Phospho) S17(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 99.9; S(11): 0.1; S(13): 0.1; T(14): 0.1; S(17): 99.8	S9; S17;	S4449; S4457	14		0.001	0	2	971.9	1943	61.75	12247
GYYPYSVSGSG\$TAGSR	PLEC	5339	plectin isoform 1d	S13(Phospho) T14(Phospho)	Y(2): 0.0; Y(3): 0.0; S(4): 0.0; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(13): 100.0; T(14): 97.7; S(17): 2.3	S13; T14;	S4453; T4454		4.9	0.001	0	2	971.9	1943	62.27	12367
SSSVGSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S13(Phospho)	S(1): 16.7; S(2): 16.7; S(3): 16.7; S(6): 16.7; S(7): 16.7; S(8): 16.7; S(9): 0.0; Y(10): 0.0; S(13): 100.0; S(17): 0.0	S13;	S4227		2.28	0.001	0	2	957.9	1915	61.67	12231
SSSVGsSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S13(Phospho)	S(1): 4.0; S(2): 4.0; S(3): 4.0; S(6): 79.9; S(7): 4.0; S(8): 4.0; S(9): 0.0; Y(10): 0.0; S(13): 99.7; S(17): 0.3	S6; S13;	S4220; S4227	11		0.003	0	2	957.9	1915	62.26	12364
SSSVGSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S13(Phospho)	S(1): 49.9; S(2): 49.9; S(3): 49.9; S(6): 25.1; S(7): 25.1; S(8): 0.1; S(9): 0.0; Y(10): 0.0; S(13): 100.0; S(17): 0.0	S13;	S4227		2.42	0.005	0	2	997.9	1995	78.65	15849
SSSVGsSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S6(Phospho) S13(Phospho)	S(1): 4.0; S(2): 4.0; S(3): 4.0; S(6): 79.9; S(7): 4.0; S(8): 4.0; S(9): 0.0; Y(10): 0.0; S(13): 99.7; S(17): 0.3	S6; S13;	S4220; S4227		2.3	0.005	0	2	957.9	1915	62.26	12364
GYySPYSVSGSG\$TAGsR	PLEC	5339	plectin isoform 1d	Y3(Phospho) S13(Phospho) S17(Phospho)	Y(2): 3.2; Y(3): 93.5; S(4): 3.2; Y(6): 0.0; S(7): 0.0; S(9): 0.0; S(11): 0.1; S(13): 96.5; T(14): 3.3; S(17): 100.0	Y3; S13; S17;	Y4443; S4453; S4457		2.98	0.007	0	2	1012	2023	79.21	15966
SSSVGSSSSYPISPAVSR	PLEC	5339	plectin isoform 1d	S9(Phospho)	S(1): 0.3; S(2): 0.3; S(3): 2.2; S(6): 34.2; S(7): 34.2; S(8): 34.2; S(9): 89.5; Y(10): 5.1; S(13): 0.0; S(17): 0.0	S9;	S4223		1.54	0.007	0	2	957.9	1915	67.9	13716

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#
GYYSPYSVsGSGStAGSR	PLEC	5339	plectin isoform 1d	S4(Phospho) S9(Phospho) T14(Phospho)	Y(2): 0.0; Y(3): 3.9; S(4): 96.1; Y(6): 0.0; S(7): 0.0; S(9): 96.1; S(11): 3.9; S(13): 3.9; T(14): 95.9; S(17): 0.2	S4; S9; T14;	S4444; S4449; T4454		1.93	0.008	0	2	1012	2023	77.54	15645
KVTsPLQsPTK	PLEKHA7	144100	pleckstrin homology domain-containing family A member 7	S4(Phospho) S8(Phospho)	T(3): 0.0; S(4): 100.0; S(8): 100.0; T(10): 0.0	S4; S8;	S903; S907	33		0	1	2	673.3	1346	31.18	5708
KVTsPLQsPTK	PLEKHA7	144100	pleckstrin homology domain-containing family A member 7	S4(Phospho) S8(Phospho)	T(3): 0.0; S(4): 100.0; S(8): 100.0; T(10): 0.0	S4; S8;	S903; S907		5.13	0	1	2	673.3	1346	31.18	5708
SSsVLsLEGSEK	PLEKHG3	26030	pleckstrin homology domain-containing family G member 3	S3(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(6): 100.0; S(10): 0.0	S3; S6;	S640; S643	34		0	0	2	691.8	1383	60.94	12078
SSsVLsLEGSEK	PLEKHG3	26030	pleckstrin homology domain-containing family G member 3	S3(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0; S(6): 100.0; S(10): 0.0	S3; S6;	S640; S643		2.06	0	0	2	691.8	1383	60.94	12078
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 10	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S470; S479	41		0	0	2	793.8	1587	53.85	10550
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 10	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S470; S479	39		0	0	2	793.8	1587	53.31	10431
VVVISSeDsDAENSSSR	PML	5371	protein PML isoform 10	S7(Phospho) S10(Phospho)	S(5): 0.1; S(6): 0.1; S(7): 99.7; S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0	S7; S10;	S514; S517	31		0	0	2	1014	2028	52.02	10136
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 10	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S470; S479		4.24	0	0	2	793.8	1587	53.85	10550
AVsPPHLDGPPsPR	PML	5371	protein PML isoform 10	S3(Phospho) S12(Phospho)	S(3): 100.0; S(12): 100.0	S3; S12;	S470; S479		3.92	0	0	2	793.8	1587	53.31	10431
VVVISSeDsDAENSSSR	PML	5371	protein PML isoform 10	S7(Phospho) S10(Phospho)	S(5): 0.1; S(6): 0.1; S(7): 99.7; S(10): 100.0; S(15): 0.0; S(16): 0.0; S(17): 0.0	S7; S10;	S514; S517		2.57	0	0	2	1014	2028	52.02	10136
LARssPEQRPSTSK	PML	5371	protein PML isoform 10	S4(Phospho) S5(Phospho)	S(4): 100.0; S(5): 100.0; S(12): 0.0; T(13): 0.0; S(14): 0.0	S4; S5;	S456; S457		3.25	0.005	1	3	600.9	1801	16.41	2571
TPESQPDtPPGTPLVSQDEKR	PNKP	11284	bifunctional polynucleotide phosphatase/kinase	T8(Phospho)	T(1): 0.0; S(4): 0.1; T(8): 97.3; T(12): 2.7; S(16): 0.0	T8;	T118	46		0	1	3	787	2359	43.84	8379
TPESQPDtPPGTPLVSQDEKR	PNKP	11284	bifunctional polynucleotide phosphatase/kinase	T8(Phospho)	T(1): 0.0; S(4): 0.1; T(8): 97.3; T(12): 2.7; S(16): 0.0	T8;	T118		5.18	0	1	3	787	2359	43.84	8379
EsRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S2;	S96	61		0	2	4	757.1	3025	37.15	6972
EsRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S2;	S96	48		0	2	4	757.1	3025	36.57	6850
ESRQEsDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S6(Phospho)	S(2): 3.8; S(6): 96.2; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S6;	S100	32		0	2	3	1009	3025	37.02	6944
QEsDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S3(Phospho)	S(3): 100.0; S(17): 0.0; S(18): 0.0; T(22): 0.0; S(23): 0.0	S3;	S100	29		0	1	3	885.1	2653	40.66	7711
ESRQEsDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S6(Phospho)	S(2): 4.4; S(6): 95.6; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S6;	S100	13		0	2	4	757.1	3025	37.8	7107
EsRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S2;	S96		7.97	0	2	4	757.1	3025	37.15	6972
EsRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S2(Phospho)	S(2): 100.0; S(6): 0.0; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S2;	S96		7.23	0	2	4	757.1	3025	36.57	6850

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#
QESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S3(Phospho)	S(3): 100.0; S(17): 0.0; S(18): 0.0; T(22): 0.0; S(23): 0.0	S3;	S100		5.77	0	1	3	885.1	2653	40.66	7711
ESRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S6(Phospho)	S(2): 3.8; S(6): 96.2; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S6;	S100		4.98	0	2	3	1009	3025	37.02	6944
ESRQESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S6(Phospho)	S(2): 4.4; S(6): 95.6; S(20): 0.0; S(21): 0.0; T(25): 0.0; S(26): 0.0	S6;	S100		4.57	0	2	4	757.1	3025	37.8	7107
QESDPEDDDVKKPALQSSVVATSK	PNN	5411	pinin	S3(Phospho)	S(3): 100.0; S(17): 0.0; S(18): 0.0; T(22): 0.0; S(23): 0.0	S3;	S100		3.67	0.005	1	4	664.1	2653	40.63	7705
TDESSPVLSPR	POC5	134359	centrosomal protein POC5 isoform 2	S5(Phospho) S9(Phospho)	T(1): 0.0; S(4): 0.0; S(5): 100.0; S(9): 100.0	S5; S9;	S80; S84	30		0	0	2	674.3	1348	44.82	8610
TDESSPVLSPR	POC5	134359	centrosomal protein POC5 isoform 2	S5(Phospho) S9(Phospho)	T(1): 0.0; S(4): 0.0; S(5): 100.0; S(9): 100.0	S5; S9;	S80; S84		2.88	0	0	2	674.3	1348	44.82	8610
SLDSEPSVPSAAKPPsPEK	POGZ	23126	pogo transposable element with ZNF domain isoform 3	S16(Phospho)	S(1): 0.0; S(4): 0.0; S(7): 0.0; S(10): 0.0; S(16): 100.0	S16;	S330	23		0	0	3	668.3	2003	45.3	8716
LSGEHSESstPRPR	POGZ	23126	pogo transposable element with ZNF domain isoform 3	S9(Phospho) T10(Phospho)	S(2): 0.0; S(6): 0.2; S(8): 2.7; S(9): 97.3; T(10): 99.8	S9; T10;	S1272; T1273		5.65	0	0	3	567.2	1700	14.24	2110
SLDSEPSVPSAAKPPsPEK	POGZ	23126	pogo transposable element with ZNF domain isoform 3	S16(Phospho)	S(1): 0.0; S(4): 0.0; S(7): 0.0; S(10): 0.0; S(16): 100.0	S16;	S330		4.6	0	0	3	668.3	2003	45.3	8716
SLDSEPSVPSAAKPPsPEK	POGZ	23126	pogo transposable element with ZNF domain isoform 3	S16(Phospho)	S(1): 0.0; S(4): 0.0; S(7): 0.0; S(10): 0.0; S(16): 100.0	S16;	S330		3.02	0	0	2	1002	2003	45.5	8761
LSGEHSESstPRPR	POGZ	23126	pogo transposable element with ZNF domain isoform 3	S9(Phospho) T10(Phospho)	S(2): 0.0; S(6): 0.2; S(8): 2.7; S(9): 97.3; T(10): 99.8	S9; T10;	S1272; T1273	24		0.001	0	3	567.2	1700	14.24	2110
AIStPEtPLTK	POLA2	23649	DNA polymerase alpha subunit B	T4(Phospho) T7(Phospho)	S(3): 0.0; T(4): 100.0; T(7): 98.0; T(10): 2.0	T4; T7;	T127; T130	21		0	0	2	659.3	1318	48.56	9402
AIStPEtPLTK	POLA2	23649	DNA polymerase alpha subunit B	T4(Phospho) T7(Phospho)	S(3): 0.0; T(4): 100.0; T(7): 98.0; T(10): 2.0	T4; T7;	T127; T130		2.93	0	0	2	659.3	1318	48.56	9402
YSPTsPTYsPtTPK	POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	S5(Phospho) T11(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): 2.1; T(11): 95.8; T(12): 2.1	S5; T11;	S1878; T1884	21		0	0	2	843.8	1687	54.27	10643
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	16		0	0	2	836.8	1673	52.38	10221
YSPTsPTYsPtTPK	POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	S5(Phospho) T11(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): 2.1; T(11): 95.8; T(12): 2.1	S5; T11;	S1878; T1884		2.9	0	0	2	843.8	1687	54.27	10643
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		2.55	0	0	2	836.8	1673	52.38	10221
YSPTsPTYsPTSPVYTPTsPK	POLR2A	5430	DNA-directed RNA polymerase II subunit RPB1	S19(Phospho)	Y(1): 0.2; S(2): 0.2; T(4): 42.6; S(5): 42.6; T(7): 2.9; Y(8): 2.9; S(9): 2.9; T(11): 2.9; S(12): 2.9; Y(15): 0.0; T(16): 0.0; T(18): 6.4; S(19): 93.5	S19;	S1906		2.31	0.006	0	2	1210	2418	74.77	15122
EREAAEAGDssQDEAEDDVK	POLR3E	55718	DNA-directed RNA polymerase III subunit RPC5 isoform 5	S11(Phospho) S12(Phospho)	S(11): 100.0; S(12): 100.0	S11; S12;	S161; S162	60		0	1	3	809	2425	27.51	4940
EAANEAGDssQDEAEDDVK	POLR3E	55718	DNA-directed RNA polymerase III subunit RPC5 isoform 5	S9(Phospho) S10(Phospho)	S(9): 100.0; S(10): 100.0	S9; S10;	S161; S162	19		0	0	2	1070	2140	34.07	6308

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#
EREAAEAGDssQDEAEDDVK	POLR3E	55718	DNA-directed RNA polymerase III subunit RPC5 isoform 5	S11(Phospho) S12(Phospho)	S(11): 100.0; S(12): 100.0	S11; S12;	S161; S162		5.03	0	1	3	809	2425	27.51	4940
EAANEAGDssQDEAEDDVK	POLR3E	55718	DNA-directed RNA polymerase III subunit RPC5 isoform 5	S9(Phospho) S10(Phospho)	S(9): 100.0; S(10): 100.0	S9; S10;	S161; S162		2.95	0	0	2	1070	2140	34.07	6308
VGGsDEEASGIPSR	PPAN	56342	suppressor of SWI4 1 homolog	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(13): 0.0	S4;	S359	94		0	0	2	720.8	1441	35.18	6558
VGGsDEEASGIPSR	PPAN	56342	suppressor of SWI4 1 homolog	S4(Phospho)	S(4): 100.0; S(9): 0.0; S(13): 0.0	S4;	S359		4.17	0	0	2	720.8	1441	35.18	6558
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 2.0; S(3): 97.9; S(6): 100.0; S(8): 0.1	S3; S6;	S239; S242	42		0	1	2	895.9	1791	30.02	5467
ssDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S1(Phospho) S2(Phospho)	S(1): 99.9; S(2): 99.9; S(5): 0.1; S(7): 0.0	S1; S2;	S238; S239	40		0	0	2	817.8	1635	39.33	7428
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 0.0; S(3): 100.0; S(6): 100.0; S(8): 0.0	S3; S6;	S239; S242	35		0	1	2	895.9	1791	30.54	5575
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 1.9; S(3): 98.1; S(6): 100.0; S(8): 0.0	S3; S6;	S239; S242	26		0	1	3	597.6	1791	30.4	5547
RSSDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S6(Phospho)	S(2): 33.4; S(3): 33.4; S(6): 99.9; S(8): 33.4	S6;	S242	21		0	1	3	597.6	1791	29.9	5441
RSSDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S6(Phospho)	S(2): 33.4; S(3): 33.4; S(6): 99.9; S(8): 33.4	S6;	S242		5.99	0	1	3	597.6	1791	29.9	5441
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 1.9; S(3): 98.1; S(6): 100.0; S(8): 0.0	S3; S6;	S239; S242		5.64	0	1	3	597.6	1791	30.4	5547
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 2.0; S(3): 97.9; S(6): 100.0; S(8): 0.1	S3; S6;	S239; S242		4.07	0	1	2	895.9	1791	30.02	5467
ssDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S1(Phospho) S2(Phospho)	S(1): 99.9; S(2): 99.9; S(5): 0.1; S(7): 0.0	S1; S2;	S238; S239		3.48	0	0	2	817.8	1635	39.33	7428
RSsDGsLSHEEDLAK	PPFIA1	8500	liprin-alpha-1 isoform a	S3(Phospho) S6(Phospho)	S(2): 0.0; S(3): 100.0; S(6): 100.0; S(8): 0.0	S3; S6;	S239; S242		3.33	0	1	2	895.9	1791	30.54	5575
CETsPPSSPR	PPFIA1	8500	liprin-alpha-1 isoform a	C1(Carbamidomethyl)S4(Phospho)	T(3): 0.1; S(4): 99.9; S(7): 50.0; S(8): 50.0	S4;	S741	20		0.002	0	2	639.2	1277	24.56	4299
SSsLGNLKK	PPFIBP1	8496	liprin-beta-1 isoform 3	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0	S3;	S313	35		0	1	2	507.3	1014	19.44	3221
SSsLGNLKK	PPFIBP1	8496	liprin-beta-1 isoform 3	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 100.0	S3;	S313		2.1	0	1	2	507.3	1014	19.44	3221
DTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	S3(Phospho)	T(2): 0.0; S(3): 97.9; S(5): 2.0; S(6): 0.0; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S3;	S157	75		0	0	2	688.8	1377	15.91	2464
tSRDTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	T1(Phospho) S6(Phospho)	T(1): 97.0; S(2): 5.7; T(5): 3.0; S(6): 94.3; S(8): 0.0; S(9): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; S(16): 0.0	T1; S6;	T152; S157	58		0	1	3	600.9	1801	15.73	2424
TSRDTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	S6(Phospho)	T(1): 50.0; S(2): 50.0; T(5): 0.0; S(6): 100.0; S(8): 0.0; S(9): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; S(16): 0.0	S6;	S157	28		0	1	2	900.9	1801	15.69	2416
tSRDTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	T1(Phospho) S6(Phospho)	T(1): 97.0; S(2): 5.7; T(5): 3.0; S(6): 94.3; S(8): 0.0; S(9): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; S(16): 0.0	T1; S6;	T152; S157		4.61	0	1	3	600.9	1801	15.73	2424
DTsPSSGSsAVSSSK	PPHLN1	51535	periphilin-1 isoform 5	S3(Phospho)	T(2): 0.0; S(3): 97.9; S(5): 2.0; S(6): 0.0; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(13): 0.0	S3;	S157		3.13	0	0	2	688.8	1377	15.91	2464

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#
TSRDTsPSSGSVAVSSSK	PPLN1	51535	periphilin-1 isoform 5	S6(Phospho)	T(1): 50.0; S(2): 50.0; T(5): 0.0; S(6): 100.0; S(8): 0.0; S(9): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; S(16): 0.0	S6;	S157		3.03	0	1	2	900.9	1801	15.69	2416
KADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S687	42		0	2	2	679.8	1359	14.71	2209
IKQsSQDNELK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S5(Phospho)	S(4): 0.0; S(5): 100.0	S5;	S696	41		0	1	2	685.3	1370	15.64	2406
ADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S687	36		0	1	2	615.8	1231	18.18	2956
KFDHessPGTDEDKsG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho) S15(Phospho)	S(6): 97.3; S(7): 2.7; T(10): 2.7; S(15): 97.3	S6; S15;	S744; S753	23		0	2	3	632.6	1896	16.99	2704
KFDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho) S7(Phospho) T10(Phospho)	S(6): 100.0; S(7): 100.0; T(10): 100.0; S(15): 0.0	S6; S7; T10;	S744; S745; T748	20		0	2	2	988.3	1976	20.51	3445
KADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S7(Phospho)	S(7): 100.0; S(10): 0.0	S7;	S687		3.7	0	2	2	679.8	1359	14.71	2209
IKQsSQDNELK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S5(Phospho)	S(4): 0.0; S(5): 100.0	S5;	S696		3.54	0	1	2	685.3	1370	15.64	2406
ADRDQsPFSK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho)	S(6): 100.0; S(9): 0.0	S6;	S687		2.87	0.001	1	2	615.8	1231	18.18	2956
KFDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	T10(Phospho)	S(6): 50.0; S(7): 50.0; T(10): 95.9; S(15): 4.1	T10;	T748	16		0.002	2	2	948.3	1896	16.92	2687
FDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	T9(Phospho)	S(5): 50.0; S(6): 50.0; T(9): 95.9; S(14): 4.1	T9;	T748	11		0.002	1	2	884.3	1768	20.09	3356
AQsRsRECDITK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	C8(Carbamidomethyl)S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(11): 0.0	S3; S5;	S544; S546	11		0.003	2	2	805.8	1611	14.18	2097
KFDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho) S7(Phospho) T10(Phospho)	S(6): 100.0; S(7): 100.0; T(10): 100.0; S(15): 0.0	S6; S7; T10;	S744; S745; T748	15		0.004	2	3	659.2	1976	20.93	3533
KFDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho) S7(Phospho) T10(Phospho)	S(6): 100.0; S(7): 100.0; T(10): 100.0; S(15): 0.0	S6; S7; T10;	S744; S745; T748		3.35	0.005	2	2	988.3	1976	20.51	3445
AQsRsRECDITK	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	C8(Carbamidomethyl)S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; T(11): 0.0	S3; S5;	S544; S546		2.15	0.007	2	2	805.8	1611	14.18	2097
KFDHessPGtDEDKSG	PPIG	9360	peptidyl-prolyl cis-trans isomerase G	S6(Phospho) S7(Phospho) T10(Phospho)	S(6): 100.0; S(7): 100.0; T(10): 100.0; S(15): 0.0	S6; S7; T10;	S744; S745; T748		4.48	0.008	2	3	659.2	1976	20.93	3533
GKYsPTVQTR	PPL	5493	periplakin	S4(Phospho)	Y(3): 0.0; S(4): 98.8; T(6): 1.2; T(9): 0.0	S4;	S14	45		0	1	2	608.8	1217	21.01	3551
GKYsPTVQTR	PPL	5493	periplakin	S4(Phospho)	Y(3): 0.0; S(4): 98.8; T(6): 1.2; T(9): 0.0	S4;	S14		2.87	0	1	2	608.8	1217	21.01	3551
SESAPTLHPYsPLsPK	PPP1R13L	10848	relA-associated inhibitor	S11(Phospho) S14(Phospho)	S(1): 0.0; S(3): 0.0; T(6): 0.0; Y(10): 3.2; S(11): 96.8; S(14): 100.0	S11; S14;	S110; S113		3.66	0	0	2	935.9	1871	61.64	12224
SEsAPTLHPYsPLsPK	PPP1R13L	10848	relA-associated inhibitor	S3(Phospho) S14(Phospho)	S(1): 2.8; S(3): 97.2; T(6): 0.0; Y(10): 0.0; S(11): 0.0; S(14): 100.0	S3; S14;	S102; S113	11		0.002	0	2	935.9	1871	64.15	12846
SEsAPTLHPYsPLsPK	PPP1R13L	10848	relA-associated inhibitor	S3(Phospho) S14(Phospho)	S(1): 2.8; S(3): 97.2; T(6): 0.0; Y(10): 0.0; S(11): 0.0; S(14): 100.0	S3; S14;	S102; S113		2.39	0.005	0	2	935.9	1871	64.15	12846
IQEQEssGEEDSLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 99.8; S(7): 100.0; S(12): 0.2; S(15): 0.0	S6; S7;	S95; S96	48		0	0	2	1162	2324	49.01	9497

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#
IQEQEssGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	46		0	0	3	775.3	2324	49.14	9524
IQEQEssGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	43		0	0	2	1162	2324	49.52	9603
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	34		0	1	3	861	2581	38.18	7183
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	23		0	1	2	1291	2581	38.31	7212
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	5.33	0	1	3	861	2581	38.18	7183	
IQEQEssGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	4.01	0	0	3	775.3	2324	49.14	9524	
IQEQEssGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 99.8; S(7): 100.0; S(12): 0.2; S(15): 0.0	S6; S7;	S95; S96	3.43	0	0	2	1162	2324	49.01	9497	
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S7(Phospho)	S(6): 4.3; S(7): 91.4; S(12): 4.3; S(15): 0.0	S7;	S96	3.26	0	1	3	834.3	2501	32.51	5984	
IQEQEssGEEDSDLSPEER	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	3.24	0	0	2	1162	2324	49.52	9603	
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; S(12): 0.0; S(15): 0.0	S6; S7;	S95; S96	3.1	0	1	2	1291	2581	38.31	7212	
IQEQEssGEEDSDLSPEEREK	PPP1R2	5504	protein phosphatase inhibitor 2 isoform 3	S7(Phospho)	S(6): 4.3; S(7): 91.4; S(12): 4.3; S(15): 0.0	S7;	S96	12	0.002	1	3	834.3	2501	32.51	5984	
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	3.11	0.003	1	2	630.3	1260	23.38	4051	
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	70		0	2	3	580.2	1739	12.62	1761
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	59		0	2	2	869.8	1739	12.61	1760
GAGQQQsQEMMEVDR	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S7(Phospho)	S(7): 100.0	S7;	S12	58		0	0	2	887.4	1774	40.88	7758
RVEsEesGDEEGK	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	48		0	1	2	805.8	1611	13.7	1998
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	6.45	0	2	3	580.2	1739	12.62	1761	
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	5.06	0	2	2	869.8	1739	12.61	1760	
GAGQQQsQEMMEVDR	PPP1R7	5510	protein phosphatase 1 regulatory subunit 7 isoform 3	S7(Phospho)	S(7): 100.0	S7;	S12	3.57	0	0	2	887.4	1774	40.88	7758	
RVEsEesGDEEGK	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	3.1	0	1	2	805.8	1611	13.7	1998	
IQQFDDDEEEDEEEAQGsGEdGEDG AWQGSQAR	PPP6R1	22870	serine/threonine-protein phosphatase 6 regulatory subunit 1	S19(Phospho) S22(Phospho)	S(19): 100.0; S(22): 100.0; S(32): 0.0	S19; S22;	S635; S638	24		0	0	3	1383	4146	81.01	16310
IQQFDDDEEEDEEEAQGsGEdGEDG AWQGSQAR	PPP6R1	22870	serine/threonine-protein phosphatase 6 regulatory subunit 1	S19(Phospho) S22(Phospho)	S(19): 100.0; S(22): 100.0; S(32): 0.0	S19; S22;	S635; S638	2.48	0	0	3	1383	4146	81.01	16310	
IQQFDDGGsDEEDIWEEK	PPP6R3	55291	serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform 3	S9(Phospho)	S(9): 100.0	S9;	S537	15		0	0	2	1110	2220	72.34	14618
IQQFDDGGsDEEDIWEEK	PPP6R3	55291	serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform 3	S9(Phospho)	S(9): 100.0	S9;	S537	2.34	0	0	2	1110	2220	72.34	14618	
IQQFDDGGsDEEDIWEEK	PPP6R3	55291	serine/threonine-protein phosphatase 6 regulatory subunit 3 isoform 3	S9(Phospho)	S(9): 100.0	S9;	S537	1.16	0.008	0	2	1110	2220	72.87	14739	
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159	32		0	1	3	776.7	2328	37.22	6985
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159	20		0	1	2	1164	2328	36.94	6928

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#
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159		5.94	0	1	3	776.7	2328	37.22	6985
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159		4.07	0	1	3	776.7	2328	36.72	6883
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159		2.69	0	1	2	1164	2328	36.94	6928
IAAPELHKGDsDEEPEPTK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0; T(19): 0.0	S11; S13;	S157; S159	13		0.001	1	3	776.7	2328	36.72	6883
IAAPELHKGDsDEEPEPTKK	PRCC	5546	proline-rich protein PRCC	S11(Phospho) S13(Phospho)	S(11): 94.7; S(13): 99.7; T(19): 5.6	S11; S13;	S157; S159		3.53	0.003	2	3	819.3	2456	30.19	5502
SIDDEITEAKsGTAtPQR	PRKAA1	5562	5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 1	S11(Phospho) T15(Phospho)	S(1): 0.0; T(7): 0.0; S(11): 99.8; T(13): 0.3; T(15): 99.8	S11; T15;	S486; T490	52		0	1	2	1040	2079	46.03	8872
SIDDEITEAKsGTAtPQR	PRKAA1	5562	5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 1	S11(Phospho) T15(Phospho)	S(1): 0.0; T(7): 0.0; S(11): 100.0; T(13): 0.1; T(15): 99.9	S11; T15;	S486; T490	39		0	1	3	693.6	2079	46.02	8871
SIDDEITEAKsGTAtPQR	PRKAA1	5562	5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 1	S11(Phospho) T15(Phospho)	S(1): 0.0; T(7): 0.0; S(11): 100.0; T(13): 0.1; T(15): 99.9	S11; T15;	S486; T490		5.53	0	1	3	693.6	2079	46.02	8871
SIDDEITEAKsGTAtPQR	PRKAA1	5562	5'-AMP-activated protein kinase catalytic subunit alpha-1 isoform 1	S11(Phospho) T15(Phospho)	S(1): 0.0; T(7): 0.0; S(11): 99.8; T(13): 0.3; T(15): 99.8	S11; T15;	S486; T490		3.92	0	1	2	1040	2079	46.03	8872
TDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	S9(Phospho)	T(1): 0.0; S(3): 0.1; S(9): 99.9	S9;	S83	11		0	1	3	686.3	2057	47.9	9264
TDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	S9(Phospho)	T(1): 2.7; S(3): 2.7; S(9): 94.5	S9;	S83	11		0	1	3	686.3	2057	47.37	9154
tDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	T1(Phospho) S9(Phospho)	T(1): 99.9; S(3): 0.1; S(9): 100.0	T1; S9;	T75; S83	10		0	1	3	713	2137	55.46	10897
tDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	T1(Phospho) S9(Phospho)	T(1): 99.9; S(3): 0.1; S(9): 100.0	T1; S9;	T75; S83		3.69	0	1	3	713	2137	55.46	10897
TDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	S9(Phospho)	T(1): 2.7; S(3): 2.7; S(9): 94.5	S9;	S83		3.26	0.001	1	3	686.3	2057	47.37	9154
TDSREDEIsPPPNPVVK	PRKAR1A	5573	cAMP-dependent protein kinase type I-alpha regulatory subunit isoform b	S9(Phospho)	T(1): 0.0; S(3): 0.1; S(9): 99.9	S9;	S83		3.17	0.001	1	3	686.3	2057	47.9	9264
SNSQSDSHDEEVsPTPPNPVVK	PRKAR1B	5575	cAMP-dependent protein kinase type I-beta regulatory subunit	S13(Phospho)	S(1): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(13): 99.9; T(15): 0.1	S13;	S83	42		0	0	3	810.7	2430	41.91	7972
SNSQSDSHDEEVsPTPPNPVVK	PRKAR1B	5575	cAMP-dependent protein kinase type I-beta regulatory subunit	S13(Phospho)	S(1): 0.0; S(3): 0.0; S(5): 0.0; S(7): 0.0; S(13): 99.9; T(15): 0.1	S13;	S83		5.79	0	0	3	810.7	2430	41.91	7972
VADAKGDsEsEEDELEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80	63		0	1	3	878.4	2633	63.46	12676
VADAKGDsEsEEDELEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80	59		0	1	3	878.4	2633	63.98	12805
VADAKGDsEsEEDELEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80	53		0	1	3	878.4	2633	65.25	13107
RVsVCAETYNPDEEEEDTDPR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	C5(Carbamidomethyl) S3(Phospho)	S(3): 100.0; T(8): 0.0; Y(9): 0.0; T(18): 0.0	S3;	S99	45		0	1	3	864.3	2591	46.53	8979

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#
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80	37		0	1	2	1317	2633	63.53	12694
GDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(17): 0.0	S3; S5;	S78; S80	31		0	0	2	1075	2149	78.62	15843
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80	23		0	1	3	878.4	2633	64.73	12994
RVsVCAETYNPDEEEEDTDPR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	C5(Carbamidomethyl) S3(Phospho)	S(3): 100.0; T(8): 0.0; Y(9): 0.0; T(18): 0.0	S3;	S99		5.55	0	1	3	864.3	2591	46.53	8979
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80		4.68	0	1	3	878.4	2633	63.46	12676
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80		3.87	0	1	3	878.4	2633	63.98	12805
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80		2.94	0	1	3	878.4	2633	64.73	12994
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80		2.93	0	1	3	878.4	2633	65.25	13107
VADAKGDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S8(Phospho) S10(Phospho)	S(8): 100.0; S(10): 100.0; S(22): 0.0	S8; S10;	S78; S80		2.67	0	1	2	1317	2633	63.53	12694
GDsEsEEDEDLEVPVPSR	PRKAR2A	5576	cAMP-dependent protein kinase type II-alpha regulatory subunit	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; S(17): 0.0	S3; S5;	S78; S80		2.31	0	0	2	1075	2149	78.62	15843
APEPLGPADQSELGPEQLEAEVGsDEEPVESR	PRKCDP	112464	protein kinase C delta-binding protein	S25(Phospho) S26(Phospho)	S(11): 0.2; S(25): 99.9; S(26): 99.9; S(33): 0.0	S25; S26;	S165; S166	23		0	0	3	1247	3738	93.51	18681
APEPLGPADQSELGPEQLEAEVGsDEEPVESR	PRKCDP	112464	protein kinase C delta-binding protein	S25(Phospho) S26(Phospho)	S(11): 0.2; S(25): 99.9; S(26): 99.9; S(33): 0.0	S25; S26;	S165; S166		2.69	0	0	3	1247	3738	93.51	18681
GAVENEEDLPeLsDsGDEAAWEDEDADLPHGK	PRMT3	10196	protein arginine N-methyltransferase 3 isoform 1	S13(Phospho) S15(Phospho)	S(13): 100.0; S(15): 100.0	S13; S15;	S25; S27		2.27	0	0	3	1239	3714	79.85	16087
AFsRGGsLEsR	PROSER2	254427	proline and serine-rich protein 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 99.9; S(10): 0.1	S3; S7;	S27; S31	17		0.002	1	2	663.8	1327	33.71	6231
AFsRGGsLEsR	PROSER2	254427	proline and serine-rich protein 2	S3(Phospho) S7(Phospho)	S(3): 100.0; S(7): 99.9; S(10): 0.1	S3; S7;	S27; S31		2.19	0.005	1	2	663.8	1327	33.71	6231
IKWDEQTSNTKGDDDEEsDEEAVK	PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	S18(Phospho)	T(7): 0.0; S(8): 0.0; T(10): 0.0; S(18): 100.0	S18;	S619	17		0	2	3	950.1	2848	39.09	7378
WDEQTSNTKGDDDEEsDEEAVKK	PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	S16(Phospho)	T(5): 0.0; S(6): 0.0; T(8): 0.0; S(16): 100.0	S16;	S619	17		0	2	3	912.4	2735	27.27	4886
WDEQTSNTKGDDDEEsDEEAVKK	PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	S16(Phospho)	T(5): 0.0; S(6): 0.0; T(8): 0.0; S(16): 100.0	S16;	S619		5	0	2	3	912.4	2735	27.27	4886
WDEQTSNTKGDDDEEsDEEAVK	PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	S16(Phospho)	T(5): 0.0; S(6): 0.0; T(8): 0.0; S(16): 100.0	S16;	S619		3.7	0.003	1	3	869.7	2607	33.14	6116
IKWDEQTSNTKGDDDEEsDEEAVK	PRPF3	9129	U4/U6 small nuclear ribonucleoprotein Prp3	S18(Phospho)	T(7): 0.0; S(8): 0.0; T(10): 0.0; S(18): 100.0	S18;	S619		3	0.003	2	3	950.1	2848	39.09	7378
VSALIEDMDDVesEEEEEEDEKLER	PRPF38A	84950	pre-mRNA-splicing factor 38A	M8(Oxidation) S13(Phospho) S14(Phospho)	S(2): 0.1; S(13): 100.0; S(14): 100.0	S13; S14;	S193; S194	15		0	1	3	1083	3246	56.89	11211
VSALIEDMDDVesEEEEEEDEKLER	PRPF38A	84950	pre-mRNA-splicing factor 38A	M8(Oxidation) S13(Phospho) S14(Phospho)	S(2): 0.1; S(13): 100.0; S(14): 100.0	S13; S14;	S193; S194		4.33	0	1	3	1083	3246	56.89	11211
VsALIEDMDDVesEEEEEEDEKLER	PRPF38A	84950	pre-mRNA-splicing factor 38A	M8(Oxidation) S2(Phospho)	S(2): 99.8; S(13): 50.1; S(14): 50.1	S2;	S182		3.14	0	1	3	1083	3246	57.43	11331

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#
RSQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(9): 0.0	S4;	S529	74		0	1	2	764.8	1529	13.68	1993
SQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(8): 0.0	S3;	S529	41		0	0	2	686.8	1373	18.05	2928
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	37		0	2	3	588.9	1765	14.07	2075
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	35		0	2	3	588.9	1765	14.58	2182
sSQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S1(Phospho)	S(1): 99.9; S(3): 0.1; S(8): 0.0	S1;	S527	28		0	0	2	686.8	1373	20.82	3510
SRsGsQGRTDSVEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 100.0; T(9): 0.0; S(11): 0.0	S3; S5;	S473; S475	24		0	2	2	827.3	1654	12.46	1719
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	19		0	2	3	588.9	1765	15.62	2401
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		7.33	0	2	3	588.9	1765	14.58	2182
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		6.32	0	2	3	588.9	1765	14.07	2075
RSQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(9): 0.0	S4;	S529		4.34	0	1	2	764.8	1529	13.68	1993
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		4.19	0	2	3	588.9	1765	15.62	2401
SRsGsQGRTDSVEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 100.0; T(9): 0.0; S(11): 0.0	S3; S5;	S473; S475		3.46	0	2	2	827.3	1654	12.46	1719
SQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(8): 0.0	S3;	S529		3.31	0	0	2	686.8	1373	18.05	2928
sSQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S1(Phospho)	S(1): 99.9; S(3): 0.1; S(8): 0.0	S1;	S527		2.71	0	0	2	686.8	1373	20.82	3510
RRsQsIEQESQEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; S(10): 0.1	S3; S5;	S527; S529		3.56	0.002	2	2	882.9	1765	14.12	2084
SRsGsQGRTDSVEK	PRPF38B	55119	pre-mRNA-splicing factor 38B	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 100.0; T(9): 0.0; S(11): 0.0	S3; S5;	S473; S475		4.63	0.006	2	3	551.9	1654	12.47	1724
SDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S6(Phospho)	S(1): 1.7; S(3): 98.3; S(6): 100.0	S3; S6;	S858; S861	27		0	1	2	755.3	1510	20.25	3390
HKSDSPesDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S8(Phospho)	S(3): 50.0; S(5): 50.0; S(8): 100.0	S8;	S861	25		0	2	3	592.2	1775	13.22	1895
HKsDSPesDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S8(Phospho)	S(3): 97.8; S(5): 2.2; S(8): 100.0	S3; S8;	S856; S861	23		0	2	2	887.8	1775	13.32	1917
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861	20		0	2	3	618.9	1855	14.89	2247
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861	20		0	2	3	618.9	1855	14.34	2132
HKSDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S5(Phospho) S8(Phospho)	S(3): 2.8; S(5): 97.2; S(8): 100.0	S5; S8;	S858; S861	17		0	2	3	592.2	1775	13.78	2013
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861	14		0	2	3	618.9	1855	15.66	2411
HKSDSPesDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S8(Phospho)	S(3): 50.0; S(5): 50.0; S(8): 100.0	S8;	S861		6.16	0	2	3	592.2	1775	13.22	1895
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861		5.54	0	2	3	618.9	1855	14.34	2132
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861		5.1	0	2	3	618.9	1855	14.89	2247
HKSDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S5(Phospho) S8(Phospho)	S(3): 2.8; S(5): 97.2; S(8): 100.0	S5; S8;	S858; S861		4.7	0	2	3	592.2	1775	13.78	2013

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#
HKsDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 100.0	S3; S5; S8;	S856; S858; S861		4.39	0	2	3	618.9	1855	15.66	2411
HKsDSPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S8(Phospho)	S(3): 97.8; S(5): 2.2; S(8): 100.0	S3; S8;	S856; S861		3.01	0	2	2	887.8	1775	13.32	1917
DSGNWDTSGsELsEGELEKR	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S10(Phospho) S13(Phospho)	S(2): 0.2; T(7): 3.7; S(8): 3.7; S(10): 92.4; S(13): 100.0	S10; S13;	S908; S911	14		0.002	1	3	786	2356	63.15	12597
SDsPEsDAEREK	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S3(Phospho) S6(Phospho)	S(1): 1.7; S(3): 98.3; S(6): 100.0	S3; S6;	S858; S861		2.45	0.003	1	2	755.3	1510	20.25	3390
DSGNWDTSGsELsEGELEKR	PRPF40A	55660	pre-mRNA-processing factor 40 homolog A	S10(Phospho) S13(Phospho)	S(2): 0.2; T(7): 3.7; S(8): 3.7; S(10): 92.4; S(13): 100.0	S10; S13;	S908; S911		2.45	0.007	1	3	786	2356	63.15	12597
KKsPIINESR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S3(Phospho)	S(3): 100.0; S(9): 0.0	S3;	S277	51		0	2	2	626.3	1252	14.77	2221
sLsPKPR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S354; S356	28		0	0	2	472.7	944.4	19.7	3273
TRsPsDDILER	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S3(Phospho) S5(Phospho)	T(1): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580	23		0	1	2	773.3	1546	52.98	10357
sRsPLLNDR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S366; S368	22		0	1	2	609.3	1218	31.54	5782
EQPEMEDANsEKsINEENGVEDQSQ NK	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S10(Phospho) S13(Phospho)	S(10): 93.0; S(13): 99.4; S(22): 7.5; S(26): 0.0	S10; S13;	S20; S23	21		0	1	3	1152	3454	41.67	7922
sRsPLLNDR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S366; S368	18		0	1	2	609.3	1218	32.06	5890
EQPEMEDANsEKsINEENGVEDQSQ NK	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	M5(Oxidation) S10(Phospho) S13(Phospho)	S(10): 98.9; S(13): 98.9; S(22): 2.2; S(26): 0.0	S10; S13;	S20; S23	18		0	1	3	1157	3470	34.36	6370
TRsPsDDILER	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S3(Phospho) S5(Phospho)	T(1): 0.0; S(3): 100.0; S(5): 100.0	S3; S5;	S578; S580		3.43	0	1	2	773.3	1546	52.98	10357
sRsPLLNDR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S366; S368		3.03	0	1	2	609.3	1218	31.54	5782
sRsPLLNDR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S366; S368		2.84	0	1	2	609.3	1218	32.06	5890
KKsPIINESR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S3(Phospho)	S(3): 100.0; S(9): 0.0	S3;	S277		2.83	0	2	2	626.3	1252	14.77	2221
EQPEMEDANsEKsINEENGVEDQSQ NK	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S10(Phospho) S13(Phospho)	S(10): 93.0; S(13): 99.4; S(22): 7.5; S(26): 0.0	S10; S13;	S20; S23		2.8	0	1	3	1152	3454	41.67	7922
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		2.61	0	1	2	545.2	1089	30.1	5483
EQPEMEDANsEKsINEENGVEDQSQ NK	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	M5(Oxidation) S10(Phospho) S13(Phospho)	S(10): 98.9; S(13): 98.9; S(22): 2.2; S(26): 0.0	S10; S13;	S20; S23		2.52	0	1	3	1157	3470	34.36	6370
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		2.51	0	1	2	545.2	1089	30.62	5592
sLsPKPR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0	S1; S3;	S354; S356		2.28	0	0	2	472.7	944.4	19.7	3273
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	20		0.002	1	2	545.2	1089	30.62	5592
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	18		0.003	1	2	545.2	1089	30.1	5483
sKDAsPINRWSPTR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 100.0; S(11): 50.0; T(13): 50.0	S1; S5;	S427; S431		3.25	0.003	2	3	618.9	1855	45.15	8685
SKDAsPINRWsPTR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S5(Phospho) S11(Phospho)	S(1): 4.4; S(5): 95.4; S(11): 95.6; T(13): 4.6	S5; S11;	S431; S437	13		0.004	2	3	592.3	1775	37.49	7043
SKDAsPINRWsPTR	PRPF4B	8899	serine/threonine-protein kinase PRP4 homolog	S11(Phospho)	S(1): 51.0; S(5): 51.0; S(11): 93.9; T(13): 4.1	S11;	S437		4.24	0.004	2	3	592.3	1775	36.96	6931

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#
KQETAAVCGEtDEEAGEsGGEGIFR	PRR12	57479	proline-rich protein 12	C8(Carbamidomethyl)T11(Phospho)S18(Phospho)	T(4): 0.0; T(11): 100.0; S(18): 100.0	T11; S18;	T1561; S1568	42		0	1	3	929.7	2787	59.56	11796
KQETAAVCGEtDEEAGEsGGEGIFR	PRR12	57479	proline-rich protein 12	C8(Carbamidomethyl)T11(Phospho)S18(Phospho)	T(4): 0.0; T(11): 100.0; S(18): 100.0	T11; S18;	T1561; S1568		4.33	0	1	3	929.7	2787	59.56	11796
NLETLPsFsDEEDSVAK	PRR12	57479	proline-rich protein 12	S9(Phospho)S10(Phospho)	T(4): 0.0; S(7): 0.4; S(9): 99.8; S(10): 99.8; S(15): 0.0	S9; S10;	S1381; S1382	10		0.003	0	2	1064	2128	88.14	17630
NLETLPsFsDEEDSVAK	PRR12	57479	proline-rich protein 12	S9(Phospho)S10(Phospho)	T(4): 0.0; S(7): 0.4; S(9): 99.8; S(10): 99.8; S(15): 0.0	S9; S10;	S1381; S1382		1.76	0.006	0	2	1064	2128	88.14	17630
SDsGGsSSEPFDR	PRRC2A	7916	protein PRRC2A	S3(Phospho)S6(Phospho)	S(1): 0.1; S(3): 99.9; S(6): 97.5; S(7): 2.5; S(8): 0.1	S3; S6;	S761; S764	49		0	0	2	744.2	1487	47.1	9098
KGNsPNSEPTPK	PRRC2A	7916	protein PRRC2A	S4(Phospho)	S(4): 100.0; S(7): 0.0; T(11): 0.0	S4;	S380	45		0	1	2	716.8	1433	15.48	2371
TAsETRSEGsEYEEIPKR	PRRC2A	7916	protein PRRC2A	S3(Phospho)S7(Phospho)S10(Phospho)	T(1): 0.0; S(3): 100.0; T(5): 4.0; S(7): 96.2; S(10): 99.8; Y(12): 0.0	S3; S7; S10;	S1085; S1089; S1092	37		0	2	3	770.3	2309	41.93	7977
LKFsDEEDGRDsDEEGAEGHR	PRRC2A	7916	protein PRRC2A	S4(Phospho)S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S342; S350	33		0	2	4	635.2	2538	32.5	5982
ERSDsGGsSSEPFDR	PRRC2A	7916	protein PRRC2A	S5(Phospho)S8(Phospho)	S(3): 0.1; S(5): 99.9; S(8): 94.4; S(9): 2.8; S(10): 2.8	S5; S8;	S761; S764	33		0	1	2	886.8	1773	32.59	6000
TAsETRSEGsEYEEIPKR	PRRC2A	7916	protein PRRC2A	S7(Phospho)S10(Phospho)	T(1): 0.0; S(3): 0.2; T(5): 3.2; S(7): 99.8; S(10): 96.8; Y(12): 0.0	S7; S10;	S1089; S1092	31		0	2	3	743.6	2229	36.16	6762
TAsETRSEGsEYEEIPK	PRRC2A	7916	protein PRRC2A	S7(Phospho)S10(Phospho)	T(1): 3.4; S(3): 3.4; T(5): 3.4; S(7): 89.8; S(10): 100.0; Y(12): 0.0	S7; S10;	S1089; S1092	21		0	1	2	1037	2073	44.92	8636
TAsETRSEGsEYEEIPK	PRRC2A	7916	protein PRRC2A	T5(Phospho)S7(Phospho)	T(1): 0.3; S(3): 3.7; T(5): 96.2; S(7): 96.3; S(10): 3.5; Y(12): 0.0	T5; S7;	T1087; S1089	16		0	1	2	1037	2073	46.45	8962
LKFsDEEDGRDsDEEGAEGHR	PRRC2A	7916	protein PRRC2A	S4(Phospho)S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S342; S350	15		0	2	3	846.7	2538	32.38	5956
TAsETRSEGsEYEEIPK	PRRC2A	7916	protein PRRC2A	S7(Phospho)	T(1): 0.0; S(3): 0.1; T(5): 50.8; S(7): 98.3; S(10): 50.8; Y(12): 0.0	S7;	S1089	15		0	1	3	691.6	2073	46.49	8972
TAsETRSEGsEYEEIPKR	PRRC2A	7916	protein PRRC2A	S3(Phospho)S7(Phospho)S10(Phospho)	T(1): 0.0; S(3): 100.0; T(5): 4.0; S(7): 96.2; S(10): 99.8; Y(12): 0.0	S3; S7; S10;	S1085; S1089; S1092		5.99	0	2	3	770.3	2309	41.93	7977
TAsETRSEGsEYEEIPK	PRRC2A	7916	protein PRRC2A	S7(Phospho)	T(1): 0.0; S(3): 0.1; T(5): 50.8; S(7): 98.3; S(10): 50.8; Y(12): 0.0	S7;	S1089		5.41	0	1	3	691.6	2073	46.49	8972
LKFsDEEDGRDsDEEGAEGHR	PRRC2A	7916	protein PRRC2A	S4(Phospho)S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S342; S350		4.91	0	2	4	635.2	2538	32.5	5982
TAsETRSEGsEYEEIPKR	PRRC2A	7916	protein PRRC2A	S7(Phospho)S10(Phospho)	T(1): 0.0; S(3): 0.2; T(5): 3.2; S(7): 99.8; S(10): 96.8; Y(12): 0.0	S7; S10;	S1089; S1092		4.84	0	2	3	743.6	2229	36.16	6762
LKFsDEEDGRDsDEEGAEGHR	PRRC2A	7916	protein PRRC2A	S4(Phospho)S12(Phospho)	S(4): 100.0; S(12): 100.0	S4; S12;	S342; S350		4.17	0	2	3	846.7	2538	32.38	5956
KGNsPNSEPTPK	PRRC2A	7916	protein PRRC2A	S4(Phospho)	S(4): 100.0; S(7): 0.0; T(11): 0.0	S4;	S380		3.58	0	1	2	716.8	1433	15.48	2371
ERSDsGGsSSEPFDR	PRRC2A	7916	protein PRRC2A	S5(Phospho)S8(Phospho)	S(3): 0.1; S(5): 99.9; S(8): 94.4; S(9): 2.8; S(10): 2.8	S5; S8;	S761; S764		3.49	0	1	2	886.8	1773	32.59	6000
SDsGGsSSEPFDR	PRRC2A	7916	protein PRRC2A	S3(Phospho)S6(Phospho)	S(1): 0.1; S(3): 99.9; S(6): 97.5; S(7): 2.5; S(8): 0.1	S3; S6;	S761; S764		2.96	0	0	2	744.2	1487	47.1	9098

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#
TASETrsEGSEYEEIPK	PRRC2A	7916	protein PRRC2A	T5(Phospho) S7(Phospho)	T(1): 0.1; S(3): 6.7; T(5): 96.5; S(7): 96.5; S(10): 0.3; Y(12): 0.0	T5; S7;	T1087; S1089		2.63	0	1	3	691.6	2073	45	8654
TASETrsEGSEyEEIPK	PRRC2A	7916	protein PRRC2A	T5(Phospho) S7(Phospho) Y12(Phospho)	T(1): 10.5; S(3): 10.5; T(5): 84.8; S(7): 94.3; S(10): 0.4; Y(12): 99.6	T5; S7; Y12;	T1087; S1089; Y1094		1.97	0	1	2	1077	2153	56.09	11029
TASETrsEGSEYEEIPK	PRRC2A	7916	protein PRRC2A	T5(Phospho) S7(Phospho)	T(1): 0.3; S(3): 3.7; T(5): 96.2; S(7): 96.3; S(10): 3.5; Y(12): 0.0	T5; S7;	T1087; S1089		2.05	0.001	1	2	1037	2073	46.45	8962
TASETrsEGsEYEEIPK	PRRC2A	7916	protein PRRC2A	S7(Phospho) S10(Phospho)	T(1): 3.4; S(3): 3.4; T(5): 3.4; S(7): 89.8; S(10): 100.0; Y(12): 0.0	S7; S10;	S1089; S1092		2.2	0.005	1	2	1037	2073	44.92	8636
STtPTSsPFR	PRRC2C	23215	protein PRRC2C	T3(Phospho) S7(Phospho)	S(1): 0.0; T(2): 0.0; T(3): 98.4; T(5): 1.6; S(6): 0.1; S(7): 100.0	T3; S7;	T2682; S2686	26		0	0	2	620.7	1240	45.79	8821
GsETDtdSEIHESASDKDSLK	PRRC2C	23215	protein PRRC2C	S2(Phospho) T6(Phospho)	S(2): 99.8; T(4): 0.5; T(6): 99.8; S(8): 0.0; S(13): 0.0; S(15): 0.0; S(19): 0.0; S(21): 0.0	S2; T6;	S1263; T1267	23		0	1	3	833.3	2498	29.82	5425
GsETDtdSEIHESASDKDSLK	PRRC2C	23215	protein PRRC2C	S2(Phospho) T6(Phospho)	S(2): 99.8; T(4): 0.5; T(6): 99.8; S(8): 0.0; S(13): 0.0; S(15): 0.0; S(19): 0.0; S(21): 0.0	S2; T6;	S1263; T1267		3.8	0	1	3	833.3	2498	29.82	5425
STtPTSsPFR	PRRC2C	23215	protein PRRC2C	T3(Phospho) S7(Phospho)	S(1): 0.0; T(2): 0.0; T(3): 98.4; T(5): 1.6; S(6): 0.1; S(7): 100.0	T3; S7;	T2682; S2686		2.93	0	0	2	620.7	1240	45.79	8821
QREEsETRSEsDFEVVPK	PRRC2C	23215	protein PRRC2C	S5(Phospho) S11(Phospho) S12(Phospho)	S(5): 90.8; T(7): 17.7; S(9): 17.7; S(11): 86.9; S(12): 86.9	S5; S11; S12;	S1242; S1248; S1249		3.41	0.003	2	3	827	2479	53.07	10379
QREEsETRSESSDFEVVPK	PRRC2C	23215	protein PRRC2C	S5(Phospho) T7(Phospho)	S(5): 100.0; T(7): 99.7; S(9): 0.2; S(11): 0.0; S(12): 0.0	S5; T7;	S1242; T1244		3.32	0.007	2	3	800.3	2399	46.2	8910
SHsPSLNPDTsPITAK	PSD3	23362	PH and SEC7 domain-containing protein 3 isoform b	S3(Phospho) S12(Phospho)	S(1): 2.7; S(3): 94.5; S(4): 2.7; S(6): 0.1; T(11): 2.8; S(12): 97.1; T(15): 0.1	S3; S12;	S476; S485		3.08	0	0	2	949.9	1899	49.37	9573
TSLMsAEsPTPR	PSEN2	5664	presenilin-2 isoform 2	S5(Phospho) S8(Phospho)	T(1): 0.0; S(2): 0.0; S(5): 100.0; S(8): 100.0; T(10): 0.0	S5; S8;	S22; S25	36		0	0	2	718.8	1437	61.03	12096
TSLMsAEsPTPR	PSEN2	5664	presenilin-2 isoform 2	S5(Phospho) S8(Phospho)	T(1): 0.0; S(2): 0.0; S(5): 100.0; S(8): 100.0; T(10): 0.0	S5; S8;	S22; S25		2.51	0.003	0	2	718.8	1437	61.03	12096
TSSAFVGKtPEAsPEPK	PSMD1	5707	26S proteasome non-ATPase regulatory subunit 1 isoform 2	T9(Phospho) S13(Phospho)	T(1): 2.9; S(2): 2.9; S(3): 0.1; T(9): 94.1; S(13): 100.0	T9; S13;	T311; S315	35		0	1	2	946.9	1893	40.75	7731
TSSAFVGKtPEAsPEPK	PSMD1	5707	26S proteasome non-ATPase regulatory subunit 1 isoform 2	T9(Phospho) S13(Phospho)	T(1): 0.0; S(2): 0.0; S(3): 0.0; T(9): 100.0; S(13): 100.0	T9; S13;	T311; S315	25		0	1	3	631.6	1893	40.84	7750
TSSAFVGKtPEAsPEPK	PSMD1	5707	26S proteasome non-ATPase regulatory subunit 1 isoform 2	T9(Phospho) S13(Phospho)	T(1): 0.0; S(2): 0.0; S(3): 0.0; T(9): 100.0; S(13): 100.0	T9; S13;	T311; S315		3.59	0	1	3	631.6	1893	40.84	7750
TSSAFVGKtPEAsPEPK	PSMD1	5707	26S proteasome non-ATPase regulatory subunit 1 isoform 2	T9(Phospho) S13(Phospho)	T(1): 2.9; S(2): 2.9; S(3): 0.1; T(9): 94.1; S(13): 100.0	T9; S13;	T311; S315		2.95	0	1	2	946.9	1893	40.75	7731
APVQPQQsPAAAPGGTDEKPSGK	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	45		0	0	3	766.7	2298	26.12	4633
DKAPVQPQQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S10(Phospho)	S(10): 100.0; T(18): 0.0; S(23): 0.0	S10;	S16	38		0	1	4	636.1	2541	25.47	4492
DKAPVQPQQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S10(Phospho)	S(10): 100.0; T(18): 0.0; S(23): 0.0	S10;	S16	28		0	1	3	847.7	2541	25.25	4446

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#
DKAPVQPQQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S10(Phospho)	S(10): 100.0; T(18): 0.0; S(23): 0.0	S10;	S16		6.66	0	1	4	636.1	2541	25.47	4492
APVQPQQsPAAAPGGTDEKPSGK	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		5.88	0	0	3	766.7	2298	26.12	4633
DKAPVQPQQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S10(Phospho)	S(10): 100.0; T(18): 0.0; S(23): 0.0	S10;	S16		4.96	0	1	3	847.7	2541	25.25	4446
APVQPQQsPAAAPGGTDEKPSGK	PSMD2	5708	26S proteasome non-ATPase regulatory subunit 2 isoform 1	S8(Phospho)	S(8): 95.1; T(16): 4.7; S(21): 0.3	S8;	S16		2.1	0.001	0	2	1150	2298	26.25	4660
ELKTDsPNQAR	PTBP1	5725	polypyrimidine tract-binding protein 1 isoform c	S7(Phospho)	T(4): 0.0; S(6): 0.0; S(7): 100.0	S7;	S141	47		0	1	2	713.3	1426	14.45	2154
ELKTDsPNQAR	PTBP1	5725	polypyrimidine tract-binding protein 1 isoform c	S7(Phospho)	T(4): 0.0; S(6): 0.0; S(7): 100.0	S7;	S141		3.5	0	1	2	713.3	1426	14.45	2154
GSEDSPPKHAGNNESSHSSR	PTDSS1	9791	phosphatidylserine synthase 1 isoform 2	S5(Phospho)	S(2): 0.1; S(5): 99.9; S(15): 0.0; S(17): 0.0; S(18): 0.0	S5;	S296	34		0	1	3	691.6	2073	12.37	1693
GSEDSPPKHAGNNESSHSSR	PTDSS1	9791	phosphatidylserine synthase 1 isoform 2	S5(Phospho)	S(2): 0.1; S(5): 99.9; S(15): 0.0; S(17): 0.0; S(18): 0.0	S5;	S296		5.87	0	1	3	691.6	2073	12.37	1693
DAGGPRPEsPVPAGR	PTDSS2	81490	phosphatidylserine synthase 2	S9(Phospho)	S(9): 100.0	S9;	S16	16		0	0	2	771.9	1543	27.24	4880
DAGGPRPEsPVPAGR	PTDSS2	81490	phosphatidylserine synthase 2	S9(Phospho)	S(9): 100.0	S9;	S16		2.94	0	0	2	771.9	1543	27.24	4880
DWEDDsDEDMSNFDR	PTGES3	10728	prostaglandin E synthase 3 isoform d	S6(Phospho)	S(6): 100.0; S(11): 0.0	S6;	S80	20		0	0	2	978.3	1956	69.46	14050
DWEDDsDEDMSNFDR	PTGES3	10728	prostaglandin E synthase 3 isoform d	M10(Oxidation) S6(Phospho)	S(6): 100.0; S(11): 0.0	S6;	S80	20		0	0	2	986.3	1972	57.05	11248
DWEDDsDEDMSNFDR	PTGES3	10728	prostaglandin E synthase 3 isoform d	S6(Phospho)	S(6): 100.0; S(11): 0.0	S6;	S80		2.48	0	0	2	978.3	1956	69.46	14050
DWEDDsDEDMSNFDR	PTGES3	10728	prostaglandin E synthase 3 isoform d	M10(Oxidation) S6(Phospho)	S(6): 100.0; S(11): 0.0	S6;	S80		2.2	0	0	2	986.3	1972	57.05	11248
YVGSsPDLVTR	PTPN14	5784	tyrosine-protein phosphatase non-receptor type 14	S5(Phospho) S6(Phospho)	Y(1): 0.0; S(3): 0.0; S(5): 100.0; S(6): 100.0; T(11): 0.0	S5; S6;	S593; S594	53		0	0	2	720.8	1441	56.7	11162
YVGSsPDLVTR	PTPN14	5784	tyrosine-protein phosphatase non-receptor type 14	S5(Phospho) S6(Phospho)	Y(1): 0.0; S(3): 0.0; S(5): 100.0; S(6): 100.0; T(11): 0.0	S5; S6;	S593; S594		2.56	0	0	2	720.8	1441	56.7	11162
GSLAPQDsDSEVSQNR	PTPN3	5774	tyrosine-protein phosphatase non-receptor type 3 isoform 6	S8(Phospho)	S(2): 0.0; S(8): 100.0; S(10): 0.0; S(13): 0.0	S8;	S93	45		0	0	2	885.4	1770	33.89	6269
GSLAPQDsDSEVSQNR	PTPN3	5774	tyrosine-protein phosphatase non-receptor type 3 isoform 6	S8(Phospho)	S(2): 0.0; S(8): 100.0; S(10): 0.0; S(13): 0.0	S8;	S93		2.74	0	0	2	885.4	1770	33.89	6269
TPGsRQAsPTEVVER	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho) S8(Phospho)	T(1): 3.7; S(4): 96.5; S(8): 99.9; T(10): 0.0	S4; S8;	S122; S126	40		0	1	3	591.9	1774	38.28	7205
GKAsPFEEDQNR	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho)	S(4): 100.0	S4;	S80	31		0	1	2	729.3	1458	22.04	3766
TPGsRQAsPTEVVER	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho) S8(Phospho)	T(1): 3.7; S(4): 96.5; S(8): 99.9; T(10): 0.0	S4; S8;	S122; S126		3.92	0	1	3	591.9	1774	38.28	7205
GKAsPFEEDQNR	PUM2	23369	pumilio homolog 2 isoform 4	S4(Phospho)	S(4): 100.0	S4;	S80		3.61	0	1	2	729.3	1458	22.04	3766
RGGGSGGGEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S304	54		0	1	2	966.3	1932	23.06	3987
GGGSGGGEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S4(Phospho)	S(4): 99.9; S(10): 0.1	S4;	S298	32		0	0	2	888.3	1776	32.14	5907
RGGGSGGGEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S11(Phospho)	S(5): 0.0; S(11): 100.0	S11;	S304		4.08	0.001	1	2	966.3	1932	23.06	3987
GGGSGGGEsEGEEVD	PURB	5814	transcriptional activator protein Pur-beta	S4(Phospho)	S(4): 99.9; S(10): 0.1	S4;	S298		3.2	0.008	0	2	888.3	1776	32.14	5907
VSPLEGsEGDGDtD	PUS1	80324	tRNA pseudouridine synthase A, mitochondrial isoform 2	S8(Phospho) T14(Phospho)	S(3): 0.0; S(8): 100.0; T(14): 100.0	S8; T14;	S392; T398	34		0	0	2	817.8	1635	84.58	16960
VSPLEGsEGDGDtD	PUS1	80324	tRNA pseudouridine synthase A, mitochondrial isoform 2	S8(Phospho) T14(Phospho)	S(3): 0.0; S(8): 100.0; T(14): 100.0	S8; T14;	S392; T398		3.61	0.003	0	2	817.8	1635	84.58	16960

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#
KAGPLGGsSYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S8(Phospho)	S(8): 97.6; S(9): 51.2; Y(10): 51.2	S8;	S434	30		0	1	3	900.3	2699	50.08	9720
AGPLGGsSYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S7(Phospho)	S(7): 97.2; S(8): 51.4; Y(9): 51.4	S7;	S434	16		0	0	3	857.6	2571	62.73	12486
AGPLGGsYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S7(Phospho) S8(Phospho)	S(7): 99.7; S(8): 95.0; Y(9): 5.3	S7; S8;	S434; S435	14		0	0	2	1286	2571	62.55	12439
AGPLGGsSYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S7(Phospho)	S(7): 97.2; S(8): 51.4; Y(9): 51.4	S7;	S434		4.09	0	0	3	857.6	2571	62.73	12486
KAGPLGGsSYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S8(Phospho)	S(8): 97.6; S(9): 51.2; Y(10): 51.2	S8;	S434		3.62	0	1	3	900.3	2699	50.08	9720
AGPLGGsYEEEEEEGGGGGER	PVRL1	5818	nectin-1 isoform 1 precursor	S7(Phospho) S8(Phospho)	S(7): 99.7; S(8): 95.0; Y(9): 5.3	S7; S8;	S434; S435		1.91	0.001	0	2	1286	2571	62.55	12439
EKLQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S10(Phospho)	S(10): 99.6; T(15): 0.1; S(17): 0.1; S(19): 0.1; S(25): 0.0	S10;	S50	66		0	1	3	973.7	2919	35.38	6598
EKLQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S10(Phospho) S17(Phospho)	S(10): 100.0; T(15): 0.0; S(17): 99.8; S(19): 0.2; S(25): 0.0	S10; S17;	S50; S57	63		0	1	3	1000	2999	39.12	7383
LQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho)	S(8): 100.0; T(13): 0.0; S(15): 0.0; S(17): 0.0; S(23): 0.0	S8;	S50	46		0	0	3	888	2662	38.99	7355
LQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho)	S(8): 96.8; T(13): 3.1; S(15): 0.1; S(17): 0.0; S(23): 0.0	S8;	S50	46		0	0	2	1332	2662	39.08	7376
LQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho) S15(Phospho)	S(8): 100.0; T(13): 0.0; S(15): 100.0; S(17): 0.0; S(23): 0.0	S8; S15;	S50; S57	40		0	0	3	914.7	2742	46.13	8894
EKLQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	M23(Oxidation) S10(Phospho)	S(10): 99.8; T(15): 0.1; S(17): 0.0; S(19): 0.0; S(25): 0.0	S10;	S50	26		0	1	3	979.1	2935	27.66	4972
EKLQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	M23(Oxidation) S10(Phospho) S17(Phospho)	S(10): 99.8; T(15): 0.2; S(17): 100.0; S(19): 0.0; S(25): 0.0	S10; S17;	S50; S57	20		0	1	3	1006	3015	31.07	5684
EKLQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S10(Phospho)	S(10): 99.6; T(15): 0.1; S(17): 0.1; S(19): 0.1; S(25): 0.0	S10;	S50		6.3	0	1	3	973.7	2919	35.38	6598
EKLQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S10(Phospho) S17(Phospho)	S(10): 100.0; T(15): 0.0; S(17): 99.8; S(19): 0.2; S(25): 0.0	S10; S17;	S50; S57		5.73	0	1	3	1000	2999	39.12	7383
EKLQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	M23(Oxidation) S10(Phospho) S17(Phospho)	S(10): 99.8; T(15): 0.2; S(17): 100.0; S(19): 0.0; S(25): 0.0	S10; S17;	S50; S57		5.72	0	1	3	1006	3015	31.07	5684
LQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho)	S(8): 100.0; T(13): 0.0; S(15): 0.0; S(17): 0.0; S(23): 0.0	S8;	S50		5	0	0	3	888	2662	38.99	7355
LQEEGGGsDEEETGsPSDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho) S15(Phospho)	S(8): 100.0; T(13): 0.0; S(15): 100.0; S(17): 0.0; S(23): 0.0	S8; S15;	S50; S57		4.38	0	0	3	914.7	2742	46.13	8894
EKLQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	M23(Oxidation) S10(Phospho)	S(10): 99.8; T(15): 0.1; S(17): 0.0; S(19): 0.0; S(25): 0.0	S10;	S50		4.21	0	1	3	979.1	2935	27.66	4972
LQEEGGGsDEEETGSPSEDGMQSAR	PWP1	11137	periodic tryptophan protein 1 homolog	S8(Phospho)	S(8): 96.8; T(13): 3.1; S(15): 0.1; S(17): 0.0; S(23): 0.0	S8;	S50		2.8	0	0	2	1332	2662	39.08	7376
sPEAVGPELEAEK	PWWP2A	114825	PWWP domain-containing protein 2A isoform c	S1(Phospho)	S(1): 100.0	S1;	S81	38		0	0	2	782.8	1565	51.38	9994

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#
sPEAVGPELEAEK	PWWP2A	114825	PWWP domain-containing protein 2A isoform c	S1(Phospho)	S(1): 100.0	S1;	S81		3.12	0	0	2	782.8	1565	51.38	9994
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	40		0	0	2	922.9	1845	30.67	5602
sSPGGQDEGGFMAQGK	PXN	5829	paxillin isoform 2	S1(Phospho)	S(1): 97.7; S(2): 2.3	S1;	S302	28		0	0	2	816.8	1633	41.57	7902
sSPGGQDEGGFMAQGK	PXN	5829	paxillin isoform 2	S1(Phospho)	S(1): 97.7; S(2): 2.3	S1;	S302		3.13	0	0	2	816.8	1633	41.57	7902
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		2.98	0	0	2	922.9	1845	30.67	5602
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): 99.9; S(16): 0.1	S13;	S106		2.62	0	0	2	922.9	1845	31.2	5713
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): 99.9; S(16): 0.1	S13;	S106	16		0.001	0	2	922.9	1845	31.2	5713
GQDtVAIEGFTDEEDTsGGEGQYR	QSER1	79832	glutamine and serine-rich protein 1	T4(Phospho) S18(Phospho)	T(4): 100.0; T(11): 0.0; T(16): 0.3; S(18): 99.7; Y(24): 0.0	T4; S18;	T1334; S1348	39		0	0	3	950.7	2850	79.89	16094
NLEHLSFsDEDDPGYSQDAYK	QSER1	79832	glutamine and serine-rich protein 1	S9(Phospho) S10(Phospho)	S(6): 11.3; S(7): 11.3; S(9): 88.7; S(10): 88.7; Y(17): 0.0; S(18): 0.0; Y(22): 0.0	S9; S10;	S1230; S1231	32		0	0	3	922	2764	68.08	13765
GQDtVAIEGFTDEEDTsGGEGQYR	QSER1	79832	glutamine and serine-rich protein 1	T4(Phospho) S18(Phospho)	T(4): 100.0; T(11): 0.0; T(16): 0.3; S(18): 99.7; Y(24): 0.0	T4; S18;	T1334; S1348		3.76	0	0	3	950.7	2850	79.89	16094
NLEHLSFsDEDDPGYSQDAYK	QSER1	79832	glutamine and serine-rich protein 1	S9(Phospho) S10(Phospho)	S(6): 11.3; S(7): 11.3; S(9): 88.7; S(10): 88.7; Y(17): 0.0; S(18): 0.0; Y(22): 0.0	S9; S10;	S1230; S1231		3.61	0	0	3	922	2764	68.08	13765
GQDtVAIEGFTDEEDTsGGEGQYR	QSER1	79832	glutamine and serine-rich protein 1	T4(Phospho) S18(Phospho)	T(4): 99.2; T(11): 5.9; T(16): 5.9; S(18): 88.9; Y(24): 0.0	T4; S18;	T1334; S1348	11		0.002	0	2	1426	2850	79.95	16106
GQDtVAIEGFTDEEDTsGGEGQYR	QSER1	79832	glutamine and serine-rich protein 1	T4(Phospho) S18(Phospho)	T(4): 99.2; T(11): 5.9; T(16): 5.9; S(18): 88.9; Y(24): 0.0	T4; S18;	T1334; S1348		2.22	0.003	0	2	1426	2850	79.95	16106
DNLLDYSADQGDsSEGGTLAR	QSOX2	169714	sulfhydryl oxidase 2 precursor	S14(Phospho)	T(6): 0.0; Y(7): 0.0; S(8): 0.0; S(14): 97.1; S(15): 2.9; T(19): 0.0	S14;	S578	45		0	0	3	789	2365	73.37	14837
DNLLDYSADQGDsSEGGTLAR	QSOX2	169714	sulfhydryl oxidase 2 precursor	S14(Phospho)	T(6): 0.0; Y(7): 0.0; S(8): 0.0; S(14): 96.6; S(15): 3.4; T(19): 0.0	S14;	S578	44		0	0	2	1183	2365	73.28	14820
DNLLDYSADQGDsSEGGTLAR	QSOX2	169714	sulfhydryl oxidase 2 precursor	S14(Phospho)	T(6): 0.0; Y(7): 0.0; S(8): 0.0; S(14): 97.1; S(15): 2.9; T(19): 0.0	S14;	S578		4.01	0	0	3	789	2365	73.37	14837
DNLLDYSADQGDsSEGGTLAR	QSOX2	169714	sulfhydryl oxidase 2 precursor	S14(Phospho)	T(6): 0.0; Y(7): 0.0; S(8): 0.0; S(14): 96.6; S(15): 3.4; T(19): 0.0	S14;	S578		3.34	0	0	2	1183	2365	73.28	14820
GEIKDsPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S13(Phospho)	S(6): 2.6; S(7): 97.4; S(9): 2.6; S(10): 0.1; S(11): 2.6; S(13): 94.8	S7; S13;	S339; S345	33		0	1	2	831.8	1663	20.16	3371
NKDSGSDTASAIHPTTPSVDSDDSEVVK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S22(Phospho)	S(4): 0.0; S(6): 0.0; T(8): 0.0; S(10): 0.0; S(15): 0.0; T(16): 0.0; T(17): 0.0; S(19): 0.0; S(22): 100.0; S(26): 0.0	S22;	S202	29		0	1	3	1001	3002	62.9	12530
GEIKDSSPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S9(Phospho)	S(6): 50.0; S(7): 50.0; S(9): 99.8; S(10): 0.0; S(11): 0.1; S(13): 0.0	S9;	S341	28		0	1	2	831.8	1663	19.62	3257

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#
DSGSDTASAIIPSTTPSVDSDESIVVK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S20(Phospho)	S(2): 0.0; S(4): 0.0; T(6): 0.0; S(8): 0.0; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(17): 0.0; S(20): 99.9; S(24): 0.1	S20;	S202	28		0	0	3	920.7	2760	77.61	15657
NKDSGSDTASAIIPSTTPSVDSDESIVVK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S22(Phospho)	S(4): 0.0; S(6): 0.0; T(8): 0.0; S(10): 0.0; S(15): 0.0; T(16): 0.0; T(17): 0.0; S(19): 0.0; S(22): 100.0; S(26): 0.0	S22;	S202		7.23	0	1	3	1001	3002	62.9	12530
DSGSDTASAIIPSTTPSVDSDESIVVK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S20(Phospho)	S(2): 0.0; S(4): 0.0; T(6): 0.0; S(8): 0.0; S(13): 0.0; T(14): 0.0; T(15): 0.0; S(17): 0.0; S(20): 99.9; S(24): 0.1	S20;	S202		6.13	0	0	3	920.7	2760	77.61	15657
GEIKDSsPSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S13(Phospho)	S(6): 2.6; S(7): 97.4; S(9): 2.6; S(10): 0.1; S(11): 2.6; S(13): 94.8	S7; S13;	S339; S345		4.09	0	1	2	831.8	1663	20.16	3371
GEIKDSSsSSSPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S9(Phospho)	S(6): 50.0; S(7): 50.0; S(9): 99.8; S(10): 0.0; S(11): 0.1; S(13): 0.0	S9;	S341		3.95	0	1	2	831.8	1663	19.62	3257
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): 97.3; S(10): 2.7; S(11): 5.5; S(13): 94.5	S7; S9; S13;	S339; S341; S345		3.41	0.001	1	2	871.8	1743	24.68	4323
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): 97.3; S(10): 2.7; S(11): 5.5; S(13): 94.5	S7; S9; S13;	S339; S341; S345	22		0.002	1	2	871.8	1743	24.68	4323
GEIKDSsPSSsPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S11(Phospho) S13(Phospho)	S(6): 0.0; S(7): 97.1; S(9): 5.5; S(10): 0.2; S(11): 97.1; S(13): 100.0	S7; S11; S13;	S339; S343; S345	21		0.003	1	2	871.8	1743	24.16	4216
GEIKDSsPSSsPsPK	RAB11FIP1	80223	rab11 family-interacting protein 1 isoform 1	S7(Phospho) S11(Phospho) S13(Phospho)	S(6): 0.0; S(7): 97.1; S(9): 5.5; S(10): 0.2; S(11): 97.1; S(13): 100.0	S7; S11; S13;	S339; S343; S345		3.95	0.003	1	2	871.8	1743	24.16	4216
KLEGNSPQGsNQGVK	RAB8A	4218	ras-related protein Rab-8A	S10(Phospho)	S(6): 0.0; S(10): 100.0	S10;	S185	20		0.001	1	2	811.9	1623	16.05	2493
KLEGNSPQGsNQGVK	RAB8A	4218	ras-related protein Rab-8A	S10(Phospho)	S(6): 0.0; S(10): 100.0	S10;	S185		3.01	0.001	1	2	811.9	1623	16.05	2493
AQsTDSLTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S3(Phospho)	S(3): 97.0; T(4): 2.9; S(6): 0.1; T(9): 0.0; S(10): 0.0; S(12): 0.0; S(15): 0.0	S3;	S364	45		0	0	2	823.9	1647	36.25	6783
RAQsTDsLGTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S4(Phospho) S7(Phospho)	S(4): 97.2; T(5): 2.8; S(7): 100.0; T(10): 0.0; S(11): 0.0; S(13): 0.0; S(16): 0.0	S4; S7;	S364; S367	39		0	1	2	941.9	1883	33.14	6114
AQSTDsLGTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S6(Phospho)	S(3): 50.0; T(4): 50.0; S(6): 100.0; T(9): 0.0; S(10): 0.0; S(12): 0.0; S(15): 0.0	S6;	S367	32		0	0	2	863.9	1727	45.32	8720
RAQsTDsLGTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S4(Phospho) S7(Phospho)	S(4): 97.2; T(5): 2.8; S(7): 100.0; T(10): 0.0; S(11): 0.0; S(13): 0.0; S(16): 0.0	S4; S7;	S364; S367		4.01	0	1	2	941.9	1883	33.14	6114
AQsTDSLTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S3(Phospho)	S(3): 97.0; T(4): 2.9; S(6): 0.1; T(9): 0.0; S(10): 0.0; S(12): 0.0; S(15): 0.0	S3;	S364		3.57	0	0	2	823.9	1647	36.25	6783
AQSTDsLGTSGSLQSK	RABEP1	9135	rab GTPase-binding effector protein 1 isoform 3	S6(Phospho)	S(3): 50.0; T(4): 50.0; S(6): 100.0; T(9): 0.0; S(10): 0.0; S(12): 0.0; S(15): 0.0	S6;	S367		3.16	0	0	2	863.9	1727	45.32	8720

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#
EsDKEEPVPTTSGGGPMSPQDDEAEES DNELSSGTGDVSK	RABGAP1L	9910	rab GTPase-activating protein 1-like isoform A	S2(Phospho)	S(2): 99.0; T(9): 0.3; T(11): 0.3; S(12): 0.3; S(18): 0.0; S(28): 0.0; S(33): 0.0; S(34): 0.0; T(36): 0.0; S(40): 0.0	S2;	S464	17		0	1	4	1077	4304	54.8	10759
EsDKEEPVPTTSGGGPMSPQDDEAEES DNELSSGTGDVSK	RABGAP1L	9910	rab GTPase-activating protein 1-like isoform A	S2(Phospho)	S(2): 99.0; T(9): 0.3; T(11): 0.3; S(12): 0.3; S(18): 0.0; S(28): 0.0; S(33): 0.0; S(34): 0.0; T(36): 0.0; S(40): 0.0	S2;	S464		3.44	0	1	4	1077	4304	54.8	10759
RADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S12(Phospho) T15(Phospho)	S(12): 100.0; T(15): 100.0	S12; T15;	S596; T599	40		0	2	4	830.8	3320	57.47	11339
RADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S12(Phospho) T15(Phospho)	S(12): 100.0; T(15): 100.0	S12; T15;	S596; T599	39		0	2	3	1107	3320	57.24	11291
ADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S11(Phospho) T14(Phospho)	S(11): 100.0; T(14): 100.0	S11; T14;	S596; T599	34		0	1	3	1055	3164	64.53	12946
GPAPAPQQCSEPEtK	RABL6	55684	rab-like protein 6 isoform 1	C9(Carbamidomethyl) T14(Phospho)	S(10): 2.0; T(14): 98.0	T14;	T496	17		0	0	2	838.9	1677	25.39	4475
RADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S12(Phospho) T15(Phospho)	S(12): 100.0; T(15): 100.0	S12; T15;	S596; T599		5.71	0	2	4	830.8	3320	57.47	11339
ADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S11(Phospho) T14(Phospho)	S(11): 100.0; T(14): 100.0	S11; T14;	S596; T599		4.52	0	1	3	1055	3164	64.53	12946
RADDFPVRDDPsDvtDEDEGPAEPPPPK	RABL6	55684	rab-like protein 6 isoform 1	S12(Phospho) T15(Phospho)	S(12): 100.0; T(15): 100.0	S12; T15;	S596; T599		4.38	0	2	3	1107	3320	57.24	11291
GPAPAPQQCSEPEtK	RABL6	55684	rab-like protein 6 isoform 1	C9(Carbamidomethyl) T14(Phospho)	S(10): 2.0; T(14): 98.0	T14;	T496		2.82	0	0	2	838.9	1677	25.39	4475
SKFsPQKEAsPAAK	RAD18	56852	E3 ubiquitin-protein ligase RAD18	S4(Phospho) S10(Phospho)	S(1): 0.0; S(4): 100.0; S(10): 100.0	S4; S10;	S158; S164		4.47	0.001	2	3	545.9	1636	22.07	3774
SKFsPQKEAsPAAK	RAD18	56852	E3 ubiquitin-protein ligase RAD18	S4(Phospho) S10(Phospho)	S(1): 0.0; S(4): 100.0; S(10): 100.0	S4; S10;	S158; S164	12		0.002	2	3	545.9	1636	22.07	3774
EDKsPSEESAPTTSPESVSGVSPSSGSSG R	RAD23A	5886	UV excision repair protein RAD23 homolog A isoform 3	S4(Phospho)	S(4): 99.4; S(6): 0.0; S(9): 0.0; T(12): 0.2; T(13): 0.2; S(14): 0.2; S(17): 0.0; S(19): 0.0; S(21): 0.0; S(24): 0.0; S(25): 0.0; S(27): 0.0; S(28): 0.0	S4;	S123	33		0	1	3	1001	3002	39.6	7484
EDKsPSEESAPTTSPESVSGVSPSSGSSG R	RAD23A	5886	UV excision repair protein RAD23 homolog A isoform 3	S4(Phospho)	S(4): 99.4; S(6): 0.0; S(9): 0.0; T(12): 0.2; T(13): 0.2; S(14): 0.2; S(17): 0.0; S(19): 0.0; S(21): 0.0; S(24): 0.0; S(25): 0.0; S(27): 0.0; S(28): 0.0	S4;	S123		5.17	0	1	3	1001	3002	39.6	7484
QEKPAEKPAEtPVATSPATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 99.8; T(15): 0.0; S(16): 0.2; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83	35		0	0	3	1009	3025	28.14	5073
QEKPAEKPAEtPVATSPATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 100.0; T(15): 0.0; S(16): 0.0; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83	29		0	0	4	757.1	3025	28.35	5119
QEKPAEKPAEtPVATSPATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 91.2; T(15): 4.4; S(16): 4.4; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83	26		0	0	3	1009	3025	28.69	5190

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#
QEKPAAEKPAETPVATSTPTATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 99.8; T(15): 0.0; S(16): 0.2; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83		5.52	0	0	3	1009	3025	28.14	5073
QEKPAAEKPAETPVATSTPTATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 100.0; T(15): 0.0; S(16): 0.0; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83		5.05	0	0	4	757.1	3025	28.35	5119
QEKPAAEKPAETPVATSTPTATDSTSGDSSR	RAD23B	5887	UV excision repair protein RAD23 homolog B isoform 3	T11(Phospho)	T(11): 91.2; T(15): 4.4; S(16): 4.4; T(18): 0.0; T(20): 0.0; S(22): 0.0; T(23): 0.0; S(24): 0.0; S(27): 0.0; S(28): 0.0	T11;	T83		4.49	0	0	3	1009	3025	28.69	5190
TPSsEEISPTK	RALBP1	10928	ralA-binding protein 1	S4(Phospho)	T(1): 0.0; S(3): 0.9; S(4): 99.1; S(8): 0.0; T(10): 0.0	S4;	S30	61		0	0	2	628.3	1256	29.08	5270
RTEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho) S13(Phospho)	T(2): 0.0; Y(5): 0.0; S(12): 99.7; S(13): 100.0; S(19): 0.3; S(21): 0.0	S12; S13;	S92; S93	57		0	1	3	841	2521	49.84	9670
RTEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho) S13(Phospho)	T(2): 0.0; Y(5): 0.0; S(12): 99.7; S(13): 100.0; S(19): 0.3; S(21): 0.0	S12; S13;	S92; S93	47		0	1	3	841	2521	50.36	9779
TEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho)	T(1): 50.0; Y(4): 50.0; S(11): 5.1; S(12): 94.9; S(18): 0.0; S(20): 0.0	S12;	S93	24		0	0	2	1183	2365	61.42	12177
RTEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho) S13(Phospho)	T(2): 0.0; Y(5): 0.0; S(12): 99.7; S(13): 100.0; S(19): 0.3; S(21): 0.0	S12; S13;	S92; S93	4.32		0	1	3	841	2521	49.84	9670
RTEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho) S13(Phospho)	T(2): 0.0; Y(5): 0.0; S(12): 99.7; S(13): 100.0; S(19): 0.3; S(21): 0.0	S12; S13;	S92; S93	3.89		0	1	3	841	2521	50.36	9779
TPSsEEISPTK	RALBP1	10928	ralA-binding protein 1	S4(Phospho)	T(1): 0.0; S(3): 0.9; S(4): 99.1; S(8): 0.0; T(10): 0.0	S4;	S30		3.65	0	0	2	628.3	1256	29.08	5270
TEGYAAFQEDssGDEAESPSK	RALBP1	10928	ralA-binding protein 1	S12(Phospho)	T(1): 50.0; Y(4): 50.0; S(11): 5.1; S(12): 94.9; S(18): 0.0; S(20): 0.0	S12;	S93		3.03	0	0	2	1183	2365	61.42	12177
TPsEEIsPTKFPGLYR	RALBP1	10928	ralA-binding protein 1	S3(Phospho) S8(Phospho)	T(1): 0.0; S(3): 94.2; S(4): 5.8; S(8): 94.2; T(10): 5.8; Y(16): 0.0	S3; S8;	S29; S34	2.31	0.001	1	3	690.3	2069	75.65	15282	
SAASREDLVGPEVGAsPQSGR	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	S16(Phospho)	S(1): 50.0; S(4): 50.0; S(16): 100.0; S(19): 0.0	S16;	S308	47		0	1	3	744	2230	51.68	10056
sAASREDLVGPEVGAsPQSGRK	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	S1(Phospho) S16(Phospho)	S(1): 99.9; S(4): 0.1; S(16): 100.0; S(19): 0.0	S1; S16;	S293; S308	23		0	2	3	786.7	2358	40.92	7765
sAASREDLVGPEVGAsPQSGRK	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	S1(Phospho) S16(Phospho)	S(1): 99.9; S(4): 0.1; S(16): 100.0; S(19): 0.0	S1; S16;	S293; S308	6.12		0	2	3	786.7	2358	40.92	7765
SAASREDLVGPEVGAsPQSGR	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	S16(Phospho)	S(1): 50.0; S(4): 50.0; S(16): 100.0; S(19): 0.0	S16;	S308	5.68		0	1	3	744	2230	51.68	10056
SVAAEGALLPQTTPsPR	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	T12(Phospho) S15(Phospho)	S(1): 0.0; T(12): 100.0; S(15): 100.0	T12; S15;	T326; S329		3.07	0	0	2	925.9	1851	75.03	15169
SVAAEGALLPQTTPsPR	RALGPS2	55103	ras-specific guanine nucleotide-releasing factor RalGPS2 isoform 2	T12(Phospho) S15(Phospho)	S(1): 0.0; T(12): 100.0; S(15): 100.0	T12; S15;	T326; S329	19		0.002	0	2	925.9	1851	75.03	15169

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#
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S14(Phospho)	T(1): 0.0; T(12): 100.0; S(14): 100.0; S(21): 50.0; T(24): 50.0	T12; S14;	T270; S272	28		0	1	4	942.6	3767	66.76	13452
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S14(Phospho)	T(1): 0.0; T(12): 100.0; S(14): 100.0; S(21): 0.0; T(24): 0.0	T12; S14;	T270; S272	28		0	1	4	922.6	3687	60.89	12066
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S14(Phospho)	T(1): 0.0; T(12): 100.0; S(14): 100.0; S(21): 50.0; T(24): 50.0	T12; S14;	T270; S272	25		0	1	3	1256	3767	66.66	13430
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	S21(Phospho) T24(Phospho)	T(1): 0.0; T(12): 54.5; S(14): 54.5; S(21): 95.5; T(24): 95.5	S21; T24;	S279; T282	20		0	1	3	1256	3767	67.17	13543
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho)	T(1): 0.0; T(12): 99.8; S(14): 0.2; S(21): 0.0; T(24): 0.0	T12;	T270	19		0	1	4	902.6	3607	58.18	11483
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	S14(Phospho)	T(1): 0.0; T(12): 5.4; S(14): 88.8; S(21): 0.4; T(24): 5.4	S14;	S272	18		0	1	3	1203	3607	58.18	11484
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S14(Phospho)	T(1): 0.0; T(12): 100.0; S(14): 100.0; S(21): 0.0; T(24): 0.0	T12; S14;	T270; S272		7.68	0	1	4	922.6	3687	60.89	12066
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho)	T(1): 0.0; T(12): 99.8; S(14): 0.2; S(21): 0.0; T(24): 0.0	T12;	T270		5.95	0	1	4	902.6	3607	58.18	11483
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	S14(Phospho) S21(Phospho) T24(Phospho)	T(1): 0.0; T(12): 7.5; S(14): 92.5; S(21): 100.0; T(24): 100.0	S14; S21; T24;	S272; S279; T282	22		0.001	1	3	1256	3767	68.56	13867
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S14(Phospho)	T(1): 0.0; T(12): 100.0; S(14): 100.0; S(21): 0.0; T(24): 0.0	T12; S14;	T270; S272	19		0.001	1	3	1230	3687	61.19	12132
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	S14(Phospho)	T(1): 0.0; T(12): 5.4; S(14): 88.8; S(21): 0.4; T(24): 5.4	S14;	S272		3.56	0.001	1	3	1203	3607	58.18	11484
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho)	T(1): 0.0; T(12): 94.1; S(14): 6.1; S(21): 49.9; T(24): 49.9	T12;	T270		3.32	0.001	1	3	1230	3687	61.71	12240
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho)	T(1): 0.0; T(12): 94.1; S(14): 6.1; S(21): 49.9; T(24): 49.9	T12;	T270	15		0.003	1	3	1230	3687	61.71	12240
TRDDGDEEGLLTHSEEELEHSQDTDADD GALQ	RALY	22913	RNA-binding protein Raly isoform 2	T12(Phospho) S21(Phospho) T24(Phospho)	T(1): 0.0; T(12): 92.6; S(14): 7.4; S(21): 100.0; T(24): 100.0	T12; S21; T24;	T270; S279; T282	11		0.003	1	4	942.6	3767	68.9	13938
DSLItPHVsR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T5(Phospho) S9(Phospho)	S(2): 0.0; T(5): 100.0; S(9): 100.0	T5; S9;	T2450; S2454	47		0	0	2	642.8	1285	53.68	10507
TAQEKDSLItPHVsR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho) S14(Phospho)	T(1): 0.0; S(7): 0.0; T(10): 100.0; S(14): 100.0	T10; S14;	T2450; S2454	34		0	1	3	614.6	1842	38.54	7261
SALsPSKsPAK	RANBP2	5903	E3 SUMO-protein ligase RanBP2	S4(Phospho) S8(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 1.5; S(8): 98.5	S4; S8;	S2276; S2280	27		0	1	2	616.8	1233	21.52	3657
SYKYSPKtPPR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T8(Phospho)	S(1): 0.0; Y(2): 0.0; Y(4): 50.0; S(5): 50.0; T(8): 100.0	T8;	T799	26		0	2	2	742.3	1484	27	4823
NADSEIKHStPSPTR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho)	S(4): 0.0; S(9): 3.2; T(10): 96.8; S(12): 50.0; T(14): 50.0	T10;	T779	13		0	1	3	600.6	1800	18.28	2977
NADSEIKHStPSPTR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho)	S(4): 0.0; S(9): 2.9; T(10): 97.1; S(12): 50.0; T(14): 50.0	T10;	T779		5.23	0	1	3	600.6	1800	17.75	2867

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#
NADSEIKHStPSPTR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho)	S(4): 0.0; S(9): 3.2; T(10): 96.8; S(12): 50.0; T(14): 50.0	T10;	T779		5.12	0	1	3	600.6	1800	18.28	2977
SALsPSKsPAK	RANBP2	5903	E3 SUMO-protein ligase RanBP2	S4(Phospho) S8(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 1.5; S(8): 98.5	S4; S8;	S2276; S2280		4.05	0	1	2	616.8	1233	21.52	3657
SYKSPKtPPR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T8(Phospho)	S(1): 0.0; Y(2): 0.0; Y(4): 50.0; S(5): 50.0; T(8): 100.0	T8;	T799		3.32	0	2	2	742.3	1484	27	4823
SYKSPKtPPR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T8(Phospho)	S(1): 0.0; Y(2): 0.0; Y(4): 50.0; S(5): 50.0; T(8): 100.0	T8;	T799	27		0.001	2	3	495.2	1484	27.01	4824
SYKSPKtPPR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T8(Phospho)	S(1): 0.0; Y(2): 0.0; Y(4): 50.0; S(5): 50.0; T(8): 100.0	T8;	T799		4.63	0.001	2	3	495.2	1484	27.01	4824
NADSEIKHStPSPTR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho)	S(4): 0.1; S(9): 0.1; T(10): 99.8; S(12): 50.0; T(14): 50.0	T10;	T779	21		0.003	1	2	900.4	1800	17.92	2903
NADSEIKHStPSPTR	RANBP2	5903	E3 SUMO-protein ligase RanBP2	T10(Phospho)	S(4): 0.1; S(9): 0.1; T(10): 99.8; S(12): 50.0; T(14): 50.0	T10;	T779		2.93	0.005	1	2	900.4	1800	17.92	2903
sAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S13(Phospho)	S(1): 99.5; S(5): 5.2; S(6): 0.5; S(13): 94.8; Y(20): 0.0	S1; S13;	S28; S40	30		0	2	3	961.7	2883	31.97	5871
sAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho)	S(1): 99.8; S(5): 91.5; S(6): 4.3; S(13): 4.3; Y(20): 0.0	S1; S5;	S28; S32	26		0	2	4	721.5	2883	32.11	5899
sAGGSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 99.7; S(5): 94.6; S(6): 5.8; S(13): 100.0; Y(20): 0.0	S1; S5; S13;	S28; S32; S40	24		0	1	3	936.3	2807	49.55	9609
sAGGSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 93.7; S(6): 6.4; S(13): 99.5; Y(20): 0.5	S1; S5; S13;	S28; S32; S40	20		0	1	3	936.3	2807	50.09	9722
SAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S13(Phospho)	S(1): 0.3; S(5): 0.0; S(6): 0.0; S(13): 99.7; Y(20): 0.0	S13;	S40	15		0	2	3	935	2803	28.39	5126
sAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 95.1; S(6): 4.9; S(13): 0.0; Y(20): 0.0	S1; S5;	S28; S32	14		0	2	3	961.7	2883	32.72	6029
SAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S13(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 0.0; S(13): 100.0; Y(20): 0.0	S13;	S40	13		0	2	4	701.5	2803	28.52	5154
SAGGSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)Y20(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 0.0; S(13): 0.2; Y(20): 99.8	Y20;	Y47	10		0	1	3	883	2647	34.43	6383
SAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S13(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 0.0; S(13): 100.0; Y(20): 0.0	S13;	S40		6.68	0	2	4	701.5	2803	28.52	5154
SAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S13(Phospho)	S(1): 0.3; S(5): 0.0; S(6): 0.0; S(13): 99.7; Y(20): 0.0	S13;	S40		5.59	0	2	3	935	2803	28.39	5126

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#
sAGGsSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho)	S(1): 99.8; S(5): 91.5; S(6): 4.3; S(13): 4.3; Y(20): 0.0	S1; S5;	S28; S32		5.42	0	2	4	721.5	2883	32.11	5899
sAGGSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S13(Phospho)	S(1): 99.5; S(5): 5.2; S(6): 0.5; S(13): 94.8; Y(20): 0.0	S1; S13;	S28; S40		5.13	0	2	3	961.7	2883	31.97	5871
sAGGsSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 100.0; S(5): 93.7; S(6): 6.4; S(13): 99.5; Y(20): 0.5	S1; S5; S13;	S28; S32; S40		4.73	0	1	3	936.3	2807	50.09	9722
SAGGSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl) Y20(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 0.0; S(13): 0.2; Y(20): 99.8	Y20;	Y47		4.49	0	1	3	883	2647	34.43	6383
sAGGsSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho) S13(Phospho)	S(1): 99.7; S(5): 94.6; S(6): 5.8; S(13): 100.0; Y(20): 0.0	S1; S5; S13;	S28; S32; S40		4.45	0	1	3	936.3	2807	49.55	9609
sAGGSPEGGEDsDREDGNYCPPVK	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S13(Phospho)	S(1): 99.3; S(5): 0.4; S(6): 0.4; S(13): 99.6; Y(20): 0.4	S1; S13;	S28; S40		3.71	0	1	3	909.7	2727	40.48	7676
sAGGsSPEGGEDsDREDGNYCPPVKR	RANBP3	8498	ran-binding protein 3 isoform 4	C21(Carbamido methyl)S1(Phospho) S5(Phospho)	S(1): 100.0; S(5): 95.1; S(6): 4.9; S(13): 0.0; Y(20): 0.0	S1; S5;	S28; S32		3.2	0	2	3	961.7	2883	32.72	6029
sETSSNPSSPEICPNK	RAP1GAP2	23108	rap1 GTPase-activating protein 2 isoform 2	C13(Carbamido methyl)S1(Phospho) S9(Phospho)	S(1): 85.3; T(3): 5.2; S(4): 4.9; S(5): 4.9; S(8): 5.5; S(9): 94.2	S1; S9;	S590; S598	12	0.002	0	2	2	947.4	1894	40.57	7694
sETSSNPSSPEICPNK	RAP1GAP2	23108	rap1 GTPase-activating protein 2 isoform 2	C13(Carbamido methyl)S1(Phospho) S9(Phospho)	S(1): 85.3; T(3): 5.2; S(4): 4.9; S(5): 4.9; S(8): 5.5; S(9): 94.2	S1; S9;	S590; S598	1.78	0.005	0	2	2	947.4	1894	40.57	7694
LTGsQLsITQVASIK	RASAL2	9462	ras GTPase-activating protein nGAP isoform 1	S4(Phospho) S7(Phospho)	T(2): 0.0; S(4): 100.0; S(7): 99.9; T(9): 0.1; S(13): 0.0	S4; S7;	S736; S739	28		0	0	2	853.4	1706	88.63	17728
LTGsQLsITQVASIK	RASAL2	9462	ras GTPase-activating protein nGAP isoform 1	S4(Phospho) S7(Phospho)	T(2): 0.0; S(4): 100.0; S(7): 99.9; T(9): 0.1; S(13): 0.0	S4; S7;	S736; S739	2.22	0	0	2	2	853.4	1706	88.63	17728
ISEGLPtPTKMtPR	RB1	5925	retinoblastoma-associated protein	T7(Phospho) T12(Phospho)	S(2): 0.0; T(7): 97.8; T(9): 2.2; T(12): 100.0	T7; T12;	T821; T826	25		0	1	2	844.4	1688	55.95	10998
ISEGLPtPTKMtPR	RB1	5925	retinoblastoma-associated protein	T7(Phospho) T12(Phospho)	S(2): 0.0; T(7): 97.8; T(9): 2.2; T(12): 100.0	T7; T12;	T821; T826	3.8	0	1	2	2	844.4	1688	55.95	10998
sPYKFPSSPLR	RB1	5925	retinoblastoma-associated protein	S1(Phospho)	S(1): 97.9; Y(3): 2.1; S(7): 50.0; S(8): 50.0	S1;	S788	16		0.002	1	2	719.8	1439	60.64	12010
sPYKFPSSPLR	RB1	5925	retinoblastoma-associated protein	S1(Phospho)	S(1): 97.9; Y(3): 2.1; S(7): 50.0; S(8): 50.0	S1;	S788	2.68	0.002	1	2	2	719.8	1439	60.64	12010
ASVSQTS PQSASSPR	RB1CC1	9821	RB1-inducible coiled-coil protein 1 isoform 2	S7(Phospho)	S(2): 3.0; S(4): 0.0; T(6): 0.1; S(7): 96.8; S(10): 0.0; S(12): 0.0; S(13): 0.0	S7;	S647	54		0	0	2	785.4	1570	21.49	3652
ASVSQTS PQSASSPR	RB1CC1	9821	RB1-inducible coiled-coil protein 1 isoform 2	S7(Phospho)	S(2): 3.0; S(4): 0.0; T(6): 0.1; S(7): 96.8; S(10): 0.0; S(12): 0.0; S(13): 0.0	S7;	S647	3.11	0	0	2	2	785.4	1570	21.49	3652

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#
NQSHSPSPVSPSR	RBBP6	5930	E3 ubiquitin-protein ligase RBBP6 isoform 2	S6(Phospho)	S(3): 0.0; S(5): 0.0; S(6): 100.0; S(8): 0.0; S(10): 50.0; S(12): 50.0	S6;	S1661	37		0	0	2	765.3	1530	15.66	2410
NQSHSPSPVSPSR	RBBP6	5930	E3 ubiquitin-protein ligase RBBP6 isoform 2	S6(Phospho)	S(3): 0.0; S(5): 0.0; S(6): 100.0; S(8): 0.0; S(10): 50.0; S(12): 50.0	S6;	S1661		3.59	0	0	2	765.3	1530	15.66	2410
VTGTGESSSTLVDTSTSTGGSPVRK	RBBP6	5930	E3 ubiquitin-protein ligase RBBP6 isoform 2	S23(Phospho)	T(2): 0.0; T(4): 0.0; S(7): 0.0; S(8): 0.0; S(9): 0.0; T(10): 0.0; Y(14): 0.0; T(15): 0.0; S(16): 0.0; T(17): 0.0; S(18): 0.0; S(19): 0.0; T(20): 0.0; S(23): 100.0	S23;	S1243	12		0.001	1	3	914.4	2741	46.94	9065
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S10(Phospho) S12(Phospho)	Y(6): 0.0; S(7): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S658; S660	40		0	0	2	1058	2116	62	12301
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S10(Phospho) S12(Phospho)	Y(6): 0.0; S(7): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S658; S660	34		0	0	2	1058	2116	62.52	12429
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S7(Phospho) S10(Phospho) S12(Phospho)	Y(6): 0.5; S(7): 99.7; S(10): 99.7; S(12): 100.0	S7; S10; S12;	S655; S658; S660	10		0	0	2	1098	2196	76.1	15359
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S10(Phospho) S12(Phospho)	Y(6): 0.0; S(7): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S658; S660		3.07	0	0	2	1058	2116	62	12301
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S10(Phospho) S12(Phospho)	Y(6): 0.0; S(7): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S658; S660		2.9	0	0	2	1058	2116	62.52	12429
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	S7(Phospho) S10(Phospho) S12(Phospho)	Y(6): 0.5; S(7): 99.7; S(10): 99.7; S(12): 100.0	S7; S10; S12;	S655; S658; S660		2.38	0	0	2	1098	2196	76.1	15359
GLVAAYSGESDsEEEQER	RBM10	8241	RNA-binding protein 10 isoform 2	Y6(Phospho) S7(Phospho)	Y(6): 96.4; S(7): 96.4; S(10): 53.6; S(12): 53.6	Y6; S7;	Y654; S655		1.47	0.001	0	2	1098	2196	75.57	15265
GGsREYDTGGGSSSSR	RBM15	64783	putative RNA-binding protein 15 isoform 2	S3(Phospho)	S(3): 100.0; Y(6): 0.0; T(8): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0	S3;	S109	80		0	1	2	820.3	1640	13.11	1872
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	19		0	1	3	648.3	1943	25.13	4420
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	16		0	1	2	971.9	1943	24.76	4339
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	14		0	1	3	648.3	1943	24.59	4304
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		5.71	0	1	3	648.3	1943	25.13	4420
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		5.43	0	1	3	648.3	1943	24.59	4304
GGsREYDTGGGSSSSR	RBM15	64783	putative RNA-binding protein 15 isoform 2	S3(Phospho)	S(3): 100.0; Y(6): 0.0; T(8): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0	S3;	S109		4.01	0	1	2	820.3	1640	13.11	1872

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#
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		3.64	0	1	2	971.9	1943	24.76	4339
RPDPDsDEDEDYER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155	42		0	0	2	909.3	1818	24.68	4322
RPDPDsDEDEDYERER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155	30		0	1	3	701.6	2103	24.72	4329
RPDPDsDEDEDYERER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155	27		0	1	3	701.6	2103	24.21	4226
RPDPDsDEDEDYERER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155		4.72	0	1	3	701.6	2103	24.72	4329
RPDPDsDEDEDYERER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155		4.29	0	1	3	701.6	2103	24.21	4226
RPDPDsDEDEDYER	RBM17	84991	splicing factor 45	S6(Phospho)	S(6): 100.0; Y(12): 0.0	S6;	S155		3.84	0	0	2	909.3	1818	24.68	4322
LGASNsPGQPNSVK	RBM25	58517	RNA-binding protein 25	S6(Phospho)	S(4): 0.0; S(6): 100.0; S(12): 0.0	S6;	S677	72		0	0	2	718.3	1436	25.17	4428
LGASNsPGQPNSVK	RBM25	58517	RNA-binding protein 25	S6(Phospho)	S(4): 0.0; S(6): 100.0; S(12): 0.0	S6;	S677		3.48	0	0	2	718.3	1436	25.17	4428
LNHsPPQSSSR	RBM26	64062	RNA-binding protein 26 isoform 3	S4(Phospho)	S(4): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0	S4;	S127	24		0	0	2	645.3	1290	13.22	1894
LNHsPPQSSSR	RBM26	64062	RNA-binding protein 26 isoform 3	S4(Phospho)	S(4): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0	S4;	S127		2.76	0	0	2	645.3	1290	13.22	1894
DIKEEsDEEEEDDEESGR	RBM33	155435	RNA-binding protein 33	S6(Phospho)	S(6): 100.0; S(16): 0.0	S6;	S205	44		0	1	3	740.6	2220	25.27	4451
DIKEEsDEEEEDDEESGR	RBM33	155435	RNA-binding protein 33	S6(Phospho)	S(6): 100.0; S(16): 0.0	S6;	S205	26		0	1	2	1110	2220	25.13	4421
DIKEEsDEEEEDDEESGR	RBM33	155435	RNA-binding protein 33	S6(Phospho)	S(6): 100.0; S(16): 0.0	S6;	S205		4.05	0	1	3	740.6	2220	25.27	4451
DIKEEsDEEEEDDEESGR	RBM33	155435	RNA-binding protein 33	S6(Phospho)	S(6): 100.0; S(16): 0.0	S6;	S205		2.99	0	1	2	1110	2220	25.13	4421
SVQGENPDDGVRGsPPEDYR	RBM34	23029	RNA-binding protein 34 isoform 2	S15(Phospho)	S(1): 0.3; S(15): 99.7; Y(20): 0.0	S15;	S28		3.98	0	1	3	795	2383	38.13	7174
DKsPVREPIDNLTPEER	RBM39	9584	RNA-binding protein 39 isoform d	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S114	48		0	2	3	692.3	2075	45.73	8808
DKsPVREPIDNLTPEER	RBM39	9584	RNA-binding protein 39 isoform d	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S114	28		0	2	3	692.3	2075	45.21	8699
DKsPVREPIDNLTPEER	RBM39	9584	RNA-binding protein 39 isoform d	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S114		5.01	0	2	3	692.3	2075	45.73	8808
DKsPVREPIDNLTPEER	RBM39	9584	RNA-binding protein 39 isoform d	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S114		3.62	0	2	3	692.3	2075	45.21	8699
MREDYDsVEQDGDPEGPQR	RBM8A	9939	RNA-binding protein 8A	S7(Phospho)	Y(5): 0.1; S(7): 99.9	S7;	S56	48		0	1	3	768.3	2303	37.94	7135
GFGsEEGSR	RBM8A	9939	RNA-binding protein 8A	S4(Phospho)	S(4): 98.4; S(8): 1.6	S4;	S42	37		0	0	2	503.2	1005	23.17	4011
MREDYDsVEQDGDPEGPQR	RBM8A	9939	RNA-binding protein 8A	S7(Phospho)	Y(5): 0.1; S(7): 99.9	S7;	S56		3.94	0	1	3	768.3	2303	37.94	7135
GFGsEEGSR	RBM8A	9939	RNA-binding protein 8A	S4(Phospho)	S(4): 98.4; S(8): 1.6	S4;	S42		2.37	0	0	2	503.2	1005	23.17	4011
ADREVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S14(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 1.4; S(14): 98.6	S14;	S188	44		0	1	3	608.6	1824	18.63	3049
ADREVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S14(Phospho)	S(11): 0.0; S(12): 2.0; S(13): 2.0; S(14): 96.0	S14;	S188	36		0	1	2	912.4	1824	18.59	3042
ADREVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S14(Phospho)	S(11): 0.0; S(12): 0.0; S(13): 1.4; S(14): 98.6	S14;	S188		4.7	0	1	3	608.6	1824	18.63	3049
ADREVQAEQPSSSsPR	RBMX2	51634	RNA-binding motif protein, X-linked 2	S14(Phospho)	S(11): 0.0; S(12): 2.0; S(13): 2.0; S(14): 96.0	S14;	S188		2.67	0.006	1	2	912.4	1824	18.59	3042
DYGHsSSRDDYPSR	RBMXL1	494115	RNA binding motif protein, X-linked-like-1	S5(Phospho)	Y(2): 0.1; S(5): 94.6; S(6): 2.7; S(7): 2.7; Y(11): 0.0; S(13): 0.0	S5;	S249		2.83	0.003	1	3	574.6	1722	19.65	3265
EREeSEDELEeANGNNPIDIEVDQNK	RCOR1	23186	REST corepressor 1	S5(Phospho)	S(5): 100.0	S5;	S260	12		0.001	1	3	1032	3095	62.84	12515
EREeSEDELEeANGNNPIDIEVDQNK	RCOR1	23186	REST corepressor 1	S5(Phospho)	S(5): 100.0	S5;	S260		2.8	0.003	1	3	1032	3095	62.84	12515
YTGEEDGAGGHsPAPPQTEELR	RECQL5	9400	ATP-dependent DNA helicase Q5 isoform 1	C21(Carbamidomethyl) S12(Phospho)	Y(1): 0.0; T(2): 0.0; S(12): 99.9; T(18): 0.1	S12;	S815	30		0	0	3	846.7	2538	38.6	7273
YTGEEDGAGGHsPAPPQTEELR	RECQL5	9400	ATP-dependent DNA helicase Q5 isoform 1	C21(Carbamidomethyl) S12(Phospho)	Y(1): 0.0; T(2): 0.0; S(12): 99.9; T(18): 0.1	S12;	S815		4.61	0	0	3	846.7	2538	38.6	7273

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#
sHSGTSPDNTAPPPPPRPQPSHSR	REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform b	S1(Phospho) T5(Phospho) S24(Phospho)	S(1): 95.7; S(3): 8.7; T(5): 95.4; S(6): 0.2; T(10): 0.0; S(22): 0.2; S(24): 99.8	S1; T5; S24;	S508; T512; S531	19		0	0	3	947.7	2841	29.36	5330
sHSGTSPDNTAPPPPPRPQPSHSR	REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform b	S1(Phospho) T5(Phospho) S24(Phospho)	S(1): 95.7; S(3): 8.7; T(5): 95.4; S(6): 0.2; T(10): 0.0; S(22): 0.2; S(24): 99.8	S1; T5; S24;	S508; T512; S531		5.54	0	0	3	947.7	2841	29.36	5330
TSADAQEPASPVVSPQQSPPTSPHTWR	REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform b	S14(Phospho)	T(1): 49.9; S(2): 49.9; S(10): 6.7; S(14): 93.5; S(18): 0.0; T(21): 48.3; S(22): 48.3; T(25): 3.3	S14;	S166		4.65	0	0	3	1033	3098	66.17	13317
TSADAQEPASPVVSPQQSPPTSPHTWR	REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform b	S14(Phospho) T21(Phospho)	T(1): 50.0; S(2): 50.0; S(10): 0.0; S(14): 93.9; S(18): 6.1; T(21): 93.9; S(22): 6.1; T(25): 0.0	S14; T21;	S166; T173		4.58	0	0	3	1033	3098	65.66	13198
SHsGTSPDNTAPPPPPRPQPSHSR	REPS1	85021	ralBP1-associated Eps domain-containing protein 1 isoform b	S3(Phospho)	S(1): 4.7; S(3): 95.0; T(5): 0.2; S(6): 0.0; T(10): 0.0; S(22): 50.0; S(24): 50.0	S3;	S510		4.04	0.001	0	3	921.1	2761	25.77	4555
NyAESDHSDEEDNDNNSATAEESTKK	RERE	473	arginine-glutamic acid dipeptide repeats protein isoform a	Y2(Phospho)	Y(2): 97.7; S(5): 51.1; S(8): 51.1; S(17): 0.0; T(19): 0.0; S(23): 0.0; T(24): 0.0	Y2;	Y50	30		0	1	3	1021	3060	22.57	3880
NyAESDHSDEEDNDNNSATAEESTKK	RERE	473	arginine-glutamic acid dipeptide repeats protein isoform a	Y2(Phospho)	Y(2): 97.7; S(5): 51.1; S(8): 51.1; S(17): 0.0; T(19): 0.0; S(23): 0.0; T(24): 0.0	Y2;	Y50		4.08	0	1	3	1021	3060	22.57	3880
EEALDDAEPEsPPPPRsPsPEPTVVDTPSHASQSAR	RERE	473	arginine-glutamic acid dipeptide repeats protein isoform a	S12(Phospho) S19(Phospho) S21(Phospho)	S(12): 89.6; S(19): 89.6; S(21): 89.6; T(25): 13.5; T(29): 13.5; S(31): 3.7; S(34): 0.3; S(36): 0.1	S12; S19; S21;	S1106; S1113; S1115		3.33	0.003	1	4	1062	4246	60.25	11931
IlyDSDsESEETLQVK	RFC1	5981	replication factor C subunit 1 isoform 1	Y3(Phospho) S7(Phospho)	Y(3): 97.4; S(5): 2.6; S(7): 99.9; S(9): 0.1; T(12): 0.0	Y3; S7;	Y67; S71	55		0	0	2	1008	2016	73.85	14927
SSPAKESVsPEDSEK	RFC1	5981	replication factor C subunit 1 isoform 1	S10(Phospho)	S(1): 50.0; S(2): 50.0; S(8): 4.3; S(10): 95.7; S(14): 0.0	S10;	S368	41		0	2	3	622.3	1865	14.64	2196
IlyDSDSESEETLQVK	RFC1	5981	replication factor C subunit 1 isoform 1	Y3(Phospho)	Y(3): 99.8; S(5): 33.4; S(7): 33.4; S(9): 33.4; T(12): 0.0	Y3;	Y67	17		0	0	2	1008	2016	73.33	14827
IlyDSDsESEETLQVK	RFC1	5981	replication factor C subunit 1 isoform 1	Y3(Phospho) S7(Phospho)	Y(3): 97.4; S(5): 2.6; S(7): 99.9; S(9): 0.1; T(12): 0.0	Y3; S7;	Y67; S71		3.88	0	0	2	1008	2016	73.85	14927
IlyDSDSESEETLQVK	RFC1	5981	replication factor C subunit 1 isoform 1	Y3(Phospho)	Y(3): 99.8; S(5): 33.4; S(7): 33.4; S(9): 33.4; T(12): 0.0	Y3;	Y67		1.82	0	0	2	1008	2016	73.33	14827
QDPVTYIsEtDEEDDFMCKK	RFC1	5981	replication factor C subunit 1 isoform 1	C18(Carbamido methyl)S8(Phospho) T10(Phospho)	T(5): 4.0; Y(6): 4.0; S(8): 92.1; T(10): 100.0	S8; T10;	S108; T110		2.29	0.005	1	3	870.7	2610	71	14362
VPAEDETQSIDSFSVPGR	RFFL	117584	E3 ubiquitin-protein ligase rififylin	T7(Phospho) S12(Phospho)	T(7): 96.6; S(9): 6.9; S(12): 96.4; S(15): 0.1	T7; S12;	T224; S229	46		0	0	2	1169	2338	74.66	15102
VPAEDETQSIDSFSVPGR	RFFL	117584	E3 ubiquitin-protein ligase rififylin	T7(Phospho) S12(Phospho)	T(7): 96.6; S(9): 6.9; S(12): 96.4; S(15): 0.1	T7; S12;	T224; S229		2.9	0	0	2	1169	2338	74.66	15102
DLELPsQEAPsFQGTEsPKPKCK	RHBDF2	79651	inactive rhomboid protein 2 isoform 2	C21(Carbamido methyl)S6(Phospho) S11(Phospho) S17(Phospho)	S(6): 100.0; S(11): 100.0; T(15): 6.6; S(17): 93.4	S6; S11; S17;	S137; S142; S148		2.68	0.003	0	3	895.7	2685	77.3	15611
GLMAGGRPEGQYsEDEDtDTDEYKEAK	RIC8A	60626	synembryn-A isoform 2	M3(Oxidation)S13(Phospho) T18(Phospho)	Y(12): 5.1; S(13): 94.9; T(18): 100.0; T(20): 0.0; Y(23): 0.0	S13; T18;	S436; T441	35		0	1	3	1056	3167	39.07	7372

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#
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	Y12(Phospho) T18(Phospho)	Y(12): 94.6; S(13): 5.4; T(18): 100.0; T(20): 0.0; Y(23): 0.0	Y12; T18;	Y435; T441	32		0	1	4	788.6	3151	45.98	8862
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	Y12(Phospho) T18(Phospho)	Y(12): 95.1; S(13): 4.9; T(18): 100.0; T(20): 0.0; Y(23): 0.0	Y12; T18;	Y435; T441	30		0	1	3	1051	3151	45.88	8841
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.0; S(13): 50.0; T(18): 100.0; T(20): 0.0; Y(23): 0.0	T18;	T441	22		0	1	3	1056	3167	39.58	7481
GLMAGGRPEGQySEDEdTDtDEYK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.1; S(13): 50.1; T(18): 99.3; T(20): 0.5; Y(23): 0.1	T18;	T441	19		0	0	3	947	2839	44.53	8536
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.0; S(13): 50.0; T(18): 99.4; T(20): 0.6; Y(23): 0.0	T18;	T441	14		0	1	3	1056	3167	46.03	8873
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	Y12(Phospho) T18(Phospho)	Y(12): 94.6; S(13): 5.4; T(18): 100.0; T(20): 0.0; Y(23): 0.0	Y12; T18;	Y435; T441		6.58	0	1	4	788.6	3151	45.98	8862
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	Y12(Phospho) T18(Phospho)	Y(12): 95.1; S(13): 4.9; T(18): 100.0; T(20): 0.0; Y(23): 0.0	Y12; T18;	Y435; T441		6.27	0	1	3	1051	3151	45.88	8841
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) S13(Phospho) T18(Phospho)	Y(12): 5.1; S(13): 94.9; T(18): 100.0; T(20): 0.0; Y(23): 0.0	S13; T18;	S436; T441		6.08	0	1	3	1056	3167	39.07	7372
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.0; S(13): 50.0; T(18): 100.0; T(20): 0.0; Y(23): 0.0	T18;	T441		4.45	0	1	3	1056	3167	39.58	7481
GLMAGGRPEGQySEDEdTDtDEYKEAK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.0; S(13): 50.0; T(18): 99.4; T(20): 0.6; Y(23): 0.0	T18;	T441		3.96	0	1	3	1056	3167	46.03	8873
GLMAGGRPEGQySEDEdTDtDEYK	RIC8A	60626	synembryon-A isoform 2	M3(Oxidation) T18(Phospho)	Y(12): 50.1; S(13): 50.1; T(18): 99.3; T(20): 0.5; Y(23): 0.1	T18;	T441		3.29	0	0	3	947	2839	44.53	8536
GLMAGGRPEGQySEDEdTDtDEYK	RIC8A	60626	synembryon-A isoform 2	T18(Phospho)	Y(12): 50.2; S(13): 50.2; T(18): 98.7; T(20): 0.8; Y(23): 0.1	T18;	T441		2.61	0.001	0	3	941.7	2823	52.47	10239
NDsGEENVPLDLTR	RICTOR	253260	rapamycin-insensitive companion of mTOR isoform 1	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S21	28		0	0	2	819.9	1639	65.38	13135
HIEDTGSTPsIGENDLK	RICTOR	253260	rapamycin-insensitive companion of mTOR isoform 1	S10(Phospho)	T(5): 49.2; S(7): 49.2; T(8): 1.7; S(10): 100.0	S10;	S1177	27		0	0	2	986.9	1973	52.44	10233
NDsGEENVPLDLTR	RICTOR	253260	rapamycin-insensitive companion of mTOR isoform 1	S3(Phospho)	S(3): 100.0; T(13): 0.0	S3;	S21		3.18	0	0	2	819.9	1639	65.38	13135
HIEDTGSTPsIGENDLK	RICTOR	253260	rapamycin-insensitive companion of mTOR isoform 1	S10(Phospho)	T(5): 49.2; S(7): 49.2; T(8): 1.7; S(10): 100.0	S10;	S1177		2.9	0	0	2	986.9	1973	52.44	10233
SQDEISsPVNK	RIF1	55183	telomere-associated protein RIF1 isoform 2	S8(Phospho)	S(1): 0.0; S(7): 1.5; S(8): 98.5	S8;	S2196	21		0	0	2	706.8	1413	28.87	5228
SQDEISsPVNK	RIF1	55183	telomere-associated protein RIF1 isoform 2	S8(Phospho)	S(1): 0.0; S(7): 1.5; S(8): 98.5	S8;	S2196		3.41	0	0	2	706.8	1413	28.87	5228
sSLSNNECGSLDKTSPEMSNSNNDR	RIF1	55183	telomere-associated protein RIF1 isoform 2	C8(Carbamidomethyl) M18(Oxidation) S1(Phospho)	S(1): 80.0; S(2): 4.0; S(4): 4.0; S(10): 4.0; T(14): 4.0; S(15): 4.0; S(19): 0.0; S(21): 0.0	S1;	S1148		2.79	0.001	1	3	990.1	2968	30.11	5486
GsPATsPHLGR	RIN1	9610	ras and Rab interactor 1	S2(Phospho) S6(Phospho)	S(2): 98.0; T(5): 3.9; S(6): 98.0	S2; S6;	S333; S337	43		0	0	2	620.2	1239	27.31	4895
GsPATsPHLGR	RIN1	9610	ras and Rab interactor 1	S2(Phospho) S6(Phospho)	S(2): 98.0; T(5): 3.9; S(6): 98.0	S2; S6;	S333; S337		3.46	0	0	2	620.2	1239	27.31	4895

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#
SQsLPNSLDYQTSDPGR	RMDN3	55177	regulator of microtubule dynamics protein 3	S3(Phospho)	S(1): 3.7; S(3): 96.1; S(7): 0.2; Y(10): 0.0; T(11): 0.0; T(13): 0.0; S(14): 0.0	S3;	S46	23		0	0	2	1023	2046	58.37	11528
SQsLPNSLDYQTSDPGR	RMDN3	55177	regulator of microtubule dynamics protein 3	S3(Phospho)	S(1): 3.7; S(3): 96.1; S(7): 0.2; Y(10): 0.0; T(11): 0.0; T(13): 0.0; S(14): 0.0	S3;	S46		2.45	0	0	2	1023	2046	58.37	11528
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	Y3(Phospho)	Y(3): 97.1; S(7): 51.5; S(8): 51.5; S(18): 0.0; Y(23): 0.0	Y3;	Y80	26		0	0	2	1403	2804	86.94	17415
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	S7(Phospho) S8(Phospho)	Y(3): 7.8; S(7): 96.1; S(8): 96.1; S(18): 0.0; Y(23): 0.0	S7; S8;	S84; S85	21		0	0	3	935.4	2804	86.89	17406
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	S7(Phospho) S8(Phospho)	Y(3): 0.2; S(7): 99.8; S(8): 100.0; S(18): 0.0; Y(23): 0.0	S7; S8;	S84; S85	18		0	0	3	935.4	2804	87.41	17505
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	S7(Phospho) S8(Phospho)	Y(3): 7.8; S(7): 96.1; S(8): 96.1; S(18): 0.0; Y(23): 0.0	S7; S8;	S84; S85		2.94	0	0	3	935.4	2804	86.89	17406
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	S7(Phospho) S8(Phospho)	Y(3): 0.2; S(7): 99.8; S(8): 100.0; S(18): 0.0; Y(23): 0.0	S7; S8;	S84; S85		2.64	0	0	3	935.4	2804	87.41	17505
AAyGDLsEEEEENEPESLGVVYK	RNF113A	7737	RING finger protein 113A	Y3(Phospho)	Y(3): 97.1; S(7): 51.5; S(8): 51.5; S(18): 0.0; Y(23): 0.0	Y3;	Y80		1.8	0	0	2	1403	2804	86.94	17415
ALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S13(Phospho)	S(11): 0.0; S(13): 100.0	S13;	S138	37		0	0	2	981.4	1962	58.12	11472
KALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S14(Phospho)	S(12): 0.0; S(14): 100.0	S14;	S138	36		0	1	3	697.3	2090	44.99	8651
ALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S136; S138	23		0	0	2	1021	2042	70.25	14212
KALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S14(Phospho)	S(12): 0.0; S(14): 100.0	S14;	S138		4.38	0	1	3	697.3	2090	44.99	8651
ALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S13(Phospho)	S(11): 0.0; S(13): 100.0	S13;	S138		3.04	0	0	2	981.4	1962	58.12	11472
KALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S14(Phospho)	S(12): 0.0; S(14): 100.0	S14;	S138		2.64	0.005	1	2	1045	2090	45.17	8690
ALVVPEPEPDSsNQER	RNF20	56254	E3 ubiquitin-protein ligase BRE1A	S11(Phospho) S13(Phospho)	S(11): 100.0; S(13): 100.0	S11; S13;	S136; S138		2.01	0.005	0	2	1021	2042	70.25	14212
TSsEAsMDAAYLDK	RNF219	79596	RING finger protein 219	S3(Phospho) S6(Phospho)	T(1): 2.4; S(2): 2.4; S(3): 95.2; S(6): 100.0; Y(11): 0.0	S3; S6;	S526; S529	27		0	0	2	824.8	1649	64.31	12889
TSsEAsMDAAYLDK	RNF219	79596	RING finger protein 219	S3(Phospho) S6(Phospho)	T(1): 2.4; S(2): 2.4; S(3): 95.2; S(6): 100.0; Y(11): 0.0	S3; S6;	S526; S529		2.3	0	0	2	824.8	1649	64.31	12889
EQDRVHsPCPTSGSEK	RNPC3	55599	RNA-binding protein 40	C9(Carbamidomethyl) S7(Phospho)	S(7): 100.0; T(11): 0.0; S(12): 0.0; S(14): 0.0	S7;	S108	26		0	1	3	631.9	1894	13.82	2023
EQDRVHsPCPTSGSEK	RNPC3	55599	RNA-binding protein 40	C9(Carbamidomethyl) S7(Phospho)	S(7): 100.0; T(11): 0.0; S(12): 0.0; S(14): 0.0	S7;	S108		4.38	0	1	3	631.9	1894	13.82	2023
sVGEAEDGPEGRGDGTCEEgSSGAEH WQDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamidomethyl) S1(Phospho)	S(1): 95.1; T(16): 68.3; S(21): 68.3; S(22): 68.3	S1;	S643		1.6	0.003	1	3	1220	3659	103.8	20803
sVGEAEDGPEGRGDGTCEEgSSGAEH WQDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamidomethyl) S1(Phospho)	S(1): 94.1; T(16): 68.6; S(21): 68.6; S(22): 68.6	S1;	S643		1.6	0.005	1	3	1220	3659	111.2	22352
sVGEAEDGPEGRGDGTCEEgSSGAEH WQDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamidomethyl) S1(Phospho)	S(1): 95.0; T(16): 68.3; S(21): 68.3; S(22): 68.3	S1;	S643		1.45	0.005	1	3	1220	3659	91.83	18350

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#
sVGAEADGPEGRGDGTCEEgssGAEHW QDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamido methyl)S1(Phospho) S21(Phospho) S22(Phospho)	S(1): 88.0; T(16): 15.9; S(21): 98.1; S(22): 98.1	S1; S21; S22;	S643; S663; S664		1.44	0.005	1	3	1220	3659	111.7	22459
sVGAEADGPEGRGDGTCEEgssGAEHW QDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamido methyl)S1(Phospho) S21(Phospho) S22(Phospho)	S(1): 88.7; T(16): 33.9; S(21): 88.7; S(22): 88.7	S1; S21; S22;	S643; S663; S664		1.56	0.007	1	3	1220	3659	106.6	21377
sVGAEADGPEGRGDGTCEEgssGAEHW QDEER	RPGR	6103	X-linked retinitis pigmentosa GTPase regulator isoform C	C17(Carbamido methyl)S1(Phospho) S22(Phospho)	S(1): 91.8; T(16): 58.2; S(21): 58.2; S(22): 91.8	S1; S22;	S643; S664		1.44	0.007	1	3	1220	3659	110.7	22238
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307	29		0	1	2	1220	2439	101.7	20348
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307	28		0	1	2	1220	2439	101.1	20236
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		4.95	0.001	1	2	1212	2423	113.7	22876
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		4.25	0.001	1	2	1220	2439	101.7	20348
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307	28		0.002	1	2	1212	2423	113.7	22876
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		5.01	0.003	1	3	813.6	2439	101.6	20344
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		4.99	0.003	1	3	813.6	2439	101.1	20232
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	M14(Oxidation) S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		4.07	0.003	1	2	1220	2439	101.1	20236
VEAKEEsEesDEDMGfGLFD	RPLP0	6175	60S acidic ribosomal protein P0	S7(Phospho) S10(Phospho)	S(7): 100.0; S(10): 100.0	S7; S10;	S304; S307		2.33	0.007	1	2	1212	2423	113.2	22770
KEEsEesDDDMGfGLFD	RPLP1	6176	60S acidic ribosomal protein P1 isoform 2	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S76; S79	45		0	1	2	1055	2110	115.2	23167
KEEsEesDDDMGfGLFD	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	27		0.001	1	2	1063	2126	105.1	21074
KEEsEesDDDMGfGLFD	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	25		0.002	1	2	1063	2126	104.1	20857
KEEsEesDDDMGfGLFD	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	22		0.002	1	2	1063	2126	104.6	20964
KEEsEesDDDMGfGLFD	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	20		0.002	1	2	1063	2126	114.2	22966
KEEsEesDDDMGfGLFD	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	22		0.003	1	2	1063	2126	113.7	22861
KEEsEesDDDMGfGLFD	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		6.02	0.003	1	2	1063	2126	103.5	20748

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#
KEEsEEsDDDMGFGLFD	RPLP1	6176	60S acidic ribosomal protein P1 isoform 2	S4(Phospho) S7(Phospho)	S(4): 100.0; S(7): 100.0	S4; S7;	S76; S79		4.77	0.003	1	2	1055	2110	115.2	23167
KEESEsDDDMGFGLFD	RPLP1	6176	60S acidic ribosomal protein P1 isoform 2	M11(Oxidation) S7(Phospho)	S(4): 0.0; S(7): 100.0	S7;	S79		3.3	0.003	1	2	1023	2046	81.91	16485
KEEsEEsDDDMGFGLFD	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	21		0.004	1	2	1063	2126	105.6	21180
KEEsEEsDDDMGFGLFD	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		3.32	0.004	1	2	1063	2126	114.2	22966
KEEsEEsDDDMGFGLFD	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	17		0.006	1	2	1063	2126	110.1	22107
KEEsEEsDDDMGFGLFD	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	25		0.007	1	2	1063	2126	106.2	21286
KEEsEEsDDDMGFGLFD	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		3.81	0.007	1	2	1063	2126	104.1	20857
KEEsEEsDDDMGFGLFD	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		2.27	0.008	1	2	1063	2126	109.5	21988
KPRPseGDEDECLPASK	RPP30	10556	ribonuclease P protein subunit p30 isoform b	C11(Carbamido methyl) S5(Phospho)	S(5): 100.0; S(15): 0.0	S5;	S251	15		0	0	3	622.6	1866	23.12	3999
KPRPseGDEDECLPASK	RPP30	10556	ribonuclease P protein subunit p30 isoform b	C11(Carbamido methyl) S5(Phospho)	S(5): 100.0; S(15): 0.0	S5;	S251		3.57	0	0	3	622.6	1866	23.12	3999
LSMEDSKsPPPKATEEK	RPRD1B	58490	regulation of nuclear pre-mRNA domain-containing protein 1B	S8(Phospho)	S(2): 0.2; S(6): 0.2; S(8): 99.6; T(14): 0.0	S8;	S134		3.65	0.001	2	3	652	1954	24.33	4250
SFNySPNSSTSEVSSTSASK	RPRD2	23248	regulation of nuclear pre-mRNA domain-containing protein 2 isoform 2	Y4(Phospho)	S(1): 0.1; Y(4): 97.0; S(5): 2.9; S(8): 0.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; T(16): 0.0; S(17): 0.0; S(19): 0.0	Y4;	Y566	55		0	0	2	1074	2147	47.36	9151
SFNySPNSSTSEVSSTSASK	RPRD2	23248	regulation of nuclear pre-mRNA domain-containing protein 2 isoform 2	Y4(Phospho)	S(1): 0.1; Y(4): 97.0; S(5): 2.9; S(8): 0.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(14): 0.0; S(15): 0.0; T(16): 0.0; S(17): 0.0; S(19): 0.0	Y4;	Y566		3.43	0	0	2	1074	2147	47.36	9151
NTGVSPASRSPSGTPTsPSNLTSGLK	RPRD2	23248	regulation of nuclear pre-mRNA domain-containing protein 2 isoform 2	S17(Phospho)	T(2): 0.0; S(5): 0.0; S(8): 0.0; S(11): 0.0; T(14): 0.0; T(16): 0.2; S(17): 95.3; S(19): 4.5; T(22): 0.0; S(23): 0.0	S17;	S459		3.03	0	0	3	864.1	2590	52.64	10277
DEILPTlPISEQK	RPS3	6188	40S ribosomal protein S3 isoform 3	T7(Phospho)	T(6): 0.0; T(7): 100.0; S(10): 0.0	T7;	T95	14		0.002	0	2	775.9	1551	65.24	13105
DEILPTlPISEQK	RPS3	6188	40S ribosomal protein S3 isoform 3	T7(Phospho)	T(6): 0.0; T(7): 100.0; S(10): 0.0	T7;	T95		2.42	0.003	0	2	775.9	1551	65.24	13105
LSsLRAsTSKSESSQK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S7(Phospho)	S(2): 3.1; S(3): 96.9; S(7): 99.9; T(8): 0.1; S(9): 0.0; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3; S7;	S236; S240	37		0	2	2	928.4	1856	19.68	3270
RLsSLRAsTSK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S8(Phospho)	S(3): 97.8; S(4): 2.2; S(8): 99.9; T(9): 0.1; S(10): 0.0	S3; S8;	S235; S240	21		0	2	2	683.3	1366	24.98	4388

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#
LSsLRASTSKSESSQK	RPS6	6194	40S ribosomal protein S6	S3(Phospho)	S(2): 5.3; S(3): 96.4; S(7): 48.3; T(8): 48.3; S(9): 1.8; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3;	S236		4.12	0	2	3	619.3	1856	19.6	3254
LSsLRaTSK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S7(Phospho)	S(2): 2.4; S(3): 97.6; S(7): 97.5; T(8): 0.1; S(9): 2.4	S3; S7;	S236; S240	23		0.001	1	2	605.3	1210	25.02	4395
LSsLRaTSKSESSQK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S7(Phospho)	S(2): 3.1; S(3): 96.9; S(7): 99.9; T(8): 0.1; S(9): 0.0; S(11): 0.0; S(13): 0.0; S(14): 0.0	S3; S7;	S236; S240		2.91	0.001	2	2	928.4	1856	19.68	3270
LSSLRASTSKsESSQK	RPS6	6194	40S ribosomal protein S6	S11(Phospho)	S(2): 0.1; S(3): 48.1; S(7): 48.1; T(8): 1.9; S(9): 1.9; S(11): 96.0; S(13): 3.8; S(14): 0.2	S11;	S244	12		0.002	2	3	619.3	1856	18.85	3094
RLssLR	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S4(Phospho)	S(3): 100.0; S(4): 100.0	S3; S4;	S235; S236	27		0.003	1	2	446.2	891.4	32.46	5974
LSsLRaTSKsESSQK	RPS6	6194	40S ribosomal protein S6	S3(Phospho) S7(Phospho) S11(Phospho)	S(2): 3.5; S(3): 96.5; S(7): 93.3; T(8): 3.4; S(9): 3.4; S(11): 99.8; S(13): 0.1; S(14): 0.0	S3; S7; S11;	S236; S240; S244	12		0.003	2	2	968.4	1936	24.08	4197
LSSLRASTSKsESSQK	RPS6	6194	40S ribosomal protein S6	S11(Phospho)	S(2): 0.2; S(3): 6.1; S(7): 65.3; T(8): 65.3; S(9): 65.3; S(11): 97.7; S(13): 0.0; S(14): 0.1	S11;	S244		3.69	0.005	2	3	645.9	1936	24.32	4248
NQsPVLEPVGR	RPS6KA3	6197	ribosomal protein S6 kinase alpha-3	S3(Phospho)	S(3): 100.0	S3;	S715	46		0	0	2	638.3	1276	46.28	8926
NQsPVLEPVGR	RPS6KA3	6197	ribosomal protein S6 kinase alpha-3	S3(Phospho)	S(3): 100.0	S3;	S715		1.92	0	0	2	638.3	1276	46.28	8926
VLDTSSTLTQsAPASPtNK	RPTOR	57521	regulatory-associated protein of mTOR isoform 2	S10(Phospho) T16(Phospho)	T(4): 0.1; S(5): 3.6; S(6): 3.6; T(8): 0.1; S(10): 92.5; S(14): 3.7; T(16): 96.3	S10; T16;	S701; T707	29		0	0	2	988.9	1977	59.25	11734
VLDTSSTLTQsAPASPtNK	RPTOR	57521	regulatory-associated protein of mTOR isoform 2	S10(Phospho) T16(Phospho)	T(4): 0.1; S(5): 3.6; S(6): 3.6; T(8): 0.1; S(10): 92.5; S(14): 3.7; T(16): 96.3	S10; T16;	S701; T707		2.82	0	0	2	988.9	1977	59.25	11734
FQEQECPPsPEPTR	RRAS2	22800	ras-related protein R-Ras2 isoform b	C6(Carbamidomethyl) S9(Phospho)	S(9): 100.0; T(13): 0.0	S9;	S109	44		0	0	2	891.4	1782	37.83	7111
KFQEQECPPsPEPTR	RRAS2	22800	ras-related protein R-Ras2 isoform b	C7(Carbamidomethyl) S10(Phospho)	S(10): 100.0; T(14): 0.0	S10;	S109	42		0	1	3	637.3	1910	30.49	5566
FQEQECPPsPEPTRK	RRAS2	22800	ras-related protein R-Ras2 isoform b	C6(Carbamidomethyl) S9(Phospho)	S(9): 97.3; T(13): 2.7	S9;	S109	20		0	1	3	637.3	1910	29.2	5297
KFQEQECPPsPEPTR	RRAS2	22800	ras-related protein R-Ras2 isoform b	C7(Carbamidomethyl) S10(Phospho)	S(10): 100.0; T(14): 0.0	S10;	S109		4.67	0	1	3	637.3	1910	30.49	5566
FQEQECPPsPEPTRK	RRAS2	22800	ras-related protein R-Ras2 isoform b	C6(Carbamidomethyl) S9(Phospho)	S(9): 97.3; T(13): 2.7	S9;	S109		3.63	0	1	3	637.3	1910	29.2	5297
FQEQECPPsPEPTR	RRAS2	22800	ras-related protein R-Ras2 isoform b	C6(Carbamidomethyl) S9(Phospho)	S(9): 100.0; T(13): 0.0	S9;	S109		3.07	0	0	2	891.4	1782	37.83	7111
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185	47		0	1	3	654.3	1961	23.86	4151
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185	44		0	1	2	981	1961	23.96	4173
NTDVAQsPEAPKQEAPAKK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185	24		0	2	3	697	2089	18.81	3087
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185		5.29	0	1	3	654.3	1961	23.86	4151
NTDVAQsPEAPKQEAPAKK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185		5.13	0	2	3	697	2089	18.81	3087
NTDVAQsPEAPKQEAPAK	RRBP1	6238	ribosome-binding protein 1	S7(Phospho)	T(2): 0.0; S(7): 100.0	S7;	S185		3.52	0	1	2	981	1961	23.96	4173
GDsIEILADSEDEEDNEEEER	RRP12	23223	RRP12-like protein isoform 3	S3(Phospho)	S(3): 99.6; S(11): 0.4	S3;	S972		1.63	0	0	2	1317	2632	75.56	15263

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#
TPTsSPASPLVAK	RRP1B	23076	ribosomal RNA processing protein 1 homolog B	S5(Phospho) S9(Phospho)	T(1): 0.0; T(3): 0.1; S(4): 2.9; S(5): 96.9; S(8): 0.2; S(9): 99.9	S5; S9;	S732; S736	19		0	0	2	751.8	1503	47.55	9189
TPTsSPASPLVAK	RRP1B	23076	ribosomal RNA processing protein 1 homolog B	S5(Phospho) S9(Phospho)	T(1): 0.0; T(3): 0.1; S(4): 2.9; S(5): 96.9; S(8): 0.2; S(9): 99.9	S5; S9;	S732; S736		3.36	0	0	2	751.8	1503	47.55	9189
VAEPGAEAtsSTGEESGSEHPPAVPMH NK	RRP1B	23076	ribosomal RNA processing protein 1 homolog B	T9(Phospho) S10(Phospho)	T(9): 79.2; S(10): 79.2; S(11): 18.1; T(12): 18.1; S(16): 2.7; S(18): 2.7	T9; S10;	T451; S452		2.43	0.003	0	3	1022	3063	41.83	7957
QGPPCsDsEEEVER	RRP8	23378	ribosomal RNA-processing protein 8	C5(Carbamidomethyl)S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S104; S106	42		0	0	2	889.8	1779	35.99	6727
QGPPCsDsEEEVER	RRP8	23378	ribosomal RNA-processing protein 8	C5(Carbamidomethyl)S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S104; S106		3.69	0	0	2	889.8	1779	35.99	6727
GRstDEYsEADEEEEEEGKPSR	RSF1	51773	remodeling and spacing factor 1	S3(Phospho) T4(Phospho) S8(Phospho)	S(3): 100.0; T(4): 100.0; Y(7): 0.1; S(8): 99.9; S(22): 0.0	S3; T4; S8;	S1277; T1278; S1282	52		0	1	3	966.7	2898	38.05	7156
GRSTDEYsEADEEEEEEGKPSR	RSF1	51773	remodeling and spacing factor 1	S8(Phospho)	S(3): 50.0; T(4): 50.0; Y(7): 4.0; S(8): 96.0; S(22): 0.0	S8;	S1282	48		0	1	3	940	2818	33.44	6177
IEsDEEEDFENVGK	RSF1	51773	remodeling and spacing factor 1	S3(Phospho)	S(3): 100.0	S3;	S1345	26		0	0	2	860.3	1720	55.79	10965
STLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)T16(Phospho) S17(Phospho)	S(1): 5.7; T(2): 5.7; S(5): 0.6; S(10): 0.6; T(16): 93.5; S(17): 94.0; S(20): 0.0	T16; S17;	T628; S629	22		0	0	4	793.3	3170	52.19	10180
GRSTDEYsEADEEEEEEGKPSR	RSF1	51773	remodeling and spacing factor 1	S8(Phospho)	S(3): 50.0; T(4): 50.0; Y(7): 4.0; S(8): 96.0; S(22): 0.0	S8;	S1282		6.55	0	1	3	940	2818	33.44	6177
STLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)T16(Phospho) S17(Phospho)	S(1): 5.7; T(2): 5.7; S(5): 0.6; S(10): 0.6; T(16): 93.5; S(17): 94.0; S(20): 0.0	T16; S17;	T628; S629		3.95	0	0	4	793.3	3170	52.19	10180
stLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)S1(Phospho)	S(1): 96.0; T(2): 49.8; S(5): 49.5; S(10): 3.7; T(16): 0.3; S(17): 0.6; S(20): 0.1	S1;	S613		3.49	0	0	3	1057	3170	52.68	10285
STLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)S10(Phospho) S17(Phospho)	S(1): 6.6; T(2): 6.6; S(5): 0.1; S(10): 86.3; T(16): 7.0; S(17): 86.8; S(20): 6.6	S10; S17;	S622; S629		3.34	0	0	3	1057	3170	52.16	10173
IEsDEEEDFENVGK	RSF1	51773	remodeling and spacing factor 1	S3(Phospho)	S(3): 100.0	S3;	S1345		2.87	0	0	2	860.3	1720	55.79	10965
stLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)S1(Phospho) T2(Phospho)	S(1): 85.5; T(2): 85.5; S(5): 9.5; S(10): 9.5; T(16): 4.7; S(17): 5.2; S(20): 0.0	S1; T2;	S613; T614	12		0.001	0	4	793.3	3170	52.77	10306
stLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)S1(Phospho)	S(1): 96.0; T(2): 49.8; S(5): 49.5; S(10): 3.7; T(16): 0.3; S(17): 0.6; S(20): 0.1	S1;	S613	11		0.002	0	3	1057	3170	52.68	10285
stLESEKPGSPAAEtSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl)S1(Phospho) T2(Phospho)	S(1): 85.5; T(2): 85.5; S(5): 9.5; S(10): 9.5; T(16): 4.7; S(17): 5.2; S(20): 0.0	S1; T2;	S613; T614		2.82	0.003	0	4	793.3	3170	52.77	10306

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#
TALSTESTCTMKGEKsPK	RSF1	51773	remodeling and spacing factor 1	C9(Carbamidomethyl) S17(Phospho)	T(1): 0.0; S(4): 0.0; S(5): 0.0; T(6): 0.0; S(8): 0.0; T(10): 0.0; S(17): 100.0	S17;	S570		2.77	0.005	2	3	717.7	2151	26.56	4727
sTLESEKPGSPEAAETSPPSNIIDHCEK	RSF1	51773	remodeling and spacing factor 1	C26(Carbamidomethyl) S10(Phospho)	S(1): 94.6; T(2): 5.4; S(5): 0.0; S(10): 0.0; T(16): 0.0; S(17): 0.0; S(20): 0.0	S1;	S613		2.22	0.006	0	3	1031	3090	48.2	9328
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	40		0	1	2	705.8	1411	12.62	1763
AAESETPGKsPEKKPK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S10(Phospho)	S(4): 0.0; T(6): 0.0; S(10): 100.0	S10;	S427	23		0	2	3	588.6	1764	12.35	1686
AtNESEDEIPLQVPIGK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	T2(Phospho)	T(2): 97.1; S(5): 2.9	T2;	T358	16		0	0	2	960.5	1920	80.87	16279
AAESETPGKsPEKKPK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	S10(Phospho)	S(4): 0.0; T(6): 0.0; S(10): 100.0	S10;	S427		5.9	0	2	3	588.6	1764	12.35	1686
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		4.77	0	1	2	705.8	1411	12.62	1763
AtNESEDEIPLQVPIGK	RSL1D1	26156	ribosomal L1 domain-containing protein 1	T2(Phospho)	T(2): 97.1; S(5): 2.9	T2;	T358		2.17	0	0	2	960.5	1920	80.87	16279
KEQSEVsVsPR	RSRC2	65117	arginine/serine-rich coiled-coil protein 2	S7(Phospho) S9(Phospho)	S(4): 0.0; S(7): 100.0; S(9): 100.0	S7; S9;	S30; S32	62		0	1	2	703.3	1406	25.51	4500
KEQSEVsVsPR	RSRC2	65117	arginine/serine-rich coiled-coil protein 2	S7(Phospho) S9(Phospho)	S(4): 0.0; S(7): 100.0; S(9): 100.0	S7; S9;	S30; S32		4.07	0	1	2	703.3	1406	25.51	4500
RfTPPSTALS PGK	RUNX1	861	runt-related transcription factor 1 isoform AML1a	T3(Phospho) S10(Phospho)	T(3): 100.0; S(6): 0.0; T(7): 0.0; S(10): 99.9	T3; S10;	T14; S21	51		0	1	2	759.8	1519	52.74	10299
RfTPPSTALS PGK	RUNX1	861	runt-related transcription factor 1 isoform AML1a	T3(Phospho) S10(Phospho)	T(3): 100.0; S(6): 0.0; T(7): 0.0; S(10): 99.9	T3; S10;	T14; S21		3.42	0.001	1	2	759.8	1519	52.74	10299
EVLVDsEGLsGEER	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	68		0	0	2	871.8	1743	67.49	13615
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	42		0	1	2	656.3	1312	15.22	2316
EVLVDsEGLsGEER	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	41		0	0	2	871.8	1743	66.99	13506
sAsPPPATSSSSSSSR	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	41		0	0	2	783.3	1566	21.22	3594
sAsPPPATSSSSSSSR	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	38		0	0	2	783.3	1566	20.68	3481
QRsPsPAPAPAPAAAAGPPTR	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	38		0	1	3	710	2128	40.8	7740
QRsPsPAPAPAPAAAAGPPTR	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	27		0	1	2	1064	2128	40.9	7762
EAASSSSGTQPAPPAPAsPWDSKK	SCAF1	58506	splicing factor, arginine/serine-rich 19	S18(Phospho)	S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; T(9): 0.0; S(18): 99.9; S(22): 0.1	S18;	S548	20		0	1	3	812	2434	43.2	8244
QRsPsPAPAPAPAAAAGPPTR	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		5.89	0	1	3	710	2128	40.8	7740
EAASSSSGTQPAPPAPAsPWDSKK	SCAF1	58506	splicing factor, arginine/serine-rich 19	S18(Phospho)	S(4): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; T(9): 0.0; S(18): 99.9; S(22): 0.1	S18;	S548		4.67	0	1	3	812	2434	43.2	8244
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		3.55	0	1	2	656.3	1312	15.22	2316
sAsPPPATSSSSSSSR	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		3.17	0	0	2	783.3	1566	21.22	3594

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#
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		2.92	0	0	2	871.8	1743	66.99	13506
QRSPsPAPAPAPAAAAGPPTR	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		2.91	0	1	2	1064	2128	40.9	7762
sAsPPPTATSSSSSR	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		2.9	0	0	2	783.3	1566	20.68	3481
RRsAsPPPATSSSSSR	SCAF1	58506	splicing factor, arginine/serine-rich 19	S3(Phospho) S5(Phospho)	S(3): 99.7; S(5): 99.7; T(10): 0.4; S(11): 0.0; S(12): 0.0; S(13): 0.0; S(14): 0.0; S(15): 0.0; S(16): 0.0	S3; S5;	S612; S614		2.19	0	2	2	939.4	1878	12.66	1772
sAsPPPTATSSSSSR	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		2.15	0	0	2	783.3	1566	20.9	3527
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		3.03	0.001	0	2	871.8	1743	67.49	13615
AETASQSQRSPISDNSGCDAPGNSNP SL SVPSSAESEK	SCAF11	9169	protein SCAF11	C18(Carbamido methyl) T3(Phospho)	T(3): 99.6; S(5): 0.3; S(7): 0.0; S(10): 0.0; S(13): 0.0; S(16): 0.0; S(24): 0.0; S(27): 0.0; S(29): 0.0; S(32): 0.0; S(33): 0.0; S(36): 0.0	T3;	T331	47		0	1	4	982.9	3929	47.41	9161
sSSNDSVDEETAESDTPVLEK	SCAF11	9169	protein SCAF11	S1(Phospho)	S(1): 93.0; S(2): 3.4; S(3): 0.1; S(6): 3.4; T(11): 0.0; S(14): 0.0; T(16): 0.0; S(17): 0.0	S1;	S400	42		0	0	2	1203	2406	51.85	10093
FHsPSTTWsPNKDPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.1; T(6): 0.0; T(7): 0.0; S(9): 99.9; T(14): 0.0	S3; S9;	S796; S802	27		0	1	3	749.6	2247	40.26	7629
FHsPsTTWSPNKDPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 89.2; T(6): 3.6; T(7): 3.6; S(9): 3.6; T(14): 0.0	S3; S5;	S796; S798	21		0	1	3	749.6	2247	40.8	7742
AETASQSQRSPISDNSGCDAPGNSNP SL SVPSSAESEK	SCAF11	9169	protein SCAF11	C18(Carbamido methyl) S10(Phospho)	T(3): 5.3; S(5): 0.3; S(7): 0.3; S(10): 93.5; S(13): 0.3; S(16): 0.3; S(24): 0.0; S(27): 0.0; S(29): 0.0; S(32): 0.0; S(33): 0.0; S(36): 0.0	S10;	S338	19		0	1	3	1310	3929	47.31	9140
FHsPSTTWsPNKDPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.1; T(6): 0.0; T(7): 0.0; S(9): 99.9; T(14): 0.0	S3; S9;	S796; S802		5.29	0	1	3	749.6	2247	40.26	7629
AETASQSQRSPISDNSGCDAPGNSNP SL SVPSSAESEK	SCAF11	9169	protein SCAF11	C18(Carbamido methyl) T3(Phospho)	T(3): 99.6; S(5): 0.3; S(7): 0.0; S(10): 0.0; S(13): 0.0; S(16): 0.0; S(24): 0.0; S(27): 0.0; S(29): 0.0; S(32): 0.0; S(33): 0.0; S(36): 0.0	T3;	T331		5.17	0	1	4	982.9	3929	47.41	9161
FHsPsTTWSPNKDPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 89.2; T(6): 3.6; T(7): 3.6; S(9): 3.6; T(14): 0.0	S3; S5;	S796; S798		3.76	0	1	3	749.6	2247	40.8	7742
sSSNDSVDEETAESDTPVLEK	SCAF11	9169	protein SCAF11	S1(Phospho)	S(1): 93.0; S(2): 3.4; S(3): 0.1; S(6): 3.4; T(11): 0.0; S(14): 0.0; T(16): 0.0; S(17): 0.0	S1;	S400		3.39	0	0	2	1203	2406	51.85	10093

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#
AETASQSQRsPISDNSGCDAPGNSNPSL SVPSSAESEK	SCAF11	9169	protein SCAF11	C18(Carbamido methyl) S10(Phospho)	T(3): 5.3; S(5): 0.3; S(7): 0.3; S(10): 93.5; S(13): 0.3; S(16): 0.3; S(24): 0.0; S(27): 0.0; S(29): 0.0; S(32): 0.0; S(33): 0.0; S(36): 0.0	S10;	S338		3.07	0	1	3	1310	3929	47.31	9140
FHsPSTTWsPNKDTPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 4.1; T(6): 4.1; T(7): 4.1; S(9): 87.6; T(14): 0.0	S3; S9;	S796; S802		2.02	0	1	2	1124	2247	40.07	7588
FHsPSTTWSPNKDTPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.4; T(6): 0.2; T(7): 0.2; S(9): 0.2; T(14): 0.0	S3; S5;	S796; S798	11		0.002	1	3	749.6	2247	39.74	7517
FHsPSTTWSPNKDTPQEK	SCAF11	9169	protein SCAF11	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.4; T(6): 0.2; T(7): 0.2; S(9): 0.2; T(14): 0.0	S3; S5;	S796; S798		3.02	0.003	1	3	749.6	2247	39.74	7517
SSEPVKETVQTTSQSPtPVEK	SCAF8	22828	protein SCAF8 isoform d	T16(Phospho)	S(1): 0.0; S(2): 0.0; T(8): 0.0; T(11): 0.0; T(12): 0.0; S(14): 0.0; T(16): 100.0	T16;	T619		2.51	0.001	1	2	1127	2252	33.53	6196
RSEACPCQPSGSLPAEEEK	SCRIB	23513	protein scribble homolog isoform b	C5(Carbamidomethyl) C7(Carbamidomethyl) S13(Phospho)	S(2): 0.0; S(11): 0.0; S(13): 100.0	S13;	S504	41		0	1	3	808.7	2424	34.59	6422
VQsPEPPAPER	SCRIB	23513	protein scribble homolog isoform b	S3(Phospho)	S(3): 100.0	S3;	S1475	37		0	0	2	643.8	1287	29.21	5300
MAESPCSPSGQQPPSPSPDEL PANVK	SCRIB	23513	protein scribble homolog isoform b	C6(Carbamidomethyl) S18(Phospho)	S(4): 0.0; S(7): 0.0; S(9): 0.0; S(15): 0.0; S(18): 100.0	S18;	S1309	10		0	0	3	962.1	2884	63.44	12670
RSEACPCQPSGSLPAEEEK	SCRIB	23513	protein scribble homolog isoform b	C5(Carbamidomethyl) C7(Carbamidomethyl) S13(Phospho)	S(2): 0.0; S(11): 0.0; S(13): 100.0	S13;	S504		5.11	0	1	3	808.7	2424	34.59	6422
MAESPCSPSGQQPPSPSPDEL PANVK	SCRIB	23513	protein scribble homolog isoform b	C6(Carbamidomethyl) S18(Phospho)	S(4): 0.0; S(7): 0.0; S(9): 0.0; S(15): 0.0; S(18): 100.0	S18;	S1309		3.67	0	0	3	962.1	2884	63.44	12670
VQsPEPPAPER	SCRIB	23513	protein scribble homolog isoform b	S3(Phospho)	S(3): 100.0	S3;	S1475		2.9	0	0	2	643.8	1287	29.21	5300
MAESPCSPSGQQPPSPSPDEL PANVK	SCRIB	23513	protein scribble homolog isoform b	M1(Oxidation) C6(Carbamidomethyl) S18(Phospho)	S(4): 0.1; S(7): 0.0; S(9): 0.0; S(15): 0.7; S(18): 99.2	S18;	S1309		2.86	0.001	0	3	967.4	2900	61.23	12139
MAESPCSPSGQQPPSPSPDEL PANVK	SCRIB	23513	protein scribble homolog isoform b	M1(Oxidation) C6(Carbamidomethyl) S15(Phospho) S18(Phospho)	S(4): 0.0; S(7): 0.0; S(9): 0.0; S(15): 100.0; S(18): 100.0	S15; S18;	S1306; S1309		2.82	0.001	0	3	994.1	2980	68.74	13899
VsPASPAGsPSADFAVHGESLGDR	SDCCAG3	10807	serologically defined colon cancer antigen 3 isoform 3	S2(Phospho) S9(Phospho)	S(2): 99.8; S(5): 0.2; S(9): 95.7; S(11): 4.3; S(20): 0.0	S2; S9;	S167; S174	20		0	0	3	824.3	2471	65.5	13160
VsPASPAGsPSADFAVHGESLGDR	SDCCAG3	10807	serologically defined colon cancer antigen 3 isoform 3	S2(Phospho) S9(Phospho)	S(2): 99.8; S(5): 0.2; S(9): 95.7; S(11): 4.3; S(20): 0.0	S2; S9;	S167; S174		3.82	0	0	3	824.3	2471	65.5	13160
ADSGPTQPPLsLsPAPETK	SEC16A	9919	protein transport protein Sec16A isoform 2	S11(Phospho) S13(Phospho)	S(3): 0.0; T(6): 0.0; S(11): 100.0; S(13): 100.0; T(18): 0.0	S11; S13;	S2081; S2083		3.1	0	0	2	1027	2053	71.23	14405
ADSGPTQPPLsLsPAPETK	SEC16A	9919	protein transport protein Sec16A isoform 2	S13(Phospho)	S(3): 0.0; T(6): 0.0; S(11): 0.2; S(13): 99.8; T(18): 0.0	S13;	S2083		2.84	0.003	0	2	987	1973	63.13	12592
AQGEVAGHeSPKIPYK	SEC31A	22872	protein transport protein Sec31A isoform 6	S11(Phospho)	S(11): 100.0; Y(16): 0.0	S11;	S760	13		0	1	3	673	2017	36.83	6905

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#
AQGEPVAGHEsPKIPYEK	SEC31A	22872	protein transport protein Sec31A isoform 6	S11(Phospho)	S(11): 100.0; Y(16): 0.0	S11;	S760	13		0	1	3	673	2017	37.36	7014
AQGEPVAGHEsPKIPYEK	SEC31A	22872	protein transport protein Sec31A isoform 6	S11(Phospho)	S(11): 100.0; Y(16): 0.0	S11;	S760		4.52	0	1	3	673	2017	36.83	6905
AQGEPVAGHEsPKIPYEK	SEC31A	22872	protein transport protein Sec31A isoform 6	S11(Phospho)	S(11): 100.0; Y(16): 0.0	S11;	S760		4.31	0	1	3	673	2017	37.36	7014
PGPTPSGTNVGSSGRsPSK	SEC61B	10952	protein transport protein Sec61 subunit beta	S16(Phospho)	T(4): 0.0; S(6): 0.0; T(8): 0.0; S(12): 0.0; S(13): 0.0; S(16): 100.0; S(18): 0.0	S16;	S17	46		0	1	2	925.4	1850	20.81	3509
PGPTPSGTNVGSSGRsPSK	SEC61B	10952	protein transport protein Sec61 subunit beta	S13(Phospho) S16(Phospho)	T(4): 0.0; S(6): 0.0; T(8): 0.0; S(12): 5.4; S(13): 94.6; S(16): 94.6; S(18): 5.4	S13; S16;	S14; S17	12		0.002	1	3	643.9	1930	25.34	4465
PGPTPSGTNVGSSGRsPSK	SEC61B	10952	protein transport protein Sec61 subunit beta	S16(Phospho)	T(4): 0.0; S(6): 0.0; T(8): 0.0; S(12): 0.0; S(13): 0.2; S(16): 99.7; S(18): 0.2	S16;	S17	11		0.003	1	2	925.4	1850	21.35	3622
EELEQQIDGDCEEDEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375	29		0	0	3	1012	3034	39.65	7498
EELEQQIDGDCEEDEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375	13		0	0	2	1518	3034	39.74	7516
EELEQQIDGDCEEDEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375		4.15	0	0	3	1012	3034	39.65	7498
EELEQQIDGDCEEDEEENDGETPK	SEC62	7095	translocation protein SEC62	C11(Carbamido methyl) T7(Phospho)	T(7): 100.0; T(23): 0.0	T7;	T375		1.98	0.001	0	2	1518	3034	39.74	7516
NHLsPQQGGATPQVPsPCCR	SEN3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl) S4(Phospho)	S(4): 100.0; T(11): 0.0; S(16): 0.0	S4;	S169	53		0	0	3	757.7	2271	41.88	7967
NHLsPQQGGATPQVPsPCCR	SEN3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl) S4(Phospho) S16(Phospho)	S(4): 100.0; T(11): 0.0; S(16): 100.0	S4; S16;	S169; S181	46		0	0	3	784.3	2351	45.45	8749
NHLsPQQGGATPQVPsPCCR	SEN3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl) S4(Phospho) T11(Phospho) S16(Phospho)	S(4): 100.0; T(11): 100.0; S(16): 100.0	S4; T11; S16;	S169; T176; S181	26		0	0	3	811	2431	50.88	9891
NHLsPQQGGATPQVPsPCCR	SEN3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl) S4(Phospho) S16(Phospho)	S(4): 100.0; T(11): 0.0; S(16): 100.0	S4; S16;	S169; S181		6.26	0	0	3	784.3	2351	45.45	8749
NHLsPQQGGATPQVPsPCCR	SEN3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl) S4(Phospho)	S(4): 100.0; T(11): 0.0; S(16): 0.0	S4;	S169		5.42	0	0	3	757.7	2271	41.88	7967

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#
NHLsPQQGGATPQVPsPCCR	SENP3	26168	sentrin-specific protease 3	C18(Carbamido methyl) C19(Carbamido methyl)S4(Phospho) T11(Phospho) S16(Phospho)	S(4): 100.0; T(11): 100.0; S(16): 100.0	S4; T11; S16;	S169; T176; S181		5.23	0	0	3	811	2431	50.88	9891
SDGsLEDGDDVHR	SERINC1	57515	serine incorporator 1 precursor	S4(Phospho)	S(1): 0.1; S(4): 99.9	S4;	S364	43		0	0	2	741.3	1482	22.83	3937
SDGsLEDGDDVHR	SERINC1	57515	serine incorporator 1 precursor	S4(Phospho)	S(1): 0.1; S(4): 99.9	S4;	S364		2.99	0	0	2	741.3	1482	22.83	3937
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7	34		0	1	2	565.8	1131	14.99	2268
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7	24		0	1	2	565.8	1131	15.52	2380
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7		4.3	0	1	2	565.8	1131	14.99	2268
RQsPLPPQK	SET	6418	protein SET isoform 1	S3(Phospho)	S(3): 100.0	S3;	S7		3.78	0	1	2	565.8	1131	15.52	2380
SsLSPSSAYER	SETD2	29072	histone-lysine N-methyltransferase SETD2	S2(Phospho)	S(1): 50.7; S(2): 98.6; S(4): 50.7; S(7): 0.0; S(8): 0.0; Y(10): 0.0	S2;	S2080	32		0	0	2	720.8	1441	52.31	10205
SSQSEGLGSeSDEDSVR	SETD2	29072	histone-lysine N-methyltransferase SETD2	S13(Phospho)	S(1): 48.9; S(2): 48.9; S(4): 2.1; S(11): 0.1; S(13): 100.0; S(17): 0.0	S13;	S323	22		0	0	2	1095	2189	78.93	15911
SSQSEGLGSeSDEDSVR	SETD2	29072	histone-lysine N-methyltransferase SETD2	S13(Phospho)	S(1): 48.9; S(2): 48.9; S(4): 2.1; S(11): 0.1; S(13): 100.0; S(17): 0.0	S13;	S323		2.8	0	0	2	1095	2189	78.93	15911
SsLSPSSAYER	SETD2	29072	histone-lysine N-methyltransferase SETD2	S2(Phospho)	S(1): 50.7; S(2): 98.6; S(4): 50.7; S(7): 0.0; S(8): 0.0; Y(10): 0.0	S2;	S2080		2.43	0	0	2	720.8	1441	52.31	10205
RSsLSPSSAYER	SETD2	29072	histone-lysine N-methyltransferase SETD2	S3(Phospho) S5(Phospho)	S(2): 0.1; S(3): 99.9; S(5): 100.0; S(8): 0.0; S(9): 0.0; Y(11): 0.0	S3; S5;	S2080; S2082	21		0.001	1	2	798.8	1597	39.83	7536
RSsLSPSSAYER	SETD2	29072	histone-lysine N-methyltransferase SETD2	S3(Phospho) S5(Phospho)	S(2): 0.1; S(3): 99.9; S(5): 100.0; S(8): 0.0; S(9): 0.0; Y(11): 0.0	S3; S5;	S2080; S2082		2.77	0.001	1	2	798.8	1597	39.83	7536
NSTLPMETsPCSSR	SETD2	29072	histone-lysine N-methyltransferase SETD2	C12(Carbamido methyl) S10(Phospho)	S(2): 0.0; T(3): 0.0; T(9): 2.4; S(10): 97.5; S(13): 0.1; S(14): 0.1	S10;	S1084		2.44	0.001	0	2	888.4	1776	46.84	9043
NSTLPMETsPCSSR	SETD2	29072	histone-lysine N-methyltransferase SETD2	C12(Carbamido methyl) S10(Phospho)	S(2): 0.0; T(3): 0.0; T(9): 2.4; S(10): 97.5; S(13): 0.1; S(14): 0.1	S10;	S1084	12		0.008	0	2	888.4	1776	46.84	9043
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 100.0; Y(21): 0.0; S(23): 0.0	S14; S16;	S80; S82	13		0	1	3	976.1	2926	68.67	13888
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 100.0; Y(21): 0.0; S(23): 0.0	S14; S16;	S80; S82	11		0	1	3	976.1	2926	68.16	13782
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 100.0; Y(21): 0.0; S(23): 0.0	S14; S16;	S80; S82		5.22	0	1	3	976.1	2926	68.67	13888
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 100.0; Y(21): 0.0; S(23): 0.0	S14; S16;	S80; S82		5.16	0	1	3	976.1	2926	68.16	13782
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 100.0; Y(21): 0.0; S(23): 0.0	S14; S16;	S80; S82		4.85	0	1	3	976.1	2926	69.19	13990
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 100.0; S(16): 99.6; Y(21): 0.5; S(23): 0.0	S14; S16;	S80; S82		3.69	0.001	1	3	976.1	2926	69.88	14144
TGDLGIPPNPEDRsPsPEIYNSEGK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 99.9; S(16): 99.3; Y(21): 0.7; S(23): 0.0	S14; S16;	S80; S82		2.97	0.001	1	3	976.1	2926	67.63	13650

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#
TGDLGIPPNPEDRsPsPEIYNSE GK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 99.9; S(16): 99.5; Y(21): 0.5; S(23): 0.0	S14; S16;	S80; S82		2.95	0.001	1	3	976.1	2926	67.57	13635
TGDLGIPPNPEDRsPsPEIYNSE GK	SF1	7536	splicing factor 1 isoform 3	S14(Phospho) S16(Phospho)	T(1): 0.0; S(14): 99.9; S(16): 99.6; Y(21): 0.5; S(23): 0.0	S14; S16;	S80; S82		2.44	0.003	1	3	976.1	2926	73.43	14847
KLSSWDQAEtPGHtPSLR	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T10(Phospho) T14(Phospho)	S(3): 0.0; S(4): 0.0; T(10): 100.0; T(14): 99.9; S(16): 0.1	T10; T14;	T223; T227	32		0	1	3	724	2170	49.75	9651
WDQTADQTPGAtPK	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T8(Phospho) T12(Phospho)	T(4): 0.0; T(8): 100.0; T(12): 100.0	T8; T12;	T207; T211	28		0	0	2	838.3	1676	41.7	7928
GGDSIGEtPTPGASK	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T8(Phospho)	S(4): 0.0; T(8): 100.0; T(10): 50.0; S(14): 50.0	T8;	T326	15		0	0	2	767.3	1534	35.9	6707
KLSSWDQAEtPGHtPSLR	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T10(Phospho) T14(Phospho)	S(3): 0.0; S(4): 0.0; T(10): 100.0; T(14): 99.9; S(16): 0.1	T10; T14;	T223; T227		4.53	0	1	3	724	2170	49.75	9651
WDQTADQTPGAtPK	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T8(Phospho) T12(Phospho)	T(4): 0.0; T(8): 100.0; T(12): 100.0	T8; T12;	T207; T211		3.85	0	0	2	838.3	1676	41.7	7928
GGDSIGEtPTPGASK	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T8(Phospho)	S(4): 0.0; T(8): 100.0; T(10): 50.0; S(14): 50.0	T8;	T326		3.49	0	0	2	767.3	1534	35.9	6707
LSSWDQAEtPGHtPSLR	SF3B1	23451	splicing factor 3B subunit 1 isoform 1	T9(Phospho) T13(Phospho)	S(2): 0.0; S(3): 0.0; T(9): 100.0; T(13): 99.9; S(15): 0.1	T9; T13;	T223; T227		3.69	0.003	0	3	681.3	2042	57.15	11272
SSLGQsAsETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S6(Phospho) S8(Phospho)	S(1): 0.0; S(2): 0.0; S(6): 100.0; S(8): 100.0; T(10): 0.0; T(14): 0.0; S(16): 0.0; S(18): 0.0	S6; S8;	S307; S309	93		0	0	2	1051	2101	54.99	10798
SSLGQsAsETEEDTVSVSKK	SF3B2	10992	splicing factor 3B subunit 2	S6(Phospho) S8(Phospho)	S(1): 0.0; S(2): 0.0; S(6): 100.0; S(8): 99.9; T(10): 0.1; T(14): 0.0; S(16): 0.0; S(18): 0.0	S6; S8;	S307; S309	43		0	1	3	743.6	2229	42.94	8188
SSLGQsAsETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S8(Phospho)	S(1): 49.9; S(2): 49.9; S(6): 7.1; S(8): 88.3; T(10): 4.8; T(14): 0.0; S(16): 0.0; S(18): 0.0	S8;	S309	33		0	0	2	1051	2101	55.41	10886
SSLGQsAsETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S8(Phospho)	S(1): 0.1; S(2): 0.1; S(6): 2.7; S(8): 94.4; T(10): 2.7; T(14): 0.0; S(16): 0.0; S(18): 0.0	S8;	S309	31		0	0	2	1011	2021	47.07	9093
ssLGQsAsETEEDTVSVSKK	SF3B2	10992	splicing factor 3B subunit 2	S1(Phospho) S2(Phospho)	S(1): 100.0; S(2): 99.8; S(6): 0.2; S(8): 0.0; T(10): 0.0; T(14): 0.0; S(16): 0.0; S(18): 0.0	S1; S2;	S302; S303	23		0	1	2	1115	2229	42.95	8190
SSLGQsAsETEEDTVSVSKK	SF3B2	10992	splicing factor 3B subunit 2	S6(Phospho) S8(Phospho)	S(1): 0.0; S(2): 0.0; S(6): 100.0; S(8): 99.9; T(10): 0.1; T(14): 0.0; S(16): 0.0; S(18): 0.0	S6; S8;	S307; S309		5.23	0	1	3	743.6	2229	42.94	8188
GFEHHKsDDssDDEQEKKPEAPK	SF3B2	10992	splicing factor 3B subunit 2	S9(Phospho) S13(Phospho) S14(Phospho)	S(9): 100.0; S(13): 100.0; S(14): 100.0	S9; S13; S14;	S431; S435; S436		4.15	0	2	3	1078	3231	24.91	4371
SSLGQsAsETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S6(Phospho) S8(Phospho)	S(1): 0.0; S(2): 0.0; S(6): 100.0; S(8): 100.0; T(10): 0.0; T(14): 0.0; S(16): 0.0; S(18): 0.0	S6; S8;	S307; S309		3.88	0	0	2	1051	2101	54.99	10798
SSLGQsAsETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S8(Phospho)	S(1): 49.9; S(2): 49.9; S(6): 7.1; S(8): 88.3; T(10): 4.8; T(14): 0.0; S(16): 0.0; S(18): 0.0	S8;	S309		3.2	0	0	2	1051	2101	55.41	10886

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#
ssLGQSASETEEDTVSVSKK	SF3B2	10992	splicing factor 3B subunit 2	S1(Phospho) S2(Phospho)	S(1): 100.0; S(2): 99.8; S(6): 0.2; S(8): 0.0; T(10): 0.0; T(14): 0.0; S(16): 0.0; S(18): 0.0	S1; S2;	S302; S303		2.88	0	1	2	1115	2229	42.95	8190
SSLGQSASETEEDTVSVSK	SF3B2	10992	splicing factor 3B subunit 2	S8(Phospho)	S(1): 0.1; S(2): 0.1; S(6): 2.7; S(8): 94.4; T(10): 2.7; T(14): 0.0; S(16): 0.0; S(18): 0.0	S8;	S309		2.54	0	0	2	1011	2021	47.07	9093
GFEHHKDsDDDssDDEQEKKPEAPK	SF3B2	10992	splicing factor 3B subunit 2	S9(Phospho) S13(Phospho) S14(Phospho)	S(9): 100.0; S(13): 100.0; S(14): 100.0	S9; S13; S14;	S431; S435; S436	20		0.001	2	3	1078	3231	24.91	4371
VKLDDDDDDDEEsKEGQESSSSAANTNP AVAPPCVVVEEK	SFSWAP	6433	splicing factor, suppressor of white-apricot homolog isoform 2	C34(Carbamido methyl) S13(Phospho)	S(7): 0.3; S(13): 79.8; S(19): 4.9; S(20): 4.9; S(21): 4.9; S(22): 4.9; T(26): 0.3	S13;	S610	15		0	2	4	1083	4328	56.57	11134
VKLDDDDDDDEEsKEGQESSSSAANTNP AVAPPCVVVEEK	SFSWAP	6433	splicing factor, suppressor of white-apricot homolog isoform 2	C34(Carbamido methyl) S13(Phospho)	S(7): 0.3; S(13): 79.8; S(19): 4.9; S(20): 4.9; S(21): 4.9; S(22): 4.9; T(26): 0.3	S13;	S610		4.16	0	2	4	1083	4328	56.57	11134
NsLTGEEGQLAR	SGPP1	81537	sphingosine-1-phosphate phosphatase 1	S2(Phospho)	S(2): 100.0; T(4): 0.0	S2;	S112	50		0	0	2	677.8	1355	43.06	8214
RNsLTGEEGQLAR	SGPP1	81537	sphingosine-1-phosphate phosphatase 1	S3(Phospho)	S(3): 100.0; T(5): 0.0	S3;	S112	41		0	1	2	755.9	1511	33.72	6233
RNsLTGEEGQLAR	SGPP1	81537	sphingosine-1-phosphate phosphatase 1	S3(Phospho)	S(3): 100.0; T(5): 0.0	S3;	S112		3.58	0	1	2	755.9	1511	33.72	6233
NsLTGEEGQLAR	SGPP1	81537	sphingosine-1-phosphate phosphatase 1	S2(Phospho)	S(2): 100.0; T(4): 0.0	S2;	S112		2.99	0	0	2	677.8	1355	43.06	8214
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	M2(Oxidation) S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 95.0; S(15): 5.0; S(19): 0.0	S8; T12;	S77; T81	16		0	2	4	719.3	2874	35.92	6712
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 100.0; S(15): 0.0; S(19): 0.0	S8; T12;	S77; T81	15		0	2	3	953.4	2858	43.53	8313
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	M2(Oxidation) S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 100.0; S(15): 0.0; S(19): 0.0	S8; T12;	S77; T81	12		0	2	3	958.7	2874	35.91	6710
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	M2(Oxidation) S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 95.0; S(15): 5.0; S(19): 0.0	S8; T12;	S77; T81		4.25	0	2	4	719.3	2874	35.92	6712
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 100.0; S(15): 0.0; S(19): 0.0	S8; T12;	S77; T81		2.95	0	2	3	953.4	2858	43	8202
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 100.0; S(15): 0.0; S(19): 0.0	S8; T12;	S77; T81		3.22	0.001	2	3	953.4	2858	43.53	8313
SRtPSASNDQQE	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	T3(Phospho)	S(1): 1.4; T(3): 98.6; S(5): 0.0; S(7): 0.0	T3;	T303	40		0.003	1	2	757.8	1515	13.64	1984
EMPQDLRsPARTPPSEEDSAEAER	SGTA	6449	small glutamine-rich tetratricopeptide repeat-containing protein alpha	M2(Oxidation) S8(Phospho) T12(Phospho)	S(8): 100.0; T(12): 100.0; S(15): 0.0; S(19): 0.0	S8; T12;	S77; T81		3.42	0.003	2	3	958.7	2874	35.91	6710
EAEEGPTGASESQDsPR	SH3PXD2A	9644	SH3 and PX domain-containing protein 2A	S15(Phospho)	T(7): 0.0; S(10): 0.0; S(12): 0.0; S(15): 100.0	S15;	S519	26		0	0	2	913.9	1827	22.49	3863
EAEEGPTGASESQDsPR	SH3PXD2A	9644	SH3 and PX domain-containing protein 2A	S15(Phospho)	T(7): 0.0; S(10): 0.0; S(12): 0.0; S(15): 100.0	S15;	S519		3.16	0	0	2	913.9	1827	22.49	3863
AQsPGsPLHAR	SHROOM2	357	protein Shroom2	S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0	S3; S6;	S1036; S1039	43		0	0	2	640.8	1281	27.41	4918
AQsPGsPLHAR	SHROOM2	357	protein Shroom2	S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0	S3; S6;	S1036; S1039		2.91	0	0	2	640.8	1281	27.41	4918

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#
TLsDEsLCSGR	SIPA1L3	23094	signal-induced proliferation-associated 1-like protein 3	C8(Carbamidomethyl)S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 100.0; S(9): 0.0	S3; S6;	S1544; S1547	49		0	0	2	692.7	1384	48.75	9442
GPPTPRTTPTMSEEPPLDLTGK	SIPA1L3	23094	signal-induced proliferation-associated 1-like protein 3	T4(Phospho)	T(4): 99.9; T(7): 50.0; T(8): 50.0; T(10): 0.0; S(12): 0.0; T(20): 0.0	T4;	T1699	26		0	1	3	828	2482	71.06	14374
TLsDEsLCSGR	SIPA1L3	23094	signal-induced proliferation-associated 1-like protein 3	C8(Carbamidomethyl)S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(6): 100.0; S(9): 0.0	S3; S6;	S1544; S1547		3.23	0	0	2	692.7	1384	48.75	9442
GPPTPRTTPTMSEEPPLDLTGK	SIPA1L3	23094	signal-induced proliferation-associated 1-like protein 3	T4(Phospho)	T(4): 99.9; T(7): 50.0; T(8): 50.0; T(10): 0.0; S(12): 0.0; T(20): 0.0	T4;	T1699		3.05	0	1	3	828	2482	71.06	14374
NSVHEQEAINsDPeLNCNCFQK	SKA3	221150	spindle and kinetochore-associated protein 3 isoform 2	C18(Carbamidomethyl)S11(Phospho)	S(2): 0.0; S(11): 96.7; S(16): 3.3	S11;	S119	14		0	0	3	923.7	2769	47.49	9178
NSVHEQEAINsDPeLNCNCFQK	SKA3	221150	spindle and kinetochore-associated protein 3 isoform 2	C18(Carbamidomethyl)S11(Phospho)	S(2): 0.0; S(11): 96.7; S(16): 3.3	S11;	S119		3.62	0	0	3	923.7	2769	47.49	9178
LtSIGSDEDEETETYQEK	SLC12A6	9990	solute carrier family 12 member 6 isoform c	T2(Phospho)	T(2): 89.2; S(3): 5.4; S(6): 5.4; T(12): 0.0; T(14): 0.0; Y(15): 0.0	T2;	T969		2.23	0.001	0	2	1077	2154	49.07	9510
TEAPGTPEGPEPERPSPGDGNPR	SLC12A7	10723	solute carrier family 12 member 7	T6(Phospho)	T(1): 0.0; T(6): 100.0; S(16): 0.0	T6;	T30	34		0	0	3	808.7	2424	33.23	6135
TEAPGTPEGPEPERPSPGDGNPR	SLC12A7	10723	solute carrier family 12 member 7	T6(Phospho)	T(1): 0.0; T(6): 100.0; S(16): 0.0	T6;	T30		3.08	0	0	3	808.7	2424	33.23	6135
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho) S9(Phospho)	S(3): 100.0; T(8): 0.1; S(9): 99.9; T(20): 0.0	S3; S9;	S461; S467	43		0	2	3	826.7	2478	31.36	5744
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 97.7; T(8): 2.3; S(9): 0.0; T(20): 0.0	S3;	S461	32		0	2	4	600.3	2398	29.98	5459
EsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S2(Phospho)	S(2): 100.0; T(7): 0.0; S(8): 0.0; T(19): 0.0	S2;	S461	29		0	1	3	757.4	2270	32.65	6014
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 100.0; T(8): 0.0; S(9): 0.0; T(20): 0.0	S3;	S461	29		0	2	4	600.3	2398	31.01	5673
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 97.6; T(8): 2.4; S(9): 0.0; T(20): 0.0	S3;	S461	26		0	2	4	600.3	2398	30.49	5565
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 93.8; T(8): 3.1; S(9): 3.1; T(20): 0.0	S3;	S461	25		0	2	3	800.1	2398	29.55	5370
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho) S9(Phospho)	S(3): 99.9; T(8): 0.1; S(9): 100.0; T(20): 0.0	S3; S9;	S461; S467	23		0	2	4	620.3	2478	31.37	5748
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 97.7; T(8): 2.3; S(9): 0.0; T(20): 0.0	S3;	S461		6.47	0	2	4	600.3	2398	29.98	5459
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 97.6; T(8): 2.4; S(9): 0.0; T(20): 0.0	S3;	S461		6.17	0	2	4	600.3	2398	30.49	5565
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho) S9(Phospho)	S(3): 100.0; T(8): 0.1; S(9): 99.9; T(20): 0.0	S3; S9;	S461; S467		5.5	0	2	3	826.7	2478	31.36	5744
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 100.0; T(8): 0.0; S(9): 0.0; T(20): 0.0	S3;	S461		5.25	0	2	4	600.3	2398	31.01	5673
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho)	S(3): 93.8; T(8): 3.1; S(9): 3.1; T(20): 0.0	S3;	S461		4.93	0	2	3	800.1	2398	29.55	5370
EsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S2(Phospho)	S(2): 100.0; T(7): 0.0; S(8): 0.0; T(19): 0.0	S2;	S461		4.49	0	1	3	757.4	2270	32.65	6014
KEsKEEETsIDVAGKPNEVTk	SLC16A1	6566	monocarboxylate transporter 1	S3(Phospho) S9(Phospho)	S(3): 99.9; T(8): 0.1; S(9): 100.0; T(20): 0.0	S3; S9;	S461; S467		4.36	0	2	4	620.3	2478	31.37	5748
DVEMGNsVIEENEMK	SLC1A3	6507	excitatory amino acid transporter 1 isoform 5	M4(Oxidation) S7(Phospho)	S(7): 100.0	S7;	S400	29		0	0	2	910.4	1820	52.48	10243
DVEMGNsVIEENEMK	SLC1A3	6507	excitatory amino acid transporter 1 isoform 5	S7(Phospho)	S(7): 100.0	S7;	S400	14		0	0	2	902.4	1804	63.7	12736

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#
DVEMGNsVIEENEMK	SLC1A3	6507	excitatory amino acid transporter 1 isoform 5	M4(Oxidation) S7(Phospho)	S(7): 100.0	S7;	S400		2.2	0	0	2	910.4	1820	52.48	10243
DVEMGNsVIEENEMK	SLC1A3	6507	excitatory amino acid transporter 1 isoform 5	S7(Phospho)	S(7): 100.0	S7;	S400		1.98	0.001	0	2	902.4	1804	63.7	12736
EIKCsPSEsPLMEK	SLC20A1	6574	sodium-dependent phosphate transporter 1	C4(Carbamidomethyl)S5(Phospho) S9(Phospho)	S(5): 97.4; S(7): 2.6; S(9): 100.0	S5; S9;	S265; S269	20		0	1	2	897.9	1795	44.9	8630
EIKCsPSEsPLMEK	SLC20A1	6574	sodium-dependent phosphate transporter 1	C4(Carbamidomethyl)S5(Phospho) S9(Phospho)	S(5): 97.4; S(7): 2.6; S(9): 100.0	S5; S9;	S265; S269		3.02	0	1	2	897.9	1795	44.9	8630
EIKCsPSEsPLMEK	SLC20A1	6574	sodium-dependent phosphate transporter 1	C4(Carbamidomethyl) M12(Oxidation) S5(Phospho) S9(Phospho)	S(5): 100.0; S(7): 3.2; S(9): 96.8	S5; S9;	S265; S269		2.25	0.007	1	2	905.9	1811	37.37	7018
sLTNSHLEK	SLC38A1	81539	sodium-coupled neutral amino acid transporter 1 isoform 1	S1(Phospho)	S(1): 98.9; T(3): 1.1; S(5): 0.0	S1;	S52	34		0	0	2	554.8	1109	21.22	3596
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	29		0	0	2	594.7	1188	26.34	4679
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		3.61	0	0	2	594.7	1188	26.34	4679
sLTNSHLEK	SLC38A1	81539	sodium-coupled neutral amino acid transporter 1 isoform 1	S1(Phospho)	S(1): 98.9; T(3): 1.1; S(5): 0.0	S1;	S52		2.83	0	0	2	554.8	1109	21.22	3596
RsLTNSHLEK	SLC38A1	81539	sodium-coupled neutral amino acid transporter 1 isoform 1	S2(Phospho)	S(2): 100.0; T(4): 50.0; S(6): 50.0	S2;	S52		3.62	0.001	1	2	672.8	1345	19.19	3167
EKQssEEEEKETR	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	55		0	2	2	884.8	1769	12.44	1712
EKQssEEEEKETR	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	37		0	2	3	590.2	1769	12.44	1715
EKQssEEEEKETR	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		4.68	0	2	3	590.2	1769	12.44	1715
EKQssEEEEKETR	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		4.01	0	2	2	884.8	1769	12.44	1712
ESDKEDGRsPSYDTPSQR	SLC4A7	9497	sodium bicarbonate cotransporter 3 isoform c	S10(Phospho)	S(2): 0.0; S(10): 100.0; S(12): 0.0; Y(13): 0.0; T(15): 0.0; S(17): 0.0	S10;	S84	26		0	2	3	755	2263	19.96	3329
ESDKEDGRsPSYDTPSQR	SLC4A7	9497	sodium bicarbonate cotransporter 3 isoform c	S10(Phospho)	S(2): 0.0; S(10): 100.0; S(12): 0.0; Y(13): 0.0; T(15): 0.0; S(17): 0.0	S10;	S84		5.17	0	2	3	755	2263	19.96	3329
VSAsSFHFVGENDENQDR	SLC6A14	11254	sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	S4(Phospho)	S(2): 0.1; S(4): 97.7; S(5): 2.2	S4;	S21	44		0	0	3	738.6	2214	37.48	7039
VSAsSFHFVGENDENQDR	SLC6A14	11254	sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	S4(Phospho)	S(2): 2.3; S(4): 95.4; S(5): 2.3	S4;	S21	30		0	0	2	1107	2214	37.58	7060
VSAsSFHFVGENDENQDR	SLC6A14	11254	sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	S4(Phospho)	S(2): 0.1; S(4): 97.7; S(5): 2.2	S4;	S21		6.47	0	0	3	738.6	2214	37.48	7039
VSAsSFHFVGENDENQDR	SLC6A14	11254	sodium- and chloride-dependent neutral and basic amino acid transporter B(0+)	S4(Phospho)	S(2): 2.3; S(4): 95.4; S(5): 2.3	S4;	S21		2.81	0	0	2	1107	2214	37.58	7060
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	50		0	0	2	891.4	1782	43.91	8394
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 97.7; S(5): 2.3; T(15): 0.0	S1;	S31	43		0	0	2	891.4	1782	42.68	8133
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	14		0	0	2	891.4	1782	43.03	8207

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#
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		4.37	0	0	2	891.4	1782	43.91	8394
sADGSAPAGEGEGVTLQR	SLC7A5	8140	large neutral amino acids transporter small subunit 1	S1(Phospho)	S(1): 97.7; S(5): 2.3; T(15): 0.0	S1;	S31		3.87	0	0	2	891.4	1782	42.68	8133
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		3.13	0	0	2	891.4	1782	43.03	8207
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 0.0; T(4): 0.0; S(5): 0.0; S(6): 0.0; T(9): 0.0; T(14): 0.0; S(18): 0.0; S(20): 97.8; S(22): 2.1; S(23): 0.0	S20;	S785	38		0	1	3	887.4	2660	45.34	8725
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 48.2; T(4): 1.8; S(5): 48.2; S(6): 1.8; T(9): 0.1; T(14): 0.0; S(18): 0.0; S(20): 99.8; S(22): 0.1; S(23): 0.0	S20;	S785	23		0	1	3	914	2740	52.39	10222
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 0.0; T(4): 0.0; S(5): 0.0; S(6): 0.0; T(9): 0.0; T(14): 0.0; S(18): 0.2; S(20): 99.7; S(22): 0.2; S(23): 0.0	S20;	S785	15		0	1	2	1331	2660	45.46	8752
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 0.0; T(4): 0.0; S(5): 0.0; S(6): 0.0; T(9): 0.0; T(14): 0.0; S(18): 0.0; S(20): 97.8; S(22): 2.1; S(23): 0.0	S20;	S785		7	0	1	3	887.4	2660	45.34	8725
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S23(Phospho)	S(1): 0.0; T(4): 0.0; S(5): 0.0; S(6): 0.0; T(9): 0.0; T(14): 0.0; S(18): 0.1; S(20): 51.1; S(22): 51.1; S(23): 97.6	S23;	S788		4.53	0	1	3	914	2740	54.22	10634
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 48.2; T(4): 1.8; S(5): 48.2; S(6): 1.8; T(9): 0.1; T(14): 0.0; S(18): 0.0; S(20): 99.8; S(22): 0.1; S(23): 0.0	S20;	S785		4.25	0	1	3	914	2740	52.39	10222
SKETSSPGTDDVFTAPSDsPSSQR	SLC9A1	6548	sodium/hydrogen exchanger 1	S20(Phospho)	S(1): 0.0; T(4): 0.0; S(5): 0.0; S(6): 0.0; T(9): 0.0; T(14): 0.0; S(18): 0.2; S(20): 99.7; S(22): 0.2; S(23): 0.0	S20;	S785		2.45	0	1	2	1331	2660	45.46	8752
DSGsISLQETR	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(6): 0.0; T(10): 0.0	S4;	S779	76		0	0	2	636.8	1273	41.62	7912
VEDESAEDTQsNDGKEVVEVGQK	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S11(Phospho)	S(5): 0.0; T(9): 3.2; S(11): 96.8	S11;	S571	36		0	1	3	853.4	2558	38.07	7162
VEDESAEDTQsNDGKEVVEVGQK	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S5(Phospho) S11(Phospho)	S(5): 100.0; T(9): 5.0; S(11): 95.0	S5; S11;	S565; S571	15		0	1	3	880	2638	44.01	8415
VEDESAEDTQsNDGKEVVEVGQK	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S11(Phospho)	S(5): 0.0; T(9): 3.2; S(11): 96.8	S11;	S571		4.84	0	1	3	853.4	2558	38.07	7162
VEDESAEDTQsNDGKEVVEVGQK	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S5(Phospho) S11(Phospho)	S(5): 100.0; T(9): 5.0; S(11): 95.0	S5; S11;	S565; S571		4.06	0	1	3	880	2638	44.01	8415
DSGsISLQETR	SLK	9748	STE20-like serine/threonine-protein kinase isoform 2	S4(Phospho)	S(2): 0.0; S(4): 100.0; S(6): 0.0; T(10): 0.0	S4;	S779		3.26	0	0	2	636.8	1273	41.62	7912
DGQDAIAQSPEKEsK	SLTM	79811	SAFB-like transcription modulator isoform b	S14(Phospho)	S(9): 0.0; S(14): 100.0	S14;	S276	23		0	1	2	841.9	1683	22	3758
IsKSPGHMVILDQTK	SLTM	79811	SAFB-like transcription modulator isoform b	M9(Oxidation) S2(Phospho)	S(2): 98.5; S(3): 50.8; S(5): 50.8; T(15): 0.0	S2;	S532	21		0	1	3	639.6	1917	37.28	6998
DGQDAIAQSPEKEsK	SLTM	79811	SAFB-like transcription modulator isoform b	S14(Phospho)	S(9): 0.0; S(14): 100.0	S14;	S276		4.35	0	1	2	841.9	1683	22	3758

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#
IsSKSPGHMVILDQTK	SLTM	79811	SAFB-like transcription modulator isoform b	M9(Oxidation)S2(Phospho)	S(2): 98.5; S(3): 50.8; S(5): 50.8; T(15): 0.0	S2;	S532		3.22	0	1	3	639.6	1917	37.28	6998
IAKEEEsEDEsNEEEEEDEEsESEA	SMARCA2	6595	probable global transcription activator SNF2L2 isoform d	S7(Phospho)S11(Phospho)S23(Phospho)	S(7): 100.0; S(11): 100.0; S(23): 95.1; S(25): 4.9	S7; S11; S23;	S170; S174; S186	18		0.002	1	3	1176	3527	39.99	7572
IAKEEEsEDEsNEEEEEDEEsESEA	SMARCA2	6595	probable global transcription activator SNF2L2 isoform d	S7(Phospho)S11(Phospho)S23(Phospho)	S(7): 100.0; S(11): 100.0; S(23): 95.1; S(25): 4.9	S7; S11; S23;	S170; S174; S186	4.48	0.003		1	3	1176	3527	39.99	7572
DSDAGSStPTTSTR	SMARCA4	6597	transcription activator BRG1 isoform F	T8(Phospho)	S(2): 0.0; S(6): 0.0; S(7): 1.8; T(8): 96.3; T(10): 1.8; T(11): 0.0; S(12): 0.0; T(13): 0.0	T8;	T1390	48		0	0	2	731.8	1463	15.74	2426
QKIEKEDDsEGEEsEEEEEGEEGsESES	SMARCA4	6597	transcription activator BRG1 isoform F	S9(Phospho)S14(Phospho)S25(Phospho)	S(9): 100.0; S(14): 100.0; S(25): 99.1; S(27): 0.8; S(29): 0.0	S9; S14; S25;	S1536; S1541; S1552	30		0	2	3	1229	3684	31.94	5866
DSDAGSStPTTSTR	SMARCA4	6597	transcription activator BRG1 isoform F	T8(Phospho)	S(2): 0.0; S(6): 0.0; S(7): 1.8; T(8): 96.3; T(10): 1.8; T(11): 0.0; S(12): 0.0; T(13): 0.0	T8;	T1390		3.75	0	0	2	731.8	1463	15.74	2426
KAENAEGQTPAIGPDGEPLDETSQMSDL PVK	SMARCA4	6597	transcription activator BRG1 isoform F	T9(Phospho)S26(Phospho)	T(9): 89.3; T(22): 5.3; S(23): 5.3; S(26): 100.0	T9; S26;	T596; S613	12		0.001	1	3	1129	3384	75.72	15296
QKIEKEDDsEGEEsEEEEEGEEGsESES	SMARCA4	6597	transcription activator BRG1 isoform F	S9(Phospho)S14(Phospho)S25(Phospho)	S(9): 100.0; S(14): 100.0; S(25): 99.1; S(27): 0.8; S(29): 0.0	S9; S14; S25;	S1536; S1541; S1552	3.34	0.001		2	3	1229	3684	31.94	5866
KAENAEGQTPAIGPDGEPLDETSQMSDL PVK	SMARCA4	6597	transcription activator BRG1 isoform F	T9(Phospho)S26(Phospho)	T(9): 89.3; T(22): 5.3; S(23): 5.3; S(26): 100.0	T9; S26;	T596; S613		3.17	0.001	1	3	1129	3384	75.72	15296
KLsssSEPYEEDFNDDQSIKK	SMARCAD1	56916	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 isoform b	S3(Phospho)S4(Phospho)S5(Phospho)	S(3): 100.0; S(4): 100.0; S(5): 99.7; S(6): 0.4; Y(9): 0.0; S(19): 0.0	S3; S4; S5;	S211; S212; S213		3.97	0	2	3	939	2815	55.67	10940
KLSSsSEPYEEDFNDDQSIK	SMARCAD1	56916	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 isoform b	S5(Phospho)	S(3): 51.1; S(4): 51.1; S(5): 93.1; S(6): 4.7; Y(9): 0.0; S(19): 0.0	S5;	S213		3.57	0	1	3	869.7	2607	59.09	11703
ANtPDSITEKtEDSSVPETPDNER	SMARCAD1	56916	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A containing DEAD/H box 1 isoform b	T3(Phospho)T12(Phospho)	T(3): 99.4; S(6): 6.0; T(9): 5.5; T(12): 78.1; S(15): 5.5; S(16): 5.5; T(20): 0.0	T3; T12;	T54; T63		2.51	0	1	3	969.7	2907	50.96	9907
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	39		0	1	3	592.3	1775	20.84	3513
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	35		0	1	3	592.3	1775	20.33	3405
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	27		0	1	2	887.9	1775	20.26	3392
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	25		0	1	2	887.9	1775	20.8	3506
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		6.35	0	1	3	592.3	1775	20.84	3513
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		5.94	0	1	3	592.3	1775	20.33	3405

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#
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		3.6	0	1	2	887.9	1775	20.8	3506
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		3.46	0	1	2	887.9	1775	20.26	3392
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	30		0	2	3	514.6	1542	13.38	1930
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; S(7): 0.0; T(9): 0.0	S3; S5;	S302; S304	28		0	2	2	771.3	1542	13.34	1921
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	22		0	2	2	771.3	1542	13.86	2030
KRsPsPsPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0; T(9): 0.0	S3; S5; S7;	S302; S304; S306	21		0	2	3	541.2	1622	15.39	2353
RsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 0.0; T(8): 0.0	S2; S4;	S302; S304	21		0	1	2	707.3	1414	18.64	3051
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		6.19	0	2	3	514.6	1542	13.38	1930
KRsPsPsPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0; T(9): 0.0	S3; S5; S7;	S302; S304; S306		6.13	0	2	3	541.2	1622	15.39	2353
KRsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; S(7): 0.0; T(9): 0.0	S3; S5;	S302; S304		4.86	0	2	2	771.3	1542	13.34	1921
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		3.96	0	2	2	771.3	1542	13.86	2030
RsPsPSPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S2(Phospho) S4(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 0.0; T(8): 0.0	S2; S4;	S302; S304		3.93	0	1	2	707.3	1414	18.64	3051
KRsPsPsPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0; T(9): 0.0	S3; S5; S7;	S302; S304; S306		3.88	0	2	2	811.3	1622	15.37	2349
KRsPsPsPTPEAK	SMARCC2	6601	SWI/SNF complex subunit SMARCC2 isoform b	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0; T(9): 0.0	S3; S5; S7;	S302; S304; S306	14		0.009	2	2	811.3	1622	15.37	2349
GtMDDISQEEGSSQGEDSVSGSQR	SMC1A	8243	structural maintenance of chromosomes protein 1A isoform 2	T2(Phospho)	T(2): 95.2; S(7): 0.2; S(12): 0.0; S(13): 0.0; S(18): 0.2; S(20): 4.2; S(22): 0.2	T2;	T924	32		0	0	3	856	2566	45.37	8732
GtMDDISQEEGSSQGEDSVSGSQR	SMC1A	8243	structural maintenance of chromosomes protein 1A isoform 2	T2(Phospho)	T(2): 95.2; S(7): 0.2; S(12): 0.0; S(13): 0.0; S(18): 0.2; S(20): 4.2; S(22): 0.2	T2;	T924		4	0	0	3	856	2566	45.37	8732
KGDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S9(Phospho)	S(7): 0.1; S(9): 99.9; S(16): 0.0; S(19): 0.0	S9;	S1067	79		0	1	2	1124	2247	15.65	2409
KGDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S9(Phospho)	S(7): 2.0; S(9): 98.0; S(16): 0.0; S(19): 0.0	S9;	S1067	58		0	1	3	749.6	2247	15.73	2425
GDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S6(Phospho)	S(6): 99.9; S(8): 0.1; S(15): 0.0; S(18): 0.0	S6;	S1065	38		0	0	2	1060	2119	20.48	3438
KGDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S9(Phospho)	S(7): 2.0; S(9): 98.0; S(16): 0.0; S(19): 0.0	S9;	S1067		5.61	0	1	3	749.6	2247	15.73	2425
KGDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S9(Phospho)	S(7): 0.1; S(9): 99.9; S(16): 0.0; S(19): 0.0	S9;	S1067		4.21	0	1	2	1124	2247	15.65	2409
GDVEGSQsQDEGEGSGESER	SMC3	9126	structural maintenance of chromosomes protein 3	S6(Phospho)	S(6): 99.9; S(8): 0.1; S(15): 0.0; S(18): 0.0	S6;	S1065		2.7	0	0	2	1060	2119	20.48	3438
REEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S15(Phospho)	S(9): 0.1; S(14): 3.1; S(15): 96.8; S(23): 0.0	S15;	S28	67		0	1	3	865.7	2595	37.89	7124

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#
tESPATAETAASELDNR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	T1(Phospho)	T(1): 95.7; S(3): 2.1; T(6): 2.1; T(10): 0.0; S(12): 0.0	T1;	T39	62		0	0	2	986.4	1972	63.99	12807
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S16(Phospho)	S(10): 0.0; S(15): 0.1; S(16): 99.9; S(24): 0.0	S16;	S28	57		0	2	3	917.7	2751	34.68	6441
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 100.0; S(15): 4.5; S(16): 95.5; S(24): 0.0	S10; S16;	S22; S28	43		0	2	3	944.4	2831	36.4	6814
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S16(Phospho)	S(10): 0.0; S(15): 3.1; S(16): 96.9; S(24): 0.0	S16;	S28	40		0	2	3	917.7	2751	34.13	6320
RREEGPPPPSPDGASSDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho)	S(10): 93.1; S(15): 3.5; S(16): 3.5; S(24): 0.0	S10;	S22	36		0	2	3	917.7	2751	33.62	6214
REEGPPPPSPDGASSDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S9(Phospho)	S(9): 100.0; S(14): 50.0; S(15): 50.0; S(23): 0.0	S9;	S22	35		0	1	3	892.4	2675	41.41	7869
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 99.8; S(15): 0.3; S(16): 99.8; S(24): 0.0	S10; S16;	S22; S28	34		0	2	3	944.4	2831	36.92	6922
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 100.0; S(15): 5.5; S(16): 94.5; S(24): 0.0	S10; S16;	S22; S28	18		0	2	3	944.4	2831	35.82	6692
EEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S13(Phospho) S14(Phospho)	S(8): 11.9; S(13): 94.0; S(14): 94.0; S(22): 0.0	S13; S14;	S27; S28	16		0	0	3	840.3	2519	50.85	9884
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 100.0; S(15): 4.5; S(16): 95.5; S(24): 0.0	S10; S16;	S22; S28		7.36	0	2	3	944.4	2831	36.4	6814
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S16(Phospho)	S(10): 0.0; S(15): 3.1; S(16): 96.9; S(24): 0.0	S16;	S28		5.61	0	2	3	917.7	2751	34.13	6320
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 99.8; S(15): 0.3; S(16): 99.8; S(24): 0.0	S10; S16;	S22; S28		5.06	0	2	3	944.4	2831	36.92	6922
REEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S15(Phospho)	S(9): 0.1; S(14): 3.1; S(15): 96.8; S(23): 0.0	S15;	S28		4.75	0	1	3	865.7	2595	37.89	7124
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S16(Phospho)	S(10): 0.0; S(15): 0.1; S(16): 99.9; S(24): 0.0	S16;	S28		4.61	0	2	3	917.7	2751	34.68	6441
REEGPPPPSPDGASSDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S9(Phospho)	S(9): 100.0; S(14): 50.0; S(15): 50.0; S(23): 0.0	S9;	S22		4.53	0	1	3	892.4	2675	41.41	7869
tESPATAETAASELDNR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	T1(Phospho)	T(1): 95.7; S(3): 2.1; T(6): 2.1; T(10): 0.0; S(12): 0.0	T1;	T39		4.25	0	0	2	986.4	1972	63.99	12807
RREEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho) S16(Phospho)	S(10): 100.0; S(15): 5.5; S(16): 94.5; S(24): 0.0	S10; S16;	S22; S28		4.24	0	2	3	944.4	2831	35.82	6692
EEGPPPPSPDGASsDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S13(Phospho) S14(Phospho)	S(8): 11.9; S(13): 94.0; S(14): 94.0; S(22): 0.0	S13; S14;	S27; S28		3.21	0	0	3	840.3	2519	50.85	9884
RREEGPPPPSPDGASSDAEPEPPSGR	SMC4	10051	structural maintenance of chromosomes protein 4 isoform 1	S10(Phospho)	S(10): 93.1; S(15): 3.5; S(16): 3.5; S(24): 0.0	S10;	S22		3.69	0.003	2	3	917.7	2751	33.62	6214
FYLPGTSRPPiIVsEFR	SMC6	79677	structural maintenance of chromosomes protein 6	S14(Phospho)	Y(2): 6.6; T(6): 0.6; S(7): 6.6; S(14): 86.2	S14;	S565		1.4	0.008	0	2	1030	2059	51.97	10121

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#
NLATsAdtPPSTVPGTGK	SMG1	23049	serine/threonine-protein kinase SMG1	S5(Phospho) T8(Phospho)	T(4): 7.4; S(5): 96.3; T(8): 96.3; S(11): 0.0; T(12): 0.0; T(16): 0.0	S5; T8;	S3570; T3573	27		0	0	2	937.4	1874	57.84	11413
NLATsAdtPPSTVPGTGK	SMG1	23049	serine/threonine-protein kinase SMG1	S5(Phospho) T8(Phospho)	T(4): 7.4; S(5): 96.3; T(8): 96.3; S(11): 0.0; T(12): 0.0; T(16): 0.0	S5; T8;	S3570; T3573		3	0	0	2	937.4	1874	57.84	11413
ELVGDTGSQEGDHEPsGsETEEDTSSSP HR	SMIM13	221710	small integral membrane protein 13	S16(Phospho) S18(Phospho)	T(6): 1.2; S(8): 1.2; S(16): 98.3; S(18): 92.0; T(20): 7.4; T(24): 0.0; S(25): 0.0; S(26): 0.0; S(27): 0.0	S16; S18;	S58; S60	47		0	0	3	1106	3316	35.26	6575
ELVGDTGSQEGDHEPsGsETEEDTSSSPH R	SMIM13	221710	small integral membrane protein 13	T6(Phospho) S16(Phospho)	T(6): 98.8; S(8): 9.1; S(16): 91.3; S(18): 50.4; T(20): 50.4; T(24): 0.0; S(25): 0.0; S(26): 0.0; S(27): 0.0	T6; S16;	T48; S58	28		0	0	3	1133	3396	40.97	7777
ELVGDTGSQEGDHEPsGsETEEDTSSSP HR	SMIM13	221710	small integral membrane protein 13	S16(Phospho) S18(Phospho)	T(6): 1.2; S(8): 1.2; S(16): 98.3; S(18): 92.0; T(20): 7.4; T(24): 0.0; S(25): 0.0; S(26): 0.0; S(27): 0.0	S16; S18;	S58; S60		3.87	0	0	3	1106	3316	35.26	6575
ELVGDTGSQEGDHEPsGsETEEDTSSSPH R	SMIM13	221710	small integral membrane protein 13	T6(Phospho) S16(Phospho)	T(6): 98.8; S(8): 9.1; S(16): 91.3; S(18): 50.4; T(20): 50.4; T(24): 0.0; S(25): 0.0; S(26): 0.0; S(27): 0.0	T6; S16;	T48; S58		3.02	0	0	3	1133	3396	40.97	7777
GtGQSDSDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	T2(Phospho)	T(2): 92.9; S(5): 3.5; S(8): 3.5; T(14): 0.0	T2;	T25	19		0	0	2	1009	2017	86.02	17229
GtGQSDSDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	T2(Phospho)	T(2): 92.9; S(5): 3.5; S(8): 3.5; T(14): 0.0	T2;	T25		3.64	0	0	2	1009	2017	86.02	17229
GtGQsDDSDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	T2(Phospho) S5(Phospho)	T(2): 100.0; S(5): 95.9; S(8): 4.1; T(14): 0.0	T2; S5;	T25; S28		3.39	0	0	2	1049	2097	103.3	20683
GtGQsDDSDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	T2(Phospho) S5(Phospho)	T(2): 100.0; S(5): 94.9; S(8): 5.1; T(14): 0.0	T2; S5;	T25; S28		3.21	0	0	2	1049	2097	103.8	20796
RGTGQsDDsDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	S6(Phospho) S9(Phospho)	T(3): 5.0; S(6): 95.0; S(9): 100.0; T(15): 0.0	S6; S9;	S28; S31	14		0.002	1	2	1127	2253	82.77	16639
RGTGQsDDsDIWDDTALIK	SMN2	6607	survival motor neuron protein isoform c	S6(Phospho) S9(Phospho)	T(3): 5.0; S(6): 95.0; S(9): 100.0; T(15): 0.0	S6; S9;	S28; S31		1.9	0.003	1	2	1127	2253	82.77	16639
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho)	S(5): 0.0; S(8): 100.0; S(10): 0.0; T(13): 0.0; S(14): 0.0	S8;	S52	57		0	0	3	638	1912	17.79	2876
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 0.1; S(8): 99.9; S(10): 99.9; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54	48		0	0	3	664.6	1992	19.99	3333
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 5.1; S(8): 97.5; S(10): 97.5; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54	37		0	0	3	664.6	1992	19.48	3227
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 3.2; S(8): 96.9; S(10): 99.9; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54	27		0	0	2	996.4	1992	19.92	3320
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 0.2; S(8): 99.8; S(10): 100.0; T(13): 50.0; S(14): 50.0	S8; S10;	S52; S54		6.2	0	0	3	691.3	2072	23.68	4114
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 0.1; S(8): 99.9; S(10): 99.9; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54		5.8	0	0	3	664.6	1992	19.99	3333
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 5.1; S(8): 97.5; S(10): 97.5; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54		5.7	0	0	3	664.6	1992	19.48	3227

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#
RPDHSGGsPSPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho)	S(5): 0.0; S(8): 100.0; S(10): 0.0; T(13): 0.0; S(14): 0.0	S8;	S52		5.41	0	0	3	638	1912	17.79	2876
RPDHSGGsPsPPTSEPAR	SNIP1	79753	smad nuclear-interacting protein 1	S8(Phospho) S10(Phospho)	S(5): 3.2; S(8): 96.9; S(10): 99.9; T(13): 0.0; S(14): 0.0	S8; S10;	S52; S54		3.37	0	0	2	996.4	1992	19.92	3320
RTsNERPGSGQGQGR	SNIP1	79753	smad nuclear-interacting protein 1	S3(Phospho)	T(2): 3.7; S(3): 96.3; S(9): 0.0	S3;	S153		3.68	0.005	1	3	556.2	1667	12.35	1688
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 98.5; S(14): 1.5	S4; S12;	S224; S232	51		0	0	2	837.4	1674	46.84	9042
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	39		0	0	3	558.6	1674	46.66	9006
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	35		0	0	3	563.9	1690	35.83	6693
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	30		0	0	3	558.6	1674	46.15	8899
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	28		0	0	3	563.9	1690	36.36	6805
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224	28		0	0	2	845.3	1690	35.95	6719
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0; S(14): 0.0	S4; S12;	S224; S232	22		0	1	3	601.3	1802	36.28	6789
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 99.9; S(14): 0.1	S4; S12;	S224; S232	16		0	1	3	606.6	1818	27.37	4909
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		5.69	0	0	3	558.6	1674	46.66	9006
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 99.9; S(14): 0.1	S4; S12;	S224; S232		5.67	0	1	3	606.6	1818	27.37	4909
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 100.0; S(14): 0.0	S4; S12;	S224; S232		5.54	0	1	3	601.3	1802	36.28	6789
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		5.28	0	0	3	563.9	1690	36.36	6805
GPPsPPAPVMHsPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 98.5; S(14): 1.5	S4; S12;	S224; S232		4.82	0	0	2	837.4	1674	46.84	9042
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		4.26	0	0	3	563.9	1690	35.83	6693
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 97.5; S(14): 2.5	S4; S12;	S224; S232		4.08	0	1	3	601.3	1802	35.73	6673
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 97.5; S(14): 2.5	S4; S12;	S224; S232		3.66	0	1	3	601.3	1802	36.85	6910
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		3.41	0	0	3	558.6	1674	46.15	8899
GPPsPPAPVMHsPSRK	SNW1	22938	SNW domain-containing protein 1	S4(Phospho) S12(Phospho)	S(4): 100.0; S(12): 97.5; S(14): 2.5	S4; S12;	S224; S232	10		0.001	1	3	601.3	1802	36.85	6910
GPPsPPAPVMHSPSR	SNW1	22938	SNW domain-containing protein 1	M10(Oxidation) S4(Phospho)	S(4): 100.0; S(12): 50.0; S(14): 50.0	S4;	S224		3.02	0.005	0	2	845.3	1690	35.95	6719
AEsCGsFDETESEESSK	SNX24	28966	sorting nexin-24	C4(Carbamidomethyl)S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0; T(10): 0.0; S(12): 0.0; S(15): 0.0; S(16): 0.0	S3; S6;	S113; S116	51		0	0	2	1020	2039	40.56	7691
AEsCGsFDETESEESSK	SNX24	28966	sorting nexin-24	C4(Carbamidomethyl)S3(Phospho) S6(Phospho)	S(3): 100.0; S(6): 100.0; T(10): 0.0; S(12): 0.0; S(15): 0.0; S(16): 0.0	S3; S6;	S113; S116		2.97	0	0	2	1020	2039	40.56	7691
APsPTSSAGEEGTK	SOGA1	140710	protein SOGA1 isoform 1	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(6): 0.0; S(7): 0.0; T(13): 0.0	S3;	S1541	14		0.005	0	2	699.8	1399	18.75	3073

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#
APsPTSSAGEEGTK	SOGA1	140710	protein SOGA1 isoform 1	S3(Phospho)	S(3): 100.0; T(5): 0.0; S(6): 0.0; S(7): 0.0; T(13): 0.0	S3;	S1541		3.3	0.008	0	2	699.8	1399	18.75	3073
SVESTSPPEpSk	SON	6651	protein SON isoform E	S10(Phospho)	S(1): 0.0; S(4): 0.0; T(5): 0.0; S(6): 0.0; S(10): 100.0	S10;	S287	37		0	0	2	614.3	1228	17.25	2758
EMEHTVCAAGTsPVGEIGEEK	SON	6651	protein SON isoform E	M2(Oxidation) C8(Carbamidomethyl) S13(Phospho)	T(6): 0.0; T(12): 0.1; S(13): 99.9	S13;	S1556	37		0	0	3	814.3	2441	43.71	8351
EMEHTVCAAGTsPVGEIGEEK	SON	6651	protein SON isoform E	C8(Carbamidomethyl) S13(Phospho)	T(6): 0.0; T(12): 0.1; S(13): 99.9	S13;	S1556	30		0	0	3	809	2425	47.17	9112
EMEHTVCAAGTsPVGEIGEEK	SON	6651	protein SON isoform E	C8(Carbamidomethyl) S13(Phospho)	T(6): 0.0; T(12): 0.1; S(13): 99.9	S13;	S1556		4.56	0	0	3	809	2425	47.17	9112
EMEHTVCAAGTsPVGEIGEEK	SON	6651	protein SON isoform E	M2(Oxidation) C8(Carbamidomethyl) S13(Phospho)	T(6): 0.0; T(12): 0.1; S(13): 99.9	S13;	S1556		4.52	0	0	3	814.3	2441	43.71	8351
SVESTSPPEpSk	SON	6651	protein SON isoform E	S10(Phospho)	S(1): 0.0; S(4): 0.0; T(5): 0.0; S(6): 0.0; S(10): 100.0	S10;	S287		3.05	0	0	2	614.3	1228	17.25	2758
SGYHDDsDEDLLE	SORT1	6272	sortilin isoform 2	S7(Phospho)	S(1): 0.0; Y(3): 0.0; S(7): 100.0	S7;	S688	28		0.002	0	2	787.8	1575	55.76	10959
SVCPGGSSPGSSSGGGR	SOWAHC	65124	ankyrin repeat domain-containing protein SOWAHC	C3(Carbamidomethyl) S8(Phospho)	S(1): 0.0; S(7): 0.0; S(8): 98.0; S(11): 1.9; S(12): 0.0; S(13): 0.0	S8;	S226	53		0	0	2	786.8	1573	18.53	3029
SVCPGGSSPGSSSGGGR	SOWAHC	65124	ankyrin repeat domain-containing protein SOWAHC	C3(Carbamidomethyl) S8(Phospho)	S(1): 0.0; S(7): 0.0; S(8): 98.0; S(11): 1.9; S(12): 0.0; S(13): 0.0	S8;	S226		3.66	0	0	2	786.8	1573	18.53	3029
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho)	S(9): 95.7; S(11): 95.7; S(12): 8.7; S(21): 0.0; S(22): 0.0	S9; S11;	S372; S374	24		0	0	3	960.1	2878	60.58	11996
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho) S12(Phospho)	S(9): 100.0; S(11): 100.0; S(12): 100.0; S(21): 0.0; S(22): 0.0	S9; S11; S12;	S372; S374; S375	22		0	0	3	986.7	2958	67.89	13713
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho) S12(Phospho)	S(9): 100.0; S(11): 100.0; S(12): 100.0; S(21): 0.0; S(22): 0.0	S9; S11; S12;	S372; S374; S375	14		0	0	3	986.7	2958	67.26	13565
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho) S12(Phospho)	S(9): 100.0; S(11): 100.0; S(12): 100.0; S(21): 0.0; S(22): 0.0	S9; S11; S12;	S372; S374; S375		2.99	0	0	3	986.7	2958	67.89	13713
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho) S12(Phospho)	S(9): 100.0; S(11): 100.0; S(12): 100.0; S(21): 0.0; S(22): 0.0	S9; S11; S12;	S372; S374; S375		2.85	0	0	3	986.7	2958	67.26	13565
VIGQDHDFsEsEEEEAPAEASSGALR	SP100	6672	nuclear autoantigen Sp-100 isoform 6	S9(Phospho) S11(Phospho)	S(9): 95.7; S(11): 95.7; S(12): 8.7; S(21): 0.0; S(22): 0.0	S9; S11;	S372; S374		2.72	0	0	3	960.1	2878	60.58	11996
SASQsSLDKLDQELK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S6(Phospho)	S(1): 1.7; S(3): 50.0; S(5): 50.0; S(6): 98.3	S6;	S733	29		0	1	2	904.9	1809	61.68	12234
sASQsSLDKLDQELKEQQK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S1(Phospho) S6(Phospho)	S(1): 96.5; S(3): 3.5; S(5): 3.5; S(6): 96.5	S1; S6;	S728; S733	23		0	2	3	774.7	2322	54.28	10648
AVEQEDELsDVSQGGSK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S9(Phospho)	S(9): 100.0; S(12): 50.0; S(16): 50.0	S9;	S265	22		0	0	2	969.4	1938	44.62	8559
sASQsSLDKLDQELKEQQK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S1(Phospho) S6(Phospho)	S(1): 95.6; S(3): 4.4; S(5): 4.4; S(6): 95.6	S1; S6;	S728; S733	11		0	2	3	774.7	2322	54.79	10757
sASQsSLDKLDQELKEQQK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S1(Phospho) S6(Phospho)	S(1): 96.5; S(3): 3.5; S(5): 3.5; S(6): 96.5	S1; S6;	S728; S733		4.07	0	2	3	774.7	2322	54.28	10648
sASQsSLDKLDQELKEQQK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S1(Phospho) S6(Phospho)	S(1): 95.6; S(3): 4.4; S(5): 4.4; S(6): 95.6	S1; S6;	S728; S733		3.65	0	2	3	774.7	2322	54.79	10757

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#
SASQSSLDKLDQELK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S6(Phospho)	S(1): 1.7; S(3): 50.0; S(5): 50.0; S(6): 98.3	S6;	S733		2.66	0	1	2	904.9	1809	61.68	12234
sAsQSSLDKLDQELK	SPAG9	9043	C-Jun-amino-terminal kinase-interacting protein 4 isoform 1	S1(Phospho) S3(Phospho)	S(1): 99.3; S(3): 91.0; S(5): 4.8; S(6): 4.8	S1; S3;	S728; S730		2.34	0	1	2	904.9	1809	61.53	12201
SQGSGNEAEPLGK	SPATS2L	26010	SPATS2-like protein isoform b	S4(Phospho)	S(1): 0.0; S(4): 100.0	S4;	S386	75		0	0	2	677.3	1354	25.9	4584
SQGSGNEAEPLGK	SPATS2L	26010	SPATS2-like protein isoform b	S4(Phospho)	S(1): 0.0; S(4): 100.0	S4;	S386		3.78	0	0	2	677.3	1354	25.9	4584
EsGVVAVSPEKsESPQKEDGLSSQLK	SPEN	23013	msx2-interacting protein	S2(Phospho) S12(Phospho)	S(2): 100.0; S(8): 0.0; S(12): 94.8; S(14): 5.2; S(22): 0.0; S(23): 0.0	S2; S12;	S2114; S2124	25		0	2	3	959.1	2875	51.19	9955
EsGVVAVSPEKsESPQKEDGLSSQLK	SPEN	23013	msx2-interacting protein	S2(Phospho) S12(Phospho)	S(2): 100.0; S(8): 0.0; S(12): 94.8; S(14): 5.2; S(22): 0.0; S(23): 0.0	S2; S12;	S2114; S2124		4.36	0	2	3	959.1	2875	51.19	9955
VHsTSsLDSQK	SPG11	80208	spatacsin isoform 1	S3(Phospho) S6(Phospho)	S(3): 95.9; T(4): 2.1; S(5): 4.1; S(6): 97.9; S(9): 0.0	S3; S6;	S1955; S1958	22		0.003	0	2	674.8	1349	17.76	2868
VHsTSsLDSQK	SPG11	80208	spatacsin isoform 1	S3(Phospho) S6(Phospho)	S(3): 95.9; T(4): 2.1; S(5): 4.1; S(6): 97.9; S(9): 0.0	S3; S6;	S1955; S1958		2.71	0.005	0	2	674.8	1349	17.76	2868
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	36		0	0	2	588.3	1176	13.4	1934
TSSKESsPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S7(Phospho) S11(Phospho)	T(1): 33.3; S(2): 33.3; S(3): 33.3; S(6): 0.2; S(7): 99.9; S(11): 96.4; T(13): 3.6; S(14): 0.0	S7; S11;	S2165; S2169	29		0	1	2	958.4	1916	40.53	7686
TSsKESsPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S7(Phospho) S11(Phospho)	T(1): 3.6; S(2): 3.6; S(3): 92.9; S(6): 3.6; S(7): 96.2; S(11): 99.8; T(13): 0.2; S(14): 0.0	S3; S7; S11;	S2161; S2165; S2169	28		0	2	2	1022	2044	27.76	4992
TSsKESSPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 99.8; S(6): 50.0; S(7): 50.0; S(11): 0.0; T(13): 0.0; S(14): 0.0	S3;	S2161	25		0	2	3	655.3	1964	26.03	4613
TSsKESsPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S6(Phospho) S11(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 99.8; S(6): 97.2; S(7): 2.8; S(11): 99.9; T(13): 0.1; S(14): 0.0	S3; S6; S11;	S2161; S2164; S2169	23		0	2	2	1022	2044	28.29	5105
ESSPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S7(Phospho)	S(2): 50.0; S(3): 50.0; S(7): 100.0; T(9): 0.0; S(10): 0.0	S7;	S2169	20		0	0	2	716.8	1433	43.94	8400
TSSKESSPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	T13(Phospho)	T(1): 33.3; S(2): 33.3; S(3): 33.3; S(6): 50.0; S(7): 50.0; S(11): 0.0; T(13): 97.4; S(14): 2.6	T13;	T2171	19		0	2	3	681.9	2044	28.08	5060
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		4.31	0	0	2	588.3	1176	13.4	1934
TSSKESsPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S7(Phospho) S11(Phospho)	T(1): 33.3; S(2): 33.3; S(3): 33.3; S(6): 0.2; S(7): 99.9; S(11): 96.4; T(13): 3.6; S(14): 0.0	S7; S11;	S2165; S2169		3.86	0	1	2	958.4	1916	40.53	7686
TSsKESSPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 99.8; S(6): 50.0; S(7): 50.0; S(11): 0.0; T(13): 0.0; S(14): 0.0	S3;	S2161		3.78	0	2	3	655.3	1964	26.03	4613
TSsKESsPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S7(Phospho)	T(1): 3.9; S(2): 3.9; S(3): 92.2; S(6): 4.1; S(7): 95.7; S(11): 0.2; T(13): 0.0; S(14): 0.0	S3; S7;	S2161; S2165		3.16	0	1	2	918.4	1836	35.77	6681
TSsKESsPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S7(Phospho) S11(Phospho)	T(1): 3.6; S(2): 3.6; S(3): 92.9; S(6): 3.6; S(7): 96.2; S(11): 99.8; T(13): 0.2; S(14): 0.0	S3; S7; S11;	S2161; S2165; S2169		2.45	0	2	2	1022	2044	27.76	4992

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#
ESSPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S7(Phospho)	S(2): 50.0; S(3): 50.0; S(7): 100.0; T(9): 0.0; S(10): 0.0	S7;	S2169		2.04	0	0	2	716.8	1433	43.94	8400
TSSKESSPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	T13(Phospho)	T(1): 33.3; S(2): 33.3; S(3): 33.3; S(6): 50.0; S(7): 50.0; S(11): 0.0; T(13): 97.4; S(14): 2.6	T13;	T2171		4.27	0.001	2	3	681.9	2044	28.08	5060
TSSKESSPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	T13(Phospho)	T(1): 49.5; S(2): 49.5; S(3): 2.0; S(6): 49.5; S(7): 49.5; S(11): 3.9; T(13): 96.1; S(14): 0.0	T13;	T2171		3.33	0.001	1	3	639.2	1916	40.19	7614
TSsKESsPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S7(Phospho)	T(1): 3.9; S(2): 3.9; S(3): 92.2; S(6): 4.1; S(7): 95.7; S(11): 0.2; T(13): 0.0; S(14): 0.0	S3; S7;	S2161; S2165	13	0.002	1	2	2	918.4	1836	35.77	6681
TSsKESsPIPsPTSDRK	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	S3(Phospho) S6(Phospho) S11(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 99.8; S(6): 97.2; S(7): 2.8; S(11): 99.9; T(13): 0.1; S(14): 0.0	S3; S6; S11;	S2161; S2164; S2169		2.84	0.002	2	2	1022	2044	28.29	5105
tsSKESSPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	T1(Phospho) S2(Phospho) S11(Phospho)	T(1): 100.0; S(2): 100.0; S(3): 0.0; S(6): 0.0; S(7): 0.0; S(11): 95.6; T(13): 4.2; S(14): 0.2	T1; S2; S11;	T2159; S2160; S2169		2.64	0.003	1	2	958.4	1916	40.02	7578
TSSKESSPIPsPTSDR	SPTBN1	6711	spectrin beta chain, non-erythrocytic 1 isoform 1	T13(Phospho)	T(1): 49.5; S(2): 49.5; S(3): 2.0; S(6): 49.5; S(7): 49.5; S(11): 3.9; T(13): 96.1; S(14): 0.0	T13;	T2171	16	0.005	1	3	3	639.2	1916	40.19	7614
SRLtPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho) S7(Phospho)	S(1): 2.2; T(4): 97.8; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188	42	0	1	3	3	631.9	1894	34.1	6314
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	31	0	1	2	2	947.4	1894	34.02	6298
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	29	0	1	2	2	947.4	1894	34.55	6411
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	27	0	0	0	2	785.8	1571	36.19	6769
SRLtPVsPESSSTEEK	SQSTM1	8878	sequestosome-1 isoform 2	T4(Phospho) S7(Phospho)	S(1): 2.2; T(4): 97.8; S(7): 100.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; T(13): 0.0	T4; S7;	T185; S188		6.07	0	1	3	631.9	1894	34.1	6314
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		3.54	0	1	2	947.4	1894	34.55	6411
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		3.14	0	1	2	947.4	1894	34.02	6298
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		2.31	0	0	2	785.8	1571	36.19	6769
LQPPsPLGPEGsVEESEAEASGEEEEGDGTPR	SRCAP	10847	helicase SRCAP	S5(Phospho) S12(Phospho)	S(5): 80.2; S(12): 80.2; S(16): 19.8; S(21): 19.8; T(30): 0.0	S5; S12;	S3161; S3168	24	0	0	3	3	1143	3426	78.9	15904

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#
LQPPsPLGPEGsVEESEAEASGEEEGDG TPR	SRCAP	10847	helicase SRCAP	S5(Phospho) S12(Phospho)	S(5): 80.2; S(12): 80.2; S(16): 19.8; S(21): 19.8; T(30): 0.0	S5; S12;	S3161; S3168		2.58	0	0	3	1143	3426	78.9	15904
LQPPsPLGPEGsVEESEAEASGEEEGDG TPR	SRCAP	10847	helicase SRCAP	S5(Phospho) S21(Phospho)	S(5): 98.5; S(12): 8.4; S(16): 1.5; S(21): 91.6; T(30): 0.0	S5; S21;	S3161; S3177		1.8	0.005	0	3	1143	3426	77.11	15571
GSAPHSESDLPEQEEIILGsDDDEQEDP NDYCK	SRPK1	6732	SRSF protein kinase 1	C32(Carbamido methyl) S20(Phospho)	S(2): 0.0; S(6): 0.0; S(8): 0.0; S(20): 100.0; Y(31): 0.0	S20;	S51	12		0	0	4	954.4	3814	61.87	12272
GSAPHSESDLPEQEEIILGsDDDEQEDP NDYCK	SRPK1	6732	SRSF protein kinase 1	C32(Carbamido methyl) S20(Phospho)	S(2): 0.1; S(6): 0.6; S(8): 0.6; S(20): 98.7; Y(31): 0.0	S20;	S51		3.39	0	0	3	1272	3814	61.79	12256
GSAPHSESDLPEQEEIILGsDDDEQEDP NDYCK	SRPK1	6732	SRSF protein kinase 1	C32(Carbamido methyl) S20(Phospho)	S(2): 0.0; S(6): 0.0; S(8): 0.0; S(20): 100.0; Y(31): 0.0	S20;	S51		3.3	0	0	4	954.4	3814	61.87	12272
GsAPHsESDLPEQEEIILGsDDDEQEDPN DYCK	SRPK1	6732	SRSF protein kinase 1	C32(Carbamido methyl)S2(Phospho) S6(Phospho) S20(Phospho)	S(2): 99.9; S(6): 98.8; S(8): 2.4; S(20): 98.8; Y(31): 0.0	S2; S6; S20;	S33; S37; S51		1.89	0.001	0	3	1325	3974	79.77	16071
TVsASsTGDLPK	SRPK2	6733	SRSF protein kinase 2 isoform b precursor	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(5): 0.0; S(6): 100.0; T(7): 0.0	S3; S6;	S494; S497	63		0	0	2	661.8	1323	45.9	8846
TVsASsTGDLPK	SRPK2	6733	SRSF protein kinase 2 isoform b precursor	S3(Phospho) S6(Phospho)	T(1): 0.0; S(3): 100.0; S(5): 0.0; S(6): 100.0; T(7): 0.0	S3; S6;	S494; S497		3.8	0	0	2	661.8	1323	45.9	8846
GtGGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)	T(2): 99.3; S(4): 0.8; S(14): 66.6; S(15): 66.6; S(16): 66.6; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256	40		0	0	3	1137	3409	49.09	9514
GtGGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl) T2(Phospho)	T(2): 94.7; S(4): 5.3; S(14): 0.0; S(15): 0.0; S(16): 0.0; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256	33		0	0	3	1084	3249	39.5	7463
GTGGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)S15(Phospho) S16(Phospho)	T(2): 50.0; S(4): 50.0; S(14): 8.3; S(15): 92.4; S(16): 99.3; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	S15; S16;	S269; S270	27		0	0	3	1137	3409	48.58	9406
GtGsGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho) S4(Phospho)	T(2): 99.8; S(4): 98.3; S(14): 0.6; S(15): 0.6; S(16): 0.6; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2; S4;	T256; S258	21		0	0	3	1110	3329	44.65	8566
GtGGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)	T(2): 93.0; S(4): 7.0; S(14): 66.7; S(15): 66.7; S(16): 66.7; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256	21		0	0	3	1137	3409	49.62	9623
GtGGGQLQDLDCSSsDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)	T(2): 99.3; S(4): 0.8; S(14): 66.6; S(15): 66.6; S(16): 66.6; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256		5.44	0	0	3	1137	3409	49.09	9514

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#
GtGSGGQLQDLDCSSDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)	T(2): 94.7; S(4): 5.3; S(14): 0.0; S(15): 0.0; S(16): 0.0; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256		5	0	0	3	1084	3249	39.5	7463
GTGSGGQLQDLDCSSDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)S15(Phospho)S16(Phospho)	T(2): 50.0; S(4): 50.0; S(14): 8.3; S(15): 92.4; S(16): 99.3; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	S15; S16;	S269; S270		4.77	0	0	3	1137	3409	48.58	9406
GtGSGGQLQDLDCSSDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)	T(2): 93.0; S(4): 7.0; S(14): 66.7; S(15): 66.7; S(16): 66.7; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2;	T256		3.99	0	0	3	1137	3409	49.62	9623
GtGsGGQLQDLDCSSDDEGAQNSTK PSATK	SRPR	6734	signal recognition particle receptor subunit alpha isoform 2	C13(Carbamido methyl)T2(Phospho)S4(Phospho)	T(2): 99.8; S(4): 98.3; S(14): 0.6; S(15): 0.6; S(16): 0.6; S(25): 0.0; T(26): 0.0; S(29): 0.0; T(31): 0.0	T2; S4;	T256; S258		2.7	0	0	3	1110	3329	44.65	8566
APQTSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho)	T(4): 0.0; S(5): 1.5; S(6): 97.1; S(7): 1.5	S6;	S668	63		0	0	2	652.3	1304	25.42	4482
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	61		0	2	2	847.9	1695	21.26	3603
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(3): 0.0; S(5): 100.0	S5;	S847	55		0	1	2	972.9	1945	48.66	9423
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	51		0	2	2	847.9	1695	20.75	3495
APQTSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)S7(Phospho)	T(4): 0.0; S(5): 99.9; S(6): 2.5; S(7): 97.6	S5; S7;	S667; S669	51		0	0	2	692.3	1384	32.27	5933
APQTSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)S7(Phospho)	T(4): 3.3; S(5): 93.5; S(6): 6.5; S(7): 96.7	S5; S7;	S667; S669	51		0	0	2	692.3	1384	31.76	5826
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	51		0	2	3	565.6	1695	20.72	3488
KAAAsPsQSVr	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	1288	17.66	2847
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho)S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847	50		0	1	2	1013	2025	55.19	10838
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(3): 0.0; S(5): 100.0	S5;	S847	49		0	1	3	648.9	1945	48.33	9356
REsPsPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S409; S411	49		0	1	3	461.2	1382	13.02	1854
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	47		0	2	3	565.6	1695	21.26	3604
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	47		0	1	2	604.3	1208	18.7	3063
KAAAsPsQsVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho)S6(Phospho)S9(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 100.0	S4; S6; S9;	S711; S713; S716	47		0	1	2	684.3	1368	21.49	3651
KAAAsPSPQSVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho)	S(4): 100.0; S(6): 0.0; S(9): 0.0	S4;	S711	45		0	1	2	604.3	1208	14.67	2201
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho)S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847	43		0	1	3	675.6	2025	55.23	10847
RRsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho)S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535	42		0	2	3	459.9	1378	13.55	1965
HRPpPAtPPPK	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	42		0	0	3	481.2	1442	19.3	3189

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#
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 3.4; S(13): 93.2; S(15): 3.4; T(16): 0.0; S(19): 0.0	S7; S13;	S742; S748	42		0	0	3	915.1	2743	67.32	13579
KEtEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847	42		0	1	2	1013	2025	55.7	10946
RAspSPPPK	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	41		0	1	2	548.7	1096	13.1	1869
HRPSPPAtpPPPK	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	38		0	0	3	481.2	1442	18.79	3081
RYsSPPPK	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	1	2	594.7	1188	23.42	4059
RYsSPPPK	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	22.35	3834
HRPSPPAtpPPPK	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	1442	18.27	2975
RYsSPPPK	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	36		0	1	2	594.7	1188	21.85	3726
KAAspPQsVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho) S9(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 100.0	S4; S6; S9;	S711; S713; S716	36		0	1	2	684.3	1368	22.23	3808
RRspSPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535	35		0	2	3	459.9	1378	14.08	2076
RRtspPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T554; S556	34		0	2	3	408.5	1224	13.4	1935
EKtPELPEPSVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho)	T(3): 100.0; S(10): 0.0	T3;	T181	33		0	1	2	717.4	1434	42.52	8100
TAsPPPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho)	T(1): 1.3; S(3): 98.7	S3;	S589	33		0	1	2	564.3	1128	16.25	2536
RYsSPPPKR	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	33		0	2	2	672.8	1345	16.87	2676
RLspASPPR	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	33		0	1	2	614.3	1228	30.25	5516
HRPSPPAtpPPPK	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	33		0	0	3	481.2	1442	19.84	3303
HRPSPPAtpPPPK	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	32		0	0	3	481.2	1442	17.72	2861
SRVsSPGR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 100.0	S4; S6;	S390; S392	32		0	1	2	552.7	1104	19.64	3262
RRtAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589	31		0	2	3	455.2	1364	15.28	2331
GTEKREsSPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S9(Phospho)	T(2): 0.0; S(7): 100.0; S(9): 100.0	S7; S9;	S409; S411	31		0	2	3	599.6	1797	12.51	1733
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 0.2; S(13): 99.7; S(15): 0.2; T(16): 0.0; S(19): 0.0	S7; S13;	S742; S748	31		0	1	3	957.8	2871	56.54	11127
RLspAsPPR	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	30		0	1	2	654.3	1307	36.79	6897
RLspAsPPR	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	30		0	1	2	654.3	1307	35.25	6572
REsSPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S409; S411	30		0	1	2	691.3	1382	12.83	1814
RQsPSPSTRPIR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho)	S(3): 100.0; S(5): 50.0; S(7): 0.0; T(8): 50.0	S3;	S686	29		0	1	2	771.4	1542	19.21	3171
VPKPEPIPEKPEsPEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S14(Phospho)	S(14): 100.0	S14;	S221	29		0	1	3	660	1978	39.54	7471
RtPtPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T2(Phospho) T4(Phospho)	T(2): 100.0; T(4): 100.0	T2; T4;	T545; T547	29		0	1	2	541.2	1081	16.28	2543

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#
HRPSPPAAtPPPK	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	28		0	0	2	721.3	1442	18.79	3082
RAsPsPPPKR	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	2	2	626.8	1253	12.32	1678
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho) S19(Phospho)	S(7): 100.0; S(11): 5.1; S(13): 94.9; S(15): 0.0; T(16): 0.0; S(19): 100.0	S7; S13; S19;	S742; S748; S754	28		0	0	3	941.8	2823	76.88	15511
HRPSPPAAtPPPK	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	28		0	0	2	721.3	1442	19.3	3190
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	27		0	1	2	594.7	1188	23.94	4169
HRPSPPAAtPPPK	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	27		0	0	2	721.3	1442	18.27	2974
RVsHsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S609; S611	26		0	1	2	582.8	1164	12.3	1672
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	25		0	1	2	614.3	1228	29.2	5298
RQSPSPStRPIR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T8(Phospho)	S(3): 50.0; S(5): 50.0; S(7): 0.1; T(8): 99.9	T8;	T691	24		0	1	2	771.4	1542	18.68	3059
VsSSRSVsGsPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S8(Phospho) S10(Phospho)	S(2): 94.6; S(3): 2.7; S(4): 2.7; S(6): 0.2; S(8): 99.9; S(10): 100.0	S2; S8; S10;	S721; S727; S729	21		0	1	2	893.3	1786	23.03	3980
VPKPEPIPEKPEsPEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S14(Phospho)	S(14): 100.0	S14;	S221	20		0	1	3	660	1978	39	7359
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	20		0	1	2	611.3	1222	18	2919
RVsSSRsVsGsPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S7(Phospho) S9(Phospho) S11(Phospho)	S(3): 2.6; S(4): 97.3; S(5): 0.2; S(7): 99.9; S(9): 100.0; S(11): 100.0	S4; S7; S9; S11;	S722; S725; S727; S729	19		0	2	3	674.6	2022	22.86	3943
RVsSSRsVsGsPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S7(Phospho) S9(Phospho) S11(Phospho)	S(3): 99.9; S(4): 0.1; S(5): 0.1; S(7): 99.9; S(9): 100.0; S(11): 100.0	S3; S7; S9; S11;	S721; S725; S727; S729	16		0	2	3	674.6	2022	23.52	4079
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S19(Phospho)	S(7): 99.9; S(11): 27.4; S(13): 27.4; S(15): 27.4; T(16): 27.4; S(19): 90.5	S7; S19;	S742; S754	16		0	0	3	941.8	2823	76.34	15399
RVsSSRsVSGSPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 94.5; S(4): 11.2; S(5): 91.9; S(7): 96.7; S(9): 52.9; S(11): 52.9	S3; S5; S7;	S721; S723; S725	13		0	2	2	1011	2022	23.04	3984
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 5.0; S(13): 89.8; S(15): 5.0; T(16): 0.3; S(19): 0.0	S7; S13;	S742; S748	11		0	1	3	957.8	2871	56.18	11049
VPKPEPIPEKPEsPEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S14(Phospho)	S(14): 100.0	S14;	S221		6.42	0	1	3	660	1978	39.54	7471
HRPSPPAAtPPPK	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		6.26	0	0	3	481.2	1442	18.27	2975
HRPSPPAAtPPPK	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		6.21	0	0	3	481.2	1442	19.3	3189
GTEKREsPsPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S9(Phospho)	T(2): 0.0; S(7): 100.0; S(9): 100.0	S7; S9;	S409; S411		6.16	0	2	3	599.6	1797	12.51	1733
HRPSPPAAtPPPK	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		6.09	0	0	3	481.2	1442	18.79	3081
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		6.08	0	2	3	565.6	1695	21.26	3604
KPPAPPsPVQSQsPSTNWSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 3.4; S(13): 93.2; S(15): 3.4; T(16): 0.0; S(19): 0.0	S7; S13;	S742; S748		6.02	0	0	3	915.1	2743	67.32	13579

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#
RRsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535		6	0	2	3	459.9	1378	13.55	1965
RRsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535		5.79	0	2	3	459.9	1378	14.08	2076
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		5.74	0	0	3	481.2	1442	19.84	3303
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		5.71	0	2	3	565.6	1695	20.72	3488
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		5.68	0	2	2	847.9	1695	21.26	3603
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		5.61	0	0	3	481.2	1442	17.72	2861
RRTAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589		5.48	0	2	3	455.2	1364	15.28	2331
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(3): 0.0; S(5): 100.0	S5;	S847		5.31	0	1	3	648.9	1945	48.33	9356
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847		5	0	1	3	675.6	2025	55.23	10847
RAsPsPPPK	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		4.87	0	1	2	548.7	1096	13.1	1869
KAAAsPsQsVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho) S9(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 100.0	S4; S6; S9;	S711; S713; S716		4.76	0	1	2	684.3	1368	21.49	3651
KPPAPPsPVQSQsPSTNWSPAVPVKK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 0.2; S(13): 99.7; S(15): 0.2; T(16): 0.0; S(19): 0.0	S7; S13;	S742; S748		4.57	0	1	3	957.8	2871	56.54	11127
KAAAsPsQSVR	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		4.52	0	1	2	644.3	1288	17.66	2847
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		4.52	0	1	2	594.7	1188	22.35	3834
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		4.46	0	1	2	594.7	1188	23.42	4059
VPKPEPIPEKPsPEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S14(Phospho)	S(14): 100.0	S14;	S221		4.42	0	1	3	660	1978	39	7359
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		4.42	0	2	2	847.9	1695	20.75	3495
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		4.32	0	1	2	594.7	1188	22.9	3951
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		4.23	0	1	2	611.3	1222	18	2919
RVsHsPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S609; S611		4.22	0	1	2	582.8	1164	12.3	1672
REsPsPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S409; S411		4.21	0	1	2	691.3	1382	12.83	1814
RYsPsPPPKR	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		4.2	0	2	2	672.8	1345	16.87	2676
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847		4.17	0	1	2	1013	2025	55.19	10838
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		4.09	0	1	2	594.7	1188	23.94	4169
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		4.09	0	0	2	721.3	1442	18.27	2974
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T845; S847		4.07	0	1	2	1013	2025	55.7	10946
REsPsPAPKPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S409; S411		4.07	0	1	3	461.2	1382	13.02	1854
KETEsEAEDNLDDLEK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho)	T(3): 0.0; S(5): 100.0	S5;	S847		4.03	0	1	2	972.9	1945	48.66	9423

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#
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		4.02	0	1	2	611.3	1222	18.53	3027
RRsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535		3.88	0	2	2	689.3	1378	13.48	1950
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		3.79	0	0	2	721.3	1442	18.79	3082
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		3.68	0	1	2	577.7	1154	15.01	2271
KAA5PSPQSVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho)	S(4): 100.0; S(6): 0.0; S(9): 0.0	S4;	S711		3.65	0	1	2	604.3	1208	14.67	2201
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		3.65	0	1	2	577.7	1154	15.52	2379
RRtPtPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) T5(Phospho)	T(3): 100.0; T(5): 100.0	T3; T5;	T545; T547		3.6	0	2	2	619.3	1238	13.51	1956
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		3.58	0	1	2	594.7	1188	21.85	3726
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		3.54	0	0	2	721.3	1442	19.3	3190
APQTSsPPPVVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho)	T(4): 0.0; S(5): 1.5; S(6): 97.1; S(7): 1.5	S6;	S668		3.43	0	0	2	652.3	1304	25.42	4482
APQTSsPPPVVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	T(4): 3.3; S(5): 93.5; S(6): 6.5; S(7): 96.7	S5; S7;	S667; S669		3.38	0	0	2	692.3	1384	31.76	5826
VsSSRSVsGsPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho) S8(Phospho) S10(Phospho)	S(2): 94.6; S(3): 2.7; S(4): 2.7; S(6): 0.2; S(8): 99.9; S(10): 100.0	S2; S8; S10;	S721; S727; S729		3.36	0	1	2	893.3	1786	23.03	3980
KPPAPPsPVQSQsPSTNWSsPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho) S19(Phospho)	S(7): 100.0; S(11): 5.1; S(13): 94.9; S(15): 0.0; T(16): 0.0; S(19): 100.0	S7; S13; S19;	S742; S748; S754		3.35	0	0	3	941.8	2823	76.88	15511
RtPtPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T2(Phospho) T4(Phospho)	T(2): 100.0; T(4): 100.0	T2; T4;	T545; T547		3.19	0	1	2	541.2	1081	16.28	2543
KPPAPPsPVQSQsPSTNWSsPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S13(Phospho)	S(7): 100.0; S(11): 5.0; S(13): 89.8; S(15): 5.0; T(16): 0.3; S(19): 0.0	S7; S13;	S742; S748		3.19	0	1	3	957.8	2871	56.18	11049
RRtAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589		3.14	0	2	2	682.3	1364	15.26	2326
RRtAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589		3.14	0	2	2	682.3	1364	15.79	2438
KPPAPPsPVQSQsPSTNWSsPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S11(Phospho) S19(Phospho)	S(7): 100.0; S(11): 89.9; S(13): 4.9; S(15): 4.9; T(16): 0.3; S(19): 100.0	S7; S11; S19;	S742; S746; S754		3.03	0	1	3	984.5	2951	62.12	12328
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		2.81	0	1	2	604.3	1208	18.7	3063
AA5sPQSVR	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		2.77	0	0	2	580.2	1159	25.88	4580
EKTPELPEPSVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho)	T(3): 100.0; S(10): 0.0	T3;	T181		2.4	0	1	2	717.4	1434	42.52	8100
TAsPPPPPKR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho)	T(1): 1.3; S(3): 98.7	S3;	S589		2.14	0	1	2	564.3	1128	16.25	2536
RLsPAsPPR	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	32		0.001	1	2	614.3	1228	29.71	5402
AA5sPQSVR	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	29		0.001	0	2	580.2	1159	25.88	4580
RLsPAsPPR	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	25		0.001	1	2	654.3	1307	36.28	6787
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	22		0.001	1	2	604.3	1208	18.19	2957
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	19		0.001	1	2	577.7	1154	15.52	2379

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#
RRsPsPAPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S533; S535	19		0.001	2	2	689.3	1378	13.48	1950
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	17		0.001	1	2	611.3	1222	18.53	3027
RRTAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589	16		0.001	2	2	682.3	1364	15.79	2438
RQsPsPSTRPIR	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; T(8): 0.0	S3; S5;	S686; S688	14		0.001	1	3	514.6	1542	18.67	3058
RAsPsPPPKR	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		4.14	0.001	2	2	626.8	1253	12.32	1678
RRsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 98.5; T(9): 1.5	S3; S5;	S522; S524		4.01	0.001	2	2	655.8	1311	12.64	1768
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		3.65	0.001	1	2	654.3	1307	35.25	6572
RRTPsPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T554; S556		3.39	0.001	2	2	612.3	1224	13.26	1902
RRsPsLSSK	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; S(8): 0.0	S3; S5;	S626; S628		3.35	0.001	2	2	589.3	1178	12.58	1753
APQTsSsPPPVr	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	T(4): 0.0; S(5): 99.9; S(6): 2.5; S(7): 97.6	S5; S7;	S667; S669		3.04	0.001	0	2	692.3	1384	32.27	5933
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		2.19	0.001	1	2	604.3	1208	18.19	2957
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	34		0.002	1	2	594.7	1188	22.9	3951
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	26		0.002	1	2	654.3	1307	35.77	6679
KPPAPPsPVQsQSPTNwSPAVPVKK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S11(Phospho) S19(Phospho)	S(7): 100.0; S(11): 89.9; S(13): 4.9; S(15): 4.9; T(16): 0.3; S(19): 100.0	S7; S11; S19;	S742; S746; S754	20		0.002	1	3	984.5	2951	62.12	12328
RRTAsPPPPPK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T587; S589	13		0.002	2	2	682.3	1364	15.26	2326
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	0.002	2	3	437.5	1311	12.73	1792
KPPAPPsPVQsQSPTNwSPAVPVK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S19(Phospho)	S(7): 99.9; S(11): 27.4; S(13): 27.4; S(15): 27.4; T(16): 27.4; S(19): 90.5	S7; S19;	S742; S754		2.22	0.002	0	3	941.8	2823	76.34	15399
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	30		0.003	2	3	437.5	1311	12.73	1792
APQTsSsPPPVRR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho) S7(Phospho)	T(4): 2.3; S(5): 2.3; S(6): 95.5; S(7): 99.8	S6; S7;	S668; S669	23		0.003	1	3	513.9	1540	22.58	3884
RQsPsPSTRPIR	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; T(8): 0.0	S3; S5;	S686; S688	14		0.003	1	3	514.6	1542	19.22	3172
AAsPSPQsVRR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S8(Phospho)	S(3): 100.0; S(5): 2.3; S(8): 97.7	S3; S8;	S711; S716	11		0.003	1	2	658.3	1316	18.18	2955
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		4.29	0.003	1	2	654.3	1307	36.28	6787
RRTPsPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T554; S556		4.1	0.003	2	3	408.5	1224	13.4	1935
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		3.93	0.003	1	2	654.3	1307	36.79	6897
APQTsSsPPPVRR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S6(Phospho) S7(Phospho)	T(4): 2.3; S(5): 2.3; S(6): 95.5; S(7): 99.8	S6; S7;	S668; S669		3.74	0.003	1	3	513.9	1540	22.58	3884
RRTPsPPPR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T554; S556		3.45	0.003	2	2	612.3	1224	13.76	2010

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#
KPPAPPsPVQsQSPSTNwSPAVPVKK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S7(Phospho) S11(Phospho) S19(Phospho)	S(7): 100.0; S(11): 88.0; S(13): 11.2; S(15): 6.2; T(16): 6.6; S(19): 88.0	S7; S11; S19;	S742; S746; S754		3.41	0.003	1	4	738.6	2951	62.19	12347
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		3.23	0.003	1	2	614.3	1228	29.2	5298
RRsPsPPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 98.5; T(9): 1.5	S3; S5;	S522; S524	26		0.004	2	2	655.8	1311	12.64	1768
SRVsVsPGR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 100.0	S4; S6;	S390; S392	23		0.004	1	2	552.7	1104	20.16	3369
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		4.34	0.004	1	2	654.3	1307	35.77	6679
RQsPsPSTRPIR	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; T(8): 0.0	S3; S5;	S686; S688		3.74	0.004	1	3	514.6	1542	18.67	3058
RVSSRSVSQsPEPAAK	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S11(Phospho)	S(3): 50.0; S(4): 50.0; S(5): 50.0; S(7): 50.0; S(9): 3.9; S(11): 96.2	S11;	S729		4.05	0.005	2	3	647.9	1942	19.66	3267
sPsPPPTRR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(7): 0.0	S1; S3;	S522; S524	20		0.006	1	2	577.7	1154	16.04	2490
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	16		0.006	1	2	577.7	1154	15.01	2271
KAAsPsPQsVR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S4(Phospho) S6(Phospho) S9(Phospho)	S(4): 100.0; S(6): 100.0; S(9): 100.0	S4; S6; S9;	S711; S713; S716		3.67	0.006	1	2	684.3	1368	22.23	3808
KSRVsVsPGR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	S(2): 1.9; S(5): 98.1; S(7): 100.0	S5; S7;	S390; S392	20		0.007	2	2	616.8	1233	15.35	2344
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		3.58	0.007	1	2	654.3	1307	38.01	7151
RsPSPPTR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S2(Phospho)	S(2): 97.4; S(4): 51.3; T(8): 51.3	S2;	S522		2.2	0.007	1	2	577.7	1154	16.04	2490
KSRVsVsPGR	SRRM1	10250	serine/arginine repetitive matrix protein 1 isoform 3	S5(Phospho) S7(Phospho)	S(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S390; S392	16		0.009	2	2	616.8	1233	15.87	2456
sLsGSSPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 0.0; S(6): 0.0	S1; S3;	S778; S780	60		0	0	2	590.2	1179	31.68	5811
SRVsPCS NVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C7(Carbamidomethyl)S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 100.0; S(8): 0.0; S(12): 0.0	S3; S5;	S952; S954	52		0	1	2	812.8	1625	24.24	4231
SGMsPEQSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(1): 0.0; S(4): 100.0; S(8): 0.0	S4;	S1132	50		0	0	2	529.7	1058	16.93	2691
SSGHSSSEsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S10;	S1387	48		0	0	3	566.2	1697	29.13	5282
SSGHSSSEsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S10;	S1387	45		0	0	2	848.9	1697	28.95	5242
sGTPPRQGSII SPQANEQSVTPQR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T11(Phospho)	S(1): 95.1; T(3): 9.3; S(9): 4.7; T(11): 86.3; S(12): 4.6; S(19): 0.0; T(21): 0.0	S1; T11;	S846; T856	43		0	1	3	895.1	2683	42.31	8057
SVsPCS NVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S3(Phospho)	S(1): 0.0; S(3): 100.0; S(6): 0.0; S(10): 0.0	S3;	S954	42		0	0	2	651.3	1302	26.05	4617
GRSECDsPEPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S7(Phospho) S8(Phospho)	S(3): 0.0; S(7): 100.0; S(8): 100.0	S7; S8;	S1482; S1483	41		0	1	2	754.8	1509	12.76	1798

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#
SSGHSSSELSDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 1.5; S(6): 49.3; S(7): 49.3; S(10): 100.0	S10;	S1387	40		0	0	2	888.8	1777	36.67	6871
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 100.0; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694	39		0	1	2	640.3	1280	20.3	3399
QSHSGSISYPYK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S8(Phospho)	S(2): 0.0; S(4): 0.0; S(6): 0.0; S(8): 99.9; Y(10): 0.0	S8;	S994	36		0	0	2	684.3	1368	24.37	4259
RPSQPQsPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S7(Phospho)	S(3): 0.0; S(7): 100.0	S7;	S2706	35		0	0	2	551.3	1102	12.93	1836
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	35		0	0	2	691.2	1381	34.71	6449
NHsGSrTPPVAlNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) T7(Phospho)	S(3): 99.9; S(5): 2.9; T(7): 97.1; S(14): 0.0; S(15): 0.0	S3; T7;	S2100; T2104	33		0	1	3	613.9	1840	28.09	5062
NHsGSrTPPVAlNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho) T7(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 100.0; S(14): 0.0; S(15): 0.0	S3; S5; T7;	S2100; S2102; T2104	32		0	1	3	640.6	1920	35.55	6634
GRsECDsPEPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S3(Phospho) S8(Phospho)	S(3): 100.0; S(7): 0.0; S(8): 100.0	S3; S8;	S1478; S1483	32		0	1	2	754.8	1509	13.36	1925
HGGsPQPLATTPLSQEPVNPPEAsPTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S25(Phospho)	S(4): 100.0; T(10): 0.0; T(11): 0.0; S(14): 0.0; S(22): 0.1; S(25): 96.2; T(27): 3.7	S4; S25;	S377; S398	31		0	0	3	1005	3012	66.19	13320
RSLsGSsPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C9(Carbamidomethyl)S4(Phospho) S7(Phospho)	S(2): 0.0; S(4): 100.0; S(6): 0.0; S(7): 100.0	S4; S7;	S780; S783	31		0	1	2	668.3	1336	18.5	3022
RGEGDAPFsEPGTTSTQRPSSPETATK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S9(Phospho) S21(Phospho)	S(9): 99.0; T(13): 0.4; T(14): 0.4; S(15): 0.1; T(16): 0.1; S(20): 0.5; S(21): 99.0; T(24): 0.4; T(26): 0.0	S9; S21;	S311; S323	31		0	1	3	984.4	2951	41.4	7866
HAAssPESPKAPAPGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S4(Phospho) S5(Phospho)	S(3): 100.0; S(4): 100.0; S(5): 100.0; S(8): 0.0; S(17): 0.0	S3; S4; S5;	S435; S436; S437	30		0	0	3	712.9	2137	18.71	3065
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	29		0	0	2	590.2	1179	28.55	5160
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 3.9; S(2): 3.9; S(4): 96.1; S(5): 96.1; T(9): 0.0	S4; S5;	S1693; S1694	29		0	1	2	640.3	1280	20.97	3543
HSLsGSSPGMK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(2): 0.0; S(4): 96.7; S(6): 1.7; S(7): 1.7	S4;	S1460	29		0	0	2	584.2	1167	17.51	2815
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): 0.1; S(6): 99.9	S1; S3; S6;	S1497; S1499; S1502	28		0	1	2	778.3	1556	26.47	4708
SSGHSSSELSDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 48.6; S(2): 1.4; S(5): 48.6; S(6): 1.4; S(7): 0.0; S(10): 100.0	S10;	S1387	28		0	0	3	592.9	1777	36.81	6901
NHsGSrTPPVAlNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho) T7(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 100.0; S(14): 0.0; S(15): 0.0	S3; S5; T7;	S2100; S2102; T2104	28		0	1	3	640.6	1920	36.07	6742
SRsGSsPGLR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 97.7; S(6): 2.4	S3; S5;	S1441; S1443	27		0	1	2	582.2	1163	17.11	2730

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#
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 100.0; Y(4): 0.0; S(5): 100.0	S3; S5;	S2692; S2694	26		0	0	2	599.2	1197	54.11	10608
AQTTPGPSLSGSK	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	26		0	0	2	653.8	1307	34.52	6404
HAsssPeSPKPAPAPGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S4(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(4): 100.0; S(5): 100.0; S(8): 100.0; S(17): 0.0	S3; S4; S5; S8;	S435; S436; S437; S440	26		0	0	3	739.6	2217	21.53	3658
SGSsQELDVKPSASPQER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(1): 3.3; S(3): 3.3; S(4): 93.4; S(12): 0.0; S(14): 0.0	S4;	S1542	26		0	0	3	661.3	1982	33.79	6248
SATRPSPsPER	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	25		0	0	2	672.8	1345	16.4	2568
GGRsRsSSPVTLASR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 98.1; S(7): 51.0; S(8): 51.0; T(11): 0.0; S(15): 0.0	S4; S6;	S1099; S1101	25		0	2	3	629.6	1887	40.81	7743
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 1.6; S(2): 1.6; S(4): 96.9; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694	25		0	1	2	640.3	1280	21.61	3675
NHsGSrTPPVALNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) T7(Phospho)	S(3): 99.9; S(5): 2.5; T(7): 97.6; S(14): 0.0; S(15): 0.0	S3; T7;	S2100; T2104	25		0	1	3	613.9	1840	28.6	5171
sRsSPSELNNK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 50.0; S(6): 50.0	S1; S3;	S1497; S1499	24		0	1	2	778.3	1556	26.99	4819
THTTALAGRsPsPASGR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho) S12(Phospho)	T(1): 0.0; T(3): 0.0; T(4): 0.0; S(10): 100.0; S(12): 100.0; S(15): 0.0	S10; S12;	S295; S297	24		0	1	2	913.9	1827	21.87	3729
SCFESSPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl) S6(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 100.0	S6;	S876	24		0	0	2	738.3	1476	48.28	9343
NHsGSrTPPVALNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho) T7(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 100.0; S(14): 0.0; S(15): 0.0	S3; S5; T7;	S2100; S2102; T2104	23		0	1	2	960.4	1920	35.22	6566
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	23		0	1	2	530.2	1059	38.52	7255
sCFESSPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl) S1(Phospho) S6(Phospho)	S(1): 100.0; S(5): 0.1; S(6): 99.9	S1; S6;	S871; S876	23		0	0	2	778.3	1556	58.97	11677
HAsssPeSPKPAPAPGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S4(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(4): 100.0; S(5): 100.0; S(8): 100.0; S(17): 0.0	S3; S4; S5; S8;	S435; S436; S437; S440	23		0	0	3	739.6	2217	21	3549
sGTPPRQGSITSPQANEQSVtPQR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T21(Phospho)	S(1): 93.8; T(3): 6.2; S(9): 3.2; T(11): 48.4; S(12): 48.4; S(19): 0.5; T(21): 99.5	S1; T21;	S846; T866	23		0	1	3	921.7	2763	45.92	8850
NHSGsRtPPVALNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) T7(Phospho)	S(3): 5.5; S(5): 97.2; T(7): 97.2; S(14): 0.0; S(15): 0.0	S5; T7;	S2102; T2104	22		0	1	3	613.9	1840	27.57	4952
GQSQTSPDHRSDTSSPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(3): 2.7; T(5): 2.7; S(6): 94.5; S(11): 0.0; T(13): 0.0; S(14): 0.0; S(15): 0.0	S6;	S1064	21		0	1	3	717.6	2151	15.79	2439
SRtPPSAPSQSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho)	S(1): 1.6; T(3): 98.4; S(6): 0.0; S(9): 0.0; S(11): 0.0	T3;	T2409	21		0	1	2	675.8	1351	14.73	2214
HAsSPESPKPAPAPGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 99.9; S(4): 49.2; S(5): 49.2; S(8): 1.6; S(17): 0.0	S3;	S435	20		0	0	3	686.3	2057	15.06	2284
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	20		0	2	3	553.2	1658	13.65	1987

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#
RsRsVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S2(Phospho) S4(Phospho) S6(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 100.0; S(9): 0.0; S(13): 0.0	S2; S4; S6;	S950; S952; S954	19		0	2	3	620.9	1861	23.44	4065
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	19		0	2	3	553.2	1658	14.67	2200
QGSITSPQANEQSVtPQRR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T15(Phospho)	S(3): 0.0; T(5): 0.0; S(6): 0.0; S(13): 2.5; T(15): 97.5	T15;	T866	18		0	1	3	722	2164	29.33	5325
NHsGsRtPPVALN SSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho) T7(Phospho)	S(3): 100.0; S(5): 100.0; T(7): 100.0; S(14): 0.0; S(15): 0.0	S3; S5; T7;	S2100; S2102; T2104	18		0	1	3	640.6	1920	35.04	6528
AQTPPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C16(Carbamidomethyl)T3(Phospho) S14(Phospho)	T(3): 100.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 100.0	T3; S14;	T1003; S1014	18		0	1	3	738.3	2213	38.22	7192
QGSITSPQANEQSVtPQRR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) T15(Phospho)	S(3): 3.7; T(5): 3.7; S(6): 92.6; S(13): 3.9; T(15): 96.1	S6; T15;	S857; T866	17		0	1	3	748.7	2244	35.3	6582
VKAQTTPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamidomethyl)T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.0; S(14): 3.1; S(16): 96.9	T5; S16;	T1003; S1014	17		0	2	3	814	2440	32.48	5978
sRsRTSPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 50.0; S(6): 50.0; T(9): 0.0	S1; S3;	S1982; S1984	16		0	2	2	693.8	1387	13.46	1947
SSGHsSSELSDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) S10(Phospho)	S(1): 50.0; S(2): 50.0; S(5): 100.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S5; S10;	S1382; S1387	15		0	0	2	928.8	1857	48.72	9435
VKAQTTPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamidomethyl)T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.0; S(14): 0.0; S(16): 100.0	T5; S16;	T1003; S1014	14		0	2	4	610.8	2440	32.75	6035
sLTRsPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S5(Phospho)	S(1): 99.9; T(3): 2.3; S(5): 97.8	S1; S5;	S2067; S2071	14		0	1	2	629.3	1258	41.79	7949
HA sSPESPKPAPAGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 98.4; S(4): 67.2; S(5): 67.2; S(8): 67.2; S(17): 0.0	S3;	S435	14		0	0	3	712.9	2137	17.04	2715
AQTPPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C16(Carbamidomethyl) S14(Phospho)	T(3): 0.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 100.0	S14;	S1014	14		0	1	3	711.7	2133	31.94	5865
SRtsPAPWK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S4(Phospho)	S(1): 3.0; T(3): 98.5; S(4): 98.5	T3; S4;	T1856; S1857	14		0	1	2	595.2	1189	34.62	6428
SATRP sPsPERsSTGPEPPAPTPLLAER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S8(Phospho) S12(Phospho)	S(1): 5.5; T(3): 5.5; S(6): 89.1; S(8): 100.0; S(12): 93.9; S(13): 5.7; T(14): 0.4; T(22): 0.0	S6; S8; S12;	S351; S353; S357	13		0	1	3	1042	3125	66.95	13498
SRtsPAPWK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S4(Phospho)	S(1): 1.5; T(3): 98.5; S(4): 100.0	T3; S4;	T1856; S1857	10		0	1	2	595.2	1189	35.16	6554
VKAQTTPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamidomethyl)T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.0; S(14): 3.1; S(16): 96.9	T5; S16;	T1003; S1014		6.66	0	2	3	814	2440	32.48	5978
VKAQTTPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamidomethyl)T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.2; S(14): 4.4; S(16): 95.4	T5; S16;	T1003; S1014		6.49	0	2	3	814	2440	33	6086

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#
VKAQTPPGPSLGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamido methyl)T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.0; S(14): 0.0; S(16): 100.0	T5; S16;	T1003; S1014		6.3	0	2	4	610.8	2440	32.75	6035
AQTPPGPSLGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C16(Carbamido methyl)T3(Phospho) S14(Phospho)	T(3): 100.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 100.0	T3; S14;	T1003; S1014		6.17	0	1	3	738.3	2213	38.22	7192
VKPEtPPRQSHsSGSISYPYK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho) S12(Phospho)	T(5): 100.0; S(10): 0.4; S(12): 88.6; S(14): 5.3; S(16): 5.3; Y(18): 0.4	T5; S12;	T983; S990		6.1	0	1	4	588.8	2352	30.04	5471
SSGHSSSELsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S10;	S1387		5.93	0	0	3	566.2	1697	29.13	5282
sRsPSSPELNK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 50.0; S(6): 50.0	S1; S3;	S1497; S1499		5.91	0	1	2	778.3	1556	26.99	4819
GEGDAPFSEPGTTSTQRPSsPETATK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S20(Phospho)	S(8): 0.0; T(12): 0.0; T(13): 0.0; S(14): 0.0; T(15): 0.0; S(19): 4.3; S(20): 95.6; T(23): 0.0; T(25): 0.0	S20;	S323		5.74	0	0	3	905.7	2715	42.34	8062
SSGHSSSELsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 48.6; S(2): 1.4; S(5): 48.6; S(6): 1.4; S(7): 0.0; S(10): 100.0	S10;	S1387		5.51	0	0	3	592.9	1777	36.81	6901
GEGDAPFSEPGTTSTQRPSsPETATK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S19(Phospho) S20(Phospho)	S(8): 0.0; T(12): 0.3; T(13): 0.3; S(14): 5.1; T(15): 5.1; S(19): 85.2; S(20): 93.8; T(23): 9.4; T(25): 0.8	S19; S20;	S322; S323		5.16	0	0	3	932.4	2795	49.44	9586
GEGDAPFSEPGTTSTQRPSsPETATK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S20(Phospho)	S(8): 0.0; T(12): 0.0; T(13): 0.0; S(14): 0.0; T(15): 0.0; S(19): 4.0; S(20): 91.8; T(23): 4.0; T(25): 0.2	S20;	S323		5.11	0	0	3	905.7	2715	42.85	8169
HASsSPESPKPAPAGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 99.9; S(4): 49.2; S(5): 49.2; S(8): 1.6; S(17): 0.0	S3;	S435		5.11	0	0	3	686.3	2057	15.06	2284
DGSGTPSRHsLsGSSPGMK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho) S12(Phospho)	S(3): 74.9; T(5): 5.5; S(7): 9.9; S(10): 79.1; S(12): 82.7; S(14): 24.0; S(15): 24.0	S10; S12;	S1458; S1460		4.95	0	1	3	695.6	2085	29.23	5304
SSGHSSSELsPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 0.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S10;	S1387		4.93	0	0	2	848.9	1697	28.95	5242
sRsPSSPELNK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 0.1; S(6): 99.9	S1; S3; S6;	S1497; S1499; S1502		4.86	0	1	2	778.3	1556	26.47	4708
THTTALAGRsPsPASGR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho) S12(Phospho)	T(1): 0.0; T(3): 0.0; T(4): 0.0; S(10): 100.0; S(12): 100.0; S(15): 0.0	S10; S12;	S295; S297		4.82	0	1	3	609.6	1827	22.27	3816
HGGsPQPLATTPLSQEPVNPPEAsPTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S25(Phospho)	S(4): 100.0; T(10): 0.0; T(11): 0.0; S(14): 0.0; S(22): 0.1; S(25): 96.2; T(27): 3.7	S4; S25;	S377; S398		4.78	0	0	3	1005	3012	66.19	13320
VKPEtPPRQSHSGSISYPYK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho)	T(5): 100.0; S(10): 24.7; S(12): 24.7; S(14): 24.7; S(16): 24.7; Y(18): 1.0	T5;	T983		4.77	0	1	3	784.7	2352	30.35	5537

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#
RsRsVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S2(Phospho) S4(Phospho) S6(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 100.0; S(9): 0.0; S(13): 0.0	S2; S4; S6;	S950; S952; S954		4.62	0	2	3	620.9	1861	23.44	4065
GQSQTSPDHRSDTSsPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S11(Phospho) S15(Phospho)	S(3): 0.2; T(5): 47.3; S(6): 47.3; S(11): 89.4; T(13): 13.1; S(14): 13.1; S(15): 89.5	S11; S15;	S1069; S1073		4.52	0	1	3	771	2311	21.44	3640
VKPEtPPRQSHSGsIsPYPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho) S14(Phospho) S16(Phospho)	T(5): 100.0; S(10): 4.2; S(12): 4.2; S(14): 92.0; S(16): 95.5; Y(18): 4.2	T5; S14; S16;	T983; S992; S994		4.46	0	1	3	811.4	2432	33.37	6163
NHsGSRTPPVALNssR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) T7(Phospho)	S(3): 99.9; S(5): 2.9; T(7): 97.1; S(14): 0.0; S(15): 0.0	S3; T7;	S2100; T2104		4.45	0	1	3	613.9	1840	28.09	5062
RGEGDAPFsEPGTTSTQRPSsPETATK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S9(Phospho) S21(Phospho)	S(9): 99.0; T(13): 0.4; T(14): 0.4; S(15): 0.1; T(16): 0.1; S(20): 0.5; S(21): 99.0; T(24): 0.4; T(26): 0.0	S9; S21;	S311; S323		4.43	0	1	3	984.4	2951	41.4	7866
SATRPSPsPERSSTGPEPPAPTLLAER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S8(Phospho)	S(1): 0.3; T(3): 0.3; S(6): 99.5; S(8): 100.0; S(12): 0.0; S(13): 0.0; T(14): 0.0; T(22): 0.0	S6; S8;	S351; S353		4.41	0	1	3	1016	3045	58.61	11591
sGTTPRQGSITSQANEQSVtPQR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T21(Phospho)	S(1): 93.8; T(3): 6.2; S(9): 3.2; T(11): 48.4; S(12): 48.4; S(19): 0.5; T(21): 99.5	S1; T21;	S846; T866		4.36	0	1	3	921.7	2763	45.92	8850
SATRPSPsPERSSTGPEPPAPTLLAER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S8(Phospho) S12(Phospho)	S(1): 5.5; T(3): 5.5; S(6): 89.1; S(8): 100.0; S(12): 93.9; S(13): 5.7; T(14): 0.4; T(22): 0.0	S6; S8; S12;	S351; S353; S357		4.35	0	1	3	1042	3125	66.95	13498
AQTTPGSPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C16(Carbamidomethyl) S14(Phospho)	T(3): 0.0; S(8): 0.0; S(10): 0.0; S(12): 0.0; S(14): 100.0	S14;	S1014		4.32	0	1	3	711.7	2133	31.94	5865
HAsssPESPKPAPAPGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S4(Phospho) S5(Phospho)	S(3): 100.0; S(4): 100.0; S(5): 100.0; S(8): 0.0; S(17): 0.0	S3; S4; S5;	S435; S436; S437		4.29	0	0	3	712.9	2137	18.71	3065
RsRsSsPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S6(Phospho)	S(2): 2.2; S(3): 95.7; S(5): 4.3; S(6): 97.8; T(10): 0.0	S3; S6;	S1691; S1694		4.21	0	2	3	479.2	1436	15.14	2300
sGTTPRQGSITSQANEQSVTPQR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T11(Phospho)	S(1): 95.1; T(3): 9.3; S(9): 4.7; T(11): 86.3; S(12): 4.6; S(19): 0.0; T(21): 0.0	S1; T11;	S846; T856		4.12	0	1	3	895.1	2683	42.31	8057
NHsGSRTPPVALNssR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) T7(Phospho)	S(3): 99.9; S(5): 2.5; T(7): 97.6; S(14): 0.0; S(15): 0.0	S3; T7;	S2100; T2104		4.07	0	1	3	613.9	1840	28.6	5171
THTTALAGRSPsPASGR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S12(Phospho)	T(1): 32.8; T(3): 32.8; T(4): 32.8; S(10): 1.7; S(12): 99.8; S(15): 0.0	S12;	S297		3.93	0	1	3	609.6	1827	21.75	3702
GQSQTSPDHRSDTSsPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho)	S(3): 2.7; T(5): 2.7; S(6): 94.5; S(11): 0.0; T(13): 0.0; S(14): 0.0; S(15): 0.0	S6;	S1064		3.89	0	1	3	717.6	2151	15.79	2439
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 0.0; S(2): 0.0; S(4): 100.0; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694		3.85	0	1	2	640.3	1280	20.3	3399
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		3.74	0	0	2	590.2	1179	28.55	5160

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#
SRsVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C7(Carbamidomethyl)S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 100.0; S(8): 0.0; S(12): 0.0	S3; S5;	S952; S954		3.72	0	1	2	812.8	1625	24.24	4231
NHSGsRtPPVALNSSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) T7(Phospho)	S(3): 5.5; S(5): 97.2; T(7): 97.2; S(14): 0.0; S(15): 0.0	S5; T7;	S2102; T2104		3.69	0	1	3	613.9	1840	27.57	4952
sRsRTSPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 50.0; S(6): 50.0; T(9): 0.0	S1; S3;	S1982; S1984		3.64	0	2	2	693.8	1387	13.46	1947
SATRPSPsPER	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		3.61	0	0	2	672.8	1345	16.4	2568
VKPEtPPRQSHSGSIsPYPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.2; S(14): 0.2; S(16): 95.5; Y(18): 4.1	T5; S16;	T983; S994		3.58	0	1	3	784.7	2352	30.88	5646
SGSsQELDVKPSASPQER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(1): 3.3; S(3): 3.3; S(4): 93.4; S(12): 0.0; S(14): 0.0	S4;	S1542		3.57	0	0	3	661.3	1982	33.79	6248
HASsSPESPKPAPAGSHR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 98.4; S(4): 67.2; S(5): 67.2; S(8): 67.2; S(17): 0.0	S3;	S435		3.55	0	0	3	712.9	2137	17.04	2715
EKSATRPSPsPER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S8(Phospho) S10(Phospho)	S(3): 100.0; T(5): 0.0; S(8): 100.0; S(10): 100.0	S3; S8; S10;	S346; S351; S353		3.54	0	1	2	841.3	1682	15.82	2445
sLsGSSPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C8(Carbamidomethyl)S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 0.0; S(6): 0.0	S1; S3;	S778; S780		3.52	0	0	2	590.2	1179	31.68	5811
SRsGsSPGLR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 97.7; S(6): 2.4	S3; S5;	S1441; S1443		3.44	0	1	2	582.2	1163	17.11	2730
THTTALAGRSPsPASGR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho) S12(Phospho)	T(1): 0.0; T(3): 0.0; T(4): 0.0; S(10): 100.0; S(12): 100.0; S(15): 0.0	S10; S12;	S295; S297		3.39	0	1	2	913.9	1827	21.87	3729
SRtsPAPWK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S4(Phospho)	S(1): 3.0; T(3): 98.5; S(4): 98.5	T3; S4;	T1856; S1857		3.37	0	1	2	595.2	1189	34.62	6428
HSLsGSSPGMK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(2): 0.0; S(4): 96.7; S(6): 1.7; S(7): 1.7	S4;	S1460		3.32	0	0	2	584.2	1167	17.51	2815
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 3.9; S(2): 3.9; S(4): 96.1; S(5): 96.1; T(9): 0.0	S4; S5;	S1693; S1694		3.28	0	1	2	640.3	1280	20.97	3543
SSGHSSSELSPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho)	S(1): 0.0; S(2): 0.0; S(5): 1.5; S(6): 49.3; S(7): 49.3; S(10): 100.0	S10;	S1387		3.25	0	0	2	888.8	1777	36.67	6871
RPSQPSPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S7(Phospho)	S(3): 0.0; S(7): 100.0	S7;	S2706		3.19	0	0	2	551.3	1102	12.93	1836
SRtsPAPWK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S4(Phospho)	S(1): 1.5; T(3): 98.5; S(4): 100.0	T3; S4;	T1856; S1857		3.19	0	1	2	595.2	1189	35.16	6554
sLTRsPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S5(Phospho)	S(1): 100.0; T(3): 0.0; S(5): 100.0	S1; S5;	S2067; S2071		3.18	0	1	2	629.3	1258	42.33	8061
SSRssPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S5(Phospho)	S(1): 1.6; S(2): 1.6; S(4): 96.9; S(5): 100.0; T(9): 0.0	S4; S5;	S1693; S1694		3.13	0	1	2	640.3	1280	21.61	3675
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		3.08	0	0	2	691.2	1381	34.71	6449
SCFEssPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl) S6(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 100.0	S6;	S876		3.02	0	0	2	738.3	1476	48.28	9343
RsPsVsSPEPAEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S2(Phospho) S4(Phospho) S6(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 97.2; S(7): 2.8	S2; S4; S6;	S1727; S1729; S1731		2.98	0	1	2	805.8	1611	27.29	4890

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#
SATRPSPsPER	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		2.86	0	0	2	672.8	1345	15.78	2435
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		2.76	0	1	2	530.2	1059	38.52	7255
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		2.73	0	0	2	653.8	1307	34.52	6404
SVsPCSNVESR	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl) S3(Phospho)	S(1): 0.0; S(3): 100.0; S(6): 0.0; S(10): 0.0	S3;	S954		2.72	0	0	2	651.3	1302	26.05	4617
SRTPPSAPSQSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho)	S(1): 1.6; T(3): 98.4; S(6): 0.0; S(9): 0.0; S(11): 0.0	T3;	T2409		2.66	0	1	2	675.8	1351	14.73	2214
MSCFsRPSMsPTPLDR	SRRM2	23524	serine/arginine repetitive matrix protein 2	M1(Oxidation) C3(Carbamidomethyl) M9(Oxidation) S5(Phospho) S10(Phospho)	S(2): 0.0; S(5): 99.9; S(8): 3.3; S(10): 96.7; T(12): 0.1	S5; S10;	S2118; S2123		2.66	0	0	3	687.6	2061	47.94	9273
sLtrSPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho) S5(Phospho)	S(1): 100.0; T(3): 100.0; S(5): 100.0	S1; T3; S5;	S2067; T2069; S2071		2.61	0	1	2	669.3	1338	50.57	9824
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		2.6	0	1	2	530.2	1059	39.04	7366
sRtPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho)	S(1): 100.0; T(3): 100.0	S1; T3;	S2020; T2022		2.51	0	1	2	529.2	1057	26.93	4807
SGMsPEQSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho)	S(1): 0.0; S(4): 100.0; S(8): 0.0	S4;	S1132		2.49	0	0	2	529.7	1058	16.93	2691
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		2.4	0	2	2	829.4	1658	14.58	2181
SSGHsSSELSPDAVEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) S10(Phospho)	S(1): 50.0; S(2): 50.0; S(5): 100.0; S(6): 0.0; S(7): 0.0; S(10): 100.0	S5; S10;	S1382; S1387		2.36	0	0	2	928.8	1857	48.72	9435
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 100.0; Y(4): 0.0; S(5): 100.0	S3; S5;	S2692; S2694		2.35	0	0	2	599.2	1197	54.11	10608
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	27		0.001	1	2	794.7	1588	17.08	2722
sRTsPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S4(Phospho)	S(1): 98.8; T(3): 1.2; S(4): 100.0; T(7): 0.0	S1; S4;	S1984; S1987	26		0.001	1	2	532.2	1063	13.31	1914
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		0.001	1	2	530.2	1059	39.04	7366
RSsRSsPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S6(Phospho)	S(2): 2.2; S(3): 95.7; S(5): 4.3; S(6): 97.8; T(10): 0.0	S3; S6;	S1691; S1694	22		0.001	2	3	479.2	1436	15.14	2300
RSsVsSPEPAEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S2(Phospho) S4(Phospho) S6(Phospho)	S(2): 100.0; S(4): 100.0; S(6): 97.2; S(7): 2.8	S2; S4; S6;	S1727; S1729; S1731	18		0.001	1	2	805.8	1611	27.29	4890
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		0.001	2	3	553.2	1658	14.15	2091
SATRPSPsPER	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	12		0.001	0	2	672.8	1345	15.78	2435
VKAQTTPGPSLSGSKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C18(Carbamidomethyl) T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 0.0; S(12): 0.2; S(14): 4.4; S(16): 95.4	T5; S16;	T1003; S1014	11		0.001	2	3	814	2440	33	6086

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#
VKPEtPPRQSHsGSISYPYK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho) S12(Phospho)	T(5): 100.0; S(10): 0.3; S(12): 90.3; S(14): 4.6; S(16): 4.6; Y(18): 0.3	T5; S12;	T983; S990		5.49	0.001	1	4	588.8	2352	30.58	5583
GQSQTsPDHRsDTSSPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S11(Phospho)	S(3): 0.0; T(5): 6.1; S(6): 93.5; S(11): 97.4; T(13): 32.9; S(14): 35.0; S(15): 35.0	S6; S11;	S1064; S1069		4.86	0.001	1	3	771	2311	20.28	3396
SGTPPRQGSITSPQANEQSVtPQRR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T21(Phospho)	S(1): 50.0; T(3): 50.0; S(9): 33.3; T(11): 33.3; S(12): 33.3; S(19): 0.5; T(21): 99.5	T21;	T866		4.84	0.001	2	3	973.8	2919	37.44	7030
QGSITSPQANEQSVtPQRR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T15(Phospho)	S(3): 0.0; T(5): 0.0; S(6): 0.0; S(13): 2.5; T(15): 97.5	T15;	T866		4.6	0.001	1	3	722	2164	29.33	5325
GQSQTsPDHRSDTsSPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S15(Phospho)	S(3): 0.0; T(5): 3.7; S(6): 96.3; S(11): 0.1; T(13): 3.6; S(14): 3.6; S(15): 92.7	S6; S15;	S1064; S1073		4.03	0.001	1	3	744.3	2231	16.48	2586
VKsSTPPRQsPSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S10(Phospho)	S(3): 100.0; S(4): 50.0; T(5): 50.0; S(10): 100.0; S(12): 0.0	S3; S10;	S901; S908		3.9	0.001	2	2	833.8	1667	12.65	1771
GGRsRsSSPVELASR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 98.1; S(7): 51.0; S(8): 51.0; T(11): 0.0; S(15): 0.0	S4; S6;	S1099; S1101		3.63	0.001	2	3	629.6	1887	40.81	7743
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): 0.0; S(6): 100.0	S1; S3; S6;	S1497; S1499; S1502		3.62	0.001	1	2	778.3	1556	27.62	4963
RSLsGSsPCPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C9(Carbamidomethyl)S4(Phospho) S7(Phospho)	S(2): 0.0; S(4): 100.0; S(6): 0.0; S(7): 100.0	S4; S7;	S780; S783		3.12	0.001	1	2	668.3	1336	18.5	3022
QSHSGSIsPYPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S8(Phospho)	S(2): 0.0; S(4): 0.0; S(6): 0.0; S(8): 99.9; Y(10): 0.0	S8;	S994		2.76	0.001	0	2	684.3	1368	24.37	4259
sRTsPITR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S4(Phospho)	S(1): 98.0; T(3): 3.9; S(4): 98.0; T(7): 0.0	S1; S4;	S1972; S1975		2.75	0.001	1	2	539.2	1077	17.62	2838
sCFESSPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl)S1(Phospho) S6(Phospho)	S(1): 100.0; S(5): 0.1; S(6): 99.9	S1; S6;	S871; S876		2.43	0.001	0	2	778.3	1556	58.97	11677
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 99.9; Y(4): 0.1; S(5): 99.9	S3; S5;	S2692; S2694		2.21	0.001	0	2	599.2	1197	54.62	10722
sLTrsPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho) S5(Phospho)	S(1): 100.0; T(3): 100.0; S(5): 100.0	S1; T3; S5;	S2067; T2069; S2071		1.6	0.001	1	2	669.3	1338	50.04	9713
EKsATRPsPsPER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S8(Phospho) S10(Phospho)	S(3): 100.0; T(5): 0.0; S(8): 100.0; S(10): 100.0	S3; S8; S10;	S346; S351; S353	22		0.002	1	2	841.3	1682	15.82	2445
SLsYsPVER	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho)	S(1): 0.0; S(3): 99.9; Y(4): 0.1; S(5): 99.9	S3; S5;	S2692; S2694	21		0.002	0	2	599.2	1197	54.62	10722
sLTrsPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S5(Phospho)	S(1): 100.0; T(3): 0.0; S(5): 100.0	S1; S5;	S2067; S2071	17		0.002	1	2	629.3	1258	42.33	8061
sRsRtPPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho) T5(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 100.0; T(9): 0.0	S1; S3; T5;	S1923; S1925; T1927	17		0.002	2	2	698.8	1397	17.53	2820
sRtPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho)	S(1): 100.0; T(3): 100.0	S1; T3;	S2020; T2022	16		0.002	1	2	529.2	1057	26.93	4807
sRtPPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho)	S(1): 100.0; T(3): 100.0; T(7): 0.0	S1; T3;	S1925; T1927	13		0.002	1	2	537.2	1073	18.87	3099

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#
SCFEssPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl)S5(Phospho) S6(Phospho)	S(1): 0.0; S(5): 100.0; S(6): 100.0	S5; S6;	S875; S876	13		0.002	0	2	778.3	1556	59.8	11839
VKPEtPPRQSHSGSiSPYPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho)	T(5): 100.0; S(10): 24.7; S(12): 24.7; S(14): 24.7; S(16): 24.7; Y(18): 1.0	T5;	T983	12		0.002	1	3	784.7	2352	30.35	5537
GQSQTsPDHRSDTsPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) S15(Phospho)	S(3): 0.0; T(5): 3.7; S(6): 96.3; S(11): 0.1; T(13): 3.6; S(14): 3.6; S(15): 92.7	S6; S15;	S1064; S1073	12		0.002	1	3	744.3	2231	16.48	2586
DGSGTPSRHsLsGSSPGMK	SRRM2	23524	serine/arginine repetitive matrix protein 2	S10(Phospho) S12(Phospho)	S(3): 74.9; T(5): 5.5; S(7): 9.9; S(10): 79.1; S(12): 82.7; S(14): 24.0; S(15): 24.0	S10; S12;	S1458; S1460	11		0.002	1	3	695.6	2085	29.23	5304
QGSITsPQANEQSVtPQRR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S6(Phospho) T15(Phospho)	S(3): 3.7; T(5): 3.7; S(6): 92.6; S(13): 3.9; T(15): 96.1	S6; T15;	S857; T866		4.35	0.002	1	3	748.7	2244	35.3	6582
SCFEssPDPELK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C2(Carbamidomethyl)S5(Phospho) S6(Phospho)	S(1): 0.0; S(5): 100.0; S(6): 100.0	S5; S6;	S875; S876		2.13	0.002	0	2	778.3	1556	59.8	11839
GQSQTsPDHRSDTsPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T13(Phospho) S14(Phospho) S15(Phospho)	S(3): 33.3; T(5): 33.3; S(6): 33.3; S(11): 0.1; T(13): 99.9; S(14): 99.9; S(15): 100.0	T13; S14; S15;	T1071; S1072; S1073	13		0.003	1	2	1196	2391	25.04	4401
REtPsPRPMR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T2738; S2740	11		0.003	1	2	693.8	1387	18.06	2931
VKsSTPPRQSPSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 100.0; S(4): 50.0; T(5): 50.0; S(10): 50.0; S(12): 50.0	S3;	S901		5.04	0.003	2	3	556.2	1667	12.69	1781
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		3.6	0.003	1	2	794.7	1588	17.08	2722
RSSRsPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S5(Phospho) S6(Phospho)	S(2): 0.0; S(3): 3.5; S(5): 98.2; S(6): 98.2; T(10): 0.1	S5; S6;	S1693; S1694		3.3	0.003	2	2	718.3	1436	15.13	2298
sRsRtPPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho) T5(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 100.0; T(9): 0.0	S1; S3; T5;	S1923; S1925; T1927		3.21	0.003	2	2	698.8	1397	17.53	2820
VKPEtPPRQSHSGSiSPYPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	T5(Phospho) S16(Phospho)	T(5): 100.0; S(10): 3.5; S(12): 3.5; S(14): 3.5; S(16): 86.1; Y(18): 3.5	T5; S16;	T983; S994		3.1	0.003	1	3	784.7	2352	29.81	5424
sRsRTsPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho) S6(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 2.4; S(6): 97.6; T(9): 0.0	S1; S3; S6;	S1982; S1984; S1987		3	0.003	2	2	693.8	1387	14.03	2065
sLRTsPPAIR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S5(Phospho)	S(1): 99.9; T(3): 2.3; S(5): 97.8	S1; S5;	S2067; S2071		2.5	0.003	1	2	629.3	1258	41.79	7949
sRtPPVTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho)	S(1): 100.0; T(3): 100.0; T(7): 0.0	S1; T3;	S1925; T1927		2.39	0.003	1	2	537.2	1073	18.87	3099
GRsECDsPEPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S3(Phospho) S8(Phospho)	S(3): 100.0; S(7): 0.0; S(8): 100.0	S3; S8;	S1478; S1483		2.97	0.004	1	2	754.8	1509	13.36	1925
ARsRtPPSPAPSQSR	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		4.05	0.005	2	3	553.2	1658	14.15	2091

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#
GQSQTSPDHRSDTSsPEVR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S15(Phospho)	S(3): 0.2; T(5): 49.9; S(6): 49.9; S(11): 35.3; T(13): 35.3; S(14): 35.3; S(15): 94.2	S15;	S1073		4.03	0.005	1	3	771	2311	19.7	3275
AQTPPGPSLSGsKsPCPQEK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C16(Carbamidomethyl)T3(Phospho) S12(Phospho) S14(Phospho)	T(3): 100.0; S(8): 0.4; S(10): 0.4; S(12): 99.3; S(14): 100.0	T3; S12; S14;	T1003; S1012; S1014		3	0.005	1	3	765	2293	45.86	8837
REtPsRPRMR	SRRM2	23524	serine/arginine repetitive matrix protein 2	T3(Phospho) S5(Phospho)	T(3): 100.0; S(5): 100.0	T3; S5;	T2738; S2740		2.53	0.005	1	2	693.8	1387	18.06	2931
RSrSsPELTR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho) S5(Phospho) S6(Phospho)	S(2): 9.3; S(3): 95.5; S(5): 95.4; S(6): 99.5; T(10): 0.3	S3; S5; S6;	S1691; S1693; S1694		2.22	0.005	2	2	758.3	1516	19.41	3213
sRtPLLPR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) T3(Phospho)	S(1): 100.0; T(3): 100.0	S1; T3;	S2032; T2034		1.82	0.005	1	2	550.3	1100	45.07	8667
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	19		0.006	1	2	669.3	1338	12.57	1748
VKsSTPPRQSPSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S3(Phospho)	S(3): 100.0; S(4): 50.0; T(5): 50.0; S(10): 50.0; S(12): 50.0	S3;	S901	10		0.007	2	3	556.2	1667	12.69	1781
GRSECDssPEPK	SRRM2	23524	serine/arginine repetitive matrix protein 2	C5(Carbamidomethyl)S7(Phospho) S8(Phospho)	S(3): 0.0; S(7): 100.0; S(8): 100.0	S7; S8;	S1482; S1483		3.25	0.007	1	2	754.8	1509	12.76	1798
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		3.92	0.008	1	2	669.3	1338	12.57	1748
sRsRTSPVSR	SRRM2	23524	serine/arginine repetitive matrix protein 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; T(5): 50.0; S(6): 50.0; S(9): 0.0	S1; S3;	S1888; S1890		2.85	0.008	2	2	686.8	1373	12.77	1800
SRGsPRYSR	SRSF1	6426	serine/arginine-rich splicing factor 1 isoform 1	S4(Phospho)	S(1): 0.0; S(4): 100.0; Y(7): 50.0; S(8): 50.0	S4;	S234	19		0.003	2	2	661.8	1323	14.07	2073
VKVDGPRsPSYGR	SRSF1	6426	serine/arginine-rich splicing factor 1 isoform 1	S8(Phospho)	S(8): 98.6; S(10): 50.7; Y(11): 50.7	S8;	S199		4.36	0.005	2	3	526.6	1578	26.07	4622
VKVDGPRsPSYGR	SRSF1	6426	serine/arginine-rich splicing factor 1 isoform 1	S8(Phospho)	S(8): 98.6; S(10): 50.7; Y(11): 50.7	S8;	S199	14		0.007	2	3	526.6	1578	26.07	4622
SRGsPRYSR	SRSF1	6426	serine/arginine-rich splicing factor 1 isoform 1	S4(Phospho) S8(Phospho)	S(1): 0.0; S(4): 100.0; Y(7): 2.0; S(8): 98.0	S4; S8;	S234; S238	14		0.007	2	3	441.5	1323	13.95	2050
sRsFDYNYR	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; Y(6): 0.0; Y(8): 0.0	S1; S3;	S131; S133	31		0	1	2	684.2	1367	44.28	8477
sRsFDYNYR	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; Y(6): 0.0; Y(8): 0.0	S1; S3;	S131; S133		3.42	0	1	2	684.2	1367	44.28	8477
SWTsPKSSGH	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S4(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 100.0; S(7): 50.0; S(8): 50.0	S4;	S255		2.88	0	1	2	617.2	1233	27.41	4919
sRsFDYNYR	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; Y(6): 0.0; Y(8): 0.0	S1; S3;	S131; S133	27		0.002	1	2	684.2	1367	44.35	8496
SWTsPKSSGH	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S4(Phospho)	S(1): 0.0; T(3): 0.0; S(4): 100.0; S(7): 50.0; S(8): 50.0	S4;	S255	18		0.002	1	2	617.2	1233	27.41	4919
sRsFDYNYR	SRSF10	10772	serine/arginine-rich splicing factor 10 isoform 3	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; Y(6): 0.0; Y(8): 0.0	S1; S3;	S131; S133		3.75	0.002	1	2	684.2	1367	44.35	8496
TKECsVEKGTGDSLRL	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	C4(Carbamidomethyl) S5(Phospho)	T(1): 0.0; S(5): 100.0; T(10): 0.0; S(13): 0.0	S5;	S455	60		0	2	3	582.9	1747	20.42	3425
KPIETGsPK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S7(Phospho)	T(5): 0.0; S(7): 100.0	S7;	S448	30		0	0	2	518.8	1037	12.93	1835
DYDEEEQGYDsEKEK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S11(Phospho)	Y(2): 0.0; Y(9): 0.0; S(11): 100.0	S11;	S433	19		0	1	3	648.6	1944	26.39	4691

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#
TKECsVEKGTGDSLR	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	C4(Carbamidomethyl) S5(Phospho)	T(1): 0.0; S(5): 100.0; T(10): 0.0; S(13): 0.0	S5;	S455		5.3	0	2	3	582.9	1747	20.42	3425
DYDEEEQGYDsEKEKK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S11(Phospho)	Y(2): 0.0; Y(9): 0.1; S(11): 99.9	S11;	S433		3.72	0	2	3	691.3	2072	21.62	3677
DYDEEEQGYDsEKEK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S11(Phospho)	Y(2): 0.0; Y(9): 0.0; S(11): 100.0	S11;	S433		3.6	0	1	3	648.6	1944	26.39	4691
KPIETGsPK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S7(Phospho)	T(5): 0.0; S(7): 100.0	S7;	S448		3.33	0	0	2	518.8	1037	12.93	1835
DYDEEEQGYDsEKEK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S11(Phospho)	Y(2): 0.0; Y(9): 0.0; S(11): 100.0	S11;	S433	28		0.001	1	2	972.4	1944	26.38	4689
DYDEEEQGYDsEKEK	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S11(Phospho)	Y(2): 0.0; Y(9): 0.0; S(11): 100.0	S11;	S433		3.3	0.001	1	2	972.4	1944	26.38	4689
KLsRsPsPR	SRSF11	9295	serine/arginine-rich splicing factor 11 isoform 2	S3(Phospho) S5(Phospho) S7(Phospho)	S(3): 100.0; S(5): 100.0; S(7): 100.0	S3; S5; S7;	S366; S368; S370		3.19	0.005	2	2	634.3	1268	14.13	2088
sRsPPVPSK	SRSF2	6427	serine/arginine-rich splicing factor 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(8): 0.0	S1; S3;	S189; S191		2.96	0.001	1	2	557.7	1114	16.36	2560
sRsPPVPSK	SRSF2	6427	serine/arginine-rich splicing factor 2	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(8): 0.0	S1; S3;	S189; S191	12		0.004	1	2	557.7	1114	16.36	2560
IQNNDNVGKPKsRSPSR	SRSF4	6429	serine/arginine-rich splicing factor 4	S12(Phospho)	S(12): 100.0; S(14): 50.0; S(16): 50.0	S12;	S288		6.12	0	2	3	686.3	2057	12.83	1812
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.4; S(3): 98.6; S(10): 0.0	S3;	S303	54		0	0	2	601.8	1203	45.02	8657
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(10): 0.0	S3;	S303	41		0	0	2	601.8	1203	45.53	8766
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	37		0	1	2	549.7	1098	15.86	2451
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(10): 0.0	S3;	S303	36		0	0	2	601.8	1203	44.5	8531
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.5; S(3): 98.5; S(10): 0.0	S3;	S303	35		0	0	2	601.8	1203	46.08	8884
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	33		0	2	2	627.8	1255	12.87	1821
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	28		0	1	2	549.7	1098	16.4	2569
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	27		0	1	2	549.7	1098	15.02	2274
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	26		0	2	2	627.8	1255	13.73	2005
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		3.92	0	1	2	549.7	1098	15.86	2451
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		3.72	0	1	2	549.7	1098	15.02	2274
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		3.53	0	1	2	549.7	1098	16.4	2569
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		3.46	0	2	2	627.8	1255	13.73	2005
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(10): 0.0	S3;	S303		2.99	0	0	2	601.8	1203	45.53	8766
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.5; S(3): 98.5; S(10): 0.0	S3;	S303		2.94	0	0	2	601.8	1203	46.08	8884
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.4; S(3): 98.6; S(10): 0.0	S3;	S303		2.92	0	0	2	601.8	1203	45.02	8657
SNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(10): 0.0	S3;	S303		2.58	0	0	2	601.8	1203	44.5	8531
SRSQsRsNsPLPVPPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S5(Phospho) S7(Phospho) S9(Phospho)	S(1): 4.2; S(3): 4.2; S(5): 92.3; S(7): 99.6; S(9): 99.6; S(16): 0.0	S5; S7; S9;	S299; S301; S303		3.5	0.001	2	3	688.6	2064	40.23	7623

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#
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	29		0.002	2	3	418.9	1255	12.4	1701
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		3.43	0.003	2	2	627.8	1255	12.87	1821
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		3.12	0.005	2	3	418.9	1255	12.4	1701
SRSQsRsNsPLVPVPSK	SRSF6	6431	serine/arginine-rich splicing factor 6	S5(Phospho) S7(Phospho) S9(Phospho)	S(1): 0.1; S(3): 0.7; S(5): 99.7; S(7): 99.7; S(9): 99.7; S(16): 0.0	S5; S7; S9;	S299; S301; S303		2.99	0.005	2	3	688.6	2064	41.5	7887
SRYSRSPYsR	SRSF8	10929	serine/arginine-rich splicing factor 8	S4(Phospho) S9(Phospho)	S(1): 0.0; Y(3): 0.1; S(4): 99.9; S(6): 0.1; Y(8): 2.2; S(9): 97.8	S4; S9;	S156; S161		2.67	0.007	2	2	709.8	1419	16.64	2625
RPPKsPEEEGQMSS	SRSF8	10929	serine/arginine-rich splicing factor 8	S5(Phospho)	S(5): 100.0; S(13): 50.0; S(14): 50.0	S5;	S273	27		0.009	1	2	859.8	1719	23.08	3991
GRDsPYQSR	SRSF9	8683	serine/arginine-rich splicing factor 9	S4(Phospho)	S(4): 100.0; Y(6): 0.0; S(8): 0.0	S4;	S204	27		0	1	2	573.2	1145	12.75	1795
GRDsPYQSR	SRSF9	8683	serine/arginine-rich splicing factor 9	S4(Phospho)	S(4): 100.0; Y(6): 0.0; S(8): 0.0	S4;	S204		3.14	0	1	2	573.2	1145	12.75	1795
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 3.7; S(20): 96.3	S20;	S87	22		0	1	3	1075	3222	37.03	6946
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 4.2; S(20): 95.8	S20;	S87	14		0	1	4	806.3	3222	37.45	7033
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 4.2; S(20): 95.8	S20;	S87	14		0	1	4	806.3	3222	36.93	6926
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 4.2; S(20): 95.8	S20;	S87		6.61	0	1	4	806.3	3222	36.93	6926
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 4.2; S(20): 95.8	S20;	S87		5.7	0	1	4	806.3	3222	37.45	7033
APSEELHGDQTDGFGGSQsPQKQEEQR	SSH3	54961	protein phosphatase Slingshot homolog 3	S20(Phospho)	S(3): 0.0; T(12): 0.0; S(18): 3.7; S(20): 96.3	S20;	S87		4.59	0	1	3	1075	3222	37.03	6946
EGMNPYSYDEYADsDEDQHDAYLER	SSRP1	6749	FACT complex subunit SSRP1	M3(Oxidation) S13(Phospho)	S(6): 0.0; Y(7): 0.0; Y(10): 0.0; S(13): 100.0; Y(21): 0.0	S13;	S444	37		0	0	3	982.4	2945	52.21	10185
EGMNPYSYDEYADsDEDQHDAYLER	SSRP1	6749	FACT complex subunit SSRP1	S13(Phospho)	S(6): 0.0; Y(7): 0.0; Y(10): 0.0; S(13): 100.0; Y(21): 0.0	S13;	S444	33		0	0	3	977	2929	57.26	11295
SKFVssDESSSGENK	SSRP1	6749	FACT complex subunit SSRP1	S6(Phospho) S7(Phospho)	S(1): 0.0; S(6): 99.6; S(7): 99.6; S(10): 1.0; S(11): 49.9; S(12): 49.9	S6; S7;	S667; S668	19		0	1	2	978.8	1957	33.81	6253
EGMNPYSYDEYADsDEDQHDAYLER	SSRP1	6749	FACT complex subunit SSRP1	S13(Phospho)	S(6): 0.0; Y(7): 0.0; Y(10): 0.0; S(13): 100.0; Y(21): 0.0	S13;	S444		4.92	0	0	3	977	2929	57.26	11295
EGMNPYSYDEYADsDEDQHDAYLER	SSRP1	6749	FACT complex subunit SSRP1	M3(Oxidation) S13(Phospho)	S(6): 0.0; Y(7): 0.0; Y(10): 0.0; S(13): 100.0; Y(21): 0.0	S13;	S444		4.62	0	0	3	982.4	2945	52.21	10185
SKFVssDESSSGENK	SSRP1	6749	FACT complex subunit SSRP1	S6(Phospho) S7(Phospho)	S(1): 0.0; S(6): 99.6; S(7): 99.6; S(10): 1.0; S(11): 49.9; S(12): 49.9	S6; S7;	S667; S668		2.92	0.003	1	2	978.8	1957	33.81	6253
SQsVsPPPVLSPPR	ST5	6764	suppression of tumorigenicity 5 protein isoform 1	S3(Phospho) S5(Phospho)	S(1): 2.0; S(3): 98.0; S(5): 100.0; S(11): 0.0	S3; S5;	S30; S32	44		0	0	2	804.4	1608	74.86	15140
SQsVsPPPVLSPPR	ST5	6764	suppression of tumorigenicity 5 protein isoform 1	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 100.0; S(11): 0.0	S3; S5;	S30; S32	38		0	0	2	804.4	1608	75.39	15230
SQsVsPPPVLSPPR	ST5	6764	suppression of tumorigenicity 5 protein isoform 1	S3(Phospho) S5(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 100.0; S(11): 0.0	S3; S5;	S30; S32		2.56	0	0	2	804.4	1608	75.39	15230
SQsVsPPPVLSPPR	ST5	6764	suppression of tumorigenicity 5 protein isoform 1	S3(Phospho) S5(Phospho)	S(1): 2.0; S(3): 98.0; S(5): 100.0; S(11): 0.0	S3; S5;	S30; S32		2.51	0	0	2	804.4	1608	74.86	15140
GSSPTPPCSPVQPsK	STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform d	C8(Carbamidomethyl) S14(Phospho)	S(2): 33.3; S(3): 33.3; T(5): 33.3; S(9): 0.0; S(14): 100.0	S14;	S325	19		0	0	2	843.3	1686	37.97	7143

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)S14(Phospho)	S(2): 33.3; S(3): 33.3; T(5): 33.3; S(9): 0.0; S(14): 100.0	S14;	S325		2.55	0	0	2	843.3	1686	37.97	7143
GSSPTPPCSPVQPsK	STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform d	C8(Carbamidomethyl)T5(Phospho) S14(Phospho)	S(2): 50.8; S(3): 50.8; T(5): 98.4; S(9): 0.1; S(14): 99.9	T5; S14;	T316; S325		2.49	0	0	2	883.3	1766	46.71	9016
GSSPTPPCSPVQPsK	STAU2	27067	double-stranded RNA-binding protein Staufen homolog 2 isoform d	C8(Carbamidomethyl)T5(Phospho) S14(Phospho)	S(2): 50.8; S(3): 50.8; T(5): 98.4; S(9): 0.1; S(14): 99.9	T5; S14;	T316; S325	21	0.001	0	0	2	883.3	1766	46.71	9016
SHsPSSDPDTPSPVGDSR	STIM1	6786	stromal interaction molecule 1 isoform 2 precursor	S3(Phospho)	S(1): 2.1; S(3): 97.8; S(5): 0.0; S(6): 0.0; T(11): 0.0; S(13): 0.0; S(18): 0.0	S3;	S618	59		0	0	3	667.9	2002	31.64	5802
SHsPSSDPDTPSPVGDSR	STIM1	6786	stromal interaction molecule 1 isoform 2 precursor	S3(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 0.0; S(6): 0.0; T(11): 0.0; S(13): 0.0; S(18): 0.0	S3;	S618	26		0	0	2	1001	2002	31.68	5812
SHsPSSDPDTPSPVGDSR	STIM1	6786	stromal interaction molecule 1 isoform 2 precursor	S3(Phospho)	S(1): 2.1; S(3): 97.8; S(5): 0.0; S(6): 0.0; T(11): 0.0; S(13): 0.0; S(18): 0.0	S3;	S618		4.88	0	0	3	667.9	2002	31.64	5802
SHsPSSDPDTPSPVGDSR	STIM1	6786	stromal interaction molecule 1 isoform 2 precursor	S3(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 0.0; S(6): 0.0; T(11): 0.0; S(13): 0.0; S(18): 0.0	S3;	S618		4.13	0	0	2	1001	2002	31.68	5812
SIVPSsPQPQR	STIM2	57620	stromal interaction molecule 2 isoform 3 precursor	S6(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 100.0	S6;	S523	33		0	0	2	638.3	1276	38.88	7332
SIVPSsPQPQR	STIM2	57620	stromal interaction molecule 2 isoform 3 precursor	S6(Phospho)	S(1): 0.0; S(5): 0.0; S(6): 100.0	S6;	S523		2.35	0	0	2	638.3	1276	38.88	7332
QVAEQGGDLsPAANR	STK10	6793	serine/threonine-protein kinase 10	S10(Phospho)	S(10): 100.0	S10;	S438	75		0	0	2	796.9	1593	31.84	5843
ASQsRPNsSALETLGGEK	STK10	6793	serine/threonine-protein kinase 10	S4(Phospho) S8(Phospho)	S(2): 3.0; S(4): 97.0; S(8): 97.0; S(9): 3.0; T(13): 0.0	S4; S8;	S450; S454	27		0	0	3	664.6	1992	49.79	9659
ASQsRPNsSALETLGGEK	STK10	6793	serine/threonine-protein kinase 10	S4(Phospho) S8(Phospho)	S(2): 0.1; S(4): 99.9; S(8): 99.9; S(9): 0.1; T(13): 0.0	S4; S8;	S450; S454	24		0	0	2	996.4	1992	49.78	9657
LSEEAECNPStPSK	STK10	6793	serine/threonine-protein kinase 10	C7(Carbamidomethyl) T12(Phospho)	S(2): 0.0; S(11): 3.0; T(12): 94.1; S(14): 3.0	T12;	T952	14		0	0	2	863.4	1726	29.85	5430
ASQsRPNsSALETLGGEK	STK10	6793	serine/threonine-protein kinase 10	S4(Phospho) S8(Phospho)	S(2): 3.0; S(4): 97.0; S(8): 97.0; S(9): 3.0; T(13): 0.0	S4; S8;	S450; S454	4.39		0	0	3	664.6	1992	49.79	9659
QVAEQGGDLsPAANR	STK10	6793	serine/threonine-protein kinase 10	S10(Phospho)	S(10): 100.0	S10;	S438		3.83	0	0	2	796.9	1593	31.84	5843
LSEEAECNPStPSK	STK10	6793	serine/threonine-protein kinase 10	C7(Carbamidomethyl) T12(Phospho)	S(2): 0.0; S(11): 3.0; T(12): 94.1; S(14): 3.0	T12;	T952		3.22	0	0	2	863.4	1726	29.85	5430
ASQsRPNsSALETLGGEK	STK10	6793	serine/threonine-protein kinase 10	S4(Phospho) S8(Phospho)	S(2): 0.1; S(4): 99.9; S(8): 99.9; S(9): 0.1; T(13): 0.0	S4; S8;	S450; S454	2.25		0	0	2	996.4	1992	49.78	9657
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	34		0	1	2	667.3	1334	15.43	2361
RASIsEPsDTDPEPR	STK11IP	114790	serine/threonine-protein kinase 11-interacting protein	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 96.9; T(10): 3.1	S3; S5; S8;	S387; S389; S392	25		0	1	2	948.8	1897	42.31	8056
RASIsEPsDTDPEPR	STK11IP	114790	serine/threonine-protein kinase 11-interacting protein	S3(Phospho) S5(Phospho) S8(Phospho)	S(3): 100.0; S(5): 100.0; S(8): 96.9; T(10): 3.1	S3; S5; S8;	S387; S389; S392		3.03	0	1	2	948.8	1897	42.31	8056
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		2.95	0	1	2	667.3	1334	15.43	2361
TEDGDWWEWSdDEMDKSEEGK	STK39	27347	STE20/SPS1-related proline-alanine-rich protein kinase	S9(Phospho)	T(1): 4.8; S(9): 95.2; S(17): 0.0	S9;	S385		2.89	0	1	3	866.3	2597	59.22	11728

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#
TEDGDWEWSDEEMDEKSEEGK	STK39	27347	STE20/SPS1-related proline-alanine-rich protein kinase	M13(Oxidation) S9(Phospho)	T(1): 4.3; S(9): 95.4; S(17): 0.2	S9;	S385		2.87	0	1	3	871.6	2613	51.82	10085
EVDQDDEENSDEEMDSGMTMR	STK4	6789	serine/threonine-protein kinase 4	S10(Phospho)	S(10): 100.0; S(17): 0.0; T(19): 0.0	S10;	S320	39		0	0	3	880.3	2639	53.72	10516
EVDQDDEENSDEEMDSGMTMR	STK4	6789	serine/threonine-protein kinase 4	M20(Oxidation) S10(Phospho)	S(10): 100.0; S(17): 0.0; T(19): 0.0	S10;	S320	16		0	0	3	885.6	2655	44.82	8608
EVDQDDEENSDEEMDSGMTMR	STK4	6789	serine/threonine-protein kinase 4	S10(Phospho)	S(10): 100.0; S(17): 0.0; T(19): 0.0	S10;	S320		3.31	0	0	3	880.3	2639	53.72	10516
EVDQDDEENSDEEMDSGMTMR	STK4	6789	serine/threonine-protein kinase 4	M20(Oxidation) S10(Phospho)	S(10): 100.0; S(17): 0.0; T(19): 0.0	S10;	S320		2.33	0	0	3	885.6	2655	44.82	8608
AA\$PPASDLIEQQQK	STRIP1	85369	striatin-interacting protein 1 isoform 2	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0	S3;	S240	23		0	0	2	910.9	1821	55.16	10834
AA\$PPASDLIEQQQK	STRIP1	85369	striatin-interacting protein 1 isoform 2	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0	S3;	S240		2.99	0	0	2	910.9	1821	55.16	10834
ENPPVEDsDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho)	S(8): 98.3; S(9): 1.7	S8;	S498	55		0	1	2	906.4	1812	19.17	3163
ENPPVEDssDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0	S8; S9;	S498; S499	31		0	1	2	946.3	1892	23.55	4086
ENPPVEDssDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0	S8; S9;	S498; S499	29		0	1	3	631.2	1892	23.26	4029
ENPPVEDssDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0	S8; S9;	S498; S499		3.82	0	1	3	631.2	1892	23.26	4029
ENPPVEDssDEDDKRNQGNLYDK	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0; Y(21): 0.0	S8; S9;	S498; S499		3.45	0	2	3	942	2824	34.31	6358
ENPPVEDsDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho)	S(8): 98.3; S(9): 1.7	S8;	S498		3.34	0	1	2	906.4	1812	19.17	3163
ENPPVEDssDEDDKR	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 100.0; S(9): 100.0	S8; S9;	S498; S499		2.5	0	1	2	946.3	1892	23.55	4086
ENPPVEDssDEDDKRNQGNLYDK	STT3B	201595	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	S8(Phospho) S9(Phospho)	S(8): 92.5; S(9): 92.5; Y(21): 15.1	S8; S9;	S498; S499		5.07	0.006	2	4	706.8	2824	34.7	6446
LGAGGGsPEKSPSAQELK	STUB1	10273	E3 ubiquitin-protein ligase CHIP isoform a	S7(Phospho)	S(7): 100.0; S(11): 0.0; S(13): 0.0	S7;	S19	37		0	1	2	896.9	1793	31.73	5821
LGAGGGsPEKSPSAQELK	STUB1	10273	E3 ubiquitin-protein ligase CHIP isoform a	S7(Phospho)	S(7): 100.0; S(11): 0.0; S(13): 0.0	S7;	S19		2.61	0	1	2	896.9	1793	31.73	5821
VsQSPSKDSEENPATEERPEK	STX18	53407	syntaxin-18	S2(Phospho)	S(2): 99.9; S(4): 0.1; S(6): 0.0; S(9): 0.0; T(15): 0.0	S2;	S187	33		0	1	3	808.7	2424	21.93	3742
VsQSPSKDSEENPATEERPEK	STX18	53407	syntaxin-18	S2(Phospho)	S(2): 99.9; S(4): 0.1; S(6): 0.0; S(9): 0.0; T(15): 0.0	S2;	S187		6.14	0	1	3	808.7	2424	21.93	3742

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#
SSSVtsIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	T5(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 1.4; T(5): 98.6; S(6): 100.0; S(11): 0.0	T5; S6;	T748; S749	51		0	1	2	728.3	1456	28	5044
SSSVtsIDKESR	STXBP5	134957	syntaxin-binding protein 5 isoform a	T5(Phospho) S6(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 1.4; T(5): 98.6; S(6): 100.0; S(11): 0.0	T5; S6;	T748; S749		3.09	0	1	2	728.3	1456	28	5044
GTGGsESSRAsGLVGR	SUN2	25777	SUN domain-containing protein 2 isoform b	S5(Phospho) S11(Phospho)	T(2): 0.0; S(5): 99.9; S(7): 0.2; S(8): 3.1; S(11): 96.8	S5; S11;	S110; S116	23		0	1	2	819.3	1638	33.32	6152
YSQGGDDGSSSSGGSSVAGSQSTLFKDs PLR	SUN2	25777	SUN domain-containing protein 2 isoform b	S28(Phospho)	Y(1): 0.0; S(2): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(15): 0.0; S(16): 0.0; S(20): 0.0; S(22): 0.0; T(23): 0.0; S(28): 100.0	S28;	S38	14		0	1	3	1054	3159	57.48	11343
YSQGGDDGSSSSGGSSVAGSQSTLFKDs PLR	SUN2	25777	SUN domain-containing protein 2 isoform b	S28(Phospho)	Y(1): 0.0; S(2): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; S(12): 0.0; S(15): 0.0; S(16): 0.0; S(20): 0.0; S(22): 0.0; T(23): 0.0; S(28): 100.0	S28;	S38		3.58	0	1	3	1054	3159	57.48	11343
GTGGsESSRAsGLVGR	SUN2	25777	SUN domain-containing protein 2 isoform b	S5(Phospho) S11(Phospho)	T(2): 0.0; S(5): 99.9; S(7): 0.2; S(8): 3.1; S(11): 96.8	S5; S11;	S110; S116		1.82	0.008	1	2	819.3	1638	33.32	6152
KDLGSTEDGDGtDDFLtDKEDK	SURF2	6835	surfeit locus protein 2 isoform 2	T12(Phospho) T17(Phospho)	S(5): 0.0; T(6): 0.0; T(12): 100.0; T(17): 100.0	T12; T17;	T190; T195	55		0	2	3	897.3	2690	48.11	9309
DLGSTEDGDGtDDFLtDKEDK	SURF2	6835	surfeit locus protein 2 isoform 2	T11(Phospho) T16(Phospho)	S(4): 0.0; T(5): 0.0; T(11): 100.0; T(16): 100.0	T11; T16;	T190; T195	22		0	1	3	854.7	2562	63.26	12626
KDLGSTEDGDGtDDFLtDKEDK	SURF2	6835	surfeit locus protein 2 isoform 2	T12(Phospho) T17(Phospho)	S(5): 0.0; T(6): 0.0; T(12): 100.0; T(17): 100.0	T12; T17;	T190; T195		5.94	0	2	3	897.3	2690	48.11	9309
DLGSTEDGDGtDDFLtDKEDK	SURF2	6835	surfeit locus protein 2 isoform 2	T11(Phospho) T16(Phospho)	S(4): 0.0; T(5): 0.0; T(11): 100.0; T(16): 100.0	T11; T16;	T190; T195		3.65	0	1	3	854.7	2562	63.26	12626
GSGDIsSDsIDHSPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho) S9(Phospho)	S(2): 0.1; S(6): 99.9; S(7): 2.9; S(9): 97.1; S(13): 0.0	S6; S9;	S141; S144	50		0	0	2	866.8	1733	32.36	5951
GSGDIsSDsIDHsPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho) S9(Phospho) S13(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 0.2; S(9): 99.8; S(13): 100.0	S6; S9; S13;	S141; S144; S148	12		0	0	2	906.8	1813	37.62	7069
GSGDIsSDsIDHSPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho) S9(Phospho)	S(2): 0.1; S(6): 99.9; S(7): 2.9; S(9): 97.1; S(13): 0.0	S6; S9;	S141; S144		3.59	0	0	2	866.8	1733	32.36	5951
GSGDIsSDsIDHsPAK	SUV39H2	79723	histone-lysine N-methyltransferase SUV39H2 isoform 4	S6(Phospho) S9(Phospho) S13(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 0.2; S(9): 99.8; S(13): 100.0	S6; S9; S13;	S141; S144; S148		2.87	0	0	2	906.8	1813	37.62	7069
DSsFTEVPRsPK	SVIL	6840	supervillin isoform 1	S3(Phospho) S10(Phospho)	S(2): 0.0; S(3): 100.0; T(5): 0.0; S(10): 100.0	S3; S10;	S238; S245	20		0	1	2	755.3	1510	43.45	8295
DSsFTEVPRsPK	SVIL	6840	supervillin isoform 1	S3(Phospho) S10(Phospho)	S(2): 0.0; S(3): 100.0; T(5): 0.0; S(10): 100.0	S3; S10;	S238; S245		3.37	0	1	2	755.3	1510	43.45	8295
QRsPAPGsPDEEGGAEPAAAGIR	SYNM	23336	synemin isoform B	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S1044; S1049	46		0	1	3	794	2380	43.67	8343
QRsPAPGsPDEEGGAEPAAAGIR	SYNM	23336	synemin isoform B	S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S1044; S1049		5.25	0	1	3	794	2380	43.67	8343
SPsPISNQPSPR	TAB3	257397	TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(6): 0.0; S(10): 0.0	S3;	S385	53		0	0	2	673.8	1347	29.69	5399
SPsPISNQPSPR	TAB3	257397	TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	S3(Phospho)	S(1): 1.7; S(3): 98.3; S(6): 0.0; S(10): 0.0	S3;	S385		2.85	0	0	2	673.8	1347	29.69	5399
TPEKLDNTPasPPRsPAEPNDIPIAK	TACC2	10579	transforming acidic coiled-coil-containing protein 2 isoform b	S11(Phospho) S15(Phospho)	T(1): 0.0; T(8): 4.3; S(11): 95.7; S(15): 100.0	S11; S15;	S463; S467	12		0	2	3	972.5	2915	54.64	10727
TPEKLDNTPasPPRsPAEPNDIPIAK	TACC2	10579	transforming acidic coiled-coil-containing protein 2 isoform b	S11(Phospho) S15(Phospho)	T(1): 0.0; T(8): 4.3; S(11): 95.7; S(15): 100.0	S11; S15;	S463; S467		4.42	0	2	3	972.5	2915	54.64	10727

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#
LDNTPAsPPRsPAEPNDIPIAK	TACC2	10579	transforming acidic coiled-coil-containing protein 2 isoform b	S7(Phospho) S11(Phospho)	T(4): 0.0; S(7): 100.0; S(11): 100.0	S7; S11;	S463; S467	11		0.002	1	3	820.7	2460	60.82	12051
LDNTPAsPPRsPAEPNDIPIAK	TACC2	10579	transforming acidic coiled-coil-containing protein 2 isoform b	S7(Phospho) S11(Phospho)	T(4): 0.0; S(7): 100.0; S(11): 100.0	S7; S11;	S463; S467		3.07	0.002	1	3	820.7	2460	60.82	12051
LsPENNQVLTK	TAF12	6883	transcription initiation factor TFIID subunit 12	S2(Phospho)	S(2): 100.0; T(10): 0.0	S2;	S51	37		0	0	2	661.8	1323	41.28	7841
LsPENNQVLTK	TAF12	6883	transcription initiation factor TFIID subunit 12	S2(Phospho)	S(2): 100.0; T(10): 0.0	S2;	S51		2.27	0	0	2	661.8	1323	41.28	7841
NFsDNQLQEGK	TAGLN2	8407	transgelin-2 isoform b	S3(Phospho)	S(3): 100.0	S3;	S163	27		0	0	2	680.3	1360	38.45	7241
NFsDNQLQEGK	TAGLN2	8407	transgelin-2 isoform b	S3(Phospho)	S(3): 100.0	S3;	S163		2.8	0	0	2	680.3	1360	38.45	7241
EYPsPPPsPLR	TANC2	26115	protein TANC2	S4(Phospho) S8(Phospho)	Y(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S1530; S1534	22		0.002	0	2	700.3	1400	62.12	12327
EYPsPPPsPLR	TANC2	26115	protein TANC2	S4(Phospho) S8(Phospho)	Y(2): 0.0; S(4): 100.0; S(8): 100.0	S4; S8;	S1530; S1534		2.03	0.005	0	2	700.3	1400	62.12	12327
TEEARSPAPGPGTPTGTPTTR	TBC1D10B	26000	TBC1 domain family member 10B	T14(Phospho)	T(1): 0.0; S(7): 0.0; T(14): 100.0; T(16): 0.0; T(18): 50.0; T(20): 50.0	T14;	T148	20		0	0	3	746.3	2237	33.54	6197
TEEARSPAPGPGTPTGTPTTR	TBC1D10B	26000	TBC1 domain family member 10B	T14(Phospho)	T(1): 0.0; S(7): 0.0; T(14): 100.0; T(16): 0.0; T(18): 50.0; T(20): 50.0	T14;	T148		5.29	0	0	3	746.3	2237	33.54	6197
ALAAGADsPKTEEARSPAPGPGTPTGTPTTR	TBC1D10B	26000	TBC1 domain family member 10B	S8(Phospho)	S(8): 93.3; T(11): 6.7; S(17): 0.0; T(24): 49.8; T(26): 49.8; T(28): 0.3; T(30): 0.0	S8;	S132		2.98	0.003	1	3	1040	3118	41.23	7831
NDsPTQIPVSSDVCR	TBC1D15	64786	TBC1 domain family member 15 isoform 3	C14(Carbamido methyl) S3(Phospho)	S(3): 100.0; T(5): 0.0; S(10): 0.0; S(11): 0.0	S3;	S658	27		0	0	2	877.9	1755	52.43	10230
NDsPTQIPVSSDVCR	TBC1D15	64786	TBC1 domain family member 15 isoform 3	C14(Carbamido methyl) S3(Phospho)	S(3): 100.0; T(5): 0.0; S(10): 0.0; S(11): 0.0	S3;	S658		2.98	0	0	2	877.9	1755	52.43	10230
YItPESSPVR	TBC1D16	125058	TBC1 domain family member 16 isoform a	T3(Phospho)	Y(1): 0.0; T(3): 100.0; S(6): 50.0; S(7): 50.0	T3;	T99		2.76	0.001	0	2	654.8	1309	48.64	9419
YItPESSPVR	TBC1D16	125058	TBC1 domain family member 16 isoform a	T3(Phospho)	Y(1): 0.0; T(3): 100.0; S(6): 50.0; S(7): 50.0	T3;	T99	26		0.009	0	2	654.8	1309	48.64	9419
RAVsEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C7(Carbamidomethyl) S4(Phospho) S9(Phospho)	S(4): 100.0; S(9): 100.0	S4; S9;	S455; S460	56		0	1	2	977.8	1955	44.09	8433
RAVsEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C7(Carbamidomethyl) S9(Phospho)	S(4): 0.0; S(9): 100.0	S9;	S460	41		0.001	1	2	937.9	1875	34.79	6472
AVsEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C6(Carbamidomethyl) S3(Phospho) S8(Phospho)	S(3): 100.0; S(8): 100.0	S3; S8;	S455; S460	33		0.002	0	2	899.8	1799	62.33	12382
RAVsEGCAsEDEVEGEA	TBC1D2	55357	TBC1 domain family member 2A isoform 3	C7(Carbamidomethyl) S4(Phospho) S9(Phospho)	S(4): 100.0; S(9): 100.0	S4; S9;	S455; S460		3.97	0.007	1	2	977.8	1955	44.09	8433
TSSTCSNeLSVGGTSTVTPR	TBC1D4	9882	TBC1 domain family member 4 isoform 3	C5(Carbamidomethyl) S9(Phospho)	T(1): 18.7; S(2): 18.7; S(3): 18.7; T(4): 73.1; S(6): 73.1; S(9): 90.2; S(11): 7.4; T(15): 0.0; S(16): 0.0; T(18): 0.0	S9;	S694	16		0	0	2	1134	2267	77.06	15555
TSSTCSNeLSVGGTSTVTPR	TBC1D4	9882	TBC1 domain family member 4 isoform 3	C5(Carbamidomethyl) S9(Phospho)	T(1): 18.7; S(2): 18.7; S(3): 18.7; T(4): 73.1; S(6): 73.1; S(9): 90.2; S(11): 7.4; T(15): 0.0; S(16): 0.0; T(18): 0.0	S9;	S694		2.32	0	0	2	1134	2267	77.06	15555

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#
NISSSPsVEsLPGGR	TBC1D5	9779	TBC1 domain family member 5 isoform b	S7(Phospho) S10(Phospho)	S(3): 0.0; S(4): 0.0; S(5): 0.0; S(7): 100.0; S(10): 100.0	S7; S10;	S541; S544	30		0	0	2	823.8	1647	59.05	11696
NISSSPsVEsLPGGR	TBC1D5	9779	TBC1 domain family member 5 isoform b	S7(Phospho) S10(Phospho)	S(3): 0.0; S(4): 0.0; S(5): 0.0; S(7): 100.0; S(10): 100.0	S7; S10;	S541; S544		2.48	0.003	0	2	823.8	1647	59.05	11696
KASVDPSTESSAPQEGSEQPASPAsPL SSR	TBC1D9B	23061	TBC1 domain family member 9B isoform b	S27(Phospho)	S(3): 0.0; S(8): 0.0; T(9): 0.0; S(11): 0.0; S(12): 0.0; S(19): 0.0; S(24): 0.0; S(27): 100.0; S(30): 0.0; S(31): 0.0	S27;	S435	50		0	1	3	1088	3261	48.72	9436
ASVVDPSSTESSAPQEGSEQPASPAsPLS SR	TBC1D9B	23061	TBC1 domain family member 9B isoform b	S26(Phospho)	S(2): 0.0; S(7): 0.0; T(8): 0.0; S(10): 0.0; S(11): 0.0; S(18): 0.0; S(23): 0.0; S(26): 100.0; S(29): 0.0; S(30): 0.0	S26;	S435	22		0	0	3	1045	3132	57.84	11414
KASVDPSTESSAPQEGSEQPASPAsPL SSR	TBC1D9B	23061	TBC1 domain family member 9B isoform b	S27(Phospho)	S(3): 0.0; S(8): 0.0; T(9): 0.0; S(11): 0.0; S(12): 0.0; S(19): 0.0; S(24): 0.0; S(27): 100.0; S(30): 0.0; S(31): 0.0	S27;	S435		5.16	0	1	3	1088	3261	48.72	9436
ASVVDPSSTESSAPQEGSEQPASPAsPLS SR	TBC1D9B	23061	TBC1 domain family member 9B isoform b	S26(Phospho)	S(2): 0.0; S(7): 0.0; T(8): 0.0; S(10): 0.0; S(11): 0.0; S(18): 0.0; S(23): 0.0; S(26): 100.0; S(29): 0.0; S(30): 0.0	S26;	S435		4.1	0	0	3	1045	3132	57.84	11414
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79	64		0	2	2	868.4	1736	17.62	2840
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79	61		0	2	3	579.3	1736	17.54	2821
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79	46		0	2	3	579.3	1736	17	2705
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79	32		0	2	2	868.4	1736	17.08	2724
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79		5.34	0	2	3	579.3	1736	17.54	2821
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79		4.76	0	2	3	579.3	1736	17	2705
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79		4.55	0	2	2	868.4	1736	17.62	2840
KKEPAITSQN\$PEAR	TCEA1	6917	transcription elongation factor A protein 1 isoform 2	S11(Phospho)	T(7): 0.0; S(8): 0.0; S(11): 100.0	S11;	S79		3.67	0	2	2	868.4	1736	17.08	2724
NEGNLENEGKPEDEVEPDDEGKsDEEEK PDVEGK	TCEAL3	85012	transcription elongation factor A protein-like 3	S23(Phospho)	S(23): 100.0	S23;	S30	22		0	1	4	967.2	3866	38.57	7265
NEGNLENEGKPEDEVEPDDEGKsDEEEK PDVEGK	TCEAL3	85012	transcription elongation factor A protein-like 3	S23(Phospho)	S(23): 100.0	S23;	S30		7.09	0	1	4	967.2	3866	38.57	7265
NEGNLENEGKPEDEVEPDDEGKsDEEEK PDVEGK	TCEAL3	85012	transcription elongation factor A protein-like 3	S23(Phospho)	S(23): 100.0	S23;	S30		5.77	0	1	4	967.2	3866	37.65	7075
TECEGKREDEGEPEGDEGQLEDEG\$QEK	TCEAL3	85012	transcription elongation factor A protein-like 3	C3(Carbamidomethyl) S24(Phospho)	T(1): 0.0; S(24): 100.0	S24;	S65		4.17	0.001	2	3	1040	3117	27.79	4999
LNAsPAAREEAT\$PGAK	TCF20	6942	transcription factor 20 isoform 2	S4(Phospho)	S(4): 99.9; T(12): 50.1; S(13): 50.1	S4;	S574		3.4	0.003	1	2	915.4	1830	28.89	5231
LNASPAAREEAT\$PGAK	TCF20	6942	transcription factor 20 isoform 2	S13(Phospho)	S(4): 51.3; T(12): 51.3; S(13): 97.3	S13;	S583		3.94	0.005	1	3	610.6	1830	28.83	5218
GNT\$KTDGDDTETVPSEQ\$HASGK	TCF25	22980	transcription factor 25	T3(Phospho)	T(3): 99.7; S(5): 0.3; T(7): 0.0; T(12): 0.0; T(14): 0.0; S(17): 0.0; S(20): 0.0; S(23): 0.0	T3;	T102	15		0	1	3	886.4	2657	18.11	2941

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#
GNIESKTDGDDTETVPSEQSHASGK	TCF25	22980	transcription factor 25	T3(Phospho)	T(3): 99.7; S(5): 0.3; T(7): 0.0; T(12): 0.0; T(14): 0.0; S(17): 0.0; S(20): 0.0; S(23): 0.0	T3;	T102		3.62	0	1	3	886.4	2657	18.11	2941
KQEGPATQVDSAVGTLPATsPQSTSVQAK	TCOF1	6949	treacle protein isoform g	S20(Phospho)	T(7): 0.0; S(11): 0.0; T(15): 0.0; T(19): 3.6; S(20): 96.4; S(23): 0.0; T(24): 0.0; S(25): 0.0	S20;	S1073	29		0	1	3	988.5	2963	54.06	10599
TQPSSGVDSAVGTLPATsPQSTSVQAK	TCOF1	6949	treacle protein isoform d	S18(Phospho)	T(1): 0.0; S(4): 0.0; S(5): 0.0; S(9): 0.0; T(13): 0.0; T(17): 0.3; S(18): 99.5; S(21): 0.3; T(22): 0.0; S(23): 0.0	S18;	S1111	11		0	0	3	894.4	2681	57.75	11396
KQEGPATQVDSAVGTLPATsPQSTSVQAK	TCOF1	6949	treacle protein isoform g	S20(Phospho)	T(7): 0.0; S(11): 0.0; T(15): 0.0; T(19): 3.6; S(20): 96.4; S(23): 0.0; T(24): 0.0; S(25): 0.0	S20;	S1073		6.17	0	1	3	988.5	2963	54.06	10599
TQPSSGVDSAVGTLPATsPQSTSVQAK	TCOF1	6949	treacle protein isoform d	S18(Phospho)	T(1): 0.0; S(4): 0.0; S(5): 0.0; S(9): 0.0; T(13): 0.0; T(17): 0.3; S(18): 99.5; S(21): 0.3; T(22): 0.0; S(23): 0.0	S18;	S1111		4.47	0	0	3	894.4	2681	57.75	11396
TSQVGAASAPAKesPR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S381 S381	76		0	1	2	818.9	1637	19.13	3153
TSQVGAASAPAKesPR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S381 S381	63		0	1	3	546.3	1637	19.18	3164
KLsGDQPAAR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S3(Phospho)	S(3): 100.0	S3;	S1350 S1312	55		0	1	2	561.8	1123	14.11	2083
KLGAGEGGEASVsPEKTSTTSK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S13(Phospho)	S(11): 0.0; S(13): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0; T(20): 0.0; S(21): 0.0	S13;	S1378 S1340	45		0	2	3	734.4	2201	24.3	4244
LGAGEGGEASVsPEKTSTTSK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S12(Phospho)	S(10): 4.2; S(12): 95.6; T(16): 0.2; S(17): 0.0; T(18): 0.0; T(19): 0.0; S(20): 0.0	S12;	S1378 S1340	44		0	1	2	1037	2073	27.85	5012
ASSVSTKESPAR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; T(6): 0.0; S(9): 100.0	S9;	S233 S233	37		0	1	2	650.3	1300	12.6	1758
GSLGsQGAKDEPEEELQK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S5(Phospho)	S(2): 0.1; S(5): 99.9	S5;	S1410 S1372	27		0	1	3	661.3	1982	37.2	6982
DDPDGKQEAQPQAAGMLsPK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S19(Phospho)	S(19): 100.0	S19;	S1257 S1219	17		0	1	3	764.4	2291	35.99	6726
KLGAGEGGEASVsPEKTSTTSK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S13(Phospho)	S(11): 0.0; S(13): 100.0; T(17): 0.0; S(18): 0.0; T(19): 0.0; T(20): 0.0; S(21): 0.0	S13;	S1378 S1340		7.48	0	2	3	734.4	2201	24.3	4244
TSQVGAASAPAKesPR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S381 S381		6.94	0	1	3	546.3	1637	19.18	3164
DDPDGKQEAQPQAAGMLsPK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	M17(Oxidation) S19(Phospho)	S(19): 100.0	S19;	S1257 S1219		5.79	0	1	3	769.7	2307	26.29	4669
TSQVGAASAPAKesPR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S14(Phospho)	T(1): 0.0; S(2): 0.0; S(8): 0.0; S(14): 100.0	S14;	S381 S381		4.74	0	1	2	818.9	1637	19.13	3153
GSLGsQGAKDEPEEELQK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S5(Phospho)	S(2): 0.1; S(5): 99.9	S5;	S1410 S1372		4.3	0	1	3	661.3	1982	37.2	6982
KLsGDQPAAR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S3(Phospho)	S(3): 100.0	S3;	S1350 S1312		3.17	0	1	2	561.8	1123	14.11	2083

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#
LGAGEGGEASVsPEKSTTSK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S12(Phospho)	S(10): 4.2; S(12): 95.6; T(16): 0.2; S(17): 0.0; T(18): 0.0; T(19): 0.0; S(20): 0.0	S12;	S1378 S1340		3.08	0	1	2	1037	2073	27.85	5012
DDPDGKQEAQPQAAGMLSPK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S19(Phospho)	S(19): 100.0	S19;	S1257 S1219		4.25	0.001	1	3	764.4	2291	35.99	6726
DDPDGKQEAQPQAAGMLSPK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S19(Phospho)	S(19): 100.0	S19;	S1257 S1219	19		0.002	1	3	764.4	2291	36.55	6846
DDPDGKQEAQPQAAGMLSPK	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S19(Phospho)	S(19): 100.0	S19;	S1257 S1219		3.86	0.005	1	3	764.4	2291	36.55	6846
ASSVSTKESPAR	TCOF1 TCOF1	6949 6949	treacle protein isoform d treacle protein isoform g	S9(Phospho)	S(2): 0.0; S(3): 0.0; S(5): 0.0; T(6): 0.0; S(9): 100.0	S9;	S233 S233		3.56	0.005	1	2	650.3	1300	12.6	1758
TAPSSPLTsPSDTR	TEX2	55852	testis-expressed sequence 2 protein isoform 2	S9(Phospho)	T(1): 49.1; S(4): 1.8; S(5): 49.1; T(8): 3.5; S(9): 93.0; S(11): 3.5; T(13): 0.1	S9;	S270		2.48	0.001	0	2	788.8	1577	44.55	8542
SYMNPGDQsPADSNK	TFAP2C	7022	transcription factor AP-2 gamma	S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(9): 99.9; S(13): 0.1	S9;	S434	38		0	0	2	845.8	1691	33.35	6159
SYMNPGDQsPADSNK	TFAP2C	7022	transcription factor AP-2 gamma	S9(Phospho)	S(1): 0.0; Y(2): 0.0; S(9): 99.9; S(13): 0.1	S9;	S434		2.74	0	0	2	845.8	1691	33.35	6159
RTPAPPEPGsPAPGEGPSGR	TFPT	29844	TCF3 fusion partner	S10(Phospho)	T(2): 0.0; S(10): 100.0; S(18): 0.0	S10;	S180	39		0	1	3	665.3	1994	32.85	6055
RTPAPPEPGsPAPGEGPSGR	TFPT	29844	TCF3 fusion partner	S10(Phospho)	T(2): 0.0; S(10): 100.0; S(18): 0.0	S10;	S180		4.37	0	1	3	665.3	1994	32.85	6055
DsPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	S2(Phospho)	S(2): 96.7; S(4): 3.2; S(6): 0.0; S(7): 0.1; T(12): 0.0; T(16): 0.0	S2;	S66	32		0	1	3	690.3	2069	19.95	3325
tESGEETDLISPPQEEVK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	T1(Phospho)	T(1): 99.9; S(3): 0.1; T(7): 0.0; S(11): 0.0	T1;	T296	16		0	0	2	1034	2068	62.35	12388
DsPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	S2(Phospho)	S(2): 96.7; S(4): 3.2; S(6): 0.0; S(7): 0.1; T(12): 0.0; T(16): 0.0	S2;	S66		5.18	0	1	3	690.3	2069	19.95	3325
DSPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	T16(Phospho)	S(2): 0.2; S(4): 0.2; S(6): 0.0; S(7): 0.0; T(12): 4.0; T(16): 95.7	T16;	T80		3.13	0	1	2	1035	2069	19.99	3335
tESGEETDLISPPQEEVK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	T1(Phospho)	T(1): 99.9; S(3): 0.1; T(7): 0.0; S(11): 0.0	T1;	T296		2.98	0	0	2	1034	2068	62.35	12388
DSPSKSSAEAQTPEDTPNK	TGOLN2	10618	trans-Golgi network integral membrane protein 2 isoform 1 precursor	T16(Phospho)	S(2): 0.2; S(4): 0.2; S(6): 0.0; S(7): 0.0; T(12): 4.0; T(16): 95.7	T16;	T80	12		0.002	1	2	1035	2069	19.99	3335
DsGNNSGDQATEEEEGGYSCGTAESHDSK	TGS1	96764	trimethylguanosine synthase	C20(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(6): 0.0; T(11): 0.0; Y(18): 0.0; S(19): 0.0; T(22): 0.0; S(25): 0.0; S(28): 0.0	S2;	S51	40		0	0	3	1033	3098	29.39	5336
DsGNNSGDQATEEEEGGYSCGTAESHDSK	TGS1	96764	trimethylguanosine synthase	C20(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(6): 0.0; T(11): 0.0; Y(18): 0.0; S(19): 0.0; T(22): 0.0; S(25): 0.0; S(28): 0.0	S2;	S51		4.23	0	0	3	1033	3098	29.39	5336
DHsNNDREVPPDLTK	THOC2	57187	THO complex subunit 2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S1486		4.43	0	1	3	606.3	1817	30.9	5651
DHsNNDREVPPDLTK	THOC2	57187	THO complex subunit 2	S3(Phospho)	S(3): 100.0; T(14): 0.0	S3;	S1486		3.82	0	1	3	606.3	1817	31.47	5768
ALFKPPEDSQDDEsDsDAEEEQTTK	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 5.9; S(14): 94.4; S(16): 99.6; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314	29		0	0	3	991	2971	57.09	11258
ALFKPPEDSQDDEsDsDAEEEQTTKR	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 0.0; S(14): 100.0; S(16): 100.0; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314	17		0	1	3	1043	3127	48.21	9329

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#
ALFKPPEDSQDDEsDsDAEEEQTTK	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 0.6; S(14): 99.7; S(16): 99.7; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314	12		0	0	3	991	2971	56.83	11194
ALFKPPEDSQDDEsDsDAEEEQTTKR	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 0.0; S(14): 100.0; S(16): 100.0; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314		3.38	0	1	3	1043	3127	48.21	9329
ALFKPPEDSQDDEsDsDAEEEQTTK	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 5.9; S(14): 94.4; S(16): 99.6; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314		3.15	0	0	3	991	2971	57.09	11258
ALFKPPEDSQDDEsDsDAEEEQTTK	THOC5	8563	THO complex subunit 5 homolog	S14(Phospho) S16(Phospho)	S(9): 0.6; S(14): 99.7; S(16): 99.7; T(23): 0.0; T(24): 0.0	S14; S16;	S312; S314		2.42	0	0	3	991	2971	56.83	11194
ALFKPPEDSQDDESDsDAEEEQTTK	THOC5	8563	THO complex subunit 5 homolog	S9(Phospho)	S(9): 96.0; S(14): 52.0; S(16): 52.0; T(23): 0.0; T(24): 0.0	S9;	S307		2.53	0.004	0	3	991.1	2971	57.63	11371
TDSEKPFrgsQsPKR	THRAP3	9967	thyroid hormone receptor-associated protein 3	S10(Phospho) S12(Phospho)	T(1): 0.0; S(3): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S406; S408		4.71	0	2	3	627.3	1880	16.07	2497
FsGEEGIEDDESgTENREEKNiQPTTE	THRAP3	9967	thyroid hormone receptor-associated protein 3	S2(Phospho)	S(2): 100.0; S(13): 0.0; T(15): 0.0; T(27): 0.0; T(28): 0.0	S2;	S928		3.53	0	2	3	1122	3364	48.3	9348
ASAVSELsPRERSPALK	THRAP3	9967	thyroid hormone receptor-associated protein 3	S8(Phospho) S13(Phospho)	S(2): 0.0; S(5): 0.0; S(8): 100.0; S(13): 100.0	S8; S13;	S243; S248		4	0.003	2	3	653.3	1958	40.84	7749
TDSEKPFrgsQsPKR	THRAP3	9967	thyroid hormone receptor-associated protein 3	S10(Phospho) S12(Phospho)	T(1): 0.0; S(3): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S406; S408		3.97	0.003	2	3	627.3	1880	15.57	2390
TDSEKPFrgsQsPKR	THRAP3	9967	thyroid hormone receptor-associated protein 3	S10(Phospho) S12(Phospho)	T(1): 0.0; S(3): 0.0; S(10): 100.0; S(12): 100.0	S10; S12;	S406; S408		3.75	0.005	2	3	627.3	1880	16.59	2611
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	44		0	2	4	686	2741	38.53	7258
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	40		0	2	3	914.4	2741	38.48	7246
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	19		0	2	3	914.4	2741	40.14	7604
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	18		0	2	3	914.4	2741	39.51	7465
FtDKDQQPSGSEGEDDDAEaALK	THUMPd1	55623	THUMP domain-containing protein 1	T2(Phospho)	T(2): 100.0; S(9): 50.0; S(11): 50.0	T2;	T79	18		0	1	2	1307	2613	47.74	9230
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	16		0	2	3	914.4	2741	38.99	7354
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.1; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88	13		0	2	2	1371	2741	38.62	7278
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		6.43	0	2	4	686	2741	38.53	7258
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		5.74	0	2	3	914.4	2741	38.48	7246
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		4.83	0	2	3	914.4	2741	38.99	7354
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		4.01	0	2	3	914.4	2741	39.51	7465
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.0; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		3.96	0	2	3	914.4	2741	40.14	7604
FTDKDQQPsGsEGEDDDAEaALKK	THUMPd1	55623	THUMP domain-containing protein 1	S9(Phospho) S11(Phospho)	T(2): 0.1; S(9): 100.0; S(11): 100.0	S9; S11;	S86; S88		2.41	0	2	2	1371	2741	38.62	7278
FtDKDQQPSGSEGEDDDAEaALK	THUMPd1	55623	THUMP domain-containing protein 1	T2(Phospho)	T(2): 100.0; S(9): 50.0; S(11): 50.0	T2;	T79		2.38	0	1	2	1307	2613	47.74	9230
RtLsLTQR	TIAM2	26230	T-lymphoma invasion and metastasis-inducing protein 2 isoform a	T2(Phospho) S4(Phospho)	T(2): 100.0; S(4): 100.0; T(6): 0.0	T2; S4;	T751; S753		1.49	0.007	1	2	567.8	1135	35.61	6647
GLSLSPQsPPER	TICRR	90381	treslin isoform 1	S5(Phospho) S8(Phospho)	S(3): 0.0; S(5): 100.0; S(8): 100.0	S5; S8;	S1429; S1432	30		0	0	2	714.3	1428	61.55	12206

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#
LQKsPAKMTPTK	TICRR	90381	treslin isoform 1	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; T(11): 0.0	S4; T9;	S1140; T1145	28		0	2	2	745.3	1490	18.23	2966
GLSsPQsPPER	TICRR	90381	treslin isoform 1	S5(Phospho) S8(Phospho)	S(3): 0.0; S(5): 100.0; S(8): 100.0	S5; S8;	S1429; S1432		2.44	0	0	2	714.3	1428	61.55	12206
LQKsPAKMTPTK	TICRR	90381	treslin isoform 1	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; T(11): 0.0	S4; T9;	S1140; T1145		3.67	0.001	2	2	745.3	1490	18.23	2966
QLLDsDEEQEEDEGR	TIMELESS	8914	protein timeless homolog	S5(Phospho)	S(5): 100.0	S5;	S1173	67		0	0	2	936.4	1872	45.24	8705
QLLDsDEEQEEDEGR	TIMELESS	8914	protein timeless homolog	S5(Phospho)	S(5): 100.0	S5;	S1173		3.4	0	0	2	936.4	1872	45.24	8705
KDsLTQAQEQGNLLN	TJAP1	93643	tight junction-associated protein 1 isoform b	S3(Phospho)	S(3): 100.0; T(5): 0.0	S3;	S535		3.58	0.005	1	2	869.9	1739	53.36	10441
sREDLSAQPVQTK	TJP1	7082	tight junction protein ZO-1 isoform a	S1(Phospho)	S(1): 100.0; S(6): 0.0; T(12): 0.0	S1;	S617	54		0	1	2	769.9	1539	26.49	4712
sVASSQPAKPTK	TJP1	7082	tight junction protein ZO-1 isoform a	S1(Phospho)	S(1): 100.0; S(4): 50.0; S(5): 50.0; T(11): 0.0	S1;	S175	51		0	0	2	680.8	1361	17.46	2805
IDsPGFKPASQKQ	TJP1	7082	tight junction protein ZO-1 isoform a	S3(Phospho)	S(3): 100.0; S(10): 0.0	S3;	S912	14		0	0	2	741.9	1483	28.47	5144
sVASSQPAKPTK	TJP1	7082	tight junction protein ZO-1 isoform a	S1(Phospho)	S(1): 100.0; S(4): 50.0; S(5): 50.0; T(11): 0.0	S1;	S175		4.04	0	0	2	680.8	1361	17.46	2805
sREDLSAQPVQTK	TJP1	7082	tight junction protein ZO-1 isoform a	S1(Phospho)	S(1): 100.0; S(6): 0.0; T(12): 0.0	S1;	S617		3.75	0	1	2	769.9	1539	26.49	4712
IDsPGFKPASQKQ	TJP1	7082	tight junction protein ZO-1 isoform a	S3(Phospho)	S(3): 100.0; S(10): 0.0	S3;	S912		2.04	0	0	2	741.9	1483	28.47	5144
KsREDLSAQPVQTK	TJP1	7082	tight junction protein ZO-1 isoform a	S2(Phospho)	S(2): 100.0; S(7): 0.0; T(13): 0.0	S2;	S617	15		0.003	2	2	833.9	1667	20.68	3480
GSYGsDAEEEEYR	TJP2	9414	tight junction protein ZO-2 isoform 1	S5(Phospho)	S(2): 0.0; Y(3): 0.1; S(5): 99.9; Y(12): 0.0	S5;	S1159	52		0	0	2	786.3	1572	37.44	7032
AASSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S11(Phospho)	S(3): 51.3; S(4): 51.3; S(11): 97.4	S11;	S986	38		0	1	3	837	2509	49.31	9558
SRsWEDsPER	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho) S7(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 100.0	S3; S7;	S170; S174	34		0	1	2	704.8	1408	27.03	4828
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 96.7; S(5): 3.3; S(12): 100.0	S4; S12;	S978; S986	32		0	2	4	667.1	2665	43.49	8304
GsYGSDAEEEEYRQQLSEHSK	TJP2	9414	tight junction protein ZO-2 isoform 1	S2(Phospho)	S(2): 94.8; Y(3): 2.6; S(5): 2.6; Y(12): 0.0; S(17): 0.0; S(20): 0.0	S2;	S1156	30		0	1	3	837	2509	43.75	8359
GRsIDQDYER	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho)	S(3): 100.0; Y(8): 0.0	S3;	S244	28		0	1	2	659.8	1319	22.45	3856
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 96.0; S(5): 4.0; S(12): 100.0	S4; S12;	S978; S986	27		0	2	4	667.1	2665	42.99	8198
DNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho)	S(3): 100.0	S3;	S986	25		0	0	2	800.9	1601	43.25	8254
AASsDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S11(Phospho)	S(3): 4.1; S(4): 96.1; S(11): 99.8	S4; S11;	S979; S986	24		0	1	3	837	2509	49.82	9666
SILKPSTPIPPQEGEEVGESSEEQDNAPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S20(Phospho)	S(1): 0.0; S(6): 0.0; T(7): 0.3; S(20): 99.4; S(21): 0.3	S20;	S1067	16		0	0	3	1058	3172	57.42	11330
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 99.8; S(5): 0.2; S(12): 100.0	S4; S12;	S978; S986	15		0	2	3	889.1	2665	43.28	8259
AASSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S11(Phospho)	S(3): 51.3; S(4): 51.3; S(11): 97.4	S11;	S986		6.05	0	1	3	837	2509	49.31	9558
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 96.7; S(5): 3.3; S(12): 100.0	S4; S12;	S978; S986		5.84	0	2	4	667.1	2665	43.49	8304
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 96.0; S(5): 4.0; S(12): 100.0	S4; S12;	S978; S986		5.34	0	2	4	667.1	2665	42.99	8198
AASsDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S11(Phospho)	S(3): 4.1; S(4): 96.1; S(11): 99.8	S4; S11;	S979; S986		5.1	0	1	3	837	2509	49.82	9666
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 99.8; S(5): 0.2; S(12): 100.0	S4; S12;	S978; S986		4.92	0	2	3	889.1	2665	43.28	8259

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#
GsYSGDAEEEEYRQLSEHSK	TJP2	9414	tight junction protein ZO-2 isoform 1	S2(Phospho)	S(2): 94.8; Y(3): 2.6; S(5): 2.6; Y(12): 0.0; S(17): 0.0; S(20): 0.0	S2;	S1156		4.49	0	1	3	837	2509	43.75	8359
SRsWEDsPER	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho) S7(Phospho)	S(1): 0.0; S(3): 100.0; S(7): 100.0	S3; S7;	S170; S174		4.3	0	1	2	704.8	1408	27.03	4828
RAAsSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S4(Phospho) S12(Phospho)	S(4): 95.5; S(5): 4.5; S(12): 100.0	S4; S12;	S978; S986		3.47	0	2	3	889.1	2665	43.8	8371
SILKPSTPIPPQEGEEVGESSEEQDNAPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S20(Phospho)	S(1): 0.0; S(6): 0.0; T(7): 0.3; S(20): 99.4; S(21): 0.3	S20;	S1067		3.4	0	0	3	1058	3172	57.42	11330
GRsIDQDYER	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho)	S(3): 100.0; Y(8): 0.0	S3;	S244		3.31	0	1	2	659.8	1319	22.45	3856
GSYGsDAEEEEYR	TJP2	9414	tight junction protein ZO-2 isoform 1	S5(Phospho)	S(2): 0.0; Y(3): 0.1; S(5): 99.9; Y(12): 0.0	S5;	S1159		3.09	0	0	2	786.3	1572	37.44	7032
SILKPSTPIPPQEGEEVGESSEEQDNAPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S21(Phospho)	S(1): 0.0; S(6): 0.0; T(7): 0.0; S(20): 4.7; S(21): 95.3	S21;	S1068		3	0	0	3	1058	3172	56.88	11209
DNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S3(Phospho)	S(3): 100.0	S3;	S986		2.52	0	0	2	800.9	1601	43.25	8254
AASSDQLRDNsPPPAFKPEPPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S11(Phospho)	S(3): 50.1; S(4): 50.1; S(11): 99.8	S11;	S986		2.49	0.003	1	4	628	2509	49.5	9600
sILKPSTPIPPQEGEEVGESSEEQDNAPK	TJP2	9414	tight junction protein ZO-2 isoform 1	S1(Phospho) S20(Phospho)	S(1): 99.0; S(6): 0.5; T(7): 0.5; S(20): 93.6; S(21): 6.4	S1; S20;	S1048; S1067		2.61	0.005	0	3	1085	3252	61.32	12158
SSEPVADESQsPR	TJP3	27134	tight junction protein ZO-3 isoform 1	S12(Phospho)	S(1): 0.0; S(2): 0.0; S(10): 0.0; S(12): 100.0	S12;	S856	43		0	0	2	798.8	1597	23.34	4044
HAQRsPEAsQTDSPVESPR	TJP3	27134	tight junction protein ZO-3 isoform 1	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 93.4; T(11): 3.3; S(13): 3.3; S(17): 0.0	S5; S9;	S319; S323	26		0	1	3	747	2239	21.14	3579
ASPSsPGRQDsDEDDGPQRVEEVDQGR	TJP3	27134	tight junction protein ZO-3 isoform 1	S5(Phospho) S11(Phospho)	S(2): 13.0; S(4): 13.0; S(5): 87.0; S(11): 87.0	S5; S11;	S106; S112	19		0	2	3	1025	3073	38.87	7329
HAQRsPEAsQTDSPVESPR	TJP3	27134	tight junction protein ZO-3 isoform 1	S5(Phospho) S9(Phospho)	S(5): 100.0; S(9): 93.4; T(11): 3.3; S(13): 3.3; S(17): 0.0	S5; S9;	S319; S323	5.04	0	1	3	747	2239	21.14	3579	
ASPSsPGRQDsDEDDGPQRVEEVDQGR	TJP3	27134	tight junction protein ZO-3 isoform 1	S5(Phospho) S11(Phospho)	S(2): 13.0; S(4): 13.0; S(5): 87.0; S(11): 87.0	S5; S11;	S106; S112	2.8	0	2	3	1025	3073	38.87	7329	
SSEPVADESQsPR	TJP3	27134	tight junction protein ZO-3 isoform 1	S12(Phospho)	S(1): 0.0; S(2): 0.0; S(10): 0.0; S(12): 100.0	S12;	S856	2.77	0	0	2	798.8	1597	23.34	4044	
ASPSSPGRQDsDEDDGPQRVEEVDQGR	TJP3	27134	tight junction protein ZO-3 isoform 1	S11(Phospho)	S(2): 0.3; S(4): 0.3; S(5): 5.2; S(11): 94.2	S11;	S112	2.71	0	2	3	998.4	2993	34.73	6454	
ESSANNSVsPSESRLR	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): 99.9; S(11): 0.1; S(13): 0.0	S9;	S147	68		0	0	2	822.3	1644	35.01	6522
DAPTSPASVASSSSTPSSK	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	48		0	0	2	922.4	1844	38.1	7168
DAPTSPAsVASSSStPSSK	TLE3	7090	transducin-like enhancer protein 3 isoform g	S8(Phospho) T15(Phospho)	T(4): 0.0; S(5): 0.3; S(8): 99.4; S(11): 0.3; S(12): 0.0; S(13): 0.0; S(14): 0.2; T(15): 90.6; S(17): 4.6; S(18): 4.6	S8; T15;	S233; T240	26		0	0	2	962.4	1924	44.75	8592
ESSANNSVsPSESRLR	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): 99.9; S(11): 0.1; S(13): 0.0	S9;	S147	3.36	0	0	2	822.3	1644	35.01	6522	
DAPTSPASVASSSSTPSSK	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	3.09	0	0	2	922.4	1844	38.1	7168	

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#
DAPTPASVASSSSstPSSK	TLE3	7090	transducin-like enhancer protein 3 isoform g	S8(Phospho) T15(Phospho)	T(4): 0.0; S(5): 0.3; S(8): 99.4; S(11): 0.3; S(12): 0.0; S(13): 0.0; S(14): 0.2; T(15): 90.6; S(17): 4.6; S(18): 4.6	S8; T15;	S233; T240		3.02	0	0	2	962.4	1924	44.75	8592
RTSPSsLPGR	TMEM201	199953	transmembrane protein 201 isoform 1	S6(Phospho)	T(2): 0.0; S(3): 50.0; S(5): 50.0; S(6): 100.0	S6;	S444	25		0	1	2	609.3	1218	25.48	4495
RTSPSsLPGR	TMEM201	199953	transmembrane protein 201 isoform 1	S6(Phospho)	T(2): 0.0; S(3): 50.0; S(5): 50.0; S(6): 100.0	S6;	S444		3.34	0.004	1	2	609.3	1218	25.48	4495
NAEREQEsEEEM	TMEM45A	55076	transmembrane protein 45A	S8(Phospho)	S(8): 100.0	S8;	S271	43		0	1	2	780.8	1561	23.16	4008
SNTEPQsPPIAsPK	TMF1	7110	TATA element modulatory factor	S7(Phospho) S12(Phospho)	S(1): 0.0; T(3): 0.0; S(7): 100.0; S(12): 100.0	S7; S12;	S72; S77	13		0	0	2	806.8	1613	42.83	8165
SNTEPQsPPIAsPK	TMF1	7110	TATA element modulatory factor	S7(Phospho) S12(Phospho)	S(1): 0.0; T(3): 0.0; S(7): 100.0; S(12): 100.0	S7; S12;	S72; S77		3.09	0	0	2	806.8	1613	42.83	8165
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67	83		0	1	3	910.7	2730	67.76	13684
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho) T14(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 100.0; S(19): 0.0	S6; S7; T14;	S66; S67; T74	60		0	1	3	937.4	2810	75.31	15216
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67	54		0	1	3	910.7	2730	67.26	13564
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho) T14(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 100.0; S(19): 0.0	S6; S7; T14;	S66; S67; T74	50		0	1	3	937.4	2810	74.8	15127
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67	48		0	1	3	910.7	2730	68.29	13809
EQGTESRsSTPLTISSAENTR	TMPO	7112	thymopoietin isoform alpha	S8(Phospho) S9(Phospho)	T(4): 0.0; S(6): 4.5; S(8): 95.4; S(9): 95.5; T(10): 4.5; T(14): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S8; S9;	S158; S159	41		0	1	3	865.7	2595	48.37	9363
SStPLTISSAENTR	TMPO	7112	thymopoietin isoform alpha	T3(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 99.9; T(7): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; T(15): 0.0	T3;	T160	38		0	0	2	864.4	1728	50.61	9833
GPPDFSSDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	T14(Phospho)	S(6): 50.0; S(7): 50.0; T(14): 100.0; S(19): 0.0	T14;	T74	35		0	1	3	910.7	2730	64.38	12908
EQGTESRsSTPLTISSAENTR	TMPO	7112	thymopoietin isoform alpha	T4(Phospho) S8(Phospho)	T(4): 99.8; S(6): 0.4; S(8): 99.5; S(9): 0.2; T(10): 0.2; T(14): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	T4; S8;	T154; S158	30		0	1	3	865.7	2595	49.57	9612
SHISDQsPLSSK	TMPO	7112	thymopoietin isoform alpha	S7(Phospho)	S(1): 0.0; S(4): 0.0; S(7): 100.0; S(10): 0.0; S(11): 0.0	S7;	S351	27		0	0	2	683.3	1366	23.6	4096
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67		6.31	0	1	3	910.7	2730	67.76	13684
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67		4.84	0	1	3	910.7	2730	67.26	13564
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho) T14(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 100.0; S(19): 0.0	S6; S7; T14;	S66; S67; T74		4.4	0	1	3	937.4	2810	75.31	15216
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 0.0; S(19): 0.0	S6; S7;	S66; S67		4.3	0	1	3	910.7	2730	68.29	13809
GPPDFssDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	S6(Phospho) S7(Phospho) T14(Phospho)	S(6): 100.0; S(7): 100.0; T(14): 100.0; S(19): 0.0	S6; S7; T14;	S66; S67; T74		4.23	0	1	3	937.4	2810	74.8	15127

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#
EQGTESRSTPLPTISSAENTR	TMPO	7112	thymopoietin isoform alpha	T4(Phospho) S8(Phospho)	T(4): 99.8; S(6): 0.4; S(8): 99.5; S(9): 0.2; T(10): 0.2; T(14): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	T4; S8;	T154; S158		4.13	0	1	3	865.7	2595	49.57	9612
SHISDQsPLSSK	TMPO	7112	thymopoietin isoform alpha	S7(Phospho)	S(1): 0.0; S(4): 0.0; S(7): 100.0; S(10): 0.0; S(11): 0.0	S7;	S351		4.12	0	0	2	683.3	1366	23.6	4096
EQGTESRSTPLPTISSAENTR	TMPO	7112	thymopoietin isoform alpha	S8(Phospho) S9(Phospho)	T(4): 0.0; S(6): 4.5; S(8): 95.4; S(9): 95.5; T(10): 4.5; T(14): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0; T(22): 0.0	S8; S9;	S158; S159		4.09	0	1	3	865.7	2595	48.37	9363
GPPDFSSDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	T14(Phospho)	S(6): 50.0; S(7): 50.0; T(14): 100.0; S(19): 0.0	T14;	T74		3.55	0	1	3	910.7	2730	64.38	12908
SSSTPLPTISSAENTR	TMPO	7112	thymopoietin isoform alpha	T3(Phospho)	S(1): 0.0; S(2): 0.0; T(3): 99.9; T(7): 0.0; S(9): 0.0; S(10): 0.0; S(11): 0.0; T(15): 0.0	T3;	T160		3.34	0	0	2	864.4	1728	50.61	9833
SSSTPLPTISSAENTR	TMPO	7112	thymopoietin isoform alpha	T3(Phospho)	S(1): 2.4; S(2): 2.4; T(3): 95.2; T(7): 0.0; S(9): 1.2; S(10): 48.8; S(11): 48.8; T(15): 1.2	T3;	T160		3.01	0	0	2	904.4	1808	61.15	12122
GPPDFSSDEEREPTVLGSGAAAAAGR	TMPO	7112	thymopoietin isoform alpha	T14(Phospho)	S(6): 0.0; S(7): 0.0; T(14): 100.0; S(19): 0.0	T14;	T74		2.48	0.003	1	3	884.1	2650	57.16	11275
KVEEEQEADEEDVsEEEEASK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0	S14;	S247	46		0	1	2	1260	2518	31.76	5827
KVEEEQEADEEDVsEEEEASK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0	S14;	S247	46		0	1	3	840	2518	31.75	5825
KVEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0; T(24): 0.0	S14;	S247	43		0	2	3	1016	3047	31.5	5773
KVEEEQEADEEDVsEEEEASK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 99.9; S(20): 0.1	S14;	S247	36		0	1	3	840	2518	32.37	5955
VEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S13(Phospho)	S(13): 100.0; S(19): 0.0; T(23): 0.0	S13;	S247	35		0	1	3	973.7	2919	34.59	6420
KVEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0; T(24): 0.0	S14;	S247	33		0	2	3	1016	3047	30.95	5660
VEEEQEADEEDVsEEEEASK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S13(Phospho)	S(13): 100.0; S(19): 0.0	S13;	S247	22		0	0	2	1195	2390	37.24	6989
KVEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0; T(24): 0.0	S14;	S247		7.05	0	2	3	1016	3047	31.5	5773
KVEEEQEADEEDVsEEEEASK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0	S14;	S247		6.56	0	1	3	840	2518	31.75	5825
KVEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0; T(24): 0.0	S14;	S247		5.44	0	2	3	1016	3047	30.95	5660
VEEEQEADEEDVsEEEEASKEGTNK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S13(Phospho)	S(13): 100.0; S(19): 0.0; T(23): 0.0	S13;	S247		5.25	0	1	3	973.7	2919	34.59	6420

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KVEEEQEAEEDVsEEEAESK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 100.0; S(20): 0.0	S14;	S247		4.39	0	1	2	1260	2518	31.76	5827
KVEEEQEAEEDVsEEEAESK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S14(Phospho)	S(14): 99.9; S(20): 0.1	S14;	S247		4.1	0	1	3	840	2518	32.37	5955
VEEEQEAEEDVsEEEAESK	TMX1	81542	thioredoxin-related transmembrane protein 1 precursor	S13(Phospho)	S(13): 100.0; S(19): 0.0	S13;	S247		3.63	0	0	2	1195	2390	37.24	6989
AGDNIPEEQPVASTPTTVsDGENKKDK	TMX2	51075	thioredoxin-related transmembrane protein 2 isoform 2	S19(Phospho)	S(13): 0.0; T(14): 0.0; T(16): 0.2; T(17): 0.2; S(19): 99.6	S19;	S250	16		0	2	3	969.8	2907	38.96	7350
AGDNIPEEQPVASTPTTVsDGENKKDK	TMX2	51075	thioredoxin-related transmembrane protein 2 isoform 2	S19(Phospho)	S(13): 0.0; T(14): 0.0; T(16): 0.2; T(17): 0.2; S(19): 99.6	S19;	S250		3.43	0.005	2	3	969.8	2907	38.96	7350
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	77		0	0	2	923.9	1847	53.82	10542
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	62		0	0	2	923.9	1847	54.35	10662
sQEADVQDWEFR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S1(Phospho)	S(1): 100.0	S1;	S836	59		0	0	2	795.3	1590	68.88	13932
NRsAEEGELAESK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; S(12): 0.0	S3;	S1666	58		0	1	2	750.3	1500	20.21	3381
AsPEPPGPRESSR	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	50		0	0	2	689.3	1378	25.69	4537
RDsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893	50		0	1	3	768.3	2303	45.29	8714
RDsLGAYASQDANEQGQDLGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893	46		0	2	3	820.4	2459	41.2	7825
ASRVPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0; S(17): 0.0	S6; S7;	S1620; S1621	41		0	1	3	721	2161	43.6	8328
DsLGAYASQDANEQGQDLGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; Y(6): 0.0; S(8): 0.0	S2;	S893	40		0	1	3	768.3	2303	47.61	9204
TEAQDLCRAsPEPPGPRESSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C7(Carbamidomethyl) S10(Phospho)	T(1): 0.0; S(10): 100.0; S(18): 0.0; S(19): 0.0; S(20): 0.0	S10;	S672	39		0	1	3	784.3	2351	37.39	7021
DsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; Y(6): 0.0; S(8): 0.0	S2;	S893	38		0	0	2	1074	2147	55.37	10877
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	33		0	0	2	923.9	1847	53.29	10426
QQAGAQGPGsADLEDGEMGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S10(Phospho)	S(10): 100.0	S10;	S1073	30		0	1	3	728	2182	36.63	6863
ASRVPssDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0; S(17): 0.0	S6; S7;	S1620; S1621	30		0	1	2	1081	2161	43.67	8344
TEAQDLCRAsPEPPGPRESSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C7(Carbamidomethyl) S10(Phospho)	T(1): 0.0; S(10): 100.0; S(18): 0.0; S(19): 0.0; S(20): 0.0	S10;	S672	28		0	1	3	784.3	2351	36.88	6914
NMAPGAVCSPGESK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C8(Carbamidomethyl) S13(Phospho)	S(9): 2.0; S(13): 98.0	S13;	S1301	25		0	0	2	742.8	1485	33.57	6203
RFsEGLVQsPSQDQEK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0; S(11): 0.0	S3; S9;	S429; S435	23		0	1	2	997.9	1995	50.26	9760
RDsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893	21		0	1	2	1152	2303	45.49	8759
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	17		0	0	2	923.9	1847	54.08	10602
RDsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893		6.14	0	1	3	768.3	2303	45.29	8714

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#
RDsLGAYASQDANEQGQDLGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893		5.32	0	2	3	820.4	2459	41.2	7825
DsLGAYASQDANEQGQDLGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; Y(6): 0.0; S(8): 0.0	S2;	S893		5.3	0	1	3	768.3	2303	47.61	9204
TEAQLCLCRAsPEPPGPRESSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C7(Carbamidomethyl) S10(Phospho)	T(1): 0.0; S(10): 100.0; S(18): 0.0; S(19): 0.0; S(20): 0.0	S10;	S672		5.17	0	1	3	784.3	2351	37.39	7021
NRsAEEGELAESK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; S(12): 0.0	S3;	S1666		5.08	0	1	2	750.3	1500	20.21	3381
QQAGAQQPGsADLEDGEMGKR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S10(Phospho)	S(10): 100.0	S10;	S1073		4.95	0	1	3	728	2182	36.63	6863
ASRVPsDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0; S(17): 0.0	S6; S7;	S1620; S1621		4.77	0	1	3	721	2161	43.6	8328
TEAQLCLCRAsPEPPGPRESSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C7(Carbamidomethyl) S10(Phospho)	T(1): 0.0; S(10): 100.0; S(18): 0.0; S(19): 0.0; S(20): 0.0	S10;	S672		4.6	0	1	3	784.3	2351	36.88	6914
VPsDEEVVEEPQSR	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		4.5	0	0	2	923.9	1847	53.82	10542
VPsDEEVVEEPQSR	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		4.42	0	0	2	923.9	1847	54.35	10662
DsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S2(Phospho)	S(2): 100.0; Y(6): 0.0; S(8): 0.0	S2;	S893		4.27	0	0	2	1074	2147	55.37	10877
VPsDEEVVEEPQSR	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		4.1	0	0	2	923.9	1847	54.08	10602
RDsLGAYASQDANEQGQDLGK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho)	S(3): 100.0; Y(7): 0.0; S(9): 0.0	S3;	S893		4	0	1	2	1152	2303	45.49	8759
ASRVPsDEEVVEEPQSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S6(Phospho) S7(Phospho)	S(2): 0.0; S(6): 100.0; S(7): 100.0; S(17): 0.0	S6; S7;	S1620; S1621		3.7	0	1	2	1081	2161	43.67	8344
RfSEGLVQsPSQDQEK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S3(Phospho) S9(Phospho)	S(3): 100.0; S(9): 100.0; S(11): 0.0	S3; S9;	S429; S435		3.45	0	1	2	997.9	1995	50.26	9760
VPsDEEVVEEPQSR	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		3.31	0	0	2	923.9	1847	53.29	10426
sQEADVQDWEFR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	S1(Phospho)	S(1): 100.0	S1;	S836		3.18	0	0	2	795.3	1590	68.88	13932
NMAPGAVCSPGEsK	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C8(Carbamidomethyl) S13(Phospho)	S(9): 2.0; S(13): 98.0	S13;	S1301		3.05	0	0	2	742.8	1485	33.57	6203
TEAQLCLCRAsPEPPGPRESSR	TNKS1BP1	85456	182 kDa tankyrase-1-binding protein	C7(Carbamidomethyl) S10(Phospho)	T(1): 0.1; S(10): 99.9; S(18): 0.0; S(19): 0.0; S(20): 0.0	S10;	S672		2.43	0	1	2	1176	2351	37.14	6970
AsPEPPGPRESSR	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		2.23	0	0	2	689.3	1378	25.69	4537
GVGSGPHPPDTQQPsPSK	TNS3	64759	tensin-3	S15(Phospho)	S(4): 0.0; T(11): 0.1; S(15): 97.6; S(17): 2.4	S15;	S660	29		0	0	3	618.3	1853	25.51	4501
GVGSGPHPPDTQQPsPSK	TNS3	64759	tensin-3	S15(Phospho)	S(4): 0.0; T(11): 0.1; S(15): 97.6; S(17): 2.4	S15;	S660		5.73	0	0	3	618.3	1853	25.51	4501
GVGSGPHPPDTQQPsPSK	TNS3	64759	tensin-3	S17(Phospho)	S(4): 0.0; T(11): 0.0; S(15): 2.9; S(17): 97.1	S17;	S662		2.52	0.005	0	2	926.9	1853	25.36	4470
GVGSGPHPPDTQQPsPSK	TNS3	64759	tensin-3	S17(Phospho)	S(4): 0.0; T(11): 0.0; S(15): 2.9; S(17): 97.1	S17;	S662	10		0.008	0	2	926.9	1853	25.36	4470
ASSPHGLGsPLVAsPR	TNS4	84951	tensin-4 precursor	S9(Phospho) S14(Phospho)	S(2): 50.0; S(3): 50.0; S(9): 100.0; S(14): 100.0	S9; S14;	S248; S253	33		0	0	2	886.9	1773	64.61	12965
ASSPHGLGsPLVAsPR	TNS4	84951	tensin-4 precursor	S9(Phospho) S14(Phospho)	S(2): 50.0; S(3): 50.0; S(9): 100.0; S(14): 100.0	S9; S14;	S248; S253		3.01	0.006	0	2	886.9	1773	64.61	12965
AADsDDGAVSAPAsDGGVSK	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	61		0	0	2	964.4	1928	36.8	6899

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#
EATNTTSEPSAPSQDLLDLSpsPR	TOM1L1	10040	TOM1-like protein 1	S22(Phospho)	T(3): 0.0; T(5): 0.0; T(6): 0.0; S(7): 0.0; S(10): 0.0; S(13): 0.0; S(20): 0.0; S(22): 100.0	S22;	S323	31		0	0	3	865.1	2593	75.44	15239
EATNTTSEPSAPSQDLLDLSpsPR	TOM1L1	10040	TOM1-like protein 1	S22(Phospho)	T(3): 0.0; T(5): 0.0; T(6): 0.0; S(7): 0.0; S(10): 0.0; S(13): 0.0; S(20): 0.0; S(22): 100.0	S22;	S323		3.17	0	0	3	865.1	2593	75.44	15239
NRVPsAGDVEK	TOMM34	10953	mitochondrial import receptor subunit TOM34	S5(Phospho)	S(5): 100.0	S5;	S186	36		0	1	2	626.3	1252	25	4392
NRVPsAGDVEK	TOMM34	10953	mitochondrial import receptor subunit TOM34	S5(Phospho)	S(5): 100.0	S5;	S186		3.54	0	1	2	626.3	1252	25	4392
AsPAPGSGHPEGPGAHLDMSNLSR	TOMM70A	9868	mitochondrial import receptor subunit TOM70	M19(Oxidation) S2(Phospho)	S(2): 100.0; S(7): 0.0; S(21): 0.0	S2;	S91		2.94	0.005	0	3	822.7	2466	37.62	7070
EAQKVPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S15(Phospho)	S(15): 100.0; T(21): 0.0	S15;	S1106	33		0	2	4	704.3	2814	21.81	3717
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106	30		0	1	3	744	2230	19.82	3298
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106	30		0	1	2	1115	2230	19.39	3208
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106	29		0	1	3	744	2230	19.31	3191
IKNENTEGsPQEDGVELEGLK	TOP2A	7153	DNA topoisomerase 2-alpha	S9(Phospho)	T(6): 0.2; S(9): 99.8	S9;	S1247	26		0	1	3	789.4	2366	51.89	10100
KPstSDDsDSNF EK	TOP2A	7153	DNA topoisomerase 2-alpha	S3(Phospho) T4(Phospho) S8(Phospho)	S(3): 100.0; T(4): 99.9; S(5): 0.1; S(8): 100.0; S(10): 0.0	S3; T4; S8;	S1469; T1470; S1474	23		0	0	2	898.8	1797	30.81	5633
EAQKVPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S15(Phospho)	S(15): 100.0; T(21): 0.0	S15;	S1106	10		0	2	3	938.7	2814	21.64	3681
EAQKVPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S15(Phospho)	S(15): 100.0; T(21): 0.0	S15;	S1106		5.71	0	2	4	704.3	2814	21.81	3717
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106		5.54	0	1	3	744	2230	19.82	3298
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106		5.12	0	1	3	744	2230	19.31	3191
EAQKVPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S15(Phospho)	S(15): 100.0; T(21): 0.0	S15;	S1106		3.9	0	2	3	938.7	2814	21.64	3681
IKNENTEGsPQEDGVELEGLK	TOP2A	7153	DNA topoisomerase 2-alpha	S9(Phospho)	T(6): 0.2; S(9): 99.8	S9;	S1247		3.79	0	1	3	789.4	2366	51.89	10100
VPDEEENEesDNEKETEK	TOP2A	7153	DNA topoisomerase 2-alpha	S10(Phospho)	S(10): 100.0; T(16): 0.0	S10;	S1106		3.24	0	1	2	1115	2230	19.39	3208
KPstSDDsDSNF EK	TOP2A	7153	DNA topoisomerase 2-alpha	S3(Phospho) T4(Phospho) S8(Phospho)	S(3): 100.0; T(4): 99.9; S(5): 0.1; S(8): 100.0; S(10): 0.0	S3; T4; S8;	S1469; T1470; S1474		2.8	0	0	2	898.8	1797	30.81	5633
KAsGsENEGDYNPGR	TOP2B	7155	DNA topoisomerase 2-beta	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(11): 0.0	S3; S5;	S1545; S1547	61		0	1	2	870.8	1741	21.98	3753
VVEAVNsDsDSEFGIPK	TOP2B	7155	DNA topoisomerase 2-beta	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 99.9; S(11): 0.1	S7; S9;	S1517; S1519	59		0	0	2	976.9	1953	79.6	16037
KASGsENEGDYNPGR	TOP2B	7155	DNA topoisomerase 2-beta	S5(Phospho)	S(3): 0.0; S(5): 100.0; Y(11): 0.0	S5;	S1547	37		0	1	2	830.8	1661	16.96	2696
KAsGsENEGDYNPGRK	TOP2B	7155	DNA topoisomerase 2-beta	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(11): 0.0	S3; S5;	S1545; S1547	31		0	2	3	623.6	1869	15.58	2394
VVEAVNsDsDSEFGIPK	TOP2B	7155	DNA topoisomerase 2-beta	S7(Phospho) S9(Phospho)	S(7): 95.8; S(9): 95.8; S(11): 8.3	S7; S9;	S1517; S1519	14		0	0	2	976.9	1953	79.08	15941
KAsGsENEGDYNPGR	TOP2B	7155	DNA topoisomerase 2-beta	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(11): 0.0	S3; S5;	S1545; S1547		4.33	0	1	2	870.8	1741	21.98	3753
KAsGsENEGDYNPGRK	TOP2B	7155	DNA topoisomerase 2-beta	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(11): 0.0	S3; S5;	S1545; S1547		4.19	0	2	3	623.6	1869	15.58	2394
VVEAVNsDsDSEFGIPK	TOP2B	7155	DNA topoisomerase 2-beta	S7(Phospho) S9(Phospho)	S(7): 100.0; S(9): 99.9; S(11): 0.1	S7; S9;	S1517; S1519		3.91	0	0	2	976.9	1953	79.6	16037
KASGsENEGDYNPGR	TOP2B	7155	DNA topoisomerase 2-beta	S5(Phospho)	S(3): 0.0; S(5): 100.0; Y(11): 0.0	S5;	S1547		2.8	0	1	2	830.8	1661	16.96	2696
VVEAVNsDsDSEFGIPK	TOP2B	7155	DNA topoisomerase 2-beta	S7(Phospho) S9(Phospho)	S(7): 95.8; S(9): 95.8; S(11): 8.3	S7; S9;	S1517; S1519		1.83	0.001	0	2	976.9	1953	79.08	15941
VKAsPITNDGEDEFVpsDGLDKDEYTFsP GK	TOP2B	7155	DNA topoisomerase 2-beta	S4(Phospho) S17(Phospho) S28(Phospho)	S(4): 99.2; T(7): 0.9; S(17): 99.9; Y(25): 0.1; T(26): 0.8; S(28): 99.1	S4; S17; S28;	S1395; S1408; S1419		3.35	0.002	2	3	1200	3597	79.85	16088
ASPTITNDGEDEFVpsDGLDKDEYTFsPGK	TOP2B	7155	DNA topoisomerase 2-beta	Y23(Phospho) S26(Phospho)	S(2): 0.0; T(5): 0.0; S(15): 6.0; Y(23): 93.6; T(24): 0.5; S(26): 100.0	Y23; S26;	Y1416; S1419		2.54	0.004	1	3	1097	3290	82.65	16617

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#
VVEAVNsDsSEFGIPK	TOP2B	7155	DNA topoisomerase 2-beta	S7(Phospho) S9(Phospho)	S(7): 94.4; S(9): 94.4; S(11): 11.2	S7; S9;	S1517; S1519		1.71	0.005	0	2	976.9	1953	80.13	16143
VKAsPITNDGEDEFVPsDGLDKDEYTFsPGK	TOP2B	7155	DNA topoisomerase 2-beta	S4(Phospho) S17(Phospho) S28(Phospho)	S(4): 99.4; T(7): 0.6; S(17): 92.7; Y(25): 7.3; T(26): 7.3; S(28): 92.7	S4; S17; S28;	S1395; S1408; S1419		3.23	0.006	2	4	900.1	3597	79.89	16095
DSHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 0.1; S(4): 99.9; S(5): 99.9; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157	68		0	0	3	847.7	2541	52.04	10140
DSHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 5.2; S(4): 97.4; S(5): 97.4; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157	64		0	0	3	847.7	2541	51.5	10019
DSHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho)	S(2): 2.7; S(4): 2.7; S(5): 94.6; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S5;	S157	58		0	0	3	821	2461	43.75	8361
DSHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho)	S(2): 50.0; S(4): 50.0; S(5): 100.0; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S5;	S157	57		0	0	2	1271	2541	51.63	10046
GLRDsHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho) S7(Phospho) S8(Phospho)	S(5): 100.0; S(7): 100.0; S(8): 100.0; S(14): 0.0; S(15): 0.0; T(17): 0.0; S(20): 0.0; T(22): 0.0; S(24): 0.0	S5; S7; S8;	S154; S156; S157	40		0	1	3	983	2947	52.8	10314
VNFsEEGETEEDDQSSHSVVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215	38		0	0	3	946.1	2836	43.97	8406
VNFsEEGETEEDDQSSHSVVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220	37		0	0	3	972.7	2916	48.25	9339
VNFsEEGETEEDDQSSHSVVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	T9(Phospho)	S(4): 3.4; T(9): 96.6; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	T9;	T220	36		0	0	3	946.1	2836	43.16	8235
GLRDShssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S7(Phospho) S8(Phospho)	S(5): 0.2; S(7): 99.8; S(8): 100.0; S(14): 0.0; S(15): 0.0; T(17): 0.0; S(20): 0.0; T(22): 0.0; S(24): 0.0	S7; S8;	S156; S157	34		0	1	3	956.4	2867	45.91	8847
LQQQHSEQPPLQPsPVMTR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S14(Phospho)	S(6): 0.0; S(14): 100.0; T(18): 0.0	S14;	S143	30		0	0	3	761	2281	45.69	8799
VNFsEEGETEEDDQSSHSVVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215	25		0	0	3	946.1	2836	44.49	8527
DSHssEEDEASSQTDLSTQISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 5.1; S(4): 95.1; S(5): 99.7; S(11): 2.5; S(12): 48.7; T(14): 48.7; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157	25		0	0	3	874.3	2621	59.57	11800
LQQQHSEQPPLQPsPVMTR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	M17(Oxidation) S14(Phospho)	S(6): 0.0; S(14): 100.0; T(18): 0.0	S14;	S143	21		0	0	3	766.4	2297	38.19	7188

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#
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 99.4; T(9): 33.5; S(16): 33.5; S(17): 33.5; S(19): 0.2; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215	18		0	0	2	1459	2916	48.29	9346
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; S(16): 0.1; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220	18		0	0	3	972.7	2916	50.24	9754
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 98.6; T(9): 98.6; S(16): 1.4; S(17): 1.4; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220	17		0	0	3	972.7	2916	49.67	9633
DSHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 0.1; S(4): 99.9; S(5): 99.9; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157		7.55	0	0	3	847.7	2541	52.04	10140
GLRDsHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho) S7(Phospho) S8(Phospho)	S(5): 100.0; S(7): 100.0; S(8): 100.0; S(14): 0.0; S(15): 0.0; S(17): 0.0; S(20): 0.0; T(22): 0.0; S(24): 0.0	S5; S7; S8;	S154; S156; S157		7.44	0	1	3	983	2947	52.8	10314
GLRDShsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S7(Phospho) S8(Phospho)	S(5): 0.2; S(7): 99.8; S(8): 100.0; S(14): 0.0; S(15): 0.0; T(17): 0.0; S(20): 0.0; T(22): 0.0; S(24): 0.0	S7; S8;	S156; S157		6.7	0	1	3	956.4	2867	45.91	8847
DSHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 5.2; S(4): 97.4; S(5): 97.4; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157		6.38	0	0	3	847.7	2541	51.5	10019
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215		5.56	0	0	3	946.1	2836	43.97	8406
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220		5.16	0	0	3	972.7	2916	48.25	9339
VNFSEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	T9(Phospho)	S(4): 3.4; T(9): 96.6; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	T9;	T220		5.04	0	0	3	946.1	2836	43.16	8235
DSHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho)	S(2): 50.0; S(4): 50.0; S(5): 100.0; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S5;	S157		4.95	0	0	2	1271	2541	51.63	10046
DSHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S5(Phospho)	S(2): 2.7; S(4): 2.7; S(5): 94.6; S(11): 0.0; S(12): 0.0; T(14): 0.0; S(17): 0.0; T(19): 0.0; S(21): 0.0	S5;	S157		4.67	0	0	3	821	2461	43.75	8361
LQQQHSEQLPLQPpVPMTR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	M17(Oxidation) S14(Phospho)	S(6): 0.0; S(14): 100.0; T(18): 0.0	S14;	S143		4.48	0	0	3	766.4	2297	38.19	7188
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 100.0; T(9): 0.0; S(16): 0.0; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215		4.26	0	0	3	946.1	2836	44.49	8527

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#
DSHsEEDEASSQTDLSTISK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) S5(Phospho)	S(2): 5.1; S(4): 95.1; S(5): 99.7; S(11): 2.5; S(12): 48.7; T(14): 48.7; S(17): 0.0; T(19): 0.0; S(21): 0.0	S4; S5;	S156; S157		4.13	0	0	3	874.3	2621	59.57	11800
LQQQHSEQPLQPsPVMTR	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S14(Phospho)	S(6): 0.0; S(14): 100.0; T(18): 0.0	S14;	S143		4.06	0	0	3	761	2281	45.69	8799
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 100.0; T(9): 100.0; S(16): 0.1; S(17): 0.0; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220		2.2	0	0	3	972.7	2916	50.24	9754
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho)	S(4): 99.4; T(9): 33.5; S(16): 33.5; S(17): 33.5; S(19): 0.2; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4;	S215		1.9	0	0	2	1459	2916	48.29	9346
VNFsEEGETEEDDQDSSHSSVTTVK	TOR1AIP1	26092	torsin-1A-interacting protein 1 isoform 2	S4(Phospho) T9(Phospho)	S(4): 98.6; T(9): 98.6; S(16): 1.4; S(17): 1.4; S(19): 0.0; S(20): 0.0; T(22): 0.0; T(23): 0.0	S4; T9;	S215; T220		2.41	0.001	0	3	972.7	2916	49.67	9633
LSTTPsPTSSLHEDGVDFRR	TOX4	9878	TOX high mobility group box family member 4 isoform 2	S6(Phospho) S10(Phospho)	S(2): 2.6; T(3): 48.7; T(4): 48.7; S(6): 90.8; T(8): 5.0; S(9): 9.2; S(10): 95.0	S6; S10;	S155; S159	30		0	1	3	857.7	2571	58.8	11639
LSTTPsPTSSLHEDGVDFRR	TOX4	9878	TOX high mobility group box family member 4 isoform 2	S6(Phospho)	S(2): 0.0; T(3): 0.0; T(4): 0.4; S(6): 97.4; T(8): 32.9; S(9): 34.7; S(10): 34.7	S6;	S155	16		0	1	3	831	2491	53.92	10567
LSTTPsPTSSLHEDGVDFRR	TOX4	9878	TOX high mobility group box family member 4 isoform 2	S6(Phospho) S10(Phospho)	S(2): 2.6; T(3): 48.7; T(4): 48.7; S(6): 90.8; T(8): 5.0; S(9): 9.2; S(10): 95.0	S6; S10;	S155; S159		4.7	0	1	3	857.7	2571	58.8	11639
LSTTPsPTSSLHEDGVDFRR	TOX4	9878	TOX high mobility group box family member 4 isoform 2	S6(Phospho)	S(2): 0.0; T(3): 0.0; T(4): 0.4; S(6): 97.4; T(8): 32.9; S(9): 34.7; S(10): 34.7	S6;	S155		3.51	0	1	3	831	2491	53.92	10567
ALPNTSSsPQPK	TP53	7157	cellular tumor antigen p53 isoform k	S9(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 1.7; S(9): 98.2	S9;	S156	47		0	0	2	710.8	1421	23.94	4167
ALPNTSSsPQPK	TP53	7157	cellular tumor antigen p53 isoform k	S9(Phospho)	T(6): 0.0; S(7): 0.0; S(8): 1.7; S(9): 98.2	S9;	S156		3.77	0	0	2	710.8	1421	23.94	4167
GGPGKLSPR	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S7(Phospho)	S(7): 100.0	S7;	S1362	58		0	1	2	474.7	948.5	16.29	2545
TSSGtsLSAMHSSGSSGK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	T5(Phospho) S6(Phospho)	T(1): 0.0; S(2): 0.0; S(3): 0.3; T(5): 99.4; S(6): 95.4; S(8): 4.8; S(12): 0.0; S(13): 0.0; S(15): 0.0; S(16): 0.0	T5; S6;	T1319; S1320	28		0	0	2	914.8	1829	28.86	5224
LITsEEERsPAK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S4(Phospho) S9(Phospho)	T(3): 0.1; S(4): 99.9; S(9): 100.0	S4; S9;	S1673; S1678	27		0	1	2	760.3	1520	33.77	6244
NsPEDLGLSLTGDSCK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	C15(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0; T(11): 0.0; S(14): 0.0	S2;	S500	21		0	0	2	886.9	1773	69.4	14032
QSQQPMKPIsPVKDPVsPASQK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	M6(Oxidation) S10(Phospho) S17(Phospho)	S(2): 0.0; S(10): 100.0; S(17): 99.9; S(20): 0.1	S10; S17;	S1094; S1101	21		0	1	3	851.7	2553	38.73	7300
STPFIVSPsPTEQEGR	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	T11(Phospho)	S(1): 0.0; T(2): 0.0; S(8): 0.0; S(9): 2.3; T(11): 97.7	T11;	T382	21		0	0	2	906.4	1812	64.98	13047
QSQQPMKPIsPVKDPVsPASQK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	M6(Oxidation) S10(Phospho) S17(Phospho)	S(2): 0.0; S(10): 100.0; S(17): 99.9; S(20): 0.1	S10; S17;	S1094; S1101		6.01	0	1	3	851.7	2553	38.73	7300
TSSGtsLSAMHSSGSSGK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	T5(Phospho) S6(Phospho)	T(1): 0.0; S(2): 0.0; S(3): 0.3; T(5): 99.4; S(6): 95.4; S(8): 4.8; S(12): 0.0; S(13): 0.0; S(15): 0.0; S(16): 0.0	T5; S6;	T1319; S1320		2.79	0	0	2	914.8	1829	28.86	5224

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#
NsPEDLGLSLTGDSCK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	C15(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(9): 0.0; T(11): 0.0; S(14): 0.0	S2;	S500		2.47	0	0	2	886.9	1773	69.4	14032
IDEDGENTQIEDTEPMSPVLNsK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S22(Phospho)	T(8): 0.0; T(13): 0.0; S(17): 5.2; S(22): 94.8	S22;	S557	12		0.001	0	2	1321	2641	67.77	13686
GGPGKLSPR	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S7(Phospho)	S(7): 100.0	S7;	S1362		3.29	0.001	1	2	474.7	948.5	16.29	2545
STPFIVSSPTEQEGR	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	T11(Phospho)	S(1): 0.0; T(2): 0.0; S(8): 0.0; S(9): 2.3; T(11): 97.7	T11;	T382		2.32	0.001	0	2	906.4	1812	64.98	13047
IDEDGENTQIEDTEPMSPVLNsK	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S22(Phospho)	T(8): 0.0; T(13): 0.0; S(17): 5.2; S(22): 94.8	S22;	S557		1.88	0.003	0	2	1321	2641	67.77	13686
LITSEERsPAKR	TP53BP1	7158	tumor suppressor p53-binding protein 1 isoform 3	S4(Phospho) S9(Phospho)	T(3): 2.6; S(4): 97.4; S(9): 100.0	S4; S9;	S1673; S1678		3.23	0.008	2	3	559.3	1676	26.92	4806
KNQsSEDILR	TP53BP2	7159	apoptosis-stimulating of p53 protein 2 isoform 2	S4(Phospho)	S(4): 100.0; S(5): 0.0	S4;	S357	59		0	1	2	635.3	1270	26.79	4778
KNQsSEDILR	TP53BP2	7159	apoptosis-stimulating of p53 protein 2 isoform 2	S4(Phospho)	S(4): 100.0; S(5): 0.0	S4;	S357		3.54	0	1	2	635.3	1270	26.79	4778
QTSIQSPSSYGNSsPPLNK	TP63	8626	tumor protein 63 isoform 5	S14(Phospho)	T(2): 0.0; S(3): 0.0; S(6): 0.0; S(8): 0.0; S(9): 0.0; Y(10): 0.0; S(13): 4.2; S(14): 95.8	S14;	S369		2.39	0.003	0	2	1036	2072	47.59	9198
NSPTFKsFEEK	TPD52	7163	tumor protein D52 isoform 7	S7(Phospho)	S(2): 0.0; T(4): 0.0; S(7): 100.0	S7;	S136	20		0	1	2	697.3	1394	40.63	7704
NSATFKsFEDR	TPD52L2	7165	tumor protein D54 isoform h	S7(Phospho)	S(2): 0.0; T(4): 0.0; S(7): 100.0	S7;	S123	56		0	1	2	691.3	1382	38.3	7210
NSATFKsFEDR	TPD52L2	7165	tumor protein D54 isoform h	S7(Phospho)	S(2): 0.0; T(4): 0.0; S(7): 100.0	S7;	S123	49		0	1	2	691.3	1382	37.79	7104
NSATFKsFEDR	TPD52L2	7165	tumor protein D54 isoform h	S7(Phospho)	S(2): 0.0; T(4): 0.0; S(7): 100.0	S7;	S123		3.38	0	1	2	691.3	1382	38.3	7210
NSATFKsFEDR	TPD52L2	7165	tumor protein D54 isoform h	S7(Phospho)	S(2): 0.0; T(4): 0.0; S(7): 100.0	S7;	S123		2.84	0	1	2	691.3	1382	37.79	7104
AADSQNSGEGNTGAAESsFSQEVSR	TPR	7175	nucleoprotein TPR	S18(Phospho)	S(4): 0.0; S(7): 0.1; T(12): 0.0; S(17): 0.0; S(18): 99.7; S(20): 0.1; S(24): 0.0	S18;	S2048	52		0	0	3	856	2566	44.41	8511
AADSQNSGEGNTGAAESsFSQEVSR	TPR	7175	nucleoprotein TPR	S18(Phospho)	S(4): 0.0; S(7): 0.1; T(12): 0.0; S(17): 0.0; S(18): 99.7; S(20): 0.1; S(24): 0.0	S18;	S2048		5.29	0	0	3	856	2566	44.41	8511
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262	33		0	2	3	476.9	1429	19.86	3307
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	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;	S260; S262	32		0	1	2	636.7	1272	24.97	4386
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	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;	S260; S262	31		0	1	2	636.7	1272	24.46	4277
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262	28		0	2	3	476.9	1429	21.55	3663
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262	24		0	2	3	476.9	1429	18.8	3084
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262	24		0	2	3	476.9	1429	19.34	3198
sRShsPMSNR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S1(Phospho) S3(Phospho) S5(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 100.0; S(8): 0.0	S1; S3; S5;	S96; S98; S100	23		0	1	2	699.7	1398	13.22	1896

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#
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262		4.53	0	2	3	476.9	1429	19.86	3307
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262		4.4	0	2	3	476.9	1429	19.34	3198
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262		4.34	0	2	3	476.9	1429	18.8	3084
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262		4.15	0	2	3	476.9	1429	21.55	3663
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	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;	S260; S262		3.82	0	1	2	636.7	1272	24.97	4386
RsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	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;	S260; S262		3.51	0	1	2	636.7	1272	24.46	4277
sRsHsPMSNR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S1(Phospho) S3(Phospho) S5(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 100.0; S(8): 0.0	S1; S3; S5;	S96; S98; S100		3.14	0	1	2	699.7	1398	13.22	1896
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262	15		0.001	2	2	714.8	1429	20.29	3397
RRsPSPYYsR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.0; Y(7): 0.0; Y(8): 0.0; S(9): 99.9	S3; S9;	S260; S266	15		0.002	2	2	714.8	1429	19.77	3288
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 95.8; Y(7): 2.1; Y(8): 2.1; S(9): 0.0	S3; S5;	S260; S262	11		0.002	2	2	714.8	1429	20.81	3508
RRsPSPYYsR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S9(Phospho)	S(3): 100.0; S(5): 0.0; Y(7): 0.0; Y(8): 0.0; S(9): 99.9	S3; S9;	S260; S266		3.5	0.003	2	2	714.8	1429	19.77	3288
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 99.9; Y(7): 0.0; Y(8): 0.0; S(9): 0.0	S3; S5;	S260; S262		3.36	0.003	2	2	714.8	1429	20.29	3397
RRsPSPYYsR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho)	S(3): 100.0; S(5): 49.1; Y(7): 0.9; Y(8): 0.9; S(9): 49.1	S3;	S260		3.95	0.005	2	2	714.8	1429	19.25	3180
RRsPsPYYSR	TRA2A	29896	transformer-2 protein homolog alpha isoform 1	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 95.8; Y(7): 2.1; Y(8): 2.1; S(9): 0.0	S3; S5;	S260; S262		2.69	0.006	2	2	714.8	1429	20.81	3508
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	40		0	0	2	675.3	1350	15.36	2348
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		2.73	0	0	2	675.3	1350	15.36	2348
EtEEQSDSsAEQGDPAGEGK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 100.0; S(7): 0.0; S(9): 0.0	T2;	T55	53		0	0	2	1080	2159	21.53	3659
EtEEQSDSsAEQGDPAGEGK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 100.0; S(7): 0.0; S(9): 0.0	T2;	T55	36		0	0	3	720.3	2159	21.58	3668
AtAQPPAPLSPDSGSPSPDSGSASPVEEE DVGSSSEK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 99.5; S(10): 0.0; S(13): 0.0; S(15): 0.0; S(17): 0.4; S(20): 0.0; S(22): 0.0; S(24): 0.0; S(33): 0.0; S(34): 0.0	T2;	T16	13		0	0	3	1183	3546	60.73	12030
EtEEQSDSsAEQGDPAGEGK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 100.0; S(7): 0.0; S(9): 0.0	T2;	T55		4.85	0	0	3	720.3	2159	21.58	3668
EtEEQSDSsAEQGDPAGEGK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 100.0; S(7): 0.0; S(9): 0.0	T2;	T55		3.6	0	0	2	1080	2159	21.53	3659

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#
ATAQPAPLSPDSGSPSPDSGSASPVEEE DVGSSSEK	TRIM16	10626	tripartite motif-containing protein 16	T2(Phospho)	T(2): 99.5; S(10): 0.0; S(13): 0.0; S(15): 0.0; S(17): 0.4; S(20): 0.0; S(22): 0.0; S(24): 0.0; S(33): 0.0; S(34): 0.0	T2;	T16		3.45	0	0	3	1183	3546	60.73	12030
NEsEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S3(Phospho) S12(Phospho)	S(3): 95.5; S(9): 9.1; S(12): 95.5	S3; S12;	S985; S994	60		0	1	3	840.3	2519	55.61	10928
NESEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S9(Phospho) S12(Phospho)	S(3): 9.0; S(9): 95.5; S(12): 95.5	S9; S12;	S991; S994	47		0	1	2	1260	2519	55.71	10949
NEsEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S3(Phospho) S12(Phospho)	S(3): 99.8; S(9): 0.4; S(12): 99.8	S3; S12;	S985; S994	32		0	1	3	840.3	2519	56.17	11047
NEsEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S3(Phospho) S12(Phospho)	S(3): 95.5; S(9): 9.1; S(12): 95.5	S3; S12;	S985; S994		3.85	0	1	3	840.3	2519	55.61	10928
NESEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S9(Phospho) S12(Phospho)	S(3): 9.0; S(9): 95.5; S(12): 95.5	S9; S12;	S991; S994		3.49	0	1	2	1260	2519	55.71	10949
NEsEDNKFSDsDDDFVQPR	TRIM24	8805	transcription intermediary factor 1-alpha isoform b	S3(Phospho) S12(Phospho)	S(3): 99.8; S(9): 0.4; S(12): 99.8	S3; S12;	S985; S994		2.97	0	1	3	840.3	2519	56.17	11047
AsAPSPNAQVACDHCLK	TRIM25	7706	E3 ubiquitin/ISG15 ligase TRIM25	C12(Carbamido methyl) C15(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(5): 0.0	S2;	S97	32		0	0	3	635.9	1906	33.75	6240
AsAPSPNAQVACDHCLK	TRIM25	7706	E3 ubiquitin/ISG15 ligase TRIM25	C12(Carbamido methyl) C15(Carbamido methyl) S2(Phospho)	S(2): 100.0; S(5): 0.0	S2;	S97		4.59	0	0	3	635.9	1906	33.75	6240
LASPSGSTSSGLEVVAPEGTsAPGGGPGT LDDSATICR	TRIM28	10155	transcription intermediary factor 1-beta	C37(Carbamido methyl) T20(Phospho)	S(3): 0.3; S(5): 0.3; S(7): 5.2; T(8): 0.3; S(9): 0.3; S(10): 5.2; T(20): 83.0; S(21): 5.2; T(29): 0.0; S(33): 0.0; T(35): 0.0	T20;	T611	19		0	0	3	1214	3639	78.67	15857
LASPSGSTSSGLEVVAPEGTsAPGGGPGT LDDSATICR	TRIM28	10155	transcription intermediary factor 1-beta	C37(Carbamido methyl) T20(Phospho)	S(3): 0.3; S(5): 0.3; S(7): 5.2; T(8): 0.3; S(9): 0.3; S(10): 5.2; T(20): 83.0; S(21): 5.2; T(29): 0.0; S(33): 0.0; T(35): 0.0	T20;	T611		2.91	0	0	3	1214	3639	78.67	15857
TSYQPSsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 1.6; S(7): 98.4	S7;	S489	38		0	0	2	580.2	1159	21.41	3634
TSYQPSsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 1.9; S(7): 98.1	S7;	S489	36		0	0	2	580.2	1159	20.89	3524
TSYQPSsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 1.9; S(7): 98.1	S7;	S489		2.42	0	0	2	580.2	1159	20.89	3524
TSYQPSsPGR	TRIM29	23650	tripartite motif-containing protein 29	S7(Phospho)	T(1): 0.0; S(2): 0.0; Y(3): 0.0; S(6): 1.6; S(7): 98.4	S7;	S489		2.22	0	0	2	580.2	1159	21.41	3634
APsDSSLGTPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho)	S(3): 99.9; S(5): 0.1; S(6): 0.0; T(9): 0.0; S(11): 0.0	S3;	S296	36		0	0	3	641.3	1922	42.04	8001
APsDSsLGTSPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 100.0; S(5): 2.7; S(6): 97.3; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299	34		0	0	2	1001	2002	47.19	9116
APsDSsLGTSPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 96.9; S(5): 3.2; S(6): 99.9; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299	33		0	0	3	667.9	2002	47.63	9207
APsDSsLGTSPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 96.0; S(5): 4.2; S(6): 99.8; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299	20		0	0	3	667.9	2002	47.1	9097
APsDSsLGTSPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 96.9; S(5): 3.2; S(6): 99.9; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299		4.69	0	0	3	667.9	2002	47.63	9207
APsDSSLGTPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho)	S(3): 99.9; S(5): 0.1; S(6): 0.0; T(9): 0.0; S(11): 0.0	S3;	S296		3.75	0	0	3	641.3	1922	42.04	8001

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#
APsDSsLGTPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 96.0; S(5): 4.2; S(6): 99.8; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299		3.36	0	0	3	667.9	2002	47.1	9097
APsDSsLGTPSDGRPELR	TRIP10	9322	cdc42-interacting protein 4 isoform 2	S3(Phospho) S6(Phospho)	S(3): 100.0; S(5): 2.7; S(6): 97.3; T(9): 0.0; S(11): 0.0	S3; S6;	S296; S299		2.31	0.006	0	2	1001	2002	47.19	9116
DDSLDLsPQGR	TRIP12	9320	E3 ubiquitin-protein ligase TRIP12 isoform d	S7(Phospho)	S(3): 0.0; S(7): 100.0	S7;	S721	33		0	0	2	641.8	1283	51.7	10060
DDSLDLsPQGR	TRIP12	9320	E3 ubiquitin-protein ligase TRIP12 isoform d	S7(Phospho)	S(3): 0.0; S(7): 100.0	S7;	S721		2.11	0.003	0	2	641.8	1283	51.7	10060
EKGsPGQNDQELK	TRIT1	54802	tRNA dimethylallyltransferase, mitochondrial isoform 3	S4(Phospho)	S(4): 100.0	S4;	S373	25		0	1	2	755.3	1510	14.55	2176
EKGsPGQNDQELK	TRIT1	54802	tRNA dimethylallyltransferase, mitochondrial isoform 3	S4(Phospho)	S(4): 100.0	S4;	S373		3.05	0	1	2	755.3	1510	14.55	2176
KHsEEAEFTPLKCsPK	TWISTNB	221830	DNA-directed RNA polymerase I subunit RPA43	C14(Carbamido methyl)S3(Phospho) S15(Phospho)	S(3): 96.5; T(9): 3.5; S(15): 100.0	S3; S15;	S316; S328		4.76	0	2	3	715.6	2145	41.69	7927
KHsEEAEFTPLKCsPK	TWISTNB	221830	DNA-directed RNA polymerase I subunit RPA43	C14(Carbamido methyl)S3(Phospho) S15(Phospho)	S(3): 96.4; T(9): 3.6; S(15): 100.0	S3; S15;	S316; S328		4.03	0	2	3	715.6	2145	41.15	7814
RPEGPGAQAPSSsPR	TXLNA	200081	alpha-taxilin	S12(Phospho)	S(11): 2.3; S(12): 97.7	S12;	S515	30		0	0	2	743.8	1487	18.54	3030
RPEGPGAQAPSSsPR	TXLNA	200081	alpha-taxilin	S12(Phospho)	S(11): 2.3; S(12): 97.7	S12;	S515		3.71	0.001	0	2	743.8	1487	18.54	3030
NPSDSAVHsPFTK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 100.0; T(12): 0.0	S9;	S409	53		0	0	2	733.8	1467	30.27	5519
RYPSsISSSPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S7(Phospho)	Y(2): 1.6; S(4): 49.2; S(5): 49.2; S(7): 99.8; S(8): 0.0; S(9): 0.1; T(15): 0.0	S7;	S600	38		0	2	3	718.3	2153	44.86	8621
RYPSsISSSPQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S4(Phospho) S5(Phospho)	Y(2): 0.0; S(4): 88.9; S(5): 94.3; S(7): 5.6; S(8): 2.9; S(9): 8.2	S4; S5;	S597; S598	27		0	1	2	748.8	1497	29.15	5286
RYPSsISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	Y(2): 0.0; S(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.1; S(9): 99.9; T(15): 0.0	S9;	S602	27		0	2	3	691.7	2073	39.51	7466
STSAQMSPGSSDNQSSsPQPAQKQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S18(Phospho)	S(1): 33.3; T(2): 33.3; S(3): 33.3; S(8): 0.1; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.3; S(18): 99.7	S18;	S470	24		0	0	3	898	2692	37.05	6949
RYPSsISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	Y(2): 0.0; S(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.1; S(9): 99.9; T(15): 0.0	S9;	S602	22		0	2	3	691.7	2073	40.06	7585
RYPSsISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S5(Phospho)	Y(2): 0.3; S(4): 5.0; S(5): 94.4; S(7): 33.4; S(8): 33.4; S(9): 33.4; T(15): 0.0	S5;	S598	19		0	2	2	1077	2153	44.81	8606
STSAQMSPGSSDNQSSsPQPAQKQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S18(Phospho)	S(1): 0.0; T(2): 0.0; S(3): 0.0; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.2; S(18): 99.8	S18;	S470	13		0	0	3	871.4	2612	30.67	5603
YPSSISSsPQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S8(Phospho)	Y(1): 0.0; S(3): 0.0; S(4): 0.0; S(6): 1.9; S(7): 0.0; S(8): 98.1	S8;	S602	12		0	0	2	630.8	1261	30.64	5597
RYPSsISSSPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S7(Phospho)	Y(2): 1.6; S(4): 49.2; S(5): 49.2; S(7): 99.8; S(8): 0.0; S(9): 0.1; T(15): 0.0	S7;	S600		4.79	0	2	3	718.3	2153	44.86	8621

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#
STSA PQMSPGSSDNQSSsPQPAQQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S18(Phospho)	S(1): 33.3; T(2): 33.3; S(3): 33.3; S(8): 0.1; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.3; S(18): 99.7	S18;	S470		4.32	0	0	3	898	2692	37.05	6949
STSA PQMSPGSSDNQSSsPQPAQQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	M7(Oxidation)S11(Phospho)S18(Phospho)	S(1): 5.6; T(2): 5.6; S(3): 0.4; S(8): 5.6; S(11): 82.3; S(12): 0.0; S(16): 0.4; S(17): 6.4; S(18): 93.5	S11; S18;	S463; S470		4.16	0	0	3	903.4	2708	25.35	4466
NPSDSAVHsPFTK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	S(3): 0.0; S(5): 0.0; S(9): 100.0; T(12): 0.0	S9;	S409		3.92	0	0	2	733.8	1467	30.27	5519
STSA PQMSPGSSDNQSSsPQPAQQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S18(Phospho)	S(1): 0.0; T(2): 0.0; S(3): 0.0; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.2; S(18): 99.8	S18;	S470		3.91	0	0	3	871.4	2612	30.67	5603
RYPSISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	Y(2): 0.0; S(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.1; S(9): 99.9; T(15): 0.0	S9;	S602		3.46	0	2	3	691.7	2073	39.51	7466
RYPSISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S9(Phospho)	Y(2): 0.0; S(4): 0.0; S(5): 0.0; S(7): 0.0; S(8): 0.1; S(9): 99.9; T(15): 0.0	S9;	S602		3.14	0	2	3	691.7	2073	40.06	7585
YPSISSsPQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S8(Phospho)	Y(1): 0.0; S(3): 0.0; S(4): 0.0; S(6): 1.9; S(7): 0.0; S(8): 98.1	S8;	S602		2.69	0	0	2	630.8	1261	30.64	5597
sTSA PQMSPGSSDNQSSsPQPAQQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S1(Phospho)	S(1): 92.1; T(2): 3.9; S(3): 3.9; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S1;	S453	19		0.001	0	2	1307	2612	31.59	5793
RYPSISSsPQKDLTQAK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S5(Phospho)	Y(2): 0.3; S(4): 5.0; S(5): 94.4; S(7): 33.4; S(8): 33.4; S(9): 33.4; T(15): 0.0	S5;	S598		2.37	0.001	2	2	1077	2153	44.81	8606
sTSA PQMSPGSSDNQSSsPQPAQQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S1(Phospho)	S(1): 92.1; T(2): 3.9; S(3): 3.9; S(8): 0.0; S(11): 0.0; S(12): 0.0; S(16): 0.0; S(17): 0.0; S(18): 0.0	S1;	S453		2.66	0.003	0	2	1307	2612	31.59	5793
RYPSISSsPQK	UBAP2L	9898	ubiquitin-associated protein 2-like isoform c	S4(Phospho)S5(Phospho)	Y(2): 0.0; S(4): 88.9; S(5): 94.3; S(7): 5.6; S(8): 2.9; S(9): 8.2	S4; S5;	S597; S598		3.39	0.005	1	2	748.8	1497	29.15	5286
QRsDDESPSTSSGSSDADQRDPAAPEPEEQEER	UBE2E3	10477	ubiquitin-conjugating enzyme E2 E3	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(12): 0.0; S(14): 0.0; S(15): 0.0	S3;	S8	18		0	2	3	1224	3669	29.27	5312
QRsDDESPSTSSGSSDADQRDPAAPEPEEQEER	UBE2E3	10477	ubiquitin-conjugating enzyme E2 E3	S3(Phospho)	S(3): 100.0; S(7): 0.0; S(9): 0.0; T(10): 0.0; S(11): 0.0; S(12): 0.0; S(14): 0.0; S(15): 0.0	S3;	S8		4.11	0	2	3	1224	3669	29.27	5312
LIHGEDsDsEGEEEGEGR	UBE2O	63893	(E3-independent) E2 ubiquitin-conjugating enzyme	S7(Phospho)S9(Phospho)	S(7): 100.0; S(9): 100.0	S7; S9;	S87; S89	45		0	0	2	959.8	1919	27.96	5035
LIHGEDsDsEGEEEGEGR	UBE2O	63893	(E3-independent) E2 ubiquitin-conjugating enzyme	S7(Phospho)S9(Phospho)	S(7): 100.0; S(9): 100.0	S7; S9;	S87; S89		4.02	0	0	2	959.8	1919	27.96	5035
SQSsEGVSSLSsSPsNSLETQSLSLR	UBE4B	10277	ubiquitin conjugation factor E4 B isoform 2	S4(Phospho)S15(Phospho)	S(1): 0.3; S(3): 4.5; S(4): 81.3; S(8): 4.7; S(9): 4.7; S(11): 4.7; S(12): 4.9; S(13): 4.9; S(15): 84.9; S(17): 4.7; T(20): 0.3; S(22): 0.0; S(24): 0.0; S(26): 0.0	S4; S15;	S79; S90	35		0	0	3	972.7	2916	65.91	13258

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#
SQsEGVSSLSsSPsNSLETQSQSLSR	UBE4B	10277	ubiquitin conjugation factor E4 B isoform 2	S4(Phospho) S15(Phospho)	S(1): 0.3; S(3): 4.5; S(4): 81.3; S(8): 4.7; S(9): 4.7; S(11): 4.7; S(12): 4.9; S(13): 4.9; S(15): 84.9; S(17): 4.7; T(20): 0.3; S(22): 0.0; S(24): 0.0; S(26): 0.0	S4; S15;	S79; S90		3.44	0	0	3	972.7	2916	65.91	13258
QAsEsEDDFIKEK	UBN1	29855	ubiquitin-1 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S173; S175	18		0	1	2	843.3	1686	46.98	9073
QAsEsEDDFIKEK	UBN1	29855	ubiquitin-1 isoform b	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S173; S175		2.79	0	1	2	843.3	1686	46.98	9073
ERDSELSDTDSGCCLGQSESDK	UHRF1	29128	E3 ubiquitin-protein ligase UHRF1 isoform 1	C13(Carbamido methyl) C14(Carbamido methyl) S7(Phospho)	S(4): 0.1; S(7): 99.9; T(9): 0.1; S(11): 0.0; S(18): 0.0; S(20): 0.0	S7;	S91	64		0	1	3	852.3	2555	36.32	6797
DsELSDTDSGCCLGQSESDK	UHRF1	29128	E3 ubiquitin-protein ligase UHRF1 isoform 1	C11(Carbamido methyl) C12(Carbamido methyl) S2(Phospho)	S(2): 97.4; S(5): 2.6; T(7): 0.0; S(9): 0.0; S(16): 0.0; S(18): 0.0	S2;	S88	40		0	0	2	1135	2270	46.37	8947
ERDSELSDTDSGCCLGQSESDK	UHRF1	29128	E3 ubiquitin-protein ligase UHRF1 isoform 1	C13(Carbamido methyl) C14(Carbamido methyl) S7(Phospho)	S(4): 0.1; S(7): 99.9; T(9): 0.1; S(11): 0.0; S(18): 0.0; S(20): 0.0	S7;	S91		6.12	0	1	3	852.3	2555	36.32	6797
DsELSDTDSGCCLGQSESDK	UHRF1	29128	E3 ubiquitin-protein ligase UHRF1 isoform 1	C11(Carbamido methyl) C12(Carbamido methyl) S2(Phospho)	S(2): 97.4; S(5): 2.6; T(7): 0.0; S(9): 0.0; S(16): 0.0; S(18): 0.0	S2;	S88		3.24	0	0	2	1135	2270	46.37	8947
TVsQQsFDGVSLDSSGPEDR	UHRF1BP1	54887	UHRF1-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 4.1; S(3): 95.9; S(6): 95.9; S(11): 4.1; S(14): 0.0; S(15): 0.0	S3; S6;	S1103; S1106	21		0	0	2	1136	2271	78.68	15858
TVsQQsFDGVSLDSSGPEDR	UHRF1BP1	54887	UHRF1-binding protein 1	S3(Phospho) S6(Phospho)	T(1): 4.1; S(3): 95.9; S(6): 95.9; S(11): 4.1; S(14): 0.0; S(15): 0.0	S3; S6;	S1103; S1106		2.19	0	0	2	1136	2271	78.68	15858
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 0.1; S(7): 99.9; S(10): 100.0	S7; S10;	S547; S550	31		0	0	4	1067	4264	56.81	11190
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 1.9; S(7): 99.0; S(10): 99.0	S7; S10;	S547; S550	18		0	0	4	1067	4264	57.36	11317
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 8.9; S(7): 91.2; S(10): 99.9	S7; S10;	S547; S550	11		0	0	3	1422	4264	56.42	11098
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 0.1; S(7): 99.9; S(10): 100.0	S7; S10;	S547; S550		4.89	0	0	4	1067	4264	56.81	11190
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 1.9; S(7): 99.0; S(10): 99.0	S7; S10;	S547; S550		3.3	0	0	4	1067	4264	57.36	11317
YLEEDNsDEsDAEGEHGDGAEEEEAPPA GPRPGPEPAGLGR	UNC93B1	81622	protein unc-93 homolog B1	S7(Phospho) S10(Phospho)	Y(1): 8.9; S(7): 91.2; S(10): 99.9	S7; S10;	S547; S550		2.58	0	0	3	1422	4264	56.42	11098
APAGQEEPGtPPsPLSAEQLDR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T10(Phospho) S14(Phospho)	T(10): 100.0; S(13): 3.6; S(14): 96.4; S(17): 0.0	T10; S14;	T60; S64	40		0	0	3	832	2494	67.37	13590
KAPAGQEEPGtPPsPLSAEQLDR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T11(Phospho) S15(Phospho)	T(11): 100.0; S(14): 0.2; S(15): 99.9; S(18): 0.0	T11; S15;	T60; S64	35		0	1	3	874.7	2622	56.07	11025
HAPsPEPAVQGTGVAGVPEESGDAAAI PAK	UNG	7374	uracil-DNA glycosylase isoform UNG2	S4(Phospho)	S(4): 100.0; T(12): 0.0; S(21): 0.0	S4;	S23	33		0	0	3	964.1	2890	56.85	11199
KAPAGQEEPGtPPsPLSAEQLDR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T11(Phospho) S15(Phospho)	T(11): 99.9; S(14): 3.8; S(15): 96.4; S(18): 0.0	T11; S15;	T60; S64	22		0	1	3	874.7	2622	55.49	10902
HAPsPEPAVQGTGVAGVPEESGDAAAI PAK	UNG	7374	uracil-DNA glycosylase isoform UNG2	S4(Phospho)	S(4): 100.0; T(12): 0.0; S(21): 0.0	S4;	S23		6.29	0	0	3	964.1	2890	56.85	11199

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#
KAPAGQEEPGtPPsPLSAEQLDLR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T11(Phospho) S15(Phospho)	T(11): 100.0; S(14): 0.2; S(15): 99.9; S(18): 0.0	T11; S15;	T60; S64		6	0	1	3	874.7	2622	56.07	11025
KAPAGQEEPGtPPsPLSAEQLDLR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T11(Phospho) S15(Phospho)	T(11): 99.9; S(14): 3.8; S(15): 96.4; S(18): 0.0	T11; S15;	T60; S64		4.99	0	1	3	874.7	2622	55.49	10902
APAGQEEPGtPPsPLSAEQLDLR	UNG	7374	uracil-DNA glycosylase isoform UNG2	T10(Phospho) S14(Phospho)	T(10): 100.0; S(13): 3.6; S(14): 96.4; S(17): 0.0	T10; S14;	T60; S64		4.37	0	0	3	832	2494	67.37	13590
SQIDVALsQDsTYQGER	UPF1	5976	regulator of nonsense transcripts 1 isoform 2	S8(Phospho) S11(Phospho)	S(1): 0.0; S(8): 100.0; S(11): 94.6; T(12): 2.7; Y(13): 2.7	S8; S11;	S1096; S1099	32		0	0	2	1029	2057	66.35	13358
SQIDVALsQDsTYQGER	UPF1	5976	regulator of nonsense transcripts 1 isoform 2	S8(Phospho) S11(Phospho)	S(1): 0.0; S(8): 100.0; S(11): 94.6; T(12): 2.7; Y(13): 2.7	S8; S11;	S1096; S1099		2.99	0	0	2	1029	2057	66.35	13358
LLTEISSAVFILTDNIsKK	URGCP	55665	up-regulator of cell proliferation isoform 2	S17(Phospho)	T(3): 66.6; S(6): 66.6; S(7): 66.6; T(13): 7.4; S(17): 92.7	S17;	S323		2.85	0.005	1	3	778	2332	33.41	6171
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 0.0; S(16): 100.0	S16;	S576	77		0	0	3	1036	3107	50.74	9860
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 3.4; S(16): 96.6	S16;	S576	33		0	0	3	1036	3107	50.2	9747
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 0.0; S(16): 100.0	S16;	S576	29		0	0	3	1036	3107	51.25	9968
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 0.0; S(16): 100.0	S16;	S576		6.49	0	0	3	1036	3107	50.74	9860
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 0.0; S(16): 100.0	S16;	S576		4.02	0	0	3	1036	3107	51.25	9968
NHVSNEEEQEEQGEsEDEWEQVGPR	USP10	9100	ubiquitin carboxyl-terminal hydrolase 10 isoform 2	S16(Phospho)	S(3): 3.4; S(16): 96.6	S16;	S576		3.71	0	0	3	1036	3107	50.2	9747
GPStPKKPLEQSC	USP15	9958	ubiquitin carboxyl-terminal hydrolase 15 isoform 3	C13(Carbamidomethyl) T4(Phospho)	S(3): 2.2; T(4): 97.8; S(12): 0.0	T4;	T226		2.64	0	1	2	754.8	1509	21.32	3615
KTVEDEDQDsEEKDNDSYIK	USP16	10600	ubiquitin carboxyl-terminal hydrolase 16 isoform b	S10(Phospho)	T(2): 0.0; S(10): 100.0; S(18): 0.0; Y(19): 0.0	S10;	S414	37		0	2	3	866	2596	29.51	5362
KTVEDEDQDsEEKDNDSYIK	USP16	10600	ubiquitin carboxyl-terminal hydrolase 16 isoform b	S10(Phospho)	T(2): 0.0; S(10): 100.0; S(18): 0.0; Y(19): 0.0	S10;	S414		5.2	0	2	3	866	2596	29.51	5362
TVEDEDQDsEEKDNDSYIK	USP16	10600	ubiquitin carboxyl-terminal hydrolase 16 isoform b	S9(Phospho)	T(1): 0.0; S(9): 100.0; S(17): 0.0; Y(18): 0.0	S9;	S414		3.65	0	1	3	823.3	2468	35.42	6607
AVPIAIAVEGEsEsEDDDLKPR	USP20	10868	ubiquitin carboxyl-terminal hydrolase 20	S12(Phospho) S14(Phospho)	S(12): 100.0; S(14): 100.0	S12; S14;	S132; S134	42		0	0	3	834.7	2502	65.45	13149
SSsPCrTPEPDNDAHLR	USP20	10868	ubiquitin carboxyl-terminal hydrolase 20	C5(Carbamidomethyl)S3(Phospho) T7(Phospho)	S(1): 2.5; S(2): 0.1; S(3): 97.5; T(7): 100.0	S3; T7;	S373; T377	37		0	1	3	700.3	2099	26.42	4696
SSsPCrTPEPDNDAHLR	USP20	10868	ubiquitin carboxyl-terminal hydrolase 20	C5(Carbamidomethyl)S3(Phospho) T7(Phospho)	S(1): 2.5; S(2): 0.1; S(3): 97.5; T(7): 100.0	S3; T7;	S373; T377		5.13	0	1	3	700.3	2099	26.42	4696
AVPIAIAVEGEsEsEDDDLKPR	USP20	10868	ubiquitin carboxyl-terminal hydrolase 20	S12(Phospho) S14(Phospho)	S(12): 100.0; S(14): 100.0	S12; S14;	S132; S134		3.89	0	0	3	834.7	2502	65.45	13149
AVPIAIAVEGEsEsEDDDLKPR	USP20	10868	ubiquitin carboxyl-terminal hydrolase 20	S12(Phospho) S14(Phospho)	S(12): 100.0; S(14): 100.0	S12; S14;	S132; S134		1.6	0.005	0	2	1252	2502	65.72	13212
VSDQNspVLPK	USP24	23358	ubiquitin carboxyl-terminal hydrolase 24	S6(Phospho)	S(2): 0.0; S(6): 100.0	S6;	S2047	56		0	0	2	632.3	1264	36.88	6915
VSDQNspVLPK	USP24	23358	ubiquitin carboxyl-terminal hydrolase 24	S6(Phospho)	S(2): 0.0; S(6): 100.0	S6;	S2047		3.58	0	0	2	632.3	1264	36.88	6915
AVsPAPQSSSR	USP36	57602	ubiquitin carboxyl-terminal hydrolase 36	S3(Phospho)	S(3): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0	S3;	S742	42		0	0	2	583.8	1167	15.92	2465
AVsPAPQSSSR	USP36	57602	ubiquitin carboxyl-terminal hydrolase 36	S3(Phospho)	S(3): 100.0; S(8): 0.0; S(9): 0.0; S(10): 0.0	S3;	S742		2.83	0	0	2	583.8	1167	15.92	2465

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#
EREVDEdSEPEREVR	USP39	10713	U4/U6.U5 tri-snRNP-associated protein 2 isoform 2	S8(Phospho)	S(8): 100.0	S8;	S82		3.15	0.006	2	3	651.9	1954	24.37	4258
HQQDsDLsAACsDADLHR	USP42	84132	ubiquitin carboxyl-terminal hydrolase 42	C11(Carbamido methyl)S5(Phospho) S8(Phospho) S12(Phospho)	S(5): 100.0; S(8): 100.0; S(12): 100.0	S5; S8; S12;	S1219; S1222; S1226	34		0	0	3	755.9	2266	43.29	8262
GPPEDRDAEPQPGsPAAESLEEPDAAA GLSSTK	USP42	84132	ubiquitin carboxyl-terminal hydrolase 42	S14(Phospho)	S(14): 95.8; S(19): 4.2; S(30): 0.0; S(31): 0.0; T(32): 0.0	S14;	S754	10		0	1	3	1120	3356	57.72	11391
HQQDsDLsAACsDADLHR	USP42	84132	ubiquitin carboxyl-terminal hydrolase 42	C11(Carbamido methyl)S5(Phospho) S8(Phospho) S12(Phospho)	S(5): 100.0; S(8): 100.0; S(12): 100.0	S5; S8; S12;	S1219; S1222; S1226		4.69	0	0	3	755.9	2266	43.29	8262
GPPEDRDAEPQPGsPAAESLEEPDAAA GLSSTK	USP42	84132	ubiquitin carboxyl-terminal hydrolase 42	S14(Phospho)	S(14): 95.8; S(19): 4.2; S(30): 0.0; S(31): 0.0; T(32): 0.0	S14;	S754		3.88	0	1	3	1120	3356	57.72	11391
SYsSPDITQAIQEEK	USP8	9101	ubiquitin carboxyl-terminal hydrolase 8 isoform b	S3(Phospho)	S(1): 2.7; Y(2): 2.7; S(3): 91.8; S(4): 2.7; T(8): 0.0	S3;	S612	21		0	0	2	952.9	1905	67.85	13701
SYsSPDITQAIQEEK	USP8	9101	ubiquitin carboxyl-terminal hydrolase 8 isoform b	S3(Phospho)	S(1): 2.7; Y(2): 2.7; S(3): 91.8; S(4): 2.7; T(8): 0.0	S3;	S612		2.65	0	0	2	952.9	1905	67.85	13701
DYLLsEsEDEGDNDGER	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31	51		0	0	2	1052	2103	73.62	14885
DYLLsEsEDEGDNDGER	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31	26		0	0	2	1052	2103	73.08	14784
DYLLsEsEDEGDNDGERK	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31	21		0	1	3	744.3	2231	55.42	10888
DYLLsEsEDEGDNDGERK	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31		3.88	0	1	3	744.3	2231	55.42	10888
DYLLsEsEDEGDNDGER	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31		2.86	0	0	2	1052	2103	73.62	14885
DYLLsEsEDEGDNDGER	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31		2.29	0	0	2	1052	2103	73.08	14784
DYLLsEsEDEGDNDGERK	UTP14A	10813	U3 small nucleolar RNA-associated protein 14 homolog A isoform 2	S5(Phospho) S7(Phospho)	Y(2): 0.0; S(5): 100.0; S(7): 100.0	S5; S7;	S29; S31		2.16	0	1	2	1116	2231	55.59	10924
KTsSDDesEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S4(Phospho) S8(Phospho)	T(2): 0.1; S(3): 2.9; S(4): 97.1; S(8): 100.0	S4; S8;	S206; S210	64		0	1	2	1136	2271	50.92	9900
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	50		0	0	2	1031	2062	26.87	4793
tsSDDesEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	T1(Phospho) S2(Phospho)	T(1): 99.9; S(2): 99.9; S(3): 0.2; S(7): 0.0	T1; S2;	T204; S205	47		0	0	2	1072	2143	66.96	13499
KtsSDDesEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	T2(Phospho) S3(Phospho) S8(Phospho)	T(2): 100.0; S(3): 96.0; S(4): 4.1; S(8): 100.0	T2; S3; S8;	T204; S205; S210	47		0	1	3	784.3	2351	64.02	12815
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	35		0	0	3	687.9	2062	26.87	4794
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	20		0	0	2	1031	2062	27.1	4844
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	20		0	0	2	1031	2062	27.42	4922

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#
KTSSDDEsEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S3(Phospho) S8(Phospho)	T(2): 51.3; S(3): 97.4; S(4): 51.3; S(8): 100.0	S3; S8;	S205; S210	18		0	1	2	1176	2351	63.93	12793
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		6.88	0	0	3	687.9	2062	26.87	4794
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		4.88	0	0	2	1031	2062	27.1	4844
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		4.75	0	0	2	1031	2062	26.87	4793
KTSSDDEsEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S4(Phospho) S8(Phospho)	T(2): 0.1; S(3): 2.9; S(4): 97.1; S(8): 100.0	S4; S8;	S206; S210		4.39	0	1	2	1136	2271	50.92	9900
KtsSDDEsEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	T2(Phospho) S3(Phospho) S8(Phospho)	T(2): 100.0; S(3): 96.0; S(4): 4.1; S(8): 100.0	T2; S3; S8;	T204; S205; S210		3.93	0	1	3	784.3	2351	64.02	12815
tsSDDESEEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	T1(Phospho) S2(Phospho)	T(1): 99.9; S(2): 99.9; S(3): 0.2; S(7): 0.0	T1; S2;	T204; S205		3.26	0	0	2	1072	2143	66.96	13499
KTSSDDEsEEDEDDLQR	UTP18	51096	U3 small nucleolar RNA-associated protein 18 homolog	S3(Phospho) S8(Phospho)	T(2): 51.3; S(3): 97.4; S(4): 51.3; S(8): 100.0	S3; S8;	S205; S210		2.95	0	1	2	1176	2351	63.93	12793
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		2.7	0.001	0	2	1031	2062	27.42	4922
TSAAACAVTDLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.2; S(12): 99.8; S(15): 100.0	S12; S15;	S365; S368	39		0	1	3	826.3	2477	58.26	11501
TSAAACAVTDLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.0; S(12): 100.0; S(15): 100.0	S12; S15;	S365; S368	30		0	1	3	826.3	2477	57.72	11389
TSAAACAVTDLSDDsDFDEK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.0; S(12): 100.0; S(15): 100.0	S12; S15;	S365; S368	26		0	0	2	1139	2278	69.57	14079
TSAAACAVtLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)T9(Phospho) S15(Phospho)	T(1): 0.3; S(2): 0.3; T(9): 94.5; S(12): 4.9; S(15): 100.0	T9; S15;	T362; S368	22		0	1	2	1239	2477	57.8	11406
TSAAACAVTDLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.0; S(12): 100.0; S(15): 100.0	S12; S15;	S365; S368		5.22	0	1	3	826.3	2477	57.72	11389
TSAAACAVTDLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.2; S(12): 99.8; S(15): 100.0	S12; S15;	S365; S368		4.78	0	1	3	826.3	2477	58.26	11501
TSAAACAVTDLSDDsDFDEK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)S12(Phospho) S15(Phospho)	T(1): 0.0; S(2): 0.0; T(9): 0.0; S(12): 100.0; S(15): 100.0	S12; S15;	S365; S368		3.79	0	0	2	1139	2278	69.57	14079
TSAAACAVtLSDDsDFDEKAK	UTP3	57050	something about silencing protein 10	C6(Carbamidomethyl)T9(Phospho) S15(Phospho)	T(1): 0.3; S(2): 0.3; T(9): 94.5; S(12): 4.9; S(15): 100.0	T9; S15;	T362; S368		3.22	0	1	2	1239	2477	57.8	11406
ASSRsPVFTPR	VAV2	7410	guanine nucleotide exchange factor VAV2 isoform 2	S5(Phospho)	S(2): 50.0; S(3): 50.0; S(5): 100.0; T(9): 0.0	S5;	S771	30		0	1	2	682.8	1365	39.24	7409
ASSRsPVFTPR	VAV2	7410	guanine nucleotide exchange factor VAV2 isoform 2	S5(Phospho)	S(2): 50.0; S(3): 50.0; S(5): 100.0; T(9): 0.0	S5;	S771		2.96	0	1	2	682.8	1365	39.24	7409
SREssPSHGLLK	VCPIP1	80124	deubiquitinating protein VCIP135	S4(Phospho) S5(Phospho)	S(1): 0.1; S(4): 99.9; S(5): 99.9; S(7): 0.1	S4; S5;	S997; S998	25		0	1	2	729.3	1458	28.51	5152
SREssPSHGLLK	VCPIP1	80124	deubiquitinating protein VCIP135	S4(Phospho) S5(Phospho)	S(1): 0.1; S(4): 99.9; S(5): 99.9; S(7): 0.1	S4; S5;	S997; S998		3.77	0	1	2	729.3	1458	28.51	5152

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#
SLYASSPGGVYATR	VIM	7431	vimentin	S6(Phospho)	S(1): 0.0; Y(3): 0.0; S(5): 0.1; S(6): 99.8; Y(11): 0.1; T(13): 0.0	S6;	S56	40		0	0	2	754.8	1509	53.98	10580
SLYASSPGGVYATR	VIM	7431	vimentin	S6(Phospho)	S(1): 0.0; Y(3): 0.0; S(5): 0.1; S(6): 99.8; Y(11): 0.1; T(13): 0.0	S6;	S56		2.72	0	0	2	754.8	1509	53.98	10580
EVQDKDYPLTPPPsPTVDEPK	VPS13D	55187	vacuolar protein sorting-associated protein 13D isoform 2	T10(Phospho) S14(Phospho)	Y(7): 0.1; T(10): 99.9; S(14): 96.9; T(16): 3.1	T10; S14;	T1761; S1765	14		0	1	3	838	2512	60.52	11983
EVQDKDYPLTPPPsPTVDEPK	VPS13D	55187	vacuolar protein sorting-associated protein 13D isoform 2	T10(Phospho) S14(Phospho)	Y(7): 0.1; T(10): 99.9; S(14): 96.9; T(16): 3.1	T10; S14;	T1761; S1765		4.86	0	1	3	838	2512	60.52	11983
EGQSPADEKGNDS DGEGESDDPEK	VPS4B	9525	vacuolar protein sorting-associated protein 4B	S14(Phospho)	S(5): 0.1; S(14): 99.9; S(20): 0.0	S14;	S102	29		0	1	3	890.3	2669	22.85	3942
EGQSPADEKGNDS DGEGESDDPEKK	VPS4B	9525	vacuolar protein sorting-associated protein 4B	S14(Phospho)	S(5): 0.0; S(14): 99.7; S(20): 0.3	S14;	S102		3.69	0	2	3	933	2797	19.06	3139
EGQSPADEKGNDS DGEGESDDPEK	VPS4B	9525	vacuolar protein sorting-associated protein 4B	S14(Phospho)	S(5): 0.1; S(14): 99.9; S(20): 0.0	S14;	S102		3.52	0	1	3	890.3	2669	22.85	3942
GsSPGIQDTLEAEDGAFETDEAPEDR	WDR3	10885	WD repeat-containing protein 3	S2(Phospho)	S(2): 89.2; S(3): 5.2; T(9): 5.2; T(19): 0.3	S2;	S240	25		0	0	3	939.4	2816	77.01	15545
GsSPGIQDTLEAEDGAFETDEAPEDR	WDR3	10885	WD repeat-containing protein 3	S2(Phospho)	S(2): 89.2; S(3): 5.2; T(9): 5.2; T(19): 0.3	S2;	S240		2.79	0	0	3	939.4	2816	77.01	15545
LQAKESQQR	WDR43	23160	WD repeat-containing protein 43	S6(Phospho)	S(6): 100.0	S6;	S77	39		0	1	2	568.8	1137	12.63	1764
LQAKESQQR	WDR43	23160	WD repeat-containing protein 43	S6(Phospho)	S(6): 100.0	S6;	S77		3.36	0	1	2	568.8	1137	12.63	1764
TKEYVSNDAAsDDEEKLQSQTDTDG GR	WDR44	54521	WD repeat-containing protein 44 isoform 3	S12(Phospho)	T(1): 0.0; Y(4): 0.0; S(6): 0.0; S(12): 100.0; S(20): 0.0; T(23): 0.0; T(25): 0.0	S12;	S378	59		0	2	3	1089	3264	35.39	6601
EYVSNDAAsDDEEKLQSQTDTDGGR	WDR44	54521	WD repeat-containing protein 44 isoform 3	S10(Phospho)	Y(2): 0.2; S(4): 4.0; S(10): 95.8; S(18): 0.0; T(21): 0.0; T(23): 0.0	S10;	S378	36		0	1	3	1012	3035	39.98	7568
TKEYVSNDAAsDDEEKLQSQTDTDG GR	WDR44	54521	WD repeat-containing protein 44 isoform 3	S12(Phospho)	T(1): 0.0; Y(4): 0.0; S(6): 0.0; S(12): 100.0; S(20): 0.0; T(23): 0.0; T(25): 0.0	S12;	S378		4.79	0	2	3	1089	3264	35.39	6601
EYVSNDAAsDDEEKLQSQTDTDGGR	WDR44	54521	WD repeat-containing protein 44 isoform 3	S10(Phospho)	Y(2): 0.2; S(4): 4.0; S(10): 95.8; S(18): 0.0; T(21): 0.0; T(23): 0.0	S10;	S378		4.07	0	1	3	1012	3035	39.98	7568
TCEERPAEDGsDEEDPDSMEAPTR	WDR55	54853	WD repeat-containing protein 55	C2(Carbamidomethyl) S11(Phospho)	T(1): 0.0; S(11): 100.0; S(18): 0.0; T(23): 0.0	S11;	S14	58		0	0	3	935	2803	37.57	7058
TCEERPAEDGsDEEDPDSMEAPTR	WDR55	54853	WD repeat-containing protein 55	C2(Carbamidomethyl) M19(Oxidation) S11(Phospho)	T(1): 0.1; S(11): 99.9; S(18): 0.0; T(23): 0.0	S11;	S14	32		0	0	3	940.3	2819	28.81	5214
TCEERPAEDGsDEEDPDSMEAPTR	WDR55	54853	WD repeat-containing protein 55	C2(Carbamidomethyl) M19(Oxidation) S11(Phospho)	T(1): 0.1; S(11): 99.9; S(18): 0.0; T(23): 0.0	S11;	S14		4.55	0	0	3	940.3	2819	28.81	5214
TCEERPAEDGsDEEDPDSMEAPTR	WDR55	54853	WD repeat-containing protein 55	C2(Carbamidomethyl) S11(Phospho)	T(1): 0.0; S(11): 100.0; S(18): 0.0; T(23): 0.0	S11;	S14		4.48	0	0	3	935	2803	37.57	7058
EIPEDVDMEEKEsEDsDEENDFTEK	WDR75	84128	WD repeat-containing protein 75 isoform 2	S14(Phospho) S17(Phospho)	S(14): 100.0; S(17): 100.0; T(24): 0.0	S14; S17;	S715; S718		2.89	0.005	1	3	1093	3277	65.77	13225
EIPEDVDMEEKEsEDsDEENDFTEK	WDR75	84128	WD repeat-containing protein 75 isoform 2	M8(Oxidation) S14(Phospho) S17(Phospho)	S(14): 100.0; S(17): 100.0; T(24): 0.0	S14; S17;	S715; S718		2.48	0.005	1	3	1098	3293	58.79	11638

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#
DVDDGSGSPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S11(Phospho)	S(6): 0.0; S(8): 0.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S11;	S1784	43		0	0	3	643.9	1930	20.16	3370
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S8(Phospho) S11(Phospho)	S(6): 0.1; S(8): 99.9; S(11): 100.0; S(16): 0.0; S(17): 0.0	S8; S11;	S1781; S1784	38		0	0	2	1005	2010	22.63	3894
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S8(Phospho) S11(Phospho)	S(6): 0.1; S(8): 99.9; S(11): 100.0; S(16): 0.0; S(17): 0.0	S8; S11;	S1781; S1784	35		0	0	3	670.6	2010	22.53	3872
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho) S11(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S6; S8; S11;	S1779; S1781; S1784	29		0	0	3	697.2	2090	26.75	4771
DVDDGSGsPHSPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 0.0; S(16): 0.0; S(17): 0.0	S6; S8;	S1779; S1781	25		0	0	3	670.6	2010	23.09	3993
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho) S11(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S6; S8; S11;	S1779; S1781; S1784	17		0	0	2	1045	2090	26.84	4788
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho) S11(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S6; S8; S11;	S1779; S1781; S1784		5.3	0	0	3	697.2	2090	26.75	4771
DVDDGSGSPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S11(Phospho)	S(6): 0.0; S(8): 0.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S11;	S1784		5.23	0	0	3	643.9	1930	20.16	3370
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S8(Phospho) S11(Phospho)	S(6): 0.1; S(8): 99.9; S(11): 100.0; S(16): 0.0; S(17): 0.0	S8; S11;	S1781; S1784		5.22	0	0	3	670.6	2010	22.53	3872
DVDDGSGsPHSPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 0.0; S(16): 0.0; S(17): 0.0	S6; S8;	S1779; S1781		4.33	0	0	3	670.6	2010	23.09	3993
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S8(Phospho) S11(Phospho)	S(6): 0.1; S(8): 99.9; S(11): 100.0; S(16): 0.0; S(17): 0.0	S8; S11;	S1781; S1784		3.45	0	0	2	1005	2010	22.63	3894
DVDDGSGsPHsPHQLSSK	WNK1	65125	serine/threonine-protein kinase WNK1 isoform 2	S6(Phospho) S8(Phospho) S11(Phospho)	S(6): 100.0; S(8): 100.0; S(11): 100.0; S(16): 0.0; S(17): 0.0	S6; S8; S11;	S1779; S1781; S1784		2.73	0	0	2	1045	2090	26.84	4788
VDKETNTETPAPsPTVVRPK	WWC1	23286	protein KIBRA isoform 3	S13(Phospho)	T(5): 33.3; T(7): 33.3; T(9): 33.3; S(13): 100.0; T(15): 0.0	S13;	S899	20		0	1	3	776	2326	33.66	6222
VDKETNTETPAPsPTVVRPK	WWC1	23286	protein KIBRA isoform 3	S13(Phospho)	T(5): 33.3; T(7): 33.3; T(9): 33.3; S(13): 100.0; T(15): 0.0	S13;	S899		5.26	0	1	3	776	2326	33.66	6222
yAGLDDTDESELPpGWEER	WWOX	51741	WW domain-containing oxidoreductase isoform 2	Y1(Phospho)	Y(1): 99.9; T(7): 50.1; S(9): 50.1	Y1;	Y6	27		0	0	2	1227	2454	93.19	18616
yAGLDDTDESELPpGWEER	WWOX	51741	WW domain-containing oxidoreductase isoform 2	Y1(Phospho)	Y(1): 99.9; T(7): 50.1; S(9): 50.1	Y1;	Y6		2.19	0	0	2	1227	2454	93.19	18616
TTPATGEQsPGAR	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	48		0	0	2	676.8	1353	16.91	2685
TTPATGEQsPGAR	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		3.38	0	0	2	676.8	1353	16.91	2685
SEAAAPHTDAGGGLsDEEEGTSSQAEAR	XPC	7508	DNA repair protein complementing XP-C cells	S15(Phospho) S16(Phospho)	S(1): 0.0; T(8): 0.0; S(15): 100.0; S(16): 100.0; T(22): 0.0; S(23): 0.0; S(24): 0.0	S15; S16;	S883; S884	64		0	0	3	1017	3048	41.84	7958
SEAAAPHTDAGGGLsDEEEGTSSQAEAR	XPC	7508	DNA repair protein complementing XP-C cells	S15(Phospho) S16(Phospho)	S(1): 0.0; T(8): 0.0; S(15): 100.0; S(16): 100.0; T(22): 0.0; S(23): 0.0; S(24): 0.0	S15; S16;	S883; S884	57		0	0	3	1017	3048	41.31	7847

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#
SEAAAPHTDAGGGLsDEEEGTSSQAEAR	XPC	7508	DNA repair protein complementing XP-C cells	S15(Phospho) S16(Phospho)	S(1): 0.0; T(8): 0.0; S(15): 100.0; S(16): 100.0; T(22): 0.0; S(23): 0.0; S(24): 0.0	S15; S16;	S883; S884		5.92	0	0	3	1017	3048	41.84	7958
SEAAAPHTDAGGGLsDEEEGTSSQAEAR	XPC	7508	DNA repair protein complementing XP-C cells	S15(Phospho) S16(Phospho)	S(1): 0.0; T(8): 0.0; S(15): 100.0; S(16): 100.0; T(22): 0.0; S(23): 0.0; S(24): 0.0	S15; S16;	S883; S884		5.23	0	0	3	1017	3048	41.31	7847
SKPsssEEDEGPQDKQEK	XPC	7508	DNA repair protein complementing XP-C cells	S4(Phospho) S5(Phospho) S6(Phospho)	S(1): 0.3; S(4): 99.7; S(5): 100.0; S(6): 100.0	S4; S5; S6;	S397; S398; S399		4.49	0	1	3	725.3	2174	14.63	2193
SKPsssEEDEGPQDKQEK	XPC	7508	DNA repair protein complementing XP-C cells	S4(Phospho) S5(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(5): 100.0; S(6): 100.0	S4; S5; S6;	S397; S398; S399		3.65	0	1	3	725.3	2174	15.45	2367
SEAAAPHTDAGGGLsDEEEGTSSQAEAR	XPC	7508	DNA repair protein complementing XP-C cells	S15(Phospho) S16(Phospho)	S(1): 0.0; T(8): 0.2; S(15): 80.2; S(16): 80.2; T(22): 18.6; S(23): 18.6; S(24): 2.4	S15; S16;	S883; S884		1.95	0.003	0	2	1525	3048	41.49	7885
AIGSTSKPQEsPK	XRCC1	7515	DNA repair protein XRCC1	S11(Phospho)	S(4): 0.0; T(5): 0.0; S(6): 0.0; S(11): 100.0	S11;	S241	52		0	0	2	705.3	1410	15.14	2301
TKPTQAAGPSSPQKPPTPEETK	XRCC1	7515	DNA repair protein XRCC1	T21(Phospho)	T(1): 0.0; T(4): 0.0; S(10): 50.0; S(11): 50.0; T(17): 0.1; T(21): 99.9	T21;	T457	19		0	0	3	813	2437	26.11	4631
TKPTQAAGPSsPQKPPtPEETK	XRCC1	7515	DNA repair protein XRCC1	S11(Phospho) T17(Phospho)	T(1): 0.1; T(4): 0.1; S(10): 2.9; S(11): 96.9; T(17): 97.1; T(21): 2.9	S11; T17;	S447; T453	18		0	0	4	610	2437	26	4606
TKPTQAAGPSSPQKPPTPEETK	XRCC1	7515	DNA repair protein XRCC1	T21(Phospho)	T(1): 0.0; T(4): 0.0; S(10): 50.0; S(11): 50.0; T(17): 0.1; T(21): 99.9	T21;	T457		5.91	0	0	3	813	2437	26.11	4631
AIGSTSKPQEsPK	XRCC1	7515	DNA repair protein XRCC1	S11(Phospho)	S(4): 0.0; T(5): 0.0; S(6): 0.0; S(11): 100.0	S11;	S241		3.88	0	0	2	705.3	1410	15.14	2301
TKPTQAAGPSsPQKPPPTPEETK	XRCC1	7515	DNA repair protein XRCC1	S11(Phospho)	T(1): 0.0; T(4): 0.0; S(10): 4.5; S(11): 90.8; T(17): 0.2; T(21): 4.5	S11;	S447		3.81	0	0	3	786.4	2357	24.5	4286
TKPtQAAGPSSPQKPPPTPEETK	XRCC1	7515	DNA repair protein XRCC1	T4(Phospho) T21(Phospho)	T(1): 0.2; T(4): 99.4; S(10): 0.2; S(11): 0.2; T(17): 4.0; T(21): 96.0	T4; T21;	T440; T457		3.49	0	0	3	813	2437	25.61	4521
EAQSSQATPVQTSQPDSSNIVKVsPR	XRN1	54464	5'-3' exoribonuclease 1 isoform c	S24(Phospho)	S(4): 0.0; S(5): 0.0; T(8): 0.0; T(12): 0.0; S(13): 0.0; S(17): 0.0; S(18): 0.0; S(24): 100.0	S24;	S1633	11		0	1	3	941.1	2821	47.23	9124
EAQSSQATPVQTSQPDSSNIVKVsPR	XRN1	54464	5'-3' exoribonuclease 1 isoform c	S24(Phospho)	S(4): 0.0; S(5): 0.0; T(8): 0.0; T(12): 0.0; S(13): 0.0; S(17): 0.0; S(18): 0.0; S(24): 100.0	S24;	S1633		3.79	0.001	1	3	941.1	2821	47.23	9124
NsPGSQVASNPR	XRN2	22803	5'-3' exoribonuclease 2	S2(Phospho)	S(2): 100.0; S(5): 0.0; S(9): 0.0	S2;	S448	77		0	0	2	647.3	1294	19.26	3181
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	48		0	1	2	988.9	1977	27.87	5016
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	43		0	1	2	988.9	1977	28.37	5123
RKAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S499; S501	43		0	2	3	711.6	2133	22.32	3827
AEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S499; S501	40		0	0	2	924.8	1849	38.62	7277
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	37		0	1	3	659.6	1977	28.01	5046
RKAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S499; S501	31		0	2	2	1067	2133	22.42	3849
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501	24		0	1	2	988.9	1977	27.93	5029

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#
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		5.09	0	1	2	988.9	1977	27.87	5016
RKAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S499; S501		5.02	0	2	3	711.6	2133	22.32	3827
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		4.75	0	1	2	988.9	1977	28.37	5123
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		4.43	0	1	3	659.6	1977	28.01	5046
KAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S5(Phospho) S7(Phospho)	S(5): 100.0; S(7): 100.0	S5; S7;	S499; S501		4	0	1	2	988.9	1977	27.93	5029
NsPGSQVASNPR	XRN2	22803	5'-3' exoribonuclease 2	S2(Phospho)	S(2): 100.0; S(5): 0.0; S(9): 0.0	S2;	S448		3.89	0	0	2	647.3	1294	19.26	3181
AEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S4(Phospho) S6(Phospho)	S(4): 100.0; S(6): 100.0	S4; S6;	S499; S501		3.53	0	0	2	924.8	1849	38.62	7277
RKAEDsDsEPEPEDNVR	XRN2	22803	5'-3' exoribonuclease 2	S6(Phospho) S8(Phospho)	S(6): 100.0; S(8): 100.0	S6; S8;	S499; S501		3.24	0	2	2	1067	2133	22.42	3849
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S9(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 96.2; S(11): 3.8; S(18): 0.0; S(20): 0.0	S9;	S165	50		0	1	3	1113	3337	27.09	4843
NEGSESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S6(Phospho)	S(4): 2.0; S(6): 98.0	S6;	S176	50		0	0	2	834.3	1668	16.45	2579
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S20(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 0.0; S(11): 0.0; S(18): 0.0; S(20): 100.0	S20;	S176	49		0	1	3	1113	3337	27.63	4966
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S18(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 3.6; S(11): 3.6; S(18): 89.2; S(20): 3.6	S18;	S174	33		0	1	4	835.1	3337	27.92	5026
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S20(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 2.6; S(11): 50.0; S(18): 50.0; S(20): 97.4	S20;	S176	32		0	1	3	1140	3417	31.1	5690
NEGSESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 100.0; S(6): 0.0	S4;	S174	32		0	0	2	834.3	1668	17.16	2740
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S9(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 96.2; S(11): 3.8; S(18): 0.0; S(20): 0.0	S9;	S165		5.79	0	1	3	1113	3337	27.09	4843
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S20(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 0.0; S(11): 0.0; S(18): 0.0; S(20): 100.0	S20;	S176		5.59	0	1	3	1113	3337	27.63	4966
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S18(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 3.6; S(11): 3.6; S(18): 89.2; S(20): 3.6	S18;	S174		5.13	0	1	4	835.1	3337	27.92	5026
NYQQNYQNSeSGEKNEGSESAPEGQA QQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S20(Phospho)	Y(2): 0.0; Y(6): 0.0; S(9): 2.6; S(11): 50.0; S(18): 50.0; S(20): 97.4	S20;	S176		4.03	0	1	3	1140	3417	31.1	5690
NEGSESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S4(Phospho)	S(4): 100.0; S(6): 0.0	S4;	S174		3.72	0	0	2	834.3	1668	17.16	2740
NEGSESAPEGQAQQR	YBX1	4904	nuclease-sensitive element-binding protein 1	S6(Phospho)	S(4): 2.0; S(6): 98.0	S6;	S176		3.14	0	0	2	834.3	1668	16.45	2579
NYAGEEEEEGsGSEGFDPPTDR	YBX3	8531	Y-box-binding protein 3 isoform a	S11(Phospho) S13(Phospho)	Y(2): 9.2; S(11): 90.8; S(13): 90.8; S(14): 9.2; T(22): 0.0	S11; S13;	S201; S203		1.63	0.001	0	2	1345	2690	62.49	12422
NYAGEEEEEGsGSEGFDPPTDR	YBX3	8531	Y-box-binding protein 3 isoform a	S11(Phospho) S13(Phospho)	Y(2): 9.2; S(11): 90.8; S(13): 90.8; S(14): 9.2; T(22): 0.0	S11; S13;	S201; S203	16		0.003	0	2	1345	2690	62.49	12422
SSsPTQYGLTK	ZAK	51776	mitogen-activated protein kinase kinase kinase MLT isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 98.5; T(5): 1.5; Y(7): 0.0; T(10): 0.0	S3;	S637	42		0	0	2	624.8	1249	36.8	6898

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#
SSsPTQYGLTK	ZAK	51776	mitogen-activated protein kinase kinase kinase MLT isoform 1	S3(Phospho)	S(1): 0.0; S(2): 0.0; S(3): 98.5; T(5): 1.5; Y(7): 0.0; T(10): 0.0	S3;	S637		2.41	0	0	2	624.8	1249	36.8	6898
VTDKDCNEstDNDELEDEPEEPFYR	ZBTB1	22890	zinc finger and BTB domain-containing protein 1 isoform 2	C6(Carbamidomethyl)S9(Phospho) T10(Phospho)	T(2): 0.2; S(9): 99.8; T(10): 100.0; Y(24): 0.0	S9; T10;	S355; T356	29		0	1	3	1069	3206	67.16	13542
VTDKDCNEstDNDELEDEPEEPFYR	ZBTB1	22890	zinc finger and BTB domain-containing protein 1 isoform 2	C6(Carbamidomethyl)S9(Phospho) T10(Phospho)	T(2): 0.2; S(9): 99.8; T(10): 100.0; Y(24): 0.0	S9; T10;	S355; T356		3.32	0	1	3	1069	3206	67.16	13542
SFsASQSTDREGAsPVTEVR	ZBTB21	49854	zinc finger and BTB domain-containing protein 21 isoform S	S3(Phospho) S14(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 0.0; S(7): 0.1; T(8): 3.3; S(14): 96.5; T(17): 0.0	S3; S14;	S411; S422		3.75	0	1	3	757.7	2271	47.32	9145
SFsASQSTDREGAsPVTEVR	ZBTB21	49854	zinc finger and BTB domain-containing protein 21 isoform S	S3(Phospho) S14(Phospho)	S(1): 0.1; S(3): 99.9; S(5): 0.0; S(7): 0.1; T(8): 3.3; S(14): 96.5; T(17): 0.0	S3; S14;	S411; S422	13		0.005	1	3	757.7	2271	47.32	9145
GGADPSPGATATPGAPAQSPDAR	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): 3.3; S(22): 96.7	S22;	S526	25		0	0	3	804	2410	43.79	8368
GGADPSPGATATPGAPAQSPDAR	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): 3.3; S(22): 96.7	S22;	S526		5.78	0	0	3	804	2410	43.79	8368
SLsPSHLTEDR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; T(8): 0.0	S3;	S877	56		0	0	2	661.3	1322	36.12	6755
sLsPSHLTEDR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 0.0; T(8): 0.0	S1; S3;	S875; S877	51		0	0	2	701.3	1402	46.97	9070
STsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho) S10(Phospho)	S(1): 2.1; T(2): 2.1; S(3): 95.7; S(10): 100.0; S(13): 0.0; S(14): 0.0	S3; S10;	S318; S325	39		0	0	3	570.2	1709	15.1	2291
GNIETTSsEDGQVFsPK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S7(Phospho) S14(Phospho)	T(5): 0.1; T(6): 0.1; S(7): 99.8; S(14): 100.0	S7; S14;	S986; S993	36		0	0	2	934.9	1869	61.28	12148
STsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho) S10(Phospho)	S(1): 2.5; T(2): 2.5; S(3): 95.1; S(10): 100.0; S(13): 0.0; S(14): 0.0	S3; S10;	S318; S325	33		0	0	2	854.8	1709	15.11	2294
sAsPYPSHLSsPQR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho) S12(Phospho)	S(1): 99.9; S(3): 99.9; Y(5): 0.2; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(12): 100.0	S1; S3; S12;	S370; S372; S381	25		0	0	2	920.8	1841	47.43	9166
sAsPYPSHLSsPQR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho) S12(Phospho)	S(1): 100.0; S(3): 100.0; Y(5): 0.0; S(7): 0.0; S(9): 0.0; S(11): 2.6; S(12): 97.4	S1; S3; S12;	S370; S372; S381	25		0	0	3	614.2	1841	47.7	9221
tPsPPPIPEDIALGK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	T1(Phospho) S3(Phospho)	T(1): 100.0; S(3): 100.0	T1; S3;	T263; S265	23		0	0	2	894.9	1789	94.8	18949
GPRTpSPPPPIPEDIALGK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T263; S265	15		0	1	3	700.3	2099	75.14	15185
DKPRsTsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S5(Phospho) S7(Phospho) S14(Phospho)	S(5): 99.9; T(6): 0.2; S(7): 99.9; S(14): 100.0; S(17): 0.0; S(18): 0.0	S5; S7; S14;	S316; S318; S325	10		0	1	3	762.3	2285	15.02	2276
GPRTpSPPPPIPEDIALGK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	T4(Phospho) S6(Phospho)	T(4): 100.0; S(6): 100.0	T4; S6;	T263; S265		4.69	0	1	3	700.3	2099	75.14	15185
STsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho) S10(Phospho)	S(1): 2.1; T(2): 2.1; S(3): 95.7; S(10): 100.0; S(13): 0.0; S(14): 0.0	S3; S10;	S318; S325		4.62	0	0	3	570.2	1709	15.1	2291
DKPRsTsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S5(Phospho) S7(Phospho) S14(Phospho)	S(5): 99.9; T(6): 0.2; S(7): 99.9; S(14): 100.0; S(17): 0.0; S(18): 0.0	S5; S7; S14;	S316; S318; S325		4.2	0	1	3	762.3	2285	15.02	2276

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#
sAsPYPSHSLsPQR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho) S12(Phospho)	S(1): 100.0; S(3): 100.0; Y(5): 0.0; S(7): 0.0; S(9): 0.0; S(11): 2.6; S(12): 97.4	S1; S3; S12;	S370; S372; S381		3.95	0	0	3	614.2	1841	47.7	9221
GNIETTSedGQVFsPK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S7(Phospho) S14(Phospho)	T(5): 0.1; T(6): 0.1; S(7): 99.8; S(14): 100.0	S7; S14;	S986; S993		3.48	0	0	2	934.9	1869	61.28	12148
sAsPYPSHSLsPQR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho) S12(Phospho)	S(1): 99.9; S(3): 99.9; Y(5): 0.2; S(7): 0.0; S(9): 0.0; S(11): 0.0; S(12): 100.0	S1; S3; S12;	S370; S372; S381		3.15	0	0	2	920.8	1841	47.43	9166
SLsPSHLTEDR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho)	S(1): 0.0; S(3): 100.0; S(5): 0.0; T(8): 0.0	S3;	S877		2.99	0	0	2	661.3	1322	36.12	6755
sLsPSHLTEDR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S1(Phospho) S3(Phospho)	S(1): 100.0; S(3): 100.0; S(5): 0.0; T(8): 0.0	S1; S3;	S875; S877		2.85	0	0	2	701.3	1402	46.97	9070
tPsPPPIPEDIALGK	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	T1(Phospho) S3(Phospho)	T(1): 100.0; S(3): 100.0	T1; S3;	T263; S265		2.65	0	0	2	894.9	1789	94.8	18949
STsPAGQHHSPISSR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S3(Phospho) S10(Phospho)	S(1): 2.5; T(2): 2.5; S(3): 95.1; S(10): 100.0; S(13): 0.0; S(14): 0.0	S3; S10;	S318; S325		2.7	0.001	0	2	854.8	1709	15.11	2294
SKLsPpsSLR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S4(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 99.9; S(8): 0.1	S4; S6;	S207; S209	15		0.005	1	2	616.3	1232	37	6940
SKLsPpsSLR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S4(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 99.9; S(8): 0.1	S4; S6;	S207; S209		2.73	0.005	1	2	616.3	1232	37	6940
SKLsPpsSLR	ZC3H13	23091	zinc finger CCCH domain-containing protein 13	S4(Phospho) S6(Phospho)	S(1): 0.0; S(4): 100.0; S(6): 100.0; S(8): 0.0	S4; S6;	S207; S209		2.08	0.005	1	2	616.3	1232	36.49	6833
DLVQDPKPApPK	ZC3H14	79882	zinc finger CCCH domain-containing protein 14 isoform 6	S10(Phospho)	S(10): 100.0	S10;	S515	38		0	0	2	687.8	1375	30.66	5600
DLVQDPKPApPK	ZC3H14	79882	zinc finger CCCH domain-containing protein 14 isoform 6	S10(Phospho)	S(10): 100.0	S10;	S515		4.25	0	0	2	687.8	1375	30.66	5600
NGDECAVHHPIsPCK	ZC3H14	79882	zinc finger CCCH domain-containing protein 14 isoform 6	C5(Carbamidomethyl) C14(Carbamidomethyl) S12(Phospho)	Y(7): 0.0; S(12): 100.0	S12;	S615		3.35	0.004	0	3	622.2	1865	24.39	4263
GPpQEEEDNHSDEEDRASEPKsQDQDS EVNELSR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S3(Phospho) S22(Phospho)	S(3): 100.0; S(11): 50.0; S(18): 50.0; S(22): 91.3; S(27): 8.7; S(33): 0.0	S3; S22;	S59; S78	40		0	2	4	1029	4113	38.52	7256
GPSQEEEDNHsDEEDRASEPK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S11(Phospho)	S(3): 4.1; S(11): 95.9; S(18): 0.0	S11;	S67	34		0	1	3	822.3	2465	17.54	2822
GPSQEEEDNHsDEEDRASePK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S11(Phospho) S18(Phospho)	S(3): 0.0; S(11): 100.0; S(18): 100.0	S11; S18;	S67; S74	31		0	1	3	849	2545	18.36	2993
DSGSQDLDGAGVRAsDLEDEESAAR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S16(Phospho)	S(2): 0.0; S(4): 0.0; S(16): 100.0; S(23): 0.0	S16;	S46	20		0	1	3	915.7	2745	58.52	11567
GPSQEEEDNHsDEEDRASEPK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S11(Phospho)	S(3): 4.1; S(11): 95.9; S(18): 0.0	S11;	S67		6.74	0	1	3	822.3	2465	17.54	2822
GPpQEEEDNHSDEEDRASEPKsQDQDS EVNELSR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S3(Phospho) S22(Phospho)	S(3): 100.0; S(11): 50.0; S(18): 50.0; S(22): 91.3; S(27): 8.7; S(33): 0.0	S3; S22;	S59; S78		4.78	0	2	4	1029	4113	38.52	7256
DSGSQDLDGAGVRAsDLEDEESAAR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S16(Phospho)	S(2): 0.0; S(4): 0.0; S(16): 100.0; S(23): 0.0	S16;	S46		4.64	0	1	3	915.7	2745	58.52	11567
GPTSSPCEEEGDEGEEDRTsDLRDEASSV TR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	C7(Carbamidomethyl) S20(Phospho)	T(3): 33.3; S(4): 33.3; S(5): 33.3; T(19): 6.5; S(20): 93.5; S(27): 0.0; S(28): 0.0; T(30): 0.0	S20;	S110		2.76	0	2	3	1186	3557	50.8	9874
GPpQEEEDNHsDEEDRASEPKsQDQDSE VNELSR	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S3(Phospho) S11(Phospho) S22(Phospho)	S(3): 99.9; S(11): 92.9; S(18): 14.1; S(22): 92.3; S(27): 0.7; S(33): 0.0	S3; S11; S22;	S59; S67; S78		2.66	0	2	3	1372	4113	38.35	7220
GPSQEEEDNHsDEEDRASePK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S11(Phospho) S18(Phospho)	S(3): 0.0; S(11): 100.0; S(18): 100.0	S11; S18;	S67; S74		6.22	0.001	1	3	849	2545	18.36	2993

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#
YEPSDKDRQsPPPAK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S10(Phospho)	Y(1): 0.0; S(4): 0.0; S(10): 100.0	S10;	S842	10		0.004	2	3	598.9	1795	15.3	2334
YEPSDKDRQsPPPAK	ZC3H18	124245	zinc finger CCCH domain-containing protein 18 isoform 2	S10(Phospho)	Y(1): 0.0; S(4): 0.0; S(10): 100.0	S10;	S842		3.4	0.005	2	3	598.9	1795	15.3	2334
AAKPGPAEAPSPTASPSGDAsPPATAPY DPR	ZC3H4	23211	zinc finger CCCH domain-containing protein 4	S21(Phospho)	S(11): 0.0; T(13): 0.0; S(15): 0.0; S(17): 4.8; S(21): 95.2; T(25): 0.0; Y(28): 0.0	S21;	S1114	18		0	0	3	1004	3011	49.18	9531
AAKPGPAEAPSPTASPSGDAsPPATAPY DPR	ZC3H4	23211	zinc finger CCCH domain-containing protein 4	S21(Phospho)	S(11): 48.3; T(13): 48.3; S(15): 9.8; S(17): 6.9; S(21): 86.7; T(25): 0.0; Y(28): 0.0	S21;	S1114	17		0	0	3	1031	3091	54.44	10682
AAKPGPAEAPSPTASPSGDAsPPATAPY DPR	ZC3H4	23211	zinc finger CCCH domain-containing protein 4	S21(Phospho)	S(11): 0.0; T(13): 0.0; S(15): 0.0; S(17): 4.8; S(21): 95.2; T(25): 0.0; Y(28): 0.0	S21;	S1114		4.02	0	0	3	1004	3011	49.18	9531
AAKPGPAEAPSPTASPSGDAsPPATAPY DPR	ZC3H4	23211	zinc finger CCCH domain-containing protein 4	S21(Phospho)	S(11): 48.3; T(13): 48.3; S(15): 9.8; S(17): 6.9; S(21): 86.7; T(25): 0.0; Y(28): 0.0	S21;	S1114		3.66	0	0	3	1031	3091	54.44	10682
tGSGSPFAGNsPAREGEQDAASLK	ZC3H4	23211	zinc finger CCCH domain-containing protein 4	T1(Phospho) S11(Phospho)	T(1): 99.5; S(3): 0.3; S(5): 0.3; S(11): 100.0; S(22): 0.0	T1; S11;	T1265; S1275		3.21	0.002	1	3	832	2494	55.62	10929
SKDYDVVsDNDICsQESEDNFAK	ZC3H8	84524	zinc finger CCCH domain-containing protein 8	C13(Carbamidomethyl) S8(Phospho)	S(1): 0.0; Y(4): 0.0; Y(7): 3.7; S(8): 96.1; S(14): 0.2; S(17): 0.0	S8;	S77	29		0	1	3	937	2809	56.37	11087
SKDYDVVsDNDICsQESEDNFAK	ZC3H8	84524	zinc finger CCCH domain-containing protein 8	C13(Carbamidomethyl) S8(Phospho)	S(1): 0.0; Y(4): 0.0; Y(7): 3.7; S(8): 96.1; S(14): 0.2; S(17): 0.0	S8;	S77		4.52	0	1	3	937	2809	56.37	11087
SCtPsPDQISHR	ZC3HAV1	56829	zinc finger CCCH-type antiviral protein 1 isoform 2	C2(Carbamidomethyl)T3(Phospho) S5(Phospho)	S(1): 0.0; T(3): 100.0; S(5): 100.0; S(10): 0.0	T3; S5;	T273; S275	47		0	0	2	772.8	1545	31.53	5780
SCtPsPDQISHR	ZC3HAV1	56829	zinc finger CCCH-type antiviral protein 1 isoform 2	C2(Carbamidomethyl)T3(Phospho) S5(Phospho)	S(1): 0.0; T(3): 100.0; S(5): 100.0; S(10): 0.0	T3; S5;	T273; S275		2.51	0	0	2	772.8	1545	31.53	5780
SQDATFsPGSEQAEKsPGPIVSR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho) S16(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 0.0; S(16): 100.0; S(22): 0.0	S7; S16;	S314; S323	43		0	1	3	845.7	2535	53.82	10543
SQDATFsPGSEQAEK	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 99.9; S(10): 0.1	S7;	S314	36		0	0	2	831.3	1662	34.73	6456
SQDATFsPGsEQAEKsPGPIVSR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho) S16(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 100.0; S(16): 100.0; S(22): 0.0	S7; S10; S16;	S314; S317; S323	17		0	1	3	872.4	2615	63.26	12625
SQDATFsPGSEQAEKsPGPIVSR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho) S16(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 0.0; S(16): 100.0; S(22): 0.0	S7; S16;	S314; S323		6.4	0	1	3	845.7	2535	53.82	10543
SQDATFsPGsEQAEKsPGPIVSR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho) S10(Phospho) S16(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 100.0; S(10): 100.0; S(16): 100.0; S(22): 0.0	S7; S10; S16;	S314; S317; S323		4.71	0	1	3	872.4	2615	63.26	12625
SQDATFsPGSEQAEKsPGPIVSR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S16(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 0.0; S(10): 0.0; S(16): 100.0; S(22): 0.0	S16;	S323		4.43	0	1	3	819	2455	47.01	9079
SQDATFsPGSEQAEK	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S7(Phospho)	S(1): 0.0; T(5): 0.0; S(7): 99.9; S(10): 0.1	S7;	S314		2.89	0	0	2	831.3	1662	34.73	6456

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SWDSSsPVD RPEE AASPTR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S6(Phospho)	S(1): 0.0; S(4): 0.1; S(5): 3.5; S(6): 96.4; S(17): 33.3; T(19): 33.3; T(20): 33.3	S6;	S338	19		0.002	0	3	811.3	2432	50.16	9737
SWDSSsPVD RPEE AASPTR	ZC3HC1	51530	nuclear-interacting partner of ALK isoform 2	S6(Phospho)	S(1): 0.0; S(4): 0.1; S(5): 3.5; S(6): 96.4; S(17): 33.3; T(19): 33.3; T(20): 33.3	S6;	S338		3.77	0.004	0	3	811.3	2432	50.16	9737
SLGSASPGGQPPLSsPTR	ZDHHC5	25921	palmitoyltransferase ZDHHC5	S16(Phospho)	S(1): 33.3; S(4): 33.3; S(6): 33.3; S(15): 3.8; S(16): 92.4; T(18): 3.8	S16;	S694		3.07	0	0	2	976.9	1953	61.19	12130
SLGSASPGGQPPLSsPTR	ZDHHC5	25921	palmitoyltransferase ZDHHC5	S16(Phospho)	S(1): 33.3; S(4): 33.3; S(6): 33.3; S(15): 3.8; S(16): 92.4; T(18): 3.8	S16;	S694	17		0.001	0	2	976.9	1953	61.19	12130
KPISDNFssDEEQSTGPIK	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S9(Phospho) S10(Phospho)	S(4): 0.0; S(7): 0.0; S(9): 100.0; S(10): 100.0; S(15): 0.0; T(16): 0.0	S9; S10;	S1303; S1304	59		0	0	3	776	2326	52.23	10189
TSSsSPANsDVEIDGIGR	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S4(Phospho) S9(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 3.0; S(4): 96.7; S(5): 0.1; S(9): 100.0	S4; S9;	S804; S809	50		0	0	2	976.4	1952	64.99	13049
KPISDNFssDEEQSTGPIK	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S9(Phospho) S10(Phospho)	S(4): 0.0; S(7): 0.2; S(9): 99.8; S(10): 100.0; S(15): 0.0; T(16): 0.0	S9; S10;	S1303; S1304	48		0	0	2	1163	2326	52.36	10217
KPISDNFssDEEQSTGPIK	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S9(Phospho) S10(Phospho)	S(4): 0.0; S(7): 0.0; S(9): 100.0; S(10): 100.0; S(15): 0.0; T(16): 0.0	S9; S10;	S1303; S1304		4.6	0	0	3	776	2326	52.23	10189
KPISDNFssDEEQSTGPIK	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S9(Phospho) S10(Phospho)	S(4): 0.0; S(7): 0.2; S(9): 99.8; S(10): 100.0; S(15): 0.0; T(16): 0.0	S9; S10;	S1303; S1304		3.5	0	0	2	1163	2326	52.36	10217
TSSsSPANsDVEIDGIGR	ZFC3H1	196441	zinc finger C3H1 domain-containing protein	S4(Phospho) S9(Phospho)	T(1): 0.1; S(2): 0.1; S(3): 3.0; S(4): 96.7; S(5): 0.1; S(9): 100.0	S4; S9;	S804; S809		2.69	0	0	2	976.4	1952	64.99	13049
RsSPSARPPDVP GQQPAAKsPsPVQG K	ZFP91	80829	E3 ubiquitin-protein ligase ZFP91 isoform 2	S3(Phospho) S21(Phospho) S23(Phospho)	S(2): 6.6; S(3): 93.0; S(5): 0.5; S(21): 100.0; S(23): 100.0	S3; S21; S23;	S83; S101; S103		4.1	0.004	2	3	1032	3094	34.96	6512
LPDsDDDEDEETAIQR	ZFYVE19	84936	abscission/NoCut checkpoint regulator isoform 2	S4(Phospho)	S(4): 100.0; T(12): 0.0	S4;	S286	37		0	0	2	964.4	1928	47.28	9135
LPDsDDDEDEETAIQR	ZFYVE19	84936	abscission/NoCut checkpoint regulator isoform 2	S4(Phospho)	S(4): 100.0; T(12): 0.0	S4;	S286		3.29	0	0	2	964.4	1928	47.28	9135
WsPPQNYK	ZFYVE19	84936	abscission/NoCut checkpoint regulator isoform 2	S2(Phospho)	S(2): 100.0; Y(7): 0.0	S2;	S144	10		0.005	0	2	550.2	1099	45.83	8830
RVTQHEsDNENEIQNK	ZMYM4	9202	zinc finger MYM-type protein 4	S7(Phospho)	T(3): 0.0; S(7): 100.0	S7;	S122	48		0	1	3	754.7	2262	26.79	4777
VTQHEsDNENEIQNK	ZMYM4	9202	zinc finger MYM-type protein 4	S6(Phospho)	T(2): 0.0; S(6): 100.0	S6;	S122	28		0	0	2	1053	2106	29.46	5350
RVTQHEsDNENEIQNK	ZMYM4	9202	zinc finger MYM-type protein 4	S7(Phospho)	T(3): 0.0; S(7): 100.0	S7;	S122		7.69	0	1	3	754.7	2262	26.79	4777
VTQHEsDNENEIQNK	ZMYM4	9202	zinc finger MYM-type protein 4	S6(Phospho)	T(2): 0.0; S(6): 100.0	S6;	S122		2.75	0	0	2	1053	2106	29.46	5350
STsPAsEKADPGAVK	ZMYND8	23613	protein kinase C-binding protein 1 isoform n	S3(Phospho) S6(Phospho)	S(1): 0.1; T(2): 0.1; S(3): 99.8; S(6): 100.0	S3; S6;	S404; S407	40		0	1	2	802.8	1605	23.38	4050
DKAsPEPEKDFSEK	ZMYND8	23613	protein kinase C-binding protein 1 isoform n	S4(Phospho)	S(4): 100.0; S(12): 0.0	S4;	S420	23		0	2	3	562.9	1687	24.26	4236
DKAsPEPEKDFSEK	ZMYND8	23613	protein kinase C-binding protein 1 isoform n	S4(Phospho)	S(4): 100.0; S(12): 0.0	S4;	S420		4.6	0	2	3	562.9	1687	24.26	4236
STsPAsEKADPGAVK	ZMYND8	23613	protein kinase C-binding protein 1 isoform n	S3(Phospho) S6(Phospho)	S(1): 0.1; T(2): 0.1; S(3): 99.8; S(6): 100.0	S3; S6;	S404; S407		2.86	0	1	2	802.8	1605	23.38	4050
DKAsPEPEKDFSEK	ZMYND8	23613	protein kinase C-binding protein 1 isoform n	S4(Phospho)	S(4): 100.0; S(12): 0.0	S4;	S420		2.21	0.003	2	2	843.9	1687	24.38	4260
ATGDGssPELPSLER	ZNF106	64397	zinc finger protein 106 isoform 2	S6(Phospho) S7(Phospho)	T(2): 3.0; S(6): 97.1; S(7): 99.9; S(12): 0.0	S6; S7;	S210; S211	57		0	0	2	838.3	1676	70.06	14176

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#
NRENSPSSQSAGLSSINK	ZNF106	64397	zinc finger protein 106 isoform 2	S5(Phospho)	S(5): 100.0; S(7): 0.0; S(8): 0.0; S(10): 0.0; S(14): 0.0; S(15): 0.0	S5;	S464	57		0	1	3	652.6	1956	29.86	5435
SLsESsVIMDR	ZNF106	64397	zinc finger protein 106 isoform 2	M9(Oxidation)S3(Phospho)S6(Phospho)	S(1): 0.1; S(3): 97.5; S(5): 2.5; S(6): 99.9	S3; S6;	S46; S49	13		0	0	2	700.3	1400	58.93	11666
NRENSPSSQSAGLSSINK	ZNF106	64397	zinc finger protein 106 isoform 2	S5(Phospho)	S(5): 100.0; S(7): 0.0; S(8): 0.0; S(10): 0.0; S(14): 0.0; S(15): 0.0	S5;	S464		3.96	0	1	3	652.6	1956	29.86	5435
ATGDGssPELPSLER	ZNF106	64397	zinc finger protein 106 isoform 2	S6(Phospho)S7(Phospho)	T(2): 3.0; S(6): 97.1; S(7): 99.9; S(12): 0.0	S6; S7;	S210; S211		2.77	0	0	2	838.3	1676	70.06	14176
SLsESsVIMDR	ZNF106	64397	zinc finger protein 106 isoform 2	M9(Oxidation)S3(Phospho)S6(Phospho)	S(1): 0.1; S(3): 97.5; S(5): 2.5; S(6): 99.9	S3; S6;	S46; S49		1.51	0.005	0	2	700.3	1400	58.93	11666
QSSPSGSEQLVR	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	64		0	0	2	677.8	1355	32.32	5943
RsSTSGDTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)T8(Phospho)	S(2): 96.1; S(3): 3.7; T(4): 0.2; S(5): 0.2; T(8): 99.8; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158	28		0	1	3	997.4	2990	64.72	12993
RsSTSGDTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)	S(2): 94.9; S(3): 2.5; T(4): 2.5; S(5): 0.1; T(8): 0.0; S(20): 0.0; S(21): 0.0	S2;	S152	23		0	1	3	970.7	2910	55.97	11004
GGQGDPVPTQQPADPSTPEQQNsPSGSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	S24(Phospho)	T(10): 0.0; S(17): 50.0; T(18): 50.0; S(24): 100.0; S(26): 0.0; S(28): 0.0	S24;	S520	21		0	0	4	889.1	3553	66.21	13325
RsSTSGDTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)T8(Phospho)	S(2): 96.0; S(3): 3.9; T(4): 0.2; S(5): 0.0; T(8): 100.0; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158	19		0	1	3	997.4	2990	65.23	13102
sSTSGDTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S1(Phospho)	S(1): 86.3; S(2): 74.3; T(3): 13.1; S(4): 13.1; T(7): 13.1; S(19): 0.0; S(20): 0.0	S1;	S152	18		0	1	3	997.4	2990	66.88	13481
RsSTSGDTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)	S(2): 94.1; S(3): 2.9; T(4): 2.9; S(5): 0.1; T(8): 0.0; S(20): 0.0; S(21): 0.0	S2;	S152	16		0	2	3	1023	3066	49.8	9661
GGQGDPVPTQQPADPSTPEQQNsPSGSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	S24(Phospho)	T(10): 0.3; S(17): 49.9; T(18): 49.9; S(24): 99.5; S(26): 0.5; S(28): 0.0	S24;	S520	12		0	0	3	1185	3553	65.98	13274
RsSTSGDTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)T8(Phospho)	S(2): 95.5; S(3): 4.3; T(4): 0.4; S(5): 4.3; T(8): 95.5; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158	12		0	2	3	1049	3146	56.77	11177
GGQGDPVPTQQPADPSTPEQQNsPSGSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	T18(Phospho)	T(10): 0.0; S(17): 5.6; T(18): 94.3; S(24): 0.0; S(26): 0.0; S(28): 0.0	T18;	T514	11		0	0	3	1159	3474	56.68	11156
RSSTSGDTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	T8(Phospho)	S(2): 48.8; S(3): 48.8; T(4): 2.4; S(5): 0.1; T(8): 100.0; S(20): 0.0; S(21): 0.0	T8;	T158	10		0	2	3	1049	3146	56.23	11059
RsSTSGDTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)T8(Phospho)	S(2): 96.1; S(3): 3.7; T(4): 0.2; S(5): 0.2; T(8): 99.8; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158		5.86	0	1	3	997.4	2990	64.72	12993
GGQGDPVPTQQPADPSTPEQQNsPSGSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	S24(Phospho)	T(10): 0.0; S(17): 50.0; T(18): 50.0; S(24): 100.0; S(26): 0.0; S(28): 0.0	S24;	S520		5.49	0	0	4	889.1	3553	66.21	13325
RsSTSGDTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)	S(2): 94.9; S(3): 2.5; T(4): 2.5; S(5): 0.1; T(8): 0.0; S(20): 0.0; S(21): 0.0	S2;	S152		5.08	0	1	3	970.7	2910	55.97	11004

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#
GGQGDPVPTQQPADPSTPEQQNsPS GSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	S24(Phospho)	T(10): 0.0; S(17): 0.0; T(18): 0.0; S(24): 100.0; S(26): 0.0; S(28): 0.0	S24;	S520		4.87	0	0	3	1159	3474	58.12	11471
RsSTSGDTTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho) T8(Phospho)	S(2): 95.5; S(3): 4.3; T(4): 0.4; S(5): 4.3; T(8): 95.5; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158		4.85	0	2	3	1049	3146	56.77	11177
RSSTSGDTTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	T8(Phospho)	S(2): 48.8; S(3): 48.8; T(4): 2.4; S(5): 0.1; T(8): 100.0; S(20): 0.0; S(21): 0.0	T8;	T158		4.7	0	2	3	1049	3146	56.23	11059
GGQGDPVPTQQPADPSTPEQQNsPS GSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	S24(Phospho)	T(10): 0.3; S(17): 49.9; T(18): 49.9; S(24): 99.5; S(26): 0.5; S(28): 0.0	S24;	S520		4.2	0	0	3	1185	3553	65.98	13274
RsSTSGDTTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho)	S(2): 94.1; S(3): 2.9; T(4): 2.9; S(5): 0.1; T(8): 0.0; S(20): 0.0; S(21): 0.0	S2;	S152		4.16	0	2	3	1023	3066	49.8	9661
GGQGDPVPTQQPADPSTPEQQNsPS GSEQFVR	ZNF185	7739	zinc finger protein 185 isoform 3	T18(Phospho)	T(10): 0.0; S(17): 5.6; T(18): 94.3; S(24): 0.0; S(26): 0.0; S(28): 0.0	T18;	T514		4.11	0	0	3	1159	3474	56.68	11156
GGQGDPVPAQQPADPSTPER	ZNF185	7739	zinc finger protein 185 isoform 3	T18(Phospho)	S(17): 2.8; T(18): 97.2	T18;	T448		3.64	0	0	2	1078	2155	39.2	7401
RsSTSGDTTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho) T8(Phospho)	S(2): 96.0; S(3): 3.9; T(4): 0.2; S(5): 0.0; T(8): 100.0; S(20): 0.0; S(21): 0.0	S2; T8;	S152; T158		3.63	0	1	3	997.4	2990	65.23	13102
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		3.57	0	0	2	677.8	1355	32.32	5943
sSTSGDTTEEEEEEVVPFSSDEQKR	ZNF185	7739	zinc finger protein 185 isoform 3	S1(Phospho)	S(1): 86.3; S(2): 74.3; T(3): 13.1; S(4): 13.1; T(7): 13.1; S(19): 0.0; S(20): 0.0	S1;	S152		2.59	0	1	3	997.4	2990	66.88	13481
GGQGDPVPAQQPADPSTPER	ZNF185	7739	zinc finger protein 185 isoform 3	T18(Phospho)	S(17): 2.8; T(18): 97.2	T18;	T448	19		0.001	0	2	1078	2155	39.2	7401
RsSTSGDTTEEEEEEVVPFSSDEQK	ZNF185	7739	zinc finger protein 185 isoform 3	S2(Phospho) T8(Phospho)	S(2): 87.9; S(3): 5.8; T(4): 5.8; S(5): 0.5; T(8): 99.4; S(20): 0.5; S(21): 0.0	S2; T8;	S152; T158		1.9	0.001	1	2	1496	2990	64.8	13010
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	20.52	3446
sPGLCSDSLEK	ZNF318	24149	zinc finger protein 318	C5(Carbamidomethyl) S1(Phospho)	S(1): 100.0; S(6): 0.0; S(8): 0.0	S1;	S136	23		0	0	2	636.8	1273	41.23	7830
TKsPKPAEsPQSATK	ZNF318	24149	zinc finger protein 318	S3(Phospho) S9(Phospho)	T(1): 0.0; S(3): 100.0; S(9): 99.9; S(12): 0.0; T(14): 0.1	S3; S9;	S1037; S1043	12		0	1	3	572.9	1717	13.73	2004
TKsPKPAEsPQSATK	ZNF318	24149	zinc finger protein 318	S3(Phospho) S9(Phospho)	T(1): 0.0; S(3): 100.0; S(9): 99.9; S(12): 0.0; T(14): 0.1	S3; S9;	S1037; S1043		4.79	0	1	3	572.9	1717	13.73	2004
RVsPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81		3.1	0	1	2	528.2	1055	20.52	3446
sPGLCSDSLEK	ZNF318	24149	zinc finger protein 318	C5(Carbamidomethyl) S1(Phospho)	S(1): 100.0; S(6): 0.0; S(8): 0.0	S1;	S136		3.05	0	0	2	636.8	1273	41.23	7830
RVsPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81	24		0.002	1	2	528.2	1055	21.05	3559
RVsPsPPR	ZNF318	24149	zinc finger protein 318	S3(Phospho) S5(Phospho)	S(3): 100.0; S(5): 100.0	S3; S5;	S79; S81		2.89	0.003	1	2	528.2	1055	21.05	3559
TEEPLGSPHPSGTVESPGEGPQDTR	ZNF446	55663	zinc finger protein 446 isoform 2	S7(Phospho) S16(Phospho)	T(1): 0.0; S(7): 100.0; S(11): 0.3; T(13): 0.0; S(16): 99.7; T(24): 0.0	S7; S16;	S137; S146	37		0	0	3	907.7	2721	49.4	9578

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#
TEEPGLSPHPSGTVESPGEGPQDTR	ZNF446	55663	zinc finger protein 446 isoform 2	S7(Phospho)	T(1): 0.2; S(7): 99.8; S(11): 0.0; T(13): 0.0; S(16): 0.0; T(24): 0.0	S7;	S137	25		0	0	3	881	2641	44.67	8571
TEEPGLSPHPSGTVESPGEGPQDTR	ZNF446	55663	zinc finger protein 446 isoform 2	S7(Phospho) S16(Phospho)	T(1): 0.0; S(7): 100.0; S(11): 0.3; T(13): 0.0; S(16): 99.7; T(24): 0.0	S7; S16;	S137; S146		4.06	0	0	3	907.7	2721	49.4	9578
TEEPGLSPHPSGTVESPGEGPQDTR	ZNF446	55663	zinc finger protein 446 isoform 2	S7(Phospho)	T(1): 0.2; S(7): 99.8; S(11): 0.0; T(13): 0.0; S(16): 0.0; T(24): 0.0	S7;	S137		3.62	0	0	3	881	2641	44.67	8571
TNSPAYSDIsDAGEDGEGKVDsvk	ZNF609	23060	zinc finger protein 609	S7(Phospho) S10(Phospho)	T(1): 50.0; S(3): 50.0; Y(6): 6.8; S(7): 99.5; S(10): 93.7; S(22): 0.0	S7; S10;	S846; S849	42		0	1	3	894.3	2681	58.08	11462
TNSPAYSDIsDAGEDGEGKVDsvk	ZNF609	23060	zinc finger protein 609	S7(Phospho) S10(Phospho)	T(1): 50.0; S(3): 50.0; Y(6): 6.8; S(7): 99.5; S(10): 93.7; S(22): 0.0	S7; S10;	S846; S849		5.11	0	1	3	894.3	2681	58.08	11462
TQsPEFEAQSSK	ZNF768	79724	zinc finger protein 768	S3(Phospho)	T(1): 0.0; S(3): 100.0; S(10): 0.0; S(11): 0.0	S3;	S160	37		0	0	2	709.8	1419	28.68	5186
YEPQsPGYEPSPGYEPR	ZNF768	79724	zinc finger protein 768	S5(Phospho) S12(Phospho)	Y(1): 0.0; S(5): 100.0; Y(8): 0.0; S(12): 97.0; Y(15): 3.0	S5; S12;	S125; S132		4.09	0	1	3	757	2269	48.28	9344
TQsPEFEAQSSK	ZNF768	79724	zinc finger protein 768	S3(Phospho)	T(1): 0.0; S(3): 100.0; S(10): 0.0; S(11): 0.0	S3;	S160		2.83	0	0	2	709.8	1419	28.68	5186
VKQDSPEsPKsPSAAGGQK	ZNF800	168850	zinc finger protein 800	T11(Phospho) S12(Phospho)	S(5): 0.2; S(7): 0.0; S(10): 4.1; T(11): 95.8; S(12): 99.8; S(14): 0.2	T11; S12;	T461; S462	31		0	2	3	759.7	2277	13.27	1905
VKQDSPEsPKsPSAAGGQK	ZNF800	168850	zinc finger protein 800	T11(Phospho) S12(Phospho)	S(5): 0.2; S(7): 0.0; S(10): 4.1; T(11): 95.8; S(12): 99.8; S(14): 0.2	T11; S12;	T461; S462		4.53	0	2	3	759.7	2277	13.27	1905
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153	46		0	1	3	807.3	2420	29.81	5422
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153	40		0	1	3	807.3	2420	30.31	5528
YNLDAsEEEDSNK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S6(Phospho)	Y(1): 0.0; S(6): 99.9; S(11): 0.1	S6;	S188	30		0	0	2	797.3	1594	36.84	6908
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153	24		0	1	2	1210	2420	29.89	5440
tRsRsPESQVIGENTK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	T1(Phospho) S3(Phospho) S5(Phospho)	T(1): 100.0; S(3): 100.0; S(5): 100.0; S(8): 0.0; T(15): 0.0	T1; S3; S5;	T303; S305; S307	19		0	2	3	676.9	2029	35.62	6649
TRsRsPESQVIGENTK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S3(Phospho) S5(Phospho)	T(1): 1.9; S(3): 98.1; S(5): 100.0; S(8): 0.0; T(15): 0.0	S3; S5;	S305; S307	19		0	2	3	650.3	1949	27.84	5009
EVEDKsEGEEDEDEDLSKYK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0; Y(21): 0.0	S7;	S153	14		0	2	3	904.4	2711	38.8	7315
YNLDAsEEEDSNKKK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S6(Phospho)	Y(1): 0.0; S(6): 100.0; S(11): 0.0	S6;	S188	14		0	2	3	617.3	1850	22.96	3966
TRsRsPESQVIGENTK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S3(Phospho) S5(Phospho)	T(1): 1.9; S(3): 98.1; S(5): 100.0; S(8): 0.0; T(15): 0.0	S3; S5;	S305; S307		6.11	0	2	3	650.3	1949	27.84	5009
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153		4.36	0	1	3	807.3	2420	29.81	5422
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153		3.94	0	1	3	807.3	2420	30.31	5528
tRsRsPESQVIGENTK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	T1(Phospho) S3(Phospho) S5(Phospho)	T(1): 100.0; S(3): 100.0; S(5): 100.0; S(8): 0.0; T(15): 0.0	T1; S3; S5;	T303; S305; S307		3.71	0	2	3	676.9	2029	35.62	6649
YNLDAsEEEDSNKKK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S6(Phospho)	Y(1): 0.0; S(6): 100.0; S(11): 0.0	S6;	S188		3.62	0	2	3	617.3	1850	22.96	3966
EVEDKsEGEEDEDEDLSK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0	S7;	S153		3.51	0	1	2	1210	2420	29.89	5440

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#
EVEDKEsEGEEDEDEDLSKYK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S7(Phospho)	S(7): 100.0; S(19): 0.0; Y(21): 0.0	S7;	S153		2.88	0	2	3	904.4	2711	38.8	7315
YNLDAsEEEDSNK	ZRANB2	9406	zinc finger Ran-binding domain-containing protein 2 isoform 2	S6(Phospho)	Y(1): 0.0; S(6): 99.9; S(11): 0.1	S6;	S188		2.8	0	0	2	797.3	1594	36.84	6908
FsPGAPGGSGSQPNQK	ZYX	7791	zyxin	S2(Phospho)	S(2): 100.0; S(9): 0.0; S(11): 0.0	S2;	S281	51		0	0	2	798.3	1596	30.63	5594
GPPASsPAPAPK	ZYX	7791	zyxin	S6(Phospho)	S(5): 1.5; S(6): 98.5	S6;	S259	25		0	0	2	578.8	1157	21.67	3686
FTPVAAsKFSPGAPGGSGSQPNQK	ZYX	7791	zyxin	S6(Phospho)	T(2): 0.2; S(6): 95.4; S(9): 4.4; S(16): 0.0; S(18): 0.0	S6;	S278	25		0	1	3	776	2326	46.54	8981
FTPVAAsKFSPGAPGGSGSQPNQK	ZYX	7791	zyxin	S6(Phospho)	T(2): 0.2; S(6): 95.4; S(9): 4.4; S(16): 0.0; S(18): 0.0	S6;	S278		4.33	0	1	3	776	2326	46.54	8981
FsPGAPGGSGSQPNQK	ZYX	7791	zyxin	S2(Phospho)	S(2): 100.0; S(9): 0.0; S(11): 0.0	S2;	S281		3.62	0	0	2	798.3	1596	30.63	5594
GPPASsPAPAPK	ZYX	7791	zyxin	S6(Phospho)	S(5): 1.5; S(6): 98.5	S6;	S259		2.93	0	0	2	578.8	1157	21.67	3686