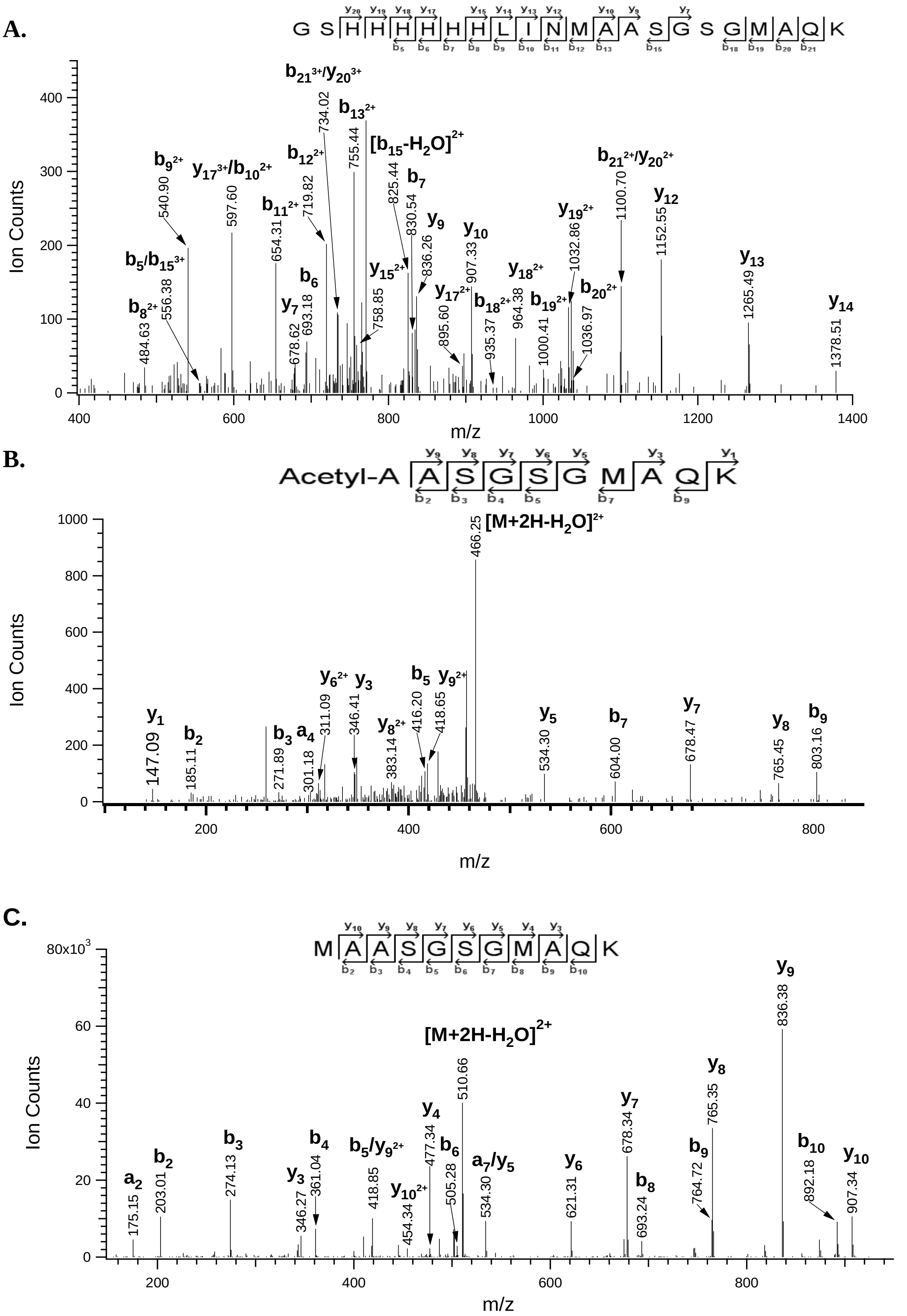
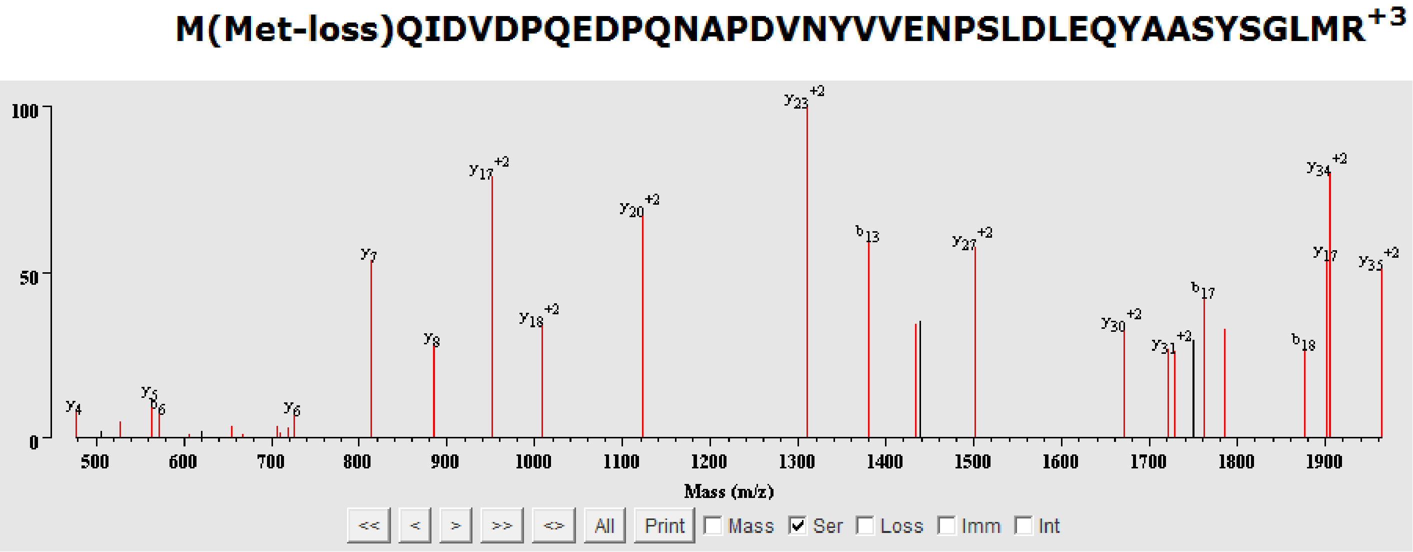


Supplemental Figure 1

Supplemental Figure 2: MS/MS Spectra of the Identified N-terminal Peptides in Table 2.

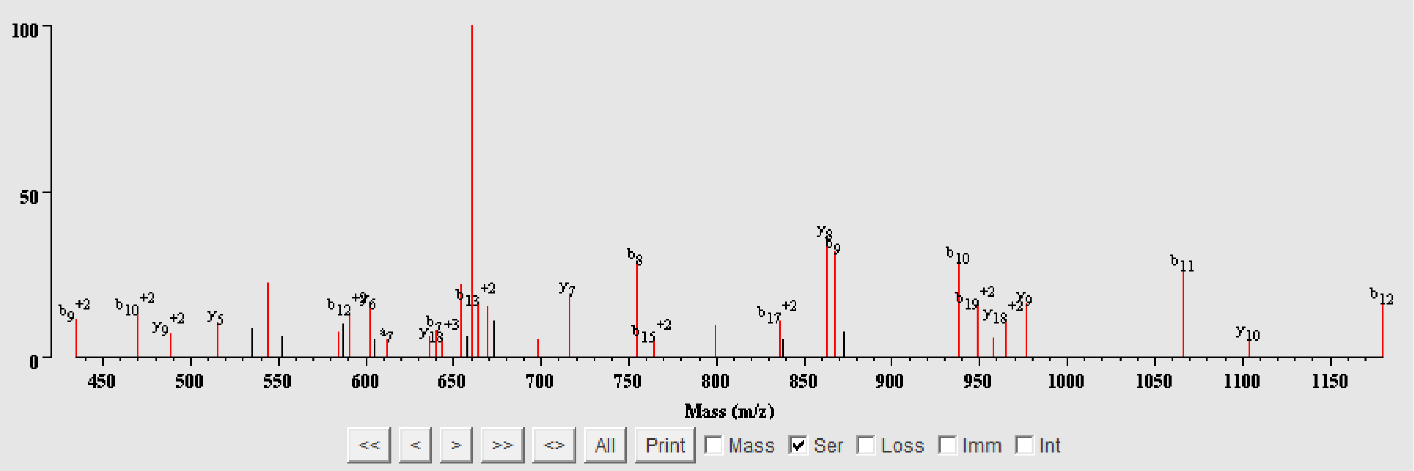
A. N-terminal Peptide of Subunit CSN1 (MH_3^{3+} 1460.6798, LTQ MS/MS)



m/z	Ion Type	m/z	Ion Type	m/z	Ion Type
476.602	NYVV	884.612	QNAPDVNY-H2O	1761.73	QIDVDPQEDPQNAPDV
	VNYV		IDVDPQED-28		b17
	y4		y8		YVVENPSLDLEQYAAS-H2O
527.35	NPSLD		YVVENPSL-H2O		VVENPSLDLEQYAASY-H2O
	VENPS	950.898	VVENPSLDL-NH3	1784.7	y32-NH3+2
	DVDPQ-28		y17+2		QEDPQNAPDVNYVVEN-28
563.195	EQYAA	1008.18	y18+2		PDVNYVVENPSLDLEQ-28
	DVNYV-28		ENPSLDLEQ-H2O	1875.73	QIDVDPQEDPQNAPDVN
	y5	1122.02	y20+2		b18
571.325	PDVNY-H2O	1310.54	y23+2		NYVVENPSLDLEQYAAS-H2O
	QIDVD		SLDLEQYAASYS-H2O	1900.93	y17
	b6		PDVNYVVENPSL-NH3	1905.75	y34+2
	LDLEQ-28		PSLDLEQYAASY-28		VVENPSLDLEQYAASYSG-H2O
605.518	PQNAPD-H2O	1379.3	QIDVDPQEDPQN		VNYVVENPSLDLEQYAA
	DPQNAP-H2O		b13	1963.22	y35+2
	YVVEN	1433.57	QIDVDPQEDPQNA-NH3	1728.21	QNAPDVNYVVENPSLD-28
	LEQYA		b14-NH3		APDVNYVVENPSLDLE-28
	NYVVE	1501.47	y27+2		y31+2
655.245	EDPQNA		VDPQEDPQNAPDVN-H2O	813.419	EQYAASY
	PSLDLE		a15-H2O		YAASYSGL
666.37	DVDPQE-H2O		NYVVENPSLDLEQ		y7
	VDPQED-H2O		VVENPSLDLEQYAA-28		
	QYAASY-H2O	1671.11	QEDPQNAPDVNYVVE-28		
705.593	PQNAPDV-NH3		y30+2		
709.12	y6-NH3	1720.26	IDVDPQEDPQNAPDVN-28		
719.33	NYVVEN		y31-NH3+2		
726.452	y6		PQNAPDVNYVVENPSL-H2O		

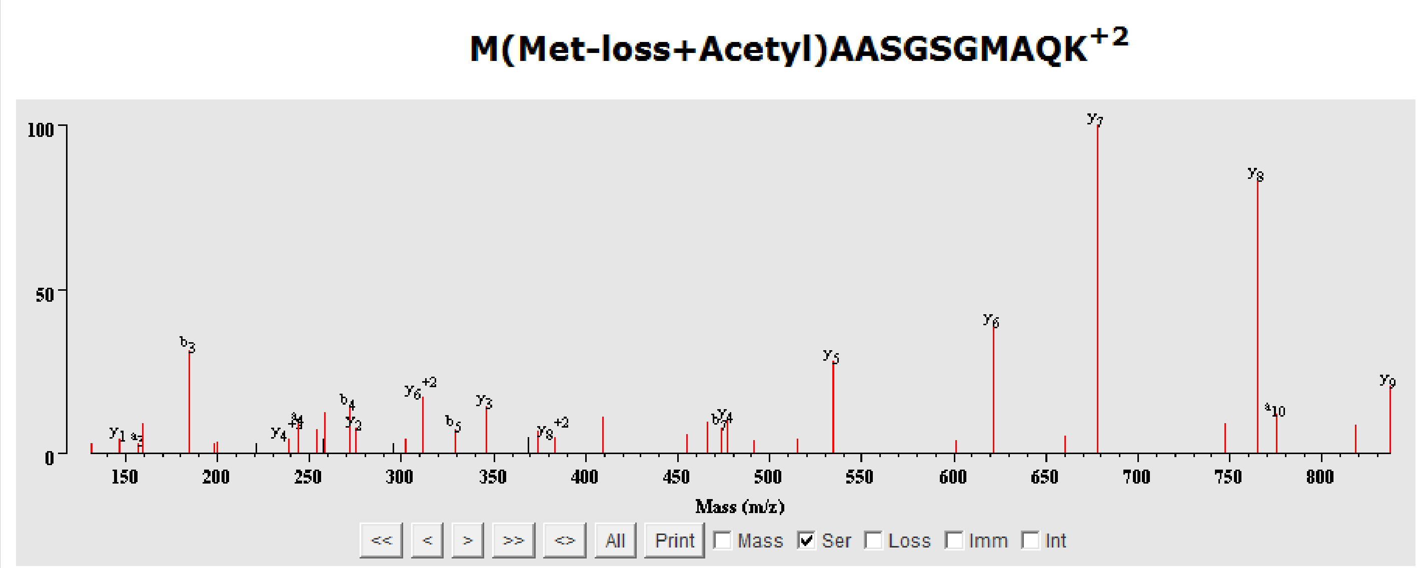
B. N-terminal Peptide of Subunit CSN4 (MH$_3^{3+}$ 681.3410, LTQ MS/MS)

M(Met-loss+Acetyl)AAAVRQDLAQLM(Oxidation)NSSGSHK^{+3}



m/z	Ion Type	m/z	Ion Type
434.263	b9+2	863.234	y8
469.742	b10+2	867.309	b9
488.682	y9+2	938.275	b10
515.32	y5	948.48	b19+2
543.991	y10-H2O+2	957.872	y9-H2O
	y10-NH3+2	965.185	y18+2
584.245	y6-H2O	976.165	y9
590.284	y16-H2O+3	1066.323	b11
	b12+2	1104.146	y10
	y16-NH3+3	1179.482	b12
602.408	a19-SOCH4+3		
	y6		
612.053	b19-SOCH4+3		
	a7		
	y12-SOCH4+2		
636.13	y12-H2O+2		
	y12-NH3+2		
639.438	b7		
643.267	y18+3		
654.363	b13-H2O+2		
660.024	MH-SOCH4+3		
664.032	b13+2		
669.545	y13-SOCH4+2		
698.251	y7-H2O		
716.366	y7		
754.303	b8		
764.484	b15+2		
799.326	b16-H2O+2		
	y8-SOCH4		
	b16-NH3+2		
835.83	y15-H2O+2		
	y15-NH3+2		
	b17+2		

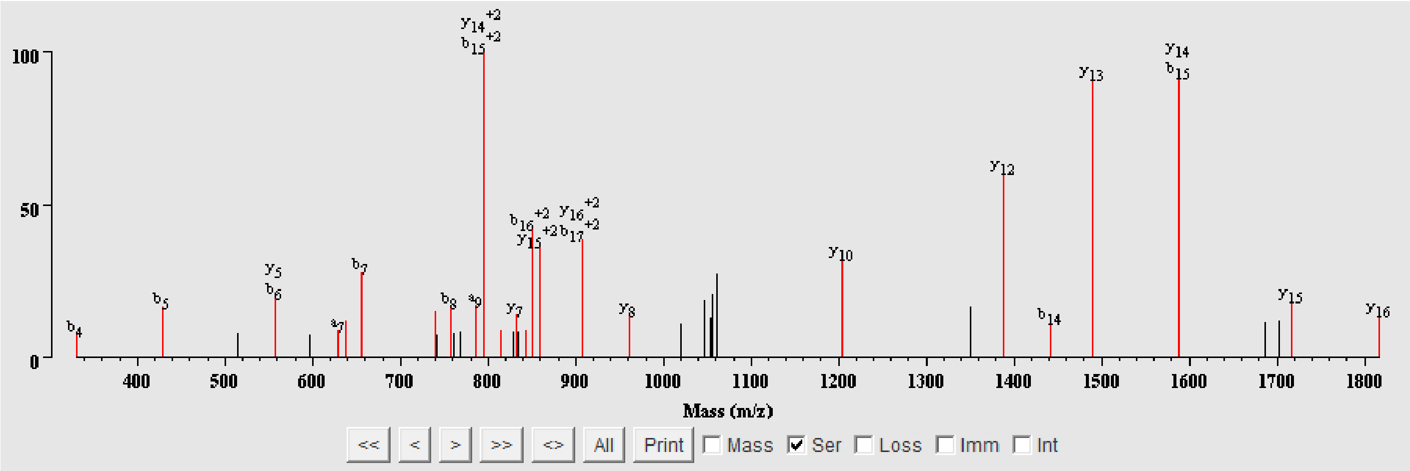
C. N-terminal Peptide of CSN 5 (MH_2^{2+} 475.22, QSTAR MS/MS)



m/z	Ion Type	m/z	Ion Type
131.0716	AS-28	534.2647	ASGSGMA-28
147.109	y1		AASGSGM-28
157.0967	a3		y5
159.0691	AS	601.2244	SGSGMAQ-H2O
185.0829	b3	621.2808	y6
198.087	ASG-H2O	660.3011	y7-H2O
200.0968	AQ	678.3201	y7
239.1042	y4+2	747.3458	y8-H2O
244.1178	a4	765.3396	y8
254.098	b4-H2O	775.348	a10
258.1307	SGM-H2O	818.3866	y9-H2O
	y2-NH3	836.3979	y9
272.1124	b4		
275.1584	ASGS-28		
	y2		
302.1439	y6-H2O+2		
311.1264	b5-H2O		
329.134	SGMA-H2O		
	b5		
	y3-NH3		
346.1907	AASGS-28		
	y3		
374.1608	AASGS		
	y8-H2O+2		
383.1947	y8+2		
409.6824	y9-H2O+2		
455.1769	b7-H2O		
466.2173	MH-H2O+2		
473.1855	SGSGMA-H2O		
	ASGSGM-H2O		
	b7		
477.2262	y4		
491.1653	ASGSGM		
	SGSGMA		
515.1458	GSGMAQ-NH3		

D. N-terminal Peptide of CSN7a (MH_2^{2+} 1073.0811, LTQ MSMS)

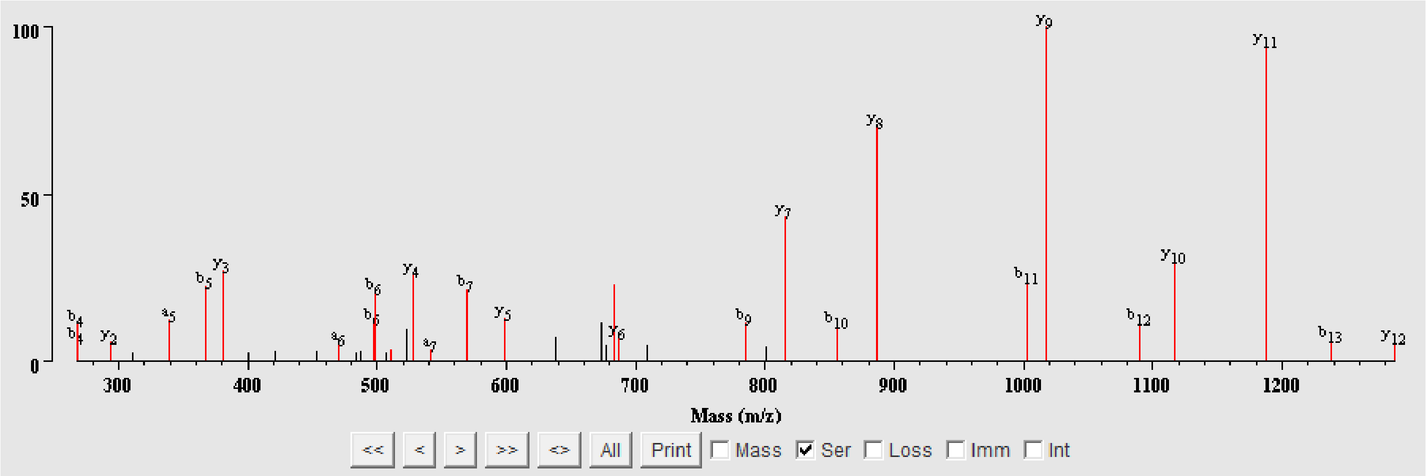
M(Met-loss+Acetyl)SAEVKVTGQNQEQFLLLAK^{+2}



m/z	Ion Type
331.262	y3
429.234	b5
557.372	b6
	y5
628.31	a7
638.446	b7-H2O
656.313	b7
739.367	b8-H2O
786.43	b15-NH3+2
	y14-NH3+2
	a9
795.082	b15+2
	y14+2
815.488	y7-NH3
832.485	y7
843.053	b16-NH3+2
851.215	b16+2
858.971	y15+2
908.209	b17+2
961.547	y8
1203.492	y10
1388.753	y12
1441.58	b14
1489.611	y13
1588.796	b15
	y14
1717.026	y15
1815.883	y16

E. N-terminal Peptide of Subunit CSN8 (MH_2^{2+} 692.3525, LTQ MSMS)

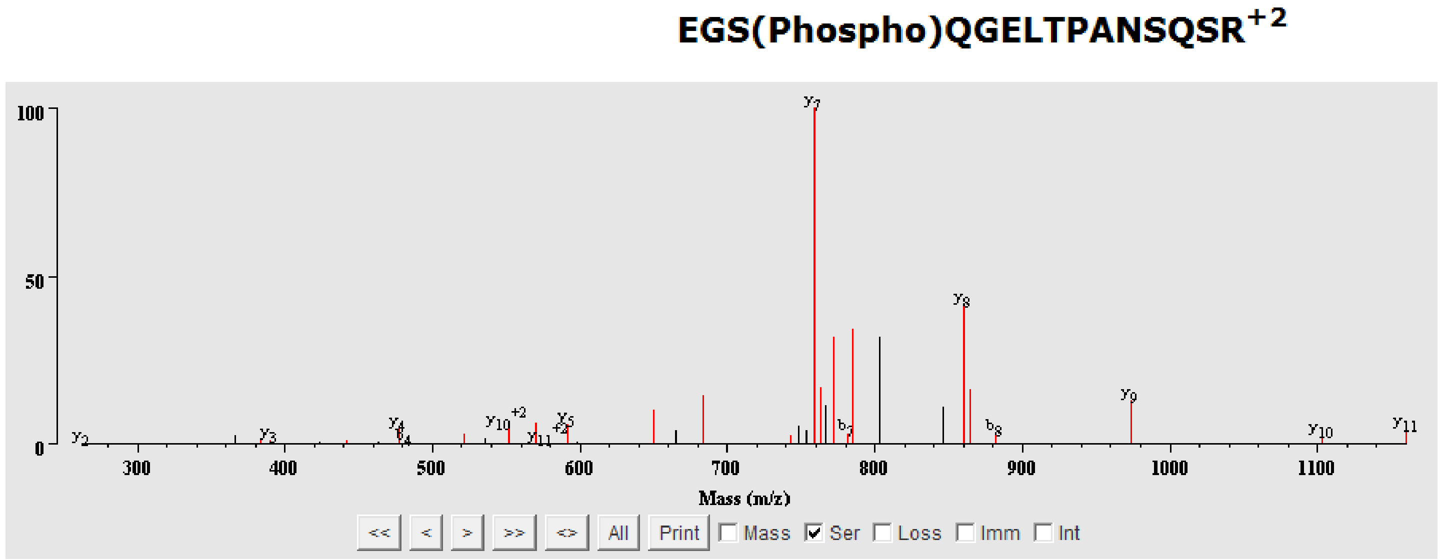
M(Met-loss)PVAVMAESAFSFK^{+2}



m/z	Ion Type
267.669	b4
268.281	b4
294.3	y2
339.195	a5
367.156	b5
381.181	y3
470.335	a6
498.318	b6
510.381	y4-H2O
528.286	y4
540.956	a7
569.238	b7
599.207	y5
683.182	y13-H2O+2 MH-H2O+2 y13-NH3+2 MH-NH3+2
686.488	y6
785.162	b9
815.412	y7
856.068	b10
886.235	y8
1003.298	b11
1017.279	y9
1090.347	b12
1116.256	y10
1187.278	y11
1238.326	b13
1286.263	y12

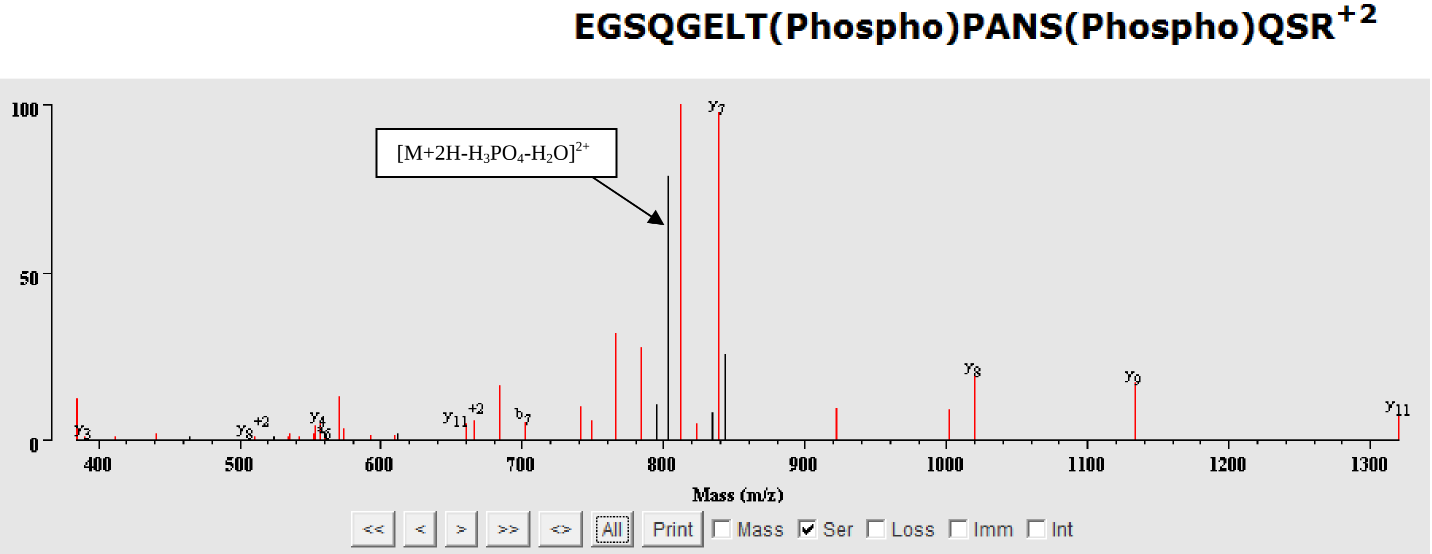
Supplemental Figure 3. MS/MS Spectra of the Identified Phosphopeptides in Table 3.

A. MH_2^{2+} 820.8492 (LTQ MSMS)



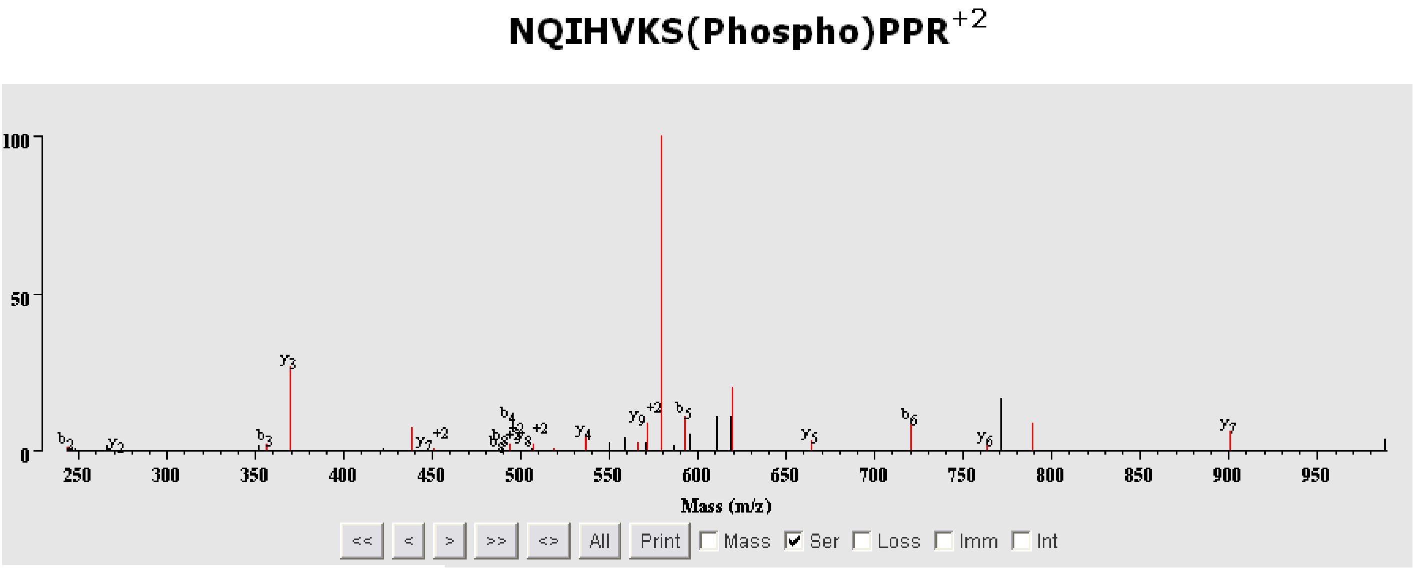
m/z	Ion Type	m/z	Ion Type
262.224	y2	1159.609	y11
384.08	b4-H3PO4		
390.348	y3		
441.293	b5-H3PO4		
459.471	y4-H2O		
	y4-NH3		
463.547	b4-H2O		
477.368	y4		
482.233	b4		
521.238	b5-H2O		
552.208	y10+2		
570.307	b6-H3PO4		
580.356	y11+2		
591.435	y5		
650.159	b6-H2O		
683.265	b7-H3PO4		
742.471	y7-NH3		
748.315	y14-NH3+2		
753.883	a7		
759.45	y7		
763.109	b7-H2O		
771.953	MH-H3PO4+2		
781.097	b7		
784.341	b8-H3PO4		
860.472	y8		
864.195	b8-H2O		
882.259	b8		
973.487	y9		
1102.648	y10		

B. MH_2^{2+} 860.8324(LTQ MSMS)



m/z	Ion Type
384.192	b4-H2O
390.254	y3
411.177	y7-H2O+2
	y7-NH3+2
441.051	b5-H2O
511.148	y8+2
557.157	y4
560.634	a6
570.12	b6-H2O
573.302	y5-H3PO4
660.29	y11+2
683.296	b7-H2O
701.418	b7
741.394	y7-H3PO4
784.311	b8-H3PO4
802.936	MH-H3PO4-H2O+2
811.934	MH-H3PO4+2
822.633	y7-NH3
839.258	y7
922.41	y8-H3PO4
1002.381	y8-H2O
1020.266	y8
1133.395	y9
1319.462	y11

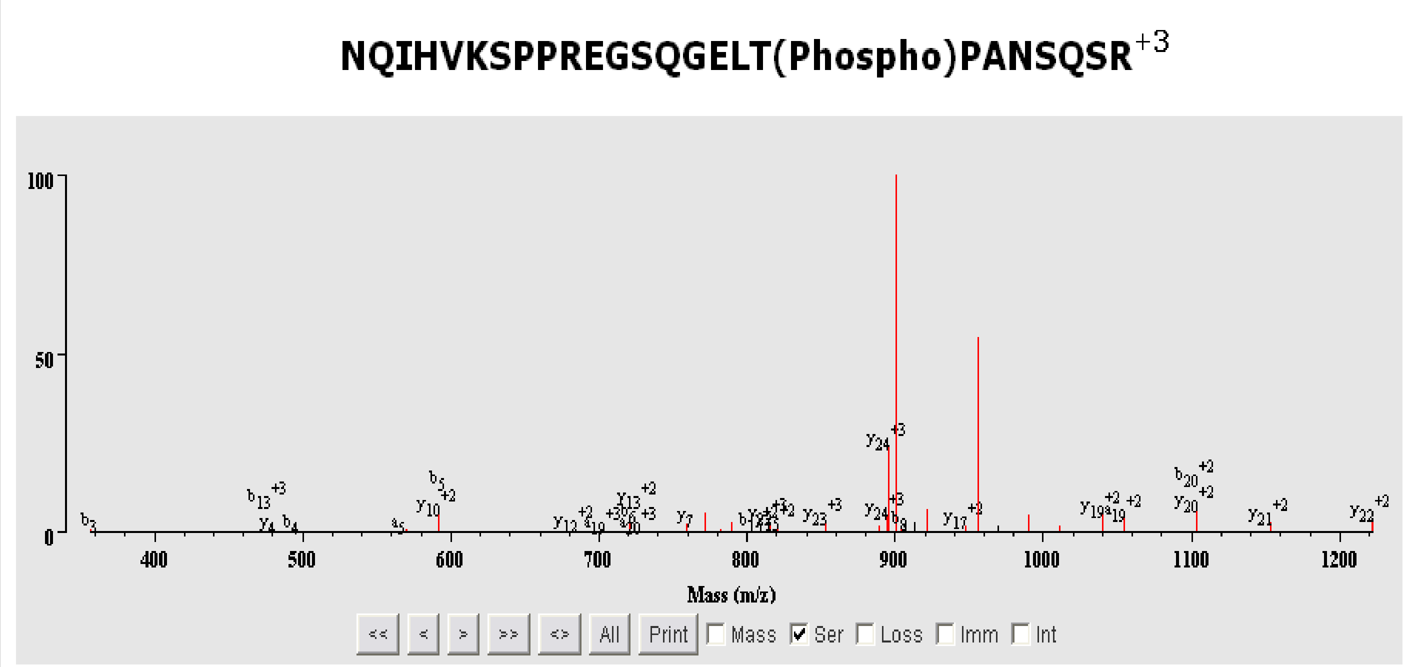
C. MH$_2^{2+}$ 628.3220 (LTQ MSMS)



☐ Mass ☑ Ser ☐ Loss ☐ Imm ☐ Int

m/z	Ion Type
243.174	b2
272.362	y2
356.139	b3
369.265	y3
401.822	y7-H3PO4+2
438.319	y4-H3PO4
450.728	y7+2
492.069	b9-H3PO4+2
	b8+2
493.325	b8+2
	b4
507.391	y8+2
518.404	y4-NH3
536.366	y4
566.297	y5-H3PO4
570.958	y9+2
579.393	MH-H3PO4+2
592.327	b5
619.804	MH-NH3+2
664.334	y5
720.391	b6
763.431	y6
789.317	b7-H3PO4
900.423	y7

D. MH$_3^{3+}$ 933.1158(LTQ MSMS)



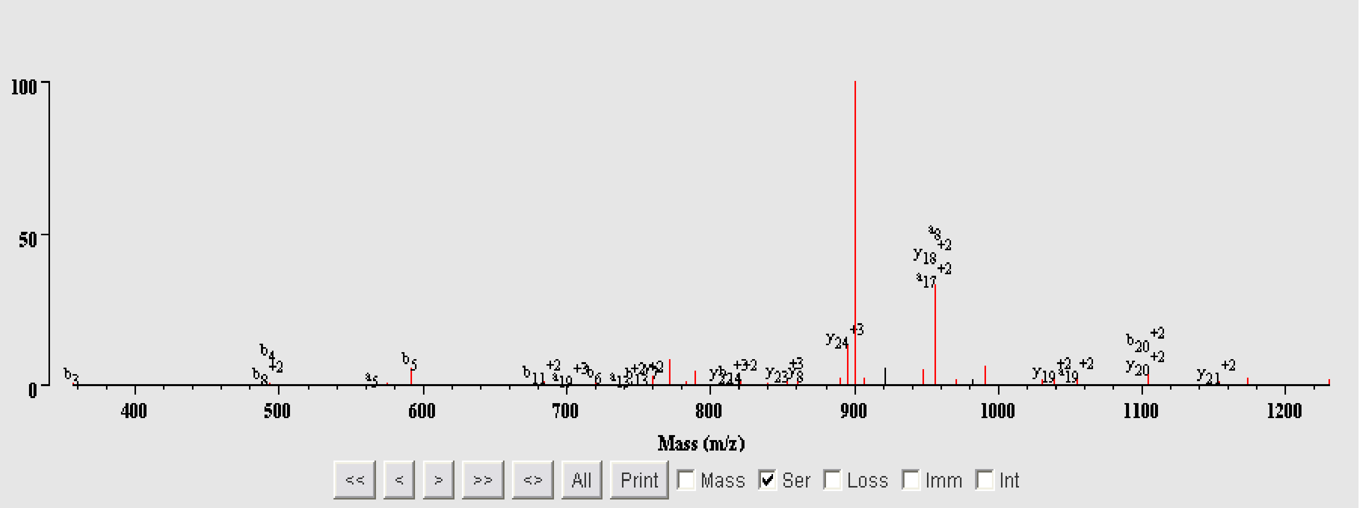
NQIHVKSPPREGSQGELT(Phospho)PANSQSR^{+3}

☐ Mass ☑ Ser ☐ Loss ☐ Imm ☐ Int

m/z	Ion Type
356.253	b3
477.353	y4
	b13+3
493.086	b9-NH3+2
	b4
564.46	a5
570.417	b10-H2O+2
	b10-NH3+2
573.995	y5-H2O
	y5-NH3
592.289	y10+2
	b5
684.197	y12+2
703.525	a19+3
	y20-H3PO4+3
	b6-NH3
	b20-H3PO4+3
720.407	b6
727.269	a20+3
	y13+2
741.042	y7-H2O
	b21-H3PO4+3
745.138	
759.462	y7
771.362	b22-H3PO4+3
	b14-H2O+2
	b14-NH3+2
	y15-H3PO4+2
782.042	y22-H3PO4+3
789.256	b7-H2O
808.937	b15+2
	y22-H2O+3
	y22-NH3+3
815.147	y22+3
820.218	y23-H3PO4+3
	y15+2
852.65	y23+3
889.294	y24-H2O+3
	y24-NH3+3
	y16-H2O+2
894.439	y24+3
895.115	y24+3
900.217	MH-H3PO4+3
900.827	MH-H3PO4+3
903.973	b8
921.674	b17-NH3+2
	y8-H2O
947.133	y18-H3PO4+2
	y17+2
956.239	y9-H3PO4
	a18-H3PO4+2
990.446	y19-H3PO4+2
1010.948	b18-H2O+2
	b18-NH3+2
1039.745	y19+2
1054.586	a19+2
	y20-H3PO4+2
	b20-H3PO4+2
1103.737	y20+2
	b20+2
	y21-H3PO4+2
1153.214	b21-NH3+2
	y21+2
1221.551	y11-H2O
	y22+2

E. MH_3^{3+} 933.1221(LTQ MSMS)

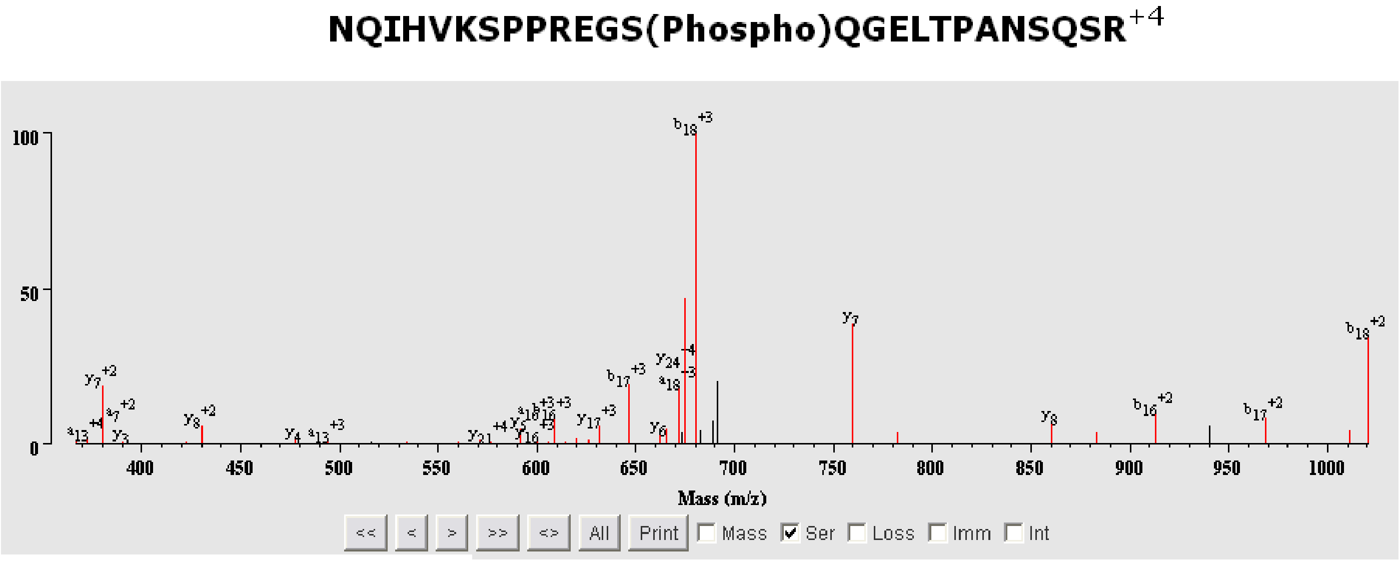
NQIHVKS(Phospho)PPREGSQGELTPANSQSR^{+3}



☐ Mass ☑ Ser ☐ Loss ☐ Imm ☐ Int

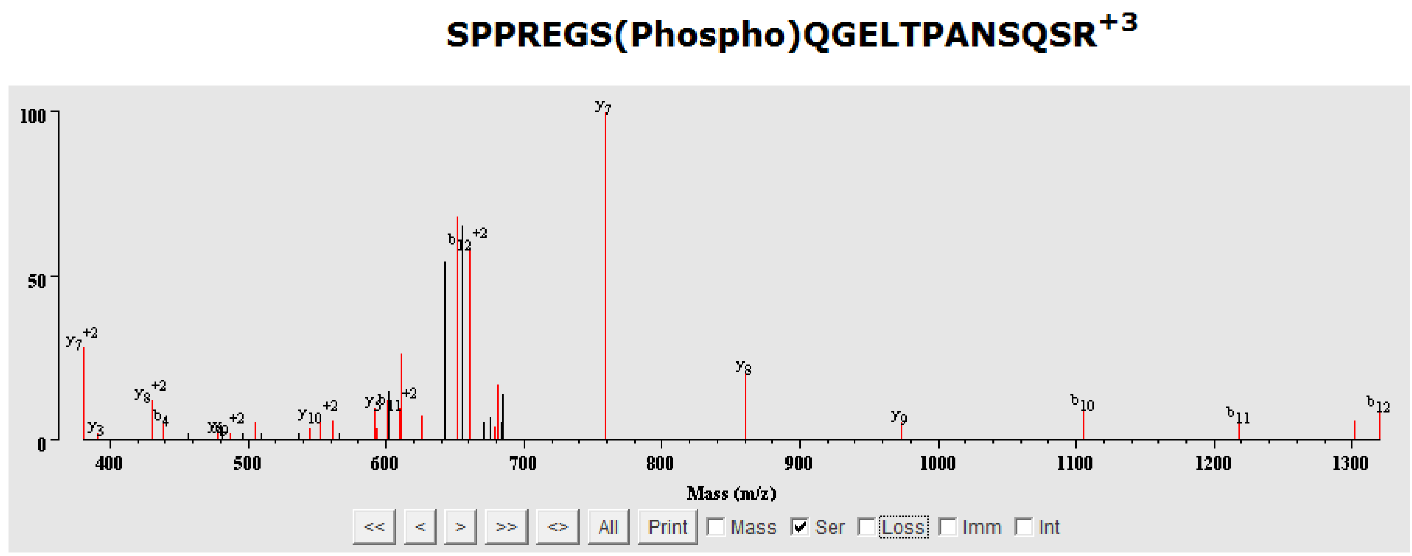
m/z	Ion Type
356.239	b9-NH3+3
	b3
493.222	b8+2
	b4
564.579	a5
575.266	b5-NH3
592.25	b5
684.096	b11+2
703.486	b12-H2O+2
	a19+3
	y20-H3PO4+3
	b6-NH3
	b20-H3PO4+3
	b12-NH3+2
720.034	b6
742.587	a13+2
	y7-NH3
755.497	b13+2
759.424	y7
771.38	b22-H3PO4+3
	b14-H3PO4+2
	y15-H2O+2
782.437	y22-H3PO4+3
789.383	b7-H3PO4
809.344	y22-H2O+3
	y22-NH3+3
814.855	y22+3
820.325	y23-H3PO4+3
	b14+2
839.385	b15-H2O+2
	b15-NH3+2
	b23-H2O+3
846.999	y23-H2O+3
	y23-NH3+3
852.91	y23+3
860.597	y8
889.679	y24-H2O+3
	y24-NH3+3
894.792	y24+3
900.169	MH-H3PO4+3
900.82	MH-H3PO4+3
906.642	a17-H3PO4+2
921.344	
947.223	y18-H2O+2
	y18-NH3+2
956.035	a17+2
	y9-H2O
	a9-H3PO4
	y18+2
	a8
	y9-NH3
971.205	b18-H3PO4+2
981.917	
990.764	y19-H3PO4+2
1030.587	y19-H2O+2
	y19-NH3+2
1039.404	y19+2
1054.555	a19+2
	y20-H3PO4+2
	b20-H3PO4+2
1103.929	y20+2
	b20+2
	y21-H3PO4+2
1153.192	b21-NH3+2
	y21+2
1172.926	y22-H3PO4+2
1229.514	y23-H3PO4+2

F. MH$_4^{4+}$ 700.0887(LTQ MSMS)


NQIHVKSPPREGS(Phospho)QGELTPANSQSR^{+4}

m/z	Ion Type
366.345	TPAN-H2O
	PRE-NH3
	a13-H2O+4
371.877	y7-H2O+2
	a10-H2O+3
	a13+4
	a10-NH3+3
	y7-NH3+2
	y3-H2O
380.265	y7+2
	b10-H2O+3
	b10-NH3+3
390.08	y3
	a7+2
422.3	y8-H2O+2
	y8-NH3+2
	PREG-H2O
430.584	a8-NH3+2
	y8+2
477.294	y4
494.147	ELTPA-H2O
	a13+3
533.847	b15-H3PO4+3
560.283	b15-H2O+3
	b15-NH3+3
570.691	b10-H2O+2
	b10-NH3+2
	TPANSQ-28
	y11-H2O+2
	a22-H3PO4+4
576.676	b16-H3PO4+3
	b21-H2O+4
	b21-NH3+4
	y21+4
	S(Phospho)QGEL-H2O
591.337	y5
	a22-H2O+4
	a22-NH3+4
599.894	TPANSQ
	y17-H3PO4+3
	y16+3
	a16+3
605.612	SPPREG-H2O
	QIHVK
609.033	QGELTP-H2O
	ELTPAN-H2O
	b16+3
	ELTPAN-NH3
	QGELTP-NH3
614.419	b17-H3PO4+3
	y23-H3PO4+4
619.868	REGS(Phospho)Q-H2O
626.074	y17-H2O+3
	y17-NH3+3
	QGELTP
	ELTPAN
631.679	a17-H2O+3
	a17-NH3+3
	y18-H3PO4+3
	y17+3
	b24-H3PO4+4
646.808	HVKSPP
	b17+3
	y24-H3PO4+4
	VKSPPR-H2O
662.417	y6
	IHVKSP
665.378	a18-H2O+3
	a18-NH3+3
	GELTPAN-H2O
	QIHVKS-28
	VKSPPR
671.334	a19-H3PO4+3
	a18+3
	y24+4
674.427	b18-H2O+3
	b18-NH3+3
680.413	b19-H3PO4+3
	QGELTPA-NH3
	b18+3
759.276	a21-H2O+3
	a21-NH3+3
	y7
	IHVKSPP
782.377	y22-H3PO4+3
	LTPANSQS-NH3
860.347	a24-H2O+3
	a24-NH3+3
	y8
882.736	EGS(Phospho)QGELT
913.02	b16+2
	HVKSPPRE-H2O
968.981	GELTPANSQS-NH3
	b17+2
1010.909	REGS(Phospho)QGELT-28
	b18-H2O+2
	b18-NH3+2
1020.128	KSPPREGS(Phospho)Q-28
	b19-H3PO4+2
	b18+2
	REGS(Phospho)QGELT-H2O

G. MH$_3^{3+}$ 693.3148 (LTQ MSMS)



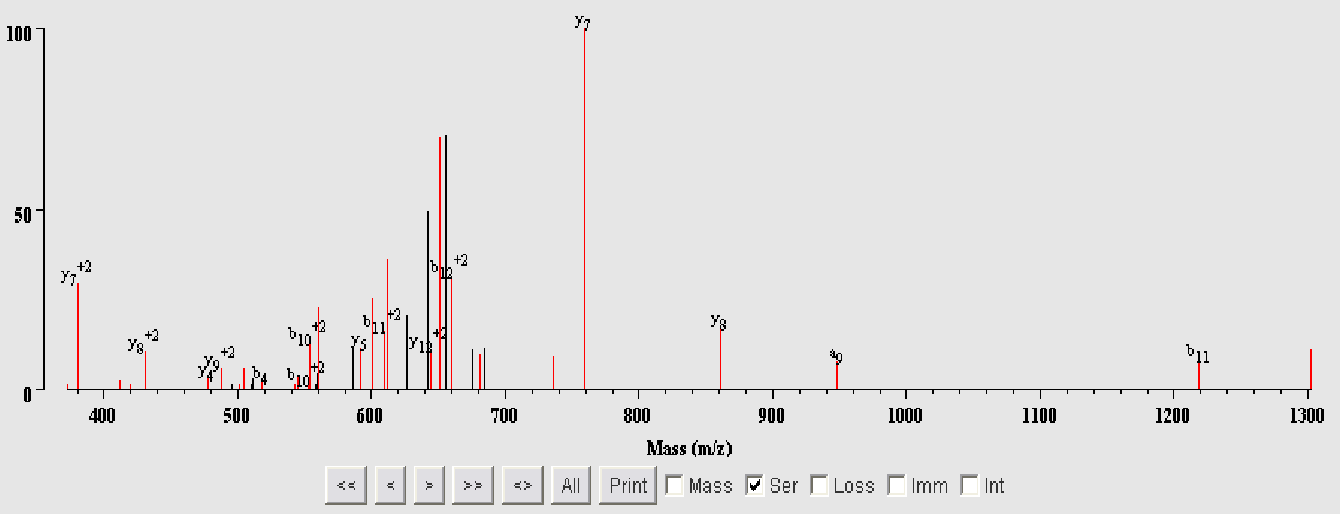
SPPREGS(Phospho)QGELTPANSQSR^{+3}

☐ Mass ☑ Ser ☐ Loss ☐ Imm ☐ Int

m/z	Ion Type
380.211	y7+2
390.392	y3
430.841	y8+2
438.329	b4
477.375	y4
487.439	y9+2
504.43	b10-H3PO4+2
544.535	b10-H2O+2
	b10-NH3+2
552.007	y10+2
560.974	b11-H3PO4+2
591.38	y5
593.362	y16-H2O+3
600.717	b11-H2O+2
609.791	b11+2
611.152	b12-H3PO4+2
626.045	y17-H2O+3
	y17-NH3+3
651.285	b12-H2O+2
	b12-NH3+2
660.538	b12+2
	MH-H3PO4+3
678.772	y13-H3PO4+2
681.456	a14-H3PO4+2
759.4	y7
860.425	y8
973.401	y9
1105.454	b10
1218.269	b11
1301.526	b12-H2O
1319.379	b12

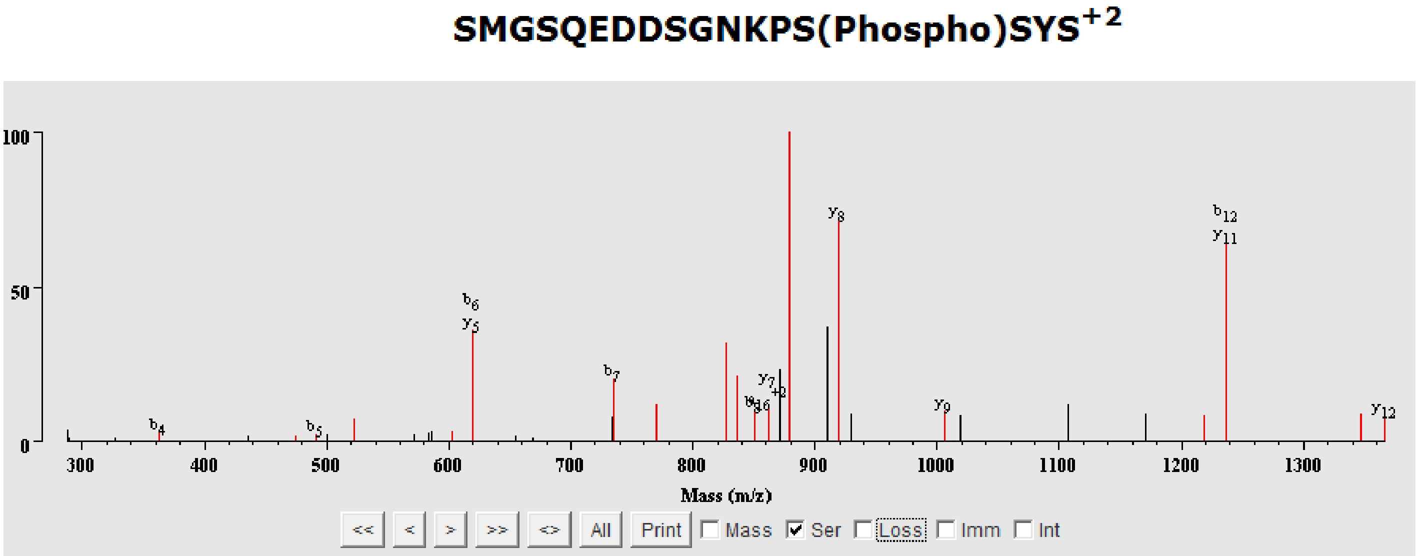
H. MH_3^{3+} 693.3160(LTQ MSMS)

S(Phospho)PPREGSQGELTPANSQSR^{+3}



m/z	Ion Type	m/z	Ion Type
372.08	y7-NH3+2	660.279	b13-H3PO4+2
	y3-H2O		b12+2
380.285	y7+2		MH-H3PO4+3
411.308	b8-H3PO4+2	681.363	a14-H3PO4+2
420.068	b4-H3PO4	735.559	b14-H2O+2
430.817	y8+2		b14-NH3+2
477.265	y4	759.506	y7
487.675	y9+2	860.648	b17-H3PO4+2
501.186	b4-NH3		y8
504.286	b10-H3PO4+2	947.806	y18-NH3+2
517.819	b4		a9
542.482	y10-H2O+2	1218.685	b11
	y10-NH3+2	1301.703	b12-H2O
544.537	b10-H2O+2		
	b10-NH3+2		
552.653	b10+2		
553.306	b10+2		
557.688			
559.605			
560.855	b11-H3PO4+2		
591.37	y5		
600.955	b11-H2O+2		
	b11-NH3+2		
609.991	b11+2		
611.533	b12-H3PO4+2		
644.422	y6-H2O		
	y12+2		
651.316	b12-H2O+2		
	b12-NH3+2		

I. MH_2^{2+} 928.3361(LTQ MSMS)

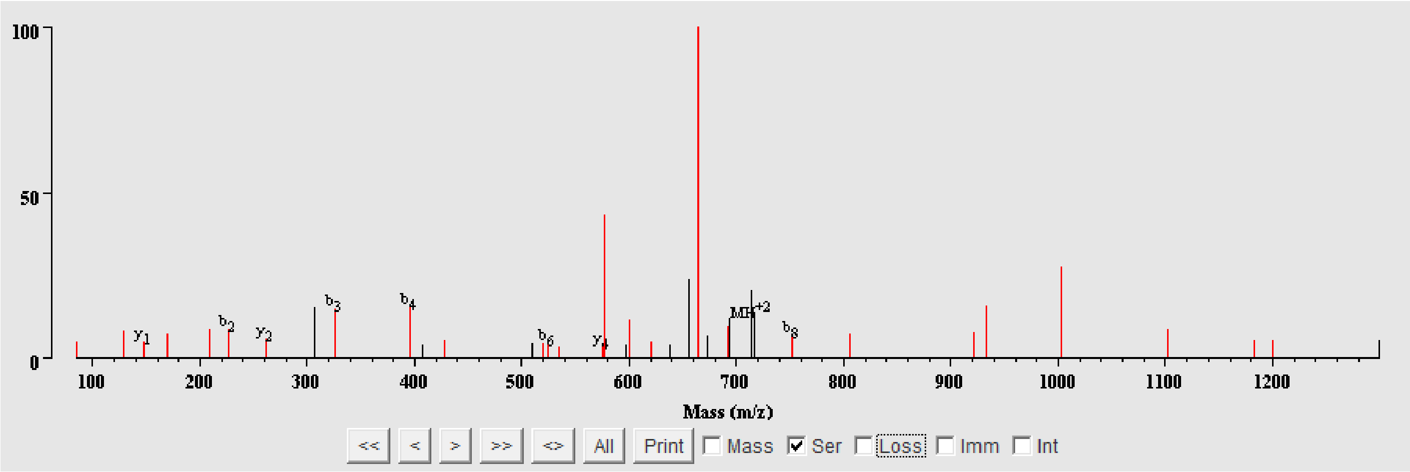


☐ Mass ☑ Ser ☐ Loss ☐ Imm ☐ Int

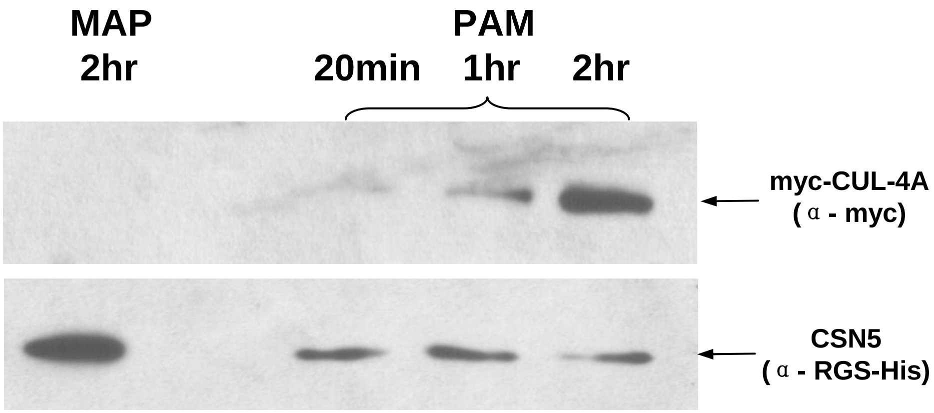
m/z	Ion Type
363.003	b4
474.471	b5-NH3
491.327	b5
522.145	y5-H3PO4
602.424	y5-H2O
	b6-H2O
	b6-NH3
620.221	y5
	b6
735.083	b7
770.316	y15-H3PO4+2
827.073	b16-H3PO4+2
835.897	y16-H3PO4+2
850.304	b8
862.216	a16+2
	y7
879.29	MH-H3PO4+2
919.333	b9-H2O
	MH-H2O+2
	y8
	MH-NH3+2
1006.372	y9
1218.551	y11-H2O
	b12-H2O
1236.341	y11
	b12
1347.481	y12-H2O
1365.795	y12

J. MH_2^{2+} 713.4 (QSTAR MSMS)

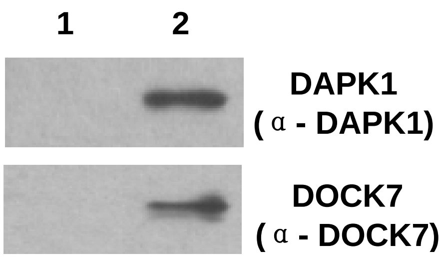
KPVAGALDVS(Phospho)FNK^{+2}



m/z	Ion Type
84.0856	K
129.1005	GA
	AG
	K
147.1084	y1
169.1394	PV-28
209.101	b2-NH3
226.1669	b2
261.1613	y2
325.2287	PVAG
	b3
396.2796	PVAGA
	b4
428.3447	GALDV-28
520.3711	a11-H3PO4+2
524.2754	b6
534.3184	b11-H3PO4+2
575.2794	y4
576.3469	y5-H3PO4
600.4085	y12-H3PO4+2
620.4748	b7-NH3
664.4596	MH-H3PO4+2
691.3847	y6-H3PO4
713.4734	ALDVS(Phospho)F
	MH+2
752.3213	GALDVS(Phospho)F-H2O
	b8
805.5167	a9-H2O
920.5723	b10-H3PO4
932.6546	y9-H3PO4
1003.5808	y10-H3PO4
1102.7568	y11-H3PO4
1181.8746	b12-H3PO4
1199.64	y12-H3PO4



Supplemental Figure 4



Supplemental Figure 5

Supplemental Table 1. Protein Reports of the Identified CSN Interacting Proteins Using MAP-SILA

	MAP-SILAC(1)				MAP-SILAC(2)				
Acc #	Num Uniqu	% Cov	Best Disc	Best Expe	Num Uniqu	% Cov	Best Disc	Best Expe	Num Uniqu
P08107	36	45.7	5.78	4.20E-10	50	44.3	5.16	6.50E-09	43
Q96N67	60	28.8	4.86	2.20E-08	39	20.3	3.79	9.50E-07	54
Q4VCS5	37	32.6	4.57	7.50E-08	37	29.3	3.63	4.00E-06	27
Q16531	19	21.1	4.45	1.20E-07	33	25.7	4.92	5.20E-07	8
O43491	15	15.7	4.35	1.90E-07	39	38.1	4.09	7.80E-07	15
P35580	15	10.4	5.33	2.90E-09	29	19.5	5.22	2.20E-07	5
P34931	21	26.5	5.78	4.20E-10	29	27.8	5.16	6.50E-09	24
P11021	18	27.1	4.7	4.20E-08	33	38.4	3.7	2.10E-06	18
Q13620	15	20.1	3.81	1.90E-06	31	35.1	3.96	1.60E-06	9
O75955	21	43.1	4.26	2.80E-07	6	15.9	3.35	2.50E-06	22
P08238	31	30.8	5.85	3.10E-10	22	21.3	4.83	4.80E-08	18
P28289	14	47.1	4.22	3.30E-07	18	55.4	3.68	2.10E-06	21
P35579	6	3.8	2.78	5.10E-05	21	14.5	3.9	1.10E-06	1
Q6WCQ1	24	24.2	4.19	3.80E-07	10	13.3	3.23	4.60E-06	10
O75970	23	14.6	4.41	1.50E-07	17	12.9	3.67	6.40E-06	11
Q13618	6	13.3	3.45	8.70E-06	15	23.7	4.78	5.50E-08	
P17066	11	13.4	4.56	7.80E-08	12	11.2	4.85	2.20E-08	13
Q5VUJ6	14	18.8	4.77	3.10E-08	11	17.4	3.33	3.60E-05	8
O15085	2	2.6	3.93	1.10E-06	12	12.2	4.71	1.00E-07	3
P53355	15	10.7	4.44	1.30E-07	10	10.6	5.03	3.40E-08	17
Q8N3R9	9	18.5	4.43	1.30E-07	16	27.6	3.21	8.30E-06	9
P11171	13	16.4	4.44	1.30E-07	13	15.3	2.5	1.40E-05	10
O14974	14	13.8	4.44	1.30E-07	11	12.7	4.52	1.40E-07	9
Q9UJZ1	7	27	4.45	1.20E-07	2	9.3	4.11	5.10E-07	9
Q13617	5	6.4	2.33	1.70E-05	13	17.6	3.58	1.00E-05	
Q92466	4	8.7	1.55	2.40E-04	9	28.1	4.69	7.80E-09	3
Q13616	1	2.4	1.87	1.40E-04	11	18.3	3.99	3.80E-06	
P25705	12	23	4.72	3.90E-08	8	19.5	4.43	1.30E-07	9
P13639	5	6.9	3.86	1.60E-06	3	4.8	3.12	3.50E-05	11
Q9Y2D5	11	12.6	4.54	8.30E-08	5	10.8	3.44	6.10E-07	6
Q13619	9	12.3	2.5	2.60E-05	8	10.7	2.82	9.80E-06	4
Q9P0K7	10	11.1	4.86	2.20E-08	4	4.8	2.21	1.20E-04	4
Q9NZQ3	11	15.7	3.72	2.70E-06	7	8.9	3.41	3.70E-06	9
P48741	7	14.2	4.55	7.90E-08	7	10.9	4.5	2.20E-08	8
P60660	6	35.1	4.02	7.70E-07	12	48.3	2.91	7.30E-06	6
Q9P2K6	2	7.7	3.06	2.00E-05	7	20	4.06	6.10E-07	2
Q9UDY2	7	8.2	3.86	1.50E-06	3	4.3	2.01	3.70E-04	9
O75477	7	14.7	3.66	3.70E-06	2	7.5	1.88	1.40E-04	8
Q8NI35	5	3.1	5.37	2.50E-09	5	3.9	3.54	1.10E-05	7
P04843	7	10.7	4.22	3.30E-07	2	4	0.41	0.005	6
Q9Y4B6	4	3.1	2.6	7.50E-05	6	5.6	3.85	5.40E-06	5
Q14651	6	4.1	3.3	1.70E-05	5	5.6	2.88	6.30E-05	6
P80723	5	48	2.94	3.60E-05	6	57.3	3.17	2.10E-05	5
Q14315	5	1.7	2.82	1.20E-05	7	3.7	3.03	3.90E-06	7
Q8IY63	6	7.6	3.48	7.70E-06	6	7.1	2.23	1.00E-04	4
Q13561	5	10.7	3.74	2.60E-06	5	15.5	3.02	9.70E-06	
P62877	3	18.5	4.15	4.40E-07	7	18.5	2.37	1.40E-05	2
Q6PJ61	4	13	2.71	1.30E-05	1	4.5	2.78	3.90E-05	3

P36957	2	6	3.46	8.50E-06	2	3.1	3.86	2.00E-06	1
Q9NUP9	2	14.2	4.24	3.10E-07	1	8.1	1.65	3.80E-04	2
P63167	2	12.4	3.55	5.70E-06	3	20.2	2.25	2.20E-05	1
Q9NNW5	3	5.2	0.85	5.90E-04					2

C and PAM-SILAC Approaches

PAM-SILAC(1)			PAM-SILAC(2)						
% Cov	Best Disc	Best Expe	Num Uniq	% Cov	Best Disc	Best Expe	Protein M	Species	Protein Na
36.7	5.28	3.90E-09	33	34.6	4.41	1.50E-07	70052.8	HUMAN	Heat shock
21.2	4.88	8.50E-10	26	11.1	4.42	1.40E-07	242562.8	HUMAN	Dedicator
25.1	3.62	4.30E-06	40	36.5	4.39	1.40E-07	118086.4	HUMAN	Angiomoti
10.4	4.94	1.40E-08	13	12.9	3.63	4.10E-06	126969	HUMAN	DNA dama
16.7	3.76	2.30E-07	23	22.9	3.71	3.00E-06	112589	HUMAN	Band 4.1-li
3.5	2.11	1.40E-05	2	1.2	2.7	1.40E-04	228941	HUMAN	Myosin-10
22.8	4.91	3.90E-09	18	18.1	4.3	2.30E-07	70375.6	HUMAN	Heat shock
26.3	4.33	1.30E-07	15	17	3.89	1.40E-06	72333.5	HUMAN	78 kDa glu
7.5	2.82	1.50E-05	13	14.5	3.62	4.20E-06	102300	HUMAN	Cullin-4B -
42.6	5.55	2.20E-09	3	9.8	3.18	2.80E-05	47355.7	HUMAN	Flotillin-1 -
22.1	4.24	5.70E-08	4	5.5	3.69	2.40E-06	83264.9	HUMAN	Heat shock
46.5	4.2	1.50E-07	12	39.6	3	6.10E-05	40569.5	HUMAN	Tropomodu
0.6	1.77	9.60E-05	2	1.1	1.61	9.20E-04	226534.2	HUMAN	Myosin-9 -
12.3	2.65	2.90E-06	4	5	2.17	1.60E-04	116447.1	HUMAN	Myosin pho
6.2	4.15	1.00E-06	8	4.4	2.7	1.70E-05	218598.4	HUMAN	Multiple PD
			3	4.4	3.47	8.00E-06	88931	HUMAN	Cullin-3 -
14.2	4.77	6.80E-09	9	10	4.3	2.30E-07	71028.7	HUMAN	Heat shock
12.8	4.8	1.50E-07	10	13.5	3.09	4.00E-05	84589.1	HUMAN	Leucine-ric
2.9	4.67	8.60E-09	2	2.2	1.39	0.001	167705.9	HUMAN	Rho guanin
9.8	3.6	1.90E-07	7	6.2	3.88	1.40E-06	160287.8	HUMAN	Death-asso
17.5	4.04	1.20E-08	7	11.4	4.32	2.10E-07	77294.2	HUMAN	MAGUK p5
13.3	5.03	6.30E-08	3	3.1	2.6	3.30E-04	97017.7	HUMAN	Protein 4.1
7.4	3.34	5.30E-07	3	3.2	2.88	1.00E-04	115281.6	HUMAN	Protein pho
29.8	4.99	2.70E-08	1	4.5	1.28	1.80E-04	38534.4	HUMAN	Stomatin-li
			3	4	3.67	3.10E-06	86983.9	HUMAN	Cullin-2 -
7.3	2	4.90E-05	4	9.8	2.68	7.10E-06	47864.4	HUMAN	DNA dama
			1	1.3	2.96	2.90E-06	89679.3	HUMAN	Cullin-1 -
15.6	3.06	1.40E-06	4	6.1	2.95	3.80E-05	59751.1	HUMAN	ATP syntha
12.9	4.05	5.60E-07					95339	HUMAN	Elongation
10.7	2.22	3.20E-06	3	3.7	3.52	6.40E-06	96102	HUMAN	A-kinase a
4.5	2.6	5.70E-05	2	3.2	2.49	5.40E-04	87681	HUMAN	Cullin-4A -
5.2	2.36	1.50E-05	2	2.2	1.52	7.30E-04	110042.2	HUMAN	Ankycorbin
13.2	3.11	1.60E-05	9	9.3	2.63	2.90E-04	78960.9	HUMAN	SH3 adapt
13.1	4.43	6.80E-09	8	13.1	4.3	2.30E-07	40244.8	HUMAN	Putative he
29.1	3.57	1.80E-07	2	8.6	3.31	5.30E-06	16930.2	HUMAN	Myosin ligh
2.2	0.79	4.80E-04	3	11.1	3.62	4.20E-06	56868.3	HUMAN	Kelch dom
7.4	3.48	3.40E-07	5	6.7	2.93	8.20E-05	133973.1	HUMAN	Tight juncti
13.6	3.6	1.90E-07	1	3.5	1.7	2.00E-04	38926.2	HUMAN	Erlin-1 pre
4.1	3.82	4.00E-07	2	2.1	1.46	2.10E-04	196369.7	HUMAN	InaD-like p
9.2	4.11	2.10E-07					68570	HUMAN	Dolichyl-di
4.2	2.94	7.80E-07	5	4.5	2.38	9.40E-05	169008.7	HUMAN	Protein VP
7	3.28	7.70E-07	4	4.1	3.78	2.20E-06	70353.2	HUMAN	Plastin-1 -
51.1	4.35	2.80E-08	5	35.7	1.66	3.30E-04	22693.6	HUMAN	Brain acid
2.5	2.98	8.40E-08	4	1.3	2.35	1.30E-04	290961.6	HUMAN	Filamin-C -
4.9	2.11	2.10E-05	2	1	2.43	7.50E-05	106575.1	HUMAN	Angiomoti
			4	10.5	2.98	2.20E-06	44231.4	HUMAN	Dynactin s
18.5	1.48	6.90E-05	6	18.5	2.29	5.20E-06	12274.1	HUMAN	RING-box
7.9	5.44	3.00E-09	3	8.8	3.38	1.20E-05	69031.4	HUMAN	F-box only

2	0.88	3.30E-04	3	6	1.88	1.50E-04	48640.6	HUMAN	Dihydrolipo
14.2	0.26	0.0063	4	20.8	2.36	5.50E-04	21834.2	HUMAN	Lin-7 homo
12.4	2.35	2.30E-05	2	12.4	3.12	3.60E-05	10366	HUMAN	Dynein ligh
5.7	2.9	2.50E-06					121725.7	HUMAN	WD repeat

me
70 kDa protein 1 - Homo sapiens (Human)
f cytokinesis protein 7 - Homo sapiens (Human)
- Homo sapiens (Human)
ge-binding protein 1 - Homo sapiens (Human)
ke protein 2 - Homo sapiens (Human)
- Homo sapiens (Human)
70 kDa protein 1L - Homo sapiens (Human)
cose-regulated protein precursor - Homo sapiens (Human)
Homo sapiens (Human)
Homo sapiens (Human)
protein HSP 90-beta - Homo sapiens (Human)
lin-1 - Homo sapiens (Human)
Homo sapiens (Human)
sphatase Rho-interacting protein - Homo sapiens (Human)
Z domain protein - Homo sapiens (Human)
omo sapiens (Human)
70 kDa protein 6 - Homo sapiens (Human)
h repeat and calponin homology domain-containing protein 2 - Homo sapiens (Human)
e nucleotide exchange factor 11 - Homo sapiens (Human)
ciated protein kinase 1 - Homo sapiens (Human)
5 subfamily member 5 - Homo sapiens (Human)
- Homo sapiens (Human)
sphatase 1 regulatory subunit 12A - Homo sapiens (Human)
ke protein 2 - Homo sapiens (Human)
omo sapiens (Human)
ge-binding protein 2 - Homo sapiens (Human)
omo sapiens (Human)
ase subunit alpha, mitochondrial precursor - Homo sapiens (Human)
factor 2 - Homo sapiens (Human)
nchor protein 2 - Homo sapiens (Human)
Homo sapiens (Human)
- Homo sapiens (Human)
er protein SPIN90 - Homo sapiens (Human)
at shock 70 kDa protein 7 - Homo sapiens (Human)
t polypeptide 6 - Homo sapiens (Human)
ain-containing protein 5 - Homo sapiens (Human)
ion protein ZO-2 - Homo sapiens (Human)
cursor - Homo sapiens (Human)
rotein - Homo sapiens (Human)
phosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor - Homo sapiens (Human)
RBP - Homo sapiens (Human)
Homo sapiens (Human)
soluble protein 1 - Homo sapiens (Human)
- Homo sapiens (Human)
-like protein 1 - Homo sapiens (Human)
ubunit 2 - Homo sapiens (Human)
protein 1 - Homo sapiens (Human)
protein 46 - Homo sapiens (Human)

›yllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial prec
›log C - Homo sapiens (Human)
ıt chain 1, cytoplasmic - Homo sapiens (Human)
:-containing protein 6 - Homo sapiens (Human)

cursor - Homo sapiens (Human)

Supplemental Table 2. Quantification of Putative PIPs Using MAP-SILAC and Tc-PAM-SILAC Approache

A. Stable Interactors*

	MAP-SILAC(1)			PAM-SILAC(1)			MAP-SILAC(2)		
Acc	n	avg	std	n	avg	std	n	avg	std
Q4VCS5	36	high	n/a	38	high	n/a	26	high	n/a
Q9Y4B6	4	high	n/a	4	high	n/a	2	high	-
P80723	3	9.4	2.2	-	-	-	3	6.9	1.6
Q8IY63	5	7.2	1.8	2	4.3	0.5	3	6.6	1.4
P28289	11	5.7	1.5	16	4.0	0.7	8	6.0	1.1
P63167	2	4.7	0.7	1	4.2	-	3	3.2	0.4
Q9UJZ1	6	3.9	1	9	2.3	0.3	2	3.7	0.3
Q96N67	52	3.9	0.9	48	2.5	0.3	14	2.7	0.5
O75955	17	2.7	0.5	21	2.0	0.4	4	2.8	0.7
O43491	13	3.0	0.8	13	2.7	0.6	15	2.2	0.9
P48741	4	2.9	0.6	6	1.7	0.1	6	2.7	0.6
Q9NZQ3	9	2.9	0.8	9	3.4	0.7	2	3.0	0.7
P34931	16	2.6	0.6	18	2.2	0.5	27	2.5	0.6
P25705	7	2.5	0.5	6	1.8	0.3	5	1.6	0.1
P08107	33	2.5	0.7	42	2.0	0.4	47	2.8	0.4
P17066	9	2.5	0.7	10	1.8	0.3	7	2.8	0.6
P35579	6	2.3	0.3	1	2.5	-	15	2.2	0.6
Q9NNW5	3	high	n/a	2	high	n/a	-	-	-
P11021	13	2.1	0.5	8	1.7	0.2	17	1.6	0.4
P08238	17	2.0	0.4	11	1.8	0.2	21	2.1	0.5

B. Putative CSN Interacting Proteins**

MAP-SILAC(1)			PAM-SILAC(1)			MAP-SILAC(2)			P
Acc	n	avg	std	n	avg	std	n	avg	std
O75477	7	2.5	0.9	8	1.4	0.1	-	-	-
Q13561	2	2.4	0.5	3	1.3	0.2	5	2.0	0.6
P60660	4	2.2	0.3	6	1.4	0.1	2	2.8	0.2
P36957	2	2.1	0.3	1	1.5	-	4	1.6	0.2
Q6WCQ1	16	2.0	0.4	8	1.3	0.2	9	1.7	0.5
P13639	3	2.0	0.4	-	-	-	-	-	-
P11171	5	1.9	0.6	7	1.1	0.1	2	1.8	0.1
Q14651	6	1.8	0.3	6	1.3	0.2	5	1.9	0.3
Q9P0K7	10	1.7	0.5	4	1.0	0.2	3	1.7	0.3
Q14315	5	1.7	0.2	7	0.9	0.1	3	1.9	0.2
Q9UDY2	2	1.7	0.2	2	1.0	0.0	2	1.8	0.3
P04843	6	1.7	0.3	6	1.1	0.1	-	-	-

Note:

*Stable interactors are the ones with similar MAP-SILAC and PAM-SILAC ratios (< 2 fold difference).

**These proteins have MAP-SILAC ratios >1.5, whereas their PAM-SILAC ratios =<1.5 or not determined.
MAP-SILAC ratios are higher than PAM-SILAC ratios but less than 2-fold increase.

n: number of unique peptides used for quantitation; avg: average value of SILAC ratios (L/H), high SILAC ratios
that the heavy labeled peaks of the peptide pairs were not detected; std: standard deviation of SILAC ratios in

es

PAM-SILAC(2)			
n	avg	std	Protein Name
22	high	n/a	Angiomotin
-	-	-	Protein VPRBP
4	4.8	0.7	Brain acid soluble protein 1
1	4.5	-	Angiomotin-like protein 1
10	3.5	0.6	Tropomodulin-1
3	2.2	0.2	Dynein light chain 1, cytoplasmic
1	3.1	-	Stomatin-like protein 2
3	1.7	0.4	Dedicator of cytokinesis protein 7
1	1.7	-	Flotillin-1
17	1.8	0.3	Band 4.1-like protein 2
7	2.2	0.4	Putative heat shock 70 kDa protein 7
2	1.8	0.1	SH3 adapter protein SPIN90
16	2.0	0.5	Heat shock 70 kDa protein 1L
4	1.6	0.3	ATP synthase subunit alpha, mitochondrial precursor
32	2.3	0.4	Heat shock 70 kDa protein 1
10	2.2	0.7	Heat shock 70 kDa protein 6
1	1.6	-	Myosin-9
-	-	-	WD repeat-containing protein 6
14	1.7	0.3	78 kDa glucose-regulated protein precursor - Homo sapiens (Human)
4	1.8	0.2	Heat shock protein HSP 90-beta - Homo sapiens (Human)

AM-SILAC(2)			
n	avg	std	protein name
-	-	-	Erlin-1 precursor - Homo sapiens (Human)
1	1.3	-	Dynactin subunit 2 - Homo sapiens (Human)
2	1.5	0.3	Myosin light polypeptide 6 - Homo sapiens (Human)
3	1.2	0.1	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydroge
5	0.9	0.1	Myosin phosphatase Rho-interacting protein - Homo sapiens (Human)
-	-	-	Elongation factor 2
2	0.9	0.1	Protein 4.1 - Homo sapiens (Human)
4	1.2	0.2	Plastin-1 - Homo sapiens (Human)
2	1.0	0.1	Ankycorbin - Homo sapiens (Human)
2	1.0	0.1	Filamin-C - Homo sapiens (Human)
3	0.9	0.1	Tight junction protein ZO-2 - Homo sapiens (Human)
-	-	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precurs

s indicate
each experiment.

enase complex, mitochondrial precursor - Homo sapiens (Human)

or - Homo sapiens (Human)