Supplementary Table S3. The list of phosphopeptides identified from Fresh tissues.

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
1	AAETPAVASCWSGPQVSPEHK	57.021465@C:10, 79.966331@S:17	58.6	763.6714	3	2287.992	-0.0008	43.629	K	E	+		@S:17		AAETPAVA[s]CW[s]GPQV[s]PEHK	SRRM2_MOUSE;S1269
2	AAETPAVASCWSGPQVSPEHK	57.021465@C:10, 79.966331@S:9	31.7	763.672	3	2287.994	0.0008	35.389	K	E	+		@S:9		AAETPAVA[s]CW[s]GPQV[s]PEHK	SRRM2_MOUSE;S1261
3	AAPGGASPTIFSR	79.966331@S:7	20.7	656.3081	2	1310.602	-0.0003	34.985	K	I	+		@S:7		AAPGGA[s]P[t]IF[s]R	HINT2_MOUSE;S52
4	AAQSPQQHSSGDPTEEESPV	79.966331@S:18	40.2	1080.937	2	2159.859	-0.005	21.638	K	-	+		@S:18		AAQSPQQHSSGDPTEEE[pS]PV	MOT1_MOUSE;S491
5	AASADSTTEGTPTDGFTVLSTK	79.966331@S:3	52.8	1118.996	2	2235.976	-0.002	44.976	K	S	+	ambiguos		@S:3orS:6	AA[s]AD[s][t][t]EGTPTDGFTVLSTK	H2AY_MOUSE;S170orS173
6	AASADSTTEGTPTDGFTVLSTK	79.966331@S:6	63.3	1118.995	2	2235.975	-0.0034	44.887	K	S	+		@S:6		AA[s]AD[s][t][t]EGTPTDGFTVLSTK	H2AY_MOUSE;S173
7	AASADSTTEGTPTDGFTVLSTK	79.966332@T:8	27.3	1118.994	2	2235.973	-0.0054	44.366	K	S	+		@T:8		AA[s]AD[s][t][t]EG[t]PTDGFTVLSTK	H2AY_MOUSE;T175
8	AASLTEDRGRDPVK	79.966331@S:3	32.2	532.2573	3	1593.75	-0.0012	19.715	K	R	+		@S:3		AA[s]L[t]EDRGRDPVK	IF4G1_MOUSE;S1211
9	AASLTEDRGRDPVK	79.966332@T:5	20.2	532.2568	3	1593.749	-0.0025	19.714	K	R	+		@T:5		AA[s]L[t]EDRGRDPVK	IF4G1_MOUSE;T1213
10	AASPPASASDLIEQQQK	79.966331@S:3	77.1	910.9261	2	1819.838	0.0023	43.781	R	R	+		@S:3		AA[pS]PPASASDLIEQQQK	FA40A_MOUSE;S335
11	AAVQELSGSILTSEDPEER	79.966331@S:9,79.966332@T:12	29.4	1095.963	2	2189.912	-0.001	48.548	R	G	+		@S:9,@T:12		AAVQEL[s]G[s]IL[t][s]EDPEER	PSN1_MOUSE;S367,PSN1_MOUSE;T370
12	AAVQMEFLASSESV	15.994915@M:5,79.966331@S:13	57.4	782.8337	2	1563.653	0.0001	54.865	K	-	+		@S:13		AAVQMEFLASSE[pS]V	GTR2_MOUSE;S522
13	AAVQMEFLASSESV	79.966331@S:13	44.7	774.837	2	1547.659	0.0015	57.285	K	-	+		@S:13		AAVQMEFLAS[s]E[s]V	GTR2_MOUSE;S522
14	ADSDGDLSENDDGAGDLR	79.966331@S:3,79.966331@S:8	53.3	991.3364	2	1980.658	-0.0042	33.101	R	S	+		@S:3,@S:8		AD[pS]DGDL[pS]ENDDGAGDLR	AKAP8_MOUSE;S320,AKAP8_MOUSE;S325
15	ADSDQDSKMSFKEIK	79.966331@S:10	39.9	904.8898	2	1807.765	-0.0049	49.301	R	S	+		@S:10		ADSDQD[s]KM[s]FKEIK	PLCD3_MOUSE;S199
16	ADSHGELDLAR	79.966331@S:3	30.4	421.8502	3	1262.529	-0.0005	26.024	R	T	+		@S:3		AD[pS]HGELDLAR	ACOT1_MOUSE;S56,ACOT4_MOUSE;S56,ACOT5_MOUSE;S56,ACOT6_MOUSE;S56,ACOT3_MOUSE;S67
17	ADSVPNLEPSEESLVTK	79.966331@S:3	30.4	947.9381	2	1893.862	0.0009	44.086	R	-	+		@S:3		AD[pS]VPNLEPSEESLVTK	LNP_MOUSE;S411
18	AEAKEESEESDEDMGFGLFD	15.994915@M:14, 79.966331@S:10	23.4	1165.928	2	2329.841	-0.0044	52.409	K	-	+		@S:10		AEAKEE[s]EE[s]DEDMGFGLFD	RLA0_MOUSE;S307
19	AEAKEESEESDEDMGFGLFD	15.994915@M:14, 79.966331@S:7,79.966331@S:10	35.4	804.2778	3	2409.812	-0.0004	61.044	K	-	+		@S:7,@S:10		AEAKEE[pS]EE[pS]DEDMGFGLFD	RLA0_MOUSE;S304,RLA0_MOUSE;S307
20	AEAKEESEESDEDMGFGLFD	79.966331@S:10	32.9	1157.93	2	2313.846	-0.0052	59.022	K	-	+		@S:10		AEAKEE[s]EE[s]DEDMGFGLFD	RLA0_MOUSE;S307
21	AEAKEESEESDEDMGFGLFD	79.966331@S:7	50.9	1157.93	2	2313.845	-0.0058	60.502	K	-	+		@S:7		AEAKEE[pS]EE[pS]DEDMGFGLFD	RLA0_MOUSE;S304
22	AEAKEESEESDEDMGFGLFD	79.966331@S:7,79.966331@S:10	39.5	1197.912	2	2393.81	-0.007	68.781	K	-	+		@S:7,@S:10		AEAKEE[s]EE[s]DEDMGFGLFD	RLA0_MOUSE;S304,RLA0_MOUSE;S307
23	AEALSSLHGDDQDSEDEVLTVPEVK	79.966331@S:14	46.3	921.7455	3	2762.215	-0.0023	46.236	K	V			@S:14		AEALSSLHGDDQD[pS]EDEVLTVPEVK	MPRI_MOUSE;S2401
24	AEALSSLHGDDQDSEDEVLTVPEVK	79.966331@S:6	57.1	921.7459	3	2762.216	-0.0011	46.525	K	V			@S:6		AEAL[s][s]LHGDDQD[s]EDEVLTVPEVK	MPRI_MOUSE;S2393
25	AEEDEILNRSPR	79.966331@S:10	48.3	503.5627	3	1507.666	-0.0005	26.125	K	N	+		@S:10		AEEDEILNR[pS]PR	CALX_MOUSE;S582
26	AEEPAPRTSHK	79.966331@S:9	20.1	434.8664	3	1301.577	0.0009	25.84	R	S	+		@S:9		AEEPAPR[t][s]HK	BHLH9_MOUSE;S157
27	AELGMNDSPSQSPPVK	79.966331@S:12	21	868.8805	2	1735.746	-0.0023	32.397	R	R	+		@S:12		AELGMND[s]P[s]Q[s]PPVK	ACSA_MOUSE;S267
28	AEQSLHDLQER	79.966331@S:4	38.1	469.2084	3	1404.603	0.0001	29.669	R	L	+		@S:4		AEQ[pS]LHDLQER	STIM1_MOUSE;S257
29	AERLSPPASSGSER	79.966331@S:5	29.2	508.5659	3	1522.676	-0.0018	20.618	K	R	+		@S:5		AERL[s]PPA[s][s]G[s]ER	MLXPL_MOUSE;S614
30	AESPETSAVESTQSTPQK	79.966331@S:3	85.1	978.9226	2	1955.831	-0.0054	24.167	R	G	+		@S:3		AE[s]PE[t]SAVESTQSTPQK	PDS5B_MOUSE;S1356
31	AESPETSAVESTQSTPQK	79.966331@S:7	53.5	652.9535	3	1955.839	0.0024	30.204	R	G			@S:7		AE[s]PE[t][s]AVESTQSTPQK	PDS5B_MOUSE;S1360
32	AESSDSGAESEEEEAQEELK	79.966331@S:6	65.8	1117.426	2	2232.837	-0.0056	36.262	K	G	+		@S:6		AE[s][s]D[s]GAE[s]EEEEAQEELK	ACBD5_MOUSE;S187
33	AESSDSGAESEEEEAQEELK	79.966331@S:6,79.966331@S:10	45.1	1157.409	2	2312.804	-0.0053	38.036	K	G	+		@S:6,@S:10		AE[s][s]D[s]GAESEEEEAQEELK	ACBD5_MOUSE;S187,ACBD5_MOUSE;S191
34	AETSESSGSAPAVPEASASPK	79.966331@S:19	84.5	1020.441	2	2038.868	-0.0055	25.014	K	Q			@S:19		AETSESSGSAPAVPEA[s]A[s]PK	MECP2_MOUSE;S80
35	AGDVLEDSPK	79.966331@S:8	70.5	555.7388	2	1109.463	-0.0012	22.74	R	R	+		@S:8		AGDVLED[pS]PK	HDGF_MOUSE;S165
36	AGDVLEDSPKRPK	79.966331@S:8	60.8	497.9113	3	1490.712	-0.0009	19.051	R	E	+		@S:8		AGDVLED[pS]PKRPK	HDGF_MOUSE;S165
37	AGLEDSEEDVEEAEVEAEDKDH	79.966331@S:6	73.7	842.3285	3	2523.964	-0.0015	39.371	R	-	+		@S:6		AGLED[pS]EEDVEEAEVEAEDKDH	TBB1_MOUSE;S435
38	AGNSDSEEDDANERVDLILEPK	79.966331@S:4,79.966331@S:6	34.8	859.3533	3	2575.038	0.0017	52.244	K	D	+		@S:4,@S:6		AGN[pS]D[pS]EEDDANERVDLILEPK	FAM21_MOUSE;S157,FAM21_MOUSE;S159
39	AGSMVLPYILSSTLRR	15.994915@M:4,79.966332@T:13,79.966331@Y:8	25.9	647.3093	3	1938.906	0.0023	37.029	R	L	+	ambiguos	@Y:8	@S:12orT:13	AG[s]MVLP[y]IL[s][s][t]LRR	DOCK5_MOUSE;Y1661,DOCK5_MOUSE;S1665orT1666
40	AGSPQLDDIR	79.966331@S:3	55.5	576.2582	2	1150.502	-0.0002	29.91	R	V	+		@S:3		AG[pS]PQLDDIR	EI2BE_MOUSE;S540
41	AHNLQDGQLSDTGDLGEDIASN	79.966332@T:12	25.8	783.9993	3	2348.976	0.0004	43.347	K	-	+	ambiguos		@S:10orT:12	AHNLQDGQL[s]D[t]GDLGEDIASN	KI21A_MOUSE;S1660orT1662
42	AITSLLGGGSPK	79.966331@S:10	54.9	590.8025	2	1179.59	0.0004	50.702	K	N	+		@S:10		AITSLLGGG[pS]PK	NIPBL_MOUSE;S2652
43	AKDSTYQTLI	79.966331@S:4,79.966332@T:5	25.2	433.8468	3	1298.519	-0.0009	23.293	K	-	+		@S:4,@T:5		AKD[s][t][y]Q[t]LI	C16L2_MOUSE;S166,C16L2_MOUSE;T167
44	AKDSTYQTLI	79.966332@T:5,79.966331@Y:6	29	433.8469	3	1298.519	-0.0008	23.144	K	-			@T:5,@Y:6		AKD[s][t][y]Q[t]LI	C16L2_MOUSE;T167,C16L2_MOUSE;Y168
45	AKPAAQSEEETATSPAASPTPQSAER	79.966331@S:14, 79.966331@S:18	64.8	924.7278	3	2771.162	-0.0074	21.768	R	S	+		@S:14,@S:18		AKPAAQSEEETAT[s]PAA[s]P[t]PQSAER	EIF3B_MOUSE;S75,EIF3B_MOUSE;S79

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
46	AKPAAQSEEETATSPAASPTPQSAER	79.966331@S:18	73	898.073	3	2691.197	-0.0052	21.051	R	S	+		@S:18		AKPAAQSEEETATSPAA[pS]PTPQSAER	EIF3B_MOUSE;S79
47	AKPAAQSEEETATSPAASPTPQSAER	79.966331@S:7,79.966331@S:23	45.8	924.7284	3	2771.163	-0.0055	22.932	R	S	+		@S:7,@S:23		AKPAAQ[s]EEE[t]AT[s]PAA[s]P[t]PQSAER	EIF3B_MOUSE;S68,EIF3B_MOUSE;S84
48	AKPAAQSEEETATSPAASPTPQSAER	79.966332@T:13, 79.966331@S:14, 79.966331@S:18	51.2	951.3845	3	2851.132	-0.0035	23.215	R	S	+		@T:13,@S:14, @S:18		AKPAAQ[s]EEE[t]AT[s]PAA[s]P[t]PQSAER	EIF3B_MOUSE;T74,EIF3B_MOUSE;S75,EIF3B_MOUSE;S79
49	AKPAAQSEEETATSPAASPTPQSAER	79.966332@T:20	58.6	898.0752	3	2691.204	0.0013	27.116	R	S	+		@T:20		AKPAAQSEEETATSPAA[s]P[t]PQSAER	EIF3B_MOUSE;T81
50	AKSAIESDVDFWDK	79.966331@S:3	22.5	564.2501	3	1689.728	-0.0001	45.816	R	L			@S:3		AK[s]AIE[s]DVDFWDK	PEX5_MOUSE;S281
51	AKSFLEYCISLNK	57.021465@C:8,79.966331@S:10,79.966331@Y:7	19.9	578.2528	3	1731.737	0.0021	27.321	R	L			@Y:7,@S:10		AK[s]FLE[y]CI[s]LNK	VRTN_MOUSE;Y417,VRTN_MOUSE;S420
52	ALDESLAEPHLEDR	79.966331@S:5	29.9	558.9187	3	1673.734	0.0046	36.974	K	T	+		@S:5		ALDE[pS]LAEPHLEDR	PML_MOUSE;S609
53	ALELYEQLRQR	79.966331@Y:5	27.9	749.8731	2	1497.732	-0.0024	58.999	K	T	+		@Y:5		ALEL[pY]EQLRQR	DYHC2_MOUSE;Y1966
54	ALFKPPEDSQDDESDSDAEEEQTTK	79.966331@S:14, 79.966331@S:16	23.9	991.0468	3	2970.119	-0.003	38.13	K	R	+		@S:14,@S:16		ALFKPPED[s]QDDE[s]D[s]DAEEEQ[t][t]K	THOC5_MOUSE;S312,THOC5_MOUSE;S314
55	ALLSPTFTSGK	79.966331@S:4	41.4	601.2971	2	1200.58	0.0005	41.691	R	L	+		@S:4		ALL[s]P[t]F[t][s]GK	CP3AB_MOUSE;S134,CP341_MOUSE;S134
56	ALLSPTFTSGK	79.966331@S:9	28	601.2969	2	1200.579	0.0001	39.77	R	L	+	ambiguos		@T:8orS:9	ALLSP[t]F[t][s]GK	CP3AB_MOUSE;T138orS139,CP341_MOUSE;T138orS139
57	ALSTDPASPNLK	79.966331@S:8	40.6	647.3087	2	1292.603	0.0016	27.794	K	S	+		@S:8		ALSTDPA[pS]PNLK	TLN1_MOUSE;S1328
58	ALVVPEPEPDSDSNQER	79.966331@S:13	34.2	981.4292	2	1960.844	0.0024	35.746	K	K	+		@S:13		ALVVPEPEPD[s]D[s]NQER	BRE1A_MOUSE;S138
59	AMSGSWER	15.994915@M:2,79.966331@S:3	44	510.1859	2	1018.357	-0.0007	20.267	R	D	+		@S:3		AM[pS]GSWER	F134C_MOUSE;S26
60	APKEELASDLEEMATSSAK	79.966331@S:8	48.8	696.3131	3	2085.917	-0.0002	50.716	K	R	+		@S:8		APKEELA[pS]DLEEMATSSAK	NOP56_MOUSE;S513
61	APKPEPVPEPKEPSPEK	79.966331@S:14	41	645.9872	3	1934.94	0.0009	28.924	K	N	+		@S:14		APKPEPVPEPKEP[pS]PEK	SRRM1_MOUSE;S260
62	APNSPDVLEIEFK	79.966331@S:4	59.9	769.8602	2	1537.706	-0.0007	51.467	K	K	+		@S:4		APN[pS]PDVLEIEFK	ASSY_MOUSE;S219
63	APNSPDVLEIEFKK	79.966331@S:4	68.4	556.2742	3	1665.801	-0.0007	42.853	K	G	+		@S:4		APN[pS]PDVLEIEFKK	ASSY_MOUSE;S219
64	APSSSSVGISEWLDQK	79.966331@S:5	68	885.902	2	1769.789	0.0022	53.653	K	L	+	ambiguos		@S:3orS:4orS:5	AP[s][s][s][s]VGISEWLDQK	ETFA_MOUSE;S190orS191orS192
65	APSSSSVGISEWLDQK	79.966331@S:6	38.1	885.9005	2	1769.786	-0.0008	53.048	K	L	+	ambiguos		@S:3orS:4orS:5orS:6	AP[s][s][s][s]VGI[s]EWLDQK	ETFA_MOUSE;S190orS191orS192orS193
66	APTAALSPEPQDSK	79.966331@S:7	74.2	746.3391	2	1490.664	-0.0017	23.323	R	E	+		@S:7		APTAAL[pS]PEPQDSK	SAFB1_MOUSE;S366,SAFB2_MOUSE;S387
67	APTAALSPEPQDSKEDVK	79.966331@S:7	64.4	654.9736	3	1961.899	0.0008	23.856	R	K	+		@S:7		APTAAL[pS]PEPQDSKEDVK	SAFB1_MOUSE;S366,SAFB2_MOUSE;S387
68	APTAALSPEPQDSKEDVKK	79.966331@S:7	53.7	697.6705	3	2089.99	-0.0036	20.975	R	F	+		@S:7		APTAAL[s]PEPQD[s]KEDVKK	SAFB1_MOUSE;S366,SAFB2_MOUSE;S387
69	AQEHTDTGDRSESPEEPALEKPPLDK	79.966331@S:13	47.7	739.8351	4	2955.311	-0.002	26.885	R	A	+		@S:13		AQEH[t]D[t]GDR[s]E[s]PEEPALEKPPLDK	TOIP2_MOUSE;S83
70	AQLSPGLYDDSSAR	79.966331@S:4	55.6	780.3397	2	1558.665	-0.0015	34.801	K	R	+		@S:4		AQL[pS]PGLYDDSSAR	NCOR1_MOUSE;S1481
71	AQRLSQETEALGR	79.966331@S:5	62.9	769.8686	2	1537.723	-0.0023	27.465	R	S	+		@S:5		AQRL[pS]QETEALGR	NUCB1_MOUSE;S368
72	ARPAQAPVSEELPPSPKPGK	79.966331@S:15	52	712.6986	3	2135.074	-0.0036	24.033	R	K	+		@S:15		ARPAQAPVSEELPP[pS]PKPGK	FAM21_MOUSE;S388
73	ASEPVKEPVQTAQSPAPVEK	79.966331@S:14	41.8	724.6914	3	2171.052	0.0012	30.699	K	E	+		@S:14		ASEPVKEPVQ[t]AQ[s]PAPVEK	SCAF8_MOUSE;S617
74	ASGTKLTEPR	79.966332@T:7	20.6	380.5206	3	1138.54	0.0016	29.444	R	K	+		@T:7		A[s]G[t]KL[t]EPR	EVI1_MOUSE;T601
75	ASPALGSGHHDGSGDSLEMSSLDR	15.994915@M:19, 79.966331@S:16	28.9	620.5095	4	2478.009	-0.0032	27.203	R	A	+		@S:16		A[s]PALG[s]GHHDG[s]GD[s]LEMSSLDR	TOM70_MOUSE;S108
76	ASPALGSGHHDGSGDSLEMSSLDR	15.994915@M:19, 79.966331@S:2	20.9	827.0112	3	2478.012	-0.0002	34.828	R	A	+		@S:2		A[s]PALG[s]GHHDG[s]GDSLEMSSLDR	TOM70_MOUSE;S94
77	ASPALGSGHHDGSGDSLEMSSLDR	79.966331@S:16	32.4	616.5116	4	2462.017	0.0005	33.065	R	A			@S:16		A[s]PALG[s]GHHDG[s]GD[s]LEMSSLDR	TOM70_MOUSE;S108
78	ASPALGSGHHDGSGDSLEMSSLDR	79.966331@S:2	88.3	821.6792	3	2462.016	-0.0012	33.017	R	A	+		@S:2		A[pS]PALGSGHHDGSGDSLEMSSLDR	TOM70_MOUSE;S94
79	ASPALGSGHHDGSGDSLEMSSLDR	79.966331@S:7	24.2	616.5114	4	2462.016	-0.0003	34.821	R	A	+	ambiguos		@S:2orS:7	A[s]PALG[s]GHHDG[s]GD[s]LEMSSLDR	TOM70_MOUSE;S94orS99
80	ASQRPDVLTTGGGNPIGDK	79.966331@S:2	35.7	654.9814	3	1961.922	0.0017	31.515	R	L	+		@S:2		A[s]QRPDVL[t][t]GGGNPIGDK	CATA_MOUSE;S21
81	ASRVPSSDEEVVEEPQSR	79.966331@S:2,79.966331@S:7	26.5	720.9656	3	2159.875	-0.0022	28.867	R	R	+	ambiguos	@S:2	@S:6orS:7	A[s]RVP[s][s]DEEVVEEPQSR	TB182_MOUSE;S1607,TB182_MOUSE;S1611orS1612
82	ASRVPSSDEEVVEEPQSR	79.966331@S:7	28.2	694.31	3	2079.908	-0.0028	26.587	R	R	+		@S:7		A[s]RVP[s][s]DEEVVEEPQSR	TB182_MOUSE;S1612
83	ASSPNISSYSESGVYSQESLTSSLSTTPQGK	79.966331@S:16, 79.966331@S:19, 79.966331@Y:9	21.9	855.6033	4	3418.384	0.0062	31.087	R	R	+	ambiguos	@S:16,@S:19	@Y:9orS:10	A[s][s]PNI[s][s][y][s]E[s]GV[y][s]QE[s]L[t][s][s]L[s][t][t]PQGK	F179B_MOUSE;S1030,F179B_MOUSE;S1033,F179B_MOUSE;Y1023orS1024
84	ASSPPDRIDIFGR	79.966331@S:3	40.1	504.2396	3	1509.697	-0.0008	41.833	R	T			@S:3		A[s][s]PPDRIDIFGR	ARGL1_MOUSE;S75
85	ASVSDLSPRERSPALK	79.966331@S:7,79.966331@S:12	27.6	624.9589	3	1871.855	0.0006	33.948	R	S	+		@S:7,@S:12		ASVSDL[pS]PRER[pS]PALK	TR150_MOUSE;S243,TR150_MOUSE;S248
86	ASWRACCPPASPSASHVPAR	57.021465@C:6,57.021465@C:7,79.966331@S:11,79.966331@S:13,79.966331@S:15	19.4	802.3079	3	2403.902	-0.0025	30.072	R	A			@S:11,@S:13, @S:15		A[s]WRACCPPA[s]P[s]A[s]HVPAR	GP124_MOUSE;S1085,GP124_MOUSE;S1087,GP124_MOUSE;S1089

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
87	ATDSHSDSEEELAAFCPQLDDSTVAR	57.021465@C:16,79.966331@S:4,79.966331@S:6,79.966331@S:8	48.7	1031.048	3	3090.121	-0.0029	58.977	R	E	+		@S:4,@S:6,@S:8		A[t]D[s]H[s]D[s]EEELAAFCPQLDDSTVAR	F134C_MOUSE;S256,F134C_MOUSE;S258,F134C_MOUSE;S260
88	ATDSHSDSEEELAAFCPQLDDSTVAR	57.021465@C:16,79.966331@S:6,79.966331@S:8	48.7	1004.392	3	3010.154	-0.0043	54.376	R	E		ambiguos	@S:8	@T:2orS:4orS:6	A[t]D[s]H[s]D[s]EEELAAFCPQLDDSTVAR	F134C_MOUSE;S260,F134C_MOUSE;T254orS256orS258
89	ATNLAGETESVSDCADNVSEAPATSEQK	57.021465@C:14,79.966331@S:10	25.9	987.746	3	2960.216	-0.0068	44.331	K	I			@S:10		A[t]NLAGE[t]E[s]V[s]DCADNVSEAPATSEQK	LRBA_MOUSE;S1219
90	ATSPPHLDGTSNPESTVPEK	79.966331@S:11	40.6	715.3228	3	2142.947	-0.0006	29.04	K	K			@S:11		A[t][s]PPHLDG[t][s]NPESTVPEK	PML_MOUSE;S536
91	ATSPPHLDGTSNPESTVPEK	79.966331@S:3	30.2	715.3228	3	2142.947	-0.0006	29.183	K	K			@S:3		A[t][s]PPHLDG[t][s]NPESTVPEK	PML_MOUSE;S528
92	ATSPSTLVSTGPSSR	79.966331@S:3	51	764.3553	2	1526.696	-0.0017	28.491	K	S	+		@S:3		A[t][s]P[s][t]LVSTGPSSR	MAP4_MOUSE;S785
93	ATSPSTLVSTGPSSR	79.966332@T:2	76.7	764.3541	2	1526.694	-0.0041	28.629	K	S	+	ambiguos		@T:2orS:3	A[t][s]P[s][t]LVSTGPSSR	MAP4_MOUSE;T784orS785
94	ATWGDGGDNSPSNVVSK	79.966331@S:10	86.3	885.8692	2	1769.724	-0.002	38.747	K	Q	+		@S:10		ATWGDGGDN[s]P[s]NVVSK	SNP23_MOUSE;S110
95	AVTCDISEDEED	57.021465@C:4,79.966331@S:7	21.2	731.7505	2	1461.486	0.0011	35.745	R	-	+		@S:7		AV[t]CDI[s]EDEED	PCY1A_MOUSE;S362
96	AVYQGPGSSPVK	79.966331@S:9	26.6	635.297	2	1268.579	-0.0007	24.584	K	S			@S:9		AVYQGPG[s][s]PVK	COMT_MOUSE;S261
97	AVYQGPGSSPVKS	79.966331@S:9	43.9	678.8133	2	1355.612	-0.0001	31.862	K	-	+		@S:9		AVYQGPG[s][s]PVKS	COMT_MOUSE;S261
98	AYSGSDLPSGTGSGGGGADGAR	79.966331@S:3	62.9	988.9026	2	1975.791	-0.0002	27.564	R	A	+		@S:3		A[y][s]G[s]DLPSGTGSGGGGADGAR	ZNRF2_MOUSE;S18
99	CDGSPRTPPSTPPATANLSADDDFQNTDLR	57.021465@C:1,79.966331@S:4,79.966332@T:7,79.966331@S:10	36.7	1152.787	3	3455.34	-0.0012	48.123	R	T	+		@S:4,@T:7,@S:10		CDG[s]PR[t]PP[s][t]PPA[t]ANLSADDDFQNTDLR	SAMH1_MOUSE;S18,SAMH1_MOUSE;T21,SAMH1_MOUSE;S24
100	CGSGPVHISGQHLVAVEEDAESEDEDEEDVK	57.021465@C:1,79.966331@S:22	82.2	1149.478	3	3445.413	-0.0012	47.037	K	L	+		@S:22		CGSGPVHISGQHLVAVEEDAE[pS]EDEDEEDVK	NPM_MOUSE;S125
101	CSLSQPGPSVSSPK	57.021465@C:1,79.966331@S:9,79.966331@S:11	25.8	530.8816	3	1589.623	0.0033	39.186	K	S	+		@S:9,@S:11		C[s]L[s]QPGP[s]V[s][s]PK	SYNE1_MOUSE;S8713,SYNE1_MOUSE;S8715
102	CTGGDGAMGDPGSAGKK	57.021465@C:1,15.994915@M:8,79.966331@S:13	17.4	554.5491	3	1660.625	0.0033	36.888	K	G	+		@S:13		C[t]GGDGAMGDPG[s]AGKK	CO6A6_MOUSE;S1401
103	CTHSSSIEDLALGR	57.021465@C:1,79.966331@S:4,79.966331@S:5	31.8	569.2266	3	1704.658	0	42.486	K	C	+	ambiguos		@T:2orS:4orS:5, @T:2orS:4orS:	C[t]H[s][s][s]IEDLALGR	C1GLT_MOUSE;T233orS235orS236,C1GLT_MOUSE;T233orS235orS236
104	CTHSSSIEDLALGR	57.021465@C:1,79.966331@S:4,79.966331@S:6	35.9	853.3363	2	1704.658	0.0001	42.529	K	C	+		@S:4,@S:6		C[t]H[s][s][s]IEDLALGR	C1GLT_MOUSE;S235,C1GLT_MOUSE;S237
105	CTHSSSIEDLALGR	57.021465@C:1,79.966332@T:2,79.966331@S:4	34.4	569.2263	3	1704.657	-0.0008	41.825	K	C	+		@T:2,@S:4		C[t]H[s][s][s]IEDLALGR	C1GLT_MOUSE;T233,C1GLT_MOUSE;S235
106	DAIHLGMSSAPLVK	15.994915@M:7,79.966331@S:9	27.4	512.2506	3	1533.73	0.0038	20.715	M	H	+		@S:9		DAIHLGM[s][s]APLVK	IRK15_MOUSE;S10
107	DAQSPLLEVDAASVK	79.966331@S:4	53.9	811.887	2	1621.759	-0.0005	44.925	K	Y	+		@S:4		DAQ[pS]PLLEVDAASVK	F208A_MOUSE;S836
108	DASPINRWSPTR	79.966331@S:3,79.966331@S:9	17.8	780.3235	2	1558.632	-0.0006	32.396	K	R	+		@S:3,@S:9		DA[s]PINRW[s]P[t]R	PRP4B_MOUSE;S431,PRP4B_MOUSE;S437
109	DDDDIDLFGSDDEEESEEAK	79.966331@S:10	77.7	1176.921	2	2351.827	-0.0058	53.425	K	K	+		@S:10		DDDDIDLFG[pS]DDEEESEEAK	EF1B_MOUSE;S106
110	DDDDIDLFGSDDEEESEEAKK	79.966331@S:10	80.3	827.6489	3	2479.925	-0.0027	45.666	K	L	+		@S:10		DDDDIDLFG[pS]DDEEESEEAKK	EF1B_MOUSE;S106
111	DDGDEEGLLTHSEEELEHSQDTDAEDGALQ	79.966331@S:12	36	1122.106	3	3363.296	-0.0097	45.648	R	-			@S:12		DDGDEEGLL[t]H[s]EEELEH[s]QD[t]DAEDGALQ	RALY_MOUSE;S294
112	DDGDEEGLLTHSEEELEHSQDTDAEDGALQ	79.966332@T:10	61	1122.107	3	3363.298	-0.0081	45.658	R	-	+		@T:10		DDGDEEGLL[t]H[s]EEELEH[s]QD[t]DAEDGALQ	RALY_MOUSE;T292
113	DDGSWEVIEGYR	79.966331@S:4	67.8	753.3007	2	1504.587	-0.0003	50.245	R	A	+		@S:4		DDG[pS]WEVIEGYR	DHE3_MOUSE;S128
114	DEILPTTPISEQK	79.966331@S:10	26.7	775.8706	2	1549.727	-0.0009	39.374	K	G			@S:10		DEILP[t][t]PI[s]EQK	RS3_MOUSE;S224
115	DEILPTTPISEQK	79.966332@T:6	49.1	775.8711	2	1549.728	0	46.925	K	G			@T:6		DEILP[t][t]PISEQK	RS3_MOUSE;T220
116	DEILPTTPISEQK	79.966332@T:7	68.8	775.871	2	1549.727	-0.0002	47.265	K	G			@T:7		DEILP[t][t]PISEQK	RS3_MOUSE;T221
117	DEKKEESEESDDDMGFGLFD	15.994915@M:14,79.966331@S:7,79.966331@S:10	35.5	833.2883	3	2496.843	-0.0012	57.042	K	-	+		@S:7,@S:10		DEKKEE[pS]EE[pS]DDDMGFGLFD	RLA2_MOUSE;S102,RLA2_MOUSE;S105
118	DEKKEESEESDDDMGFGLFD	79.966331@S:7,79.966331@S:10	35.8	827.9566	3	2480.848	-0.0014	65.102	K	-	+		@S:7,@S:10		DEKKEE[pS]EE[pS]DDDMGFGLFD	RLA2_MOUSE;S102,RLA2_MOUSE;S105
119	DFDISEQNDSSDEEK	79.966331@S:10,79.966331@S:11	42.7	959.317	2	1916.619	-0.0043	39.677	K	Q	+		@S:10,@S:11		DFDISEQND[pS][pS]DEEK	DNJC1_MOUSE;S477,DNJC1_MOUSE;S478
120	DFKSVSGGIQEPGFQR	79.966331@S:4,79.966331@S:6	30.2	637.9385	3	1910.794	-0.0027	40.326	R	G	+		@S:4,@S:6		DFK[pS]V[pS]GGIQEPGFQR	IGFN1_MOUSE;S1893,IGFN1_MOUSE;S1895
121	DFSATDLTEFAAR	79.966331@S:3	68.2	762.324	2	1522.633	-0.0006	57.301	K	A	+		@S:3		DF[s]A[t]DLTEFAAR	THIM_MOUSE;S28
122	DFSLEQLR	79.966331@S:3	45.5	544.2446	2	1086.475	-0.0001	47.744	R	Q	+		@S:3		DF[pS]LEQLR	PGRC2_MOUSE;S98
123	DFTPAELR	79.966332@T:3	21	514.7261	2	1027.438	0.0001	38.051	R	R	+		@T:3		DF[pT]PAELR	PGRC1_MOUSE;T74
124	DFTPVCTTELGR	57.021465@C:6,79.966332@T:3	47.3	738.3151	2	1474.616	-0.0007	41.823	R	A	+		@T:3		DF[pT]PVCTTELGR	PRDX6_MOUSE;T44

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
125	DFYMTDSISRASQTMAK	15.994915@M:4,79.966332@T:5,79.966331@Y:3	21	709.9438	3	2126.81	0.0003	47.765	K	C	+		@Y:3,@T:5		DF[y]M[t]D[s]I[s]RA[s]Q[t]MAK	NDUS1_MOUSE;Y695,NDUS1_MOUSE;T697
126	DGSFEGLTVK	79.966331@S:3	59.5	566.7496	2	1131.485	-0.0003	48.502	K	K	+		@S:3		DG[pS]FEGLTVK	TTC7A_MOUSE;S648
127	DGSSGHSTLPRSPR	79.966331@S:3	21.1	767.3461	2	1532.678	0.0044	27.303	R	D	+	ambiguos		@S:3orS:4	DG[s][s]GH[s]TLPRSPR	TENC1_MOUSE;S883orS884
128	DGTAPPPQSPSSPGSGQDEDWSDEESPRK	79.966331@S:22	85.1	1040.759	3	3119.254	-0.0088	29.94	R	V	+		@S:22		DGTAPPPQSPSSPGSGQDEDW[pS]DEESPRK	PACN3_MOUSE;S354
129	DHSPTPSVFNSDEER	79.966331@S:3	31.9	599.5759	3	1795.706	0.0008	37.515	R	Y	+		@S:3		DH[s]P[t]P[s]VFNSDEER	FIP1_MOUSE;S479
130	DHSPTPSVFNSDEERYR	79.966331@S:3	35.1	705.9625	3	2114.866	-0.0038	31.538	R	Y	+		@S:3		DH[s]P[t]P[s]VFN[s]DEER[y]R	FIP1_MOUSE;S479
131	DHSPTPSVFNSDEERYR	79.966331@S:3,79.966331@S:7	23.2	732.6188	3	2194.835	-0.0011	35.155	R	Y	+	ambiguos	@S:3	@S:7orS:11	DH[s]P[t]P[s]VFN[s]DEERYR	FIP1_MOUSE;S479,FIP1_MOUSE;S483orS487
132	DHSSQSEEEVVEGEK	79.966331@S:4	29.8	590.2357	3	1767.685	0.0016	22.495	R	E	+	ambiguos		@S:3orS:4	DH[s][s]Q[s]EEEVVEGEK	BNI3L_MOUSE;S116orS117
133	DHSSQSEEEVVEGEK	79.966331@S:6	31.2	590.2351	3	1767.683	-0.0001	28.994	R	E	+		@S:6		DH[s][s]Q[s]EEEVVEGEK	BNI3L_MOUSE;S119
134	DIDLFGSDEEEEDK	79.966331@S:7	78.9	860.8268	2	1719.639	-0.001	50.986	K	E	+		@S:7		DIDLFG[pS]DEEEEDK	EF1D_MOUSE;S162
135	DIDLFGSDEEEEDKEAAR	79.966331@S:7	76	1074.436	2	2146.858	0.0001	45.066	K	L	+		@S:7		DIDLFG[pS]DEEEEDKEAAR	EF1D_MOUSE;S162
136	DIIRQPSEEEIIK	79.966331@S:7	51.8	825.4098	2	1648.805	-0.0022	37.776	K	L	+		@S:7		DIIRQP[pS]EEEIIK	PEA15_MOUSE;S116
137	DIKEESDEEDDDDEESGRLR	79.966331@S:6	79.7	820.9887	3	2459.944	-0.0007	23.055	K	F	+		@S:6		DIKEE[pS]DEEDDDDEESGRLR	RBM33_MOUSE;S243
138	DIQAFLNQCGASPGEAR	57.021465@C:9,79.966331@S:12	49.7	638.6122	3	1912.815	0.0009	51.037	R	H	+		@S:12		DIQAFLNQCGA[pS]PGEAR	NAGS_MOUSE;S109
139	DISLSEYK	79.966331@S:5	22.2	517.7256	2	1033.437	-0.0002	38.717	K	G	+		@S:5		DI[s]L[s]E[y]K	PRDX1_MOUSE;S32
140	DKFSPTQDRPESSTVLK	79.966331@S:4	39.3	672.3199	3	2013.938	-0.0029	27.559	R	V	+		@S:4		DKF[s]P[t]QDRPESSTVLK	SRRM2_MOUSE;S1151
141	DKFSPTQDRPESSTVLK	79.966332@T:6	31.8	672.3213	3	2013.942	0.0013	35.373	R	V	+		@T:6		DKF[s]P[t]QDRPESSTVLK	SRRM2_MOUSE;T1153
142	DKSPVREPIDNLTPEER	79.966331@S:3	67.8	692.3314	3	2073.972	-0.0009	31.332	K	D	+		@S:3		DK[pS]PVREPIDNLTPEER	RBM39_MOUSE;S136
143	DLLEMSRESDPHGAESSSSGR	79.966331@S:6,79.966331@S:9,79.966331@S:16,79.966331@S:18,79.966331@S:19	13.6	882.948	3	2645.822	0.0038	41.863	K	N	+		@S:6,@S:9,@S:16,@S:18,@S:19		DLLEM[s]RE[s]DPHGAE[s][s][s][s]GR	ZBBX_MOUSE;S664,ZBBX_MOUSE;S667,ZBBX_MOUSE;S674,ZBBX_MOUSE;S676,ZBBX_MOUSE;S677
144	DLLSDLQDISDSER	79.966331@S:12	34.4	843.3652	2	1684.716	-0.0035	60.814	R	K	+	ambiguos		@S:10orS:12	DLLSDLQDI[s]D[s]ER	CDK11_MOUSE;S270orS272
145	DLQYITISK	79.966331@S:8	25.7	580.7836	2	1159.553	0.0001	42.327	K	E	+	ambiguos		@T:6orS:8	DLQYI[t]I[s]K	AFAD_MOUSE;T1497orS1499
146	DLTHSDSESSLHMSDR	15.994915@M:13,79.966331@S:7	28	638.2512	3	1911.732	0.0012	26.524	R	Q	+		@S:7		DL[t]H[s]D[s]E[s][s]LHMSDR	STIM1_MOUSE;S521
147	DLTHSDSESSLHMSDR	79.966331@S:7	26.2	632.9185	3	1895.734	-0.0022	26.153	R	Q	+		@S:7		DLTH[s]D[s]E[s][s]LHMSDR	STIM1_MOUSE;S521
148	DLVQPDKPASPK	79.966331@S:10	20.7	687.8352	2	1373.656	-0.0034	22.077	R	F	+		@S:10		DLVQPDKPA[pS]PK	ZC3HE_MOUSE;S515
149	DMDEPSPVPNVEEVTLPK	15.994915@M:2,79.966331@S:6	30.2	1046.461	2	2090.907	-0.0053	49.453	K	T	+		@S:6		DMDEP[pS]PVPNVEEVTLPK	SMRC2_MOUSE;S347
150	DMDEPSPVPNVEEVTLPK	79.966331@S:6	34.4	1038.465	2	2074.914	-0.0025	51.94	K	T	+		@S:6		DMDEP[pS]PVPNVEEVTLPK	SMRC2_MOUSE;S347
151	DMSPLPESEVTLGK	15.994915@M:2,79.966331@S:3	22.3	799.8538	2	1597.693	-0.0015	38.554	K	D	+		@S:3		DM[pS]PLPESEVTLGK	MAP4_MOUSE;S475
152	DMSPLPESEVTLGK	79.966331@S:3	45.4	791.8575	2	1581.7	0.0008	44.834	K	D	+		@S:3		DM[pS]PLPESEVTLGK	MAP4_MOUSE;S475
153	DMSPSAETEAPLAK	15.994915@M:2,79.966331@S:3	44.5	771.8228	2	1541.631	-0.0009	27.006	K	N	+		@S:3		DM[s]P[s]AETEAPLAK	MAP4_MOUSE;S517
154	DMSPSAETEAPLAK	79.966331@S:3	44.2	763.8254	2	1525.636	-0.0008	32.092	K	N	+		@S:3		DM[s]P[s]AETEAPLAK	MAP4_MOUSE;S517
155	DNLGNSNVPDSPIPAECEAAGR	57.021465@C:17,79.966331@S:11	50.3	1182.003	2	2361.99	0.0009	44.428	K	G	+		@S:11		DNLGNSNVPD[pS]PIPAECEAAGR	CTGE5_MOUSE;S654
156	DNPSPEPQLDDIKR	79.966331@S:4	37.6	568.5919	3	1702.754	-0.0023	30.071	K	E	+		@S:4		DNP[pS]PEPQLDDIKR	EAF1_MOUSE;S165
157	DPDSALGISDGETSPSSK	79.966331@S:14	65.5	921.8855	2	1841.756	-0.0004	36.629	K	G	+	ambiguos		@T:13orS:14	DPDSALGISDGE[t][s]P[s][s]K	COBL1_MOUSE;T550orS551
158	DPDSALGISDGETSPSSK	79.966331@S:9	76.2	921.8855	2	1841.756	-0.0004	42.443	K	G	+		@S:9		DPDSALGI[s]DGE[t][s]P[s][s]K	COBL1_MOUSE;S546
159	DPDSALGISDGETSPSSK	79.966331@S:9,79.966331@S:14	19.4	961.8669	2	1921.719	-0.0039	40.605	K	G	+		@S:9,@S:14		DPDSALGI[s]DGE[t][s]PSSK	COBL1_MOUSE;S546,COBL1_MOUSE;S551
160	DPDSALGISDGETSPSSK	79.966332@T:13	38.3	921.8859	2	1841.757	0.0005	35.287	K	G	+		@T:13		DPDSALGI[s]DGE[t][s]P[s][s]K	COBL1_MOUSE;T550
161	DPDSALGISDGETSPSSK	79.966332@T:13,79.966331@S:14	39.4	961.8688	2	1921.723	0	39.379	K	G	+		@T:13,@S:14		DPDSALGI[s]DGE[t][s]P[s][s]K	COBL1_MOUSE;T550,COBL1_MOUSE;S551
162	DQLRDASPPPAFKPEPPK	79.966331@S:7	22.9	690.674	3	2069	0.0018	32.072	R	A	+		@S:7		DQLRDA[pS]PPPAFKPEPPK	ZO2_MOUSE;S968
163	DQQPSGSEGEDDDAEAALKK	79.966331@S:5,79.966331@S:7	26.2	1125.426	2	2248.837	-0.004	28.707	K	E	+		@S:5,@S:7		DQQP[pS]G[pS]EGEDDDAEAALKK	THUM1_MOUSE;S86,THUM1_MOUSE;S88
164	DQYFLALASNR	79.966331@S:9,79.966331@Y:3	17	729.2954	2	1456.576	-0.0026	43.782	K	S	+		@Y:3,@S:9		DQ[pY]FLALA[pS]NR	SC5AB_MOUSE;Y236,SC5AB_MOUSE;S242
165	DRASPESLDLTR	79.966331@S:4	60.4	720.3295	2	1438.644	-0.0009	29.865	K	D	+		@S:4		DRA[pS]PESLDLTR	PROX1_MOUSE;S511
166	DRESRSPFLKPDER	79.966331@S:6	27.2	453.7161	4	1810.835	-0.001	21.698	R	A	+		@S:6		DRE[s]R[s]PFLKPDER	SFR19_MOUSE;S821
167	DRGGDTSDTESSIIIR	79.966331@S:7	21	601.2706	3	1800.79	0.0009	40.341	R	R	+		@S:7		DRGGD[t][s]D[t]ESSIIIR	SP100_MOUSE;S314
168	DRGGDTSDTESSIIIR	79.966332@T:9	27.2	601.2704	3	1800.789	0.0003	40.388	R	R	+		@T:9		DRGGD[t][s]D[t]ESSIIIR	SP100_MOUSE;T316
169	DRSPSPLRGNVVPSPLPTR	79.966331@S:3,79.966331@S:5	59.8	735.6907	3	2204.05	-0.0001	39.431	R	R	+		@S:3,@S:5		DR[pS]P[pS]PLRGNVVP[pS]PLPTR	CHSP1_MOUSE;S31,CHSP1_MOUSE;S33

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
170	DRSPSPLRGNVVPSPLPTR	79.966331@S:3,79.966331@S:5,79.966331@S:14	29.3	762.3453	3	2284.014	-0.0026	41.218	R	R	+		@S:3,@S:5,@S:14		DR[pS]P[pS]PLRGNVVPSPLPTR	CHSP1_MOUSE;S31,CHSP1_MOUSE;S33,CHSP1_MOUSE;S42
171	DSDQVAQSDGEESPAAEEQLLGER	79.966331@S:13	62.1	880.7022	3	2639.085	-0.0026	50.875	K	I	+		@S:13		DSDQVAQSDGEE[pS]PAAEEQLLGER	SC31A_MOUSE;S531
172	DSDQVAQSDGEESPAAEEQLLGER	79.966331@S:2	61.8	1320.548	2	2639.081	-0.006	44.805	K	I	+		@S:2		D[s]DQVAQ[s]DGEESPAAEEQLLGER	SC31A_MOUSE;S520
173	DSDQVAQSDGEESPAAEEQLLGER	79.966331@S:8	87.5	880.7031	3	2639.087	0.0004	53.049	K	I	+		@S:8		DSDQVAQ[pS]DGEE[pS]PAAEEQLLGER	SC31A_MOUSE;S526
174	DSDQVAQSDGEESPAAEEQLLGER	79.966331@S:8,79.966331@S:13	69.3	907.3579	3	2719.052	-0.0017	47.678	K	I	+		@S:8,@S:13		DSDQVAQ[pS]DGEESPAAEEQLLGER	SC31A_MOUSE;S526,SC31A_MOUSE;S531
175	DSLPSGPREEAKPASPSSVQDR	79.966331@S:15	33.6	797.3705	3	2389.09	-0.0015	24.242	R	S	+		@S:15		DSLPSGPREEAKPA[s]P[s][s]VQDR	MIA3_MOUSE;S1915
176	DSQDTSAEQSDHDDEVASLASASGGFGSK	79.966331@S:10	71.9	993.3984	3	2977.173	-0.0002	44.545	R	I	+		@S:10		D[s]QD[t][s]AEQ[s]DHDDEVASLASASGGFGSK	EDC4_MOUSE;S884
177	DSQDTSAEQSDHDDEVASLASASGGFGSK	79.966331@S:6	64.4	993.3963	3	2977.167	-0.0063	43.694	R	I			@S:6		D[s]QD[t][s]AEQ[s]DHDDEVA[s]LASASGGFGSK	EDC4_MOUSE;S880
178	DSSTSPGDYVLSVSENSR	79.966331@S:2	43.4	990.4156	2	1978.817	0.001	48.722	R	V	+	ambiguos		@S:2orS:3	D[s][s][t][s]PGDYVLSVSENSR	CRK_MOUSE;S40orS41
179	DSSTSPGDYVLSVSENSR	79.966331@S:5	47.8	990.4148	2	1978.815	-0.0007	48.752	R	V	+	ambiguos		@S:3orT:4orS:5	D[s][s][t][s]PGDYVLSVSENSR	CRK_MOUSE;S41orT42orS43
180	DSVINLSESVEDGPR	79.966331@S:7	66.2	848.8754	2	1695.736	0.0009	44.514	R	G	+		@S:7		DSVINL[pS]ESVEDGPR	MA2A1_MOUSE;S80
181	DTIALCTAESIDNLR	57.021465@C:6,79.966331@S:10	26.6	591.2699	3	1770.788	0.0019	48.596	R	A			@S:10		D[t]IALC[t]AE[s]IDNLR	AT11C_MOUSE;S201
182	DTSPDKGELVSDEEEDT	79.966331@S:11	35	973.3744	2	1944.734	-0.0019	30.398	R	-	+		@S:11		DTSPDKGELV[pS]DEEEDT	TBD2B_MOUSE;S959
183	DVQDAIAQSPEK	79.966331@S:9	79.8	690.806	2	1379.597	0.0004	32.122	K	E	+		@S:9		DVQDAIAQ[pS]PEK	SLTM_MOUSE;S289
184	DVYLSPR	79.966331@S:5	31	465.2104	2	928.4062	0.0007	34.645	R	D			@S:5		DVYL[pS]PR	RMXL1_MOUSE;S205,RBMX_MOUSE;S208
185	DVYLSPRDDGYSTK	79.966331@S:5	33.2	848.3665	2	1694.718	-0.0005	30.997	R	D	+		@S:5		DV[y]L[s]PRDDGYSTK	RMXL1_MOUSE;S205,RBMX_MOUSE;S208
186	DWDKESEGEEPAGGR	79.966331@S:6	24.7	581.2282	3	1740.663	0.0001	23.44	K	A	+		@S:6		DWDKE[pS]EGEEPAGGR	RRP15_MOUSE;S265
187	DWEDDSDEDMSNFDR	15.994915@M:10, 79.966331@S:6	93.8	986.3137	2	1970.613	-0.0021	38.257	K	F	+		@S:6		DWEDD[pS]DEDMSNFDR	TEBP_MOUSE;S113
188	DWEDDSDEDMSNFDR	79.966331@S:6	88.1	978.3157	2	1954.617	-0.0032	46.74	K	F	+		@S:6		DWEDD[pS]DEDMSNFDR	TEBP_MOUSE;S113
189	DYEEVGADSAEGDDEGEEY	79.966331@S:9	69.1	1079.858	2	2157.702	-0.0036	40.21	K	-	+		@S:9		DYEEVGAD[pS]AEGDDEGEEY	TBA1C_MOUSE;S439
190	EAEEELAASGGQSPTGEQIPQFQQR	79.966331@S:13	39.4	923.0782	3	2766.213	-0.0007	49.554	R	Q	+		@S:13		EAEEELAA[s]GGQ[s]P[t]GEQIPQFQQR	MACF1_MOUSE;S5551
191	EAEEESSGGEEEDEDENIEVVYSK	79.966331@S:6,79.966331@S:7	58.5	1431.516	2	2861.018	-0.0035	44.543	K	T	+		@S:6,@S:7		EAEEE[pS][pS]GGEEEDEDENIEVVYSK	IF5_MOUSE;S387,IF5_MOUSE;S388
192	EAEEESSGGEEEDEDENIEVVYSK	79.966331@S:7	22.6	928.0253	3	2781.054	-0.001	39.447	K	T	+	ambiguos		@S:6orS:7	EAEEE[s][s]GGEEEDEDENIEVVYSK	IF5_MOUSE;S387orS388
193	EAGIVHSDAEKEQEEEEQK	79.966331@S:7	44.6	755.6552	3	2263.944	-0.0044	20.824	K	Q	+		@S:7		EAGIVH[pS]DAEKEQEEEEQK	PININ_MOUSE;S346
194	EALVEPASESPRPALAR	79.966331@S:10	28.3	624.9787	3	1871.914	0	38.938	R	S			@S:10		EALVEPA[s]E[s]PRPALAR	NHRF1_MOUSE;S275
195	EATEGTTVTLR	79.966332@T:3	19.6	629.2906	2	1256.567	0.0017	27.343	K	C	+		@T:3		EA[t]EG[t][t]V[t]LR	OBSCN_MOUSE;T3718
196	EAYNDSSDEESSSHHGPGVQCAHQ	57.021465@C:21, 79.966331@S:6,79.966331@S:7	37.7	929.9903	3	2786.949	-0.0051	20.773	R	-	+		@S:6,@S:7		EA[y]ND[s][s]DEE[s][s][s]HHGPGVQCAHQ	DNJA2_MOUSE;S394,DNJA2_MOUSE;S395
197	ECNRSNSSSPVDK	57.021465@C:2,79.966331@S:8	34.4	520.5439	3	1558.61	0.0015	39.29	K	L	+		@S:8		ECNR[s]N[s][s][s]PVDK	GPBP1_MOUSE;S275
198	EDEEKPKIEDVGSDEEDDSGK	79.966331@S:13	32	810.6627	3	2428.966	0.002	30.863	K	D	+		@S:13		EDEEKPKIEDVG[pS]DEEDDSGK	HS90B_MOUSE;S255
199	EDSGTFSLGK	79.966331@S:3	42.6	560.7315	2	1119.448	-0.0001	31.945	R	M			@S:3		ED[s]G[t]FSLGK	PRKRA_MOUSE;S18
200	EDSGTFSLGK	79.966332@T:5	25.5	560.7314	2	1119.448	-0.0002	32.284	R	M			@T:5		ED[s]G[t]F[s]LGK	PRKRA_MOUSE;T20
201	EDSGTPLVTPSLLQMVR	15.994915@M:15, 79.966331@S:3,79.966332@T:5,79.966332@T:9	20.3	700.2899	3	2097.848	-0.0018	17.878	R	L	+		@S:3,@T:5,@T:9		ED[s]G[t]PLV[t]P[s]LLQMVR	K1522_MOUSE;S795,K1522_MOUSE;T797,K1522_MOUSE;T801
202	EELASDLEEMATSSAK	15.994915@M:10, 79.966331@S:5	27.5	903.8701	2	1805.726	-0.0021	47.271	K	R	+		@S:5		EELA[s]DLEEMA[t][s][s]AK	NOP56_MOUSE;S513
203	EELASDLEEMATSSAK	79.966331@S:5	80.7	895.8741	2	1789.734	0.0008	60.953	K	R	+		@S:5		EELA[pS]DLEEMATSSAK	NOP56_MOUSE;S513
204	EELEQQTDGDCDEEDDDKDGEVPK	57.021465@C:11, 79.966332@T:7	89	959.0253	3	2874.054	-0.0005	31.688	K	S	+		@T:7		EELEQQ[pT]DGDCDEEDDDKDGEVPK	SEC62_MOUSE;T375
205	EEVASEPEEAASPTTPK	79.966331@S:12	30	926.3965	2	1850.778	-0.0037	24.754	K	K	+		@S:12		EEVA[s]EPEEAA[s]P[t][t]PK	NOP56_MOUSE;S543
206	EEVASEPEEAASPTTPK	79.966331@S:5	82.2	926.3979	2	1850.781	-0.0009	32.777	K	K	+		@S:5		EEVA[s]EPEEAA[s]P[t][t]PK	NOP56_MOUSE;S536
207	EEVASEPEEAASPTTPK	79.966331@S:5,79.966331@S:12	30.2	966.3793	2	1930.744	-0.0046	26.993	K	K	+		@S:5,@S:12		EEVA[pS]EPEEAASPTTPK	NOP56_MOUSE;S536,NOP56_MOUSE;S543
208	EFDELSPSAQR	79.966331@S:8	37.6	679.7848	2	1357.555	0	40.075	R	D	+		@S:8		EFDEL[s]P[s]AQR	AT2A2_MOUSE;S663
209	EFDYDSPHGLDSD	79.966331@S:12	32.7	788.7772	2	1575.54	-0.0004	39.12	K	-	+		@S:12		EFDYD[s]PHGLD[s]D	S7A6O_MOUSE;S305
210	EFDYDSPHGLDSD	79.966331@S:6	23.1	788.777	2	1575.539	-0.0009	39.734	K	-	+		@S:6		EFD[y]D[s]PHGLD[s]D	S7A6O_MOUSE;S299
211	EFESGDFQDFTR	79.966331@S:4	31.3	779.2982	2	1556.582	-0.0003	48.463	K	Q	+		@S:4		EFE[s]GDFQDF[t]R	SYNRG_MOUSE;S974
212	EFGASECISPQDFSK	57.021465@C:7,79.966331@S:14	42.6	891.3572	2	1780.7	-0.0017	49.732	K	S	+		@S:14		EFGASECISPQDF[pS]K	ADHX_MOUSE;S247
213	EFITGDVEPTDAESAWHSENEEEDK	79.966331@S:18	62.8	982.059	3	2943.155	-0.0055	45.194	R	L			@S:18		EFITGDVEPTDAE[s]AWH[s]ENEEEDK	NP1L4_MOUSE;S125
214	EGEEPTVYSDDEEPK	79.966331@S:9	37.6	902.3435	2	1802.672	-0.0047	27.77	K	D	+		@S:9		EGEEPTV[y][s]DDEEPK	PGRC1_MOUSE;S181

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
215	EGEEPTVYSDDEEPK	79.966332@T:6	45	902.3451	2	1802.676	-0.0014	34.263	K	D	+		@T:6		EGEEPTV[y][s]DDEEPK	PGRC1_MOUSE;T178
216	EGEEPTVYSDDEEPKDETAR	79.966331@S:9	77.1	792.6492	3	2374.926	-0.0068	26.627	K	K	+		@S:9		EGEEPTV[y][s]DDEEPKDETAR	PGRC1_MOUSE;S181
217	EGEEPTVYSDDEEPKDETARK	79.966331@S:9	79.8	835.3483	3	2503.023	-0.0045	23.496	K	N	+		@S:9		EGEEP[t]V[y][s]DDEEPKDETARK	PGRC1_MOUSE;S181
218	EGINPGYDDYADSDEDQHDAYLER	79.966331@S:13	61.4	956.3691	3	2866.085	-0.0025	41.065	K	M	+		@S:13		EGINPG[y]DD[y]AD[s]DEDQHDA[y]LER	SSRP1_MOUSE;S444
219	EGVILTNENAASPEQPGDEDAK	79.966331@S:12	59.5	788.6795	3	2363.017	-0.0001	41.22	K	Q	+		@S:12		EGVILTNENAA[pS]PEQPGDEDAK	NSUN2_MOUSE;S723
220	EIITEEPSEEEADMPKPK	79.966331@S:8	19.3	717.985	3	2150.933	0.0003	34.851	K	K			@S:8		EII[t]EEP[s]EEEADMPKPK	DDX21_MOUSE;S118
221	EISDDEAEEEKGEKEEEDK	79.966331@S:3	33.1	773.3061	3	2316.896	-0.004	21.041	K	E	+		@S:3		EI[pS]DDEAEEEKGEKEEEDK	HS90B_MOUSE;S226
222	EKEEKESDDKPEIEDVGSDEEEEEK	79.966331@S:18	37.9	758.5632	4	3030.224	0.0001	24.776	K	K	+		@S:18		EKEEKESDDKPEIEDVG[pS]DEEEEEK	HS90A_MOUSE;S263
223	EKEEKESDDKPEIEDVGSDEEEEEK	79.966331@S:7	40.7	758.5625	4	3030.221	-0.0026	24.483	K	K	+		@S:7		EKEEKESDDKPEIEDVG[pS]DEEEEEK	HS90A_MOUSE;S252
224	EKSPELPEPSVR	79.966331@S:3	31.2	724.3449	2	1446.675	-0.0003	35.614	K	M	+		@S:3		EK[s]PELPEP[s]VR	SRRM1_MOUSE;S220
225	EKTPSPKEEDEEAESPPEK	79.966332@T:3,79.966331@S:5	29.7	772.6442	3	2314.911	-0.0021	20.166	K	K	+		@T:3,@S:5		EK[pT]P[pS]PKEEDEEAESPPEK	NUCKS_MOUSE;T202,NUCKS_MOUSE;S204
226	ELFDYSPPLHK	79.966331@S:6	27.5	475.8864	3	1424.637	-0.0003	43.651	K	S			@S:6		ELFD[y][s]PPLHK	BCLF1_MOUSE;S510
227	ELPRPGASPPAEK	79.966331@S:8	30.3	476.9007	3	1427.68	-0.0007	22.647	R	S	+		@S:8		ELPRPGA[pS]PPAEK	GCH1_MOUSE;S24
228	ELSHSPPRENSFESSLEFK	79.966331@S:5	26.8	767.3454	3	2299.014	-0.0015	39.664	K	N	+		@S:5		EL[s]H[s]PPREN[s]FE[s][s]LEFK	SRRM2_MOUSE;S1278
229	ELSVEEQIK	79.966331@S:3	34.4	577.7706	2	1153.527	0	32.239	R	R	+		@S:3		EL[pS]VEEQIK	LIMA1_MOUSE;S735
230	ELVGDTGSQEGDNEQPSGSETEEDPSASPQK	79.966331@S:17,79.966331@S:19	64.1	1122.099	3	3363.275	-0.008	31.193	R	I	+		@S:17,@S:19		ELVGDTGSQEGDNEQP[s]G[s]E[t]EEDPSASPQK	CF228_MOUSE;S59,CF228_MOUSE;S61
231	ELVGDTGSQEGDNEQPSGSETEEDPSASPQK	79.966332@T:21	39.1	1095.445	3	3283.314	-0.0021	29.235	R	I	+		@T:21		ELVGDTGSQEGDNEQP[s]G[s]E[t]EEDPSASPQK	CF228_MOUSE;T63
232	ELWDSPEPASAPRTPQSPVSR	79.966332@T:14,79.966331@S:17	42.6	823.028	3	2466.062	0.0003	41.455	R	I	+		@T:14,@S:17		ELWDSPEPA[s]APR[t]PQ[s]PV[s]R	FHOD1_MOUSE;T499,FHOD1_MOUSE;S502
233	ENPPSPPTSPAAPQPR	79.966331@S:5	51.1	861.8942	2	1721.774	-0.0035	27.311	R	E	+		@S:5		ENPP[s]PP[t][s]PAAPQPR	SFR1_MOUSE;S67
234	ENPPSPPTSPAAPQPR	79.966331@S:5,79.966331@S:9	40.4	901.8781	2	1801.742	-0.0021	31.981	R	E	+		@S:5,@S:9		ENPP[s]PP[t][s]PAAPQPR	SFR1_MOUSE;S67,SFR1_MOUSE;S71
235	ENPPSPPTSPAAPQPR	79.966332@T:8,79.966331@S:9	32.5	601.5887	3	1801.744	0.0005	32.077	R	E	+		@T:8,@S:9		ENPP[s]PP[t][s]PAAPQPR	SFR1_MOUSE;T70,SFR1_MOUSE;S71
236	ENPPVEDSSDEDDKRNPGNLYDK	79.966331@S:8,79.966331@S:9	64	931.7021	3	2792.084	-0.0005	34.879	R	A	+		@S:8,@S:9		ENPPVED[pS][pS]DEDDKRNPGNLYDK	STT3B_MOUSE;S495,STT3B_MOUSE;S496
237	ENPPVEDSSDEDDKRNPGNLYDK	79.966331@S:9	57.1	905.045	3	2712.113	-0.0057	26.081	R	A	+		@S:9		ENPPVED[s][s]DEDDKRNPGNLYDK	STT3B_MOUSE;S496
238	ENVEYIEREESDGEYDEFGR	79.966331@S:11	62.1	849.0062	3	2543.997	0.0002	41.652	R	K	+		@S:11		ENVE[y]IEREE[s]DGEYDEFGR	ZRAB2_MOUSE;S120
239	ENYEDQEPLVGHESPITLAAR	79.966332@T:17	25.8	816.7077	3	2447.101	0.0006	43.17	K	E	+	ambiguos		@S:14orT:17	ENYEDQEPLVGHE[s]PI[t]LAAR	TB182_MOUSE;S602orT605
240	EQESSGEEDNDLSPEEREK	79.966331@S:4,79.966331@S:5	21.2	789.6222	3	2365.845	-0.0023	24.061	R	K	+		@S:4,@S:5		EQE[pS][pS]GEEDNDLSPEEREK	IPP2_MOUSE;S122,IPP2_MOUSE;S123
241	EQLSEVEGSGEDDQGDDHSESAQK	79.966331@S:9	31.1	886.0097	3	2655.007	-0.002	29.145	K	V	+		@S:9		EQLSEVEG[pS]GEDDQGDDHSESAQK	UBP4_MOUSE;S680
242	ERDHSPTPSVFNSDEER	79.966332@T:7	25.2	694.6238	3	2080.85	0.0008	25	R	Y	+		@T:7		ERDH[s]P[t]P[s]VFNSDEER	FIP1_MOUSE;T481
243	ERDTSPDKGELVSDEEEDT	79.966331@S:13	23.6	744.3007	3	2229.88	0.0006	33.413	R	-	+		@S:13		ERDTSPDKGELV[pS]DEEEDT	TBD2B_MOUSE;S959
244	ERIQQFDDGGSDEEDIWEEK	79.966331@S:11	70.4	835.6747	3	2504.002	0.0006	44.775	K	H	+		@S:11		ERIQQFDDGG[pS]DEEDIWEEK	PP6R3_MOUSE;S588
245	ERKNSASLHVLK	79.966331@S:5	22.6	366.1949	4	1460.75	0.0006	25.59	K	T	+		@S:5		ERKN[s]A[s]LHVLK	SO1B2_MOUSE;S288
246	ERSDSGGSSSEPFER	79.966331@S:3	30.8	569.5596	3	1705.657	-0.0012	21.228	R	H	+		@S:3		ER[s]D[s]GG[s][s][s]EPFER	PRC2A_MOUSE;S759
247	ERSPALKSPLQSVVVR	79.966331@S:3,79.966331@S:8	31.4	642.6588	3	1924.955	0.0009	44.942	R	R	+		@S:3,@S:8		ER[pS]PALK[pS]PLQSVVVR	TR150_MOUSE;S248,TR150_MOUSE;S253
248	ERSSTFLER	79.966331@S:3	18.3	402.1838	3	1203.53	0.001	23.491	R	H			@S:3		ER[s][s][t]FLER	S4A4_MOUSE;S1069
249	ESAEFSVLEYSEMGSSFNGSPKGESAMLVENTK	15.994915@M:13,79.966331@S:11,79.966331@S:15	24.1	930.1374	4	3716.52	0.0016	64.672	R	E	+		@S:11,@S:15		E[s]AEF[s]VLE[y][s]EMG[s][s]FNG[s]PKGE[s]AMLVEN[t]K	RTN4_MOUSE;S282,RTN4_MOUSE;S286
250	ESALSRASDESLRK	79.966331@S:5	29.7	543.5925	3	1627.756	-0.001	20.152	K	V	+		@S:5		E[s]AL[s]RA[s]DE[s]LRK	S20A2_MOUSE;S253
251	ESDDKPEIEDVGSDEEEEEK	79.966331@S:13	72.4	1194.46	2	2386.905	-0.0015	36.473	K	K	+		@S:13		ESDDKPEIEDVG[pS]DEEEEEK	HS90A_MOUSE;S263
252	ESDDKPEIEDVGSDEEEEEK	79.966331@S:2	28.7	796.6428	3	2386.907	0.0005	28.964	K	K	+		@S:2		ESDDKPEIEDVG[pS]DEEEEEK	HS90A_MOUSE;S252
253	ESDDKPEIEDVGSDEEEEEKK	79.966331@S:13	78.4	839.3404	3	2514.999	-0.0017	27.119	K	D	+		@S:13		ESDDKPEIEDVG[pS]DEEEEEKK	HS90A_MOUSE;S263
254	ESDDKPEIEDVGSDEEEEEKK	79.966331@S:2	20.1	629.7579	4	2515.002	0.0015	34.107	K	D			@S:2		E[s]DDKPEIEDVG[s]DEEEEEKK	HS90A_MOUSE;S252
255	ESDDKPEIEDVGSDEEEEEKKDGDK	79.966331@S:13	69.1	977.731	3	2930.171	-0.0003	32.516	K	K	+		@S:13		ESDDKPEIEDVG[pS]DEEEEEKKDGDK	HS90A_MOUSE;S263
256	ESDDKPEIEDVGSDEEEEEKKDGDK	79.966331@S:2	26.4	733.5503	4	2930.172	0.0009	30.548	K	K			@S:2		E[s]DDKPEIEDVG[s]DEEEEEKKDGDK	HS90A_MOUSE;S252
257	ESLKEEDESDDDNM	15.994915@M:14,79.966331@S:2	43	876.2951	2	1750.576	-0.0007	23.504	K	-	+		@S:2		ESLKEEDE[pS]DDDNM	PSA3_MOUSE;S243
258	ESLKEEDESDDDNM	15.994915@M:14,79.966331@S:9	58	876.2953	2	1750.576	-0.0004	19.008	K	-	+		@S:9		ESLKEEDE[pS]DDDNM	PSA3_MOUSE;S250
259	ESLKEEDESDDDNM	79.966331@S:9	37.7	868.297	2	1734.579	-0.0021	24.305	K	-	+		@S:9		ESLKEEDE[pS]DDDNM	PSA3_MOUSE;S250
260	ESLPLDLSDDQSNSK	79.966331@S:8	37.1	864.3724	2	1726.73	0.0005	43.254	K	K	+		@S:8		ESLPLDL[s]DDQ[s]N[s]K	NVL_MOUSE;S190
261	ESPRPPAAAEAPAGSDGEDGGRR	79.966331@S:15	39	777.3433	3	2329.008	-0.0002	26.403	R	D	+		@S:15		ESPRPPAAAEAPAG[pS]DGEDGGRR	LARP1_MOUSE;S81
262	ESPRPPAAAEAPAGSDGEDGGRR	79.966331@S:2	27.2	583.259	4	2329.007	-0.0016	20.747	R	D	+		@S:2		E[s]PRPPAAAEAPAG[s]DGEDGGRR	LARP1_MOUSE;S68
263	ESSPVPSPTLDRK	79.966331@S:3,79.966332@T:9	20.4	524.8954	3	1571.664	0.001	25.366	K	A	+	ambiguos	@S:3	@S:7orT:9	E[s][s]PVP[s]P[t]LDRK	SPTB2_MOUSE;S2164,SPTB2_MOUSE;S2168orT2170
264	ETLWLLSGVKK	79.966331@S:7	22.1	451.9096	3	1352.707	-0.0036	28.285	R	M	+		@S:7		E[t]LWLL[s]GVKK	GCP5_MOUSE;S279
265	ETMTMILKAK	79.966332@T:2	26.8	415.8707	3	1244.59	-0.0008	20.444	K	L	+		@T:2		E[t]M[t]MILKAK	KS6A3_MOUSE;T276

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
266	EVDDILGEGSDDSDIEK	79.966331@S:10, 79.966331@S:13	23.7	998.371	2	1994.727	-0.0008	47.862	K	K	+		@S:10,@S:13		EVDDILGEG[pS]DD[pS]DIEK	CTDP1_MOUSE;S860,CTDP1_MOUSE;S863
267	EVEDKESEGEEEDEDEDLSK	79.966331@S:7	72.8	807.3041	3	2418.89	-0.0054	23.33	K	Y	+		@S:7		EVEDKE[pS]EGEEEDEDEDLSK	ZRAB2_MOUSE;S153
268	EVGIHLNYKEDSCVR	57.021465@C:13, 79.966331@S:12	22.7	633.6211	3	1897.841	0.0021	40.218	K	L	+		@S:12		EVGIHLN[y]KED[s]CVR	CRRY_MOUSE;S454
269	EVIEASDKEGLSPAK	79.966331@S:6,79.966331@S:12	21.3	578.2529	3	1731.737	0.0001	27.512	K	R			@S:6,@S:12		EVIEA[pS]DKEGL[pS]PAK	PRP4B_MOUSE;S88,PRP4B_MOUSE;S94
270	EVSDDEAEEKEEKEEEK	79.966331@S:3	59.3	1066.423	2	2130.831	-0.0059	18.523	K	E	+		@S:3		EV[pS]DDEAEEKEEKEEEK	HS90A_MOUSE;S231
271	EVYLSGSFNNWSK	79.966331@S:7	41	805.8485	2	1609.682	0.0011	47.979	K	L	+		@S:7		EVYL[s]G[s]FNNWSK	AAKB1_MOUSE;S96
272	EWFLEAAKDPSAVAK	79.966331@S:11	21.7	581.279	3	1740.815	0.0028	47.888	K	H			@S:11		EWFLEAAKDP[pS]AVAK	G6PI_MOUSE;S237
273	FAVLNDSDKSDDEASSCNDQLK	57.021465@C:17, 79.966331@S:7,79.966331@S:10	33.6	873.3378	3	2616.992	-0.0011	38.934	K	G	+		@S:7,@S:10		FAVLND[pS]DK[pS]DDEASSCNDQLK	IFIH1_MOUSE;S645,IFIH1_MOUSE;S648
274	FGSADNIPNLK	79.966331@S:3	45.7	628.2896	2	1254.565	0.0002	39.208	K	D	+		@S:3		FG[pS]ADNIPNLK	TMCC1_MOUSE;S378
275	FGSSPQRDPNWIGDR	79.966331@S:4	46.8	604.5998	3	1810.778	-0.0013	34.68	R	S	+		@S:4		FG[s][s]PQRDPNWIGDR	CASC3_MOUSE;S263
276	FHDSEGDDTEETEDYR	79.966331@S:4	37.4	675.5729	3	2023.697	0.0013	31.166	K	Q			@S:4		FHD[s]EGDD[t]EETEDYR	BCLF1_MOUSE;S395
277	FHDSEGDDTEETEDYR	79.966332@T:9	16.1	675.5715	3	2023.693	-0.0031	24.556	K	Q			@T:9		FHD[s]EGDD[t]EE[t]ED[y]R	BCLF1_MOUSE;T400
278	FHLEPTSPPTTDGFK	79.966331@S:7	42.4	877.3938	2	1752.773	-0.0029	39.704	K	Y	+		@S:7		FHLEP[t][s]PP[t][t]DGFK	GYS2_MOUSE;S627
279	FHLEPTSPPTTDGFK	79.966332@T:6	28.9	877.3938	2	1752.773	-0.0029	39.721	K	Y	+		@T:6		FHLEP[t][s]PP[t][t]DGFK	GYS2_MOUSE;T626
280	FHSGNKSPEVLR	79.966331@S:3,79.966331@S:7	18.9	510.8881	3	1529.642	-0.0006	20.857	R	A	+		@S:3,@S:7		FH[pS]GNK[pS]PEVLR	CLCC1_MOUSE;S429,CLCC1_MOUSE;S433
281	FHSGNKSPEVLR	79.966331@S:7	22.2	484.2327	3	1449.676	-0.0004	19.216	R	A	+		@S:7		FHSGNK[pS]PEVLR	CLCC1_MOUSE;S433
282	FIDKDQQPSGSEGEDDDAEAALKK	79.966331@S:9,79.966331@S:11	40.1	918.378	3	2752.112	-0.0033	30.259	K	E	+		@S:9,@S:11		FIDKDQQP[pS]G[pS]EGEDDDAEAALKK	THUM1_MOUSE;S86,THUM1_MOUSE;S88
283	FLNRSSQESLDIK	79.966331@S:6,79.966331@S:9	23.8	566.2494	3	1695.726	-0.0006	37.407	K	E	+		@S:6,@S:9		FLNR[s][s]QE[s]LDIK	KS6C1_MOUSE;S423,KS6C1_MOUSE;S426
284	FLTEELSLDQDR	79.966331@S:7	56.9	773.3457	2	1544.677	0.001	47.455	K	I	+		@S:7		FLTEEL[pS]LDQDR	DOPD_MOUSE;S90
285	FRRSETPPHWR	79.966331@S:4,79.966332@T:6	29.7	407.9276	4	1627.681	0.0004	23.854	R	Q	+		@S:4,@T:6		FRR[pS]E[pT]PPHWR	PPIG_MOUSE;S354,PPIG_MOUSE;T356
286	FSGEEGEIEDDESGTENREEK	79.966331@S:13	40.3	822.6534	3	2464.938	-0.0006	32.962	K	D	+		@S:13		FSGEEGEIEDDE[s]G[t]ENREEK	TR150_MOUSE;S935
287	FSHSYLSDSDTEAK	79.966331@S:9	63.8	833.8343	2	1665.654	-0.002	26.757	R	L	+		@S:9		F[s]H[s][y]L[s]D[s]D[t]EAK	MY18A_MOUSE;S2039
288	FSHSYLSDSDTEAK	79.966331@S:9,79.966331@Y:5	16.4	873.8186	2	1745.623	0.0004	30.72	R	L	+	ambiguos	@S:9	@S:4orY:5	FSHSYL[s]D[s]DTEAK	MY18A_MOUSE;S2039,MY18A_MOUSE;S2034orY2035
289	FVVDGVEVSITTSKIISEDEK	79.966332@T:11	30.3	792.3944	3	2374.161	0.0057	67.418	R	K			@T:11		FVVDGVEV[s]I[t][t][s]KII[s]EDEK	STK10_MOUSE;T542
290	GAAEEADSEDSDAEEKPVKQEDFPK	79.966331@S:8,79.966331@S:11	44.6	961.048	3	2880.122	-0.0041	28.85	K	D	+		@S:8,@S:11		GAAEEAD[pS]ED[pS]DAEEKPVKQEDFPK	TFP11_MOUSE;S96,TFP11_MOUSE;S99
291	GAEDYPDPPLPHSYSSDR	79.966331@S:13	37.3	694.9534	3	2081.838	0.0015	43.994	K	I			@S:13		GAEDYPDPPLPH[s][y][s][s]DR	SRBS2_MOUSE;S1095
292	GAEDYPDPPLPHSYSSDR	79.966331@S:16	51.8	694.9532	3	2081.838	0.0009	35.647	K	I		ambiguos		@S:13orY:14orS:15orS:16	GAED[y]PDPPLPH[s][y][s][s]DR	SRBS2_MOUSE;S1095orY1096orS1097orS1098
293	GAEEEEEEEDDDSEEEIK	79.966331@S:13	84.4	1095.881	2	2189.748	-0.0049	24.504	K	A	+		@S:13		GAEEEEEEEDDD[pS]EEEIK	DEMA_MOUSE;S226
294	GAPSSPAAGVLPSPQGK	79.966331@S:5	29.2	800.8893	2	1599.764	-0.0018	32.596	R	A			@S:5		GAP[s][s]PAAGVLPSPQGK	NU188_MOUSE;S1719
295	GATPAEDDEDKDIDLFGSDEEEEDK	79.966331@S:18	92.9	950.3728	3	2848.097	-0.0007	52.23	K	E	+		@S:18		GATPAEDDEDKDIDLFG[pS]DEEEEDK	EF1D_MOUSE;S162
296	GATPAEDDEDKDIDLFGSDEEEEDKEAAR	79.966331@S:18	74.6	819.8346	4	3275.309	-0.0056	40.91	K	L			@S:18		GA[t]PAEDDEDKDIDLFG[s]DEEEEDKEAAR	EF1D_MOUSE;S162
297	GDGGSTPTPGDSLQNPDTASEALSEPESQRR	79.966331@S:5,79.966331@S:28	42.3	1106.124	3	3315.35	-0.0067	37.779	R	E	+	ambiguos	@S:5	@S:24orS:28	GDGG[s][t]P[t]PGD[s]LQNPD[t]A[s]EAL[s]EPE[s]QRR	FA73B_MOUSE;S205,FA73B_MOUSE;S224orS228
298	GDGGSTPTPGDSLQNPDTASEALSEPESQRR	79.966332@T:6	122.9	1079.469	3	3235.386	-0.0042	37.681	R	E			@T:6		GDGG[s][t]P[t]PGDSLQNPDTASEALSEPESQRR	FA73B_MOUSE;T206
299	GDQVLNFSDAEDLIDDSK	79.966331@S:8	71.3	1030.937	2	2059.86	-0.0022	65.11	K	L	+		@S:8		GDQVLNF[pS]DAEDLIDDSK	MCRS1_MOUSE;S282
300	GDSIEEILADSEDEDEEEERGR	79.966331@S:11	57.7	868.0146	3	2601.022	-0.002	46.087	K	G			@S:11		GDSIEEILAD[pS]EDEDEEEERGR	RRP12_MOUSE;S1081
301	GDSLILEHQWELEK	79.966331@S:3	26.4	888.9128	2	1775.811	-0.002	49.304	R	L	+		@S:3		GD[pS]LILEHQWELEK	KIF1B_MOUSE;S1487
302	GEPNVSYICSR	57.021465@C:9,79.966331@Y:7	61.1	681.2814	2	1360.548	0	37.35	R	Y			@Y:7		GEPNV[s][y]ICSR	GSK3A_MOUSE;Y279,GSK3B_MOUSE;Y216
303	GFDTSPEHSLDLGISGR	79.966331@S:9	27	623.2794	3	1866.816	0.0016	45.338	K	K			@S:9		GFD[t][s]PEH[s]LDLGISGR	EP400_MOUSE;S927
304	GGDVSPSPYSSSSWR	79.966331@S:5	62	824.8357	2	1647.657	0.0003	34.898	R	R	+		@S:5		GGDV[s]P[s]PYSSSSWR	CDK13_MOUSE;S384
305	GGNVFEALIQDDSEEEEEEEENR	79.966331@S:13	78.3	916.367	3	2746.079	0.0026	59.55	K	V	+		@S:13		GGNVFEALIQDD[pS]EEEEEEEENR	ABCF1_MOUSE;S138
306	GGSSGEELEDEEPVK	79.966331@S:3,79.966331@S:4	61.1	861.3115	2	1720.608	-0.0033	34.732	R	K	+		@S:3,@S:4		GG[pS][pS]GEELEDEEPVK	HDGR2_MOUSE;S366,HDGR2_MOUSE;S367
307	GGSSGEELEDEEPVKK	79.966331@S:3,79.966331@S:4	49.3	925.3588	2	1848.703	-0.0036	27.328	R	R	+		@S:3,@S:4		GG[pS][pS]GEELEDEEPVKK	HDGR2_MOUSE;S366,HDGR2_MOUSE;S367
308	GHGTYMGEEKLIASVAGSVER	79.966331@S:14, 79.966331@S:18, 79.966331@Y:5	20	608.4989	4	2429.966	-0.0064	24.082	R	V	+	ambiguos	@S:14,@S:18	@T:4orY:5	GHG[t][y]MGEEKLIA[s]VAG[s]VER	EXOS2_MOUSE;S55,EXOS2_MOUSE;S59,EXOS2_MOUSE;T45orY46
309	GHPSAGAEEEGGSDGSAAEAEPR	79.966331@S:13	79.8	749.9631	3	2246.867	-0.0038	19.832	R	A	+		@S:13		GHPSAGAEEEGG[pS]DG[pS]AAEAEPR	EIF3B_MOUSE;S120
310	GHPSAGAEEEGGSDGSAAEAEPR	79.966331@S:13, 79.966331@S:16	62.4	776.618	3	2326.832	-0.0055	20.313	R	A	+		@S:13,@S:16		GHP[s]AGAEEEGG[s]DG[s]AAEAEPR	EIF3B_MOUSE;S120,EIF3B_MOUSE;S123

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
311	GHPSAGAEEEGGSDGSAAEAEPR	79.966331@S:4,79.966331@S:16	33.5	776.6206	3	2326.84	0.0023	25.121	R	A	+		@S:4,@S:16		GHP[s]AGAEEEGG[s]DG[s]AAEAEPR	EIF3B_MOUSE;S111,EIF3B_MOUSE;S123
312	GIITDSFGR	79.966331@S:6	27.1	523.2392	2	1044.464	-0.0003	38.28	R	H	+		@S:6		GIITD[pS]FGR	CCM2_MOUSE;S393
313	GILAADESTGSIAK	79.966331@S:11	21.4	706.8367	2	1411.659	-0.0008	34.946	K	R	+	ambiguos		@S:8orT:9orS:11	GILAADE[s][t]G[s]IAK	ALDOA_MOUSE;S36orT37orS39
314	GILAADESTGSIAK	79.966331@S:8	19.1	706.8361	2	1411.658	-0.0019	34.962	K	R	+	ambiguos		@S:8orT:9orS:11	GILAADE[s][t]G[s]IAK	ALDOA_MOUSE;S36orT37orS39
315	GILAADESTGSIAK	79.966332@T:9	26.9	706.8365	2	1411.658	-0.0012	34.757	K	R	+		@T:9		GILAADE[s][t]G[s]IAK	ALDOA_MOUSE;T37
316	GILAADESVGTMGNR	15.994915@M:12,79.966331@S:8	73	793.8477	2	1585.681	0.0001	39.658	K	L	+		@S:8		GILAADE[pS]VGTMGNR	ALDOB_MOUSE;S36
317	GILAADESVGTMGNR	15.994915@M:12,79.966332@T:11	90.6	793.8479	2	1585.681	0.0005	39.224	K	L	+		@T:11		GILAADESVG[pT]MGNR	ALDOB_MOUSE;T39
318	GILAADESVGTMGNR	79.966331@S:8	59.2	785.8502	2	1569.686	0.0001	46.363	K	L	+		@S:8		GILAADE[s]VG[t]MGNR	ALDOB_MOUSE;S36
319	GILAADESVGTMGNR	79.966332@T:11	88.7	785.851	2	1569.687	0.0016	45.634	K	L	+		@T:11		GILAADESVG[pT]MGNR	ALDOB_MOUSE;T39
320	GILRTPDTIR	79.966332@T:5	22.5	407.8837	3	1220.629	0.0013	29.132	K	R	+		@T:5		GILR[t]PD[t]IR	CLH_MOUSE;T394
321	GIPLPTGDTSPEPELLPGDPLPPPK	79.966331@S:10	21.1	872.1075	3	2613.301	0.0029	68.014	K	E	+		@S:10		GIPLP[t]GD[t][s]PEPELLPGDPLPPPK	EIF3G_MOUSE;S42
322	GIPLPTGDTSPEPELLPGDPLPPPK	79.966332@T:9,79.966331@S:10	33.3	898.7614	3	2693.262	-0.0019	66.013	K	E			@T:9,@S:10		GIPLP[t]GD[t][s]PEPELLPGDPLPPPK	EIF3G_MOUSE;T41,EIF3G_MOUSE;S42
323	GKSPQLALR	79.966331@S:3	55.2	525.2785	2	1048.542	-0.0006	21.945	K	Q	+		@S:3		GK[pS]PQLALR	UBXN6_MOUSE;S36
324	GLLFSASK	79.966331@S:7	22.5	451.723	2	901.4314	0.0005	40.772	K	Q	+		@S:7		GLLF[s]A[s]K	S14L2_MOUSE;S116
325	GLPSPYNMSAPGSR	79.966331@S:13	20.7	757.3277	2	1512.641	-0.0024	39.18	K	S	+		@S:13		GLPSP[y]NM[s]APG[s]R	DESP_MOUSE;S2836
326	GLSASTVDLSSSS	79.966331@S:5	42	645.7768	2	1289.539	0.0003	47.557	R	-	+		@S:5		GL[s]A[s][t]VDLSSSS	KLC4_MOUSE;S611
327	GLSASTVDLSSSS	79.966332@T:6	30.9	645.7769	2	1289.539	0.0004	47.537	R	-	+		@T:6		GL[s]A[s][t]VDLSSSS	KLC4_MOUSE;T612
328	GLVAAYSGESDSEEEQER	79.966331@S:10,79.966331@S:12	40.6	1058.391	2	2114.768	-0.0037	38.135	R	G	+		@S:10,@S:12		GLVAAYSGE[pS]D[pS]EEEQER	RBM10_MOUSE;S736,RBM10_MOUSE;S738
329	GMSHSPSVALR	15.994915@M:2,79.966331@S:3	24.6	413.1849	3	1236.533	0.0006	26.428	R	G	+		@S:3		GM[s]H[s]P[s]VALR	PROX1_MOUSE;S177
330	GMSHSPSVALR	79.966331@S:5	23.8	407.8537	3	1220.539	0.0018	22.247	R	G	+	ambiguos		@S:3orS:5	GM[s]H[s]P[s]VALR	PROX1_MOUSE;S177orS179
331	GPLPAAPPTAPERQPSWER	79.966331@S:16	27.8	713.0116	3	2136.013	-0.0024	36.225	R	S	+	ambiguos		@T:9orS:16	GPLPAAPP[t]APERQP[s]WER	RTN4_MOUSE;T98orS105
332	GPLPAAPPTAPERQPSWER	79.966332@T:9	44.3	713.0119	3	2136.014	-0.0013	35.973	R	S	+		@T:9		GPLPAAPP[t]APERQP[s]WER	RTN4_MOUSE;T98
333	GPPDFSSDEEREPTPVLGSGASVGR	79.966331@S:6,79.966331@S:7	23	901.7153	3	2702.124	-0.002	44.141	K	G	+		@S:6,@S:7		GPPDF[s][s]DEEREP[t]PVLG[s]GASVGR	LAP2A_MOUSE;S66,LAP2A_MOUSE;S67,LAP2B_MOUSE;S66,LAP2B_MOUSE;S67
334	GPPSPPAPVMHSPSRK	15.994915@M:10,79.966331@S:4,79.966331@S:12	23.4	606.5978	3	1816.772	-0.0016	13.972	R	M	+		@S:4,@S:12		GPP[s]PPAPVMH[s]P[s]RK	SNW1_MOUSE;S224,SNW1_MOUSE;S232
335	GPPSPPAPVMHSPSRK	15.994915@M:10,79.966331@S:4,79.966331@S:14	23.8	606.5977	3	1816.771	-0.0021	20.353	R	M	+		@S:4,@S:14		GPP[s]PPAPVMH[s]P[s]RK	SNW1_MOUSE;S224,SNW1_MOUSE;S234
336	GPPSPPAPVMHSPSRK	79.966331@S:4,79.966331@S:12	30.3	601.2662	3	1800.777	-0.0017	24.196	R	M	+		@S:4,@S:12		GPP[s]PPAPVMH[s]P[s]RK	SNW1_MOUSE;S224,SNW1_MOUSE;S232
337	GPPSPPAPVMHSPSRK	79.966331@S:4,79.966331@S:14	24.1	601.2663	3	1800.777	-0.0013	24.095	R	M	+		@S:4,@S:14		GPP[s]PPAPVMH[s]P[s]RK	SNW1_MOUSE;S224,SNW1_MOUSE;S234
338	GPQPRPSSPVSAPVRPK	79.966331@S:7,79.966331@S:11	34.6	639.6421	3	1915.904	-0.0026	22.092	R	T	+		@S:7,@S:11		GPQPRP[s][s]PV[s]APVRPK	AAKG2_MOUSE;S86,AAKG2_MOUSE;S90
339	GPQPRPSSPVSAPVRPK	79.966331@S:8,79.966331@S:11	29.5	639.6421	3	1915.904	-0.0025	21.671	R	T	+		@S:8,@S:11		GPQPRP[s][s]PV[s]APVRPK	AAKG2_MOUSE;S87,AAKG2_MOUSE;S90
340	GQAMLHVTWGSKVR	79.966332@T:8	33.4	550.6043	3	1648.791	0.0002	20.984	R	L			@T:8		GQAMLHV[t]WG[s]KVR	TM143_MOUSE;T20
341	GQQDPGSEASESHGLEAR	79.966331@S:10	21.2	967.8994	2	1933.784	0.004	34.999	R	S	+		@S:10		GQQDPG[s]EA[s]E[s]HGLEAR	RAB44_MOUSE;S406
342	GQTPLTEGSEDLDGHSDPEESFAR	79.966331@S:16	32.6	885.3661	3	2653.076	-0.0054	39.955	R	D	+		@S:16		GQTPLTEG[s]EDLDGH[s]DPEE[s]FAR	F134C_MOUSE;S320
343	GQTPLTEGSEDLDGHSDPEESFAR	79.966331@S:21	39.6	885.3669	3	2653.079	-0.0028	40.037	R	D	+		@S:21		GQTPLTEG[s]EDLDGH[s]DPEE[s]FAR	F134C_MOUSE;S325
344	GQTPLTEGSEDLDGHSDPEESFAR	79.966331@S:9,79.966331@S:16	47	912.0224	3	2733.045	-0.0025	43.142	R	D	+		@S:9,@S:16		GQTPL[t]EG[s]EDLDGH[s]DPEE[s]FAR	F134C_MOUSE;S313,F134C_MOUSE;S320
345	GRADGDWDDQEVLDYFSDK	79.966331@S:17	46.3	770.9775	3	2309.911	-0.0007	54.207	K	E	+		@S:17		GRADGDWDDQEVLDYF[pS]DK	BCLF1_MOUSE;S383
346	GRADGDWDDQEVLDYFSDKESAK	79.966331@S:17	59	909.3795	3	2725.117	-0.0014	49.973	K	Q	+		@S:17		GRADGDWDDQEVLD[y]F[s]DKE[s]AK	BCLF1_MOUSE;S383
347	GRLSPVPVPR	79.966331@S:4	29.4	579.3131	2	1156.612	-0.0002	35.188	R	A	+		@S:4		GRL[pS]PVPVPR	RALY_MOUSE;S135
348	GRLTPSPDIIVLSDNEASSPR	79.966332@T:4,79.966331@S:6,79.966331@S:19	35.1	822.024	3	2463.05	0.0017	53.194	R	S			@T:4,@S:6,@S:19		GRL[t]P[s]PDIIVLSDNEA[s][s]PR	P66B_MOUSE;T121,P66B_MOUSE;S123,P66B_MOUSE;S136
349	GRRSPVLLPK	79.966331@S:4	19.5	401.5639	3	1201.67	0.0004	20.729	R	G	+		@S:4		GRR[pS]PVLLPK	BICD2_MOUSE;S578
350	GSAEGSSDEEGKLVIDEPAK	79.966331@S:6,79.966331@S:7	64.5	1089.445	2	2176.876	-0.0056	34.947	K	E	+		@S:6,@S:7		G[s]AEG[s][s]DEEGKLVIDEPAK	HDGF_MOUSE;S132,HDGF_MOUSE;S133
351	GSAEGSSDEEGKLVIDEPAK	79.966331@S:7	48.2	699.979	3	2096.915	0	39.033	K	E			@S:7		GSAEG[s][s]DEEGKLVIDEPAK	HDGF_MOUSE;S133
352	GSGTASDDEFENLR	79.966331@S:6	82.2	789.3083	2	1576.602	-0.0023	35.742	R	I	+		@S:6		G[s]G[t]A[s]DDEFENLR	HUWE1_MOUSE;S1907
353	GSGTGHPVPGVAQAPDSPAGVR	79.966331@S:17	37.6	698.6636	3	2092.969	-0.0002	26.937	R	T	+		@S:17		GSGTGHPVPGVAQAPD[pS]PAGVR	SNTB1_MOUSE;S86
354	GSLASLDSLR	79.966331@S:5	52.7	549.7627	2	1097.511	-0.0009	42.547	R	K	+		@S:5		GSLA[pS]LDSLR	CTND1_MOUSE;S349
355	GSLASLDSLRK	79.966331@S:5	38.4	409.5429	3	1225.607	0.0003	33.954	R	G	+		@S:5		GSLA[s]LD[s]LRK	CTND1_MOUSE;S349

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
356	GSLSRSSSPVTELTAR	79.966331@S:6,79.966331@S:7	26.2	603.2714	3	1806.792	0.001	35.574	K	S	+	ambiguos	@S:6	@S:7orS:8	G[s]L[s]R[s][s][s]PVTELTAR	SRRM2_MOUSE;S1066,SRRM2_MOUSE;S1067orS1068
357	GSPGALSSDSELPENPYSQVK	79.966331@S:10	45.8	748.003	3	2240.987	0.0033	51.11	R	G			@S:10		G[s]PGAL[s][s]D[s]ELPENPYSQVK	CING_MOUSE;S92
358	GSPGALSSDSELPENPYSQVK	79.966331@S:8	66.8	1121.499	2	2240.983	-0.0009	50.997	R	G	+		@S:8		GSPGAL[s][s]DSELPENPYSQVK	CING_MOUSE;S90
359	GSPVSEIGWETPPPESPR	79.966331@S:16	41.8	1001.451	2	2000.888	-0.0004	45.164	K	L	+		@S:16		GSPVSEIGWETPPPE[pS]PR	SNTB1_MOUSE;S218
360	GSSQPNLSTSYSEQEYGK	79.966331@S:3	67.4	1021.423	2	2040.831	-0.0006	32.81	R	A			@S:3		G[s][s]QPNLSTSYSEQEYGK	EPN2_MOUSE;S173
361	GSYQDSLRASIR	79.966331@S:10	34.8	478.224	3	1431.65	-0.0007	27.9	R	Q	+		@S:10		GSYQD[s]LRA[s]IR	ABCBB_MOUSE;S696
362	GTFASLSELHCDK	57.021465@C:11, 79.966331@S:5	50.2	515.5535	3	1543.639	0.0008	47.553	K	L			@S:5		GTFA[s]L[s]ELHCDK	HBB2_MOUSE;S88,HBB1_MOUSE;S88
363	GTFASLSELHCDK	57.021465@C:11, 79.966332@T:2	34.2	772.8266	2	1543.639	0.0008	47.534	K	L	+		@T:2		G[t]FA[s]L[s]ELHCDK	HBB2_MOUSE;T85,HBB1_MOUSE;T85
364	GTGPGGQLQDLDCSSSDDEGATQNTKPSATK	57.021465@C:13, 79.966331@S:14, 79.966331@S:15	45.4	1094.775	3	3281.303	-0.0037	33.427	R	G	+		@S:14,@S:15		GTGPGGQLQDLDC[pS][pS][pS]DDEGATQNTKPSATK	SRPR_MOUSE;S295,SRPR_MOUSE;S296
365	GTGPGGQLQDLDCSSSDDEGATQNTKPSATK	57.021465@C:13, 79.966331@S:14, 79.966331@S:15, 79.966331@S:16	26.1	1121.429	3	3361.265	-0.0082	36.578	R	G	+		@S:14,@S:15, @S:16		GTGPGGQLQDLDC[s][s][s]DDEGATQNTKPSATK	SRPR_MOUSE;S295,SRPR_MOUSE;S296,SRPR_MOUSE;S297
366	GTGPGGQLQDLDCSSSDDEGATQNTKPSATK	57.021465@C:13, 79.966331@S:15, 79.966331@S:16	50	1094.775	3	3281.302	-0.0047	33.331	R	G	+	ambiguos	@S:16	@S:14orS:15	GTGPGGQLQDLDC[s][s][s]DDEGATQNTKPSATK	SRPR_MOUSE;S297,SRPR_MOUSE;S295orS296
367	GTLDEEDEEADSDTDDIDHR	79.966331@S:12	51.1	786.2906	3	2355.85	-0.0001	36.481	R	V	+		@S:12		GTLDEEDEEAD[pS]DTDDIDHR	GPN1_MOUSE;S338
368	GTLDEEDEEADSDTDDIDHR	79.966332@T:14	25.8	786.2901	3	2355.848	-0.0016	29.77	R	V	+	ambiguos		@S:12orT:14	GTLDEEDEEAD[s]D[t]DDIDHR	GPN1_MOUSE;S338orT340
369	GWLRDPNASPGDAGEQAIR	79.966331@S:9	58.5	697.32	3	2088.938	0.0005	45.815	K	Q	+		@S:9		GWLRDPNA[pS]PGDAGEQAIR	VINC_MOUSE;S290
370	GWSPPPEVR	79.966331@S:3	35.8	552.7471	2	1103.48	-0.0005	35.69	R	R	+		@S:3		GW[pS]PPPEVR	ACSA_MOUSE;S30
371	GWSPPPEVRR	79.966331@S:3	29.5	420.8678	3	1259.582	0.0005	30.353	R	S	+		@S:3		GW[pS]PPPEVRR	ACSA_MOUSE;S30
372	GYYSPYSVSGSGSTAGSR	79.966331@S:11	56.6	931.882	2	1861.749	-0.0025	33.065	K	T	+		@S:11		GYYSPYSV[s]G[s]G[s][t]AG[s]R	PLEC_MOUSE;S4627
373	GYYSPYSVSGSGSTAGSR	79.966331@S:13	66.2	931.882	2	1861.749	-0.0026	33.24	K	T	+		@S:13		GYYSPYSV[s]G[s]G[s][t]AG[s]R	PLEC_MOUSE;S4629
374	GYYSPYSVSGSGSTAGSR	79.966331@S:17	60.5	931.883	2	1861.751	-0.0006	41.208	K	T	+		@S:17		GYYSPYSVSGSG[s][t]AG[s]R	PLEC_MOUSE;S4633
375	GYYSPYSVSGSGSTAGSR	79.966331@S:7	49.7	931.8824	2	1861.75	-0.0018	33.442	K	T	+		@S:7		GYYSPY[s]V[s]G[s]G[s][t]AG[s]R	PLEC_MOUSE;S4623
376	HAFSPVASVESASGETLHSPK	79.966331@S:11	46.4	740.0113	3	2217.012	0.0018	39.207	R	V	+		@S:11		HAFSPVASVE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S312
377	HAFSPVASVESASGETLHSPK	79.966331@S:11, 79.966331@S:13	57.4	766.6662	3	2296.977	0.0002	44.698	R	V	+		@S:11,@S:13		HAFSPVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S312,FETUA_MOUSE;S314
378	HAFSPVASVESASGETLHSPK	79.966331@S:11, 79.966332@T:16	34.3	766.6659	3	2296.976	-0.0006	44.349	R	V	+		@S:11,@T:16		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S312,FETUA_MOUSE;T317
379	HAFSPVASVESASGETLHSPK	79.966331@S:13	69	740.0101	3	2217.008	-0.0017	33.931	R	V	+		@S:13		HAFSPVASVESA[s]GETLH[s]PK	FETUA_MOUSE;S314
380	HAFSPVASVESASGETLHSPK	79.966331@S:4	39.3	740.0112	3	2217.012	0.0014	47.617	R	V	+		@S:4		HAFSPVA[s]VE[s]A[s]GETLHSPK	FETUA_MOUSE;S305
381	HAFSPVASVESASGETLHSPK	79.966331@S:8	62.4	740.009	3	2217.005	-0.005	33.277	R	V	+		@S:8		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S309
382	HAFSPVASVESASGETLHSPK	79.966331@S:8,79.966331@S:11	58.2	766.6653	3	2296.974	-0.0026	35.185	R	V	+		@S:8,@S:11		HAFSPVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S309,FETUA_MOUSE;S312
383	HAFSPVASVESASGETLHSPK	79.966331@S:8,79.966331@S:11,79.966331@S:13	23.2	793.3205	3	2376.94	-0.0034	38.837	R	V	+		@S:8,@S:11,@S:13		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S309,FETUA_MOUSE;S312,FETUA_MOUSE;S314
384	HAFSPVASVESASGETLHSPK	79.966331@S:8,79.966331@S:19	51.3	766.6665	3	2296.978	0.0011	34.865	R	V	+		@S:8,@S:19		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S309,FETUA_MOUSE;S320
385	HAFSPVASVESASGETLHSPK	79.966331@S:8,79.966332@T:16	43.6	766.6664	3	2296.977	0.0009	43.03	R	V	+		@S:8,@T:16		HAFSPVASVE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;S309,FETUA_MOUSE;T317
386	HAFSPVASVESASGETLHSPK	79.966332@T:16	71.3	740.0097	3	2217.007	-0.0029	32.899	R	V	+		@T:16		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;T317
387	HAFSPVASVESASGETLHSPK	79.966332@T:16, 79.966331@S:19	43.9	766.6658	3	2296.976	-0.001	39.112	R	V	+		@T:16,@S:19		HAF[s]PVA[s]VE[s]A[s]GE[t]LH[s]PK	FETUA_MOUSE;T317,FETUA_MOUSE;S320
388	HASSSPESLKPTPAPGSR	79.966331@S:3,79.966331@S:4	38.9	655.9533	3	1964.838	-0.0013	21.914	R	R	+		@S:3,@S:4		HA[s][s][s]PE[s]LKPTPAPGSR	SRRM2_MOUSE;S433,SRRM2_MOUSE;S434
389	HASSSPESLKPTPAPGSR	79.966331@S:5,79.966331@S:8	26.2	655.9537	3	1964.839	-0.0001	21.131	R	R	+		@S:5,@S:8		HA[s][s][s]PE[s]LKPTPAPGSR	SRRM2_MOUSE;S435,SRRM2_MOUSE;S438
390	HGESAWNLENR	79.966331@S:4	22.9	464.8609	3	1391.561	-0.0011	29.47	R	F	+		@S:4		HGE[pS]AWNLENR	PGAM1_MOUSE;S14
391	HGGGGIVANLSEQSLK	79.966331@S:11	47.2	823.8985	2	1645.782	0	33.886	K	D	+		@S:11		HGGGGIVANL[s]EQ[s]LK	PP1R7_MOUSE;S45
392	HGGGGIVANLSEQSLKDGVDR	79.966331@S:11, 79.966331@S:14	41.1	757.0049	3	2267.993	-0.0008	36.123	K	G	+		@S:11,@S:14		HGGGGIVANL[pS]EQ[pS]LKDGVDR	PP1R7_MOUSE;S45,PP1R7_MOUSE;S48
393	HGLTHEELKSPREPGYK	79.966331@S:10	51.9	515.2507	4	2056.974	0.0005	27.066	K	A	+		@S:10		HGLTHEELK[s]PREPG[y]K	TR150_MOUSE;S695
394	HGSDPAFGPSPR	79.966331@S:3	47.4	652.7736	2	1303.533	-0.002	21.899	R	G	+		@S:3		HG[pS]DPAFGPSPR	FA83H_MOUSE;S522
395	HGSPTAPIGAGSPEFTEQGR	79.966331@S:3	47.2	692.6448	3	2074.913	0.0015	40.349	R	S	+		@S:3		HG[s]P[t]APIGAGSPEFTEQGR	PKHA7_MOUSE;S533
396	HGSPTAPIGAGSPEFTEQGR	79.966332@T:5	59.5	692.6445	3	2074.912	0.0007	40.261	R	S	+		@T:5		HG[s]P[t]APIGAGSPEFTEQGR	PKHA7_MOUSE;T535
397	HIKEEPLSEEEPCTSTAVPSPEK	57.021465@C:13, 79.966331@S:8	92.6	892.0696	3	2673.187	-0.0011	38.366	K	K	+		@S:8		HIKEEPL[pS]EEEPCTSTAVP[pS]PEK	NOP58_MOUSE;S509
398	HIKEEPLSEEEPCTSTAVPSPEK	57.021465@C:13, 79.966331@S:8,79.966331@S:20	37.2	918.7258	3	2753.156	0.0012	39.805	K	K	+		@S:8,@S:20		HIKEEPL[pS]EEEPCTSTAVPSPEK	NOP58_MOUSE;S509,NOP58_MOUSE;S521
399	HLQILTEFKEKAR	79.966332@T:6	21.5	423.9767	4	1691.878	0.0015	31.265	K	A			@T:6		HLQIL[pT]EFKEKAR	SPA3A_MOUSE;T151

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
400	HLSHPEPEQQHVIQR	79.966331@S:3	48.9	479.4801	4	1913.891	0.0015	26.757	R	L	+		@S:3		HL[pS]HPEPEQQHVIQR	ACINU_MOUSE;S710
401	HNLTKTLGTLK	79.966332@T:4	21.4	435.902	3	1304.684	-0.0012	39.31	R	S			@T:4		HNL[t]K[t]LG[t]LK	E2F8_MOUSE;T187
402	HNQDSQHCSLSGDEEDELFK	57.021465@C:8,79.966331@S:11	78.7	818.9879	3	2453.942	-0.0013	43.362	R	G	+		@S:11		HNQDSQHCSL[pS]GDEEDELFK	FKB15_MOUSE;S1159
403	HNQDSQHCSLSGDEEDELFK	57.021465@C:8,79.966331@S:9,79.966331@S:11	40.5	845.6429	3	2533.907	-0.0026	37.719	R	G	+		@S:9,@S:11		HNQDSQHC[pS]L[pS]GDEEDELFK	FKB15_MOUSE;S1157,FKB15_MOUSE;S1159
404	HRAEAPPLQREDSGTFSLGK	79.966331@S:13	34.9	569.7756	4	2275.073	-0.0014	30.116	R	M	+		@S:13		HRAEAPPLQRED[s]G[t]F[s]LGK	PRKRA_MOUSE;S18
405	HRAEAPPLQREDSGTFSLGK	79.966332@T:15	33.2	569.7763	4	2275.076	0.0017	37.927	R	M	+		@T:15		HRAEAPPLQRED[s]G[t]F[s]LGK	PRKRA_MOUSE;T20
406	HRSEEENQVNLPK	79.966331@S:3	66.1	553.9203	3	1658.739	-0.0023	20.341	R	L	+		@S:3		HR[pS]EEENQVNLPK	GCH1_MOUSE;S51
407	HRSGDALTTVVVK	79.966331@S:3	53.7	488.2518	3	1461.734	-0.0004	24.725	R	Q	+		@S:3		HR[pS]GDALTTVVVK	SNIP1_MOUSE;S18
408	HSSLPTESDEDIAPAQR	79.966331@S:8	98.3	966.9194	2	1931.824	-0.002	29.368	R	V	+		@S:8		HSSLPTE[pS]DEDIAPAQR	AP3D1_MOUSE;S760
409	HTGPNSPDTANDGFVR	79.966331@S:6	41.9	588.9164	3	1763.727	0.0007	30.357	K	L	+		@S:6		H[t]GPN[s]PD[t]ANDGFVR	HNRH1_MOUSE;S104,HNRH2_MOUSE;S104
410	HTGPNSPDTANDGFVR	79.966332@T:2	41.3	588.917	3	1763.729	0.0026	31.374	K	L	+		@T:2		H[t]GPN[s]PDTANDGFVR	HNRH1_MOUSE;T100,HNRH2_MOUSE;T100
411	HTGPNSPDTANDGFVR	79.966332@T:9	36.8	882.8694	2	1763.724	-0.0023	31.463	K	L	+		@T:9		HTGPN[s]PD[t]ANDGFVR	HNRH1_MOUSE;T107,HNRH2_MOUSE;T107
412	HTQLVEQLDESSV	79.966331@S:12	69.2	782.8479	2	1563.681	-0.0005	38.141	K	-	+		@S:12		HTQLVEQLDE[s][s]V	SEM4G_MOUSE;S836
413	IACDEEFSDSEDEGEGGRR	57.021465@C:3,79.966331@S:8,79.966331@S:10	23	773.2687	3	2316.784	-0.0037	26.706	R	N	+		@S:8,@S:10		IACDEEF[pS]D[pS]EDEGEGGRR	HDAC2_MOUSE;S422,HDAC2_MOUSE;S424
414	IACEEEFSDSDEEGEGGRK	57.021465@C:3,79.966331@S:8,79.966331@S:10	16.8	768.6057	3	2302.795	-0.0022	26.445	R	N	+		@S:8,@S:10		IACEEEF[pS]D[pS]DEEGEGGRK	HDAC1_MOUSE;S421,HDAC1_MOUSE;S423
415	IDISPSALR	79.966331@S:4	37.7	526.263	2	1050.511	0.0005	39.844	R	K	+		@S:4		IDI[s]P[s]ALR	BCLF1_MOUSE;S656
416	IDISPSTFR	79.966331@S:4	44.1	558.2605	2	1114.506	0.0004	51.476	R	K	+		@S:4		IDI[s]P[s][t]FR	TR150_MOUSE;S679
417	IDISPSTFRK	79.966331@S:4	21.2	415.2081	3	1242.602	0.0015	34.354	R	H	+		@S:4		IDI[s]P[s][t]FRK	TR150_MOUSE;S679
418	IEDVGSDEEDDSGK	79.966331@S:6	71.5	787.7904	2	1573.566	-0.0008	21.696	K	D	+		@S:6		IEDVG[pS]DEEDDSGK	HS90B_MOUSE;S255
419	IEDVGSDEEDDSGKDK	79.966331@S:6	60.7	909.3496	2	1816.685	-0.0041	19.677	K	K	+		@S:6		IEDVG[pS]DEEDDSGKDK	HS90B_MOUSE;S255
420	IEFEGQSVDFVDPNK	79.966331@S:7	47.6	902.3951	2	1802.776	-0.0008	55.277	K	Q	+		@S:7		IEFEGQ[pS]VDFVDPNK	CPSM_MOUSE;S189
421	IESPKLER	79.966331@S:3	26.9	351.178	3	1050.512	0.001	20.547	K	T	+		@S:3		IE[pS]PKLER	HS105_MOUSE;S810
422	IGHHSTSDDSSAYRSVDEVNYWDK	79.966331@S:15	77	712.801	4	2847.175	-0.0025	34.146	R	Q	+		@S:15		IGHHSTSDDSSA[y]R[s]VDEVNYWDK	ODBA_MOUSE;S344
423	IGHHSTSDDSSAYRSVDEVNYWDK	79.966331@S:5,79.966331@Y:13	37.5	976.7206	3	2927.14	-0.0037	36.779	R	Q	+		@S:5,@Y:13		IGHH[s][t][s]DD[s][s]A[y]R[s]VDEVNYWDK	ODBA_MOUSE;S334,ODBA_MOUSE;Y342
424	IGHHSTSDDSSAYRSVDEVNYWDK	79.966331@S:7,79.966331@S:15	36.4	732.7931	4	2927.143	-0.0005	36.719	R	Q	+	ambiguos	@S:15	@T:6orS:7	IGHH[s][t][s]DD[s][s]A[y]R[s]VDEVN[y]WDK	ODBA_MOUSE;S344,ODBA_MOUSE;T335orS336
425	IGHHSTSDDSSAYRSVDEVNYWDK	79.966332@T:6,79.966331@S:15	58.2	732.7933	4	2927.144	0.0004	36.815	R	Q	+	ambiguos	@S:15	@S:5orT:6	IGHH[s][t][s]DDSSA[y]R[s]VDEVNYWDK	ODBA_MOUSE;S344,ODBA_MOUSE;S334orT335
426	IHRSSSSEEASQELESDDG	79.966331@S:4	96.8	714.954	3	2141.84	0.0015	29.516	R	-			@S:4		IHR[s][s][s][s]EEASQELESDDG	PCLI1_MOUSE;S202
427	IHRSSSSEEASQELESDDG	79.966331@S:5	92.6	714.9537	3	2141.839	0.0005	29.647	R	-		ambiguos		@S:4orS:5	IHR[s][s][s][s]EEASQELESDDG	PCLI1_MOUSE;S202orS203
428	IHRSSSSEEASQELESDDG	79.966331@S:6	75.1	714.952	3	2141.834	-0.0044	22.709	R	-		ambiguos		@S:4orS:5orS:6	IHR[s][s][s][s]EEASQELESDDG	PCLI1_MOUSE;S202orS203orS204
429	IHRSSSSEEASQELESDDG	79.966331@S:7	42.4	714.953	3	2141.837	-0.0013	22.812	R	-	+	ambiguos		@S:4orS:5orS:6orS:7	IHR[s][s][s][s]EEASQELESDDG	PCLI1_MOUSE;S202orS203orS204orS205
430	ILLDAQHESGRSSSK	79.966331@S:12	22.5	569.9396	3	1706.797	-0.0019	20.817	K	S	+		@S:12		ILLDAQHE[s]GR[s][s][s]K	BNIP3_MOUSE;S51
431	IPNQFQGSPPAPSDESVK	79.966331@S:8	29.2	989.4499	2	1976.885	-0.0029	33.367	R	I	+		@S:8		IPNQFQG[pS]PPAPSDESVK	HEBP1_MOUSE;S111
432	IPNQFQGSPPAPSDESVKIEER	79.966331@S:8	27.3	835.7266	3	2504.158	-0.0004	36.912	R	E	+		@S:8		IPNQFQG[s]PPAP[s]DE[s]VKIEER	HEBP1_MOUSE;S111
433	IQEFCEQHYHCAEGSQEECDK	57.021465@C:5,57.021465@C:11,57.021465@C:19,79.966331@S:15	51.6	922.0066	3	2762.998	-0.0057	25.029	R	-	+		@S:15		IQEFCEQHYHCAEG[pS]QEECDK	ATTY_MOUSE;S448
434	IQQFDDGGSDEEDIWEEK	79.966331@S:9	88.3	1110.436	2	2218.857	-0.0007	48.134	R	H	+		@S:9		IQQFDDGG[pS]DEEDIWEEK	PP6R3_MOUSE;S588
435	IRTSPTFR	79.966331@S:4	33.8	529.2625	2	1056.51	-0.0012	21.012	K	R	+		@S:4		IR[t][s]P[t]FR	RL23A_MOUSE;S43
436	IRTSPTFR	79.966332@T:6	39.8	529.2628	2	1056.511	-0.0007	21.025	K	R	+		@T:6		IR[t][s]P[t]FR	RL23A_MOUSE;T45
437	ISSCTHRASPSSDEDKPEVPPR	57.021465@C:4,79.966332@T:5,79.966331@S:11	28.7	653.7759	4	2611.074	-0.0029	20.199	R	V	+	ambiguos	@S:11	@S:2orS:3orT:5	I[s][s]C[t]HRA[s]P[s][s]DEDKPEVPPR	ERRFI_MOUSE;S274,ERRFI_MOUSE;S265orS266orT268
438	ISYTPPESPVASHR	79.966331@S:8,79.966331@Y:3	30.7	567.5749	3	1699.703	0.002	37.62	R	S	+		@Y:3,@S:8		IS[y][t]PPE[s]PVASHR	ETV6_MOUSE;Y17,ETV6_MOUSE;S22
439	ISYTPPESPVASHR	79.966332@T:4,79.966331@S:8	28.3	567.5744	3	1699.701	0.0006	37.714	R	S	+		@T:4,@S:8		I[s][y][t]PPE[s]PVA[s]HR	ETV6_MOUSE;T18,ETV6_MOUSE;S22
440	ITHSPDSVKSKAAYGNSQAVGER	79.966331@S:7,79.966331@S:10,79.966331@Y:14	24.6	881.3708	3	2641.091	-0.0069	44.698	K	R	+		@S:7,@S:10,@Y:14		I[t]H[s]PD[s]VK[s]KAA[y]GN[s]QAVGER	JHD2C_MOUSE;S474,JHD2C_MOUSE;S477,JHD2C_MOUSE;Y481
441	ITVEKDPDSALGISDGETSPSSK	79.966331@S:14	51	805.0391	3	2412.095	0.0011	36.272	R	G	+		@S:14		ITVEKDPDSALGI[s]DGE[t][s]P[s][s]K	COBL1_MOUSE;S546
442	ITVEKDPDSALGISDGETSPSSK	79.966331@S:14,79.966332@T:18	35.7	831.6936	3	2492.059	-0.0019	39.799	R	G	+		@S:14,@T:18		ITVEKDPDSALGI[pS]DGETSPSSK	COBL1_MOUSE;S546,COBL1_MOUSE;T550

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
443	ITVEKDPDSALGISDGETSPSSK	79.966332@T:18, 79.966331@S:19	39.6	831.6938	3	2492.06	-0.0013	39.687	R	G	+		@T:18,@S:19		ITVEKDPDSALGI[s]DGE[t][s]P[s][s]K	COBL1_MOUSE;T550,COBL1_MOUSE;S551
444	IVEPEVVGESDSEVEGDAWR	79.966331@S:10, 79.966331@S:12	44.1	1181.477	2	2360.94	-0.0048	53.001	K	L	+		@S:10,@S:12		IVEPEVVGE[pS]D[pS]EVEGDAWR	MFAP1_MOUSE;S116,MFAP1_MOUSE;S118
445	IVETINSDSDSEFGIPKK	79.966331@S:7,79.966331@S:9	24.8	713.6485	3	2137.924	0.0017	42.24	K	T	+		@S:7,@S:9		IVE[t]IN[s]D[s]D[s]EFGIPKK	TOP2B_MOUSE;S1509,TOP2B_MOUSE;S1511
446	IVSAQSLAEDDVE	79.966331@S:3	35.7	728.3162	2	1454.618	0	51.671	R	-	+		@S:3		IV[s]AQ[s]LAEDDVE	TOM20_MOUSE;S135
447	IWLVDSK	79.966331@S:6	28.2	470.7302	2	939.4458	-0.0008	45.777	K	G	+		@S:6		IWLVD[pS]K	MAOX_MOUSE;S336
448	IYHLPDAESDEDEDFK	79.966331@S:9	72.8	1001.901	2	2001.788	-0.0003	49.047	K	E	+		@S:9		IYHLPDAE[pS]DEDEDFK	SEPT2_MOUSE;S218
449	IYHLPDAESDEDEDFKEQTR	79.966331@S:9	56.8	630.0165	4	2516.037	-0.0011	36.961	K	L	+		@S:9		IYHLPDAE[pS]DEDEDFKEQTR	SEPT2_MOUSE;S218
450	IYQFPDCDSDEDEDFK	57.021465@C:7,79.966331@S:9	24.4	1051.882	2	2101.749	-0.0007	46.561	K	L	+		@S:9		IYQFPDCD[pS]DEDEDFK	SEPT4_MOUSE;S325
451	IYQFPDCDSDEDEDFKLQDQALK	57.021465@C:7,79.966331@S:9	29.3	967.072	3	2898.194	-0.0001	50.731	K	E	+		@S:9		IYQFPDCD[pS]DEDEDFKLQDQALK	SEPT4_MOUSE;S325
452	IYQYIQSR	79.966331@Y:4	34	575.768	2	1149.521	-0.0005	31.87	R	F			@Y:4		IYQ[pY]IQSR	DYR1A_MOUSE;Y321,DYR1B_MOUSE;Y273
453	KAANANAAAAPSTASVAAPDSDAGGGGGPGTR	79.966331@S:12, 79.966331@S:21, 79.966332@T:31	21.3	745.3056	4	2977.193	-0.0072	38.731	R	G	+		@S:12,@S:21, @T:31		KAANANAAAAP[s][t]A[s]VAAPD[s]DAGGGGGPG[t]R	SCRT1_MOUSE;S138,SCRT1_MOUSE;S147,SCRT1_MOUSE;T157
454	KAEGEPQEESPLK	79.966331@S:10	31.4	761.3434	2	1520.672	-0.0036	19.061	K	S	+		@S:10		KAEGEPQEE[pS]PLK	BCLF1_MOUSE;S177
455	KAPKEELASDLEEMATSSAK	15.994915@M:14, 79.966331@S:9	23	744.343	3	2230.007	-0.0004	47.88	K	R	+		@S:9		KAPKEELA[s]DLEEMA[t][s][s]AK	NOP56_MOUSE;S513
456	KAPKEELASDLEEMATSSAK	79.966331@S:9	54.9	739.0106	3	2214.01	-0.0027	48.116	K	R	+		@S:9		KAPKEELA[pS]DLEEMATSSAK	NOP56_MOUSE;S513
457	KASEEEYVIRK	79.966331@S:3	27.1	477.9006	3	1430.68	-0.0007	20.558	R	S	+		@S:3		KA[pS]EEEYVIRK	ARHG6_MOUSE;S639
458	KDSEEEVSLLGNQDIEEGNSR	79.966331@S:3	51.5	810.0216	3	2427.043	-0.0009	40.004	R	M	+		@S:3		KD[s]EEEV[s]LLGNQDIEEGNSR	VPP2_MOUSE;S695
459	KDSEGYSESPDLEFEYADTDK	79.966331@S:7	35	835.6666	3	2503.978	-0.0012	42.623	R	W	+		@S:7		KD[s]EG[y][s]E[s]PDLEFEYADTDK	FA40A_MOUSE;S63
460	KDSEGYSESPDLEFEYADTDK	79.966331@Y:6	33.9	835.6668	3	2503.979	-0.0007	42.801	R	W		ambiguos		@S:3orY:6	KD[s]EG[y][s]ESPDLEFEYADTDK	FA40A_MOUSE;S59orY62
461	KEEENVDSDDEGELQDLLSQDWR	79.966331@S:8	62.1	943.7288	3	2828.165	-0.0017	61.351	K	V			@S:8		KEEENVD[pS]DDEGELQDLLSQDWR	ZN830_MOUSE;S342
462	KEESEESDDDMGFGLFD	15.994915@M:11, 79.966331@S:4	61.2	1023.363	2	2044.712	-0.0011	63.178	K	-	+		@S:4		KEE[pS]EE[pS]DDDMGFGLFD	RLA2_MOUSE;S102
463	KEESEESDDDMGFGLFD	15.994915@M:11, 79.966331@S:4,79.966331@S:7	64.2	1063.346	2	2124.678	-0.002	61.764	K	-	+		@S:4,@S:7		KEE[pS]EESDDDMGFGLFD	RLA2_MOUSE;S102,RLA2_MOUSE;S105
464	KEESEESDDDMGFGLFD	15.994915@M:11, 79.966331@S:7	78.5	1023.364	2	2044.714	0.0003	53.354	K	-	+		@S:7		KEESEE[pS]DDDMGFGLFD	RLA2_MOUSE;S105
465	KEESEESDDDMGFGLFD	79.966331@S:4	59.6	1015.366	2	2028.716	-0.002	61.887	K	-	+		@S:4		KEE[pS]EE[pS]DDDMGFGLFD	RLA2_MOUSE;S102
466	KEESEESDDDMGFGLFD	79.966331@S:4,79.966331@S:7	69.6	1055.348	2	2108.682	-0.0026	70.589	K	-	+		@S:4,@S:7		KEE[pS]EESDDDMGFGLFD	RLA2_MOUSE;S102,RLA2_MOUSE;S105
467	KEESEESDDDMGFGLFD	79.966331@S:7	50.7	1015.366	2	2028.716	-0.0019	60.868	K	-	+		@S:7		KEESEE[pS]DDDMGFGLFD	RLA2_MOUSE;S105
468	KEESEESEDDMGFGLFD	15.994915@M:11, 79.966331@S:4	50.6	1030.37	2	2058.726	-0.0028	54.157	K	-	+		@S:4		KEE[pS]EE[pS]EDDMGFGLFD	RLA1_MOUSE;S101
469	KEESEESEDDMGFGLFD	15.994915@M:11, 79.966331@S:4,79.966331@S:7	59.4	1070.354	2	2138.694	-0.0011	61.116	K	-	+		@S:4,@S:7		KEE[pS]EESEDDMGFGLFD	RLA1_MOUSE;S101,RLA1_MOUSE;S104
470	KEESEESEDDMGFGLFD	15.994915@M:11, 79.966331@S:7	49.4	1030.371	2	2058.727	-0.0018	52.59	K	-	+		@S:7		KEE[s]EE[s]EDDMGFGLFD	RLA1_MOUSE;S104
471	KEESEESEDDMGFGLFD	79.966331@S:4	72.5	1022.373	2	2042.731	-0.0026	61.519	K	-	+		@S:4		KEE[pS]EE[pS]EDDMGFGLFD	RLA1_MOUSE;S101
472	KEESEESEDDMGFGLFD	79.966331@S:4,79.966331@S:7	53	1062.355	2	2122.696	-0.0047	70.22	K	-	+		@S:4,@S:7		KEE[pS]EESEDDMGFGLFD	RLA1_MOUSE;S101,RLA1_MOUSE;S104
473	KEESEESEDDMGFGLFD	79.966331@S:7	47.7	1022.373	2	2042.73	-0.0036	60.509	K	-	+		@S:7		KEESEE[pS]EDDMGFGLFD	RLA1_MOUSE;S104
474	KEKSPELPEPSVR	79.966331@S:4	27.1	525.9308	3	1574.771	0.0002	31.63	K	M			@S:4		KEK[pS]PELPEPSVR	SRRM1_MOUSE;S220
475	KETESEAEDDNLDDLER	79.966331@S:5	90.2	1044.418	2	2086.821	-0.0005	40.09	R	H	+		@S:5		KE[t]E[s]EAEDDNLDDLER	SRRM1_MOUSE;S915
476	KETESEAEDDNLDDLER	79.966332@T:3	74.1	1044.417	2	2086.819	-0.0027	31.88	R	H	+		@T:3		KE[pT]E[pS]EAEDDNLDDLER	SRRM1_MOUSE;T913
477	KETESEAEDDNLDDLER	79.966332@T:3,79.966331@S:5	82.3	1084.401	2	2166.787	-0.0008	35.558	R	H	+		@T:3,@S:5		KE[t]E[s]EAEDDNLDDLER	SRRM1_MOUSE;T913,SRRM1_MOUSE;S915
478	KFQEQECPPSPEPTRK	57.021465@C:7,79.966331@S:10	38	679.9736	3	2036.899	-0.0038	20.045	R	E	+		@S:10		KFQEQECPP[pS]PEPTRK	RRAS2_MOUSE;S186
479	KGATPAEDDEDKDIDLFGSDEEEEDK	79.966331@S:19	97.6	993.0691	3	2976.185	-0.0066	38.99	K	E	+		@S:19		KGATPAEDDEDKDIDLFG[pS]DEEEEDK	EF1D_MOUSE;S162
480	KGATPAEDDEDKDIDLFGSDEEEEDK	79.966332@T:4,79.966331@S:19	49.5	1019.725	3	3056.152	-0.006	41.916	K	E	+		@T:4,@S:19		KGA[pT]PAEDDEDKDIDLFG[pS]DEEEEDK	EF1D_MOUSE;T147,EF1D_MOUSE;S162
481	KGGEFDEFVNDDTDDDLPVSK	79.966332@T:13	29.1	808.0041	3	2420.99	0.0007	46.606	K	K	+		@T:13		KGGEFDEFVNDD[pT]DDDLPVSK	CTR9_MOUSE;T925
482	KGSAEGSSDEEGKLVIDEPAK	79.966331@S:3,79.966331@S:7,79.966331@S:8	48.6	795.9871	3	2384.939	-0.0031	34.08	K	E	+		@S:3,@S:7,@S:8		KG[pS]AEG[pS][pS]DEEGKLVIDEPAK	HDGF_MOUSE;S128,HDGF_MOUSE;S132,HDGF_MOUSE;S133
483	KGSAEGSSDEEGKLVIDEPAK	79.966331@S:7	47.7	742.6762	3	2225.007	-0.0033	26.595	K	E	+		@S:7		KG[s]AEG[s][s]DEEGKLVIDEPAK	HDGF_MOUSE;S132
484	KGSAEGSSDEEGKLVIDEPAK	79.966331@S:7,79.966331@S:8	77.8	769.3324	3	2304.975	-0.001	29.923	K	E	+		@S:7,@S:8		KG[s]AEG[s][s]DEEGKLVIDEPAK	HDGF_MOUSE;S132,HDGF_MOUSE;S133
485	KGSAEGSSDEEGKLVIDEPAK	79.966331@S:8	55.9	742.6762	3	2225.007	-0.0032	26.64	K	E	+		@S:8		KG[s]AEG[s][s]DEEGKLVIDEPAK	HDGF_MOUSE;S133
486	KGSITEYTATEEK	79.966331@S:3	71.1	768.8431	2	1535.672	-0.0039	22.834	R	G	+		@S:3		KG[s]I[t]EYTATEEK	BNIP2_MOUSE;S114

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
487	KGSLNINEFK	79.966331@S:3	30.6	615.3001	2	1228.586	0.0003	33.497	R	E	+		@S:3		KG[pS]LNINEFK	S10AD_MOUSE;S32
488	KGSPTPAYPER	79.966331@S:3	43.1	641.7944	2	1281.574	-0.0011	18.747	R	K	+		@S:3		KG[s]P[t]PA[y]PER	FA83H_MOUSE;S871
489	KGSPVSEIGWETPPPESPR	79.966331@S:17	25.1	710.6684	3	2128.983	0.0005	38.605	K	L	+		@S:17		KGSPVSEIGWE[t]PPPE[s]PR	SNTB1_MOUSE;S218
490	KGSPVSEIGWETPPPESPR	79.966332@T:12, 79.966331@S:17	34.4	737.3234	3	2208.948	-0.001	42.431	K	L	+		@T:12,@S:17		KGSPVSEIGWE[pT]PPPE[pS]PR	SNTB1_MOUSE;T213,SNTB1_MOUSE;S218
491	KGSSTDISEDWEK	79.966331@S:3	74.3	781.3244	2	1560.634	-0.0002	28.969	K	D	+		@S:3		KG[s][s][t]DISEDWEK	BSDC1_MOUSE;S384
492	KGSSTTPQTSRMPVPMTSK	15.994915@M:16, 79.966332@T:5,79.966332@T:6	25.2	549.992	4	2195.939	0.0032	41.924	R	N		ambiguos	@T:6	@S:3orS:4orT:5	KG[s][s][t][t]PQ[t][s]RMPVPM[t][s]K	SKT_MOUSE;T1744,SKT_MOUSE;S1741orS1742orT1743
493	KGTIGDWK	79.966332@T:3	44.9	492.7311	2	983.4476	-0.0001	23.965	R	N	+		@T:3		KG[pT]IGDWK	ST1A1_MOUSE;T256,ST2A1_MOUSE;T250
494	KGTTPPRSPESSPK	79.966331@S:12	22.1	516.9191	3	1547.735	0.001	25.392	R	Q	+		@S:12		KG[t][t]PPR[s]PE[s][s]PK	JPH1_MOUSE;S469
495	KGTTPPRSPESSPK	79.966332@T:4	21.7	516.9182	3	1547.733	-0.0017	19.097	R	Q	+		@T:4		KG[t][t]PPR[s]PESSPK	JPH1_MOUSE;T461
496	KHGGGGIVANLSEQSLKDGVDR	79.966331@S:12, 79.966331@S:15	37.4	600.0297	4	2396.09	0.0012	32.299	K	G	+		@S:12,@S:15		KHGGGGIVANL[pS]EQ[pS]LKDGVDR	PP1R7_MOUSE;S45,PP1R7_MOUSE;S48
497	KHSLEGDEGSDFITK	79.966331@S:3	37.6	581.5927	3	1741.756	0.0004	35.321	K	N	+		@S:3		KH[pS]LEGDEGSDFITK	TXLNG_MOUSE;S79
498	KISPPSYAR	79.966331@S:3	20.1	549.7702	2	1097.526	-0.0012	23.821	R	R	+		@S:3		KI[pS]PPSYAR	CLASR_MOUSE;S285
499	KITEDTVEFGS	79.966331@S:11	25.2	653.2842	2	1304.554	0.0001	36.243	K	-	+		@S:11		KITEDTVEFG[pS]	ABCD3_MOUSE;S659
500	KKSPNELVDDLFK	79.966331@S:3	46.7	538.2706	3	1611.79	-0.0009	44.928	R	G	+		@S:3		KK[pS]PNELVDDLFK	NSF1C_MOUSE;S114
501	KLEKEEEEGISQESSEEEQ	79.966331@S:11	69.6	772.9899	3	2315.948	-0.0051	22.156	K	-	+		@S:11		KLEKEEEEGISQE[s][s]EEEQ	HMGA1_MOUSE;S99
502	KLEKEEEEGISQESSEEEQ	79.966331@S:14	68.7	1158.983	2	2315.952	-0.0008	28.211	K	-	+		@S:14		KLEKEEEEGISQE[pS][pS]EEEQ	HMGA1_MOUSE;S102
503	KLEKEEEEGISQESSEEEQ	79.966331@S:14, 79.966331@S:15	77.8	799.6476	3	2395.921	0.0018	29.601	K	-	+		@S:14,@S:15		KLEKEEEEGISQE[s][s]EEEQ	HMGA1_MOUSE;S102,HMGA1_MOUSE;S103
504	KLEKEEEEGISQESSEEEQ	79.966331@S:15	60.9	772.9903	3	2315.949	-0.0038	21.963	K	-	+		@S:15		KLEKEEEEGISQE[s][s]EEEQ	HMGA1_MOUSE;S103
505	KLGVSVSPSR	79.966331@S:5	28.9	555.2893	2	1108.564	-0.0001	29.212	K	A	+		@S:5		KLGV[s]V[s]P[s]R	ZCH18_MOUSE;S528
506	KLSCSLEDLRR	57.021465@C:4,79.966331@S:3	36.4	486.2371	3	1455.689	-0.0009	27.074	K	E	+		@S:3		KL[s]C[s]LEDLRR	LIPB2_MOUSE;S384
507	KLSVGAYVSSVR	79.966331@S:3	57.5	673.3472	2	1344.68	-0.0004	38.07	R	V	+		@S:3		KL[pS]VGAYVSSVR	S23IP_MOUSE;S748
508	KMSDDDEDDEEEYGKEEHEK	15.994915@M:2,79.966331@S:3	39	638.9832	4	2551.904	-0.0019	18.137	K	E	+		@S:3		KM[pS]DDDEDDEEEYGKEEHEK	SPT6H_MOUSE;S125
509	KNIFEKPFMARYVR	15.994915@M:9,79.966331@Y:12	19.1	632.3197	3	1893.937	0.0049	20.051	K	V	+		@Y:12		KNIFEKPFMAR[pY]VR	MFGM_MOUSE;Y442
510	KNSASLHVLK	79.966331@S:3	52.5	588.8098	2	1175.605	-0.0012	19.965	R	T	+		@S:3		KN[pS]A[pS]LHVLK	SO1B2_MOUSE;S288
511	KNSASLHVLK	79.966331@S:3,79.966331@S:5	30.9	419.5314	3	1255.572	-0.0004	22.702	R	T	+		@S:3,@S:5		KN[s]A[s]LHVLK	SO1B2_MOUSE;S288,SO1B2_MOUSE;S290
512	KNSATIPESDDL	79.966331@S:3	56.4	685.2978	2	1368.581	0.0001	41.853	R	-	+		@S:3		KN[s]A[t]IPESDDL	HUTH_MOUSE;S648
513	KPASVSPTTPTSPTEGEAS	79.966331@S:12	48.8	962.4309	2	1922.847	-0.0038	22.977	R	-	+		@S:12		KPASVSPTTP[t][s]P[t]EGEA[s]	DC1L1_MOUSE;S516
514	KPKSSQTLVSAK	79.966332@T:7	24.8	451.9095	3	1352.707	0.0003	28.017	K	T	+		@T:7		KPK[s][s]Q[t]LV[s]AK	M10L1_MOUSE;T410
515	KPPAPPSPVQSQSPSTNWSPAVPAK	79.966331@S:7,79.966331@S:11	34.8	905.7563	3	2714.247	-0.0036	38.357	K	K	+	ambiguos	@S:7	@S:11orS:13	KPPAPP[s]PVQ[s]Q[s]P[s][t]NW[s]PAVPAK	SRRM1_MOUSE;S810,SRRM1_MOUSE;S814orS816
516	KPPAPPSPVQSQSPSTNWSPAVPAK	79.966331@S:7,79.966331@S:11,79.966331@S:19	43.2	932.4112	3	2794.212	-0.005	40.99	K	K	+	ambiguos	@S:7,@S:19	@S:11orS:13	KPPAPP[s]PVQ[s]Q[s]P[s][t]NWSPAVPAK	SRRM1_MOUSE;S810,SRRM1_MOUSE;S822,SRRM1_MOUSE;S814orS816
517	KPPAPPSPVQSQSPSTNWSPAVPAK	79.966331@S:7,79.966331@S:13	39.2	905.7552	3	2714.244	-0.0068	38.471	K	K	+		@S:7,@S:13		KPPAPP[s]PVQ[s]Q[s]P[s][t]NW[s]PAVPAK	SRRM1_MOUSE;S810,SRRM1_MOUSE;S816
518	KPPAPPSPVQSQSPSTNWSPAVPAK	79.966331@S:7,79.966332@T:16,79.966331@S:19	28	932.4126	3	2794.216	-0.0011	39.702	K	K	+		@S:7,@T:16,@S:19		KPPAPP[s]PVQ[s]Q[s]P[s][t]NW[s]PAVPAK	SRRM1_MOUSE;S810,SRRM1_MOUSE;T819,SRRM1_MOUSE;S822
519	KQSQQLELLESELRK	79.966331@S:3	32.8	636.9976	3	1907.971	-0.0007	42.454	R	E	+		@S:3		KQ[pS]QQLELLESELRK	PLXC1_MOUSE;S984
520	KQSQSQDVLVLEDSK	79.966331@S:3	35.4	595.2878	3	1782.842	0.0015	41.067	K	K	+		@S:3		KQ[s]Q[s]QDVLVLEDSK	MRP2_MOUSE;S279
521	KQSQSQDVLVLEDSKK	79.966331@S:3	67.3	637.9854	3	1910.934	-0.0005	26.876	K	K	+		@S:3		KQ[s]Q[s]QDVLVLEDSKK	MRP2_MOUSE;S279
522	KQSQSQDVLVLEDSKK	79.966331@S:5	34.8	637.9853	3	1910.934	-0.0009	26.489	K	K	+		@S:5		KQ[s]Q[s]QDVLVLEDSKK	MRP2_MOUSE;S281
523	KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	79.966332@T:3,79.966331@S:19	69.7	1136.524	3	3406.55	-0.0027	43.579	K	A	+		@T:3,@S:19		KQ[t]PPASPSPQPIEDRPP[s][s]PI[y]EDAAPFK	SRC8_MOUSE;T401,SRC8_MOUSE;S417
524	KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	79.966332@T:3,79.966331@S:20	29.1	852.6452	4	3406.552	-0.0005	51.95	K	A			@T:3,@S:20		KQ[t]PPA[s]PSPQPIEDRPP[s][s]PI[y]EDAAPFK	SRC8_MOUSE;T401,SRC8_MOUSE;S418
525	KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	79.966332@T:3,79.966331@S:9	50.2	852.6452	4	3406.552	-0.0008	44.176	K	A	+		@T:3,@S:9		KQ[t]PPA[s]P[s]PQPIEDRPP[s][s]PI[y]EDAAPFK	SRC8_MOUSE;T401,SRC8_MOUSE;S407
526	KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	79.966332@T:3,79.966331@S:9,79.966331@S:20	45.1	1163.179	3	3486.516	-0.0023	46.726	K	A	+	ambiguos	@T:3,@S:9	@S:19orS:20	KQ[t]PPA[s]P[s]PQPIEDRPP[s][s]PI[y]EDAAPFK	SRC8_MOUSE;T401,SRC8_MOUSE;S407,SRC8_MOUSE;S417orS418
527	KQTPPASPSPQPIEDRPPSSPIYEDAAPFK	79.966332@T:3,79.966331@S:9,79.966331@Y:23	65.5	1163.18	3	3486.518	-0.0002	54.977	K	A	+		@T:3,@S:9,@Y:23		KQ[t]PPA[s]P[s]PQPIEDRPP[s][s]PIYEDAAPFK	SRC8_MOUSE;T401,SRC8_MOUSE;S407,SRC8_MOUSE;Y421
528	KRDFSLEQLR	79.966331@S:5	34.7	457.8973	3	1370.67	-0.0005	31.078	K	Q	+		@S:5		KRDF[pS]LEQLR	PGRC2_MOUSE;S98
529	KREEAAPPTPAPDDLAQLK	79.966332@T:9	48.5	709.6863	3	2126.037	-0.0037	31.79	R	N	+		@T:9		KREEAAPP[pT]PAPDDLAQLK	LYRIC_MOUSE;T96
530	KSLDSDESEDEDDDYQQK	79.966331@S:2,79.966331@S:5	44	769.2683	3	2304.783	-0.0001	24.668	K	R	+		@S:2,@S:5		K[s]LD[s]DE[s]EDEDDDYQQK	HAP28_MOUSE;S57,HAP28_MOUSE;S60

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
531	KSLDSDESEDEDDDYQQK	79.966331@S:5	34	742.6124	3	2224.815	-0.0016	22.797	K	R			@S:5		K[s]LD[s]DE[s]EDEDDDYQQK	HAP28_MOUSE;S60
532	KSLDSDESEDEDDDYQQK	79.966331@S:5,79.966331@S:8	42.8	1153.4	2	2304.784	0.0013	24.184	K	R	+		@S:5,@S:8		K[s]LD[s]DE[s]EDEDDDYQQK	HAP28_MOUSE;S60,HAP28_MOUSE;S63
533	KSLDSDESEDEDDDYQQK	79.966331@S:8	56.8	742.6115	3	2224.813	-0.0043	22.445	K	R			@S:8		K[s]LD[s]DE[s]EDEDDDYQQK	HAP28_MOUSE;S63
534	KSPVGKSPPATGSAYGSSQK	79.966331@S:2,79.966331@S:7	65.5	698.6479	3	2092.922	-0.0011	19.252	K	E	+		@S:2,@S:7		K[s]PVGK[s]PPA[t]GSAYGSSQK	TR150_MOUSE;S315,TR150_MOUSE;S320
535	KSPVGKSPPATGSAYGSSQK	79.966331@S:2,79.966332@T:11	37.1	698.6488	3	2092.925	0.0013	24.736	K	E	+		@S:2,@T:11		K[s]PVGK[s]PPA[t]G[s]A[y]GSSQK	TR150_MOUSE;S315,TR150_MOUSE;T324
536	KSPVGKSPPATGSAYGSSQK	79.966331@S:7	28.8	671.992	3	2012.954	-0.0025	19.008	K	E	+		@S:7		K[s]PVGK[s]PPA[t]G[s]A[y]G[s][s]QK	TR150_MOUSE;S320
537	KSPVGKSPPATGSAYGSSQK	79.966332@T:11	33.1	671.9927	3	2012.956	-0.0005	19.022	K	E	+		@T:11		KSPVGK[s]PPA[t]G[s]A[y]G[s]SQK	TR150_MOUSE;T324
538	KSSPKEEVASEPEEAASPTTPK	79.966331@S:2,79.966331@S:10	43.1	820.3594	3	2458.056	0.0009	30.372	K	K	+		@S:2,@S:10		K[s][s]PKEEVA[s]EPEEAASPTTPK	NOP56_MOUSE;S528,NOP56_MOUSE;S536
539	KSSPKEEVASEPEEAASPTTPK	79.966331@S:3,79.966331@S:10	52.5	820.3568	3	2458.049	-0.0068	23.652	K	K	+		@S:3,@S:10		K[s][s]PKEEVA[s]EPEEAASPTTPK	NOP56_MOUSE;S529,NOP56_MOUSE;S536
540	KSSREGDFLAPK	79.966331@S:3	39.1	472.2292	3	1413.666	0.0005	30.235	R	Q	+		@S:3		K[s][s]REGDFLAPK	MLXPL_MOUSE;S196
541	KSSVEGLEPAENK	79.966331@S:3	57.6	734.339	2	1466.663	-0.0019	21.146	R	C	+		@S:3		K[s][s]VEGLEPAENK	SRP14_MOUSE;S45
542	KTSFDENDSEELEDKDSK	79.966331@S:3	23	732.6341	3	2194.88	0.0014	29.859	K	S	+		@S:3		K[t][s]FDEND[s]EELEDKDSK	IF2P_MOUSE;S108
543	KTSFDENDSEELEDKDSK	79.966331@S:3,79.966331@S:9	19.7	759.2883	3	2274.843	-0.0023	24.068	K	S	+		@S:3,@S:9		K[t][s]FDEND[s]EELEDKDSK	IF2P_MOUSE;S108,IF2P_MOUSE;S114
544	KTSFDENDSEELEDKDSK	79.966331@S:9	32.1	732.6329	3	2194.877	-0.0023	22.614	K	S	+		@S:9		K[t][s]FDEND[s]EELEDKDSK	IF2P_MOUSE;S114
545	KVEEEQEADEEDVSEEEAEDR	79.966331@S:14	64.8	858.6672	3	2572.98	-0.0014	24.919	K	E	+		@S:14		KVEEEQEADEEDV[pS]EEEAEDR	TMX1_MOUSE;S245
546	KVEEEQEADEEDVSEEEAEDREGASK	79.966331@S:14	39.1	762.3098	4	3045.21	0.0008	30.39	K	A	+		@S:14		KVEEEQEADEEDV[s]EEEAEDREGA[s]K	TMX1_MOUSE;S245
547	KVPEQPPELPQLDSQHL	79.966331@S:14	40.5	679.0025	3	2033.986	0.0033	53.539	K	-	+		@S:14		KVPEQPPELPQLD[pS]QHL	NUCB1_MOUSE;S456
548	KVSKQEEASGGPLAPK	79.966331@S:3	22.1	569.2891	3	1704.845	0.0007	18.451	R	A	+		@S:3		KV[s]KQEEA[s]GGPLAPK	VASP_MOUSE;S235
549	KVSVEPQDSHQDAQPR	79.966331@S:3	58.7	634.2892	3	1899.846	-0.002	18.151	R	G	+		@S:3		KV[pS]VEPQDSHQDAQPR	SO2B1_MOUSE;S21
550	KVSVEPQDSHQDAQPR	79.966331@S:9	35	634.2899	3	1899.848	0.0004	18.107	R	G	+		@S:9		KV[s]VEPQD[s]HQDAQPR	SO2B1_MOUSE;S27
551	KYQAIASNSK	79.966331@S:9	19.4	397.1919	3	1188.554	-0.0001	25.934	K	I		ambiguos		@S:7orS:9	K[y]QAIA[s]N[s]K	ERLN1_MOUSE;S291orS293
552	KYVISDEEEEEDD	79.966331@S:5	46.3	840.3133	2	1678.612	-0.0013	31.187	K	-	+		@S:5		KYVI[pS]DEEEEEDD	LEO1_MOUSE;S659
553	LAGISQGVYR	79.966331@Y:9	25.4	572.2814	2	1142.548	-0.0003	28.677	K	R	+		@Y:9		LAGI[s]QGV[y]R	ACD11_MOUSE;Y323
554	LASTDDGYIDLQFK	79.966331@S:3	82	833.3741	2	1664.734	0.0001	53.245	R	K	+		@S:3		LA[s][t]DDGYIDLQFK	CT030_MOUSE;S24
555	LASTDDGYIDLQFK	79.966332@T:4	49.3	833.3738	2	1664.733	-0.0004	52.635	R	K	+	ambiguos		@S:3orT:4	LA[s][t]DDG[y]IDLQFK	CT030_MOUSE;S24orT25
556	LATTVSAPDLK	79.966331@S:6	46.3	598.3017	2	1194.589	-0.0009	33.248	R	S	+		@S:6		LAT[t]V[s]APDLK	MAP4_MOUSE;S901
557	LDGETASDSESRAETAPLPTSVDDTPEVLNR	79.966331@S:7	95.7	1118.173	3	3351.496	-0.0029	46.462	K	A	+		@S:7		LDGE[t]A[s]D[s]ESRAETAPLPTSVDDTPEVLNR	CDS2_MOUSE;S32
558	LDLQRKTETK	79.966332@T:9	28.6	437.8932	3	1310.658	-0.0018	30.447	K	E			@T:9		LDLQRK[t]E[t]K	GORAB_MOUSE;T244
559	LDNTPASPPRSPTEPSDTPIAK	79.966331@S:7,79.966331@S:11	42.9	817.6995	3	2450.077	-0.0001	37.729	K	G	+		@S:7,@S:11		LDNTPA[s]PPR[s]P[t]EPSDTPIAK	TACC2_MOUSE;S510,TACC2_MOUSE;S514
560	LDNTPASPPRSPTEPSDTPIAK	79.966331@S:7,79.966332@T:13	27.6	817.6979	3	2450.072	-0.0049	31.577	K	G	+		@S:7,@T:13		LDN[t]PA[s]PPR[s]P[t]EP[s]DTPIAK	TACC2_MOUSE;S510,TACC2_MOUSE;T516
561	LENQSLKSVK	79.966331@S:5	22.6	613.3129	2	1224.611	-0.0002	35.145	K	F	+		@S:5		LENQ[s]LK[s]VK	MMP2_MOUSE;S646
562	LEREDSSEEEEEEIDDEEIER	79.966331@S:6,79.966331@S:7	53.5	923.6762	3	2768.007	-0.0043	36.431	R	R	+		@S:6,@S:7		LERED[pS][pS]EEEEEEIDDEEIER	MFAP1_MOUSE;S132,MFAP1_MOUSE;S133
563	LFDDSDERGTVGNVK	79.966331@S:5	33.6	577.9248	3	1730.753	0.0013	31.732	K	E	+		@S:5		LFDD[s]DERG[t]VGNVK	HTSF1_MOUSE;S724
564	LGPGLPQDGSDEEDEEWPTLEK	79.966331@S:10	26.7	841.0272	3	2520.06	0.0015	53.831	R	A	+		@S:10		LGPGLPQDG[pS]DEEDEEWPTLEK	BYST_MOUSE;S97
565	LGTGGGGSPDKSPSAQELK	79.966331@S:8	72.9	622.6267	3	1864.858	0.0013	22.577	R	E	+		@S:8		LGTGGGG[pS]PDKSPSAQELK	CHIP_MOUSE;S20
566	LGVPVGVLSAK	79.966331@S:9	19.4	560.3118	2	1118.609	-0.0011	24.086	R	V			@S:9		LGVPVGVL[pS]AK	FANCA_MOUSE;S113
567	LGVSVSPSR	79.966331@S:6	36.2	491.2417	2	980.4688	-0.0004	25.466	K	A	+		@S:6		LGVSV[s]P[s]R	ZCH18_MOUSE;S530
568	LGVSVSPSR	79.966331@S:8	40	491.2421	2	980.4696	0.0004	25.423	K	A	+		@S:8		LGV[s]V[s]P[s]R	ZCH18_MOUSE;S532
569	LHCSGEEVVKSPGTAKK	57.021465@C:3,79.966332@T:14	22.8	477.4832	4	1905.904	0.0019	20.211	K	D			@T:14		LHC[s]GEEVVK[s]PG[t]AKK	TNR8_MOUSE;T139
570	LIEDERSDREETESSEGEETAAGAGAK	79.966331@S:7,79.966331@S:14,79.966331@S:15	27.3	1036.063	3	3105.167	-0.0068	26.018	K	S	+		@S:7,@S:14,@S:15		LIEDER[s]DREE[t]E[s][s]EGEETAAGAGAK	CERS2_MOUSE;S341,CERS2_MOUSE;S348,CERS2_MOUSE;S349
571	LIEDERSDREETESSEGEETAAGAGAK	79.966331@S:7,79.966332@T:12,79.966331@S:14	31.9	1036.063	3	3105.167	-0.0063	26.654	K	S	+		@S:7,@T:12,@S:14		LIEDER[s]DREE[t]E[s][s]EGEETAAGAGAK	CERS2_MOUSE;S341,CERS2_MOUSE;T346,CERS2_MOUSE;S348
572	LKFSDEEDGRDSDEEGAEGHK	79.966331@S:4,79.966331@S:12	26.6	628.2397	4	2508.93	-0.0021	23.484	K	D	+		@S:4,@S:12		LKF[pS]DEEDGRD[pS]DEEGAEGHK	PRC2A_MOUSE;S342,PRC2A_MOUSE;S350
573	LKSEDELRPDVDEHTQK	79.966331@S:3	23.9	530.4978	4	2117.962	-0.0011	22.621	R	T	+		@S:3		LK[pS]EDELRPDVDEHTQK	REPS1_MOUSE;S708
574	LKSGETTTAEEIK	79.966331@S:3	24.8	496.2381	3	1485.692	-0.0038	27.751	R	A			@S:3		LK[s]GE[t][t][t]AEEIK	ACSF2_MOUSE;S560
575	LLHEDLDESDDDVDEK	79.966331@S:9	34.9	656.2653	3	1965.774	0.0014	38.236	R	L	+		@S:9		LLHEDLDE[pS]DDDVDEK	ASAP2_MOUSE;S704
576	LLKEGEEPTVYSDDEEPKDETAR	79.966331@S:12	91.8	910.7377	3	2729.191	-0.0043	29.264	K	K	+		@S:12		LLKEGEEP[t]V[y][s]DDEEPKDETAR	PGRC1_MOUSE;S181
577	LLKPGEEPSEYTDEEDTK	79.966331@S:9	52.4	1080.466	2	2158.918	-0.0012	36.058	R	D	+		@S:9		LLKPGEEP[s]E[y][t]DEED[t]K	PGRC2_MOUSE;S202
578	LLKPGEEPSEYTDEEDTK	79.966331@S:9,79.966331@Y:11	21.9	747.3019	3	2238.884	-0.002	31.502	R	D	+		@S:9,@Y:11		LLKPGEEP[s]E[y][t]DEEDTK	PGRC2_MOUSE;S202,PGRC2_MOUSE;Y204

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
579	LLKPGEEPSEYTDEEDTK	79.966331@S:9,79.966332@T:12	33.4	747.3024	3	2238.885	-0.0004	31.873	R	D	+		@S:9,@T:12		LLKPGEEP[s]E[y][t]DEEDTK	PGRC2_MOUSE;S202,PGRC2_MOUSE;T205
580	LLKPGEEPSEYTDEEDTK	79.966331@Y:11	45.3	720.6464	3	2158.917	-0.002	35.806	R	D	+		@Y:11		LLKPGEEPSE[y][t]DEEDTK	PGRC2_MOUSE;Y204
581	LLKPGEEPSEYTDEEDTK	79.966332@T:12	80.9	720.6466	3	2158.918	-0.0015	28.573	R	D	+		@T:12		LLKPGEEP[s]E[y][t]DEED[t]K	PGRC2_MOUSE;T205
582	LLKPGEEPSEYTDEEDTK	79.966332@T:12,79.966331@Y:11	20	747.3011	3	2238.881	-0.0044	31.884	R	D	+	ambiguos		@S:9orY:11orT:12,@S:9orY:11orT:12	LLKPGEEPSE[y][t]DEEDTK	PGRC2_MOUSE;S202orY204orT205,PGRC2_MOUSE;S202orY204orT205
583	LLKPGEEPSEYTDEEDTKDHSKQD	79.966332@T:12	32.3	718.3119	4	2869.218	0.0005	24.493	R	-	+		@T:12		LLKPGEEP[s]E[y][t]DEED[t]KDH[s]KQD	PGRC2_MOUSE;T205
584	LLLDPSSTPTK	79.966331@S:7	21.5	626.315	2	1250.615	-0.0005	36.093	K	A	+		@S:7		LLLDP[s][s][t]P[t]K	LTOR1_MOUSE;S27
585	LLQSVKNSMLQMK	15.994915@M:9,79.966331@S:4	19.6	539.2706	3	1614.79	0.0025	23.312	R	K	+		@S:4		LLQ[s]VKN[s]MLQMK	DOK5_MOUSE;S240
586	LLSEQDGSLK	79.966331@S:8	29.6	585.2765	2	1168.538	0.0008	33.793	K	D	+		@S:8		LLSEQDG[pS]LK	CXB1_MOUSE;S258
587	LLTTQSEDTQGPGLKMPSQR	15.994915@M:16,79.966331@S:6,79.966331@S:18	22.8	788.3479	3	2362.022	-0.0058	27.051	R	A	+		@S:6,@S:18		LL[t][t]Q[s]ED[t]QGPGLKMP[s]QR	IL16_MOUSE;S942,IL16_MOUSE;S954
588	LLTTQSEDTQGPGLKMPSQR	15.994915@M:16,79.966331@S:6,79.966332@T:9	26.8	788.3498	3	2362.028	0	34.883	R	A	+		@S:6,@T:9		LL[t][t]Q[s]ED[t]QGPGLKMP[s]QR	IL16_MOUSE;S942,IL16_MOUSE;T945
589	LMGEDEKPAAKENSEGAGAKASSAGVLVS	15.994915@M:2,79.966331@S:14,79.966331@S:22,79.966331@S:23	27.1	1020.427	3	3058.259	-0.0048	23.237	R	-	+		@S:14,@S:22,@S:23		LMGEDEKPAAKEN[s]EGAGAKA[s][s]AGVLV[s]	PFD2_MOUSE;S139,PFD2_MOUSE;S147,PFD2_MOUSE;S148
590	LNDPFQPFPGNDSPK	79.966331@S:13	25.2	876.8849	2	1751.755	-0.0004	49.899	K	E	+		@S:13		LNDPFQPFPGND[pS]PK	EPS15_MOUSE;S816
591	LPEEPSSEDEQQPEK	79.966331@S:7	43.7	911.3733	2	1820.732	-0.0033	23.55	R	K	+		@S:7		LPEEP[s][s]EDEQQPEK	ITSN1_MOUSE;S335
592	LQLSDEESVFEDALVCPDAR	57.021465@C:16,79.966331@S:8	26.4	791.6813	3	2372.022	-0.0021	67.417	K	Y		ambiguos		@S:4orS:8	LQL[s]DEE[s]VFEDALVCPDAR	PHLB2_MOUSE;S486orS490
593	LQRPKEESSEDENEVSNILR	79.966331@S:8,79.966331@S:9	62.5	844.7045	3	2531.092	-0.0025	38.814	R	S	+		@S:8,@S:9		LQRPKEE[pS][pS]EDENEVSNILR	OTUD4_MOUSE;S1016,OTUD4_MOUSE;S1017
594	LRLSPSPTSQR	79.966331@S:4,79.966331@S:6	19.4	467.881	3	1400.621	-0.0003	25.817	R	S	+		@S:4,@S:6		LRL[s]P[s]P[t]SQR	LMNA_MOUSE;S390,LMNA_MOUSE;S392
595	LSASSTGSTR	79.966331@S:5	17.2	349.4885	3	1045.444	-0.0005	15.915	R	S	+		@S:5		L[s]A[s][s][t]G[s][t]R	BCAR1_MOUSE;S435
596	LSEEQGSTPKGPR	79.966331@S:2,79.966331@S:7	27.8	773.32	2	1544.625	-0.0018	27.744	K	R	+		@S:2,@S:7		L[s]EEQG[s][t]PKGPR	FA13C_MOUSE;S368,FA13C_MOUSE;S373
597	LSRGDSLKEPTSIADSSR	79.966331@S:6	31.8	666.9868	3	1997.939	-0.0033	26.161	K	H	+		@S:6		L[s]RGD[s]LKEPTSIADSSR	ZDHC5_MOUSE;S380
598	LSRSRTASLTSAASIDGSR	79.966331@S:4,79.966332@T:6,79.966331@S:8	32	725.978	3	2174.912	0	31.525	R	S	+	ambiguos	@S:8	@S:2orS:4orT:6,@S:2orS:4orT:6	L[s]R[s]R[t]A[s]L[t][s]AA[s]IDGSR	NDRG2_MOUSE;S332,NDRG2_MOUSE;S326orS328orT330,NDRG2_MOUSE;S326orS328orT330
599	LSSSDEEDFLYVDIK	79.966331@S:2	58.7	920.399	2	1838.783	-0.0029	58.057	R	G	+	ambiguos		@S:2orS:3orS:4	L[s][s][s]DEEDFLYVDIK	MUG1_MOUSE;S95orS96orS97
600	LSSSDEEDFLYVDIK	79.966331@S:4	54.2	920.4008	2	1838.787	0.0007	58.114	R	G	+	ambiguos		@S:3orS:4	L[s][s][s]DEEDFLYVDIK	MUG1_MOUSE;S96orS97
601	LSTSFVLETFIHSK	79.966332@T:3,79.966331@S:4,79.966332@T:9	21.4	616.9263	3	1847.757	0.0023	36.42	K	E		ambiguos		@S:2orT:3orS:4,@S:2orT:3orS:4, @T:9orS:13	L[s][t][s]FVLE[t]FIH[s]K	UBP34_MOUSE;S2345orT2346orS2347,UBP34_MOUSE;S2345orT2346orS2347,UBP34_MOUSE;T2352orS2356
602	LSVQDPVVVVAEDSQEK	79.966331@S:14	23.4	961.4613	2	1920.908	-0.0001	44.402	R	L	+		@S:14		LSVQDPVVVVAED[pS]QEK	S38AA_MOUSE;S441
603	LTLSDGESGEEKPTKPK	79.966331@S:4,79.966331@S:8	26.3	659.2936	3	1974.859	0.0003	30.418	K	E	+		@S:4,@S:8		L[t]L[s]DGE[s]GEEKP[t]KPK	ATRX_MOUSE;S1335,ATRX_MOUSE;S1339
604	LVDSDGSLAEVPK	79.966331@S:7	27.6	705.3315	2	1408.648	-0.0003	33.969	R	E	+		@S:7		LVD[s]DG[s]LAEVPK	STEA3_MOUSE;S20
605	MAQALSEEEFQR	15.994915@M:1,79.966331@S:6	17.4	512.2134	3	1533.618	0.0015	57.738	-	M			@S:6		MAQAL[pS]EEEFQR	GRAP1_MOUSE;S6
606	MGSLGGLALCLLR	57.021465@C:10,15.994915@M:1,79.966331@S:3	22.4	728.8543	2	1455.694	-0.0038	53.622	-	L	+		@S:3		MG[pS]LGGLALCLLR	PTPRT_MOUSE;S3
607	MKDQGPDKENSGAVEASVK	15.994915@M:1,79.966331@S:17	24.4	522.2356	4	2084.913	0.0049	19.773	R	L	+		@S:17		MKDQGPDKEN[s]GAVEA[s]VK	VIR_MOUSE;S382
608	MLAESDDSGDEESVSQTDKTELQSTLR	15.994915@M:1,79.966331@S:5,79.966331@S:8	88.3	1049.758	3	3146.251	-0.0015	40.955	K	T	+		@S:5,@S:8		MLAE[s]DD[s]GDEE[s]VSQTDKTELQSTLR	OSBP1_MOUSE;S134,OSBP1_MOUSE;S137
609	MLLEYTDSSYDEK	79.966331@Y:10	26.8	837.3355	2	1672.656	-0.0015	42.84	R	R	+	ambiguos		@S:8orS:9orY:10	MLLE[y][t]D[s][s][y]DEK	GSTM1_MOUSE;S26orS27orY28
610	MMLPSPVTSTPFSVK	79.966331@S:5,79.966331@S:9,79.966331@S:13	18.9	621.2489	3	1860.725	0.0004	23.006	-	D	+		@S:5,@S:9,@S:13		MMLP[s]PV[t][s][t]PF[s]VK	NKX23_MOUSE;S5,NKX23_MOUSE;S9,NKX23_MOUSE;S13
611	MNSVLCSR	57.021465@C:6,15.994915@M:1,79.966331@S:3,79.966331@S:7	20.1	381.4635	3	1141.369	-0.0013	17.085	-	A			@S:3,@S:7		MN[pS]VLC[pS]R	CSMT1_MOUSE;S3,CSMT1_MOUSE;S7
612	MQAESQSPTNVDLEDK	15.994915@M:1,79.966331@S:7	62.3	944.3853	2	1886.756	-0.0044	25.979	R	E	+		@S:7		MQAESQ[s]P[t]NVDLEDK	TB182_MOUSE;S1063

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
613	MSGFIYQGK	15.994915@M:1,79.966331@S:2	42.2	563.7359	2	1125.457	0.0006	39.114	R	L	+		@S:2		M[pS]GFIYQGK	ARHG7_MOUSE;S497
614	MSQAYSSSQRVSSYR	15.994915@M:1,79.966331@S:6,79.966331@S:7,79.966331@S:8	16.2	664.905	3	1991.693	0.0046	21.501	-	R	+		@S:6,@S:7,@S:8		M[s]QA[y][s][s][s]QRV[s][s][y]R	DESM_MOUSE;S6,DESM_MOUSE;S7,DESM_MOUSE;S8
615	MTKYSIMQGEYRDTFTIETDPK	15.994915@M:7,79.966332@T:16,79.966331@Y:4	23.4	944.0621	3	2829.164	-0.0034	61.377	R	R	+		@Y:4,@T:16		M[t]K[y][s]IMQGE[y]RD[t]F[t]IE[t]DPK	CADH5_MOUSE;Y293,CADH5_MOUSE;T305
616	MTVTYTARVANAR	15.994915@M:1,79.966332@T:4,79.966332@T:6	22.2	543.9016	3	1628.683	0.0047	32.048	-	F	+		@T:4,@T:6		M[t]V[t][y][t]ARVANAR	BEST2_MOUSE;T4,BEST2_MOUSE;T6
617	MVKATRLHGEETMPHSGR	79.966332@T:5,79.966332@T:12	27.2	549.9921	4	2195.939	0.0023	40.509	R	I			@T:5,@T:12		MVKA[t]RLHGEE[t]MPH[s]GR	KCNH7_MOUSE;T962,KCNH7_MOUSE;T969
618	NASVPNLR	79.966331@S:3	31.1	475.7263	2	949.438	-0.0001	25.812	R	G	+		@S:3		NA[pS]VPNLR	FA54B_MOUSE;S100
619	NDSWGSFDLR	79.966331@S:3	54.9	638.7536	2	1275.493	0.0005	50.226	R	A	+		@S:3		ND[pS]WGSFDLR	NUFP2_MOUSE;S649
620	NFSDNQLQEGK	79.966331@S:3	56.5	680.2825	2	1358.55	0.0001	34.461	R	N	+		@S:3		NF[pS]DNQLQEGK	TAGL2_MOUSE;S163
621	NFYESEEEEEEK	79.966331@S:5	72.8	821.2936	2	1640.573	-0.004	30.462	K	E	+		@S:5		NFYE[pS]EEEEEEK	AP3B1_MOUSE;S276
622	NFYESEEEEEEKEK	79.966331@S:5	20.4	633.5789	3	1897.715	0.0007	35.904	K	S	+		@S:5		NF[y]E[s]EEEEEEKEK	AP3B1_MOUSE;S276
623	NGCYGIYITSRVLK	57.021465@C:3,79.966332@T:9	20.4	431.7109	4	1722.814	-0.002	22.247	K	A			@T:9		NGC[y]GI[y]I[t][s]RVLK	FREM1_MOUSE;T1670
624	NHSGSRTPPVALSSSR	79.966331@S:3,79.966331@S:5,79.966332@T:7	19.7	631.5858	3	1891.736	-0.0023	24.554	R	M	+		@S:3,@S:5,@T:7		NH[pS]G[pS]R[pT]PPVALSSSR	SRRM2_MOUSE;S2052,SRRM2_MOUSE;S2054,SRRM2_MOUSE;T2056
625	NHSGSRTPPVALSSSR	79.966331@S:3,79.966332@T:7	29.6	604.9315	3	1811.773	0.0009	28.572	R	M	+		@S:3,@T:7		NH[s]G[s]R[t]PPVALSSSR	SRRM2_MOUSE;S2052,SRRM2_MOUSE;T2056
626	NHSGSRTPPVALSSSR	79.966331@S:5,79.966332@T:7	25.9	604.9311	3	1811.771	-0.0002	28.195	R	M	+		@S:5,@T:7		NH[s]G[s]R[t]PPVALSSSR	SRRM2_MOUSE;S2054,SRRM2_MOUSE;T2056
627	NISLSSEEEAEGLAGHPR	79.966331@S:5	30.1	659.2965	3	1974.868	-0.0009	36.39	K	V	+		@S:5		NI[s]L[s][s]EEEAEGLAGHPR	PARF_MOUSE;S482
628	NISLSSEEEAEGLAGHPR	79.966331@S:5,79.966331@S:6	57.5	1028.424	2	2054.833	-0.0014	41.637	K	V	+		@S:5,@S:6		NI[s]L[s][s]EEEAEGLAGHPR	PARF_MOUSE;S482,PARF_MOUSE;S483
629	NISLSSEEEAEGLAGHPR	79.966331@S:6	22.4	659.2963	3	1974.867	-0.0014	36.464	K	V			@S:6		NI[s]L[s][s]EEEAEGLAGHPR	PARF_MOUSE;S483
630	NITGSSPVADFSAIK	79.966331@S:6	57	793.877	2	1585.739	0.0006	55.261	K	E			@S:6		NITG[s][s]PVADFSAIK	EPS15_MOUSE;S324
631	NKFGSADNIPNLK	79.966331@S:5	27.2	749.3585	2	1496.702	0.0001	33.227	R	D	+		@S:5		NKFG[pS]ADNIPNLK	TMCC1_MOUSE;S378
632	NKLEGDSDVDSELEDRVDGVK	79.966331@S:7	60.7	800.3588	3	2398.055	0.0008	39.341	K	S	+		@S:7		NKLEGD[pS]DVD[pS]ELEDRVDGVK	MY18A_MOUSE;S1966
633	NKLEGDSDVDSELEDRVDGVK	79.966331@S:7,79.966331@S:11	37	827.014	3	2478.02	0.0001	42.416	K	S	+		@S:7,@S:11		NKLEGD[s]DVD[s]ELEDRVDGVK	MY18A_MOUSE;S1966,MY18A_MOUSE;S1970
634	NKSEVDLYNSDPLVCR	57.021465@C:15,79.966331@S:3	26	663.6311	3	1987.871	0.0006	50.1	R	A	+		@S:3		NK[pS]EVDLYNSDPLVCR	MGLL_MOUSE;S189
635	NLAKPGVTSTSDSEDEDDQEGEKK	79.966331@S:11,79.966331@S:13	46.7	913.6995	3	2738.077	-0.0078	21.356	K	R	+		@S:11,@S:13		NLAKPGV[t][s][t][s]D[s]EDEDDQEGEKK	PSIP1_MOUSE;S272,PSIP1_MOUSE;S274
636	NLGSINTELQDVQR	79.966331@S:4	98.2	833.893	2	1665.771	-0.0009	45.312	R	I	+		@S:4		NLG[pS]INTELQDVQR	SC22B_MOUSE;S137
637	NLLEDDSDEEEDFFLR	79.966331@S:7	84.5	1033.416	2	2064.816	-0.0036	64.845	R	G	+		@S:7		NLLEDD[pS]DEEEDFFLR	VAMP4_MOUSE;S30
638	NLLNHPTANSGASILR	79.966332@T:7	21	586.6262	3	1756.857	-0.0052	55.512	R	E			@T:7		NLLNHP[t]AN[s]GA[s]ILR	FOLC_MOUSE;T549
639	NLNLVSSTASIK	79.966331@S:10	41	663.8362	2	1325.658	-0.0013	37.988	R	D	+	ambiguos		@S:7orT:8orS:10	NLNLV[s][s][t]A[s]IK	RHG35_MOUSE;S770orT771orS773
640	NLSFEIK	79.966331@S:3	25.4	465.7202	2	929.4258	-0.0001	41.705	R	K	+		@S:3		NL[pS]FEIK	PTN12_MOUSE;S434
641	NLSFNITEDELK	79.966331@S:3	36.5	751.8425	2	1501.67	0.0004	53.068	K	E	+		@S:3		NL[s]FNI[t]EDELK	NUCL_MOUSE;S403
642	NLSIYDGPEQR	79.966331@S:3	20.8	686.2999	2	1370.585	-0.0015	35.473	R	F	+		@S:3		NL[s]I[y]DGPEQR	ETFD_MOUSE;S550
643	NLTSSSLNDISDKPEK	79.966331@S:4	37.3	914.4222	2	1826.83	-0.0001	36.605	R	D	+		@S:4		NL[t][s][s][s]LNDISDKPEK	S4A4_MOUSE;S255
644	NLTSSSLNDISDKPEK	79.966331@S:4,79.966331@S:6	35.8	954.4036	2	1906.793	-0.0036	31.626	R	D	+		@S:4,@S:6		NL[t][s][s][s]LNDI[s]DKPEK	S4A4_MOUSE;S255,S4A4_MOUSE;S257
645	NLTSSSLNDISDKPEK	79.966331@S:6	66.9	914.4214	2	1826.828	-0.0017	28.739	R	D	+		@S:6		NLT[s][s][s]LNDISDKPEK	S4A4_MOUSE;S257
646	NLTSSSLNDISDKPEK	79.966332@T:3,79.966331@S:6	45.8	954.4039	2	1906.793	-0.0029	32.019	R	D	+		@T:3,@S:6		NL[t][s][s][s]LNDI[s]DKPEK	S4A4_MOUSE;T254,S4A4_MOUSE;S257
647	NPPPQDYESDDESYEVLDLTEYAR	79.966331@S:9	77.3	975.7367	3	2924.188	-0.0031	59.747	R	R			@S:9		NPPPQD[y]E[s]DDE[s][y]EVLDLTEYAR	FUND1_MOUSE;S13
648	NQPEPTAPATPMTSLLR	79.966332@T:10	49.9	952.4527	2	1902.891	-0.0002	47.249	K	L	+		@T:10		NQPEP[t]APA[t]PM[t]SLLR	S6A13_MOUSE;T587
649	NREPVQLETLSIR	79.966331@S:11	24.4	409.4623	4	1633.82	0.0013	27.557	K	G	+		@S:11		NREPVQLE[t]L[s]IR	SMD1_MOUSE;S59
650	NSASLHVLK	79.966331@S:2	45.2	524.7628	2	1047.511	-0.0003	22.933	K	T	+		@S:2		N[s]A[s]LHVLK	SO1B2_MOUSE;S288
651	NSASLHVLK	79.966331@S:4	37.5	524.7632	2	1047.512	0.0005	32.646	K	T	+		@S:4		NSA[pS]LHVLK	SO1B2_MOUSE;S290
652	NSASVGIIQR	79.966331@S:4	70.5	562.7761	2	1123.538	-0.001	27.096	K	D	+		@S:4		NSA[pS]VGIIQR	GPAT3_MOUSE;S68
653	NSATCHSEDSDLEID	57.021465@C:5,79.966331@S:7,79.966331@S:10	16.5	926.8023	2	1851.59	-0.0007	33.619	R	-	+		@S:7,@S:10		N[s]A[t]CH[s]ED[s]DLEID	PHLP_MOUSE;S293,PHLP_MOUSE;S296
654	NSATCHSEDSDLEID	57.021465@C:5,79.966332@T:4,79.966331@S:10	13.9	926.8016	2	1851.589	-0.002	33.719	R	-	+	ambiguos	@S:10	@S:2orT:4	N[s]A[t]CH[s]ED[s]DLEID	PHLP_MOUSE;S296,PHLP_MOUSE;S288orT290
655	NSATIPESDDL	79.966331@S:2	31.2	621.2502	2	1240.486	-0.0001	48.239	K	-	+		@S:2		N[s]A[t]IPESDDL	HUTH_MOUSE;S648

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
656	NSATIPESDDL	79.966332@T:4	25.2	621.2504	2	1240.486	0.0003	48.255	K	-			@T:4		N[s]A[t]IPESDDL	HUTH_MOUSE;T650
657	NSGPVSEVNTGFSPEVK	79.966331@S:13	39.6	914.4101	2	1826.806	-0.0031	39.362	K	E	+		@S:13		NSGPVSEVN[t]GF[s]PEVK	SRRM2_MOUSE;S1305
658	NSGSFSSPSISPR	79.966331@S:11	77.4	701.8044	2	1401.594	0.0016	29.677	R	-	+		@S:11		NSGSFSSP[s]I[s]PR	MTUS1_MOUSE;S1208
659	NSHSDSSIYIR	79.966331@S:4	16.3	453.529	3	1357.565	-0.0012	23.025	R	R	+		@S:4		N[s]H[s]D[s]SIYIR	CLMN_MOUSE;S925
660	NSTLSEEDYIER	79.966331@S:5	67.6	768.3164	2	1534.618	-0.0006	35.367	K	R	+		@S:5		NS[t]L[s]EEDYIER	BNIP3_MOUSE;S88
661	NTFTAWSEEDSDYEIDDRDVNK	79.966331@S:7	65.3	910.3668	3	2728.079	-0.0028	45.898	K	I			@S:7		NTFTAW[s]EED[s]D[y]EIDDRDVNK	LARP1_MOUSE;S604
662	NTFTAWSEEDSDYEIDDRDVNK	79.966331@S:7,79.966331@S:11	82.3	937.0226	3	2808.046	-0.0017	48.336	K	I	+		@S:7,@S:11		N[t]F[t]AW[s]EED[s]D[y]EIDDRDVNK	LARP1_MOUSE;S604,LARP1_MOUSE;S608
663	NTFTAWSEEDSDYEIDDRDVNK	79.966331@S:7,79.966331@Y:13	34.6	937.0237	3	2808.049	0.0016	51.568	K	I	+	ambiguos	@S:7	@S:11orY:13	NTFTAW[s]EED[s]D[y]EIDDRDVNK	LARP1_MOUSE;S604,LARP1_MOUSE;S608orY610
664	NVPGLAAPSSPTQK	79.966331@S:10	40.3	723.8533	2	1445.692	0.0005	36.726	R	E	+		@S:10		NVPGLAAP[s][s]P[t]QK	PP6R2_MOUSE;S670
665	NVPGLAAPSSPTQK	79.966331@S:9	39.3	723.8533	2	1445.692	0.0005	36.73	R	E			@S:9		NVPGLAAP[s][s]P[t]QK	PP6R2_MOUSE;S669
666	NVPGLAAPSSPTQK	79.966332@T:12	30.7	723.8528	2	1445.691	-0.0005	29.116	R	E	+	ambiguos		@S:9orS:10orT:12	NVPGLAAP[s][s]P[t]QK	PP6R2_MOUSE;S669orS670orT672
667	NVPQEESLEDSDVDADFK	79.966331@S:11	83.9	1058.931	2	2115.848	-0.0042	42.226	R	A	+		@S:11		NVPQEESLED[pS]DVDADFK	IMA3_MOUSE;S60
668	NWTEDIEGGISSPVK	79.966331@S:12	80.2	856.3825	2	1710.75	0.0002	47.605	R	K			@S:12		NWTEDIEGGI[s][s]PVK	NFIC_MOUSE;S323
669	PGPTPSGTNVGSSGRSPSK	79.966331@S:16	35.9	617.2853	3	1848.834	-0.0027	18.265	M	A	+		@S:16		PGP[t]P[s]G[t]NVG[s][s]GR[s]P[s]K	SC61B_MOUSE;S17
670	QADVADQQTTELPAENGETENQSPASEEEK	79.966331@S:26	48	1109.131	3	3324.372	-0.007	32.101	K	E	+		@S:26		QADVADQQTTELPAENGETENQ[s]PA[s]EEEK	HMGN1_MOUSE;S87
671	QAGDQMLSYNLGR	79.966331@S:8	19.1	511.5566	3	1531.648	-0.0009	30.465	R	R	+	ambiguos		@S:8orY:9	QAGDQML[s][y]NLGR	HECW2_MOUSE;S299orY300
672	QASTDAGTAGALTPQHVR	79.966331@S:3	81.5	620.9581	3	1859.852	-0.0003	24.759	R	A	+		@S:3		QA[s][t]DAG[t]AGALTPQHVR	YAP1_MOUSE;S94
673	QDFLKTDSDSDLQLYK	79.966331@S:8	30.4	665.9703	3	1994.889	0.0018	45.098	K	E	+		@S:8		QDFLK[t]D[s]D[s]DLQLYK	AMPD2_MOUSE;S109
674	QGDNISDDEDEVR	79.966331@S:6	39.5	786.2958	2	1570.577	-0.0014	25.729	R	V	+		@S:6		QGDNI[pS]DDEDEVR	STX4_MOUSE;S15
675	QGGITSEQAAVISKFWKSHK	79.966332@T:5,79.966331@S:6,79.966331@S:13	23.3	814.6947	3	2441.062	0.0039	17.259	K	I			@T:5,@S:6,@S:13		QGGI[t][s]EQAAVI[s]KFWK[s]HK	COMD1_MOUSE;T86,COMD1_MOUSE;S87,COMD1_MOUSE;S94
676	QGPTPAGLPRQPPSR	79.966332@T:4,79.966331@S:14	24.8	573.597	3	1717.769	-0.001	39.756	K	S	+		@T:4,@S:14		QGP[pT]PAGLPRQPP[pS]R	MRCKB_MOUSE;T1625,MRCKB_MOUSE;S1635
677	QGSGQGQASGSGRCGASSGQTSGCGSG	57.021465@C:14, 57.021465@C:24, 79.966331@S:26	22.2	628.2399	4	2508.93	-0.0038	23.414	R	-	+		@S:26		QG[s]GQGQA[s]G[s]GRCGA[s][s]GQ[t][s]GCG[s]G	HORN_MOUSE;S760
678	QHRESGEGEEEVADSAR	79.966331@S:5	53.4	655.9356	3	1964.785	-0.0011	18.396	K	L			@S:5		QHRE[pS]GEGEEEVADSAR	LRC47_MOUSE;S293
679	QKSDAEEDGVTGSQDEEDSKPK	79.966331@S:13	72.6	820.3399	3	2457.998	-0.0041	17.592	K	A	+		@S:13		QK[s]DAEEDGV[t]G[s]QDEEDSKPK	CALX_MOUSE;S563
680	QKSDAEEDGVTGSQDEEDSKPK	79.966331@S:19	30.6	615.508	4	2458.003	0.001	17.443	K	A			@S:19		QK[s]DAEEDGV[t]G[s]QDEED[s]KPK	CALX_MOUSE;S569
681	QKSDAEEDGVTGSQDEEDSKPK	79.966331@S:3	84.3	820.3412	3	2458.002	-0.0003	22.917	K	A			@S:3		QK[s]DAEEDGV[t]G[s]QDEED[s]KPK	CALX_MOUSE;S553
682	QKSDAEEDGVTGSQDEEDSKPK	79.966331@S:3,79.966331@S:13	83	846.9954	3	2537.964	-0.0041	18.546	K	A	+		@S:3,@S:13		QK[pS]DAEEDGVTGSQDEEDSKPK	CALX_MOUSE;S553,CALX_MOUSE;S563
683	QKSDAEEDGVTGSQDEEDSKPK	79.966332@T:11	23.1	820.3404	3	2457.999	-0.0027	17.42	K	A	+		@T:11		QK[s]DAEEDGV[t]G[s]QDEED[s]KPK	CALX_MOUSE;T561
684	QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR	79.966331@S:13	26.6	882.8839	4	3527.506	0.0006	37.139	K	S	+		@S:13		QK[s]DAEEDGV[t]G[s]QDEED[s]KPKAEEDEILNR	CALX_MOUSE;S563
685	QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR	79.966331@S:3,79.966331@S:13	22	902.8755	4	3607.473	0.0006	40.222	K	S	+		@S:3,@S:13		QK[s]DAEEDGV[t]G[s]QDEED[s]KPKAEEDEILNR	CALX_MOUSE;S553,CALX_MOUSE;S563
686	QLGSECLHVSPK	57.021465@C:6,79.966331@S:10	22.3	478.8863	3	1433.637	-0.0004	27.693	K	I			@S:10		QLGSECLHV[pS]PK	ACOT1_MOUSE;S416
687	QLHIEGASLELSDDDTESK	79.966331@S:12	28	722.9862	3	2165.937	0.0004	44.892	R	T	+		@S:12		QLHIEGASLEL[s]DDD[t]E[s]K	MYH10_MOUSE;S1956
688	QLSSGVSEIR	79.966331@S:3	56.3	578.2739	2	1154.533	0.0001	28.596	R	Q	+		@S:3		QL[s][s]GVSEIR	HSPB1_MOUSE;S86
689	QLSTEQAALQESLEK	79.966331@S:3	63.5	877.9136	2	1753.813	-0.0009	53.599	R	E	+		@S:3		QL[s][t]EQAALQESLEK	MTUS1_MOUSE;S1143
690	QLSTEQAALQESLEK	79.966332@T:4	71.1	877.9133	2	1753.812	-0.0015	45.157	R	E	+	ambiguos		@S:3orT:4	QL[s][t]EQAALQESLEK	MTUS1_MOUSE;S1143orT1144
691	QLSVPASDEEDEVPAPIPR	79.966331@S:7	62.4	1064.992	2	2127.969	-0.0034	52.667	K	G	+		@S:7		QLSVPA[pS]DEEDEVPAPIPR	ABCF1_MOUSE;S107
692	QLSVVVPSYNEEK	79.966331@S:8,79.966331@Y:9	23.5	551.24	3	1650.698	0.004	34.94	K	R	+		@S:8,@Y:9		QL[s]VVVP[s][y]NEEK	ALG5_MOUSE;S73,ALG5_MOUSE;Y74
693	QMRTTLEKIR	15.994915@M:2,79.966332@T:5	18.4	457.8974	3	1370.67	-0.0037	31.503	R	N	+		@T:5		QMR[t][t]LEKIR	CCD68_MOUSE;T43
694	QNQPTSCVSAPASSETSRSPK	57.021465@C:7,79.966331@S:19	51.8	767.0039	3	2297.99	-0.0047	20.406	K	S	+		@S:19		QNQPTSCVSAPA[s][s]E[t][s]R[s]PK	RBP2_MOUSE;S1605
695	QNSDFPSPSRR	79.966331@S:3	23.8	457.5336	3	1369.579	0.0013	40.716	R	K	+		@S:3		QN[s]DFP[s]P[s]RR	CENPL_MOUSE;S40
696	QPEVPTSSKK	79.966331@S:7	27.9	394.1924	3	1179.555	0.0016	21.798	K	E	+	ambiguos		@T:6orS:7	QPEVP[t][s][s]KK	EFCB5_MOUSE;T618orS619
697	QPLLLSEDEEDTK	79.966331@S:6	64.5	798.8558	2	1595.697	0.0003	46.301	K	R	+		@S:6		QPLLL[pS]EDEEDTK	EIF3C_MOUSE;S39
698	QPLLLSEDEEDTKR	79.966331@S:6	24.1	584.9402	3	1751.799	0.001	41.198	K	V			@S:6		QPLLL[s]EDEED[t]KR	EIF3C_MOUSE;S39
699	QPTPPFFGR	79.966332@T:3	24.9	563.7578	2	1125.501	0.0001	51.528	R	D			@T:3		QP[pT]PPFFGR	RBM14_MOUSE;T206
700	QQSEEDLLLQDFSR	79.966331@S:3	60.1	894.3956	2	1786.777	-0.0008	57.317	K	N	+		@S:3		QQ[pS]EEDLLLQDFSR	SSRG_MOUSE;S11
701	QREMLLEDVGSEEEPEEDDEAPFQEK	79.966331@S:11	32.3	1053.437	3	3157.29	-0.0061	48.917	K	D	+		@S:11		QREMLLEDVG[pS]EEEPEEDDEAPFQEK	NUCKS_MOUSE;S113
702	QRSPIALPVK	79.966331@S:3	27.7	396.8883	3	1187.643	0.0004	37.491	R	Q	+		@S:3		QR[pS]PIALPVK	PNISR_MOUSE;S211
703	QSQSQDVLVLEDSK	79.966331@S:13	23.4	828.3791	2	1654.744	-0.0014	37.18	K	K	+		@S:13		Q[s]Q[s]QDVLVLED[s]K	MRP2_MOUSE;S290

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
704	QVESFLK	79.966331@S:4	20.3	465.7205	2	929.4264	0.0006	51.609	K	A	+		@S:4		QVE[pS]FLK	KIF22_MOUSE;S642
705	QVSAGDLFR	79.966331@S:3	38	536.7447	2	1071.475	-0.0002	42.22	K	S			@S:3		QV[pS]AGDLFR	EPIPL_MOUSE;S1537
706	QVSASELCTSGILDR	57.021465@C:8,79.966331@S:3	58.1	858.3865	2	1714.758	-0.0012	45.089	R	D	+		@S:3		QV[s]A[s]ELCTSGILDR	EPIPL_MOUSE;S2705
707	QYKQSLAIESDGKK	79.966331@S:10	21.6	558.943	3	1673.807	0.0047	17.031	K	G			@S:10		Q[y]KQ[s]LAIE[s]DGKK	PPCT_MOUSE;S163
708	RAEAQALLQDYVSTQSAEE	79.966331@S:16	94.3	1094.99	2	2187.964	-0.0041	48.418	R	-	+		@S:16		RAEAQALLQDYVSTQ[pS]AEE	AASD1_MOUSE;S409
709	RAGDVLEDSPKRPK	79.966331@S:9	33.7	549.9448	3	1646.813	-0.0015	18.491	R	E	+		@S:9		RAGDVLED[pS]PKRPK	HDGF_MOUSE;S165
710	RASRSLDGAAAAESTDR	79.966331@S:3,79.966331@S:5	53.2	631.9324	3	1892.775	-0.0025	20.96	K	S	+		@S:3,@S:5		RA[pS]R[pS]LDGAAAAESTDR	41_MOUSE;S541,41_MOUSE;S543
711	RDESDEEPPRVER	79.966331@S:4	24.8	565.2434	3	1692.708	-0.0021	18.67	R	T	+		@S:4		RDE[pS]DEEPPRVER	K1671_MOUSE;S205
712	RDIMRSSFLNLR	15.994915@M:4,79.966331@S:6	22.3	401.6991	4	1602.767	-0.0027	28.655	R	D			@S:6		RDIMR[s][s]FLNLR	MYCS_MOUSE;S366
713	RDSFDDRGPSLNPVLDYDHGSR	79.966331@S:3	41.8	650.2897	4	2597.13	0	39.801	R	S	+		@S:3		RD[s]FDDRGP[s]LNPVLDYDHGSR	MATR3_MOUSE;S188
714	RDSSDDWEIPDGQITVGQR	79.966331@S:4	69.6	751.9973	3	2252.97	0.0001	46.342	R	I			@S:4		RD[s][s]DDWEIPDGQITVGQR	BRAF_MOUSE;S484
715	REEQTDTSDGESVTHHIR	79.966331@S:12	28.3	544.987	4	2175.919	0.0006	25.781	R	R	+		@S:12		REEQTD[t][s]DGE[s]V[t]HHIR	GNL1_MOUSE;S55
716	REEQTDTSDGESVTHHIR	79.966331@S:8	36.3	544.9864	4	2175.916	-0.0017	19.661	R	R			@S:8		REEQTD[t][s]DGE[s]V[t]HHIR	GNL1_MOUSE;S51
717	REESVPPSSTAR	79.966332@T:10	20.1	465.8807	3	1394.62	0.001	21.71	K	S	+		@T:10		REE[s]VPP[s][s][t]AR	NOG1_MOUSE;T564
718	RFESEDDIDALAFGK	79.966331@S:4	76.3	896.8913	2	1791.768	-0.0036	49.327	R	Q	+		@S:4		RFE[pS]EDDIDALAFGK	STAB2_MOUSE;S2503
719	RFSIATLR	79.966331@S:3	31.7	522.2733	2	1042.532	-0.0005	35.479	R	D	+		@S:3		RF[s]IA[t]LR	CP2AC_MOUSE;S130,CP2A5_MOUSE;S131
720	RFSSGGEEEDFDR	79.966331@S:3,79.966331@S:4	26.7	845.791	2	1689.567	-0.0034	31.102	R	S	+		@S:3,@S:4		RF[pS][pS]GGEEEDFDR	ABLM3_MOUSE;S502,ABLM3_MOUSE;S503
721	RFSVSTLR	79.966331@S:3	48.3	523.2632	2	1044.512	0.0001	38.951	R	N	+		@S:3		RF[s]V[s][t]LR	CP2DB_MOUSE;S138,CP2DA_MOUSE;S138,CP2DQ_MOUSE;S138,CP2D9_MOUSE;S138
722	RGASASPQGRQSPSPSTRPIR	79.966331@S:4,79.966331@S:6,79.966332@T:17	36.2	811.6891	3	2432.045	-0.0058	19.389	R	R	+		@S:4,@S:6,@T:17		RGA[s]A[s]PQGRQ[s]P[s]P[s][t]RPIR	SRRM1_MOUSE;S723,SRRM1_MOUSE;S725,SRRM1_MOUSE;T736
723	RGSGDTSISMDTEASIR	15.994915@M:10,79.966331@S:7	46.9	626.9348	3	1877.783	0.0001	33.492	R	E	+		@S:7		RG[s]GD[t][s]ISMDTEASIR	LRRF1_MOUSE;S92
724	RGSGDTSSLIDPDTSLSELR	79.966331@S:8	23.9	729.3373	3	2184.99	0	47.425	R	E		ambiguos		@S:3orT:6orS:7orS:8	RG[s]GD[t][s][s]LIDPDTSLSELR	LRRF2_MOUSE;S111orT114orS115orS116
725	RGSLELGNPSAAHLGDELK	79.966331@S:3	48	682.0005	3	2042.98	0.001	47.678	R	E	+		@S:3		RG[pS]LELGNPSAAHLGDELK	SVIL_MOUSE;S960
726	RGSLTFAGESSK	79.966331@S:3	50.9	660.3025	2	1318.59	-0.0013	23.878	R	T	+		@S:3		RG[s]L[t]FAGESSK	FA83H_MOUSE;S970
727	RGSPVPPVPER	79.966331@S:3	24.9	635.818	2	1269.621	-0.0016	21.592	R	R	+		@S:3		RG[pS]PVPPVPER	FA83H_MOUSE;S948
728	RGSPVPPVPERR	79.966331@S:3	44.9	476.2483	3	1425.723	-0.0011	19.494	R	G	+		@S:3		RG[pS]PVPPVPERR	FA83H_MOUSE;S948
729	RGTSPRPPEGGLGYSQLGDDDLK	79.966332@T:3,79.966331@S:4	49.8	859.0454	3	2574.114	-0.0009	38.739	K	E	+		@T:3,@S:4		RG[pT][pS]PRPPEGGLGYSQLGDDDLK	CDK11_MOUSE;T740,CDK11_MOUSE;S741
730	RGVSAHGLSHEERR	79.966331@S:4,79.966331@S:9	19.2	584.2566	3	1749.748	0.0018	21.286	M	Q	+		@S:4,@S:9		RGV[pS]AHGL[pS]HEERR	RRNAD_MOUSE;S5,RRNAD_MOUSE;S10
731	RHLPGSGQQPSPPAR	79.966331@S:11	31.9	555.6048	3	1663.793	-0.0019	19.237	K	S	+		@S:11		RHLPGSGQQP[pS]PPAR	TENC1_MOUSE;S1087
732	RHSGQDVHVVLK	79.966331@S:3	55.2	364.4373	4	1453.72	0.0008	19.117	R	L	+		@S:3		RH[pS]GQDVHVVLK	NSF1C_MOUSE;S176
733	RIACDEEFSDSEDEGEGGRR	57.021465@C:4,79.966331@S:9,79.966331@S:11	40.6	825.3019	3	2472.884	-0.0052	25.191	K	N	+		@S:9,@S:11		RIACDEEF[pS]D[pS]EDEGEGGRR	HDAC2_MOUSE;S422,HDAC2_MOUSE;S424
734	RIDFIPVSPAPSPTR	79.966331@S:8,79.966332@T:14	37.1	604.9533	3	1811.838	0.0008	48.664	K	G	+	ambiguos	@S:8	@S:12orT:14	RIDFIPV[s]PAP[s]P[t]R	F122A_MOUSE;S140,F122A_MOUSE;S144orT146
735	RIDISPSALR	79.966331@S:5	34.5	604.3133	2	1206.612	-0.0001	34.918	R	K	+		@S:5		RIDI[s]P[s]ALR	BCLF1_MOUSE;S656
736	RIDISPSTFR	79.966331@S:5	22.1	636.3111	2	1270.608	0.0005	46.083	R	K	+		@S:5		RIDI[s]P[s][t]FR	TR150_MOUSE;S679
737	RIPYTPGEIPK	79.966332@T:5	34.3	450.8988	3	1349.675	0.0001	34.288	K	F	+		@T:5		RIP[y][t]PGEIPK	UGDH_MOUSE;T474
738	RISGLIYEETR	79.966331@S:3	64.6	708.8469	2	1415.679	-0.0017	37.675	K	G	+		@S:3		RI[pS]GLIYEETR	H4_MOUSE;S48
739	RKAEDSDSEPEPEDNVR	79.966331@S:6,79.966331@S:8	32	711.6095	3	2131.807	-0.0029	19.17	K	L	+		@S:6,@S:8		RKAED[pS]D[pS]EPEPEDNVR	XRN2_MOUSE;S499,XRN2_MOUSE;S501
740	RKASPEPPDSAESALK	79.966331@S:4	40.4	588.2837	3	1761.829	-0.0004	20.967	K	L	+		@S:4		RKA[pS]PEPPDSAESALK	I2BPL_MOUSE;S526
741	RKEDELSIGSAPLGK	79.966331@S:7,79.966331@S:10	27.1	587.2725	3	1758.796	0.0003	35.543	R	Q	+		@S:7,@S:10		RKEDEL[pS]IG[pS]APLGK	VP13B_MOUSE;S998,VP13B_MOUSE;S1001
742	RKGSLDYLK	79.966331@S:4	28.1	387.2008	3	1158.581	0.0007	20.839	K	Q	+		@S:4		RKG[s]LD[y]LK	LUZP1_MOUSE;S261
743	RKLSGDLEAGAPK	79.966331@S:4	31.9	474.576	3	1420.706	-0.0014	20.786	K	N	+		@S:4		RKL[pS]GDLEAGAPK	TCOF_MOUSE;S1191
744	RKLSVGAYVSSVR	79.966331@S:4	47.2	501.2681	3	1500.782	0.001	41.285	K	V	+		@S:4		RKL[pS]VGAYVSSVR	S23IP_MOUSE;S748
745	RKPSPSPPPPTATESR	79.966331@S:4,79.966331@S:6	26.9	622.2824	3	1863.825	-0.0027	17.758	K	K	+		@S:4,@S:6		RKP[pS]P[pS]PPPPTATESR	SMRC1_MOUSE;S327,SMRC1_MOUSE;S329
746	RKTSGPPVSELITK	79.966331@S:4	21	531.6185	3	1591.834	0.0001	27.011	K	A	+	ambiguos		@T:3orS:4	RK[t][s]GPPV[s]ELI[t]K	H14_MOUSE;T35orS36
747	RLQSLIK	79.966331@S:4	27.1	469.265	2	936.5154	-0.0002	32.4	R	N	+		@S:4		RLQ[pS]LIK	HLTF_MOUSE;S629
748	RLSAGTTVADVQK	79.966331@S:3	29.1	713.3578	2	1424.701	-0.0015	25.052	R	I	+		@S:3		RL[s]AG[t][t]VADVQK	PHLB2_MOUSE;S465
749	RLSPSASPPR	79.966331@S:3,79.966331@S:7	19.7	614.2672	2	1226.52	-0.0011	21.066	R	R	+		@S:3,@S:7		RL[s]P[s]A[s]PPR	SRRM1_MOUSE;S387,SRRM1_MOUSE;S391

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
750	RLSQSDEDVIR	79.966331@S:5	31.1	466.5522	3	1396.635	-0.0001	24.754	K	L	+		@S:5		RL[s]Q[s]DEDVIR	WDR26_MOUSE;S103
751	RLSRTDLTDYLNR	79.966331@S:3	28.8	568.2803	3	1701.819	-0.0009	39.149	R	H	+		@S:3		RL[s]R[t]DL[t]D[y]LNR	QCR1_MOUSE;S212
752	RLSRTDLTDYLNR	79.966332@T:5	35	568.2806	3	1701.82	0.0002	47.565	R	H	+		@T:5		RL[s]R[t]DLTDYLNR	QCR1_MOUSE;T214
753	RLSSLRASTSK	79.966331@S:3,79.966331@S:4	21.3	455.881	3	1364.621	-0.0002	21.788	R	S	+		@S:3,@S:4		RL[pS][pS]LRASTSK	RS6_MOUSE;S235,RS6_MOUSE;S236
754	RMSPKPELTEDQK	15.994915@M:2,79.966331@S:3	24.8	552.2545	3	1653.742	-0.0017	17.452	K	Q	+		@S:3		RM[pS]PKPELTEDQK	CETN2_MOUSE;S20
755	RNPPELSQNSFK	79.966331@S:10	22.3	499.5679	3	1495.682	0	22.944	K	K	+		@S:10		RNPPEL[s]QN[s]FK	CB078_MOUSE;S554
756	RNSLTGEEGELVK	79.966331@S:3	73.2	756.3582	2	1510.702	-0.0009	28.524	R	V	+		@S:3		RN[s]L[t]GEEGELVK	SGPP1_MOUSE;S101
757	RNSLTGEEGELVK	79.966332@T:5	26.5	504.5749	3	1510.703	0.0001	36.922	R	V			@T:5		RN[s]L[t]GEEGELVK	SGPP1_MOUSE;T103
758	RNVPQEESLEDSDVDADFK	79.966331@S:12	57.2	758.3255	3	2271.955	0.0015	44.798	K	A	+		@S:12		RNVPQEESLED[pS]DVDADFK	IMA3_MOUSE;S60
759	RPASPSSPEHLPATPAESPAQR	79.966331@S:4,79.966331@S:7	42.7	815.0298	3	2442.068	-0.0053	27.136	K	F	+		@S:4,@S:7		RPA[s]P[s][s]PEHLPA[t]PAE[s]PAQR	SDS3_MOUSE;S234,SDS3_MOUSE;S237
760	RPASPSSPEHLPATPAESPAQR	79.966331@S:4,79.966332@T:14	40.5	815.0317	3	2442.073	0.0003	27.133	K	F	+		@S:4,@T:14		RPA[s]P[s][s]PEHLPA[t]PAE[s]PAQR	SDS3_MOUSE;S234,SDS3_MOUSE;T244
761	RPDPDSDEDEDYERER	79.966331@S:6	82.1	701.602	3	2101.784	-0.002	20.165	R	R	+		@S:6		RPDPD[pS]DEDEDYERER	SPF45_MOUSE;S155
762	RPESRGSGVNAAGDGTIR	79.966331@S:4	22.7	627.2961	3	1878.866	-0.0034	18.568	R	E	+		@S:4		RPE[s]RG[s]GVNAAGDG[t]IR	TGM1_MOUSE;S91
763	RPESRGSGVNAAGDGTIR	79.966331@S:7	30	627.2973	3	1878.87	0.0005	18.489	R	E	+		@S:7		RPE[s]RG[s]GVNAAGDGTIR	TGM1_MOUSE;S94
764	RPGLEKASDEEPED	79.966331@S:8	33.4	826.3474	2	1650.68	0.0028	20.424	K	-	+		@S:8		RPGLEKA[pS]DEEPED	DI3L2_MOUSE;S864
765	RPHTPTPGIYMGRPTYGSSR	15.994915@M:11,79.966332@T:4	29.2	582.5237	4	2326.066	-0.0022	23.47	K	R	+		@T:4		RPH[t]P[t]PGI[y]MGRP[t][y]G[s][s]R	TRA2B_MOUSE;T201
766	RPHTPTPGIYMGRPTYGSSR	15.994915@M:11,79.966332@T:6	22.3	582.5238	4	2326.066	-0.0016	23.586	K	R	+		@T:6		RPH[t]P[t]PGI[y]MGRP[t][y]G[s][s]R	TRA2B_MOUSE;T203
767	RPSTSPDVLQGQPPR	79.966331@S:5	31.9	572.2811	3	1713.821	0.0015	33.654	R	A			@S:5		RP[s][t][s]PDVLQGQPPR	UB2J1_MOUSE;S268
768	RPSTSPDVLQGQPPR	79.966332@T:4	38.5	572.2805	3	1713.82	-0.0001	33.701	R	A	+		@T:4		RP[s][t][s]PDVLQGQPPR	UB2J1_MOUSE;T267
769	RQDSAGPILDGAR	79.966331@S:4	20	479.2276	3	1434.661	-0.0005	22.924	R	S	+		@S:4		RQD[pS]AGPILDGAR	CGNL1_MOUSE;S284
770	RQGSFSEDVISHK	79.966331@S:4	46.8	523.9058	3	1568.696	-0.0028	24.656	K	G	+		@S:4		RQG[s]F[s]EDVISHK	MACF1_MOUSE;S3889
771	RQGSFSEDVISHK	79.966331@S:6	39.9	523.9067	3	1568.698	-0.0002	32.925	K	G	+		@S:6		RQG[s]F[s]EDVISHK	MACF1_MOUSE;S3891
772	RQSSLTFQSSDPEHVR	79.966331@S:3	50.3	651.9657	3	1952.875	0.001	33.759	K	Q	+		@S:3		RQ[s][s]L[t]FQSSDPEHVR	COBL1_MOUSE;S1214
773	RQSSLTFQSSDPEHVR	79.966331@S:4	53.7	651.9655	3	1952.875	0.0005	33.762	K	Q	+		@S:4		RQ[s][s]L[t]FQSSDPEHVR	COBL1_MOUSE;S1215
774	RQSSLTFQSSDPEHVR	79.966332@T:6	39.4	651.9646	3	1952.872	-0.0022	25.596	K	Q	+		@T:6		RQ[s][s]L[t]FQSSDPEHVR	COBL1_MOUSE;T1217
775	RQSSSYEDPWK	79.966331@S:3,79.966331@S:4	40.2	771.7861	2	1541.558	-0.0013	33.292	R	I	+		@S:3,@S:4		RQ[s][s][s][y]EDPWK	REPS1_MOUSE;S272,REPS1_MOUSE;S273
776	RQSSSYEDPWK	79.966331@S:3,79.966331@Y:6	35.3	771.7874	2	1541.56	0.0014	33.329	R	I	+		@S:3,@Y:6		RQ[s][s][s][y]EDPWK	REPS1_MOUSE;S272,REPS1_MOUSE;Y275
777	RQSSTADAPEAQHEPGITITEWK	79.966331@S:4	27	878.0718	3	2631.194	-0.0032	37.26	K	N	+	ambiguos		@S:3orS:4	RQ[s][s][t]ADAPEAQHEPGITITEWK	KPBB_MOUSE;S692orS693
778	RRAGDVLEDSPK	79.966331@S:10	46.8	474.8959	3	1421.666	-0.0006	19.223	K	R	+		@S:10		RRAGDVLED[pS]PK	HDGF_MOUSE;S165
779	RRHSGQDVHVVLK	79.966331@S:4	54.1	403.4625	4	1609.821	0.0005	24.448	R	L	+		@S:4		RRH[pS]GQDVHVVLK	NSF1C_MOUSE;S176
780	RRNSEEFGVK	79.966331@S:4	48.4	434.5381	3	1300.592	0	17.701	K	L	+		@S:4		RRN[pS]EEFGVK	ZO3_MOUSE;S195
781	RRSESSGNLPSVADTR	79.966331@S:3	45.9	604.618	3	1810.832	0	29.524	R	S	+		@S:3		RR[s]E[s][s]GNLPSVADTR	AKAP1_MOUSE;S101
782	RRSESSGNLPSVADTR	79.966331@S:5	24.4	604.6183	3	1810.833	0.0007	29.379	R	S	+		@S:5		RR[s]E[s][s]GNLPSVADTR	AKAP1_MOUSE;S103
783	RRSFSISPVR	79.966331@S:3,79.966331@S:5	27.9	455.546	3	1363.616	-0.0002	27.061	R	L	+		@S:3,@S:5		RR[pS]F[pS]I[pS]PVR	SON_MOUSE;S2027,SON_MOUSE;S2029
784	RRSFSISPVR	79.966331@S:3,79.966331@S:5,79.966331@S:7	20.4	482.201	3	1443.581	-0.0013	30.06	R	L	+		@S:3,@S:5,@S:7		RR[s]F[s]I[s]PVR	SON_MOUSE;S2027,SON_MOUSE;S2029,SON_MOUSE;S2031
785	RRSFSISPVR	79.966331@S:3,79.966331@S:7	27.4	455.5462	3	1363.617	0.0005	35.897	R	L	+		@S:3,@S:7		RR[s]F[s]I[s]PVR	SON_MOUSE;S2027,SON_MOUSE;S2031
786	RRSGSNGSVVSLEQQQK	79.966331@S:5,79.966331@S:8	26.1	673.9701	3	2018.888	-0.0052	23.261	K	I	+	ambiguos	@S:8	@S:3orS:5	RR[s]G[s]NG[s]VVSLEQQQK	KIF7_MOUSE;S903,KIF7_MOUSE;S898orS900
787	RRSPSPAPPPPPPPPPPR	79.966331@S:3,79.966331@S:5	80.7	686.3338	3	2055.98	-0.0012	22.895	R	R	+		@S:3,@S:5		RR[pS]P[pS]PAPPPPPPPPPPR	SRRM1_MOUSE;S572,SRRM1_MOUSE;S574
788	RRSPSPDFYK	79.966331@S:3,79.966331@S:5	23.8	471.5299	3	1411.568	-0.0009	21.937	R	R	+		@S:3,@S:5		RR[s]P[s]PDF[y]K	U2AFM_MOUSE;S387,U2AFM_MOUSE;S389
789	RRSPSPYYSR	79.966331@S:3	34.2	450.21	3	1347.608	-0.0003	17.117	R	G	+		@S:3		RR[pS]P[pS]PYYSR	TRA2A_MOUSE;S259,TRA2B_MOUSE;S264
790	RRSPSPYYSR	79.966331@S:3,79.966331@S:5	37	476.8652	3	1427.574	-0.0012	17.604	R	Y	+		@S:3,@S:5		RR[s]P[s]P[y][y][s]R	TRA2A_MOUSE;S259,TRA2A_MOUSE;S261,TRA2B_MOUSE;S264,TRA2B_MOUSE;S266
791	RRSPSPYYSR	79.966331@S:3,79.966331@Y:7	34	714.7942	2	1427.574	-0.001	17.773	R	G	+		@S:3,@Y:7		RR[pS]PSPYYSR	TRA2A_MOUSE;S259,TRA2A_MOUSE;Y263,TRA2B_MOUSE;S264,TRA2B_MOUSE;Y268
792	RSASADNLILPR	79.966331@S:4	47.8	696.8532	2	1391.692	-0.0003	41.377	K	W	+		@S:4		R[s]A[s]ADNLILPR	CCNY_MOUSE;S326
793	RSASPDDDLGSSNWEAADLGNEER	79.966331@S:12	76.1	891.0341	3	2670.08	-0.0027	41.706	K	K			@S:12		R[s]A[s]PDDDLG[s][s]NWEAADLGNEER	SMAP_MOUSE;S25
794	RSASPDDDLGSSNWEAADLGNEER	79.966331@S:4	65.2	891.0354	3	2670.084	0.0012	42.017	K	K			@S:4		R[s]A[s]PDDDLGSSNWEAADLGNEER	SMAP_MOUSE;S17

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
795	RSASPDDDLGSSNWEAADLGNEERK	79.966331@S:4	88.1	933.7326	3	2798.176	-0.0019	37.522	K	Q	+		@S:4		R[s]A[s]PDDDLGS[s]NWEAADLGNEERK	SMAP_MOUSE;S17
796	RSDSLLSFR	79.966331@S:4	37.3	580.7766	2	1159.539	-0.0001	45.917	R	F	+		@S:4		RSD[s]LL[s]FR	BORG5_MOUSE;S207
797	RSLAALDALNTDDENDEEEYEAWK	79.966332@T:11	97.3	959.7409	3	2876.201	-0.0018	51.459	K	V	+		@T:11		RSLAALDALN[pT]DDENDEEEYEAWK	MFAP1_MOUSE;T267
798	RSPLPGEPQRPK	79.966331@S:2	45.5	481.2484	3	1440.723	-0.0005	19.231	R	R	+		@S:2		R[pS]PLPGEPQRPK	DFFA_MOUSE;S314
799	RSPSPAPPPPPPPPPPR	79.966331@S:2,79.966331@S:4	21.8	634.3005	3	1899.88	0	25.927	R	R	+		@S:2,@S:4		R[pS]P[pS]PAPPPPPPPPPPR	SRRM1_MOUSE;S572,SRRM1_MOUSE;S574
800	RSPVPARPLPPTSQK	79.966331@S:2	26.6	570.9737	3	1709.899	0.0015	20.008	R	A	+		@S:2		R[pS]PVPARPLPPTSQK	LS14A_MOUSE;S216
801	RSSDPALTGLSTSVSDNNFSSEEPSR	79.966331@S:2	73.4	940.7474	3	2819.22	-0.0045	41.939	R	K	+		@S:2		R[s][s]DPAL[t]GLSTSVSDNNFSSEEPSR	PARD3_MOUSE;S143
802	RSSDPALTGLSTSVSDNNFSSEEPSR	79.966331@S:3	67.4	940.747	3	2819.219	-0.0054	42.371	R	K	+		@S:3		R[s][s]DPAL[t]GL[s][t]SVSDNNFSSEEPSR	PARD3_MOUSE;S144
803	RSSDPALTGLSTSVSDNNFSSEEPSRK	79.966331@S:3	51.3	983.4455	3	2947.315	-0.0049	38.203	R	N	+		@S:3		R[s][s]DPALTGLSTSVSDNNFSSEEPSRK	PARD3_MOUSE;S144
804	RSSSELSPEVVEK	79.966331@S:3	68	763.8573	2	1525.7	-0.0025	25.121	R	V	+		@S:3		R[s][s][s]EL[s]PEVVEK	SRRM2_MOUSE;S1339
805	RSSSELSPEVVEK	79.966331@S:3,79.966331@S:7	47.1	803.8393	2	1605.664	-0.0047	27.95	R	V	+		@S:3,@S:7		R[s][s][s]ELSPEVVEK	SRRM2_MOUSE;S1339,SRRM2_MOUSE;S1343
806	RSSSELSPEVVEK	79.966331@S:4,79.966331@S:7	37	803.8418	2	1605.669	0.0003	35.286	R	V	+		@S:4,@S:7		R[s][s][s]EL[s]PEVVEK	SRRM2_MOUSE;S1340,SRRM2_MOUSE;S1343
807	RSSSPAELELKDDLQQAHGR	79.966331@S:3,79.966331@S:4	55.7	600.021	4	2396.055	0.0028	33.957	R	C	+		@S:3,@S:4		R[s][s][s]PAELELKDDLQQAHGR	RGPA2_MOUSE;S819,RGPA2_MOUSE;S820
808	RSYSSPDITQALQEEEK	79.966331@S:2	21.9	687.6439	3	2059.91	0	40.081	K	R	+	ambiguos		@S:2orY:3orS:4orS:5	R[s][y][s][s]PDI[t]QALQEEEK	UBP8_MOUSE;S678orY679orS680orS681
809	RSYSSPDITQALQEEEK	79.966331@S:4	47.7	687.6443	3	2059.911	0.0011	48.822	K	R	+		@S:4		R[s][y][s][s]PDITQALQEEEK	UBP8_MOUSE;S680
810	RSYSSPDITQALQEEEK	79.966331@Y:3	35.7	687.644	3	2059.91	0.0002	39.992	K	R	+	ambiguos		@S:2orY:3	R[s][y][s][s]PDITQALQEEEK	UBP8_MOUSE;S678orY679
811	RTEGYAAFQEDSSGDEAESPSK	79.966331@S:12,79.966331@S:13	60.3	840.9857	3	2519.935	-0.0014	33.233	K	V	+		@S:12,@S:13		RTEGYAAFQED[pS][pS]GDEAESPSK	RBP1_MOUSE;S92,RBP1_MOUSE;S93
812	RTGSNISGASSDVSLDEQYK	79.966331@S:4,79.966331@S:7	76	758.6494	3	2272.926	0.0012	41.228	K	H	+		@S:4,@S:7		R[t]G[s]NI[s]GA[s]SDVSLDEQYK	OSBP1_MOUSE;S323,OSBP1_MOUSE;S326
813	RTSMGGTQQQFVEGVR	15.994915@M:4,79.966331@S:3	24.1	626.2846	3	1875.832	0.002	34.255	R	M	+		@S:3		R[t][s]MGG[t]QQQFVEGVR	CTNB1_MOUSE;S552
814	RTSMGGTQQQFVEGVR	15.994915@M:4,79.966332@T:7	32.4	626.2836	3	1875.829	-0.0009	26.059	R	M	+		@T:7		R[t][s]MGG[t]QQQFVEGVR	CTNB1_MOUSE;T556
815	RVPSPTPVPK	79.966331@S:4	40.1	579.307	2	1156.599	-0.0011	19.931	K	E	+		@S:4		RVP[s]P[t]PVPK	SRRM2_MOUSE;S2535
816	RVSSGSCFALE	57.021465@C:7,79.966331@S:3	18.6	646.7705	2	1291.526	-0.0004	35.02	R	-	+		@S:3		RV[s][s]G[s]CFALE	MTCH1_MOUSE;S381
817	RVSVCAETFNPDEEEEDNDPR	57.021465@C:5,79.966331@S:3	61	863.3449	3	2587.013	-0.0042	35.734	R	V			@S:3		RV[s]VCAE[t]FNPDEEEEDNDPR	KAP2_MOUSE;S96
818	RVSVCAETFNPDEEEEDNDPR	57.021465@C:5,79.966332@T:8	30.7	863.3451	3	2587.013	-0.0036	35.757	R	V			@T:8		RV[s]VCAE[t]FNPDEEEEDNDPR	KAP2_MOUSE;T101
819	RVSVCAETFNPDEEEEDNDPRVVHPK	57.021465@C:5,79.966331@S:3	47.5	787.8474	4	3147.36	-0.0002	41.849	R	T			@S:3		RV[s]VCAE[t]FNPDEEEEDNDPRVVHPK	KAP2_MOUSE;S96
820	RWPGVYTFLSDK	79.966331@S:10,79.966331@Y:6	24.9	407.9274	4	1627.68	-0.0031	24.199	R	H	+		@Y:6,@S:10		RWPGV[y][t]FL[s]DK	GRAA_MOUSE;Y241,GRAA_MOUSE;S245
821	RWPGVYTFLSDK	79.966332@T:7,79.966331@Y:6	19	407.9277	4	1627.682	-0.002	32.033	R	H	+		@Y:6,@T:7		RWPGV[y][t]FL[s]DK	GRAA_MOUSE;Y241,GRAA_MOUSE;T242
822	RWSGELRR	79.966331@S:3	25.5	380.5205	3	1138.54	-0.0002	21.125	R	S	+		@S:3		RW[pS]GELRR	PLIN5_MOUSE;S155
823	RYSPPIQR	79.966331@S:3	27.3	366.1817	3	1095.523	0.0006	20.793	R	R	+		@S:3		R[y][s]PPIQR	SRRM1_MOUSE;S616
824	SAASPVVISIPER	79.966331@S:4	40.7	703.3576	2	1404.701	-0.0008	41.523	K	A	+		@S:4		[s]AA[s]PVVISIPER	SON_MOUSE;S1794
825	SAEDLTDGSYDDILNAEQLK	79.966331@S:1	88.4	1138.993	2	2275.972	-0.0013	56.933	R	K	+		@S:1		[s]AEDL[t]DGSYDDILNAEQLK	ARM10_MOUSE;S43
826	SAEDLTDGSYDDILNAEQLKK	79.966331@S:1	39.3	802.3636	3	2404.069	0.0007	49.751	R	L	+		@S:1		[s]AEDL[t]DG[s][y]DDILNAEQLKK	ARM10_MOUSE;S43
827	SAFTPATATGSSPSPVLGQGEK	79.966331@S:12	72.4	1085.506	2	2168.997	-0.0025	37.56	R	V	+		@S:12		SAFTPATATG[s][s]P[s]PVLGQGEK	ITSN1_MOUSE;S895
828	SAFTPATATGSSPSPVLGQGEK	79.966331@S:14	85.3	1085.507	2	2169	0.0005	37.16	R	V	+		@S:14		SAFTPATATG[s][s]P[s]PVLGQGEK	ITSN1_MOUSE;S897
829	SAPETLTLPDPEK	79.966331@S:1	30.6	739.345	2	1476.675	0.0005	42.108	K	K	+		@S:1		[s]APE[t]L[t]LPDPEK	PITC1_MOUSE;S299
830	SAQAQMRAMLDQLMGTSR	15.994915@M:14,79.966331@S:1	21	697.6442	3	2089.911	-0.0001	47.465	M	D	+		@S:1		[s]AQAQMRAMLDQLMG[t][s]R	LC7L2_MOUSE;S2
831	SARATRPR	79.966331@S:1	18.8	332.1688	3	993.4846	-0.0023	17.775	M	S	+		@S:1		[s]ARA[t]RPR	USBP1_MOUSE;S2
832	SASADNLILPR	79.966331@S:1	31.7	618.8035	2	1235.592	0.0013	48.609	R	W	+		@S:1		[s]A[s]ADNLILPR	CCNY_MOUSE;S324
833	SASADNLILPR	79.966331@S:3	28.4	618.8031	2	1235.592	0.0005	48.611	R	W	+		@S:3		[s]A[s]ADNLILPR	CCNY_MOUSE;S326
834	SASPDDDLGSSNWEAADLGNEER	79.966331@S:3	95.4	1257.996	2	2513.977	-0.0053	47.507	R	K	+		@S:3		[s]A[s]PDDDLGSSNWEAADLGNEER	SMAP_MOUSE;S17
835	SASPDDDLGSSNWEAADLGNEERK	79.966331@S:3	58.5	881.6997	3	2642.077	0.0003	41.64	R	Q	+		@S:3		[s]A[s]PDDDLGSSNWEAADLGNEERK	SMAP_MOUSE;S17
836	SASQSSLDKLDQELK	79.966331@S:1,79.966331@S:6	37.6	904.8887	2	1807.763	-0.0014	40.801	R	E	+		@S:1,@S:6		[s]A[s]Q[s][s]LDKLDQELK	JIP4_MOUSE;S728,JIP4_MOUSE;S733
837	SASQSSLDKLDQELK	79.966331@S:3,79.966331@S:6	29.3	904.8895	2	1807.764	0.0002	40.579	R	E	+		@S:3,@S:6		[s]A[s]Q[s][s]LDKLDQELK	JIP4_MOUSE;S730,JIP4_MOUSE;S733
838	SASQSSLDKLDQELK	79.966331@S:6	31	864.9056	2	1727.797	-0.0012	35.304	R	E	+	ambiguos		@S:5orS:6	[s]A[s]Q[s][s]LDKLDQELK	JIP4_MOUSE;S732orS733
839	SASSDTSEELNSQDSPK	79.966331@S:3	85.7	931.37	2	1860.725	-0.0007	29.215	R	R	+		@S:3		[s]A[s][s]DTSEELNSQDSPK	NHRF1_MOUSE;S285
840	SASSDTSEELNSQDSPK	79.966331@S:4	71.2	931.3705	2	1860.726	0.0002	29.094	R	R	+		@S:4		[s]A[s][s]D[t]SEELNSQDSPK	NHRF1_MOUSE;S286

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
841	SASSDTSEELNSQDSPK	79.966332@T:6	47.9	621.2492	3	1860.726	-0.0005	23.477	R	R			@T:6		[s]A[s][s]D[t][s]EELNSQDSPK	NHRF1_MOUSE;T288
842	SASSDTSEELNSQDSPKR	79.966331@S:3	36.2	673.2825	3	2016.826	-0.0015	20.864	R	Q	+		@S:3		[s]A[s][s]DTSEELNSQDSPKR	NHRF1_MOUSE;S285
843	SATPPPAEPASLPQEPPK	79.966332@T:3	47	947.4517	2	1892.889	-0.0033	32.166	K	A	+		@T:3		[s]A[t]PPPAEPASLPQEPPK	G3BP2_MOUSE;T227
844	SATSGDIWPGLSAYDNSPR	79.966331@S:17	44.2	1037.448	2	2072.882	-0.0018	53.891	K	S	+		@S:17		SATSGDIWPGL[s]A[y]DN[s]PR	BCLF1_MOUSE;S221
845	SAVQCSHLWDIAGR	57.021465@C:5,79.966331@S:6	24.2	560.584	3	1678.73	0.0014	25.643	K	F	+		@S:6		[s]AVQC[s]HLWDIAGR	K1984_MOUSE;S313
846	SAYQDYDSDSDVPEELKR	79.966331@S:10	28	732.9705	3	2195.89	0	36.517	K	D	+		@S:10		SAYQD[y]D[s]D[s]DVPEELKR	CC132_MOUSE;S561
847	SAYQDYDSDSDVPEELKR	79.966331@S:8	29.6	732.9707	3	2195.89	0.0007	36.667	K	D	+		@S:8		[s]A[y]QD[y]D[s]D[s]DVPEELKR	CC132_MOUSE;S559
848	SAYQDYDSDSDVPEELKR	79.966331@Y:6	27.4	732.9695	3	2195.887	-0.003	36.196	K	D	+		@Y:6		SA[y]QD[y]D[s]D[s]DVPEELKR	CC132_MOUSE;Y557
849	SDAEEDGVTGSQDEEDSKPK	79.966331@S:11	43.9	734.9574	3	2201.85	0.0018	24.096	K	A	+		@S:11		SDAEEDGV[t]G[s]QDEED[s]KPK	CALX_MOUSE;S563
850	SDEEDEDSDFGEEQR	79.966331@S:8	52.5	933.8105	2	1865.606	-0.0047	25.599	R	D	+		@S:8		SDEEDED[pS]DFGEEQR	GPAT1_MOUSE;S694
851	SDEEDEDSDFGEEQRDCYLK	57.021465@C:17,79.966331@S:8	77.5	849.3105	3	2544.91	-0.0016	36.436	R	V	+		@S:8		SDEEDED[pS]DFGEEQRDCYLK	GPAT1_MOUSE;S694
852	SDISERPSVDDVESETGSTGALETR	79.966331@S:14	47.4	906.3963	3	2716.167	-0.004	37.591	R	S	+		@S:14		SDISERPSVDDVE[s]E[t]G[s][t]GALETR	C2C2L_MOUSE;S619
853	SDISERPSVDDVESETGSTGALETR	79.966331@S:8,79.966331@S:14	43.8	933.0532	3	2796.138	0.0001	38.164	R	S	+		@S:8,@S:14		SDI[s]ERP[s]VDDVE[s]E[t]G[s][t]GALETR	C2C2L_MOUSE;S613,C2C2L_MOUSE;S619
854	SDISERPSVDDVESETGSTGALETR	79.966332@T:16,79.966331@S:18	23.4	933.0518	3	2796.134	-0.0041	38.859	R	S	+		@T:16,@S:18		SDISERP[s]VDDVE[s]E[t]G[s][t]GALETR	C2C2L_MOUSE;T621,C2C2L_MOUSE;S623
855	SDLIEDEELEDTGKGSEDEWEQVGPK	79.966331@S:16	93.3	1005.427	3	3013.259	-0.0009	48.38	R	N	+		@S:16		SDLIEDEELEDTGKG[pS]EDEWEQVGPK	UBP10_MOUSE;S570
856	SDNEETLGRPAQPPNAGESPHSPGVEDAPIAK	79.966331@S:22	33.8	837.6348	4	3346.51	0	38.788	K	V			@S:22		SDNEETLGRPAQPPNAGE[s]PH[s]PGVEDAPIAK	LIMA1_MOUSE;S488
857	SEDDSAKFDSNEEDTASVFAPSFGLK	79.966331@S:10	47.2	958.4064	3	2872.197	0.001	55.333	K	Q	+		@S:10		SEDD[s]AKFD[s]NEED[t]A[s]VFAPSFGLK	TOP2B_MOUSE;S1453
858	SEDDSAKFDSNEEDTASVFAPSFGLK	79.966332@T:15	25.8	958.4055	3	2872.195	-0.0018	56.156	K	Q	+		@T:15		[s]EDD[s]AKFD[s]NEED[t]A[s]VFAPSFGLK	TOP2B_MOUSE;T1458
859	SEDRPSSPQVSVAAVETK	79.966331@S:6	54.6	656.3082	3	1965.903	-0.0015	28.536	R	E	+		@S:6		[s]EDRP[s][s]PQVSVAAVETK	TP53B_MOUSE;S261
860	SEDSGIGLSASSPELSEHLR	79.966331@S:4	75.9	717.658	3	2149.952	-0.0005	41.675	K	V	+		@S:4		[s]ED[s]GIGLSASSPELSEHLR	DOP2_MOUSE;S589
861	SEQPLSQVLPSLSPEHK	79.966331@S:11	57.4	652.6544	3	1954.941	0.0013	56.026	K	E	+		@S:11		SEQPLSQVLP[s]L[s]PEHK	SRRM2_MOUSE;S1214
862	SEQPLSQVLPSLSPEHK	79.966331@S:13	52.6	652.654	3	1954.94	0.0002	46.172	K	E	+		@S:13		SEQPLSQVLP[s]L[s]PEHK	SRRM2_MOUSE;S1216
863	SESPKEPEQLR	79.966331@S:3	38.7	460.5448	3	1378.613	-0.0005	20.486	K	K	+		@S:3		[s]E[s]PKEPEQLR	ROA1_MOUSE;S6
864	SESPPPLSEPK	79.966331@S:3	38.4	624.2807	2	1246.547	-0.0014	25.416	R	Q	+		@S:3		SE[pS]PPPLSEPK	BRD3_MOUSE;S262
865	SETNWESPK	79.966331@S:7	22.4	579.229	2	1156.443	-0.0004	23.193	K	Q	+		@S:7		SETNWE[pS]PK	LYRIC_MOUSE;S565
866	SFDQLTPEESK	79.966331@S:10	36.9	680.7871	2	1359.56	0.0001	41.129	K	E	+		@S:10		SFDQLTPEE[pS]K	CALU_MOUSE;S69
867	SFDQLTPEESKER	79.966331@S:10	33.1	549.2416	3	1644.703	-0.0002	28.602	K	L	+		@S:10		SFDQL[t]PEE[s]KER	CALU_MOUSE;S69
868	SFISSSPSSPSR	79.966331@S:11	42.2	659.7877	2	1317.561	0.0006	34.905	K	A			@S:11		SFI[s][s][s]P[s][s]P[s]R	SRBS2_MOUSE;S384
869	SFISSSPSSPSR	79.966331@S:9	45.6	659.7864	2	1317.558	-0.0019	27.191	K	A			@S:9		SFISSSP[s][s]P[s]R	SRBS2_MOUSE;S382
870	SFLSEPSSPGR	79.966331@S:8	48.9	622.2712	2	1242.528	-0.0004	32.728	R	S	+		@S:8		SFLSEP[s][s]PGR	VIR_MOUSE;S1578
871	SFSISPVR	79.966331@S:1,79.966331@S:5	25.6	526.7141	2	1051.414	-0.0005	41.277	R	L	+		@S:1,@S:5		[s]F[s]I[s]PVR	SON_MOUSE;S2027,SON_MOUSE;S2031
872	SFSLASSGNSPISQR	79.966331@S:10	68.4	809.3666	2	1616.719	-0.0009	36.357	R	R	+		@S:10		SFSLAS[s]GN[s]PISQR	OSB11_MOUSE;S186
873	SFSLDPLMER	15.994915@M:8,79.966331@S:3	42.5	645.7746	2	1289.535	-0.0017	48.587	R	R	+		@S:3		[s]F[s]LDPLMER	TENC1_MOUSE;S120
874	SFTSGPGAR	79.966331@S:1	22.9	480.2022	2	958.3898	-0.0011	18.964	R	I	+		@S:1		[s]F[t][s]GPGAR	K2C8_MOUSE;S24
875	SGEGEVSGLLR	79.966331@S:1	87.6	592.2711	2	1182.528	-0.0006	37.887	R	K	+		@S:1		[pS]GEGEVSGLLR	TIF1B_MOUSE;S473
876	SGEGEVSGLLRK	79.966331@S:1	39.2	656.3186	2	1310.623	-0.0005	31.451	R	V	+		@S:1		[pS]GEGEVSGLLRK	TIF1B_MOUSE;S473
877	SGKLSQELDFVSHNVR	79.966331@S:5	85.9	632.6381	3	1894.892	-0.0012	36.006	K	T	+		@S:5		[s]GKL[s]QELDFVSHNVR	NUCB1_MOUSE;S85
878	SGSPKLDPSEVYLK	79.966331@S:3	29.5	533.9274	3	1598.76	0.0011	46.449	R	S			@S:3		[s]G[s]PKLDPSEVYLK	MAGI3_MOUSE;S702
879	SGVAVPTSPK	79.966331@S:8	19.3	511.7496	2	1021.485	0	22.71	R	G	+	ambiguos		@T:7orS:8	[s]GVAVP[t][s]PK	PDCD4_MOUSE;T93orS94
880	SGYHDDSDEDLLE	79.966331@S:7	16.8	787.7802	2	1573.546	0.0001	35.664	K	-	+		@S:7		[s]G[y]HDD[s]DEDLLE	SORT_MOUSE;S819
881	SGYHDDSDEDLLE	79.966331@Y:3	17	787.7803	2	1573.546	0.0004	35.512	K	-	+		@Y:3		[s]G[y]HDD[s]DEDLLE	SORT_MOUSE;Y815
882	SHFTPNSRSPTEPK	79.966331@S:7	23.1	555.5859	3	1663.736	0.0005	23.792	R	-	+		@S:7		SHF[t]PN[s]R[s]P[t]EPK	HGD_MOUSE;S438
883	SHFTPNSRSPTEPK	79.966332@T:4	20.4	555.586	3	1663.736	0.0007	18.121	R	-	+		@T:4		SHF[t]PN[s]R[s]P[t]EPK	HGD_MOUSE;T435
884	SHGQDYLVGNR	79.966331@S:1	34.8	663.2853	2	1324.556	-0.0001	23.29	K	L	+		@S:1		[pS]HGQDYLVGNR	GSTA1_MOUSE;S142,GSTA3_MOUSE;S142,GSTA2_MOUSE;S142
885	SHSGPAGSFNKPAIR	79.966331@S:3	37.1	535.9224	3	1604.745	-0.0007	22.367	R	I	+		@S:3		[s]H[s]GPAGSFNKPAIR	ERRFI_MOUSE;S251
886	SHSLDDLQGDADVGK	79.966331@S:1	22.1	546.2333	3	1635.678	0.0003	38.036	R	N			@S:1		[s]H[s]LDDLQGDADVGK	SASH1_MOUSE;S829
887	SHSLDDLQGDADVGK	79.966331@S:3	53.5	818.8449	2	1635.675	-0.0026	30.367	R	N	+		@S:3		[s]H[s]LDDLQGDADVGK	SASH1_MOUSE;S831
888	SHSLPNSLDYAQASER	79.966331@S:1	68.8	618.9384	3	1853.793	-0.0011	32.804	R	G			@S:1		[s]H[s]LPN[s]LDYAQASER	RMD3_MOUSE;S44
889	SHSLPNSLDYAQASER	79.966331@S:1,79.966331@S:3	43.8	645.5942	3	1933.761	0.0001	34.486	R	G	+		@S:1,@S:3		[s]H[s]LPN[s]LDYAQASER	RMD3_MOUSE;S44,RMD3_MOUSE;S46
890	SHSLPNSLDYAQASER	79.966331@S:1,79.966331@S:7	46.6	645.5941	3	1933.76	-0.0002	34.072	R	G	+		@S:1,@S:7		[s]H[s]LPN[s]LDYAQASER	RMD3_MOUSE;S44,RMD3_MOUSE;S50
891	SHSLPNSLDYAQASER	79.966331@S:3	87.1	927.9022	2	1853.79	-0.0047	32.628	R	G	+		@S:3		[s]H[s]LPN[s]LDYAQASER	RMD3_MOUSE;S46

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
892	SHSLPNSLDYAQASER	79.966331@S:3,79.966331@S:7	42.8	645.5935	3	1933.759	-0.0022	34.421	R	G	+		@S:3,@S:7		[s]H[s]LPNSLDYAQASER	RMD3_MOUSE;S46,RMD3_MOUSE;S50
893	SHSLPNSLDYAQASER	79.966331@S:7	64.3	618.9388	3	1853.795	0	40.872	R	G			@S:7		[s]H[s]LPN[s]LDYAQASER	RMD3_MOUSE;S50
894	SHSRQASTDAGTAGALTPQHVR	79.966331@S:3,79.966331@S:7	44.3	602.768	4	2407.043	-0.0002	29.184	K	A	+		@S:3,@S:7		[s]H[s]RQA[s][t]DAG[t]AGAL[t]PQHVR	YAP1_MOUSE;S90,YAP1_MOUSE;S94
895	SHSRQASTDAGTAGALTPQHVR	79.966331@S:3,79.966332@T:8	42.5	602.768	4	2407.043	-0.0003	21.619	K	A	+		@S:3,@T:8		[s]H[s]RQA[s][t]DAG[t]AGALTPQHVR	YAP1_MOUSE;S90,YAP1_MOUSE;T95
896	SIAAELDELADDR	79.966331@S:1	98.7	749.3269	2	1496.639	-0.0003	56.699	R	M	+		@S:1		[pS]IAAELDELADDR	STX16_MOUSE;S41
897	SIFREESPLR	79.966331@S:7	30.5	438.5468	3	1312.619	0.0009	31.04	K	I	+		@S:7		SIFREE[pS]PLR	BCLF1_MOUSE;S529
898	SISFPEVPRSPK	79.966331@S:3,79.966331@S:10	35.2	501.8931	3	1502.657	0.0002	41.298	R	Q	+		@S:3,@S:10		[s]I[s]FPEVPR[s]PK	SVIL_MOUSE;S220,SVIL_MOUSE;S227
899	SISSRSSLSR	79.966331@S:9	20.7	580.2785	2	1158.542	0.003	21.003	R	H	+	ambiguos		@S:7orS:9	[s]I[s][s]R[s][s]L[s]R	F178A_MOUSE;S221orS223
900	SISTVDLTEK	79.966331@S:3	43.5	586.7759	2	1171.537	0	32.751	R	S	+		@S:3		[s]I[s][t]VDLTEK	BI2L1_MOUSE;S421
901	SKESLQEAGKSDANTDLIGGSPK	79.966331@S:11	47.9	603.7882	4	2411.124	0.0018	35.534	K	G			@S:11		[s]KE[s]LQEAGK[s]DAN[t]DLIGGSPK	MOT1_MOUSE;S220
902	SKESLQEAGKSDANTDLIGGSPK	79.966331@S:4	80.5	804.7129	3	2411.117	-0.0047	27.777	K	G	+		@S:4		[s]KE[s]LQEAGKSDANTDLIGGSPK	MOT1_MOUSE;S213
903	SKFDSDEEDEDAENLEAVSSGK	79.966331@S:1	51.3	827.6653	3	2479.974	-0.001	38.37	R	V	+	ambiguos		@S:1orS:5	[s]KFD[s]DEEDEDAENLEAVSSGK	PNISR_MOUSE;S286orS290
904	SKFDSDEEDEDAENLEAVSSGK	79.966331@S:5	31.9	827.6649	3	2479.973	-0.0021	38.512	R	V	+		@S:5		[s]KFD[s]DEEDEDAENLEAVSSGK	PNISR_MOUSE;S290
905	SKPVFSESLSD	79.966331@S:10	47.9	638.2789	2	1274.543	0	43.191	K	-	+		@S:10		SKPVF[s]E[s]L[s]D	TIM8A_MOUSE;S96
906	SKPVFSESLSD	79.966331@S:6	32.4	638.2789	2	1274.543	0.0001	34.295	K	-	+		@S:6		SKPVF[s]E[s]L[s]D	TIM8A_MOUSE;S92
907	SKPVFSESLSD	79.966331@S:8	40.4	638.2788	2	1274.543	-0.0001	34.222	K	-	+		@S:8		SKPVF[s]E[s]L[s]D	TIM8A_MOUSE;S94
908	SKSEEAHAEDSVMDHHFR	79.966331@S:3	22.1	548.7269	4	2190.878	-0.0006	25.994	K	K	+		@S:3		[s]K[s]EEAHAED[s]VMDHHFR	PAIRB_MOUSE;S329
909	SLAALDALNTDDENDEEEYEAWK	79.966332@T:10	53	907.7073	3	2720.1	-0.0014	58.431	R	V	+		@T:10		SLAALDALN[pT]DDENDEEEYEAWK	MFAP1_MOUSE;T267
910	SLALTFAIGGSLLAGMKYFKK	15.994915@M:16,79.966332@T:5,79.966331@Y:18	34.3	598.7993	4	2391.168	-0.0032	28.997	K	E		ambiguos	@Y:18	@S:1orT:5	[s]LAL[t]FAIGG[s]LLAGMK[y]FKK	SCO1_MOUSE;Y97,SCO1_MOUSE;S80orT84
911	SLDSDESEDEDDDYQQK	79.966331@S:1	98.7	1049.365	2	2096.716	-0.0063	26.279	K	R	+	ambiguos		@S:1orS:4	SLD[pS]DESEDEDDDYQQK	HAP28_MOUSE;S57orS60
912	SLDSDESEDEDDDYQQK	79.966331@S:4	83.4	1049.366	2	2096.717	-0.0048	25.899	K	R	+		@S:4		[s]LD[s]DE[s]EDEDDDYQQK	HAP28_MOUSE;S60
913	SLDSDESEDEDDDYQQK	79.966331@S:4,79.966331@S:7	81.7	1089.348	2	2176.682	-0.0061	27.701	K	R	+		@S:4,@S:7		[s]LD[s]DESEDEDDDYQQK	HAP28_MOUSE;S60,HAP28_MOUSE;S63
914	SLEELFQVK	79.966331@S:1	35.3	586.7845	2	1171.554	0.0018	54.684	K	M	+		@S:1		[pS]LEELFQVK	CGNL1_MOUSE;S679
915	SLERAEAGDNLGALVR	79.966331@S:1	32.1	584.2877	3	1749.841	0.0003	39.029	K	G	+		@S:1		[pS]LERAEAGDNLGALVR	EFTU_MOUSE;S312
916	SLGLSDDDIVK	79.966331@S:1	23.5	621.2868	2	1240.559	0.0002	33.656	K	F	+		@S:1		[s]LGL[s]DDDIVK	SYLC_MOUSE;S165
917	SLGQWLQEEK	79.966331@S:1	56.1	649.2949	2	1296.575	0.0002	48.99	K	V	+		@S:1		[pS]LGQWLQEEK	CPSM_MOUSE;S148
918	SLLDASEEAIKK	79.966331@S:1	38.1	692.3415	2	1382.668	-0.0009	35.065	K	D	+		@S:1		[pS]LLDASEEAIKK	VINC_MOUSE;S721
919	SLPEESGEETDTVDPVTLYSYK	79.966331@S:6	58.1	1270.053	2	2538.092	-0.0017	60.427	R	V	+		@S:6		[s]LPEE[s]GEE[t]DTVDPVTLYSYK	ITIH2_MOUSE;S60
920	SLPTTVPESPNYR	79.966331@S:9	38.3	770.8564	2	1539.698	0.0012	41.539	R	N	+		@S:9		SLPTTVPE[pS]PNYR	LARP1_MOUSE;S751
921	SLPVSICR	57.021465@C:7,79.966331@S:1	22.9	506.2381	2	1010.462	-0.0004	43.873	R	S	+		@S:1		[s]LPV[s]ICR	SASH1_MOUSE;S805
922	SLQSLLGPSSK	79.966331@S:1	46	598.7997	2	1195.585	-0.0001	41.696	R	F	+		@S:1		[s]LQ[s]LLGPSSK	CORO7_MOUSE;S459
923	SLSPLGGRDESPVSHR	79.966331@S:3,79.966331@S:11	36.4	618.6033	3	1852.788	0.001	34.902	R	A	+		@S:3,@S:11		[s]L[s]PLGGRDE[s]PV[s]HR	CDK13_MOUSE;S318,CDK13_MOUSE;S326
924	SLSPLSGTTDTK	79.966331@S:3	62.7	643.7971	2	1285.58	-0.0007	28.703	R	A	+		@S:3		SL[pS]PLSGTTDTK	ACINU_MOUSE;S479
925	SLSPLSGTTDTKAESPAGR	79.966331@S:1,79.966331@S:15	43.3	678.9643	3	2033.871	0.0003	38.142	R	V	+		@S:1,@S:15		[s]L[s]PL[s]G[t][t]D[t]KAE[s]PAGR	ACINU_MOUSE;S477,ACINU_MOUSE;S491
926	SLSPLSGTTDTKAESPAGR	79.966331@S:15	36	652.3076	3	1953.901	-0.0034	27.844	R	V	+		@S:15		SLSPL[s]G[t][t]D[t]KAE[s]PAGR	ACINU_MOUSE;S491
927	SLSPLSGTTDTKAESPAGR	79.966331@S:3,79.966331@S:6	38.8	678.9641	3	2033.87	-0.0002	31.175	R	V	+		@S:3,@S:6		[s]L[s]PL[s]G[t][t]D[t]KAE[s]PAGR	ACINU_MOUSE;S479,ACINU_MOUSE;S482
928	SLSPLSGTTDTKAESPAGR	79.966332@T:11	44.4	652.3081	3	1953.902	-0.0019	27.53	R	V	+		@T:11		SL[s]PL[s]G[t][t]D[t]KAE[s]PAGR	ACINU_MOUSE;T487
929	SLSPPWEQDR	79.966331@S:3	28.7	647.7772	2	1293.54	0.0007	42.516	R	R	+		@S:3		[s]L[s]PPWEQDR	CTGE5_MOUSE;S573
930	SLSPPWEQDRR	79.966331@S:3	40.6	484.2208	3	1449.641	0.0003	45.461	R	M	+		@S:3		SL[pS]PPWEQDRR	CTGE5_MOUSE;S573
931	SLSSAFRAVSNDPRIITWR	79.966331@S:1,79.966331@S:3,79.966331@S:4,79.966331@S:10,79.966332@T:17	19.4	859.3348	3	2574.983	-0.0041	45.407	M	I	+		@S:1,@S:3,@S:4,@S:10,@T:17		[pS]L[pS][pS]AFRAV[pS]NDPRII[pT]WR	AVIL_MOUSE;S2,AVIL_MOUSE;S4,AVIL_MOUSE;S5,AVIL_MOUSE;S11,AVIL_MOUSE;T18
932	SLSTSGESLYHVLGLDK	79.966331@S:3	27.8	629.303	3	1884.887	0.0002	60.414	R	N	+		@S:3		[s]L[s][t][s]GE[s]L[y]HVLGLDK	DNJC5_MOUSE;S10
933	SLSVTSLGGLPVWEAER	79.966331@S:3,79.966331@S:6	79.1	980.9427	2	1959.871	-0.0036	67.19	R	L	+		@S:3,@S:6		[s]L[s]V[t][s]LGGLPVWEAER	GYS2_MOUSE;S8,GYS2_MOUSE;S11
934	SLSYSPVER	79.966331@S:3,79.966331@S:5	24.7	599.233	2	1196.451	-0.0002	32.472	R	R	+		@S:3,@S:5		[s]L[s][y][s]PVER	SRRM2_MOUSE;S2646,SRRM2_MOUSE;S2648
935	SLSYSPVER	79.966331@S:3,79.966331@Y:4	21.5	599.2331	2	1196.452	0.0001	38.668	R	R	+		@S:3,@Y:4		[s]L[s][y][s]PVER	SRRM2_MOUSE;S2646,SRRM2_MOUSE;Y2647
936	SLSYSPVER	79.966331@S:5	27.9	559.2496	2	1116.485	-0.0005	28.467	R	R	+		@S:5		SL[s][y][s]PVER	SRRM2_MOUSE;S2648
937	SNSSEASSGDFLDLK	79.966331@S:3	71	818.8405	2	1635.666	0	46.018	R	G	+		@S:3		[s]N[s][s]EASSGDFLDLK	HN1_MOUSE;S87
938	SPFNSPSPQDSPR	79.966331@S:7	61.3	748.3136	2	1494.613	-0.0014	27.155	K	L	+		@S:7		SPFNSP[s]PQD[s]PR	NFIC_MOUSE;S339
939	SPGETSKPRPFAGGGYR	79.966331@S:1	22.7	615.2875	3	1842.841	-0.0008	21.99	K	L	+		@S:1		[s]PGE[t][s]KPRPFAGGG[y]R	NSF1C_MOUSE;S140

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
940	SPLQSVVVR	79.966331@S:1	32.1	532.7787	2	1063.543	0.0002	40.269	K	R	+		@S:1		[pS]PLQSVVVR	TR150_MOUSE;S253
941	SPSGGAAGPLLTPSQSLDGSR	79.966331@S:1	49.9	1017.977	2	2033.939	-0.0027	42.718	R	R	+		@S:1		[s]P[s]GGAAGPLLTPSQSLDGSR	KCD12_MOUSE;S187
942	SPSKEPHFTDFEGK	79.966331@S:3	31	562.5786	3	1684.714	0.0006	38.457	K	T	+		@S:3		[s]P[s]KEPHFTDFEGK	S38A3_MOUSE;S53
943	SPSPAPPPPPPPPPR	79.966331@S:1,79.966331@S:3	24.3	582.2665	3	1743.778	-0.0011	31.123	R	R	+		@S:1,@S:3		[pS]P[pS]PAPPPPPPPPPR	SRRM1_MOUSE;S572,SRRM1_MOUSE;S574
944	SPSPGRREEDGDELAR	79.966331@S:3	22.6	617.605	3	1849.793	-0.0023	19.335	R	R	+		@S:3		[s]P[s]PGRREEDGDELAR	HEM6_MOUSE;S101
945	SPSPVHLPEDPK	79.966331@S:3	26.3	461.5498	3	1381.628	-0.0002	27.858	R	V	+		@S:3		[s]P[s]PVHLPEDPK	LAR4B_MOUSE;S603
946	SPVGKSPPATGSAYGSSQK	79.966332@T:10	33	629.295	3	1884.863	0.0012	26.819	K	E	+		@T:10		[s]PVGK[s]PPA[t]G[s]AYGSSQK	TR150_MOUSE;T324
947	SQDATVSPGSEQSEKSPGPIVSR	79.966331@S:16	36.3	808.3722	3	2422.095	-0.0066	25.373	R	T	+		@S:16		SQDATV[s]PG[s]EQ[s]EK[s]PGPIV[s]R	NIPA_MOUSE;S343
948	SQEPISNDQKVSDDDKEK	79.966331@S:6	23.6	714.645	3	2140.913	-0.0029	18.198	K	G	+		@S:6		SQEPI[s]NDQKV[s]DDDKEK	LYRIC_MOUSE;S417
949	SQGPEASGRSLTDR	79.966331@S:1	19.9	514.2294	3	1539.666	-0.0014	33.56	R	Q			@S:1		[s]QGPEA[s]GR[s]L[t]DR	CXA10_MOUSE;S389
950	SQKNGMESLSKYKPSSSFTVSK	79.966331@S:8,79.966331@S:10,79.966331@S:15	29	665.7821	4	2659.099	-0.0049	17.379	K	V	+		@S:8,@S:10,@S:15		[s]QKNGME[s]L[s]K[y]KP[s][s][s]F[t]V[s]K	CRLD2_MOUSE;S367,CRLD2_MOUSE;S369,CRLD2_MOUSE;S374
951	SQLSPVKTK	79.966331@S:4	21.1	534.2771	2	1066.54	-0.0027	21.624	R	K			@S:4		[s]QL[s]PVK[t]K	IF2M_MOUSE;S83
952	SQNNFVAILDLPEGEHQYK	79.966331@S:1	43.3	1141.526	2	2281.038	-0.0034	55.639	R	F	+		@S:1		[pS]QNNFVAILDLPEGEHQYK	AAKB1_MOUSE;S108
953	SQSGEDESLNQPGPIK	79.966331@S:1	36.1	589.2595	3	1764.757	0.0001	35.629	R	T			@S:1		[s]Q[s]GEDE[s]LNQPGPIK	PEX1_MOUSE;S1210
954	SQSGEDESLNQPGPIK	79.966331@S:3	99.3	883.385	2	1764.755	-0.0012	35.624	R	T	+		@S:3		[s]Q[s]GEDESLNQPGPIK	PEX1_MOUSE;S1212
955	SQSLIIR	79.966331@S:3	34.1	448.7337	2	895.4528	0.0001	28.962	R	T	+		@S:3		[s]Q[s]LIIR	P3C2A_MOUSE;S339
956	SQSLPTTLLSPVR	79.966331@S:1,79.966331@S:3	26.9	779.8669	2	1557.719	-0.0012	56.996	R	V	+		@S:1,@S:3		[s]Q[s]LP[t][t]LLSPVR	SSFA2_MOUSE;S736,SSFA2_MOUSE;S738
957	SQSPLRGGMTEAAQTDK	79.966331@S:3	34	619.6106	3	1855.81	-0.0034	25.27	R	Q	+		@S:3		[s]Q[s]PLRGGMTEAAQTDK	BAG3_MOUSE;S138
958	SQSPSPPPLPEDLEK	79.966331@S:1	26.6	850.8931	2	1699.772	0.0011	39.667	K	A	+	ambiguos		@S:1orS:3	[s]Q[s]P[s]PPPLPEDLEK	ACINU_MOUSE;S387orS389
959	SQSPSPPPLPEDLEK	79.966331@S:1,79.966331@S:5	31.4	890.875	2	1779.735	-0.0015	51.594	K	A	+		@S:1,@S:5		[s]Q[s]P[s]PPPLPEDLEK	ACINU_MOUSE;S387,ACINU_MOUSE;S391
960	SQSPSPPPLPEDLEK	79.966331@S:3	59.2	850.8922	2	1699.77	-0.0007	47.811	K	A	+		@S:3		SQ[pS]P[pS]PPPLPEDLEK	ACINU_MOUSE;S389
961	SQSPSPPPLPEDLEK	79.966331@S:3,79.966331@S:5	51.6	890.8753	2	1779.736	-0.0009	45.354	K	A	+		@S:3,@S:5		[s]Q[s]PSPPPLPEDLEK	ACINU_MOUSE;S389,ACINU_MOUSE;S391
962	SQSPSPPPLPEDLEK	79.966331@S:5	52.2	850.8917	2	1699.769	-0.0017	39.476	K	A	+		@S:5		[s]Q[s]P[s]PPPLPEDLEK	ACINU_MOUSE;S391
963	SQSSHSYDDSTLPLIDR	79.966331@S:6	25.6	667.6241	3	1999.85	-0.002	38.934	R	N		ambiguos		@S:1orS:3orS:4orS:6	[s]Q[s][s]H[s][y]DD[s][t]LPLIDR	CTND1_MOUSE;S859orS861orS862orS864
964	SQSSHSYDDSTLPLIDR	79.966331@Y:7	27.1	667.6248	3	1999.853	0.0001	48.042	R	N			@Y:7		[s]Q[s][s]H[s][y]DDSTLPLIDR	CTND1_MOUSE;Y865
965	SQVDNGSMKGGER	79.966331@S:7	19.6	482.202	3	1443.584	0.0029	24.787	K	L	+	ambiguos		@S:1orS:7	[s]QVDNG[s]MKGGER	TTF2_MOUSE;S772orS778
966	SRDDLYDPDDPRDLPHSR	79.966331@S:1	27.7	562.9955	4	2247.953	-0.0016	30.412	R	D	+		@S:1		[s]RDDL[y]DPDDPRDLPHSR	LSR_MOUSE;S473
967	SRGSPSSYTSASSSPR	79.966331@S:4	19.6	565.2439	3	1692.71	-0.0005	18.652	R	Y	+		@S:4		[s]RG[s]P[s][s][y][t][s]A[s][s][s]PR	EPN3_MOUSE;S175
968	SRLIQLK	79.966331@S:1	28.7	469.2652	2	936.5158	0.0001	43.227	K	K	+		@S:1		[pS]RLIQLK	ASH1L_MOUSE;S2001
969	SRPSAGERRAGSQR	79.966331@S:12	26.4	532.2579	3	1593.752	0.0035	25.937	R	A	+		@S:12		[s]RP[s]AGERRAG[s]QR	SUV92_MOUSE;S57
970	SRSGEGEVSGLLR	79.966331@S:3	30.7	476.2275	3	1425.661	-0.0007	31.235	R	K		ambiguos		@S:1orS:3	[s]R[s]GEGEVSGLLR	TIF1B_MOUSE;S471orS473
971	SRSPVDSPVPASMFAPEPSSPGAAR	79.966331@S:3,79.966331@S:20	55.7	886.3862	3	2656.137	-0.0027	47.706	R	A			@S:3,@S:20		[s]R[s]PVDSPVPASMFAPEP[s][s]PGAAR	GTPB1_MOUSE;S8,GTPB1_MOUSE;S25
972	SRSRDDLYDPDDPR	79.966331@S:3	17.4	596.251	3	1785.731	-0.0008	23.367	R	D	+		@S:3		[s]R[s]RDDL[y]DPDDPR	LSR_MOUSE;S473
973	SRTASGSSVTSLEGTR	79.966331@S:1,79.966332@T:3	29.6	585.9153	3	1754.724	0.0003	34.294	R	S			@S:1,@T:3		[s]R[t]A[s]GSSVTSLEGTR	NDRG1_MOUSE;S326,NDRG1_MOUSE;T328
974	SRTASGSSVTSLEGTR	79.966332@T:3,79.966331@S:5	34.7	585.9148	3	1754.723	-0.0012	26.831	R	S	+	ambiguos	@S:5	@S:1orT:3	[s]R[t]A[s]G[s][s]VTSLEGTR	NDRG1_MOUSE;S330,NDRG1_MOUSE;S326orT328
975	SRTPLLPR	79.966331@S:1,79.966332@T:3	20	367.1734	3	1098.498	-0.0005	27.835	R	K	+		@S:1,@T:3		[pS]R[pT]PLLPR	SRRM2_MOUSE;S1984,SRRM2_MOUSE;T1986
976	SRTSVQTEDDQLIAGQSAR	79.966331@S:4	30.9	714.6654	3	2140.974	-0.0007	28.136	R	A		ambiguos		@T:3orS:4	[s]R[t][s]VQ[t]EDDQLIAGQSAR	CTNA2_MOUSE;T653orS654,CTNA1_MOUSE;T654orS655
977	SRTSVQTEDDQLIAGQSAR	79.966331@S:4,79.966332@T:7	45.5	741.3212	3	2220.942	0.0004	38.327	R	A			@S:4,@T:7		[s]R[t][s]VQ[t]EDDQLIAGQSAR	CTNA2_MOUSE;S654,CTNA2_MOUSE;T657,CTNA1_MOUSE;S655,CTNA1_MOUSE;T658
978	SRTSVQTEDDQLIAGQSAR	79.966332@T:3,79.966331@S:4	46.6	741.3217	3	2220.943	0.0019	38.251	R	A			@T:3,@S:4		[s]R[t][s]VQ[t]EDDQLIAGQSAR	CTNA2_MOUSE;T653,CTNA2_MOUSE;S654,CTNA1_MOUSE;T654,CTNA1_MOUSE;S655
979	SRTSVQTEDDQLIAGQSAR	79.966332@T:7	45.7	714.6658	3	2140.976	0.0006	36.227	R	A			@T:7		[s]R[t][s]VQ[t]EDDQLIAGQSAR	CTNA2_MOUSE;T657,CTNA1_MOUSE;T658
980	SSGSLSPGLETEDPLEAR	79.966331@S:2,79.966331@S:6	30.6	1002.913	2	2003.811	-0.0011	50.699	K	E	+	ambiguos	@S:6	@S:2orS:4	[s][s]G[s]L[s]PGLE[t]EDPLEAR	TB182_MOUSE;S1375,TB182_MOUSE;S1371orS1373
981	SSGSLSPGLETEDPLEAR	79.966331@S:4,79.966331@S:6	34.8	1002.915	2	2003.815	0.0024	49.8	K	E	+		@S:4,@S:6		[s][s]G[s]L[s]PGLETEDPLEAR	TB182_MOUSE;S1373,TB182_MOUSE;S1375
982	SSGSLSPGLETEDPLEAR	79.966331@S:6	53.4	962.9304	2	1923.846	0	45.268	K	E	+		@S:6		[s][s]G[s]L[s]PGLETEDPLEAR	TB182_MOUSE;S1375
983	SSGSPYGGGYGSGGGSGGYGSR	79.966331@S:12	23.6	664.2571	3	1989.749	0.0003	25.623	R	R	+		@S:12		[s][s]G[s]P[y]GGG[y]G[s]GGG[s]GG[y]G[s]R	ROA3_MOUSE;S367

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
984	SSGSPYGGGYGSGGGSGGYGSR	79.966331@S:4	53.1	664.2571	3	1989.749	0.0004	32.025	R	R	+		@S:4		[s][s]G[s]P[y]GGG[y]G[s]GGGSGGYGSR	ROA3_MOUSE;S359
985	SSGSPYGGGYGSGGGSGGYGSR	79.966331@Y:6	61.4	664.2573	3	1989.75	0.001	31.95	R	R	+		@Y:6		[s][s]G[s]P[y]GGG[y]G[s]GGGSGGYGSR	ROA3_MOUSE;Y361
986	SSLPHSQENLPK	79.966331@S:6	27.4	708.8283	2	1415.642	-0.0025	21.55	K	L	+		@S:6		SSLPH[pS]QENLPK	IRF3_MOUSE;S135
987	SSLVLSMLQQMLMEDK	15.994915@M:11,15.994915@M:13,79.966331@S:2	24.1	491.9748	4	1963.87	-0.0004	27.394	R	A	+		@S:2		[s][s]LVL[s]MLQQMLMEDK	K1468_MOUSE;S638
988	SSMSGLHLVK	15.994915@M:3,79.966331@S:4	23.6	577.7678	2	1153.521	0.0009	32.588	R	Q	+		@S:4		[s][s]M[s]GLHLVK	ACACA_MOUSE;S79
989	SSMSGLHLVK	79.966331@S:4	30.2	569.7693	2	1137.524	-0.0012	31.073	R	Q	+		@S:4		[s][s]M[s]GLHLVK	ACACA_MOUSE;S79
990	SSPFKVSPLSFGR	79.966331@S:2,79.966331@S:7	24.1	523.5692	3	1567.686	0.0022	51.146	K	K	+	ambiguos	@S:7	@S:1orS:2	[s][s]PFKV[s]PL[s]FGR	SDPR_MOUSE;S293,SDPR_MOUSE;S287orS288
991	SSPKEEVASEPEEAASPTTPK	79.966331@S:2	63.9	751.0032	3	2249.988	-0.0063	24.009	K	K	+	ambiguos		@S:1orS:2	[s][s]PKEEVA[s]EPEEAASPTTPK	NOP56_MOUSE;S528orS529
992	SSPKEEVASEPEEAASPTTPK	79.966331@S:2,79.966331@S:9	48.8	1165.985	2	2329.955	-0.0055	27.198	K	K	+	ambiguos	@S:9	@S:1orS:2	[s][s]PKEEVA[s]EPEEAASPTTPK	NOP56_MOUSE;S536,NOP56_MOUSE;S528orS529
993	SSPKEEVASEPEEAASPTTPK	79.966331@S:9	83	751.0044	3	2249.991	-0.0027	23.982	K	K	+		@S:9		[s][s]PKEEVA[s]EPEEAA[s]P[t][t]PK	NOP56_MOUSE;S536
994	SSPKEEVASEPEEAASPTTPK	79.966331@S:9,79.966331@S:16	36.2	777.6597	3	2329.957	-0.0031	24.707	K	K	+		@S:9,@S:16		[s][s]PKEEVA[s]EPEEAASPTTPK	NOP56_MOUSE;S536,NOP56_MOUSE;S543
995	SSPPPLSGASEVDAGELGSER	79.966331@S:2	91.2	1061.469	2	2120.923	-0.0028	40.316	R	T	+		@S:2		[s][s]PPPLSGASEVDAGELGSER	D19L1_MOUSE;S23
996	SSPQLDPLRK	79.966331@S:2	29.7	407.5396	3	1219.597	0.0008	26.905	R	S	+		@S:2		[s][s]PQLDPLRK	LS14A_MOUSE;S183
997	SSRRSSSELSPEVVEK	79.966331@S:1,79.966331@S:7,79.966331@S:10	23.3	672.9409	3	2015.801	0.0007	26.517	R	V	+	ambiguos	@S:7,@S:10	@S:1orS:2	[s][s]RR[s][s][s]EL[s]PEVVEK	SRRM2_MOUSE;S1340,SRRM2_MOUSE;S1343,SRRM2_MOUSE;S1334orS1335
998	SSRRSSSELSPEVVEK	79.966331@S:2,79.966331@S:6	43.8	646.2845	3	1935.832	-0.0023	24.616	R	V	+		@S:2,@S:6		[s][s]RR[s][s][s]ELSPEVVEK	SRRM2_MOUSE;S1335,SRRM2_MOUSE;S1339
999	SSRRSSSELSPEVVEK	79.966331@S:5,79.966331@S:6	42.2	646.2854	3	1935.834	0.0005	32.604	R	V	+		@S:5,@S:6		[s][s]RR[s][s][s]ELSPEVVEK	SRRM2_MOUSE;S1338,SRRM2_MOUSE;S1339
1000	SSRRSSSELSPEVVEK	79.966331@S:6,79.966331@S:7	30.2	646.2847	3	1935.832	-0.0017	24.569	R	V	+		@S:6,@S:7		[s][s]RR[s][s][s]ELSPEVVEK	SRRM2_MOUSE;S1339,SRRM2_MOUSE;S1340
1001	SSSLGDLLR	79.966331@S:3	53.5	514.2444	2	1026.474	-0.0005	44.499	R	E	+		@S:3		[s][s][s]LGDLLR	PKHO2_MOUSE;S395
1002	SSSPTQYGLSR	79.966331@S:3	44.3	631.7741	2	1261.534	-0.0003	25.348	R	N			@S:3		[s][s][s]P[t]QYGLSR	MLTK_MOUSE;S638
1003	SSSPVTELTAR	79.966331@S:3	26.3	614.2845	2	1226.554	0	38.519	R	S	+		@S:3		[s][s][s]PV[t]ELTAR	SRRM2_MOUSE;S1068
1004	SSSPVTELTARSPVK	79.966331@S:2,79.966331@S:12	35.9	859.8911	2	1717.768	-0.0012	32.071	R	Q	+		@S:2,@S:12		[s][s][s]PVTELTAR[s]PVK	SRRM2_MOUSE;S1067,SRRM2_MOUSE;S1077
1005	SSSPVTELTARSPVK	79.966331@S:3,79.966331@S:12	32.5	859.891	2	1717.767	-0.0014	32.051	R	Q	+		@S:3,@S:12		[s][s][s]PV[t]EL[t]AR[s]PVK	SRRM2_MOUSE;S1068,SRRM2_MOUSE;S1077
1006	SSSPVTELTARSPVKQDK	79.966331@S:3,79.966331@S:12	46.6	697.3236	3	2088.949	-0.0005	35.608	R	S	+		@S:3,@S:12		[s][s][s]PV[t]EL[t]AR[s]PVKQDK	SRRM2_MOUSE;S1068,SRRM2_MOUSE;S1077
1007	SSSPVTELTARSPVKQDK	79.966331@S:3,79.966332@T:9	22.8	697.3239	3	2088.95	0.0004	35.538	R	S	+		@S:3,@T:9		[s][s][s]PV[t]EL[t]AR[s]PVKQDK	SRRM2_MOUSE;S1068,SRRM2_MOUSE;T1074
1008	SSSSSQESLNRPFSSK	79.966331@S:5	20.2	603.2663	3	1806.777	-0.0014	24.148	R	W	+		@S:5		[s][s][s][s][s]QE[s]LNRPF[s][s]K	CLAP2_MOUSE;S333
1009	SSSVGSSSSYPISSAGPR	79.966331@S:3	94.6	896.8901	2	1791.766	-0.002	30.211	R	T	+		@S:3		[s][s][s]VG[s][s][s]SYPISSAGPR	PLEC_MOUSE;S4393
1010	SSSVGSSSSYPISSAGPR	79.966331@S:3,79.966331@S:6	74.2	936.8754	2	1871.736	0.0023	41.39	R	T	+		@S:3,@S:6		[s][s][s]VGSSSSYPISSAGPR	PLEC_MOUSE;S4393,PLEC_MOUSE;S4396
1011	SSSVLSLEGSDK	79.966331@S:10	21.9	644.7871	2	1287.56	0.0001	33.751	R	G	+		@S:10		SSSVLSLEG[pS]DK	PKHG3_MOUSE;S766
1012	SSTPLPTVSSSAENTR	79.966332@T:3	46.7	857.3871	2	1712.76	-0.0021	27.582	R	Q	+		@T:3		[s][s][t]PLP[t]VSSSAENTR	LAP2A_MOUSE;T159,LAP2B_MOUSE;T159
1013	SSVLTVSNVYSSK	79.966331@S:1,79.966331@S:2,79.966332@T:5,79.966331@S:11	16	564.1983	3	1689.573	-0.0013	28.747	K	S	+		@S:1,@S:2,@T:5,@S:11		[s][s]VL[t]V[s]NV[y][s][s]K	ZN638_MOUSE;S1378,ZN638_MOUSE;S1379,ZN638_MOUSE;T1382,ZN638_MOUSE;S1388
1014	STPERRTVQMIMETR	79.966332@T:7	23.3	479.4796	4	1913.889	0.0039	20.468	K	Q	+		@T:7		[s][t]PERR[t]VQMIME[t]R	PLCG2_MOUSE;T42
1015	STSATDTHHVELAR	79.966332@T:2	30.1	535.5736	3	1603.699	-0.0003	19.916	R	E	+	ambiguos		@S:1orT:2	[s][t][s]ATDTHHVELAR	BCKD_MOUSE;S31orT32
1016	STSPAPADVAPAQEDLR	79.966331@S:3	85.4	902.9091	2	1803.804	-0.0003	38.931	K	T	+		@S:3		[s][t][s]PAPADVAPAQEDLR	G3BP1_MOUSE;S231
1017	STSPIIGSPPVR	79.966331@S:3	24.3	645.8257	2	1289.637	-0.0013	31.966	R	A	+		@S:3		[s][t][s]PIIG[s]PPVR	PATL1_MOUSE;S179
1018	STSQGSINSPVYSR	79.966331@S:3	60.3	781.8447	2	1561.675	-0.0025	27.166	R	H	+		@S:3		[s][t][s]QG[s]INSPVYSR	ABLM1_MOUSE;S496
1019	STTFSTNYR	79.966332@T:2	36	578.7374	2	1155.46	0.0004	34.898	R	S	+		@T:2		[s][t][t]FSTNYR	K1C18_MOUSE;T8
1020	SVDALDDINRPGSTESGRSSPPSSGR	79.966331@S:16	22.7	908.7439	3	2723.21	-0.0051	29.945	R	R	+		@S:16		SVDALDDINRPG[s][t]E[s]GR[s][s]PP[s][s]GR	LSR_MOUSE;S451
1021	SVDALDDINRPGSTESGRSSPPSSGR	79.966331@S:19	47.5	908.7455	3	2723.215	-0.0001	29.764	R	R	+		@S:19		SVDALDDINRPG[s][t]E[s]GR[s][s]PP[s][s]GR	LSR_MOUSE;S454
1022	SVDALDDINRPGSTESGRSSPPSSGR	79.966331@S:20	45.3	908.7436	3	2723.209	-0.0059	29.807	R	R	+		@S:20		SVDALDDINRPG[s][t]E[s]GR[s][s]PP[s][s]GR	LSR_MOUSE;S455
1023	SVDALDDINRPGSTESGRSSPPSSGR	79.966331@S:24	46.7	908.7453	3	2723.214	-0.0008	37.698	R	R	+		@S:24		SVDALDDINRPG[s][t]E[s]GR[s][s]PP[s][s]GR	LSR_MOUSE;S459
1024	SVDEIIR	79.966331@S:1	28.5	456.2154	2	910.4162	0.0002	38.435	R	L	+		@S:1		[pS]VDEIIR	PRDX1_MOUSE;S152
1025	SVDLDAFVAR	79.966331@S:1	66.5	586.7709	2	1171.527	-0.0003	50.556	K	N	+		@S:1		[pS]VDLDAFVAR	CD2AP_MOUSE;S458
1026	SVEDEMDSPGEEPFYTGQGR	79.966331@S:8	33	1155.446	2	2308.878	-0.0049	44.703	K	S	+		@S:8		[s]VEDEMD[s]PGEEPFYTGQGR	NFIA_MOUSE;S310

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
1027	SVENLPECGITHEQR	57.021465@C:8,79.966331@S:1	42.3	616.9365	3	1847.788	0.0005	37.796	R	A	+		@S:1		[pS]VENLPECGITHEQR	PI4KB_MOUSE;S428
1028	SVGEVLQSVLRYEK	79.966331@S:1,79.966331@S:8	25.2	589.6104	3	1765.809	0.0039	42.032	R	E	+		@S:1,@S:8		[s]VGEVLQ[s]VLR[y]EK	AKAP3_MOUSE;S827,AKAP3_MOUSE;S834
1029	SVNEILGLAESSPKEPK	79.966331@S:11	40.5	626.6471	3	1876.919	0.0011	43.851	K	V	+	ambiguos		@S:11orS:12	SVNEILGLAE[s][s]PKEPK	CI082_MOUSE;S306orS307
1030	SVNEILGLAESSPKEPK	79.966331@S:12	41.6	626.6462	3	1876.917	-0.0015	43.826	K	V	+	ambiguos		@S:11orS:12	SVNEILGLAE[s][s]PKEPK	CI082_MOUSE;S306orS307
1031	SVPTVDSGNEDDDSSFK	79.966331@S:7	80.4	939.8695	2	1877.724	0.0041	38.038	K	I	+		@S:7		SVPTVD[pS]GNEDDDSSFK	IF2P_MOUSE;S215
1032	SVSEAALAQPEGLLGTDTLK	79.966331@S:3	37.8	1040.514	2	2079.014	0.0006	55.071	R	K	+	ambiguos		@S:1orS:3	[s]V[s]EAALAQPEGLLGTDTLK	LIPS_MOUSE;S557orS559
1033	SVSELSLQGR	79.966331@S:3	38.2	578.2729	2	1154.531	-0.0019	33.575	R	R	+		@S:3		[s]V[s]EL[s]LQGR	RAIN_MOUSE;S322
1034	SVVFTSAR	79.966331@S:1	28.4	473.7234	2	945.4322	0.0001	26.544	K	A	+		@S:1		[pS]VVFTSAR	CAH14_MOUSE;S325
1035	SWHSRLSIDLSDK	79.966331@S:7	21.8	541.9237	3	1622.749	0.0039	32.596	K	T		ambiguos		@S:1orS:4orS:7	[s]WH[s]RL[s]IDL[s]DK	UN13C_MOUSE;S774orS777orS780
1036	SWVEENR	79.966331@S:1	28.3	500.2003	2	998.386	0.0002	31.508	K	A	+		@S:1		[pS]WVEENR	3HAO_MOUSE;S9
1037	SYEDLTELEDR	79.966331@S:1	56.6	725.2927	2	1448.571	0	43.785	R	E	+	ambiguos		@S:1orY:2	[s][y]EDLTELEDR	MON1A_MOUSE;S56orY57
1038	SYEDLTELEDREASGDSPK	79.966331@S:1	49	740.9778	3	2219.912	0.001	48.995	R	E	+		@S:1		[s][y]EDLTELEDREASGDSPK	MON1A_MOUSE;S56
1039	SYEDLTELEDREASGDSPK	79.966331@Y:2	36.3	740.9772	3	2219.91	-0.0011	41.249	R	E	+	ambiguos		@S:1orY:2	[s][y]EDL[t]ELEDREASGDSPK	MON1A_MOUSE;S56orY57
1040	SYELPDGQVITIGNER	79.966331@S:1	71.8	935.9333	2	1869.852	0.0011	54.211	K	F	+	ambiguos		@S:1orY:2	[s][y]ELPDGQVITIGNER	ACTS_MOUSE;S241orY242,ACTH_MOUSE;S240orY241,ACTG_MOUSE;S239orY240,ACTC_MOUSE;S241orY242,ACTBL_MOUSE;S240orY241,ACTA_MOUSE;S241orY242,ACTB_MOUSE;S239orY240
1041	SYGSQPNSPTSEDLAK	79.966331@S:8	31.5	880.8717	2	1759.729	-0.0014	25.138	K	T	+		@S:8		SYGSQPN[s]P[t][s]EDLAK	CGNL1_MOUSE;S203
1042	TANASLEEIIDK	79.966331@S:5	52.5	692.3236	2	1382.633	-0.0004	42.665	K	A	+		@S:5		TANA[pS]LEEIIDK	VP13C_MOUSE;S736
1043	TANKFEGLSQQASTSSAKTALGPR	79.966332@T:14, 79.966331@S:15, 79.966331@S:16, 79.966332@T:19	25.6	924.0461	3	2769.116	-0.0049	31.149	K	V	+	ambiguos	@S:16,@T:19	@S:13orT:14orS:15, @S:13orT:14orS:15	[t]ANKFEGL[s]QQA[s][t][s][s]AK[t]ALGPR	ASAP1_MOUSE;S899,ASAP1_MOUSE;T902,ASAP1_MOUSE;S896orT897orS898,ASAP1_MOUSE;S896orT897orS898
1044	TARPNSEAPLSGSEDADDSNK	79.966331@S:11	81	747.647	3	2239.919	-0.0037	20.81	K	L	+		@S:11		TARPNSEAPL[pS]GSEDADDSNK	IF2P_MOUSE;S137
1045	TASDSDEQQWPEEK	79.966331@S:3	78.8	865.3316	2	1728.649	-0.003	27.791	R	R	+		@S:3		[t]A[s]DSDEQQWPEEK	PDS5B_MOUSE;S1255
1046	TASDSDEQQWPEEK	79.966331@S:5	45.5	865.3322	2	1728.65	-0.0018	28.017	R	R	+	ambiguos		@S:3orS:5	[t]A[s]D[s]DEQQWPEEK	PDS5B_MOUSE;S1255orS1257
1047	TASDSDEQQWPEEK	79.966332@T:1	46	865.3324	2	1728.65	-0.0014	28.186	R	R	+	ambiguos		@T:1orS:3	[t]A[s]D[s]DEQQWPEEK	PDS5B_MOUSE;T1253orS1255
1048	TASETRSEGSEYEEIPK	79.966332@T:5	28	664.9518	3	1991.834	-0.0026	26.721	R	R	+		@T:5		[t]A[s]E[t]R[s]EG[s]E[y]EEIPK	PRC2A_MOUSE;T1085
1049	TASFSESRADEVAPAK	79.966331@S:3	64.1	873.3894	2	1744.764	-0.0026	25.138	R	K	+		@S:3		[t]A[s]F[s]ESRADEVAPAK	ACLY_MOUSE;S455
1050	TASFSESRADEVAPAKK	79.966331@S:3	56.7	625.2938	3	1872.86	-0.0023	22.077	R	A	+		@S:3		[t]A[s]F[s]ESRADEVAPAKK	ACLY_MOUSE;S455
1051	TASGSSVTSLEGTR	79.966332@T:1	57.2	716.8182	2	1431.622	-0.0025	27.894	R	S	+		@T:1		[t]A[s]G[s][s]VTSLEGTR	NDRG1_MOUSE;T328
1052	TASISSSPSEGTPAVGSYGCTPQSLPK	57.021465@C:20, 79.966331@S:7	22.5	916.0803	3	2745.219	-0.0013	46.798	R	F	+	ambiguos		@S:5orS:6orS:7	[t]A[s]I[s][s][s]P[s]EG[t]PAVGSYGCTPQSLPK	LARP1_MOUSE;S826orS827orS828
1053	TASISSSPSEGTPAVGSYGCTPQSLPK	57.021465@C:20, 79.966332@T:12	55.6	916.08	3	2745.218	-0.0022	46.716	R	F	+		@T:12		[t]A[s]I[s][s][s]P[s]EG[t]PAVGSYGCTPQSLPK	LARP1_MOUSE;T833
1054	TASLTSAASIDGSR	79.966331@S:3	76.1	708.8221	2	1415.63	0.0004	38.995	R	S	+		@S:3		[t]A[s]L[t]SAASIDGSR	NDRG2_MOUSE;S332
1055	TASLTSAASIDGSR	79.966331@S:9	77.7	708.8216	2	1415.629	-0.0006	37.058	R	S	+		@S:9		TASLTSAA[pS]IDGSR	NDRG2_MOUSE;S338
1056	TASLTSAASIDGSR	79.966332@T:1	62.2	708.8213	2	1415.628	-0.0013	31.377	R	S	+	ambiguos		@T:1orS:3	[t]A[s]L[t][s]AA[s]IDG[s]R	NDRG2_MOUSE;T330orS332
1057	TASLTSAASIDGSR	79.966332@T:1,79.966331@S:9	25.7	748.8043	2	1495.594	-0.0016	32.973	R	S	+		@T:1,@S:9		[t]A[s]L[t][s]AASIDGSR	NDRG2_MOUSE;T330,NDRG2_MOUSE;S338
1058	TCPAIIR	57.021465@C:2,79.966332@T:1	14.8	455.7144	2	909.4142	-0.0001	46.46	R	A	+		@T:1		[pT]CPAIIR	RASL2_MOUSE;T432
1059	TDGSISGDRQPVTVADYISR	79.966331@S:4,79.966331@S:6	40	766.3333	3	2295.978	0.0006	47.116	R	A	+		@S:4,@S:6		[t]DG[s]I[s]GDRQPVTVADYISR	FXR2_MOUSE;S602,FXR2_MOUSE;S604
1060	TDSDSDLQLYK	79.966331@S:3	69.5	682.7843	2	1363.554	-0.0003	34.429	K	E	+		@S:3		[t]D[s]D[s]DLQLYK	AMPD2_MOUSE;S109
1061	TDSREDEISPPPPNPVVK	79.966331@S:3	38.1	686.3248	3	2055.953	0.0012	38.374	R	G	+		@S:3		[t]D[s]REDEI[s]PPPPNPVVK	KAP0_MOUSE;S77
1062	TDSREDEISPPPPNPVVK	79.966331@S:9	25.6	686.3245	3	2055.952	0.0002	30.188	R	G	+		@S:9		[t]D[s]REDEI[s]PPPPNPVVK	KAP0_MOUSE;S83
1063	TDWSSGDASRPSSDSADSPK	79.966331@S:12	55.8	711.6177	3	2131.831	-0.0018	22.94	R	S			@S:12		TDWSSGDASRP[s][s]D[s]AD[s]PK	ARHGC_MOUSE;S303
1064	TEDGGWEWSDDEFDEESEEGR	79.966331@S:9	68.5	1292.448	2	2582.882	-0.0054	53.987	K	A	+		@S:9		TEDGGWEW[pS]DDEFDEESEEGR	OXSR1_MOUSE;S339
1065	TEEVLSPDGSPSKSPSK	79.966331@S:16	28.2	608.9469	3	1823.819	-0.0002	22.236	R	K	+	ambiguos		@S:14orS:16	TEEVL[s]PDG[s]P[s]K[s]P[s]K	ADDG_MOUSE;S681orS683
1066	TESGETLAGDSDFSLKPEK	79.966331@S:3	67.5	697.6429	3	2089.907	-0.0025	38.926	K	G	+		@S:3		[t]E[s]GETLAGDSDFSLKPEK	TGON1_MOUSE;S210,TGON2_MOUSE;S220
1067	TGDLGIPPNPEDRSPSPEPIYNSEGK	79.966331@S:14, 79.966331@S:16	58.8	976.0881	3	2925.242	-0.0045	42.093	R	R	+		@S:14,@S:16		TGDLGIPPNPEDR[s]P[s]PEPI[y]N[s]EGK	SF01_MOUSE;S80,SF01_MOUSE;S82
1068	TGDLGIPPNPEDRSPSPEPIYNSEGK	79.966331@S:14, 79.966331@S:23	53.3	976.0872	3	2925.24	-0.0073	46.071	R	R	+	ambiguos	@S:14	@Y:21orS:23	TGDLGIPPNPEDR[s]P[s]PEPI[y]N[s]EGK	SF01_MOUSE;S80,SF01_MOUSE;Y87orS89
1069	TGDLGIPPNPEDRSPSPEPIYNSEGK	79.966331@S:14, 79.966331@Y:21	56.9	976.0887	3	2925.244	-0.0026	42.296	R	R	+		@S:14,@Y:21		TGDLGIPPNPEDR[s]P[s]PEPI[y]N[s]EGK	SF01_MOUSE;S80,SF01_MOUSE;Y87
1070	TGEPDEEEGTFRSSIR	79.966331@S:13	27.6	630.6022	3	1888.785	0.0009	35.065	R	R	+		@S:13		TGEPDEEEG[t]FR[s][s]IR	PLM_MOUSE;S82

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
1071	TGEPDEEEGTFRSSIR	79.966331@S:14	57.4	945.3982	2	1888.782	-0.0022	27.535	R	R	+		@S:14		TGEPDEEEGTFR[s][s]IR	PLM_MOUSE;S83
1072	TGEPDEEEGTFRSSIR	79.966332@T:10	26.3	630.6022	3	1888.785	0.0008	34.988	R	R	+		@T:10		TGEPDEEEG[pT]FRSSIR	PLM_MOUSE;T79
1073	TGEPDEEEGTFRSSIRR	79.966331@S:13	34.9	682.636	3	2044.886	0.0012	31.235	R	L	+		@S:13		TGEPDEEEG[t]FR[s][s]IRR	PLM_MOUSE;S82
1074	TGEPDEEEGTFRSSIRR	79.966331@S:14	32.7	682.6361	3	2044.886	0.0013	31.135	R	L	+		@S:14		TGEPDEEEG[t]FR[s][s]IRR	PLM_MOUSE;S83
1075	TGEPDEEEGTFRSSIRR	79.966332@T:10	49.4	682.6347	3	2044.882	-0.0027	23.924	R	L	+		@T:10		TGEPDEEEG[t]FR[s][s]IRR	PLM_MOUSE;T79
1076	TGSYGALAEISASK	79.966332@T:1	67.2	717.8293	2	1433.644	0.0001	41.389	K	E	+	ambiguos		@T:1orS:3orY:4	[t]G[s][y]GALAEISASK	MYPT1_MOUSE;T443orS445orY446
1077	TGTGSPFAGNSPAREGEQDAGSLK	79.966331@S:5,79.966331@S:11	67.1	832.014	3	2493.02	-0.0009	42.87	K	D	+		@S:5,@S:11		[t]G[t]G[s]PFAGN[s]PAREGEQDAGSLK	ZC3H4_MOUSE;S1270,ZC3H4_MOUSE;S1276
1078	TGVLTVASYRVSK	79.966331@S:8,79.966331@Y:9	21.3	385.9359	4	1539.714	0.0046	20.379	K	S	+		@S:8,@Y:9		TGVL[t]VA[s][y]RV[s]K	P4HA2_MOUSE;S380,P4HA2_MOUSE;Y381
1079	THAEIKTLSTQMNITK	79.966332@T:7,79.966332@T:10,79.966332@T:15	20.4	685.9577	3	2054.851	-0.0037	34.408	K	G	+	ambiguos	@T:7,@T:15	@S:9orT:10	[t]HAEIK[t]L[s][t]QMNI[t]K	TITIN_MOUSE;T34832,TITIN_MOUSE;T34840,TITIN_MOUSE;S34834orT34835
1080	THSDQFLVSFK	79.966331@S:3	29.6	694.8154	2	1387.616	-0.001	41.568	R	D	+		@S:3		TH[pS]DQFLVSFK	ATPG_MOUSE;S146
1081	TIDIEPDIETLLSQQSGNS	79.966331@S:19	46.6	713.9941	3	2138.96	-0.0016	72.933	R	-	+		@S:19		TIDIEPDIETLLSQQ[s]GN[s]	GPX1_MOUSE;S201
1082	TITFHSNGDTSFPDPDIMAAMK	15.994915@M:18, 15.994915@M:21, 79.966332@T:3,79.966331@S:6,79.966331@S:11	20.5	889.9953	3	2666.964	-0.0073	50.092	K	N	+		@T:3,@S:6,@S:11		[t]I[t]FH[s]NGD[t][s]FPDPDIMAAMK	SMKZ_MOUSE;T283,SMKZ_MOUSE;S286,SMKZ_MOUSE;S291
1083	TKPPRPDSPTTTPNISVK	79.966331@S:16	24.2	672.6766	3	2015.008	-0.0009	24.271	K	K	+		@S:16		TKPPRPD[s]P[t][t][t]PNI[s]VK	ELF1_MOUSE;S195
1084	TKSPAEEELTPSAVVR	79.966331@S:3	36.4	598.6277	3	1792.861	0.0004	39.72	R	R	+		@S:3		[t]K[s]PAEEELTPSAVVR	PKHA6_MOUSE;S901
1085	TLDQSPELR	79.966332@T:1	19	569.7607	2	1137.507	0.0001	50.99	R	S	+		@T:1		[t]LDQ[s]PELR	MTOR_MOUSE;T1162
1086	TLFLGIPDENFEDHSAPPSPEEK	79.966331@S:15, 79.966331@S:19	26.3	910.3838	3	2728.13	-0.005	60.099	R	D			@S:15,@S:19		TLFLGIPDENFEDH[pS]APP[pS]PEEK	M3K5_MOUSE;S1036,M3K5_MOUSE;S1040
1087	TLSDESIYSSQR	79.966331@S:3	34.7	733.3134	2	1464.612	-0.001	32.174	R	E	+		@S:3		[t]L[s]DE[s]I[y][s][s]QR	SI1L1_MOUSE;S1564
1088	TNPSPTNPFSSDLQK	79.966331@S:4	60.2	856.8793	2	1711.744	-0.0013	39.772	R	T	+		@S:4		[t]NP[s]P[t]NPFSSDLQK	NUMB_MOUSE;S636
1089	TNSPSISPSMLSNAEHK	79.966331@S:3,79.966331@S:7	22.6	653.9365	3	1958.788	0.0029	40.056	K	R	+		@S:3,@S:7		[t]N[s]P[s]I[s]P[s]ML[s]NAEHK	ATX2_MOUSE;S832,ATX2_MOUSE;S836
1090	TNTNVNCPIECFMPLDVQADRDDSRE	57.021465@C:7,57.021465@C:11,79.966331@S:24	93.2	1059.44	3	3175.297	-0.0074	56.714	R	-	+		@S:24		TNTNVNCPIECFMPLDVQADRDD[pS]RE	FINC_MOUSE;S2475
1091	TPEELDDSDFETEDFDVR	79.966331@S:8	94.1	1119.931	2	2237.848	-0.0046	50.624	R	S	+		@S:8		TPEELDD[pS]DFETEDFDVR	CTNA1_MOUSE;S641
1092	TPEELDDSDFETEDFDVRSR	79.966331@S:8,79.966331@S:19	41.1	854.6567	3	2560.948	-0.0036	50.775	R	T	+		@S:8,@S:19		[t]PEELDD[s]DFE[t]EDFDVR[s]R	CTNA1_MOUSE;S641,CTNA1_MOUSE;S652
1093	TPFTTSGSLENN	79.966331@S:8	34.5	674.2772	2	1346.54	0.0008	42.931	R	-	+		@S:8		TPFT[t][s]G[s]LENN	CDO1_MOUSE;S196
1094	TPRCSLPDLPPGAQSR	57.021465@C:4,79.966332@T:1,79.966331@S:5	25.5	637.9462	3	1910.817	0.0056	32.611	K	R			@T:1,@S:5		[pT]PRC[pS]LPDLPPGAQSR	MMP17_MOUSE;T106,MMP17_MOUSE;S110
1095	TPSPKEEDEEAESPPEK	79.966331@S:13	48.7	660.2758	3	1977.806	-0.0037	19.84	K	K	+		@S:13		TPSPKEEDEEAE[pS]PPEK	NUCKS_MOUSE;S214
1096	TPSQEGCQDLTQEQR	57.021465@C:7,79.966331@S:3	93.5	928.8761	2	1855.738	-0.0031	24.87	R	D	+		@S:3		[t]P[s]QEGCQDLTQEQR	PEX1_MOUSE;S1182
1097	TPSQEGCQDLTQEQR	57.021465@C:7,79.966332@T:1	82.5	928.8759	2	1855.737	-0.0036	24.361	R	D	+	ambiguos		@T:1orS:3	[t]P[s]QEGCQDLTQEQR	PEX1_MOUSE;T1180orS1182
1098	TPVDYIDLPYSSSPSR	79.966331@S:13	48.7	938.9215	2	1875.828	-0.0007	50.605	K	S	+	ambiguos		@S:11orS:12orS:13	TPVDYIDLP[y][s][s][s]P[s]R	SRBS1_MOUSE;S1199orS1200orS1201
1099	TPVDYIDLPYSSSPSR	79.966331@S:15	53.5	938.9227	2	1875.831	0.0016	51.289	K	S	+	ambiguos		@S:11orS:12orS:13orS:15	TPVDYIDLP[y][s][s][s]P[s]R	SRBS1_MOUSE;S1199orS1200orS1201orS1203
1100	TQAAGPSSPPRPPTPK	79.966331@S:8,79.966332@T:14	27.8	583.5969	3	1747.769	-0.0006	23.929	K	E	+		@S:8,@T:14		TQAAGP[s][s]PPRPP[t]PK	XRCC1_MOUSE;S446,XRCC1_MOUSE;T452
1101	TQSSGQDGRPQEEPHAEDLQK	79.966331@S:3	26.3	806.3488	3	2416.025	-0.0045	20.309	R	I	+		@S:3		[t]Q[s][s]GQDGRPQEEPHAEDLQK	PI51C_MOUSE;S554
1102	TQTPPLGQTPQLGLK	79.966332@T:3	27.6	829.9295	2	1657.844	0.0004	41.847	R	T	+		@T:3		[t]Q[t]PPLGQ[t]PQLGLK	IF4G2_MOUSE;T507
1103	TRGAEDDLNTVAAGTMTGMLYK	15.994915@M:19, 79.966332@T:1,79.966332@T:10,79.966331@Y:21	22.5	643.505	4	2569.991	0.0036	38.495	K	C		ambiguos	@T:1,@T:10	@T:17orY:21	[t]RGAEDDLN[t]VAAG[t]M[t]GML[y]K	TIM23_MOUSE;T148,TIM23_MOUSE;T157,TIM23_MOUSE;T164orY168
1104	TRVVEDNHNYYVSRVYGPGEK	79.966331@Y:10, 79.966331@Y:11, 79.966331@Y:16	22.4	908.0409	3	2721.101	-0.0017	58.532	R	Q	+		@Y:10,@Y:11, @Y:16		[t]RVVEDNHN[y][y]V[s]RV[y]GPGEK	PLDX1_MOUSE;Y92,PLDX1_MOUSE;Y93,PLDX1_MOUSE;Y98
1105	TSFDENDSEELEDK	79.966331@S:8	73.8	869.322	2	1736.629	-0.0007	38.114	K	D	+		@S:8		TSFDEND[pS]EELEDK	IF2P_MOUSE;S114
1106	TSFDENDSEELEDKDSK	79.966331@S:8	22.1	689.936	3	2066.786	0.0019	33.343	K	S	+		@S:8		TSFDEND[pS]EELEDKDSK	IF2P_MOUSE;S114
1107	TSPGRADLPGSSSTFTK	79.966331@S:2	25.1	596.944	3	1787.81	0.0012	36.783	R	S	+		@S:2		[t][s]PGRADLPGSSSTFTK	SRBS2_MOUSE;S358
1108	TSPGRADLPGSSSTFTK	79.966332@T:1	21.6	596.9436	3	1787.809	0	28.7	R	S	+		@T:1		[t][s]PGRADLPGSSSTFTK	SRBS2_MOUSE;T357
1109	TSPLMLDR	15.994915@M:5,79.966331@S:2	19.5	514.7275	2	1027.44	-0.0005	28.257	R	A	+	ambiguos		@T:1orS:2	[t][s]PLMLDR	SRRM2_MOUSE;T2350orS2351
1110	TSPTPSVFVELGEEELEAVTARPEAVER	79.966331@S:2	67.2	1041.503	3	3121.487	0.0015	74.782	K	A	+	ambiguos		@T:1orS:2	[t][s]P[t]P[s]VFVELGEEELEAVTARPEAVER	B2L13_MOUSE;T342orS343

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
1111	TSSKESSPVPSPTLDRK	79.966331@S:6,79.966331@S:7,79.966331@S:11	21.5	685.9525	3	2054.836	-0.0007	24.04	R	A	+		@S:6,@S:7,@S:11		[t][s][s]KE[s][s]PVP[s]P[t]LDRK	SPTB2_MOUSE;S2163,SPTB2_MOUSE;S2164,SPTB2_MOUSE;S2168
1112	TSSVVTLEVAK	79.966331@S:3	58.8	607.3071	2	1212.6	-0.0006	33.058	R	Q			@S:3		[t][s][s]VVTLEVAK	AFAD_MOUSE;S1083
1113	TTQSGFEGFLK	79.966331@S:4	30.2	647.7892	2	1293.564	-0.0004	47.692	K	D	+		@S:4		[t][t]Q[s]GFEGFLK	URIC_MOUSE;S168
1114	TTQSLQDFPVADSEEEAEEEFQK	79.966331@S:13	28.3	913.0506	3	2736.13	-0.0027	48.478	R	E	+		@S:13		TTQSLQDFPVAD[pS]EEEAEEEFQK	TFP11_MOUSE;S211
1115	TTRTPEVSGYTYEKTER	79.966332@T:2,79.966332@T:4	23	545.2332	4	2176.904	-0.0043	22.428	K	S	+		@T:2,@T:4		[t][t]R[t]PEV[s]G[y][t][y]EK[t]ER	MAP1B_MOUSE;T1960,MAP1B_MOUSE;T1962
1116	TTSPATDAGHVQETSEPSLQALESR	79.966331@S:3	25.2	898.075	3	2691.203	0.0007	40.116	K	Q			@S:3		[t][t][s]PA[t]DAGHVQETSEPSLQALESR	AIMP2_MOUSE;S36
1117	TTVKSSELQQL	79.966331@S:6	29.2	657.3211	2	1312.628	0.0001	42.627	R	-		ambiguos		@S:5orS:6	TTVK[s][s]ELQQL	SO2B1_MOUSE;S677orS678
1118	TVYLQSALSSSSSAEK	79.966331@S:12	52.1	869.4003	2	1736.786	-0.0009	37.545	K	F		ambiguos		@S:12orS:13	TVYLQSALS[s][s][s][s][s]AEK	EI24_MOUSE;S319orS320
1119	TVYLQSALSSSSSAEK	79.966331@S:13	78.8	869.3993	2	1736.784	-0.0028	37.584	K	F			@S:13		TVYLQSALSS[s][s][s]AEK	EI24_MOUSE;S320
1120	TYSECEDGTYSPEISWHHGK	57.021465@C:5,79.966331@S:3	61.5	821.6575	3	2461.951	-0.0017	34.617	K	G	+		@S:3		[t][y][s]ECEDGTYSPEISWHHGK	PTSS1_MOUSE;S417
1121	VAGSEGSSSTLVDYTSTSSTGGSPVRK	79.966331@S:18	69	899.7452	3	2696.214	-0.004	31.142	K	S	+		@S:18		VAGSEGSSS[t]LVD[y][t][s][t][s][s][t]GG[s]PVRK	RBBP6_MOUSE;S1273
1122	VASGSDLHLTDIDSDSNR	79.966331@S:3	34.3	661.2885	3	1980.844	0.0011	37.101	K	G	+		@S:3		VA[s]G[s]DLHL[t]DIDSDSNR	MY18A_MOUSE;S72
1123	VATLNSEEENDPPTYK	79.966331@S:6	40.7	943.9055	2	1885.796	-0.0017	29.967	K	D	+		@S:6		VATLN[pS]EEENDPPTYK	VIGLN_MOUSE;S31
1124	VDIITEEMPENALPSDEDDKDPNDPYR	79.966331@S:15	96.1	1066.454	3	3196.339	-0.0043	50.533	R	A			@S:15		VDIITEEMPENALP[pS]DEDDKDPNDPYR	AP3D1_MOUSE;S784
1125	VDNARVSPEVGSADVASIAQK	79.966331@S:7	22.6	731.6891	3	2192.045	-0.0019	36.138	K	E	+		@S:7		VDNARV[s]PEVG[s]ADVA[s]IAQK	FAM21_MOUSE;S747
1126	VDNLTYRTSPDTLR	79.966331@S:9	55.3	577.6083	3	1729.803	-0.0006	30.583	K	R			@S:9		VDNL[t][y]R[t][s]PDTLR	SRSF2_MOUSE;S26
1127	VDNLTYRTSPDTLR	79.966332@T:8	42.6	577.6088	3	1729.805	0.001	38.621	K	R	+		@T:8		VDNLT[y]R[t][s]PD[t]LR	SRSF2_MOUSE;T25
1128	VDNLTYRTSPDTLRR	79.966331@S:9	43.4	629.6426	3	1885.906	0.0014	34.758	K	V	+		@S:9		VDNL[t][y]R[t][s]PD[t]LRR	SRSF2_MOUSE;S26
1129	VDNLTYRTSPDTLRR	79.966331@Y:6	23	472.4833	4	1885.904	-0.0006	27.021	K	V			@Y:6		VDNL[t][y]R[t][s]PD[t]LRR	SRSF2_MOUSE;Y23
1130	VDSTTCLFPVEEK	57.021465@C:6,79.966331@S:3	80.5	802.8495	2	1603.684	0.0003	54.699	R	A	+		@S:3		VD[s][t][t]CLFPVEEK	GFPT1_MOUSE;S259
1131	VDSTTCLFPVEEK	57.021465@C:6,79.966332@T:4	69.5	802.8494	2	1603.684	0.0001	54.641	R	A	+	ambiguos		@S:3orT:4	VD[s][t][t]CLFPVEEK	GFPT1_MOUSE;S259orT260
1132	VEPAWHDQDETSSVKSDGAGGAR	79.966331@S:13	32.2	827.0213	3	2478.042	-0.0028	24.69	K	A	+		@S:13		VEPAWHDQDE[t][s][s]VK[s]DGAGGAR	LARP1_MOUSE;S299
1133	VETAEVCSRPQELPQSPR	57.021465@C:7,79.966331@S:16	25.9	721.6674	3	2161.98	-0.0023	27.907	K	I			@S:16		VETAEVC[s]RPQELPQ[s]PR	FA63A_MOUSE;S103
1134	VFDDDSDDIEEEEEADEK	79.966331@S:6	71.5	1104.894	2	2207.773	-0.0065	38.532	R	E	+		@S:6		VFDDD[pS]DDIEEEEEADEK	HTSF1_MOUSE;S645
1135	VGSLTPPSSPK	79.966332@T:5,79.966331@S:9	27	615.2647	2	1228.515	0.0007	33.817	K	T	+		@T:5,@S:9		VG[s]L[t]PP[s][s]PK	AAK1_MOUSE;T618,AAK1_MOUSE;S622
1136	VKSWVEENR	79.966331@S:3	23	409.5237	3	1225.549	0.0002	23.32	R	A	+		@S:3		VK[pS]WVEENR	3HAO_MOUSE;S9
1137	VKVDGPRSPSYGR	79.966331@S:8,79.966331@Y:11	22.4	526.5671	3	1576.679	-0.0005	20.386	R	S	+		@S:8,@Y:11		VKVDGPR[s]P[s][y]GR	SRSF1_MOUSE;S199,SRSF1_MOUSE;Y202
1138	VMHTQCHSTPDSAEDVR	57.021465@C:6,15.994915@M:2,79.966331@S:12	31.9	689.2741	3	2064.8	-0.0027	17.234	R	K	+		@S:12		VMHTQCHSTPD[pS]AEDVR	FETUA_MOUSE;S138
1139	VMHTQCHSTPDSAEDVRK	57.021465@C:6,15.994915@M:2,79.966331@S:12	45.1	731.9722	3	2192.895	-0.0032	14.244	R	L	+		@S:12		VMHTQCH[s][t]PD[s]AEDVRK	FETUA_MOUSE;S138
1140	VMHTQCHSTPDSAEDVRK	57.021465@C:6,79.966331@S:12	35.8	726.6404	3	2176.899	-0.0038	17.266	R	L	+		@S:12		VMHTQCHS[t]PD[s]AEDVRK	FETUA_MOUSE;S138
1141	VMHTQCHSTPDSAEDVRK	57.021465@C:6,79.966332@T:9	23.5	545.2324	4	2176.9	-0.0025	17.241	R	L	+		@T:9		VMH[t]QCH[s][t]PD[s]AEDVRK	FETUA_MOUSE;T135
1142	VPSRQSLEDRGYSPDTR	79.966331@S:3,79.966331@S:6	35.6	708.303	3	2121.887	-0.001	25.847	R	V	+		@S:3,@S:6		VP[s]RQ[s]LEDRG[y][s]PD[t]R	ZO3_MOUSE;S356,ZO3_MOUSE;S359
1143	VQISPDSGGLPER	79.966331@S:4	40.7	717.8346	2	1433.655	-0.0006	32.028	K	S	+		@S:4		VQI[s]PD[s]GGLPER	FUBP2_MOUSE;S182
1144	VQVAPLQGSPPLSHDDR	79.966331@S:9	29.8	632.6389	3	1894.895	0.001	34.601	K	G	+		@S:9		VQVAPLQG[s]PPL[s]HDDR	ZO2_MOUSE;S107
1145	VRGWSPPPEVR	79.966331@S:5	39.1	680.3314	2	1358.648	-0.0013	32.129	R	R	+		@S:5		VRGW[pS]PPPEVR	ACSA_MOUSE;S30
1146	VRPASSAASVYAGAGGSGSR	79.966331@S:17	88.5	629.9613	3	1886.862	-0.0014	23.171	R	I	+		@S:17		VRPASSAASVYAGAGG[pS]GSR	K1C18_MOUSE;S43
1147	VRPASSAASVYAGAGGSGSR	79.966331@S:5	57	629.9614	3	1886.862	-0.0013	31.28	R	I	+		@S:5		VRPA[s][s]AA[s]V[y]AGAGGSGSR	K1C18_MOUSE;S31
1148	VSGRTSPLMLDR	15.994915@M:9,79.966331@S:6	26.7	476.5616	3	1426.663	-0.0011	24.914	R	A	+		@S:6		V[s]GR[t][s]PLMLDR	SRRM2_MOUSE;S2351
1149	VSGRTSPLMLDR	79.966331@S:6	26.7	471.23	3	1410.668	-0.0007	27.55	R	A	+		@S:6		V[s]GR[t][s]PLMLDR	SRRM2_MOUSE;S2351
1150	VSSLSPEQEQGLWK	79.966331@S:5	25.8	834.3867	2	1666.759	-0.0014	42.554	K	Q	+		@S:5		V[s][s]L[s]PEQEQGLWK	FA76B_MOUSE;S193
1151	VSSPVLETVQQR	79.966331@S:2	52.1	711.8529	2	1421.691	-0.0004	38.599	K	T			@S:2		V[s][s]PVLETVQQR	SRRM2_MOUSE;S1359
1152	VSSPVLETVQQR	79.966331@S:3	47.9	711.8528	2	1421.691	-0.0005	38.595	K	T			@S:3		V[s][s]PVLETVQQR	SRRM2_MOUSE;S1360
1153	VSSPVLETVQQRTPSR	79.966331@S:3,79.966332@T:8	42.3	648.6377	3	1942.891	-0.0004	30.307	K	E	+		@S:3,@T:8		V[s][s]PVLE[t]VQQR[t]PSR	SRRM2_MOUSE;S1360,SRRM2_MOUSE;T1365
1154	VSSPVLETVQQRTPSRER	79.966331@S:3,79.966332@T:13	32.4	743.6845	3	2228.032	-0.0035	26.948	K	S	+		@S:3,@T:13		V[s][s]PVLE[t]VQQR[t]P[s]RER	SRRM2_MOUSE;S1360,SRRM2_MOUSE;T1370
1155	VSSPVLETVQQRTPSRER	79.966331@S:3,79.966332@T:8	21.8	743.684	3	2228.03	-0.005	27.212	K	S	+		@S:3,@T:8		V[s][s]PVLE[t]VQQR[t]P[s]RER	SRRM2_MOUSE;S1360,SRRM2_MOUSE;T1365

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions
1156	VTLQDYHLPDSDEDEETAIQR	79.966331@S:11	59	852.0377	3	2553.091	0.0004	44.819	R	V	+		@S:11		VTLQDYHLPD[pS]DEDEETAIQR	ZFY19_MOUSE;S280
1157	VVDYSQFQESDDADEDYGR	79.966331@S:10	77.4	1159.439	2	2316.864	-0.0055	40.1	K	D	+		@S:10		VVDYSQFQE[pS]DDADEDYGR	NUCKS_MOUSE;S19
1158	VVDYSQFQESDDADEDYGRDSGPPAK	79.966331@S:10	94.9	990.7345	3	2969.182	-0.0059	35.998	K	K	+		@S:10		VVDY[s]QFQE[s]DDADEDYGRDSGPPAK	NUCKS_MOUSE;S19
1159	VVDYSQFQESDDADEDYGRDSGPPAKK	79.966331@S:10	23.4	775.327	4	3097.279	-0.0036	32.393	K	I	+		@S:10		VVD[y][s]QFQE[s]DDADED[y]GRD[s]GPPAKK	NUCKS_MOUSE;S19
1160	VVPSPDSDSDTDLEDPSPR	79.966331@S:7,79.966331@S:9	59.8	1094.42	2	2186.825	-0.0042	37.262	R	R	+		@S:7,@S:9		VVP[s]PD[s]D[s]D[t]DLEDPSPR	MLXPL_MOUSE;S23,MLXPL_MOUSE;S25
1161	VVPSPDSDSDTDLEDPSPR	79.966331@S:9	56.5	1054.436	2	2106.858	-0.0049	33.782	R	R	+		@S:9		VVPSPD[s]D[s]D[t]DLEDPSPR	MLXPL_MOUSE;S25
1162	VWTSGQVEEYDLDADDINSR	79.966331@S:4	37.6	1196.503	2	2390.992	0.0018	49.093	K	V	+	ambiguos		@T:3orS:4	VW[t][s]GQVEE[y]DLDADDINSR	AQP1_MOUSE;T246orS247
1163	VYLTRWGIQGR	79.966332@T:4	25.1	476.9089	3	1427.705	-0.0025	34.628	K	W			@T:4		V[y]L[t]RWGIQGR	K1644_MOUSE;T132
1164	WAHDKFSGEEGEIEDDESGTENREEK	79.966331@S:7	56.3	776.5661	4	3102.235	-0.0009	31.936	K	D	+		@S:7		WAHDKF[s]GEEGEIEDDE[s]G[t]ENREEK	TR150_MOUSE;S924
1165	WAHDKFSGEEGEIEDDESGTENREEK	79.966331@S:7,79.966331@S:18	36.8	796.5571	4	3182.199	-0.0035	32.226	K	D	+		@S:7,@S:18		WAHDKF[pS]GEEGEIEDDESGTENREEK	TR150_MOUSE;S924,TR150_MOUSE;S935
1166	WDKDDFESEEEDVK	79.966331@S:8	42.8	925.8519	2	1849.689	-0.0038	36.295	K	T	+		@S:8		WDKDDFE[pS]EEEDVK	RBBP6_MOUSE;S1329
1167	WLDESDAEMELR	15.994915@M:9,79.966331@S:5	60.5	795.3127	2	1588.611	-0.0007	47.834	R	A	+		@S:5		WLDE[pS]DAEMELR	HACD3_MOUSE;S114
1168	WLDESDAEMELR	79.966331@S:5	70.7	787.3154	2	1572.616	-0.0004	51.356	R	A	+		@S:5		WLDE[pS]DAEMELR	HACD3_MOUSE;S114
1169	WRSLQQLAEER	79.966331@S:3	40.7	748.356	2	1494.697	-0.0006	39.21	R	S	+		@S:3		WR[pS]LQQLAEER	SPTA2_MOUSE;S1217
1170	YAALSVDGEDEDEGDDCTE	57.021465@C:17, 79.966331@S:5	30.1	1085.371	2	2168.726	0.0012	40.022	K	-	+		@S:5		[y]AAL[s]VDGEDEDEGDDCTE	IF4B_MOUSE;S597
1171	YDERPGPSPLPHR	79.966331@S:8	22.8	534.2473	3	1599.72	0.0005	21.91	R	D	+		@S:8		[y]DERPGP[s]PLPHR	RU17_MOUSE;S226
1172	YFLGLVDMTTVYGFR	15.994915@M:8,79.966332@T:10	24.4	626.6217	3	1876.843	-0.0038	30.044	R	K	+	ambiguos		@T:9orT:10	[y]FLGLVDM[t][t]V[y]GFR	PI5L1_MOUSE;T351orT352
1173	YFQISQDEDGSESED	79.966331@S:11	57.3	914.8255	2	1827.636	0.0004	49.787	R	-	+		@S:11		YFQI[s]QDEDG[s]E[s]ED	RL22L_MOUSE;S118
1174	YFQISQDEDGSESED	79.966331@S:11, 79.966331@S:13	20.5	954.8069	2	1907.599	-0.0031	50.215	R	-	+		@S:11,@S:13		YFQISQDEDG[pS]ESED	RL22L_MOUSE;S118,RL22L_MOUSE;S120
1175	YGMGTSVER	15.994915@M:3,79.966332@T:5	49.6	548.212	2	1094.409	-0.0009	18.638	R	A	+		@T:5		YGMG[t][s]VER	ODPA_MOUSE;T231
1176	YGMGTSVER	79.966331@S:6	29.5	540.2147	2	1078.415	-0.0007	24.154	R	A	+		@S:6		YGMG[t][s]VER	ODPA_MOUSE;S232
1177	YGSIVDDER	79.966331@S:3	22.5	567.2288	2	1132.443	-0.0008	27.545	R	L	+		@S:3		[y]G[s]IVDDER	IQGA2_MOUSE;S16
1178	YHGHSMSDPGVSYR	15.994915@M:6,79.966331@S:12,79.966331@Y:1	25.6	590.2113	3	1767.612	0.0009	26.069	R	T	+		@Y:1,@S:12		[y]HGH[s]M[s]DPGV[s][y]R	ODPA_MOUSE;Y289,ODPA_MOUSE;S300
1179	YHGHSMSDPGVSYR	15.994915@M:6,79.966331@S:5	38.7	563.5555	3	1687.645	-0.0002	18.791	R	T	+		@S:5		[y]HGH[s]M[s]DPGV[s][y]R	ODPA_MOUSE;S293
1180	YHGHSMSDPGVSYR	15.994915@M:6,79.966331@S:5,79.966331@S:12	24.6	590.2106	3	1767.61	-0.0012	20.089	R	T	+		@S:5,@S:12		[y]HGH[s]M[s]DPGV[s][y]R	ODPA_MOUSE;S293,ODPA_MOUSE;S300
1181	YHGHSMSDPGVSYR	15.994915@M:6,79.966331@S:5,79.966331@Y:13	24.7	590.2104	3	1767.609	-0.0019	20.144	R	T	+		@S:5,@Y:13		YHGH[s]M[s]DPGVSYR	ODPA_MOUSE;S293,ODPA_MOUSE;Y301
1182	YHGHSMSDPGVSYR	79.966331@S:12, 79.966331@Y:1	39	584.8791	3	1751.615	-0.0011	23.796	R	T	+		@Y:1,@S:12		[y]HGH[s]M[s]DPGV[s][y]R	ODPA_MOUSE;Y289,ODPA_MOUSE;S300
1183	YHGHSMSDPGVSYR	79.966331@S:5	34.5	836.8304	2	1671.646	-0.0039	21.869	R	T	+		@S:5		[y]HGH[s]MSDPGV[s][y]R	ODPA_MOUSE;S293
1184	YHGHSMSDPGVSYR	79.966331@S:5,79.966331@Y:13	26.5	584.8798	3	1751.618	0.0013	31.112	R	T	+		@S:5,@Y:13		[y]HGH[s]M[s]DPGVSYR	ODPA_MOUSE;S293,ODPA_MOUSE;Y301
1185	YHGHSMSDPGVSYR	79.966331@S:7	48.4	558.2235	3	1671.649	-0.0013	21.819	R	T	+		@S:7		YHGH[s]M[s]DPGVSYR	ODPA_MOUSE;S295
1186	YISGSSFK	79.966331@S:3	27.9	484.7099	2	967.4052	0.0001	36.02	R	D	+		@S:3		YI[s]G[s]SFK	DHB5_MOUSE;S307
1187	YLSFTPPEK	79.966331@S:3	31.6	581.2657	2	1160.517	0.0013	40.954	K	D	+		@S:3		[y]L[s]F[t]PPEK	PAK2_MOUSE;S141
1188	YNLDASEEEDSNK	79.966331@S:6	58.8	797.2999	2	1592.585	-0.0026	25.957	K	K	+		@S:6		YNLDA[pS]EEEDSNK	ZRAB2_MOUSE;S188
1189	YQDEVFGGFVTEPQEESEEEVEEPEER	79.966331@S:17	44.9	1099.446	3	3295.317	-0.0067	56.058	R	Q	+		@S:17		YQDEVFGGFV[t]EPQEE[s]EEEVEEPEER	G3BP1_MOUSE;S149
1190	YQLQSQENFEPFMK	15.994915@M:13, 79.966331@S:5	45.2	942.8965	2	1883.778	-0.0016	45.835	K	A	+		@S:5		[y]QLQ[s]QENFEPFMK	FABPL_MOUSE;S11
1191	YQLQSQENFEPFMK	79.966331@S:5	70.1	934.8988	2	1867.783	-0.0022	51.682	K	A	+		@S:5		YQLQ[pS]QENFEPFMK	FABPL_MOUSE;S11
1192	YRADSHGELDLAR	79.966331@S:5	50.4	528.2383	3	1581.693	-0.0005	25.842	R	T	+		@S:5		[y]RAD[s]HGELDLAR	ACOT1_MOUSE;S56,ACOT4_MOUSE;S56,ACOT5_MOUSE;S56,ACOT6_MOUSE;S56,ACOT3_MOUSE;S67
1193	YRSPYSGPK	79.966331@S:3	24.4	567.7518	2	1133.489	-0.0015	18.251	R	F	+		@S:3		[y]R[s]P[y]SGPK	RBM39_MOUSE;S97
1194	YRSQSGEDESLNQPGPIK	79.966331@S:3	25.7	695.6479	3	2083.922	0.0007	33.319	R	T	+		@S:3		[y]R[s]Q[s]GEDESLNQPGPIK	PEX1_MOUSE;S1210
1195	YRSQSGEDESLNQPGPIK	79.966331@S:5	31.5	695.6469	3	2083.919	-0.0023	25.862	R	T	+		@S:5		[y]R[s]Q[s]GEDE[s]LNQPGPIK	PEX1_MOUSE;S1212
1196	YRSQSGEDESLNQPGPIK	79.966331@Y:1	28.4	695.6474	3	2083.92	-0.0006	33.356	R	T	+		@Y:1		[y]R[s]Q[s]GEDESLNQPGPIK	PEX1_MOUSE;Y1208
1197	YTDQSGEEEEDYESEEQLQHR	79.966331@S:5	74.2	894.343	3	2680.007	-0.0013	29.758	R	I	+		@S:5		YTDQ[pS]GEEEEDYESEEQLQHR	COQ9_MOUSE;S81

[a] Each Mascot phosphorylation assignment was confirmed and accpeted as umambiguous depending on the presence of site-determining ions supporting the phosphorylation site (see Experimental procedure).

No.	Peptide sequence	Modification	Peptide score	Observed m/z	Charge	Observed mass	Mass error	Retention time (min)	Forward residue	Backword residue	Precursor origin neutral loss peak	Manual confirmation[a]	Confirmed phospho-site	Ambiguous phospho-site	Best guess by Phoscalc[b]	P-positions

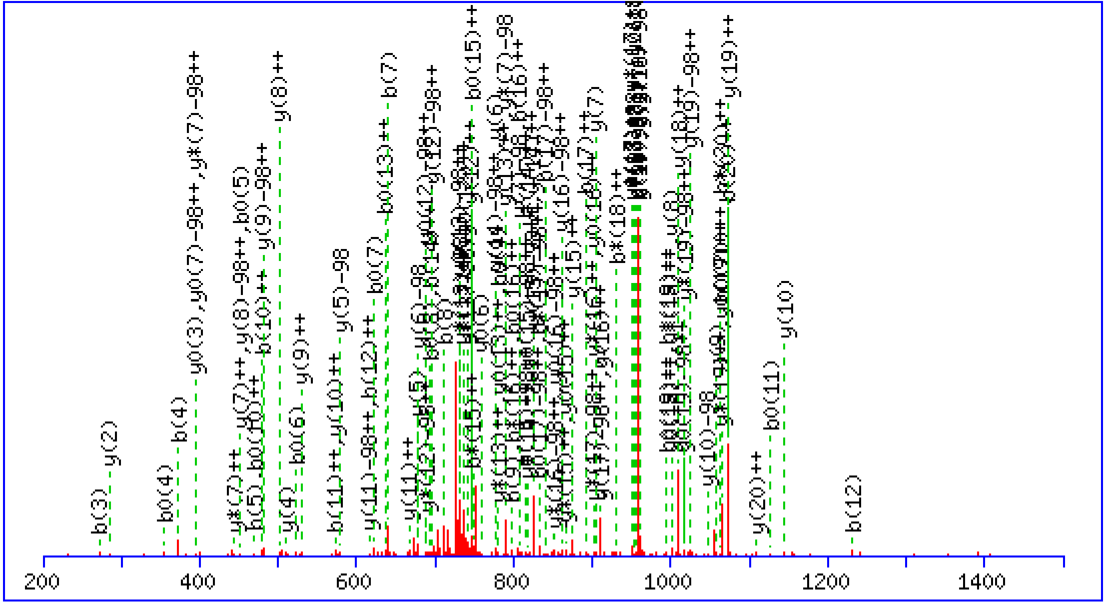
[b] The Phoscalc assigned sites of phosphorylation are indicated as [pS], [pT] or [pY], while ambiguous sites are represented as [s], [t] or [y].

Peptide No.1

AAETPAVASCWSGPQVSPEHK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **AAETPAVASCWSGPQVSPEHK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5777: 2287.992453 from(763.671427,3+) index(5235)
Title: Elution from: 43.629 to 43.629 scan no 3541 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2287.9933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 8.4e-006
Matched b ions: b(3), b(4), b(5), b(7), b(8), b(9), b(10), b(10)++, b(11)++, b(12), b(12)++, b(14)++, b(16)++, b(17)-98++, b(17)++, b(19)-98++, b(20)++
Matched y ions: y(2), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(9)-98++, y(9)-98, y(9), y(9)++, y(10)++, y(10), y(10)-98, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++

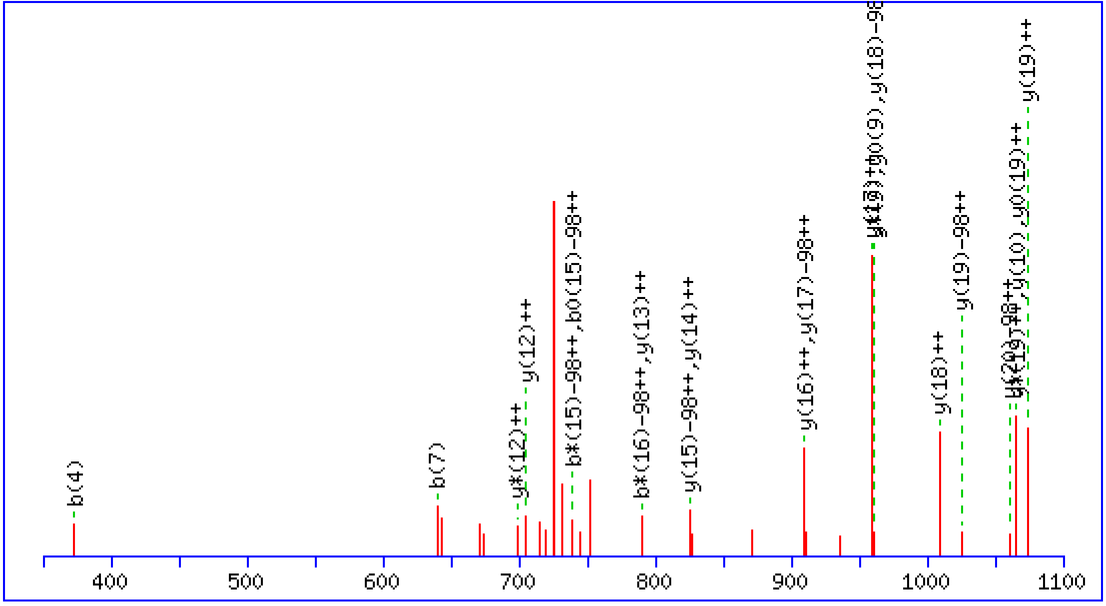
Peptide No.2

AAETPAVASCWSGPQVSPEHK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **AAETPAVASCWSGPQVSPEHK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus

GN=Srrm2 PE=1 SV=3

Match to Query 4905: 2287.994079 from(763.671969,3+) index(4747)
Title: Elution from: 35.389 to 35.389 scan no 3213 cid35.00 polarity:+:m1s



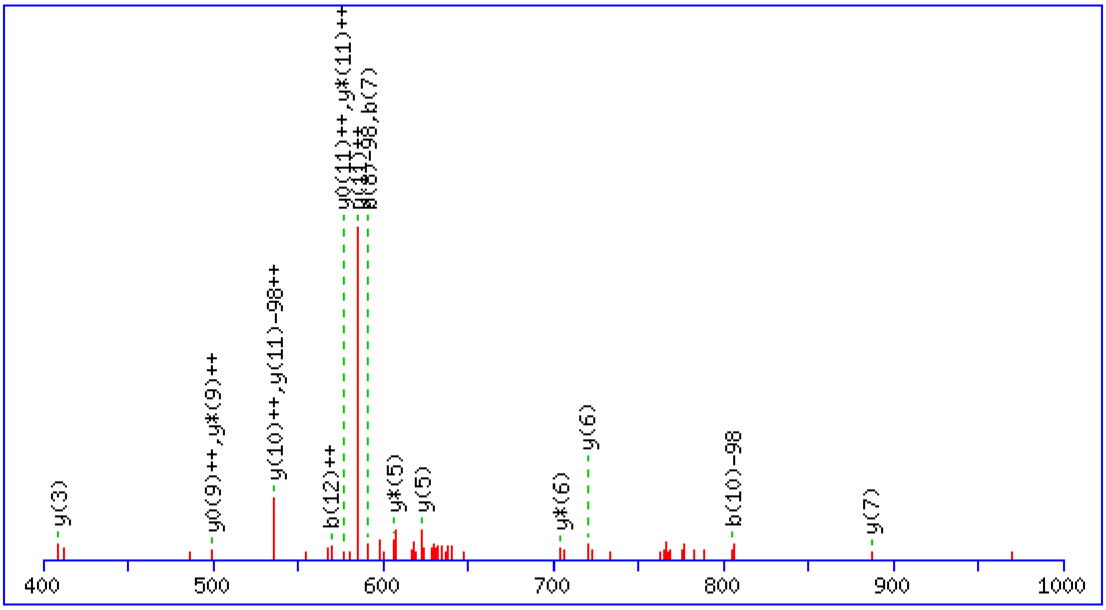
Monoisotopic mass of neutral peptide Mr(calc): 2287.9933
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0041
Matched b ions: b(4), b(7)
Matched y ions: y(10), y(12)++, y(13)++, y(14)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++

Peptide No.3

AAPGGASPTIFSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **AAPGGASPTIFSR**
Found in **HINT2_MOUSE** in **SwissProt**, Histidine triad nucleotide-binding protein 2, mitochondrial OS=Mus musculus GN=Hint2 PE=2 SV=1

Match to Query 2039: 1310.601710 from(656.308131,2+) index(2019)
Title: Elution from: 34.985 to 34.985 scan no 3273 cid35.00 polarity:+



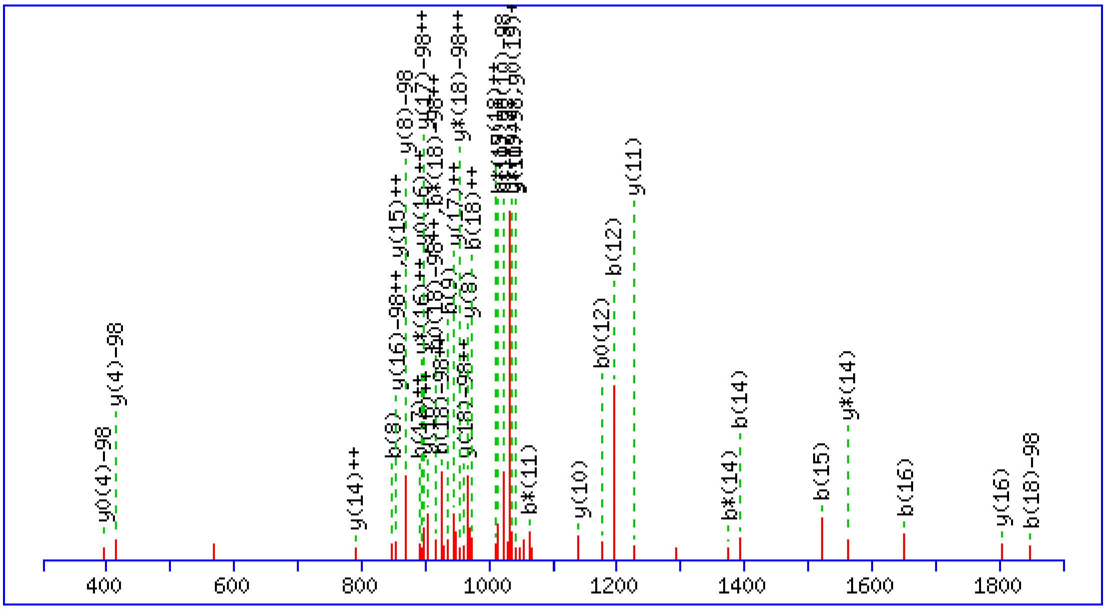
Monoisotopic mass of neutral peptide Mr(calc): 1310.6020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.049
Matched b ions: b(7), b(8)-98, b(10)-98, b(12)++
Matched y ions: y(3), y(5), y(6), y(7), y(10)++, y(11)++, y(11)-98++

Peptide No.4

AAQSPQQHSSGDPTEEESPV
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **AAQSPQQHSSGDPTEEESPV**
Found in **MOT1_MOUSE** in **SwissProt**, Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1

Match to Query 4632: 2159.859414 from(1080.936983,2+) index(3627)
Title: Elution from: 21.638 to 21.638 scan no 1438 cid35.00 polarity:+:m1s



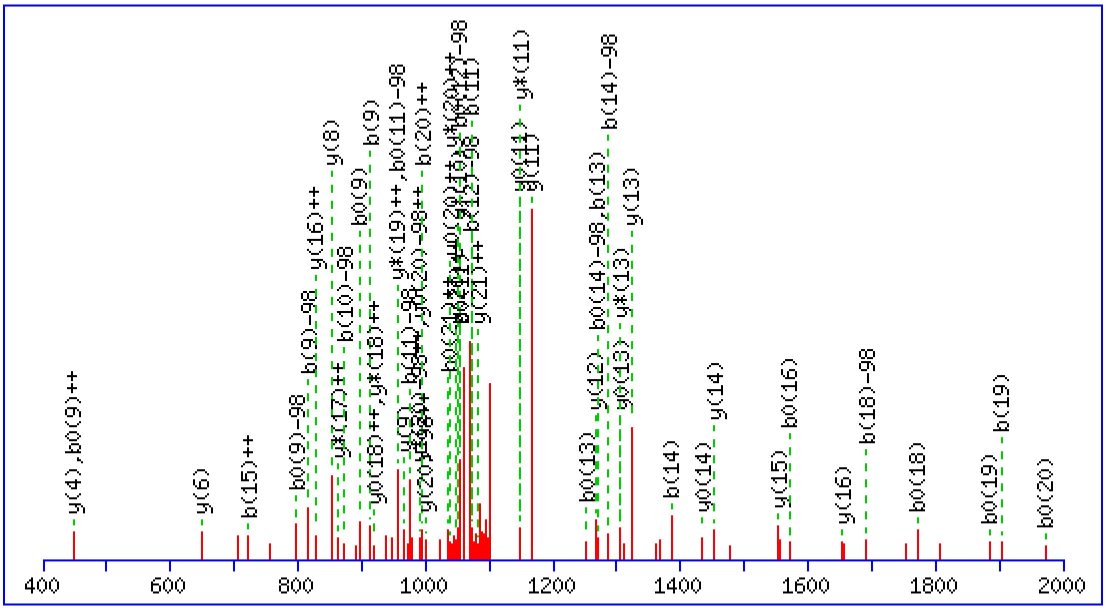
Monoisotopic mass of neutral peptide Mr(calc): 2159.8644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00033
Matched b ions: b(8), b(9), b(10), b(12), b(14), b(15), b(16), b(17)++, b(18)-98++, b(18)-98, b(18)++, b(19)++
Matched y ions: y(4)-98, y(8)-98, y(8), y(10), y(10)-98, y(11), y(14)++, y(15)++, y(16)-98++, y(16), y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++

Peptide No.5

AASADSTTEGTPTDGFTVLSTK
Confirmed sites:
Ambiguous sites: @S:3orS:6

MS/MS Fragmentation of **AASADSTTEGTPTDGFTVLSTK**
Found in **H2AY_MOUSE** in **SwissProt**, Core histone macro-H2A.1 OS=Mus musculus GN=H2afy PE=1 SV=3

Match to Query 5699: 2235.976404 from(1118.995478,2+) index(6359)
Title: Elution from: 44.976 to 44.976 scan no 4565 cid35.00 polarity:+:m1s



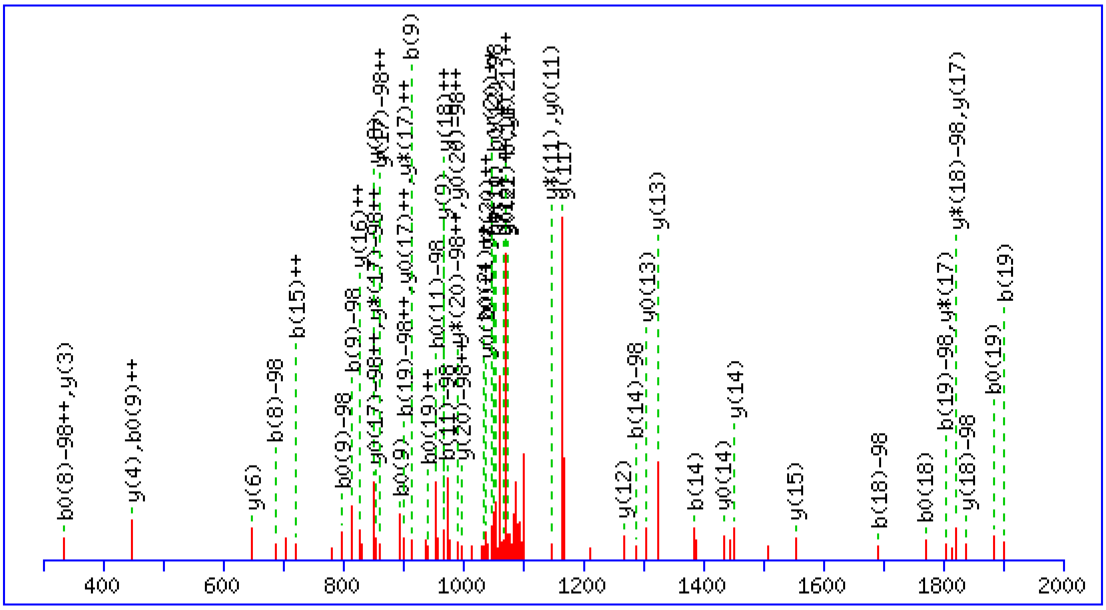
Monoisotopic mass of neutral peptide Mr(calc): 2235.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 3.4e-005
Matched b ions: b(9)-98, b(9), b(10)-98, b(11)-98, b(11), b(12)-98, b(13), b(14), b(14)-98, b(15)++, b(18)-98, b(19), b(20)++
Matched y ions: y(4), y(6), y(8), y(9), y(11), y(12), y(13), y(14), y(15), y(16), y(16)++, y(20)-98++, y(20)++, y(21)++

Peptide No.6

AASADSTTEGTPTDGFTVLSTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **AASADSTTEGTPTDGFTVLSTK**
Found in **H2AY_MOUSE** in **SwissProt**, Core histone macro-H2A.1 OS=Mus musculus GN=H2afy PE=1 SV=3

Match to Query 5840: 2235.975016 from(1118.994784,2+) index(6513)
Title: Elution from: 44.887 to 44.887 scan no 4585 cid35.00 polarity:+:m1s



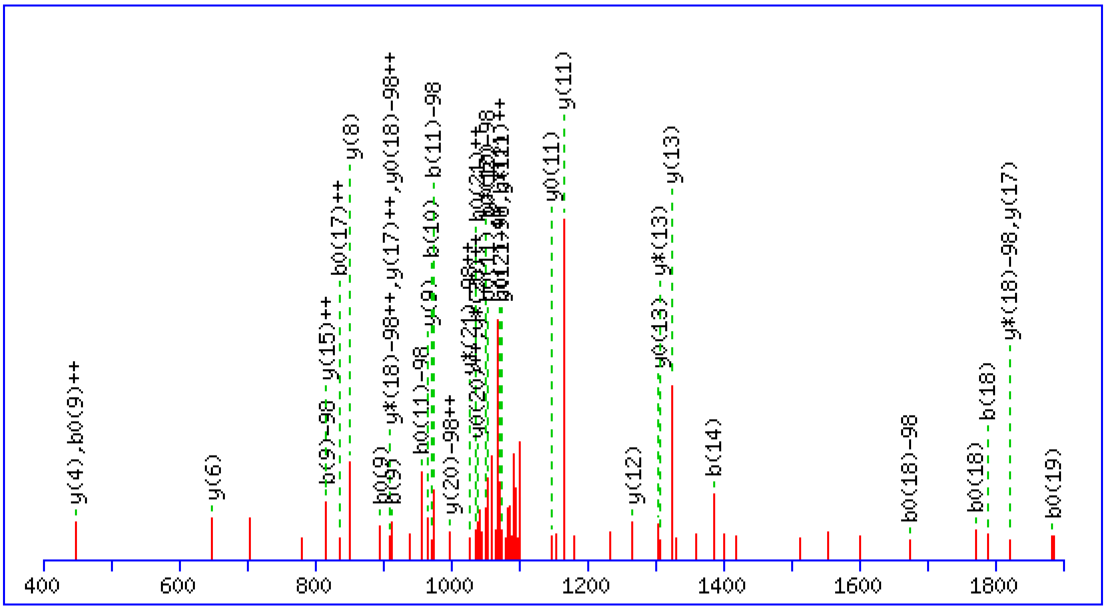
Monoisotopic mass of neutral peptide Mr(calc): 2235.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 **Expect:** 2.8e-006
Matched b ions: b(8)-98, b(9)-98, b(9), b(11)-98, b(11), b(14), b(14)-98, b(15)++, b(18)-98, b(19), b(19)-98, b(19)-98++
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16)++, y(17), y(17)-98++, y(18)-98, y(18)++, y(20)-98++, y(20)++

Peptide No.7

AASADSTTEGTPTDGFTVLSTK
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of **AASADSTTEGTPTDGFTVLSTK**
Found in **H2AY_MOUSE** in **SwissProt**, Core histone macro-H2A.1 OS=Mus musculus GN=H2afy PE=1 SV=3

Match to Query 4885: 2235.972998 from(1118.993775,2+) index(5618)
Title: Elution from: 44.366 to 44.366 scan no 4320 cid35.00 polarity:+:m1s



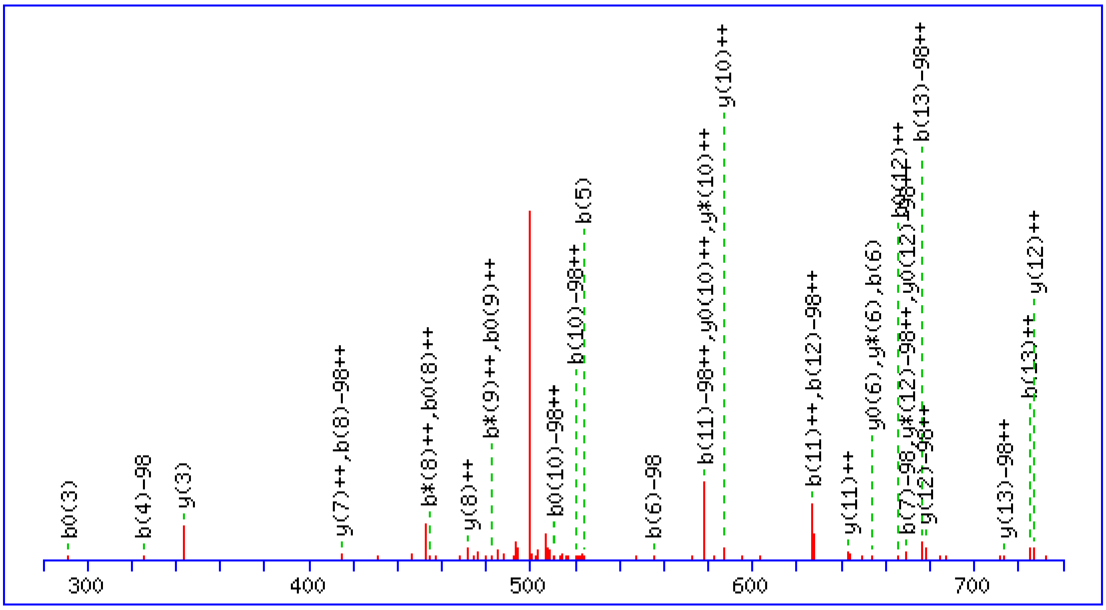
Monoisotopic mass of neutral peptide Mr(calc): 2235.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(9)-98, b(9), b(10), b(11)-98, b(11), b(12)-98, b(14), b(18)
Matched y ions: y(4), y(6), y(8), y(9), y(11), y(12), y(13), y(15)++, y(17), y(17)++, y(20)-98++

Peptide No.8

AASLTEDRGRDPVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AASLTEDRGRDPVK**
Found in **IF4G1_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1

Match to Query 3398: 1593.749979 from(532.257269,3+) index(425)
Title: Elution from: 19.715 to 19.715 scan no 1236 cid35.00 polarity:+



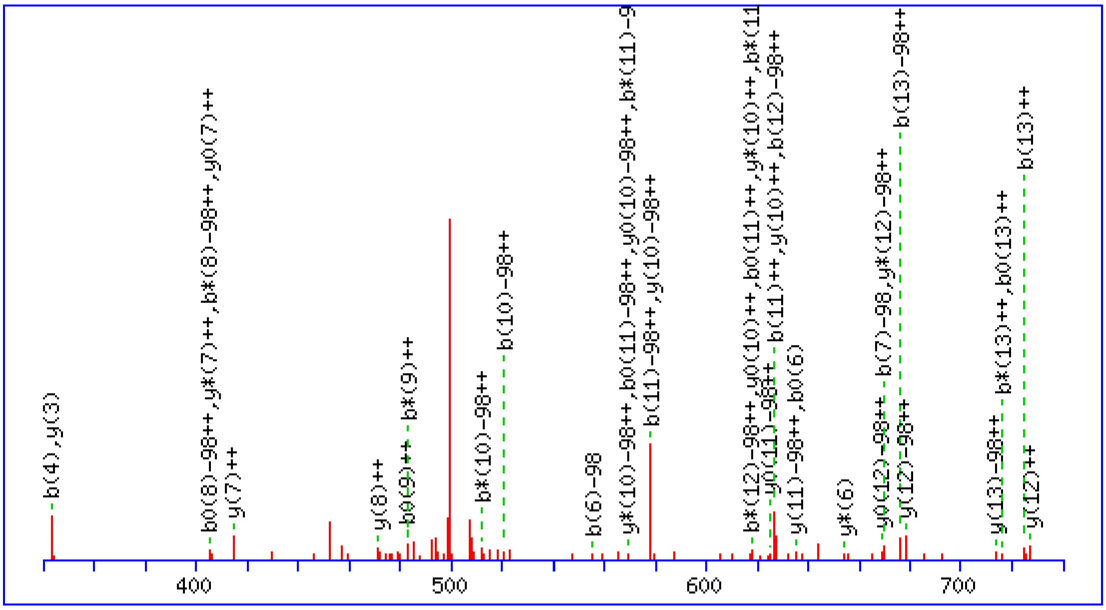
Monoisotopic mass of neutral peptide Mr(calc): 1593.7512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0029
Matched b ions: b(4)-98, b(5), b(6), b(6)-98, b(7)-98, b(8)-98++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(3), y(7)++, y(8)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++

Peptide No.9

AASLTEDRGRDPVK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **AASLTEDRGRDPVK**
Found in **IF4G1_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1

Match to Query 2784: 1593.748695 from(532.256841,3+) index(302)
Title: Elution from: 19.714 to 19.714 scan no 1179 cid35.00 polarity:+



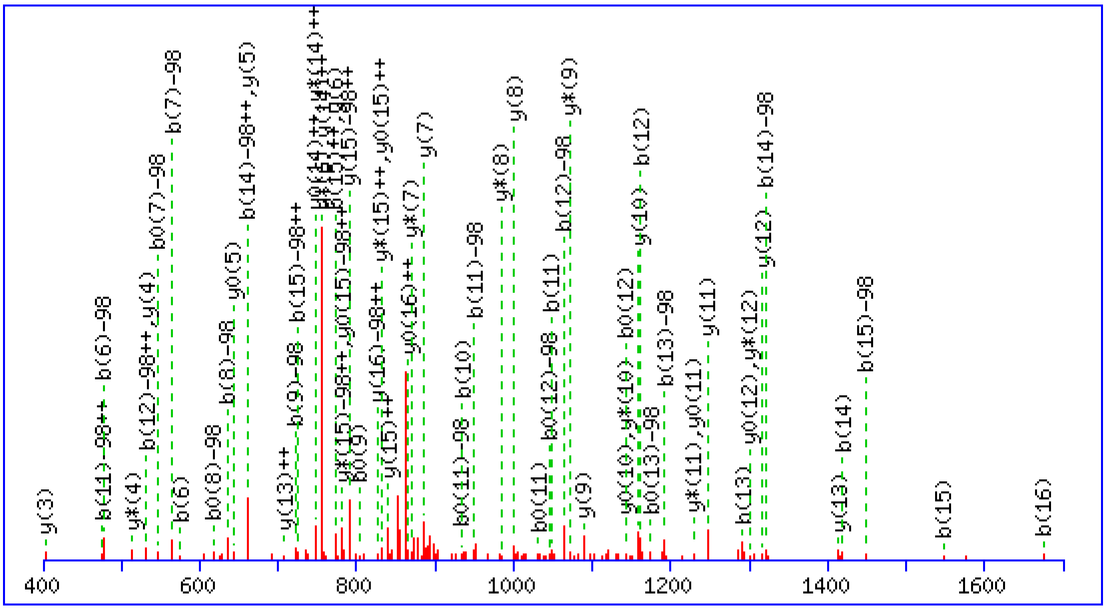
Monoisotopic mass of neutral peptide Mr(calc): 1593.7512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.05
Matched b ions: b(4), b(6)-98, b(7)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(13)++
Matched y ions: y(3), y(7)++, y(8)++, y(10)-98++, y(10)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++

Peptide No.10

AASPPASASDLIEQQQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AASPPASASDLIEQQQK**
Found in **FA40A_MOUSE** in **SwissProt**, Protein FAM40A OS=Mus musculus GN=Fam40a PE=1 SV=2

Match to Query 3975: 1819.837570 from(910.926061,2+) index(4509)
Title: Elution from: 43.781 to 43.781 scan no 3374 cid35.00 polarity:+:m1s



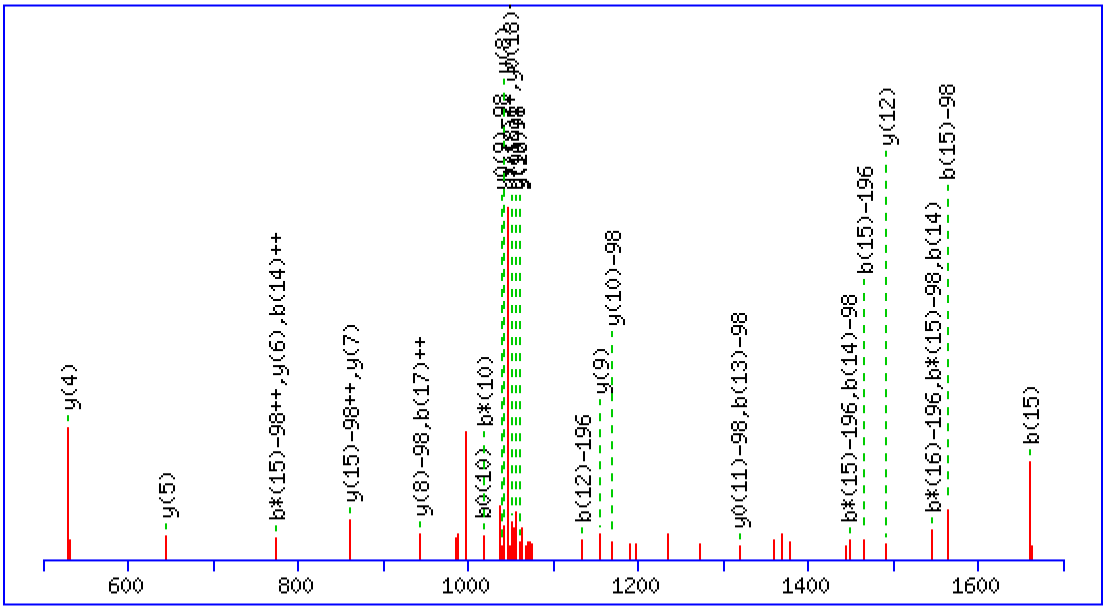
Monoisotopic mass of neutral peptide Mr(calc): 1819.8353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 **Expect:** 1.3e-007
Matched b ions: b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(10), b(11)-98++, b(11)-98, b(11), b(12)-98, b(12)-98++, b(12), b(13), b(13)-98, b(14)-98++, b(14)-98, b(14), b(15), b(15)-98, b(15)++, b(15)-98++, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++

Peptide No.11

AAVQELSGSILTSEDPEER
Confirmed sites: @S:9,@T:12
Ambiguous sites:

MS/MS Fragmentation of **AAVQELSGSILTSEDPEER**
Found in **PSN1_MOUSE** in **SwissProt**, Presenilin-1 OS=Mus musculus GN=Psen1 PE=1 SV=1

Match to Query 5700: 2189.911950 from(1095.963251,2+) index(6735)
Title: Elution from: 48.548 to 48.548 scan no 5025 cid35.00 polarity:+:m1s



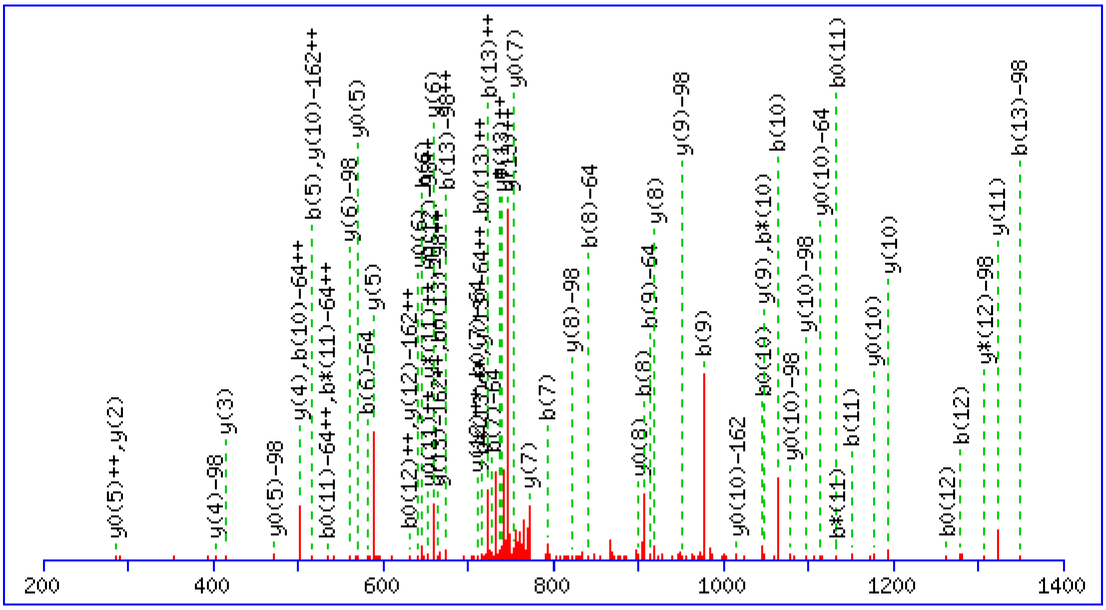
Monoisotopic mass of neutral peptide Mr(calc): 2189.9130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0063
Matched b ions: b(11)-98, b(12)-196, b(13)-98, b(14)++, b(14), b(14)-98, b(15)-98, b(15), b(15)-196, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(12), y(15)-98++, y(18)++

Peptide No.12

AAVQMEFLASSESV
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **AAVQMEFLASSESV**
Found in **GTR2_MOUSE** in **SwissProt**, Solute carrier family 2, facilitated glucose transporter member 2 OS=Mus musculus GN=Slc2a2 PE=1 SV=3

Match to Query 3735: 1563.652926 from(782.833739,2+) index(2371)
Title: Elution from: 54.865 to 54.865 scan no 4610 cid35.00 polarity:+



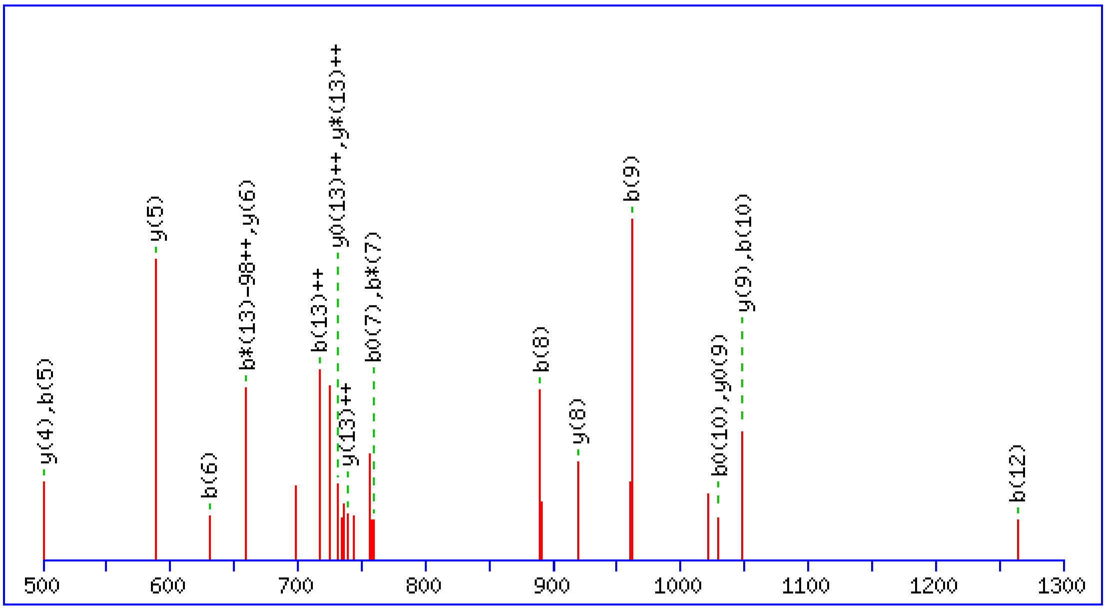
Monoisotopic mass of neutral peptide Mr(calc): 1563.6528
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 7.5e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13)-98, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(6), y(6)-98, y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(12)++, y(13)++

Peptide No.13

AAVQMEFLASSESV
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **AAVQMEFLASSESV**
Found in **GTR2_MOUSE** in **SwissProt**, Solute carrier family 2, facilitated glucose transporter member 2 OS=Mus musculus GN=Slc2a2 PE=1 SV=3

Match to Query 2767: 1547.659404 from(774.836978,2+) index(5801)
Title: Elution from: 57.285 to 57.285 scan no 5610 cid35.00 polarity:+:m1s



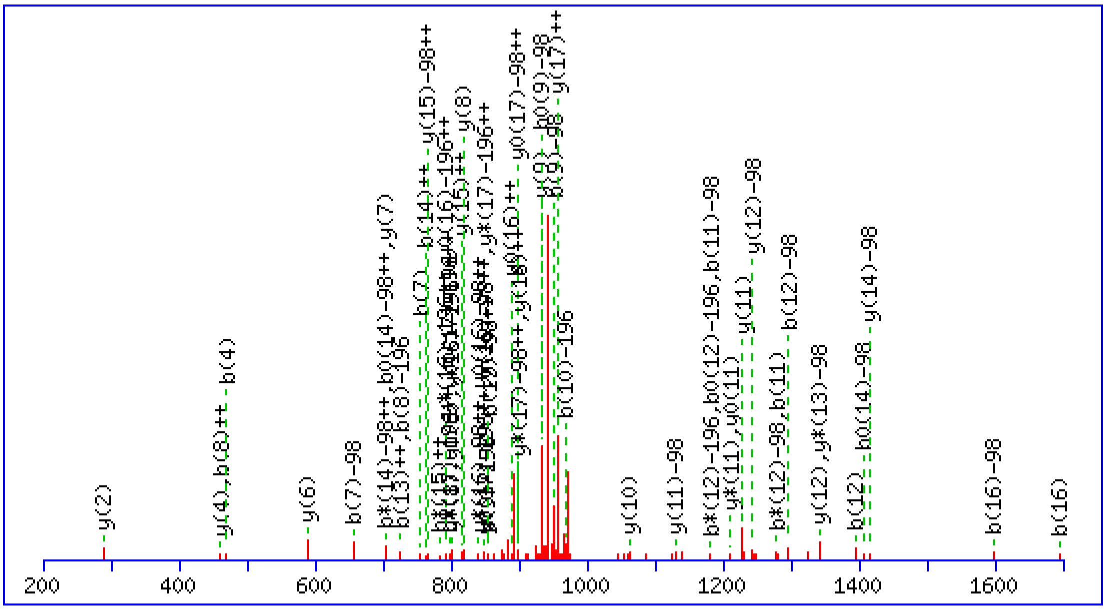
Monoisotopic mass of neutral peptide Mr(calc): 1547.6579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00016
Matched b ions: b(5), b(6), b(8), b(9), b(10), b(12), b(13)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(13)++

Peptide No.14

ADSDGDLSENDDGAGDLR
Confirmed sites: @S:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of **ADSDGDLSENDDGAGDLR**
Found in **AKAP8_MOUSE** in **SwissProt**, A-kinase anchor protein 8 OS=Mus musculus GN=Akap8 PE=1 SV=1

Match to Query 4119: 1980.658148 from(991.336350,2+) index(4789)
Title: Elution from: 33.101 to 33.101 scan no 2965 cid35.00 polarity:+:m1s



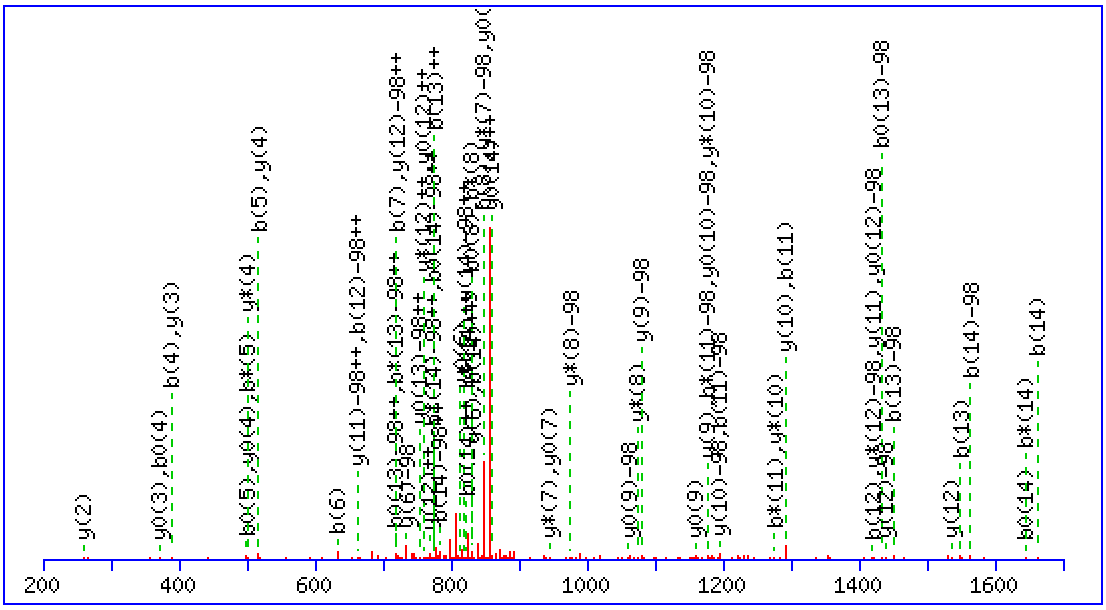
Monoisotopic mass of neutral peptide Mr(calc): 1980.6623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 5.2e-006
Matched b ions: b(4), b(7)-98, b(7), b(8)++, b(8)-196, b(9)-98, b(9)-196, b(10)-196, b(11), b(11)-98, b(12), b(12)-98, b(13)++, b(14)++, b(16)-98, b(16), b(17)-98++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(14)-98, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)++

Peptide No.15

ADSDQDSKMSFKEIK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **ADSDQDSKMSFKEIK**
Found in **PLCD3_MOUSE** in **SwissProt**, 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-3 OS=Mus musculus GN=Plcd3 PE=1 SV=2

Match to Query 3940: 1807.764972 from(904.889762,2+) index(4761)
Title: Elution from: 49.301 to 49.301 scan no 3890 cid35.00 polarity:+:m1s



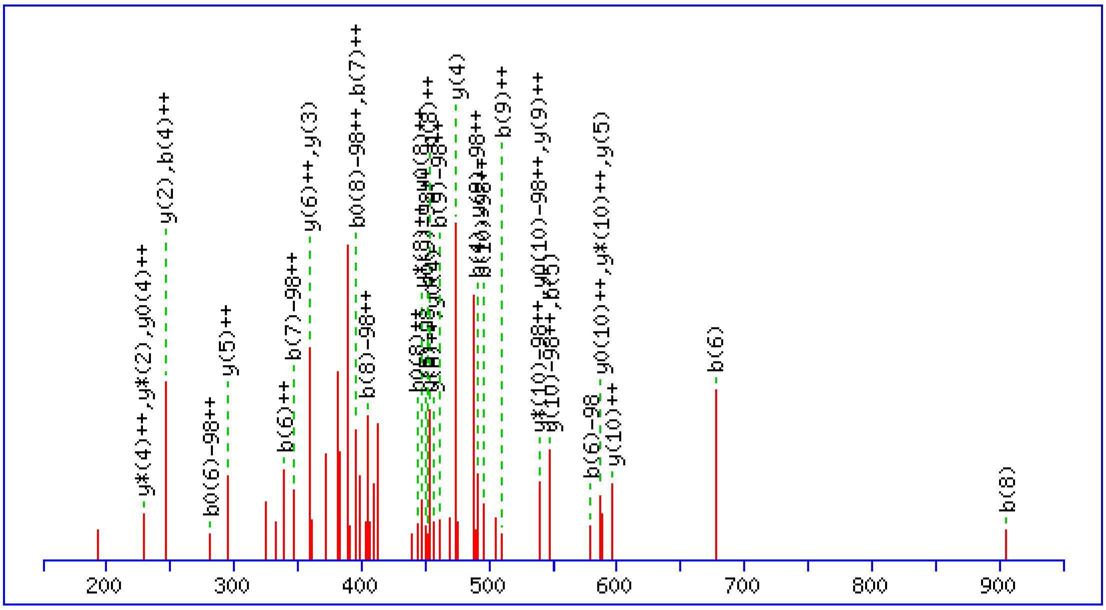
Monoisotopic mass of neutral peptide Mr(calc): 1807.7699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00068
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(11)-98, b(11), b(12), b(12)-98++, b(13)-98, b(13), b(13)++, b(14)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(6)-98, y(6), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98++, y(12), y(12)-98, y(12)-98++, y(12)++, y(14)-98++

Peptide No.16

ADSHGELDLAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ADSHGELDLAR**
Found in **ACOT1_MOUSE** in **SwissProt**, Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1 PE=1 SV=1

Match to Query 1792: 1262.528703 from(421.850177,3+) index(1116)
Title: Elution from: 26.024 to 26.024 scan no 2057 cid35.00 polarity:+



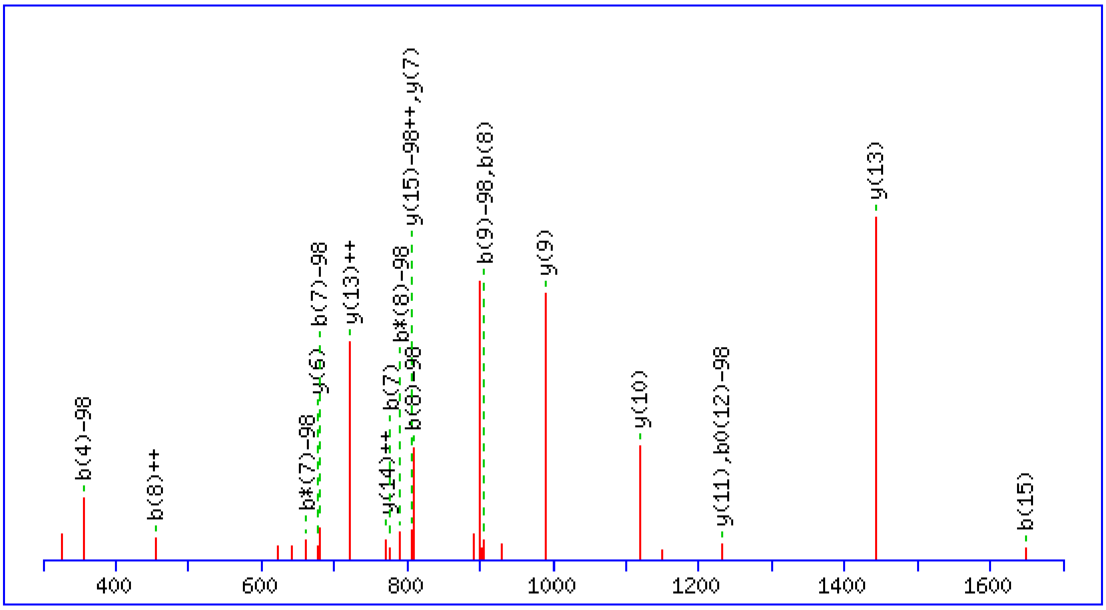
Monoisotopic mass of neutral peptide Mr(calc): 1262.5292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0037
Matched b ions: b(4)++, b(4), b(5), b(5)-98, b(6), b(6)++, b(6)-98, b(7)++, b(7)-98++, b(8), b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++

Peptide No.17

ADSVPNLEPSEESLVTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ADSVPNLEPSEESLVTK**
Found in **LNP_MOUSE** in **SwissProt**, Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1

Match to Query 4563: 1893.861684 from(947.938118,2+) index(6456)
Title: Elution from: 44.086 to 44.086 scan no 4484 cid35.00 polarity:+:m1s



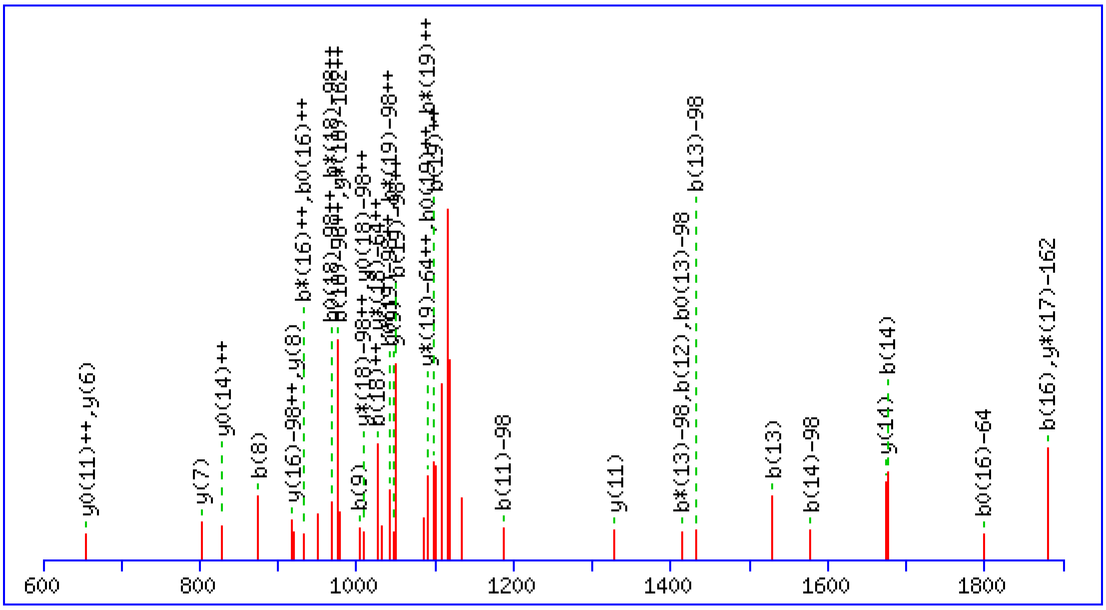
Monoisotopic mass of neutral peptide Mr(calc): 1893.8608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0047
Matched b ions: b(4)-98, b(7)-98, b(7), b(8)++, b(8)-98, b(8), b(9)-98, b(15)
Matched y ions: y(6), y(7), y(9), y(10), y(11), y(13)++, y(13), y(14)++, y(15)-98++

Peptide No.18

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **AEAKEESEESDEDMGFGLFD**
Found in **RLA0_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5060: 2329.841318 from(1165.927935,2+) index(5933)
Title: Elution from: 52.409 to 52.409 scan no 5125 cid35.00 polarity:+:m1s



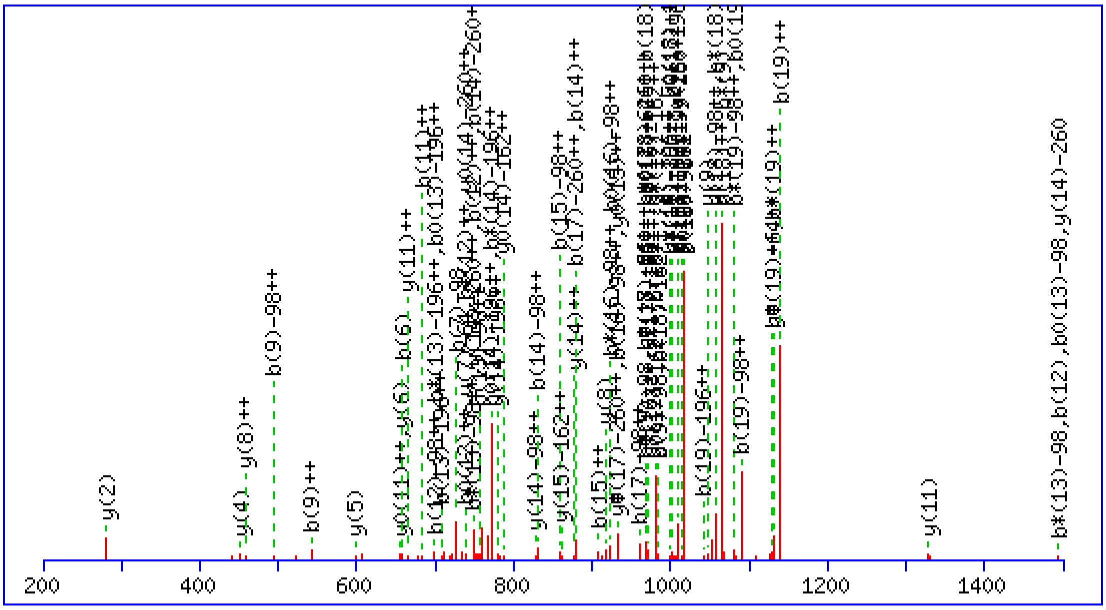
Monoisotopic mass of neutral peptide Mr(calc): 2329.8457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.017
Matched b ions: b(8), b(9), b(11)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(16), b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(6), y(7), y(8), y(9), y(11), y(14), y(16)-98++

Peptide No.19

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **AEAKEESEESDEDMGFGLFD**
Found in **RLA0_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 6211: 2409.811599 from(804.277809,3+) index(7123)
Title: Elution from: 61.044 to 61.044 scan no 6223 cid35.00 polarity:+:m1s



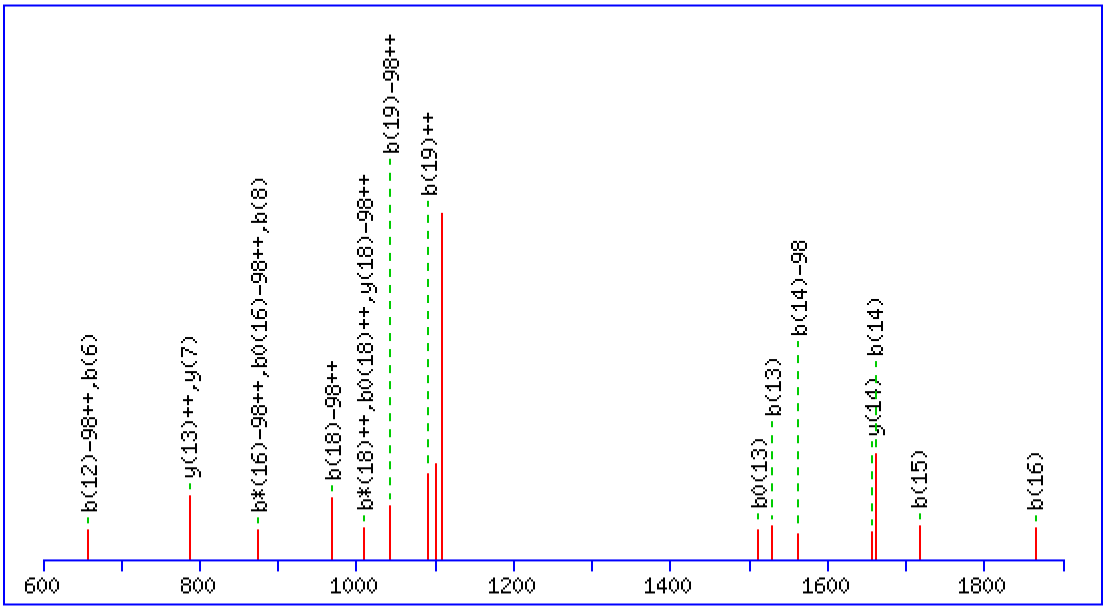
Monoisotopic mass of neutral peptide Mr(calc): 2409.8120
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.0006
Matched b ions: b(6), b(7)-98, b(9)++, b(9)-98++, b(9)-98, b(11)++, b(12), b(12)++, b(12)-98++, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(4), y(5), y(6), y(8)++, y(8), y(9), y(11), y(11)++, y(14)-98++, y(14)++, y(14)-196++, y(17)-196++, y(18)-98++, y(18)-196++

Peptide No.20

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **AEAKEESEESDEDMGFGLFD**
Found in **RLA0_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5029: 2313.845622 from(1157.930087,2+) index(6055)
Title: Elution from: 59.022 to 59.022 scan no 5644 cid35.00 polarity:+:m1s



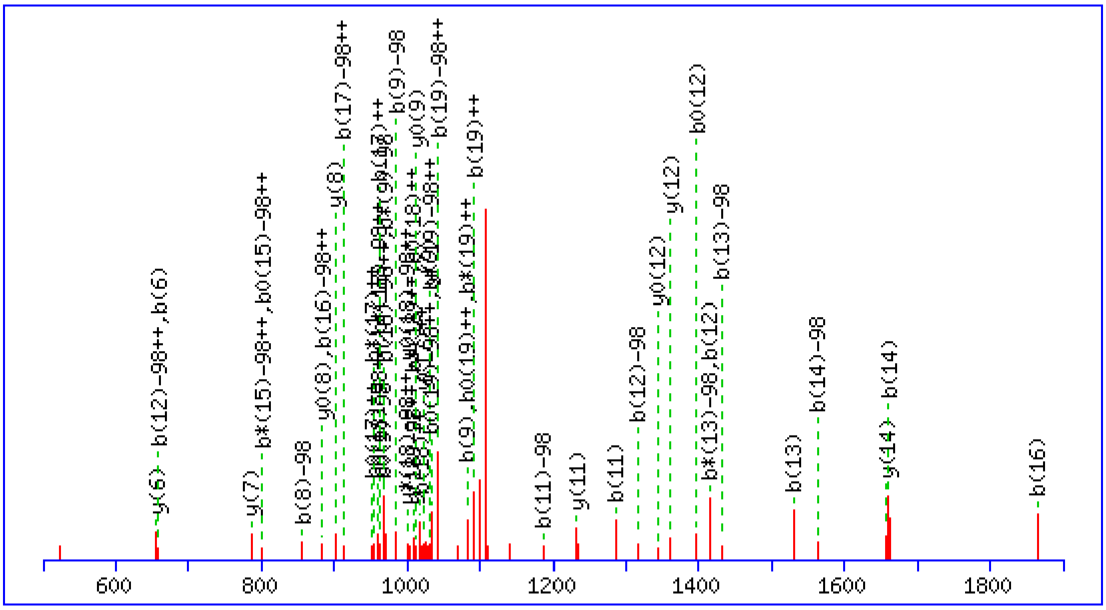
Monoisotopic mass of neutral peptide Mr(calc): 2313.8508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0015
Matched b ions: b(6), b(8), b(12)-98++, b(13), b(14), b(14)-98, b(15), b(16), b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(7), y(13)++, y(14), y(18)-98++

Peptide No.21

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **AEAKEESEESDEDMGFGLFD**
Found in **RLA0_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5851: 2313.844998 from(1157.929775,2+) index(6897)
Title: Elution from: 60.502 to 60.502 scan no 6104 cid35.00 polarity:+:m1s



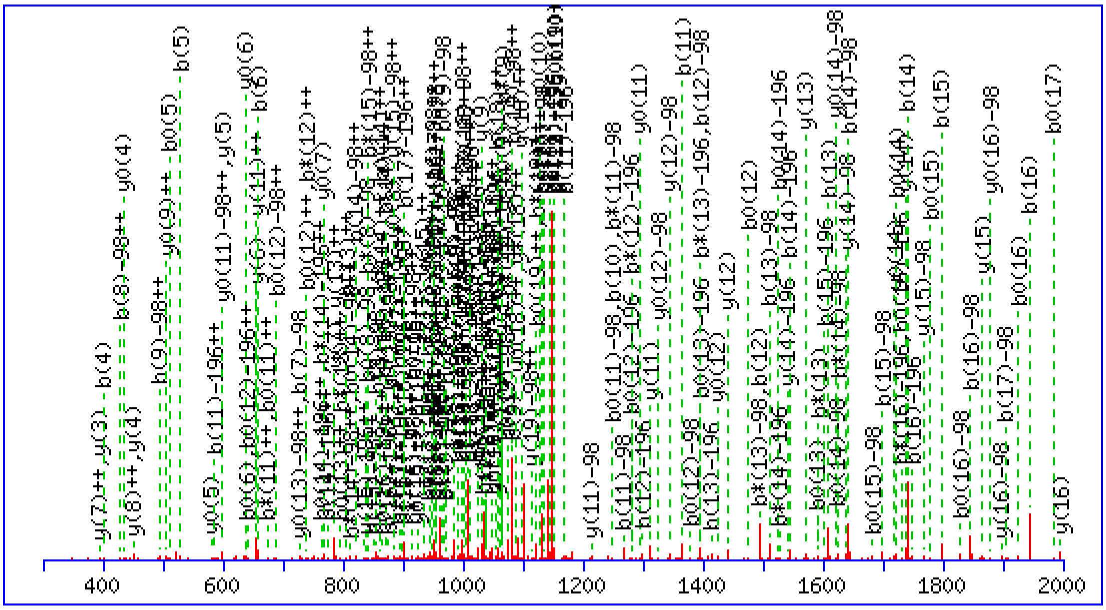
Monoisotopic mass of neutral peptide Mr(calc): 2313.8508
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 2.3e-005
Matched b ions: b(6), b(8)-98, b(9)-98, b(9), b(11), b(11)-98, b(12), b(12)-98++, b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(16), b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(6), y(7), y(8), y(9), y(11), y(12), y(14), y(17)++, y(18)-98++

Peptide No.22

AEAKEESEESDEDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **AEAKEESEESDEDMGFGLFD**
Found in **RLA0_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3

Match to Query 5987: 2393.810098 from(1197.912325,2+) index(6985)
Title: Elution from: 68.781 to 68.781 scan no 6655 cid35.00 polarity:+:m1s



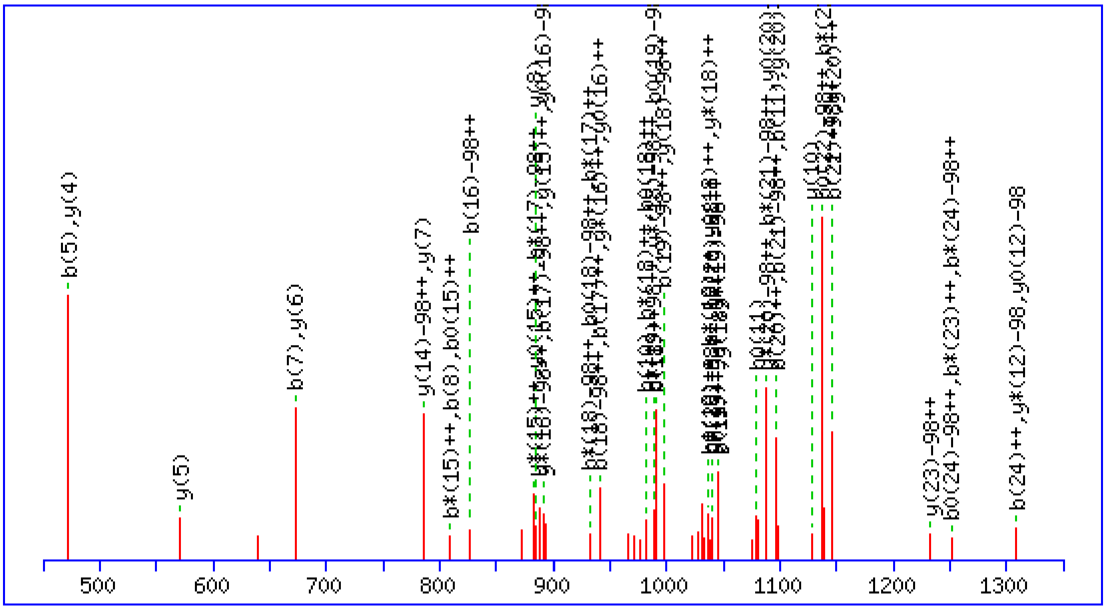
Monoisotopic mass of neutral peptide Mr(calc): 2393.8171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.0002
Matched b ions: b(4), b(5), b(6), b(7)-98, b(8)-98, b(8)-98++, b(8), b(9), b(9)-98, b(9)-98++, b(10)-98, b(10)-196, b(10), b(11), b(11)-98, b(11)-196, b(11)-196++, b(12), b(12)-98, b(12)-196, b(13)-98, b(13), b(13)-196, b(13)++, b(14)-98, b(14), b(14)-98++, b(14)-196, b(14)-196++, b(14)++, b(15), b(15)-98, b(15)-98++, b(15)++, b(15)-196, b(16)-98, b(16), b(16)-196, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)-98, b(17)++, b(18)-98++, b(18)-196++, b(18)++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(10), y(11), y(11)++, y(11)-98, y(12), y(12)-98, y(13)++, y(13), y(14), y(14)-98, y(14)-196, y(15)++, y(15), y(15)-98, y(15)-196++, y(15)-98++, y(16), y(16)-98, y(16)-196++, y(16)-98++, y(17)-196++, y(17)-98++, y(17)++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++

Peptide No.23

AEALSSLHGDDQDSEDEVLTVPEVK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **AEALSSLHGDDQDSEDEVLTVPEVK**
Found in **MPRI_MOUSE** in **SwissProt**, Cation-independent mannose-6-phosphate receptor OS=Mus musculus GN=Igf2r PE=1 SV=1

Match to Query 5525: 2762.214810 from(921.745546,3+) index(5501)
Title: Elution from: 46.236 to 46.236 scan no 4557 cid35.00 polarity:+:m1s



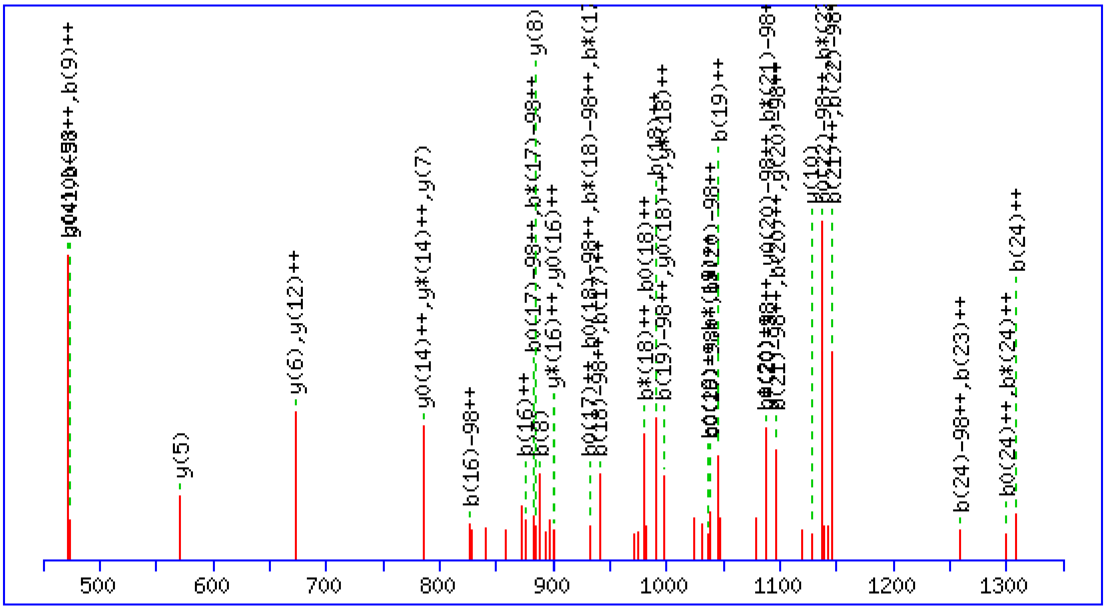
Monoisotopic mass of neutral peptide Mr(calc): 2762.2171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 0.00016
Matched b ions: b(5), b(7), b(8), b(10), b(11), b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(24)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(14)-98++, y(15)++, y(18)++, y(18)-98++, y(20)++, y(20)-98++, y(23)-98++

Peptide No.24

AEALSSLHGDDQDSEDEVLTVPEVK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **AEALSSLHGDDQDSEDEVLTVPEVK**
Found in **MPRI_MOUSE** in **SwissProt**, Cation-independent mannose-6-phosphate receptor OS=Mus musculus GN=Igf2r PE=1 SV=1

Match to Query 6551: 2762.216007 from(921.745945,3+) index(6448)
Title: Elution from: 46.525 to 46.525 scan no 4746 cid35.00 polarity:+:m1s



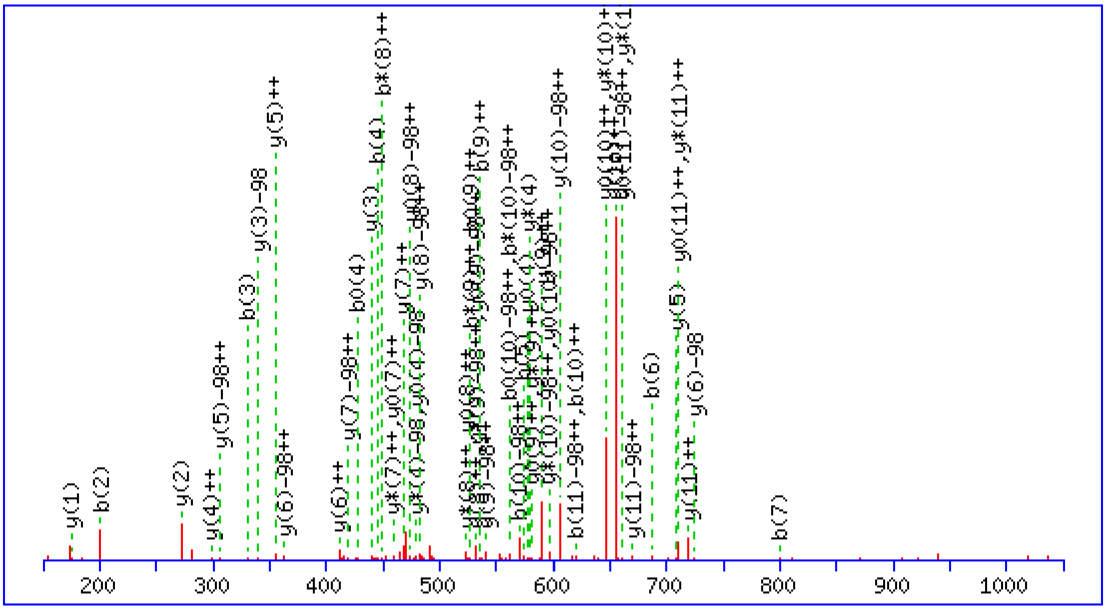
Monoisotopic mass of neutral peptide Mr(calc): 2762.2171
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.4e-005
Matched b ions: b(5), b(8), b(9)++, b(16)-98++, b(16)++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(23)++, b(24)-98++, b(24)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(12)++, y(20)++, y(20)-98++

Peptide No.25

AEEDEILNRSPR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **AEEDEILNRSPR**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 3012: 1507.666206 from(503.562678,3+) index(1175)
Title: Elution from: 26.125 to 26.125 scan no 2106 cid35.00 polarity:+



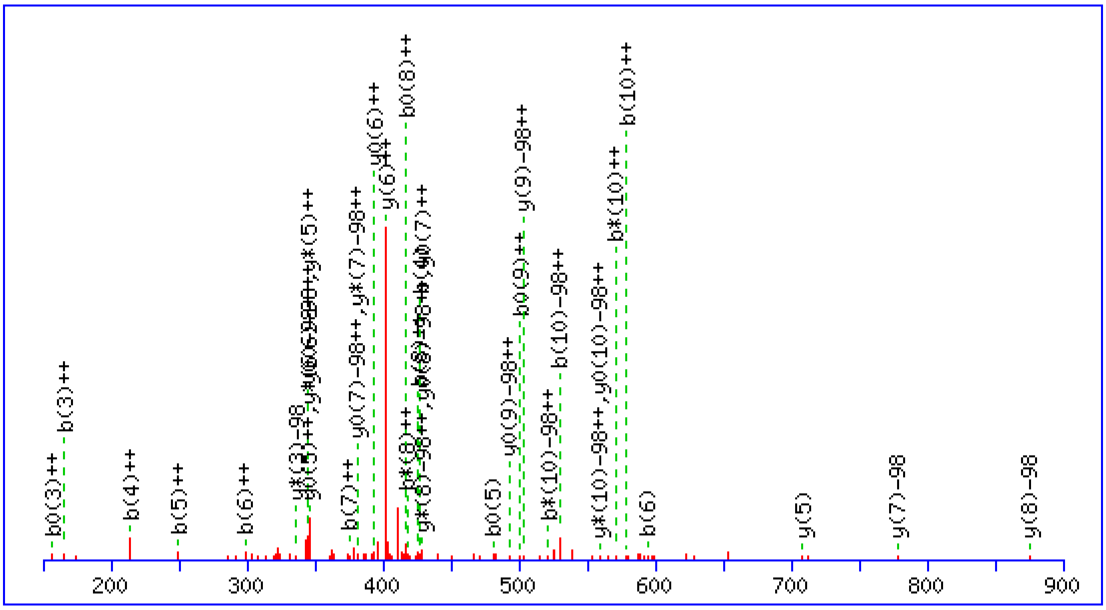
Monoisotopic mass of neutral peptide Mr(calc): 1507.6667
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 5.8e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(9)++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(3)-98, y(4)++, y(5)++, y(5)-98++, y(5), y(6)++, y(6)-98++, y(6)-98, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.26

AEEPAPRTSHK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **AEEPAPRTSHK**
Found in **BHLH9_MOUSE** in **SwissProt**, Protein BHLHb9 OS=Mus musculus GN=Bhlhb9 PE=1 SV=1

Match to Query 2485: 1301.577375 from(434.866401,3+) index(211)
Title: Elution from: 25.840 to 25.840 scan no 1349 cid35.00 polarity:+



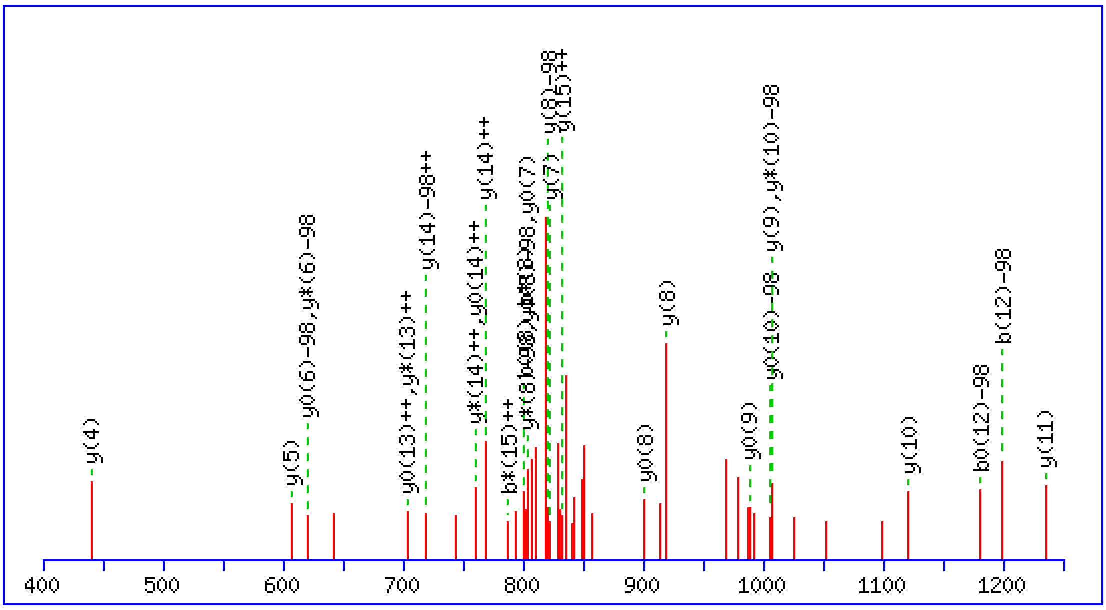
Monoisotopic mass of neutral peptide Mr(calc): 1301.5765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.048
Matched b ions: b(3)++, b(4)++, b(4), b(5)++, b(6), b(6)++, b(7)++, b(8)++, b(10)-98++, b(10)++
Matched y ions: y(5), y(6)++, y(7)-98, y(8)-98, y(9)-98++

Peptide No.27

AELGMNDSPSQSPPVK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **AELGMNDSPSQSPPVK**
Found in **ACSA_MOUSE** in **SwissProt**, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2

Match to Query 3972: 1735.746478 from(868.880515,2+) index(1792)
Title: Elution from: 32.397 to 32.397 scan no 2957 cid35.00 polarity:+



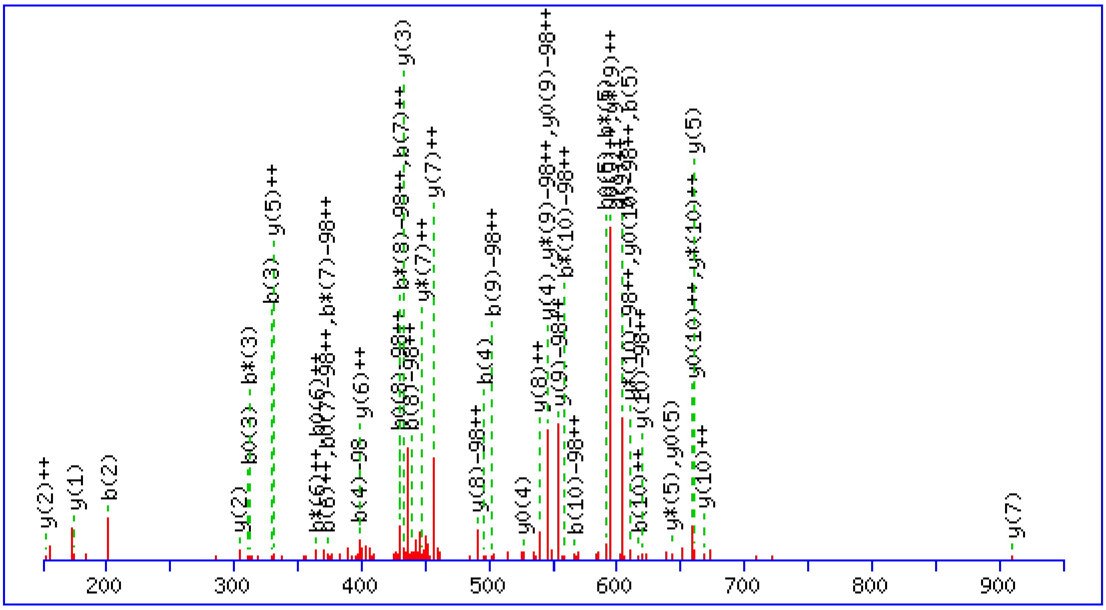
Monoisotopic mass of neutral peptide Mr(calc): 1735.7488
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.044
Matched b ions: b(12)-98
Matched y ions: y(4), y(5), y(7), y(8), y(8)-98, y(9), y(10), y(11), y(14)-98++, y(14)++, y(15)++

Peptide No.28

AEQSLHDLQER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **AEQSLHDLQER**
Found in **STIM1_MOUSE** in **SwissProt**, Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=2

Match to Query 2769: 1404.603495 from(469.208441,3+) index(499)
Title: Elution from: 29.669 to 29.669 scan no 1766 cid35.00 polarity:+



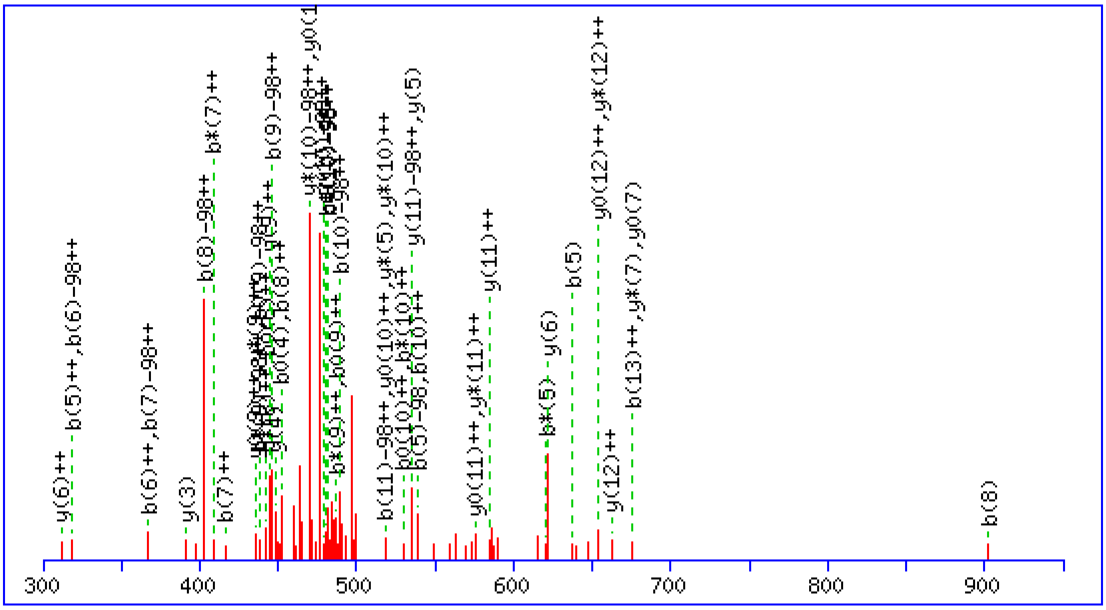
Monoisotopic mass of neutral peptide Mr(calc): 1404.6034
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00064
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(6)++, b(7)++, b(8)-98++, b(9)-98++, b(10)-98++, b(10)++
Matched y ions: y(1), y(2), y(2)++, y(3), y(4), y(5), y(5)++, y(6)++, y(7), y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++

Peptide No.29

AERLSPPASSGSER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **AERLSPPASSGSER**
Found in **MLXPL_MOUSE** in **SwissProt**, Carbohydrate-responsive element-binding protein OS=Mus musculus GN=Mlxipl PE=1 SV=1

Match to Query 3078: 1522.675875 from(508.565901,3+) index(534)
Title: Elution from: 20.618 to 20.618 scan no 1358 cid35.00 polarity:+



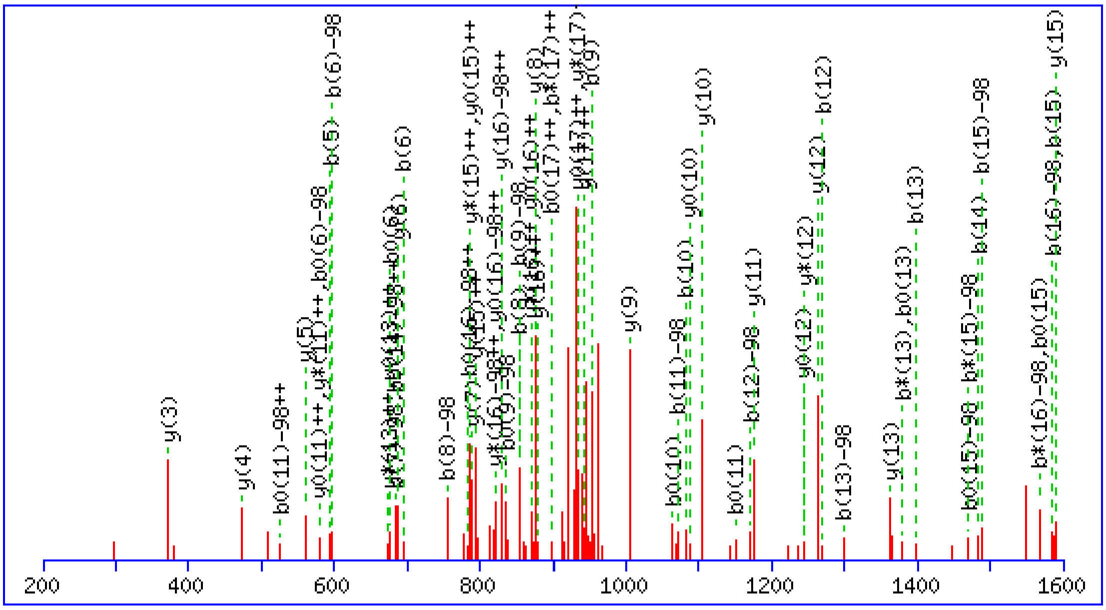
Monoisotopic mass of neutral peptide Mr(calc): 1522.6777
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0049
Matched b ions: b(4), b(5)-98, b(5)++, b(5), b(6)++, b(6)-98++, b(7)-98++, b(7)++, b(8)-98++, b(8), b(8)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++

Peptide No.30

AESPETSAVESTQSTPQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AESPETSAVESTQSTPQK**
Found in **PDS5B_MOUSE** in **SwissProt**, Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1

Match to Query 4680: 1955.830748 from(978.922650,2+) index(4429)
Title: Elution from: 24.167 to 24.167 scan no 1805 cid35.00 polarity:+:m1s



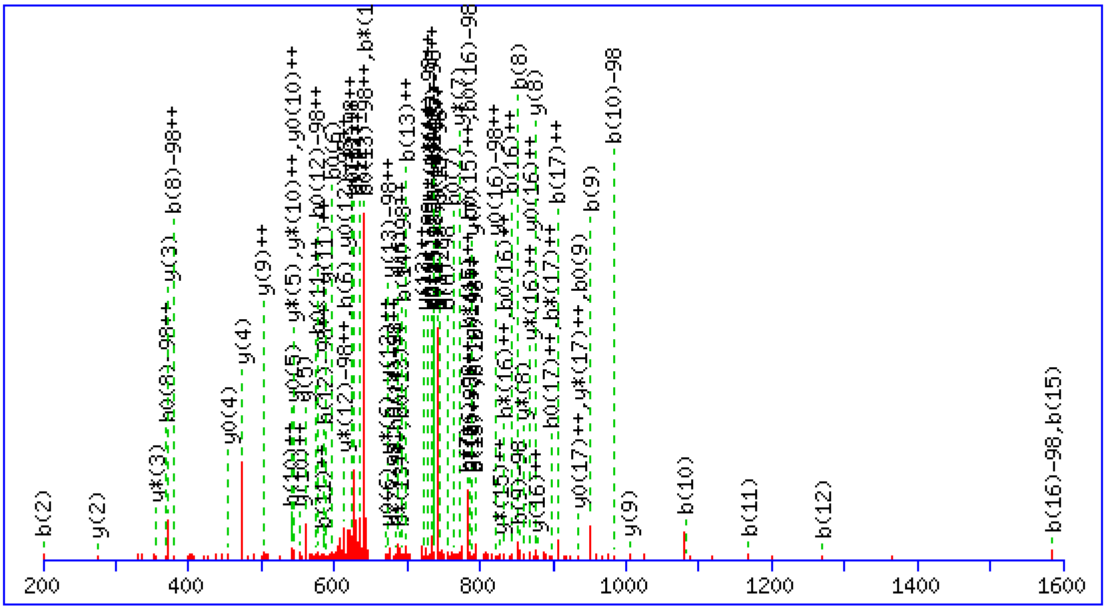
Monoisotopic mass of neutral peptide Mr(calc): 1955.8361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 **Expect:** 2.1e-008
Matched b ions: b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10), b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14), b(15)-98, b(15), b(16)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15)++, y(15), y(16)-98++, y(16)++, y(17)++

Peptide No.31

AESPETSAVESTQSTPQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **AESPETSAVESTQSTPQK**
Found in **PDS5B_MOUSE** in **SwissProt**, Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1

Match to Query 4961: 1955.838546 from(652.953458,3+) index(4079)
Title: Elution from: 30.204 to 30.204 scan no 1911 cid35.00 polarity:+:m1s



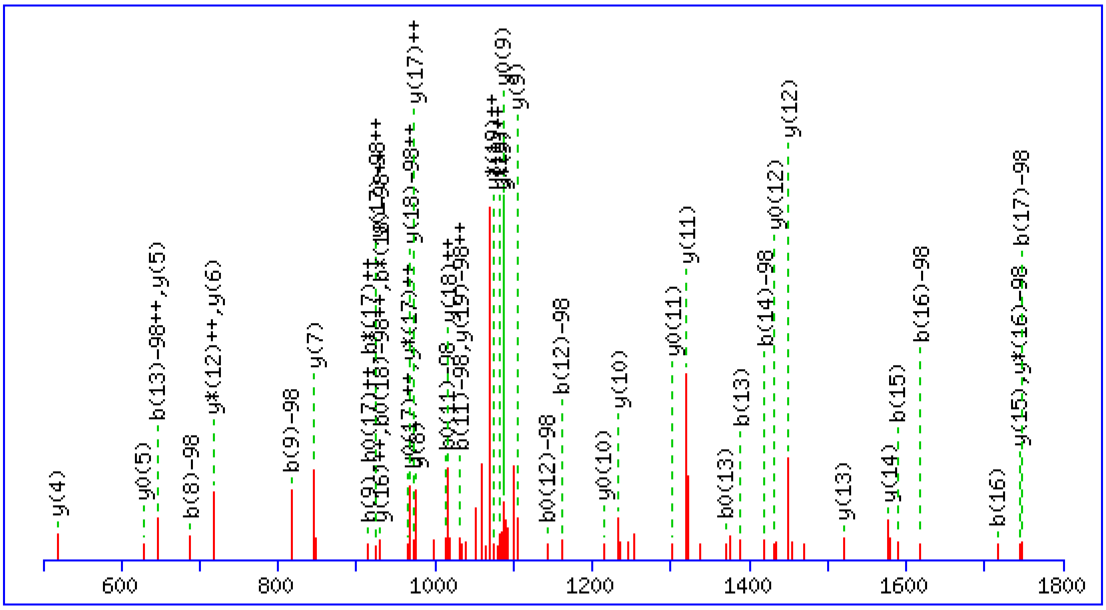
Monoisotopic mass of neutral peptide Mr(calc): 1955.8361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 2.4e-005
Matched b ions: b(2), b(6), b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9), b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(11)++, b(12), b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(15), b(15)++, b(15)-98++, b(16)-98, b(16)-98++, b(16)++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++

Peptide No.32

AESSDSGAESEEEEAQEELK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **AESSDSGAESEEEEAQEELK**
Found in **ACBD5_MOUSE** in **SwissProt**, Acyl-CoA-binding domain-containing protein 5 OS=Mus musculus GN=Acbd5 PE=1 SV=1

Match to Query 5828: 2232.837410 from(1117.425981,2+) index(5837)
Title: Elution from: 36.262 to 36.262 scan no 3475 cid35.00 polarity:+:m1s



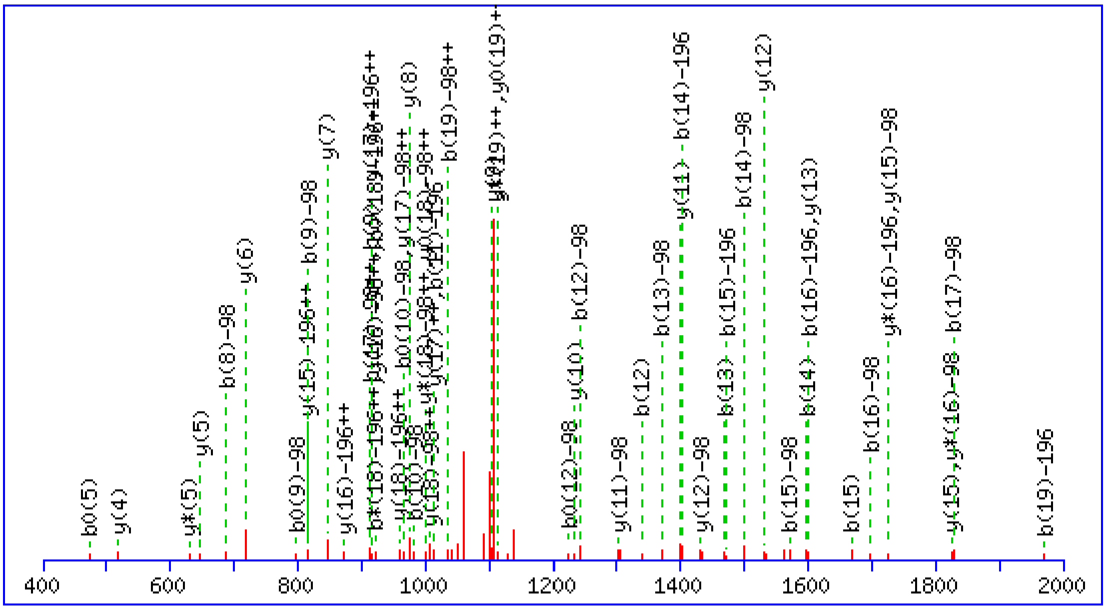
Monoisotopic mass of neutral peptide Mr(calc): 2232.8430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 9.3e-007
Matched b ions: b(8)-98, b(9)-98, b(9), b(11)-98, b(12)-98, b(13)-98++, b(13), b(14)-98, b(15), b(16)-98, b(16), b(17)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++

Peptide No.33

AESSDSGAESEEEEAQEELK
Confirmed sites: @S:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of **AESSDSGAESEEEEAQEELK**
Found in **ACBD5_MOUSE** in **SwissProt**, Acyl-CoA-binding domain-containing protein 5 OS=Mus musculus GN=Acbd5 PE=1 SV=1

Match to Query 4931: 2312.804082 from(1157.409317,2+) index(4987)
Title: Elution from: 38.036 to 38.036 scan no 3557 cid35.00 polarity:+:m1s



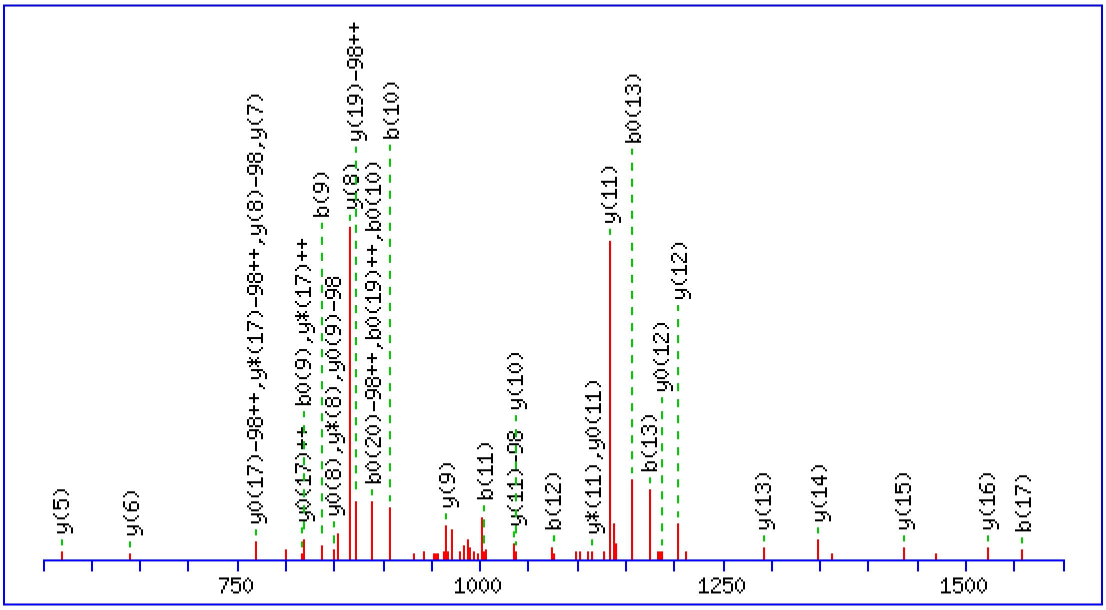
Monoisotopic mass of neutral peptide Mr(calc): 2312.8094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 5.8e-005
Matched b ions: b(8)-98, b(9), b(9)-98, b(10)-98, b(11)-196, b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(14)-196, b(14), b(15), b(15)-98, b(15)-196, b(16)-98, b(16)-196, b(17)-98++, b(17)-98, b(19)-196, b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98, y(12), y(13), y(15)-98, y(15), y(15)-196++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)-196++, y(17)++, y(18)-196++, y(18)-98++

Peptide No.34

AETSESSGSAPAVPEASASPK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **AETSESSGSAPAVPEASASPK**
Found in **MECP2_MOUSE** in **SwissProt**, Methyl-CpG-binding protein 2 OS=Mus musculus GN=Mecp2 PE=1 SV=1

Match to Query 4978: 2038.867650 from(1020.441101,2+) index(1003)
Title: Elution from: 25.014 to 25.014 scan no 1919 cid35.00 polarity:+



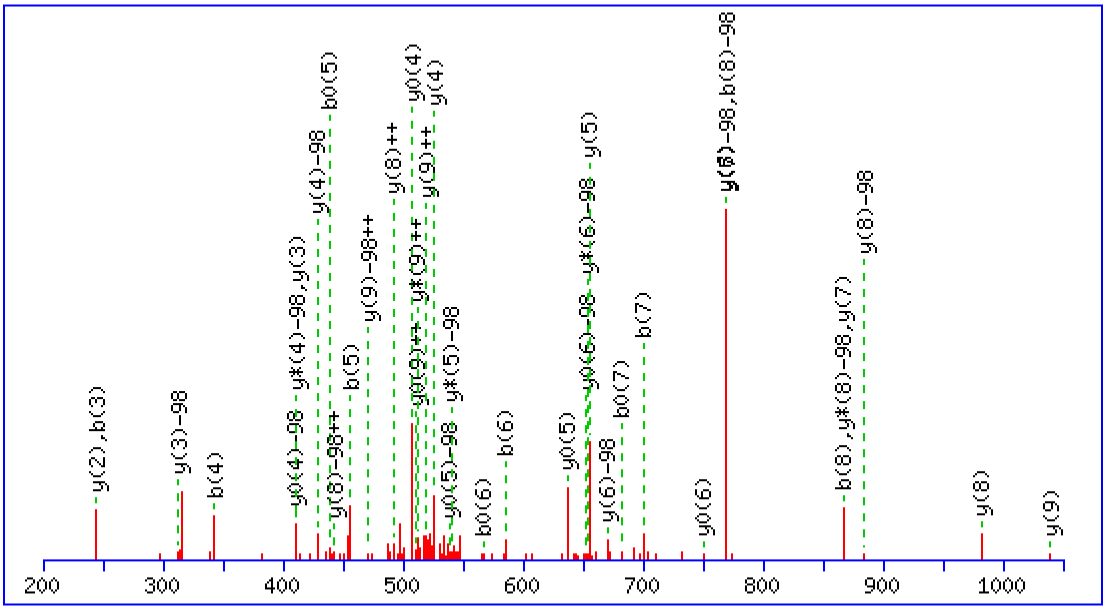
Monoisotopic mass of neutral peptide Mr(calc): 2038.8732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 **Expect:** 2e-008
Matched b ions: b(9), b(10), b(11), b(12), b(13), b(17)
Matched y ions: y(5), y(6), y(7), y(8)-98, y(8), y(9), y(10), y(11), y(11)-98, y(12), y(13), y(14), y(15), y(16), y(19)-98++

Peptide No.35

AGDVLEDSPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **AGDVLEDSPK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 1277: 1109.462970 from(555.738761,2+) index(781)
Title: Elution from: 22.740 to 22.740 scan no 1646 cid35.00 polarity:+



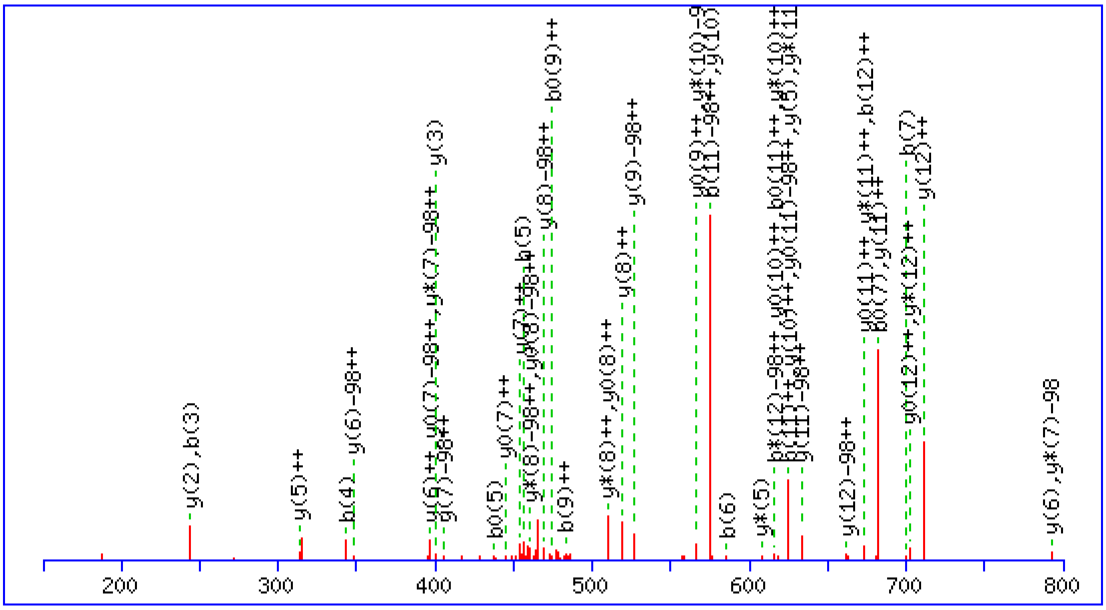
Monoisotopic mass of neutral peptide Mr(calc): 1109.4642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 **Expect:** 2.1e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(8)-98
Matched y ions: y(2), y(3), y(3)-98, y(4)-98, y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-98++, y(8)++, y(9), y(9)++, y(9)-98++

Peptide No.36

AGDVLEDSPKRPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **AGDVLEDSPKRPK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 2770: 1490.712111 from(497.911313,3+) index(282)
Title: Elution from: 19.051 to 19.051 scan no 1113 cid35.00 polarity:+



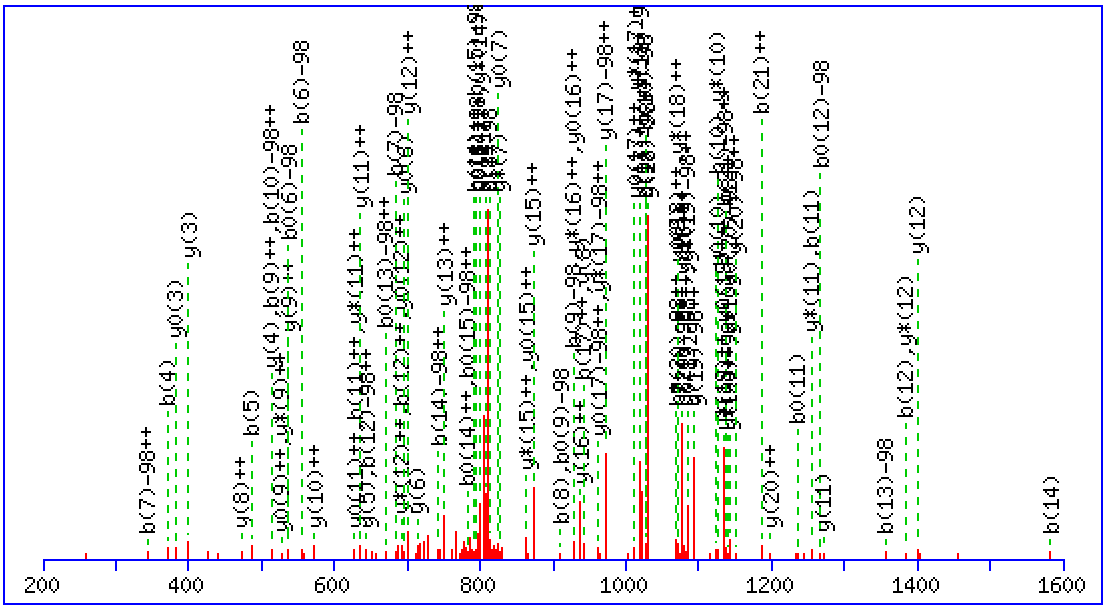
Monoisotopic mass of neutral peptide Mr(calc): 1490.7130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 4e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(5), y(5)++, y(6), y(6)++, y(6)-98++, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++

Peptide No.37

AGLEDSEEDVEEAEVEAEDKDH
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **AGLEDSEEDVEEAEVEAEDKDH**
Found in **TBB1_MOUSE** in **SwissProt**, Tubulin beta-1 chain OS=Mus musculus GN=Tubb1 PE=1 SV=1

Match to Query 5413: 2523.963531 from(842.328453,3+) index(5314)
Title: Elution from: 39.371 to 39.371 scan no 3750 cid35.00 polarity:+:m1s



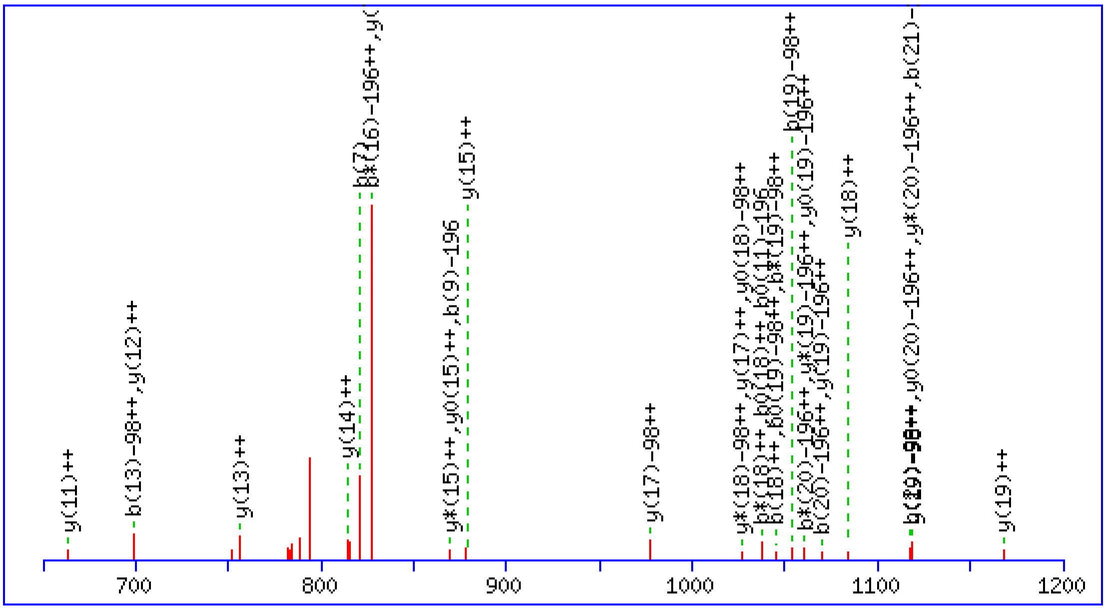
Monoisotopic mass of neutral peptide Mr(calc): 2523.9650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 **Expect:** 1.7e-007
Matched b ions: b(4), b(5), b(6)-98, b(7)-98++, b(7)-98, b(8), b(8)-98, b(9)++, b(9)-98, b(9), b(10)-98++, b(10)-98, b(10), b(11), b(11)++, b(12)-98++, b(12), b(12)++, b(13)-98, b(14), b(14)-98++, b(14)++, b(15)-98++, b(17)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(20)-98++

Peptide No.38

AGNSDSEEDDANERVDLILEPK
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **AGNSDSEEDDANERVDLILEPK**
Found in **FAM21_MOUSE** in **SwissProt**, WASH complex subunit FAM21 OS=Mus musculus GN=Fam21 PE=1 SV=1

Match to Query 6507: 2575.038114 from(859.353314,3+) index(6893)
Title: Elution from: 52.244 to 52.244 scan no 5423 cid35.00 polarity:+:m1s



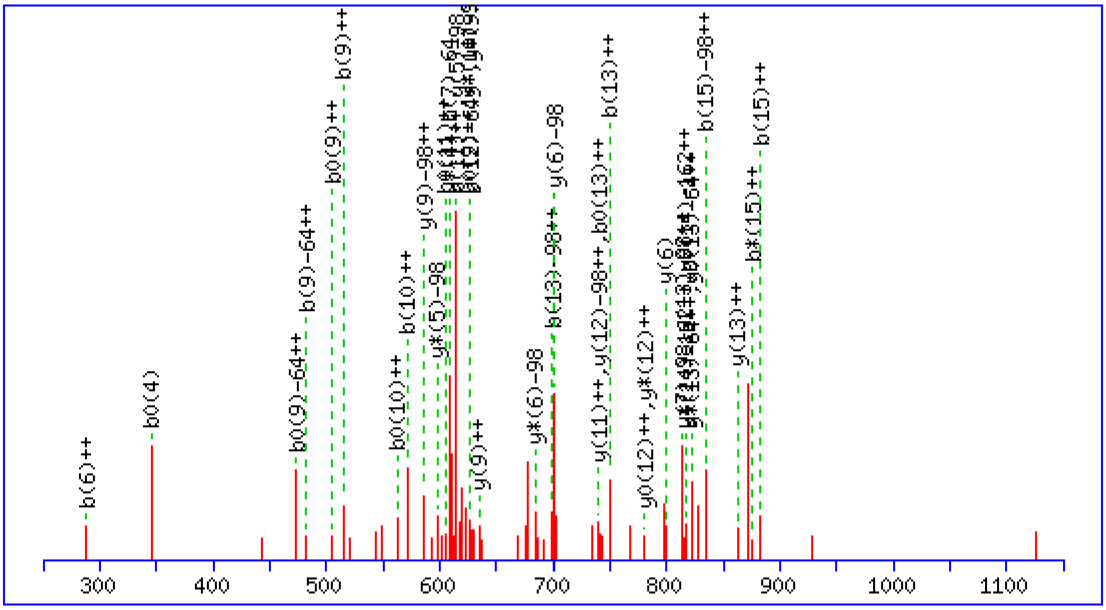
Monoisotopic mass of neutral peptide Mr(calc): 2575.0364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0019
Matched b ions: b(7), b(9)-196, b(13)-98++, b(15)-98++, b(18)++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-196++
Matched y ions: y(7), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(17)-98++, y(17)++, y(18)++, y(19)-98++, y(19)++, y(19)-196++

Peptide No.39

AGSMVLPYILSSTLRR
Confirmed sites: @Y:8
Ambiguous sites: @S:12orT:13

MS/MS Fragmentation of **AGSMVLPYILSSTLRR**
Found in **DOCK5_MOUSE** in **SwissProt**, Dedicator of cytokinesis protein 5 OS=Mus musculus GN=Dock5 PE=1 SV=2

Match to Query 4055: 1938.906183 from(647.309337,3+) index(4902)
Title: Elution from: 37.029 to 37.029 scan no 3429 cid35.00 polarity:+:m1s



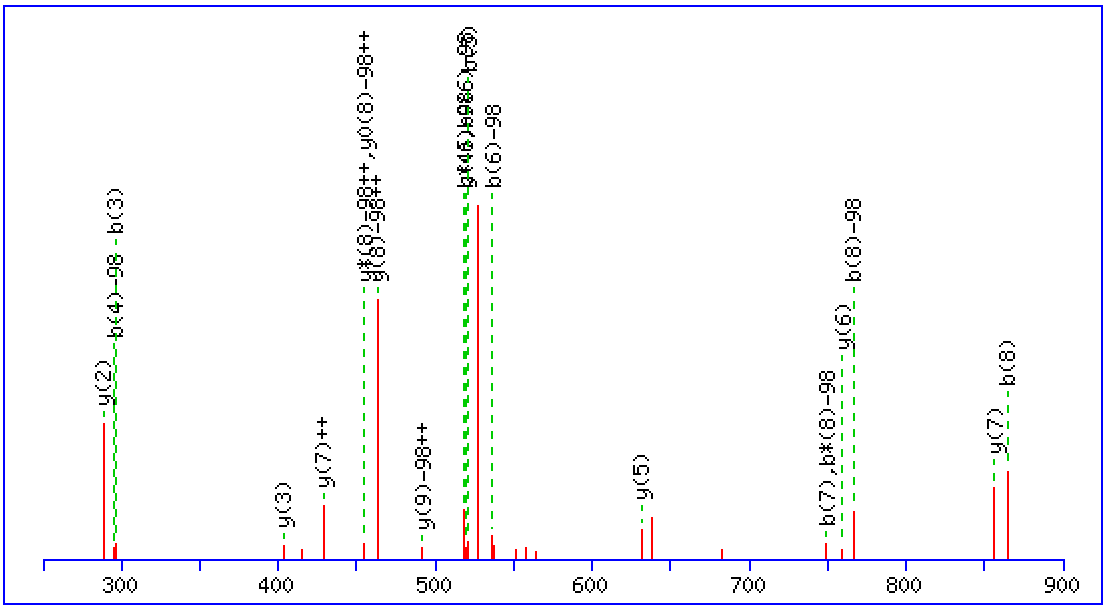
Monoisotopic mass of neutral peptide Mr(calc): 1938.9039
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y8 : Phospho (Y)
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.015
Matched b ions: b(6)++, b(9)++, b(10)++, b(11)++, b(13)++, b(13)-98++, b(15)-98++, b(15)++
Matched y ions: y(5)-98, y(6)-98, y(6), y(7)-98, y(9)-98++, y(9)++, y(11)++, y(12)-98++, y(13)-98++, y(13)++

Peptide No.40

AGSPQLDDIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AGSPQLDDIR**
Found in **EI2BE_MOUSE** in **SwissProt**, Translation initiation factor eIF-2B subunit epsilon OS=Mus musculus GN=Eif2b5 PE=1 SV=1

Match to Query 1306: 1150.501792 from(576.258172,2+) index(1495)
Title: Elution from: 29.910 to 29.910 scan no 2588 cid35.00 polarity:+



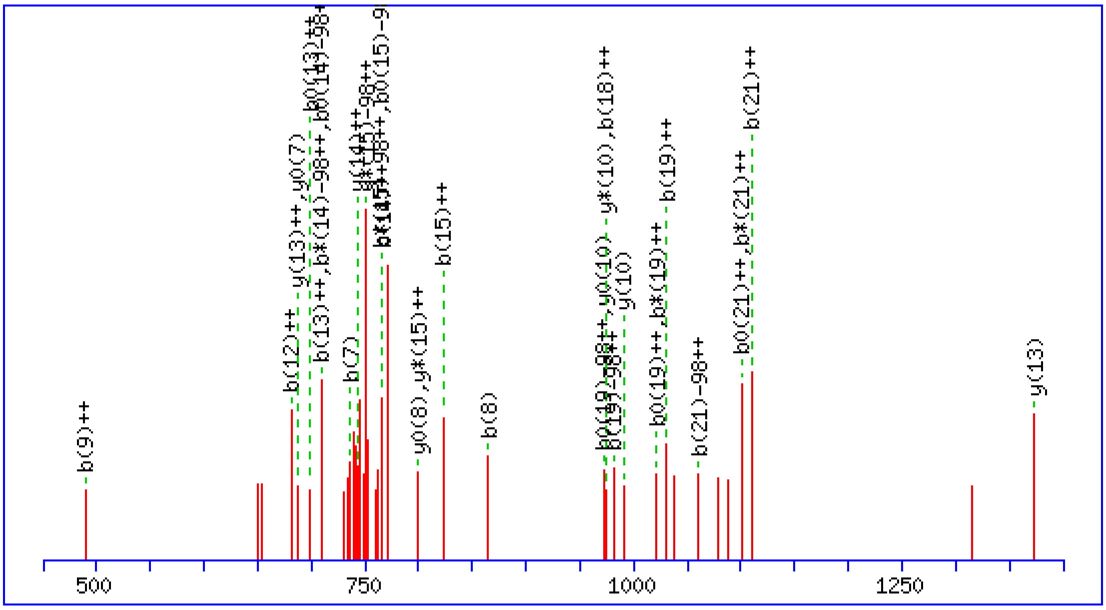
Monoisotopic mass of neutral peptide Mr(calc): 1150.5020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 **Expect:** 5.2e-006
Matched b ions: b(3), b(4)-98, b(5), b(6)-98, b(7), b(8)-98, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)-98++, y(9)-98++

Peptide No.41

AHNLQDGQLSDTGDLGEDIASN
Confirmed sites:
Ambiguous sites: @S:10orT:12

MS/MS Fragmentation of **AHNLQDGQLSDTGDLGEDIASN**
Found in **KI21A_MOUSE** in **SwissProt**, Kinesin-like protein KIF21A OS=Mus musculus GN=Kif21a PE=1 SV=2

Match to Query 5081: 2348.976198 from(783.999342,3+) index(5557)
Title: Elution from: 43.347 to 43.347 scan no 4205 cid35.00 polarity:+:m1s



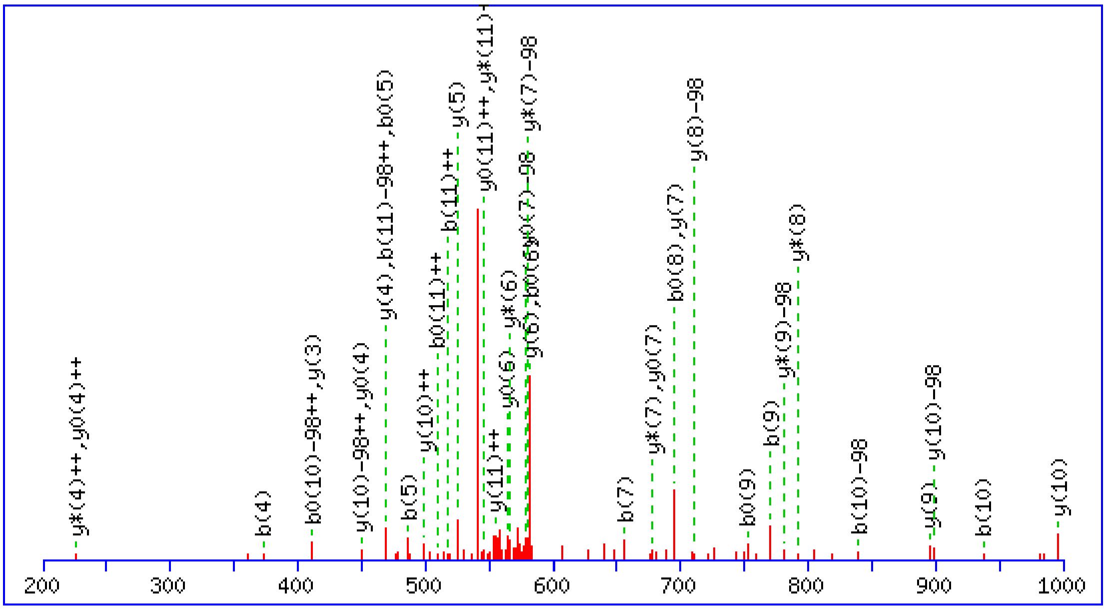
Monoisotopic mass of neutral peptide Mr(calc): 2348.9758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.017
Matched b ions: b(7), b(8), b(9)++, b(12)++, b(13)++, b(14)++, b(15)++, b(18)++, b(19)-98++, b(19)++, b(21)++, b(21)-98++
Matched y ions: y(10), y(13), y(13)++, y(14)++

Peptide No.42

AITSLLGGGSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **AITSLLGGGSPK**
Found in **NIPBL_MOUSE** in **SwissProt**, Nipped-B-like protein OS=Mus musculus GN=Nipbl PE=1 SV=1

Match to Query 1867: 1179.590392 from(590.802472,2+) index(1869)
Title: Elution from: 50.702 to 50.702 scan no 4001 cid35.00 polarity:+



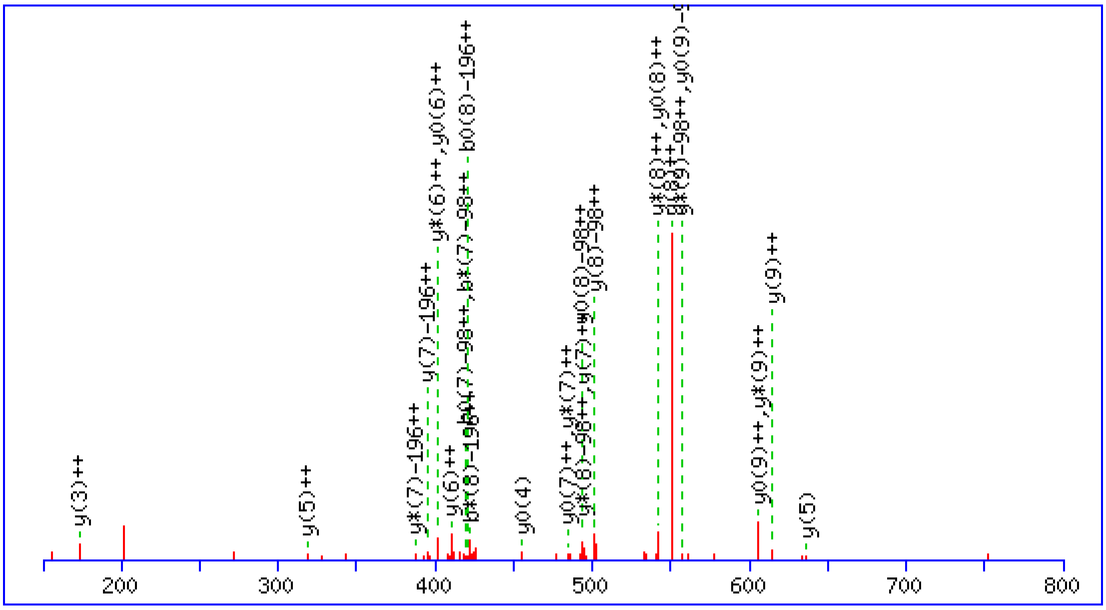
Monoisotopic mass of neutral peptide Mr(calc): 1179.5900
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 **Expect:** 1.9e-005
Matched b ions: b(4), b(5), b(7), b(9), b(10)-98, b(10), b(11)-98++, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10), y(10)-98, y(10)++, y(10)-98++, y(11)++

Peptide No.43

AKDSTYQTLI
Confirmed sites: @S:4,@T:5
Ambiguous sites:

MS/MS Fragmentation of **AKDSTYQTLI**
Found in **C16L2_MOUSE** in **SwissProt**, CD164 sialomucin-like 2 protein OS=Mus musculus GN=Cd164l2 PE=2 SV=1

Match to Query 1961: 1298.518689 from(433.846839,3+) index(792)
Title: Elution from: 23.293 to 23.293 scan no 1685 cid35.00 polarity:+



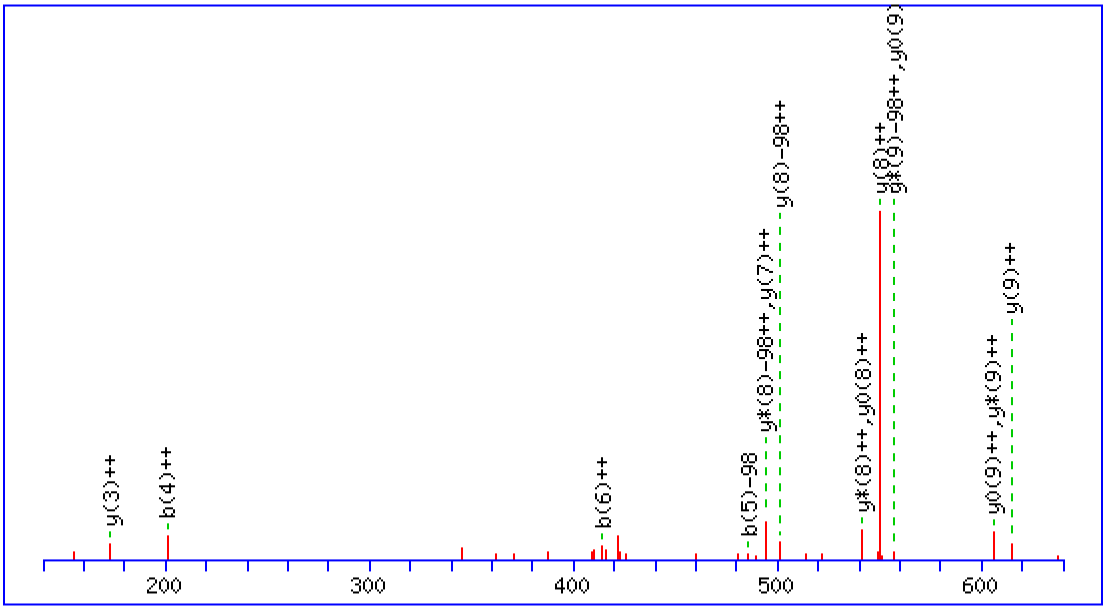
Monoisotopic mass of neutral peptide Mr(calc): 1298.5196
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.011
Matched b ions:
Matched y ions: y(3)++, y(5)++, y(5), y(6)++, y(7)++, y(7)-196++, y(8)++, y(8)-98++, y(9)++

Peptide No.44

AKDSTYQTLI
Confirmed sites: @T:5,@Y:6
Ambiguous sites:

MS/MS Fragmentation of **AKDSTYQTLI**
Found in **C16L2_MOUSE** in **SwissProt**, CD164 sialomucin-like 2 protein OS=Mus musculus GN=Cd164l2 PE=2 SV=1

Match to Query 1941: 1298.518797 from(433.846875,3+) index(542)
Title: Elution from: 23.144 to 23.144 scan no 1540 cid35.00 polarity:+



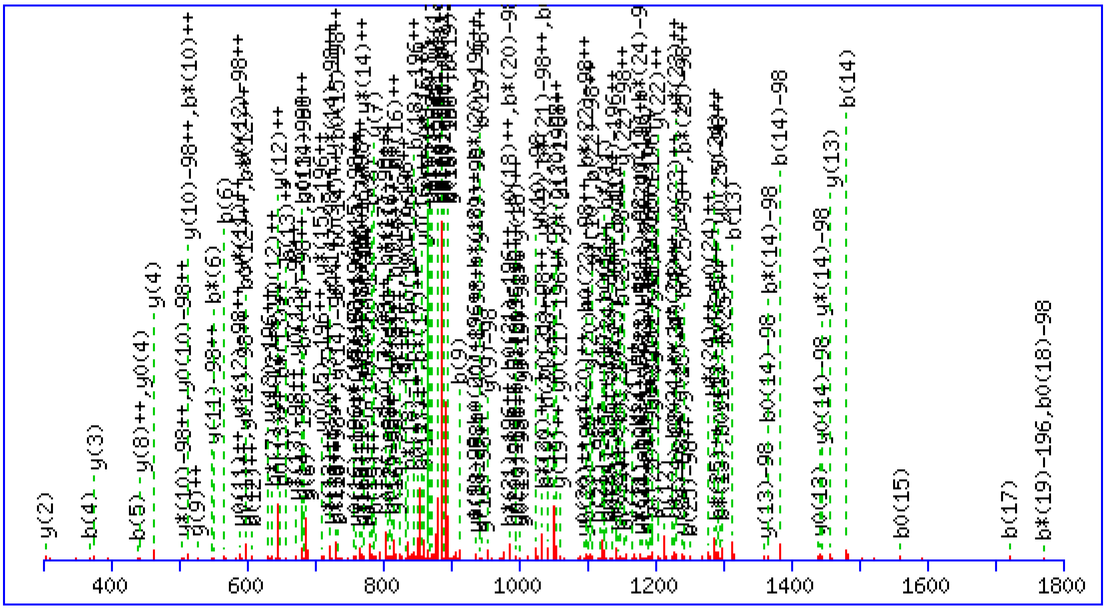
Monoisotopic mass of neutral peptide Mr(calc): 1298.5196
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y6 : Phospho (Y)
Ions Score: 29 **Expect:** 0.0041
Matched b ions: b(4)++, b(5)-98, b(6)++
Matched y ions: y(3)++, y(7)++, y(8)++, y(8)-98++, y(9)++

Peptide No.45

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @S:14,@S:18
Ambiguous sites:

MS/MS Fragmentation of **AKPAAQSEEETATSPAASPTPQSAER**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 6556: 2771.161446 from(924.727758,3+) index(4144)
Title: Elution from: 21.768 to 21.768 scan no 1477 cid35.00 polarity:+:m1s



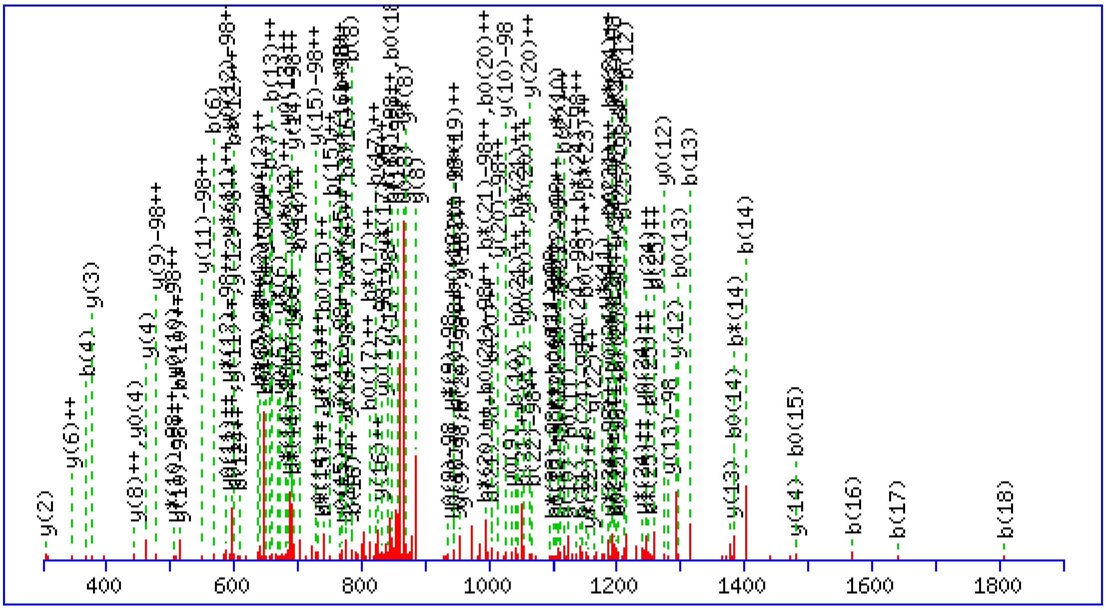
Monoisotopic mass of neutral peptide Mr(calc): 2771.1688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 2.4e-006
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(10), b(11), b(12), b(12)++, b(13), b(13)++, b(14), b(14)-98, b(15)++, b(16)++, b(17), b(17)-98++, b(17)++, b(18)-98++, b(18)-196++, b(19)-196++, b(19)-98++, b(20)-98++, b(21)-98++, b(21)-196++, b(22)++, b(22)-98++, b(23)-196++, b(23)-98++, b(24)-196++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(8)++, y(9), y(9)-98, y(9)++, y(10), y(10)-98++, y(10)-98, y(11)++, y(11), y(11)-98++, y(12)-98++, y(12)++, y(12), y(12)-98, y(13)++, y(13), y(13)-98++, y(13)-196++, y(13)-98, y(14)++, y(14)-196++, y(14)-98++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(24)++, y(24)-98++

Peptide No.46

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **AKPAAQSEEETATSPAASPTPQSAER**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5623: 2691.197226 from(898.073018,3+) index(3558)
Title: Elution from: 21.051 to 21.051 scan no 1359 cid35.00 polarity:+:m1s



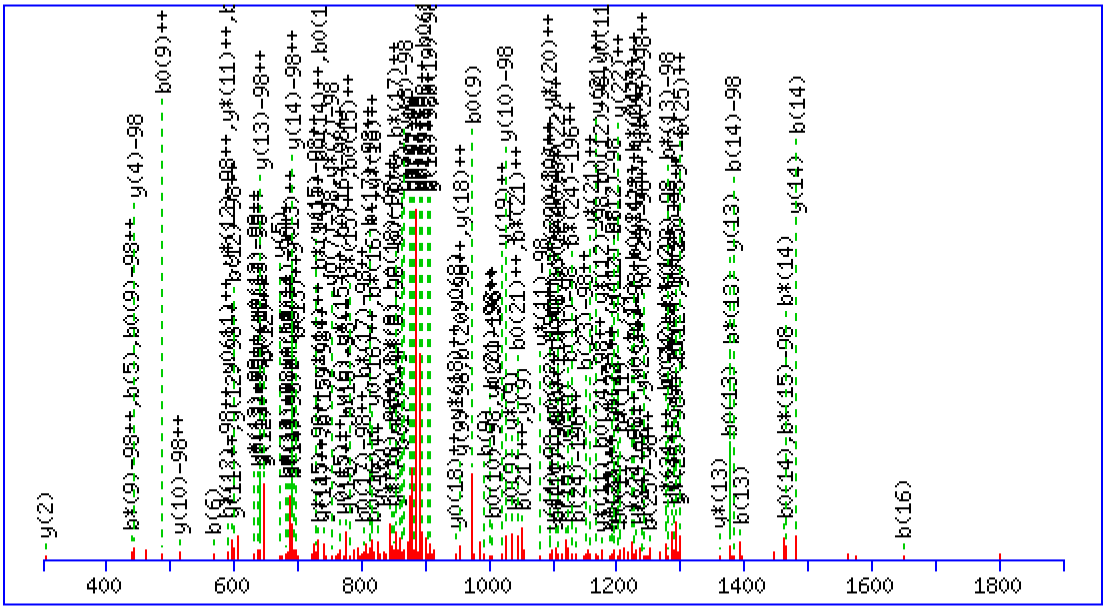
Monoisotopic mass of neutral peptide Mr(calc): 2691.2024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 **Expect:** 3.8e-007
Matched b ions: b(4), b(6), b(7), b(8), b(10), b(11), b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15)++, b(16), b(16)++, b(17), b(17)++, b(18), b(18)-98++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(8)++, y(8), y(9), y(9)-98++, y(9)-98, y(10)-98++, y(10), y(10)-98, y(11)++, y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12)++, y(12)-98, y(12), y(13)++, y(13), y(13)-98++, y(13)-98, y(14), y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(20)-98++, y(20)++, y(22)++, y(23)++, y(24)++, y(24)-98++

Peptide No.47

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @S:7,@S:23
Ambiguous sites:

MS/MS Fragmentation of **AKPAAQSEEETATSPAASPTPQSAER**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5538: 2771.163303 from(924.728377,3+) index(3507)
Title: Elution from: 22.932 to 22.932 scan no 1511 cid35.00 polarity:+:m1s



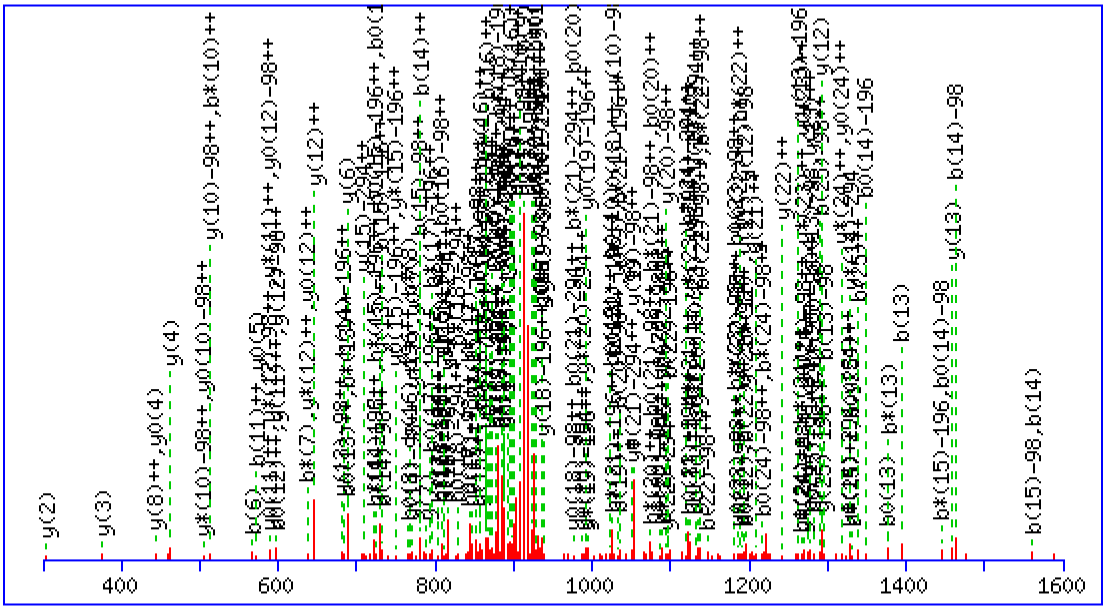
Monoisotopic mass of neutral peptide Mr(calc): 2771.1688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S23 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00019
Matched b ions: b(5), b(6), b(8), b(9), b(10), b(11), b(11)-98, b(12)-98++, b(12)-98, b(12), b(12)++, b(13), b(13)++, b(14), b(14)-98++, b(14)-98, b(15)-98++, b(16)-98++, b(16), b(17)-98++, b(17)++, b(18)++, b(19)-98++, b(20)-98++, b(21)++, b(21)-98++, b(23)-98++, b(24)-196++, b(25)++, b(25)-98++
Matched y ions: y(2), y(4)-98, y(5), y(6), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(11)++, y(11), y(11)-98, y(12)-98++, y(12)++, y(12), y(12)-98, y(13)++, y(13), y(13)-98++, y(14)++, y(14), y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(20)++, y(20)-196++, y(21)++, y(22)++, y(23)++, y(24)++, y(24)-98++

Peptide No.48

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @T:13,@S:14,@S:18
Ambiguous sites:

MS/MS Fragmentation of **AKPAAQSEEETATSPAASPTPQSAER**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5611: 2851.131582 from(951.384470,3+) index(3541)
Title: Elution from: 23.215 to 23.215 scan no 1550 cid35.00 polarity:+:m1s



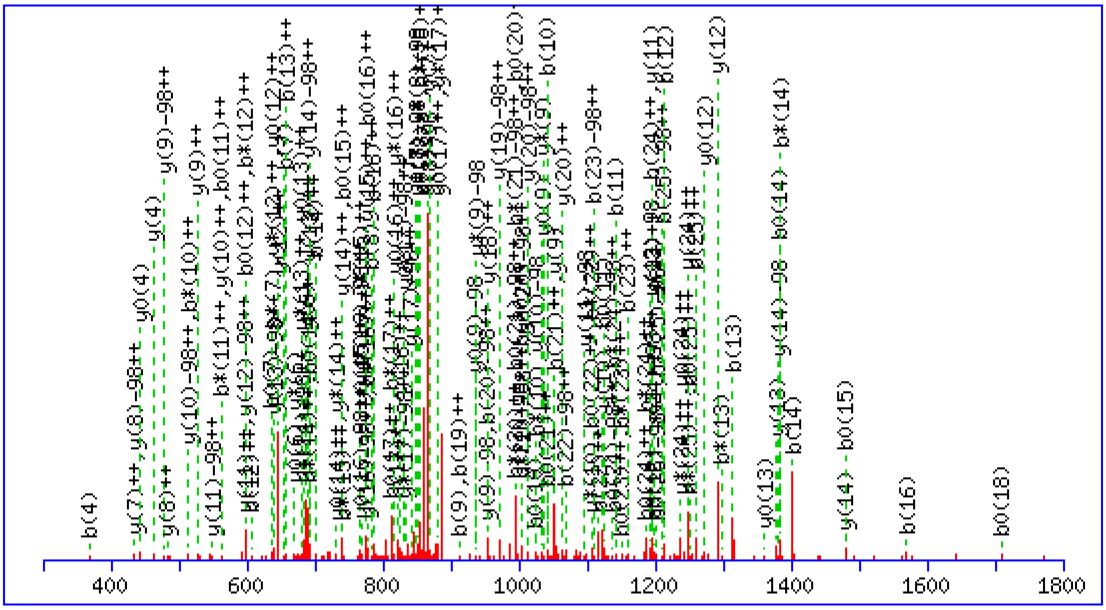
Monoisotopic mass of neutral peptide Mr(calc): 2851.1351
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 **Expect:** 4e-005
Matched b ions: b(6), b(9), b(11)++, b(13), b(13)-98, b(14)-98, b(14), b(14)-196++, b(14)-98++, b(14)++, b(15)-98, b(15)-98++, b(15)-196++, b(16)-98++, b(16)-196++, b(16)++, b(17)++, b(17)-196++, b(17)-98++, b(18)-196++, b(18)-98++, b(19)-294++, b(19)-196++, b(19)++, b(20)-98++, b(20)-294++, b(21)-196++, b(21)++, b(22)++, b(22)-98++, b(22)-196++, b(23)-98++, b(24)++, b(25)++, b(25)-98++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8)++, y(8), y(9), y(10)-98, y(10), y(10)-98++, y(11)++, y(11), y(12)-98++, y(12)++, y(12), y(12)-98, y(13)++, y(13), y(13)-98++, y(13)-196, y(14)-196++, y(14)-98++, y(15)-294++, y(15)-98++, y(15)++, y(16)++, y(16)-196++, y(16)-98++, y(17)-98++, y(17)-196++, y(18)-294++, y(18)-196++, y(19)-98++, y(20)-98++, y(21)++, y(22)-98++, y(22)-294++, y(22)++, y(23)++, y(23)-294++, y(24)++, y(24)-98++, y(25)-196++

Peptide No.49

AKPAAQSEEETATSPAASPTPQSAER
Confirmed sites: @T:20
Ambiguous sites:

MS/MS Fragmentation of **AKPAAQSEEETATSPAASPTPQSAER**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 6435: 2691.203673 from(898.075167,3+) index(3796)
Title: Elution from: 27.116 to 27.116 scan no 1537 cid35.00 polarity:+:m1s



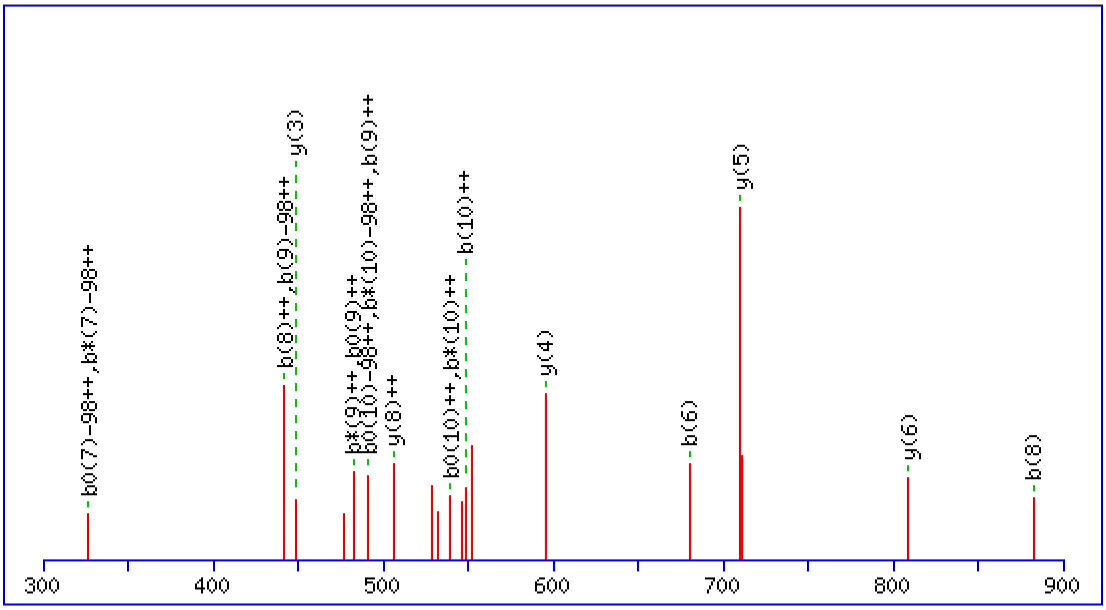
Monoisotopic mass of neutral peptide Mr(calc): 2691.2024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 1e-005
Matched b ions: b(4), b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(16), b(16)++, b(17)++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++, b(23)++, b(24)++, b(25)++, b(25)-98++
Matched y ions: y(4), y(6), y(7)++, y(7), y(8)-98++, y(8)++, y(8)-98, y(9)++, y(9), y(9)-98, y(9)-98++, y(10), y(10)-98++, y(10)++, y(10)-98, y(11)++, y(11), y(11)-98++, y(11)-98, y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++, y(13), y(14), y(14)++, y(14)-98++, y(14)-98, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(19)-98++, y(20)++, y(20)-98++, y(23)++, y(24)++, y(24)-98++

Peptide No.50

AKSAIESDVDFWDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AKSAIESDVDFWDK**
Found in **PEX5_MOUSE** in **SwissProt**, Peroxisomal targeting signal 1 receptor OS=Mus musculus GN=Pex5 PE=2 SV=2

Match to Query 3765: 1689.728562 from(564.250130,3+) index(2943)
Title: Elution from: 45.816 to 45.816 scan no 4706 cid35.00 polarity:+



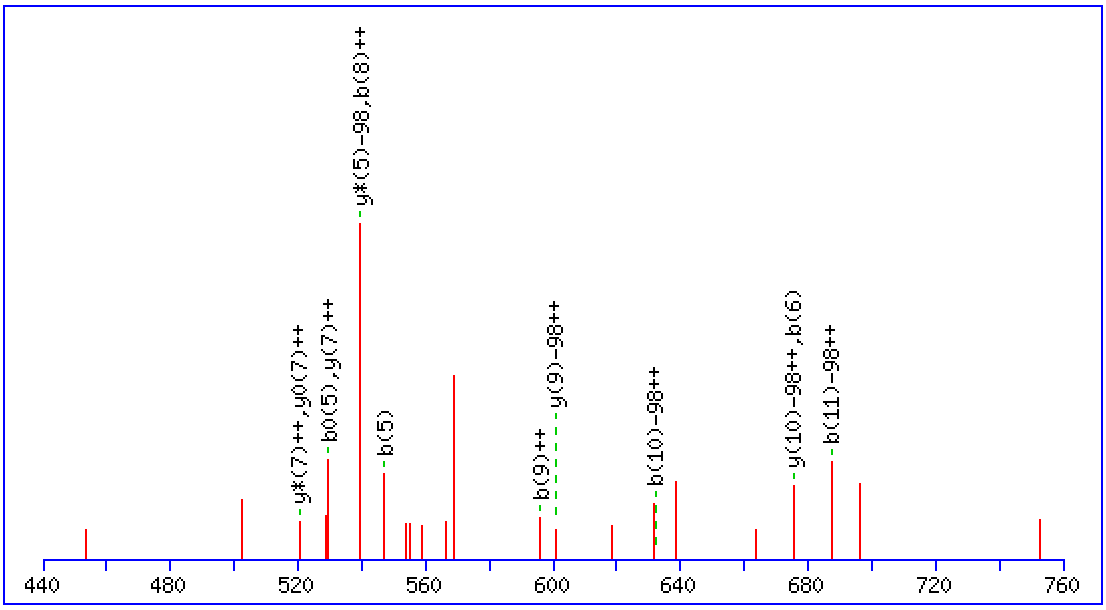
Monoisotopic mass of neutral peptide Mr(calc): 1689.7287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.035
Matched b ions: b(6), b(8)++, b(8), b(9)-98++, b(9)++, b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++

Peptide No.51

AKSFLEYCISLNK
Confirmed sites: @Y:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **AKSFLEYCISLNK**
Found in **VRTN_MOUSE** in **SwissProt**, Vertnin OS=Mus musculus GN=Vrtn PE=2 SV=1

Match to Query 3401: 1731.736536 from(578.252788,3+) index(4009)
Title: Elution from: 27.321 to 27.321 scan no 2115 cid35.00 polarity:+:m1s



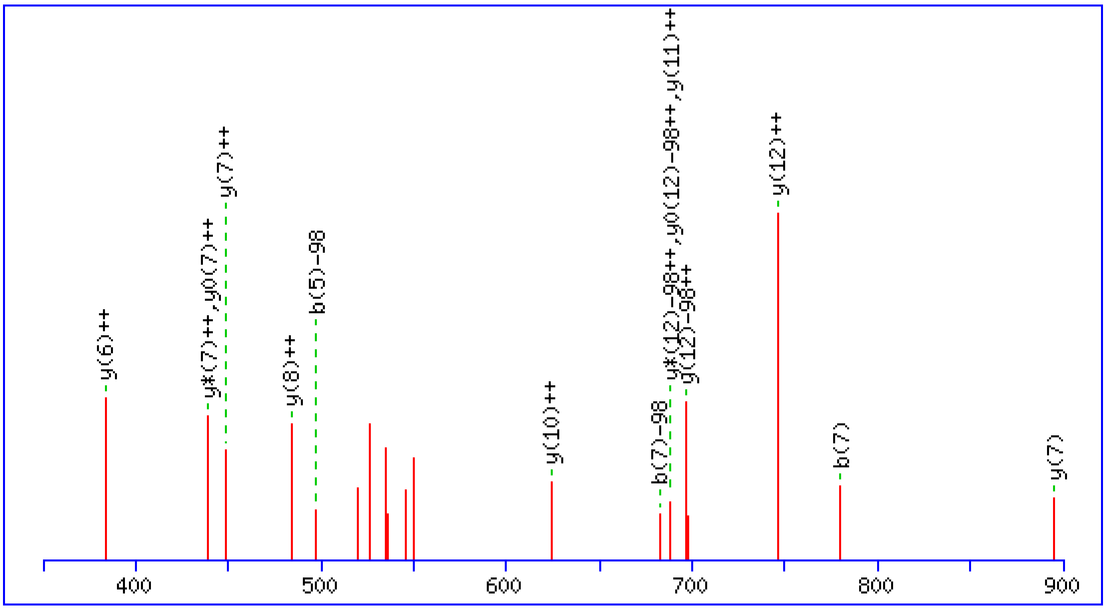
Monoisotopic mass of neutral peptide Mr(calc): 1731.7344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y7 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.048
Matched b ions: b(5), b(6), b(8)++, b(9)++, b(10)-98++, b(11)-98++
Matched y ions: y(7)++, y(9)-98++, y(10)-98++

Peptide No.52

ALDESLAEPHLEDR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **ALDESLAEPHLEDR**
Found in **PML_MOUSE** in **SwissProt**, Protein PML OS=Mus musculus GN=Pml PE=1 SV=3

Match to Query 3693: 1673.734365 from(558.918731,3+) index(5899)
Title: Elution from: 36.974 to 36.974 scan no 3567 cid35.00 polarity:+:m1s



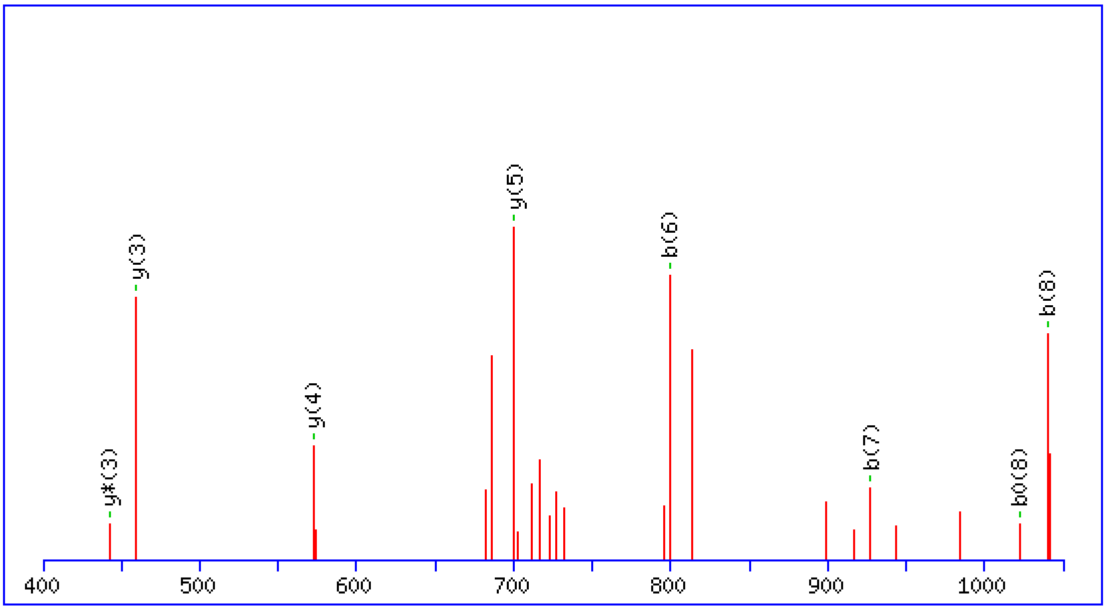
Monoisotopic mass of neutral peptide Mr(calc): 1673.7298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0058
Matched b ions: b(5)-98, b(7)-98, b(7)
Matched y ions: y(6)++, y(7), y(7)++, y(8)++, y(10)++, y(11)++, y(12)++, y(12)-98++

Peptide No.53

ALELYEQLRQR
Confirmed sites: @Y:5
Ambiguous sites:

MS/MS Fragmentation of **ALELYEQLRQR**
Found in **DYHC2_MOUSE** in **SwissProt**, Cytoplasmic dynein 2 heavy chain 1 OS=Mus musculus GN=Dync2h1 PE=1 SV=1

Match to Query 2579: 1497.731610 from(749.873081,2+) index(5829)
Title: Elution from: 58.999 to 58.999 scan no 5744 cid35.00 polarity:+:m1s



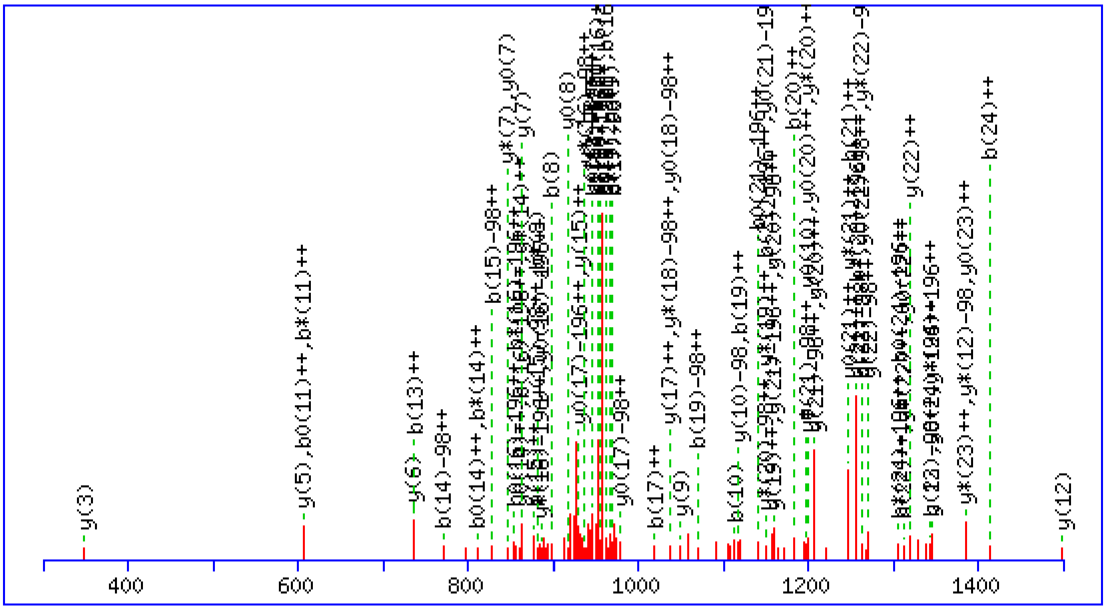
Monoisotopic mass of neutral peptide Mr(calc): 1497.7340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y5 : Phospho (Y)
Ions Score: 28 **Expect:** 0.0075
Matched b ions: b(6), b(7), b(8)
Matched y ions: y(3), y(4), y(5)

Peptide No.54

ALFKPPEDSQDDESDSDAEEEQTTK
Confirmed sites: @S:14,@S:16
Ambiguous sites:

MS/MS Fragmentation of **ALFKPPEDSQDDESDSDAEEEQTTK**
Found in **THOC5_MOUSE** in **SwissProt**, THO complex subunit 5 homolog OS=Mus musculus GN=Thoc5 PE=1 SV=2

Match to Query 6704: 2970.118647 from(991.046825,3+) index(5845)
Title: Elution from: 38.130 to 38.130 scan no 3691 cid35.00 polarity:+:m1s



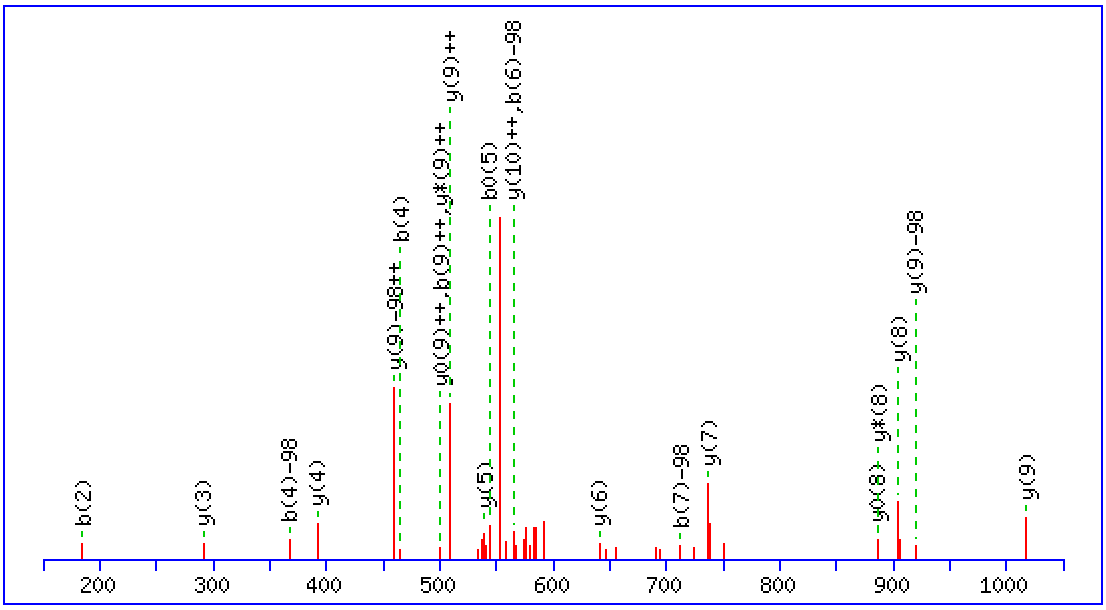
Monoisotopic mass of neutral peptide Mr(calc): 2970.1216
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.023
Matched b ions: b(8), b(10), b(12), b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-196++, b(17)-98++, b(17)++, b(18)-196++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(21)-196++, b(22)-98++, b(22)++, b(24)++
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10)-98, y(12), y(15)++, y(15)-98++, y(16)-98++, y(17)++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)-98++, y(22)++, y(23)-98++

Peptide No.55

ALLSPTFTSGK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **ALLSPTFTSGK**
Found in **CP341_MOUSE** in **SwissProt**, Cytochrome P450 3A41 OS=Mus musculus GN=Cyp3a41a PE=2 SV=2

Match to Query 1403: 1200.579602 from(601.297077,2+) index(5458)
Title: Elution from: 41.691 to 41.691 scan no 4016 cid35.00 polarity:+:m1s



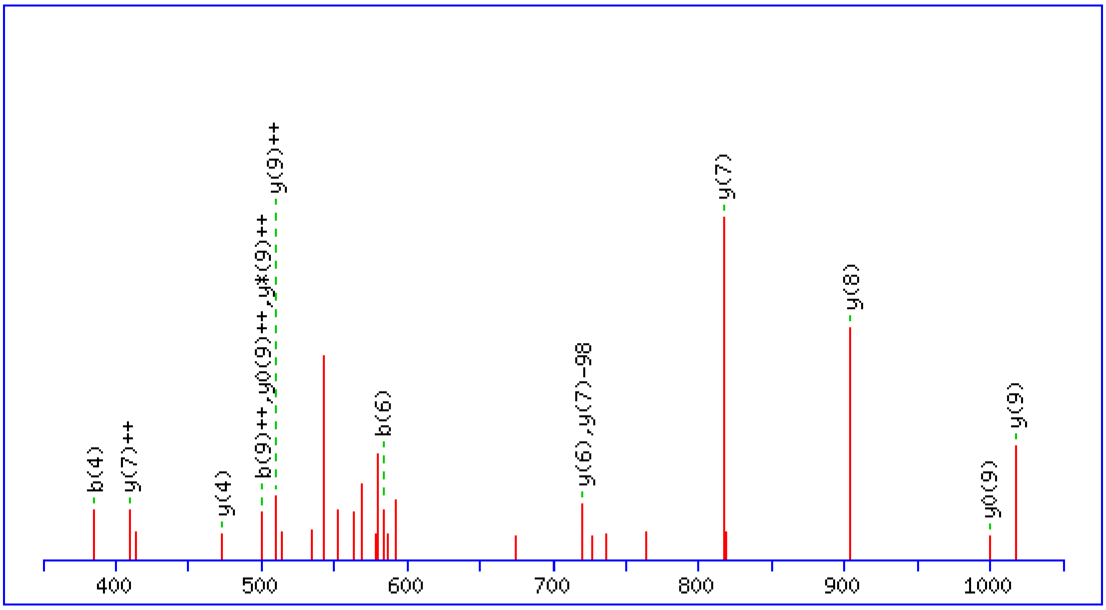
Monoisotopic mass of neutral peptide Mr(calc): 1200.5791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00033
Matched b ions: b(2), b(4)-98, b(4), b(6)-98, b(7)-98, b(9)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9), y(9)++, y(9)-98, y(10)++

Peptide No.56

ALLSPTFTSGK
Confirmed sites:
Ambiguous sites: @T:8orS:9

MS/MS Fragmentation of **ALLSPTFTSGK**
Found in **CP341_MOUSE** in **SwissProt**, Cytochrome P450 3A41 OS=Mus musculus GN=Cyp3a41a PE=2 SV=2

Match to Query 1402: 1200.579226 from(601.296889,2+) index(2244)
Title: Elution from: 39.770 to 39.770 scan no 3794 cid35.00 polarity:+



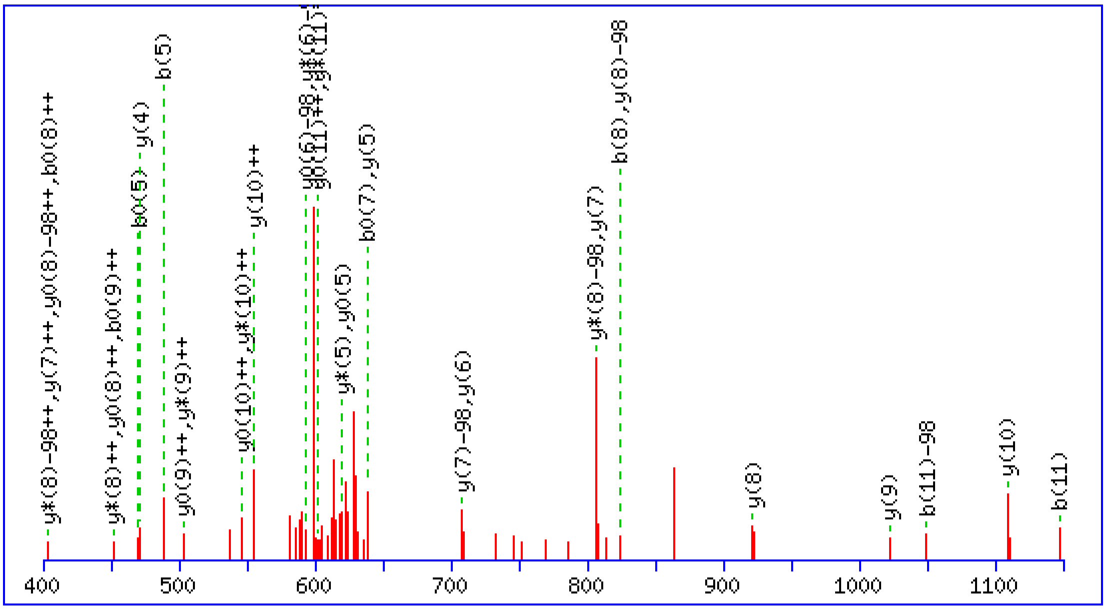
Monoisotopic mass of neutral peptide Mr(calc): 1200.5791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0071
Matched b ions: b(4), b(6), b(9)++
Matched y ions: y(4), y(6), y(7)-98, y(7), y(7)++, y(8), y(9), y(9)++

Peptide No.57

ALSTDPASPNLK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **ALSTDPASPNLK**
Found in **TLN1_MOUSE** in **SwissProt**, Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=2

Match to Query 1908: 1292.602932 from(647.308742,2+) index(4069)
Title: Elution from: 27.794 to 27.794 scan no 2181 cid35.00 polarity:+:m1s



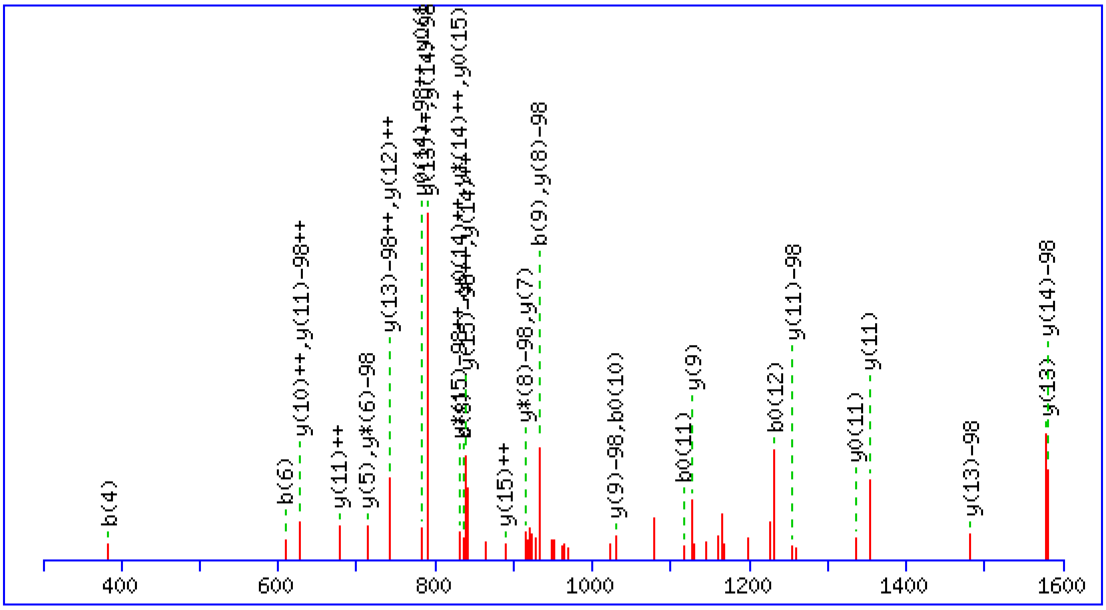
Monoisotopic mass of neutral peptide Mr(calc): 1292.6013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00034
Matched b ions: b(5), b(8), b(11)-98, b(11)
Matched y ions: y(4), y(5), y(6), y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(9), y(10), y(10)++

Peptide No.58

ALVVPEPEPDSDSNQER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **ALVVPEPEPDSDSNQER**
Found in **BRE1A_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase BRE1A OS=Mus musculus GN=Rnf20 PE=1 SV=2

Match to Query 4109: 1960.843916 from(981.429234,2+) index(4776)
Title: Elution from: 35.746 to 35.746 scan no 3258 cid35.00 polarity:+:m1s



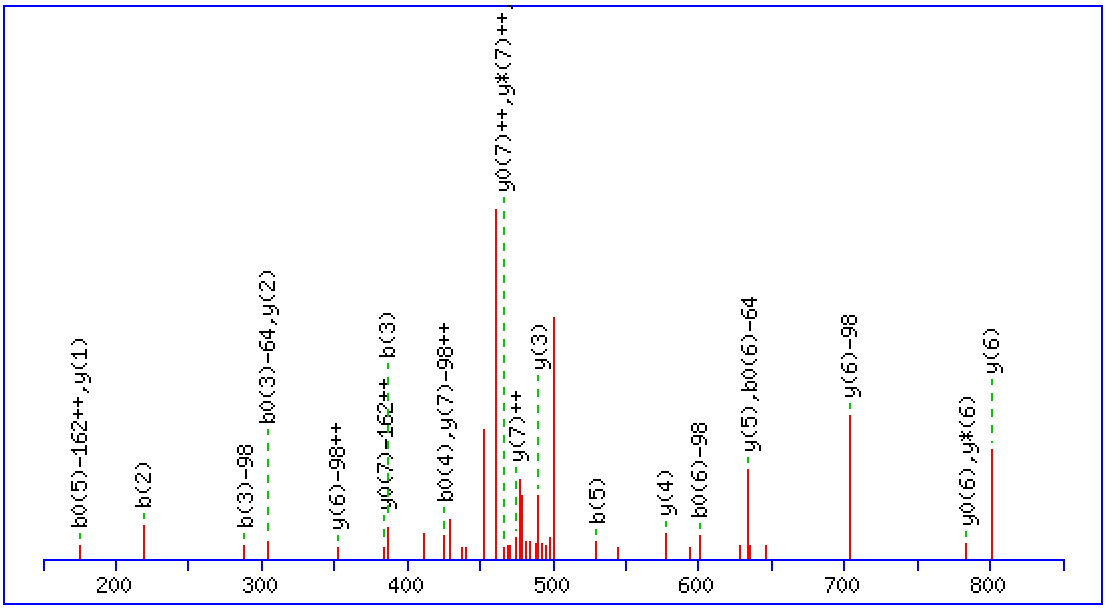
Monoisotopic mass of neutral peptide Mr(calc): 1960.8415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0026
Matched b ions: b(4), b(6), b(8), b(9)
Matched y ions: y(5), y(7), y(8)-98, y(9), y(9)-98, y(10)++, y(11)-98++, y(11), y(11)++, y(11)-98, y(12)++, y(13)-98++, y(13)++, y(13)-98, y(13), y(14)-98++, y(14)++, y(14)-98, y(15)-98++, y(15)++

Peptide No.59

AMSGSWER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AMSGSWER**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 973: 1018.357182 from(510.185867,2+) index(491)
Title: Elution from: 20.267 to 20.267 scan no 1310 cid35.00 polarity:+



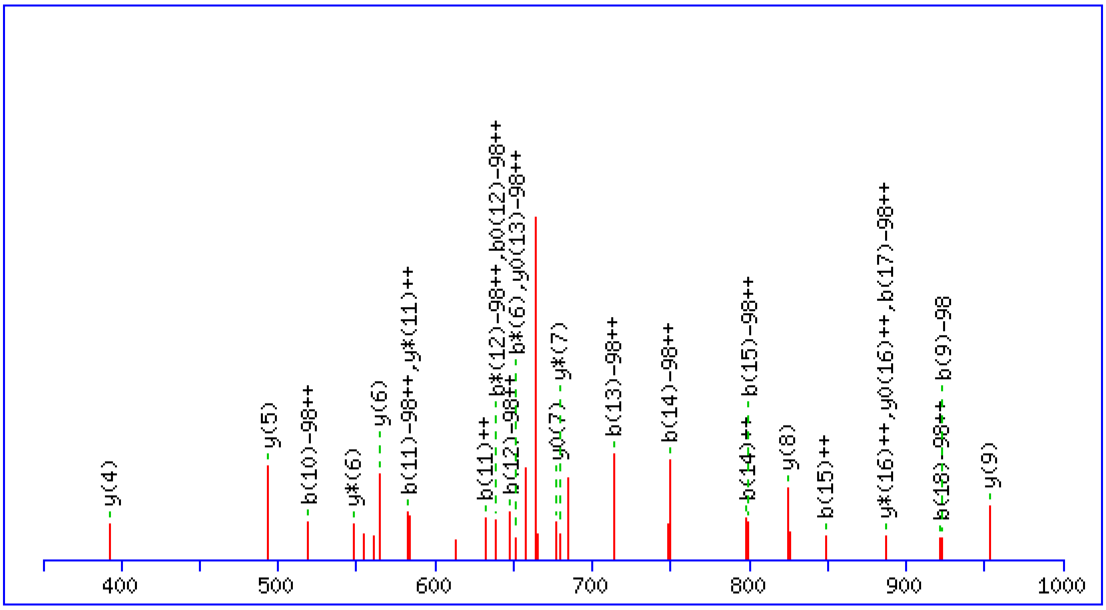
Monoisotopic mass of neutral peptide Mr(calc): 1018.3579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 4.2e-005
Matched b ions: b(2), b(3)-98, b(3), b(5)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)-98++, y(7)-98++, y(7)++

Peptide No.60

APKEELASDLEEMATSSAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **APKEELASDLEEMATSSAK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4396: 2085.917460 from(696.313096,3+) index(5902)
Title: Elution from: 50.716 to 50.716 scan no 4960 cid35.00 polarity:+:m1s



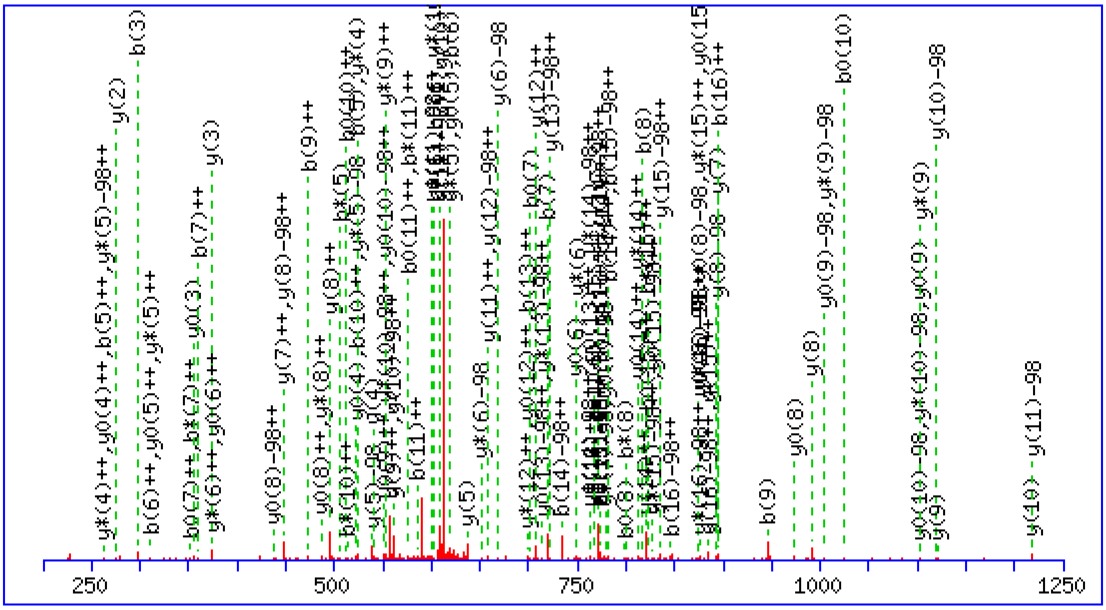
Monoisotopic mass of neutral peptide Mr(calc): 2085.9177
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 0.00011
Matched b ions: b(9)-98, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(17)-98++, b(18)-98++
Matched y ions: y(4), y(5), y(6), y(8), y(9)

Peptide No.61

APKPEPVPEPKEPSPEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **APKPEPVPEPKEPSPEK**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 4260: 1934.939868 from(645.987232,3+) index(3369)
Title: Elution from: 28.924 to 28.924 scan no 1678 cid35.00 polarity:+:m1s



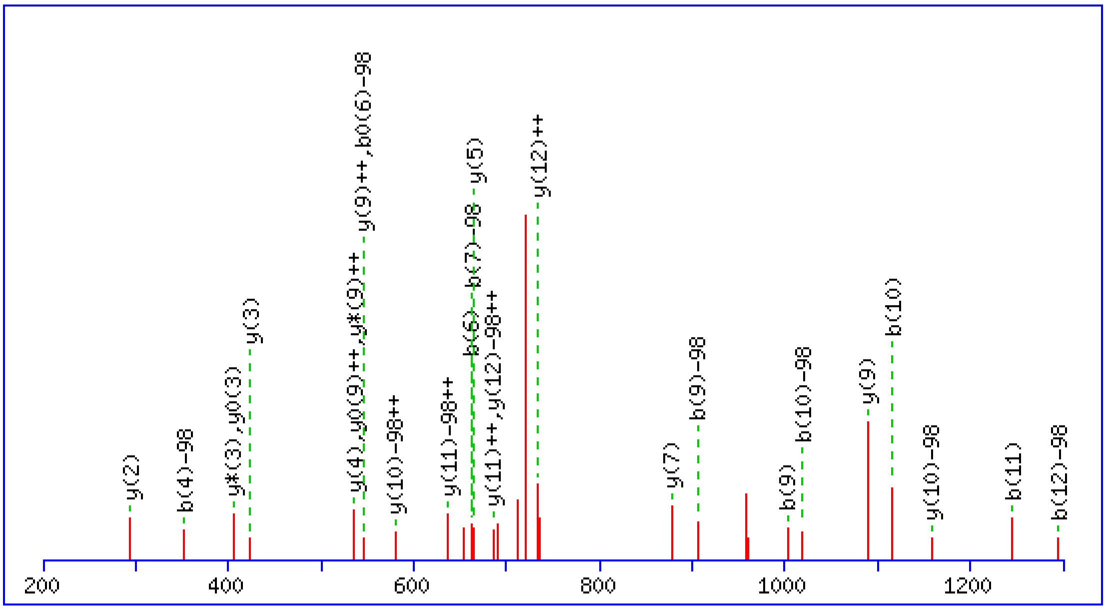
Monoisotopic mass of neutral peptide Mr(calc): 1934.9390
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.0005
Matched b ions: b(3), b(5), b(5)++, b(6)++, b(6), b(7), b(7)++, b(8), b(9), b(9)++, b(10)++, b(11)++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7)++, y(7), y(8)++, y(8)-98++, y(8), y(8)-98, y(9), y(9)++, y(10)-98, y(10), y(10)++, y(10)-98++, y(11)-98, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++

Peptide No.62

APNSPDVLEIEFK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **APNSPDVLEIEFK**
Found in **ASSY_MOUSE** in **SwissProt**, Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1

Match to Query 2702: 1537.705754 from(769.860153,2+) index(2707)
Title: Elution from: 51.467 to 51.467 scan no 5102 cid35.00 polarity:+



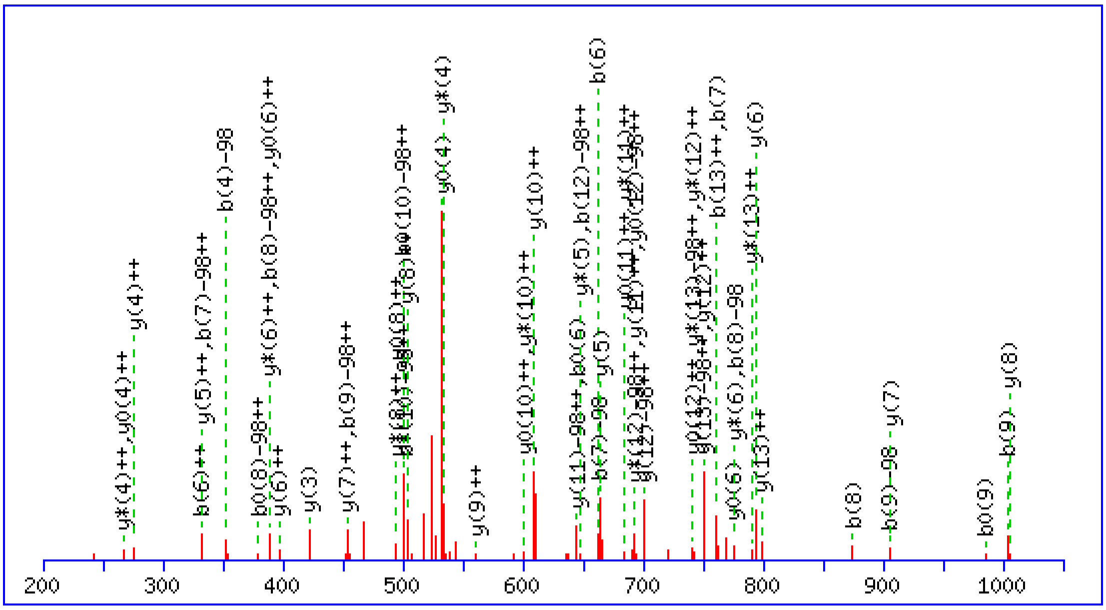
Monoisotopic mass of neutral peptide Mr(calc): 1537.7065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 **Expect:** 5.1e-006
Matched b ions: b(4)-98, b(6), b(7)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(9), y(9)++, y(10)-98++, y(10)-98, y(11)-98++, y(11)++, y(12)++, y(12)-98++

Peptide No.63

APNSPDVLEIEFKK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **APNSPDVLEIEFKK**
Found in **ASSY_MOUSE** in **SwissProt**, Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1

Match to Query 3161: 1665.800760 from(556.274196,3+) index(5309)
Title: Elution from: 42.853 to 42.853 scan no 4162 cid35.00 polarity:+:m1s



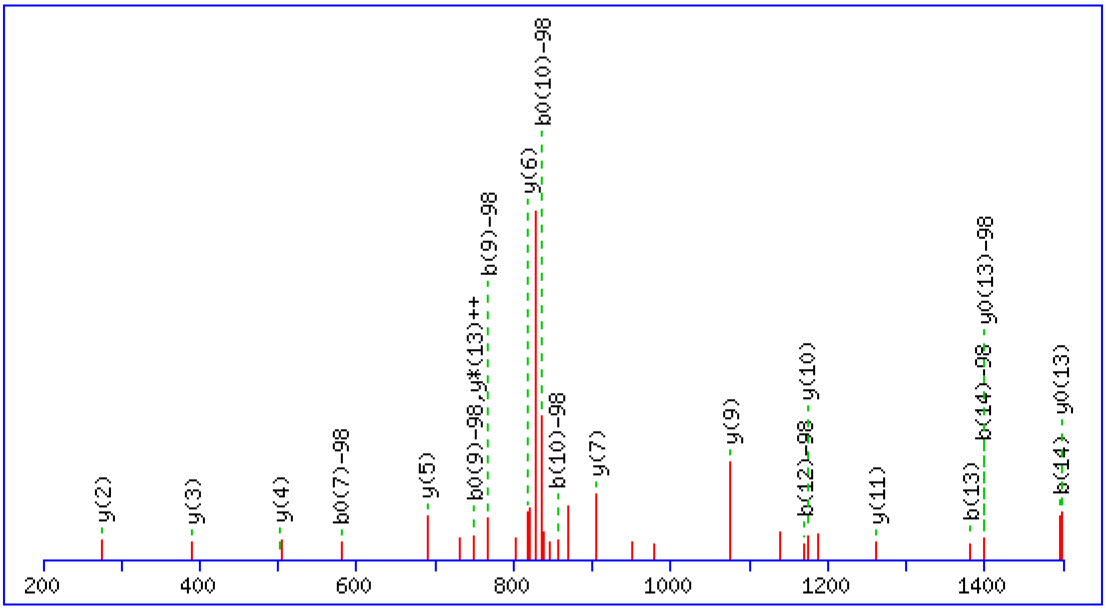
Monoisotopic mass of neutral peptide Mr(calc): 1665.8015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 7.2e-007
Matched b ions: b(4)-98, b(6)++, b(6), b(7)-98++, b(7), b(7)-98, b(8), b(8)-98++, b(8)-98, b(9), b(9)-98, b(9)-98++, b(12)-98++, b(13)++
Matched y ions: y(3), y(4)++, y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++

Peptide No.64

APSSSSVGISEWLDQK
Confirmed sites:
Ambiguous sites: @S:3orS:4orS:5

MS/MS Fragmentation of **APSSSSVGISEWLDQK**
Found in **ETFA_MOUSE** in **SwissProt**, Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2

Match to Query 3982: 1769.789450 from(885.902001,2+) index(6739)
Title: Elution from: 53.653 to 53.653 scan no 5528 cid35.00 polarity:+:m1s



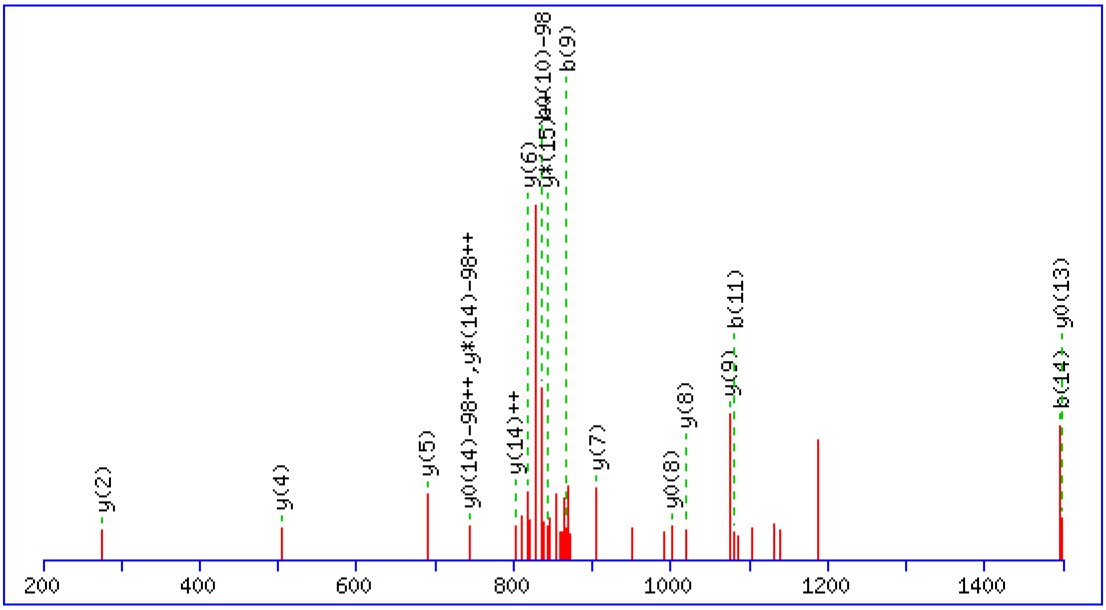
Monoisotopic mass of neutral peptide Mr(calc): 1769.7873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 1e-006
Matched b ions: b(9)-98, b(10)-98, b(12)-98, b(13), b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11)

Peptide No.65

APSSSSVGISEWLDQK
Confirmed sites:
Ambiguous sites: @S:3orS:4orS:5orS:6

MS/MS Fragmentation of **APSSSSVGISEWLDQK**
Found in **ETFA_MOUSE** in **SwissProt**, Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2

Match to Query 3522: 1769.786470 from(885.900511,2+) index(5728)
Title: Elution from: 53.048 to 53.048 scan no 5264 cid35.00 polarity:+:m1s



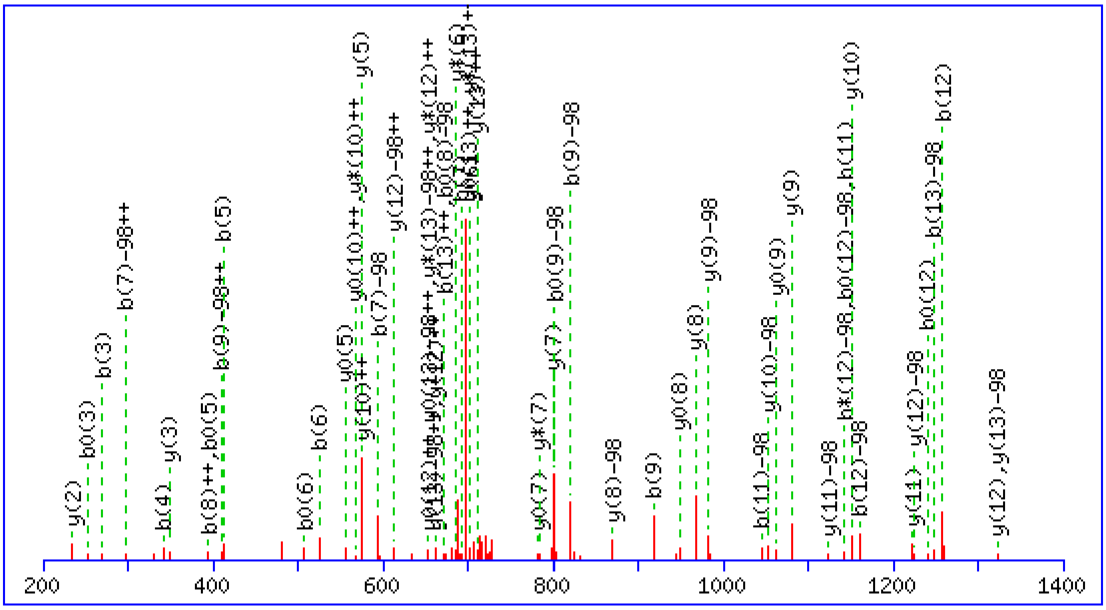
Monoisotopic mass of neutral peptide Mr(calc): 1769.7873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.00093
Matched b ions: b(9), b(11), b(14)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(14)++

Peptide No.66

APTAALSPEPQDSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **APTAALSPEPQDSK**
Found in **SAFB1_MOUSE** in **SwissProt**, Scaffold attachment factor B1 OS=Mus musculus GN=Safb PE=1 SV=2

Match to Query 2547: 1490.663656 from(746.339104,2+) index(563)
Title: Elution from: 23.323 to 23.323 scan no 1565 cid35.00 polarity:+



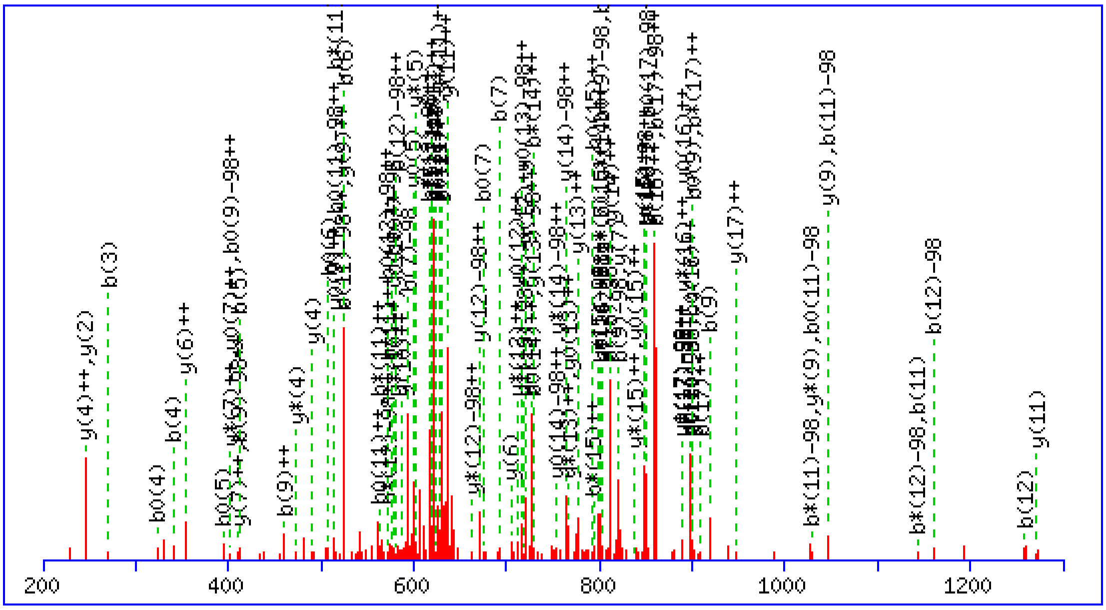
Monoisotopic mass of neutral peptide Mr(calc): 1490.6654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 **Expect:** 1.6e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98++, b(7)-98, b(7), b(8)++, b(9), b(9)-98, b(9)-98++, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13)++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(11), y(11)-98, y(12)-98++, y(12)-98, y(12), y(12)++, y(13)-98, y(13)-98++, y(13)++

Peptide No.67

APTAALSPEPQDSKEDVK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **APTAALSPEPQDSKEDVK**
Found in **SAFB1_MOUSE** in **SwissProt**, Scaffold attachment factor B1 OS=Mus musculus GN=Safb PE=1 SV=2

Match to Query 4115: 1961.899116 from(654.973648,3+) index(3619)
Title: Elution from: 23.856 to 23.856 scan no 1638 cid35.00 polarity:+:m1s



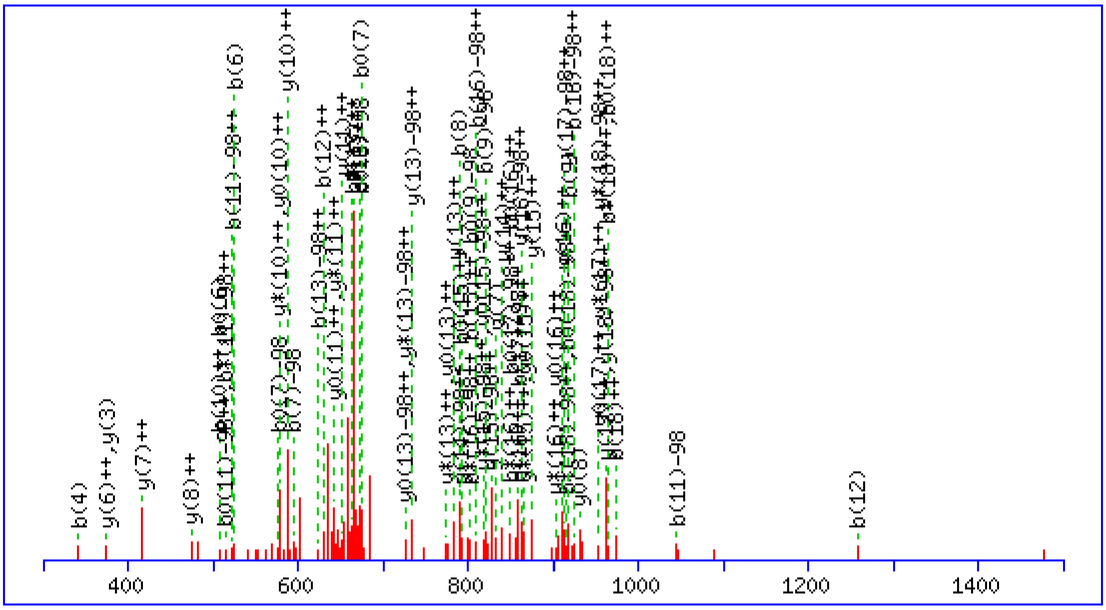
Monoisotopic mass of neutral peptide Mr(calc): 1961.8983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 **Expect:** 2.1e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(7), b(9)++, b(9)-98, b(9)-98++, b(9), b(11)-98++, b(11)-98, b(11), b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(2), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(9)++, y(9), y(10)++, y(11)++, y(11), y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++

Peptide No.68

APTAALSPEPQDSKEDVKK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **APTAALSPEPQDSKEDVKK**
Found in **SAFB1_MOUSE** in **SwissProt**, Scaffold attachment factor B1 OS=Mus musculus GN=Safb PE=1 SV=2

Match to Query 5271: 2089.989558 from(697.670462,3+) index(576)
Title: Elution from: 20.975 to 20.975 scan no 1406 cid35.00 polarity:+



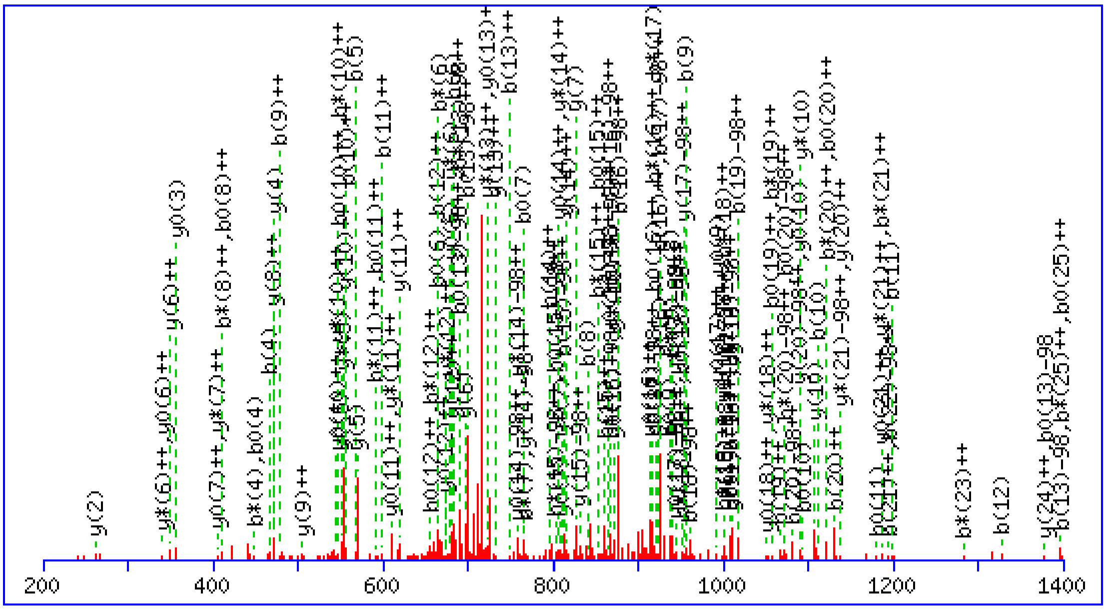
Monoisotopic mass of neutral peptide Mr(calc): 2089.9932
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 2.3e-005
Matched b ions: b(4), b(6), b(7)-98, b(8), b(9)-98, b(9), b(10)++, b(11)-98, b(11)-98++, b(12), b(12)++, b(13)++, b(13)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(3), y(6)++, y(7)++, y(7), y(8)++, y(10)++, y(11)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++

Peptide No.69

AQEHTDTGDRSESPEEPALEKPPLDK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **AQEHTDTGDRSESPEEPALEKPPLDK**
Found in **TOIP2_MOUSE** in **SwissProt**, Torsin-1A-interacting protein 2 OS=Mus musculus GN=Tor1aip2 PE=1 SV=1

Match to Query 6697: 2955.311480 from(739.835146,4+) index(4711)
Title: Elution from: 26.885 to 26.885 scan no 2173 cid35.00 polarity:+:m1s



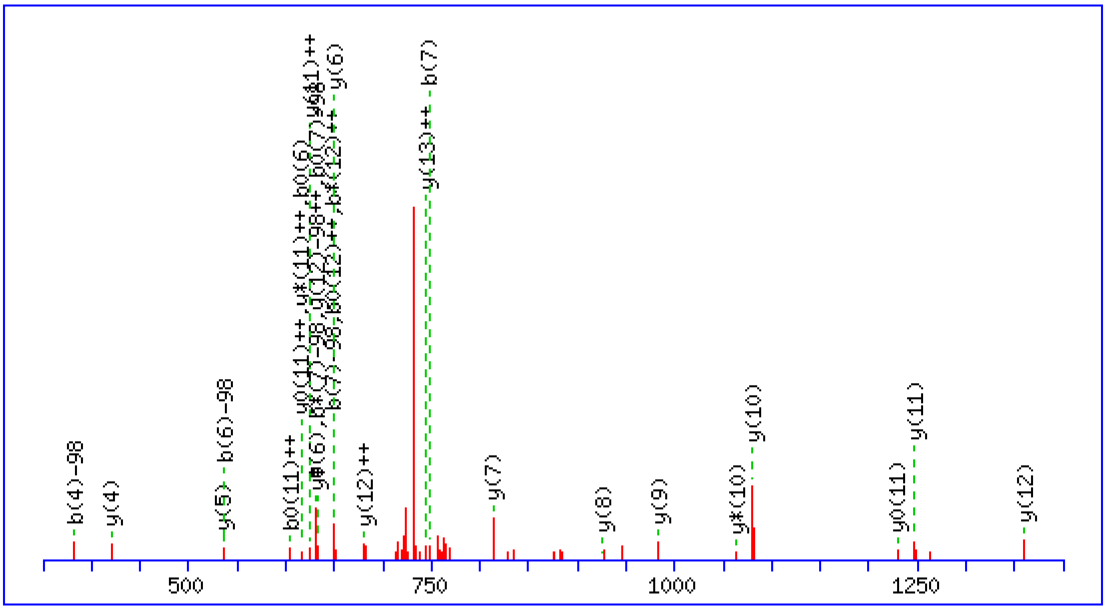
Monoisotopic mass of neutral peptide Mr(calc): 2955.3135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.00017
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(9)++, b(10)++, b(10), b(11), b(11)++, b(12), b(12)++, b(13)-98, b(13)-98++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(22)-98++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(20)-98++, y(20)++, y(24)++

Peptide No.70

AQLSPGLYDDSSAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **AQLSPGLYDDSSAR**
Found in **NCOR1_MOUSE** in **SwissProt**, Nuclear receptor corepressor 1 OS=Mus musculus GN=Ncor1 PE=1 SV=1

Match to Query 2807: 1558.664920 from(780.339736,2+) index(4693)
Title: Elution from: 34.801 to 34.801 scan no 3135 cid35.00 polarity:+:m1s



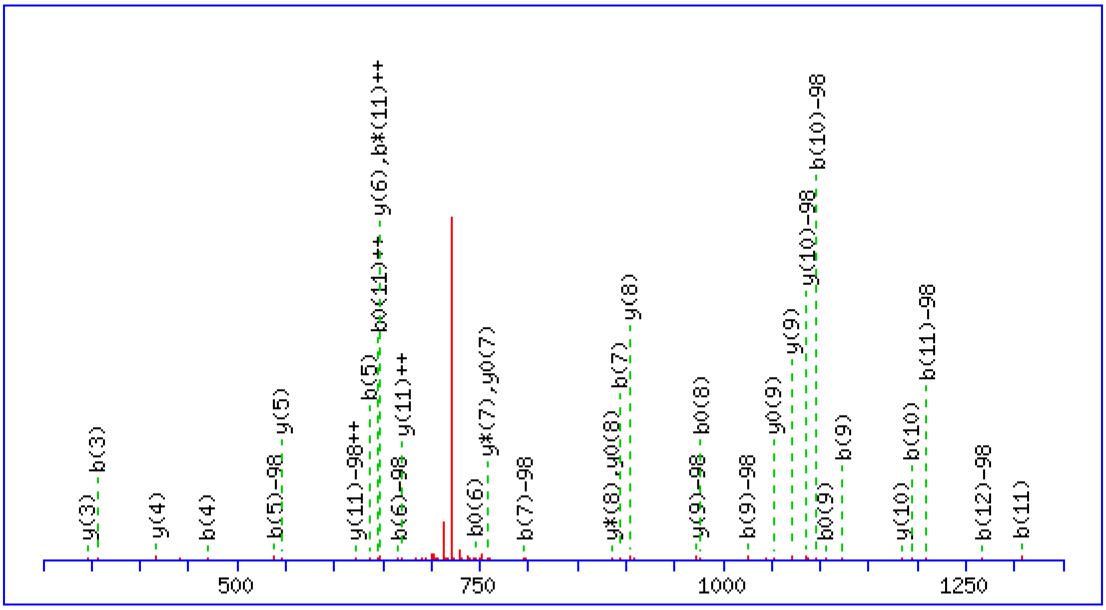
Monoisotopic mass of neutral peptide Mr(calc): 1558.6664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 9.9e-006
Matched b ions: b(4)-98, b(6)-98, b(7)-98, b(7)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)-98++, y(12), y(12)++, y(13)++

Peptide No.71

AQRLSQETEALGR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **AQRLSQETEALGR**
Found in **NUCB1_MOUSE** in **SwissProt**, Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2

Match to Query 2703: 1537.722600 from(769.868576,2+) index(1036)
Title: Elution from: 27.465 to 27.465 scan no 2135 cid35.00 polarity:+



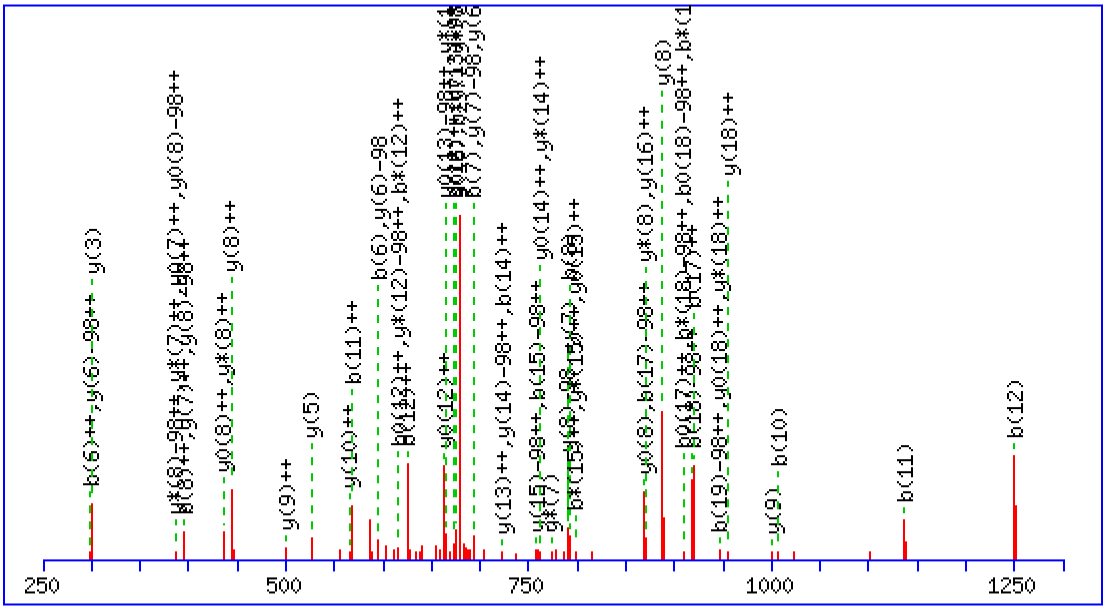
Monoisotopic mass of neutral peptide Mr(calc): 1537.7249
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 **Expect:** 2.7e-006
Matched b ions: b(3), b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11)-98++, y(11)++

Peptide No.72

ARPAQAPVSEELPPSPKPGK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **ARPAQAPVSEELPPSPKPGK**
Found in **FAM21_MOUSE** in **SwissProt**, WASH complex subunit FAM21 OS=Mus musculus GN=Fam21 PE=1 SV=1

Match to Query 5495: 2135.074035 from(712.698621,3+) index(4583)
Title: Elution from: 24.033 to 24.033 scan no 1822 cid35.00 polarity:+:m1s



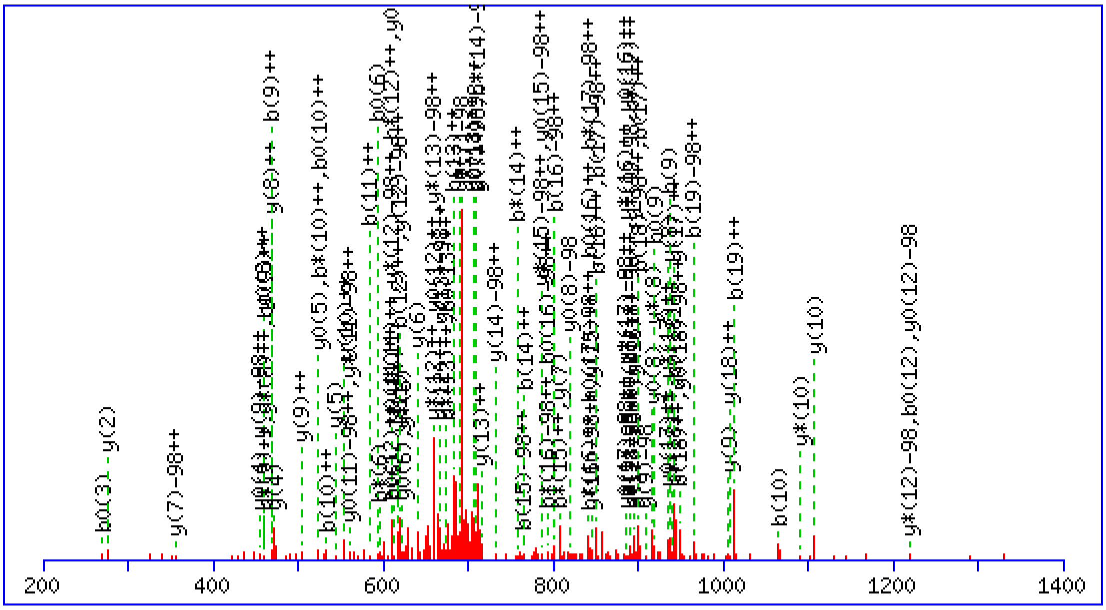
Monoisotopic mass of neutral peptide Mr(calc): 2135.0776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 4e-005
Matched b ions: b(6)++, b(6), b(7), b(8)++, b(8), b(10), b(11)++, b(11), b(12), b(12)++, b(13)++, b(14)++, b(15)-98++, b(17)++, b(17)-98++, b(18)-98++, b(19)-98++
Matched y ions: y(3), y(5), y(6)-98++, y(6)-98, y(6), y(7)++, y(7), y(7)-98, y(8)++, y(8)-98, y(8), y(8)-98++, y(9), y(9)++, y(10)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(15)-98++, y(16)++, y(18)++

Peptide No.73

ASEPVKEPVQTAQSPAPVEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **ASEPVKEPVQTAQSPAPVEK**
Found in **SCAF8_MOUSE** in **SwissProt**, Protein SCAF8 OS=Mus musculus GN=Scaf8 PE=1 SV=1

Match to Query 5497: 2171.052282 from(724.691370,3+) index(4131)
Title: Elution from: 30.699 to 30.699 scan no 1977 cid35.00 polarity:+:m1s



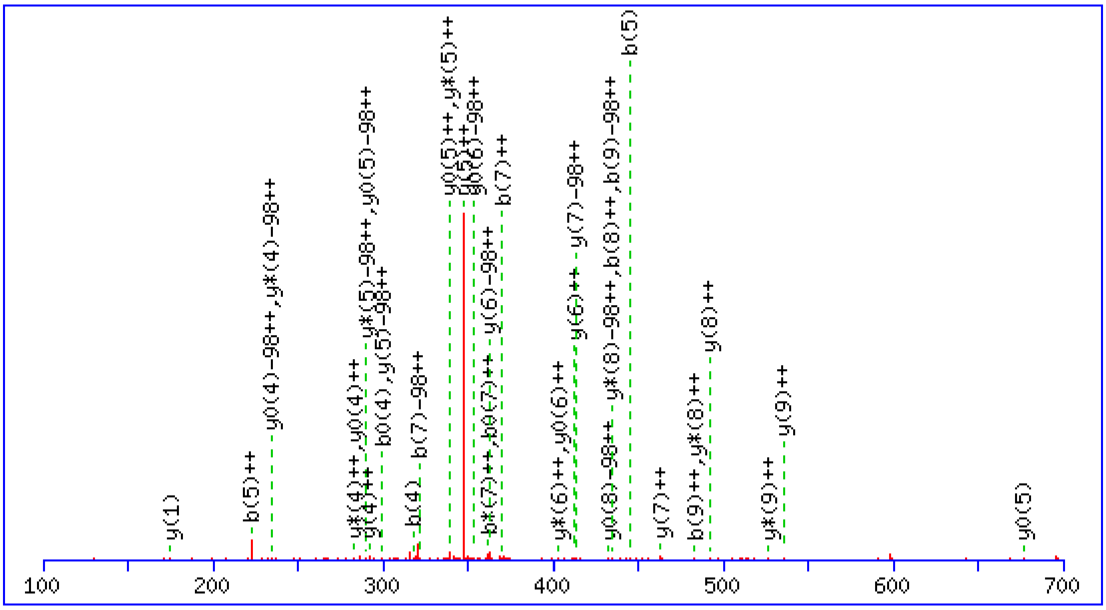
Monoisotopic mass of neutral peptide Mr(calc): 2171.0511
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00043
Matched b ions: b(6), b(9)++, b(9), b(10), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(7)-98++, y(7)-98, y(8)++, y(8), y(9)-98++, y(9), y(9)++, y(9)-98, y(10), y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++

Peptide No.74

ASGTKLTEPR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **ASGTKLTEPR**
Found in **EVI1_MOUSE** in **SwissProt**, MDS1 and EVI1 complex locus protein EVI1 OS=Mus musculus GN=Mecom PE=1 SV=1

Match to Query 1859: 1138.539912 from(380.520580,3+) index(603)
Title: Elution from: 29.444 to 29.444 scan no 1826 cid35.00 polarity:+



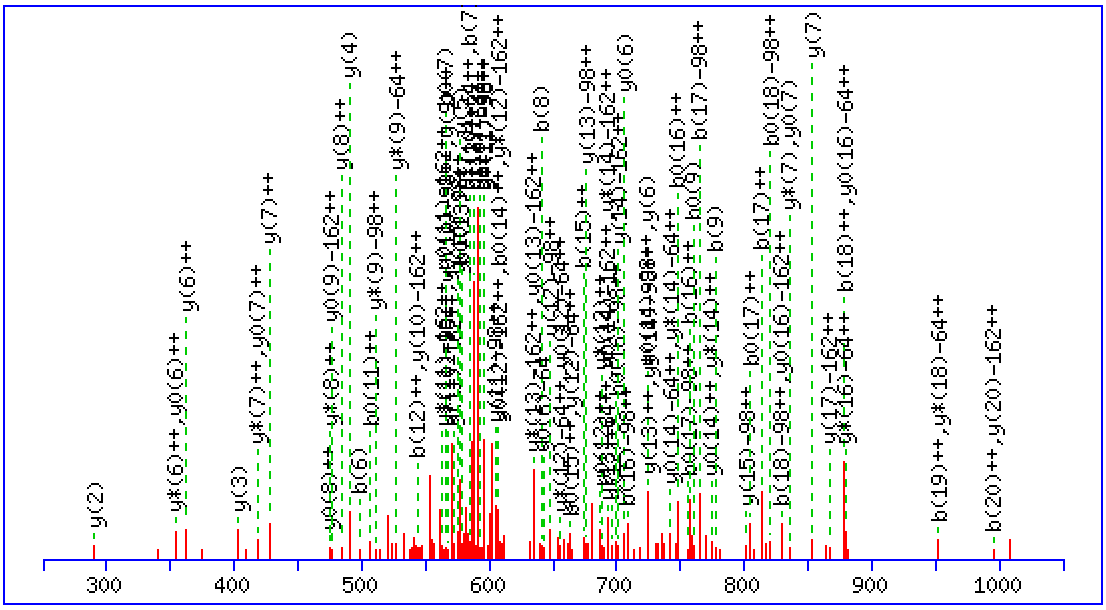
Monoisotopic mass of neutral peptide Mr(calc): 1138.5383
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.044
Matched b ions: b(4), b(5)++, b(5), b(7)-98++, b(7)++, b(8)++, b(9)++, b(9)-98++
Matched y ions: y(1), y(4)++, y(5)++, y(5)-98++, y(6)-98++, y(6)++, y(7)++, y(7)-98++, y(8)++, y(9)++

Peptide No.75

ASPALGSGHHDGSGDSLEMSSLDR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **ASPALGSGHHDGSGDSLEMSSLDR**
Found in **TOM70_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=2

Match to Query 6325: 2478.008696 from(620.509450,4+) index(4929)
Title: Elution from: 27.203 to 27.203 scan no 2254 cid35.00 polarity:+:m1s



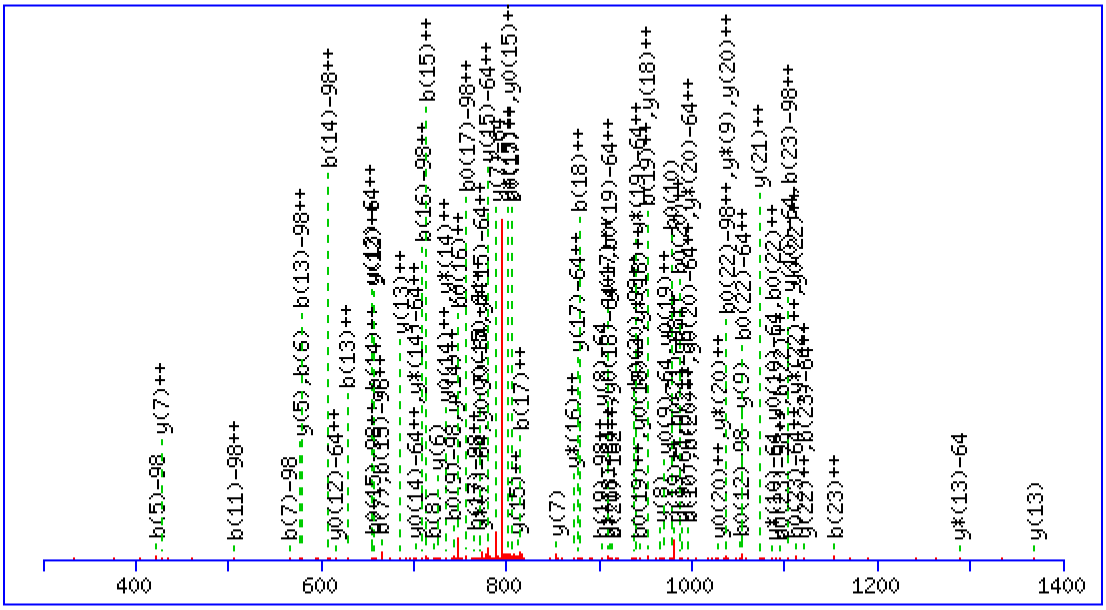
Monoisotopic mass of neutral peptide Mr(calc): 2478.0119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 **Expect:** 0.0089
Matched b ions: b(6), b(7), b(8), b(9), b(12)++, b(13)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(10)-98++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(15)-98++

Peptide No.76

ASPALGSGHHDGSGDSLEMSSLDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ASPALGSGHHDGSGDSLEMSSLDR**
Found in **TOM70_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=2

Match to Query 5363: 2478.011667 from(827.011165,3+) index(3865)
Title: Elution from: 34.828 to 34.828 scan no 2376 cid35.00 polarity:+:m1s



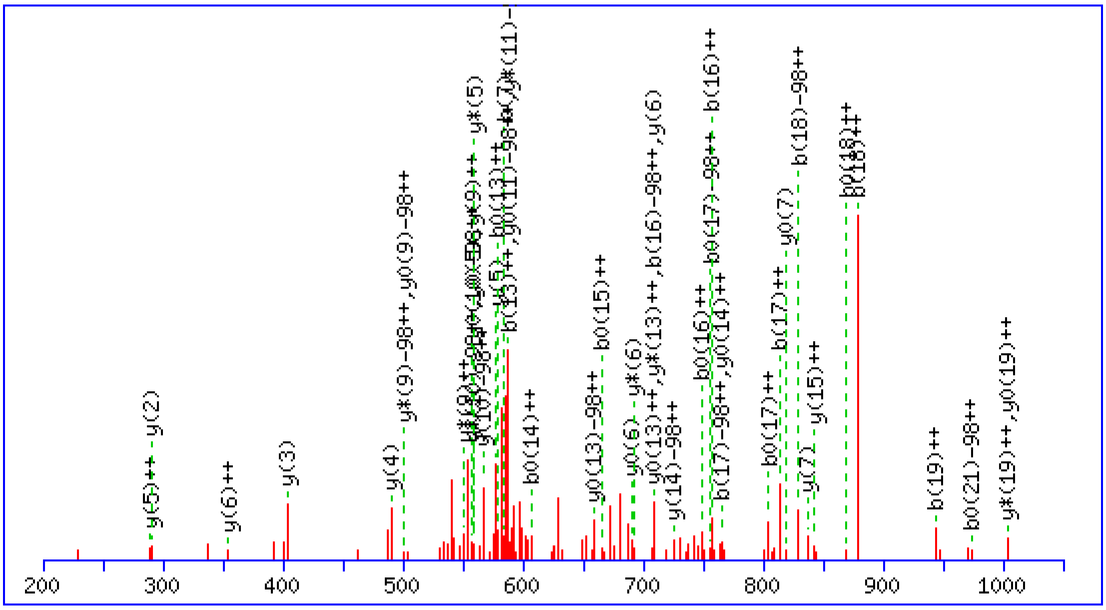
Monoisotopic mass of neutral peptide Mr(calc): 2478.0119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 21 **Expect:** 0.05
Matched b ions: b(5)-98, b(6), b(7), b(7)-98, b(8), b(10), b(11)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++
Matched y ions: y(5), y(6), y(7), y(7)++, y(8), y(9), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++

Peptide No.77

ASPALGSGHHDGSGDSLEMSSLDR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **ASPALGSGHHDGSGDSLEMSSLDR**
Found in **TOM70_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=2

Match to Query 6135: 2462.017412 from(616.511629,4+) index(5345)
Title: Elution from: 33.065 to 33.065 scan no 3014 cid35.00 polarity:+:m1s



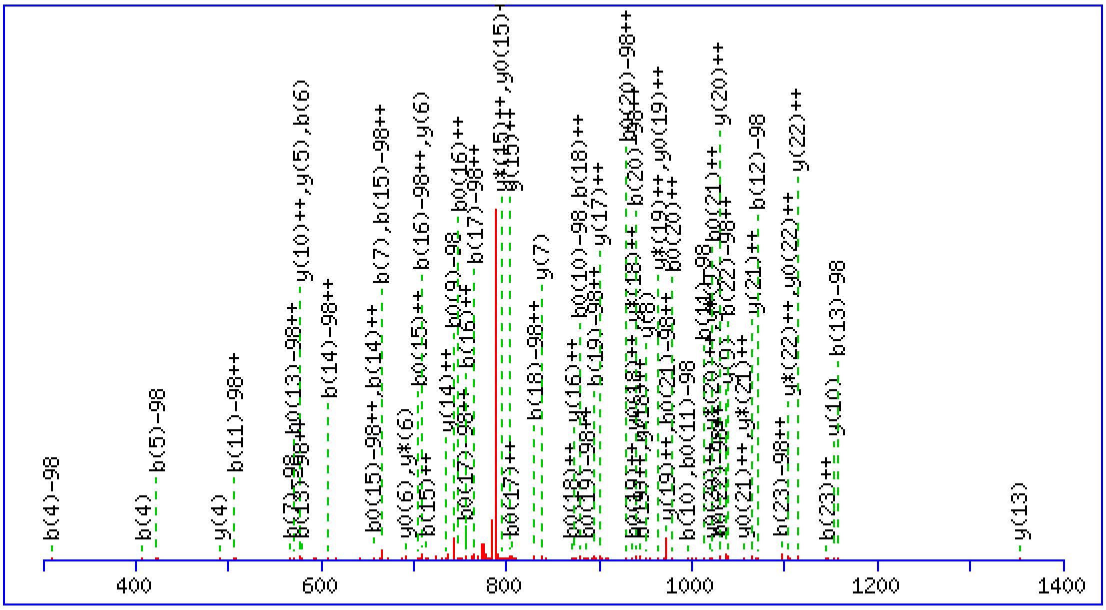
Monoisotopic mass of neutral peptide Mr(calc): 2462.0169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0049
Matched b ions: b(7), b(13)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(9)++, y(10)-98++, y(14)-98++, y(15)++

Peptide No.78

ASPALGSGHHDGSGDSLEMSSLDR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ASPALGSGHHDGSGDSLEMSSLDR**
Found in **TOM70_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=2

Match to Query 6309: 2462.015688 from(821.679172,3+) index(5512)
Title: Elution from: 33.017 to 33.017 scan no 3041 cid35.00 polarity:+:m1s



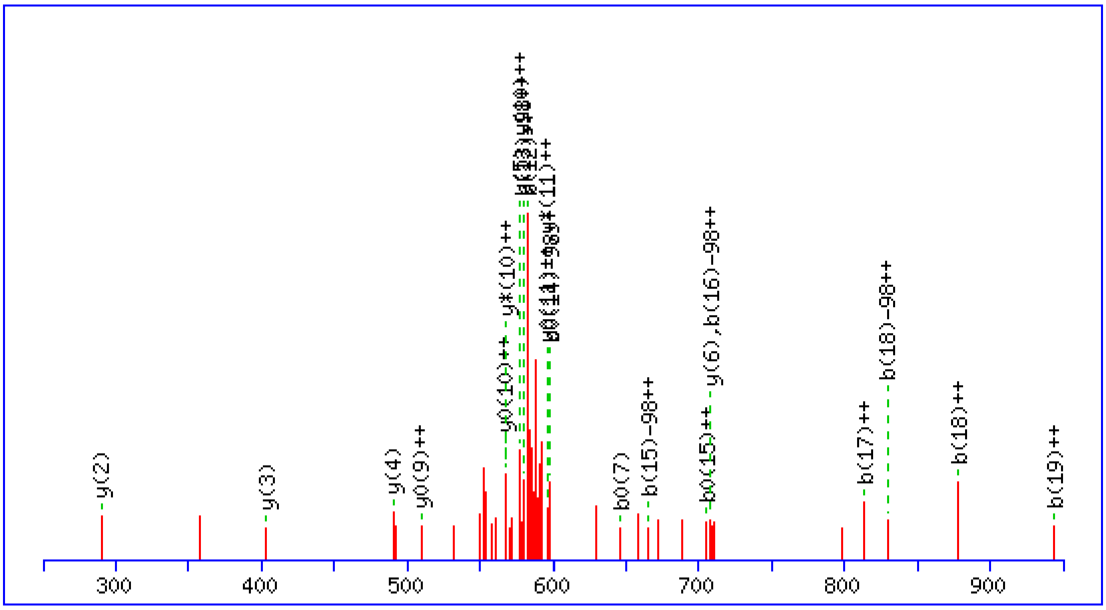
Monoisotopic mass of neutral peptide Mr(calc): 2462.0169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 1.1e-008
Matched b ions: b(4)-98, b(4), b(5)-98, b(6), b(7), b(7)-98, b(10), b(11)-98++, b(11)-98, b(12)-98, b(13)-98++, b(13)-98, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(13), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++

Peptide No.79

ASPALGSGHHDGSGDSLEMSSLDR
Confirmed sites:
Ambiguous sites: @S:2orS:7

MS/MS Fragmentation of **ASPALGSGHHDGSGDSLEMSSLDR**
Found in **TOM70_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=2

Match to Query 6133: 2462.016608 from(616.511428,4+) index(5531)
Title: Elution from: 34.821 to 34.821 scan no 3251 cid35.00 polarity:+:m1s



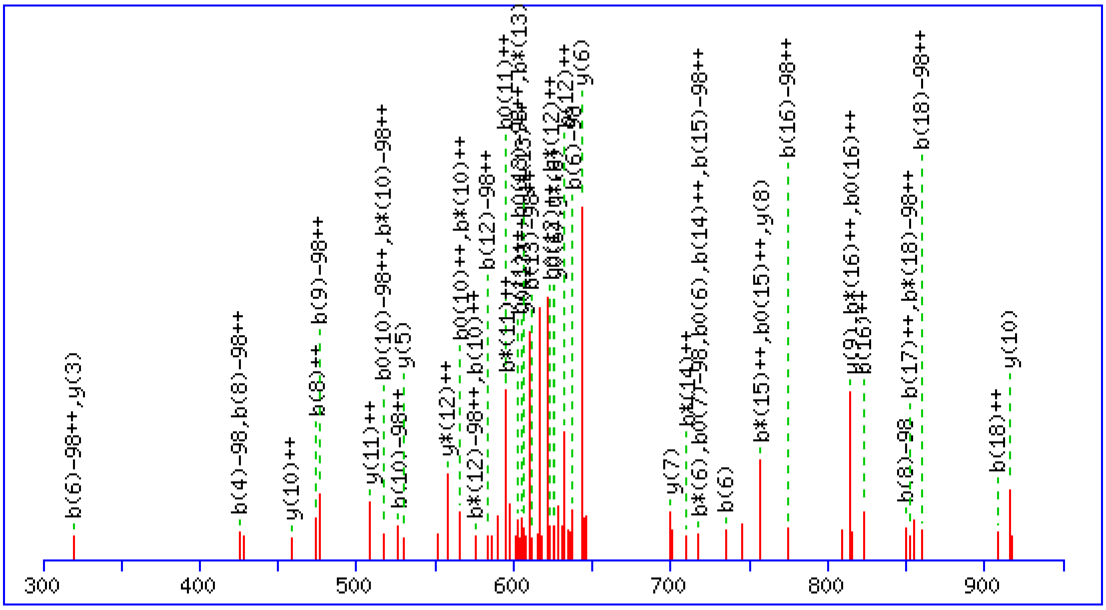
Monoisotopic mass of neutral peptide Mr(calc): 2462.0169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.028
Matched b ions: b(12)++, b(13)-98++, b(15)-98++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(10)++

Peptide No.80

ASQRPDVLTTGGGNPIGDK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ASQRPDVLTTGGGNPIGDK**
Found in **CATA_MOUSE** in **SwissProt**, Catalase OS=Mus musculus GN=Cat PE=1 SV=4

Match to Query 4710: 1961.922459 from(654.981429,3+) index(5177)
Title: Elution from: 31.515 to 31.515 scan no 2804 cid35.00 polarity:+:m1s



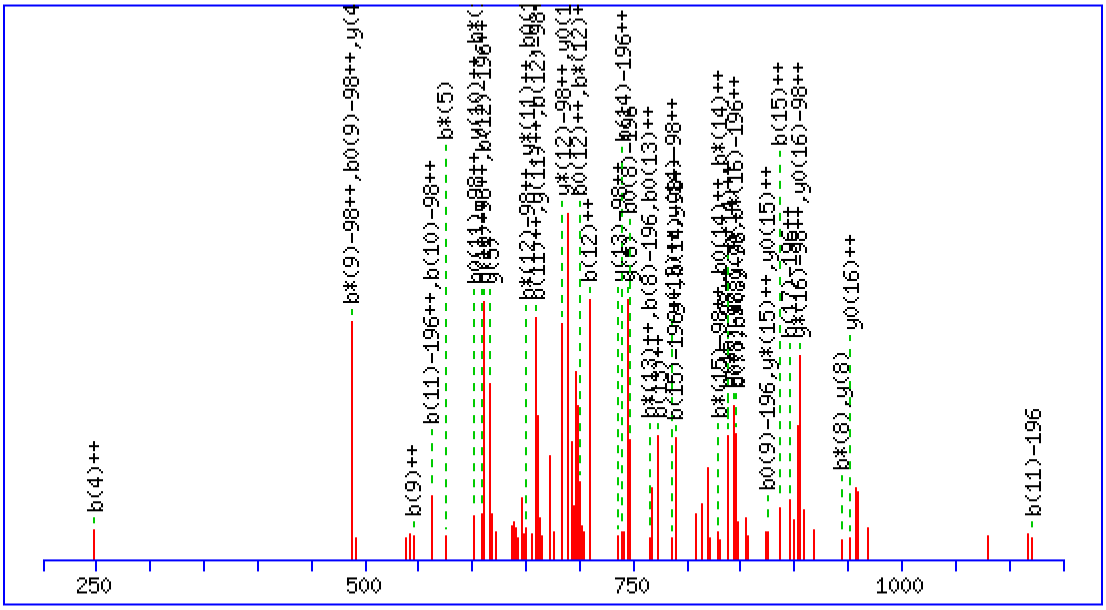
Monoisotopic mass of neutral peptide Mr(calc): 1961.9208
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0019
Matched b ions: b(4)-98, b(6)-98++, b(6)-98, b(6), b(8)++, b(8)-98++, b(8)-98, b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)++

Peptide No.81

ASRVPSSDEEVVEEPQSR
Confirmed sites: @S:2
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of **ASRVPSSDEEVVEEPQSR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4633: 2159.875113 from(720.965647,3+) index(4438)
Title: Elution from: 28.867 to 28.867 scan no 2417 cid35.00 polarity:+:m1s



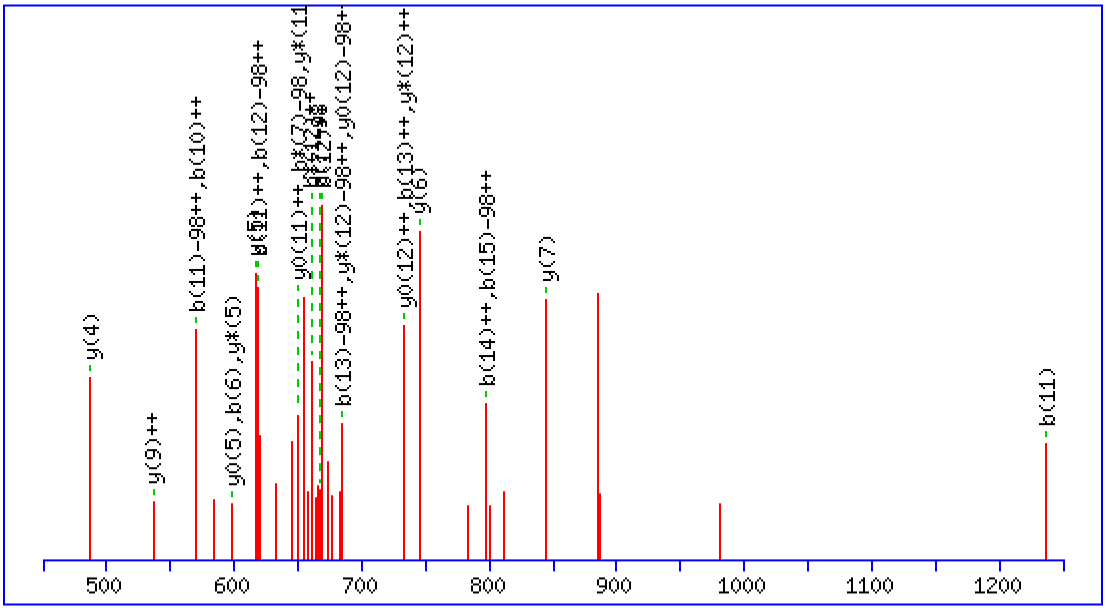
Monoisotopic mass of neutral peptide Mr(calc): 2159.8773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.013
Matched b ions: b(4)++, b(7), b(8)-196, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)-196++, b(11)-196, b(11)++, b(12)-196++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-196++, b(15)-98++, b(17)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(13)-98++, y(13)++, y(14)-98++

Peptide No.82

ASRVPSSDEEVVEEPQSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **ASRVPSSDEEVVEEPQSR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4377: 2079.908205 from(694.310011,3+) index(1086)
Title: Elution from: 26.587 to 26.587 scan no 2108 cid35.00 polarity:+



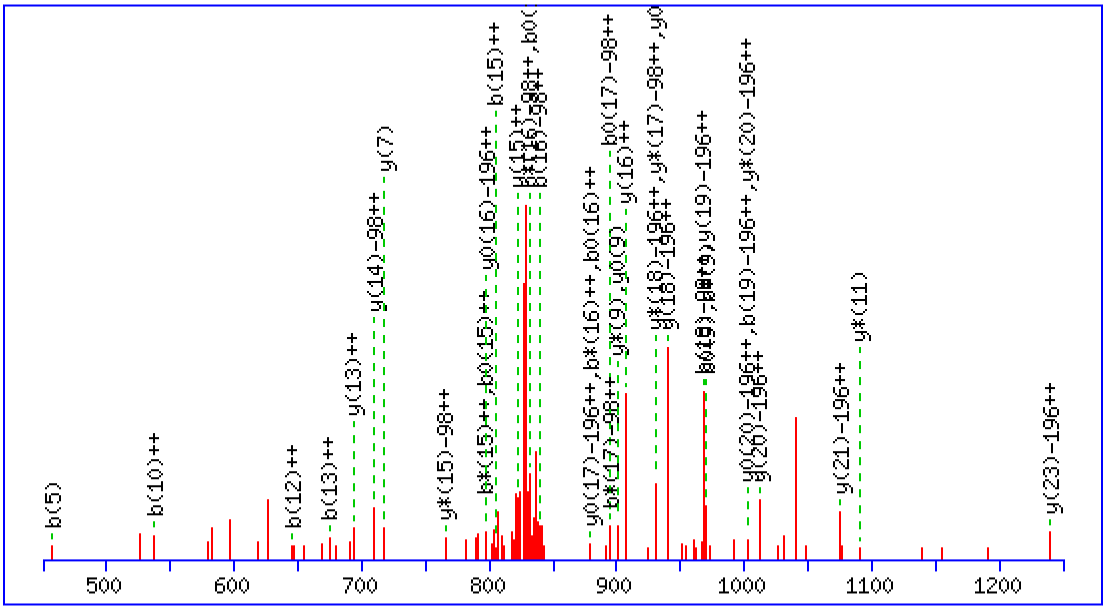
Monoisotopic mass of neutral peptide Mr(calc): 2079.9110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(6), b(7)-98, b(10)++, b(11)-98++, b(11), b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(9)++

Peptide No.83

ASSPNISSYSESGVYSQESLTSSLSTTPQGK
Confirmed sites: @S:16,@S:19
Ambiguous sites: @Y:9orS:10

MS/MS Fragmentation of **ASSPNISSYSESGVYSQESLTSSLSTTPQGK**
Found in **F179B_MOUSE** in **SwissProt**, Protein FAM179B OS=Mus musculus GN=Fam179b PE=2 SV=2

Match to Query 7145: 3418.384088 from(855.603298,4+) index(5297)
Title: Elution from: 31.087 to 31.087 scan no 2780 cid35.00 polarity:+:m1s



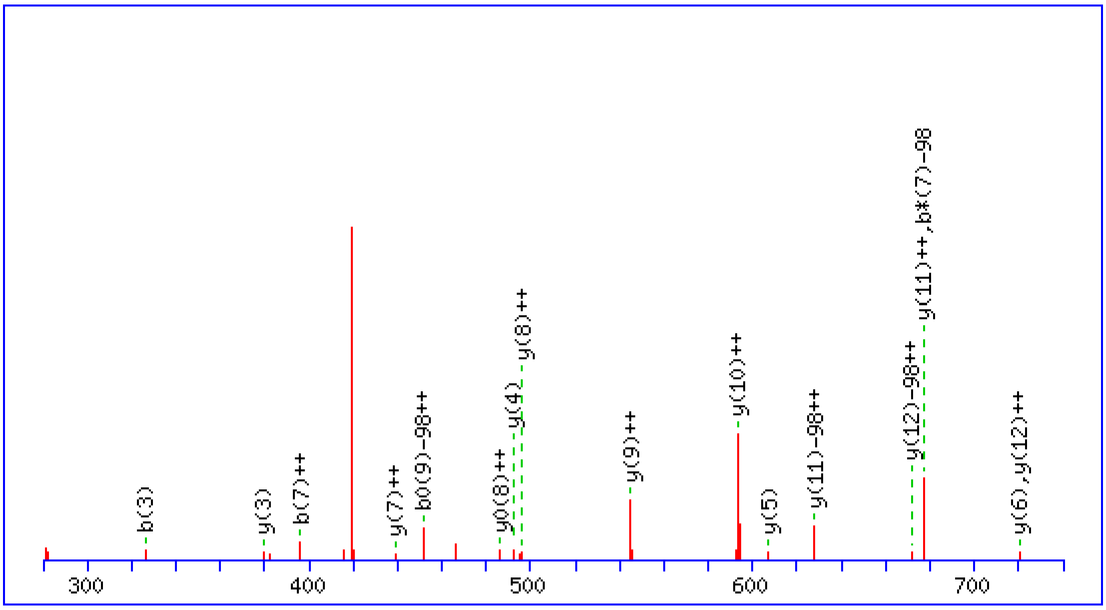
Monoisotopic mass of neutral peptide Mr(calc): 3418.3779
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y9 : Phospho (Y)
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.046
Matched b ions: b(5), b(10)++, b(12)++, b(13)++, b(15)++, b(16)-98++, b(18)-98++, b(19)-196++
Matched y ions: y(7), y(8), y(13)++, y(14)-98++, y(15)++, y(16)++, y(18)-196++, y(19)-196++, y(20)-196++, y(21)-196++, y(23)-196++

Peptide No.84

ASSPPDRIDIFGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ASSPPDRIDIFGR**
Found in **ARGL1_MOUSE** in **SwissProt**, Arginine and glutamate-rich protein 1 OS=Mus musculus GN=Arglu1 PE=1 SV=2

Match to Query 2488: 1509.696894 from(504.239574,3+) index(2369)
Title: Elution from: 41.833 to 41.833 scan no 4031 cid35.00 polarity:+



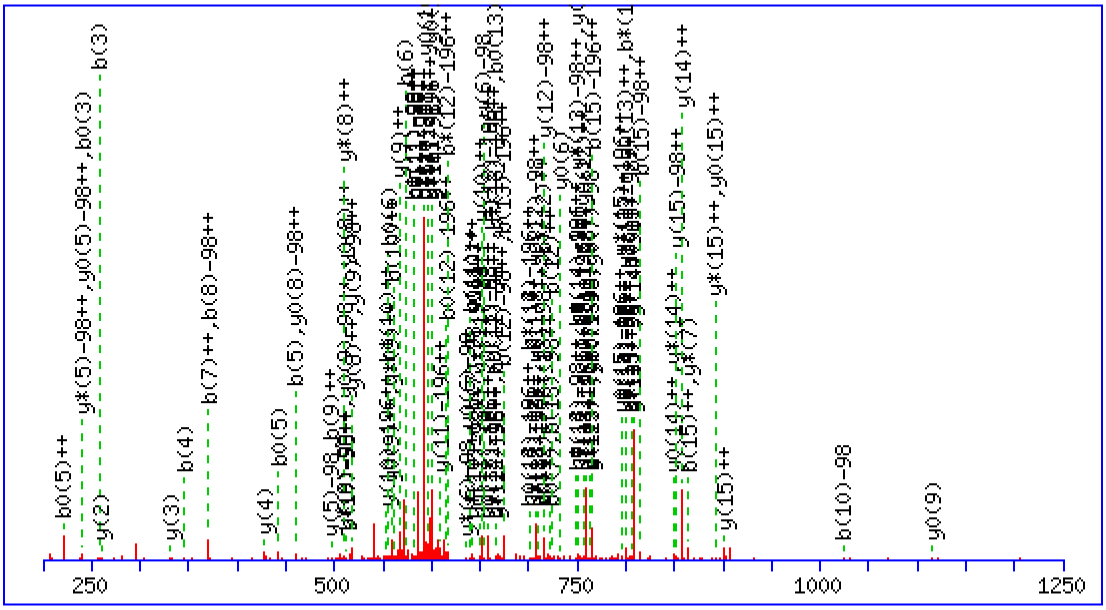
Monoisotopic mass of neutral peptide Mr(calc): 1509.6977
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00041
Matched b ions: b(3), b(7)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++

Peptide No.85

ASVSDLSPRERSPALK
Confirmed sites: @S:7,@S:12
Ambiguous sites:

MS/MS Fragmentation of **ASVSDLSPRERSPALK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4083: 1871.854899 from(624.958909,3+) index(848)
Title: Elution from: 33.948 to 33.948 scan no 2267 cid35.00 polarity:+



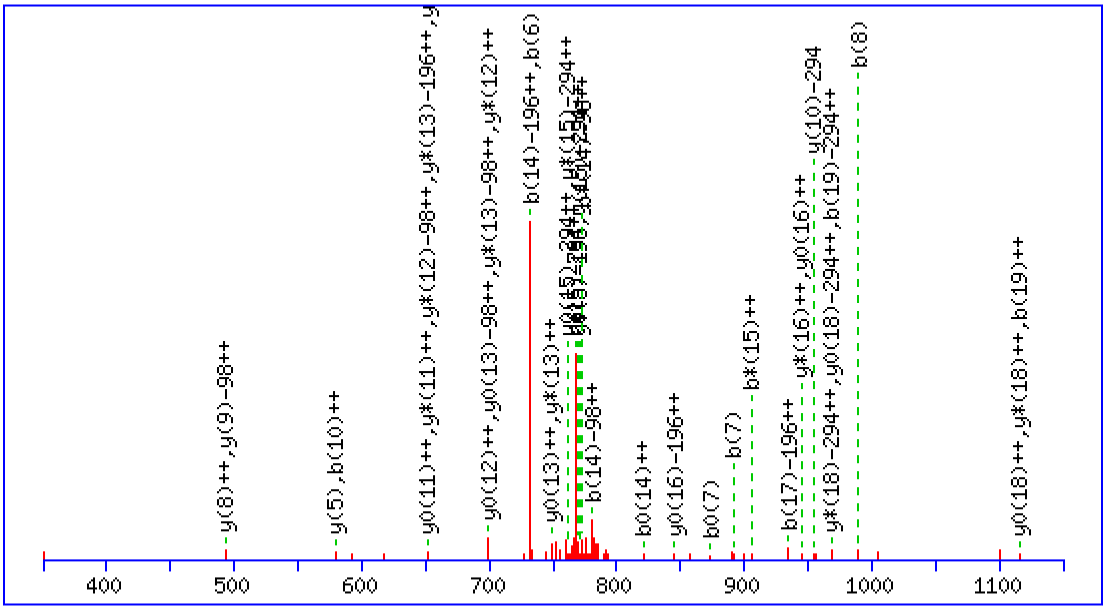
Monoisotopic mass of neutral peptide Mr(calc): 1871.8543
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7)-98, b(8)-98++, b(9)++, b(10)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(15)++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-196++, y(10)-98++, y(11)-98++, y(11)++, y(11)-196++, y(12)++, y(12)-98++, y(12)-196++, y(13)-98++, y(13)++, y(13)-196++, y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-98++

Peptide No.86

ASWRACCPPASPSASHVPAR
Confirmed sites: @S:11,@S:13,@S:15
Ambiguous sites:

MS/MS Fragmentation of **ASWRACCPPASPSASHVPAR**
Found in **GP124_MOUSE** in **SwissProt**, G-protein coupled receptor 124 OS=Mus musculus GN=Gpr124 PE=2 SV=2

Match to Query 5260: 2403.901878 from(802.307902,3+) index(3466)
Title: Elution from: 30.072 to 30.072 scan no 1812 cid35.00 polarity:+:m1s



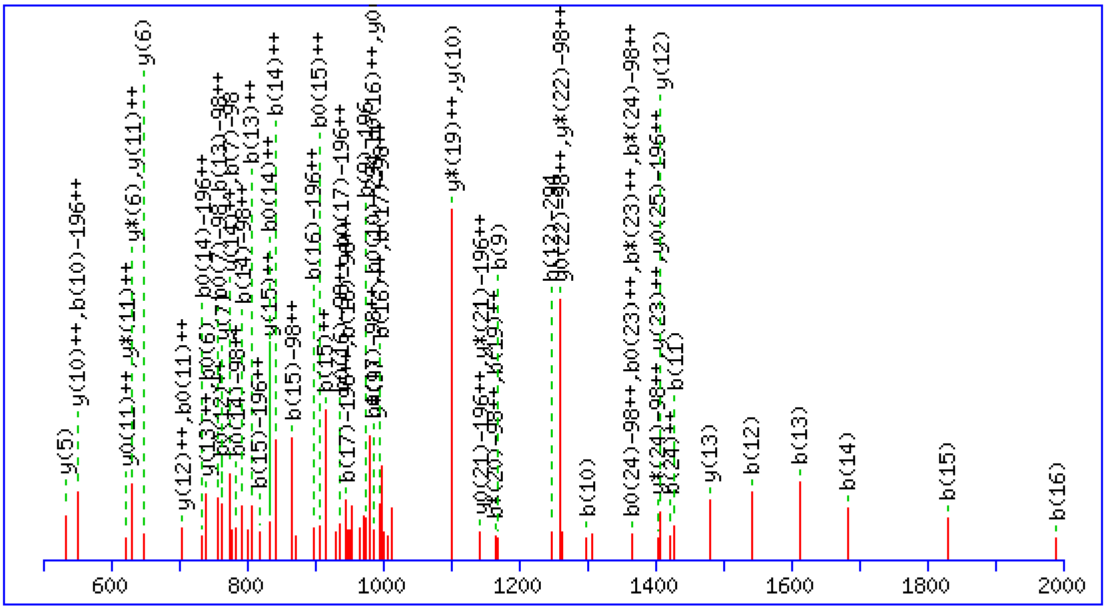
Monoisotopic mass of neutral peptide Mr(calc): 2403.9044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.046
Matched b ions: b(6), b(7), b(8), b(10)++, b(14)-196++, b(14)-98++, b(15)-294++, b(17)-196++, b(19)-294++, b(19)++
Matched y ions: y(5), y(8)++, y(9)-98++, y(10)-294, y(15)-294++

Peptide No.87

ATDSHSDSEEELAAFCPQLDDSTVAR
Confirmed sites: @S:4,@S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of **ATDSHSDSEEELAAFCPQLDDSTVAR**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 6951: 3090.121077 from(1031.047635,3+) index(7084)
Title: Elution from: 58.977 to 58.977 scan no 6052 cid35.00 polarity:+:m1s



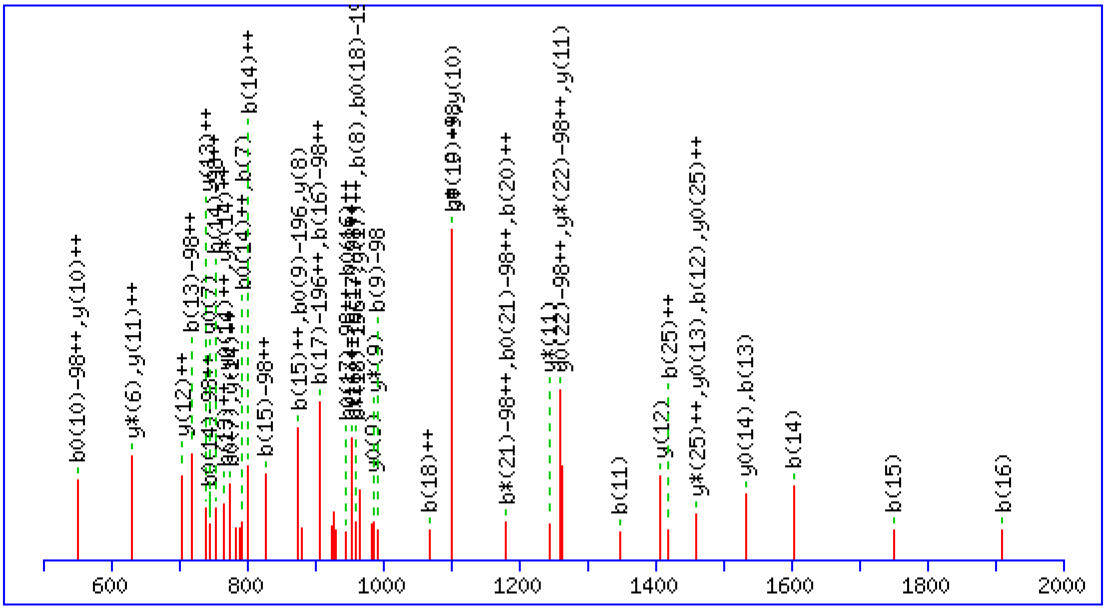
Monoisotopic mass of neutral peptide Mr(calc): 3090.1240
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 5.5e-005
Matched b ions: b(7)-98, b(9), b(9)-196, b(10)-196++, b(10), b(11), b(12)-294, b(12), b(13), b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(15)-196++, b(16), b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)-98++, b(19)++, b(24)++
Matched y ions: y(5), y(6), y(7), y(10), y(10)++, y(11)++, y(11), y(12)++, y(12), y(13), y(13)++, y(14)++, y(15)++, y(23)++

Peptide No.88

ATDSHSDSEEELAAFCPQLDDSTVAR
Confirmed sites: @S:8
Ambiguous sites: @T:2orS:4orS:6

MS/MS Fragmentation of **ATDSHSDSEEELAAFCPQLDDSTVAR**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 6919: 3010.153434 from(1004.391754,3+) index(6951)
Title: Elution from: 54.376 to 54.376 scan no 5647 cid35.00 polarity:+:m1s



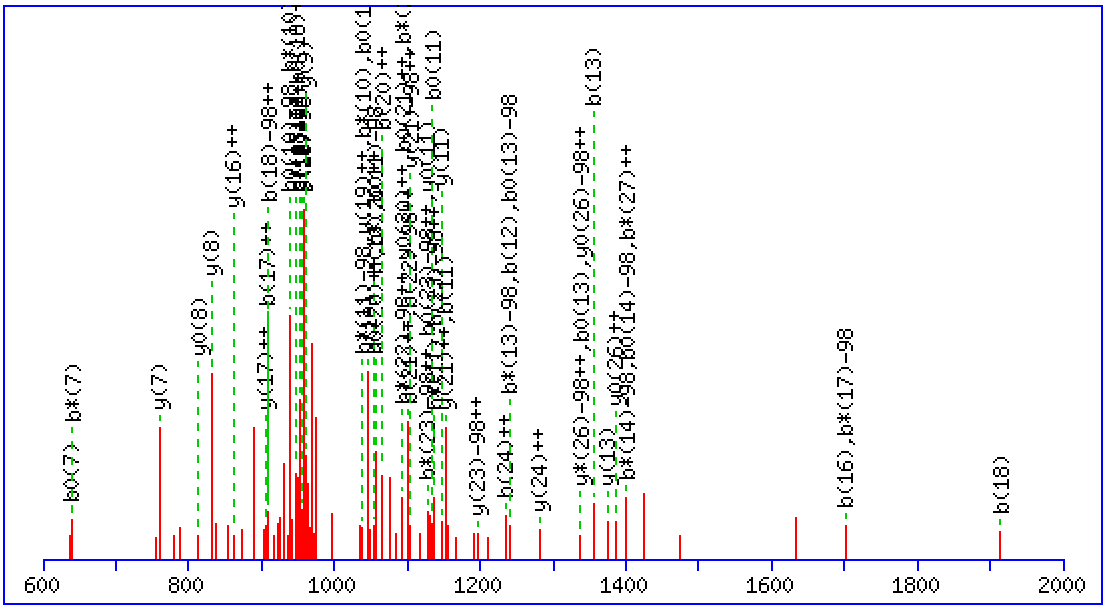
Monoisotopic mass of neutral peptide Mr(calc): 3010.1577
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 7.6e-005
Matched b ions: b(7), b(8), b(9)-98, b(11), b(12), b(13)-98++, b(13), b(13)++, b(14)++, b(14), b(14)-98++, b(15), b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(16), b(17)-196++, b(17)-98++, b(18)++, b(20)++, b(25)++
Matched y ions: y(8), y(10), y(10)++, y(11)++, y(11), y(12), y(12)++, y(13)++, y(14)++, y(17)++

Peptide No.89

ATNLAGETESVSDCADNVSEAPATSEQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **ATNLAGETESVSDCADNVSEAPATSEQK**
Found in **LRBA_MOUSE** in **SwissProt**, Lipopolysaccharide-responsive and beige-like anchor protein OS=Mus musculus GN=Lrba PE=1 SV=1

Match to Query 6573: 2960.216235 from(987.746021,3+) index(5283)
Title: Elution from: 44.331 to 44.331 scan no 3619 cid35.00 polarity:+:m1s



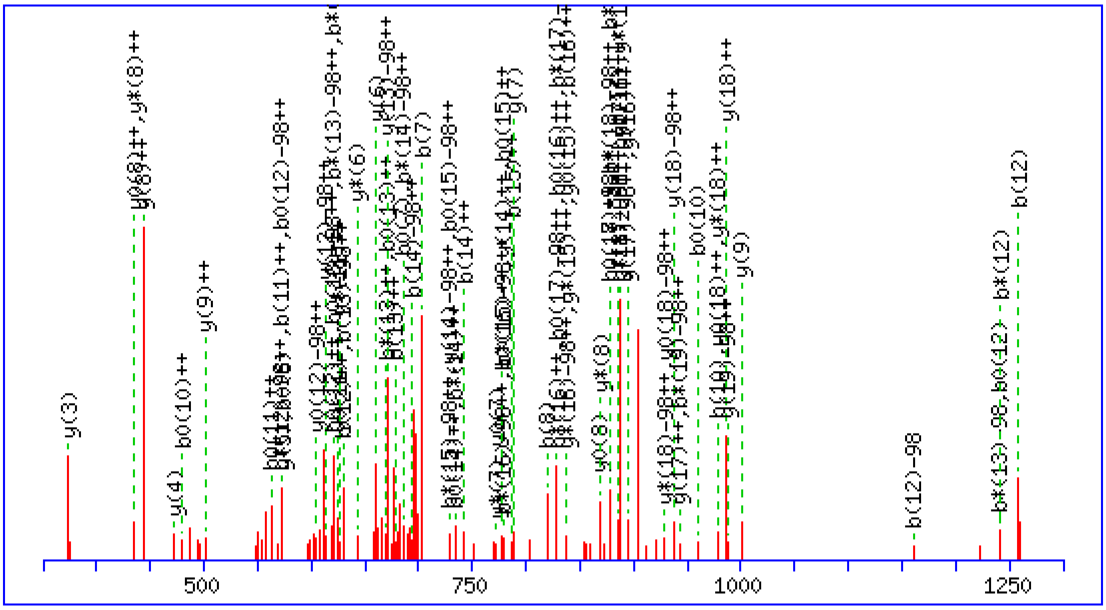
Monoisotopic mass of neutral peptide Mr(calc): 2960.2230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.017
Matched b ions: b(10)-98, b(10), b(11), b(11)-98, b(12), b(13), b(16), b(17)++, b(18)++, b(18), b(18)-98++, b(19)-98++, b(20)++, b(21)++, b(22)-98++, b(23)-98++, b(24)++
Matched y ions: y(7), y(8), y(9), y(10), y(11), y(13), y(16)++, y(17)++, y(18)++, y(19)++, y(21)++, y(21)-98++, y(23)-98++, y(24)++

Peptide No.90

ATSPPHLDGTSNPESTVPEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **ATSPPHLDGTSNPESTVPEK**
Found in **PML_MOUSE** in **SwissProt**, Protein PML OS=Mus musculus GN=Pml PE=1 SV=3

Match to Query 4608: 2142.946539 from(715.322789,3+) index(4455)
Title: Elution from: 29.040 to 29.040 scan no 2440 cid35.00 polarity:+:m1s



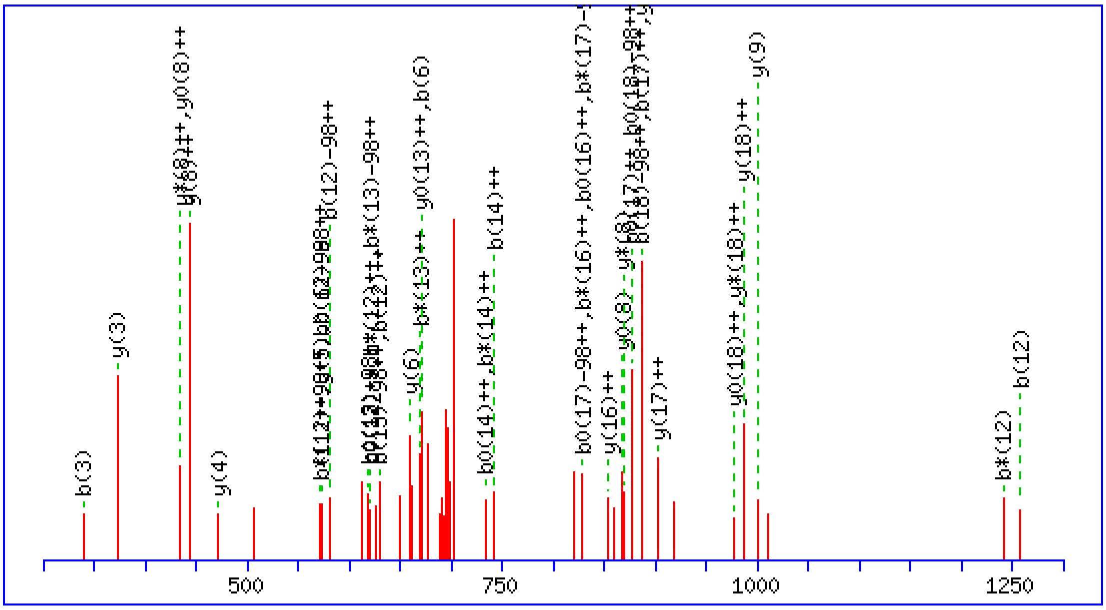
Monoisotopic mass of neutral peptide Mr(calc): 2142.9471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00049
Matched b ions: b(7), b(8), b(10), b(11)++, b(12)-98, b(12), b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(12)-98++, y(13)-98++, y(14)++, y(14)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++

Peptide No.91

ATSPPHLDGTSNPESTVPEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ATSPPHLDGTSNPESTVPEK**
Found in **PML_MOUSE** in **SwissProt**, Protein PML OS=Mus musculus GN=Pml PE=1 SV=3

Match to Query 4593: 2142.946467 from(715.322765,3+) index(4219)
Title: Elution from: 29.183 to 29.183 scan no 2373 cid35.00 polarity:+:m1s



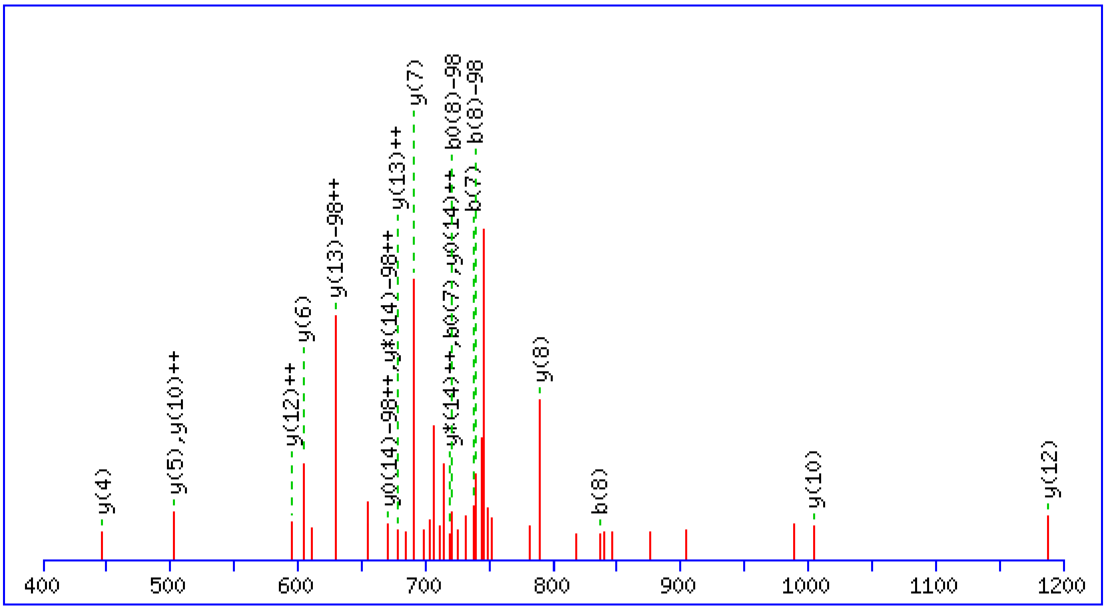
Monoisotopic mass of neutral peptide Mr(calc): 2142.9471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0054
Matched b ions: b(3), b(6), b(6)-98, b(11)++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(14)++, b(17)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++, y(8), y(9), y(16)++, y(17)++, y(18)++

Peptide No.92

ATSPSTLVSTGPSSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ATSPSTLVSTGPSSR**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2544: 1526.696082 from(764.355317,2+) index(1300)
Title: Elution from: 28.491 to 28.491 scan no 2366 cid35.00 polarity:+



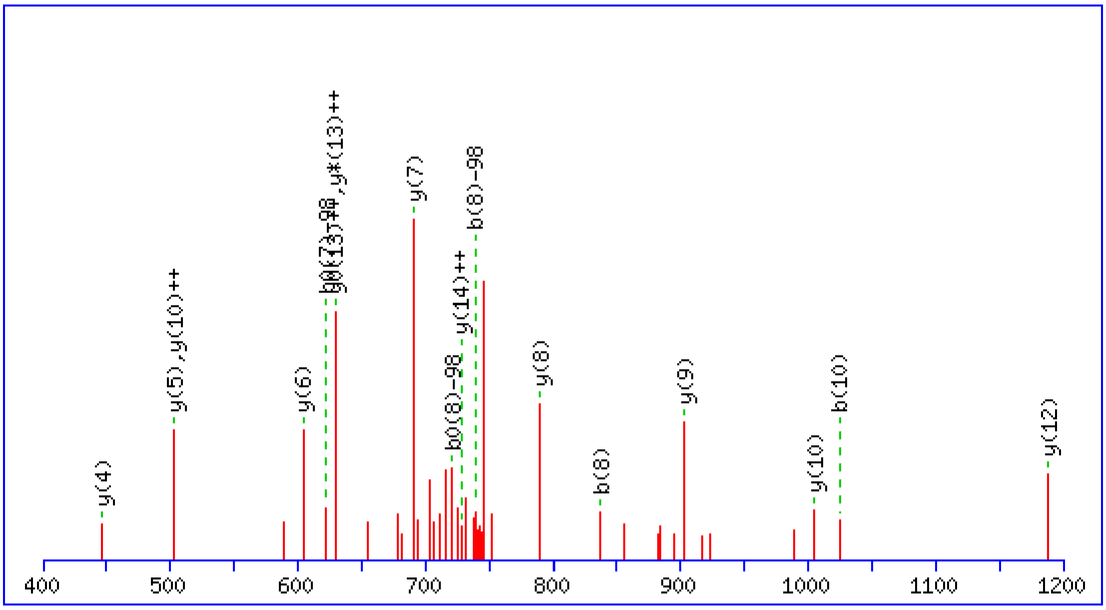
Monoisotopic mass of neutral peptide Mr(calc): 1526.6978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 3.7e-005
Matched b ions: b(7), b(8)-98, b(8)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)++, y(10), y(12), y(12)++, y(13)-98++, y(13)++

Peptide No.93

ATSPSTLVSTGPSSR
Confirmed sites:
Ambiguous sites: @T:2orS:3

MS/MS Fragmentation of **ATSPSTLVSTGPSSR**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2665: 1526.693736 from(764.354144,2+) index(1174)
Title: Elution from: 28.629 to 28.629 scan no 2297 cid35.00 polarity:+



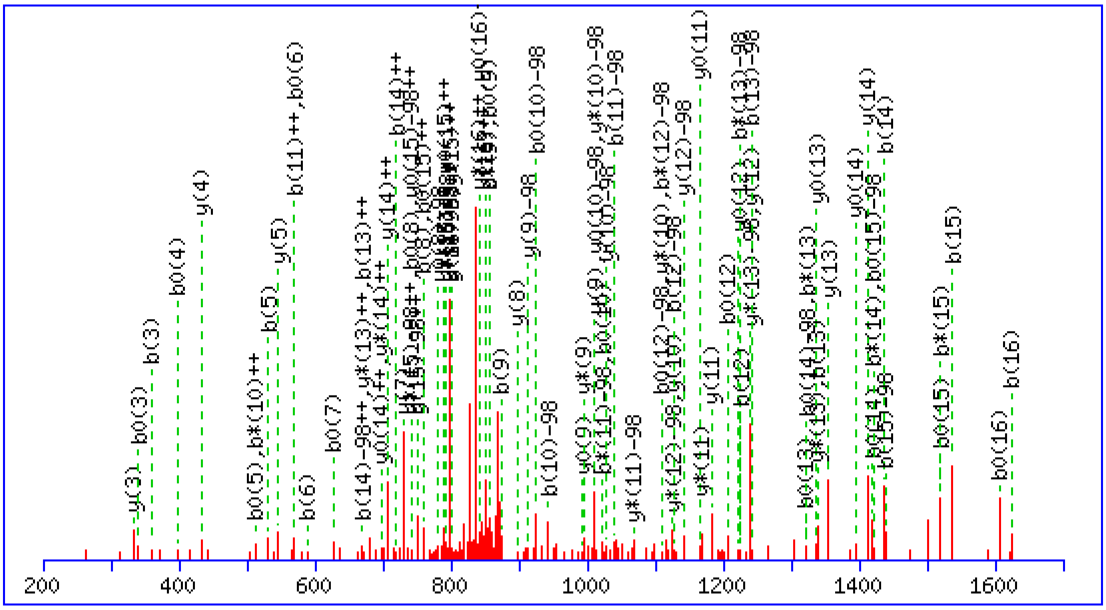
Monoisotopic mass of neutral peptide Mr(calc): 1526.6978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 **Expect:** 1.2e-007
Matched b ions: b(8), b(8)-98, b(10)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(12), y(14)++

Peptide No.94

ATWGDGGDNSPSNVVSK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **ATWGDGGDNSPSNVVSK**
Found in **SNP23_MOUSE** in **SwissProt**, Synaptosomal-associated protein 23 OS=Mus musculus GN=Snap23 PE=1 SV=1

Match to Query 4464: 1769.723810 from(885.869181,2+) index(1473)
Title: Elution from: 38.747 to 38.747 scan no 2981 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1769.7258
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 86 **Expect:** 1.1e-008
Matched b ions: b(3), b(5), b(6), b(8), b(9), b(10)-98, b(11)++, b(11)-98, b(12), b(12)-98, b(13), b(13)++, b(13)-98, b(14), b(14)-98++, b(14)++, b(15), b(15)-98, b(16)
Matched y ions: y(3), y(4), y(5), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(12), y(12)-98, y(13), y(14), y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.95

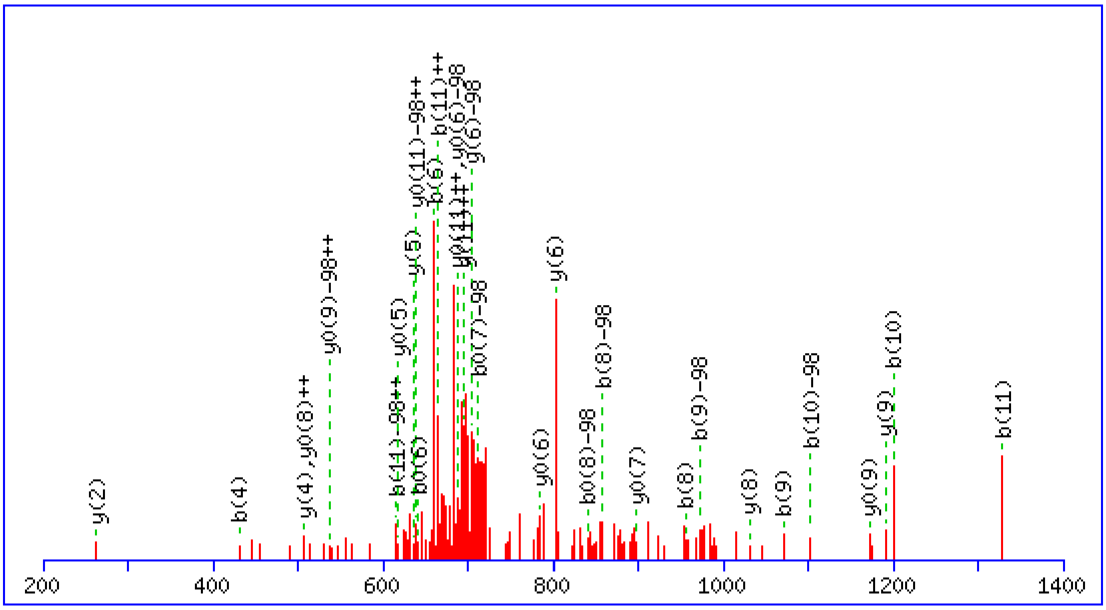
AVTCDISEDEED

Confirmed sites: @S:7

Ambiguous sites:

MS/MS Fragmentation of **AVTCDISEDEED**
Found in **PCY1A_MOUSE** in **SwissProt**, Choline-phosphate cytidylyltransferase A OS=Mus musculus GN=Pcyt1a PE=1 SV=1

Match to Query 2947: 1461.486520 from(731.750536,2+) index(1017)
Title: Elution from: 35.745 to 35.745 scan no 2488 cid35.00 polarity:+



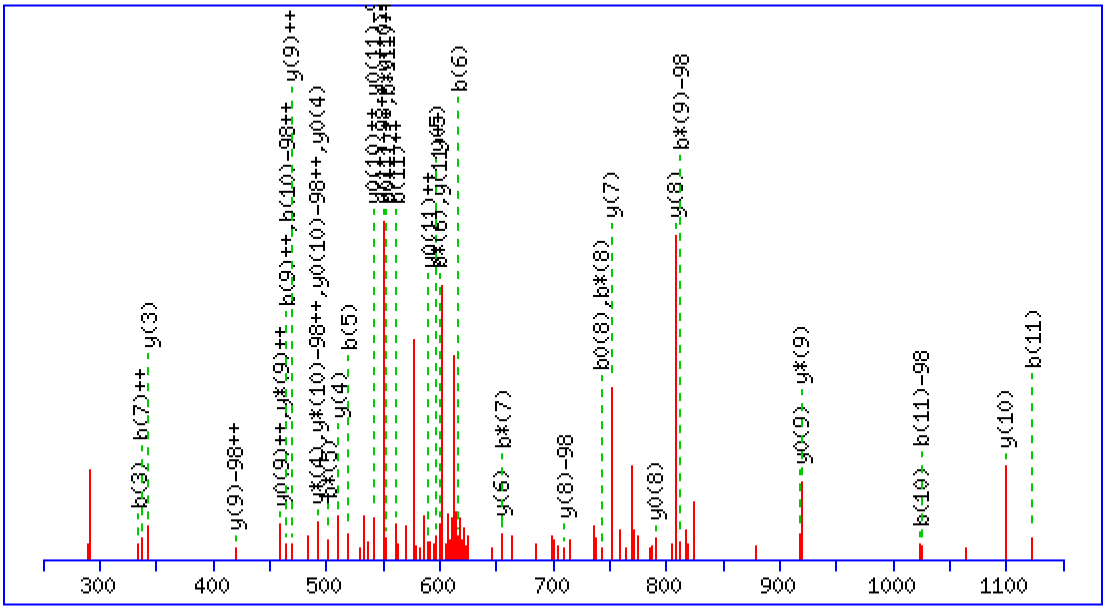
Monoisotopic mass of neutral peptide Mr(calc): 1461.4854
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.012
Matched b ions: b(4), b(6), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98++, b(11)++
Matched y ions: y(2), y(4), y(5), y(6), y(6)-98, y(8), y(9), y(11)++

Peptide No.96

AVYQGPGSSPVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **AVYQGPGSSPVK**
Found in **COMT_MOUSE** in **SwissProt**, Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=1

Match to Query 1971: 1268.579450 from(635.297001,2+) index(999)
Title: Elution from: 24.584 to 24.584 scan no 1896 cid35.00 polarity:+



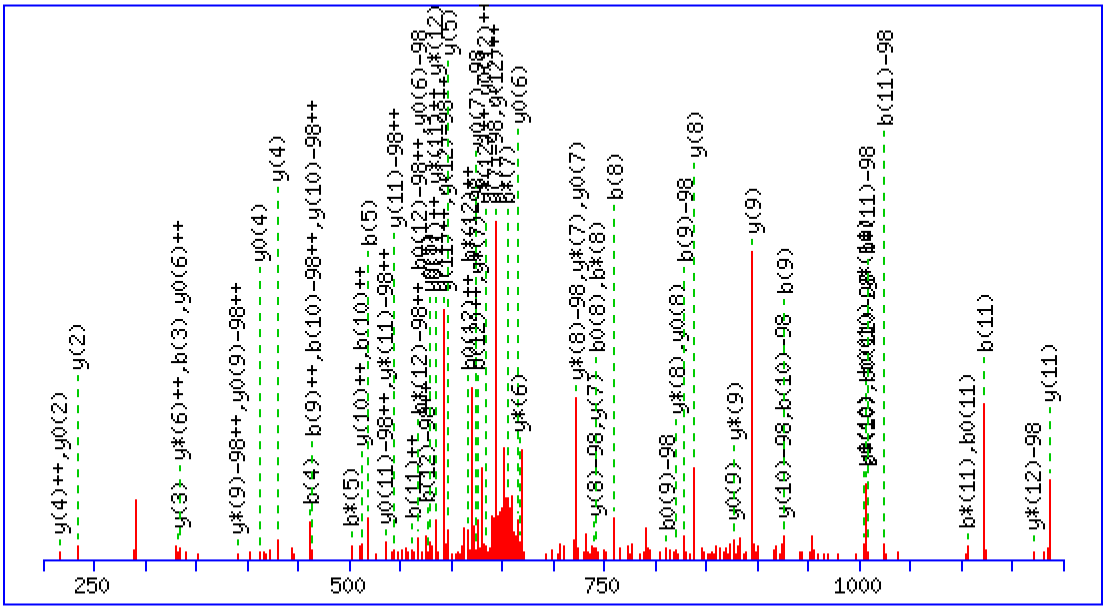
Monoisotopic mass of neutral peptide Mr(calc): 1268.5802
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0084
Matched b ions: b(3), b(5), b(6), b(7)++, b(9)++, b(10), b(10)-98++, b(11)-98, b(11), b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)++, y(9)-98++, y(10)++, y(10), y(11)-98++, y(11)++

Peptide No.97

AVYQGPGSSPVKS
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **AVYQGPGSSPVKS**
Found in **COMT_MOUSE** in **SwissProt**, Catechol O-methyltransferase OS=Mus musculus GN=Comt PE=1 SV=1

Match to Query 3009: 1355.612074 from(678.813313,2+) index(820)
Title: Elution from: 31.862 to 31.862 scan no 2118 cid35.00 polarity:+



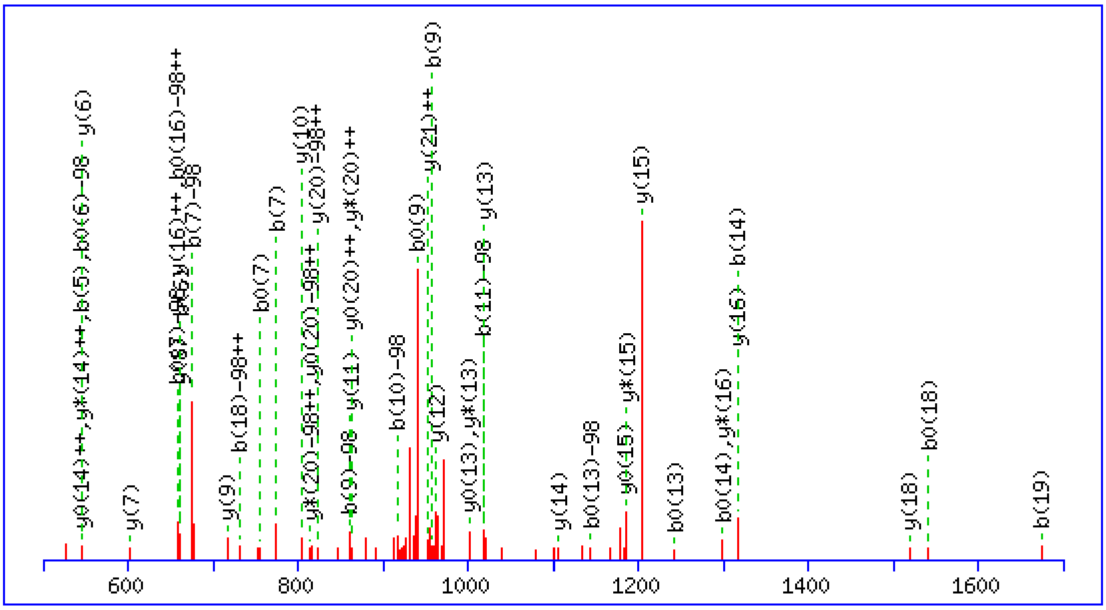
Monoisotopic mass of neutral peptide Mr(calc): 1355.6122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.0002
Matched b ions: b(3), b(4), b(5), b(8), b(9)-98, b(9), b(9)++, b(10)++, b(10)-98++, b(10)-98, b(11)-98, b(11), b(11)++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(7)-98, y(7), y(8), y(8)-98, y(9), y(10)++, y(10)-98++, y(10)-98, y(11)++, y(11), y(11)-98++, y(12)-98++, y(12)++

Peptide No.98

AYSGSDLPSGTGSGGGGADGAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **AYSGSDLPSGTGSGGGGADGAR**
Found in **ZNRF2_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase ZNRF2 OS=Mus musculus GN=Znrf2 PE=1 SV=1

Match to Query 4780: 1975.790680 from(988.902616,2+) index(4798)
Title: Elution from: 27.564 to 27.564 scan no 2266 cid35.00 polarity:+:m1s



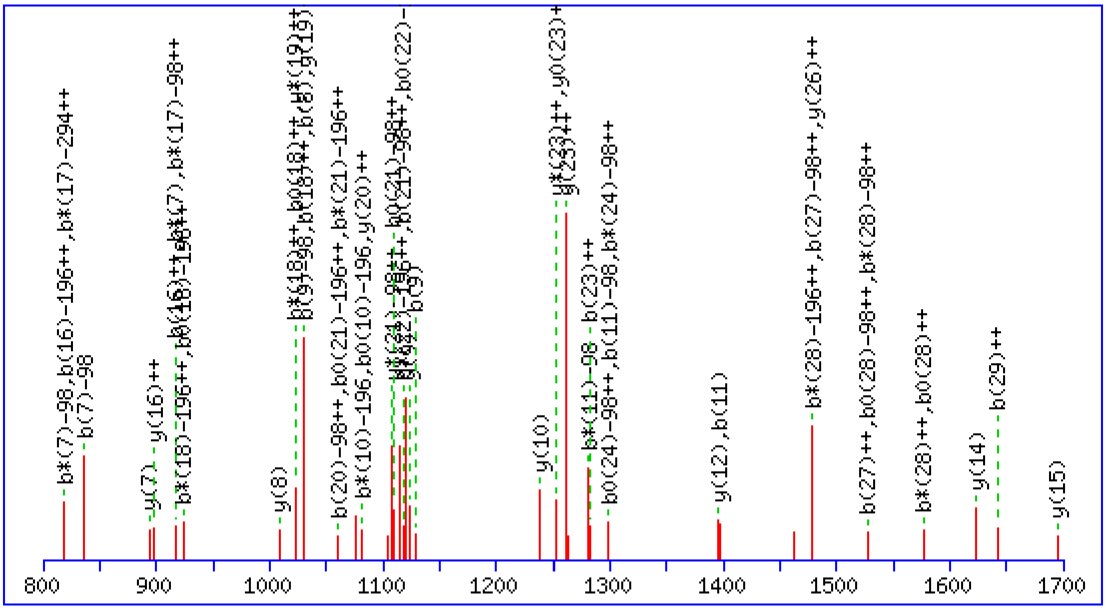
Monoisotopic mass of neutral peptide Mr(calc): 1975.7909
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 **Expect:** 2.5e-006
Matched b ions: b(5), b(6), b(7)-98, b(7), b(9)-98, b(9), b(10)-98, b(11)-98, b(14), b(18)-98++, b(19)
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(16), y(16)++, y(18), y(20)-98++, y(21)++

Peptide No.99

CDGSPRTPPSTPPATANLSADDDFQNTDLR
Confirmed sites: @S:4,@T:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **CDGSPRTPPSTPPATANLSADDDFQNTDLR**
Found in **SAMH1_MOUSE** in **SwissProt**, SAM domain and HD domain-containing protein 1 OS=Mus musculus GN=Samhd1 PE=1 SV=2

Match to Query 5855: 3455.340303 from(1152.787377,3+) index(5588)
Title: Elution from: 48.123 to 48.123 scan no 4759 cid35.00 polarity:+:m1s



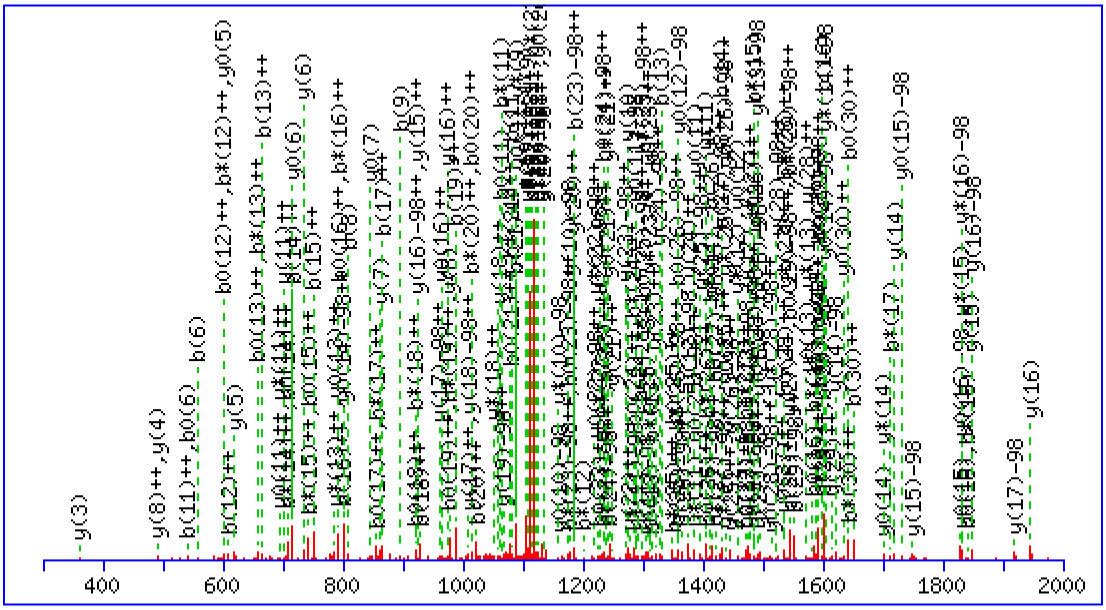
Monoisotopic mass of neutral peptide Mr(calc): 3455.3415
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0017
Matched b ions: b(7)-98, b(8), b(9)-98, b(9), b(11), b(11)-98, b(16)-196++, b(16)++, b(18)++, b(20)-98++, b(21)-98++, b(23)++, b(27)-98++, b(27)++, b(29)++
Matched y ions: y(7), y(8), y(9), y(10), y(12), y(14), y(15), y(16)++, y(19)++, y(20)++, y(23)++, y(26)++

Peptide No.100

CGSGPVHISGQHLVAVEEDAESEDEDEEDVK
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of **CGSGPVHISGQHLVAVEEDAESEDEDEEDVK**
Found in **NPM_MOUSE** in **SwissProt**, Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1

Match to Query 6710: 3445.412910 from(1149.478246,3+) index(5453)
Title: Elution from: 47.037 to 47.037 scan no 3904 cid35.00 polarity:+:m1s



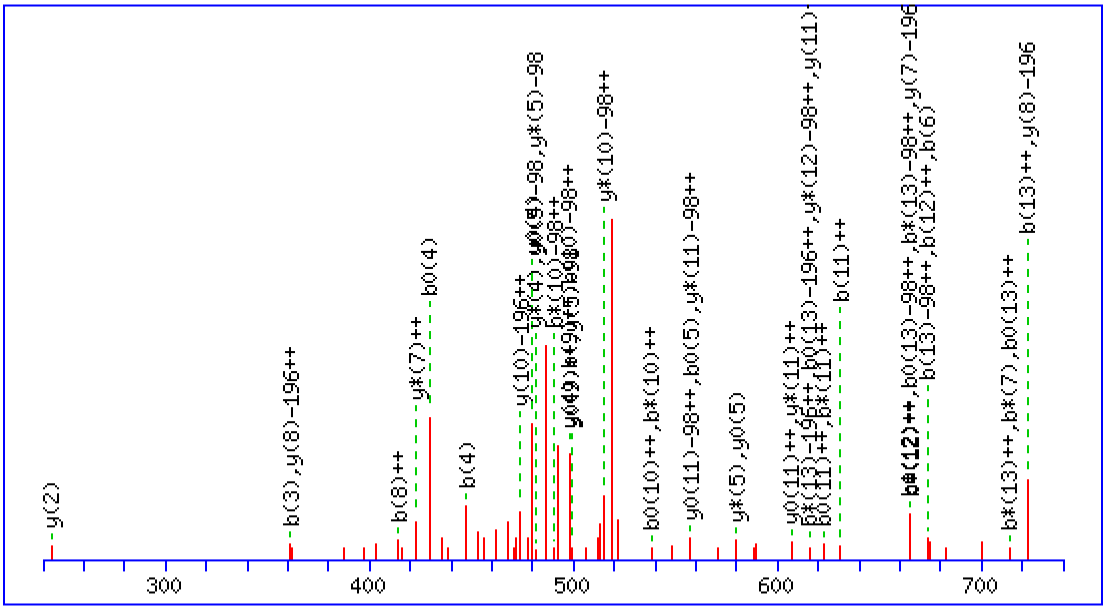
Monoisotopic mass of neutral peptide Mr(calc): 3445.4141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S22 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 6e-008
Matched b ions: b(6), b(8), b(9), b(11)++, b(11), b(12)++, b(13)++, b(13), b(14)++, b(14), b(15)++, b(16)++, b(16), b(17)++, b(18)++, b(19)++, b(20)++, b(21)++, b(22)-98++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)++, b(25)-98++, b(26)++, b(26)-98++, b(27)-98++, b(27)++, b(28)++, b(28)-98++, b(29)++, b(29)-98++, b(30)-98++, b(30)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10), y(10)-98, y(11)++, y(11)-98, y(11), y(12)-98, y(12), y(13)-98, y(13), y(14), y(14)-98, y(15)-98, y(15), y(15)++, y(16), y(16)-98, y(16)-98++, y(16)++, y(17)-98, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(24)-98++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)++, y(27)-98++, y(28)-98++, y(28)++, y(29)++

Peptide No.101

CSLSQPGPSVSSPK
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of **CSLSQPGPSVSSPK**
Found in **SYNE1_MOUSE** in **SwissProt**, Nesprin-1 OS=Mus musculus GN=Syne1 PE=1 SV=2

Match to Query 2774: 1589.623059 from(530.881629,3+) index(2203)
Title: Elution from: 39.186 to 39.186 scan no 3727 cid35.00 polarity:+



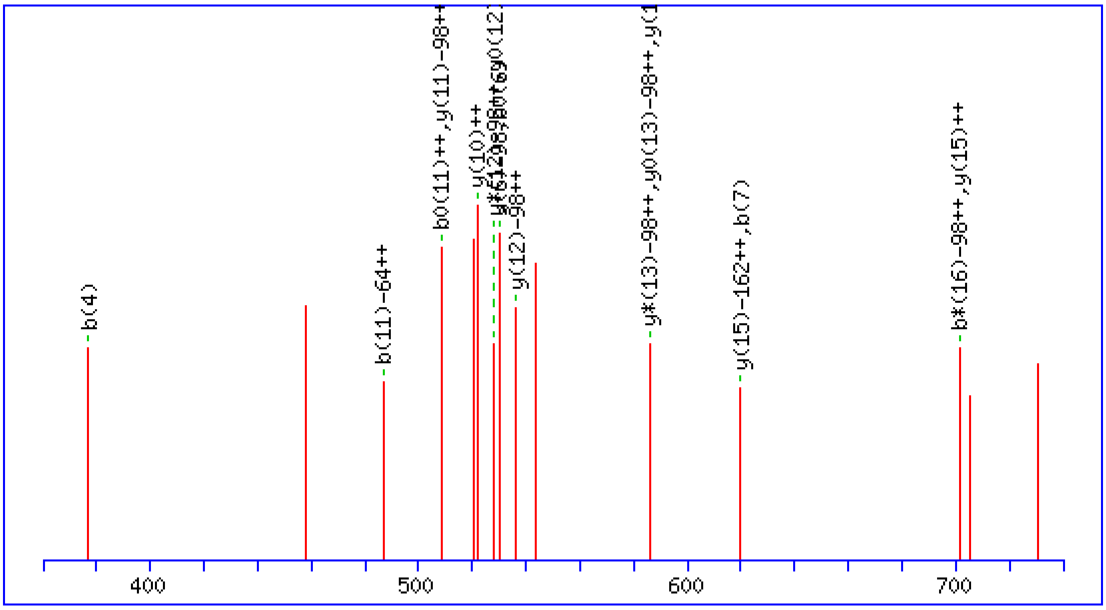
Monoisotopic mass of neutral peptide Mr(calc): 1589.6198
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0075
Matched b ions: b(3), b(4), b(6), b(8)++, b(9)++, b(10)-98++, b(11)++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(4), y(5)-98, y(7)-196, y(8)-196, y(8)-196++, y(10)-196++, y(11)++

Peptide No.102

CTGGDGAMGDPGSAGKK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **CTGGDGAMGDPGSAGKK**
Found in **CO6A6_MOUSE** in **SwissProt**, Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=1 SV=2

Match to Query 3135: 1660.625613 from(554.549147,3+) index(4888)
Title: Elution from: 36.888 to 36.888 scan no 3410 cid35.00 polarity:+:m1s



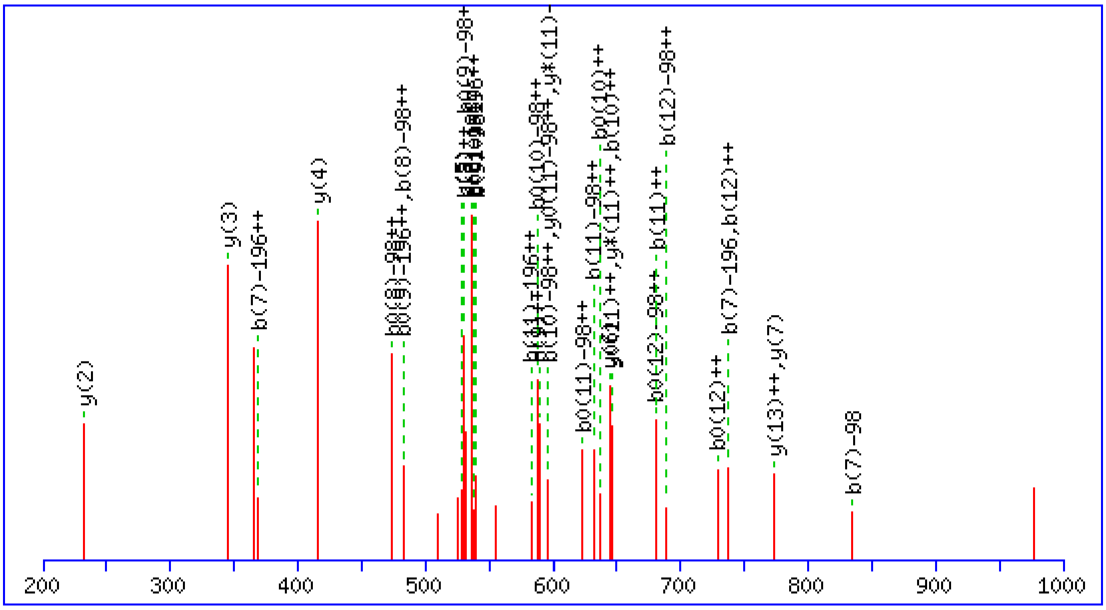
Monoisotopic mass of neutral peptide Mr(calc): 1660.6223
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.04
Matched b ions: b(4), b(7)
Matched y ions: y(6)-98, y(10)++, y(11)-98++, y(12)++, y(12)-98++, y(15)++

Peptide No.103

CTHSSSIEDLALGR
Confirmed sites:
Ambiguous sites: @T:2orS:4orS:5, @T:2orS:4orS:5

MS/MS Fragmentation of **CTHSSSIEDLALGR**
Found in **C1GLT_MOUSE** in **SwissProt**, Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1 OS=Mus musculus GN=C1galt1 PE=1 SV=1

Match to Query 3658: 1704.657942 from(569.226590,3+) index(6202)
Title: Elution from: 42.486 to 42.486 scan no 4269 cid35.00 polarity:+:m1s



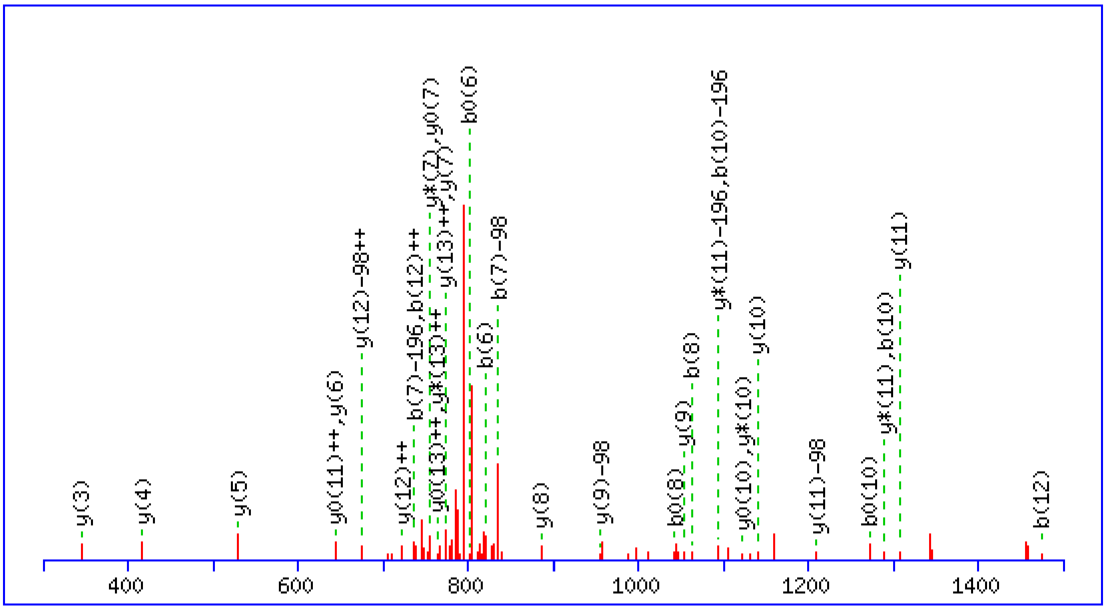
Monoisotopic mass of neutral peptide Mr(calc): 1704.6579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0026
Matched b ions: b(5)-196, b(7)-196, b(7)-98, b(7)-196++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(11)-196++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(13)++

Peptide No.104

CTHSSSIEDLALGR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **CTHSSSIEDLALGR**
Found in **C1GLT_MOUSE** in **SwissProt**, Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1 OS=Mus musculus GN=C1galt1 PE=1 SV=1

Match to Query 3819: 1704.658014 from(853.336283,2+) index(6363)
Title: Elution from: 42.529 to 42.529 scan no 4296 cid35.00 polarity:+:m1s



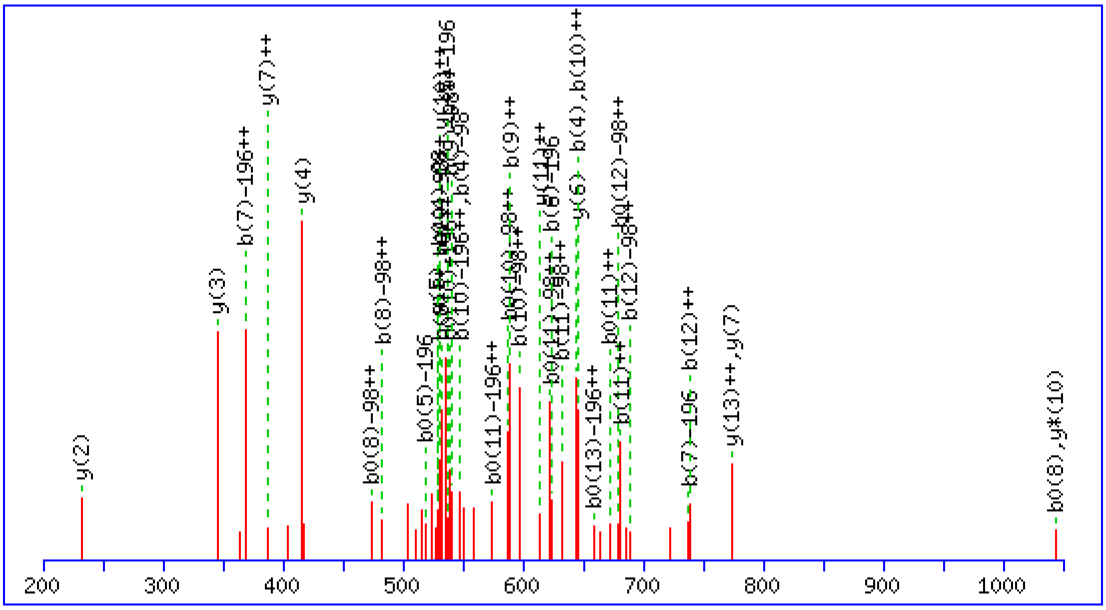
Monoisotopic mass of neutral peptide Mr(calc): 1704.6579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.001
Matched b ions: b(6), b(7)-196, b(7)-98, b(8), b(10)-196, b(10), b(12)++, b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10), y(11)-98, y(11), y(12)++, y(12)-98++, y(13)++

Peptide No.105

CTHSSSIEDLALGR
Confirmed sites: @T:2,@S:4
Ambiguous sites:

MS/MS Fragmentation of **CTHSSSIEDLALGR**
Found in **C1GLT_MOUSE** in **SwissProt**, Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase 1 OS=Mus musculus GN=C1galt1 PE=1 SV=1

Match to Query 3197: 1704.657108 from(569.226312,3+) index(2368)
Title: Elution from: 41.825 to 41.825 scan no 4030 cid35.00 polarity:+



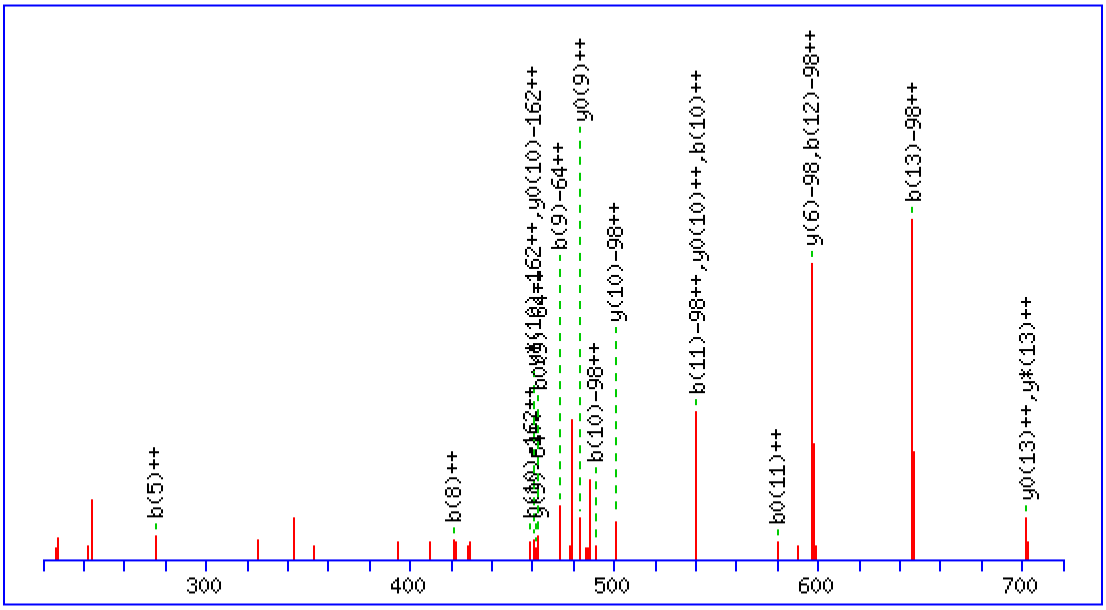
Monoisotopic mass of neutral peptide Mr(calc): 1704.6579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0014
Matched b ions: b(4), b(4)-98, b(5)-196, b(6)-196, b(7)-196++, b(7)-196, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(10)-196++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(10)++, y(11)++, y(13)++

Peptide No.106

DAIHLGMSSAPLVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **DAIHLGMSSAPLVK**
Found in **IRK15_MOUSE** in **SwissProt**, ATP-sensitive inward rectifier potassium channel 15 OS=Mus musculus GN=Kcnj15 PE=2 SV=1

Match to Query 2685: 1533.730032 from(512.250620,3+) index(277)
Title: Elution from: 20.715 to 20.715 scan no 1215 cid35.00 polarity:+



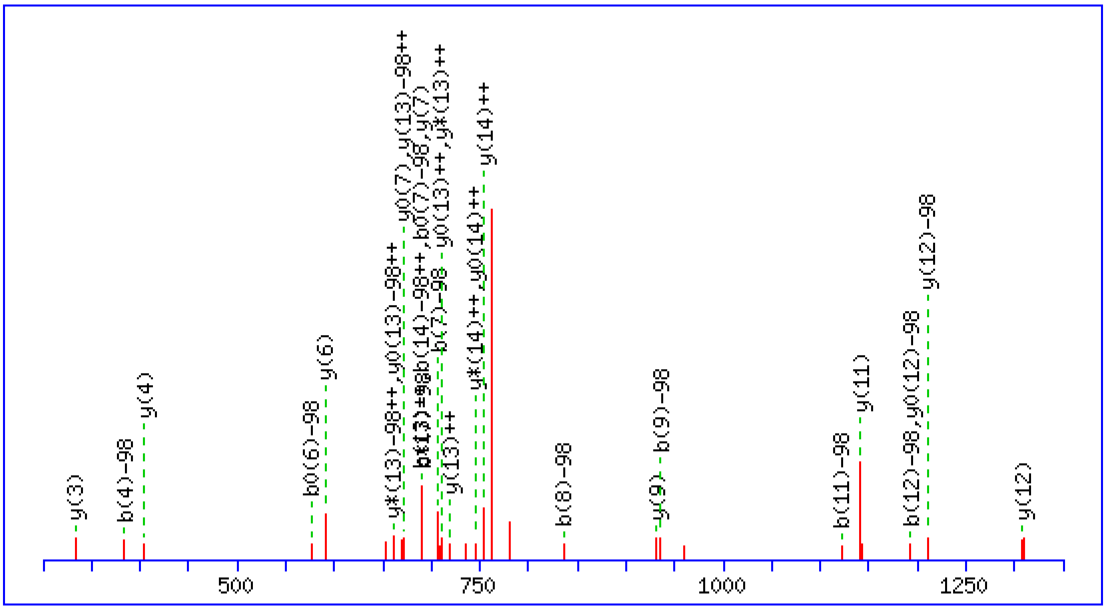
Monoisotopic mass of neutral peptide Mr(calc): 1533.7262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0097
Matched b ions: b(5)++, b(8)++, b(10)++, b(10)-98++, b(11)-98++, b(12)-98++, b(13)-98++
Matched y ions: y(6)-98, y(10)-98++

Peptide No.107

DAQSPLLEVDAASVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **DAQSPLLEVDAASVK**
Found in **F208A_MOUSE** in **SwissProt**, Protein FAM208A OS=Mus musculus GN=Fam208a PE=2 SV=2

Match to Query 3494: 1621.759476 from(811.887014,2+) index(6516)
Title: Elution from: 44.925 to 44.925 scan no 4590 cid35.00 polarity:+:m1s



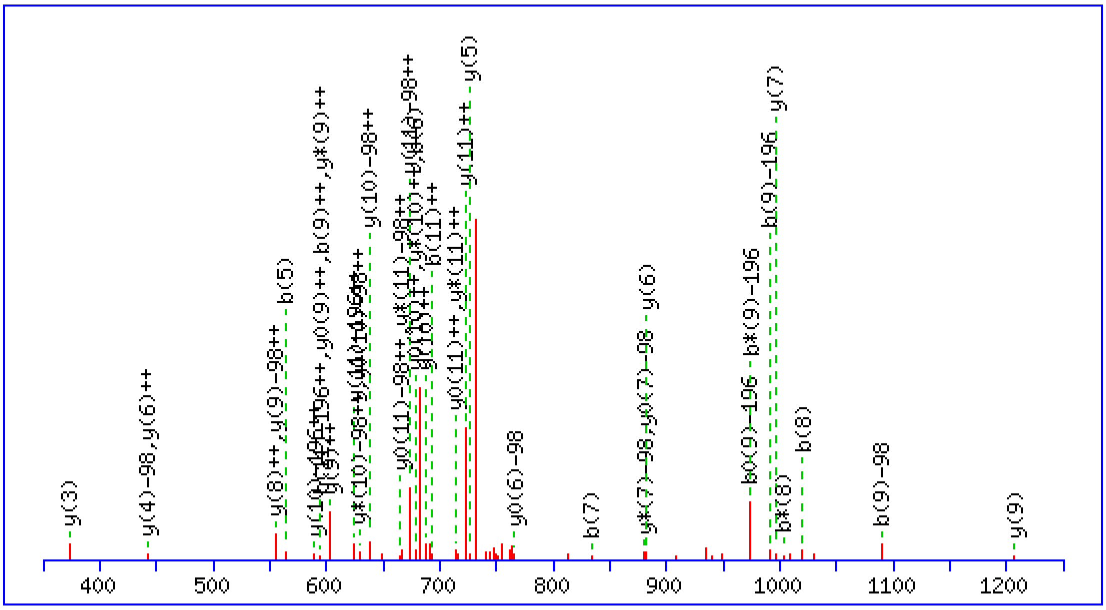
Monoisotopic mass of neutral peptide Mr(calc): 1621.7600
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 **Expect:** 2.1e-005
Matched b ions: b(4)-98, b(7)-98, b(8)-98, b(9)-98, b(11)-98, b(12)-98, b(13)++, b(14)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(9), y(11), y(12)-98, y(12), y(13)-98++, y(13)++, y(14)++

Peptide No.108

DASPINRWSPTR
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of **DASPINRWSPTR**
Found in **PRP4B_MOUSE** in **SwissProt**, Serine/threonine-protein kinase PRP4 homolog OS=Mus musculus GN=Prpf4b PE=1 SV=3

Match to Query 2806: 1558.632350 from(780.323451,2+) index(1479)
Title: Elution from: 32.396 to 32.396 scan no 2812 cid35.00 polarity:+



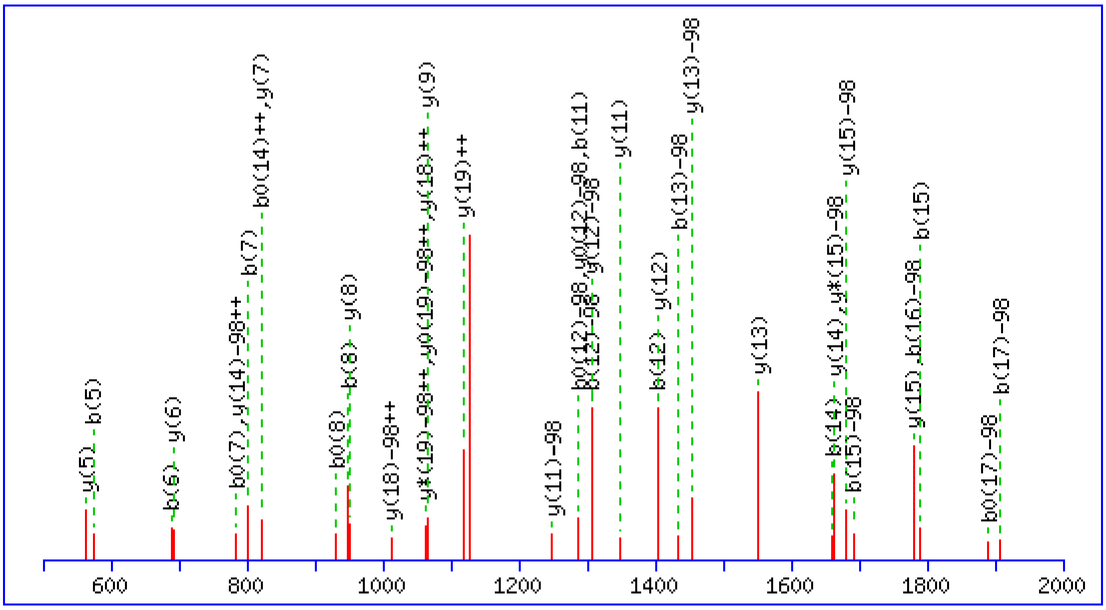
Monoisotopic mass of neutral peptide Mr(calc): 1558.6330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 18 **Expect:** 0.048
Matched b ions: b(5), b(6), b(7), b(8), b(9)-196, b(9)-98, b(9)++, b(11)-196++, b(11)++
Matched y ions: y(3), y(4)-98, y(5), y(6)++, y(6), y(7), y(8)++, y(9)-98++, y(9)++, y(9), y(10)-98++, y(10)++, y(10)-196++, y(11)-196++, y(11)++, y(11)-98++

Peptide No.109

DDDDIDLFGSDDEEESEEAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DDDDIDLFGSDDEEESEEAK**
Found in **EF1B_MOUSE** in **SwissProt**, Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5

Match to Query 5913: 2351.826776 from(1176.920664,2+) index(6736)
Title: Elution from: 53.425 to 53.425 scan no 5507 cid35.00 polarity:+:m1s



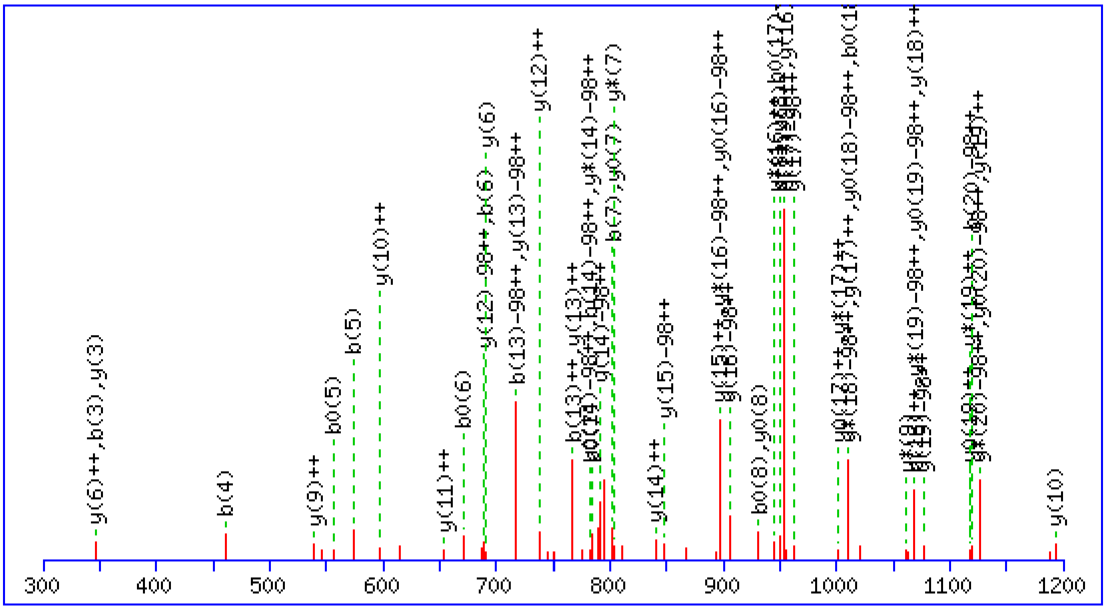
Monoisotopic mass of neutral peptide Mr(calc): 2351.8326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 **Expect:** 3.2e-008
Matched b ions: b(5), b(6), b(7), b(8), b(11), b(12)-98, b(12), b(13)-98, b(14), b(15), b(15)-98, b(16)-98, b(17)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98++, y(15), y(15)-98, y(18)++, y(18)-98++, y(19)++

Peptide No.110

DDDDIDLFGSDDEEESEEAKK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DDDDIDLFGSDDEEESEEAKK**
Found in **EF1B_MOUSE** in **SwissProt**, Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5

Match to Query 6339: 2479.924764 from(827.648864,3+) index(6579)
Title: Elution from: 45.666 to 45.666 scan no 4686 cid35.00 polarity:+:m1s



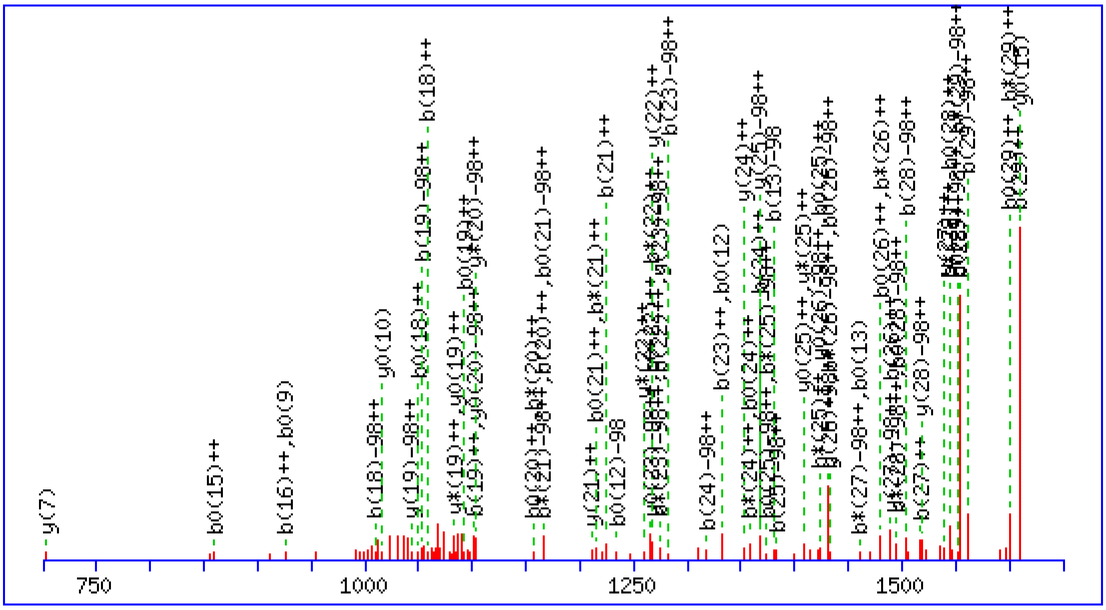
Monoisotopic mass of neutral peptide Mr(calc): 2479.9275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 **Expect:** 4.3e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(13)-98++, b(13)++, b(14)-98++, b(17)-98++, b(18)++, b(20)-98++
Matched y ions: y(3), y(6)++, y(6), y(8), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++

Peptide No.111

DDGDEEGLLTHSEEELEHSQDTDAEDGALQ
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **DDGDEEGLLTHSEEELEHSQDTDAEDGALQ**
Found in **RALY_MOUSE** in **SwissProt**, RNA-binding protein Raly OS=Mus musculus GN=Raly PE=1 SV=3

Match to Query 6000: 3363.296304 from(1122.106044,3+) index(5690)
Title: Elution from: 45.648 to 45.648 scan no 4459 cid35.00 polarity:+:m1s



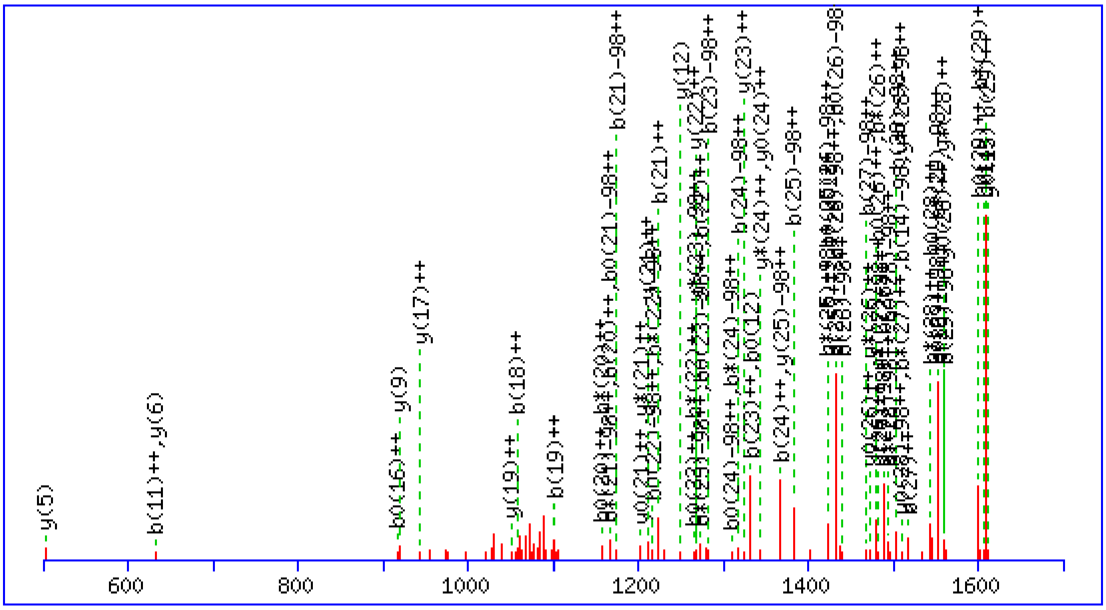
Monoisotopic mass of neutral peptide Mr(calc): 3363.3060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0012
Matched b ions: b(13)-98, b(16)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(21)++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(25)-98++, b(26)++, b(27)++, b(28)++, b(28)-98++, b(29)++, b(29)-98++
Matched y ions: y(7), y(19)-98++, y(21)++, y(22)++, y(23)-98++, y(24)++, y(25)-98++, y(26)-98++, y(27)-98++, y(27)++, y(28)-98++

Peptide No.112

DDGDEEGLLTHSEEELEHSQDTDAEDGALQ
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **DDGDEEGLLTHSEEELEHSQDTDAEDGALQ**
Found in **RALY_MOUSE** in **SwissProt**, RNA-binding protein Raly OS=Mus musculus GN=Raly PE=1 SV=3

Match to Query 7109: 3363.297945 from(1122.106591,3+) index(6578)
Title: Elution from: 45.658 to 45.658 scan no 4685 cid35.00 polarity:+:m1s



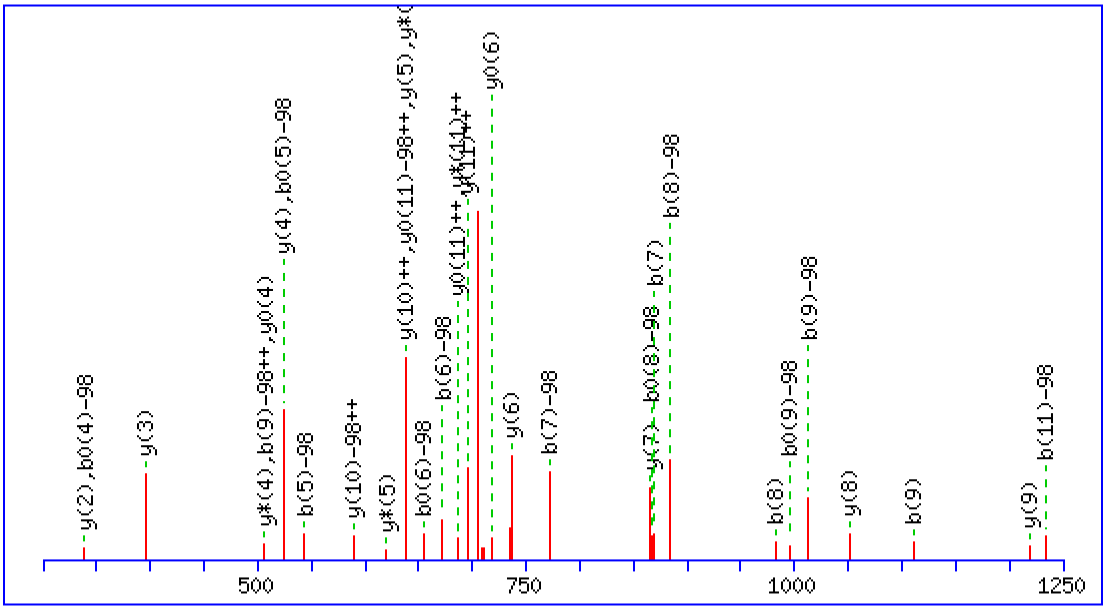
Monoisotopic mass of neutral peptide Mr(calc): 3363.3060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 3.6e-006
Matched b ions: b(11)++, b(14), b(14)-98, b(18)++, b(19)++, b(20)++, b(21)++, b(21)-98++, b(22)++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(25)-98++, b(26)++, b(26)-98++, b(27)++, b(27)-98++, b(28)++, b(28)-98++, b(29)++, b(29)-98++
Matched y ions: y(5), y(6), y(9), y(12), y(17)++, y(19)++, y(21)++, y(22)++, y(23)++, y(25)-98++, y(26)++, y(27)-98++

Peptide No.113

DDGSWEVIEGYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **DDGSWEVIEGYR**
Found in **DHE3_MOUSE** in **SwissProt**, Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1

Match to Query 2595: 1504.586828 from(753.300690,2+) index(2678)
Title: Elution from: 50.245 to 50.245 scan no 4979 cid35.00 polarity:+



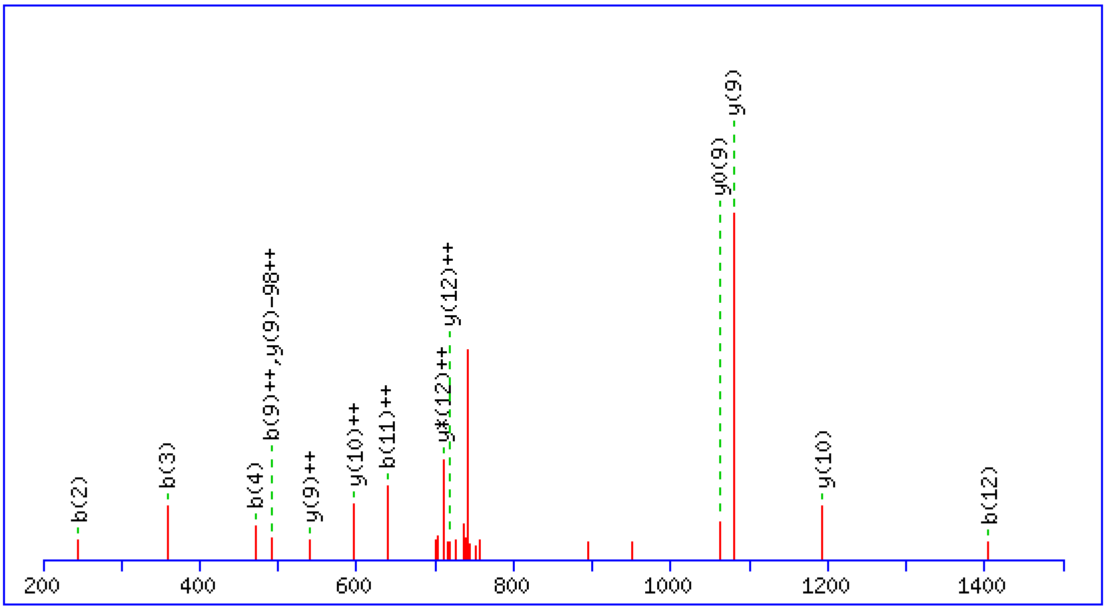
Monoisotopic mass of neutral peptide Mr(calc): 1504.5871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 5.4e-007
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10)-98++, y(11)++

Peptide No.114

DEILPTTPISEQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DEILPTTPISEQK**
Found in **RS3_MOUSE** in **SwissProt**, 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1

Match to Query 3220: 1549.726718 from(775.870635,2+) index(2473)
Title: Elution from: 39.374 to 39.374 scan no 3884 cid35.00 polarity:+



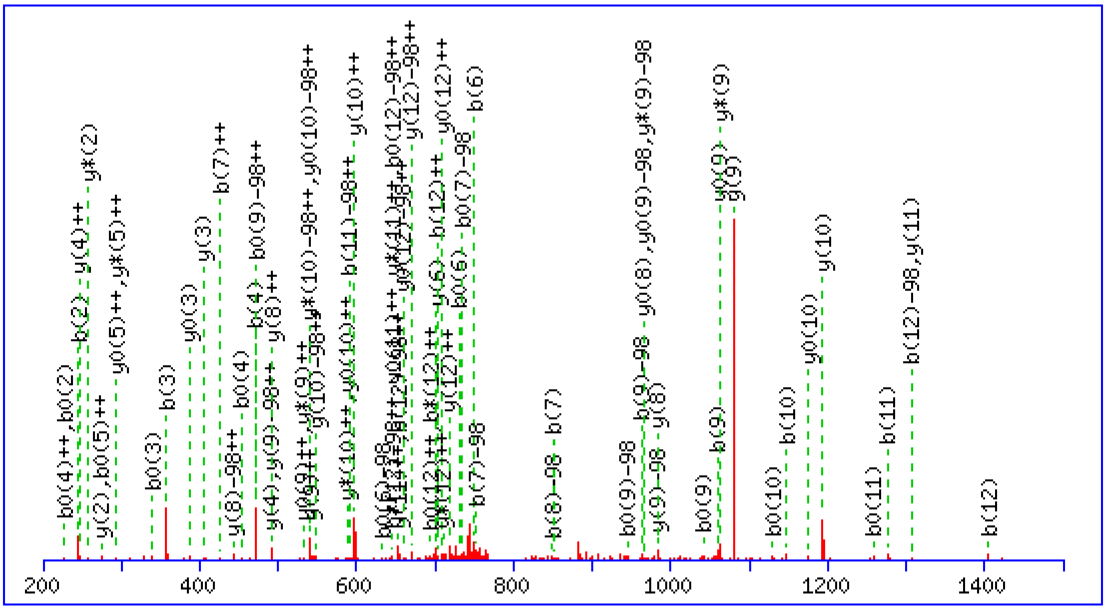
Monoisotopic mass of neutral peptide Mr(calc): 1549.7276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.012
Matched b ions: b(2), b(3), b(4), b(9)++, b(11)++, b(12)
Matched y ions: y(9), y(9)-98++, y(9)++, y(10), y(10)++, y(12)++

Peptide No.115

DEILPTTPISEQK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **DEILPTTPISEQK**
Found in **RS3_MOUSE** in **SwissProt**, 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1

Match to Query 3711: 1549.727588 from(775.871070,2+) index(5447)
Title: Elution from: 46.925 to 46.925 scan no 3893 cid35.00 polarity:+:m1s



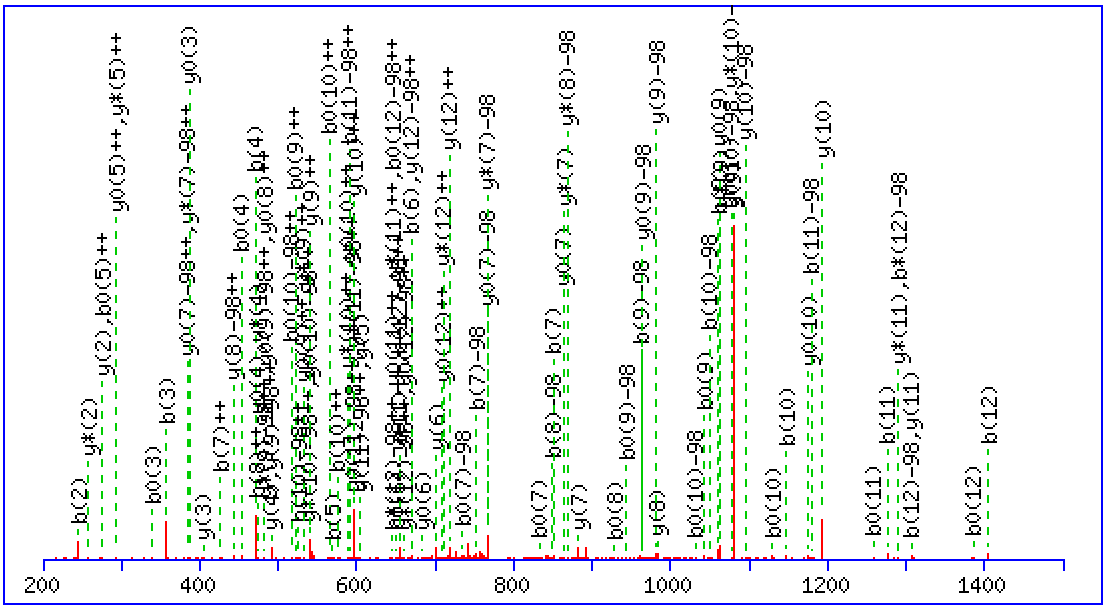
Monoisotopic mass of neutral peptide Mr(calc): 1549.7276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 6.2e-005
Matched b ions: b(2), b(3), b(4), b(6), b(7)++, b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10), b(11), b(11)-98++, b(12), b(12)-98++, b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(6), y(8), y(8)-98++, y(8)++, y(9), y(9)-98++, y(9)++, y(9)-98, y(10)++, y(10), y(10)-98++, y(11)++, y(11), y(12)++, y(12)-98++

Peptide No.116

DEILPTTPISEQK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **DEILPTTPISEQK**
Found in **RS3_MOUSE** in **SwissProt**, 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1

Match to Query 3710: 1549.727434 from(775.870993,2+) index(2053)
Title: Elution from: 47.265 to 47.265 scan no 3928 cid35.00 polarity:+



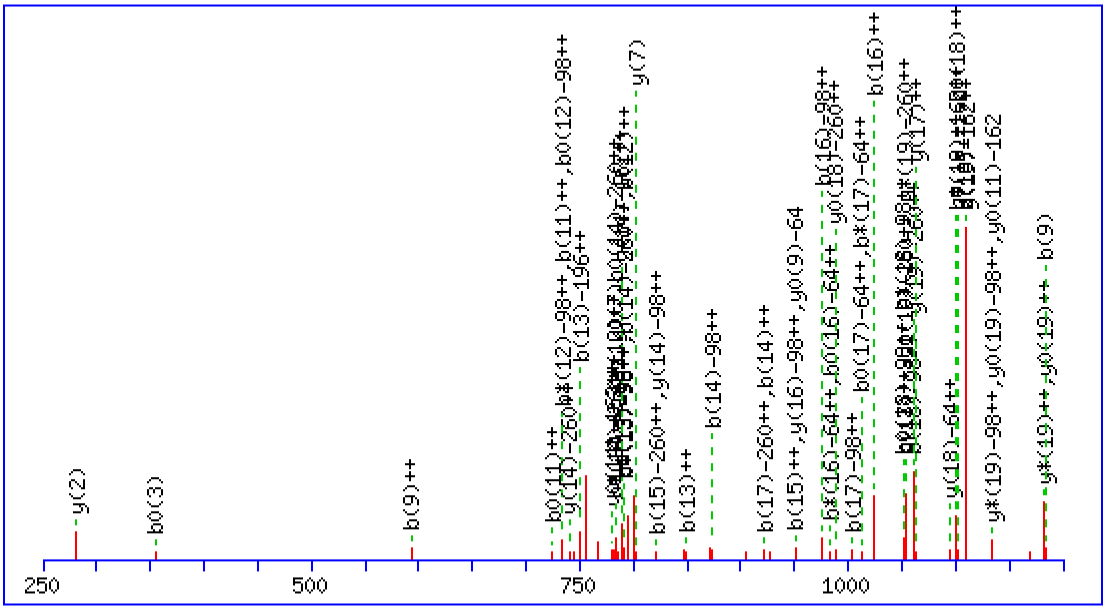
Monoisotopic mass of neutral peptide Mr(calc): 1549.7276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 7.3e-007
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)++, b(7), b(7)-98, b(8)++, b(8)-98, b(9)-98, b(9), b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12), b(12)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98++, y(9)-98, y(9), y(9)-98++, y(9)++, y(10)++, y(10), y(10)-98, y(11)++, y(11), y(11)-98++, y(12)++, y(12)-98++

Peptide No.117

DEKKEESEESDDDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **DEKKEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6363: 2496.842937 from(833.288255,3+) index(7038)
Title: Elution from: 57.042 to 57.042 scan no 5896 cid35.00 polarity:+:m1s



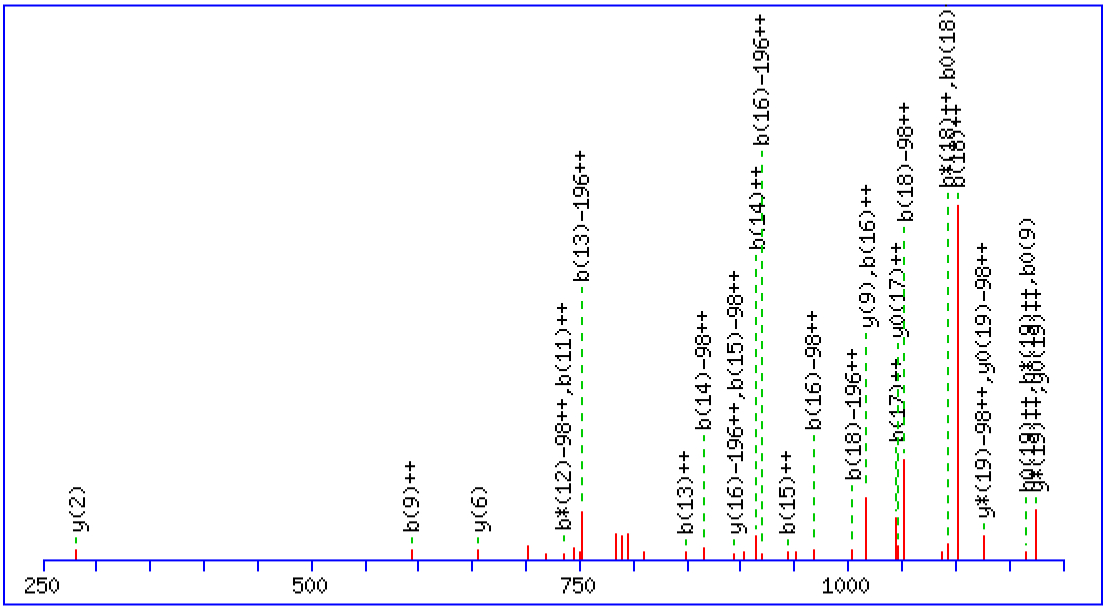
Monoisotopic mass of neutral peptide Mr(calc): 2496.8441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 35 **Expect:** 0.00038
Matched b ions: b(9)++, b(9), b(11)++, b(12)++, b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(7), y(14)-98++, y(16)-98++, y(17)++

Peptide No.118

DEKKEESEESDDDMGFGLFD
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **DEKKEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 6340: 2480.847831 from(827.956553,3+) index(7176)
Title: Elution from: 65.102 to 65.102 scan no 6514 cid35.00 polarity:+:m1s



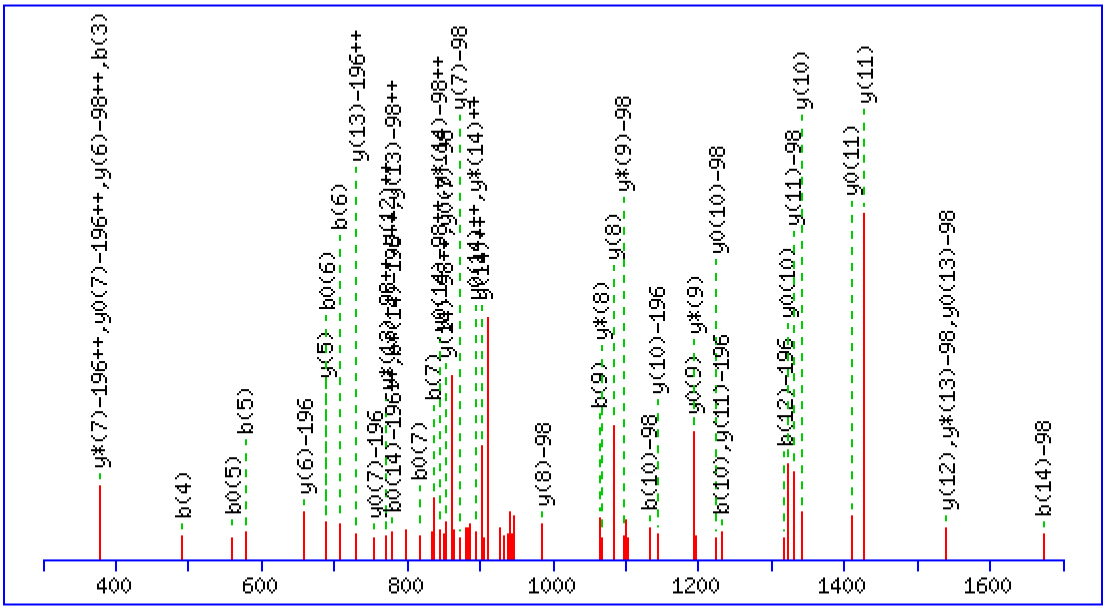
Monoisotopic mass of neutral peptide Mr(calc): 2480.8492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0004
Matched b ions: b(9)++, b(11)++, b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(16)-196++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++
Matched y ions: y(2), y(6), y(9), y(16)-196++

Peptide No.119

DFDISEQNDSSDEEK
Confirmed sites: @S:10,@S:11
Ambiguous sites:

MS/MS Fragmentation of **DFDISEQNDSSDEEK**
Found in **DNJC1_MOUSE** in **SwissProt**, DnaJ homolog subfamily C member 1 OS=Mus musculus GN=Dnajc1 PE=1 SV=1

Match to Query 4522: 1916.619536 from(959.317044,2+) index(2454)
Title: Elution from: 39.677 to 39.677 scan no 3898 cid35.00 polarity:+



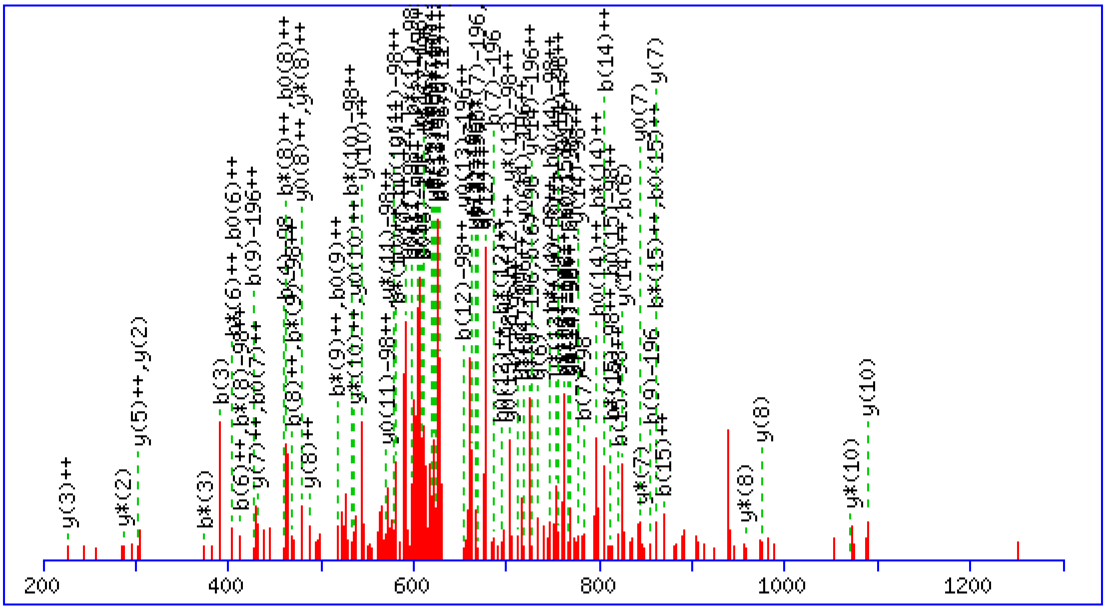
Monoisotopic mass of neutral peptide Mr(calc): 1916.6238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 5.4e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(9), b(10)-98, b(10), b(12)-196, b(14)-98
Matched y ions: y(5), y(6)-98++, y(6)-196, y(7)-98, y(8), y(8)-98, y(10), y(10)-196, y(11), y(11)-98, y(11)-196, y(12), y(12)++, y(13)-196++, y(13)-98++, y(14)++, y(14)-98++

Peptide No.120

DFKSVSGGIQEPGFQR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **DFKSVSGGIQEPGFQR**
Found in **IGFN1_MOUSE** in **SwissProt**, Immunoglobulin-like and fibronectin type III domain-containing protein 1 OS=Mus musculus GN=Igfn1 PE=1 SV=3

Match to Query 4175: 1910.793783 from(637.938537,3+) index(4310)
Title: Elution from: 40.326 to 40.326 scan no 3019 cid35.00 polarity:+:m1s



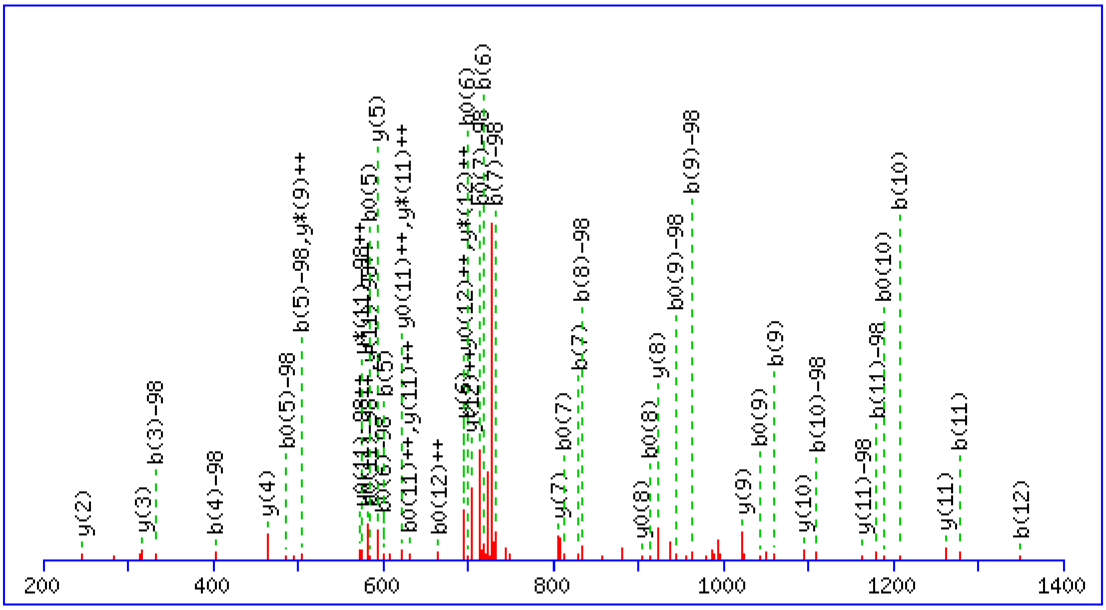
Monoisotopic mass of neutral peptide Mr(calc): 1910.7965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0046
Matched b ions: b(3), b(4)-98, b(6)++, b(6)-196, b(6), b(6)-98, b(7)-196, b(7)-98, b(8)++, b(9)-196++, b(9)-196, b(10)++, b(11)-98++, b(12)-196++, b(12)++, b(12)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3)++, y(5), y(5)++, y(6), y(7)++, y(7), y(8), y(8)++, y(10), y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-196++, y(13)-98++, y(14)++, y(14)-196++, y(14)-98++

Peptide No.121

DFSATDLTEFAAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DFSATDLTEFAAR**
Found in **THIM_MOUSE** in **SwissProt**, 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=3

Match to Query 3077: 1522.633520 from(762.324036,2+) index(3391)
Title: Elution from: 57.301 to 57.301 scan no 5914 cid35.00 polarity:+



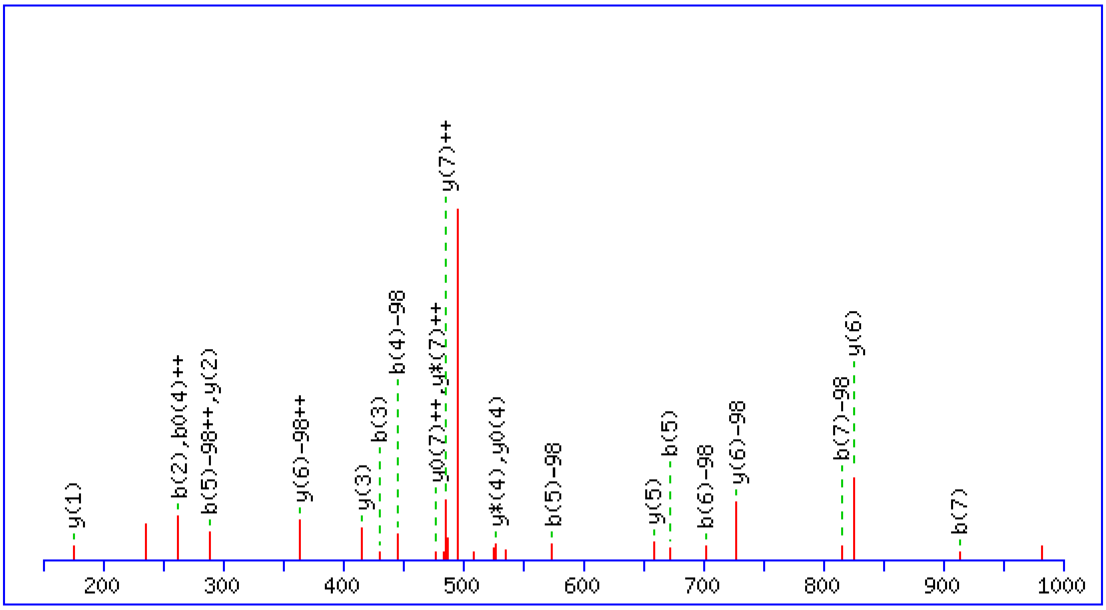
Monoisotopic mass of neutral peptide Mr(calc): 1522.6341
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 6.4e-007
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11), y(11)-98, y(11)++, y(12)++

Peptide No.122

DFSLEQLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DFSLEQLR**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 1073: 1086.474570 from(544.244561,2+) index(2989)
Title: Elution from: 47.744 to 47.744 scan no 4893 cid35.00 polarity:+



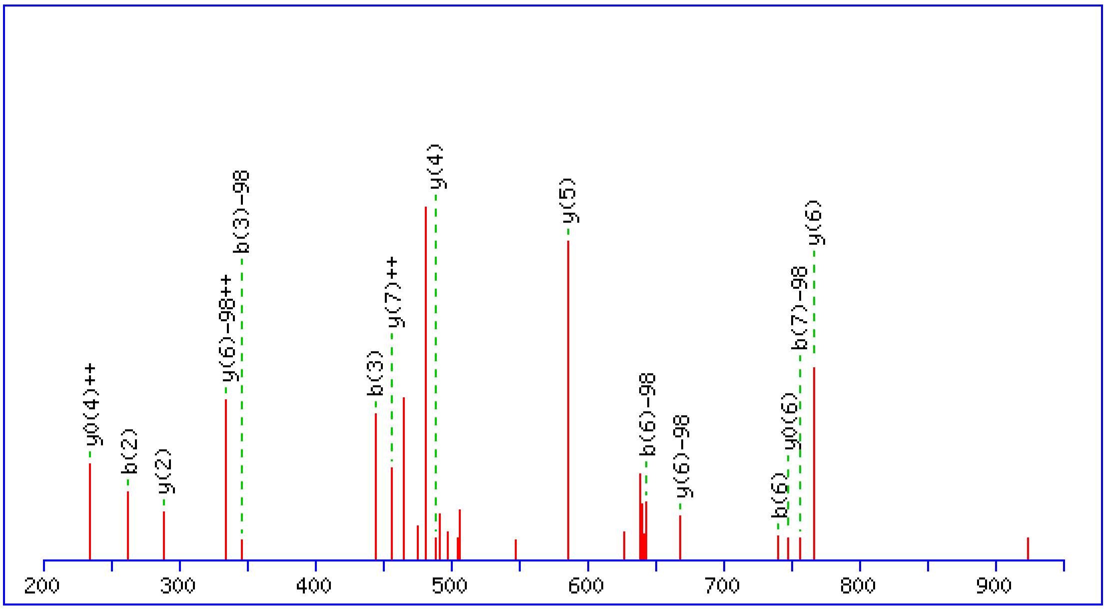
Monoisotopic mass of neutral peptide Mr(calc): 1086.4747
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 0.00012
Matched b ions: b(2), b(3), b(4)-98, b(5)-98++, b(5), b(5)-98, b(6)-98, b(7), b(7)-98
Matched y ions: y(1), y(2), y(3), y(5), y(6)-98++, y(6)-98, y(6), y(7)++

Peptide No.123

DFTPAELR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **DFTPAELR**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 995: 1027.437720 from(514.726136,2+) index(2348)
Title: Elution from: 38.051 to 38.051 scan no 3710 cid35.00 polarity:+



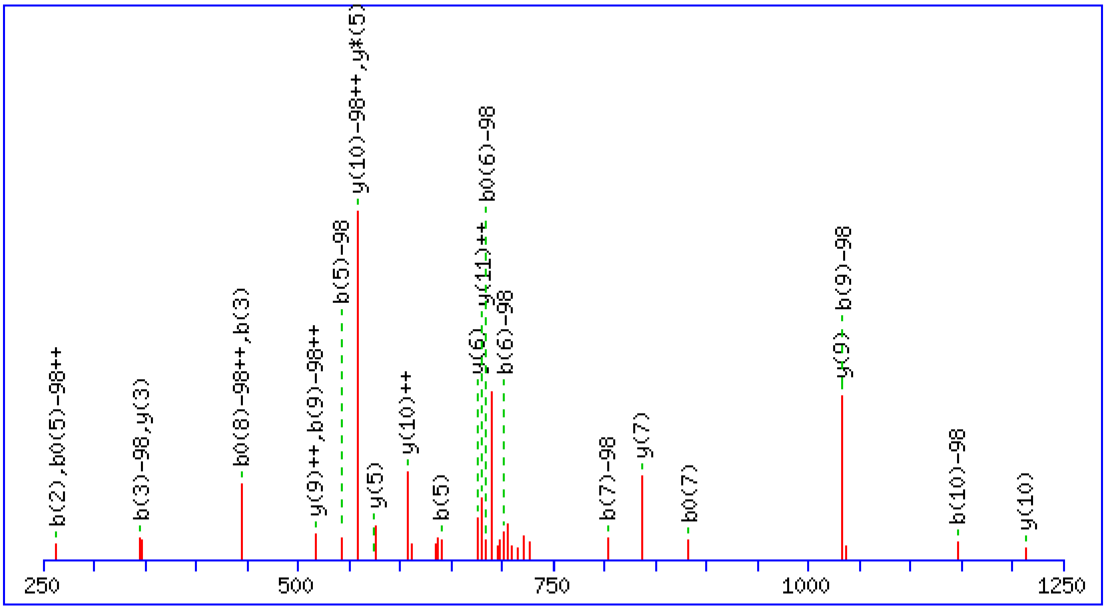
Monoisotopic mass of neutral peptide Mr(calc): 1027.4376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.016
Matched b ions: b(2), b(3)-98, b(3), b(6)-98, b(6), b(7)-98
Matched y ions: y(2), y(4), y(5), y(6)-98++, y(6), y(6)-98, y(7)++

Peptide No.124

DFTPVCTTELGR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **DFTPVCTTELGR**
Found in **PRDX6_MOUSE** in **SwissProt**, Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3

Match to Query 2715: 1474.615738 from(738.315145,2+) index(6141)
Title: Elution from: 41.823 to 41.823 scan no 4180 cid35.00 polarity:+:m1s



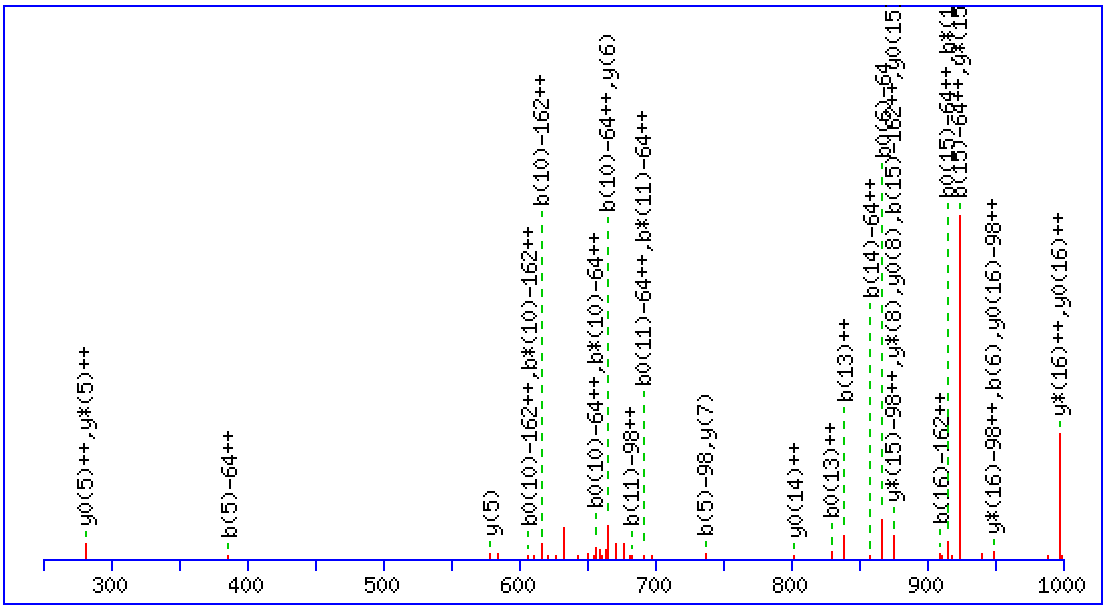
Monoisotopic mass of neutral peptide Mr(calc): 1474.6164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 6.1e-005
Matched b ions: b(2), b(3)-98, b(3), b(5)-98, b(5), b(6)-98, b(7)-98, b(9)-98++, b(9)-98, b(10)-98
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(9)++, y(10)-98++, y(10)++, y(10), y(11)++

Peptide No.125

DFYMTDSISRASQTMAK
Confirmed sites: @Y:3,@T:5
Ambiguous sites:

MS/MS Fragmentation of **DFYMTDSISRASQTMAK**
Found in **NDUS1_MOUSE** in **SwissProt**, NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=2

Match to Query 4537: 2126.809422 from(709.943750,3+) index(2693)
Title: Elution from: 47.765 to 47.765 scan no 4678 cid35.00 polarity:+



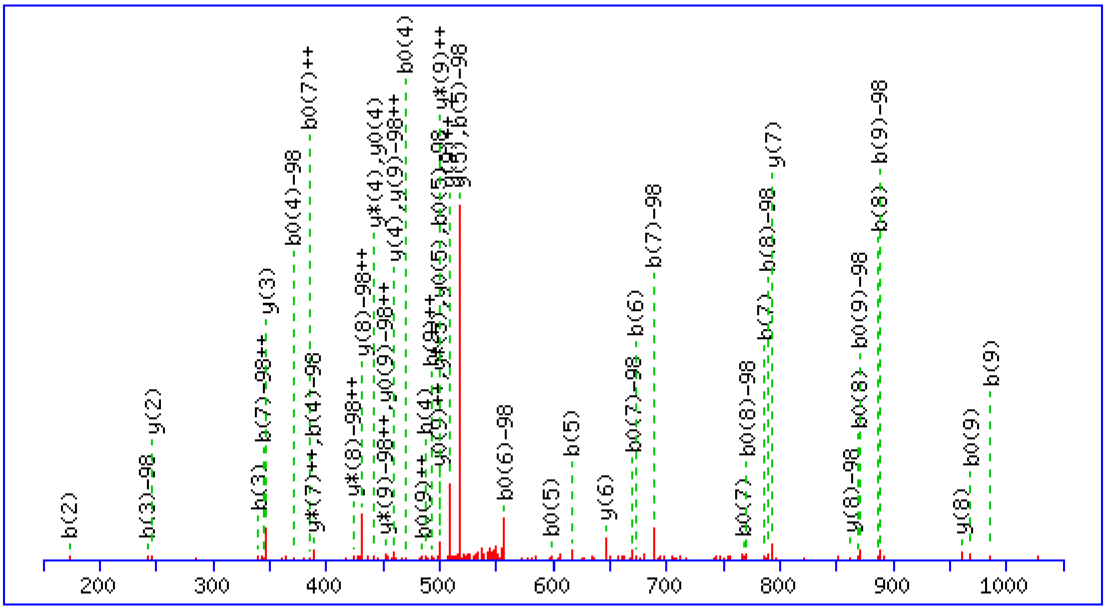
Monoisotopic mass of neutral peptide Mr(calc): 2126.8091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y3 : Phospho (Y)
M4 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.028
Matched b ions: b(5)-98, b(6), b(11)-98++, b(13)++
Matched y ions: y(5), y(6), y(7)

Peptide No.126

DGSFEGLTVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DGSFEGLTVK**
Found in **TTC7A_MOUSE** in **SwissProt**, Tetratricopeptide repeat protein 7A OS=Mus musculus GN=Ttc7a PE=1 SV=1

Match to Query 1829: 1131.484586 from(566.749569,2+) index(2117)
Title: Elution from: 48.502 to 48.502 scan no 4049 cid35.00 polarity:+



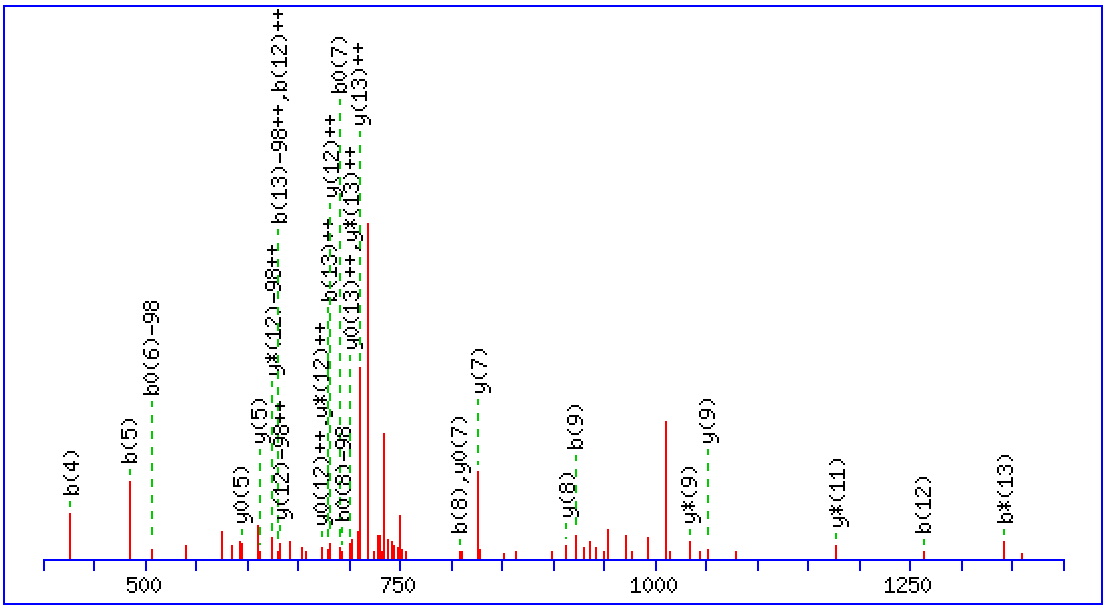
Monoisotopic mass of neutral peptide Mr(calc): 1131.4849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 4.6e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(7)-98, b(7), b(7)-98++, b(8)-98, b(8), b(9)-98, b(9), b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(8)-98, y(9)++, y(9)-98++

Peptide No.127

DGSSGHSTLPRSPR
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of **DGSSGHSTLPRSPR**
Found in **TENC1_MOUSE** in **SwissProt**, Tensin-like C1 domain-containing phosphatase OS=Mus musculus GN=Tenc1 PE=1 SV=1

Match to Query 3106: 1532.677728 from(767.346140,2+) index(4942)
Title: Elution from: 27.303 to 27.303 scan no 2268 cid35.00 polarity:+:m1s



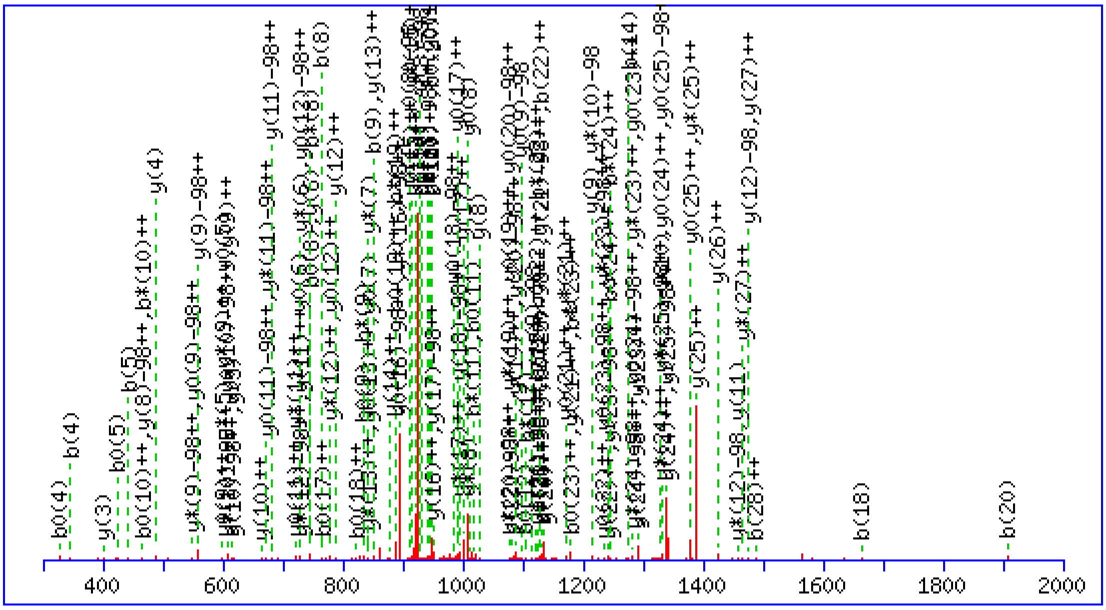
Monoisotopic mass of neutral peptide Mr(calc): 1532.6733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.042
Matched b ions: b(4), b(5), b(8), b(9), b(12), b(12)++, b(13)-98++, b(13)++
Matched y ions: y(5), y(7), y(8), y(9), y(12)-98++, y(12)++, y(13)++

Peptide No.128

DGTAPPPQSPSSPGSGQDEDWSDEESPRK
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of **DGTAPPPQSPSSPGSGQDEDWSDEESPRK**
Found in **PACN3_MOUSE** in **SwissProt**, Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1

Match to Query 6781: 3119.254122 from(1040.758650,3+) index(5028)
Title: Elution from: 29.940 to 29.940 scan no 2592 cid35.00 polarity:+:m1s



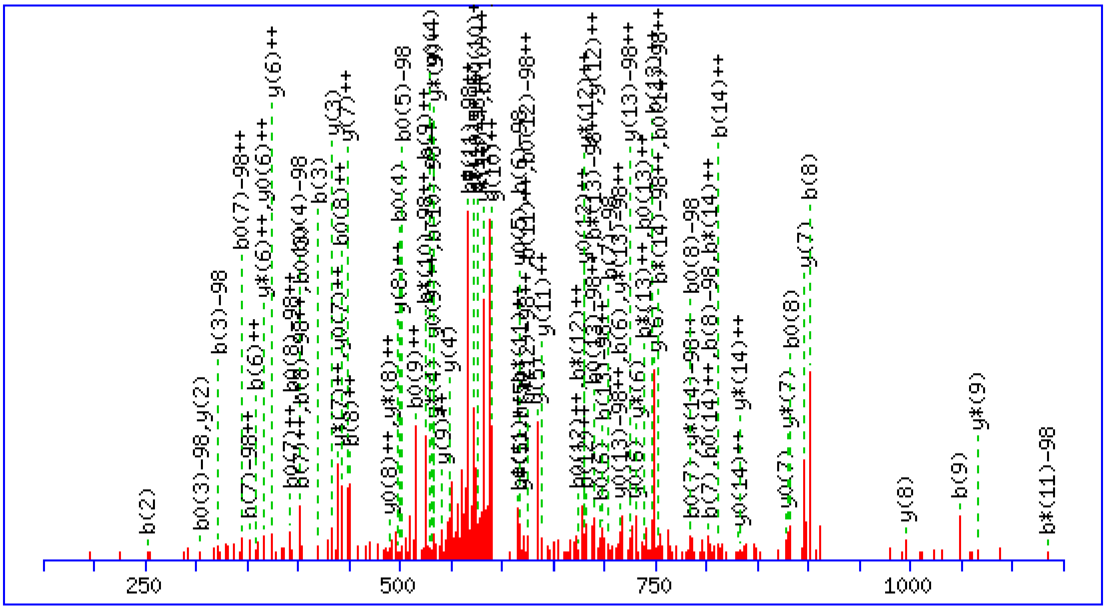
Monoisotopic mass of neutral peptide Mr(calc): 3119.2629
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 **Expect:** 2.5e-008
Matched b ions: b(4), b(5), b(8), b(9), b(10), b(12), b(14), b(18), b(20), b(22)++, b(22)-98++, b(28)++
Matched y ions: y(3), y(4), y(5), y(6), y(8)-98++, y(8), y(8)-98, y(9)-98++, y(9)++, y(9)-98, y(9), y(10)-98++, y(10)++, y(10), y(11)-98++, y(11)++, y(11), y(12)-98, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++, y(24)-98++, y(24)++, y(25)++, y(25)-98++, y(26)++, y(27)++

Peptide No.129

DHSPTPSVFNSDEER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DHSPTPSVFNSDEER**
Found in **FIP1_MOUSE** in **SwissProt**, Pre-mRNA 3'-end-processing factor FIP1 OS=Mus musculus GN=Fip1l1 PE=1 SV=1

Match to Query 4513: 1795.705800 from(599.575876,3+) index(1357)
Title: Elution from: 37.515 to 37.515 scan no 2828 cid35.00 polarity:+



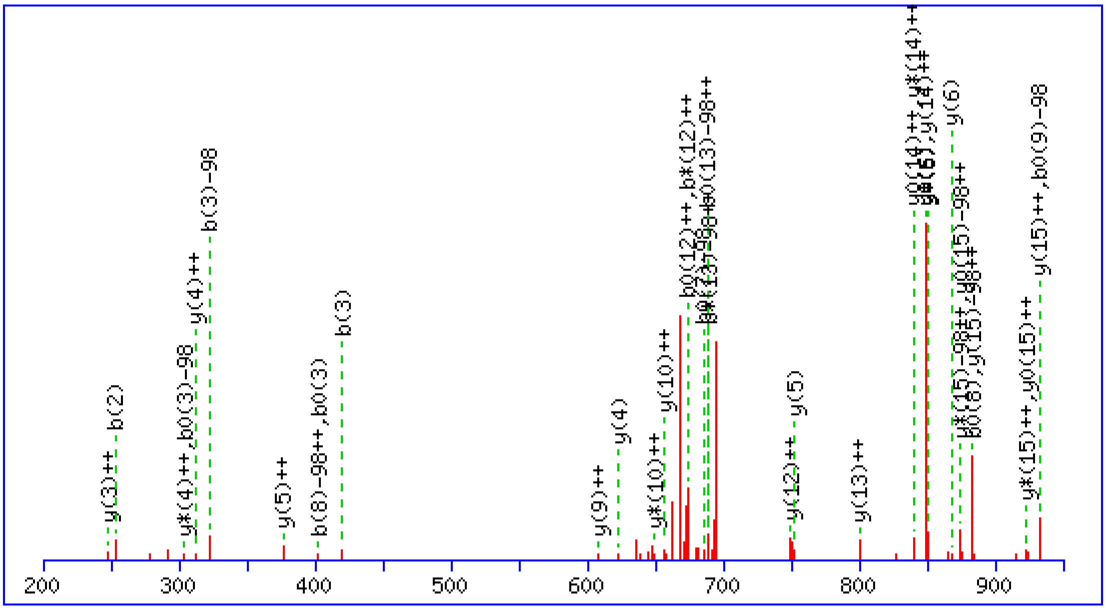
Monoisotopic mass of neutral peptide Mr(calc): 1795.7050
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.002
Matched b ions: b(2), b(3)-98, b(3), b(5), b(6), b(6)++, b(6)-98, b(7), b(7)-98++, b(7)++, b(7)-98, b(8), b(8)++, b(8)-98, b(8)-98++, b(9), b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)-98++

Peptide No.130

DHSPTPSVFNSDEERYR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DHSPTPSVFNSDEERYR**
Found in **FIP1_MOUSE** in **SwissProt**, Pre-mRNA 3'-end-processing factor FIP1 OS=Mus musculus GN=Fip1l1 PE=1 SV=1

Match to Query 5252: 2114.865699 from(705.962509,3+) index(5179)
Title: Elution from: 31.538 to 31.538 scan no 2807 cid35.00 polarity:+:m1s



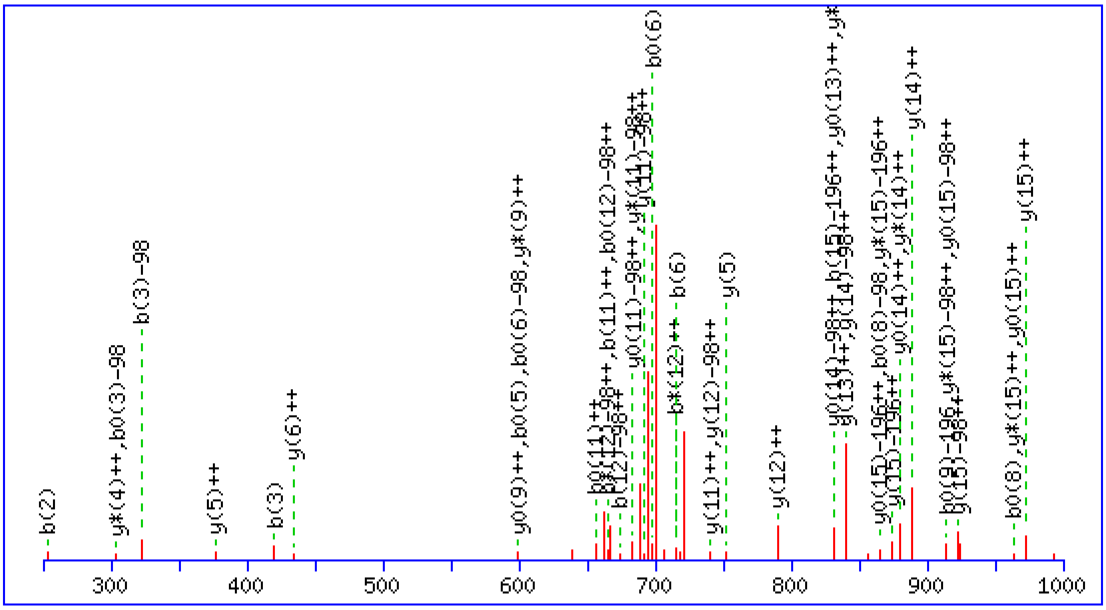
Monoisotopic mass of neutral peptide Mr(calc): 2114.8695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0017
Matched b ions: b(2), b(3)-98, b(3), b(8)-98++, b(15)-98++
Matched y ions: y(3)++, y(4), y(4)++, y(5)++, y(5), y(6), y(9)++, y(10)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++

Peptide No.131

DHSPTPSVFNSDEERYR
Confirmed sites: @S:3
Ambiguous sites: @S:7orS:11

MS/MS Fragmentation of **DHSPTPSVFNSDEERYR**
Found in **FIP1_MOUSE** in **SwissProt**, Pre-mRNA 3'-end-processing factor FIP1 OS=Mus musculus GN=Fip1l1 PE=1 SV=1

Match to Query 5596: 2194.834662 from(732.618830,3+) index(2032)
Title: Elution from: 35.155 to 35.155 scan no 3296 cid35.00 polarity:+



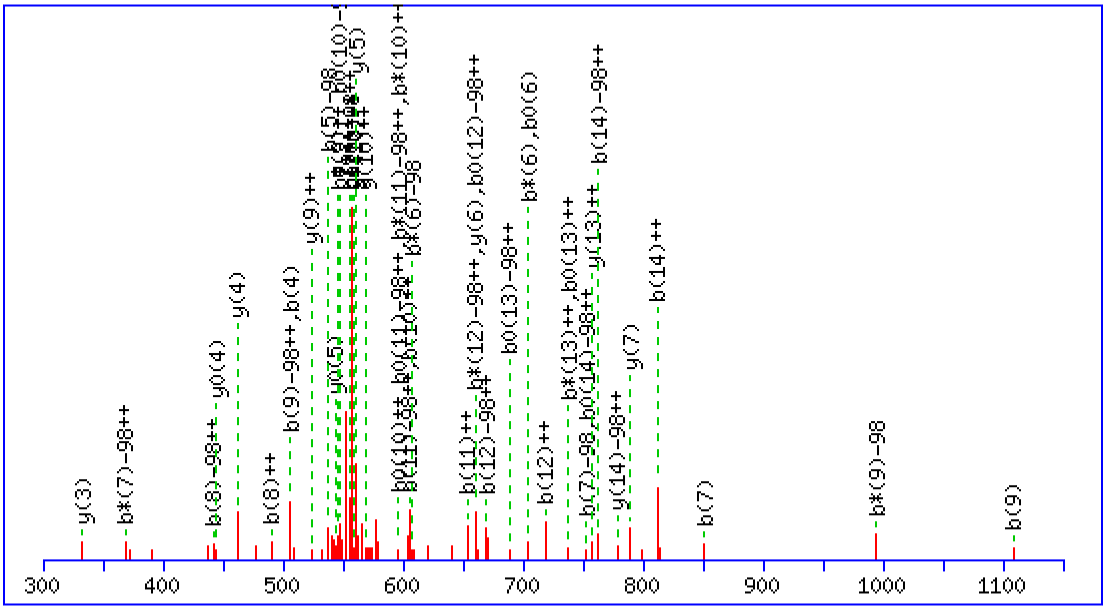
Monoisotopic mass of neutral peptide Mr(calc): 2194.8358
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.019
Matched b ions: b(2), b(3)-98, b(3), b(6), b(11)++, b(12)-98++, b(15)-196++
Matched y ions: y(5)++, y(5), y(6)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(15)-196++

Peptide No.132

DHSSQSEEEVVEGEK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of **DHSSQSEEEVVEGEK**
Found in **BNI3L_MOUSE** in **SwissProt**, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like OS=Mus musculus GN=Bnip3l PE=1 SV=1

Match to Query 3446: 1767.685227 from(590.235685,3+) index(637)
Title: Elution from: 22.495 to 22.495 scan no 1553 cid35.00 polarity:+



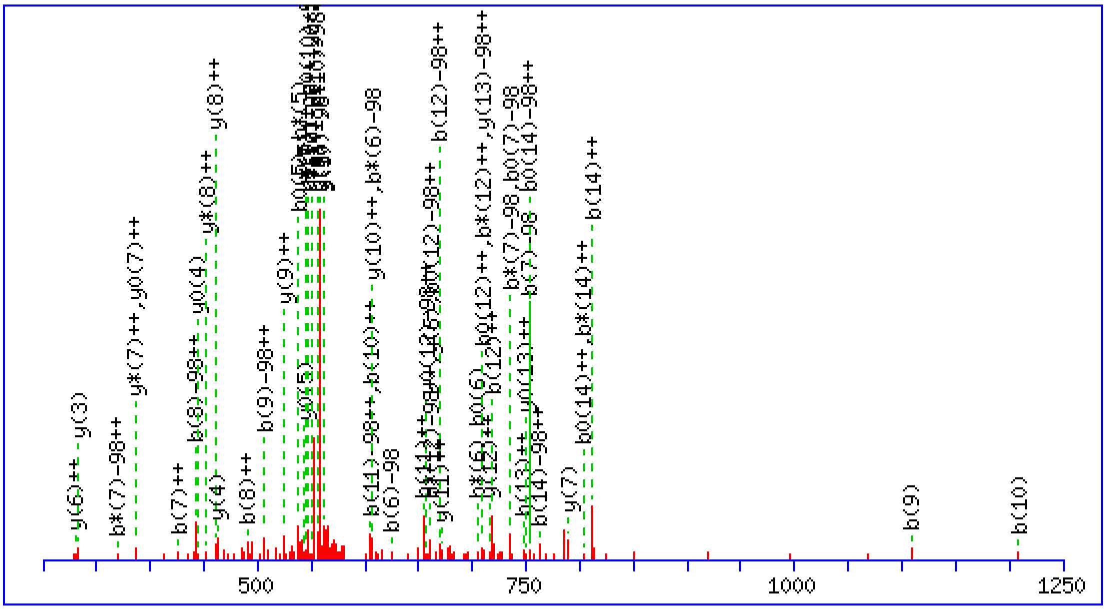
Monoisotopic mass of neutral peptide Mr(calc): 1767.6836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0046
Matched b ions: b(4), b(5)-98, b(7), b(7)-98, b(8)++, b(8)-98++, b(9)-98++, b(9), b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)++, y(10)++, y(13)++, y(14)-98++

Peptide No.133

DHSSQSEEEVVEGEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DHSSQSEEEVVEGEK**
Found in **BNI3L_MOUSE** in **SwissProt**, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like OS=Mus musculus GN=Bnip3l PE=1 SV=1

Match to Query 3873: 1767.683466 from(590.235098,3+) index(441)
Title: Elution from: 28.994 to 28.994 scan no 1687 cid35.00 polarity:+



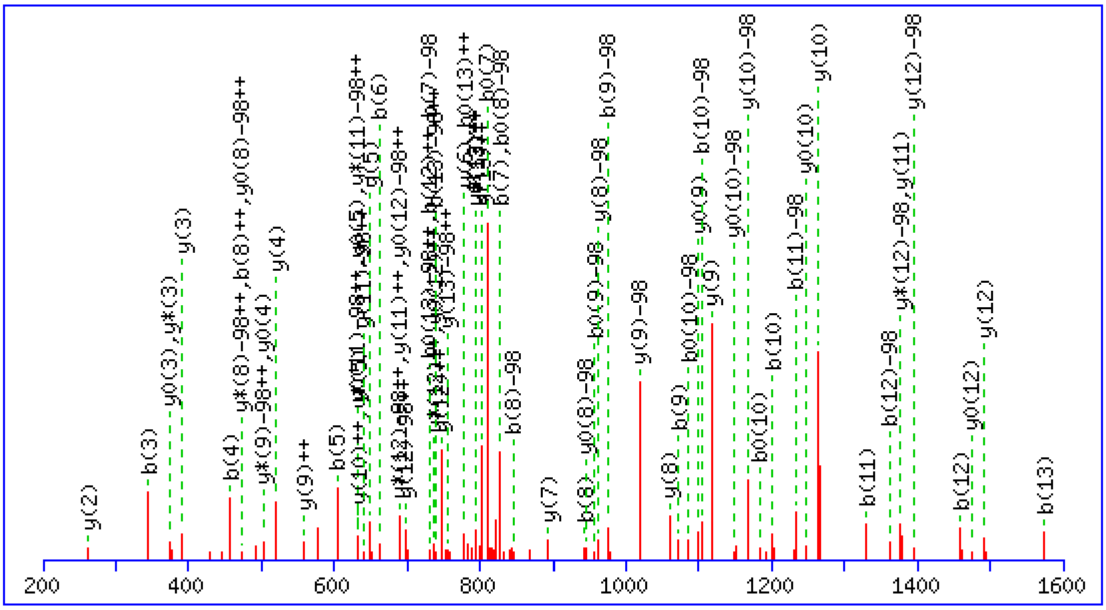
Monoisotopic mass of neutral peptide Mr(calc): 1767.6836
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0034
Matched b ions: b(5), b(6)-98, b(7)++, b(7)-98, b(8)-98++, b(8)++, b(9), b(9)-98++, b(9)++, b(10), b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(9)++, y(10)-98++, y(10)++, y(11)++, y(12)++, y(13)-98++

Peptide No.134

DIDLFGSDEEEEDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DIDLFGSDEEEEDK**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 3251: 1719.639014 from(860.826783,2+) index(5910)
Title: Elution from: 50.986 to 50.986 scan no 4988 cid35.00 polarity:+:m1s



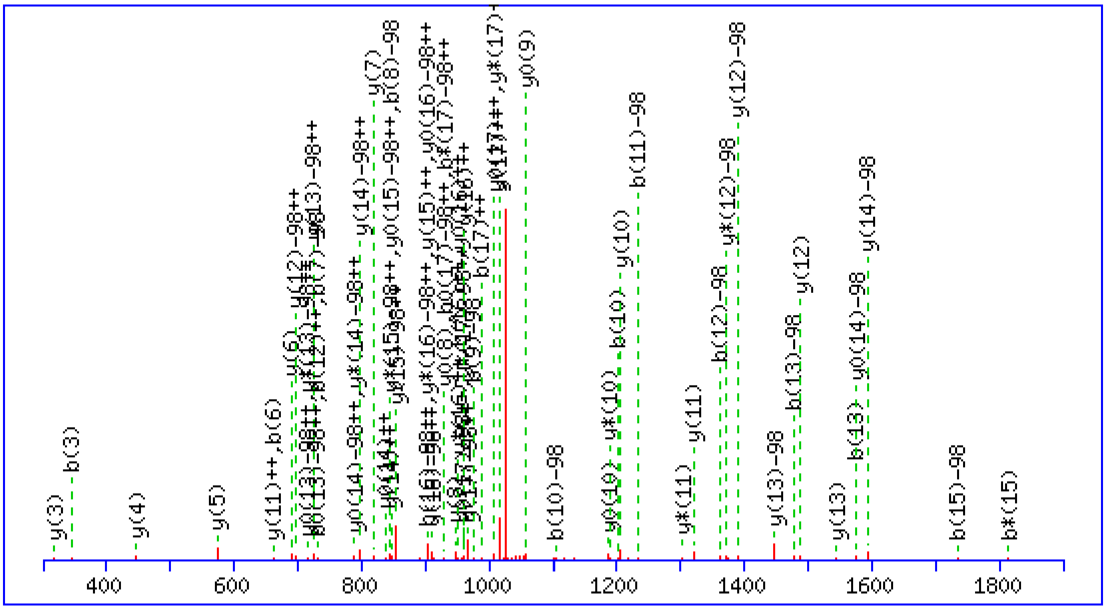
Monoisotopic mass of neutral peptide Mr(calc): 1719.6400
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 **Expect:** 4e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8), b(8)++, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)++, b(13), b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)++, y(10)-98, y(10), y(10)++, y(11), y(11)++, y(11)-98++, y(12)++, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++

Peptide No.135

DIDLFGSDEEEEDKEAAR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DIDLFGSDEEEEDKEAAR**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 4599: 2146.857992 from(1074.436272,2+) index(5438)
Title: Elution from: 45.066 to 45.066 scan no 4421 cid35.00 polarity:+:m1s



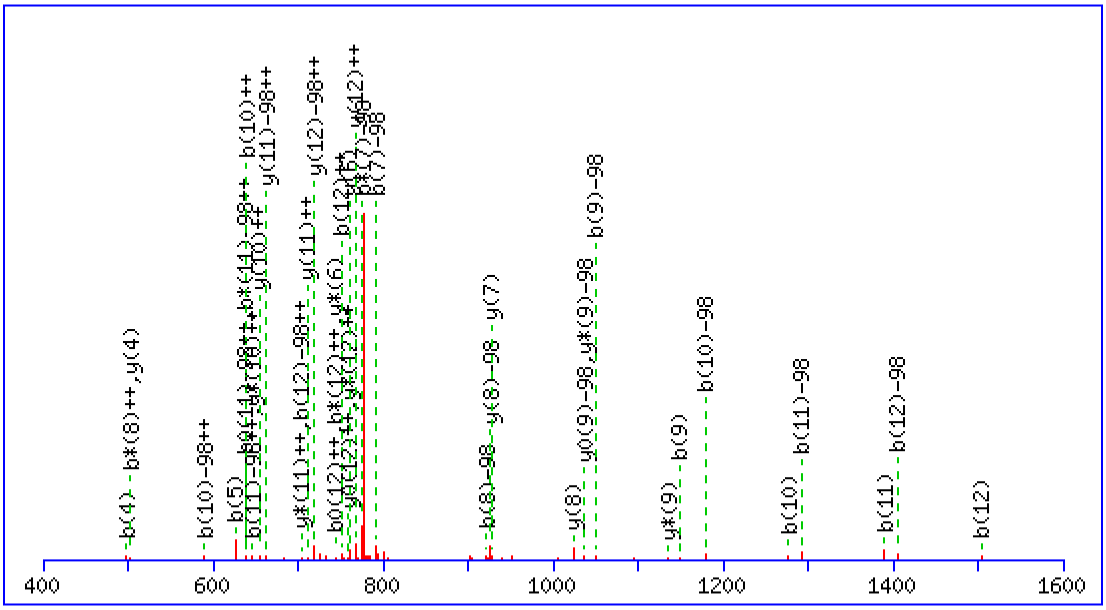
Monoisotopic mass of neutral peptide Mr(calc): 2146.8579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 **Expect:** 1.3e-007
Matched b ions: b(3), b(6), b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98, b(11)-98, b(12)-98, b(12)++, b(13), b(13)-98, b(15)-98, b(16)-98++, b(16)++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)++, y(12)-98++, y(12)-98, y(12), y(13)-98, y(13)-98++, y(13), y(14)-98++, y(14)-98, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.136

DIIRQPSEEEIIK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DIIRQPSEEEIIK**
Found in **PEA15_MOUSE** in **SwissProt**, Astrocytic phosphoprotein PEA-15 OS=Mus musculus GN=Pea15 PE=1 SV=1

Match to Query 2962: 1648.805142 from(825.409847,2+) index(2084)
Title: Elution from: 37.776 to 37.776 scan no 3551 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1648.8073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 3.7e-005
Matched b ions: b(4), b(5), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(10)++, b(11)-98, b(11), b(11)-98++, b(12)-98, b(12), b(12)++, b(12)-98++
Matched y ions: y(4), y(6), y(7), y(8)-98, y(8), y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++

Peptide No.137

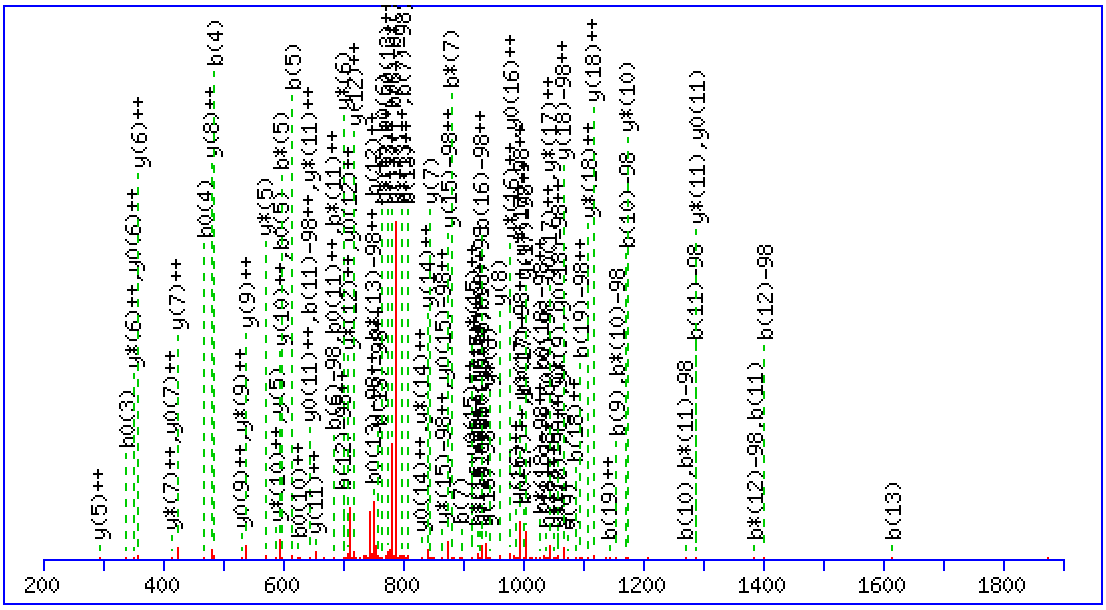
DIKEESDEEDDDDEESGRLR

Confirmed sites: @S:6

Ambiguous sites:

MS/MS Fragmentation of **DIKEESDEEDDDDEESGRLR**
Found in **RBM33_MOUSE** in **SwissProt**, RNA-binding protein 33 OS=Mus musculus GN=Rbm33 PE=1 SV=2

Match to Query 5313: 2459.944236 from(820.988688,3+) index(3791)
Title: Elution from: 23.055 to 23.055 scan no 1627 cid35.00 polarity:+:m1s



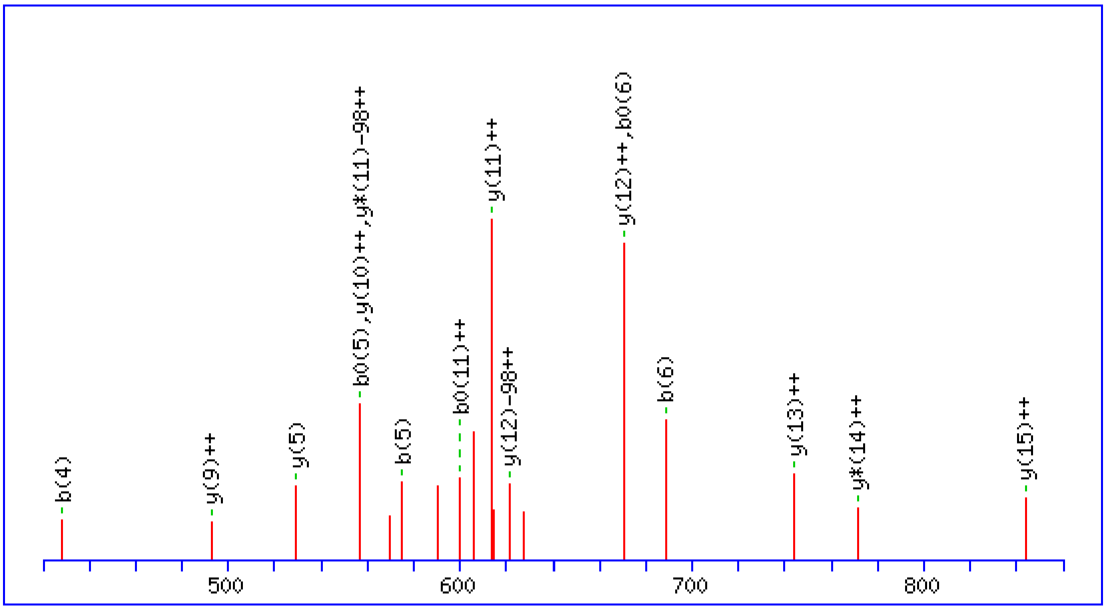
Monoisotopic mass of neutral peptide Mr(calc): 2459.9449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 **Expect:** 4.6e-008
Matched b ions: b(4), b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(11)-98++, b(12)-98, b(12)++, b(12)-98++, b(13), b(13)++, b(13)-98++, b(16)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(5)++, y(5), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++

Peptide No.138

DIQAFLNQCGASPGEAR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **DIQAFLNQCGASPGEAR**
Found in **NAGS_MOUSE** in **SwissProt**, N-acetylglutamate synthase, mitochondrial OS=Mus musculus GN=Nags PE=1 SV=2

Match to Query 4506: 1912.814832 from(638.612220,3+) index(6672)
Title: Elution from: 51.037 to 51.037 scan no 5250 cid35.00 polarity:+:m1s



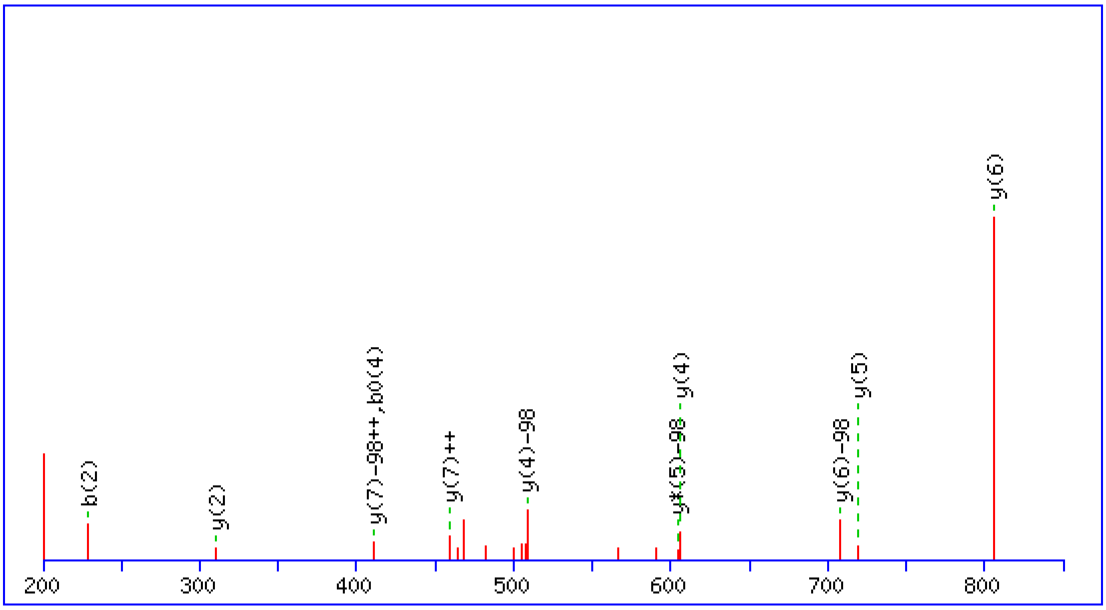
Monoisotopic mass of neutral peptide Mr(calc): 1912.8139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 5.5e-005
Matched b ions: b(4), b(5), b(6)
Matched y ions: y(5), y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(15)++

Peptide No.139

DISLSEYK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **DISLSEYK**
Found in **PRDX1_MOUSE** in **SwissProt**, Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1

Match to Query 822: 1033.436674 from(517.725613,2+) index(2166)
Title: Elution from: 38.717 to 38.717 scan no 3668 cid35.00 polarity:+



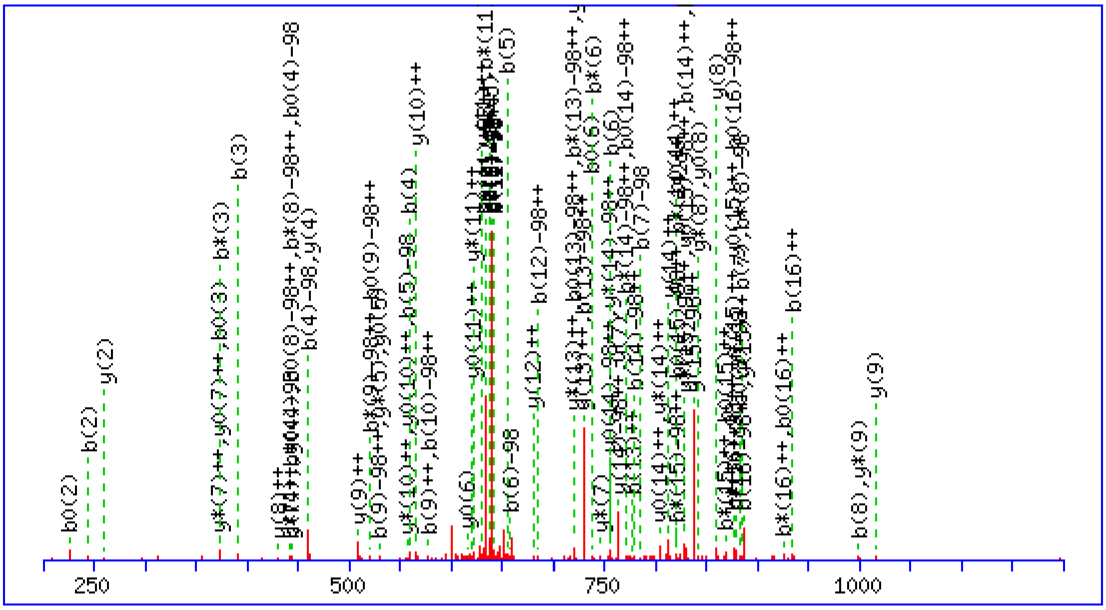
Monoisotopic mass of neutral peptide Mr(calc): 1033.4369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.02
Matched b ions: b(2)
Matched y ions: y(2), y(4)-98, y(4), y(5), y(6)-98, y(6), y(7)++, y(7)-98++

Peptide No.140

DKFSPTQDRPESSTVLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **DKFSPTQDRPESSTVLK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5052: 2013.937893 from(672.319907,3+) index(1323)
Title: Elution from: 27.559 to 27.559 scan no 2303 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 2013.9408

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 39 **Expect:** 0.00065

Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7)-98, b(7), b(8), b(9)++, b(9)-98++, b(10)-98++, b(11)-98++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++

Matched y ions: y(2), y(4), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++

Peptide No.141

DKFSPTQDRPESSTVLK

Confirmed sites: @T:6

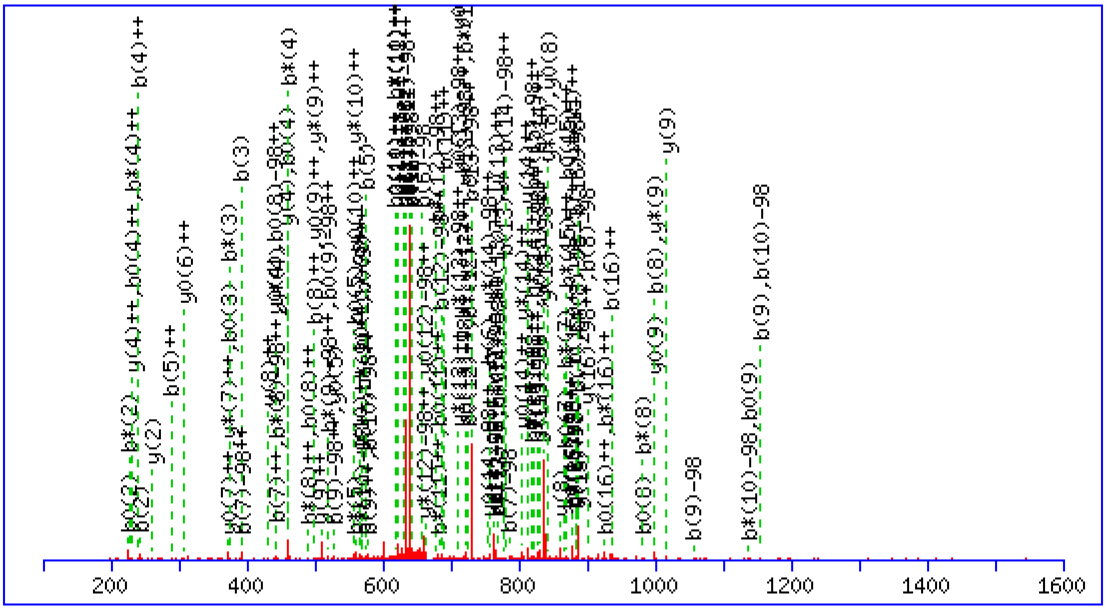
Ambiguous sites:

MS/MS Fragmentation of **DKFSPTQDRPESSTVLK**

Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5158: 2013.942123 from(672.321317,3+) index(4580)

Title: Elution from: 35.373 to 35.373 scan no 2562 cid35.00 polarity:+:m1s



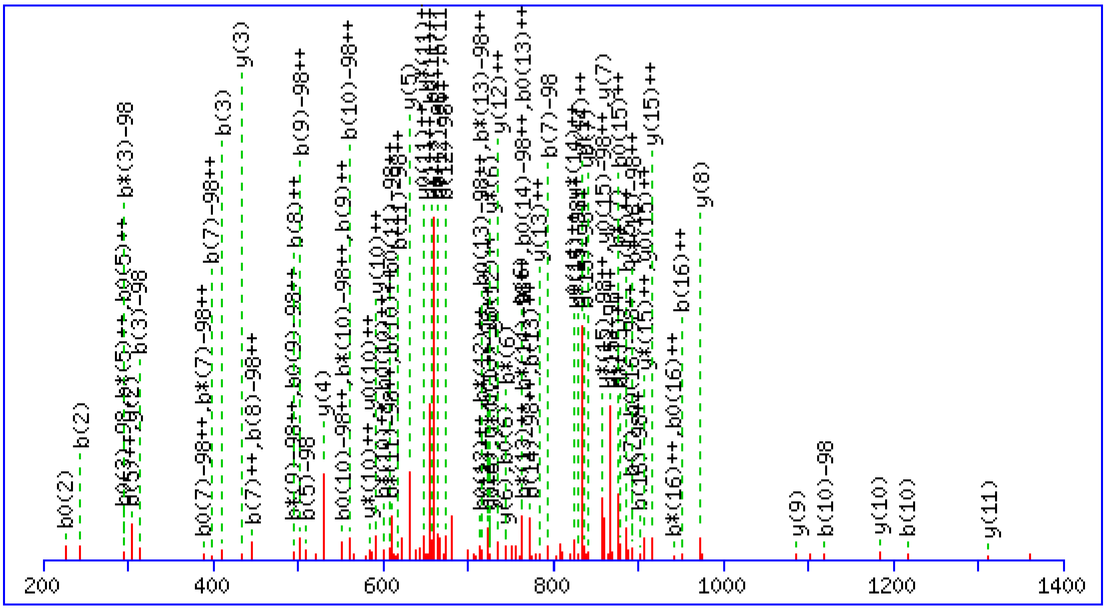
Monoisotopic mass of neutral peptide Mr(calc): 2013.9408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0035
Matched b ions: b(2), b(3), b(4)++, b(5)++, b(5), b(6), b(6)-98, b(7)++, b(7)-98, b(7)-98++, b(7), b(8), b(8)-98, b(8)++, b(9), b(9)++, b(9)-98, b(9)-98++, b(10)-98, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(4), y(4)++, y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++

Peptide No.142

DKSPVREPIDNLTPEER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DKSPVREPIDNLTPEER**
Found in **RBM39_MOUSE** in **SwissProt**, RNA-binding protein 39 OS=Mus musculus GN=Rbm39 PE=1 SV=2

Match to Query 4401: 2073.972318 from(692.331382,3+) index(4380)
Title: Elution from: 31.332 to 31.332 scan no 2669 cid35.00 polarity:+:m1s



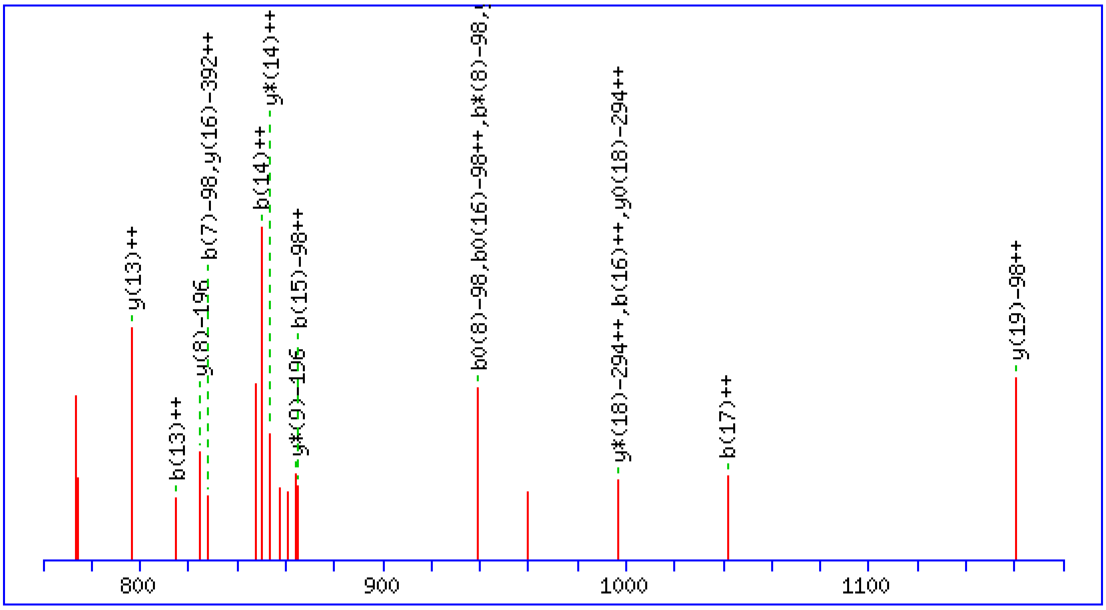
Monoisotopic mass of neutral peptide Mr(calc): 2073.9732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 1.1e-006
Matched b ions: b(2), b(3), b(3)-98, b(5)++, b(5)-98, b(6)-98, b(6), b(7)++, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++

Peptide No.143

DLLEMSRESDPHGAESSSSGR
Confirmed sites: @S:6,@S:9,@S:16,@S:18,@S:19
Ambiguous sites:

MS/MS Fragmentation of **DLLEMSRESDPHGAESSSSGR**
Found in **ZBBX_MOUSE** in **SwissProt**, Zinc finger B-box domain-containing protein 1 OS=Mus musculus GN=Zbbx PE=2 SV=1

Match to Query 5404: 2645.822289 from(882.948039,3+) index(2256)
Title: Elution from: 41.863 to 41.863 scan no 4037 cid35.00 polarity:+



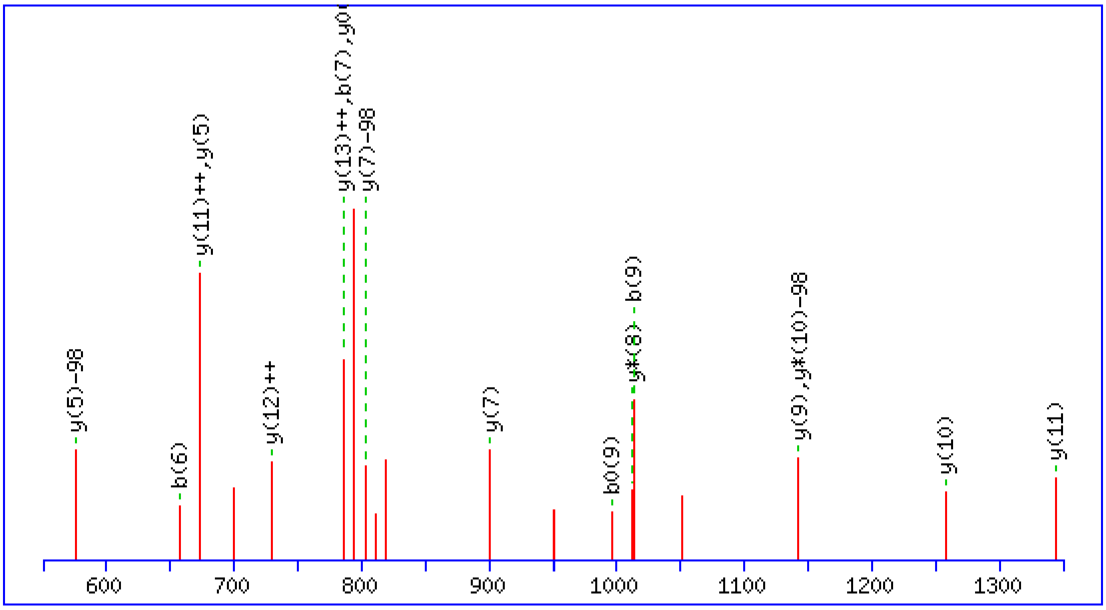
Monoisotopic mass of neutral peptide Mr(calc): 2645.8185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 14 **Expect:** 0.05
Matched b ions: b(7)-98, b(13)++, b(14)++, b(15)-98++, b(16)++, b(17)++
Matched y ions: y(8)-196, y(13)++, y(15)++, y(16)-392++, y(19)-98++

Peptide No.144

DLLSDLQDISDSER
Confirmed sites:
Ambiguous sites: @S:10orS:12

MS/MS Fragmentation of **DLLSDLQDISDSER**
Found in **CDK11_MOUSE** in **SwissProt**, Cyclin-dependent kinase 11 OS=Mus musculus GN=Cdk11 PE=1 SV=2

Match to Query 3744: 1684.715758 from(843.365155,2+) index(3465)
Title: Elution from: 60.814 to 60.814 scan no 6201 cid35.00 polarity:+



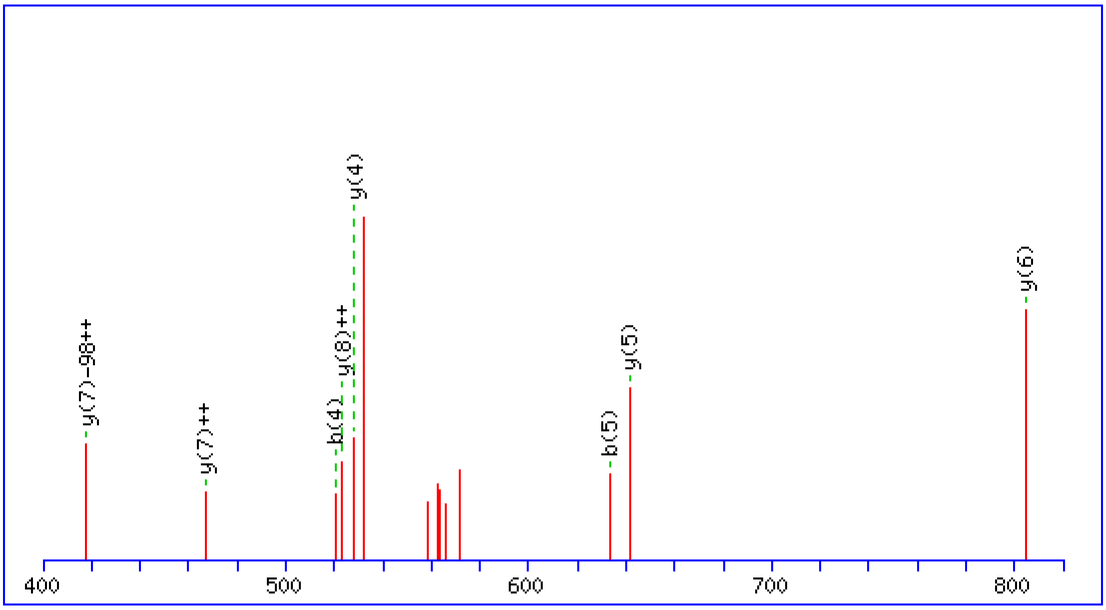
Monoisotopic mass of neutral peptide Mr(calc): 1684.7193
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0016
Matched b ions: b(6), b(7), b(9)
Matched y ions: y(5), y(5)-98, y(7), y(7)-98, y(9), y(10), y(11)++, y(11), y(12)++, y(13)++

Peptide No.145

DLQYITISK
Confirmed sites:
Ambiguous sites: @T:6orS:8

MS/MS Fragmentation of **DLQYITISK**
Found in **AFAD_MOUSE** in **SwissProt**, Afadin OS=Mus musculus GN=Mllt4 PE=1 SV=3

Match to Query 1365: 1159.552702 from(580.783627,2+) index(2657)
Title: Elution from: 42.327 to 42.327 scan no 4248 cid35.00 polarity:+



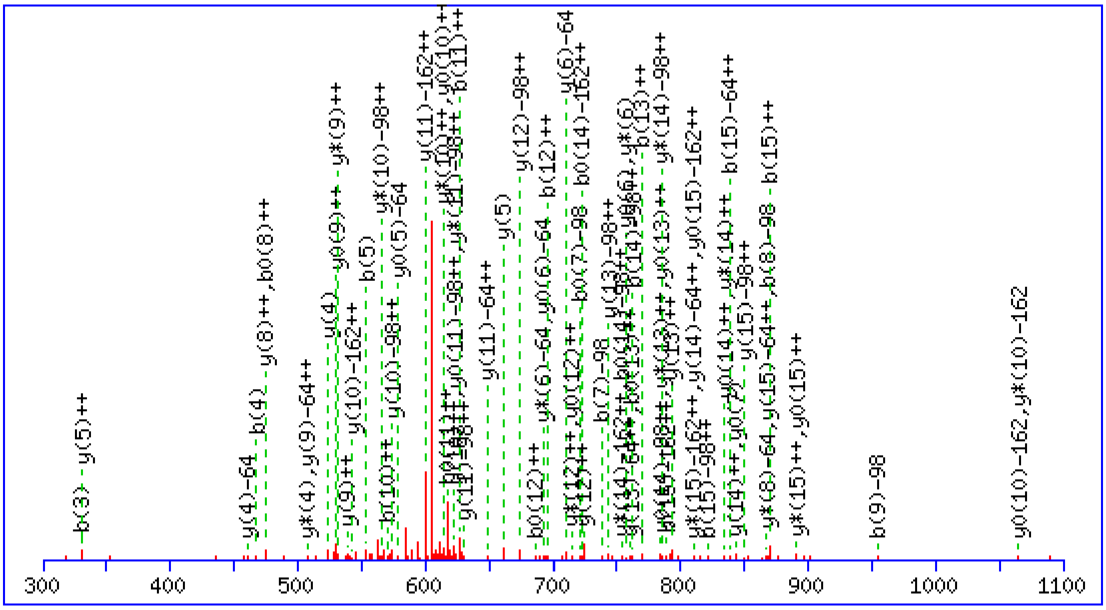
Monoisotopic mass of neutral peptide Mr(calc): 1159.5526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0098
Matched b ions: b(4), b(5)
Matched y ions: y(4), y(5), y(6), y(7)-98++, y(7)++, y(8)++

Peptide No.146

DLTHSDSESSLHMSDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DLTHSDSESSLHMSDR**
Found in **STIM1_MOUSE** in **SwissProt**, Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=2

Match to Query 4181: 1911.731790 from(638.251206,3+) index(256)
Title: Elution from: 26.524 to 26.524 scan no 1419 cid35.00 polarity:+



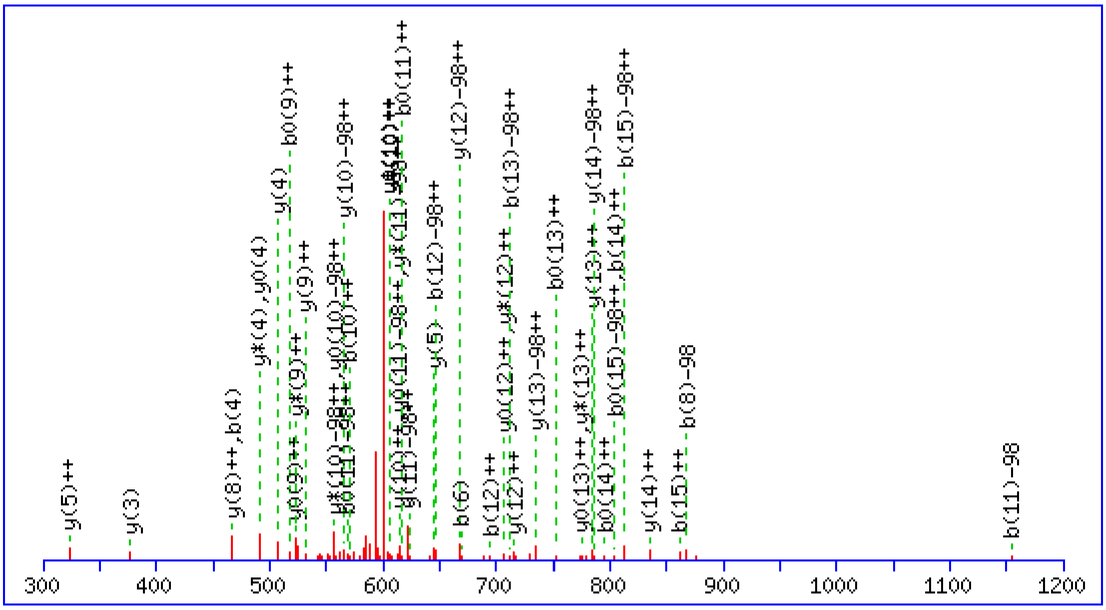
Monoisotopic mass of neutral peptide Mr(calc): 1911.7306
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 28 **Expect:** 0.0046
Matched b ions: b(3), b(4), b(5), b(7)-98, b(8)-98, b(9)-98, b(10)++, b(11)++, b(12)++, b(13)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(4), y(5)++, y(5), y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(15)-98++

Peptide No.147

DLTHSDSESSLHMSDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DLTHSDSESSLHMSDR**
Found in **STIM1_MOUSE** in **SwissProt**, Stromal interaction molecule 1 OS=Mus musculus GN=Stim1 PE=1 SV=2

Match to Query 4434: 1895.733531 from(632.918453,3+) index(4663)
Title: Elution from: 26.153 to 26.153 scan no 2075 cid35.00 polarity:+:m1s



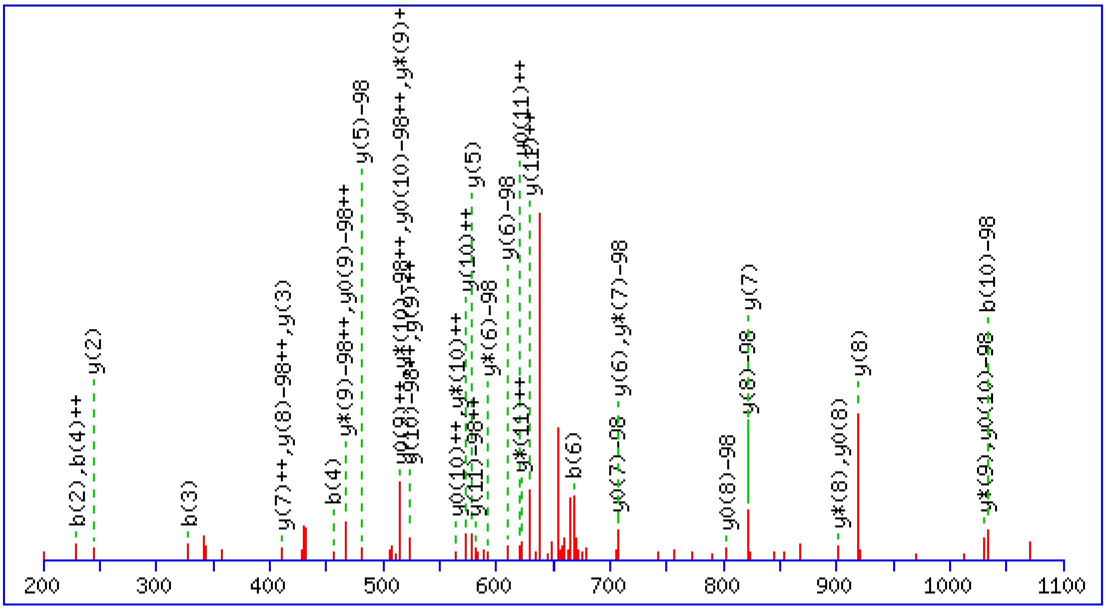
Monoisotopic mass of neutral peptide Mr(calc): 1895.7357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.0083
Matched b ions: b(4), b(6), b(8)-98, b(10)++, b(11)-98, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++

Peptide No.148

DLVQPDKPASPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DLVQPDKPASPK**
Found in **ZC3HE_MOUSE** in **SwissProt**, Zinc finger CCCH domain-containing protein 14 OS=Mus musculus GN=Zc3h14 PE=1 SV=1

Match to Query 2253: 1373.655818 from(687.835185,2+) index(655)
Title: Elution from: 22.077 to 22.077 scan no 1519 cid35.00 polarity:+



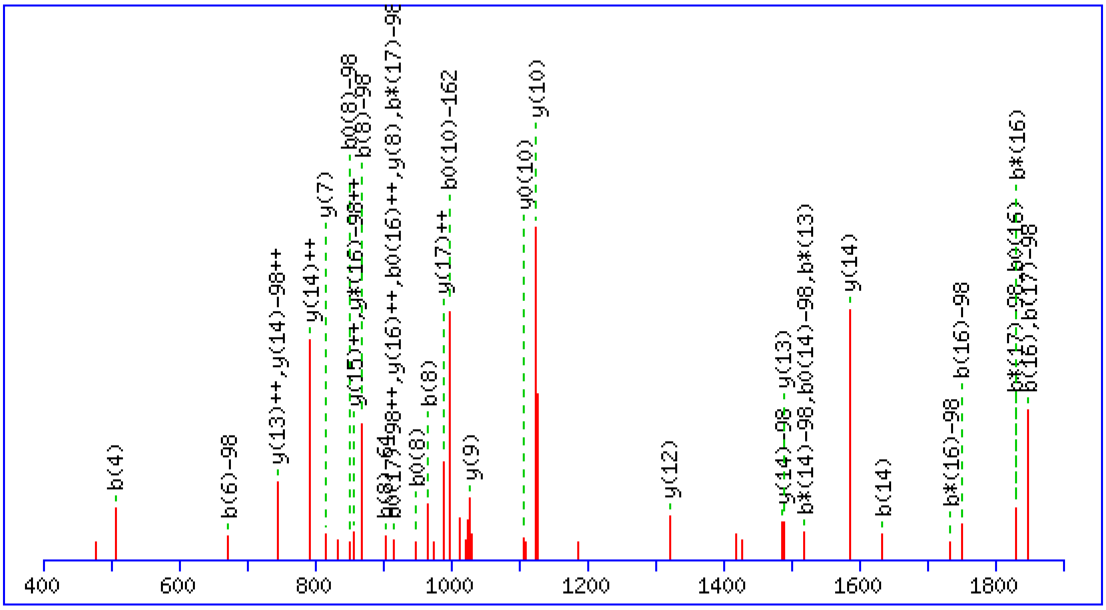
Monoisotopic mass of neutral peptide Mr(calc): 1373.6592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.045
Matched b ions: b(2), b(3), b(4)++, b(4), b(6), b(10)-98
Matched y ions: y(2), y(3), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.149

DMDEPSPVPNVEEVTLPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DMDEPSPVPNVEEVTLPK**
Found in **SMRC2_MOUSE** in **SwissProt**, SWI/SNF complex subunit SMARCC2 OS=Mus musculus GN=Smarcc2 PE=1 SV=2

Match to Query 5274: 2090.906646 from(1046.460599,2+) index(6785)
Title: Elution from: 49.453 to 49.453 scan no 5130 cid35.00 polarity:+:m1s



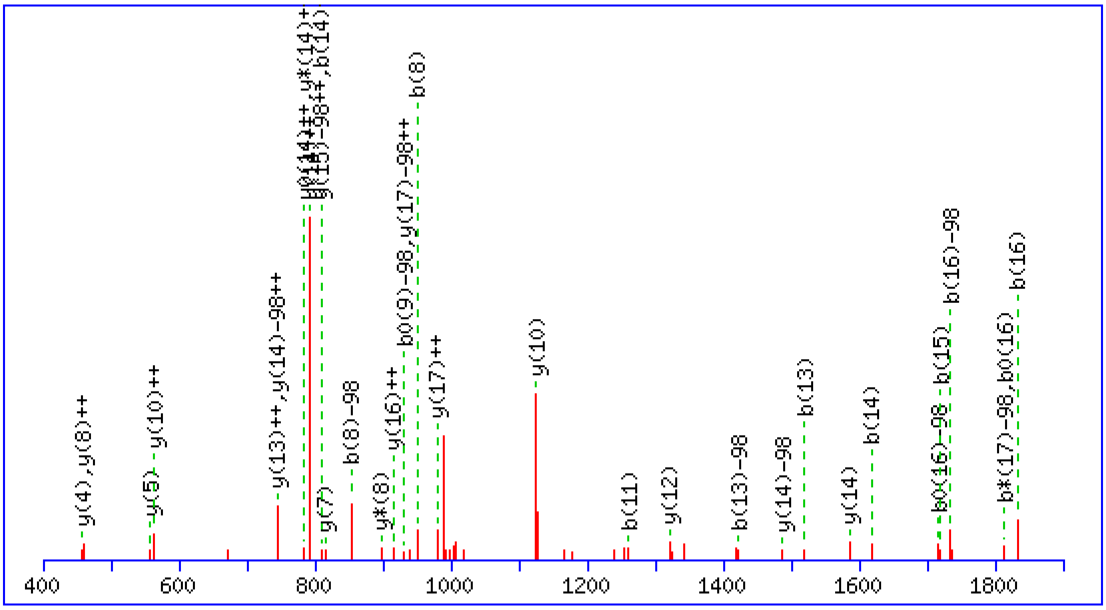
Monoisotopic mass of neutral peptide Mr(calc): 2090.9119
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.005
Matched b ions: b(4), b(6)-98, b(8), b(8)-98, b(14), b(16), b(16)-98, b(17)-98
Matched y ions: y(7), y(8), y(9), y(10), y(12), y(13)++, y(13), y(14)-98++, y(14)++, y(14), y(14)-98, y(15)++, y(16)++, y(17)++

Peptide No.150

DMDEPSPVPNVEEVTLPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DMDEPSPVPNVEEVTLPK**
Found in **SMRC2_MOUSE** in **SwissProt**, SWI/SNF complex subunit SMARCC2 OS=Mus musculus GN=Smarcc2 PE=1 SV=2

Match to Query 5227: 2074.914530 from(1038.464541,2+) index(6880)
Title: Elution from: 51.940 to 51.940 scan no 5387 cid35.00 polarity:+:m1s



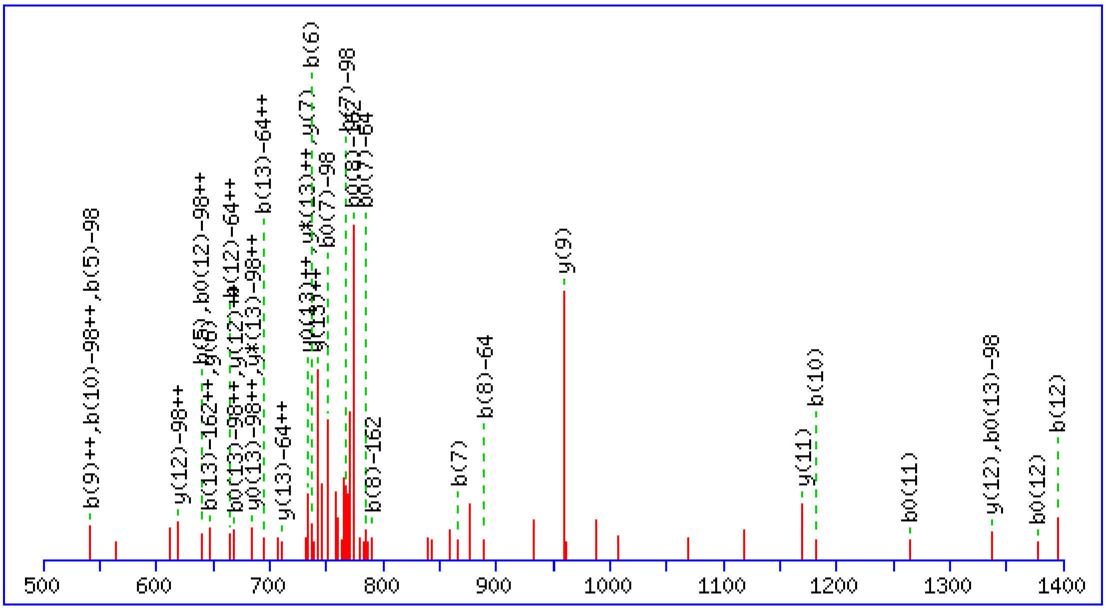
Monoisotopic mass of neutral peptide Mr(calc): 2074.9170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0022
Matched b ions: b(8), b(8)-98, b(11), b(13), b(13)-98, b(14), b(14)++, b(15), b(16)-98, b(16)
Matched y ions: y(4), y(5), y(7), y(8)++, y(10)++, y(10), y(12), y(13)++, y(14)-98++, y(14)++, y(14), y(14)-98, y(15)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.151

DMSPLPESEVTLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DMSPLPESEVTLGK**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2800: 1597.693058 from(799.853805,2+) index(2155)
Title: Elution from: 38.554 to 38.554 scan no 3650 cid35.00 polarity:+



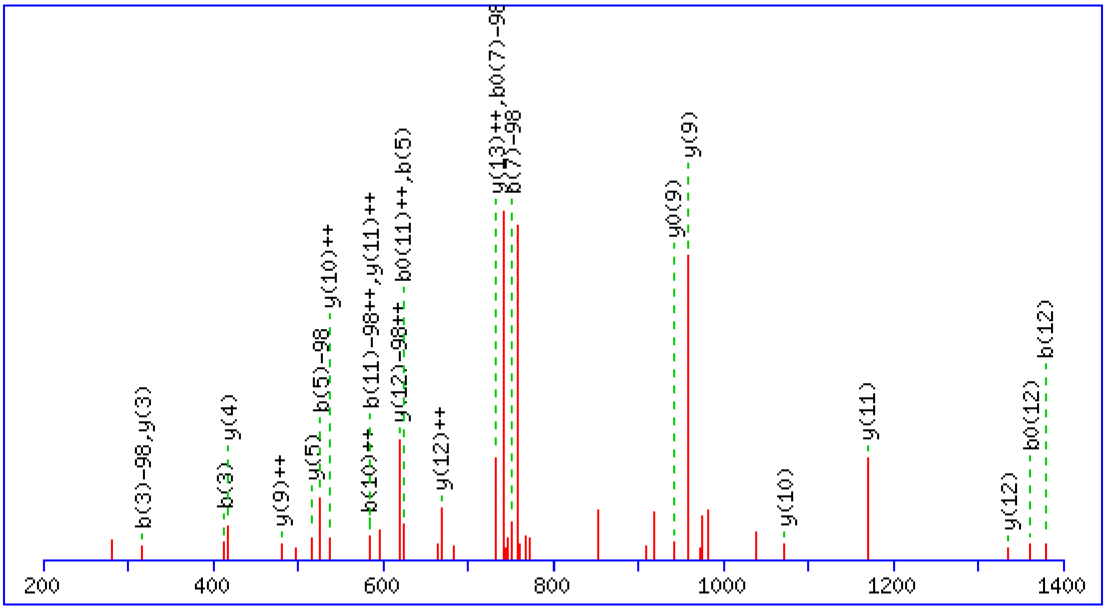
Monoisotopic mass of neutral peptide Mr(calc): 1597.6946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.032
Matched b ions: b(5)-98, b(5), b(6), b(7), b(7)-98, b(9)++, b(10)-98++, b(10), b(12)
Matched y ions: y(6), y(7), y(9), y(11), y(12)-98++, y(12), y(12)++, y(13)++

Peptide No.152

DMSPLPESEVTLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DMSPLPESEVTLGK**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 3160: 1581.700514 from(791.857533,2+) index(2817)
Title: Elution from: 44.834 to 44.834 scan no 4546 cid35.00 polarity:+



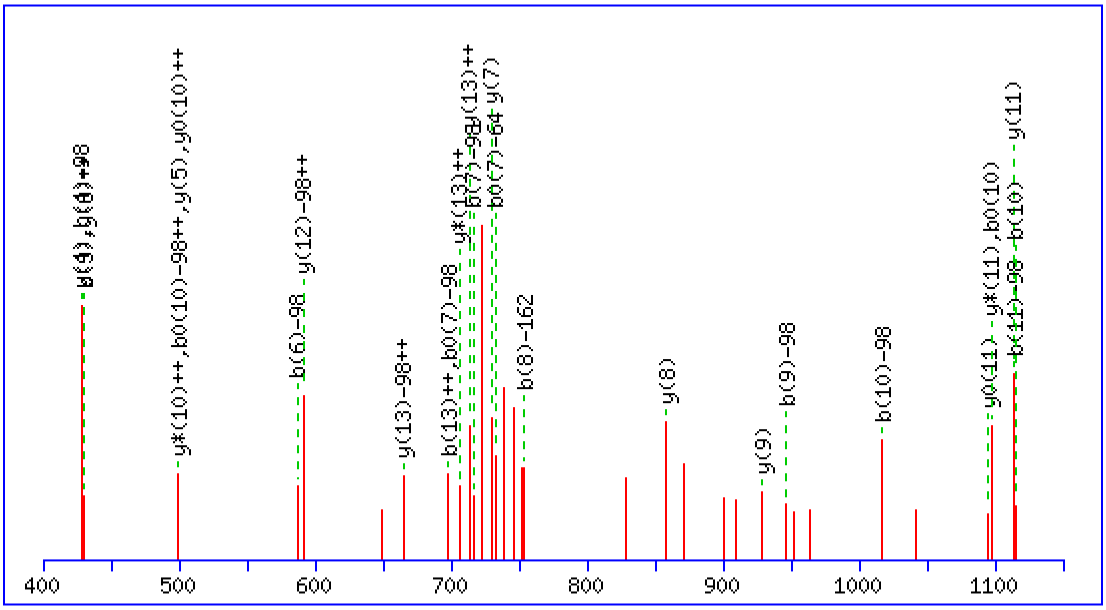
Monoisotopic mass of neutral peptide Mr(calc): 1581.6997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00014
Matched b ions: b(3)-98, b(3), b(5)-98, b(5), b(7)-98, b(10)++, b(11)-98++, b(12)
Matched y ions: y(3), y(4), y(5), y(7), y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)-98++, y(12)++, y(12), y(13)++

Peptide No.153

DMSPSAETEAPLAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DMSPSAETEAPLAK**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 3157: 1541.631144 from(771.822848,2+) index(1255)
Title: Elution from: 27.006 to 27.006 scan no 2227 cid35.00 polarity:+



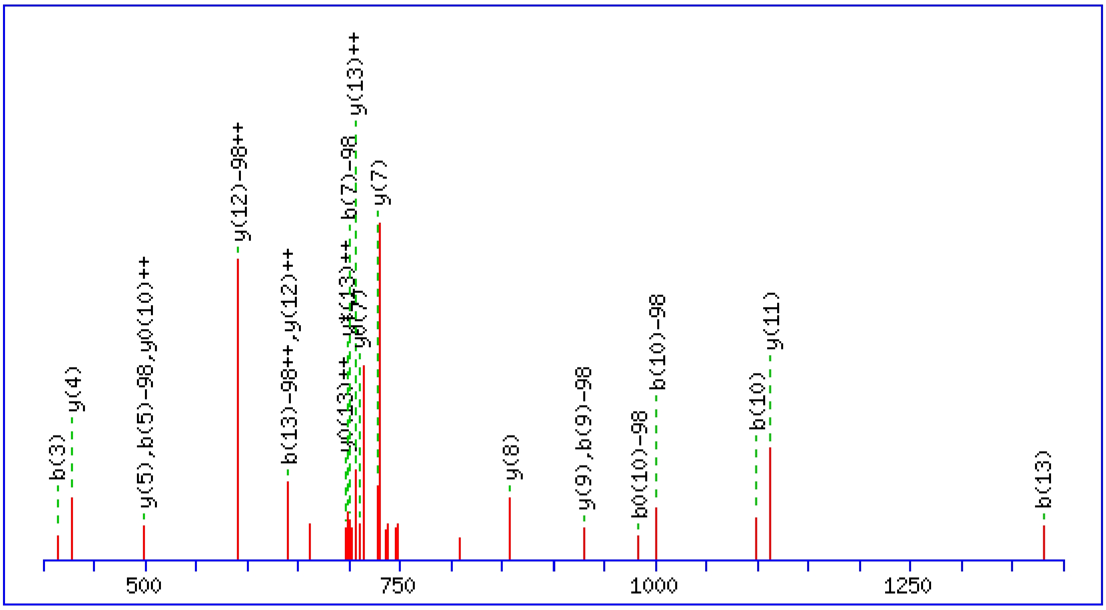
Monoisotopic mass of neutral peptide Mr(calc): 1541.6320
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00016
Matched b ions: b(3), b(4)-98, b(6)-98, b(7)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(13)++
Matched y ions: y(4), y(5), y(7), y(8), y(8)++, y(9), y(11), y(12)-98++, y(13)++, y(13)-98++

Peptide No.154

DMSPSAETEAPLAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **DMSPSAETEAPLAK**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 2920: 1525.636304 from(763.825428,2+) index(1708)
Title: Elution from: 32.092 to 32.092 scan no 2882 cid35.00 polarity:+



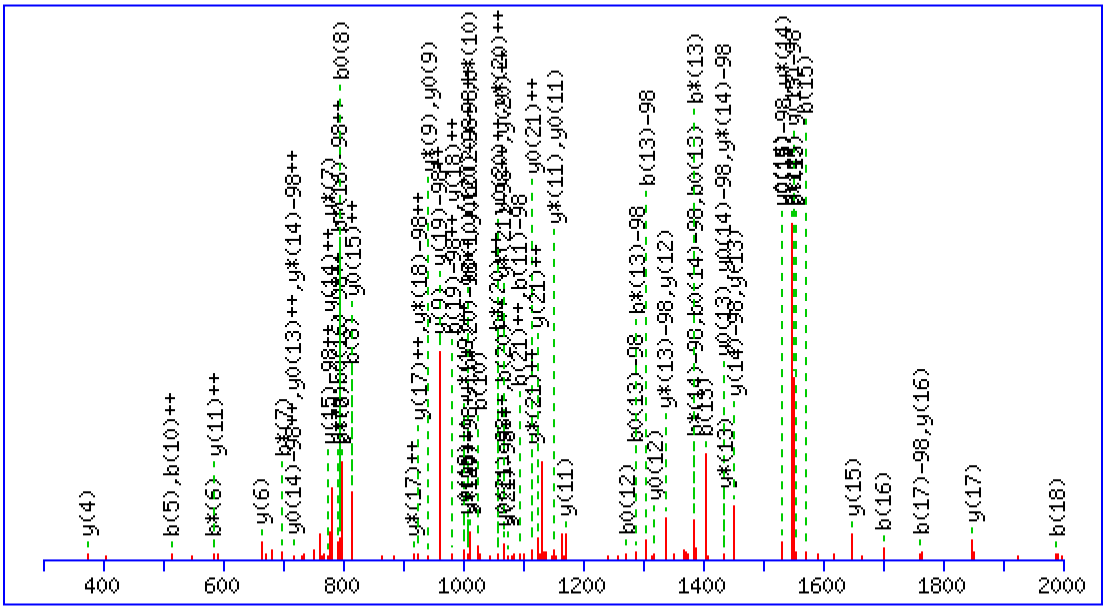
Monoisotopic mass of neutral peptide Mr(calc): 1525.6371
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00018
Matched b ions: b(3), b(5)-98, b(7)-98, b(9)-98, b(10)-98, b(10), b(13), b(13)-98++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(11), y(12)-98++, y(12)++, y(13)++

Peptide No.155

DNLGNSNVPDSPIPAECEAAGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **DNLGNSNVPDSPIPAECEAAGR**
Found in **CTGE5_MOUSE** in **SwissProt**, Cutaneous T-cell lymphoma-associated antigen 5 homolog OS=Mus musculus GN=Ctage5 PE=1 SV=1

Match to Query 5166: 2361.990500 from(1182.002526,2+) index(4547)
Title: Elution from: 44.428 to 44.428 scan no 3442 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2361.9896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 5.6e-005
Matched b ions: b(5), b(8), b(10)++, b(10), b(11)-98, b(13), b(13)-98, b(15), b(16), b(17)-98, b(18), b(19)-98++, b(20)++, b(21)++
Matched y ions: y(4), y(6), y(7), y(9), y(11)++, y(11), y(12), y(13), y(14), y(14)-98, y(14)++, y(15), y(15)-98, y(15)-98++, y(16), y(17), y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++

Peptide No.156

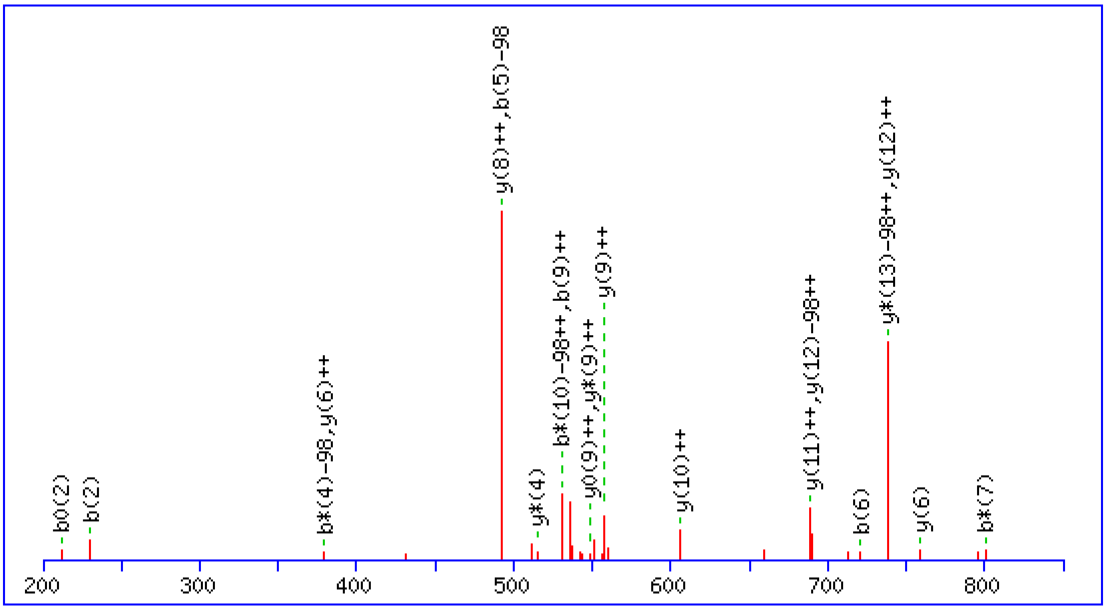
DNPSPEPQLDDIKR

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of **DNPSPEPQLDDIKR**
Found in **EAF1_MOUSE** in **SwissProt**, ELL-associated factor 1 OS=Mus musculus GN=Eaf1 PE=1 SV=2

Match to Query 3189: 1702.754019 from(568.591949,3+) index(4529)
Title: Elution from: 30.071 to 30.071 scan no 2573 cid35.00 polarity:+:m1s



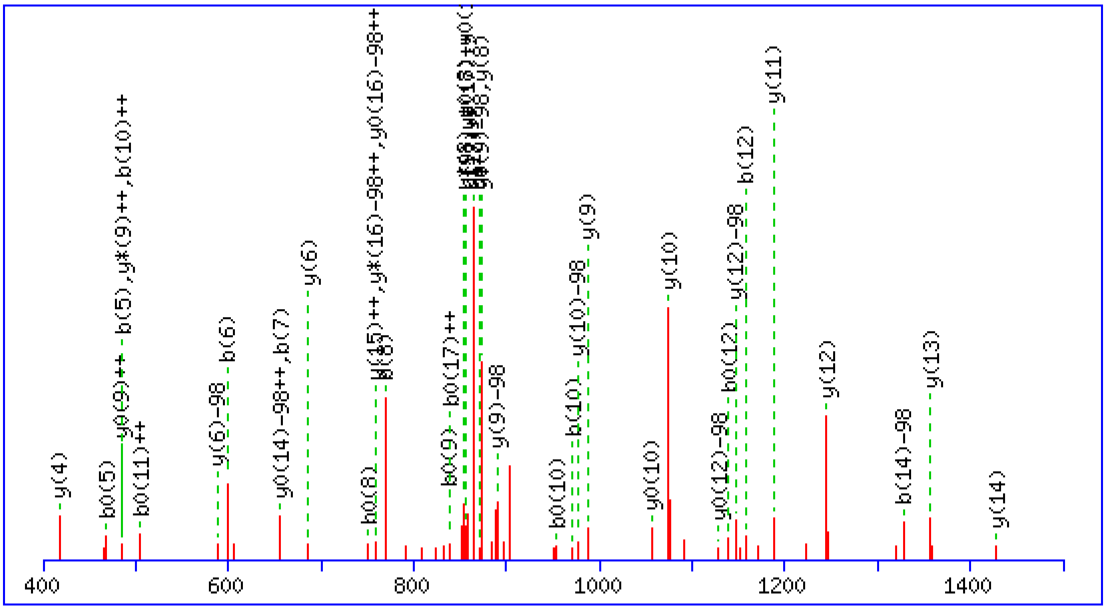
Monoisotopic mass of neutral peptide Mr(calc): 1702.7563
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.001
Matched b ions: b(2), b(5)-98, b(6), b(9)++
Matched y ions: y(6)++, y(6), y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++

Peptide No.157

DPDSALGISDGETSPSSK
Confirmed sites:
Ambiguous sites: @T:13orS:14

MS/MS Fragmentation of **DPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4215: 1841.756370 from(921.885461,2+) index(5707)
Title: Elution from: 36.629 to 36.629 scan no 3494 cid35.00 polarity:+:m1s



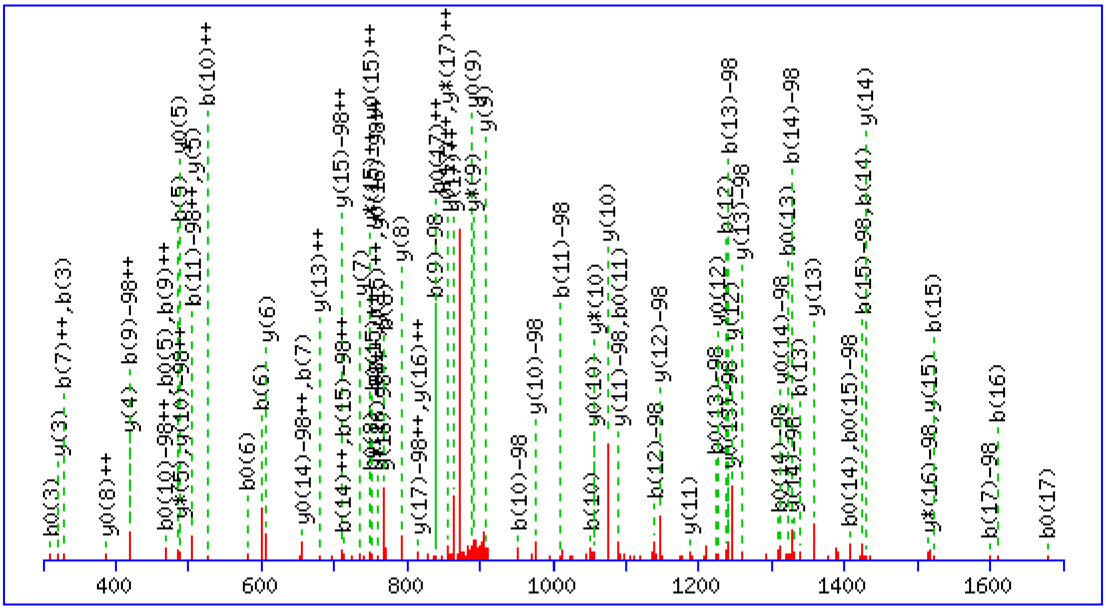
Monoisotopic mass of neutral peptide Mr(calc): 1841.7568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 9.5e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)++, b(10), b(12), b(14)-98
Matched y ions: y(4), y(6), y(6)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11), y(12), y(12)-98, y(13), y(14), y(15)++, y(17)++

Peptide No.158

DPDSALGISDGETSPSSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **DPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4001: 1841.756428 from(921.885490,2+) index(4441)
Title: Elution from: 42.443 to 42.443 scan no 3245 cid35.00 polarity:+:m1s



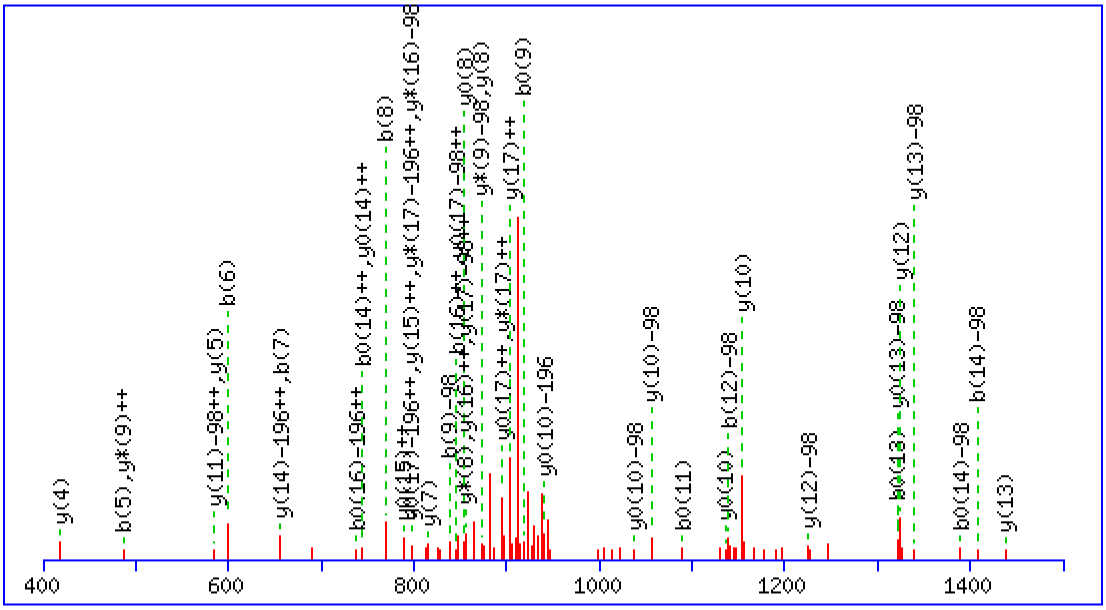
Monoisotopic mass of neutral peptide Mr(calc): 1841.7568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 **Expect:** 8.1e-008
Matched b ions: b(3), b(5), b(6), b(7)++, b(7), b(8), b(9)++, b(9)-98++, b(9)-98, b(10)-98, b(10), b(10)++, b(11)-98++, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(14), b(14)-98, b(14)++, b(15)-98, b(15), b(15)-98++, b(16), b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(10)-98++, y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)++, y(13)-98, y(14), y(14)-98, y(15)-98++, y(15), y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.159

DPDSALGISDGETSPSSK
Confirmed sites: @S:9,@S:14
Ambiguous sites:

MS/MS Fragmentation of **DPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4559: 1921.719250 from(961.866901,2+) index(6060)
Title: Elution from: 40.605 to 40.605 scan no 4020 cid35.00 polarity:+:m1s



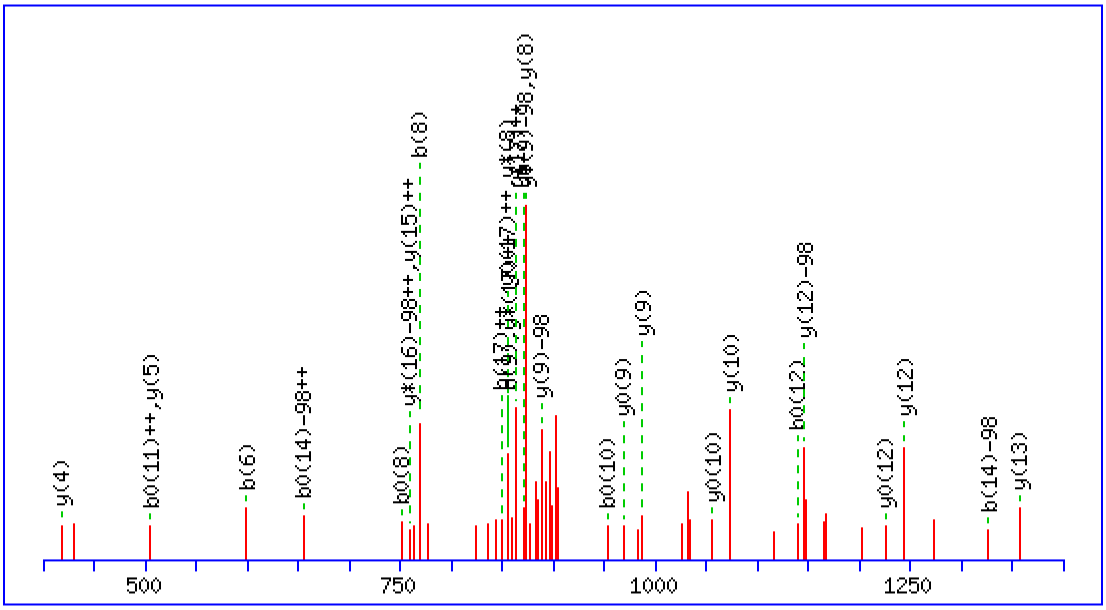
Monoisotopic mass of neutral peptide Mr(calc): 1921.7231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.039
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(12)-98, b(14)-98, b(16)++
Matched y ions: y(4), y(5), y(7), y(8), y(10)-98, y(10), y(11)-98++, y(12), y(12)-98, y(13), y(13)-98, y(14)-196++, y(15)++, y(16)++, y(17)++, y(17)-98++

Peptide No.160

DPDSALGISDGETSPSSK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of **DPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4216: 1841.757318 from(921.885935,2+) index(2045)
Title: Elution from: 35.287 to 35.287 scan no 3314 cid35.00 polarity:+



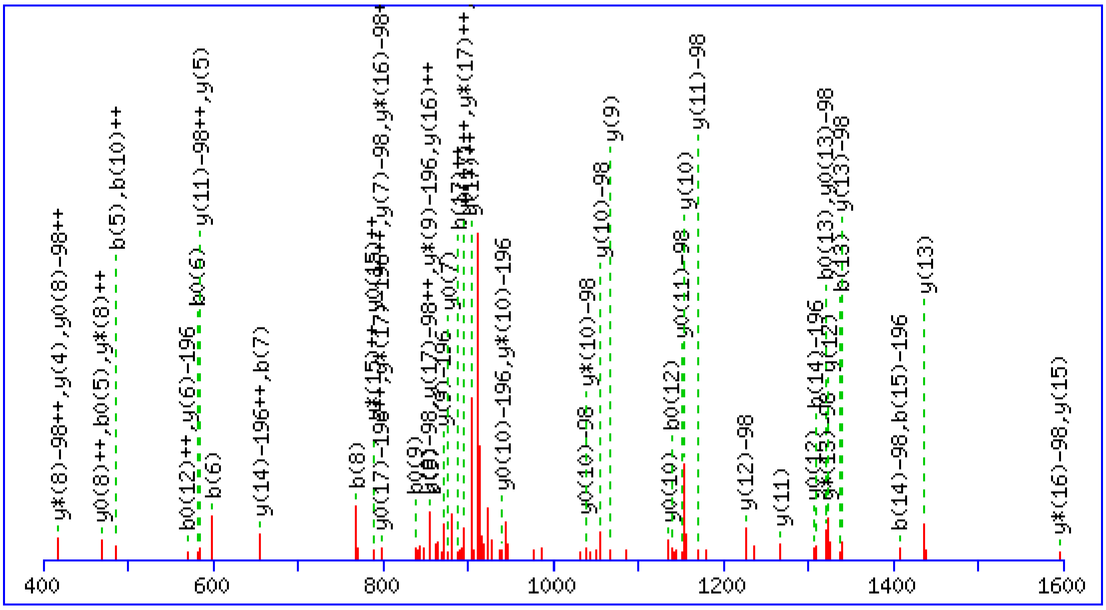
Monoisotopic mass of neutral peptide Mr(calc): 1841.7568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0005
Matched b ions: b(6), b(8), b(9), b(14)-98, b(17)++
Matched y ions: y(4), y(5), y(8), y(9), y(9)-98, y(10), y(12)-98, y(12), y(13), y(15)++, y(17)++

Peptide No.161

DPDSALGISDGETSPSSK
Confirmed sites: @T:13,@S:14
Ambiguous sites:

MS/MS Fragmentation of **DPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 3935: 1921.723056 from(961.868804,2+) index(5315)
Title: Elution from: 39.379 to 39.379 scan no 3751 cid35.00 polarity:+:m1s



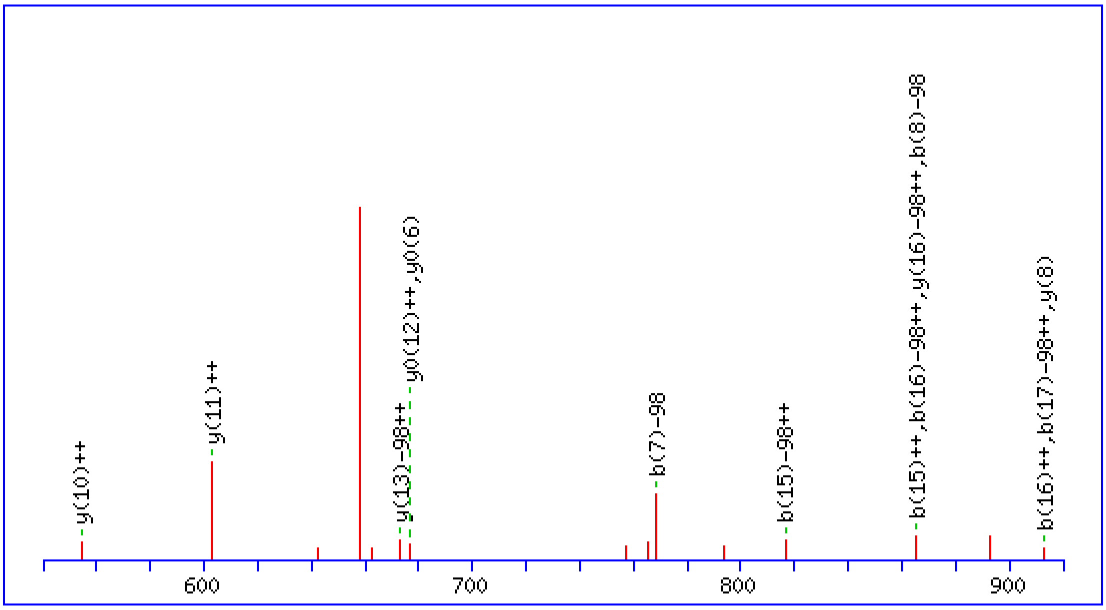
Monoisotopic mass of neutral peptide Mr(calc): 1921.7231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00026
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10)++, b(13), b(14)-196, b(14)-98, b(15)-196, b(17)++
Matched y ions: y(4), y(5), y(6)-196, y(7)-98, y(7), y(8)-98, y(9), y(9)-196, y(10)-98, y(10), y(11)-98++, y(11), y(11)-98, y(12)-98, y(12), y(13), y(13)-98, y(14)-196++, y(15), y(15)++, y(16)++, y(17)++, y(17)-98++

Peptide No.162

DQLRDASPPPAFKPEPPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DQLRDASPPPAFKPEPPK**
Found in **ZO2_MOUSE** in **SwissProt**, Tight junction protein ZO-2 OS=Mus musculus GN=Tjp2 PE=1 SV=2

Match to Query 4394: 2069.000076 from(690.673968,3+) index(4443)
Title: Elution from: 32.072 to 32.072 scan no 2768 cid35.00 polarity:+:m1s



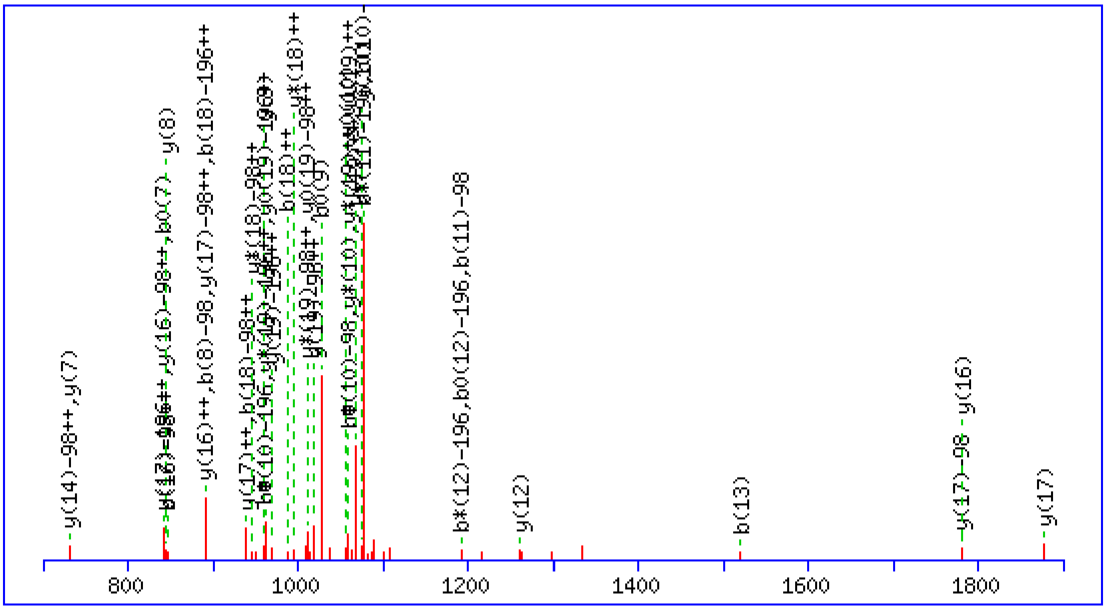
Monoisotopic mass of neutral peptide Mr(calc): 2068.9983
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.035
Matched b ions: b(7)-98, b(8)-98, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++
Matched y ions: y(8), y(10)++, y(11)++, y(13)-98++, y(16)-98++

Peptide No.163

DQQPSGSEGEDDDAEAALKK
Confirmed sites: @S:5,@S:7
Ambiguous sites:

MS/MS Fragmentation of **DQQPSGSEGEDDDAEAALKK**
Found in **THUM1_MOUSE** in **SwissProt**, THUMP domain-containing protein 1 OS=Mus musculus GN=Thumpd1 PE=1 SV=1

Match to Query 5745: 2248.836956 from(1125.425754,2+) index(4921)
Title: Elution from: 28.707 to 28.707 scan no 2423 cid35.00 polarity:+:m1s



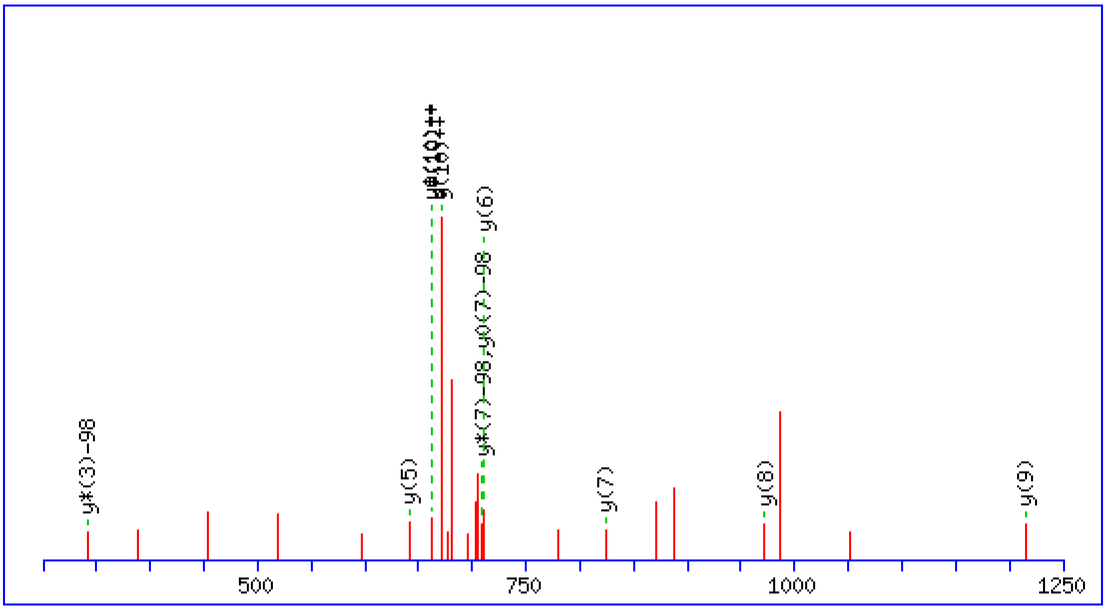
Monoisotopic mass of neutral peptide Mr(calc): 2248.8410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0086
Matched b ions: b(8)-98, b(10)-98, b(11)-98, b(13), b(16)-98++, b(18)-196++, b(18)-98++, b(18)++
Matched y ions: y(7), y(8), y(9), y(10), y(12), y(14)-98++, y(16)++, y(16)-98++, y(16), y(17)-98++, y(17)-98, y(17), y(17)-196++, y(17)++, y(19)++, y(19)-98++, y(19)-196++

Peptide No.164

DQYFLALASNR
Confirmed sites: @Y:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of **DQYFLALASNR**
Found in **SC5AB_MOUSE** in **SwissProt**, Sodium/myo-inositol cotransporter 2 OS=Mus musculus GN=Slc5a11 PE=2 SV=1

Match to Query 2278: 1456.576338 from(729.295445,2+) index(2489)
Title: Elution from: 43.782 to 43.782 scan no 4252 cid35.00 polarity:+



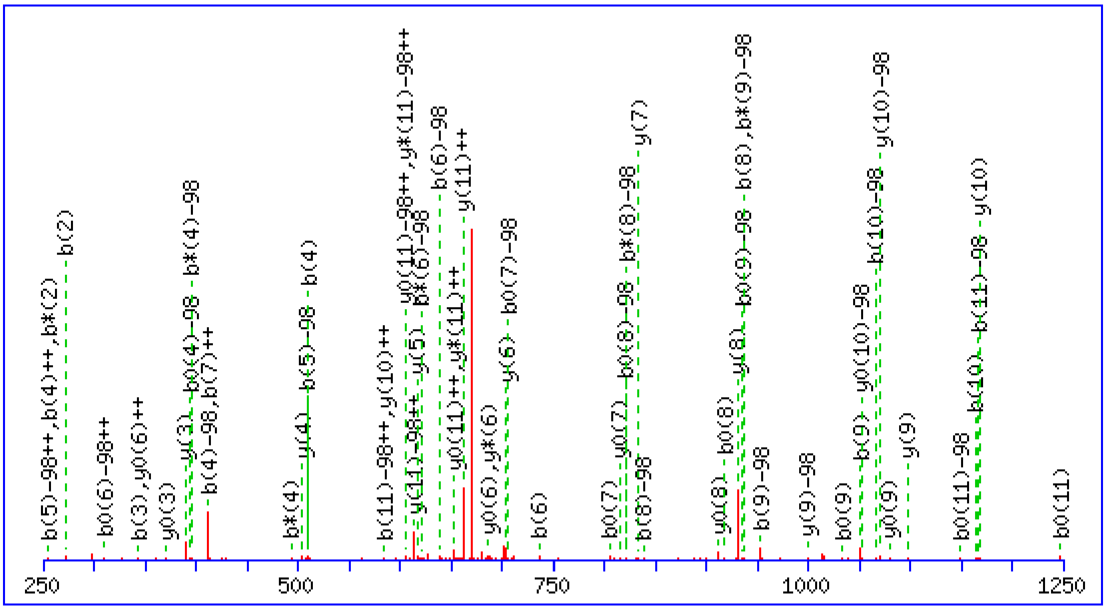
Monoisotopic mass of neutral peptide Mr(calc): 1456.5789
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y3 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.055
Matched b ions:
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)++

Peptide No.165

DRASPESLDLTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **DRASPESLDLTR**
Found in **PROX1_MOUSE** in **SwissProt**, Prospero homeobox protein 1 OS=Mus musculus GN=Prox1 PE=1 SV=2

Match to Query 2680: 1438.644444 from(720.329498,2+) index(1545)
Title: Elution from: 29.865 to 29.865 scan no 2617 cid35.00 polarity:+



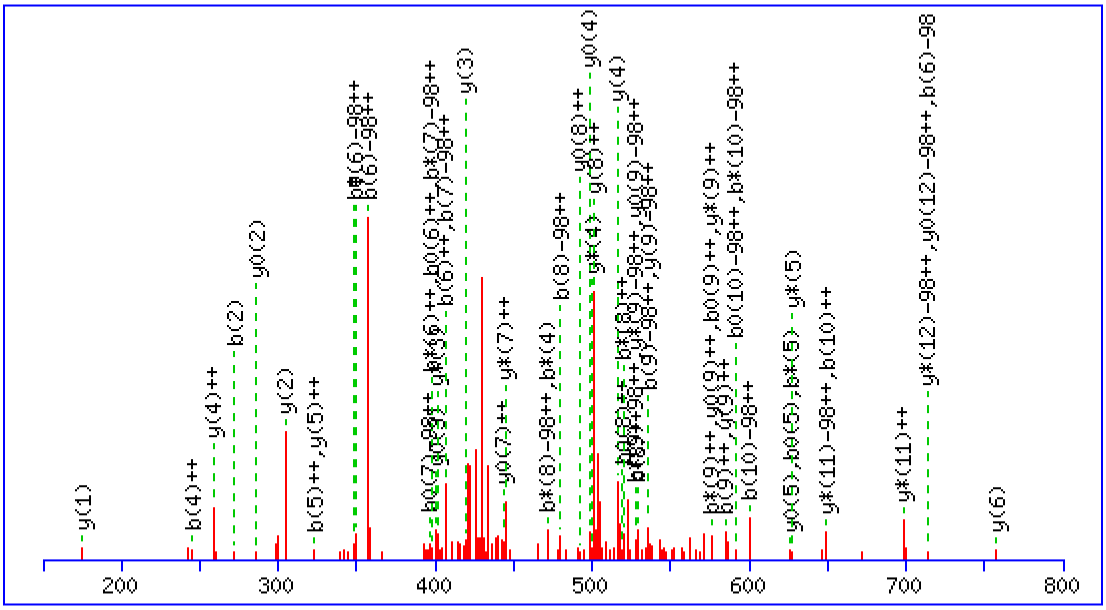
Monoisotopic mass of neutral peptide Mr(calc): 1438.6453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 **Expect:** 4.2e-006
Matched b ions: b(2), b(3), b(4)-98, b(4), b(4)++, b(5)-98++, b(5)-98, b(6)-98, b(6), b(7)++, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(11)-98++, y(11)++

Peptide No.166

DRESRSPFLKPDER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DRESRSPFLKPDER**
Found in **SFR19_MOUSE** in **SwissProt**, Splicing factor, arginine/serine-rich 19 OS=Mus musculus GN=Scaf1 PE=1 SV=1

Match to Query 3560: 1810.835348 from(453.716113,4+) index(3634)
Title: Elution from: 21.698 to 21.698 scan no 1446 cid35.00 polarity:+:m1s



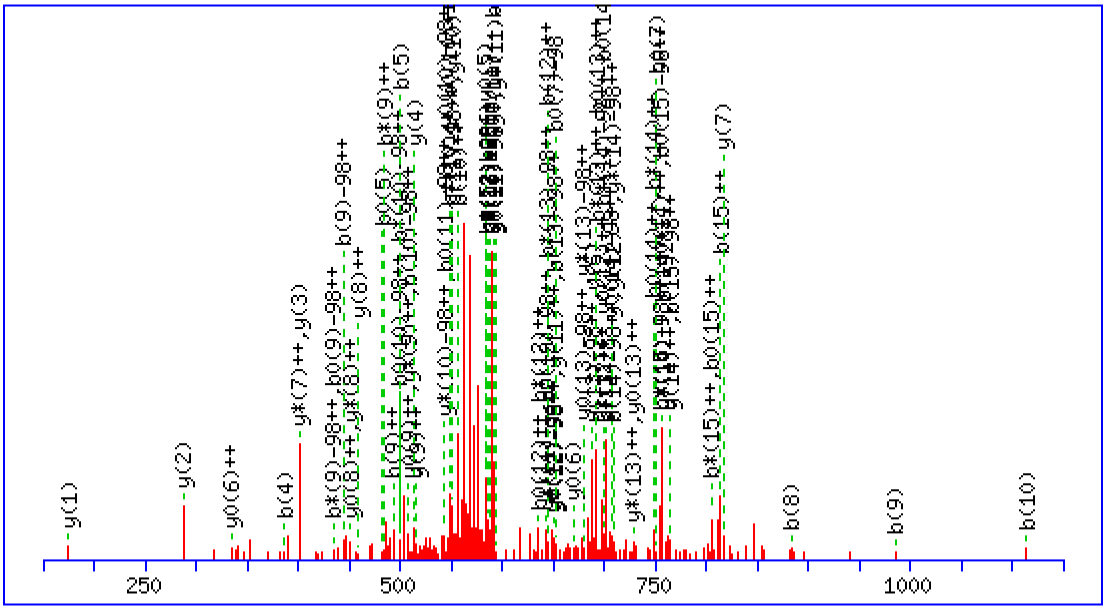
Monoisotopic mass of neutral peptide Mr(calc): 1810.8363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0093
Matched b ions: b(2), b(3), b(4)++, b(5)++, b(6)-98++, b(6)-98, b(6)++, b(7)-98++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(10)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(6), y(8)++, y(9)++, y(9)-98++

Peptide No.167

DRGGDTSDTESSIIIR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DRGGDTSDTESSIIIR**
Found in **SP100_MOUSE** in **SwissProt**, Nuclear autoantigen Sp-100 OS=Mus musculus GN=Sp100 PE=1 SV=2

Match to Query 3916: 1800.789957 from(601.270595,3+) index(1376)
Title: Elution from: 40.341 to 40.341 scan no 3021 cid35.00 polarity:+



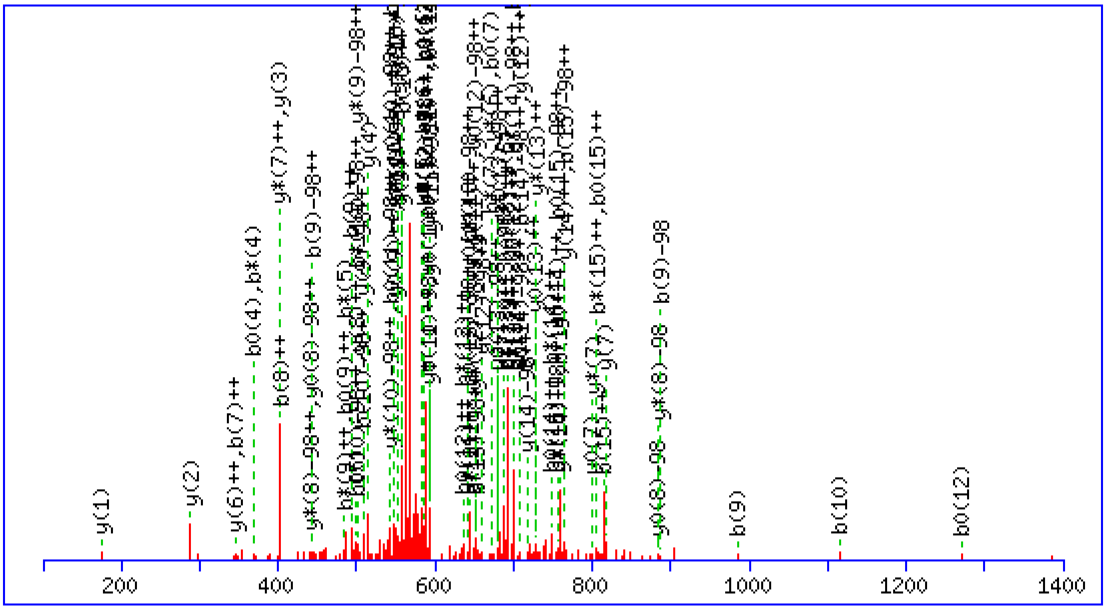
Monoisotopic mass of neutral peptide Mr(calc): 1800.7891
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.039
Matched b ions: b(4), b(5), b(8), b(9), b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(6), y(7), y(8)++, y(9)++, y(10)-98++, y(11)++, y(12)++, y(13)-98++, y(14)++

Peptide No.168

DRGGDTSDTESSIIIR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **DRGGDTSDTESSIIIR**
Found in **SP100_MOUSE** in **SwissProt**, Nuclear autoantigen Sp-100 OS=Mus musculus GN=Sp100 PE=1 SV=2

Match to Query 4523: 1800.789414 from(601.270414,3+) index(5005)
Title: Elution from: 40.388 to 40.388 scan no 3170 cid35.00 polarity:+:m1s



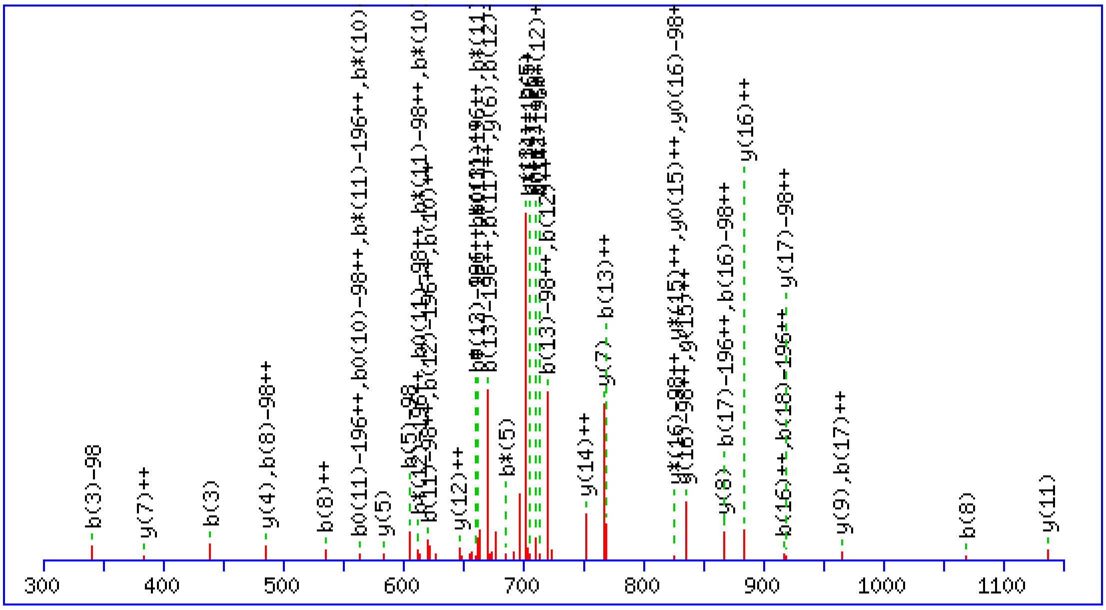
Monoisotopic mass of neutral peptide Mr(calc): 1800.7891
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0097
Matched b ions: b(5), b(7), b(7)++, b(8)++, b(9), b(9)-98, b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(6), y(6)++, y(7), y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++

Peptide No.169

DRSPSPLRGNVVPSPLPTR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **DRSPSPLRGNVVPSPLPTR**
Found in **CHSP1_MOUSE** in **SwissProt**, Calcium-regulated heat stable protein 1 OS=Mus musculus GN=Carhsp1 PE=1 SV=1

Match to Query 5762: 2204.050290 from(735.690706,3+) index(6129)
Title: Elution from: 39.431 to 39.431 scan no 3892 cid35.00 polarity:+:m1s



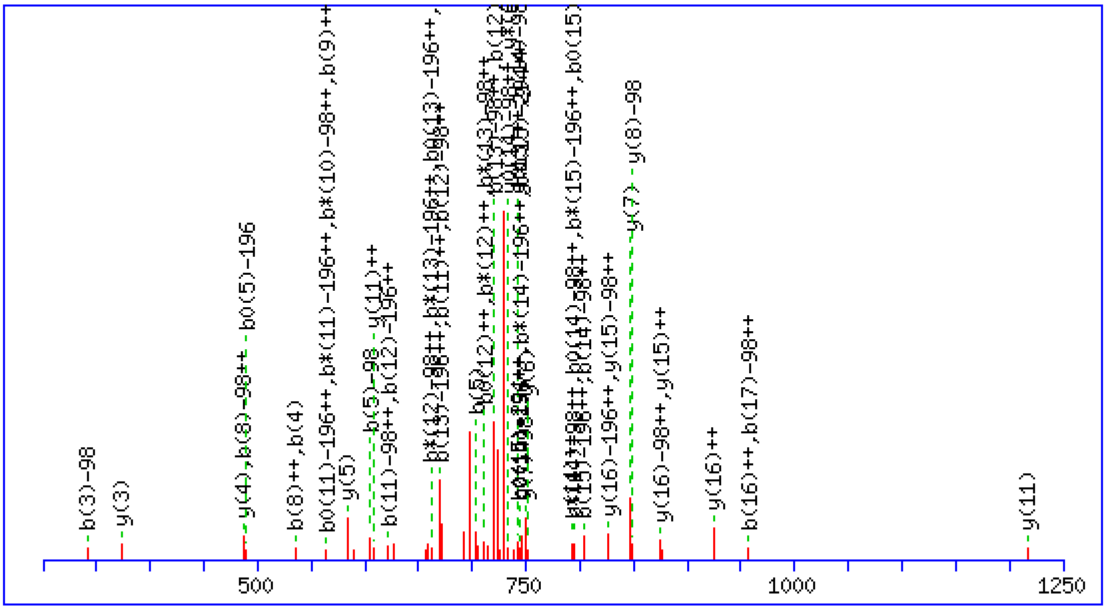
Monoisotopic mass of neutral peptide Mr(calc): 2204.0504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 7.5e-006
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(8)-98++, b(8)++, b(8), b(9)++, b(10)++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(18)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8), y(9), y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++

Peptide No.170

DRSPSPLRGNVVPSPLPTR
Confirmed sites: @S:3,@S:5,@S:14
Ambiguous sites:

MS/MS Fragmentation of **DRSPSPLRGNVVPSPLPTR**
Found in **CHSP1_MOUSE** in **SwissProt**, Calcium-regulated heat stable protein 1 OS=Mus musculus GN=Carhsp1 PE=1 SV=1

Match to Query 5954: 2284.014060 from(762.345296,3+) index(6253)
Title: Elution from: 41.218 to 41.218 scan no 4125 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2284.0167

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 29 **Expect:** 0.0083

Matched b ions: b(3)-98, b(4), b(5)-98, b(5), b(8)-98++, b(8)++, b(9)++, b(11)-98++, b(11)++, b(12)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)-196++, b(14)-98++, b(15)-196++, b(16)++, b(17)-98++

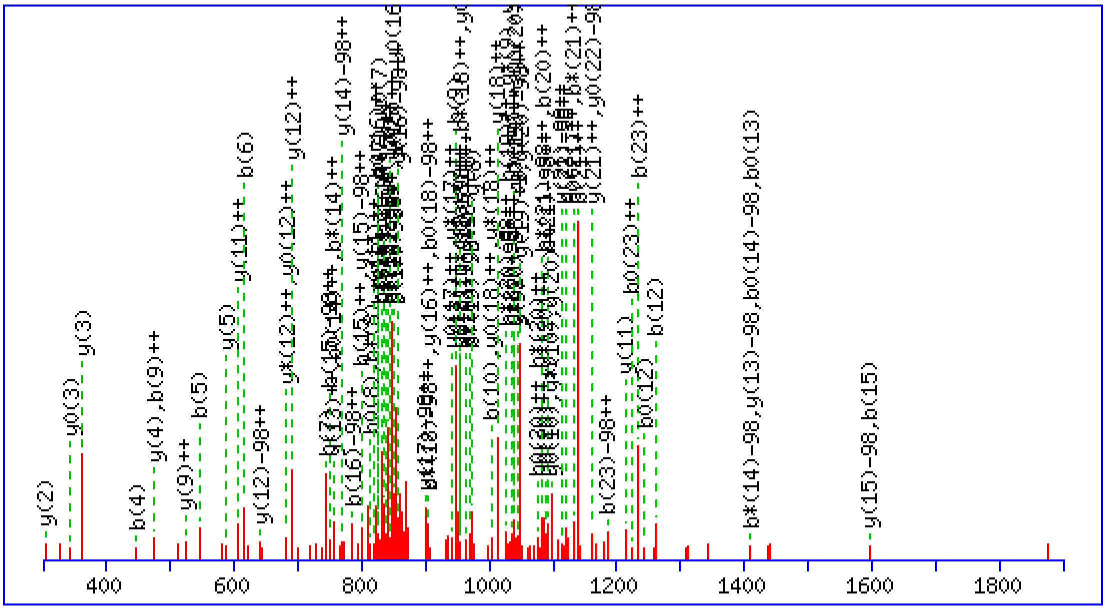
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(11), y(11)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++

Peptide No.171

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **DSDQVAQSDGEESPAAEEQLLGER**
Found in **SC31A_MOUSE** in **SwissProt**, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 5495: 2639.084637 from(880.702155,3+) index(4809)
Title: Elution from: 50.875 to 50.875 scan no 4015 cid35.00 polarity:+:m1s



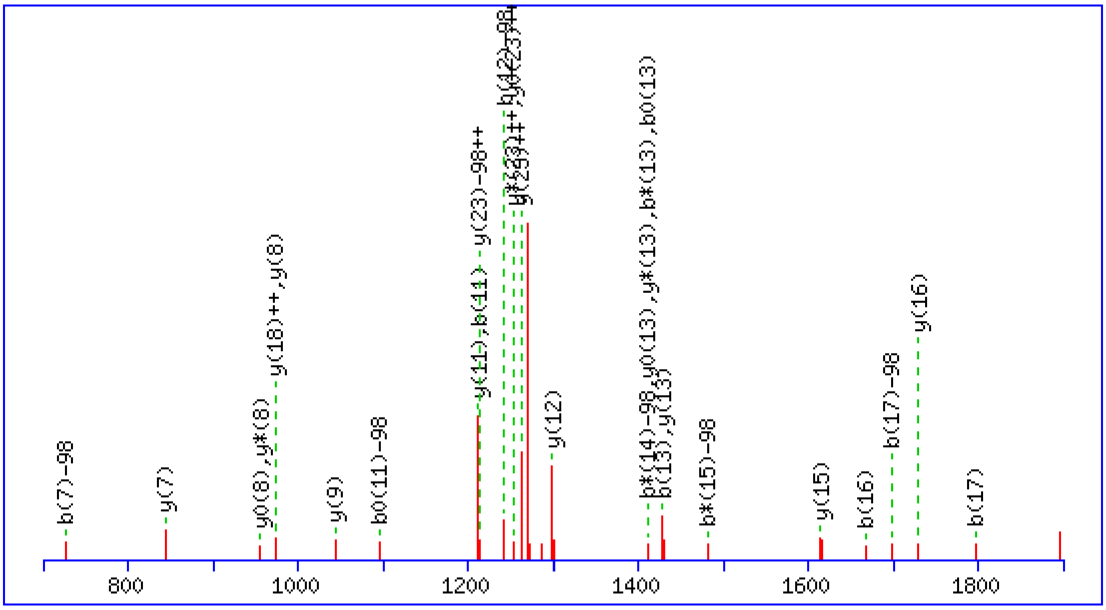
Monoisotopic mass of neutral peptide Mr(calc): 2639.0872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 **Expect:** 4.2e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)++, b(9), b(10), b(11), b(12), b(15), b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9)++, y(9), y(11)++, y(11), y(12)++, y(12)-98++, y(13)++, y(13)-98, y(14)-98++, y(14)++, y(15)++, y(15)-98, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++

Peptide No.172

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **DSDQVAQSDGEESPAAEEQLLGER**
Found in **SC31A_MOUSE** in **SwissProt**, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 5393: 2639.081206 from(1320.547879,2+) index(5417)
Title: Elution from: 44.805 to 44.805 scan no 4388 cid35.00 polarity:+:m1s



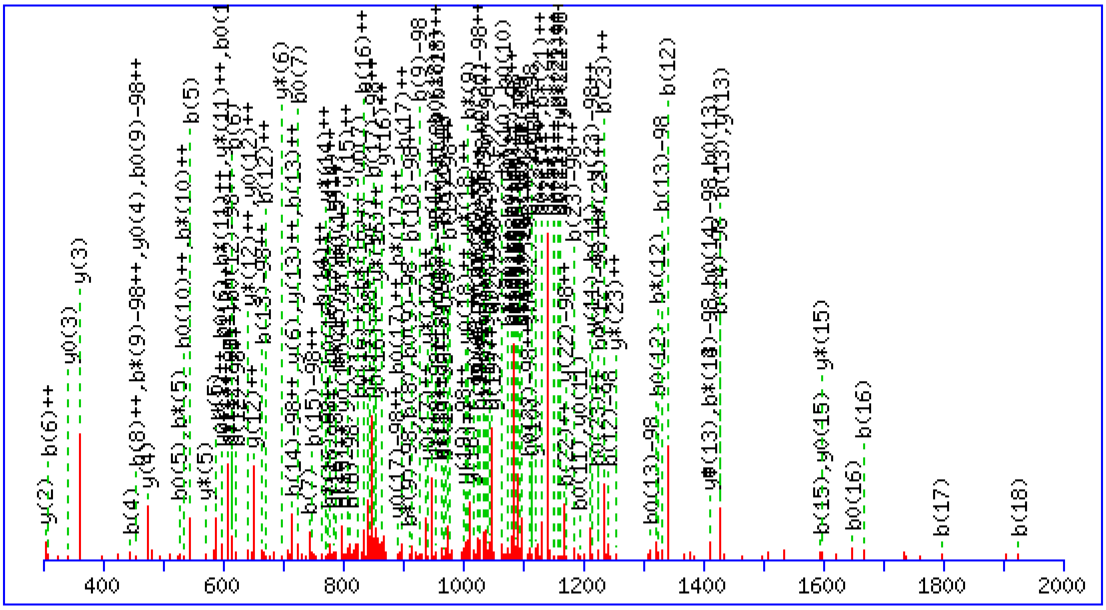
Monoisotopic mass of neutral peptide Mr(calc): 2639.0872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 4.5e-006
Matched b ions: b(7)-98, b(11), b(12)-98, b(13), b(16), b(17)-98, b(17)
Matched y ions: y(7), y(8), y(9), y(11), y(12), y(13), y(15), y(16), y(18)++, y(23)-98++, y(23)++

Peptide No.173

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **DSDQVAQSDGEESPAAEEQLLGER**
Found in **SC31A_MOUSE** in **SwissProt**, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 5499: 2639.087595 from(880.703141,3+) index(4891)
Title: Elution from: 53.049 to 53.049 scan no 4202 cid35.00 polarity:+:m1s



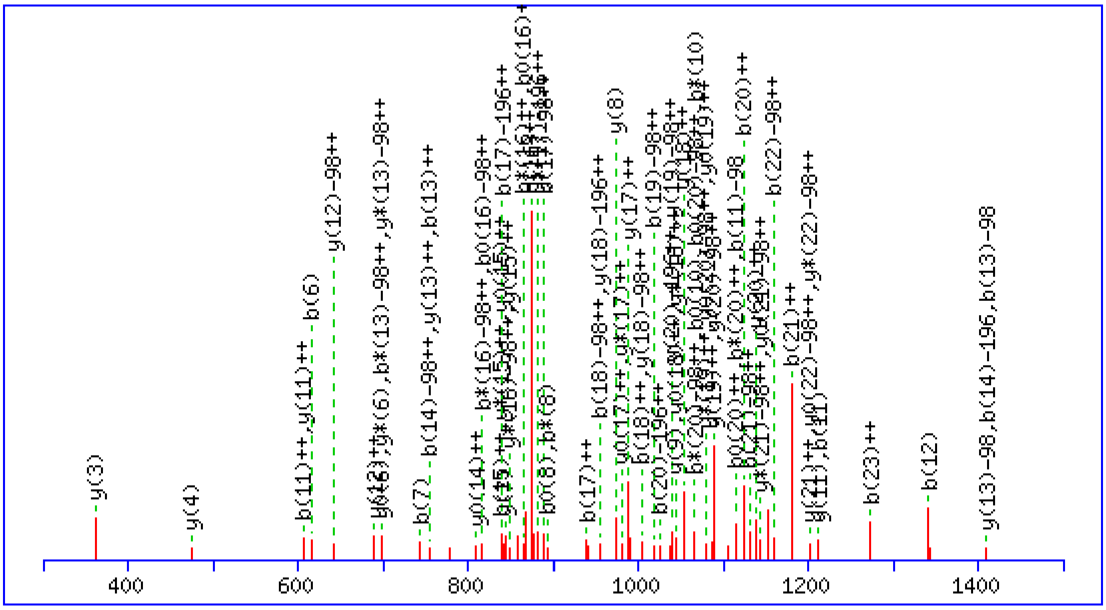
Monoisotopic mass of neutral peptide Mr(calc): 2639.0872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 87 **Expect:** 1.3e-008
Matched b ions: b(4), b(5), b(6), b(6)++, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)-98, b(10), b(11)++, b(11), b(11)-98, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)++, b(13), b(13)-98++, b(13)-98, b(14)-98++, b(14)-98, b(14)++, b(15)++, b(15), b(15)-98++, b(16), b(16)++, b(16)-98++, b(17), b(17)-98++, b(17)++, b(18), b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(12)++, y(13)++, y(13), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(22)-98++, y(23)-98++

Peptide No.174

DSDQVAQSDGEESPAAEEQLLGER
Confirmed sites: @S:8,@S:13
Ambiguous sites:

MS/MS Fragmentation of **DSDQVAQSDGEESPAAEEQLLGER**
Found in **SC31A_MOUSE** in **SwissProt**, Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2

Match to Query 5646: 2719.051785 from(907.357871,3+) index(5786)
Title: Elution from: 47.678 to 47.678 scan no 4672 cid35.00 polarity:+:m1s



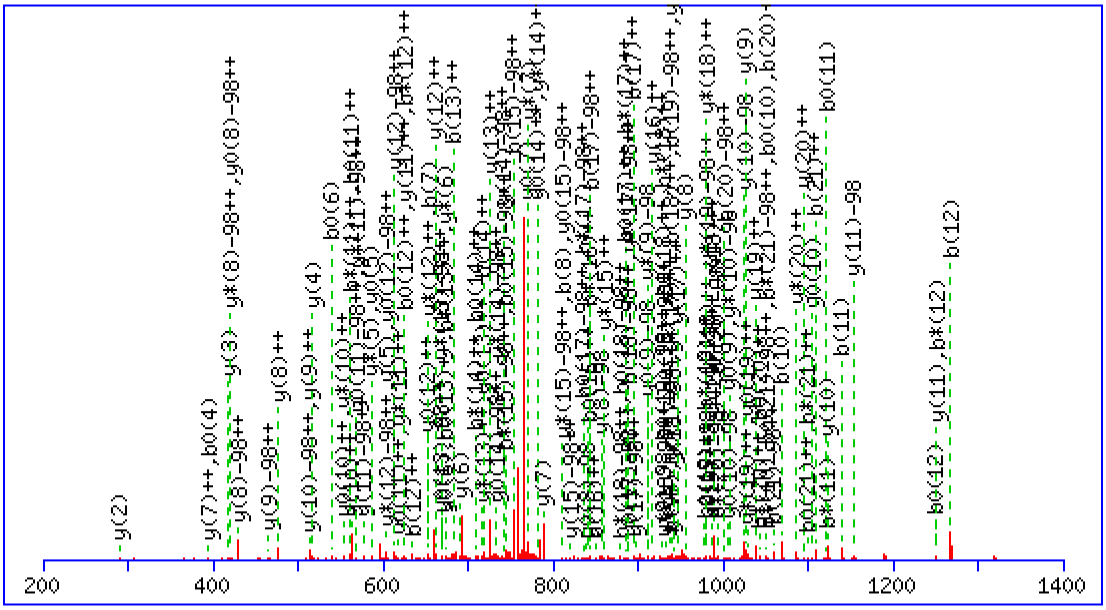
Monoisotopic mass of neutral peptide Mr(calc): 2719.0535
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 6.2e-007
Matched b ions: b(6), b(7), b(11)++, b(11), b(11)-98, b(12), b(13)-98, b(13)++, b(14)-196, b(14)-98++, b(15)++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-98++, b(18)++, b(19)-98++, b(20)++, b(20)-196++, b(21)++, b(21)-98++, b(22)-98++, b(23)++
Matched y ions: y(3), y(4), y(7), y(8), y(9), y(11)++, y(11), y(12)++, y(12)-98++, y(13)-98, y(13)++, y(15)++, y(17)++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++, y(21)++

Peptide No.175

DSLPSGPREEAKPASPSSVQDR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **DSLPSGPREEAKPASPSSVQDR**
Found in **MIA3_MOUSE** in **SwissProt**, Melanoma inhibitory activity protein 3 OS=Mus musculus GN=Mia3 PE=1 SV=2

Match to Query 5166: 2389.089624 from(797.370484,3+) index(3931)
Title: Elution from: 24.242 to 24.242 scan no 1789 cid35.00 polarity:+:m1s



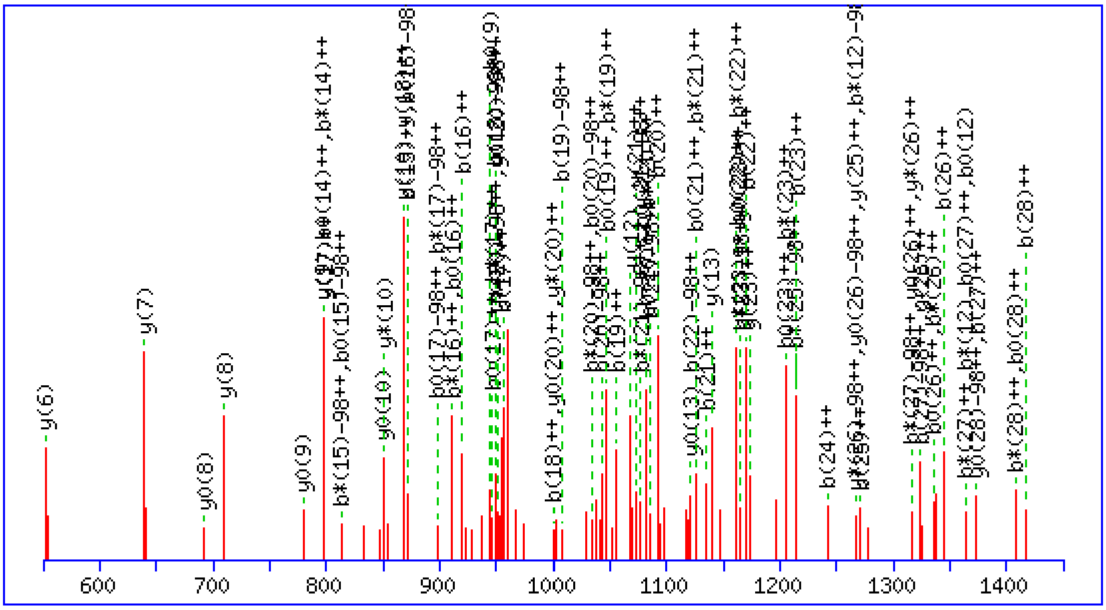
Monoisotopic mass of neutral peptide Mr(calc): 2389.0911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0035
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(13)++, b(14)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)-98++, y(8)-98, y(8)++, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10)++, y(10), y(10)-98++, y(10)-98, y(11), y(11)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(15)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++

Peptide No.176

DSQDTSAEQSDHDDEVASLASASGGFGSK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DSQDTSAEQSDHDDEVASLASASGGFGSK**
Found in **EDC4_MOUSE** in **SwissProt**, Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2

Match to Query 6718: 2977.173246 from(993.398358,3+) index(6331)
Title: Elution from: 44.545 to 44.545 scan no 4512 cid35.00 polarity:+:m1s



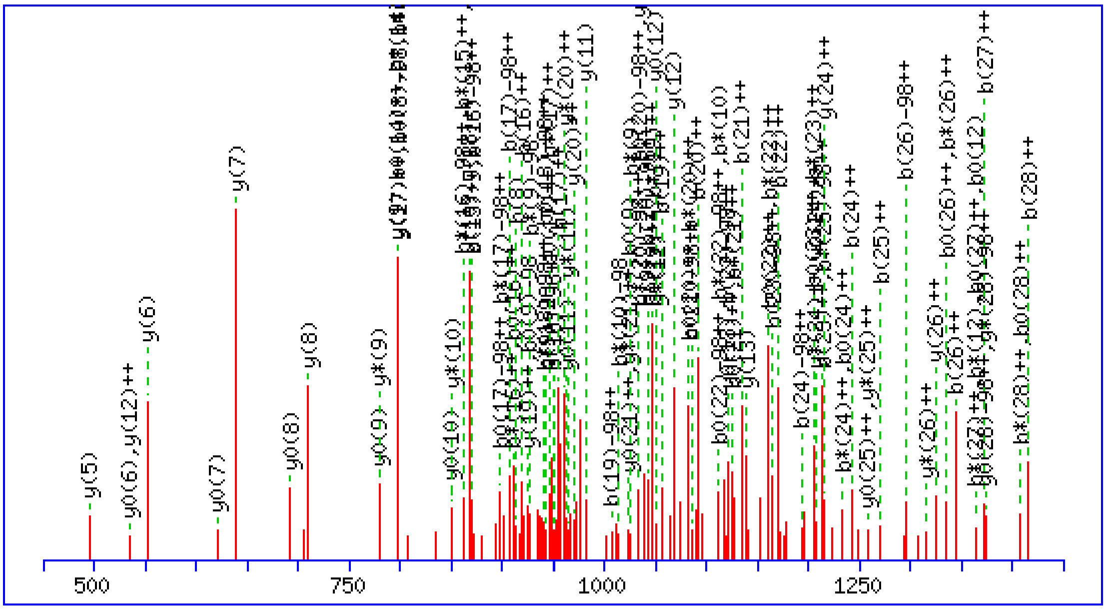
Monoisotopic mass of neutral peptide Mr(calc): 2977.1734
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 **Expect:** 4.2e-007
Matched b ions: b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(25)++, b(26)++, b(27)-98++, b(27)++, b(28)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(12), y(13), y(17)++, y(18)++, y(21)++, y(23)++, y(25)++, y(26)++

Peptide No.177

DSQDTSAEQSDHDDEVASLASASGGFGSK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DSQDTSAEQSDHDDEVASLASASGGFGSK**
Found in **EDC4_MOUSE** in **SwissProt**, Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2

Match to Query 5873: 2977.167120 from(993.396316,3+) index(5580)
Title: Elution from: 43.694 to 43.694 scan no 4244 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2977.1734

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 64 **Expect:** 2.3e-006

Matched b ions: b(8), b(9), b(9)-98, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(24)-98++, b(25)++, b(26)++, b(26)-98++, b(27)++, b(28)++

Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(24)++, y(26)++

Peptide No.178

DSSTSPGDYVLSVSENSR

Confirmed sites:

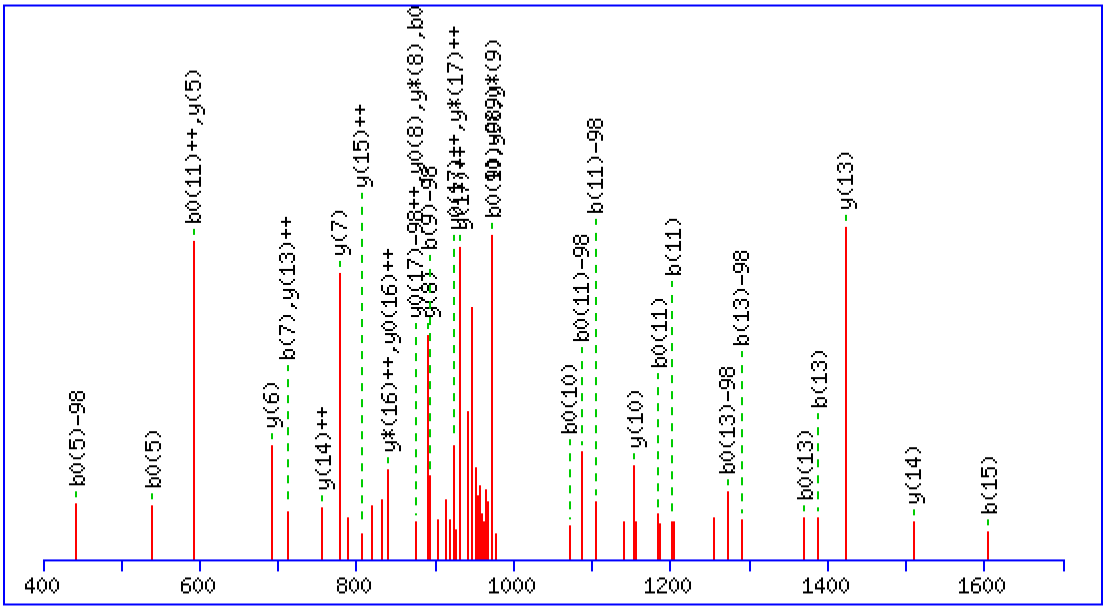
Ambiguous sites: @S:2orS:3

MS/MS Fragmentation of **DSSTSPGDYVLSVSENSR**

Found in **CRK_MOUSE** in **SwissProt**, Adapter molecule crk OS=Mus musculus GN=Crk PE=1 SV=1

Match to Query 4930: 1978.816742 from(990.415647,2+) index(6744)

Title: Elution from: 48.722 to 48.722 scan no 5044 cid35.00 polarity:+:m1s



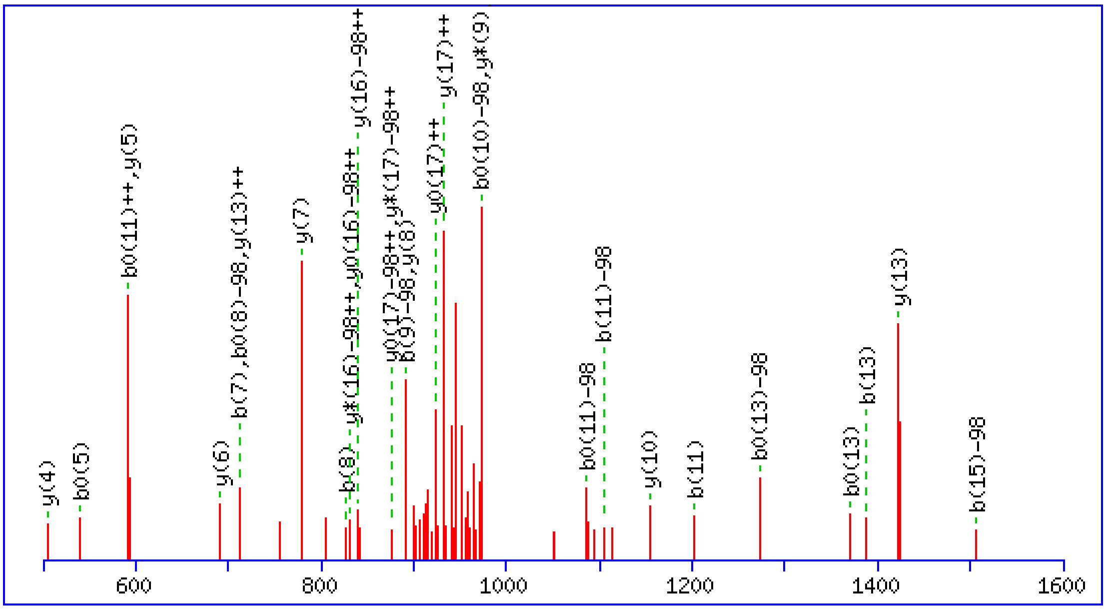
Monoisotopic mass of neutral peptide Mr(calc): 1978.8157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00025
Matched b ions: b(7), b(9)-98, b(11)-98, b(11), b(13)-98, b(13), b(15)
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(13), y(13)++, y(14), y(14)++, y(15)++, y(17)++

Peptide No.179

DSSTSPGDYVLSVSENSR
Confirmed sites:
Ambiguous sites: @S:3orT:4orS:5

MS/MS Fragmentation of **DSSTSPGDYVLSVSENSR**
Found in **CRK_MOUSE** in **SwissProt**, Adapter molecule crk OS=Mus musculus GN=Crk PE=1 SV=1

Match to Query 4793: 1978.814980 from(990.414766,2+) index(6568)
Title: Elution from: 48.752 to 48.752 scan no 5006 cid35.00 polarity:+:m1s



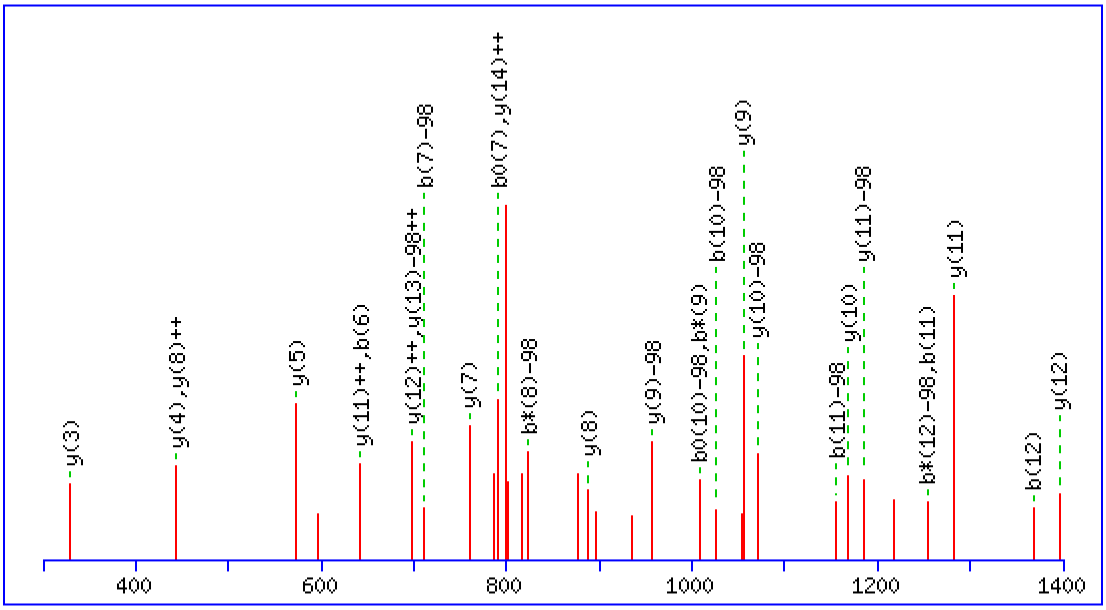
Monoisotopic mass of neutral peptide Mr(calc): 1978.8157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 9e-005
Matched b ions: b(7), b(8), b(9)-98, b(11), b(11)-98, b(13), b(15)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(13), y(13)++, y(16)-98++, y(17)++

Peptide No.180

DSVINLSESVEDGPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **DSVINLSESVEDGPR**
Found in **MA2A1_MOUSE** in **SwissProt**, Alpha-mannosidase 2 OS=Mus musculus GN=Man2a1 PE=1 SV=2

Match to Query 3169: 1695.736170 from(848.875361,2+) index(2531)
Title: Elution from: 44.514 to 44.514 scan no 4334 cid35.00 polarity:+



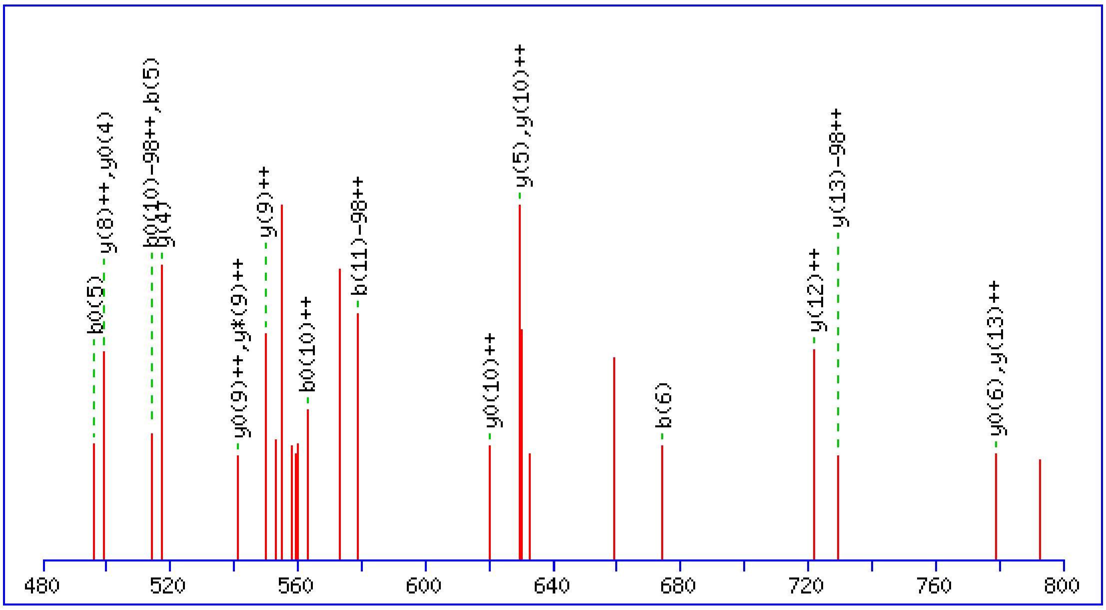
Monoisotopic mass of neutral peptide Mr(calc): 1695.7353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 1.1e-006
Matched b ions: b(6), b(7)-98, b(10)-98, b(11), b(11)-98, b(12)
Matched y ions: y(3), y(4), y(5), y(7), y(8)++, y(8), y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)++, y(11)-98, y(12)++, y(12), y(13)-98++, y(14)++

Peptide No.181

DTIALCTAESIDNLR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **DTIALCTAESIDNLR**
Found in **AT11C_MOUSE** in **SwissProt**, Probable phospholipid-transporting ATPase 11C OS=Mus musculus GN=Atp11c PE=1 SV=2

Match to Query 3454: 1770.787755 from(591.269861,3+) index(5838)
Title: Elution from: 48.596 to 48.596 scan no 4773 cid35.00 polarity:+:m1s



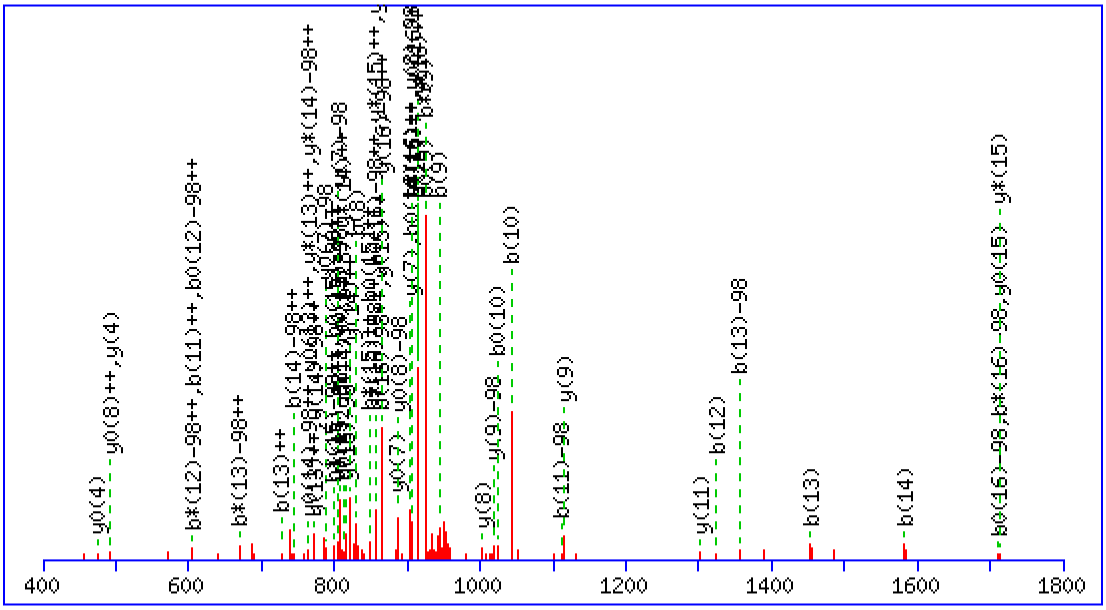
Monoisotopic mass of neutral peptide Mr(calc): 1770.7859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(5), b(6), b(11)-98++
Matched y ions: y(4), y(5), y(8)++, y(9)++, y(10)++, y(12)++, y(13)++, y(13)-98++

Peptide No.182

DTSPDKGELVSDEEEDT
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **DTSPDKGELVSDEEEDT**
Found in **TBD2B_MOUSE** in **SwissProt**, TBC1 domain family member 2B OS=Mus musculus GN=Tbc1d2b PE=1 SV=2

Match to Query 3991: 1944.734238 from(973.374395,2+) index(4553)
Title: Elution from: 30.398 to 30.398 scan no 2612 cid35.00 polarity:+:m1s



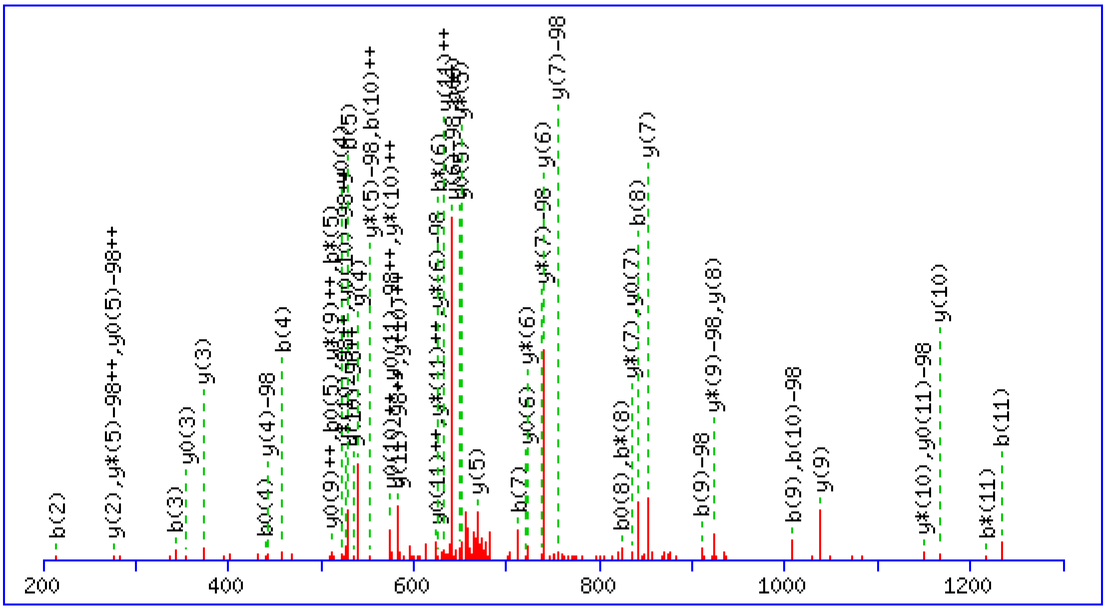
Monoisotopic mass of neutral peptide Mr(calc): 1944.7361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.001
Matched b ions: b(8), b(9), b(10), b(11)++, b(11)-98, b(12), b(13), b(13)-98, b(13)++, b(14), b(14)-98++, b(15)-98++, b(15), b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(11), y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.183

DVQDAIAQSPEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **DVQDAIAQSPEK**
Found in **SLTM_MOUSE** in **SwissProt**, SAFB-like transcription modulator OS=Mus musculus GN=Sltm PE=1 SV=1

Match to Query 2730: 1379.597398 from(690.805975,2+) index(699)
Title: Elution from: 32.122 to 32.122 scan no 2054 cid35.00 polarity:+



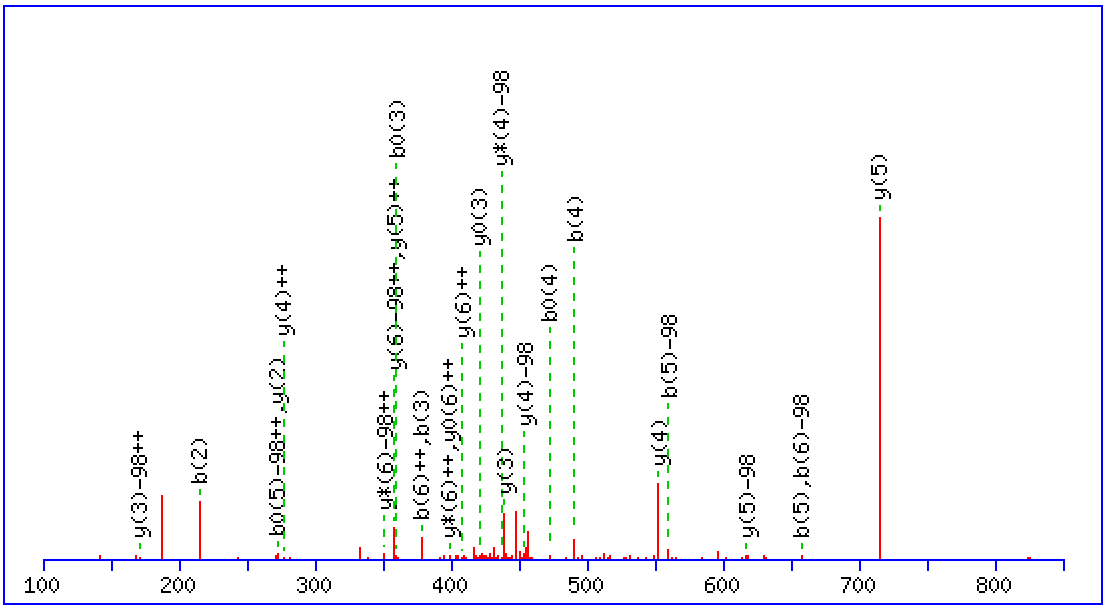
Monoisotopic mass of neutral peptide Mr(calc): 1379.5970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 **Expect:** 4.8e-008
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)-98, b(10)-98, b(10)++, b(11)
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(10)++, y(10), y(10)-98++, y(11)-98++, y(11)++

Peptide No.184

DVYLSPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **DVYLSPR**
Found in **RMXL1_MOUSE** in **SwissProt**, RNA binding motif protein, X-linked-like-1 OS=Mus musculus GN=Rbmxl1 PE=1 SV=1

Match to Query 583: 928.406212 from(465.210382,2+) index(915)
Title: Elution from: 34.645 to 34.645 scan no 2354 cid35.00 polarity:+



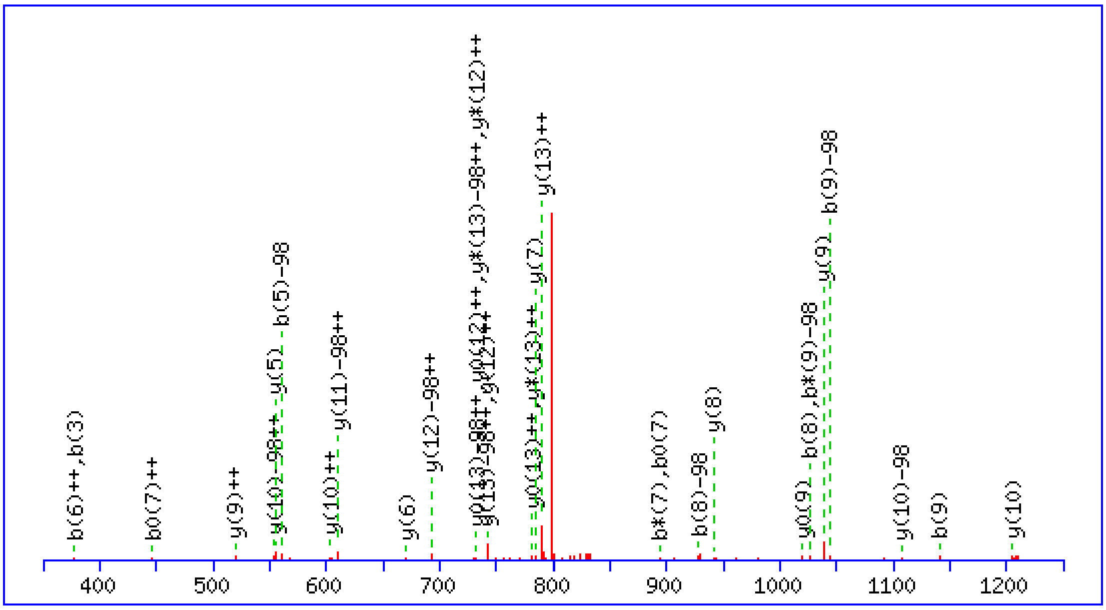
Monoisotopic mass of neutral peptide Mr(calc): 928.4055
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0042
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(6)++
Matched y ions: y(2), y(3), y(3)-98++, y(4), y(4)++, y(4)-98, y(5), y(5)++, y(5)-98, y(6)-98++, y(6)++

Peptide No.185

DVYLSPRDDGYSTK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **DVYLSPRDDGYSTK**
Found in **RMXL1_MOUSE** in **SwissProt**, RNA binding motif protein, X-linked-like-1 OS=Mus musculus GN=Rbmxl1 PE=1 SV=1

Match to Query 3621: 1694.718360 from(848.366456,2+) index(5116)
Title: Elution from: 30.997 to 30.997 scan no 2734 cid35.00 polarity:+:m1s



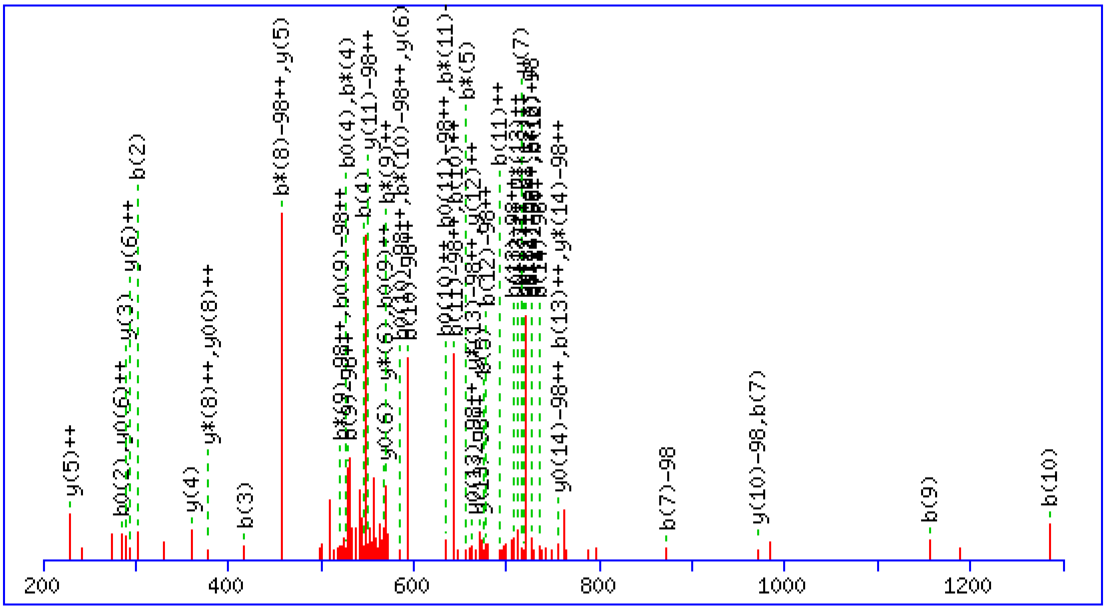
Monoisotopic mass of neutral peptide Mr(calc): 1694.7189
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.002
Matched b ions: b(3), b(5)-98, b(6)++, b(8)-98, b(8), b(9), b(9)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++

Peptide No.186

DWDKESEGEEPAGGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DWDKESEGEEPAGGR**
Found in **RRP15_MOUSE** in **SwissProt**, RRP15-like protein OS=Mus musculus GN=Rrp15 PE=2 SV=2

Match to Query 3445: 1740.662898 from(581.228242,3+) index(3568)
Title: Elution from: 23.440 to 23.440 scan no 1581 cid35.00 polarity:+:m1s



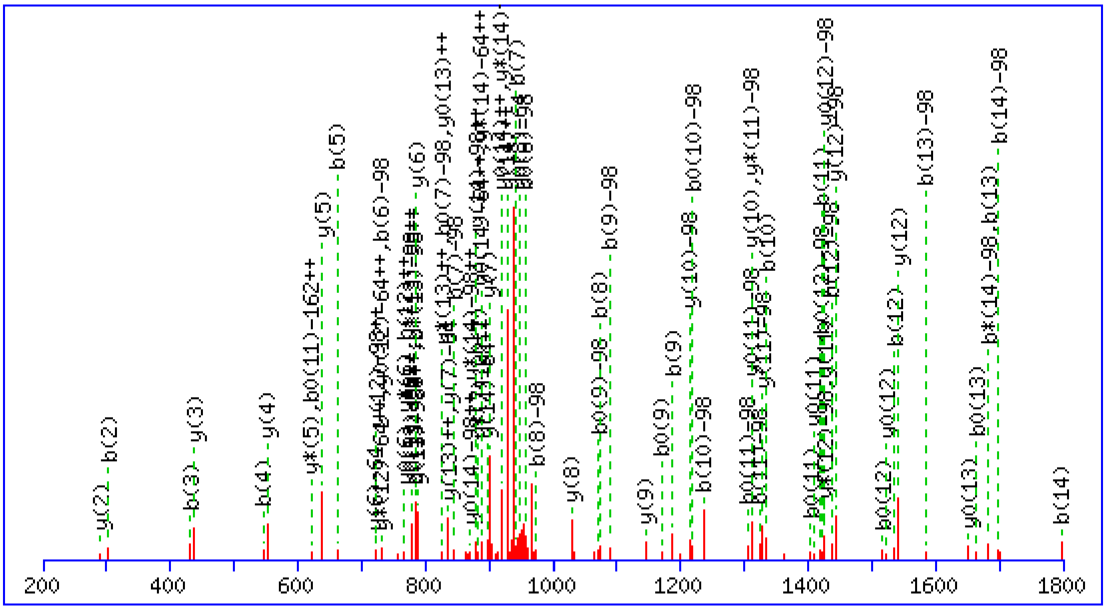
Monoisotopic mass of neutral peptide Mr(calc): 1740.6628
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.013
Matched b ions: b(2), b(3), b(4), b(5), b(7)-98, b(7), b(9), b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(10)-98, y(11)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.187

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DWEDDSDEDMSNFDR**
Found in **TEBP_MOUSE** in **SwissProt**, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 4753: 1970.612908 from(986.313730,2+) index(2328)
Title: Elution from: 38.257 to 38.257 scan no 3708 cid35.00 polarity:+



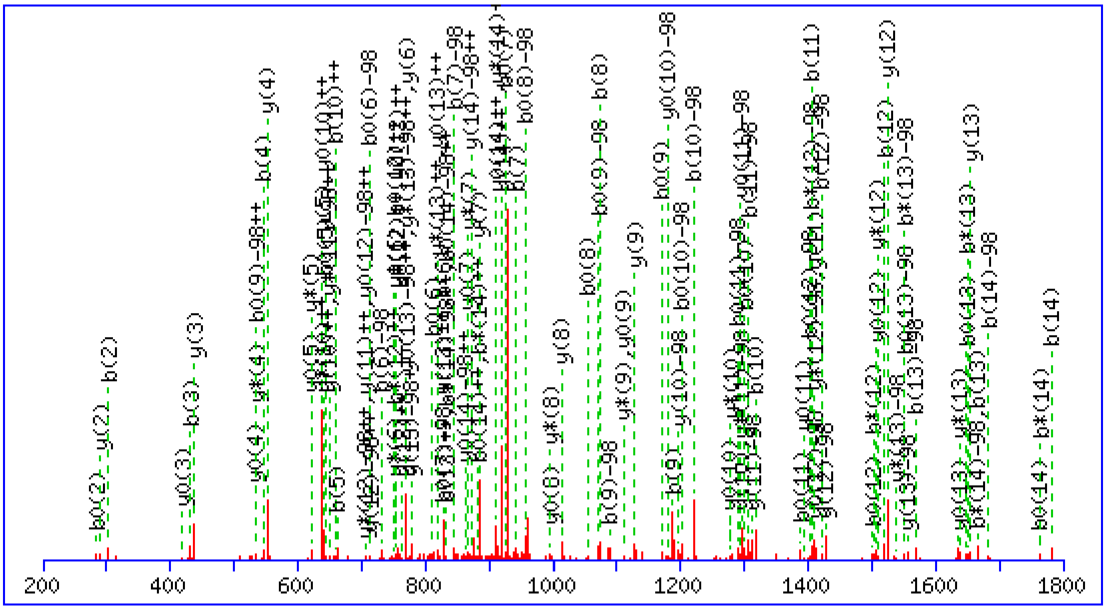
Monoisotopic mass of neutral peptide Mr(calc): 1970.6150
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 94 **Expect:** 4.2e-010
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(11), y(12)-98, y(12), y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++

Peptide No.188

DWEDDSDEDMSNFDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **DWEDDSDEDMSNFDR**
Found in **TEBP_MOUSE** in **SwissProt**, Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1

Match to Query 4670: 1954.616792 from(978.315672,2+) index(6464)
Title: Elution from: 46.740 to 46.740 scan no 4774 cid35.00 polarity:+:m1s



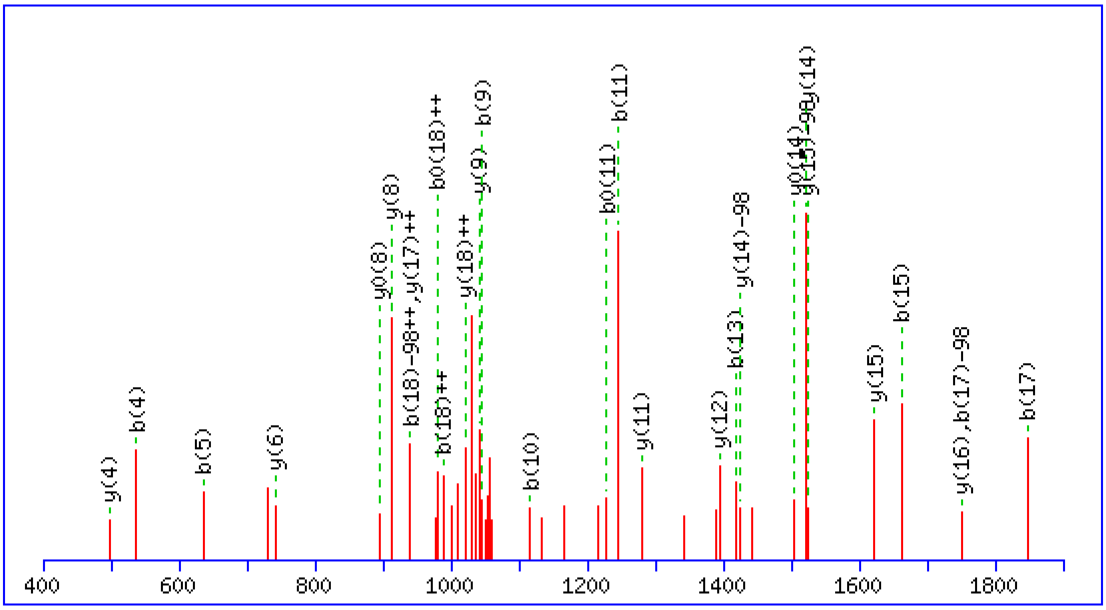
Monoisotopic mass of neutral peptide Mr(calc): 1954.6200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 88 **Expect:** 1.6e-009
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)-98, b(7)-98, b(7), b(8), b(9)-98, b(9), b(10)-98, b(10), b(10)++, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(13)++, b(14), b(14)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(13), y(13)-98, y(14)++, y(14)-98++

Peptide No.189

DYEEVGADSAEGDDEGEEY
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **DYEEVGADSAEGDDEGEEY**
Found in **TBA1C_MOUSE** in **SwissProt**, Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1

Match to Query 4613: 2157.702316 from(1079.858434,2+) index(5153)
Title: Elution from: 40.210 to 40.210 scan no 3834 cid35.00 polarity:+:m1s



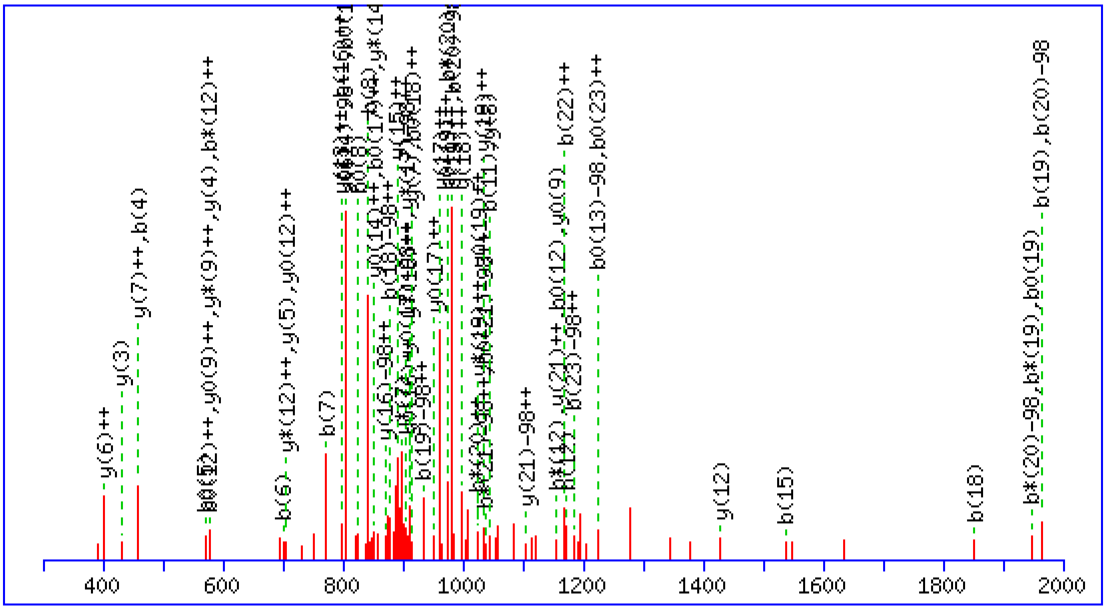
Monoisotopic mass of neutral peptide Mr(calc): 2157.7059
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 1.7e-007
Matched b ions: b(4), b(5), b(9), b(10), b(11), b(13), b(15), b(17)-98, b(17), b(18)-98++, b(18)++
Matched y ions: y(4), y(6), y(8), y(9), y(11), y(12), y(14), y(14)-98, y(15), y(15)-98, y(16), y(17)++, y(18)++

Peptide No.190

EAEEELAASGGQSPTGEQIPQFQQR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **EAEEELAASGGQSPTGEQIPQFQQR**
Found in **MACF1_MOUSE** in **SwissProt**, Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=2

Match to Query 5605: 2766.212655 from(923.078161,3+) index(4773)
Title: Elution from: 49.554 to 49.554 scan no 3915 cid35.00 polarity:+:m1s



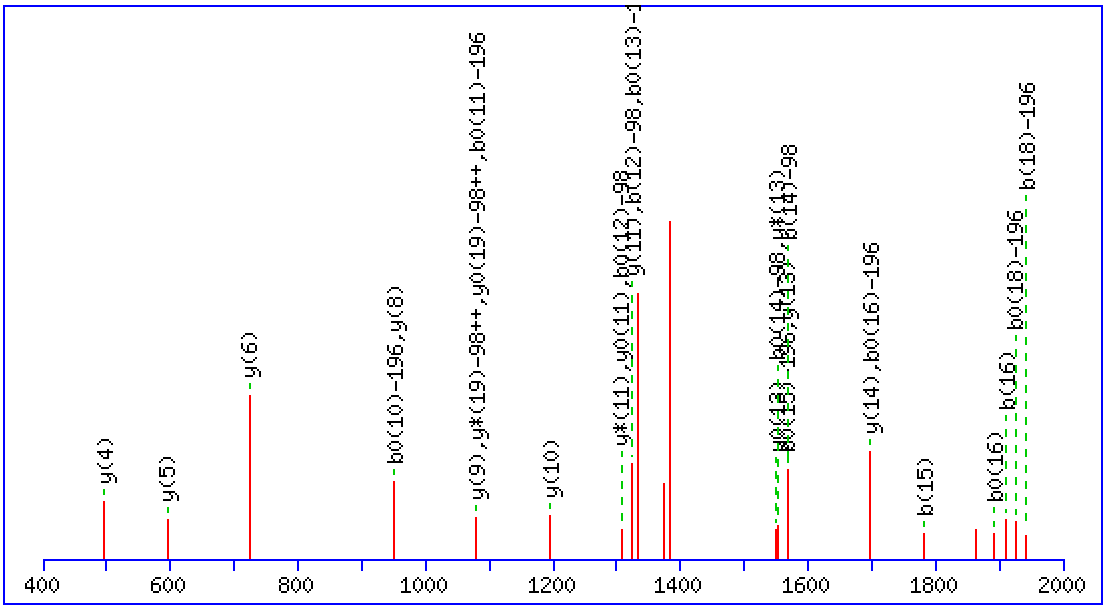
Monoisotopic mass of neutral peptide Mr(calc): 2766.2134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.001
Matched b ions: b(4), b(6), b(7), b(8), b(11), b(12), b(15), b(16)++, b(18), b(18)-98++, b(19)++, b(19), b(19)-98++, b(20)-98++, b(20)-98, b(22)++, b(23)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(12), y(13)++, y(15)++, y(16)-98++, y(17)++, y(18)++, y(19)++, y(21)++, y(21)-98++

Peptide No.191

EAEEESSGGEEEDEDENIEVVYSK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **EAEEESSGGEEEDEDENIEVVYSK**
Found in **IF5_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Eif5 PE=1 SV=1

Match to Query 5615: 2861.017656 from(1431.516104,2+) index(5401)
Title: Elution from: 44.543 to 44.543 scan no 4355 cid35.00 polarity:+:m1s



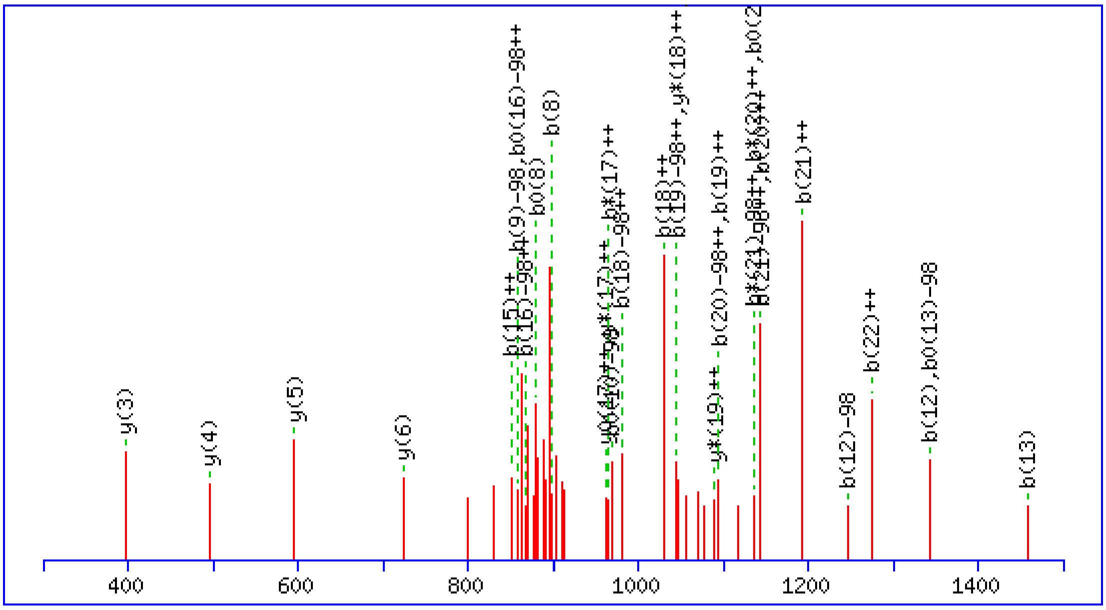
Monoisotopic mass of neutral peptide Mr(calc): 2861.0212
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 **Expect:** 5e-006
Matched b ions: b(12)-98, b(14)-98, b(15), b(16), b(18)-196
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(13), y(14)

Peptide No.192

EAEEESSGGEEEDEDENIEVVYSK
Confirmed sites:
Ambiguous sites: @S:6orS:7

MS/MS Fragmentation of **EAEEESSGGEEEDEDENIEVVYSK**
Found in **IF5_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5 OS=Mus musculus GN=Eif5 PE=1 SV=1

Match to Query 5734: 2781.053937 from(928.025255,3+) index(5322)
Title: Elution from: 39.447 to 39.447 scan no 3760 cid35.00 polarity:+:m1s



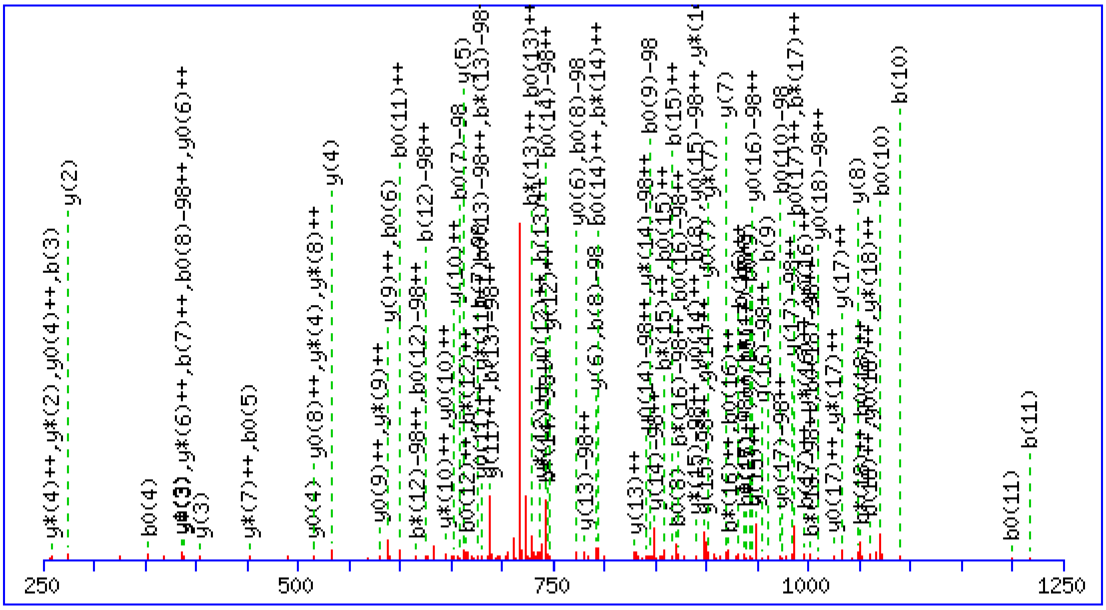
Monoisotopic mass of neutral peptide Mr(calc): 2781.0549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.029
Matched b ions: b(8), b(9)-98, b(12), b(12)-98, b(13), b(15)++, b(16)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++
Matched y ions: y(3), y(4), y(5), y(6)

Peptide No.193

EAGIVHSDAEKEQEEEEQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **EAGIVHSDAEKEQEEEEQK**
Found in **PININ_MOUSE** in **SwissProt**, Pinin OS=Mus musculus GN=Pnn PE=1 SV=4

Match to Query 5767: 2263.943655 from(755.655161,3+) index(4028)
Title: Elution from: 20.824 to 20.824 scan no 1349 cid35.00 polarity:+:m1s



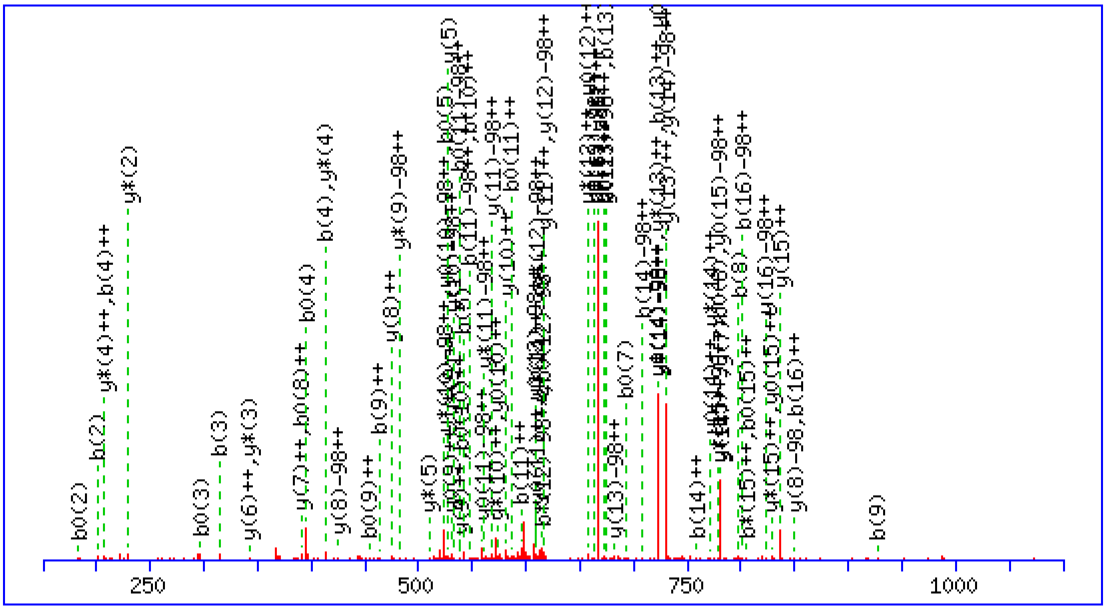
Monoisotopic mass of neutral peptide Mr(calc): 2263.9481
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00018
Matched b ions: b(3), b(7)++, b(7)-98, b(8)-98, b(8), b(9), b(10), b(11), b(12)-98++, b(13)-98++, b(13)++, b(15)++, b(16)++, b(17)++, b(18)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.194

EALVEPASESPRPALAR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **EALVEPASESPRPALAR**
Found in **NHRF1_MOUSE** in **SwissProt**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3

Match to Query 4710: 1871.914164 from(624.978664,3+) index(4901)
Title: Elution from: 38.938 to 38.938 scan no 3004 cid35.00 polarity:+:m1s



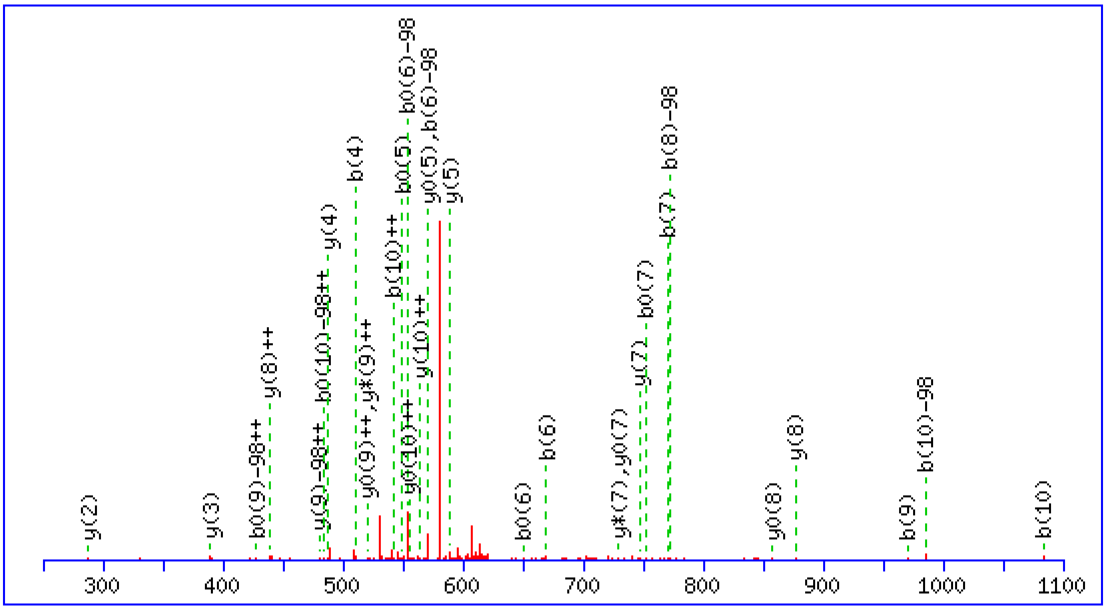
Monoisotopic mass of neutral peptide Mr(calc): 1871.9142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0084
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(8), b(9), b(9)++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(16)-98++, b(16)++
Matched y ions: y(5), y(6)++, y(7)++, y(7), y(8)++, y(8)-98++, y(8)-98, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)-98++

Peptide No.195

EATEGTTVTLR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **EATEGTTVTLR**
Found in **OBSCN_MOUSE** in **SwissProt**, Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2

Match to Query 1772: 1256.566656 from(629.290604,2+) index(1241)
Title: Elution from: 27.343 to 27.343 scan no 2236 cid35.00 polarity:+



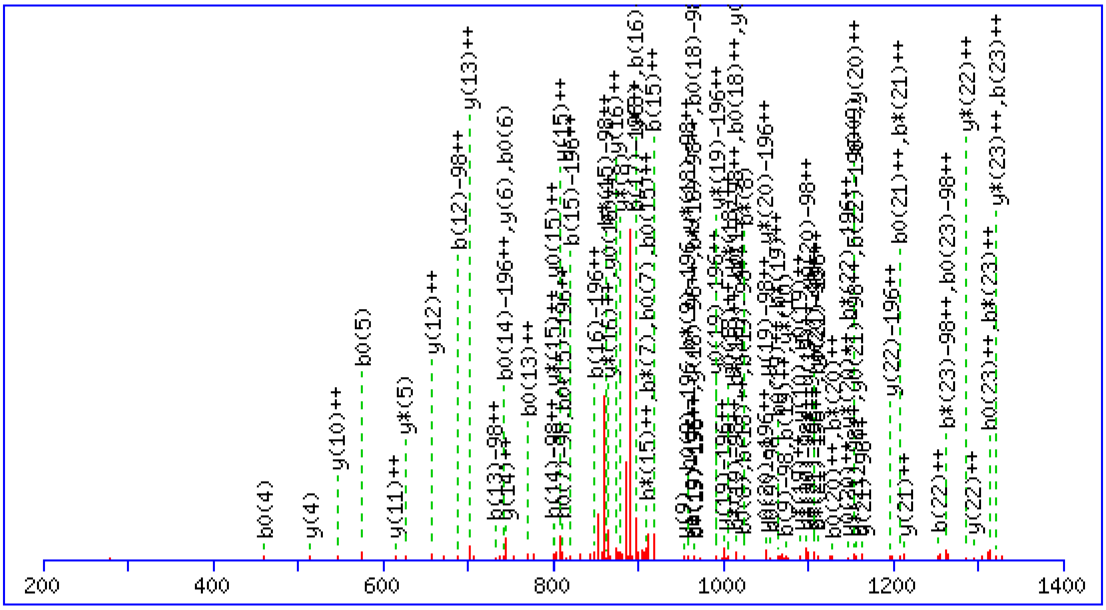
Monoisotopic mass of neutral peptide Mr(calc): 1256.5650
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.049
Matched b ions: b(4), b(6)-98, b(6), b(7), b(8)-98, b(9), b(10)-98, b(10), b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)++, y(8), y(9)-98++, y(10)++

Peptide No.196

EAYNDSSDEESSSHHGPGVQCAHQ
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **EAYNDSSDEESSSHHGPGVQCAHQ**
Found in **DNJA2_MOUSE** in **SwissProt**, DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1

Match to Query 5742: 2786.949036 from(929.990288,3+) index(3526)
Title: Elution from: 20.773 to 20.773 scan no 1322 cid35.00 polarity:+:m1s



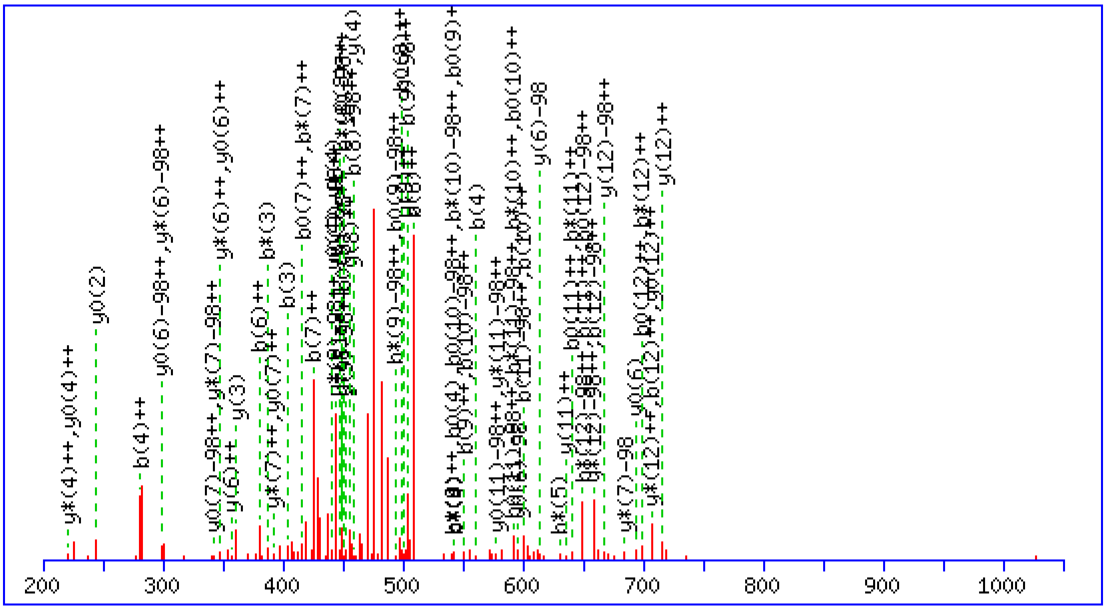
Monoisotopic mass of neutral peptide Mr(calc): 2786.9541
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00033
Matched b ions: b(9)-98, b(12)-98++, b(13)-98++, b(14)-98++, b(15)++, b(15)-196++, b(16)-98++, b(16)-196++, b(17)-196++, b(18)++, b(19)++, b(19)-98++, b(22)-196++, b(22)++, b(23)++
Matched y ions: y(4), y(6), y(8), y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(18)++, y(18)-98++, y(19)-196++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-196++

Peptide No.197

ECNRSNSSSPVDK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **ECNRSNSSSPVDK**
Found in **GPBP1_MOUSE** in **SwissProt**, Vasculin OS=Mus musculus GN=Gpbp1 PE=1 SV=1

Match to Query 2682: 1558.609776 from(520.543868,3+) index(2210)
Title: Elution from: 39.290 to 39.290 scan no 3739 cid35.00 polarity:+



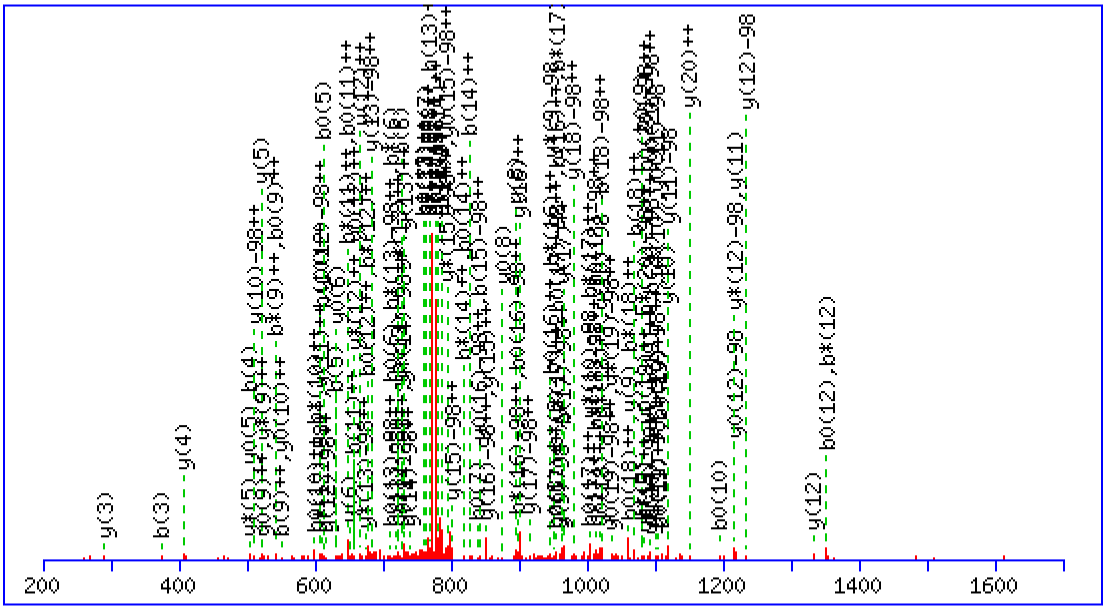
Monoisotopic mass of neutral peptide Mr(calc): 1558.6083
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0014
Matched b ions: b(3), b(4)++, b(4), b(6)++, b(7)++, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(3), y(4), y(6)++, y(6)-98, y(8)++, y(9)-98++, y(9)++, y(11)++, y(12)++, y(12)-98++

Peptide No.198

EDEEKPKIEDVGSDEEDDSGK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **EDEEKPKIEDVGSDEEDDSGK**
Found in **HS90B_MOUSE** in **SwissProt**, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3

Match to Query 6149: 2428.966236 from(810.662688,3+) index(4146)
Title: Elution from: 30.863 to 30.863 scan no 1998 cid35.00 polarity:+:m1s



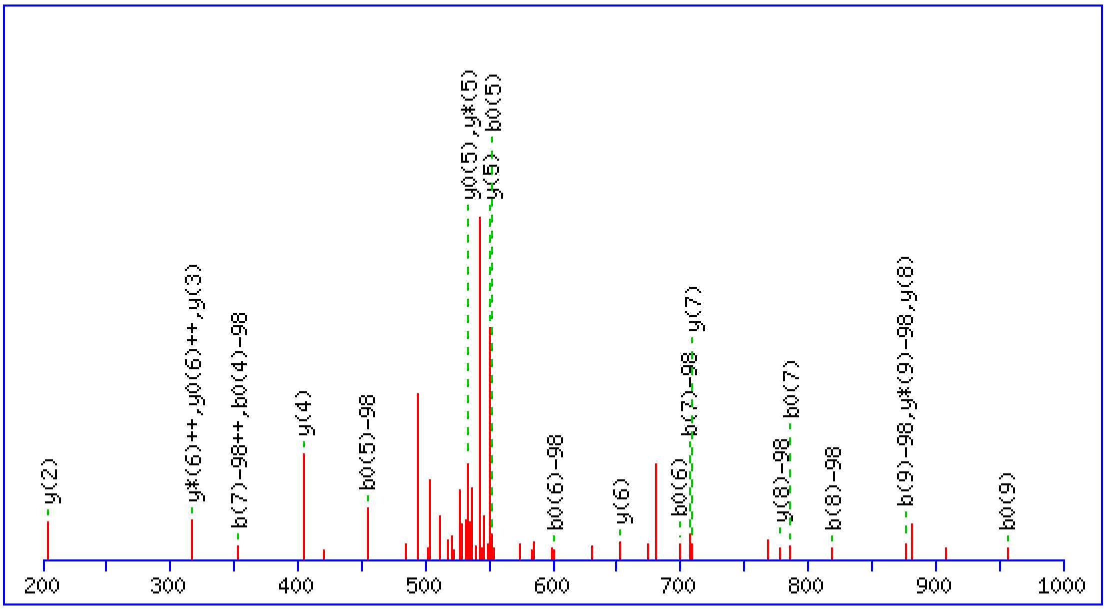
Monoisotopic mass of neutral peptide Mr(calc): 2428.9642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0033
Matched b ions: b(3), b(4), b(5), b(6), b(9)++, b(10)++, b(11)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(10)-98++, y(11), y(11)-98, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(19)++, y(20)-98++, y(20)++

Peptide No.199

EDSGTFSLGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **EDSGTFSLGK**
Found in **PRKRA_MOUSE** in **SwissProt**, Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1

Match to Query 1077: 1119.448400 from(560.731476,2+) index(1591)
Title: Elution from: 31.945 to 31.945 scan no 2815 cid35.00 polarity:+



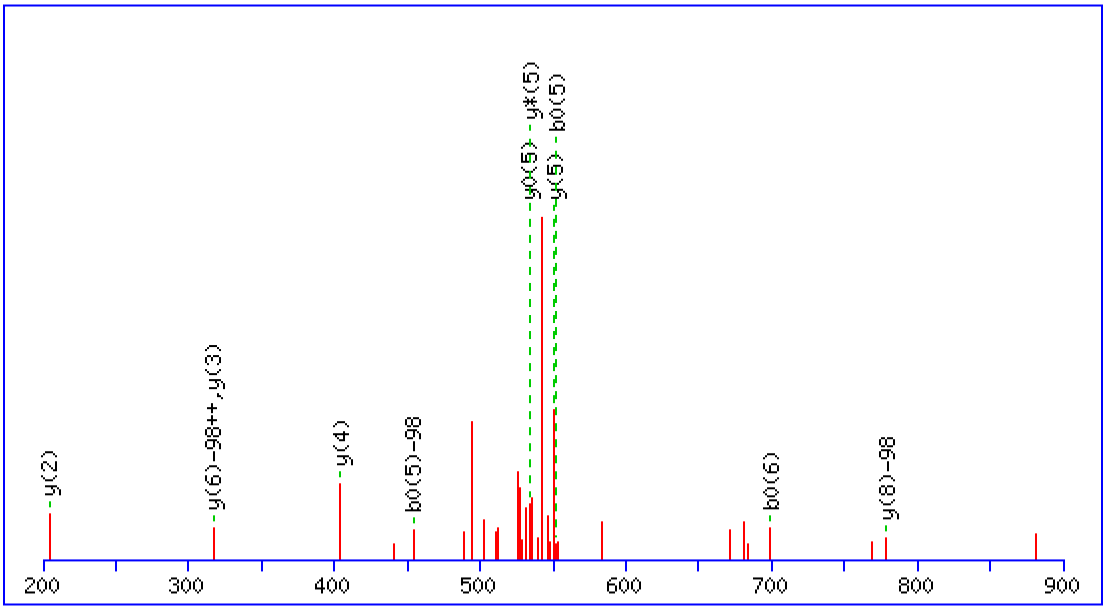
Monoisotopic mass of neutral peptide Mr(calc): 1119.4485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00022
Matched b ions: b(7)-98, b(7)-98++, b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98

Peptide No.200

EDSGTFSLGK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **EDSGTFSLGK**
Found in **PRKRA_MOUSE** in **SwissProt**, Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1

Match to Query 1169: 1119.448258 from(560.731405,2+) index(1728)
Title: Elution from: 32.284 to 32.284 scan no 2908 cid35.00 polarity:+



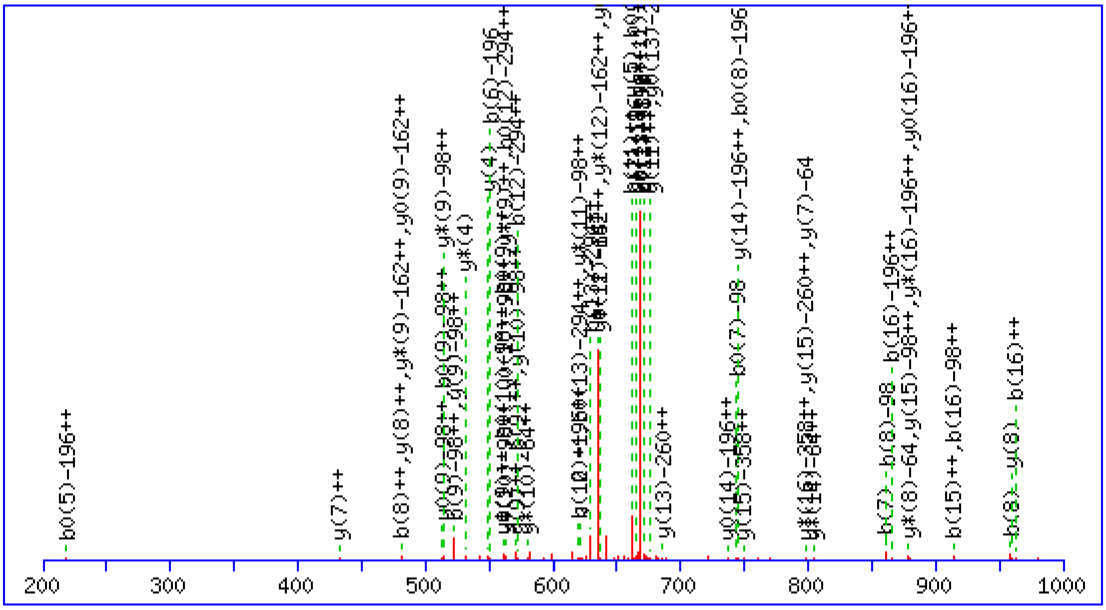
Monoisotopic mass of neutral peptide Mr(calc): 1119.4485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.011
Matched b ions:
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98++, y(8)-98

Peptide No.201

EDSGTPLVTPSLLQMVR
Confirmed sites: @S:3,@T:5,@T:9
Ambiguous sites:

MS/MS Fragmentation of **EDSGTPLVTPSLLQMVR**
Found in **K1522_MOUSE** in **SwissProt**, Uncharacterized protein KIAA1522 OS=Mus musculus GN=Kiaa1522 PE=1 SV=1

Match to Query 5298: 2097.847773 from(700.289867,3+) index(209)
Title: Elution from: 17.878 to 17.878 scan no 995 cid35.00 polarity:+



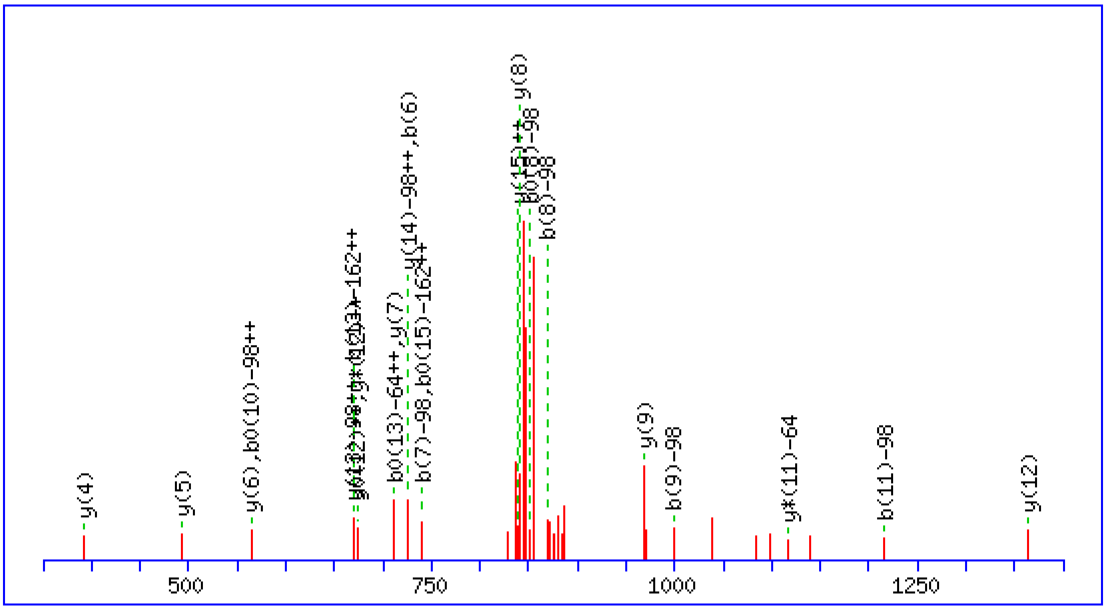
Monoisotopic mass of neutral peptide Mr(calc): 2097.8496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M15 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.036
Matched b ions: b(6)-196, b(7), b(7)-196, b(8), b(8)++, b(8)-98, b(9)-98++, b(9)++, b(11)++, b(12)-98++, b(12)-294++, b(12)-196++, b(13)-294++, b(15)++, b(16)++, b(16)-98++, b(16)-196++
Matched y ions: y(4), y(5), y(7)++, y(8)++, y(8), y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(11)++, y(12)-98++, y(14)-196++, y(15)-98++

Peptide No.202

EELASDLEEMATSSAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **EELASDLEEMATSSAK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4225: 1805.725722 from(903.870137,2+) index(6660)
Title: Elution from: 47.271 to 47.271 scan no 4872 cid35.00 polarity:+:m1s



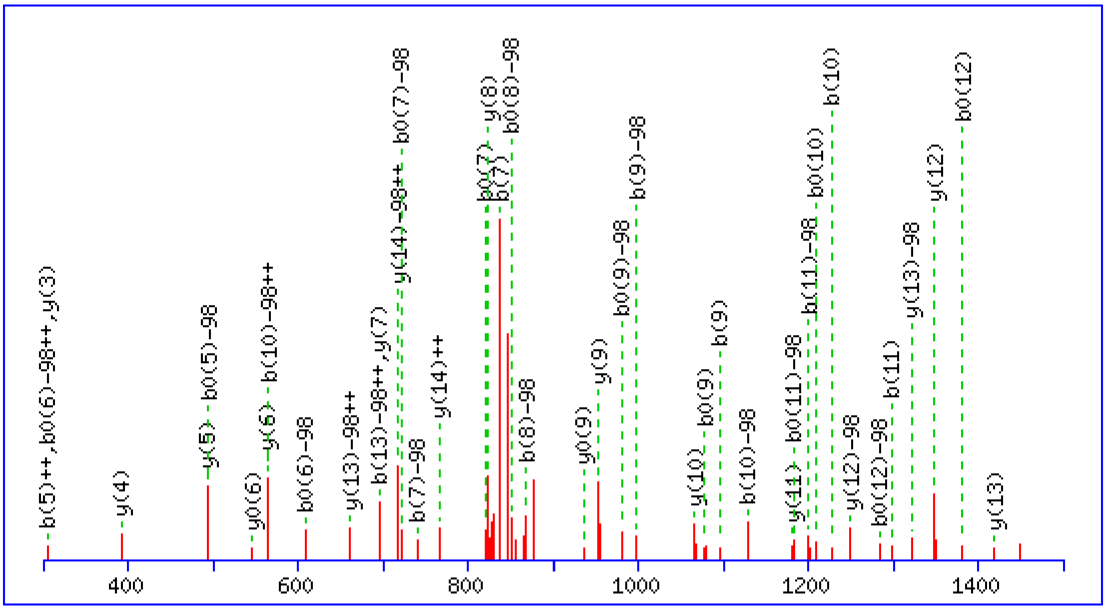
Monoisotopic mass of neutral peptide Mr(calc): 1805.7278
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.0078
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)-98, b(11)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12), y(13)-98++, y(14)-98++, y(15)++

Peptide No.203

EELASDLEEMATSSAK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **EELASDLEEMATSSAK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4165: 1789.733596 from(895.874074,2+) index(7121)
Title: Elution from: 60.953 to 60.953 scan no 6215 cid35.00 polarity:+:m1s



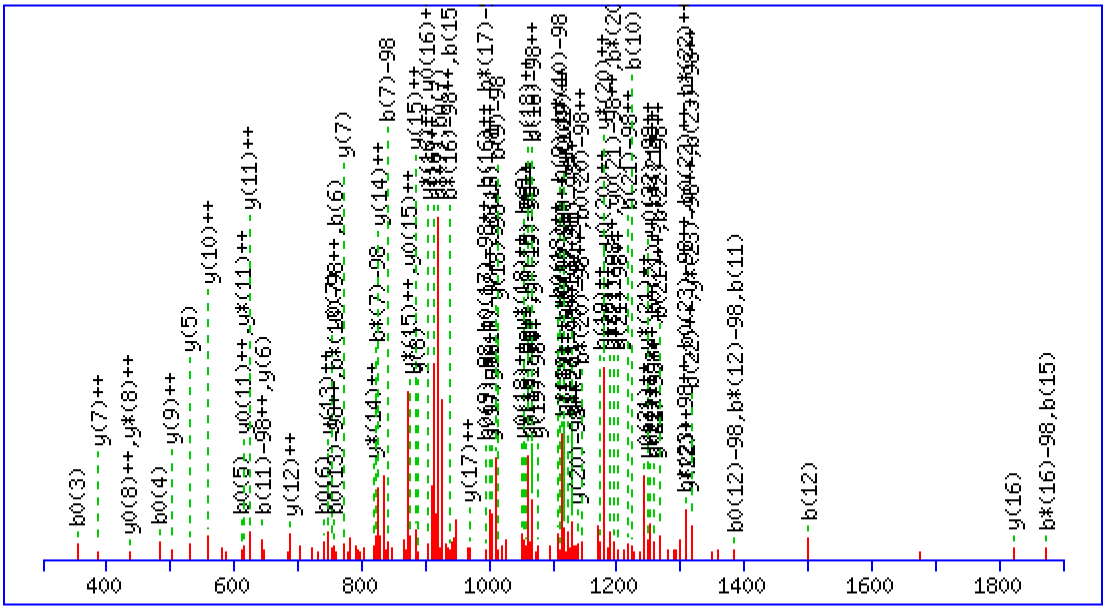
Monoisotopic mass of neutral peptide Mr(calc): 1789.7328
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 **Expect:** 3.8e-008
Matched b ions: b(5)++, b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(11)-98, b(11), b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)-98++, y(13)-98, y(13), y(14)-98++, y(14)++

Peptide No.204

EELEQQTDGDCDEEDDDKDGEVPK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **EELEQQTDGDCDEEDDDKDGEVPK**
Found in **SEC62_MOUSE** in **SwissProt**, Translocation protein SEC62 OS=Mus musculus GN=Sec62 PE=1 SV=1

Match to Query 5649: 2874.054111 from(959.025313,3+) index(3596)
Title: Elution from: 31.688 to 31.688 scan no 2000 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2874.0546

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 89 **Expect:** 5.1e-009

Matched b ions: b(6), b(7)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98++, b(12), b(15), b(15)++, b(16)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)-98++

Matched y ions: y(5), y(6), y(7)++, y(7), y(8), y(9), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16), y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-98++

Peptide No.205

EEVASEPEEAASPTTPK

Confirmed sites: @S:12

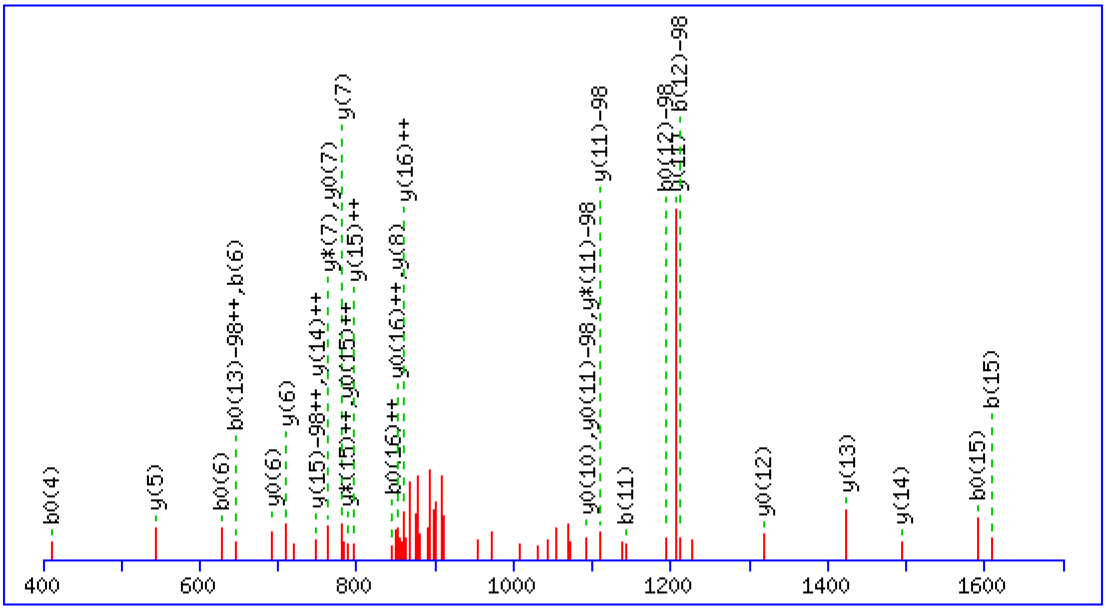
Ambiguous sites:

MS/MS Fragmentation of **EEVASEPEEAASPTTPK**

Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4254: 1850.778540 from(926.396546,2+) index(971)

Title: Elution from: 24.754 to 24.754 scan no 1884 cid35.00 polarity:+



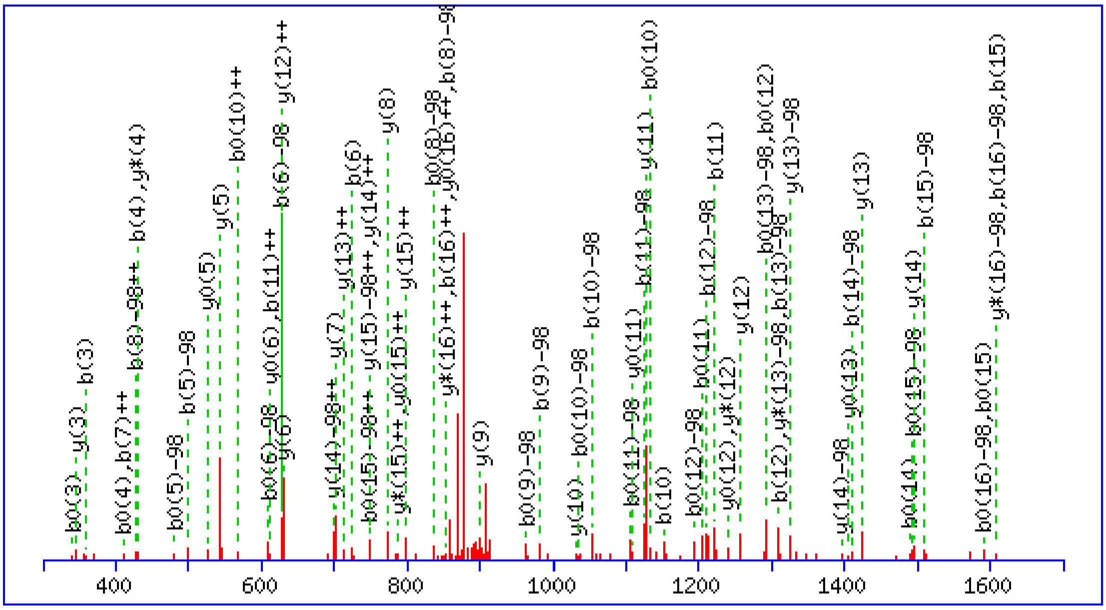
Monoisotopic mass of neutral peptide Mr(calc): 1850.7822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0049
Matched b ions: b(6), b(11), b(12)-98, b(15)
Matched y ions: y(5), y(6), y(7), y(8), y(11), y(11)-98, y(13), y(14), y(14)++, y(15)-98++, y(15)++, y(16)++

Peptide No.206

EEVASEPEEAASPTTPK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **EEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4645: 1850.781318 from(926.397935,2+) index(4324)
Title: Elution from: 32.777 to 32.777 scan no 2233 cid35.00 polarity:+:m1s



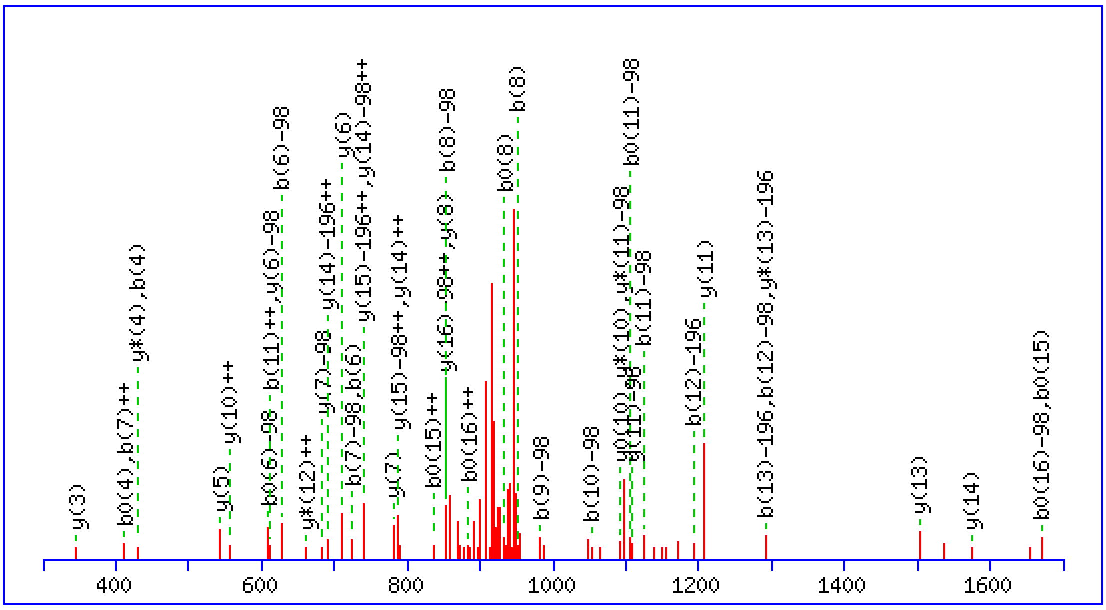
Monoisotopic mass of neutral peptide Mr(calc): 1850.7822
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 2.7e-008
Matched b ions: b(3), b(4), b(5)-98, b(6)-98, b(6), b(7)++, b(8)-98++, b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)++, b(12)-98, b(12), b(13)-98, b(14)-98, b(15)-98, b(15), b(16)-98, b(16)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13), y(13)++, y(13)-98, y(14), y(14)-98++, y(14)++, y(14)-98, y(15)++, y(15)-98++

Peptide No.207

EEVASEPEEAASPTTPK
Confirmed sites: @S:5,@S:12
Ambiguous sites:

MS/MS Fragmentation of **EEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 3951: 1930.743974 from(966.379263,2+) index(4229)
Title: Elution from: 26.993 to 26.993 scan no 2163 cid35.00 polarity:+:m1s



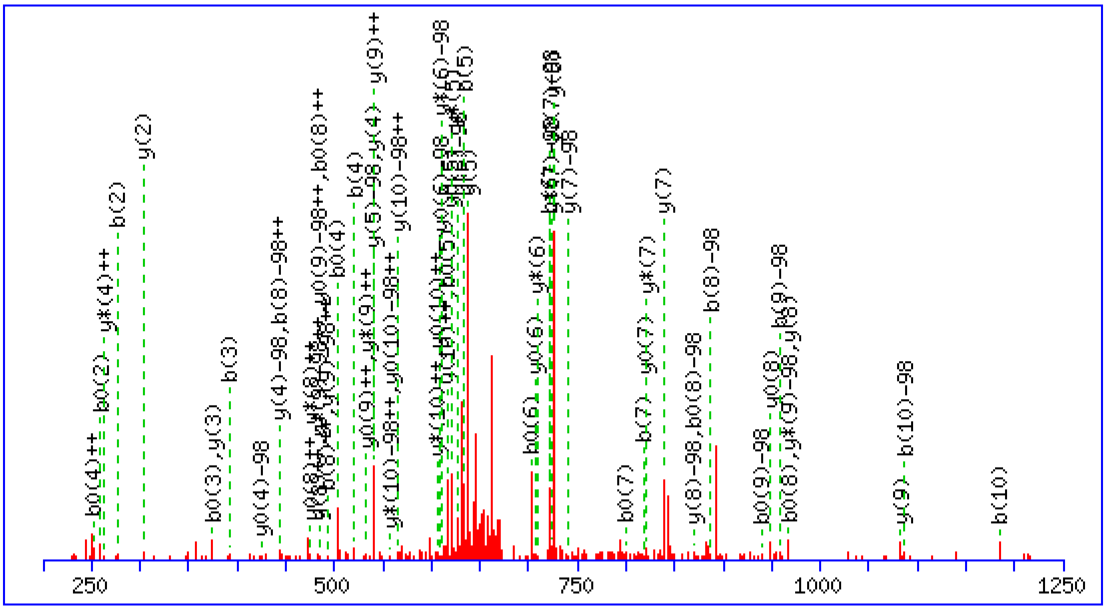
Monoisotopic mass of neutral peptide Mr(calc): 1930.7486
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0028
Matched b ions: b(4), b(6)-98, b(6), b(7)++, b(7)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(11)-98, b(11)++, b(12)-98, b(12)-196, b(13)-196
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(10)++, y(11), y(11)-98, y(13), y(14)-98++, y(14)++, y(14), y(14)-196++, y(15)-196++, y(15)-98++, y(16)-98++

Peptide No.208

EFDELSPSAQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **EFDELSPSAQR**
Found in **AT2A2_MOUSE** in **SwissProt**, Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2

Match to Query 3016: 1357.555070 from(679.784811,2+) index(1566)
Title: Elution from: 40.075 to 40.075 scan no 3131 cid35.00 polarity:+



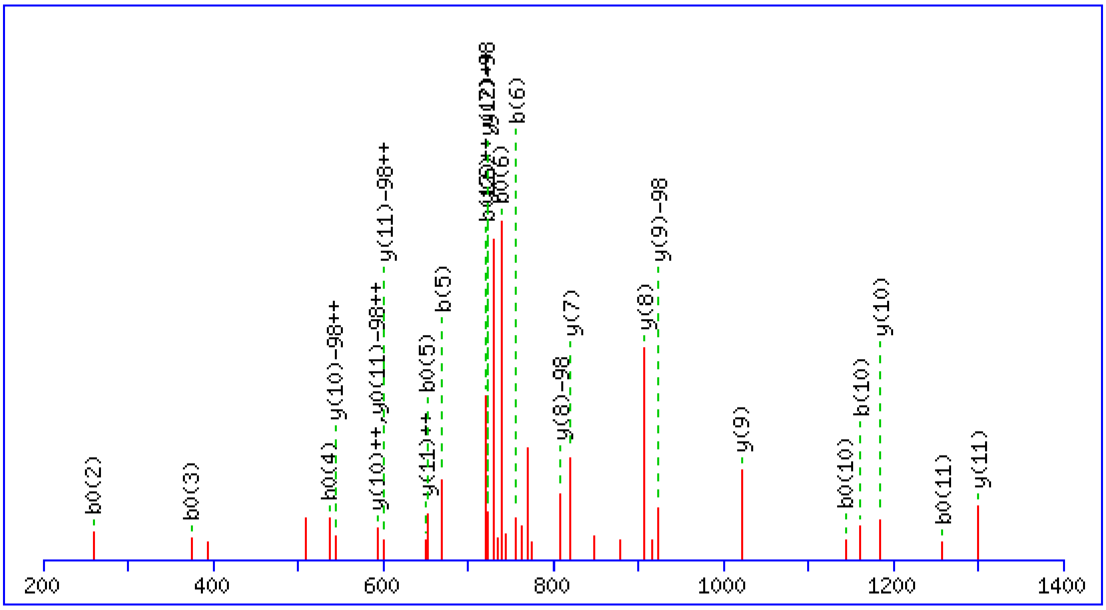
Monoisotopic mass of neutral peptide Mr(calc): 1357.5551
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00055
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8)-98++, b(8)++, b(8)-98, b(9)-98, b(10), b(10)-98
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)++, y(9)-98++, y(10)++, y(10)-98++

Peptide No.209

EFDYDSPHGLDSD
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **EFDYDSPHGLDSD**
Found in **S7A6O_MOUSE** in **SwissProt**, Probable RNA polymerase II nuclear localization protein SLC7A6OS OS=Mus musculus GN=Slc7a6os PE=1 SV=1

Match to Query 2733: 1575.539902 from(788.777227,2+) index(2195)
Title: Elution from: 39.120 to 39.120 scan no 3718 cid35.00 polarity:+



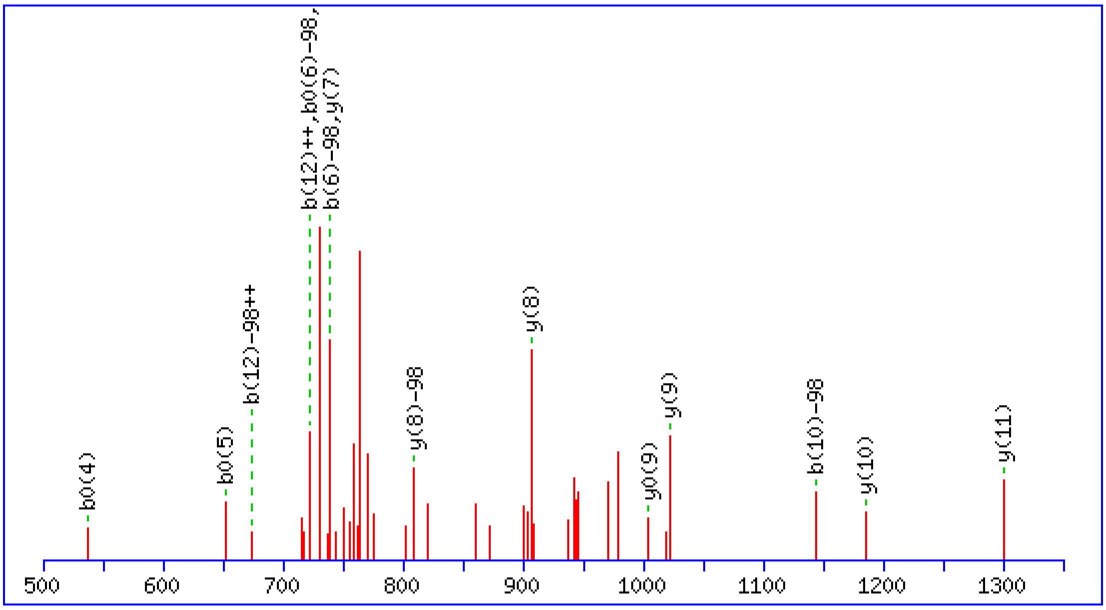
Monoisotopic mass of neutral peptide Mr(calc): 1575.5403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.00075
Matched b ions: b(5), b(6), b(10), b(12)++
Matched y ions: y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)++, y(10)-98++, y(11), y(11)++, y(11)-98++, y(12)++

Peptide No.210

EFDYDSPHGLDSD
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **EFDYDSPHGLDSD**
Found in **S7A6O_MOUSE** in **SwissProt**, Probable RNA polymerase II nuclear localization protein SLC7A6OS OS=Mus musculus GN=Slc7a6os PE=1 SV=1

Match to Query 3324: 1575.539448 from(788.777000,2+) index(2498)
Title: Elution from: 39.734 to 39.734 scan no 3932 cid35.00 polarity:+



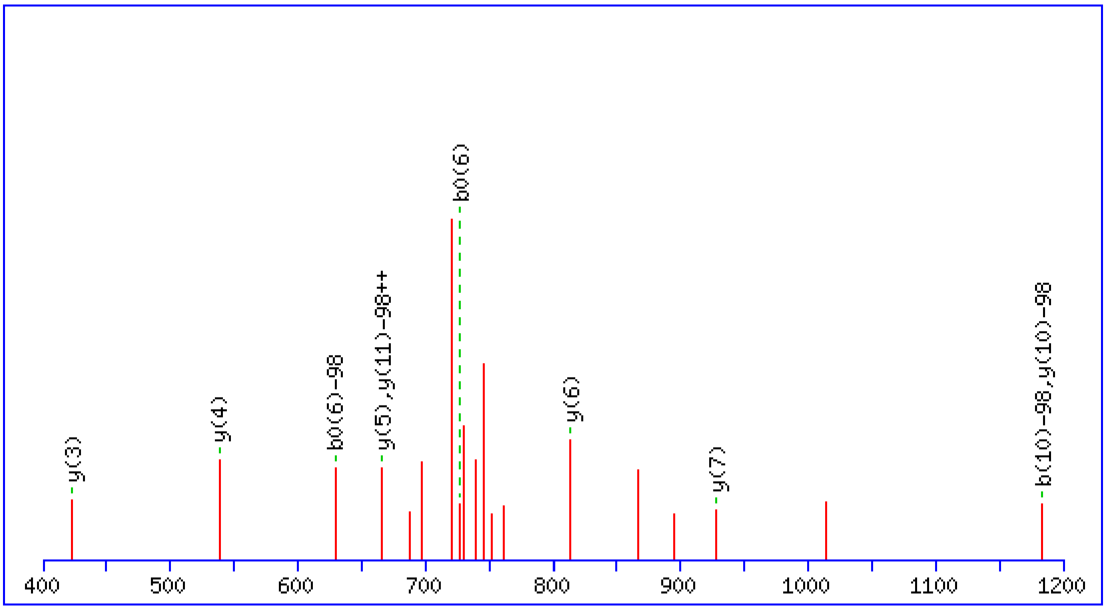
Monoisotopic mass of neutral peptide Mr(calc): 1575.5403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.0054
Matched b ions: b(6)-98, b(10)-98, b(12)++, b(12)-98++
Matched y ions: y(7), y(8), y(8)-98, y(9), y(10), y(11)

Peptide No.211

EFESGDFQDFTR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **EFESGDFQDFTR**
Found in **SYNRG_MOUSE** in **SwissProt**, Synergin gamma OS=Mus musculus GN=Synrg PE=1 SV=1

Match to Query 3240: 1556.581826 from(779.298189,2+) index(3079)
Title: Elution from: 48.463 to 48.463 scan no 5014 cid35.00 polarity:+



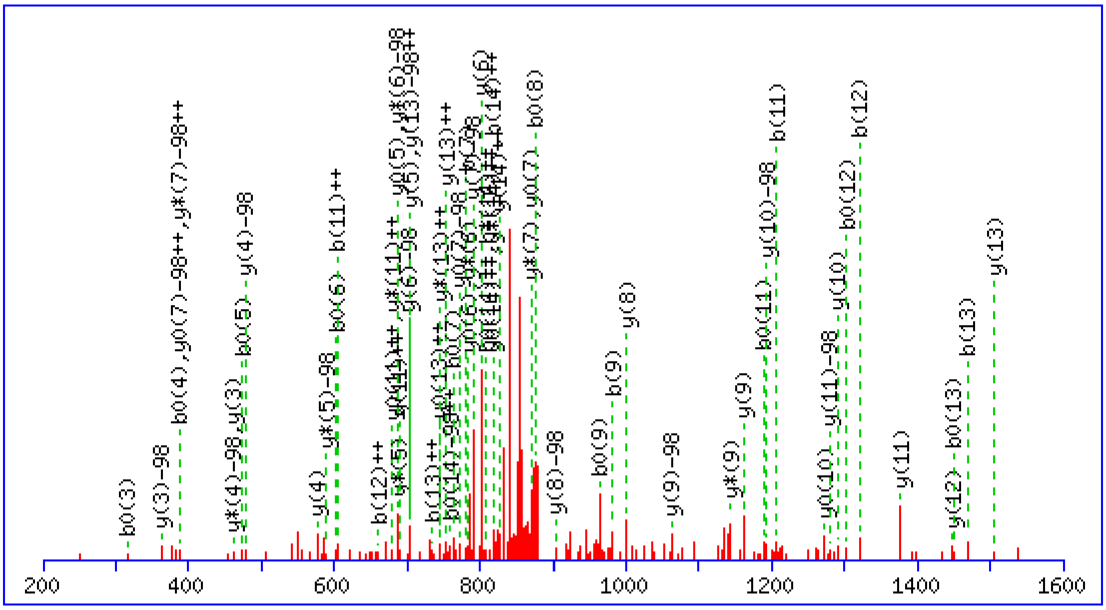
Monoisotopic mass of neutral peptide Mr(calc): 1556.5821
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0022
Matched b ions: b(10)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(10)-98, y(11)-98++

Peptide No.212

EFGASECISPQDFSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **EFGASECISPQDFSK**
Found in **ADHX_MOUSE** in **SwissProt**, Alcohol dehydrogenase class-3 OS=Mus musculus GN=Adh5 PE=1 SV=3

Match to Query 3887: 1780.699840 from(891.357196,2+) index(1841)
Title: Elution from: 49.732 to 49.732 scan no 3927 cid35.00 polarity:+



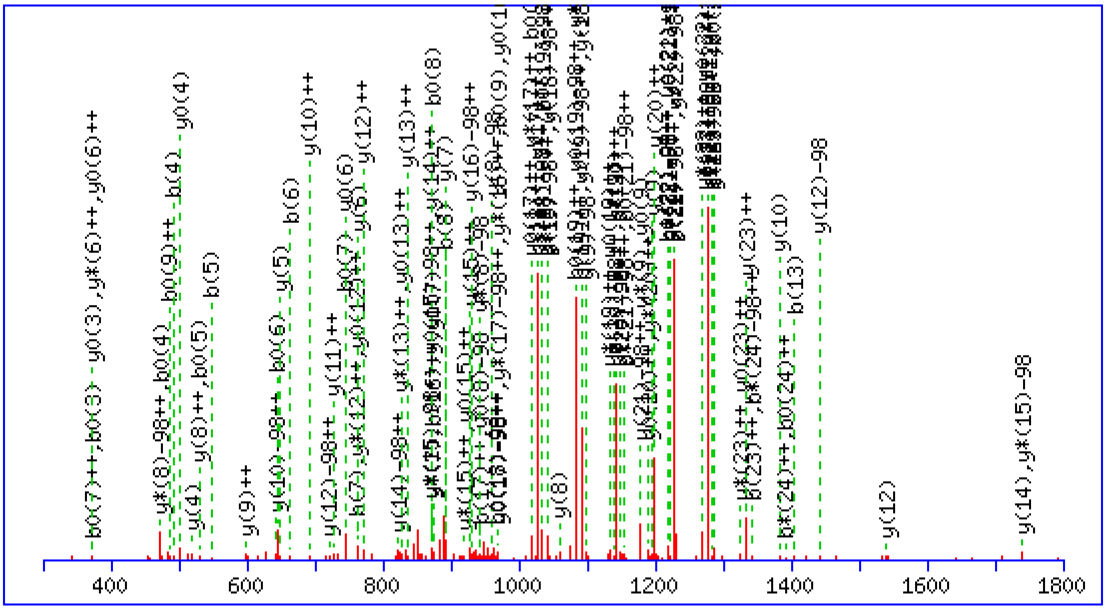
Monoisotopic mass of neutral peptide Mr(calc): 1780.7015
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00023
Matched b ions: b(7), b(9), b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14)++
Matched y ions: y(3)-98, y(3), y(4), y(4)-98, y(5), y(6)-98, y(6), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12), y(13), y(13)-98++, y(13)++, y(14)++

Peptide No.213

EFITGDVEPTDAESAWHSENEEEDK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **EFITGDVEPTDAESAWHSENEEEDK**
Found in **NP1L4_MOUSE** in **SwissProt**, Nucleosome assembly protein 1-like 4 OS=Mus musculus GN=Nap1l4 PE=1 SV=1

Match to Query 6877: 2943.155235 from(982.059021,3+) index(6538)
Title: Elution from: 45.194 to 45.194 scan no 4626 cid35.00 polarity:+:m1s



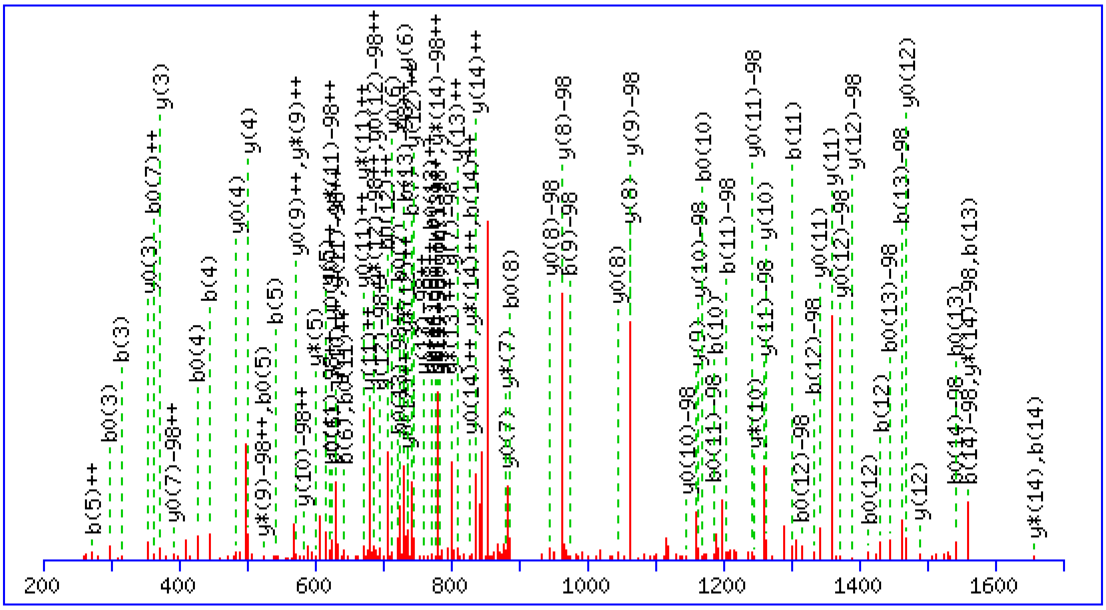
Monoisotopic mass of neutral peptide Mr(calc): 2943.1607
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 **Expect:** 3.7e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(13), b(16)++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(22)++, b(22)-98++, b(23)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9)++, y(9)-98, y(9), y(10)-98++, y(10), y(10)++, y(10)-98, y(11)++, y(12), y(12)++, y(12)-98, y(12)-98++, y(13)++, y(14), y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++

Peptide No.214

EGEEPTVYSDDEEPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **EGEEPTVYSDDEEPK**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 4209: 1802.672394 from(902.343473,2+) index(1348)
Title: Elution from: 27.770 to 27.770 scan no 2332 cid35.00 polarity:+



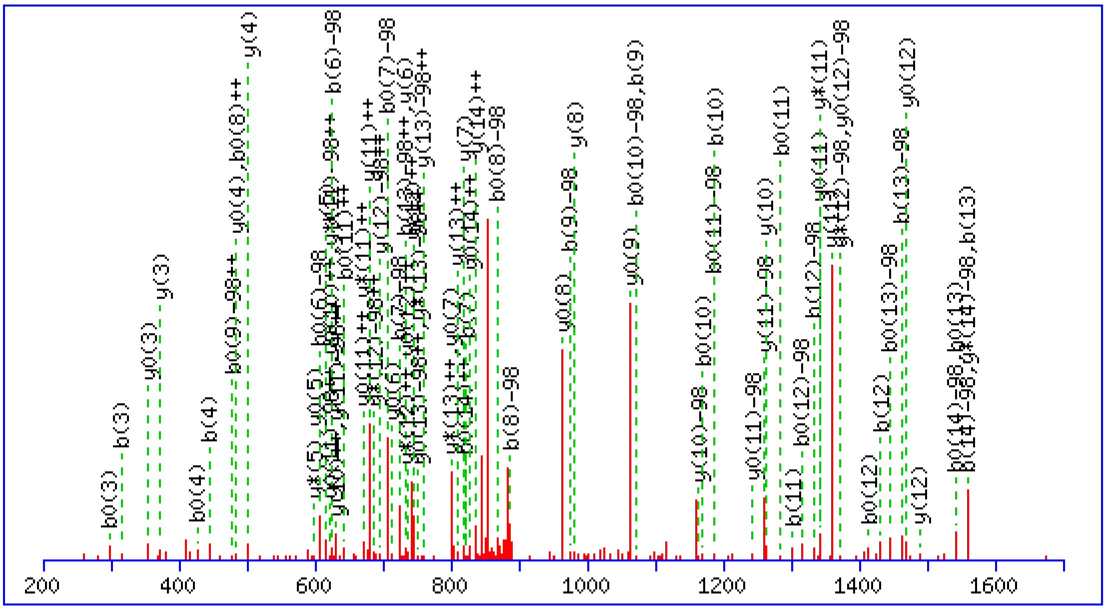
Monoisotopic mass of neutral peptide Mr(calc): 1802.6771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0005
Matched b ions: b(3), b(4), b(5)++, b(5), b(6), b(7), b(9)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(13)++, b(13)-98++, b(14)-98, b(14)-98++, b(14), b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(8)-98, y(8), y(9)-98, y(9), y(10)++, y(10), y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(11)-98, y(11), y(12), y(12)++, y(12)-98, y(12)-98++, y(13)++, y(13)-98++, y(14)++

Peptide No.215

EGEEPTVYSDDEEPK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **EGEEPTVYSDDEEPK**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 4531: 1802.675728 from(902.345140,2+) index(1049)
Title: Elution from: 34.263 to 34.263 scan no 2415 cid35.00 polarity:+



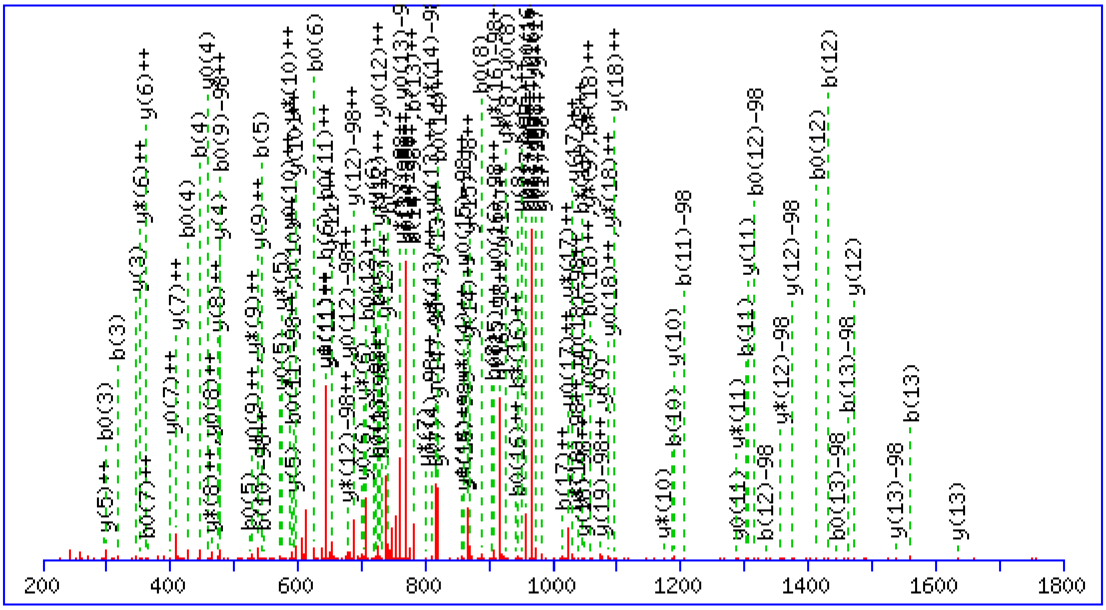
Monoisotopic mass of neutral peptide Mr(calc): 1802.6771
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 0.00012
Matched b ions: b(3), b(4), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10), b(11), b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)++, y(10), y(10)-98, y(11)++, y(11)-98, y(11), y(11)-98++, y(12)++, y(12), y(12)-98++, y(13)-98++, y(13)++, y(14)++

Peptide No.216

EGEEPTVYSDDEEPKDETAR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **EGEEPTVYSDDEEPKDETAR**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 6118: 2374.925847 from(792.649225,3+) index(4862)
Title: Elution from: 26.627 to 26.627 scan no 2175 cid35.00 polarity:+:m1s



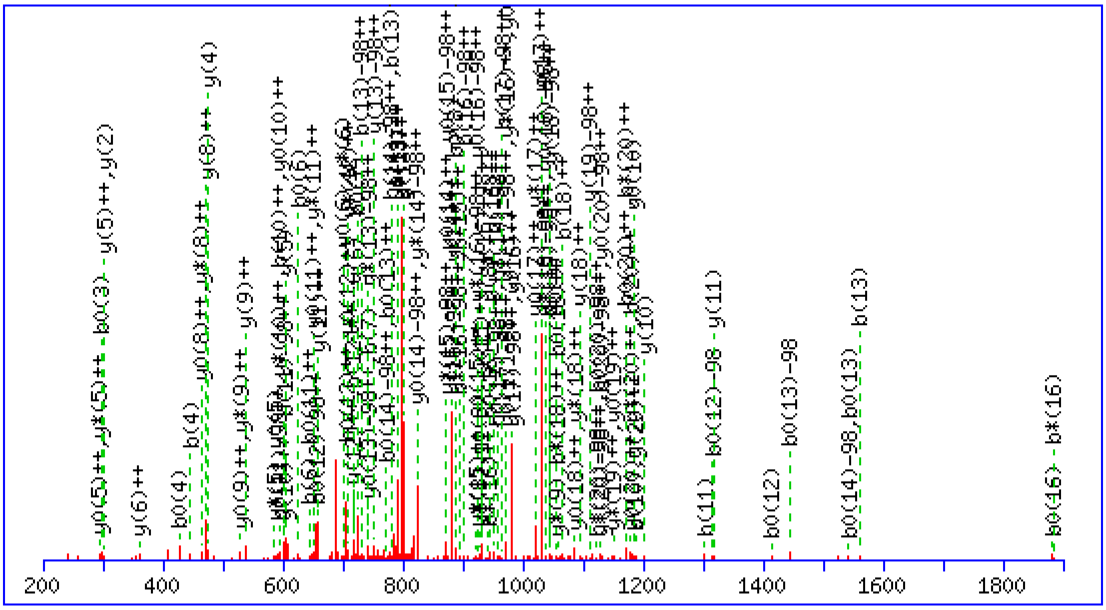
Monoisotopic mass of neutral peptide Mr(calc): 2374.9326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 **Expect:** 7.9e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10), b(10)-98++, b(10)++, b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(13)++, b(13)-98++, b(14)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)-98++, y(12)++, y(12)-98, y(12), y(13)-98++, y(13), y(13)-98, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++

Peptide No.217

EGEEPTVYSDDEEPKDETARK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **EGEEPTVYSDDEEPKDETARK**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 6381: 2503.023012 from(835.348280,3+) index(4517)
Title: Elution from: 23.496 to 23.496 scan no 1749 cid35.00 polarity:+:m1s



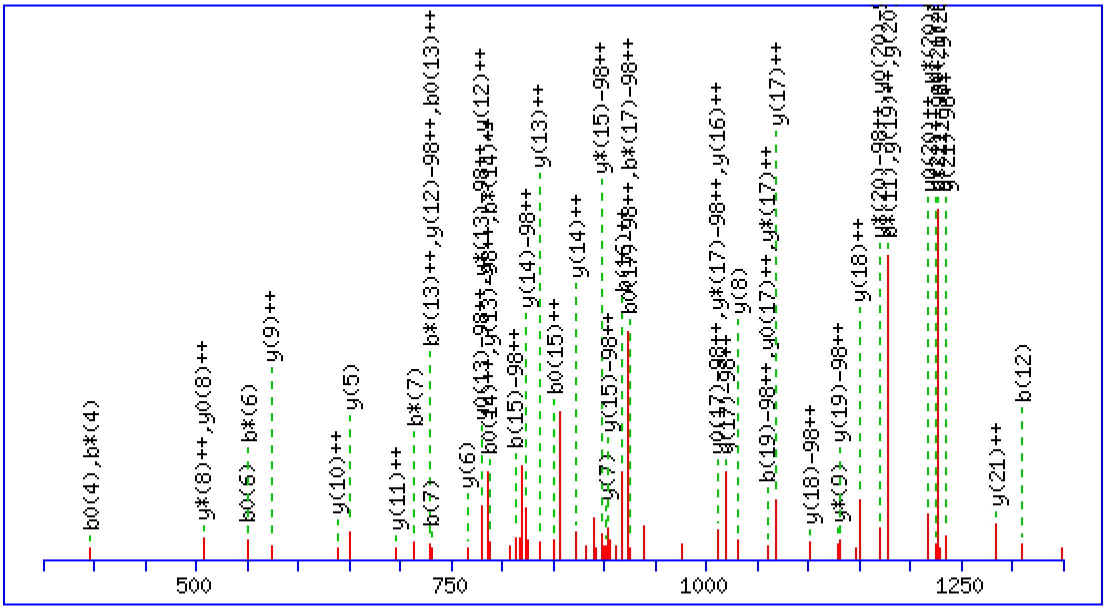
Monoisotopic mass of neutral peptide Mr(calc): 2503.0275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 **Expect:** 7.3e-008
Matched b ions: b(4), b(6), b(7), b(10)++, b(10), b(11), b(11)-98++, b(12)++, b(13), b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(4), y(5), y(5)++, y(6)++, y(6), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(20)++

Peptide No.218

EGINPGYDDYADSDEDQHDAYLER
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **EGINPGYDDYADSDEDQHDAYLER**
Found in **SSRP1_MOUSE** in **SwissProt**, FACT complex subunit SSRP1 OS=Mus musculus GN=Ssrp1 PE=1 SV=2

Match to Query 6622: 2866.085352 from(956.369060,3+) index(6088)
Title: Elution from: 41.065 to 41.065 scan no 4082 cid35.00 polarity:+:m1s



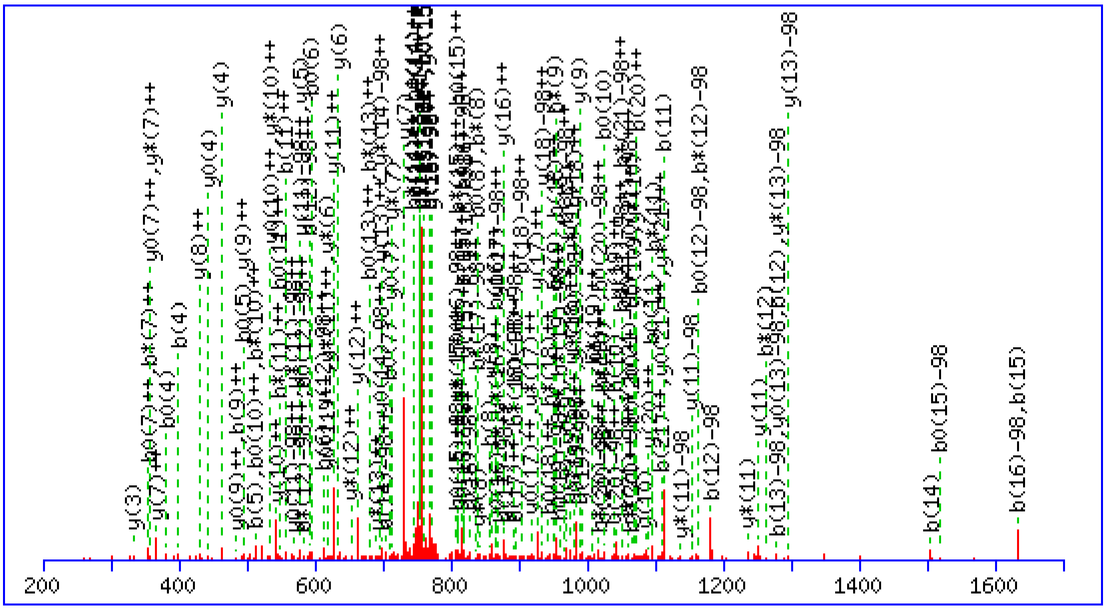
Monoisotopic mass of neutral peptide Mr(calc): 2866.0879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 **Expect:** 4.2e-006
Matched b ions: b(7), b(12), b(15)-98++, b(16)++, b(19)-98++, b(21)++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++

Peptide No.219

EGVILTNENAASPEQPGDEDAK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **EGVILTNENAASPEQPGDEDAK**
Found in **NSUN2_MOUSE** in **SwissProt**, tRNA (cytosine(34)-C(5))-methyltransferase OS=Mus musculus GN=Nsun2 PE=1 SV=2

Match to Query 5174: 2363.016540 from(788.679456,3+) index(4364)
Title: Elution from: 41.220 to 41.220 scan no 3115 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2363.0166
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 7.6e-006
Matched b ions: b(4), b(5), b(6), b(8), b(9), b(9)++, b(10), b(11), b(11)++, b(12)-98, b(12), b(12)-98++, b(13)-98, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15), b(15)++, b(16)-98, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12)++, y(13)-98, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++

Peptide No.220

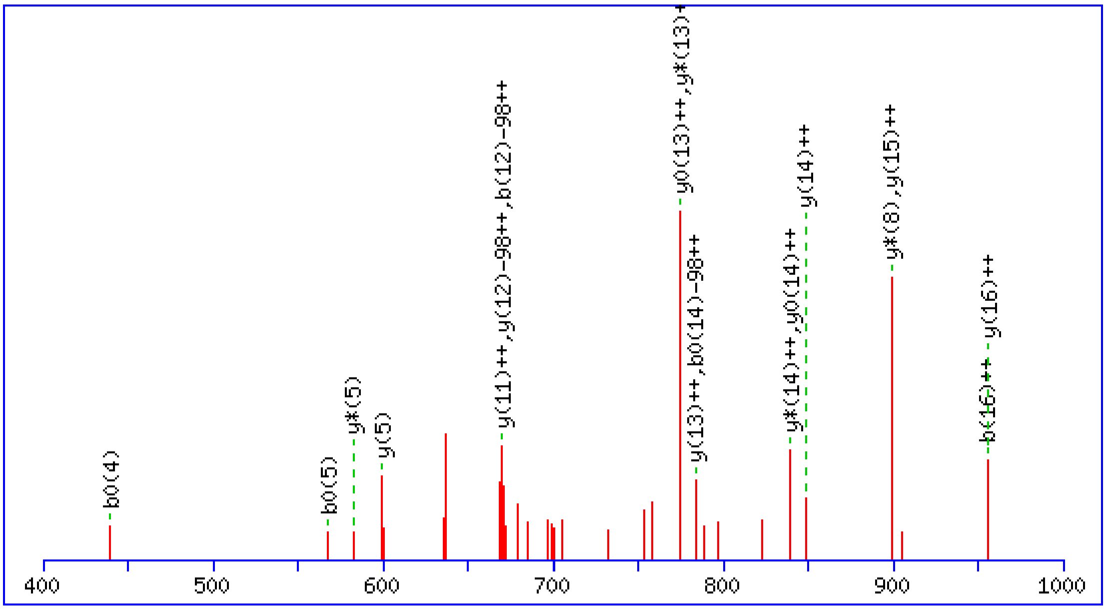
EIITEEPSEEEADMPKPK

Confirmed sites: @S:8

Ambiguous sites:

MS/MS Fragmentation of **EIITEEPSEEEADMPKPK**
Found in **DDX21_MOUSE** in **SwissProt**, Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3

Match to Query 5426: 2150.933271 from(717.985033,3+) index(5534)
Title: Elution from: 34.851 to 34.851 scan no 3255 cid35.00 polarity:+:m1s



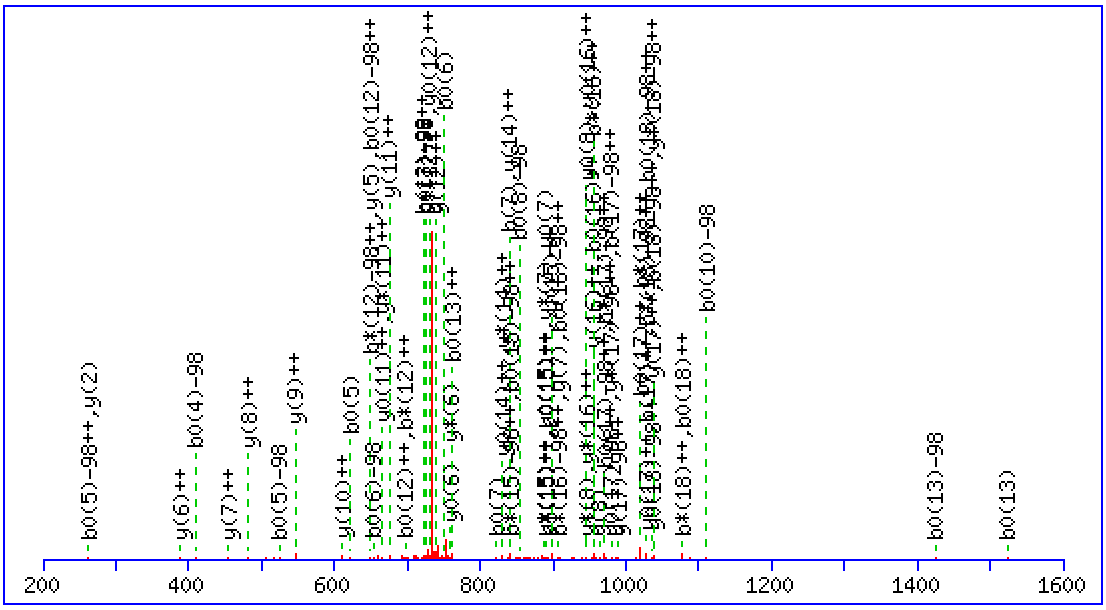
Monoisotopic mass of neutral peptide Mr(calc): 2150.9330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.059
Matched b ions: b(12)-98++, b(16)++
Matched y ions: y(5), y(11)++, y(12)-98++, y(13)++, y(14)++, y(15)++, y(16)++

Peptide No.221

EISDDEAEEEKGEKEEEDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **EISDDEAEEEKGEKEEEDK**
Found in **HS90B_MOUSE** in **SwissProt**, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3

Match to Query 6017: 2316.896499 from(773.306109,3+) index(4236)
Title: Elution from: 21.041 to 21.041 scan no 1415 cid35.00 polarity:+:m1s



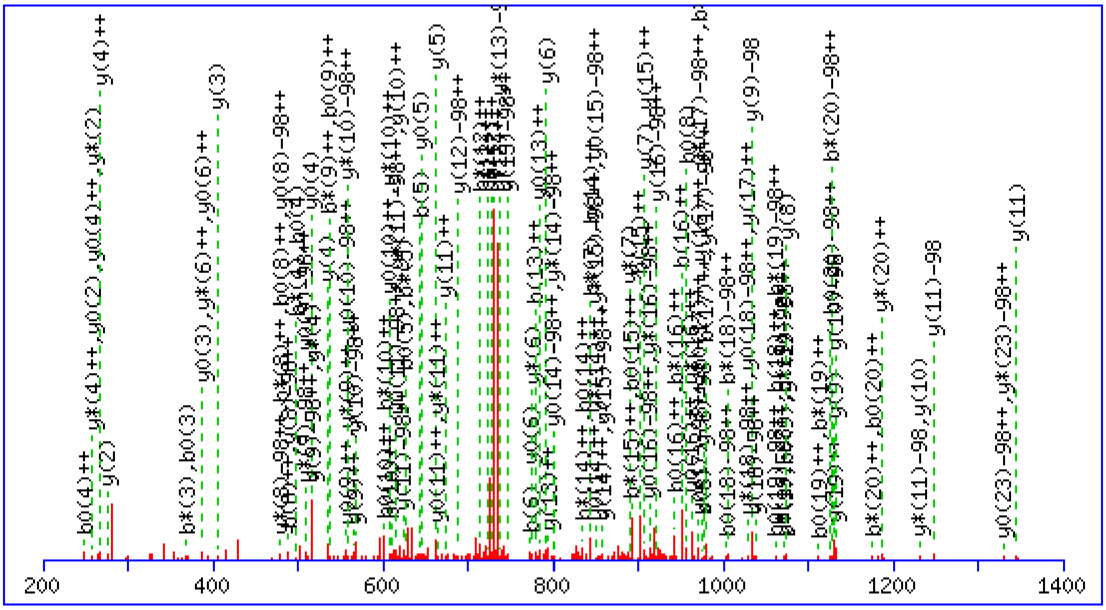
Monoisotopic mass of neutral peptide Mr(calc): 2316.9005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0023
Matched b ions: b(7), b(13)-98++, b(17)++, b(17)-98++, b(18)-98++
Matched y ions: y(2), y(5), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-98++

Peptide No.222

EKEEKESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **EKEEKESDDKPEIEDVGSDEEEEEK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5707: 3030.223780 from(758.563221,4+) index(3721)
Title: Elution from: 24.776 to 24.776 scan no 1764 cid35.00 polarity:+:m1s



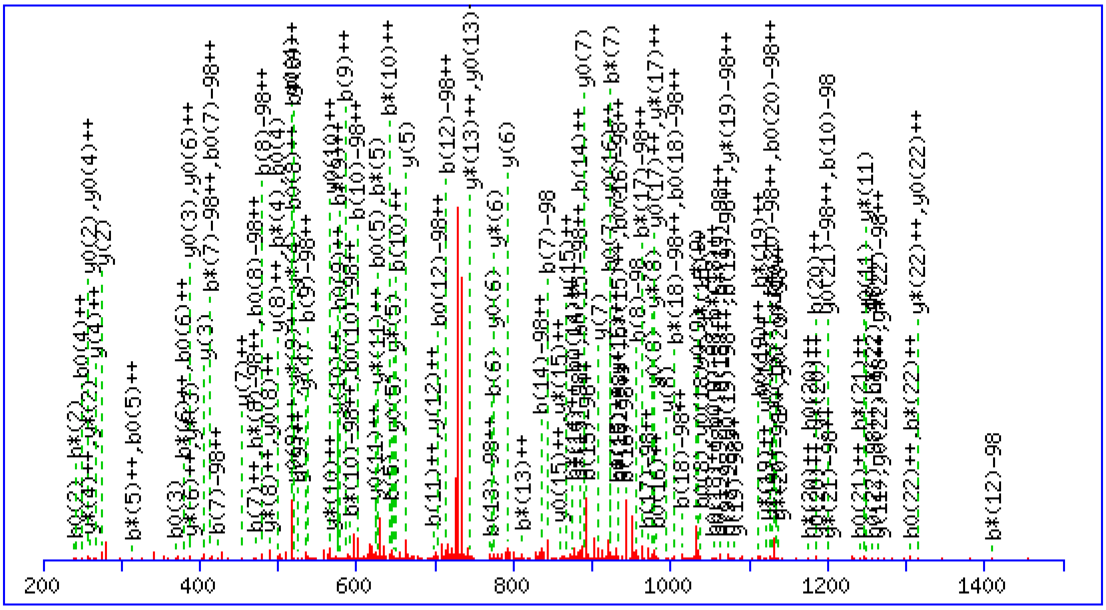
Monoisotopic mass of neutral peptide Mr(calc): 3030.2237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0011
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6)++, b(6), b(8)++, b(8), b(10)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(19)-98++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(8), y(8)-98++, y(8)-98, y(9)-98++, y(9), y(9)-98, y(9)++, y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(19)++

Peptide No.223

EKEEKESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **EKEEKESDDKPEIEDVGSDEEEEEK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5893: 3030.221056 from(758.562540,4+) index(3954)
Title: Elution from: 24.483 to 24.483 scan no 1821 cid35.00 polarity:+:m1s



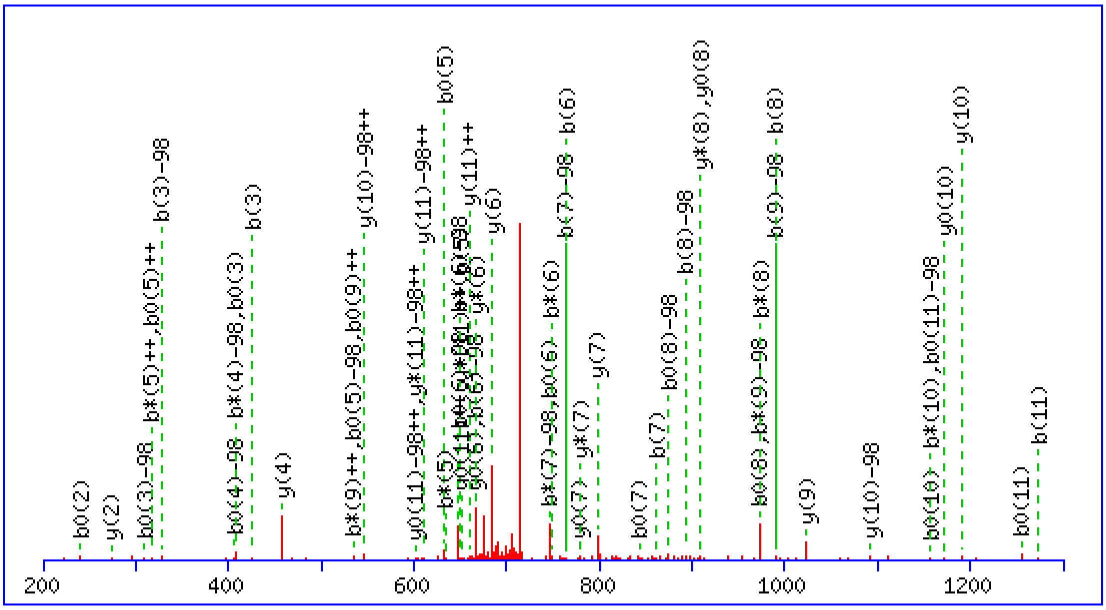
Monoisotopic mass of neutral peptide Mr(calc): 3030.2237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00052
Matched b ions: b(2), b(3), b(4)++, b(4), b(5), b(6)++, b(6), b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8)-98, b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)-98, b(10)++, b(11)++, b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(16)-98++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(20)++, b(21)-98++, b(22)++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(11), y(12)++, y(15)++, y(16)++, y(19)-98++, y(19)++

Peptide No.224

EKSPELPEPSVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **EKSPELPEPSVR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 2885: 1446.675220 from(724.344886,2+) index(1010)
Title: Elution from: 35.614 to 35.614 scan no 2475 cid35.00 polarity:+



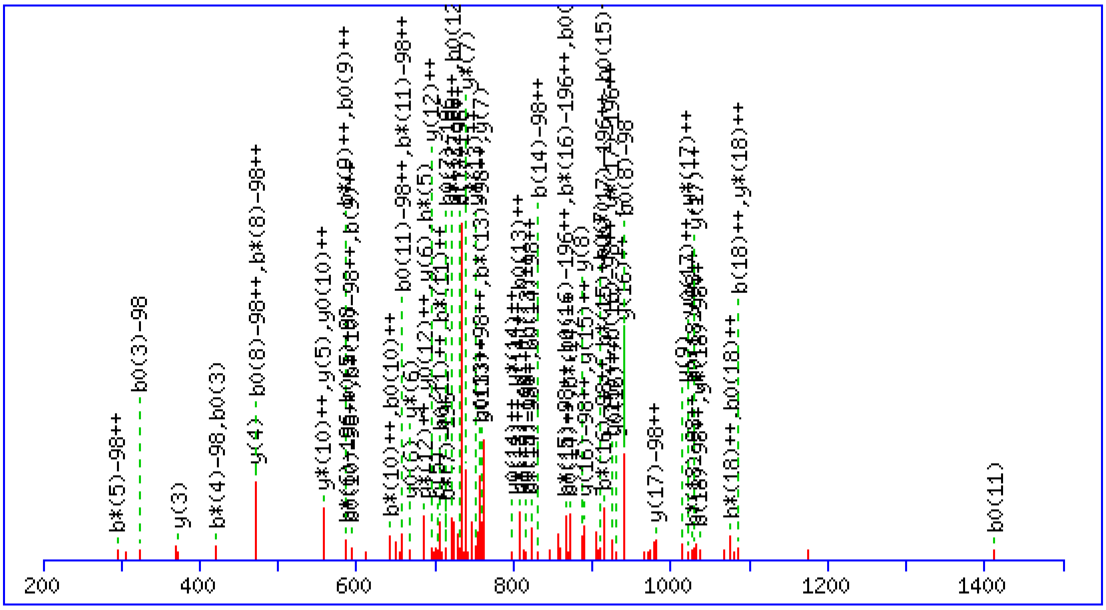
Monoisotopic mass of neutral peptide Mr(calc): 1446.6755
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0032
Matched b ions: b(3)-98, b(3), b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)-98, b(11)
Matched y ions: y(2), y(4), y(6), y(7), y(9), y(10)-98++, y(10), y(10)-98, y(11)-98++, y(11)++

Peptide No.225

EKTPSPKEEDEEAESPPEK
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **EKTPSPKEEDEEAESPPEK**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 5856: 2314.910853 from(772.644227,3+) index(3947)
Title: Elution from: 20.166 to 20.166 scan no 1261 cid35.00 polarity:+:m1s



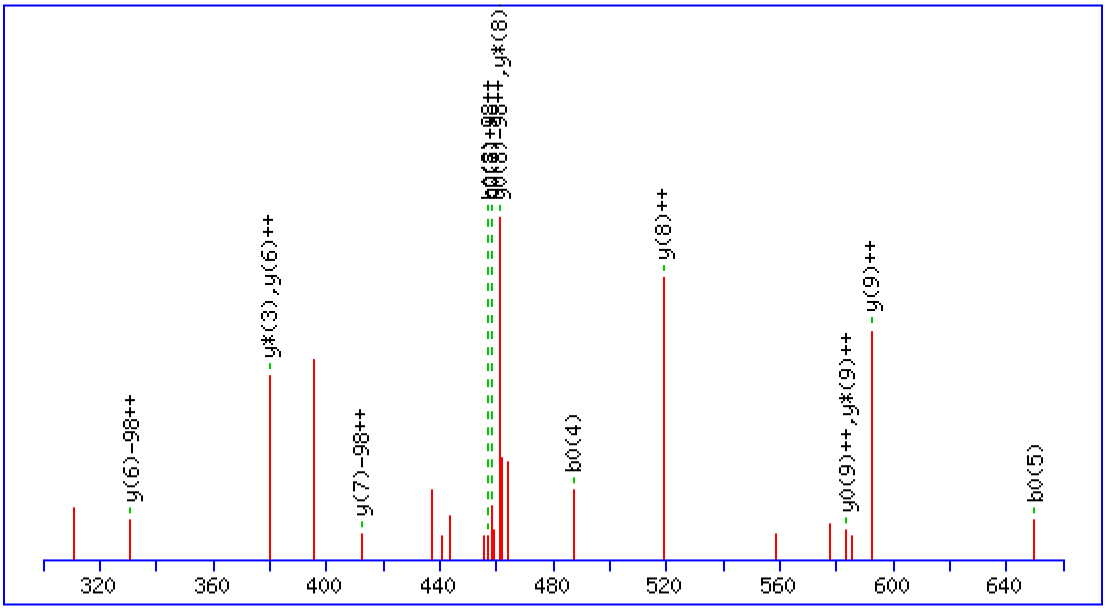
Monoisotopic mass of neutral peptide Mr(calc): 2314.9130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0065
Matched b ions: b(5), b(7)-196, b(9)++, b(12)-98++, b(13)++, b(14)-98++, b(15)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.226

ELFDYSPPLHK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **ELFDYSPPLHK**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 2623: 1424.637387 from(475.886405,3+) index(2780)
Title: Elution from: 43.651 to 43.651 scan no 4431 cid35.00 polarity:+



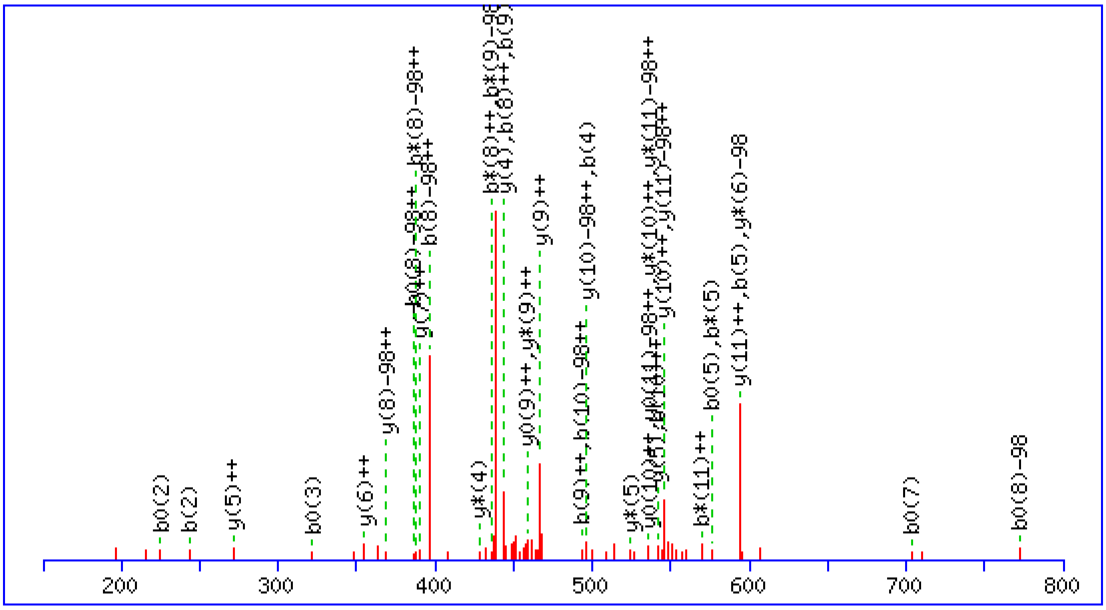
Monoisotopic mass of neutral peptide Mr(calc): 1424.6377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0082
Matched b ions:
Matched y ions: y(6)++, y(6)-98++, y(7)++, y(7)-98++, y(8)++, y(9)++

Peptide No.227

ELPRPGASPPAEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **ELPRPGASPPAEK**
Found in **GCH1_MOUSE** in **SwissProt**, GTP cyclohydrolase 1 OS=Mus musculus GN=Gch1 PE=2 SV=1

Match to Query 2643: 1427.680341 from(476.900723,3+) index(770)
Title: Elution from: 22.647 to 22.647 scan no 1633 cid35.00 polarity:+



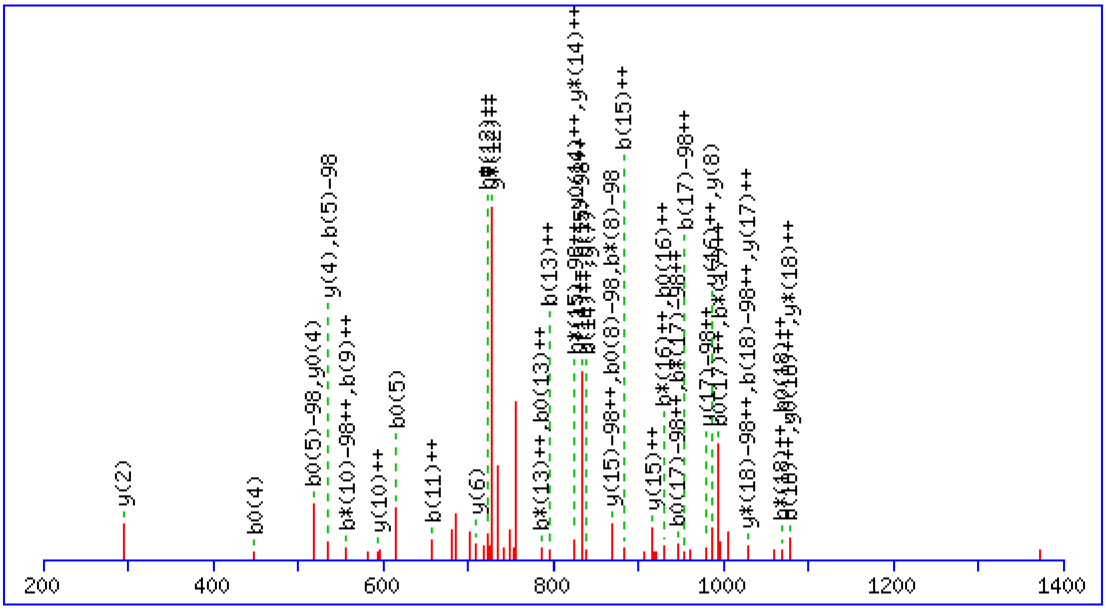
Monoisotopic mass of neutral peptide Mr(calc): 1427.6810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0054
Matched b ions: b(2), b(4), b(5), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++
Matched y ions: y(4), y(5)++, y(5), y(6)++, y(7)++, y(8)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.228

ELSHSPPRENSFESSLEFK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **ELSHSPPRENSFESSLEFK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5005: 2299.014252 from(767.345360,3+) index(5333)
Title: Elution from: 39.664 to 39.664 scan no 3782 cid35.00 polarity:+:m1s



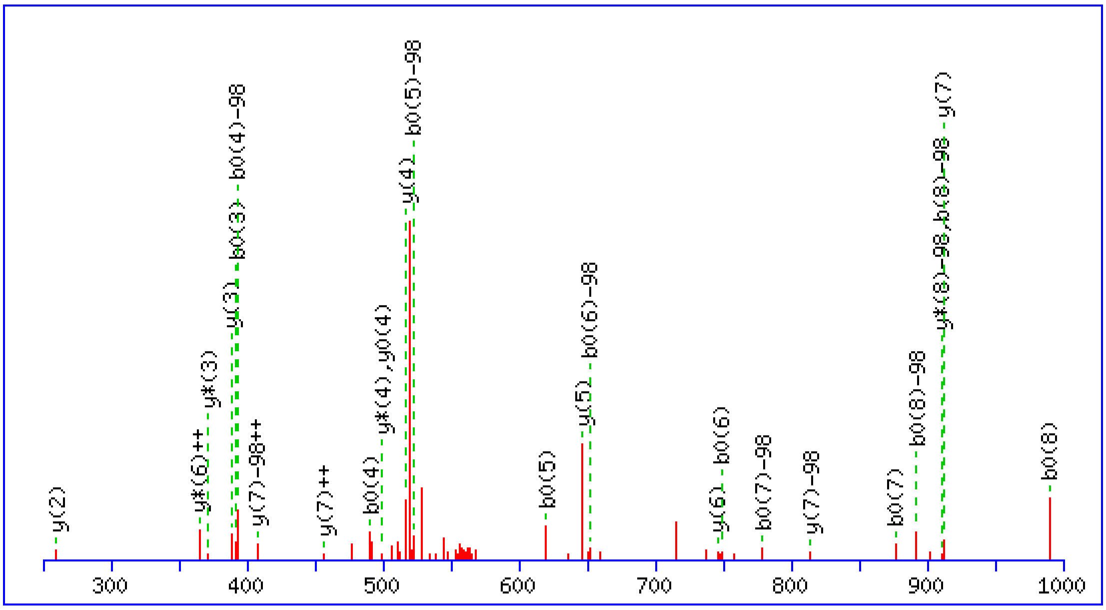
Monoisotopic mass of neutral peptide Mr(calc): 2299.0158
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.014
Matched b ions: b(5)-98, b(9)++, b(11)++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(10)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)-98++, y(17)++

Peptide No.229

ELSVEEQIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ELSVEEQIK**
Found in **LIMA1_MOUSE** in **SwissProt**, LIM domain and actin-binding protein 1 OS=Mus musculus GN=Lima1 PE=1 SV=3

Match to Query 1222: 1153.526716 from(577.770634,2+) index(1611)
Title: Elution from: 32.239 to 32.239 scan no 2851 cid35.00 polarity:+



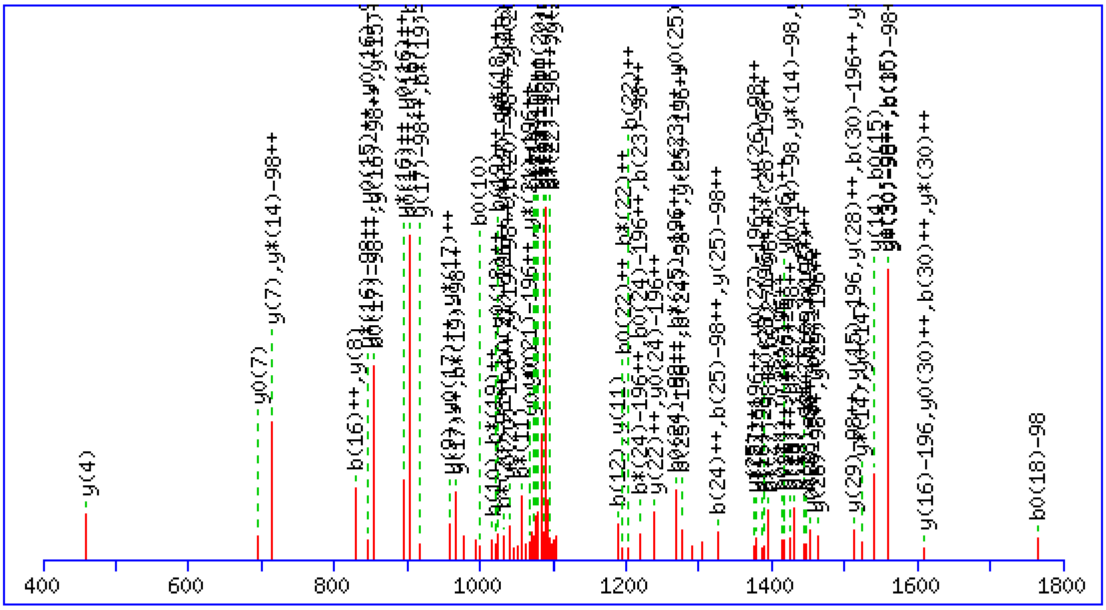
Monoisotopic mass of neutral peptide Mr(calc): 1153.5267
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0017
Matched b ions: b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(7)-98++, y(7)++

Peptide No.230

ELVGDTGSQEGDNEQPSGSETEEDPSASPQK
Confirmed sites: @S:17,@S:19
Ambiguous sites:

MS/MS Fragmentation of **ELVGDTGSQEGDNEQPSGSETEEDPSASPQK**
Found in **CF228_MOUSE** in **SwissProt**, UPF0766 protein C6orf228 homolog OS=Mus musculus PE=3 SV=1

Match to Query 5999: 3363.274545 from(1122.098791,3+) index(4608)
Title: Elution from: 31.193 to 31.193 scan no 2715 cid35.00 polarity:+:m1s



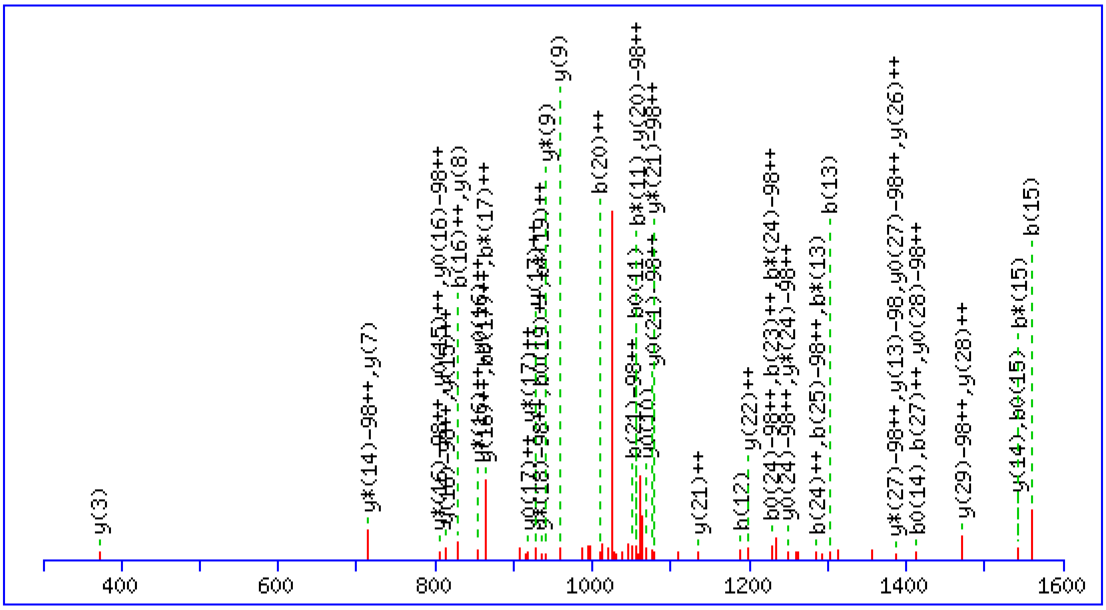
Monoisotopic mass of neutral peptide Mr(calc): 3363.2825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 **Expect:** 1.6e-006
Matched b ions: b(10), b(11), b(12), b(14), b(15), b(16)++, b(19)++, b(20)++, b(20)-98++, b(22)++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(25)-196++, b(25)-98++, b(26)++, b(27)++, b(28)-98++, b(29)-196++, b(30)-196++, b(30)-98++, b(30)++
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(11), y(13)-98, y(14), y(15)++, y(15)-196, y(16)-98++, y(16)++, y(16)-196, y(17)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(21)-196++, y(22)++, y(25)-196++, y(25)-98++, y(25)++, y(26)-98++, y(26)++, y(28)++, y(28)-98++, y(28)-196++, y(29)-98++, y(29)++, y(29)-196++

Peptide No.231

ELVGDTGSQEGDNEQPSGSETEEDPSASPQK
Confirmed sites: @T:21
Ambiguous sites:

MS/MS Fragmentation of **ELVGDTGSQEGDNEQPSGSETEEDPSASPQK**
Found in **CF228_MOUSE** in **SwissProt**, UPF0766 protein C6orf228 homolog OS=Mus musculus PE=3 SV=1

Match to Query 5780: 3283.313961 from(1095.445263,3+) index(4222)
Title: Elution from: 29.235 to 29.235 scan no 2380 cid35.00 polarity:+:m1s



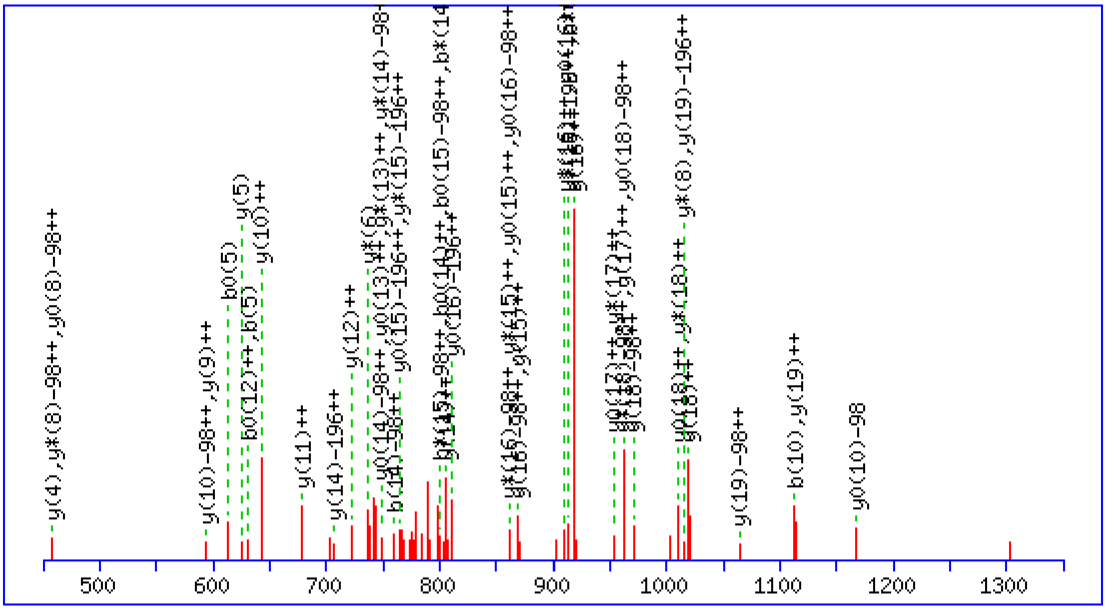
Monoisotopic mass of neutral peptide Mr(calc): 3283.3161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00069
Matched b ions: b(12), b(13), b(15), b(16)++, b(20)++, b(21)-98++, b(23)++, b(24)++, b(25)-98++, b(27)++
Matched y ions: y(3), y(7), y(8), y(9), y(13)-98, y(14), y(15)++, y(16)++, y(16)-98++, y(17)++, y(20)-98++, y(21)++, y(22)++, y(26)++, y(28)++, y(29)-98++

Peptide No.232

ELWDSPEPASAPRTPQSPVSR
Confirmed sites: @T:14,@S:17
Ambiguous sites:

MS/MS Fragmentation of **ELWDSPEPASAPRTPQSPVSR**
Found in **FHOD1_MOUSE** in **SwissProt**, FH1/FH2 domain-containing protein 1 OS=Mus musculus GN=Fhod1 PE=2 SV=3

Match to Query 6147: 2466.062112 from(823.027980,3+) index(6109)
Title: Elution from: 41.455 to 41.455 scan no 4131 cid35.00 polarity:+:m1s



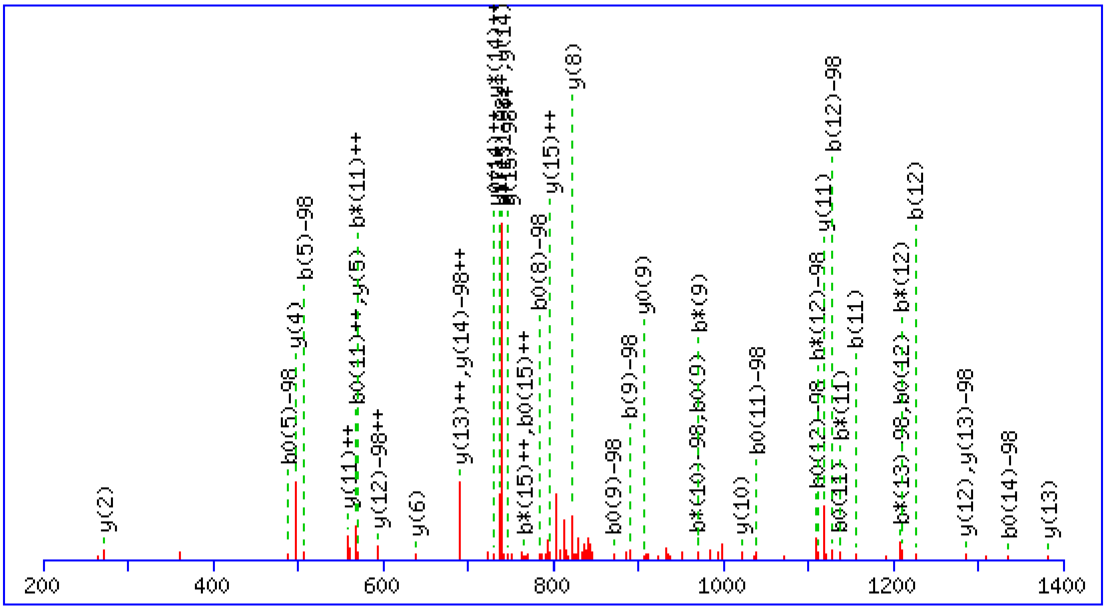
Monoisotopic mass of neutral peptide Mr(calc): 2466.0618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00049
Matched b ions: b(5), b(10), b(14)-98++
Matched y ions: y(4), y(5), y(9)++, y(10)++, y(10)-98++, y(11)++, y(12)++, y(14)++, y(14)-196++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(19)-196++

Peptide No.233

ENPPSPPTSPAAPQPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **ENPPSPPTSPAAPQPR**
Found in **SFR1_MOUSE** in **SwissProt**, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Sfr1 PE=1 SV=2

Match to Query 3870: 1721.773856 from(861.894204,2+) index(4943)
Title: Elution from: 27.311 to 27.311 scan no 2269 cid35.00 polarity:+:m1s



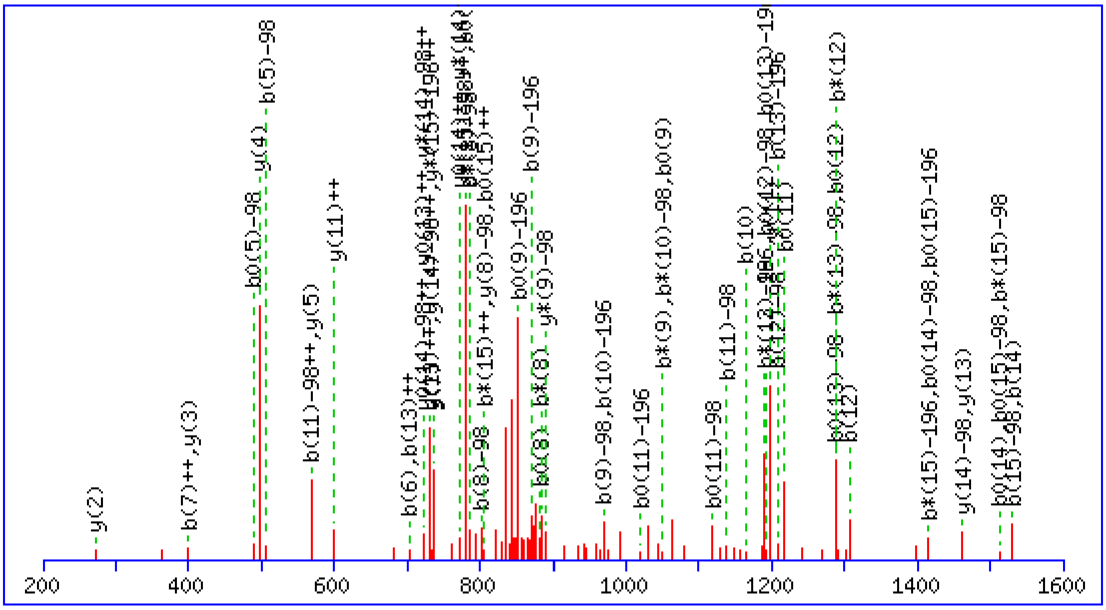
Monoisotopic mass of neutral peptide Mr(calc): 1721.7774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 3.9e-005
Matched b ions: b(5)-98, b(9)-98, b(11), b(12), b(12)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)++, y(12), y(12)-98++, y(13)-98, y(13), y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++

Peptide No.234

ENPPSPPTSPAAPQPR
Confirmed sites: @S:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of **ENPPSPPTSPAAPQPR**
Found in **SFR1_MOUSE** in **SwissProt**, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Sfr1 PE=1 SV=2

Match to Query 3918: 1801.741576 from(901.878064,2+) index(689)
Title: Elution from: 31.981 to 31.981 scan no 2038 cid35.00 polarity:+



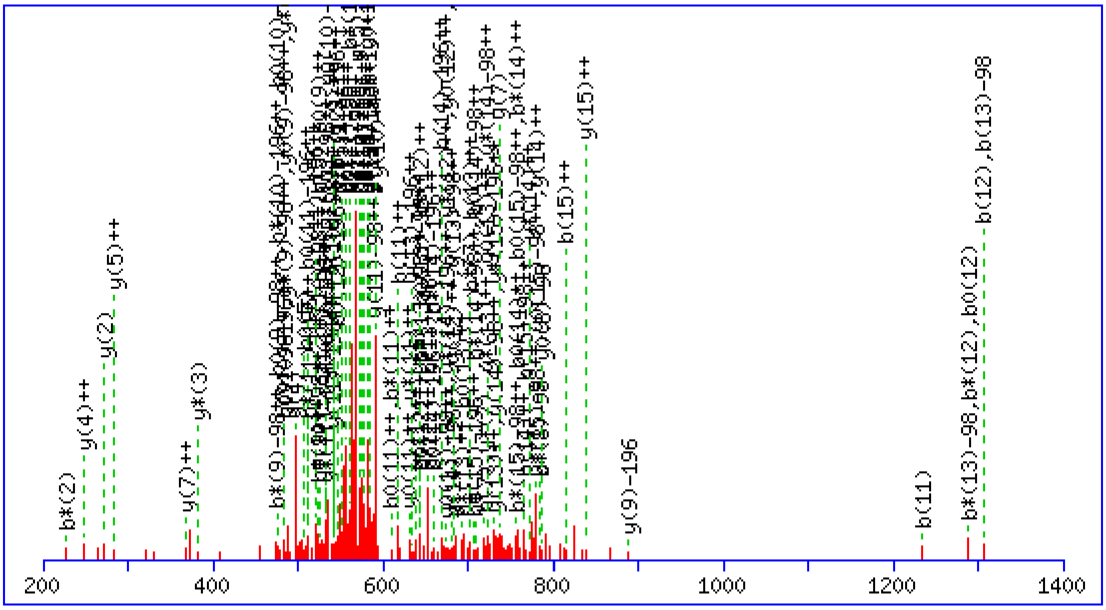
Monoisotopic mass of neutral peptide Mr(calc): 1801.7437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00037
Matched b ions: b(5)-98, b(6), b(7)++, b(8)-98, b(9)-98, b(9)-196, b(10)-196, b(10), b(11)-98++, b(11)-98, b(12), b(12)-98, b(13)++, b(13)-196, b(14), b(15)-98
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)-98, y(11)++, y(11), y(13)++, y(13), y(14)-98++, y(14)++, y(14)-98

Peptide No.235

ENPPSPPTSPAAPQPR
Confirmed sites: @T:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of **ENPPSPPTSPAAPQPR**
Found in **SFR1_MOUSE** in **SwissProt**, Swi5-dependent recombination DNA repair protein 1 homolog OS=Mus musculus GN=Sfr1 PE=1 SV=2

Match to Query 3920: 1801.744164 from(601.588664,3+) index(697)
Title: Elution from: 32.077 to 32.077 scan no 2050 cid35.00 polarity:+



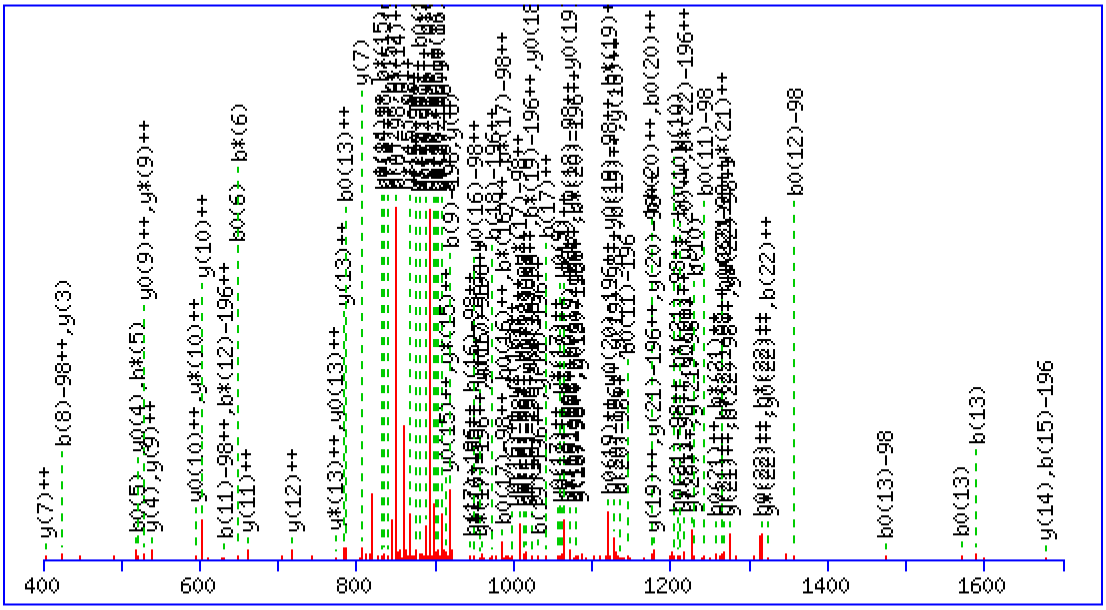
Monoisotopic mass of neutral peptide Mr(calc): 1801.7437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.003
Matched b ions: b(5), b(7), b(9)-98++, b(9)++, b(10)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)-196++, b(11), b(11)++, b(12)++, b(12), b(12)-196++, b(13)-98++, b(13)-98, b(13)++, b(14)++, b(14)-196++, b(15)-98++, b(15)++
Matched y ions: y(2), y(4)++, y(4), y(5), y(5)++, y(6), y(7)++, y(7), y(9)-196, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-196++, y(11)-98++, y(12)-196++, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)++, y(14)-98++, y(14)-196++, y(15)++

Peptide No.236

ENPPVEDSSDEDDKRNPGNLYDK
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of **ENPPVEDSSDEDDKRNPGNLYDK**
Found in **STT3B_MOUSE** in **SwissProt**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus GN=Stt3b PE=1 SV=2

Match to Query 6502: 2792.084577 from(931.702135,3+) index(4527)
Title: Elution from: 34.879 to 34.879 scan no 2497 cid35.00 polarity:+:m1s



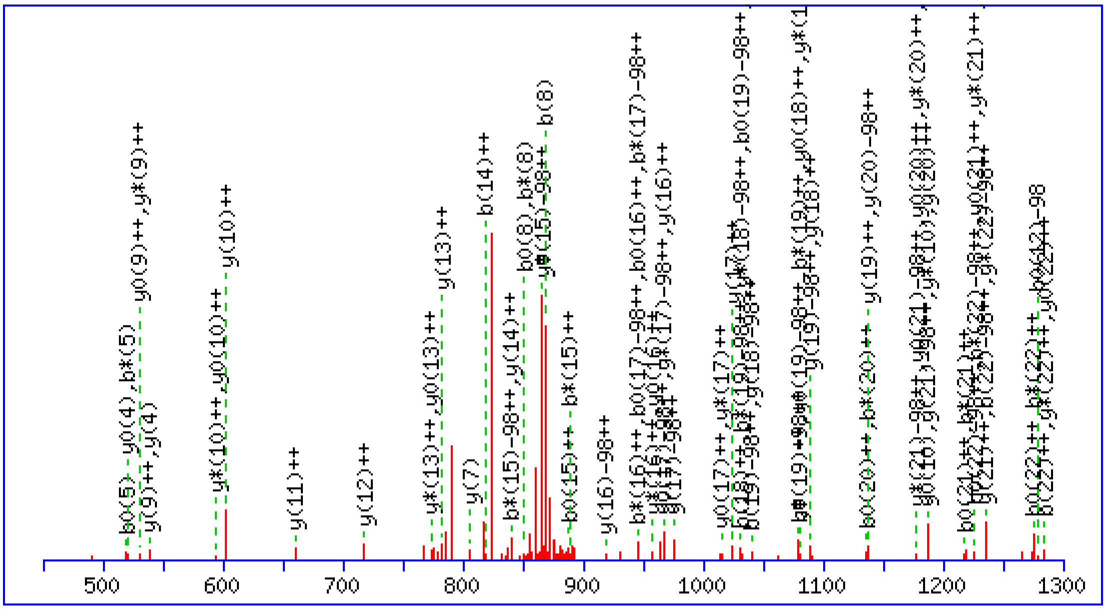
Monoisotopic mass of neutral peptide Mr(calc): 2792.0851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 **Expect:** 2.4e-006
Matched b ions: b(8)-98, b(8)-98++, b(9)-196, b(10), b(11)-98++, b(13), b(15)-196, b(15)-98++, b(15)-196++, b(16)-98++, b(17)-196++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(3), y(4), y(7)++, y(7), y(8), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14), y(14)++, y(15)-98++, y(16)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-196++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++

Peptide No.237

ENPPVEDSSDEDDKRNPGNLYDK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **ENPPVEDSSDEDDKRNPGNLYDK**
Found in **STT3B_MOUSE** in **SwissProt**, Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus GN=Stt3b PE=1 SV=2

Match to Query 6666: 2712.113109 from(905.044979,3+) index(4821)
Title: Elution from: 26.081 to 26.081 scan no 2100 cid35.00 polarity:+:m1s



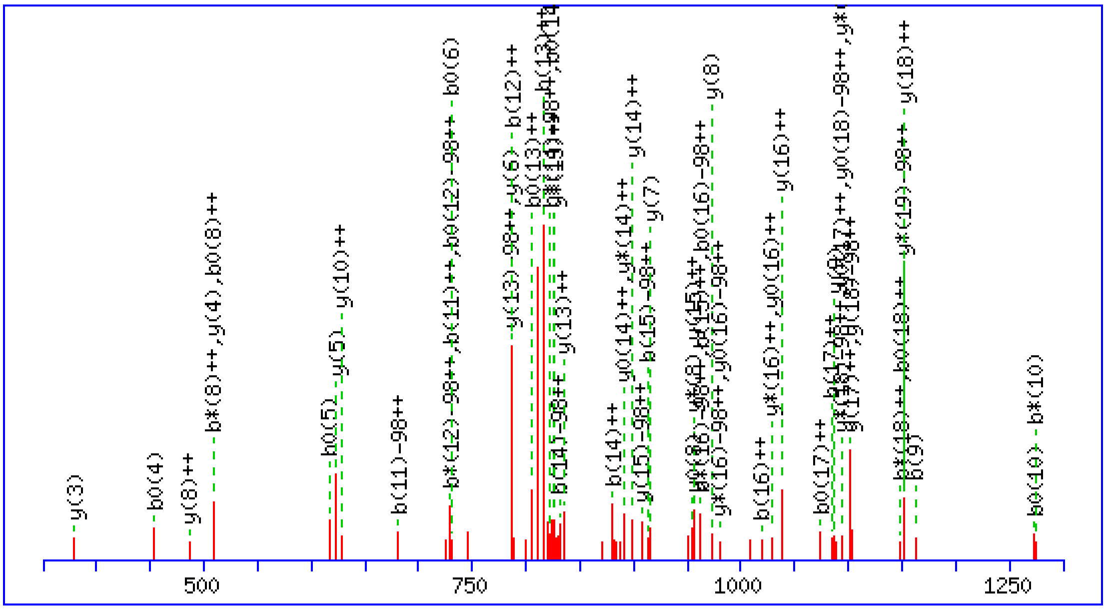
Monoisotopic mass of neutral peptide Mr(calc): 2712.1188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.8e-005
Matched b ions: b(8), b(14)++, b(18)++, b(19)-98++, b(21)-98++, b(21)++, b(22)-98++, b(22)++
Matched y ions: y(4), y(7), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++

Peptide No.238

ENVEYIEREESDGEYDEFGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **ENVEYIEREESDGEYDEFGR**
Found in **ZRAB2_MOUSE** in **SwissProt**, Zinc finger Ran-binding domain-containing protein 2 OS=Mus musculus GN=Zranb2 PE=1 SV=2

Match to Query 6459: 2543.996742 from(849.006190,3+) index(6295)
Title: Elution from: 41.652 to 41.652 scan no 4183 cid35.00 polarity:+:m1s



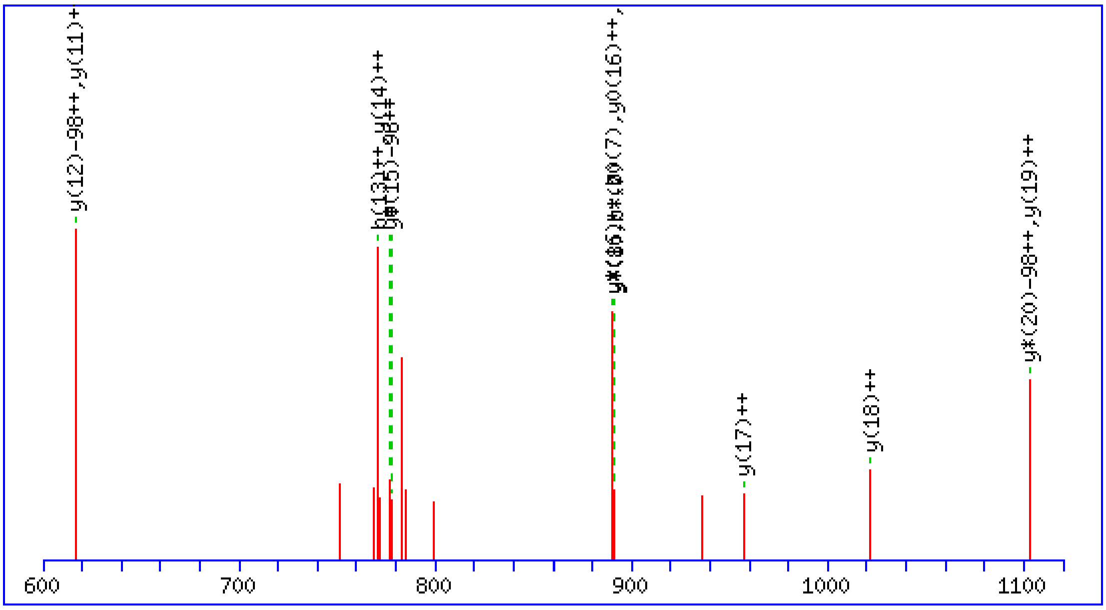
Monoisotopic mass of neutral peptide Mr(calc): 2543.9965
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 **Expect:** 3.2e-006
Matched b ions: b(9), b(11)++, b(11)-98++, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(18)-98++, y(18)++

Peptide No.239

ENYEDQEPLVGHESPITLAAR
Confirmed sites:
Ambiguous sites: @S:14orT:17

MS/MS Fragmentation of **ENYEDQEPLVGHESPITLAAR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 6115: 2447.101173 from(816.707667,3+) index(2725)
Title: Elution from: 43.170 to 43.170 scan no 4352 cid35.00 polarity:+



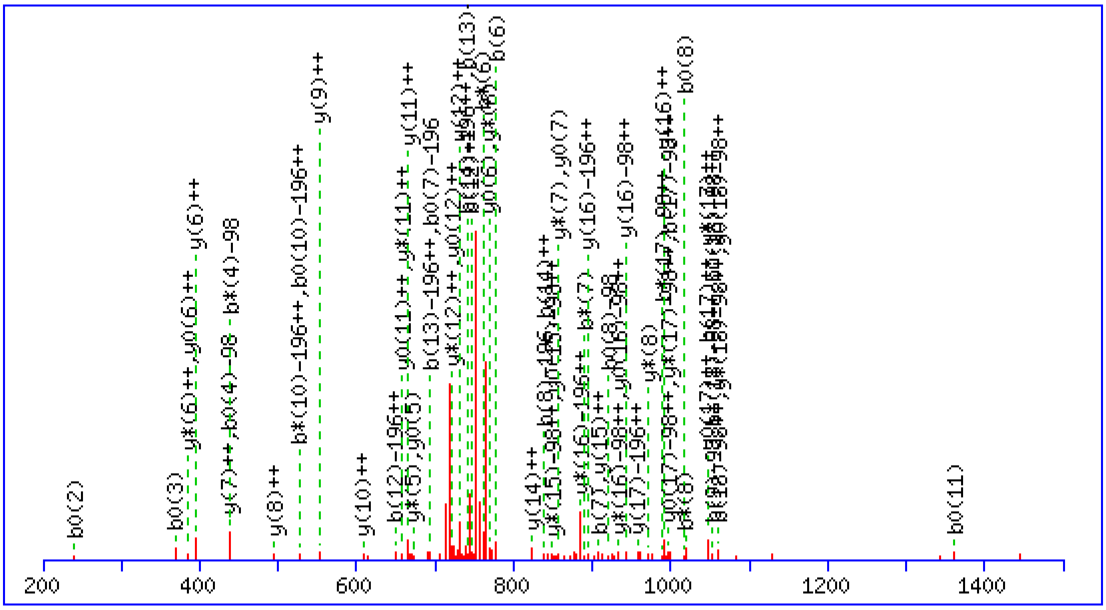
Monoisotopic mass of neutral peptide Mr(calc): 2447.1006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.021
Matched b ions: b(13)++
Matched y ions: y(11)++, y(12)-98++, y(14)++, y(17)++, y(18)++, y(19)++

Peptide No.240

EQESSGEEDNDLSPEEREK
Confirmed sites: @S:4,@S:5
Ambiguous sites:

MS/MS Fragmentation of **EQESSGEEDNDLSPEEREK**
Found in **IPP2_MOUSE** in **SwissProt**, Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3

Match to Query 5113: 2365.844892 from(789.622240,3+) index(3909)
Title: Elution from: 24.061 to 24.061 scan no 1764 cid35.00 polarity:+:m1s



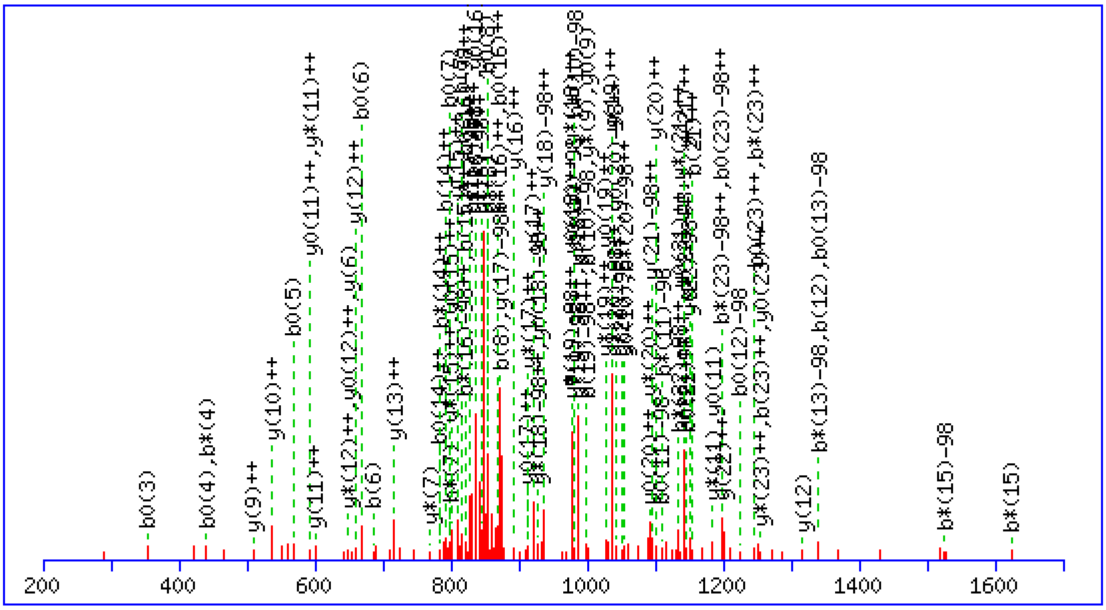
Monoisotopic mass of neutral peptide Mr(calc): 2365.8472
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.019
Matched b ions: b(6), b(7), b(8)-196, b(9)-98, b(12)-196++, b(12)++, b(13)-196++, b(13)-98++, b(14)-196++, b(14)++, b(17)++, b(17)-98++, b(18)-98++
Matched y ions: y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)-196++

Peptide No.241

EQLSEVEGSGEDDQGDDHSESAQK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **EQLSEVEGSGEDDQGDDHSESAQK**
Found in **UBP4_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 4 OS=Mus musculus GN=Usp4 PE=1 SV=3

Match to Query 6399: 2655.007326 from(886.009718,3+) index(3983)
Title: Elution from: 29.145 to 29.145 scan no 1787 cid35.00 polarity:+:m1s



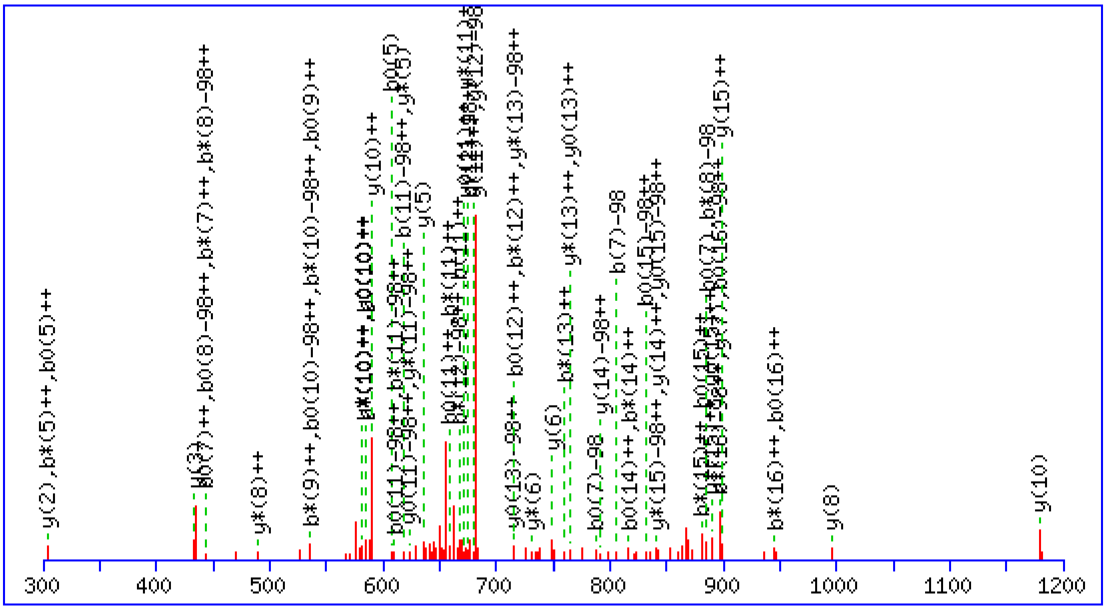
Monoisotopic mass of neutral peptide Mr(calc): 2655.0093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0036
Matched b ions: b(6), b(7), b(8), b(10)-98, b(12), b(14)++, b(15)++, b(16)-98++, b(19)-98++, b(21)++, b(22)-98++, b(23)++
Matched y ions: y(6), y(9)++, y(10)++, y(11)++, y(12), y(12)++, y(13)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++

Peptide No.242

ERDHSPTPSVFNSDEER
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **ERDHSPTPSVFNSDEER**
Found in **FIP1_MOUSE** in **SwissProt**, Pre-mRNA 3'-end-processing factor FIP1 OS=Mus musculus GN=Fip1l1 PE=1 SV=1

Match to Query 4379: 2080.849521 from(694.623783,3+) index(4015)
Title: Elution from: 25.000 to 25.000 scan no 1892 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2080.8487

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 25 **Expect:** 0.015

Matched b ions: b(7)-98, b(11)-98++, b(11)++, b(12)-98++, b(15)++, b(15)-98++

Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(10)++, y(10), y(11)++, y(12)-98++, y(14)-98++, y(14)++, y(15)++

Peptide No.243

ERDTSPDKGELVSDEEEDT

Confirmed sites: @S:13

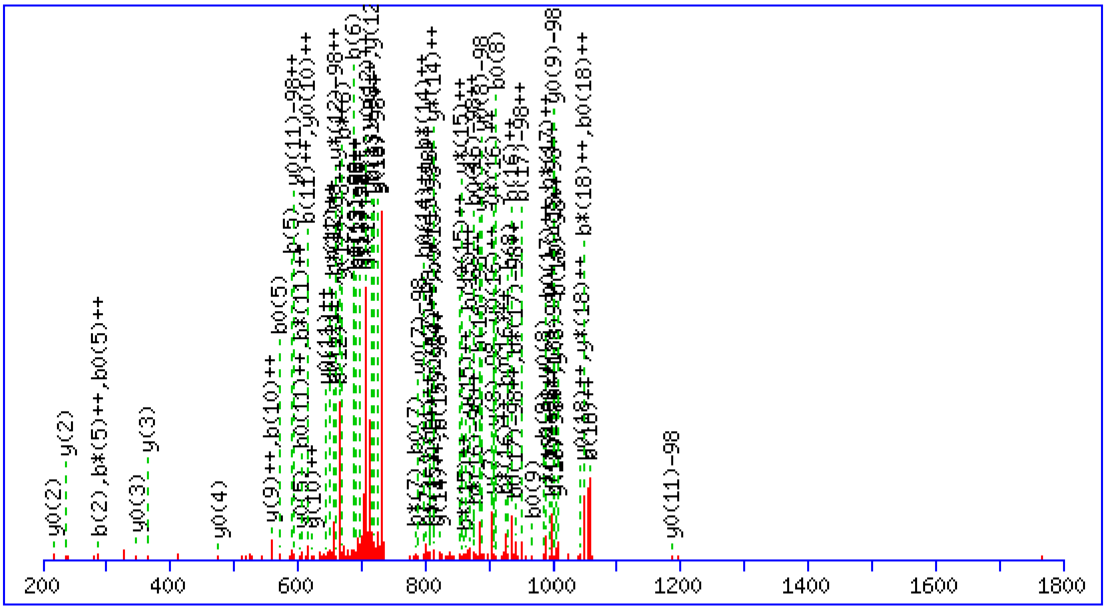
Ambiguous sites:

MS/MS Fragmentation of **ERDTSPDKGELVSDEEEDT**

Found in **TBD2B_MOUSE** in **SwissProt**, TBC1 domain family member 2B OS=Mus musculus GN=Tbc1d2b PE=1 SV=2

Match to Query 4867: 2229.880356 from(744.300728,3+) index(3734)

Title: Elution from: 33.413 to 33.413 scan no 2202 cid35.00 polarity:+:m1s



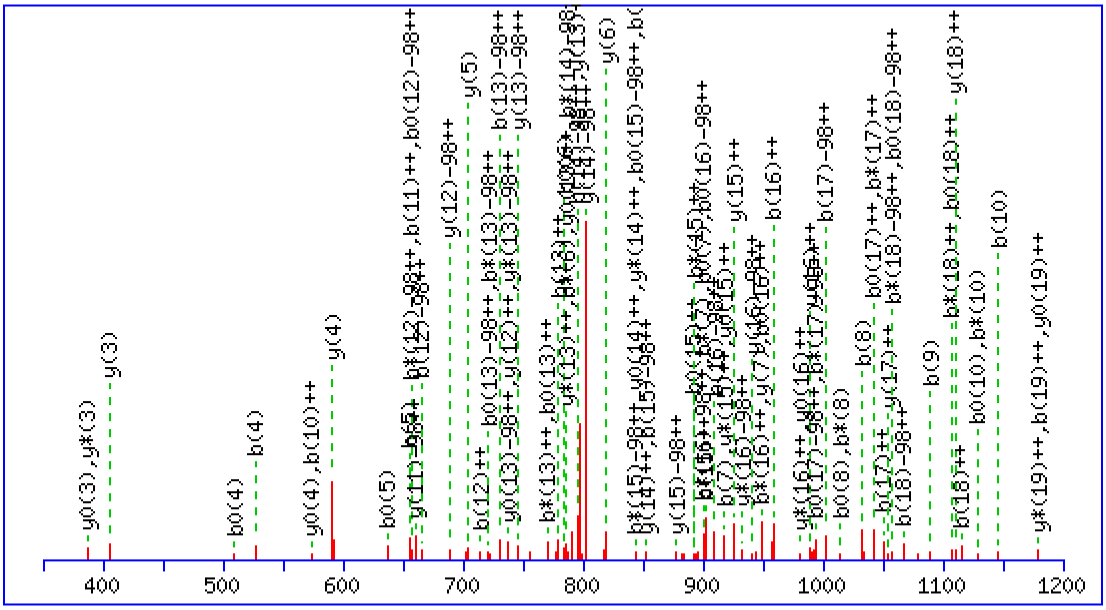
Monoisotopic mass of neutral peptide Mr(calc): 2229.8798
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.023
Matched b ions: b(2), b(5), b(6), b(7), b(8), b(9), b(10)++, b(11)++, b(12)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(7), y(7)-98, y(8)-98, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(14)++, y(15)++, y(18)-98++

Peptide No.244

ERIQQFDDGGSDEEDIWEEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **ERIQQFDDGGSDEEDIWEEK**
Found in **PP6R3_MOUSE** in **SwissProt**, Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Mus musculus GN=Ppp6r3 PE=1 SV=1

Match to Query 5234: 2504.002173 from(835.674667,3+) index(5414)
Title: Elution from: 44.775 to 44.775 scan no 4384 cid35.00 polarity:+:m1s



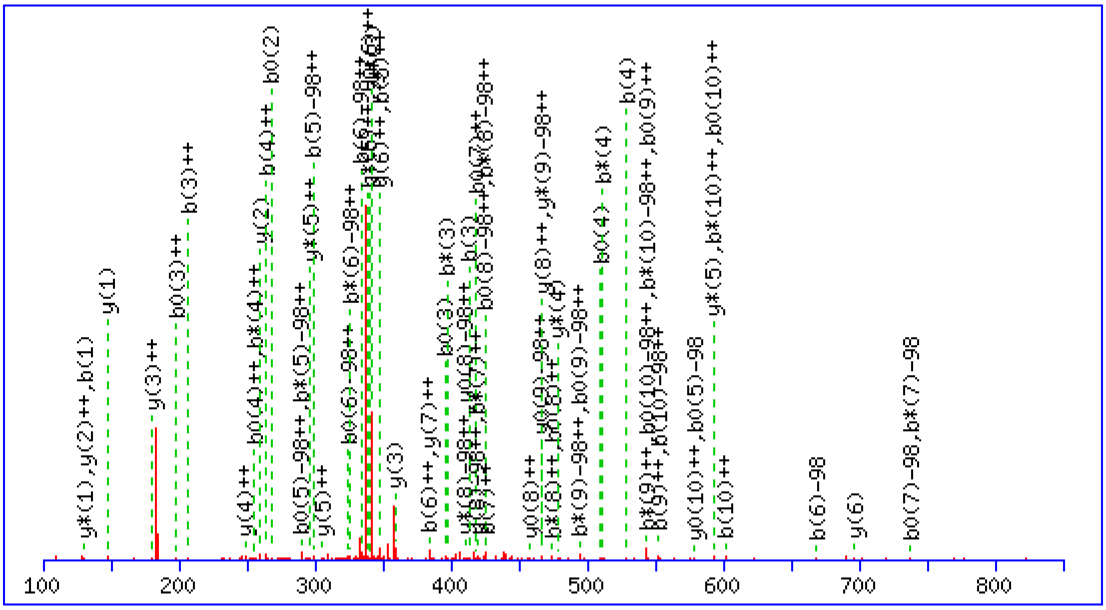
Monoisotopic mass of neutral peptide Mr(calc): 2504.0016
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 **Expect:** 5.5e-007
Matched b ions: b(4), b(5), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)++

Peptide No.245

ERKNSASLHVLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **ERKNSASLHVLK**
Found in **SO1B2_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 2945: 1460.750580 from(366.194921,4+) index(190)
Title: Elution from: 25.590 to 25.590 scan no 1320 cid35.00 polarity:+



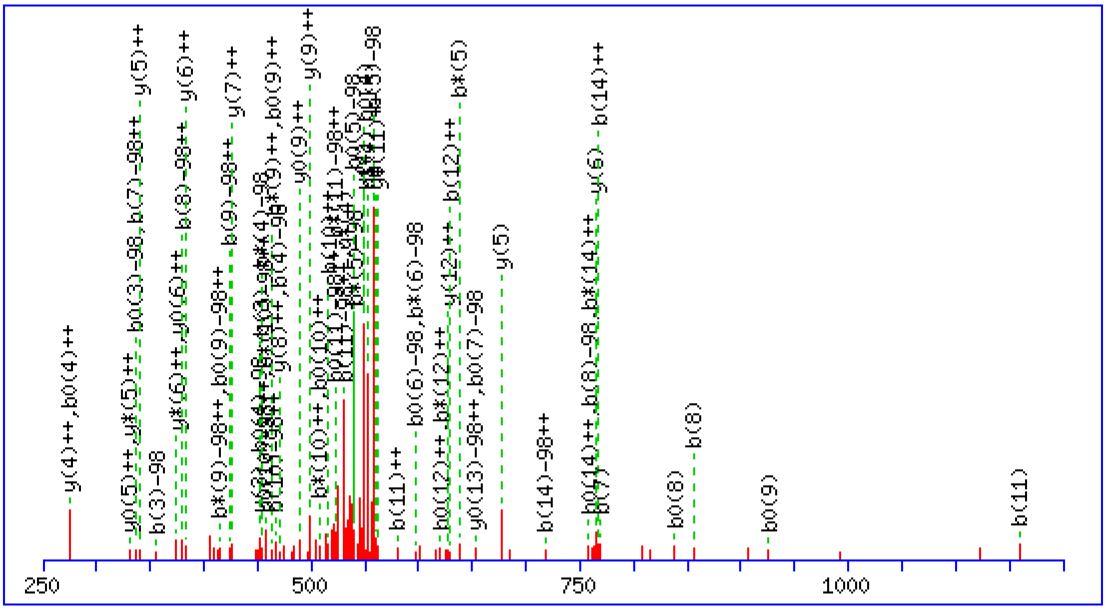
Monoisotopic mass of neutral peptide Mr(calc): 1460.7500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.023
Matched b ions: b(1), b(3)++, b(3), b(4)++, b(4), b(5)-98++, b(5)++, b(6)-98, b(6)++, b(6)-98++, b(7)++, b(9)++, b(10)-98++, b(10)++
Matched y ions: y(1), y(2), y(2)++, y(3), y(3)++, y(4)++, y(5)++, y(6), y(6)++, y(7)++, y(8)-98++, y(8)++

Peptide No.246

ERSDSGGSSSEPFER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ERSDSGGSSSEPFER**
Found in **PRC2A_MOUSE** in **SwissProt**, Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1

Match to Query 3203: 1705.656861 from(569.559563,3+) index(3578)
Title: Elution from: 21.228 to 21.228 scan no 1383 cid35.00 polarity:+:m1s



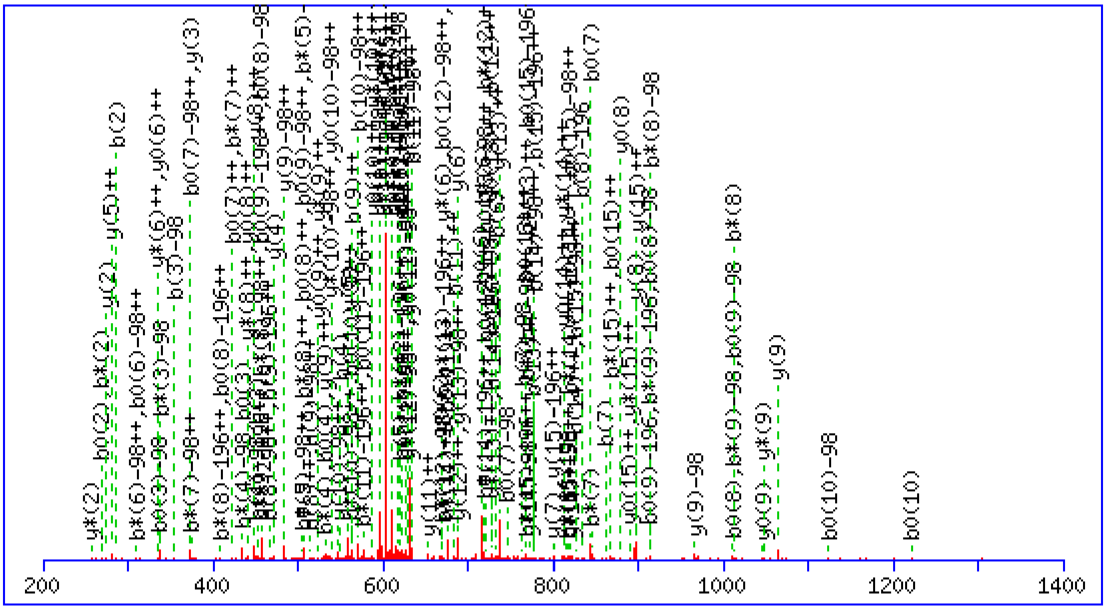
Monoisotopic mass of neutral peptide Mr(calc): 1705.6581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0039
Matched b ions: b(3)-98, b(3), b(4)-98, b(5)-98, b(7)-98++, b(7), b(8), b(8)-98++, b(8)-98, b(9)-98++, b(10)-98++, b(10)++, b(11), b(11)-98++, b(11)++, b(12)++, b(13)-98++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(8)++, y(9)++, y(12)++

Peptide No.247

ERSPALKSPLQSVVVR
Confirmed sites: @S:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of **ERSPALKSPLQSVVVR**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4875: 1924.954485 from(642.658771,3+) index(5326)
Title: Elution from: 44.942 to 44.942 scan no 3686 cid35.00 polarity:+:m1s



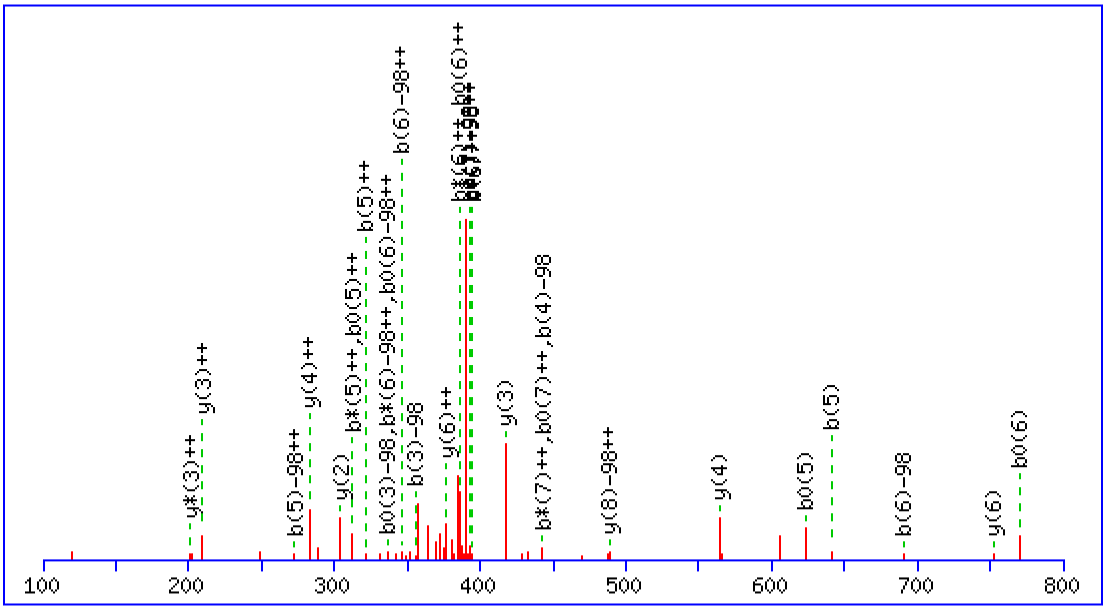
Monoisotopic mass of neutral peptide Mr(calc): 1924.9536
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.004
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6), b(7)-98, b(7), b(8)-98++, b(8)++, b(8)-196, b(9)-196++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(9)-98, y(9), y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-196++

Peptide No.248

ERSSTFLER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **ERSSTFLER**
Found in **S4A4_MOUSE** in **SwissProt**, Electrogenic sodium bicarbonate cotransporter 1 OS=Mus musculus GN=Slc4a4 PE=1 SV=2

Match to Query 1448: 1203.529527 from(402.183785,3+) index(584)
Title: Elution from: 23.491 to 23.491 scan no 1588 cid35.00 polarity:+



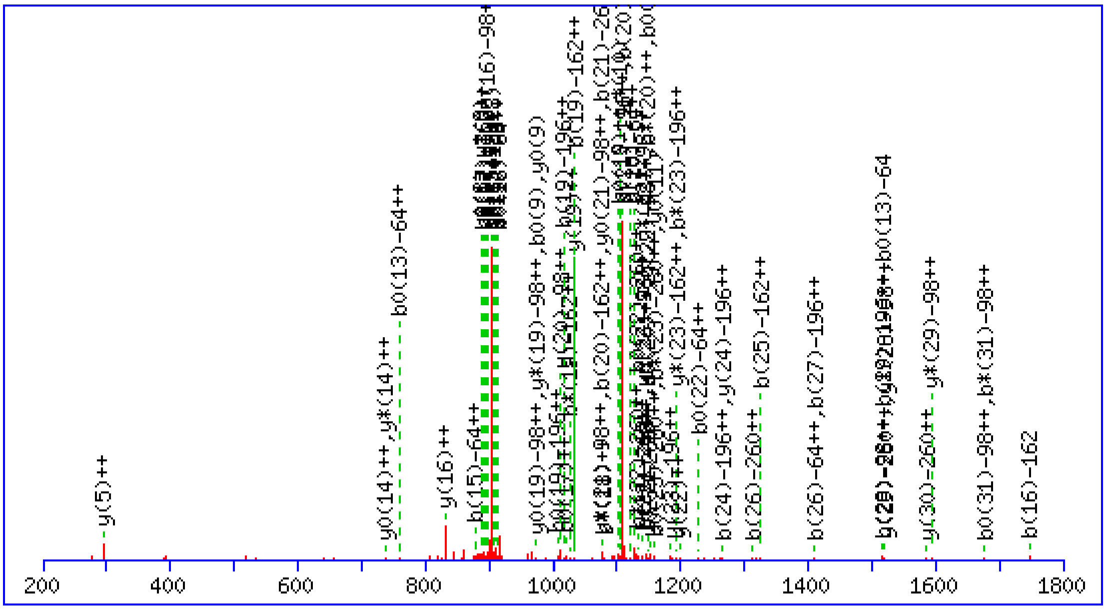
Monoisotopic mass of neutral peptide Mr(calc): 1203.5285
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 18 **Expect:** 0.054
Matched b ions: b(3)-98, b(4)-98, b(5), b(5)-98++, b(5)++, b(6)-98, b(6)-98++, b(6)++
Matched y ions: y(2), y(3)++, y(3), y(4)++, y(4), y(6), y(6)++, y(8)-98++

Peptide No.249

ESAEFSVLEYSEMGSSFNGSPKGESAMLVENTK
Confirmed sites: @S:11,@S:15
Ambiguous sites:

MS/MS Fragmentation of **ESAEFSVLEYSEMGSSFNGSPKGESAMLVENTK**
Found in **RTN4_MOUSE** in **SwissProt**, Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2

Match to Query 6754: 3716.520420 from(930.137381,4+) index(2676)
Title: Elution from: 64.672 to 64.672 scan no 5396 cid35.00 polarity:+



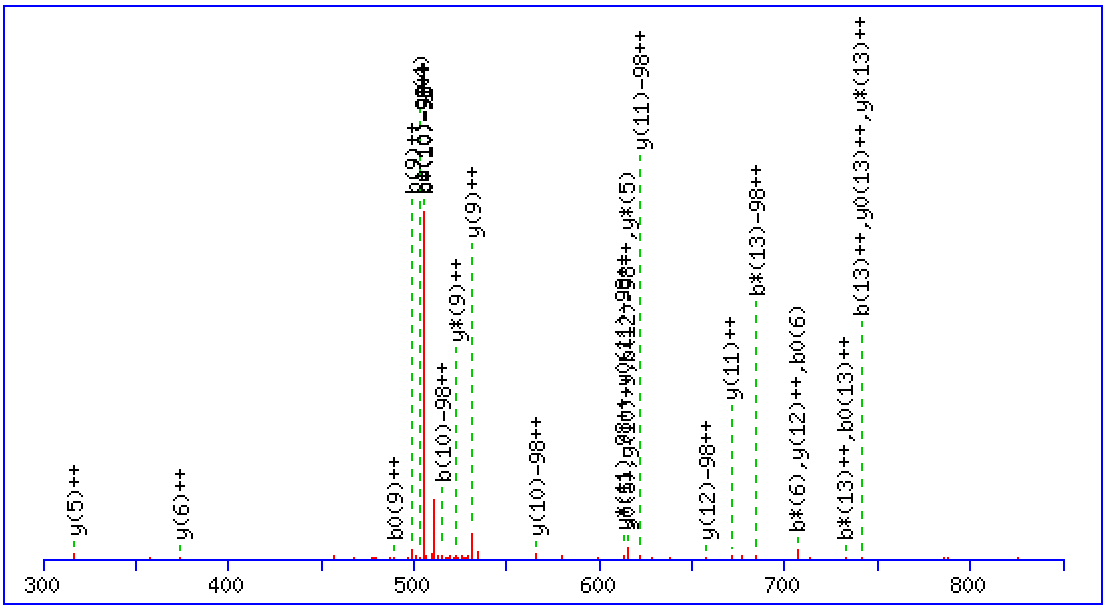
Monoisotopic mass of neutral peptide Mr(calc): 3716.5188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.038
Matched b ions: b(15)++, b(16)-98++, b(19)-196++, b(20)-98++, b(21)-196++, b(24)-196++, b(27)-196++, b(28)-98++, b(29)-196++
Matched y ions: y(5)++, y(8), y(10), y(16)++, y(17)++, y(19)++, y(20)-98++, y(22)++, y(22)-98++, y(23)-196++, y(24)-196++

Peptide No.250

ESALSRASDESLRK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **ESALSRASDESLRK**
Found in **S20A2_MOUSE** in **SwissProt**, Sodium-dependent phosphate transporter 2 OS=Mus musculus GN=Slc20a2 PE=1 SV=2

Match to Query 3326: 1627.755645 from(543.592491,3+) index(415)
Title: Elution from: 20.152 to 20.152 scan no 1259 cid35.00 polarity:+



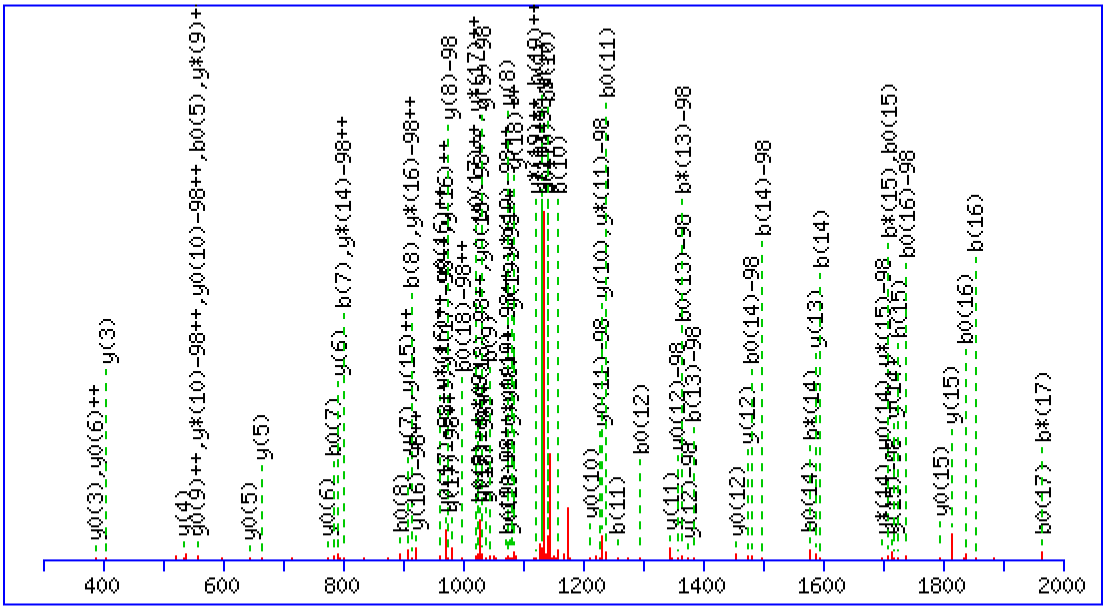
Monoisotopic mass of neutral peptide Mr(calc): 1627.7566
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.005
Matched b ions: b(9)++, b(10)-98++, b(12)-98++, b(13)++
Matched y ions: y(4), y(5)++, y(6)++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++

Peptide No.251

ESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6047: 2386.904558 from(1194.459555,2+) index(4682)
Title: Elution from: 36.473 to 36.473 scan no 2701 cid35.00 polarity:+:m1s



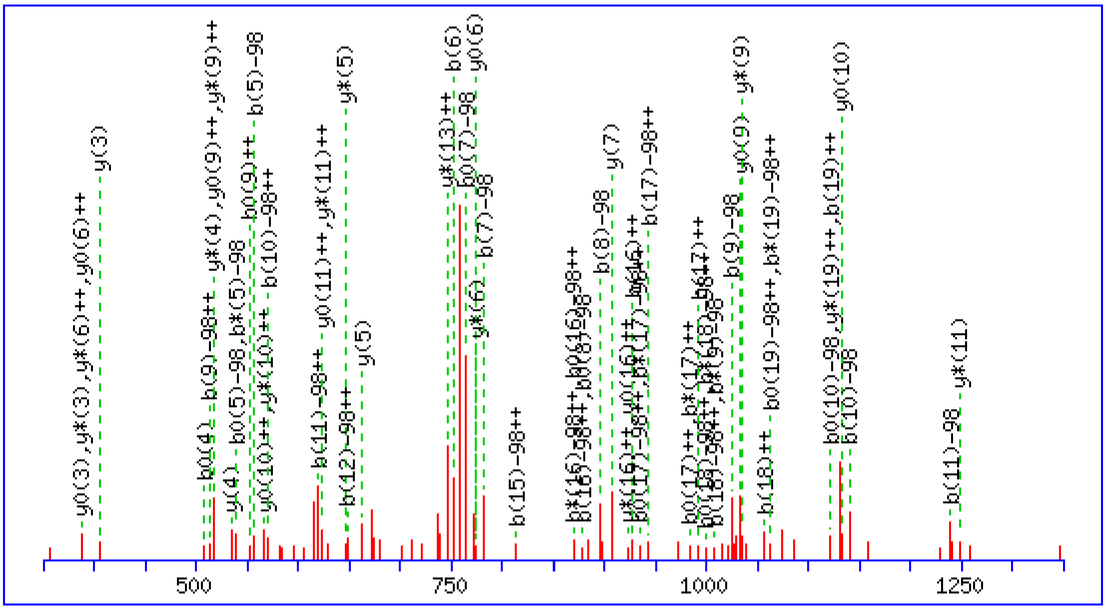
Monoisotopic mass of neutral peptide Mr(calc): 2386.9061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 **Expect:** 2.7e-007
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(13)-98, b(14), b(14)-98, b(15), b(16), b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(12), y(12)-98, y(13), y(14), y(15)-98, y(15), y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++, y(19)++

Peptide No.252

ESDDKPEIEDVGSDEEEEEK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5160: 2386.906608 from(796.642812,3+) index(4448)
Title: Elution from: 28.964 to 28.964 scan no 2430 cid35.00 polarity:+:m1s



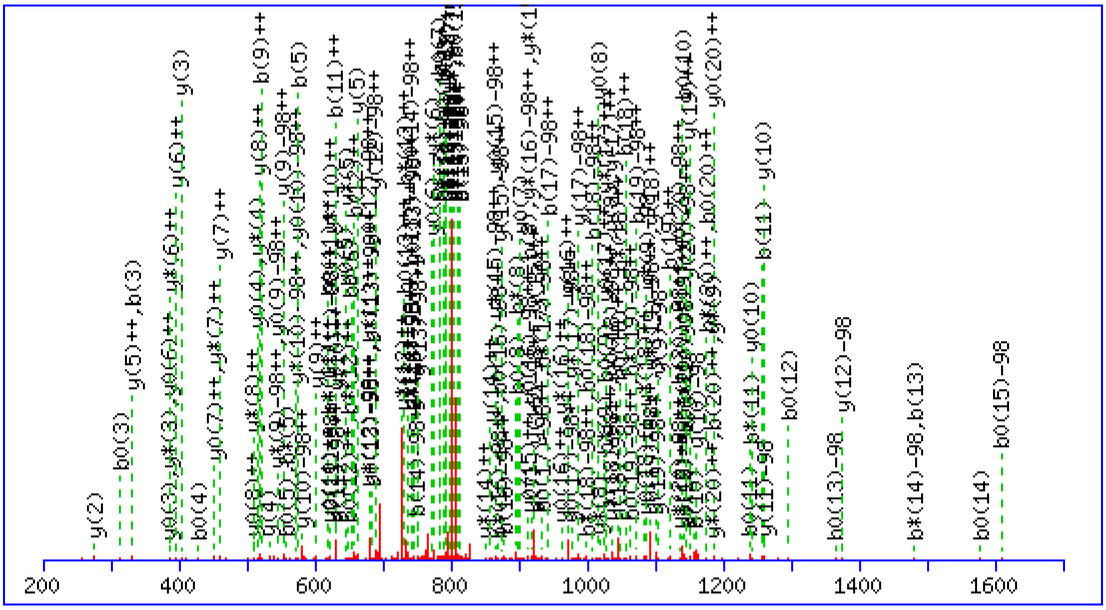
Monoisotopic mass of neutral peptide Mr(calc): 2386.9061
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0065
Matched b ions: b(5)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(9)-98++, b(10)-98, b(10)-98++, b(11)-98++, b(11)-98, b(12)-98++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(7)

Peptide No.253

ESDDKPEIEDVGSDEEEEEKK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEKK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6237: 2514.999255 from(839.340361,3+) index(4742)
Title: Elution from: 27.119 to 27.119 scan no 2205 cid35.00 polarity:+:m1s



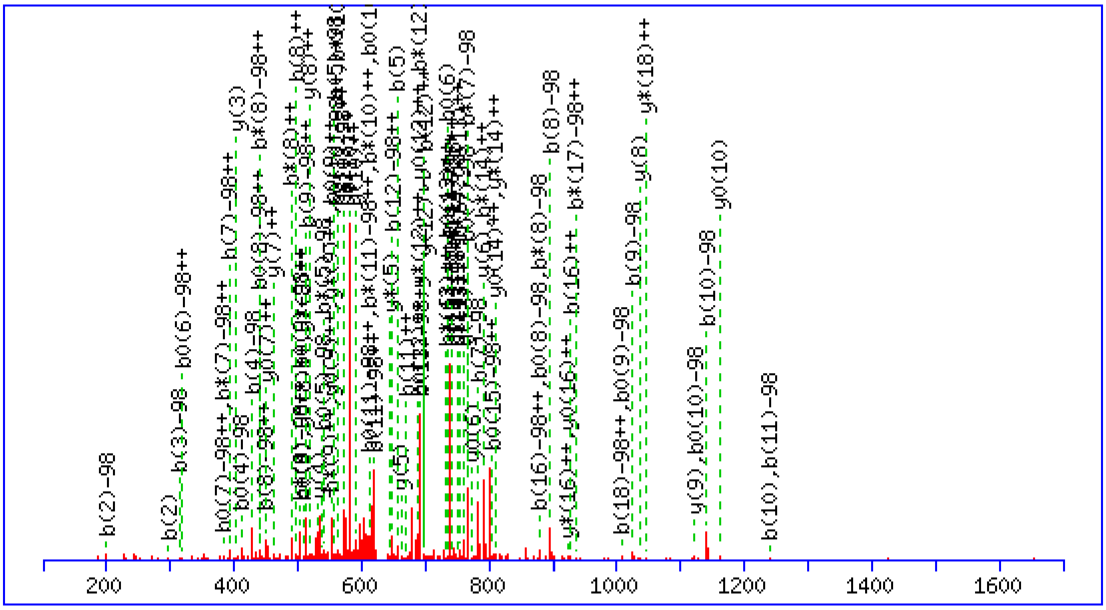
Monoisotopic mass of neutral peptide Mr(calc): 2515.0010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 **Expect:** 7.9e-008
Matched b ions: b(3), b(5), b(7), b(8), b(9)++, b(10), b(11), b(11)++, b(12)++, b(13), b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)-98++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)-98++, y(9)++, y(9)-98, y(10)++, y(10)-98, y(10), y(10)-98++, y(11)-98++, y(11)-98, y(11)++, y(12)-98, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++

Peptide No.254

ESDDKPEIEDVGSDEEEEEKK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEKK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6242: 2515.002480 from(629.757896,4+) index(4445)
Title: Elution from: 34.107 to 34.107 scan no 2394 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2515.0010
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.055
Matched b ions: b(2)-98, b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(7)-98++, b(7)-98, b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10)-98, b(10), b(10)-98++, b(11)-98++, b(11)-98, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(16)++, b(16)-98++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)++, y(13)++

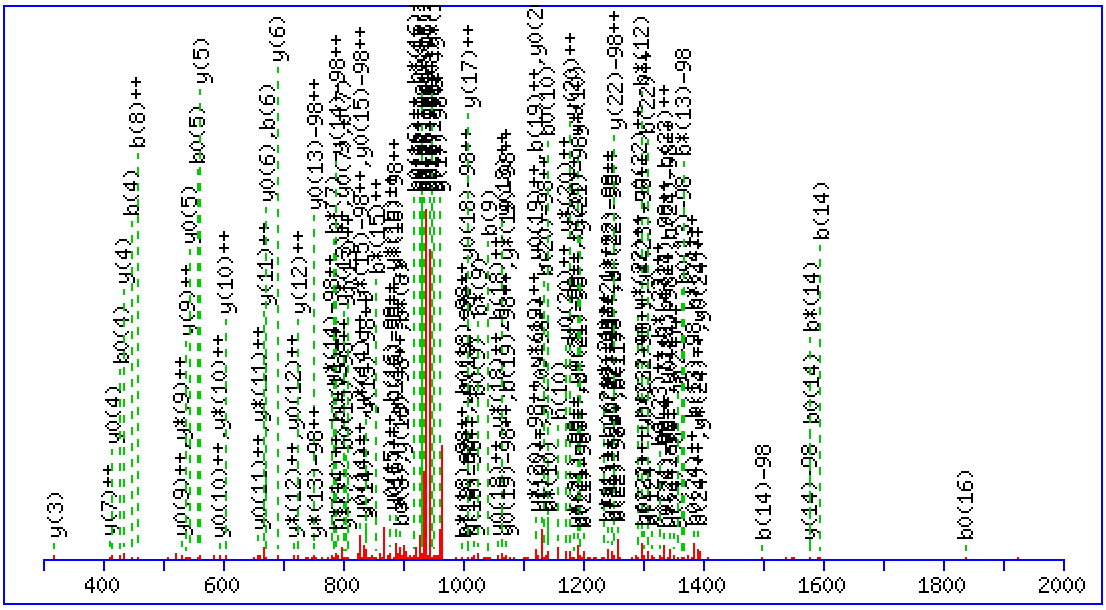
Peptide No.255

ESDDKPEIEDVGSDEEEEEKKDGDK

Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEKKDGDK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6537: 2930.171043 from(977.730957,3+) index(4296)
Title: Elution from: 32.516 to 32.516 scan no 2199 cid35.00 polarity:+:m1s



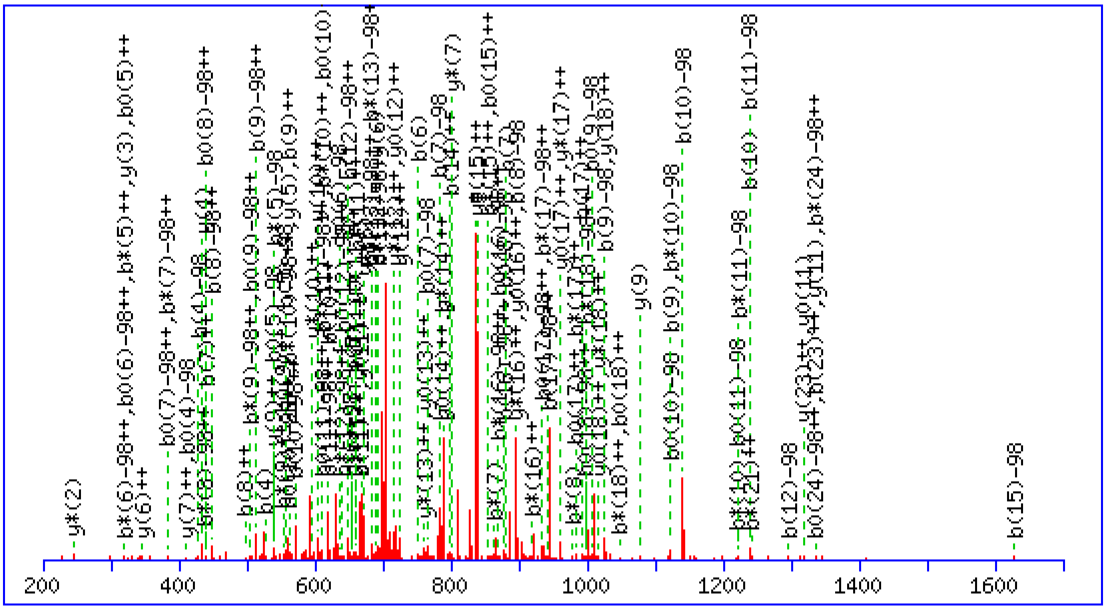
Monoisotopic mass of neutral peptide Mr(calc): 2930.1713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 9.1e-007
Matched b ions: b(4), b(6), b(7), b(8)++, b(9), b(10), b(11), b(12), b(13)-98, b(14)-98, b(14), b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(24)++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(8), y(9)++, y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14)-98++, y(14)-98, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++, y(24)-98++

Peptide No.256

ESDDKPEIEDVGSDEEEEEKKDGDK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ESDDKPEIEDVGSDEEEEEKKDGDK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 6540: 2930.172240 from(733.550336,4+) index(4116)
Title: Elution from: 30.548 to 30.548 scan no 1957 cid35.00 polarity:+:m1s



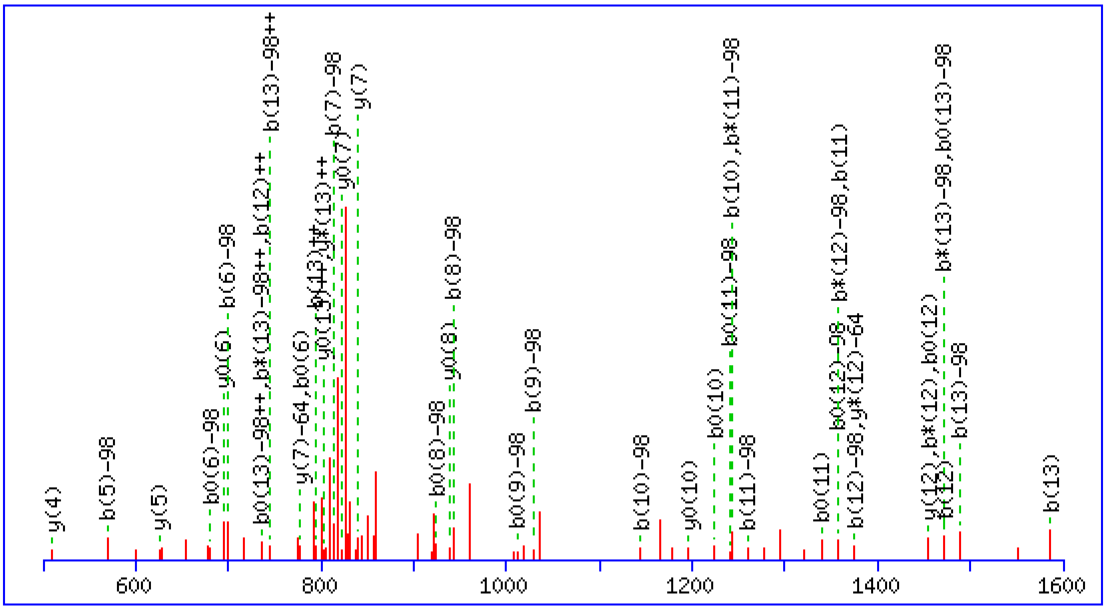
Monoisotopic mass of neutral peptide Mr(calc): 2930.1713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.017
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)++, b(7), b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(9), b(9)-98, b(9)++, b(10)-98, b(10)++, b(10)-98++, b(10), b(11)-98, b(11)-98++, b(11)++, b(12)-98, b(12)-98++, b(13)-98++, b(14)++, b(15)-98, b(16)-98++, b(17)-98++, b(17)++, b(23)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(9), y(9)++, y(10)++, y(11), y(11)++, y(12)++, y(18)++, y(23)++

Peptide No.257

ESLKEEDESDDDNM
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ESLKEEDESDDDNM**
Found in **PSA3_MOUSE** in **SwissProt**, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3826: 1750.575658 from(876.295105,2+) index(87)
Title: Elution from: 23.504 to 23.504 scan no 1131 cid35.00 polarity:+



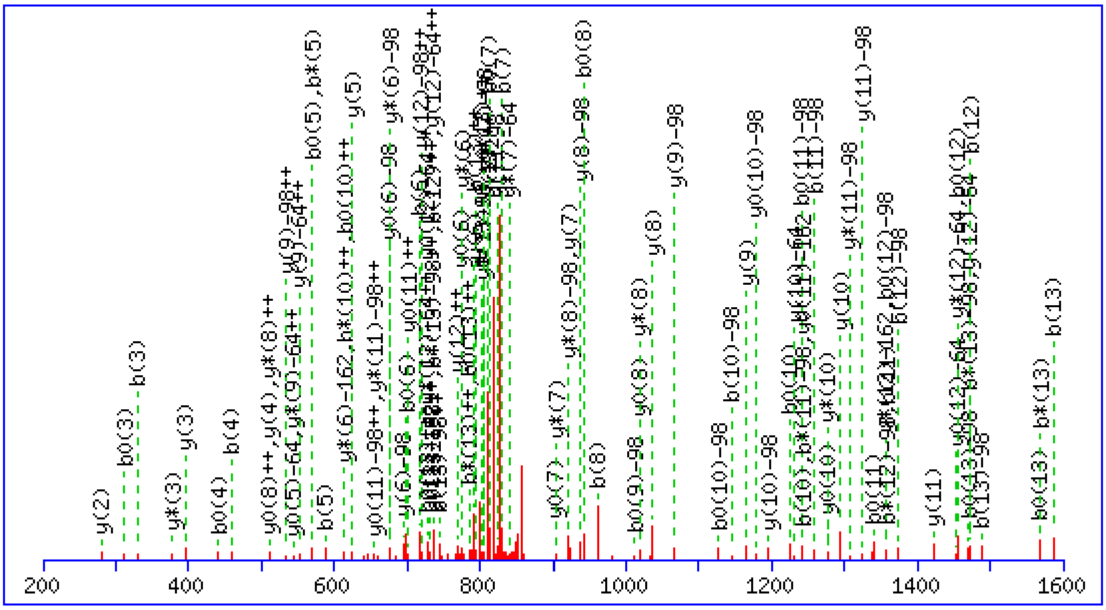
Monoisotopic mass of neutral peptide Mr(calc): 1750.5764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 43 **Expect:** 5.7e-005
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(13)-98, b(13), b(13)-98++, b(13)++
Matched y ions: y(4), y(5), y(7), y(12)

Peptide No.258

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **ESLKEEDESDDDNM**
Found in **PSA3_MOUSE** in **SwissProt**, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3391: 1750.575950 from(876.295251,2+) index(218)
Title: Elution from: 19.008 to 19.008 scan no 1085 cid35.00 polarity:+



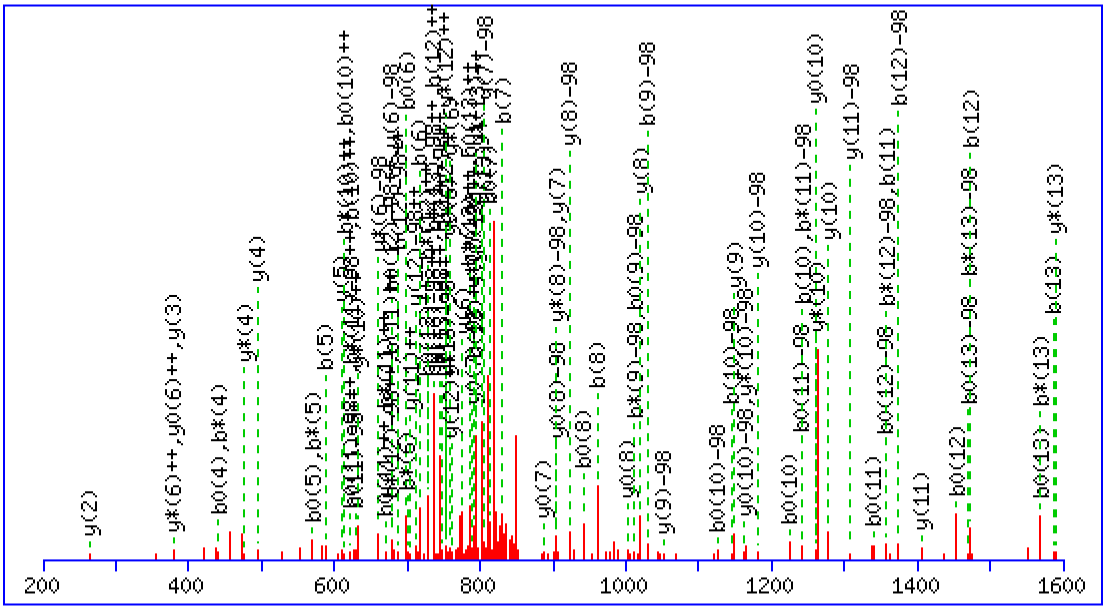
Monoisotopic mass of neutral peptide Mr(calc): 1750.5764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 58 **Expect:** 1.8e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(10), b(10)-98, b(11)-98, b(11), b(12)++, b(12)-98, b(12), b(13), b(13)-98, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(9)-98++, y(10), y(10)-98, y(11), y(11)-98, y(12)++, y(12)-98++, y(13)++

Peptide No.259

ESLKEEDESDDDNM
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **ESLKEEDESDDDNM**
Found in **PSA3_MOUSE** in **SwissProt**, Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3

Match to Query 3962: 1734.579356 from(868.296954,2+) index(964)
Title: Elution from: 24.305 to 24.305 scan no 1859 cid35.00 polarity:+



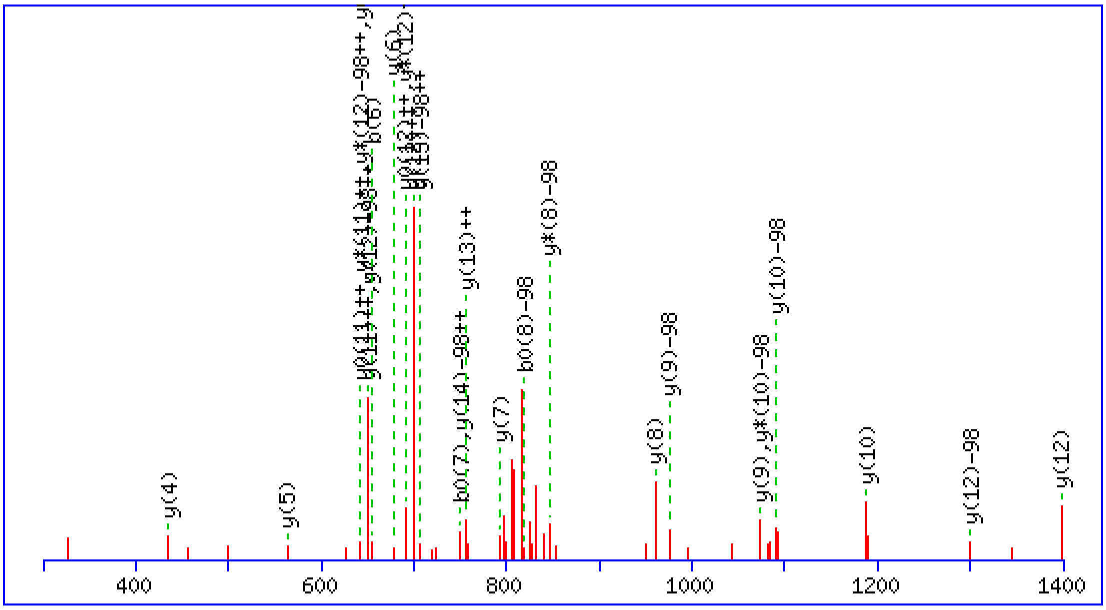
Monoisotopic mass of neutral peptide Mr(calc): 1734.5815
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00017
Matched b ions: b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(10), b(10)++, b(11), b(11)++, b(11)-98++, b(12)++, b(12), b(12)-98, b(12)-98++, b(13)-98++, b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++

Peptide No.260

ESLPLDLSDDQSNSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **ESLPLDLSDDQSNSK**
Found in **NVL_MOUSE** in **SwissProt**, Nuclear valosin-containing protein-like OS=Mus musculus GN=Nvl PE=1 SV=1

Match to Query 3735: 1726.730304 from(864.372428,2+) index(6263)
Title: Elution from: 43.254 to 43.254 scan no 4363 cid35.00 polarity:+:m1s



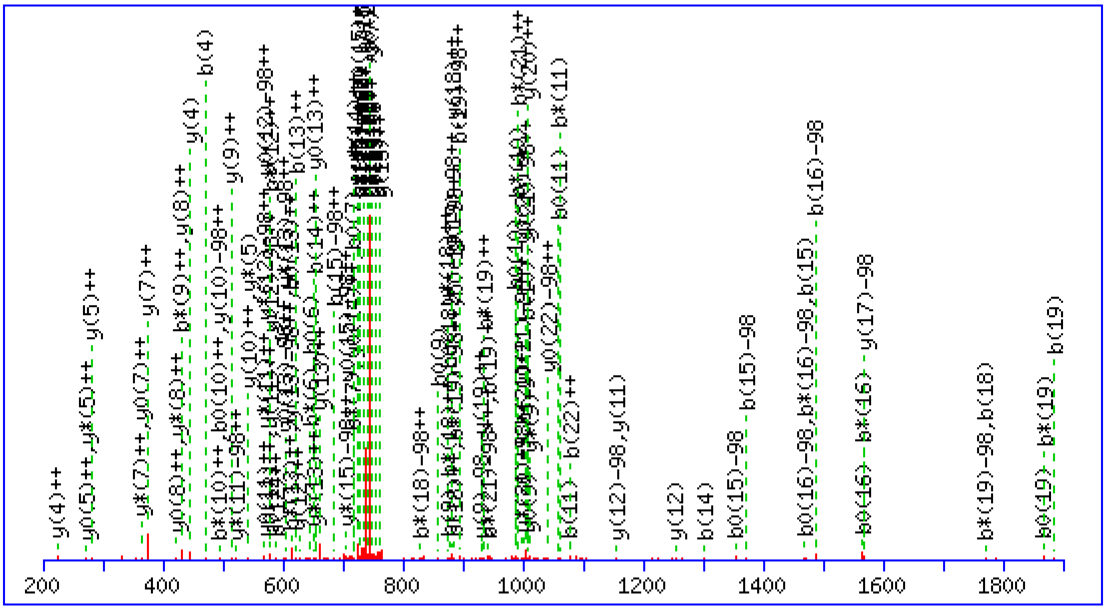
Monoisotopic mass of neutral peptide Mr(calc): 1726.7298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.00092
Matched b ions: b(6), b(12)++, b(12)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)++, y(12)++, y(12)-98, y(12), y(12)-98++, y(13)++, y(13)-98++, y(14)-98++

Peptide No.261

ESPRPPAAAEAPAGSDGEDGGRR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **ESPRPPAAAEAPAGSDGEDGGRR**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 5833: 2329.008213 from(777.343347,3+) index(3735)
Title: Elution from: 26.403 to 26.403 scan no 1454 cid35.00 polarity:+:m1s



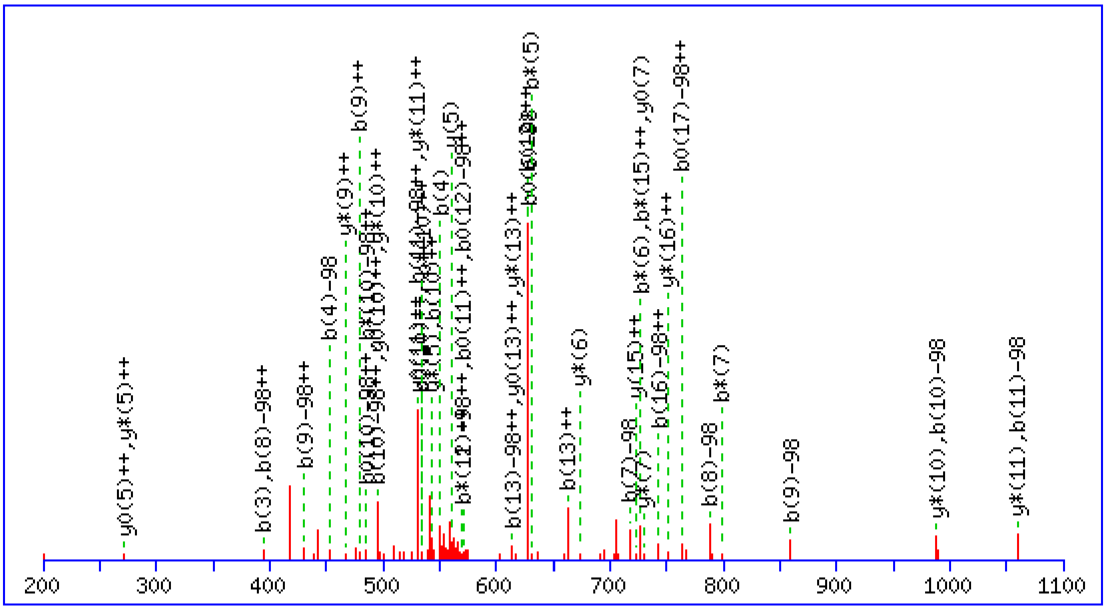
Monoisotopic mass of neutral peptide Mr(calc): 2329.0084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00089
Matched b ions: b(4), b(7), b(9), b(10), b(11), b(12)++, b(13)++, b(14), b(14)++, b(15)-98, b(15), b(15)++, b(15)-98++, b(16)-98, b(16)-98++, b(18), b(18)++, b(19)++, b(19), b(19)-98++, b(21)++, b(22)++
Matched y ions: y(4)++, y(4), y(5)++, y(7)++, y(7), y(8)++, y(9)++, y(9)-98, y(10)-98++, y(10)++, y(11), y(11)++, y(12)-98, y(12)-98++, y(12), y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(17)-98, y(18)++, y(19)-98++, y(19)++, y(20)++, y(21)-98++

Peptide No.262

ESPRPPAAAEAPAGSDGEDGGRR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **ESPRPPAAAEAPAGSDGEDGGRR**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 5883: 2329.006764 from(583.258967,4+) index(4019)
Title: Elution from: 20.747 to 20.747 scan no 1339 cid35.00 polarity:+:m1s



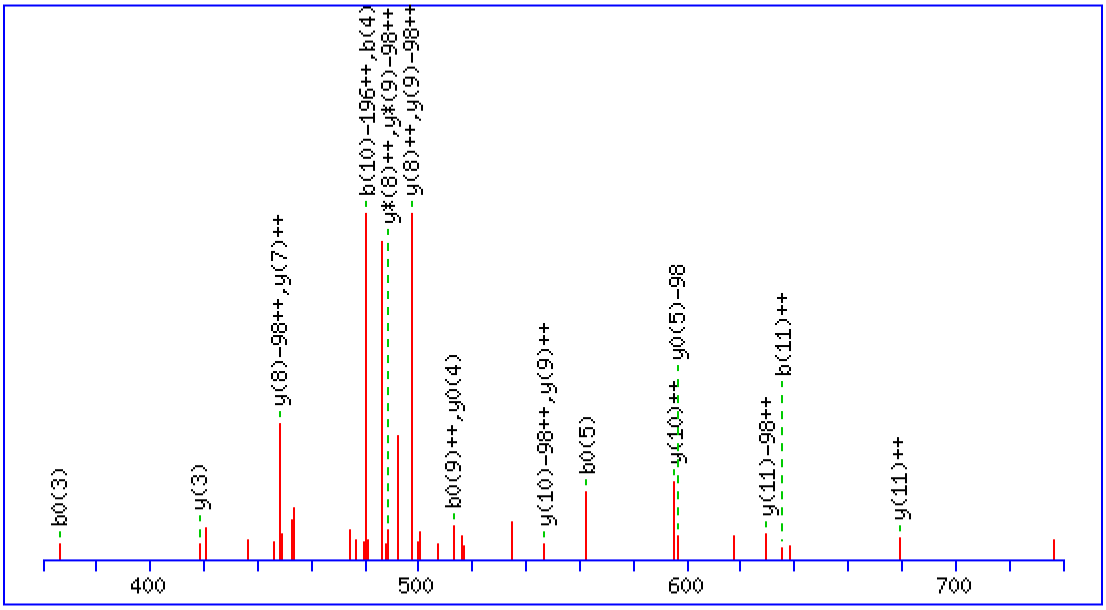
Monoisotopic mass of neutral peptide Mr(calc): 2329.0084
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.013
Matched b ions: b(3), b(4), b(4)-98, b(7)-98, b(8)-98++, b(8)-98, b(9)-98, b(9)-98++, b(9)++, b(10)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)-98, b(12)++, b(13)++, b(13)-98++, b(16)-98++
Matched y ions: y(5), y(15)++

Peptide No.263

ESSPVPSPTLDRK
Confirmed sites: @S:3
Ambiguous sites: @S:7orT:9

MS/MS Fragmentation of **ESSPVPSPTLDRK**
Found in **SPTB2_MOUSE** in **SwissProt**, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 3123: 1571.664324 from(524.895384,3+) index(4566)
Title: Elution from: 25.366 to 25.366 scan no 1967 cid35.00 polarity:+:m1s



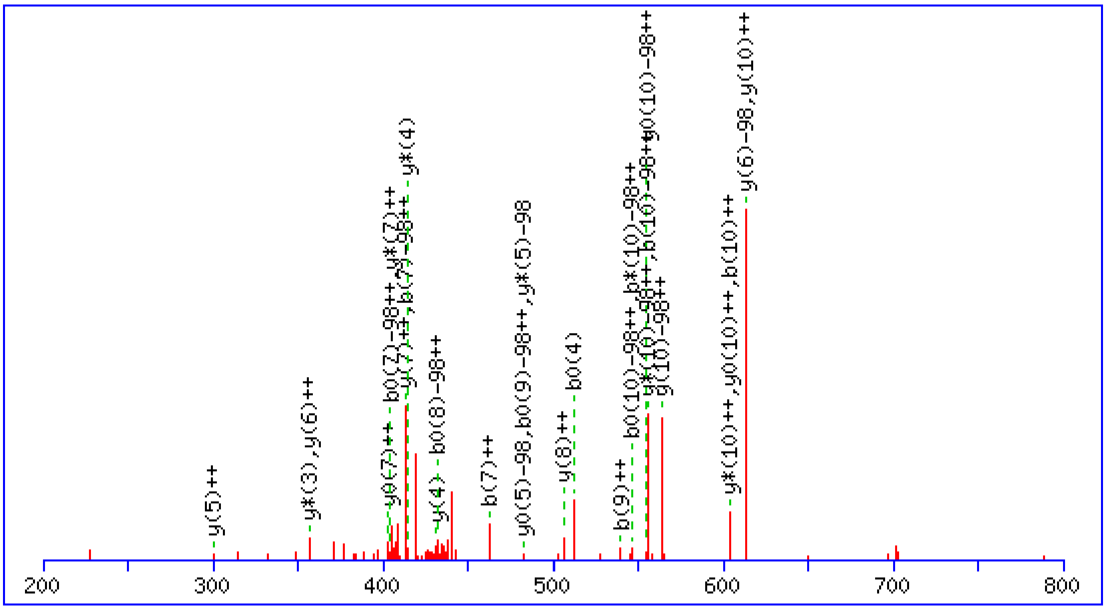
Monoisotopic mass of neutral peptide Mr(calc): 1571.6633
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.035
Matched b ions: b(4), b(10)-196++, b(11)++
Matched y ions: y(3), y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.264

ETLWLLSGVKK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **ETLWLLSGVKK**
Found in **GCP5_MOUSE** in **SwissProt**, Gamma-tubulin complex component 5 OS=Mus musculus GN=Tubgcp5 PE=2 SV=2

Match to Query 2095: 1352.706903 from(451.909577,3+) index(1134)
Title: Elution from: 28.285 to 28.285 scan no 2249 cid35.00 polarity:+



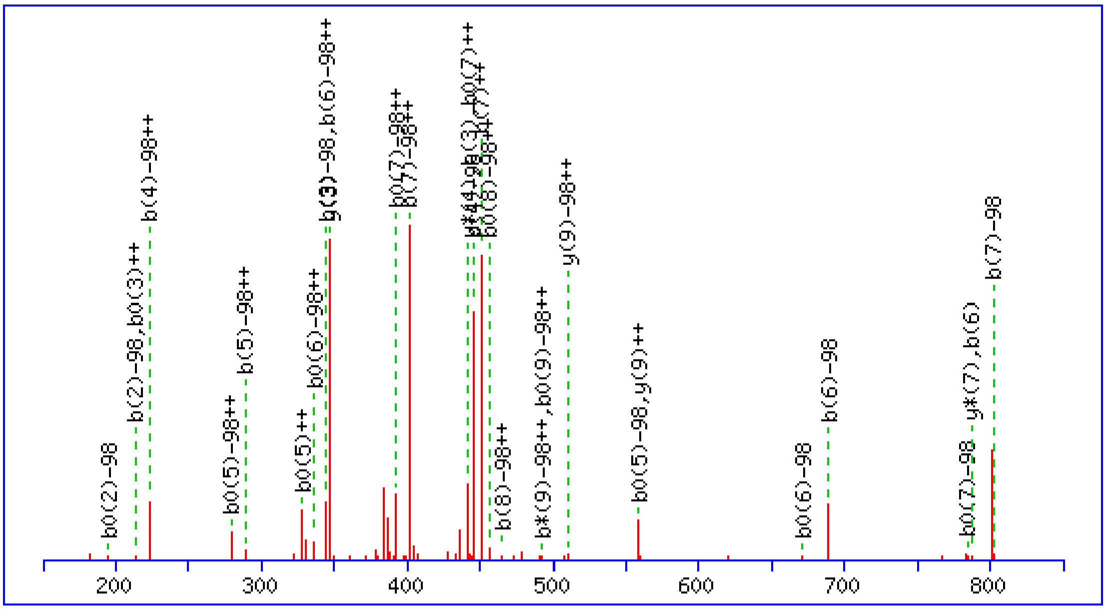
Monoisotopic mass of neutral peptide Mr(calc): 1352.7105
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.026
Matched b ions: b(7)-98++, b(7)++, b(9)++, b(10)-98++, b(10)++
Matched y ions: y(4), y(5)++, y(6)-98, y(6)++, y(7)++, y(8)++, y(10)++, y(10)-98++

Peptide No.265

ETMTMILKAK
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of **ETMTMILKAK**
Found in **KS6A3_MOUSE** in **SwissProt**, Ribosomal protein S6 kinase alpha-3 OS=Mus musculus GN=Rps6ka3 PE=1 SV=2

Match to Query 1866: 1244.590149 from(415.870659,3+) index(512)
Title: Elution from: 20.444 to 20.444 scan no 1334 cid35.00 polarity:+



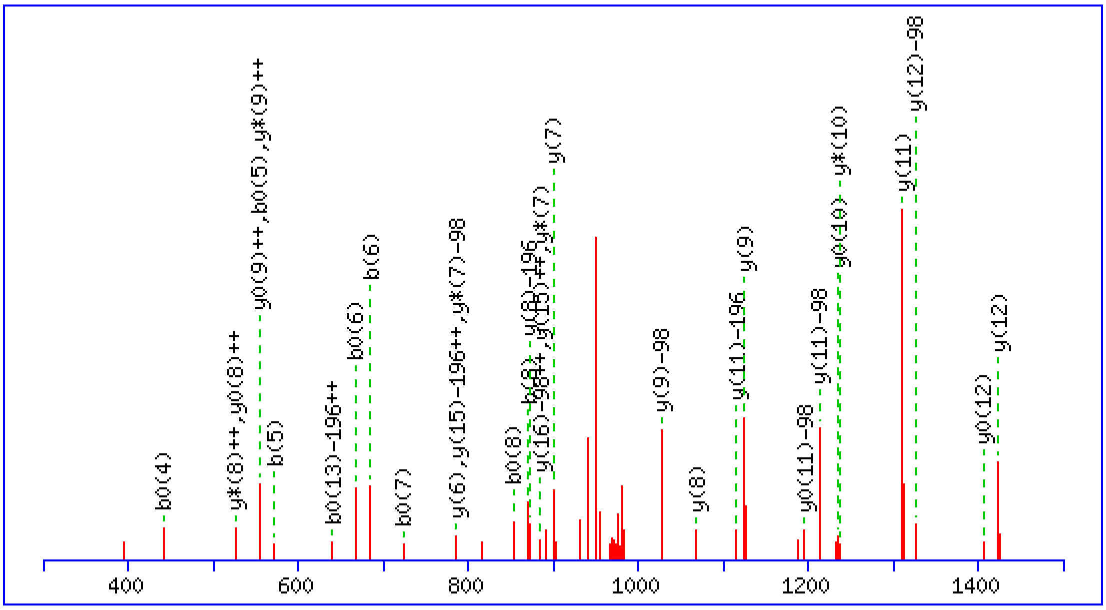
Monoisotopic mass of neutral peptide Mr(calc): 1244.5909
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(2)-98, b(3)-98, b(3), b(4)-98++, b(4)-98, b(5)-98++, b(6)-98++, b(6)-98, b(6), b(7)-98++, b(7)++, b(7)-98, b(8)-98++
Matched y ions: y(3), y(9)++, y(9)-98++

Peptide No.266

EVDDILGEGSDDSDIEK
Confirmed sites: @S:10,@S:13
Ambiguous sites:

MS/MS Fragmentation of **EVDDILGEGSDDSDIEK**
Found in **CTDP1_MOUSE** in **SwissProt**, RNA polymerase II subunit A C-terminal domain phosphatase OS=Mus musculus GN=Ctdp1 PE=1 SV=1

Match to Query 4207: 1994.727486 from(998.371019,2+) index(5579)
Title: Elution from: 47.862 to 47.862 scan no 4733 cid35.00 polarity:+:m1s



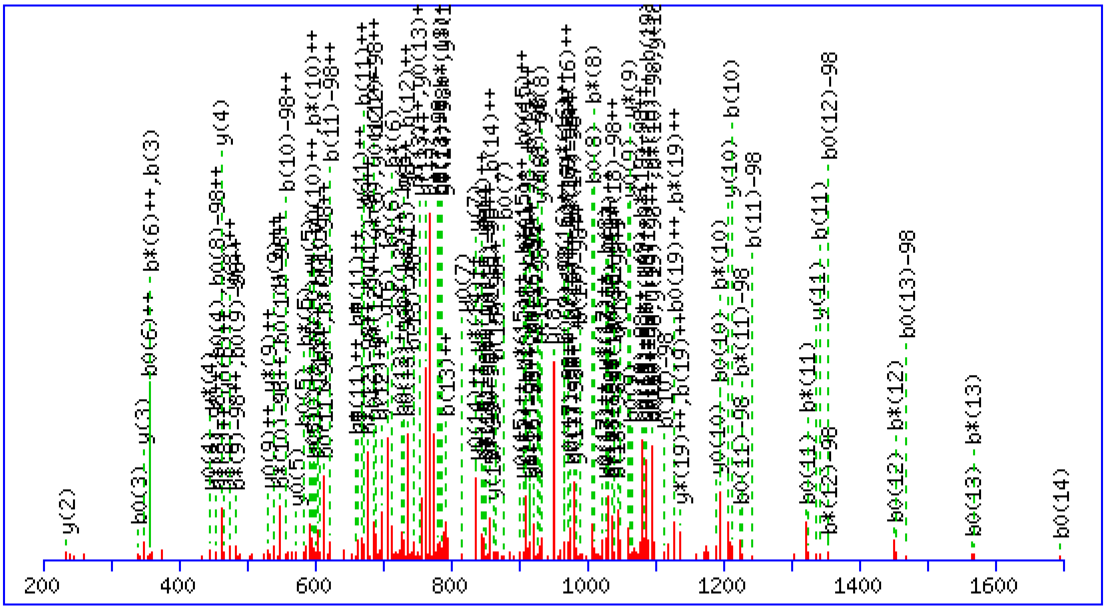
Monoisotopic mass of neutral peptide Mr(calc): 1994.7283
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.0098
Matched b ions: b(5), b(6), b(8)
Matched y ions: y(6), y(7), y(8), y(8)-196, y(9)-98, y(9), y(11)-98, y(11), y(11)-196, y(12), y(12)-98, y(15)-196++, y(15)++, y(16)-98++

Peptide No.267

EVEDKESEGEEEDEDEDLSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **EVEDKESEGEEEDEDEDLSK**
Found in **ZRAB2_MOUSE** in **SwissProt**, Zinc finger Ran-binding domain-containing protein 2 OS=Mus musculus GN=Zranb2 PE=1 SV=2

Match to Query 6061: 2418.890475 from(807.304101,3+) index(4326)
Title: Elution from: 23.330 to 23.330 scan no 1690 cid35.00 polarity:+:m1s



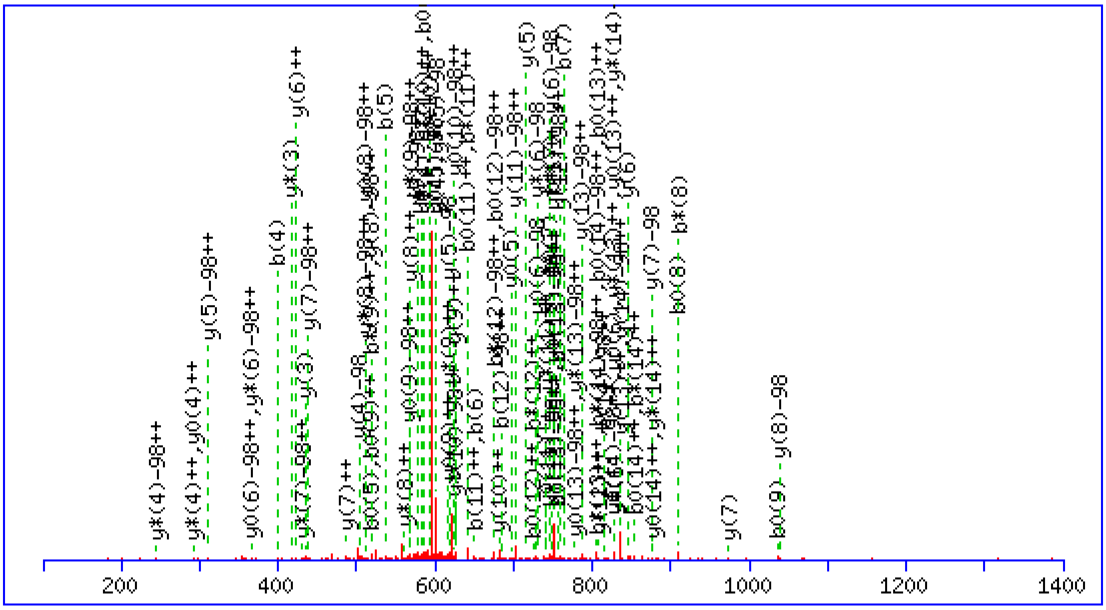
Monoisotopic mass of neutral peptide Mr(calc): 2418.8959
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 **Expect:** 2e-007
Matched b ions: b(3), b(5), b(6), b(8), b(8)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++

Peptide No.268

EVGIHLNYKEDSCVR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **EVGIHLNYKEDSCVR**
Found in **CRRY_MOUSE** in **SwissProt**, Complement regulatory protein Crry OS=Mus musculus GN=Crry PE=1 SV=1

Match to Query 4147: 1897.841367 from(633.621065,3+) index(4306)
Title: Elution from: 40.218 to 40.218 scan no 3009 cid35.00 polarity:+:m1s



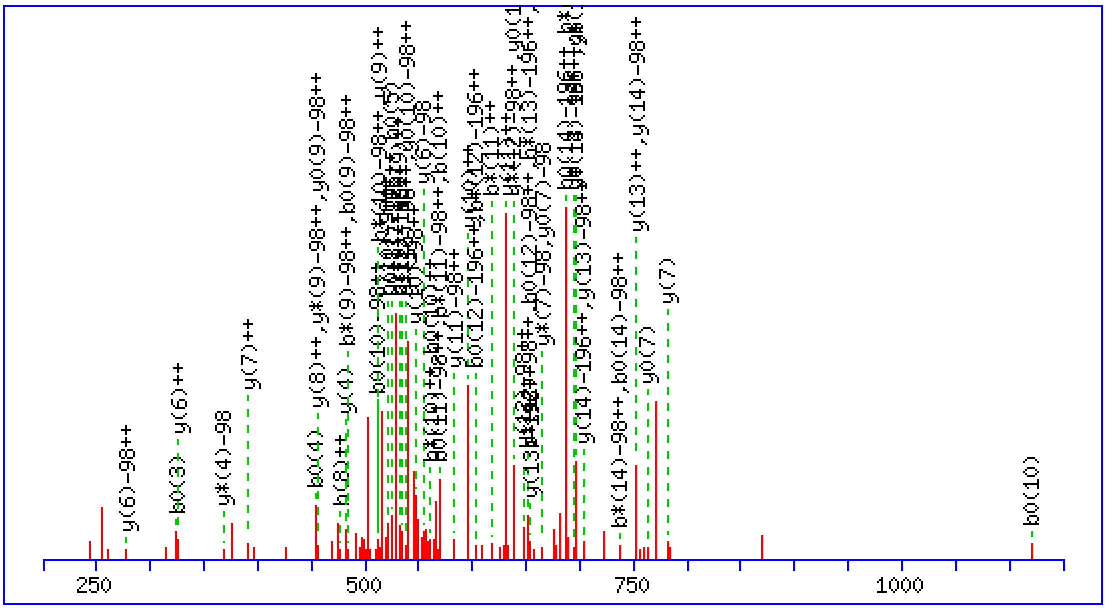
Monoisotopic mass of neutral peptide Mr(calc): 1897.8393
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.029
Matched b ions: b(4), b(5), b(6), b(7), b(10)++, b(11)++, b(12)-98++, b(14)-98++
Matched y ions: y(3), y(4), y(4)-98, y(5)-98++, y(5), y(5)-98, y(6)-98, y(6), y(6)++, y(7)-98++, y(7), y(7)++, y(7)-98, y(8)-98, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++

Peptide No.269

EVIEASDKEGLSPAK
Confirmed sites: @S:6,@S:12
Ambiguous sites:

MS/MS Fragmentation of **EVIEASDKEGLSPAK**
Found in **PRP4B_MOUSE** in **SwissProt**, Serine/threonine-protein kinase PRP4 homolog OS=Mus musculus GN=Prpf4b PE=1 SV=3

Match to Query 3790: 1731.736962 from(578.252930,3+) index(4791)
Title: Elution from: 27.512 to 27.512 scan no 2259 cid35.00 polarity:+:m1s



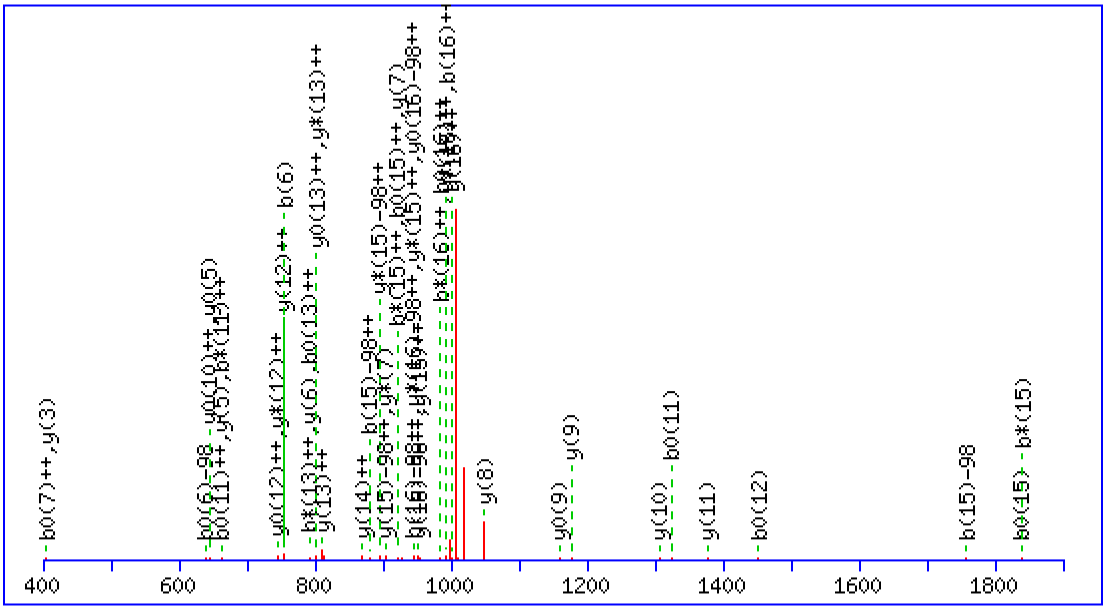
Monoisotopic mass of neutral peptide Mr(calc): 1731.7369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.034
Matched b ions: b(8)++, b(10)++, b(10)-98++, b(14)-196++
Matched y ions: y(4), y(6)++, y(6), y(6)-98++, y(6)-98, y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-196++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)-196++

Peptide No.270

EVSDDEAEEKEEKEEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **EVSDDEAEEKEEKEEEK**
Found in **HS90A_MOUSE** in **SwissProt**, Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4

Match to Query 5359: 2130.830560 from(1066.422556,2+) index(3750)
Title: Elution from: 18.523 to 18.523 scan no 1043 cid35.00 polarity:+:m1s



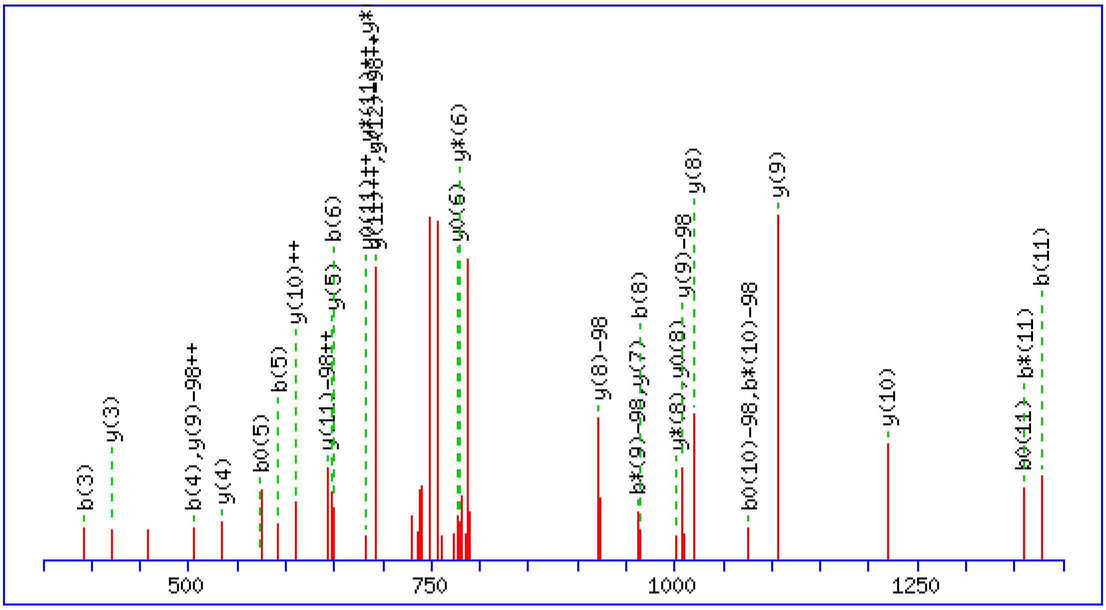
Monoisotopic mass of neutral peptide Mr(calc): 2130.8365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 4.8e-006
Matched b ions: b(6), b(15)-98, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++

Peptide No.271

EVYLSGSFNNWSK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **EVYLSGSFNNWSK**
Found in **AAKB1_MOUSE** in **SwissProt**, 5'-AMP-activated protein kinase subunit beta-1 OS=Mus musculus GN=Prkab1 PE=1 SV=2

Match to Query 2823: 1609.682508 from(805.848530,2+) index(5801)
Title: Elution from: 47.979 to 47.979 scan no 4704 cid35.00 polarity:+:m1s



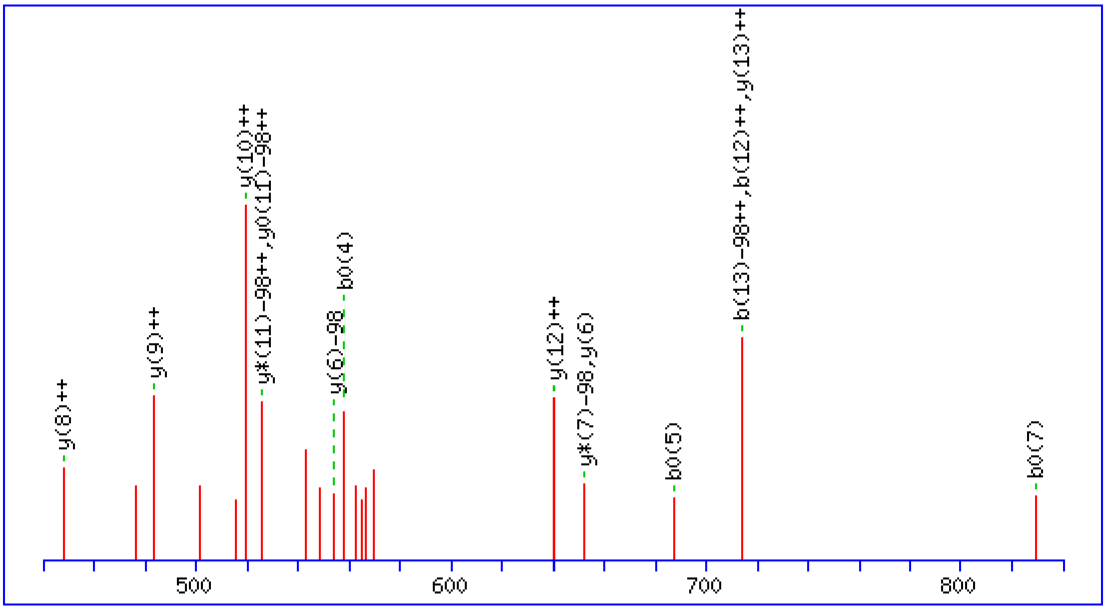
Monoisotopic mass of neutral peptide Mr(calc): 1609.6814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00035
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(11), b(12)-98++
Matched y ions: y(3), y(4), y(5), y(7), y(8)-98, y(8), y(9), y(9)-98, y(9)-98++, y(10), y(10)++, y(11)++, y(11)-98++, y(12)-98++

Peptide No.272

EWFLEAAKDPSAVAK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **EWFLEAAKDPSAVAK**
Found in **G6PI_MOUSE** in **SwissProt**, Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4

Match to Query 3839: 1740.815190 from(581.279006,3+) index(6528)
Title: Elution from: 47.888 to 47.888 scan no 4910 cid35.00 polarity:+:m1s



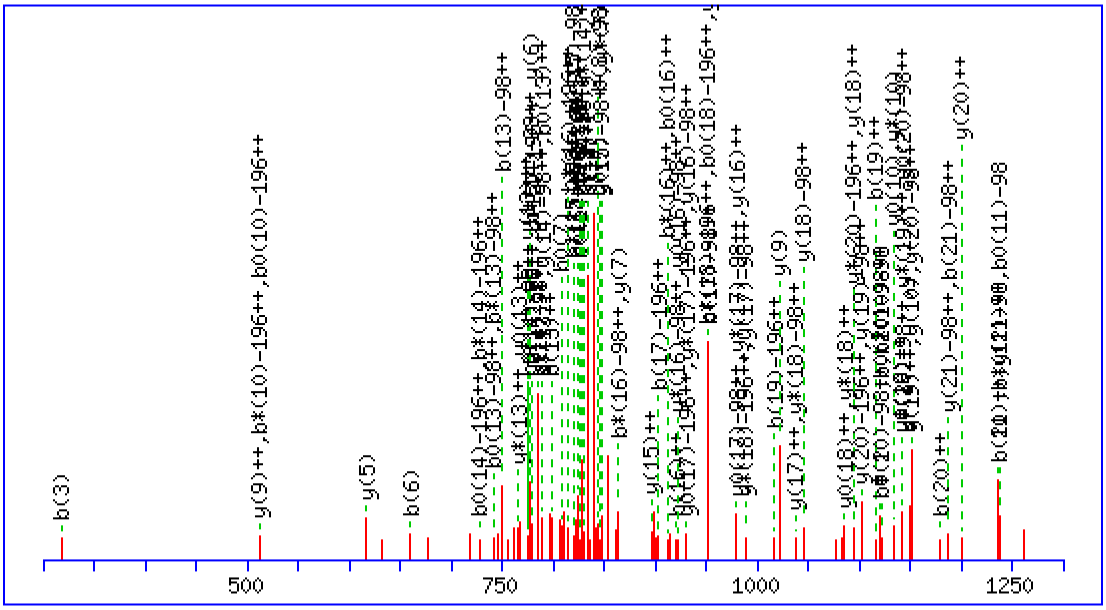
Monoisotopic mass of neutral peptide Mr(calc): 1740.8124
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.033
Matched b ions: b(12)++, b(13)-98++
Matched y ions: y(6), y(6)-98, y(8)++, y(9)++, y(10)++, y(12)++, y(13)++

Peptide No.273

FAVLNDSDKSDDEASSCNDQLK
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **FAVLNDSDKSDDEASSCNDQLK**
Found in **IFIH1_MOUSE** in **SwissProt**, Interferon-induced helicase C domain-containing protein 1 OS=Mus musculus GN=Ifih1 PE=1 SV=1

Match to Query 5373: 2616.991692 from(873.337840,3+) index(5064)
Title: Elution from: 38.934 to 38.934 scan no 3672 cid35.00 polarity:+:m1s



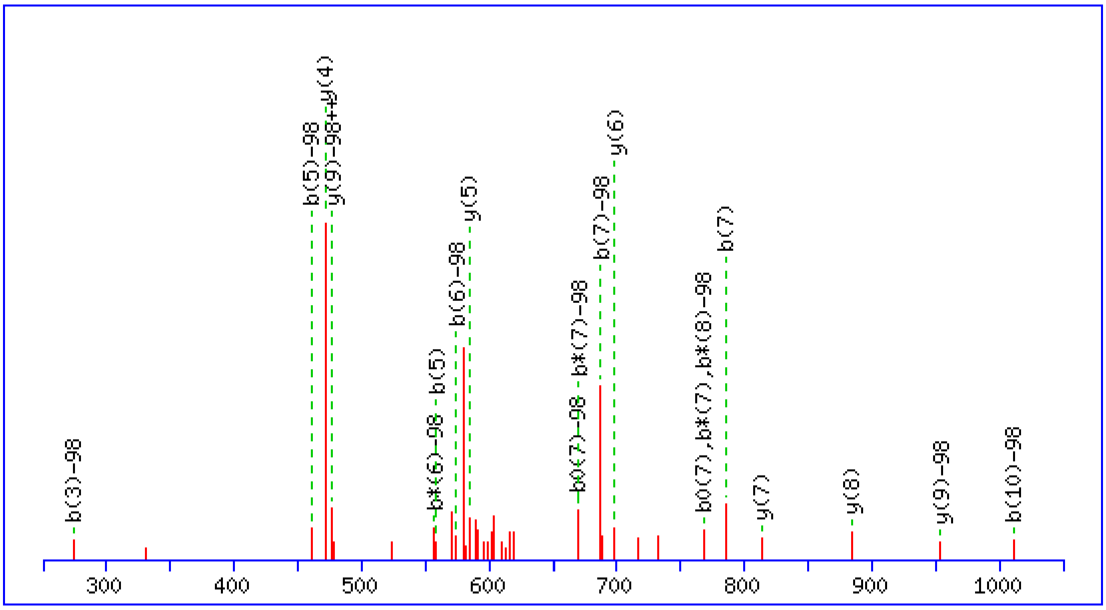
Monoisotopic mass of neutral peptide Mr(calc): 2616.9928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.002
Matched b ions: b(3), b(6), b(8)-98, b(10), b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(16)-196++, b(16)++, b(17)-98++, b(17)-196++, b(19)-196++, b(19)++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(13)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)-196++, y(20)++, y(21)++, y(21)-98++

Peptide No.274

FGSADNIPNLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **FGSADNIPNLK**
Found in **TMCC1_MOUSE** in **SwissProt**, Transmembrane and coiled-coil domains protein 1 OS=Mus musculus GN=Tmcc1 PE=1 SV=2

Match to Query 1616: 1254.564714 from(628.289633,2+) index(2205)
Title: Elution from: 39.208 to 39.208 scan no 3730 cid35.00 polarity:+



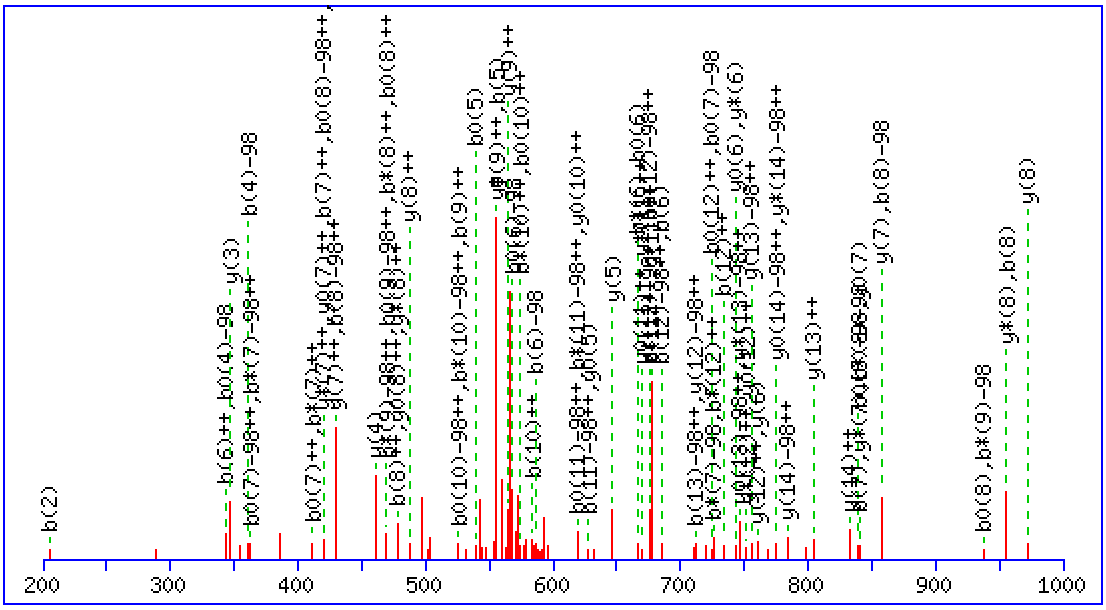
Monoisotopic mass of neutral peptide Mr(calc): 1254.5645
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 9.8e-005
Matched b ions: b(3)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(10)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9)-98

Peptide No.275

FGSSPQRDPNWIGDR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **FGSSPQRDPNWIGDR**
Found in **CASC3_MOUSE** in **SwissProt**, Protein CASC3 OS=Mus musculus GN=Casc3 PE=1 SV=3

Match to Query 4123: 1810.777545 from(604.599791,3+) index(1984)
Title: Elution from: 34.680 to 34.680 scan no 3232 cid35.00 polarity:+



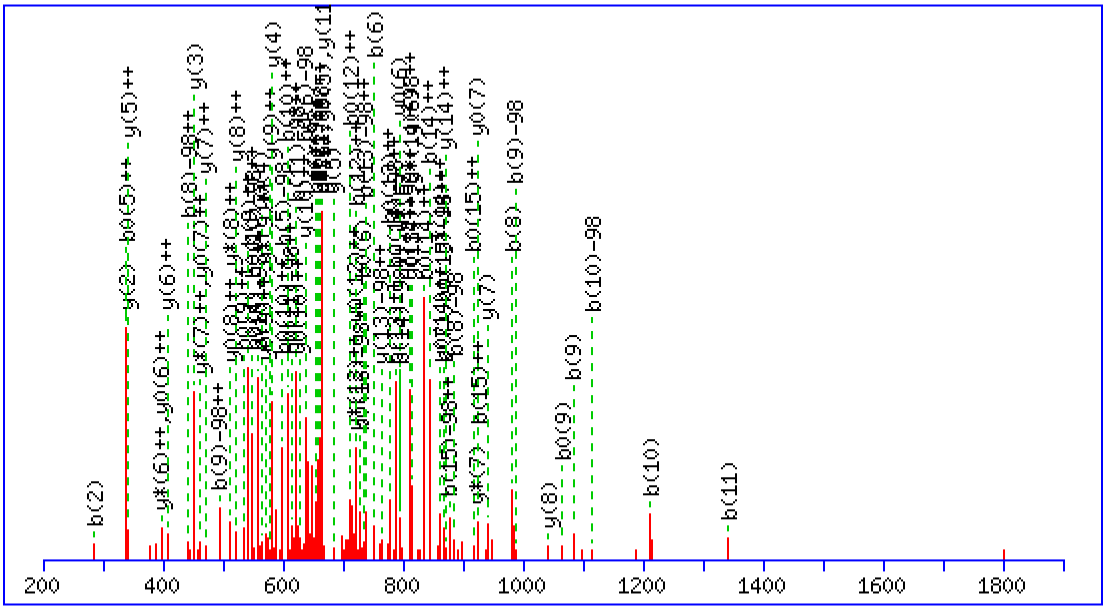
Monoisotopic mass of neutral peptide Mr(calc): 1810.7788
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 0.00011
Matched b ions: b(2), b(4)-98, b(5), b(6)++, b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8)-98++, b(8)-98, b(8), b(8)++, b(9)-98++, b(9)++, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++

Peptide No.276

FHDSEGDDTEETEDYR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **FHDSEGDDTEETEDYR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 5172: 2023.696950 from(675.572926,3+) index(4174)
Title: Elution from: 31.166 to 31.166 scan no 2036 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2023.6956

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 37 **Expect:** 0.00029

Matched b ions: b(2), b(5)-98, b(6), b(6)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9)++, b(9), b(9)-98++, b(9)-98, b(10)-98, b(10), b(10)-98++, b(10)++, b(11), b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++

Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(13)++, y(13)-98++, y(14)++

Peptide No.277

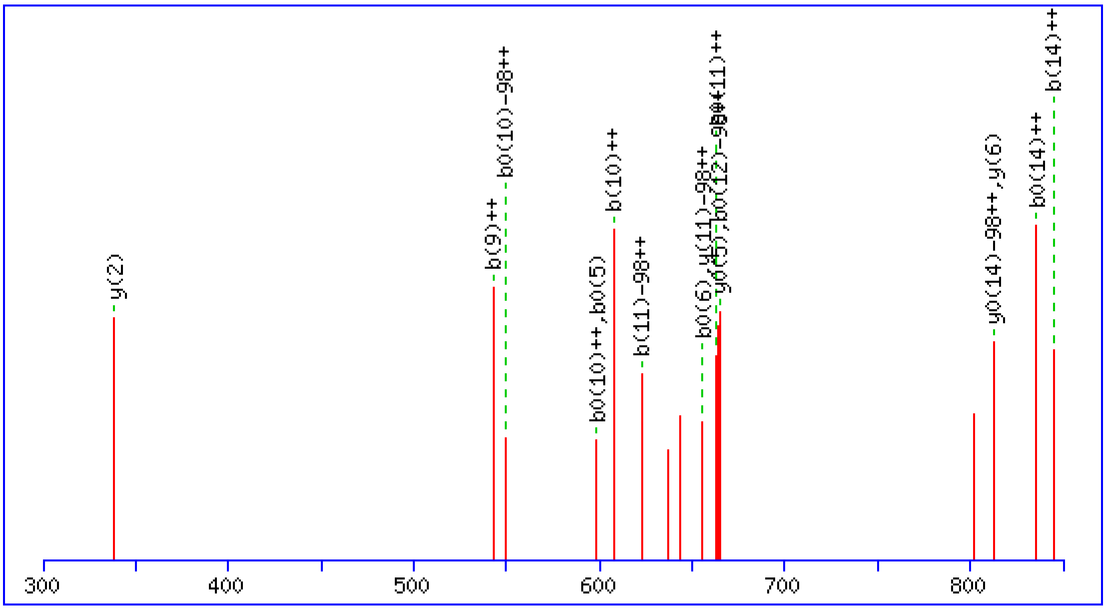
FHDSEGDDTEETEDYR

Confirmed sites: @T:9

Ambiguous sites:

MS/MS Fragmentation of **FHDSEGDDTEETEDYR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 4946: 2023.692522 from(675.571450,3+) index(4476)
Title: Elution from: 24.556 to 24.556 scan no 1857 cid35.00 polarity:+:m1s



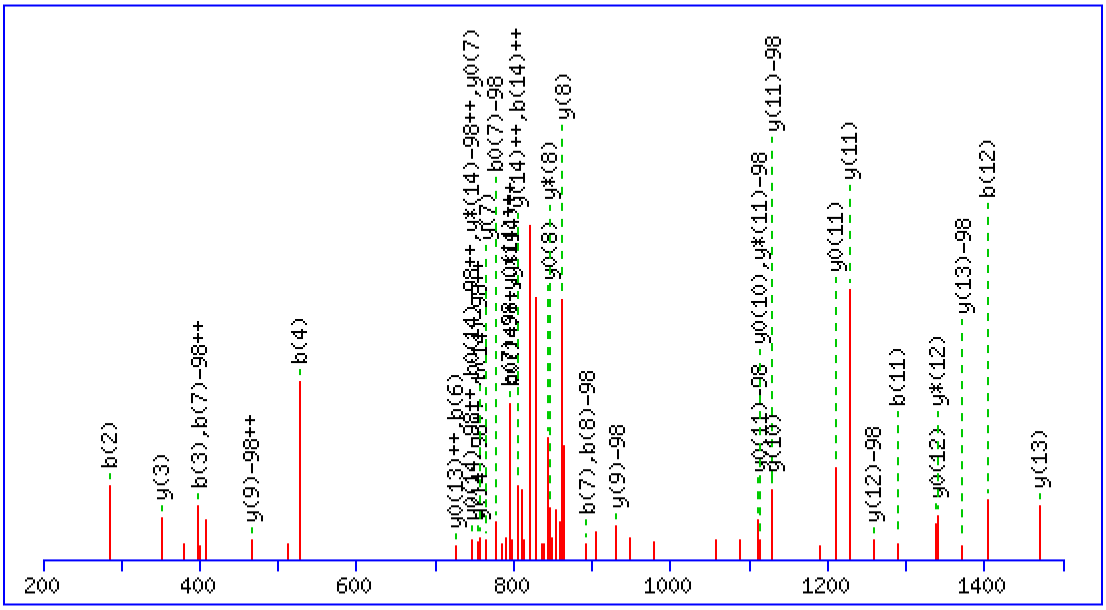
Monoisotopic mass of neutral peptide Mr(calc): 2023.6956
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 16 **Expect:** 0.04
Matched b ions: b(9)++, b(10)++, b(11)-98++, b(14)++
Matched y ions: y(2), y(6), y(11)-98++

Peptide No.278

FHLEPTSPPTTDGFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **FHLEPTSPPTTDGFK**
Found in **GYS2_MOUSE** in **SwissProt**, Glycogen [starch] synthase, liver OS=Mus musculus GN=Gys2 PE=1 SV=2

Match to Query 4057: 1752.773102 from(877.393827,2+) index(6146)
Title: Elution from: 39.704 to 39.704 scan no 3928 cid35.00 polarity:+:m1s



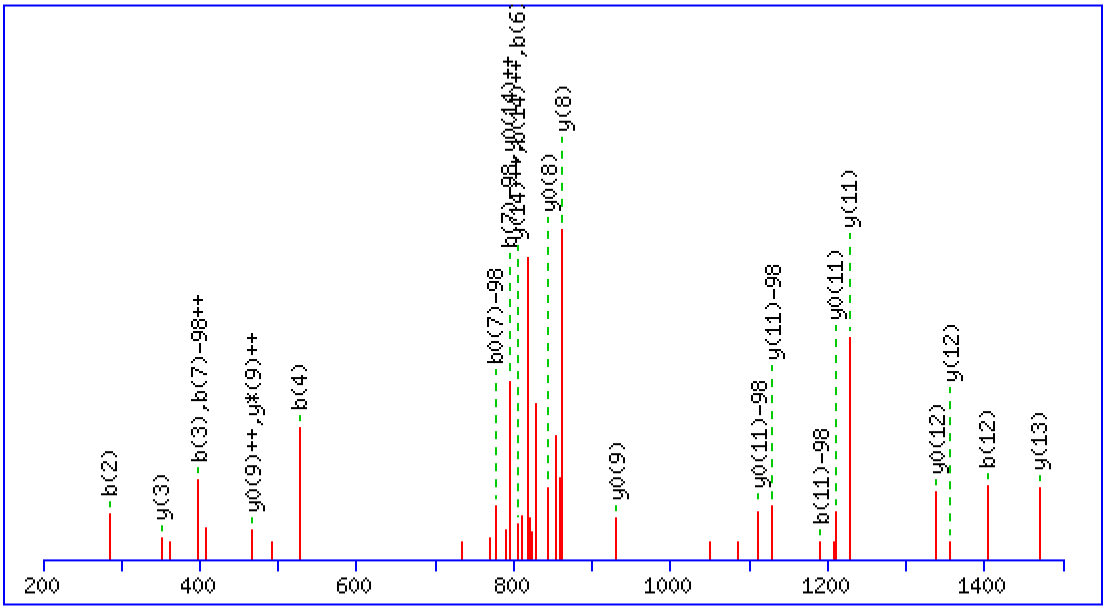
Monoisotopic mass of neutral peptide Mr(calc): 1752.7760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 **Expect:** 0.00026
Matched b ions: b(2), b(3), b(4), b(6), b(7)-98++, b(7)-98, b(7), b(8)-98, b(11), b(12), b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(7), y(8), y(9)-98, y(9)-98++, y(10), y(11)-98, y(11), y(12)-98, y(13), y(13)-98, y(14)-98++, y(14)++

Peptide No.279

FHLEPTSPPTTDGFK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **FHLEPTSPPTTDGFK**
Found in **GYS2_MOUSE** in **SwissProt**, Glycogen [starch] synthase, liver OS=Mus musculus GN=Gys2 PE=1 SV=2

Match to Query 3915: 1752.773052 from(877.393802,2+) index(2458)
Title: Elution from: 39.721 to 39.721 scan no 3904 cid35.00 polarity:+



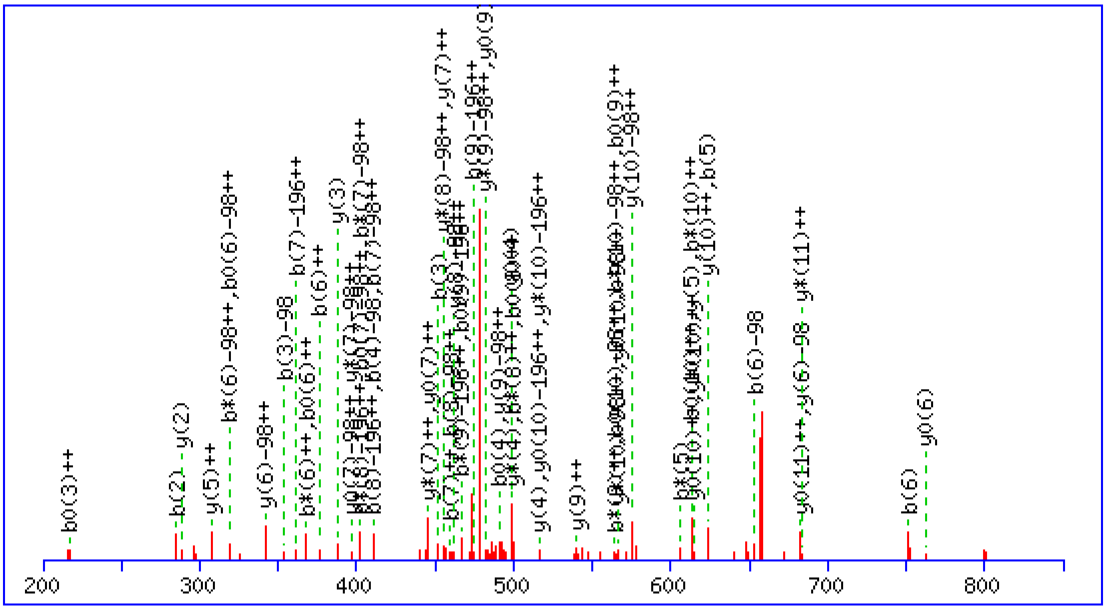
Monoisotopic mass of neutral peptide Mr(calc): 1752.7760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0057
Matched b ions: b(2), b(3), b(4), b(6), b(7)-98++, b(7)-98, b(11)-98, b(12), b(14)++
Matched y ions: y(3), y(4), y(8), y(11)-98, y(11), y(12), y(13), y(14)++

Peptide No.280

FHSGNKSPEVLR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **FHSGNKSPEVLR**
Found in **CLCC1_MOUSE** in **SwissProt**, Chloride channel CLIC-like protein 1 OS=Mus musculus GN=Clcc1 PE=1 SV=1

Match to Query 2551: 1529.642346 from(510.888058,3+) index(441)
Title: Elution from: 20.857 to 20.857 scan no 1333 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1529.6429

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 19 **Expect:** 0.049

Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(6), b(6)-98, b(6)++, b(7)-98++, b(7)-196++, b(7)++, b(8)-196++, b(8)-98++, b(9)-196++

Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)-98++, y(6)-98, y(7)++, y(8)-98++, y(9)++, y(9)-98++, y(10)-98++, y(10)++

Peptide No.281

FHSGNKSPEVLR

Confirmed sites: @S:7

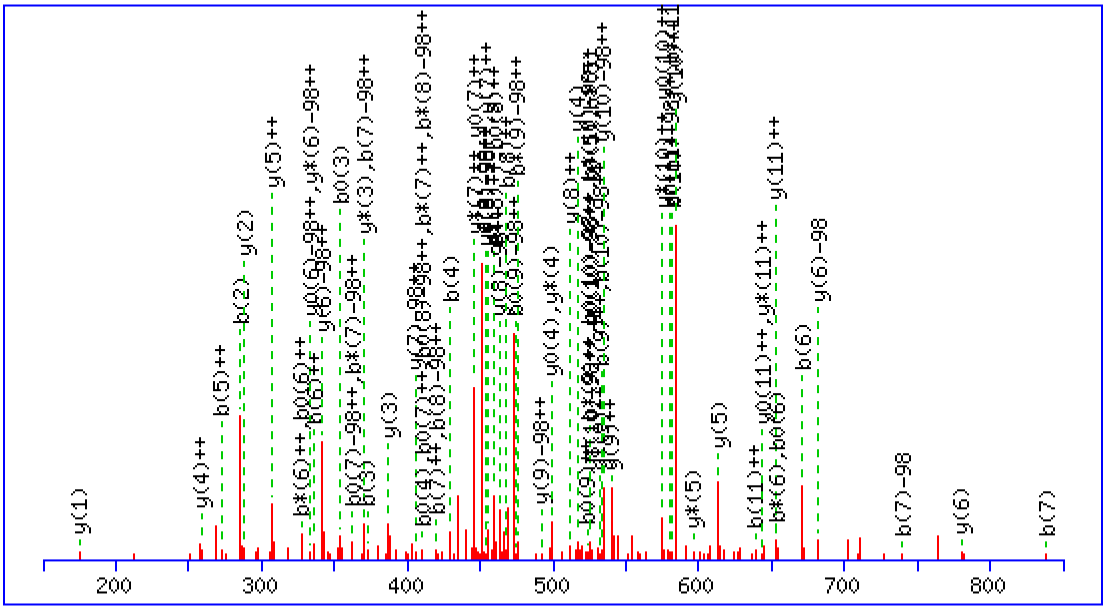
Ambiguous sites:

MS/MS Fragmentation of **FHSGNKSPEVLR**

Found in **CLCC1_MOUSE** in **SwissProt**, Chloride channel CLIC-like protein 1 OS=Mus musculus GN=Clcc1 PE=1 SV=1

Match to Query 2258: 1449.676245 from(484.232691,3+) index(242)

Title: Elution from: 19.216 to 19.216 scan no 1113 cid35.00 polarity:+



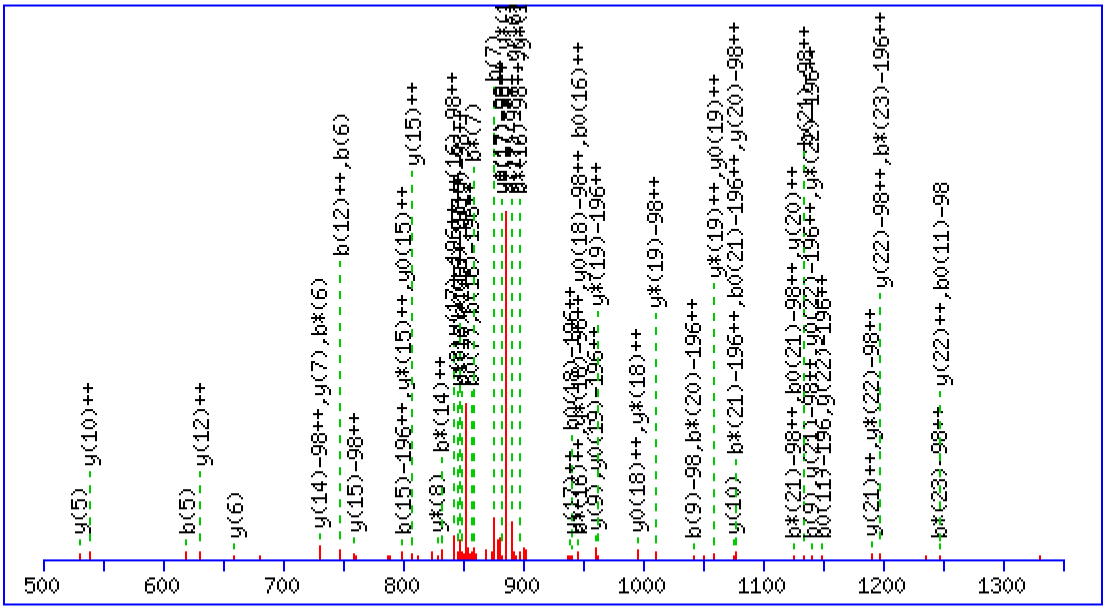
Monoisotopic mass of neutral peptide Mr(calc): 1449.6766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.03
Matched b ions: b(2), b(3), b(4), b(5)++, b(6), b(6)++, b(7), b(7)-98++, b(7)-98, b(7)++, b(8)-98++, b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)-98++, y(6)-98, y(7)++, y(7)-98++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++

Peptide No.282

FIDKDQQPSGSEGEDDDAEAALKK
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of **FIDKDQQPSGSEGEDDDAEAALKK**
Found in **THUM1_MOUSE** in **SwissProt**, THUMP domain-containing protein 1 OS=Mus musculus GN=Thumpd1 PE=1 SV=1

Match to Query 5515: 2752.112112 from(918.377980,3+) index(4296)
Title: Elution from: 30.259 to 30.259 scan no 2522 cid35.00 polarity:+:m1s



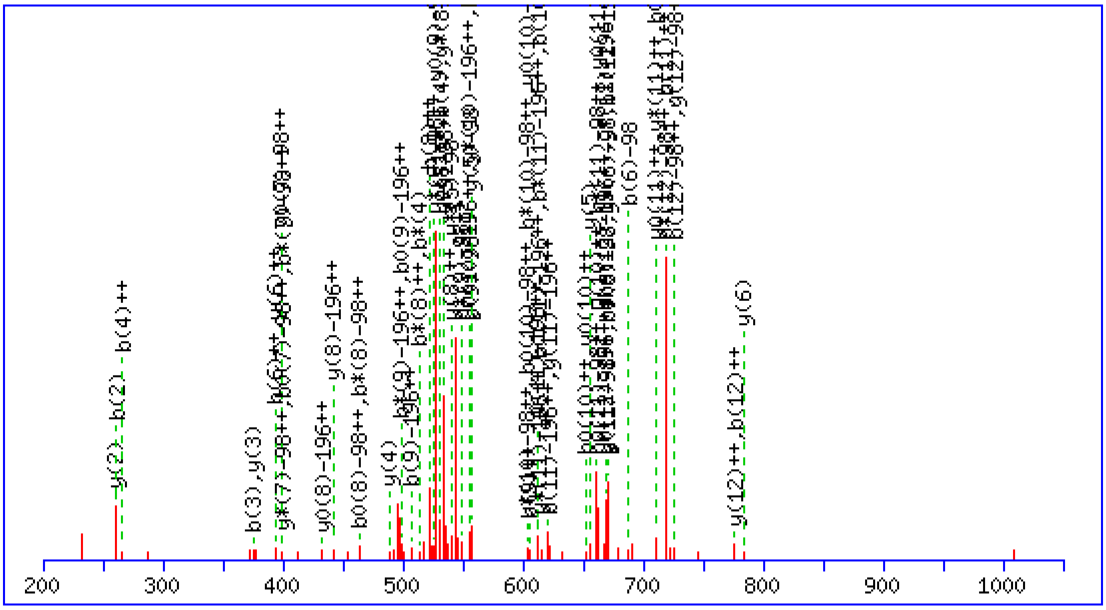
Monoisotopic mass of neutral peptide Mr(calc): 2752.1154
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.0006
Matched b ions: b(5), b(6), b(7), b(9), b(9)-98, b(12)++, b(15)-196++, b(15)-98++, b(15)++, b(16)-196++, b(21)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(12)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)-196++, y(17)++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(22)-196++

Peptide No.283

FLNRSSQESLDIK
Confirmed sites: @S:6,@S:9
Ambiguous sites:

MS/MS Fragmentation of **FLNRSSQESLDIK**
Found in **KS6C1_MOUSE** in **SwissProt**, Ribosomal protein S6 kinase delta-1 OS=Mus musculus GN=Rps6kc1 PE=1 SV=2

Match to Query 3256: 1695.726399 from(566.249409,3+) index(4937)
Title: Elution from: 37.407 to 37.407 scan no 3478 cid35.00 polarity:+:m1s



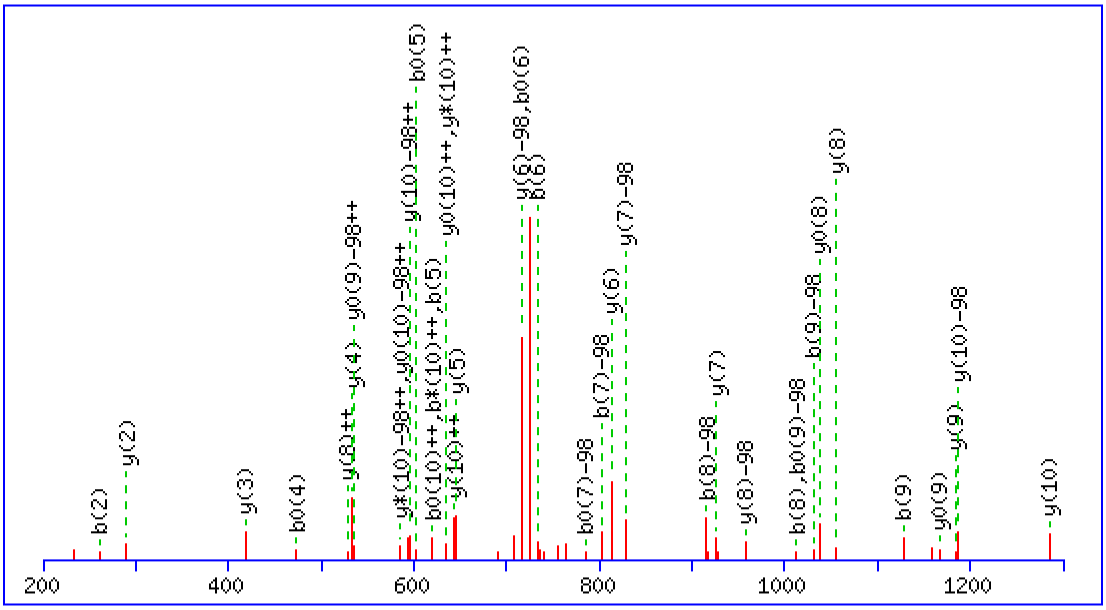
Monoisotopic mass of neutral peptide Mr(calc): 1695.7270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.024
Matched b ions: b(2), b(3), b(4)++, b(4), b(6)++, b(6)-98, b(8)++, b(9)-98++, b(9)-196++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(11)-196++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)++, y(6), y(8)++, y(8)-196++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(11)-196++, y(12)++, y(12)-98++

Peptide No.284

FLTEELSLDQDR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **FLTEELSLDQDR**
Found in **DOPD_MOUSE** in **SwissProt**, D-dopachrome decarboxylase OS=Mus musculus GN=Ddt PE=1 SV=3

Match to Query 3001: 1544.676872 from(773.345712,2+) index(6498)
Title: Elution from: 47.455 to 47.455 scan no 4857 cid35.00 polarity:+:m1s



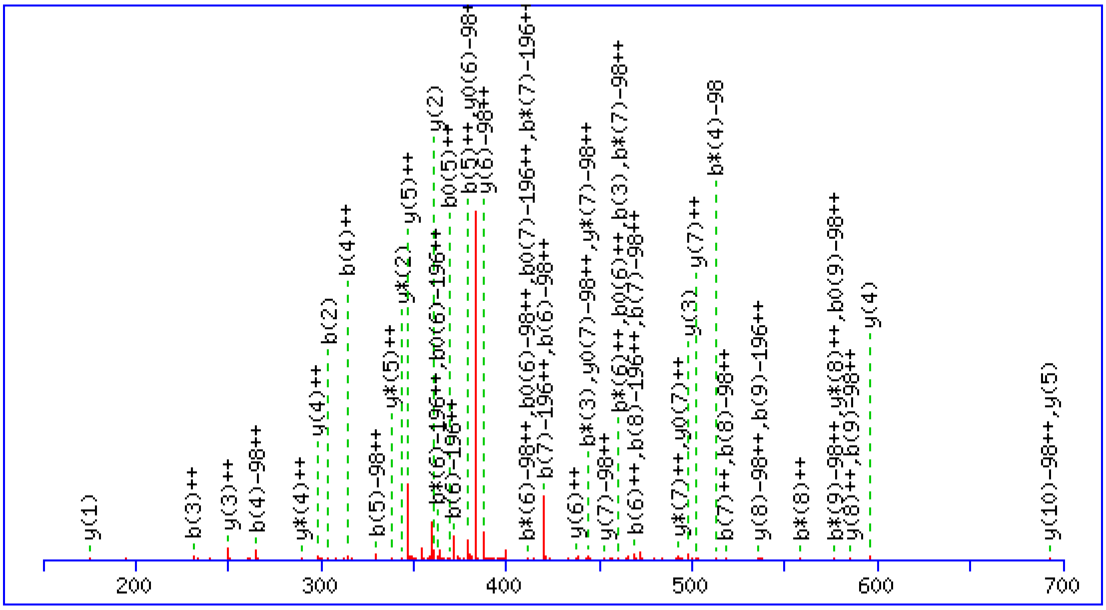
Monoisotopic mass of neutral peptide Mr(calc): 1544.6759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.1e-005
Matched b ions: b(2), b(5), b(6), b(7)-98, b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7)-98, y(7), y(8)-98, y(8)++, y(8), y(9), y(10)-98, y(10), y(10)-98++, y(10)++

Peptide No.285

FRRSETPPHWR
Confirmed sites: @S:4,@T:6
Ambiguous sites:

MS/MS Fragmentation of **FRRSETPPHWR**
Found in **PPIG_MOUSE** in **SwissProt**, Peptidyl-prolyl cis-trans isomerase G OS=Mus musculus GN=Ppig PE=1 SV=1

Match to Query 3322: 1627.681400 from(407.927626,4+) index(861)
Title: Elution from: 23.854 to 23.854 scan no 1762 cid35.00 polarity:+



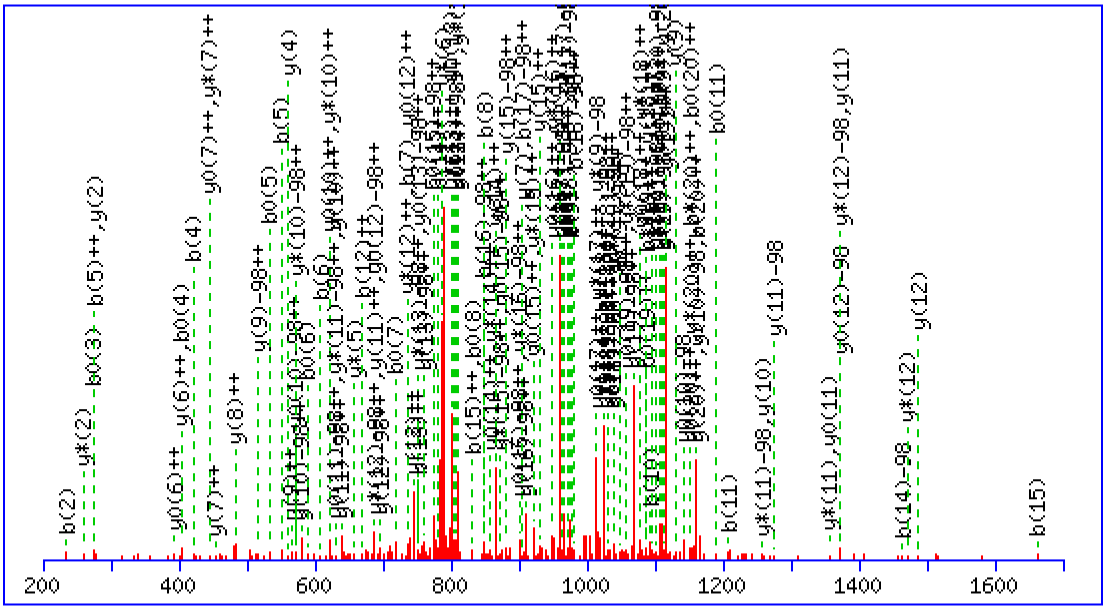
Monoisotopic mass of neutral peptide Mr(calc): 1627.6810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0051
Matched b ions: b(2), b(3)++, b(3), b(4)-98++, b(4)++, b(5)++, b(5)-98++, b(6)-98++, b(6)-196++, b(6)++, b(7)-196++, b(7)++, b(7)-98++, b(8)-98++, b(8)-196++, b(9)-98++, b(9)-196++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(4)++, y(5)++, y(5), y(6)-98++, y(6)++, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(10)-98++

Peptide No.286

FSGEEGEIEDDESGTENREEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **FSGEEGEIEDDESGTENREEK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 5355: 2464.938465 from(822.653431,3+) index(3701)
Title: Elution from: 32.962 to 32.962 scan no 2151 cid35.00 polarity:+:m1s



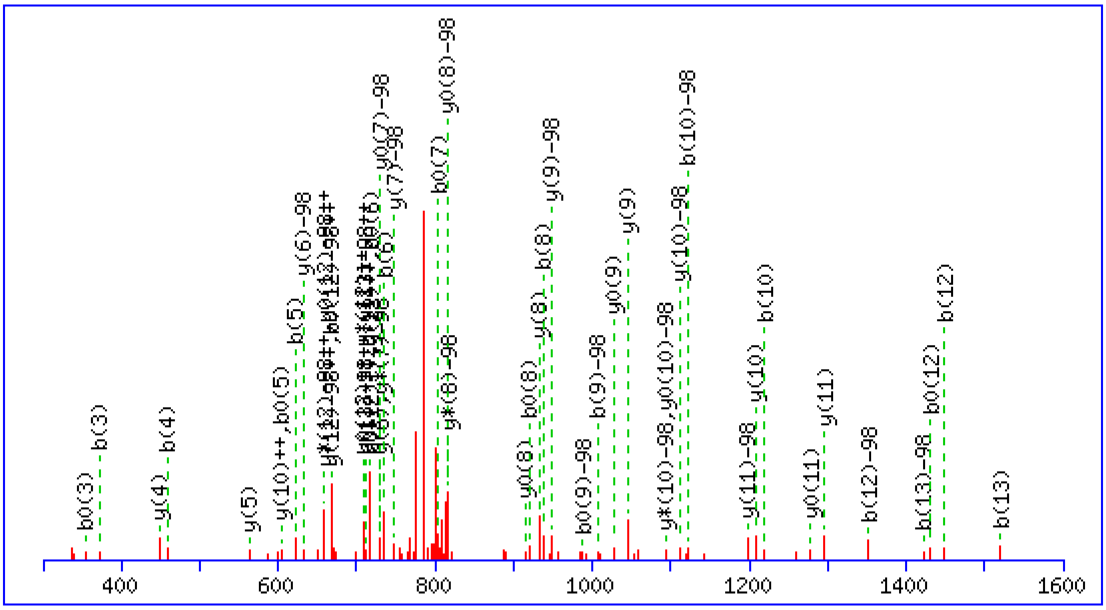
Monoisotopic mass of neutral peptide Mr(calc): 2464.9391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00037
Matched b ions: b(2), b(4), b(5)++, b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(13)++, b(14)-98, b(14)++, b(15), b(15)++, b(16)-98++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(4), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10)-98, y(10), y(10)++, y(11)++, y(11), y(11)-98++, y(11)-98, y(12)-98++, y(12), y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.287

FSHSYLSDSDTEAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **FSHSYLSDSDTEAK**
Found in **MY18A_MOUSE** in **SwissProt**, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 3667: 1665.653950 from(833.834251,2+) index(1223)
Title: Elution from: 26.757 to 26.757 scan no 2193 cid35.00 polarity:+



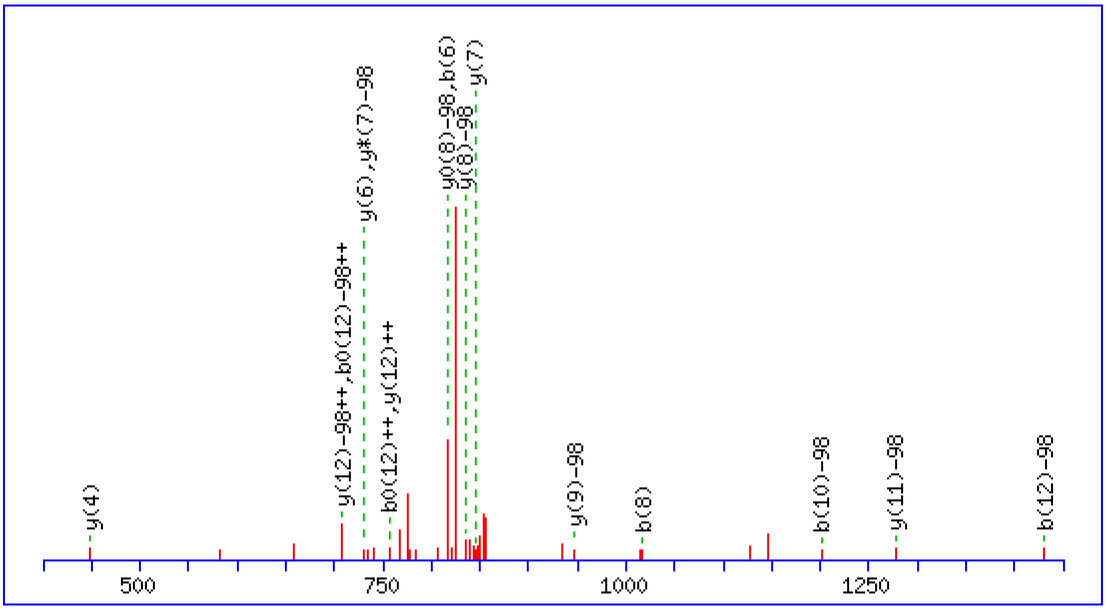
Monoisotopic mass of neutral peptide Mr(calc): 1665.6559
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 **Expect:** 1.4e-006
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9)-98, b(10)-98, b(10), b(12)-98, b(12), b(13), b(13)-98, b(13)-98++
Matched y ions: y(4), y(5), y(6)-98, y(6), y(7)-98, y(8), y(9)-98, y(9), y(10), y(10)-98, y(10)++, y(11), y(11)-98, y(12)++, y(12)-98++, y(13)-98++

Peptide No.288

FSHSYLSDSDTEAK
Confirmed sites: @S:9
Ambiguous sites: @S:4orY:5

MS/MS Fragmentation of **FSHSYLSDSDTEAK**
Found in **MY18A_MOUSE** in **SwissProt**, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 3457: 1745.622712 from(873.818632,2+) index(1331)
Title: Elution from: 30.720 to 30.720 scan no 2586 cid35.00 polarity:+



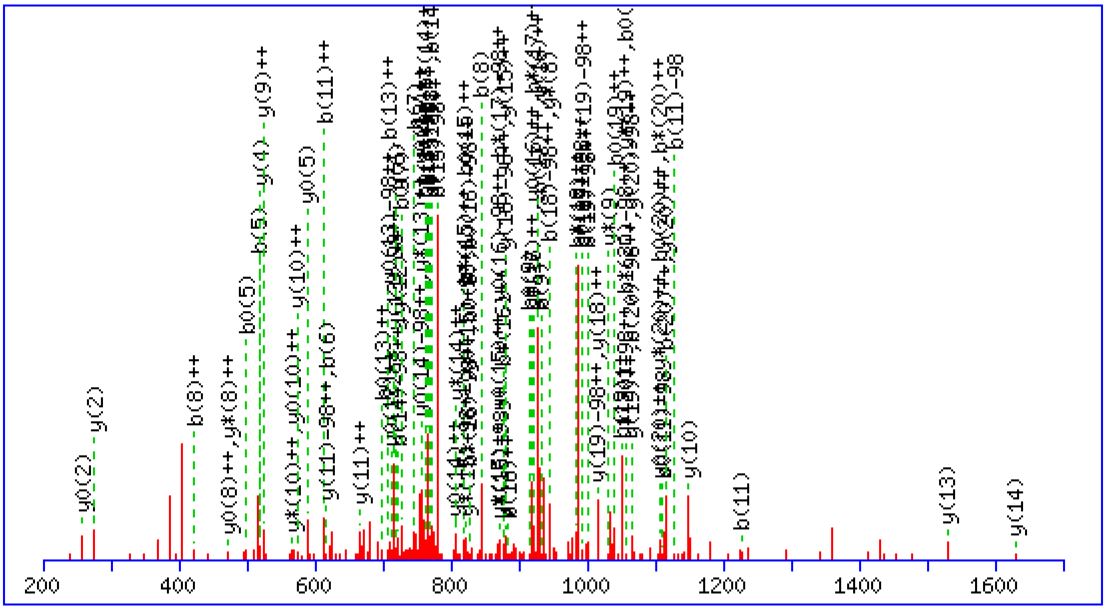
Monoisotopic mass of neutral peptide Mr(calc): 1745.6223
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y5 : Phospho (Y)
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 **Expect:** 0.046
Matched b ions: b(6), b(8), b(10)-98, b(12)-98
Matched y ions: y(4), y(6), y(7), y(8)-98, y(9)-98, y(11)-98, y(12)-98++, y(12)++

Peptide No.289

FVVDGVEVSITTSKIISEDEK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **FVVDGVEVSITTSKIISEDEK**
Found in **STK10_MOUSE** in **SwissProt**, Serine/threonine-protein kinase 10 OS=Mus musculus GN=Stk10 PE=1 SV=2

Match to Query 6014: 2374.161399 from(792.394409,3+) index(2725)
Title: Elution from: 67.418 to 67.418 scan no 5580 cid35.00 polarity:+



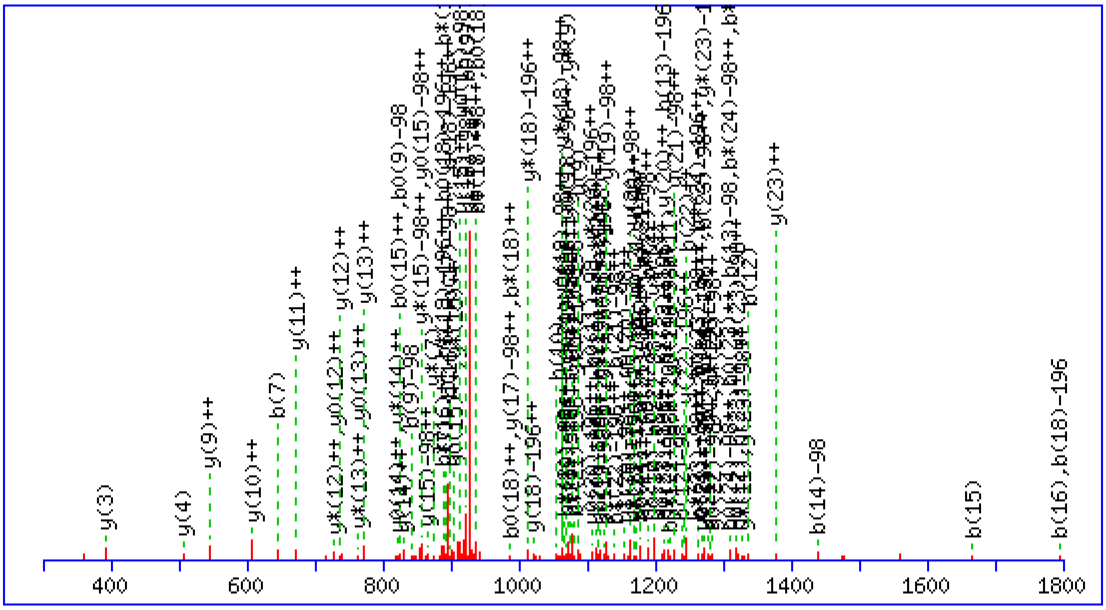
Monoisotopic mass of neutral peptide Mr(calc): 2374.1557
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.006
Matched b ions: b(5), b(6), b(7), b(8)++, b(8), b(9), b(11)++, b(11), b(11)-98, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(2), y(4), y(6), y(9)++, y(10), y(10)++, y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(13), y(14), y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(20)-98++

Peptide No.290

GAAEEADSEDSDAEEKPVKQEDFPK
Confirmed sites: @S:8,@S:11
Ambiguous sites:

MS/MS Fragmentation of **GAAEEADSEDSDAEEKPVKQEDFPK**
Found in **TFP11_MOUSE** in **SwissProt**, Tuftelin-interacting protein 11 OS=Mus musculus GN=Tfip11 PE=1 SV=1

Match to Query 6828: 2880.122169 from(961.047999,3+) index(5113)
Title: Elution from: 28.850 to 28.850 scan no 2480 cid35.00 polarity:+:m1s



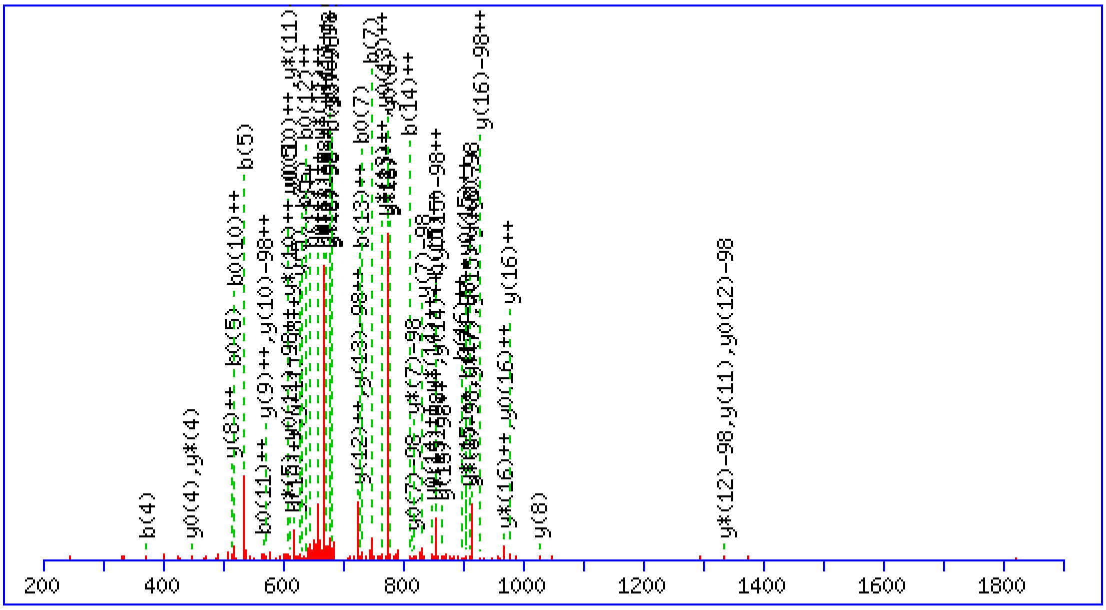
Monoisotopic mass of neutral peptide Mr(calc): 2880.1263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00021
Matched b ions: b(7), b(9)-98, b(10), b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(13)-196, b(14)-98, b(15), b(16), b(16)++, b(17)-98++, b(18)-196, b(18)-196++, b(20)-98++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(23)-196++, b(24)-196++
Matched y ions: y(3), y(4), y(7), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(17)-98++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++, y(19)-98++, y(19)++, y(20)-98++, y(20)-196++, y(20)++, y(21)-196++, y(21)++, y(21)-98++, y(22)-196++, y(23)++, y(23)-196++, y(23)-98++

Peptide No.291

GAEDYPDPPLPHSYSSDR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GAEDYPDPPLPHSYSSDR**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 5295: 2081.838291 from(694.953373,3+) index(5260)
Title: Elution from: 43.994 to 43.994 scan no 3581 cid35.00 polarity:+:m1s



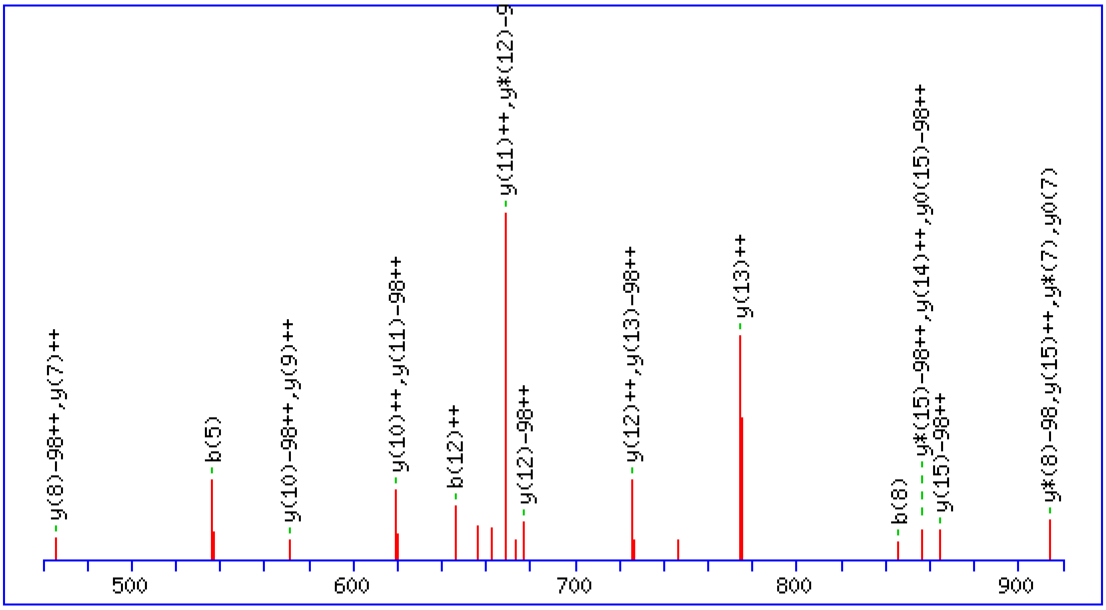
Monoisotopic mass of neutral peptide Mr(calc): 2081.8368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.00088
Matched b ions: b(4), b(5), b(6), b(7), b(12)++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)-98++
Matched y ions: y(5), y(7)-98, y(8), y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(11), y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.292

GAEDYPDPPLPHSYSSDR
Confirmed sites:
Ambiguous sites: @S:13orY:14orS:15orS:16

MS/MS Fragmentation of **GAEDYPDPPLPHSYSSDR**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 4380: 2081.837676 from(694.953168,3+) index(4996)
Title: Elution from: 35.647 to 35.647 scan no 3279 cid35.00 polarity:+:m1s



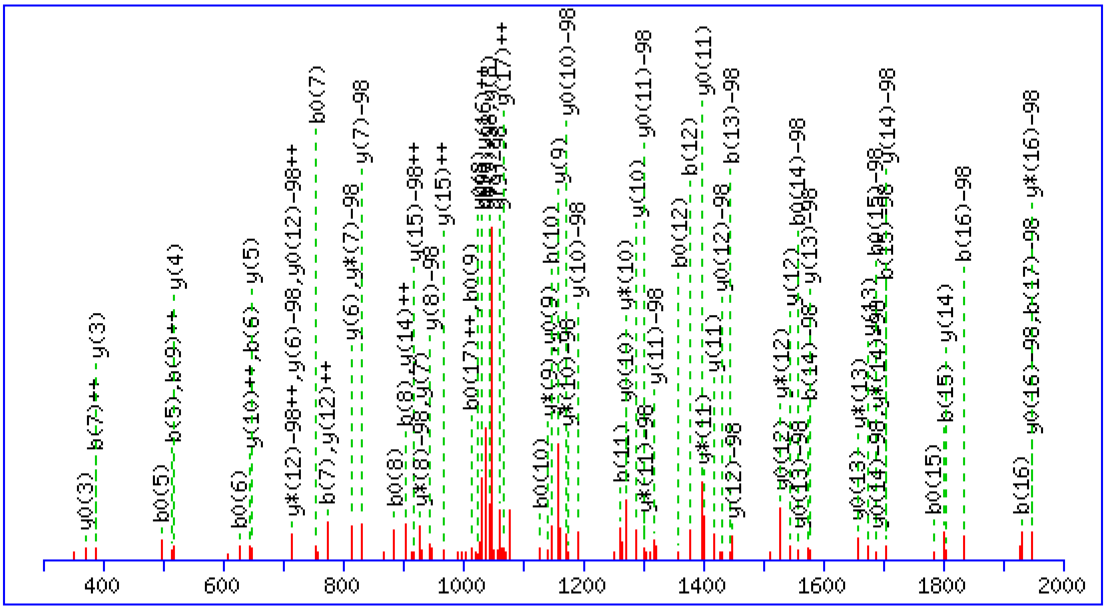
Monoisotopic mass of neutral peptide Mr(calc): 2081.8368
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 3.2e-005
Matched b ions: b(5), b(8), b(12)++
Matched y ions: y(7)++, y(8)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++

Peptide No.293

GAEEEEEEEEDDDSEEEIK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GAEEEEEEEEDDDSEEEIK**
Found in **DEMA_MOUSE** in **SwissProt**, Dematin OS=Mus musculus GN=Epb49 PE=1 SV=1

Match to Query 4767: 2189.748296 from(1095.881424,2+) index(3957)
Title: Elution from: 24.504 to 24.504 scan no 1824 cid35.00 polarity:+:m1s



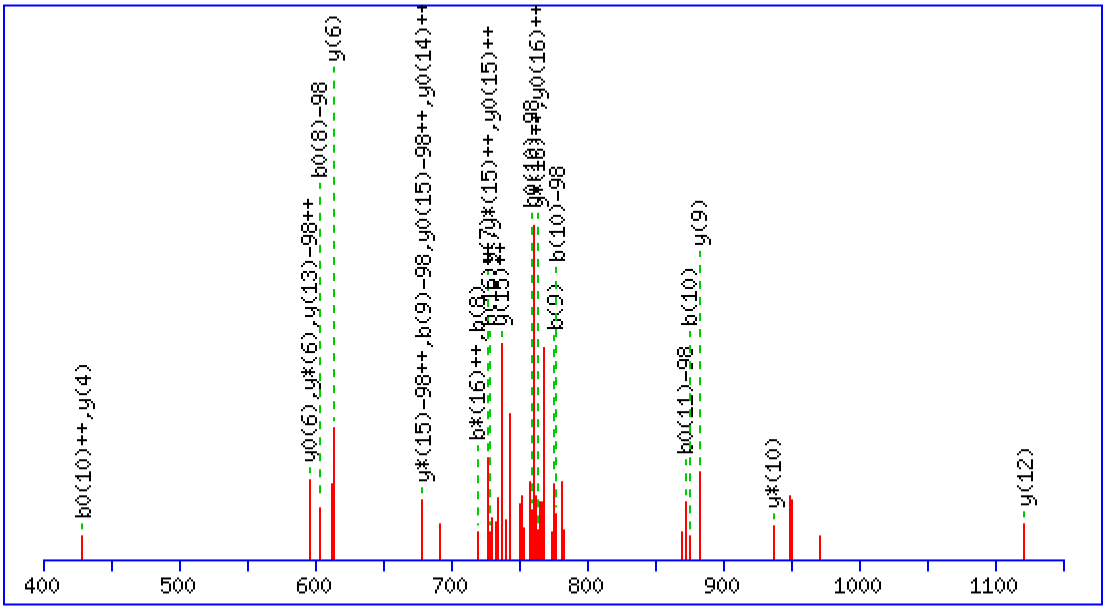
Monoisotopic mass of neutral peptide Mr(calc): 2189.7532
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 84 **Expect:** 8.5e-009
Matched b ions: b(5), b(6), b(7), b(7)++, b(8), b(9)++, b(9), b(10), b(11), b(12), b(13)-98, b(14)-98, b(15), b(15)-98, b(16), b(16)-98, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6)-98, y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)++, y(10)-98, y(10), y(11), y(11)-98, y(12)++, y(12), y(12)-98, y(13)-98, y(13), y(14)++, y(14)-98, y(14), y(15)-98++, y(15)++, y(16)++, y(17)++

Peptide No.294

GAPSSPAAGVLPSPQGK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GAPSSPAAGVLPSPQGK**
Found in **NU188_MOUSE** in **SwissProt**, Nucleoporin NUP188 homolog OS=Mus musculus GN=Nup188 PE=1 SV=2

Match to Query 3234: 1599.763968 from(800.889260,2+) index(1762)
Title: Elution from: 32.596 to 32.596 scan no 2951 cid35.00 polarity:+



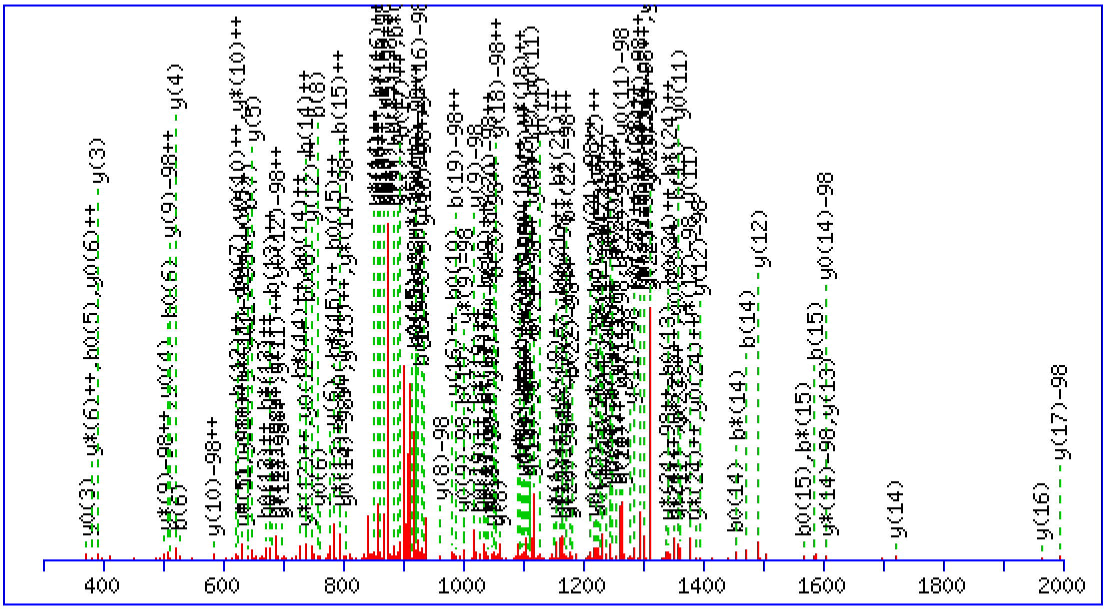
Monoisotopic mass of neutral peptide Mr(calc): 1599.7658
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0071
Matched b ions: b(8), b(9)-98, b(9), b(10), b(10)-98, b(16)-98++, b(16)++
Matched y ions: y(4), y(6), y(7), y(9), y(12), y(13)-98++, y(15)++

Peptide No.295

GATPAEDDDEDKDIDLFGSDEEEEDK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **GATPAEDDDEDKDIDLFGSDEEEEDK**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 5641: 2848.096443 from(950.372757,3+) index(4869)
Title: Elution from: 52.230 to 52.230 scan no 4139 cid35.00 polarity:+:m1s



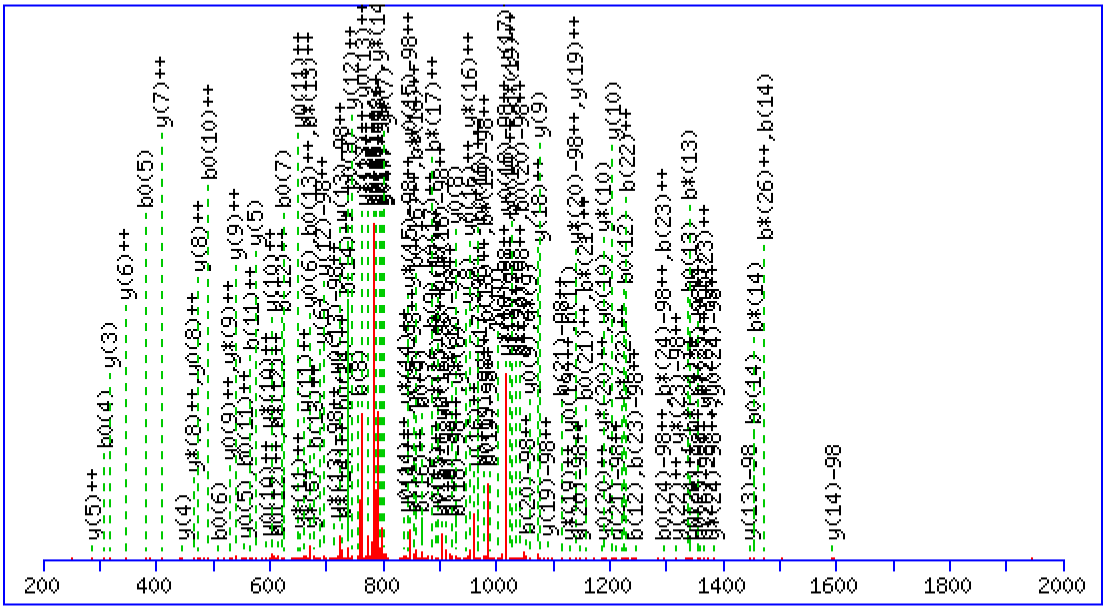
Monoisotopic mass of neutral peptide Mr(calc): 2848.0971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 93 **Expect:** 2.8e-009
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(12), b(13)++, b(13), b(14)++, b(14), b(15), b(15)++, b(16)++, b(17)++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(9)-98++, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)++, y(11), y(11)-98++, y(11)-98, y(12), y(12)++, y(12)-98, y(12)-98++, y(13), y(13)++, y(14), y(14)++, y(15)-98++, y(15)++, y(16), y(16)++, y(16)-98++, y(17)-98, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++

Peptide No.296

GATPAEDDEDKDIDLFGSDEEEEDKEAAR
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **GATPAEDDEDKDIDLFGSDEEEEDKEAAR**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 6848: 3275.309376 from(819.834620,4+) index(6080)
Title: Elution from: 40.910 to 40.910 scan no 4061 cid35.00 polarity:+:m1s



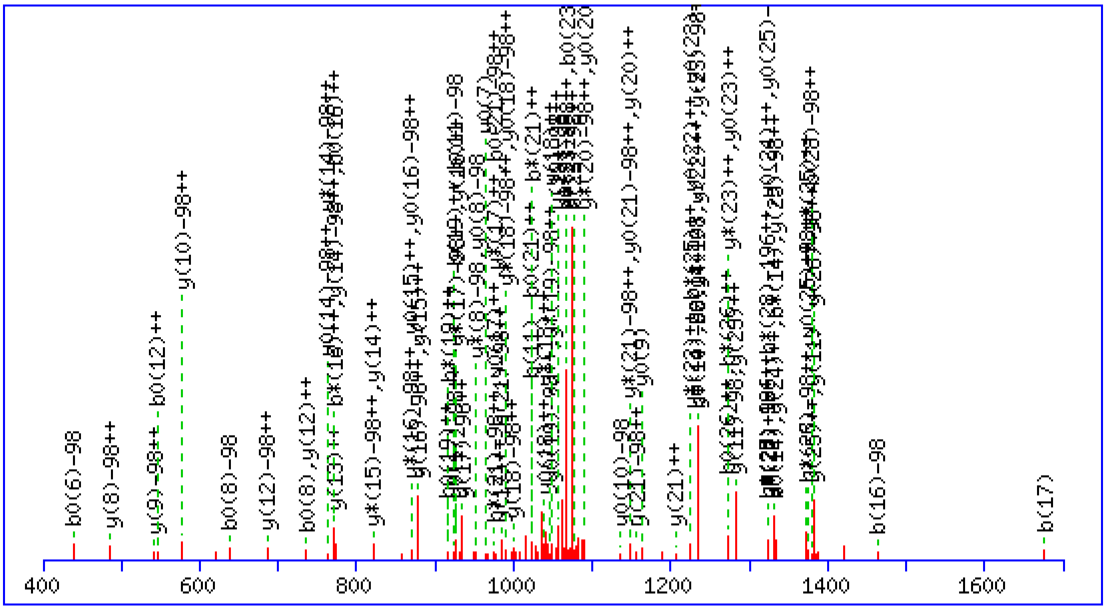
Monoisotopic mass of neutral peptide Mr(calc): 3275.3150
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 **Expect:** 2e-007
Matched b ions: b(8), b(9), b(10), b(11), b(11)++, b(12)++, b(12), b(13), b(13)++, b(14), b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(21)-98++, b(22)++, b(23)++, b(23)-98++, b(25)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)-98, y(13)++, y(14)-98, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(21)-98++, y(22)++

Peptide No.297

GDGGSTPTPGDSLQNPDTASEALSEPESQRR
Confirmed sites: @S:5
Ambiguous sites: @S:24orS:28

MS/MS Fragmentation of **GDGGSTPTPGDSLQNPDTASEALSEPESQRR**
Found in **FA73B_MOUSE** in **SwissProt**, Protein FAM73B OS=Mus musculus GN=Fam73b PE=1 SV=1

Match to Query 7077: 3315.349935 from(1106.123921,3+) index(5973)
Title: Elution from: 37.779 to 37.779 scan no 3674 cid35.00 polarity:+:m1s



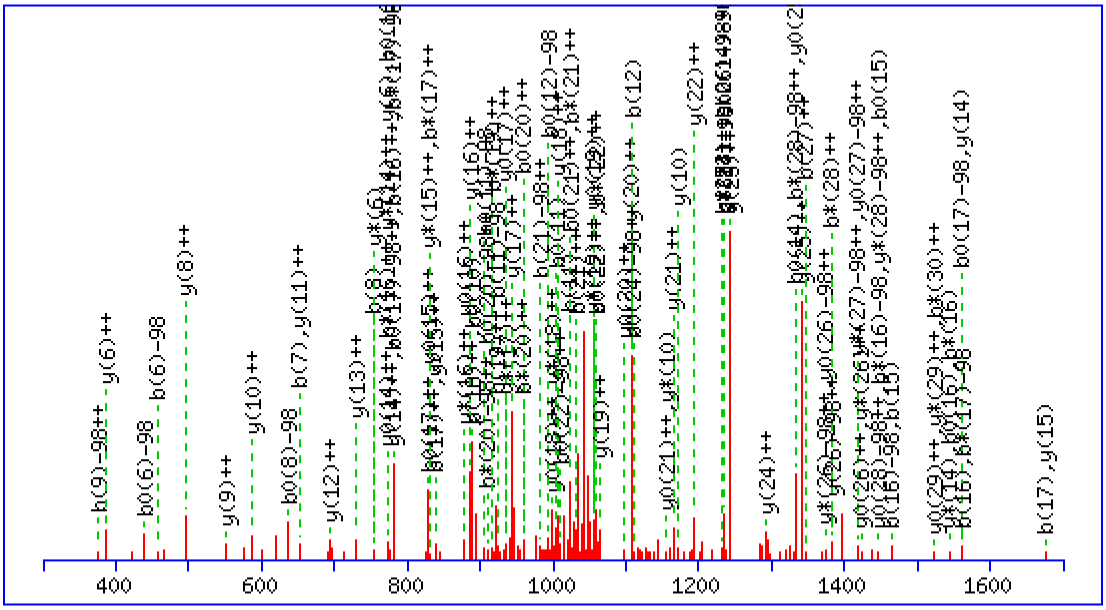
Monoisotopic mass of neutral peptide Mr(calc): 3315.3566
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S28 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00046
Matched b ions: b(11), b(11)-98, b(16)-98, b(17), b(19)++, b(21)-98++, b(22)++, b(23)-98++, b(28)-98++
Matched y ions: y(8)-98++, y(8), y(9)-98++, y(10)-98++, y(11)-98, y(11), y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(25)++, y(25)-98++, y(26)-98++

Peptide No.298

GDGGSTPTPGDSLQNPDTASEALSEPESQRR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **GDGGSTPTPGDSLQNPDTASEALSEPESQRR**
Found in **FA73B_MOUSE** in **SwissProt**, Protein FAM73B OS=Mus musculus GN=Fam73b PE=1 SV=1

Match to Query 7037: 3235.386042 from(1079.469290,3+) index(5964)
Title: Elution from: 37.681 to 37.681 scan no 3661 cid35.00 polarity:+:m1s



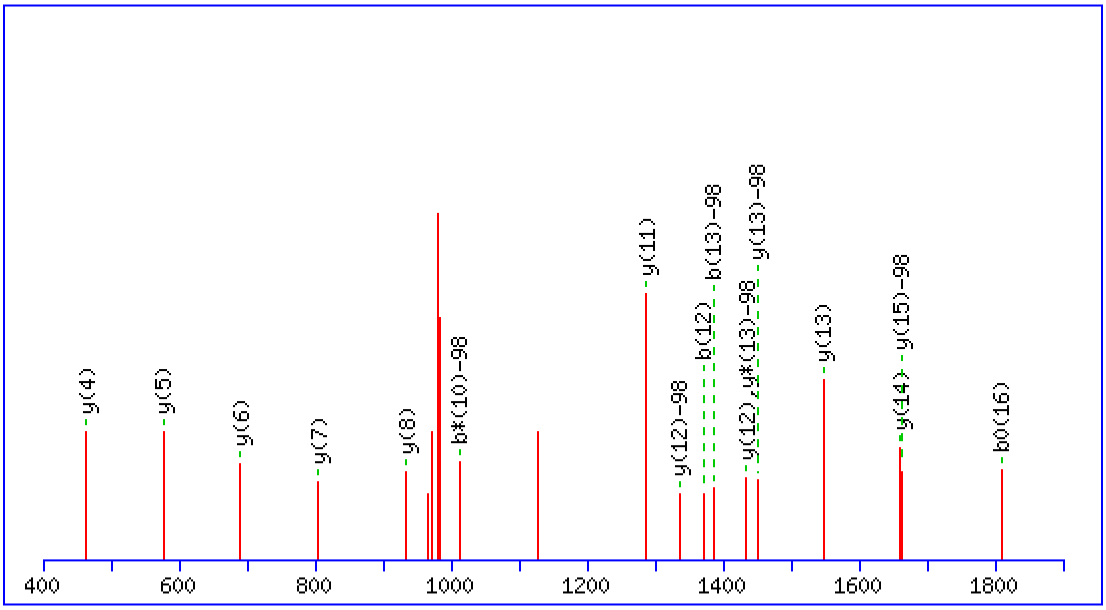
Monoisotopic mass of neutral peptide Mr(calc): 3235.3902
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 123 **Expect:** 4.7e-012
Matched b ions: b(6)-98, b(7), b(8), b(9)-98++, b(11), b(11)-98, b(12), b(15), b(16)++, b(16), b(16)-98, b(17), b(17)++, b(18)++, b(19)++, b(21)-98++, b(21)++, b(25)++, b(26)-98++, b(27)++
Matched y ions: y(6)++, y(6), y(8)++, y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(14), y(15), y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++, y(24)++, y(25)++, y(26)-98++

Peptide No.299

GDQVLNFSDAEDLIDDSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **GDQVLNFSDAEDLIDDSK**
Found in **MCRS1_MOUSE** in **SwissProt**, Microspherule protein 1 OS=Mus musculus GN=Mcrs1 PE=1 SV=1

Match to Query 5181: 2059.860118 from(1030.937335,2+) index(7177)
Title: Elution from: 65.110 to 65.110 scan no 6515 cid35.00 polarity:+:m1s



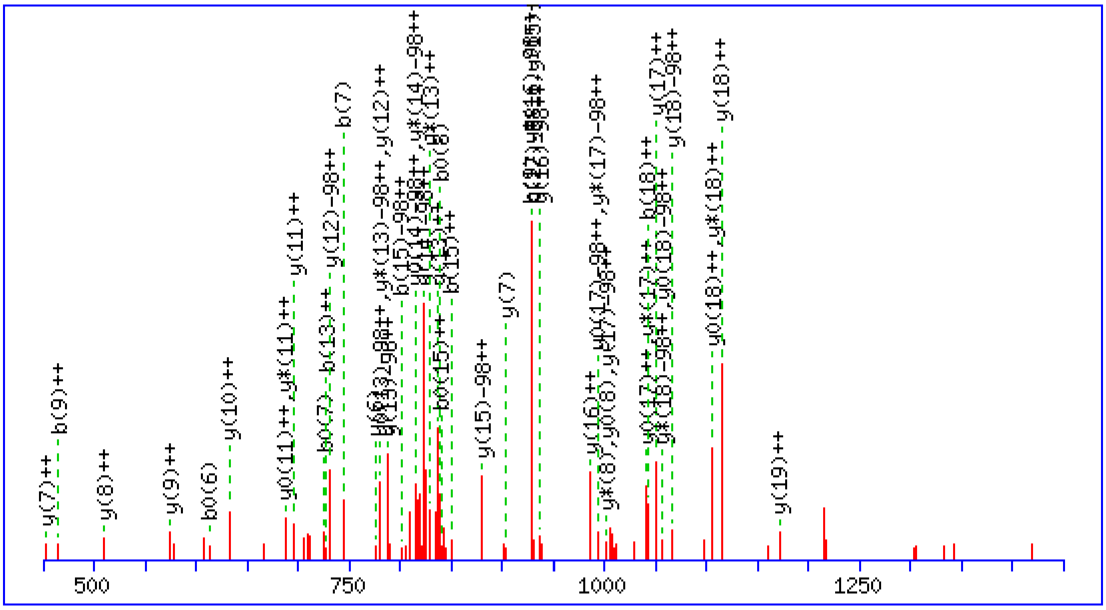
Monoisotopic mass of neutral peptide Mr(calc): 2059.8623
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 **Expect:** 4.3e-007
Matched b ions: b(12), b(13)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(11), y(12), y(12)-98, y(13), y(13)-98, y(14), y(15)-98

Peptide No.300

GDSIEEILADSEDEDEEEERGR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **GDSIEEILADSEDEDEEEERGR**
Found in **RRP12_MOUSE** in **SwissProt**, RRP12-like protein OS=Mus musculus GN=Rrp12 PE=1 SV=1

Match to Query 6355: 2601.021918 from(868.014582,3+) index(6436)
Title: Elution from: 46.087 to 46.087 scan no 4703 cid35.00 polarity:+:m1s



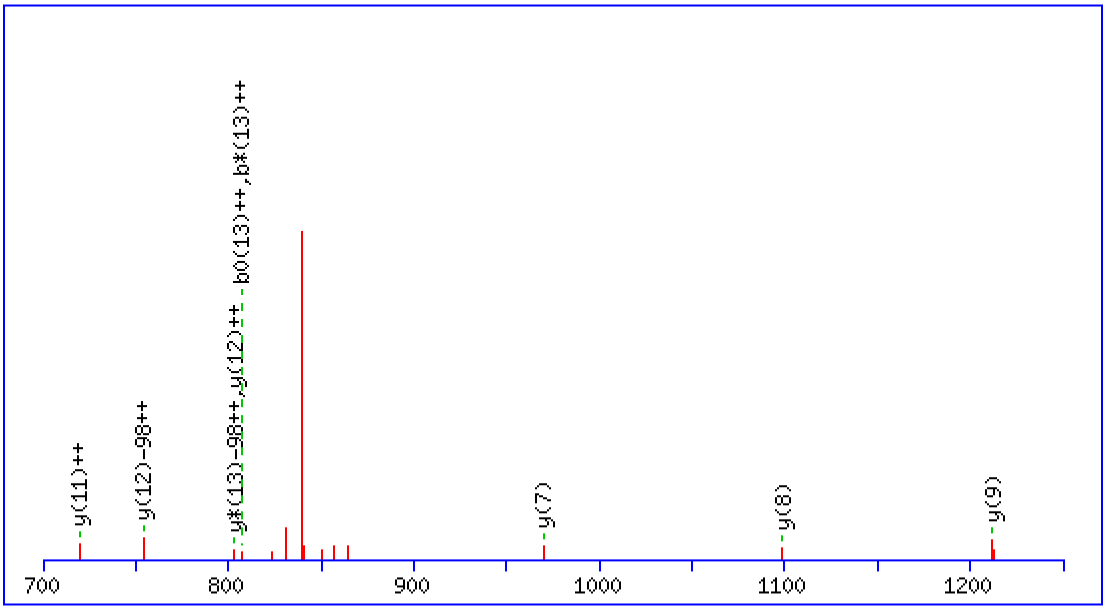
Monoisotopic mass of neutral peptide Mr(calc): 2601.0239
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 **Expect:** 8.1e-006
Matched b ions: b(7), b(9)++, b(9), b(13)++, b(15)-98++, b(15)++, b(17)-98++, b(18)++
Matched y ions: y(6), y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++

Peptide No.301

GDSLILEHQWELEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GDSLILEHQWELEK**
Found in **KIF1B_MOUSE** in **SwissProt**, Kinesin-like protein KIF1B OS=Mus musculus GN=Kif1b PE=1 SV=2

Match to Query 4122: 1775.811078 from(888.912815,2+) index(6773)
Title: Elution from: 49.304 to 49.304 scan no 5112 cid35.00 polarity:+:m1s



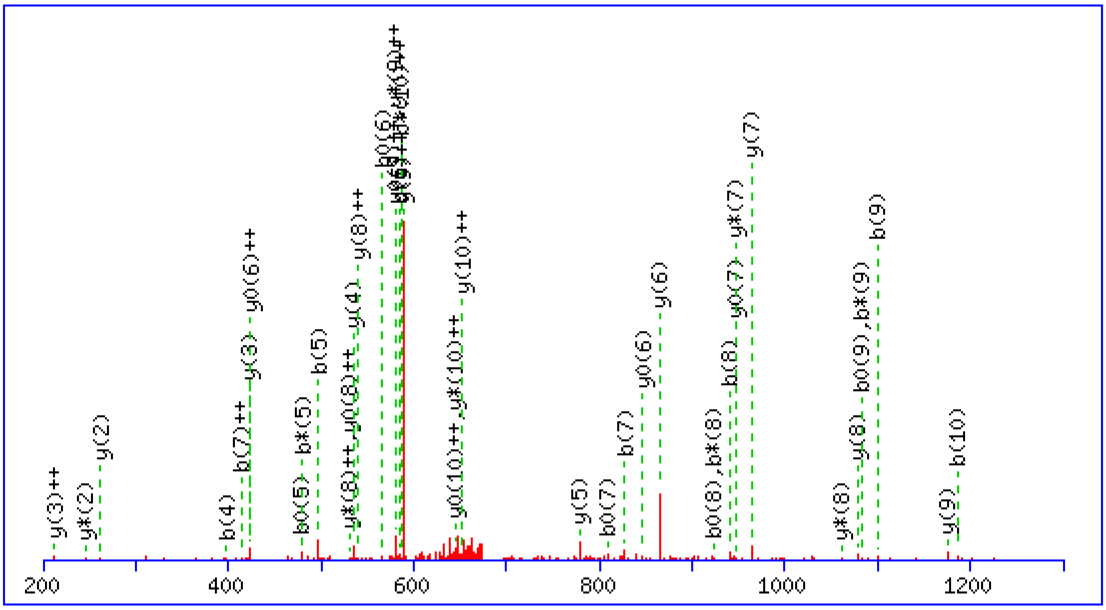
Monoisotopic mass of neutral peptide Mr(calc): 1775.8131
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.014
Matched b ions:
Matched y ions: y(7), y(8), y(9), y(11)++, y(12)-98++, y(12)++

Peptide No.302

GEPNVSYICSR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of **GEPNVSYICSR**
Found in **GSK3A_MOUSE** in **SwissProt**, Glycogen synthase kinase-3 alpha OS=Mus musculus GN=Gsk3a PE=1 SV=2

Match to Query 3031: 1360.548240 from(681.281396,2+) index(1342)
Title: Elution from: 37.350 to 37.350 scan no 2808 cid35.00 polarity:+



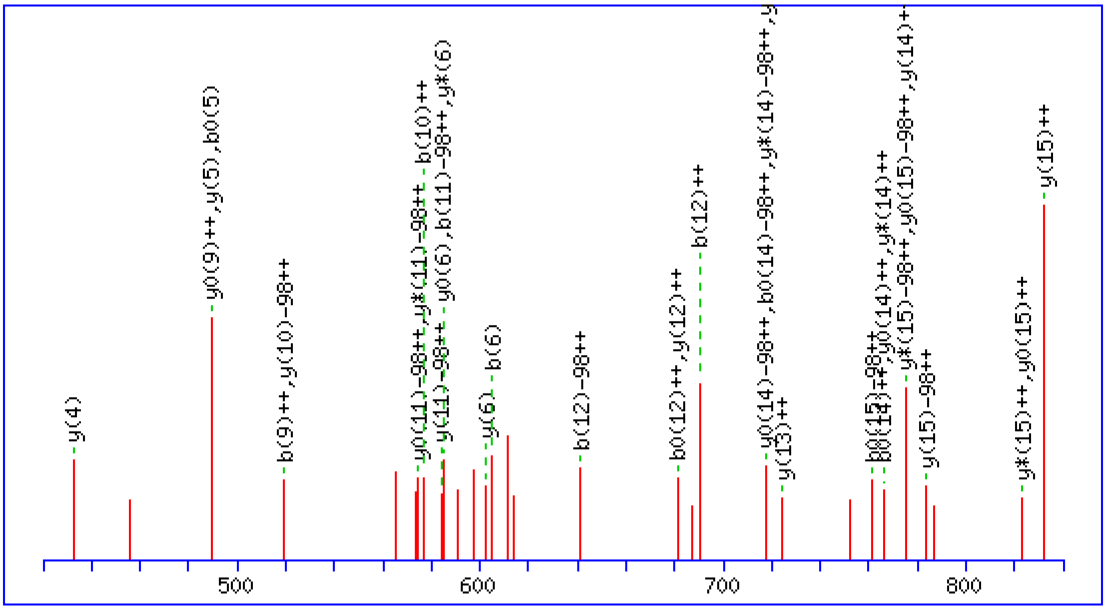
Monoisotopic mass of neutral peptide Mr(calc): 1360.5482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 61 **Expect:** 2.2e-006
Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(8), b(9), b(10)
Matched y ions: y(2), y(3)++, y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10)++

Peptide No.303

GFDTSPEHSLDLGISGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **GFDTSPEHSLDLGISGR**
Found in **EP400_MOUSE** in **SwissProt**, E1A-binding protein p400 OS=Mus musculus GN=Ep400 PE=1 SV=3

Match to Query 4324: 1866.816483 from(623.279437,3+) index(2857)
Title: Elution from: 45.338 to 45.338 scan no 4611 cid35.00 polarity:+



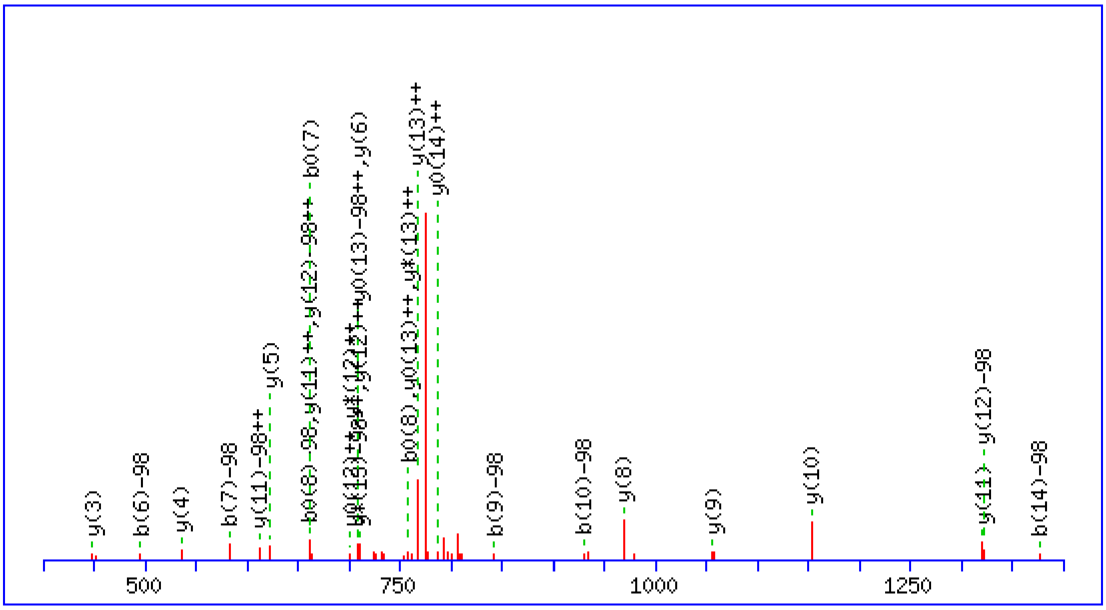
Monoisotopic mass of neutral peptide Mr(calc): 1866.8149
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(6), b(9)++, b(10)++, b(11)-98++, b(12)++, b(12)-98++, b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(10)-98++, y(11)-98++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++

Peptide No.304

GGDVSPSPYSSSSWR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GGDVSPSPYSSSSWR**
Found in **CDK13_MOUSE** in **SwissProt**, Cyclin-dependent kinase 13 OS=Mus musculus GN=Cdk13 PE=1 SV=3

Match to Query 3578: 1647.656934 from(824.835743,2+) index(5704)
Title: Elution from: 34.898 to 34.898 scan no 3293 cid35.00 polarity:+:m1s



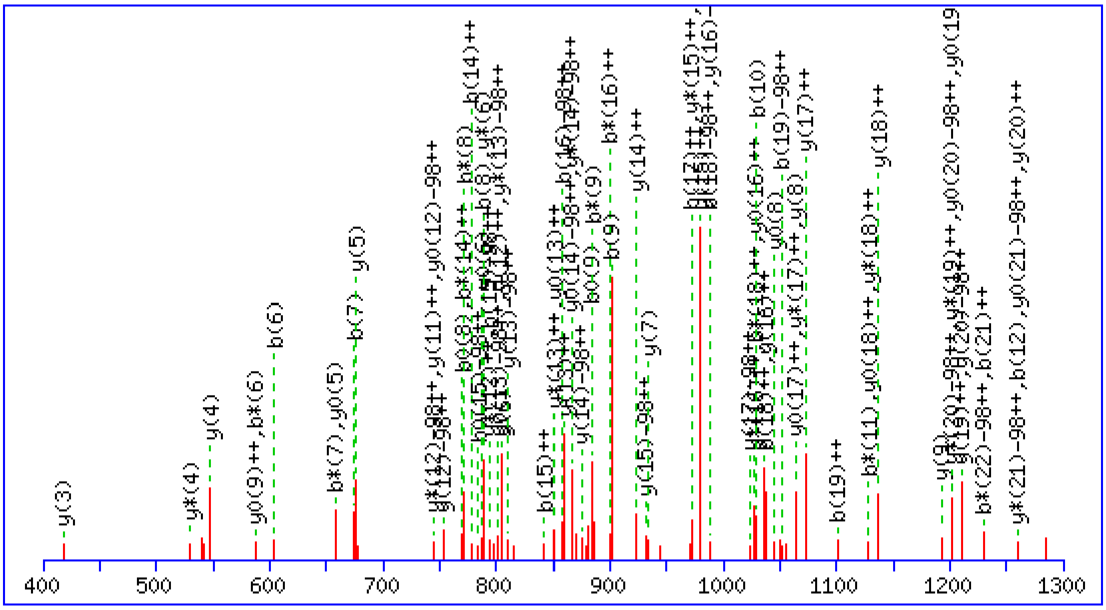
Monoisotopic mass of neutral peptide Mr(calc): 1647.6566
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 2.4e-006
Matched b ions: b(6)-98, b(7)-98, b(9)-98, b(10)-98, b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11)++, y(11), y(11)-98++, y(12)-98++, y(12)++, y(12)-98, y(13)++

Peptide No.305

GGNVFEALIQDDSEEEEEEEEENR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GGNVFEALIQDDSEEEEEEEEENR**
Found in **ABCF1_MOUSE** in **SwissProt**, ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1

Match to Query 5685: 2746.079184 from(916.367004,3+) index(6060)
Title: Elution from: 59.550 to 59.550 scan no 5680 cid35.00 polarity:+:m1s



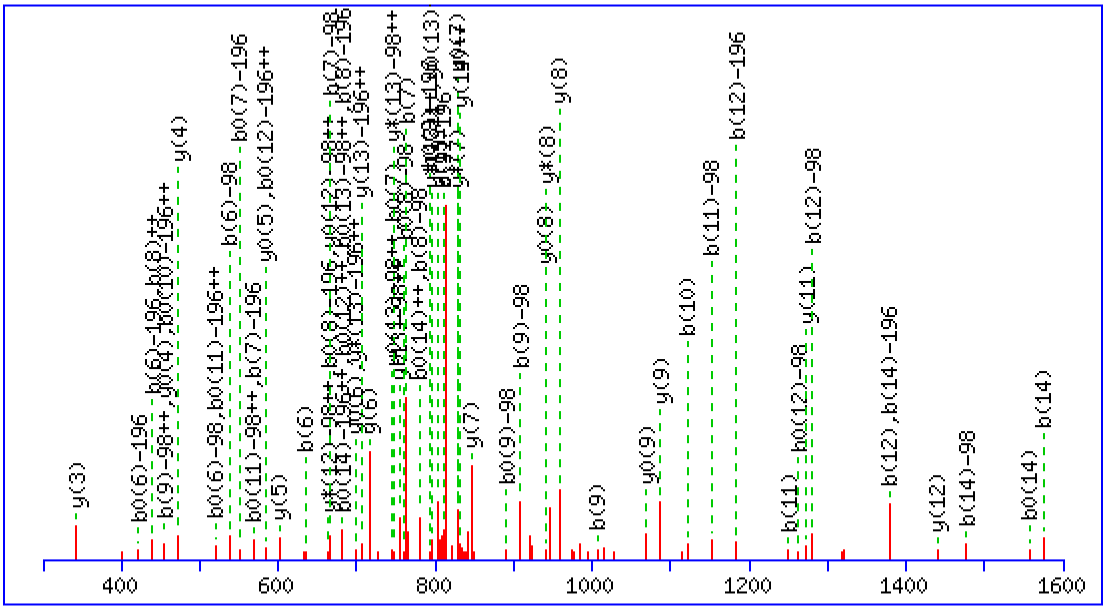
Monoisotopic mass of neutral peptide Mr(calc): 2746.0766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 **Expect:** 8.2e-008
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(12), b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(21)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(20)-98++, y(20)++

Peptide No.306

GGSSGEELEDEEPVK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **GGSSGEELEDEEPVK**
Found in **HDGR2_MOUSE** in **SwissProt**, Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1

Match to Query 3703: 1720.608452 from(861.311502,2+) index(1991)
Title: Elution from: 34.732 to 34.732 scan no 3239 cid35.00 polarity:+



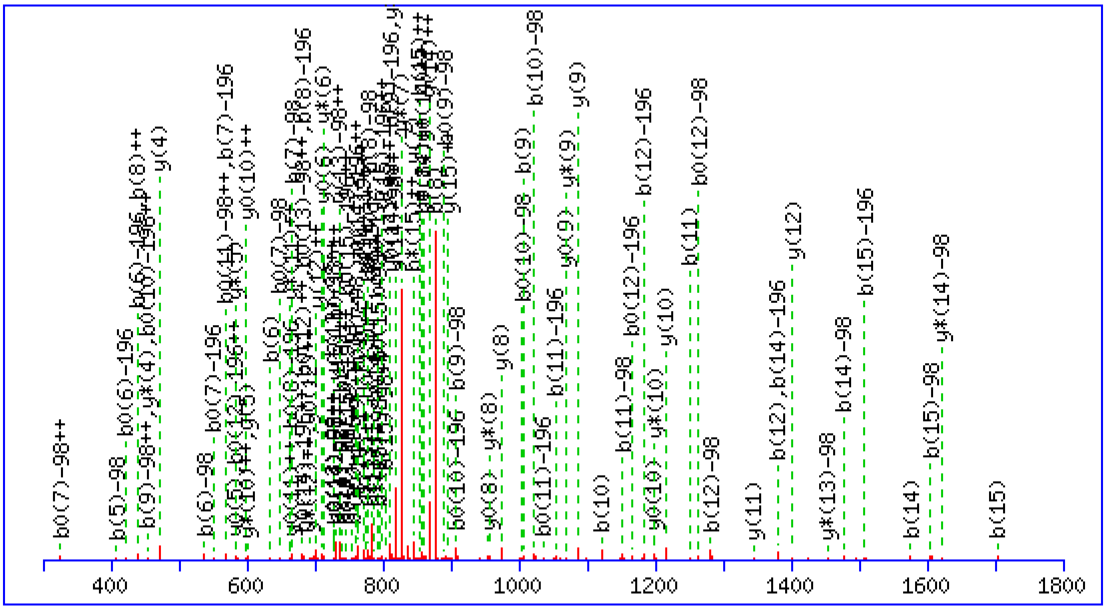
Monoisotopic mass of neutral peptide Mr(calc): 1720.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 1.4e-006
Matched b ions: b(6)-98, b(6)-196, b(6), b(7)-196, b(7), b(7)-98, b(8)++, b(8)-196, b(8)-98, b(9)-98, b(9)-98++, b(9), b(9)-196, b(10), b(11)-98, b(11), b(12)-98, b(12), b(12)-196, b(14)-196, b(14)-98, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(12), y(13)-196++, y(13)-98++, y(13)++, y(14)++

Peptide No.307

GGSSGEELEDEEPVKK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **GGSSGEELEDEEPVKK**
Found in **HDGR2_MOUSE** in **SwissProt**, Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1

Match to Query 3749: 1848.703054 from(925.358803,2+) index(4010)
Title: Elution from: 27.328 to 27.328 scan no 2116 cid35.00 polarity:+:m1s



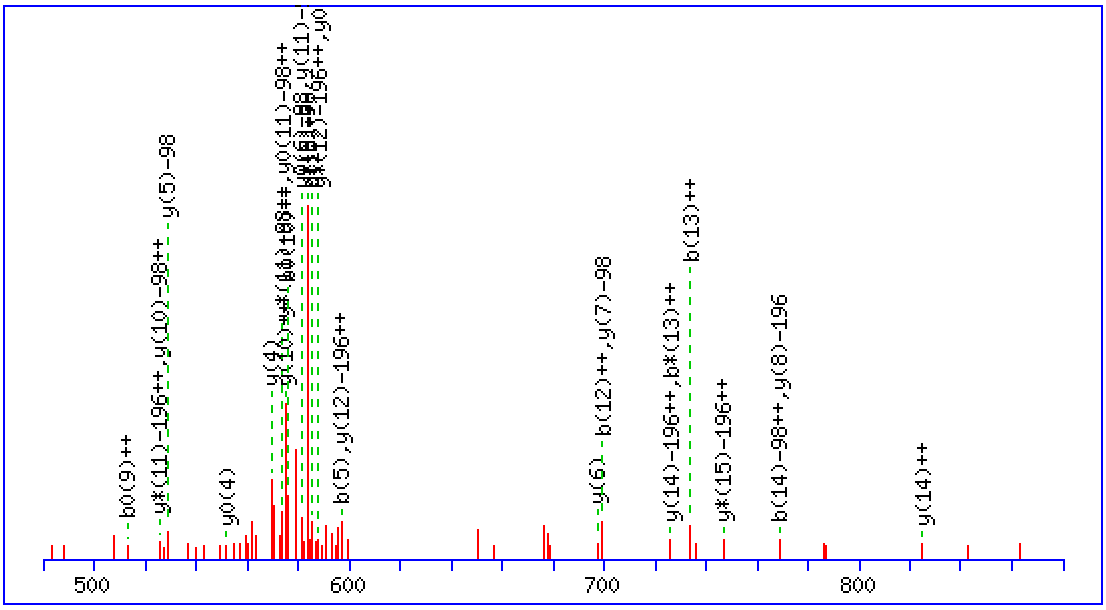
Monoisotopic mass of neutral peptide Mr(calc): 1848.7067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 3.6e-005
Matched b ions: b(5)-98, b(6)-98, b(6)-196, b(6), b(7)-196, b(7)-98, b(7), b(8), b(8)++, b(8)-196, b(8)-98, b(9)-98++, b(9)-196, b(9)-98, b(9), b(10)-98, b(10), b(11)-196, b(11)-98, b(11), b(12)-98, b(12), b(12)-196, b(13)++, b(14)-196, b(14)-98, b(14), b(14)-98++, b(14)++, b(15), b(15)-98, b(15)-196, b(15)-196++, b(15)-98++, b(15)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)++

Peptide No.308

GHGTYMGEEKLIASVAGSVER
Confirmed sites: @S:14,@S:18
Ambiguous sites: @T:4orY:5

MS/MS Fragmentation of **GHGTYMGEEKLIASVAGSVER**
Found in **EXOS2_MOUSE** in **SwissProt**, Exosome complex component RRP4 OS=Mus musculus GN=Exosc2 PE=2 SV=1

Match to Query 5260: 2429.966548 from(608.498913,4+) index(817)
Title: Elution from: 24.082 to 24.082 scan no 1767 cid35.00 polarity:+



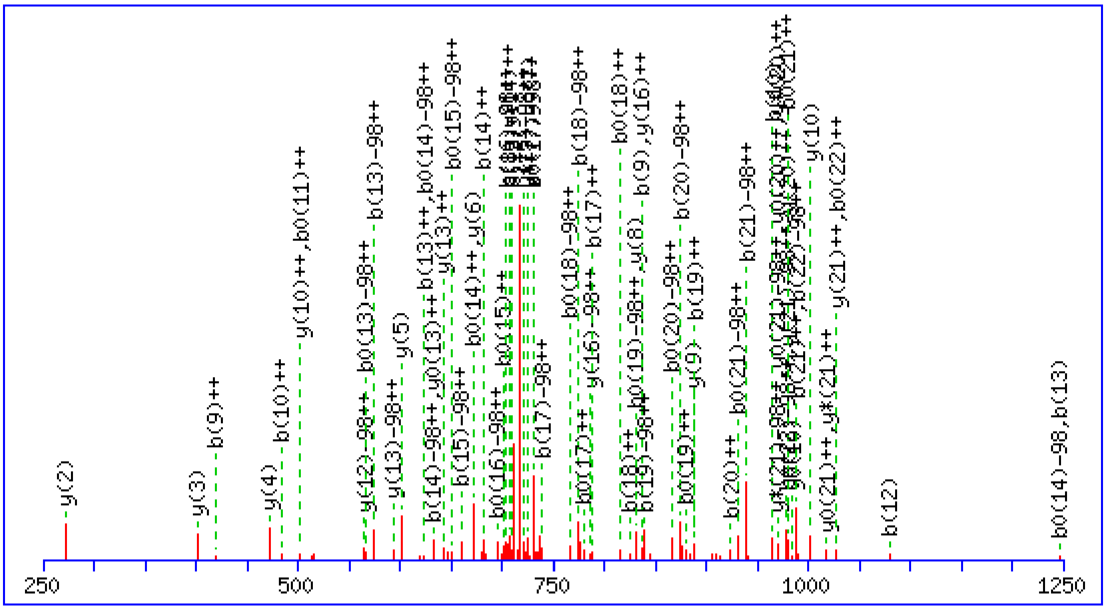
Monoisotopic mass of neutral peptide Mr(calc): 2429.9729
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y5 : Phospho (Y)
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.047
Matched b ions: b(5), b(10)++, b(12)++, b(13)++, b(14)-98++
Matched y ions: y(4), y(5)-98, y(6), y(7)-98, y(8)-196, y(10)++, y(10)-98++, y(11)-98++, y(12)-196++, y(14)++, y(14)-196++

Peptide No.309

GHPSAGAEEEGGSDGSAAEAEPR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GHPSAGAEEEGGSDGSAAEAEPR**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5885: 2246.867496 from(749.963108,3+) index(4089)
Title: Elution from: 19.832 to 19.832 scan no 1252 cid35.00 polarity:+:m1s



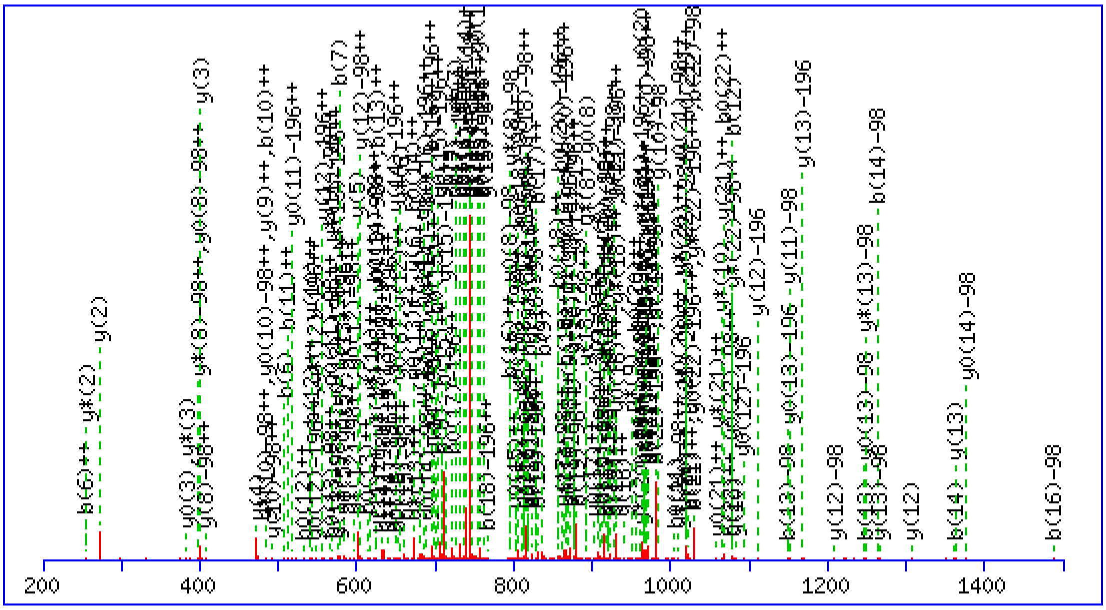
Monoisotopic mass of neutral peptide Mr(calc): 2246.8713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 **Expect:** 3.4e-008
Matched b ions: b(8), b(9)++, b(9), b(10)++, b(10), b(12), b(13), b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(10)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(15)-98++, y(16)++, y(16)-98++, y(20)++, y(21)-98++, y(21)++

Peptide No.310

GHPSAGAEEEGGSDGSAAEAEPR
Confirmed sites: @S:13,@S:16
Ambiguous sites:

MS/MS Fragmentation of **GHPSAGAEEEGGSDGSAAEAEPR**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5053: 2326.832067 from(776.617965,3+) index(3470)
Title: Elution from: 20.313 to 20.313 scan no 1260 cid35.00 polarity:+:m1s



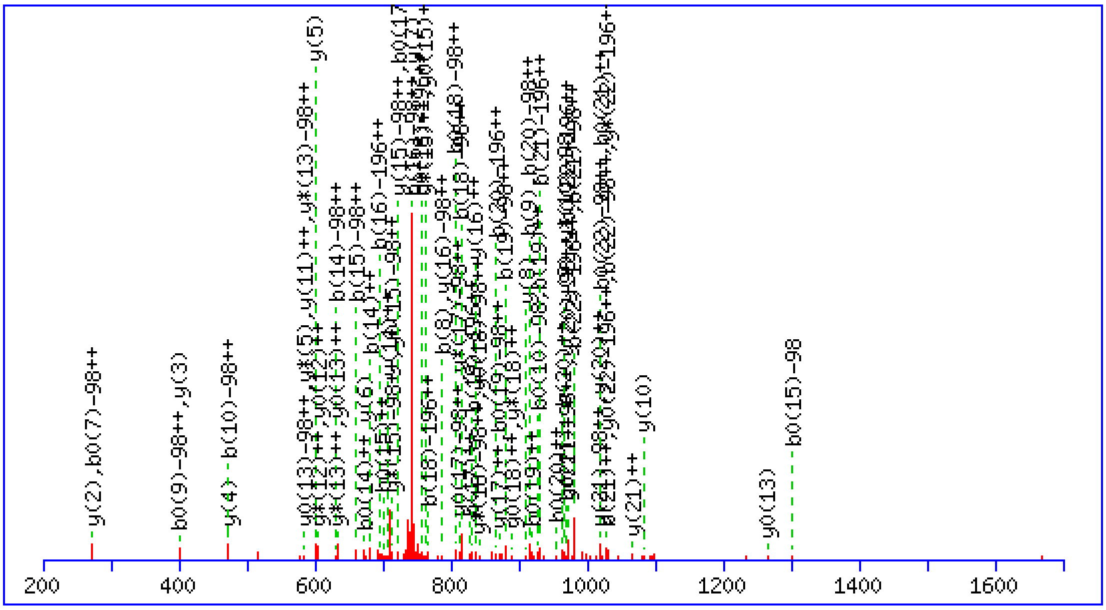
Monoisotopic mass of neutral peptide Mr(calc): 2326.8376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 1.1e-006
Matched b ions: b(6)++, b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)++, b(11), b(12), b(12)++, b(13), b(13)-98, b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)-98, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)-98, b(16)-196++, b(16)++, b(17)-196++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)-196++, b(21)++, b(22)-196++, b(22)-98++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8)-98, y(8), y(9)++, y(9)-98, y(9), y(10), y(10)-98++, y(10)++, y(10)-98, y(11)-98, y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)-196++, y(12)++, y(12)-196, y(13)-98, y(13)-98++, y(13), y(13)-196++, y(13)-196, y(13)++, y(14)-196++, y(14)-98++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(21)-196++

Peptide No.311

GHPSAGAEEEGGSDGSAAEAEPR
Confirmed sites: @S:4,@S:16
Ambiguous sites:

MS/MS Fragmentation of **GHPSAGAEEEGGSDGSAAEAEPR**
Found in **EIF3B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1

Match to Query 5827: 2326.839924 from(776.620584,3+) index(3636)
Title: Elution from: 25.121 to 25.121 scan no 1316 cid35.00 polarity:+:m1s



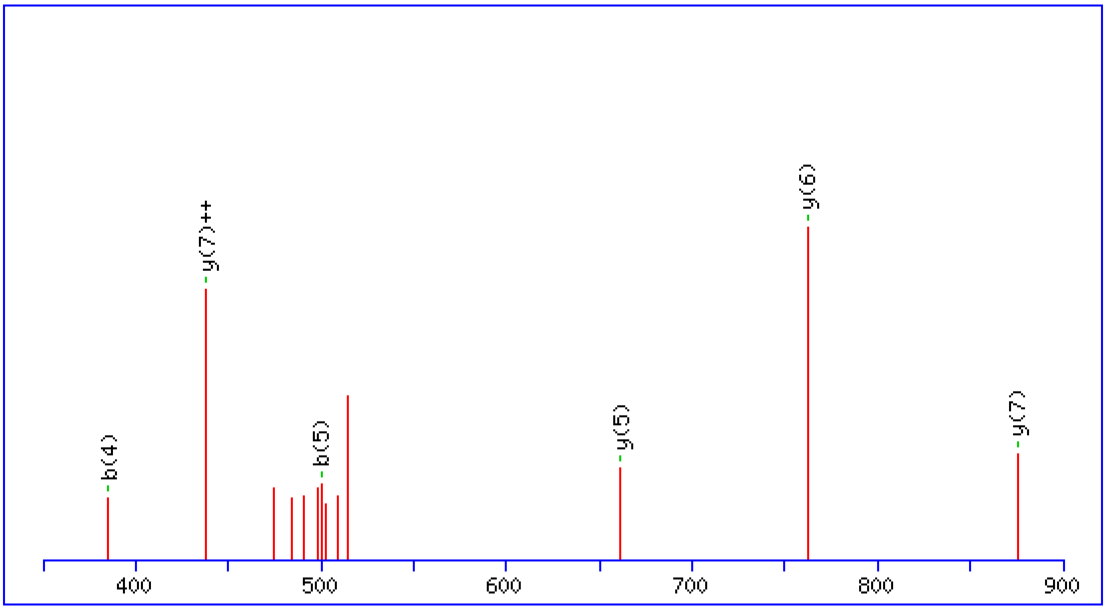
Monoisotopic mass of neutral peptide Mr(calc): 2326.8376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0014
Matched b ions: b(8), b(9), b(10)-98++, b(14)-98++, b(14)++, b(15)-98++, b(16)-98++, b(16)-196++, b(17)++, b(18)-98++, b(18)-196++, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(20)-196++, b(21)-98++, b(21)-196++, b(21)++, b(22)-196++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(14)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++

Peptide No.312

GIITDSFGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **GIITDSFGR**
Found in **CCM2_MOUSE** in **SwissProt**, Malcavernin OS=Mus musculus GN=Ccm2 PE=1 SV=1

Match to Query 929: 1044.463798 from(523.239175,2+) index(2331)
Title: Elution from: 38.280 to 38.280 scan no 3711 cid35.00 polarity:+



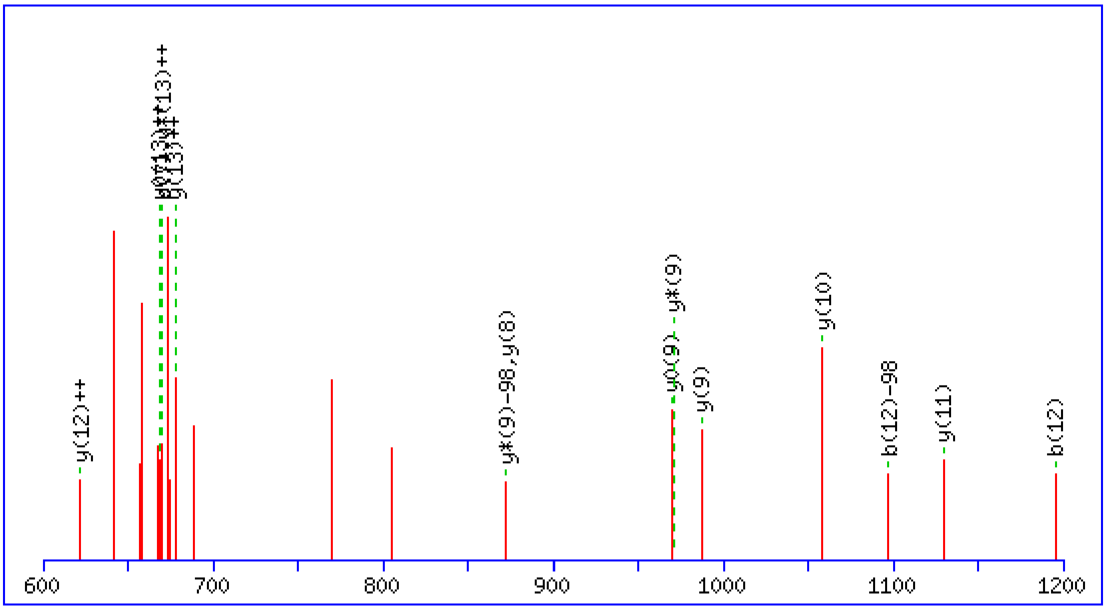
Monoisotopic mass of neutral peptide Mr(calc): 1044.4641
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(4), b(5)
Matched y ions: y(5), y(6), y(7)++, y(7)

Peptide No.313

GILAADESTGSIAK
Confirmed sites:
Ambiguous sites: @S:8orT:9orS:11

MS/MS Fragmentation of **GILAADESTGSIAK**
Found in **ALDOA_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2556: 1411.658808 from(706.836680,2+) index(2057)
Title: Elution from: 34.946 to 34.946 scan no 3298 cid35.00 polarity:+



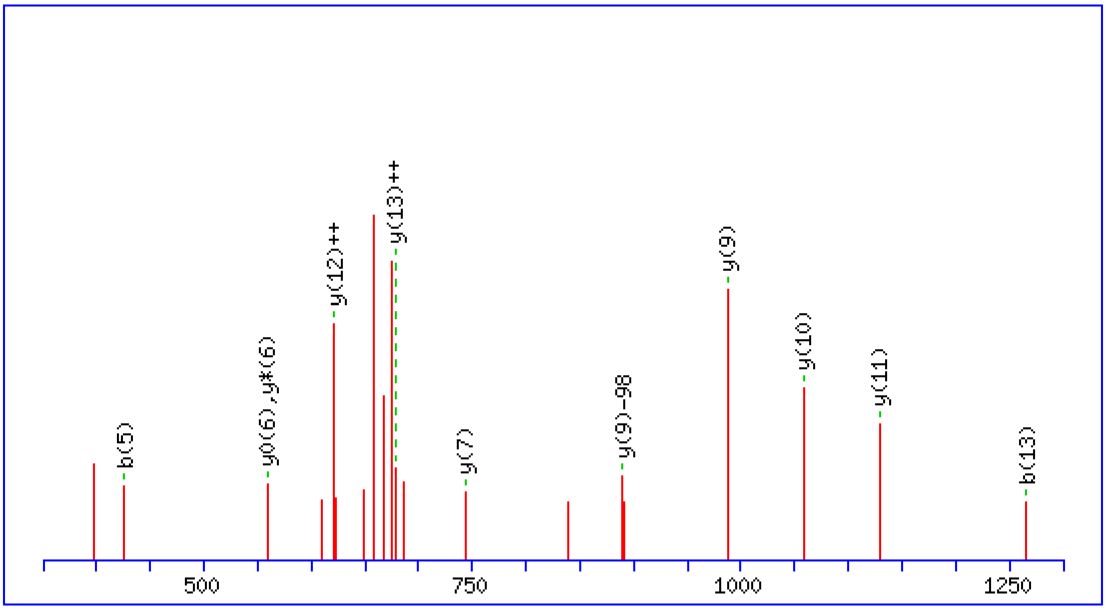
Monoisotopic mass of neutral peptide Mr(calc): 1411.6596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.035
Matched b ions: b(7), b(12)-98, b(12)
Matched y ions: y(8), y(9), y(10), y(11), y(12)++, y(13)++

Peptide No.314

GILAADESTGSIAK
Confirmed sites:
Ambiguous sites: @S:8orT:9orS:11

MS/MS Fragmentation of **GILAADESTGSIAK**
Found in **ALDOA_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2397: 1411.657746 from(706.836149,2+) index(5547)
Title: Elution from: 34.962 to 34.962 scan no 3270 cid35.00 polarity:+:m1s



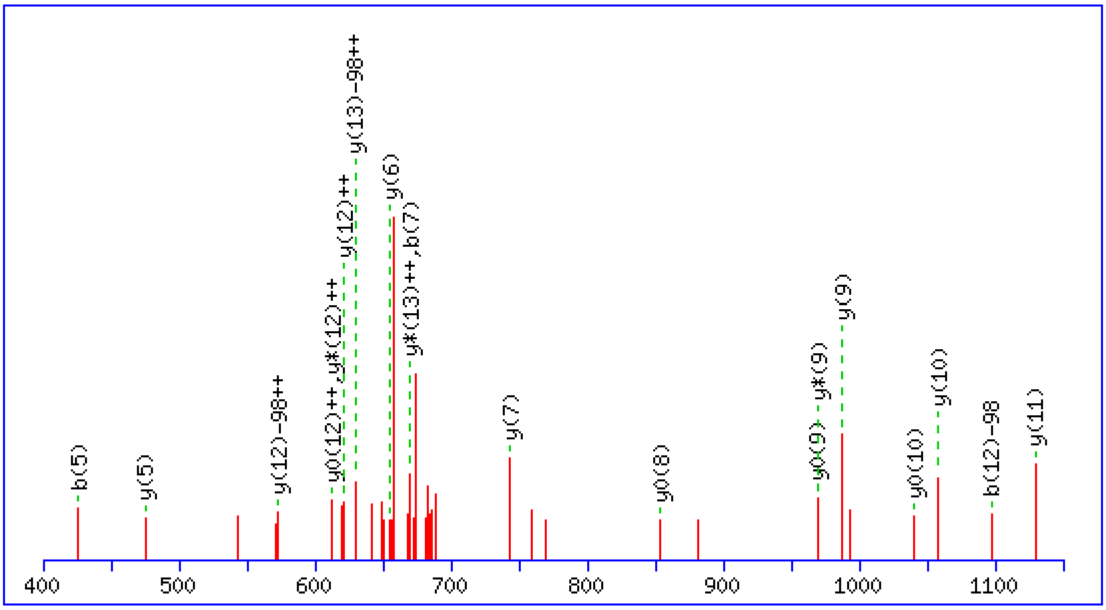
Monoisotopic mass of neutral peptide Mr(calc): 1411.6596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.058
Matched b ions: b(5), b(13)
Matched y ions: y(7), y(9)-98, y(9), y(10), y(11), y(12)++, y(13)++

Peptide No.315

GILAADESTGSIAK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **GILAADESTGSIAK**
Found in **ALDOA_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2

Match to Query 2254: 1411.658412 from(706.836482,2+) index(1697)
Title: Elution from: 34.757 to 34.757 scan no 3129 cid35.00 polarity:+



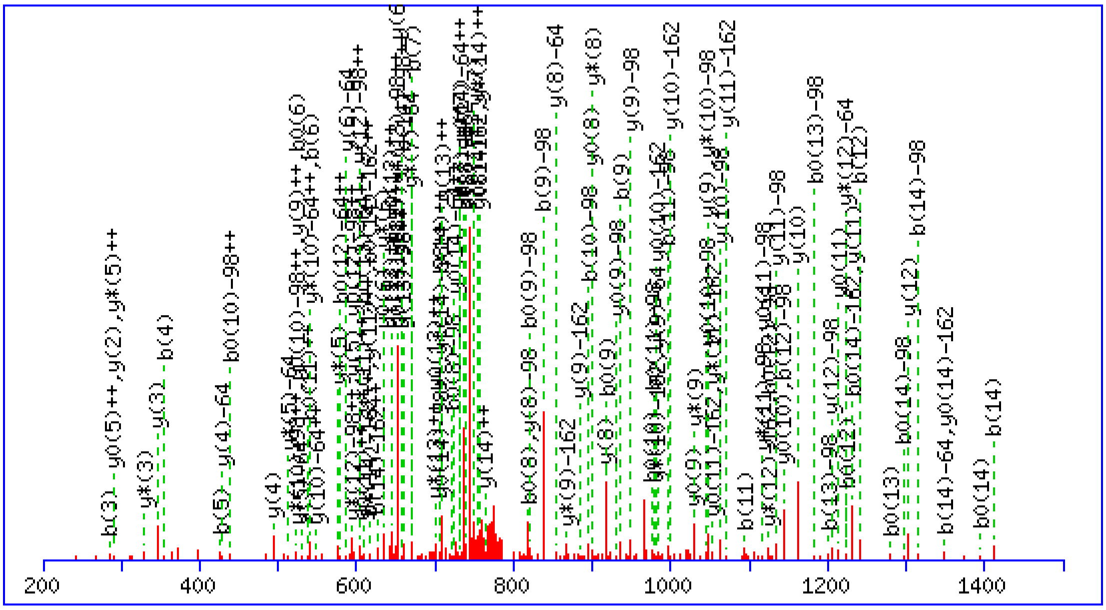
Monoisotopic mass of neutral peptide Mr(calc): 1411.6596
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.01
Matched b ions: b(5), b(7), b(12)-98
Matched y ions: y(5), y(6), y(7), y(9), y(10), y(11), y(12)++, y(12)-98++, y(13)-98++

Peptide No.316

GILAADESVGTMGNR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **GILAADESVGTMGNR**
Found in **ALDOB_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3

Match to Query 3801: 1585.680824 from(793.847688,2+) index(1535)
Title: Elution from: 39.658 to 39.658 scan no 3082 cid35.00 polarity:+



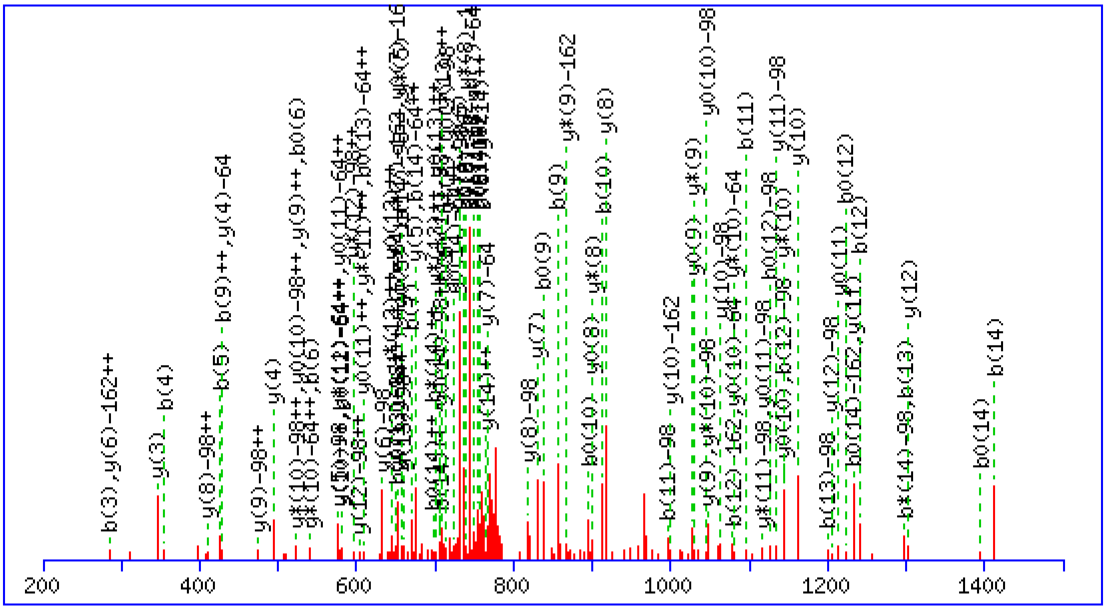
Monoisotopic mass of neutral peptide Mr(calc): 1585.6807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 73 **Expect:** 2.3e-007
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(13)-98, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)++, y(12), y(12)-98++, y(12)++, y(12)-98, y(13)++, y(13)-98++, y(14)++

Peptide No.317

GILAADESVGTMGNR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **GILAADESVGTMGNR**
Found in **ALDOB_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3

Match to Query 3296: 1585.681154 from(793.847853,2+) index(1302)
Title: Elution from: 39.224 to 39.224 scan no 2897 cid35.00 polarity:+



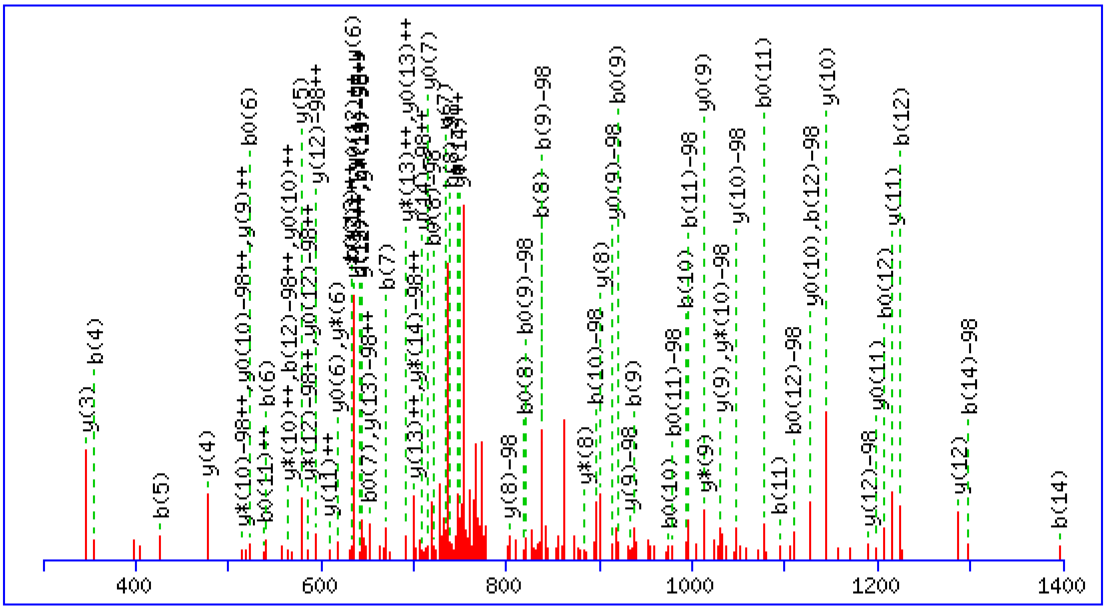
Monoisotopic mass of neutral peptide Mr(calc): 1585.6807
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M12 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 91 **Expect:** 4e-009
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(8)-98++, y(9), y(9)++, y(9)-98++, y(10), y(10)++, y(10)-98, y(11), y(11)-98, y(12), y(12)++, y(12)-98, y(12)-98++, y(13)-98++, y(13)++, y(14)++

Peptide No.318

GILAADESVGTMGNR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **GILAADESVGTMGNR**
Found in **ALDOB_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3

Match to Query 3254: 1569.685864 from(785.850208,2+) index(1708)
Title: Elution from: 46.363 to 46.363 scan no 3629 cid35.00 polarity:+



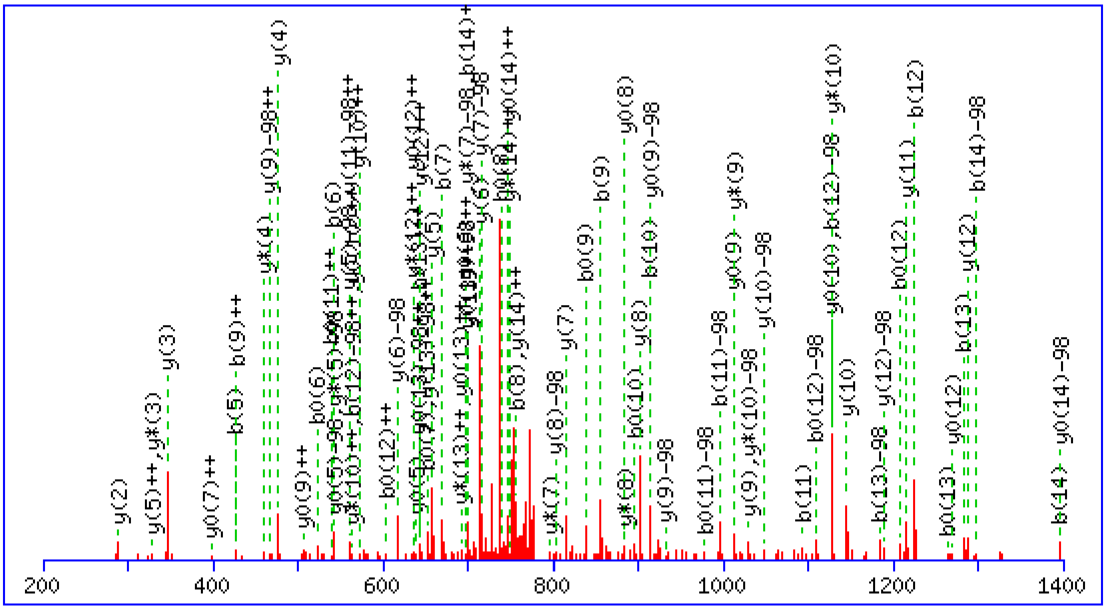
Monoisotopic mass of neutral peptide Mr(calc): 1569.6858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 6.3e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(12)-98++, b(13)++, b(14), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)++, y(9)-98, y(10), y(10)-98, y(11), y(11)++, y(12), y(12)++, y(12)-98, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++

Peptide No.319

GILAADESVGTMGNR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **GILAADESVGTMGNR**
Found in **ALDOB_MOUSE** in **SwissProt**, Fructose-bisphosphate aldolase B OS=Mus musculus GN=Aldob PE=1 SV=3

Match to Query 3255: 1569.687382 from(785.850967,2+) index(4602)
Title: Elution from: 45.634 to 45.634 scan no 3553 cid35.00 polarity:+:m1s



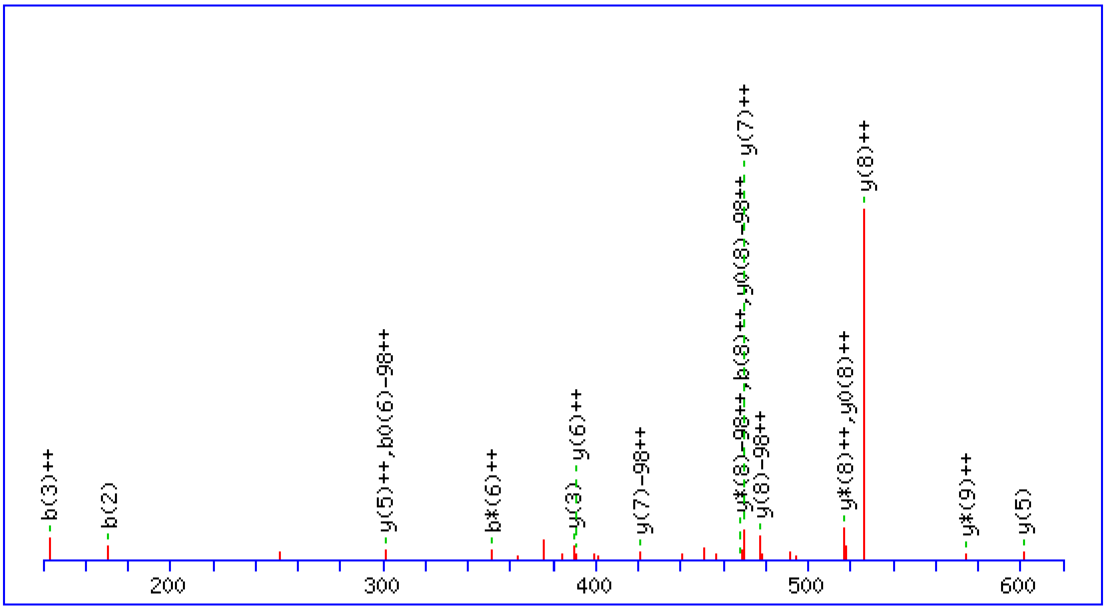
Monoisotopic mass of neutral peptide Mr(calc): 1569.6858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 89 **Expect:** 6.8e-009
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(9)++, b(10), b(11)-98, b(11), b(12)-98, b(12), b(12)-98++, b(13), b(13)-98, b(13)++, b(14), b(14)-98, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(5)++, y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98++, y(9)-98, y(10), y(10)-98, y(10)++, y(11)-98++, y(11), y(12), y(12)++, y(12)-98, y(13)-98++, y(13)++, y(14)++

Peptide No.320

GILRTPDTIR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **GILRTPDTIR**
Found in **CLH_MOUSE** in **SwissProt**, Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3

Match to Query 1735: 1220.629128 from(407.883652,3+) index(1492)
Title: Elution from: 29.132 to 29.132 scan no 2518 cid35.00 polarity:+



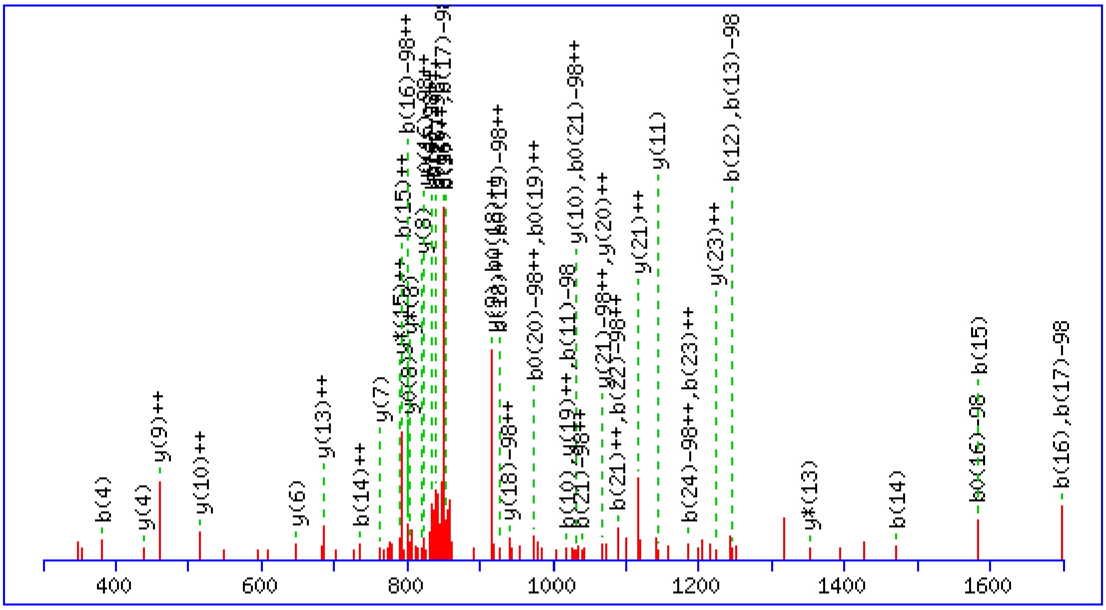
Monoisotopic mass of neutral peptide Mr(calc): 1220.6278
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.023
Matched b ions: b(2), b(3)++, b(8)++
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(7)++, y(7)-98++, y(8)++, y(8)-98++

Peptide No.321

GIPLPTGDTSPEPELLPGDPLPPPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **GIPLPTGDTSPEPELLPGDPLPPPK**
Found in **EIF3G_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=2

Match to Query 6334: 2613.300756 from(872.107528,3+) index(6145)
Title: Elution from: 68.014 to 68.014 scan no 5615 cid35.00 polarity:+:m1s



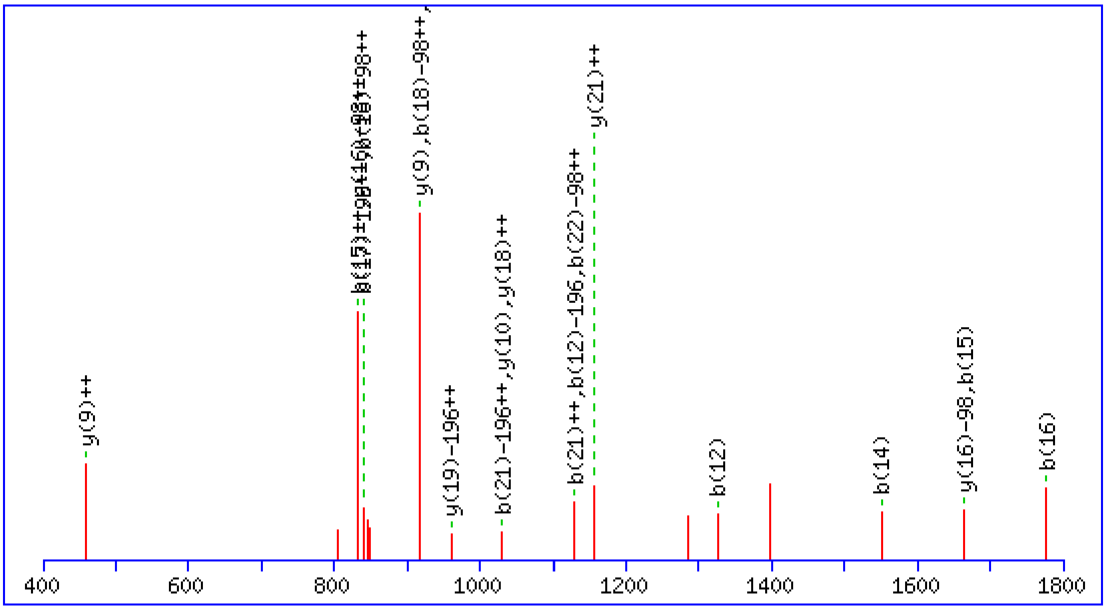
Monoisotopic mass of neutral peptide Mr(calc): 2613.2979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.042
Matched b ions: b(4), b(9), b(10), b(11)-98, b(12), b(13)-98, b(14), b(14)++, b(15)++, b(15), b(16)++, b(16), b(16)-98++, b(17)-98++, b(17)-98, b(18)++, b(21)++, b(21)-98++, b(22)-98++, b(23)++, b(24)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(13)++, y(16)-98++, y(18)-98++, y(19)++, y(20)++, y(21)++, y(21)-98++, y(23)++

Peptide No.322

GIPLPTGDTSPEPELLPGDPLPPPK
Confirmed sites: @T:9,@S:10
Ambiguous sites:

MS/MS Fragmentation of **GIPLPTGDTSPEPELLPGDPLPPPK**
Found in **EIF3G_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=2

Match to Query 6473: 2693.262303 from(898.761377,3+) index(6972)
Title: Elution from: 66.013 to 66.013 scan no 6494 cid35.00 polarity:+:m1s



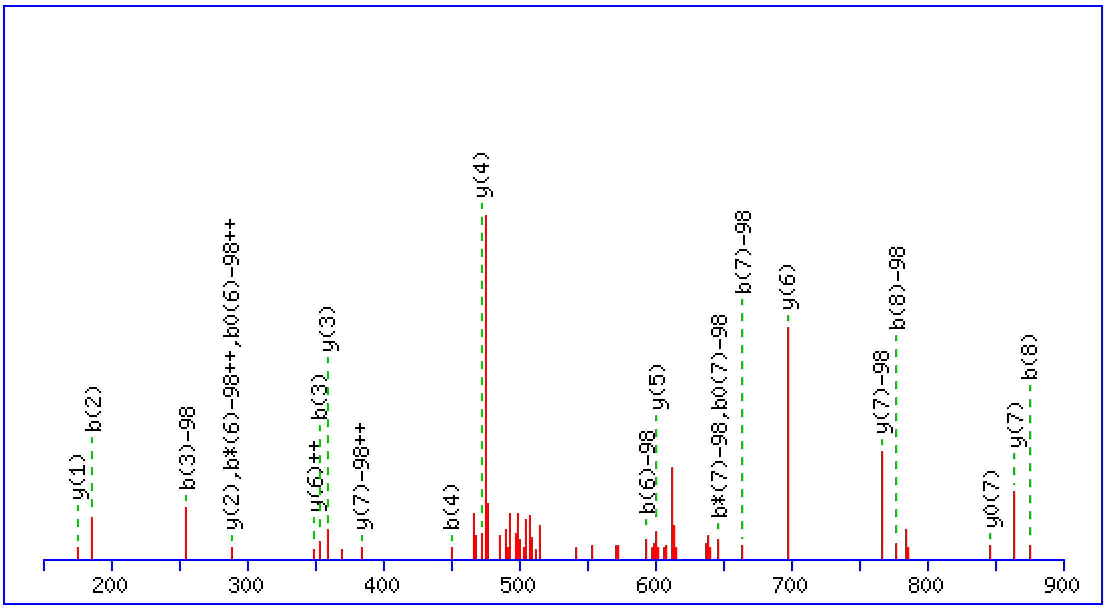
Monoisotopic mass of neutral peptide Mr(calc): 2693.2642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0037
Matched b ions: b(12), b(12)-196, b(14), b(15)++, b(15), b(16), b(16)-98++, b(17)-196++, b(18)-98++, b(21)-196++, b(21)++, b(22)-98++
Matched y ions: y(9)++, y(9), y(10), y(16)-98++, y(16)-98, y(18)++, y(19)-196++, y(21)++

Peptide No.323

GKSPQLALR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GKSPQLALR**
Found in **UBXN6_MOUSE** in **SwissProt**, UBX domain-containing protein 6 OS=Mus musculus GN=Ubxn6 PE=1 SV=1

Match to Query 1080: 1048.542426 from(525.278489,2+) index(695)
Title: Elution from: 21.945 to 21.945 scan no 1537 cid35.00 polarity:+



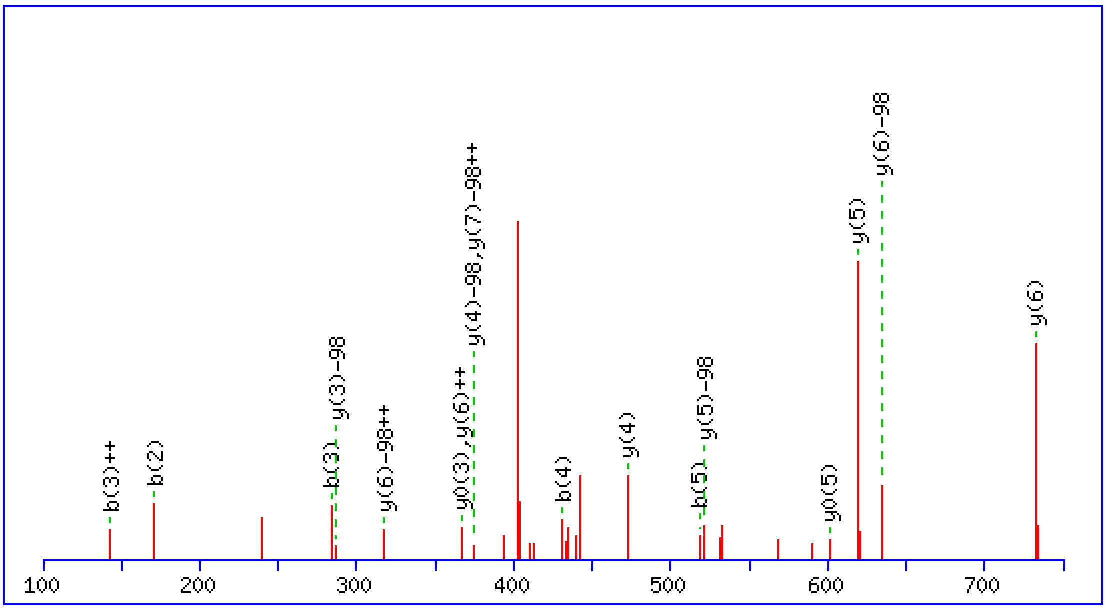
Monoisotopic mass of neutral peptide Mr(calc): 1048.5430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 **Expect:** 1.2e-005
Matched b ions: b(2), b(3)-98, b(3), b(4), b(6)-98, b(7)-98, b(8), b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)-98, y(7)-98++

Peptide No.324

GLLFSASK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **GLLFSASK**
Found in **S14L2_MOUSE** in **SwissProt**, SEC14-like protein 2 OS=Mus musculus GN=Sec14l2 PE=2 SV=1

Match to Query 489: 901.431486 from(451.723019,2+) index(2199)
Title: Elution from: 40.772 to 40.772 scan no 3904 cid35.00 polarity:+



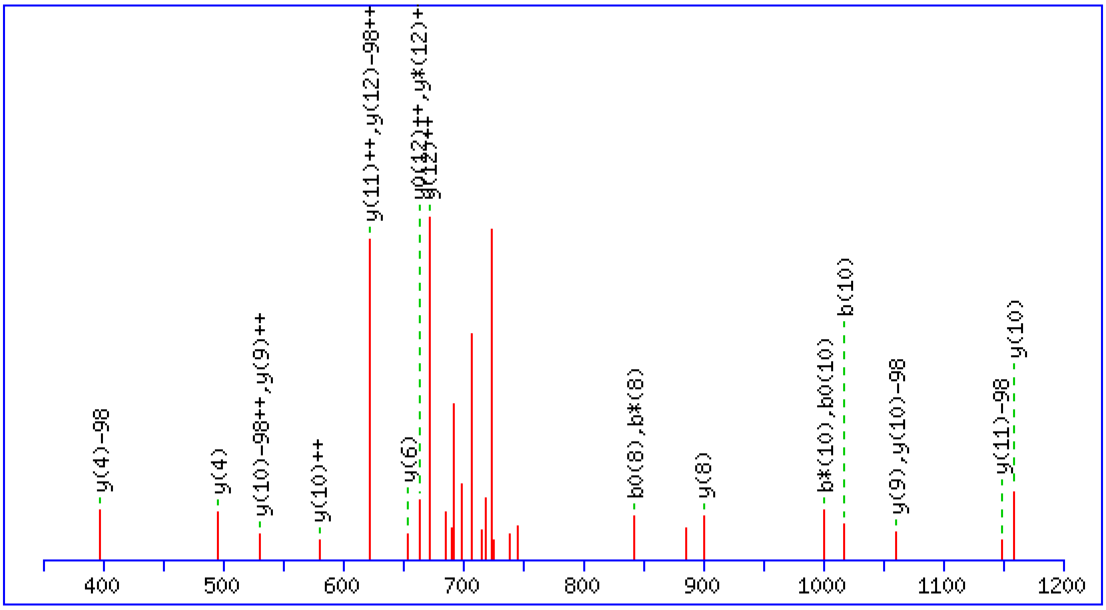
Monoisotopic mass of neutral peptide Mr(calc): 901.4310
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.024
Matched b ions: b(2), b(3), b(3)++, b(4), b(5)
Matched y ions: y(3)-98, y(4), y(4)-98, y(5), y(5)-98, y(6), y(6)-98++, y(6)-98, y(6)++, y(7)-98++

Peptide No.325

GLPSPYNMSAPGSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GLPSPYNMSAPGSR**
Found in **DESP_MOUSE** in **SwissProt**, Desmoplakin OS=Mus musculus GN=Dsp PE=3 SV=1

Match to Query 3041: 1512.640810 from(757.327681,2+) index(2455)
Title: Elution from: 39.180 to 39.180 scan no 3858 cid35.00 polarity:+



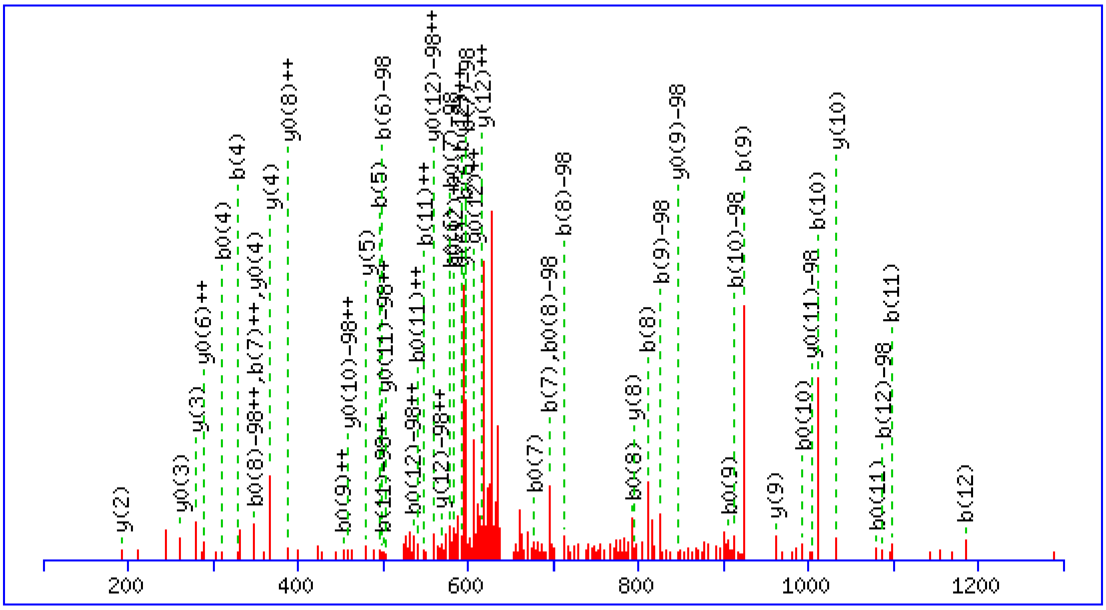
Monoisotopic mass of neutral peptide Mr(calc): 1512.6432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.052
Matched b ions: b(10)
Matched y ions: y(4)-98, y(4), y(6), y(8), y(9)++, y(9), y(10)-98++, y(10), y(10)++, y(10)-98, y(11)++, y(11)-98, y(12)++, y(12)-98++

Peptide No.326

GLSASTVDLSSSS
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GLSASTVDLSSSS**
Found in **KLC4_MOUSE** in **SwissProt**, Kinesin light chain 4 OS=Mus musculus GN=Klc4 PE=1 SV=1

Match to Query 2744: 1289.539124 from(645.776838,2+) index(2069)
Title: Elution from: 47.557 to 47.557 scan no 3959 cid35.00 polarity:+



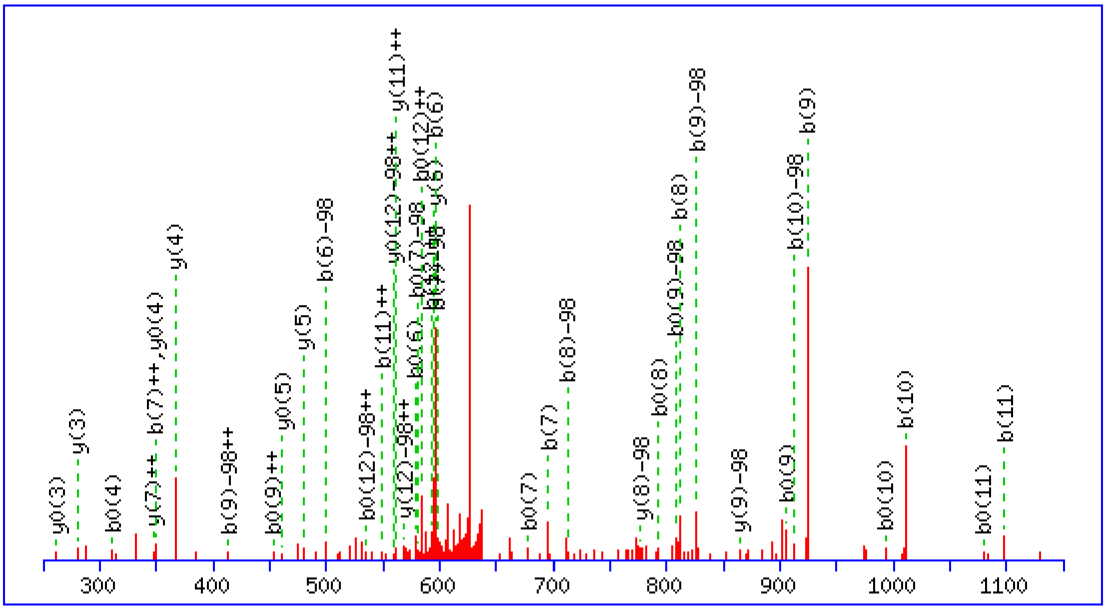
Monoisotopic mass of neutral peptide Mr(calc): 1289.5388
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.0002
Matched b ions: b(4), b(5), b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98++, b(11)++, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(12)-98++, y(12)++

Peptide No.327

GLSASTVDLSSSS
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **GLSASTVDLSSSS**
Found in **KLC4_MOUSE** in **SwissProt**, Kinesin light chain 4 OS=Mus musculus GN=Klc4 PE=1 SV=1

Match to Query 2437: 1289.539170 from(645.776861,2+) index(1763)
Title: Elution from: 47.537 to 47.537 scan no 3742 cid35.00 polarity:+



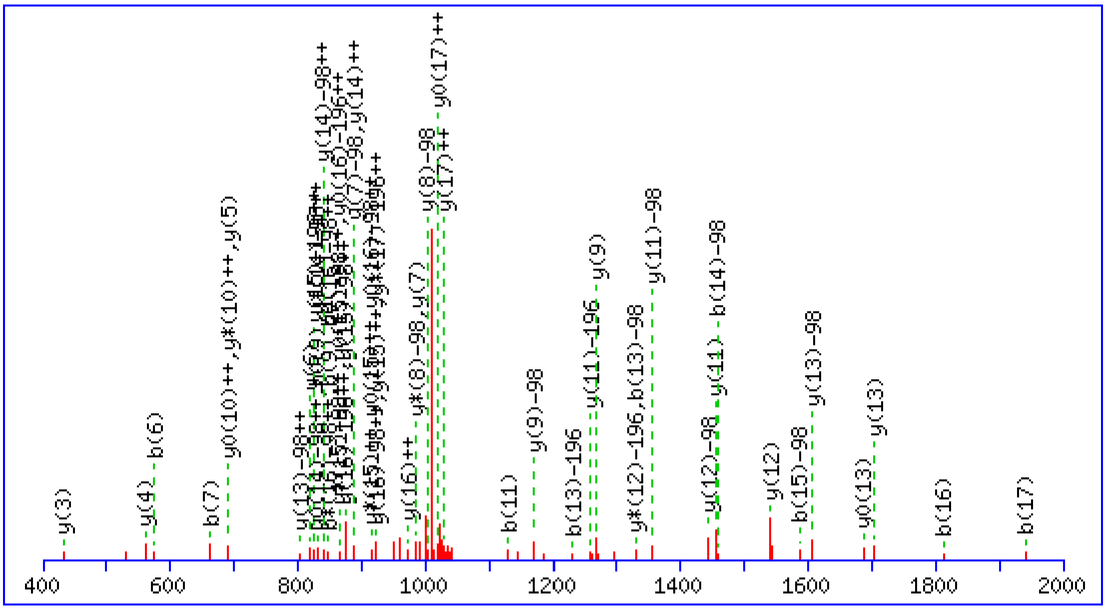
Monoisotopic mass of neutral peptide Mr(calc): 1289.5388
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0025
Matched b ions: b(6)-98, b(6), b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(9)-98++, b(10), b(10)-98, b(11), b(11)++, b(12)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(8)-98, y(9)-98, y(11)++, y(12)-98++

Peptide No.328

GLVAAYSGESDSEEEQER
Confirmed sites: @S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of **GLVAAYSGESDSEEEQER**
Found in **RBM10_MOUSE** in **SwissProt**, RNA-binding protein 10 OS=Mus musculus GN=Rbm10 PE=1 SV=1

Match to Query 5385: 2114.768106 from(1058.391329,2+) index(6007)
Title: Elution from: 38.135 to 38.135 scan no 3721 cid35.00 polarity:+:m1s



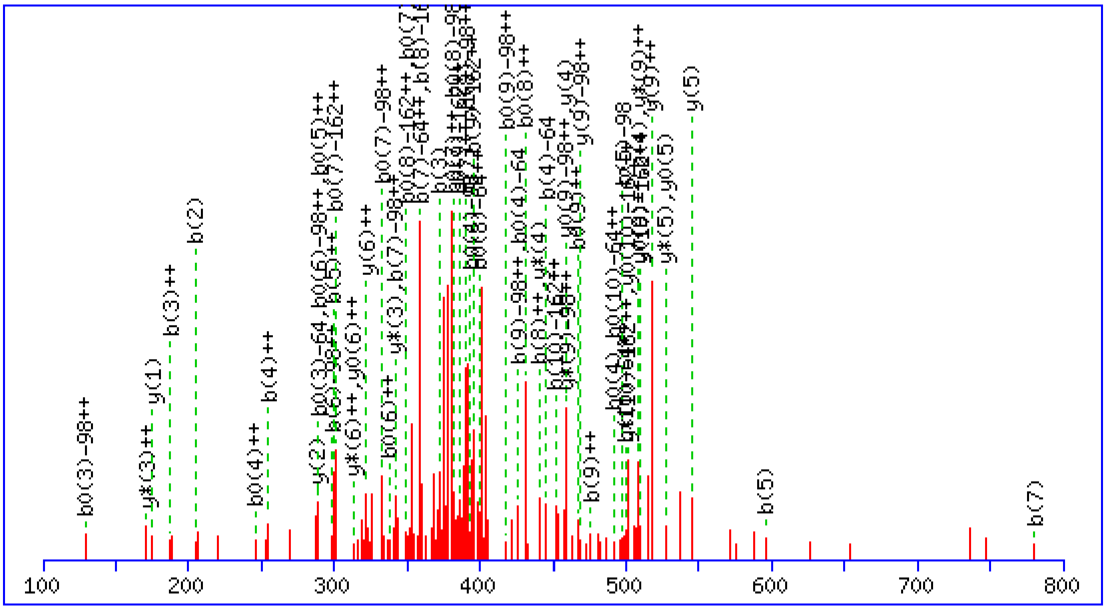
Monoisotopic mass of neutral peptide Mr(calc): 2114.7718
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00027
Matched b ions: b(6), b(7), b(9), b(11), b(13)-98, b(13)-196, b(14)-98, b(15)-98, b(16), b(17)
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(9)-98, y(9), y(11)-98, y(11), y(11)-196, y(12), y(12)-98, y(13), y(13)-98, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(15)-196++, y(16)-196++, y(16)-98++, y(16)++, y(17)++

Peptide No.329

GMSHSPSVALR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GMSHSPSVALR**
Found in **PROX1_MOUSE** in **SwissProt**, Prospero homeobox protein 1 OS=Mus musculus GN=Prox1 PE=1 SV=2

Match to Query 2167: 1236.532785 from(413.184871,3+) index(250)
Title: Elution from: 26.428 to 26.428 scan no 1409 cid35.00 polarity:+



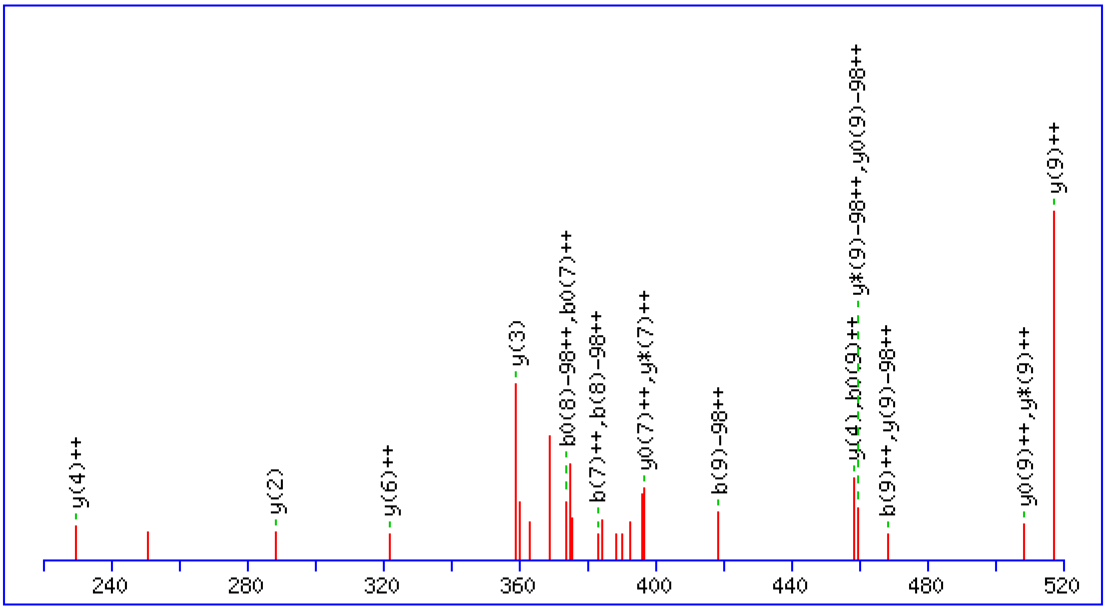
Monoisotopic mass of neutral peptide Mr(calc): 1236.5322
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.011
Matched b ions: b(2), b(3)++, b(3), b(4), b(4)++, b(5)++, b(5), b(5)-98, b(6)-98++, b(7), b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(9)++, y(9)-98++

Peptide No.330

GMSHSPSVALR
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of **GMSHSPSVALR**
Found in **PROX1_MOUSE** in **SwissProt**, Prospero homeobox protein 1 OS=Mus musculus GN=Prox1 PE=1 SV=2

Match to Query 1733: 1220.539143 from(407.853657,3+) index(4385)
Title: Elution from: 22.247 to 22.247 scan no 1579 cid35.00 polarity:+:m1s



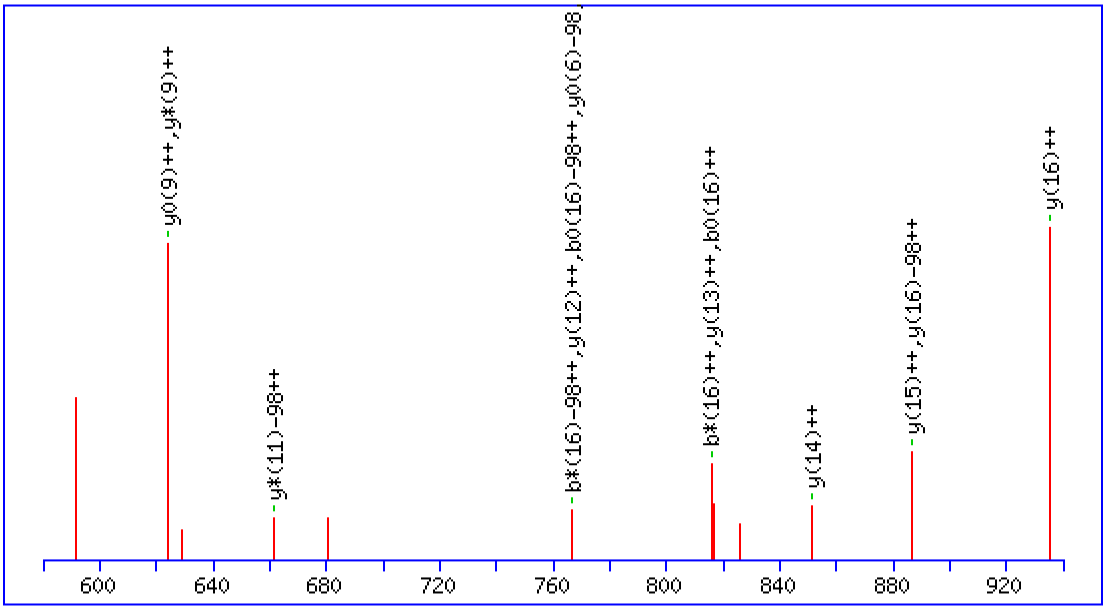
Monoisotopic mass of neutral peptide Mr(calc): 1220.5373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.014
Matched b ions: b(7)++, b(8)-98++, b(9)++, b(9)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(6)++, y(9)++, y(9)-98++

Peptide No.331

GPLPAAPPTAPERQPSWER
Confirmed sites:
Ambiguous sites: @T:9orS:16

MS/MS Fragmentation of **GPLPAAPPTAPERQPSWER**
Found in **RTN4_MOUSE** in **SwissProt**, Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2

Match to Query 5496: 2136.012888 from(713.011572,3+) index(5833)
Title: Elution from: 36.225 to 36.225 scan no 3470 cid35.00 polarity:+:m1s



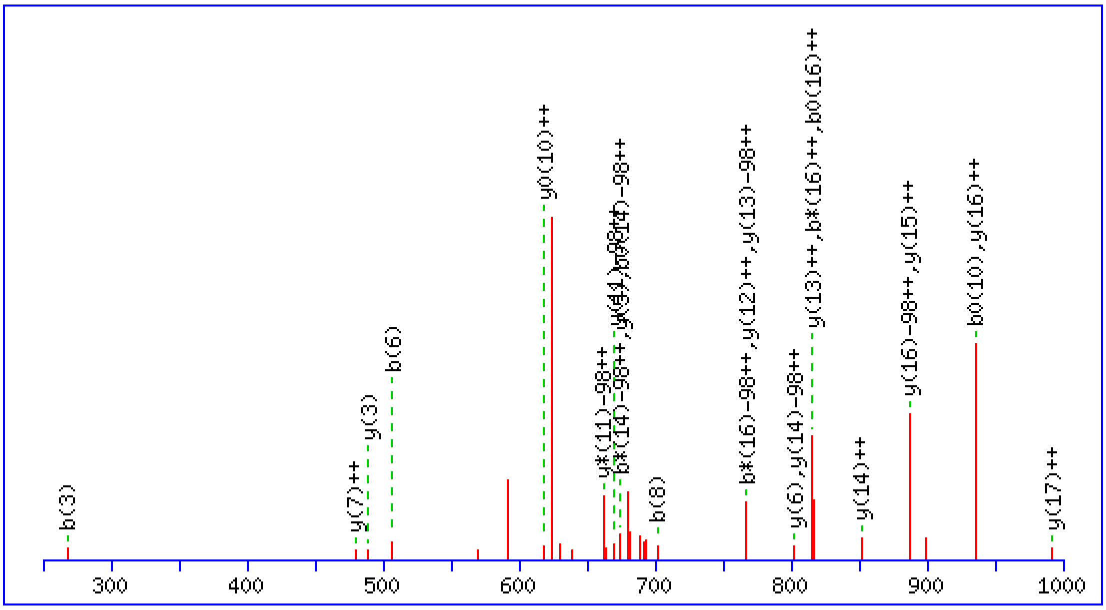
Monoisotopic mass of neutral peptide Mr(calc): 2136.0153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.012
Matched b ions:
Matched y ions: y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++

Peptide No.332

GPLPAAPPTAPERQPSWER
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **GPLPAAPPTAPERQPSWER**
Found in **RTN4_MOUSE** in **SwissProt**, Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2

Match to Query 4562: 2136.013959 from(713.011929,3+) index(5022)
Title: Elution from: 35.973 to 35.973 scan no 3319 cid35.00 polarity:+:m1s



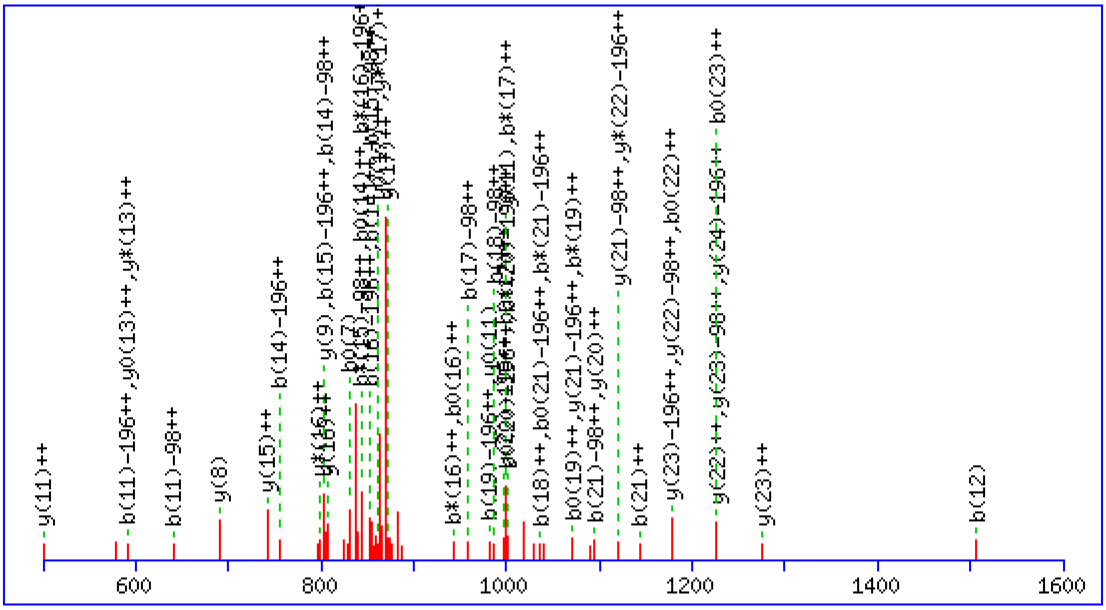
Monoisotopic mass of neutral peptide Mr(calc): 2136.0153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00027
Matched b ions: b(3), b(6), b(8)
Matched y ions: y(3), y(5), y(6), y(7)++, y(11)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++

Peptide No.333

GPPDFSSDEEREPTPVLGSGASVGR
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **GPPDFSSDEEREPTPVLGSGASVGR**
Found in **LAP2B_MOUSE** in **SwissProt**, Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4

Match to Query 5635: 2702.124162 from(901.715330,3+) index(5603)
Title: Elution from: 44.141 to 44.141 scan no 4292 cid35.00 polarity:+:m1s



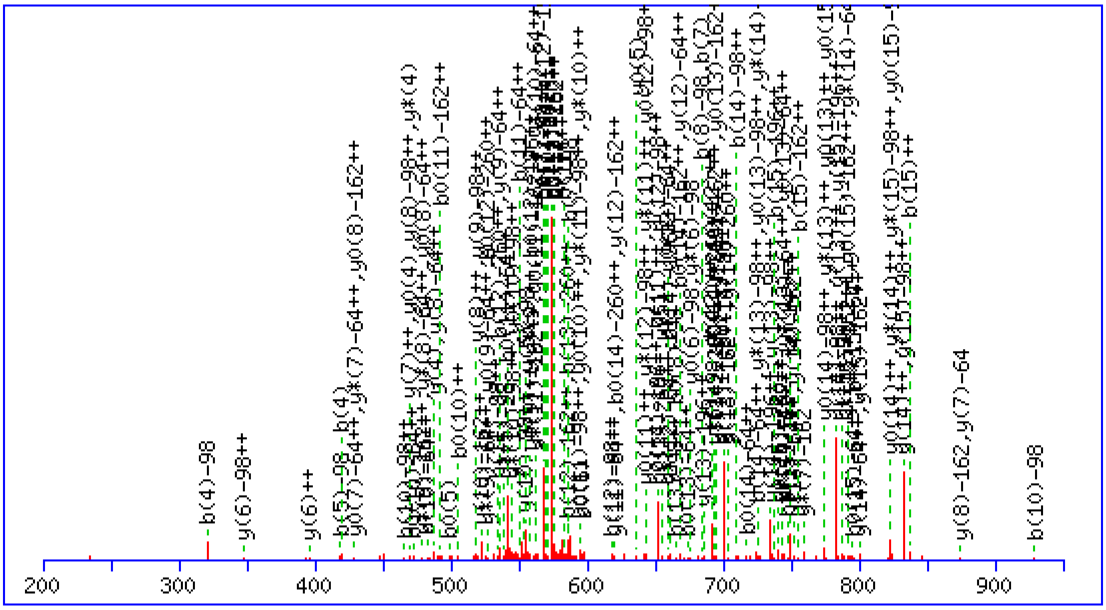
Monoisotopic mass of neutral peptide Mr(calc): 2702.1262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.039
Matched b ions: b(11)-196++, b(11)-98++, b(12), b(14)-196++, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(16)-196++, b(17)-98++, b(18)++, b(18)-98++, b(19)-196++, b(21)++, b(21)-98++
Matched y ions: y(8), y(9), y(11), y(11)++, y(15)++, y(16)++, y(17)++, y(20)-196++, y(20)++, y(21)-98++, y(21)-196++, y(22)-98++, y(22)++, y(23)-196++, y(23)-98++, y(23)++, y(24)-196++

Peptide No.334

GPPSPPAPVMHSPSRK
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of **GPPSPPAPVMHSPSRK**
Found in **SNW1_MOUSE** in **SwissProt**, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 3659: 1816.771668 from(606.597832,3+) index(85)
Title: Elution from: 13.972 to 13.972 scan no 722 cid35.00 polarity:+



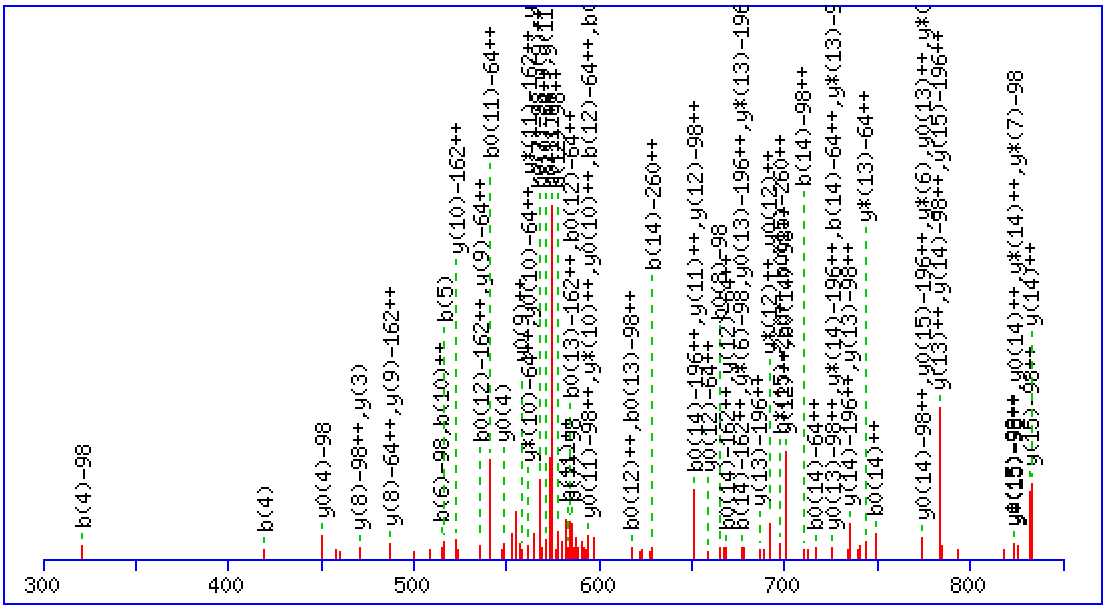
Monoisotopic mass of neutral peptide Mr(calc): 1816.7733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.025
Matched b ions: b(4)-98, b(4), b(5)-98, b(7)-98, b(7), b(8)-98, b(10)-98, b(10)-98++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(13)-98++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++
Matched y ions: y(4), y(5)-98, y(5), y(6)-98++, y(6)++, y(6)-98, y(6), y(7)++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)-98++

Peptide No.335

GPPSPPAPVMHSPSRK
Confirmed sites: @S:4,@S:14
Ambiguous sites:

MS/MS Fragmentation of **GPPSPPAPVMHSPSRK**
Found in **SNW1_MOUSE** in **SwissProt**, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 4273: 1816.771167 from(606.597665,3+) index(502)
Title: Elution from: 20.353 to 20.353 scan no 1322 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1816.7733

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 24 **Expect:** 0.023

Matched b ions: b(4)-98, b(4), b(5), b(6)-98, b(7)-98, b(10)++, b(11)++, b(12)-98++, b(14)-98++

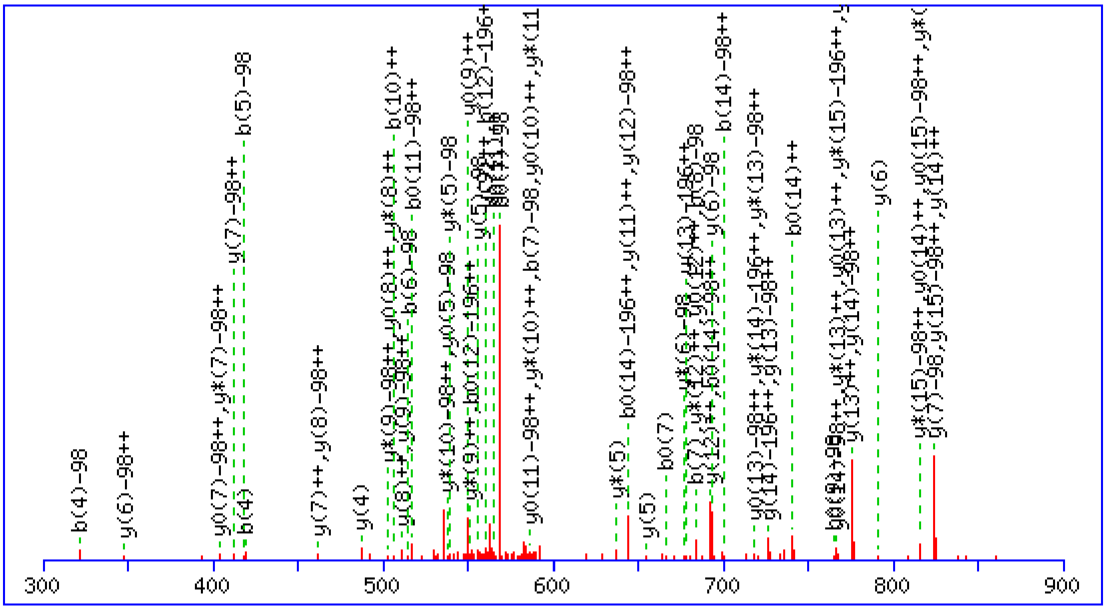
Matched y ions: y(3), y(4), y(8)-98++, y(9)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)-98++

Peptide No.336

GPPSPPAPVMHSPSRK
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of **GPPSPPAPVMHSPSRK**
Found in **SNW1_MOUSE** in **SwissProt**, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 4204: 1800.776643 from(601.266157,3+) index(4602)
Title: Elution from: 24.196 to 24.196 scan no 1844 cid35.00 polarity:+:m1s



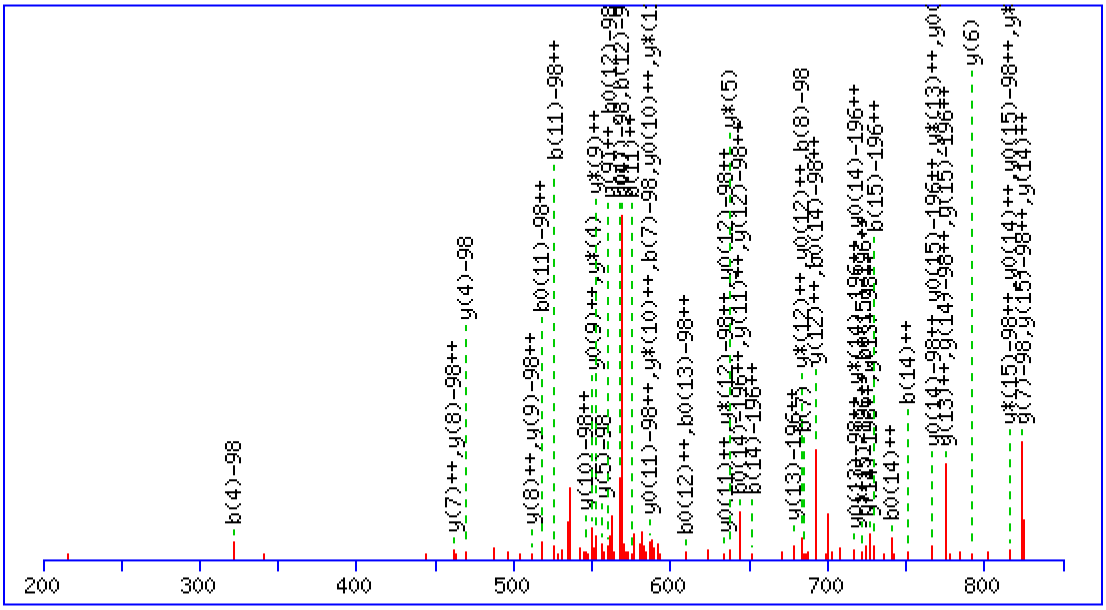
Monoisotopic mass of neutral peptide Mr(calc): 1800.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0053
Matched b ions: b(4)-98, b(4), b(5)-98, b(6)-98, b(7), b(7)-98, b(8)-98, b(10)++, b(12)-196++, b(14)-98++
Matched y ions: y(4), y(5)-98, y(5), y(6)-98, y(6)-98++, y(6), y(7)-98, y(7)-98++, y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(15)-98++

Peptide No.337

GPPSPPAPVMHSPSRK
Confirmed sites: @S:4,@S:14
Ambiguous sites:

MS/MS Fragmentation of **GPPSPPAPVMHSPSRK**
Found in **SNW1_MOUSE** in **SwissProt**, SNW domain-containing protein 1 OS=Mus musculus GN=Snw1 PE=1 SV=3

Match to Query 4078: 1800.777036 from(601.266288,3+) index(890)
Title: Elution from: 24.095 to 24.095 scan no 1795 cid35.00 polarity:+



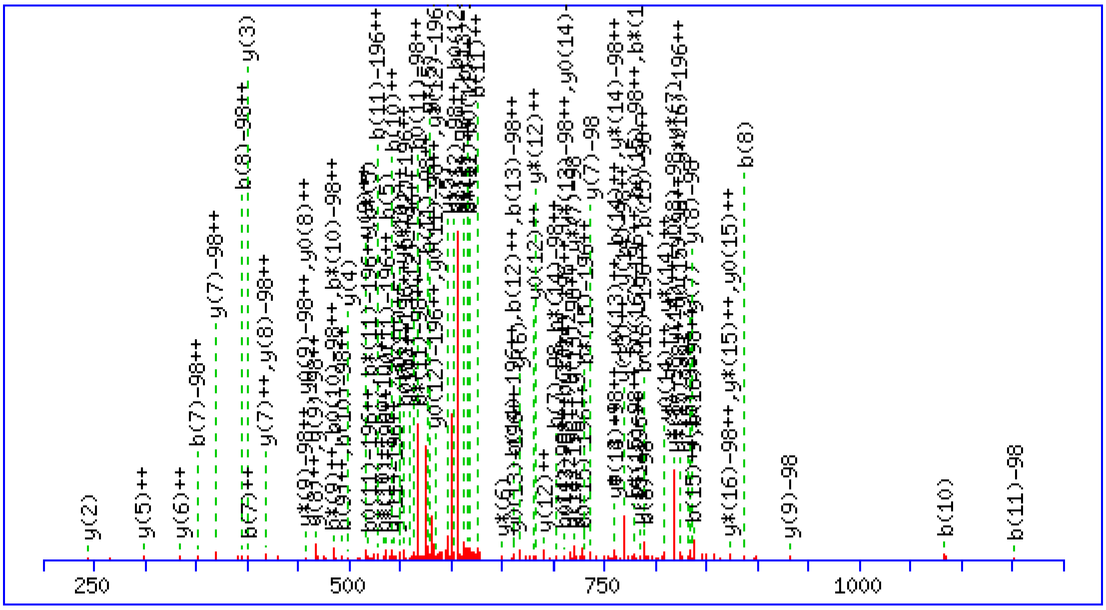
Monoisotopic mass of neutral peptide Mr(calc): 1800.7783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.021
Matched b ions: b(4)-98, b(7)-98, b(7), b(8)-98, b(11)-98++, b(11)++, b(12)-98++, b(14)-196++, b(14)++, b(15)-196++
Matched y ions: y(4), y(4)-98, y(5)-98, y(6), y(7)-98, y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)-98++

Peptide No.338

GPQPRPSSPVSAPVRPK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of **GPQPRPSSPVSAPVRPK**
Found in **AAKG2_MOUSE** in **SwissProt**, 5'-AMP-activated protein kinase subunit gamma-2 OS=Mus musculus GN=Prkag2 PE=1 SV=2

Match to Query 3911: 1915.904388 from(639.642072,3+) index(589)
Title: Elution from: 22.092 to 22.092 scan no 1500 cid35.00 polarity:+



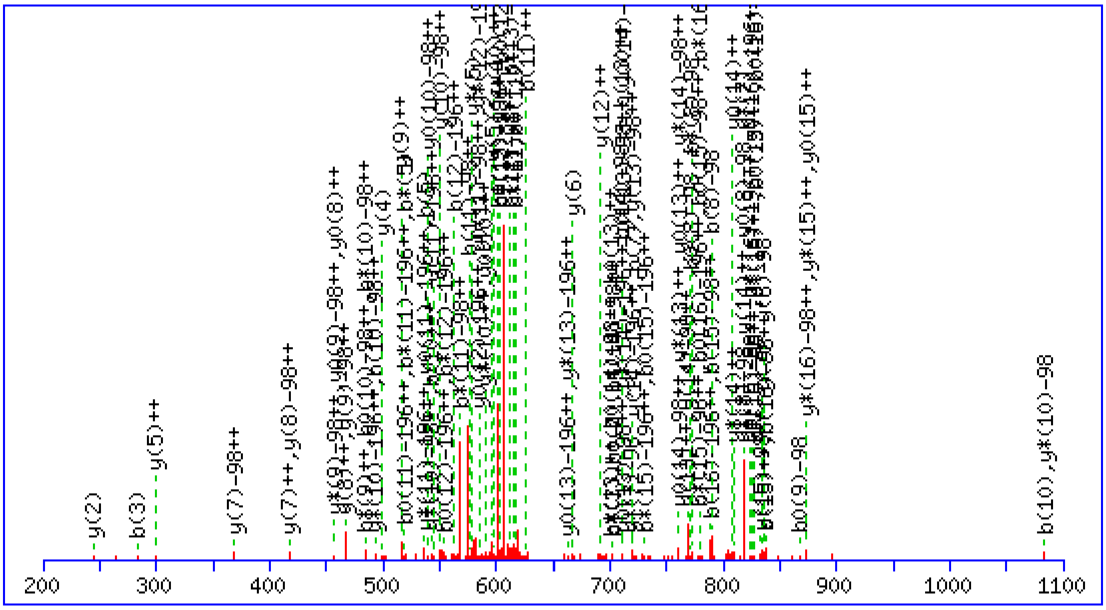
Monoisotopic mass of neutral peptide Mr(calc): 1915.9070
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0023
Matched b ions: b(5), b(7)++, b(7)-98++, b(7)-98, b(8)-98, b(8)-98++, b(8), b(9)++, b(10), b(10)++, b(10)-98++, b(11)-98, b(11)-196++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(12)-196++, b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)-98++, y(7)++, y(7)-98, y(7), y(8)++, y(8)-98++, y(8)-98, y(9)-98++, y(9)++, y(9)-98, y(10)++, y(11)-196++, y(12)++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(14)-98++, y(15)-196++, y(15)-98++

Peptide No.339

GPQPRPSSPVSAPVRPK
Confirmed sites: @S:8,@S:11
Ambiguous sites:

MS/MS Fragmentation of **GPQPRPSSPVSAPVRPK**
Found in **AAKG2_MOUSE** in **SwissProt**, 5'-AMP-activated protein kinase subunit gamma-2 OS=Mus musculus GN=Prkag2 PE=1 SV=2

Match to Query 3961: 1915.904508 from(639.642112,3+) index(3368)
Title: Elution from: 21.671 to 21.671 scan no 1343 cid35.00 polarity:+:m1s



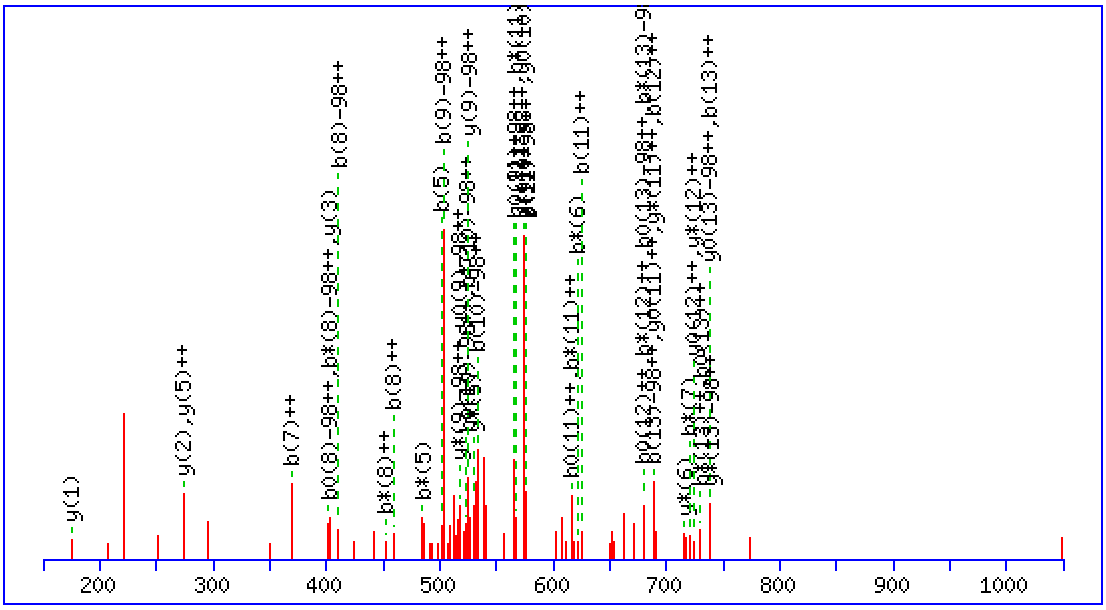
Monoisotopic mass of neutral peptide Mr(calc): 1915.9070
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0075
Matched b ions: b(3), b(5), b(7), b(8)-98, b(10), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-196++, b(16)-98++
Matched y ions: y(2), y(4), y(5)++, y(5), y(6), y(7)++, y(7)-98++, y(7), y(8)-98++, y(8)++, y(8)-98, y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(11)-196++, y(12)++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(14)-98++, y(15)-98++

Peptide No.340

GQAMLHVTWGSKVR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of **GQAMLHVTWGSKVR**
Found in **TM143_MOUSE** in **SwissProt**, Transmembrane protein 143 OS=Mus musculus GN=Tmem143 PE=2 SV=1

Match to Query 3084: 1648.791066 from(550.604298,3+) index(305)
Title: Elution from: 20.984 to 20.984 scan no 1251 cid35.00 polarity:+



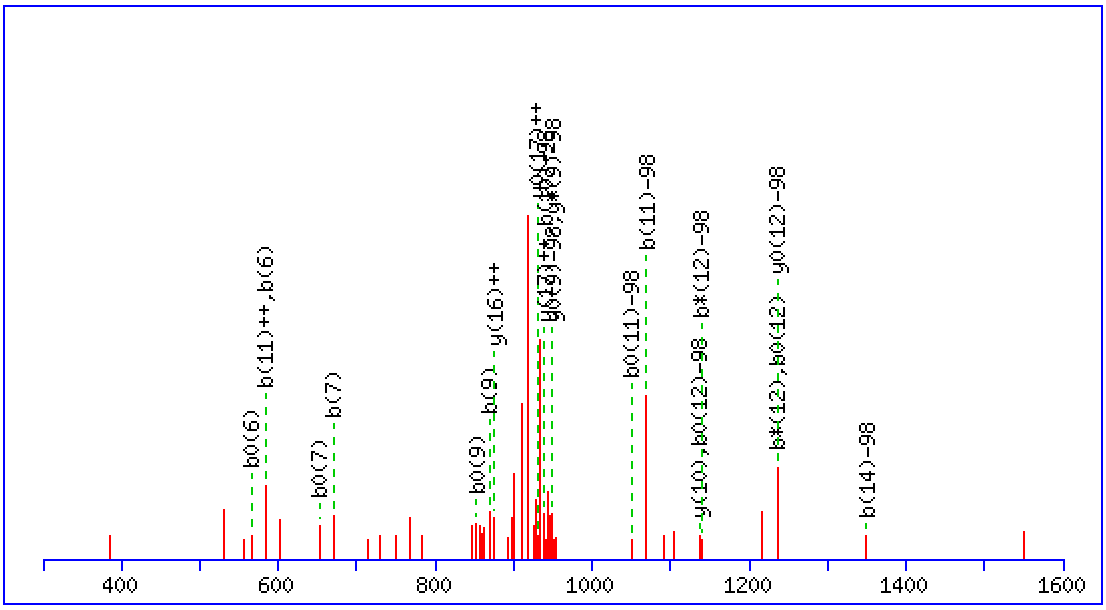
Monoisotopic mass of neutral peptide Mr(calc): 1648.7909
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0027
Matched b ions: b(5), b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(13)-98++, b(13)++
Matched y ions: y(1), y(2), y(3), y(5)++, y(9)-98++, y(9)++

Peptide No.341

GQQDPGSEASESHGLEAR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **GQQDPGSEASESHGLEAR**
Found in **RAB44_MOUSE** in **SwissProt**, Ras-related protein Rab-44 OS=Mus musculus GN=Rab44 PE=2 SV=1

Match to Query 4036: 1933.784266 from(967.899409,2+) index(1722)
Title: Elution from: 34.999 to 34.999 scan no 3162 cid35.00 polarity:+



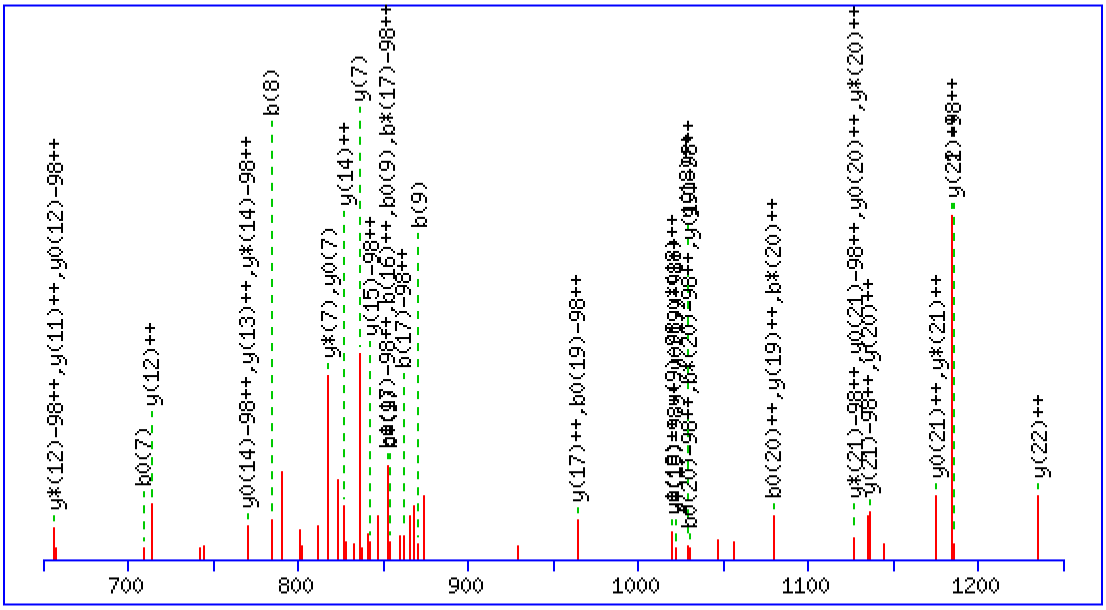
Monoisotopic mass of neutral peptide Mr(calc): 1933.7803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.041
Matched b ions: b(6), b(7), b(9), b(10)-98, b(11)++, b(11)-98, b(14)-98
Matched y ions: y(10), y(16)++, y(17)++

Peptide No.342

GQTPLTEGSEDLDGHSDPEESFAR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **GQTPLTEGSEDLDGHSDPEESFAR**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 6607: 2653.076340 from(885.366056,3+) index(6168)
Title: Elution from: 39.955 to 39.955 scan no 3962 cid35.00 polarity:+:m1s



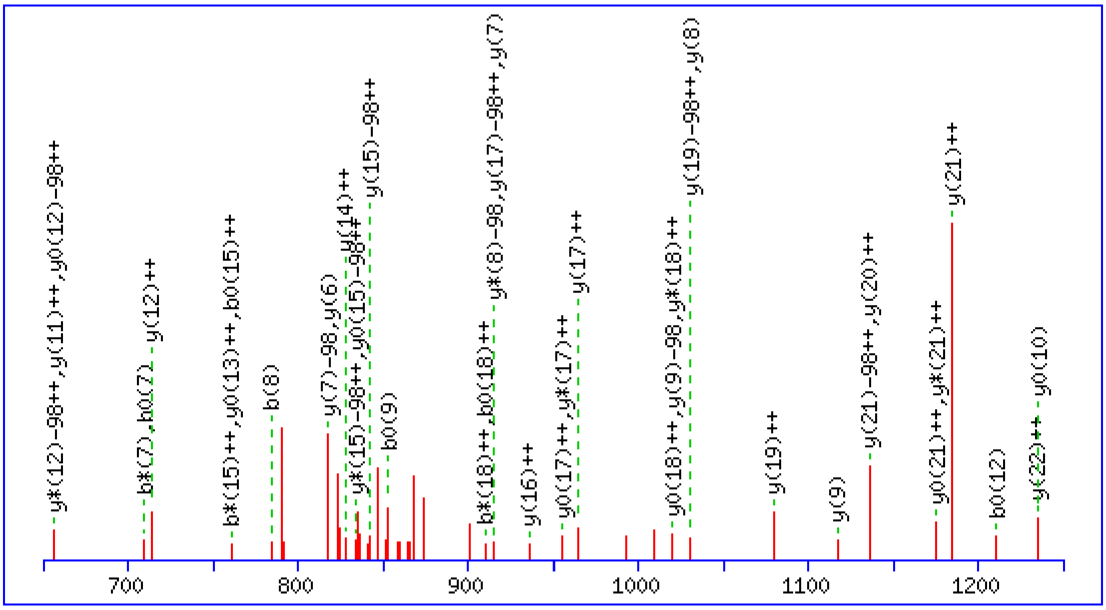
Monoisotopic mass of neutral peptide Mr(calc): 2653.0817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0041
Matched b ions: b(8), b(9), b(16)++, b(17)-98++
Matched y ions: y(7), y(9)-98, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-98++

Peptide No.343

GQTPLTEGSEDLDGHSDPEESFAR
Confirmed sites: @S:21
Ambiguous sites:

MS/MS Fragmentation of **GQTPLTEGSEDLDGHSDPEESFAR**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 5576: 2653.078929 from(885.366919,3+) index(5356)
Title: Elution from: 40.037 to 40.037 scan no 3824 cid35.00 polarity:+:m1s



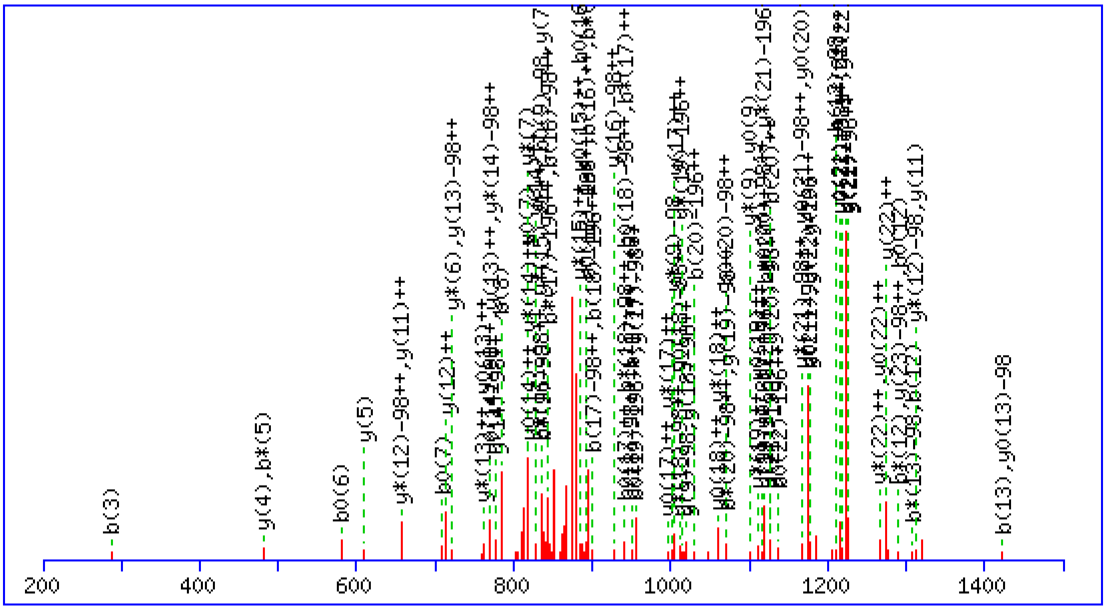
Monoisotopic mass of neutral peptide Mr(calc): 2653.0817
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00078
Matched b ions: b(8)
Matched y ions: y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(11)++, y(12)++, y(14)++, y(15)-98++, y(16)++, y(17)++, y(17)-98++, y(19)++, y(19)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++

Peptide No.344

GQTPLTEGSEDLDGHSDPEESFAR
Confirmed sites: @S:9,@S:16
Ambiguous sites:

MS/MS Fragmentation of **GQTPLTEGSEDLDGHSDPEESFAR**
Found in **F134C_MOUSE** in **SwissProt**, Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1

Match to Query 6695: 2733.045519 from(912.022449,3+) index(6405)
Title: Elution from: 43.142 to 43.142 scan no 4372 cid35.00 polarity:+:m1s



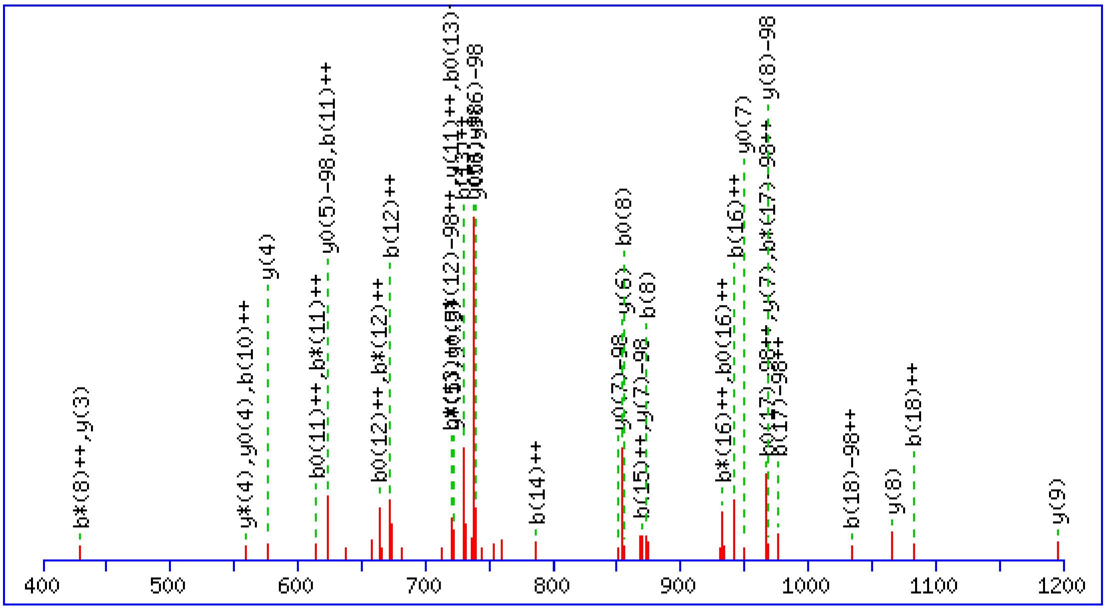
Monoisotopic mass of neutral peptide Mr(calc): 2733.0480
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 9.8e-005
Matched b ions: b(3), b(8), b(12), b(12)-98, b(13), b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)-196++, b(20)-196++, b(20)++
Matched y ions: y(4), y(5), y(7), y(8), y(9)-98, y(9), y(11)++, y(11), y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)++, y(22)-98++, y(22)-196++, y(23)-98++

Peptide No.345

GRADGDWDDQEVLDYFSDK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **GRADGDWDDQEVLDYFSDK**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 5023: 2309.910690 from(770.977506,3+) index(5987)
Title: Elution from: 54.207 to 54.207 scan no 5296 cid35.00 polarity:+:m1s



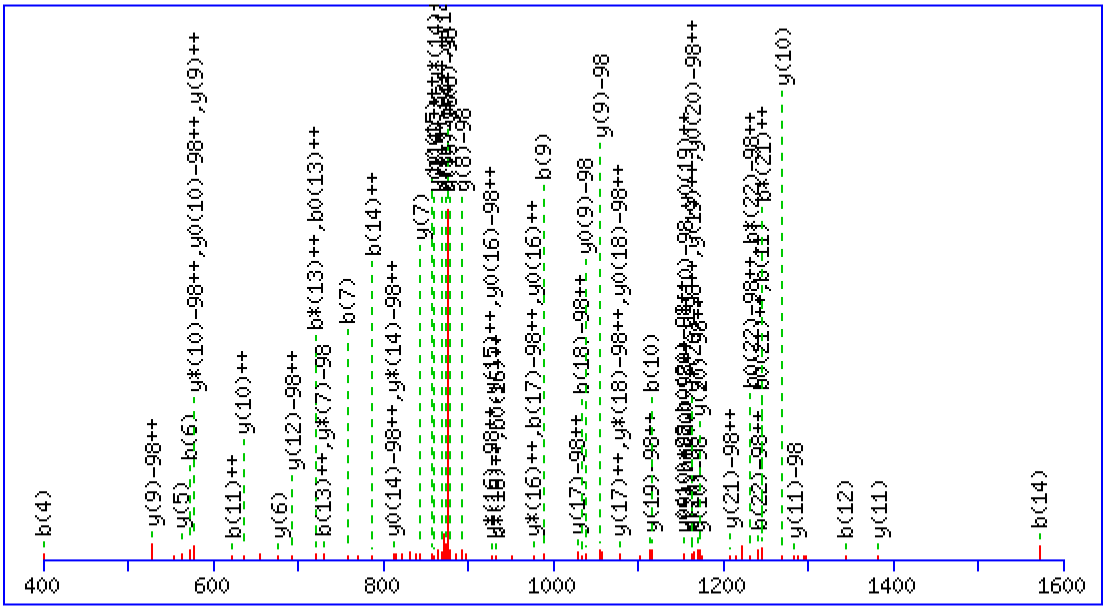
Monoisotopic mass of neutral peptide Mr(calc): 2309.9114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00014
Matched b ions: b(8), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(11)++

Peptide No.346

GRADGDWDDQEVLDYFSDKESAK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **GRADGDWDDQEVLDYFSDKESAK**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 6499: 2725.116666 from(909.379498,3+) index(6630)
Title: Elution from: 49.973 to 49.973 scan no 5140 cid35.00 polarity:+:m1s



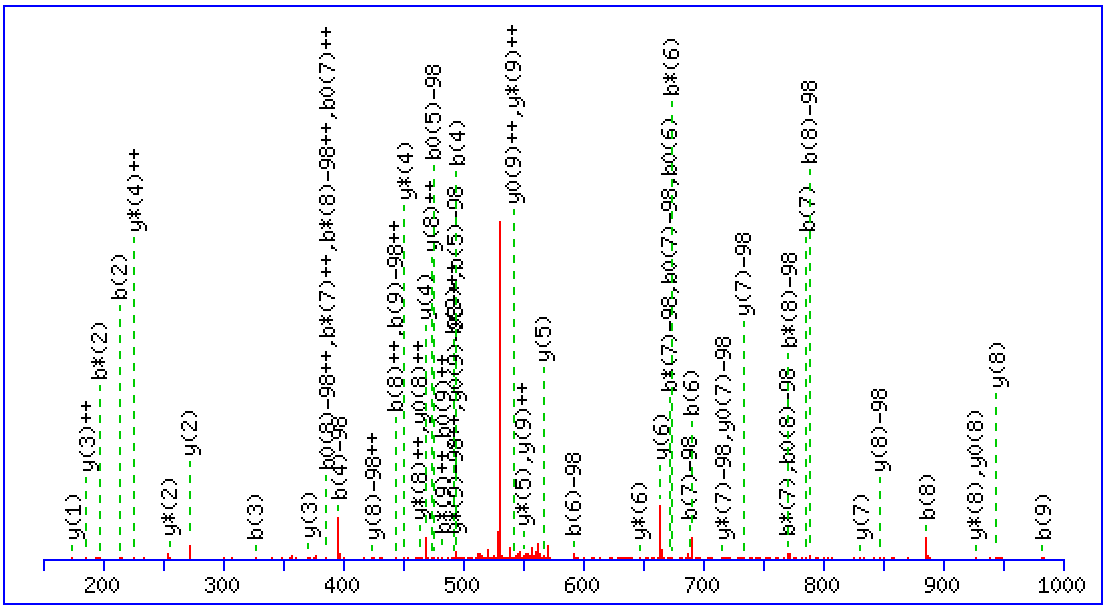
Monoisotopic mass of neutral peptide Mr(calc): 2725.1181
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 9.5e-006
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10), b(11)++, b(11), b(12), b(13)++, b(14), b(14)++, b(17)-98++, b(18)-98++, b(20)-98++, b(22)-98++
Matched y ions: y(5), y(6), y(7), y(8)-98, y(9)-98++, y(9)-98, y(9)++, y(9), y(10)-98, y(10)++, y(10), y(11), y(11)-98, y(12)-98++, y(14)++, y(15)++, y(15)-98++, y(17)-98++, y(17)++, y(19)-98++, y(19)++, y(20)-98++, y(21)-98++

Peptide No.347

GRLSPVPVPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **GRLSPVPVPR**
Found in **RALY_MOUSE** in **SwissProt**, RNA-binding protein Raly OS=Mus musculus GN=Raly PE=1 SV=3

Match to Query 1975: 1156.611608 from(579.313080,2+) index(1145)
Title: Elution from: 35.188 to 35.188 scan no 2537 cid35.00 polarity:+



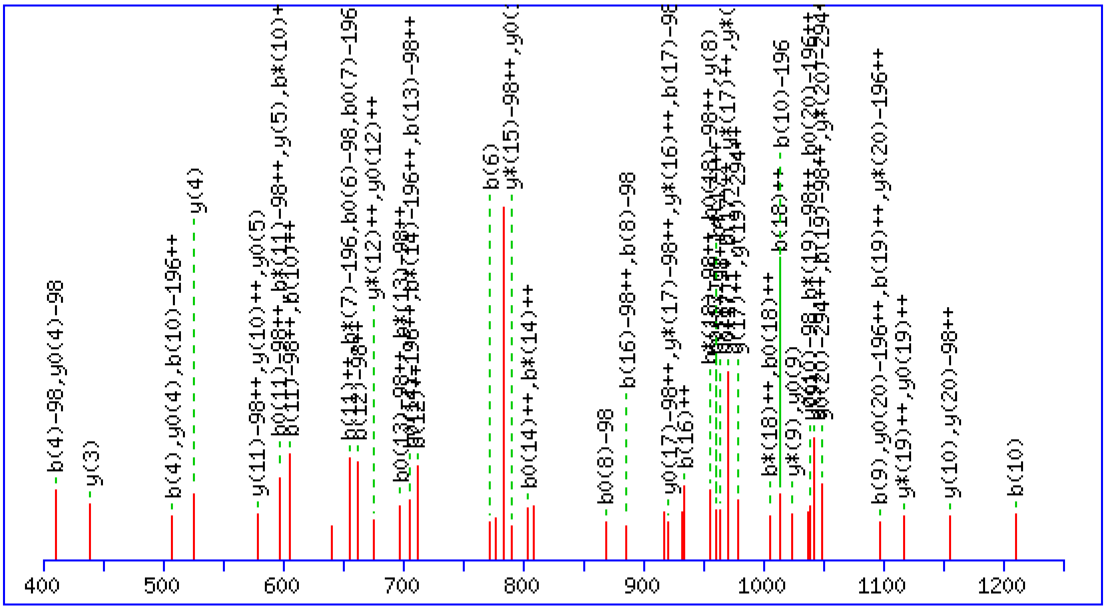
Monoisotopic mass of neutral peptide Mr(calc): 1156.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0041
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(8)++, b(9), b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(8)-98++, y(8)++, y(9)++

Peptide No.348

GRLTPSPDIIVLSDNEASSPR
Confirmed sites: @T:4,@S:6,@S:19
Ambiguous sites:

MS/MS Fragmentation of **GRLTPSPDIIVLSDNEASSPR**
Found in **P66B_MOUSE** in **SwissProt**, Transcriptional repressor p66-beta OS=Mus musculus GN=Gatad2b PE=1 SV=1

Match to Query 5324: 2463.050175 from(822.024001,3+) index(5954)
Title: Elution from: 53.194 to 53.194 scan no 5200 cid35.00 polarity:+:m1s



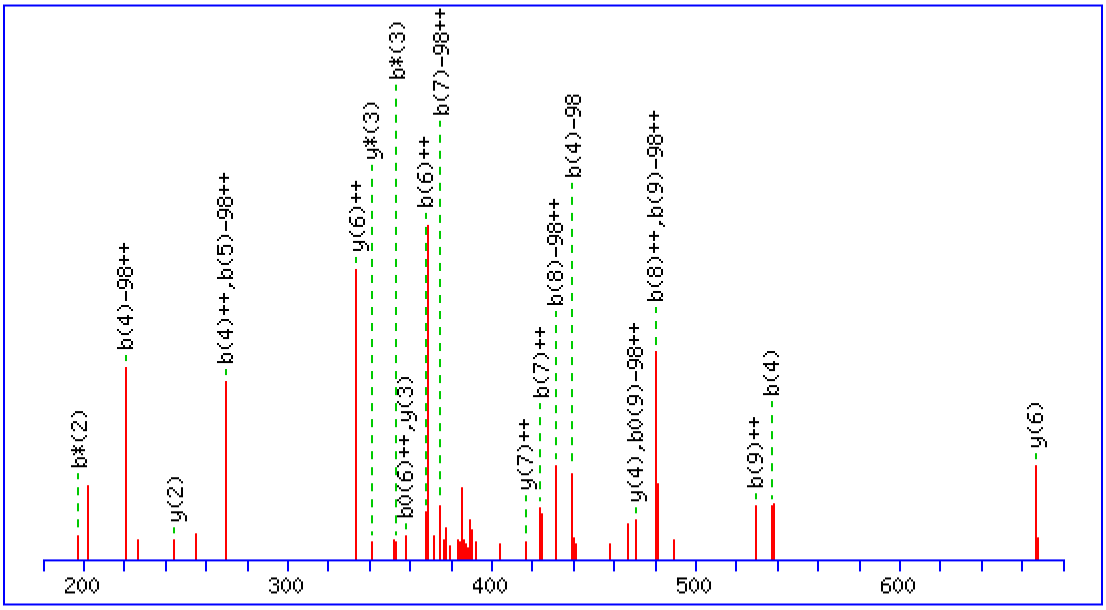
Monoisotopic mass of neutral peptide Mr(calc): 2463.0485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0023
Matched b ions: b(4)-98, b(4), b(6), b(8)-98, b(9), b(10)++, b(10), b(10)-196++, b(10)-196, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(8), y(9), y(10), y(10)++, y(11)-98++, y(17)++, y(19)-294++, y(20)-98++

Peptide No.349

GRRSPVLLPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **GRRSPVLLPK**
Found in **BICD2_MOUSE** in **SwissProt**, Protein bicaudal D homolog 2 OS=Mus musculus GN=Bicd2 PE=1 SV=1

Match to Query 1408: 1201.669986 from(401.563938,3+) index(426)
Title: Elution from: 20.729 to 20.729 scan no 1316 cid35.00 polarity:+



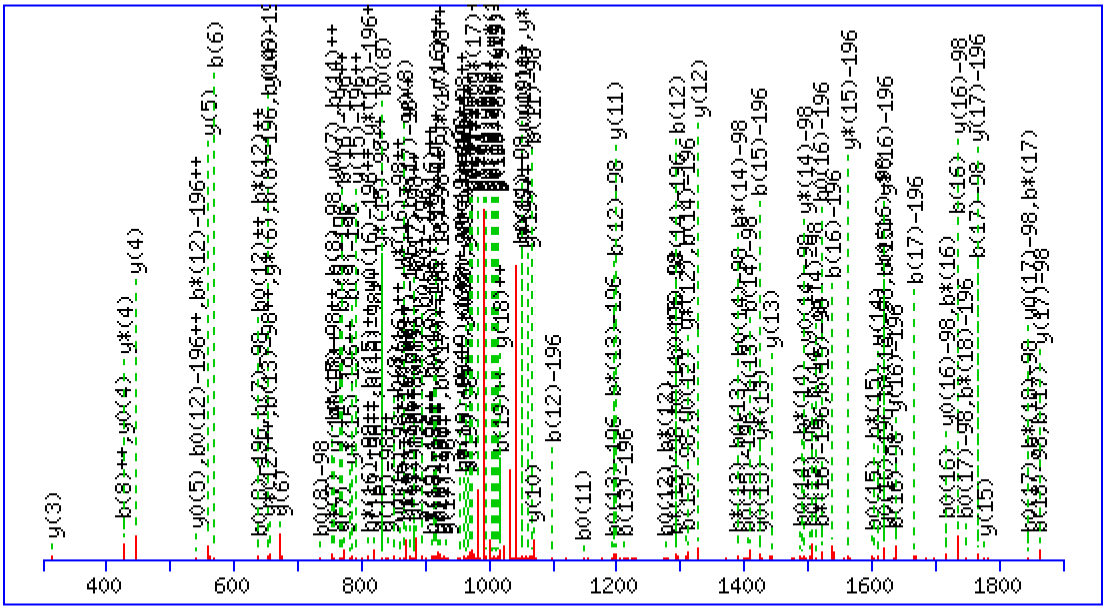
Monoisotopic mass of neutral peptide Mr(calc): 1201.6696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.039
Matched b ions: b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98++, b(6)++, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(6), y(6)++, y(7)++

Peptide No.350

GSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **GSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 4700: 2176.875778 from(1089.445165,2+) index(4941)
Title: Elution from: 34.947 to 34.947 scan no 3194 cid35.00 polarity:+:m1s



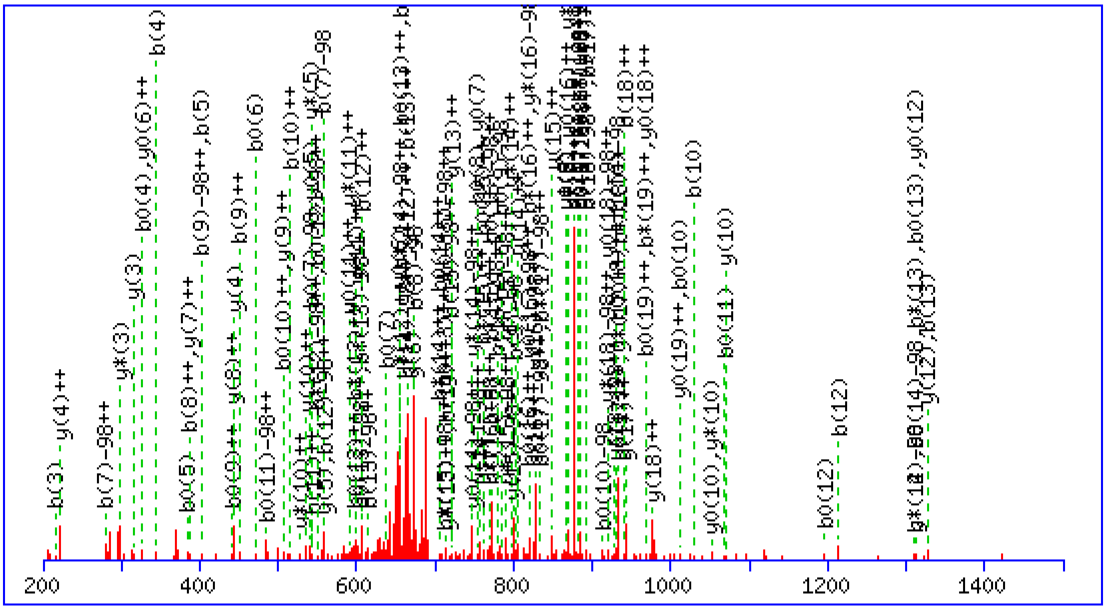
Monoisotopic mass of neutral peptide Mr(calc): 2176.8814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 **Expect:** 2.4e-006
Matched b ions: b(6), b(7)-98, b(8)++, b(8)-196, b(8)-98, b(8), b(9)-196, b(9)-98, b(10)-196, b(10)-98, b(11)-196, b(11)-98, b(12)-98, b(12), b(12)-196, b(13)-98++, b(13)-196, b(13)-98, b(13), b(14)-196, b(14), b(14)-196++, b(14)++, b(14)-98, b(15)-196, b(15), b(15)++, b(15)-98, b(16)-196, b(16)-98, b(16), b(16)++, b(16)-98++, b(16)-196++, b(17), b(17)-98, b(17)-196, b(17)-98++, b(18)-98, b(18)-196++, b(19)++, b(19)-196++, b(19)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)-98++, y(14)-98, y(15), y(15)-196++, y(15)-98++, y(16)-98++, y(16)-98, y(16)-196++, y(16)-196, y(16)++, y(17)-196++, y(17)-98, y(17)-196, y(17)-98++, y(17)++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(19)++

Peptide No.351

GSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **GSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 4645: 2096.915097 from(699.978975,3+) index(1295)
Title: Elution from: 39.033 to 39.033 scan no 2881 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 2096.9151

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 48 **Expect:** 9.1e-005

Matched b ions: b(3), b(4), b(5), b(7), b(7)-98++, b(7)-98, b(8), b(8)-98, b(8)++, b(9)++, b(9)-98++, b(9)-98, b(10)-98, b(10)++, b(10), b(11)++, b(12), b(12)-98++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++

Matched y ions: y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(10), y(11)++, y(12), y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++

Peptide No.352

GSGTASDDEFENLR

Confirmed sites: @S:6

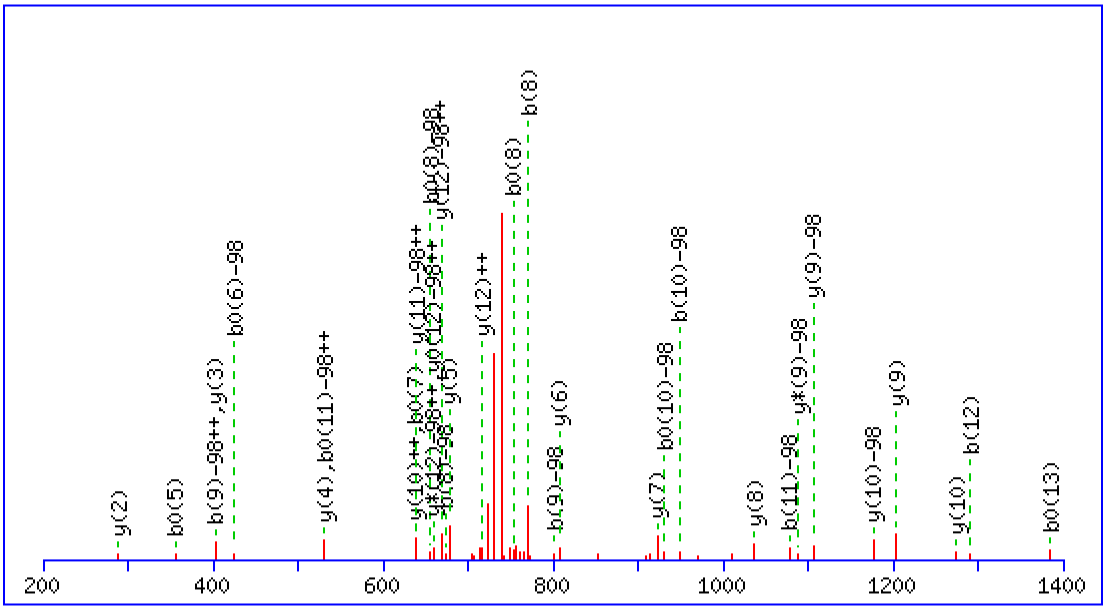
Ambiguous sites:

MS/MS Fragmentation of **GSGTASDDEFENLR**

Found in **HUWE1_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase HUWE1 OS=Mus musculus GN=Huwe1 PE=1 SV=5

Match to Query 3327: 1576.601948 from(789.308250,2+) index(2140)

Title: Elution from: 35.742 to 35.742 scan no 3405 cid35.00 polarity:+



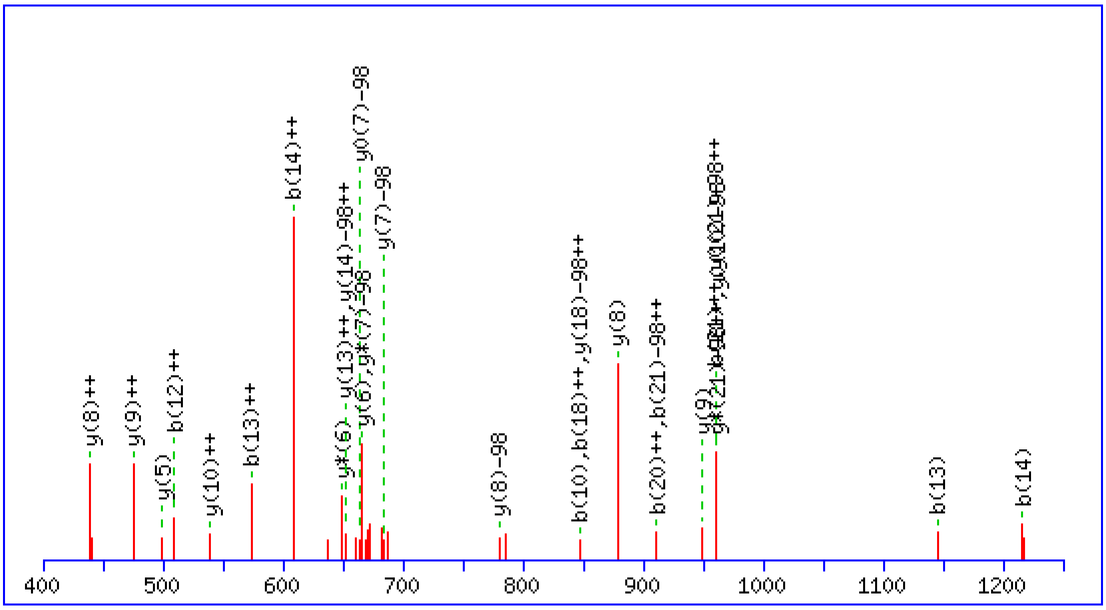
Monoisotopic mass of neutral peptide Mr(calc): 1576.6042
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 2.2e-008
Matched b ions: b(8), b(8)-98, b(9)-98++, b(9)-98, b(10)-98, b(11)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(10)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.353

GSGTGHPVPGVAQAPDSPAGVR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **GSGTGHPVPGVAQAPDSPAGVR**
Found in **SNTB1_MOUSE** in **SwissProt**, Beta-1-syntrophin OS=Mus musculus GN=Sntb1 PE=1 SV=4

Match to Query 5152: 2092.969035 from(698.663621,3+) index(4719)
Title: Elution from: 26.937 to 26.937 scan no 2180 cid35.00 polarity:+:m1s



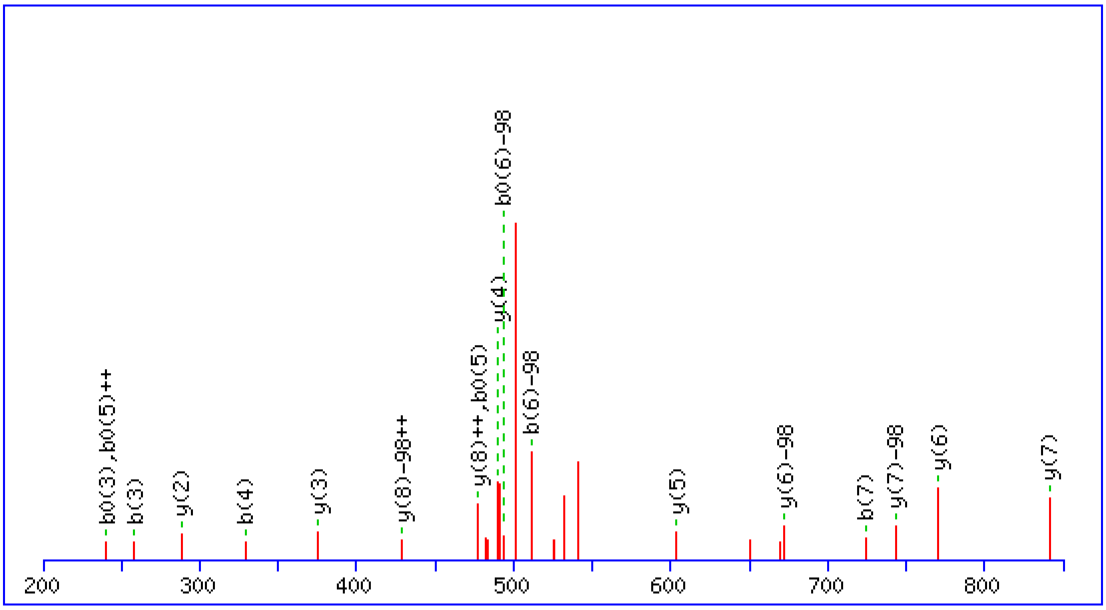
Monoisotopic mass of neutral peptide Mr(calc): 2092.9692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0013
Matched b ions: b(10), b(12)++, b(13)++, b(13), b(14)++, b(14), b(18)++, b(20)++, b(21)++, b(21)-98++
Matched y ions: y(5), y(6), y(7)-98, y(8), y(8)++, y(8)-98, y(9)++, y(9), y(10)++, y(13)++, y(14)-98++, y(18)-98++

Peptide No.354

GSLASLDSLR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GSLASLDSLR**
Found in **CTND1_MOUSE** in **SwissProt**, Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2

Match to Query 1120: 1097.510856 from(549.762704,2+) index(2678)
Title: Elution from: 42.547 to 42.547 scan no 4277 cid35.00 polarity:+



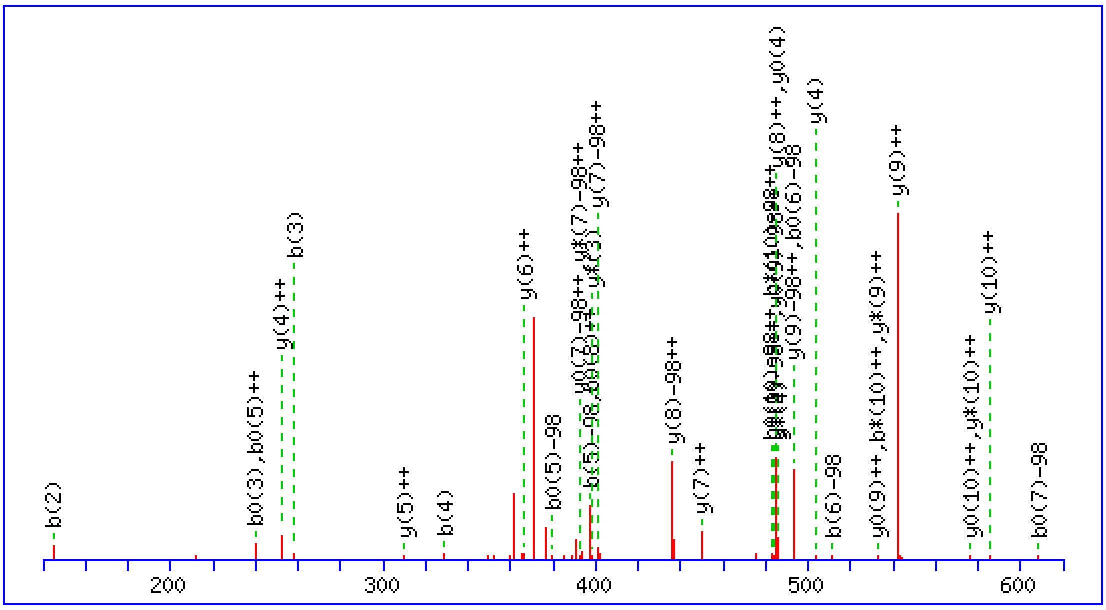
Monoisotopic mass of neutral peptide Mr(calc): 1097.5118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 2.6e-005
Matched b ions: b(3), b(4), b(6)-98, b(7)
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(7), y(7)-98, y(8)-98++, y(8)++

Peptide No.355

GSLASLDSLRK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GSLASLDSLRK**
Found in **CTND1_MOUSE** in **SwissProt**, Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2

Match to Query 1766: 1225.606983 from(409.542937,3+) index(1954)
Title: Elution from: 33.954 to 33.954 scan no 3168 cid35.00 polarity:+



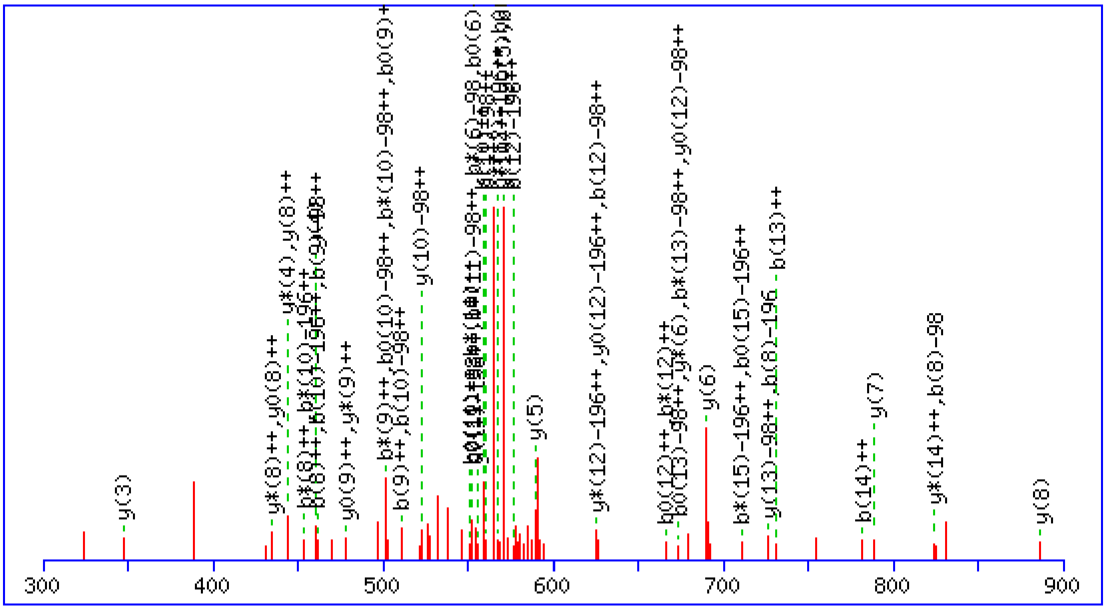
Monoisotopic mass of neutral peptide Mr(calc): 1225.6067
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00046
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98
Matched y ions: y(4)++, y(4), y(5)++, y(6)++, y(7)++, y(7)-98++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++

Peptide No.356

GSLSRSSSPVTELTAR
Confirmed sites: @S:6
Ambiguous sites: @S:7orS:8

MS/MS Fragmentation of **GSLSRSSSPVTELTAR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3542: 1806.792351 from(603.271393,3+) index(4991)
Title: Elution from: 35.574 to 35.574 scan no 3271 cid35.00 polarity:+:m1s



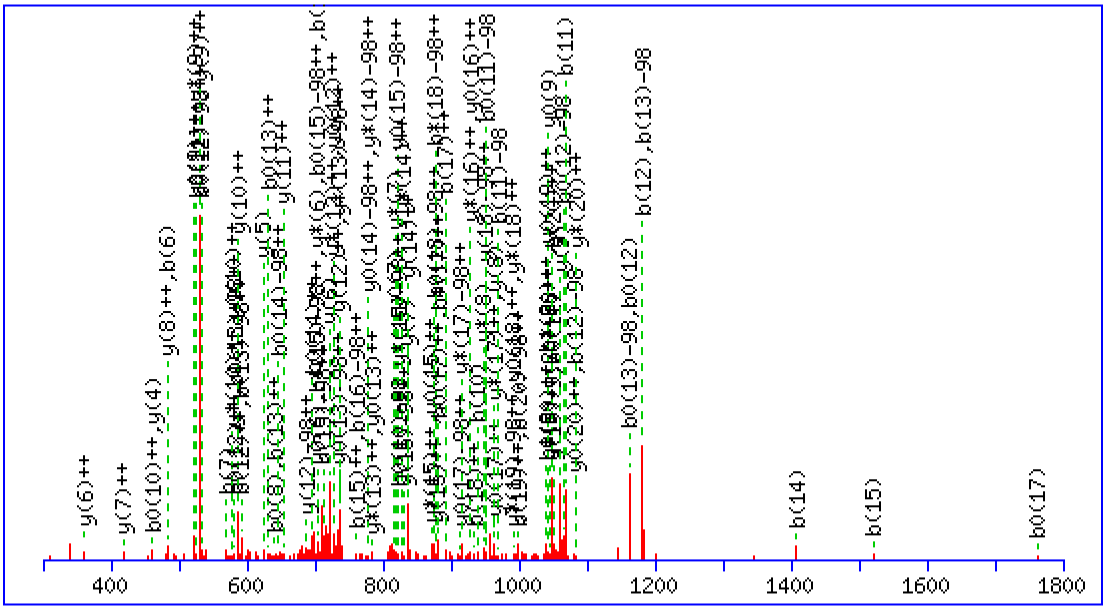
Monoisotopic mass of neutral peptide Mr(calc): 1806.7914
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.013
Matched b ions: b(5), b(6)-98, b(8)-196, b(8)-98, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(10)-196++, b(11)-98++, b(12)-98++, b(12)-196++, b(13)++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(10)++, y(10)-98++, y(11)-196++, y(13)-98++

Peptide No.357

GSPGALSSDSELPENPYSQVK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **GSPGALSSDSELPENPYSQVK**
Found in **CING_MOUSE** in **SwissProt**, Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1

Match to Query 5679: 2240.987109 from(748.002979,3+) index(5645)
Title: Elution from: 51.110 to 51.110 scan no 4287 cid35.00 polarity:+:m1s



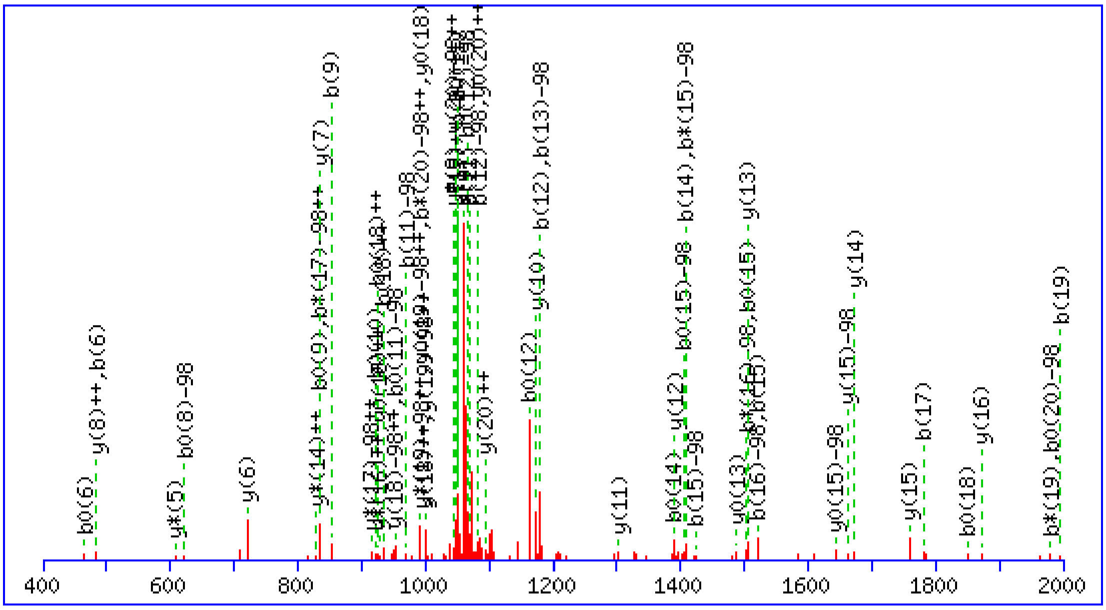
Monoisotopic mass of neutral peptide Mr(calc): 2240.9838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00018
Matched b ions: b(6), b(7), b(10), b(11), b(11)-98, b(12), b(12)++, b(12)-98, b(13)-98, b(13)-98++, b(13)++, b(14), b(14)++, b(15), b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(12)-98++, y(14)++, y(15)++, y(15)-98++, y(18)-98++, y(19)++, y(20)-98++

Peptide No.358

GSPGALSSDSELPENPYSQVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **GSPGALSSDSELPENPYSQVK**
Found in **CING_MOUSE** in **SwissProt**, Cingulin OS=Mus musculus GN=Cgn PE=1 SV=1

Match to Query 5678: 2240.982904 from(1121.498728,2+) index(2226)
Title: Elution from: 50.997 to 50.997 scan no 4276 cid35.00 polarity:+



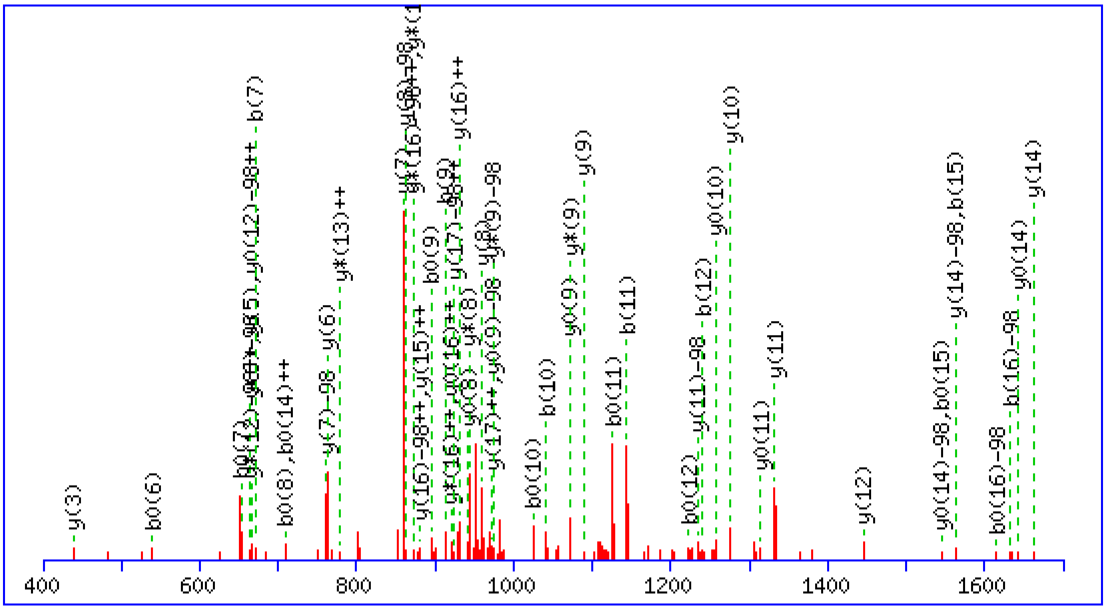
Monoisotopic mass of neutral peptide Mr(calc): 2240.9838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 **Expect:** 1.6e-006
Matched b ions: b(6), b(9), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(14), b(15), b(15)-98, b(16)-98, b(17), b(18)++, b(19), b(20)++
Matched y ions: y(6), y(7), y(8)++, y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(15)-98, y(16), y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++

Peptide No.359

GSPVSEIGWETPPPESPR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **GSPVSEIGWETPPPESPR**
Found in **SNTB1_MOUSE** in **SwissProt**, Beta-1-syntrophin OS=Mus musculus GN=Sntb1 PE=1 SV=4

Match to Query 4863: 2000.887692 from(1001.451122,2+) index(6373)
Title: Elution from: 45.164 to 45.164 scan no 4588 cid35.00 polarity:+:m1s



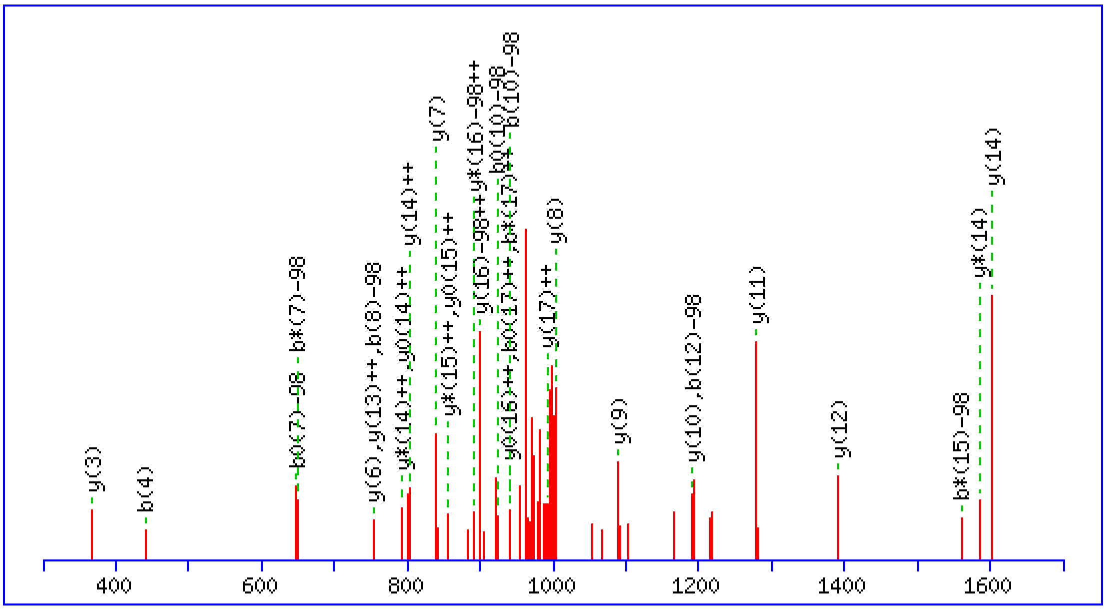
Monoisotopic mass of neutral peptide Mr(calc): 2000.8881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00046
Matched b ions: b(7), b(9), b(10), b(11), b(12), b(15), b(16)-98
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(9), y(10), y(11), y(11)-98, y(12), y(14)-98, y(14), y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++

Peptide No.360

GSSQPNLSTSYSEQEYGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GSSQPNLSTSYSEQEYGK**
Found in **EPN2_MOUSE** in **SwissProt**, Epsin-2 OS=Mus musculus GN=Epn2 PE=1 SV=1

Match to Query 4981: 2040.830686 from(1021.422619,2+) index(5317)
Title: Elution from: 32.810 to 32.810 scan no 2980 cid35.00 polarity:+:m1s



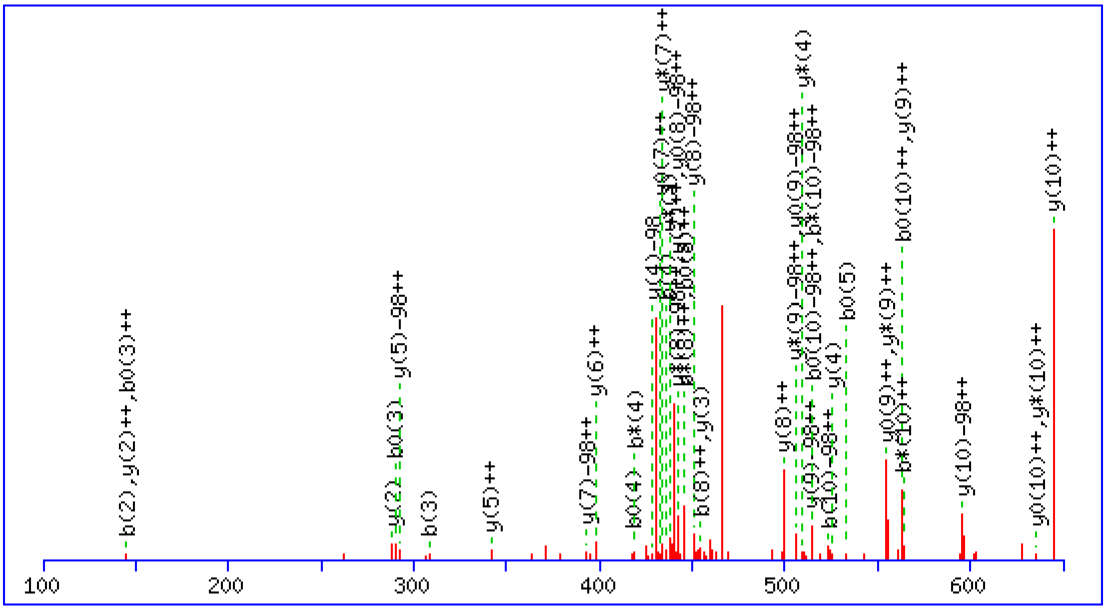
Monoisotopic mass of neutral peptide Mr(calc): 2040.8313
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 8.9e-007
Matched b ions: b(4), b(8)-98, b(10)-98, b(12)-98
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(14), y(14)++, y(16)-98++, y(17)++

Peptide No.361

GSYQDSLRASIR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **GSYQDSLRASIR**
Found in **ABCBB_MOUSE** in **SwissProt**, Bile salt export pump OS=Mus musculus GN=Abcb11 PE=1 SV=2

Match to Query 2658: 1431.650022 from(478.223950,3+) index(1365)
Title: Elution from: 27.900 to 27.900 scan no 2350 cid35.00 polarity:+



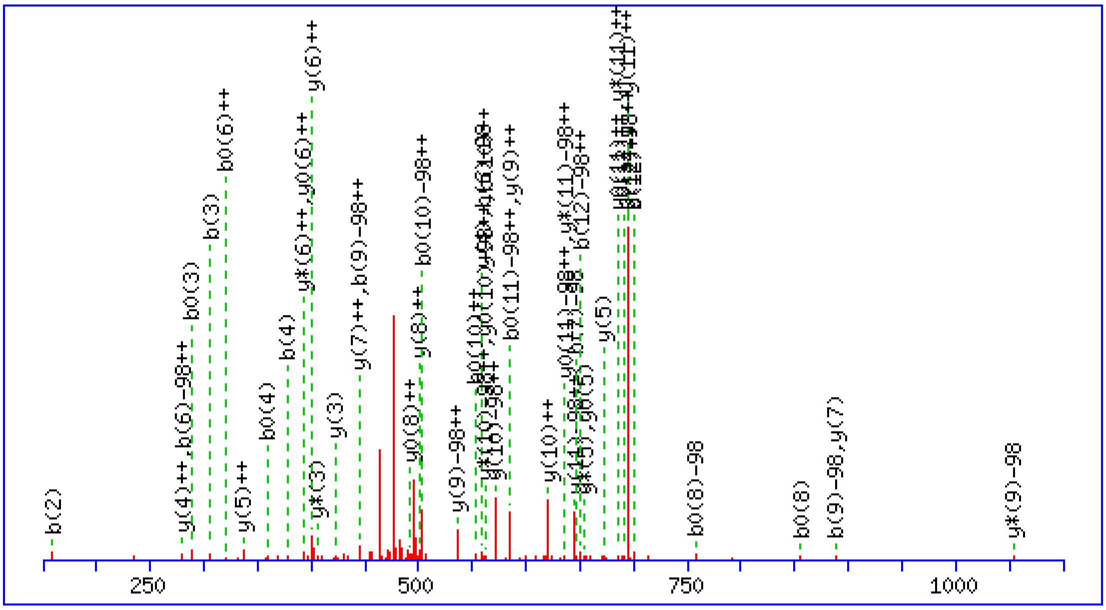
Monoisotopic mass of neutral peptide Mr(calc): 1431.6507
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.002
Matched b ions: b(2), b(3), b(4), b(8)++, b(10)-98++
Matched y ions: y(2)++, y(2), y(3), y(4)-98, y(4), y(5)-98++, y(5)++, y(6)++, y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)++, y(10)-98++

Peptide No.362

GTFASLSELHCDK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **GTFASLSELHCDK**
Found in **HBB1_MOUSE** in **SwissProt**, Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1 SV=2

Match to Query 3188: 1543.638558 from(515.553462,3+) index(1764)
Title: Elution from: 47.553 to 47.553 scan no 3744 cid35.00 polarity:+



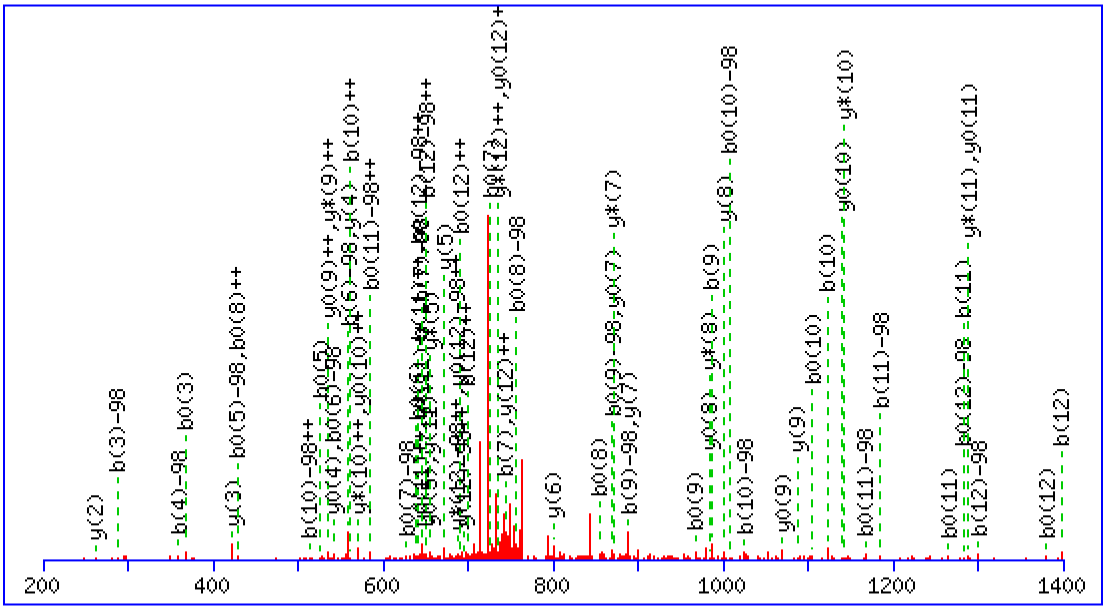
Monoisotopic mass of neutral peptide Mr(calc): 1543.6378
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 3.7e-005
Matched b ions: b(2), b(3), b(4), b(6)-98++, b(6)-98, b(7)-98, b(9)-98, b(9)-98++, b(10)++, b(12)++, b(12)-98++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(7), y(7)++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++

Peptide No.363

GTFASLSELHCDK
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of **GTFASLSELHCDK**
Found in **HBB2_MOUSE** in **SwissProt**, Hemoglobin subunit beta-2 OS=Mus musculus GN=Hbb-b2 PE=1 SV=2

Match to Query 3676: 1543.638612 from(772.826582,2+) index(2067)
Title: Elution from: 47.534 to 47.534 scan no 3956 cid35.00 polarity:+



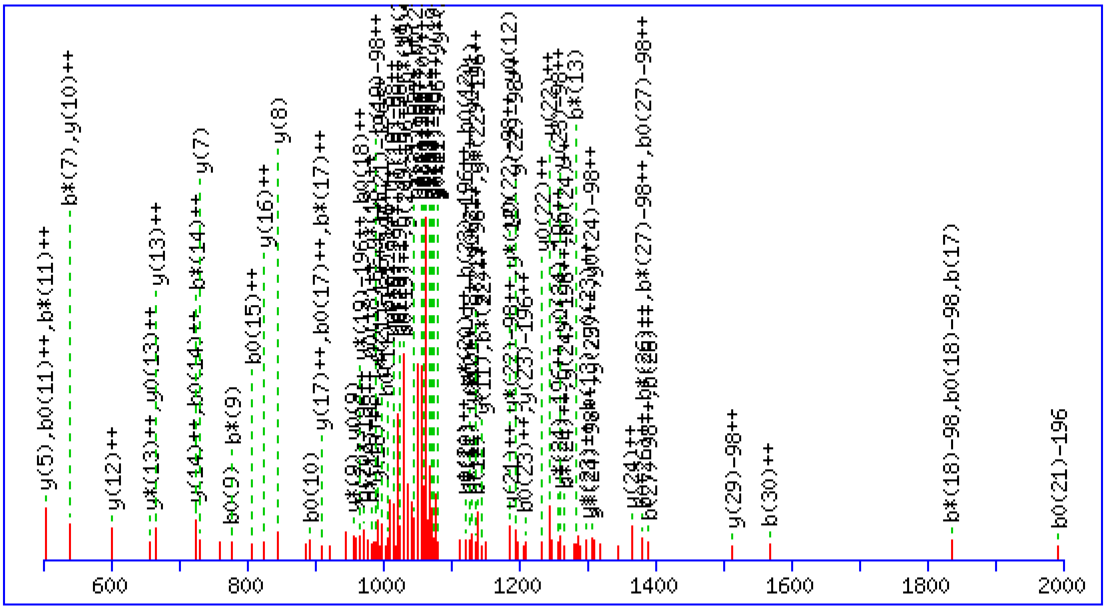
Monoisotopic mass of neutral peptide Mr(calc): 1543.6378
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0015
Matched b ions: b(3)-98, b(4)-98, b(6)-98, b(7)-98, b(7), b(9)-98, b(9), b(10), b(10)-98, b(10)-98++, b(10)++, b(11)-98, b(11), b(11)++, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(12)++, y(12)-98++

Peptide No.364

GTGPGGQLQDLDCSSSDDEGATQNTKPSATK
Confirmed sites: @S:14,@S:15
Ambiguous sites:

MS/MS Fragmentation of **GTGPGGQLQDLDCSSSDDEGATQNTKPSATK**
Found in **SRPR_MOUSE** in **SwissProt**, Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1

Match to Query 7058: 3281.303166 from(1094.774998,3+) index(5552)
Title: Elution from: 33.427 to 33.427 scan no 3097 cid35.00 polarity:+:m1s



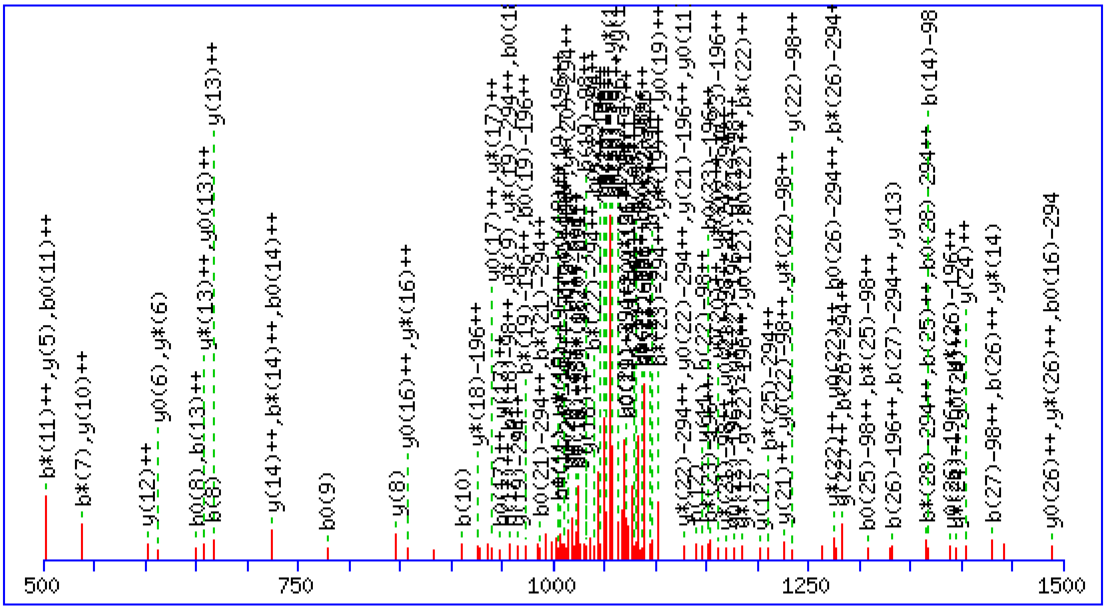
Monoisotopic mass of neutral peptide Mr(calc): 3281.3069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00018
Matched b ions: b(11), b(12), b(13), b(17), b(19)-98++, b(20)-196++, b(20)++, b(21)-98++, b(21)-196++, b(22)-196++, b(23)-196++, b(26)++, b(27)-98++, b(30)++
Matched y ions: y(5), y(7), y(8), y(10)++, y(10), y(11), y(12)++, y(13)++, y(14)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(20)-196++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(23)-196++, y(24)++, y(24)-196++, y(29)-98++

Peptide No.365

GTGPGGQLQDLDCSSSDDEGATQNTKPSATK
Confirmed sites: @S:14,@S:15,@S:16
Ambiguous sites:

MS/MS Fragmentation of **GTGPGGQLQDLDCSSSDDEGATQNTKPSATK**
Found in **SRPR_MOUSE** in **SwissProt**, Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1

Match to Query 7105: 3361.264995 from(1121.428941,3+) index(5868)
Title: Elution from: 36.578 to 36.578 scan no 3517 cid35.00 polarity:+:m1s



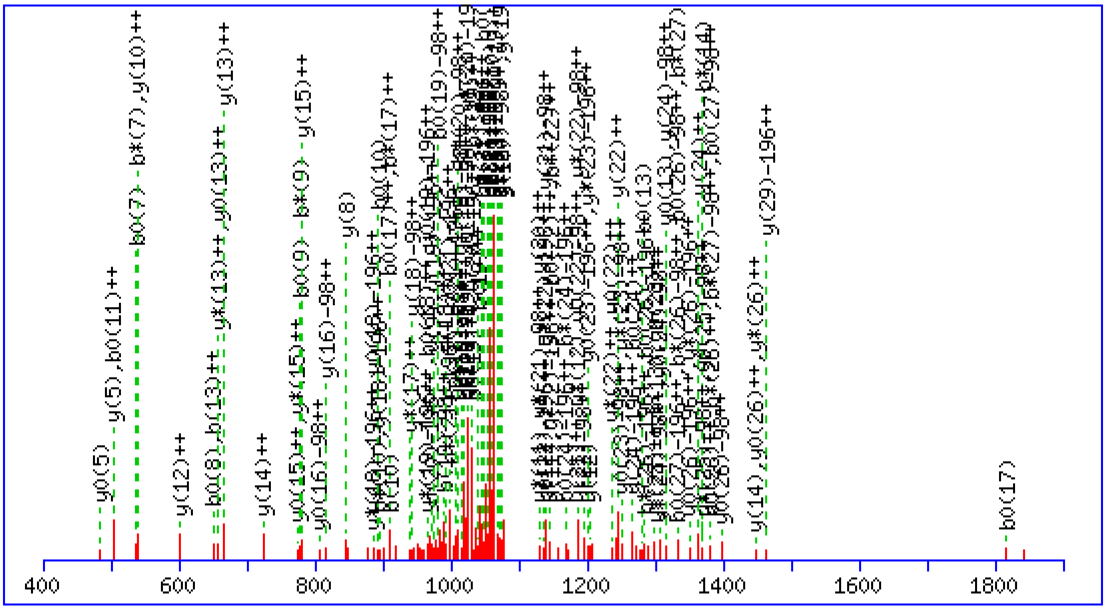
Monoisotopic mass of neutral peptide Mr(calc): 3361.2732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.011
Matched b ions: b(8), b(10), b(11), b(12), b(13)++, b(14)-98, b(17)++, b(19)-98++, b(19)++, b(20)-196++, b(21)-196++, b(21)-98++, b(22)-98++, b(22)-196++, b(23)-196++, b(24)-294++, b(25)++, b(26)-294++, b(26)++, b(26)-196++, b(27)-98++, b(27)-294++
Matched y ions: y(5), y(8), y(10)++, y(11), y(12)++, y(12), y(13)++, y(13), y(14)++, y(17)++, y(18)++, y(19)-294++, y(19)-196++, y(19)-98++, y(20)-294++, y(20)-196++, y(21)++, y(21)-196++, y(21)-98++, y(21)-294++, y(22)++, y(22)-196++, y(22)-98++, y(24)++

Peptide No.366

GTGPGGQLQDLDCSSSDDEGATQNTKPSATK
Confirmed sites: @S:16
Ambiguous sites: @S:14orS:15

MS/MS Fragmentation of **GTGPGGQLQDLDCSSSDDEGATQNTKPSATK**
Found in **SRPR_MOUSE** in **SwissProt**, Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1

Match to Query 6853: 3281.302161 from(1094.774663,3+) index(5373)
Title: Elution from: 33.331 to 33.331 scan no 3050 cid35.00 polarity:+:m1s



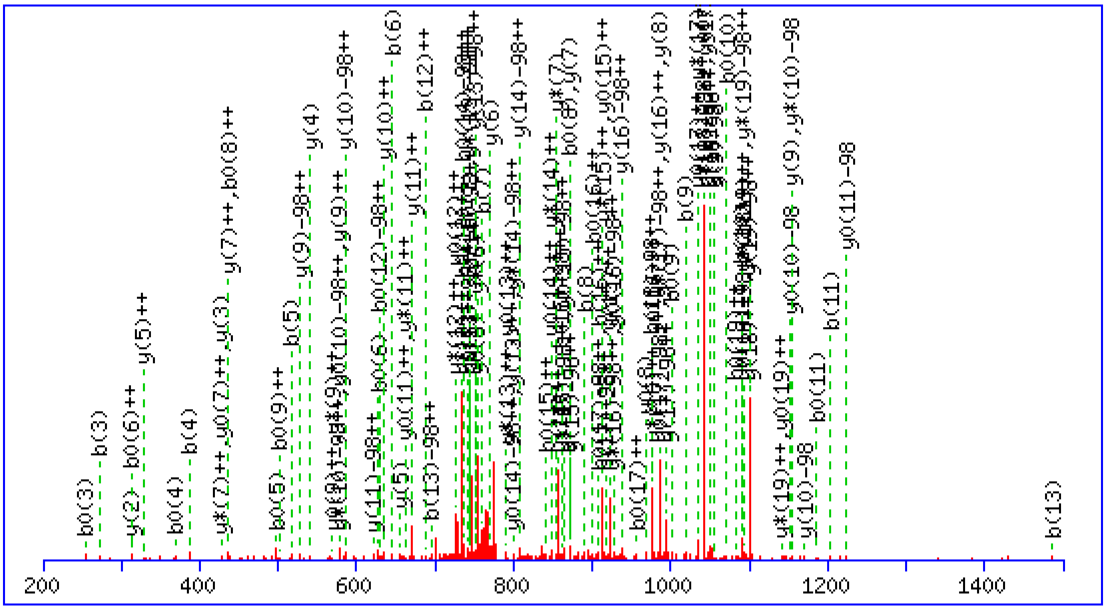
Monoisotopic mass of neutral peptide Mr(calc): 3281.3069
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 6e-005
Matched b ions: b(10), b(11), b(12), b(13)++, b(13), b(19)-98++, b(19)++, b(20)-196++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(22)-196++
Matched y ions: y(5), y(8), y(9), y(10)++, y(10), y(11), y(12)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15)++, y(16)-98++, y(18)-196++, y(18)-98++, y(18)++, y(19)-98++, y(19)-196++, y(19)++, y(20)-196++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-196++, y(22)-98++, y(24)++, y(24)-196++, y(24)-98++, y(29)-196++

Peptide No.367

GTLDEEDEEADSDTDDIDHR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **GTLDEEDEEADSDTDDIDHR**
Found in **GPN1_MOUSE** in **SwissProt**, GPN-loop GTPase 1 OS=Mus musculus GN=Gpn1 PE=1 SV=1

Match to Query 5916: 2355.849876 from(786.290568,3+) index(4683)
Title: Elution from: 36.481 to 36.481 scan no 2702 cid35.00 polarity:+:m1s



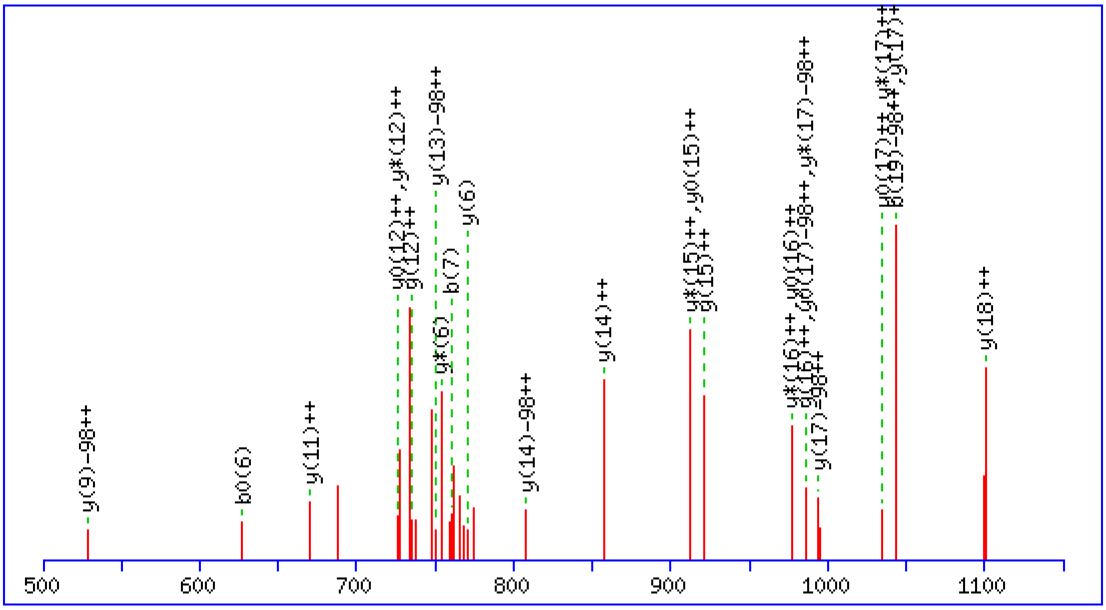
Monoisotopic mass of neutral peptide Mr(calc): 2355.8500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 2.6e-005
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(13), b(13)-98++, b(13)++, b(14)-98++, b(16)++, b(16)-98++, b(17)-98++, b(18)-98++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)++, y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)-98++

Peptide No.368

GTLDEEDEEADSDTDDIDHR
Confirmed sites:
Ambiguous sites: @S:12orT:14

MS/MS Fragmentation of **GTLDEEDEEADSDTDDIDHR**
Found in **GPN1_MOUSE** in **SwissProt**, GPN-loop GTPase 1 OS=Mus musculus GN=Gpn1 PE=1 SV=1

Match to Query 6085: 2355.848397 from(786.290075,3+) index(5185)
Title: Elution from: 29.770 to 29.770 scan no 2604 cid35.00 polarity:+:m1s



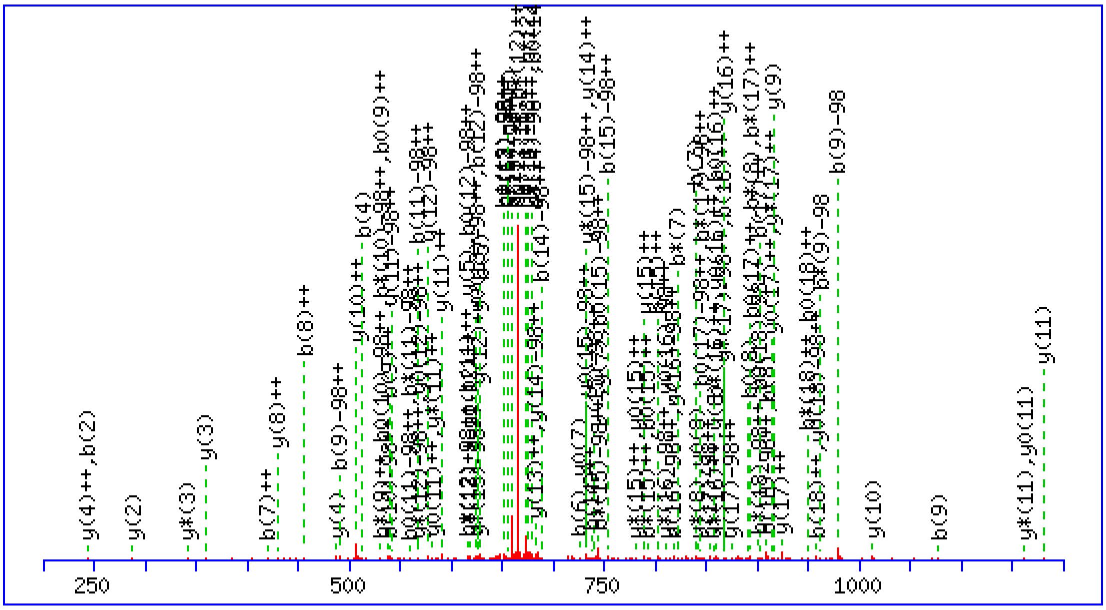
Monoisotopic mass of neutral peptide Mr(calc): 2355.8500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0094
Matched b ions: b(7), b(19)-98++
Matched y ions: y(6), y(9)-98++, y(11)++, y(12)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++

Peptide No.369

GWLRDPNASPGDAGEQAIR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **GWLRDPNASPGDAGEQAIR**
Found in **VINC_MOUSE** in **SwissProt**, Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4

Match to Query 4635: 2088.938316 from(697.320048,3+) index(4611)
Title: Elution from: 45.815 to 45.815 scan no 3571 cid35.00 polarity:+:m1s



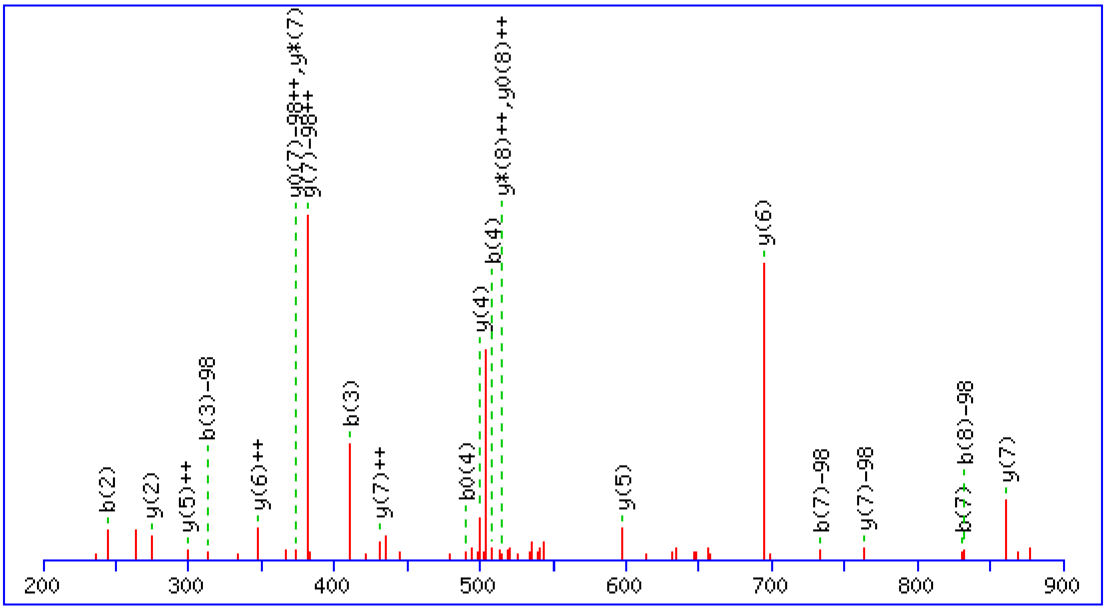
Monoisotopic mass of neutral peptide Mr(calc): 2088.9378
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 9.3e-006
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(7)++, b(8), b(8)++, b(9)-98, b(9), b(9)-98++, b(9)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11), y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.370

GWSPPPEVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GWSPPPEVR**
Found in **ACSA_MOUSE** in **SwissProt**, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2

Match to Query 1140: 1103.479644 from(552.747098,2+) index(2088)
Title: Elution from: 35.690 to 35.690 scan no 3368 cid35.00 polarity:+



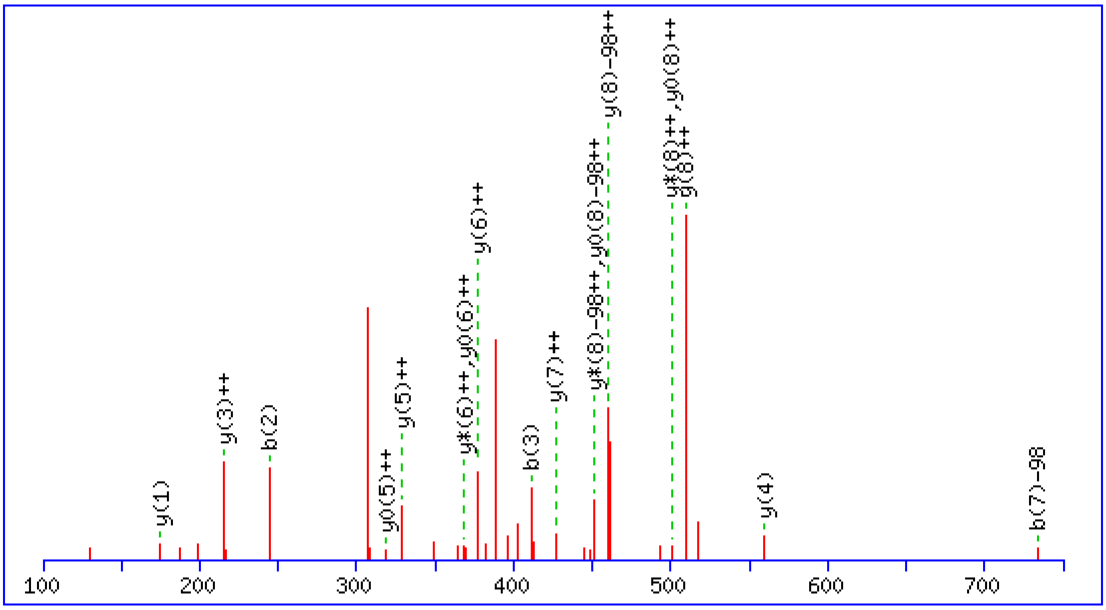
Monoisotopic mass of neutral peptide Mr(calc): 1103.4801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.00069
Matched b ions: b(2), b(3), b(3)-98, b(4), b(7)-98, b(7), b(8)-98
Matched y ions: y(2), y(4), y(5), y(5)++, y(6), y(6)++, y(7)-98++, y(7)-98, y(7), y(7)++

Peptide No.371

GWSPPPEVRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **GWSPPPEVRR**
Found in **ACSA_MOUSE** in **SwissProt**, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2

Match to Query 1628: 1259.581692 from(420.867840,3+) index(1453)
Title: Elution from: 30.353 to 30.353 scan no 2606 cid35.00 polarity:+



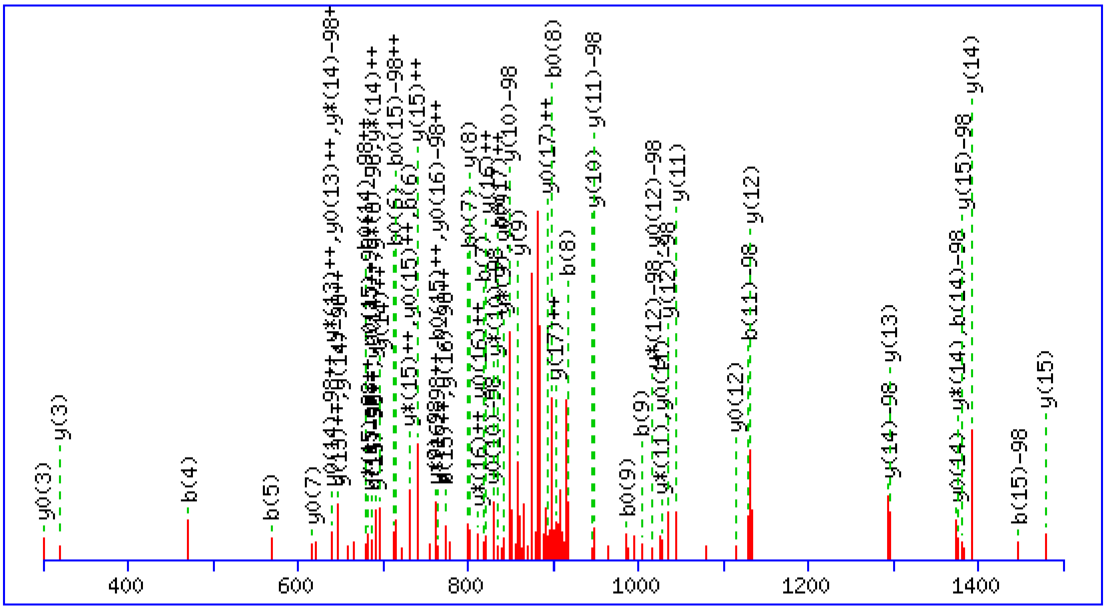
Monoisotopic mass of neutral peptide Mr(calc): 1259.5812
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0063
Matched b ions: b(2), b(3), b(7)-98
Matched y ions: y(1), y(3)++, y(4), y(5)++, y(6)++, y(7)++, y(8)++, y(8)-98++

Peptide No.372

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **GYYSPYSVSGSGSTAGSR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3726: 1861.749536 from(931.882044,2+) index(4785)
Title: Elution from: 33.065 to 33.065 scan no 2960 cid35.00 polarity:+:m1s



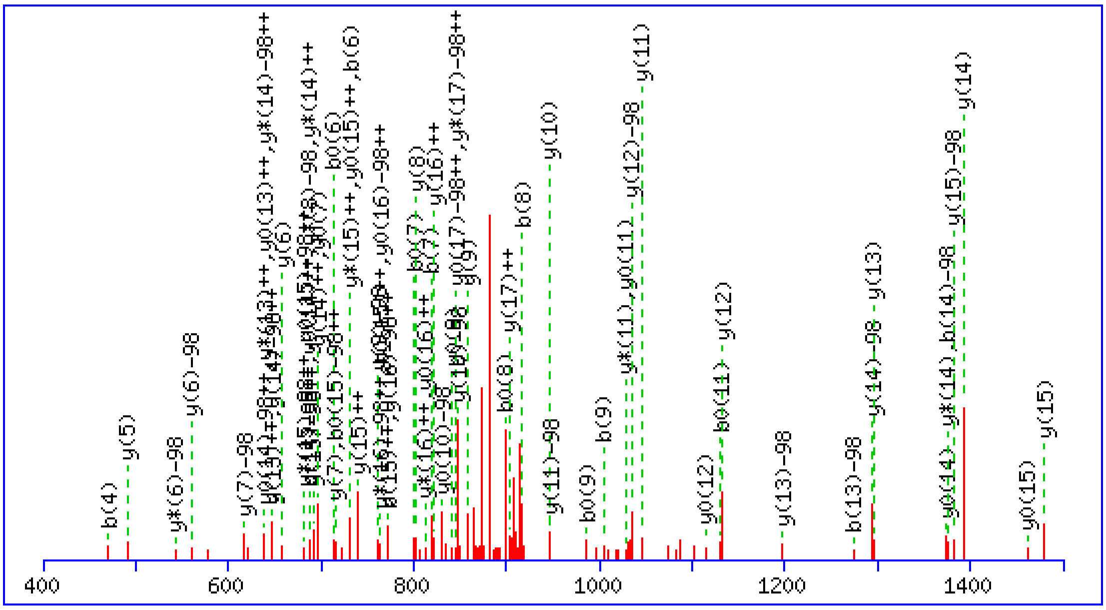
Monoisotopic mass of neutral peptide Mr(calc): 1861.7520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 8.6e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(11)-98, b(14)-98, b(14)-98++, b(15)-98, b(15)++
Matched y ions: y(3), y(8), y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)++, y(13), y(14)-98++, y(14)-98, y(14), y(14)++, y(15)++, y(15), y(15)-98++, y(15)-98, y(16)-98++, y(16)++, y(17)++

Peptide No.373

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **GYYSPYSVSGSGSTAGSR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 3794: 1861.749380 from(931.881966,2+) index(1557)
Title: Elution from: 33.240 to 33.240 scan no 2928 cid35.00 polarity:+



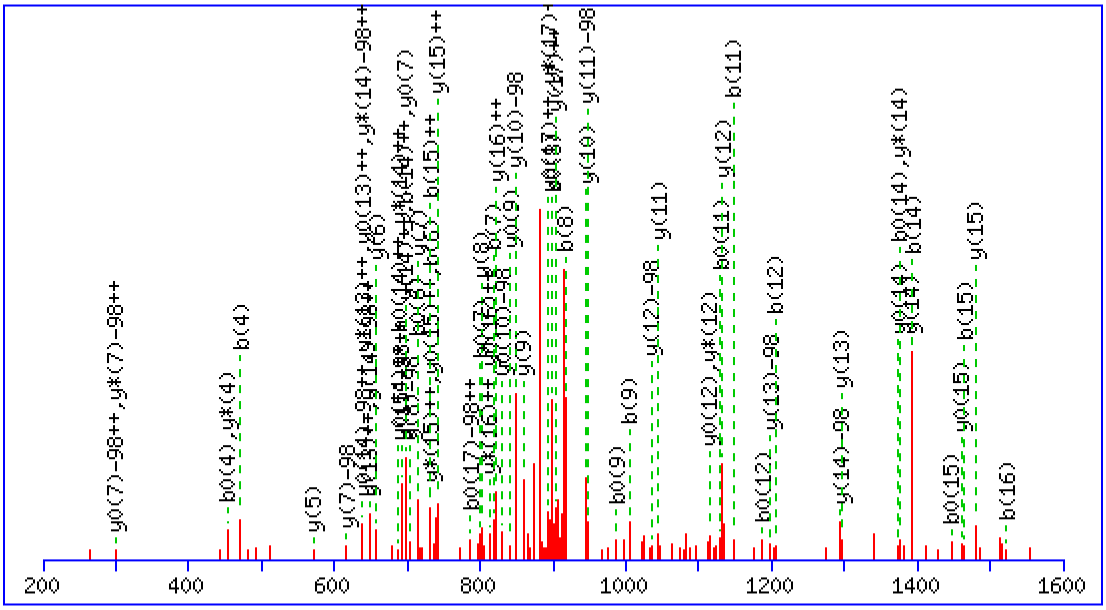
Monoisotopic mass of neutral peptide Mr(calc): 1861.7520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 9.8e-007
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(13)-98, b(14)-98, b(14)-98++, b(15)++
Matched y ions: y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(9), y(9)-98, y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(13)++, y(13)-98, y(13), y(14)-98++, y(14)-98, y(14), y(14)++, y(15)++, y(15), y(15)-98, y(15)-98++, y(16)-98++, y(16)++, y(17)++

Peptide No.374

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **GYYSPYSVSGSGSTAGSR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4695: 1861.751398 from(931.882975,2+) index(5061)
Title: Elution from: 41.208 to 41.208 scan no 3264 cid35.00 polarity:+:m1s



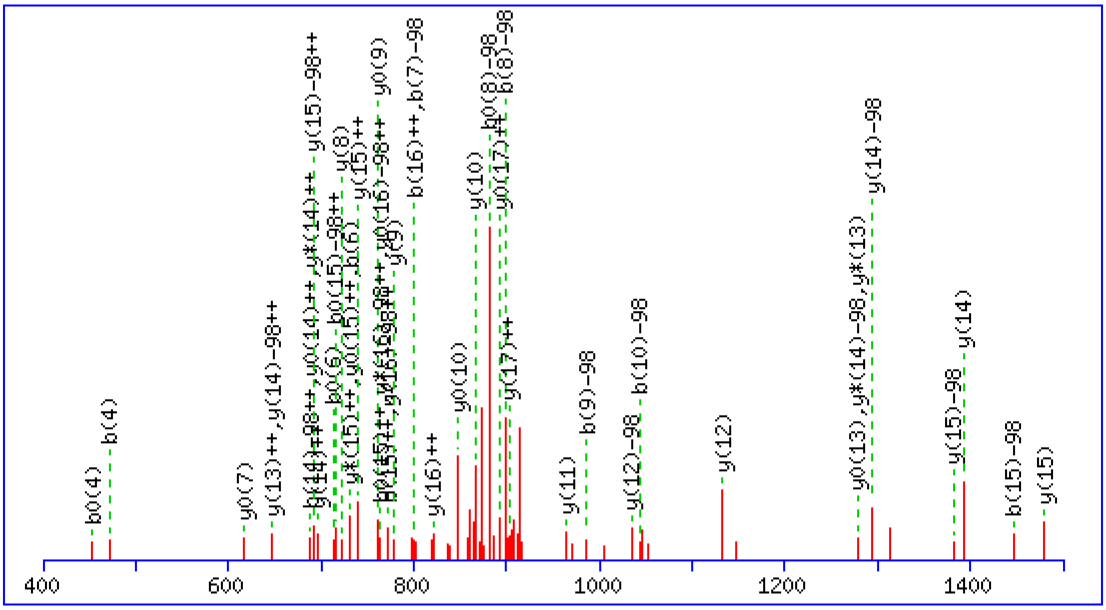
Monoisotopic mass of neutral peptide Mr(calc): 1861.7520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 3.7e-006
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(11), b(12), b(14)++, b(14), b(15), b(15)++, b(16)
Matched y ions: y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13)++, y(13)-98, y(13), y(14)-98++, y(14)++, y(14)-98, y(14), y(15), y(15)-98++, y(15)++, y(16)++, y(17)++

Peptide No.375

GYYSPYSVSGSGSTAGSR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **GYYSPYSVSGSGSTAGSR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4444: 1861.750166 from(931.882359,2+) index(1903)
Title: Elution from: 33.442 to 33.442 scan no 3099 cid35.00 polarity:+



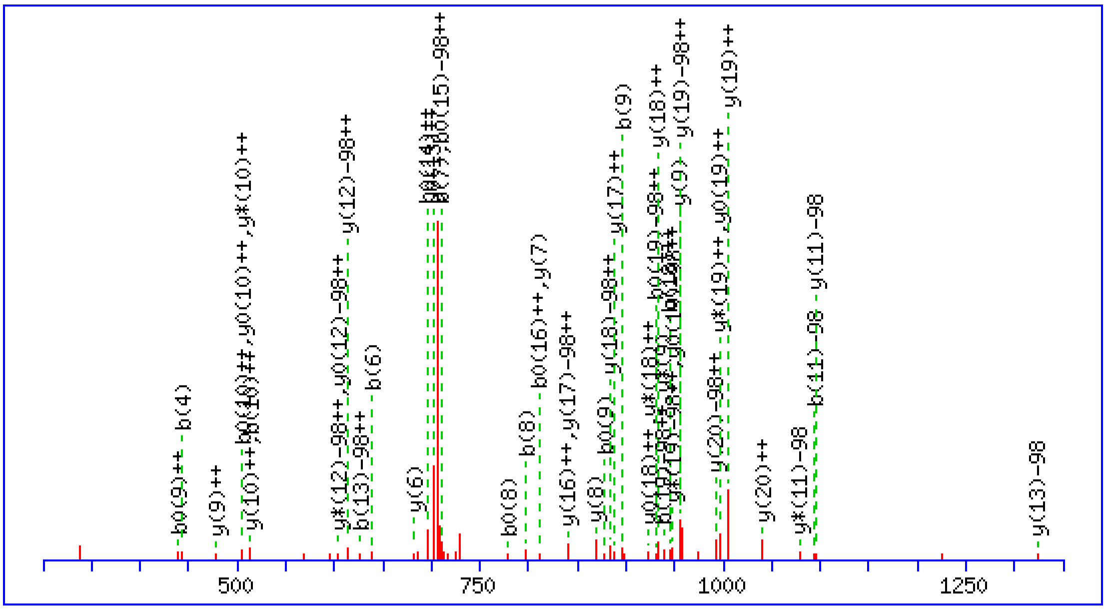
Monoisotopic mass of neutral peptide Mr(calc): 1861.7520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 4.5e-005
Matched b ions: b(4), b(6), b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(14)-98++, b(15)-98, b(15)++, b(16)++
Matched y ions: y(8), y(9), y(10), y(11), y(12)-98, y(12), y(13)++, y(14)-98++, y(14)-98, y(14), y(14)++, y(15)++, y(15), y(15)-98++, y(15)-98, y(16)-98++, y(16)++, y(17)++

Peptide No.376

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4802: 2217.012060 from(740.011296,3+) index(5079)
Title: Elution from: 39.207 to 39.207 scan no 3705 cid35.00 polarity:+:m1s



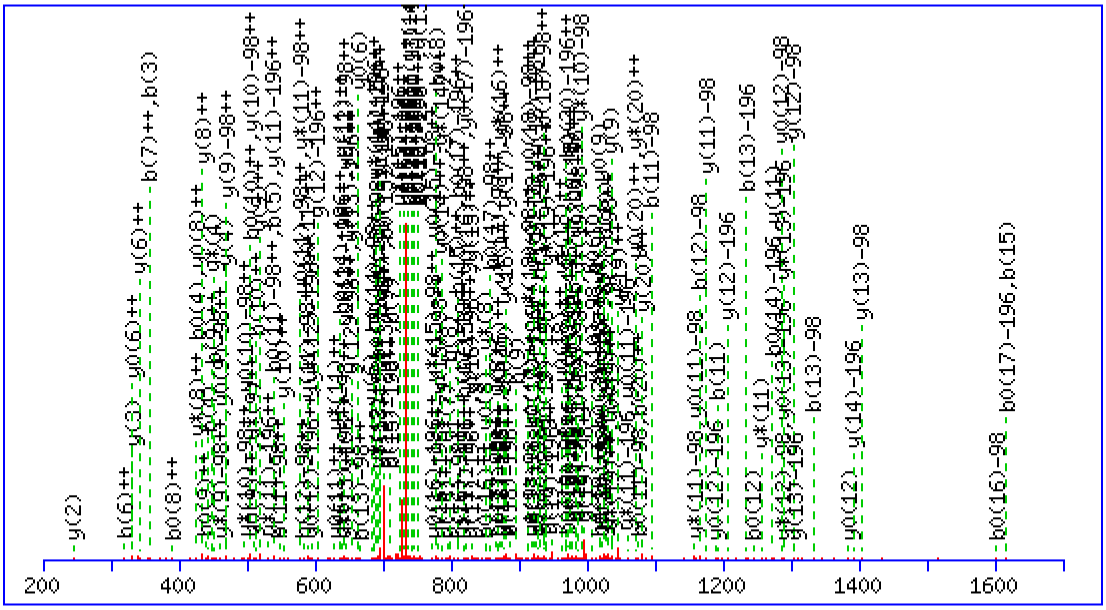
Monoisotopic mass of neutral peptide Mr(calc): 2217.0103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 0.00017
Matched b ions: b(4), b(6), b(7), b(8), b(9), b(10)++, b(11)-98, b(13)-98++, b(18)++, b(19)-98++
Matched y ions: y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(11)-98, y(12)-98++, y(13)-98, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.377

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4992: 2296.976802 from(766.666210,3+) index(4559)
Title: Elution from: 44.698 to 44.698 scan no 3465 cid35.00 polarity:+:m1s



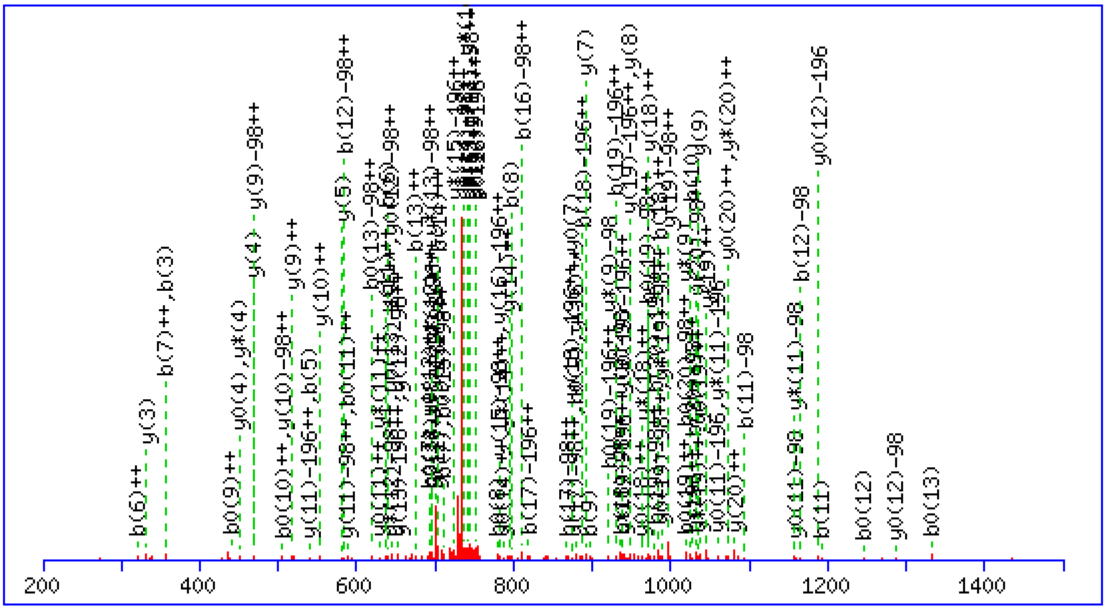
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.1e-005
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7)++, b(7), b(8), b(9), b(9)++, b(10), b(10)++, b(11)-98, b(11)-98++, b(11), b(12)-98, b(12)-98++, b(13)-98, b(13)-98++, b(13)-196, b(14)-98++, b(15), b(15)-196++, b(15)++, b(16)-98++, b(17)-196++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(20)-196++
Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(8)++, y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10)++, y(10)-98, y(11)-98++, y(11), y(11)++, y(11)-196++, y(11)-98, y(12)++, y(12)-196, y(12)-98, y(12)-196++, y(12)-98++, y(13)-98++, y(13)-98, y(13)++, y(13)-196, y(13)-196++, y(14)-98++, y(14)-196, y(14)++, y(14)-196++, y(15)++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)++, y(16)-196++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++

Peptide No.378

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:11,@T:16
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4991: 2296.975995 from(766.665941,3+) index(4541)
Title: Elution from: 44.349 to 44.349 scan no 3432 cid35.00 polarity:+:m1s



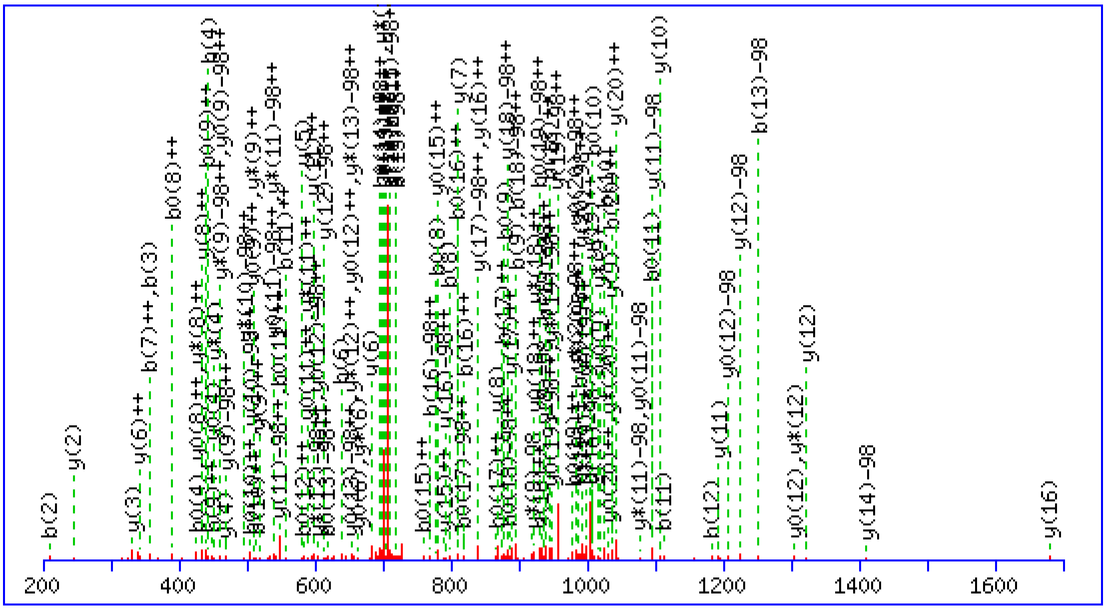
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0023
Matched b ions: b(3), b(5), b(6)++, b(6), b(7)++, b(7), b(8), b(9), b(10), b(11), b(11)-98, b(12)-98, b(12)-98++, b(13)++, b(14)++, b(16)-98++, b(17)-98++, b(17)-196++, b(18)-98++, b(18)++, b(18)-196++, b(19)-196++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9)++, y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10)++, y(11)-196++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-196++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(14)-196++, y(15)-98++, y(16)++, y(16)-196++, y(17)-98++, y(18)-196++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++

Peptide No.379

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4852: 2217.008571 from(740.010133,3+) index(4861)
Title: Elution from: 33.931 to 33.931 scan no 3071 cid35.00 polarity:+:m1s



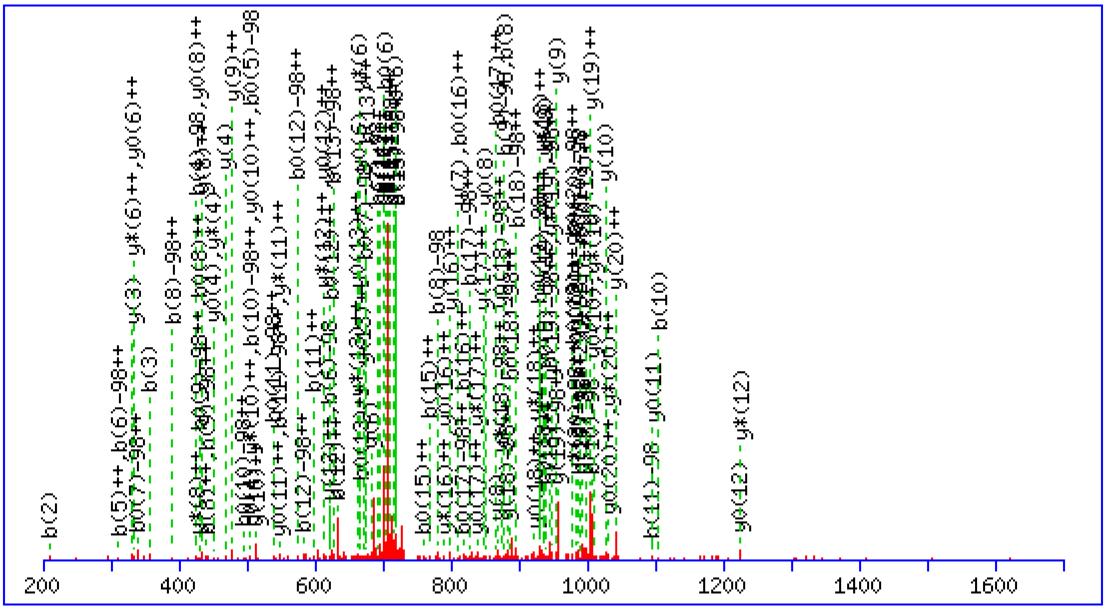
Monoisotopic mass of neutral peptide Mr(calc): 2217.0103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 **Expect:** 9e-007
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(7)++, b(8), b(9), b(9)++, b(10), b(10)++, b(11), b(11)++, b(12), b(13)-98, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(8), y(9), y(9)-98++, y(9)++, y(9)-98, y(10)-98++, y(10)-98, y(10), y(11)-98++, y(11)++, y(11)-98, y(11), y(12)-98, y(12), y(12)-98++, y(13)++, y(14)-98, y(14)-98++, y(15)++, y(16), y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.380

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5622: 2217.011700 from(740.011176,3+) index(5487)
Title: Elution from: 47.617 to 47.617 scan no 3967 cid35.00 polarity:+:m1s



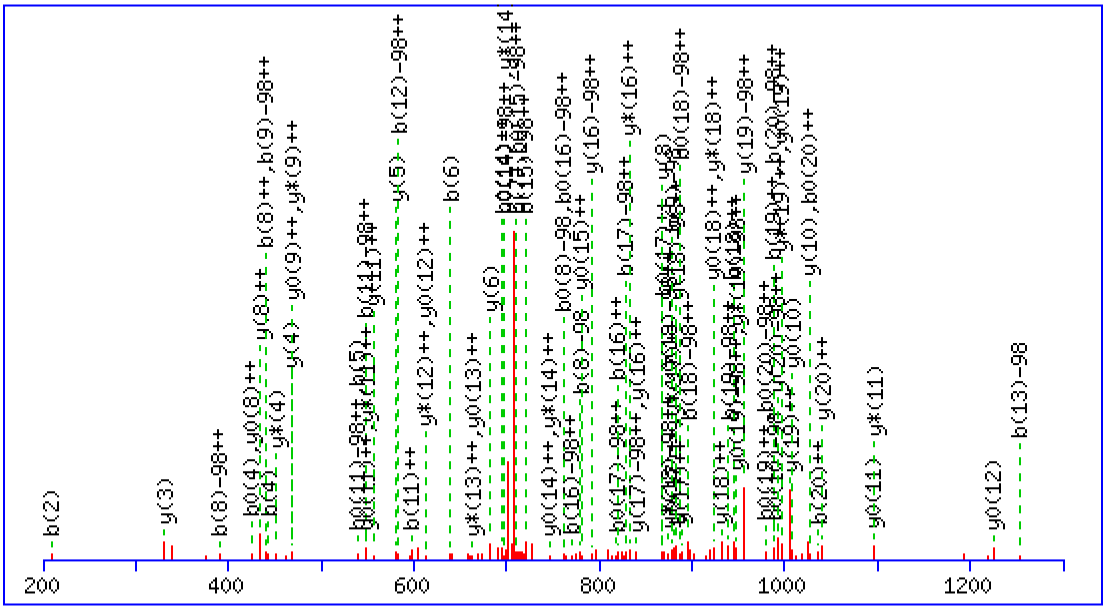
Monoisotopic mass of neutral peptide Mr(calc): 2217.0103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00084
Matched b ions: b(2), b(3), b(4)-98, b(5)++, b(6), b(6)-98++, b(6)-98, b(7)-98, b(8)++, b(8)-98++, b(8)-98, b(8), b(9)-98++, b(9)-98, b(10)-98++, b(10)-98, b(10), b(11)-98++, b(11)-98, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(12)++, y(13)++, y(14)++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.381

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4801: 2217.005271 from(740.009033,3+) index(4551)
Title: Elution from: 33.277 to 33.277 scan no 2933 cid35.00 polarity:+:m1s



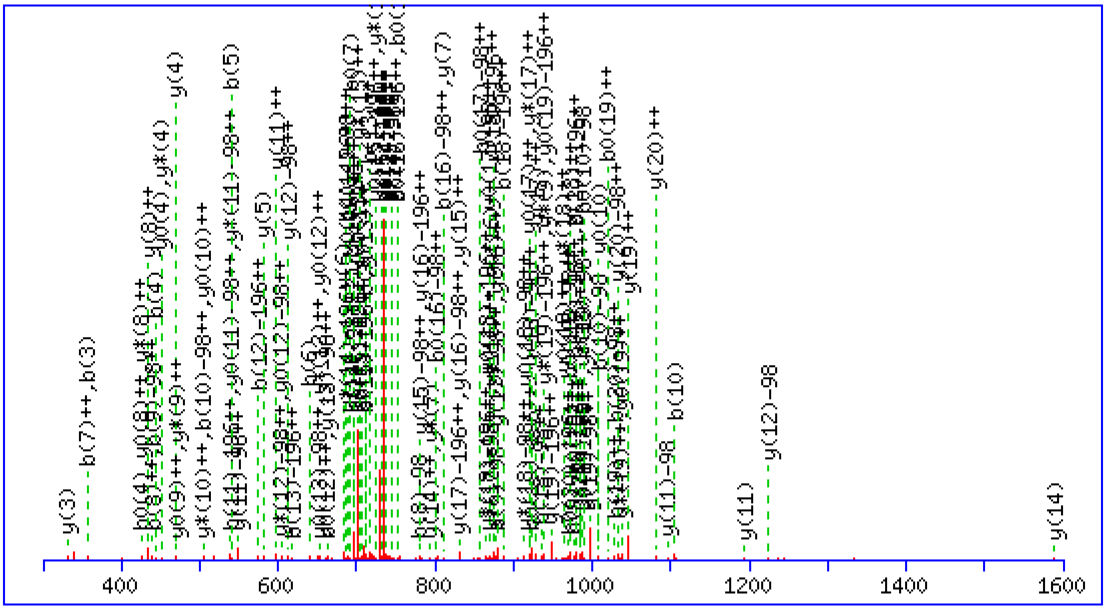
Monoisotopic mass of neutral peptide Mr(calc): 2217.0103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 4.5e-006
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8)++, b(8)-98++, b(8)-98, b(9)-98++, b(9)-98, b(11)++, b(11)-98++, b(12)-98++, b(13)-98, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)++, y(8), y(10), y(11)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++

Peptide No.382

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@S:11
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5825: 2296.974015 from(766.665281,3+) index(5566)
Title: Elution from: 35.185 to 35.185 scan no 3300 cid35.00 polarity:+:m1s



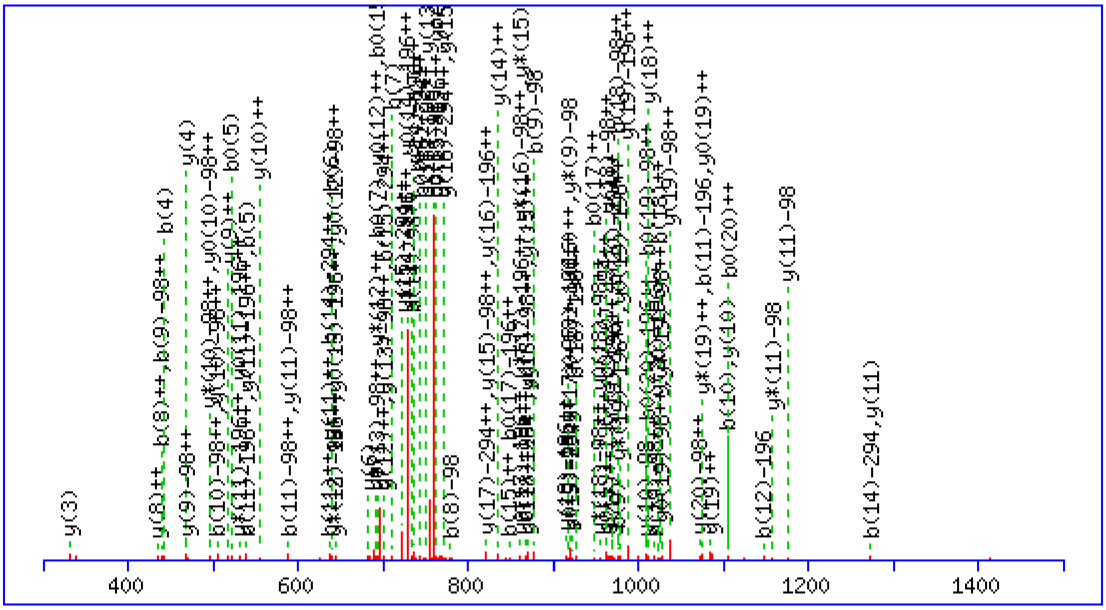
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 **Expect:** 8.9e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9), b(10), b(10)-98++, b(10)-98, b(11)-196++, b(12)-196++, b(13)-196++, b(13)++, b(14)-98++, b(15)-196++, b(16)-98++, b(18)++, b(18)-196++, b(18)-98++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(11)-98++, y(11), y(11)++, y(11)-98, y(12)-98, y(12)-98++, y(13)++, y(13)-98++, y(14), y(14)-196++, y(14)-98++, y(14)++, y(15)++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)++, y(16)-196++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(20)-98++, y(20)++, y(20)-196++

Peptide No.383

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5151: 2376.939576 from(793.320468,3+) index(5269)
Title: Elution from: 38.837 to 38.837 scan no 3684 cid35.00 polarity:+:m1s



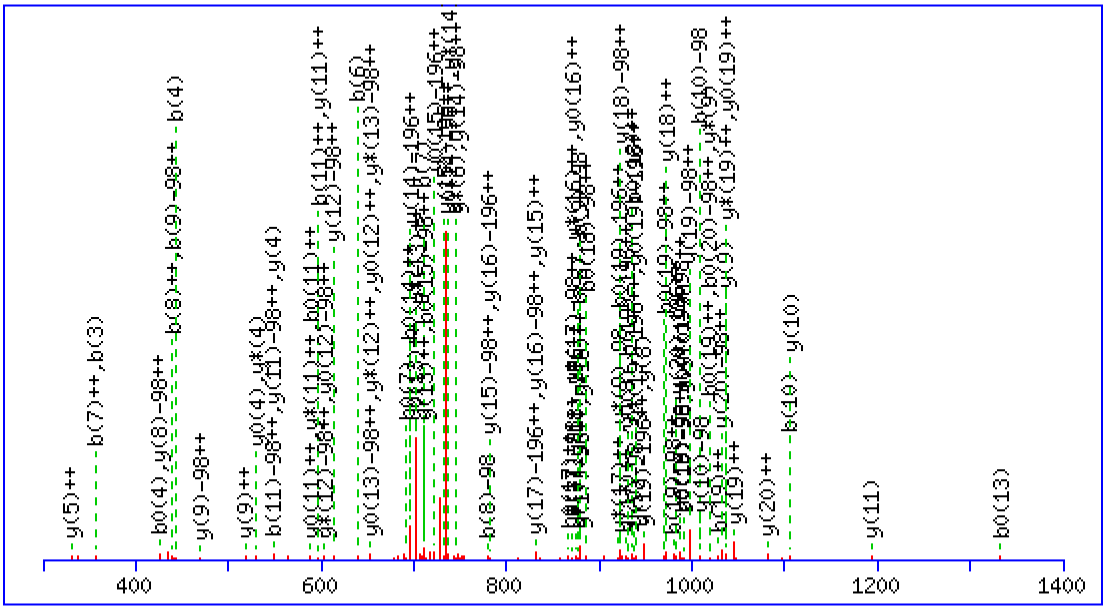
Monoisotopic mass of neutral peptide Mr(calc): 2376.9430
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.021
Matched b ions: b(4), b(5), b(6), b(7), b(8)++, b(8)-98, b(9)-98, b(9)-98++, b(9), b(10)-98++, b(10), b(11)-98++, b(11)-196++, b(11)-196, b(11)++, b(12)-196, b(14)-294, b(14)-294++, b(14)-98++, b(15)-294++, b(15)-196++, b(15)++, b(18)-98++, b(18)-196++, b(18)++, b(19)-98++, b(19)-294++, b(19)-196++, b(20)-294++
Matched y ions: y(3), y(4), y(6), y(8)++, y(8), y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(10), y(10)-98, y(11)-98++, y(11), y(11)-196++, y(11)-98, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-196++, y(14)++, y(15)++, y(15)-98++, y(15)-294++, y(15)-196++, y(16)++, y(16)-98++, y(16)-196++, y(16)-294++, y(17)-98++, y(17)-196++, y(17)-294++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-196++, y(19)-98++, y(19)++, y(20)-98++, y(20)-196++

Peptide No.384

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@S:19
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4996: 2296.977726 from(766.666518,3+) index(4933)
Title: Elution from: 34.865 to 34.865 scan no 3183 cid35.00 polarity:+:m1s



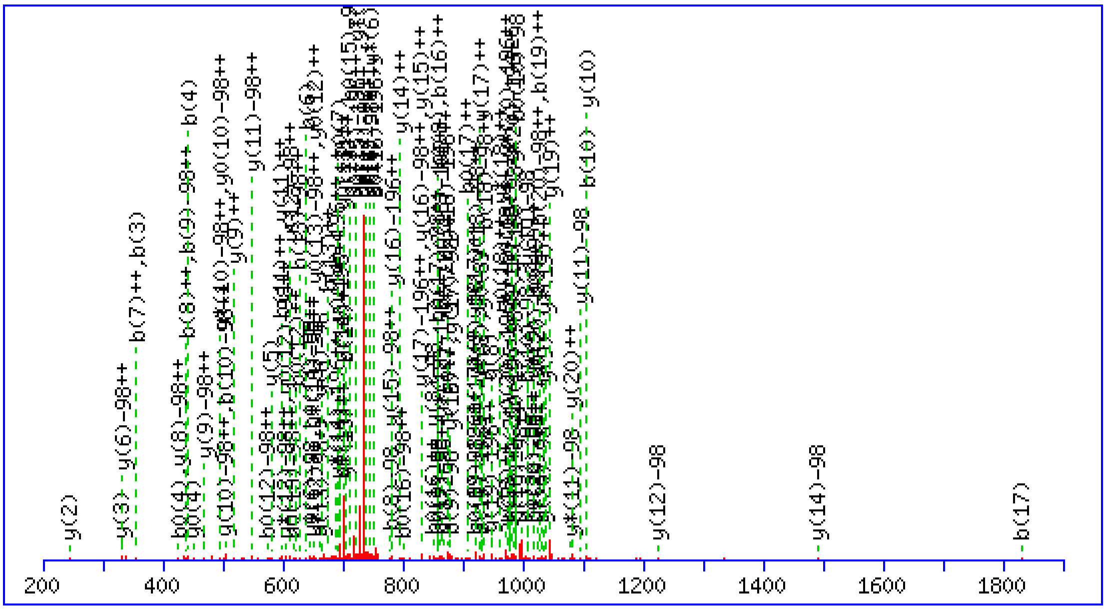
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 **Expect:** 4.6e-005
Matched b ions: b(3), b(4), b(6), b(7)++, b(7), b(8)++, b(8)-98, b(8), b(9)-98++, b(9)-98, b(10), b(10)-98, b(11)-98++, b(11)++, b(19)-98++, b(19)-196++, b(19)++
Matched y ions: y(4), y(5)++, y(8)-98++, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10), y(10)-98, y(11)-98++, y(11), y(11)++, y(12)-98++, y(13)++, y(14)-196++, y(14)-98++, y(15)++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)-196++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(20)-98++, y(20)++, y(20)-196++

Peptide No.385

HAFSPVASVESASGETLHSPK
Confirmed sites: @S:8,@T:16
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4993: 2296.977501 from(766.666443,3+) index(4467)
Title: Elution from: 43.030 to 43.030 scan no 3299 cid35.00 polarity:+:m1s



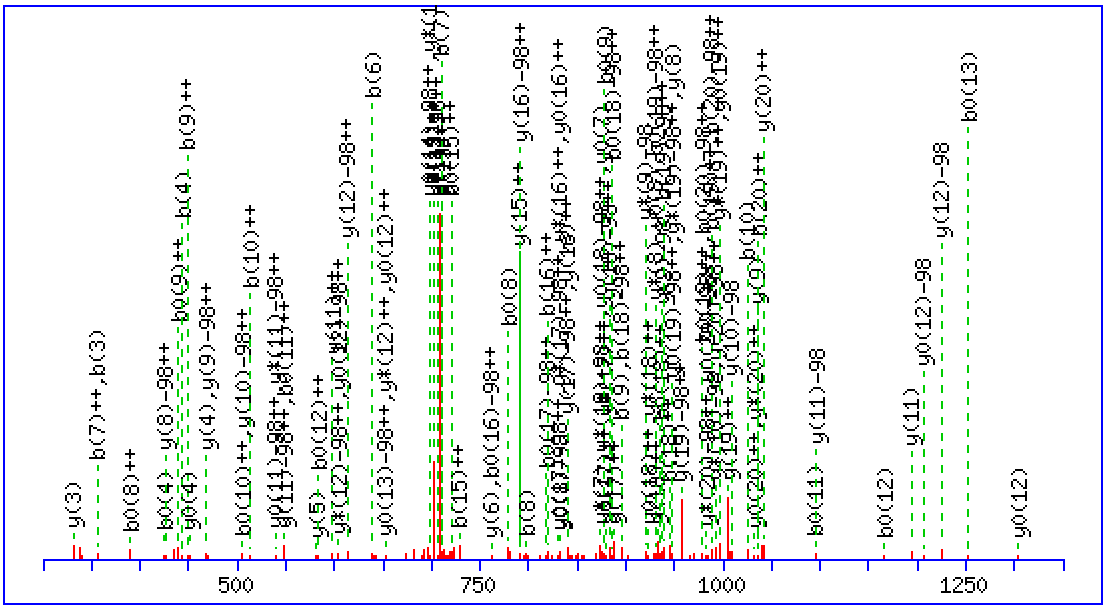
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00027
Matched b ions: b(3), b(4), b(6), b(7)++, b(7), b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9), b(10)-98++, b(10), b(10)-98, b(11)++, b(13)-98++, b(13)++, b(14)++, b(16)++, b(17), b(17)-98++, b(18)-98++, b(18)++, b(19)-196++, b(19)-98++, b(19)++, b(20)-196++, b(20)-98++
Matched y ions: y(2), y(3), y(5), y(6)-98++, y(6)-98, y(8)-98++, y(8), y(8)-98, y(9)-98++, y(9)++, y(9), y(10)-98++, y(10), y(10)-98, y(11)++, y(11)-98++, y(11)-98, y(12)-98, y(12)-98++, y(13)-98++, y(13)++, y(14)-98, y(14)-98++, y(14)-196++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(16)-196++, y(17)-196++, y(17)-98++, y(17)++, y(18)-98++, y(18)-196++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-196++, y(20)-98++

Peptide No.386

HAFSPVASVESASGETLHSPK
Confirmed sites: @T:16
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5650: 2217.007407 from(740.009745,3+) index(5328)
Title: Elution from: 32.899 to 32.899 scan no 2992 cid35.00 polarity:+:m1s



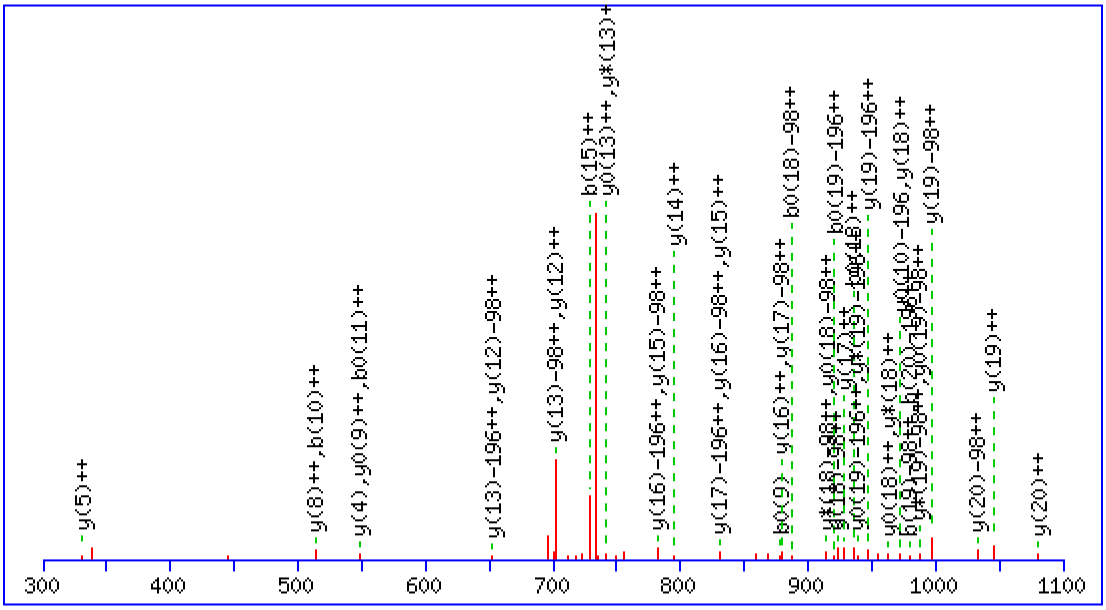
Monoisotopic mass of neutral peptide Mr(calc): 2217.0103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 5.2e-007
Matched b ions: b(3), b(4), b(6), b(7)++, b(7), b(8), b(9), b(9)++, b(10)++, b(10), b(15)++, b(16)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8)-98++, y(8), y(9)-98++, y(9), y(9)-98, y(10)-98++, y(10)-98, y(11)-98++, y(11), y(11)-98, y(11)++, y(12)-98, y(12)-98++, y(13)++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.387

HAFSPVASVESASGETLHSPK
Confirmed sites: @T:16,@S:19
Ambiguous sites:

MS/MS Fragmentation of **HAFSPVASVESASGETLHSPK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4993: 2296.975611 from(766.665813,3+) index(5289)
Title: Elution from: 39.112 to 39.112 scan no 3717 cid35.00 polarity:+:m1s



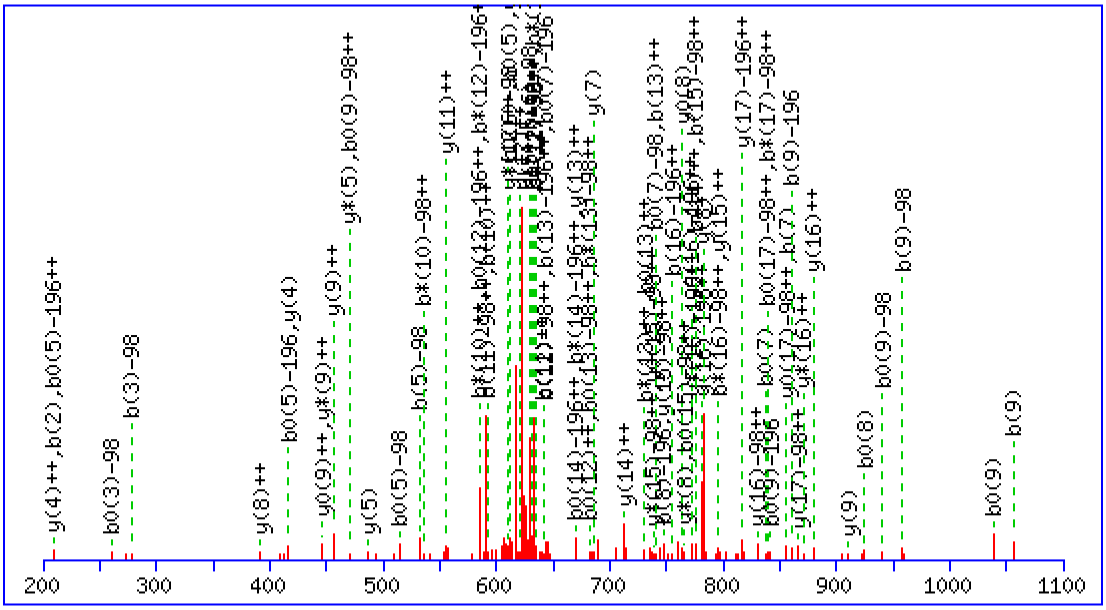
Monoisotopic mass of neutral peptide Mr(calc): 2296.9766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00026
Matched b ions: b(10)++, b(15)++, b(19)-98++, b(20)-196++
Matched y ions: y(4), y(5)++, y(8)++, y(12)++, y(12)-98++, y(13)-98++, y(13)-196++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(19)-196++, y(20)-98++, y(20)++

Peptide No.388

HASSSPESLKPTPAPGSR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **HASSSPESLKPTPAPGSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4720: 1964.838066 from(655.953298,3+) index(4162)
Title: Elution from: 21.914 to 21.914 scan no 1497 cid35.00 polarity:+:m1s



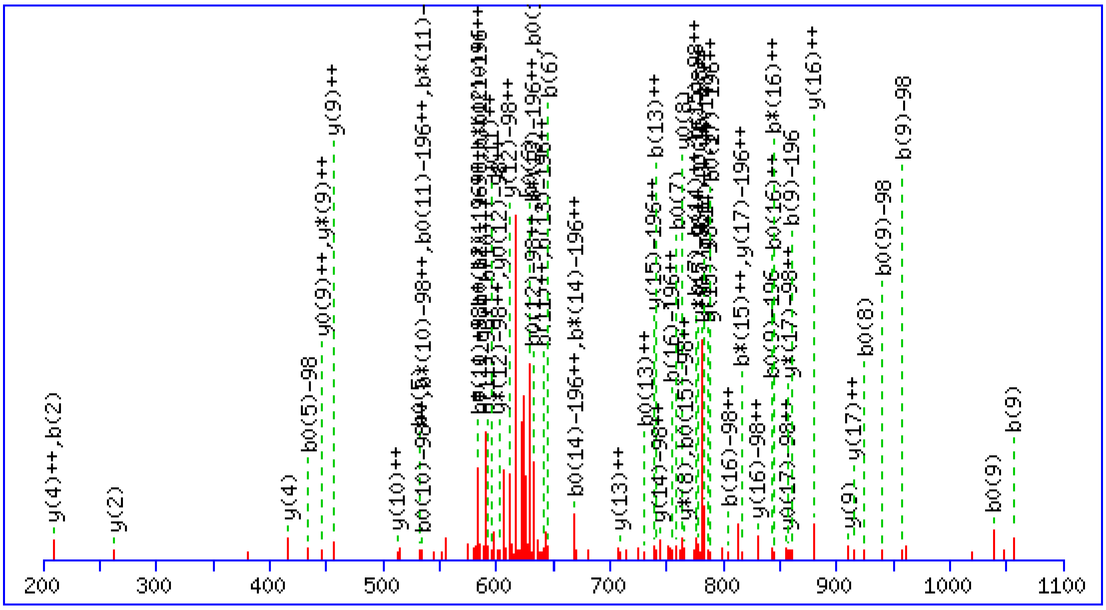
Monoisotopic mass of neutral peptide Mr(calc): 1964.8394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00087
Matched b ions: b(2), b(3)-98, b(5)-98, b(5), b(6)-98, b(7), b(8)-196, b(9)-98, b(9), b(9)-196, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(13)-196++, b(13)++, b(14)++, b(15)-98++, b(16)-196++
Matched y ions: y(4)++, y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++

Peptide No.389

HASSSPESLKPTPAPGSR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of **HASSSPESLKPTPAPGSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4868: 1964.839332 from(655.953720,3+) index(4248)
Title: Elution from: 21.131 to 21.131 scan no 1427 cid35.00 polarity:+:m1s



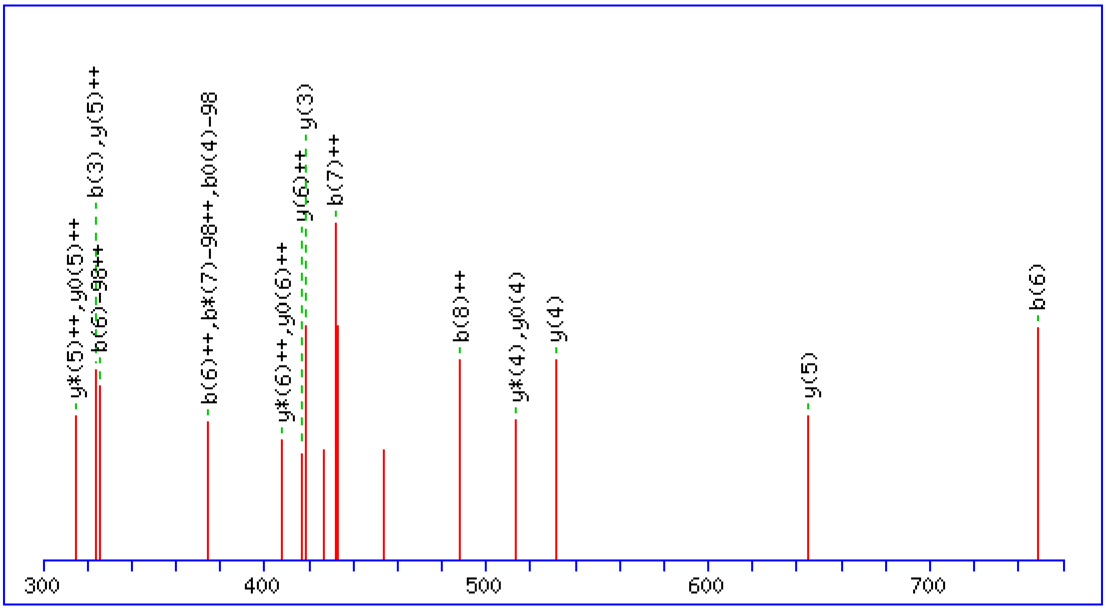
Monoisotopic mass of neutral peptide Mr(calc): 1964.8394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.015
Matched b ions: b(2), b(6), b(7), b(9), b(9)-98, b(9)-196, b(10)++, b(11)-98++, b(11)++, b(13)-196++, b(13)++, b(14)++, b(15)-98++, b(16)-196++, b(16)-98++
Matched y ions: y(2), y(4)++, y(4), y(6), y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)-98++, y(13)++, y(14)-98++, y(15)-196++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-196++

Peptide No.390

HGESAWNLENR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **HGESAWNLENR**
Found in **PGAM1_MOUSE** in **SwissProt**, Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3

Match to Query 2293: 1391.560836 from(464.860888,3+) index(4998)
Title: Elution from: 29.470 to 29.470 scan no 2527 cid35.00 polarity:+:m1s



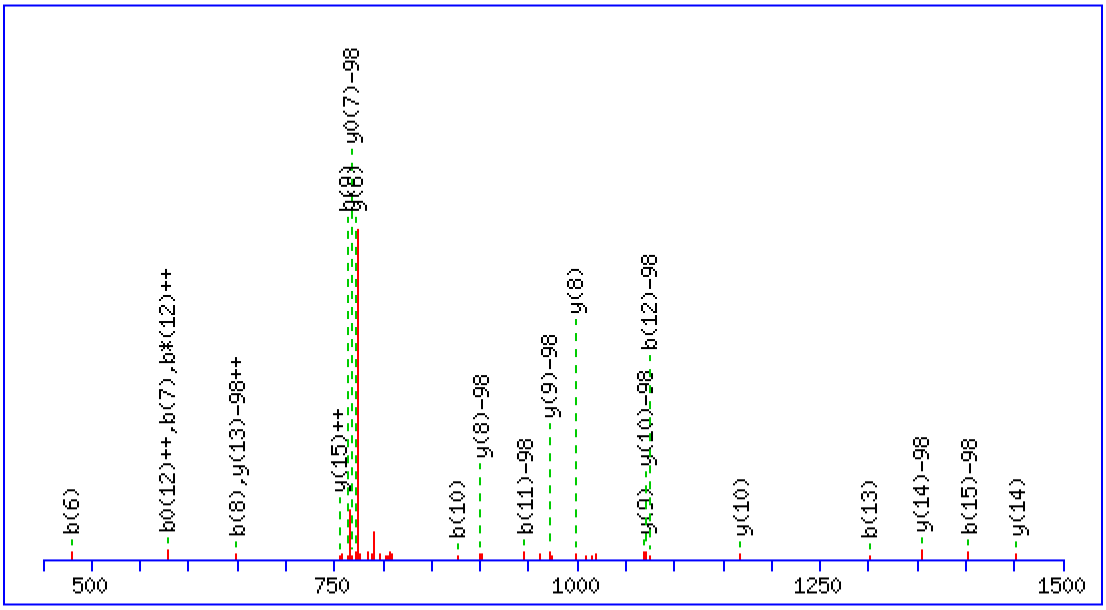
Monoisotopic mass of neutral peptide Mr(calc): 1391.5619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.014
Matched b ions: b(3), b(6), b(6)-98++, b(6)++, b(7)++, b(8)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++

Peptide No.391

HGGGGIVANLSEQSLK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **HGGGGIVANLSEQSLK**
Found in **PP1R7_MOUSE** in **SwissProt**, Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2

Match to Query 3379: 1645.782488 from(823.898520,2+) index(1899)
Title: Elution from: 33.886 to 33.886 scan no 3125 cid35.00 polarity:+



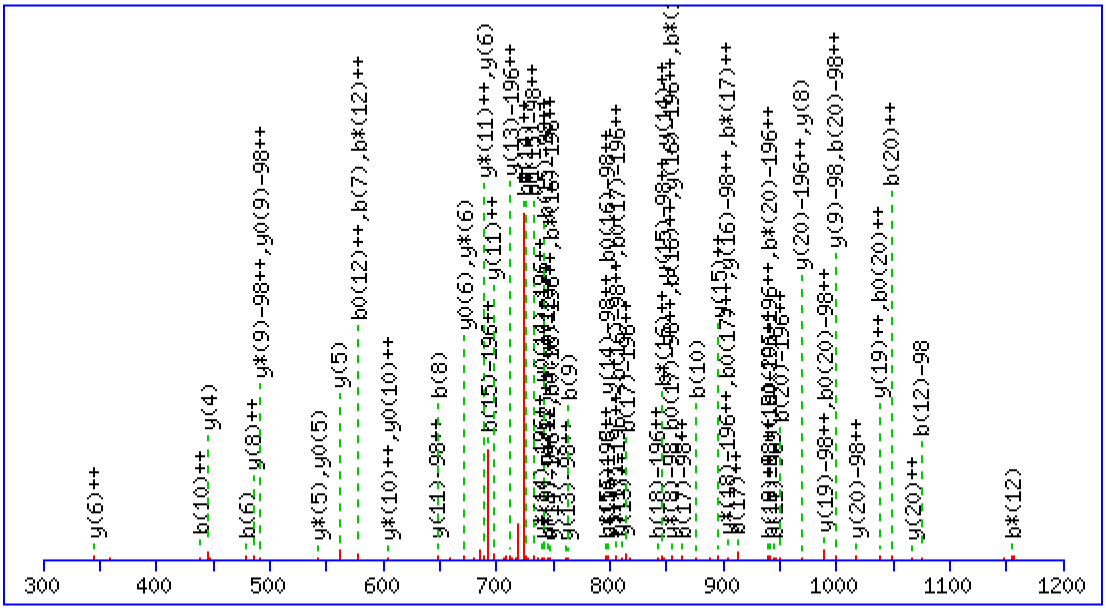
Monoisotopic mass of neutral peptide Mr(calc): 1645.7825
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 9.7e-005
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11)-98, b(12)-98, b(13), b(15)-98
Matched y ions: y(6), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(13)-98++, y(14)-98, y(14), y(15)++

Peptide No.392

HGGGGIVANLSEQSLKDGVDR
Confirmed sites: @S:11,@S:14
Ambiguous sites:

MS/MS Fragmentation of **HGGGGIVANLSEQSLKDGVDR**
Found in **PP1R7_MOUSE** in **SwissProt**, Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2

Match to Query 5771: 2267.992896 from(757.004908,3+) index(5660)
Title: Elution from: 36.123 to 36.123 scan no 3427 cid35.00 polarity:+:m1s



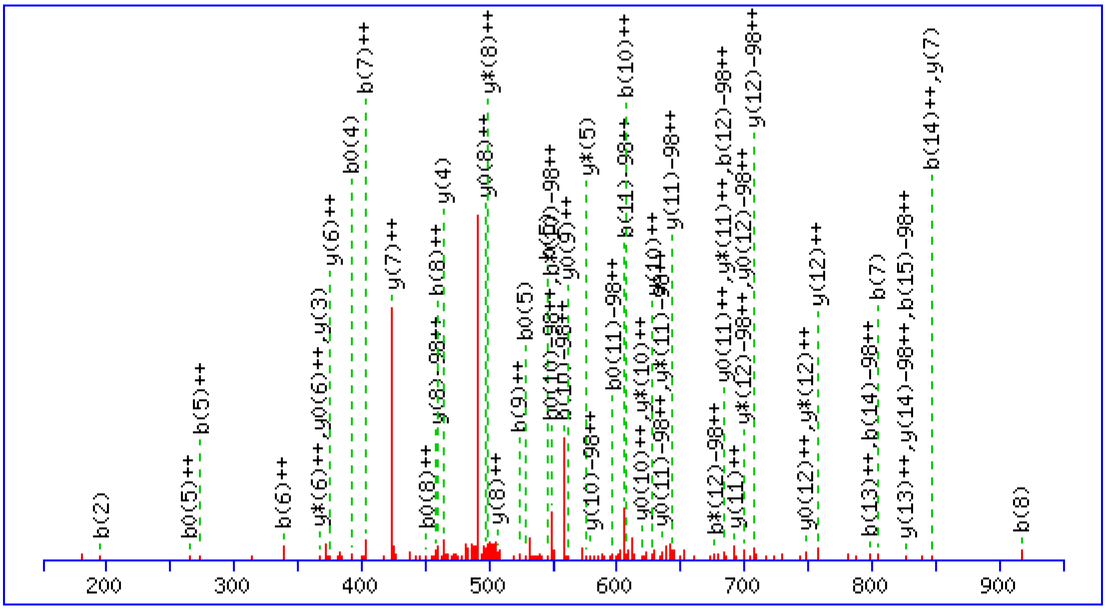
Monoisotopic mass of neutral peptide Mr(calc): 2267.9937
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.0006
Matched b ions: b(6), b(7), b(8), b(9), b(10)++, b(10), b(11)-98, b(12)-98, b(15)-196++, b(15)-98++, b(16)-98++, b(16)++, b(17)-196++, b(17)++, b(17)-98++, b(18)++, b(18)-196++, b(19)-98++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(4), y(5), y(6)++, y(6), y(8)++, y(8), y(9)-98, y(11)++, y(11)-98++, y(13)-196++, y(13)-98++, y(13)++, y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)++, y(15)-98++, y(16)-196++, y(16)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)++, y(20)-98++, y(20)-196++

Peptide No.393

HGLTHEELKSPREPGYK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **HGLTHEELKSPREPGYK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4557: 2056.973608 from(515.250678,4+) index(3234)
Title: Elution from: 27.066 to 27.066 scan no 1478 cid35.00 polarity:+:m1s



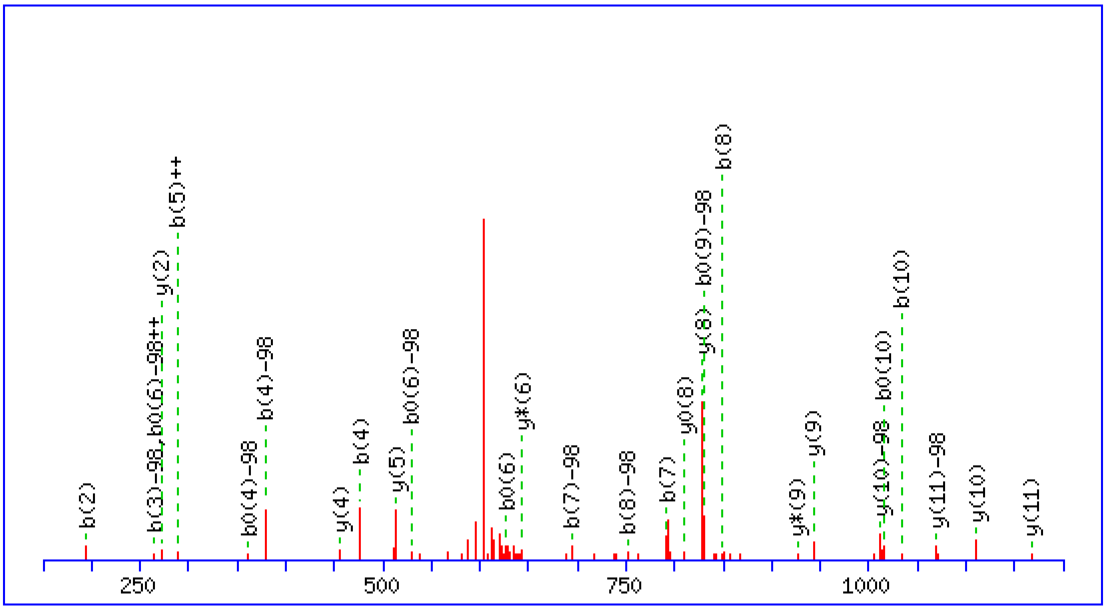
Monoisotopic mass of neutral peptide Mr(calc): 2056.9731
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 3.9e-005
Matched b ions: b(2), b(5)++, b(5), b(6)++, b(7)++, b(7), b(8), b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++
Matched y ions: y(3), y(4), y(6)++, y(7)++, y(7), y(8)-98++, y(8)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(14)-98++

Peptide No.394

HGSDPAFGPSPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **HGSDPAFGPSPR**
Found in **FA83H_MOUSE** in **SwissProt**, Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1

Match to Query 1984: 1303.532682 from(652.773617,2+) index(630)
Title: Elution from: 21.899 to 21.899 scan no 1495 cid35.00 polarity:+



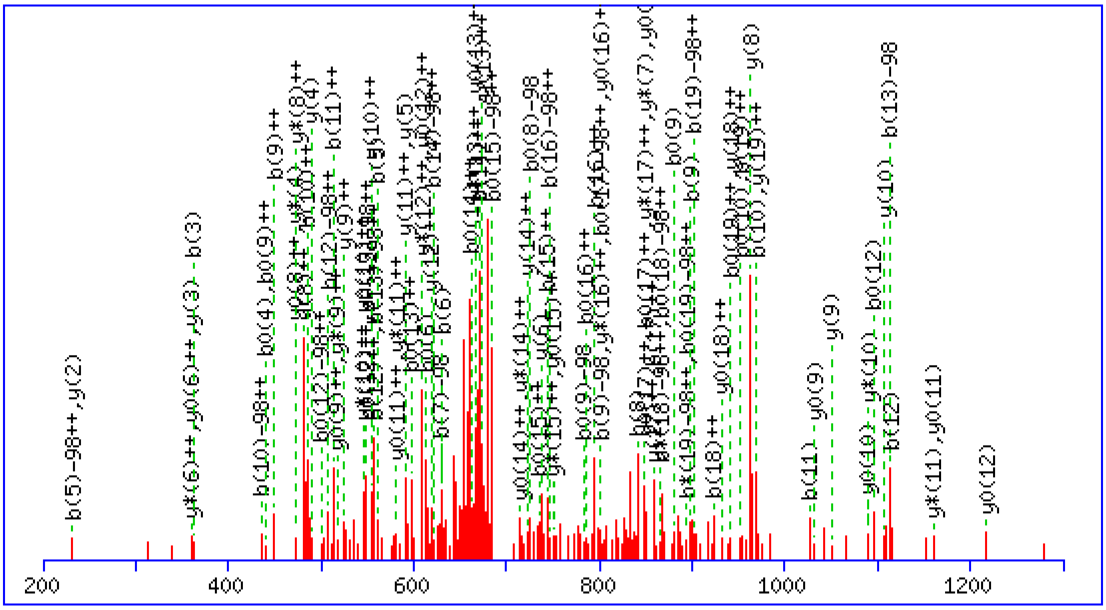
Monoisotopic mass of neutral peptide Mr(calc): 1303.5347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 5.6e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)++, b(7), b(7)-98, b(8)-98, b(8), b(10)
Matched y ions: y(2), y(4), y(5), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98

Peptide No.395

HGSPTAPIGAGSPEFTEQGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **HGSPTAPIGAGSPEFTEQGR**
Found in **PKHA7_MOUSE** in **SwissProt**, Pleckstrin homology domain-containing family A member 7 OS=Mus musculus GN=Plekha7 PE=1 SV=2

Match to Query 4590: 2074.912524 from(692.644784,3+) index(4312)
Title: Elution from: 40.349 to 40.349 scan no 3022 cid35.00 polarity:+:m1s



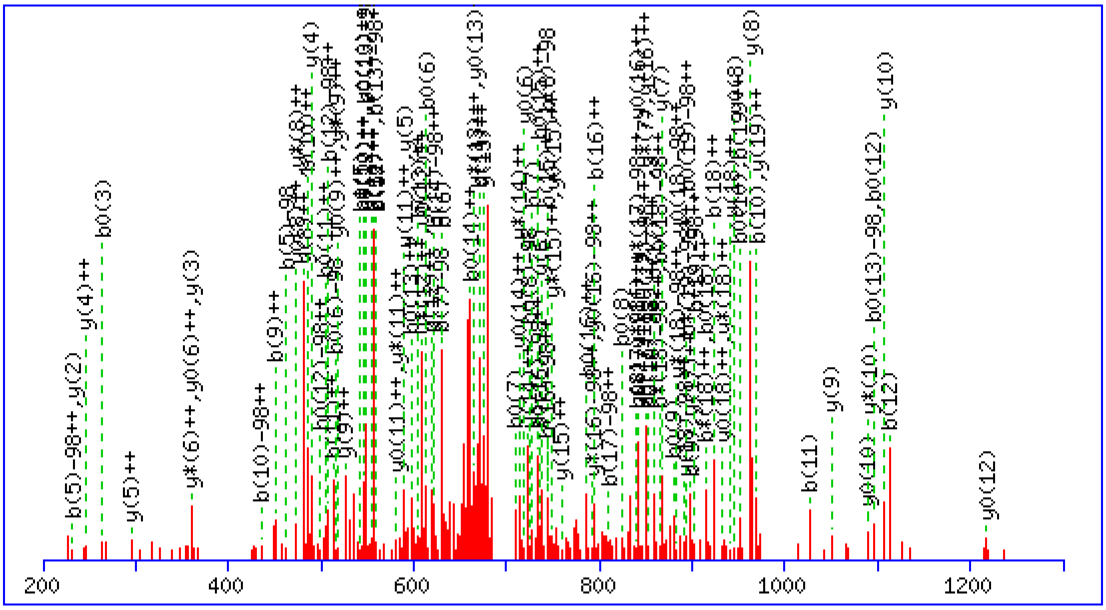
Monoisotopic mass of neutral peptide Mr(calc): 2074.9110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00011
Matched b ions: b(3), b(5)-98++, b(5), b(6), b(7)-98, b(8), b(9)++, b(9)-98, b(9), b(10)++, b(10), b(10)-98++, b(11)++, b(11), b(12), b(12)++, b(12)-98++, b(13)-98++, b(13)-98, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++, y(17)++, y(18)++, y(19)++

Peptide No.396

HGSPTAPIGAGSPEFTEQGR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **HGSPTAPIGAGSPEFTEQGR**
Found in **PKHA7_MOUSE** in **SwissProt**, Pleckstrin homology domain-containing family A member 7 OS=Mus musculus GN=Plekha7 PE=1 SV=2

Match to Query 5285: 2074.911708 from(692.644512,3+) index(4996)
Title: Elution from: 40.261 to 40.261 scan no 3155 cid35.00 polarity:+:m1s



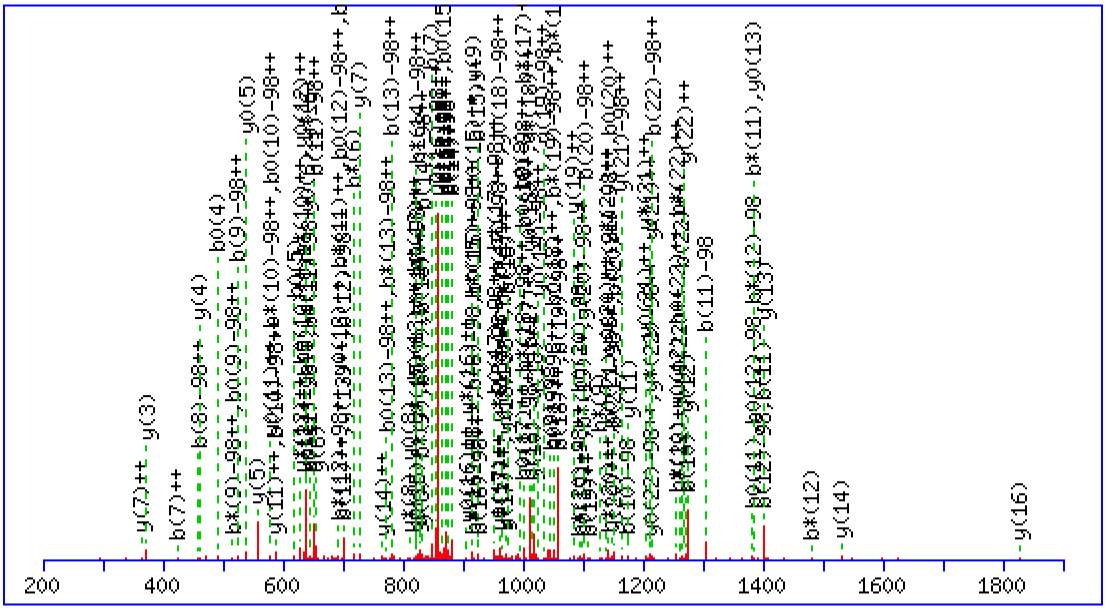
Monoisotopic mass of neutral peptide Mr(calc): 2074.9110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 6.6e-006
Matched b ions: b(5)-98++, b(5)-98, b(5), b(6), b(7)-98, b(7), b(8), b(8)-98, b(9)++, b(9), b(10)++, b(10), b(10)-98++, b(11), b(11)++, b(12)++, b(12), b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++

Peptide No.397

HIKEEPLSEEEPCTSTAVPSPEK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **HIKEEPLSEEEPCTSTAVPSPEK**
Found in **NOP58_MOUSE** in **SwissProt**, Nucleolar protein 58 OS=Mus musculus GN=Nop58 PE=1 SV=1

Match to Query 6429: 2673.186936 from(892.069588,3+) index(4851)
Title: Elution from: 38.366 to 38.366 scan no 2933 cid35.00 polarity:+:m1s



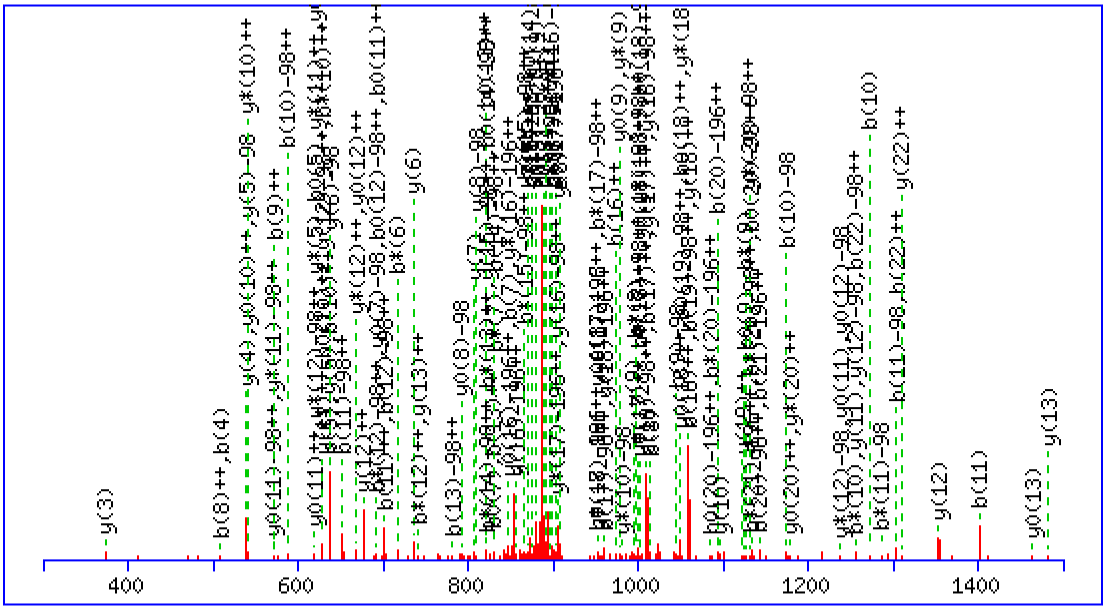
Monoisotopic mass of neutral peptide Mr(calc): 2673.1880
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 **Expect:** 4.9e-009
Matched b ions: b(5), b(7)++, b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11)++, b(11)-98, b(11), b(11)-98++, b(12)-98++, b(12)-98, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(22)-98++, b(22)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9), y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(13), y(14), y(14)++, y(16), y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)++

Peptide No.398

HIKEEPLSEEEPCTSTAVPSPEK
Confirmed sites: @S:8,@S:20
Ambiguous sites:

MS/MS Fragmentation of **HIKEEPLSEEEPCTSTAVPSPEK**
Found in **NOP58_MOUSE** in **SwissProt**, Nucleolar protein 58 OS=Mus musculus GN=Nop58 PE=1 SV=1

Match to Query 6485: 2753.155629 from(918.725819,3+) index(4962)
Title: Elution from: 39.805 to 39.805 scan no 3102 cid35.00 polarity:+:m1s



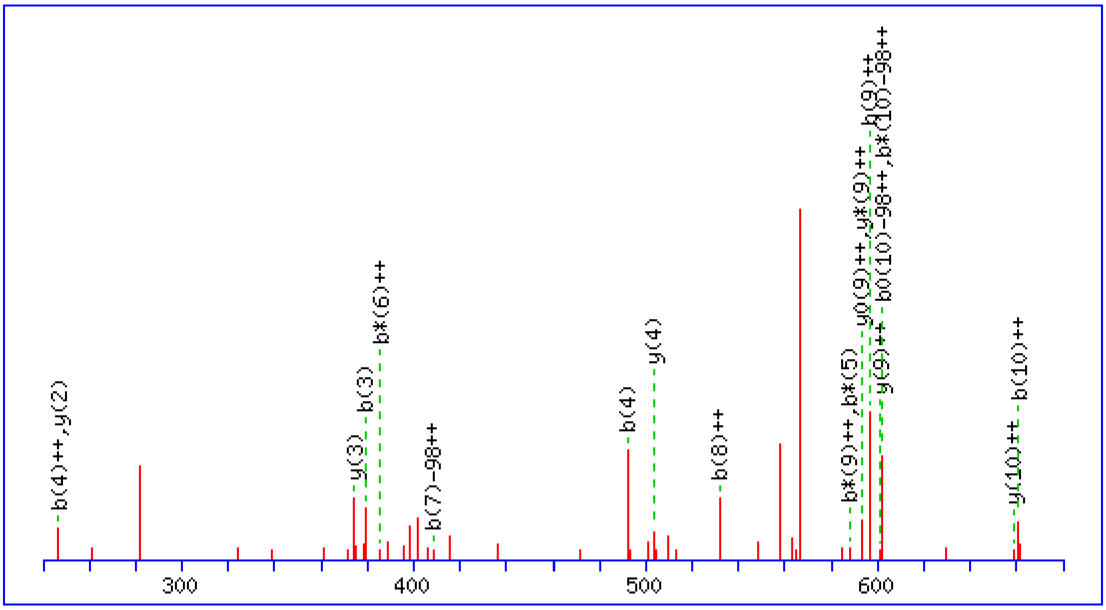
Monoisotopic mass of neutral peptide Mr(calc): 2753.1544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0018
Matched b ions: b(4), b(5), b(7), b(8)++, b(8), b(9)++, b(9)-98, b(10)++, b(10)-98, b(10), b(10)-98++, b(11), b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-196++, b(22)-98++, b(22)++
Matched y ions: y(3), y(4), y(5)-98, y(5), y(6), y(6)-98, y(7), y(8)-98, y(8), y(9)-98, y(9), y(10), y(11), y(11)++, y(12)++, y(12), y(12)-98, y(12)-98++, y(13), y(13)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(22)++

Peptide No.399

HLQILTEFKEKAR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **HLQILTEFKEKAR**
Found in **SPA3A_MOUSE** in **SwissProt**, Serine protease inhibitor A3A OS=Mus musculus GN=Serpina3a PE=2 SV=2

Match to Query 3607: 1691.877532 from(423.976659,4+) index(5148)
Title: Elution from: 31.265 to 31.265 scan no 2770 cid35.00 polarity:+:m1s



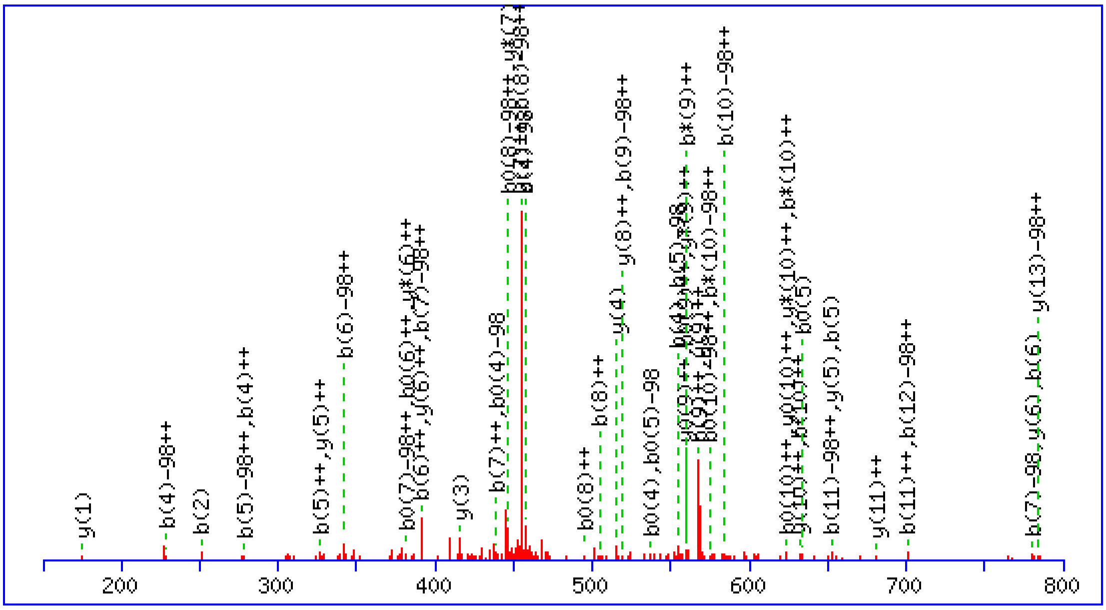
Monoisotopic mass of neutral peptide Mr(calc): 1691.8760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.025
Matched b ions: b(3), b(4), b(4)++, b(7)-98++, b(8)++, b(9)++, b(10)++
Matched y ions: y(2), y(3), y(4), y(9)++, y(10)++

Peptide No.400

HLSHPEPEQQHVIQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **HLSHPEPEQQHVIQR**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4847: 1913.891212 from(479.480079,4+) index(3764)
Title: Elution from: 26.757 to 26.757 scan no 1495 cid35.00 polarity:+:m1s



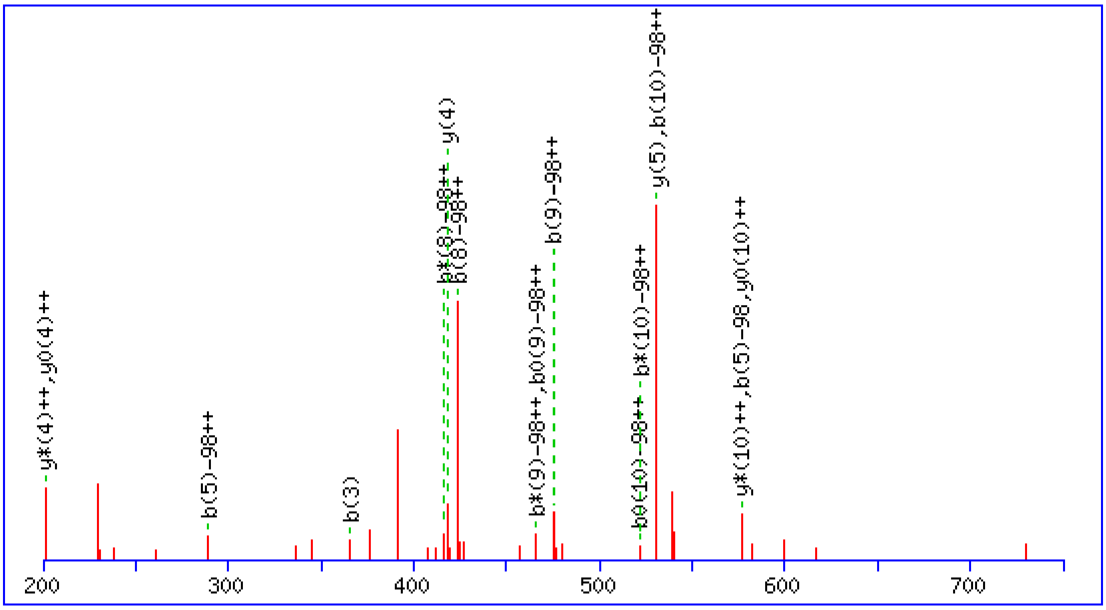
Monoisotopic mass of neutral peptide Mr(calc): 1913.8897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 7.4e-005
Matched b ions: b(2), b(4)-98++, b(4), b(4)-98, b(4)++, b(5), b(5)++, b(5)-98, b(5)-98++, b(6)-98++, b(6), b(6)++, b(7)-98, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)-98++
Matched y ions: y(1), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(13)-98++

Peptide No.401

HNLTKTLGTLK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **HNLTKTLGTLK**
Found in **E2F8_MOUSE** in **SwissProt**, Transcription factor E2F8 OS=Mus musculus GN=E2f8 PE=1 SV=1

Match to Query 2006: 1304.684133 from(435.901987,3+) index(5956)
Title: Elution from: 39.310 to 39.310 scan no 3849 cid35.00 polarity:+:m1s



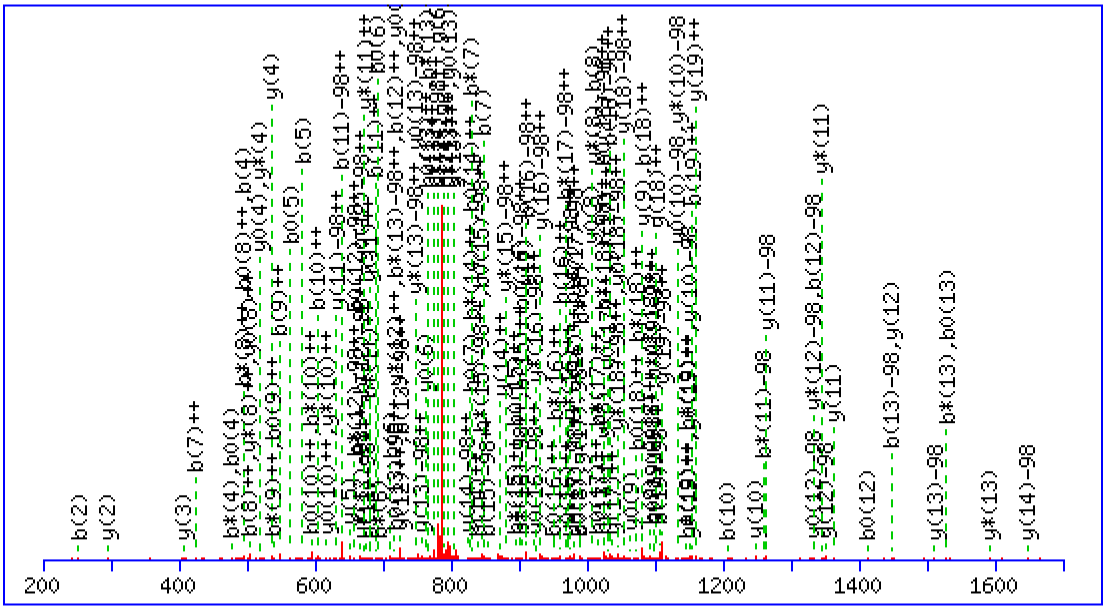
Monoisotopic mass of neutral peptide Mr(calc): 1304.6853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.037
Matched b ions: b(3), b(5)-98++, b(5)-98, b(8)-98++, b(9)-98++, b(10)-98++
Matched y ions: y(4), y(5)

Peptide No.402

HNQDSQHCSLSGDEEDELFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **HNQDSQHCSLSGDEEDELFK**
Found in **FKB15_MOUSE** in **SwissProt**, FK506-binding protein 15 OS=Mus musculus GN=Fkbp15 PE=1 SV=2

Match to Query 6167: 2453.941833 from(818.987887,3+) index(5213)
Title: Elution from: 43.362 to 43.362 scan no 3506 cid35.00 polarity:+:m1s



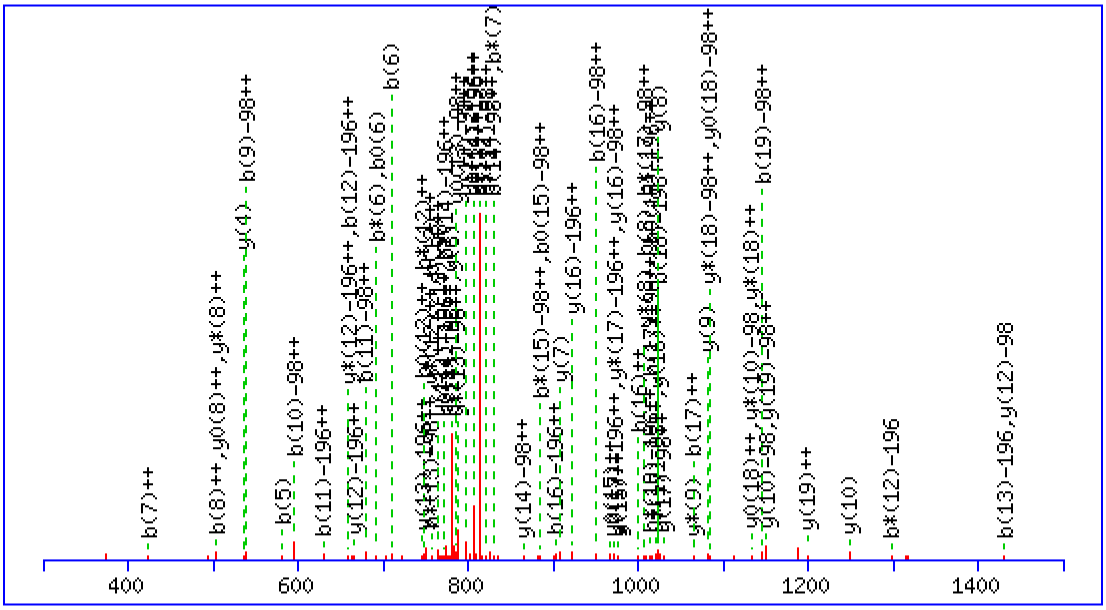
Monoisotopic mass of neutral peptide Mr(calc): 2453.9431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 **Expect:** 4.7e-008
Matched b ions: b(2), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(11)++, b(12)-98++, b(12)-98, b(12)++, b(13)-98++, b(13)-98, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12), y(12)-98++, y(13)-98, y(13)-98++, y(13)++, y(14)-98, y(14)++, y(14)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++

Peptide No.403

HNQDSQHCSLSGDEEDELFK
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of **HNQDSQHCSLSGDEEDELFK**
Found in **FKB15_MOUSE** in **SwissProt**, FK506-binding protein 15 OS=Mus musculus GN=Fkbp15 PE=1 SV=2

Match to Query 6444: 2533.906785 from(845.642871,3+) index(5968)
Title: Elution from: 37.719 to 37.719 scan no 3666 cid35.00 polarity:+:m1s



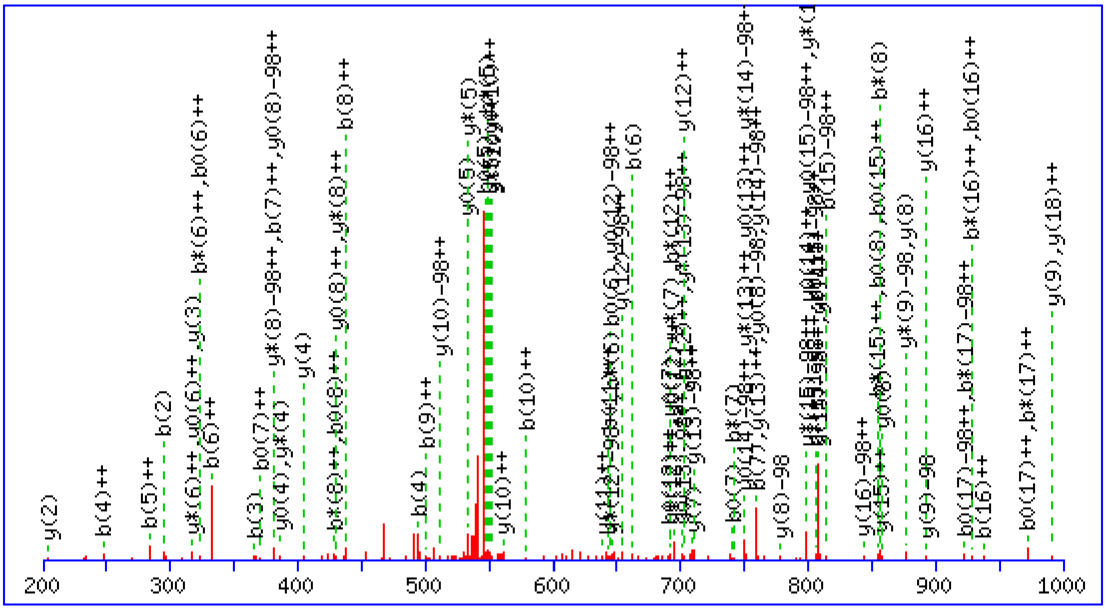
Monoisotopic mass of neutral peptide Mr(calc): 2533.9094
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00023
Matched b ions: b(5), b(6), b(7)++, b(8)++, b(8), b(9)-98++, b(10)-98++, b(11)-196++, b(11)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-196, b(13)-98++, b(14)-196++, b(14)-98++, b(16)-98++, b(16)-196++, b(16)++, b(17)-98++, b(17)++, b(18)-196++, b(19)-98++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(12)-98, y(12)++, y(12)-196++, y(13)-98++, y(13)-196++, y(14)-98++, y(15)++, y(16)-196++, y(16)++, y(16)-98++, y(17)-98++, y(19)-98++, y(19)++

Peptide No.404

HRAEAPPLQREDSGTFSLGK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **HRAEAPPLQREDSGTFSLGK**
Found in **PRKRA_MOUSE** in **SwissProt**, Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1

Match to Query 5785: 2275.073216 from(569.775580,4+) index(5046)
Title: Elution from: 30.116 to 30.116 scan no 2616 cid35.00 polarity:+:m1s



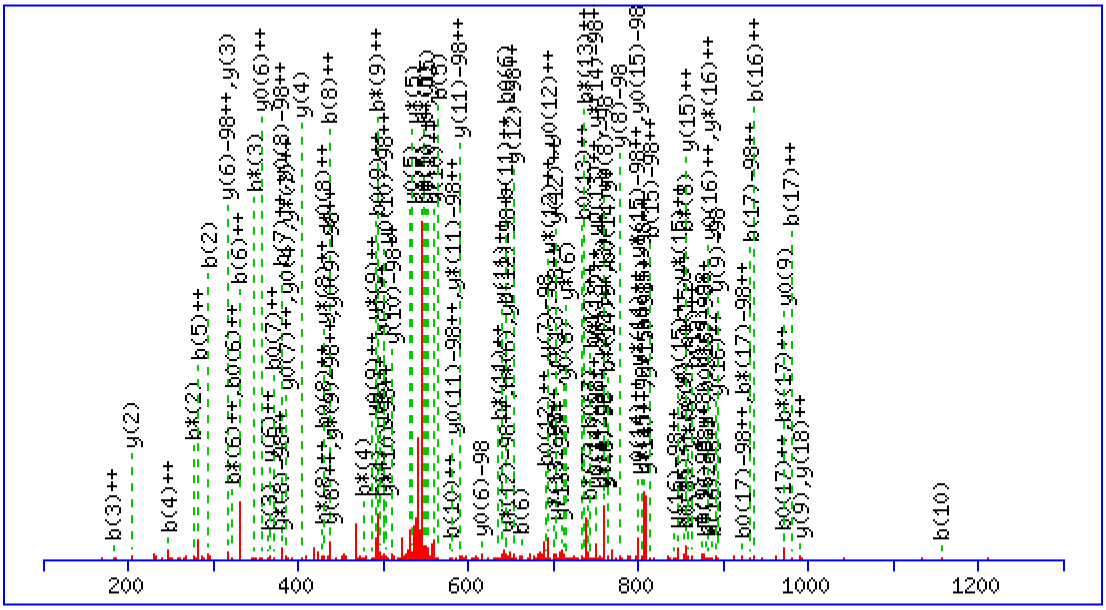
Monoisotopic mass of neutral peptide Mr(calc): 2275.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0023
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)++, b(6)++, b(6), b(7), b(7)++, b(8)++, b(9)++, b(10)++, b(11)++, b(12)++, b(15)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(18)++

Peptide No.405

HRAEAPPLQREDSGTFSLGK
Confirmed sites: @T:15
Ambiguous sites:

MS/MS Fragmentation of **HRAEAPPLQREDSGTFSLGK**
Found in **PRKRA_MOUSE** in **SwissProt**, Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Mus musculus GN=Prkra PE=1 SV=1

Match to Query 4947: 2275.076256 from(569.776340,4+) index(4149)
Title: Elution from: 37.927 to 37.927 scan no 2755 cid35.00 polarity:+:m1s



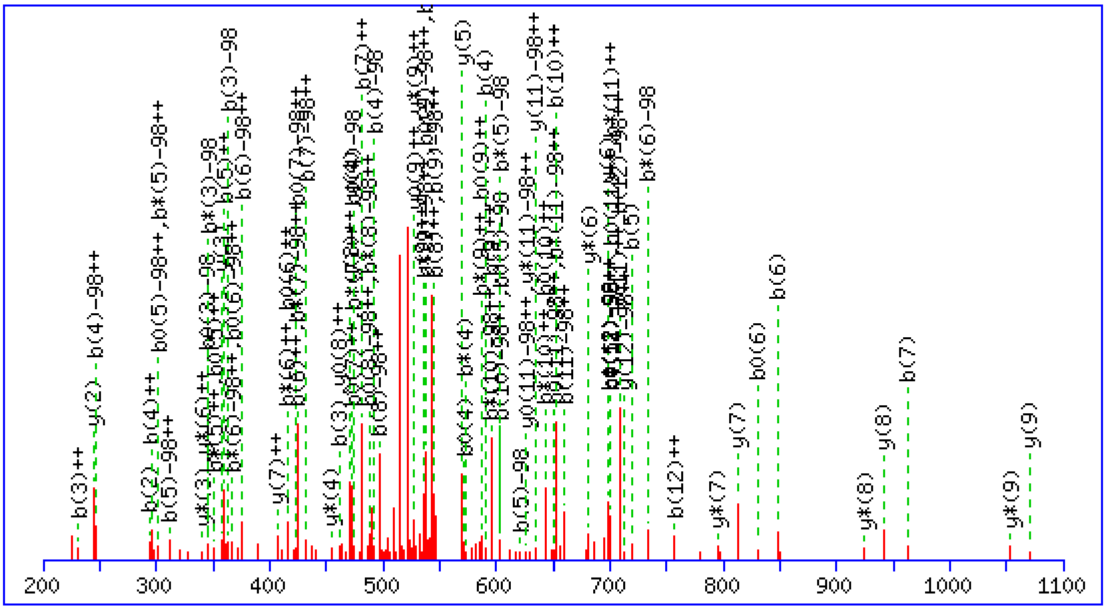
Monoisotopic mass of neutral peptide Mr(calc): 2275.0746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.003
Matched b ions: b(2), b(3)++, b(3), b(4)++, b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(9)++, b(10), b(10)++, b(11)++, b(13)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98++, y(6)++, y(7)-98, y(8), y(8)-98, y(8)++, y(9), y(9)++, y(9)-98, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(18)++

Peptide No.406

HRSEEENQVNLPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **HRSEEENQVNLPK**
Found in **GCH1_MOUSE** in **SwissProt**, GTP cyclohydrolase 1 OS=Mus musculus GN=Gch1 PE=2 SV=1

Match to Query 3455: 1658.738970 from(553.920266,3+) index(437)
Title: Elution from: 20.341 to 20.341 scan no 1284 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1658.7413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 66 **Expect:** 1.2e-006
Matched b ions: b(2), b(3)++, b(3)-98, b(3), b(4)-98++, b(4)++, b(4)-98, b(4), b(5)++, b(5)-98++, b(5)-98, b(5), b(6)++, b(6), b(6)-98++, b(7), b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(11)-98++, y(12)-98++

Peptide No.407

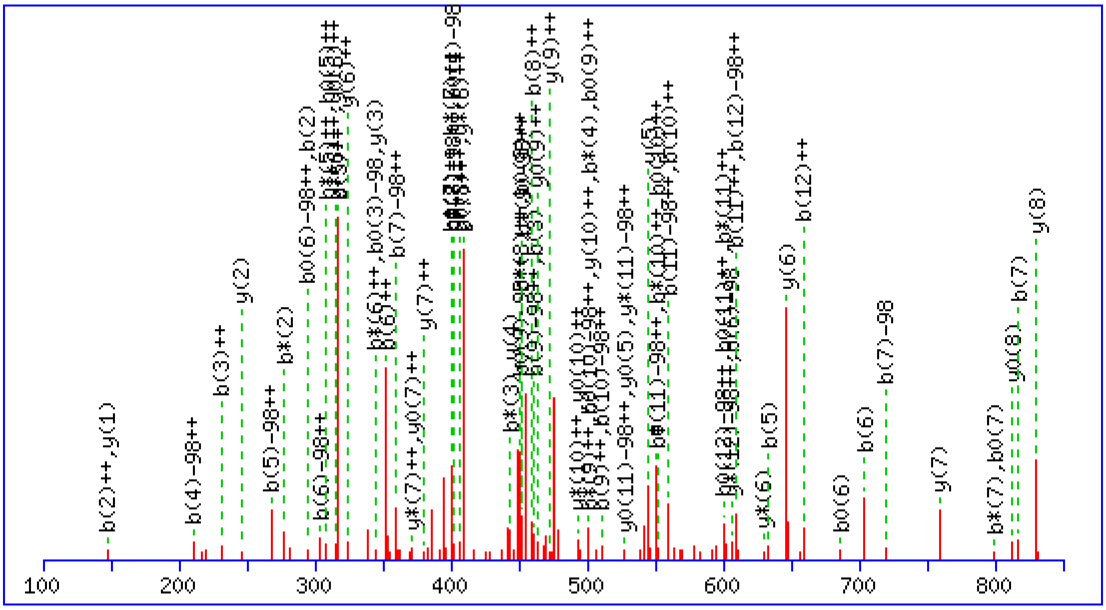
HRSGDALTTVVVK

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **HRSGDALTTVVVK**
Found in **SNIP1_MOUSE** in **SwissProt**, Smad nuclear-interacting protein 1 OS=Mus musculus GN=Snip1 PE=1 SV=1

Match to Query 2455: 1461.733695 from(488.251841,3+) index(724)
Title: Elution from: 24.725 to 24.725 scan no 1757 cid35.00 polarity:+



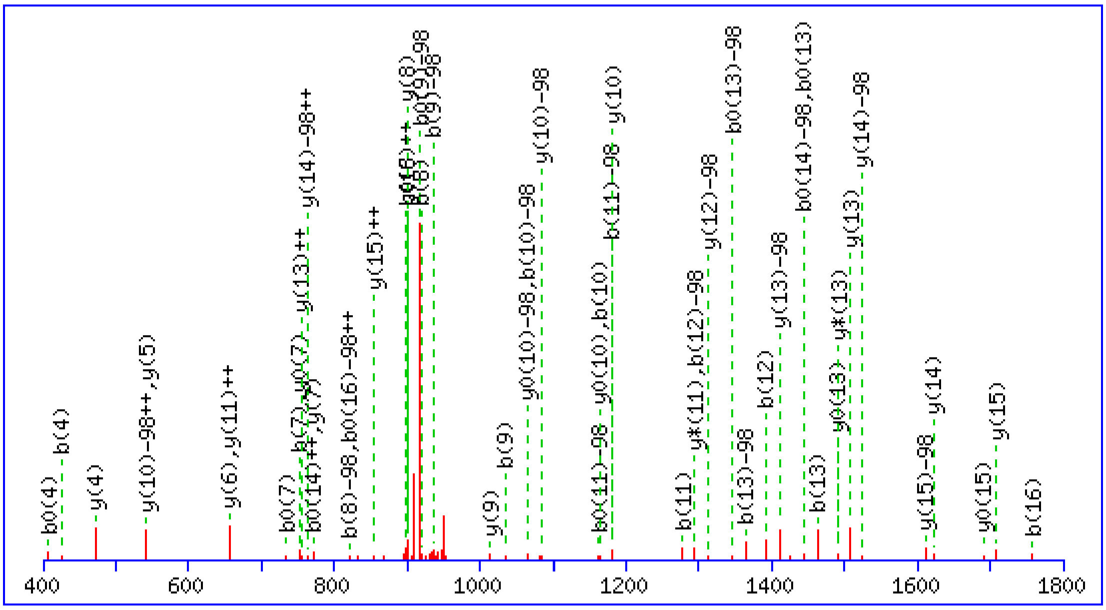
Monoisotopic mass of neutral peptide Mr(calc): 1461.7341
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 1.6e-005
Matched b ions: b(2)++, b(2), b(3)++, b(3), b(4)-98++, b(5)++, b(5)-98++, b(5), b(6), b(6)++, b(6)-98++, b(6)-98, b(7)++, b(7), b(7)-98, b(7)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(9)++, y(10)++

Peptide No.408

HSSLPTESDEDIAPAQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **HSSLPTESDEDIAPAQR**
Found in **AP3D1_MOUSE** in **SwissProt**, AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1

Match to Query 4737: 1931.824232 from(966.919392,2+) index(1512)
Title: Elution from: 29.368 to 29.368 scan no 2550 cid35.00 polarity:+



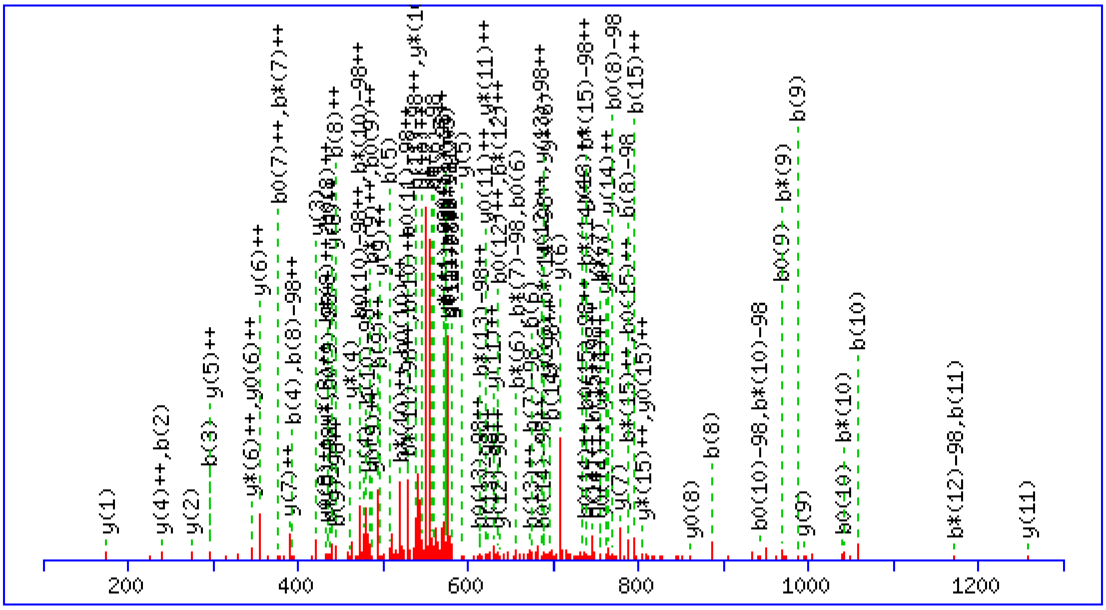
Monoisotopic mass of neutral peptide Mr(calc): 1931.8262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 **Expect:** 6.8e-010
Matched b ions: b(4), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13), b(13)-98, b(16)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(10)-98, y(11)++, y(12)-98, y(13), y(13)-98, y(13)++, y(14)-98, y(14), y(14)-98++, y(15)-98, y(15), y(15)++, y(16)++

Peptide No.409

HTGPNSPDTANDGFVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **HTGPNSPDTANDGFVR**
Found in **HNRH1_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3

Match to Query 4443: 1763.727231 from(588.916353,3+) index(4097)
Title: Elution from: 30.357 to 30.357 scan no 1932 cid35.00 polarity:+:m1s



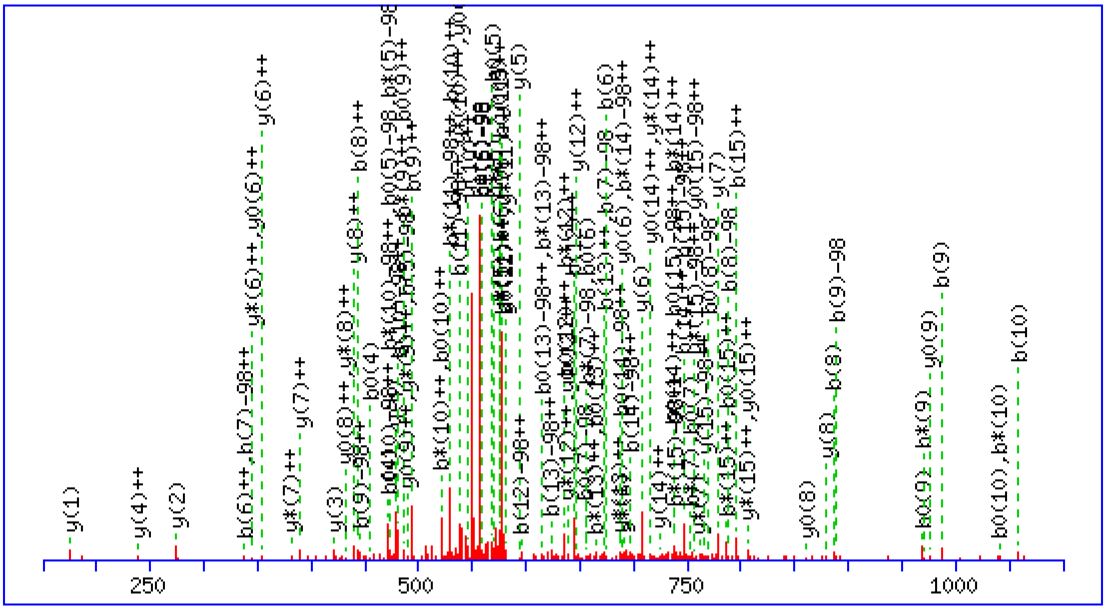
Monoisotopic mass of neutral peptide Mr(calc): 1763.7265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00026
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(9), b(10), b(10)++, b(10)-98++, b(11), b(11)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(9), y(9)++, y(10)++, y(11), y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++

Peptide No.410

HTGPNSPDTANDGFVR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of **HTGPNSPDTANDGFVR**
Found in **HNRH1_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3

Match to Query 4444: 1763.729079 from(588.916969,3+) index(4194)
Title: Elution from: 31.374 to 31.374 scan no 2061 cid35.00 polarity:+:m1s



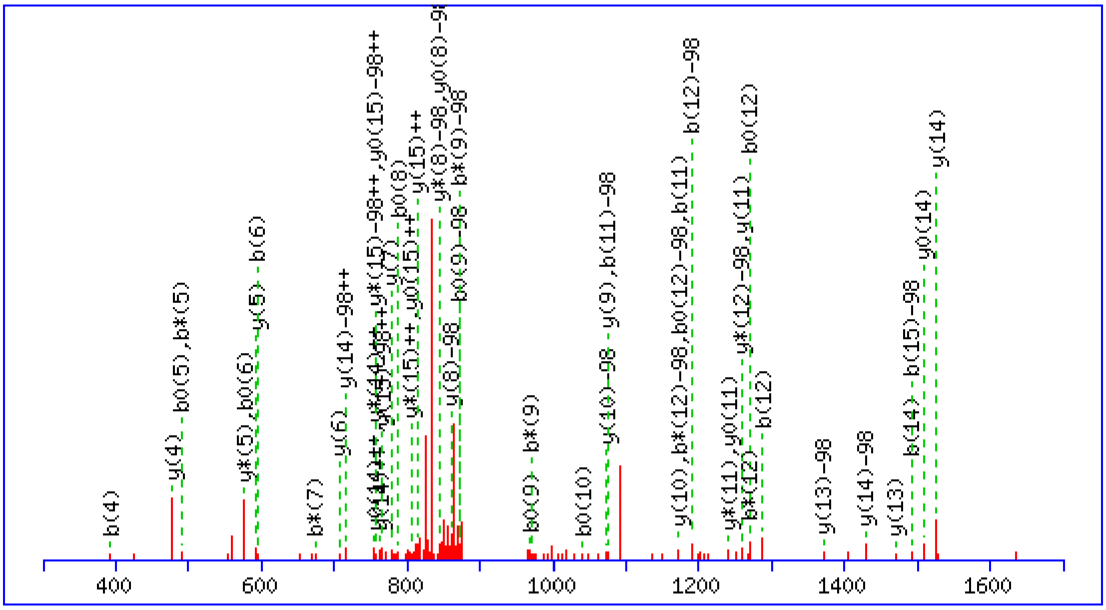
Monoisotopic mass of neutral peptide Mr(calc): 1763.7265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00035
Matched b ions: b(4), b(5)-98, b(6)++, b(6)-98, b(6), b(7)-98++, b(7)-98, b(8), b(8)++, b(8)-98, b(9), b(9)-98, b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(10)++, y(12)++, y(14)++, y(15)-98++

Peptide No.411

HTGPNSPDTANDGFVR
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **HTGPNSPDTANDGFVR**
Found in **HNRH1_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3

Match to Query 4442: 1763.724228 from(882.869390,2+) index(787)
Title: Elution from: 31.463 to 31.463 scan no 2071 cid35.00 polarity:+



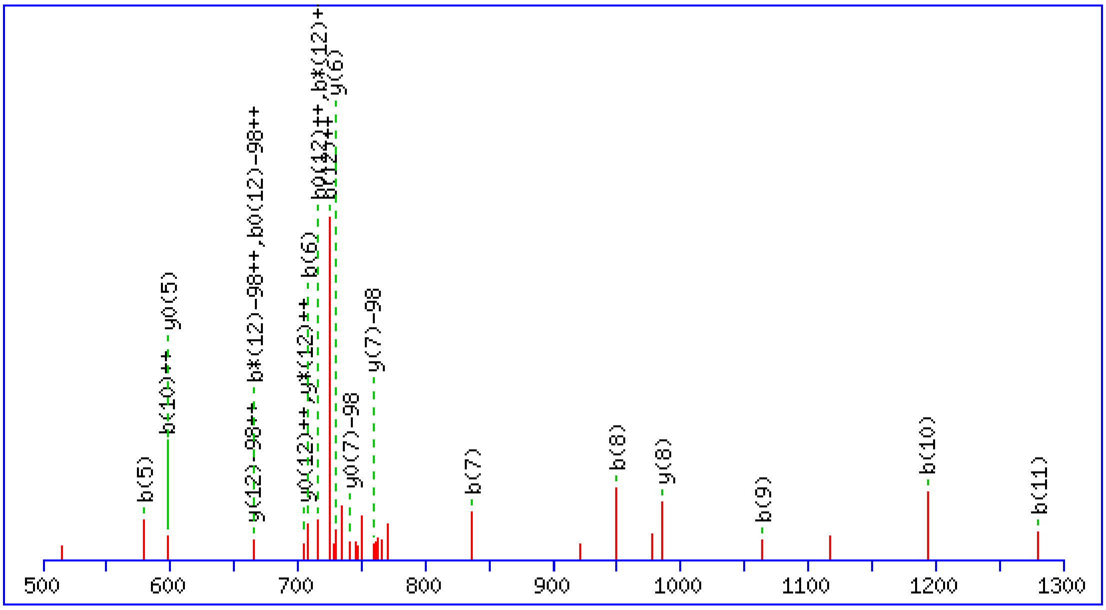
Monoisotopic mass of neutral peptide Mr(calc): 1763.7265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.00068
Matched b ions: b(4), b(6), b(11), b(11)-98, b(12)-98, b(12), b(14), b(15)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10), y(10)-98, y(11), y(13)-98, y(13), y(14)-98++, y(14)-98, y(14), y(14)++, y(15)-98++, y(15)++

Peptide No.412

HTQLVEQLDESSV
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **HTQLVEQLDESSV**
Found in **SEM4G_MOUSE** in **SwissProt**, Semaphorin-4G OS=Mus musculus GN=Sema4g PE=1 SV=1

Match to Query 2687: 1563.681298 from(782.847925,2+) index(2111)
Title: Elution from: 38.141 to 38.141 scan no 3594 cid35.00 polarity:+



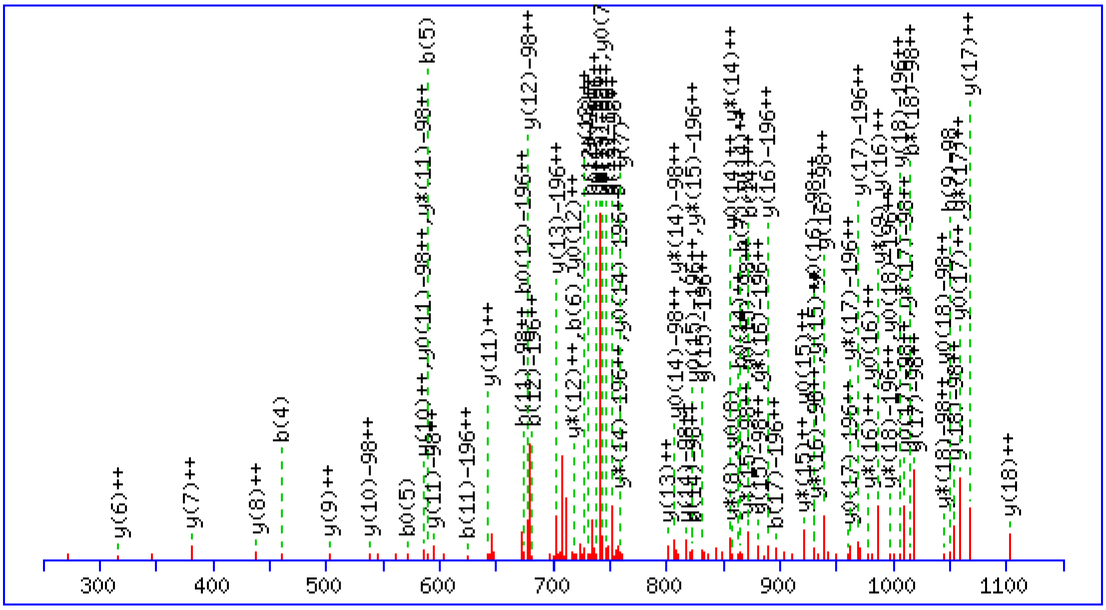
Monoisotopic mass of neutral peptide Mr(calc): 1563.6818
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 **Expect:** 5.8e-007
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(11), b(12)++
Matched y ions: y(6), y(7)-98, y(8), y(12)-98++

Peptide No.413

IACDEEFSDSEDEGEGGRR
Confirmed sites: @S:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of **IACDEEFSDSEDEGEGGRR**
Found in **HDAC2_MOUSE** in **SwissProt**, Histone deacetylase 2 OS=Mus musculus GN=Hdac2 PE=1 SV=1

Match to Query 5035: 2316.784224 from(773.268684,3+) index(4195)
Title: Elution from: 26.706 to 26.706 scan no 2124 cid35.00 polarity:+:m1s



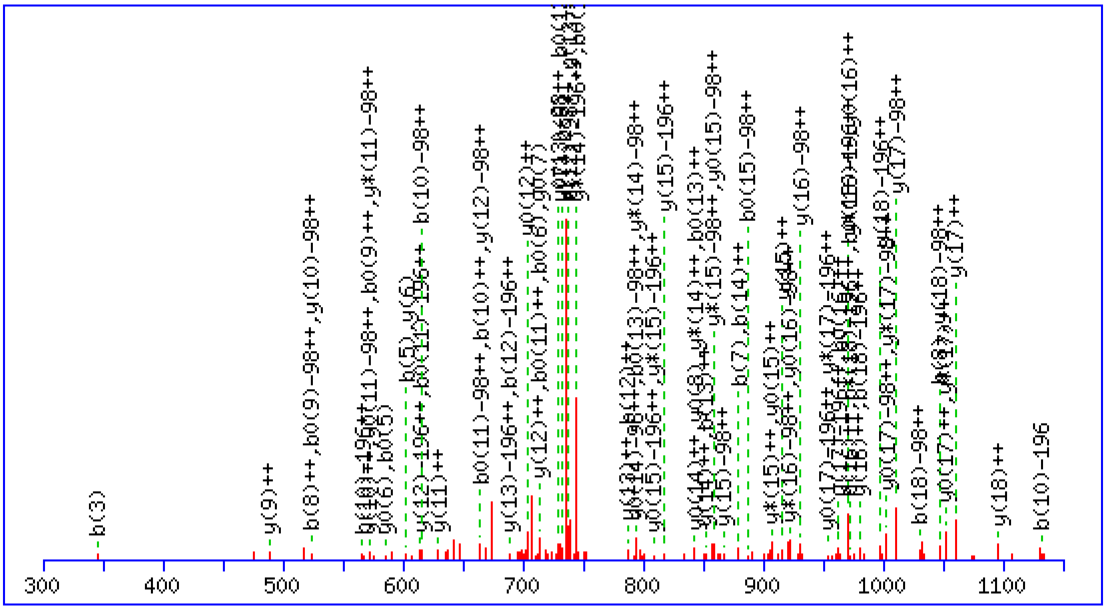
Monoisotopic mass of neutral peptide Mr(calc): 2316.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.008
Matched b ions: b(4), b(5), b(6), b(7), b(9)-98, b(11)-196++, b(11)-98++, b(12)-196++, b(12)-98++, b(13)-196++, b(14)-98++, b(14)++, b(17)-196++
Matched y ions: y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(13)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)-196++, y(15)++, y(16)-98++, y(16)++, y(16)-196++, y(17)-98++, y(17)-196++, y(17)++, y(18)++, y(18)-98++, y(18)-196++

Peptide No.414

IACEEEFSDSDEEGEGGRK
Confirmed sites: @S:8,@S:10
Ambiguous sites:

MS/MS Fragmentation of **IACEEEFSDSDEEGEGGRK**
Found in **HDAC1_MOUSE** in **SwissProt**, Histone deacetylase 1 OS=Mus musculus GN=Hdac1 PE=1 SV=1

Match to Query 5009: 2302.795197 from(768.605675,3+) index(4164)
Title: Elution from: 26.445 to 26.445 scan no 2088 cid35.00 polarity:+:m1s



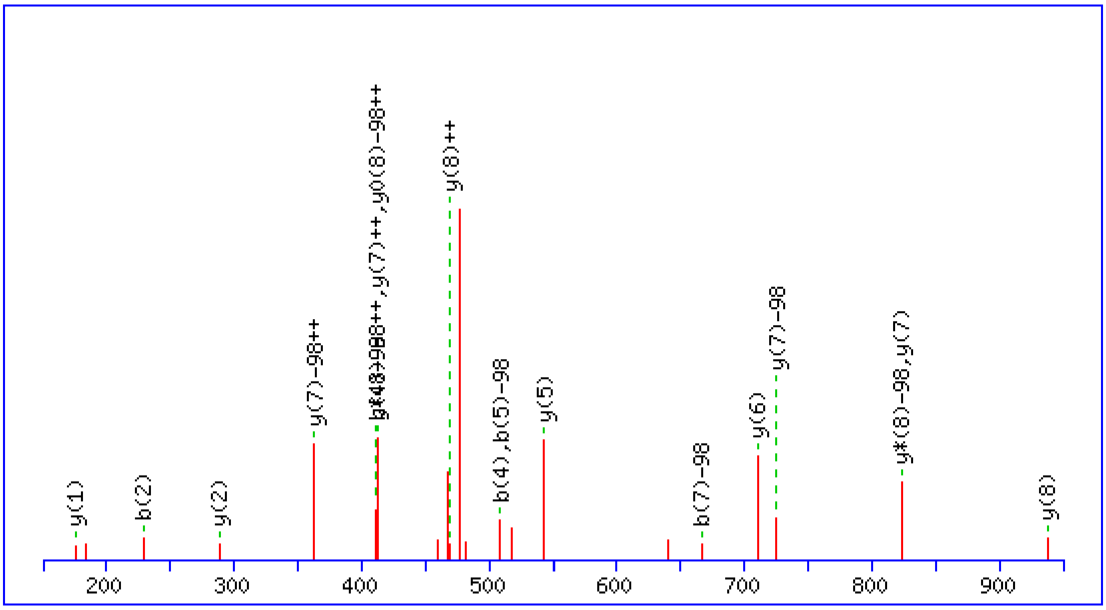
Monoisotopic mass of neutral peptide Mr(calc): 2302.7974
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.049
Matched b ions: b(3), b(5), b(6), b(7), b(8)++, b(8), b(10)-98++, b(10)-196, b(10)-196++, b(10)++, b(12)++, b(12)-98++, b(12)-196++, b(13)++, b(14)++, b(16)++, b(18)-196++, b(18)-98++
Matched y ions: y(6), y(7), y(9)++, y(10)-98++, y(10)++, y(11)++, y(12)-196++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++, y(14)++, y(15)++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++

Peptide No.415

IDISPSALR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **IDISPSALR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 888: 1050.511496 from(526.263024,2+) index(2248)
Title: Elution from: 39.844 to 39.844 scan no 3802 cid35.00 polarity:+



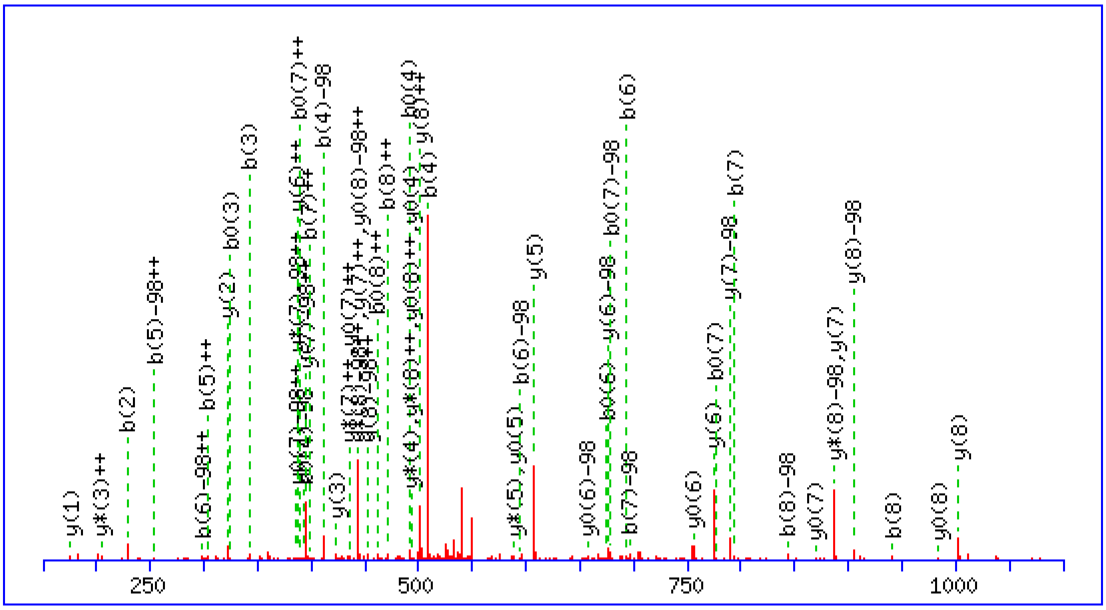
Monoisotopic mass of neutral peptide Mr(calc): 1050.5110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00071
Matched b ions: b(2), b(4)-98, b(4), b(5)-98, b(7)-98
Matched y ions: y(1), y(2), y(5), y(6), y(7)-98++, y(7)++, y(7), y(7)-98, y(8), y(8)++

Peptide No.416

IDISPSTFR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **IDISPSTFR**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 1734: 1114.506382 from(558.260467,2+) index(2245)
Title: Elution from: 51.476 to 51.476 scan no 4318 cid35.00 polarity:+



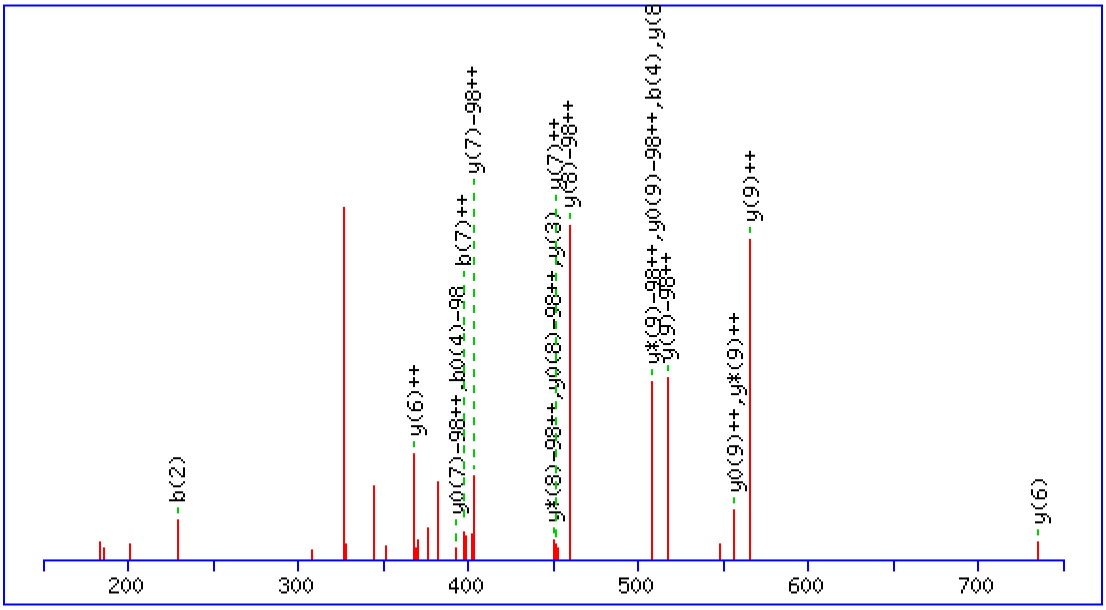
Monoisotopic mass of neutral peptide Mr(calc): 1114.5060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00017
Matched b ions: b(2), b(3), b(4), b(4)-98, b(5)-98++, b(5)++, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(7)++, b(8)-98, b(8)++, b(8)
Matched y ions: y(1), y(2), y(3), y(5), y(6), y(6)-98, y(6)++, y(7)++, y(7)-98, y(7), y(7)-98++, y(8), y(8)-98, y(8)-98++, y(8)++

Peptide No.417

IDISPSTFRK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **IDISPSTFRK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 1650: 1242.602412 from(415.208080,3+) index(1658)
Title: Elution from: 34.354 to 34.354 scan no 3075 cid35.00 polarity:+



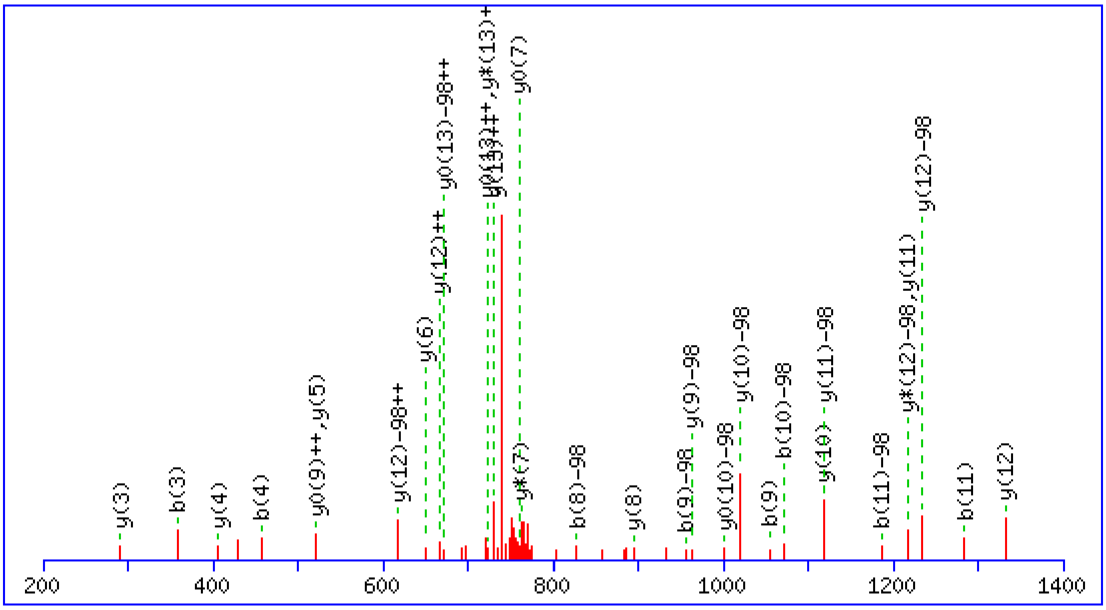
Monoisotopic mass of neutral peptide Mr(calc): 1242.6009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.033
Matched b ions: b(2), b(4), b(5)-98, b(7)++
Matched y ions: y(3), y(6), y(6)++, y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++

Peptide No.418

IEDVGSDEEDDSGK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **IEDVGSDEEDDSGK**
Found in **HS90B_MOUSE** in **SwissProt**, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3

Match to Query 3317: 1573.566150 from(787.790351,2+) index(665)
Title: Elution from: 21.696 to 21.696 scan no 1503 cid35.00 polarity:+



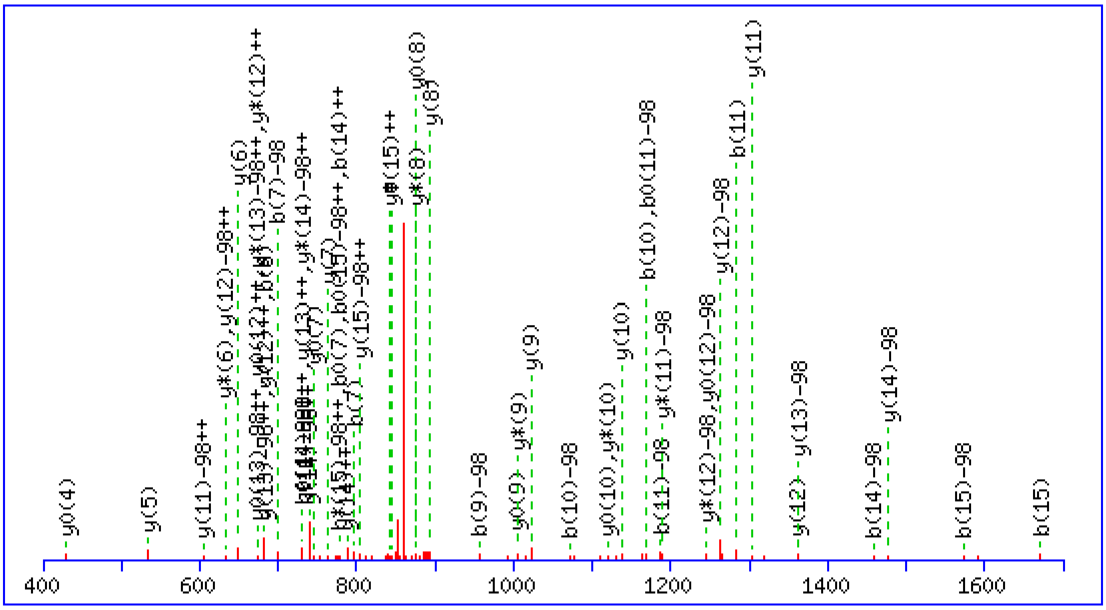
Monoisotopic mass of neutral peptide Mr(calc): 1573.5669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 1.2e-007
Matched b ions: b(3), b(4), b(8)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)-98, y(10)-98, y(10), y(11)-98, y(11), y(12)-98++, y(12)-98, y(12), y(12)++, y(13)++

Peptide No.419

IEDVGSDEEDDSGKDK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **IEDVGSDEEDDSGKDK**
Found in **HS90B_MOUSE** in **SwissProt**, Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=3

Match to Query 4271: 1816.684676 from(909.349614,2+) index(421)
Title: Elution from: 19.677 to 19.677 scan no 1231 cid35.00 polarity:+



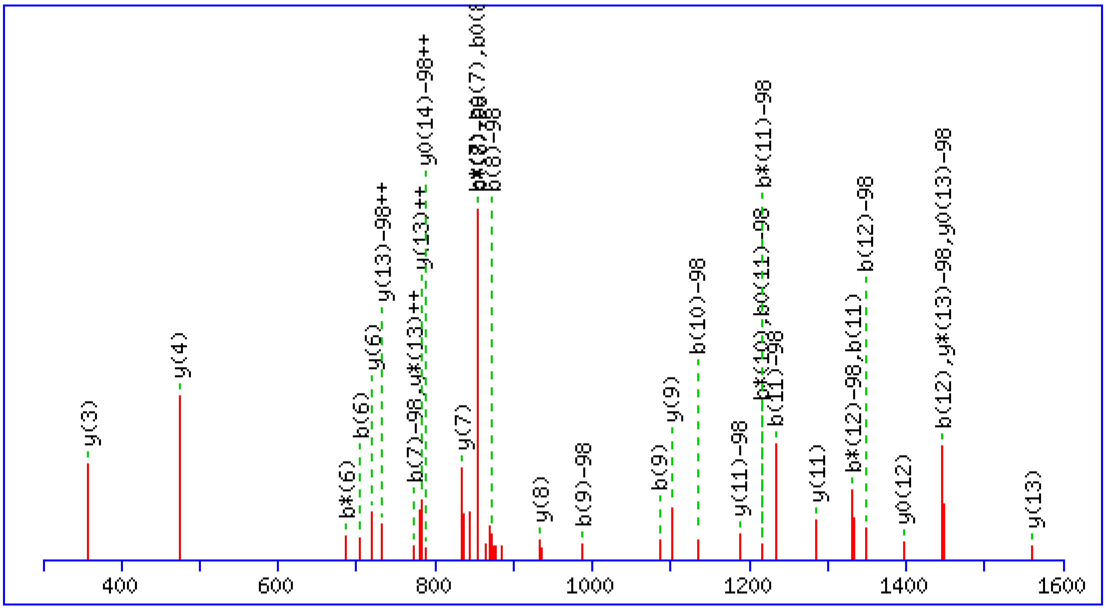
Monoisotopic mass of neutral peptide Mr(calc): 1816.6888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 **Expect:** 2.9e-006
Matched b ions: b(6), b(7)-98, b(7), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(14)-98, b(14)-98++, b(14)++, b(15), b(15)-98
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11), y(12)++, y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13)-98, y(13)++, y(14)-98++, y(14)-98, y(14)++, y(15)-98++

Peptide No.420

IEFEGQSVDFVDPNK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **IEFEGQSVDFVDPNK**
Found in **CPSM_MOUSE** in **SwissProt**, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Match to Query 4088: 1802.775568 from(902.395060,2+) index(6789)
Title: Elution from: 55.277 to 55.277 scan no 5689 cid35.00 polarity:+:m1s



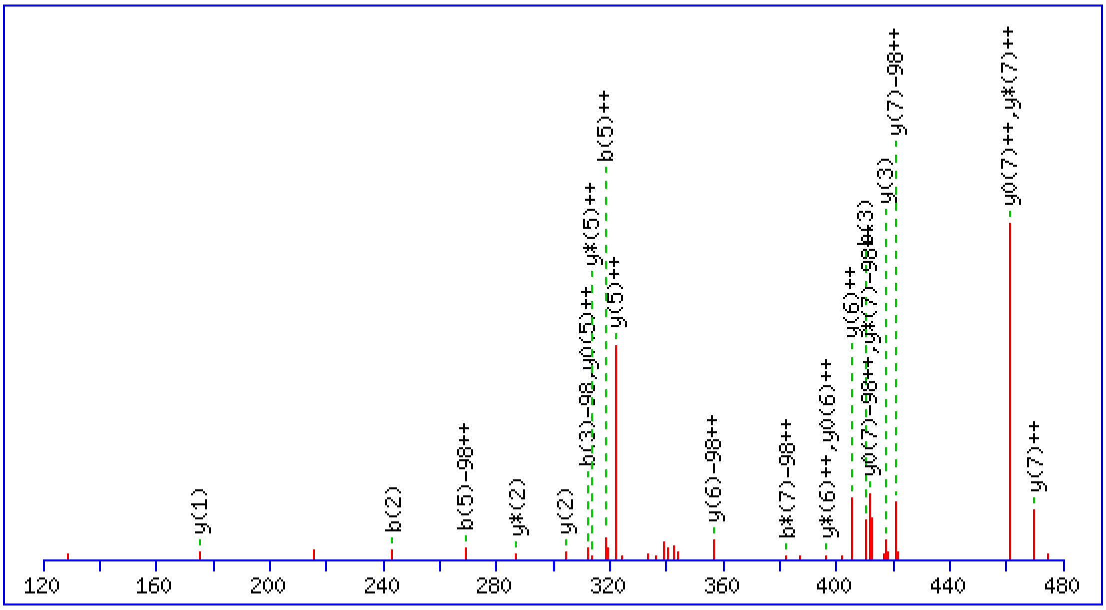
Monoisotopic mass of neutral peptide Mr(calc): 1802.7764
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.0001
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(11)-98, y(11), y(13), y(13)-98++, y(13)++

Peptide No.421

IESPKLER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **IESPKLER**
Found in **HS105_MOUSE** in **SwissProt**, Heat shock protein 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=2

Match to Query 968: 1050.512046 from(351.177958,3+) index(463)
Title: Elution from: 20.547 to 20.547 scan no 1312 cid35.00 polarity:+



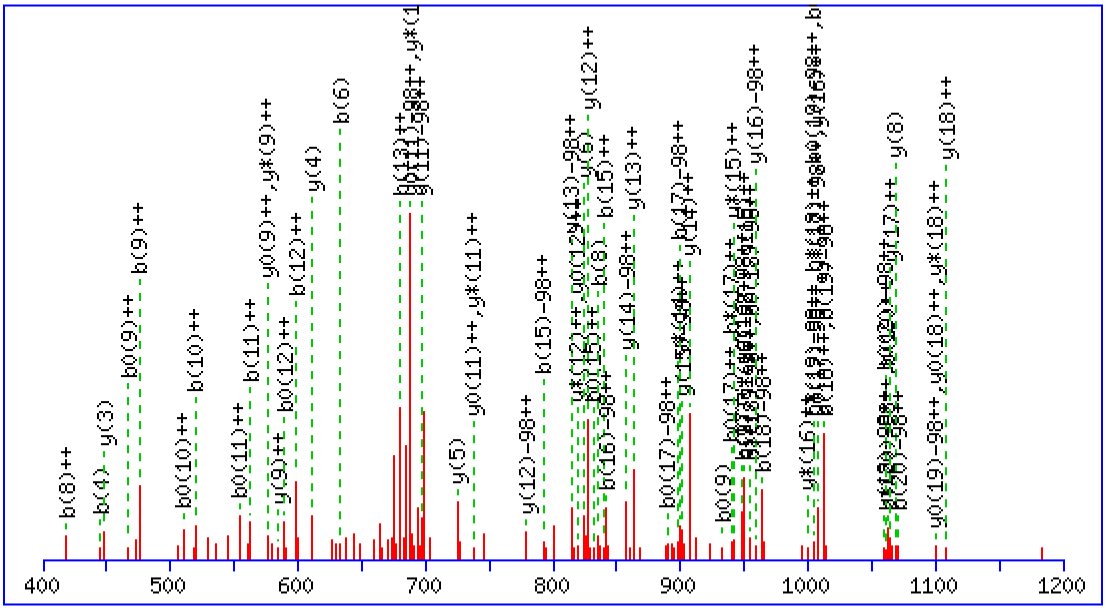
Monoisotopic mass of neutral peptide Mr(calc): 1050.5110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0087
Matched b ions: b(2), b(3)-98, b(3), b(5)++, b(5)-98++
Matched y ions: y(1), y(2), y(3), y(5)++, y(6)++, y(6)-98++, y(7)++, y(7)-98++

Peptide No.422

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **IGHHSTSDDSSAYRSVDEVNYWDK**
Found in **ODBA_MOUSE** in **SwissProt**, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6606: 2847.174836 from(712.800985,4+) index(5456)
Title: Elution from: 34.146 to 34.146 scan no 3160 cid35.00 polarity:+:m1s



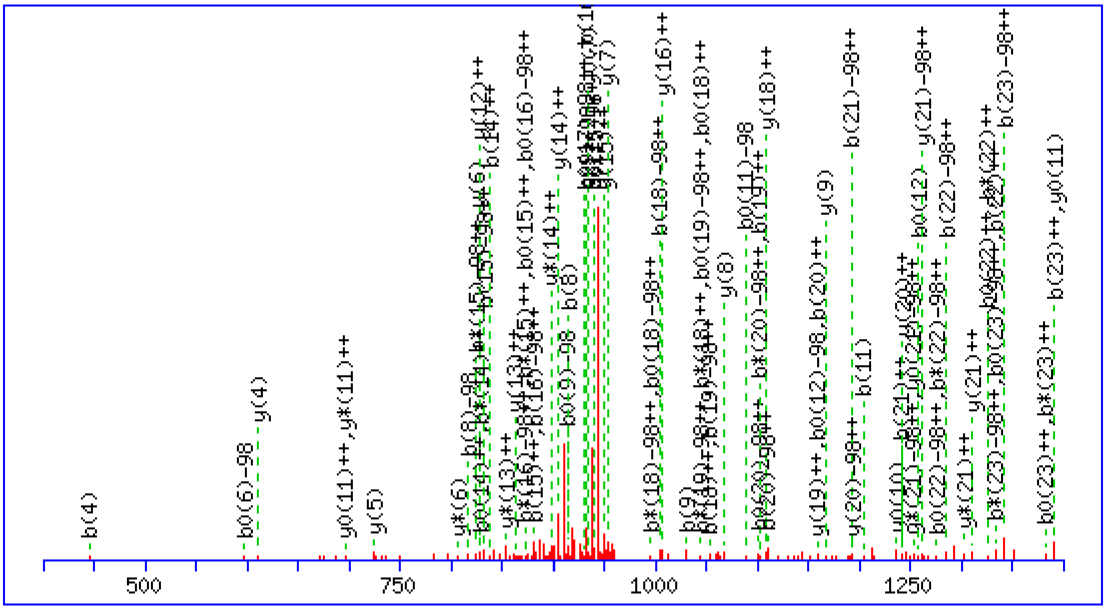
Monoisotopic mass of neutral peptide Mr(calc): 2847.1773
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 **Expect:** 1.6e-007
Matched b ions: b(4), b(6), b(8)++, b(8), b(9)++, b(9), b(10)++, b(11)++, b(12)++, b(13)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++

Peptide No.423

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:5,@Y:13
Ambiguous sites:

MS/MS Fragmentation of **IGHHSTSDDSSAYRSVDEVNYWDK**
Found in **ODBA_MOUSE** in **SwissProt**, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6852: 2927.139975 from(976.720601,3+) index(5886)
Title: Elution from: 36.779 to 36.779 scan no 3544 cid35.00 polarity:+:m1s



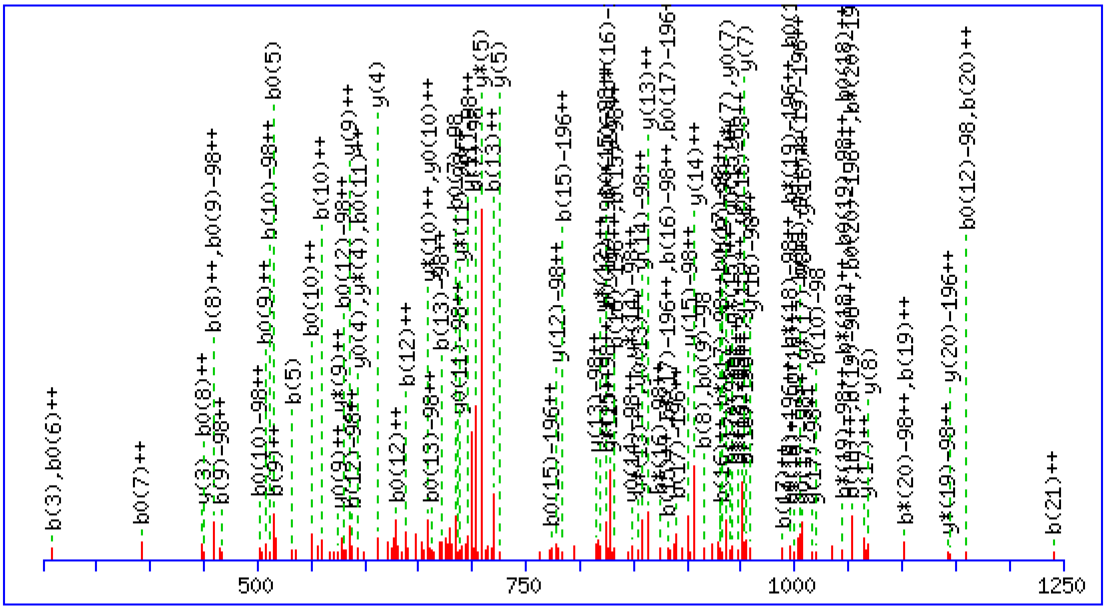
Monoisotopic mass of neutral peptide Mr(calc): 2927.1437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
Ions Score: 37 **Expect:** 0.0011
Matched b ions: b(4), b(8)-98, b(8), b(9)-98, b(9), b(11), b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(18)++, b(18)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(18)++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++

Peptide No.424

IGHHSTSDDSSAYRSVDEVNYWDK
Confirmed sites: @S:15
Ambiguous sites: @T:6orS:7

MS/MS Fragmentation of **IGHHSTSDDSSAYRSVDEVNYWDK**
Found in **ODBA_MOUSE** in **SwissProt**, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6853: 2927.143236 from(732.793085,4+) index(5879)
Title: Elution from: 36.719 to 36.719 scan no 3536 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2927.1437

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 36 **Expect:** 0.0012

Matched b ions: b(3), b(5), b(7)-98, b(8)++, b(8), b(9)++, b(9)-98++, b(9)-98, b(10)++, b(10)-98, b(10)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(15)-196++, b(15)-98++, b(15)++, b(16)-196++, b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(21)++

Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(20)-196++

Peptide No.425

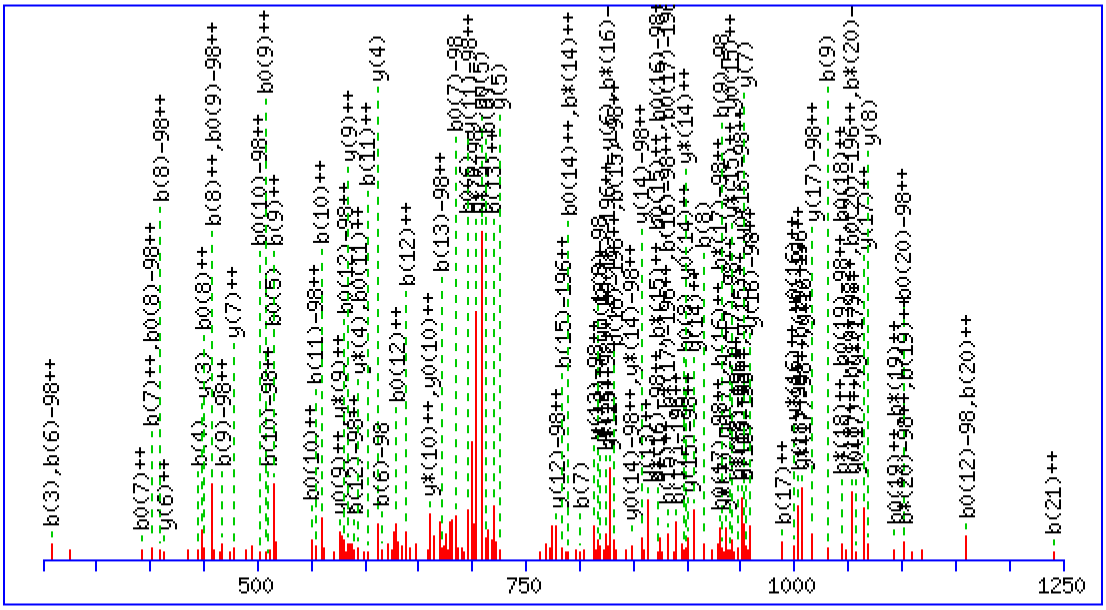
IGHHSTSDDSSAYRSVDEVNYWDK

Confirmed sites: @S:15

Ambiguous sites: @S:5orT:6

MS/MS Fragmentation of **IGHHSTSDDSSAYRSVDEVNYWDK**
Found in **ODBA_MOUSE** in **SwissProt**, 2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Mus musculus GN=Bckdha PE=1 SV=1

Match to Query 6661: 2927.144068 from(732.793293,4+) index(5723)
Title: Elution from: 36.815 to 36.815 scan no 3519 cid35.00 polarity:+:m1s



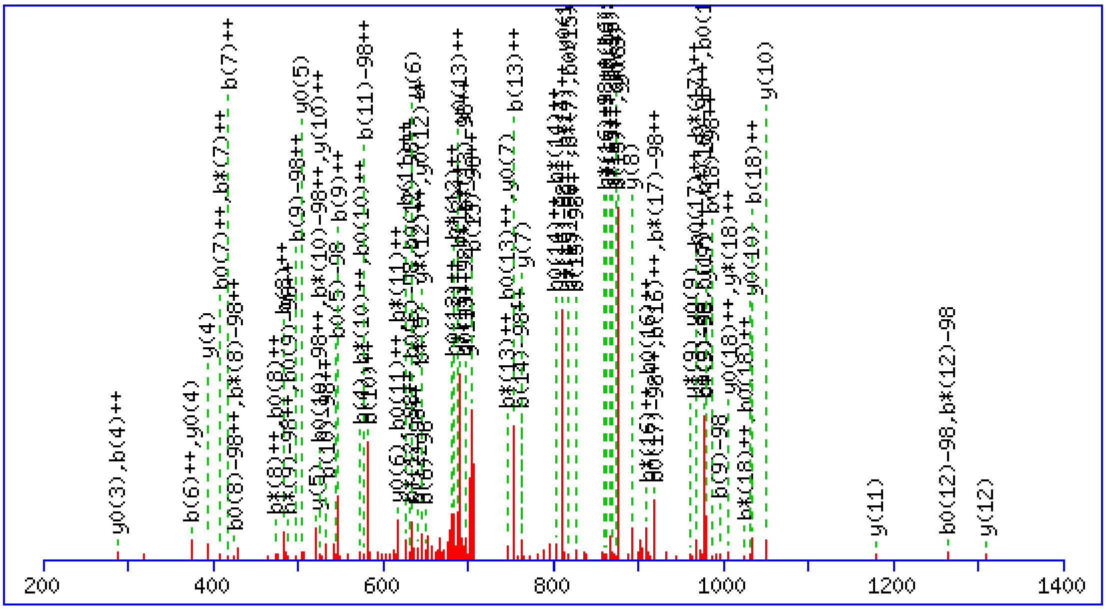
Monoisotopic mass of neutral peptide Mr(calc): 2927.1437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 **Expect:** 9.1e-006
Matched b ions: b(3), b(4), b(6)-98++, b(6), b(6)-98, b(7)++, b(7)-98, b(7), b(8)++, b(8)-98++, b(8)-98, b(8), b(9)++, b(9)-98++, b(9), b(9)-98, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(16)-98++, b(16)-196++, b(17)-196++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(19)++, b(20)++, b(21)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(9)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.426

IHRSSSSEEASQELESDDG
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **IHRSSSSEEASQELESDDG**
Found in **PCLI1_MOUSE** in **SwissProt**, PTB-containing, cubilin and LRP1-interacting protein OS=Mus musculus GN=Pid1 PE=1 SV=2

Match to Query 4713: 2141.840067 from(714.953965,3+) index(3424)
Title: Elution from: 29.516 to 29.516 scan no 1750 cid35.00 polarity:+:m1s



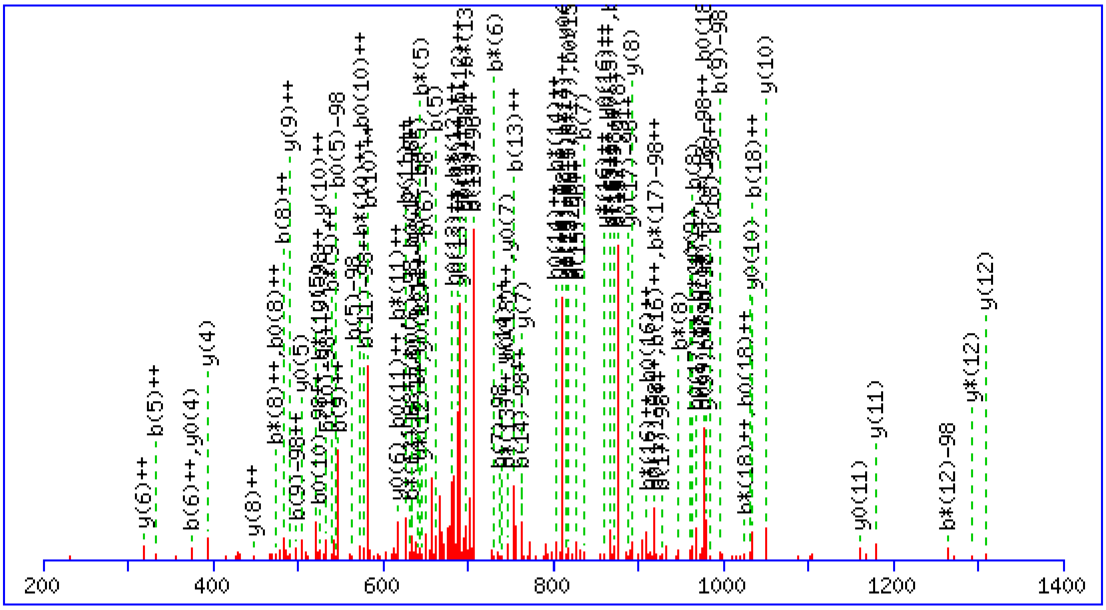
Monoisotopic mass of neutral peptide Mr(calc): 2141.8386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 **Expect:** 9.9e-010
Matched b ions: b(4)++, b(4), b(6)++, b(6)-98, b(7)++, b(8)++, b(8)-98, b(9)++, b(9)-98, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(12), y(13)++, y(16)++

Peptide No.427

IHRSSSSEEASQELESDDG
Confirmed sites:
Ambiguous sites: @S:4orS:5

MS/MS Fragmentation of **IHRSSSSEEASQELESDDG**
Found in **PCLI1_MOUSE** in **SwissProt**, PTB-containing, cubilin and LRP1-interacting protein OS=Mus musculus GN=Pid1 PE=1 SV=2

Match to Query 5440: 2141.839137 from(714.953655,3+) index(617)
Title: Elution from: 29.647 to 29.647 scan no 1849 cid35.00 polarity:+



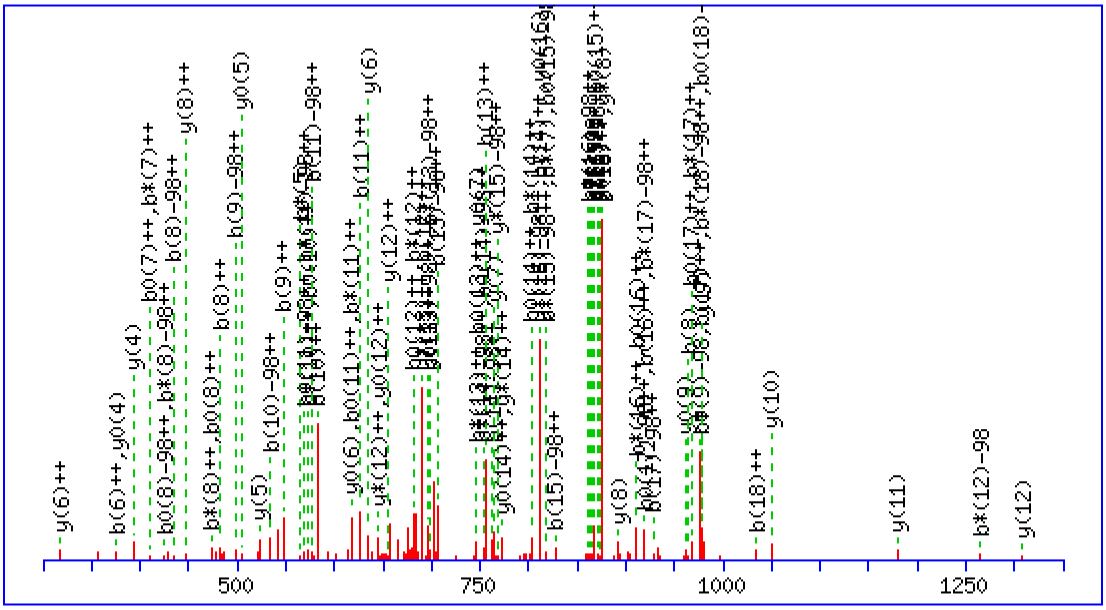
Monoisotopic mass of neutral peptide Mr(calc): 2141.8386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 93 **Expect:** 2.8e-009
Matched b ions: b(5)++, b(5)-98, b(5), b(6)++, b(6)-98, b(7)-98, b(7), b(8)++, b(8)-98, b(8), b(9)++, b(9)-98++, b(9)-98, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(12), y(13)++, y(14)++, y(16)++

Peptide No.428

IHRSSSSEEASQELESDDG
Confirmed sites:
Ambiguous sites: @S:4orS:5orS:6

MS/MS Fragmentation of **IHRSSSSEEASQELESDDG**
Found in **PCLI1_MOUSE** in **SwissProt**, PTB-containing, cubilin and LRP1-interacting protein OS=Mus musculus GN=Pid1 PE=1 SV=2

Match to Query 4601: 2141.834187 from(714.952005,3+) index(3757)
Title: Elution from: 22.709 to 22.709 scan no 1582 cid35.00 polarity:+:m1s



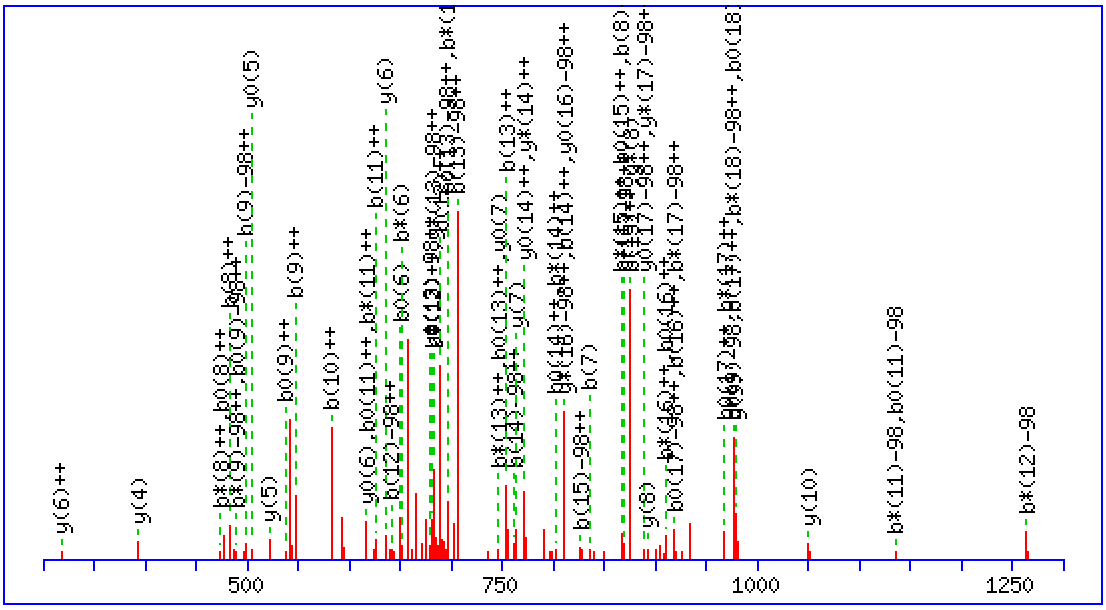
Monoisotopic mass of neutral peptide Mr(calc): 2141.8386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 75 **Expect:** 1.4e-007
Matched b ions: b(6)++, b(8)++, b(8)-98++, b(8)-98, b(8), b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(9), y(10), y(11), y(12), y(12)++, y(13)++, y(16)++

Peptide No.429

IHRSSSSEEASQELESDDG
Confirmed sites:
Ambiguous sites: @S:4orS:5orS:6orS:7

MS/MS Fragmentation of **IHRSSSSEEASQELESDDG**
Found in **PCLI1_MOUSE** in **SwissProt**, PTB-containing, cubilin and LRP1-interacting protein OS=Mus musculus GN=Pid1 PE=1 SV=2

Match to Query 5405: 2141.837277 from(714.953035,3+) index(4266)
Title: Elution from: 22.812 to 22.812 scan no 1619 cid35.00 polarity:+:m1s



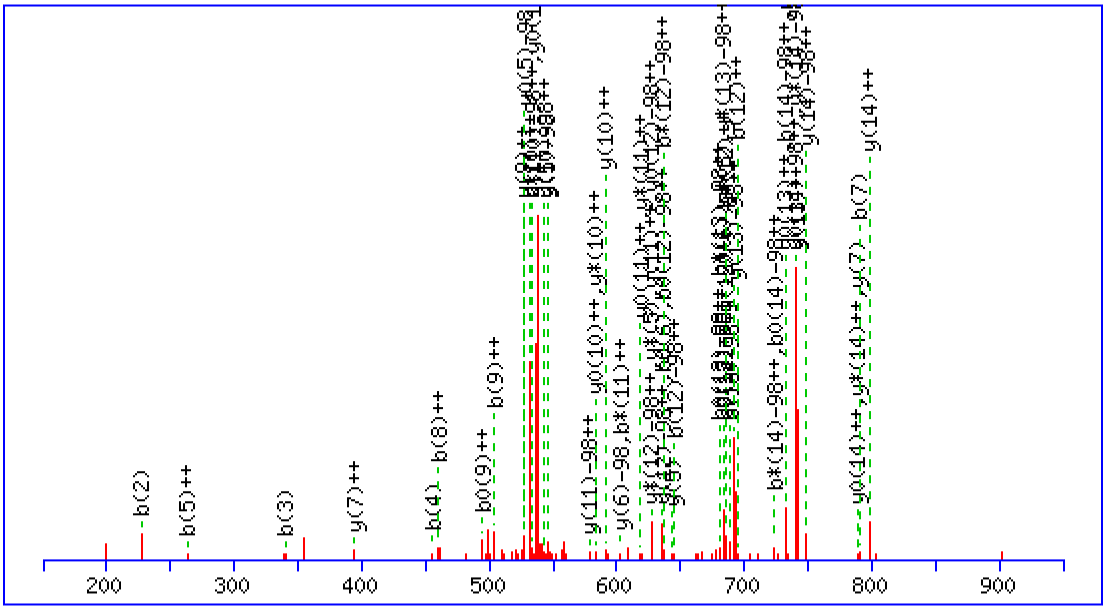
Monoisotopic mass of neutral peptide Mr(calc): 2141.8386
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00026
Matched b ions: b(7), b(8)++, b(8)-98, b(9)-98++, b(9)++, b(10)++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10)

Peptide No.430

ILLDAQHESGRSSSK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **ILLDAQHESGRSSSK**
Found in **BNIP3_MOUSE** in **SwissProt**, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Mus musculus GN=Bnip3 PE=1 SV=1

Match to Query 3668: 1706.796894 from(569.939574,3+) index(497)
Title: Elution from: 20.817 to 20.817 scan no 1348 cid35.00 polarity:+



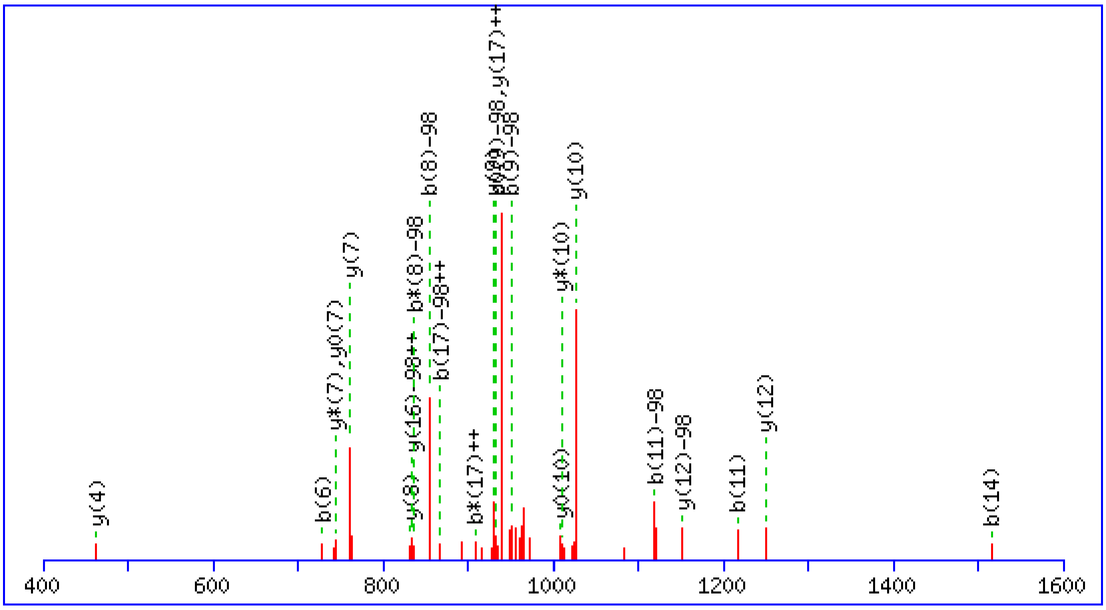
Monoisotopic mass of neutral peptide Mr(calc): 1706.7988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.031
Matched b ions: b(2), b(3), b(4), b(5)++, b(7), b(8)++, b(9)++, b(10)++, b(12)-98++, b(12)++, b(13)-98++, b(14)-98++
Matched y ions: y(5)-98, y(5), y(6)-98, y(7)++, y(7), y(9)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++

Peptide No.431

IPNQFQGSPPAPSDESVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **IPNQFQGSPPAPSDESVK**
Found in **HEBP1_MOUSE** in **SwissProt**, Heme-binding protein 1 OS=Mus musculus GN=Hebp1 PE=1 SV=1

Match to Query 4922: 1976.885158 from(989.449855,2+) index(5545)
Title: Elution from: 33.367 to 33.367 scan no 3089 cid35.00 polarity:+:m1s



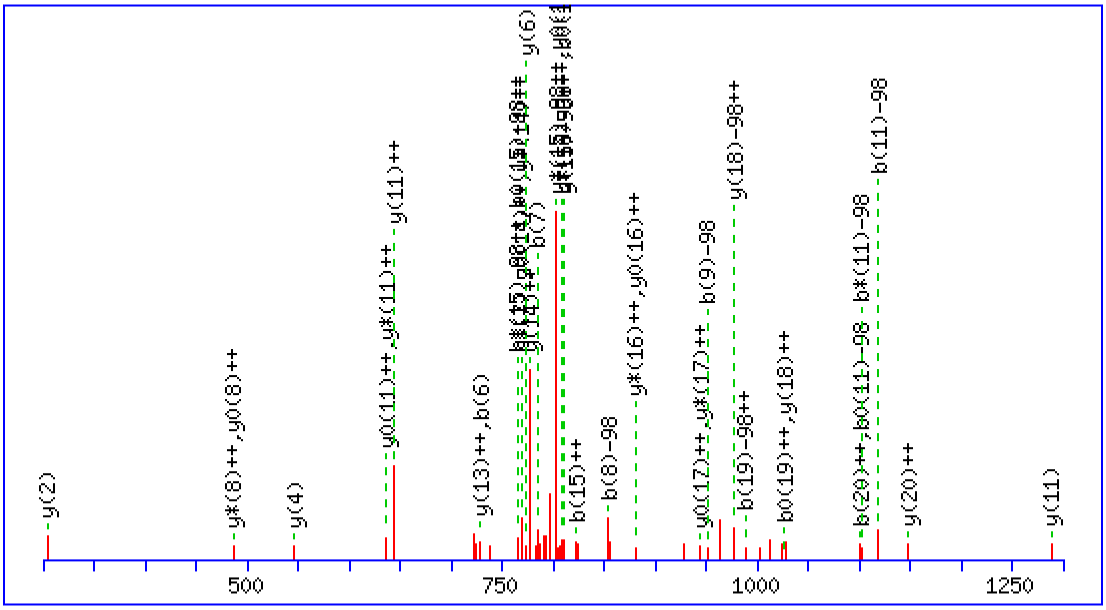
Monoisotopic mass of neutral peptide Mr(calc): 1976.8881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0076
Matched b ions: b(6), b(8)-98, b(9)-98, b(11)-98, b(11), b(14), b(17)-98++
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(12), y(12)-98, y(16)-98++, y(17)++

Peptide No.432

IPNQFQGSPPAPSDESVKIEER
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **IPNQFQGSPPAPSDESVKIEER**
Found in **HEBP1_MOUSE** in **SwissProt**, Heme-binding protein 1 OS=Mus musculus GN=Hebp1 PE=1 SV=1

Match to Query 6215: 2504.157960 from(835.726596,3+) index(5733)
Title: Elution from: 36.912 to 36.912 scan no 3532 cid35.00 polarity:+:m1s



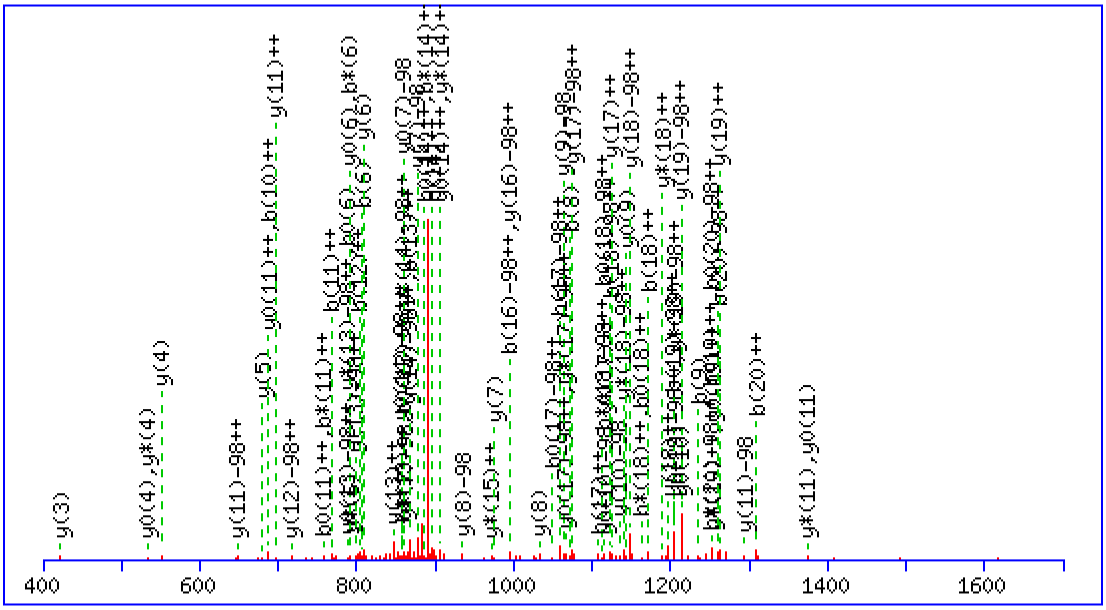
Monoisotopic mass of neutral peptide Mr(calc): 2504.1584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.013
Matched b ions: b(6), b(7), b(8)-98, b(9)-98, b(11)-98, b(15)++, b(19)-98++, b(20)++
Matched y ions: y(2), y(4), y(6), y(11)++, y(11), y(13)++, y(14)++, y(15)-98++, y(18)-98++, y(18)++, y(20)++

Peptide No.433

IQEFCEQHYHCAEGSQEECDK
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **IQEFCEQHYHCAEGSQEECDK**
Found in **ATTY_MOUSE** in **SwissProt**, Tyrosine aminotransferase OS=Mus musculus GN=Tat PE=1 SV=1

Match to Query 5526: 2762.998014 from(922.006614,3+) index(3752)
Title: Elution from: 25.029 to 25.029 scan no 1799 cid35.00 polarity:+:m1s



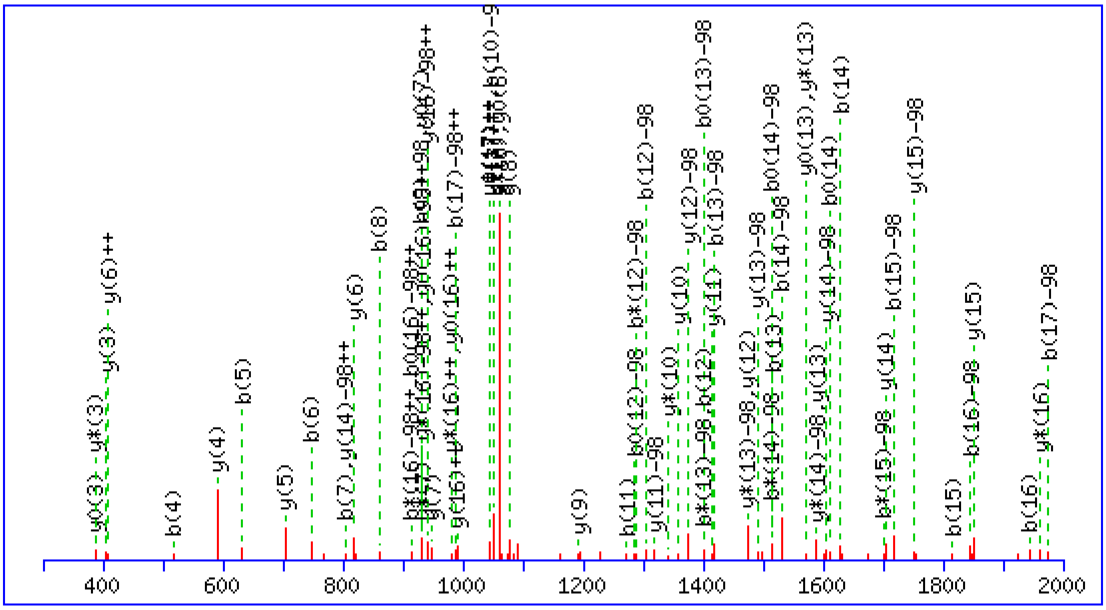
Monoisotopic mass of neutral peptide Mr(calc): 2763.0037
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 1.8e-005
Matched b ions: b(6), b(8), b(9), b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98, y(8), y(9)-98, y(10)-98, y(11)-98++, y(11)++, y(11)-98, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++

Peptide No.434

IQQFDDGGSDEEDIWEEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **IQQFDDGGSDEEDIWEEK**
Found in **PP6R3_MOUSE** in **SwissProt**, Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Mus musculus GN=Ppp6r3 PE=1 SV=1

Match to Query 4857: 2218.857330 from(1110.435941,2+) index(5807)
Title: Elution from: 48.134 to 48.134 scan no 4719 cid35.00 polarity:+:m1s



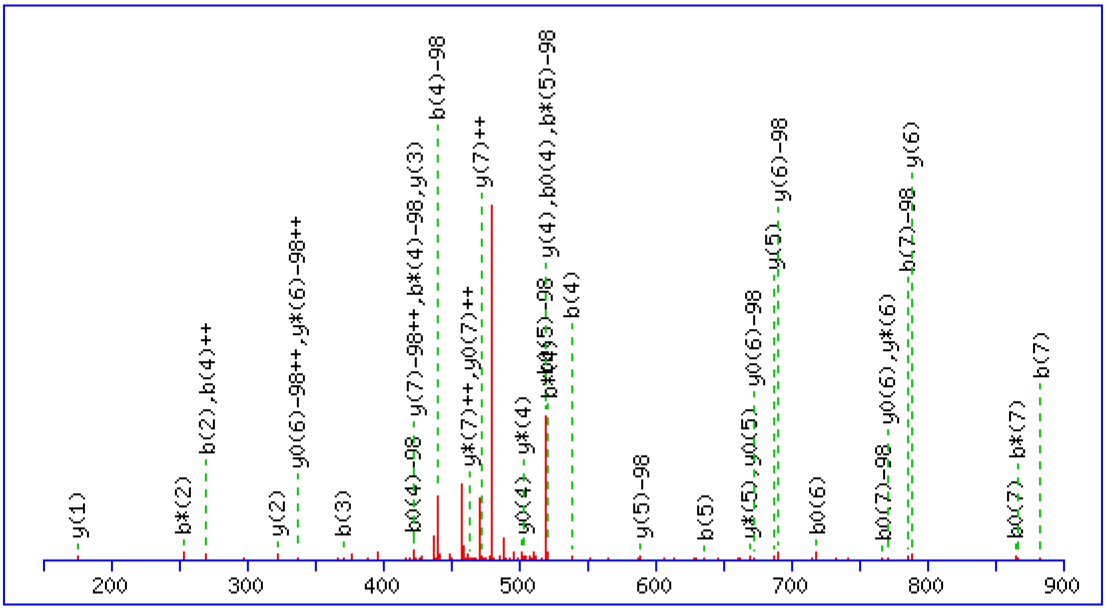
Monoisotopic mass of neutral peptide Mr(calc): 2218.8580
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 4e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(10)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15), b(16)-98, b(16), b(17)-98, b(17)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(14), y(14)-98++, y(14)-98, y(15), y(15)-98, y(16)-98++, y(16)++, y(17)++

Peptide No.435

IRTSPTFR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **IRTSPTFR**
Found in **RL23A_MOUSE** in **SwissProt**, 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1

Match to Query 1136: 1056.510462 from(529.262507,2+) index(581)
Title: Elution from: 21.012 to 21.012 scan no 1411 cid35.00 polarity:+



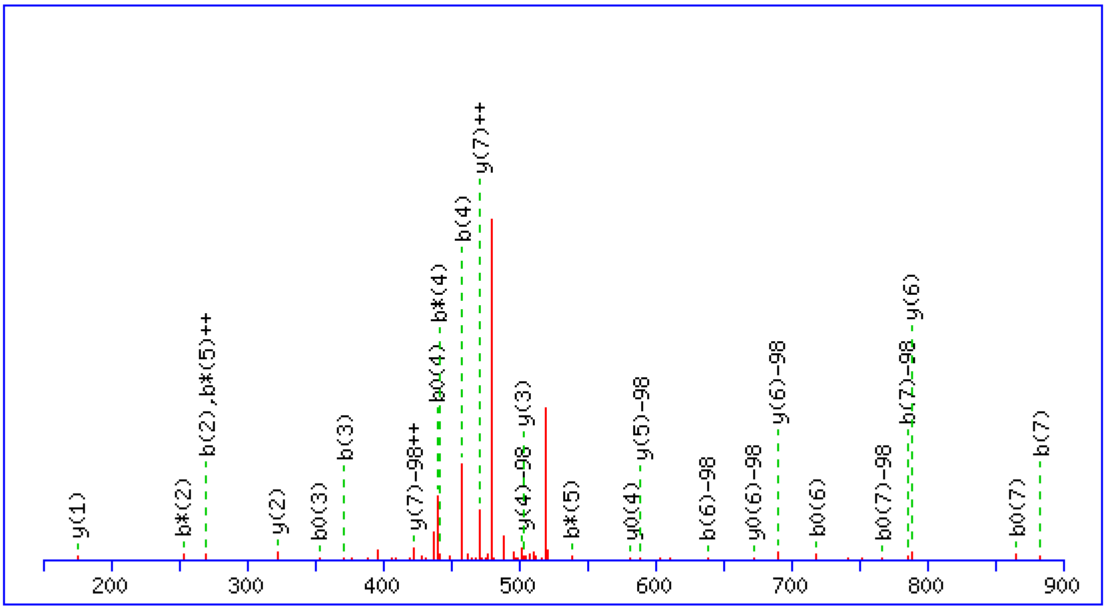
Monoisotopic mass of neutral peptide Mr(calc): 1056.5117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0018
Matched b ions: b(2), b(3), b(4)++, b(4)-98, b(4), b(5), b(7), b(7)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(6)-98, y(6), y(7)-98++, y(7)++

Peptide No.436

IRTSPTFR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **IRTSPTFR**
Found in **RL23A_MOUSE** in **SwissProt**, 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=1 SV=1

Match to Query 1001: 1056.511042 from(529.262797,2+) index(521)
Title: Elution from: 21.025 to 21.025 scan no 1376 cid35.00 polarity:+



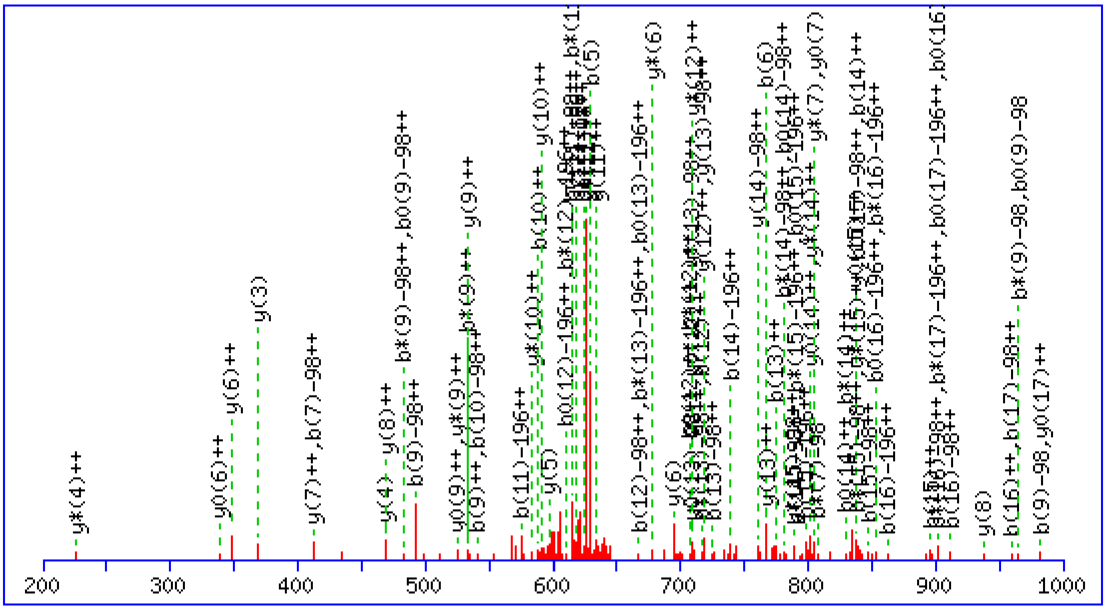
Monoisotopic mass of neutral peptide Mr(calc): 1056.5117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00045
Matched b ions: b(2), b(3), b(4), b(6)-98, b(7), b(7)-98
Matched y ions: y(1), y(2), y(3), y(4)-98, y(5)-98, y(6)-98, y(6), y(7)++, y(7)-98++

Peptide No.437

ISSCTHRASPSSDEDKPEVPPR
Confirmed sites: @S:11
Ambiguous sites: @S:2orS:3orT:5

MS/MS Fragmentation of **ISSCTHRASPSSDEDKPEVPPR**
Found in **ERRFI_MOUSE** in **SwissProt**, ERBB receptor feedback inhibitor 1 OS=Mus musculus GN=Errfi1 PE=1 SV=1

Match to Query 6369: 2611.074616 from(653.775930,4+) index(3950)
Title: Elution from: 20.199 to 20.199 scan no 1265 cid35.00 polarity:+:m1s



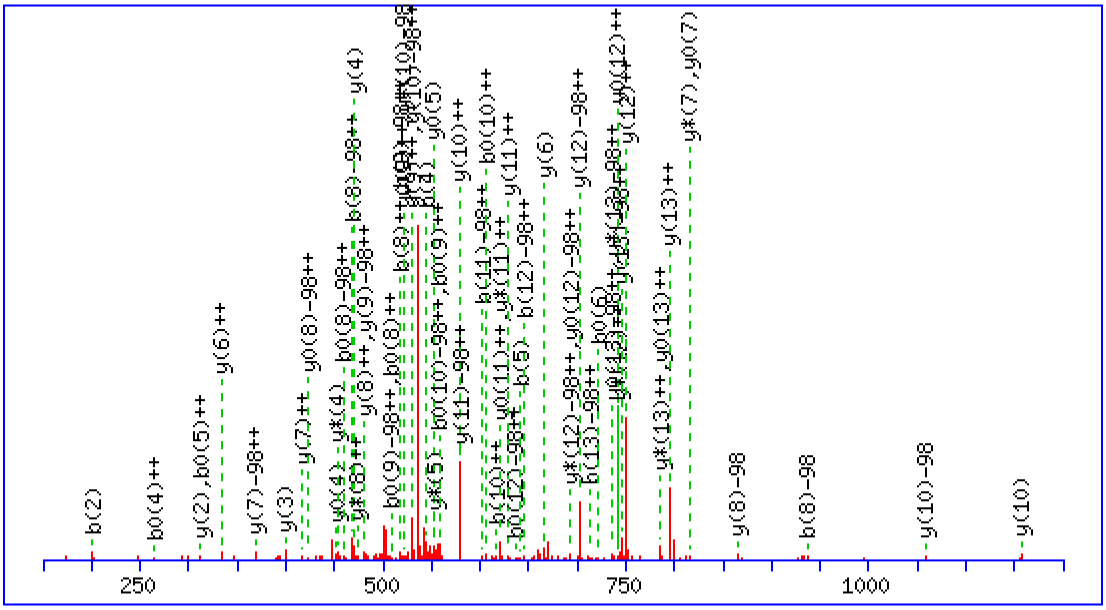
Monoisotopic mass of neutral peptide Mr(calc): 2611.0775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0092
Matched b ions: b(5), b(6), b(7)-98++, b(9)-98++, b(9)-98, b(9)++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++, b(12)-196++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-196++, b(14)-98++, b(15)-196++, b(15)++, b(15)-98++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++

Peptide No.438

ISYTPPESPVASHR
Confirmed sites: @Y:3,@S:8
Ambiguous sites:

MS/MS Fragmentation of **ISYTPPESPVASHR**
Found in **ETV6_MOUSE** in **SwissProt**, Transcription factor ETV6 OS=Mus musculus GN=Etv6 PE=1 SV=1

Match to Query 3661: 1699.702848 from(567.574892,3+) index(4118)
Title: Elution from: 37.620 to 37.620 scan no 2715 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1699.7008

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

Y3 : Phospho (Y)

S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 31 **Expect:** 0.0041

Matched b ions: b(2), b(4), b(5), b(8)-98++, b(8)-98, b(8)++, b(9)-98++, b(10)++, b(11)-98++, b(12)-98++, b(13)-98++

Matched y ions: y(2), y(3), y(4), y(6)++, y(6), y(7)-98++, y(7)++, y(8)-98, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98, y(10), y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.439

ISYTPPESPVASHR

Confirmed sites: @T:4,@S:8

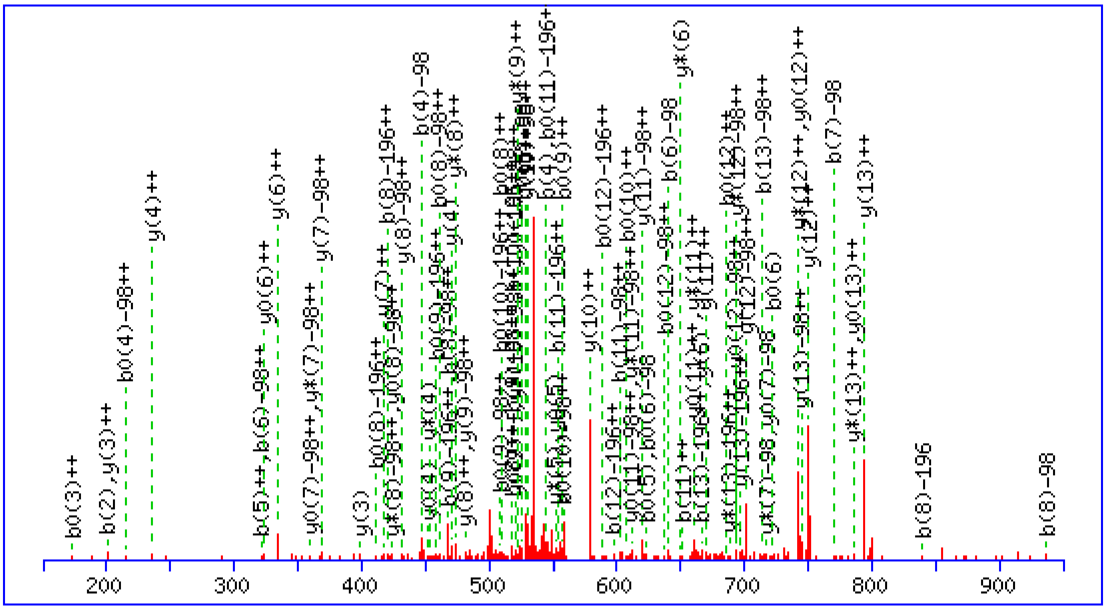
Ambiguous sites:

MS/MS Fragmentation of **ISYTPPESPVASHR**

Found in **ETV6_MOUSE** in **SwissProt**, Transcription factor ETV6 OS=Mus musculus GN=Etv6 PE=1 SV=1

Match to Query 4196: 1699.701372 from(567.574400,3+) index(1382)

Title: Elution from: 37.714 to 37.714 scan no 2855 cid35.00 polarity:+



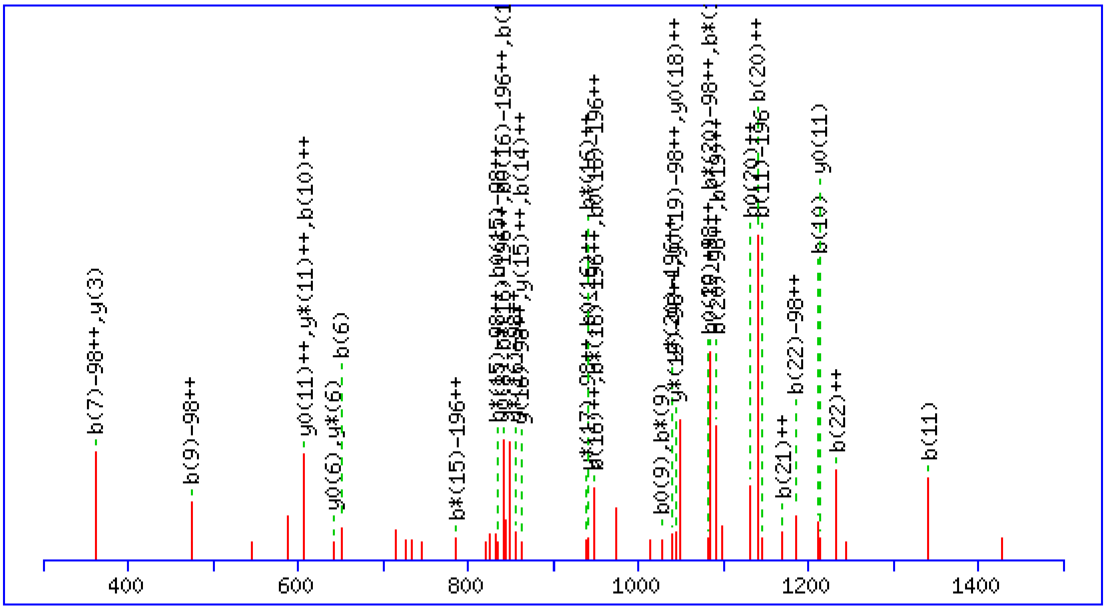
Monoisotopic mass of neutral peptide Mr(calc): 1699.7008
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0078
Matched b ions: b(2), b(4)-98, b(4), b(5)++, b(5)-98, b(6)-98++, b(6)-98, b(7)-98, b(8)-98++, b(8)-98, b(8)-196, b(8)-196++, b(8)++, b(9)-196++, b(9)-98++, b(10)-196++, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(13)-196++, b(13)-98++
Matched y ions: y(3)++, y(3), y(4)++, y(4), y(6)++, y(6), y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(13)-196++

Peptide No.440

ITHSPDSVKSKAAYGNSQAVGER
Confirmed sites: @S:7,@S:10,@Y:14
Ambiguous sites:

MS/MS Fragmentation of **ITHSPDSVKSKAAYGNSQAVGER**
Found in **JHD2C_MOUSE** in **SwissProt**, Probable JmjC domain-containing histone demethylation protein 2C OS=Mus musculus GN=Jmjd1c PE=1 SV=3

Match to Query 5400: 2641.090566 from(881.370798,3+) index(2419)
Title: Elution from: 44.698 to 44.698 scan no 4374 cid35.00 polarity:+



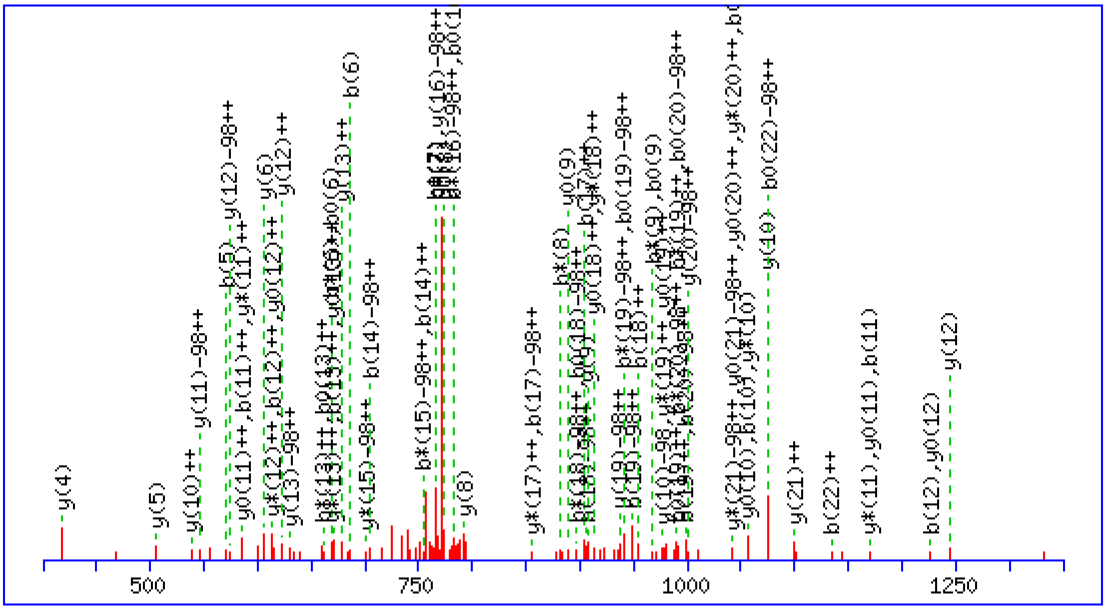
Monoisotopic mass of neutral peptide Mr(calc): 2641.0975
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y14 : Phospho (Y)
Ions Score: 25 **Expect:** 0.025
Matched b ions: b(6), b(7)-98++, b(9)-98++, b(10)++, b(10), b(11), b(11)-196, b(14)++, b(15)-98++, b(16)++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(22)++, b(22)-98++
Matched y ions: y(3), y(15)++, y(16)-98++

Peptide No.441

ITVEKDPDSALGISDGETSPSSK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **ITVEKDPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 5221: 2412.095568 from(805.039132,3+) index(5048)
Title: Elution from: 36.272 to 36.272 scan no 3357 cid35.00 polarity:+:m1s



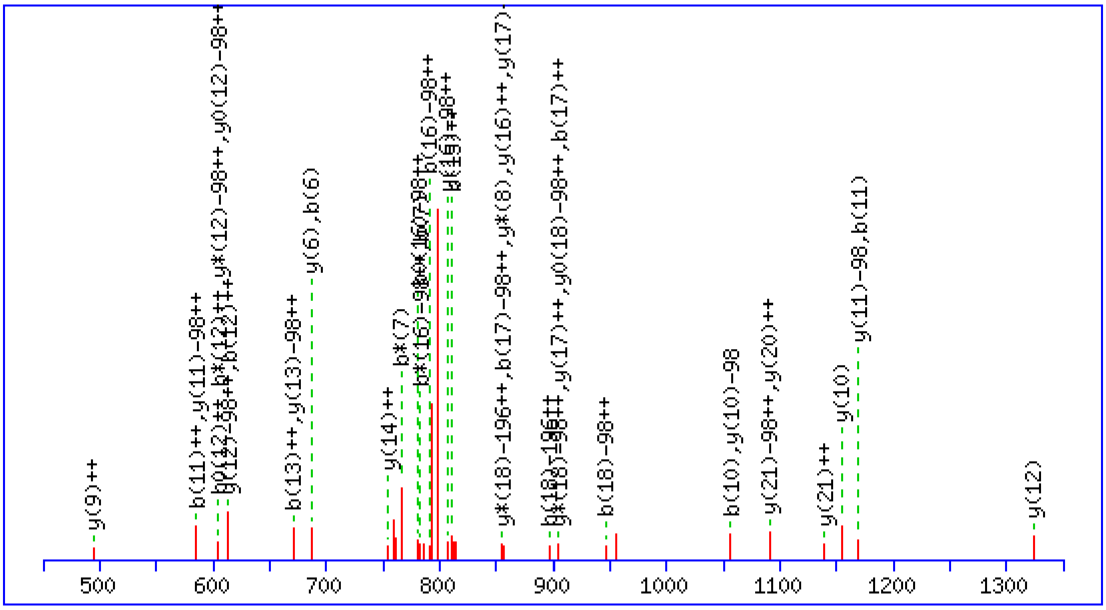
Monoisotopic mass of neutral peptide Mr(calc): 2412.0945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 6.4e-005
Matched b ions: b(5), b(6), b(10), b(11), b(11)++, b(12)++, b(12), b(13)++, b(14)-98++, b(14)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(21)-98++, b(22)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(10)++, y(10)-98, y(11)-98++, y(12), y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(16)-98++, y(19)-98++, y(20)-98++, y(21)++

Peptide No.442

ITVEKDPDSALGISDGETSPSSK
Confirmed sites: @S:14,@T:18
Ambiguous sites:

MS/MS Fragmentation of **ITVEKDPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 5211: 2492.058888 from(831.693572,3+) index(5124)
Title: Elution from: 39.799 to 39.799 scan no 3781 cid35.00 polarity:+:m1s



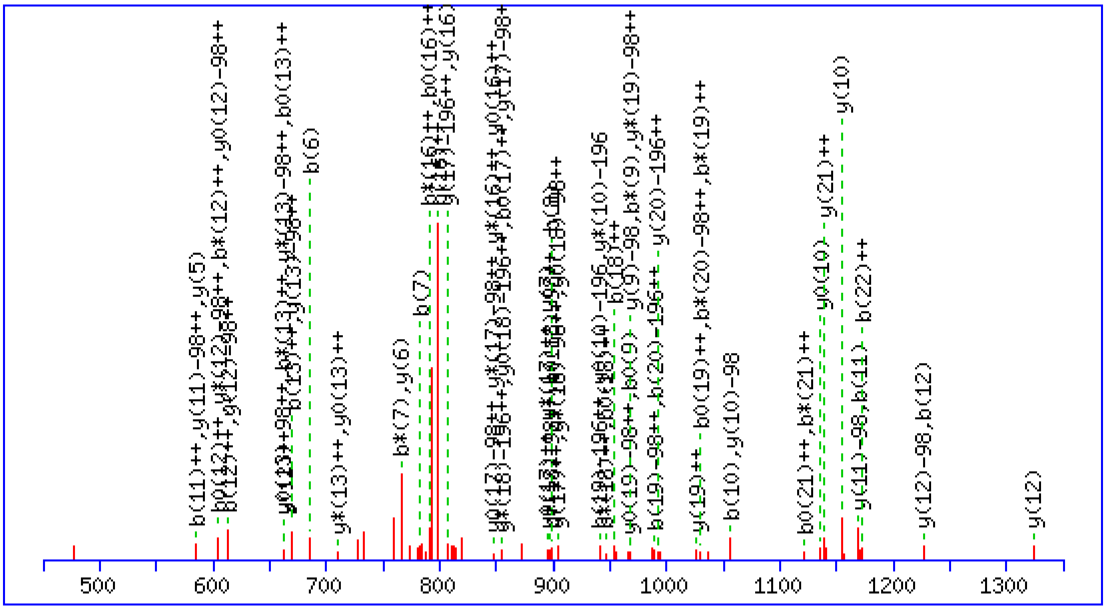
Monoisotopic mass of neutral peptide Mr(calc): 2492.0608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0019
Matched b ions: b(6), b(7), b(10), b(11)++, b(11), b(12)++, b(13)++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-196++, b(18)-98++
Matched y ions: y(6), y(9)++, y(10), y(10)-98, y(11)-98++, y(11)-98, y(12)-98++, y(12), y(13)-98++, y(14)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(20)++, y(21)-98++, y(21)++

Peptide No.443

ITVEKDPDSALGISDGETSPSSK
Confirmed sites: @T:18,@S:19
Ambiguous sites:

MS/MS Fragmentation of **ITVEKDPDSALGISDGETSPSSK**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 5351: 2492.059485 from(831.693771,3+) index(5335)
Title: Elution from: 39.687 to 39.687 scan no 3785 cid35.00 polarity:+:m1s



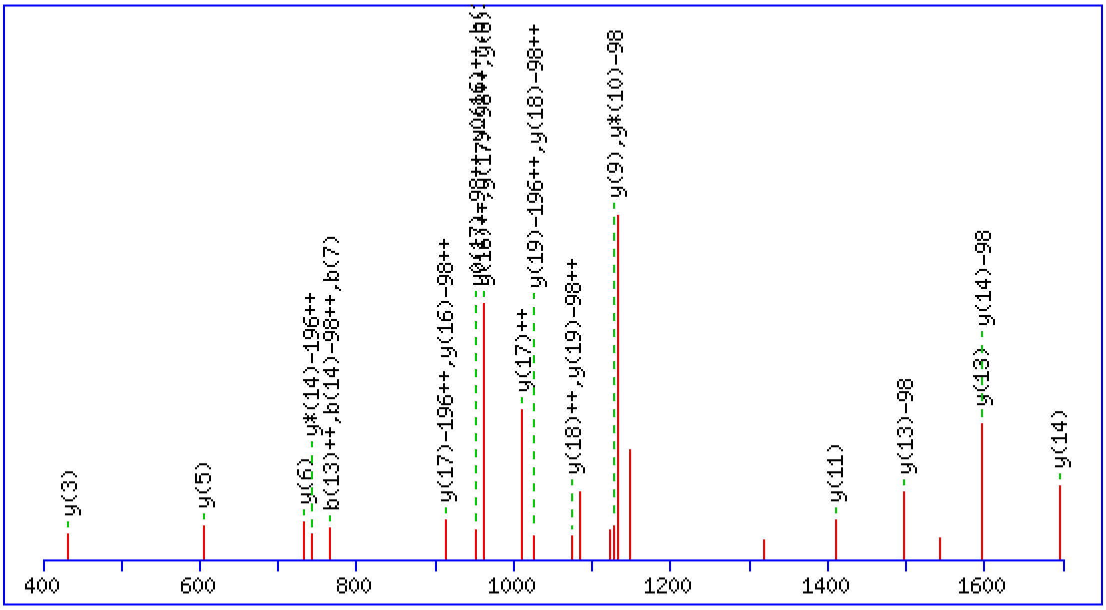
Monoisotopic mass of neutral peptide Mr(calc): 2492.0608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00076
Matched b ions: b(6), b(7), b(8), b(10), b(11), b(11)++, b(12)++, b(12), b(13)++, b(16)++, b(18)++, b(19)-196++, b(19)-98++, b(20)-196++, b(22)++
Matched y ions: y(5), y(6), y(7), y(9)-98, y(10)-98, y(10), y(11)-98, y(11)-98++, y(12)-98++, y(12)-98, y(12), y(12)++, y(13)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-196++, y(17)-98++, y(19)++, y(20)-196++, y(21)++

Peptide No.444

IVEPEVVGESDSEVEGDAWR
Confirmed sites: @S:10,@S:12
Ambiguous sites:

MS/MS Fragmentation of **IVEPEVVGESDSEVEGDAWR**
Found in **MFAP1_MOUSE** in **SwissProt**, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 6089: 2360.940314 from(1181.477433,2+) index(6901)
Title: Elution from: 53.001 to 53.001 scan no 5504 cid35.00 polarity:+:m1s



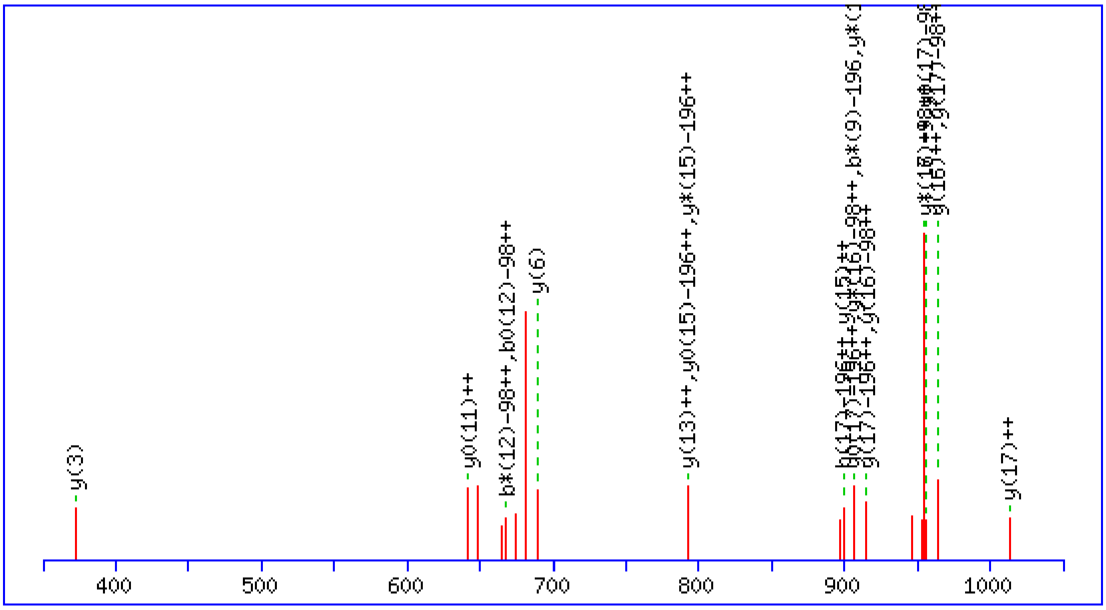
Monoisotopic mass of neutral peptide Mr(calc): 2360.9451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00026
Matched b ions: b(7), b(9), b(13)++, b(14)-98++, b(18)-98++
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(11), y(13)-98, y(13), y(14), y(14)-98, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)-196++

Peptide No.445

IVETINSDSDSEFGIPKK
Confirmed sites: @S:7,@S:9
Ambiguous sites:

MS/MS Fragmentation of **IVETINSDSDSEFGIPKK**
Found in **TOP2B_MOUSE** in **SwissProt**, DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2

Match to Query 5375: 2137.923798 from(713.648542,3+) index(6179)
Title: Elution from: 42.240 to 42.240 scan no 4236 cid35.00 polarity:+:m1s



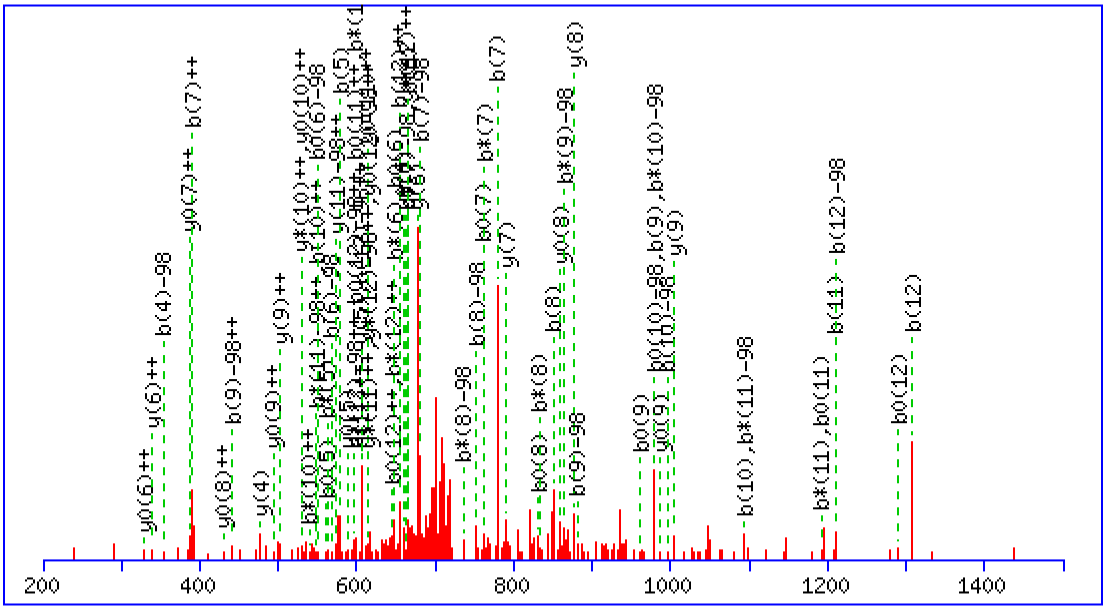
Monoisotopic mass of neutral peptide Mr(calc): 2137.9221
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.02
Matched b ions: b(17)-196++
Matched y ions: y(3), y(6), y(8), y(13)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++

Peptide No.446

IVSAQSLAEDDVE
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **IVSAQSLAEDDVE**
Found in **TOM20_MOUSE** in **SwissProt**, Mitochondrial import receptor subunit TOM20 homolog OS=Mus musculus GN=Tomm20 PE=1 SV=1

Match to Query 3345: 1454.617804 from(728.316178,2+) index(2259)
Title: Elution from: 51.671 to 51.671 scan no 4340 cid35.00 polarity:+



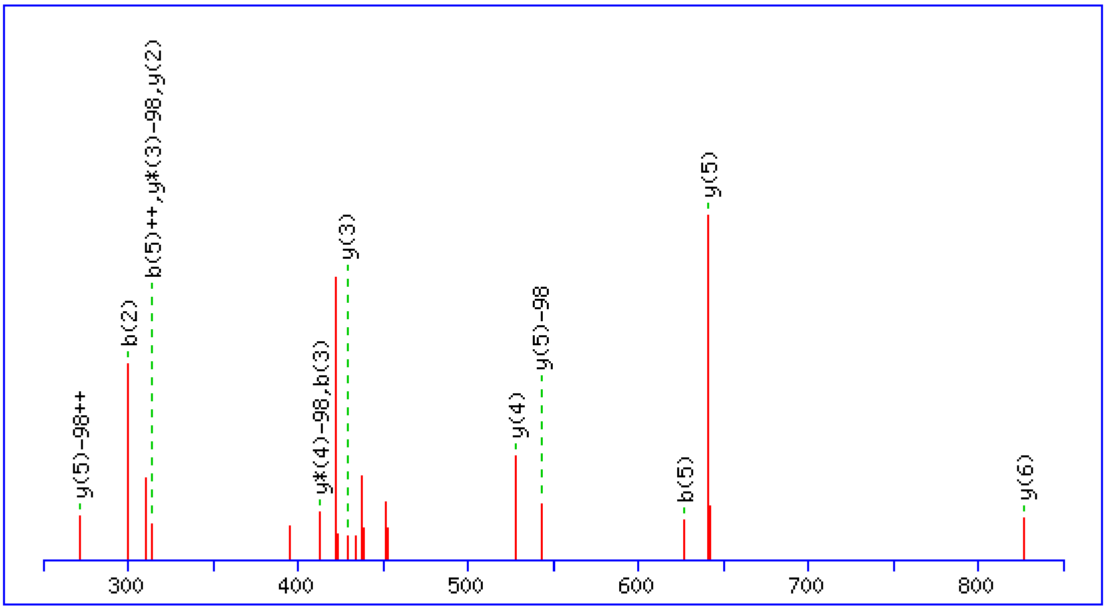
Monoisotopic mass of neutral peptide Mr(calc): 1454.6178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.00087
Matched b ions: b(4)-98, b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8), b(8)-98, b(9), b(9)-98++, b(9)-98, b(10), b(10)++, b(10)-98, b(11), b(11)++, b(12)-98++, b(12), b(12)-98, b(12)++
Matched y ions: y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(11)-98++

Peptide No.447

IWLVDSK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **IWLVDSK**
Found in **MAOX_MOUSE** in **SwissProt**, NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=2

Match to Query 652: 939.445928 from(470.730240,2+) index(2891)
Title: Elution from: 45.777 to 45.777 scan no 4666 cid35.00 polarity:+



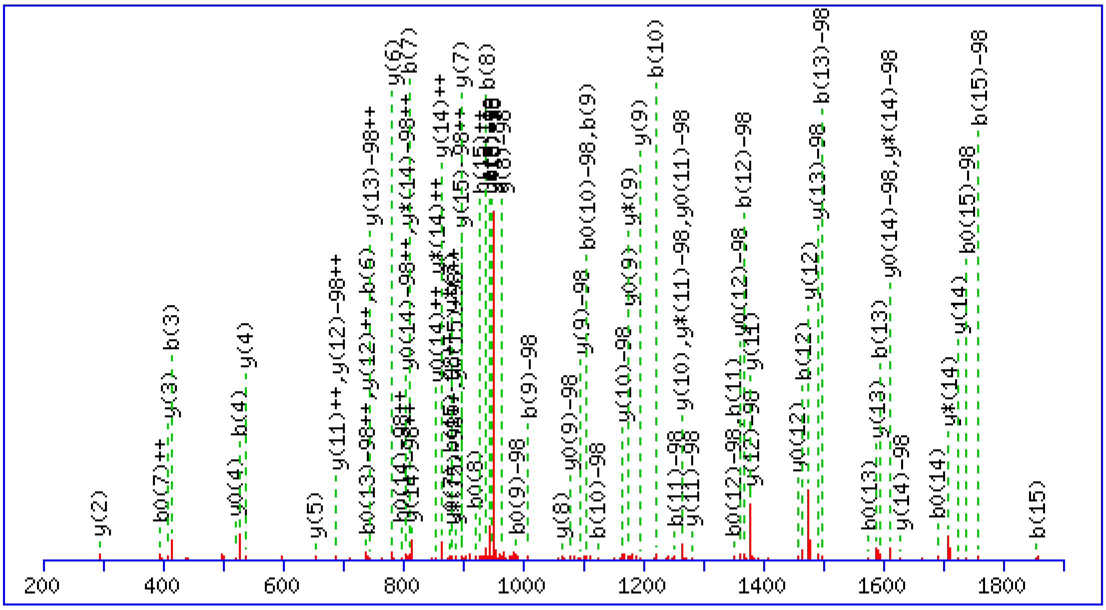
Monoisotopic mass of neutral peptide Mr(calc): 939.4467
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.005
Matched b ions: b(2), b(3), b(5), b(5)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(5)-98++, y(6)

Peptide No.448

IYHLPDAESDEDEDFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **IYHLPDAESDEDEDFK**
Found in **SEPT2_MOUSE** in **SwissProt**, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 4442: 2001.787838 from(1001.901195,2+) index(4749)
Title: Elution from: 49.047 to 49.047 scan no 3865 cid35.00 polarity:+:m1s



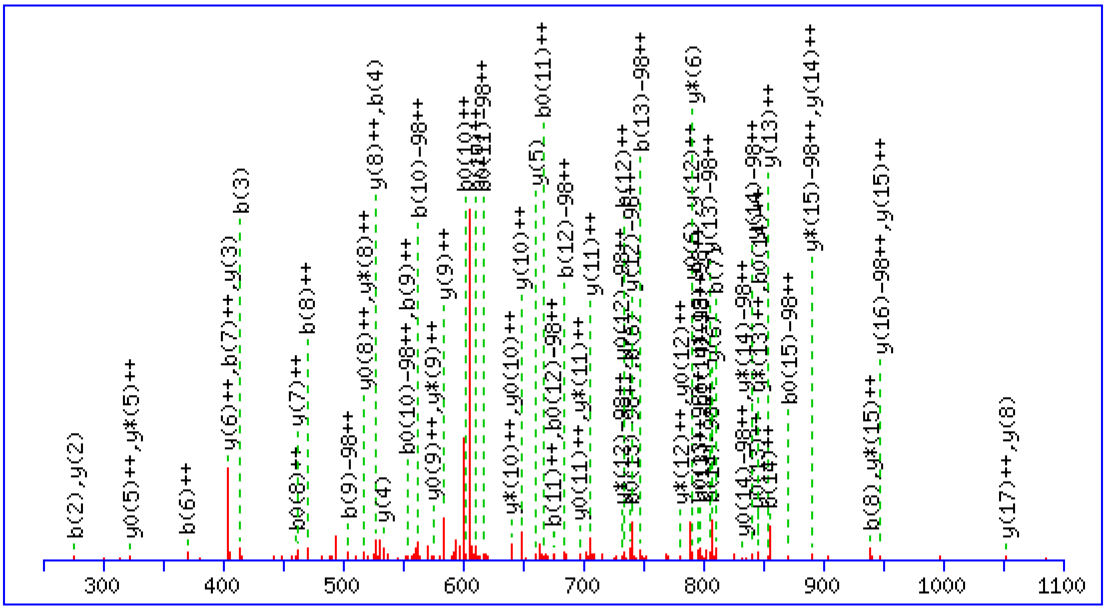
Monoisotopic mass of neutral peptide Mr(calc): 2001.7881
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 **Expect:** 2e-007
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(14), b(14)-98++, b(14)++, b(15), b(15)-98, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11), y(11)++, y(11)-98, y(12)-98, y(12), y(12)++, y(12)-98++, y(13), y(13)-98++, y(13)-98, y(14)-98++, y(14)++, y(14), y(14)-98, y(15)++, y(15)-98++

Peptide No.449

IYHLPDAESDEDEDFKEQTR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **IYHLPDAESDEDEDFKEQTR**
Found in **SEPT2_MOUSE** in **SwissProt**, Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2

Match to Query 5398: 2516.036872 from(630.016494,4+) index(5105)
Title: Elution from: 36.961 to 36.961 scan no 3445 cid35.00 polarity:+:m1s



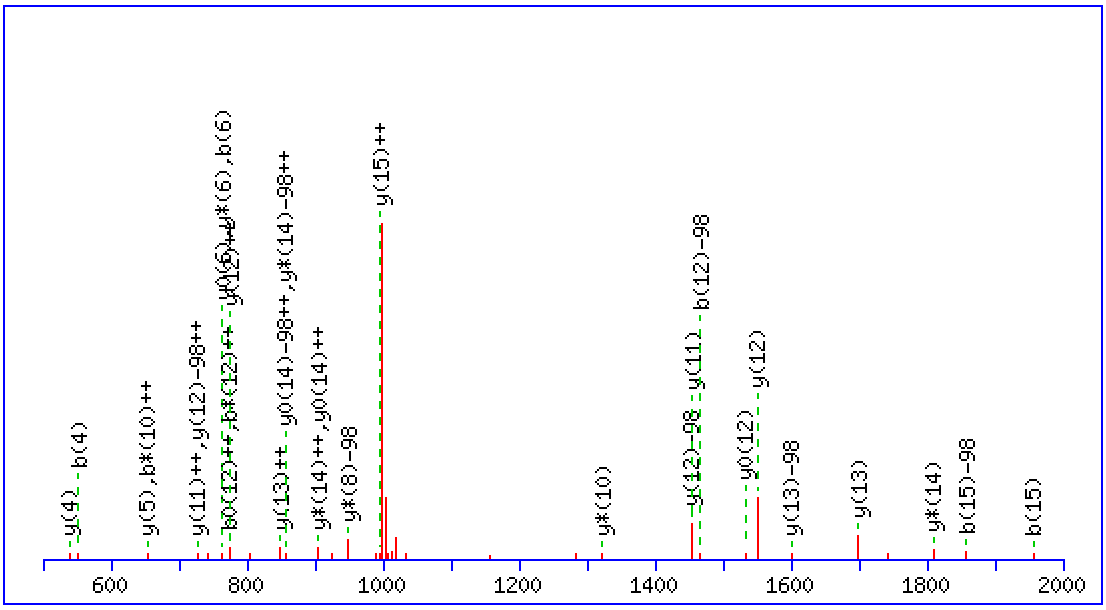
Monoisotopic mass of neutral peptide Mr(calc): 2516.0380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.2e-005
Matched b ions: b(2), b(3), b(4), b(6)++, b(6), b(7)++, b(7), b(8), b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)-98++, y(17)++

Peptide No.450

IYQFPDCDSDEDEDFK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **IYQFPDCDSDEDEDFK**
Found in **SEPT4_MOUSE** in **SwissProt**, Septin-4 OS=Mus musculus GN=Sept4 PE=1 SV=1

Match to Query 5308: 2101.749328 from(1051.881940,2+) index(2974)
Title: Elution from: 46.561 to 46.561 scan no 4790 cid35.00 polarity:+



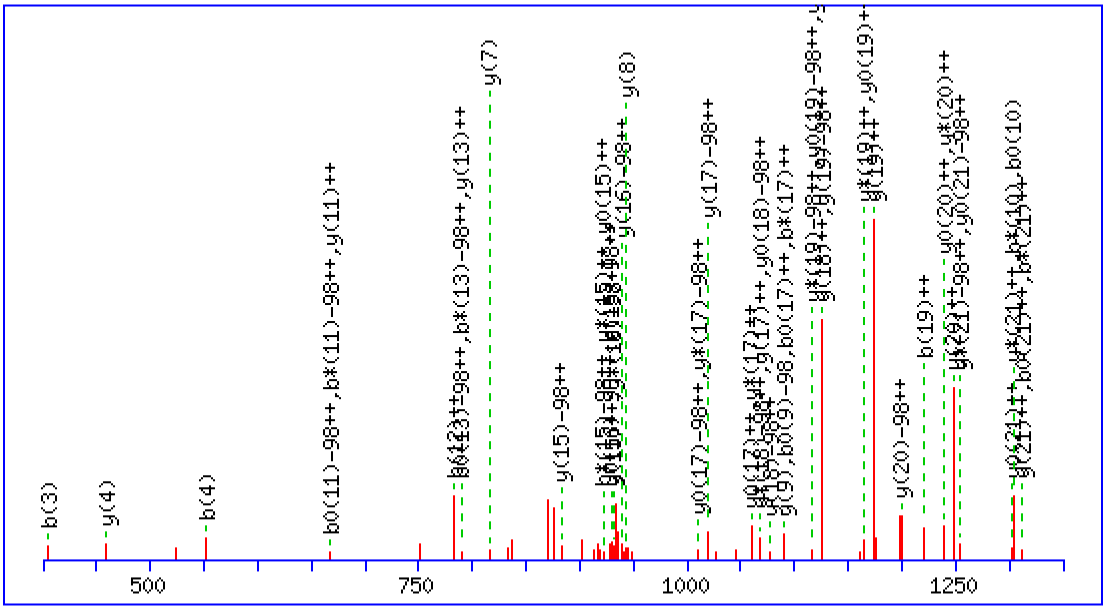
Monoisotopic mass of neutral peptide Mr(calc): 2101.7500
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.011
Matched b ions: b(4), b(6), b(12)-98, b(14), b(14)++, b(14)-98++, b(15)-98, b(15)
Matched y ions: y(4), y(5), y(11)++, y(11), y(12)++, y(12)-98, y(12), y(12)-98++, y(13)++, y(13), y(13)-98, y(15)++

Peptide No.451

IYQFPDCDSDEDEDFKLQDQALK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **IYQFPDCDSDEDEDFKLQDQALK**
Found in **SEPT4_MOUSE** in **SwissProt**, Septin-4 OS=Mus musculus GN=Sept4 PE=1 SV=1

Match to Query 6835: 2898.194166 from(967.071998,3+) index(6837)
Title: Elution from: 50.731 to 50.731 scan no 5262 cid35.00 polarity:+:m1s



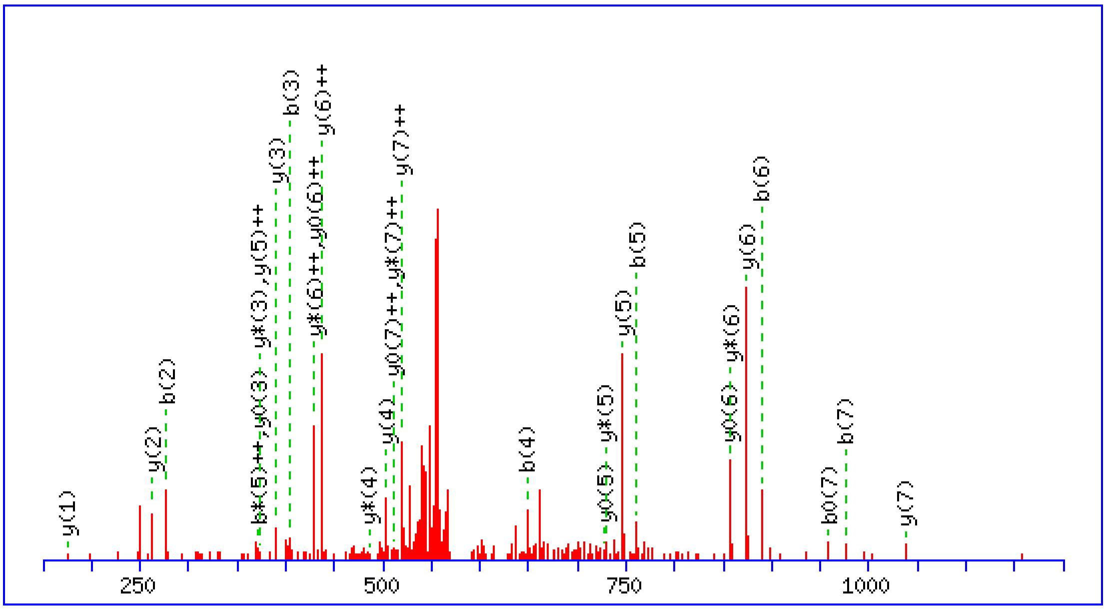
Monoisotopic mass of neutral peptide Mr(calc): 2898.1943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0069
Matched b ions: b(3), b(4), b(12)++, b(15)-98++, b(19)++
Matched y ions: y(4), y(7), y(8), y(9), y(11)++, y(13)++, y(15)-98++, y(15)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++

Peptide No.452

IYQYIQSR
Confirmed sites: @Y:4
Ambiguous sites:

MS/MS Fragmentation of **IYQYIQSR**
Found in **DYR1A_MOUSE** in **SwissProt**, Dual specificity tyrosine-phosphorylation-regulated kinase 1A OS=Mus musculus GN=Dyrk1a PE=1 SV=1

Match to Query 1929: 1149.521424 from(575.767988,2+) index(821)
Title: Elution from: 31.870 to 31.870 scan no 2119 cid35.00 polarity:+



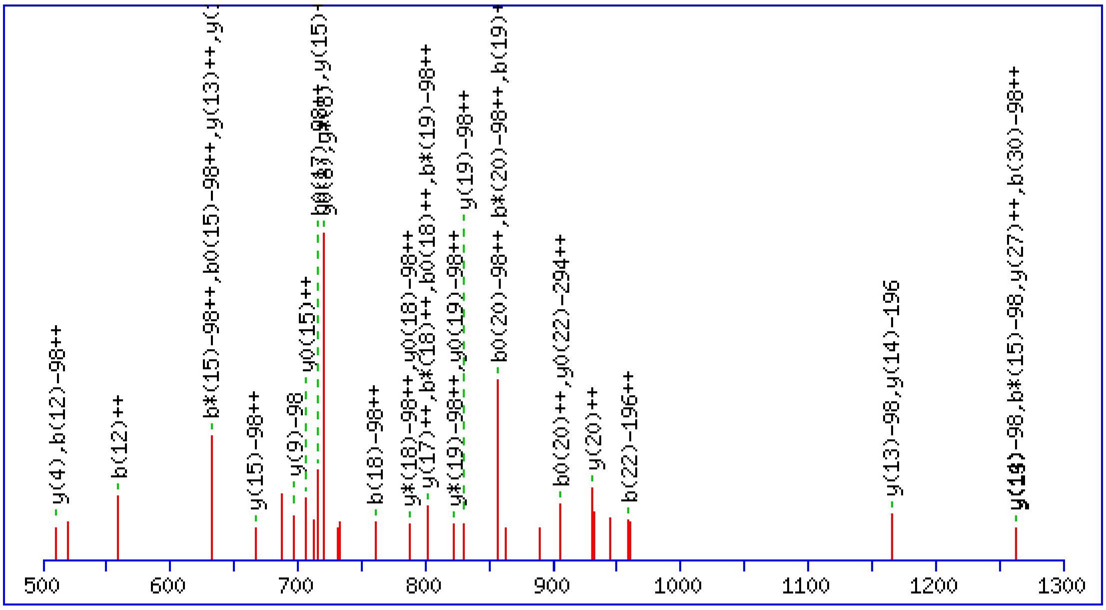
Monoisotopic mass of neutral peptide Mr(calc): 1149.5219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y4 : Phospho (Y)
Ions Score: 34 **Expect:** 0.0014
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7), y(7)++

Peptide No.453

KAANANAAAAPSTASVAAPDSDAGGGGGPGTR
Confirmed sites: @S:12,@S:21,@T:31
Ambiguous sites:

MS/MS Fragmentation of **KAANANAAAAPSTASVAAPDSDAGGGGGPGTR**
Found in **SCRT1_MOUSE** in **SwissProt**, Transcriptional repressor scratch 1 OS=Mus musculus GN=Scrt1 PE=2 SV=1

Match to Query 5875: 2977.193272 from(745.305594,4+) index(5262)
Title: Elution from: 38.731 to 38.731 scan no 3670 cid35.00 polarity:+:m1s



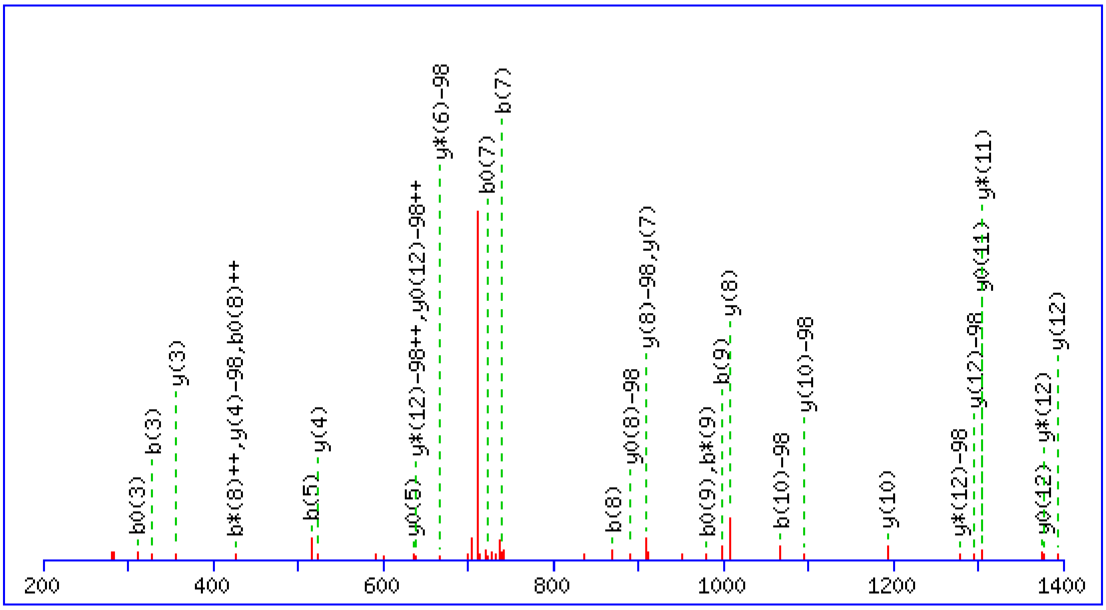
Monoisotopic mass of neutral peptide Mr(calc): 2977.2005
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T31 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.052
Matched b ions: b(12)++, b(12)-98++, b(18)-98++, b(19)++, b(22)-196++, b(30)-98++
Matched y ions: y(4), y(9)-98, y(13)++, y(13)-98, y(13), y(14)-98++, y(14)-196, y(14)-98, y(15)++, y(15)-98++, y(17)++, y(19)-98++, y(20)++, y(27)++

Peptide No.454

KAEGEPQEESPLK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **KAEGEPQEESPLK**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 3068: 1520.672284 from(761.343418,2+) index(343)
Title: Elution from: 19.061 to 19.061 scan no 1149 cid35.00 polarity:+



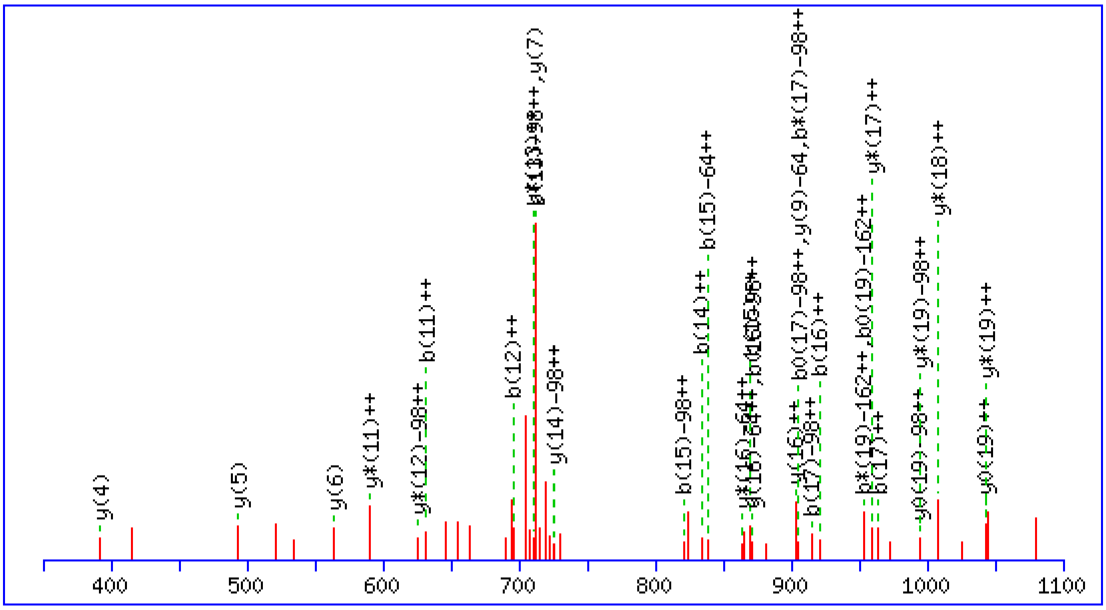
Monoisotopic mass of neutral peptide Mr(calc): 1520.6759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0033
Matched b ions: b(3), b(5), b(7), b(8), b(9), b(10)-98, b(12), b(12)-98++
Matched y ions: y(3), y(4)-98, y(4), y(7), y(8)-98, y(8), y(10)-98, y(10), y(12), y(12)-98

Peptide No.455

KAPKEELASDLEEMATSSAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **KAPKEELASDLEEMATSSAK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4874: 2230.007106 from(744.342978,3+) index(2701)
Title: Elution from: 47.880 to 47.880 scan no 4693 cid35.00 polarity:+



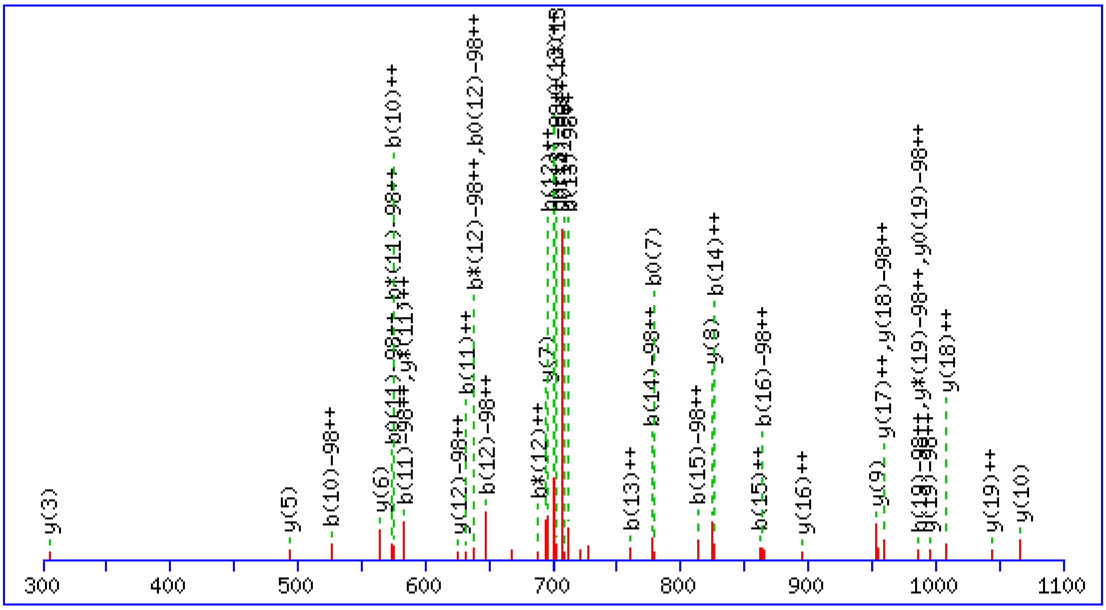
Monoisotopic mass of neutral peptide Mr(calc): 2230.0075
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M14 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 23 **Expect:** 0.04
Matched b ions: b(11)++, b(12)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(19)++, b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(14)-98++, y(16)++

Peptide No.456

KAPKEELASDLEEMATSSAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **KAPKEELASDLEEMATSSAK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 5795: 2214.009891 from(739.010573,3+) index(6715)
Title: Elution from: 48.116 to 48.116 scan no 4973 cid35.00 polarity:+:m1s



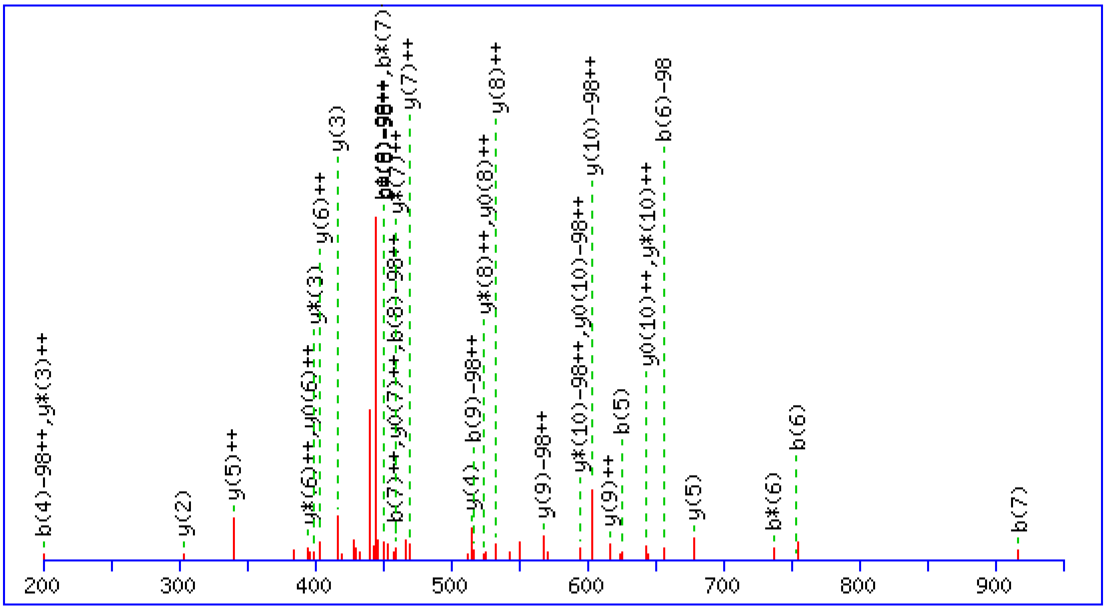
Monoisotopic mass of neutral peptide Mr(calc): 2214.0126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 **Expect:** 2.2e-005
Matched b ions: b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(19)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(12)-98++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++

Peptide No.457

KASEEEYVIRK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KASEEEYVIRK**
Found in **ARHG6_MOUSE** in **SwissProt**, Rho guanine nucleotide exchange factor 6 OS=Mus musculus GN=Arhgef6 PE=1 SV=1

Match to Query 2656: 1430.679864 from(477.900564,3+) index(527)
Title: Elution from: 20.558 to 20.558 scan no 1350 cid35.00 polarity:+



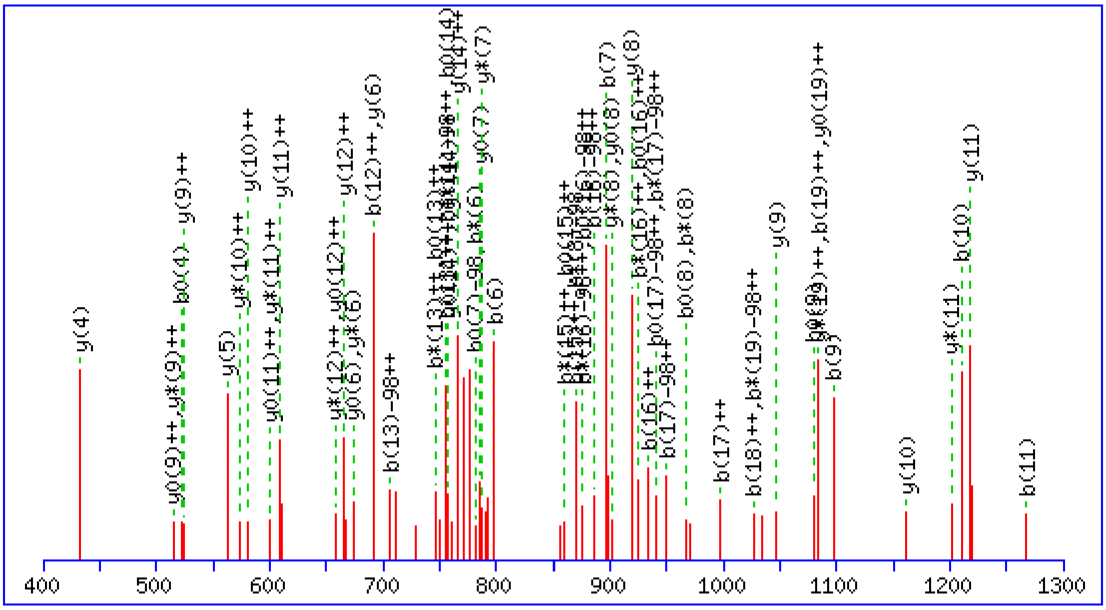
Monoisotopic mass of neutral peptide Mr(calc): 1430.6806
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.009
Matched b ions: b(2), b(4)-98++, b(5), b(6), b(6)-98, b(7), b(7)++, b(8)-98++, b(9)-98++, b(10)++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-98++

Peptide No.458

KDSEEEVSLLGNQDIEEGNSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KDSEEEVSLLGNQDIEEGNSR**
Found in **VPP2_MOUSE** in **SwissProt**, V-type proton ATPase 116 kDa subunit a isoform 2 OS=Mus musculus GN=Atp6v0a2 PE=1 SV=2

Match to Query 6069: 2427.042858 from(810.021562,3+) index(6012)
Title: Elution from: 40.004 to 40.004 scan no 3942 cid35.00 polarity:+:m1s



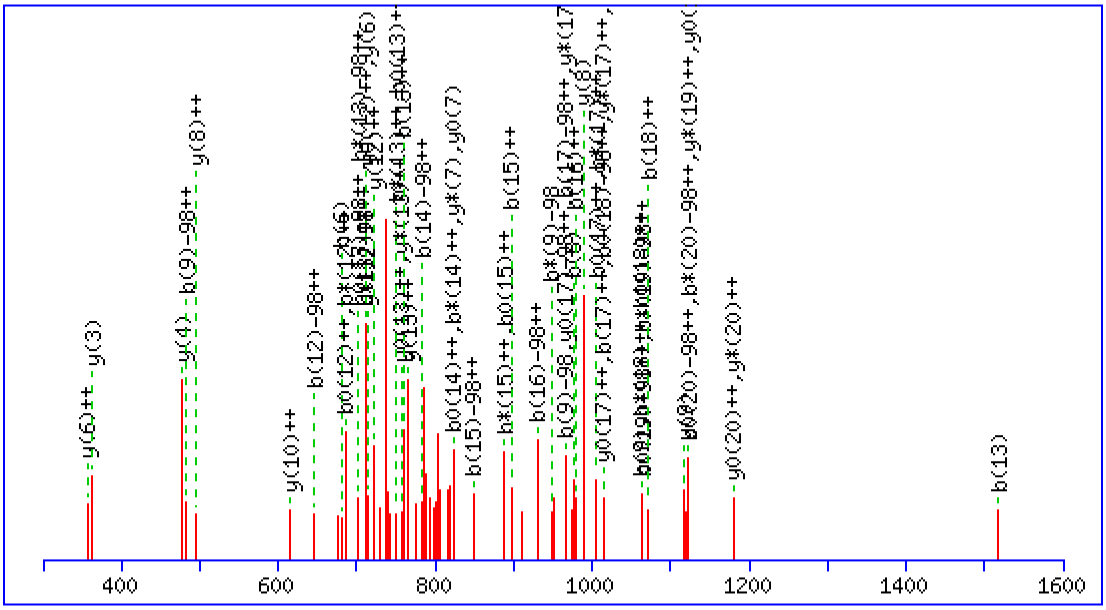
Monoisotopic mass of neutral peptide Mr(calc): 2427.0438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 5e-005
Matched b ions: b(6), b(7), b(9), b(10), b(11), b(12)++, b(13)-98++, b(13)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++, b(19)++
Matched y ions: y(4), y(5), y(6), y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(14)++

Peptide No.459

KDSEGYSESPDLEFEYADTDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KDSEGYSESPDLEFEYADTDK**
Found in **FA40A_MOUSE** in **SwissProt**, Protein FAM40A OS=Mus musculus GN=Fam40a PE=1 SV=2

Match to Query 5368: 2503.977987 from(835.666605,3+) index(5519)
Title: Elution from: 42.623 to 42.623 scan no 4127 cid35.00 polarity:+:m1s



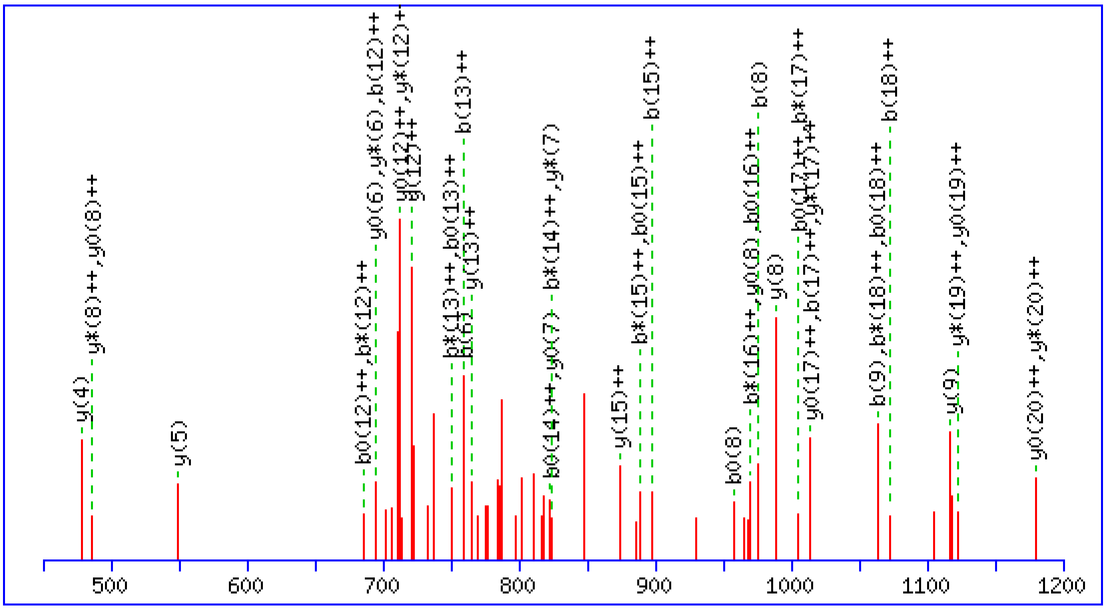
Monoisotopic mass of neutral peptide Mr(calc): 2503.9792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0015
Matched b ions: b(6), b(8), b(9)-98++, b(9)-98, b(9), b(12)-98++, b(13), b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(19)++, b(20)++
Matched y ions: y(3), y(4), y(6)++, y(6), y(8), y(8)++, y(9), y(10)++, y(12)++, y(13)++

Peptide No.460

KDSEGYSESPDLEFEYADTDK
Confirmed sites:
Ambiguous sites: @S:3orY:6

MS/MS Fragmentation of **KDSEGYSESPDLEFEYADTDK**
Found in **FA40A_MOUSE** in **SwissProt**, Protein FAM40A OS=Mus musculus GN=Fam40a PE=1 SV=2

Match to Query 5233: 2503.978470 from(835.666766,3+) index(5307)
Title: Elution from: 42.801 to 42.801 scan no 4155 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2503.9792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
Ions Score: 34 **Expect:** 0.002
Matched b ions: b(6), b(8), b(9), b(12)++, b(13)++, b(15)++, b(17)++, b(18)++, b(19)++, b(20)++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(12)++, y(13)++, y(15)++

Peptide No.461

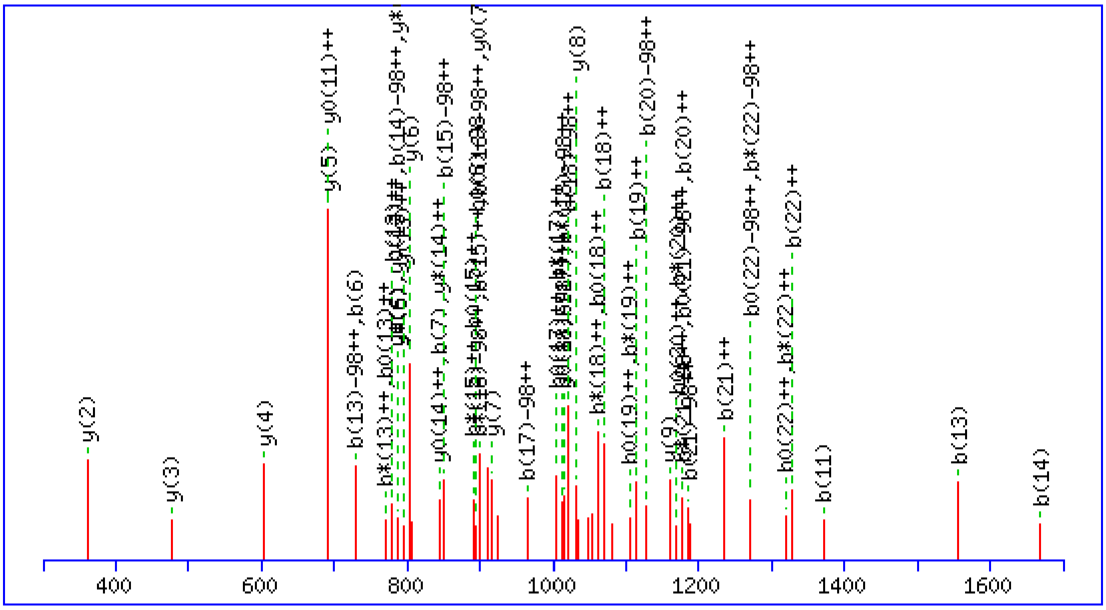
KEEENVDSDDEGELQDLLSQDWR

Confirmed sites: @S:8

Ambiguous sites:

MS/MS Fragmentation of **KEEENVDSDDEGELQDLLSQDWR**
Found in **ZN830_MOUSE** in **SwissProt**, Zinc finger protein 830 OS=Mus musculus GN=Znf830 PE=1 SV=1

Match to Query 6781: 2828.164443 from(943.728757,3+) index(7129)
Title: Elution from: 61.351 to 61.351 scan no 6248 cid35.00 polarity:+:m1s



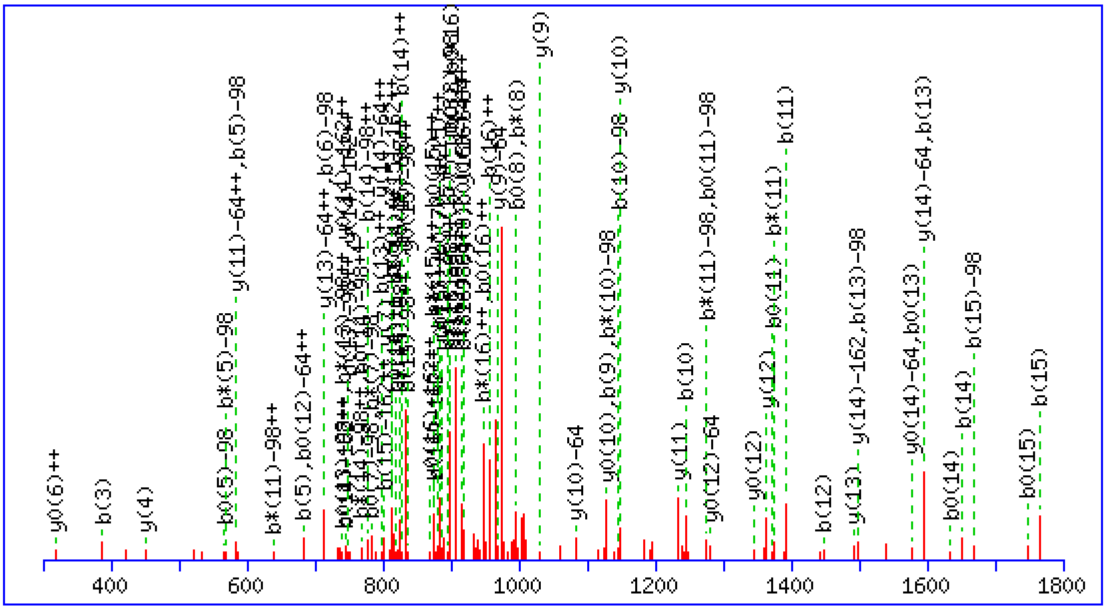
Monoisotopic mass of neutral peptide Mr(calc): 2828.1661
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 **Expect:** 3.8e-006
Matched b ions: b(6), b(7), b(11), b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(15)++, b(15)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(13)++

Peptide No.462

KEESEESDDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5217: 2044.712174 from(1023.363363,2+) index(6055)
Title: Elution from: 63.178 to 63.178 scan no 5287 cid35.00 polarity:+:m1s



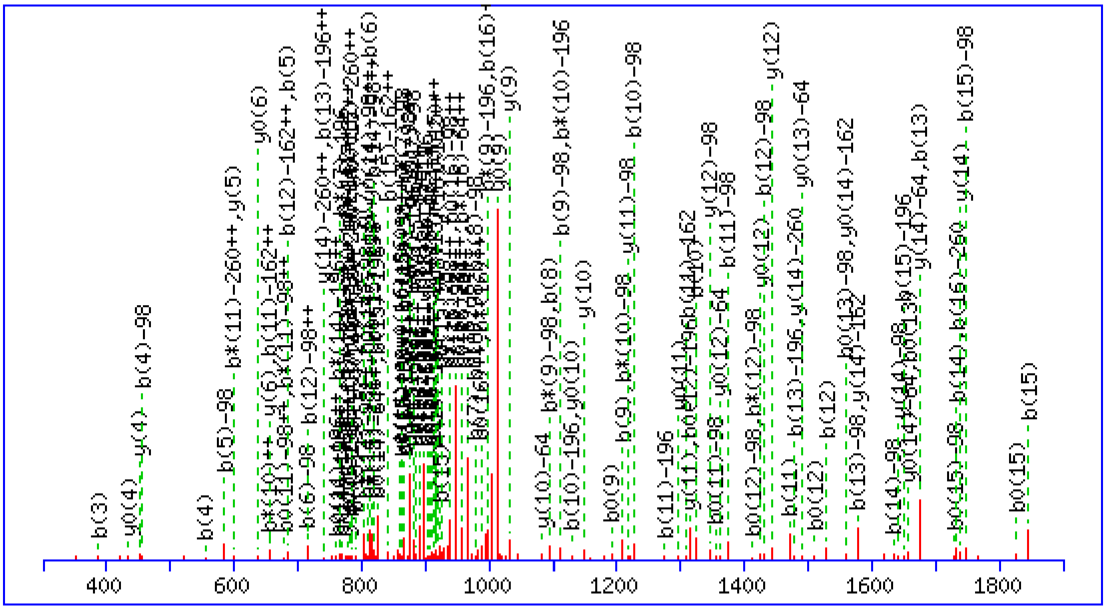
Monoisotopic mass of neutral peptide Mr(calc): 2044.7133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 61 **Expect:** 1.5e-006
Matched b ions: b(3), b(5)-98, b(5), b(6)-98, b(6), b(7), b(8)-98, b(9), b(10), b(10)-98, b(11), b(12), b(13)-98, b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(15), b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(15)++

Peptide No.463

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 4524: 2124.677612 from(1063.346082,2+) index(3006)
Title: Elution from: 61.764 to 61.764 scan no 5847 cid35.00 polarity:+



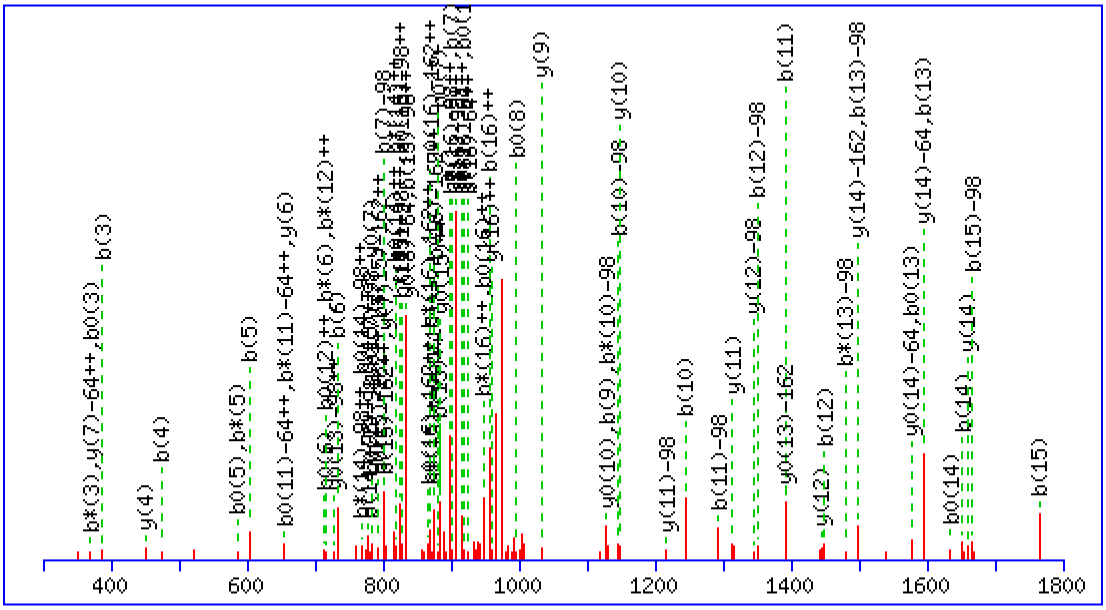
Monoisotopic mass of neutral peptide Mr(calc): 2124.6796
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 64 **Expect:** 4.9e-007
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)-196, b(7), b(8), b(8)-196, b(8)-98, b(9), b(9)-98, b(10)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-196, b(12), b(12)-98, b(12)-98++, b(13)-98, b(13), b(13)-196, b(13)-196++, b(13)-98++, b(14)-98, b(14), b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15), b(15)-98++, b(15)-98, b(15)-196, b(15)++, b(16)-98++, b(16)-196++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(14)-98, y(14), y(15)-98++

Peptide No.464

KEESEESDDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5127: 2044.713616 from(1023.364084,2+) index(6916)
Title: Elution from: 53.354 to 53.354 scan no 5543 cid35.00 polarity:+:m1s



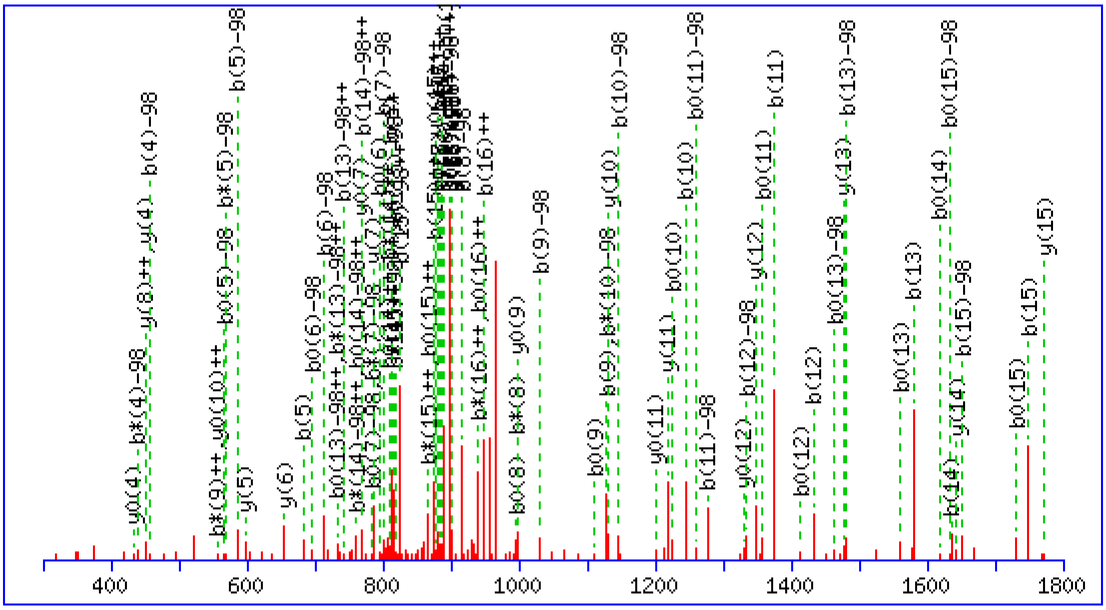
Monoisotopic mass of neutral peptide Mr(calc): 2044.7133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 79 **Expect:** 2.9e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(7)-98, b(8)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98++, b(14)++, b(15)-98++, b(15), b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12), y(12)-98, y(14), y(16)++

Peptide No.465

KEESEESDDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5085: 2028.716446 from(1015.365499,2+) index(3495)
Title: Elution from: 61.887 to 61.887 scan no 6298 cid35.00 polarity:+



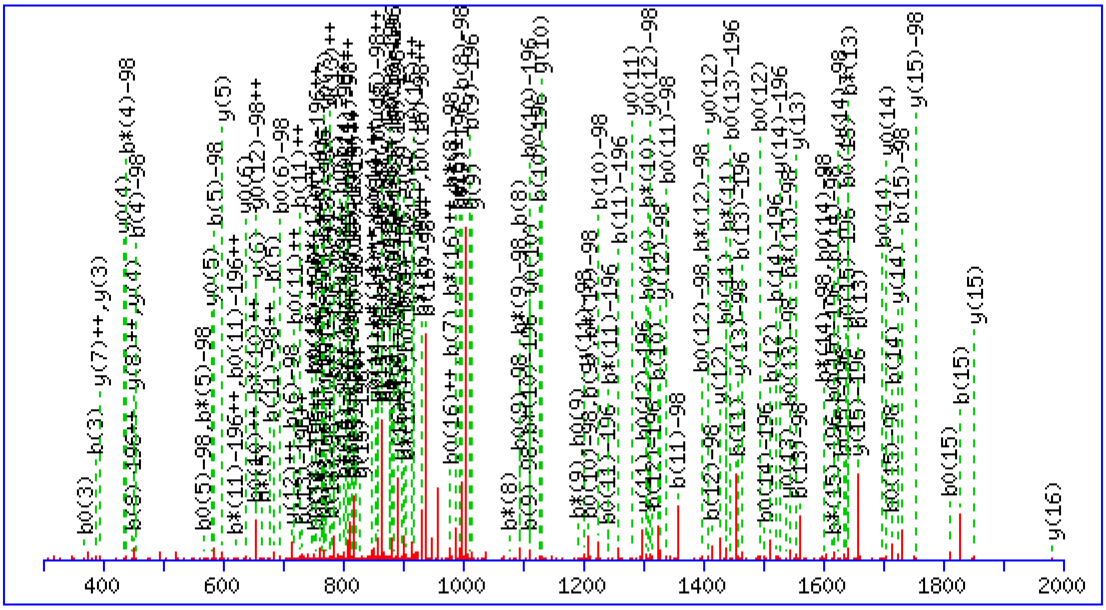
Monoisotopic mass of neutral peptide Mr(calc): 2028.7184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 3.5e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(14), b(14)-98++, b(14)++, b(15), b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(10), y(11), y(12), y(13), y(14), y(15), y(15)++, y(16)-98++

Peptide No.466

KEESEESDDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5341: 2108.682076 from(1055.348314,2+) index(3566)
Title: Elution from: 70.589 to 70.589 scan no 6848 cid35.00 polarity:+



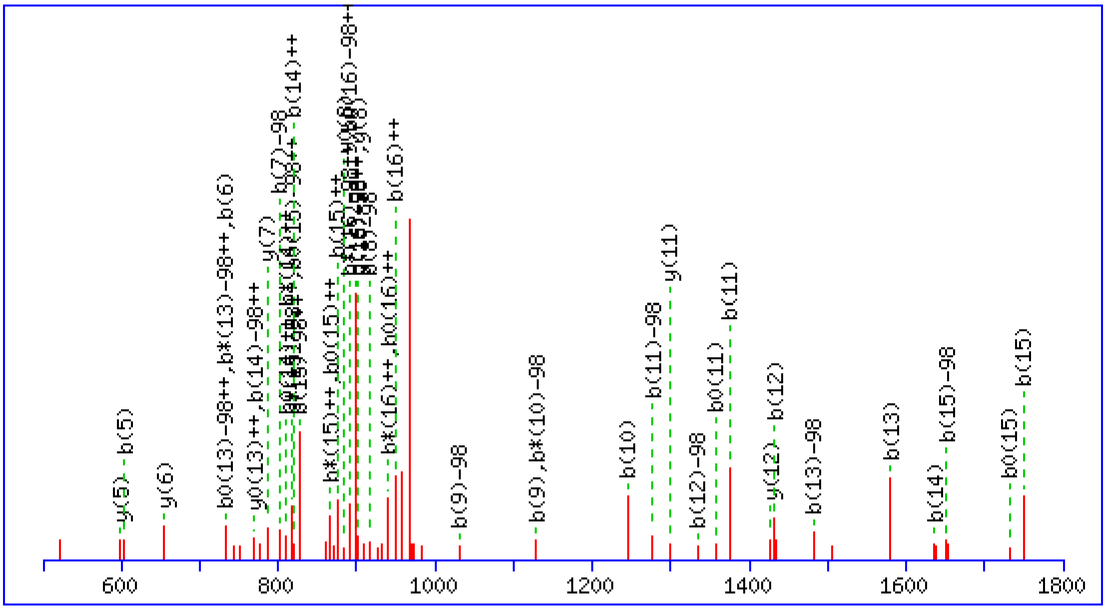
Monoisotopic mass of neutral peptide Mr(calc): 2108.6847
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 2.3e-007
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(7)-196, b(8), b(8)-196++, b(8)-98, b(8)-196, b(9)-98, b(9), b(9)-196, b(10), b(10)-98, b(10)-196, b(11)-98, b(11), b(11)-196, b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-196, b(13)-98, b(13), b(13)-196, b(13)-196++, b(13)-98++, b(14), b(14)-196++, b(14)-98, b(14)-196, b(14)-98++, b(14)++, b(15)-98++, b(15)-98, b(15), b(15)-196++, b(15)-196, b(15)++, b(16)-196++, b(16)-98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(10), y(11), y(11)-98, y(12)++, y(12), y(12)-98, y(13), y(13)-98, y(13)++, y(14), y(14)-98++, y(14)-196, y(14)-98, y(15), y(15)-98, y(15)-196++, y(15)-98++, y(15)-196, y(16), y(16)-196++

Peptide No.467

KEESEESDDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESDDDMGFGLFD**
Found in **RLA2_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3

Match to Query 5086: 2028.716510 from(1015.365531,2+) index(7118)
Title: Elution from: 60.868 to 60.868 scan no 6206 cid35.00 polarity:+:m1s



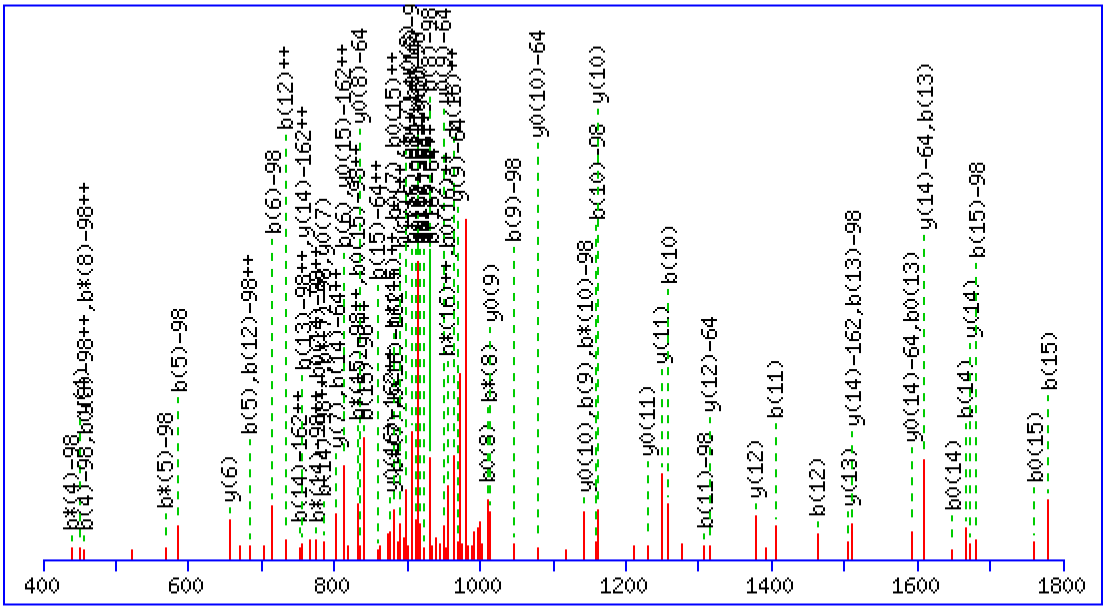
Monoisotopic mass of neutral peptide Mr(calc): 2028.7184
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 2.8e-005
Matched b ions: b(5), b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10), b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(14)-98++, b(14)++, b(15)-98, b(15), b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(5), y(6), y(7), y(8), y(11), y(12), y(16)-98++

Peptide No.468

KEESEESEDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **KEESEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 5174: 2058.726148 from(1030.370350,2+) index(3288)
Title: Elution from: 54.157 to 54.157 scan no 5624 cid35.00 polarity:+



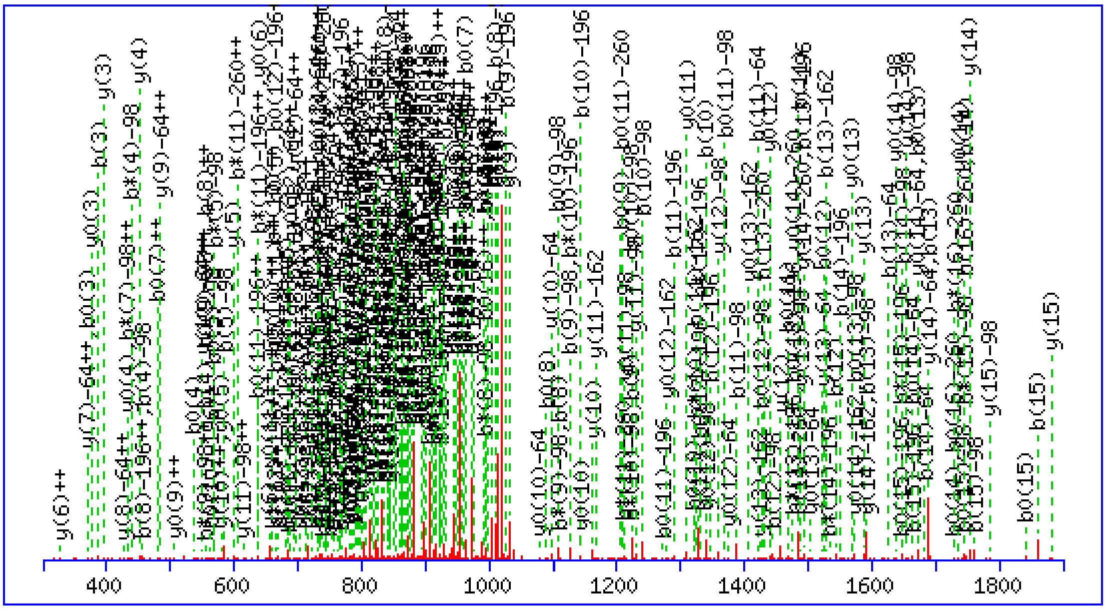
Monoisotopic mass of neutral peptide Mr(calc): 2058.7289
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 51 **Expect:** 1.7e-005
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)++, b(12)-98++, b(13)-98, b(13), b(13)-98++, b(14), b(14)-98++, b(15), b(15)-98, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(6), y(7), y(8), y(10), y(11), y(12), y(13), y(14), y(16)-98++

Peptide No.469

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4580: 2138.694130 from(1070.354341,2+) index(2997)
Title: Elution from: 61.116 to 61.116 scan no 5804 cid35.00 polarity:+



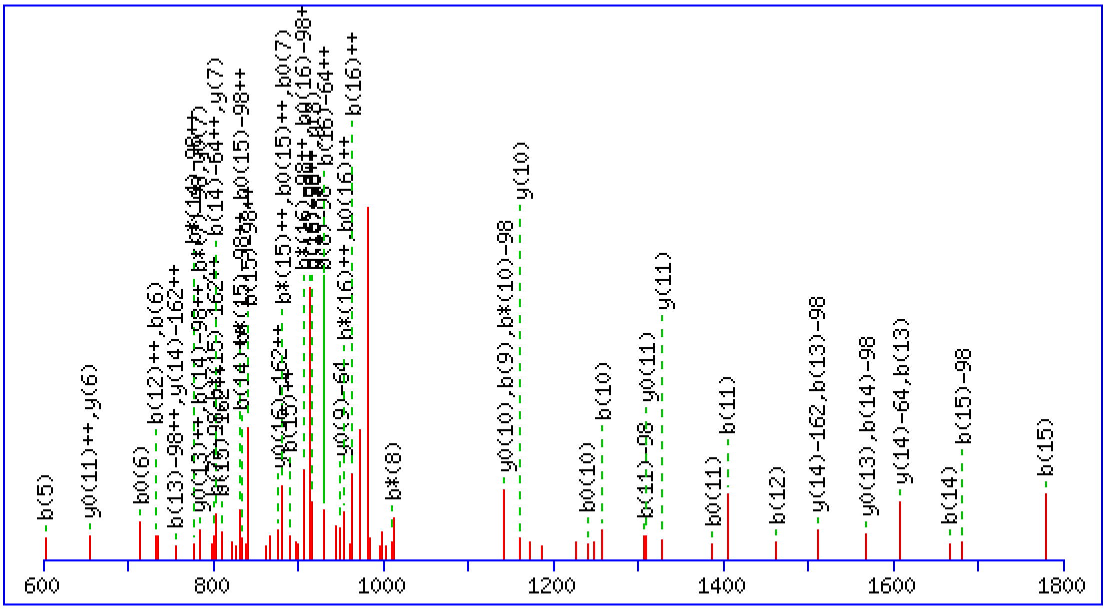
Monoisotopic mass of neutral peptide Mr(calc): 2138.6952
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 59 **Expect:** 1.7e-006
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7)-196, b(8)-196++, b(8), b(8)-98, b(8)++, b(8)-196, b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-196, b(10)++, b(11), b(11)-98, b(11)-196, b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-196, b(12)-98++, b(13)-98, b(13), b(13)-196, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98, b(14), b(14)-196, b(14)-98++, b(14)++, b(15)-98++, b(15)-98, b(15), b(15)-196++, b(15)-196, b(15)++, b(16)-98++, b(16)-196++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(13), y(13)-98, y(13)++, y(14), y(14)-98, y(14)-196++, y(14)++, y(15), y(15)-196++, y(15)-98, y(16)-196++, y(16)-98++

Peptide No.470

KEESEEESEDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4365: 2058.727096 from(1030.370824,2+) index(2720)
Title: Elution from: 52.590 to 52.590 scan no 5212 cid35.00 polarity:+



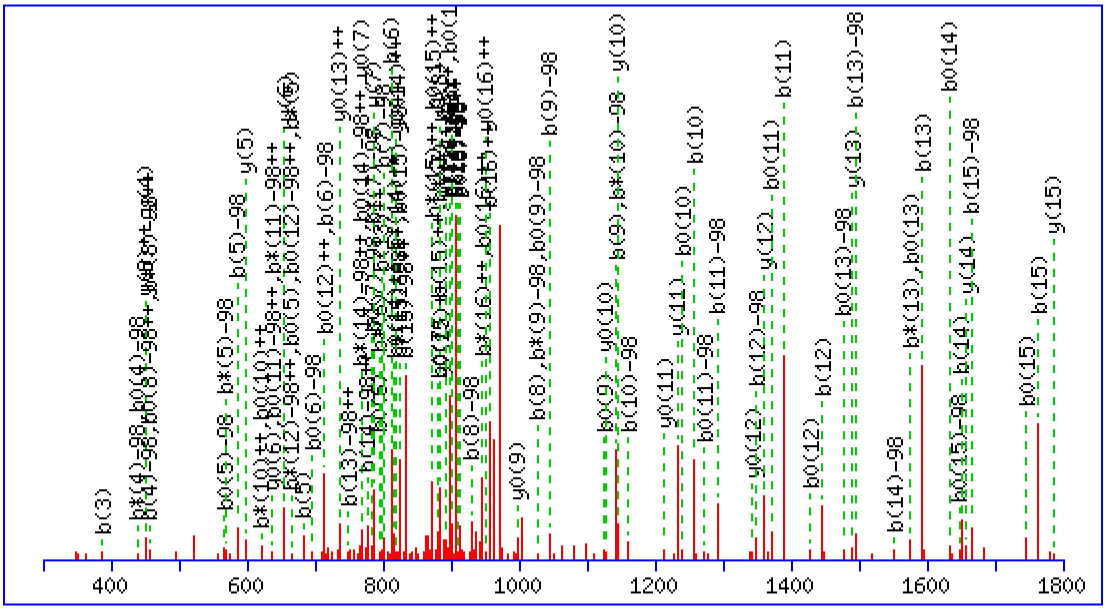
Monoisotopic mass of neutral peptide Mr(calc): 2058.7289
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 **Expect:** 2.4e-005
Matched b ions: b(5), b(6), b(7)-98, b(8)-98, b(9), b(10), b(11)-98, b(11), b(12), b(12)++, b(13)-98, b(13), b(13)-98++, b(14)-98, b(14)-98++, b(14), b(14)++, b(15)-98++, b(15), b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(6), y(7), y(8), y(10), y(11), y(16)-98++

Peptide No.471

KEESEESEDDMGFGLFD
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **KEESEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4988: 2042.731414 from(1022.372983,2+) index(3397)
Title: Elution from: 61.519 to 61.519 scan no 6192 cid35.00 polarity:+



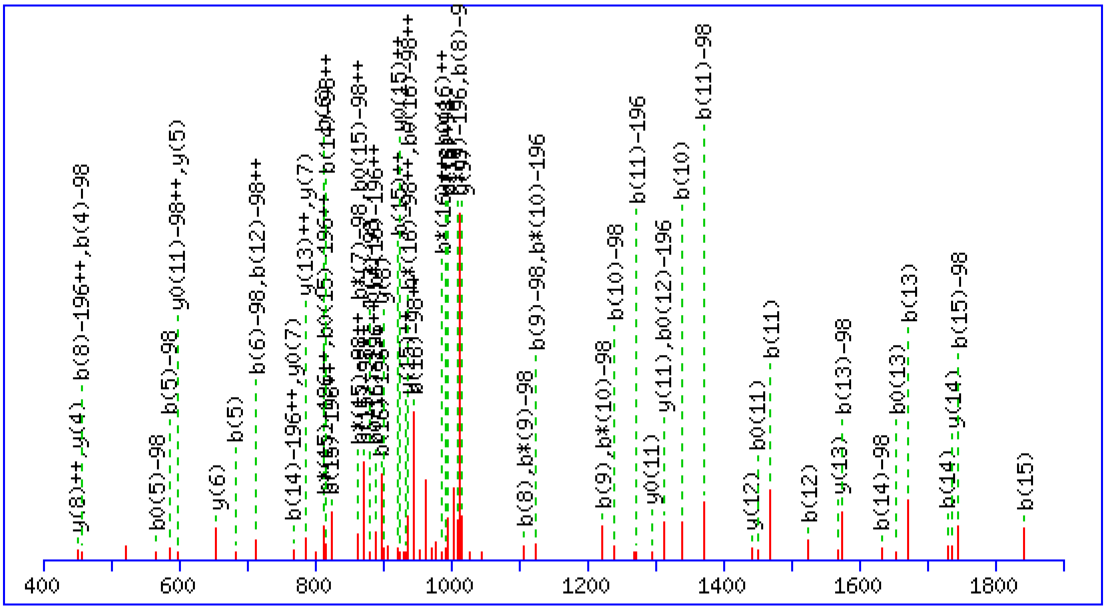
Monoisotopic mass of neutral peptide Mr(calc): 2042.7340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 **Expect:** 9.5e-008
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)-98, b(15)-98++, b(15), b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(10), y(11), y(12), y(13), y(14), y(15), y(15)++, y(16)-98++

Peptide No.472

KEESEESEDDMGFGLFD
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4503: 2122.695586 from(1062.355069,2+) index(3047)
Title: Elution from: 70.220 to 70.220 scan no 6312 cid35.00 polarity:+



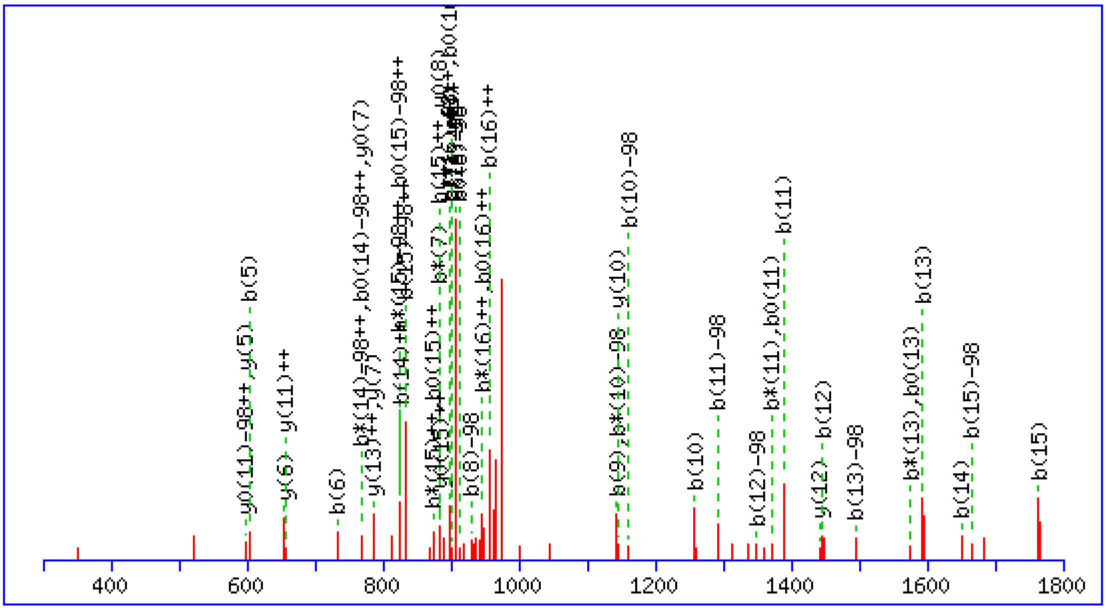
Monoisotopic mass of neutral peptide Mr(calc): 2122.7003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 5e-006
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-196++, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(11)-196, b(12)-98++, b(12), b(13)-98, b(13), b(14)-98, b(14), b(14)-98++, b(14)-196++, b(15)-196++, b(15), b(15)-98++, b(15)-98, b(15)++, b(16)-98++, b(16)-196++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(11), y(12), y(13)++, y(13), y(14), y(15)++

Peptide No.473

KEESEESEDDMGFGLFD
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KEESEESEDDMGFGLFD**
Found in **RLA1_MOUSE** in **SwissProt**, 60S acidic ribosomal protein P1 OS=Mus musculus GN=Rplp1 PE=1 SV=1

Match to Query 4987: 2042.730410 from(1022.372481,2+) index(6898)
Title: Elution from: 60.509 to 60.509 scan no 6105 cid35.00 polarity:+:m1s



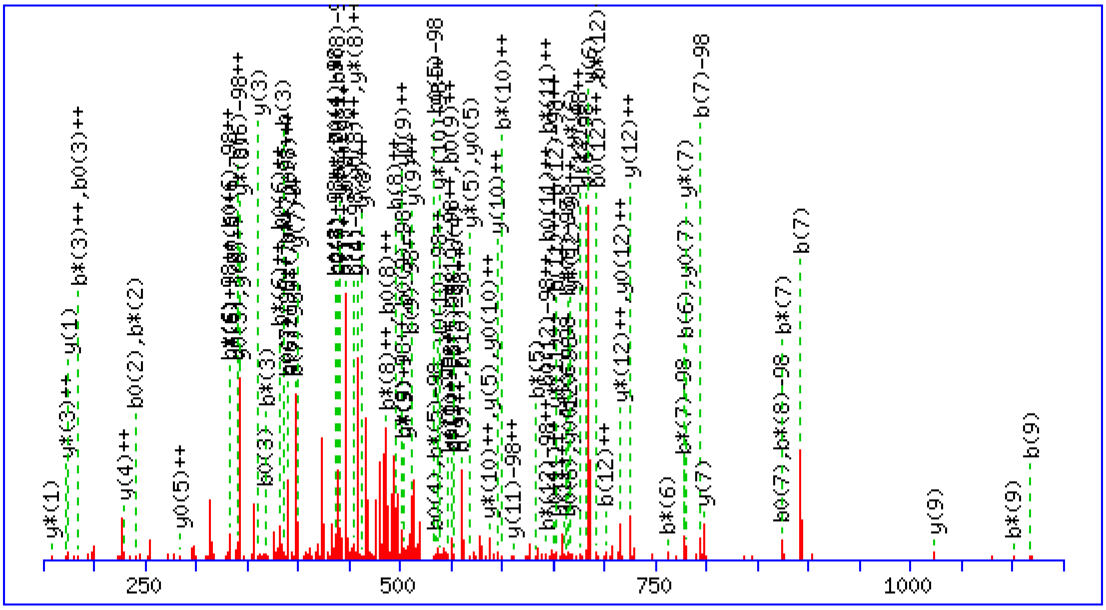
Monoisotopic mass of neutral peptide Mr(calc): 2042.7340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 3.4e-005
Matched b ions: b(5), b(6), b(7), b(8)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)++, b(15)-98++, b(15), b(15)-98, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(11)++, y(12), y(13)++

Peptide No.474

KEKSPELPEPSVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **KEKSPELPEPSVR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 3767: 1574.770671 from(525.930833,3+) index(799)
Title: Elution from: 31.630 to 31.630 scan no 2089 cid35.00 polarity:+



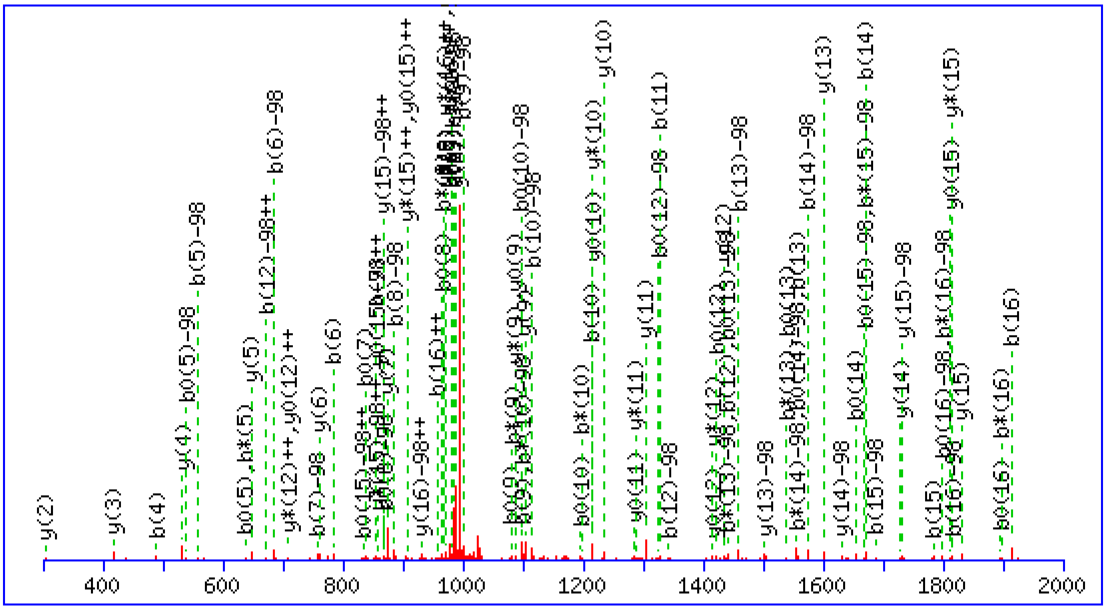
Monoisotopic mass of neutral peptide Mr(calc): 1574.7705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98++, b(6)++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)-98++, b(8)++, b(9)++, b(9), b(9)-98++, b(10)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(1), y(3), y(4), y(4)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(9), y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++

Peptide No.475

KETESEAEDDNLDDLER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KETESEAEDDNLDDLER**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 5332: 2086.821040 from(1044.417796,2+) index(4980)
Title: Elution from: 40.090 to 40.090 scan no 3133 cid35.00 polarity:+:m1s



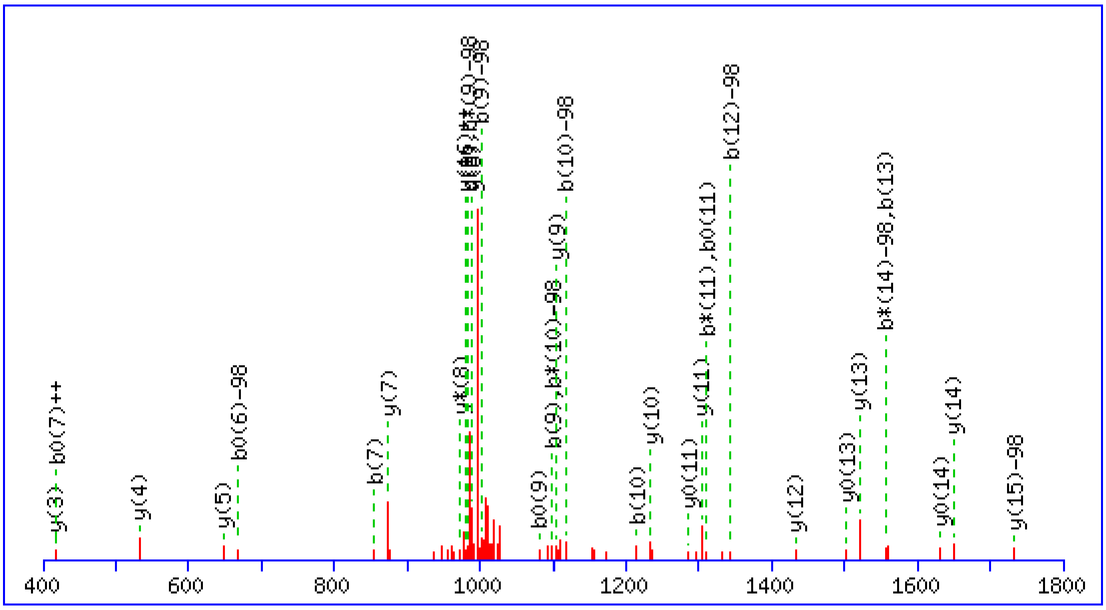
Monoisotopic mass of neutral peptide Mr(calc): 2086.8215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 90 **Expect:** 3.7e-009
Matched b ions: b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(12), b(12)-98++, b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(15), b(15)-98, b(16), b(16)-98, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15), y(15)-98, y(15)-98++, y(16)-98++, y(16)++

Peptide No.476

KETESEAEDDNLDDLER
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **KETESEAEDDNLDDLER**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 5256: 2086.818846 from(1044.416699,2+) index(5384)
Title: Elution from: 31.880 to 31.880 scan no 2887 cid35.00 polarity:+:m1s



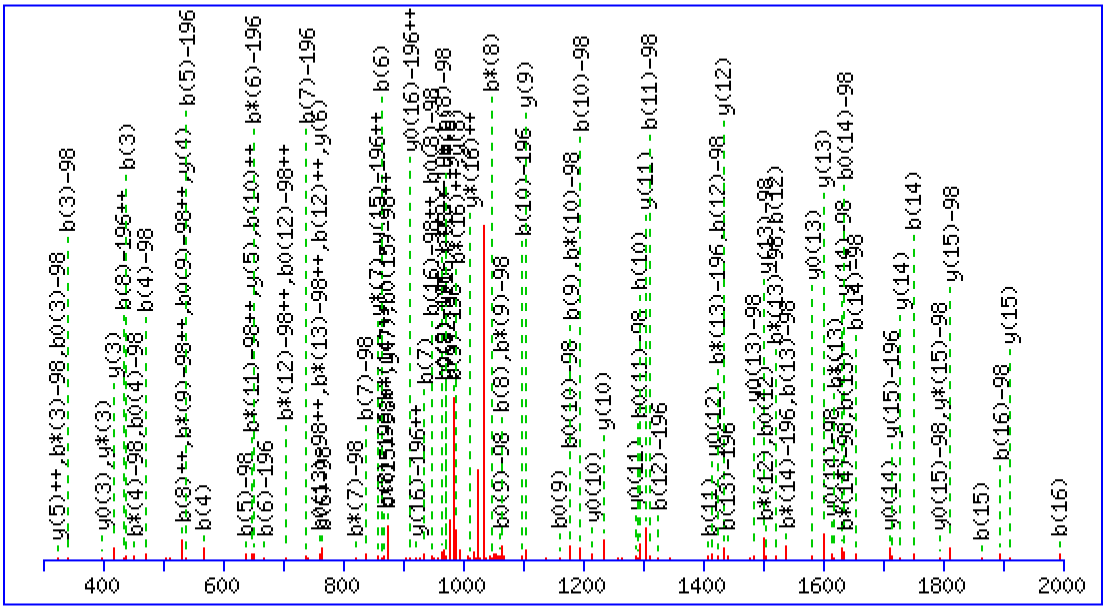
Monoisotopic mass of neutral peptide Mr(calc): 2086.8215
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 **Expect:** 1.6e-007
Matched b ions: b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(12)-98, b(13)
Matched y ions: y(3), y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15)-98, y(16)++

Peptide No.477

KETESEAEDDNLDDLER
Confirmed sites: @T:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **KETESEAEDDNLDDLER**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 4665: 2166.787066 from(1084.400809,2+) index(1895)
Title: Elution from: 35.558 to 35.558 scan no 3269 cid35.00 polarity:+



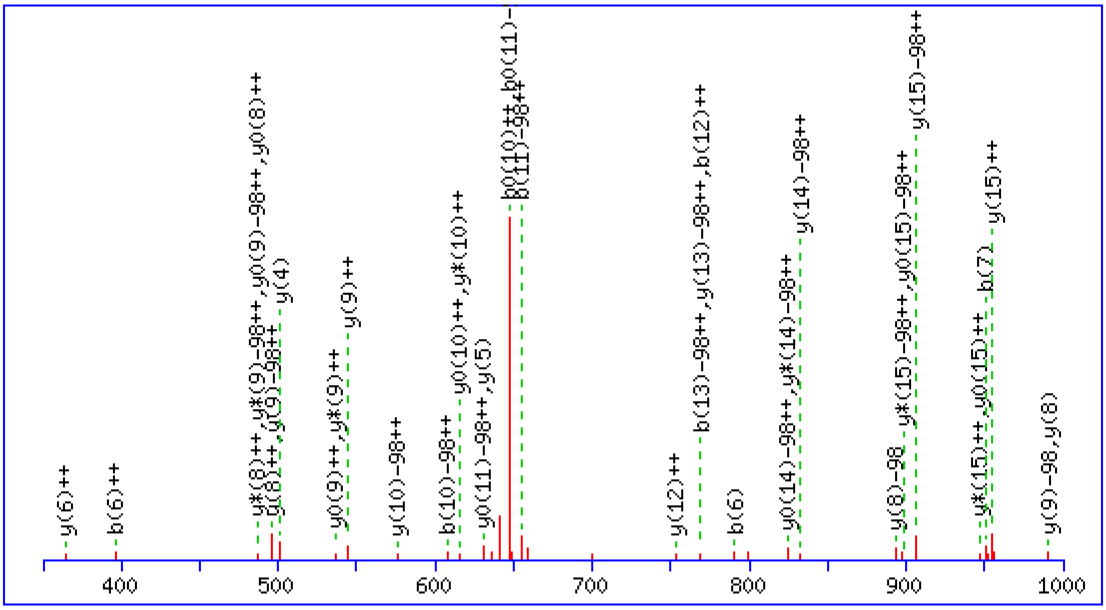
Monoisotopic mass of neutral peptide Mr(calc): 2166.7879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 1.9e-008
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)-196, b(6)-98, b(6)-196, b(6), b(7)-98, b(7)-196, b(7), b(8)++, b(8)-196++, b(8)-196, b(8), b(8)-98, b(9), b(9)-196, b(10)++, b(10)-98, b(10), b(10)-196, b(11), b(11)-98, b(12)++, b(12)-196, b(12)-98, b(12), b(13)-98, b(13), b(13)-196, b(14), b(14)-98, b(15), b(16)-98, b(16), b(16)-98++
Matched y ions: y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(15), y(15)-196++, y(15)-196, y(16)-196++, y(16)-98++

Peptide No.478

KFQEQECPPSPEPTRK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **KFQEQECPPSPEPTRK**
Found in **RRAS2_MOUSE** in **SwissProt**, Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1

Match to Query 4976: 2036.898858 from(679.973562,3+) index(404)
Title: Elution from: 20.045 to 20.045 scan no 1245 cid35.00 polarity:+



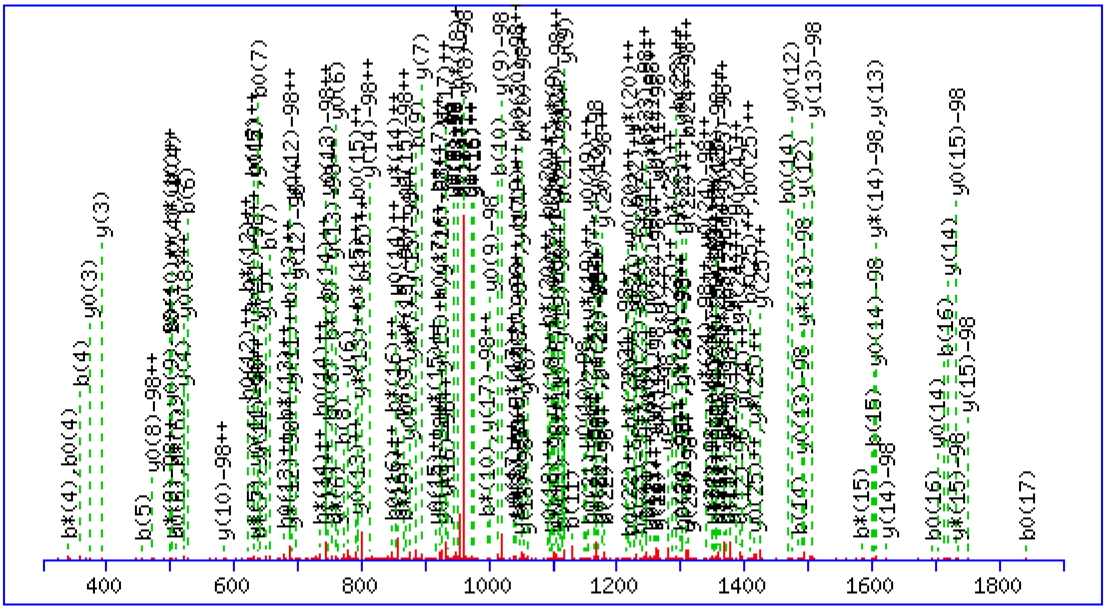
Monoisotopic mass of neutral peptide Mr(calc): 2036.9027
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.00095
Matched b ions: b(6)++, b(6), b(7), b(10)-98++, b(11)-98++, b(12)++, b(13)-98++, b(15)-98++, b(15)++
Matched y ions: y(4), y(5), y(6)++, y(8)++, y(8), y(8)-98, y(9)-98++, y(9)-98, y(9)++, y(10)-98++, y(12)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.479

KGATPAEDDEDKDIDLFGSDEEEEDK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **KGATPAEDDEDKDIDLFGSDEEEEDK**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 6909: 2976.185535 from(993.069121,3+) index(6095)
Title: Elution from: 38.990 to 38.990 scan no 3836 cid35.00 polarity:+:m1s



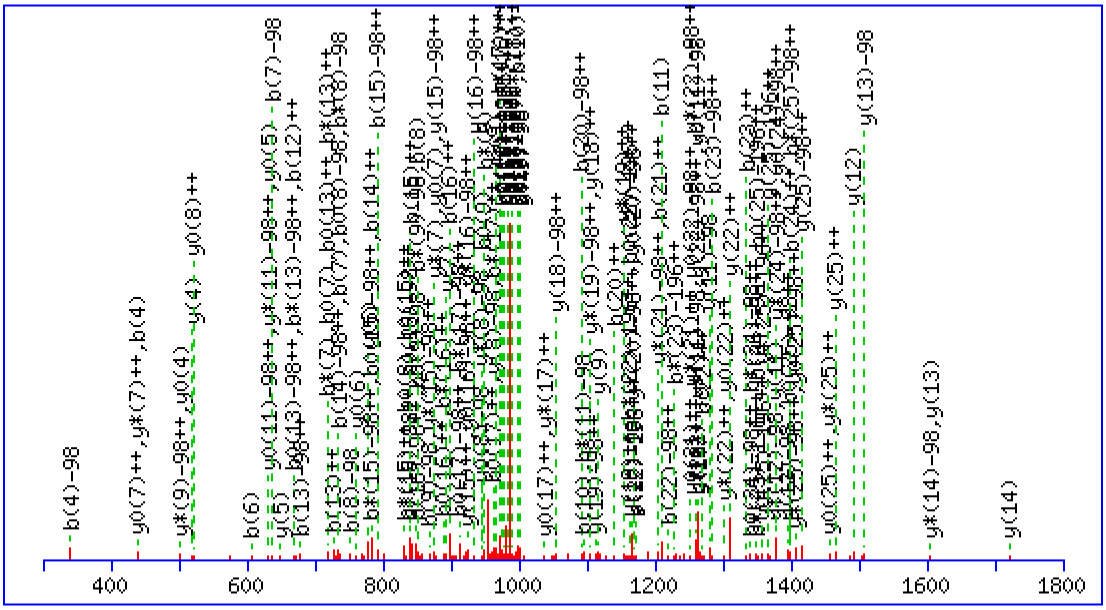
Monoisotopic mass of neutral peptide Mr(calc): 2976.1921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 **Expect:** 1e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12)++, b(12), b(13)++, b(13), b(14)++, b(14), b(15)++, b(15), b(16)++, b(16), b(17)++, b(18)++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++, b(24)++, b(25)-98++, b(25)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98, y(10), y(10)-98++, y(11)-98, y(11), y(11)-98++, y(11)++, y(12), y(12)-98, y(12)-98++, y(12)++, y(13), y(13)-98, y(13)-98++, y(14), y(14)-98, y(14)-98++, y(15)-98, y(15)-98++, y(15)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(24)-98++, y(24)++, y(25)++, y(25)-98++

Peptide No.480

KGATPAEDDDEDKDIDLFGSDEEEEDK
Confirmed sites: @T:4,@S:19
Ambiguous sites:

MS/MS Fragmentation of **KGATPAEDDDEDKDIDLFGSDEEEEDK**
Found in **EF1D_MOUSE** in **SwissProt**, Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3

Match to Query 5721: 3056.152374 from(1019.724734,3+) index(5249)
Title: Elution from: 41.916 to 41.916 scan no 4044 cid35.00 polarity:+:m1s



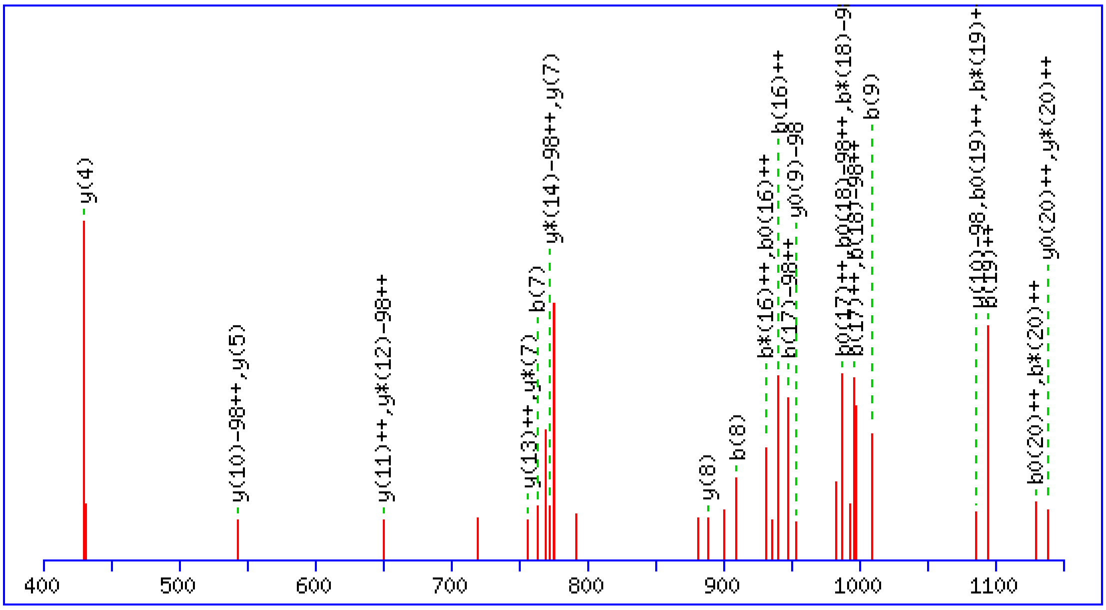
Monoisotopic mass of neutral peptide Mr(calc): 3056.1584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 4.6e-005
Matched b ions: b(4)-98, b(4), b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(20)-98++, b(20)++, b(21)++, b(22)-98++, b(22)-196++, b(22)++, b(23)-98++, b(23)++, b(24)++, b(24)-98++, b(25)-98++, b(25)++, b(25)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10)-98, y(10), y(11), y(11)-98, y(12), y(12)-98, y(13), y(13)-98, y(14), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(21)++, y(22)-98++, y(22)++, y(25)++, y(25)-98++, y(25)-196++

Peptide No.481

KGGEFDEFVNDDTDDDLPVSK
Confirmed sites: @T:13
Ambiguous sites:

MS/MS Fragmentation of **KGGEFDEFVNDDTDDDLPVSK**
Found in **CTR9_MOUSE** in **SwissProt**, RNA polymerase-associated protein CTR9 homolog OS=Mus musculus GN=Ctr9 PE=1 SV=2

Match to Query 5240: 2420.990361 from(808.004063,3+) index(5747)
Title: Elution from: 46.606 to 46.606 scan no 4574 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2420.9897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0074
Matched b ions: b(7), b(8), b(9), b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(19)++, b(20)++
Matched y ions: y(4), y(5), y(7), y(8), y(10)-98++, y(10)-98, y(11)++, y(13)++

Peptide No.482

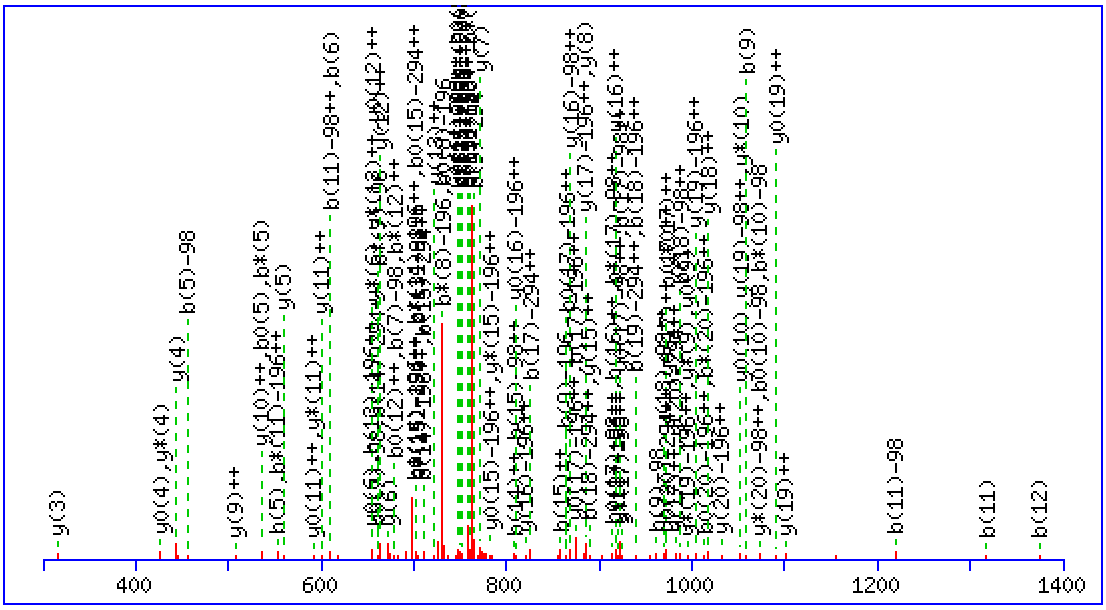
KGSAEGSSDEEGKLVIDEPAK

Confirmed sites: @S:3,@S:7,@S:8

Ambiguous sites:

MS/MS Fragmentation of **KGSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 5037: 2384.939607 from(795.987145,3+) index(4627)
Title: Elution from: 34.080 to 34.080 scan no 3040 cid35.00 polarity:+:m1s



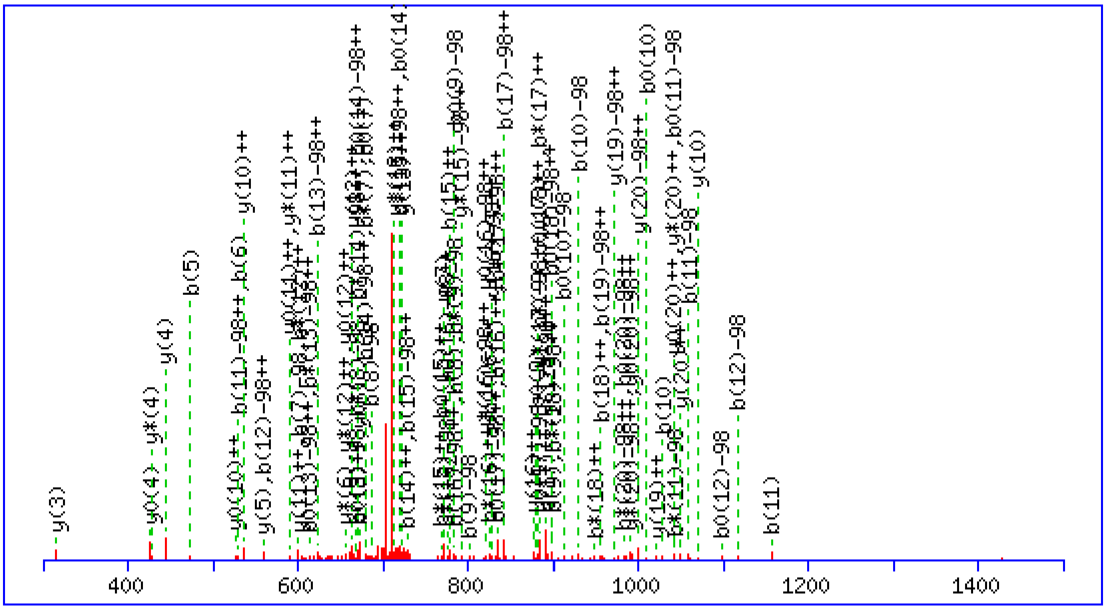
Monoisotopic mass of neutral peptide Mr(calc): 2384.9427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 9e-005
Matched b ions: b(5), b(5)-98, b(6), b(7)-98, b(8)-196, b(9)-98, b(9), b(9)-294, b(9)-196, b(11)-98, b(11), b(11)-98++, b(12), b(13)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-294++, b(14)++, b(15)++, b(15)-294++, b(15)-196++, b(15)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(17)-294++, b(18)-98++, b(18)-294++, b(18)-196++, b(19)-294++, b(20)-294++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(15)++, y(16)-98++, y(16)++, y(16)-196++, y(17)-196++, y(17)++, y(18)++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)++, y(19)-196++, y(20)-196++, y(20)-294++

Peptide No.483

KGSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KGSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 4868: 2225.006745 from(742.676191,3+) index(4182)
Title: Elution from: 26.595 to 26.595 scan no 2109 cid35.00 polarity:+:m1s



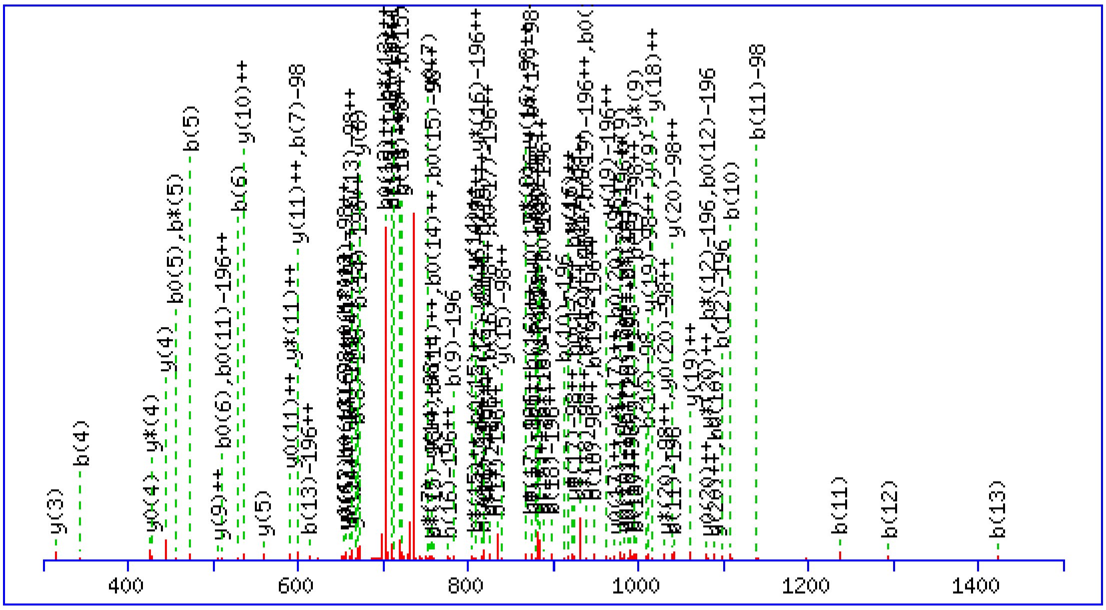
Monoisotopic mass of neutral peptide Mr(calc): 2225.0100
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.00014
Matched b ions: b(5), b(6), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)-98++, b(12)-98, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)++, y(10), y(11)++, y(12)++, y(13)++, y(16)-98++, y(16)++, y(17)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++

Peptide No.484

KGSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of **KGSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 5990: 2304.975261 from(769.332363,3+) index(5204)
Title: Elution from: 29.923 to 29.923 scan no 2625 cid35.00 polarity:+:m1s



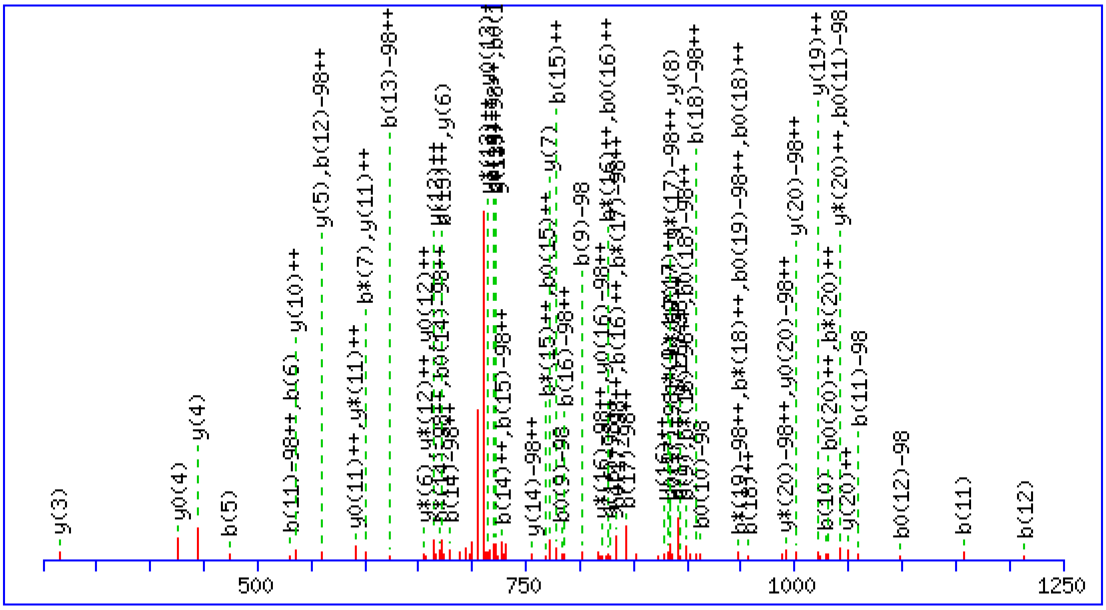
Monoisotopic mass of neutral peptide Mr(calc): 2304.9763
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 **Expect:** 1.3e-007
Matched b ions: b(4), b(5), b(6), b(7)-98, b(8)-196, b(9), b(9)-196, b(9)-98, b(10), b(10)-196, b(10)-98, b(11)-98, b(11), b(11)-196, b(12), b(12)-196, b(13), b(13)-196++, b(13)++, b(13)-98++, b(14)-98++, b(14)-196++, b(15)-196++, b(15)++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)-98++, b(19)-196++, b(20)++, b(20)-196++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(19)-196++, y(20)-196++, y(20)-98++, y(20)++

Peptide No.485

KGSAEGSSDEEGKLVIDEPAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **KGSAEGSSDEEGKLVIDEPAK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 5820: 2225.006769 from(742.676199,3+) index(4863)
Title: Elution from: 26.640 to 26.640 scan no 2177 cid35.00 polarity:+:m1s



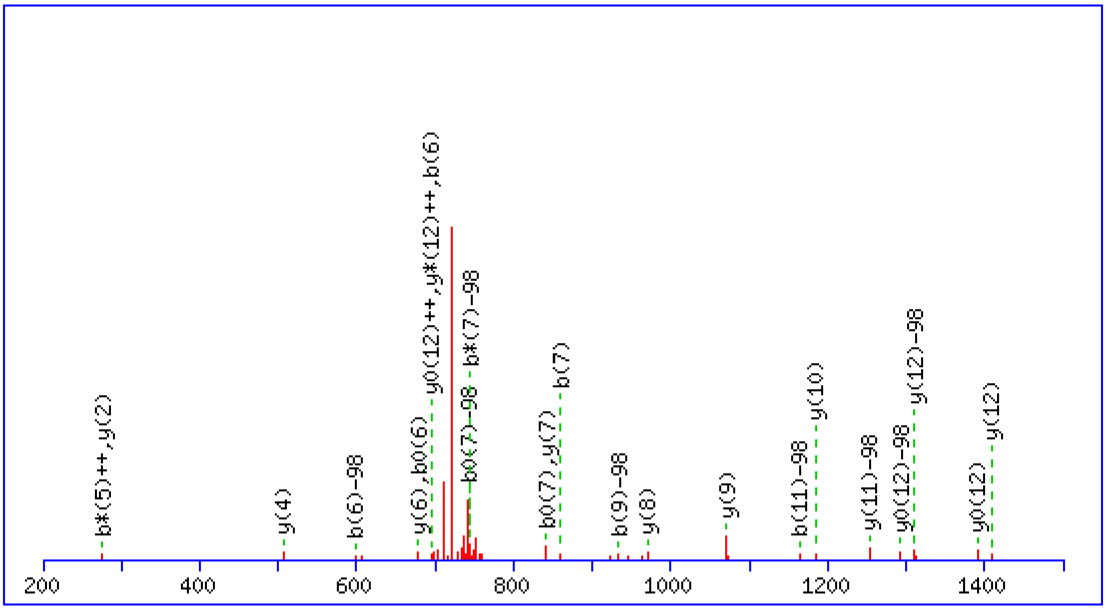
Monoisotopic mass of neutral peptide Mr(calc): 2225.0100
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 2.1e-005
Matched b ions: b(5), b(6), b(9), b(9)-98, b(10), b(11), b(11)-98, b(11)-98++, b(12), b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(16)-98++, y(16)++, y(17)-98++, y(19)++, y(20)-98++, y(20)++

Peptide No.486

KGSITEYTATEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KGSITEYTATEEK**
Found in **BNIP2_MOUSE** in **SwissProt**, BCL2/adenovirus E1B 19 kDa protein-interacting protein 2 OS=Mus musculus GN=Bnip2 PE=1 SV=2

Match to Query 3131: 1535.671686 from(768.843119,2+) index(792)
Title: Elution from: 22.834 to 22.834 scan no 1659 cid35.00 polarity:+



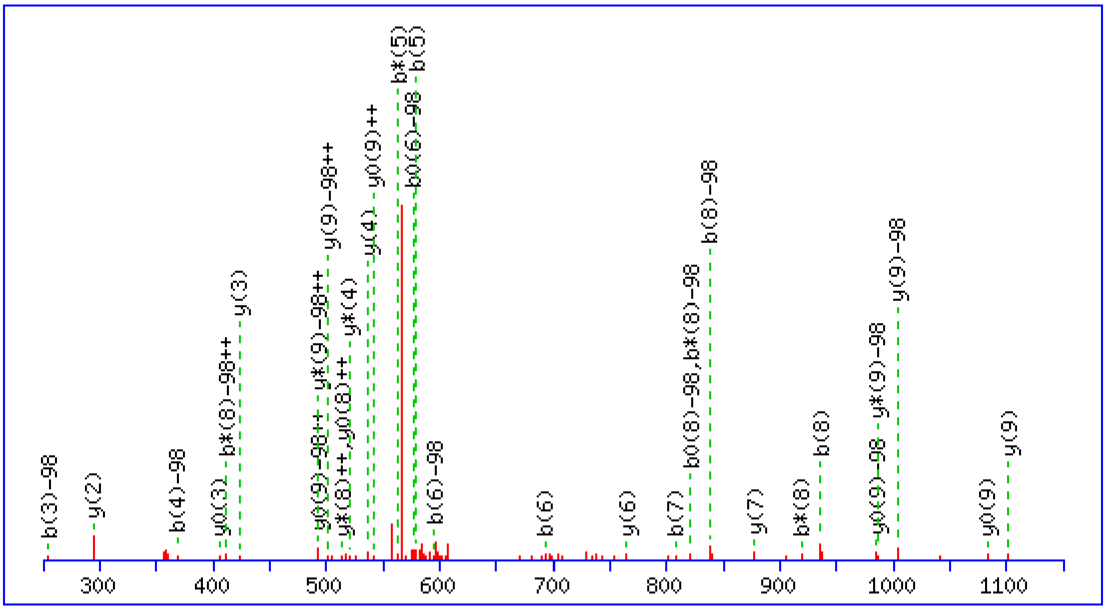
Monoisotopic mass of neutral peptide Mr(calc): 1535.6756
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 3.2e-007
Matched b ions: b(6)-98, b(6), b(7), b(9)-98, b(11)-98, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(4), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(12)-98, y(12)

Peptide No.487

KGSLNINEFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KGSLNINEFK**
Found in **S10AD_MOUSE** in **SwissProt**, Protein S100-A13 OS=Mus musculus GN=S100a13 PE=1 SV=1

Match to Query 1572: 1228.585580 from(615.300066,2+) index(4575)
Title: Elution from: 33.497 to 33.497 scan no 2963 cid35.00 polarity:+:m1s



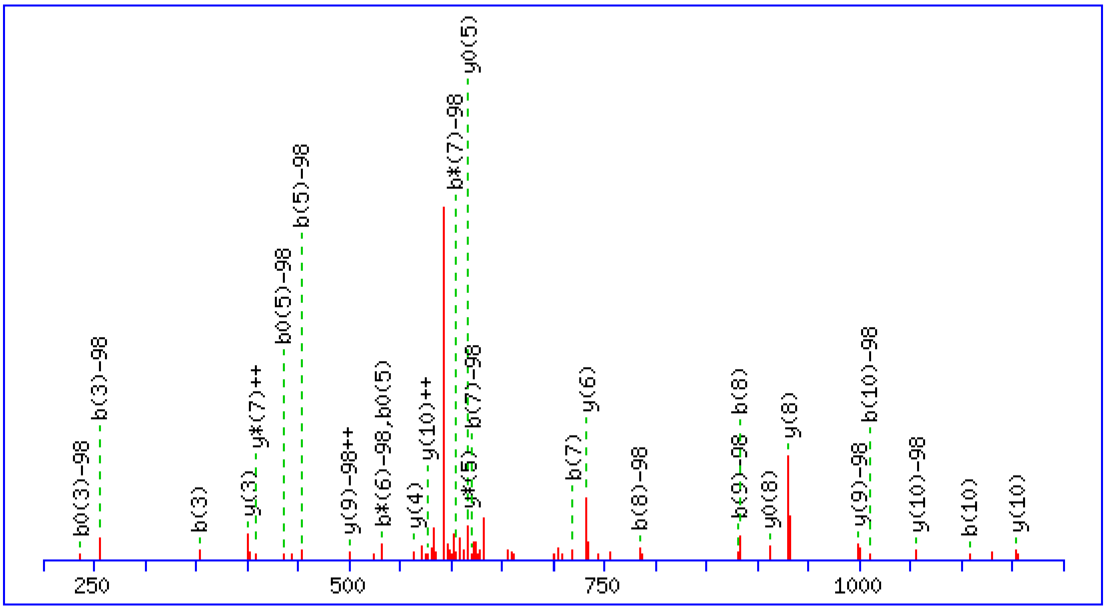
Monoisotopic mass of neutral peptide Mr(calc): 1228.5853
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0058
Matched b ions: b(3)-98, b(4)-98, b(5), b(6), b(6)-98, b(7), b(8)-98, b(8), b(9)-98++, b(9)-98, b(9), b(9)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(9)-98, y(9), y(9)-98++

Peptide No.488

KGSPTPAYPER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KGSPTPAYPER**
Found in **FA83H_MOUSE** in **SwissProt**, Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1

Match to Query 1733: 1281.574300 from(641.794426,2+) index(190)
Title: Elution from: 18.747 to 18.747 scan no 1052 cid35.00 polarity:+



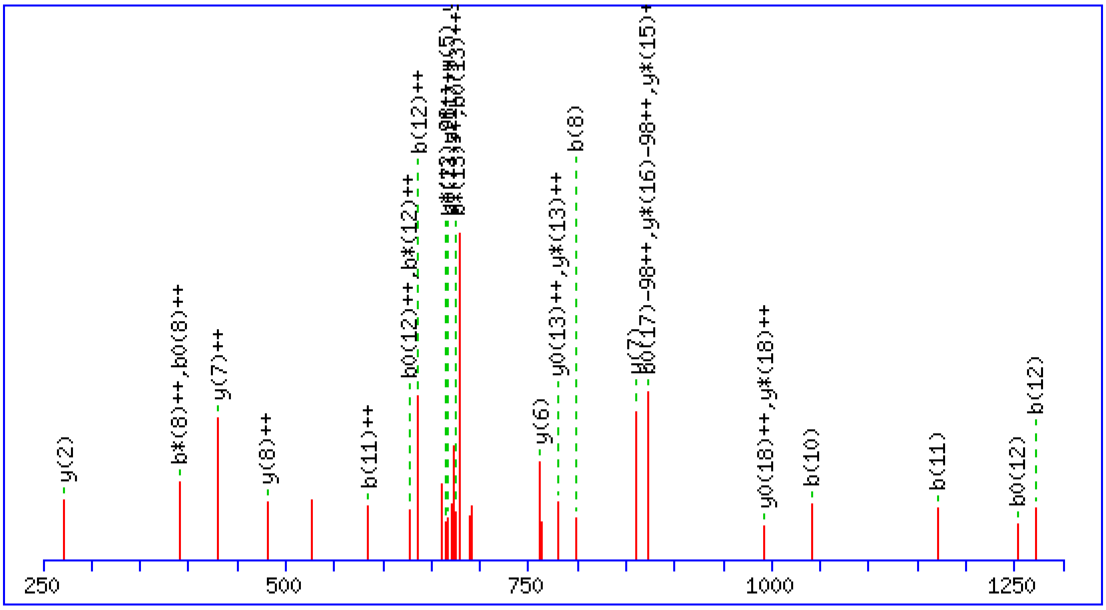
Monoisotopic mass of neutral peptide Mr(calc): 1281.5754
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00023
Matched b ions: b(3)-98, b(3), b(5)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(10)
Matched y ions: y(3), y(4), y(6), y(8), y(9)-98, y(9)-98++, y(10)-98, y(10), y(10)++

Peptide No.489

KGSPVSEIGWETPPPESPR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **KGSPVSEIGWETPPPESPR**
Found in **SNTB1_MOUSE** in **SwissProt**, Beta-1-syntrophin OS=Mus musculus GN=Sntb1 PE=1 SV=4

Match to Query 5352: 2128.983516 from(710.668448,3+) index(5893)
Title: Elution from: 38.605 to 38.605 scan no 3755 cid35.00 polarity:+:m1s



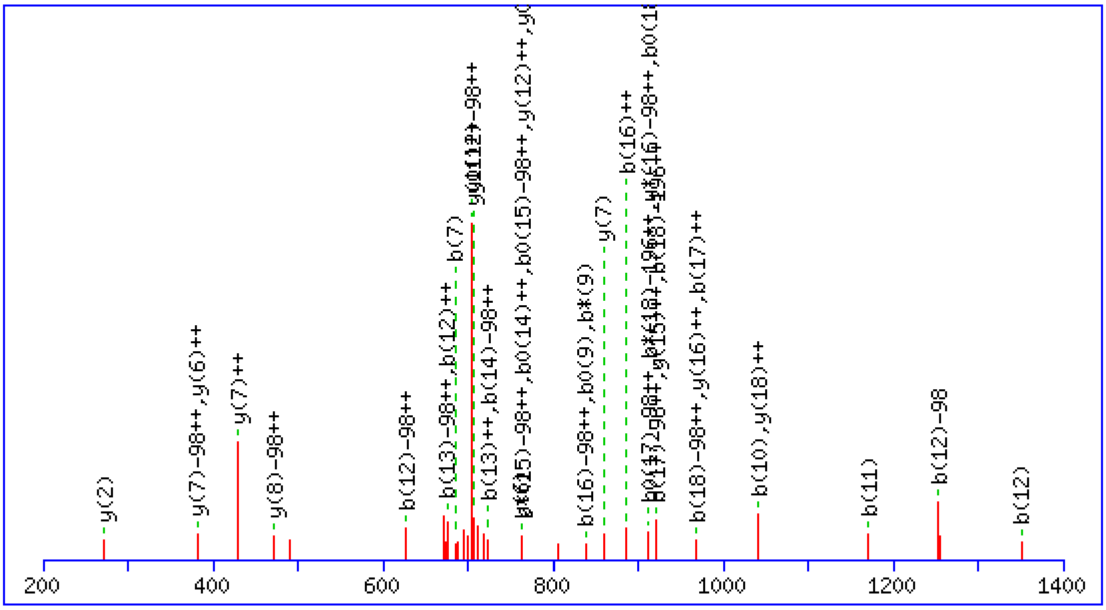
Monoisotopic mass of neutral peptide Mr(calc): 2128.9830
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.021
Matched b ions: b(8), b(10), b(11), b(11)++, b(12)++, b(12)
Matched y ions: y(2), y(5), y(6), y(7)++, y(7), y(8)++, y(11)++

Peptide No.490

KGSPVSEIGWETPPPESPR
Confirmed sites: @T:12,@S:17
Ambiguous sites:

MS/MS Fragmentation of **KGSPVSEIGWETPPPESPR**
Found in **SNTB1_MOUSE** in **SwissProt**, Beta-1-syntrophin OS=Mus musculus GN=Sntb1 PE=1 SV=4

Match to Query 5773: 2208.948381 from(737.323403,3+) index(6359)
Title: Elution from: 42.431 to 42.431 scan no 4285 cid35.00 polarity:+:m1s



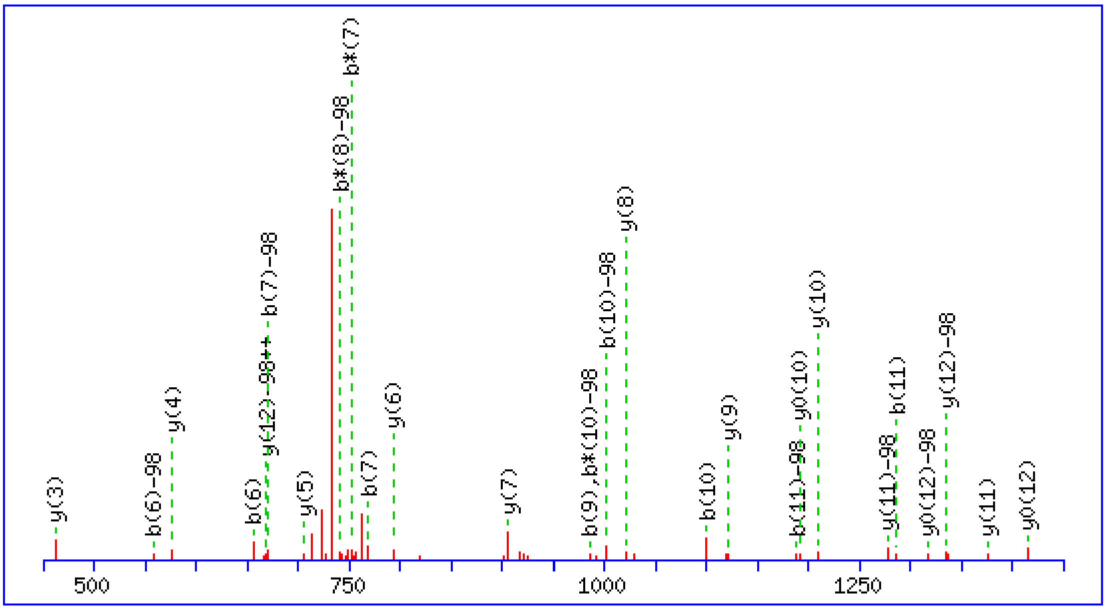
Monoisotopic mass of neutral peptide Mr(calc): 2208.9494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0022
Matched b ions: b(7), b(10), b(11), b(12)-98, b(12), b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-196++, b(18)-98++
Matched y ions: y(2), y(6)++, y(6), y(7)++, y(7), y(7)-98++, y(8)-98++, y(11)++, y(12)++, y(15)++, y(16)++, y(18)++

Peptide No.491

KGSSTDISEDWEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KGSSTDISEDWEK**
Found in **BSDC1_MOUSE** in **SwissProt**, BSD domain-containing protein 1 OS=Mus musculus GN=Bsdc1 PE=2 SV=1

Match to Query 3074: 1560.634316 from(781.324434,2+) index(1417)
Title: Elution from: 28.969 to 28.969 scan no 2458 cid35.00 polarity:+



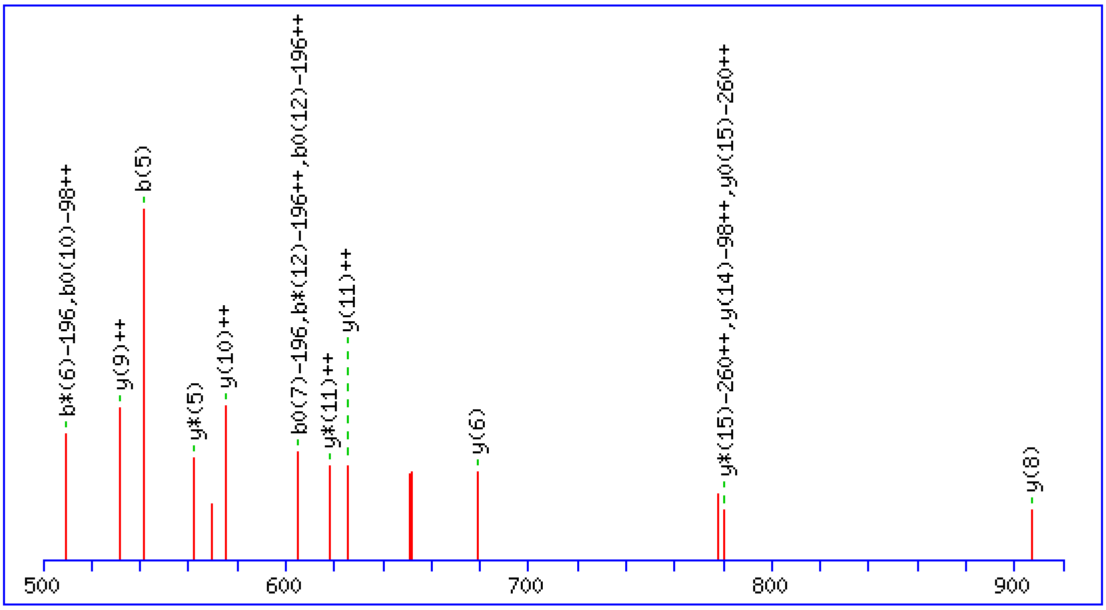
Monoisotopic mass of neutral peptide Mr(calc): 1560.6345
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 74 **Expect:** 1.3e-007
Matched b ions: b(6), b(6)-98, b(7), b(7)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12), b(12)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12)-98++

Peptide No.492

KGSSTTPQTSRMPVPMTSK
Confirmed sites: @T:6
Ambiguous sites: @S:3orS:4orT:5

MS/MS Fragmentation of **KGSSTTPQTSRMPVPMTSK**
Found in **SKT_MOUSE** in **SwissProt**, Sickle tail protein OS=Mus musculus GN=Skt PE=1 SV=1

Match to Query 4765: 2195.938920 from(549.992006,4+) index(5250)
Title: Elution from: 41.924 to 41.924 scan no 4045 cid35.00 polarity:+:m1s



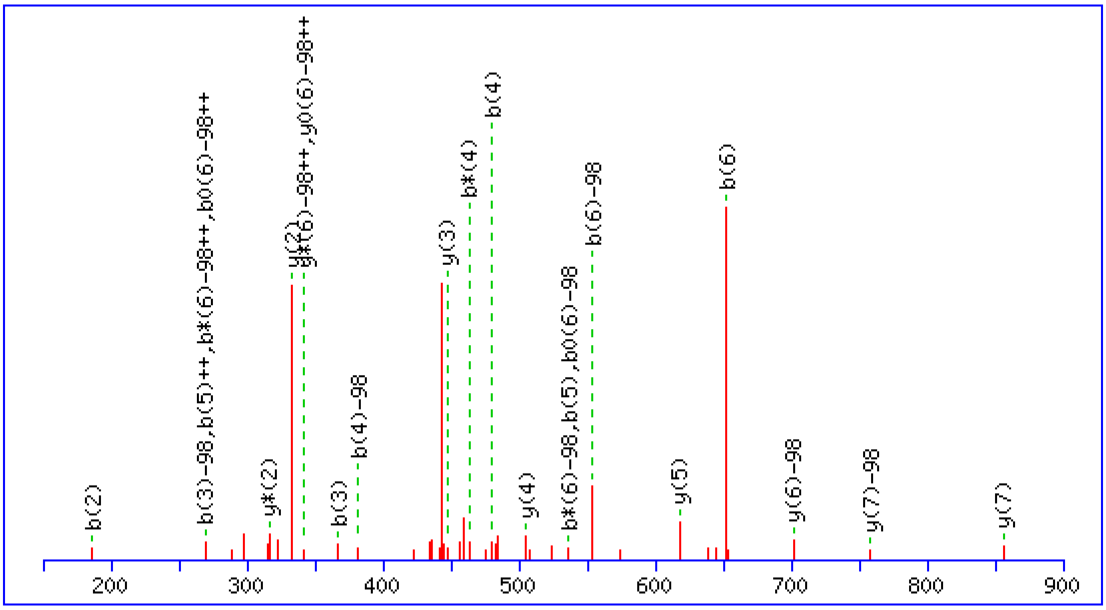
Monoisotopic mass of neutral peptide Mr(calc): 2195.9357
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 25 **Expect:** 0.022
Matched b ions: b(5)
Matched y ions: y(6), y(8), y(9)++, y(10)++, y(11)++, y(14)-98++

Peptide No.493

KGTIGDWK
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **KGTIGDWK**
Found in **ST1A1_MOUSE** in **SwissProt**, Sulfotransferase 1A1 OS=Mus musculus GN=Sult1a1 PE=2 SV=1

Match to Query 885: 983.447554 from(492.731053,2+) index(925)
Title: Elution from: 23.965 to 23.965 scan no 1813 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 983.4477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 9.8e-005
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)++, b(5), b(6)-98, b(6)
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(7), y(7)-98

Peptide No.494

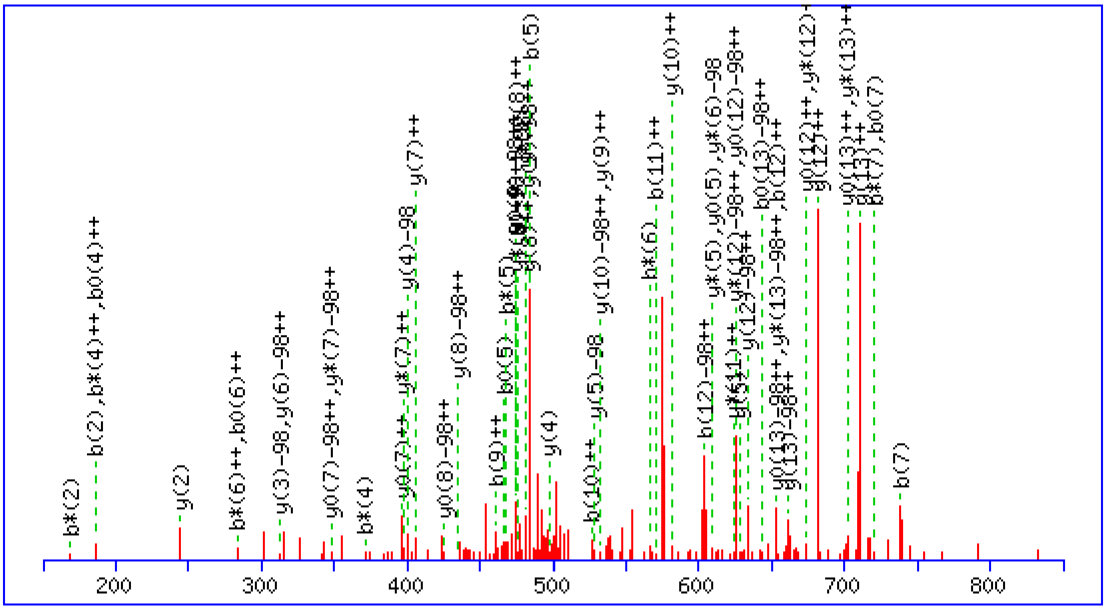
KGTTPPRSPESSPK

Confirmed sites: @S:12

Ambiguous sites:

MS/MS Fragmentation of **KGTTPPRSPESSPK**
Found in **JPH1_MOUSE** in **SwissProt**, Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1

Match to Query 3701: 1547.735493 from(516.919107,3+) index(243)
Title: Elution from: 25.392 to 25.392 scan no 1345 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1547.7345

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 22 **Expect:** 0.027

Matched b ions: b(2), b(5), b(7), b(9)++, b(10)++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++

Matched y ions: y(2), y(3)-98, y(4)-98, y(4), y(5)-98, y(5), y(6)-98++, y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)-98++, y(10)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.495

KGTTPPRSPESSPK

Confirmed sites: @T:4

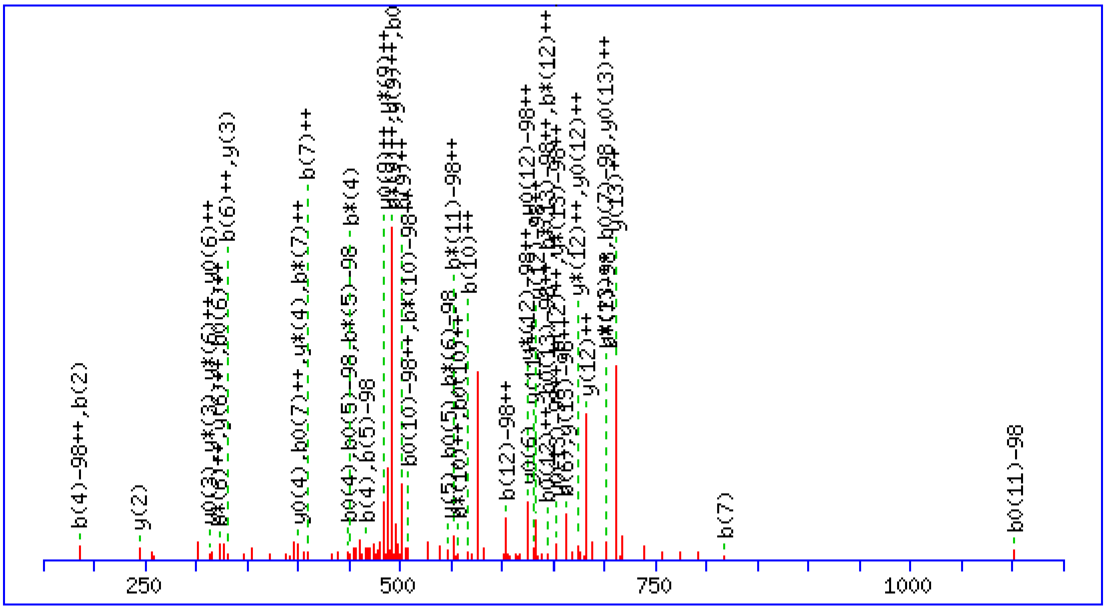
Ambiguous sites:

MS/MS Fragmentation of **KGTTPPRSPESSPK**

Found in **JPH1_MOUSE** in **SwissProt**, Junctophilin-1 OS=Mus musculus GN=Jph1 PE=1 SV=1

Match to Query 2650: 1547.732760 from(516.918196,3+) index(228)

Title: Elution from: 19.097 to 19.097 scan no 1097 cid35.00 polarity:+



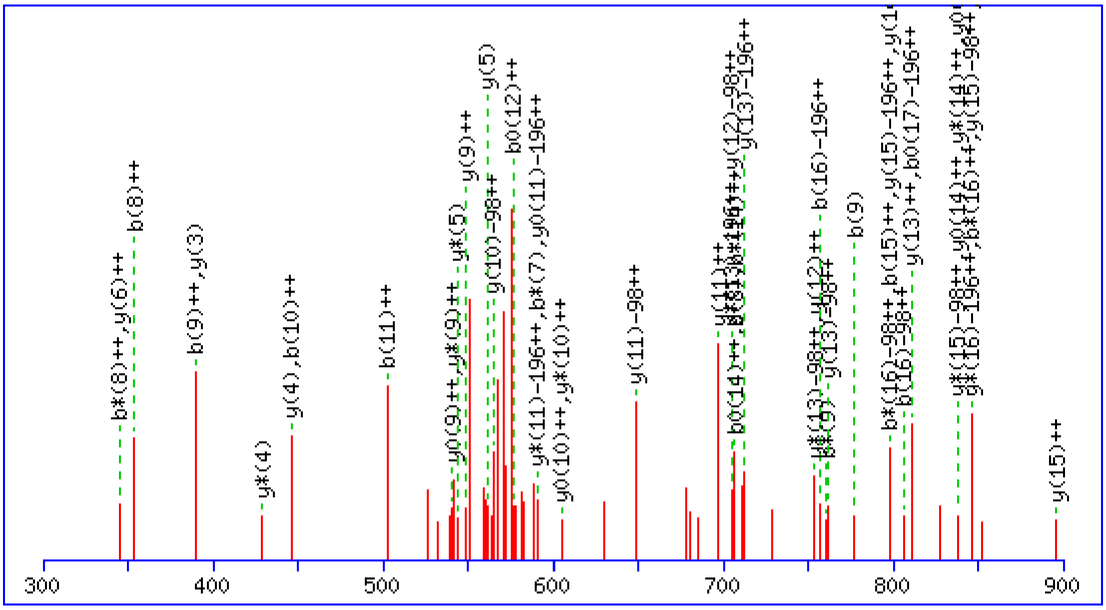
Monoisotopic mass of neutral peptide Mr(calc): 1547.7345
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.026
Matched b ions: b(2), b(4)-98++, b(4), b(5)-98, b(6), b(6)++, b(7), b(7)++, b(9)++, b(10)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(5), y(6)++, y(6), y(9)++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.496

KHGGGGIVANLSEQSLKDGVDR
Confirmed sites: @S:12,@S:15
Ambiguous sites:

MS/MS Fragmentation of **KHGGGGIVANLSEQSLKDGVDR**
Found in **PP1R7_MOUSE** in **SwissProt**, Protein phosphatase 1 regulatory subunit 7 OS=Mus musculus GN=Ppp1r7 PE=1 SV=2

Match to Query 5060: 2396.089880 from(600.029746,4+) index(4461)
Title: Elution from: 32.299 to 32.299 scan no 2799 cid35.00 polarity:+:m1s



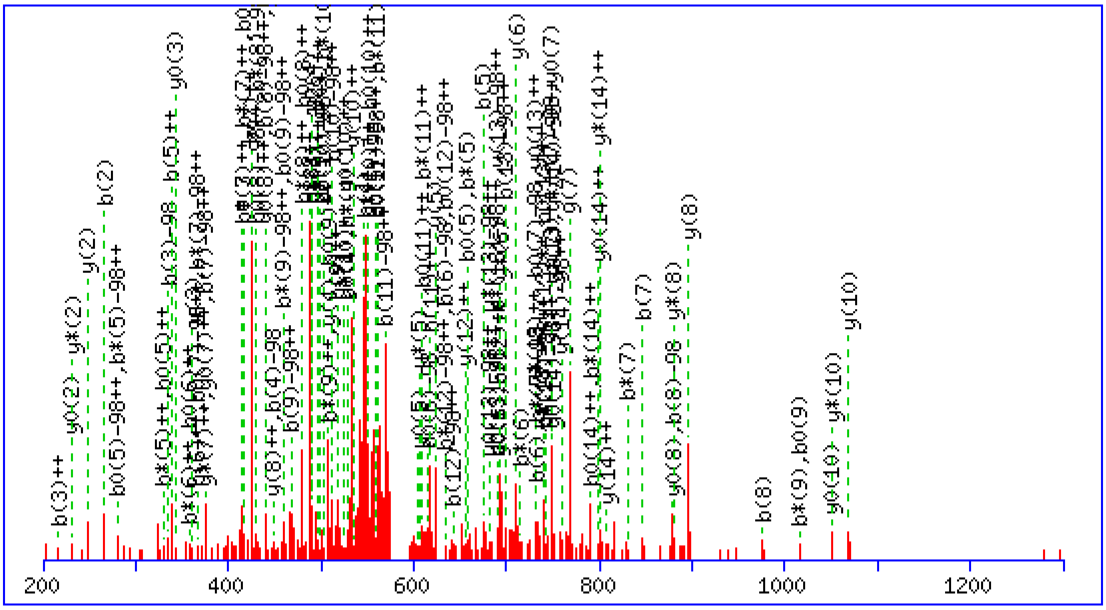
Monoisotopic mass of neutral peptide Mr(calc): 2396.0887
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0015
Matched b ions: b(8)++, b(8), b(9)++, b(9), b(10)++, b(11)++, b(15)++, b(16)-196++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(9)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-196++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)-196++, y(15)++

Peptide No.497

KHSLEGDEGSDFITK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KHSLEGDEGSDFITK**
Found in **TXLNG_MOUSE** in **SwissProt**, Gamma-taxilin OS=Mus musculus GN=Txlng PE=1 SV=1

Match to Query 4374: 1741.756371 from(581.592733,3+) index(4575)
Title: Elution from: 35.321 to 35.321 scan no 2555 cid35.00 polarity:+:m1s



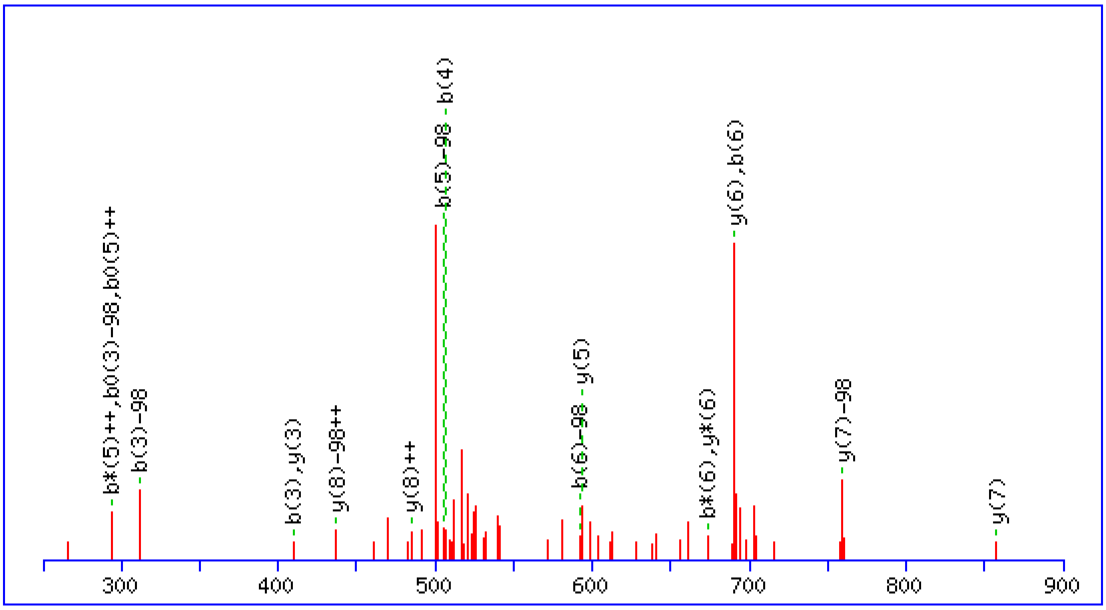
Monoisotopic mass of neutral peptide Mr(calc): 1741.7560
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00089
Matched b ions: b(2), b(3)-98, b(3)++, b(4), b(4)-98, b(5)++, b(5), b(6), b(6)++, b(6)-98, b(7)-98++, b(7)++, b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(10), y(10)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++

Peptide No.498

KISPPSYAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KISPPSYAR**
Found in **CLASR_MOUSE** in **SwissProt**, CLK4-associating serine/arginine rich protein OS=Mus musculus GN=Clasrp PE=1 SV=3

Match to Query 1245: 1097.525832 from(549.770192,2+) index(907)
Title: Elution from: 23.821 to 23.821 scan no 1793 cid35.00 polarity:+



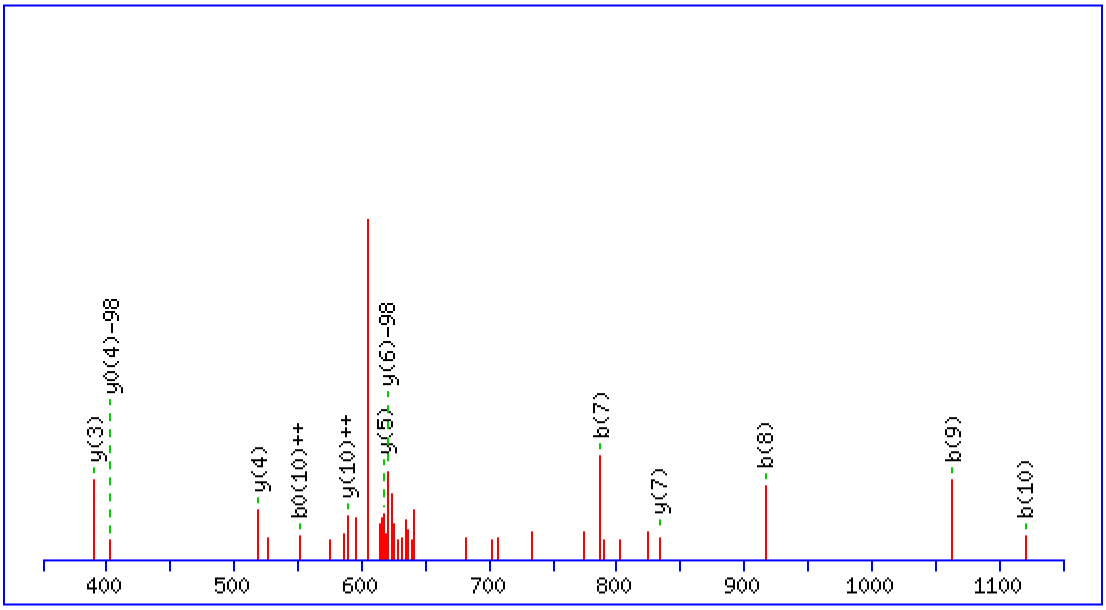
Monoisotopic mass of neutral peptide Mr(calc): 1097.5270
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.038
Matched b ions: b(3)-98, b(3), b(4), b(5)-98, b(6), b(6)-98
Matched y ions: y(3), y(5), y(6), y(7), y(7)-98, y(8)-98++, y(8)++

Peptide No.499

KITEDTVEFGS
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **KITEDTVEFGS**
Found in **ABCD3_MOUSE** in **SwissProt**, ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=2

Match to Query 1993: 1304.553806 from(653.284179,2+) index(2144)
Title: Elution from: 36.243 to 36.243 scan no 3443 cid35.00 polarity:+



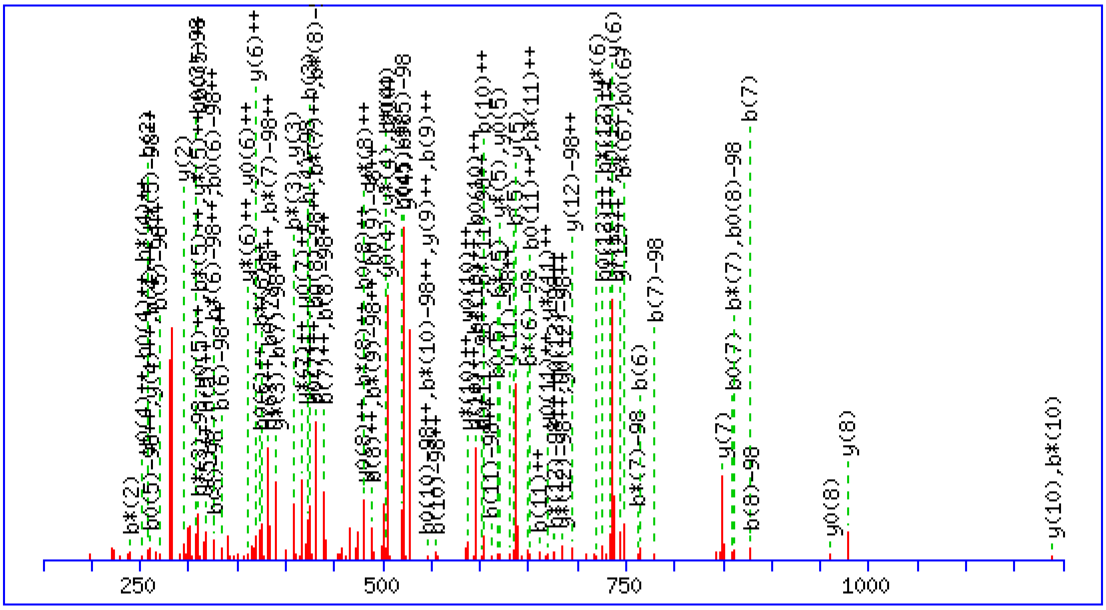
Monoisotopic mass of neutral peptide Mr(calc): 1304.5537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.013
Matched b ions: b(7), b(8), b(9), b(10)
Matched y ions: y(3), y(4), y(5), y(6)-98, y(7), y(10)++

Peptide No.500

KKSPNELVDDLFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KKSPNELVDDLFK**
Found in **NSF1C_MOUSE** in **SwissProt**, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 2832: 1611.790011 from(538.270613,3+) index(2557)
Title: Elution from: 44.928 to 44.928 scan no 4382 cid35.00 polarity:+



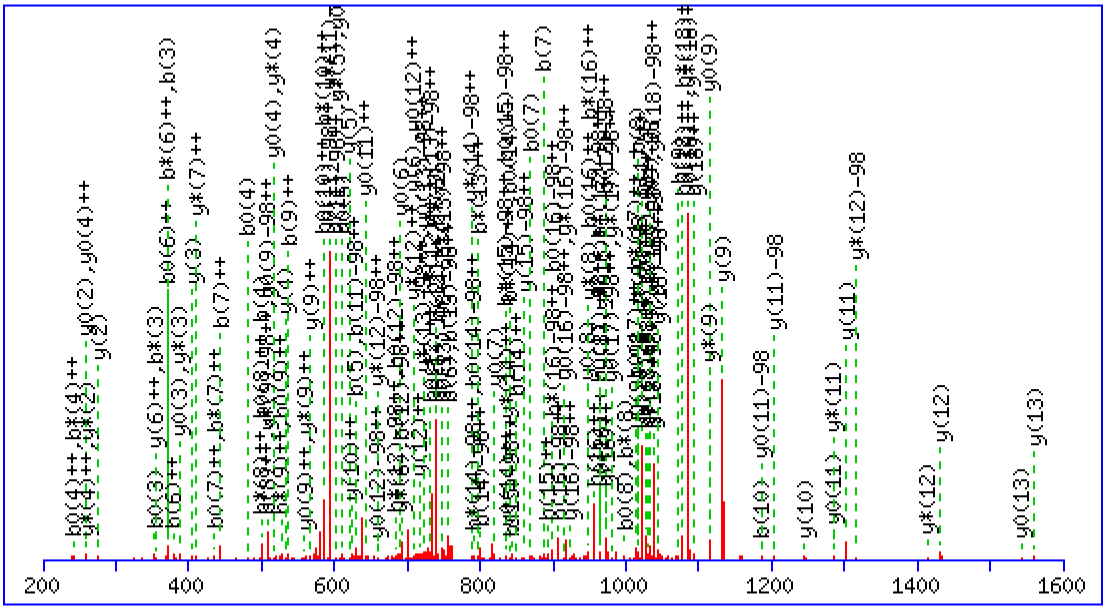
Monoisotopic mass of neutral peptide Mr(calc): 1611.7909
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00013
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)++, b(4)-98, b(5), b(5)++, b(5)-98++, b(6)++, b(6), b(6)-98++, b(7)-98++, b(7)++, b(7), b(7)-98, b(8)-98++, b(8)-98, b(8)++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(9)++, y(10), y(10)++, y(11)-98++, y(12)++, y(12)-98++

Peptide No.501

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **KLEKEEEEGISQESSEEEQ**
Found in **HMGA1_MOUSE** in **SwissProt**, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 5860: 2315.947836 from(772.989888,3+) index(4194)
Title: Elution from: 22.156 to 22.156 scan no 1530 cid35.00 polarity:+:m1s



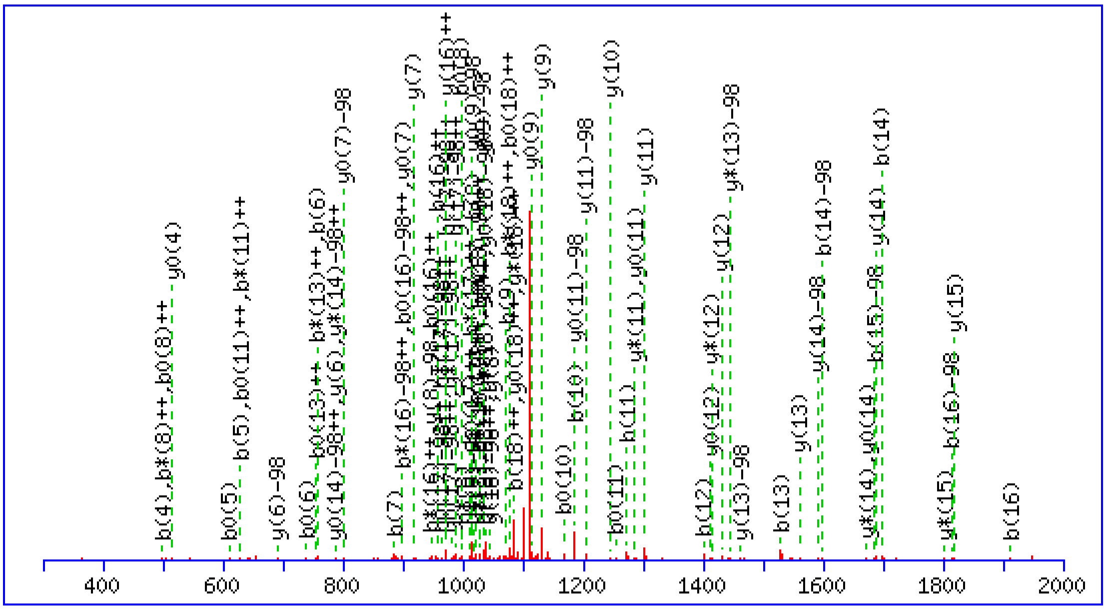
Monoisotopic mass of neutral peptide Mr(calc): 2315.9529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 **Expect:** 6.7e-007
Matched b ions: b(3), b(4), b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(8), y(9), y(9)-98, y(9)++, y(10), y(10)++, y(11), y(11)-98, y(11)-98++, y(12), y(12)++, y(13), y(13)-98++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(18)-98++, y(18)++

Peptide No.502

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **KLEKEEEEGISQESSEEEQ**
Found in **HMGA1_MOUSE** in **SwissProt**, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 5817: 2315.952118 from(1158.983335,2+) index(3892)
Title: Elution from: 28.211 to 28.211 scan no 1668 cid35.00 polarity:+:m1s



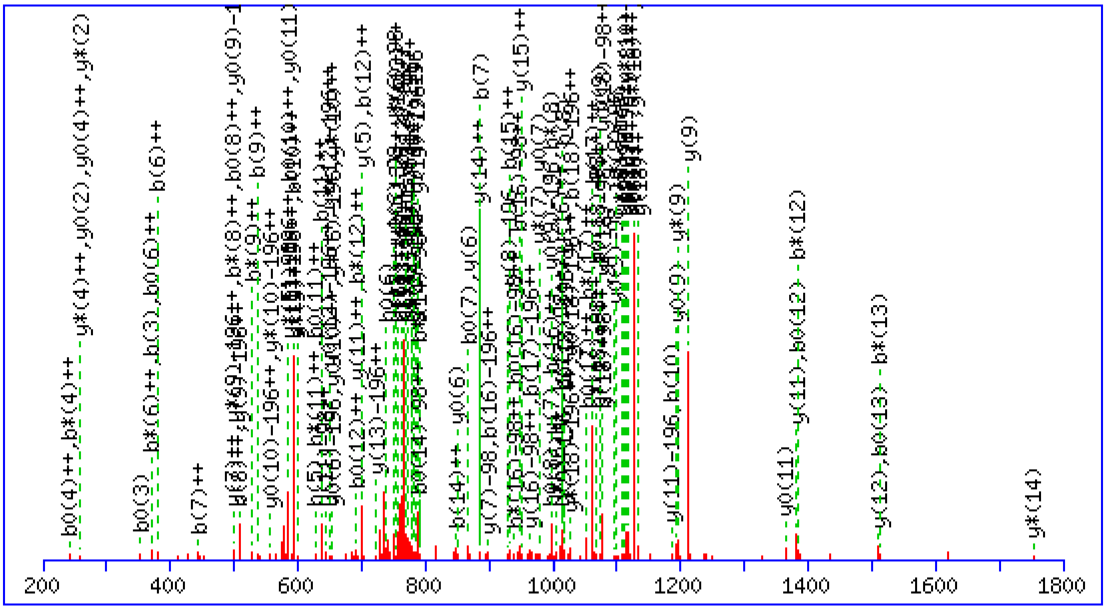
Monoisotopic mass of neutral peptide Mr(calc): 2315.9529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 **Expect:** 9.3e-007
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(14)-98, b(14), b(15)-98, b(16), b(16)-98, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(6), y(6)-98, y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)-98, y(12), y(13), y(13)-98, y(14), y(14)-98, y(15), y(16)++, y(17)-98++, y(18)-98++

Peptide No.503

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:14,@S:15
Ambiguous sites:

MS/MS Fragmentation of **KLEKEEEEGISQESSEEEQ**
Found in **HMGA1_MOUSE** in **SwissProt**, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 6067: 2395.921002 from(799.647610,3+) index(4026)
Title: Elution from: 29.601 to 29.601 scan no 1843 cid35.00 polarity:+:m1s



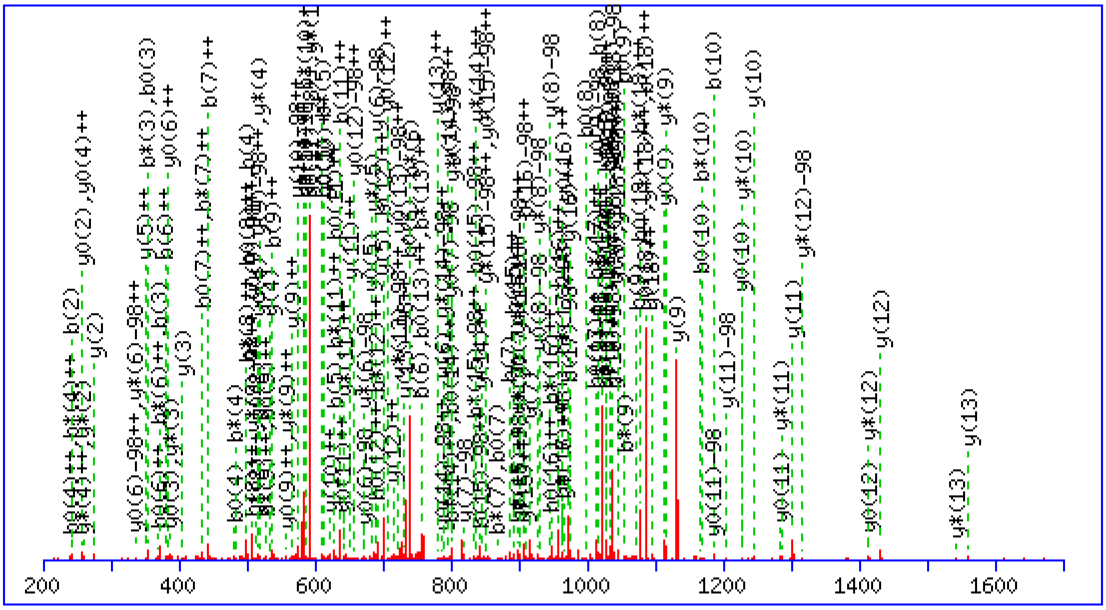
Monoisotopic mass of neutral peptide Mr(calc): 2395.9192
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 **Expect:** 8.1e-008
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(17)++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++
Matched y ions: y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)-196, y(9)-196++, y(9), y(9)-196, y(9)-98, y(11)-196++, y(11), y(11)++, y(11)-196, y(11)-98++, y(12), y(12)++, y(13)-98++, y(13)-196++, y(14)-196++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(18)++

Peptide No.504

KLEKEEEEGISQESSEEEQ
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **KLEKEEEEGISQESSEEEQ**
Found in **HMGA1_MOUSE** in **SwissProt**, High mobility group protein HMG-I/HMG-Y OS=Mus musculus GN=Hmga1 PE=1 SV=4

Match to Query 5034: 2315.949102 from(772.990310,3+) index(3667)
Title: Elution from: 21.963 to 21.963 scan no 1482 cid35.00 polarity:+:m1s



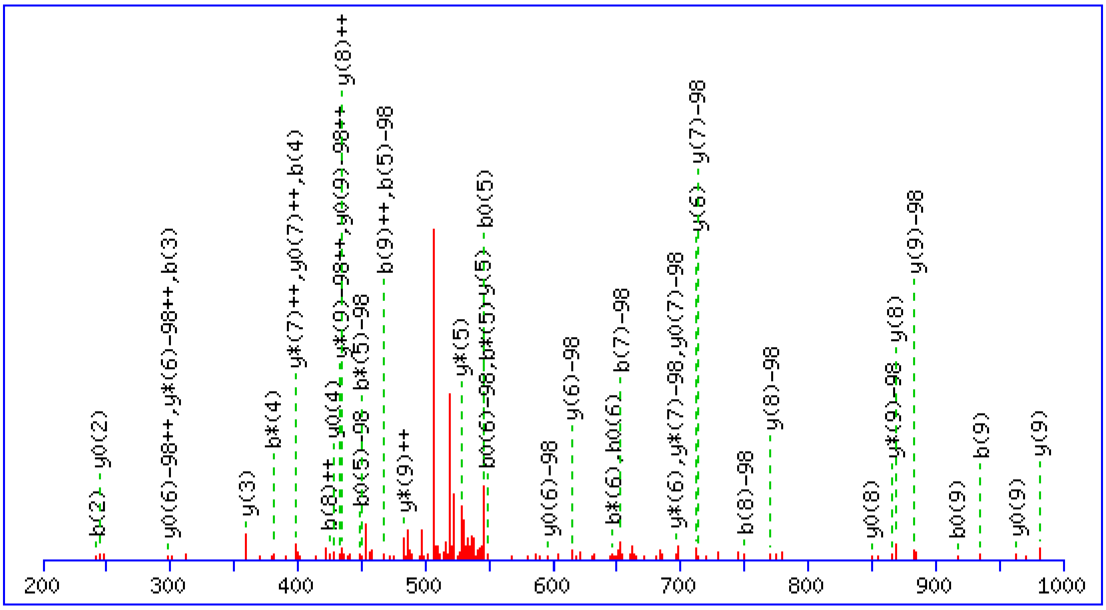
Monoisotopic mass of neutral peptide Mr(calc): 2315.9529
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 4.6e-006
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(6)++, b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(12)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)-98, y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(9)-98++, y(9)++, y(10), y(10)-98++, y(10)++, y(11), y(11)-98, y(11)++, y(12), y(12)++, y(13), y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)-98++, y(18)++

Peptide No.505

KLGVSVSPSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KLGVSVSPSR**
Found in **ZCH18_MOUSE** in **SwissProt**, Zinc finger CCCH domain-containing protein 18 OS=Mus musculus GN=Zc3h18 PE=1 SV=1

Match to Query 1484: 1108.564100 from(555.289326,2+) index(461)
Title: Elution from: 29.212 to 29.212 scan no 1713 cid35.00 polarity:+



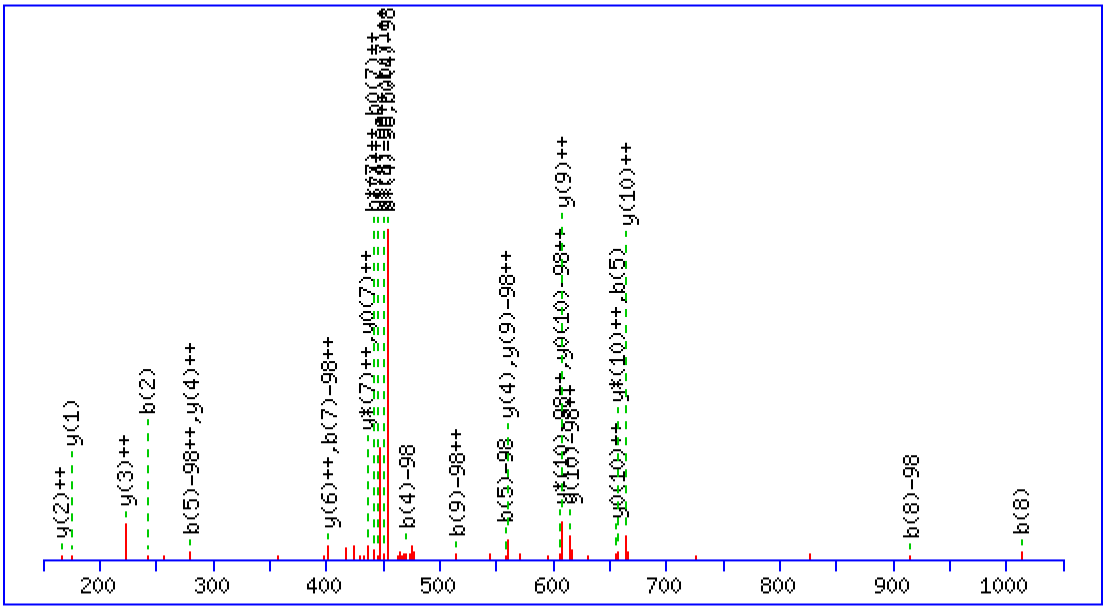
Monoisotopic mass of neutral peptide Mr(calc): 1108.5642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0071
Matched b ions: b(2), b(3), b(4), b(5)-98, b(7)-98, b(8)-98, b(8)++, b(9), b(9)++
Matched y ions: y(3), y(5), y(6), y(6)-98, y(7)-98, y(8), y(8)-98, y(8)++, y(9), y(9)-98

Peptide No.506

KLSCSLEDLRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KLSCSLEDLRR**
Found in **LIPB2_MOUSE** in **SwissProt**, Liprin-beta-2 OS=Mus musculus GN=Ppfibp2 PE=1 SV=3

Match to Query 2275: 1455.689616 from(486.237148,3+) index(1143)
Title: Elution from: 27.074 to 27.074 scan no 2174 cid35.00 polarity:+



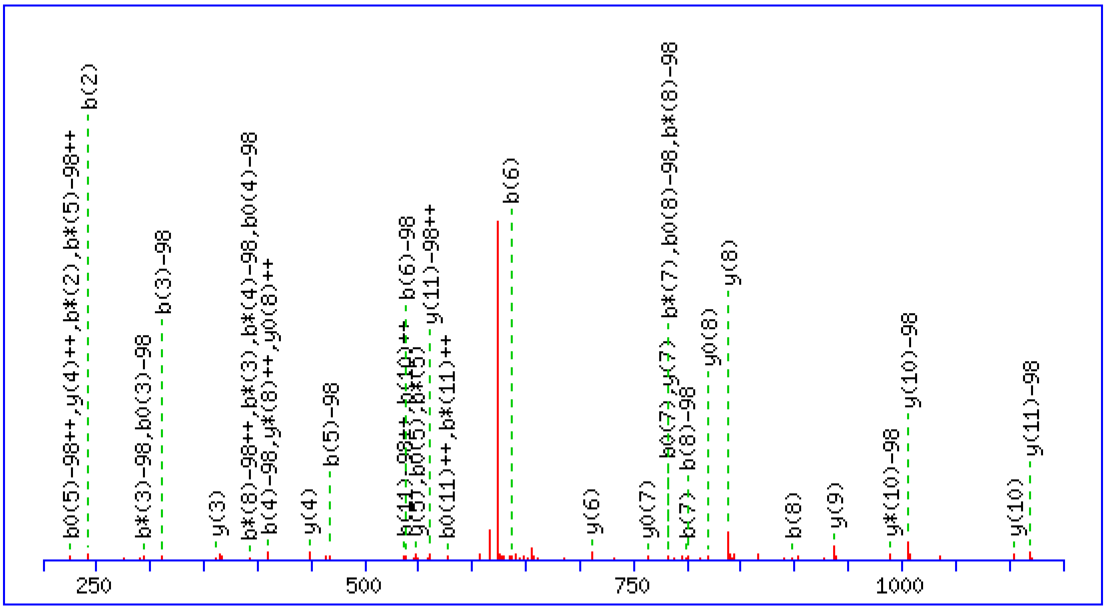
Monoisotopic mass of neutral peptide Mr(calc): 1455.6905
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.00097
Matched b ions: b(2), b(4)-98, b(5)-98++, b(5), b(5)-98, b(7)-98++, b(7)++, b(8)-98, b(8), b(9)-98++
Matched y ions: y(1), y(2)++, y(3)++, y(4)++, y(4), y(6)++, y(7)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++

Peptide No.507

KLSVGAYVSSVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KLSVGAYVSSVR**
Found in **S23IP_MOUSE** in **SwissProt**, SEC23-interacting protein OS=Mus musculus GN=Sec23ip PE=1 SV=2

Match to Query 2145: 1344.679936 from(673.347244,2+) index(2310)
Title: Elution from: 38.070 to 38.070 scan no 3683 cid35.00 polarity:+



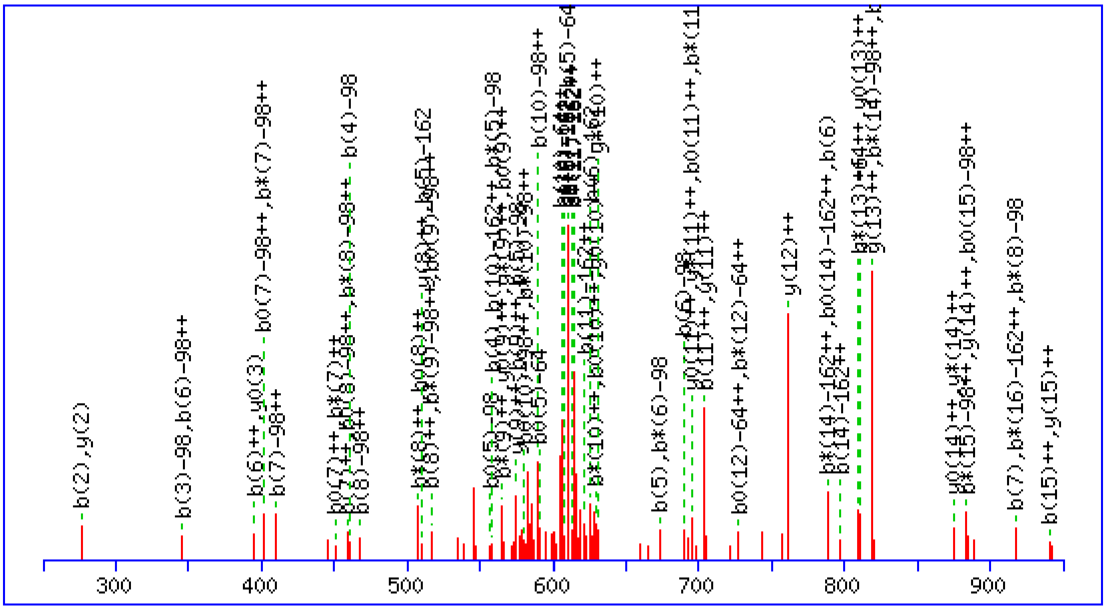
Monoisotopic mass of neutral peptide Mr(calc): 1344.6803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 6.9e-006
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(6)-98, b(6), b(7), b(8)-98, b(8), b(10)++, b(11)-98++
Matched y ions: y(3), y(4), y(4)++, y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11)-98, y(11)-98++

Peptide No.508

KMSDDDEDDEEEYGKEEHEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KMSDDDEDDEEEYGKEEHEK**
Found in **SPT6H_MOUSE** in **SwissProt**, Transcription elongation factor SPT6 OS=Mus musculus GN=Supt6h PE=1 SV=2

Match to Query 5453: 2551.903800 from(638.983226,4+) index(3231)
Title: Elution from: 18.137 to 18.137 scan no 979 cid35.00 polarity:+:m1s



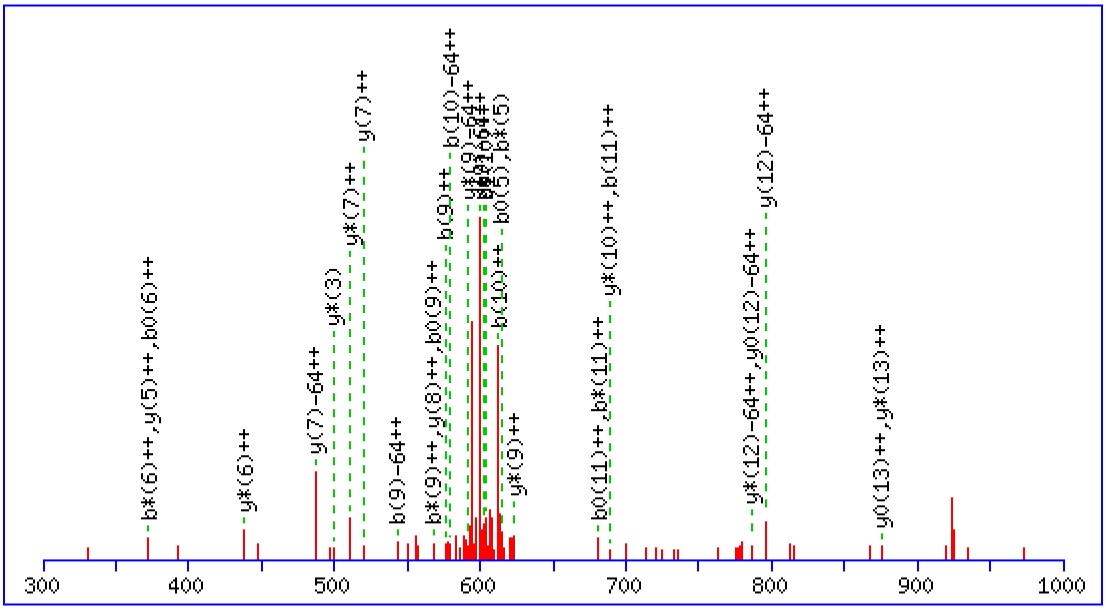
Monoisotopic mass of neutral peptide Mr(calc): 2551.9057
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00029
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98++, b(6), b(6)++, b(6)-98, b(7)-98, b(7)-98++, b(7), b(7)++, b(8)-98++, b(8)++, b(9)++, b(10)-98++, b(11)++, b(15)++
Matched y ions: y(2), y(8)++, y(9)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++

Peptide No.509

KNIFEKPFMARYVR
Confirmed sites: @Y:12
Ambiguous sites:

MS/MS Fragmentation of **KNIFEKPFMARYVR**
Found in **MFGM_MOUSE** in **SwissProt**, Lactadherin OS=Mus musculus GN=Mfge8 PE=1 SV=3

Match to Query 4566: 1893.937266 from(632.319698,3+) index(4115)
Title: Elution from: 20.051 to 20.051 scan no 1281 cid35.00 polarity:+:m1s



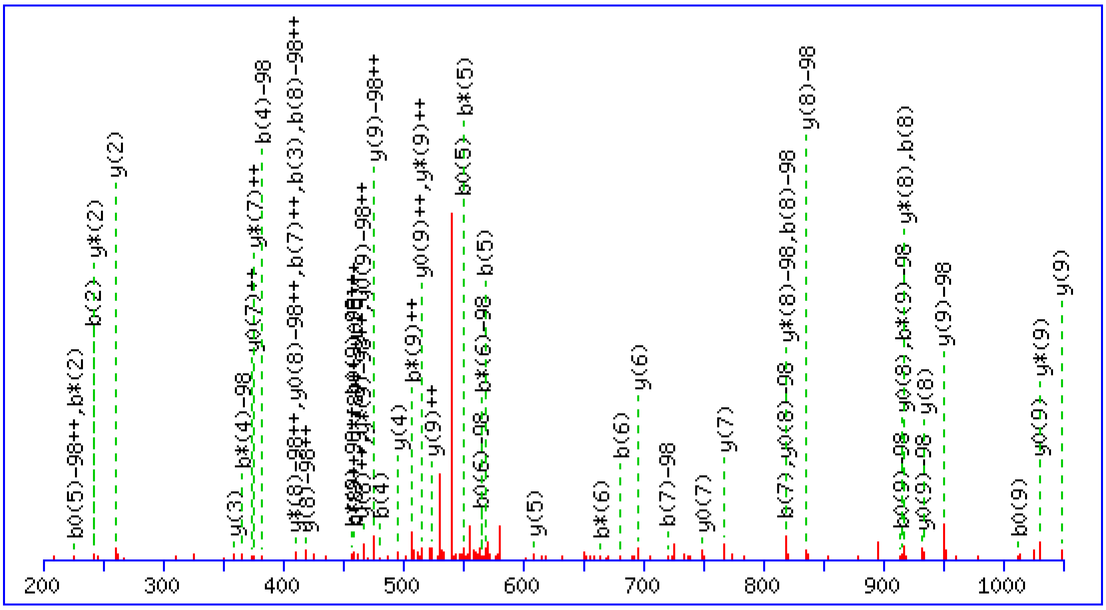
Monoisotopic mass of neutral peptide Mr(calc): 1893.9324
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M9 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Y12 : Phospho (Y)
Ions Score: 19 **Expect:** 0.06
Matched b ions: b(9)++, b(10)++, b(11)++
Matched y ions: y(5)++, y(7)++, y(8)++

Peptide No.510

KNSASLHVLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KNSASLHVLK**
Found in **SO1B2_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 1321: 1175.605144 from(588.809848,2+) index(332)
Title: Elution from: 19.965 to 19.965 scan no 1213 cid35.00 polarity:+



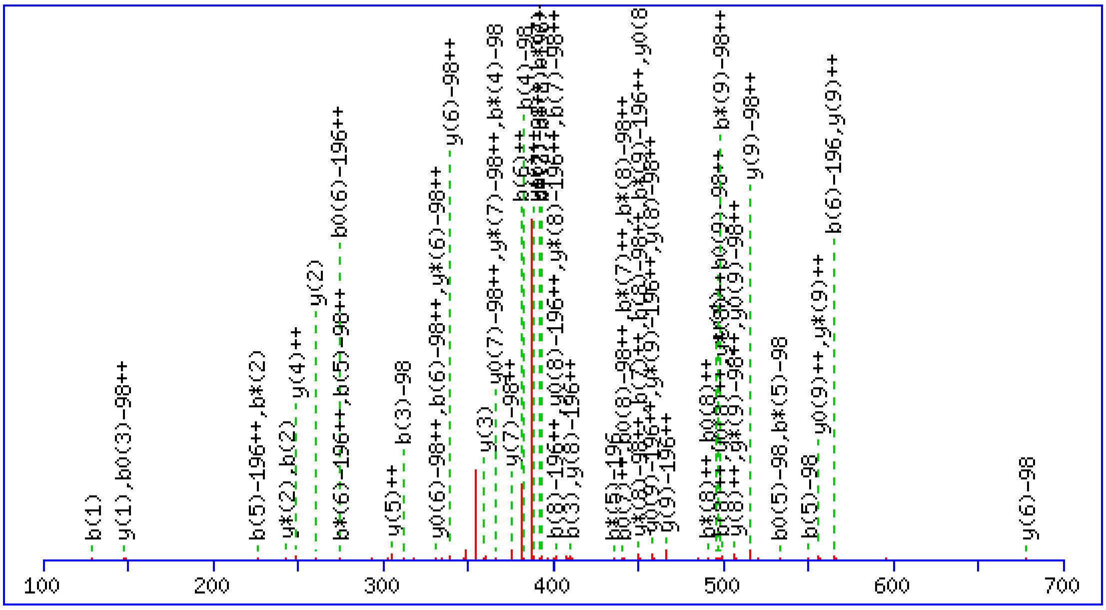
Monoisotopic mass of neutral peptide Mr(calc): 1175.6063
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 2.4e-005
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(6), b(7), b(7)-98, b(7)++, b(8)-98, b(8), b(8)++, b(8)-98++, b(9), b(9)-98++, b(9)-98, b(9)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8)-98, y(8)-98++, y(8), y(9)-98, y(9)-98++, y(9), y(9)++

Peptide No.511

KNSASLHVLK
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **KNSASLHVLK**
Found in **SO1B2_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 1619: 1255.572270 from(419.531366,3+) index(661)
Title: Elution from: 22.702 to 22.702 scan no 1581 cid35.00 polarity:+



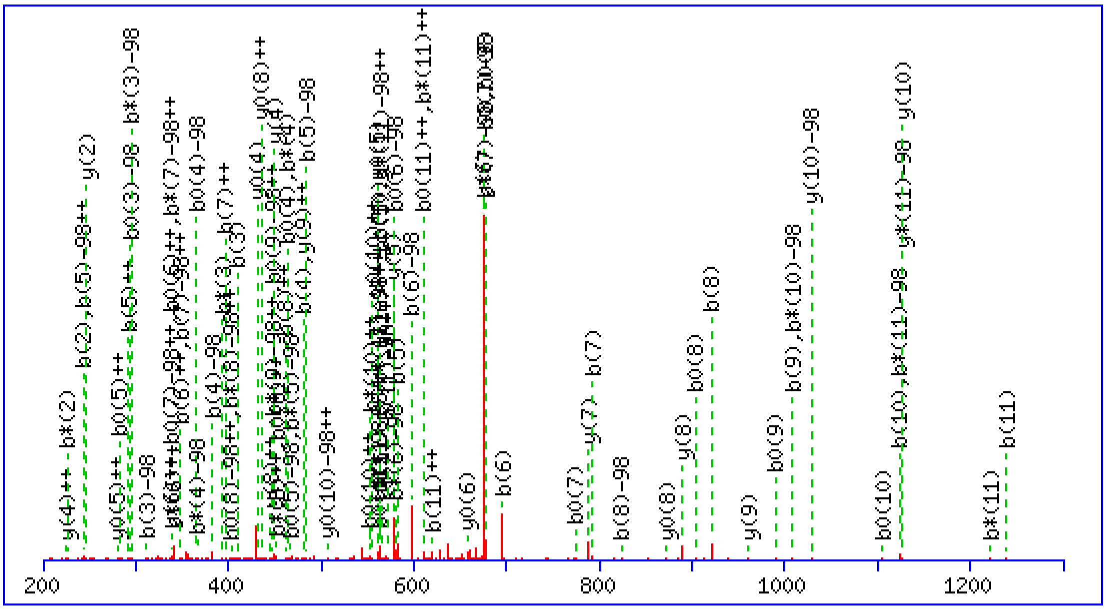
Monoisotopic mass of neutral peptide Mr(calc): 1255.5727
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0044
Matched b ions: b(1), b(2), b(3)-98, b(3), b(4)-98, b(5)-196++, b(5)-98, b(5)-98++, b(6)-196, b(6)++, b(6)-98++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(8)-196++, b(9)++, b(9)-98++, b(9)-196++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5)++, y(6)-98, y(6)++, y(6)-98++, y(7)-98++, y(8)++, y(8)-98++, y(8)-196++, y(9)-98++, y(9)++, y(9)-196++

Peptide No.512

KNSATIPESDDL
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KNSATIPESDDL**
Found in **HUTH_MOUSE** in **SwissProt**, Histidine ammonia-lyase OS=Mus musculus GN=Hal PE=1 SV=1

Match to Query 2707: 1368.581074 from(685.297813,2+) index(1477)
Title: Elution from: 41.853 to 41.853 scan no 3189 cid35.00 polarity:+



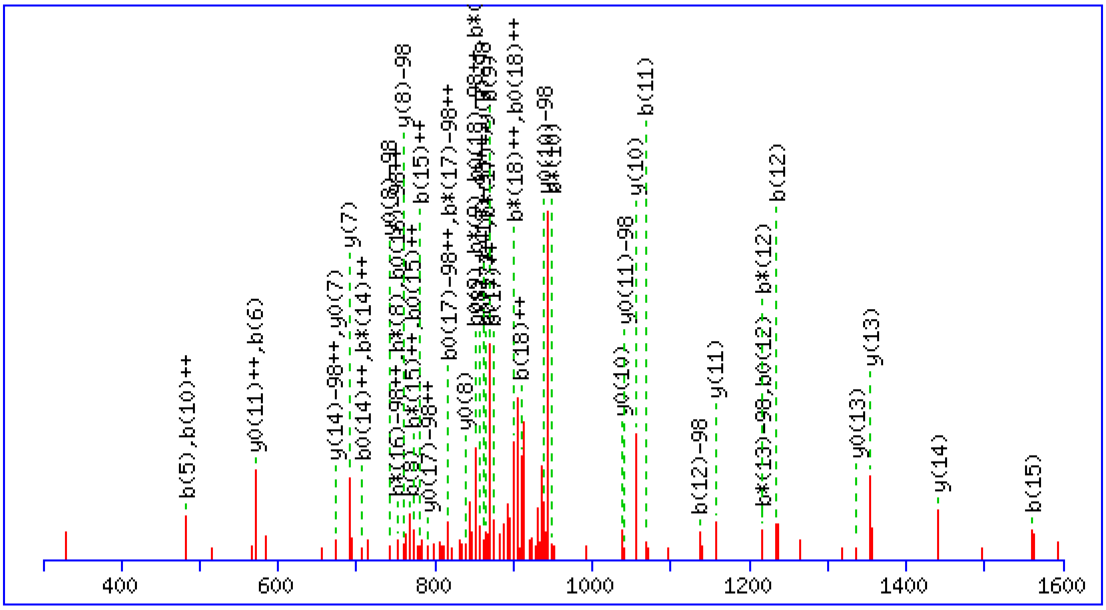
Monoisotopic mass of neutral peptide Mr(calc): 1368.5810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 7.7e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98++, b(5), b(5)-98, b(5)++, b(6)-98, b(6), b(6)++, b(7), b(7)-98++, b(7)++, b(8), b(8)-98, b(8)++, b(9), b(10), b(10)++, b(11), b(11)++, b(11)-98++
Matched y ions: y(2), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)-98, y(10), y(10)++

Peptide No.513

KPASVSPTTPTSPTEGEAS
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **KPASVSPTTPTSPTEGEAS**
Found in **DC1L1_MOUSE** in **SwissProt**, Cytoplasmic dynein 1 light intermediate chain 1 OS=Mus musculus GN=Dync1li1 PE=1 SV=1

Match to Query 3997: 1922.847224 from(962.430888,2+) index(3513)
Title: Elution from: 22.977 to 22.977 scan no 1517 cid35.00 polarity:+:m1s



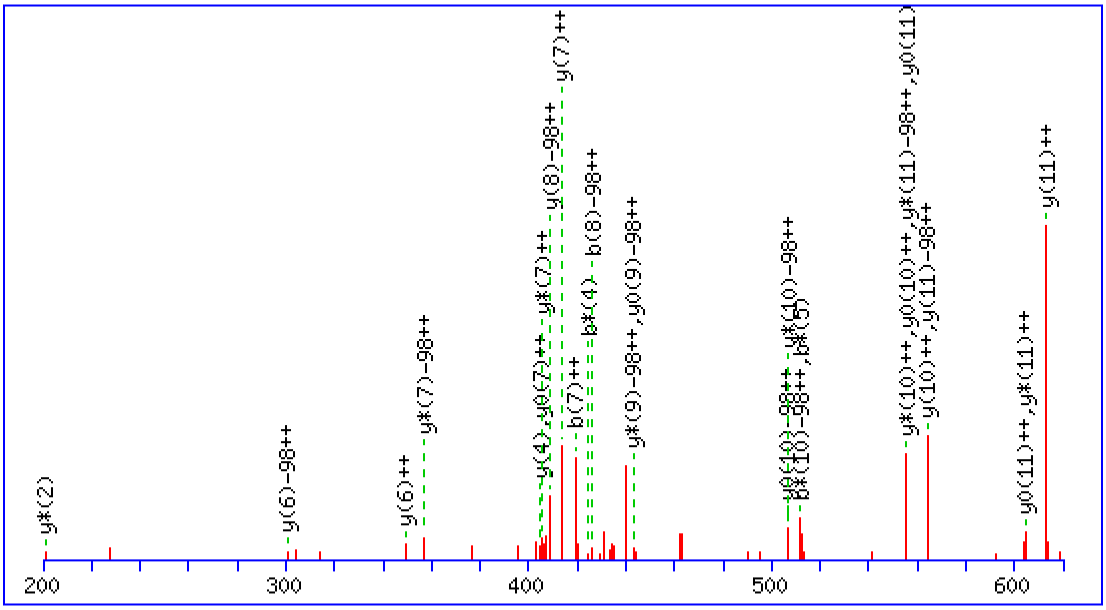
Monoisotopic mass of neutral peptide Mr(calc): 1922.8510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 9.1e-005
Matched b ions: b(5), b(6), b(8), b(9), b(10)++, b(11), b(12), b(12)-98, b(15), b(15)++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(7), y(8)-98, y(8), y(9)-98, y(10), y(11), y(13), y(14), y(14)-98++

Peptide No.514

KPKSSQTLVSAK
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **KPKSSQTLVSAK**
Found in **M10L1_MOUSE** in **SwissProt**, Putative helicase Mov10l1 OS=Mus musculus GN=Mov10l1 PE=1 SV=1

Match to Query 1972: 1352.706753 from(451.909527,3+) index(1249)
Title: Elution from: 28.017 to 28.017 scan no 2302 cid35.00 polarity:+



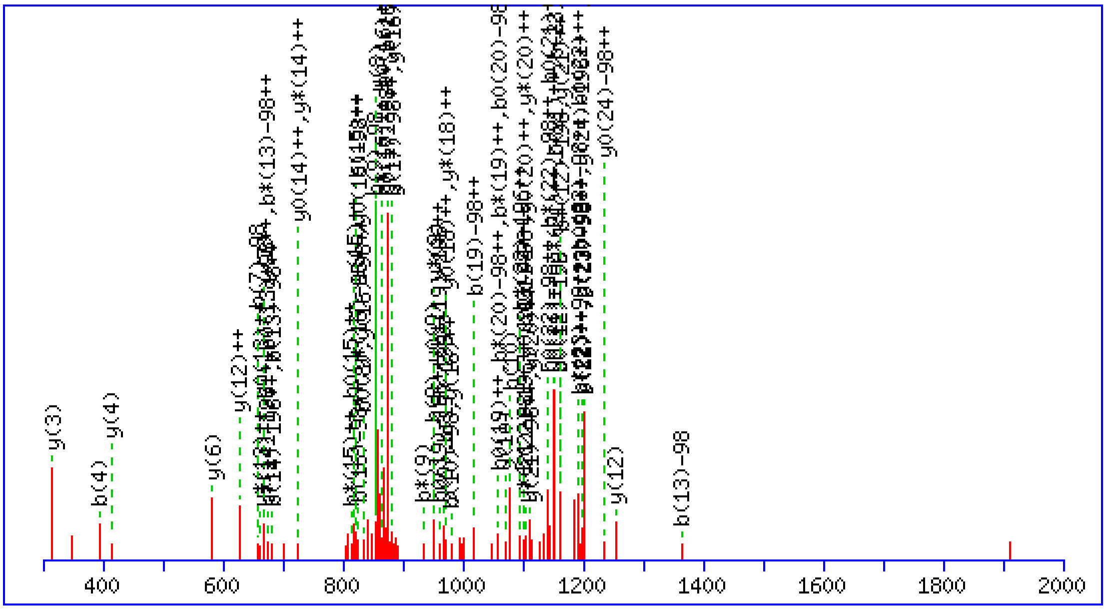
Monoisotopic mass of neutral peptide Mr(calc): 1352.7065
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.014
Matched b ions: b(7)++, b(8)-98++, b(11)-98++, b(11)++
Matched y ions: y(4), y(6)-98++, y(6)++, y(7)++, y(8)-98++, y(10)++, y(11)-98++, y(11)++

Peptide No.515

KPPAPPSPVQSQSPSTNWSPAVPAK
Confirmed sites: @S:7
Ambiguous sites: @S:11orS:13

MS/MS Fragmentation of **KPPAPPSPVQSQSPSTNWSPAVPAK**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 6671: 2714.247030 from(905.756286,3+) index(6030)
Title: Elution from: 38.357 to 38.357 scan no 3751 cid35.00 polarity:+:m1s



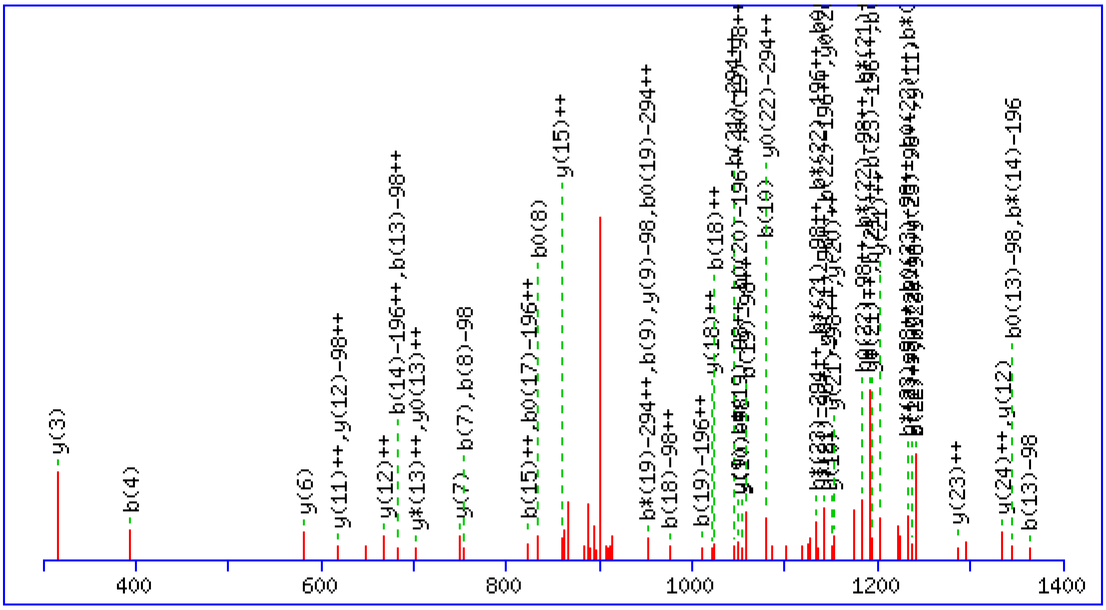
Monoisotopic mass of neutral peptide Mr(calc): 2714.2506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0023
Matched b ions: b(4), b(7)-98, b(9), b(9)-98, b(10), b(10)-98, b(13)-98, b(13)-98++, b(14)-196++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(19)-196++, b(19)-98++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(22)-196++, b(23)-196++, b(23)-98++, b(24)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(12)++, y(12), y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(23)-98++, y(24)-196++

Peptide No.516

KPPAPPSPVQSQSPSTNWSPAVPAK
Confirmed sites: @S:7,@S:19
Ambiguous sites: @S:11orS:13

MS/MS Fragmentation of **KPPAPPSPVQSQSPSTNWSPAVPAK**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 6573: 2794.211889 from(932.411239,3+) index(6085)
Title: Elution from: 40.990 to 40.990 scan no 4072 cid35.00 polarity:+:m1s



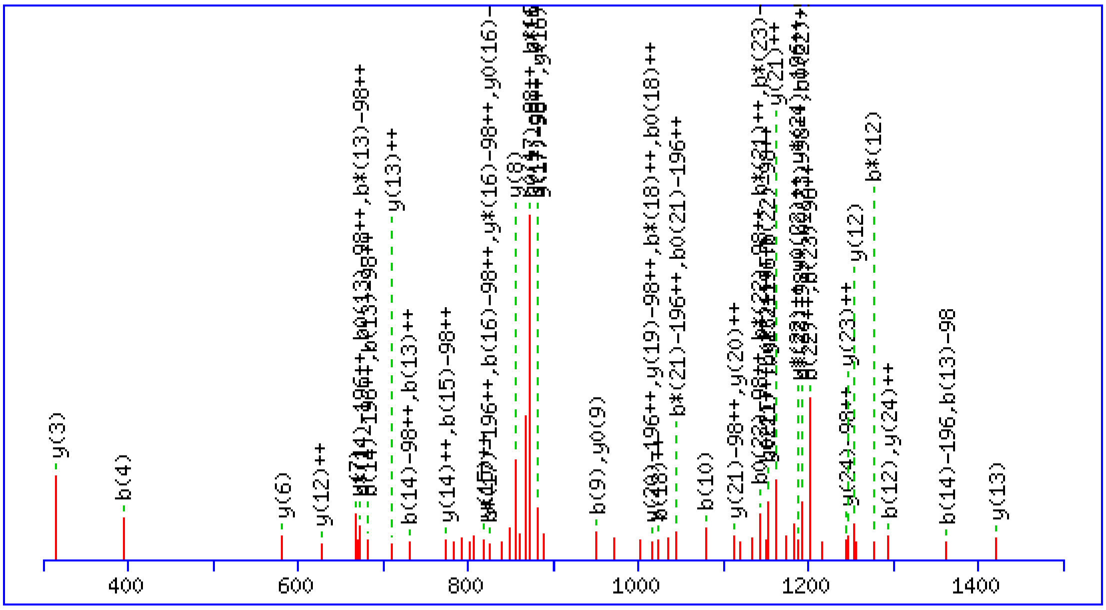
Monoisotopic mass of neutral peptide Mr(calc): 2794.2169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00031
Matched b ions: b(4), b(7), b(8)-98, b(9), b(10), b(13)-98, b(13)-98++, b(14)-196++, b(15)++, b(18)-98++, b(18)++, b(19)-98++, b(19)-196++, b(21)++, b(21)-98++, b(21)-294++, b(22)-98++, b(22)++, b(22)-196++, b(23)-196++, b(23)-98++, b(23)-294++
Matched y ions: y(3), y(6), y(7), y(9)-98, y(9), y(10)-98, y(10), y(11)++, y(11), y(12)++, y(12), y(12)-98++, y(12)-98, y(15)++, y(18)++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)-98++, y(23)++, y(24)++

Peptide No.517

KPPAPPSPVQSQSPSTNWSPAVPAK
Confirmed sites: @S:7,@S:13
Ambiguous sites:

MS/MS Fragmentation of **KPPAPPSPVQSQSPSTNWSPAVPAK**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 6479: 2714.243751 from(905.755193,3+) index(5881)
Title: Elution from: 38.471 to 38.471 scan no 3737 cid35.00 polarity:+:m1s



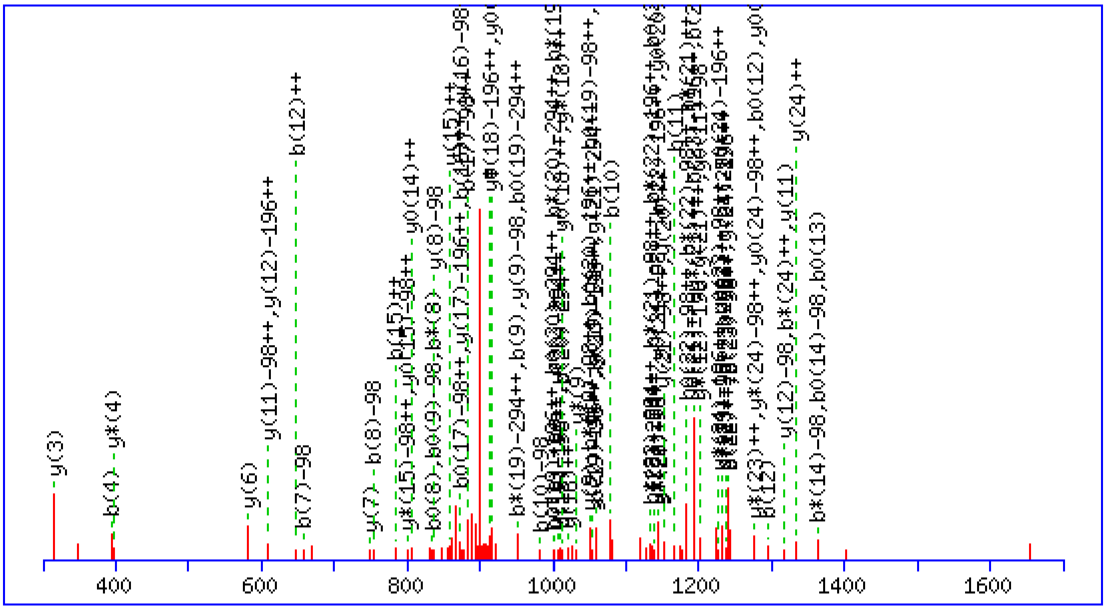
Monoisotopic mass of neutral peptide Mr(calc): 2714.2506
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.0009
Matched b ions: b(4), b(9), b(10), b(12), b(13)-98, b(13)-98++, b(13)++, b(14)-196, b(14)-196++, b(14)-98++, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)-196++, b(24)-196++
Matched y ions: y(3), y(6), y(7), y(8), y(12), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(19)-98++, y(20)++, y(20)-196++, y(21)++, y(21)-98++, y(23)++, y(24)++, y(24)-98++

Peptide No.518

KPPAPPSPVQSQSPSTNWSPAVPAK
Confirmed sites: @S:7,@T:16,@S:19
Ambiguous sites:

MS/MS Fragmentation of **KPPAPPSPVQSQSPSTNWSPAVPAK**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 5755: 2794.215831 from(932.412553,3+) index(5336)
Title: Elution from: 39.702 to 39.702 scan no 3787 cid35.00 polarity:+:m1s



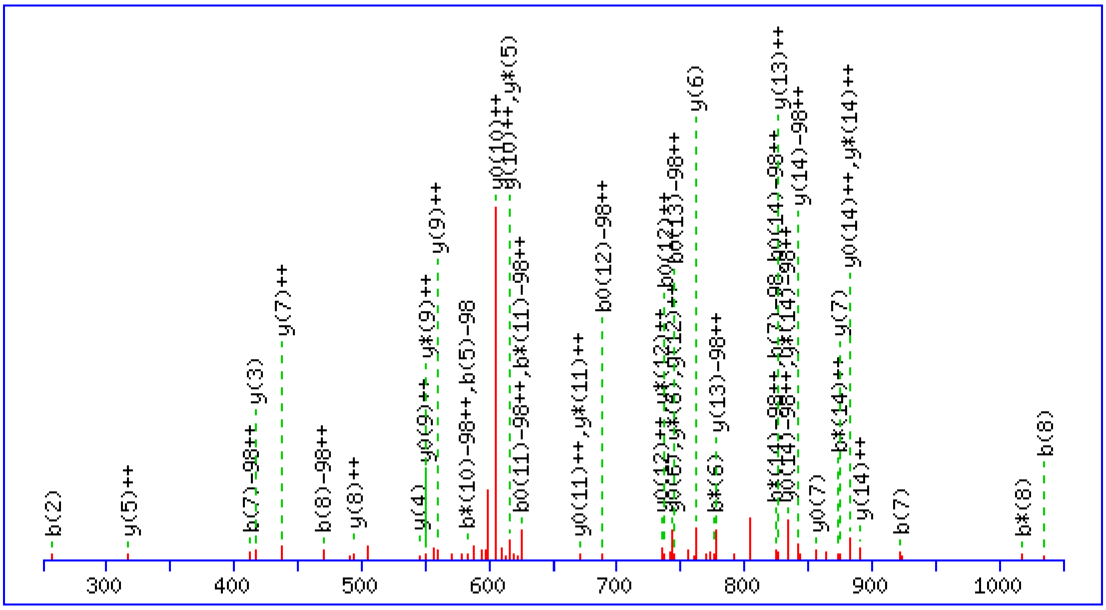
Monoisotopic mass of neutral peptide Mr(calc): 2794.2169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.012
Matched b ions: b(4), b(7)-98, b(8)-98, b(9), b(10), b(10)-98, b(11), b(12)++, b(12), b(15)++, b(16)++, b(17)-98++, b(19)-98++, b(19)-196++, b(20)-196++, b(20)-294++, b(21)-98++, b(22)-98++, b(22)++, b(22)-196++, b(23)-196++, b(23)-98++, b(23)-294++, b(24)-98++, b(24)-196++
Matched y ions: y(3), y(6), y(7), y(8)-98, y(9)-98, y(9), y(11)-98++, y(11), y(12)-196++, y(12)-98, y(15)++, y(16)-98++, y(17)-196++, y(18)++, y(19)-196++, y(19)-98++, y(20)++, y(20)-294++, y(20)-196++, y(21)++, y(21)-98++, y(21)-294++, y(22)++, y(23)-98++, y(23)-294++, y(24)++, y(24)-196++

Peptide No.519

KQSQQLELLESELRK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KQSQQLELLESELRK**
Found in **PLXC1_MOUSE** in **SwissProt**, Plexin-C1 OS=Mus musculus GN=Plxnc1 PE=1 SV=1

Match to Query 4639: 1907.971029 from(636.997619,3+) index(6360)
Title: Elution from: 42.454 to 42.454 scan no 4288 cid35.00 polarity:+:m1s



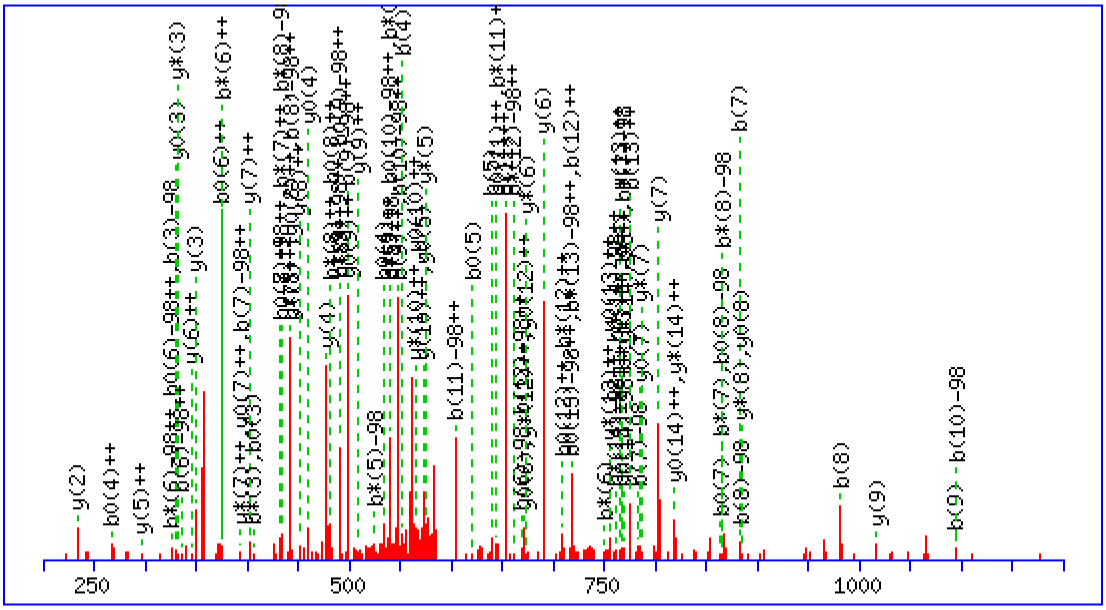
Monoisotopic mass of neutral peptide Mr(calc): 1907.9717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0027
Matched b ions: b(2), b(5)-98, b(7)-98++, b(7), b(7)-98, b(8), b(8)-98++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++

Peptide No.520

KQSQSQDVLVLEDSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KQSQSQDVLVLEDSK**
Found in **MRP2_MOUSE** in **SwissProt**, Canalicular multispecific organic anion transporter 1 OS=Mus musculus GN=Abcc2 PE=2 SV=2

Match to Query 3891: 1782.841590 from(595.287806,3+) index(4352)
Title: Elution from: 41.067 to 41.067 scan no 3097 cid35.00 polarity:+:m1s



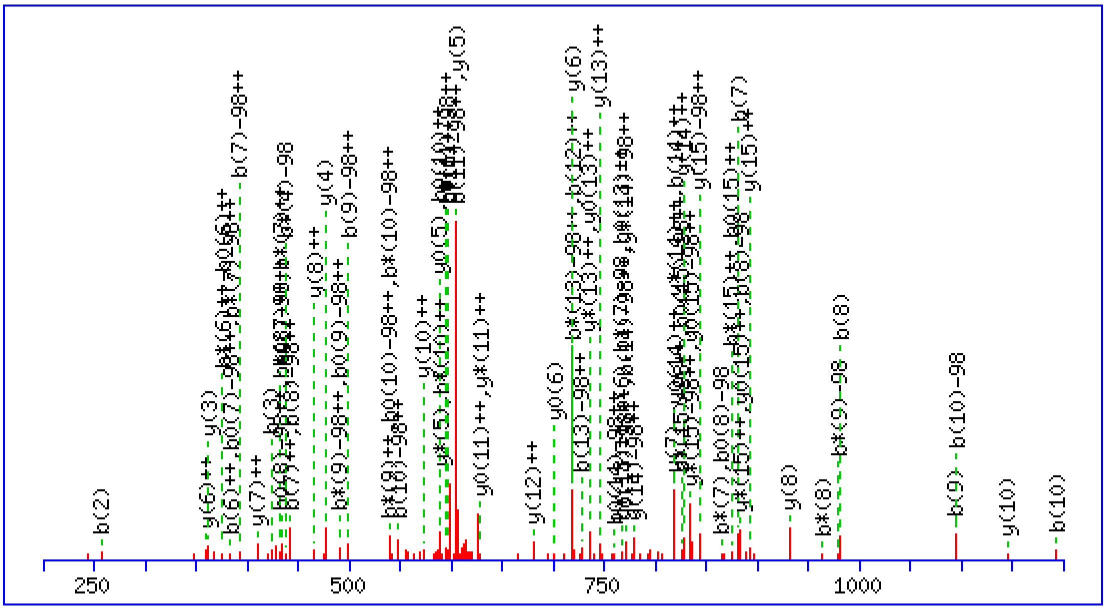
Monoisotopic mass of neutral peptide Mr(calc): 1782.8401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0019
Matched b ions: b(3)-98, b(4), b(5), b(5)-98, b(6)-98++, b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(7)-98++, b(8), b(8)-98++, b(8)++, b(8)-98, b(9)-98++, b(9)++, b(9), b(10)-98++, b(10)-98, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8)++, y(9), y(9)++, y(10)++, y(13)++

Peptide No.521

KQSQSQDVLVLEDSKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KQSQSQDVLVLEDSKK**
Found in **MRP2_MOUSE** in **SwissProt**, Canalicular multispecific organic anion transporter 1 OS=Mus musculus GN=Abcc2 PE=2 SV=2

Match to Query 3953: 1910.934507 from(637.985445,3+) index(963)
Title: Elution from: 26.876 to 26.876 scan no 2054 cid35.00 polarity:+



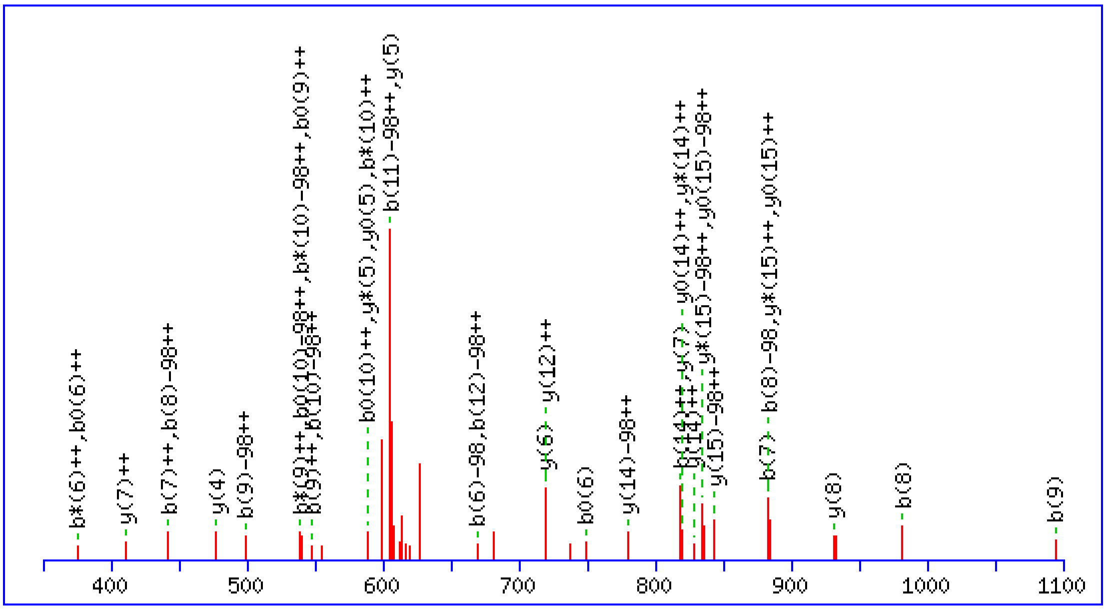
Monoisotopic mass of neutral peptide Mr(calc): 1910.9350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 1.1e-006
Matched b ions: b(2), b(3), b(6)++, b(6), b(7)++, b(7), b(7)-98++, b(8)-98++, b(8), b(8)-98, b(9), b(9)-98++, b(10), b(10)-98, b(10)-98++, b(10)++, b(11)-98++, b(12)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(10), y(10)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++

Peptide No.522

KQSQSQDVLVLEDSKK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KQSQSQDVLVLEDSKK**
Found in **MRP2_MOUSE** in **SwissProt**, Canalicular multispecific organic anion transporter 1 OS=Mus musculus GN=Abcc2 PE=2 SV=2

Match to Query 4495: 1910.934057 from(637.985295,3+) index(4682)
Title: Elution from: 26.489 to 26.489 scan no 2119 cid35.00 polarity:+:m1s



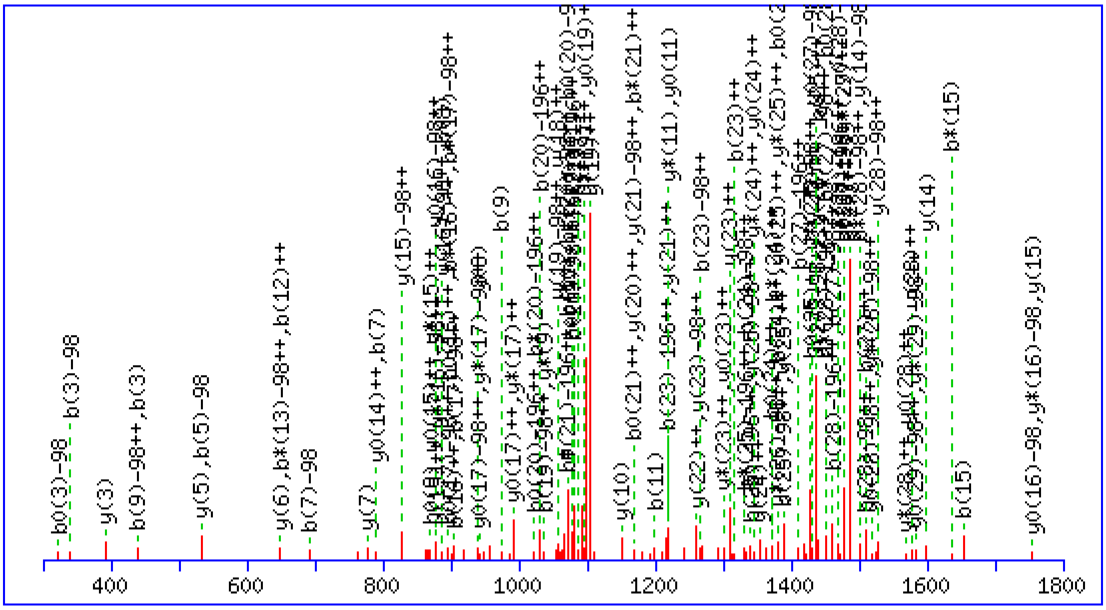
Monoisotopic mass of neutral peptide Mr(calc): 1910.9350
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0021
Matched b ions: b(6)-98, b(7)++, b(7), b(8)-98++, b(8)-98, b(8), b(9), b(9)-98++, b(9)++, b(10)-98++, b(11)-98++, b(12)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8), y(12)++, y(14)-98++, y(14)++, y(15)-98++

Peptide No.523

KQTPPASPSPQPIEDRPPSSPIYEDAAPFK
Confirmed sites: @T:3,@S:19
Ambiguous sites:

MS/MS Fragmentation of **KQTPPASPSPQPIEDRPPSSPIYEDAAPFK**
Found in **SRC8_MOUSE** in **SwissProt**, Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2

Match to Query 5825: 3406.549605 from(1136.523811,3+) index(5351)
Title: Elution from: 43.579 to 43.579 scan no 4246 cid35.00 polarity:+:m1s



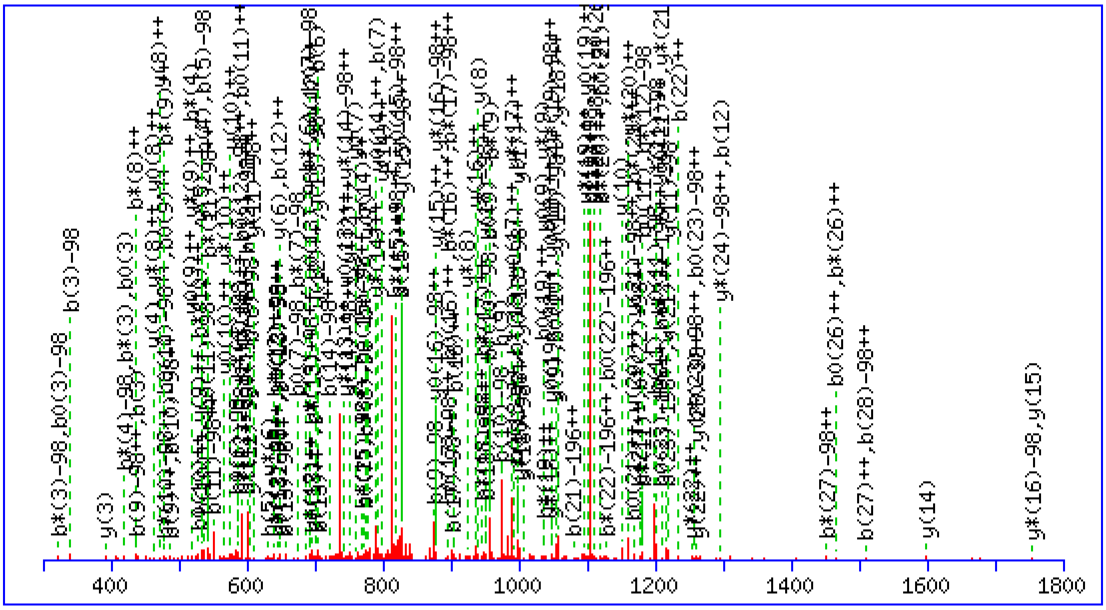
Monoisotopic mass of neutral peptide Mr(calc): 3406.5523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 1.1e-006
Matched b ions: b(3), b(3)-98, b(5)-98, b(7)-98, b(7), b(8), b(9)-98++, b(9), b(10), b(11), b(12)++, b(15), b(16)++, b(17)-98++, b(19)-98++, b(19)++, b(20)-98++, b(20)-196++, b(21)-196++, b(23)-196++, b(23)-98++, b(23)++, b(24)++, b(24)-98++, b(25)-98++, b(25)++, b(25)-196++, b(27)-98++, b(27)-196++, b(27)++, b(28)-196++, b(28)-98++, b(29)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(10), y(14), y(14)-98, y(15)-98++, y(15), y(15)++, y(16)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++, y(24)++, y(25)++, y(25)-98++, y(26)++, y(27)++, y(27)-98++, y(28)-98++, y(28)++, y(28)-196++

Peptide No.524

KQTPPASPSPQPIEDRPPSSPIYEDAAPFK
Confirmed sites: @T:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of **KQTPPASPSPQPIEDRPPSSPIYEDAAPFK**
Found in **SRC8_MOUSE** in **SwissProt**, Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2

Match to Query 6696: 3406.551848 from(852.645238,4+) index(5684)
Title: Elution from: 51.950 to 51.950 scan no 4367 cid35.00 polarity:+:m1s



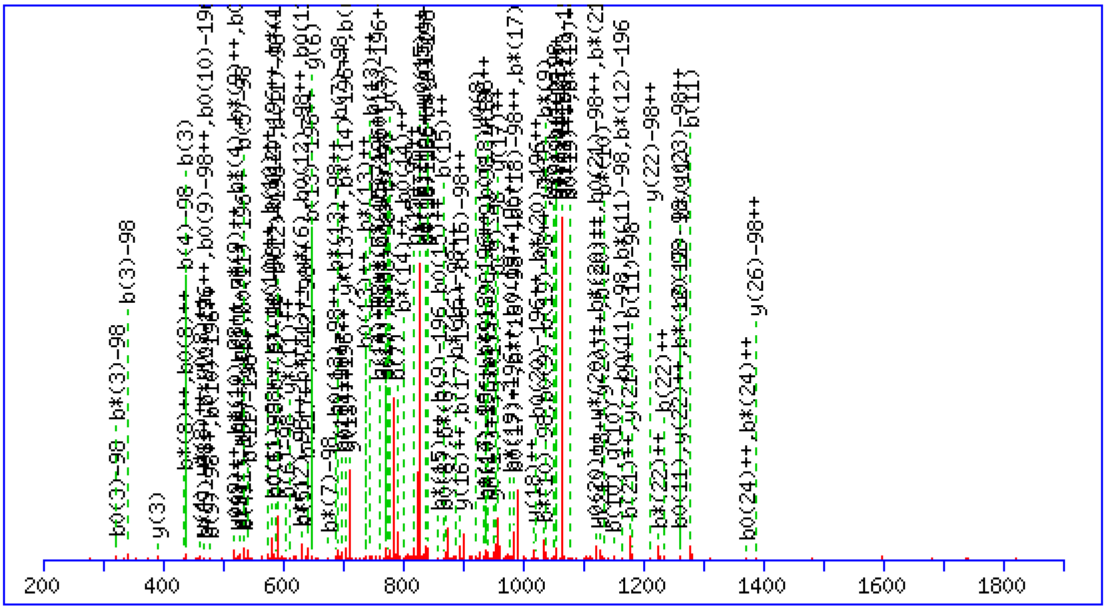
Monoisotopic mass of neutral peptide Mr(calc): 3406.5523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.012
Matched b ions: b(3)-98, b(3), b(4), b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(9)-98++, b(9), b(9)++, b(9)-98, b(10)-98++, b(10)-98, b(10)++, b(11)++, b(11), b(11)-98++, b(11)-98, b(12)-98++, b(12)++, b(12), b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(17)-98++, b(18)-98++, b(21)-196++, b(21)++, b(22)++, b(23)-196++, b(27)++, b(28)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11)-98++, y(11)-98, y(12)++, y(13)-98++, y(13)++, y(14), y(14)-98++, y(14)++, y(15), y(15)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)-98++

Peptide No.525

KQTPPASPSPQPIEDRPPSSPIYEDAAPFK
Confirmed sites: @T:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of **KQTPPASPSPQPIEDRPPSSPIYEDAAPFK**
Found in **SRC8_MOUSE** in **SwissProt**, Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2

Match to Query 5826: 3406.551528 from(852.645158,4+) index(5380)
Title: Elution from: 44.176 to 44.176 scan no 4313 cid35.00 polarity:+:m1s



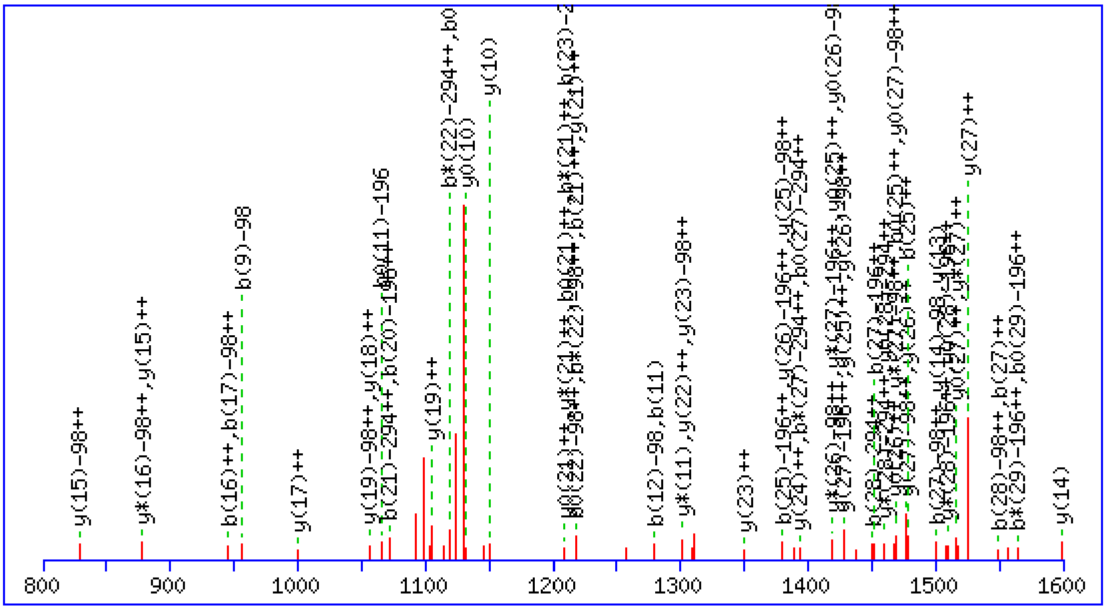
Monoisotopic mass of neutral peptide Mr(calc): 3406.5523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 9.6e-005
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(9)-98, b(9)++, b(9), b(9)-98++, b(9)-196, b(10)-98++, b(10)++, b(10), b(10)-196++, b(10)-98, b(11)-98++, b(11), b(11)-196++, b(11)-98, b(11)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)-196++, b(13)++, b(14)-98++, b(15)-196++, b(15)-98++, b(15)++, b(16)-98++, b(17)-196++, b(19)-98++, b(20)++, b(21)++, b(21)-98++, b(22)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(22)-98++, y(23)-98++, y(26)-98++

Peptide No.526

KQTPPASPSPQPIEDRPPSSPIYEDAAPFK
Confirmed sites: @T:3,@S:9
Ambiguous sites: @S:19orS:20

MS/MS Fragmentation of **KQTPPASPSPQPIEDRPPSSPIYEDAAPFK**
Found in **SRC8_MOUSE** in **SwissProt**, Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2

Match to Query 5862: 3486.516348 from(1163.179392,3+) index(5529)
Title: Elution from: 46.726 to 46.726 scan no 4615 cid35.00 polarity:+:m1s



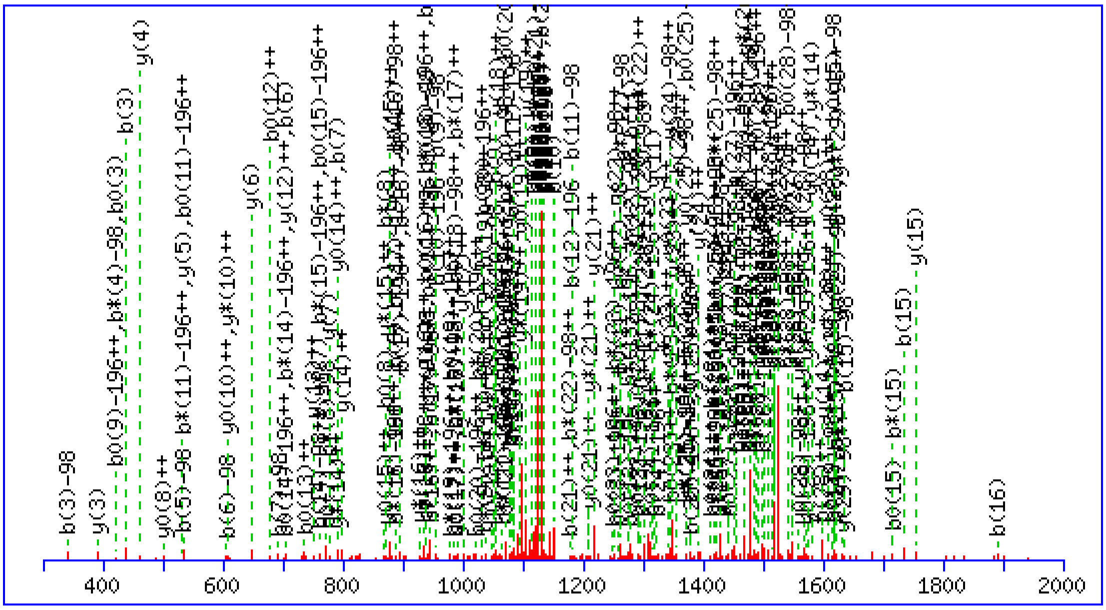
Monoisotopic mass of neutral peptide Mr(calc): 3486.5186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.0003
Matched b ions: b(9)-98, b(11), b(12)-98, b(16)++, b(17)-98++, b(20)-196++, b(21)++, b(21)-294++, b(23)-294++, b(25)-196++, b(25)++, b(27)++, b(27)-98++, b(27)-196++, b(28)-98++, b(28)-294++
Matched y ions: y(10), y(13), y(14), y(14)-98, y(15)++, y(15)-98++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(21)++, y(22)++, y(23)-98++, y(23)++, y(24)++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(26)-196++, y(27)-196++, y(27)++, y(27)-98++

Peptide No.527

KQTPPASPSPQPIEDRPPSSPIYEDAAPFK
Confirmed sites: @T:3,@S:9,@Y:23
Ambiguous sites:

MS/MS Fragmentation of **KQTPPASPSPQPIEDRPPSSPIYEDAAPFK**
Found in **SRC8_MOUSE** in **SwissProt**, Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2

Match to Query 6728: 3486.518397 from(1163.180075,3+) index(5787)
Title: Elution from: 54.977 to 54.977 scan no 4619 cid35.00 polarity:+:m1s



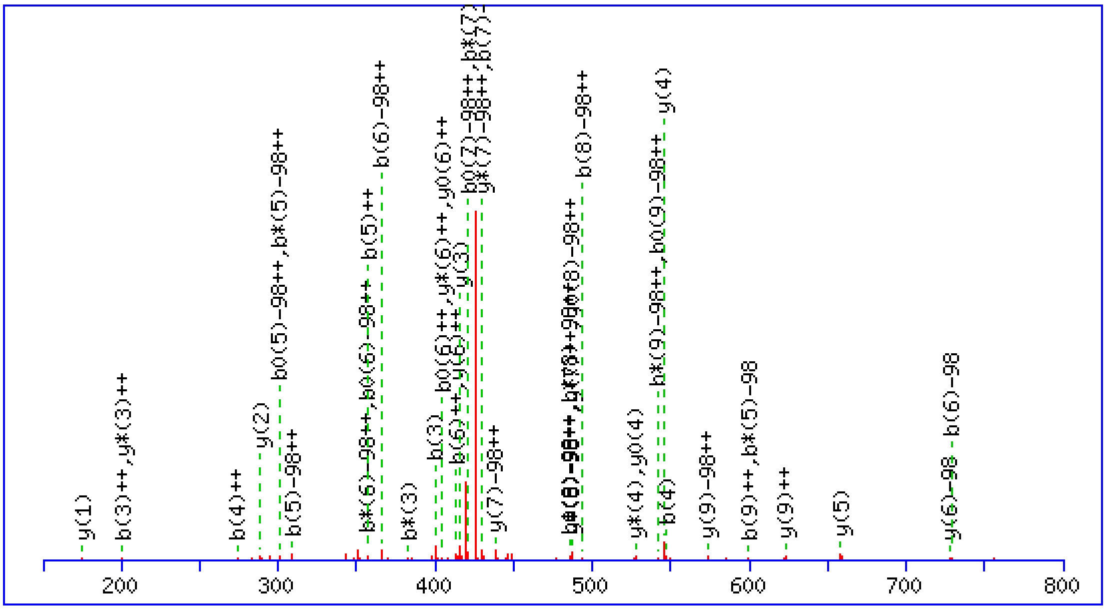
Monoisotopic mass of neutral peptide Mr(calc): 3486.5186
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y23 : Phospho (Y)
Ions Score: 65 **Expect:** 2.8e-006
Matched b ions: b(3), b(3)-98, b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(10), b(10)-196, b(10)-98, b(11), b(11)-98, b(11)-196, b(12)-98, b(12)-196, b(12), b(13)-196, b(13), b(14)-98++, b(14), b(15), b(15)-98, b(16)++, b(16), b(16)-98++, b(17)-98++, b(17)-196++, b(19)-98++, b(19)++, b(20)++, b(20)-196++, b(20)-98++, b(21)-196++, b(21)-98++, b(21)++, b(22)-196++, b(23)-196++, b(23)++, b(24)++, b(24)-98++, b(24)-196++, b(25)-98++, b(25)-196++, b(25)++, b(26)++, b(27)++, b(27)-98++, b(27)-196++, b(28)-98++, b(28)-196++, b(28)++, b(29)-196++, b(29)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(11), y(12)++, y(13)++, y(13), y(14), y(14)++, y(15)++, y(15), y(16)++, y(17)++, y(18)++, y(19)++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)-98++, y(24)++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)++, y(27)-98++, y(28)-98++, y(28)++, y(28)-196++, y(29)-98++

Peptide No.528

KRDFSLEQLR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KRDFSLEQLR**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 2239: 1370.670171 from(457.897333,3+) index(1594)
Title: Elution from: 31.078 to 31.078 scan no 2745 cid35.00 polarity:+



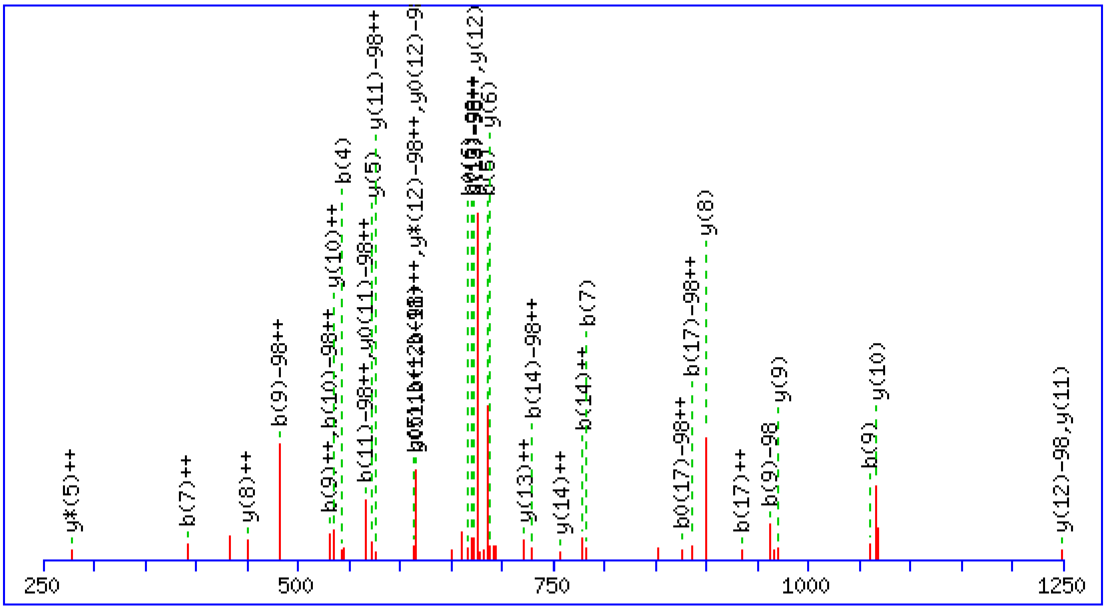
Monoisotopic mass of neutral peptide Mr(calc): 1370.6707
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0013
Matched b ions: b(3)++, b(3), b(4)++, b(4), b(5)-98++, b(5)++, b(6)-98++, b(6)-98, b(6)++, b(7)-98++, b(8)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)-98, y(6)++, y(7)++, y(7)-98++, y(9)++, y(9)-98++

Peptide No.529

KREEAAPPTPAPDDLAQLK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **KREEAAPPTPAPDDLAQLK**
Found in **LYRIC_MOUSE** in **SwissProt**, Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1

Match to Query 5341: 2126.037120 from(709.686316,3+) index(5205)
Title: Elution from: 31.790 to 31.790 scan no 2841 cid35.00 polarity:+:m1s



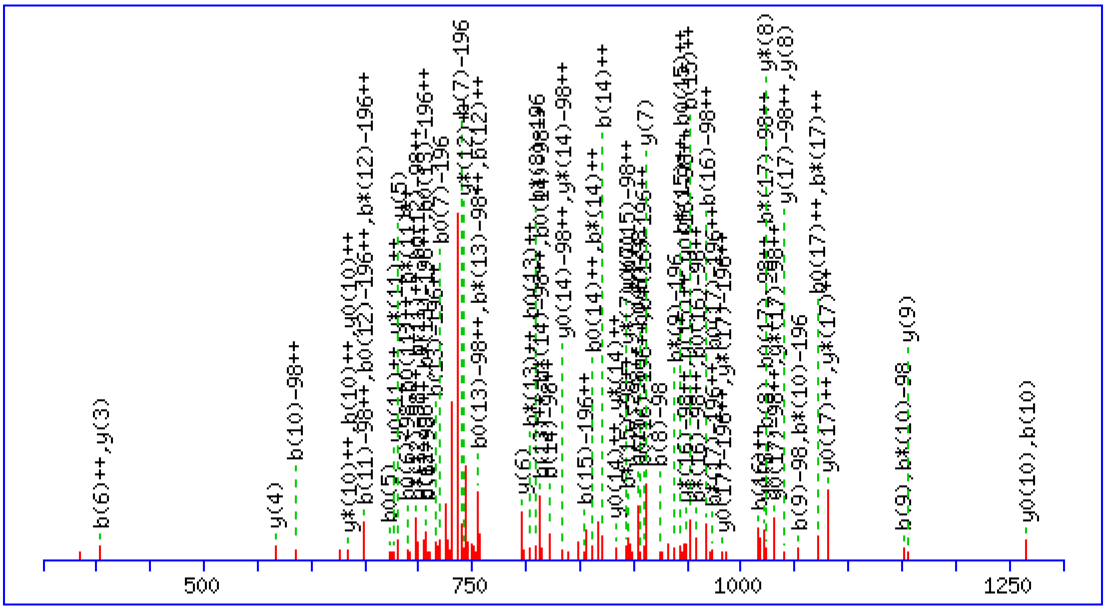
Monoisotopic mass of neutral peptide Mr(calc): 2126.0408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 7.6e-005
Matched b ions: b(4), b(5), b(6), b(7), b(7)++, b(9)-98++, b(9)-98, b(9), b(9)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++, b(17)-98++, b(17)++
Matched y ions: y(5), y(6), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(11)-98++, y(12)-98, y(12)++, y(13)++, y(13)-98++, y(14)++

Peptide No.530

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:2,@S:5
Ambiguous sites:

MS/MS Fragmentation of **KSLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5833: 2304.783081 from(769.268303,3+) index(4488)
Title: Elution from: 24.668 to 24.668 scan no 1872 cid35.00 polarity:+:m1s



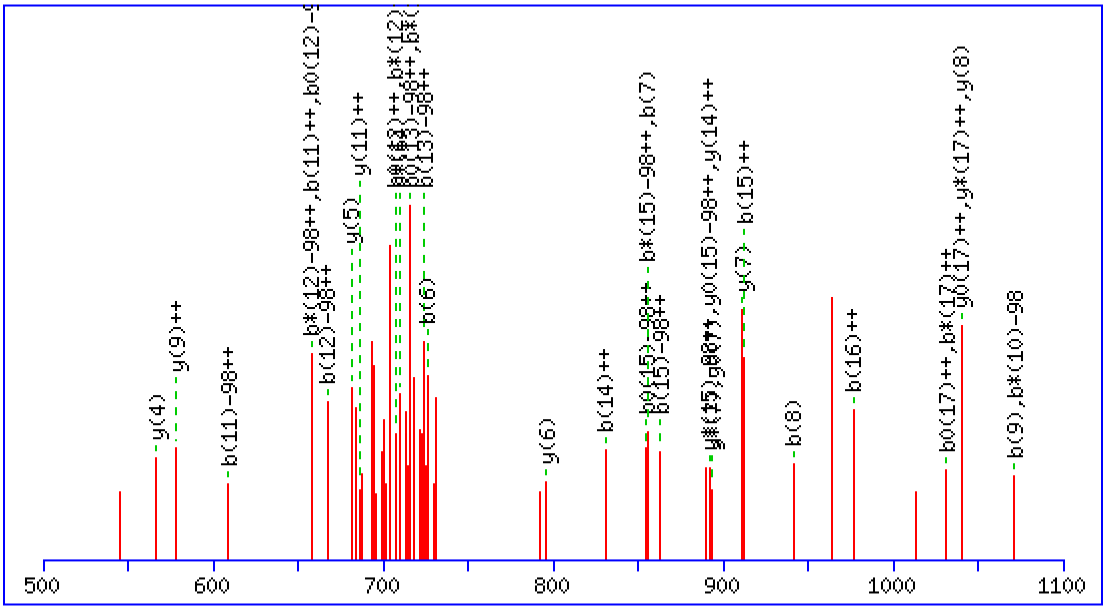
Monoisotopic mass of neutral peptide Mr(calc): 2304.7832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 7e-005
Matched b ions: b(6)++, b(6)-98, b(7)-196, b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(15)++, y(17)-98++

Peptide No.531

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KSLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5666: 2224.815330 from(742.612386,3+) index(4264)
Title: Elution from: 22.797 to 22.797 scan no 1617 cid35.00 polarity:+:m1s



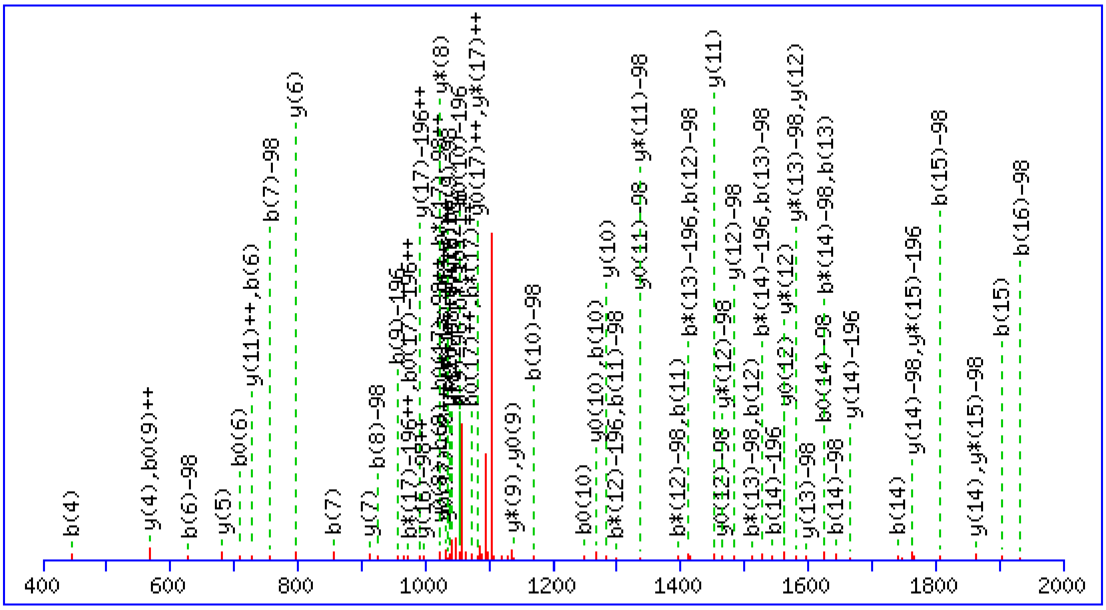
Monoisotopic mass of neutral peptide Mr(calc): 2224.8169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0011
Matched b ions: b(6), b(7), b(8), b(9), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(11)++, y(14)++

Peptide No.532

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of **KSLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5012: 2304.784454 from(1153.399503,2+) index(3925)
Title: Elution from: 24.184 to 24.184 scan no 1781 cid35.00 polarity:+:m1s



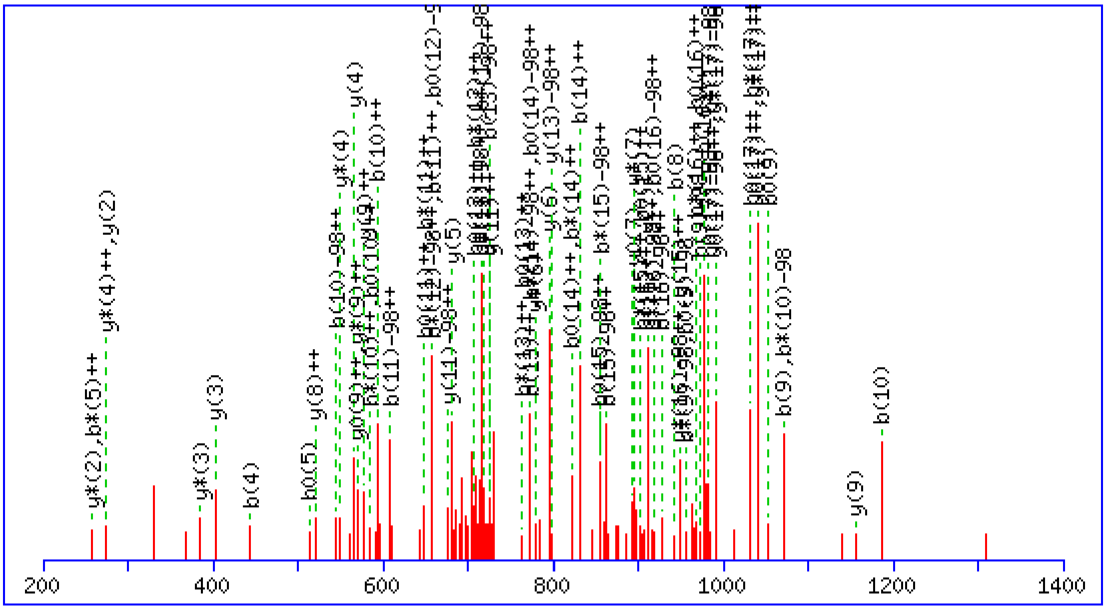
Monoisotopic mass of neutral peptide Mr(calc): 2304.7832
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00011
Matched b ions: b(4), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-196, b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98, b(14)-196, b(15)-98, b(15), b(16)-98, b(17)-98++, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(11)++, y(12)-98, y(12), y(13)-98, y(14)-98, y(14)-196, y(14), y(16)-98++, y(17)-98++, y(17)-196++

Peptide No.533

KSLDSDESEDEDDDYQQK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **KSLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 4867: 2224.812561 from(742.611463,3+) index(3726)
Title: Elution from: 22.445 to 22.445 scan no 1546 cid35.00 polarity:+:m1s



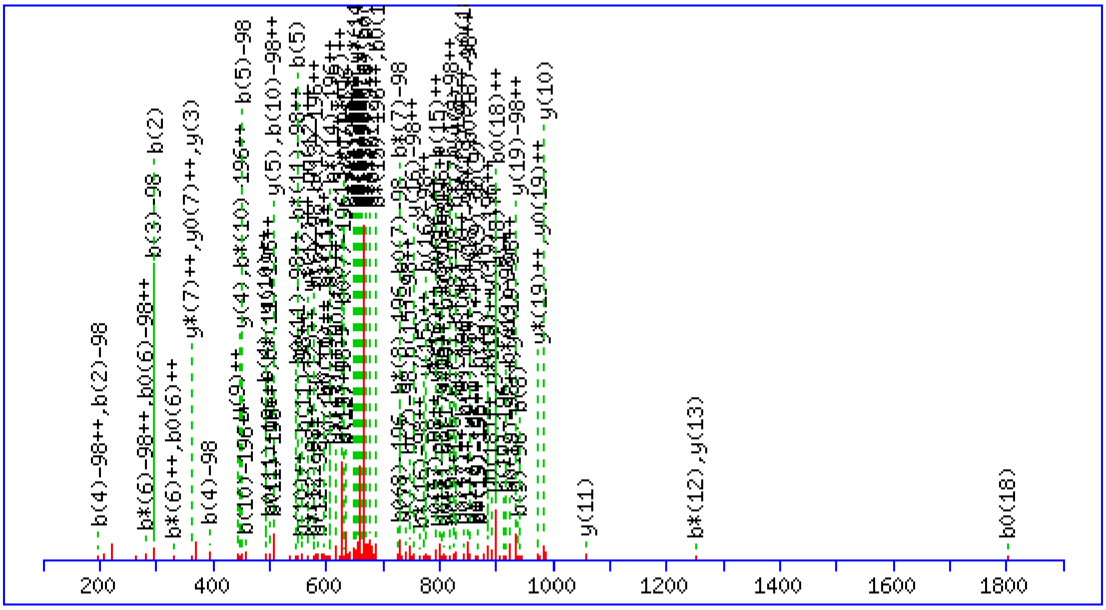
Monoisotopic mass of neutral peptide Mr(calc): 2224.8169
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 7.2e-006
Matched b ions: b(4), b(8), b(9), b(9)-98, b(10)-98++, b(10)++, b(10), b(11)-98++, b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(11)-98++, y(11)++, y(13)-98++, y(15)++

Peptide No.534

KSPVGKSPPATGSAYGSSQK
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of **KSPVGKSPPATGSAYGSSQK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4424: 2092.921959 from(698.647929,3+) index(3342)
Title: Elution from: 19.252 to 19.252 scan no 1118 cid35.00 polarity:+:m1s



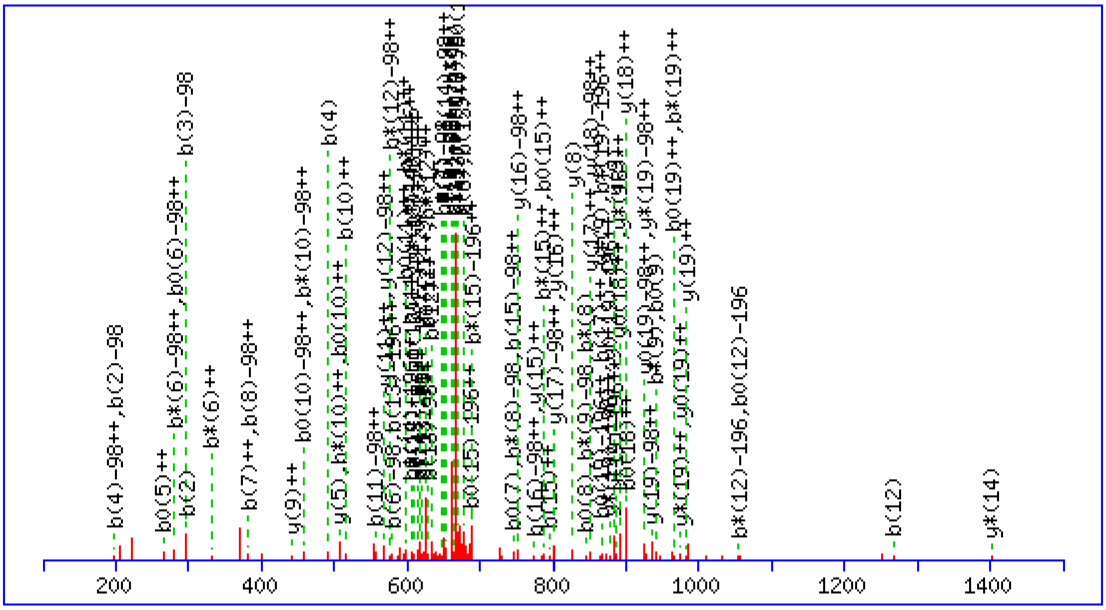
Monoisotopic mass of neutral peptide Mr(calc): 2092.9231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 66 **Expect:** 1.6e-006
Matched b ions: b(2), b(2)-98, b(3)-98, b(4)-98, b(4), b(4)-98++, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)-196, b(8), b(9)-196, b(9)-98, b(10)-196++, b(10)-98++, b(10)++, b(10)-196, b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-196++, b(13)-98++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++, b(17)++, b(19)-98++, b(19)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(12)++, y(13), y(13)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)-196++

Peptide No.535

KSPVGKSPPATGSAYGSSQK
Confirmed sites: @S:2,@T:11
Ambiguous sites:

MS/MS Fragmentation of **KSPVGKSPPATGSAYGSSQK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 5360: 2092.924425 from(698.648751,3+) index(3608)
Title: Elution from: 24.736 to 24.736 scan no 1277 cid35.00 polarity:+:m1s



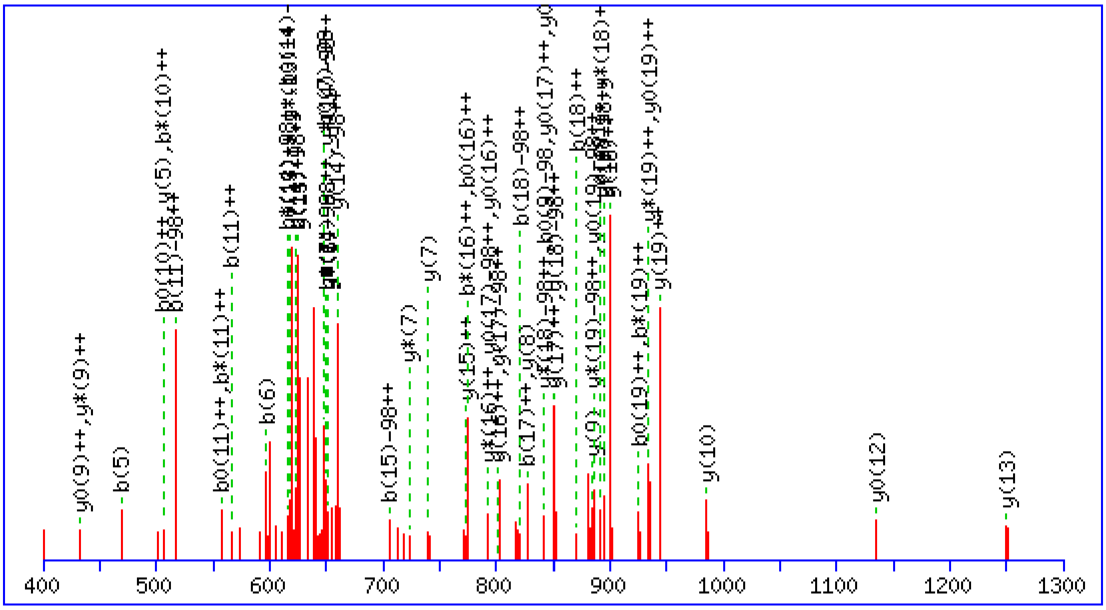
Monoisotopic mass of neutral peptide Mr(calc): 2092.9231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0011
Matched b ions: b(2), b(2)-98, b(3)-98, b(4), b(4)-98++, b(6), b(6)-98, b(7)-98, b(7)++, b(8)-98++, b(10)++, b(11)-98++, b(11)++, b(12), b(12)++, b(13)++, b(13)-196++, b(13)-98++, b(14)-196++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(19)-98++, b(19)++, b(19)-196++
Matched y ions: y(5), y(6), y(8), y(9), y(9)++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)-196++, y(19)++

Peptide No.536

KSPVGKSPPATGSAYGSSQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **KSPVGKSPPATGSAYGSSQK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4922: 2012.954298 from(671.992042,3+) index(3807)
Title: Elution from: 19.008 to 19.008 scan no 1107 cid35.00 polarity:+:m1s



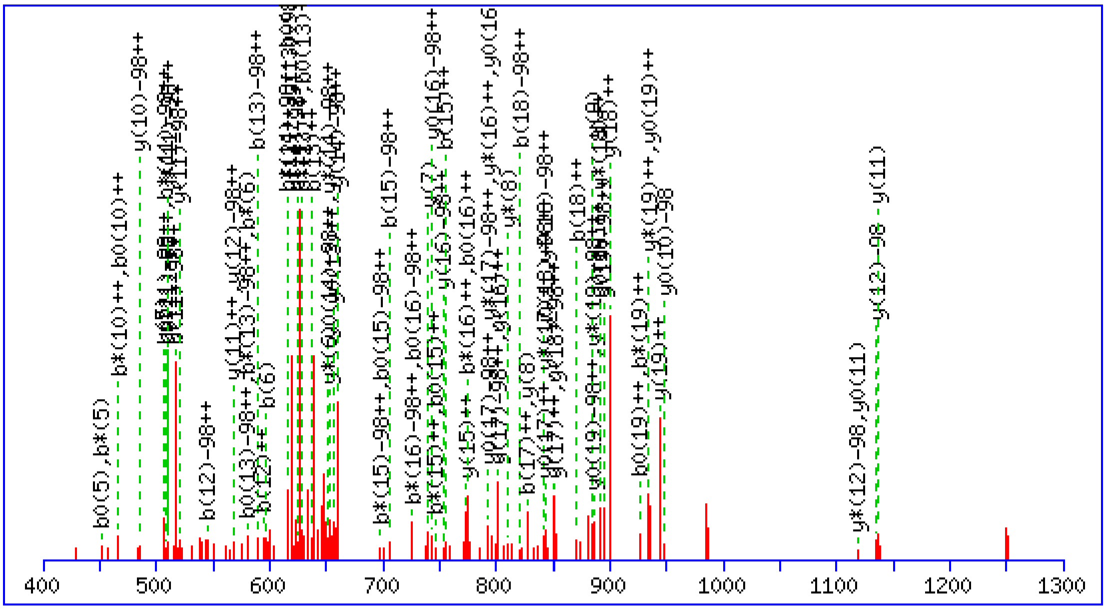
Monoisotopic mass of neutral peptide Mr(calc): 2012.9568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0082
Matched b ions: b(5), b(6), b(11)-98++, b(11)++, b(14)-98++, b(15)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(5), y(7), y(8), y(9), y(10), y(13), y(13)++, y(14)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++

Peptide No.537

KSPVGKSPPATGSAYGSSQK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **KSPVGKSPPATGSAYGSSQK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 5045: 2012.956326 from(671.992718,3+) index(3990)
Title: Elution from: 19.022 to 19.022 scan no 1144 cid35.00 polarity:+:m1s



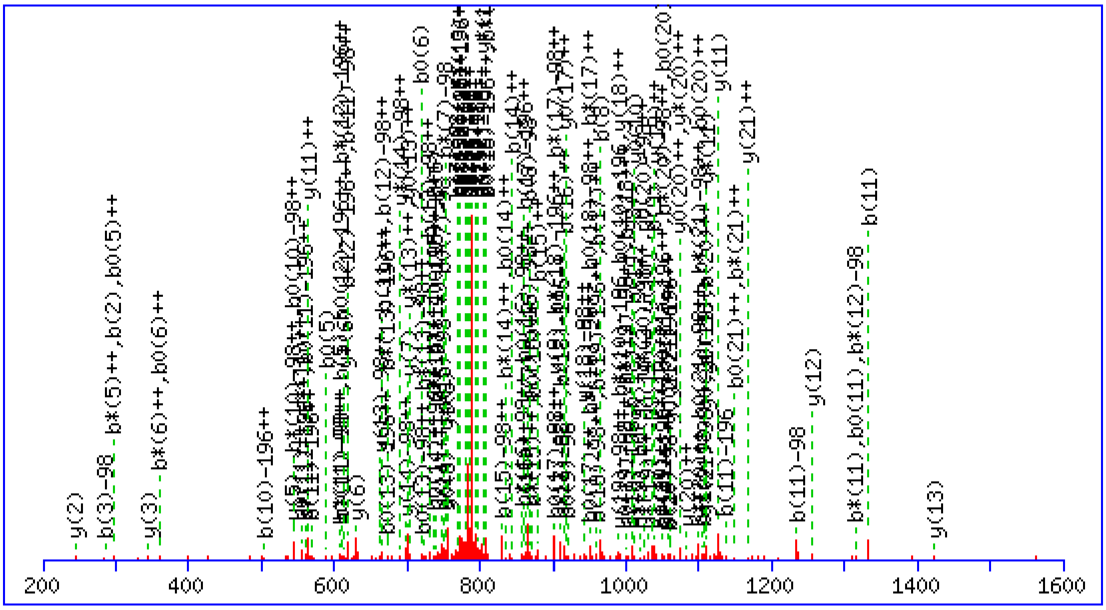
Monoisotopic mass of neutral peptide Mr(calc): 2012.9568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0028
Matched b ions: b(6), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(15)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(5), y(7), y(8), y(9), y(10)-98++, y(11), y(11)-98++, y(11)++, y(12)-98, y(12)++, y(12)-98++, y(13)-98++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++

Peptide No.538

KSSPKEEVASEPEEAASPTTPK
Confirmed sites: @S:2,@S:10
Ambiguous sites:

MS/MS Fragmentation of **KSSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 6173: 2458.056231 from(820.359353,3+) index(4099)
Title: Elution from: 30.372 to 30.372 scan no 1934 cid35.00 polarity:+:m1s



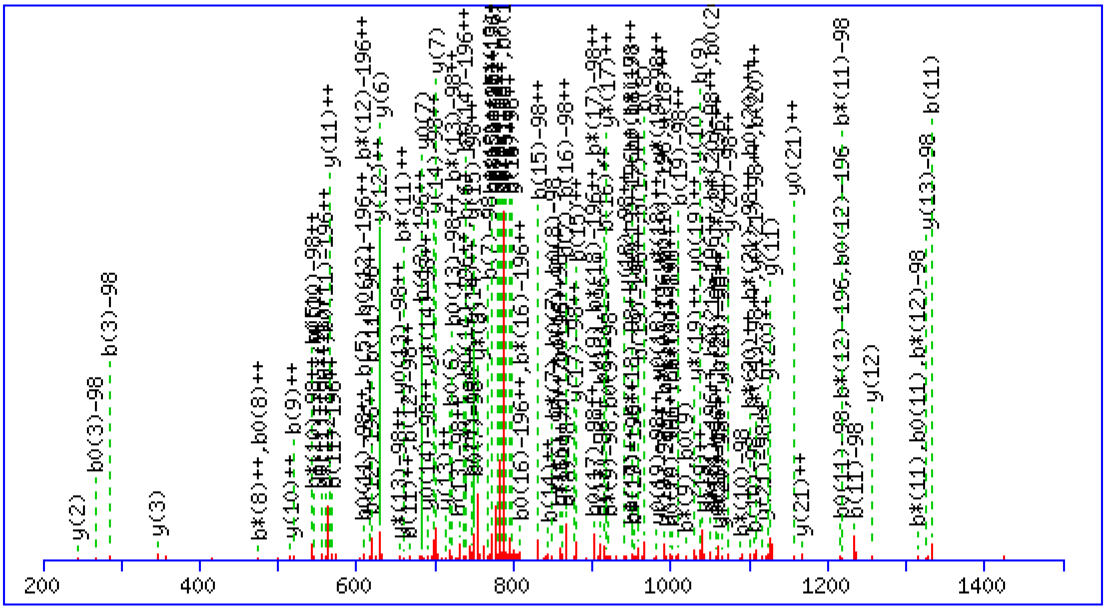
Monoisotopic mass of neutral peptide Mr(calc): 2458.0553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00039
Matched b ions: b(2), b(3)-98, b(5), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9), b(10)-196++, b(10)-196, b(10)-98, b(11)-98, b(11), b(11)-98++, b(11)++, b(11)-196++, b(11)-196, b(12)-196++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-196++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)-196++, b(17)++, b(18)-196++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)++, b(20)-98++, b(21)-98++, b(21)-196++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11), y(12), y(13), y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(21)++

Peptide No.539

KSSPKEEVASEPEEAASPTTPK
Confirmed sites: @S:3,@S:10
Ambiguous sites:

MS/MS Fragmentation of **KSSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 6299: 2458.048518 from(820.356782,3+) index(4536)
Title: Elution from: 23.652 to 23.652 scan no 1770 cid35.00 polarity:+:m1s



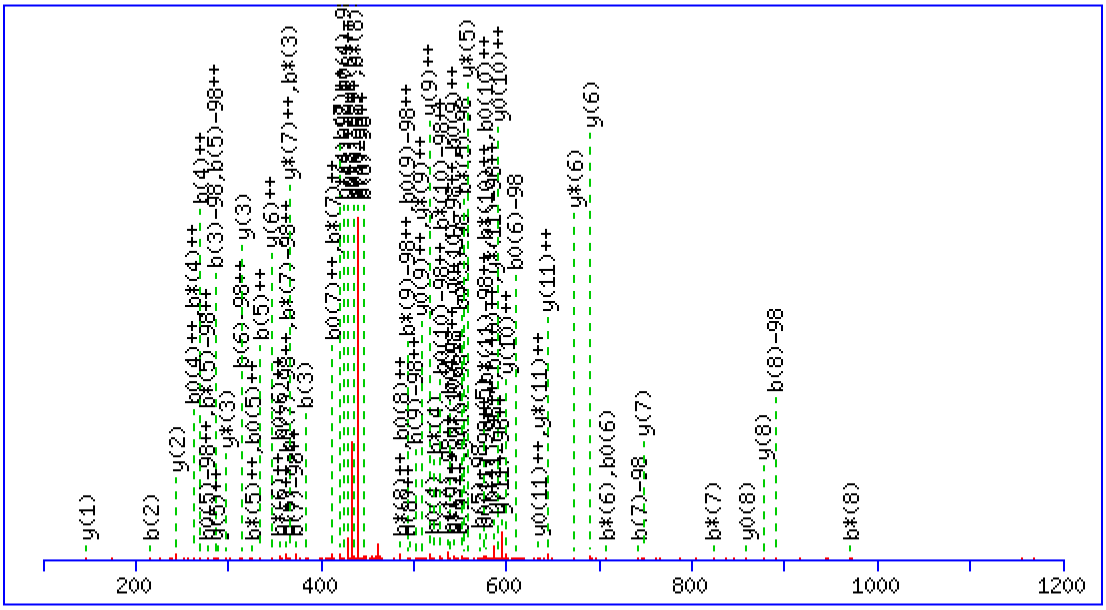
Monoisotopic mass of neutral peptide Mr(calc): 2458.0553
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 4.1e-005
Matched b ions: b(3)-98, b(5), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)++, b(9), b(10)-98, b(11)-98, b(11), b(11)-98++, b(11)-196++, b(11)++, b(12)-98++, b(12)-196++, b(13)-98++, b(13)-196++, b(13)++, b(14)-98++, b(14)++, b(14)-196++, b(15)-196++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(17)-196++, b(18)-196++, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++, b(21)++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(11), y(12), y(12)++, y(13)-98, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++

Peptide No.540

KSSREGDFLAPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KSSREGDFLAPK**
Found in **MLXPL_MOUSE** in **SwissProt**, Carbohydrate-responsive element-binding protein OS=Mus musculus GN=Mlxipl PE=1 SV=1

Match to Query 3182: 1413.665823 from(472.229217,3+) index(669)
Title: Elution from: 30.235 to 30.235 scan no 1915 cid35.00 polarity:+



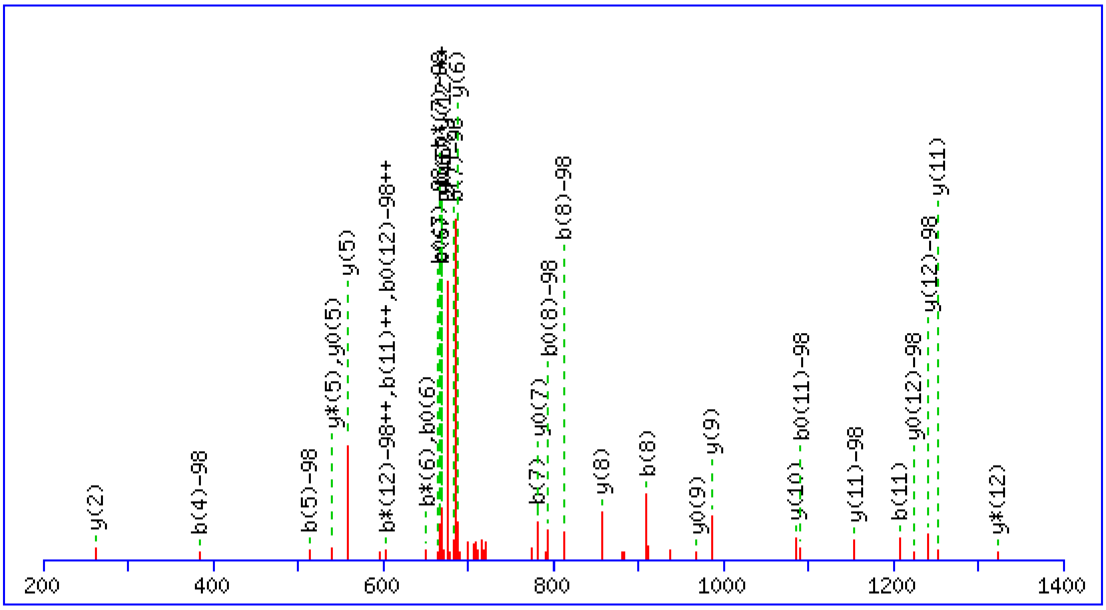
Monoisotopic mass of neutral peptide Mr(calc): 1413.6653
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00065
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4)++, b(4), b(5)++, b(5)-98++, b(5)-98, b(6)++, b(6)-98++, b(7)-98, b(7)-98++, b(7)++, b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(11)++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(8), y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(11)++

Peptide No.541

KSSVEGLEPAENK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KSSVEGLEPAENK**
Found in **SRP14_MOUSE** in **SwissProt**, Signal recognition particle 14 kDa protein OS=Mus musculus GN=Srp14 PE=1 SV=1

Match to Query 2826: 1466.663532 from(734.339042,2+) index(599)
Title: Elution from: 21.146 to 21.146 scan no 1429 cid35.00 polarity:+



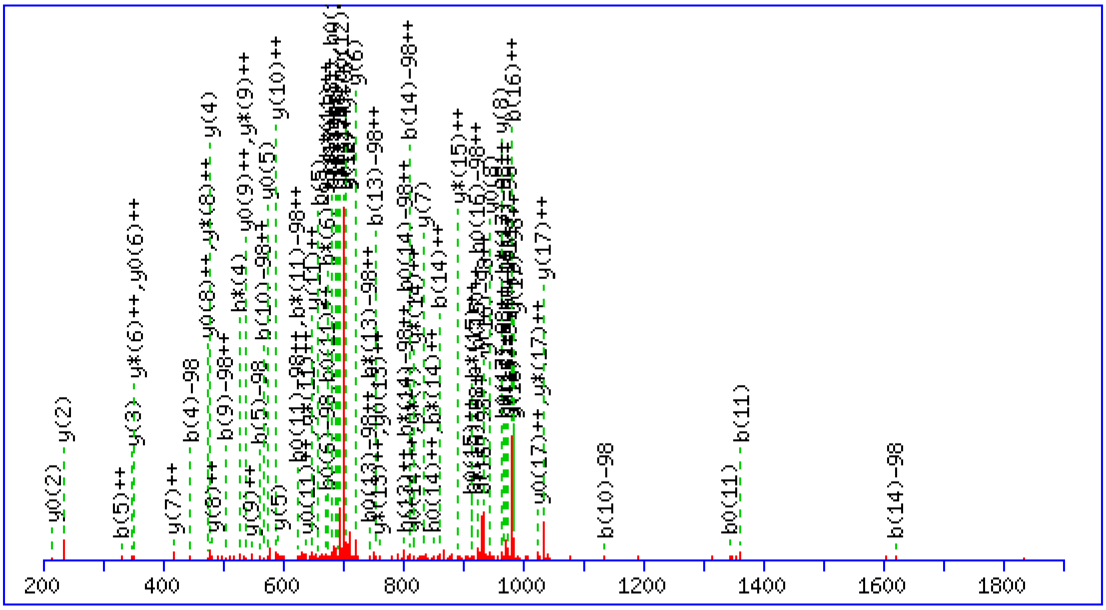
Monoisotopic mass of neutral peptide Mr(calc): 1466.6654
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 **Expect:** 8e-006
Matched b ions: b(4)-98, b(5)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(11)++, b(11), b(12)-98
Matched y ions: y(2), y(5), y(6), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12)++

Peptide No.542

KTSFDENDSEELEDKDSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KTSFDENDSEELEDKDSK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 5583: 2194.880463 from(732.634097,3+) index(4042)
Title: Elution from: 29.859 to 29.859 scan no 1869 cid35.00 polarity:+:m1s



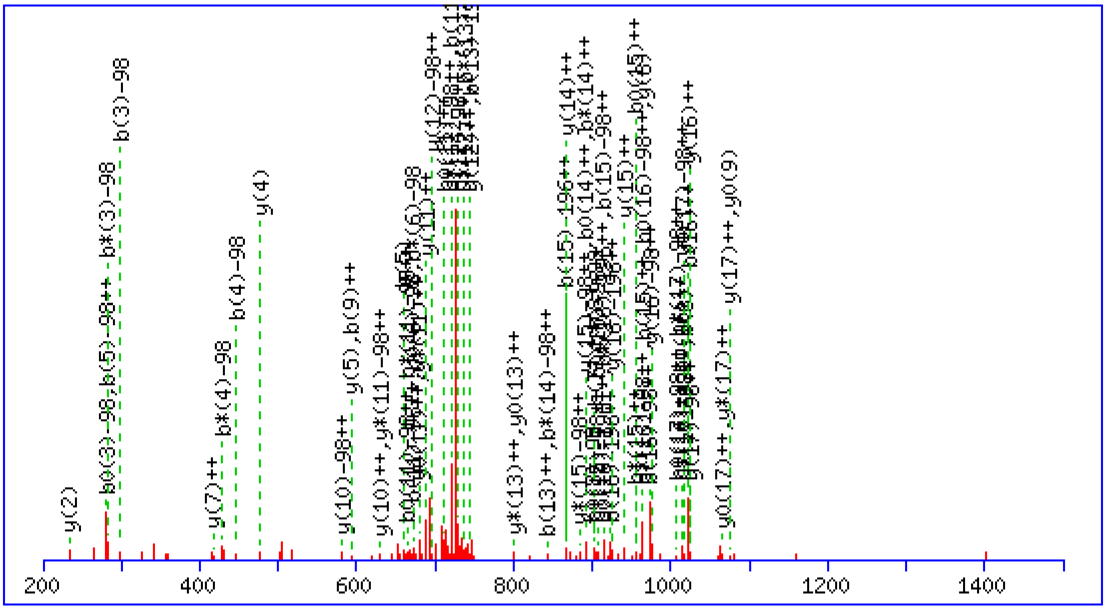
Monoisotopic mass of neutral peptide Mr(calc): 2194.8791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.028
Matched b ions: b(4)-98, b(5)++, b(5)-98, b(5), b(6)-98, b(9)-98++, b(10)-98, b(10)-98++, b(11), b(11)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98, b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.543

KTSFDENDSEELEDKDSK
Confirmed sites: @S:3,@S:9
Ambiguous sites:

MS/MS Fragmentation of **KTSFDENDSEELEDKDSK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4964: 2274.843060 from(759.288296,3+) index(815)
Title: Elution from: 24.068 to 24.068 scan no 1765 cid35.00 polarity:+



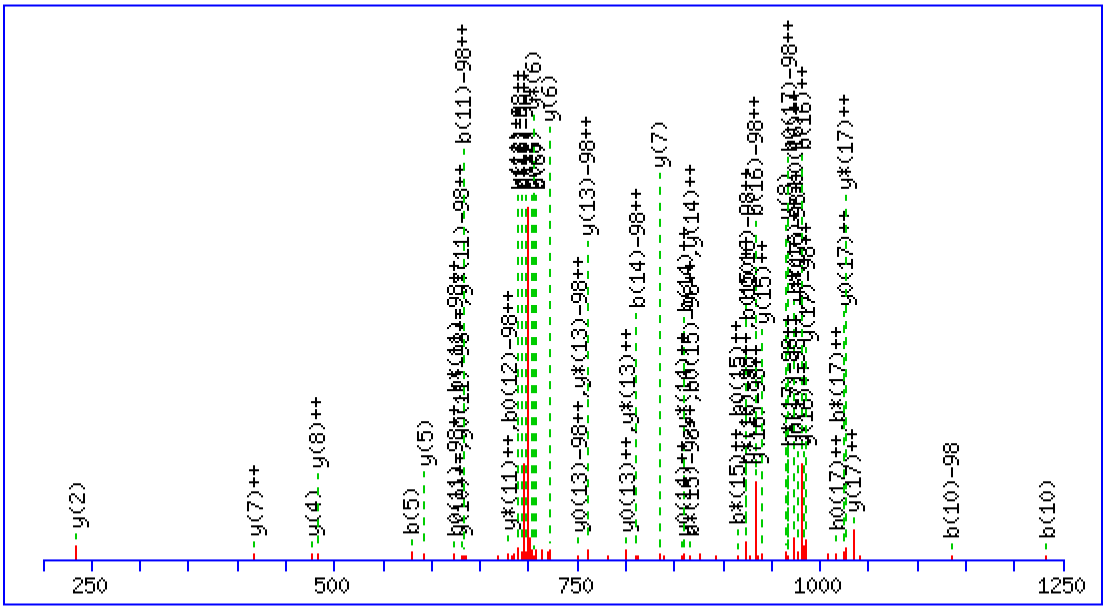
Monoisotopic mass of neutral peptide Mr(calc): 2274.8454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.033
Matched b ions: b(3)-98, b(4)-98, b(5)-98++, b(5), b(7), b(8), b(9)++, b(11)++, b(11)-98++, b(12)-98++, b(13)-196++, b(13)++, b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-196++, b(16)-98++, b(17)++, b(17)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(8), y(10)-98++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)++, y(17)-98++

Peptide No.544

KTSFDENDSEELEDKDSK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **KTSFDENDSEELEDKDSK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4805: 2194.876752 from(732.632860,3+) index(3746)
Title: Elution from: 22.614 to 22.614 scan no 1569 cid35.00 polarity:+:m1s



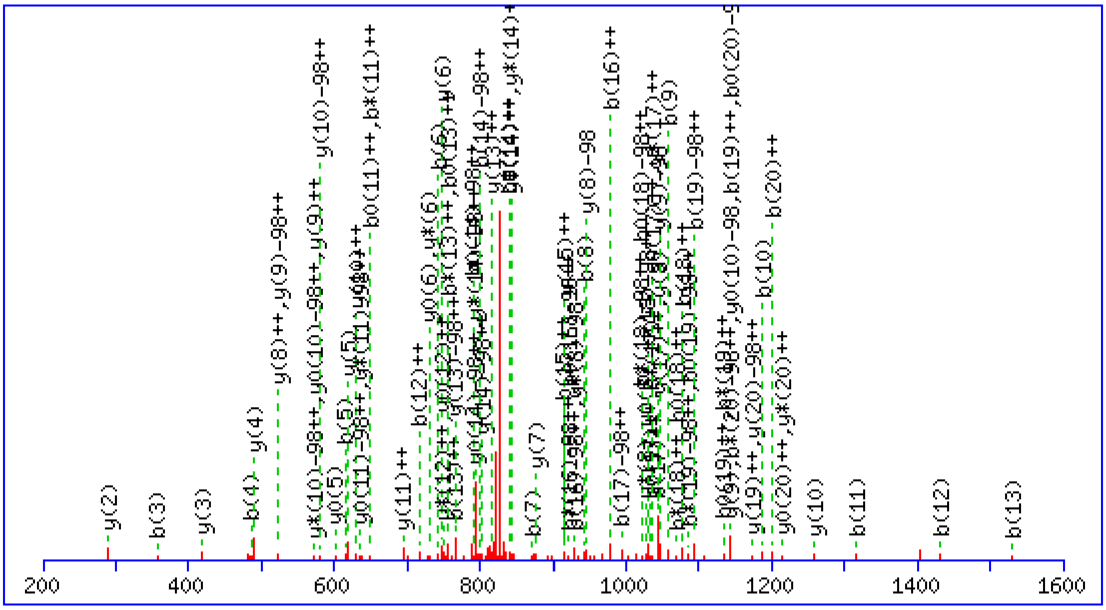
Monoisotopic mass of neutral peptide Mr(calc): 2194.8791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0028
Matched b ions: b(5), b(6), b(10)-98, b(10), b(11)-98++, b(12)-98++, b(14)-98++, b(14)++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(10)++, y(11)++, y(12)-98++, y(13)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.545

KVEEEQEADEEDVSEEEAEDR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **KVEEEQEADEEDVSEEEAEDR**
Found in **TMX1_MOUSE** in **SwissProt**, Thioredoxin-related transmembrane protein 1 OS=Mus musculus GN=Tmx1 PE=1 SV=1

Match to Query 6323: 2572.979892 from(858.667240,3+) index(4521)
Title: Elution from: 24.919 to 24.919 scan no 1906 cid35.00 polarity:+:m1s



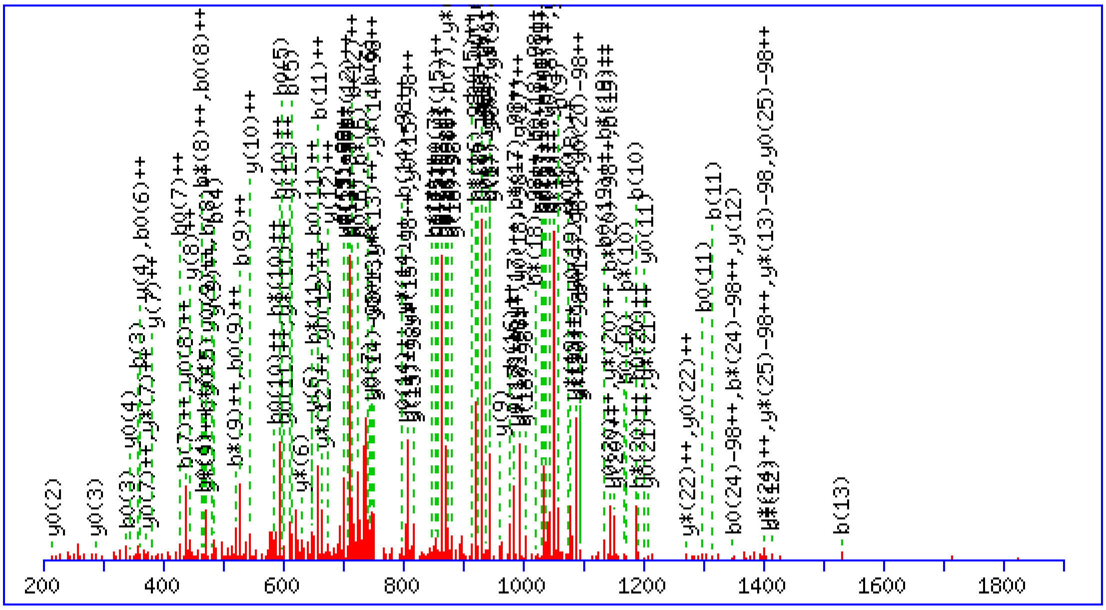
Monoisotopic mass of neutral peptide Mr(calc): 2572.9813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 **Expect:** 1.9e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11), b(12), b(12)++, b(13)++, b(13), b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(8)-98, y(9), y(9)-98++, y(9)++, y(9)-98, y(10), y(10)-98++, y(10)++, y(11)++, y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(17)++, y(19)++, y(20)-98++

Peptide No.546

KVEEEQEADEEDVSEEEAEDREGASK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **KVEEEQEADEEDVSEEEAEDREGASK**
Found in **TMX1_MOUSE** in **SwissProt**, Thioredoxin-related transmembrane protein 1 OS=Mus musculus GN=Tmx1 PE=1 SV=1

Match to Query 5704: 3045.210276 from(762.309845,4+) index(3493)
Title: Elution from: 30.390 to 30.390 scan no 1851 cid35.00 polarity:+:m1s



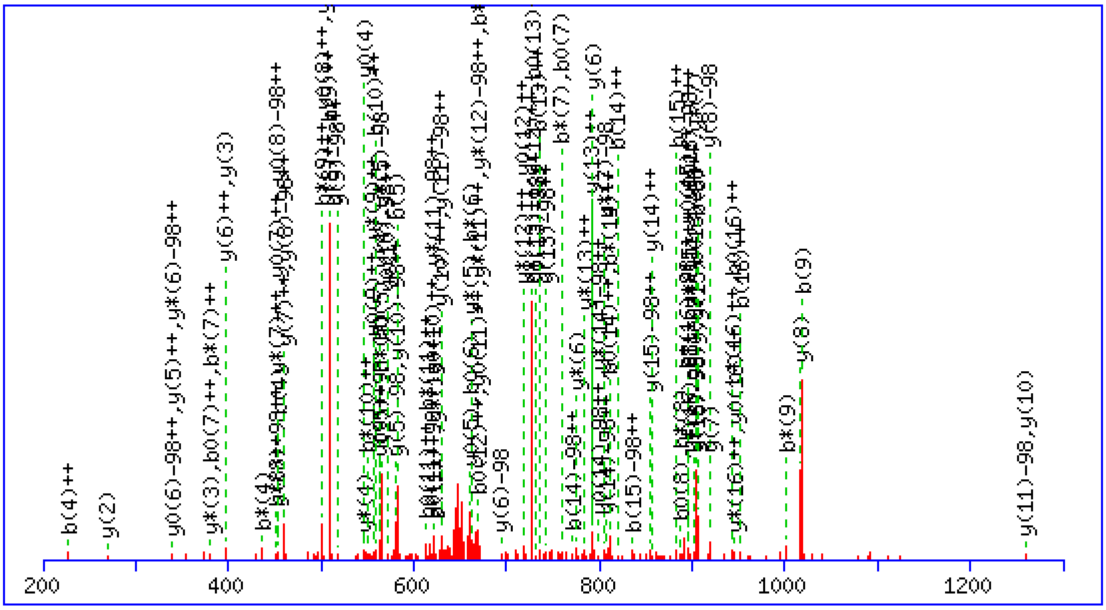
Monoisotopic mass of neutral peptide Mr(calc): 3045.2095
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00092
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11)++, b(11), b(12)++, b(13), b(14)-98++, b(14)++, b(15)++, b(16)++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(25)-98++
Matched y ions: y(4), y(6), y(7)++, y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(12), y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(20)++

Peptide No.547

KVPEQPPELPQLDSQHL
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **KVPEQPPELPQLDSQHL**
Found in **NUCB1_MOUSE** in **SwissProt**, Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2

Match to Query 5200: 2033.985585 from(679.002471,3+) index(5743)
Title: Elution from: 53.539 to 53.539 scan no 4504 cid35.00 polarity:+:m1s



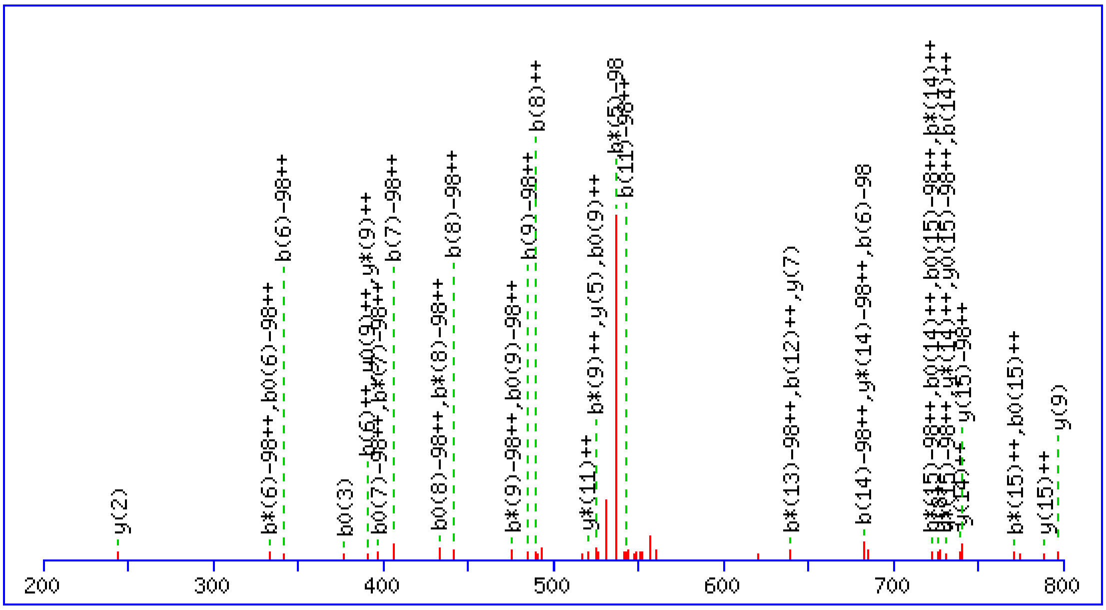
Monoisotopic mass of neutral peptide Mr(calc): 2033.9823
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00059
Matched b ions: b(4)++, b(4), b(5), b(8), b(8)++, b(9)++, b(9), b(10)++, b(11)++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5)++, y(6)++, y(6), y(6)-98, y(7)++, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9)++, y(9)-98++, y(10), y(10)-98++, y(10)++, y(11)-98, y(11)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++

Peptide No.548

KVSKQEEASGGPLAPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KVSKQEEASGGPLAPK**
Found in **VASP_MOUSE** in **SwissProt**, Vasodilator-stimulated phosphoprotein OS=Mus musculus GN=Vasp PE=1 SV=4

Match to Query 3662: 1704.845388 from(569.289072,3+) index(213)
Title: Elution from: 18.451 to 18.451 scan no 1034 cid35.00 polarity:+



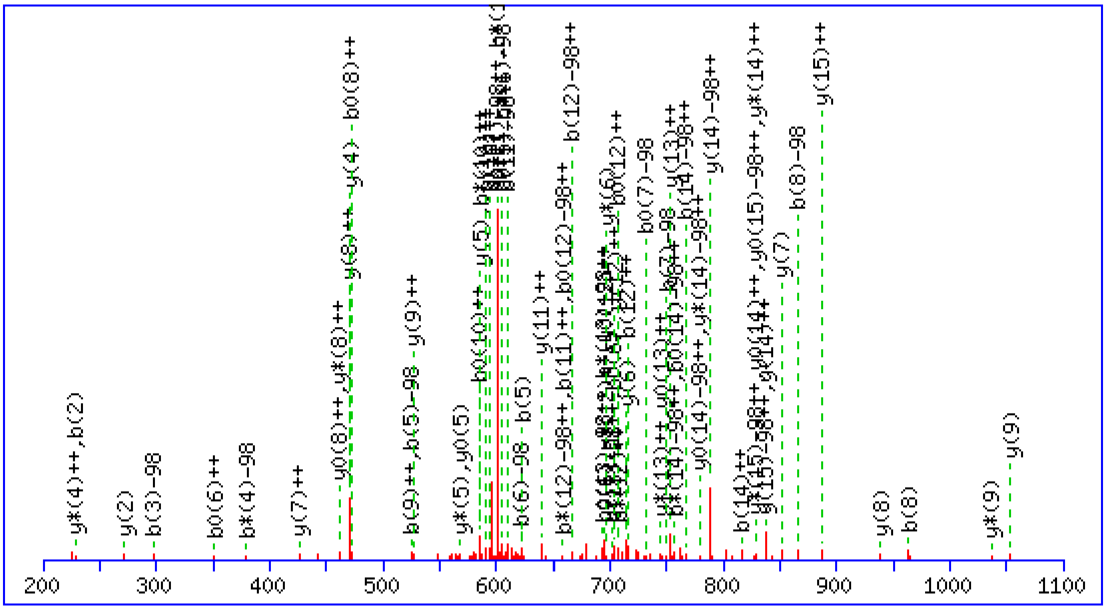
Monoisotopic mass of neutral peptide Mr(calc): 1704.8447
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.032
Matched b ions: b(6)-98, b(6)-98++, b(6)++, b(7)-98++, b(8)-98++, b(8)++, b(9)-98++, b(11)-98++, b(12)++, b(14)-98++, b(14)++, b(15)-98++
Matched y ions: y(2), y(5), y(7), y(8), y(9), y(14)++, y(15)-98++, y(15)++

Peptide No.549

KVSVEPQDSHQDAQPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **KVSVEPQDSHQDAQPR**
Found in **SO2B1_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 2B1 OS=Mus musculus GN=Slco2b1 PE=1 SV=1

Match to Query 4586: 1899.845628 from(634.289152,3+) index(235)
Title: Elution from: 18.151 to 18.151 scan no 1028 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1899.8476

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 59 **Expect:** 6.5e-006

Matched b ions: b(2), b(3)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(8), b(8)-98, b(9)++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++

Matched y ions: y(2), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++

Peptide No.550

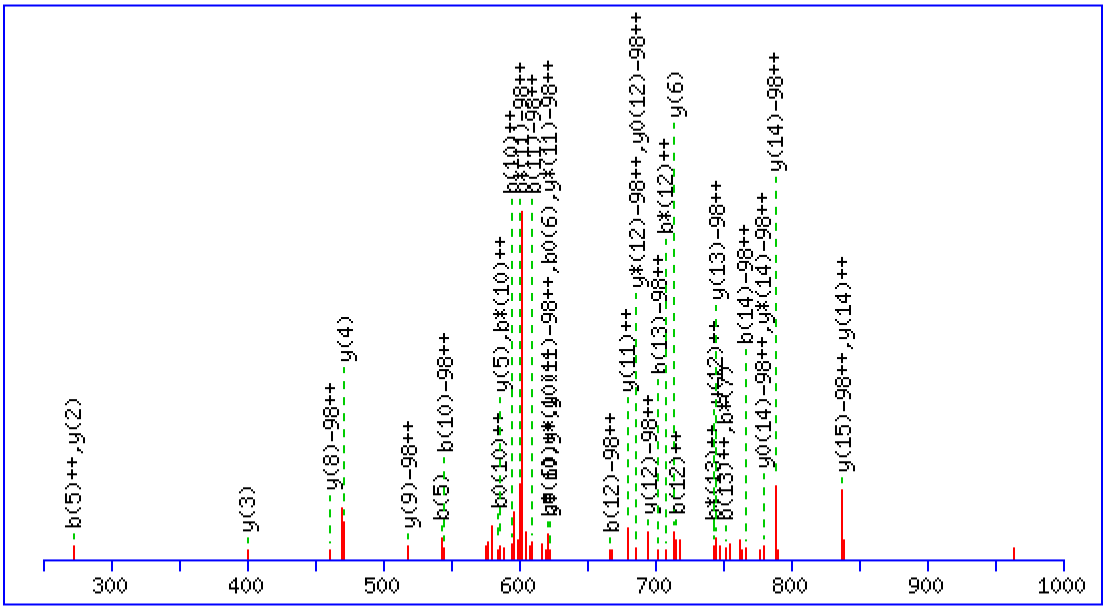
KVSVEPQDSHQDAQPR

Confirmed sites: @S:9

Ambiguous sites:

MS/MS Fragmentation of **KVSVEPQDSHQDAQPR**
Found in **SO2B1_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 2B1 OS=Mus musculus GN=Slco2b1 PE=1 SV=1

Match to Query 4451: 1899.848001 from(634.289943,3+) index(3705)
Title: Elution from: 18.107 to 18.107 scan no 991 cid35.00 polarity:+:m1s



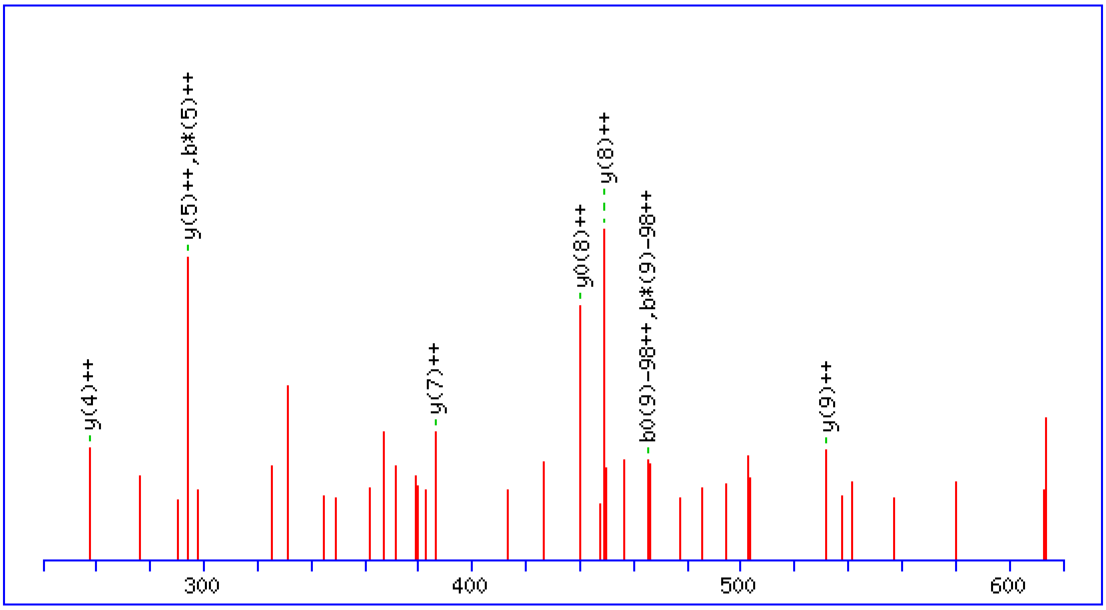
Monoisotopic mass of neutral peptide Mr(calc): 1899.8476
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.002
Matched b ions: b(5)++, b(5), b(10)-98++, b(10)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8)-98++, y(9)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++

Peptide No.551

KYQAIASNSK
Confirmed sites:
Ambiguous sites: @S:7orS:9

MS/MS Fragmentation of **KYQAIASNSK**
Found in **ERLN1_MOUSE** in **SwissProt**, Erlin-1 OS=Mus musculus GN=Erlin1 PE=2 SV=1

Match to Query 1482: 1188.553935 from(397.191921,3+) index(4636)
Title: Elution from: 25.934 to 25.934 scan no 2045 cid35.00 polarity:+:m1s



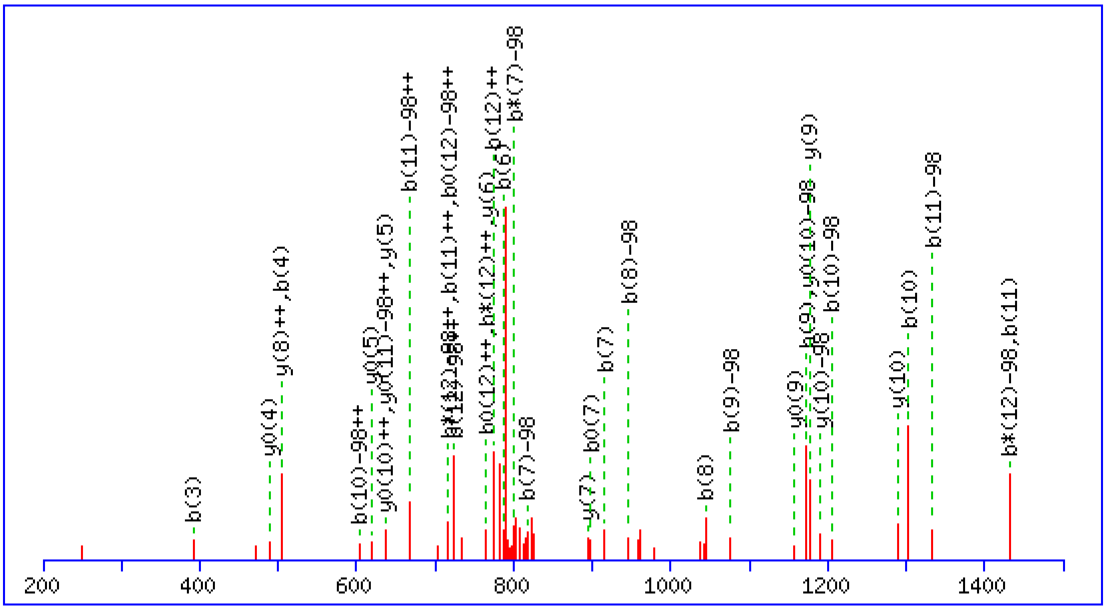
Monoisotopic mass of neutral peptide Mr(calc): 1188.5540
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.057
Matched b ions:
Matched y ions: y(4)++, y(5)++, y(7)++, y(8)++, y(9)++

Peptide No.552

KYVISDEEEEEDD
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **KYVISDEEEEEDD**
Found in **LEO1_MOUSE** in **SwissProt**, RNA polymerase-associated protein LEO1 OS=Mus musculus GN=Leo1 PE=1 SV=2

Match to Query 3195: 1678.612088 from(840.313320,2+) index(1376)
Title: Elution from: 31.187 to 31.187 scan no 2649 cid35.00 polarity:+



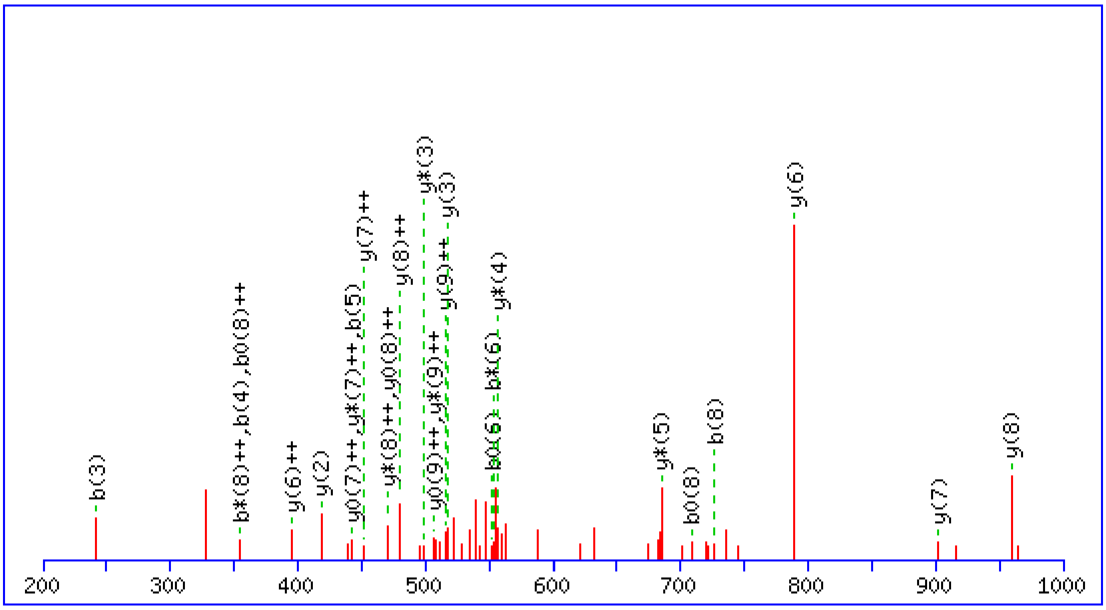
Monoisotopic mass of neutral peptide Mr(calc): 1678.6134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 5e-005
Matched b ions: b(3), b(4), b(6), b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10), b(10)-98++, b(10)-98, b(11), b(11)-98++, b(11)++, b(11)-98, b(12)-98++, b(12)++
Matched y ions: y(5), y(6), y(7), y(8)++, y(9), y(10), y(10)-98

Peptide No.553

LAGISQGVYR
Confirmed sites: @Y:9
Ambiguous sites:

MS/MS Fragmentation of **LAGISQGVYR**
Found in **ACD11_MOUSE** in **SwissProt**, Acyl-CoA dehydrogenase family member 11 OS=Mus musculus GN=Acad11 PE=1 SV=2

Match to Query 1277: 1142.548222 from(572.281387,2+) index(1388)
Title: Elution from: 28.677 to 28.677 scan no 2419 cid35.00 polarity:+



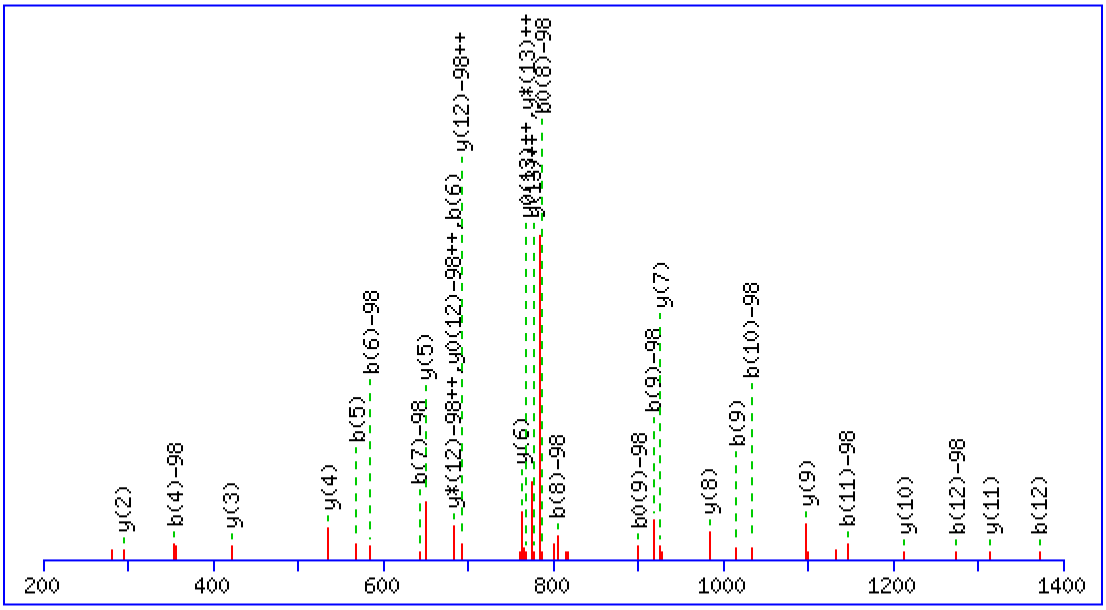
Monoisotopic mass of neutral peptide Mr(calc): 1142.5485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y9 : Phospho (Y)
Ions Score: 25 **Expect:** 0.014
Matched b ions: b(3), b(4), b(5), b(8)
Matched y ions: y(2), y(3), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++

Peptide No.554

LASTDDGYIDLQFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **LASTDDGYIDLQFK**
Found in **CT030_MOUSE** in **SwissProt**, UPF0414 transmembrane protein C20orf30 homolog OS=Mus musculus PE=1 SV=1

Match to Query 3481: 1664.733570 from(833.374061,2+) index(6729)
Title: Elution from: 53.245 to 53.245 scan no 5487 cid35.00 polarity:+:m1s



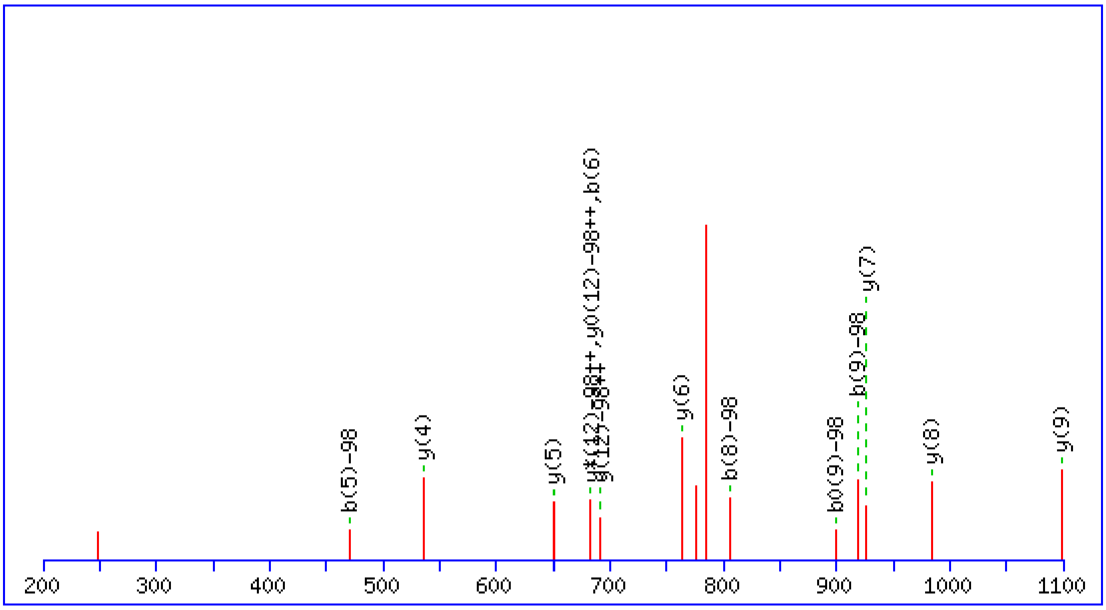
Monoisotopic mass of neutral peptide Mr(calc): 1664.7335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 3.4e-008
Matched b ions: b(4)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(12)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++, y(13)++

Peptide No.555

LASTDDGYIDLQFK
Confirmed sites:
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of **LASTDDGYIDLQFK**
Found in **CT030_MOUSE** in **SwissProt**, UPF0414 transmembrane protein C20orf30 homolog OS=Mus musculus PE=1 SV=1

Match to Query 3031: 1664.733136 from(833.373844,2+) index(2844)
Title: Elution from: 52.635 to 52.635 scan no 5148 cid35.00 polarity:+



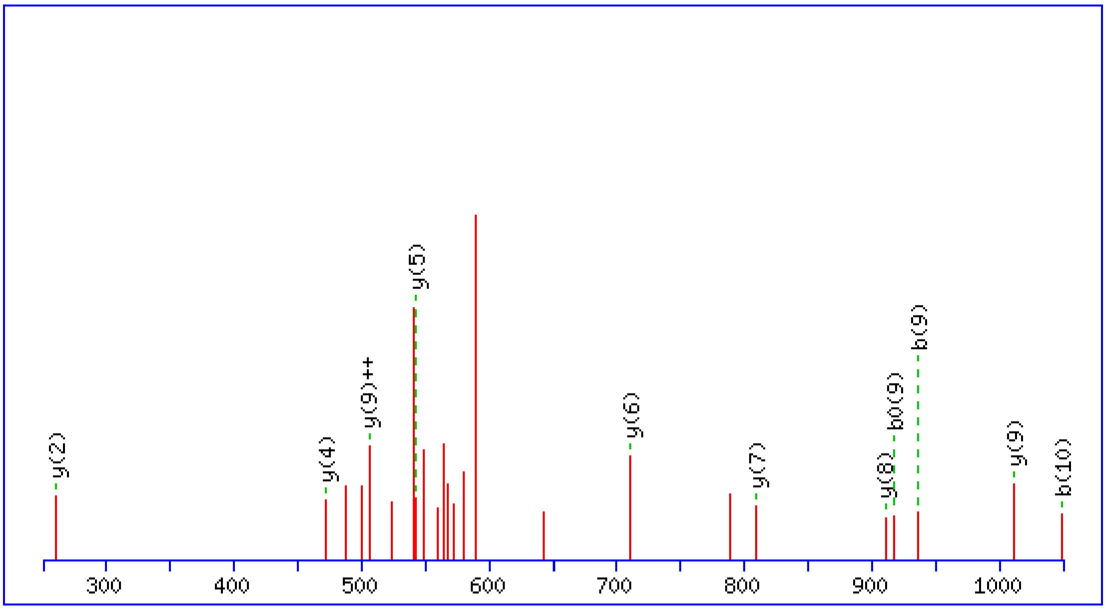
Monoisotopic mass of neutral peptide Mr(calc): 1664.7335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 5.8e-005
Matched b ions: b(5)-98, b(6), b(8)-98, b(9)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12)-98++

Peptide No.556

LATTVSAPDLK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **LATTVSAPDLK**
Found in **MAP4_MOUSE** in **SwissProt**, Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3

Match to Query 1412: 1194.588804 from(598.301678,2+) index(1558)
Title: Elution from: 33.248 to 33.248 scan no 2929 cid35.00 polarity:+



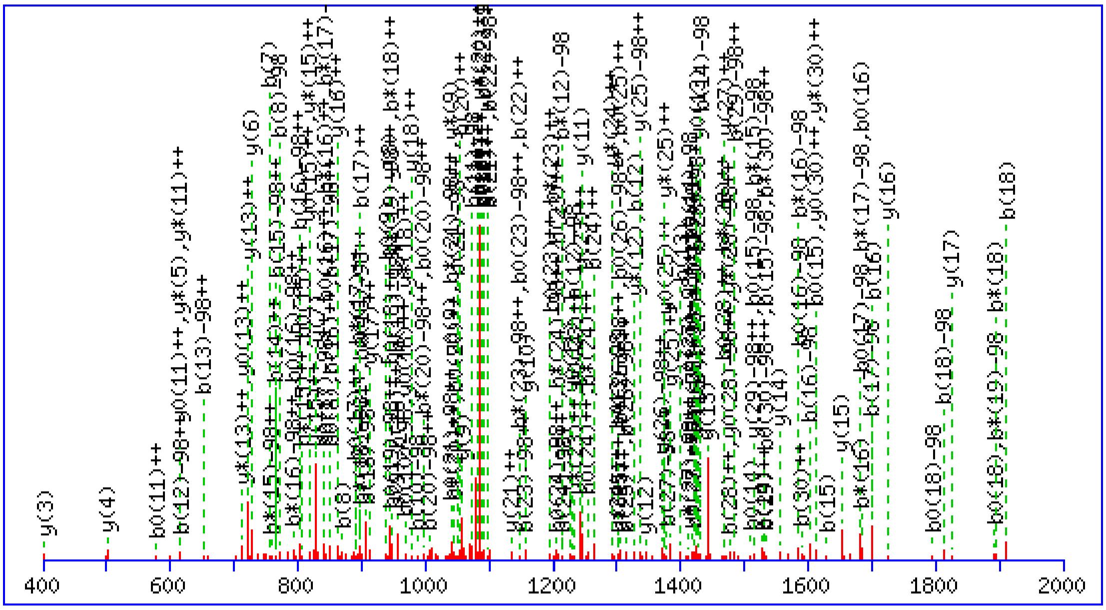
Monoisotopic mass of neutral peptide Mr(calc): 1194.5897
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00012
Matched b ions: b(9), b(10)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++

Peptide No.557

LDGETASDSESRAETAPLPTSVDDTPEVLNR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **LDGETASDSESRAETAPLPTSVDDTPEVLNR**
Found in **CDS2_MOUSE** in **SwissProt**, Phosphatidate cytidylyltransferase 2 OS=Mus musculus GN=Cds2 PE=1 SV=1

Match to Query 6881: 3351.496179 from(1118.172669,3+) index(6443)
Title: Elution from: 46.462 to 46.462 scan no 4738 cid35.00 polarity:+:m1s



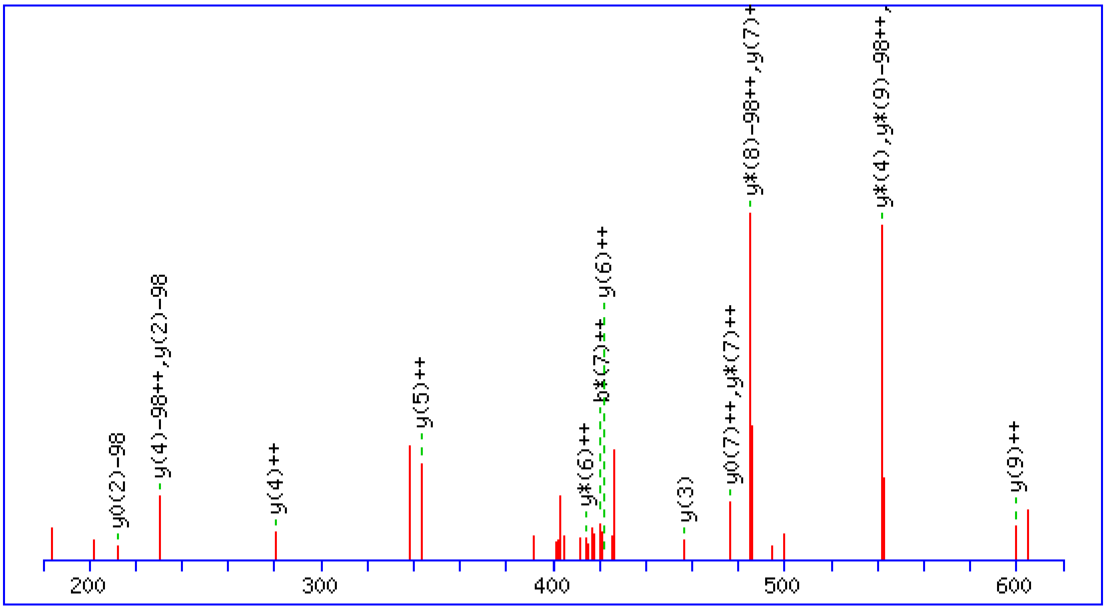
Monoisotopic mass of neutral peptide Mr(calc): 3351.4991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 96 **Expect:** 2.6e-009
Matched b ions: b(7), b(8)-98, b(8), b(9), b(10), b(10)-98, b(11)-98, b(12)-98++, b(12), b(12)-98, b(13)-98++, b(13), b(13)-98, b(14), b(14)-98, b(14)++, b(15)-98, b(15)-98++, b(15), b(16), b(16)-98++, b(16)-98, b(16)++, b(17)-98++, b(17)++, b(17)-98, b(18)-98++, b(18)-98, b(18), b(18)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)-98++, b(23)++, b(24)++, b(24)-98++, b(25)++, b(26)-98++, b(27)++, b(27)-98++, b(28)++, b(28)-98++, b(29)-98++, b(29)++, b(30)++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)++, y(13), y(14), y(15)++, y(15), y(16), y(16)++, y(17)++, y(17), y(18)++, y(20)++, y(21)++, y(23)++, y(24)++, y(25)++, y(25)-98++, y(26)-98++, y(26)++, y(27)-98++, y(27)++, y(29)-98++

Peptide No.558

LDLQRKTETK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **LDLQRKTETK**
Found in **GORAB_MOUSE** in **SwissProt**, RAB6-interacting golgin OS=Mus musculus GN=Gorab PE=1 SV=1

Match to Query 2223: 1310.657745 from(437.893191,3+) index(1600)
Title: Elution from: 30.447 to 30.447 scan no 2697 cid35.00 polarity:+



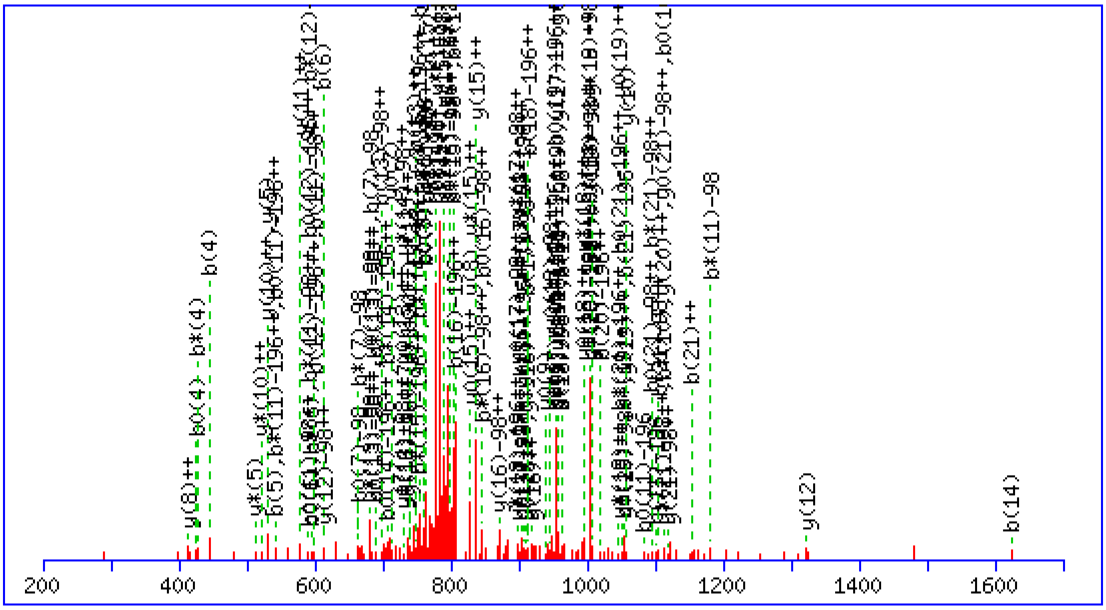
Monoisotopic mass of neutral peptide Mr(calc): 1310.6595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0054
Matched b ions:
Matched y ions: y(2)-98, y(3), y(4)-98++, y(4)++, y(5)++, y(6)++, y(7)++, y(8)++, y(9)++

Peptide No.559

LDNTPASPPRSPTEPSDTPIAK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of **LDNTPASPPRSPTEPSDTPIAK**
Found in **TACC2_MOUSE** in **SwissProt**, Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2

Match to Query 6165: 2450.076645 from(817.699491,3+) index(4797)
Title: Elution from: 37.729 to 37.729 scan no 2857 cid35.00 polarity:+:m1s



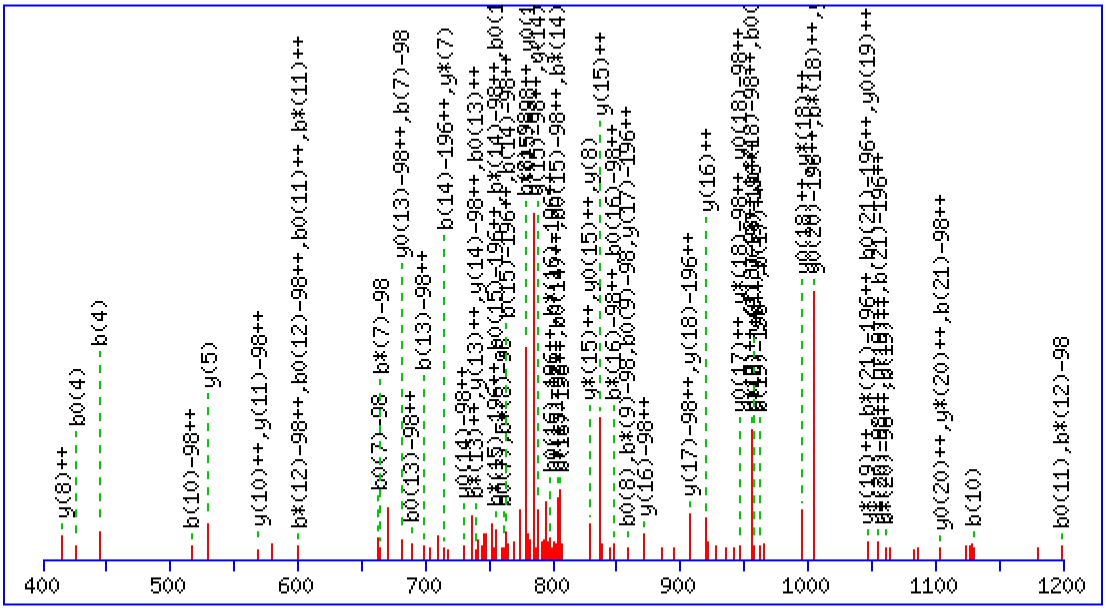
Monoisotopic mass of neutral peptide Mr(calc): 2450.0767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00039
Matched b ions: b(4), b(5), b(6), b(7)-98, b(7), b(8)-98, b(11)-196, b(11)-98++, b(12)-196++, b(13)-98++, b(13)++, b(14), b(14)-98++, b(15)-196++, b(16)-196++, b(16)++, b(17)-98++, b(18)-196++, b(18)-98++, b(19)-196++, b(20)-196++, b(21)-196++, b(21)-98++, b(21)++
Matched y ions: y(5), y(7), y(8)++, y(8), y(9), y(10)++, y(10), y(11)++, y(12), y(12)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(18)-196++, y(19)-196++, y(19)++, y(19)-98++, y(20)++, y(21)-98++

Peptide No.560

LDNTPASPPRSPTEPSDTPIAK
Confirmed sites: @S:7,@T:13
Ambiguous sites:

MS/MS Fragmentation of **LDNTPASPPRSPTEPSDTPIAK**
Found in **TACC2_MOUSE** in **SwissProt**, Transforming acidic coiled-coil-containing protein 2 OS=Mus musculus GN=Tacc2 PE=1 SV=2

Match to Query 6287: 2450.071758 from(817.697862,3+) index(5352)
Title: Elution from: 31.577 to 31.577 scan no 2846 cid35.00 polarity:+:m1s



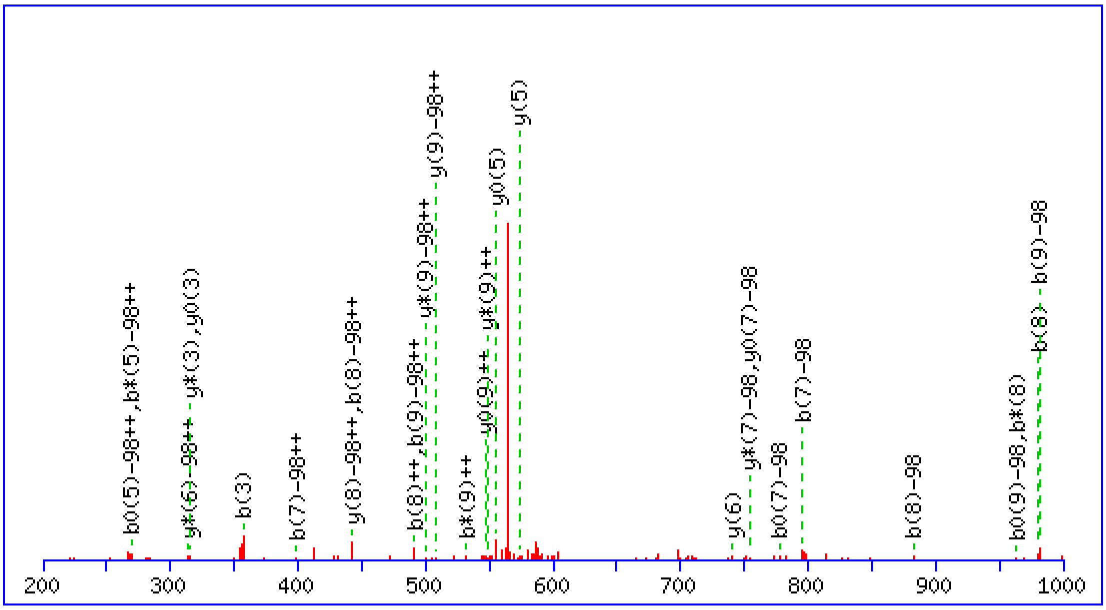
Monoisotopic mass of neutral peptide Mr(calc): 2450.0767
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.015
Matched b ions: b(4), b(7), b(7)-98, b(8)-98, b(10)-98++, b(10), b(13)-98++, b(14)-196++, b(14)-98++, b(15)-196++, b(16)-196++, b(17)++, b(19)++, b(19)-196++, b(21)-196++, b(21)-98++
Matched y ions: y(5), y(8)++, y(8), y(9), y(10)++, y(11)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(17)-196++, y(18)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-196++

Peptide No.561

LENQSLKSVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **LENQSLKSVK**
Found in **MMP2_MOUSE** in **SwissProt**, 72 kDa type IV collagenase OS=Mus musculus GN=Mmp2 PE=2 SV=1

Match to Query 1491: 1224.611300 from(613.312926,2+) index(1864)
Title: Elution from: 35.145 to 35.145 scan no 3219 cid35.00 polarity:+



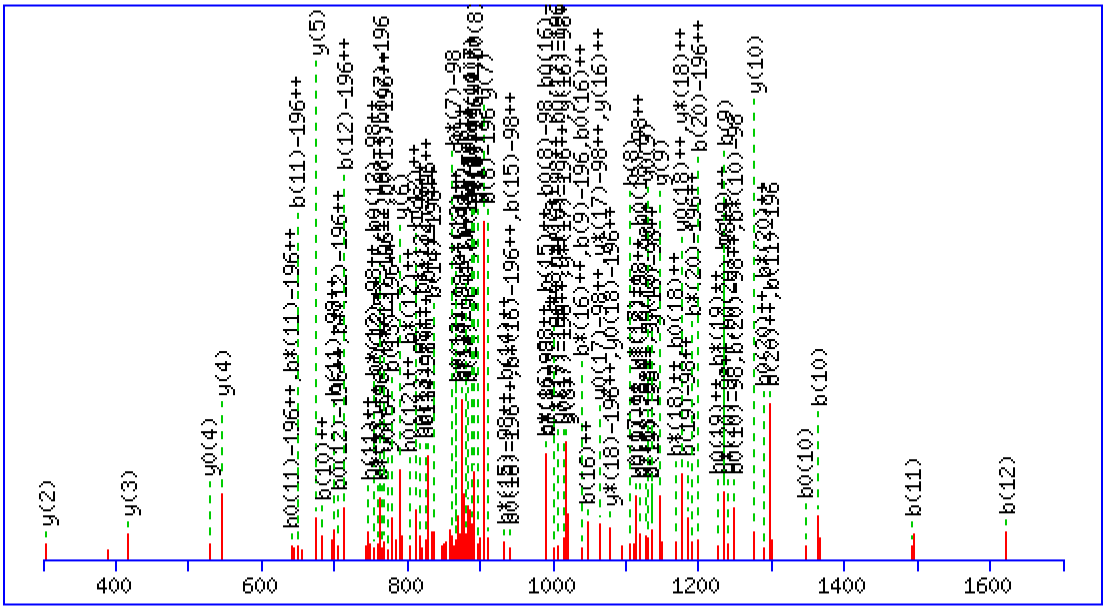
Monoisotopic mass of neutral peptide Mr(calc): 1224.6115
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.027
Matched b ions: b(3), b(7)-98, b(7)-98++, b(8)-98++, b(8)-98, b(8)++, b(8), b(9)-98, b(9)-98++
Matched y ions: y(5), y(6), y(8)-98++, y(9)-98++

Peptide No.562

LEREDSSEEEEEEIDDEEIER
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **LEREDSSEEEEEEIDDEEIER**
Found in **MFAP1_MOUSE** in **SwissProt**, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 5530: 2768.006664 from(923.676164,3+) index(4842)
Title: Elution from: 36.431 to 36.431 scan no 3348 cid35.00 polarity:+:m1s



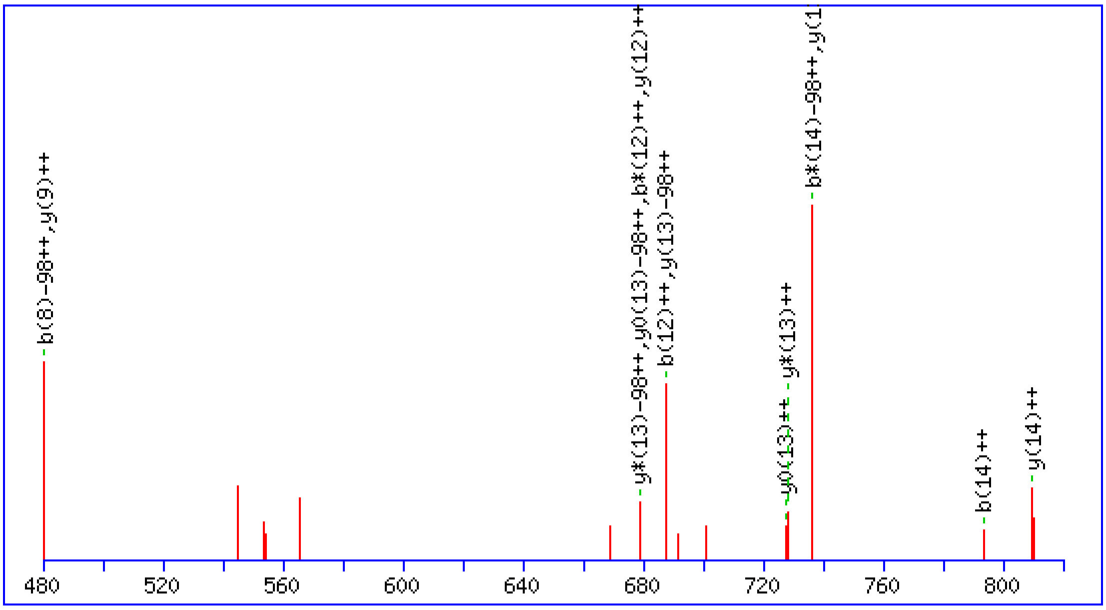
Monoisotopic mass of neutral peptide Mr(calc): 2768.0110
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 1.5e-005
Matched b ions: b(4), b(7)-98, b(8)-196, b(8), b(9), b(9)-196, b(10), b(10)++, b(11)-196, b(11)-98++, b(11), b(11)-196++, b(11)++, b(12), b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-98++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-196++, b(18)-98++, b(19)++, b(19)-98++, b(19)-196++, b(20)++, b(20)-98++, b(20)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(14)++, y(16)++, y(16)-98++, y(18)-98++

Peptide No.563

LFDDSDERGTVGNVK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **LFDDSDERGTVGNVK**
Found in **HTSF1_MOUSE** in **SwissProt**, HIV Tat-specific factor 1 homolog OS=Mus musculus GN=Htatsf1 PE=1 SV=1

Match to Query 3942: 1730.752593 from(577.924807,3+) index(5370)
Title: Elution from: 31.732 to 31.732 scan no 2867 cid35.00 polarity:+:m1s



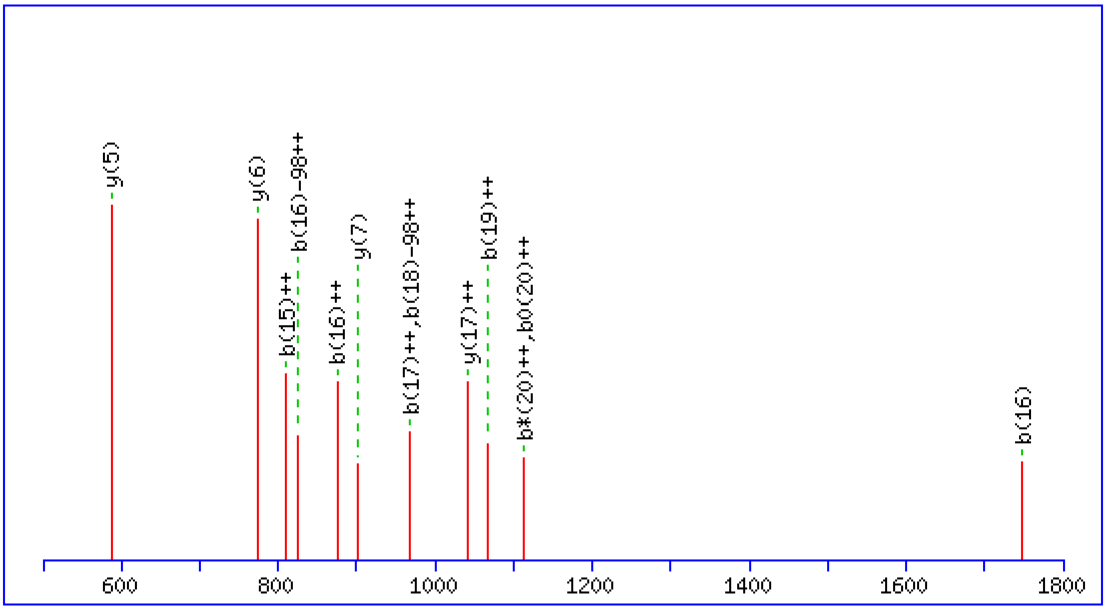
Monoisotopic mass of neutral peptide Mr(calc): 1730.7513
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0028
Matched b ions: b(8)-98++, b(12)++, b(14)++
Matched y ions: y(9)++, y(12)++, y(13)++, y(13)-98++, y(14)++

Peptide No.564

LGPGLPQDGSDEEDEEWPTLEK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **LGPGLPQDGSDEEDEEWPTLEK**
Found in **BYST_MOUSE** in **SwissProt**, Bystin OS=Mus musculus GN=Bysl PE=1 SV=3

Match to Query 6434: 2520.059646 from(841.027158,3+) index(6927)
Title: Elution from: 53.831 to 53.831 scan no 5589 cid35.00 polarity:+:m1s



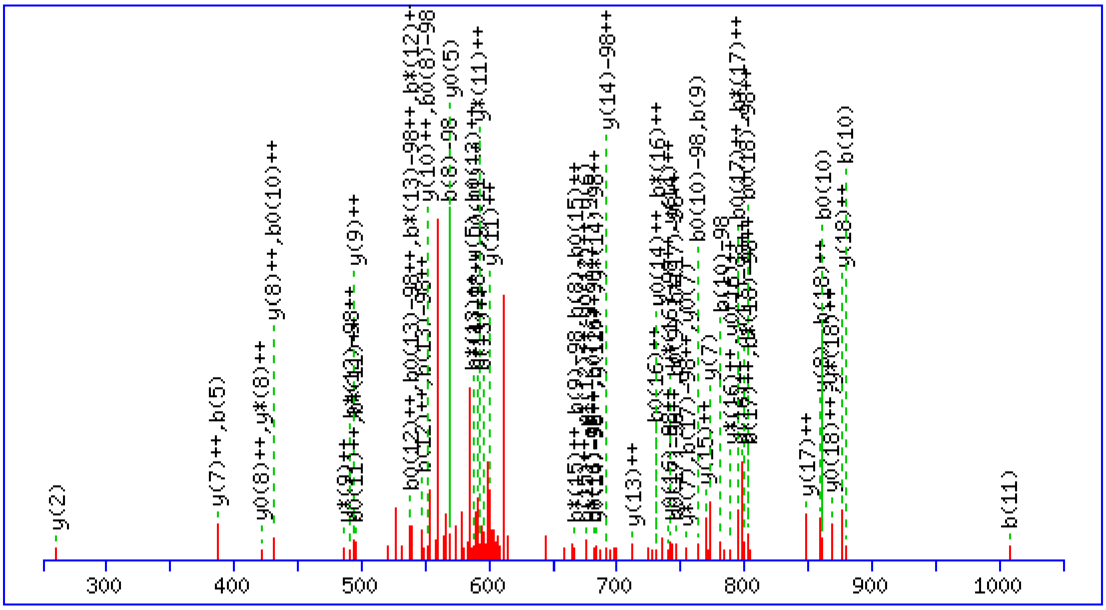
Monoisotopic mass of neutral peptide Mr(calc): 2520.0581
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.017
Matched b ions: b(15)++, b(16), b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(19)++
Matched y ions: y(5), y(6), y(7), y(17)++

Peptide No.565

LGTGGGGSPDKSPSAQELK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **LGTGGGGSPDKSPSAQELK**
Found in **CHIP_MOUSE** in **SwissProt**, STIP1 homology and U box-containing protein 1 OS=Mus musculus GN=Stub1 PE=1 SV=1

Match to Query 3734: 1864.858125 from(622.626651,3+) index(3741)
Title: Elution from: 22.577 to 22.577 scan no 1564 cid35.00 polarity:+:m1s



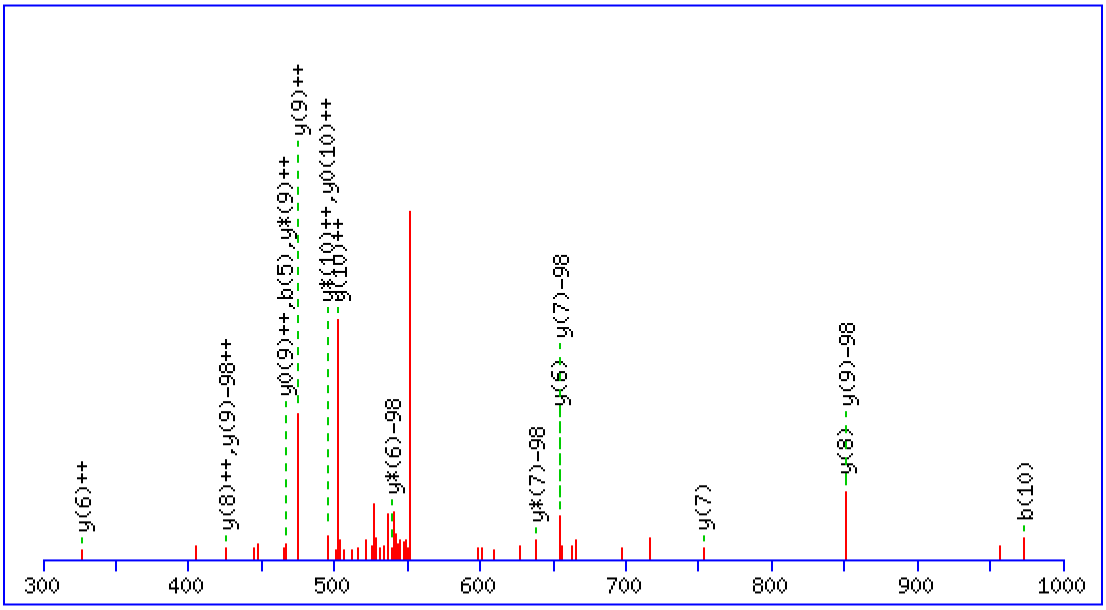
Monoisotopic mass of neutral peptide Mr(calc): 1864.8568
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 **Expect:** 2.7e-007
Matched b ions: b(5), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11), b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(17)++, b(17)-98++, b(18)++
Matched y ions: y(2), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++

Peptide No.566

LGVPVGVLSAK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **LGVPVGVLSAK**
Found in **FANCA_MOUSE** in **SwissProt**, Fanconi anemia group A protein homolog OS=Mus musculus GN=Fanca PE=2 SV=2

Match to Query 1294: 1118.609038 from(560.311795,2+) index(4589)
Title: Elution from: 24.086 to 24.086 scan no 1829 cid35.00 polarity:+:m1s



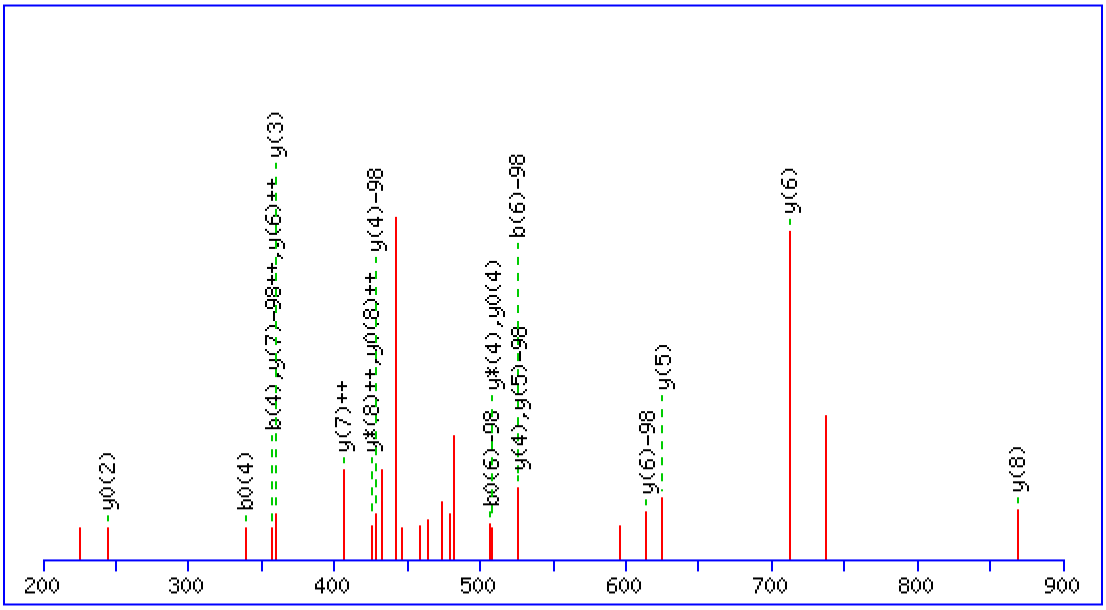
Monoisotopic mass of neutral peptide Mr(calc): 1118.6101
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.05
Matched b ions: b(5), b(10)
Matched y ions: y(6), y(6)++, y(7), y(7)-98, y(8), y(8)++, y(9)-98++, y(9)-98, y(9)++, y(10)++

Peptide No.567

LGVSVSPSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **LGVSVSPSR**
Found in **ZCH18_MOUSE** in **SwissProt**, Zinc finger CCCH domain-containing protein 18 OS=Mus musculus GN=Zc3h18 PE=1 SV=1

Match to Query 761: 980.468832 from(491.241692,2+) index(1048)
Title: Elution from: 25.466 to 25.466 scan no 1981 cid35.00 polarity:+



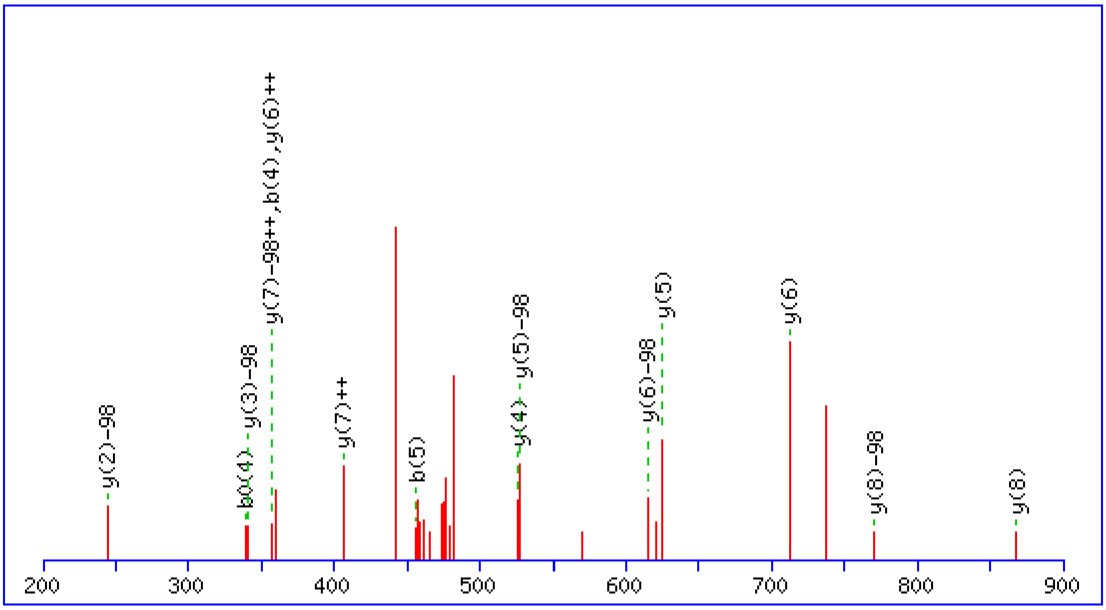
Monoisotopic mass of neutral peptide Mr(calc): 980.4692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0013
Matched b ions: b(4), b(6)-98
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)-98, y(6)++, y(7)++, y(7)-98++, y(8)

Peptide No.568

LGVSVSPSR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **LGVSVSPSR**
Found in **ZCH18_MOUSE** in **SwissProt**, Zinc finger CCCH domain-containing protein 18 OS=Mus musculus GN=Zc3h18 PE=1 SV=1

Match to Query 875: 980.469606 from(491.242079,2+) index(1092)
Title: Elution from: 25.423 to 25.423 scan no 2010 cid35.00 polarity:+



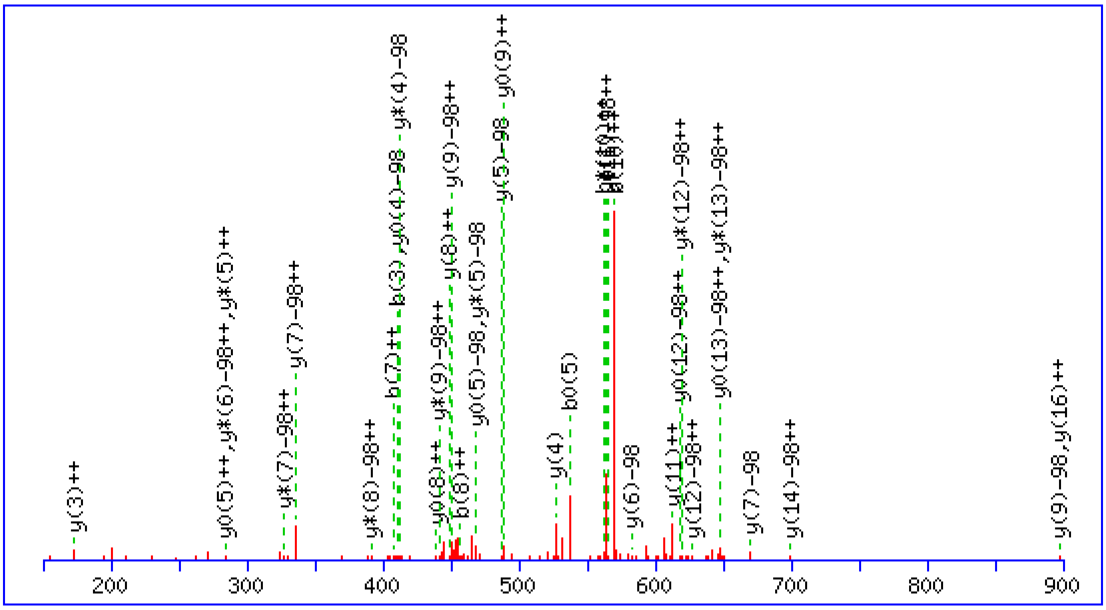
Monoisotopic mass of neutral peptide Mr(calc): 980.4692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00055
Matched b ions: b(4), b(5)
Matched y ions: y(2)-98, y(3)-98, y(4), y(5), y(5)-98, y(6), y(6)-98, y(6)++, y(7)++, y(7)-98++, y(8)-98, y(8)

Peptide No.569

LHCSGEEVVKSPGTAKK
Confirmed sites: @T:14
Ambiguous sites:

MS/MS Fragmentation of **LHCSGEEVVKSPGTAKK**
Found in **TNR8_MOUSE** in **SwissProt**, Tumor necrosis factor receptor superfamily member 8 OS=Mus musculus GN=Tnfrsf8 PE=2 SV=1

Match to Query 3870: 1905.903784 from(477.483222,4+) index(3457)
Title: Elution from: 20.211 to 20.211 scan no 1246 cid35.00 polarity:+:m1s



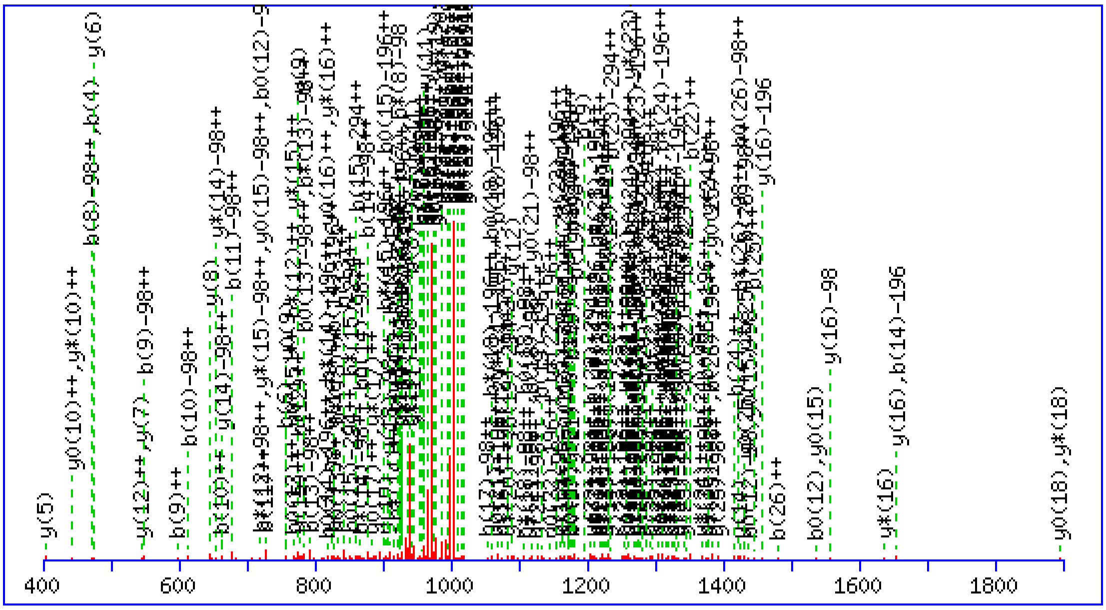
Monoisotopic mass of neutral peptide Mr(calc): 1905.9019
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.037
Matched b ions: b(3), b(7)++, b(8)++, b(10)++
Matched y ions: y(3)++, y(4), y(5)-98, y(6)-98, y(7)-98++, y(7)-98, y(8)++, y(9)-98, y(9)-98++, y(11)-98++, y(11)++, y(12)-98++, y(14)-98++, y(16)++

Peptide No.570

LIEDERSDREETESSEGEETAAGAGAK
Confirmed sites: @S:7,@S:14,@S:15
Ambiguous sites:

MS/MS Fragmentation of **LIEDERSDREETESSEGEETAAGAGAK**
Found in **CERS2_MOUSE** in **SwissProt**, Ceramide synthase 2 OS=Mus musculus GN=Cers2 PE=1 SV=1

Match to Query 5917: 3105.166947 from(1036.062925,3+) index(4129)
Title: Elution from: 26.018 to 26.018 scan no 2030 cid35.00 polarity:+:m1s



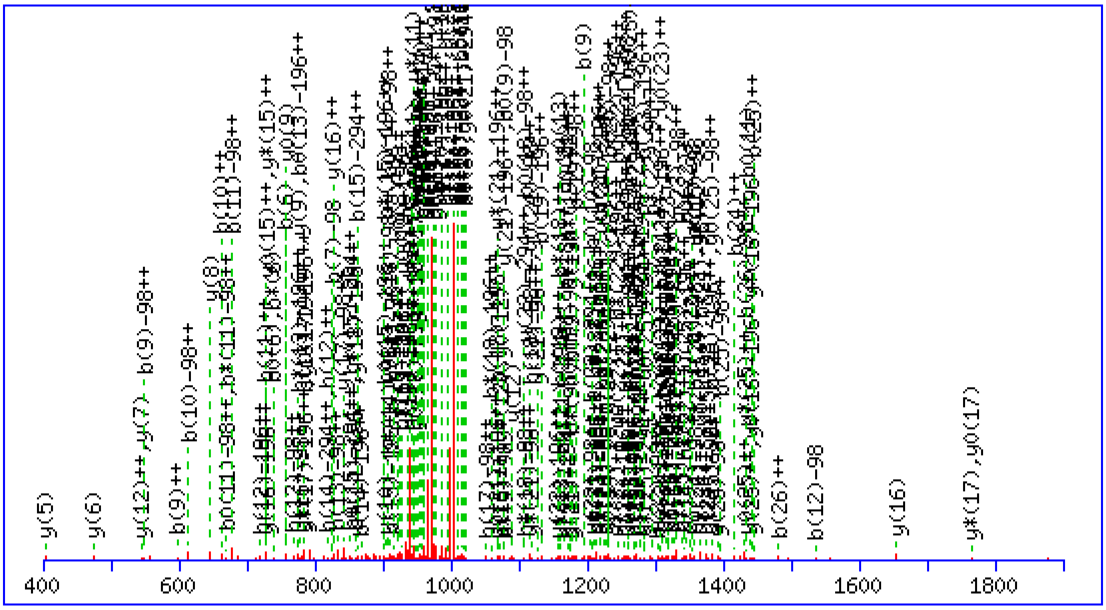
Monoisotopic mass of neutral peptide Mr(calc): 3105.1737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0064
Matched b ions: b(4), b(6), b(7)-98, b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(9), b(10)++, b(10)-98++, b(10), b(10)-98, b(11)-98++, b(11)++, b(12)++, b(13)-98++, b(13)++, b(14)-196, b(14)-98++, b(14)-196++, b(14)++, b(15)-294++, b(15)-196++, b(15)-98++, b(15)++, b(16)-294++, b(16)-196++, b(16)++, b(17)-196++, b(17)-294++, b(17)-98++, b(18)-196++, b(18)-98++, b(18)-294++, b(18)++, b(19)-98++, b(19)++, b(19)-294++, b(19)-196++, b(20)++, b(21)-196++, b(21)-98++, b(21)++, b(22)-294++, b(22)-98++, b(22)++, b(22)-196++, b(23)-98++, b(23)-294++, b(24)++, b(24)-196++, b(24)-98++, b(24)-294++, b(25)++, b(26)-98++, b(26)-196++, b(26)++, b(26)-294++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)-98, y(13), y(14), y(14)-98++, y(14)-98, y(14)-196, y(15)++, y(16), y(16)-98, y(16)++, y(16)-196, y(18)-98++, y(18)++, y(19)-98++, y(19)-196++, y(20)-196++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(22)-196++, y(23)-196++, y(23)++, y(23)-294++, y(23)-98++, y(24)-98++, y(24)-294++, y(24)-196++, y(24)++, y(25)-98++, y(25)-294++, y(25)-196++

Peptide No.571

LIEDERSDREETESSEGEETAAGAGAK
Confirmed sites: @S:7,@T:12,@S:14
Ambiguous sites:

MS/MS Fragmentation of **LIEDERSDREETESSEGEETAAGAGAK**
Found in **CERS2_MOUSE** in **SwissProt**, Ceramide synthase 2 OS=Mus musculus GN=Cers2 PE=1 SV=1

Match to Query 6773: 3105.167373 from(1036.063067,3+) index(4694)
Title: Elution from: 26.654 to 26.654 scan no 2142 cid35.00 polarity:+:m1s



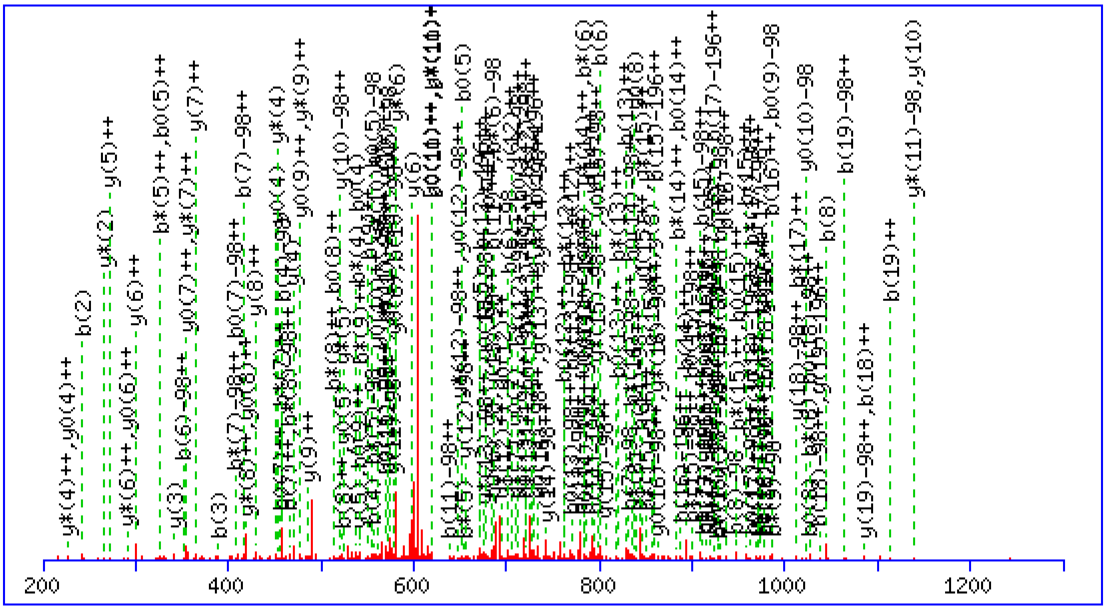
Monoisotopic mass of neutral peptide Mr(calc): 3105.1737
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0025
Matched b ions: b(6), b(7)-98, b(8)-98, b(9)++, b(9)-98++, b(9), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(11)-98, b(12)-98, b(12)-98++, b(12)-196++, b(12)++, b(13)-196++, b(13)-98++, b(14)++, b(14)-196++, b(14)-294++, b(14)-98++, b(15)-294++, b(15)-196++, b(15)-98++, b(15)++, b(16)-196++, b(16)-294++, b(16)++, b(17)-196++, b(17)-98++, b(17)-294++, b(18)-98++, b(18)-294++, b(18)-196++, b(18)++, b(19)-98++, b(19)++, b(19)-196++, b(20)-98++, b(21)-196++, b(21)-98++, b(21)++, b(22)++, b(22)-196++, b(22)-294++, b(22)-98++, b(23)-196++, b(23)-98++, b(24)-98++, b(24)++, b(24)-294++, b(24)-196++, b(25)++, b(25)-98++, b(26)-98++, b(26)-196++, b(26)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13), y(14), y(15)-98, y(16), y(16)++, y(16)-196++, y(16)-98++, y(17)-98++, y(18)-196++, y(18)-98++, y(18)++, y(19)-196++, y(19)-98++, y(20)-196++, y(21)-196++, y(21)-98++, y(21)++, y(22)++, y(22)-196++, y(22)-294++, y(22)-98++, y(23)-98++, y(23)++, y(23)-294++, y(23)-196++, y(24)++, y(24)-294++, y(24)-98++, y(24)-196++, y(25)++, y(25)-196++, y(25)-98++

Peptide No.572

LKFSDEEDGRDSDEEGAEGHK
Confirmed sites: @S:4,@S:12
Ambiguous sites:

MS/MS Fragmentation of **LKFSDEEDGRDSDEEGAEGHK**
Found in **PRC2A_MOUSE** in **SwissProt**, Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1

Match to Query 5248: 2508.929772 from(628.239719,4+) index(3574)
Title: Elution from: 23.484 to 23.484 scan no 1587 cid35.00 polarity:+:m1s



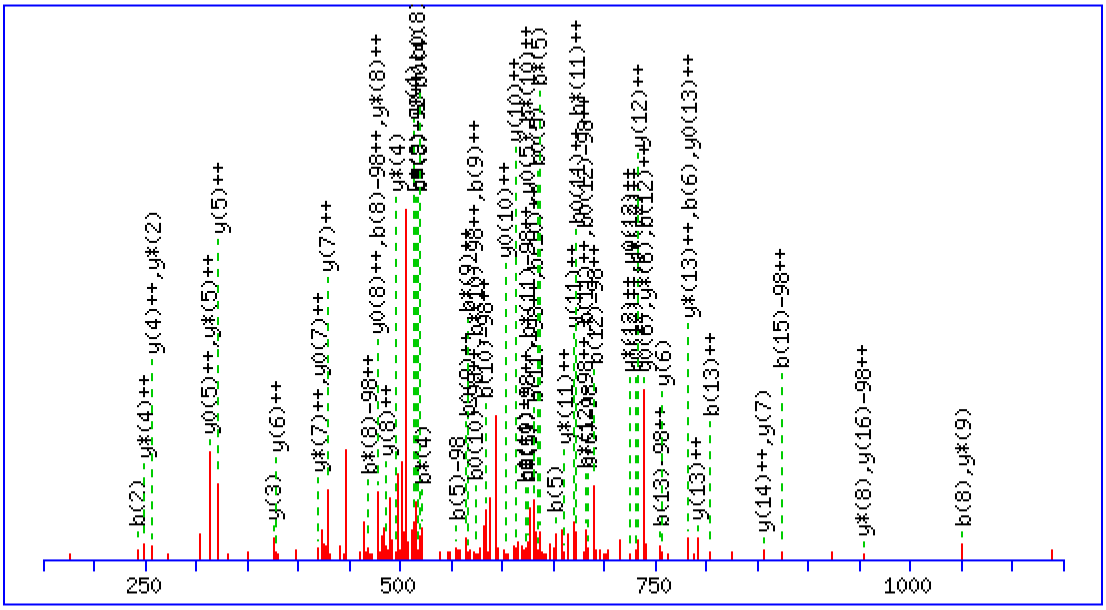
Monoisotopic mass of neutral peptide Mr(calc): 2508.9319
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0068
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(6)-98++, b(7)-98++, b(7)-98, b(7)++, b(7), b(8)-98, b(8), b(8)++, b(9)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-196++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-98++, b(16)-196++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)-98++, y(10)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)-196++, y(19)-98++, y(19)-196++

Peptide No.573

LKSEDELRPDVDEHTQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **LKSEDELRPDVDEHTQK**
Found in **REPS1_MOUSE** in **SwissProt**, RalBP1-associated Eps domain-containing protein 1 OS=Mus musculus GN=Reps1 PE=1 SV=2

Match to Query 4484: 2117.961944 from(530.497762,4+) index(3747)
Title: Elution from: 22.621 to 22.621 scan no 1570 cid35.00 polarity:+:m1s



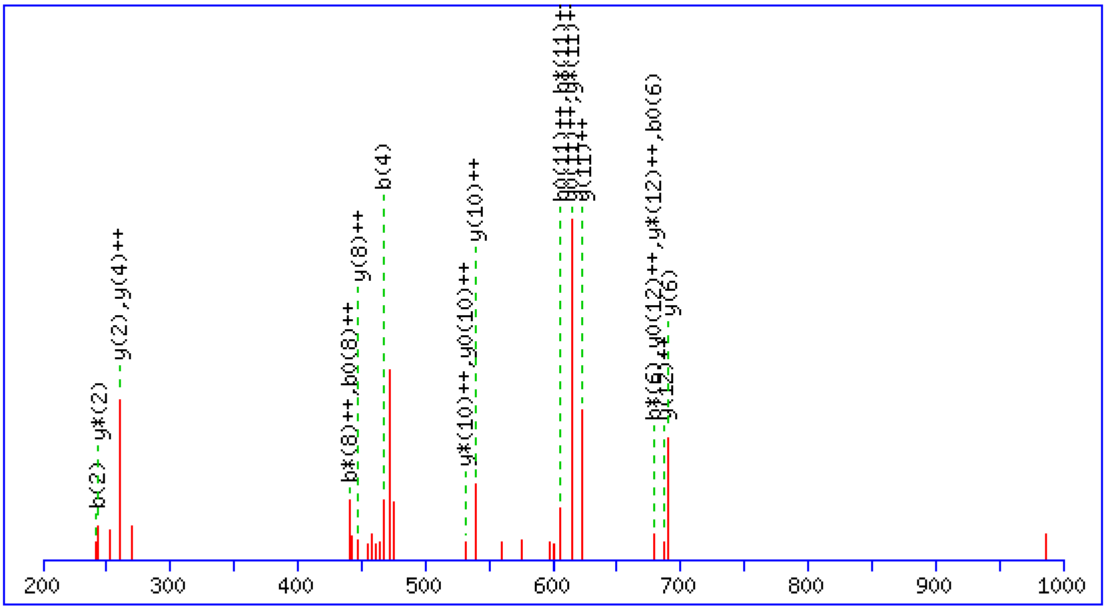
Monoisotopic mass of neutral peptide Mr(calc): 2117.9630
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.023
Matched b ions: b(2), b(5)-98, b(5), b(6), b(6)-98, b(8), b(8)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(15)-98++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(6)++, y(6), y(7)++, y(7), y(8)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(16)-98++

Peptide No.574

LKSGETTTAEEIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **LKSGETTTAEEIK**
Found in **ACSF2_MOUSE** in **SwissProt**, Acyl-CoA synthetase family member 2, mitochondrial OS=Mus musculus GN=Acsf2 PE=2 SV=1

Match to Query 2536: 1485.692496 from(496.238108,3+) index(4063)
Title: Elution from: 27.751 to 27.751 scan no 2175 cid35.00 polarity:+:m1s



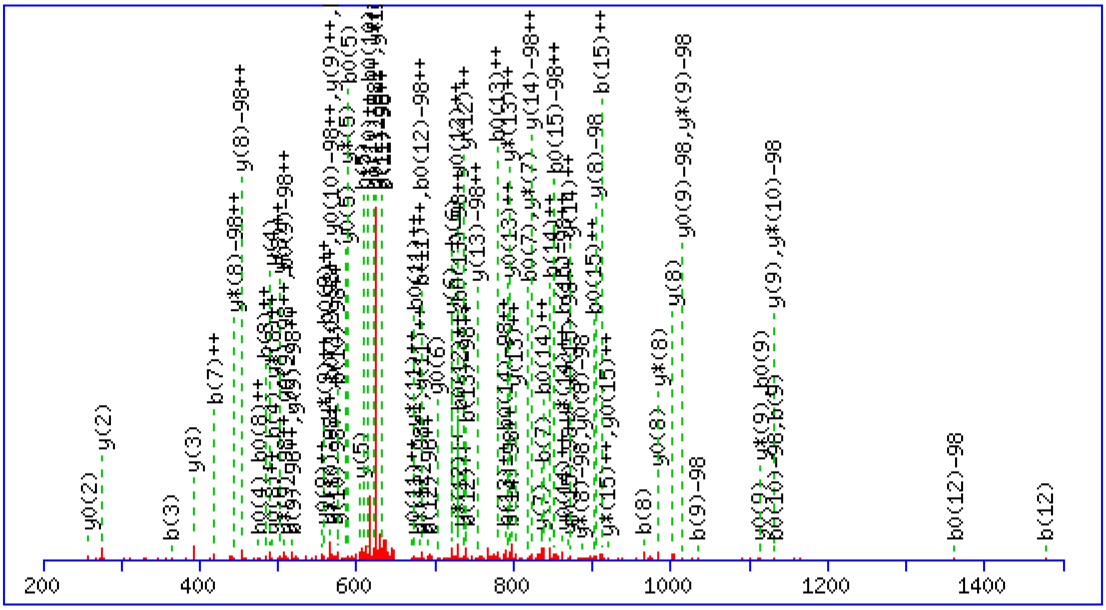
Monoisotopic mass of neutral peptide Mr(calc): 1485.6963
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.016
Matched b ions: b(2), b(4), b(11)++
Matched y ions: y(2), y(4)++, y(6), y(8)++, y(10)++, y(11)++, y(12)++

Peptide No.575

LLHEDLDESDDDVDEK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **LLHEDLDESDDDVDEK**
Found in **ASAP2_MOUSE** in **SwissProt**, Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 OS=Mus musculus GN=Asap2 PE=1 SV=3

Match to Query 5018: 1965.774186 from(656.265338,3+) index(4843)
Title: Elution from: 38.236 to 38.236 scan no 2920 cid35.00 polarity:+:m1s



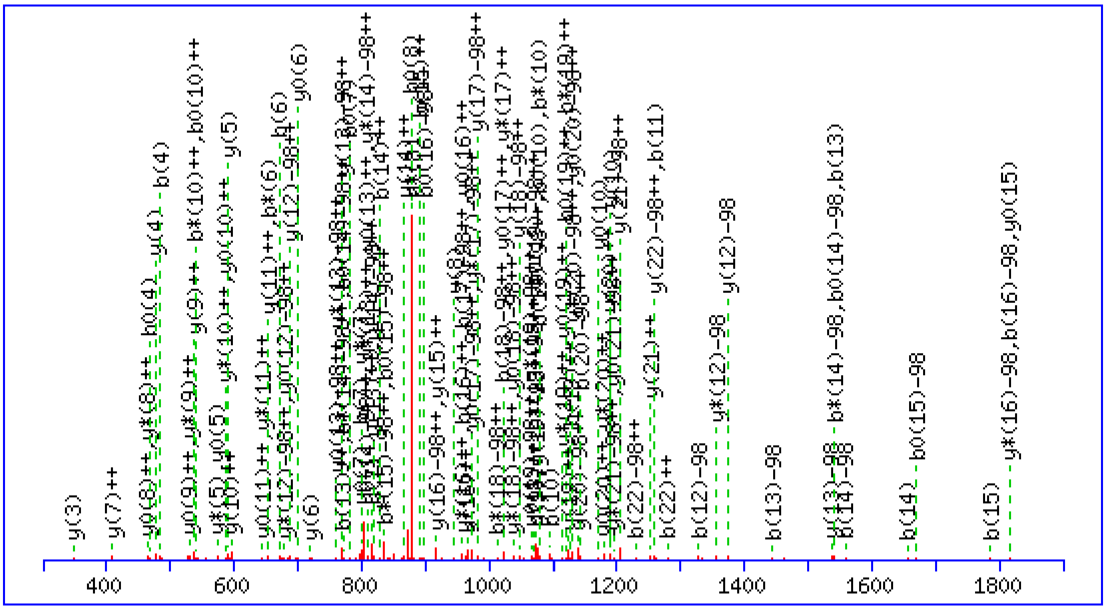
Monoisotopic mass of neutral peptide Mr(calc): 1965.7728
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0011
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(8)++, b(9)-98++, b(9)++, b(9)-98, b(9), b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12), b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(8)-98, y(8)++, y(9)-98++, y(9)++, y(9), y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++

Peptide No.576

LLKEGEEPTVYSDDEEPKDETAR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **LLKEGEEPTVYSDDEEPKDETAR**
Found in **PGRC1_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4

Match to Query 5484: 2729.191266 from(910.737698,3+) index(4224)
Title: Elution from: 29.264 to 29.264 scan no 2384 cid35.00 polarity:+:m1s



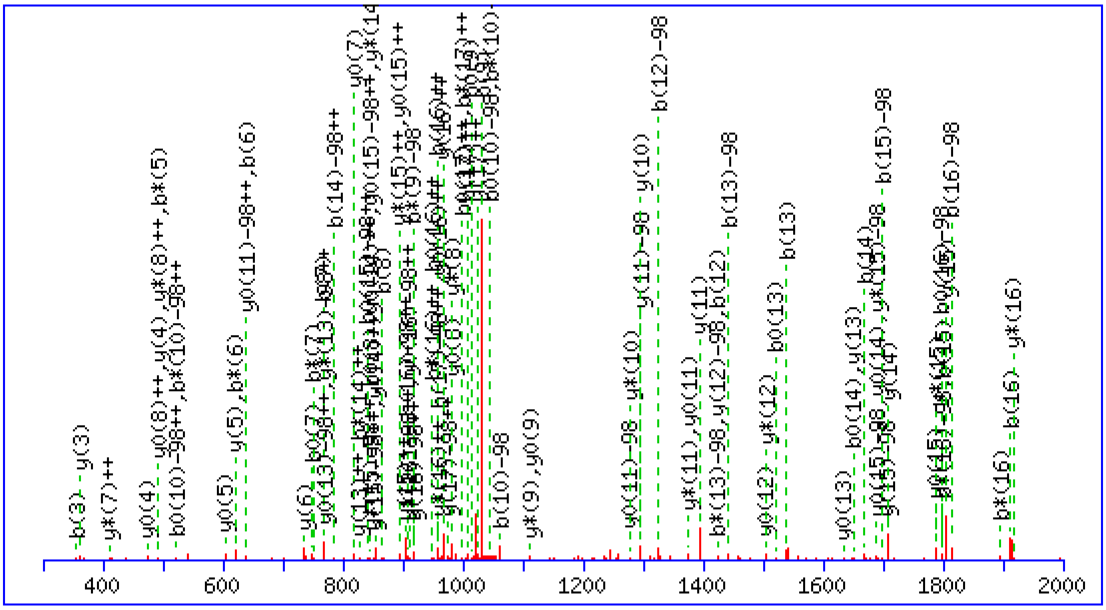
Monoisotopic mass of neutral peptide Mr(calc): 2729.1956
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 92 **Expect:** 5.1e-009
Matched b ions: b(4), b(6), b(7), b(10), b(11), b(12)-98, b(13), b(13)-98, b(13)++, b(14), b(14)-98, b(14)++, b(15), b(15)++, b(16)-98, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++, b(22)++, b(22)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)-98++, y(12)-98, y(13)-98, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++

Peptide No.577

LLKPGEEPSEYTDEEDTK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 5467: 2158.918346 from(1080.466449,2+) index(4646)
Title: Elution from: 36.058 to 36.058 scan no 2651 cid35.00 polarity:+:m1s



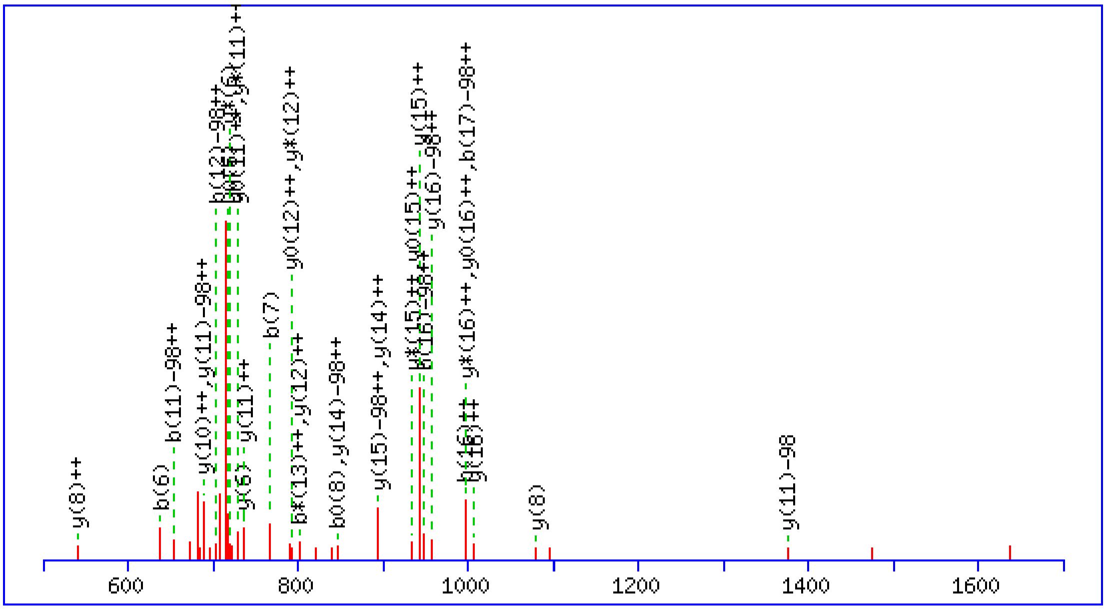
Monoisotopic mass of neutral peptide Mr(calc): 2158.9195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 3.7e-005
Matched b ions: b(3), b(6), b(7), b(8), b(9), b(10)-98, b(12)-98, b(12), b(13), b(13)-98, b(14), b(14)-98++, b(15), b(15)-98, b(16), b(16)-98, b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4), y(5), y(6), y(10), y(11)-98, y(11), y(12)-98, y(13), y(13)++, y(14)++, y(14), y(15)++, y(15)-98, y(15), y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.578

LLKPGEEPSEYTDEEDTK
Confirmed sites: @S:9,@Y:11
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 4829: 2238.883833 from(747.301887,3+) index(4393)
Title: Elution from: 31.502 to 31.502 scan no 2692 cid35.00 polarity:+:m1s



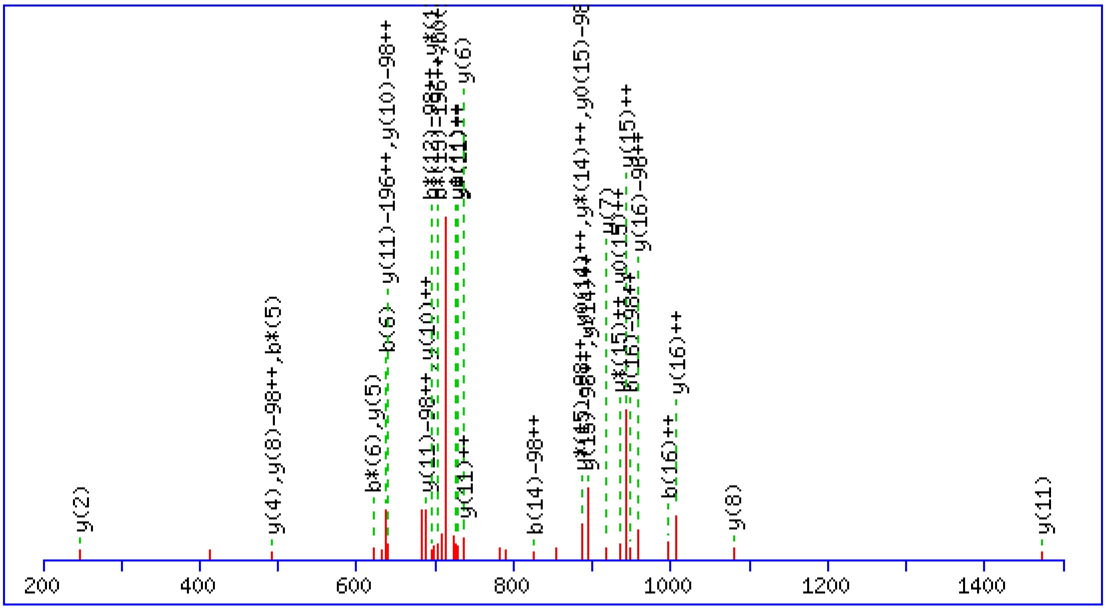
Monoisotopic mass of neutral peptide Mr(calc): 2238.8858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y11 : Phospho (Y)
Ions Score: 22 **Expect:** 0.031
Matched b ions: b(6), b(7), b(11)-98++, b(12)-98++, b(16)++, b(16)-98++, b(17)-98++
Matched y ions: y(6), y(8), y(8)++, y(10)++, y(11)-98, y(11)-98++, y(11)++, y(12)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++

Peptide No.579

LLKPGEEPSEYTDEEDTK
Confirmed sites: @S:9,@T:12
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 5855: 2238.885393 from(747.302407,3+) index(5383)
Title: Elution from: 31.873 to 31.873 scan no 2886 cid35.00 polarity:+:m1s



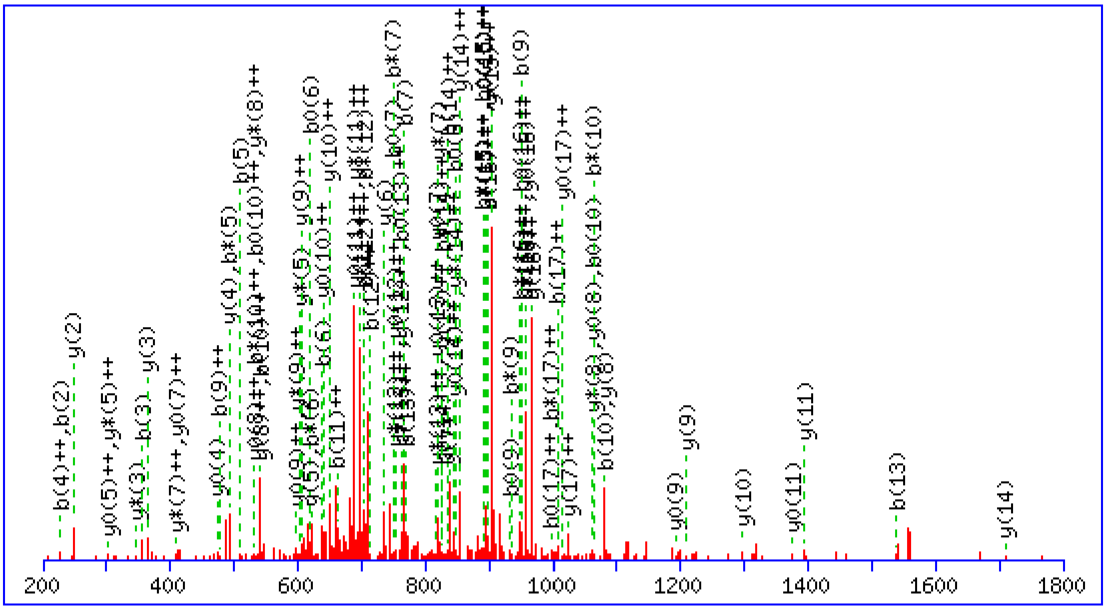
Monoisotopic mass of neutral peptide Mr(calc): 2238.8858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0019
Matched b ions: b(6), b(12)-98++, b(14)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)-98++, y(8), y(10)-98++, y(10)++, y(11), y(11)-196++, y(11)-98++, y(11)++, y(12)-196++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.580

LLKPGEEPSEYTDEEDTK
Confirmed sites: @Y:11
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 4739: 2158.917459 from(720.646429,3+) index(3958)
Title: Elution from: 35.806 to 35.806 scan no 2496 cid35.00 polarity:+:m1s



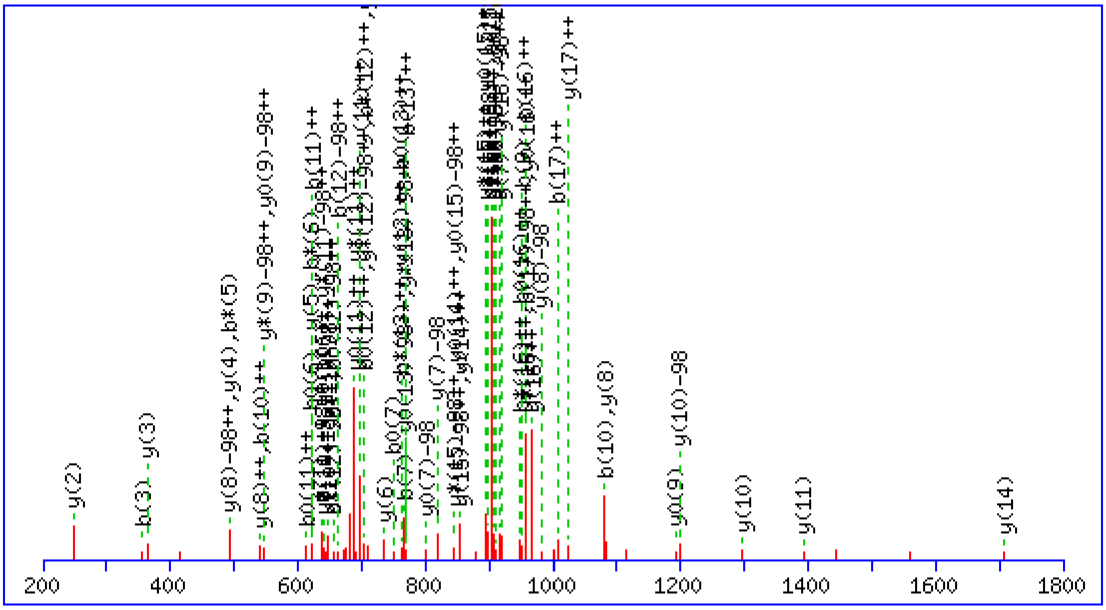
Monoisotopic mass of neutral peptide Mr(calc): 2158.9195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y11 : Phospho (Y)
Ions Score: 45 **Expect:** 0.0002
Matched b ions: b(2), b(3), b(4)++, b(5), b(6), b(7), b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)++, b(13), b(13)++, b(14)++, b(15)++, b(16)++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(11), y(12)++, y(13)++, y(14), y(14)++, y(15)++, y(16)++, y(17)++

Peptide No.581

LLKPGEEPSEYTDEEDTK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 5583: 2158.918026 from(720.646618,3+) index(5083)
Title: Elution from: 28.573 to 28.573 scan no 2442 cid35.00 polarity:+:m1s



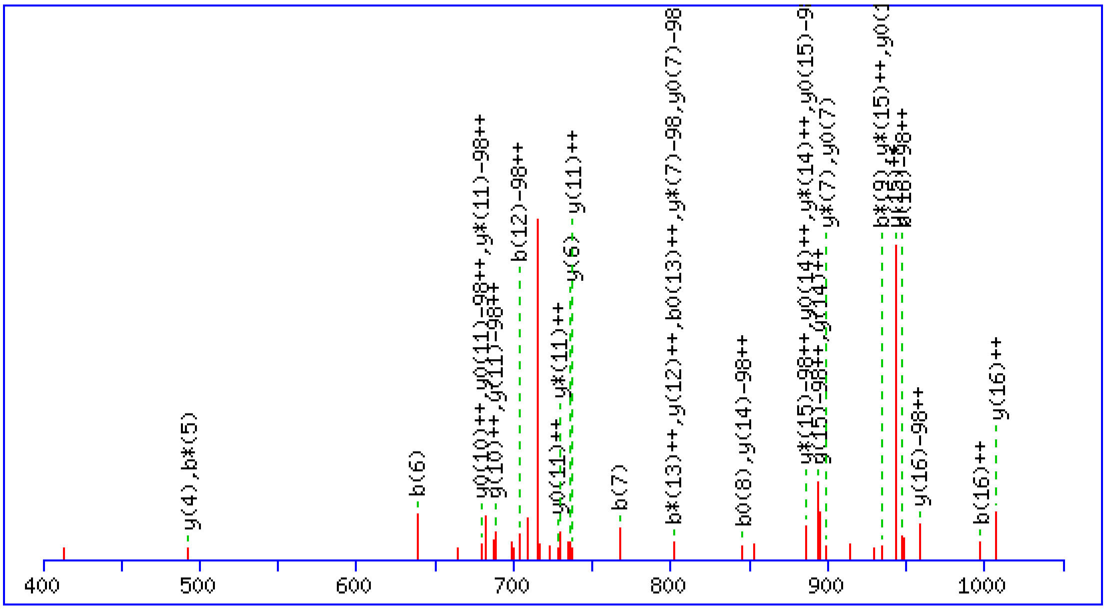
Monoisotopic mass of neutral peptide Mr(calc): 2158.9195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 **Expect:** 5.2e-008
Matched b ions: b(3), b(6), b(7), b(9), b(10), b(10)++, b(11)++, b(12)-98++, b(13)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8)-98++, y(8), y(8)++, y(8)-98, y(10)-98, y(10), y(10)++, y(11)++, y(11), y(11)-98++, y(12)++, y(14), y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++

Peptide No.582

LLKPGEEPSEYTDEEDTK
Confirmed sites:
Ambiguous sites: @S:9orY:11orT:12, @S:9orY:11orT:12

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTK**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 5713: 2238.881352 from(747.301060,3+) index(5214)
Title: Elution from: 31.884 to 31.884 scan no 2854 cid35.00 polarity:+:m1s



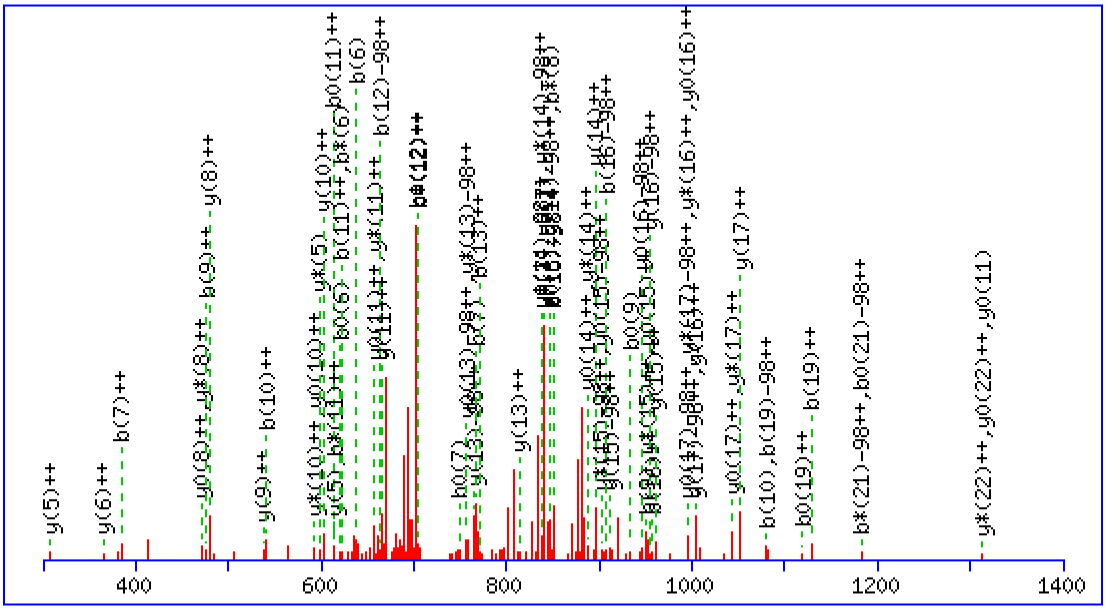
Monoisotopic mass of neutral peptide Mr(calc): 2238.8858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y11 : Phospho (Y)
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.048
Matched b ions: b(6), b(7), b(12)-98++, b(16)-98++, b(16)++
Matched y ions: y(4), y(6), y(10)++, y(11)-98++, y(11)++, y(12)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.583

LLKPGEEPSEYTDEEDTKDHSKQD
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of **LLKPGEEPSEYTDEEDTKDHSKQD**
Found in **PGRC2_MOUSE** in **SwissProt**, Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2

Match to Query 6813: 2869.218320 from(718.311856,4+) index(4639)
Title: Elution from: 24.493 to 24.493 scan no 1884 cid35.00 polarity:+:m1s



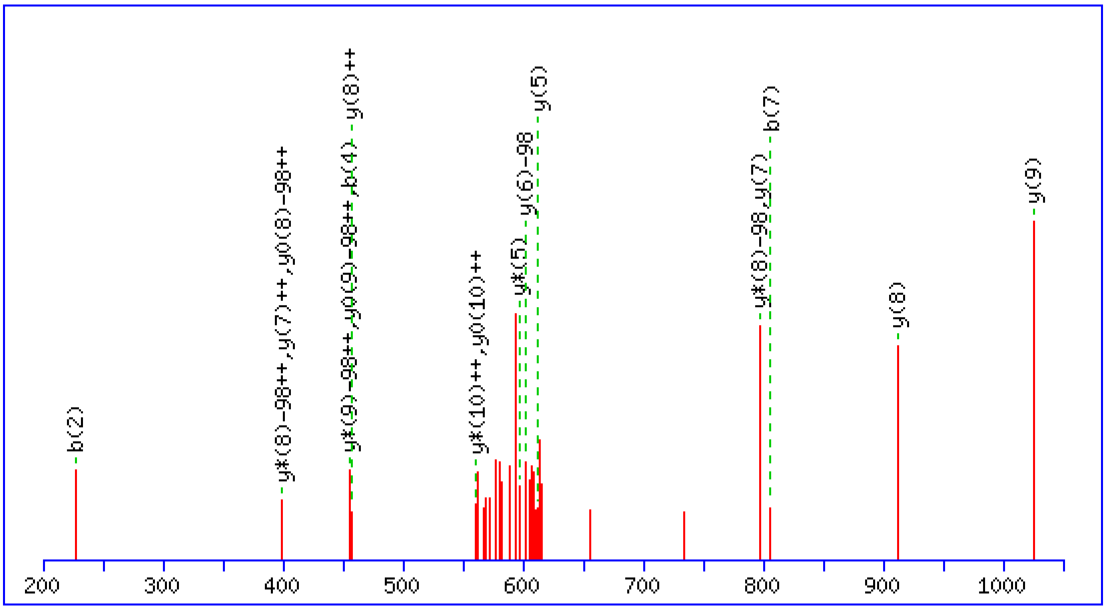
Monoisotopic mass of neutral peptide Mr(calc): 2869.2178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0054
Matched b ions: b(6), b(7)++, b(7), b(9), b(9)++, b(10)++, b(10), b(11)++, b(12)-98++, b(13)++, b(15)-98++, b(16)-98++, b(16)++, b(19)++, b(19)-98++
Matched y ions: y(5)++, y(5), y(6)++, y(8)++, y(9)++, y(10)++, y(11)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++

Peptide No.584

LLLDPSSTPTK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **LLLDPSSTPTK**
Found in **LTOR1_MOUSE** in **SwissProt**, Ragulator complex protein LAMTOR1 OS=Mus musculus GN=Lamtor1 PE=1 SV=1

Match to Query 1761: 1250.615380 from(626.314966,2+) index(2128)
Title: Elution from: 36.093 to 36.093 scan no 3423 cid35.00 polarity:+



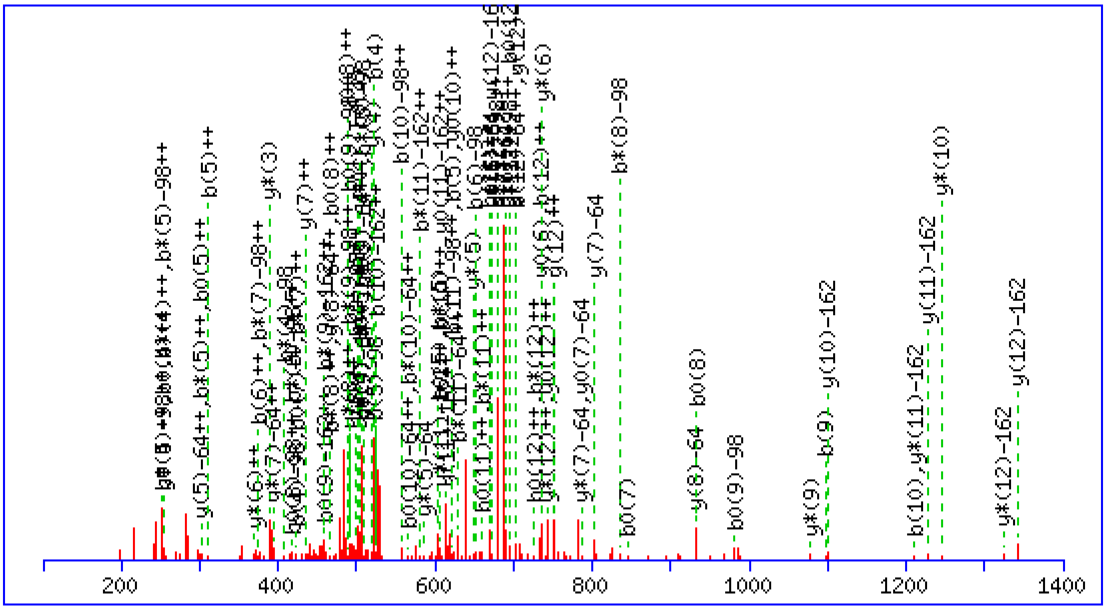
Monoisotopic mass of neutral peptide Mr(calc): 1250.6159
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.044
Matched b ions: b(2), b(4), b(7)
Matched y ions: y(5), y(6)-98, y(7)++, y(7), y(8), y(8)++, y(9)

Peptide No.585

LLQSVKNSMLQMK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **LLQSVKNSMLQMK**
Found in **DOK5_MOUSE** in **SwissProt**, Docking protein 5 OS=Mus musculus GN=Dok5 PE=1 SV=1

Match to Query 2841: 1614.789912 from(539.270580,3+) index(3821)
Title: Elution from: 23.312 to 23.312 scan no 1662 cid35.00 polarity:+:m1s



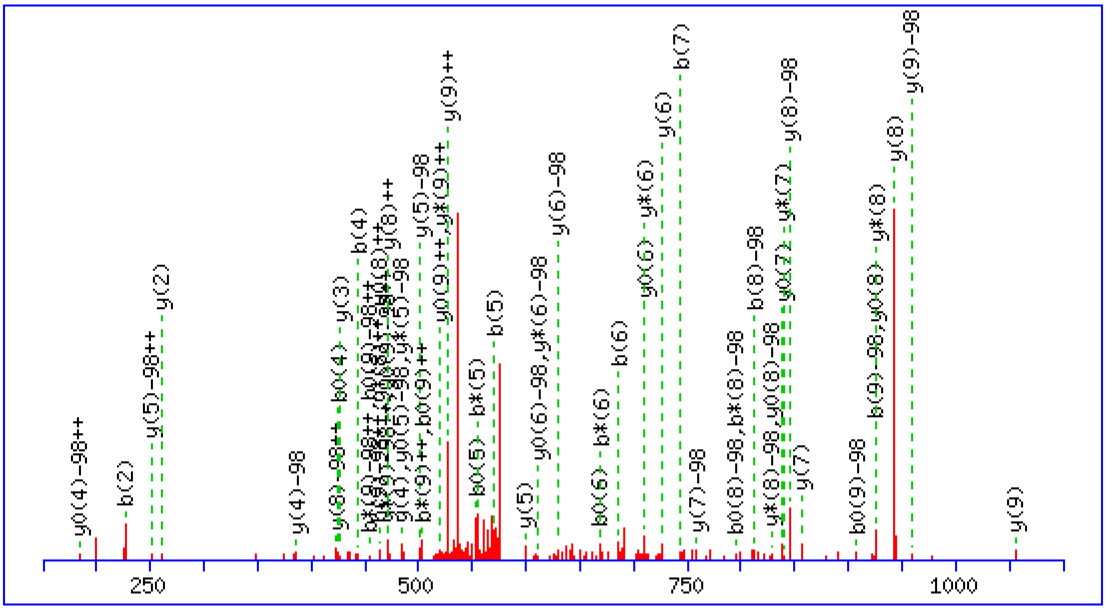
Monoisotopic mass of neutral peptide Mr(calc): 1614.7874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.054
Matched b ions: b(4), b(4)-98, b(5)++, b(5)-98, b(5), b(6)++, b(6)-98, b(9), b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++
Matched y ions: y(4), y(7)++, y(8)++, y(11)++, y(12)++, y(12)-98++

Peptide No.586

LLSEQDGSLK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **LLSEQDGSLK**
Found in **CXB1_MOUSE** in **SwissProt**, Gap junction beta-1 protein OS=Mus musculus GN=Gjb1 PE=1 SV=3

Match to Query 1803: 1168.538464 from(585.276508,2+) index(838)
Title: Elution from: 33.793 to 33.793 scan no 2250 cid35.00 polarity:+



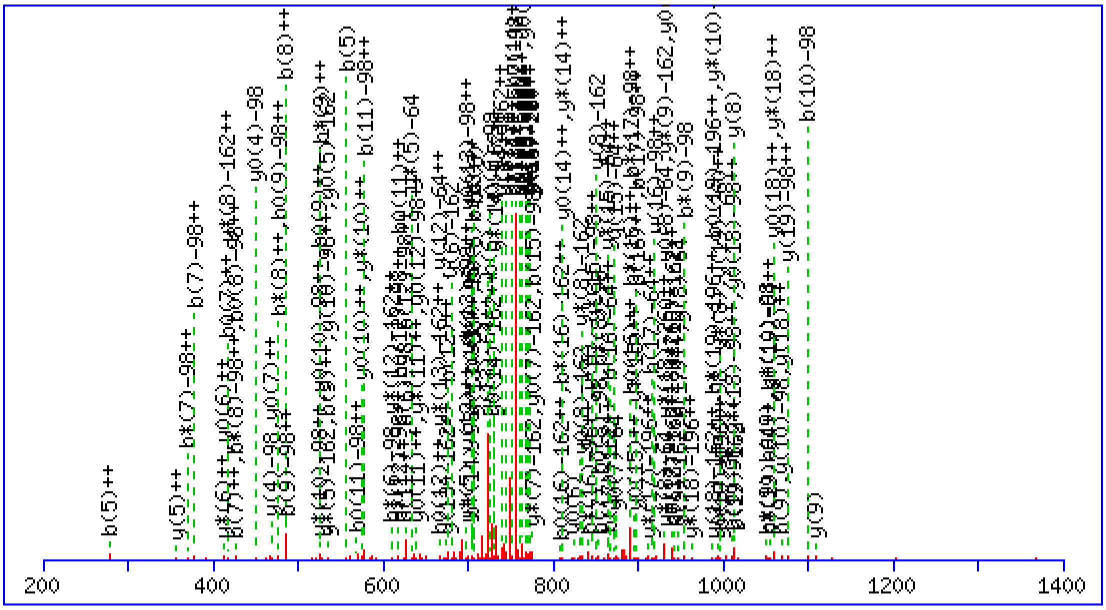
Monoisotopic mass of neutral peptide Mr(calc): 1168.5377
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0054
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(9)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5), y(5)-98++, y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8)++, y(8)-98, y(8), y(8)-98++, y(9), y(9)-98, y(9)++

Peptide No.587

LLTTQSEDTQGPGLKMPSQR
Confirmed sites: @S:6,@S:18
Ambiguous sites:

MS/MS Fragmentation of **LLTTQSEDTQGPGLKMPSQR**
Found in **IL16_MOUSE** in **SwissProt**, Pro-interleukin-16 OS=Mus musculus GN=Il16 PE=1 SV=3

Match to Query 4993: 2362.021947 from(788.347925,3+) index(985)
Title: Elution from: 27.051 to 27.051 scan no 2078 cid35.00 polarity:+



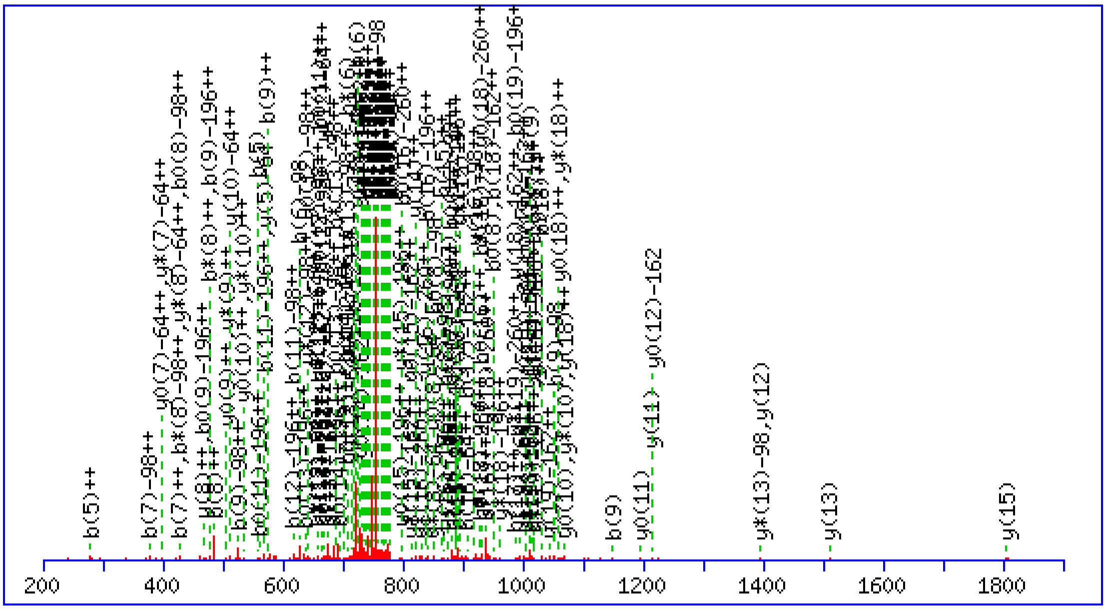
Monoisotopic mass of neutral peptide Mr(calc): 2362.0277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.043
Matched b ions: b(5)++, b(5), b(6)-98, b(6), b(7)++, b(7)-98, b(7)-98++, b(7), b(8)++, b(9)-98++, b(9), b(9)++, b(10)-98, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(19)-196++
Matched y ions: y(4)-98, y(5)++, y(6), y(6)-98, y(8), y(9), y(9)-98, y(10)-98, y(10)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(16)-98++, y(18)++, y(19)-98++

Peptide No.588

LLTTQSEDTQGPGLKMPSQR
Confirmed sites: @S:6,@T:9
Ambiguous sites:

MS/MS Fragmentation of **LLTTQSEDTQGPGLKMPSQR**
Found in **IL16_MOUSE** in **SwissProt**, Pro-interleukin-16 OS=Mus musculus GN=Il16 PE=1 SV=3

Match to Query 5169: 2362.027692 from(788.349840,3+) index(936)
Title: Elution from: 34.883 to 34.883 scan no 2383 cid35.00 polarity:+



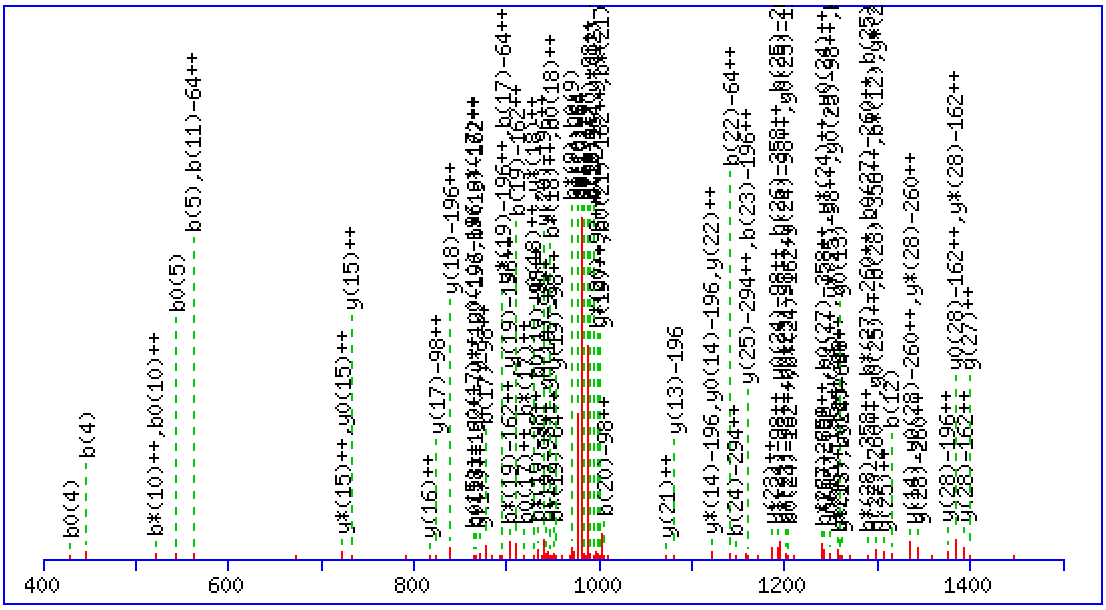
Monoisotopic mass of neutral peptide Mr(calc): 2362.0277
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.017
Matched b ions: b(5)++, b(5), b(6)-98, b(6), b(7)++, b(7)-98, b(7)-98++, b(8)++, b(8)-98, b(9)-98++, b(9)-98, b(9), b(9)-196++, b(9)++, b(11)-98++, b(11)-196++, b(11)++, b(12)-196++, b(12)++, b(12)-98++, b(13)++, b(14)-98++, b(14)-196++, b(15)-196++, b(15)++, b(16)++, b(16)-98++, b(16)-196++, b(17)-196++, b(17)++, b(18)++
Matched y ions: y(7), y(8)++, y(11), y(12), y(13)++, y(13), y(13)-98++, y(14)-98++, y(14)++, y(15), y(16)-196++, y(16)-98++, y(17)++, y(18)++, y(18)-98++

Peptide No.589

LMGEDEKPAAKENSEGAGAKASSAGVLVS
Confirmed sites: @S:14,@S:22,@S:23
Ambiguous sites:

MS/MS Fragmentation of **LMGEDEKPAAKENSEGAGAKASSAGVLVS**
Found in **PFD2_MOUSE** in **SwissProt**, Prefoldin subunit 2 OS=Mus musculus GN=Pfdn2 PE=2 SV=2

Match to Query 5903: 3058.259607 from(1020.427145,3+) index(3813)
Title: Elution from: 23.237 to 23.237 scan no 1652 cid35.00 polarity:+:m1s



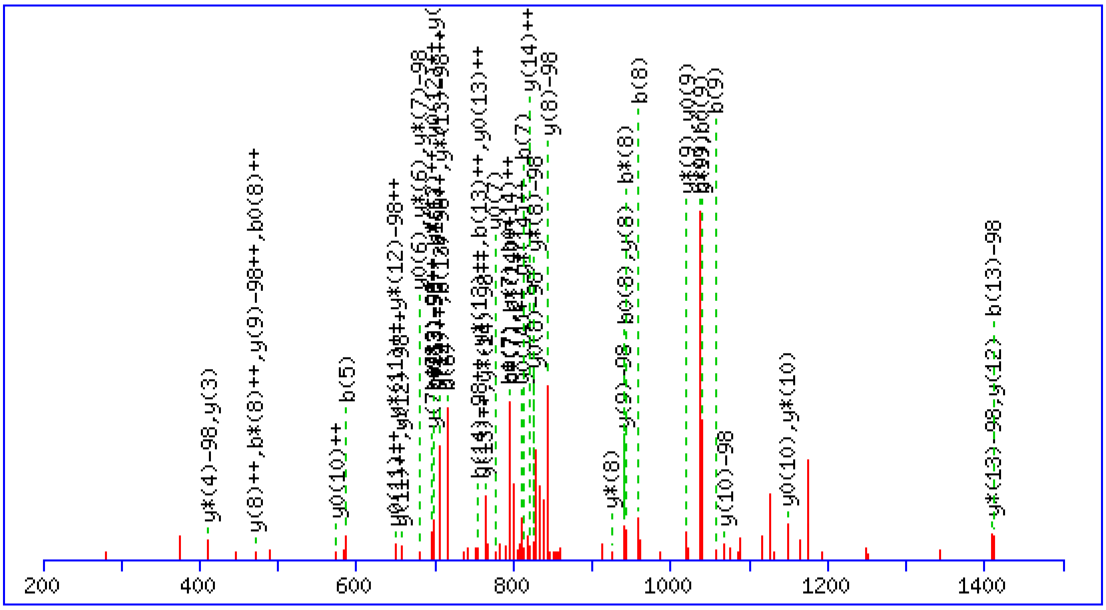
Monoisotopic mass of neutral peptide Mr(calc): 3058.2644
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S23 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.016
Matched b ions: b(4), b(5), b(9), b(12), b(15)++, b(17)-98++, b(19)-98++, b(19)++, b(20)-98++, b(23)++, b(23)-196++, b(24)-294++
Matched y ions: y(13)-196, y(14), y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-196++, y(19)-196++, y(19)-98++, y(19)++, y(20)-98++, y(20)-196++, y(21)++, y(22)++, y(23)++, y(24)-98++, y(24)++, y(25)-98++, y(25)++, y(25)-294++, y(27)++, y(28)-196++

Peptide No.590

LNDPFQPFPGNDSPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **LNDPFQPFPGNDSPK**
Found in **EPS15_MOUSE** in **SwissProt**, Epidermal growth factor receptor substrate 15 OS=Mus musculus GN=Eps15 PE=1 SV=1

Match to Query 4051: 1751.755204 from(876.884878,2+) index(6803)
Title: Elution from: 49.899 to 49.899 scan no 5178 cid35.00 polarity:+:m1s



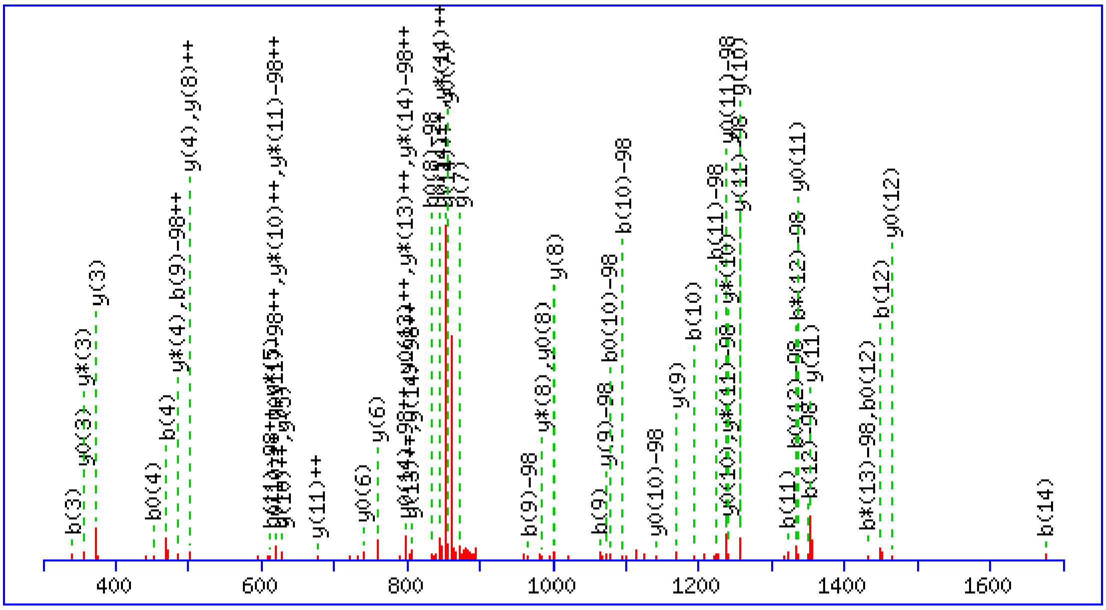
Monoisotopic mass of neutral peptide Mr(calc): 1751.7556
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.016
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(13)-98++, b(13)-98, b(13)++, b(14)-98++
Matched y ions: y(3), y(6), y(7), y(7)-98, y(8)-98, y(8)++, y(8), y(9), y(9)-98++, y(9)-98, y(10)-98, y(11)++, y(12), y(12)++, y(12)-98++, y(13)++, y(14)++

Peptide No.591

LPEEPSSEDEQQPEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **LPEEPSSEDEQQPEK**
Found in **ITSN1_MOUSE** in **SwissProt**, Intersectin-1 OS=Mus musculus GN=Itsn1 PE=1 SV=1

Match to Query 3675: 1820.731974 from(911.373263,2+) index(3581)
Title: Elution from: 23.550 to 23.550 scan no 1596 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1820.7353
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00015
Matched b ions: b(3), b(4), b(9), b(9)-98++, b(9)-98, b(10)-98, b(10), b(11)-98++, b(11), b(11)-98, b(12), b(12)-98, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98, y(9), y(10)++, y(10), y(11)-98, y(11), y(11)++, y(13)++, y(14)-98++, y(14)++

Peptide No.592

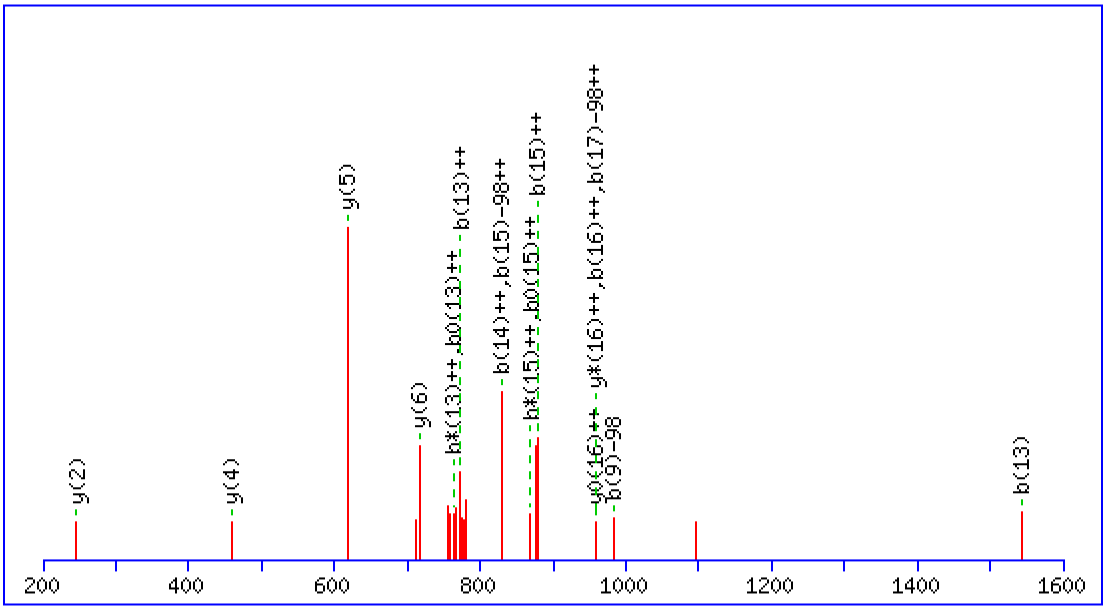
LQLSDEESVFEDALVCPDAR

Confirmed sites:

Ambiguous sites: @S:4orS:8

MS/MS Fragmentation of **LQLSDEESVFEDALVCPDAR**
Found in **PHLB2_MOUSE** in **SwissProt**, Pleckstrin homology-like domain family B member 2 OS=Mus musculus GN=Phldb2 PE=1 SV=2

Match to Query 6109: 2372.022159 from(791.681329,3+) index(7188)
Title: Elution from: 67.417 to 67.417 scan no 6651 cid35.00 polarity:+:m1s



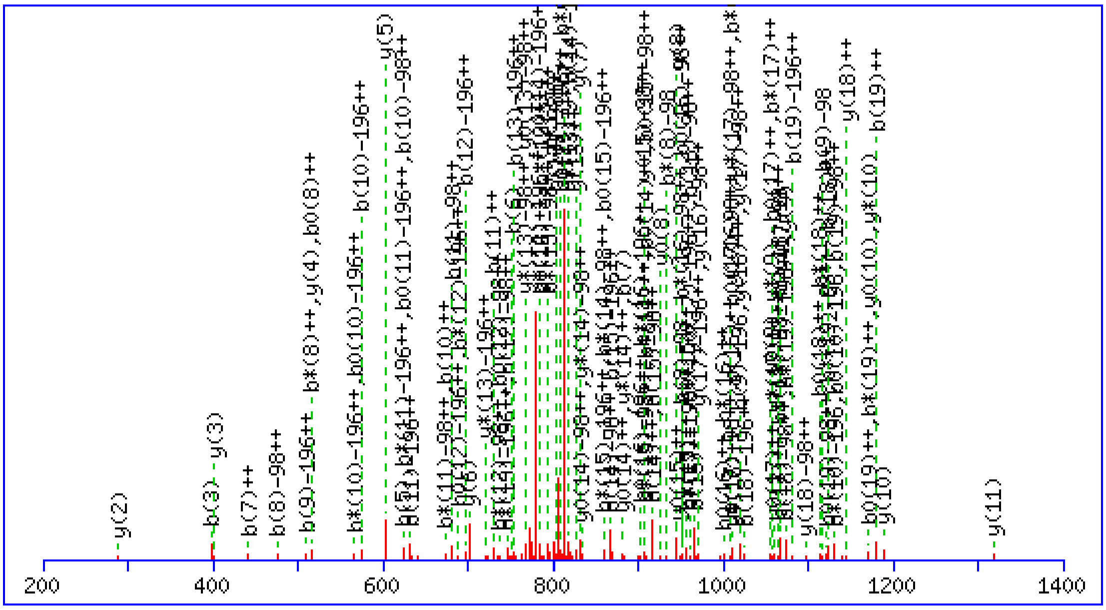
Monoisotopic mass of neutral peptide Mr(calc): 2372.0243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.017
Matched b ions: b(9)-98, b(13), b(13)++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(17)-98++
Matched y ions: y(2), y(4), y(5), y(6)

Peptide No.593

LQRPKEESSEDENEVSNILR
Confirmed sites: @S:8,@S:9
Ambiguous sites:

MS/MS Fragmentation of **LQRPKEESSEDENEVSNILR**
Found in **OTUD4_MOUSE** in **SwissProt**, OTU domain-containing protein 4 OS=Mus musculus GN=Otud4 PE=1 SV=1

Match to Query 6441: 2531.091597 from(844.704475,3+) index(6075)
Title: Elution from: 38.814 to 38.814 scan no 3812 cid35.00 polarity:+:m1s



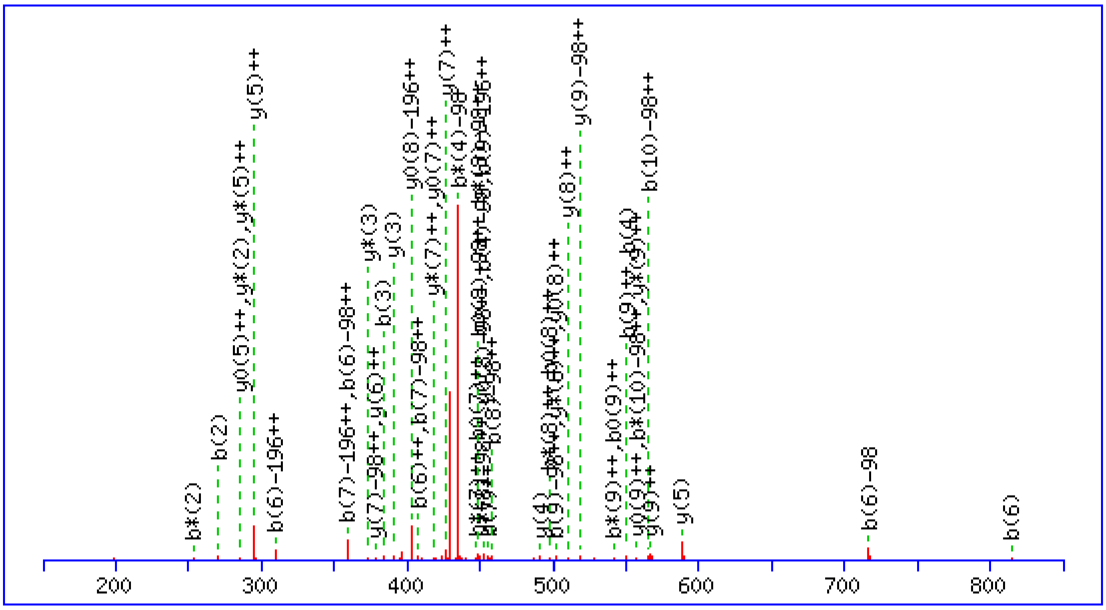
Monoisotopic mass of neutral peptide Mr(calc): 2531.0941
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 4.7e-006
Matched b ions: b(3), b(5), b(6), b(7)++, b(7), b(8)-98++, b(8)-98, b(9)-196++, b(9)-196, b(9)-98, b(10)-196++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(12)-196++, b(13)-196++, b(13)-98++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(17)-196++, y(18)-98++, y(18)++

Peptide No.594

LRLSPSPTSQR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **LRLSPSPTSQR**
Found in **LMNA_MOUSE** in **SwissProt**, Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2

Match to Query 2083: 1400.621061 from(467.880963,3+) index(1012)
Title: Elution from: 25.817 to 25.817 scan no 2002 cid35.00 polarity:+



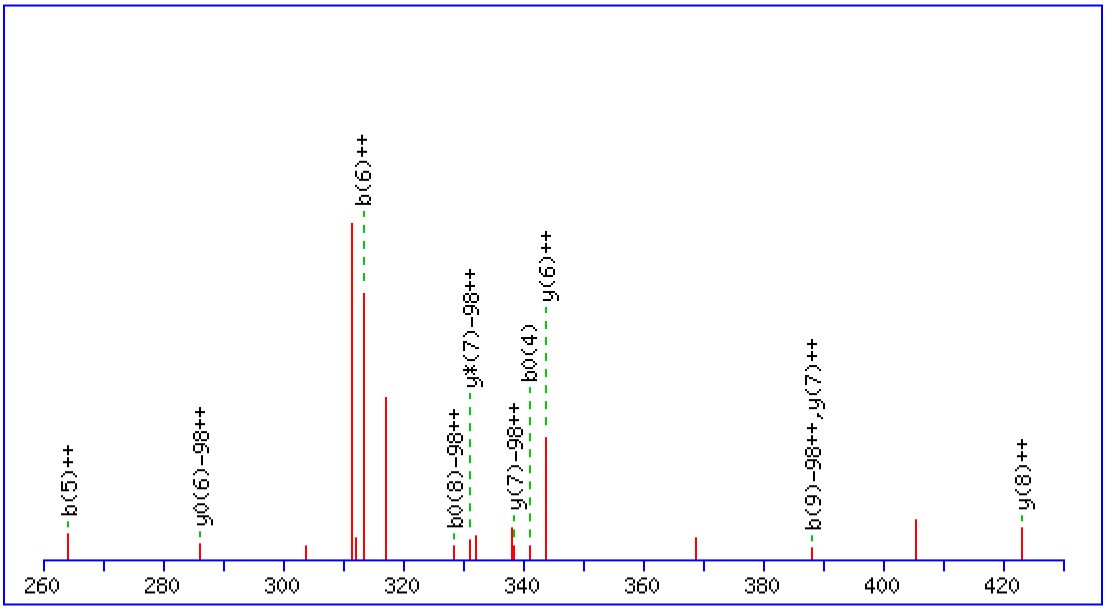
Monoisotopic mass of neutral peptide Mr(calc): 1400.6214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.05
Matched b ions: b(2), b(3), b(4), b(4)-98, b(6)-98++, b(6)-98, b(6), b(6)-196++, b(6)++, b(7)-196++, b(7)-98++, b(7)++, b(8)-98++, b(9)++, b(9)-196++, b(9)-98++, b(10)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(7)++, y(7)-98++, y(8)++, y(9)++, y(9)-98++

Peptide No.595

LSASSTGSTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **LSASSTGSTR**
Found in **BCAR1_MOUSE** in **SwissProt**, Breast cancer anti-estrogen resistance protein 1 OS=Mus musculus GN=Bcar1 PE=1 SV=2

Match to Query 848: 1045.443630 from(349.488486,3+) index(3126)
Title: Elution from: 15.915 to 15.915 scan no 783 cid35.00 polarity:+:m1s



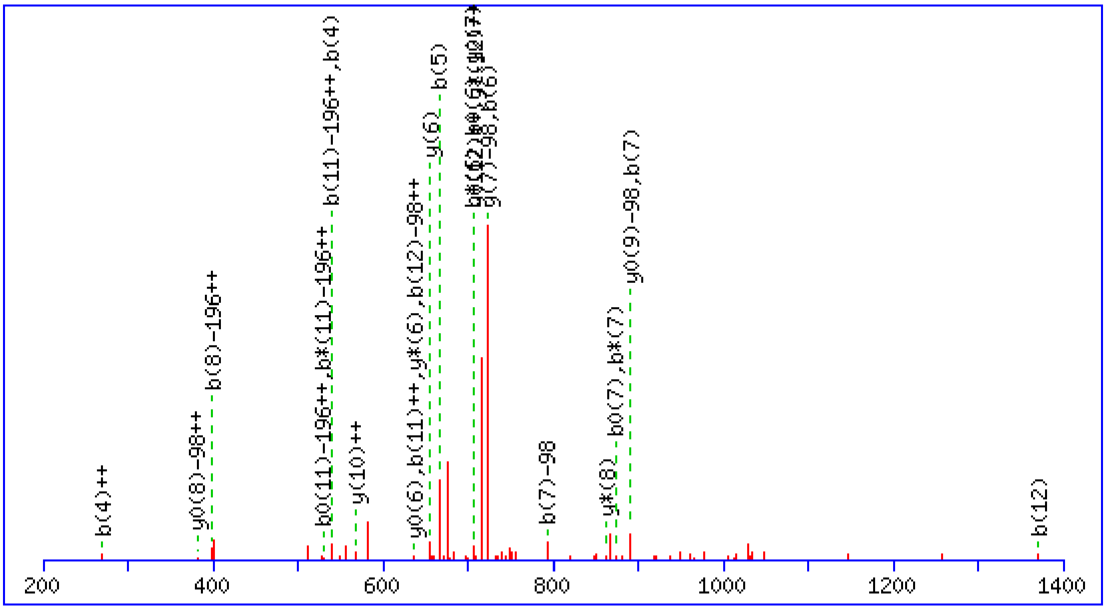
Monoisotopic mass of neutral peptide Mr(calc): 1045.4441
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.028
Matched b ions: b(5)++, b(6)++, b(9)-98++
Matched y ions: y(6)++, y(7)++, y(7)-98++, y(8)++

Peptide No.596

LSEEQGSTPKGPR
Confirmed sites: @S:2,@S:7
Ambiguous sites:

MS/MS Fragmentation of **LSEEQGSTPKGPR**
Found in **FA13C_MOUSE** in **SwissProt**, Protein FAM13C OS=Mus musculus GN=Fam13c PE=1 SV=2

Match to Query 2743: 1544.625502 from(773.320027,2+) index(1071)
Title: Elution from: 27.744 to 27.744 scan no 2174 cid35.00 polarity:+



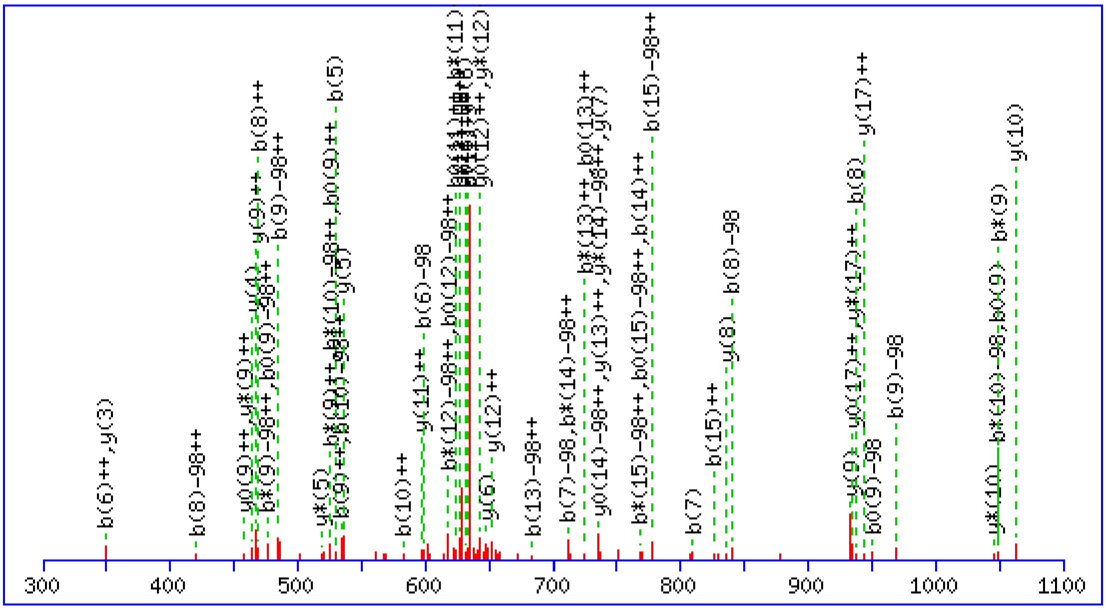
Monoisotopic mass of neutral peptide Mr(calc): 1544.6273
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0053
Matched b ions: b(4)++, b(4), b(5), b(6), b(7), b(7)-98, b(8)-196++, b(11)-196++, b(11)++, b(12), b(12)-98++
Matched y ions: y(6), y(7)-98, y(10)++

Peptide No.597

LSRGDSLKEPTSIADSSR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **LSRGDSLKEPTSIADSSR**
Found in **ZDHC5_MOUSE** in **SwissProt**, Palmitoyltransferase ZDHHC5 OS=Mus musculus GN=Zdhhc5 PE=1 SV=1

Match to Query 4852: 1997.938641 from(666.986823,3+) index(4664)
Title: Elution from: 26.161 to 26.161 scan no 2076 cid35.00 polarity:+:m1s



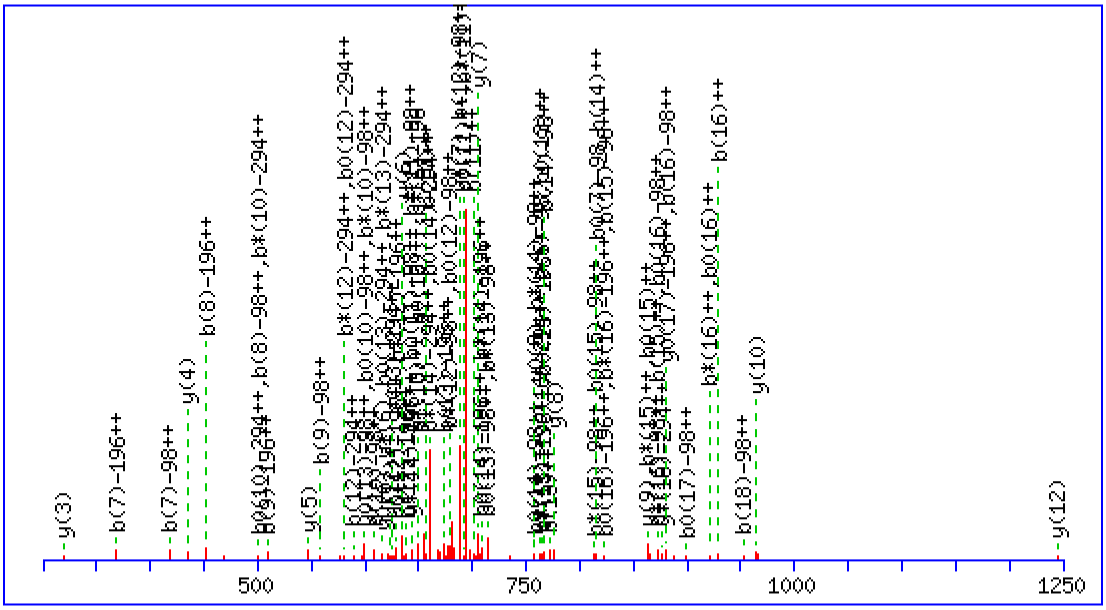
Monoisotopic mass of neutral peptide Mr(calc): 1997.9419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0042
Matched b ions: b(5), b(6)++, b(6)-98, b(7)-98, b(7), b(8)-98++, b(8)-98, b(8), b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(12)-98++, b(13)-98++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11)++, y(12)++, y(13)++, y(17)++

Peptide No.598

LSRSRTASLTSAASIDGSR
Confirmed sites: @S:8
Ambiguous sites: @S:2orS:4orT:6, @S:2orS:4orT:6

MS/MS Fragmentation of **LSRSRTASLTSAASIDGSR**
Found in **NDRG2_MOUSE** in **SwissProt**, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 5628: 2174.912313 from(725.978047,3+) index(5346)
Title: Elution from: 31.525 to 31.525 scan no 2839 cid35.00 polarity:+:m1s



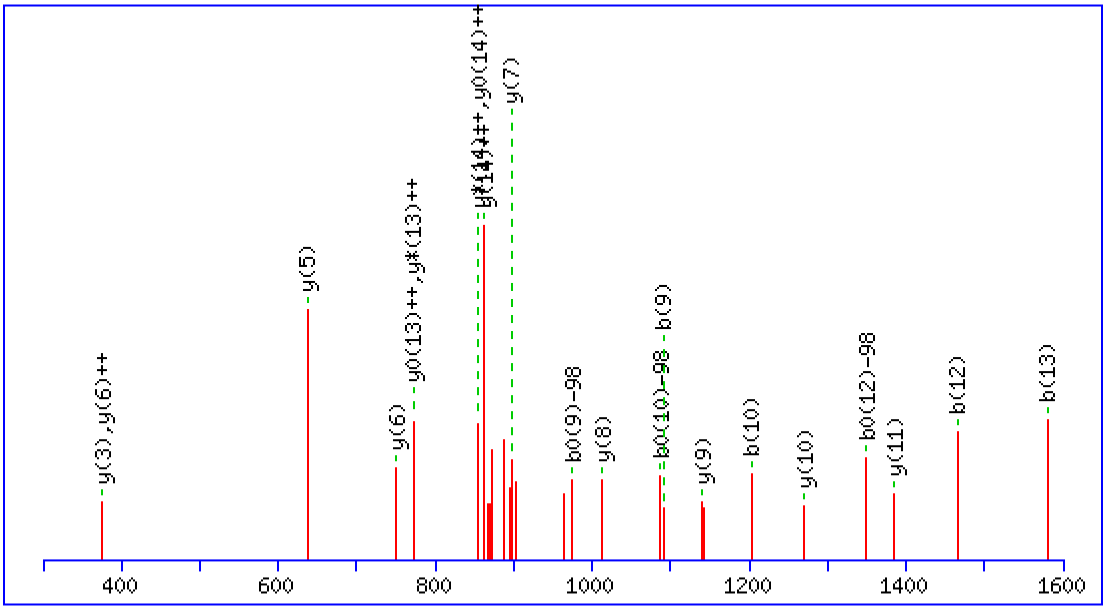
Monoisotopic mass of neutral peptide Mr(calc): 2174.9123
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0041
Matched b ions: b(6)-98, b(7)-196++, b(7)-98++, b(8)-196++, b(8)-98++, b(9)-196++, b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(12)-98++, b(12)-294++, b(12)-196++, b(13)++, b(13)-196++, b(13)-294++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12), y(12)++, y(16)-294++

Peptide No.599

LSSSDEEDFLYVDIK
Confirmed sites:
Ambiguous sites: @S:2orS:3orS:4

MS/MS Fragmentation of **LSSSDEEDFLYVDIK**
Found in **MUG1_MOUSE** in **SwissProt**, Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3

Match to Query 4331: 1838.783388 from(920.398970,2+) index(7058)
Title: Elution from: 58.057 to 58.057 scan no 5973 cid35.00 polarity:+:m1s



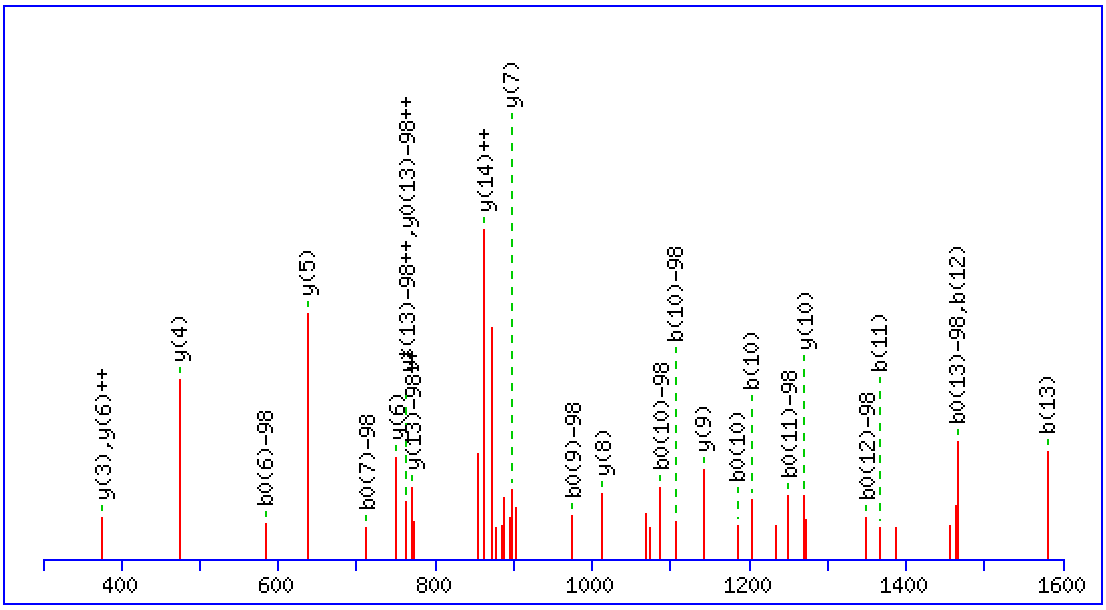
Monoisotopic mass of neutral peptide Mr(calc): 1838.7863
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 7.1e-006
Matched b ions: b(9), b(10), b(12), b(13)
Matched y ions: y(3), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(14)++

Peptide No.600

LSSSDEEDFLYVDIK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of **LSSSDEEDFLYVDIK**
Found in **MUG1_MOUSE** in **SwissProt**, Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3

Match to Query 4209: 1838.787048 from(920.400800,2+) index(6850)
Title: Elution from: 58.114 to 58.114 scan no 5912 cid35.00 polarity:+:m1s



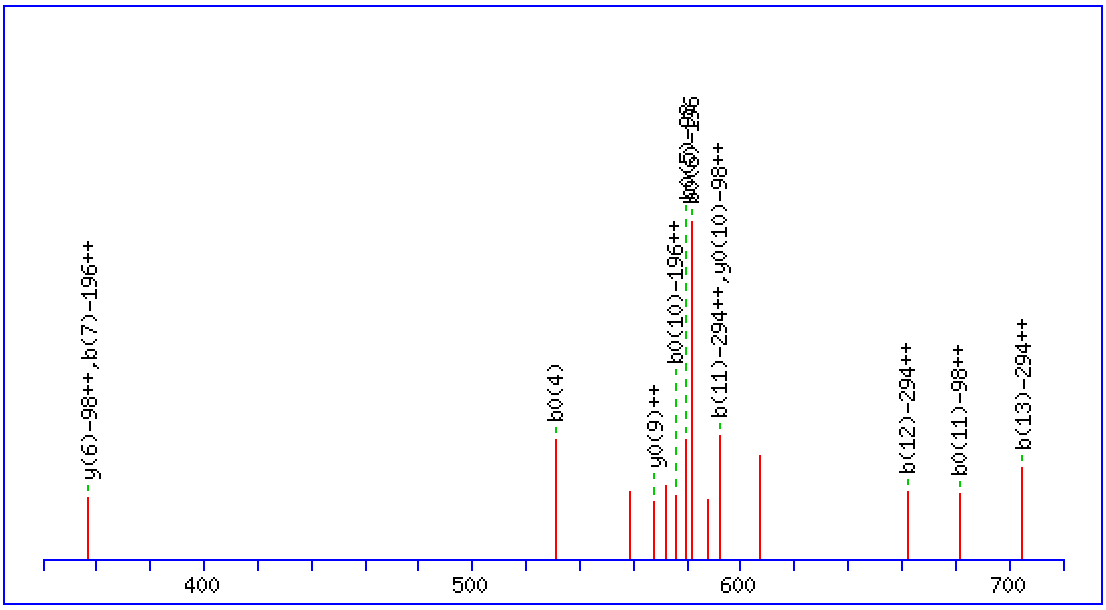
Monoisotopic mass of neutral peptide Mr(calc): 1838.7863
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 2e-005
Matched b ions: b(10)-98, b(10), b(11), b(12), b(13)
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(13)-98++, y(14)++

Peptide No.601

LSTSFVLETFIHSK
Confirmed sites:
Ambiguous sites: @S:2orT:3orS:4, @S:2orT:3orS:4, @T:9orS:13

MS/MS Fragmentation of **LSTSFVLETFIHSK**
Found in **UBP34_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 34 OS=Mus musculus GN=Usp34 PE=1 SV=3

Match to Query 4368: 1847.757165 from(616.926331,3+) index(2203)
Title: Elution from: 36.420 to 36.420 scan no 3496 cid35.00 polarity:+



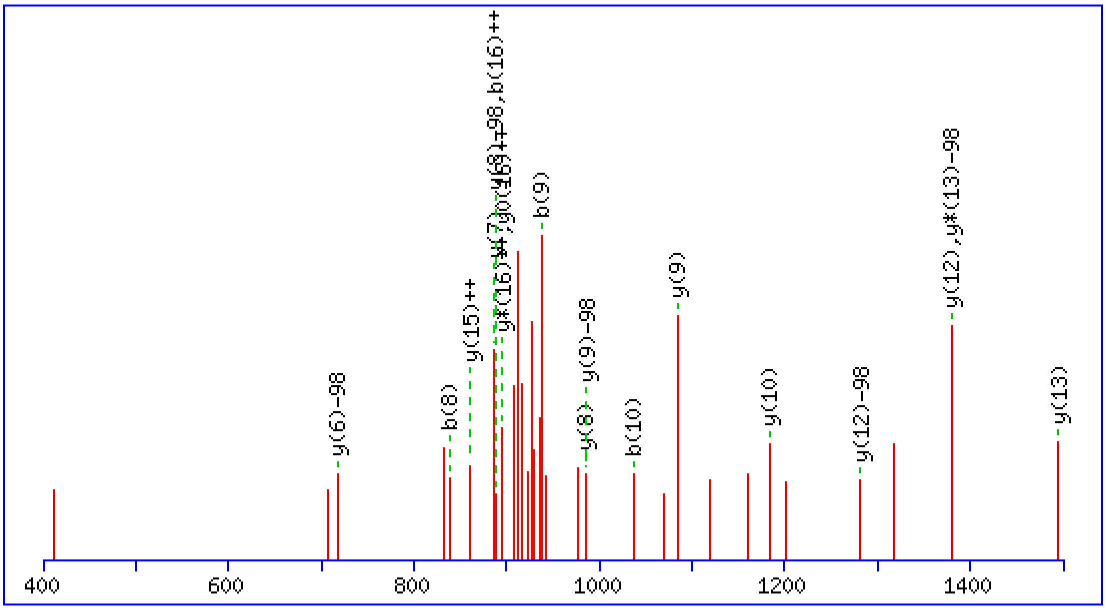
Monoisotopic mass of neutral peptide Mr(calc): 1847.7549
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.03
Matched b ions: b(7)-196++, b(11)-294++, b(12)-294++, b(13)-294++
Matched y ions: y(6)-98++

Peptide No.602

LSVQDPVVVVAEDSQEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **LSVQDPVVVVAEDSQEK**
Found in **S38AA_MOUSE** in **SwissProt**, Putative sodium-coupled neutral amino acid transporter 10 OS=Mus musculus GN=Slc38a10 PE=1 SV=2

Match to Query 3989: 1920.908078 from(961.461315,2+) index(2400)
Title: Elution from: 44.402 to 44.402 scan no 4338 cid35.00 polarity:+



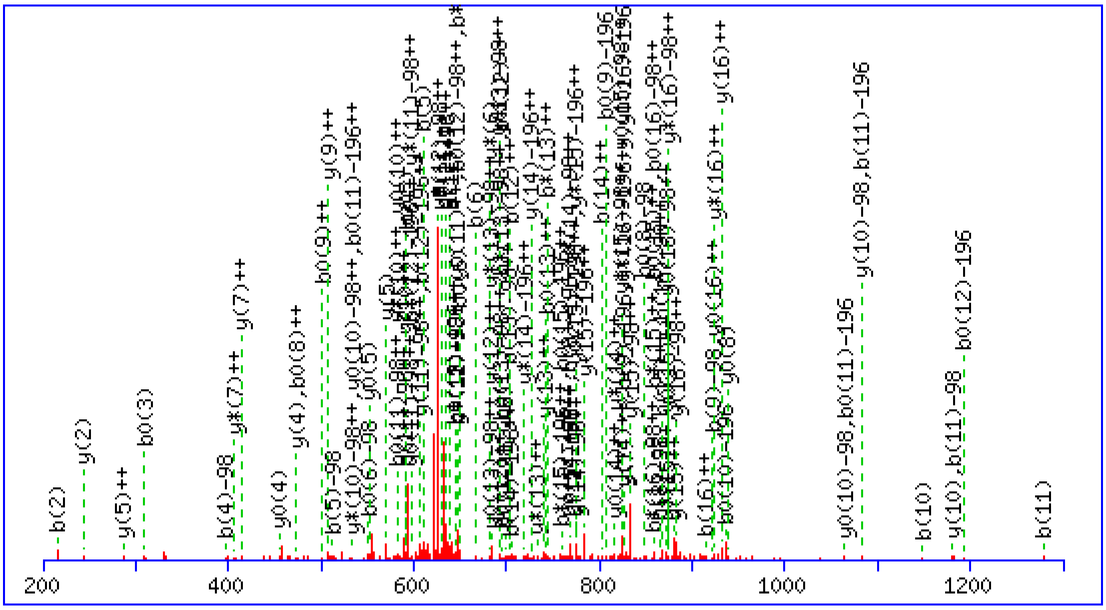
Monoisotopic mass of neutral peptide Mr(calc): 1920.9082
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.032
Matched b ions: b(8), b(9), b(10), b(16)++
Matched y ions: y(6)-98, y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(12)-98, y(12), y(13), y(15)++

Peptide No.603

LTLSDGESGEEKPTKPK
Confirmed sites: @S:4,@S:8
Ambiguous sites:

MS/MS Fragmentation of **LTLSDGESGEEKPTKPK**
Found in **ATRX_MOUSE** in **SwissProt**, Transcriptional regulator ATRX OS=Mus musculus GN=Atrx PE=1 SV=3

Match to Query 5042: 1974.859122 from(659.293650,3+) index(4104)
Title: Elution from: 30.418 to 30.418 scan no 1940 cid35.00 polarity:+:m1s



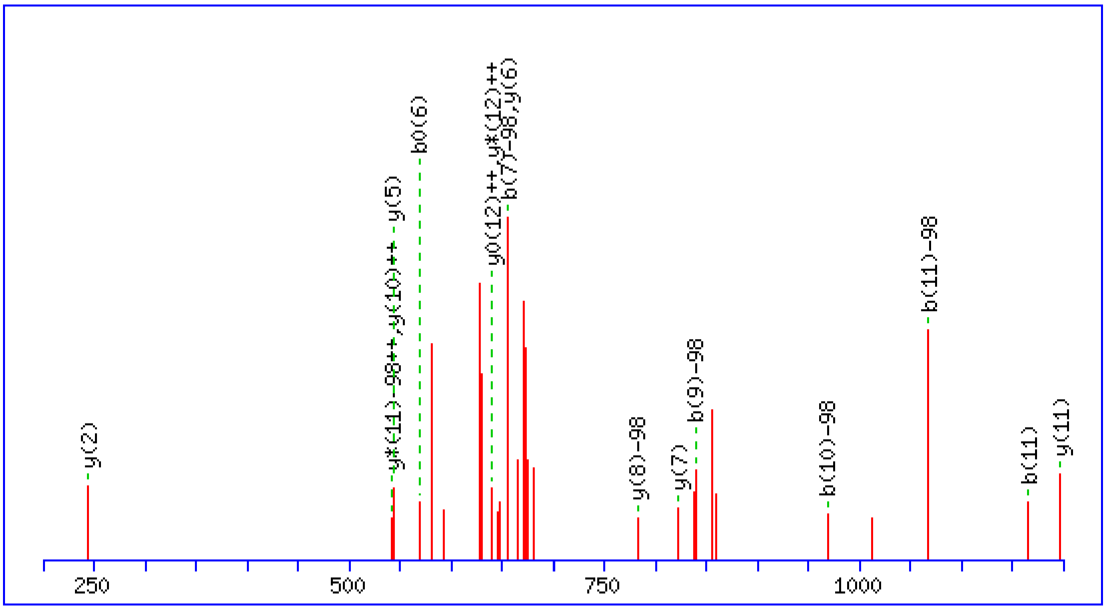
Monoisotopic mass of neutral peptide Mr(calc): 1974.8588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.013
Matched b ions: b(2), b(4)-98, b(5)-98, b(5), b(6), b(7)-98, b(8)-196, b(8)-98, b(9)-196, b(9)-98, b(10), b(11)-196, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)-196++, b(12)++, b(13)-98++, b(14)-196++, b(14)++, b(15)-196++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(4), y(5)++, y(5), y(6), y(7)++, y(7), y(9)++, y(10)-98, y(10), y(10)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.604

LVDSDGSLAEVPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **LVDSDGSLAEVPK**
Found in **STEA3_MOUSE** in **SwissProt**, Metalloreductase STEAP3 OS=Mus musculus GN=Steap3 PE=1 SV=1

Match to Query 2096: 1408.648446 from(705.331499,2+) index(1770)
Title: Elution from: 33.969 to 33.969 scan no 3076 cid35.00 polarity:+



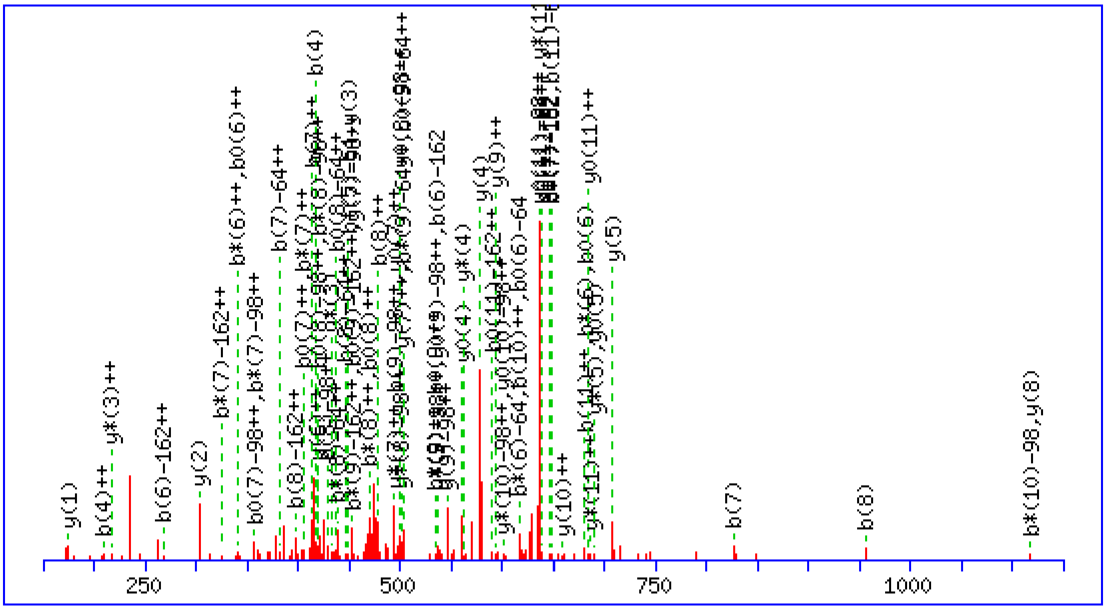
Monoisotopic mass of neutral peptide Mr(calc): 1408.6487
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(7)-98, b(9)-98, b(10)-98, b(11)-98, b(11)
Matched y ions: y(2), y(5), y(6), y(7), y(8)-98, y(10)++, y(11)

Peptide No.605

MAQALSEEEFQR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **MAQALSEEEFQR**
Found in **GRAP1_MOUSE** in **SwissProt**, GRIP1-associated protein 1 OS=Mus musculus GN=Gripap1 PE=1 SV=1

Match to Query 3619: 1533.618486 from(512.213438,3+) index(2483)
Title: Elution from: 57.738 to 57.738 scan no 4865 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1533.6170

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 17 **Expect:** 0.056

Matched b ions: b(4)++, b(4), b(7), b(7)++, b(8), b(8)++, b(8)-98++, b(9)-98++, b(10)++, b(11)++

Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(7)-98++, y(7)++, y(8), y(9)-98++, y(9)++, y(10)++

Peptide No.606

MGSLGGLALCLLR

Confirmed sites: @S:3

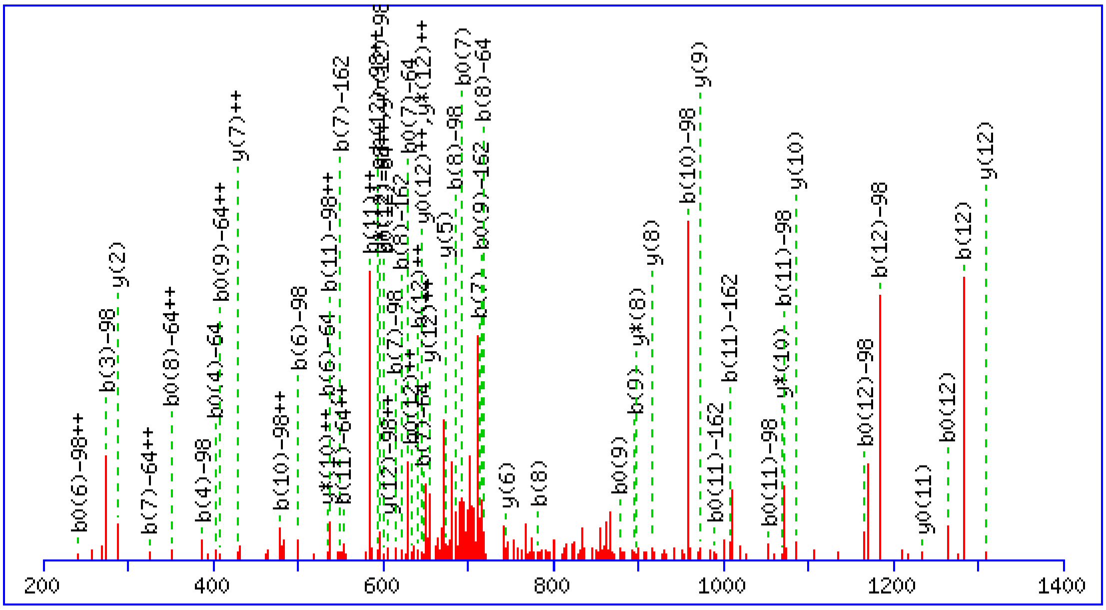
Ambiguous sites:

MS/MS Fragmentation of **MGSLGGLALCLLR**

Found in **PTPRT_MOUSE** in **SwissProt**, Receptor-type tyrosine-protein phosphatase T OS=Mus musculus GN=Ptprt PE=2 SV=2

Match to Query 3350: 1455.694128 from(728.854340,2+) index(5750)

Title: Elution from: 53.622 to 53.622 scan no 4515 cid35.00 polarity:+:m1s



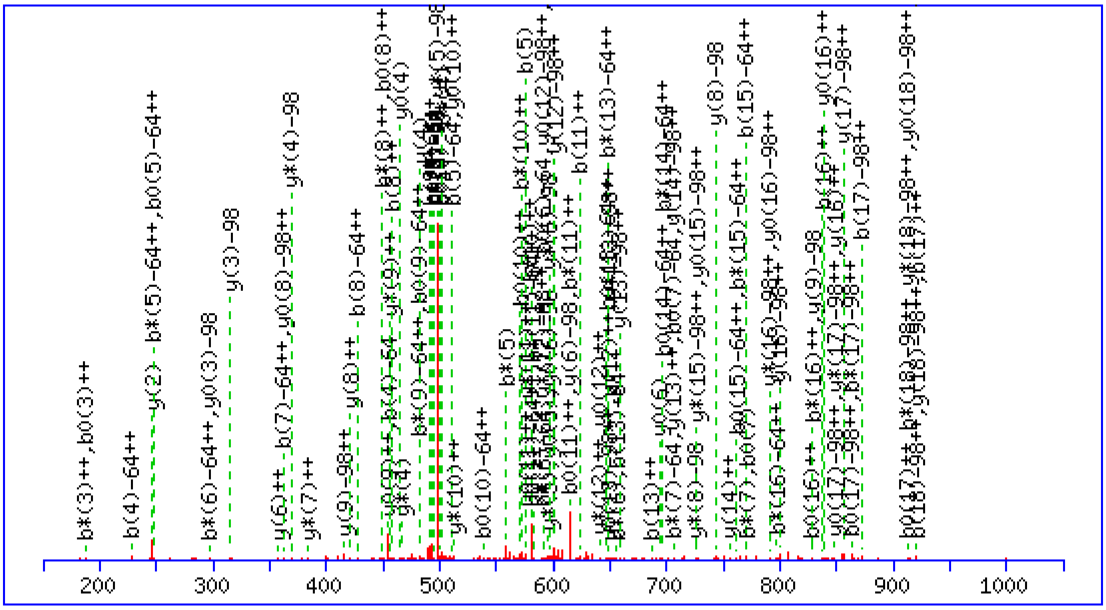
Monoisotopic mass of neutral peptide Mr(calc): 1455.6979
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.029
Matched b ions: b(3)-98, b(4)-98, b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9), b(10)-98, b(10)-98++, b(11)-98++, b(11)++, b(11)-98, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(5), y(6), y(7)++, y(8), y(9), y(10), y(12), y(12)++, y(12)-98++

Peptide No.607

MKDQGPDKENSGAVEASVK
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **MKDQGPDKENSGAVEASVK**
Found in **VIR_MOUSE** in **SwissProt**, Protein virilizer homolog OS=Mus musculus GN=Kiaa1429 PE=1 SV=1

Match to Query 4389: 2084.913416 from(522.235630,4+) index(308)
Title: Elution from: 19.773 to 19.773 scan no 1187 cid35.00 polarity:+



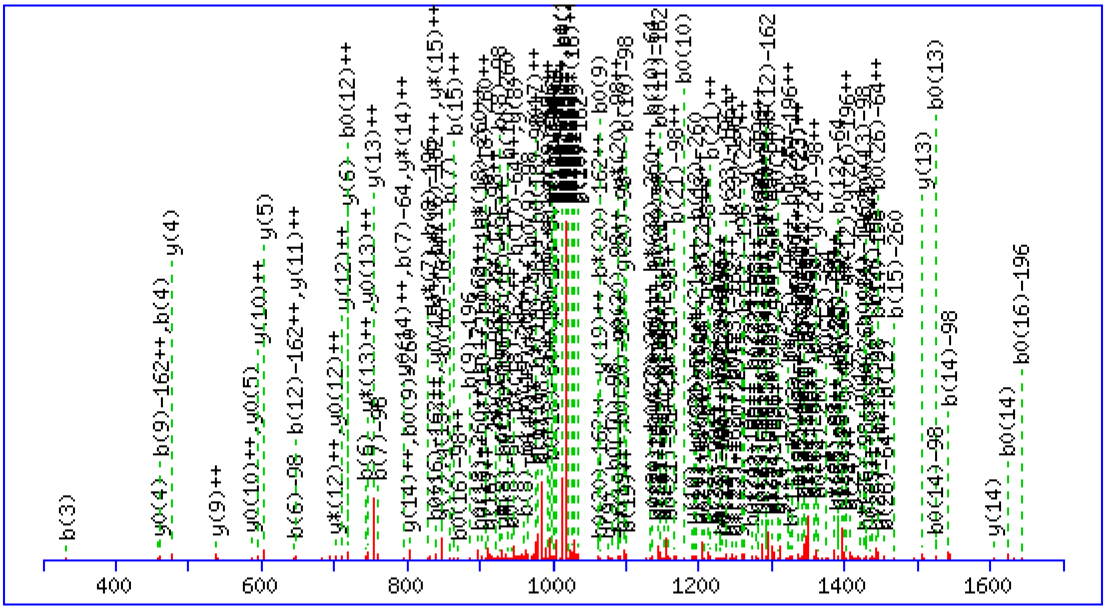
Monoisotopic mass of neutral peptide Mr(calc): 2084.9085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.021
Matched b ions: b(5), b(8)++, b(10)++, b(11)++, b(13)++, b(16)++, b(17)++, b(17)-98++, b(18)-98++
Matched y ions: y(2), y(3)-98, y(4), y(6)-98, y(6)++, y(8)-98, y(8)++, y(9)-98++, y(9)-98, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(16)-98++, y(16)++, y(17)-98++, y(18)-98++

Peptide No.608

MLAESDDSGDEESVSQTDKTELQSTLR
Confirmed sites: @S:5,@S:8
Ambiguous sites:

MS/MS Fragmentation of **MLAESDDSGDEESVSQTDKTELQSTLR**
Found in **OSBP1_MOUSE** in **SwissProt**, Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1 SV=2

Match to Query 5925: 3146.250795 from(1049.757541,3+) index(5419)
Title: Elution from: 40.955 to 40.955 scan no 3937 cid35.00 polarity:+:m1s



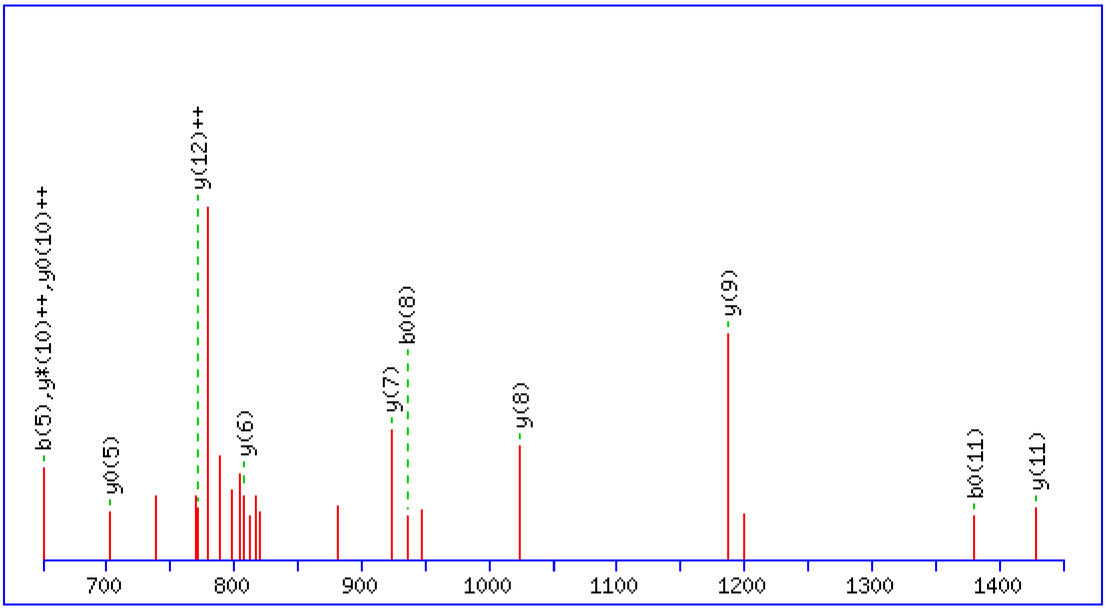
Monoisotopic mass of neutral peptide Mr(calc): 3146.2523
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 9.5e-009
Matched b ions: b(3), b(4), b(6), b(6)-98, b(7)-98, b(7), b(8)-196, b(8)-98, b(8), b(9)-98, b(9)-196, b(10)-98, b(10)-196, b(10), b(11)-98, b(11), b(12), b(12)-196, b(12)-98, b(13)-98, b(13)-196, b(14)-98, b(14)-196, b(15)++, b(17)++, b(17)-98++, b(19)-196++, b(19)++, b(20)++, b(21)++, b(21)-98++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(23)-196++, b(24)-196++, b(25)++, b(26)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(13), y(14)++, y(14), y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(23)-98++, y(23)++, y(23)-196++, y(24)-196++, y(24)-98++, y(24)++, y(25)++, y(25)-98++, y(25)-196++, y(26)-196++

Peptide No.609

MLLEYTDSSYDEK
Confirmed sites:
Ambiguous sites: @S:8orS:9orY:10

MS/MS Fragmentation of **MLLEYTDSSYDEK**
Found in **GSTM1_MOUSE** in **SwissProt**, Glutathione S-transferase Mu 1 OS=Mus musculus GN=Gstm1 PE=1 SV=2

Match to Query 3514: 1672.656410 from(837.335481,2+) index(2701)
Title: Elution from: 42.840 to 42.840 scan no 4312 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1672.6579
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y10 : Phospho (Y)
Ions Score: 27 **Expect:** 0.008
Matched b ions: b(5)
Matched y ions: y(6), y(7), y(8), y(9), y(11), y(12)++

Peptide No.610

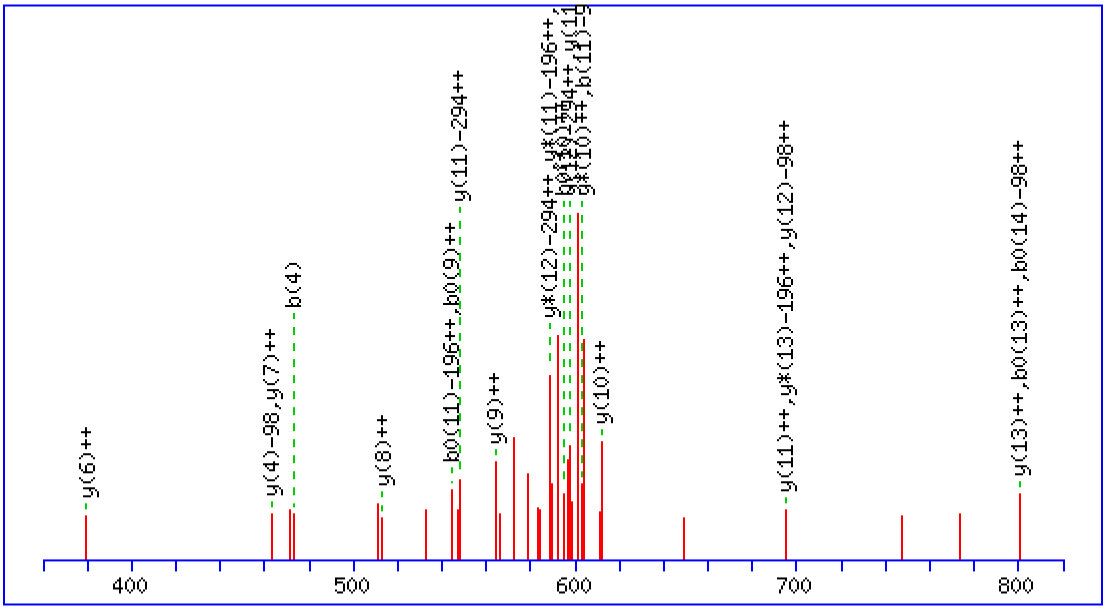
MMLPSPVTSTPFSVK

Confirmed sites: @S:5,@S:9,@S:13

Ambiguous sites:

MS/MS Fragmentation of **MMLPSPVTSTPFSVK**
Found in **NKX23_MOUSE** in **SwissProt**, Homeobox protein Nkx-2.3 OS=Mus musculus GN=Nkx2-3 PE=2 SV=2

Match to Query 3787: 1860.724893 from(621.248907,3+) index(525)
Title: Elution from: 23.006 to 23.006 scan no 1521 cid35.00 polarity:+



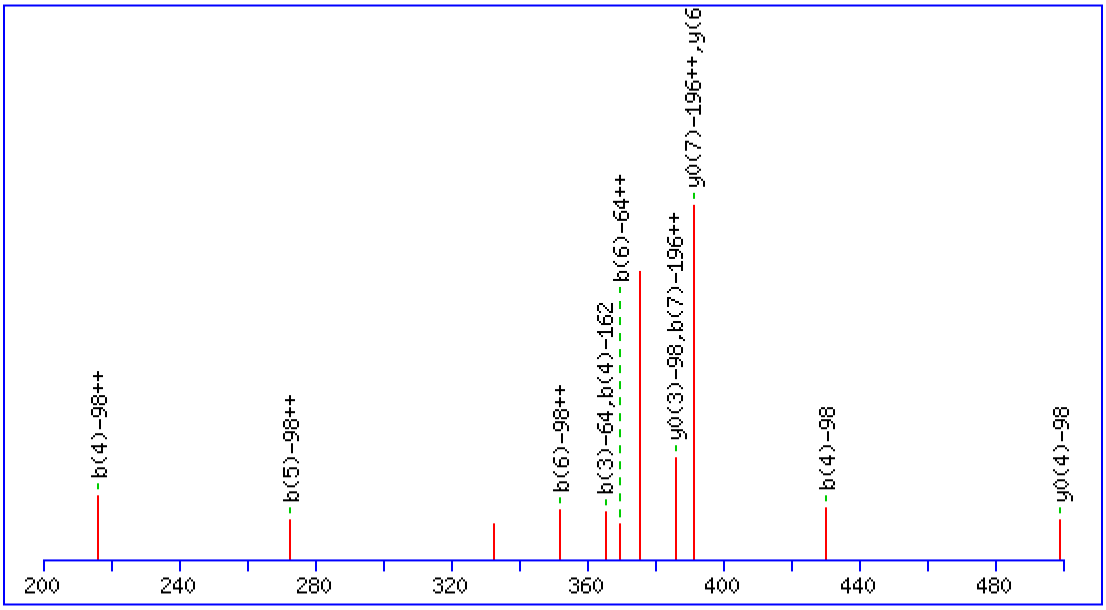
Monoisotopic mass of neutral peptide Mr(calc): 1860.7245
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.046
Matched b ions: b(4), b(10)++, b(11)-98++
Matched y ions: y(4)-98, y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(11)-294++, y(11)-196++, y(12)-98++, y(12)-294++, y(13)++

Peptide No.611

MNSVLCSR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **MNSVLCSR**
Found in **CSMT1_MOUSE** in **SwissProt**, Protein CCSMST1 OS=Mus musculus GN=Ccsmst1 PE=3 SV=1

Match to Query 1406: 1141.368537 from(381.463455,3+) index(3780)
Title: Elution from: 17.085 to 17.085 scan no 895 cid35.00 polarity:+:m1s



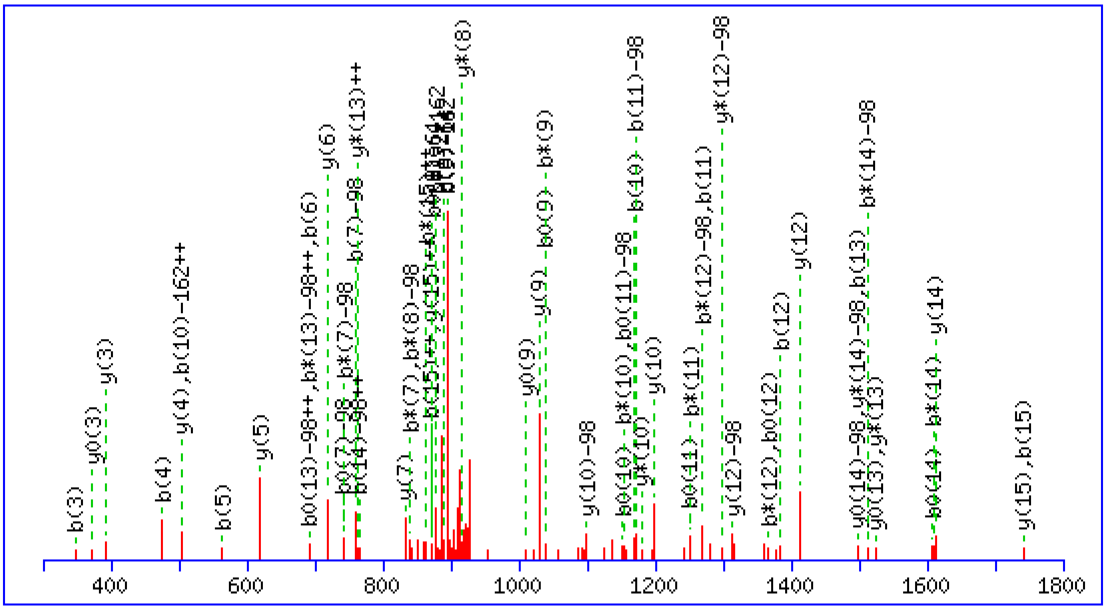
Monoisotopic mass of neutral peptide Mr(calc): 1141.3698
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.0099
Matched b ions: b(4)-98++, b(4)-98, b(5)-98++, b(6)-98++, b(7)-196++
Matched y ions: y(6)-98++

Peptide No.612

MQAESQSPTNVDLEDK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **MQAESQSPTNVDLEDK**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 3874: 1886.756134 from(944.385343,2+) index(3866)
Title: Elution from: 25.979 to 25.979 scan no 1931 cid35.00 polarity:+:m1s



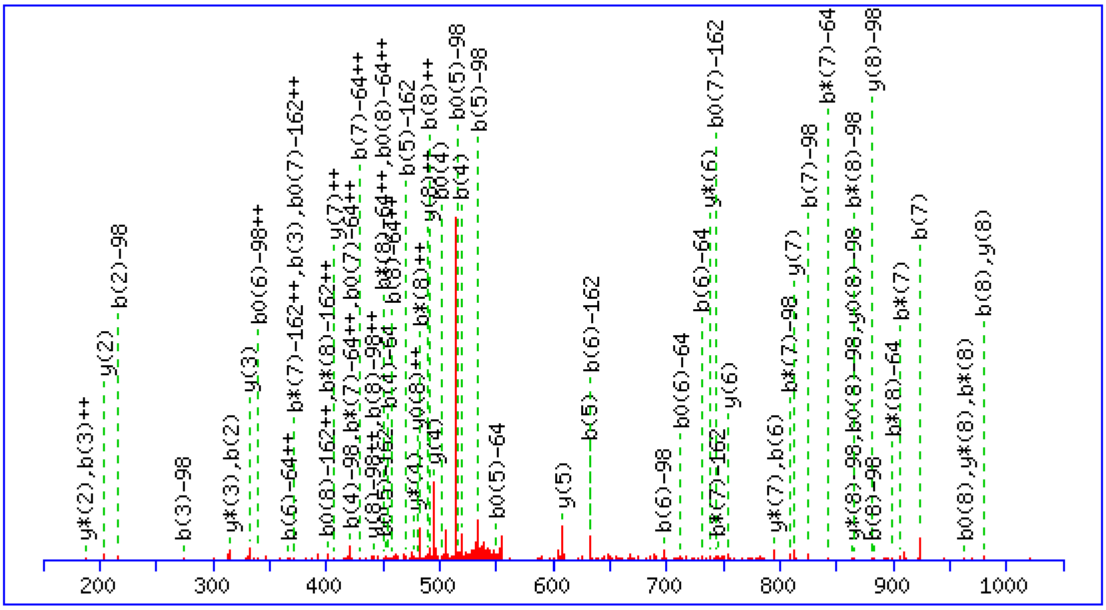
Monoisotopic mass of neutral peptide Mr(calc): 1886.7605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 **Expect:** 2.7e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98, b(10), b(11), b(11)-98, b(12), b(13), b(14)-98++, b(15), b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10)-98, y(10), y(12), y(12)-98, y(14), y(15), y(15)++

Peptide No.613

MSGFIYQGK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **MSGFIYQGK**
Found in **ARHG7_MOUSE** in **SwissProt**, Rho guanine nucleotide exchange factor 7 OS=Mus musculus GN=Arhgef7 PE=1 SV=2

Match to Query 1778: 1125.457180 from(563.735866,2+) index(1501)
Title: Elution from: 39.114 to 39.114 scan no 3024 cid35.00 polarity:+



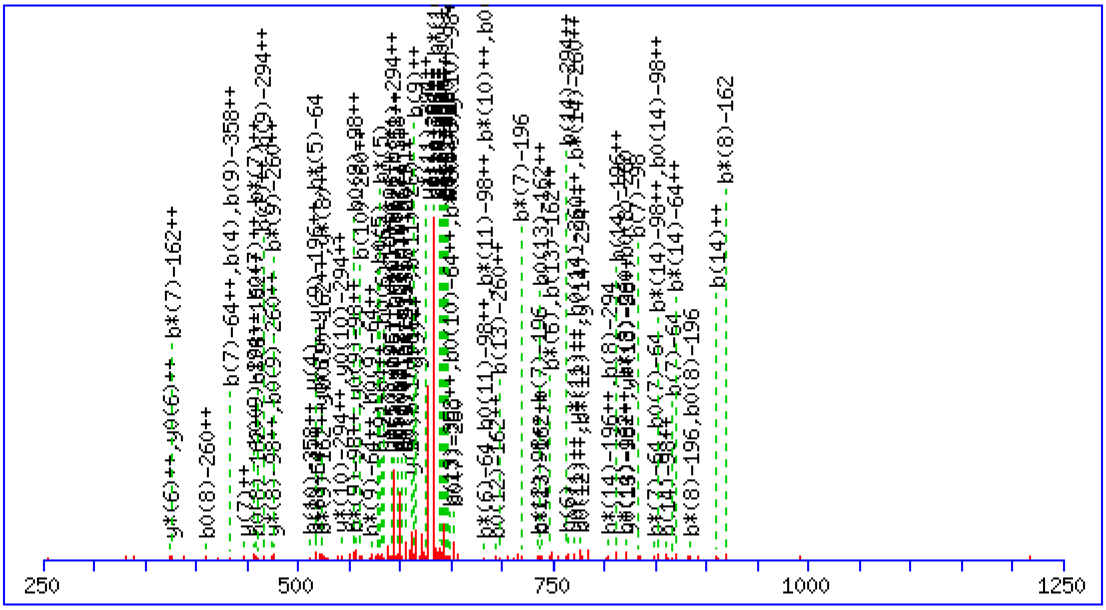
Monoisotopic mass of neutral peptide Mr(calc): 1125.4566
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 **Expect:** 9.9e-005
Matched b ions: b(2)-98, b(2), b(3)-98, b(3)++, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98++, b(8)-98, b(8)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)-98, y(8)-98++, y(8)++

Peptide No.614

MSQAYSSSQRVSSYR
Confirmed sites: @S:6,@S:7,@S:8
Ambiguous sites:

MS/MS Fragmentation of **MSQAYSSSQRVSSYR**
Found in **DESM_MOUSE** in **SwissProt**, Desmin OS=Mus musculus GN=Des PE=1 SV=3

Match to Query 4967: 1991.693178 from(664.905002,3+) index(4292)
Title: Elution from: 21.501 to 21.501 scan no 1477 cid35.00 polarity:+:m1s



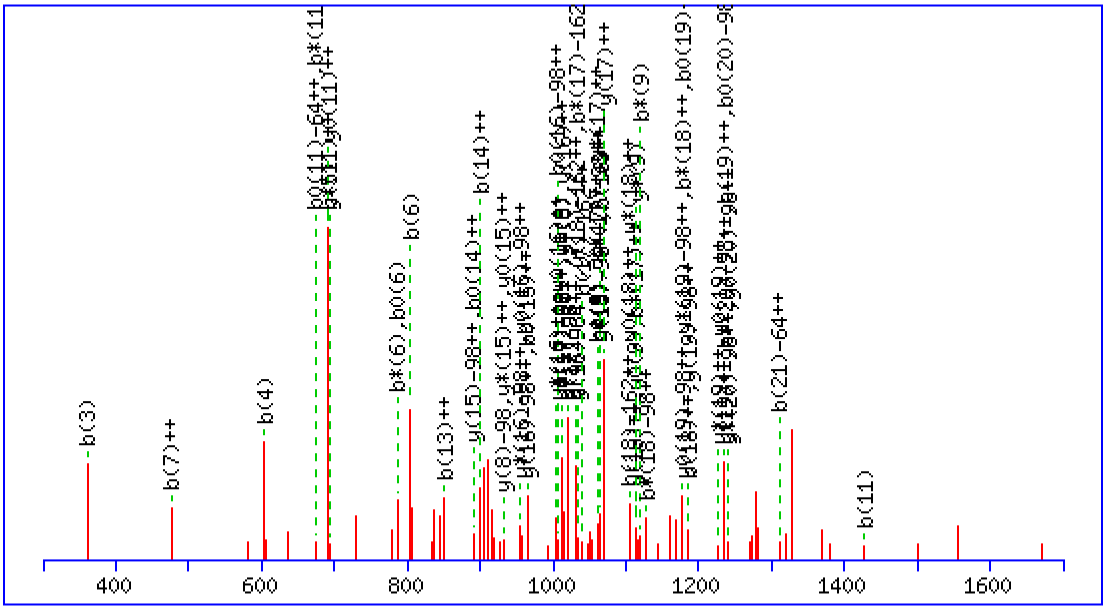
Monoisotopic mass of neutral peptide Mr(calc): 1991.6886
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 **Expect:** 0.047
Matched b ions: b(4), b(5), b(6), b(7)-196, b(7)++, b(7)-98, b(8)-294, b(9)-294++, b(9)++, b(10)-196++, b(10)-98++, b(11)-294++, b(11)-196++, b(12)-98++, b(12)-294++, b(14)-98++, b(14)-196++, b(14)++, b(14)-294++
Matched y ions: y(4), y(5), y(7)++, y(9)-196++, y(9)++, y(10)-196++, y(10)-98++, y(11)-294++, y(14)-294++

Peptide No.615

MTKYSIMQGEYRDTFTIETDPK
Confirmed sites: @Y:4,@T:16
Ambiguous sites:

MS/MS Fragmentation of **MTKYSIMQGEYRDTFTIETDPK**
Found in **CADH5_MOUSE** in **SwissProt**, Cadherin-5 OS=Mus musculus GN=Cdh5 PE=1 SV=2

Match to Query 6596: 2829.164511 from(944.062113,3+) index(6922)
Title: Elution from: 61.377 to 61.377 scan no 6178 cid35.00 polarity:+:m1s



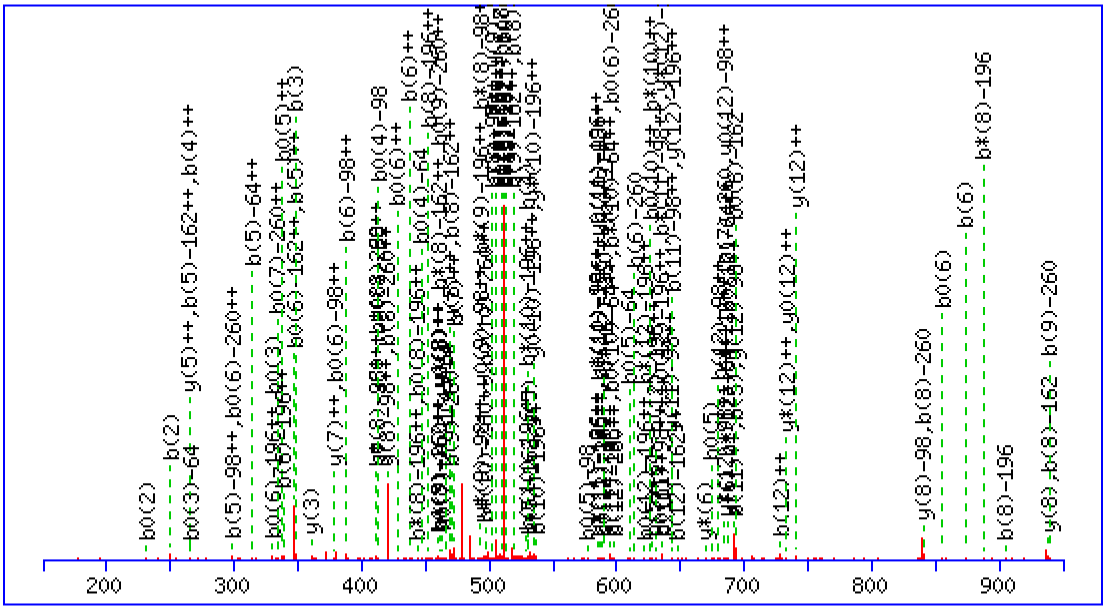
Monoisotopic mass of neutral peptide Mr(calc): 2829.1679
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y4 : Phospho (Y)
M7 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.037
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(11), b(13)++, b(14)++, b(16)++, b(18)++, b(19)++
Matched y ions: y(8)-98, y(9)-98, y(15)-98++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++

Peptide No.616

MTVTYTARVANAR
Confirmed sites: @T:4,@T:6
Ambiguous sites:

MS/MS Fragmentation of **MTVTYTARVANAR**
Found in **BEST2_MOUSE** in **SwissProt**, Bestrophin-2 OS=Mus musculus GN=Best2 PE=2 SV=1

Match to Query 3937: 1628.682954 from(543.901594,3+) index(839)
Title: Elution from: 32.048 to 32.048 scan no 2142 cid35.00 polarity:+



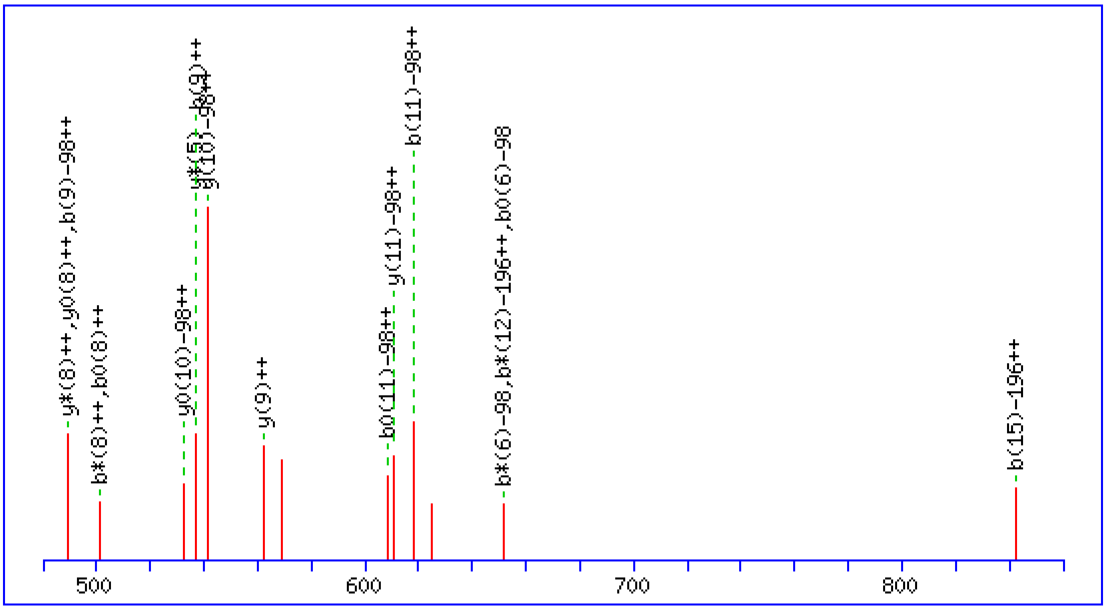
Monoisotopic mass of neutral peptide Mr(calc): 1628.6783
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.028
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)++, b(5), b(5)-98++, b(6)-98++, b(6), b(6)-196++, b(6)++, b(7)++, b(8)-196, b(8)-196++, b(8)-98++, b(9)-196++, b(10)++, b(10)-196++, b(10)-98++, b(11)-196++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(12)-196++
Matched y ions: y(3), y(5)++, y(5), y(6), y(7)++, y(8)-98++, y(8)-98, y(8), y(8)++, y(9)-98++, y(11)-98++, y(12)-98++, y(12)++, y(12)-196++

Peptide No.617

MVKATRLHGEETMPHSGR
Confirmed sites: @T:5,@T:12
Ambiguous sites:

MS/MS Fragmentation of **MVKATRLHGEETMPHSGR**
Found in **KCNH7_MOUSE** in **SwissProt**, Potassium voltage-gated channel subfamily H member 7 OS=Mus musculus GN=Kcnh7 PE=2 SV=2

Match to Query 5747: 2195.939316 from(549.992105,4+) index(6211)
Title: Elution from: 40.509 to 40.509 scan no 4032 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2195.9370

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

T12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 27 **Expect:** 0.012

Matched b ions: b(9)-98++, b(9)++, b(11)-98++, b(15)-196++

Matched y ions: y(9)++, y(10)-98++, y(11)-98++

Peptide No.618

NASVPNLR

Confirmed sites: @S:3

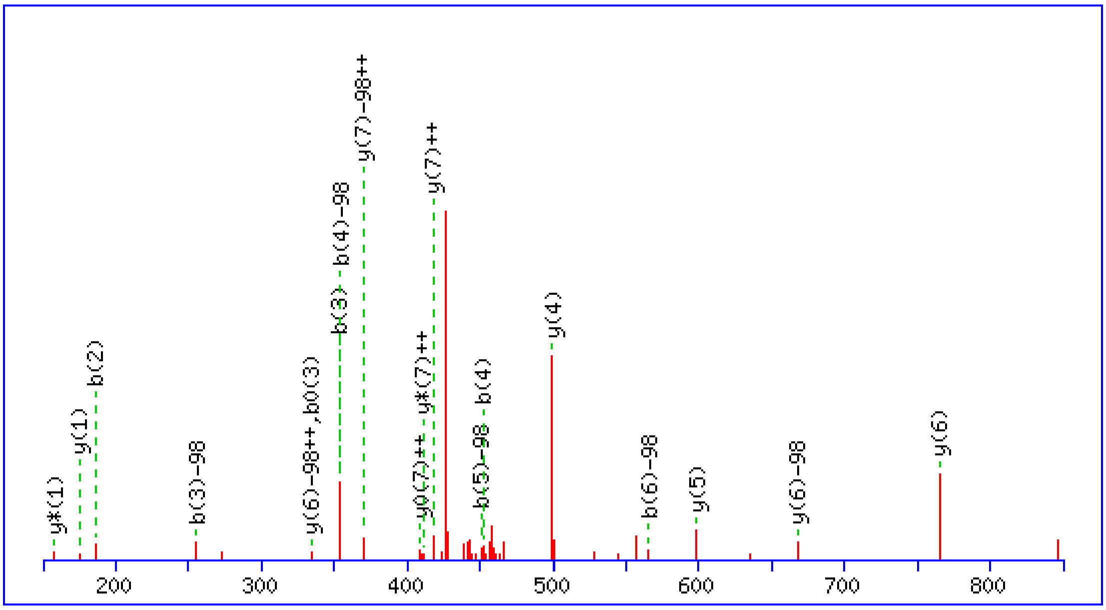
Ambiguous sites:

MS/MS Fragmentation of **NASVPNLR**

Found in **FA54B_MOUSE** in **SwissProt**, Protein FAM54B OS=Mus musculus GN=Fam54b PE=1 SV=1

Match to Query 798: 949.438094 from(475.726323,2+) index(1138)

Title: Elution from: 25.812 to 25.812 scan no 2063 cid35.00 polarity:+



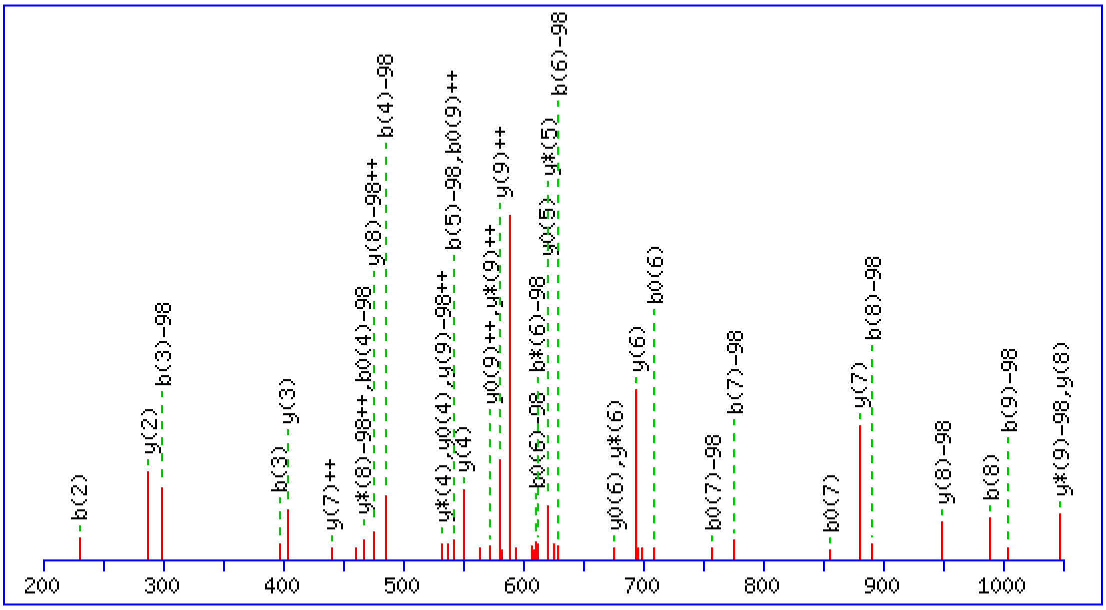
Monoisotopic mass of neutral peptide Mr(calc): 949.4382
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0017
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(6)-98
Matched y ions: y(1), y(4), y(5), y(6)-98, y(6), y(6)-98++, y(7)++, y(7)-98++

Peptide No.619

NDSWGSFDLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NDSWGSFDLR**
Found in **NUFP2_MOUSE** in **SwissProt**, Nuclear fragile X mental retardation-interacting protein 2 OS=Mus musculus GN=Nufip2 PE=1 SV=1

Match to Query 1856: 1275.492558 from(638.753555,2+) index(3110)
Title: Elution from: 50.226 to 50.226 scan no 5165 cid35.00 polarity:+



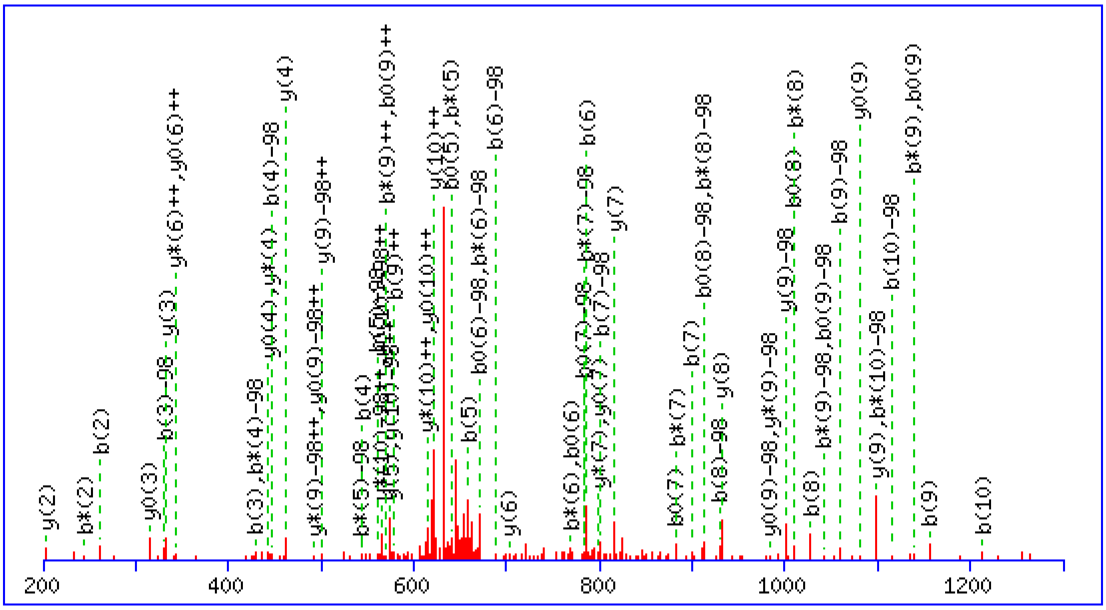
Monoisotopic mass of neutral peptide Mr(calc): 1275.4921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 **Expect:** 9.2e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(6)-98, b(7)-98, b(8), b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)++, y(8), y(8)-98++, y(8)-98, y(9)++, y(9)-98++

Peptide No.620

NFSDNQLQEGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NFSDNQLQEGK**
Found in **TAGL2_MOUSE** in **SwissProt**, Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4

Match to Query 2655: 1358.550504 from(680.282528,2+) index(898)
Title: Elution from: 34.461 to 34.461 scan no 2332 cid35.00 polarity:+



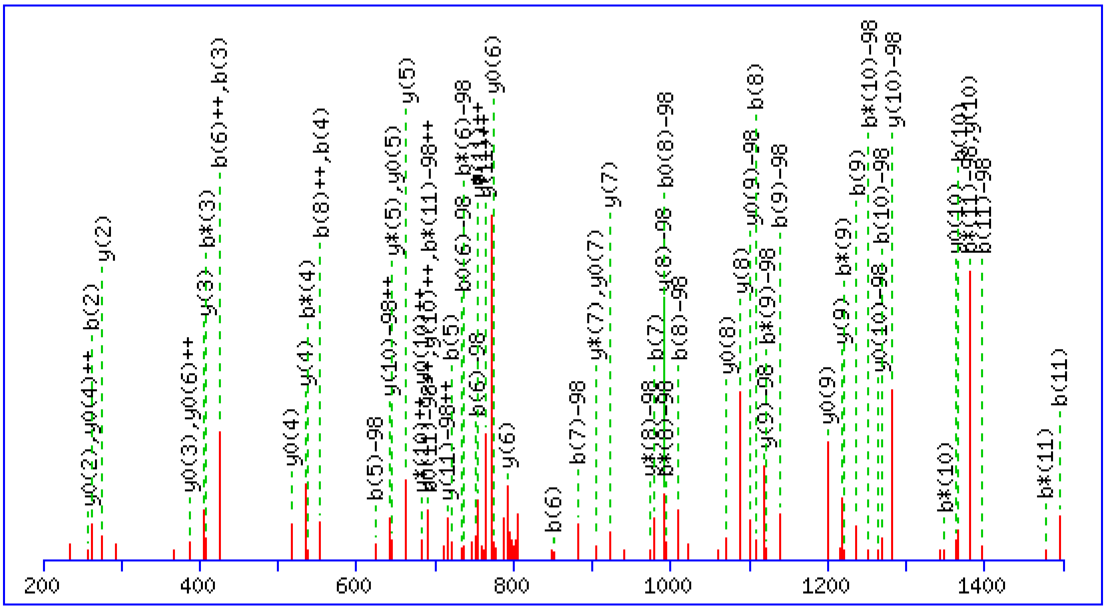
Monoisotopic mass of neutral peptide Mr(calc): 1358.5504
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 6.4e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)++, b(9)-98, b(10), b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98, y(9)-98++, y(10)-98++, y(10)++

Peptide No.621

NFYESEEEEEEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **NFYESEEEEEEK**
Found in **AP3B1_MOUSE** in **SwissProt**, AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=2

Match to Query 3560: 1640.572642 from(821.293597,2+) index(1601)
Title: Elution from: 30.462 to 30.462 scan no 2699 cid35.00 polarity:+



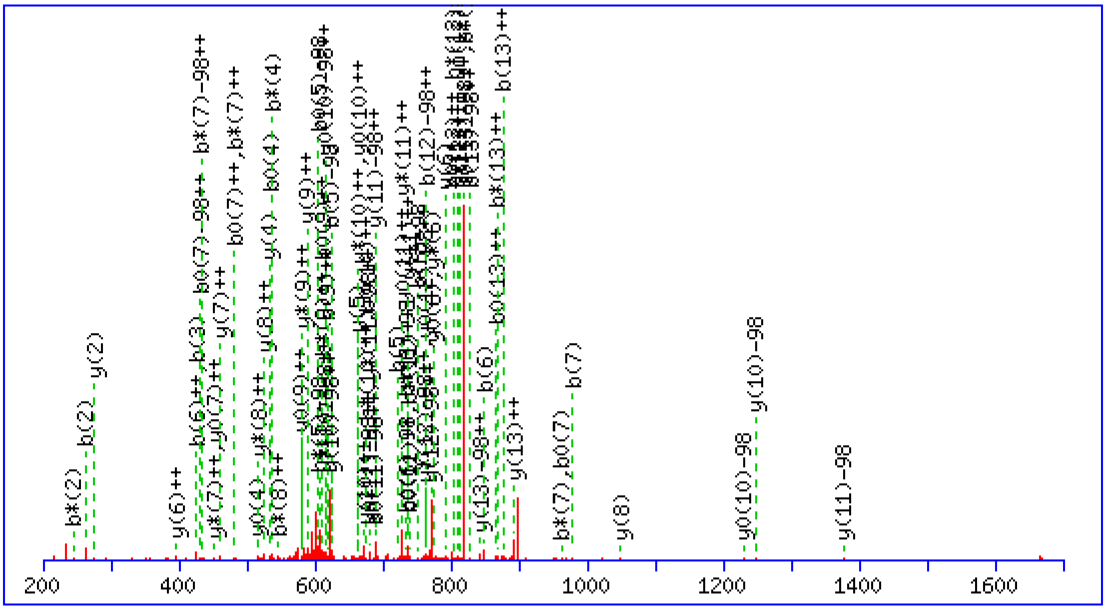
Monoisotopic mass of neutral peptide Mr(calc): 1640.5766
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 **Expect:** 1.1e-007
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)++, b(6), b(6)-98, b(7)-98, b(7), b(8)++, b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.622

NFYESEEEEEEKEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **NFYESEEEEEEKEK**
Found in **AP3B1_MOUSE** in **SwissProt**, AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=2

Match to Query 4146: 1897.714938 from(633.578922,3+) index(1034)
Title: Elution from: 35.904 to 35.904 scan no 2509 cid35.00 polarity:+



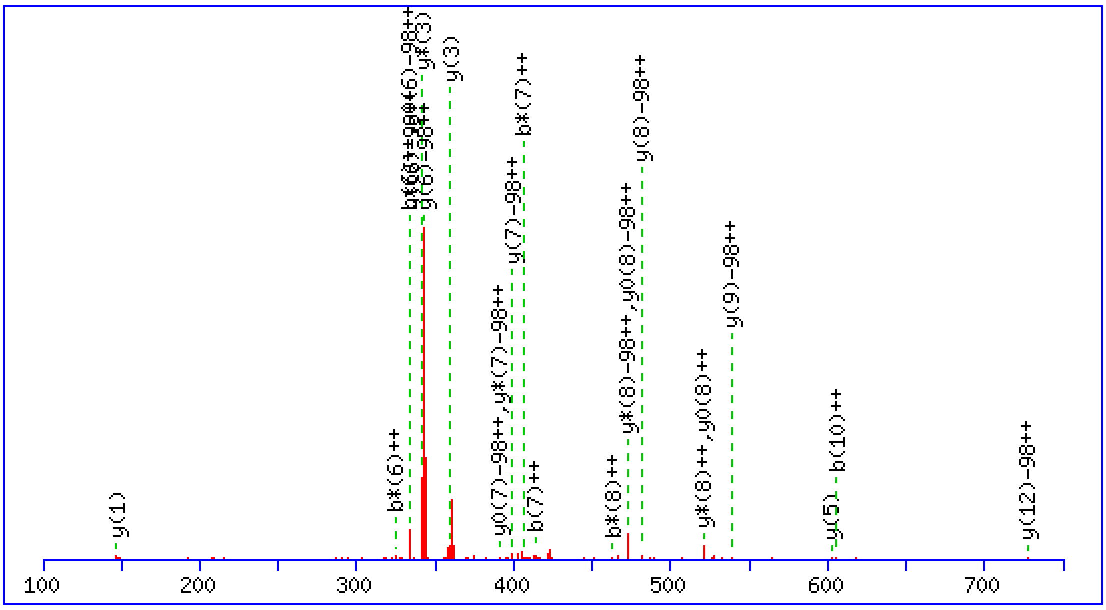
Monoisotopic mass of neutral peptide Mr(calc): 1897.7142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.027
Matched b ions: b(2), b(3), b(5)-98, b(5), b(6)++, b(6), b(6)-98, b(7), b(9)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7)++, y(8), y(8)++, y(9)++, y(10)-98, y(10)++, y(10)-98++, y(11)-98, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.623

NGCYGIYITSRVLK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **NGCYGIYITSRVLK**
Found in **FREM1_MOUSE** in **SwissProt**, FRAS1-related extracellular matrix protein 1 OS=Mus musculus GN=Frem1 PE=1 SV=1

Match to Query 4266: 1722.814408 from(431.710878,4+) index(3470)
Title: Elution from: 22.247 to 22.247 scan no 1050 cid35.00 polarity:+:m1s



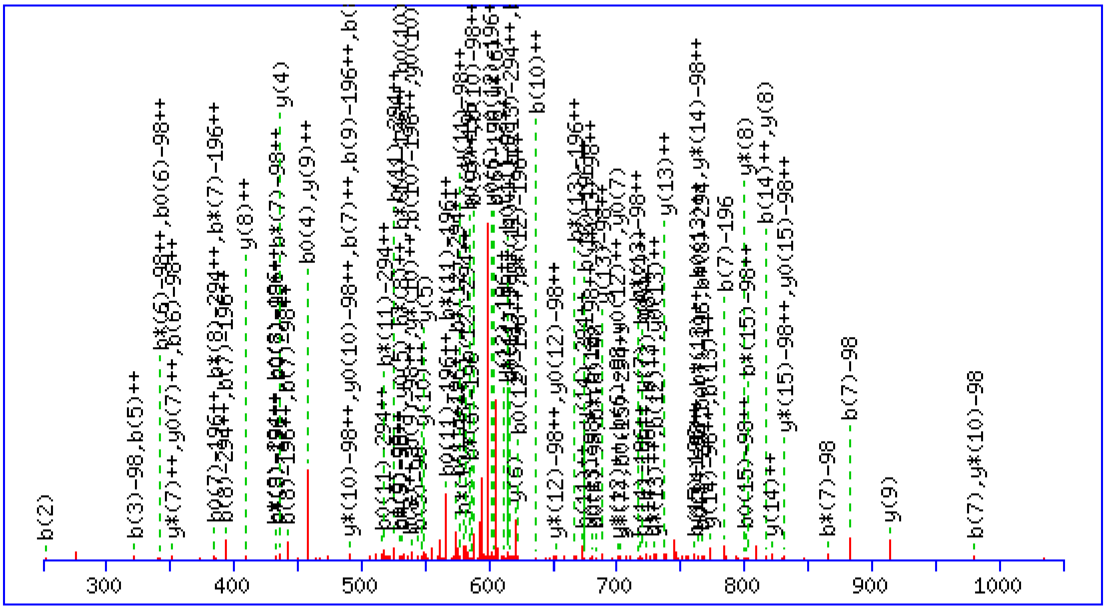
Monoisotopic mass of neutral peptide Mr(calc): 1722.8164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.045
Matched b ions: b(6)++, b(7)++, b(10)++
Matched y ions: y(1), y(3), y(5), y(6)-98++, y(7)-98++, y(8)-98++, y(9)-98++, y(12)-98++

Peptide No.624

NHSGSRTPPVALSSSR
Confirmed sites: @S:3,@S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of **NHSGSRTPPVALSSSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4553: 1891.735653 from(631.585827,3+) index(995)
Title: Elution from: 24.554 to 24.554 scan no 1892 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1891.7380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.048
Matched b ions: b(2), b(3)-98, b(5)++, b(5)-98, b(6)-98++, b(6)-196, b(6)-98, b(7)-196++, b(7)-98, b(7), b(7)-98++, b(7)-196, b(7)++, b(8)-294++, b(8)-196++, b(8)++, b(8)-98++, b(9)-98++, b(9)-196++, b(9)++, b(10)-196++, b(10)-294++, b(10)-98++, b(10)++, b(11)-294++, b(11)++, b(11)-196++, b(12)++, b(12)-294++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-196++, b(15)-196++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)-98++, y(12)-196++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(14)-196++, y(14)-294++

Peptide No.625

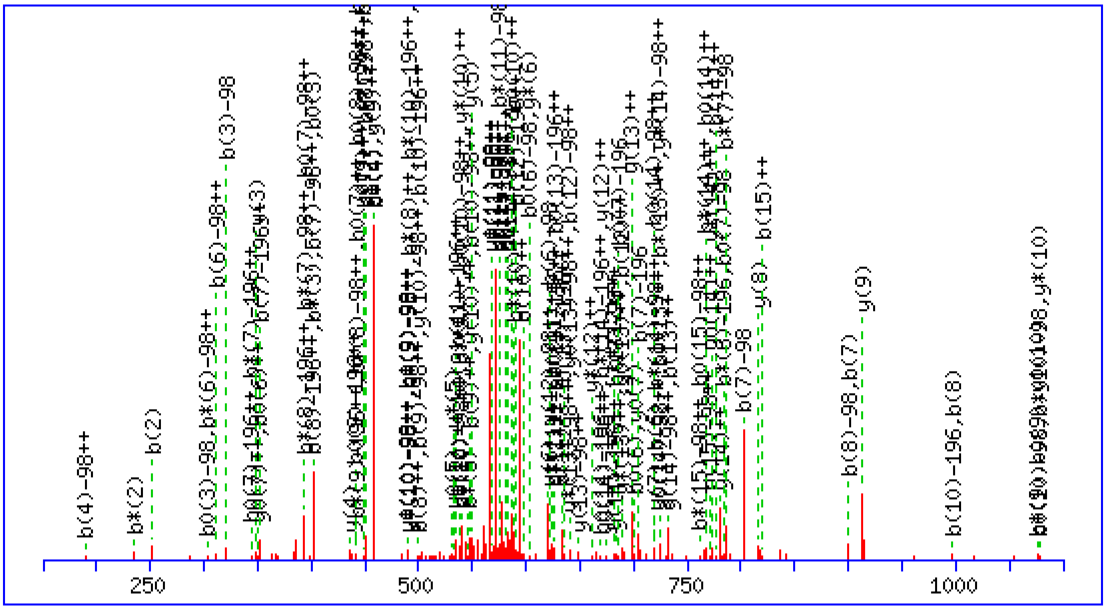
NHSGSRTPPVALSSSR

Confirmed sites: @S:3,@T:7

Ambiguous sites:

MS/MS Fragmentation of **NHSGSRTPPVALSSSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3960: 1811.772588 from(604.931472,3+) index(406)
Title: Elution from: 28.572 to 28.572 scan no 1640 cid35.00 polarity:+



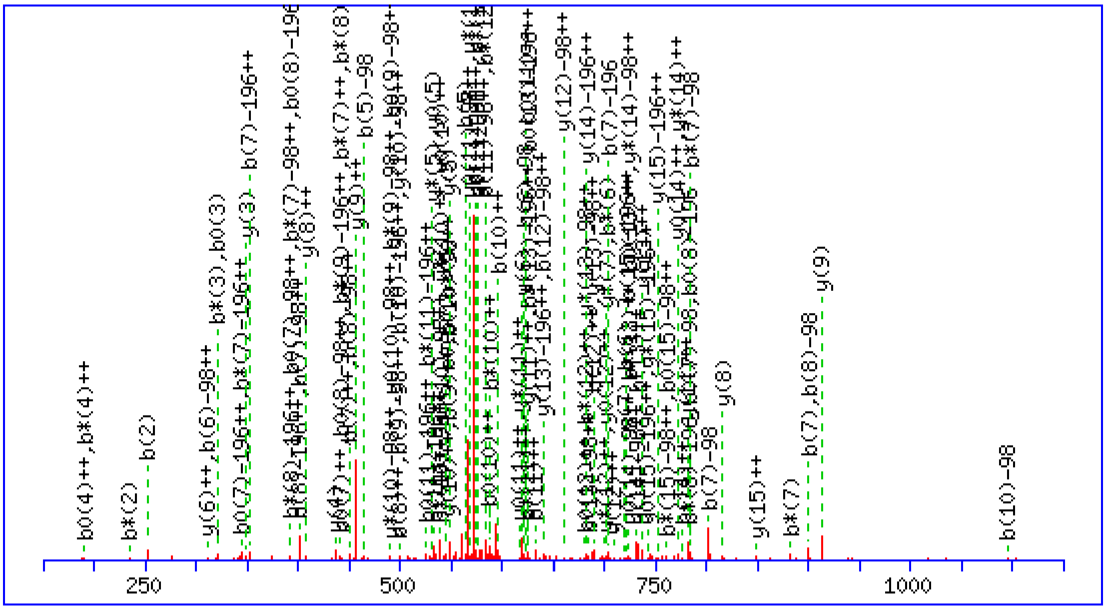
Monoisotopic mass of neutral peptide Mr(calc): 1811.7717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0068
Matched b ions: b(2), b(3)-98, b(4)-98++, b(6)-98++, b(6)-98, b(6), b(7)-196++, b(7)-98, b(7)-98++, b(7), b(7)++, b(7)-196, b(8), b(8)-196++, b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-196, b(10)-98++, b(10)-196++, b(10)++, b(11)++, b(11)-98++, b(11)-196++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-196++, b(13)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(14)-196++

Peptide No.626

NHSGSRTPPVALSSSR
Confirmed sites: @S:5,@T:7
Ambiguous sites:

MS/MS Fragmentation of **NHSGSRTPPVALSSSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3959: 1811.771469 from(604.931099,3+) index(382)
Title: Elution from: 28.195 to 28.195 scan no 1600 cid35.00 polarity:+



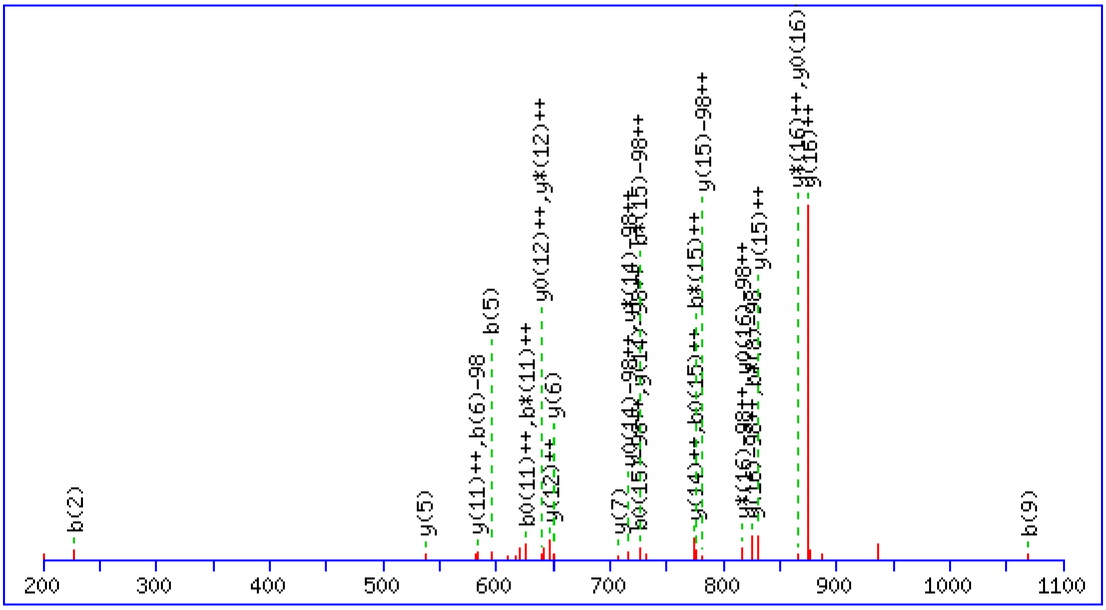
Monoisotopic mass of neutral peptide Mr(calc): 1811.7717
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.017
Matched b ions: b(2), b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(7)-196++, b(7)-98, b(7)-98++, b(7), b(7)++, b(7)-196, b(8)-196++, b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98, b(10)-98++, b(10)++, b(10)-196++, b(11)-98++, b(11)++, b(11)-196++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(15)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(13)-196++, y(14)++, y(14)-98++, y(14)-196++, y(15)++, y(15)-196++

Peptide No.627

NISLSSEEEAEGLAGHPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **NISLSSEEEAEGLAGHPR**
Found in **PARF_MOUSE** in **SwissProt**, Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2

Match to Query 4909: 1974.867549 from(659.296459,3+) index(5850)
Title: Elution from: 36.390 to 36.390 scan no 3492 cid35.00 polarity:+:m1s



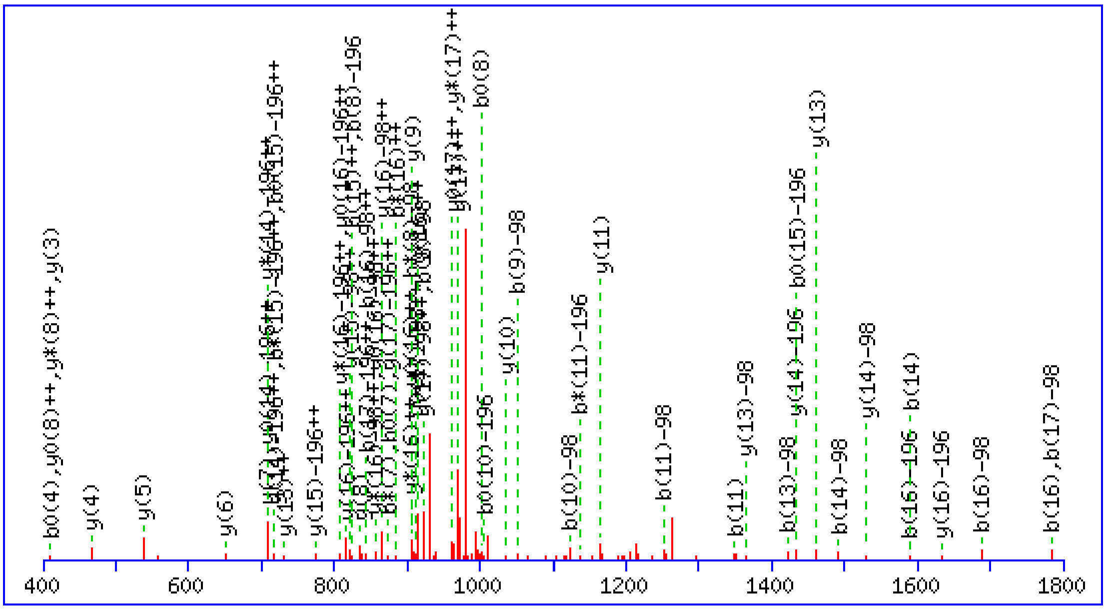
Monoisotopic mass of neutral peptide Mr(calc): 1974.8684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0067
Matched b ions: b(2), b(5), b(6)-98, b(9)
Matched y ions: y(5), y(6), y(7), y(11)++, y(12)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.628

NISLSSEEEAEGLAGHPR
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of **NISLSSEEEAEGLAGHPR**
Found in **PARF_MOUSE** in **SwissProt**, Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2

Match to Query 5158: 2054.833334 from(1028.423943,2+) index(6292)
Title: Elution from: 41.637 to 41.637 scan no 4181 cid35.00 polarity:+:m1s



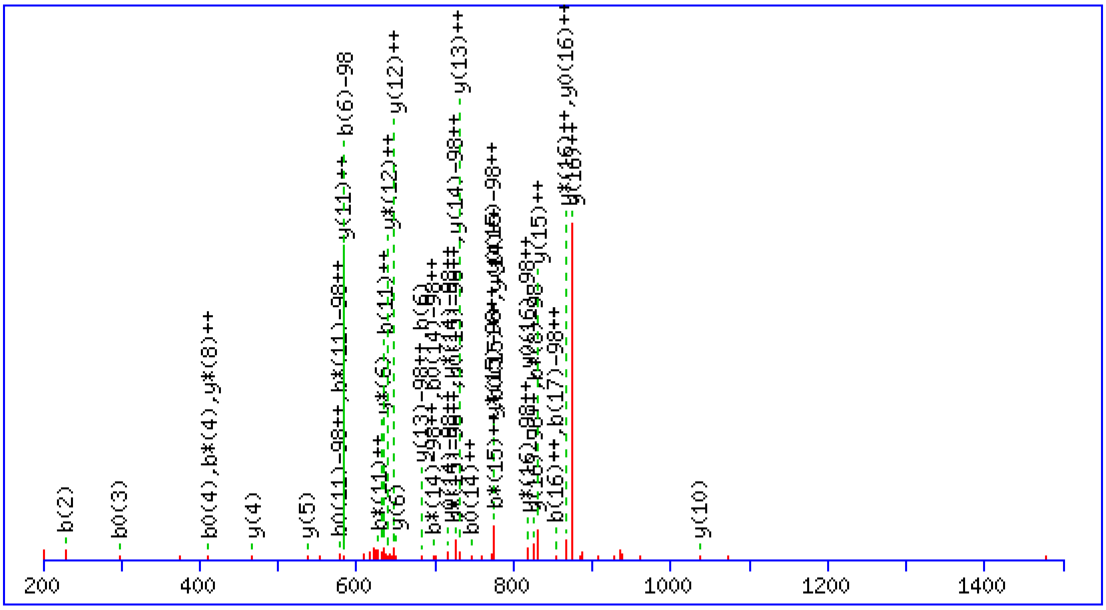
Monoisotopic mass of neutral peptide Mr(calc): 2054.8347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 **Expect:** 9.1e-006
Matched b ions: b(8)-98, b(8)-196, b(9)-98, b(10)-98, b(11), b(11)-98, b(13)-98, b(14), b(14)-98, b(15)++, b(16)-98, b(16), b(16)-196, b(16)-98++, b(17)-98, b(17)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(13)-98, y(13)++, y(14)-196, y(14)-98, y(14)-196++, y(15)-196++, y(15)-98++, y(16)-98++, y(16)-196++, y(16)-196, y(16)++, y(17)++, y(17)-98++, y(17)-196++

Peptide No.629

NISLSSEEEAEGLAGHPR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **NISLSSEEEAEGLAGHPR**
Found in **PARF_MOUSE** in **SwissProt**, Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2

Match to Query 4774: 1974.867006 from(659.296278,3+) index(5694)
Title: Elution from: 36.464 to 36.464 scan no 3472 cid35.00 polarity:+:m1s



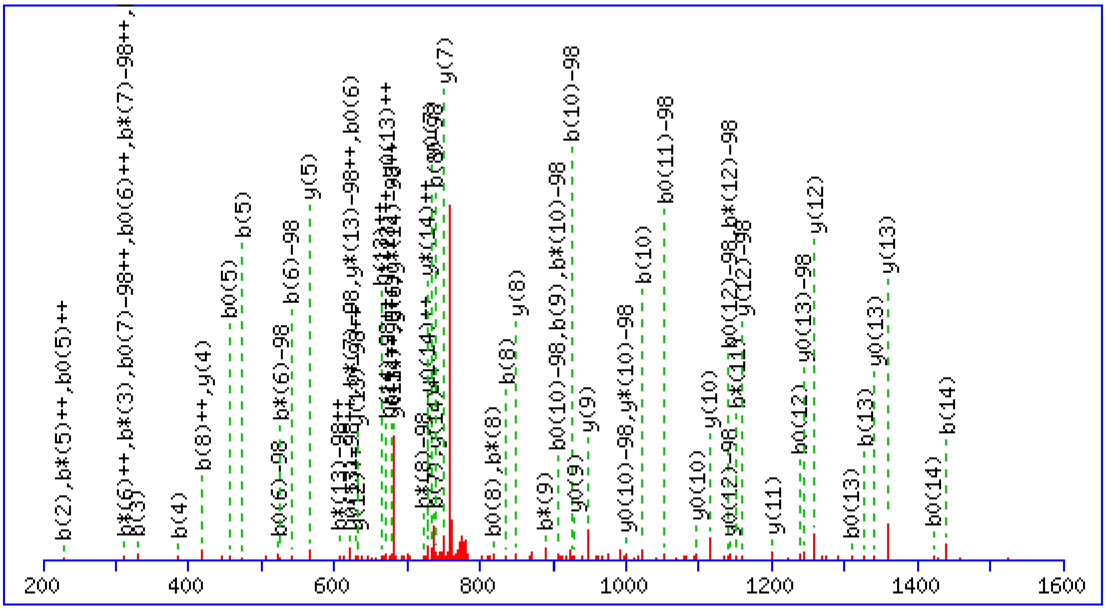
Monoisotopic mass of neutral peptide Mr(calc): 1974.8684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.041
Matched b ions: b(2), b(6)-98, b(6), b(11)++, b(16)++, b(17)-98++
Matched y ions: y(4), y(5), y(6), y(10), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.630

NITGSSPVADFSAIK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **NITGSSPVADFSAIK**
Found in **EPS15_MOUSE** in **SwissProt**, Epidermal growth factor receptor substrate 15 OS=Mus musculus GN=Eps15 PE=1 SV=1

Match to Query 3804: 1585.739468 from(793.877010,2+) index(2383)
Title: Elution from: 55.261 to 55.261 scan no 4643 cid35.00 polarity:+



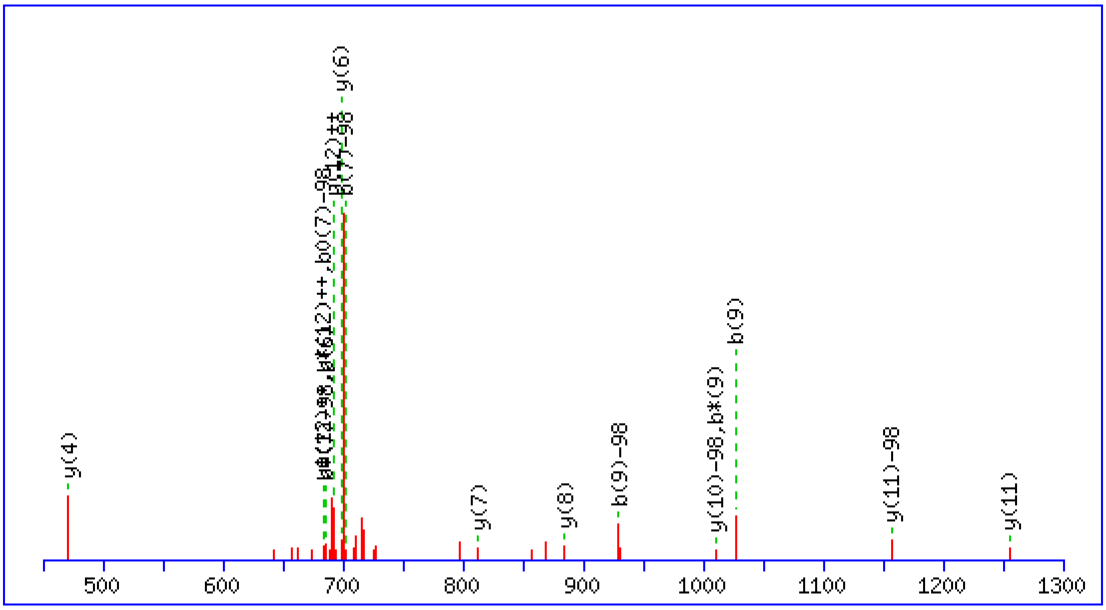
Monoisotopic mass of neutral peptide Mr(calc): 1585.7389
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(10), b(10)-98, b(13), b(13)++, b(14), b(14)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)-98, y(12)++, y(13)++, y(13), y(13)-98++, y(14)++

Peptide No.631

NKFGSADNIPNLK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **NKFGSADNIPNLK**
Found in **TMCC1_MOUSE** in **SwissProt**, Transmembrane and coiled-coil domains protein 1 OS=Mus musculus GN=Tmcc1 PE=1 SV=2

Match to Query 2961: 1496.702456 from(749.358504,2+) index(1880)
Title: Elution from: 33.227 to 33.227 scan no 3070 cid35.00 polarity:+



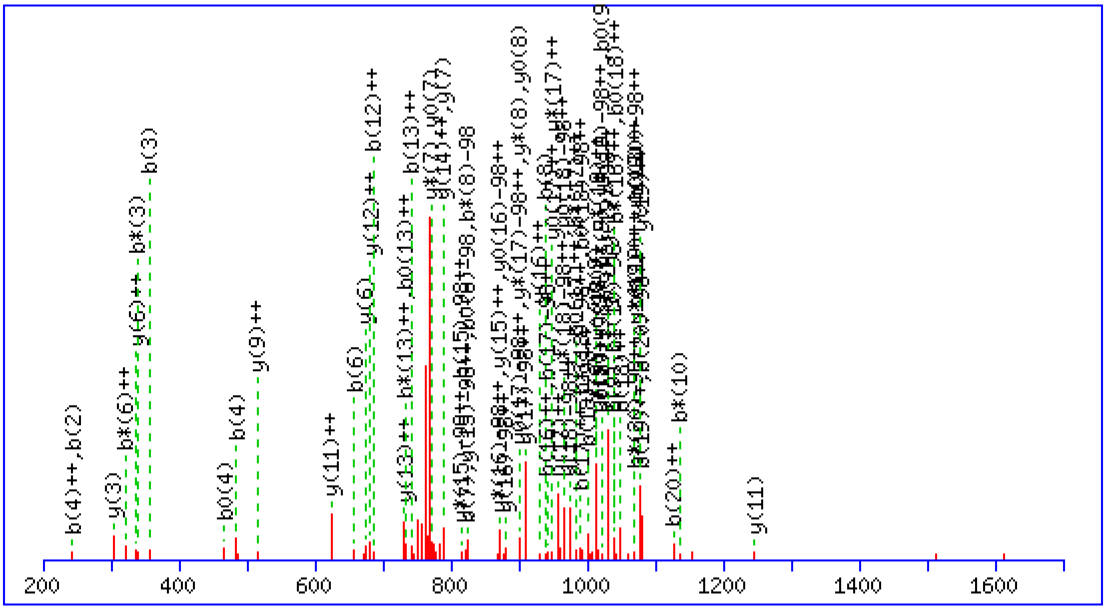
Monoisotopic mass of neutral peptide Mr(calc): 1496.7024
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0088
Matched b ions: b(6), b(7)-98, b(9)-98, b(9)
Matched y ions: y(4), y(6), y(7), y(8), y(10)-98, y(11)-98, y(11), y(12)++

Peptide No.632

NKLEGDSDVDSELEDRVDGVK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **NKLEGDSDVDSELEDRVDGVK**
Found in **MY18A_MOUSE** in **SwissProt**, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 5070: 2398.054494 from(800.358774,3+) index(5087)
Title: Elution from: 39.341 to 39.341 scan no 3723 cid35.00 polarity:+:m1s



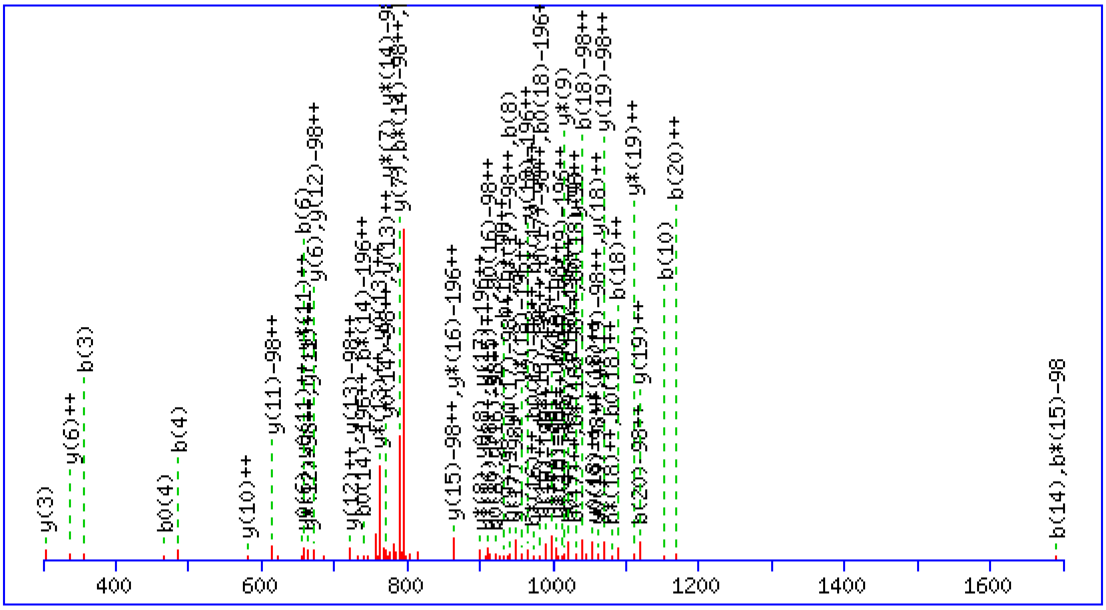
Monoisotopic mass of neutral peptide Mr(calc): 2398.0537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 **Expect:** 5.4e-006
Matched b ions: b(2), b(3), b(4), b(4)++, b(6), b(7), b(8), b(9), b(12)++, b(13)++, b(15)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(20)-98++
Matched y ions: y(3), y(6)++, y(6), y(7), y(9), y(9)++, y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++

Peptide No.633

NKLEGDSDVDSELEDRVDGVK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of **NKLEGDSDVDSELEDRVDGVK**
Found in **MY18A_MOUSE** in **SwissProt**, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 6328: 2478.020094 from(827.013974,3+) index(6357)
Title: Elution from: 42.416 to 42.416 scan no 4283 cid35.00 polarity:+:m1s



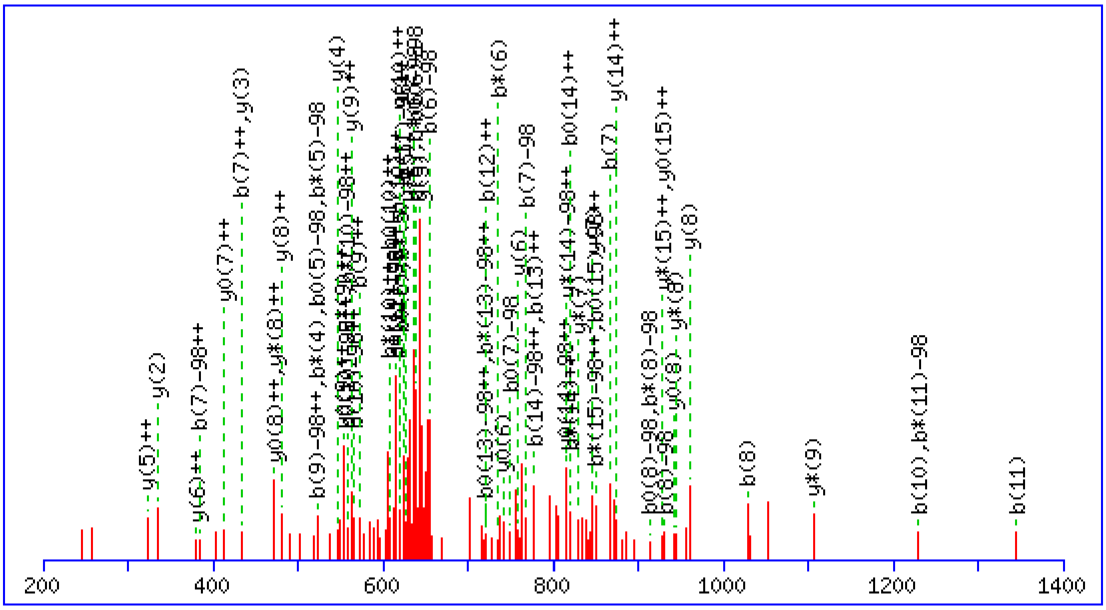
Monoisotopic mass of neutral peptide Mr(calc): 2478.0200
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0012
Matched b ions: b(3), b(4), b(6), b(8), b(9)-98, b(10), b(14), b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)-196++, b(18)++, b(20)-98++, b(20)++
Matched y ions: y(3), y(6)++, y(6), y(7), y(9), y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(15)-98++, y(15)++, y(16)-98++, y(17)++, y(17)-196++, y(17)-98++, y(18)-196++, y(18)++, y(19)++, y(19)-196++, y(19)-98++

Peptide No.634

NKSEVDLYNSDPLVCR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NKSEVDLYNSDPLVCR**
Found in **MGLL_MOUSE** in **SwissProt**, Monoglyceride lipase OS=Mus musculus GN=Mgll PE=1 SV=1

Match to Query 4416: 1987.871580 from(663.631136,3+) index(1856)
Title: Elution from: 50.100 to 50.100 scan no 3959 cid35.00 polarity:+



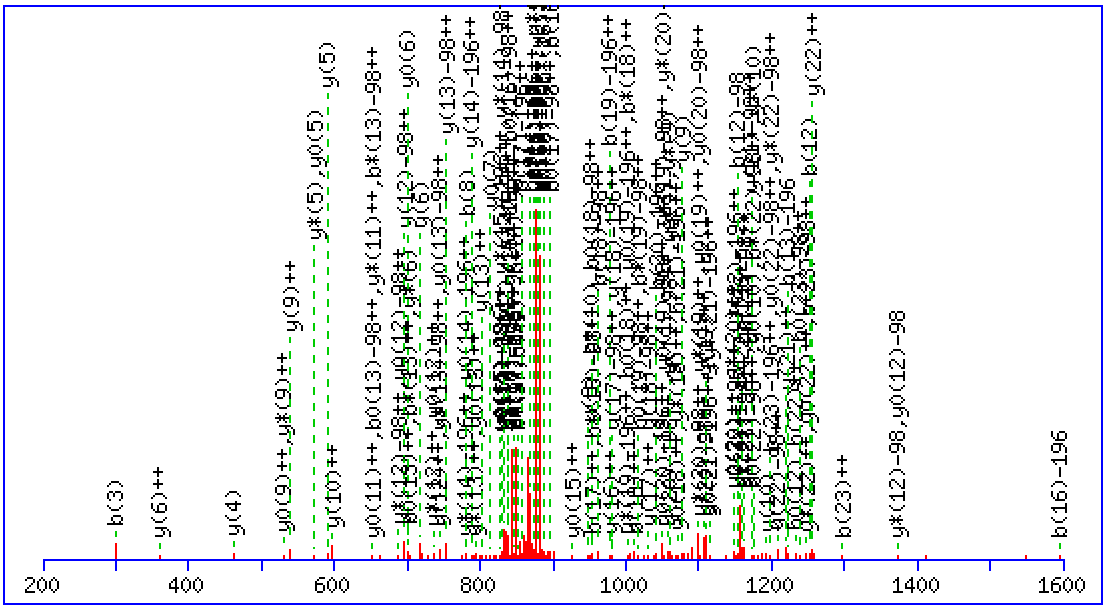
Monoisotopic mass of neutral peptide Mr(calc): 1987.8710
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.015
Matched b ions: b(5), b(6)-98, b(7), b(7)++, b(7)-98++, b(7)-98, b(8), b(8)-98, b(9)-98++, b(9)++, b(10), b(10)-98++, b(10)++, b(11), b(11)-98++, b(12)++, b(13)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6), y(7), y(8), y(8)++, y(9)++, y(10)++, y(14)++

Peptide No.635

NLAKPGVTSTSTSDSEDEDDQEGEKK
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of **NLAKPGVTSTSTSDSEDEDDQEGEKK**
Found in **PSIP1_MOUSE** in **SwissProt**, PC4 and SFRS1-interacting protein OS=Mus musculus GN=Psip1 PE=1 SV=1

Match to Query 5677: 2738.076708 from(913.699512,3+) index(3593)
Title: Elution from: 21.356 to 21.356 scan no 1400 cid35.00 polarity:+:m1s



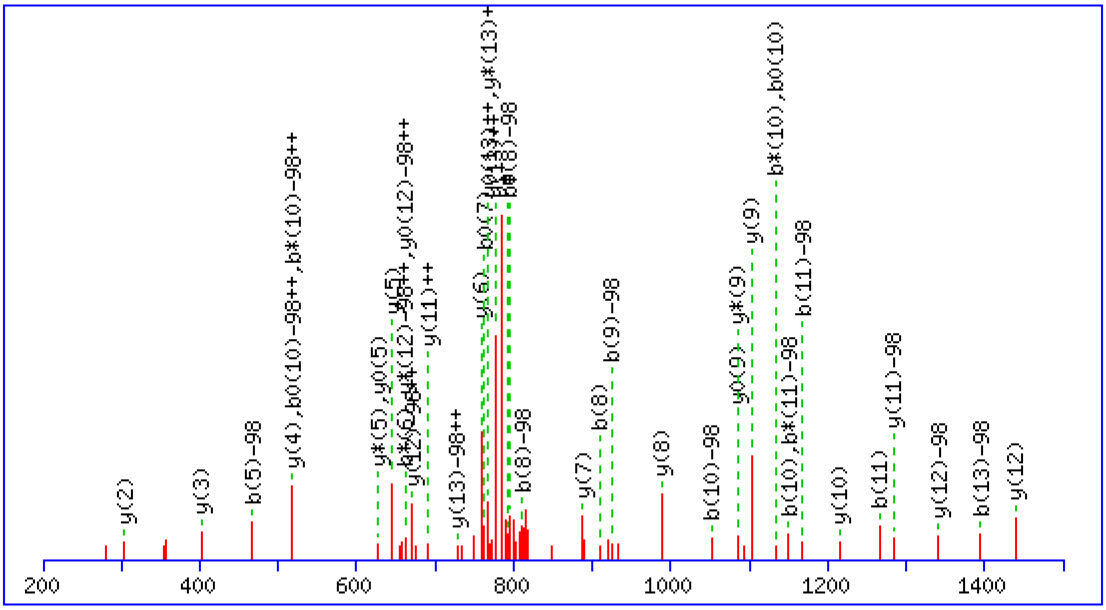
Monoisotopic mass of neutral peptide Mr(calc): 2738.0845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 0.00011
Matched b ions: b(3), b(8), b(9), b(12), b(12)-98, b(13)-196, b(15)++, b(16)-196, b(16)-98++, b(16)++, b(17)++, b(17)-196++, b(18)-98++, b(18)++, b(19)-196++, b(20)-196++, b(21)-196++, b(22)++, b(23)-98++, b(23)++, b(23)-196++
Matched y ions: y(4), y(5), y(6), y(6)++, y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)-98++, y(16)-196++, y(16)++, y(17)-98++, y(17)++, y(18)-196++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(20)-196++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(22)-196++

Peptide No.636

NLGSINTELQDVQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **NLGSINTELQDVQR**
Found in **SC22B_MOUSE** in **SwissProt**, Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3

Match to Query 3041: 1665.771392 from(833.892972,2+) index(2575)
Title: Elution from: 45.312 to 45.312 scan no 4422 cid35.00 polarity:+



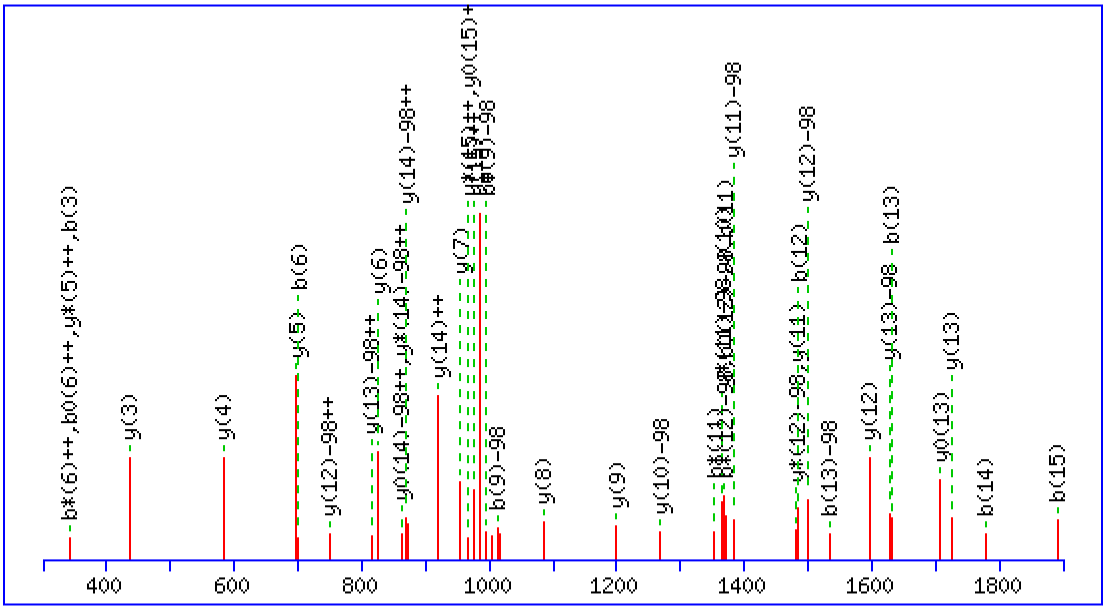
Monoisotopic mass of neutral peptide Mr(calc): 1665.7723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 98 **Expect:** 1e-009
Matched b ions: b(5)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(13)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11)++, y(12)-98, y(12), y(12)-98++, y(13)++, y(13)-98++

Peptide No.637

NLLEDDSDEEEDFFLR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **NLLEDDSDEEEDFFLR**
Found in **VAMP4_MOUSE** in **SwissProt**, Vesicle-associated membrane protein 4 OS=Mus musculus GN=Vamp4 PE=1 SV=1

Match to Query 5054: 2064.816524 from(1033.415538,2+) index(6963)
Title: Elution from: 64.845 to 64.845 scan no 6421 cid35.00 polarity:+:m1s



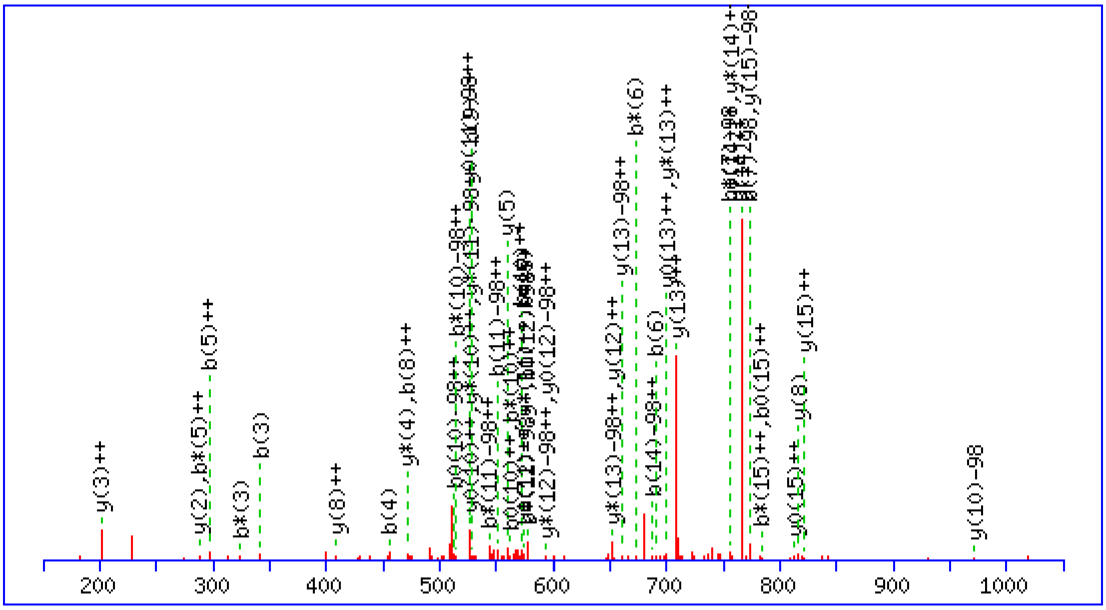
Monoisotopic mass of neutral peptide Mr(calc): 2064.8201
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 **Expect:** 2.2e-008
Matched b ions: b(3), b(6), b(9)-98, b(11), b(12), b(13), b(13)-98, b(14), b(15)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98, y(10), y(11), y(11)-98, y(12)-98, y(12), y(12)-98++, y(13)-98++, y(13)-98, y(13), y(14)++, y(14)-98++, y(15)++

Peptide No.638

NLLNHPTANSGASILR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **NLLNHPTANSGASILR**
Found in **FOLC_MOUSE** in **SwissProt**, Folylpolyglutamate synthase, mitochondrial OS=Mus musculus GN=Fpgs PE=1 SV=3

Match to Query 4423: 1756.856856 from(586.626228,3+) index(5809)
Title: Elution from: 55.512 to 55.512 scan no 4668 cid35.00 polarity:+:m1s



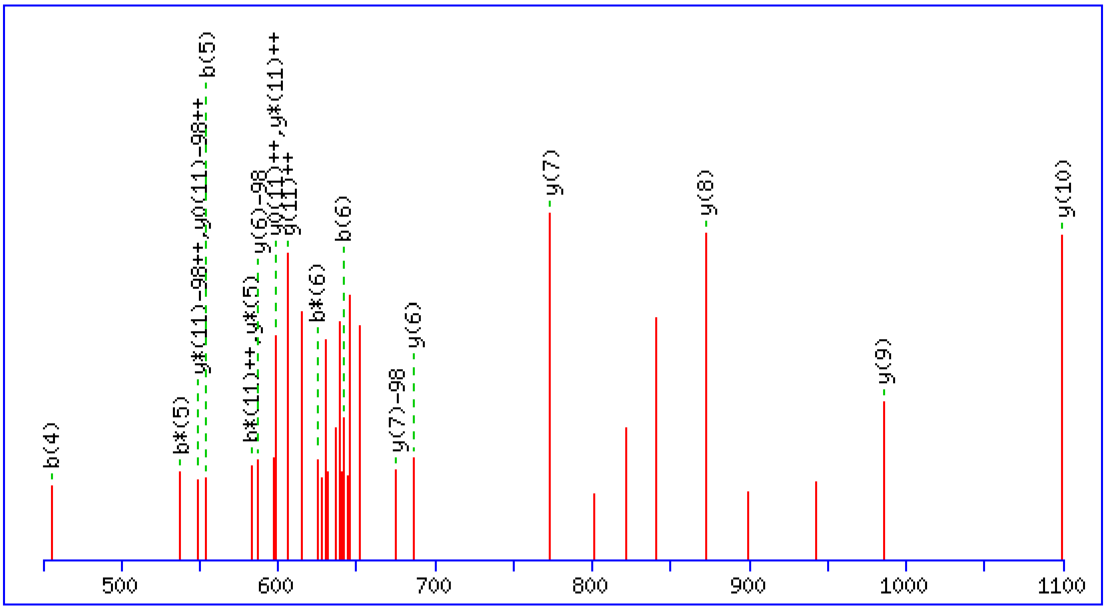
Monoisotopic mass of neutral peptide Mr(calc): 1756.8621
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.052
Matched b ions: b(3), b(4), b(5)++, b(6), b(7)-98, b(8)++, b(9)++, b(10)++, b(11)-98++, b(14)-98++
Matched y ions: y(2), y(3)++, y(5), y(8), y(8)++, y(10)-98, y(12)++, y(13)++, y(13)-98++, y(14)++, y(15)-98++, y(15)++

Peptide No.639

NLNLVSSTASIK
Confirmed sites:
Ambiguous sites: @S:7orT:8orS:10

MS/MS Fragmentation of **NLNLVSSTASIK**
Found in **RHG35_MOUSE** in **SwissProt**, Rho GTPase-activating protein 35 OS=Mus musculus GN=Arhgap35 PE=1 SV=3

Match to Query 2104: 1325.657882 from(663.836217,2+) index(2301)
Title: Elution from: 37.988 to 37.988 scan no 3672 cid35.00 polarity:+



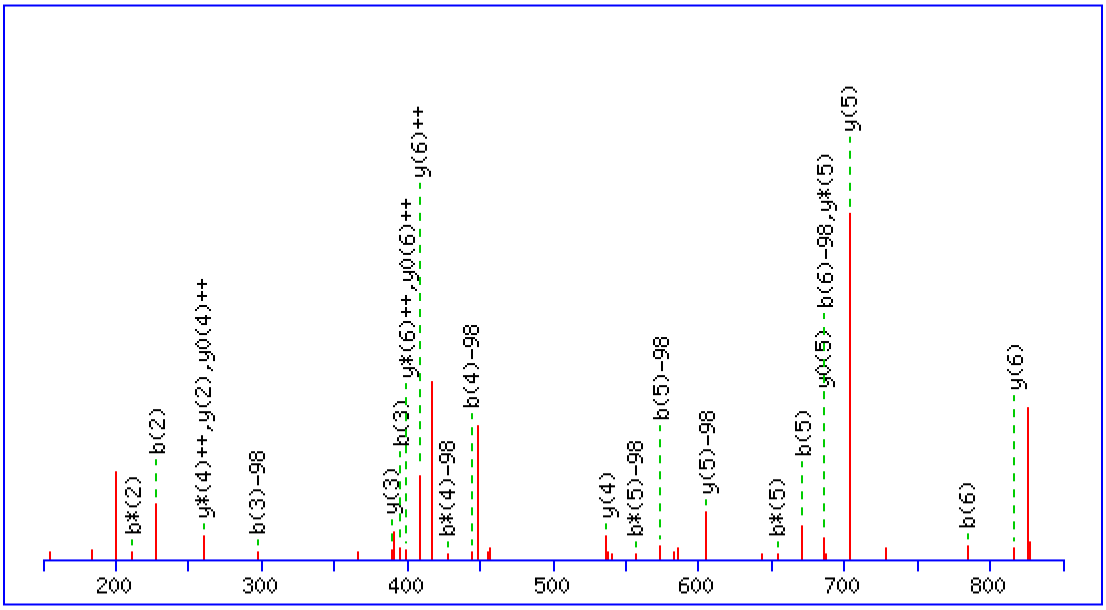
Monoisotopic mass of neutral peptide Mr(calc): 1325.6592
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.0003
Matched b ions: b(4), b(5), b(6)
Matched y ions: y(6), y(6)-98, y(7), y(7)-98, y(8), y(9), y(10), y(11)++

Peptide No.640

NLSFEIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NLSFEIK**
Found in **PTN12_MOUSE** in **SwissProt**, Tyrosine-protein phosphatase non-receptor type 12 OS=Mus musculus GN=Ptpn12 PE=1 SV=3

Match to Query 719: 929.425772 from(465.720162,2+) index(2649)
Title: Elution from: 41.705 to 41.705 scan no 4190 cid35.00 polarity:+



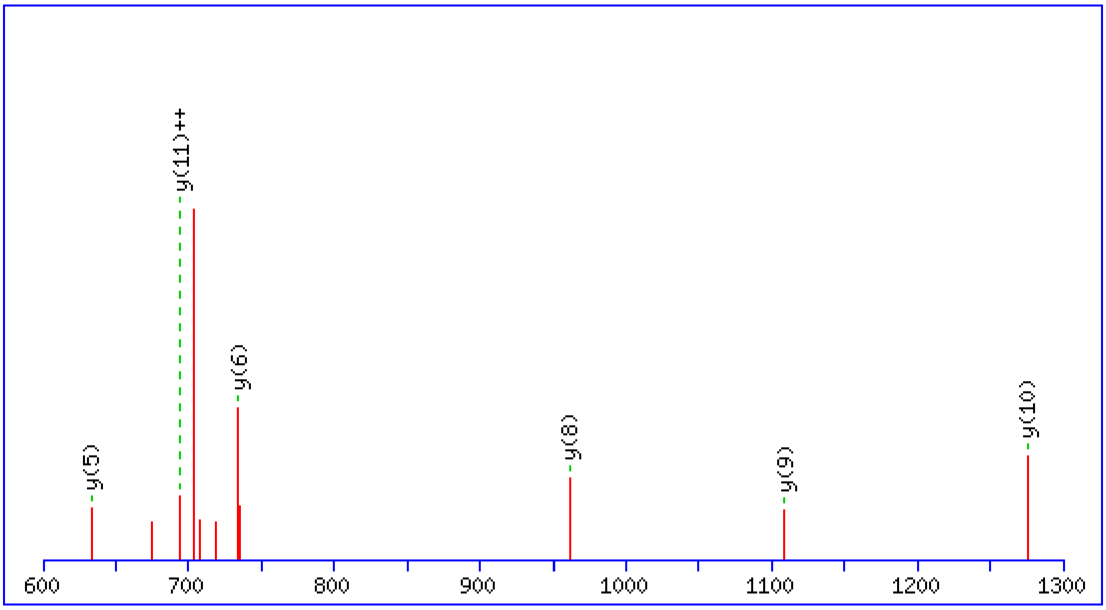
Monoisotopic mass of neutral peptide Mr(calc): 929.4259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.014
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6), b(6)-98
Matched y ions: y(2), y(3), y(4), y(5)-98, y(5), y(6)++, y(6)

Peptide No.641

NLSFNITEDELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NLSFNITEDELK**
Found in **NUCL_MOUSE** in **SwissProt**, Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2

Match to Query 2981: 1501.670450 from(751.842501,2+) index(3252)
Title: Elution from: 53.068 to 53.068 scan no 5511 cid35.00 polarity:+



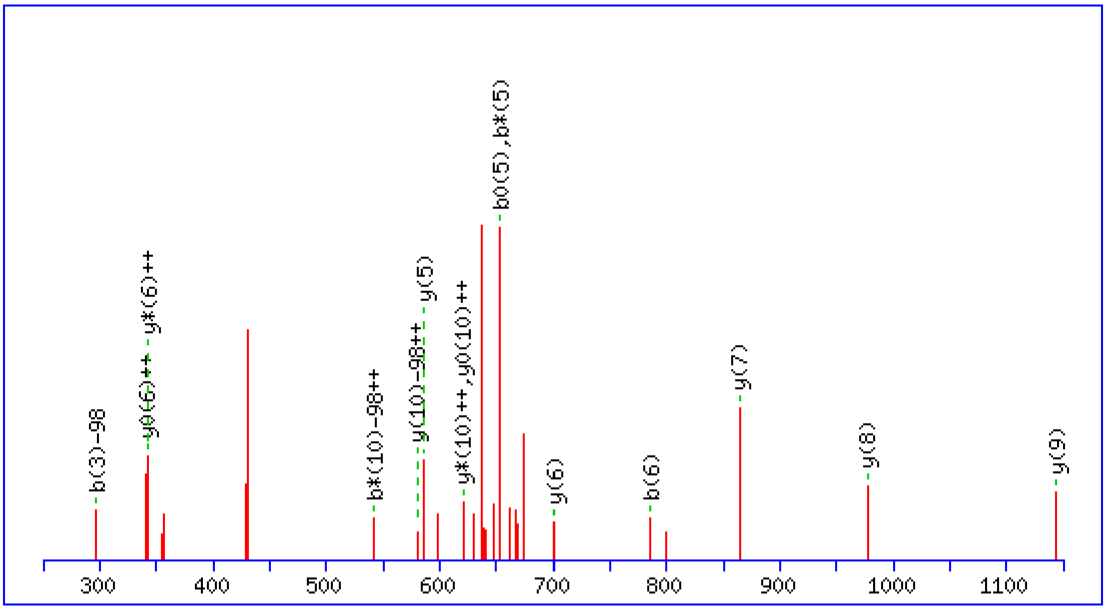
Monoisotopic mass of neutral peptide Mr(calc): 1501.6701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0013
Matched b ions:
Matched y ions: y(5), y(6), y(8), y(9), y(10), y(11)++

Peptide No.642

NLSIYDGPEQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **NLSIYDGPEQR**
Found in **ETFD_MOUSE** in **SwissProt**, Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Mus musculus GN=Etfdh PE=1 SV=1

Match to Query 2406: 1370.585246 from(686.299899,2+) index(2112)
Title: Elution from: 35.473 to 35.473 scan no 3369 cid35.00 polarity:+



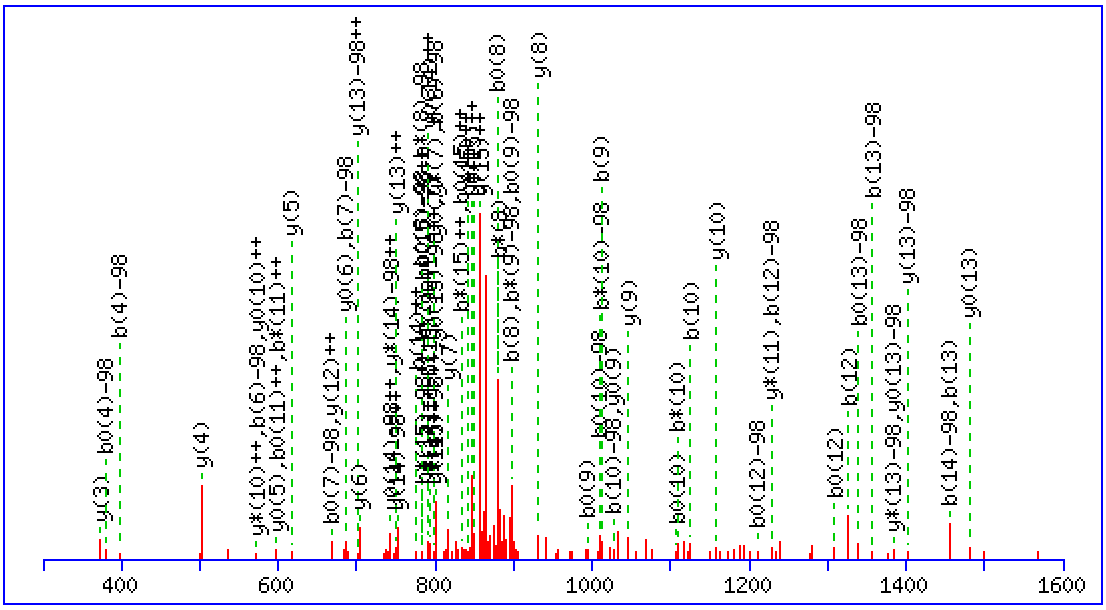
Monoisotopic mass of neutral peptide Mr(calc): 1370.5867
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.025
Matched b ions: b(3)-98, b(6)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)-98++

Peptide No.643

NLTSSSLNDISDKPEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **NLTSSSLNDISDKPEK**
Found in **S4A4_MOUSE** in **SwissProt**, Electrogenic sodium bicarbonate cotransporter 1 OS=Mus musculus GN=Slc4a4 PE=1 SV=2

Match to Query 3985: 1826.829842 from(914.422197,2+) index(1092)
Title: Elution from: 36.605 to 36.605 scan no 2588 cid35.00 polarity:+



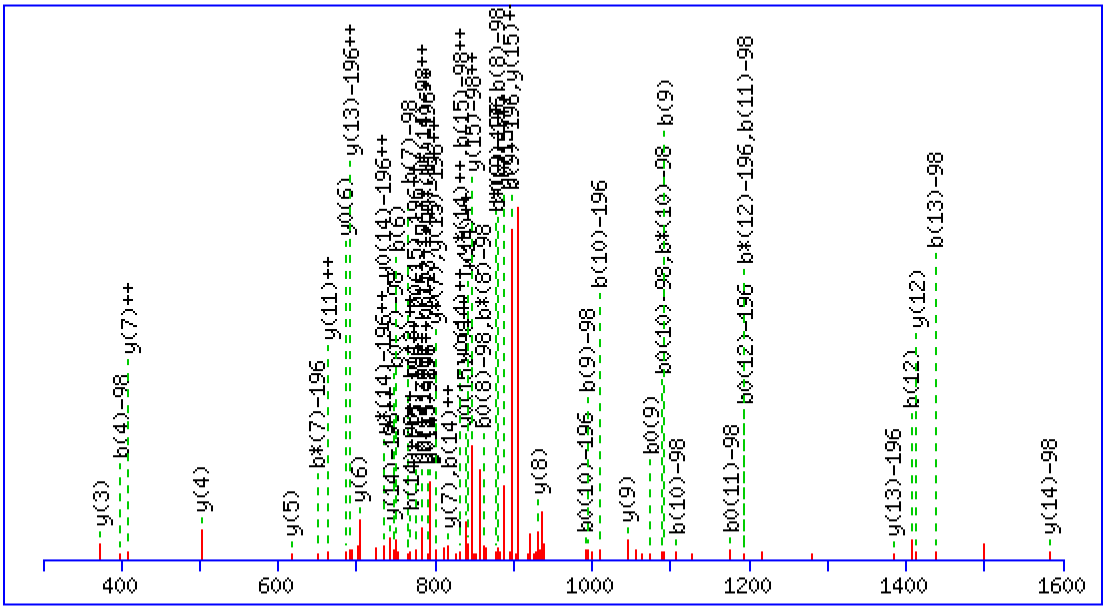
Monoisotopic mass of neutral peptide Mr(calc): 1826.8299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.0011
Matched b ions: b(4)-98, b(6)-98, b(7)-98, b(7), b(8), b(8)-98, b(9), b(10), b(10)-98, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(13)-98, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++

Peptide No.644

NLTSSSLNDISDKPEK
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **NLTSSSLNDISDKPEK**
Found in **S4A4_MOUSE** in **SwissProt**, Electrogenic sodium bicarbonate cotransporter 1 OS=Mus musculus GN=Slc4a4 PE=1 SV=2

Match to Query 3940: 1906.792616 from(954.403584,2+) index(1410)
Title: Elution from: 31.626 to 31.626 scan no 2709 cid35.00 polarity:+



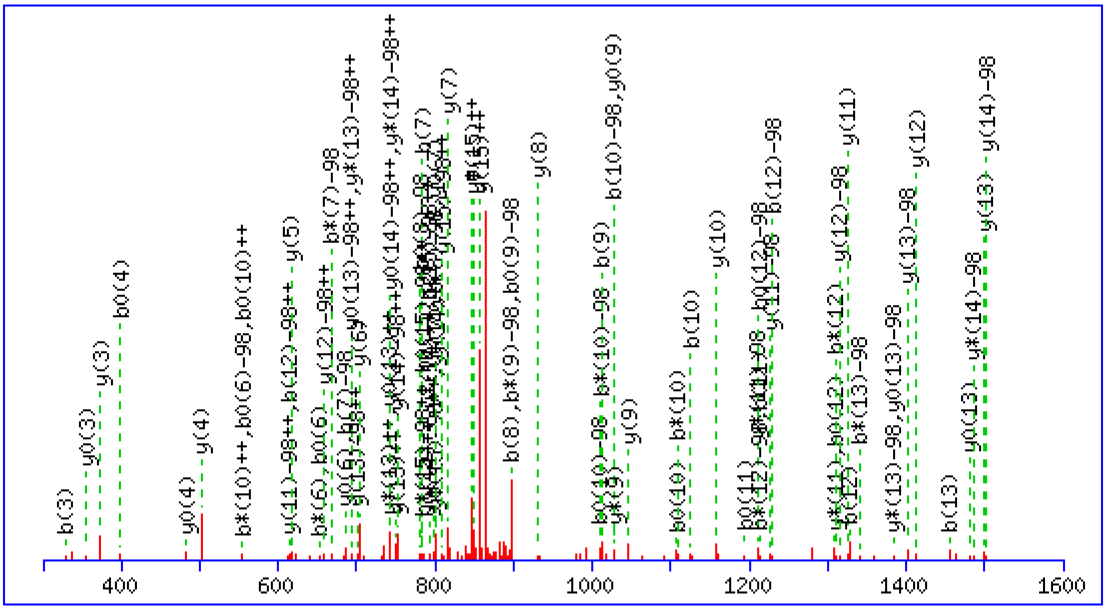
Monoisotopic mass of neutral peptide Mr(calc): 1906.7962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0013
Matched b ions: b(4)-98, b(6), b(7)-98, b(8)-98, b(9)-196, b(9), b(9)-98, b(10)-98, b(10)-196, b(11)-98, b(12), b(13)-98, b(13)++, b(14)++, b(14)-98++, b(15)-196++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(11)++, y(12), y(13)-196, y(13)-196++, y(13)++, y(14)-98, y(14)-196++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-196++

Peptide No.645

NLTSSSLNDISDKPEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **NLTSSSLNDISDKPEK**
Found in **S4A4_MOUSE** in **SwissProt**, Electrogenic sodium bicarbonate cotransporter 1 OS=Mus musculus GN=Slc4a4 PE=1 SV=2

Match to Query 4307: 1826.828166 from(914.421359,2+) index(5103)
Title: Elution from: 28.739 to 28.739 scan no 2465 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1826.8299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 1.2e-006
Matched b ions: b(3), b(7)-98, b(7), b(8), b(8)-98, b(9), b(10)-98, b(10), b(11), b(12), b(12)-98++, b(12)-98, b(13), b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11)-98, y(11), y(12), y(12)-98++, y(12)-98, y(13)-98, y(13), y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(14)-98, y(15)++, y(15)-98++

Peptide No.646

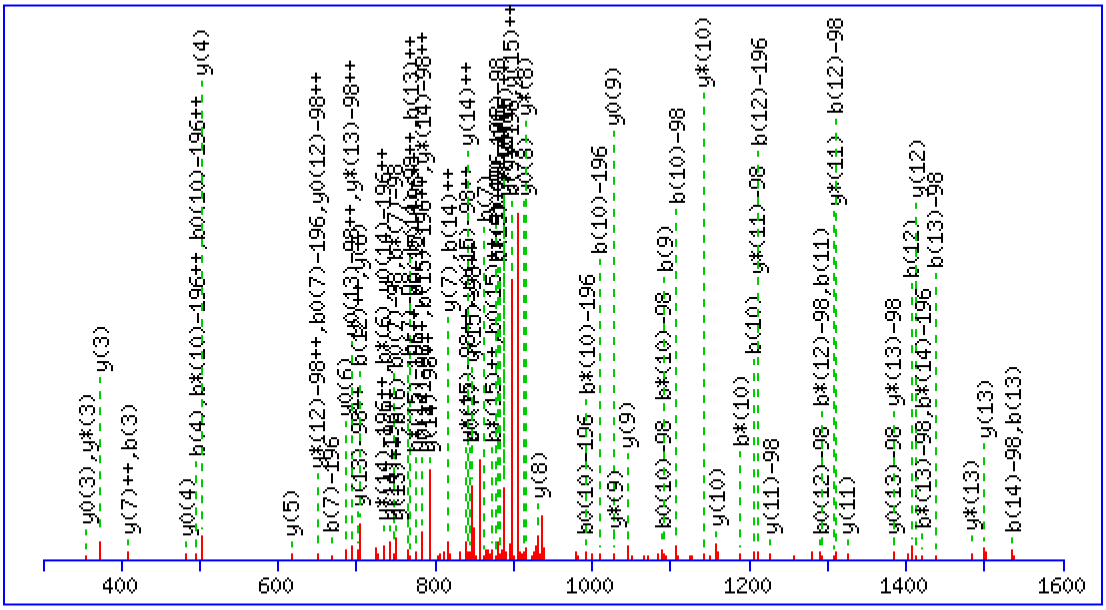
NLTSSSLNDISDKPEK

Confirmed sites: @T:3,@S:6

Ambiguous sites:

MS/MS Fragmentation of **NLTSSSLNDISDKPEK**
Found in **S4A4_MOUSE** in **SwissProt**, Electrogenic sodium bicarbonate cotransporter 1 OS=Mus musculus GN=Slc4a4 PE=1 SV=2

Match to Query 4481: 1906.793308 from(954.403930,2+) index(5231)
Title: Elution from: 32.019 to 32.019 scan no 2872 cid35.00 polarity:+:m1s



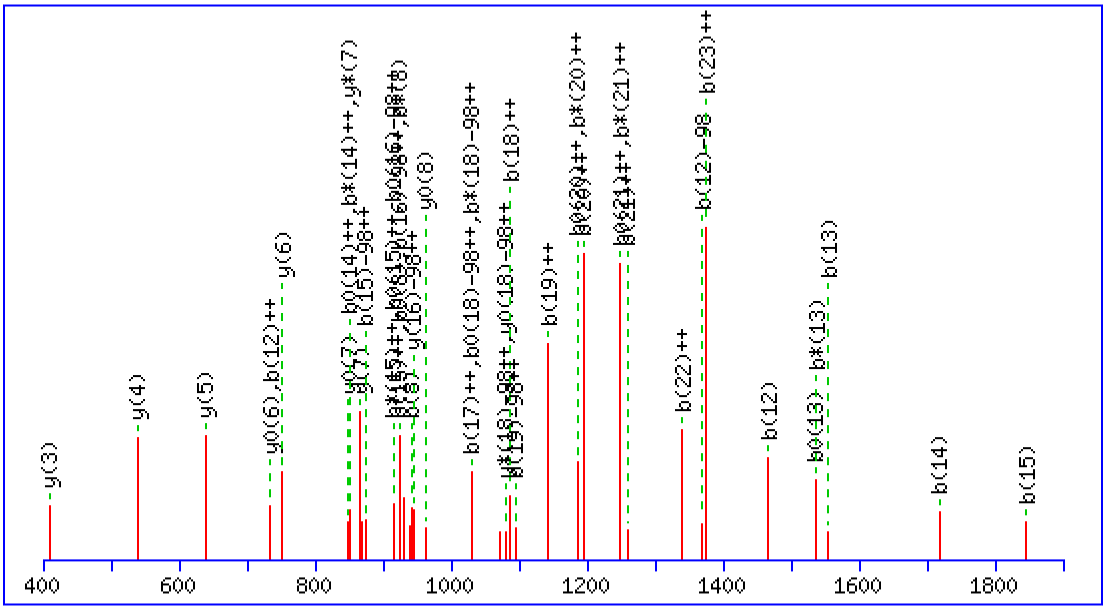
Monoisotopic mass of neutral peptide Mr(calc): 1906.7962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00013
Matched b ions: b(3), b(4), b(6), b(7)-98, b(7)-196, b(7), b(8)-98, b(9)-196, b(9), b(10)-98, b(10), b(10)-196, b(11), b(12)++, b(12), b(12)-196, b(12)-98, b(13), b(13)-98, b(13)++, b(14)-98, b(14)++, b(14)-98++, b(15)-196++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12), y(13), y(13)++, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)-98++, y(15)++

Peptide No.647

NPPPQDYESDDESYEVLDLTEYAR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **NPPPQDYESDDESYEVLDLTEYAR**
Found in **FUND1_MOUSE** in **SwissProt**, FUN14 domain-containing protein 1 OS=Mus musculus GN=Fundc1 PE=2 SV=1

Match to Query 5817: 2924.188215 from(975.736681,3+) index(6062)
Title: Elution from: 59.747 to 59.747 scan no 5693 cid35.00 polarity:+:m1s



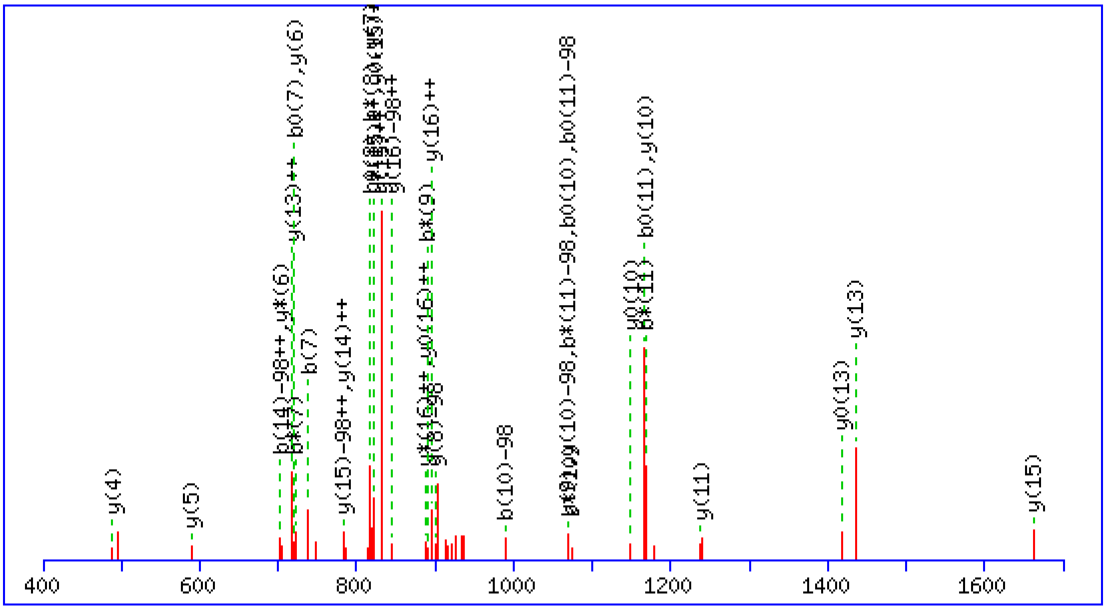
Monoisotopic mass of neutral peptide Mr(calc): 2924.1913
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 **Expect:** 1.3e-007
Matched b ions: b(8), b(12), b(12)++, b(12)-98, b(13), b(14), b(15)++, b(15), b(15)-98++, b(16)-98++, b(17)++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(21)++, b(22)++, b(23)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(16)-98++

Peptide No.648

NQPEPTAPATPMTSLLR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **NQPEPTAPATPMTSLLR**
Found in **S6A13_MOUSE** in **SwissProt**, Sodium- and chloride-dependent GABA transporter 2 OS=Mus musculus GN=Slc6a13 PE=1 SV=1

Match to Query 4597: 1902.890788 from(952.452670,2+) index(6658)
Title: Elution from: 47.249 to 47.249 scan no 4869 cid35.00 polarity:+:m1s



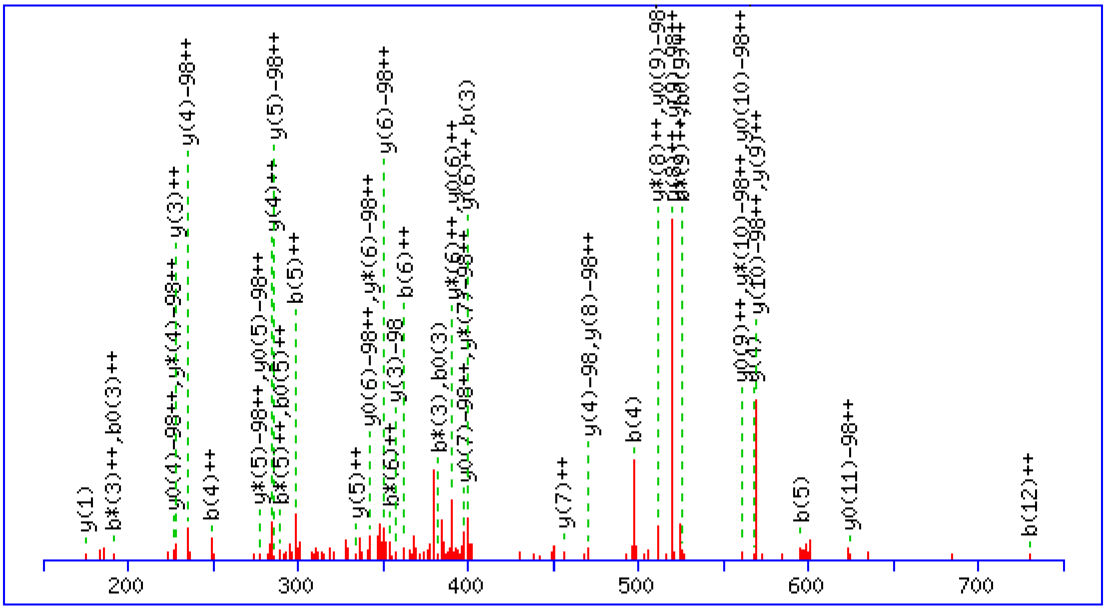
Monoisotopic mass of neutral peptide Mr(calc): 1902.8910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 7.2e-005
Matched b ions: b(7), b(10)-98, b(14)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(9), y(10)-98, y(10), y(11), y(13)++, y(13), y(14)++, y(15)++, y(15), y(15)-98++, y(16)++, y(16)-98++

Peptide No.649

NREPVQLETLSIR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **NREPVQLETLSIR**
Found in **SMD1_MOUSE** in **SwissProt**, Small nuclear ribonucleoprotein Sm D1 OS=Mus musculus GN=Snrpd1 PE=2 SV=1

Match to Query 3430: 1633.820072 from(409.462294,4+) index(334)
Title: Elution from: 27.557 to 27.557 scan no 1528 cid35.00 polarity:+



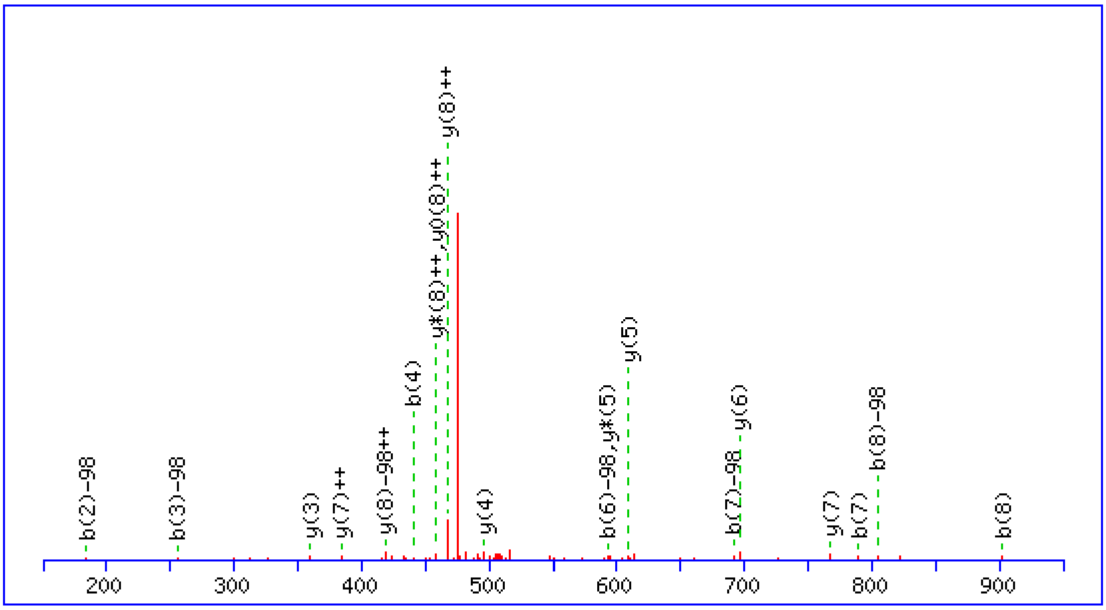
Monoisotopic mass of neutral peptide Mr(calc): 1633.8188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.019
Matched b ions: b(3), b(4)++, b(4), b(5)++, b(5), b(6)++, b(12)++
Matched y ions: y(1), y(3)++, y(3)-98, y(4)-98++, y(4)++, y(4)-98, y(4), y(5)-98++, y(5)++, y(6)++, y(6)-98++, y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)-98++

Peptide No.650

NSASLHVLK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **NSASLHVLK**
Found in **SO1B2_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 1070: 1047.511056 from(524.762804,2+) index(803)
Title: Elution from: 22.933 to 22.933 scan no 1672 cid35.00 polarity:+



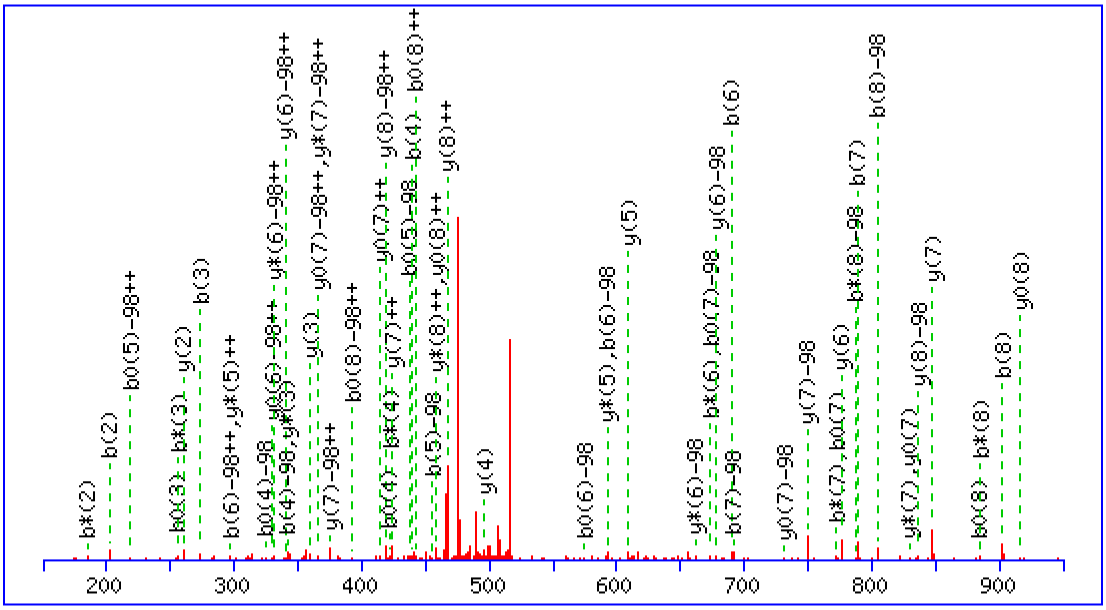
Monoisotopic mass of neutral peptide Mr(calc): 1047.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 0.00014
Matched b ions: b(2)-98, b(3)-98, b(4), b(6)-98, b(7), b(7)-98, b(8), b(8)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8)-98++

Peptide No.651

NSASLHVLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **NSASLHVLK**
Found in **SO1B2_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 1B2 OS=Mus musculus GN=Slco1b2 PE=1 SV=1

Match to Query 1355: 1047.511894 from(524.763223,2+) index(898)
Title: Elution from: 32.646 to 32.646 scan no 2216 cid35.00 polarity:+



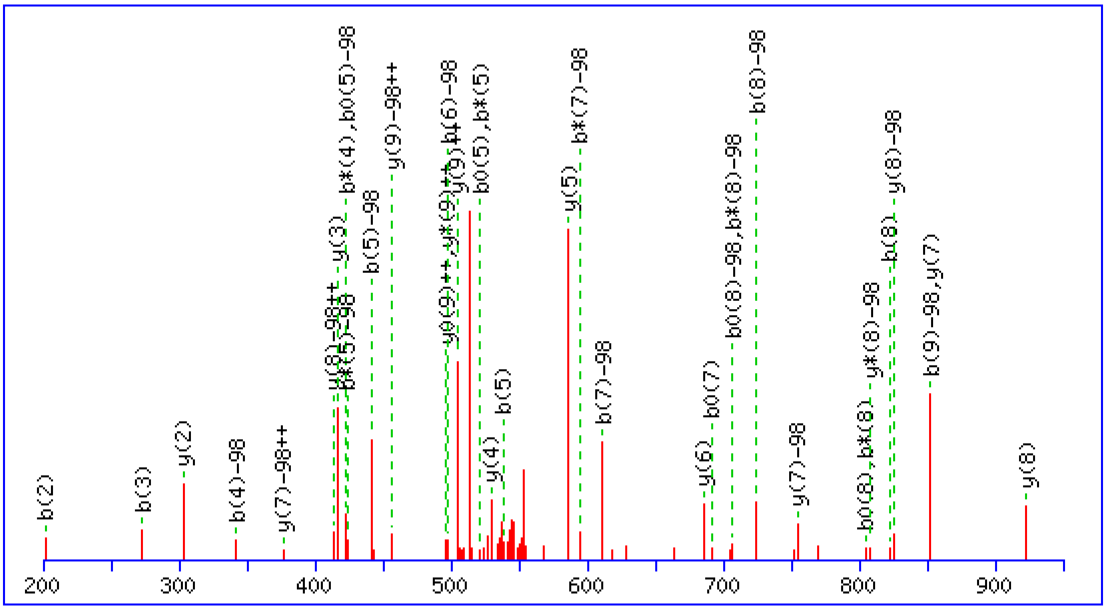
Monoisotopic mass of neutral peptide Mr(calc): 1047.5114
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.00068
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(6)-98++, b(7)-98, b(7), b(8), b(8)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(6)-98++, y(7)-98, y(7), y(7)++, y(7)-98++, y(8)++, y(8)-98++, y(8)-98

Peptide No.652

NSASVGIIQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **NSASVGIIQR**
Found in **GPAT3_MOUSE** in **SwissProt**, Glycerol-3-phosphate acyltransferase 3 OS=Mus musculus GN=Agpat9 PE=1 SV=1

Match to Query 1100: 1123.537692 from(562.776122,2+) index(1146)
Title: Elution from: 27.096 to 27.096 scan no 2177 cid35.00 polarity:+



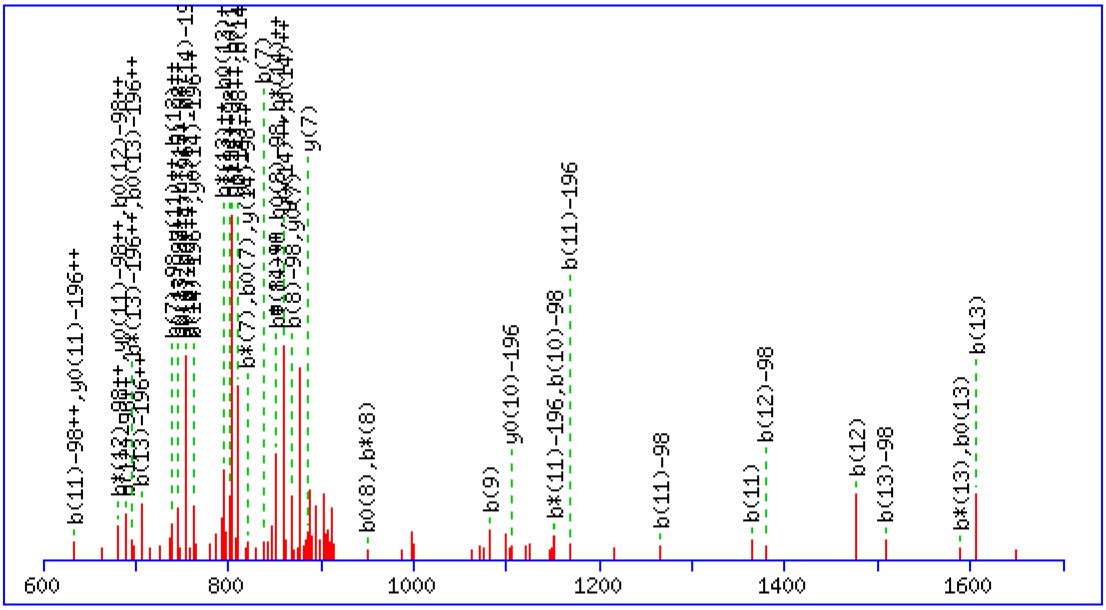
Monoisotopic mass of neutral peptide Mr(calc): 1123.5387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 4.4e-007
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(7)-98++, y(8), y(8)-98, y(8)-98++, y(9)++, y(9)-98++

Peptide No.653

NSATCHSEDSDLEID
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **NSATCHSEDSDLEID**
Found in **PHLP_MOUSE** in **SwissProt**, Phosducin-like protein OS=Mus musculus GN=Pdcl PE=1 SV=1

Match to Query 3679: 1851.589980 from(926.802266,2+) index(1734)
Title: Elution from: 33.619 to 33.619 scan no 3031 cid35.00 polarity:+



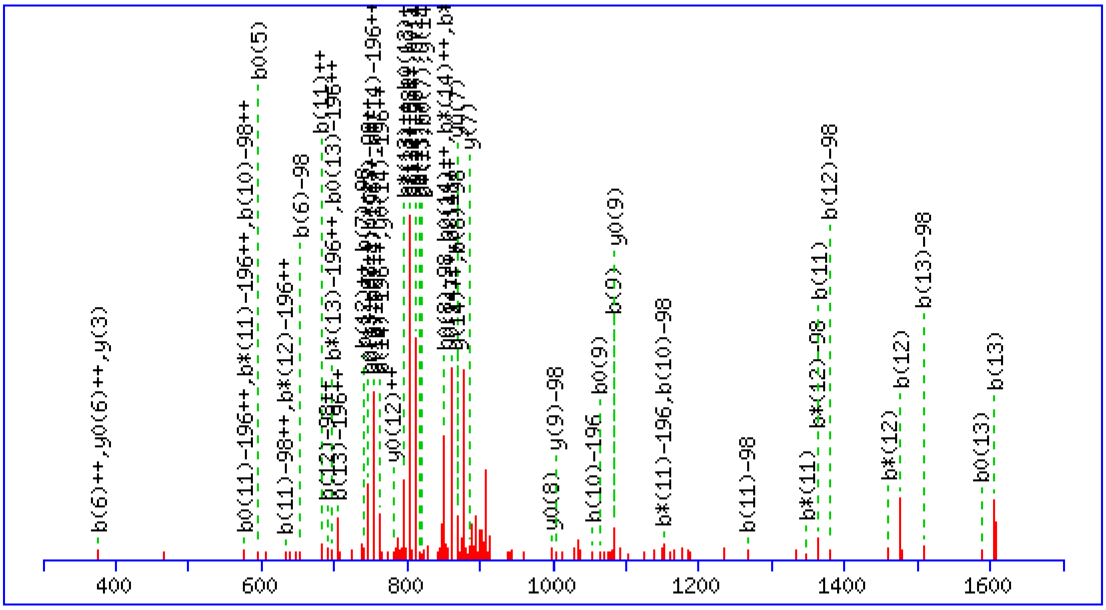
Monoisotopic mass of neutral peptide Mr(calc): 1851.5907
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.022
Matched b ions: b(7)-98, b(7), b(8)-98, b(9), b(10)-98, b(11)-98, b(11), b(11)-196, b(11)-98++, b(12), b(12)-98++, b(12)-98, b(12)++, b(13)-196++, b(13)++, b(13), b(13)-98++, b(13)-98, b(14)++, b(14)-98++, b(14)-196++
Matched y ions: y(7), y(11)++, y(14)-98++

Peptide No.654

NSATCHSEDSDLEID
Confirmed sites: @S:10
Ambiguous sites: @S:2orT:4

MS/MS Fragmentation of **NSATCHSEDSDLEID**
Found in **PHLP_MOUSE** in **SwissProt**, Phosducin-like protein OS=Mus musculus GN=Pdcl PE=1 SV=1

Match to Query 3757: 1851.588732 from(926.801642,2+) index(4597)
Title: Elution from: 33.719 to 33.719 scan no 2993 cid35.00 polarity:+:m1s



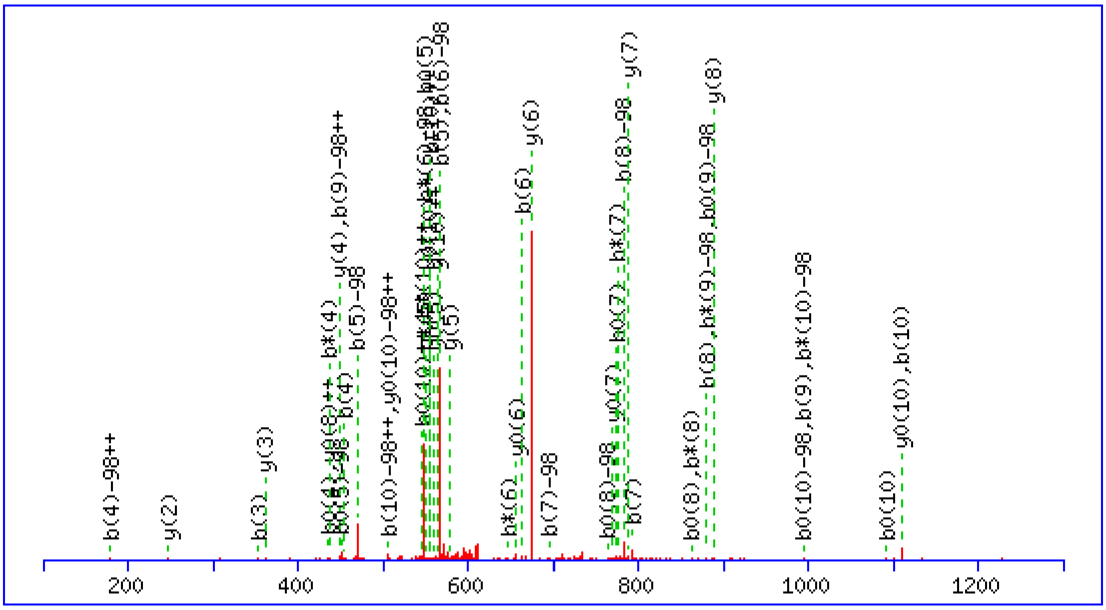
Monoisotopic mass of neutral peptide Mr(calc): 1851.5907
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 14 **Expect:** 0.041
Matched b ions: b(6)++, b(6)-98, b(7)-98, b(8)-98, b(9), b(10)-98++, b(10)-98, b(10)-196, b(11), b(11)-98++, b(11)-98, b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(13), b(13)-98, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++
Matched y ions: y(3), y(7), y(9)-98, y(14)++, y(14)-98++

Peptide No.655

NSATIPESDDL
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **NSATIPESDDL**
Found in **HUTH_MOUSE** in **SwissProt**, Histidine ammonia-lyase OS=Mus musculus GN=Hal PE=1 SV=1

Match to Query 2451: 1240.485904 from(621.250228,2+) index(2105)
Title: Elution from: 48.239 to 48.239 scan no 4026 cid35.00 polarity:+



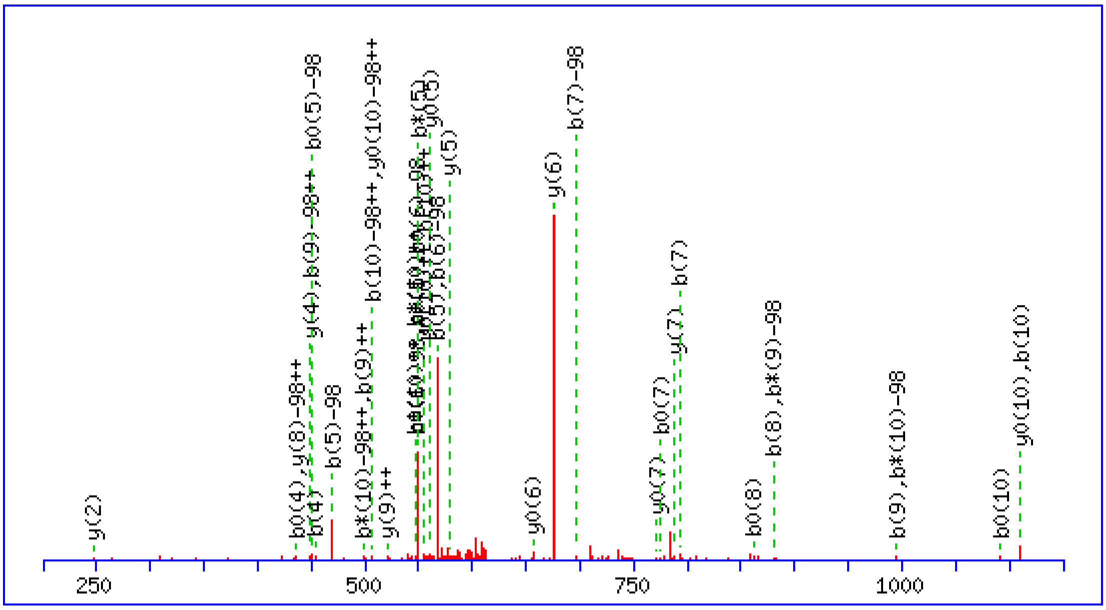
Monoisotopic mass of neutral peptide Mr(calc): 1240.4860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0018
Matched b ions: b(3), b(4)-98++, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98++, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10)++

Peptide No.656

NSATIPESDDL
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **NSATIPESDDL**
Found in **HUTH_MOUSE** in **SwissProt**, Histidine ammonia-lyase OS=Mus musculus GN=Hal PE=1 SV=1

Match to Query 2182: 1240.486336 from(621.250444,2+) index(1794)
Title: Elution from: 48.255 to 48.255 scan no 3806 cid35.00 polarity:+



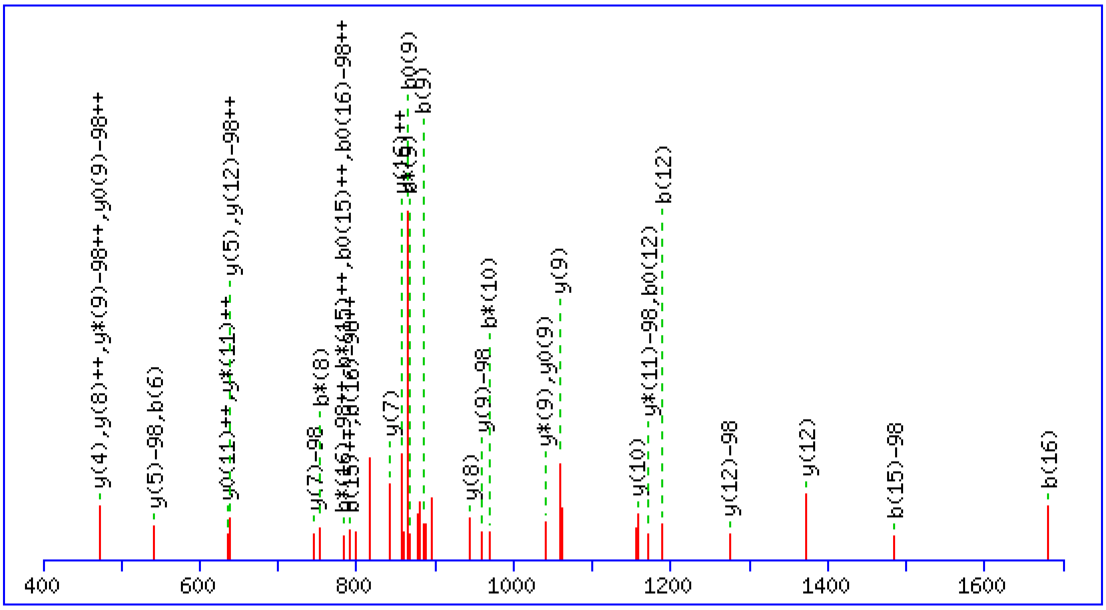
Monoisotopic mass of neutral peptide Mr(calc): 1240.4860
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.0062
Matched b ions: b(4), b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8), b(9), b(9)-98++, b(9)++, b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8)-98++, y(9)++

Peptide No.657

NSGPVSEVNTGFSPEVK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **NSGPVSEVNTGFSPEVK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4188: 1826.805718 from(914.410135,2+) index(2431)
Title: Elution from: 39.362 to 39.362 scan no 3856 cid35.00 polarity:+



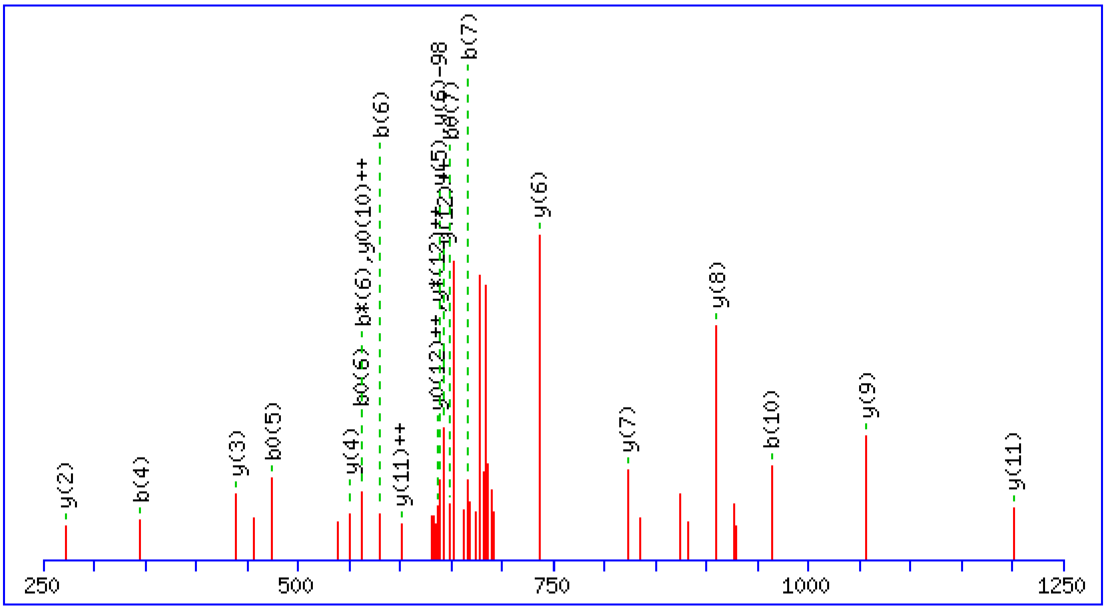
Monoisotopic mass of neutral peptide Mr(calc): 1826.8088
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00054
Matched b ions: b(6), b(9), b(12), b(15)-98, b(15)++, b(16), b(16)-98++
Matched y ions: y(4), y(5), y(5)-98, y(7)-98, y(7), y(8)++, y(8), y(9), y(9)-98, y(10), y(12)-98++, y(12)-98, y(12), y(16)++

Peptide No.658

NSGSFSSPSISPR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **NSGSFSSPSISPR**
Found in **MTUS1_MOUSE** in **SwissProt**, Microtubule-associated tumor suppressor 1 homolog OS=Mus musculus GN=Mtus1 PE=1 SV=2

Match to Query 2085: 1401.594244 from(701.804398,2+) index(4507)
Title: Elution from: 29.677 to 29.677 scan no 2523 cid35.00 polarity:+:m1s



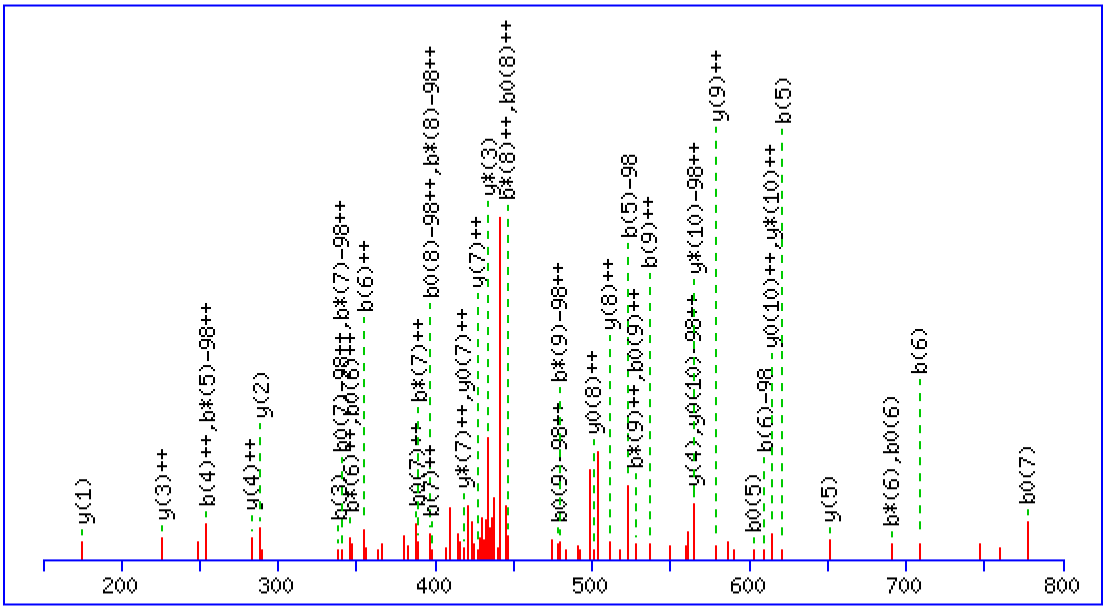
Monoisotopic mass of neutral peptide Mr(calc): 1401.5926
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 77 **Expect:** 7.1e-008
Matched b ions: b(4), b(6), b(7), b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9), y(11), y(11)++, y(12)++

Peptide No.659

NSHSDSSIYIR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **NSHSDSSIYIR**
Found in **CLMN_MOUSE** in **SwissProt**, Calmin OS=Mus musculus GN=Clmn PE=1 SV=2

Match to Query 1983: 1357.565142 from(453.528990,3+) index(693)
Title: Elution from: 23.025 to 23.025 scan no 1623 cid35.00 polarity:+



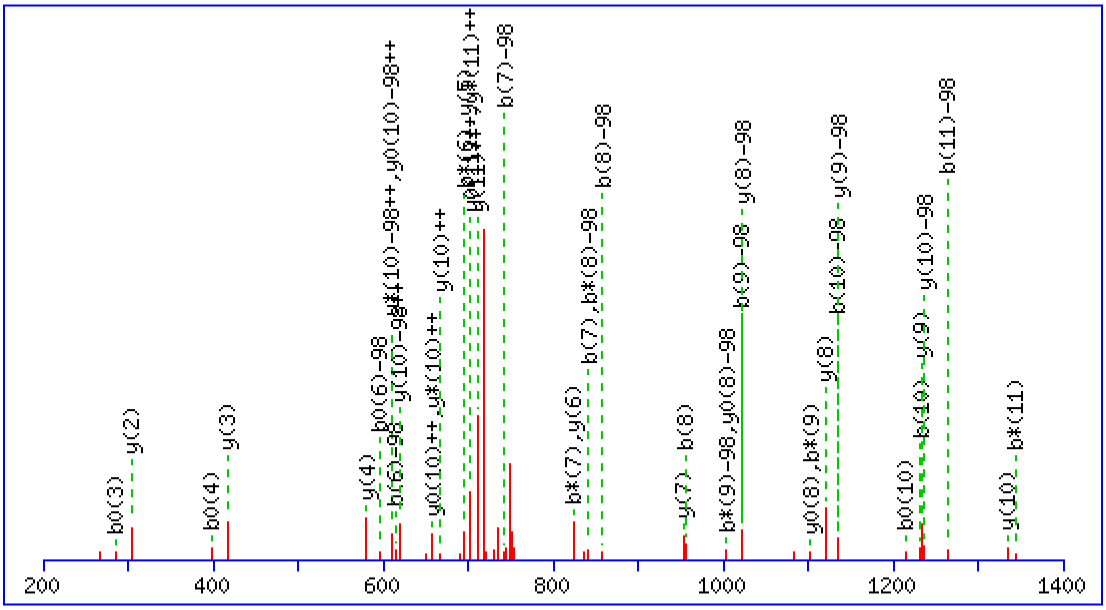
Monoisotopic mass of neutral peptide Mr(calc): 1357.5663
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 16 **Expect:** 0.058
Matched b ions: b(3), b(4)++, b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7)++, b(9)++
Matched y ions: y(1), y(2), y(3)++, y(4)++, y(4), y(5), y(7)++, y(8)++, y(9)++

Peptide No.660

NSTLSEEDYIER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **NSTLSEEDYIER**
Found in **BNIP3_MOUSE** in **SwissProt**, BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 OS=Mus musculus GN=Bnip3 PE=1 SV=1

Match to Query 2689: 1534.618232 from(768.316392,2+) index(1753)
Title: Elution from: 35.367 to 35.367 scan no 3210 cid35.00 polarity:+



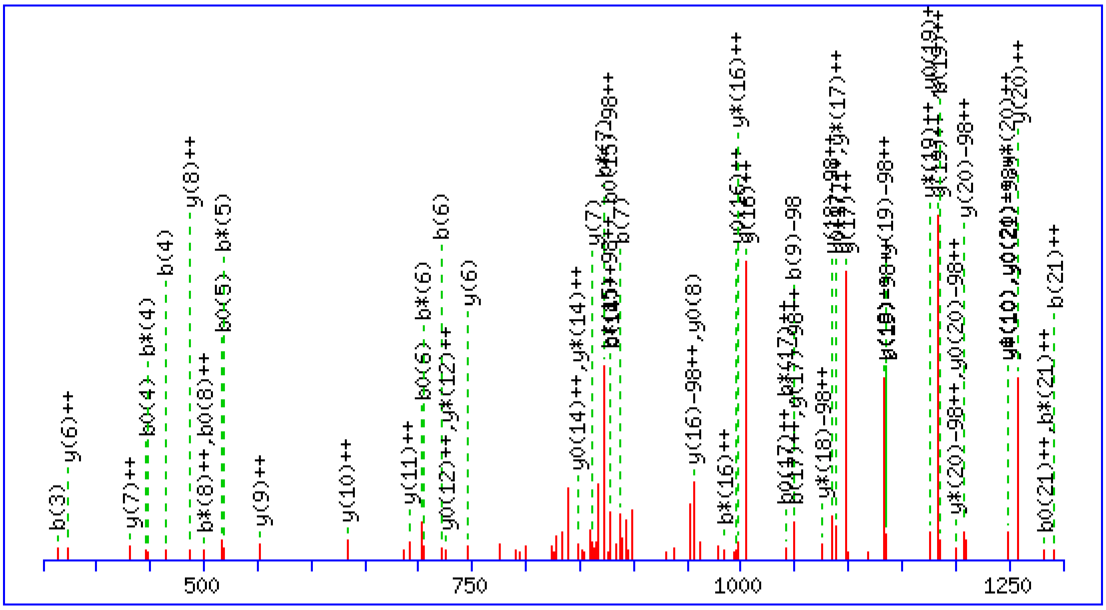
Monoisotopic mass of neutral peptide Mr(calc): 1534.6188
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 7.5e-007
Matched b ions: b(6)-98, b(7), b(7)-98, b(8), b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10), y(10)-98++, y(10)-98, y(10)++, y(11)++

Peptide No.661

NTFTAWSEEDSDYEIDDRDVNK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **NTFTAWSEEDSDYEIDDRDVNK**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 5659: 2728.078551 from(910.366793,3+) index(5707)
Title: Elution from: 45.898 to 45.898 scan no 4490 cid35.00 polarity:+:m1s



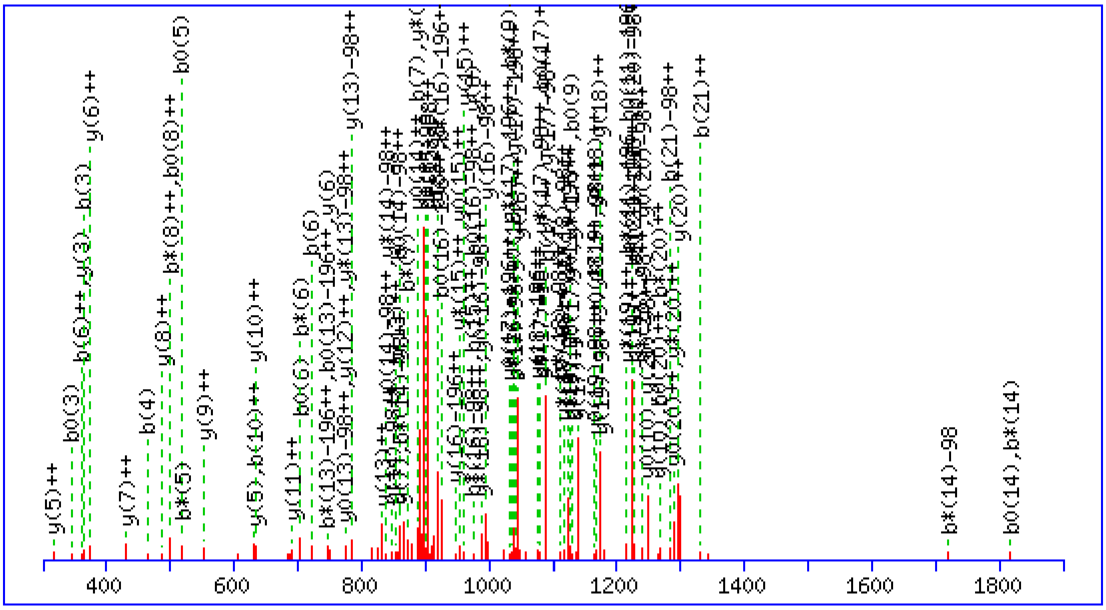
Monoisotopic mass of neutral peptide Mr(calc): 2728.0814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 1.6e-006
Matched b ions: b(3), b(4), b(6), b(7), b(9)-98, b(14)++, b(17)++, b(19)-98++, b(19)++, b(21)++
Matched y ions: y(6)++, y(6), y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(11)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++

Peptide No.662

NTFTAWSEEDSDYEIDDRDVNK
Confirmed sites: @S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of **NTFTAWSEEDSDYEIDDRDVNK**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 5583: 2808.046029 from(937.022619,3+) index(5601)
Title: Elution from: 48.336 to 48.336 scan no 4786 cid35.00 polarity:+:m1s



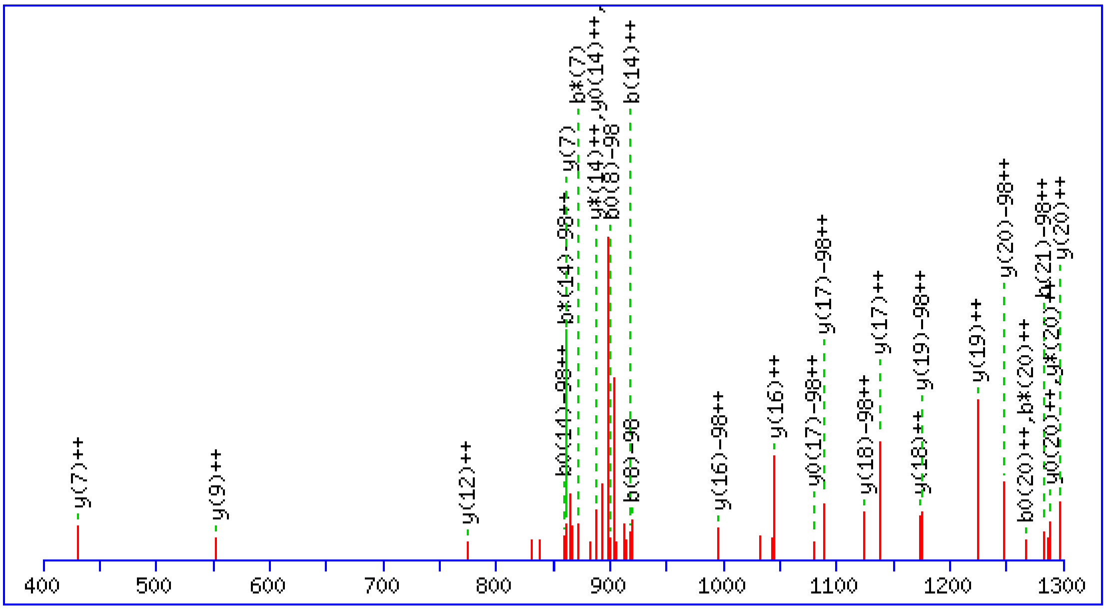
Monoisotopic mass of neutral peptide Mr(calc): 2808.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 **Expect:** 2.2e-008
Matched b ions: b(3), b(4), b(6), b(6)++, b(7), b(8)-98, b(10)++, b(13)++, b(15)-98++, b(15)++, b(17)++, b(17)-98++, b(19)++, b(20)-98++, b(21)++, b(21)-98++
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(16)++, y(16)-98++, y(16)-196++, y(17)-98++, y(17)++, y(17)-196++, y(18)++, y(18)-98++, y(18)-196++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(20)-98++

Peptide No.663

NTFTAWSEEDSDYEIDDRDVNK
Confirmed sites: @S:7
Ambiguous sites: @S:11orY:13

MS/MS Fragmentation of **NTFTAWSEEDSDYEIDDRDVNK**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 6769: 2808.049260 from(937.023696,3+) index(6871)
Title: Elution from: 51.568 to 51.568 scan no 5353 cid35.00 polarity:+:m1s



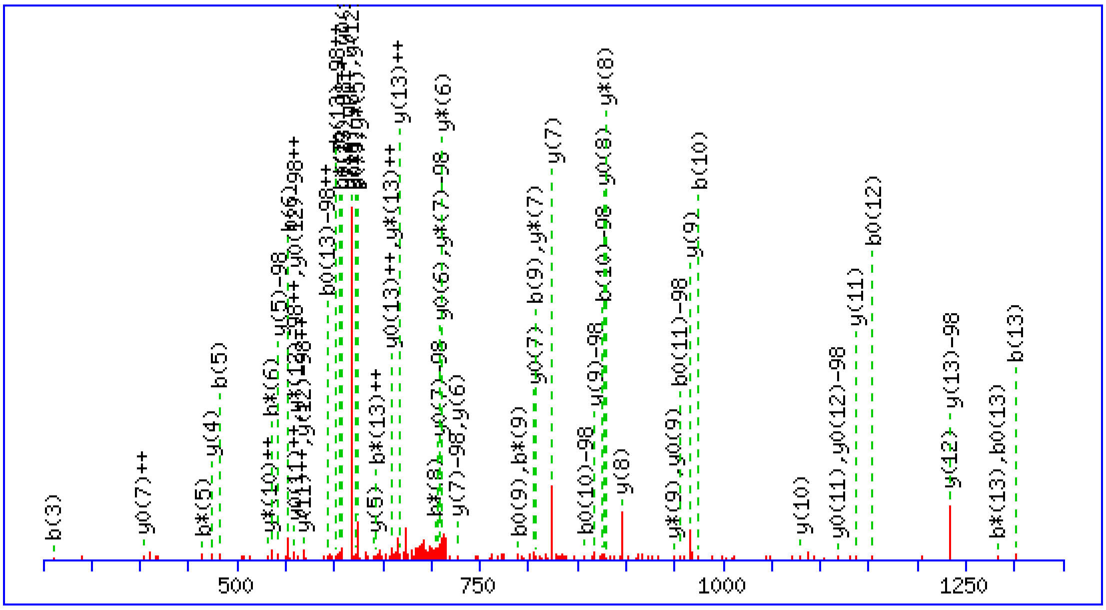
Monoisotopic mass of neutral peptide Mr(calc): 2808.0477
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y13 : Phospho (Y)
Ions Score: 35 **Expect:** 0.0014
Matched b ions: b(7), b(8)-98, b(14)++, b(21)-98++
Matched y ions: y(7)++, y(7), y(9)++, y(12)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++

Peptide No.664

NVPGLAAPSSPTQK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **NVPGLAAPSSPTQK**
Found in **PP6R2_MOUSE** in **SwissProt**, Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Mus musculus GN=Ppp6r2 PE=1 SV=1

Match to Query 2882: 1445.691968 from(723.853260,2+) index(1104)
Title: Elution from: 36.726 to 36.726 scan no 2604 cid35.00 polarity:+



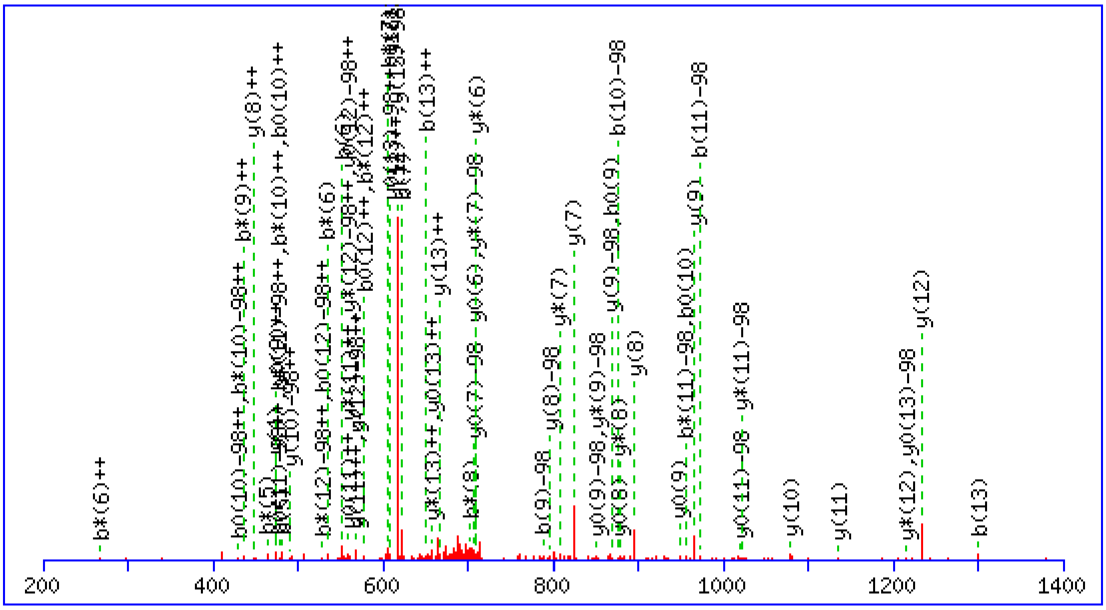
Monoisotopic mass of neutral peptide Mr(calc): 1445.6915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00045
Matched b ions: b(3), b(5), b(6), b(7), b(9), b(10)-98, b(10), b(13), b(13)-98++
Matched y ions: y(4), y(5)-98, y(5), y(6), y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)++, y(12)++, y(12), y(12)-98++, y(13)-98++, y(13)-98, y(13)++

Peptide No.665

NVPGLAAPSSPTQK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **NVPGLAAPSSPTQK**
Found in **PP6R2_MOUSE** in **SwissProt**, Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Mus musculus GN=Ppp6r2 PE=1 SV=1

Match to Query 3297: 1445.692028 from(723.853290,2+) index(1287)
Title: Elution from: 36.730 to 36.730 scan no 2731 cid35.00 polarity:+



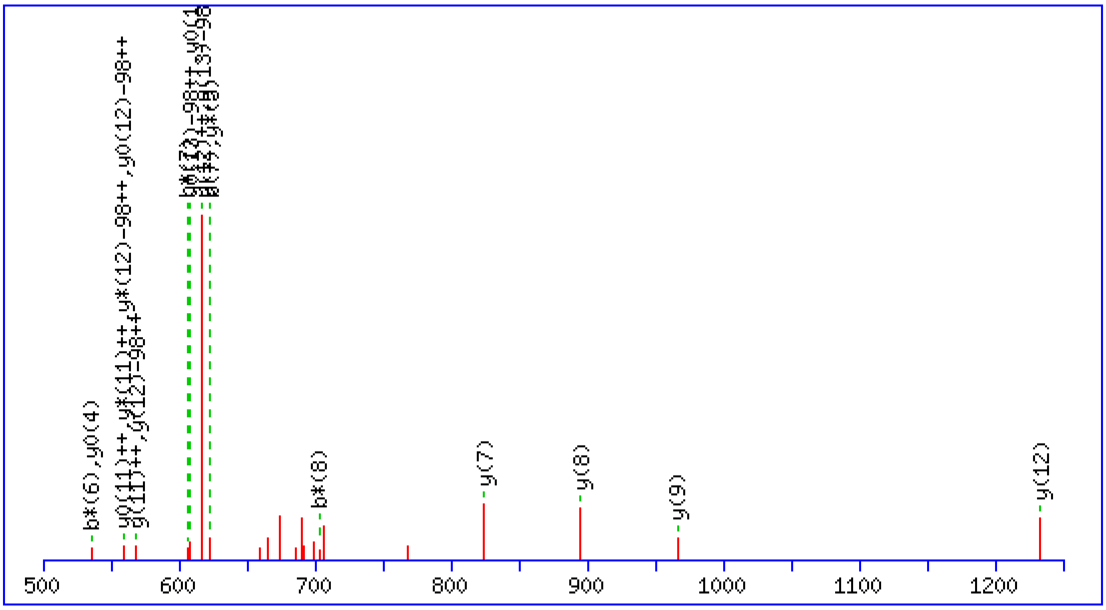
Monoisotopic mass of neutral peptide Mr(calc): 1445.6915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00052
Matched b ions: b(5), b(6), b(7), b(9)-98, b(10)-98, b(11)-98, b(13), b(13)++
Matched y ions: y(4), y(7), y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(10), y(10)-98++, y(11), y(11)++, y(12)++, y(12), y(12)-98++, y(13)-98++, y(13)++

Peptide No.666

NVPGLAAPSSPTQK
Confirmed sites:
Ambiguous sites: @S:9orS:10orT:12

MS/MS Fragmentation of **NVPGLAAPSSPTQK**
Found in **PP6R2_MOUSE** in **SwissProt**, Serine/threonine-protein phosphatase 6 regulatory subunit 2 OS=Mus musculus GN=Ppp6r2 PE=1 SV=1

Match to Query 2559: 1445.691000 from(723.852776,2+) index(1435)
Title: Elution from: 29.116 to 29.116 scan no 2478 cid35.00 polarity:+



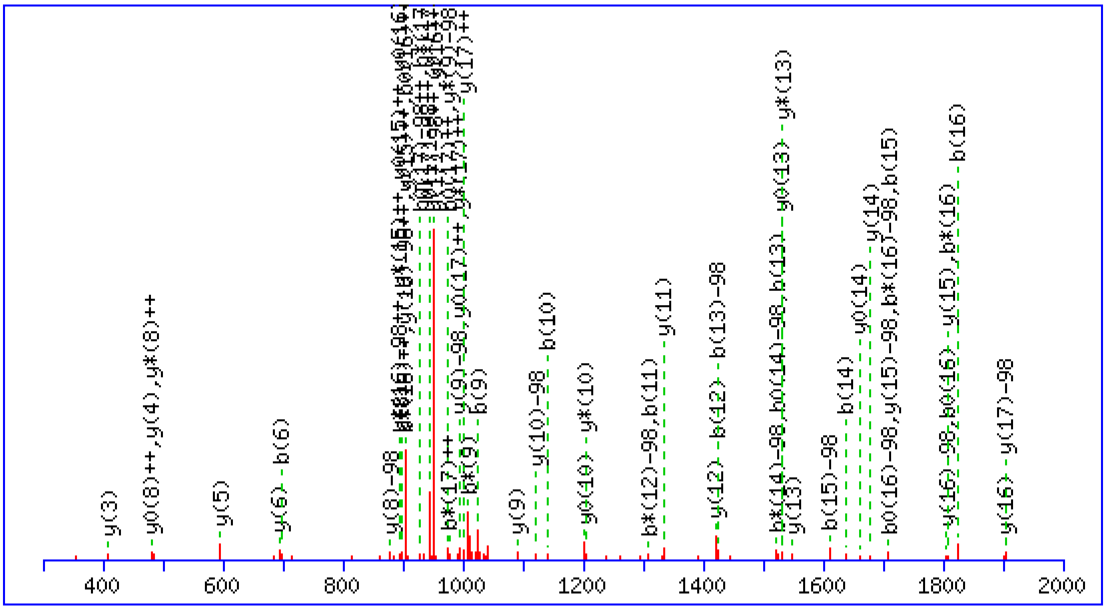
Monoisotopic mass of neutral peptide Mr(calc): 1445.6915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0038
Matched b ions: b(7)
Matched y ions: y(7), y(8), y(9), y(11)++, y(12)++, y(12), y(12)-98++, y(13)-98++

Peptide No.667

NVPQEESLEDSDVDADFK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **NVPQEESLEDSDVDADFK**
Found in **IMA3_MOUSE** in **SwissProt**, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5392: 2115.847888 from(1058.931220,2+) index(6342)
Title: Elution from: 42.226 to 42.226 scan no 4260 cid35.00 polarity:+:m1s



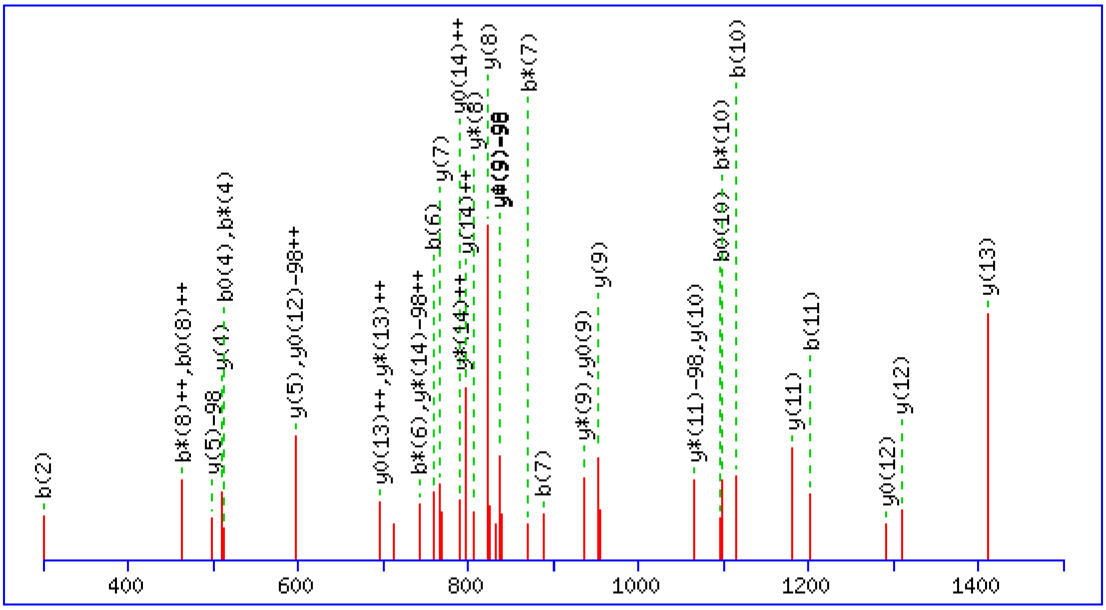
Monoisotopic mass of neutral peptide Mr(calc): 2115.8521
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 **Expect:** 1.8e-008
Matched b ions: b(6), b(8), b(9), b(10), b(11), b(12), b(13), b(13)-98, b(14), b(15)-98, b(15), b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(8)-98, y(8), y(9), y(9)-98, y(10)-98, y(11), y(12), y(13), y(14), y(15)-98, y(15)++, y(15), y(16)++, y(16), y(16)-98++, y(16)-98, y(17)-98++, y(17)-98, y(17)++

Peptide No.668

NWTEDIEGGISSPVK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **NWTEDIEGGISSPVK**
Found in **NFIC_MOUSE** in **SwissProt**, Nuclear factor 1 C-type OS=Mus musculus GN=Nfic PE=1 SV=1

Match to Query 3837: 1710.750352 from(856.382452,2+) index(6680)
Title: Elution from: 47.605 to 47.605 scan no 4912 cid35.00 polarity:+:m1s



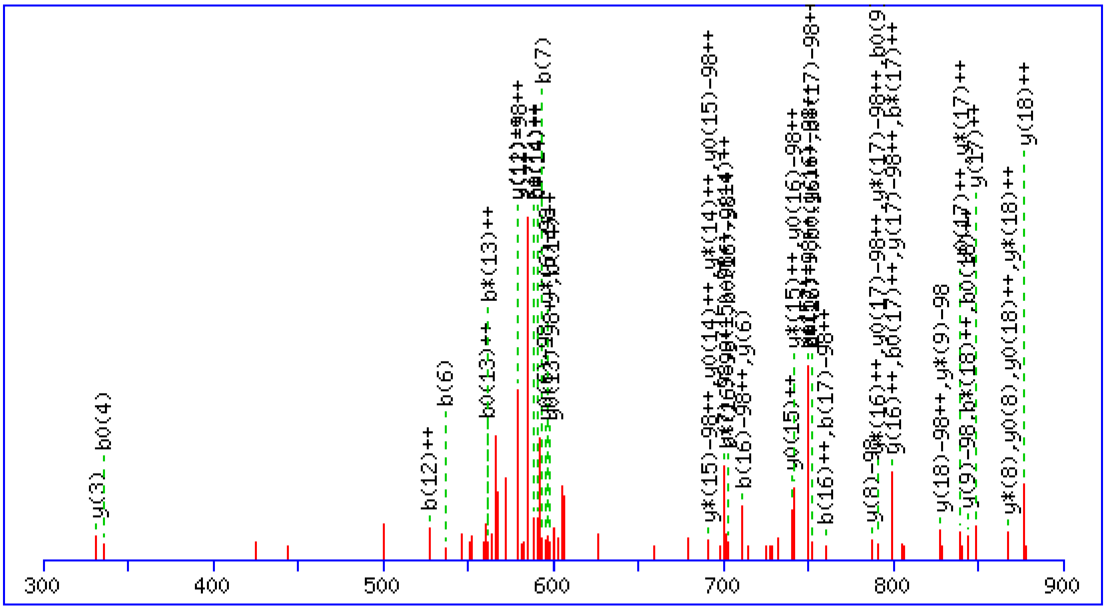
Monoisotopic mass of neutral peptide Mr(calc): 1710.7502
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 80 **Expect:** 5.9e-008
Matched b ions: b(2), b(6), b(7), b(10), b(11)
Matched y ions: y(4), y(5), y(5)-98, y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++

Peptide No.669

PGPTPSGTNVGSSGRSPSK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **PGPTPSGTNVGSSGRSPSK**
Found in **SC61B_MOUSE** in **SwissProt**, Protein transport protein Sec61 subunit beta OS=Mus musculus GN=Sec61b PE=1 SV=3

Match to Query 3670: 1848.834000 from(617.285276,3+) index(3241)
Title: Elution from: 18.265 to 18.265 scan no 994 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1848.8367

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 36 **Expect:** 0.0015

Matched b ions: b(6), b(7), b(12)++, b(14)++, b(16)-98++, b(16)++, b(17)-98++

Matched y ions: y(3), y(6), y(7)-98, y(8)-98, y(9)-98, y(11)++, y(12)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++

Peptide No.670

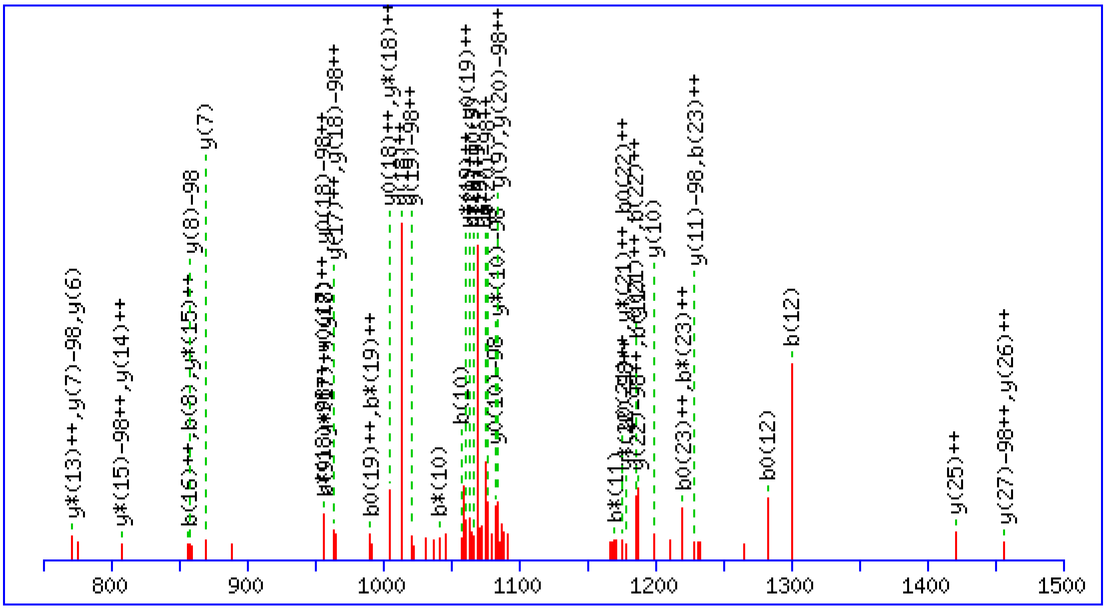
QADVADQQTTELPAENGETENQSPASEEEK

Confirmed sites: @S:26

Ambiguous sites:

MS/MS Fragmentation of **QADVADQQTTELPAENGETENQSPASEEEK**
Found in **HMGN1_MOUSE** in **SwissProt**, Non-histone chromosomal protein HMG-14 OS=Mus musculus GN=Hmgn1 PE=1 SV=2

Match to Query 5787: 3324.371967 from(1109.131265,3+) index(4445)
Title: Elution from: 32.101 to 32.101 scan no 2772 cid35.00 polarity:+:m1s



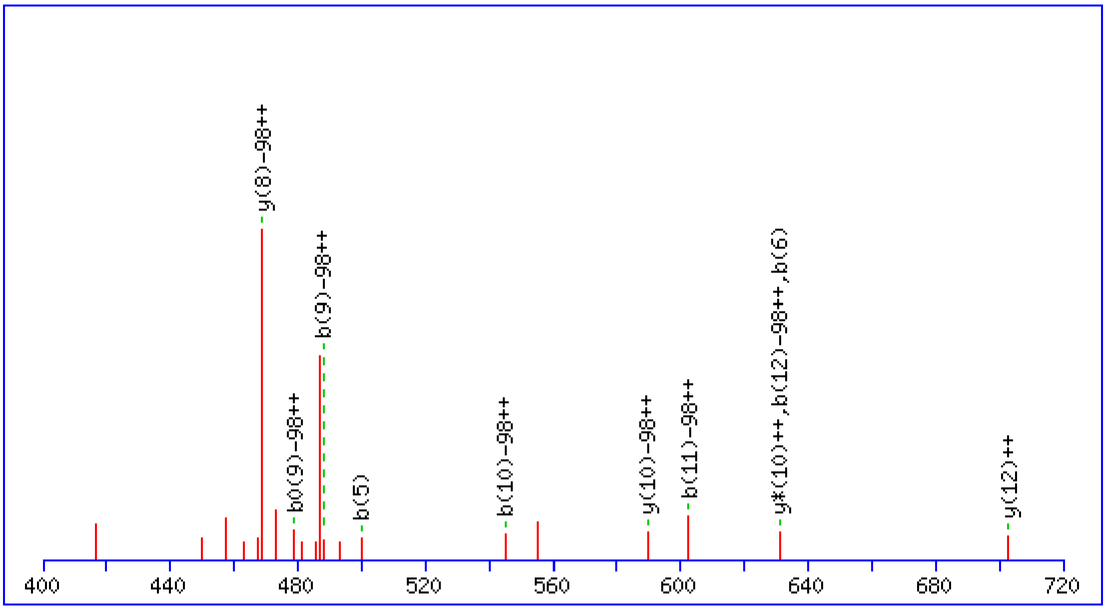
Monoisotopic mass of neutral peptide Mr(calc): 3324.3790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00012
Matched b ions: b(8), b(9), b(10), b(11), b(12), b(16)++, b(20)++, b(22)++, b(23)++
Matched y ions: y(6), y(7)-98, y(7), y(8), y(8)-98, y(9), y(10), y(11)-98, y(14)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(21)++, y(22)-98++, y(25)++, y(26)++, y(27)-98++

Peptide No.671

QAGDQMLSYNLGR
Confirmed sites:
Ambiguous sites: @S:8orY:9

MS/MS Fragmentation of **QAGDQMLSYNLGR**
Found in **HECW2_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase HECW2 OS=Mus musculus GN=Hecw2 PE=2 SV=1

Match to Query 2937: 1531.648119 from(511.556649,3+) index(5081)
Title: Elution from: 30.465 to 30.465 scan no 2663 cid35.00 polarity:+:m1s



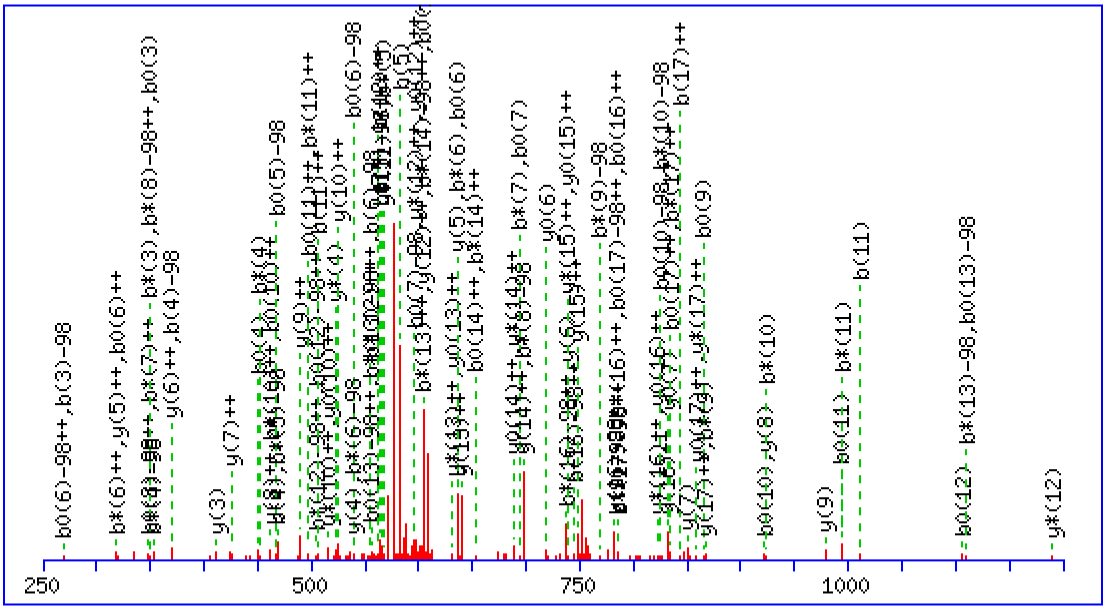
Monoisotopic mass of neutral peptide Mr(calc): 1531.6490
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.048
Matched b ions: b(5), b(6), b(9)-98++, b(10)-98++, b(11)-98++, b(12)-98++
Matched y ions: y(8)-98++, y(10)-98++, y(12)++

Peptide No.672

QASTDAGTAGALTPQHVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QASTDAGTAGALTPQHVR**
Found in **YAP1_MOUSE** in **SwissProt**, Yorkie homolog OS=Mus musculus GN=Yap1 PE=1 SV=2

Match to Query 3714: 1859.852409 from(620.958079,3+) index(892)
Title: Elution from: 24.759 to 24.759 scan no 1859 cid35.00 polarity:+



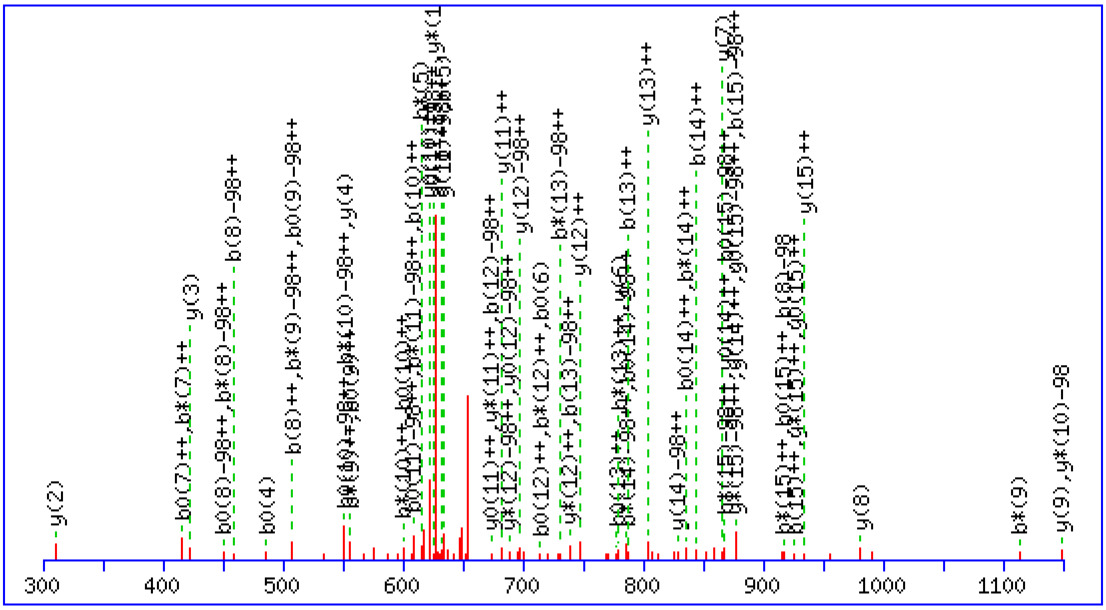
Monoisotopic mass of neutral peptide Mr(calc): 1859.8527
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 **Expect:** 5.1e-008
Matched b ions: b(3)-98, b(4), b(4)-98, b(5), b(6)-98, b(9)-98, b(11), b(11)++, b(12)++, b(13)-98++, b(16)-98++, b(17)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)++

Peptide No.673

QDFLKTDSDSDLQLYK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **QDFLKTDSDSDLQLYK**
Found in **AMPD2_MOUSE** in **SwissProt**, AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1

Match to Query 4978: 1994.889156 from(665.970328,3+) index(6529)
Title: Elution from: 45.098 to 45.098 scan no 4613 cid35.00 polarity:+:m1s



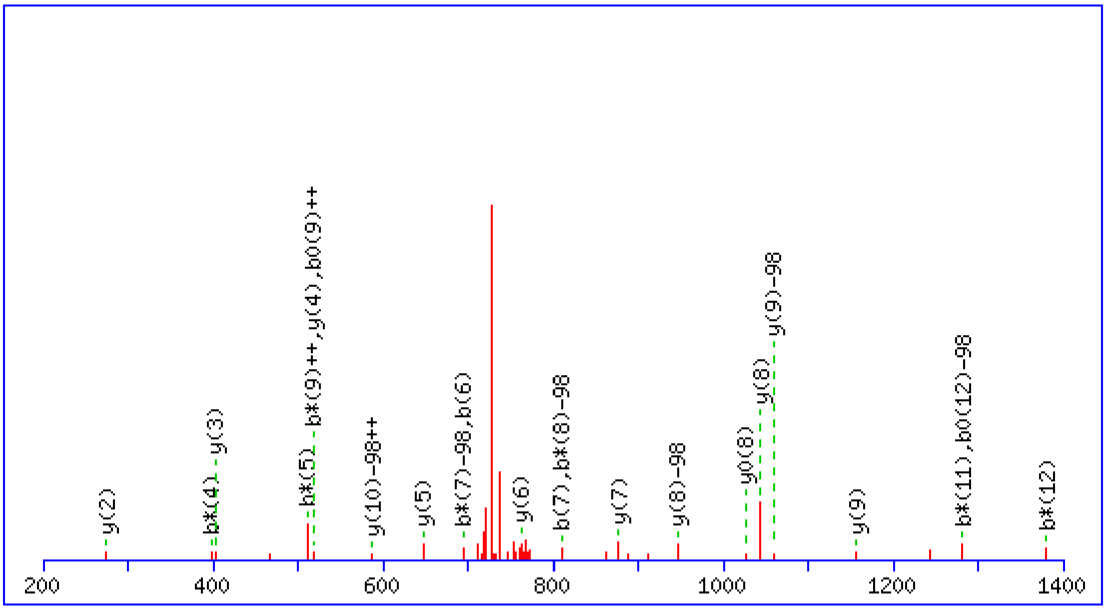
Monoisotopic mass of neutral peptide Mr(calc): 1994.8874
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0053
Matched b ions: b(5), b(8)++, b(8)-98, b(8)-98++, b(10)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(8), y(9), y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++

Peptide No.674

QGDNISDDEDEVR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **QGDNISDDEDEVR**
Found in **STX4_MOUSE** in **SwissProt**, Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1

Match to Query 2709: 1570.576968 from(786.295760,2+) index(1002)
Title: Elution from: 25.729 to 25.729 scan no 1990 cid35.00 polarity:+



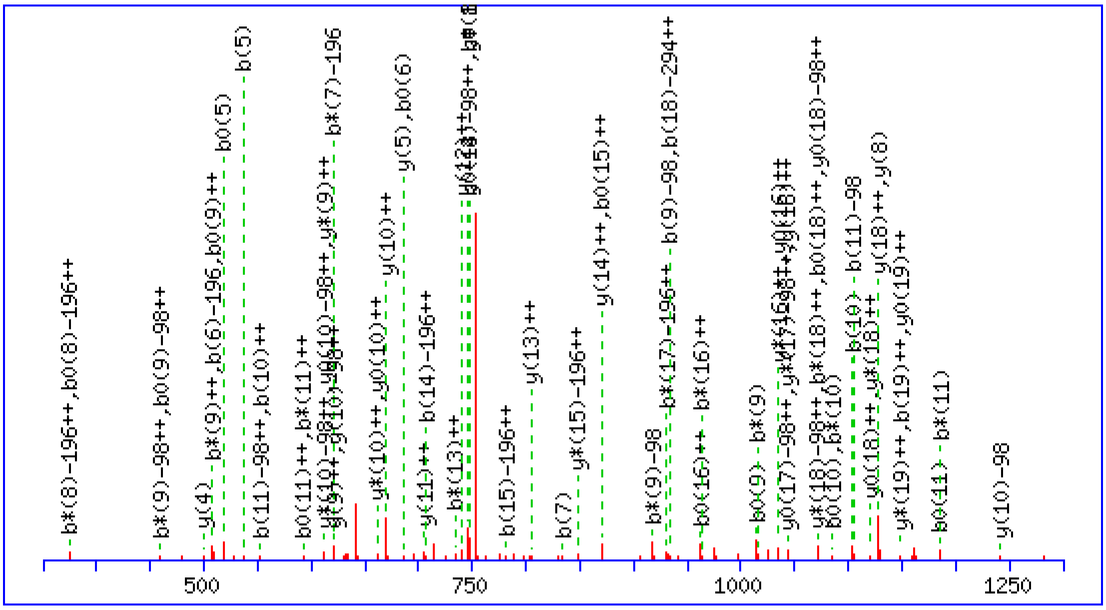
Monoisotopic mass of neutral peptide Mr(calc): 1570.5784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00022
Matched b ions: b(6), b(7)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(9)-98, y(10)-98++

Peptide No.675

QGGITSEQAAVISKFWKSHK
Confirmed sites: @T:5,@S:6,@S:13
Ambiguous sites:

MS/MS Fragmentation of **QGGITSEQAAVISKFWKSHK**
Found in **COMD1_MOUSE** in **SwissProt**, COMM domain-containing protein 1 OS=Mus musculus GN=Commd1 PE=2 SV=2

Match to Query 6262: 2441.062188 from(814.694672,3+) index(147)
Title: Elution from: 17.259 to 17.259 scan no 917 cid35.00 polarity:+



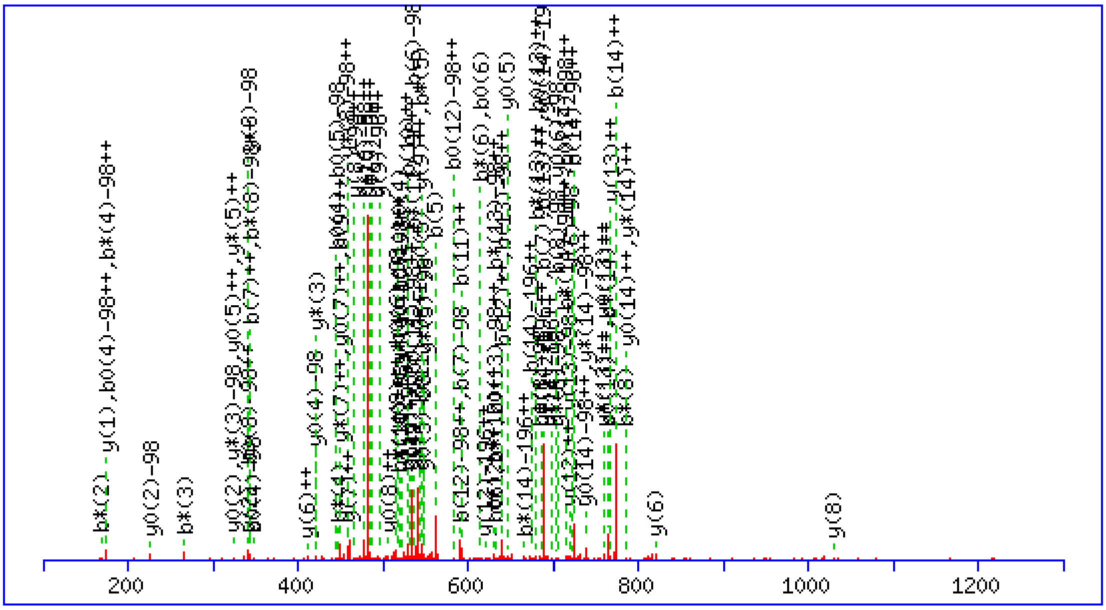
Monoisotopic mass of neutral peptide Mr(calc): 2441.0583
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.038
Matched b ions: b(5), b(6)-196, b(7), b(9)-98, b(10), b(10)++, b(11)-98++, b(11)-98, b(14)-196++, b(15)-196++, b(18)-294++, b(19)++
Matched y ions: y(4), y(5), y(8), y(9)++, y(10)++, y(10)-98++, y(10)-98, y(11)++, y(12)++, y(13)++, y(14)++, y(16)++, y(18)++

Peptide No.676

QGPTPAGLPRQPPSR
Confirmed sites: @T:4,@S:14
Ambiguous sites:

MS/MS Fragmentation of **QGPTPAGLPRQPPSR**
Found in **MRCKB_MOUSE** in **SwissProt**, Serine/threonine-protein kinase MRCK beta OS=Mus musculus GN=Cdc42bpb PE=1 SV=2

Match to Query 3704: 1717.769196 from(573.597008,3+) index(1336)
Title: Elution from: 39.756 to 39.756 scan no 2955 cid35.00 polarity:+



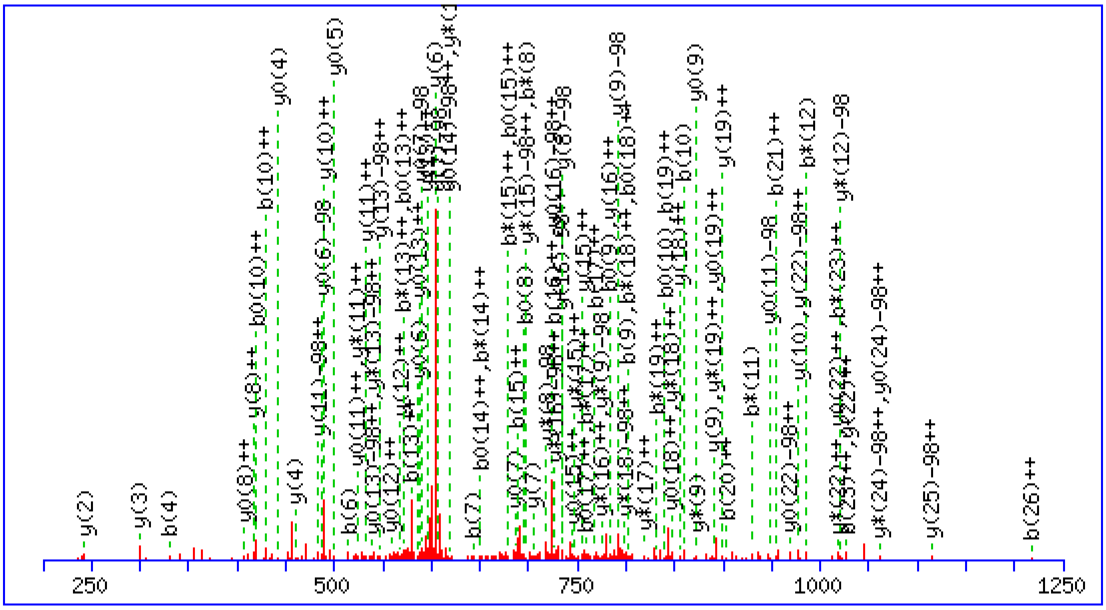
Monoisotopic mass of neutral peptide Mr(calc): 1717.7702
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.019
Matched b ions: b(5), b(6)-98, b(6), b(7), b(7)-98, b(7)++, b(8)-98, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(14)-196++
Matched y ions: y(1), y(2), y(3)-98, y(4), y(6), y(6)++, y(6)-98, y(7)++, y(8)++, y(8), y(8)-98++, y(9)++, y(9)-98++, y(10)-98++, y(12)++, y(12)-196++, y(13)++, y(13)-98++, y(14)-196++

Peptide No.677

QGSGQGQASGSGRCGASSGQTSGCGSG
Confirmed sites: @S:26
Ambiguous sites:

MS/MS Fragmentation of **QGSGQGQASGSGRCGASSGQTSGCGSG**
Found in **HORN_MOUSE** in **SwissProt**, Hornerin OS=Mus musculus GN=Hrnr PE=1 SV=1

Match to Query 5376: 2508.930620 from(628.239931,4+) index(3834)
Title: Elution from: 23.414 to 23.414 scan no 1676 cid35.00 polarity:+:m1s



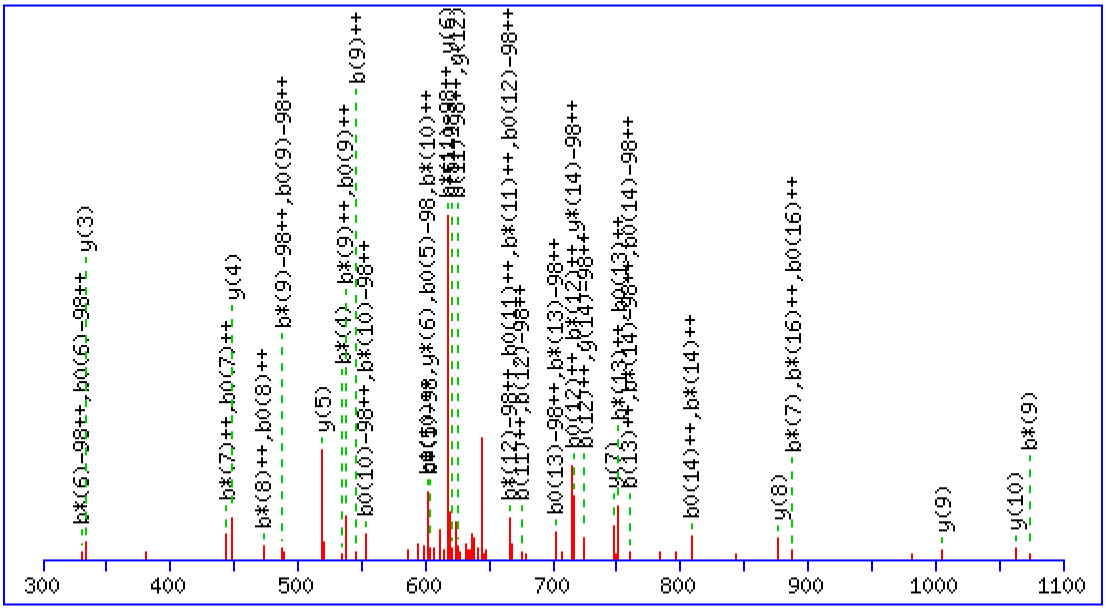
Monoisotopic mass of neutral peptide Mr(calc): 2508.9344
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S26 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.019
Matched b ions: b(4), b(6), b(7), b(9), b(10)++, b(10), b(13)++, b(15)++, b(16)++, b(17)++, b(19)++, b(20)++, b(21)++, b(23)++, b(26)++
Matched y ions: y(2), y(3), y(4), y(6), y(7)-98, y(7), y(8)++, y(8)-98, y(9)-98, y(9), y(10)++, y(10), y(11)-98++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(15)++, y(16)-98++, y(16)++, y(18)++, y(19)++, y(22)-98++, y(22)++, y(25)-98++

Peptide No.678

QHRESGEGEEEVADSAR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **QHRESGEGEEEVADSAR**
Found in **LRC47_MOUSE** in **SwissProt**, Leucine-rich repeat-containing protein 47 OS=Mus musculus GN=Lrrc47 PE=1 SV=1

Match to Query 4070: 1964.784960 from(655.935596,3+) index(3256)
Title: Elution from: 18.396 to 18.396 scan no 1011 cid35.00 polarity:+:m1s



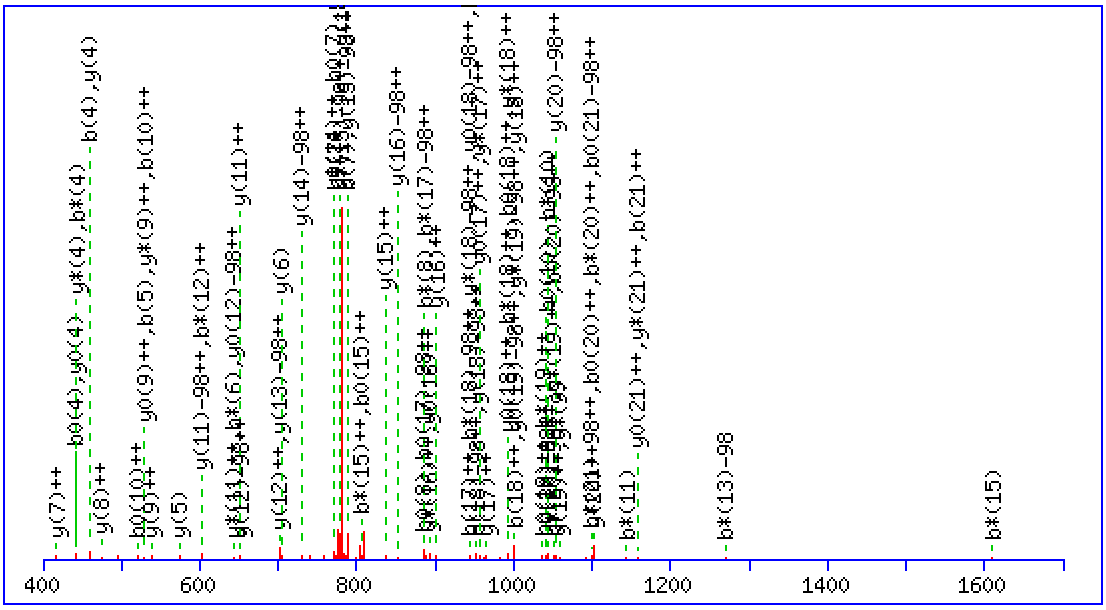
Monoisotopic mass of neutral peptide Mr(calc): 1964.7861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 2.2e-005
Matched b ions: b(5)-98, b(9)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(14)-98++

Peptide No.679

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 6125: 2457.997923 from(820.339917,3+) index(3658)
Title: Elution from: 17.592 to 17.592 scan no 926 cid35.00 polarity:+:m1s



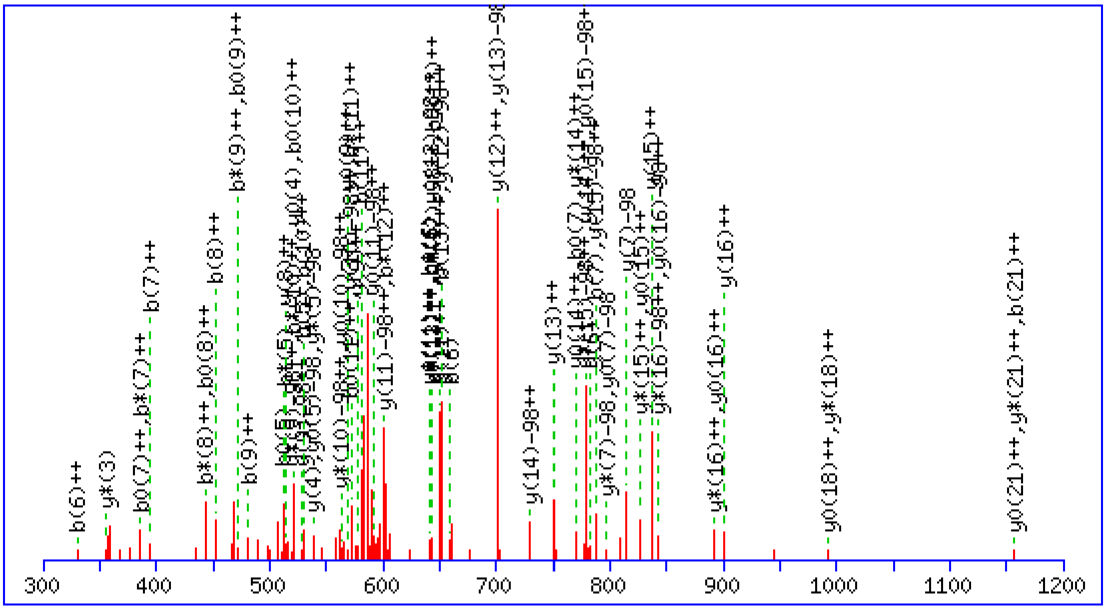
Monoisotopic mass of neutral peptide Mr(calc): 2458.0020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 **Expect:** 3.6e-007
Matched b ions: b(4), b(5), b(7), b(10)++, b(17)++, b(18)++, b(18)-98++, b(21)++
Matched y ions: y(4), y(5), y(6), y(7)++, y(8)++, y(9)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(20)++, y(20)-98++

Peptide No.680

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 5300: 2458.002992 from(615.508024,4+) index(3173)
Title: Elution from: 17.443 to 17.443 scan no 900 cid35.00 polarity:+:m1s



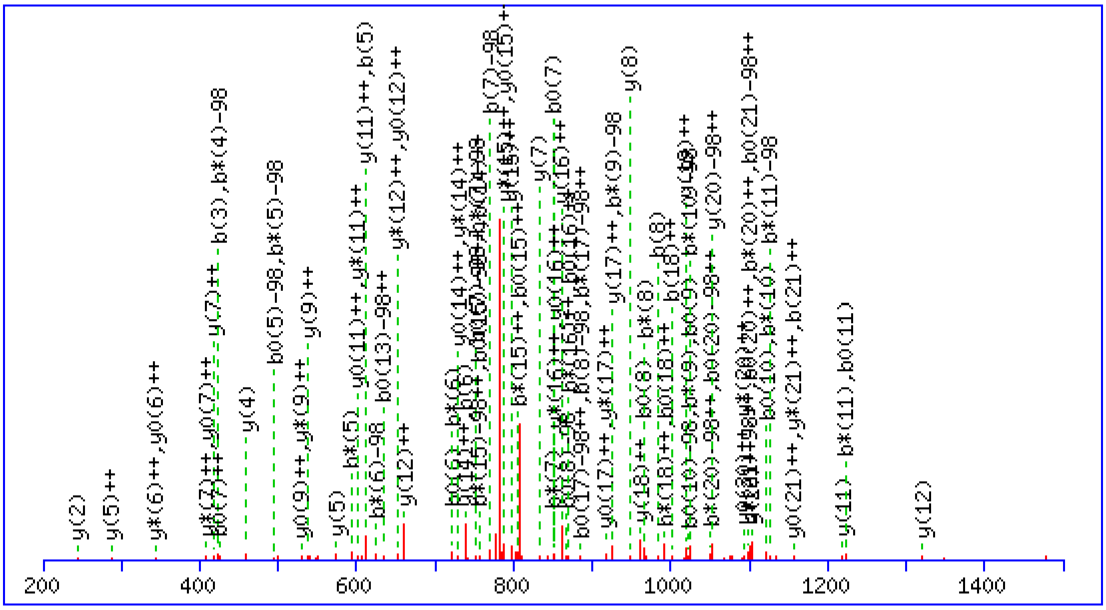
Monoisotopic mass of neutral peptide Mr(calc): 2458.0020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0058
Matched b ions: b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(9)++, b(10)++, b(11)++, b(13)++, b(21)++
Matched y ions: y(4), y(6), y(7)-98, y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++

Peptide No.681

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 5337: 2458.001667 from(820.341165,3+) index(2994)
Title: Elution from: 22.917 to 22.917 scan no 1082 cid35.00 polarity:+:m1s



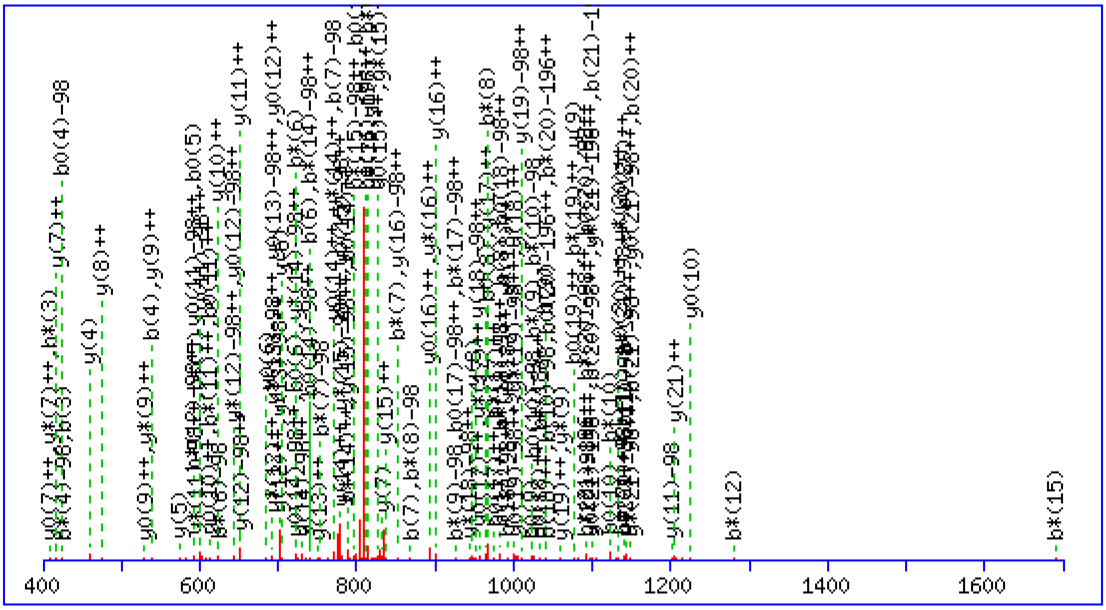
Monoisotopic mass of neutral peptide Mr(calc): 2458.0020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 84 **Expect:** 2.3e-008
Matched b ions: b(3), b(5), b(6), b(7)-98, b(8)-98, b(8), b(14)++, b(18)++, b(21)++
Matched y ions: y(2), y(4), y(5)++, y(5), y(7)++, y(7), y(8), y(9)++, y(11)++, y(11), y(12), y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(20)-98++

Peptide No.682

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:3,@S:13
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 5427: 2537.964288 from(846.995372,3+) index(3271)
Title: Elution from: 18.546 to 18.546 scan no 1030 cid35.00 polarity:+:m1s



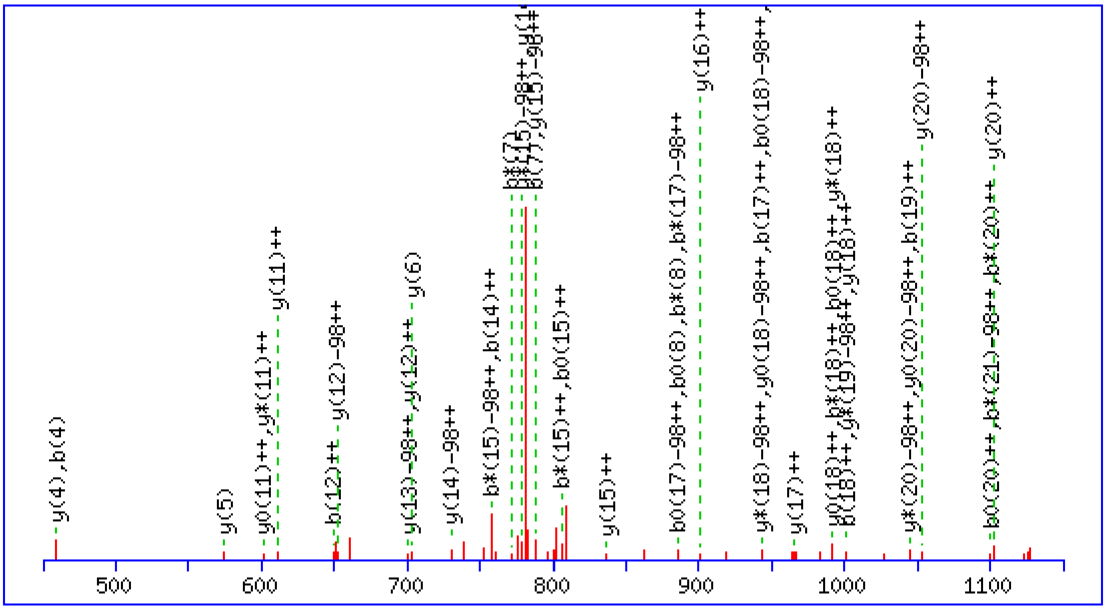
Monoisotopic mass of neutral peptide Mr(calc): 2537.9684
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 83 **Expect:** 2.5e-008
Matched b ions: b(3), b(4), b(6), b(7)-98, b(7), b(8), b(9), b(10), b(10)-98, b(11)-98, b(14)++, b(17)++, b(18)++, b(18)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)-196++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)-98++, y(11)++, y(11)-98, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++

Peptide No.683

QKSDAEEDGVTGSQDEEDSKPK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 6297: 2457.999321 from(820.340383,3+) index(3813)
Title: Elution from: 17.420 to 17.420 scan no 935 cid35.00 polarity:+:m1s



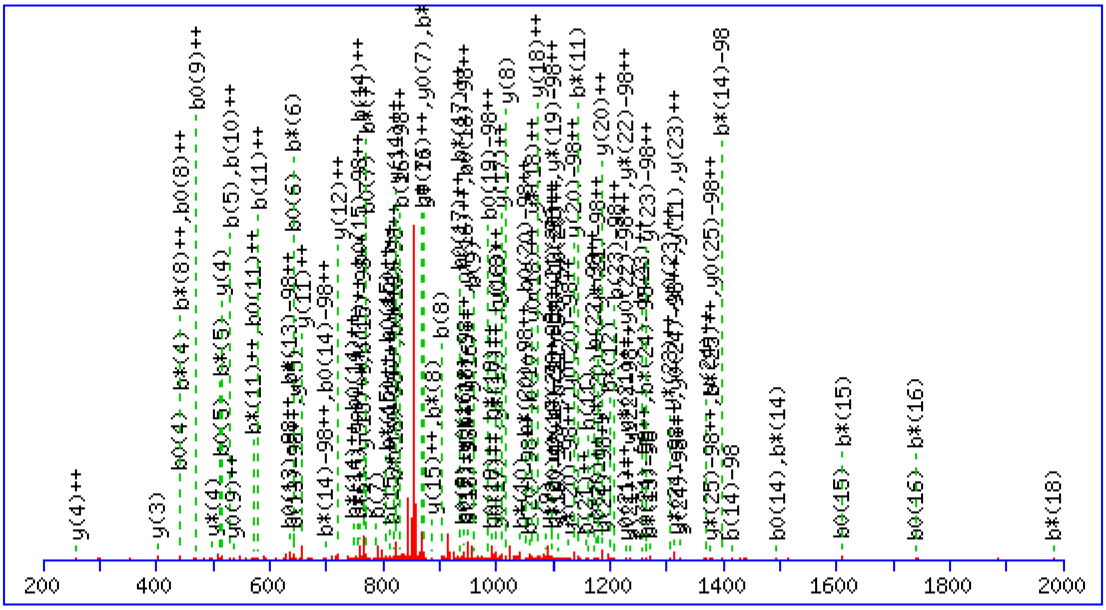
Monoisotopic mass of neutral peptide Mr(calc): 2458.0020
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.03
Matched b ions: b(4), b(7), b(12)++, b(14)++, b(17)++, b(18)++, b(19)++
Matched y ions: y(4), y(5), y(6), y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(17)++, y(18)++, y(20)++, y(20)-98++

Peptide No.684

QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 5803: 3527.506612 from(882.883929,4+) index(4074)
Title: Elution from: 37.139 to 37.139 scan no 2656 cid35.00 polarity:+:m1s



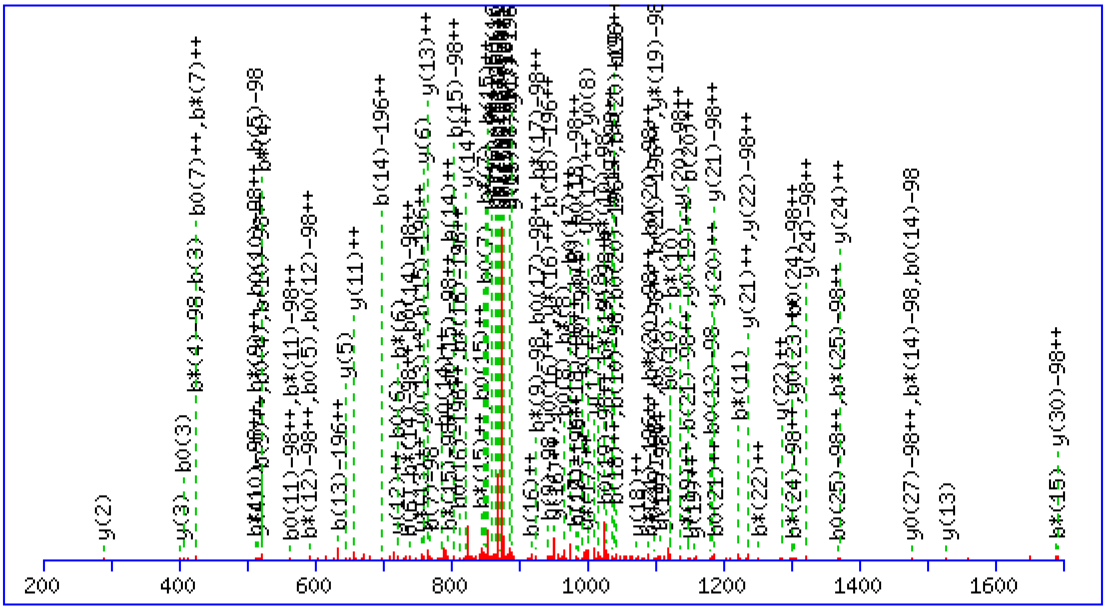
Monoisotopic mass of neutral peptide Mr(calc): 3527.5060
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.021
Matched b ions: b(5), b(7), b(8), b(9), b(10), b(10)++, b(11)++, b(11), b(13)-98++, b(14)-98, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(23)-98++, b(23)++
Matched y ions: y(3), y(4)++, y(4), y(5), y(6), y(8), y(9), y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(23)++, y(23)-98++, y(24)++, y(24)-98++

Peptide No.685

QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR
Confirmed sites: @S:3,@S:13
Ambiguous sites:

MS/MS Fragmentation of **QKSDAEEDGVTGSQDEEDSKPKAEEDEILNR**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 6743: 3607.472904 from(902.875502,4+) index(4992)
Title: Elution from: 40.222 to 40.222 scan no 3150 cid35.00 polarity:+:m1s



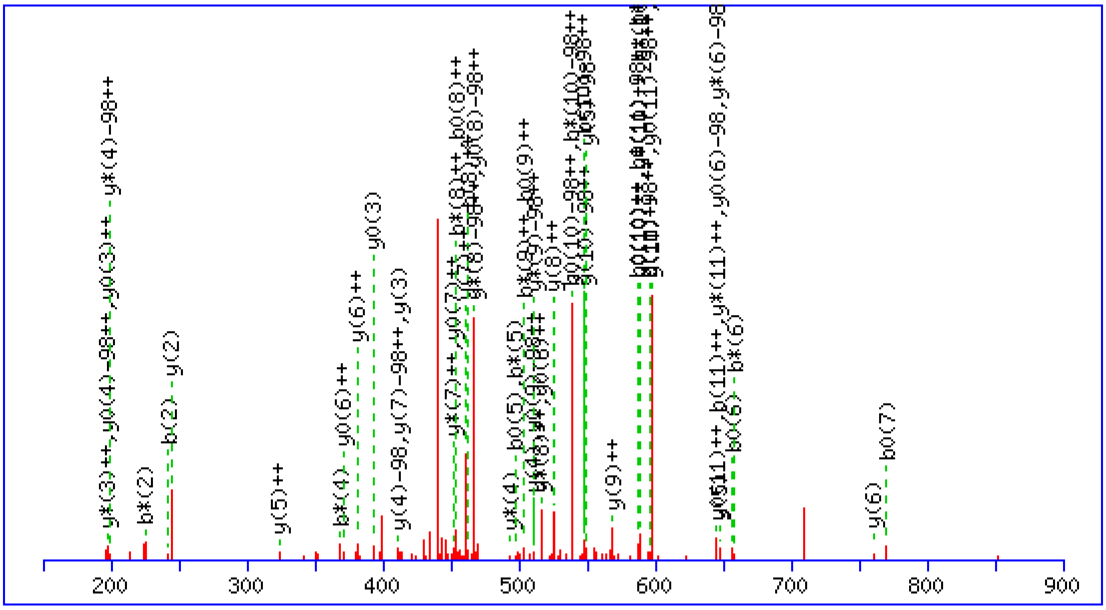
Monoisotopic mass of neutral peptide Mr(calc): 3607.4723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.048
Matched b ions: b(3), b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)++, b(9)-98, b(9), b(10)-98++, b(10)-98, b(13)-196++, b(14)-196++, b(14)++, b(15)++, b(15)-196++, b(15)-98++, b(16)-98++, b(16)++, b(17)-196++, b(17)++, b(18)++, b(18)-196++, b(18)-98++, b(19)-196++, b(19)-98++, b(20)-98++, b(20)++, b(21)-196++, b(21)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(11)++, y(12)++, y(13)++, y(13), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)-98++, y(22)++, y(24)-98++, y(24)++, y(30)-98++

Peptide No.686

QLGSECLHVSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **QLGSECLHVSPK**
Found in **ACOT1_MOUSE** in **SwissProt**, Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1 PE=1 SV=1

Match to Query 2665: 1433.636991 from(478.886273,3+) index(1339)
Title: Elution from: 27.693 to 27.693 scan no 2321 cid35.00 polarity:+



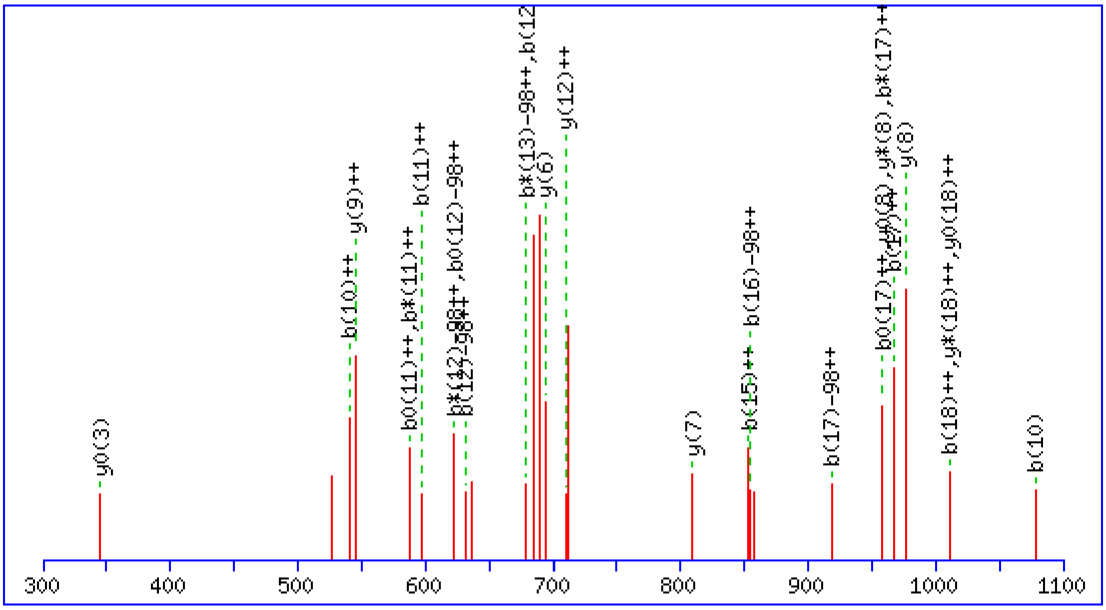
Monoisotopic mass of neutral peptide Mr(calc): 1433.6374
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.031
Matched b ions: b(2), b(8)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++
Matched y ions: y(2), y(3), y(4)-98, y(4), y(5), y(5)++, y(5)-98, y(6)++, y(6), y(7)++, y(7)-98++, y(8)++, y(9)++, y(10)++, y(10)-98++

Peptide No.687

QLHIEGASLELSDDDTESK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **QLHIEGASLELSDDDTESK**
Found in **MYH10_MOUSE** in **SwissProt**, Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2

Match to Query 5461: 2165.936898 from(722.986242,3+) index(6352)
Title: Elution from: 44.892 to 44.892 scan no 4554 cid35.00 polarity:+:m1s



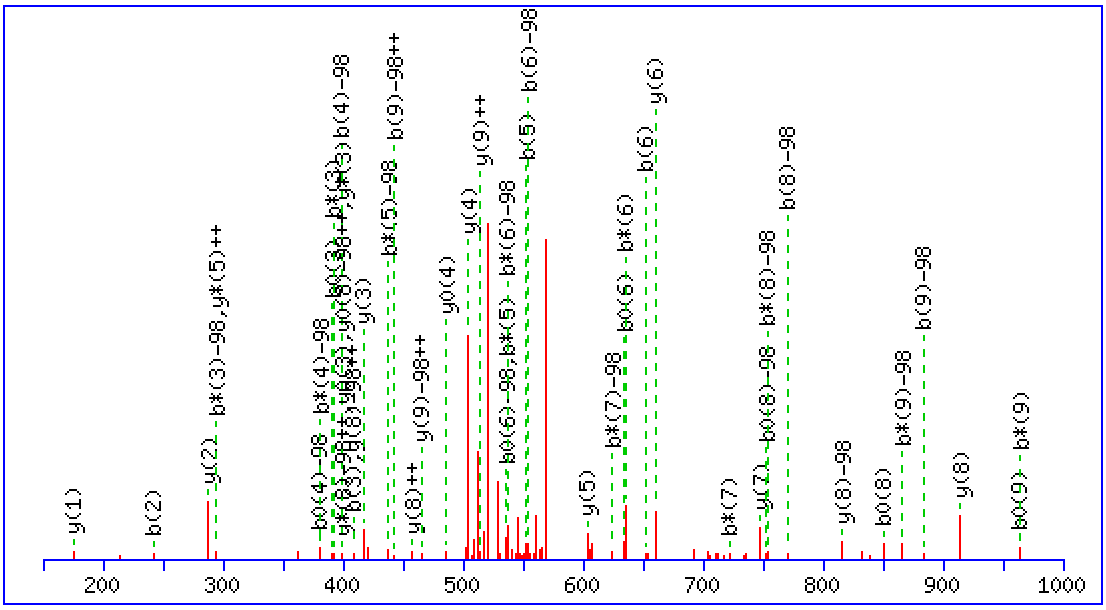
Monoisotopic mass of neutral peptide Mr(calc): 2165.9365
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(6), b(10)++, b(10), b(11)++, b(12)-98++, b(12)++, b(15)++, b(16)-98++, b(17)-98++, b(17)++, b(18)++
Matched y ions: y(6), y(7), y(8), y(9)++, y(12)++

Peptide No.688

QLSSGVSEIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QLSSGVSEIR**
Found in **HSPB1_MOUSE** in **SwissProt**, Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3

Match to Query 1226: 1154.533312 from(578.273932,2+) index(1312)
Title: Elution from: 28.596 to 28.596 scan no 2380 cid35.00 polarity:+



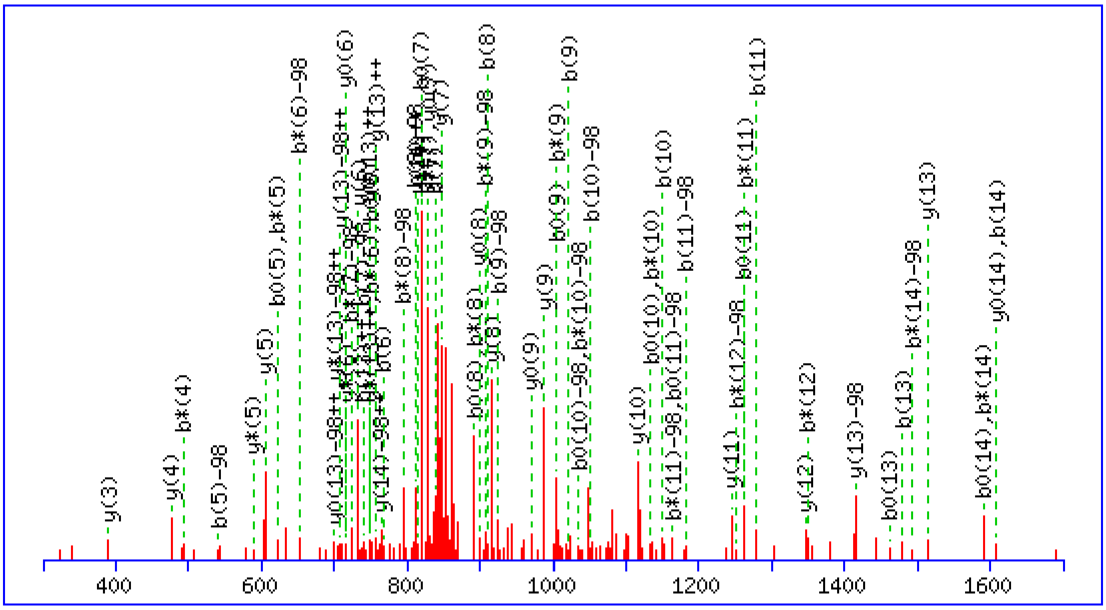
Monoisotopic mass of neutral peptide Mr(calc): 1154.5332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 **Expect:** 1.2e-005
Matched b ions: b(2), b(3), b(4)-98, b(5), b(6), b(6)-98, b(8)-98, b(9)-98, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(8)++, y(8)-98++, y(9)-98++, y(9)++

Peptide No.689

QLSTEQAALQESLEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QLSTEQAALQESLEK**
Found in **MTUS1_MOUSE** in **SwissProt**, Microtubule-associated tumor suppressor 1 homolog OS=Mus musculus GN=Mtus1 PE=1 SV=2

Match to Query 4415: 1753.812578 from(877.913565,2+) index(2335)
Title: Elution from: 53.599 to 53.599 scan no 4512 cid35.00 polarity:+



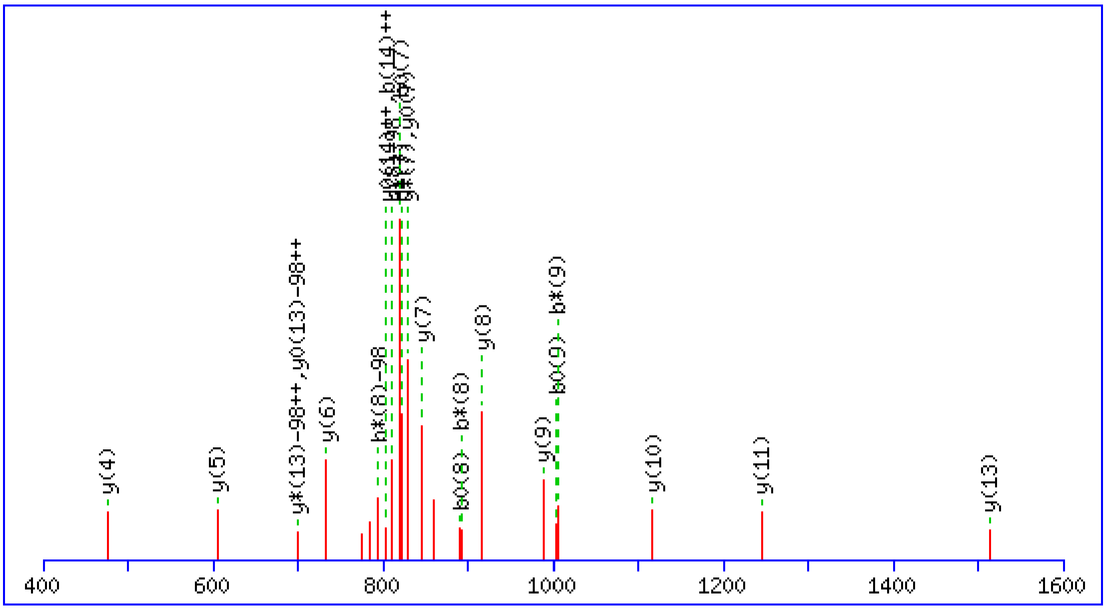
Monoisotopic mass of neutral peptide Mr(calc): 1753.8135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 **Expect:** 2.4e-006
Matched b ions: b(5)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98, b(13), b(13)++, b(14)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(13)-98++, y(13)++, y(14)-98++, y(14)++

Peptide No.690

QLSTEQAALQESLEK
Confirmed sites:
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of **QLSTEQAALQESLEK**
Found in **MTUS1_MOUSE** in **SwissProt**, Microtubule-associated tumor suppressor 1 homolog OS=Mus musculus GN=Mtus1 PE=1 SV=2

Match to Query 4064: 1753.811968 from(877.913260,2+) index(2883)
Title: Elution from: 45.157 to 45.157 scan no 4621 cid35.00 polarity:+



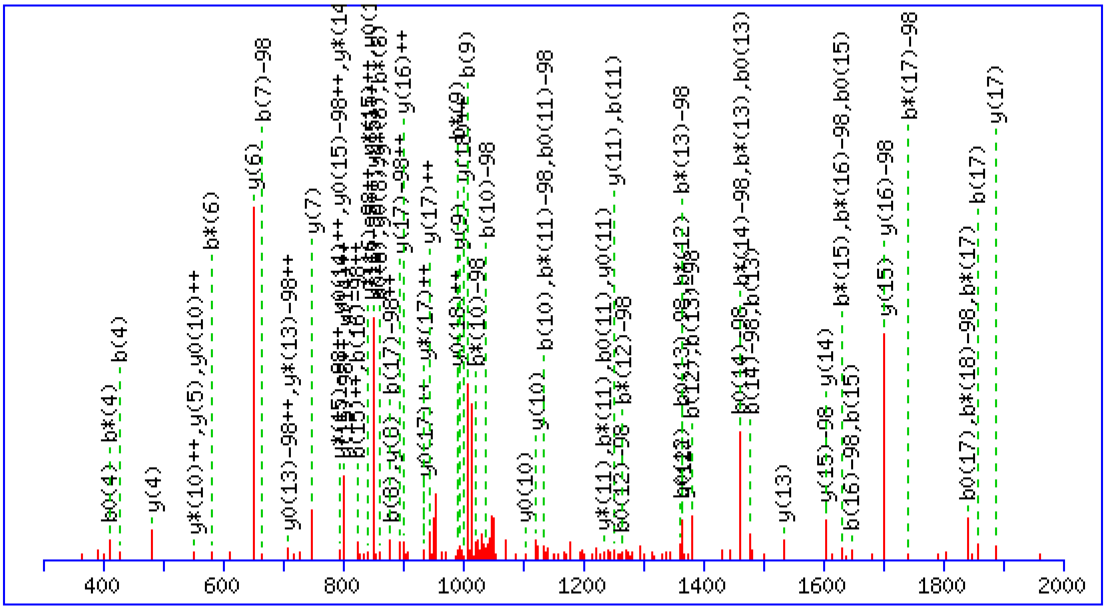
Monoisotopic mass of neutral peptide Mr(calc): 1753.8135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 71 **Expect:** 4.7e-007
Matched b ions: b(8)-98, b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13)

Peptide No.691

QLSVPASDEEDEVPAPIPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **QLSVPASDEEDEVPAPIPR**
Found in **ABCF1_MOUSE** in **SwissProt**, ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1

Match to Query 5413: 2127.969114 from(1064.991833,2+) index(5710)
Title: Elution from: 52.667 to 52.667 scan no 4428 cid35.00 polarity:+:m1s



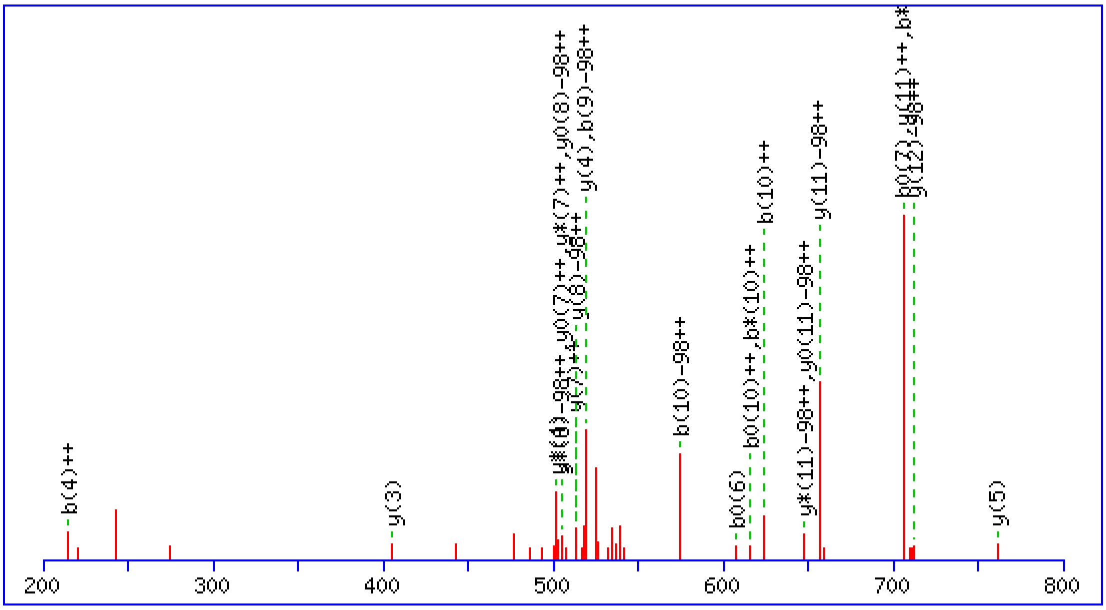
Monoisotopic mass of neutral peptide Mr(calc): 2127.9725
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 **Expect:** 4.4e-006
Matched b ions: b(4), b(7)-98, b(8), b(9), b(10), b(10)-98, b(11), b(12), b(13), b(13)-98, b(14)-98, b(15)++, b(15), b(16)-98++, b(16)-98, b(17), b(17)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)++, y(14), y(15)++, y(15)-98, y(15), y(15)-98++, y(16)-98++, y(16)-98, y(16)++, y(17), y(17)++, y(17)-98++, y(18)++

Peptide No.692

QLSVVVPSYNEEK
Confirmed sites: @S:8,@Y:9
Ambiguous sites:

MS/MS Fragmentation of **QLSVVVPSYNEEK**
Found in **ALG5_MOUSE** in **SwissProt**, Dolichyl-phosphate beta-glucosyltransferase OS=Mus musculus GN=Alg5 PE=2 SV=1

Match to Query 3414: 1650.698319 from(551.240049,3+) index(5544)
Title: Elution from: 34.940 to 34.940 scan no 3267 cid35.00 polarity:+:m1s



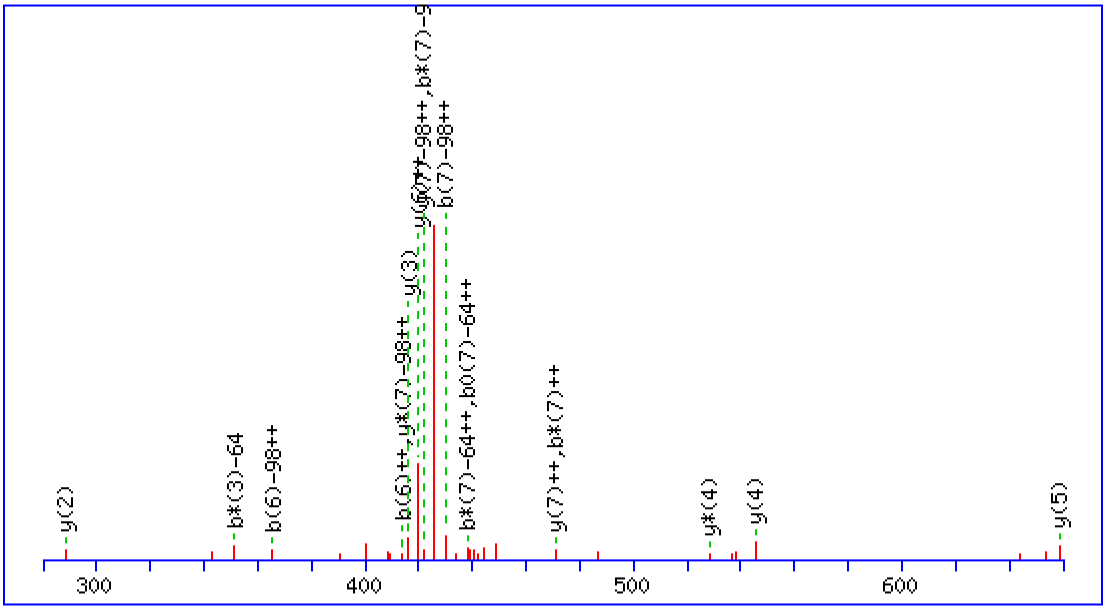
Monoisotopic mass of neutral peptide Mr(calc): 1650.6943
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y9 : Phospho (Y)
Ions Score: 24 **Expect:** 0.02
Matched b ions: b(4)++, b(9)-98++, b(10)-98++, b(10)++
Matched y ions: y(3), y(4), y(5), y(7)++, y(8)-98++, y(11)++, y(11)-98++, y(12)-98++

Peptide No.693

QMRTTLEKIR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **QMRTTLEKIR**
Found in **CCD68_MOUSE** in **SwissProt**, Coiled-coil domain-containing protein 68 OS=Mus musculus GN=Ccdc68 PE=2 SV=1

Match to Query 2018: 1370.670396 from(457.897408,3+) index(1546)
Title: Elution from: 31.503 to 31.503 scan no 2757 cid35.00 polarity:+



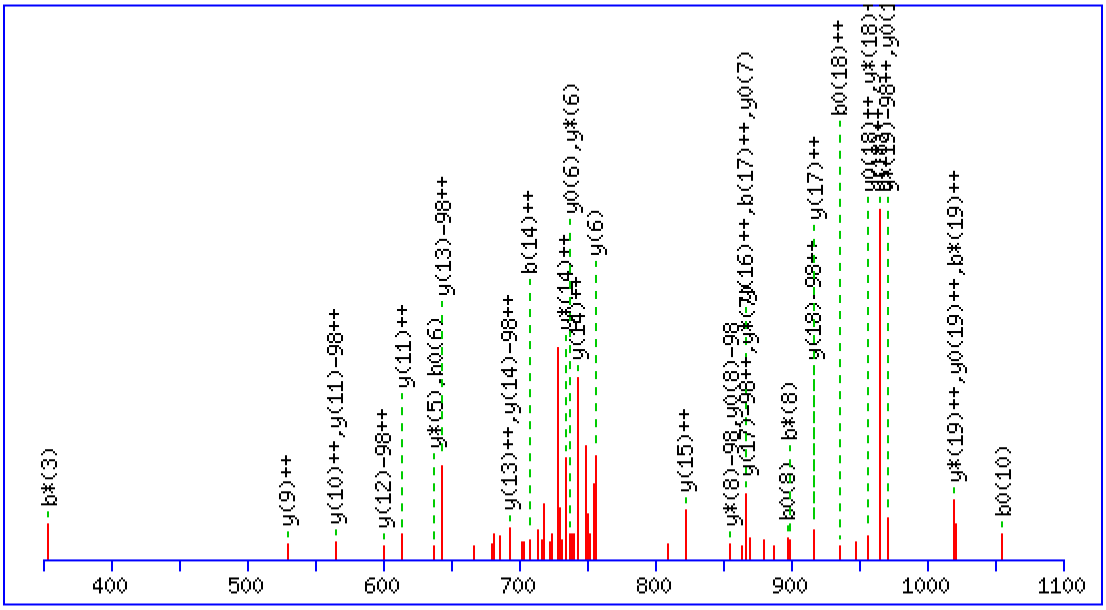
Monoisotopic mass of neutral peptide Mr(calc): 1370.6741
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 18 **Expect:** 0.055
Matched b ions: b(6)-98++, b(6)++, b(7)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(7)-98++, y(7)++

Peptide No.694

QNQPTSCVSAPASSETSRSPK
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **QNQPTSCVSAPASSETSRSPK**
Found in **RBP2_MOUSE** in **SwissProt**, E3 SUMO-protein ligase RanBP2 OS=Mus musculus GN=Ranbp2 PE=1 SV=2

Match to Query 5978: 2297.989965 from(767.003931,3+) index(4159)
Title: Elution from: 20.406 to 20.406 scan no 1329 cid35.00 polarity:+:m1s



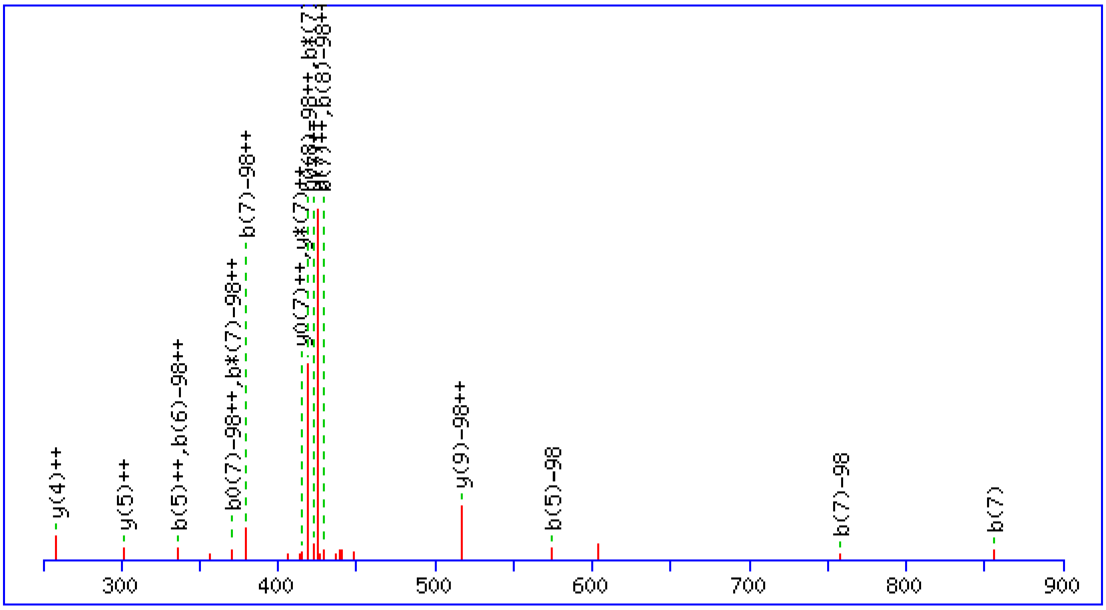
Monoisotopic mass of neutral peptide Mr(calc): 2297.9947
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 5.2e-005
Matched b ions: b(14)++, b(17)++
Matched y ions: y(6), y(8), y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++

Peptide No.695

QNSDFPSPSRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QNSDFPSPSRR**
Found in **CENPL_MOUSE** in **SwissProt**, Centromere protein L OS=Mus musculus GN=Cenpl PE=2 SV=2

Match to Query 2232: 1369.578861 from(457.533563,3+) index(6070)
Title: Elution from: 40.716 to 40.716 scan no 4035 cid35.00 polarity:+:m1s



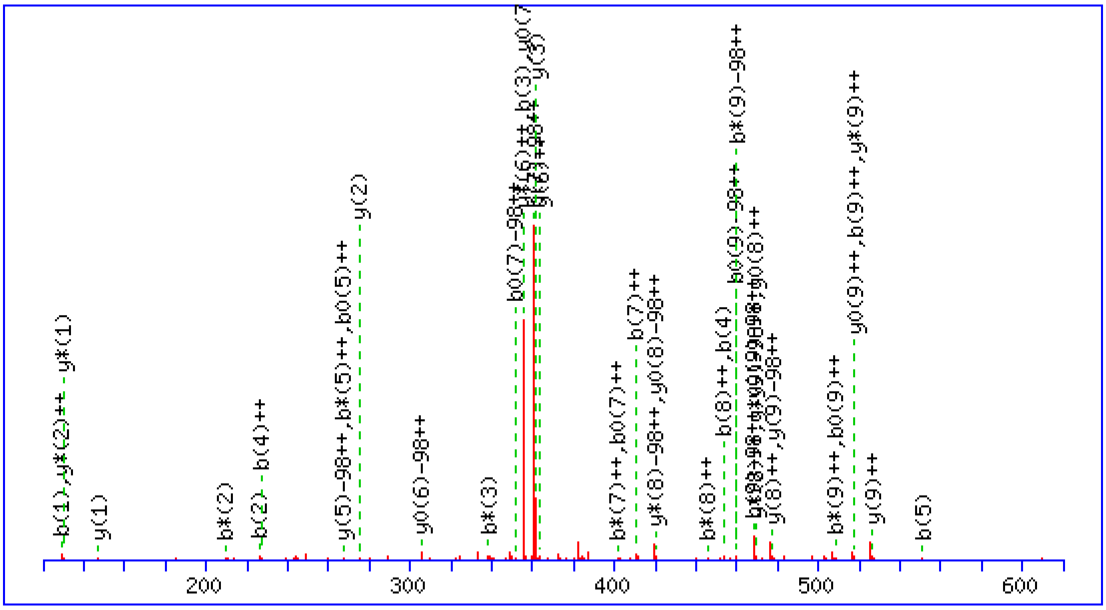
Monoisotopic mass of neutral peptide Mr(calc): 1369.5776
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.015
Matched b ions: b(5)-98, b(5)++, b(6)-98++, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)-98++
Matched y ions: y(4)++, y(5)++, y(7)++, y(9)-98++

Peptide No.696

QPEVPTSSKK
Confirmed sites:
Ambiguous sites: @T:6orS:7

MS/MS Fragmentation of **QPEVPTSSKK**
Found in **EFCB5_MOUSE** in **SwissProt**, EF-hand calcium-binding domain-containing protein 5 OS=Mus musculus GN=Efcab5 PE=2 SV=2

Match to Query 1443: 1179.555309 from(394.192379,3+) index(618)
Title: Elution from: 21.798 to 21.798 scan no 1481 cid35.00 polarity:+



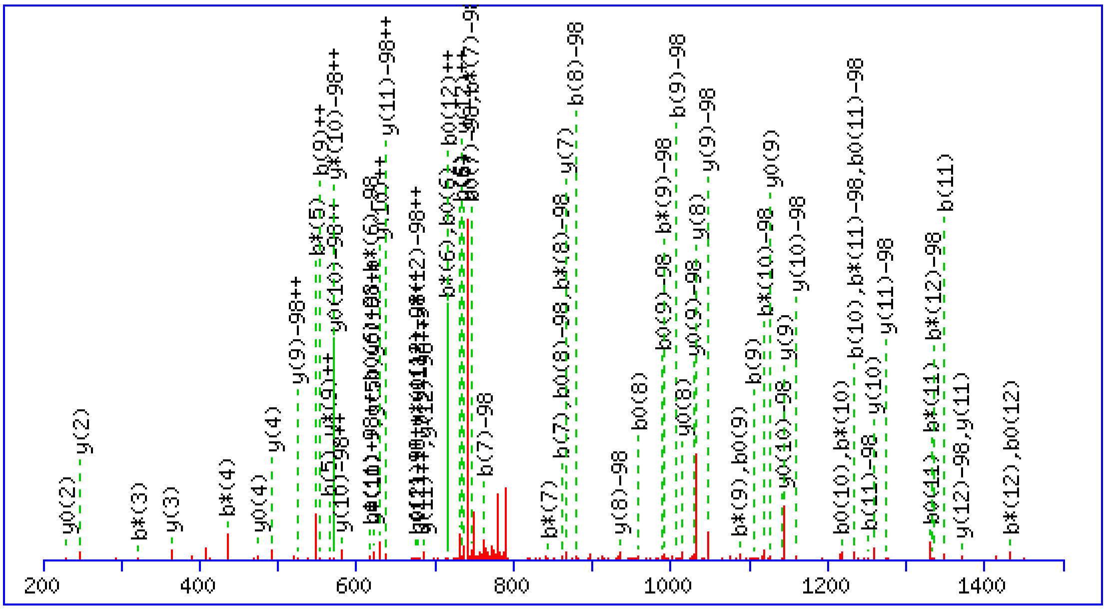
Monoisotopic mass of neutral peptide Mr(calc): 1179.5537
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0085
Matched b ions: b(1), b(2), b(3), b(4)++, b(4), b(5), b(7)-98++, b(7)++, b(8)++, b(9)-98++, b(9)++
Matched y ions: y(1), y(2), y(3), y(5)-98++, y(6)++, y(8)++, y(9)-98++, y(9)++

Peptide No.697

QPLLLSEDEEDTK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **QPLLLSEDEEDTK**
Found in **EIF3C_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1

Match to Query 3330: 1595.696952 from(798.855752,2+) index(1704)
Title: Elution from: 46.301 to 46.301 scan no 3621 cid35.00 polarity:+



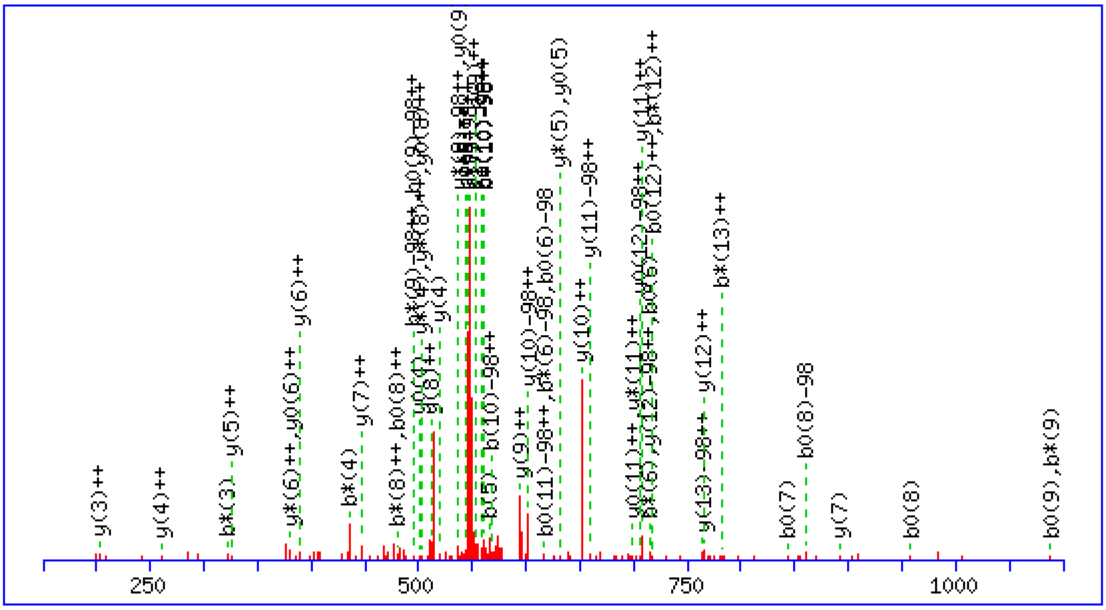
Monoisotopic mass of neutral peptide Mr(calc): 1595.6967
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 **Expect:** 1.6e-006
Matched b ions: b(5), b(6), b(7), b(7)-98, b(8)-98, b(9)++, b(9)-98, b(9), b(10), b(11), b(11)-98, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(9)-98++, y(10), y(10)++, y(10)-98++, y(10)-98, y(11)++, y(11)-98++, y(11), y(11)-98, y(12)-98++, y(12)-98, y(12)++

Peptide No.698

QPLLLSEDEEDTKR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **QPLLLSEDEEDTKR**
Found in **EIF3C_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1

Match to Query 3832: 1751.798769 from(584.940199,3+) index(4362)
Title: Elution from: 41.198 to 41.198 scan no 3112 cid35.00 polarity:+:m1s



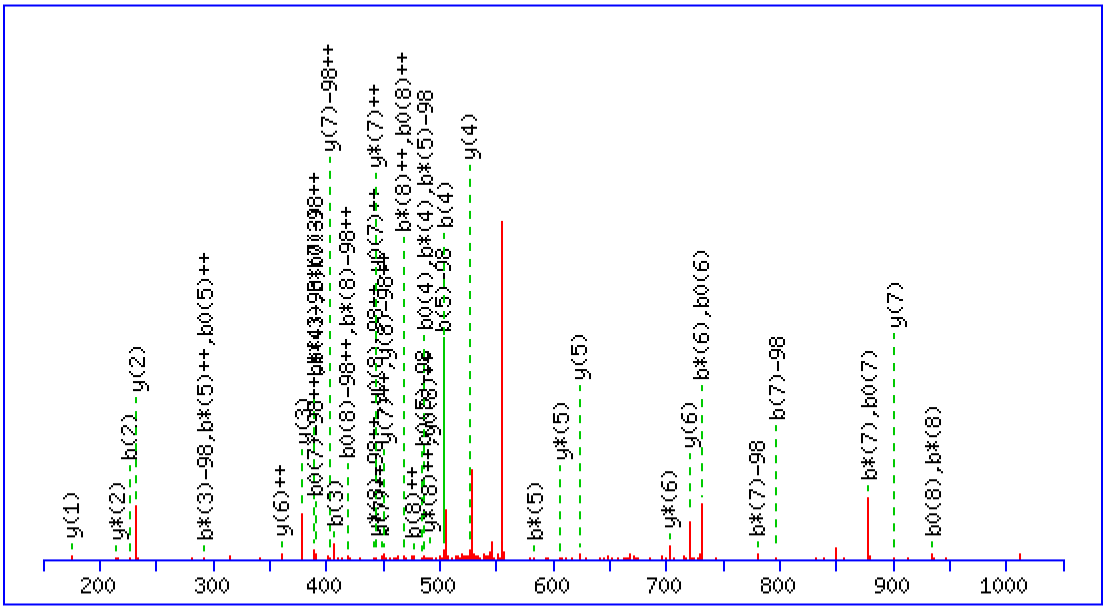
Monoisotopic mass of neutral peptide Mr(calc): 1751.7978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.023
Matched b ions: b(5), b(9)++, b(10)-98++
Matched y ions: y(3)++, y(4)++, y(4), y(5)++, y(6)++, y(7)++, y(7), y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++

Peptide No.699

QPTPPFFGR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **QPTPPFFGR**
Found in **RBM14_MOUSE** in **SwissProt**, RNA-binding protein 14 OS=Mus musculus GN=Rbm14 PE=1 SV=1

Match to Query 1782: 1125.501022 from(563.757787,2+) index(2250)
Title: Elution from: 51.528 to 51.528 scan no 4325 cid35.00 polarity:+



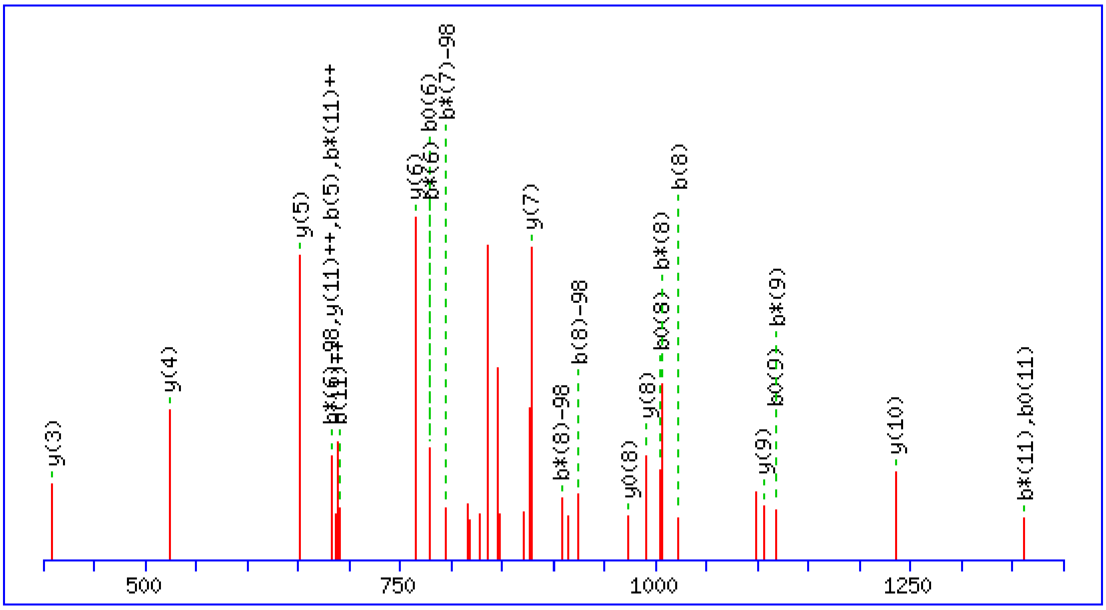
Monoisotopic mass of neutral peptide Mr(calc): 1125.5009
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.0078
Matched b ions: b(2), b(3), b(4), b(5)-98, b(7)-98, b(7)++, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(7)-98++, y(8)-98++

Peptide No.700

QQSEEDLLLQDFSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QQSEEDLLLQDFSR**
Found in **SSRG_MOUSE** in **SwissProt**, Translocon-associated protein subunit gamma OS=Mus musculus GN=Ssr3 PE=1 SV=1

Match to Query 4155: 1786.776728 from(894.395640,2+) index(3392)
Title: Elution from: 57.317 to 57.317 scan no 5916 cid35.00 polarity:+



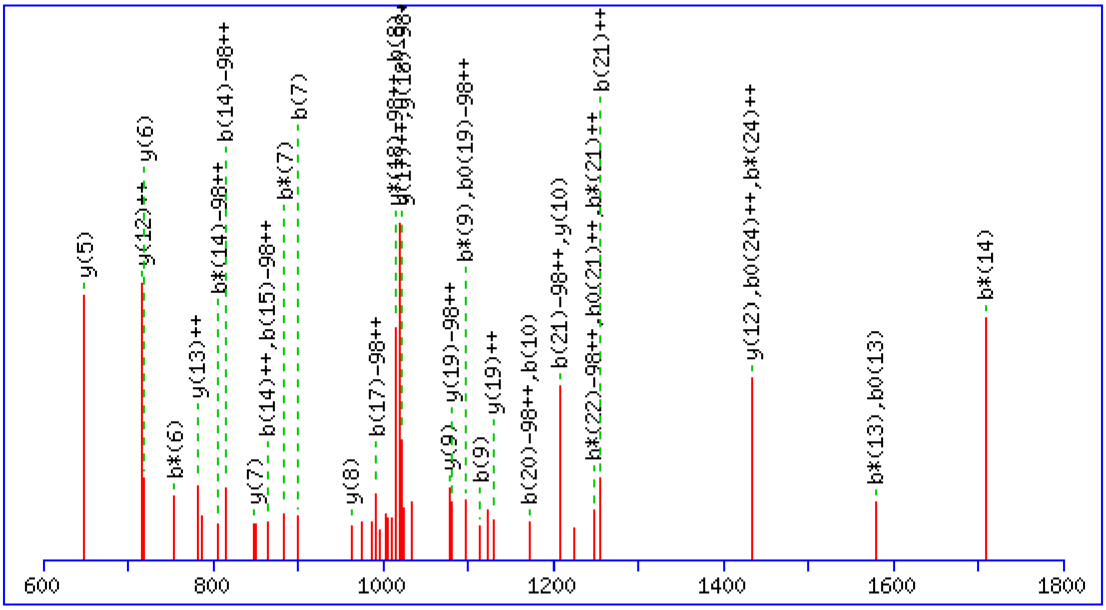
Monoisotopic mass of neutral peptide Mr(calc): 1786.7775
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 4.8e-006
Matched b ions: b(5), b(8), b(8)-98, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++

Peptide No.701

QREMLLEDVGSEEEPEEDDEAPFQEK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **QREMLLEDVGSEEEPEEDDEAPFQEK**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 6796: 3157.289673 from(1053.437167,3+) index(6579)
Title: Elution from: 48.917 to 48.917 scan no 5024 cid35.00 polarity:+:m1s



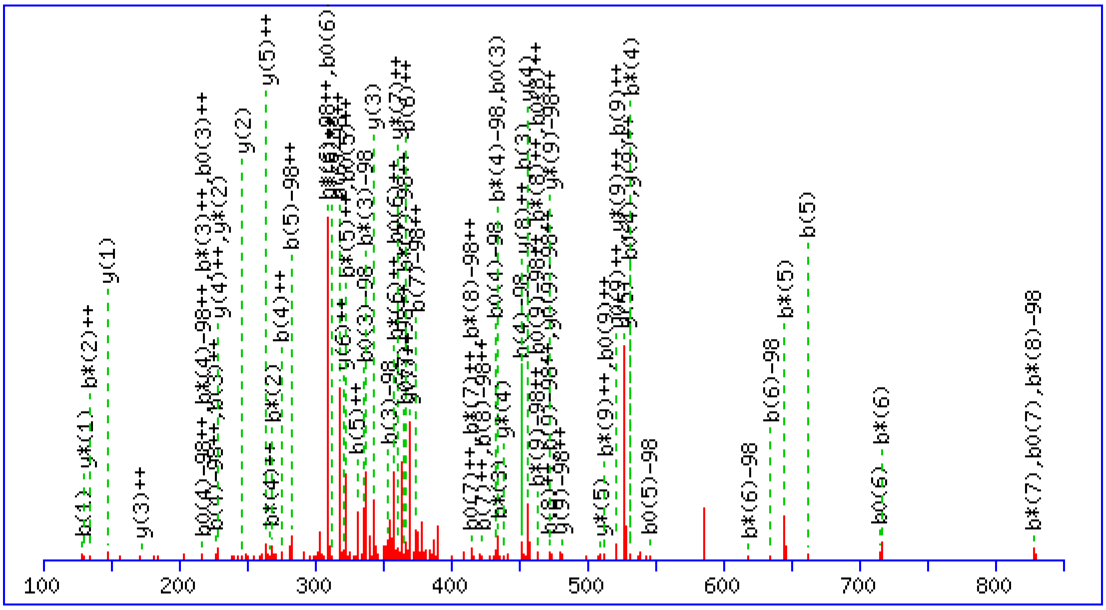
Monoisotopic mass of neutral peptide Mr(calc): 3157.2958
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0042
Matched b ions: b(7), b(8), b(9), b(10), b(14)-98++, b(14)++, b(15)-98++, b(17)-98++, b(20)-98++, b(21)-98++, b(21)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(12)++, y(12), y(13)++, y(17)++, y(18)-98++, y(19)-98++, y(19)++

Peptide No.702

QRSPIALPVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QRSPIALPVK**
Found in **PNISR_MOUSE** in **SwissProt**, Arginine/serine-rich protein PNISR OS=Mus musculus GN=Pnisr PE=1 SV=1

Match to Query 2108: 1187.643081 from(396.888303,3+) index(1355)
Title: Elution from: 37.491 to 37.491 scan no 2825 cid35.00 polarity:+



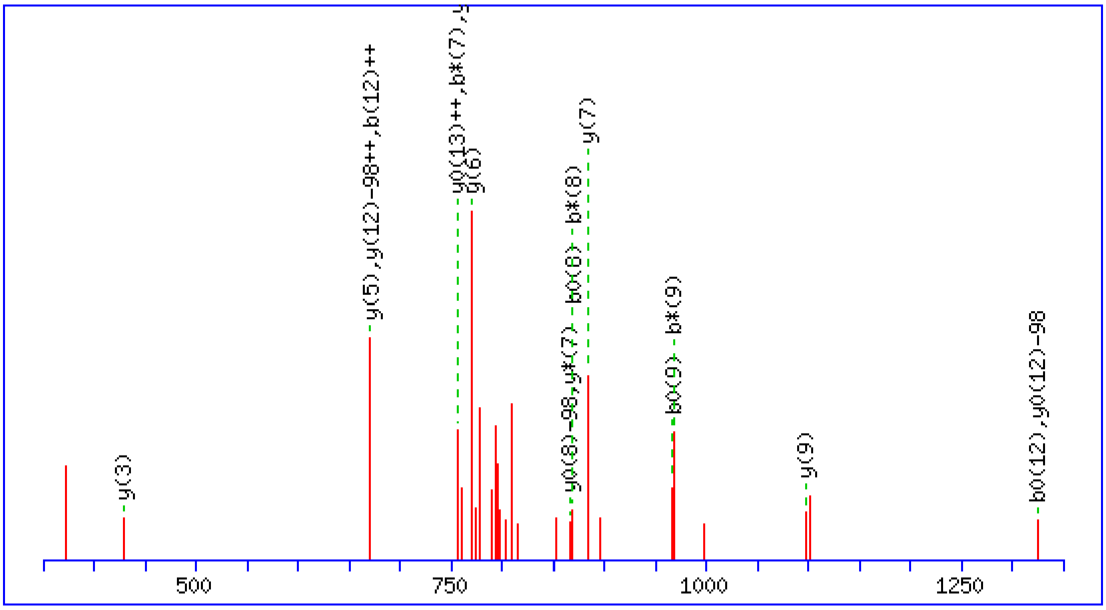
Monoisotopic mass of neutral peptide Mr(calc): 1187.6427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0084
Matched b ions: b(1), b(3)++, b(3), b(3)-98, b(4)-98++, b(4)++, b(4)-98, b(5), b(5)-98++, b(5)++, b(6)-98++, b(6)-98, b(6)++, b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)++, b(9)-98++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4)++, y(4), y(5), y(5)++, y(6)++, y(7)++, y(8)++, y(9)++, y(9)-98++

Peptide No.703

QSQSQDVLVLEDSK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **QSQSQDVLVLEDSK**
Found in **MRP2_MOUSE** in **SwissProt**, Canalicular multispecific organic anion transporter 1 OS=Mus musculus GN=Abcc2 PE=2 SV=2

Match to Query 3442: 1654.743652 from(828.379102,2+) index(2229)
Title: Elution from: 37.180 to 37.180 scan no 3566 cid35.00 polarity:+



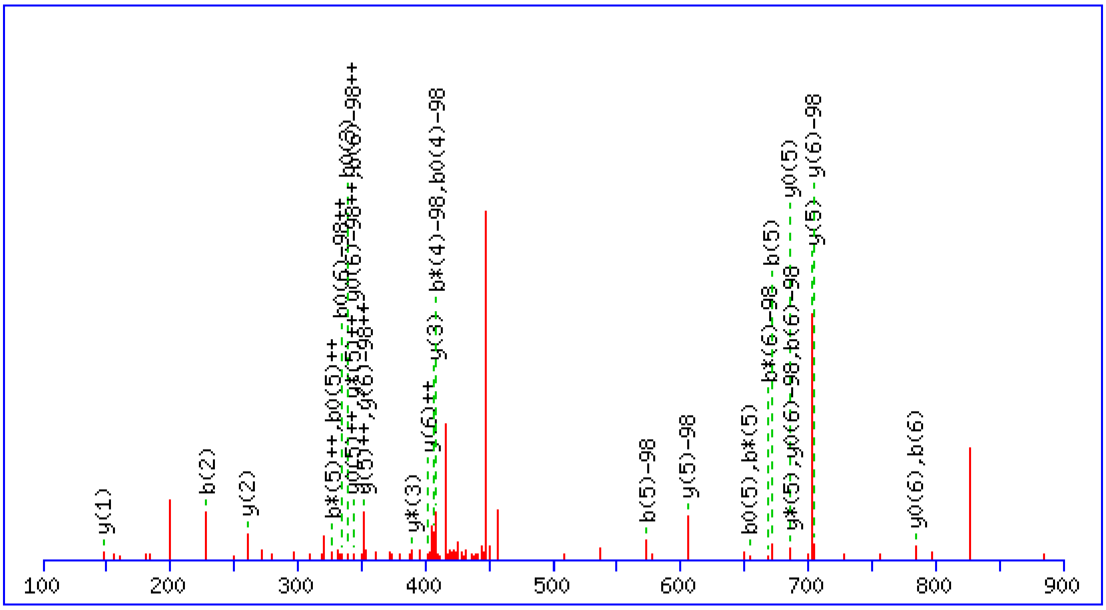
Monoisotopic mass of neutral peptide Mr(calc): 1654.7451
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.022
Matched b ions: b(12)++
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(12)-98++

Peptide No.704

QVESFLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **QVESFLK**
Found in **KIF22_MOUSE** in **SwissProt**, Kinesin-like protein KIF22 OS=Mus musculus GN=Kif22 PE=2 SV=2

Match to Query 586: 929.426460 from(465.720506,2+) index(1909)
Title: Elution from: 51.609 to 51.609 scan no 4084 cid35.00 polarity:+



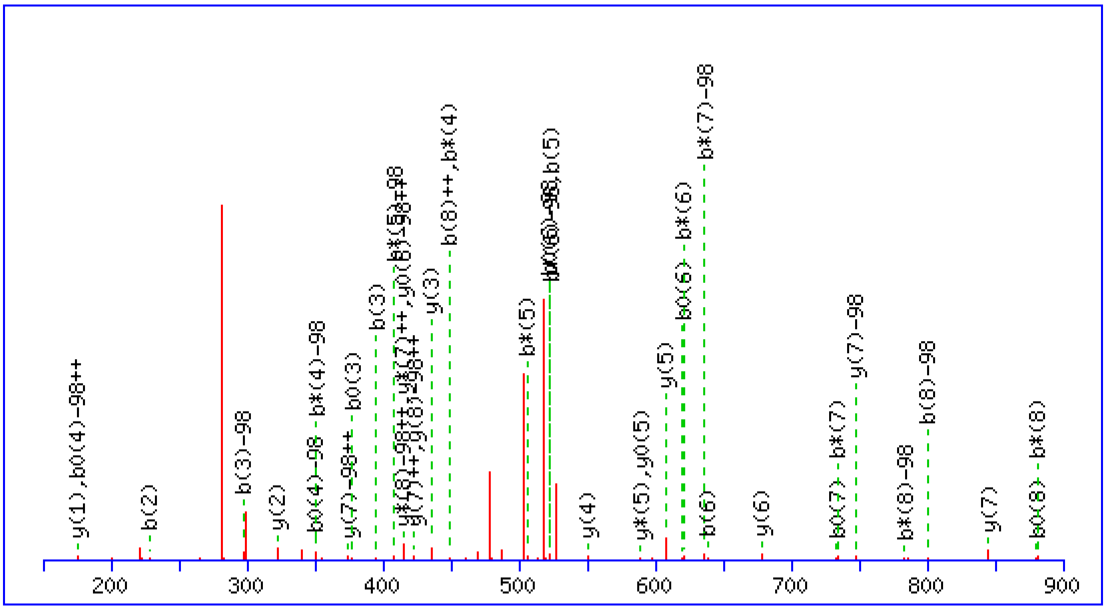
Monoisotopic mass of neutral peptide Mr(calc): 929.4259
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.043
Matched b ions: b(2), b(5)-98, b(5), b(6), b(6)-98, b(6)-98++
Matched y ions: y(1), y(2), y(3), y(5)-98, y(5), y(5)++, y(6)-98, y(6)-98++, y(6)++

Peptide No.705

QVSAGDLFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QVSAGDLFR**
Found in **EPIPL_MOUSE** in **SwissProt**, Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2

Match to Query 949: 1071.474752 from(536.744652,2+) index(2397)
Title: Elution from: 42.220 to 42.220 scan no 4079 cid35.00 polarity:+



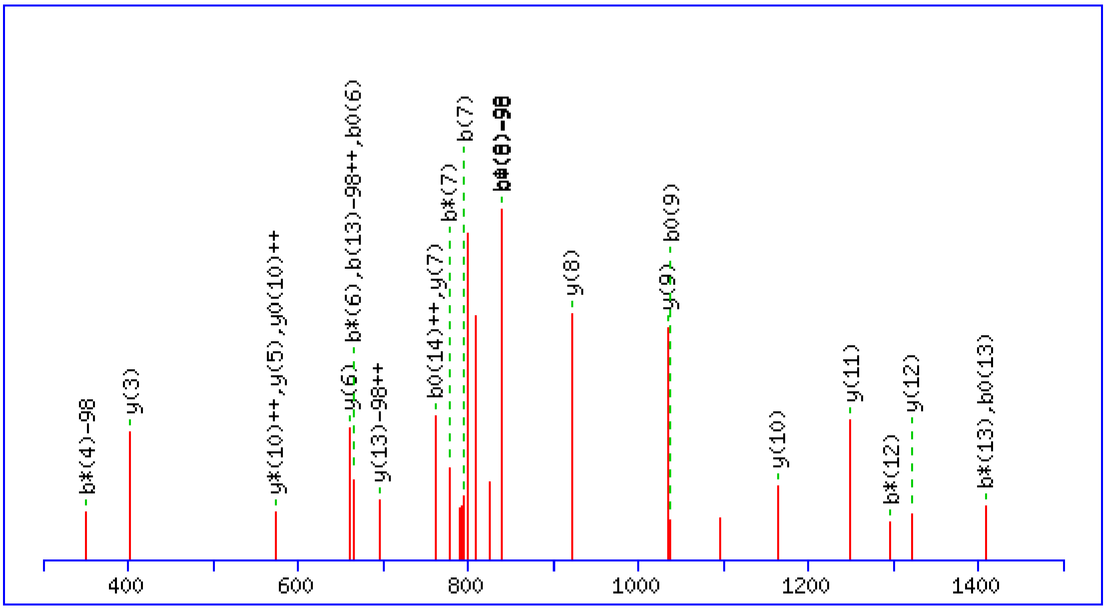
Monoisotopic mass of neutral peptide Mr(calc): 1071.4750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00041
Matched b ions: b(2), b(3)-98, b(3), b(5), b(6), b(8)-98, b(8)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(7)++, y(7)-98++, y(8)-98++

Peptide No.706

QVSASELCTSGILDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **QVSASELCTSGILDR**
Found in **EPIPL_MOUSE** in **SwissProt**, Epiplakin OS=Mus musculus GN=Eppk1 PE=1 SV=2

Match to Query 3685: 1714.758526 from(858.386539,2+) index(2837)
Title: Elution from: 45.089 to 45.089 scan no 4578 cid35.00 polarity:+



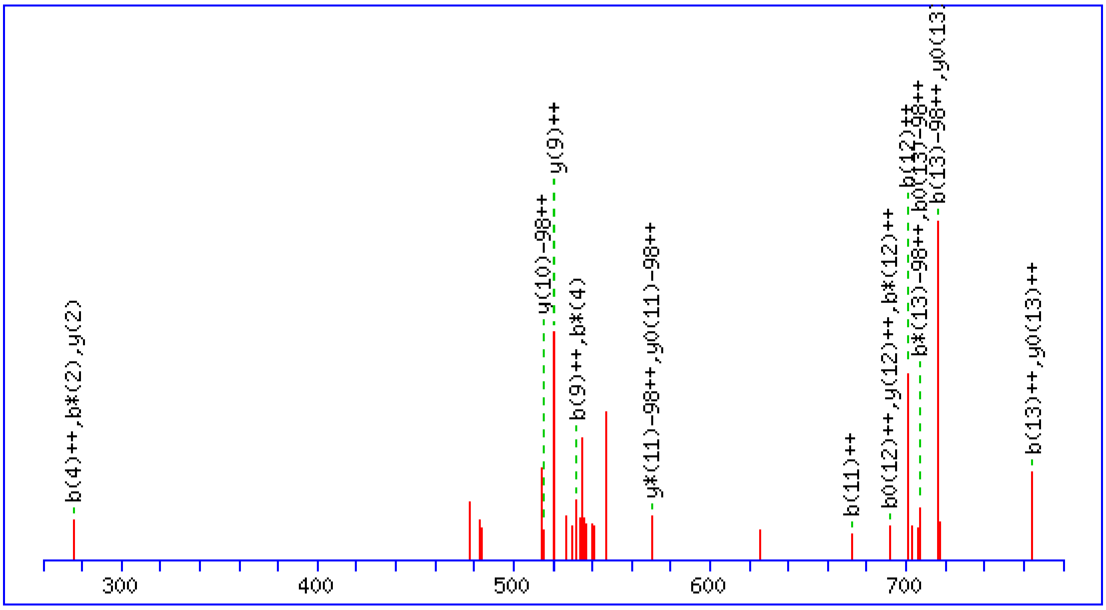
Monoisotopic mass of neutral peptide Mr(calc): 1714.7597
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 **Expect:** 8.9e-006
Matched b ions: b(7), b(13)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98++

Peptide No.707

QYKQSLAIESDGKK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **QYKQSLAIESDGKK**
Found in **PPCT_MOUSE** in **SwissProt**, Phosphatidylcholine transfer protein OS=Mus musculus GN=Pctp PE=1 SV=2

Match to Query 3695: 1673.807184 from(558.943004,3+) index(122)
Title: Elution from: 17.031 to 17.031 scan no 888 cid35.00 polarity:+



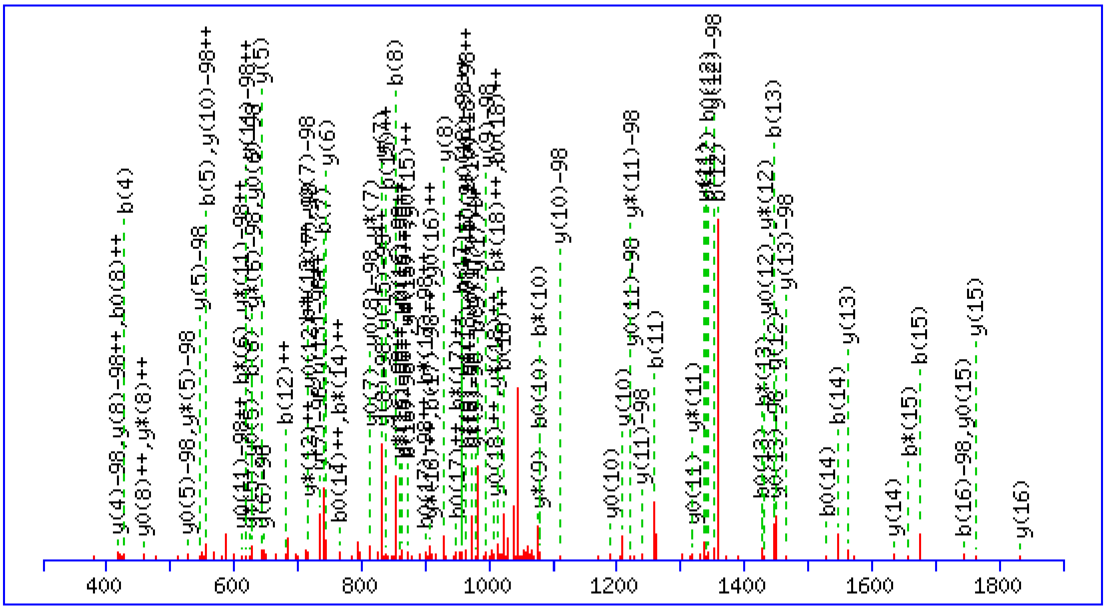
Monoisotopic mass of neutral peptide Mr(calc): 1673.8025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.038
Matched b ions: b(4)++, b(9)++, b(11)++, b(12)++, b(13)-98++, b(13)++
Matched y ions: y(2), y(9)++, y(10)-98++, y(12)++

Peptide No.708

RAEAQALLQDYVSTQSAEE
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **RAEAQALLQDYVSTQSAEE**
Found in **AASD1_MOUSE** in **SwissProt**, Alanyl-tRNA editing protein Aarsd1 OS=Mus musculus GN=Aarsd1 PE=1 SV=2

Match to Query 4729: 2187.964380 from(1094.989466,2+) index(5605)
Title: Elution from: 48.418 to 48.418 scan no 4797 cid35.00 polarity:+:m1s



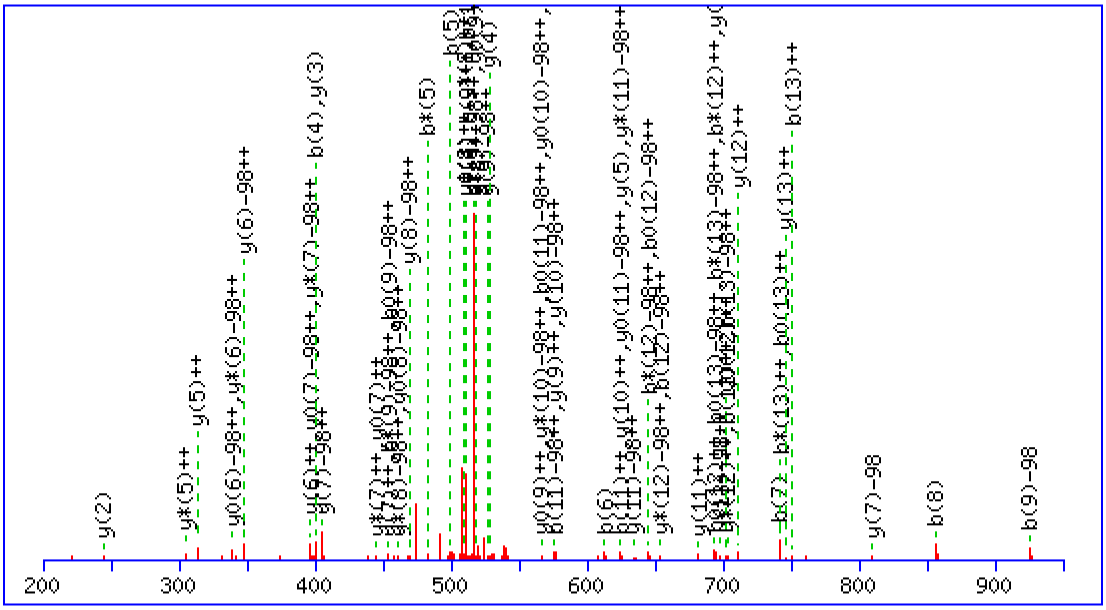
Monoisotopic mass of neutral peptide Mr(calc): 2187.9685
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 **Expect:** 2.6e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(12), b(12)++, b(13), b(14), b(15), b(15)++, b(16)-98, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++
Matched y ions: y(4)-98, y(5), y(5)-98, y(6)-98, y(6), y(7), y(7)-98, y(8)-98++, y(8), y(8)-98, y(9)-98, y(10)-98++, y(10)-98, y(10), y(11), y(11)-98, y(11)-98++, y(12), y(12)-98, y(13)-98++, y(13), y(13)-98, y(14), y(15), y(15)-98++, y(16), y(17)++

Peptide No.709

RAGDVLEDSPKRPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **RAGDVLEDSPKRPK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 3387: 1646.812635 from(549.944821,3+) index(217)
Title: Elution from: 18.491 to 18.491 scan no 1039 cid35.00 polarity:+



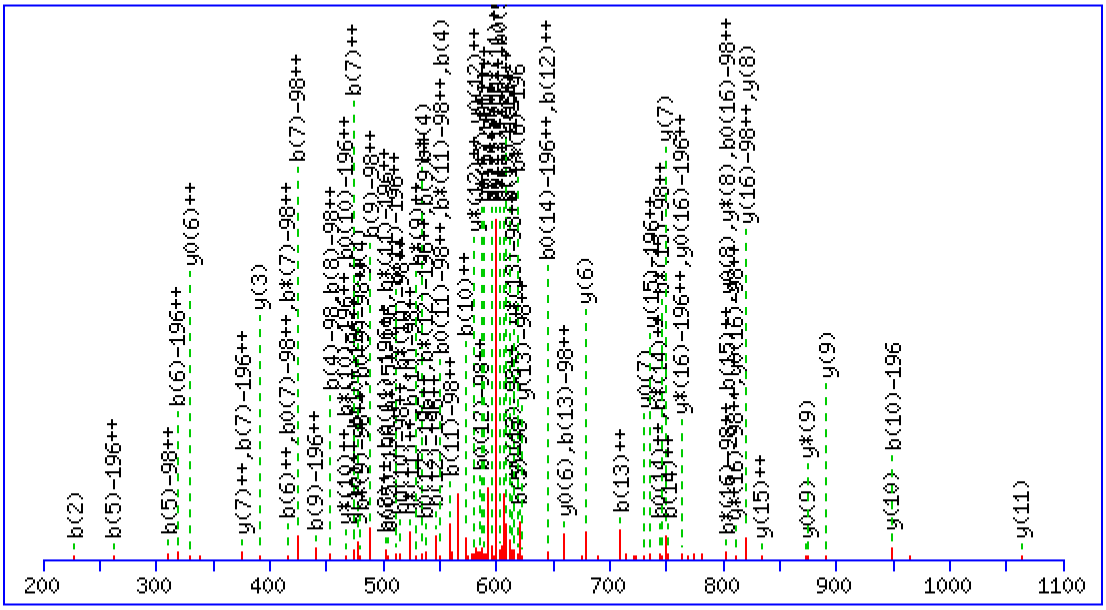
Monoisotopic mass of neutral peptide Mr(calc): 1646.8141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0019
Matched b ions: b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)-98, y(6)-98++, y(6)++, y(7)-98++, y(7)-98, y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.710

RASRSLDGAAAAESTDR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **RASRSLDGAAAAESTDR**
Found in **41_MOUSE** in **SwissProt**, Protein 4.1 OS=Mus musculus GN=Epb41 PE=1 SV=2

Match to Query 3828: 1892.775291 from(631.932373,3+) index(454)
Title: Elution from: 20.960 to 20.960 scan no 1347 cid35.00 polarity:+



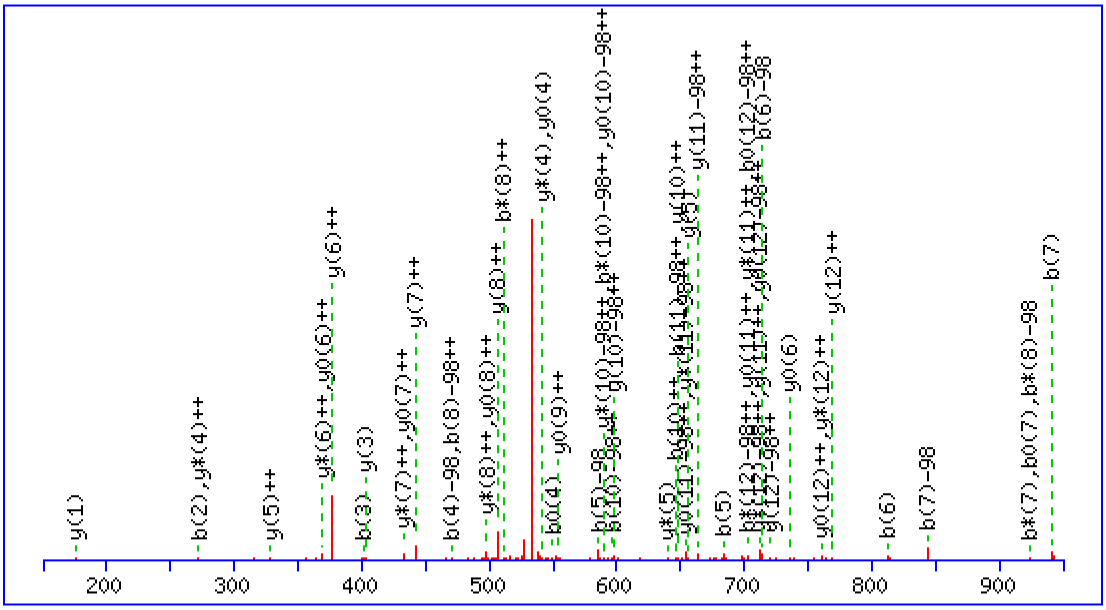
Monoisotopic mass of neutral peptide Mr(calc): 1892.7778
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 1.9e-005
Matched b ions: b(2), b(4)-98, b(4), b(5)-98++, b(5)-196++, b(5)-98, b(6)-196++, b(6)++, b(7)-98++, b(7)-196++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)-196++, b(9)++, b(10)-98++, b(10)-196, b(10)-196++, b(10)++, b(11)++, b(11)-196++, b(11)-98++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(15)++, b(16)-196++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9), y(10), y(10)++, y(11), y(12)++, y(13)-98++, y(15)++, y(15)-196++, y(16)-98++

Peptide No.711

RDESDEEPPRVER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RDESDEEPPRVER**
Found in **K1671_MOUSE** in **SwissProt**, Uncharacterized protein KIAA1671 OS=Mus musculus GN=Kiaa1671 PE=2 SV=1

Match to Query 3613: 1692.708339 from(565.243389,3+) index(236)
Title: Elution from: 18.670 to 18.670 scan no 1062 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1692.7104

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 25 **Expect:** 0.017

Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(12)++

Matched y ions: y(1), y(3), y(5)++, y(5), y(6)++, y(7)++, y(8)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.712

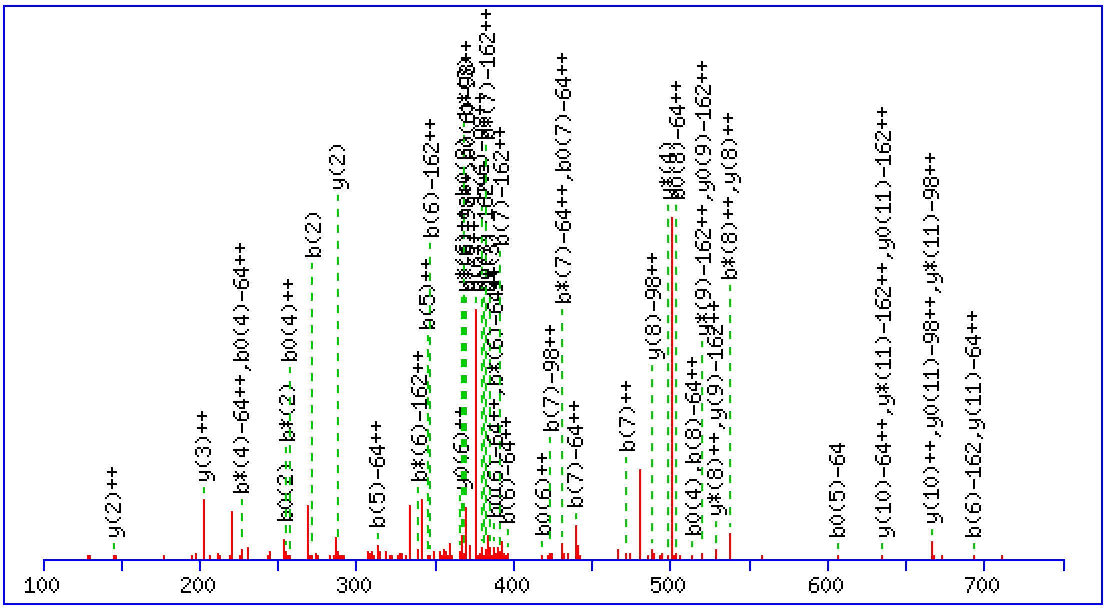
RDIMRSSFLNLR

Confirmed sites: @S:6

Ambiguous sites:

MS/MS Fragmentation of **RDIMRSSFLNLR**
Found in **MYCS_MOUSE** in **SwissProt**, Protein S-Myc OS=Mus musculus GN=Mycs PE=2 SV=2

Match to Query 3854: 1602.767356 from(401.699115,4+) index(522)
Title: Elution from: 28.655 to 28.655 scan no 1724 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1602.7701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.035
Matched b ions: b(2), b(3), b(5)++, b(6)-98++, b(7)-98++, b(7)++, b(11)-98++
Matched y ions: y(2)++, y(2), y(3)++, y(6)++, y(8)++, y(8)-98++, y(10)++

Peptide No.713

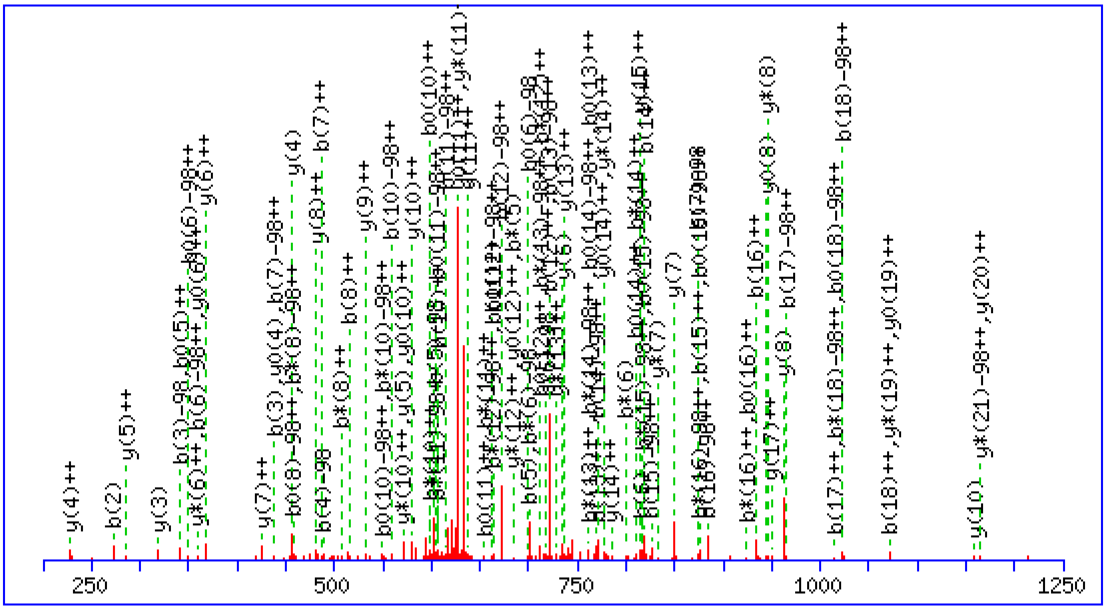
RDSFDDRGPSLNPVLDYDHGSR

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **RDSFDDRGPSLNPVLDYDHGSR**
Found in **MATR3_MOUSE** in **SwissProt**, Matrin-3 OS=Mus musculus GN=Matr3 PE=1 SV=1

Match to Query 5514: 2597.129604 from(650.289677,4+) index(5341)
Title: Elution from: 39.801 to 39.801 scan no 3798 cid35.00 polarity:+:m1s



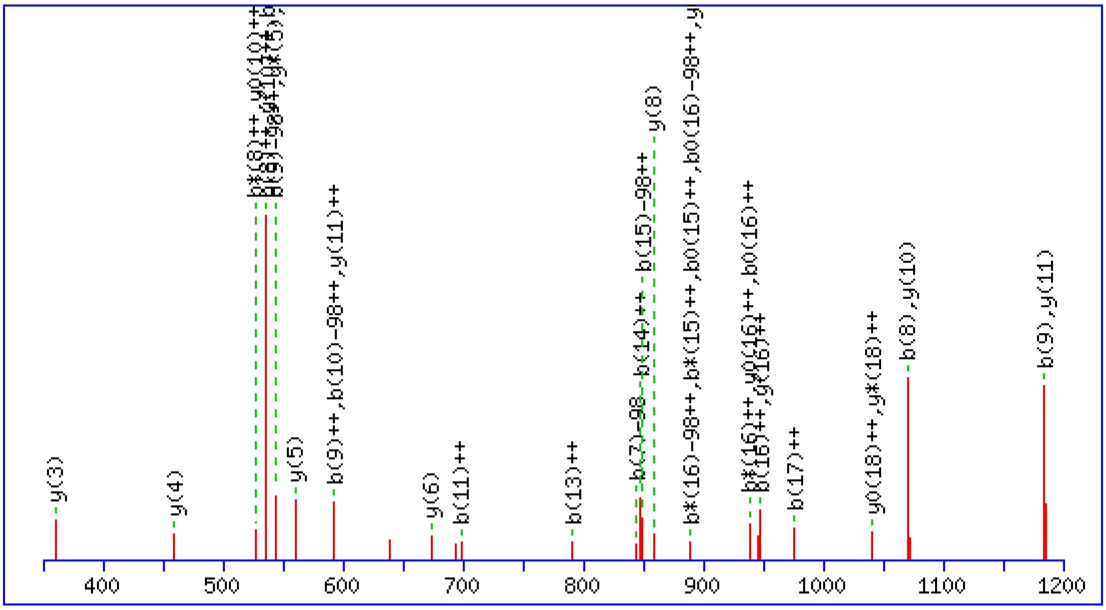
Monoisotopic mass of neutral peptide Mr(calc): 2597.1296
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 **Expect:** 0.00044
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98++, b(6), b(6)-98, b(7)-98, b(7)-98++, b(7)++, b(8)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(10), y(10)++, y(11)++, y(13)++, y(14)++, y(15)++, y(17)++, y(20)++

Peptide No.714

RDSSDDWEIPDGQITVGQR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RDSSDDWEIPDGQITVGQR**
Found in **BRAF_MOUSE** in **SwissProt**, Serine/threonine-protein kinase B-raf OS=Mus musculus GN=Braf PE=1 SV=3

Match to Query 5905: 2252.970036 from(751.997288,3+) index(6613)
Title: Elution from: 46.342 to 46.342 scan no 4763 cid35.00 polarity:+:m1s



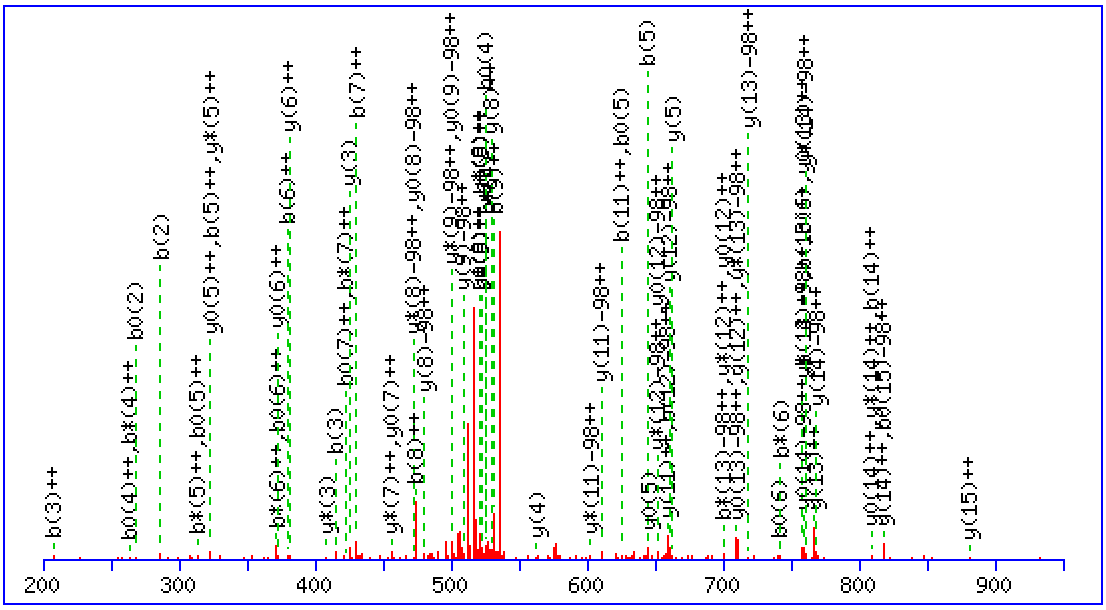
Monoisotopic mass of neutral peptide Mr(calc): 2252.9699
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 70 **Expect:** 8.8e-007
Matched b ions: b(5)-98, b(7)-98, b(8)++, b(8), b(9), b(9)-98++, b(9)++, b(10)-98++, b(11)++, b(13)++, b(14)++, b(15)-98++, b(16)++, b(17)++, b(18)++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(10)++, y(10), y(11), y(11)++, y(16)++

Peptide No.715

REEQTDTSDGESVTHHIR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **REEQTDTSDGESVTHHIR**
Found in **GNL1_MOUSE** in **SwissProt**, Guanine nucleotide-binding protein-like 1 OS=Mus musculus GN=Gnl1 PE=1 SV=4

Match to Query 5506: 2175.918836 from(544.986985,4+) index(3680)
Title: Elution from: 25.781 to 25.781 scan no 1383 cid35.00 polarity:+:m1s



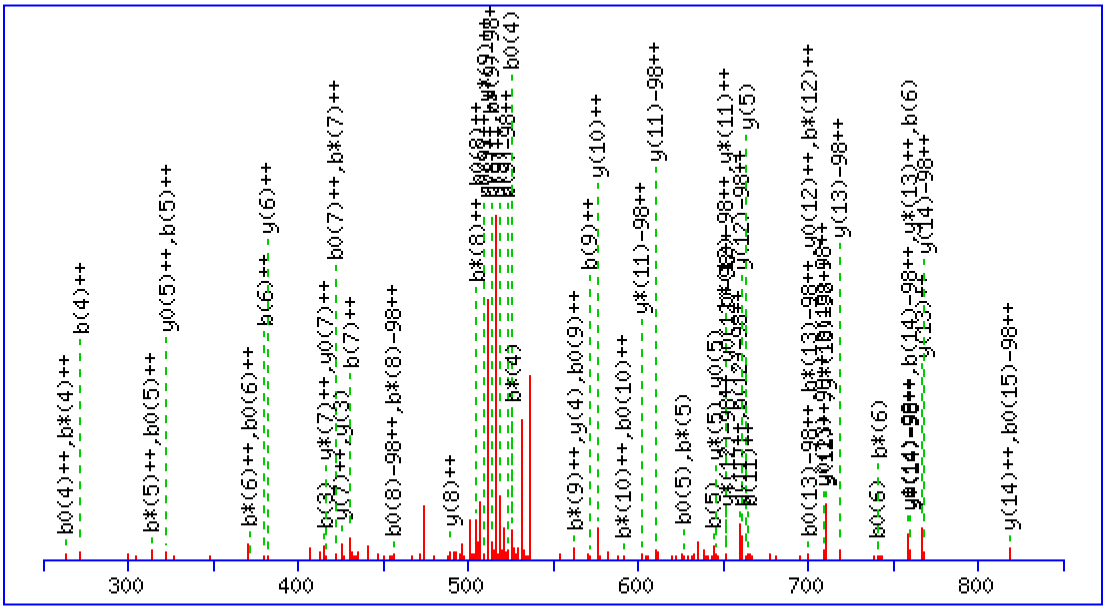
Monoisotopic mass of neutral peptide Mr(calc): 2175.9182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0084
Matched b ions: b(2), b(3)++, b(3), b(5)++, b(5), b(6)++, b(6), b(7)++, b(8)++, b(9)++, b(11)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(8)-98++, y(8)++, y(9)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++

Peptide No.716

REEQTDTSDGESVTHHIR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **REEQTDTSDGESVTHHIR**
Found in **GNL1_MOUSE** in **SwissProt**, Guanine nucleotide-binding protein-like 1 OS=Mus musculus GN=Gnl1 PE=1 SV=4

Match to Query 5636: 2175.916480 from(544.986396,4+) index(4070)
Title: Elution from: 19.661 to 19.661 scan no 1229 cid35.00 polarity:+:m1s



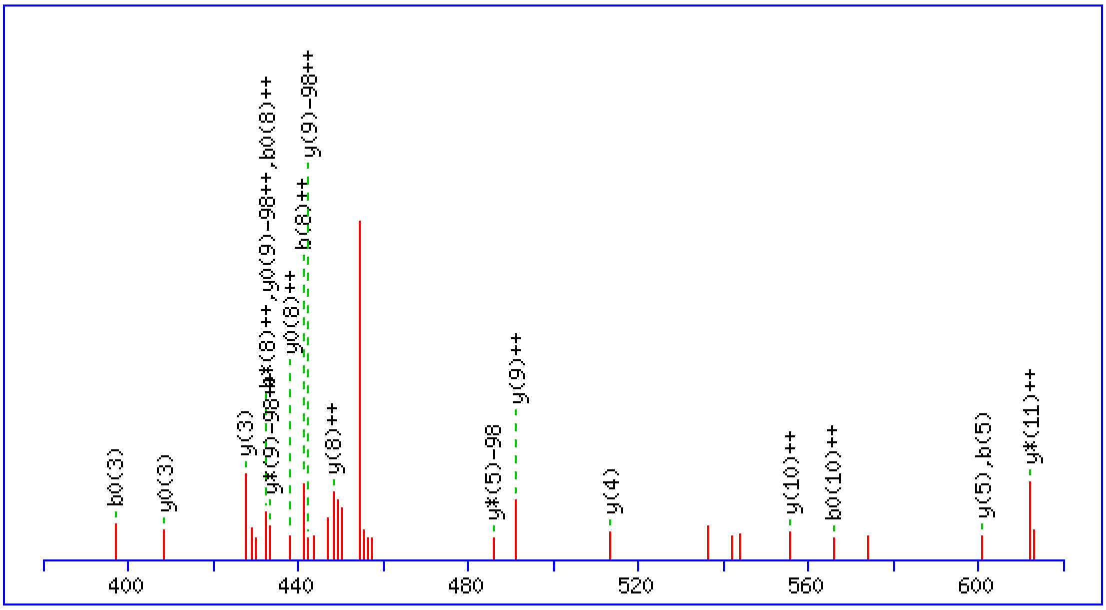
Monoisotopic mass of neutral peptide Mr(calc): 2175.9182
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0014
Matched b ions: b(3), b(4)++, b(5)++, b(5), b(6), b(6)++, b(7)++, b(8)++, b(9)-98++, b(9)++, b(11)++, b(12)-98++, b(13)-98++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(7)++, y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++

Peptide No.717

REESVPPSSTAR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **REESVPPSSTAR**
Found in **NOG1_MOUSE** in **SwissProt**, Nucleolar GTP-binding protein 1 OS=Mus musculus GN=Gtpbp4 PE=2 SV=3

Match to Query 2489: 1394.620128 from(465.880652,3+) index(666)
Title: Elution from: 21.710 to 21.710 scan no 1505 cid35.00 polarity:+



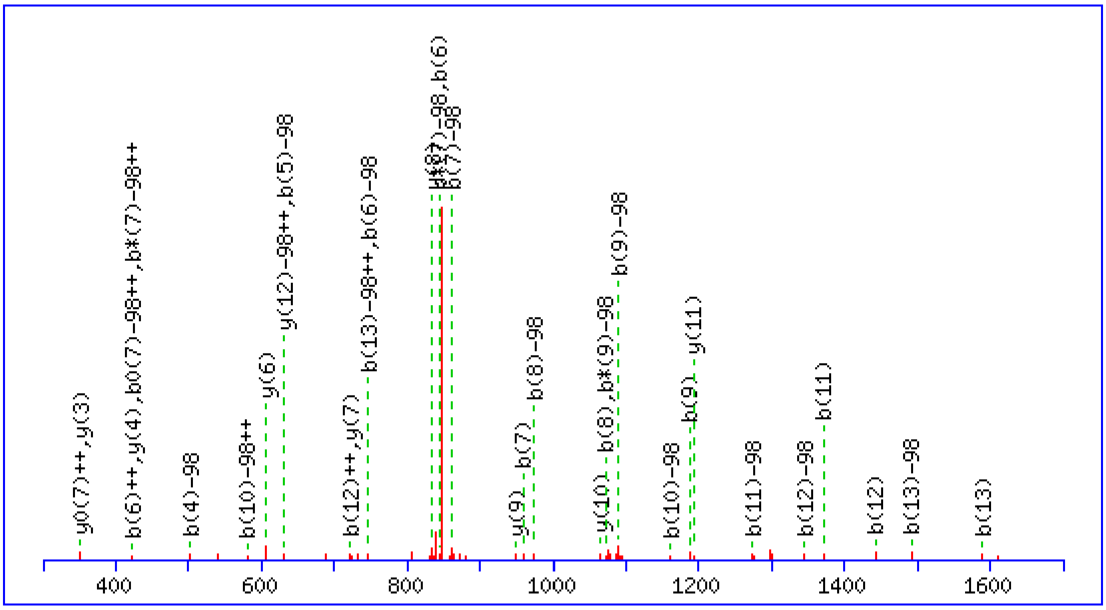
Monoisotopic mass of neutral peptide Mr(calc): 1394.6191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.036
Matched b ions: b(5), b(8)++
Matched y ions: y(3), y(4), y(5), y(8)++, y(9)++, y(9)-98++, y(10)++

Peptide No.718

RFESEDDIDALAFGK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RFESEDDIDALAFGK**
Found in **STAB2_MOUSE** in **SwissProt**, Stabilin-2 OS=Mus musculus GN=Stab2 PE=1 SV=1

Match to Query 4175: 1791.767968 from(896.891260,2+) index(3124)
Title: Elution from: 49.327 to 49.327 scan no 5115 cid35.00 polarity:+



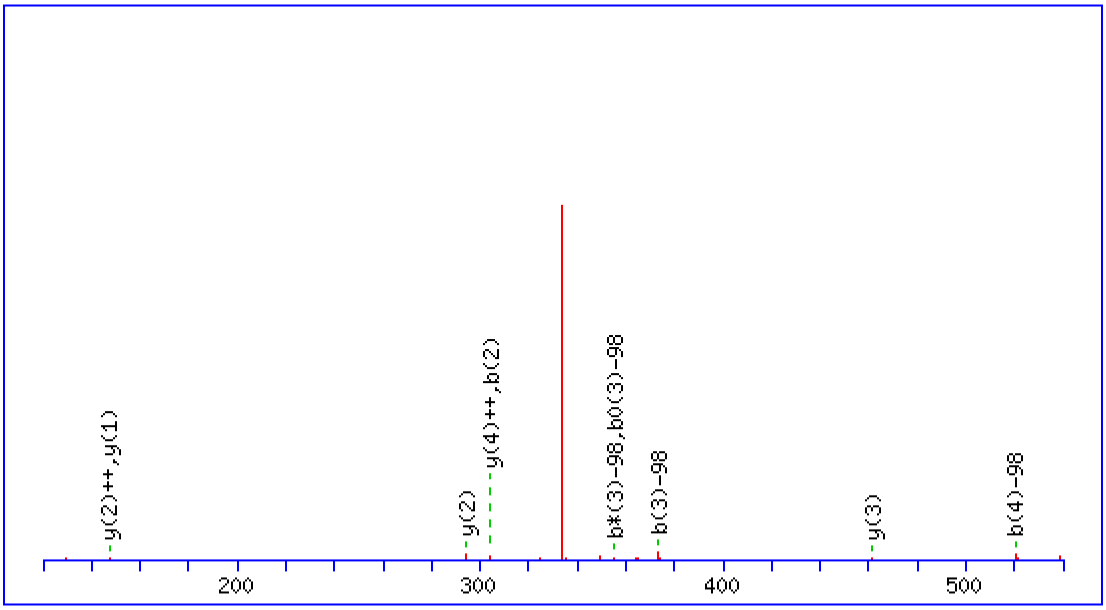
Monoisotopic mass of neutral peptide Mr(calc): 1791.7716
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 **Expect:** 1.4e-007
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6)++, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10)-98++, b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(13)-98++, b(13)-98, b(13)
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(11), y(12)-98++

Peptide No.719

RFSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RFSFK**
Found in **C2C2L_MOUSE** in **SwissProt**, C2 domain-containing protein 2-like OS=Mus musculus GN=C2cd2l PE=1 SV=2

Match to Query 254: 763.342128 from(382.678340,2+) index(851)
Title: Elution from: 23.783 to 23.783 scan no 1752 cid35.00 polarity:+



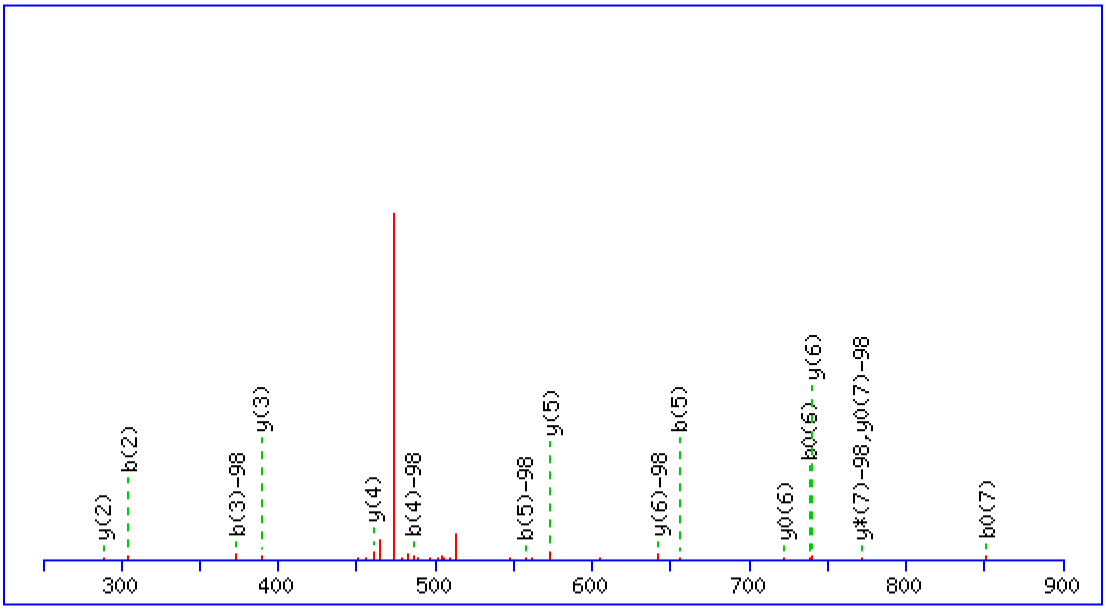
Monoisotopic mass of neutral peptide Mr(calc): 763.3418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.015
Matched b ions: b(2), b(3)-98, b(4)-98
Matched y ions: y(1), y(2), y(2)++, y(3), y(4)++

Peptide No.720

RFSIATLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RFSIATLR**
Found in **CP2AC_MOUSE** in **SwissProt**, Cytochrome P450 2A12 OS=Mus musculus GN=Cyp2a12 PE=1 SV=2

Match to Query 844: 1042.532032 from(522.273292,2+) index(1764)
Title: Elution from: 35.479 to 35.479 scan no 3225 cid35.00 polarity:+



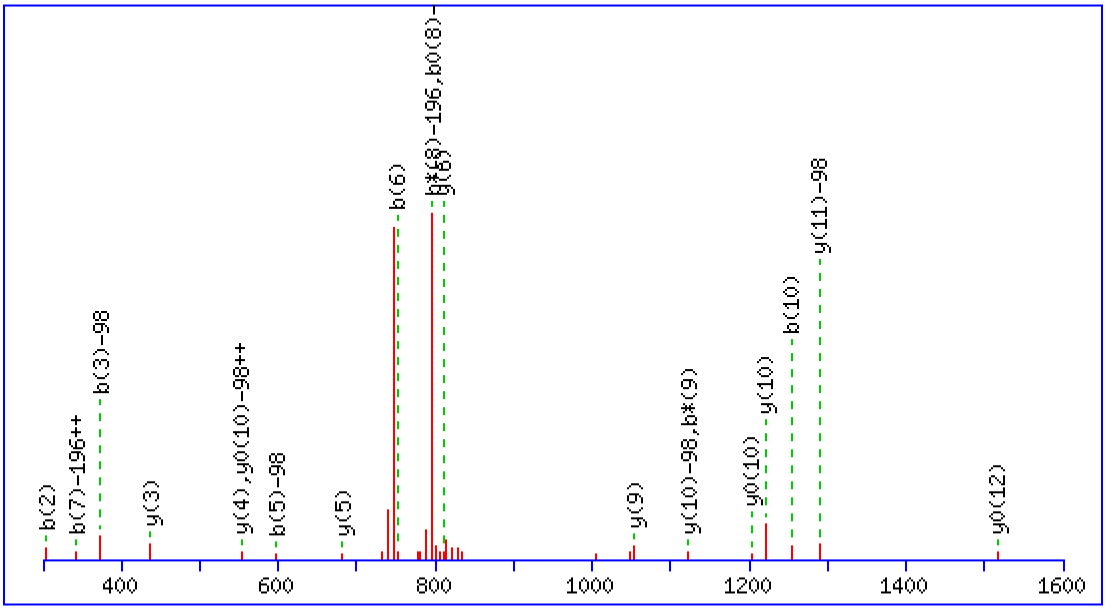
Monoisotopic mass of neutral peptide Mr(calc): 1042.5325
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0028
Matched b ions: b(2), b(3)-98, b(4)-98, b(5), b(5)-98, b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6)

Peptide No.721

RFSSGGEEEDFDR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **RFSSGGEEEDFDR**
Found in **ABLM3_MOUSE** in **SwissProt**, Actin-binding LIM protein 3 OS=Mus musculus GN=Ablim3 PE=1 SV=2

Match to Query 3762: 1689.567486 from(845.791019,2+) index(1648)
Title: Elution from: 31.102 to 31.102 scan no 2782 cid35.00 polarity:+



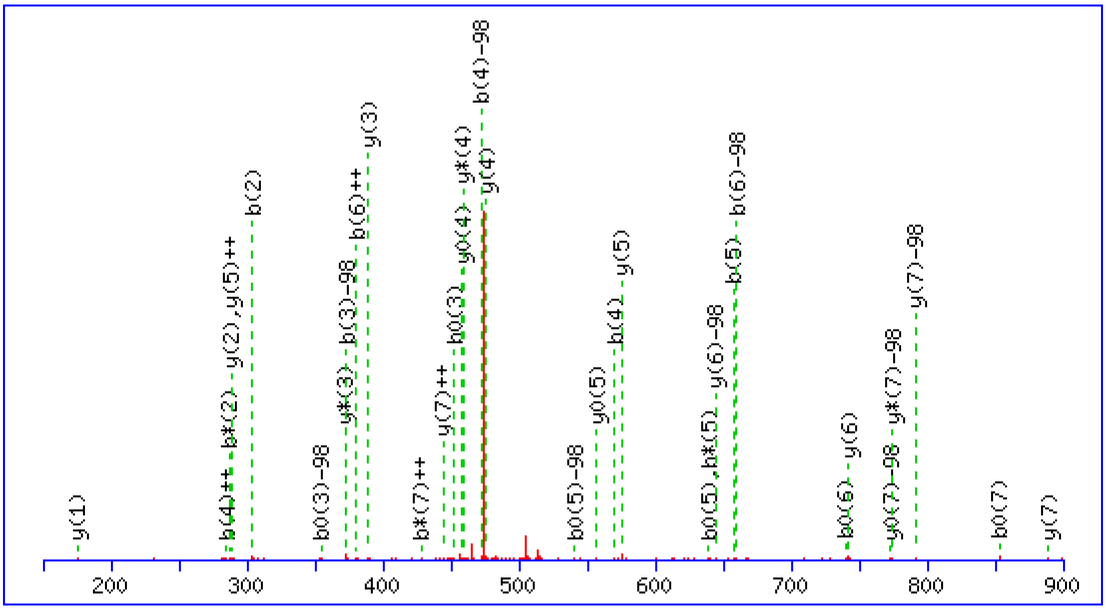
Monoisotopic mass of neutral peptide Mr(calc): 1689.5709
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0028
Matched b ions: b(2), b(3)-98, b(5)-98, b(6), b(7)-196++, b(10), b(12)
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(10)-98, y(10), y(11)-98

Peptide No.722

RFSVSTLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RFSVSTLR**
Found in **CP2DA_MOUSE** in **SwissProt**, Cytochrome P450 2D10 OS=Mus musculus GN=Cyp2d10 PE=2 SV=2

Match to Query 1164: 1044.511836 from(523.263194,2+) index(1289)
Title: Elution from: 38.951 to 38.951 scan no 2872 cid35.00 polarity:+



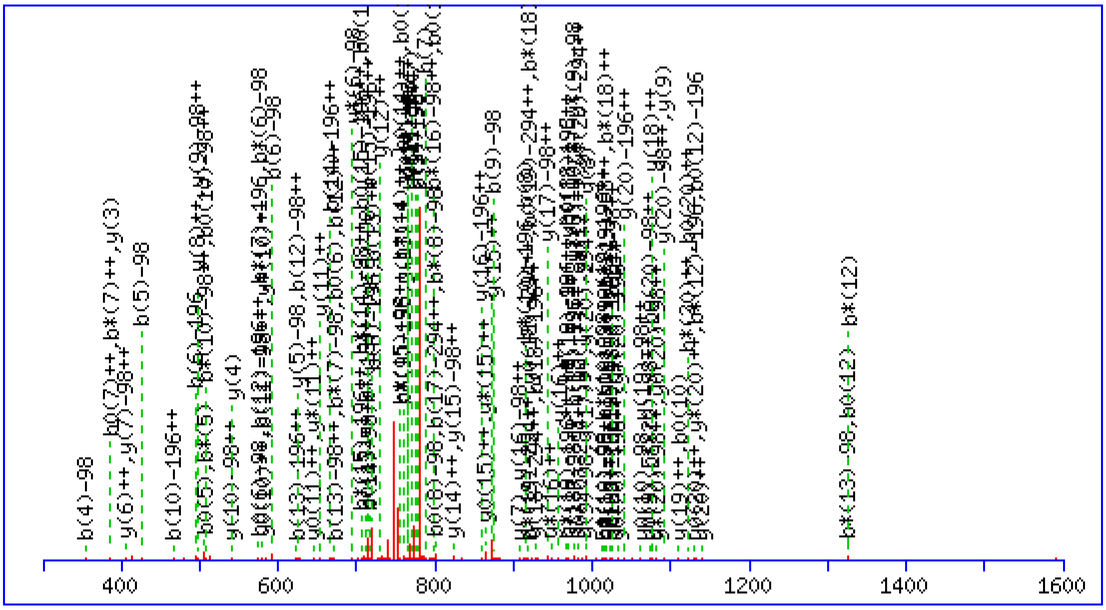
Monoisotopic mass of neutral peptide Mr(calc): 1044.5117
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 6e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(4)++, b(4), b(5), b(6)-98, b(6)++, b(7)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)-98, y(7), y(7)-98, y(7)++

Peptide No.723

RGASASPQGRQSPSPSTRPIR
Confirmed sites: @S:4,@S:6,@T:17
Ambiguous sites:

MS/MS Fragmentation of **RGASASPQGRQSPSPSTRPIR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 6249: 2432.045436 from(811.689088,3+) index(4037)
Title: Elution from: 19.389 to 19.389 scan no 1193 cid35.00 polarity:+:m1s



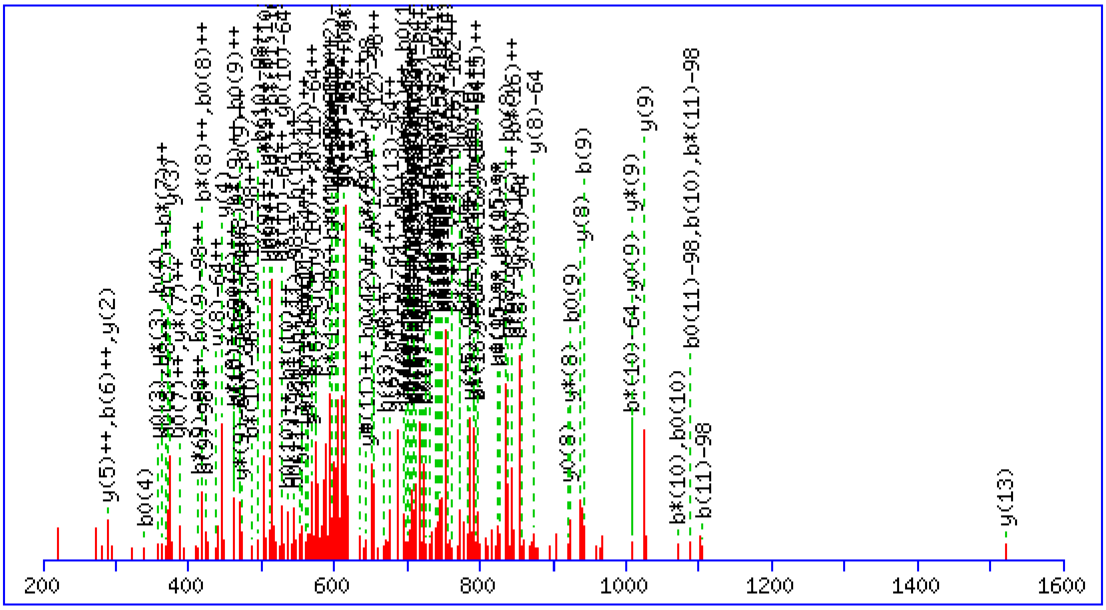
Monoisotopic mass of neutral peptide Mr(calc): 2432.0512
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0018
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6)-196, b(7), b(8)-196, b(8), b(9)-98, b(9)-196, b(10)-196++, b(11)-98++, b(12)-98++, b(12)-196++, b(12)++, b(13)++, b(13)-196++, b(13)-98++, b(14)-98++, b(14)-196++, b(14)++, b(15)-196++, b(17)-294++, b(18)-98++, b(18)-196++, b(18)++, b(19)-196++, b(19)-98++, b(20)++, b(20)-196++, b(20)-98++, b(20)-294++
Matched y ions: y(3), y(4), y(5)-98, y(6)++, y(6)-98, y(7)-98++, y(7), y(8)++, y(8), y(9), y(9)-98, y(9)-98++, y(10)-98++, y(11)++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++, y(17)++, y(17)-98++, y(18)-294++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(19)-196++, y(20)-98++, y(20)-294++, y(20)-196++, y(20)++

Peptide No.724

RGSGDTSISMDTEASIR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **RGSGDTSISMDTEASIR**
Found in **LRRF1_MOUSE** in **SwissProt**, Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfip1 PE=1 SV=2

Match to Query 4099: 1877.782719 from(626.934849,3+) index(3742)
Title: Elution from: 33.492 to 33.492 scan no 2212 cid35.00 polarity:+:m1s



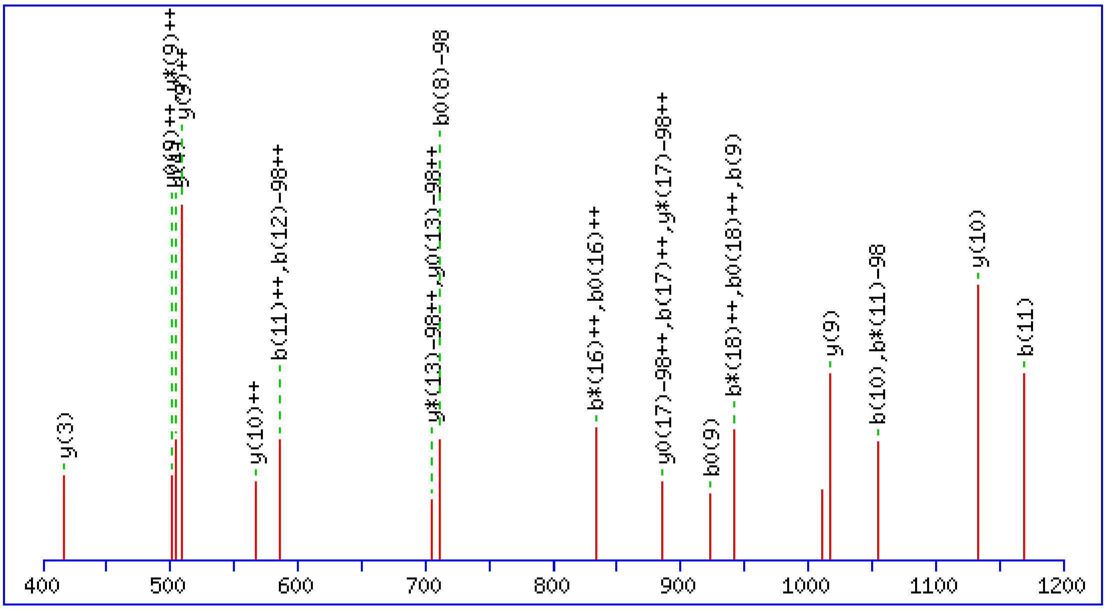
Monoisotopic mass of neutral peptide Mr(calc): 1877.7826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 47 **Expect:** 0.00012
Matched b ions: b(4), b(6)++, b(6), b(7)++, b(7), b(7)-98, b(8), b(9)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)-98, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13), y(13)-98++, y(14)-98++, y(15)-98++

Peptide No.725

RGSGDTSSLIDPDTSLSELR
Confirmed sites:
Ambiguous sites: @S:3orT:6orS:7orS:8

MS/MS Fragmentation of **RGSGDTSSLIDPDTSLSELR**
Found in **LRRF2_MOUSE** in **SwissProt**, Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfip2 PE=1 SV=1

Match to Query 5543: 2184.990015 from(729.337281,3+) index(6495)
Title: Elution from: 47.425 to 47.425 scan no 4853 cid35.00 polarity:+:m1s



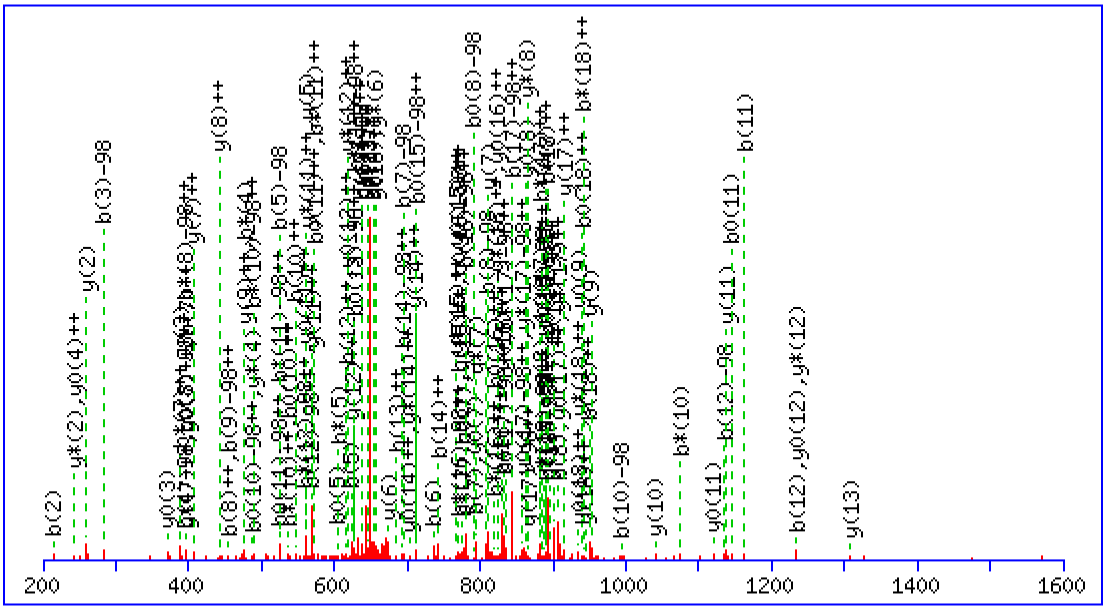
Monoisotopic mass of neutral peptide Mr(calc): 2184.9900
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.03
Matched b ions: b(9), b(10), b(11)++, b(11), b(12)-98++, b(17)++
Matched y ions: y(3), y(4), y(9)++, y(9), y(10), y(10)++

Peptide No.726

RGSLELGNPSAAHLGDELK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RGSLELGNPSAAHLGDELK**
Found in **SVIL_MOUSE** in **SwissProt**, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 4527: 2042.979606 from(682.000478,3+) index(4708)
Title: Elution from: 47.678 to 47.678 scan no 3758 cid35.00 polarity:+:m1s



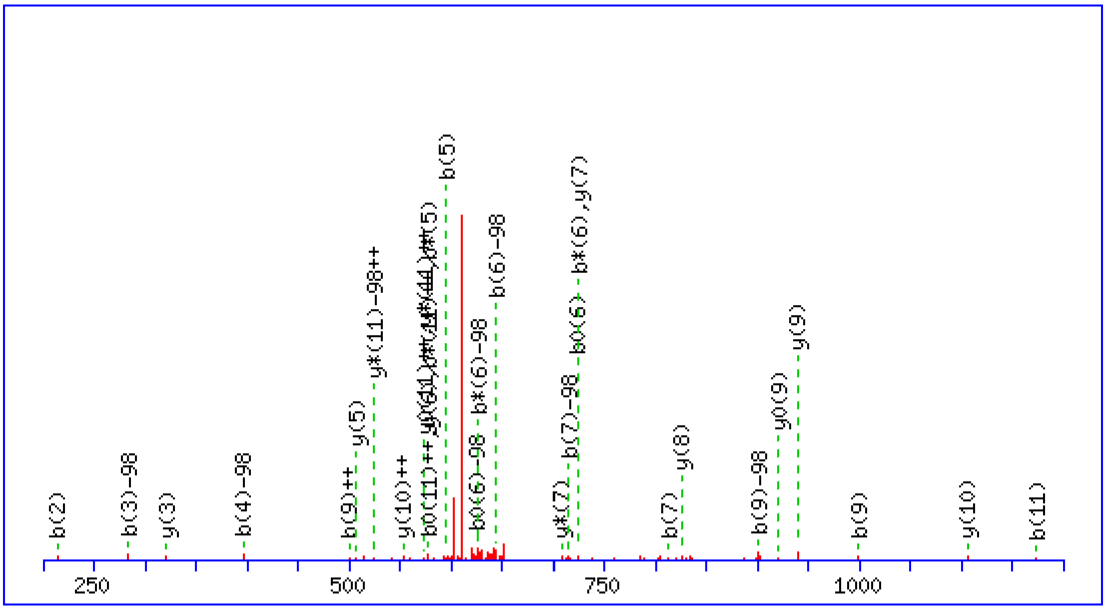
Monoisotopic mass of neutral peptide Mr(calc): 2042.9786
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 0.0001
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)++, b(9)-98++, b(10)++, b(10)-98, b(11), b(12), b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(11)++, y(11), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++

Peptide No.727

RGSLTFAGESSK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RGSLTFAGESSK**
Found in **FA83H_MOUSE** in **SwissProt**, Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1

Match to Query 2251: 1318.590466 from(660.302509,2+) index(914)
Title: Elution from: 23.878 to 23.878 scan no 1801 cid35.00 polarity:+



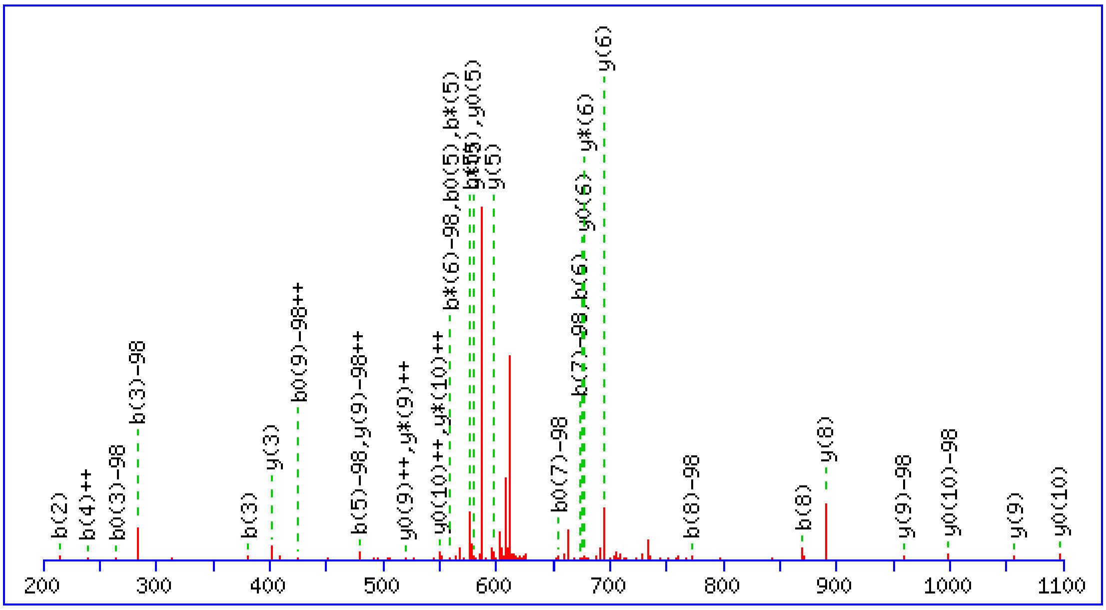
Monoisotopic mass of neutral peptide Mr(calc): 1318.5918
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 3.5e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(5), b(6)-98, b(7)-98, b(7), b(9)-98, b(9)++, b(9), b(11)
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++

Peptide No.728

RGSPVPPVPER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RGSPVPPVPER**
Found in **FA83H_MOUSE** in **SwissProt**, Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1

Match to Query 1979: 1269.621482 from(635.818017,2+) index(652)
Title: Elution from: 21.592 to 21.592 scan no 1489 cid35.00 polarity:+



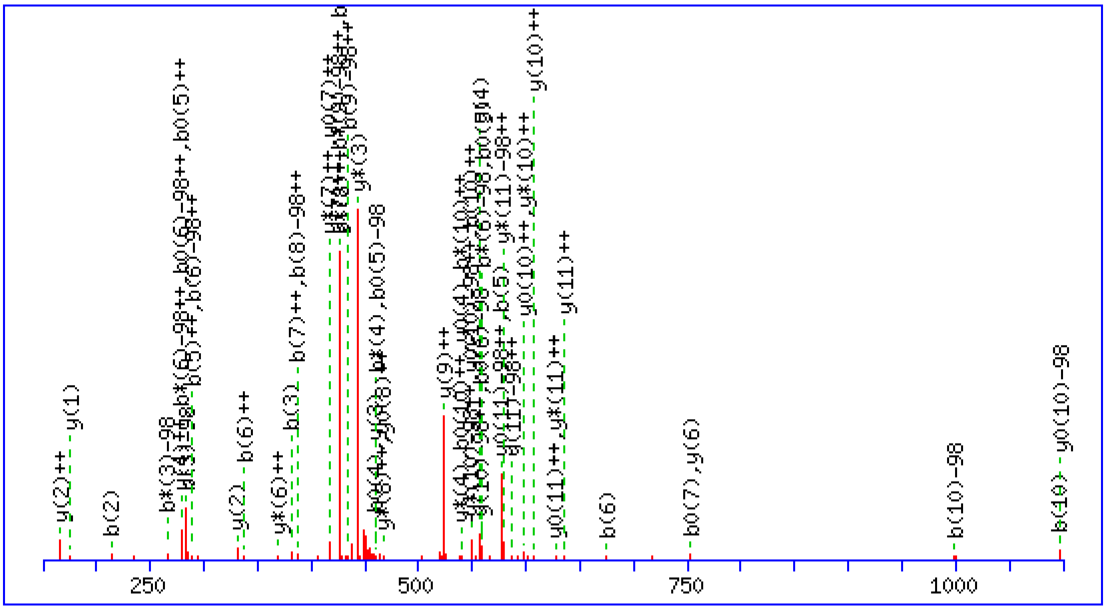
Monoisotopic mass of neutral peptide Mr(calc): 1269.6231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.012
Matched b ions: b(2), b(3)-98, b(3), b(4)++, b(5)-98, b(5), b(6), b(7)-98, b(8)-98, b(8), b(10)-98, b(10), b(10)++
Matched y ions: y(3), y(5), y(6), y(8), y(9)-98++, y(9)-98, y(9)

Peptide No.729

RGSPVPPVPERR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RGSPVPPVPERR**
Found in **FA83H_MOUSE** in **SwissProt**, Protein FAM83H OS=Mus musculus GN=Fam83h PE=1 SV=1

Match to Query 2473: 1425.723147 from(476.248325,3+) index(340)
Title: Elution from: 19.494 to 19.494 scan no 1172 cid35.00 polarity:+



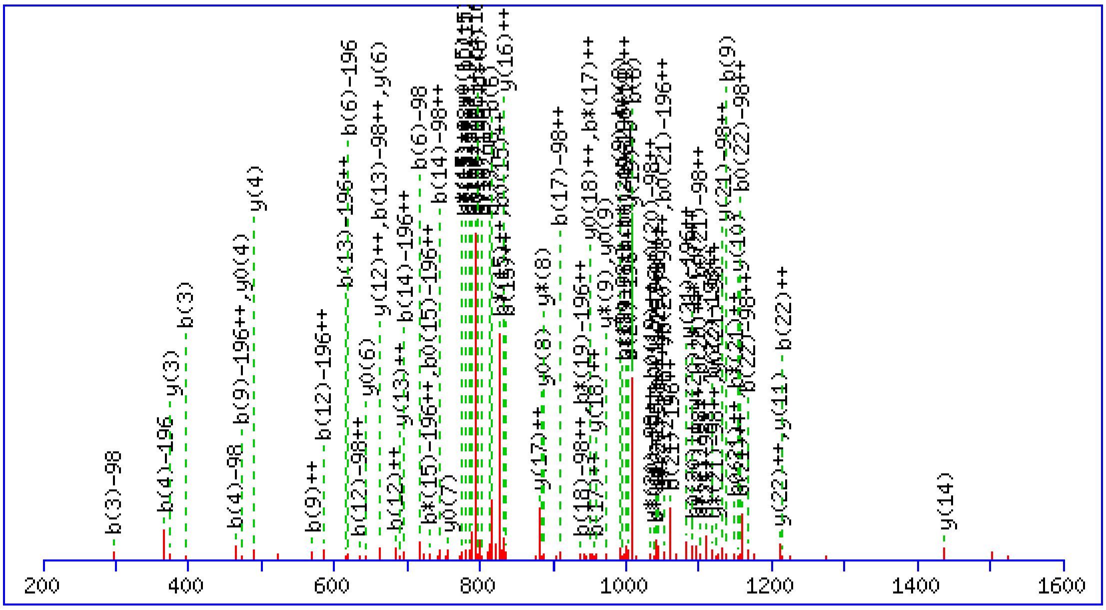
Monoisotopic mass of neutral peptide Mr(calc): 1425.7242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 0.00012
Matched b ions: b(2), b(3)-98, b(3), b(5), b(5)++, b(6), b(6)-98++, b(6)++, b(7)++, b(8)-98++, b(9)-98++, b(10)-98, b(10), b(10)++, b(11)-98++, b(11)++
Matched y ions: y(1), y(2)++, y(2), y(3), y(4)++, y(4), y(6), y(7)++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++

Peptide No.730

RGTSPRPPEGGLGYSQLGDDDLK
Confirmed sites: @T:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **RGTSPRPPEGGLGYSQLGDDDLK**
Found in **CDK11_MOUSE** in **SwissProt**, Cyclin-dependent kinase 11 OS=Mus musculus GN=Cdk11 PE=1 SV=2

Match to Query 5480: 2574.114372 from(859.045400,3+) index(5263)
Title: Elution from: 38.739 to 38.739 scan no 3671 cid35.00 polarity:+:m1s



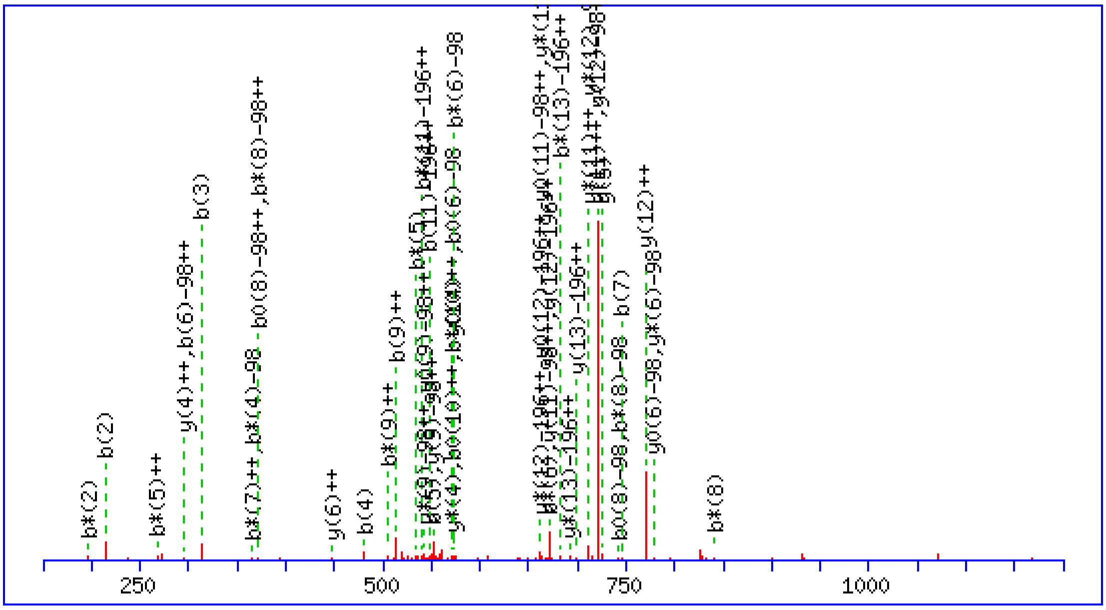
Monoisotopic mass of neutral peptide Mr(calc): 2574.1153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 8e-005
Matched b ions: b(3)-98, b(3), b(4)-196, b(4)-98, b(6), b(6)-196, b(6)-98, b(7)-98, b(8), b(9)++, b(9)-196++, b(9), b(10)-196, b(12)-196++, b(12)++, b(12)-98++, b(13)-98++, b(13)-196++, b(14)++, b(14)-196++, b(14)-98++, b(15)-98++, b(15)++, b(16)-196++, b(17)-98++, b(17)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-196++, b(20)-98++, b(21)++, b(21)-196++, b(21)-98++, b(22)++, b(22)-196++, b(22)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(9), y(10), y(11), y(12)++, y(13)++, y(14), y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)-196++, y(22)++

Peptide No.731

RGVSAHGLSHEERR
Confirmed sites: @S:4,@S:9
Ambiguous sites:

MS/MS Fragmentation of **RGVSAHGLSHEERR**
Found in **RRNAD_MOUSE** in **SwissProt**, Protein RRNAD1 OS=Mus musculus GN=Rrnad1 PE=2 SV=1

Match to Query 4041: 1749.747876 from(584.256568,3+) index(4266)
Title: Elution from: 21.286 to 21.286 scan no 1448 cid35.00 polarity:+:m1s



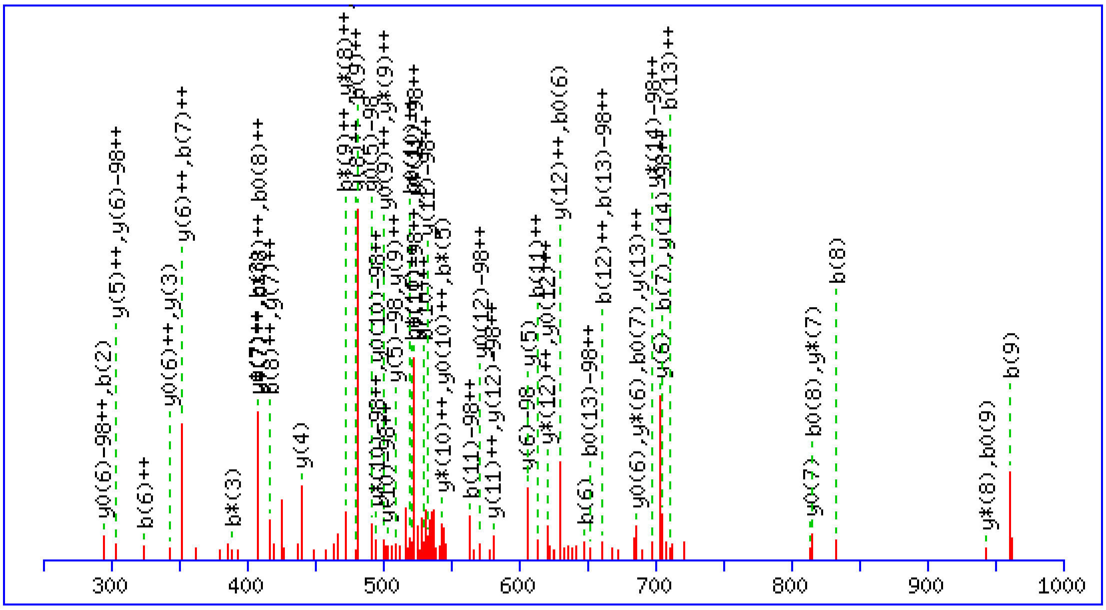
Monoisotopic mass of neutral peptide Mr(calc): 1749.7461
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.059
Matched b ions: b(2), b(3), b(4), b(5), b(6)-98++, b(7), b(9)++, b(11)-196++, b(12)-98++
Matched y ions: y(4)++, y(5), y(6)++, y(9)-98++, y(11)-98++, y(11)++, y(12)-196++, y(12)-98++, y(12)++, y(13)-196++

Peptide No.732

RHLPGSGQQPSPPAR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **RHLPGSGQQPSPPAR**
Found in **TENC1_MOUSE** in **SwissProt**, Tensin-like C1 domain-containing phosphatase OS=Mus musculus GN=Tenc1 PE=1 SV=1

Match to Query 3023: 1663.792467 from(555.604765,3+) index(245)
Title: Elution from: 19.237 to 19.237 scan no 1116 cid35.00 polarity:+



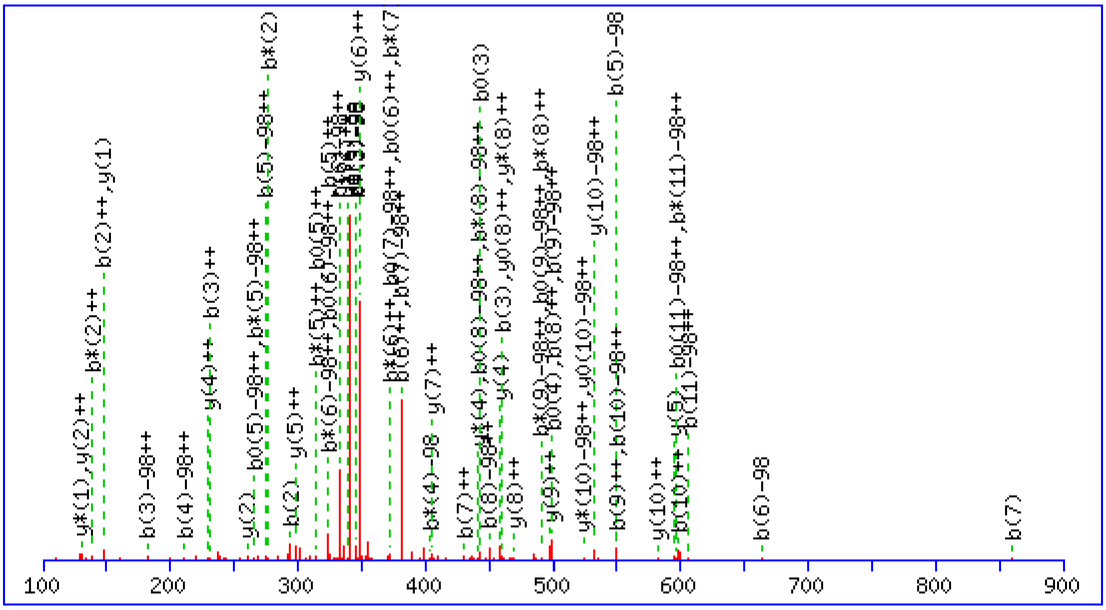
Monoisotopic mass of neutral peptide Mr(calc): 1663.7944
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0033
Matched b ions: b(2), b(3), b(6)++, b(6), b(7)++, b(7), b(8), b(8)++, b(9)++, b(9), b(10)++, b(11)-98++, b(11)++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(5)-98, y(6)++, y(6), y(6)-98, y(6)-98++, y(7)++, y(8)++, y(9)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)-98++

Peptide No.733

RHSGQDVHVVLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RHSGQDVHVVLK**
Found in **NSF1C_MOUSE** in **SwissProt**, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 2606: 1453.719916 from(364.437255,4+) index(290)
Title: Elution from: 19.117 to 19.117 scan no 1122 cid35.00 polarity:+



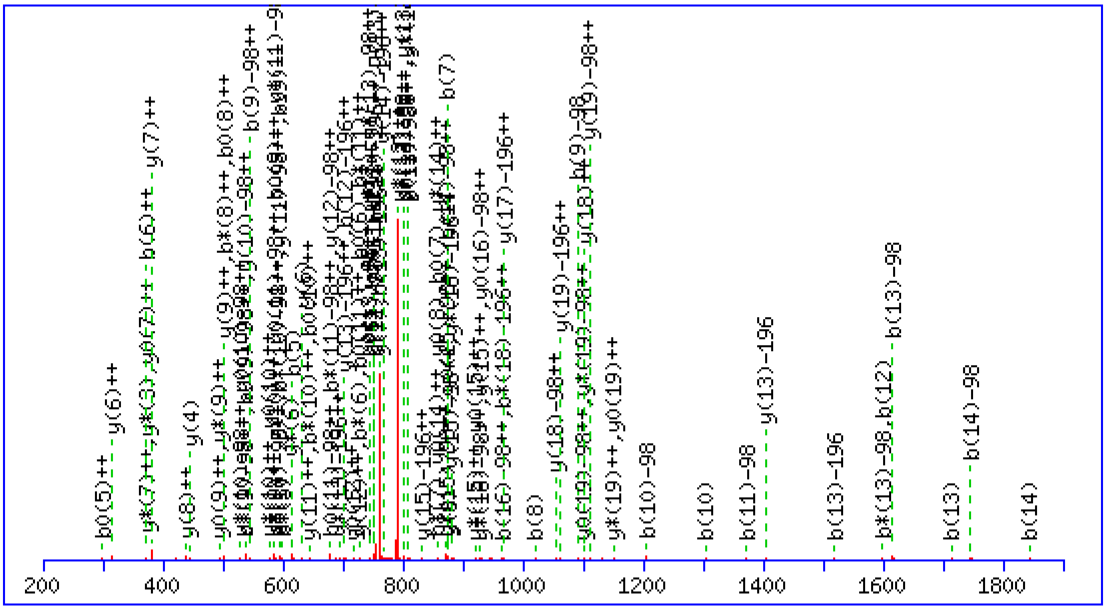
Monoisotopic mass of neutral peptide Mr(calc): 1453.7191
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 **Expect:** 1.7e-005
Matched b ions: b(2)++, b(2), b(3)-98++, b(3)++, b(3), b(4)-98++, b(5)-98, b(5)++, b(5)-98++, b(6)-98, b(6)++, b(6)-98++, b(7), b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2)++, y(2), y(4), y(4)++, y(5)++, y(5), y(6)++, y(7)++, y(8)++, y(9)++, y(10)-98++, y(10)++

Peptide No.734

RIACDEEFSDSEDEGEGGRR
Confirmed sites: @S:9,@S:11
Ambiguous sites:

MS/MS Fragmentation of **RIACDEEFSDSEDEGEGGRR**
Found in **HDAC2_MOUSE** in **SwissProt**, Histone deacetylase 2 OS=Mus musculus GN=Hdac2 PE=1 SV=1

Match to Query 6157: 2472.883833 from(825.301887,3+) index(4547)
Title: Elution from: 25.191 to 25.191 scan no 1943 cid35.00 polarity:+:m1s



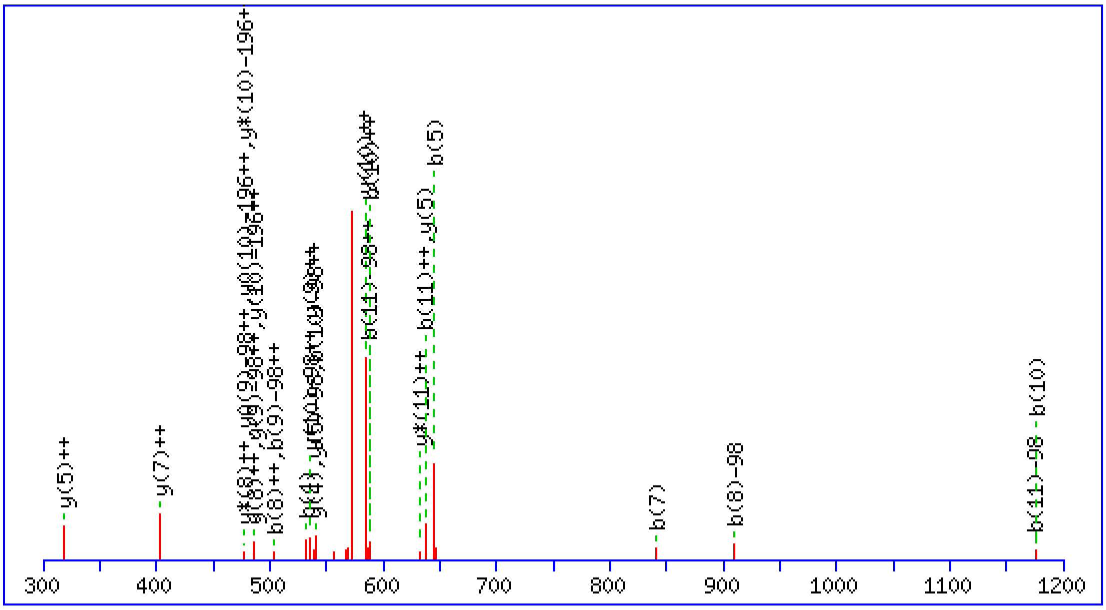
Monoisotopic mass of neutral peptide Mr(calc): 2472.8890
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00025
Matched b ions: b(5), b(6)++, b(6), b(7), b(8), b(9)-98, b(9)++, b(9)-98++, b(10)-98, b(10), b(11)-98, b(12)++, b(12), b(12)-98++, b(12)-196++, b(13)-196, b(13)-98, b(13), b(13)-196++, b(13)-98++, b(14), b(14)-98++, b(14)-98, b(16)-98++, b(19)++, b(19)-98++
Matched y ions: y(4), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)-98++, y(12)++, y(13)-196, y(13)++, y(13)-98++, y(13)-196++, y(14)-196++, y(15)++, y(15)-98++, y(15)-196++, y(17)-196++, y(18)++, y(18)-98++, y(19)-98++, y(19)-196++

Peptide No.735

RIDFIPVSPAPSPTR
Confirmed sites: @S:8
Ambiguous sites: @S:12orT:14

MS/MS Fragmentation of **RIDFIPVSPAPSPTR**
Found in **F122A_MOUSE** in **SwissProt**, Protein FAM122A OS=Mus musculus GN=Fam122a PE=1 SV=1

Match to Query 3566: 1811.838021 from(604.953283,3+) index(5844)
Title: Elution from: 48.664 to 48.664 scan no 4782 cid35.00 polarity:+:m1s



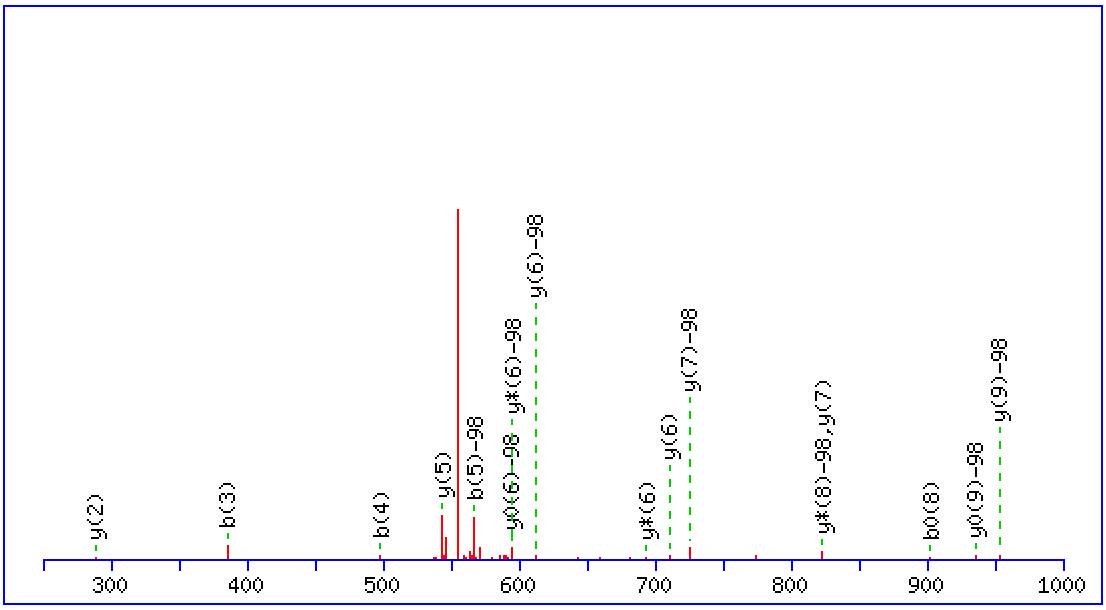
Monoisotopic mass of neutral peptide Mr(calc): 1811.8372
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.0014
Matched b ions: b(4), b(5), b(7), b(8)-98, b(8)++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)++, b(11)-98, b(11)-98++
Matched y ions: y(4), y(5)++, y(5), y(5)-98, y(7)++, y(8)++, y(9)-98++, y(9)++, y(10)-196++, y(10)++, y(10)-98++

Peptide No.736

RIDISPSALR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **RIDISPSALR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 1566: 1206.612086 from(604.313319,2+) index(2013)
Title: Elution from: 34.918 to 34.918 scan no 3264 cid35.00 polarity:+



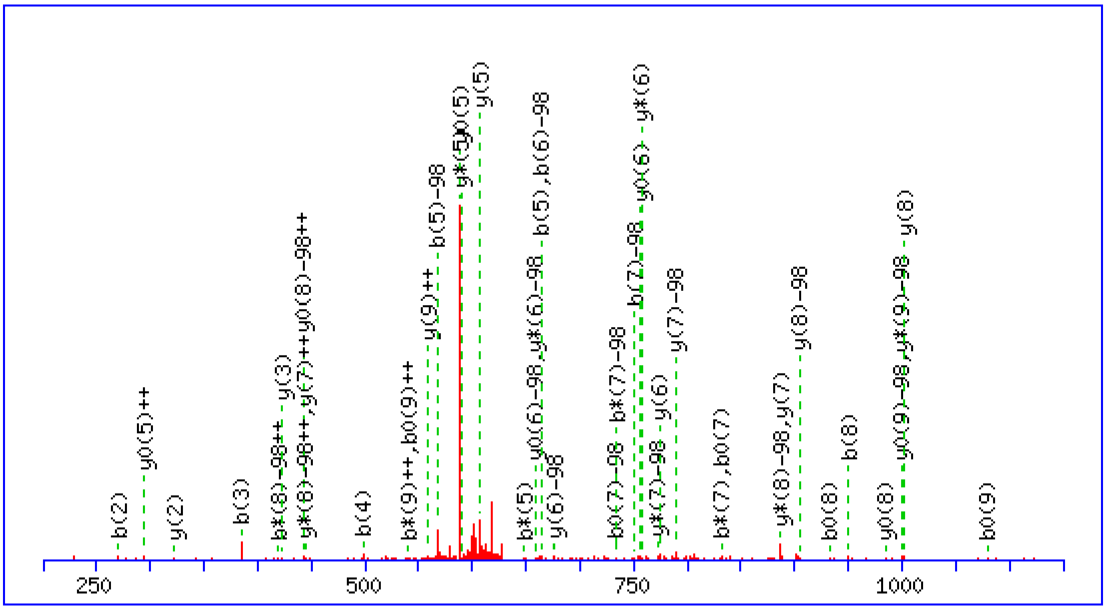
Monoisotopic mass of neutral peptide Mr(calc): 1206.6122
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0014
Matched b ions: b(3), b(4), b(5)-98, b(9)-98
Matched y ions: y(2), y(5), y(6), y(6)-98, y(7)-98, y(7), y(9)-98

Peptide No.737

RIDISPSTFR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **RIDISPSTFR**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 2592: 1270.607602 from(636.311077,2+) index(1980)
Title: Elution from: 46.083 to 46.083 scan no 3803 cid35.00 polarity:+



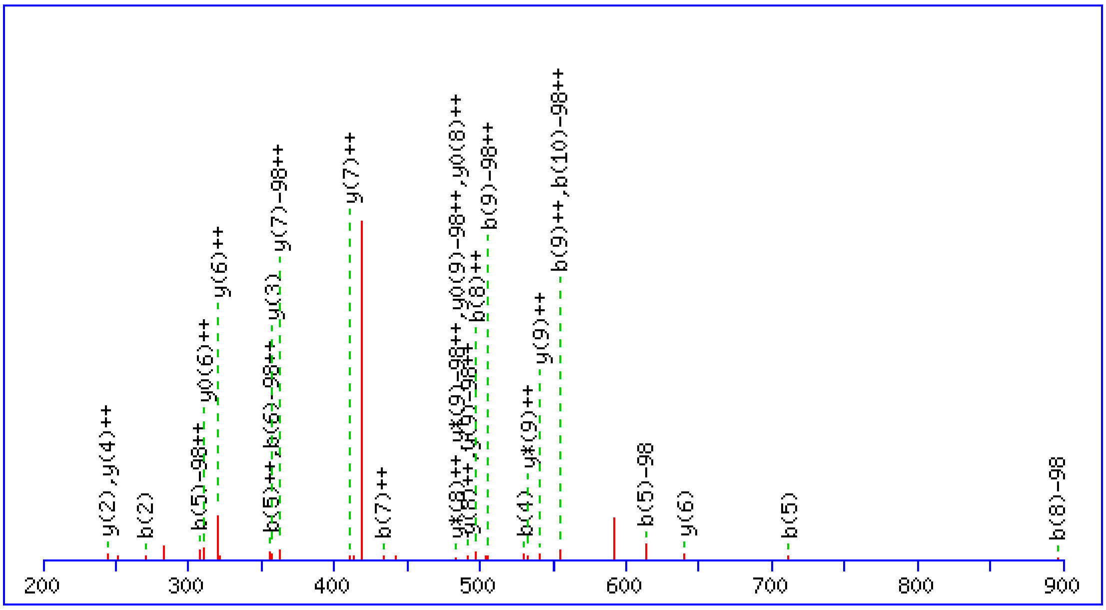
Monoisotopic mass of neutral peptide Mr(calc): 1270.6071
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.027
Matched b ions: b(2), b(3), b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(8), b(9)-98
Matched y ions: y(2), y(3), y(5), y(6)-98, y(6), y(7)-98, y(7), y(7)++, y(8), y(8)-98, y(9)++

Peptide No.738

RIPYTPGEIPK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **RIPYTPGEIPK**
Found in **UGDH_MOUSE** in **SwissProt**, UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1

Match to Query 2338: 1349.674539 from(450.898789,3+) index(1993)
Title: Elution from: 34.288 to 34.288 scan no 3213 cid35.00 polarity:+



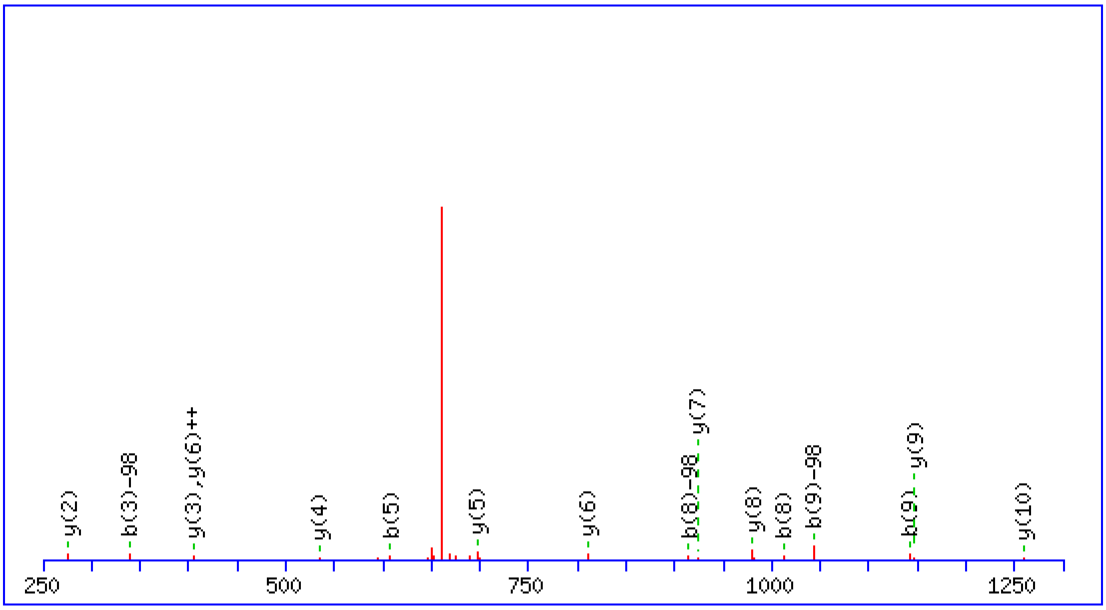
Monoisotopic mass of neutral peptide Mr(calc): 1349.6744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0015
Matched b ions: b(2), b(4), b(5), b(5)-98, b(5)++, b(5)-98++, b(6)-98++, b(7)++, b(8)++, b(8)-98, b(9)++, b(9)-98++, b(10)-98++
Matched y ions: y(2), y(3), y(4)++, y(6)++, y(6), y(7)-98++, y(7)++, y(8)++, y(9)++, y(9)-98++

Peptide No.739

RISGLIYEETR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RISGLIYEETR**
Found in **H4_MOUSE** in **SwissProt**, Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2

Match to Query 2424: 1415.679280 from(708.846916,2+) index(2275)
Title: Elution from: 37.675 to 37.675 scan no 3632 cid35.00 polarity:+



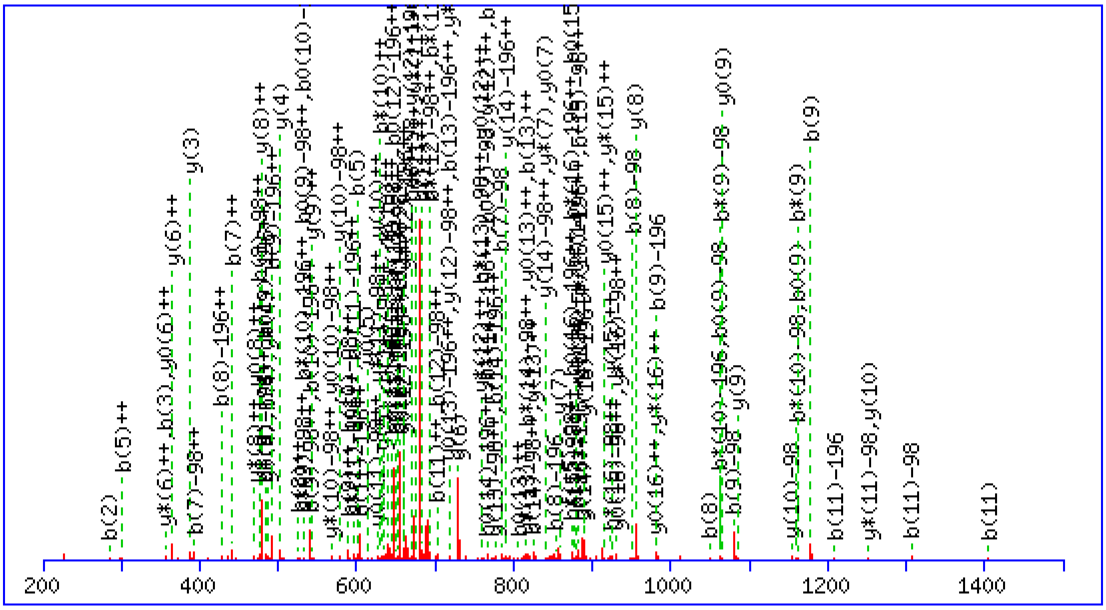
Monoisotopic mass of neutral peptide Mr(calc): 1415.6810
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 65 **Expect:** 1.9e-006
Matched b ions: b(3)-98, b(5), b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(9), y(10)

Peptide No.740

RKAEDSDSEPEPEDNVR
Confirmed sites: @S:6,@S:8
Ambiguous sites:

MS/MS Fragmentation of **RKAEDSDSEPEPEDNVR**
Found in **XRN2_MOUSE** in **SwissProt**, 5'-3' exoribonuclease 2 OS=Mus musculus GN=Xrn2 PE=1 SV=1

Match to Query 4553: 2131.806660 from(711.609496,3+) index(3332)
Title: Elution from: 19.170 to 19.170 scan no 1107 cid35.00 polarity:+:m1s



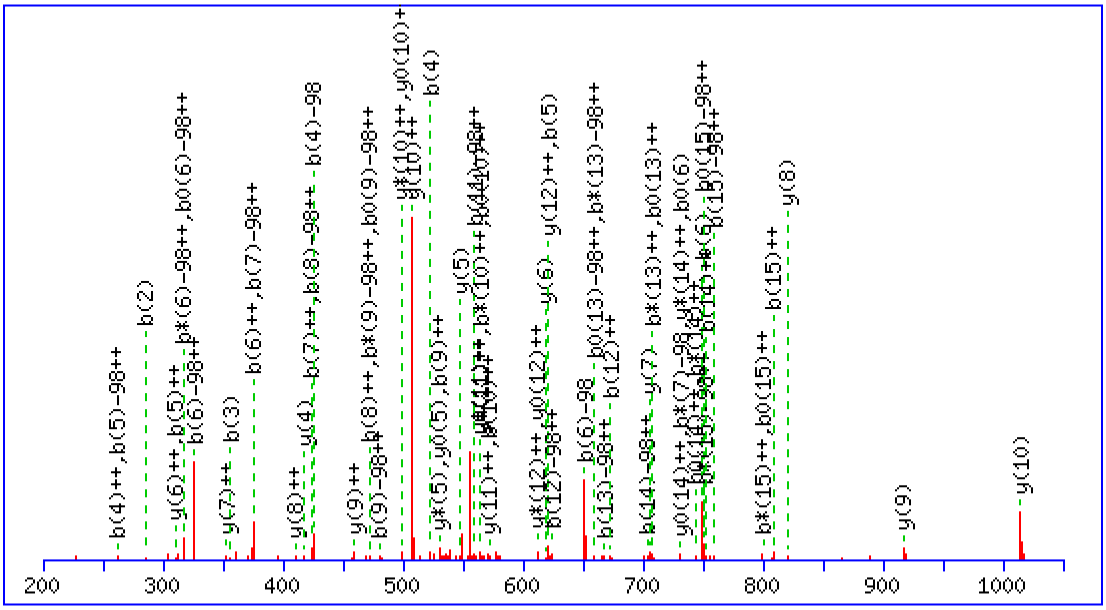
Monoisotopic mass of neutral peptide Mr(calc): 2131.8096
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0028
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6), b(6)-98, b(7)-98++, b(7)++, b(7)-98, b(7), b(8)-98++, b(8)-196++, b(8)-98, b(8), b(8)++, b(8)-196, b(9)-98++, b(9)-98, b(9), b(9)-196++, b(9)++, b(9)-196, b(10)-196++, b(10)-98++, b(10)++, b(11)-98, b(11), b(11)-196++, b(11)-98++, b(11)-196, b(11)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)-98++, b(16)-98++, b(16)-196++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)-98, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-196++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-196++, y(14)-98++, y(15)-98++, y(15)++, y(16)-196++

Peptide No.741

RKASPEPPDSAESALK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RKASPEPPDSAESALK**
Found in **I2BPL_MOUSE** in **SwissProt**, Interferon regulatory factor 2-binding protein-like OS=Mus musculus GN=Irf2bpl PE=1 SV=1

Match to Query 3942: 1761.829365 from(588.283731,3+) index(4043)
Title: Elution from: 20.967 to 20.967 scan no 1368 cid35.00 polarity:+:m1s



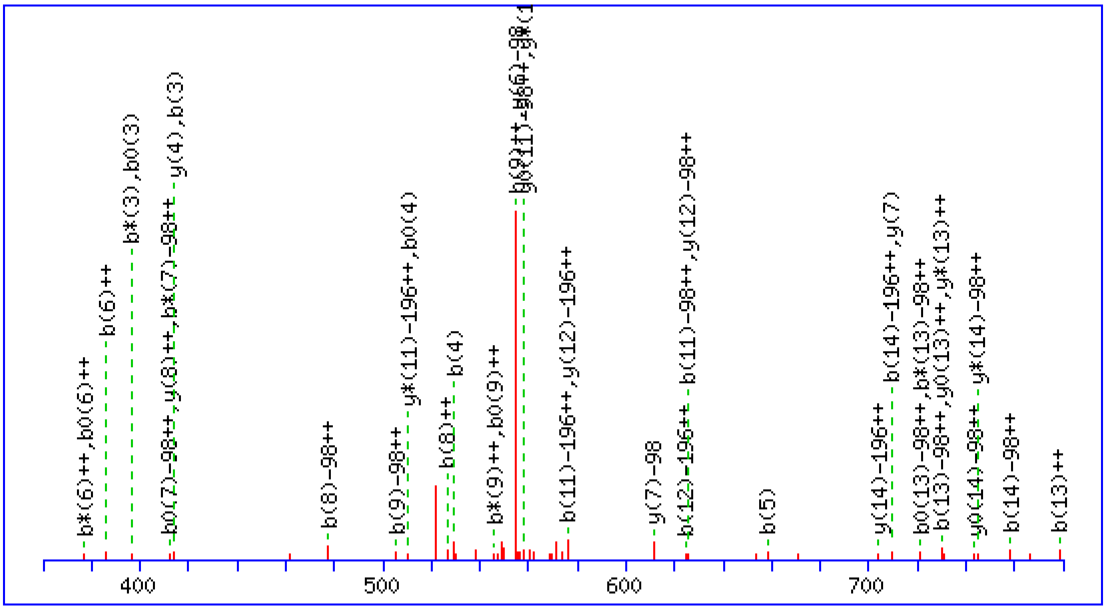
Monoisotopic mass of neutral peptide Mr(calc): 1761.8298
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00048
Matched b ions: b(2), b(3), b(4)-98, b(4), b(4)++, b(5), b(5)-98++, b(5)++, b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(11)++, y(12)++

Peptide No.742

RKEDELSIGSAPLGK
Confirmed sites: @S:7,@S:10
Ambiguous sites:

MS/MS Fragmentation of **RKEDELSIGSAPLGK**
Found in **VP13B_MOUSE** in **SwissProt**, Vacuolar protein sorting-associated protein 13B OS=Mus musculus GN=Vps13b PE=1 SV=2

Match to Query 3421: 1758.795744 from(587.272524,3+) index(1894)
Title: Elution from: 35.543 to 35.543 scan no 3267 cid35.00 polarity:+



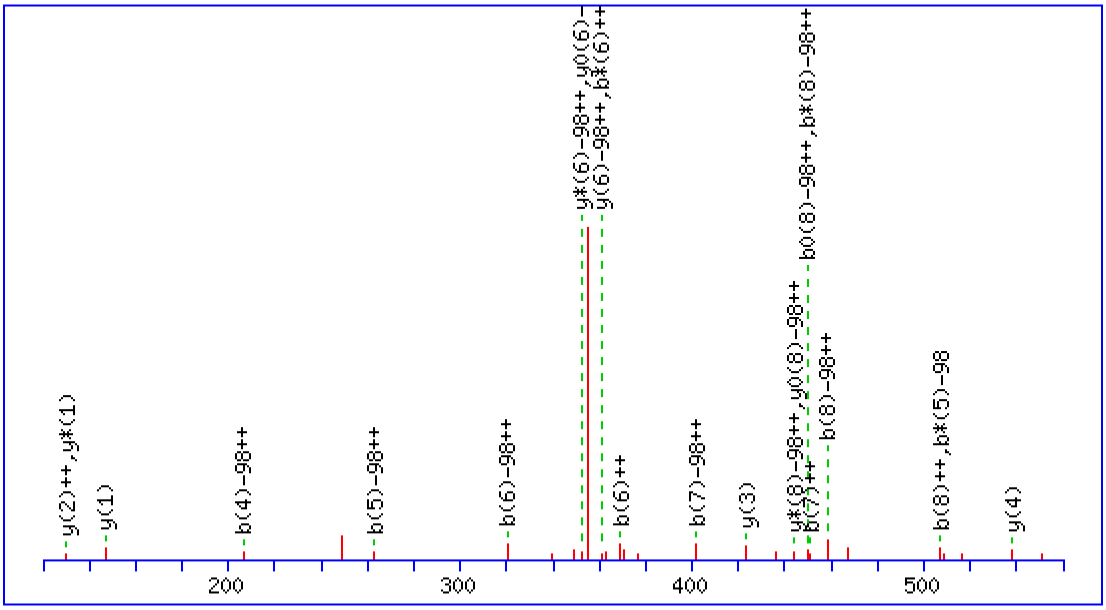
Monoisotopic mass of neutral peptide Mr(calc): 1758.7954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.012
Matched b ions: b(3), b(4), b(5), b(6)++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(11)-196++, b(11)-98++, b(12)-196++, b(13)-98++, b(13)++, b(14)-98++, b(14)-196++
Matched y ions: y(4), y(6)-98, y(7)-98, y(7), y(8)++, y(12)-196++, y(12)-98++, y(14)-196++

Peptide No.743

RKGSLDYLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RKGSLDYLK**
Found in **LUZP1_MOUSE** in **SwissProt**, Leucine zipper protein 1 OS=Mus musculus GN=Luzp1 PE=1 SV=2

Match to Query 1359: 1158.580476 from(387.200768,3+) index(500)
Title: Elution from: 20.839 to 20.839 scan no 1351 cid35.00 polarity:+



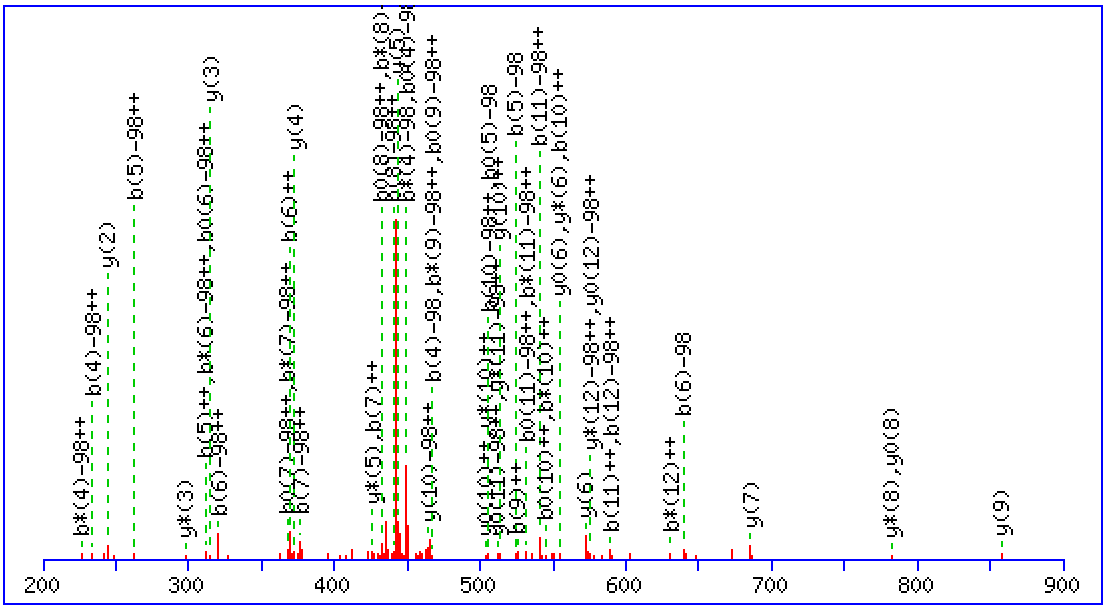
Monoisotopic mass of neutral peptide Mr(calc): 1158.5798
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0056
Matched b ions: b(4)-98++, b(5)-98++, b(6)-98++, b(6)++, b(7)-98++, b(7)++, b(8)-98++, b(8)++
Matched y ions: y(1), y(2)++, y(3), y(4), y(6)-98++

Peptide No.744

RKLSGDLEAGAPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RKLSGDLEAGAPK**
Found in **TCOF_MOUSE** in **SwissProt**, Treacle protein OS=Mus musculus GN=Tcof1 PE=1 SV=1

Match to Query 2447: 1420.706109 from(474.575979,3+) index(494)
Title: Elution from: 20.786 to 20.786 scan no 1344 cid35.00 polarity:+



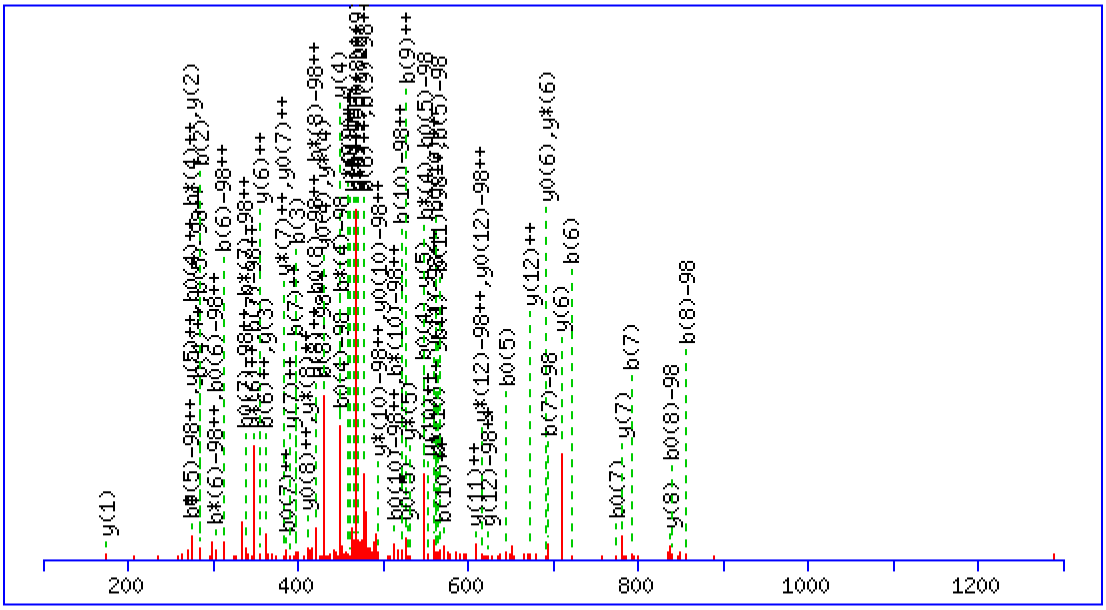
Monoisotopic mass of neutral peptide Mr(calc): 1420.7075
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0025
Matched b ions: b(4)-98++, b(4)-98, b(5)++, b(5)-98++, b(5)-98, b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(7)++, b(8)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(9), y(10)-98++, y(10)++

Peptide No.745

RKLSVGAYVSSVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RKLSVGAYVSSVR**
Found in **S23IP_MOUSE** in **SwissProt**, SEC23-interacting protein OS=Mus musculus GN=Sec23ip PE=1 SV=2

Match to Query 3520: 1500.782379 from(501.268069,3+) index(1654)
Title: Elution from: 41.285 to 41.285 scan no 3274 cid35.00 polarity:+



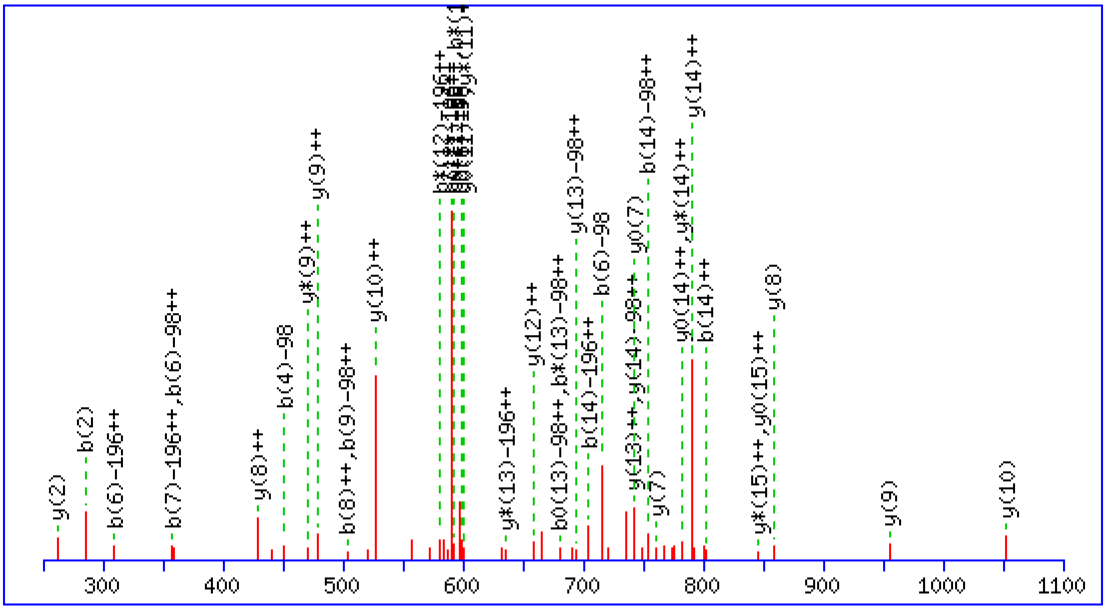
Monoisotopic mass of neutral peptide Mr(calc): 1500.7814
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 7.2e-005
Matched b ions: b(2), b(3), b(4)++, b(4)-98, b(4), b(5)-98++, b(5)-98, b(6)++, b(6)-98++, b(6), b(7)-98++, b(7)-98, b(7)++, b(7), b(8)-98++, b(8)++, b(8)-98, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.746

RKPSPSPPPPTATESR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **RKPSPSPPPPTATESR**
Found in **SMRC1_MOUSE** in **SwissProt**, SWI/SNF complex subunit SMARCC1 OS=Mus musculus GN=Smarcc1 PE=1 SV=2

Match to Query 3731: 1863.825420 from(622.282416,3+) index(3196)
Title: Elution from: 17.758 to 17.758 scan no 934 cid35.00 polarity:+:m1s



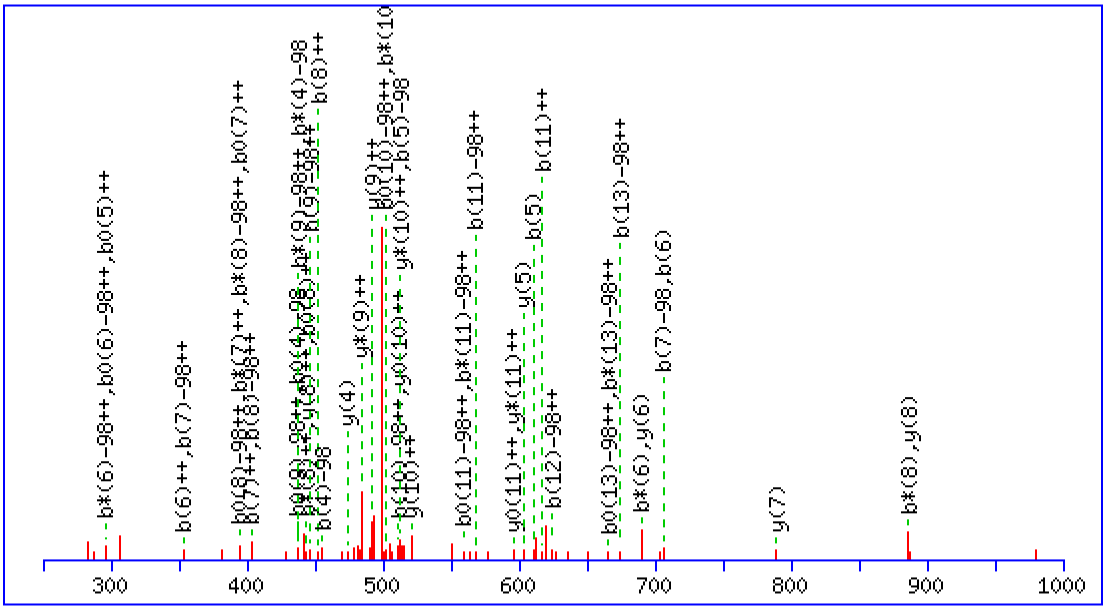
Monoisotopic mass of neutral peptide Mr(calc): 1863.8281
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.013
Matched b ions: b(2), b(4)-98, b(6)-98, b(6)-196++, b(6)-98++, b(7)-196++, b(8)++, b(9)-98++, b(10)++, b(12)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++
Matched y ions: y(2), y(7), y(8)++, y(8), y(9), y(9)++, y(10)++, y(10), y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++

Peptide No.747

RKTSGPPVSELITK
Confirmed sites:
Ambiguous sites: @T:3orS:4

MS/MS Fragmentation of **RKTSGPPVSELITK**
Found in **H14_MOUSE** in **SwissProt**, Histone H1.4 OS=Mus musculus GN=Hist1h1e PE=1 SV=2

Match to Query 3200: 1591.833579 from(531.618469,3+) index(1198)
Title: Elution from: 27.011 to 27.011 scan no 2190 cid35.00 polarity:+



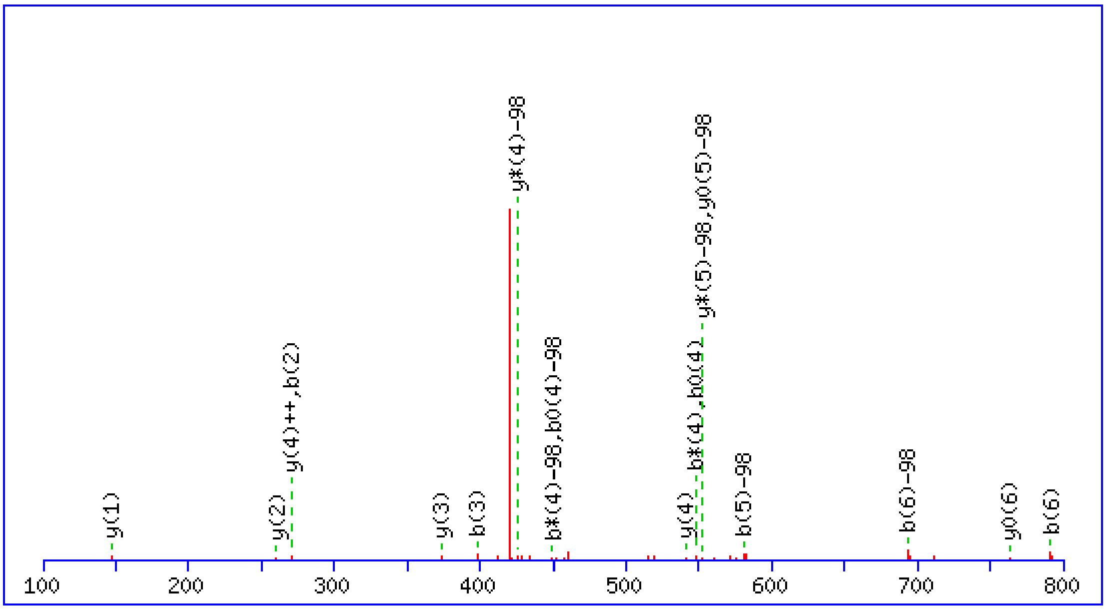
Monoisotopic mass of neutral peptide Mr(calc): 1591.8335
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.032
Matched b ions: b(4)-98, b(5), b(5)-98, b(6), b(6)++, b(7)++, b(7)-98, b(7)-98++, b(8)-98++, b(8)++, b(9)-98++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(13)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(10)++

Peptide No.748

RLQSLIK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RLQSLIK**
Found in **HLTF_MOUSE** in **SwissProt**, Helicase-like transcription factor OS=Mus musculus GN=Hltf PE=1 SV=1

Match to Query 646: 936.515464 from(469.265008,2+) index(1741)
Title: Elution from: 32.400 to 32.400 scan no 2924 cid35.00 polarity:+



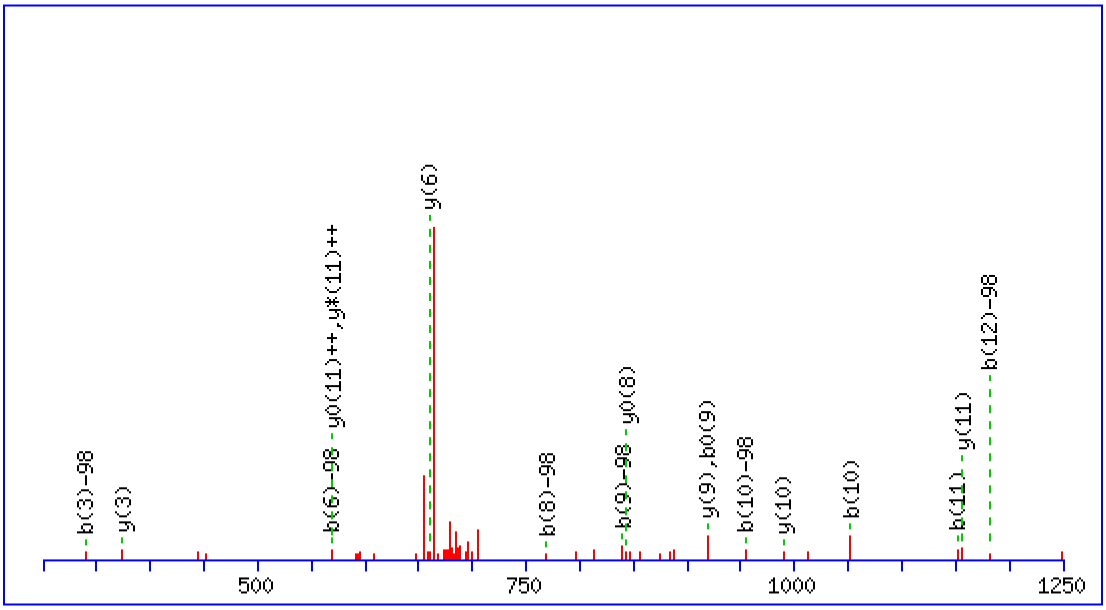
Monoisotopic mass of neutral peptide Mr(calc): 936.5157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0082
Matched b ions: b(2), b(3), b(5)-98, b(6)-98, b(6)
Matched y ions: y(1), y(2), y(3), y(4)++, y(4)

Peptide No.749

RLSAGTTVADVQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RLSAGTTVADVQK**
Found in **PHLB2_MOUSE** in **SwissProt**, Pleckstrin homology-like domain family B member 2 OS=Mus musculus GN=Phldb2 PE=1 SV=2

Match to Query 2301: 1424.701006 from(713.357779,2+) index(764)
Title: Elution from: 25.052 to 25.052 scan no 1802 cid35.00 polarity:+



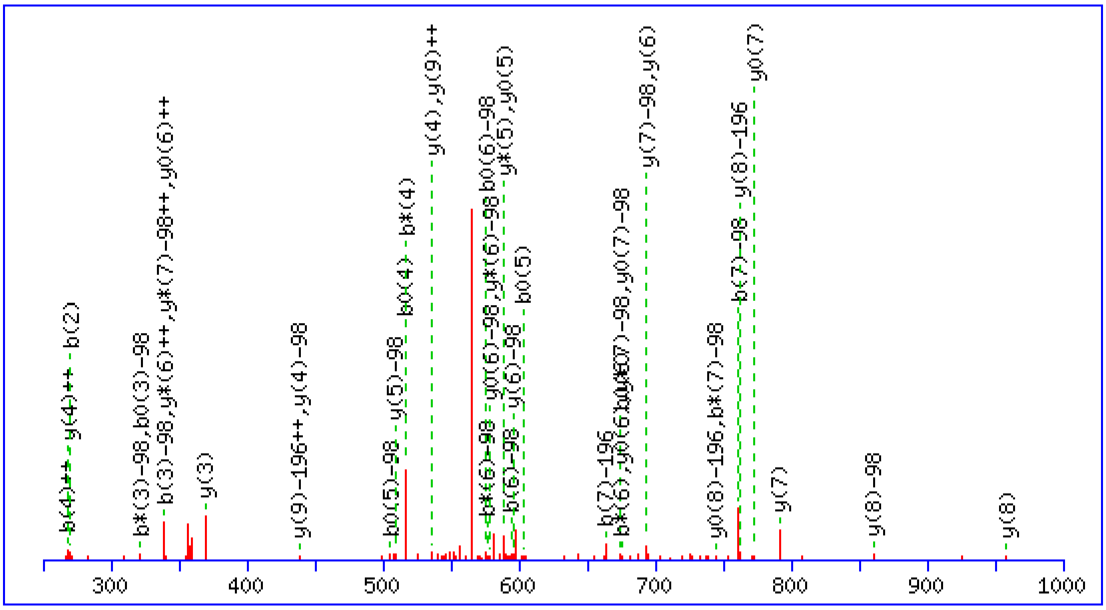
Monoisotopic mass of neutral peptide Mr(calc): 1424.7025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.007
Matched b ions: b(3)-98, b(6)-98, b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(12)-98
Matched y ions: y(3), y(6), y(9), y(10), y(11)

Peptide No.750

RLSPSASPPR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RLSPSASPPR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 1502: 1226.519930 from(614.267241,2+) index(465)
Title: Elution from: 21.066 to 21.066 scan no 1361 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1226.5210
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.037
Matched b ions: b(2), b(3)-98, b(4)++, b(6)-98, b(7)-98, b(7)-196
Matched y ions: y(3), y(4)-98, y(4)++, y(4), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(8), y(8)-98, y(8)-196, y(9)-196++, y(9)++

Peptide No.751

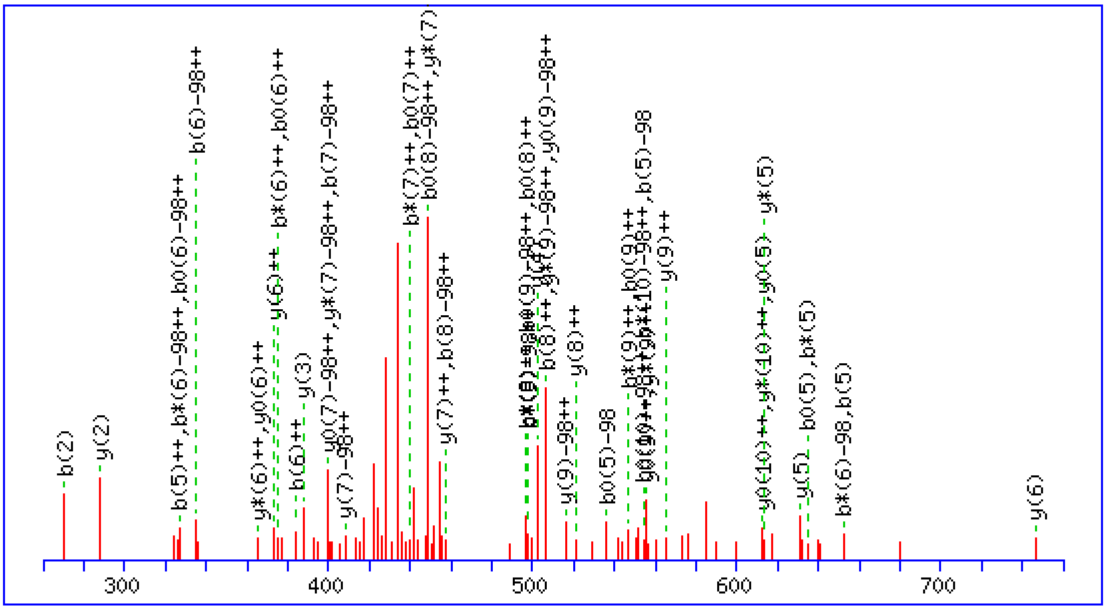
RLSQSDEDVIR

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of **RLSQSDEDVIR**
Found in **WDR26_MOUSE** in **SwissProt**, WD repeat-containing protein 26 OS=Mus musculus GN=Wdr26 PE=1 SV=3

Match to Query 2210: 1396.634634 from(466.552154,3+) index(728)
Title: Elution from: 24.754 to 24.754 scan no 1761 cid35.00 polarity:+



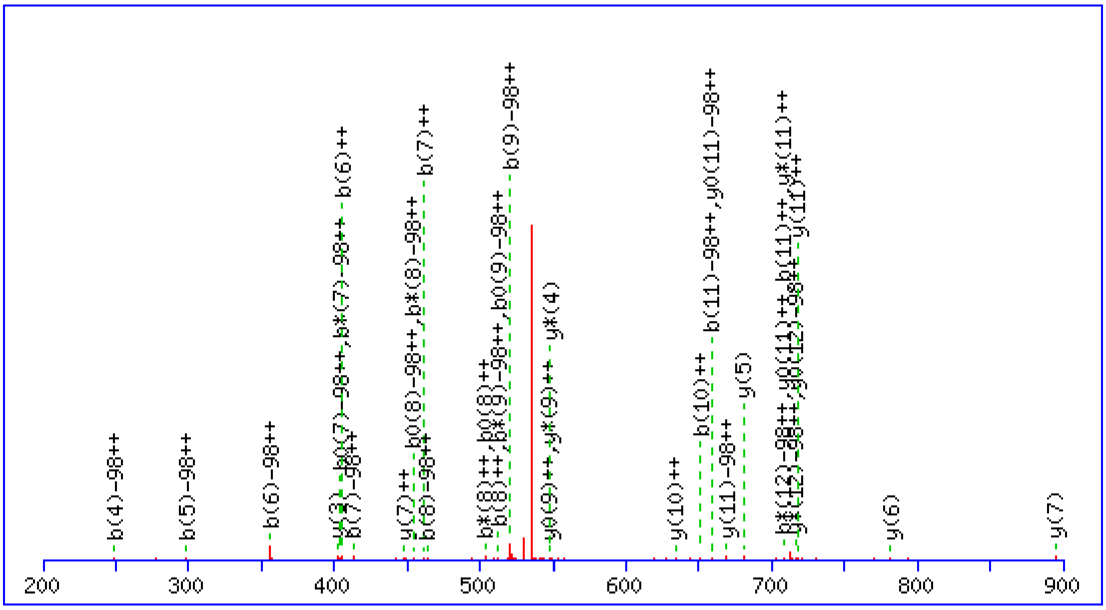
Monoisotopic mass of neutral peptide Mr(calc): 1396.6347
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0036
Matched b ions: b(2), b(5)++, b(5), b(5)-98, b(6)-98++, b(6)++, b(7)++, b(7)-98++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)-98++, y(7)++, y(8)++, y(9)-98++, y(9)++

Peptide No.752

RLSRTDLTDYLNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RLSRTDLTDYLNR**
Found in **QCR1_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2

Match to Query 3185: 1701.818991 from(568.280273,3+) index(2198)
Title: Elution from: 39.149 to 39.149 scan no 3722 cid35.00 polarity:+



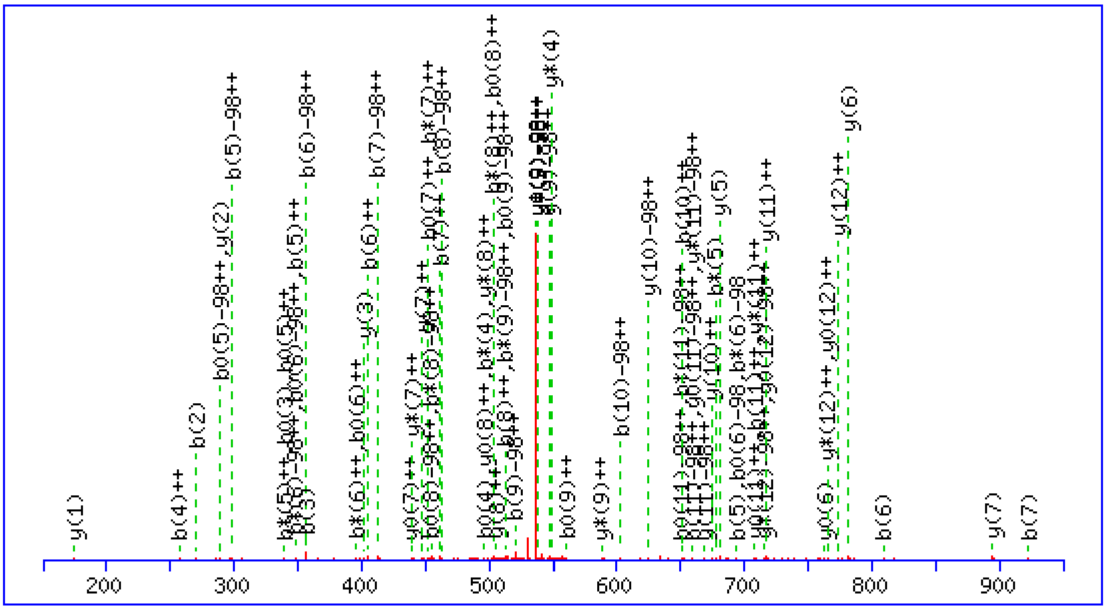
Monoisotopic mass of neutral peptide Mr(calc): 1701.8199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0085
Matched b ions: b(4)-98++, b(5)-98++, b(6)-98++, b(6)++, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++
Matched y ions: y(3), y(5), y(6), y(7), y(7)++, y(10)++, y(11)-98++, y(11)++

Peptide No.753

RLSRTDLTDYLNR
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **RLSRTDLTDYLNR**
Found in **QCR1_MOUSE** in **SwissProt**, Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=2

Match to Query 4201: 1701.820110 from(568.280646,3+) index(5483)
Title: Elution from: 47.565 to 47.565 scan no 3960 cid35.00 polarity:+:m1s



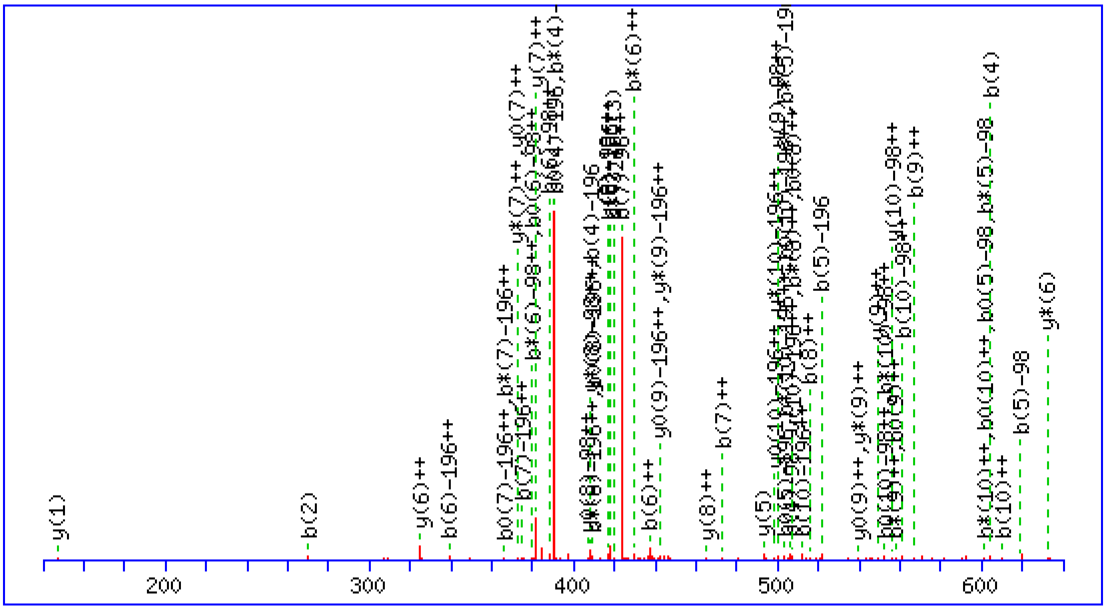
Monoisotopic mass of neutral peptide Mr(calc): 1701.8199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.002
Matched b ions: b(2), b(3), b(4)++, b(5)++, b(5)-98++, b(5), b(6)-98++, b(6)++, b(6), b(7)-98++, b(7), b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(1), y(2), y(3), y(5), y(6), y(7), y(7)++, y(8)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++

Peptide No.754

RLSSLRASTSK
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **RLSSLRASTSK**
Found in **RS6_MOUSE** in **SwissProt**, 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1

Match to Query 2002: 1364.621154 from(455.880994,3+) index(550)
Title: Elution from: 21.788 to 21.788 scan no 1458 cid35.00 polarity:+



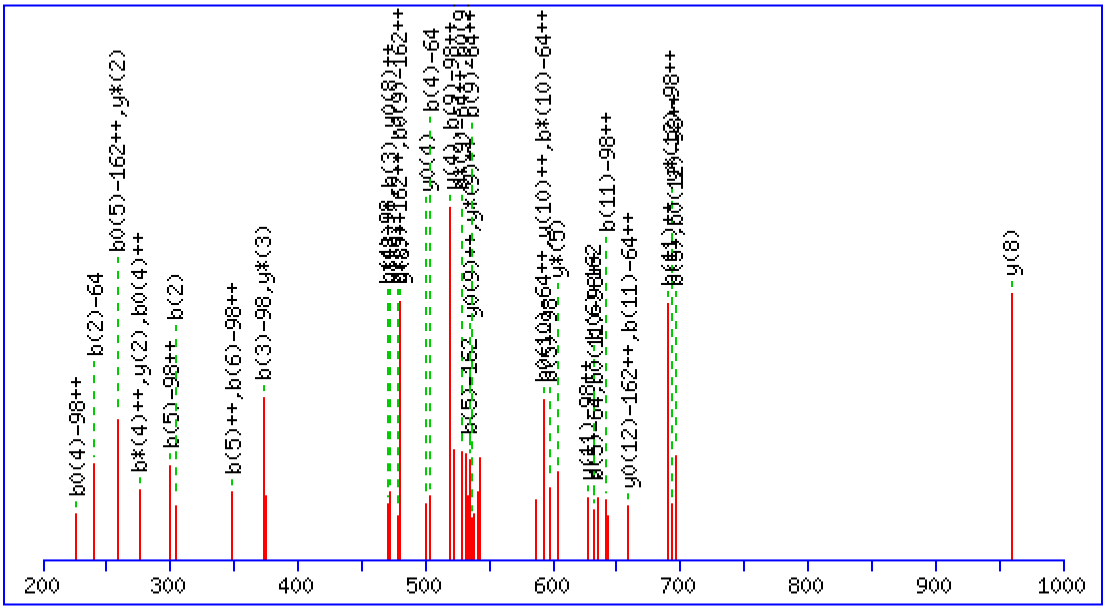
Monoisotopic mass of neutral peptide Mr(calc): 1364.6214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.03
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(4)-196, b(5)-98, b(5)-196, b(6)-196++, b(6)++, b(6)-98++, b(7)-98++, b(7)-196++, b(7)++, b(8)-196++, b(8)++, b(9)++, b(10)-196++, b(10)-98++, b(10)++
Matched y ions: y(1), y(5), y(6)++, y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)-196++, y(10)-98++

Peptide No.755

RMSPKPELTEDQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RMSPKPELTEDQK**
Found in **CETN2_MOUSE** in **SwissProt**, Centrin-2 OS=Mus musculus GN=Cetn2 PE=1 SV=1

Match to Query 3617: 1653.741555 from(552.254461,3+) index(165)
Title: Elution from: 17.452 to 17.452 scan no 939 cid35.00 polarity:+



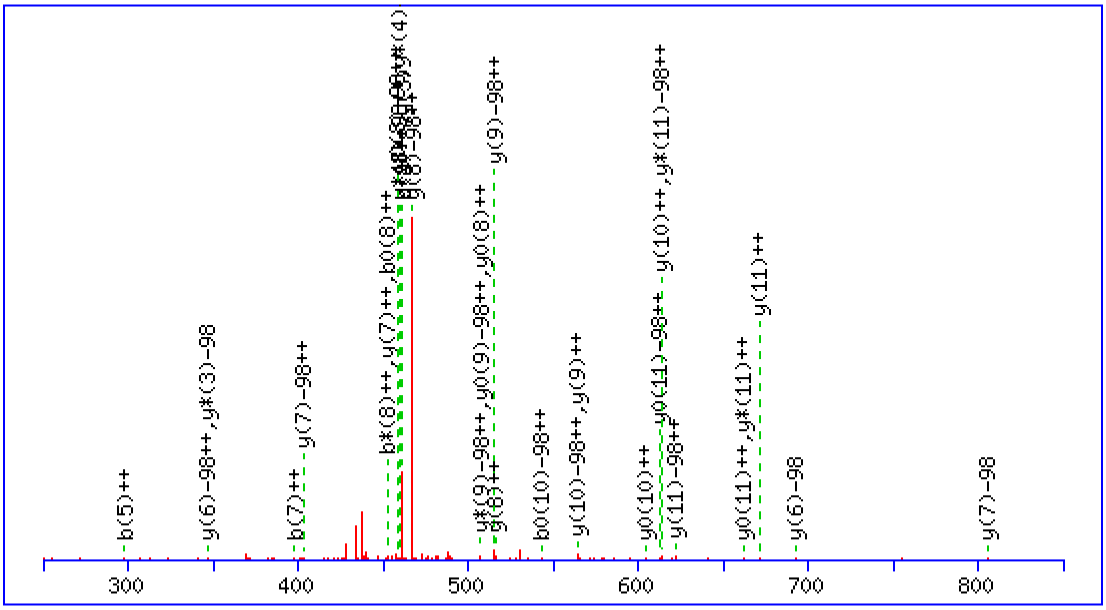
Monoisotopic mass of neutral peptide Mr(calc): 1653.7433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.021
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)++, b(5), b(5)-98++, b(5)-98, b(6)-98++, b(9)-98++, b(11)++, b(11)-98++
Matched y ions: y(2), y(4), y(8), y(8)++, y(10)++, y(11)-98++

Peptide No.756

RNPPELSQNSFK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **RNPPELSQNSFK**
Found in **CB078_MOUSE** in **SwissProt**, Uncharacterized protein C2orf78 homolog OS=Mus musculus GN=Gm5592 PE=2 SV=1

Match to Query 3053: 1495.681998 from(499.567942,3+) index(61)
Title: Elution from: 22.944 to 22.944 scan no 1085 cid35.00 polarity:+



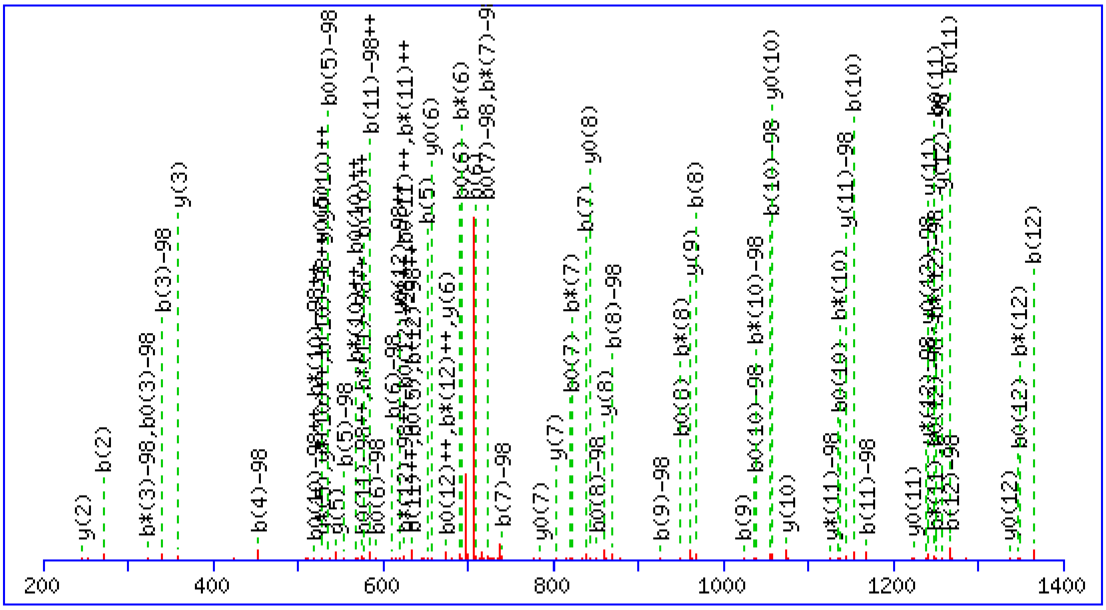
Monoisotopic mass of neutral peptide Mr(calc): 1495.6820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 **Expect:** 0.025
Matched b ions: b(5)++, b(7)++, b(8)++
Matched y ions: y(3), y(6)-98, y(6)-98++, y(7)-98, y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(10)++, y(11)-98++, y(11)++

Peptide No.757

RNSLTGEEGELVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RNSLTGEEGELVK**
Found in **SGPP1_MOUSE** in **SwissProt**, Sphingosine-1-phosphate phosphatase 1 OS=Mus musculus GN=Sgpp1 PE=1 SV=1

Match to Query 2630: 1510.701942 from(756.358247,2+) index(1161)
Title: Elution from: 28.524 to 28.524 scan no 2282 cid35.00 polarity:+



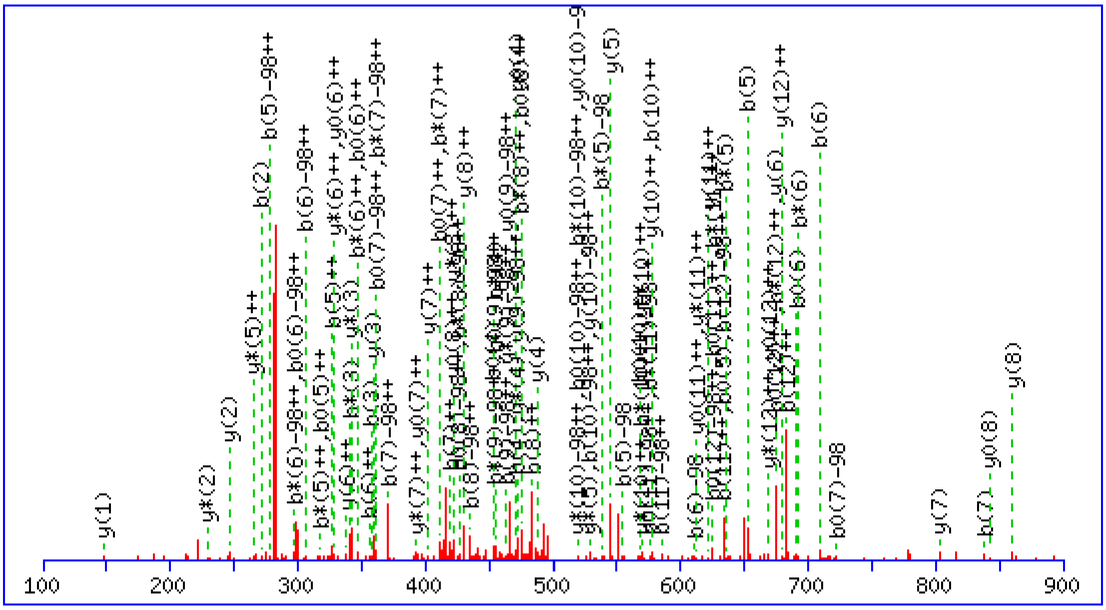
Monoisotopic mass of neutral peptide Mr(calc): 1510.7028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 73 **Expect:** 2.2e-007
Matched b ions: b(2), b(3)-98, b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(11)-98, b(11), b(12)-98++, b(12)-98, b(12)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98, y(12)-98

Peptide No.758

RNSLTGEEGELVK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **RNSLTGEEGELVK**
Found in **SGPP1_MOUSE** in **SwissProt**, Sphingosine-1-phosphate phosphatase 1 OS=Mus musculus GN=Sgpp1 PE=1 SV=1

Match to Query 3106: 1510.702935 from(504.574921,3+) index(1119)
Title: Elution from: 36.922 to 36.922 scan no 2628 cid35.00 polarity:+



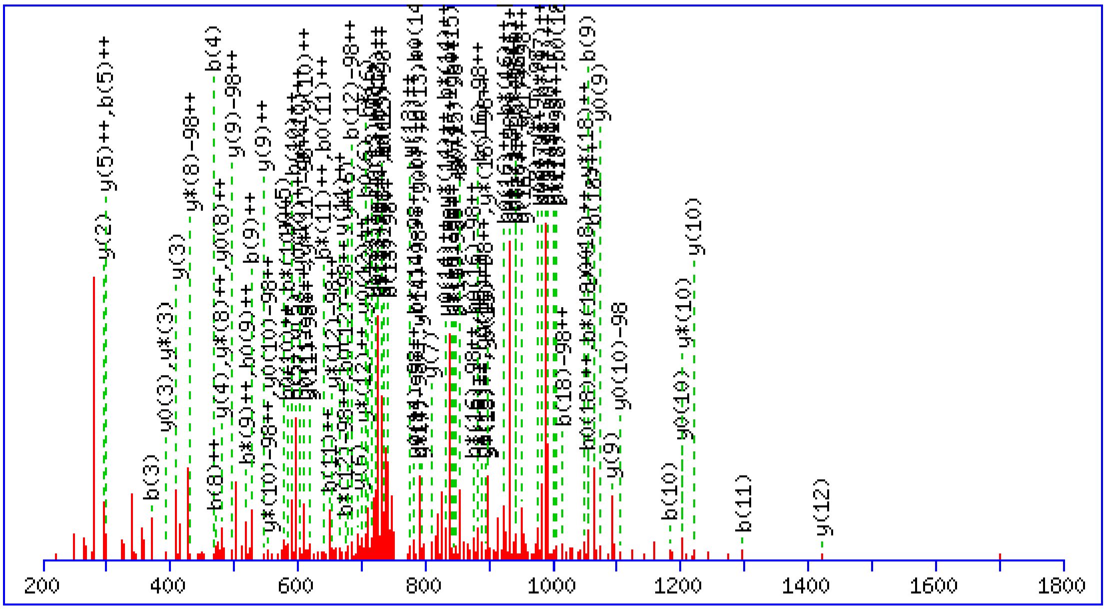
Monoisotopic mass of neutral peptide Mr(calc): 1510.7028
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.012
Matched b ions: b(2), b(3), b(4), b(5), b(5)++, b(5)-98++, b(5)-98, b(6), b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(7), b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(12)++

Peptide No.759

RNVPQEESLEDSDVDADFK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **RNVPQEESLEDSDVDADFK**
Found in **IMA3_MOUSE** in **SwissProt**, Importin subunit alpha-3 OS=Mus musculus GN=Kpna3 PE=1 SV=1

Match to Query 5725: 2271.954705 from(758.325511,3+) index(5314)
Title: Elution from: 44.798 to 44.798 scan no 3669 cid35.00 polarity:+:m1s



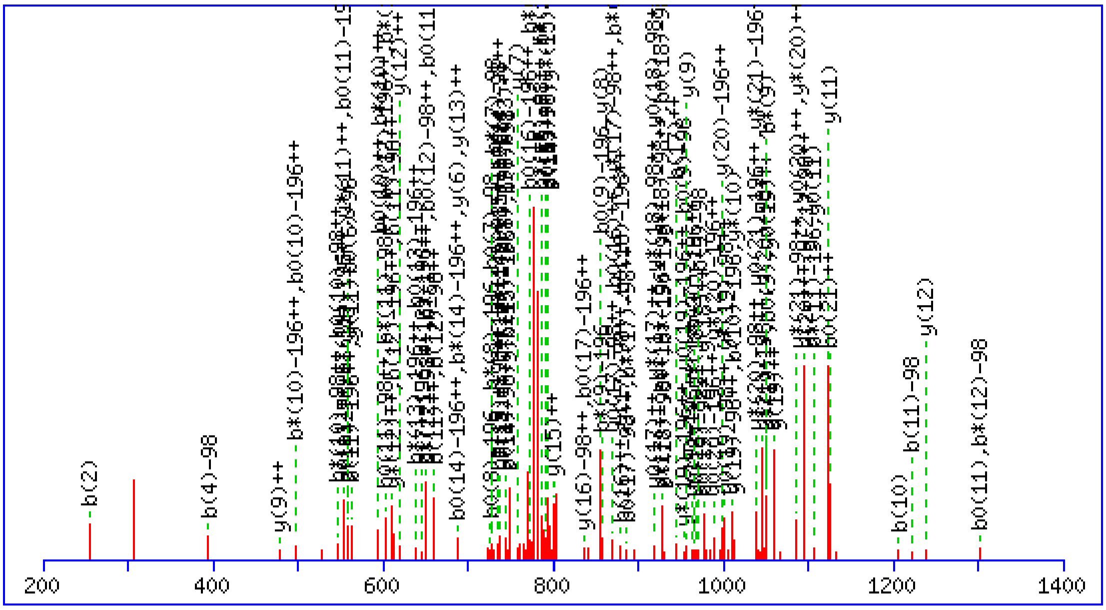
Monoisotopic mass of neutral peptide Mr(calc): 2271.9532
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.1e-005
Matched b ions: b(3), b(4), b(5), b(5)++, b(6), b(7), b(8)++, b(8), b(9)++, b(9), b(10)++, b(10), b(11), b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(7), y(8), y(9), y(9)-98++, y(9)++, y(9)-98, y(10)++, y(10), y(11)-98++, y(11)++, y(12), y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(16)++, y(17)-98++, y(17)++

Peptide No.760

RPASPSSPEHLPATPAESPAQR
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RPASPSSPEHLPATPAESPAQR**
Found in **SDS3_MOUSE** in **SwissProt**, Sin3 histone deacetylase corepressor complex component SDS3 OS=Mus musculus GN=Suds3 PE=1 SV=1

Match to Query 6270: 2442.067665 from(815.029831,3+) index(4921)
Title: Elution from: 27.136 to 27.136 scan no 2245 cid35.00 polarity:+:m1s



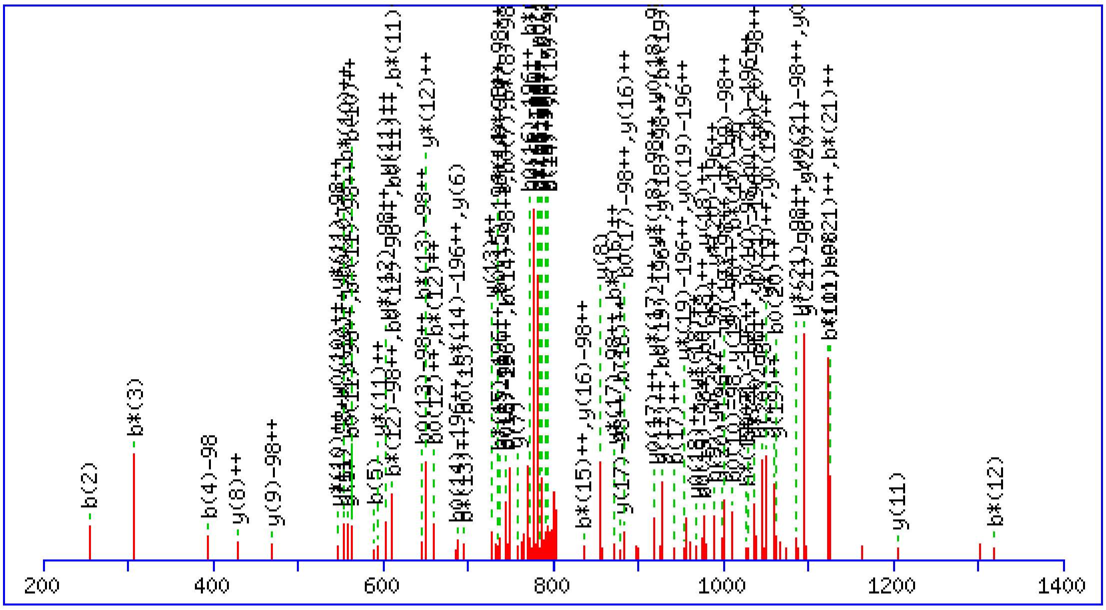
Monoisotopic mass of neutral peptide Mr(calc): 2442.0730
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00046
Matched b ions: b(2), b(4)-98, b(7)-98, b(7)-196, b(8)-196, b(9)-98, b(10), b(10)-196, b(10)-98++, b(11)-98++, b(11)++, b(11)-98, b(11)-196++, b(12)-196++, b(12)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)-196++, b(15)-98++, b(16)++, b(17)++, b(21)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(11), y(11)++, y(12), y(12)++, y(13)++, y(15)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(19)-196++, y(20)-98++, y(20)++, y(20)-196++, y(21)-196++, y(21)-98++

Peptide No.761

RPASPSSPEHLPATPAESPAQR
Confirmed sites: @S:4,@T:14
Ambiguous sites:

MS/MS Fragmentation of **RPASPSSPEHLPATPAESPAQR**
Found in **SDS3_MOUSE** in **SwissProt**, Sin3 histone deacetylase corepressor complex component SDS3 OS=Mus musculus GN=Suds3 PE=1 SV=1

Match to Query 6096: 2442.073290 from(815.031706,3+) index(4744)
Title: Elution from: 27.133 to 27.133 scan no 2207 cid35.00 polarity:+:m1s



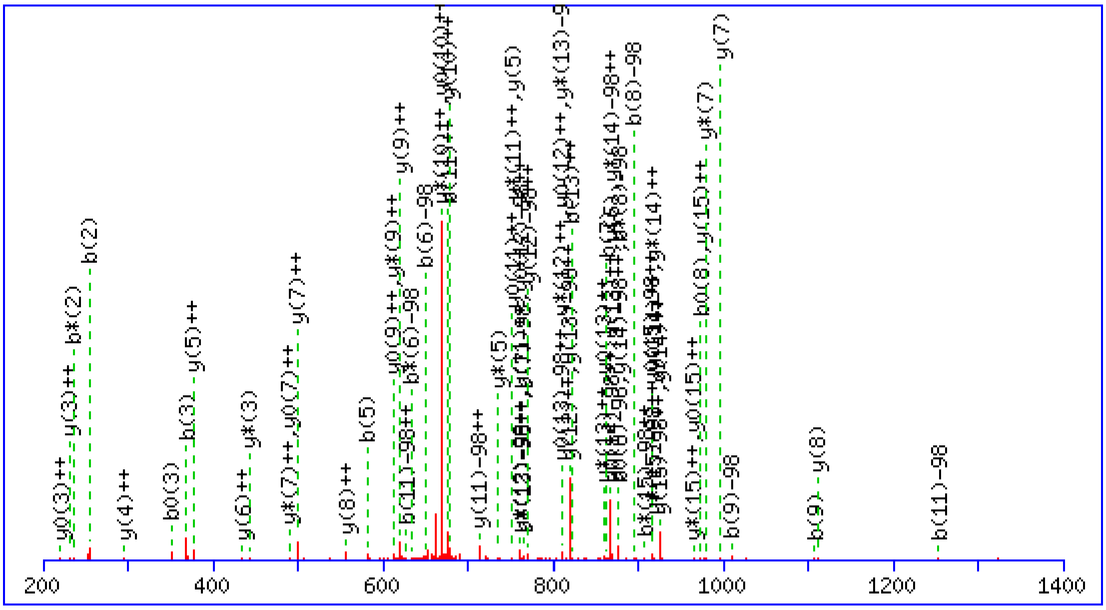
Monoisotopic mass of neutral peptide Mr(calc): 2442.0730
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00068
Matched b ions: b(2), b(4)-98, b(5), b(9), b(10), b(10)++, b(10)-98, b(14)-98++, b(14)++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(17)++, b(21)-196++, b(21)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(8)++, y(9)-98++, y(10)++, y(11)-98++, y(11), y(11)++, y(13)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(20)-196++, y(21)-98++

Peptide No.762

RPDPDSDEDEDYERER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **RPDPDSDEDEDYERER**
Found in **SPF45_MOUSE** in **SwissProt**, Splicing factor 45 OS=Mus musculus GN=Rbm17 PE=1 SV=1

Match to Query 4440: 2101.784163 from(701.601997,3+) index(3452)
Title: Elution from: 20.165 to 20.165 scan no 1240 cid35.00 polarity:+:m1s



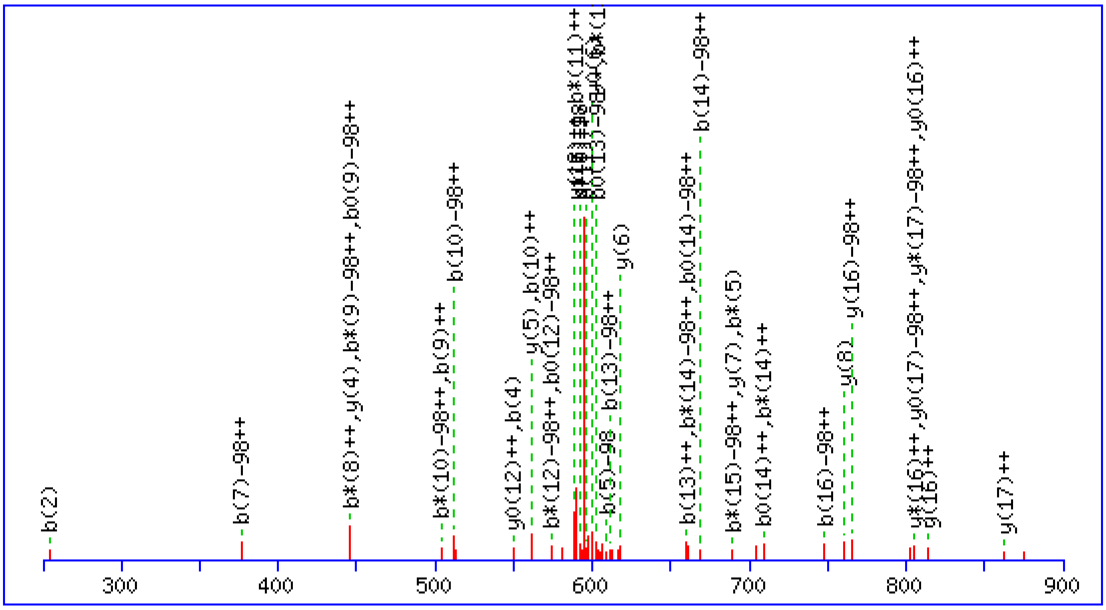
Monoisotopic mass of neutral peptide Mr(calc): 2101.7862
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 2e-008
Matched b ions: b(2), b(3), b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(11)-98, b(11)-98++, b(11)++, b(13)++, b(15)++, b(15)-98++
Matched y ions: y(3)++, y(4)++, y(5)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++

Peptide No.763

RPESRGSGVNAAGDGTIR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RPESRGSGVNAAGDGTIR**
Found in **TGM1_MOUSE** in **SwissProt**, Protein-glutamine gamma-glutamyltransferase K OS=Mus musculus GN=Tgm1 PE=1 SV=2

Match to Query 4512: 1878.866325 from(627.296051,3+) index(283)
Title: Elution from: 18.568 to 18.568 scan no 1083 cid35.00 polarity:+



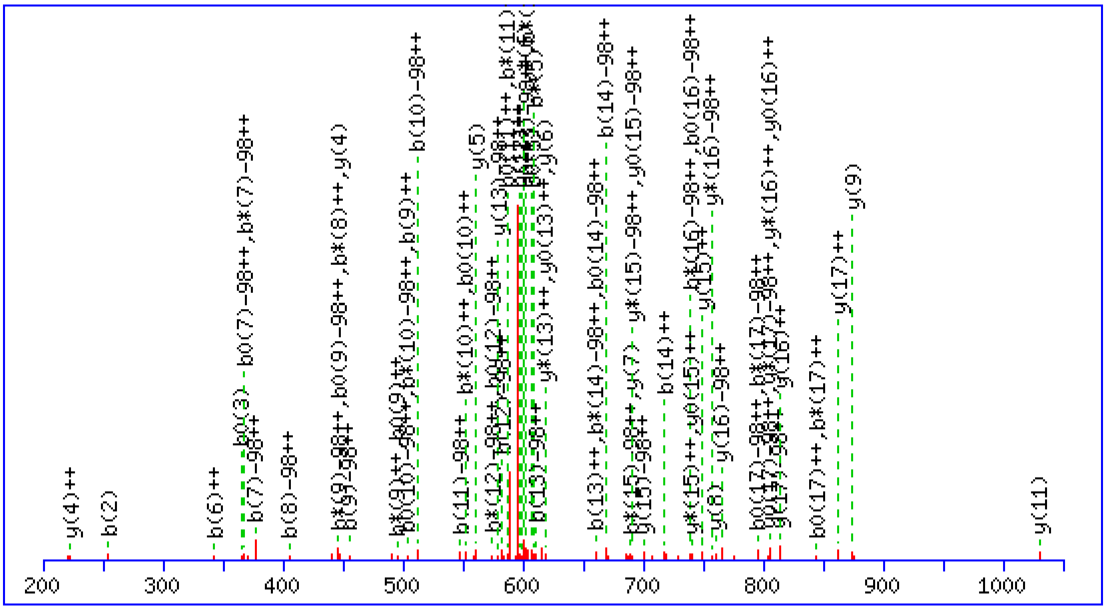
Monoisotopic mass of neutral peptide Mr(calc): 1878.8697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.031
Matched b ions: b(2), b(4), b(5)-98, b(7)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(13)++, b(13)-98++, b(14)-98++, b(16)-98++, b(17)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(13)++, y(16)-98++, y(16)++, y(17)++

Peptide No.764

RPESRGSGVNAAGDGTIR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **RPESRGSGVNAAGDGTIR**
Found in **TGM1_MOUSE** in **SwissProt**, Protein-glutamine gamma-glutamyltransferase K OS=Mus musculus GN=Tgm1 PE=1 SV=2

Match to Query 3783: 1878.870201 from(627.297343,3+) index(3266)
Title: Elution from: 18.489 to 18.489 scan no 1023 cid35.00 polarity:+:m1s



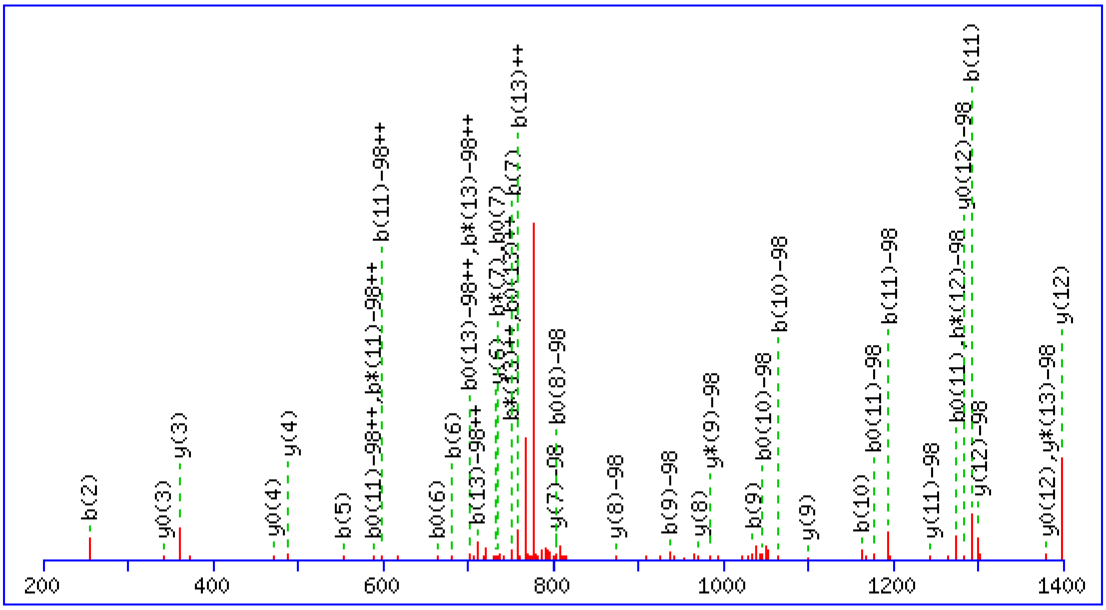
Monoisotopic mass of neutral peptide Mr(calc): 1878.8697
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.006
Matched b ions: b(2), b(6)++, b(7)-98++, b(8)-98++, b(9)++, b(9)-98++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(17)-98++
Matched y ions: y(4), y(4)++, y(5), y(6), y(7), y(8), y(9), y(11), y(12)++, y(13)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.765

RPGLEKASDEEPED
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **RPGLEKASDEEPED**
Found in **DI3L2_MOUSE** in **SwissProt**, DIS3-like exonuclease 2 OS=Mus musculus GN=Dis3l2 PE=1 SV=1

Match to Query 3413: 1650.680178 from(826.347365,2+) index(449)
Title: Elution from: 20.424 to 20.424 scan no 1295 cid35.00 polarity:+



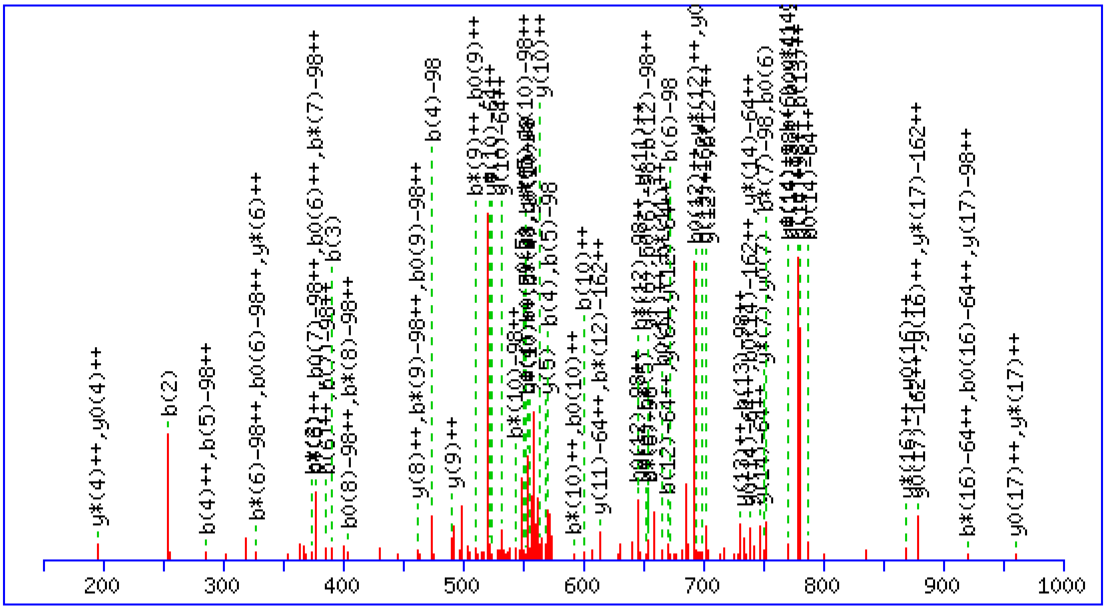
Monoisotopic mass of neutral peptide Mr(calc): 1650.6774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0023
Matched b ions: b(2), b(5), b(6), b(7), b(9)-98, b(9), b(10)-98, b(10), b(11)-98++, b(11)-98, b(11), b(13)-98++, b(13)++
Matched y ions: y(3), y(4), y(6), y(7)-98, y(8)-98, y(8), y(9), y(11)-98, y(12), y(12)-98

Peptide No.766

RPHTPTPGIYMGRPTYGSSR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **RPHTPTPGIYMGRPTYGSSR**
Found in **TRA2B_MOUSE** in **SwissProt**, Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1

Match to Query 5879: 2326.065620 from(582.523681,4+) index(4344)
Title: Elution from: 23.470 to 23.470 scan no 1709 cid35.00 polarity:+:m1s



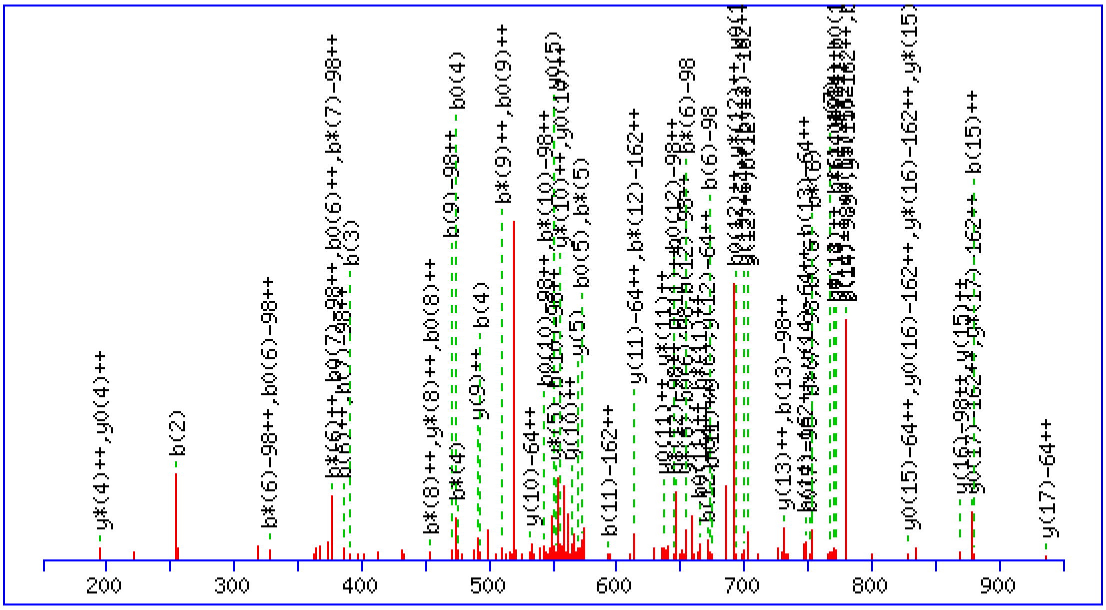
Monoisotopic mass of neutral peptide Mr(calc): 2326.0678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 29 **Expect:** 0.009
Matched b ions: b(2), b(3), b(4)-98, b(4)++, b(4), b(5)-98++, b(5)-98, b(6)++, b(6), b(6)-98, b(7)-98++, b(10)-98++, b(10)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)-98++
Matched y ions: y(5), y(6), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(16)++, y(17)-98++

Peptide No.767

RPHTPTPGIYMGRPTYGSSR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **RPHTPTPGIYMGRPTYGSSR**
Found in **TRA2B_MOUSE** in **SwissProt**, Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1

Match to Query 6035: 2326.066180 from(582.523821,4+) index(4528)
Title: Elution from: 23.586 to 23.586 scan no 1761 cid35.00 polarity:+:m1s



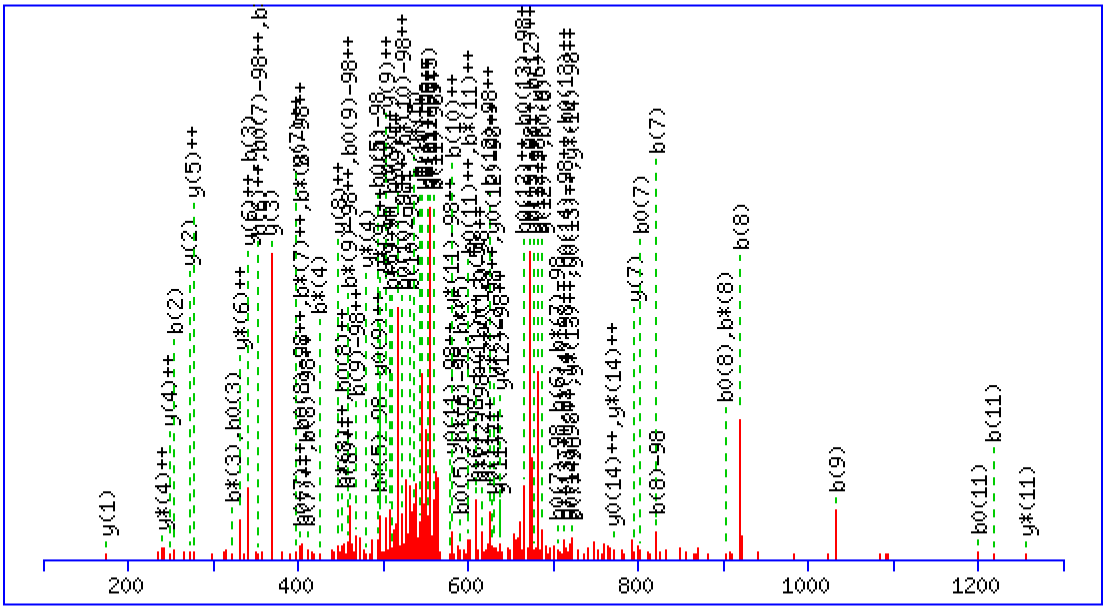
Monoisotopic mass of neutral peptide Mr(calc): 2326.0678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 22 **Expect:** 0.043
Matched b ions: b(2), b(3), b(4), b(6)++, b(6), b(6)-98, b(7)-98++, b(9)-98++, b(10)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++
Matched y ions: y(5), y(6), y(7), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++

Peptide No.768

RPSTSPDVLQGQPPR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **RPSTSPDVLQGQPPR**
Found in **UB2J1_MOUSE** in **SwissProt**, Ubiquitin-conjugating enzyme E2 J1 OS=Mus musculus GN=Ube2j1 PE=1 SV=2

Match to Query 4242: 1713.821421 from(572.281083,3+) index(4396)
Title: Elution from: 33.654 to 33.654 scan no 2335 cid35.00 polarity:+:m1s



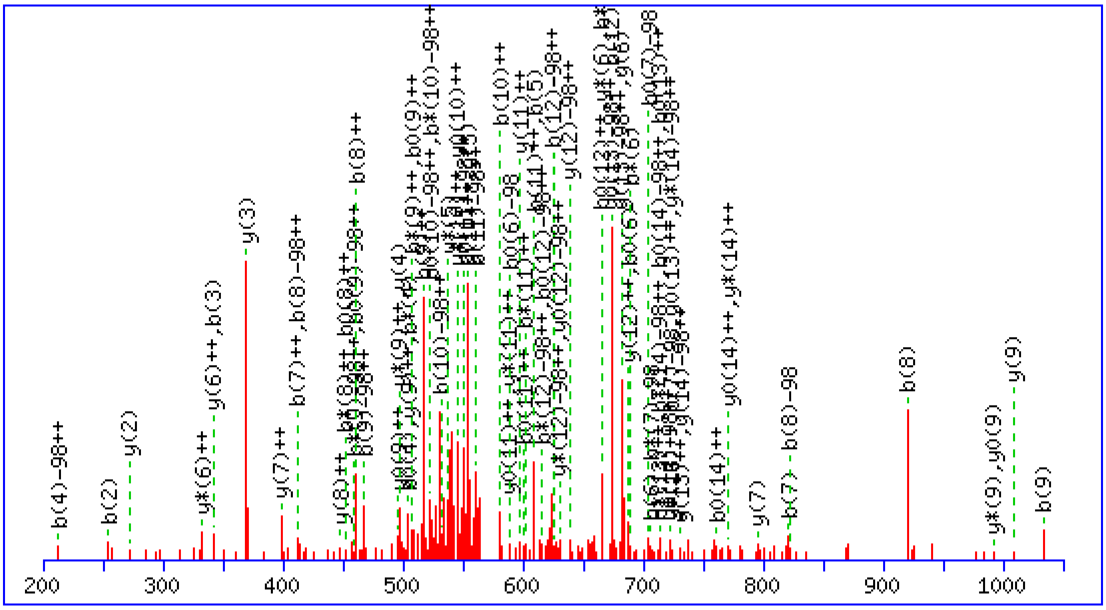
Monoisotopic mass of neutral peptide Mr(calc): 1713.8199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0032
Matched b ions: b(2), b(3), b(5), b(5)-98, b(6)++, b(6)-98, b(6), b(7), b(7)++, b(7)-98, b(8)++, b(8), b(8)-98, b(8)-98++, b(9), b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(1), y(2), y(3), y(4)++, y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++

Peptide No.769

RPSTSPDVLQGQPPR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **RPSTSPDVLQGQPPR**
Found in **UB2J1_MOUSE** in **SwissProt**, Ubiquitin-conjugating enzyme E2 J1 OS=Mus musculus GN=Ube2j1 PE=1 SV=2

Match to Query 3694: 1713.819759 from(572.280529,3+) index(3764)
Title: Elution from: 33.701 to 33.701 scan no 2238 cid35.00 polarity:+:m1s



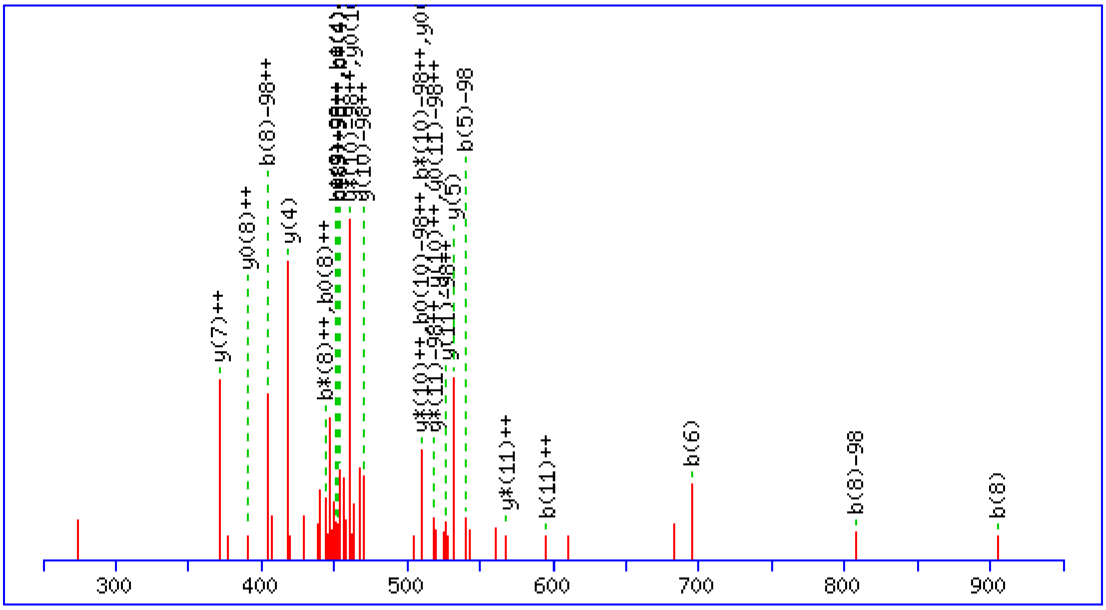
Monoisotopic mass of neutral peptide Mr(calc): 1713.8199
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0007
Matched b ions: b(2), b(3), b(4)-98++, b(4), b(5), b(6), b(7), b(7)-98, b(7)++, b(8)++, b(8), b(8)-98, b(8)-98++, b(9), b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)-98++

Peptide No.770

RQDSAGPILDGAR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RQDSAGPILDGAR**
Found in **CGNL1_MOUSE** in **SwissProt**, Cingulin-like protein 1 OS=Mus musculus GN=Cgnl1 PE=1 SV=2

Match to Query 2516: 1434.661116 from(479.227648,3+) index(750)
Title: Elution from: 22.924 to 22.924 scan no 1634 cid35.00 polarity:+



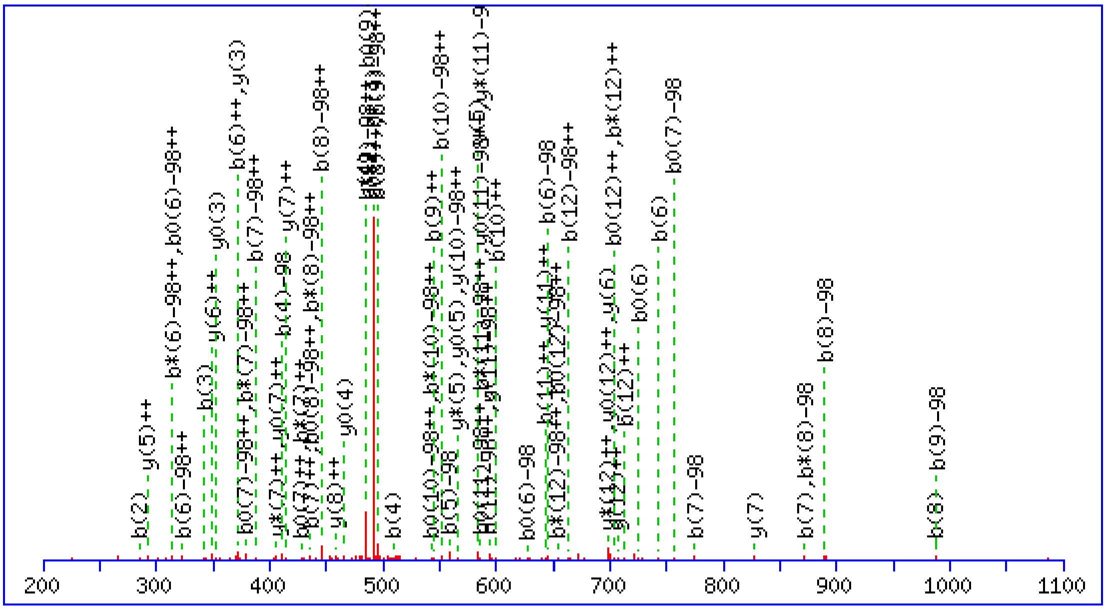
Monoisotopic mass of neutral peptide Mr(calc): 1434.6616
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.039
Matched b ions: b(5)-98, b(6), b(8)-98, b(8), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(11)++
Matched y ions: y(4), y(5), y(7)++, y(10)++, y(10)-98++, y(11)-98++

Peptide No.771

RQGSFSEDVISHK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RQGSFSEDVISHK**
Found in **MACF1_MOUSE** in **SwissProt**, Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=2

Match to Query 2700: 1568.695611 from(523.905813,3+) index(3975)
Title: Elution from: 24.656 to 24.656 scan no 1845 cid35.00 polarity:+:m1s



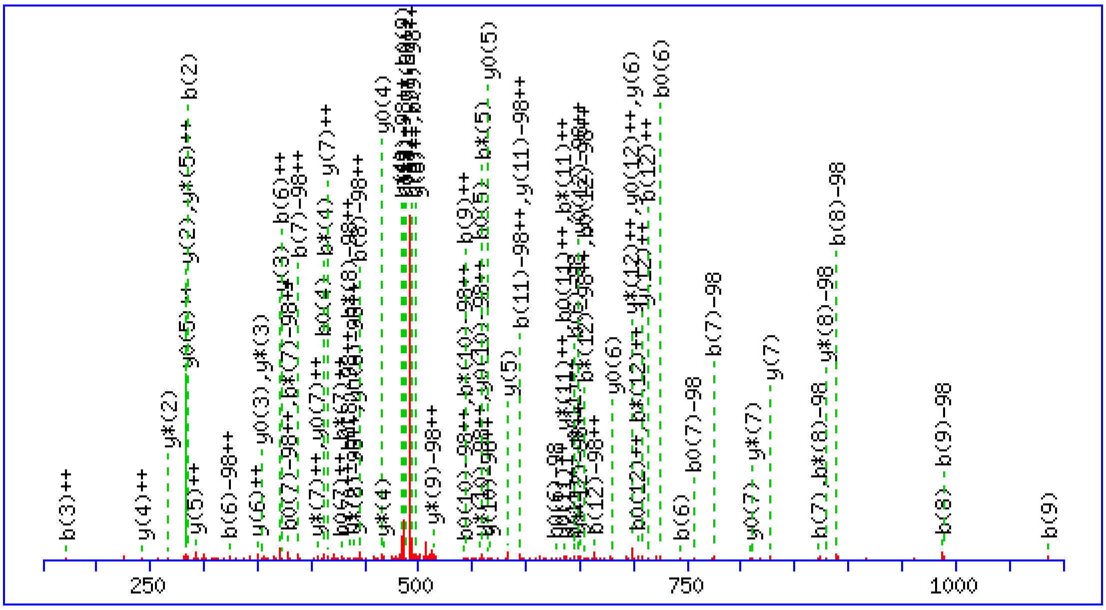
Monoisotopic mass of neutral peptide Mr(calc): 1568.6984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 8.1e-005
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(6)++, b(6)-98++, b(6), b(6)-98, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)-98, b(8), b(8)++, b(8)-98++, b(9)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++

Peptide No.772

RQGSFSEDVISHK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **RQGSFSEDVISHK**
Found in **MACF1_MOUSE** in **SwissProt**, Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=2

Match to Query 3250: 1568.698194 from(523.906674,3+) index(763)
Title: Elution from: 32.925 to 32.925 scan no 2146 cid35.00 polarity:+



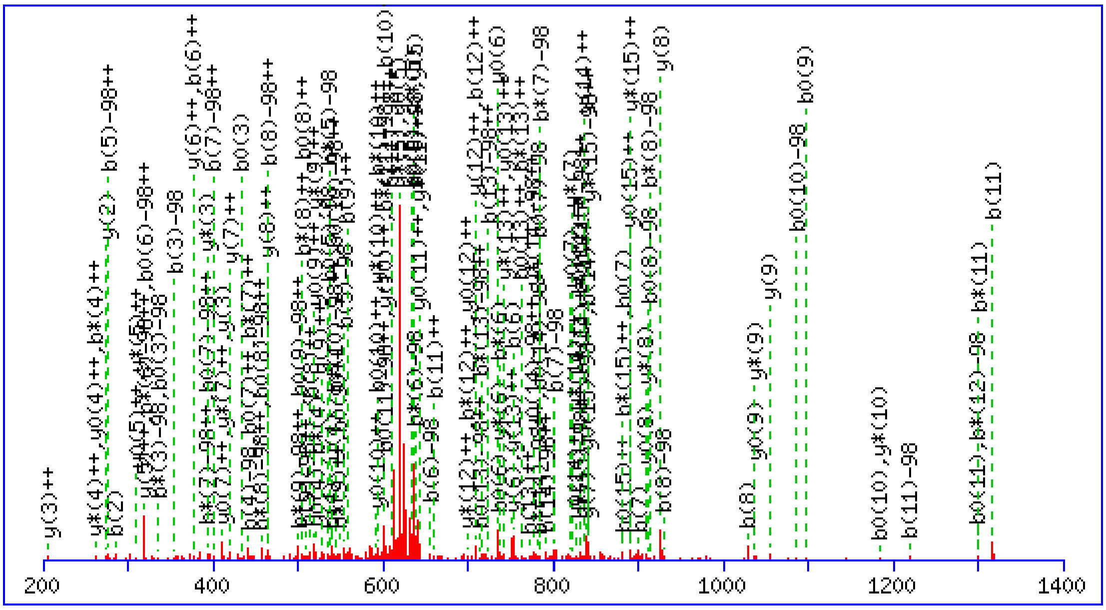
Monoisotopic mass of neutral peptide Mr(calc): 1568.6984
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00047
Matched b ions: b(2), b(3)++, b(6)-98, b(6)-98++, b(6)++, b(6), b(7)-98, b(7)-98++, b(7), b(7)++, b(8)-98, b(8), b(8)-98++, b(8)++, b(9), b(9)-98, b(9)-98++, b(9)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++

Peptide No.773

RQSSLTFQSSDPEHVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RQSSLTFQSSDPEHVR**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4947: 1952.875239 from(651.965689,3+) index(4407)
Title: Elution from: 33.759 to 33.759 scan no 2349 cid35.00 polarity:+:m1s



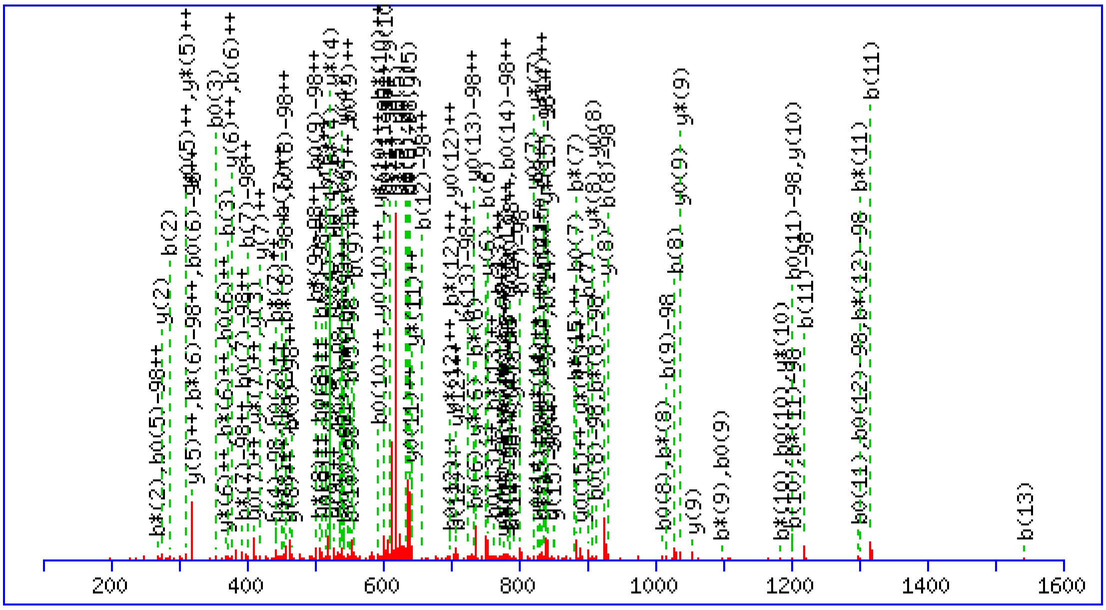
Monoisotopic mass of neutral peptide Mr(calc): 1952.8742
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 5.9e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98, b(5)-98++, b(6), b(6)++, b(6)-98, b(7), b(7)-98, b(7)-98++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(3)++, y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)++, y(13)++, y(14)++

Peptide No.774

RQSSLTFQSSDPEHVR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RQSSLTFQSSDPEHVR**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4293: 1952.874747 from(651.965525,3+) index(3770)
Title: Elution from: 33.762 to 33.762 scan no 2246 cid35.00 polarity:+:m1s



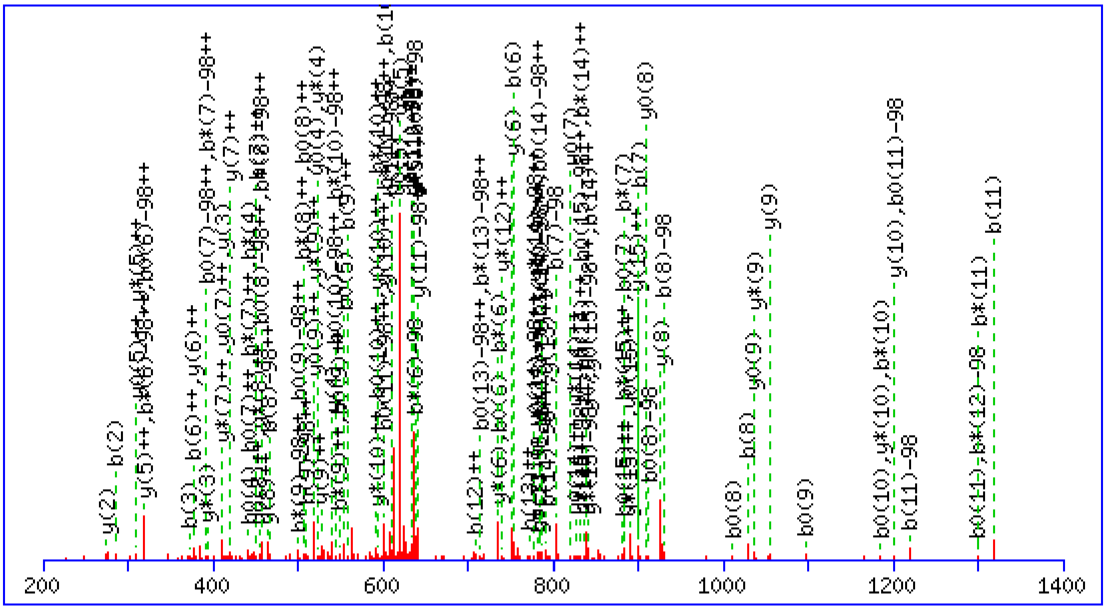
Monoisotopic mass of neutral peptide Mr(calc): 1952.8742
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 **Expect:** 2.9e-005
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)++, b(7), b(7)-98, b(7)-98++, b(7)++, b(8), b(8)-98, b(8)-98++, b(8)++, b(9)-98, b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)-98, b(11), b(11)-98++, b(12)-98++, b(12)++, b(13), b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)-98++

Peptide No.775

RQSSLTFQSSDPEHVR
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **RQSSLTFQSSDPEHVR**
Found in **COBL1_MOUSE** in **SwissProt**, Cordon-bleu protein-like 1 OS=Mus musculus GN=Cobll1 PE=1 SV=2

Match to Query 4661: 1952.872044 from(651.964624,3+) index(1066)
Title: Elution from: 25.596 to 25.596 scan no 1999 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1952.8742
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00084
Matched b ions: b(2), b(3), b(6)++, b(6), b(7), b(7)-98, b(7)++, b(8), b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(10)++, b(11)-98, b(11), b(11)-98++, b(12)++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)++, y(10), y(11)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++

Peptide No.776

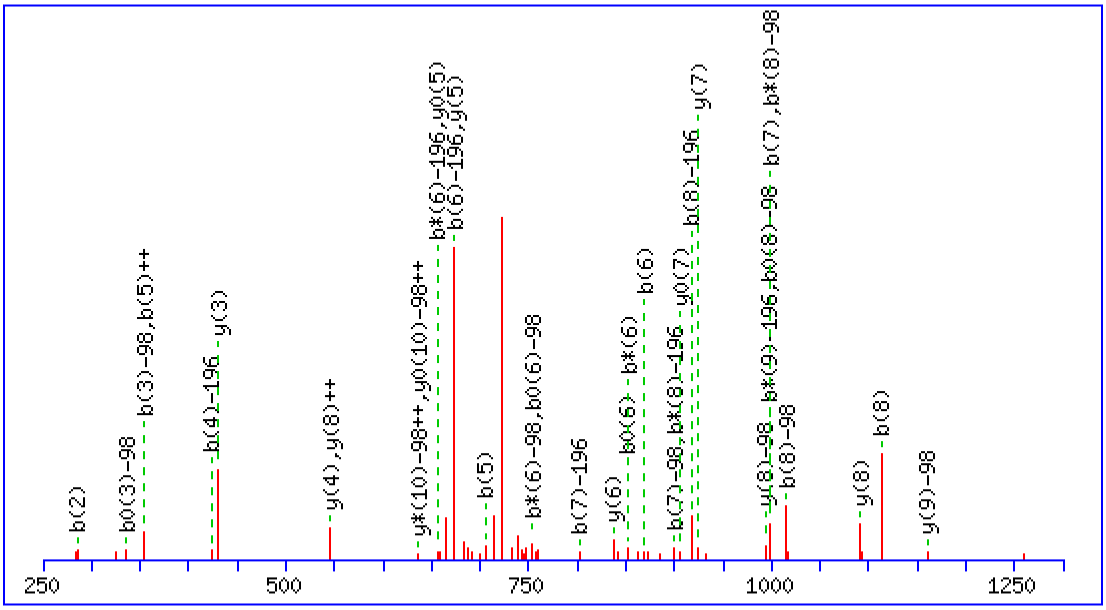
RQSSSYEDPWK

Confirmed sites: @S:3,@S:4

Ambiguous sites:

MS/MS Fragmentation of **RQSSSYEDPWK**
Found in **REPS1_MOUSE** in **SwissProt**, RalBP1-associated Eps domain-containing protein 1 OS=Mus musculus GN=Reps1 PE=1 SV=2

Match to Query 2610: 1541.557582 from(771.786067,2+) index(1713)
Title: Elution from: 33.292 to 33.292 scan no 2991 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1541.5589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00015
Matched b ions: b(2), b(3)-98, b(4)-196, b(5)++, b(5), b(6)-196, b(6), b(7), b(7)-196, b(7)-98, b(8)-196, b(8)-98, b(8)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(8)-98, y(9)-98

Peptide No.777

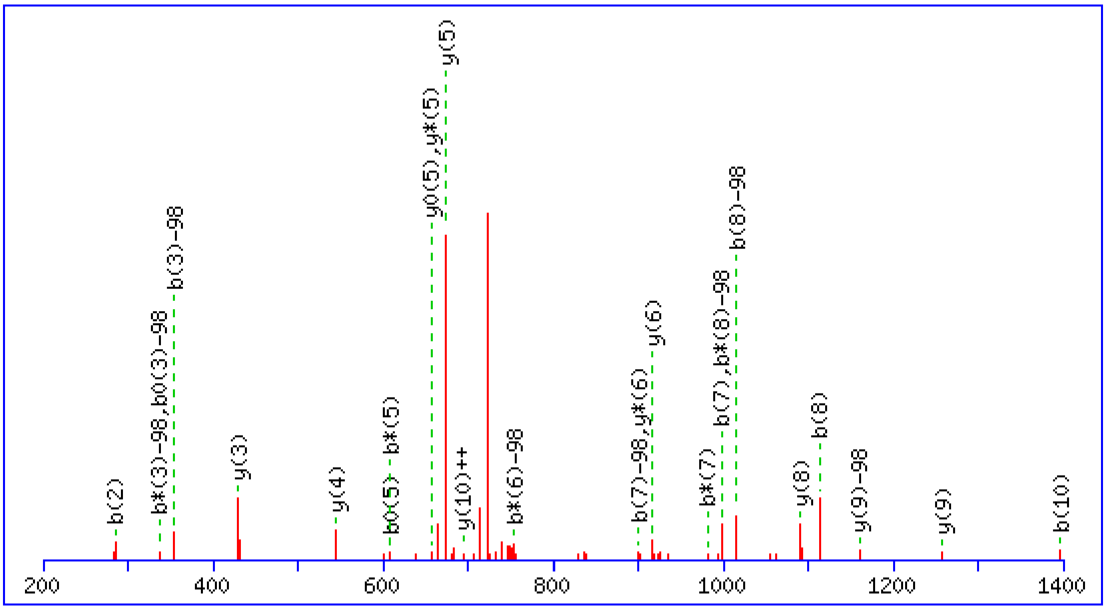
RQSSSYEDPWK

Confirmed sites: @S:3,@Y:6

Ambiguous sites:

MS/MS Fragmentation of **RQSSSYEDPWK**
Found in **REPS1_MOUSE** in **SwissProt**, RalBP1-associated Eps domain-containing protein 1 OS=Mus musculus GN=Reps1 PE=1 SV=2

Match to Query 2722: 1541.560288 from(771.787420,2+) index(4557)
Title: Elution from: 33.329 to 33.329 scan no 2940 cid35.00 polarity:+:m1s



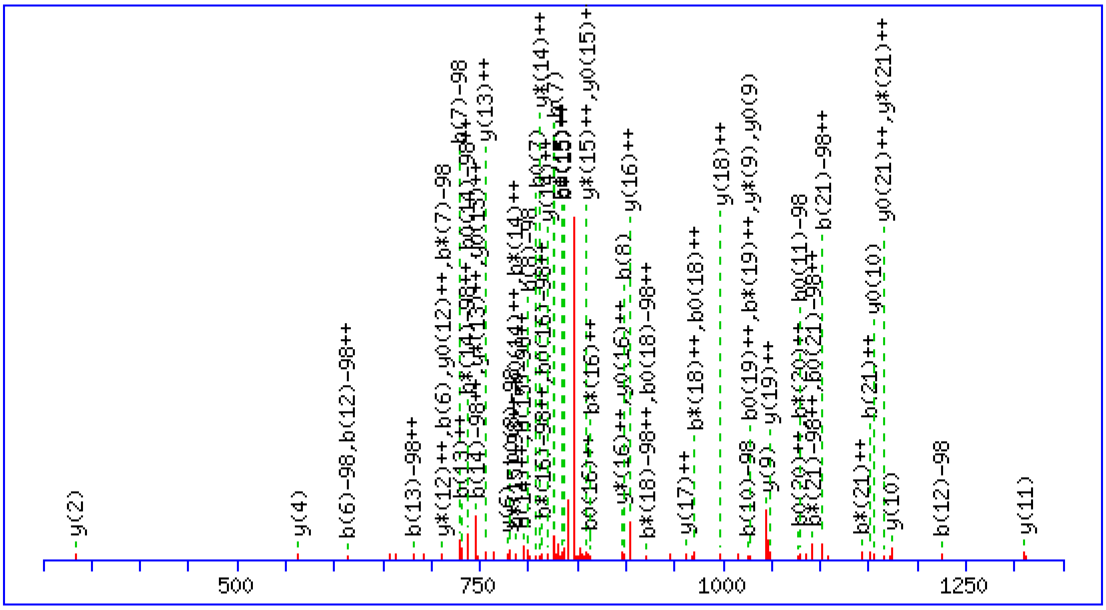
Monoisotopic mass of neutral peptide Mr(calc): 1541.5589
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y6 : Phospho (Y)
Ions Score: 35 **Expect:** 0.00056
Matched b ions: b(2), b(3)-98, b(7)-98, b(7), b(8)-98, b(8), b(10)
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(9)-98, y(10)++

Peptide No.778

RQSSTADAPEAQHEPGITITEWK
Confirmed sites:
Ambiguous sites: @S:3orS:4

MS/MS Fragmentation of **RQSSTADAPEAQHEPGITITEWK**
Found in **KPBB_MOUSE** in **SwissProt**, Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1

Match to Query 6589: 2631.193431 from(878.071753,3+) index(5926)
Title: Elution from: 37.260 to 37.260 scan no 3605 cid35.00 polarity:+:m1s



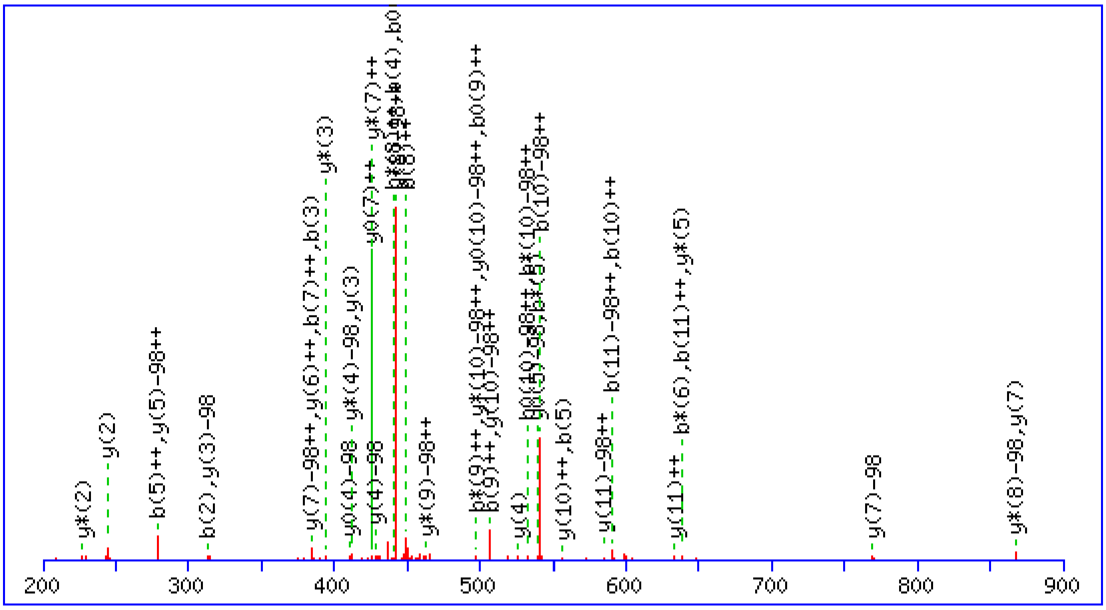
Monoisotopic mass of neutral peptide Mr(calc): 2631.1966
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.017
Matched b ions: b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(10)-98, b(12)-98++, b(12)-98, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(21)++, b(21)-98++
Matched y ions: y(2), y(4), y(6), y(9), y(10), y(11), y(13)++, y(14)++, y(16)++, y(17)++, y(18)++, y(19)++

Peptide No.779

RRAGDVLEDSPK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **RRAGDVLEDSPK**
Found in **HDGF_MOUSE** in **SwissProt**, Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2

Match to Query 2155: 1421.665767 from(474.895865,3+) index(243)
Title: Elution from: 19.223 to 19.223 scan no 1114 cid35.00 polarity:+



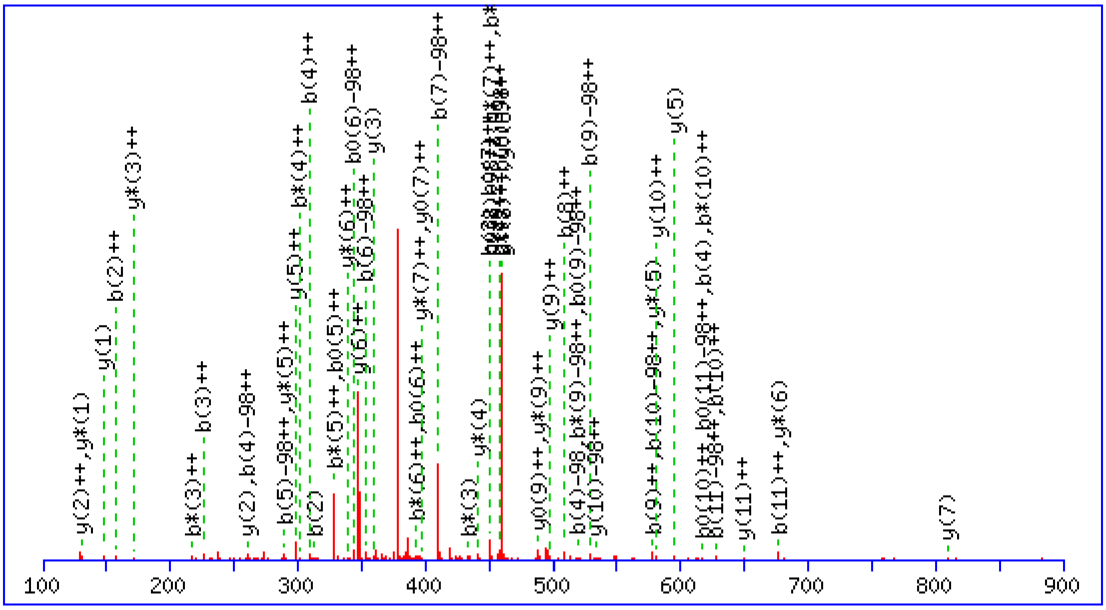
Monoisotopic mass of neutral peptide Mr(calc): 1421.6664
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 6.6e-005
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(7)++, b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++
Matched y ions: y(2), y(3)-98, y(3), y(4), y(4)-98, y(5)-98++, y(6)++, y(7)-98++, y(7)-98, y(7), y(8)-98++, y(10)-98++, y(10)++, y(11)++, y(11)-98++

Peptide No.780

RRHSGQDVHVVLK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RRHSGQDVHVVLK**
Found in **NSF1C_MOUSE** in **SwissProt**, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 3870: 1609.820708 from(403.462453,4+) index(3579)
Title: Elution from: 24.448 to 24.448 scan no 1243 cid35.00 polarity:+:m1s



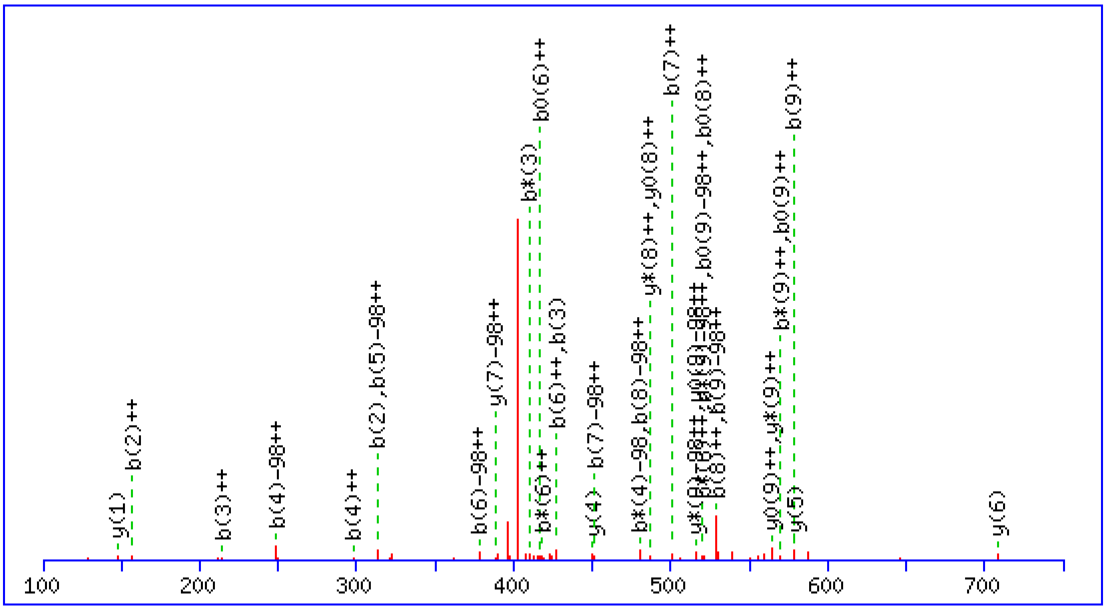
Monoisotopic mass of neutral peptide Mr(calc): 1609.8202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 **Expect:** 2.2e-005
Matched b ions: b(1), b(2)++, b(2), b(3)++, b(3), b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98++, b(6)-98++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)++, b(11)-98++
Matched y ions: y(1), y(2)++, y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(7), y(9)++, y(10)++, y(10)-98++, y(11)++

Peptide No.781

RRNSEEFGVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RRNSEEFGVK**
Found in **ZO3_MOUSE** in **SwissProt**, Tight junction protein ZO-3 OS=Mus musculus GN=Tjp3 PE=1 SV=1

Match to Query 1968: 1300.592547 from(434.538125,3+) index(136)
Title: Elution from: 17.701 to 17.701 scan no 940 cid35.00 polarity:+



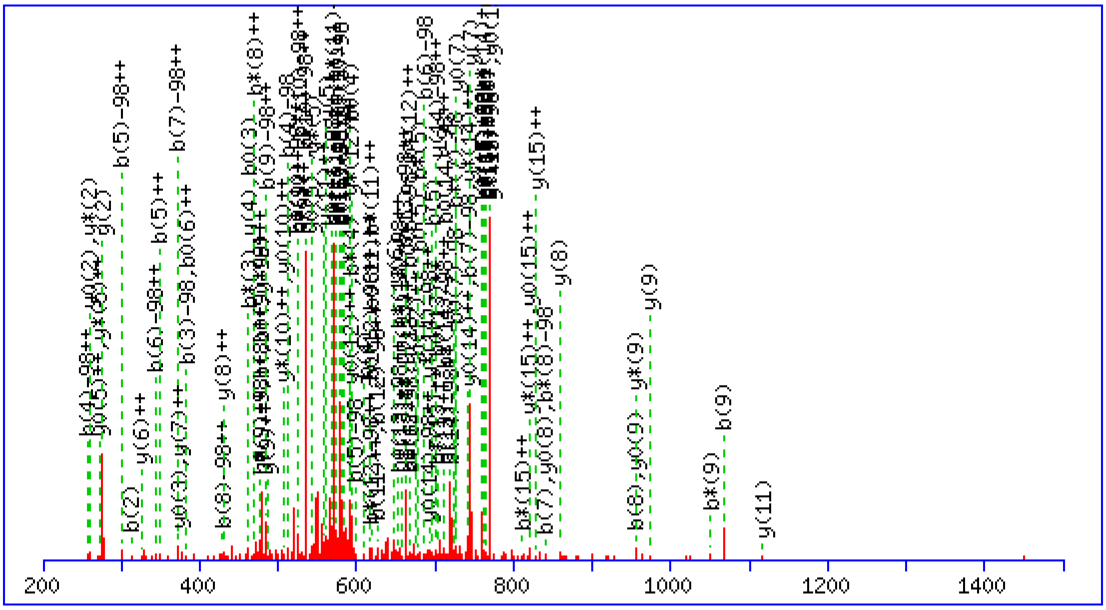
Monoisotopic mass of neutral peptide Mr(calc): 1300.5925
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 6.2e-005
Matched b ions: b(1), b(2)++, b(2), b(3), b(3)++, b(4)-98++, b(4)++, b(5)-98++, b(6)++, b(6)-98++, b(7)++, b(7)-98++, b(8)++, b(8)-98++, b(9)-98++, b(9)++
Matched y ions: y(1), y(4), y(5), y(6), y(7)-98++

Peptide No.782

RRSESSGNLPSVADTR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RRSESSGNLPSVADTR**
Found in **AKAP1_MOUSE** in **SwissProt**, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=4

Match to Query 4561: 1810.832310 from(604.618046,3+) index(609)
Title: Elution from: 29.524 to 29.524 scan no 1835 cid35.00 polarity:+



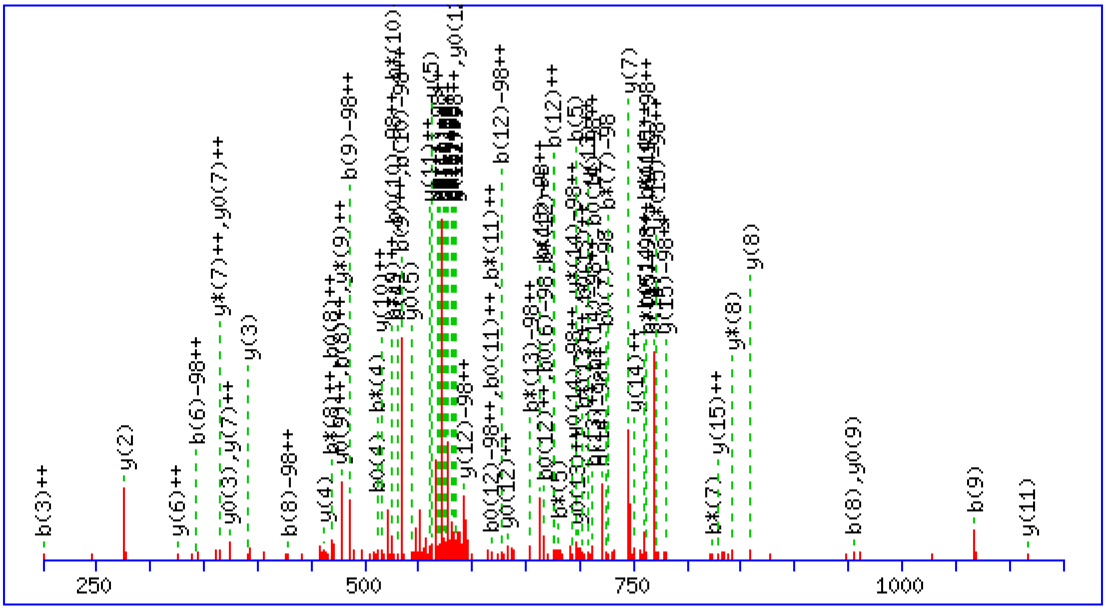
Monoisotopic mass of neutral peptide Mr(calc): 1810.8323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 0.00014
Matched b ions: b(2), b(3)-98, b(4)-98++, b(4)-98, b(4), b(5)-98++, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)-98, b(7)-98++, b(7), b(8), b(8)++, b(8)-98++, b(9)++, b(9), b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(11), y(11)++, y(13)++, y(14)-98++, y(15)++

Peptide No.783

RRSESSGNLPSVADTR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **RRSESSGNLPSVADTR**
Found in **AKAP1_MOUSE** in **SwissProt**, A-kinase anchor protein 1, mitochondrial OS=Mus musculus GN=Akap1 PE=1 SV=4

Match to Query 3957: 1810.832979 from(604.618269,3+) index(479)
Title: Elution from: 29.379 to 29.379 scan no 1735 cid35.00 polarity:+



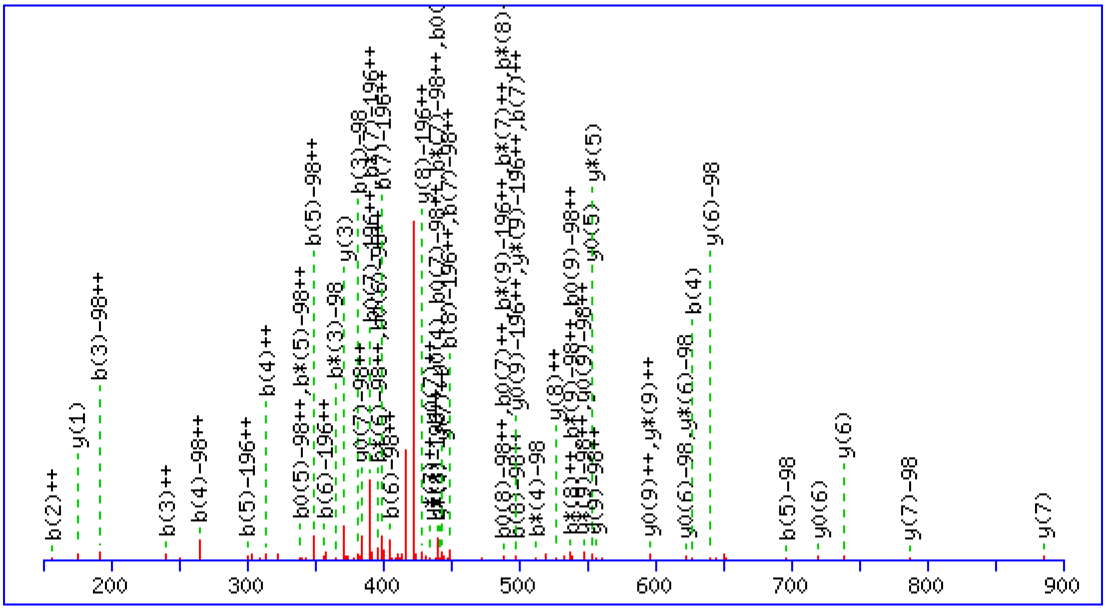
Monoisotopic mass of neutral peptide Mr(calc): 1810.8323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.02
Matched b ions: b(3)++, b(4), b(5), b(6)-98++, b(8)++, b(8), b(8)-98++, b(9), b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(7)++, y(7), y(8), y(10)++, y(11), y(11)++, y(12)-98++, y(13)++, y(14)++, y(15)++, y(15)-98++

Peptide No.784

RRSFSISPVR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **RRSFSISPVR**
Found in **SON_MOUSE** in **SwissProt**, Protein SON OS=Mus musculus GN=Son PE=1 SV=2

Match to Query 2000: 1363.616124 from(455.545984,3+) index(1141)
Title: Elution from: 27.061 to 27.061 scan no 2172 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1363.6163

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 28 **Expect:** 0.0079

Matched b ions: b(1), b(2)++, b(3)-98++, b(3)++, b(3)-98, b(4)-98++, b(4)++, b(4), b(5)-98++, b(5)-98, b(5)-196++, b(6)-196++, b(6)-98++, b(7)-196++, b(7)++, b(7)-98++, b(8)-98++, b(8)-196++, b(9)-98++, b(9)++, b(9)-196++

Matched y ions: y(1), y(3), y(6), y(6)-98, y(7)-98, y(7), y(7)++, y(8)-196++, y(8)++, y(9)-98++

Peptide No.785

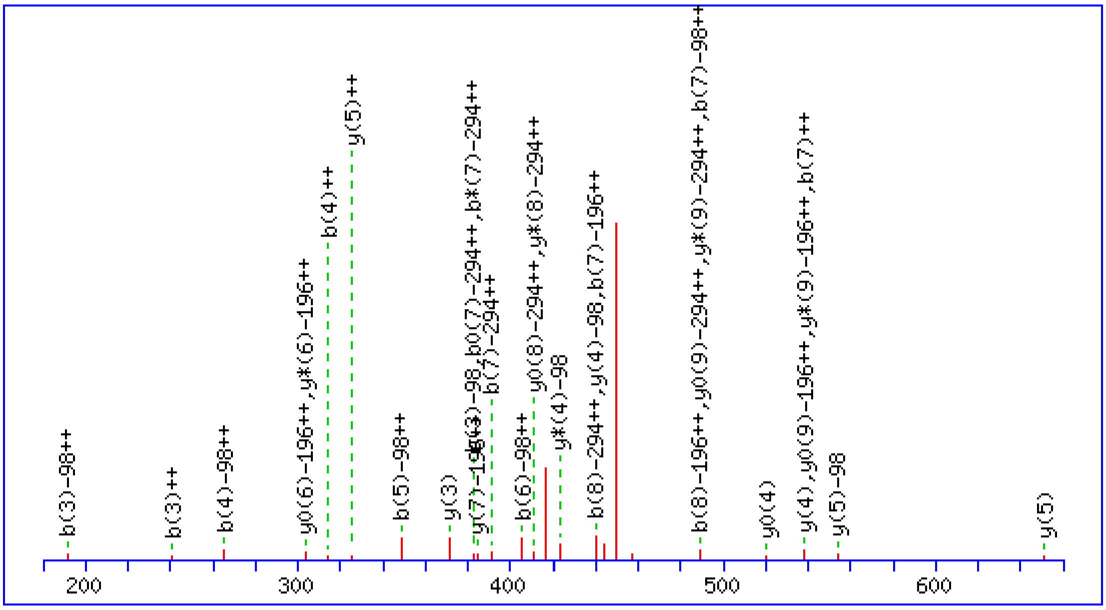
RRSFSISPVR

Confirmed sites: @S:3,@S:5,@S:7

Ambiguous sites:

MS/MS Fragmentation of **RRSFSISPVR**
Found in **SON_MOUSE** in **SwissProt**, Protein SON OS=Mus musculus GN=Son PE=1 SV=2

Match to Query 2358: 1443.581298 from(482.201042,3+) index(1286)
Title: Elution from: 30.060 to 30.060 scan no 2495 cid35.00 polarity:+



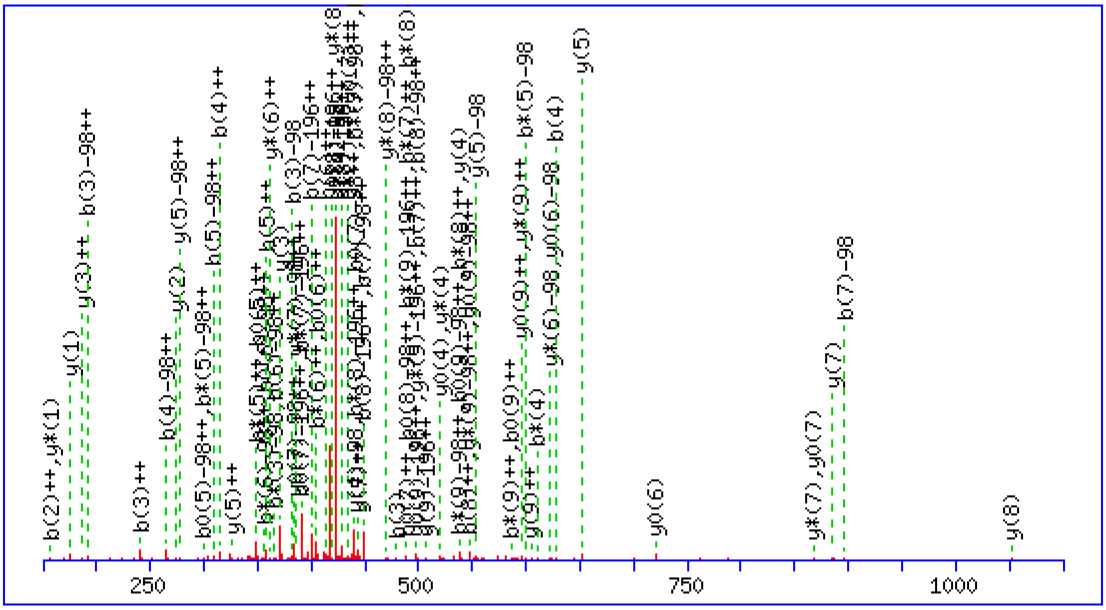
Monoisotopic mass of neutral peptide Mr(calc): 1443.5826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.035
Matched b ions: b(3)-98++, b(3)++, b(3)-98, b(4)-98++, b(4)++, b(5)-98++, b(6)-98++, b(7)++, b(7)-294++, b(7)-196++, b(7)-98++, b(8)-294++, b(8)-196++, b(9)-196++, b(9)-294++
Matched y ions: y(3), y(4), y(4)-98, y(5), y(5)-98, y(5)++, y(7)-196++

Peptide No.786

RRSFSISPVR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RRSFSISPVR**
Found in **SON_MOUSE** in **SwissProt**, Protein SON OS=Mus musculus GN=Son PE=1 SV=2

Match to Query 2668: 1363.616823 from(455.546217,3+) index(1033)
Title: Elution from: 35.897 to 35.897 scan no 2508 cid35.00 polarity:+



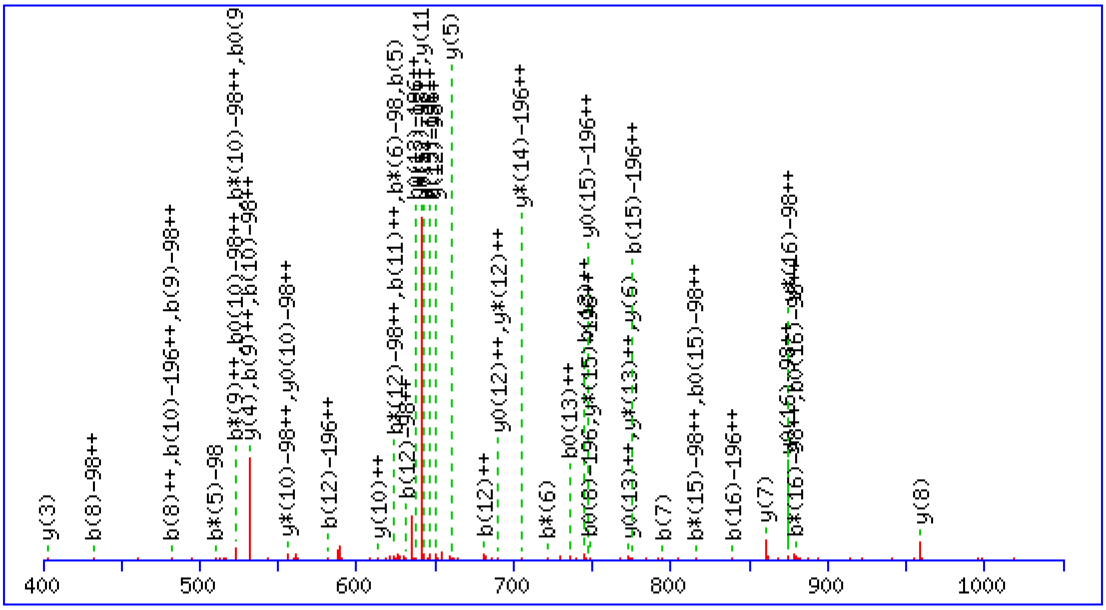
Monoisotopic mass of neutral peptide Mr(calc): 1363.6163
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.01
Matched b ions: b(1), b(2)++, b(3)++, b(3)-98++, b(3)-98, b(3), b(4)-98++, b(4)++, b(4), b(5)-98++, b(5)++, b(6)-98++, b(6)++, b(7)++, b(7)-98, b(7)-98++, b(7)-196++, b(8)++, b(8)-98++, b(8)-196++, b(9)-98++, b(9)-196++, b(9)++
Matched y ions: y(1), y(2), y(3)++, y(3), y(4), y(4)-98, y(5), y(5)-98, y(5)-98++, y(5)++, y(7), y(7)++, y(8), y(8)-196++, y(9)++, y(9)-196++

Peptide No.787

RRSGSNGSVVSLEQQQK
Confirmed sites: @S:8
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of **RRSGSNGSVVSLEQQQK**
Found in **KIF7_MOUSE** in **SwissProt**, Kinesin-like protein KIF7 OS=Mus musculus GN=Kif7 PE=1 SV=1

Match to Query 4492: 2018.888379 from(673.970069,3+) index(77)
Title: Elution from: 23.261 to 23.261 scan no 1112 cid35.00 polarity:+



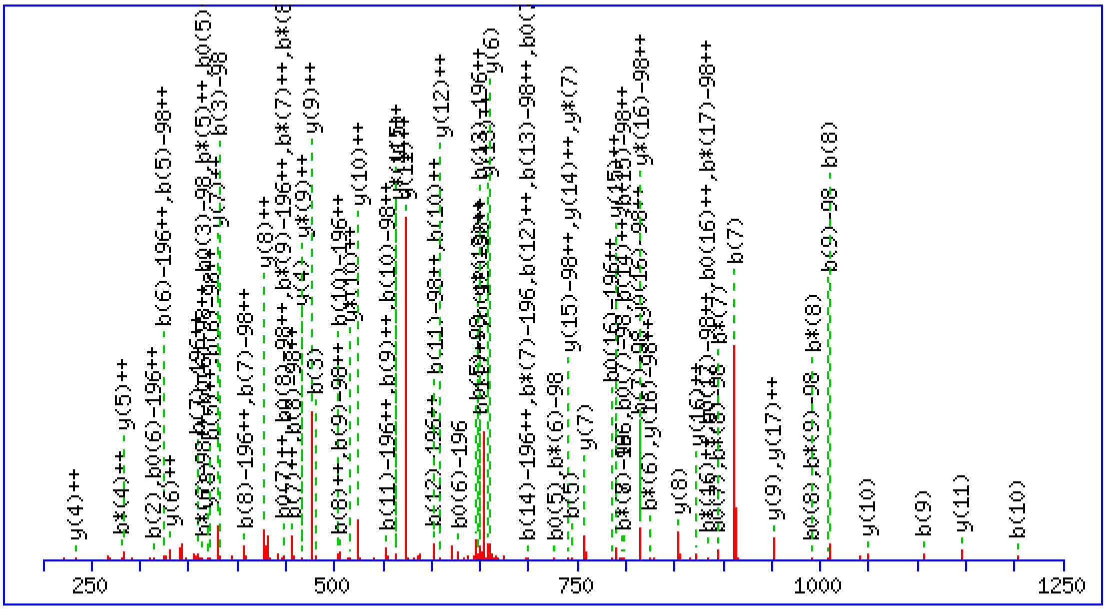
Monoisotopic mass of neutral peptide Mr(calc): 2018.8936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.015
Matched b ions: b(5), b(7), b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)-196++, b(11)++, b(12)++, b(12)-196++, b(12)-98++, b(13)++, b(13)-196++, b(15)-196++, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(12)-98++

Peptide No.788

RRSPSPAPPPPPPPPPPR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **RRSPSPAPPPPPPPPPPR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 4353: 2055.979695 from(686.333841,3+) index(3503)
Title: Elution from: 22.895 to 22.895 scan no 1506 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2055.9809
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 81 **Expect:** 6.1e-008
Matched b ions: b(2), b(3)-98, b(3), b(5)-98, b(5)-98++, b(5)++, b(5), b(6)-196++, b(6)-98++, b(7)-98, b(7), b(7)-98++, b(7)++, b(7)-196++, b(8), b(8)-196++, b(8)-98++, b(8)++, b(9), b(9)++, b(9)-98, b(9)-98++, b(10)++, b(10), b(10)-98++, b(10)-196++, b(11)-98++, b(11)-196++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(14)++, b(14)-196++, b(15)-98++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++

Peptide No.789

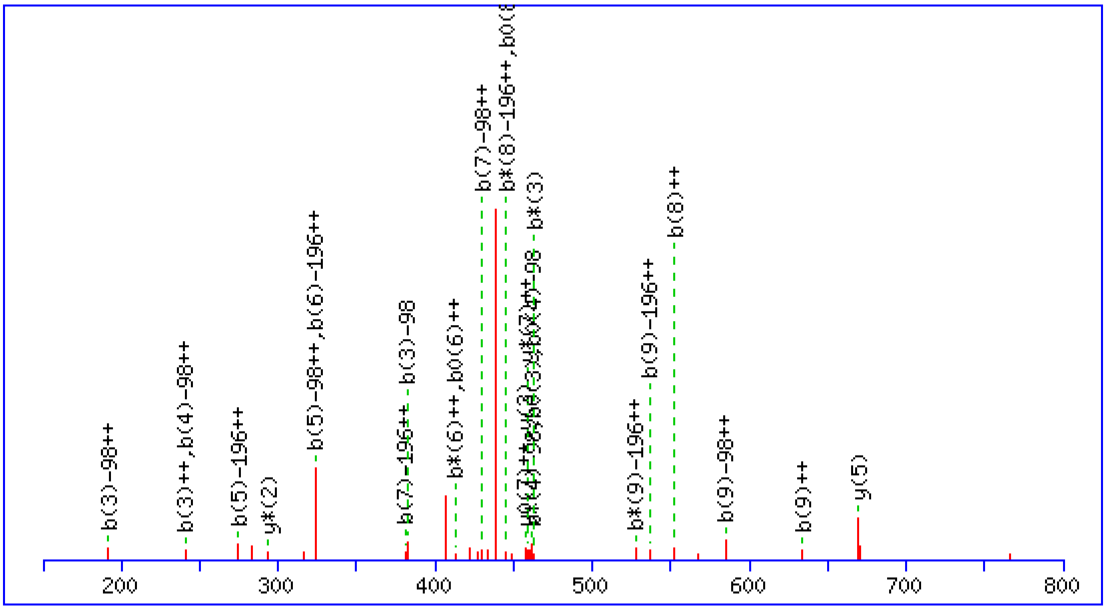
RRSPSPDFYK

Confirmed sites: @S:3,@S:5

Ambiguous sites:

MS/MS Fragmentation of **RRSPSPDFYK**
Found in **U2AFM_MOUSE** in **SwissProt**, U2 small nuclear ribonucleoprotein auxiliary factor 35 kDa subunit-related protein 2 OS=Mus musculus GN=Zrsr2 PE=2 SV=1

Match to Query 2394: 1411.567722 from(471.529850,3+) index(635)
Title: Elution from: 21.937 to 21.937 scan no 1500 cid35.00 polarity:+



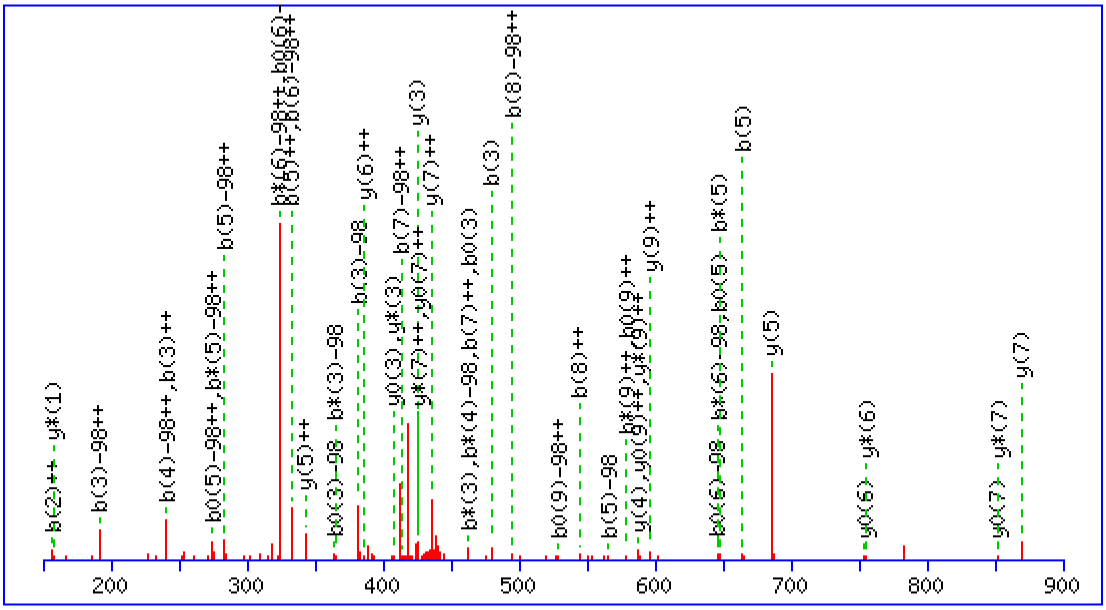
Monoisotopic mass of neutral peptide Mr(calc): 1411.5686
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(3)-98, b(3)-98++, b(3)++, b(4)-98++, b(5)-196++, b(5)-98++, b(6)-196++, b(7)-196++, b(7)-98++, b(8)++, b(9)-98++, b(9)++, b(9)-196++
Matched y ions: y(3), y(5)

Peptide No.790

RRSPSPYYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RRSPSPYYSR**
Found in **TRA2B_MOUSE** in **SwissProt**, Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1

Match to Query 2330: 1347.608169 from(450.209999,3+) index(133)
Title: Elution from: 17.117 to 17.117 scan no 899 cid35.00 polarity:+



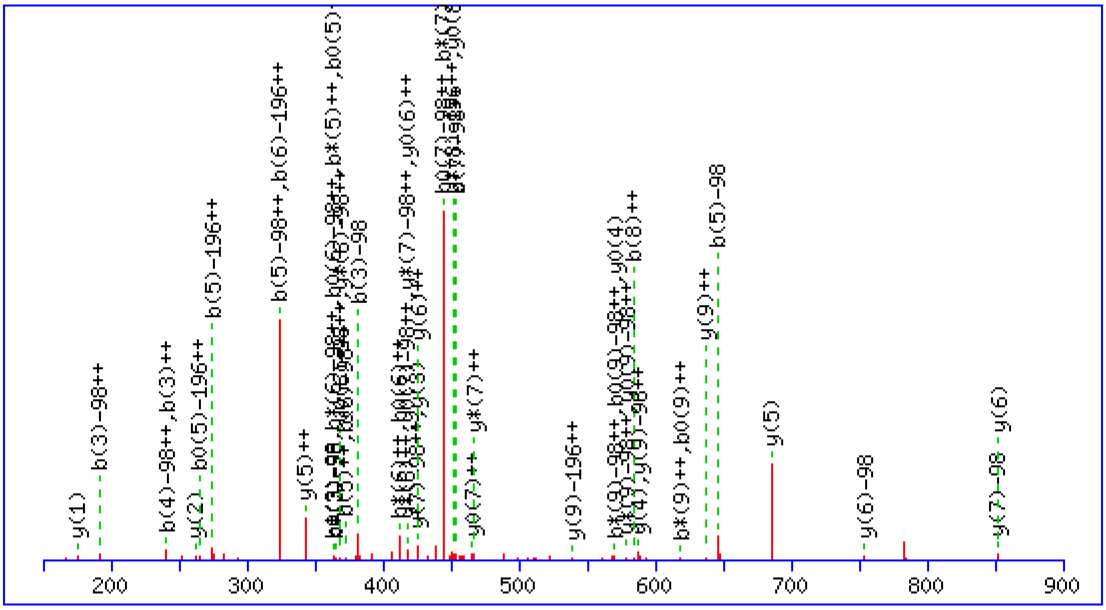
Monoisotopic mass of neutral peptide Mr(calc): 1347.6085
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0017
Matched b ions: b(1), b(2)++, b(3)++, b(3)-98++, b(3), b(3)-98, b(4)-98++, b(5)++, b(5), b(5)-98++, b(5)-98, b(6)-98++, b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++
Matched y ions: y(3), y(4), y(5), y(5)++, y(6)++, y(7), y(7)++, y(9)++

Peptide No.791

RRSPSPYYSR
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **RRSPSPYYSR**
Found in **TRA2A_MOUSE** in **SwissProt**, Transformer-2 protein homolog alpha OS=Mus musculus GN=Tra2a PE=1 SV=1

Match to Query 2184: 1427.573640 from(476.865156,3+) index(86)
Title: Elution from: 17.604 to 17.604 scan no 914 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1427.5748

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 37 **Expect:** 0.00067

Matched b ions: b(3)++, b(3)-98++, b(3)-98, b(4)-98++, b(5)-98++, b(5)-98, b(5)-196++, b(5)++, b(6)-196++, b(6)-98++, b(7)-98++, b(8)++, b(9)-98++

Matched y ions: y(1), y(2), y(3), y(4), y(5), y(5)++, y(6)-98, y(6), y(6)++, y(7)-98, y(7)-98++, y(9)-98++, y(9)-196++, y(9)++

Peptide No.792

RRSPSPYYSR

Confirmed sites: @S:3,@Y:7

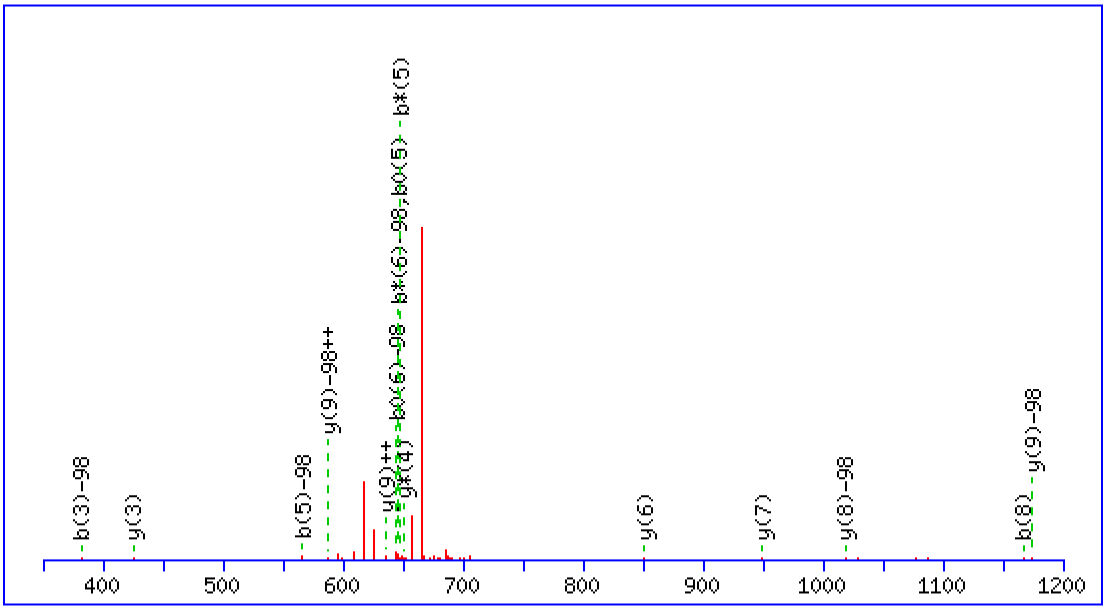
Ambiguous sites:

MS/MS Fragmentation of **RRSPSPYYSR**

Found in **TRA2B_MOUSE** in **SwissProt**, Transformer-2 protein homolog beta OS=Mus musculus GN=Tra2b PE=1 SV=1

Match to Query 2484: 1427.573768 from(714.794160,2+) index(143)

Title: Elution from: 17.773 to 17.773 scan no 949 cid35.00 polarity:+



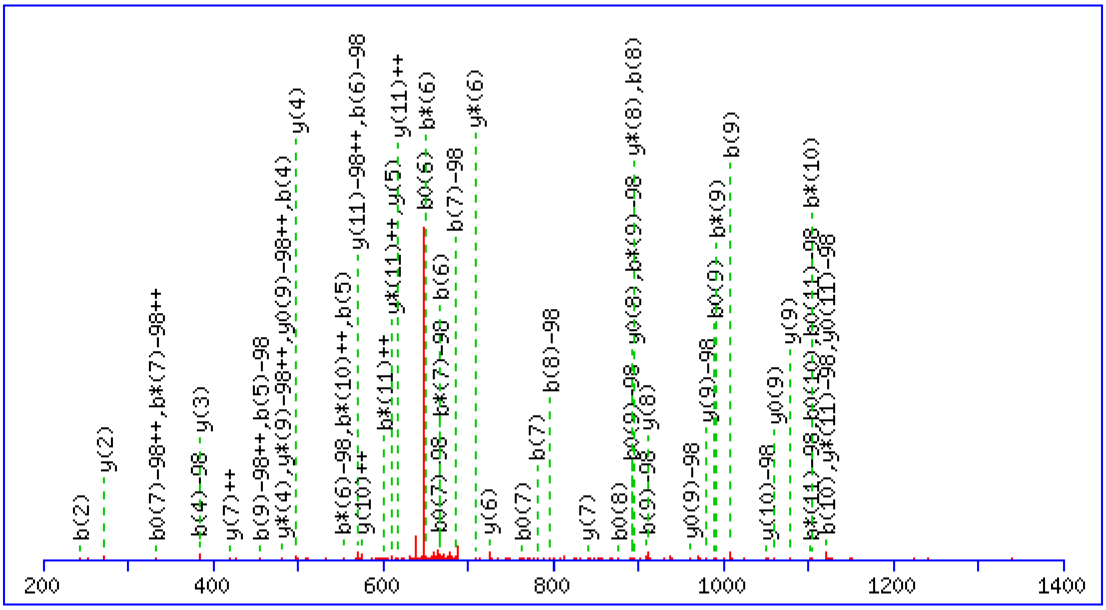
Monoisotopic mass of neutral peptide Mr(calc): 1427.5748
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y7 : Phospho (Y)
Ions Score: 34 **Expect:** 0.0013
Matched b ions: b(3)-98, b(5)-98, b(8)
Matched y ions: y(3), y(6), y(7), y(8)-98, y(9)-98, y(9)-98++, y(9)++

Peptide No.793

RSASADNLILPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RSASADNLILPR**
Found in **CCNY_MOUSE** in **SwissProt**, Cyclin-Y OS=Mus musculus GN=Ccny PE=1 SV=1

Match to Query 2741: 1391.691916 from(696.853234,2+) index(1441)
Title: Elution from: 41.377 to 41.377 scan no 3133 cid35.00 polarity:+



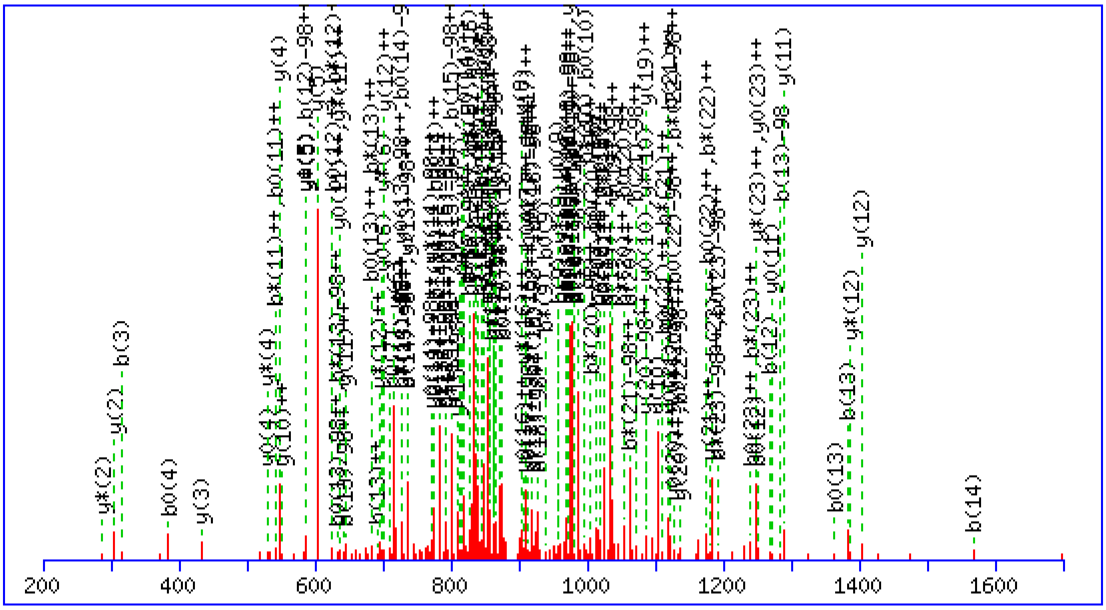
Monoisotopic mass of neutral peptide Mr(calc): 1391.6922
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 5.9e-005
Matched b ions: b(2), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9), b(9)-98, b(9)-98++, b(10), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9)-98, y(9), y(10)++, y(10)-98, y(11)-98++, y(11)++

Peptide No.794

RSASPDDDLGSSNWEAADLGNEER
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **RSASPDDDLGSSNWEAADLGNEER**
Found in **SMAP_MOUSE** in **SwissProt**, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 5420: 2670.080355 from(891.034061,3+) index(5234)
Title: Elution from: 41.706 to 41.706 scan no 4016 cid35.00 polarity:+:m1s



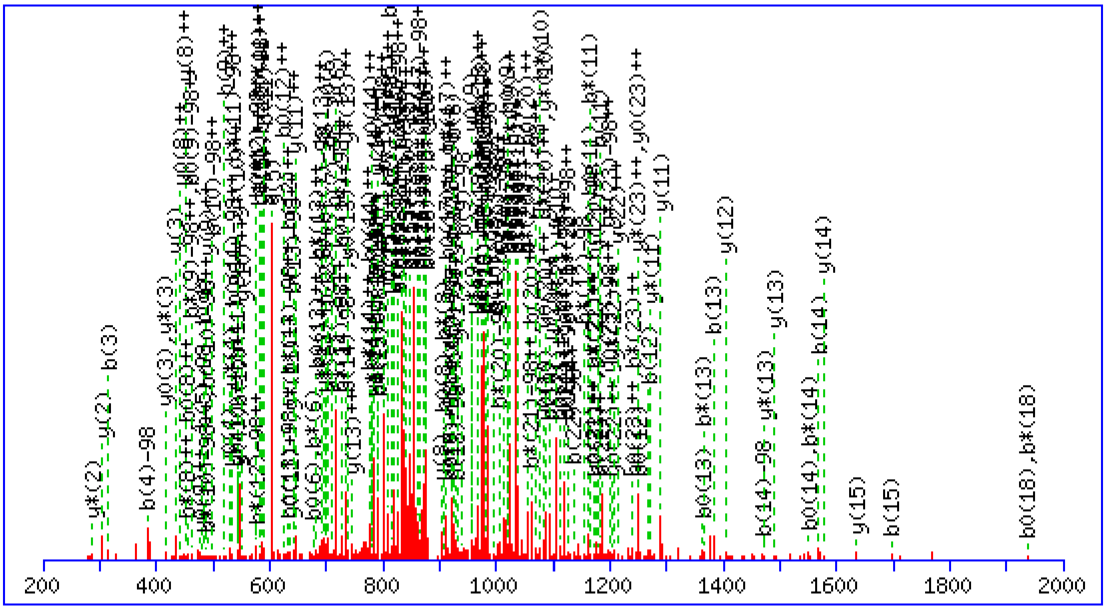
Monoisotopic mass of neutral peptide Mr(calc): 2670.0831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 **Expect:** 1.7e-007
Matched b ions: b(3), b(8), b(9), b(10), b(12)-98++, b(12), b(13), b(13)-98, b(13)-98++, b(13)++, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13)++, y(13)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)++

Peptide No.795

RSASPDDDLGSSNWEAADLGNEER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RSASPDDDLGSSNWEAADLGNEER**
Found in **SMAP_MOUSE** in **SwissProt**, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 6448: 2670.084282 from(891.035370,3+) index(6156)
Title: Elution from: 42.017 to 42.017 scan no 4206 cid35.00 polarity:+:m1s



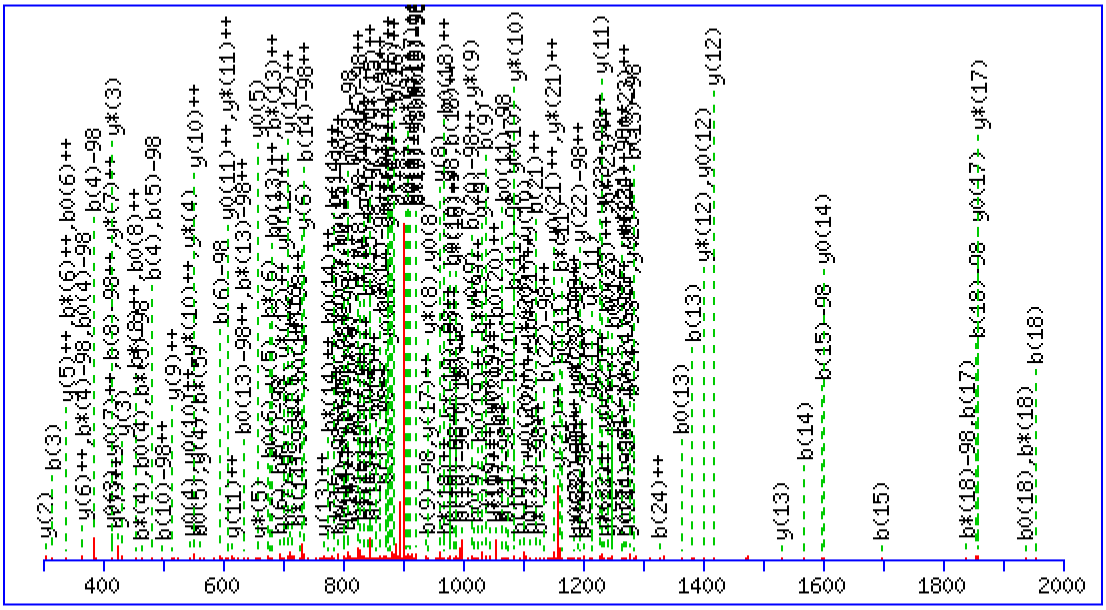
Monoisotopic mass of neutral peptide Mr(calc): 2670.0831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 **Expect:** 2.2e-006
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)++, b(9)-98, b(10)++, b(10), b(10)-98++, b(10)-98, b(11), b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(12)-98, b(12), b(13), b(13)-98++, b(13)++, b(14), b(14)-98++, b(14)++, b(14)-98, b(15), b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14), y(14)++, y(15), y(15)++, y(16)++, y(17)++, y(20)++, y(21)++, y(22)++

Peptide No.796

RSASPDDDLGSSNWEAADLGNEERK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RSASPDDDLGSSNWEAADLGNEERK**
Found in **SMAP_MOUSE** in **SwissProt**, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 6765: 2798.176101 from(933.732643,3+) index(5950)
Title: Elution from: 37.522 to 37.522 scan no 3640 cid35.00 polarity:+:m1s



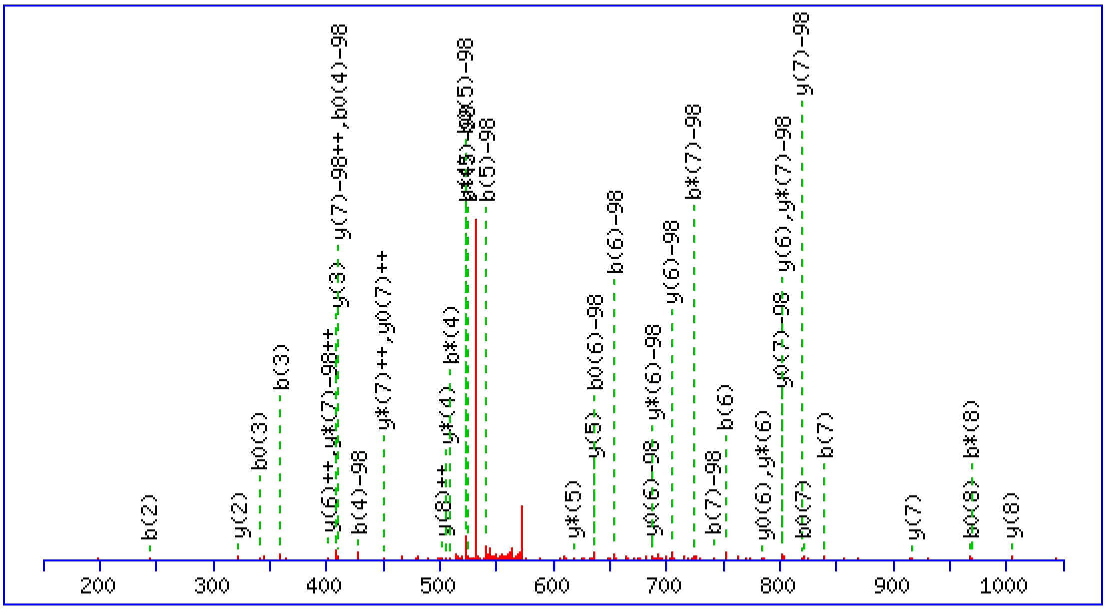
Monoisotopic mass of neutral peptide Mr(calc): 2798.1780
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 1.3e-008
Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(7)-98, b(7), b(8)-98++, b(8)-98, b(9), b(9)-98, b(10)-98, b(10)-98++, b(10), b(11)-98, b(13), b(13)-98, b(14), b(14)-98++, b(14)++, b(15), b(15)-98, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17), b(17)-98++, b(17)++, b(18)-98, b(18), b(18)++, b(19)-98++, b(20)-98++, b(21)-98++, b(21)++, b(22)-98++, b(23)-98++, b(23)++, b(24)-98++, b(24)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7)++, y(7), y(8), y(9), y(9)++, y(10)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)-98++, y(22)++, y(23)++, y(23)-98++, y(24)-98++

Peptide No.797

RSDSLLSFR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RSDSLLSFR**
Found in **BORG5_MOUSE** in **SwissProt**, Cdc42 effector protein 1 OS=Mus musculus GN=Cdc42ep1 PE=1 SV=1

Match to Query 1981: 1159.538610 from(580.776581,2+) index(1971)
Title: Elution from: 45.917 to 45.917 scan no 3785 cid35.00 polarity:+



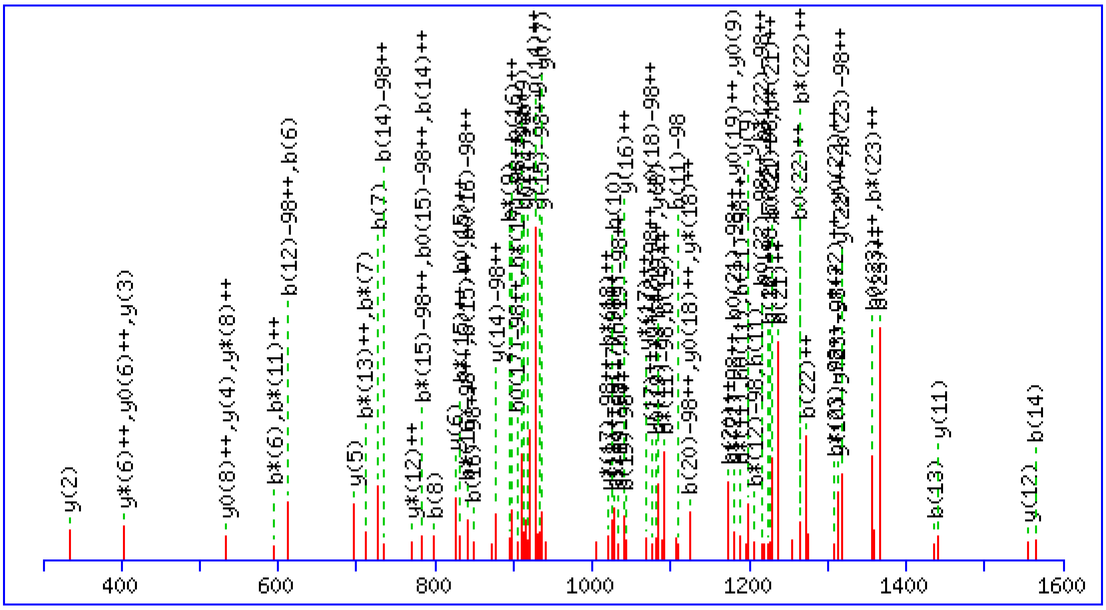
Monoisotopic mass of neutral peptide Mr(calc): 1159.5387
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.00066
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(6), b(6)-98, b(7), b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(6)++, y(7), y(7)-98++, y(7)-98, y(8), y(8)++

Peptide No.798

RSLAALDALNTDDENDEEEYEAWK
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **RSLAALDALNTDDENDEEEYEAWK**
Found in **MFAP1_MOUSE** in **SwissProt**, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 5633: 2876.200749 from(959.740859,3+) index(5697)
Title: Elution from: 51.459 to 51.459 scan no 5101 cid35.00 polarity:+:m1s



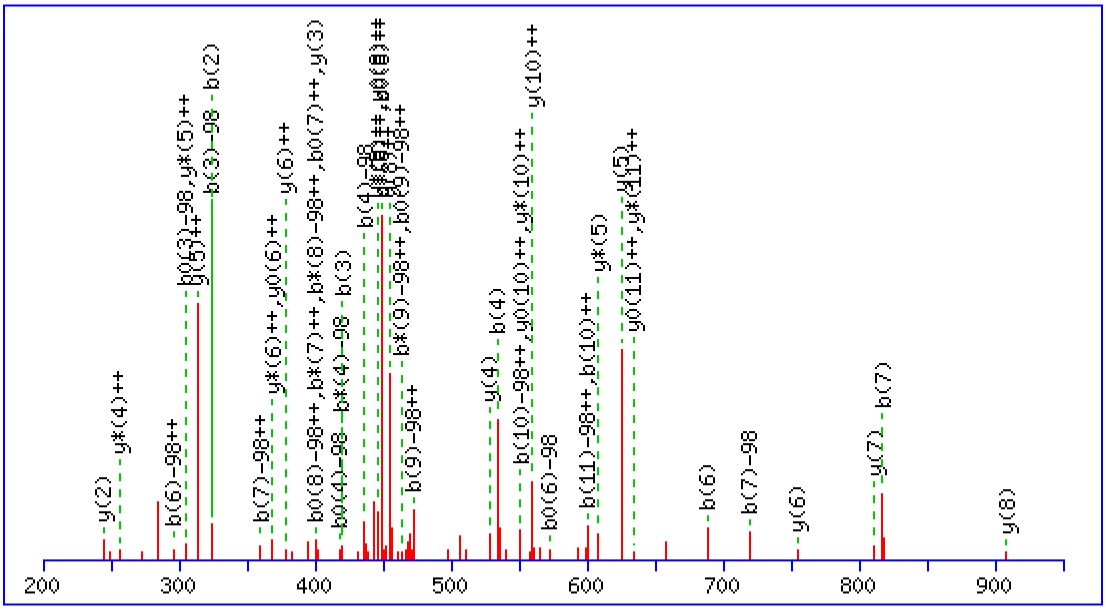
Monoisotopic mass of neutral peptide Mr(calc): 2876.2025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 97 **Expect:** 1.2e-009
Matched b ions: b(6), b(7), b(8), b(9), b(10), b(11), b(11)-98, b(12)-98++, b(12)-98, b(13), b(14), b(14)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)++, b(22)-98++, b(23)++, b(23)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(14)++, y(14)-98++, y(15)-98++, y(16)++, y(17)-98++, y(17)++, y(20)++, y(22)++, y(23)-98++

Peptide No.799

RSPLPGEPQRPK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **RSPLPGEPQRPK**
Found in **DFFA_MOUSE** in **SwissProt**, DNA fragmentation factor subunit alpha OS=Mus musculus GN=Dffa PE=1 SV=2

Match to Query 2689: 1440.723273 from(481.248367,3+) index(366)
Title: Elution from: 19.231 to 19.231 scan no 1172 cid35.00 polarity:+



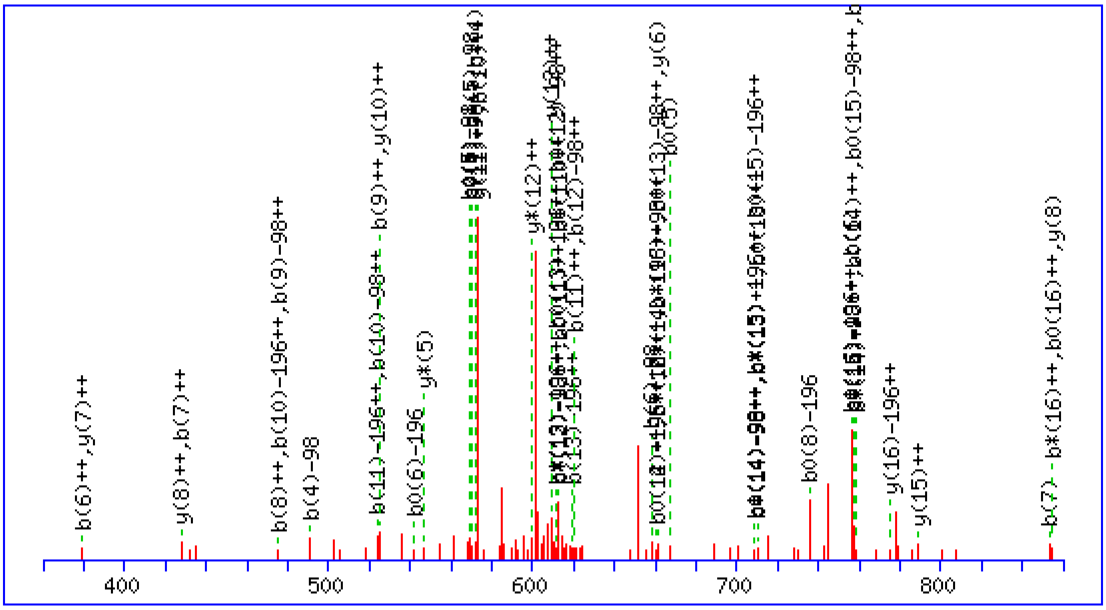
Monoisotopic mass of neutral peptide Mr(calc): 1440.7238
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 9.4e-005
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(6), b(6)-98++, b(7), b(7)-98, b(7)-98++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(10)++

Peptide No.800

RSPSPAPPPPPPPPPPR
Confirmed sites: @S:2,@S:4
Ambiguous sites:

MS/MS Fragmentation of **RSPSPAPPPPPPPPPPR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 3915: 1899.879762 from(634.300530,3+) index(3860)
Title: Elution from: 25.927 to 25.927 scan no 1924 cid35.00 polarity:+:m1s



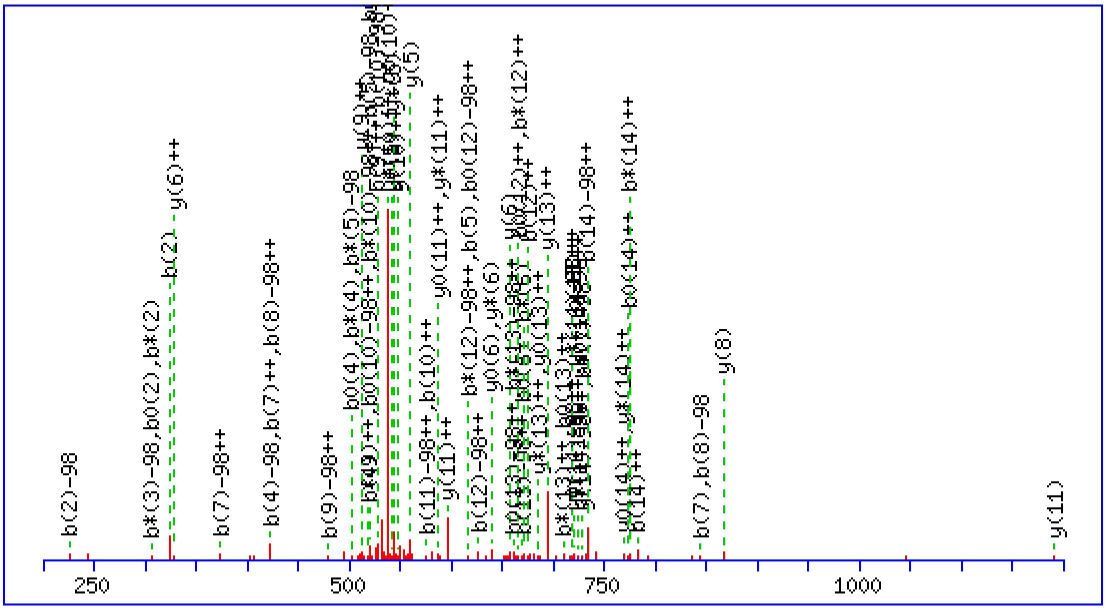
Monoisotopic mass of neutral peptide Mr(calc): 1899.8798
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.042
Matched b ions: b(4)-98, b(6), b(6)++, b(6)-98, b(7)++, b(7), b(8)++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(10)-196++, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(13)-196++
Matched y ions: y(6), y(7)++, y(7), y(8)++, y(8), y(10)++, y(11)++, y(12)++, y(15)++, y(16)-196++

Peptide No.801

RSPVPARPLPPTSQK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **RSPVPARPLPPTSQK**
Found in **LS14A_MOUSE** in **SwissProt**, Protein LSM14 homolog A OS=Mus musculus GN=Lsm14a PE=1 SV=1

Match to Query 3675: 1709.899305 from(570.973711,3+) index(3929)
Title: Elution from: 20.008 to 20.008 scan no 1240 cid35.00 polarity:+:m1s



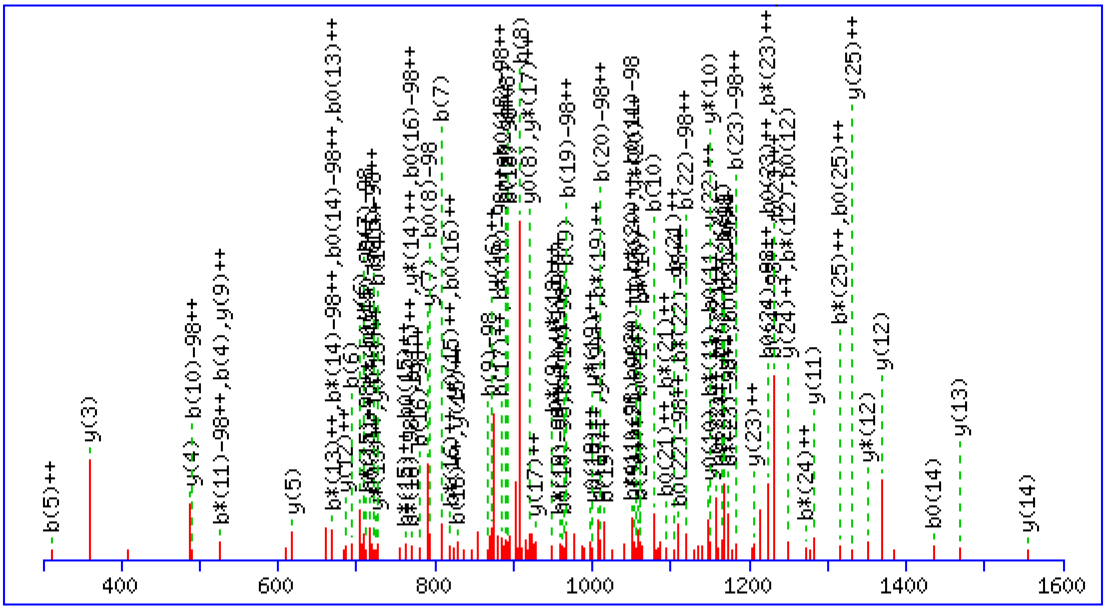
Monoisotopic mass of neutral peptide Mr(calc): 1709.8978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.007
Matched b ions: b(2), b(2)-98, b(4)-98, b(4), b(5)-98, b(5), b(7)++, b(7)-98++, b(7), b(8)-98++, b(8)-98, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(5), y(6)++, y(6), y(8), y(9)++, y(10)++, y(11), y(11)++, y(13)++, y(14)-98++

Peptide No.802

RSSDPALTGLSTSVSDNNFSSEEPSR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **RSSDPALTGLSTSVSDNNFSSEEPSR**
Found in **PARD3_MOUSE** in **SwissProt**, Partitioning defective 3 homolog OS=Mus musculus GN=Pard3 PE=1 SV=2

Match to Query 5765: 2819.220225 from(940.747351,3+) index(5471)
Title: Elution from: 41.939 to 41.939 scan no 4045 cid35.00 polarity:+:m1s



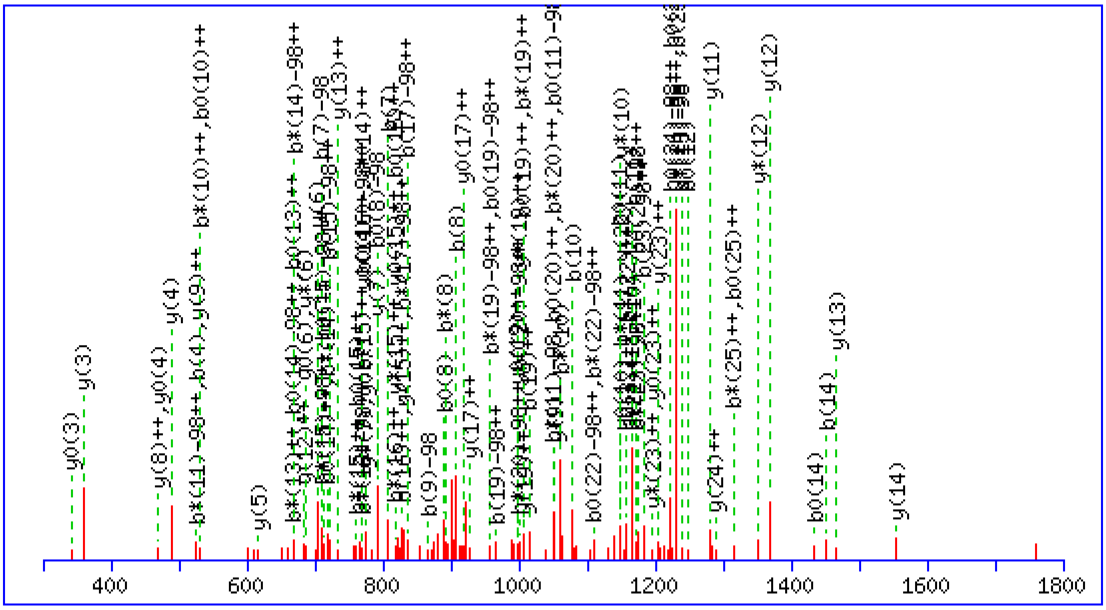
Monoisotopic mass of neutral peptide Mr(calc): 2819.2247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 73 **Expect:** 3.6e-007
Matched b ions: b(4), b(5)++, b(6), b(7), b(7)-98, b(8), b(9)-98, b(9), b(10), b(10)-98++, b(11), b(12)-98, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9)++, y(9), y(10), y(11), y(12), y(12)++, y(13), y(14), y(15)++, y(16)++, y(17)++, y(19)++, y(22)++, y(23)++, y(24)++, y(25)++

Peptide No.803

RSSDPALTGLSTSVSDNNFSSEEPSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RSSDPALTGLSTSVSDNNFSSEEPSR**
Found in **PARD3_MOUSE** in **SwissProt**, Partitioning defective 3 homolog OS=Mus musculus GN=Pard3 PE=1 SV=2

Match to Query 6586: 2819.219268 from(940.747032,3+) index(6191)
Title: Elution from: 42.371 to 42.371 scan no 4254 cid35.00 polarity:+:m1s



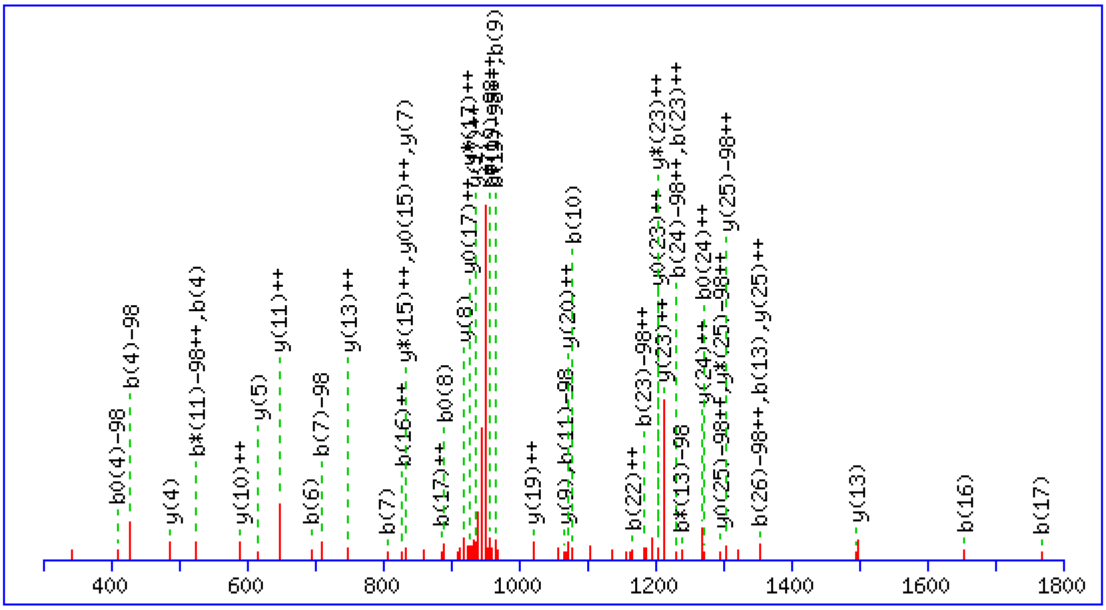
Monoisotopic mass of neutral peptide Mr(calc): 2819.2247
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 **Expect:** 1.4e-006
Matched b ions: b(4), b(7)-98, b(7), b(8), b(9)-98, b(10), b(11), b(14), b(15)-98++, b(15)++, b(16)++, b(17)-98++, b(19)++, b(19)-98++, b(22)++, b(23)++, b(23)-98++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)++, y(9)++, y(9), y(10), y(11), y(12), y(12)++, y(13), y(13)++, y(14), y(15)++, y(17)++, y(19)++, y(22)++, y(23)++, y(24)++

Peptide No.804

RSSDPALTGLSTSVSDNNFSSEEPSRK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RSSDPALTGLSTSVSDNNFSSEEPSRK**
Found in **PARD3_MOUSE** in **SwissProt**, Partitioning defective 3 homolog OS=Mus musculus GN=Pard3 PE=1 SV=2

Match to Query 6884: 2947.314660 from(983.445496,3+) index(6015)
Title: Elution from: 38.203 to 38.203 scan no 3730 cid35.00 polarity:+:m1s



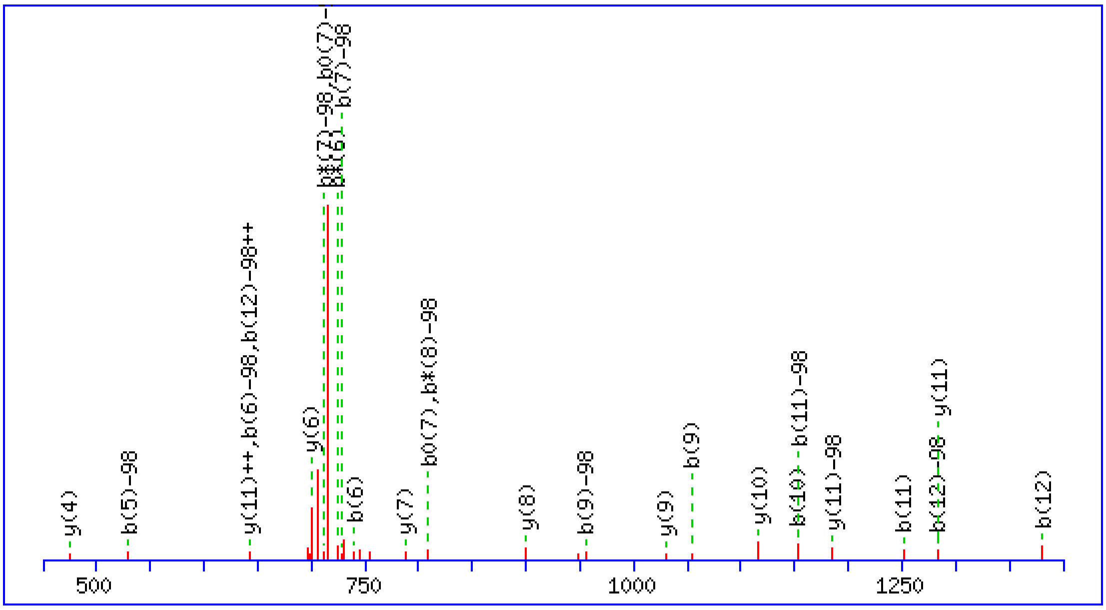
Monoisotopic mass of neutral peptide Mr(calc): 2947.3196
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 51 **Expect:** 5.6e-005
Matched b ions: b(4)-98, b(4), b(6), b(7)-98, b(7), b(9), b(10), b(11)-98, b(13), b(16), b(16)++, b(17), b(17)++, b(19)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++, b(26)-98++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10)++, y(11)++, y(13)++, y(13), y(17)++, y(19)++, y(20)++, y(23)++, y(24)++, y(25)++, y(25)-98++

Peptide No.805

RSSSELSPEVVEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3086: 1525.699970 from(763.857261,2+) index(1060)
Title: Elution from: 25.121 to 25.121 scan no 1969 cid35.00 polarity:+



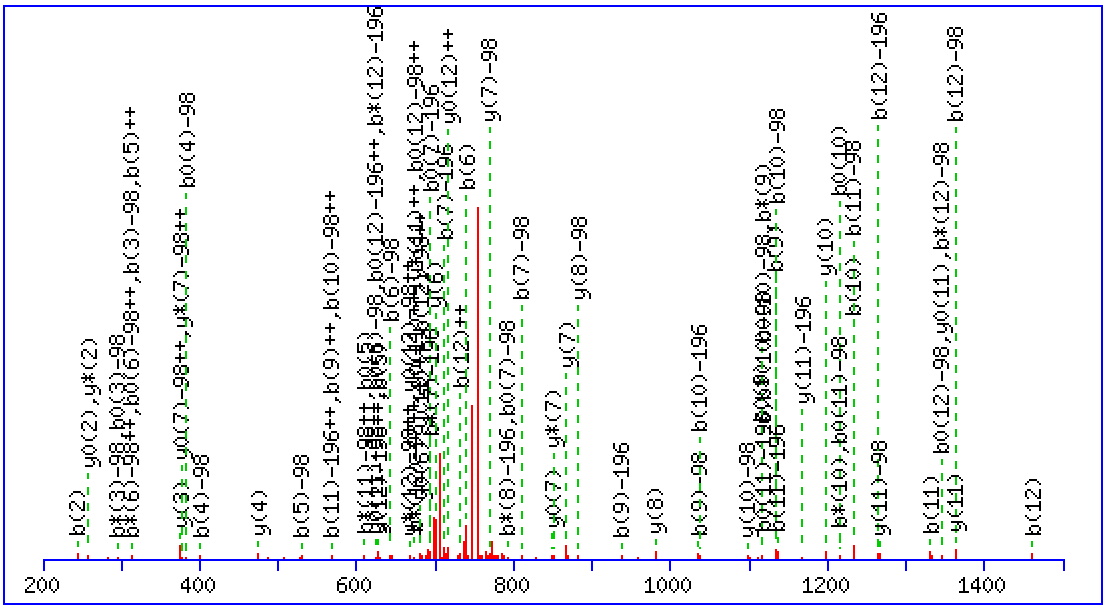
Monoisotopic mass of neutral peptide Mr(calc): 1525.7025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 7.5e-007
Matched b ions: b(5)-98, b(6)-98, b(6), b(7)-98, b(9), b(9)-98, b(10), b(11), b(11)-98, b(12)-98++, b(12), b(12)-98
Matched y ions: y(4), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11)-98, y(11)

Peptide No.806

RSSSELSPEVVEK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3246: 1605.664062 from(803.839307,2+) index(4843)
Title: Elution from: 27.950 to 27.950 scan no 2319 cid35.00 polarity:+:m1s



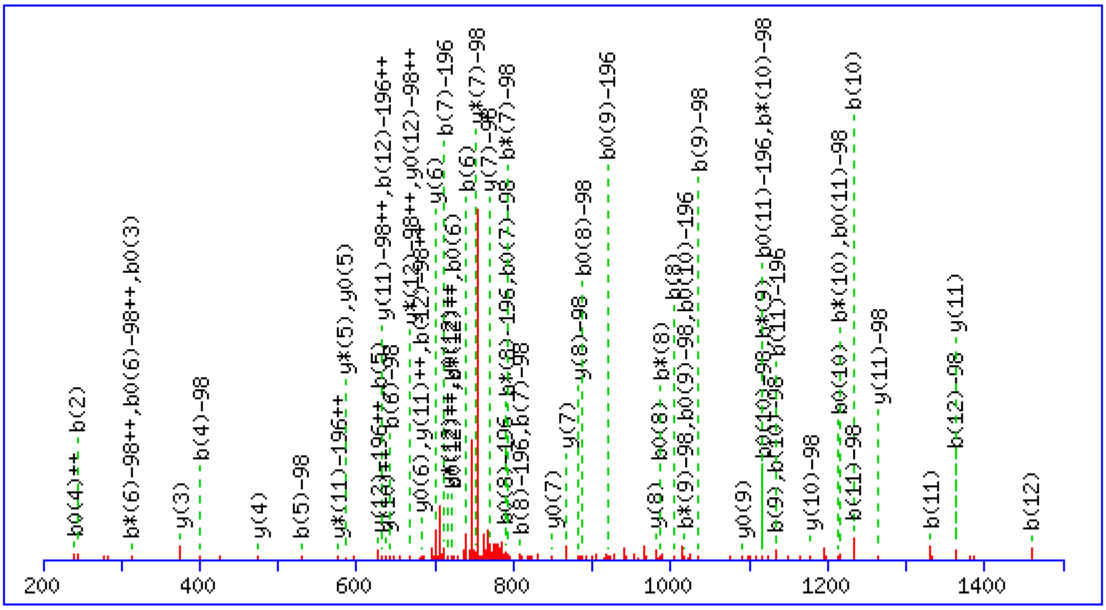
Monoisotopic mass of neutral peptide Mr(calc): 1605.6688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 7.5e-005
Matched b ions: b(2), b(3)-98, b(4)-98, b(5), b(5)-98, b(5)++, b(6)-98, b(6), b(7)-196, b(7)-98, b(9)-98, b(9)++, b(9), b(9)-196, b(10)-98, b(10), b(10)-98++, b(10)-196, b(11), b(11)-196, b(11)-98, b(11)-196++, b(12), b(12)-196, b(12)-98, b(12)-98++, b(12)++
Matched y ions: y(3), y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(10), y(10)-98, y(11), y(11)-98, y(11)-196, y(11)++, y(12)-196++

Peptide No.807

RSSSELSPEVVEK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3356: 1605.669064 from(803.841808,2+) index(982)
Title: Elution from: 35.286 to 35.286 scan no 2436 cid35.00 polarity:+



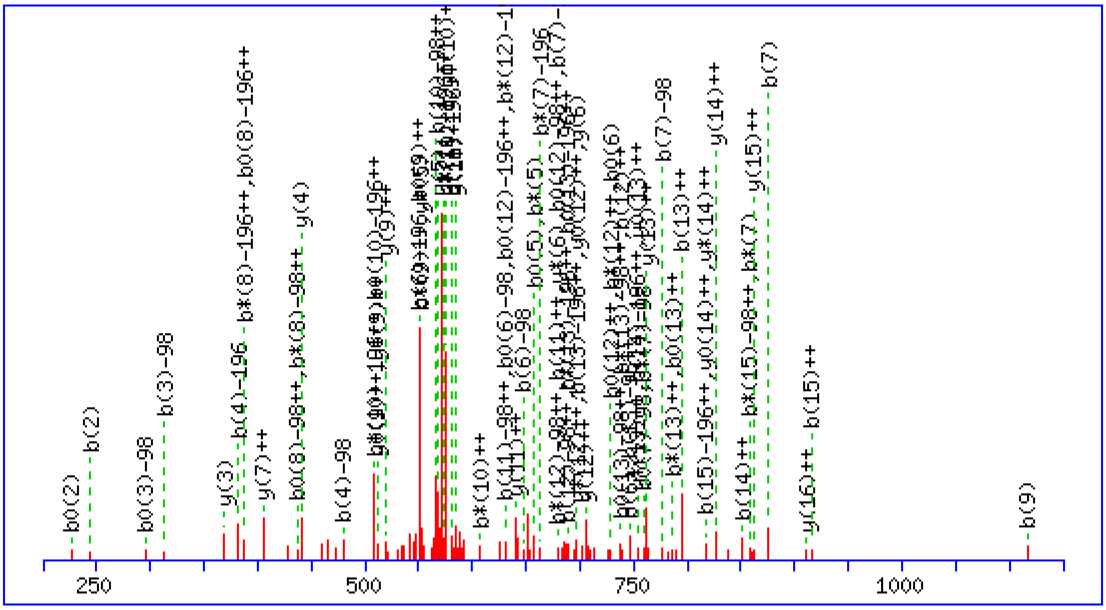
Monoisotopic mass of neutral peptide Mr(calc): 1605.6688
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 37 **Expect:** 0.00078
Matched b ions: b(2), b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7)-196, b(7)-98, b(8)-196, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)-196, b(12), b(12)-98, b(12)-196++, b(12)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(10)++, y(10)-98, y(11), y(11)-98, y(11)-98++, y(11)++, y(12)-196++

Peptide No.808

RSSSPAELELKDDLQQAHGR
Confirmed sites: @S:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **RSSSPAELELKDDLQQAHGR**
Found in **RGPA2_MOUSE** in **SwissProt**, Ral GTPase-activating protein subunit alpha-2 OS=Mus musculus GN=Ralgapa2 PE=1 SV=2

Match to Query 5058: 2396.055000 from(600.021026,4+) index(4614)
Title: Elution from: 33.957 to 33.957 scan no 3023 cid35.00 polarity:+:m1s



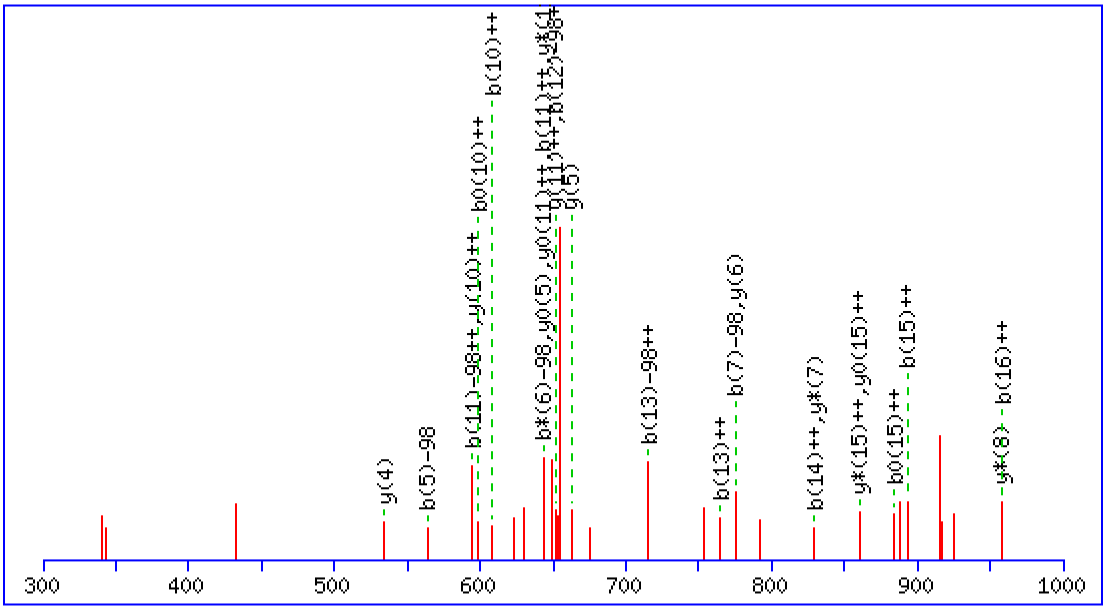
Monoisotopic mass of neutral peptide Mr(calc): 2396.0522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 **Expect:** 2.4e-005
Matched b ions: b(2), b(3)-98, b(4)-196, b(4)-98, b(6), b(6)-196, b(6)-98, b(7), b(7)-98, b(7)-196, b(9), b(10)-98++, b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-196++, b(15)-196++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++

Peptide No.809

RSYSSPDITQALQEEEK
Confirmed sites:
Ambiguous sites: @S:2orY:3orS:4orS:5

MS/MS Fragmentation of **RSYSSPDITQALQEEEK**
Found in **UBP8_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 8 OS=Mus musculus GN=Usp8 PE=1 SV=2

Match to Query 4371: 2059.909917 from(687.643915,3+) index(5143)
Title: Elution from: 40.081 to 40.081 scan no 3817 cid35.00 polarity:+:m1s



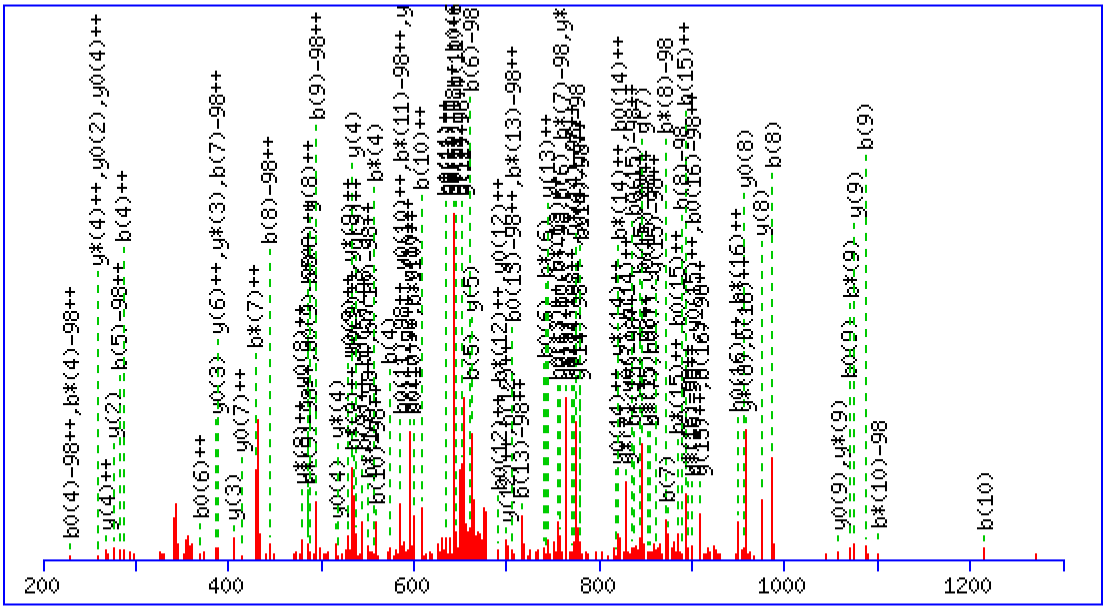
Monoisotopic mass of neutral peptide Mr(calc): 2059.9099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.038
Matched b ions: b(5)-98, b(7)-98, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(16)++
Matched y ions: y(4), y(5), y(6), y(10)++, y(11)++

Peptide No.810

RSYSSPDITQALQEEEK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RSYSSPDITQALQEEEK**
Found in **UBP8_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 8 OS=Mus musculus GN=Usp8 PE=1 SV=2

Match to Query 4573: 2059.910973 from(687.644267,3+) index(4740)
Title: Elution from: 48.822 to 48.822 scan no 3844 cid35.00 polarity:+:m1s



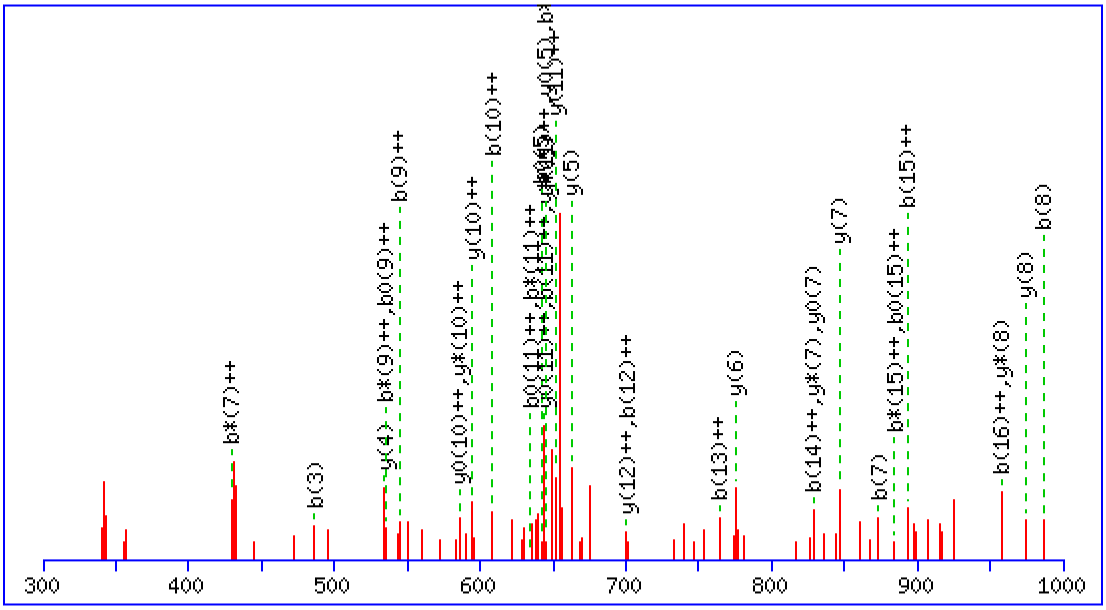
Monoisotopic mass of neutral peptide Mr(calc): 2059.9099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00011
Matched b ions: b(4)++, b(4), b(5)-98++, b(5), b(6), b(6)-98, b(7)-98, b(7), b(7)-98++, b(8), b(8)-98++, b(8)-98, b(9), b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.811

RSYSSPDITQALQEEEK
Confirmed sites:
Ambiguous sites: @S:2orY:3

MS/MS Fragmentation of **RSYSSPDITQALQEEEK**
Found in **UBP8_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 8 OS=Mus musculus GN=Usp8 PE=1 SV=2

Match to Query 4320: 2059.910133 from(687.643987,3+) index(5352)
Title: Elution from: 39.992 to 39.992 scan no 3818 cid35.00 polarity:+:m1s



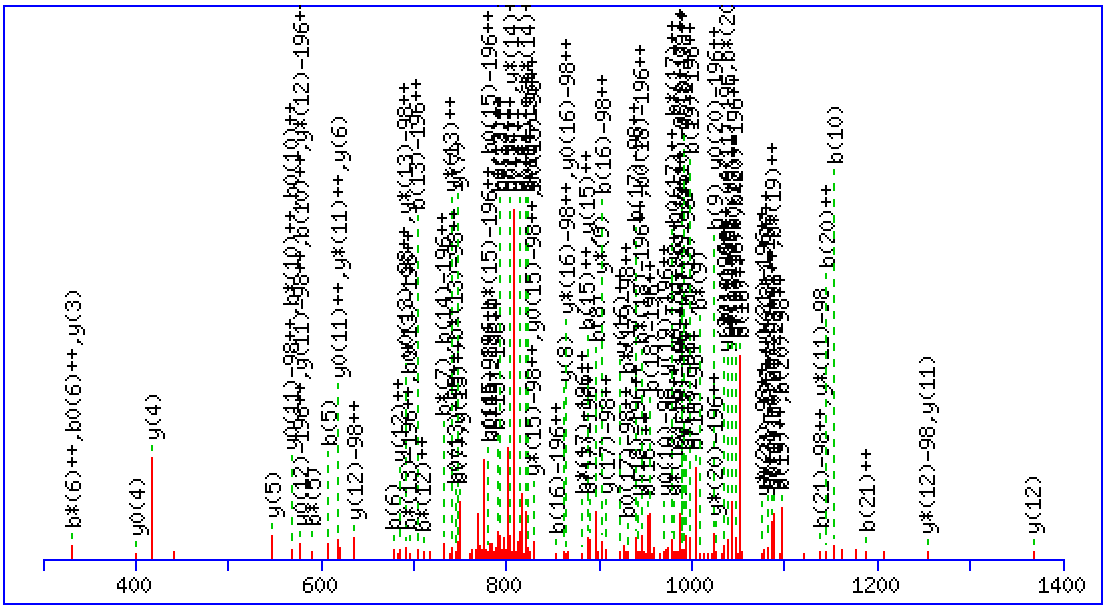
Monoisotopic mass of neutral peptide Mr(calc): 2059.9099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y3 : Phospho (Y)
Ions Score: 36 **Expect:** 0.0016
Matched b ions: b(3), b(7), b(8), b(9)++, b(10)++, b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(12)++

Peptide No.812

RTEGYAAFQEDSSGDEAESPSK
Confirmed sites: @S:12,@S:13
Ambiguous sites:

MS/MS Fragmentation of **RTEGYAAFQEDSSGDEAESPSK**
Found in **RBP1_MOUSE** in **SwissProt**, RalA-binding protein 1 OS=Mus musculus GN=Ralbp1 PE=1 SV=4

Match to Query 5275: 2519.935263 from(840.985697,3+) index(4547)
Title: Elution from: 33.233 to 33.233 scan no 2927 cid35.00 polarity:+:m1s



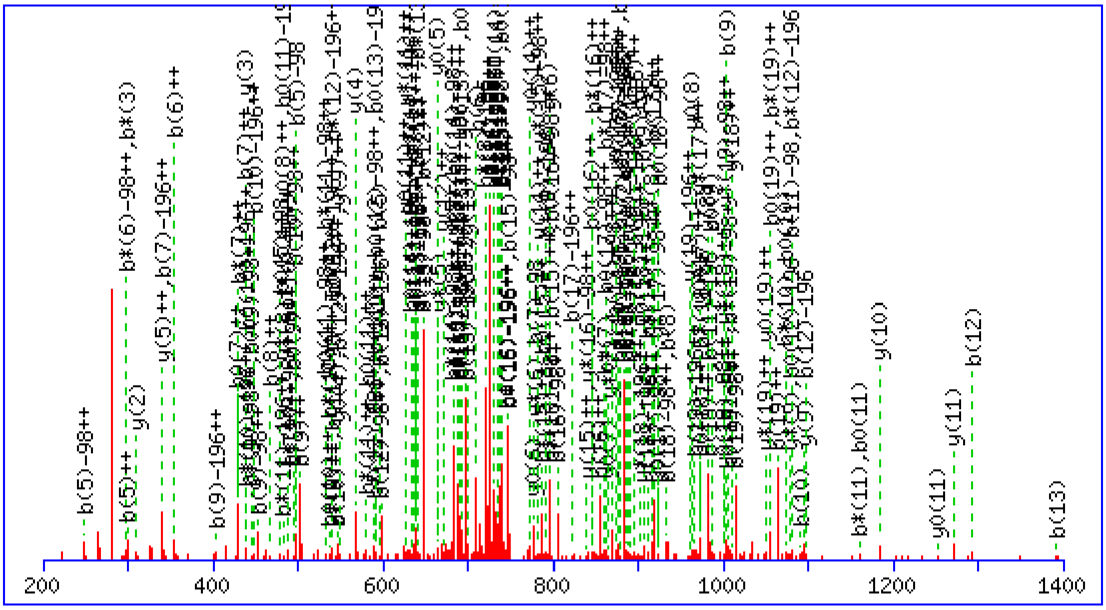
Monoisotopic mass of neutral peptide Mr(calc): 2519.9367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 2.9e-006
Matched b ions: b(5), b(6), b(7), b(8), b(9), b(10), b(10)++, b(13)++, b(13)-196++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(16)-98++, b(16)++, b(16)-196++, b(17)-196++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)++, b(20)-196++, b(21)++, b(21)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(10)-98, y(10), y(11), y(11)-98++, y(12)-98++, y(12), y(12)++, y(13)++, y(14)++, y(15)++, y(16)-196++, y(16)++, y(17)-98++, y(18)++, y(18)-196++, y(18)-98++, y(19)-196++, y(20)-196++

Peptide No.813

RTGSNISGASSDVSLDEQYK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **RTGSNISGASSDVSLDEQYK**
Found in **OSBP1_MOUSE** in **SwissProt**, Oxysterol-binding protein 1 OS=Mus musculus GN=Osbp PE=1 SV=2

Match to Query 4944: 2272.926246 from(758.649358,3+) index(4365)
Title: Elution from: 41.228 to 41.228 scan no 3116 cid35.00 polarity:+:m1s



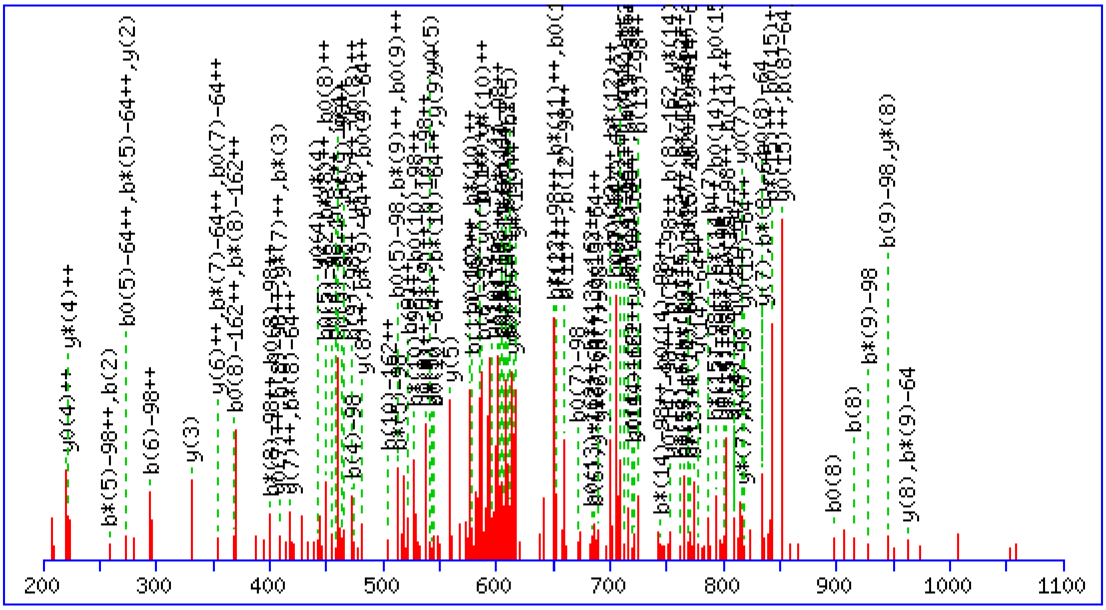
Monoisotopic mass of neutral peptide Mr(calc): 2272.9250
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 **Expect:** 1.2e-007
Matched b ions: b(4), b(5)++, b(5)-98++, b(5)-98, b(5), b(6)++, b(6), b(7)-196++, b(7)++, b(7), b(7)-98, b(8), b(8)++, b(8)-196, b(9)++, b(9)-98++, b(9), b(9)-196++, b(9)-98, b(10)++, b(10)-98++, b(10)-196++, b(10)-196, b(10), b(11)-196, b(11)++, b(11)-98++, b(11)-98, b(12)++, b(12)-98++, b(12), b(12)-196++, b(12)-196, b(13)-98++, b(13), b(13)-196++, b(13)++, b(14)++, b(14)-98++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-98++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(17)-196++, y(18)-196++, y(18)++, y(19)-196++

Peptide No.814

RTSMGGTQQQFVEGVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RTSMGGTQQQFVEGVR**
Found in **CTNB1_MOUSE** in **SwissProt**, Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Match to Query 4094: 1875.831942 from(626.284590,3+) index(3815)
Title: Elution from: 34.255 to 34.255 scan no 2307 cid35.00 polarity:+:m1s



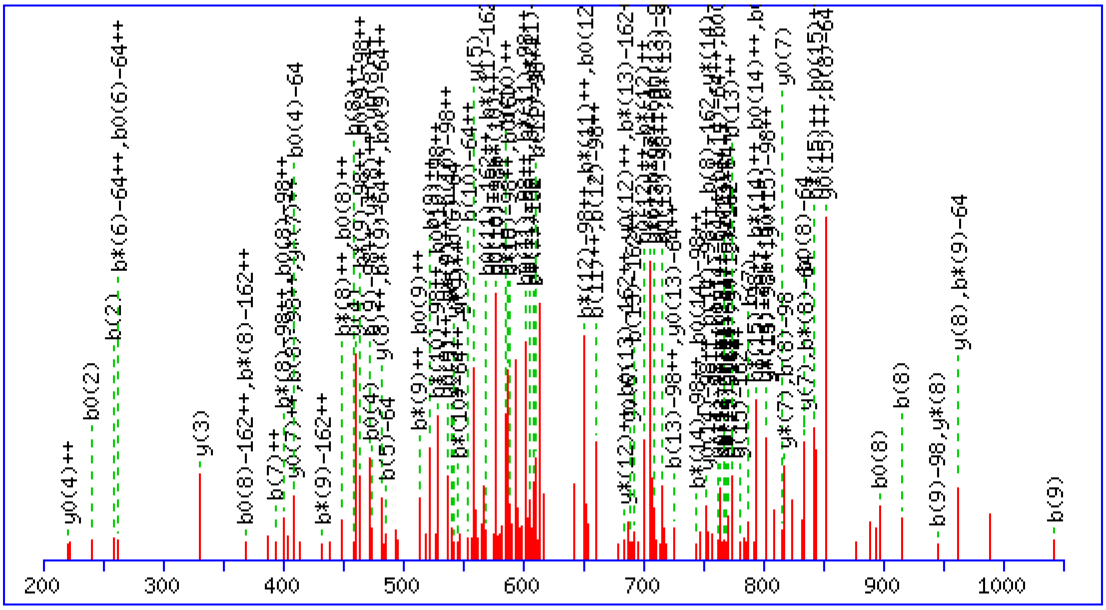
Monoisotopic mass of neutral peptide Mr(calc): 1875.8299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.023
Matched b ions: b(2), b(4)-98, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(8)-98++, b(8)++, b(9)-98, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(12)++, y(14)++

Peptide No.815

RTSMGGTQQQFVEGVR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **RTSMGGTQQQFVEGVR**
Found in **CTNB1_MOUSE** in **SwissProt**, Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1

Match to Query 4488: 1875.828996 from(626.283608,3+) index(4817)
Title: Elution from: 26.059 to 26.059 scan no 2097 cid35.00 polarity:+:m1s



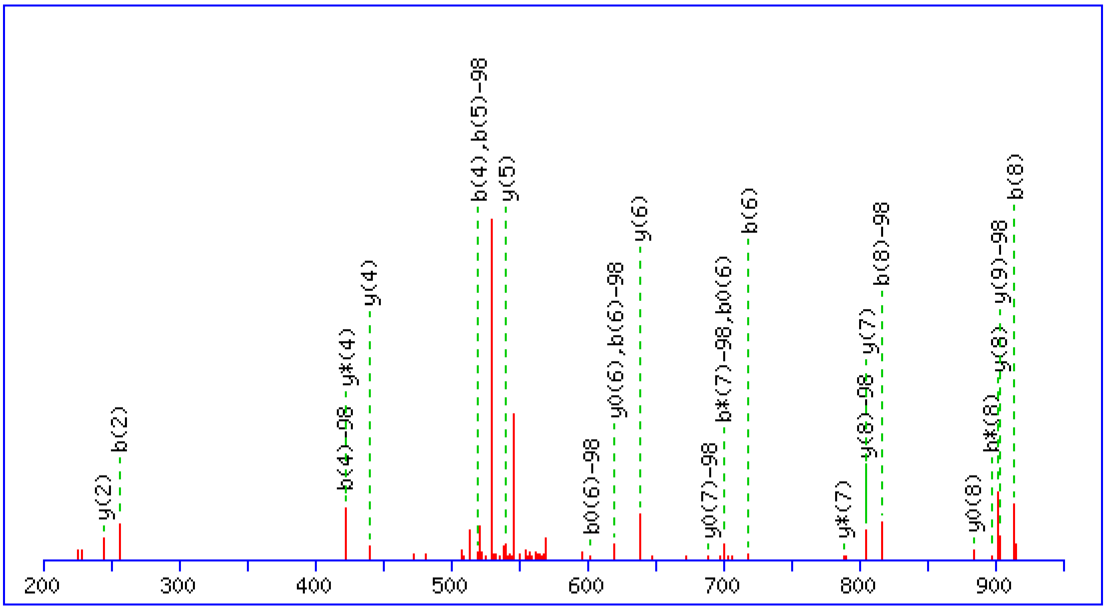
Monoisotopic mass of neutral peptide Mr(calc): 1875.8299
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M4 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0032
Matched b ions: b(2), b(6), b(7)++, b(7), b(8)-98++, b(8)-98, b(8), b(8)++, b(9), b(9)-98++, b(9)-98, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(10)-98++, y(13)++, y(14)-98++

Peptide No.816

RVPSPTPVPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **RVPSPTPVPK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 1482: 1156.599478 from(579.307015,2+) index(449)
Title: Elution from: 19.931 to 19.931 scan no 1265 cid35.00 polarity:+



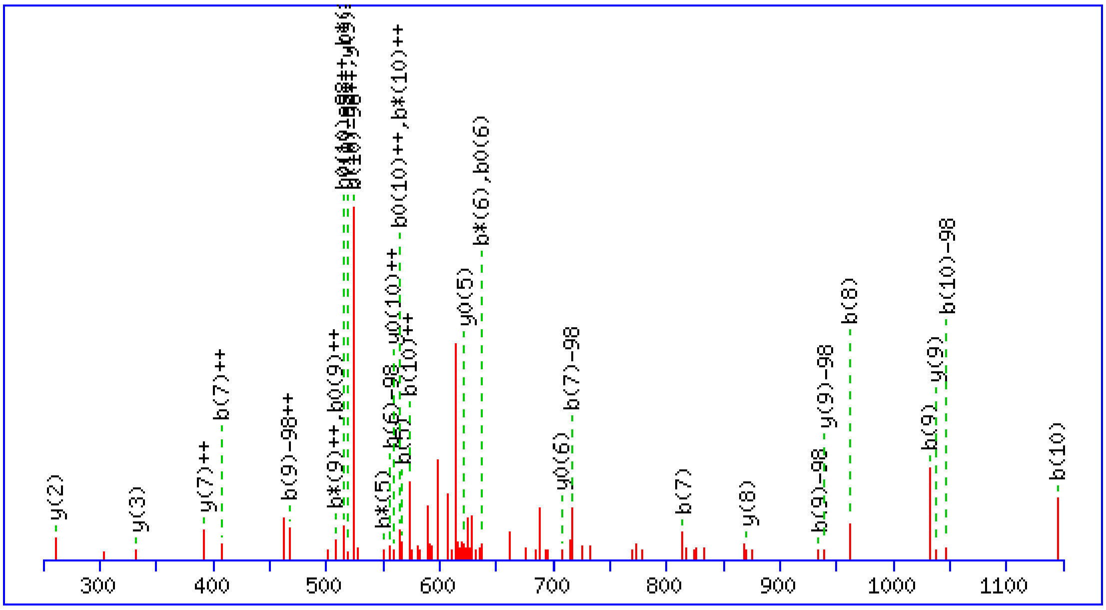
Monoisotopic mass of neutral peptide Mr(calc): 1156.6006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.0005
Matched b ions: b(2), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(8)-98, b(8)
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98

Peptide No.817

RVSSGSCFALE
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RVSSGSCFALE**
Found in **MTCH1_MOUSE** in **SwissProt**, Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1 PE=1 SV=1

Match to Query 1787: 1291.526360 from(646.770456,2+) index(1855)
Title: Elution from: 35.020 to 35.020 scan no 3204 cid35.00 polarity:+



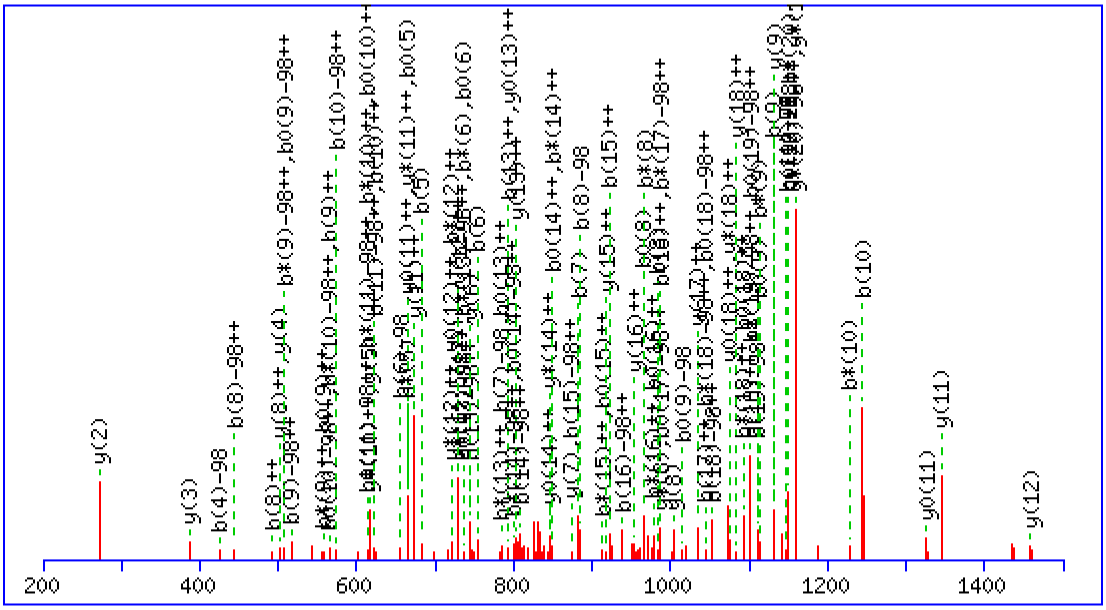
Monoisotopic mass of neutral peptide Mr(calc): 1291.5268
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.028
Matched b ions: b(5), b(6)-98, b(7)-98, b(7), b(7)++, b(8), b(9), b(9)-98, b(9)-98++, b(10)-98++, b(10), b(10)++, b(10)-98
Matched y ions: y(2), y(3), y(7)++, y(8), y(9)-98, y(9), y(9)++, y(10)-98++

Peptide No.818

RVSVCAETFNPDEEEEDNDPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RVSVCAETFNPDEEEEDNDPR**
Found in **KAP2_MOUSE** in **SwissProt**, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 6530: 2587.012815 from(863.344881,3+) index(5790)
Title: Elution from: 35.734 to 35.734 scan no 3404 cid35.00 polarity:+:m1s



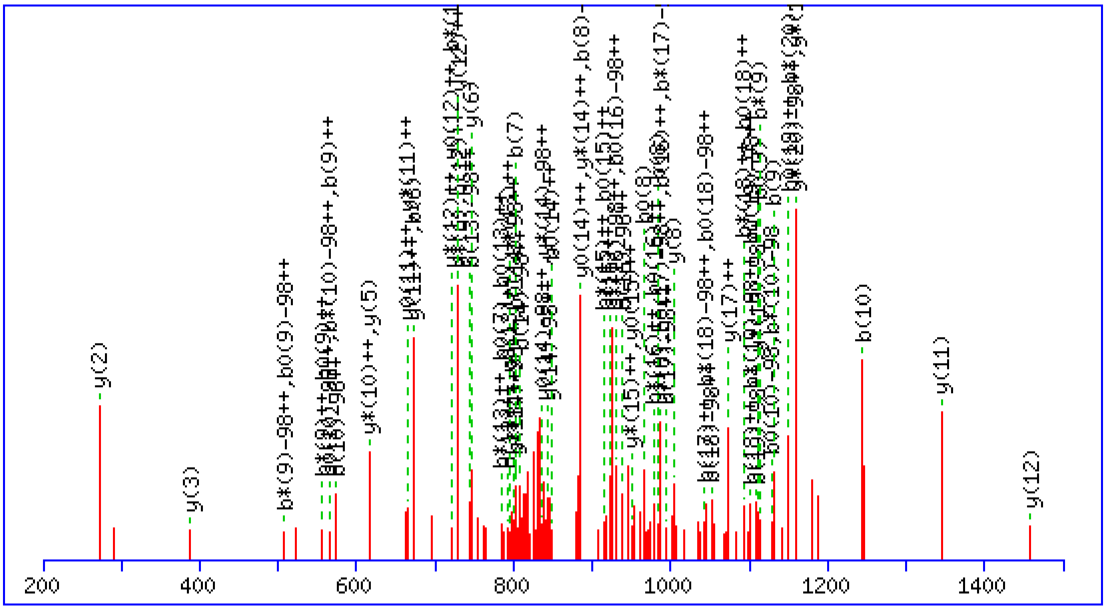
Monoisotopic mass of neutral peptide Mr(calc): 2587.0170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 61 **Expect:** 4.3e-006
Matched b ions: b(4)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98++, b(8)-98, b(8)++, b(8), b(9)-98++, b(9)++, b(9), b(10), b(10)++, b(10)-98++, b(10)-98, b(11)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(11)++, y(11), y(12)++, y(12), y(13)++, y(15)++, y(16)++, y(17)++, y(18)++

Peptide No.819

RVSVCAETFNPDEEEEDNDPR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of **RVSVCAETFNPDEEEEDNDPR**
Found in **KAP2_MOUSE** in **SwissProt**, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 6343: 2587.013376 from(863.345068,3+) index(5624)
Title: Elution from: 35.757 to 35.757 scan no 3377 cid35.00 polarity:+:m1s



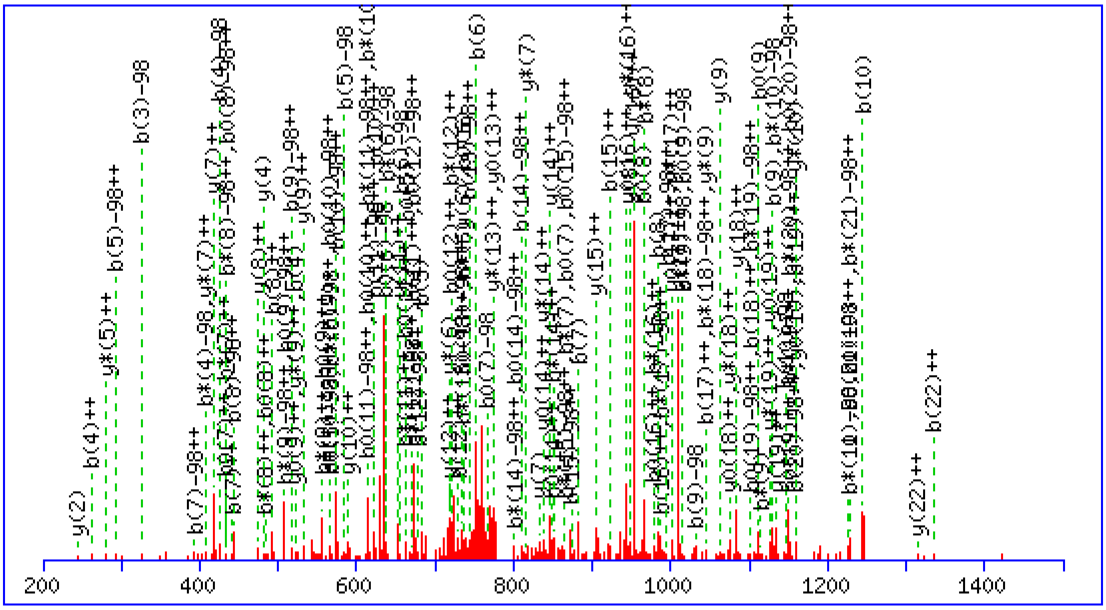
Monoisotopic mass of neutral peptide Mr(calc): 2587.0170
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0047
Matched b ions: b(6), b(7), b(8)-98, b(8), b(9)++, b(9), b(10), b(10)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)-98++
Matched y ions: y(2), y(3), y(5), y(6), y(8), y(11), y(11)++, y(12)++, y(12), y(13)++, y(14)-98++, y(17)++

Peptide No.820

RVSVCAETFNPDEEEEDNDPRVVHPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RVSVCAETFNPDEEEEDNDPRVVHPK**
Found in **KAP2_MOUSE** in **SwissProt**, cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Mus musculus GN=Prkar2a PE=1 SV=2

Match to Query 6603: 3147.360324 from(787.847357,4+) index(5109)
Title: Elution from: 41.849 to 41.849 scan no 3341 cid35.00 polarity:+:m1s



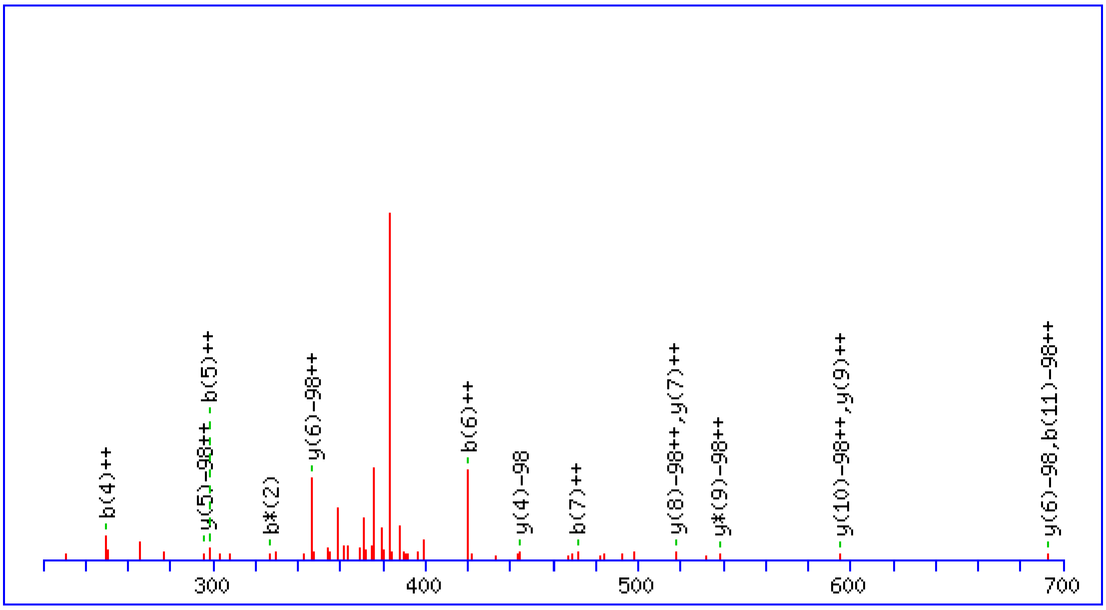
Monoisotopic mass of neutral peptide Mr(calc): 3147.3605
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00018
Matched b ions: b(3)-98, b(4)++, b(4)-98, b(4), b(5)-98++, b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98++, b(7)++, b(8)++, b(8)-98++, b(8), b(9), b(9)-98++, b(9)++, b(9)-98, b(10), b(10)-98++, b(10)++, b(10)-98, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(17)++, b(17)-98++, b(18)++, b(19)++, b(20)-98++, b(22)++
Matched y ions: y(2), y(4), y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(9), y(10)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(22)++

Peptide No.821

RWPGVYTFLSDK
Confirmed sites: @Y:6,@S:10
Ambiguous sites:

MS/MS Fragmentation of **RWPGVYTFLSDK**
Found in **GRAA_MOUSE** in **SwissProt**, Granzyme A OS=Mus musculus GN=Gzma PE=1 SV=2

Match to Query 3035: 1627.680560 from(407.927416,4+) index(666)
Title: Elution from: 24.199 to 24.199 scan no 1685 cid35.00 polarity:+



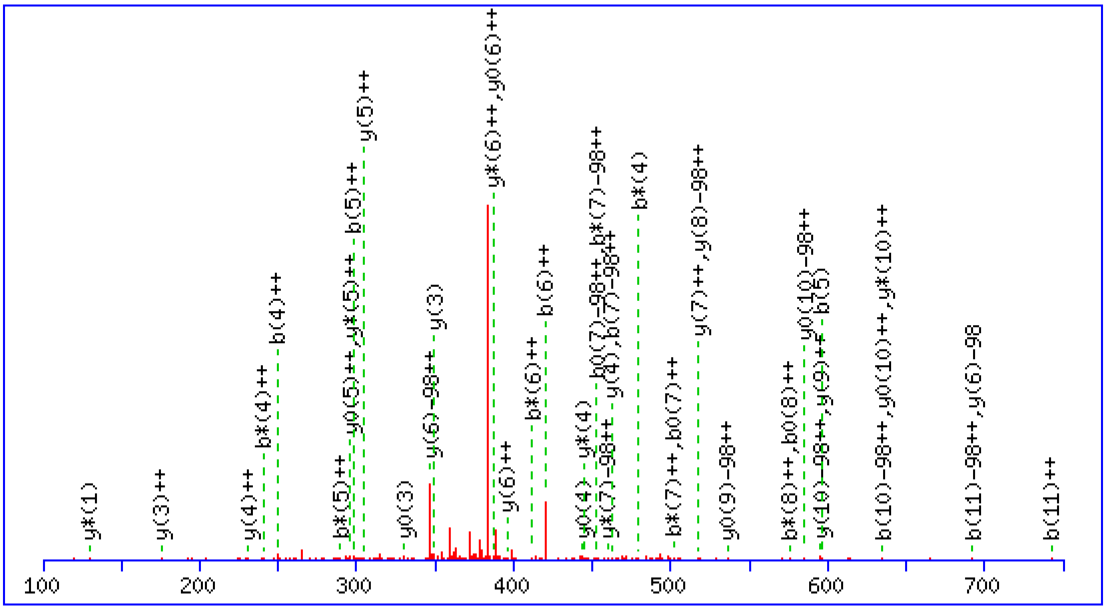
Monoisotopic mass of neutral peptide Mr(calc): 1627.6837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.016
Matched b ions: b(4)++, b(5)++, b(6)++, b(7)++, b(11)-98++
Matched y ions: y(4)-98, y(5)-98++, y(6)-98, y(6)-98++, y(7)++, y(8)-98++, y(9)++, y(10)-98++

Peptide No.822

RWPGVYTFLSDK
Confirmed sites: @Y:6,@T:7
Ambiguous sites:

MS/MS Fragmentation of **RWPGVYTFLSDK**
Found in **GRAA_MOUSE** in **SwissProt**, Granzyme A OS=Mus musculus GN=Gzma PE=1 SV=2

Match to Query 3929: 1627.681664 from(407.927692,4+) index(837)
Title: Elution from: 32.033 to 32.033 scan no 2140 cid35.00 polarity:+



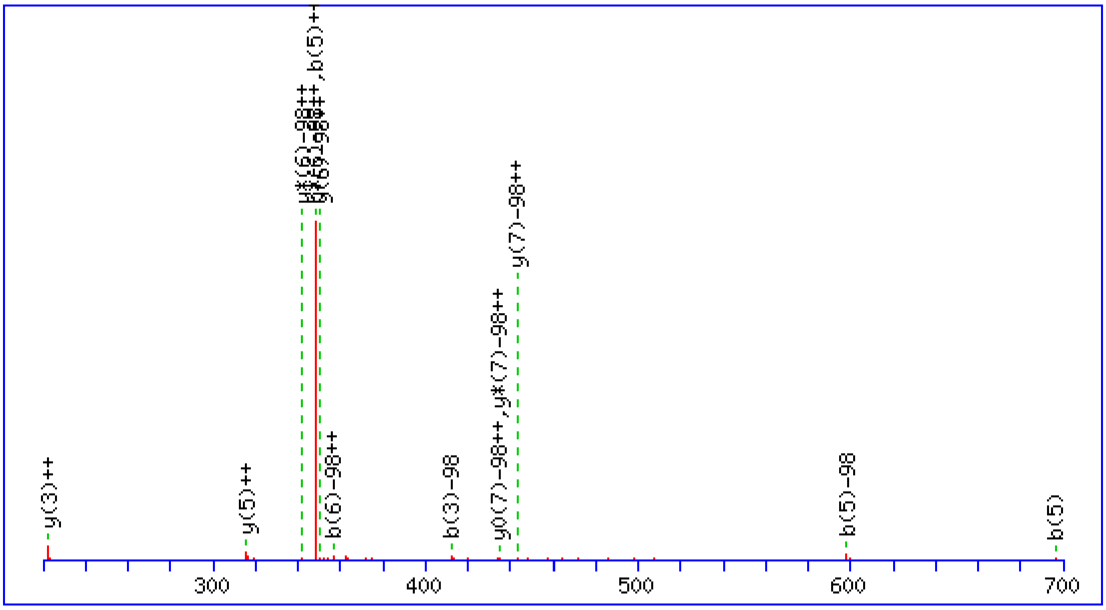
Monoisotopic mass of neutral peptide Mr(calc): 1627.6837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.06
Matched b ions: b(4)++, b(5), b(5)++, b(6)++, b(7)-98++, b(10)-98++, b(11)++, b(11)-98++
Matched y ions: y(3)++, y(3), y(4)++, y(4), y(5)++, y(6)-98++, y(6)-98, y(6)++, y(7)++, y(8)-98++, y(9)++, y(10)-98++

Peptide No.823

RWSGELRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RWSGELRR**
Found in **PLIN5_MOUSE** in **SwissProt**, Perilipin-5 OS=Mus musculus GN=Plin5 PE=1 SV=1

Match to Query 1190: 1138.539549 from(380.520459,3+) index(320)
Title: Elution from: 21.125 to 21.125 scan no 1270 cid35.00 polarity:+



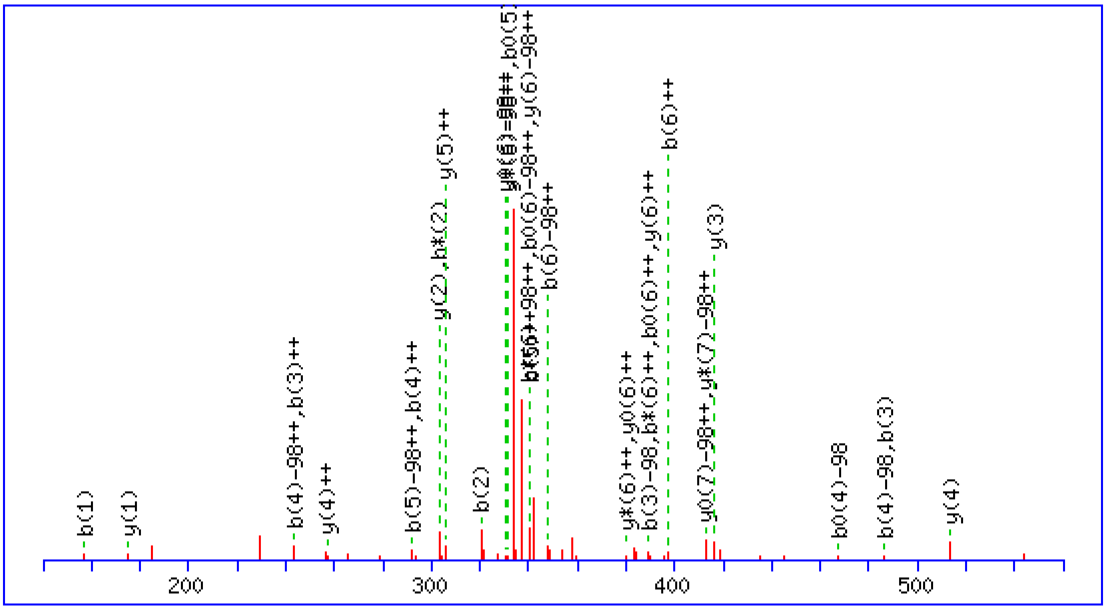
Monoisotopic mass of neutral peptide Mr(calc): 1138.5397
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 **Expect:** 0.014
Matched b ions: b(3)-98, b(5)++, b(5)-98, b(5), b(6)-98++, b(7)-98++
Matched y ions: y(3)++, y(5)++, y(6)-98++, y(7)-98++

Peptide No.824

RYSPPIQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **RYSPPIQR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 1106: 1095.523206 from(366.181678,3+) index(495)
Title: Elution from: 20.793 to 20.793 scan no 1345 cid35.00 polarity:+



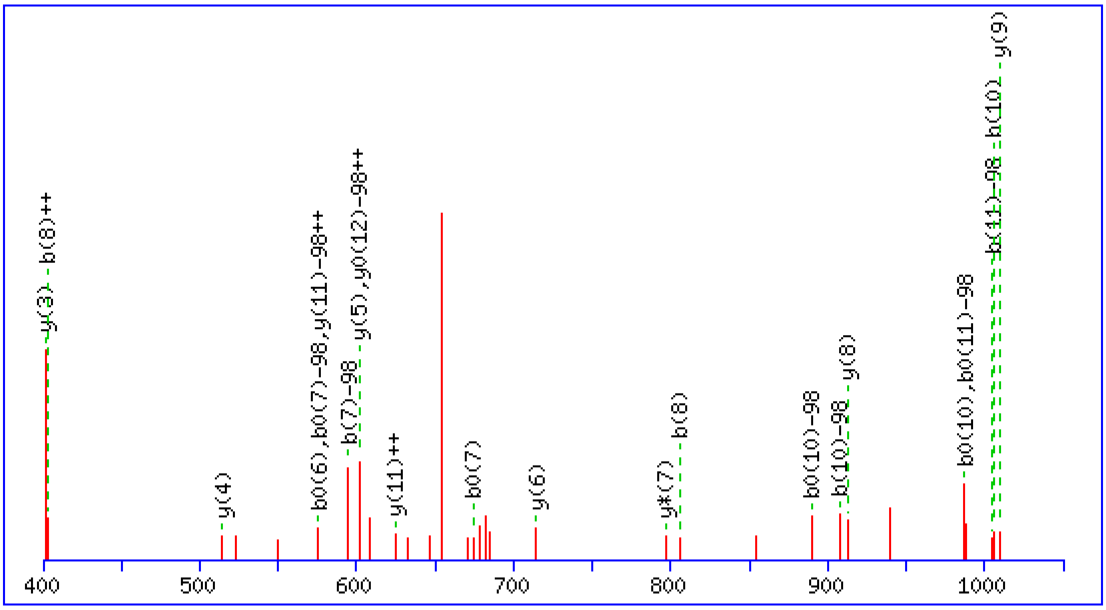
Monoisotopic mass of neutral peptide Mr(calc): 1095.5226
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.0071
Matched b ions: b(1), b(2), b(3)++, b(3), b(3)-98, b(4)-98++, b(4)-98, b(4)++, b(5)++, b(5)-98++, b(6)++, b(6)-98++, b(7)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(4)++, y(5)++, y(6)-98++, y(6)++

Peptide No.825

SAASPVVISIPER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SAASPVVISIPER**
Found in **SON_MOUSE** in **SwissProt**, Protein SON OS=Mus musculus GN=Son PE=1 SV=2

Match to Query 2361: 1404.700622 from(703.357587,2+) index(6117)
Title: Elution from: 41.523 to 41.523 scan no 4140 cid35.00 polarity:+:m1s



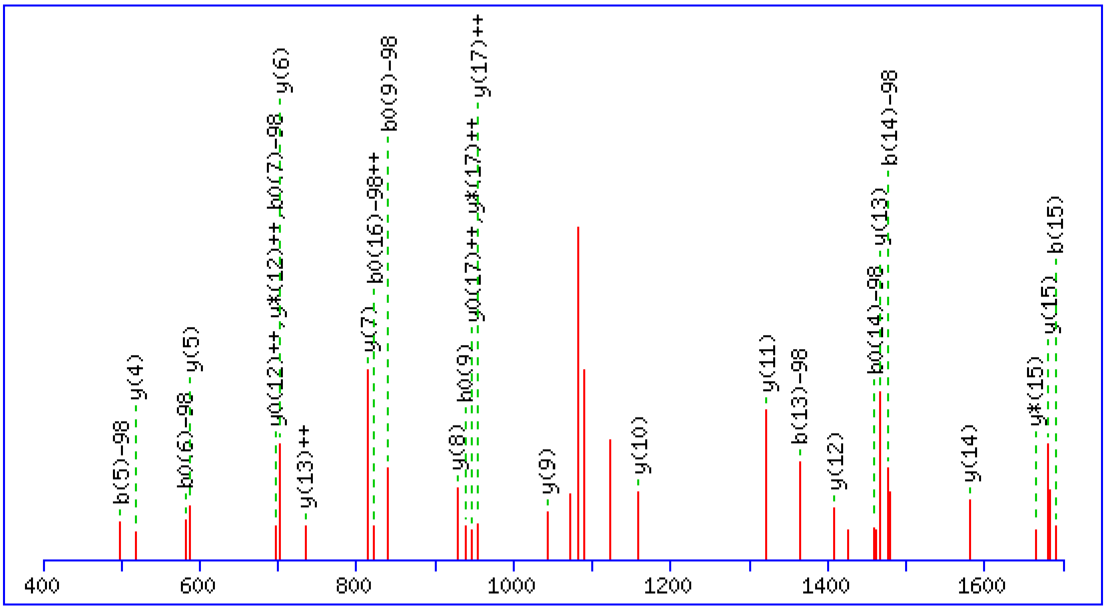
Monoisotopic mass of neutral peptide Mr(calc): 1404.7014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00033
Matched b ions: b(7)-98, b(8)++, b(8), b(10), b(10)-98, b(11)-98
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(11)-98++, y(11)++

Peptide No.826

SAEDLTDGSYDDILNAEQLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SAEDLTDGSYDDILNAEQLK**
Found in **ARM10_MOUSE** in **SwissProt**, Armadillo repeat-containing protein 10 OS=Mus musculus GN=Armc10 PE=1 SV=1

Match to Query 4967: 2275.971968 from(1138.993260,2+) index(6030)
Title: Elution from: 56.933 to 56.933 scan no 5497 cid35.00 polarity:+:m1s



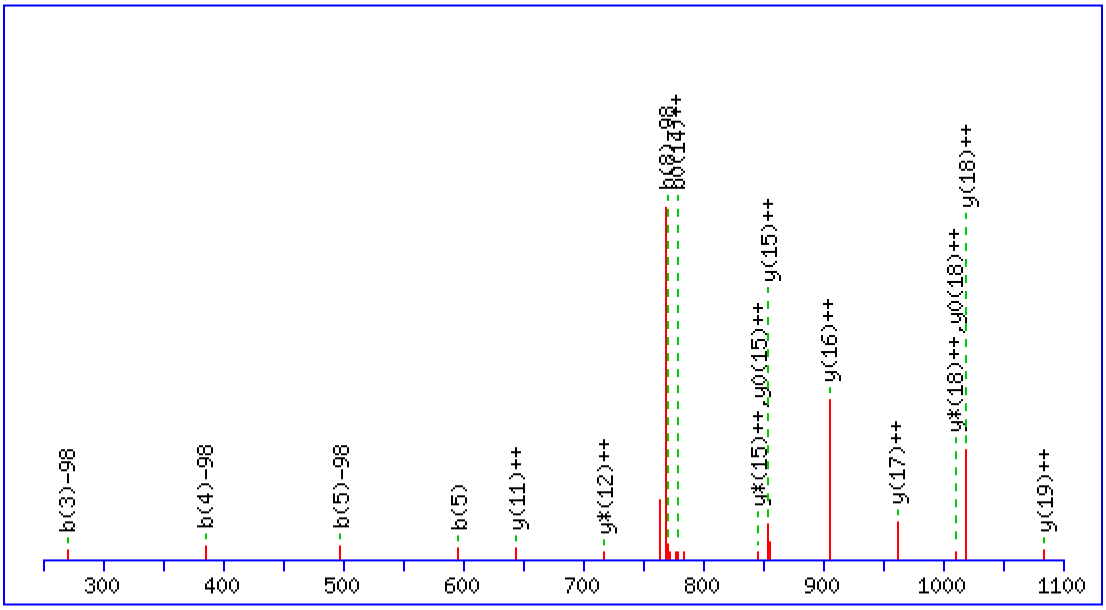
Monoisotopic mass of neutral peptide Mr(calc): 2275.9733
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 9.7e-009
Matched b ions: b(5)-98, b(13)-98, b(14)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14), y(15), y(17)++

Peptide No.827

SAEDLTDGSYDDILNAEQLKK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SAEDLTDGSYDDILNAEQLKK**
Found in **ARM10_MOUSE** in **SwissProt**, Armadillo repeat-containing protein 10 OS=Mus musculus GN=Armc10 PE=1 SV=1

Match to Query 5077: 2404.068960 from(802.363596,3+) index(5648)
Title: Elution from: 49.751 to 49.751 scan no 4926 cid35.00 polarity:+:m1s



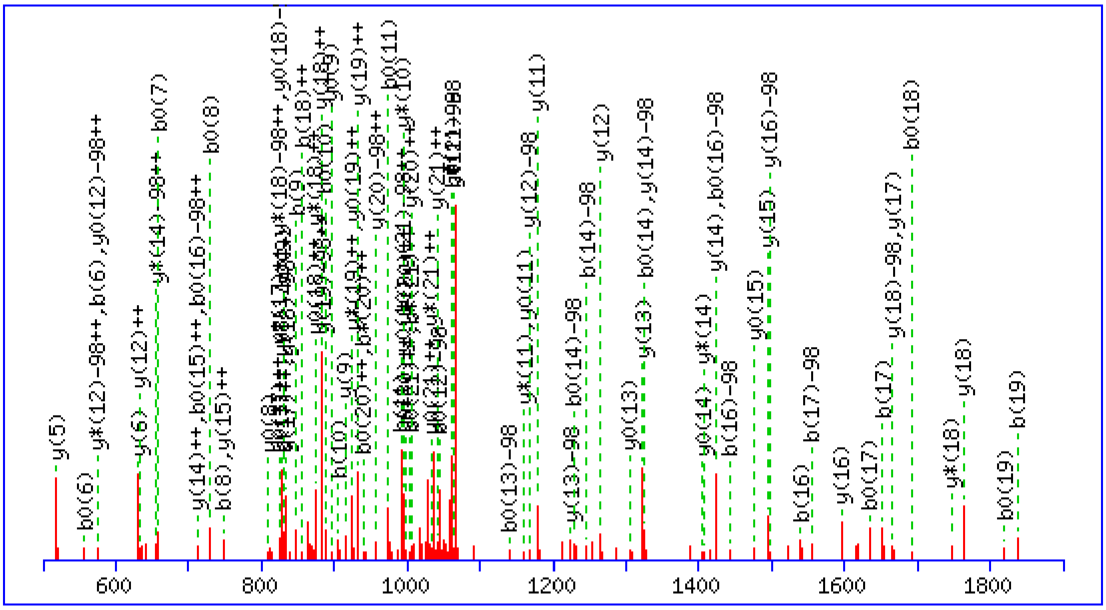
Monoisotopic mass of neutral peptide Mr(calc): 2404.0683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.001
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(8)-98
Matched y ions: y(11)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++

Peptide No.828

SAFTPATATGSSPSPVLGQGEK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **SAFTPATATGSSPSPVLGQGEK**
Found in **ITSN1_MOUSE** in **SwissProt**, Intersectin-1 OS=Mus musculus GN=Itsn1 PE=1 SV=1

Match to Query 5621: 2168.996584 from(1085.505568,2+) index(5954)
Title: Elution from: 37.560 to 37.560 scan no 3645 cid35.00 polarity:+:m1s



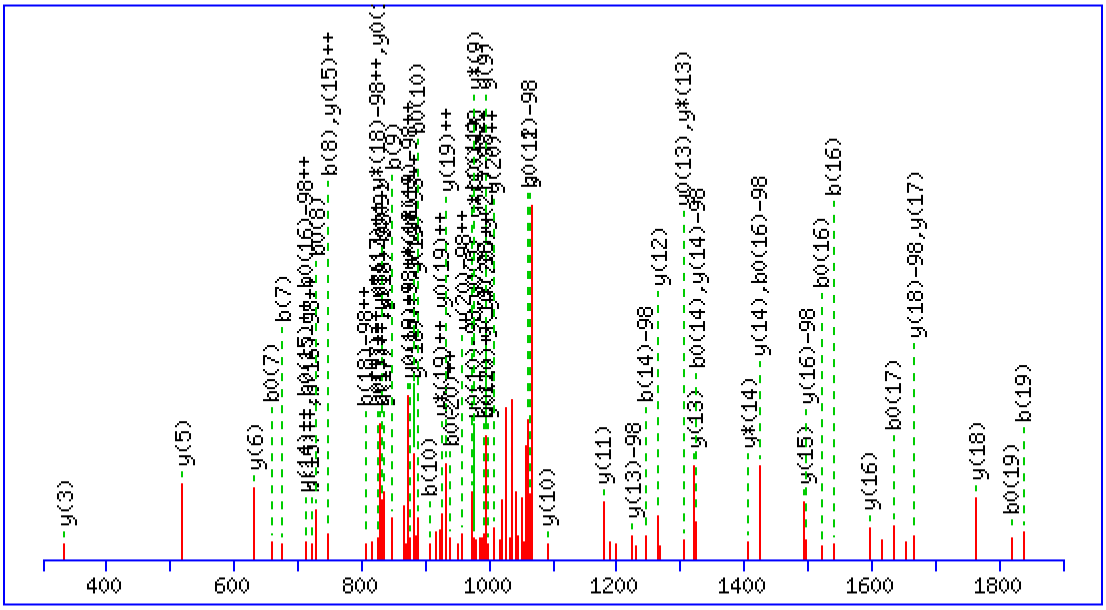
Monoisotopic mass of neutral peptide Mr(calc): 2168.9991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 72 **Expect:** 4.1e-007
Matched b ions: b(6), b(8), b(9), b(10), b(11), b(12)-98, b(14)-98, b(16), b(16)-98, b(17), b(17)++, b(17)-98, b(18)++, b(19)
Matched y ions: y(5), y(6), y(8), y(9), y(11), y(12), y(12)-98, y(12)++, y(13), y(13)-98, y(14), y(14)-98, y(14)++, y(15)++, y(15), y(16), y(16)-98, y(17)++, y(17), y(18)++, y(18), y(18)-98++, y(18)-98, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++

Peptide No.829

SAFTPATATGSSPSPVLGQGEK
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **SAFTPATATGSSPSPVLGQGEK**
Found in **ITSN1_MOUSE** in **SwissProt**, Intersectin-1 OS=Mus musculus GN=Itsn1 PE=1 SV=1

Match to Query 4660: 2168.999616 from(1085.507084,2+) index(4915)
Title: Elution from: 37.160 to 37.160 scan no 3447 cid35.00 polarity:+:m1s



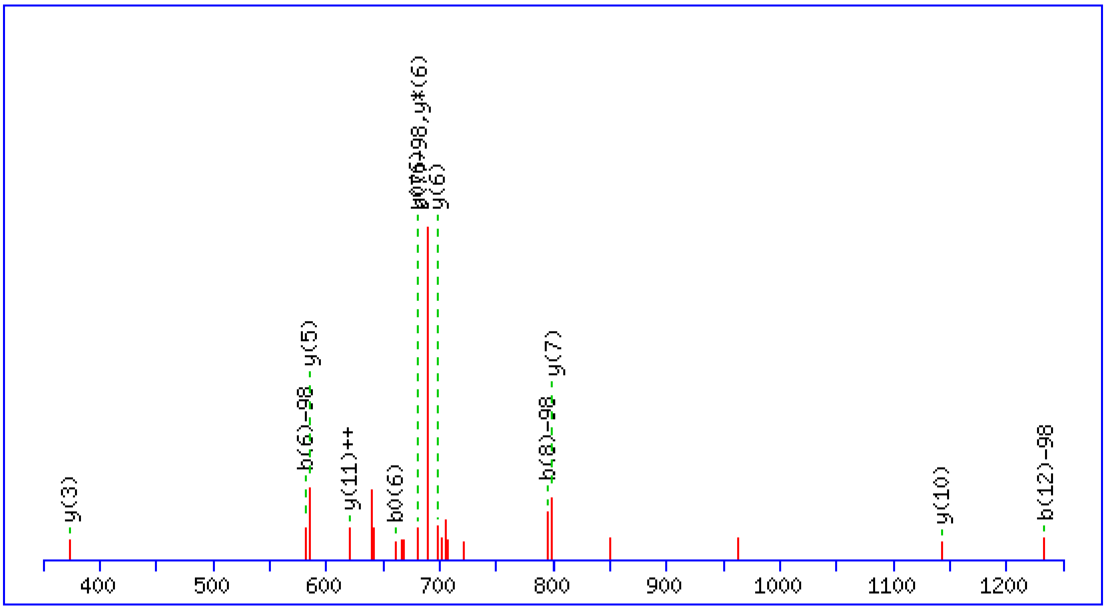
Monoisotopic mass of neutral peptide Mr(calc): 2168.9991
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 85 **Expect:** 1.9e-008
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(14)-98, b(15)++, b(16), b(16)-98++, b(17)++, b(18)-98++, b(19)
Matched y ions: y(3), y(5), y(6), y(8), y(9), y(10)-98, y(10), y(11), y(12), y(13), y(13)-98, y(14), y(14)++, y(14)-98, y(15), y(15)++, y(16), y(16)-98, y(17), y(17)++, y(18), y(18)++, y(18)-98, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)-98++

Peptide No.830

SAPETLTLPDPEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SAPETLTLPDPEK**
Found in **PITC1_MOUSE** in **SwissProt**, Cytoplasmic phosphatidylinositol transfer protein 1 OS=Mus musculus GN=Pitpnc1 PE=1 SV=1

Match to Query 2369: 1476.675384 from(739.344968,2+) index(2387)
Title: Elution from: 42.108 to 42.108 scan no 4064 cid35.00 polarity:+



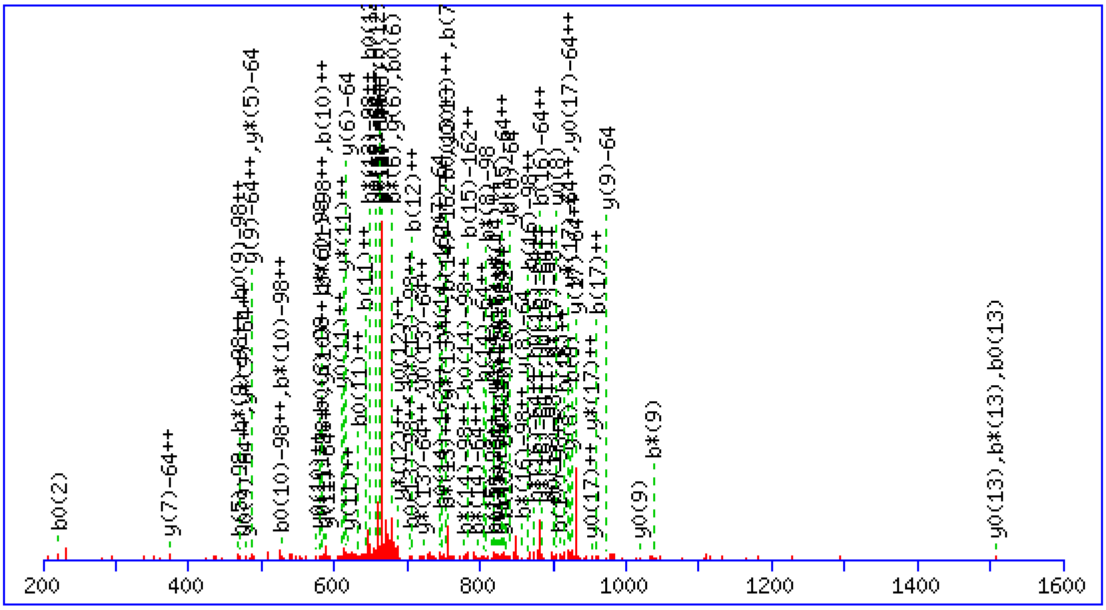
Monoisotopic mass of neutral peptide Mr(calc): 1476.6749
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0043
Matched b ions: b(6)-98, b(7)-98, b(8)-98, b(12)-98
Matched y ions: y(3), y(5), y(6), y(7), y(10), y(11)++

Peptide No.831

SAQAQMRAMLDQLMGTSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SAQAQMRAMLDQLMGTSR**
Found in **LC7L2_MOUSE** in **SwissProt**, Putative RNA-binding protein Luc7-like 2 OS=Mus musculus GN=Luc7l2 PE=1 SV=1

Match to Query 5348: 2089.910667 from(697.644165,3+) index(5474)
Title: Elution from: 47.465 to 47.465 scan no 3947 cid35.00 polarity:+:m1s



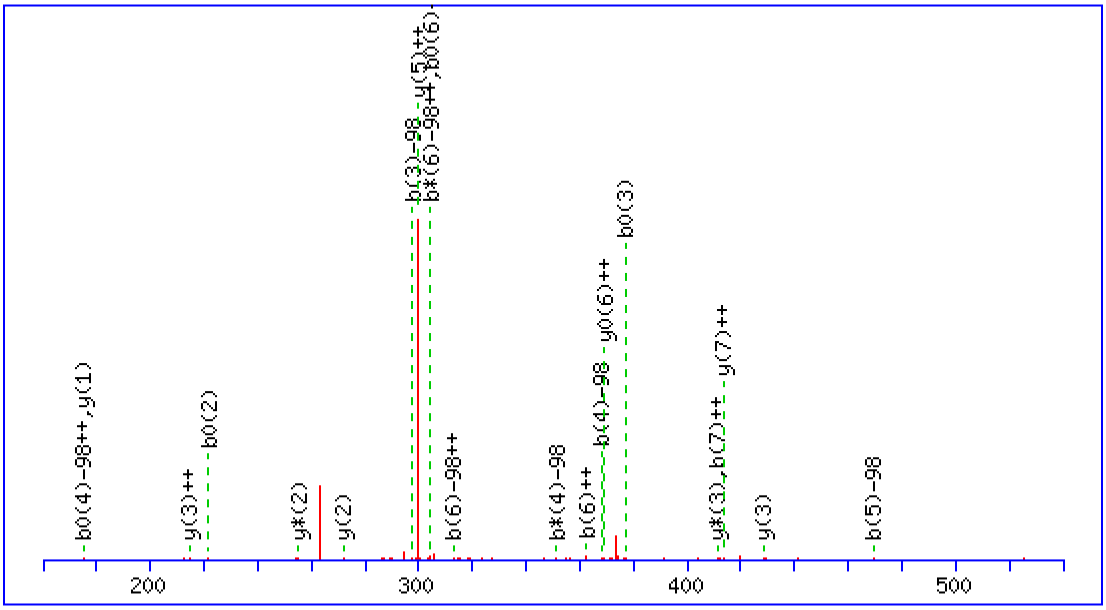
Monoisotopic mass of neutral peptide Mr(calc): 2089.9108
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M14 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.046
Matched b ions: b(5)-98, b(7)-98, b(8), b(10)++, b(11)++, b(12)-98++, b(12)++, b(15)-98++, b(16)-98++, b(16)++, b(17)-98++, b(17)++
Matched y ions: y(6), y(8), y(10)++, y(11)++, y(14)++

Peptide No.832

SARATRPR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SARATRPR**
Found in **USBP1_MOUSE** in **SwissProt**, Usher syndrome type-1C protein-binding protein 1 OS=Mus musculus GN=Ushbp1 PE=1 SV=2

Match to Query 705: 993.484587 from(332.168805,3+) index(3197)
Title: Elution from: 17.775 to 17.775 scan no 936 cid35.00 polarity:+:m1s



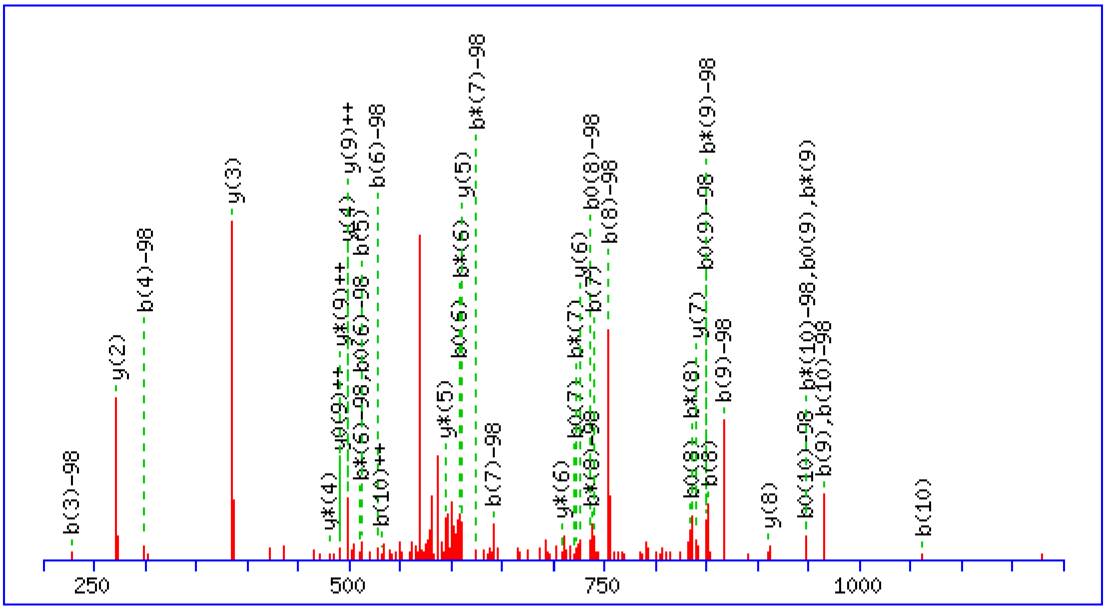
Monoisotopic mass of neutral peptide Mr(calc): 993.4869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 **Expect:** 0.019
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(6)++, b(6)-98++, b(7)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(5)++, y(7)++

Peptide No.833

SASADNLILPR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SASADNLILPR**
Found in **CCNY_MOUSE** in **SwissProt**, Cyclin-Y OS=Mus musculus GN=Ccny PE=1 SV=1

Match to Query 2163: 1235.592380 from(618.803466,2+) index(4736)
Title: Elution from: 48.609 to 48.609 scan no 3830 cid35.00 polarity:+:m1s



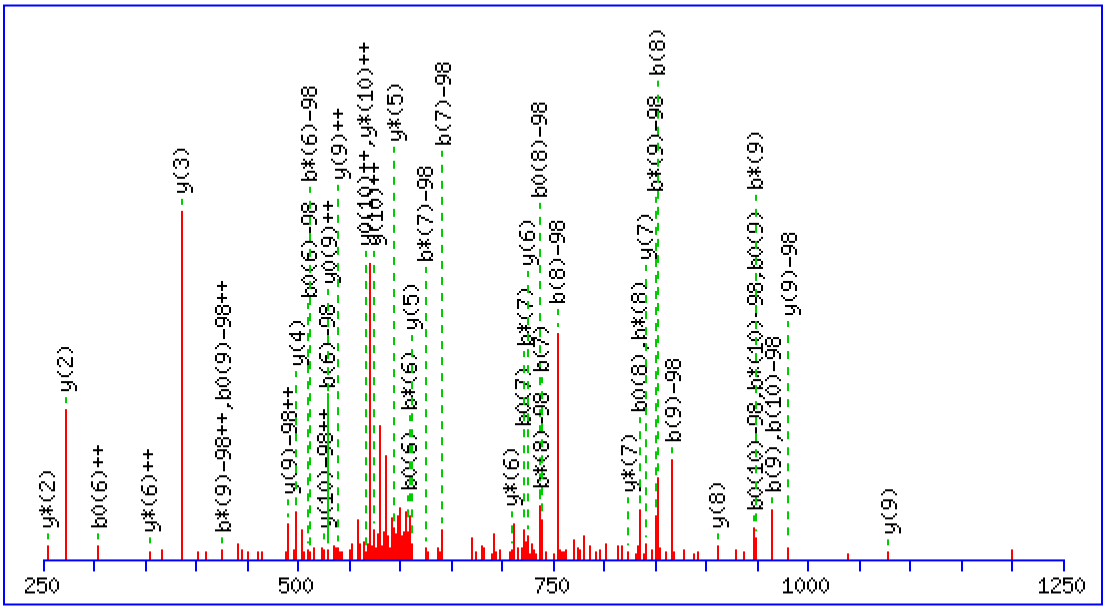
Monoisotopic mass of neutral peptide Mr(calc): 1235.5911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.003
Matched b ions: b(3)-98, b(4)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++

Peptide No.834

SASADNLILPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SASADNLILPR**
Found in **CCNY_MOUSE** in **SwissProt**, Cyclin-Y OS=Mus musculus GN=Ccny PE=1 SV=1

Match to Query 2430: 1235.591598 from(618.803075,2+) index(2125)
Title: Elution from: 48.611 to 48.611 scan no 4063 cid35.00 polarity:+



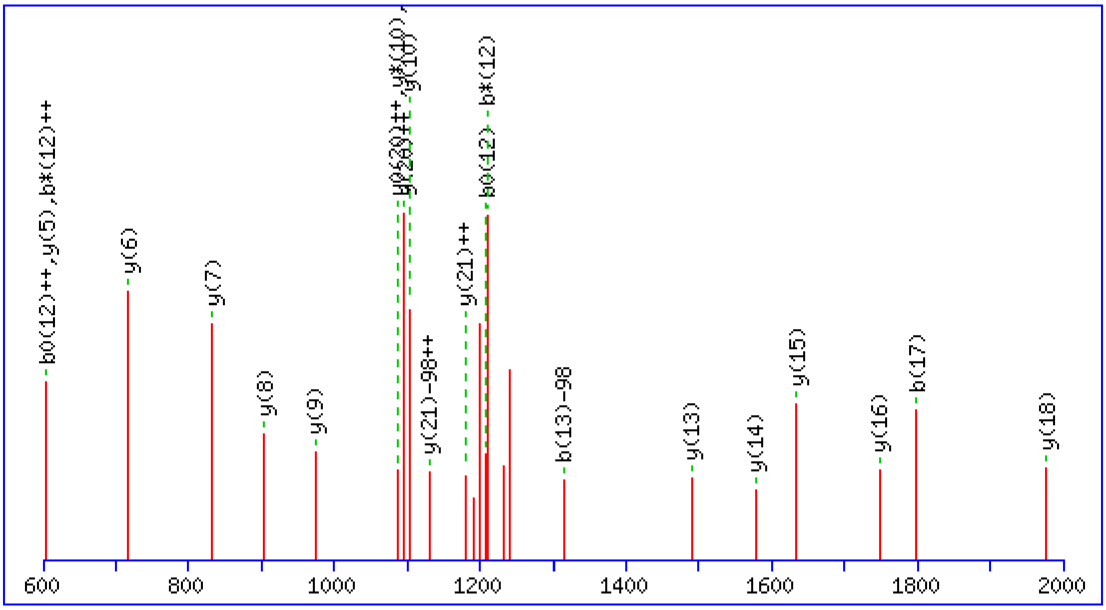
Monoisotopic mass of neutral peptide Mr(calc): 1235.5911
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0064
Matched b ions: b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)-98++, y(9)-98, y(9)++, y(10)-98++, y(10)++

Peptide No.835

SASPDDDLGSSNWEAADLGNEER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SASPDDDLGSSNWEAADLGNEER**
Found in **SMAP_MOUSE** in **SwissProt**, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 6229: 2513.976656 from(1257.995604,2+) index(6500)
Title: Elution from: 47.507 to 47.507 scan no 4862 cid35.00 polarity:+:m1s



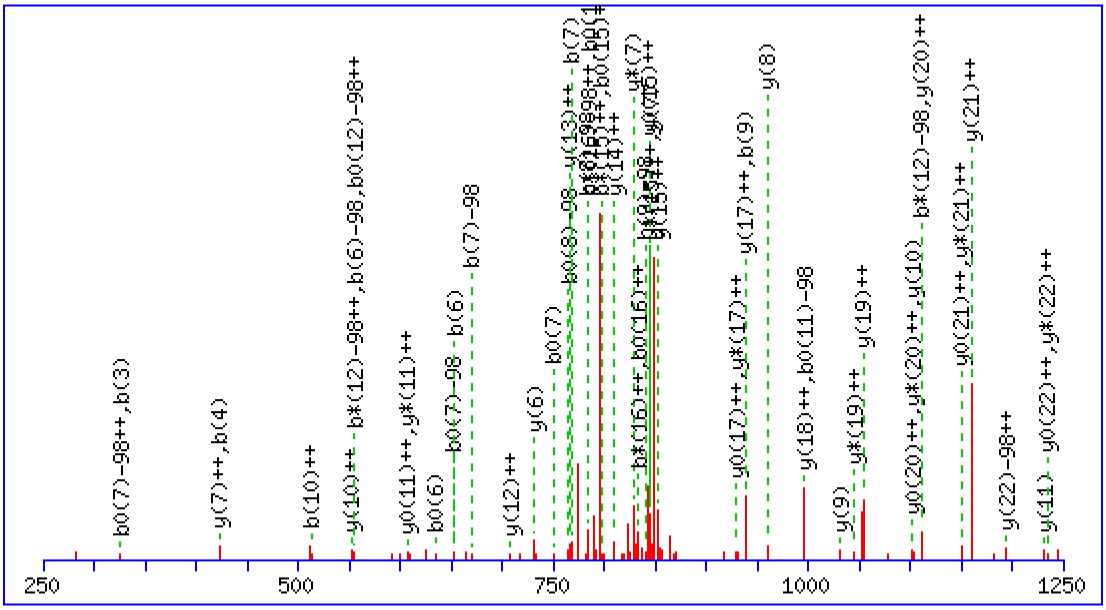
Monoisotopic mass of neutral peptide Mr(calc): 2513.9820
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 **Expect:** 1.4e-009
Matched b ions: b(13)-98, b(17)
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(13), y(14), y(15), y(16), y(18), y(20)++, y(21)-98++, y(21)++

Peptide No.836

SASPDDDLGSSNWEAADLGNEERK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SASPDDDLGSSNWEAADLGNEERK**
Found in **SMAP_MOUSE** in **SwissProt**, Small acidic protein OS=Mus musculus GN=Smap PE=1 SV=1

Match to Query 5401: 2642.077245 from(881.699691,3+) index(5230)
Title: Elution from: 41.640 to 41.640 scan no 4007 cid35.00 polarity:+:m1s



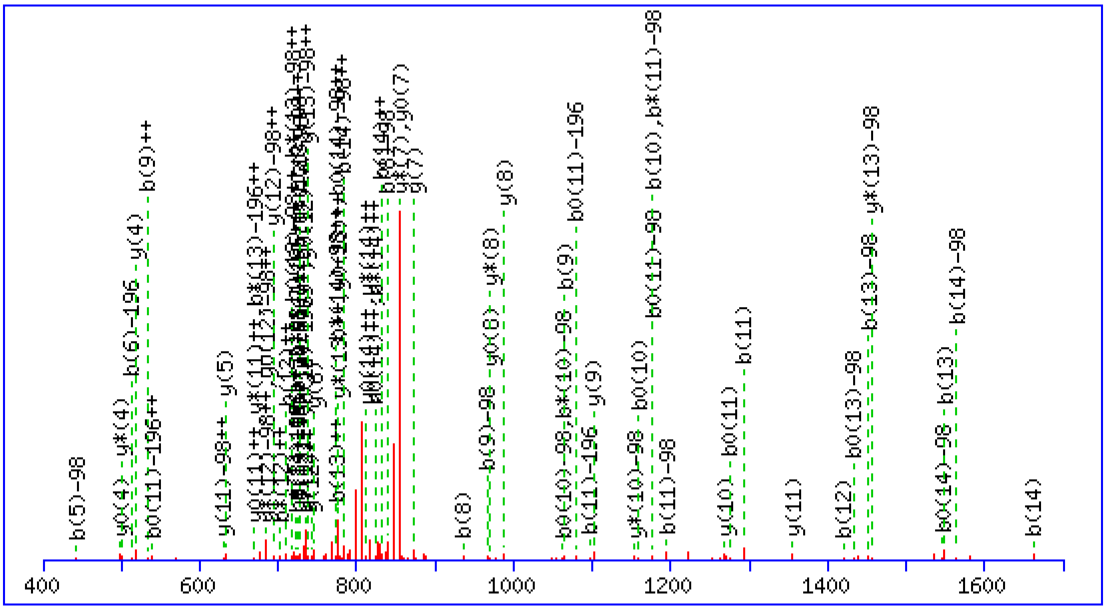
Monoisotopic mass of neutral peptide Mr(calc): 2642.0769
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 58 **Expect:** 8e-006
Matched b ions: b(3), b(4), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9), b(9)-98, b(10)++
Matched y ions: y(6), y(7)++, y(7), y(8), y(9), y(10)++, y(10), y(11), y(12)++, y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)-98++

Peptide No.837

SASQSSLDKLDQELK
Confirmed sites: @S:1,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SASQSSLDKLDQELK**
Found in **JIP4_MOUSE** in **SwissProt**, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 3626: 1807.762782 from(904.888667,2+) index(2202)
Title: Elution from: 40.801 to 40.801 scan no 3908 cid35.00 polarity:+



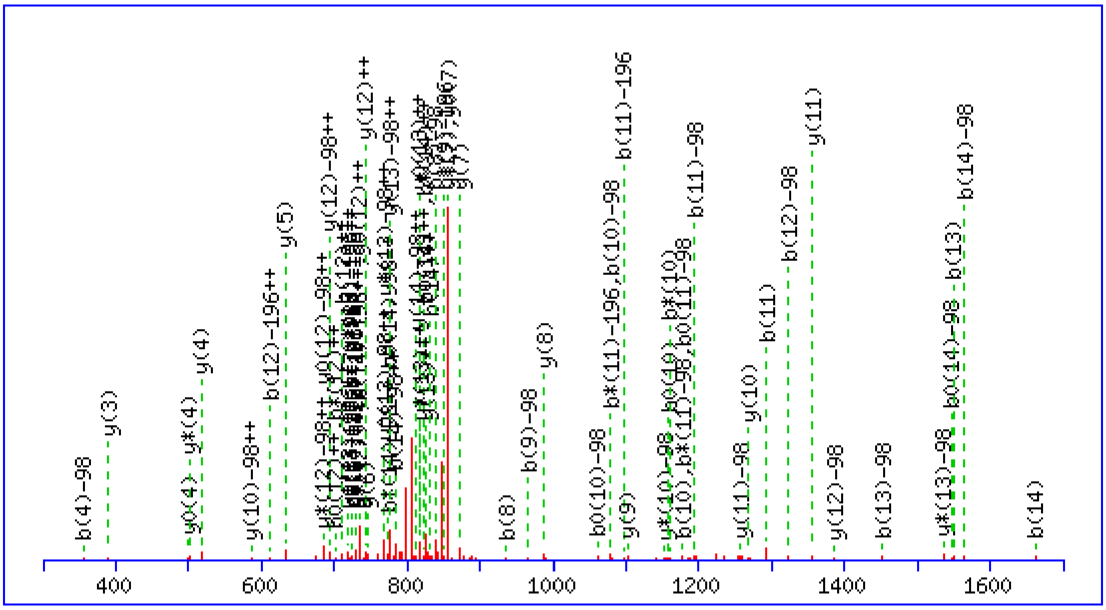
Monoisotopic mass of neutral peptide Mr(calc): 1807.7642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.0011
Matched b ions: b(5)-98, b(6)-196, b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(9)++, b(10), b(11)-98, b(11), b(11)-196, b(12), b(12)++, b(13), b(13)-98, b(13)-98++, b(13)++, b(14)-196++, b(14), b(14)-98, b(14)-98++, b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)-98++, y(12)-98++, y(12)++, y(13)-98++

Peptide No.838

SASQSSLDKLDQELK
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SASQSSLDKLDQELK**
Found in **JIP4_MOUSE** in **SwissProt**, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 3545: 1807.764436 from(904.889494,2+) index(5398)
Title: Elution from: 40.579 to 40.579 scan no 3892 cid35.00 polarity:+:m1s



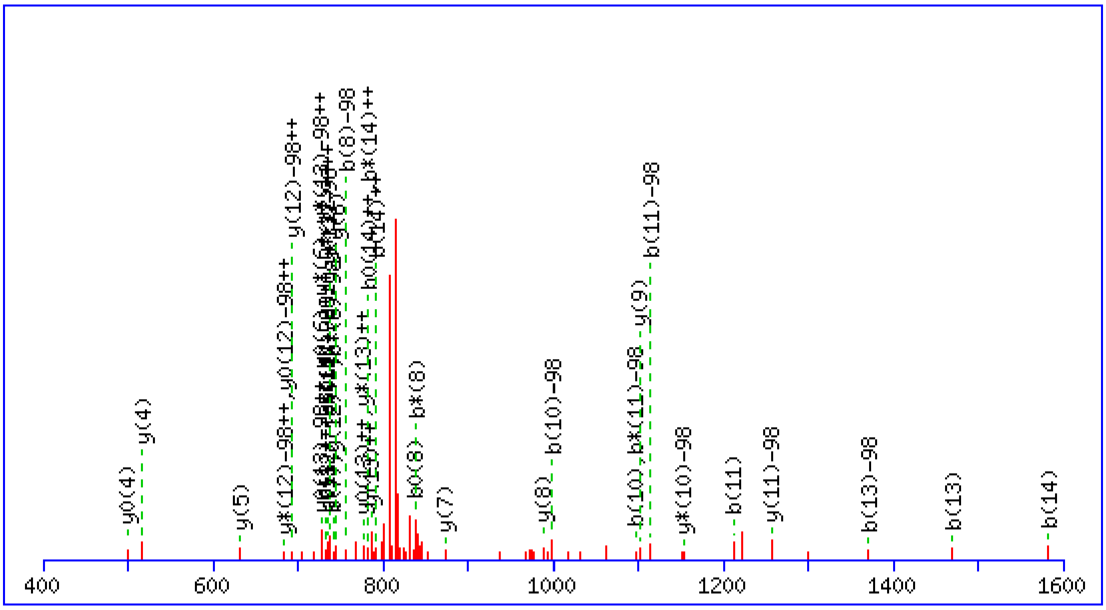
Monoisotopic mass of neutral peptide Mr(calc): 1807.7642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0072
Matched b ions: b(4)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(10)-98, b(10), b(11), b(11)-98, b(11)-196, b(12)-196++, b(12)-98, b(12)++, b(13)-98, b(13), b(14)-196++, b(14)-98, b(14), b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(11), y(11)-98, y(12)-98, y(12)-98++, y(12)++, y(13)-196++, y(13)-98++, y(13)++, y(14)-98++

Peptide No.839

SASQSSLDKLDQELK
Confirmed sites:
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of **SASQSSLDKLDQELK**
Found in **JIP4_MOUSE** in **SwissProt**, C-Jun-amino-terminal kinase-interacting protein 4 OS=Mus musculus GN=Spag9 PE=1 SV=2

Match to Query 3908: 1727.796588 from(864.905570,2+) index(2094)
Title: Elution from: 35.304 to 35.304 scan no 3346 cid35.00 polarity:+



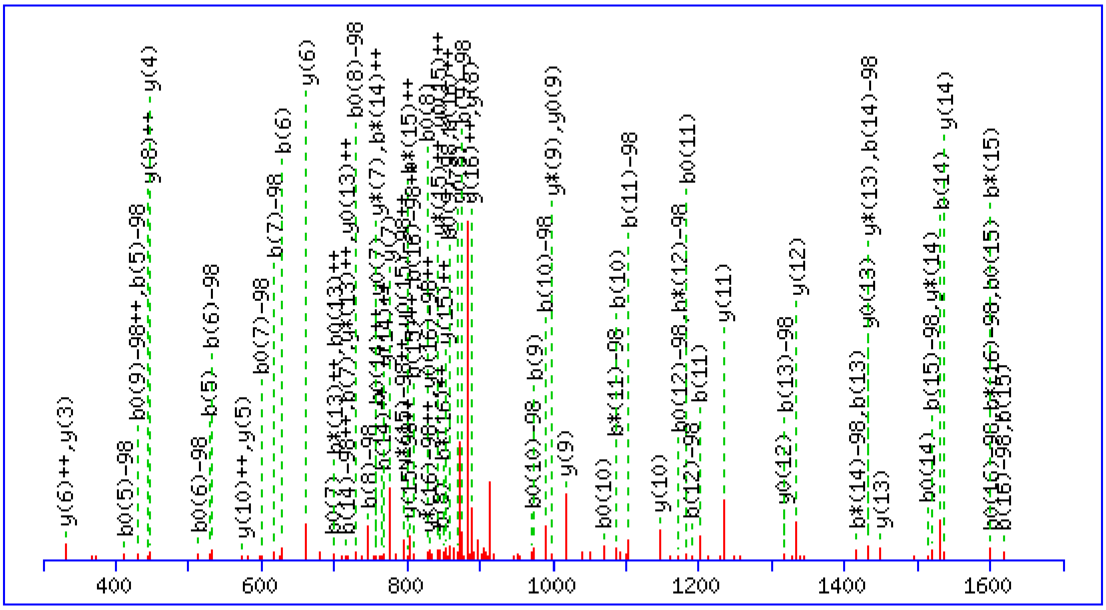
Monoisotopic mass of neutral peptide Mr(calc): 1727.7978
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.005
Matched b ions: b(7), b(8)-98, b(10)-98, b(10), b(11)-98, b(11), b(13)-98, b(13), b(13)++, b(14), b(14)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98, y(12)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.840

SASSDTSEELNSQDSPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SASSDTSEELNSQDSPK**
Found in **NHRF1_MOUSE** in **SwissProt**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3

Match to Query 4691: 1860.725508 from(931.370030,2+) index(576)
Title: Elution from: 29.215 to 29.215 scan no 1796 cid35.00 polarity:+



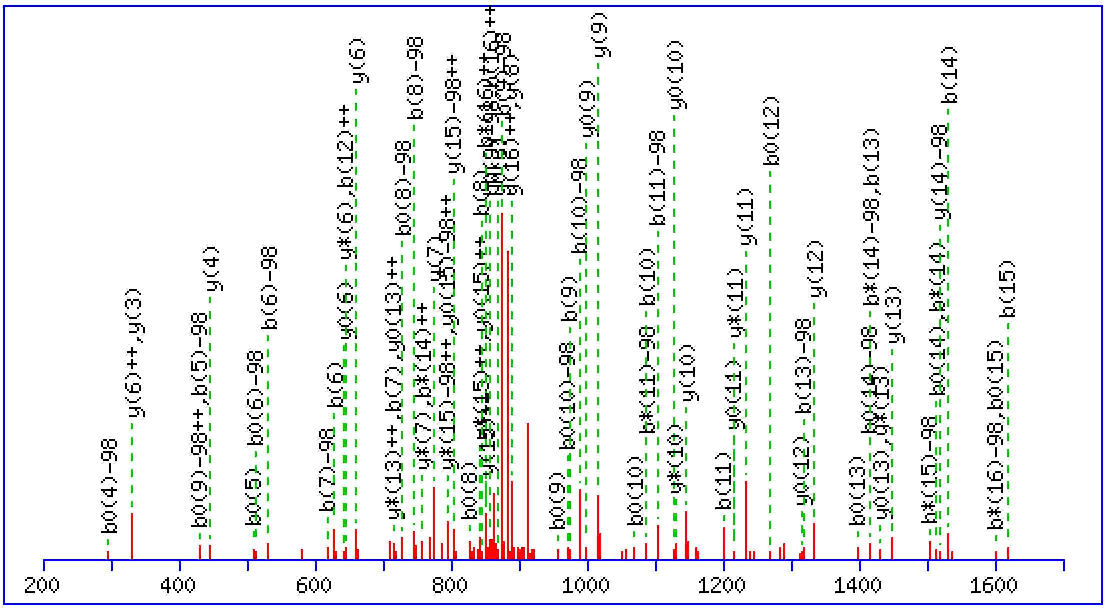
Monoisotopic mass of neutral peptide Mr(calc): 1860.7262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 **Expect:** 9.4e-009
Matched b ions: b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(14)-98++, b(14)++, b(15), b(15)-98, b(15)++, b(16)-98, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(9), y(10), y(10)++, y(11), y(12), y(13), y(14), y(14)++, y(15)-98++, y(15)++, y(16)++

Peptide No.841

SASSDTSEELNSQDSPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SASSDTSEELNSQDSPK**
Found in **NHRF1_MOUSE** in **SwissProt**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3

Match to Query 4066: 1860.726404 from(931.370478,2+) index(3386)
Title: Elution from: 29.094 to 29.094 scan no 1700 cid35.00 polarity:+:m1s



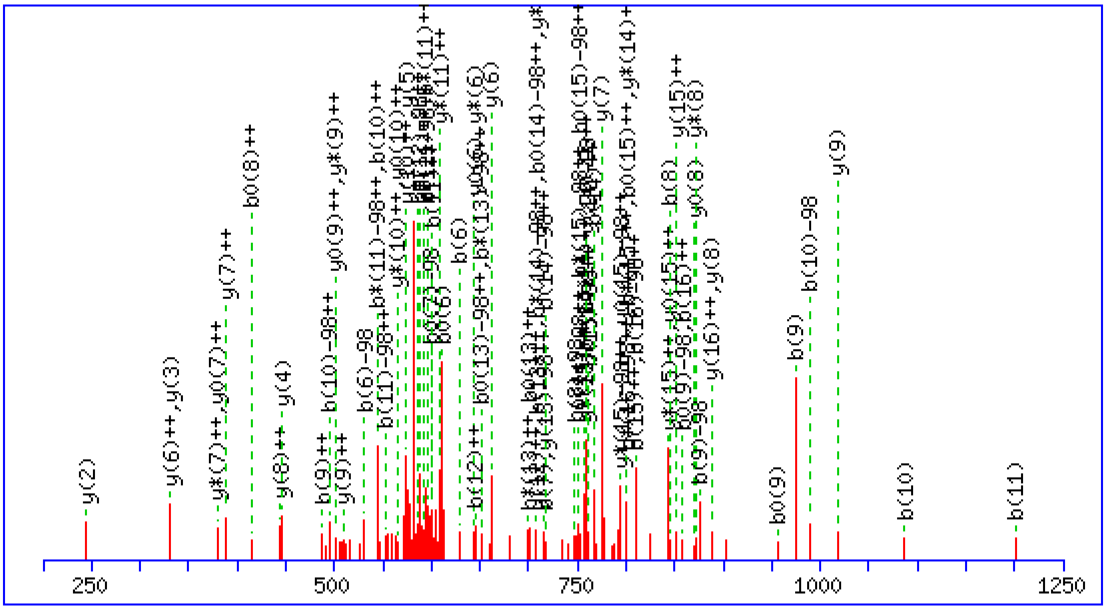
Monoisotopic mass of neutral peptide Mr(calc): 1860.7262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 2.6e-007
Matched b ions: b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(11), b(12)++, b(13), b(13)-98, b(14), b(15), b(16)++
Matched y ions: y(3), y(4), y(6)++, y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14)-98, y(15)++, y(15)-98++, y(16)++

Peptide No.842

SASSDTSEELNSQDSPK
Confirmed sites: @T:6
Ambiguous sites:

MS/MS Fragmentation of **SASSDTSEELNSQDSPK**
Found in **NHRF1_MOUSE** in **SwissProt**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3

Match to Query 4304: 1860.725691 from(621.249173,3+) index(4345)
Title: Elution from: 23.477 to 23.477 scan no 1710 cid35.00 polarity:+:m1s



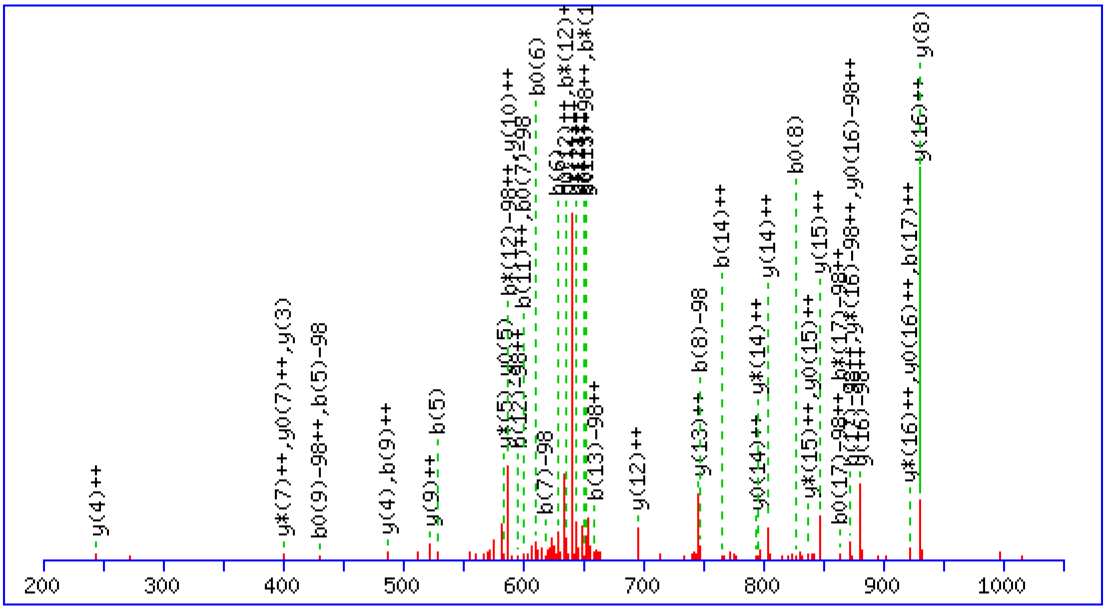
Monoisotopic mass of neutral peptide Mr(calc): 1860.7262
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 5.7e-005
Matched b ions: b(6)-98, b(6), b(7), b(8), b(8)-98, b(9)-98, b(9), b(9)++, b(10)++, b(10), b(10)-98, b(10)-98++, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(12)++, y(13)-98++, y(14)-98++, y(15)++, y(16)++

Peptide No.843

SASSDTSEELNSQDSPKR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SASSDTSEELNSQDSPKR**
Found in **NHRF1_MOUSE** in **SwissProt**, Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Mus musculus GN=Slc9a3r1 PE=1 SV=3

Match to Query 4229: 2016.825762 from(673.282530,3+) index(3537)
Title: Elution from: 20.864 to 20.864 scan no 1334 cid35.00 polarity:+:m1s



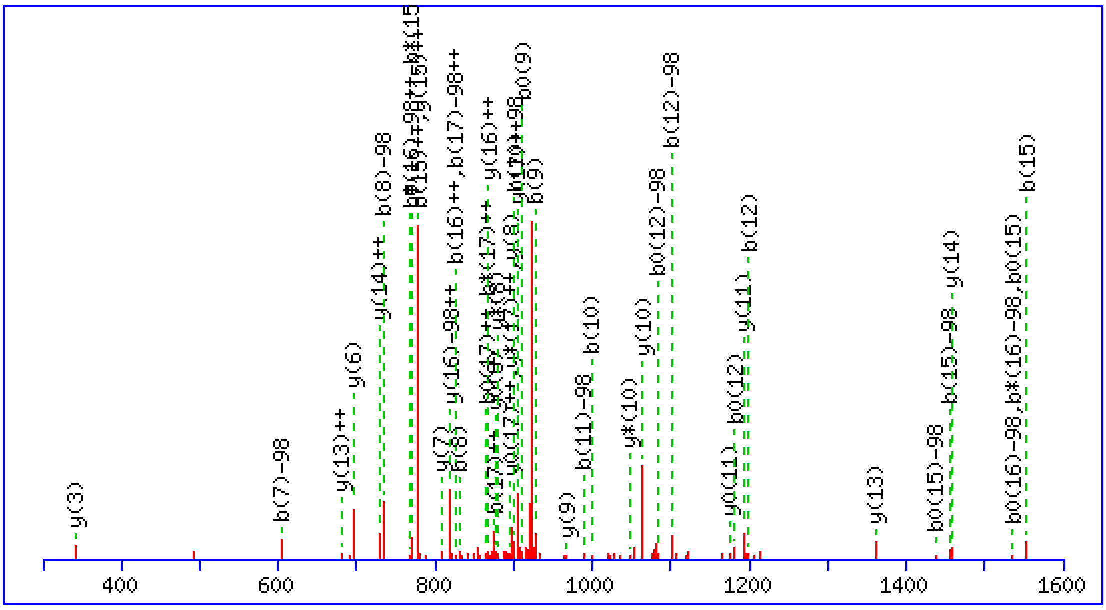
Monoisotopic mass of neutral peptide Mr(calc): 2016.8273
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0011
Matched b ions: b(5)-98, b(5), b(6), b(7)-98, b(8)-98, b(9)++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(14)++, b(17)-98++, b(17)++
Matched y ions: y(3), y(4)++, y(4), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++

Peptide No.844

SATPPPAEPASLPQEPPK
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **SATPPPAEPASLPQEPPK**
Found in **G3BP2_MOUSE** in **SwissProt**, Ras GTPase-activating protein-binding protein 2 OS=Mus musculus GN=G3bp2 PE=1 SV=2

Match to Query 4415: 1892.888772 from(947.451662,2+) index(1716)
Title: Elution from: 32.166 to 32.166 scan no 2892 cid35.00 polarity:+



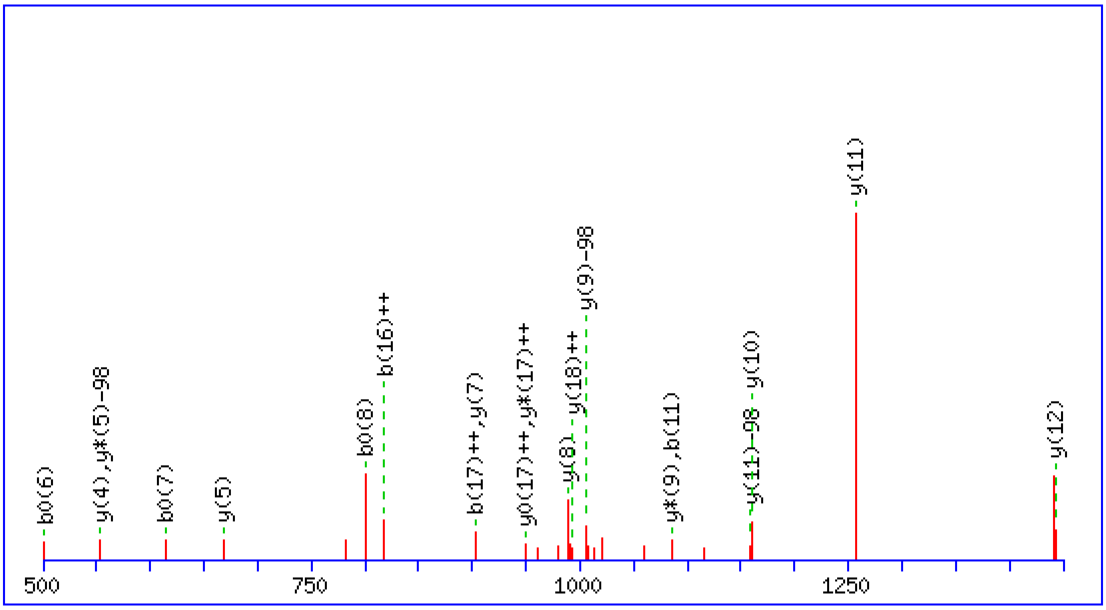
Monoisotopic mass of neutral peptide Mr(calc): 1892.8921
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 0.00011
Matched b ions: b(7)-98, b(8)-98, b(8), b(9), b(10), b(10)-98, b(11)-98, b(12)-98, b(12), b(15)++, b(15), b(15)-98, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(13)++, y(14), y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)++

Peptide No.845

SATSGDIWPGLSAYDNSPR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **SATSGDIWPGLSAYDNSPR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 5214: 2072.882222 from(1037.448387,2+) index(6930)
Title: Elution from: 53.891 to 53.891 scan no 5595 cid35.00 polarity:+:m1s



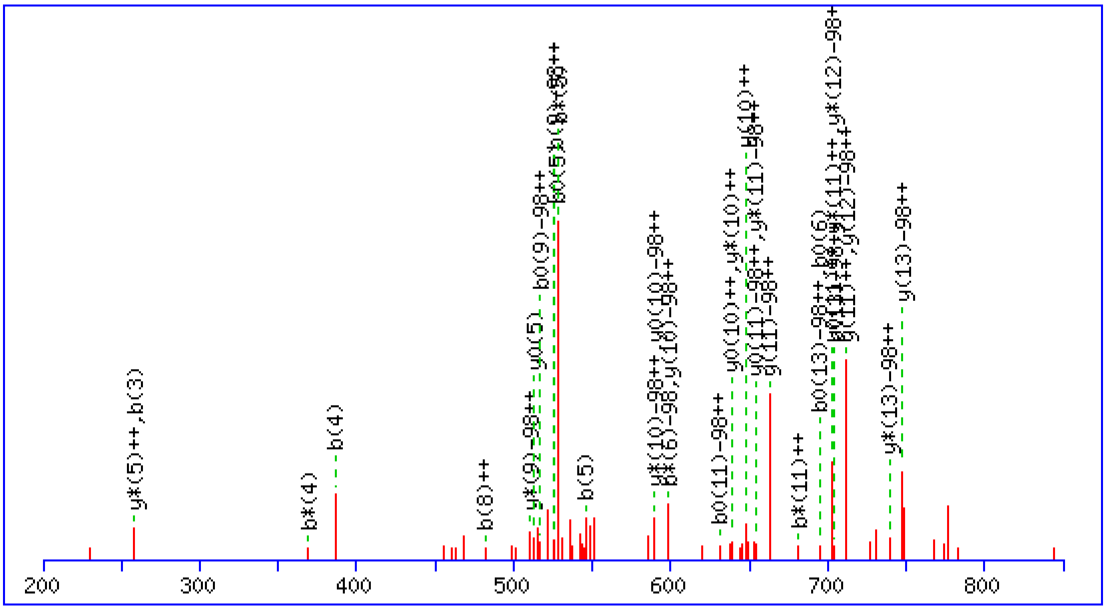
Monoisotopic mass of neutral peptide Mr(calc): 2072.8840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00028
Matched b ions: b(8), b(11), b(16)++, b(17)++
Matched y ions: y(4), y(5), y(7), y(8), y(9)-98, y(10), y(11), y(11)-98, y(12), y(18)++

Peptide No.846

SAVQCSHLWDIAGR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SAVQCSHLWDIAGR**
Found in **K1984_MOUSE** in **SwissProt**, Uncharacterized coiled-coil domain-containing protein KIAA1984 OS=Mus musculus GN=Kiaa1984 PE=2 SV=1

Match to Query 3716: 1678.730067 from(560.583965,3+) index(1119)
Title: Elution from: 25.643 to 25.643 scan no 2040 cid35.00 polarity:+



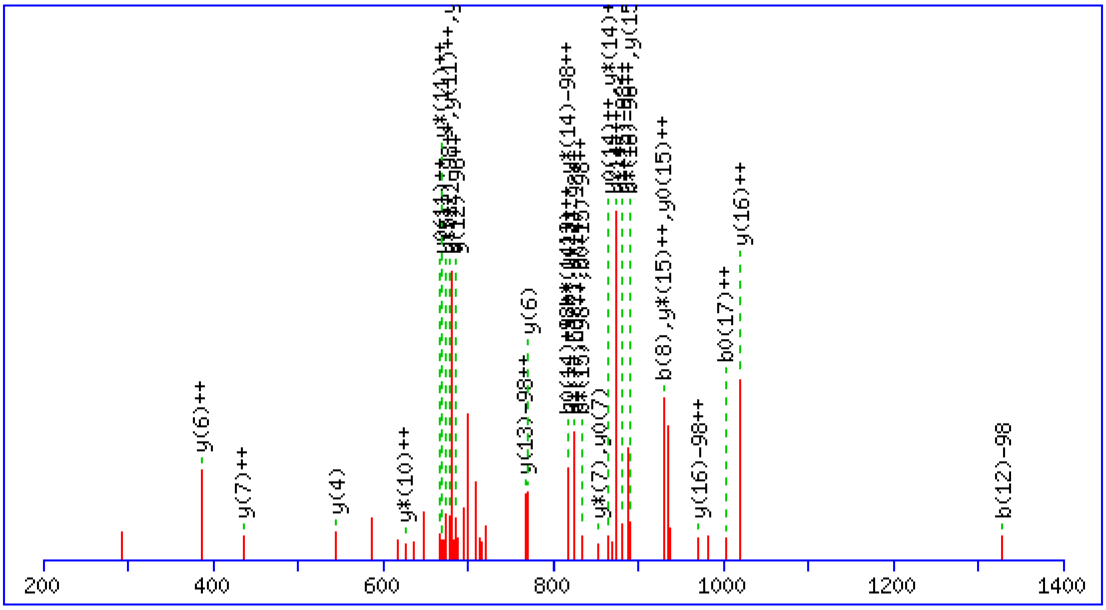
Monoisotopic mass of neutral peptide Mr(calc): 1678.7287
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(3), b(4), b(5), b(8)++, b(9)-98++, b(13)-98++
Matched y ions: y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(13)-98++

Peptide No.847

SAYQDYDSDSDVPEELKR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SAYQDYDSDSDVPEELKR**
Found in **CC132_MOUSE** in **SwissProt**, Coiled-coil domain-containing protein 132 OS=Mus musculus GN=Ccdc132 PE=1 SV=2

Match to Query 5745: 2195.889570 from(732.970466,3+) index(5862)
Title: Elution from: 36.517 to 36.517 scan no 3509 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2195.8896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0092
Matched b ions: b(8), b(12)-98
Matched y ions: y(4), y(5), y(6)++, y(6), y(7)++, y(11)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.848

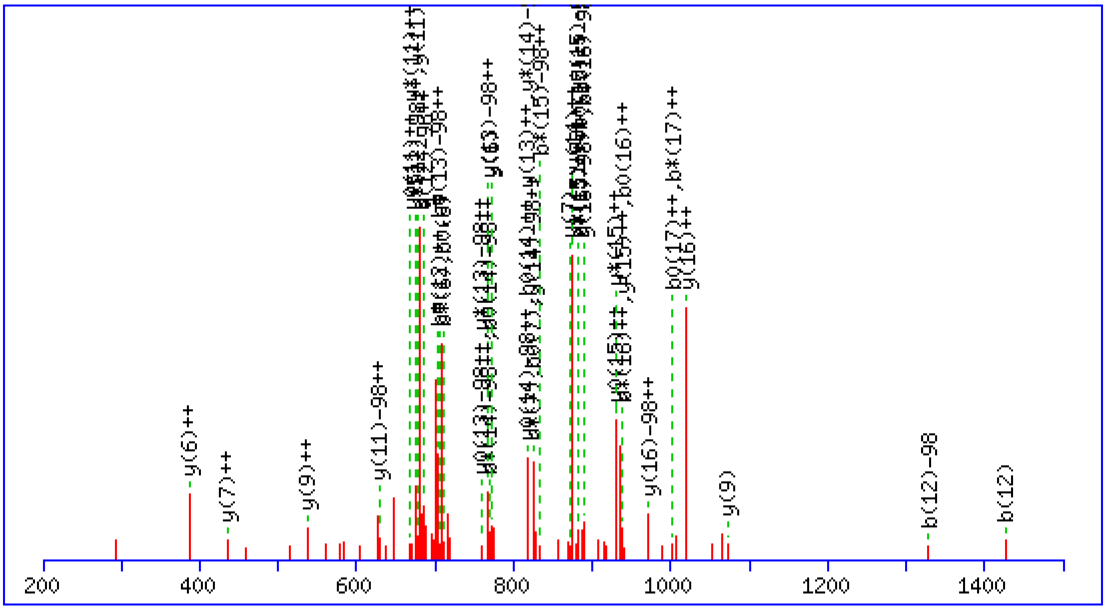
SAYQDYDSDSDVPEELKR

Confirmed sites: @S:8

Ambiguous sites:

MS/MS Fragmentation of **SAYQDYDSDSDVPEELKR**
Found in **CC132_MOUSE** in **SwissProt**, Coiled-coil domain-containing protein 132 OS=Mus musculus GN=Ccdc132 PE=1 SV=2

Match to Query 5602: 2195.890269 from(732.970699,3+) index(5711)
Title: Elution from: 36.667 to 36.667 scan no 3499 cid35.00 polarity:+:m1s



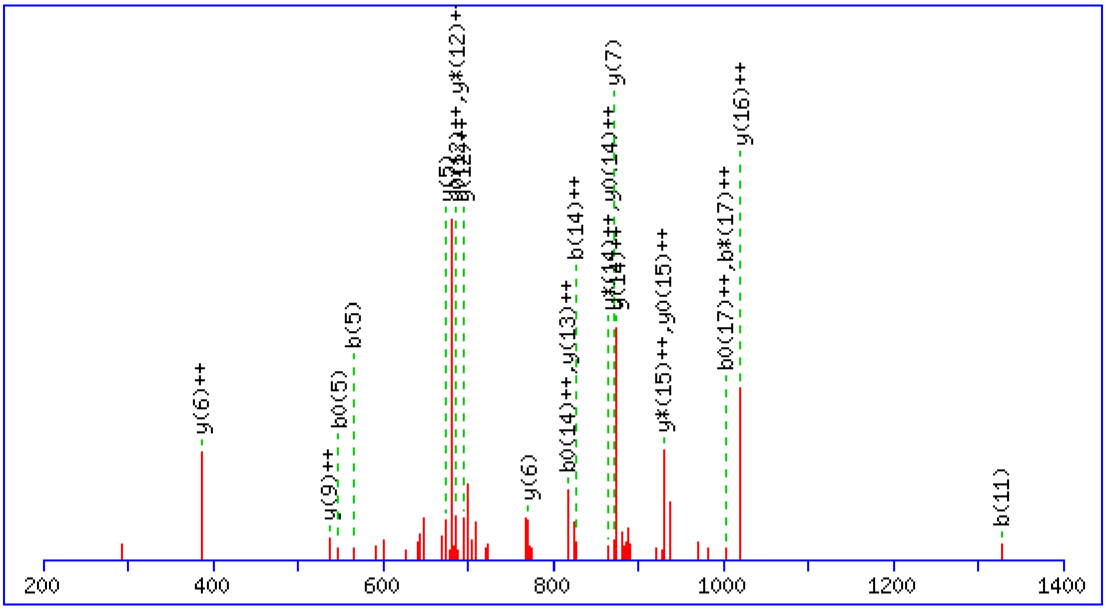
Monoisotopic mass of neutral peptide Mr(calc): 2195.8896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0063
Matched b ions: b(12)-98, b(12)
Matched y ions: y(5), y(6)++, y(6), y(7)++, y(7), y(9)++, y(9), y(11)++, y(11)-98++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.849

SAYQDYDSDSDVPEELKR
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of **SAYQDYDSDSDVPEELKR**
Found in **CC132_MOUSE** in **SwissProt**, Coiled-coil domain-containing protein 132 OS=Mus musculus GN=Ccdc132 PE=1 SV=2

Match to Query 4764: 2195.886597 from(732.969475,3+) index(4819)
Title: Elution from: 36.196 to 36.196 scan no 3316 cid35.00 polarity:+:m1s



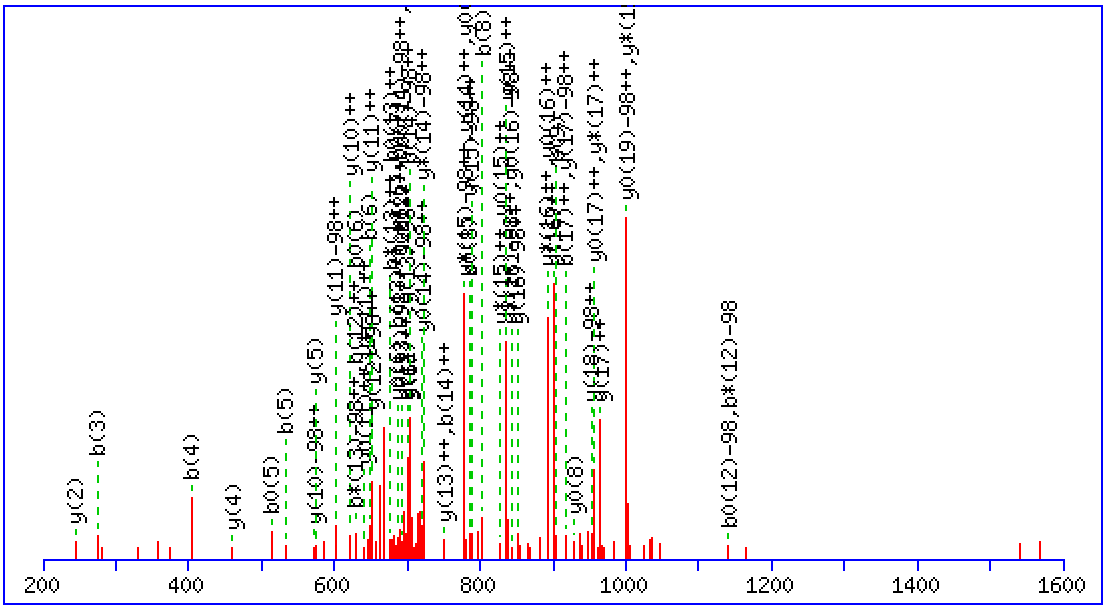
Monoisotopic mass of neutral peptide Mr(calc): 2195.8896
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
Ions Score: 27 **Expect:** 0.013
Matched b ions: b(5), b(11), b(14)++
Matched y ions: y(5), y(6)++, y(6), y(7), y(9)++, y(12)++, y(13)++, y(14)++, y(16)++

Peptide No.850

SDAEEDGVTGSQDEEDSKPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **SDAEEDGVTGSQDEEDSKPK**
Found in **CALX_MOUSE** in **SwissProt**, Calnexin OS=Mus musculus GN=Canx PE=1 SV=1

Match to Query 5593: 2201.850321 from(734.957383,3+) index(3564)
Title: Elution from: 24.096 to 24.096 scan no 1212 cid35.00 polarity:+:m1s



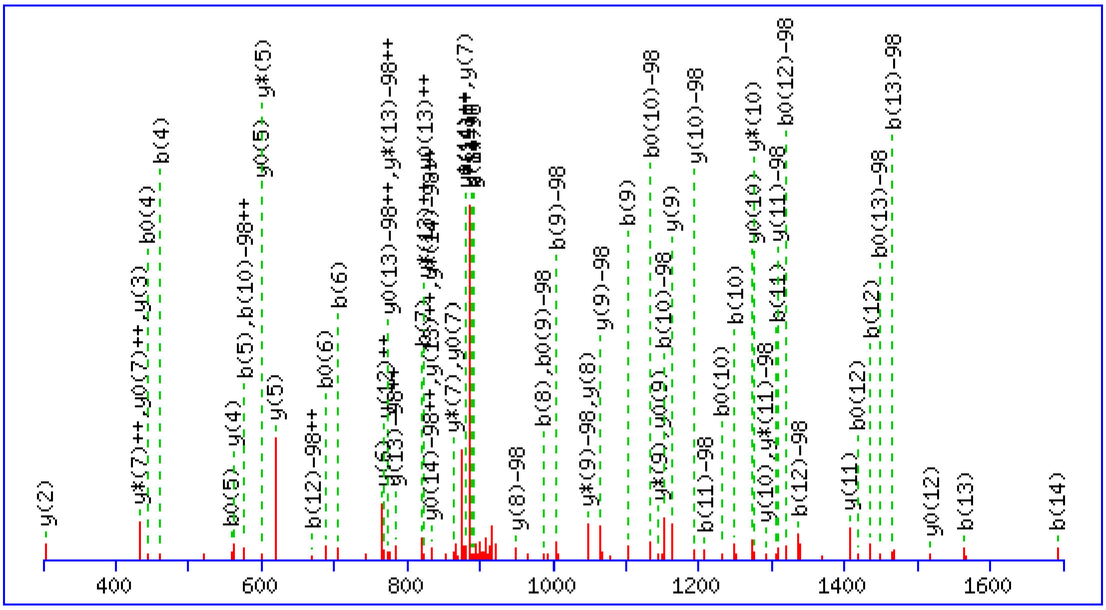
Monoisotopic mass of neutral peptide Mr(calc): 2201.8485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00018
Matched b ions: b(3), b(4), b(5), b(6), b(8), b(9), b(12)++, b(13)++, b(14)-98++, b(14)++, b(17)++
Matched y ions: y(2), y(4), y(5), y(6), y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++

Peptide No.851

SDEEDEDSDFGEEQR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SDEEDEDSDFGEEQR**
Found in **GPAT1_MOUSE** in **SwissProt**, Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Mus musculus GN=Gpam PE=1 SV=2

Match to Query 4452: 1865.606468 from(933.810510,2+) index(4765)
Title: Elution from: 25.599 to 25.599 scan no 2034 cid35.00 polarity:+:m1s



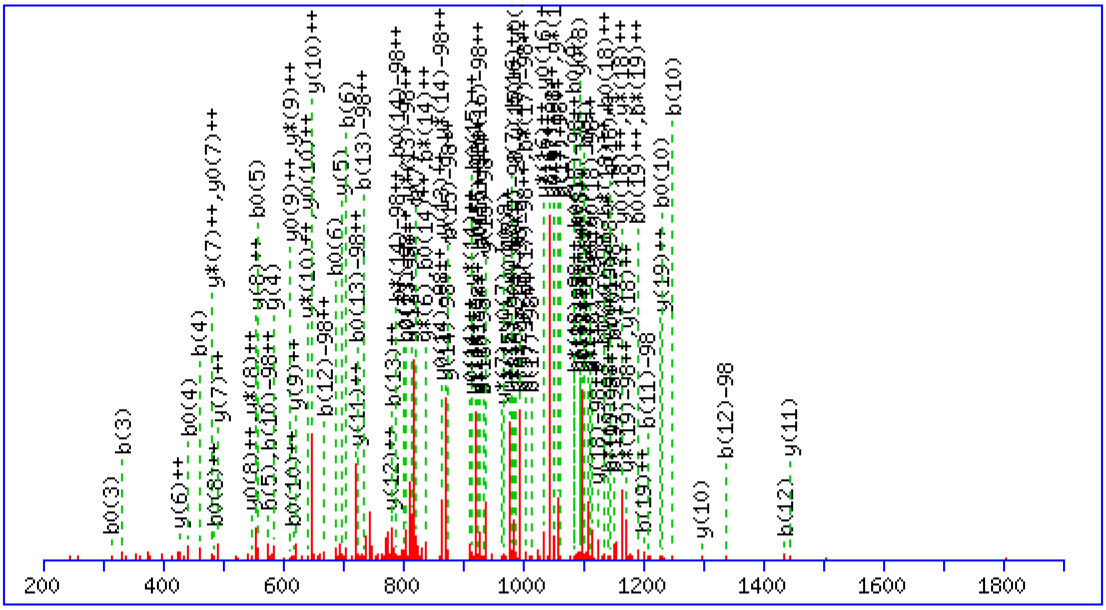
Monoisotopic mass of neutral peptide Mr(calc): 1865.6112
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 6.5e-006
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(11)-98, b(11), b(12)-98, b(12), b(12)-98++, b(13), b(13)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(10), y(10)-98, y(11), y(11)-98, y(12)++, y(13)-98++, y(13)++, y(14)++

Peptide No.852

SDEEDEDSDFGEEQRDCYLK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SDEEDEDSDFGEEQRDCYLK**
Found in **GPAT1_MOUSE** in **SwissProt**, Glycerol-3-phosphate acyltransferase 1, mitochondrial OS=Mus musculus GN=Gpam PE=1 SV=2

Match to Query 6462: 2544.909588 from(849.310472,3+) index(5855)
Title: Elution from: 36.436 to 36.436 scan no 3498 cid35.00 polarity:+:m1s



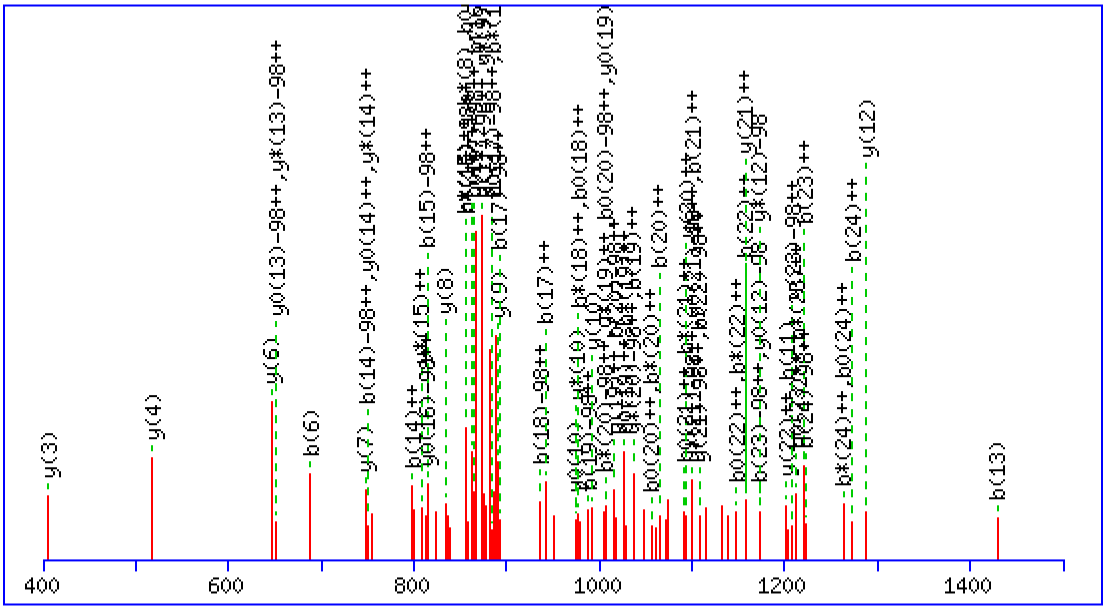
Monoisotopic mass of neutral peptide Mr(calc): 2544.9112
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 78 **Expect:** 4.4e-008
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(9), b(10), b(10)-98++, b(10)-98, b(11)-98, b(12), b(12)-98, b(12)-98++, b(13)++, b(13)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(4), y(5), y(6)++, y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(10), y(11)++, y(11), y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)++

Peptide No.853

SDISERPSVDDVESETGSTGALETR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **SDISERPSVDDVESETGSTGALETR**
Found in **C2C2L_MOUSE** in **SwissProt**, C2 domain-containing protein 2-like OS=Mus musculus GN=C2cd2l PE=1 SV=2

Match to Query 6482: 2716.167153 from(906.396327,3+) index(5797)
Title: Elution from: 37.591 to 37.591 scan no 3621 cid35.00 polarity:+:m1s



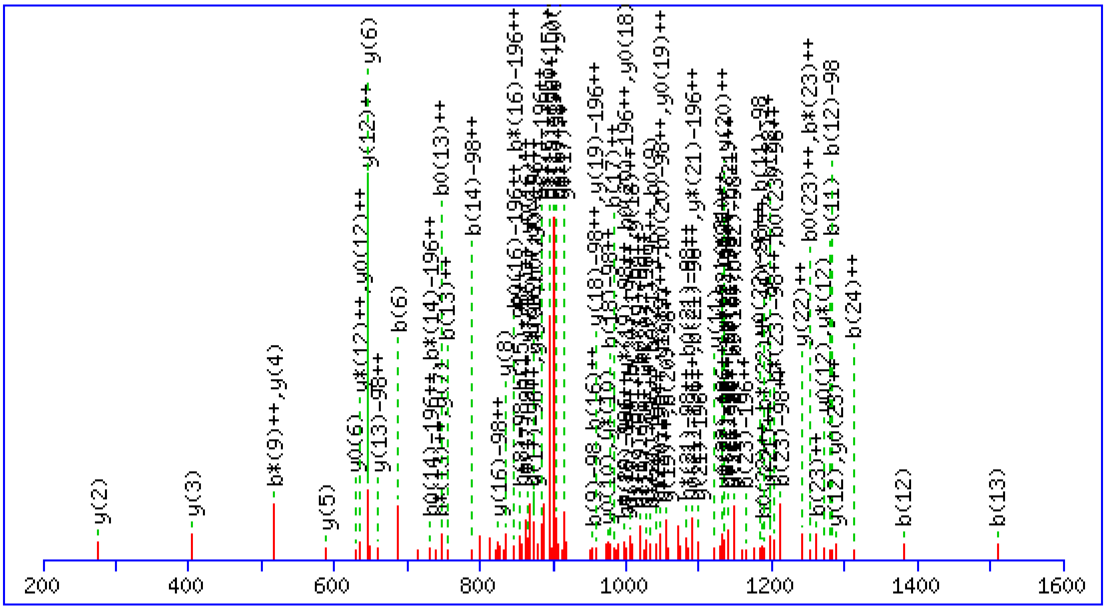
Monoisotopic mass of neutral peptide Mr(calc): 2716.1712
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00015
Matched b ions: b(6), b(11), b(13), b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)++, b(17)-98++, b(18)-98++, b(19)++, b(19)-98++, b(20)-98++, b(20)++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(24)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(12), y(16)++, y(17)-98++, y(19)++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)-98++

Peptide No.854

SDISERPSVDDVESETGSTGALETR
Confirmed sites: @S:8,@S:14
Ambiguous sites:

MS/MS Fragmentation of **SDISERPSVDDVESETGSTGALETR**
Found in **C2C2L_MOUSE** in **SwissProt**, C2 domain-containing protein 2-like OS=Mus musculus GN=C2cd2l PE=1 SV=2

Match to Query 5576: 2796.137691 from(933.053173,3+) index(4999)
Title: Elution from: 38.164 to 38.164 scan no 3574 cid35.00 polarity:+:m1s



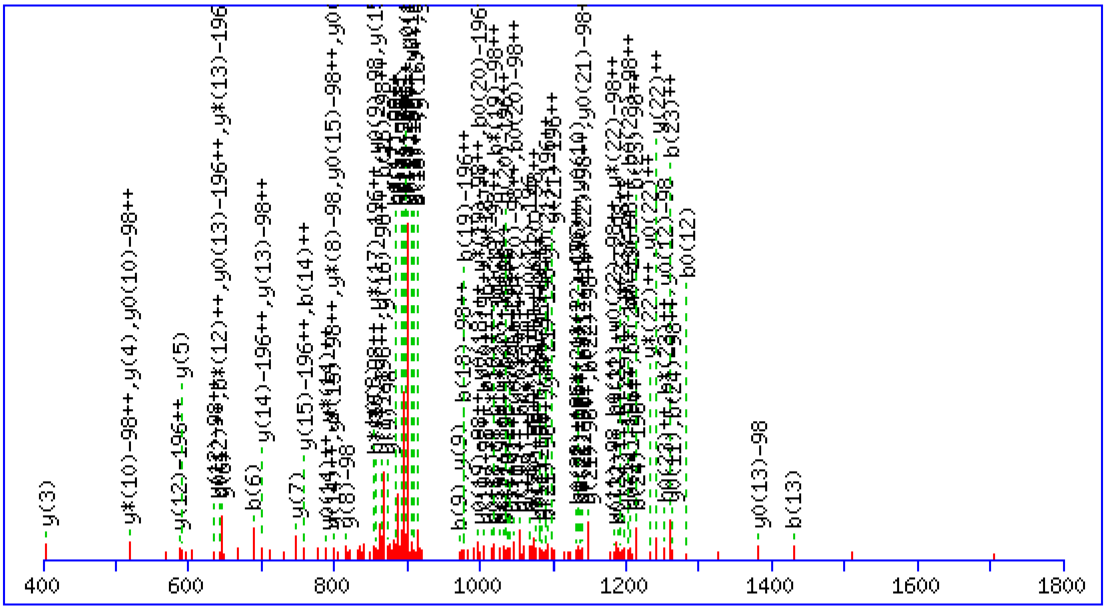
Monoisotopic mass of neutral peptide Mr(calc): 2796.1376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00029
Matched b ions: b(6), b(8)-98, b(9)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)++, b(14)-98++, b(15)-98++, b(16)-98++, b(16)++, b(17)-196++, b(17)++, b(18)-98++, b(19)-98++, b(20)-98++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(23)-196++, b(24)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(11), y(12), y(12)++, y(13)-98++, y(16)++, y(16)-98++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(19)-196++, y(20)++, y(21)-98++, y(21)-196++, y(21)++, y(22)++

Peptide No.855

SDISERPSVDDVESETGSTGALETR
Confirmed sites: @T:16,@S:18
Ambiguous sites:

MS/MS Fragmentation of **SDISERPSVDDVESETGSTGALETR**
Found in **C2C2L_MOUSE** in **SwissProt**, C2 domain-containing protein 2-like OS=Mus musculus GN=C2cd2l PE=1 SV=2

Match to Query 6763: 2796.133527 from(933.051785,3+) index(6080)
Title: Elution from: 38.859 to 38.859 scan no 3818 cid35.00 polarity:+:m1s



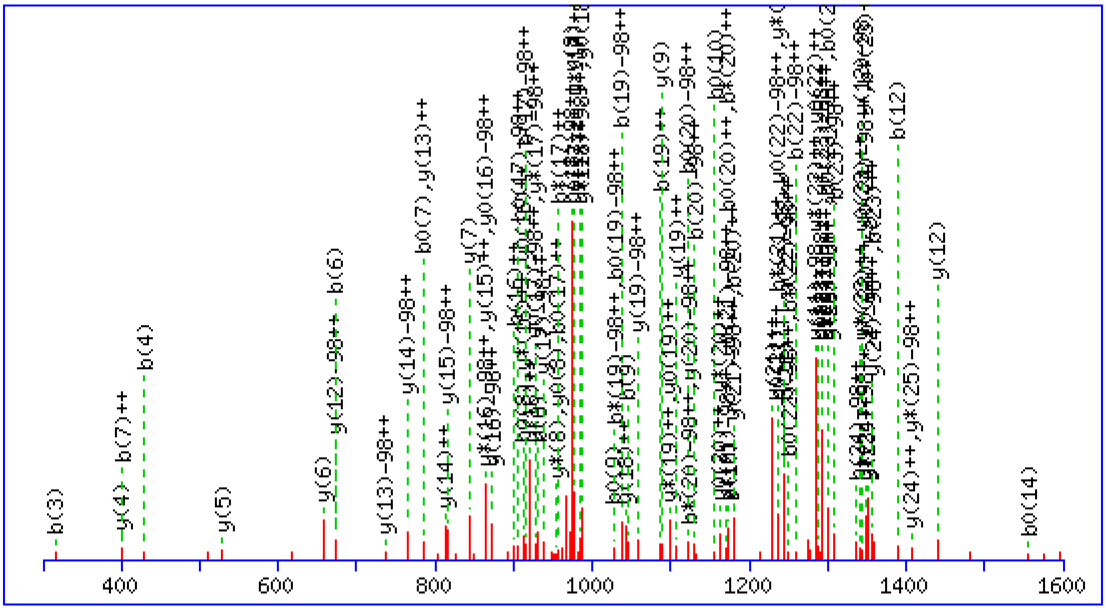
Monoisotopic mass of neutral peptide Mr(calc): 2796.1376
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.035
Matched b ions: b(6), b(9), b(13), b(14)++, b(16)++, b(16)-98++, b(17)-98++, b(18)-98++, b(19)-196++, b(19)-98++, b(19)++, b(20)-98++, b(20)-196++, b(21)-98++, b(21)++, b(21)-196++, b(22)-98++, b(22)++, b(23)++, b(23)-98++, b(24)-196++, b(24)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98, y(9), y(11)-196, y(11)-98, y(12)-196++, y(12)-98++, y(13)-98++, y(14)++, y(14)-196++, y(15)-196++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(17)-196++, y(18)-196++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-196++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)++, y(22)-98++

Peptide No.856

SDLIEDEELEDTGKGSEDEWEQVGPK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **SDLIEDEELEDTGKGSEDEWEQVGPK**
Found in **UBP10_MOUSE** in **SwissProt**, Ubiquitin carboxyl-terminal hydrolase 10 OS=Mus musculus GN=Usp10 PE=1 SV=3

Match to Query 5699: 3013.259175 from(1005.427001,3+) index(5602)
Title: Elution from: 48.380 to 48.380 scan no 4792 cid35.00 polarity:+:m1s



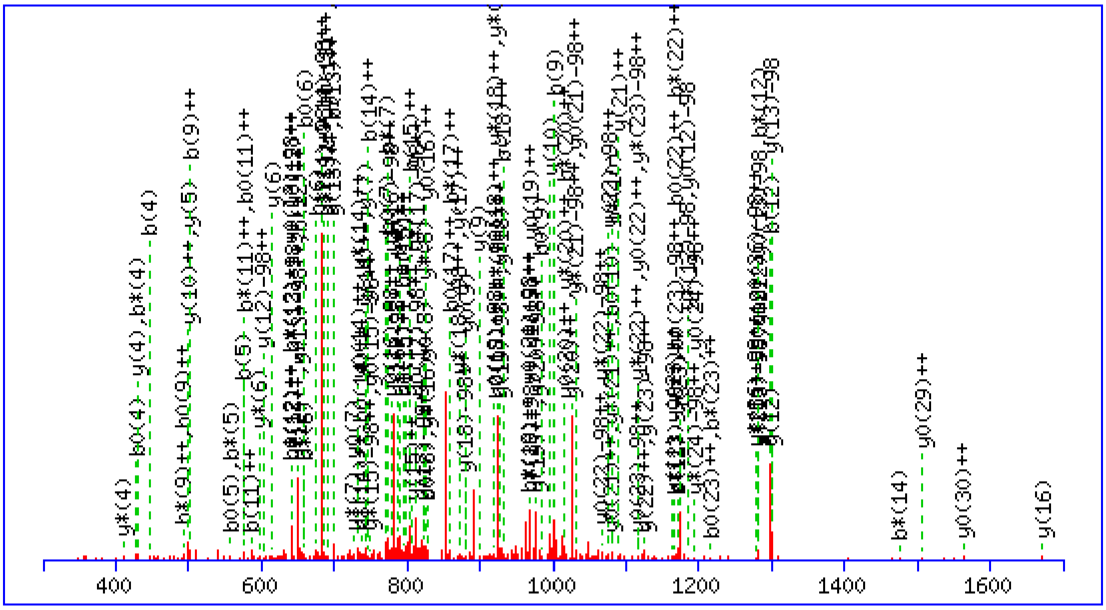
Monoisotopic mass of neutral peptide Mr(calc): 3013.2601
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 93 **Expect:** 3.8e-009
Matched b ions: b(3), b(4), b(6), b(7)++, b(8), b(9), b(10), b(11), b(12), b(16)++, b(17)-98++, b(18)-98++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11)-98, y(12), y(12)-98++, y(12)-98, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)-98++, y(24)++

Peptide No.857

SDNEETLGRPAQPPNAGESPHSPGVEDAPIAK
Confirmed sites: @S:22
Ambiguous sites:

MS/MS Fragmentation of **SDNEETLGRPAQPPNAGESPHSPGVEDAPIAK**
Found in **LIMA1_MOUSE** in **SwissProt**, LIM domain and actin-binding protein 1 OS=Mus musculus GN=Lima1 PE=1 SV=3

Match to Query 5763: 3346.510264 from(837.634842,4+) index(4211)
Title: Elution from: 38.788 to 38.788 scan no 2853 cid35.00 polarity:+:m1s



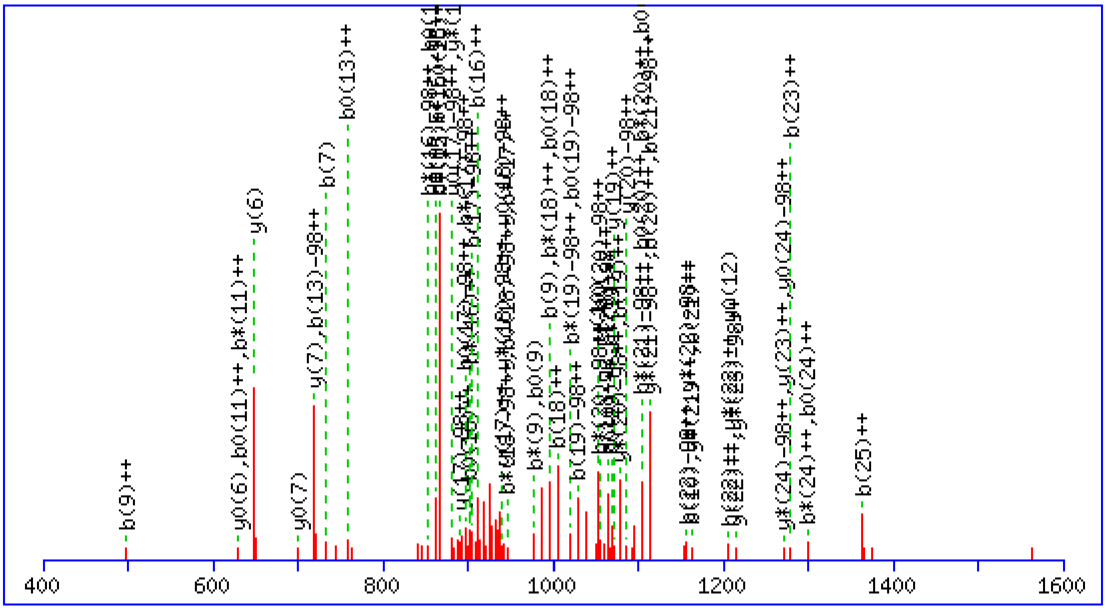
Monoisotopic mass of neutral peptide Mr(calc): 3346.5103
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0048
Matched b ions: b(4), b(5), b(6), b(7), b(9)++, b(9), b(11)++, b(11), b(12), b(12)++, b(13)++, b(14)++, b(15)++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10)++, y(10), y(11), y(12)++, y(12), y(12)-98++, y(13)-98++, y(13)-98, y(13)++, y(14)++, y(15)++, y(16), y(16)-98++, y(17)-98++, y(17)++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(25)++

Peptide No.858

SEDDSAKFDSNEEDTASVFAPSFGLK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SEDDSAKFDSNEEDTASVFAPSFGLK**
Found in **TOP2B_MOUSE** in **SwissProt**, DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2

Match to Query 5629: 2872.197366 from(958.406398,3+) index(5771)
Title: Elution from: 55.333 to 55.333 scan no 5471 cid35.00 polarity:+:m1s



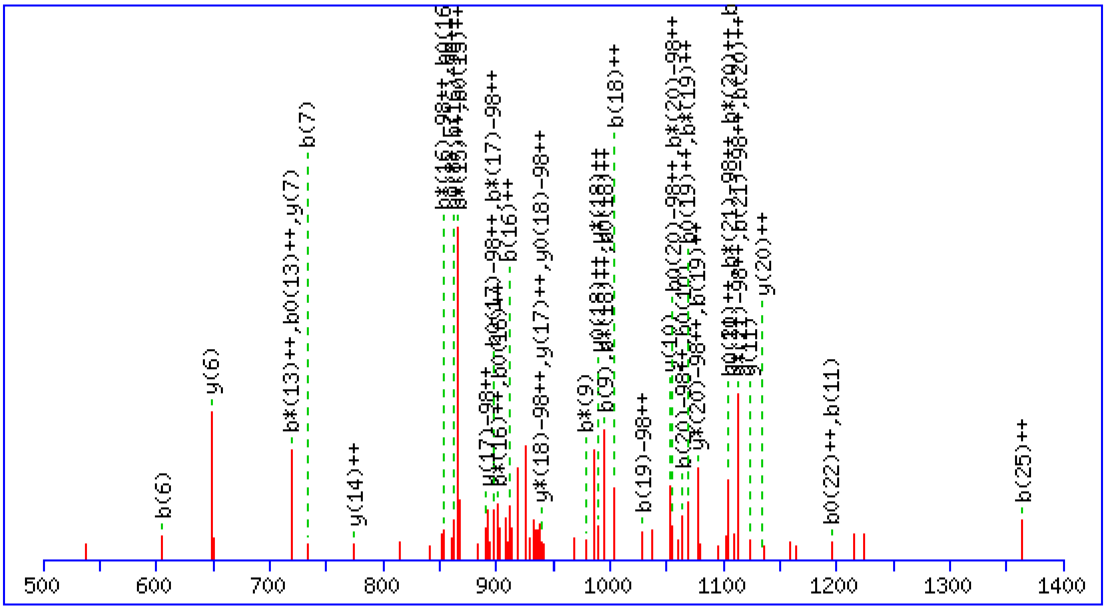
Monoisotopic mass of neutral peptide Mr(calc): 2872.1964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00016
Matched b ions: b(7), b(9)++, b(9), b(10)-98, b(10), b(13)-98++, b(16)-98++, b(16)++, b(17)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(25)++
Matched y ions: y(6), y(7), y(8), y(10), y(17)-98++, y(17)++, y(19)++, y(20)-98++, y(22)++, y(23)++

Peptide No.859

SEDDSAKFDSNEEDTASVFAPSFGLK
Confirmed sites: @T:15
Ambiguous sites:

MS/MS Fragmentation of **SEDDSAKFDSNEEDTASVFAPSFGLK**
Found in **TOP2B_MOUSE** in **SwissProt**, DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2

Match to Query 6817: 2872.194603 from(958.405477,3+) index(7011)
Title: Elution from: 56.156 to 56.156 scan no 5819 cid35.00 polarity:+:m1s



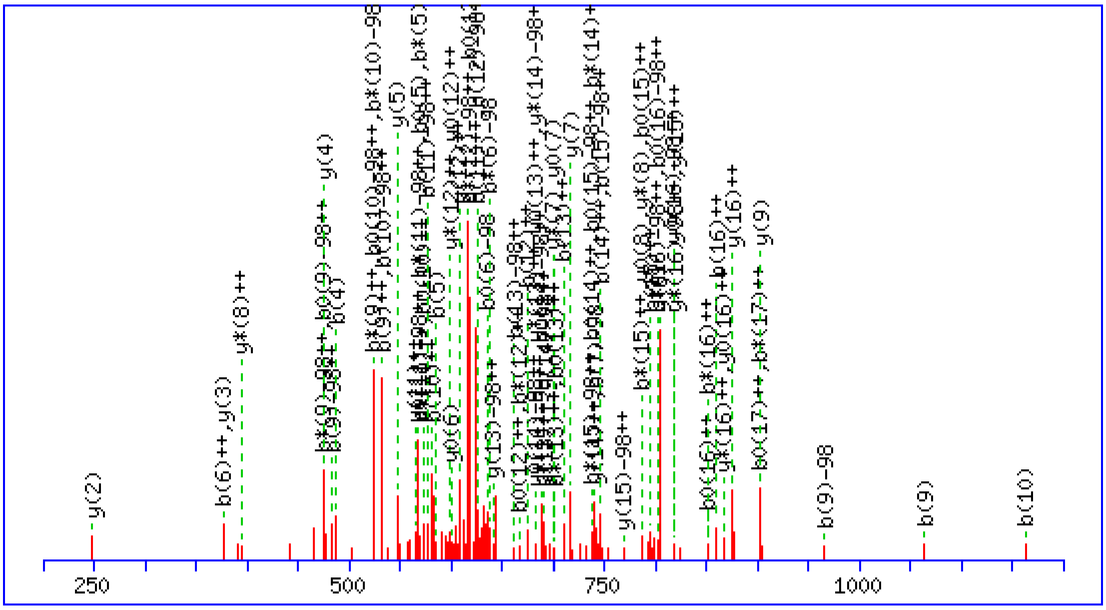
Monoisotopic mass of neutral peptide Mr(calc): 2872.1964
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.02
Matched b ions: b(6), b(7), b(9), b(11), b(16)++, b(16)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)-98++, b(25)++
Matched y ions: y(6), y(7), y(8), y(10), y(11), y(14)++, y(17)++, y(17)-98++, y(20)++

Peptide No.860

SEDRPSSPQVSVAAVETK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SEDRPSSPQVSVAAVETK**
Found in **TP53B_MOUSE** in **SwissProt**, Tumor suppressor p53-binding protein 1 OS=Mus musculus GN=Tp53bp1 PE=1 SV=2

Match to Query 4077: 1965.902889 from(656.308239,3+) index(4400)
Title: Elution from: 28.536 to 28.536 scan no 2372 cid35.00 polarity:+:m1s



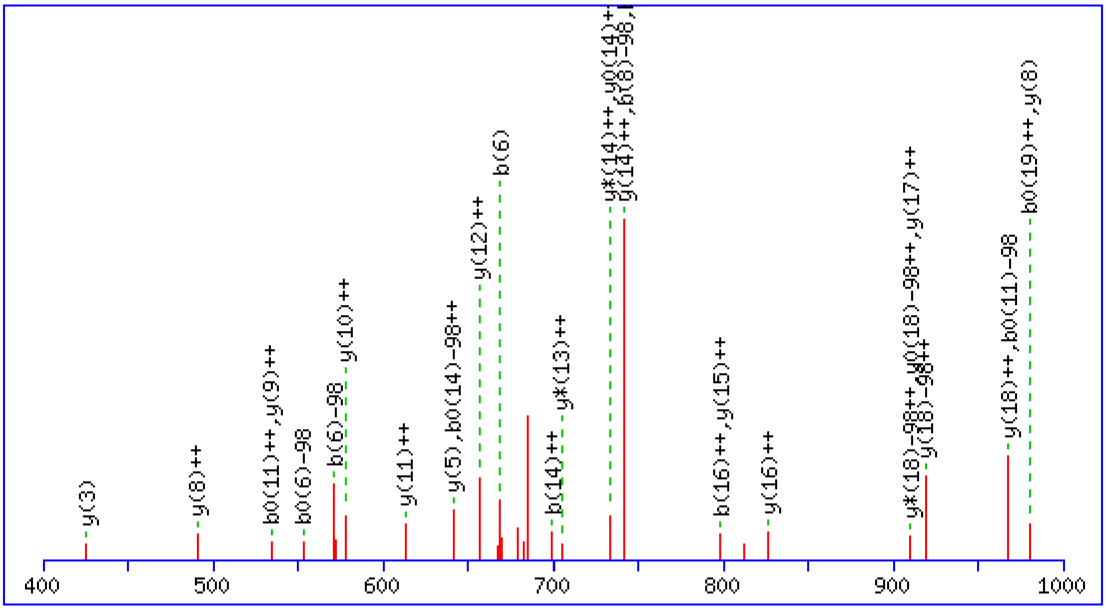
Monoisotopic mass of neutral peptide Mr(calc): 1965.9044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 **Expect:** 2.2e-005
Matched b ions: b(4), b(5), b(6)++, b(7)-98, b(9)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++

Peptide No.861

SEDSGIGLSASSPELSEHLR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SEDSGIGLSASSPELSEHLR**
Found in **DOP2_MOUSE** in **SwissProt**, Protein dopey-2 OS=Mus musculus GN=Dopey2 PE=2 SV=3

Match to Query 5569: 2149.952277 from(717.658035,3+) index(6297)
Title: Elution from: 41.675 to 41.675 scan no 4186 cid35.00 polarity:+:m1s



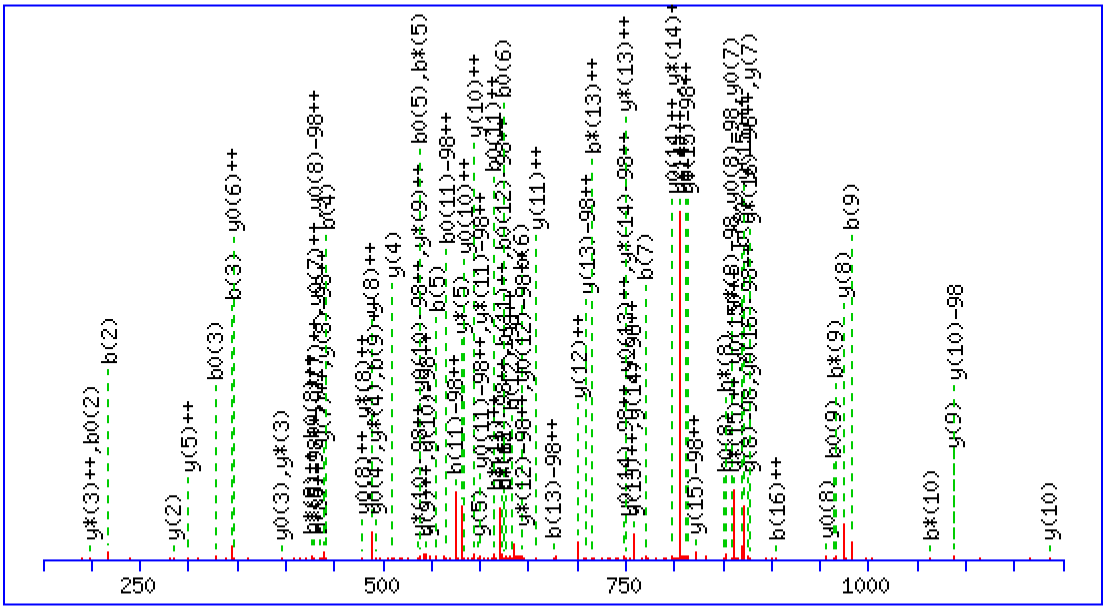
Monoisotopic mass of neutral peptide Mr(calc): 2149.9528
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 76 **Expect:** 1.7e-007
Matched b ions: b(6)-98, b(6), b(8)-98, b(14)++, b(16)++
Matched y ions: y(3), y(5), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)-98++, y(18)++

Peptide No.862

SEQPLSQVLPSLSPEHK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **SEQPLSQVLPSLSPEHK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4299: 1954.941378 from(652.654402,3+) index(4976)
Title: Elution from: 56.026 to 56.026 scan no 4433 cid35.00 polarity:+:m1s



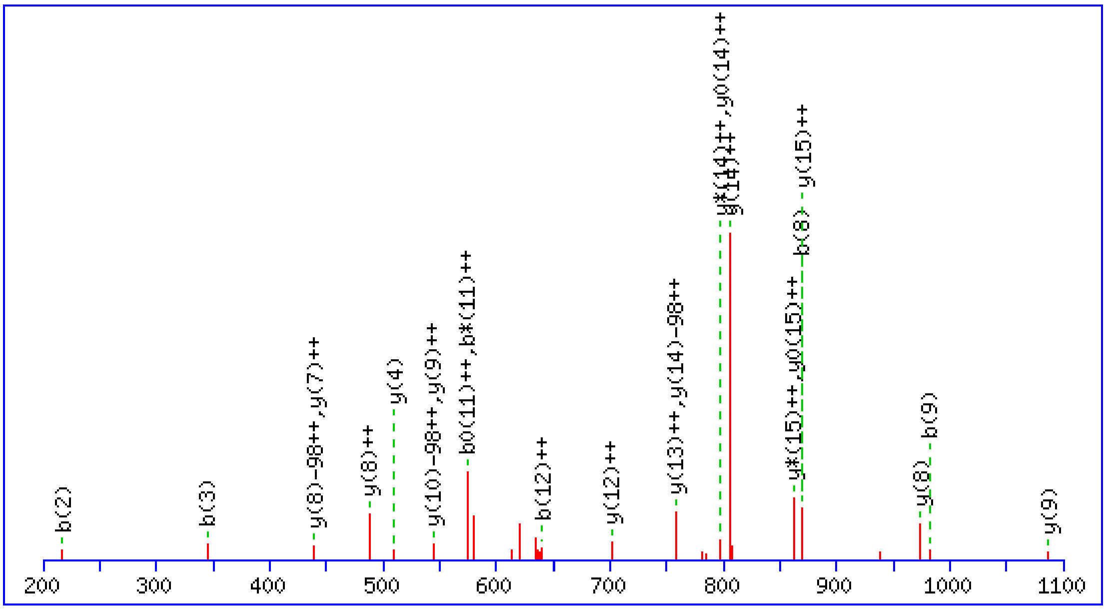
Monoisotopic mass of neutral peptide Mr(calc): 1954.9401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.1e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(16)++
Matched y ions: y(2), y(4), y(5)++, y(5), y(7)++, y(7), y(8)++, y(8), y(8)-98++, y(8)-98, y(9), y(9)++, y(10)-98, y(10)-98++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++

Peptide No.863

SEQPLSQVLPSLSPEHK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **SEQPLSQVLPSLSPEHK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4822: 1954.940313 from(652.654047,3+) index(6609)
Title: Elution from: 46.172 to 46.172 scan no 4746 cid35.00 polarity:+:m1s



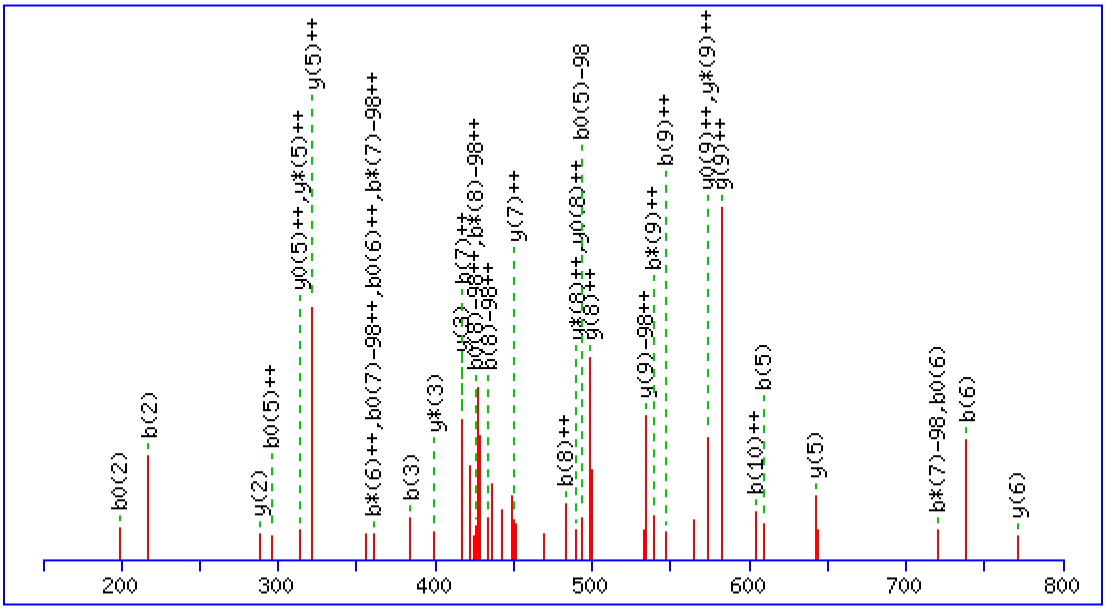
Monoisotopic mass of neutral peptide Mr(calc): 1954.9401
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 3.4e-005
Matched b ions: b(2), b(3), b(8), b(9), b(12)++
Matched y ions: y(4), y(7)++, y(8)++, y(8), y(8)-98++, y(9), y(9)++, y(10)-98++, y(12)++, y(13)++, y(14)++, y(14)-98++, y(15)++

Peptide No.864

SESPKEPEQLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SESPKEPEQLR**
Found in **ROA1_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein A1 OS=Mus musculus GN=Hnrnpa1 PE=1 SV=2

Match to Query 2442: 1378.612437 from(460.544755,3+) index(518)
Title: Elution from: 20.486 to 20.486 scan no 1340 cid35.00 polarity:+



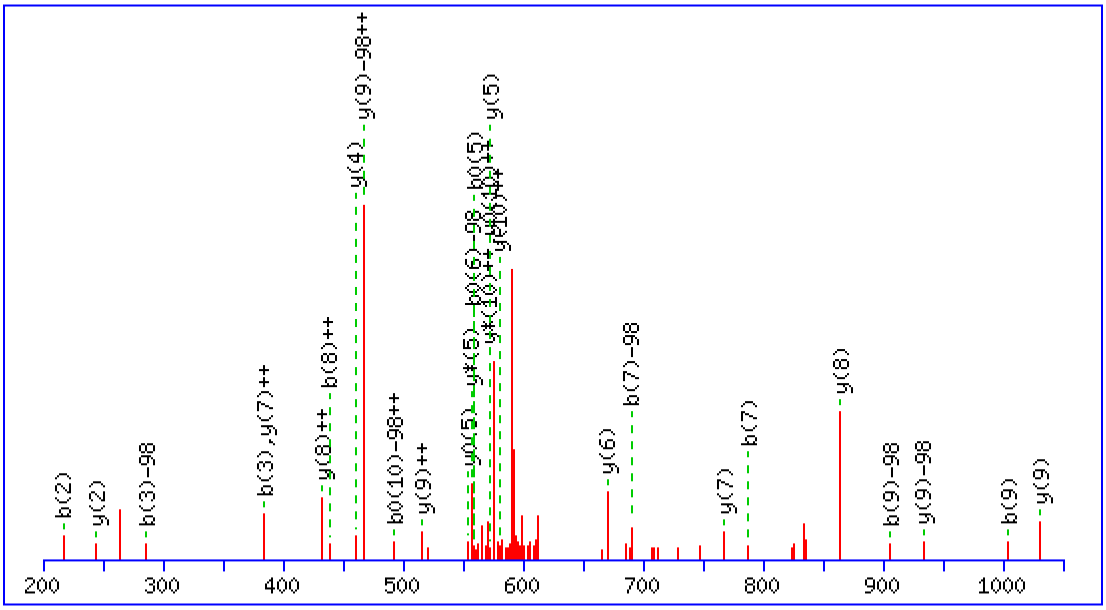
Monoisotopic mass of neutral peptide Mr(calc): 1378.6129
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00045
Matched b ions: b(2), b(3), b(5), b(6), b(7)++, b(8)++, b(8)-98++, b(9)++, b(10)++
Matched y ions: y(2), y(3), y(5)++, y(5), y(6), y(7)++, y(8)++, y(9)++, y(9)-98++

Peptide No.865

SESPPPLSEPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SESPPPLSEPK**
Found in **BRD3_MOUSE** in **SwissProt**, Bromodomain-containing protein 3 OS=Mus musculus GN=Brd3 PE=1 SV=2

Match to Query 1877: 1246.546822 from(624.280687,2+) index(1091)
Title: Elution from: 25.416 to 25.416 scan no 2009 cid35.00 polarity:+



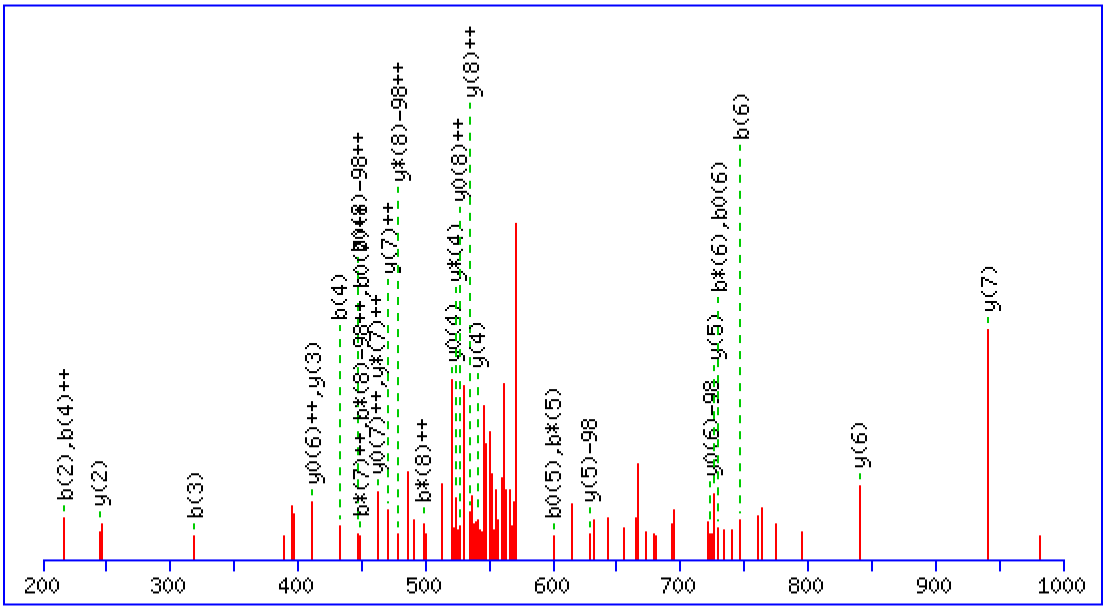
Monoisotopic mass of neutral peptide Mr(calc): 1246.5482
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.00065
Matched b ions: b(2), b(3), b(3)-98, b(7)-98, b(7), b(8)++, b(9), b(9)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7)++, y(7), y(8), y(8)++, y(9)-98++, y(9), y(9)-98, y(9)++, y(10)++

Peptide No.866

SETNWESPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SETNWESPK**
Found in **LYRIC_MOUSE** in **SwissProt**, Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1

Match to Query 1260: 1156.443380 from(579.228966,2+) index(548)
Title: Elution from: 23.193 to 23.193 scan no 1547 cid35.00 polarity:+



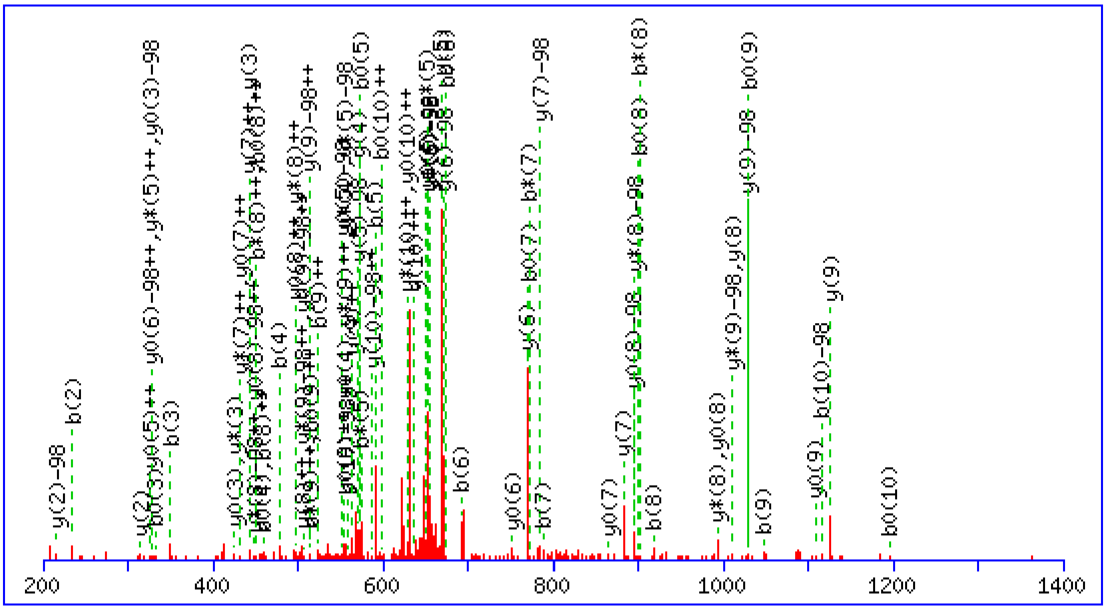
Monoisotopic mass of neutral peptide Mr(calc): 1156.4438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.009
Matched b ions: b(2), b(3), b(4)++, b(4), b(6)
Matched y ions: y(2), y(3), y(4), y(5), y(5)-98, y(6), y(7), y(7)++, y(8)++

Peptide No.867

SFDQLTPEESK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SFDQLTPEESK**
Found in **CALU_MOUSE** in **SwissProt**, Calumenin OS=Mus musculus GN=Calu PE=1 SV=1

Match to Query 2662: 1359.559622 from(680.787087,2+) index(1420)
Title: Elution from: 41.129 to 41.129 scan no 3103 cid35.00 polarity:+



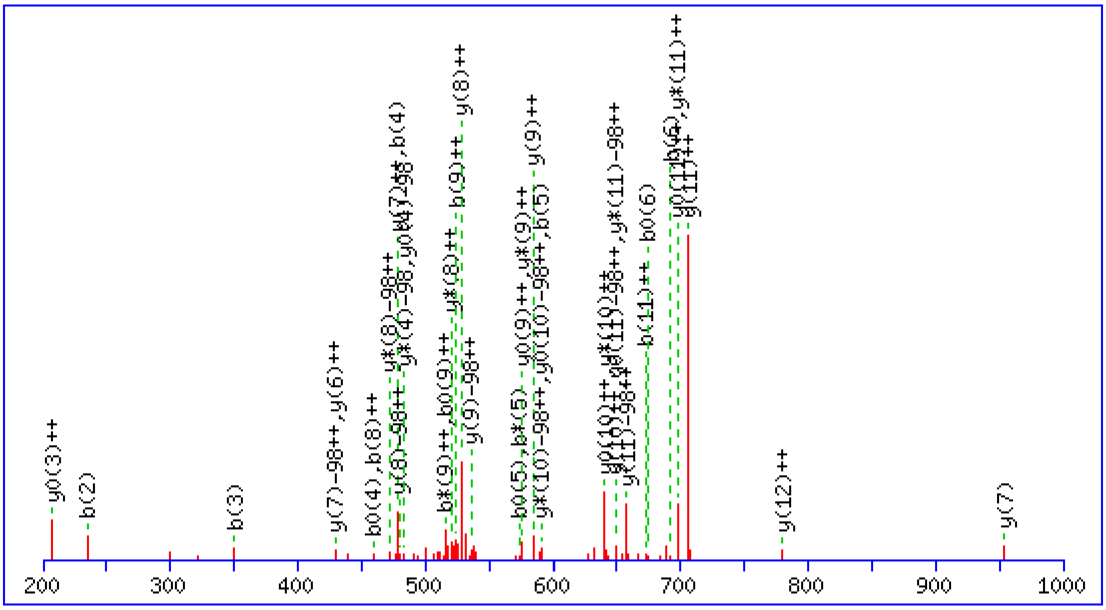
Monoisotopic mass of neutral peptide Mr(calc): 1359.5595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.00061
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(10)-98, b(10)-98++
Matched y ions: y(2), y(2)-98, y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)-98, y(7)++, y(8), y(8)++, y(9), y(9)-98, y(9)++, y(9)-98++, y(10)-98++, y(10)++

Peptide No.868

SFDQLTPEESKER
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SFDQLTPEESKER**
Found in **CALU_MOUSE** in **SwissProt**, Calumenin OS=Mus musculus GN=Calu PE=1 SV=1

Match to Query 2952: 1644.702978 from(549.241602,3+) index(1313)
Title: Elution from: 28.602 to 28.602 scan no 2381 cid35.00 polarity:+



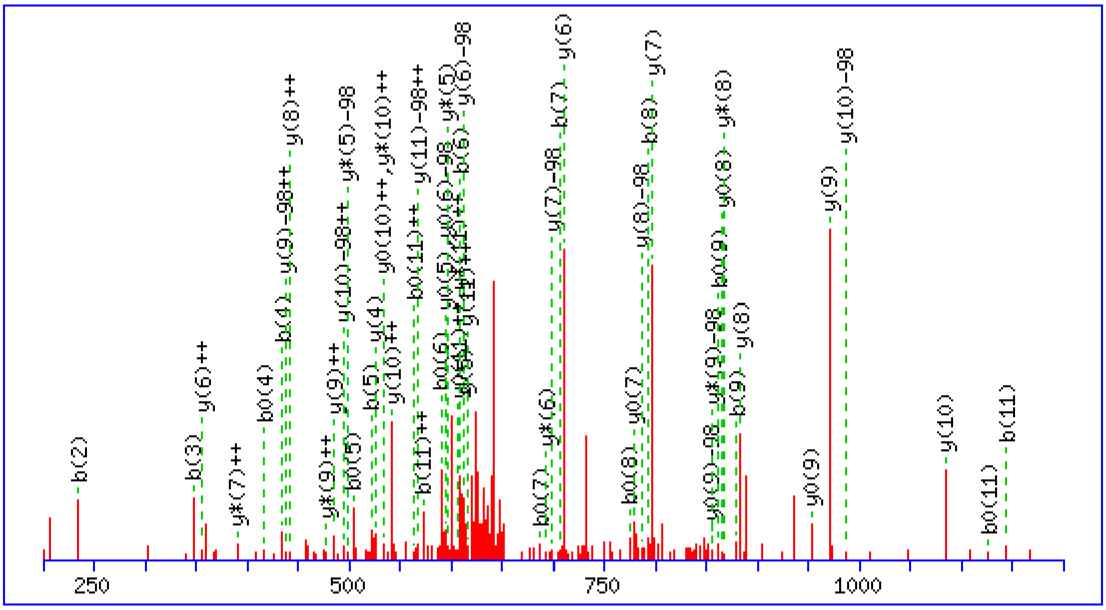
Monoisotopic mass of neutral peptide Mr(calc): 1644.7032
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0026
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8)++, b(9)++, b(11)++
Matched y ions: y(6)++, y(7)++, y(7), y(7)-98++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++

Peptide No.869

SFISSSPSSPSR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **SFISSSPSSPSR**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 2562: 1317.560830 from(659.787691,2+) index(939)
Title: Elution from: 34.905 to 34.905 scan no 2386 cid35.00 polarity:+



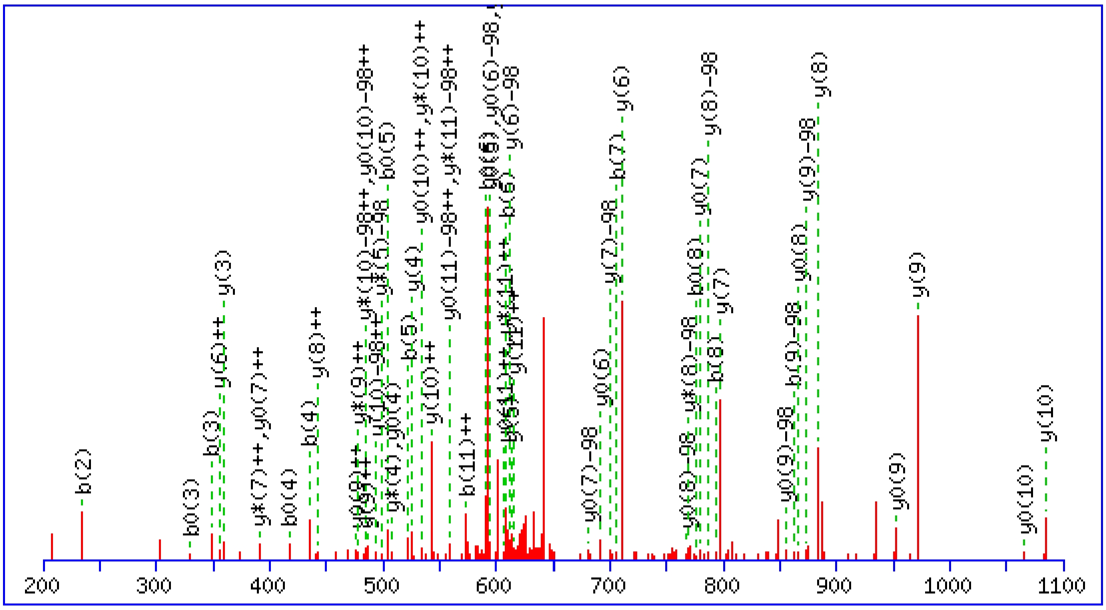
Monoisotopic mass of neutral peptide Mr(calc): 1317.5602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00021
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(11), b(11)++
Matched y ions: y(4), y(5), y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)++, y(9)-98++, y(10)++, y(10), y(10)-98++, y(10)-98, y(11)-98++, y(11)++

Peptide No.870

SFISSSPSSPSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **SFISSSPSSPSR**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 2064: 1317.558256 from(659.786404,2+) index(1221)
Title: Elution from: 27.191 to 27.191 scan no 2215 cid35.00 polarity:+



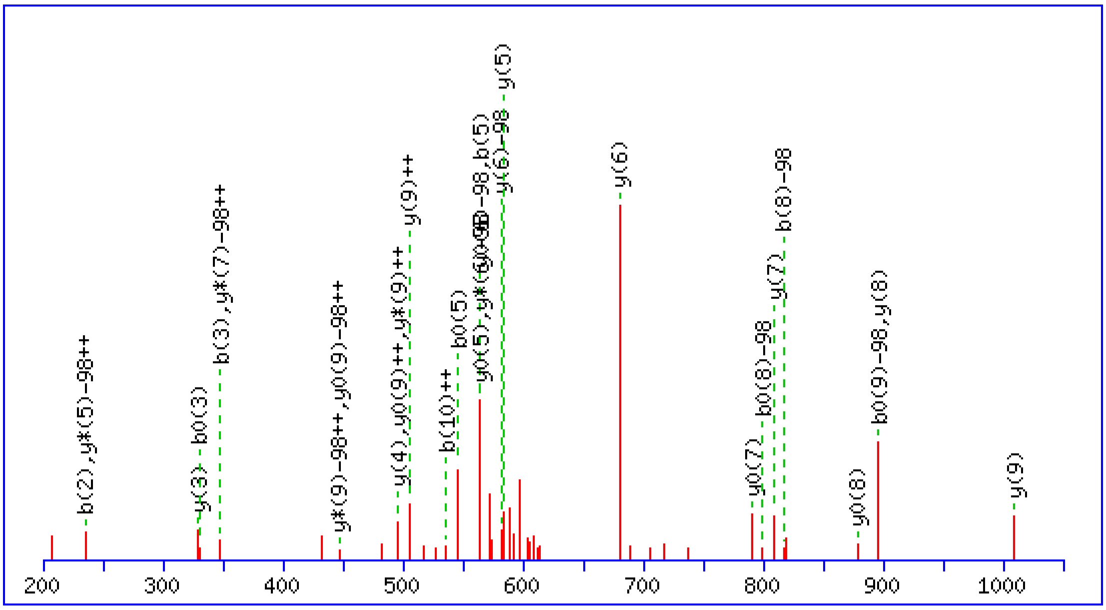
Monoisotopic mass of neutral peptide Mr(calc): 1317.5602
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 8.5e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(7), b(8), b(9)-98, b(11)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)++, y(9)-98, y(10), y(10)++, y(10)-98++, y(11)++

Peptide No.871

SFLSEPSSPGR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SFLSEPSSPGR**
Found in **VIR_MOUSE** in **SwissProt**, Protein virilizer homolog OS=Mus musculus GN=Kiaa1429 PE=1 SV=1

Match to Query 1572: 1242.527768 from(622.271160,2+) index(1662)
Title: Elution from: 32.728 to 32.728 scan no 2917 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1242.5282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 4.4e-005
Matched b ions: b(2), b(3), b(5), b(8)-98, b(10)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)-98, y(7), y(8), y(9)++, y(9)

Peptide No.872

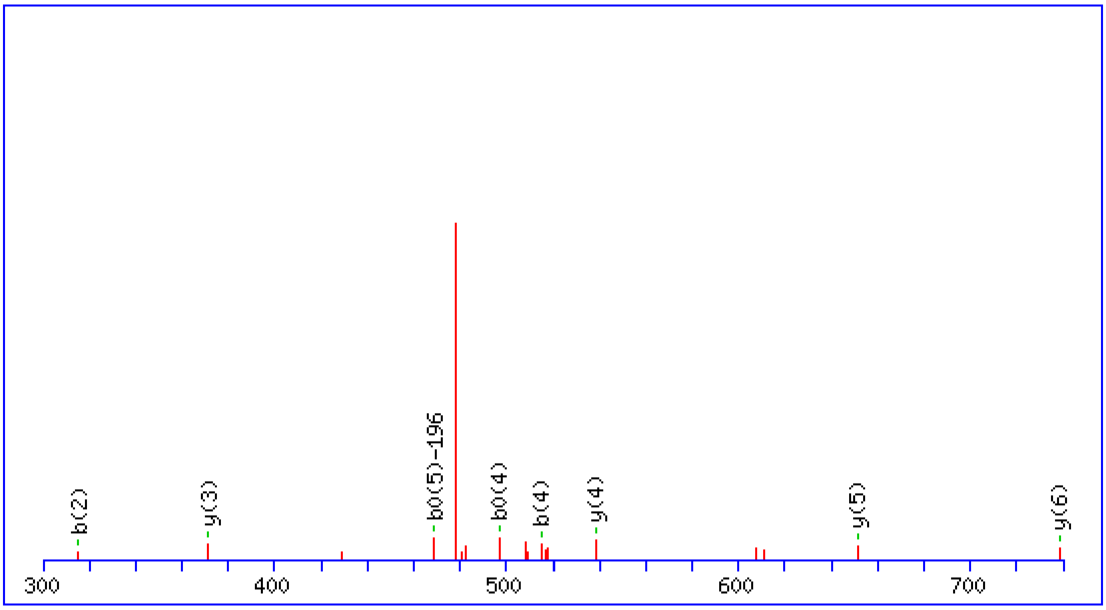
SFSISPVR

Confirmed sites: @S:1,@S:5

Ambiguous sites:

MS/MS Fragmentation of **SFSISPVR**
Found in **SON_MOUSE** in **SwissProt**, Protein SON OS=Mus musculus GN=Son PE=1 SV=2

Match to Query 898: 1051.413560 from(526.714056,2+) index(2337)
Title: Elution from: 41.277 to 41.277 scan no 3971 cid35.00 polarity:+



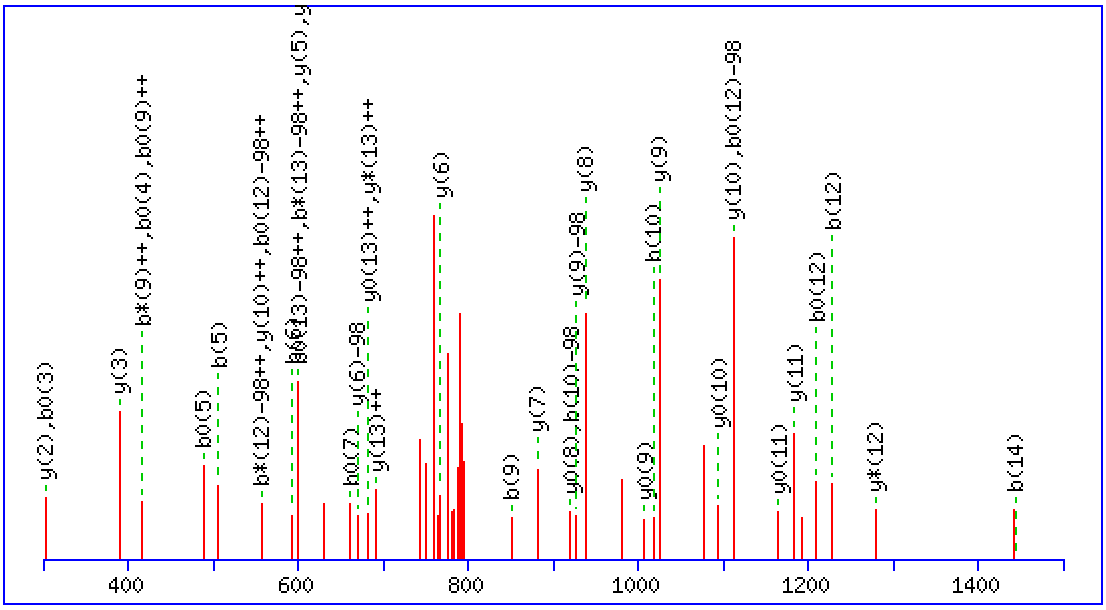
Monoisotopic mass of neutral peptide Mr(calc): 1051.4141
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0051
Matched b ions: b(2), b(4)
Matched y ions: y(3), y(4), y(5), y(6)

Peptide No.873

SFSLASSGNSPISQR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SFSLASSGNSPISQR**
Found in **OSB11_MOUSE** in **SwissProt**, Oxysterol-binding protein-related protein 11 OS=Mus musculus GN=Osbpl11 PE=1 SV=2

Match to Query 3276: 1616.718570 from(809.366561,2+) index(2155)
Title: Elution from: 36.357 to 36.357 scan no 3458 cid35.00 polarity:+



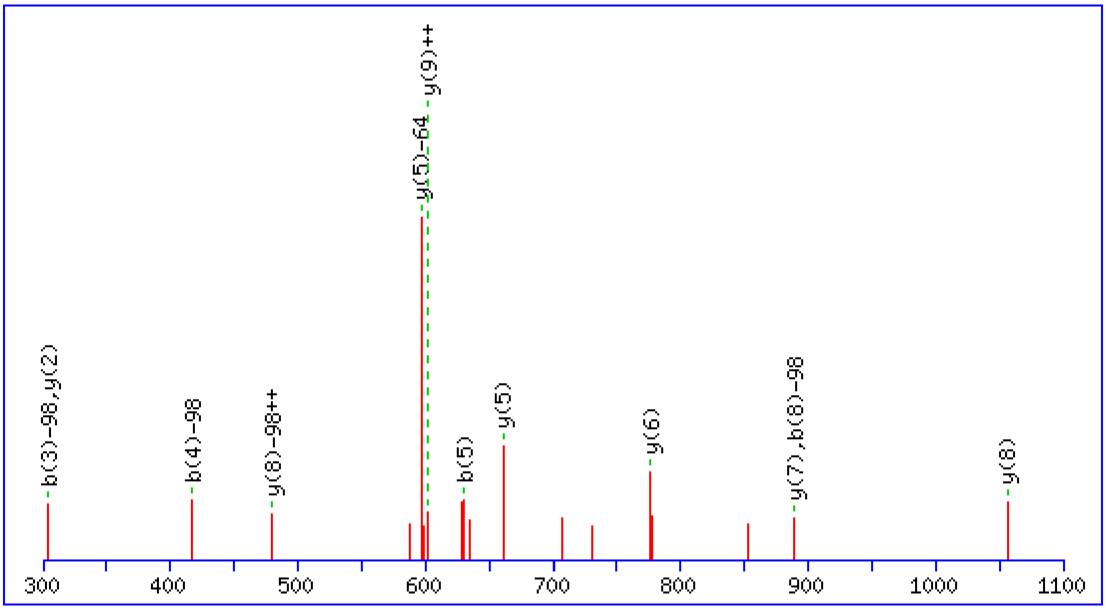
Monoisotopic mass of neutral peptide Mr(calc): 1616.7195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 68 **Expect:** 8.4e-007
Matched b ions: b(5), b(6), b(9), b(10)-98, b(10), b(12), b(14)
Matched y ions: y(2), y(3), y(5), y(6)-98, y(6), y(7), y(8), y(9), y(9)-98, y(10), y(10)++, y(11), y(12)-98++, y(13)++

Peptide No.874

SFSLDPLMER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SFSLDPLMER**
Found in **TENC1_MOUSE** in **SwissProt**, Tensin-like C1 domain-containing phosphatase OS=Mus musculus GN=Tenc1 PE=1 SV=1

Match to Query 2088: 1289.534564 from(645.774558,2+) index(3087)
Title: Elution from: 48.587 to 48.587 scan no 5030 cid35.00 polarity:+



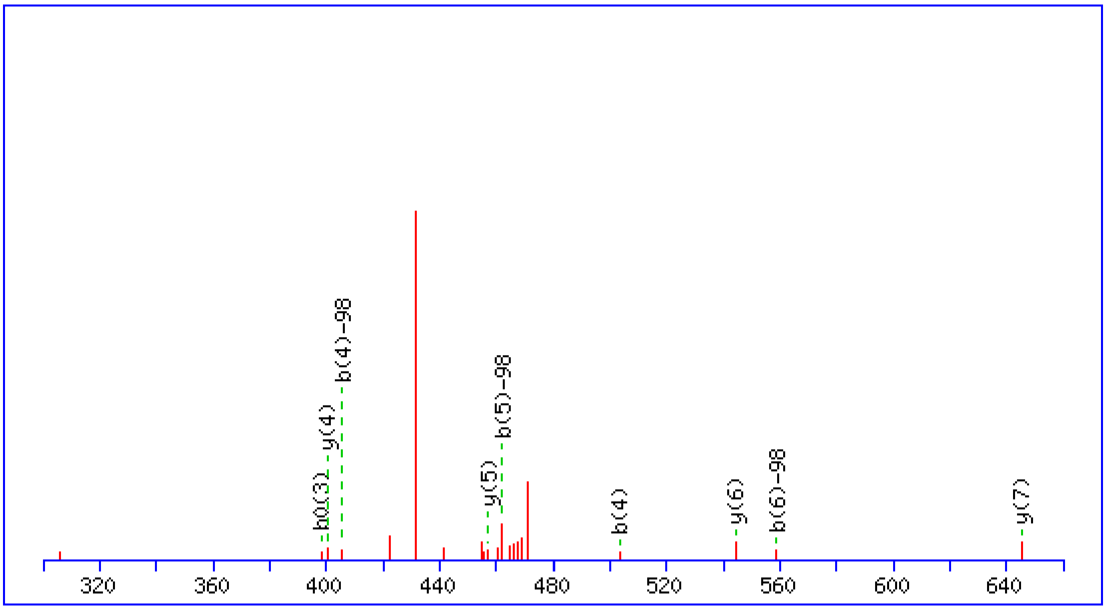
Monoisotopic mass of neutral peptide Mr(calc): 1289.5363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M8 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 43 **Expect:** 0.00015
Matched b ions: b(3)-98, b(4)-98, b(5), b(8)-98
Matched y ions: y(2), y(5), y(6), y(7), y(8), y(8)-98++, y(9)++

Peptide No.875

SFTSGPGAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SFTSGPGAR**
Found in **K2C8_MOUSE** in **SwissProt**, Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4

Match to Query 651: 958.389892 from(480.202222,2+) index(169)
Title: Elution from: 18.964 to 18.964 scan no 1031 cid35.00 polarity:+



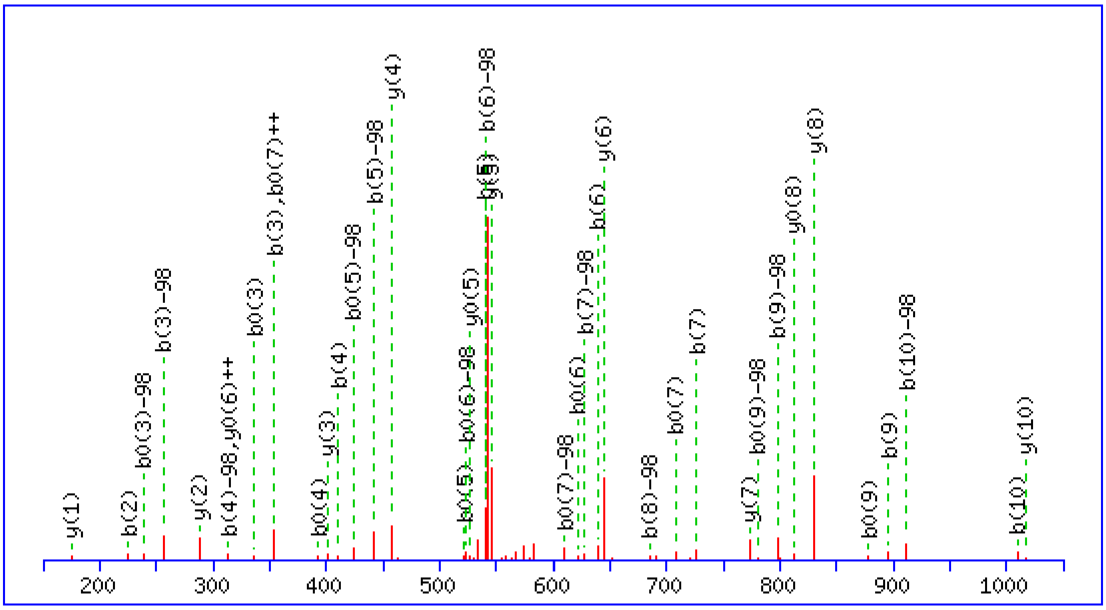
Monoisotopic mass of neutral peptide Mr(calc): 958.3910
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.012
Matched b ions: b(4)-98, b(4), b(5)-98, b(6)-98
Matched y ions: y(4), y(5), y(6), y(7)

Peptide No.876

SGEGEVSGLLR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SGEGEVSGLLR**
Found in **TIF1B_MOUSE** in **SwissProt**, Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3

Match to Query 1348: 1182.527598 from(592.271075,2+) index(2087)
Title: Elution from: 37.887 to 37.887 scan no 3560 cid35.00 polarity:+



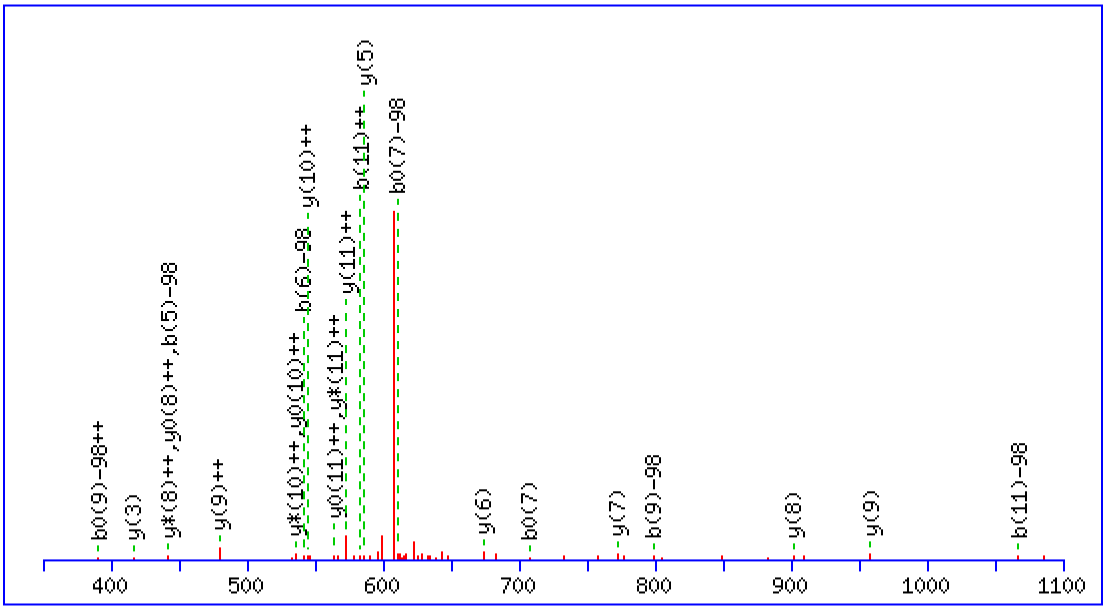
Monoisotopic mass of neutral peptide Mr(calc): 1182.5282
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 88 **Expect:** 5.7e-009
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10)
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(10)

Peptide No.877

SGEGEVSGLLRK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SGEGEVSGLLRK**
Found in **TIF1B_MOUSE** in **SwissProt**, Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3

Match to Query 1990: 1310.622640 from(656.318596,2+) index(1397)
Title: Elution from: 31.451 to 31.451 scan no 2685 cid35.00 polarity:+



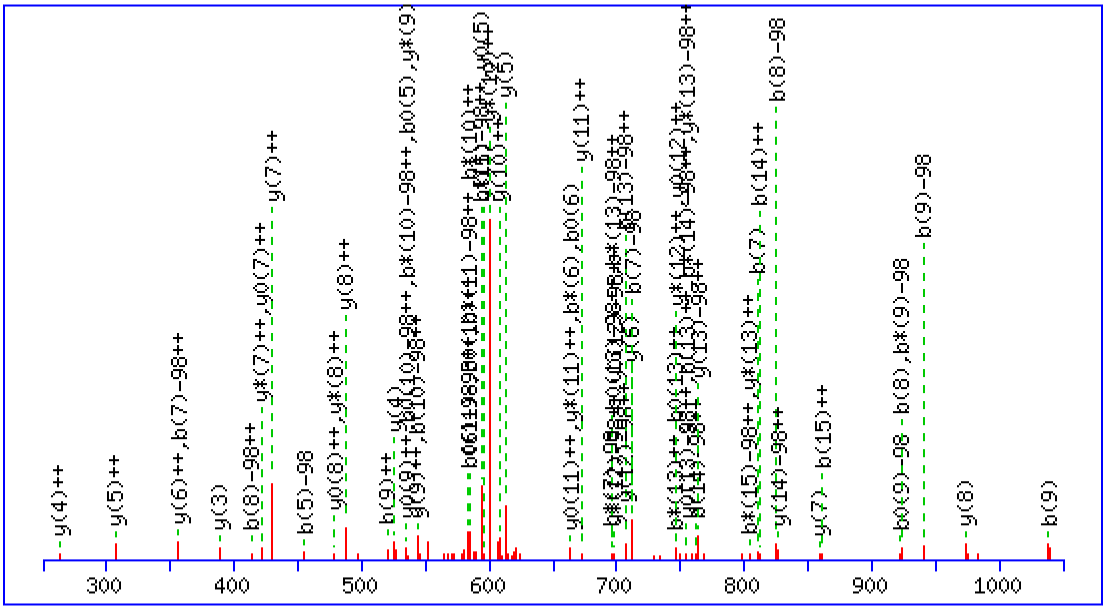
Monoisotopic mass of neutral peptide Mr(calc): 1310.6231
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00051
Matched b ions: b(5)-98, b(6)-98, b(9)-98, b(11)-98, b(11)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(11)++

Peptide No.878

SGKLSQELDFVSHNVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SGKLSQELDFVSHNVR**
Found in **NUCB1_MOUSE** in **SwissProt**, Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2

Match to Query 4430: 1894.892553 from(632.638127,3+) index(5650)
Title: Elution from: 36.006 to 36.006 scan no 3411 cid35.00 polarity:+:m1s



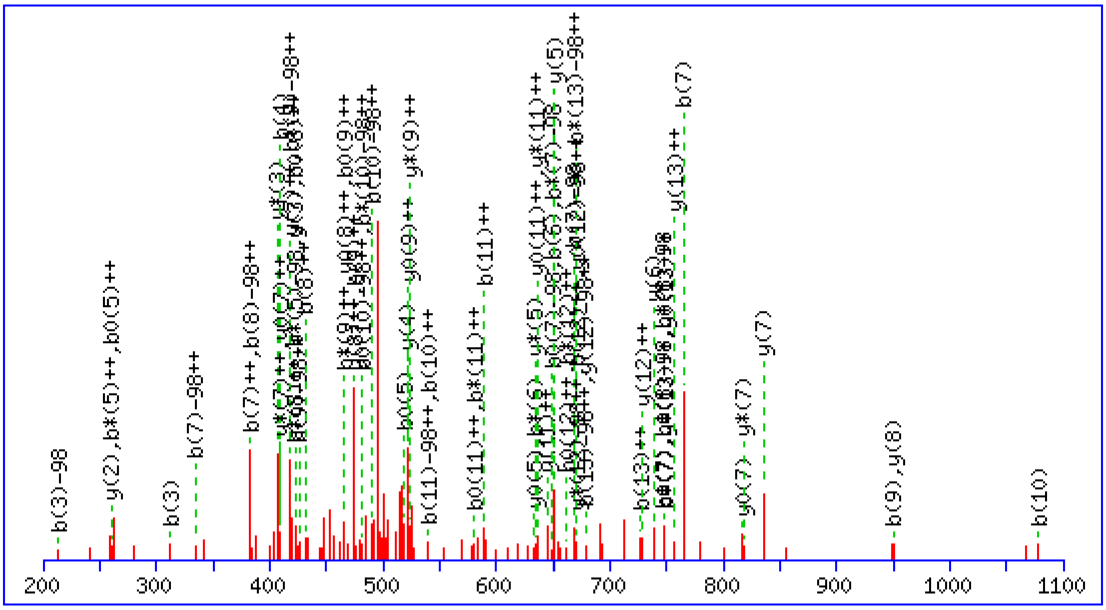
Monoisotopic mass of neutral peptide Mr(calc): 1894.8938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 86 **Expect:** 1.6e-008
Matched b ions: b(5)-98, b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)-98, b(8), b(8)-98++, b(9)-98, b(9), b(9)++, b(10)-98++, b(11)-98++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(3), y(4)++, y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)-98++, y(13)-98++, y(14)-98++

Peptide No.879

SGSPKLDPSEVYLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SGSPKLDPSEVYLK**
Found in **MAGI3_MOUSE** in **SwissProt**, Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3 OS=Mus musculus GN=Magi3 PE=1 SV=2

Match to Query 3848: 1598.760420 from(533.927416,3+) index(2001)
Title: Elution from: 46.449 to 46.449 scan no 3841 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1598.7593
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0061
Matched b ions: b(3), b(3)-98, b(4), b(6), b(7)++, b(7), b(7)-98, b(7)-98++, b(8)-98++, b(8)++, b(9), b(9)++, b(9)-98++, b(10), b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(11)++, y(12)++, y(12)-98++, y(13)++

Peptide No.880

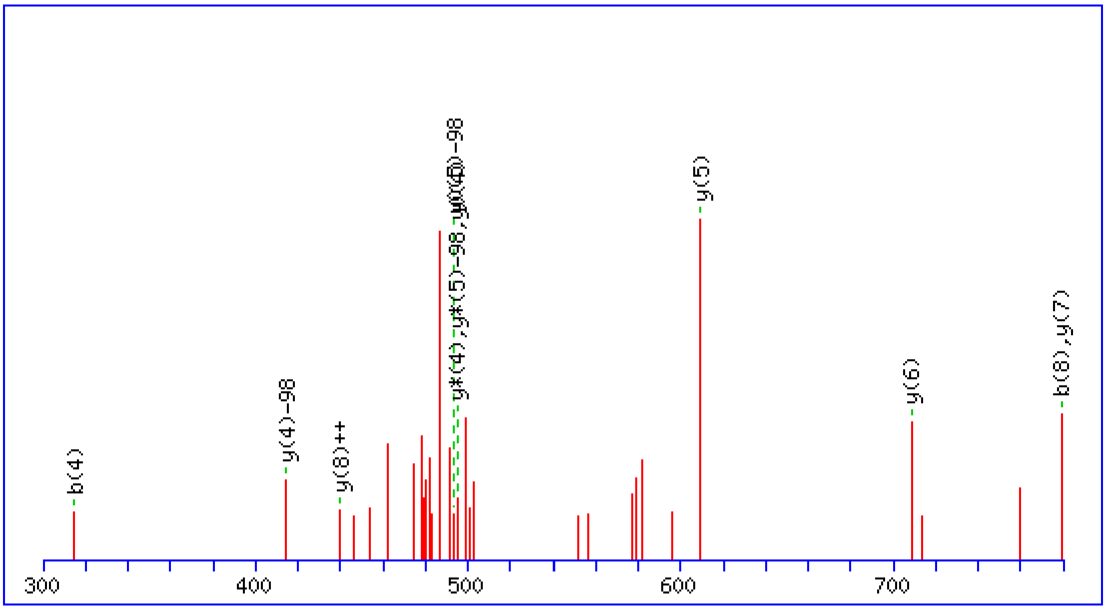
SGVAVPTSPK

Confirmed sites:

Ambiguous sites: @T:7orS:8

MS/MS Fragmentation of **SGVAVPTSPK**
Found in **PDCD4_MOUSE** in **SwissProt**, Programmed cell death protein 4 OS=Mus musculus GN=Pdcd4 PE=1 SV=1

Match to Query 855: 1021.484550 from(511.749551,2+) index(723)
Title: Elution from: 22.710 to 22.710 scan no 1605 cid35.00 polarity:+



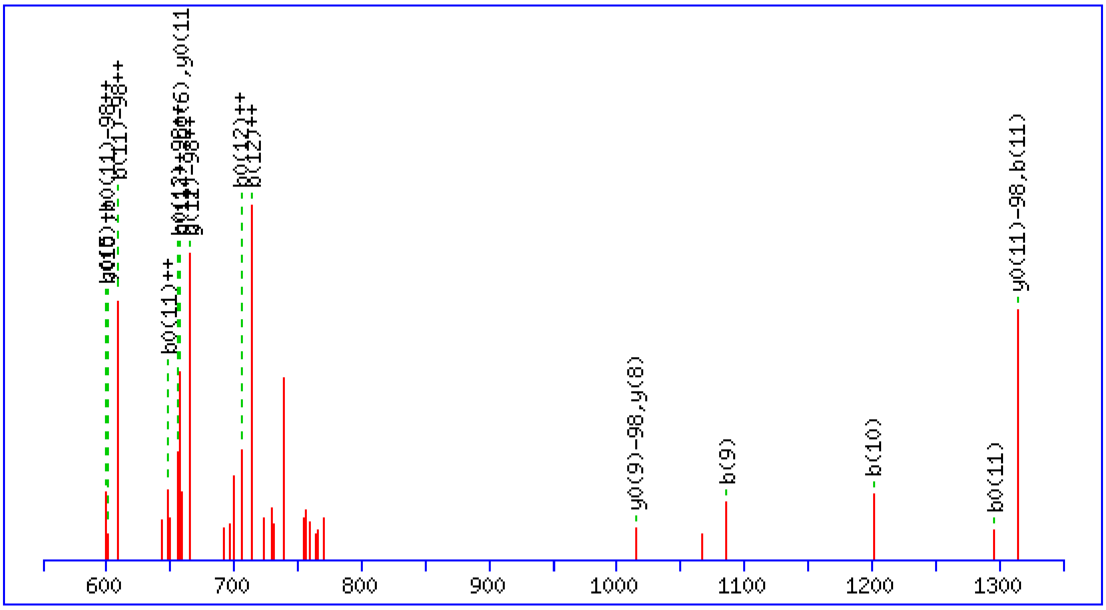
Monoisotopic mass of neutral peptide Mr(calc): 1021.4845
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.056
Matched b ions: b(4), b(5), b(8)
Matched y ions: y(4)-98, y(5), y(6), y(7), y(8)++

Peptide No.881

SGYHDDSDEDLLE
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SGYHDDSDEDLLE**
Found in **SORT_MOUSE** in **SwissProt**, Sortilin OS=Mus musculus GN=Sort1 PE=1 SV=1

Match to Query 2863: 1573.545758 from(787.780155,2+) index(4768)
Title: Elution from: 35.664 to 35.664 scan no 3247 cid35.00 polarity:+:m1s



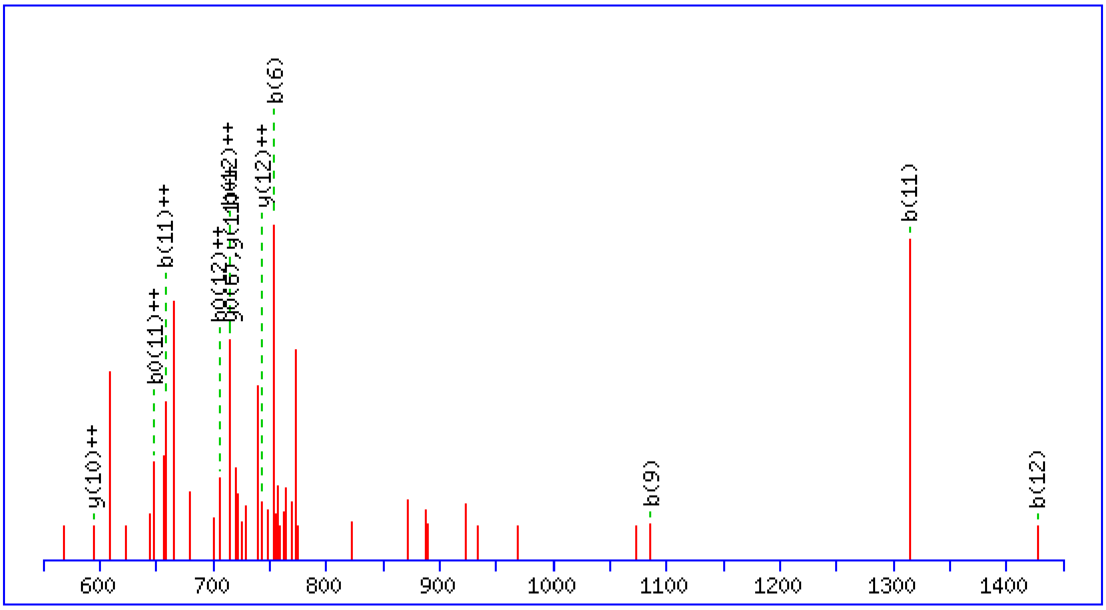
Monoisotopic mass of neutral peptide Mr(calc): 1573.5457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 17 **Expect:** 0.033
Matched b ions: b(9), b(10), b(10)++, b(11), b(11)-98++, b(11)++, b(12)-98++, b(12)++
Matched y ions: y(8), y(11)-98++

Peptide No.882

SGYHDDSDEDLLE
Confirmed sites: @Y:3
Ambiguous sites:

MS/MS Fragmentation of **SGYHDDSDEDLLE**
Found in **SORT_MOUSE** in **SwissProt**, Sortilin OS=Mus musculus GN=Sort1 PE=1 SV=1

Match to Query 2721: 1573.546078 from(787.780315,2+) index(1892)
Title: Elution from: 35.512 to 35.512 scan no 3263 cid35.00 polarity:+



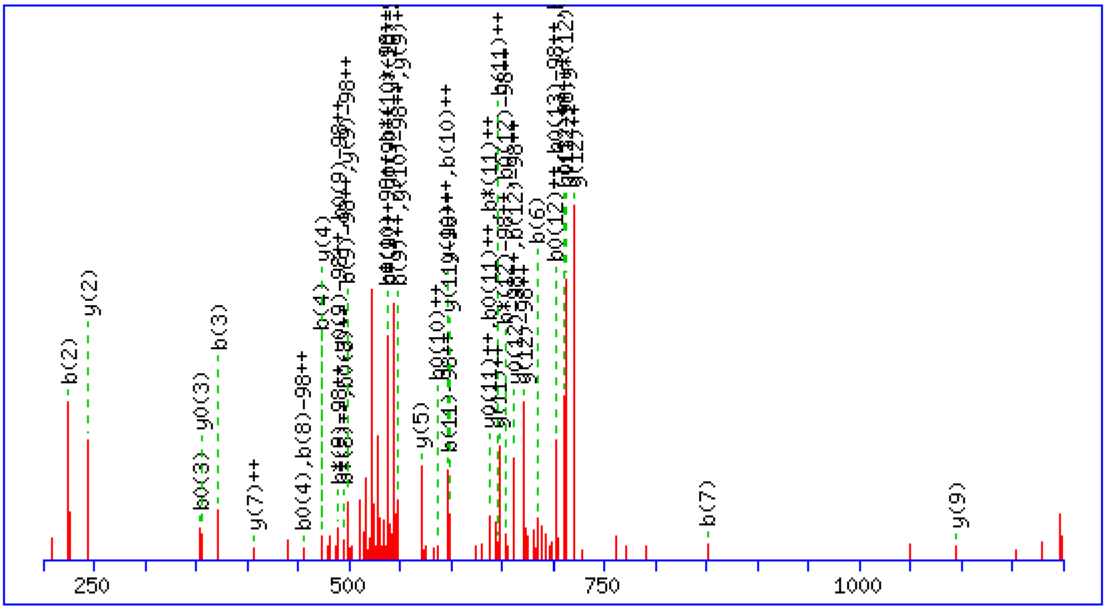
Monoisotopic mass of neutral peptide Mr(calc): 1573.5457
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y3 : Phospho (Y)
Ions Score: 17 **Expect:** 0.03
Matched b ions: b(6), b(9), b(11), b(11)++, b(12), b(12)++
Matched y ions: y(10)++, y(11)++, y(12)++

Peptide No.883

SHFTPNSRSPTEPK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SHFTPNSRSPTEPK**
Found in **HGD_MOUSE** in **SwissProt**, Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2

Match to Query 3533: 1663.735989 from(555.585939,3+) index(98)
Title: Elution from: 23.792 to 23.792 scan no 1153 cid35.00 polarity:+



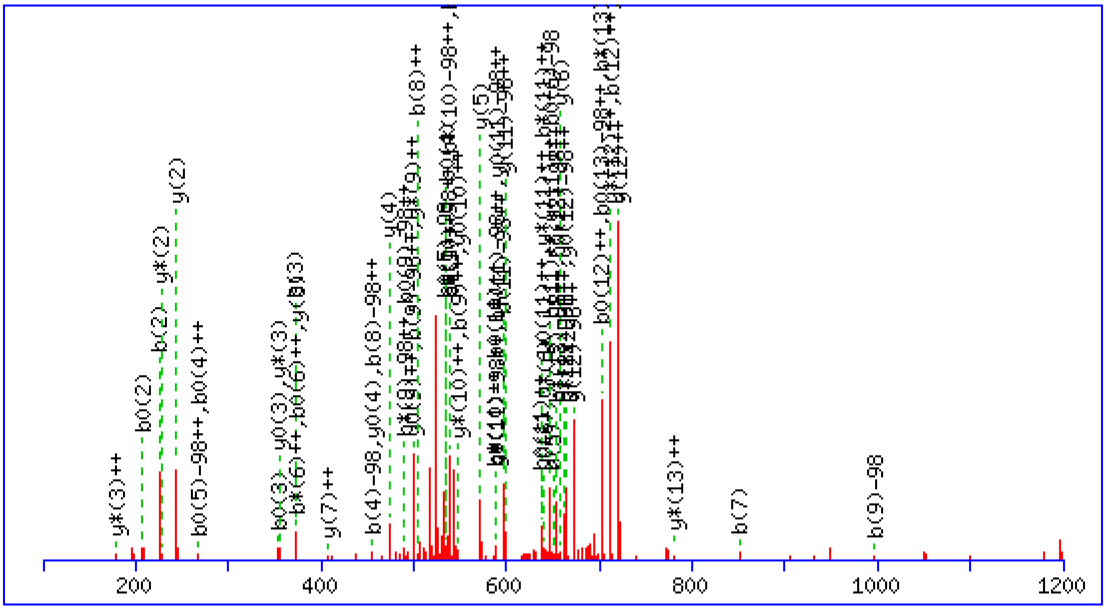
Monoisotopic mass of neutral peptide Mr(calc): 1663.7355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.029
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8)-98++, b(9)-98++, b(9)++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++
Matched y ions: y(2), y(4), y(5), y(7)++, y(9)-98++, y(9), y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.884

SHFTPNSRSPTEPK
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **SHFTPNSRSPTEPK**
Found in **HGD_MOUSE** in **SwissProt**, Homogentisate 1,2-dioxygenase OS=Mus musculus GN=Hgd PE=1 SV=2

Match to Query 3022: 1663.736220 from(555.586016,3+) index(3230)
Title: Elution from: 18.121 to 18.121 scan no 977 cid35.00 polarity:+:m1s



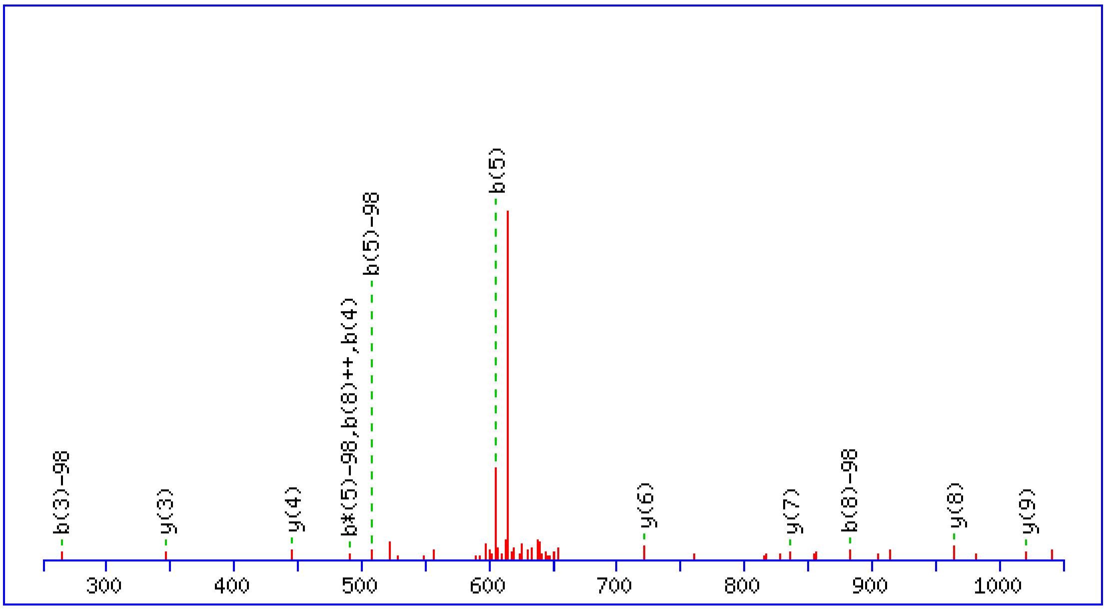
Monoisotopic mass of neutral peptide Mr(calc): 1663.7355
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.054
Matched b ions: b(2), b(3), b(4)-98, b(5), b(7), b(8)-98++, b(8)++, b(9)-98++, b(9)-98, b(9)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.885

SHGQDYLVGNR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SHGQDYLVGNR**
Found in **GSTA1_MOUSE** in **SwissProt**, Glutathione S-transferase A1 OS=Mus musculus GN=Gsta1 PE=1 SV=2

Match to Query 2284: 1324.555978 from(663.285265,2+) index(842)
Title: Elution from: 23.290 to 23.290 scan no 1721 cid35.00 polarity:+



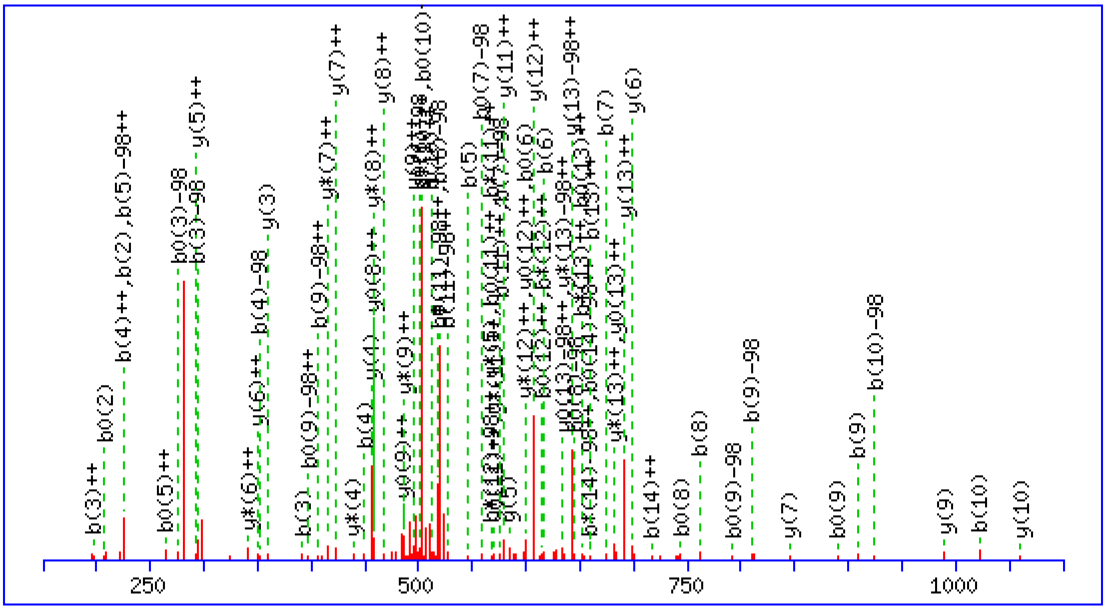
Monoisotopic mass of neutral peptide Mr(calc): 1324.5561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0016
Matched b ions: b(3)-98, b(4), b(5), b(5)-98, b(8)-98, b(8)++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9)

Peptide No.886

SHSGPAGSFNKPAIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SHSGPAGSFNKPAIR**
Found in **ERRFI_MOUSE** in **SwissProt**, ERBB receptor feedback inhibitor 1 OS=Mus musculus GN=Errfi1 PE=1 SV=1

Match to Query 3438: 1604.745276 from(535.922368,3+) index(747)
Title: Elution from: 22.367 to 22.367 scan no 1595 cid35.00 polarity:+



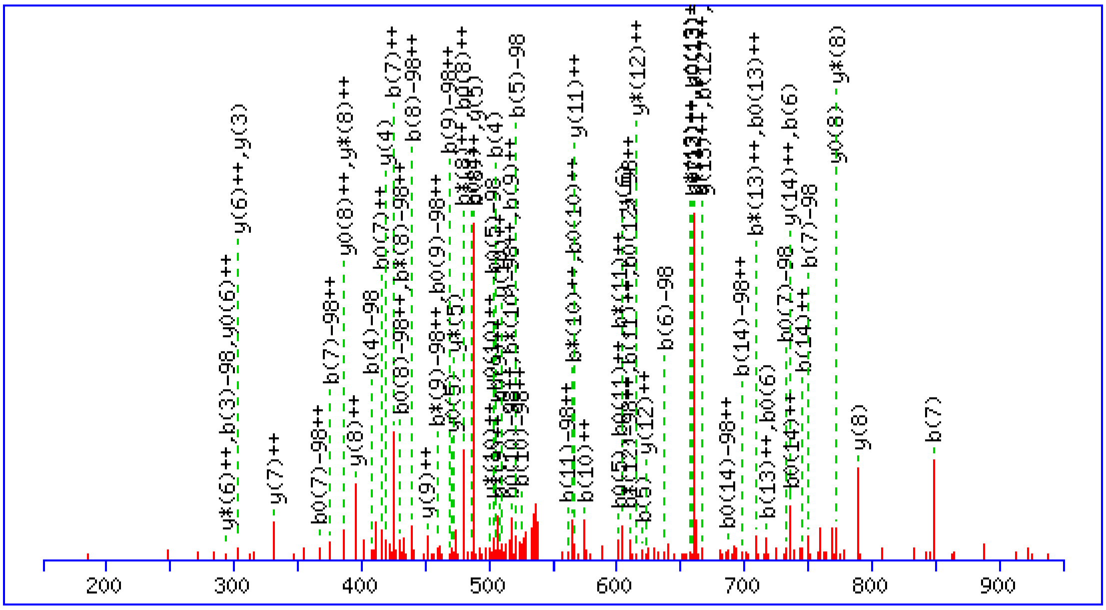
Monoisotopic mass of neutral peptide Mr(calc): 1604.7460
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.00081
Matched b ions: b(2), b(3)-98, b(3), b(3)++, b(4)++, b(4)-98, b(4), b(5)-98++, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8), b(9)-98, b(9), b(9)-98++, b(10), b(10)-98, b(10)++, b(11)-98++, b(11)++, b(13)++, b(14)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(9), y(9)++, y(10), y(11)++, y(12)++, y(13)-98++, y(13)++

Peptide No.887

SHSLDDLQGDADVGK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SHSLDDLQGDADVGK**
Found in **SASH1_MOUSE** in **SwissProt**, SAM and SH3 domain-containing protein 1 OS=Mus musculus GN=Sash1 PE=1 SV=1

Match to Query 3438: 1635.678123 from(546.233317,3+) index(1225)
Title: Elution from: 38.036 to 38.036 scan no 2769 cid35.00 polarity:+



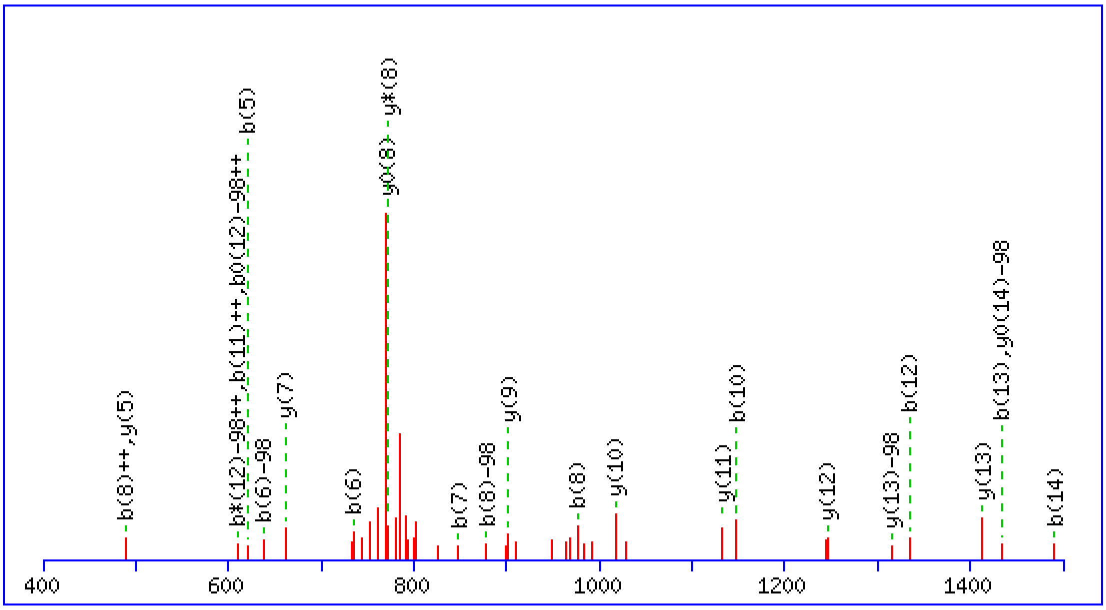
Monoisotopic mass of neutral peptide Mr(calc): 1635.6778
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.025
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)++, b(8)-98++, b(9)++, b(9)-98++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++

Peptide No.888

SHSLDDLQGDADVGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SHSLDDLQGDADVGK**
Found in **SASH1_MOUSE** in **SwissProt**, SAM and SH3 domain-containing protein 1 OS=Mus musculus GN=Sash1 PE=1 SV=1

Match to Query 3346: 1635.675204 from(818.844878,2+) index(1541)
Title: Elution from: 30.367 to 30.367 scan no 2650 cid35.00 polarity:+



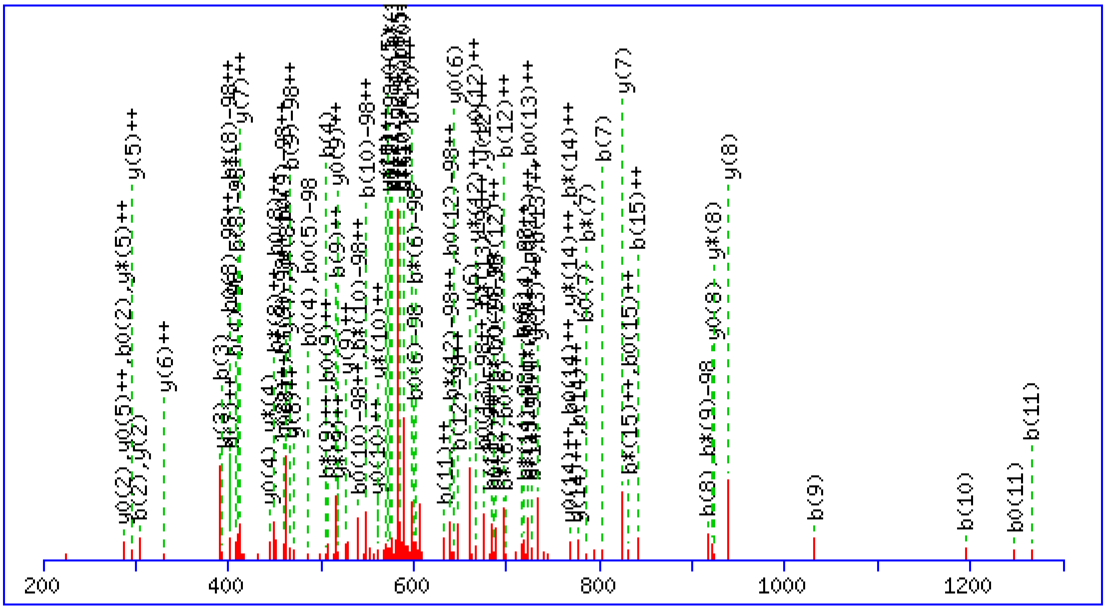
Monoisotopic mass of neutral peptide Mr(calc): 1635.6778
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 54 **Expect:** 1.7e-005
Matched b ions: b(5), b(6)-98, b(6), b(7), b(8)++, b(8), b(8)-98, b(10), b(11)++, b(12), b(13), b(14)
Matched y ions: y(5), y(7), y(9), y(10), y(11), y(12), y(13), y(13)-98

Peptide No.889

SHSLPNSLDYAQASER
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 3688: 1853.793378 from(618.938402,3+) index(1667)
Title: Elution from: 32.804 to 32.804 scan no 2927 cid35.00 polarity:+



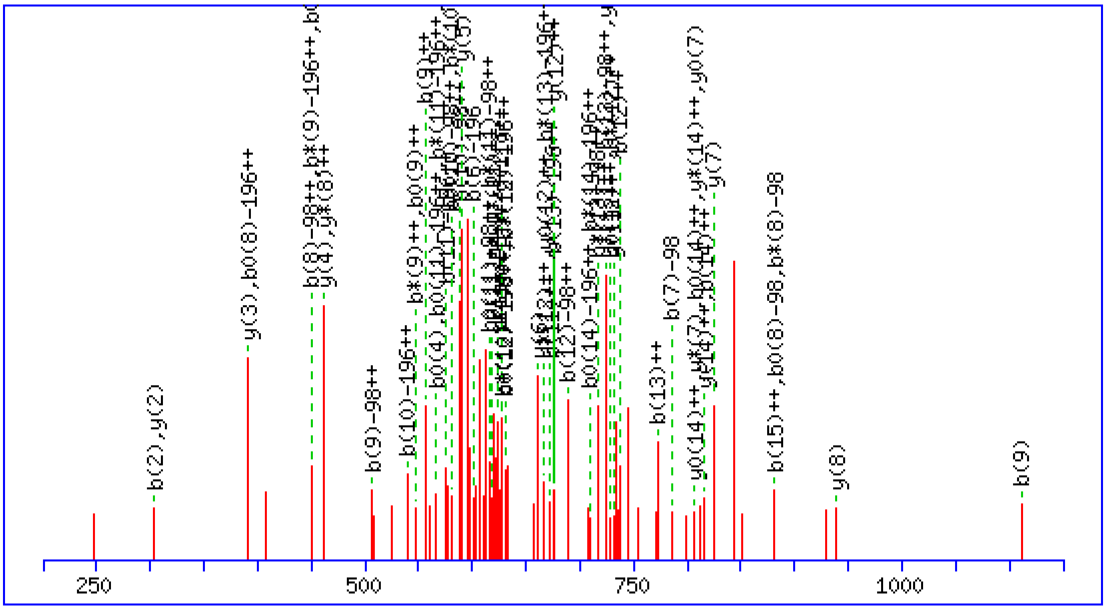
Monoisotopic mass of neutral peptide Mr(calc): 1853.7945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 7.6e-007
Matched b ions: b(2), b(3), b(4)-98, b(4), b(6), b(7), b(7)++, b(8), b(8)-98++, b(8)++, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11), b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9)++, y(10)++, y(12)++, y(13)++, y(14)++

Peptide No.890

SHSLPNSLDYAQASER
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 4604: 1933.760853 from(645.594227,3+) index(1963)
Title: Elution from: 34.486 to 34.486 scan no 3206 cid35.00 polarity:+



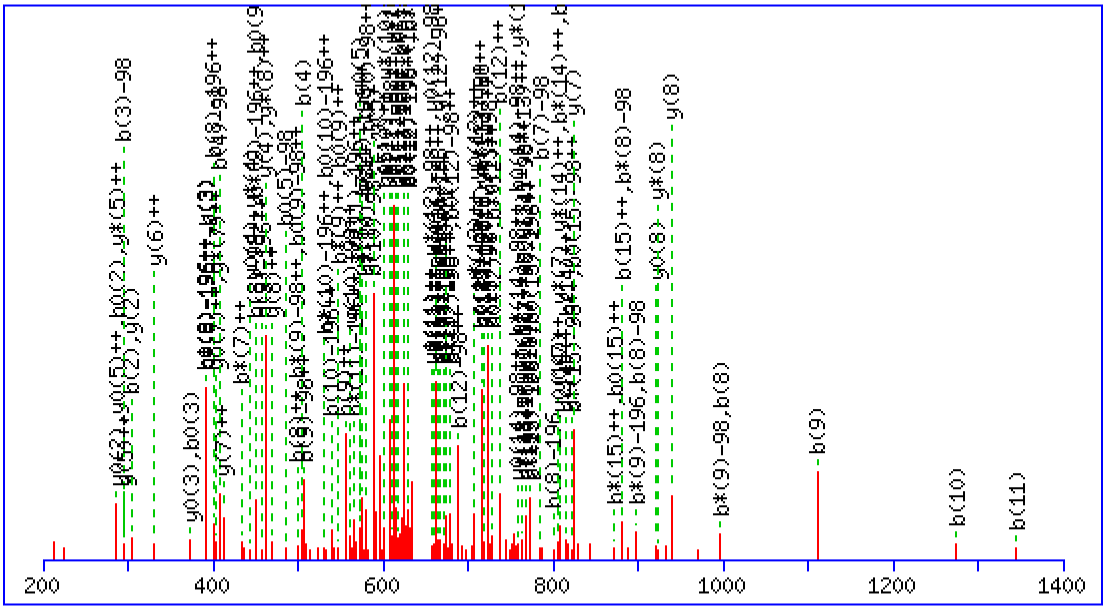
Monoisotopic mass of neutral peptide Mr(calc): 1933.7608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00017
Matched b ions: b(2), b(6)-196, b(7)-98, b(8)-98++, b(9), b(9)-98++, b(9)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)-196++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(11)++, y(12)++, y(13)++, y(14)++

Peptide No.891

SHSLPNSLDYAQASER
Confirmed sites: @S:1,@S:7
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 4035: 1933.760553 from(645.594127,3+) index(4626)
Title: Elution from: 34.072 to 34.072 scan no 3039 cid35.00 polarity:+:m1s



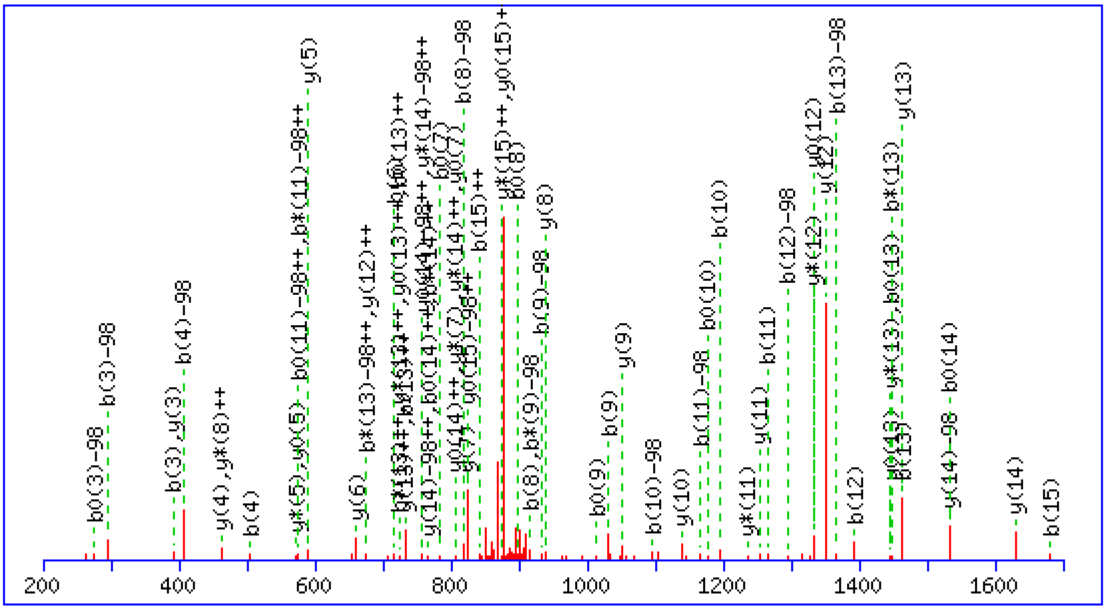
Monoisotopic mass of neutral peptide Mr(calc): 1933.7608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 8.3e-005
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5), b(6), b(6)-98, b(7)-98, b(8), b(8)-196++, b(8)-98++, b(8)-98, b(8)++, b(8)-196, b(9), b(9)-98++, b(9)++, b(9)-196++, b(10), b(10)-98++, b(10)-196++, b(11), b(11)-98++, b(11)-196++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(10)-98++, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++

Peptide No.892

SHSLPNSLDYAQASER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 3767: 1853.789780 from(927.902166,2+) index(1504)
Title: Elution from: 32.628 to 32.628 scan no 2844 cid35.00 polarity:+



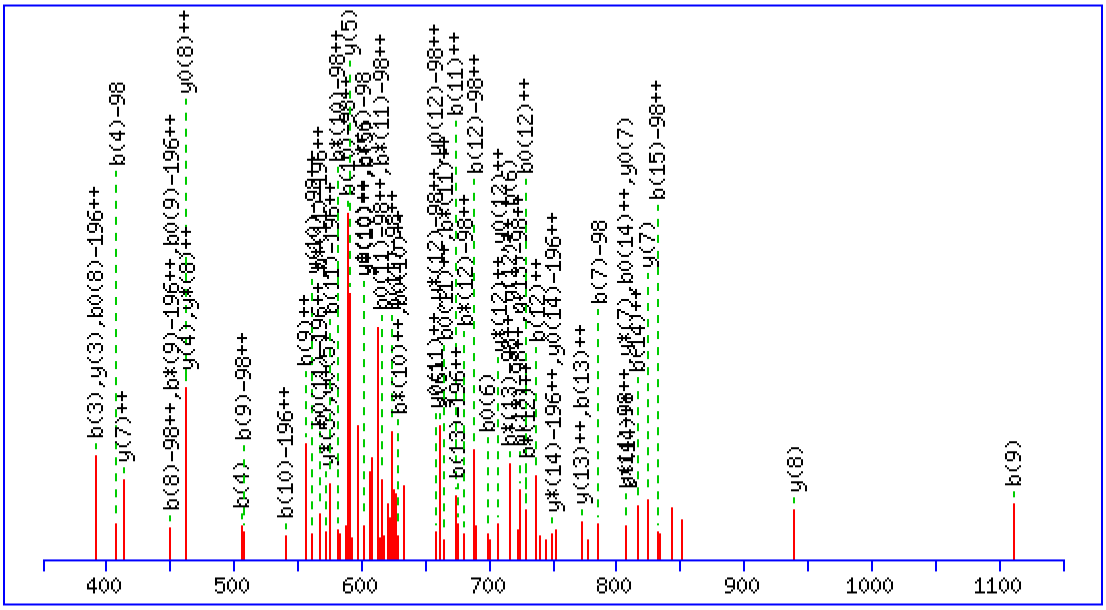
Monoisotopic mass of neutral peptide Mr(calc): 1853.7945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 87 **Expect:** 1e-008
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(6), b(8)-98, b(8), b(9), b(9)-98, b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13)++, b(13), b(13)-98, b(15), b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(12)++, y(13)++, y(13), y(14)-98, y(14), y(14)-98++

Peptide No.893

SHSLPNSLDYAQASER
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 4747: 1933.758585 from(645.593471,3+) index(5658)
Title: Elution from: 34.421 to 34.421 scan no 3231 cid35.00 polarity:+:m1s



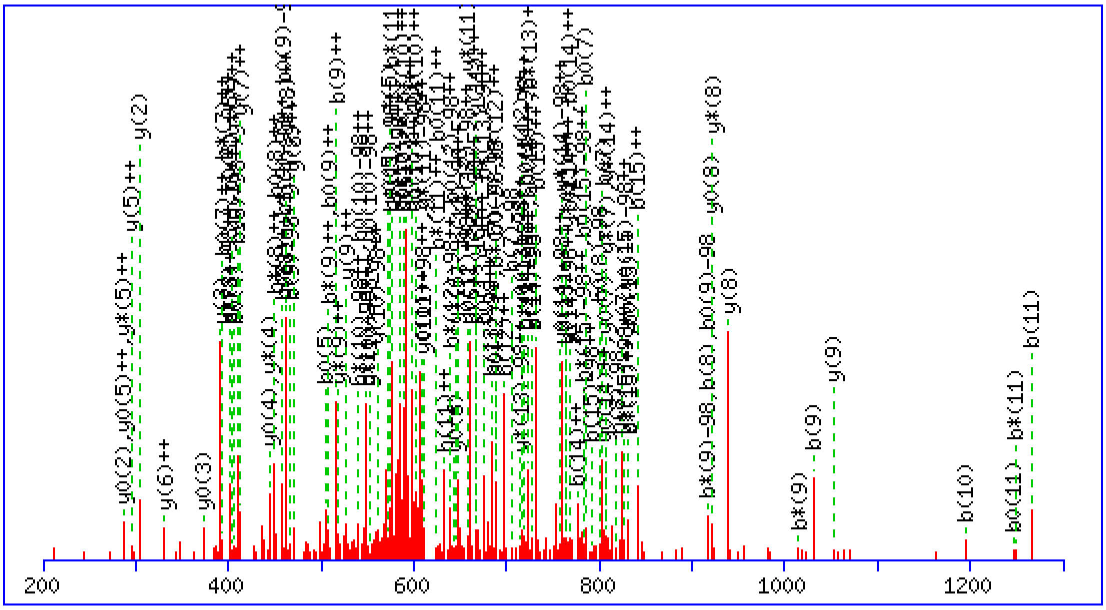
Monoisotopic mass of neutral peptide Mr(calc): 1933.7608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00022
Matched b ions: b(3), b(4)-98, b(4), b(5), b(6), b(7)-98, b(8)-98++, b(9), b(9)++, b(9)-98++, b(10)-98++, b(10)-196++, b(11)-196++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(10)-98++, y(12)++, y(13)-98++, y(13)++, y(14)-98++

Peptide No.894

SHSLPNSLDYAQASER
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SHSLPNSLDYAQASER**
Found in **RMD3_MOUSE** in **SwissProt**, Regulator of microtubule dynamics protein 3 OS=Mus musculus GN=Fam82a2 PE=1 SV=2

Match to Query 4658: 1853.794509 from(618.938779,3+) index(1621)
Title: Elution from: 40.872 to 40.872 scan no 3222 cid35.00 polarity:+



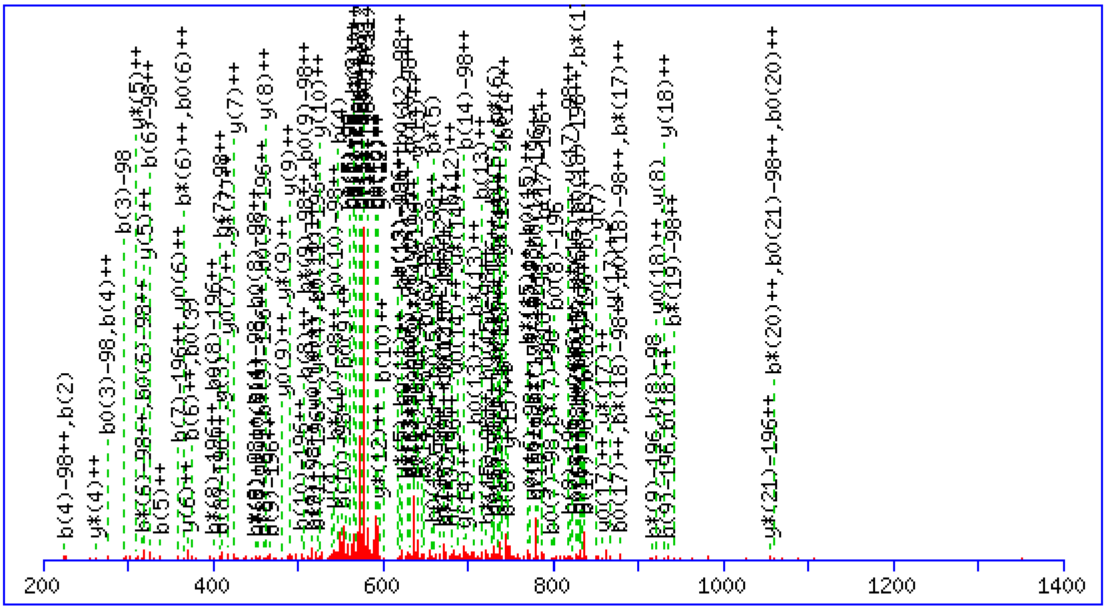
Monoisotopic mass of neutral peptide Mr(calc): 1853.7945
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 64 **Expect:** 2e-006
Matched b ions: b(7), b(7)++, b(7)-98, b(8)-98++, b(8), b(8)++, b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11), b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6), y(6)++, y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10)-98++, y(10)++, y(11)++, y(12)++, y(12)-98++, y(13)-98++, y(14)-98++

Peptide No.895

SHSRQASTDAGTAGALTPQHVR
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **SHSRQASTDAGTAGALTPQHVR**
Found in **YAP1_MOUSE** in **SwissProt**, Yorkie homolog OS=Mus musculus GN=Yap1 PE=1 SV=2

Match to Query 6089: 2407.042924 from(602.768007,4+) index(3986)
Title: Elution from: 29.184 to 29.184 scan no 1792 cid35.00 polarity:+:m1s



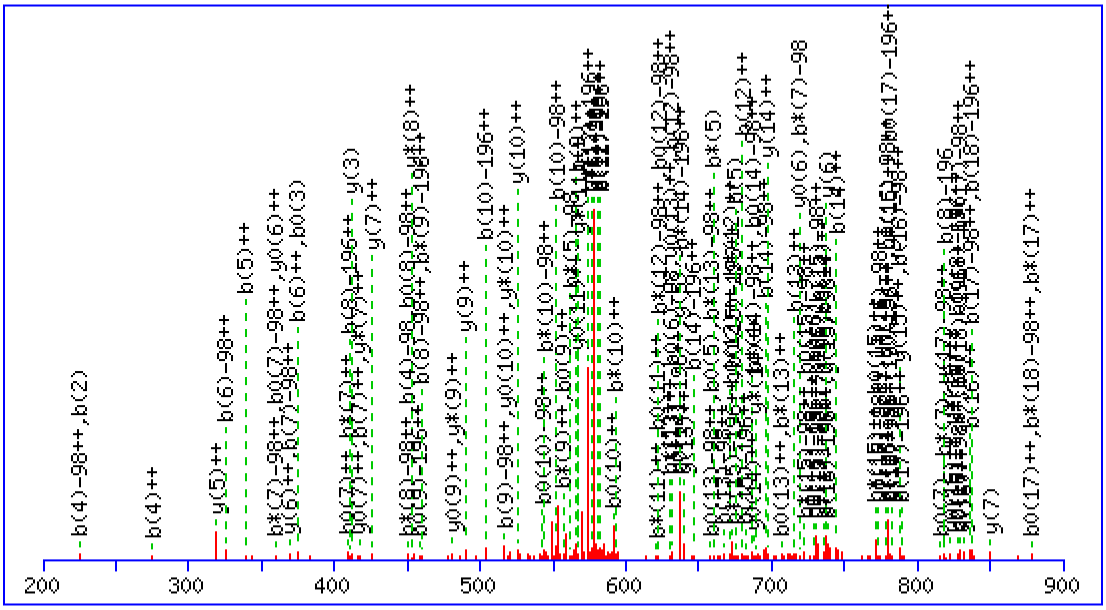
Monoisotopic mass of neutral peptide Mr(calc): 2407.0431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00027
Matched b ions: b(2), b(3)-98, b(4)-98++, b(4)++, b(4)-98, b(4), b(5)-98, b(5)++, b(6)-98++, b(6)++, b(6)-98, b(6), b(7)-98++, b(7)-196++, b(8)-196++, b(8)-98++, b(8)++, b(8)-196, b(8)-98, b(9)-98++, b(9)-196, b(9)-196++, b(9)++, b(10)-196++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)-196++, b(18)++, b(18)-196++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7)++, y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++

Peptide No.896

SHSRQASTDAGTAGALTPQHVR
Confirmed sites: @S:3,@T:8
Ambiguous sites:

MS/MS Fragmentation of **SHSRQASTDAGTAGALTPQHVR**
Found in **YAP1_MOUSE** in **SwissProt**, Yorkie homolog OS=Mus musculus GN=Yap1 PE=1 SV=2

Match to Query 5081: 2407.042808 from(602.767978,4+) index(3362)
Title: Elution from: 21.619 to 21.619 scan no 1336 cid35.00 polarity:+:m1s



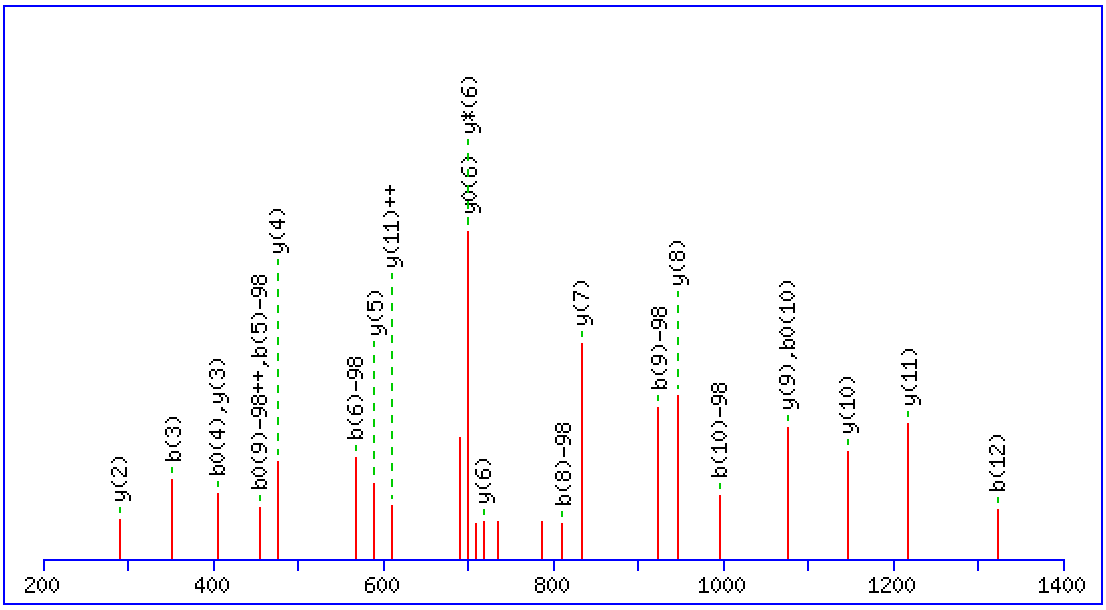
Monoisotopic mass of neutral peptide Mr(calc): 2407.0431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00042
Matched b ions: b(2), b(4)-98++, b(4)++, b(4)-98, b(5)-98, b(5)++, b(5), b(6)-98++, b(6)++, b(7)-98++, b(7)++, b(7)-98, b(8)-196++, b(8)-98++, b(8)-196, b(9)-98++, b(9)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)++, b(12)-98++, b(12)-196++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(15)-196++, b(16)++, b(16)-196++, b(16)-98++, b(17)-98++, b(17)-196++, b(18)-196++
Matched y ions: y(3), y(5)++, y(5), y(6), y(6)++, y(7), y(7)++, y(9)++, y(10)++, y(11)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-98++

Peptide No.897

SIAAELDELADDR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SIAAELDELADDR**
Found in **STX16_MOUSE** in **SwissProt**, Syntaxin-16 OS=Mus musculus GN=Stx16 PE=1 SV=3

Match to Query 2959: 1496.639232 from(749.326892,2+) index(3376)
Title: Elution from: 56.699 to 56.699 scan no 5866 cid35.00 polarity:+



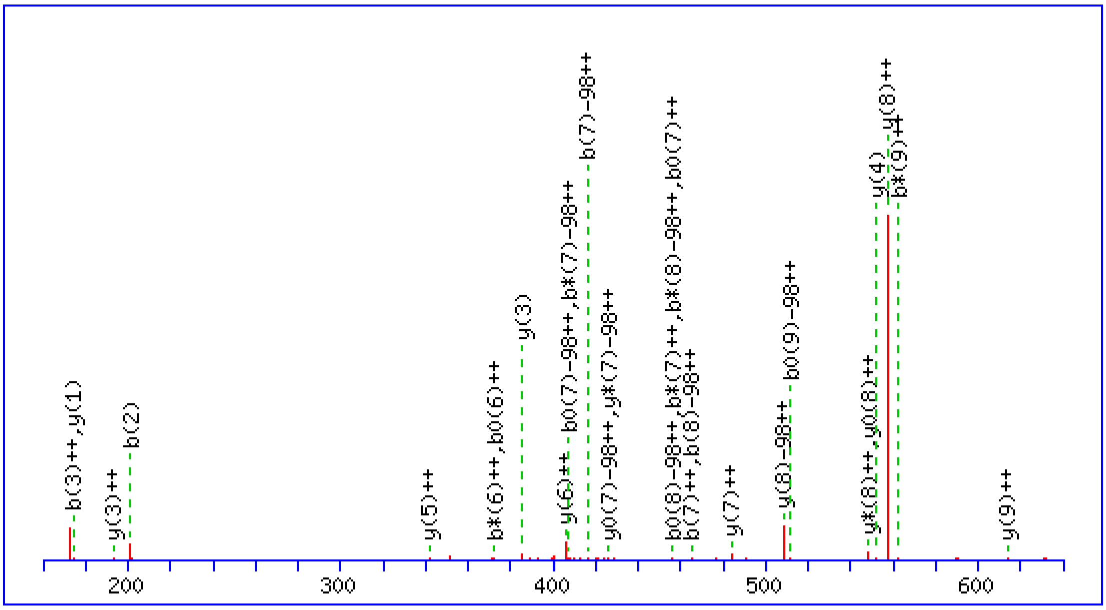
Monoisotopic mass of neutral peptide Mr(calc): 1496.6395
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 **Expect:** 7.3e-010
Matched b ions: b(3), b(5)-98, b(6)-98, b(8)-98, b(9)-98, b(10)-98, b(12)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)++, y(11)

Peptide No.898

SIFREESPLR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SIFREESPLR**
Found in **BCLF1_MOUSE** in **SwissProt**, Bcl-2-associated transcription factor 1 OS=Mus musculus GN=Bclaf1 PE=1 SV=2

Match to Query 2054: 1312.618473 from(438.546767,3+) index(1590)
Title: Elution from: 31.040 to 31.040 scan no 2740 cid35.00 polarity:+



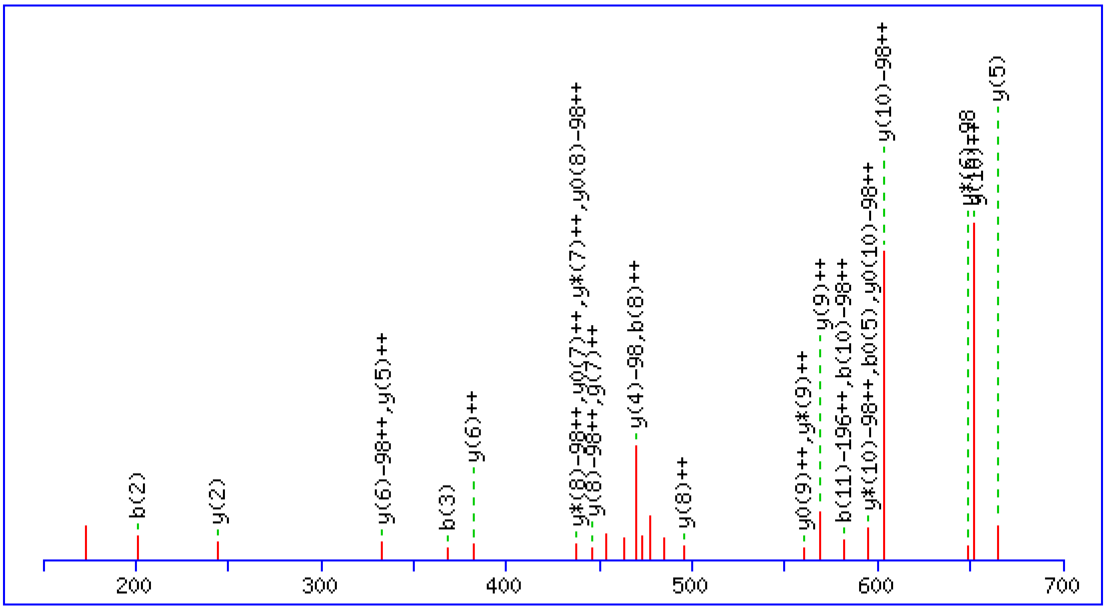
Monoisotopic mass of neutral peptide Mr(calc): 1312.6176
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0046
Matched b ions: b(2), b(3)++, b(7)-98++, b(7)++, b(8)-98++
Matched y ions: y(1), y(3), y(3)++, y(4), y(5)++, y(6)++, y(7)++, y(8)++, y(8)-98++, y(9)++

Peptide No.899

SISFPEVPRSPK
Confirmed sites: @S:3,@S:10
Ambiguous sites:

MS/MS Fragmentation of **SISFPEVPRSPK**
Found in **SVIL_MOUSE** in **SwissProt**, Supervillin OS=Mus musculus GN=Svil PE=1 SV=1

Match to Query 2588: 1502.657334 from(501.893054,3+) index(5212)
Title: Elution from: 41.298 to 41.298 scan no 3968 cid35.00 polarity:+:m1s



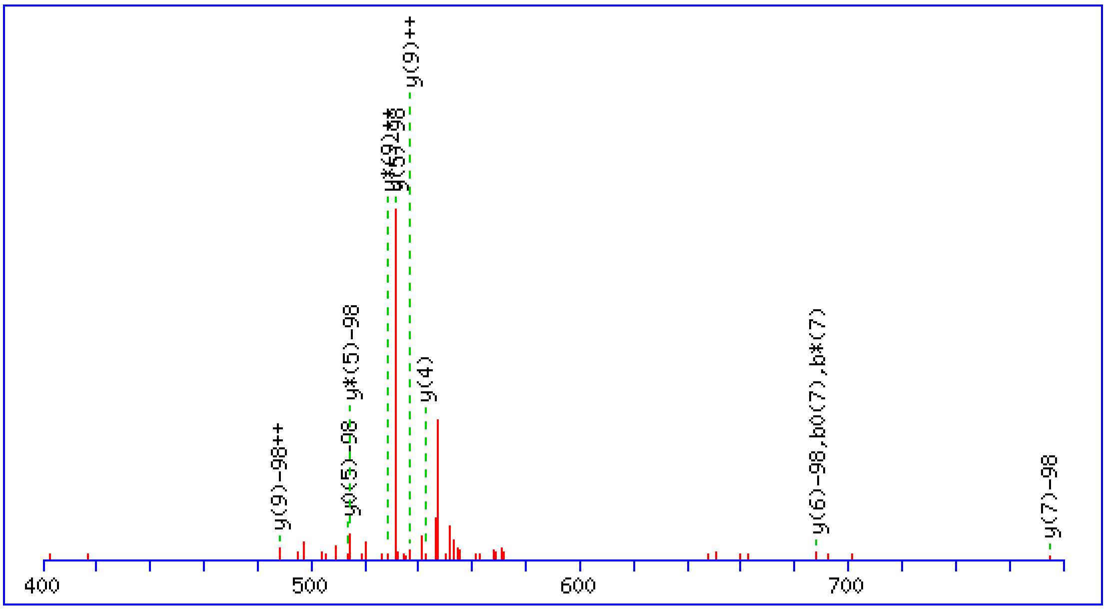
Monoisotopic mass of neutral peptide Mr(calc): 1502.6571
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0014
Matched b ions: b(2), b(3), b(8)++, b(10)-98++, b(11)-196++
Matched y ions: y(2), y(4)-98, y(5)++, y(5), y(6)-98++, y(6)++, y(7)++, y(8)++, y(8)-98++, y(9)++, y(10)++, y(10)-98++

Peptide No.900

SISSRSSLSR
Confirmed sites:
Ambiguous sites: @S:7orS:9

MS/MS Fragmentation of **SISSRSSLSR**
Found in **F178A_MOUSE** in **SwissProt**, Protein FAM178A OS=Mus musculus GN=Fam178a PE=2 SV=2

Match to Query 1357: 1158.542358 from(580.278455,2+) index(518)
Title: Elution from: 21.003 to 21.003 scan no 1373 cid35.00 polarity:+



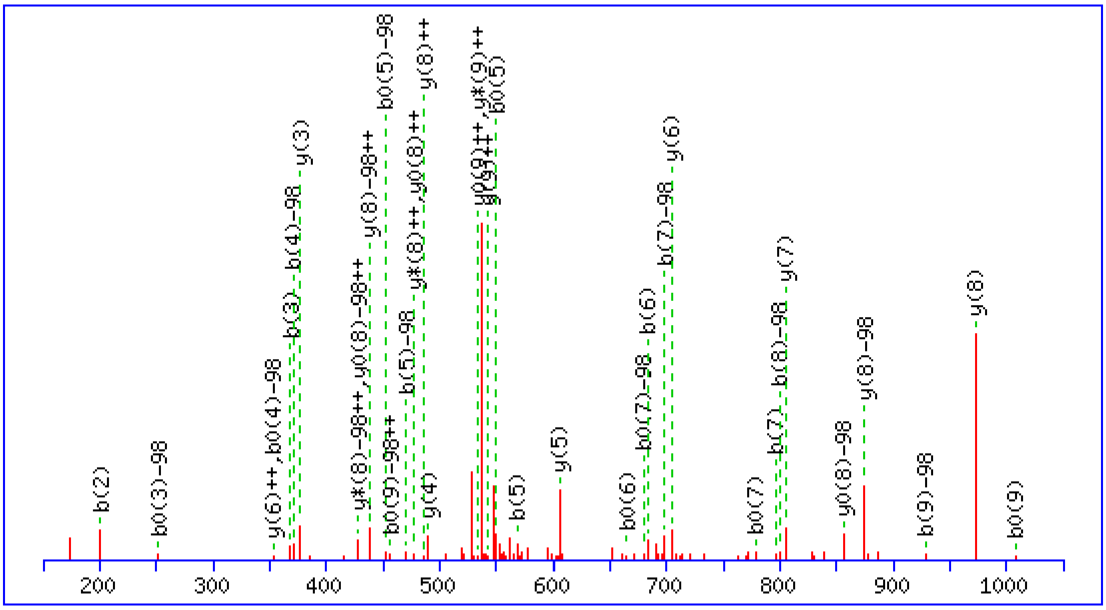
Monoisotopic mass of neutral peptide Mr(calc): 1158.5394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 **Expect:** 0.044
Matched b ions: b(5)
Matched y ions: y(4), y(5)-98, y(6)-98, y(7)-98, y(9)-98++, y(9)++

Peptide No.901

SISTVDLTEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SISTVDLTEK**
Found in **BI2L1_MOUSE** in **SwissProt**, Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Mus musculus GN=Baiap2l1 PE=1 SV=1

Match to Query 1528: 1171.537288 from(586.775920,2+) index(1832)
Title: Elution from: 32.751 to 32.751 scan no 3005 cid35.00 polarity:+



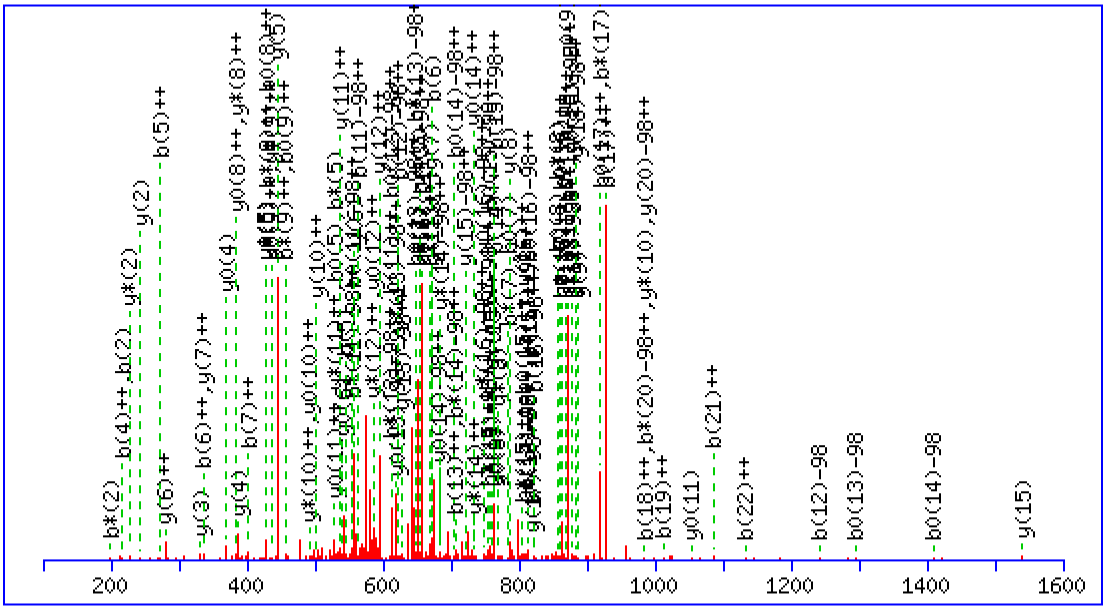
Monoisotopic mass of neutral peptide Mr(calc): 1171.5373
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00018
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(6), b(7)-98, b(7), b(8)-98, b(9)-98
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)-98++, y(8)-98, y(8)++, y(9)++

Peptide No.902

SKESLQEAGKSDANTDLIGGSPK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **SKESLQEAGKSDANTDLIGGSPK**
Found in **MOT1_MOUSE** in **SwissProt**, Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1

Match to Query 6096: 2411.123528 from(603.788158,4+) index(4597)
Title: Elution from: 35.534 to 35.534 scan no 2584 cid35.00 polarity:+:m1s



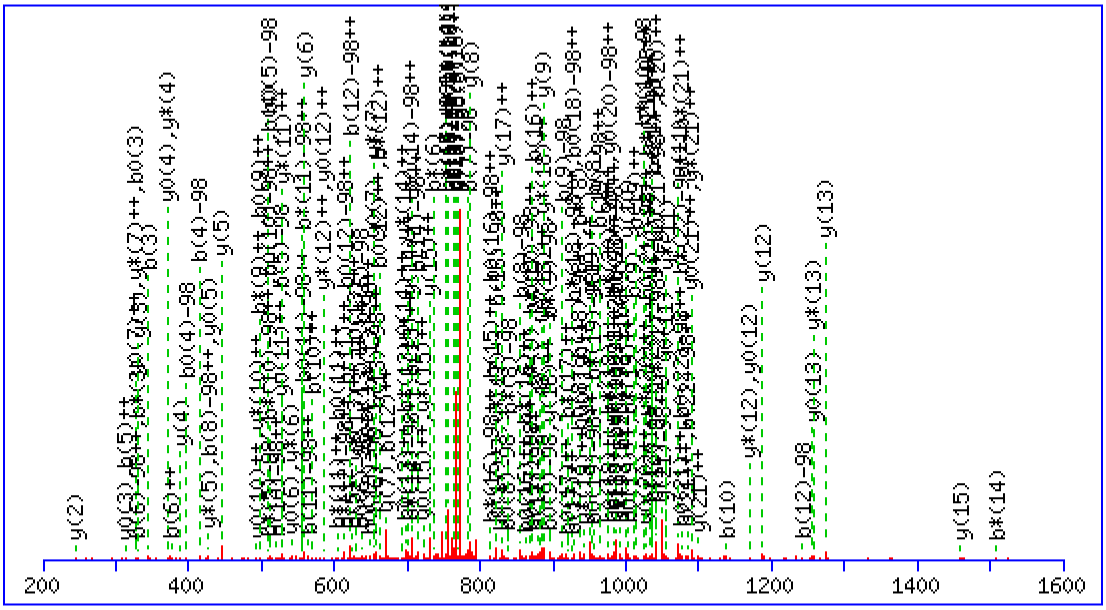
Monoisotopic mass of neutral peptide Mr(calc): 2411.1217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00014
Matched b ions: b(2), b(4)++, b(5)++, b(5), b(6)++, b(6), b(7)++, b(11)++, b(11)-98++, b(12)-98, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(19)++, b(21)++, b(22)++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7), y(8), y(9), y(10)++, y(11)++, y(12)++, y(13)-98++, y(15), y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(20)-98++

Peptide No.903

SKESLQEAGKSDANTDLIGGSPK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SKESLQEAGKSDANTDLIGGSPK**
Found in **MOT1_MOUSE** in **SwissProt**, Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1

Match to Query 6225: 2411.116959 from(804.712929,3+) index(5000)
Title: Elution from: 27.777 to 27.777 scan no 2333 cid35.00 polarity:+:m1s



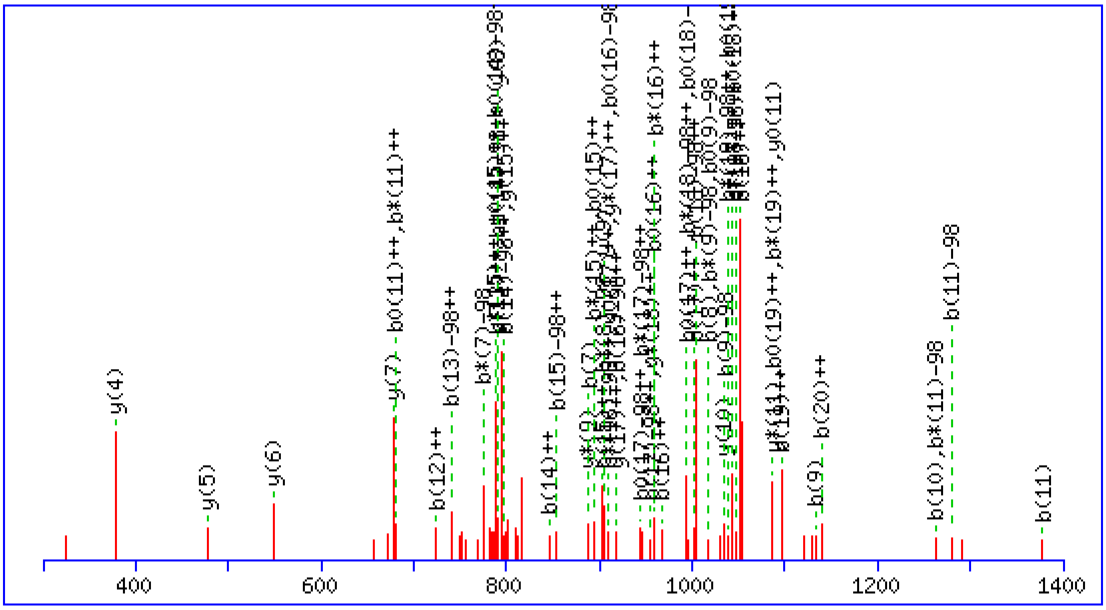
Monoisotopic mass of neutral peptide Mr(calc): 2411.1217
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 **Expect:** 8.6e-008
Matched b ions: b(3), b(4)-98, b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)++, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8)-98++, b(8), b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(12)-98, b(13)++, b(13)-98++, b(14)-98++, b(14)++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)++, b(20)-98++, b(21)++, b(21)-98++, b(22)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14)++, y(15), y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++

Peptide No.904

SKFDSDEEDEDAENLEAVSSGK
Confirmed sites:
Ambiguous sites: @S:1orS:5

MS/MS Fragmentation of **SKFDSDEEDEDAENLEAVSSGK**
Found in **PNISR_MOUSE** in **SwissProt**, Arginine/serine-rich protein PNISR OS=Mus musculus GN=Pnisr PE=1 SV=1

Match to Query 5341: 2479.974123 from(827.665317,3+) index(5231)
Title: Elution from: 38.370 to 38.370 scan no 3625 cid35.00 polarity:+:m1s



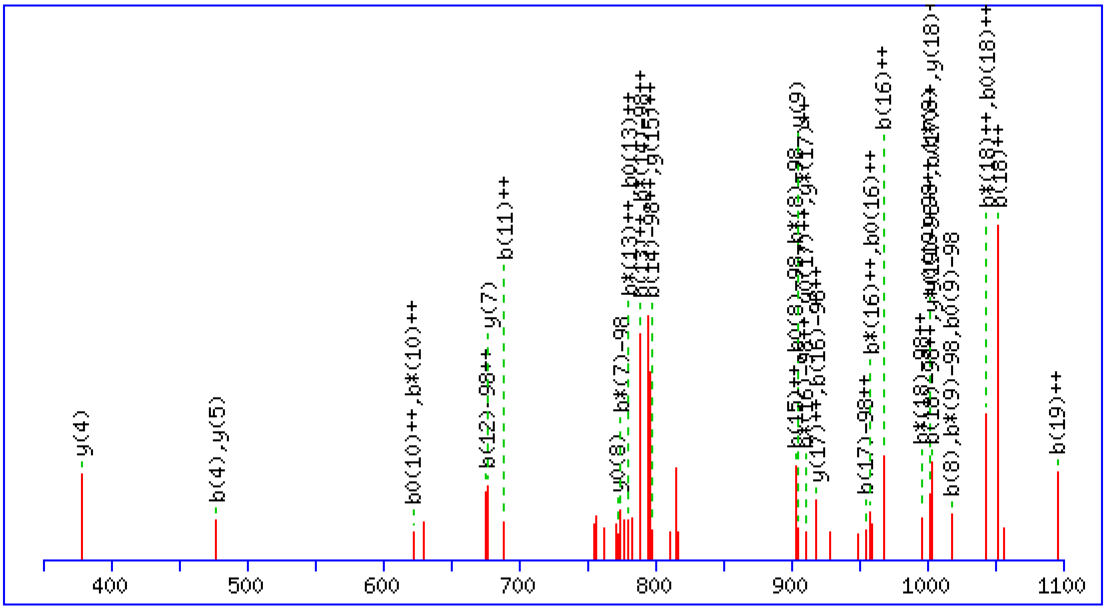
Monoisotopic mass of neutral peptide Mr(calc): 2479.9751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 51 **Expect:** 3e-005
Matched b ions: b(7), b(8), b(9), b(9)-98, b(10), b(11)-98, b(11), b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(15)++, y(17)++

Peptide No.905

SKFDSDEEDEDAENLEAVSSGK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SKFDSDEEDEDAENLEAVSSGK**
Found in **PNISR_MOUSE** in **SwissProt**, Arginine/serine-rich protein PNISR OS=Mus musculus GN=Pnisr PE=1 SV=1

Match to Query 5200: 2479.972950 from(827.664926,3+) index(5030)
Title: Elution from: 38.512 to 38.512 scan no 3619 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2479.9751

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 32 **Expect:** 0.0026

Matched b ions: b(4), b(8), b(11)++, b(12)-98++, b(13)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++

Matched y ions: y(4), y(5), y(7), y(9), y(15)++, y(17)++, y(18)++

Peptide No.906

SKPVFSESLSD

Confirmed sites: @S:10

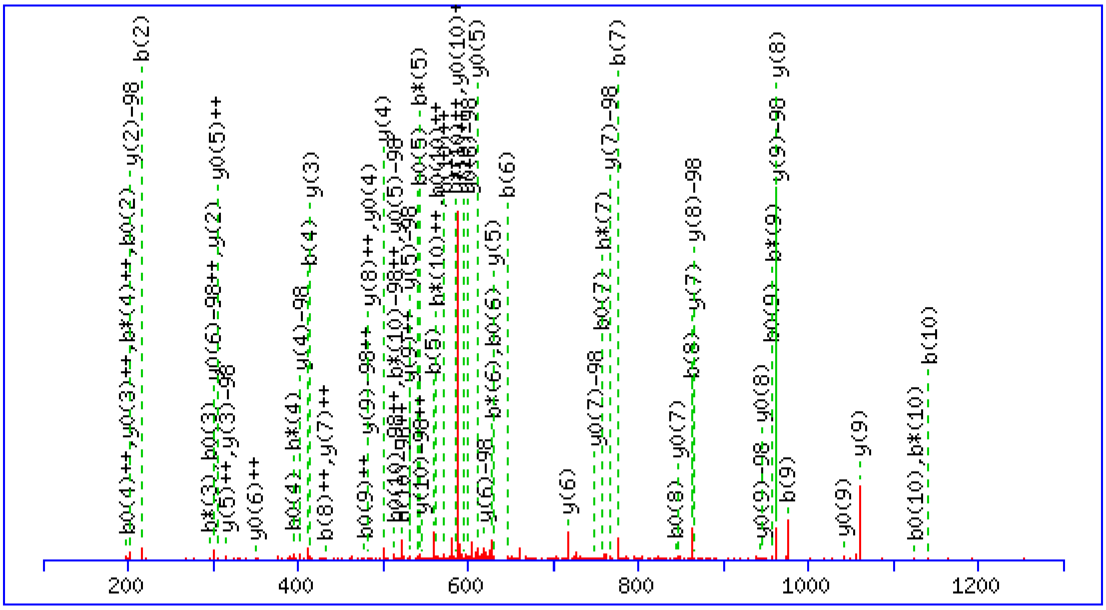
Ambiguous sites:

MS/MS Fragmentation of **SKPVFSESLSD**

Found in **TIM8A_MOUSE** in **SwissProt**, Mitochondrial import inner membrane translocase subunit Tim8 A OS=Mus musculus GN=Timm8a1 PE=1 SV=1

Match to Query 2606: 1274.543236 from(638.278894,2+) index(1785)

Title: Elution from: 43.191 to 43.191 scan no 3485 cid35.00 polarity:+



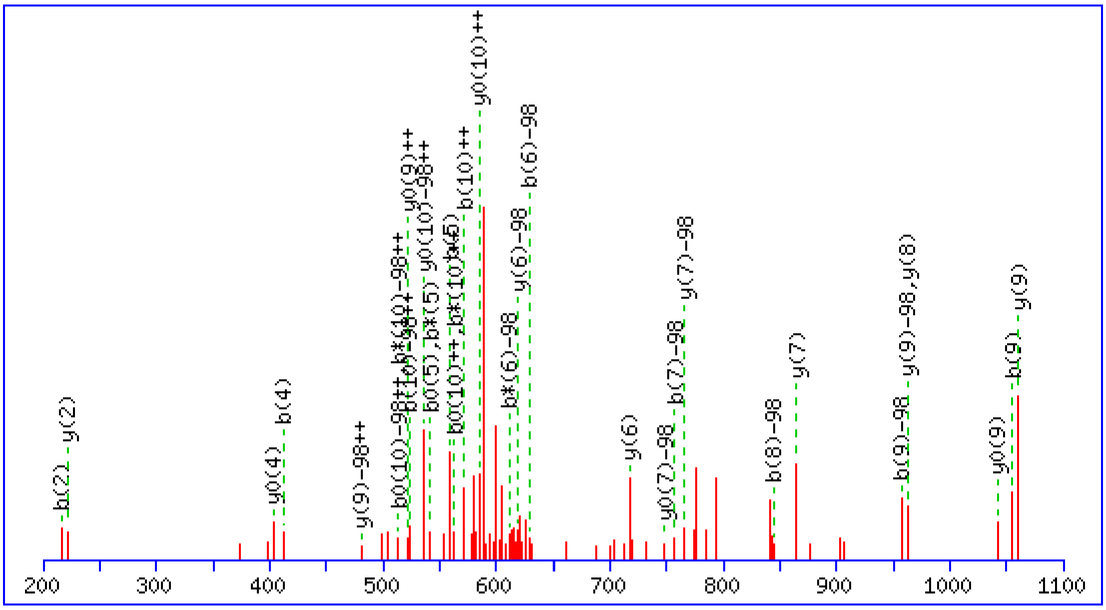
Monoisotopic mass of neutral peptide Mr(calc): 1274.5432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 6.6e-005
Matched b ions: b(2), b(4), b(5), b(6), b(7), b(8), b(8)++, b(9), b(10), b(10)-98++, b(10)++
Matched y ions: y(2), y(2)-98, y(3), y(3)-98, y(4)-98, y(4), y(5)++, y(5)-98, y(5), y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(9)-98, y(9)-98++, y(9)++, y(10)-98++, y(10)++

Peptide No.907

SKPVFSESLSD
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SKPVFSESLSD**
Found in **TIM8A_MOUSE** in **SwissProt**, Mitochondrial import inner membrane translocase subunit Tim8 A OS=Mus musculus GN=Timm8a1 PE=1 SV=1

Match to Query 1998: 1274.543300 from(638.278926,2+) index(1994)
Title: Elution from: 34.295 to 34.295 scan no 3214 cid35.00 polarity:+



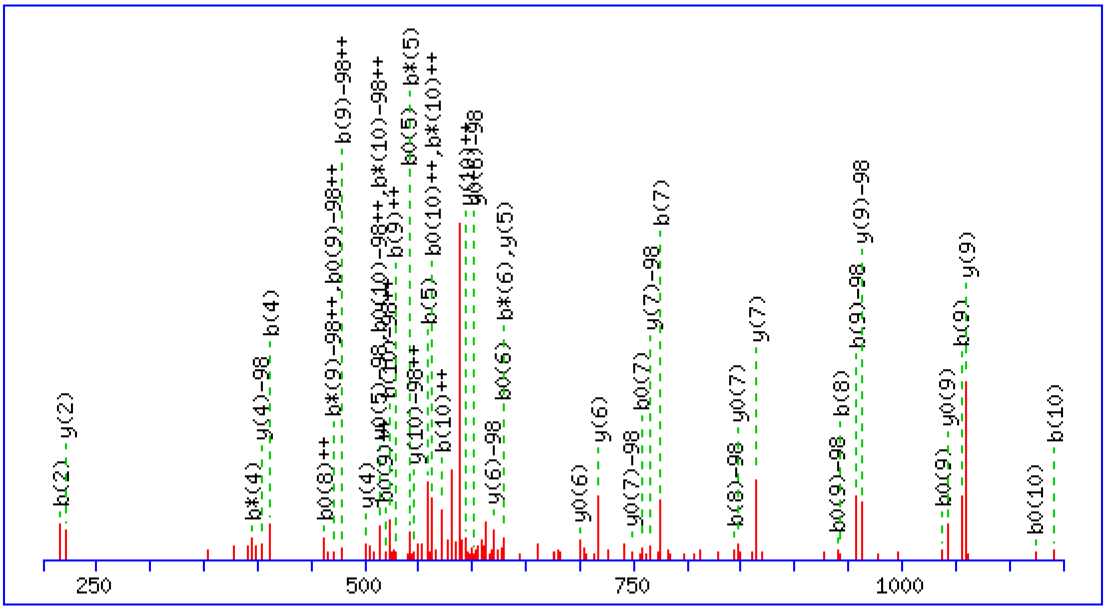
Monoisotopic mass of neutral peptide Mr(calc): 1274.5432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0023
Matched b ions: b(2), b(4), b(5), b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(9), b(10)++, b(10)-98++
Matched y ions: y(2), y(6), y(6)-98, y(7), y(7)-98, y(8), y(9), y(9)-98, y(9)-98++

Peptide No.908

SKPVFSESLSD
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SKPVFSESLSD**
Found in **TIM8A_MOUSE** in **SwissProt**, Mitochondrial import inner membrane translocase subunit Tim8 A OS=Mus musculus GN=Timm8a1 PE=1 SV=1

Match to Query 1800: 1274.543142 from(638.278847,2+) index(1648)
Title: Elution from: 34.222 to 34.222 scan no 3059 cid35.00 polarity:+



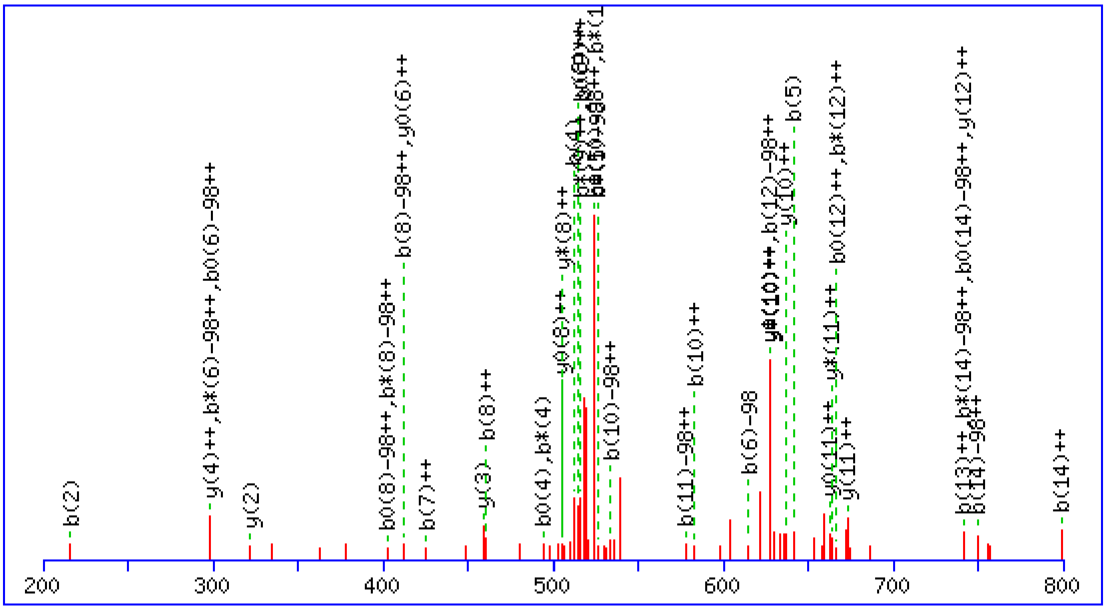
Monoisotopic mass of neutral peptide Mr(calc): 1274.5432
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00037
Matched b ions: b(2), b(4), b(5), b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(9)++, b(10), b(10)++, b(10)-98++
Matched y ions: y(2), y(4)-98, y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(9), y(9)-98, y(10)++, y(10)-98++

Peptide No.909

SKSEEAHAEDSVMDHHFR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SKSEEAHAEDSVMDHHFR**
Found in **PAIRB_MOUSE** in **SwissProt**, Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2

Match to Query 5559: 2190.878396 from(548.726875,4+) index(4642)
Title: Elution from: 25.994 to 25.994 scan no 2053 cid35.00 polarity:+:m1s



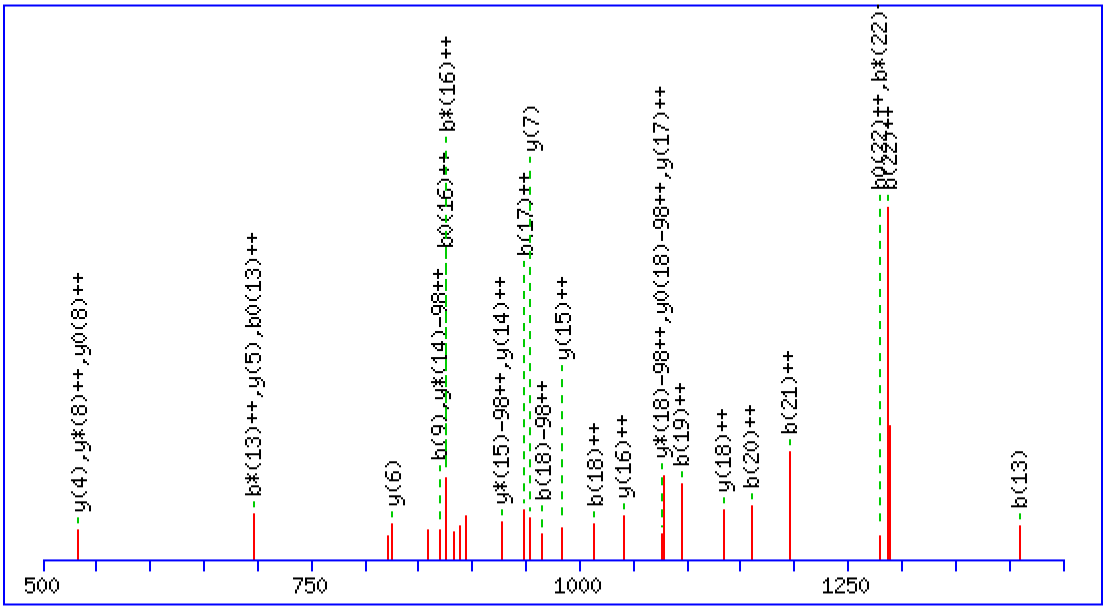
Monoisotopic mass of neutral peptide Mr(calc): 2190.8790
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.031
Matched b ions: b(2), b(4), b(5), b(6)-98, b(7)++, b(8)-98++, b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3), y(4)++, y(8)++, y(10)++, y(11)++, y(12)++

Peptide No.910

SLAALDALNTDDENDEEEYEAWK
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **SLAALDALNTDDENDEEEYEAWK**
Found in **MFAP1_MOUSE** in **SwissProt**, Microfibrillar-associated protein 1 OS=Mus musculus GN=Mfap1 PE=1 SV=1

Match to Query 6685: 2720.100021 from(907.707283,3+) index(7071)
Title: Elution from: 58.431 to 58.431 scan no 6004 cid35.00 polarity:+:m1s



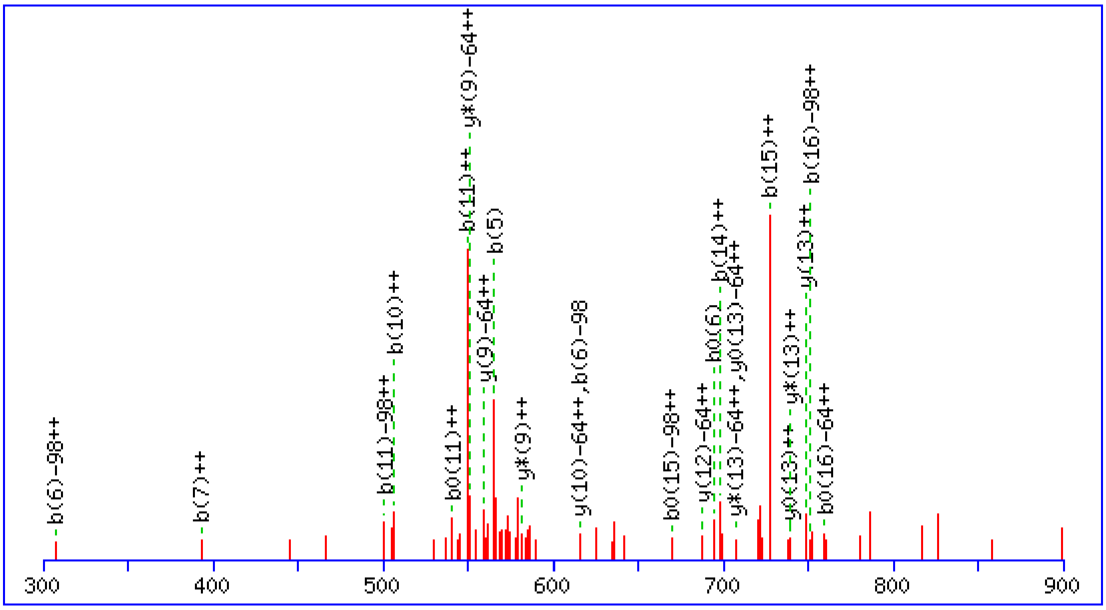
Monoisotopic mass of neutral peptide Mr(calc): 2720.1014
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 3.4e-005
Matched b ions: b(9), b(13), b(17)++, b(18)++, b(18)-98++, b(19)++, b(20)++, b(21)++, b(22)++
Matched y ions: y(4), y(5), y(6), y(7), y(14)++, y(15)++, y(16)++, y(17)++, y(18)++

Peptide No.911

SLALTFAIGGSLLAGMKYFKK
Confirmed sites: @Y:18
Ambiguous sites: @S:1orT:5

MS/MS Fragmentation of **SLALTFAIGGSLLAGMKYFKK**
Found in **SCO1_MOUSE** in **SwissProt**, Protein SCO1 homolog, mitochondrial OS=Mus musculus GN=Sco1 PE=2 SV=1

Match to Query 5979: 2391.168180 from(598.799321,4+) index(1421)
Title: Elution from: 28.997 to 28.997 scan no 2462 cid35.00 polarity:+



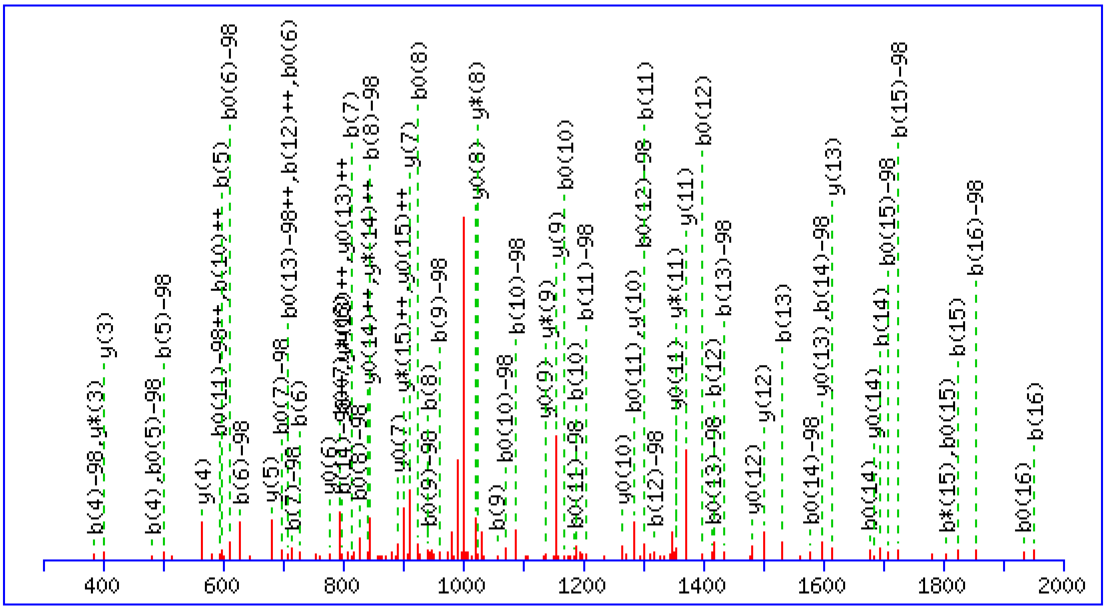
Monoisotopic mass of neutral peptide Mr(calc): 2391.1714
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y18 : Phospho (Y)
Ions Score: 34 **Expect:** 0.0023
Matched b ions: b(5), b(6)-98++, b(6)-98, b(7)++, b(10)++, b(11)++, b(11)-98++, b(14)++, b(15)++, b(16)-98++
Matched y ions: y(13)++

Peptide No.912

SLDSDESEDEDDDYQQK
Confirmed sites:
Ambiguous sites: @S:1orS:4

MS/MS Fragmentation of **SLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 5167: 2096.715640 from(1049.365096,2+) index(1144)
Title: Elution from: 26.279 to 26.279 scan no 2092 cid35.00 polarity:+



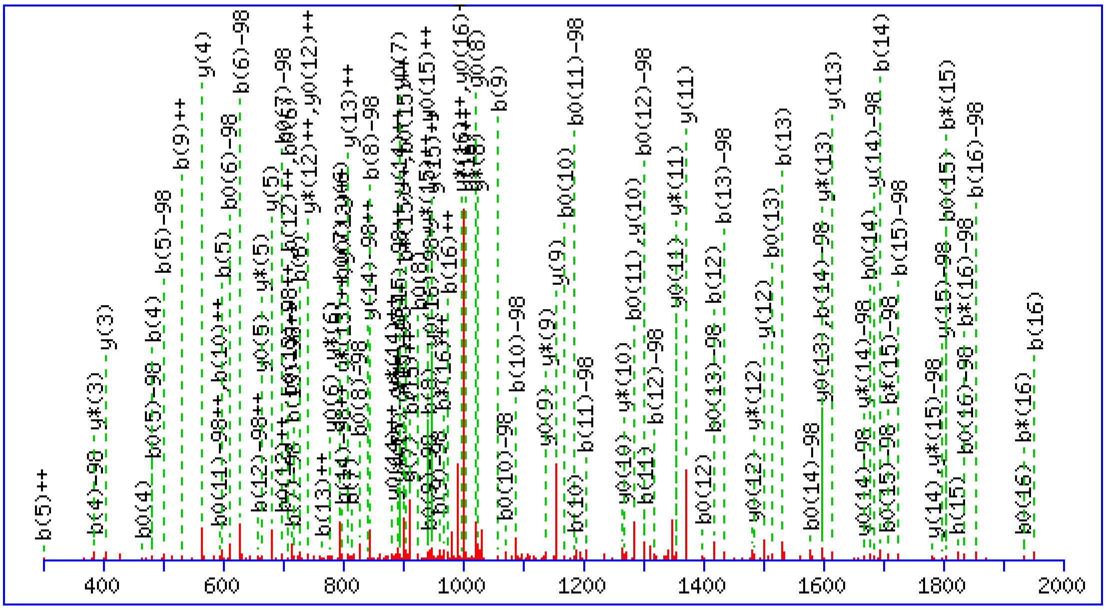
Monoisotopic mass of neutral peptide Mr(calc): 2096.7219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 **Expect:** 2.8e-010
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)-98, b(10), b(10)++, b(11), b(11)-98, b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(14)-98, b(14), b(14)-98++, b(15)-98, b(15), b(16)-98, b(16)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13)

Peptide No.913

SLDSDESEDEDDDYQQK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 4455: 2096.717084 from(1049.365818,2+) index(3856)
Title: Elution from: 25.899 to 25.899 scan no 1920 cid35.00 polarity:+:m1s



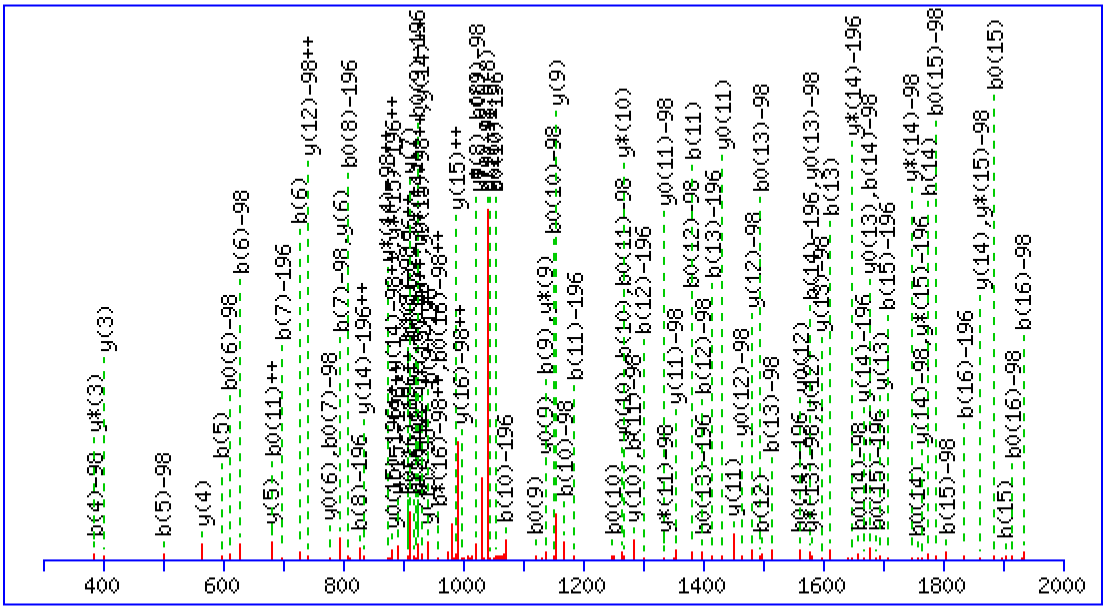
Monoisotopic mass of neutral peptide Mr(calc): 2096.7219
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 **Expect:** 9.1e-009
Matched b ions: b(4)-98, b(4), b(5)-98, b(5), b(5)++, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)++, b(9), b(10), b(10)-98, b(10)++, b(11)-98, b(11), b(12), b(12)-98++, b(12)-98, b(12)++, b(13), b(13)-98, b(13)-98++, b(13)++, b(14), b(14)-98, b(14)-98++, b(15)-98, b(15), b(15)++, b(16)-98, b(16), b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12), y(13), y(13)++, y(14)++, y(14), y(14)-98, y(14)-98++, y(15)-98++, y(15)++, y(15)-98, y(16)++

Peptide No.914

SLDSDESEDEDDDYQQK
Confirmed sites: @S:4,@S:7
Ambiguous sites:

MS/MS Fragmentation of **SLDSDESEDEDDDYQQK**
Found in **HAP28_MOUSE** in **SwissProt**, 28 kDa heat- and acid-stable phosphoprotein OS=Mus musculus GN=Pdap1 PE=1 SV=1

Match to Query 4698: 2176.682138 from(1089.348345,2+) index(1212)
Title: Elution from: 27.701 to 27.701 scan no 2259 cid35.00 polarity:+



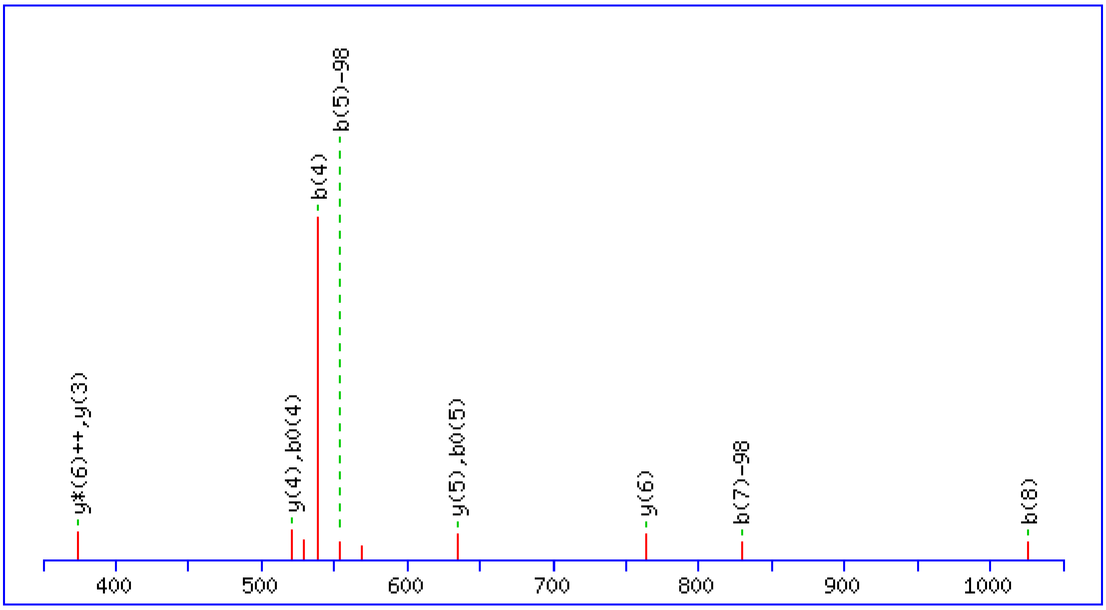
Monoisotopic mass of neutral peptide Mr(calc): 2176.6882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 **Expect:** 6.7e-009
Matched b ions: b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7)-196, b(8)-196, b(8)-98, b(8), b(9)-98, b(9), b(9)-196, b(10)-98, b(10), b(10)-196, b(11)-98, b(11), b(11)-196, b(12)-196, b(12)-98, b(12), b(13)-98, b(13), b(13)-196, b(14)-98, b(14), b(14)-196, b(15)-98, b(15)-196, b(15), b(16)-98, b(16)-196, b(16)-196++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98++, y(12)-98, y(12), y(13), y(13)-98, y(14)-98++, y(14), y(14)-196++, y(14)-98, y(14)++, y(14)-196, y(15)-98++, y(15)-196++, y(15)++, y(16)-98++, y(16)++

Peptide No.915

SLEELFQVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLEELFQVK**
Found in **CGNL1_MOUSE** in **SwissProt**, Cingulin-like protein 1 OS=Mus musculus GN=Cgnl1 PE=1 SV=2

Match to Query 1416: 1171.554446 from(586.784499,2+) index(6764)
Title: Elution from: 54.684 to 54.684 scan no 5627 cid35.00 polarity:+:m1s



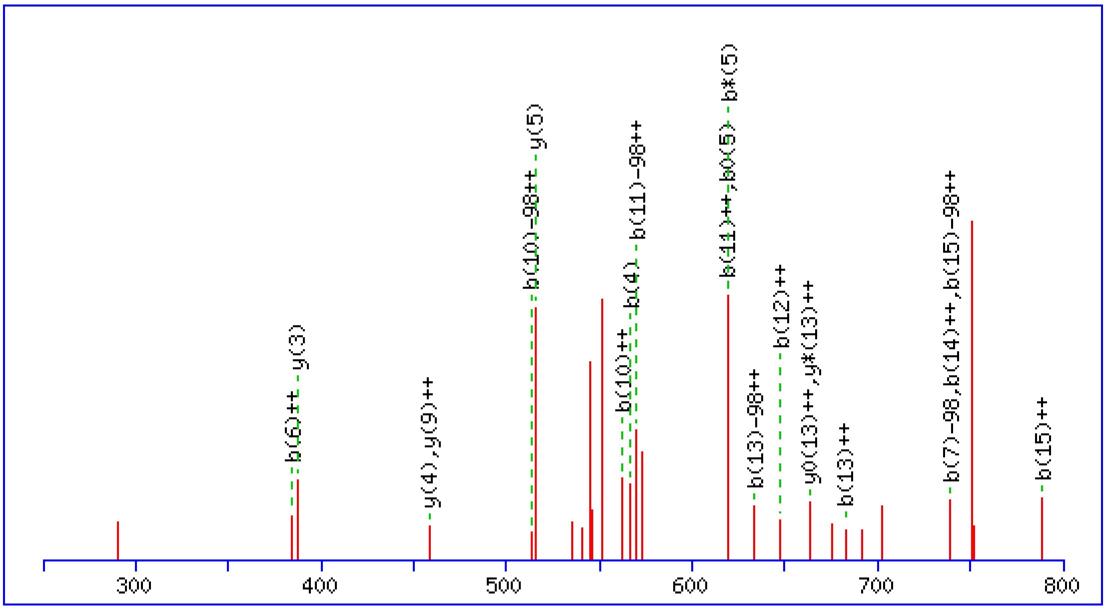
Monoisotopic mass of neutral peptide Mr(calc): 1171.5526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 **Expect:** 0.0013
Matched b ions: b(4), b(5)-98, b(7)-98, b(8)
Matched y ions: y(3), y(4), y(5), y(6)

Peptide No.916

SLERAEAGDNLGALVR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLERAEAGDNLGALVR**
Found in **EFTU_MOUSE** in **SwissProt**, Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1

Match to Query 3388: 1749.841335 from(584.287721,3+) index(5282)
Title: Elution from: 39.029 to 39.029 scan no 3706 cid35.00 polarity:+:m1s



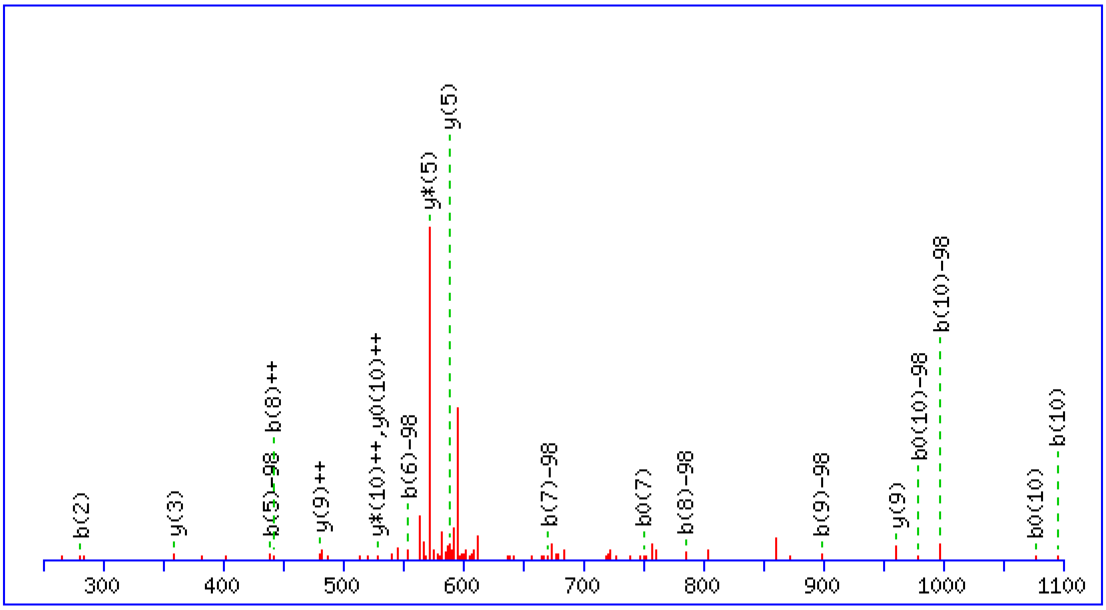
Monoisotopic mass of neutral peptide Mr(calc): 1749.8410
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0035
Matched b ions: b(4), b(6)++, b(7)-98, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(9)++

Peptide No.917

SLGLSDDDIVK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLGLSDDDIVK**
Found in **SYLC_MOUSE** in **SwissProt**, Leucine--tRNA ligase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2

Match to Query 1563: 1240.558998 from(621.286775,2+) index(1735)
Title: Elution from: 33.656 to 33.656 scan no 3034 cid35.00 polarity:+



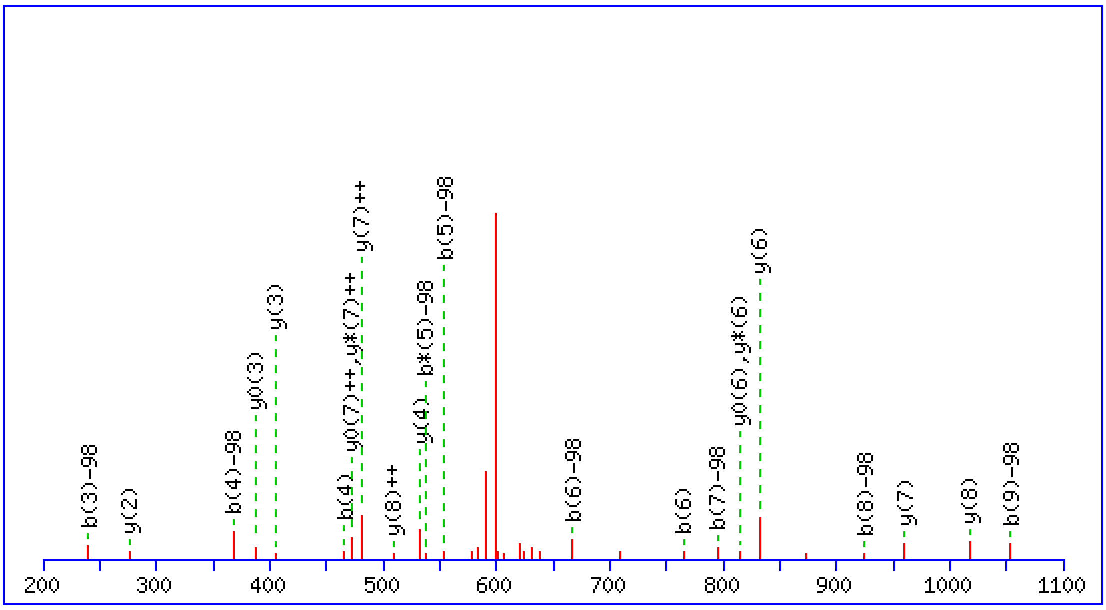
Monoisotopic mass of neutral peptide Mr(calc): 1240.5588
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.018
Matched b ions: b(2), b(5)-98, b(6)-98, b(7)-98, b(8)++, b(8)-98, b(9)-98, b(10)-98, b(10)
Matched y ions: y(3), y(5), y(9), y(9)++

Peptide No.918

SLGQWLQEEK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLGQWLQEEK**
Found in **CPSM_MOUSE** in **SwissProt**, Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2

Match to Query 1947: 1296.575274 from(649.294913,2+) index(3055)
Title: Elution from: 48.990 to 48.990 scan no 5034 cid35.00 polarity:+



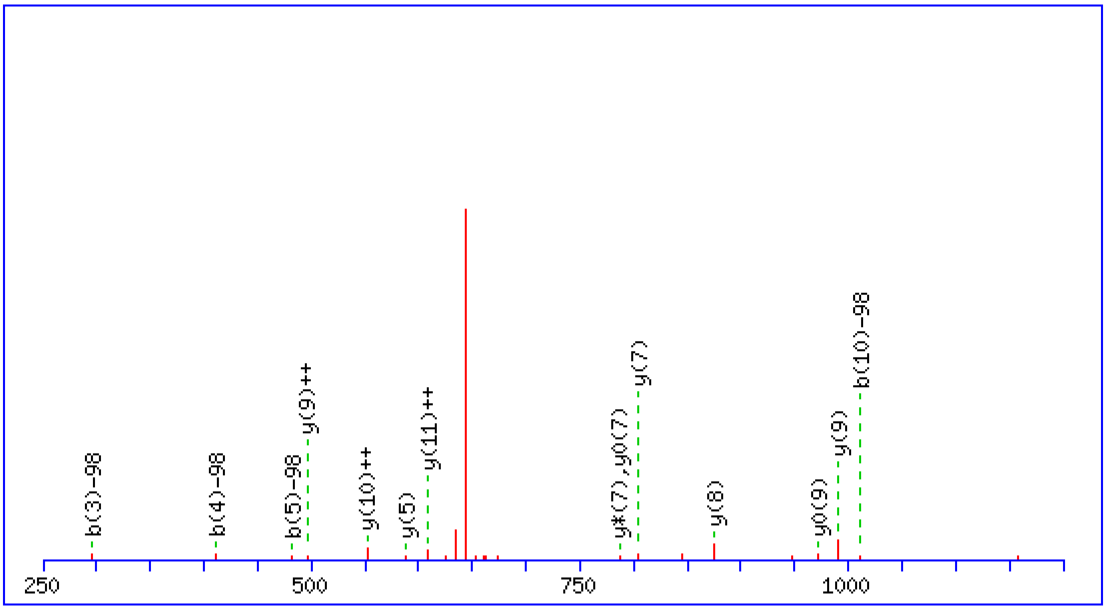
Monoisotopic mass of neutral peptide Mr(calc): 1296.5751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 **Expect:** 9.9e-006
Matched b ions: b(3)-98, b(4)-98, b(4), b(5)-98, b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(4), y(6), y(7)++, y(7), y(8), y(8)++

Peptide No.919

SLLDASEEAIKK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLLDASEEAIKK**
Found in **VINC_MOUSE** in **SwissProt**, Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4

Match to Query 2279: 1382.668484 from(692.341518,2+) index(2027)
Title: Elution from: 35.065 to 35.065 scan no 3284 cid35.00 polarity:+



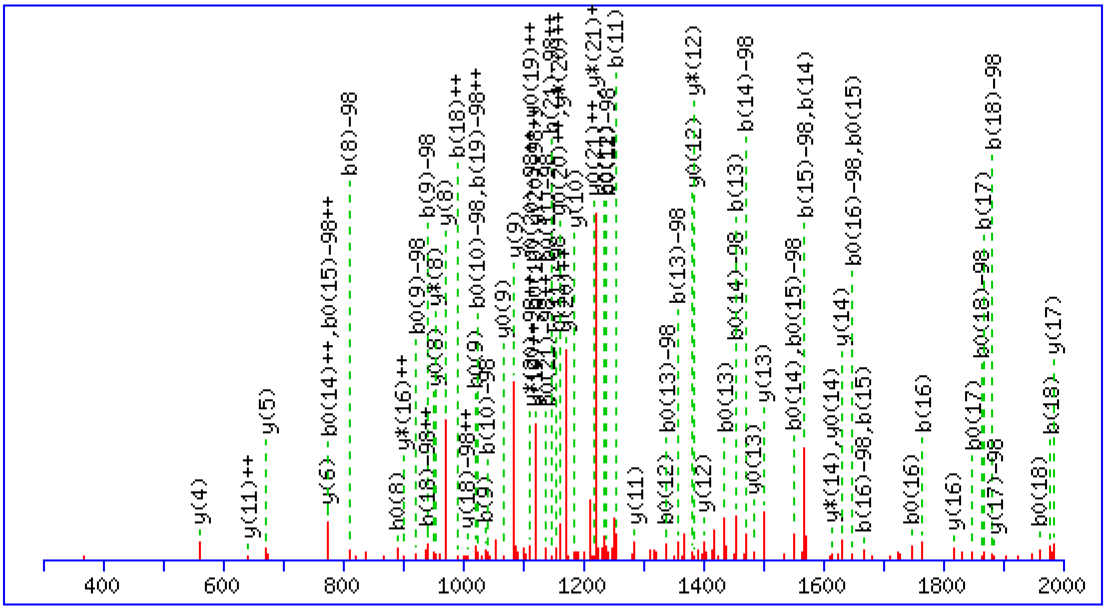
Monoisotopic mass of neutral peptide Mr(calc): 1382.6694
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.00077
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(10)-98
Matched y ions: y(5), y(7), y(8), y(9), y(9)++, y(10)++, y(11)++

Peptide No.920

SLPEESGEETDTVDPVTLYSYK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SLPEESGEETDTVDPVTLYSYK**
Found in **ITIH2_MOUSE** in **SwissProt**, Inter-alpha-trypsin inhibitor heavy chain H2 OS=Mus musculus GN=Itih2 PE=1 SV=1

Match to Query 6268: 2538.092112 from(1270.053332,2+) index(5971)
Title: Elution from: 60.427 to 60.427 scan no 5070 cid35.00 polarity:+:m1s



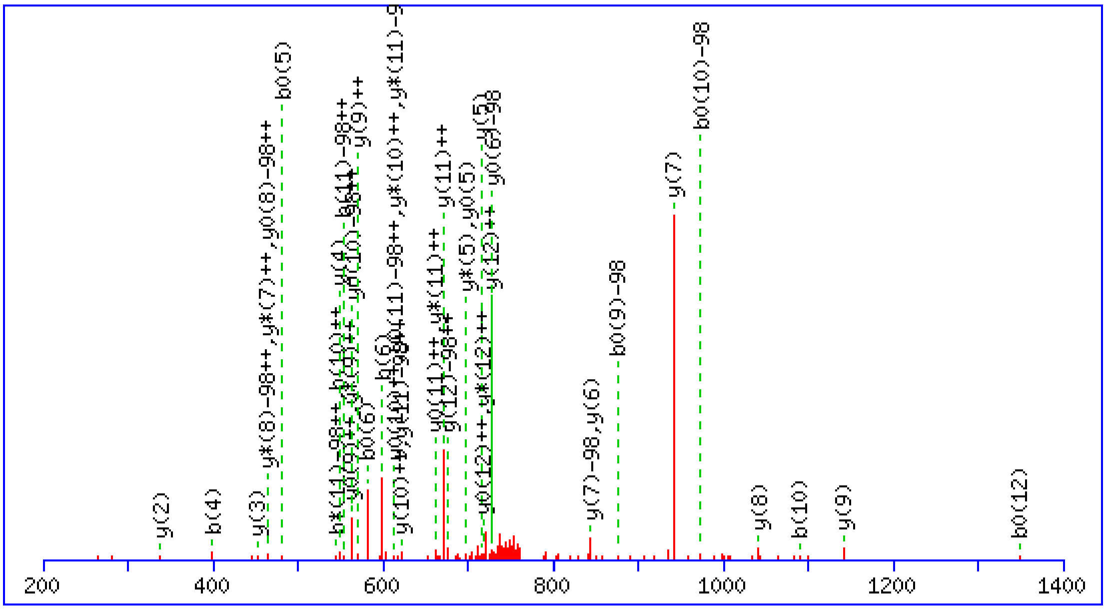
Monoisotopic mass of neutral peptide Mr(calc): 2538.0938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 58 **Expect:** 9.8e-006
Matched b ions: b(8)-98, b(9)-98, b(9), b(10)-98, b(11), b(11)-98, b(13)-98, b(13), b(14), b(14)-98, b(15)-98, b(15), b(16), b(16)-98, b(17), b(18), b(18)-98, b(18)-98++, b(18)++, b(19)-98++, b(21)-98++
Matched y ions: y(4), y(5), y(6), y(8), y(9), y(10), y(11)++, y(11), y(12), y(13), y(14), y(16), y(17), y(17)-98, y(18)-98++, y(19)++, y(20)-98++, y(20)++

Peptide No.921

SLPTTVPESPNYR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **SLPTTVPESPNYR**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 3162: 1539.698236 from(770.856394,2+) index(1452)
Title: Elution from: 41.539 to 41.539 scan no 3152 cid35.00 polarity:+



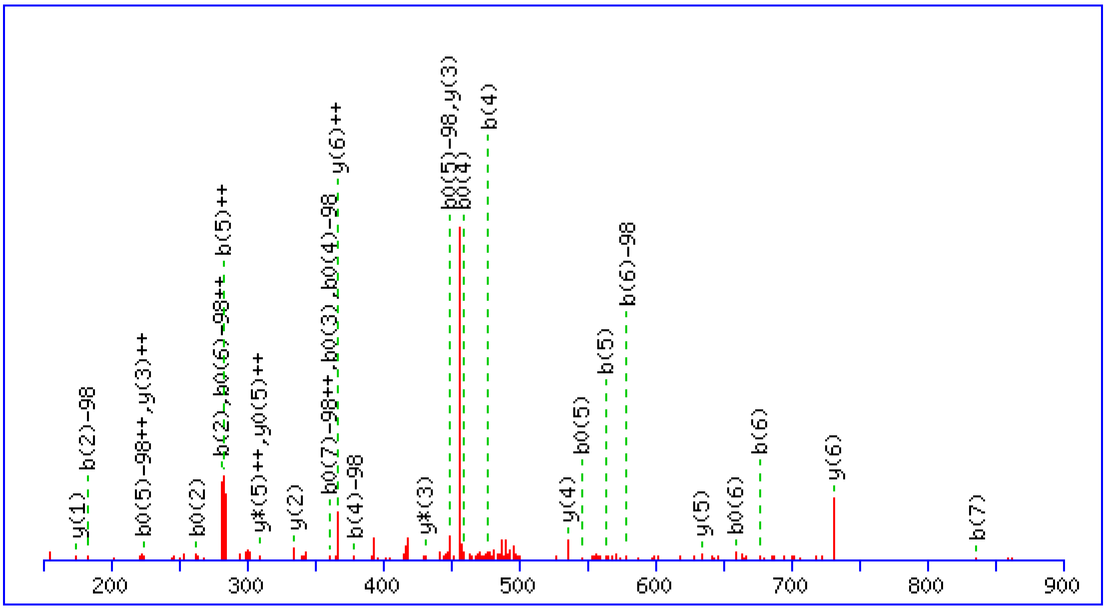
Monoisotopic mass of neutral peptide Mr(calc): 1539.6970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 **Expect:** 0.00076
Matched b ions: b(4), b(6), b(10), b(10)++, b(11)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98, y(7), y(8), y(9), y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++

Peptide No.922

SLPVSICR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLPVSICR**
Found in **SASH1_MOUSE** in **SwissProt**, SAM and SH3 domain-containing protein 1 OS=Mus musculus GN=Sash1 PE=1 SV=1

Match to Query 1140: 1010.461606 from(506.238079,2+) index(1841)
Title: Elution from: 43.873 to 43.873 scan no 3569 cid35.00 polarity:+



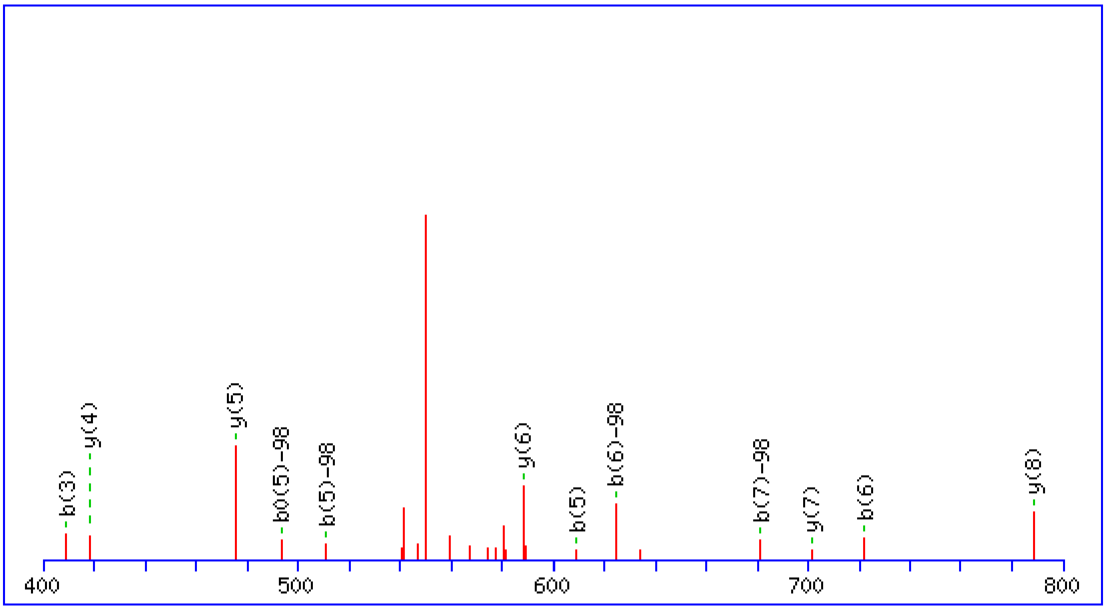
Monoisotopic mass of neutral peptide Mr(calc): 1010.4620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.02
Matched b ions: b(2), b(2)-98, b(4), b(4)-98, b(5)++, b(5), b(6), b(6)-98, b(7)
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(5), y(6)++, y(6)

Peptide No.923

SLQSLLGPSSK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SLQSLLGPSSK**
Found in **CORO7_MOUSE** in **SwissProt**, Coronin-7 OS=Mus musculus GN=Coro7 PE=2 SV=2

Match to Query 1522: 1195.584754 from(598.799653,2+) index(2600)
Title: Elution from: 41.696 to 41.696 scan no 4163 cid35.00 polarity:+



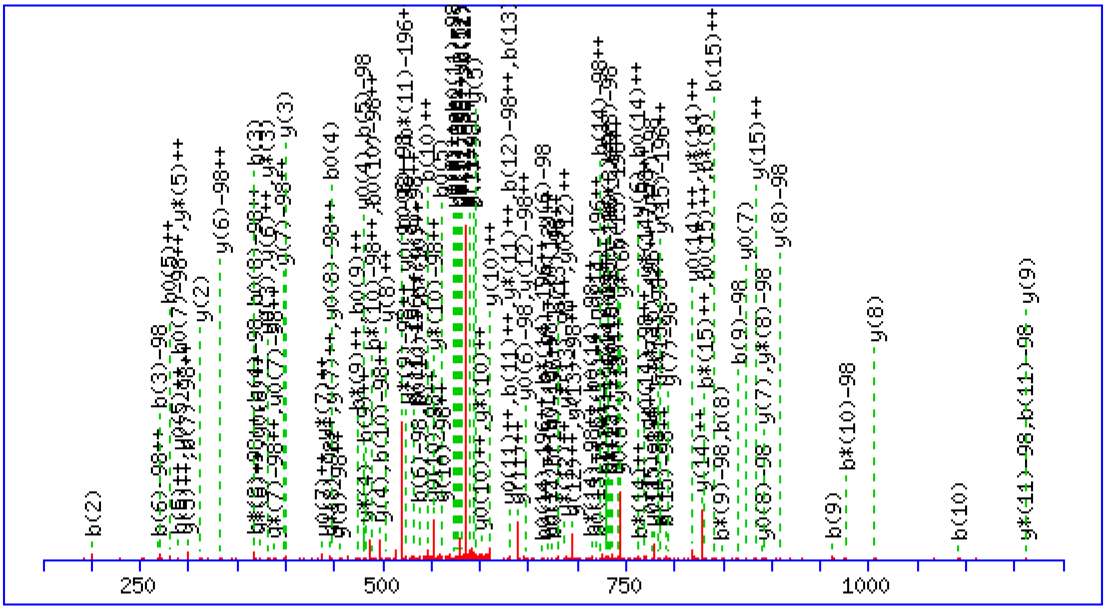
Monoisotopic mass of neutral peptide Mr(calc): 1195.5849
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 0.00012
Matched b ions: b(3), b(5), b(5)-98, b(6)-98, b(6), b(7)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8)

Peptide No.924

SLSPLGGRDESPVSHR
Confirmed sites: @S:3,@S:11
Ambiguous sites:

MS/MS Fragmentation of **SLSPLGGRDESPVSHR**
Found in **CDK13_MOUSE** in **SwissProt**, Cyclin-dependent kinase 13 OS=Mus musculus GN=Cdk13 PE=1 SV=3

Match to Query 4647: 1852.787958 from(618.603262,3+) index(4529)
Title: Elution from: 34.902 to 34.902 scan no 2500 cid35.00 polarity:+:m1s



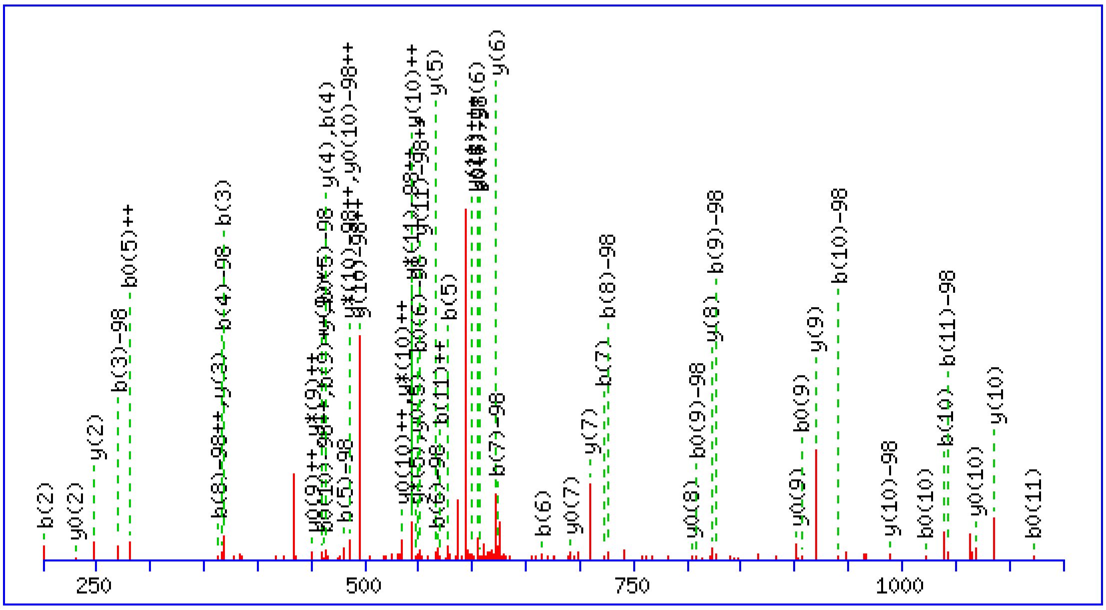
Monoisotopic mass of neutral peptide Mr(calc): 1852.7870
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0013
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(7)-98++, b(7)-98, b(8), b(9), b(9)++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)-98, b(11)-196++, b(11)-98++, b(11)++, b(12)-196++, b(12)-98++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)-98++, y(6)++, y(6)-98, y(6), y(7)++, y(7), y(7)-98++, y(7)-98, y(8), y(8)-98, y(8)-98++, y(8)++, y(9), y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)++

Peptide No.925

SLSPLSGTTDTK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SLSPLSGTTDTK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 1759: 1285.579556 from(643.797054,2+) index(1325)
Title: Elution from: 28.703 to 28.703 scan no 2395 cid35.00 polarity:+



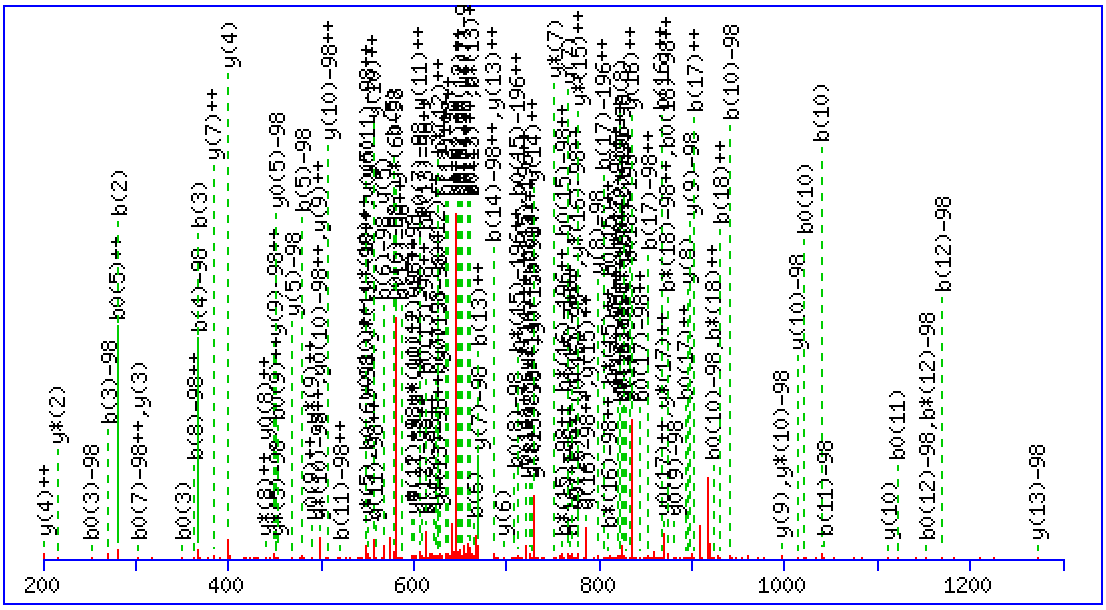
Monoisotopic mass of neutral peptide Mr(calc): 1285.5803
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 63 **Expect:** 2.2e-006
Matched b ions: b(2), b(3), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8)-98++, b(9)-98, b(9)++, b(10), b(10)-98, b(11)-98, b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10)-98++, y(10), y(10)++, y(10)-98, y(11)-98++, y(11)++

Peptide No.926

SLSPLSGTTDTKAESPAGR
Confirmed sites: @S:1,@S:15
Ambiguous sites:

MS/MS Fragmentation of **SLSPLSGTTDTKAESPAGR**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4514: 2033.871099 from(678.964309,3+) index(1232)
Title: Elution from: 38.142 to 38.142 scan no 2781 cid35.00 polarity:+



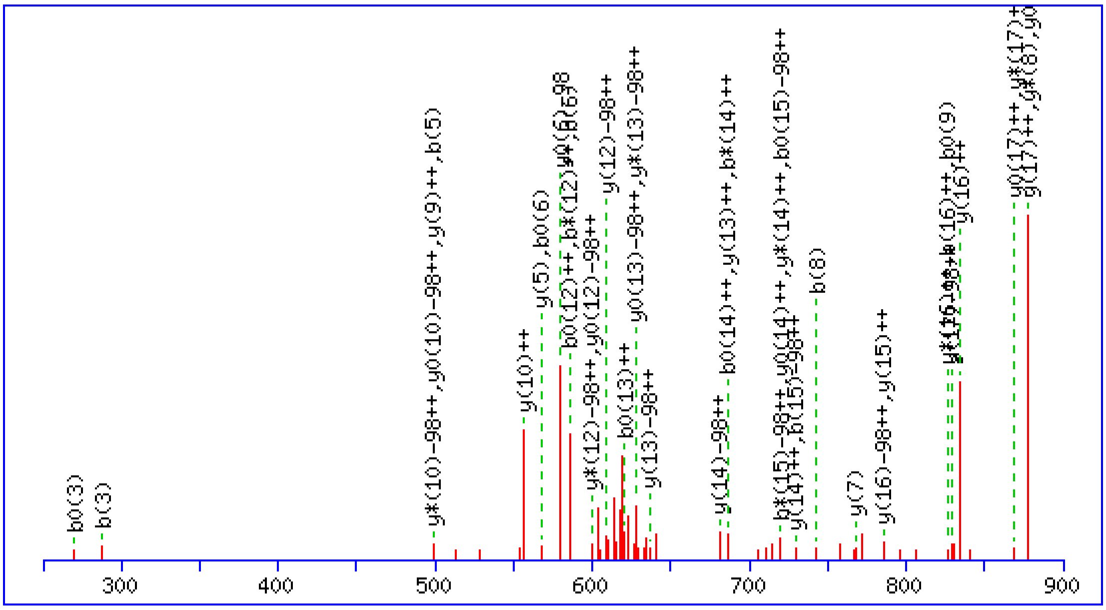
Monoisotopic mass of neutral peptide Mr(calc): 2033.8708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00022
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8)-98, b(8)-98++, b(8), b(9)-98, b(10), b(10)-98, b(11)-98, b(11)-98++, b(12)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-196++, b(15)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)-98++, b(17)++, b(18)++, b(18)-196++
Matched y ions: y(3), y(4), y(4)++, y(5), y(5)-98, y(6)-98, y(6), y(7)++, y(7), y(7)-98, y(8)-98, y(8), y(9)++, y(9)-98++, y(9), y(9)-98, y(10)++, y(10), y(10)-98, y(10)-98++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)-98, y(13)-98++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++

Peptide No.927

SLSPLSGTTDTKAESPAGR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **SLSPLSGTTDTKAESPAGR**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4087: 1953.901041 from(652.307623,3+) index(4074)
Title: Elution from: 27.844 to 27.844 scan no 2188 cid35.00 polarity:+:m1s



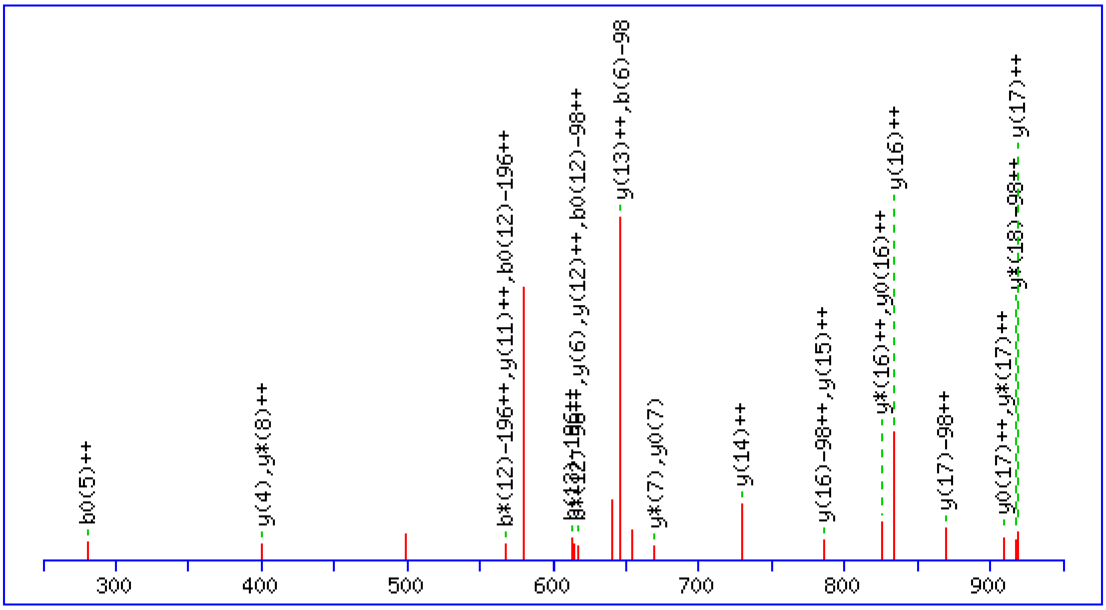
Monoisotopic mass of neutral peptide Mr(calc): 1953.9044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0015
Matched b ions: b(3), b(5), b(6), b(8), b(15)-98++, b(16)++
Matched y ions: y(5), y(7), y(9)++, y(10)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.928

SLSPLSGTTDTKAESPAGR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SLSPLSGTTDTKAESPAGR**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4969: 2033.870553 from(678.964127,3+) index(5137)
Title: Elution from: 31.175 to 31.175 scan no 2758 cid35.00 polarity:+:m1s



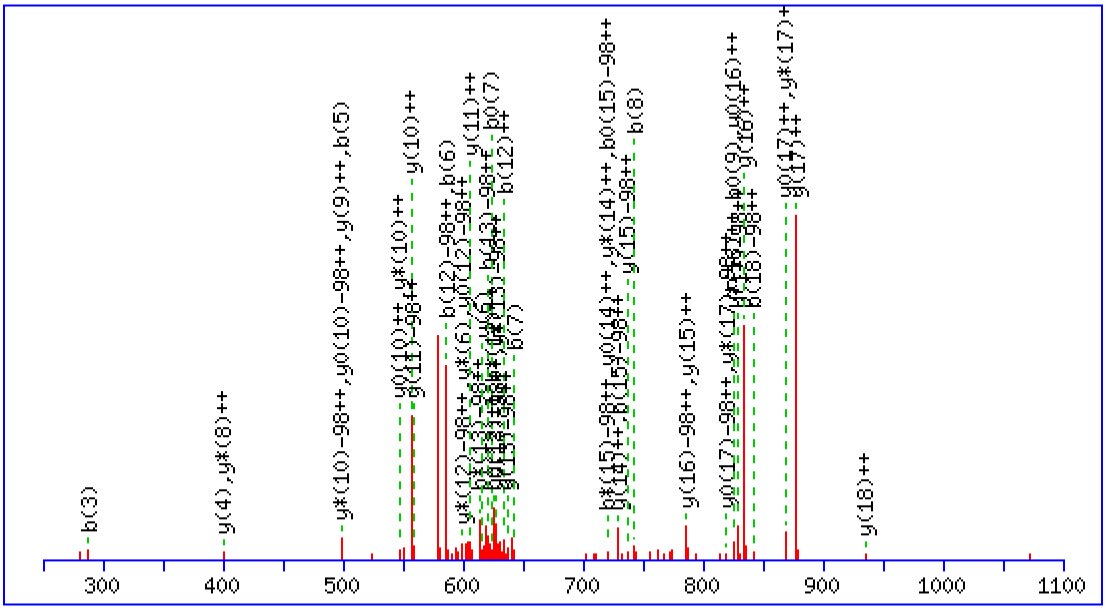
Monoisotopic mass of neutral peptide Mr(calc): 2033.8708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 **Expect:** 0.00061
Matched b ions: b(6)-98, b(13)-196++
Matched y ions: y(4), y(6), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++

Peptide No.929

SLSPLSGTTDTKAESPAGR
Confirmed sites: @T:11
Ambiguous sites:

MS/MS Fragmentation of **SLSPLSGTTDTKAESPAGR**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4025: 1953.902541 from(652.308123,3+) index(4290)
Title: Elution from: 27.530 to 27.530 scan no 2236 cid35.00 polarity:+:m1s



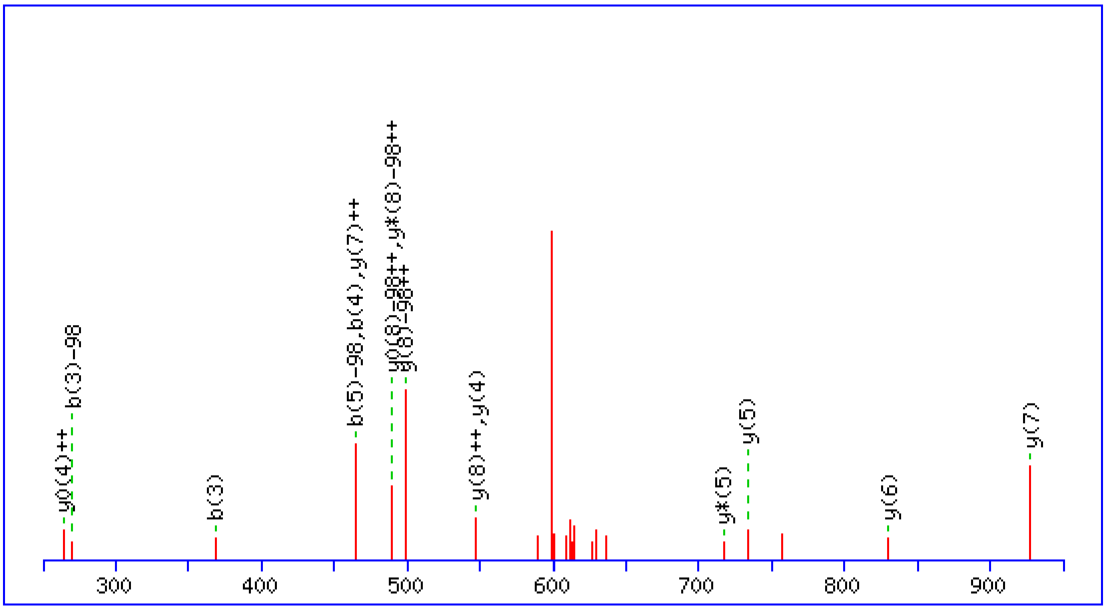
Monoisotopic mass of neutral peptide Mr(calc): 1953.9044
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00019
Matched b ions: b(3), b(5), b(6), b(7), b(8), b(12)-98++, b(12)++, b(13)-98++, b(15)-98++, b(18)-98++
Matched y ions: y(4), y(6), y(9)++, y(10)++, y(11)-98++, y(11)++, y(13)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++

Peptide No.930

SLSPPWEQDR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SLSPPWEQDR**
Found in **CTGE5_MOUSE** in **SwissProt**, Cutaneous T-cell lymphoma-associated antigen 5 homolog OS=Mus musculus GN=Ctage5 PE=1 SV=1

Match to Query 1934: 1293.539830 from(647.777191,2+) index(2675)
Title: Elution from: 42.516 to 42.516 scan no 4273 cid35.00 polarity:+



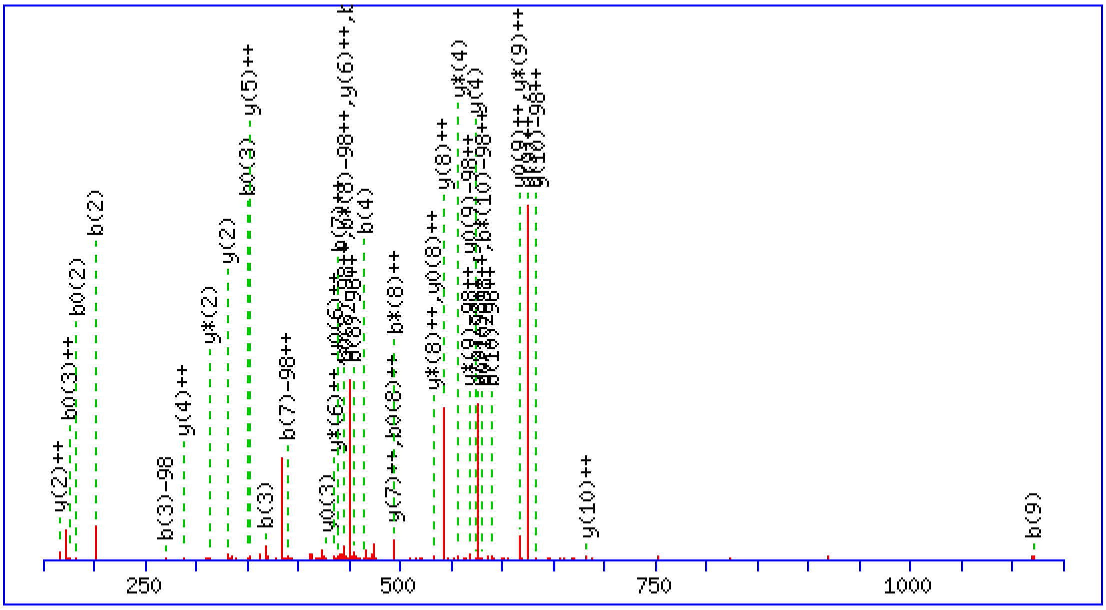
Monoisotopic mass of neutral peptide Mr(calc): 1293.5391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0039
Matched b ions: b(3)-98, b(3), b(4), b(5)-98
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8)-98++, y(8)++

Peptide No.931

SLSPPWEQDRR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SLSPPWEQDRR**
Found in **CTGE5_MOUSE** in **SwissProt**, Cutaneous T-cell lymphoma-associated antigen 5 homolog OS=Mus musculus GN=Ctage5 PE=1 SV=1

Match to Query 3315: 1449.640482 from(484.220770,3+) index(1941)
Title: Elution from: 45.461 to 45.461 scan no 3737 cid35.00 polarity:+



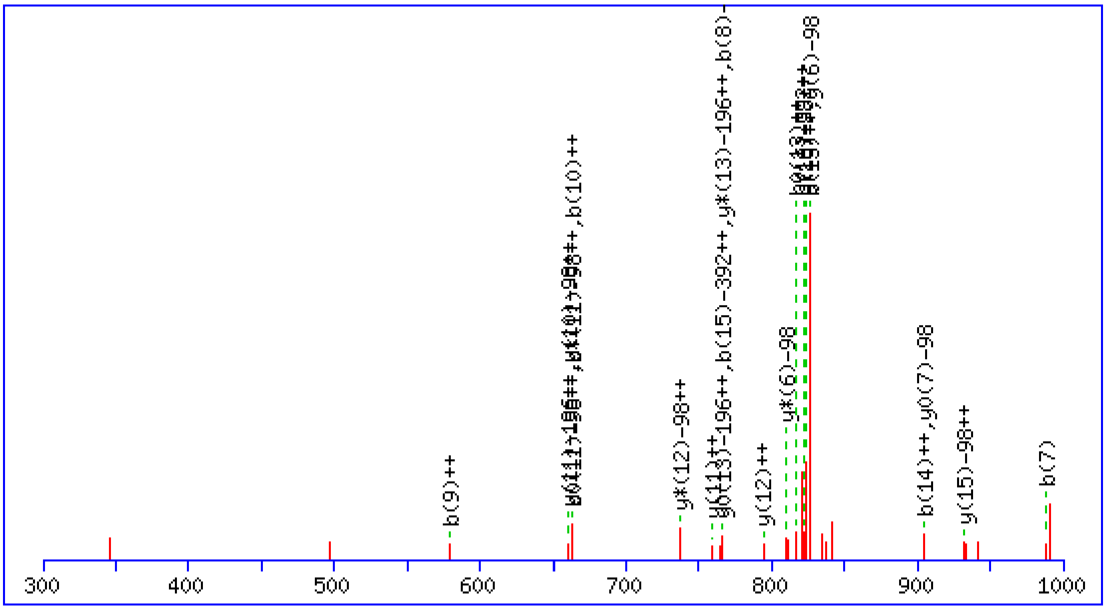
Monoisotopic mass of neutral peptide Mr(calc): 1449.6402
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00039
Matched b ions: b(2), b(3), b(3)-98, b(4), b(7)-98++, b(7)++, b(8)-98++, b(9), b(10)-98++
Matched y ions: y(2), y(2)++, y(3), y(4)++, y(4), y(5)++, y(6)++, y(7)++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++

Peptide No.932

SLSSAFRAVSNDPRIITWR
Confirmed sites: @S:1,@S:3,@S:4,@S:10,@T:17
Ambiguous sites:

MS/MS Fragmentation of **SLSSAFRAVSNDPRIITWR**
Found in **AVIL_MOUSE** in **SwissProt**, Advillin OS=Mus musculus GN=Avil PE=1 SV=2

Match to Query 6506: 2574.982443 from(859.334757,3+) index(6556)
Title: Elution from: 45.407 to 45.407 scan no 4653 cid35.00 polarity:+:m1s



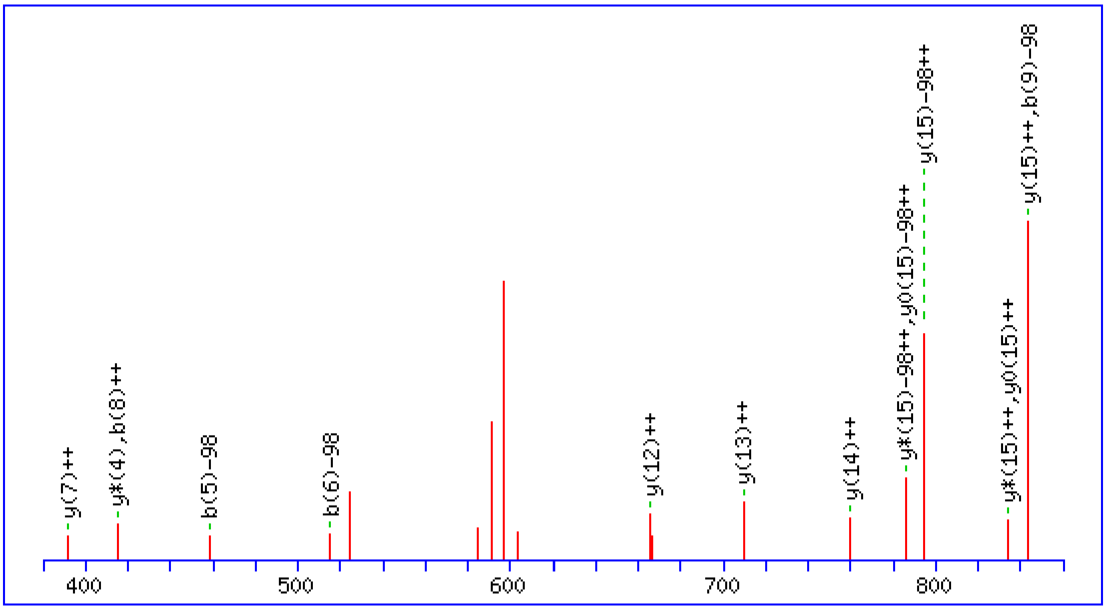
Monoisotopic mass of neutral peptide Mr(calc): 2574.9865
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 **Expect:** 0.054
Matched b ions: b(7), b(8)-294, b(9)++, b(10)++, b(13)++, b(14)++, b(15)-392++, b(16)-392++
Matched y ions: y(6)-98, y(10)-98++, y(11)-196++, y(11)++, y(12)++, y(13)-98++, y(15)-98++

Peptide No.933

SLSTSGESLYHVLGLDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SLSTSGESLYHVLGLDK**
Found in **DNJC5_MOUSE** in **SwissProt**, DnaJ homolog subfamily C member 5 OS=Mus musculus GN=Dnajc5 PE=1 SV=1

Match to Query 4529: 1884.887196 from(629.303008,3+) index(3455)
Title: Elution from: 60.414 to 60.414 scan no 6167 cid35.00 polarity:+



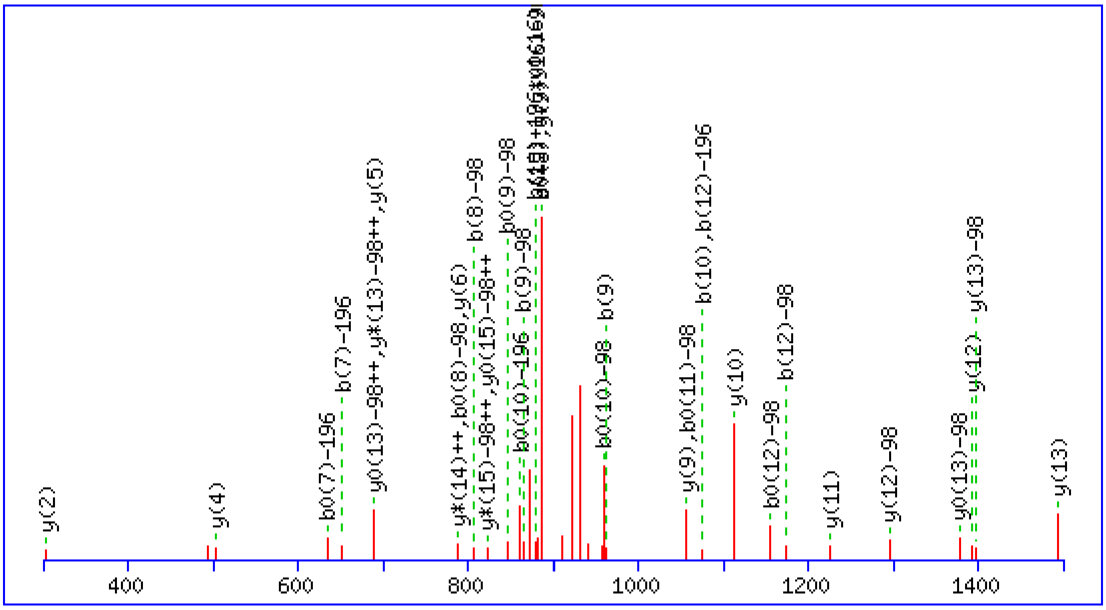
Monoisotopic mass of neutral peptide Mr(calc): 1884.8870
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.012
Matched b ions: b(5)-98, b(6)-98, b(8)++, b(9)-98
Matched y ions: y(7)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++

Peptide No.934

SLSVTSLGGLPVWEAER
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SLSVTSLGGLPVWEAER**
Found in **GYS2_MOUSE** in **SwissProt**, Glycogen [starch] synthase, liver OS=Mus musculus GN=Gys2 PE=1 SV=2

Match to Query 4048: 1959.870756 from(980.942654,2+) index(3027)
Title: Elution from: 67.190 to 67.190 scan no 6144 cid35.00 polarity:+



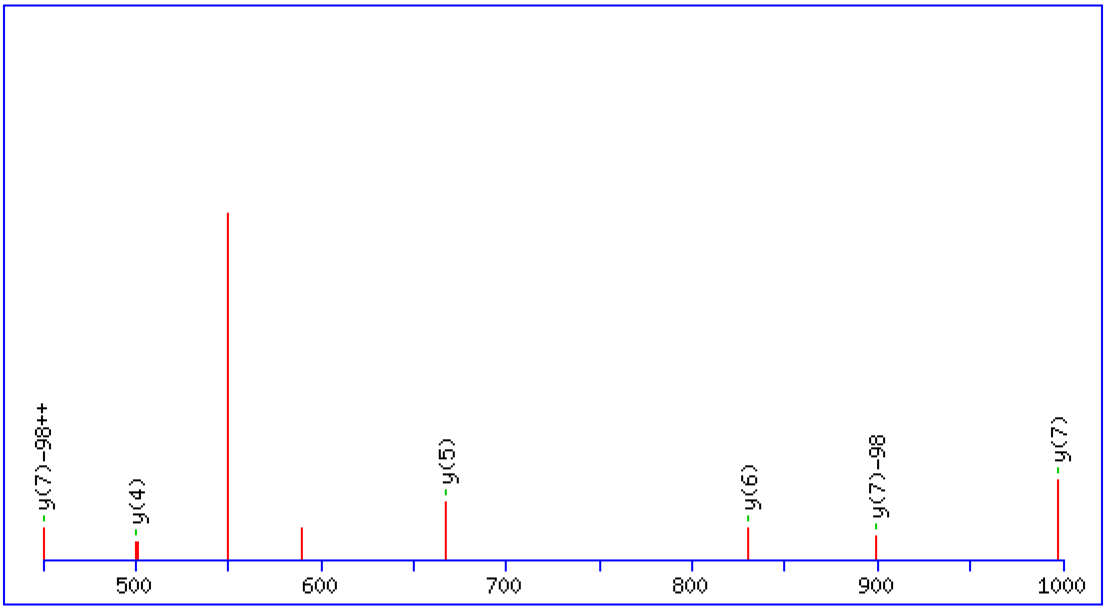
Monoisotopic mass of neutral peptide Mr(calc): 1959.8744
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 **Expect:** 8.6e-008
Matched b ions: b(7)-196, b(8)-98, b(9)-98, b(9), b(10), b(10)-196, b(12)-196, b(12)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(9), y(10), y(11), y(12)-98, y(12), y(13), y(13)-98, y(15)++

Peptide No.935

SLSYSPVER
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **SLSYSPVER**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 1524: 1196.451432 from(599.232992,2+) index(1748)
Title: Elution from: 32.472 to 32.472 scan no 2934 cid35.00 polarity:+



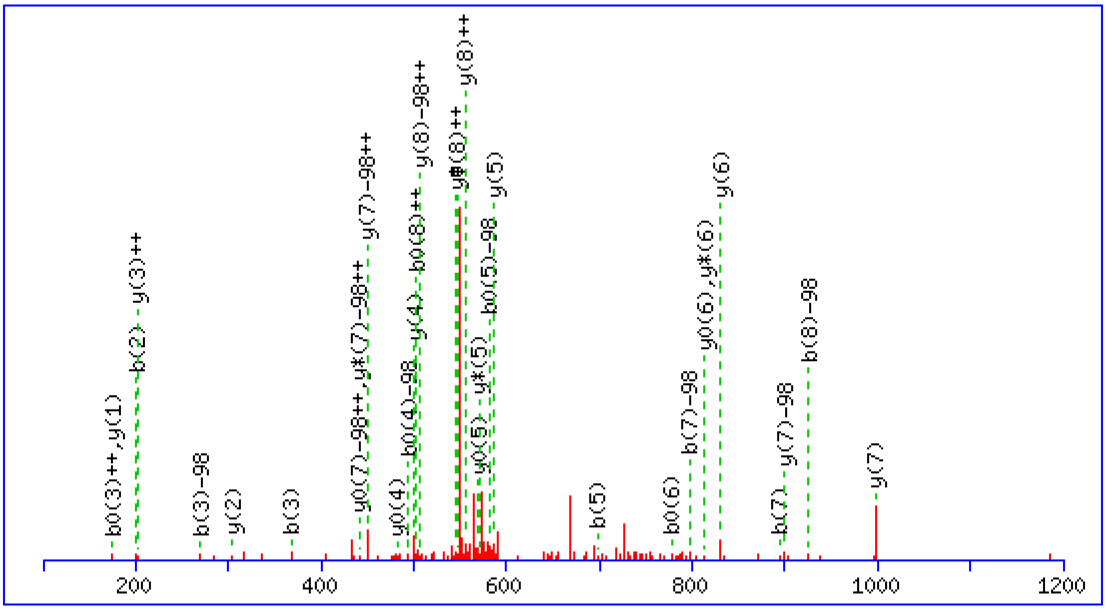
Monoisotopic mass of neutral peptide Mr(calc): 1196.4516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.0099
Matched b ions:
Matched y ions: y(4), y(5), y(6), y(7)-98, y(7), y(7)-98++

Peptide No.936

SLSYSPVER
Confirmed sites: @S:3,@Y:4
Ambiguous sites:

MS/MS Fragmentation of **SLSYSPVER**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 1959: 1196.451744 from(599.233148,2+) index(1269)
Title: Elution from: 38.668 to 38.668 scan no 2841 cid35.00 polarity:+



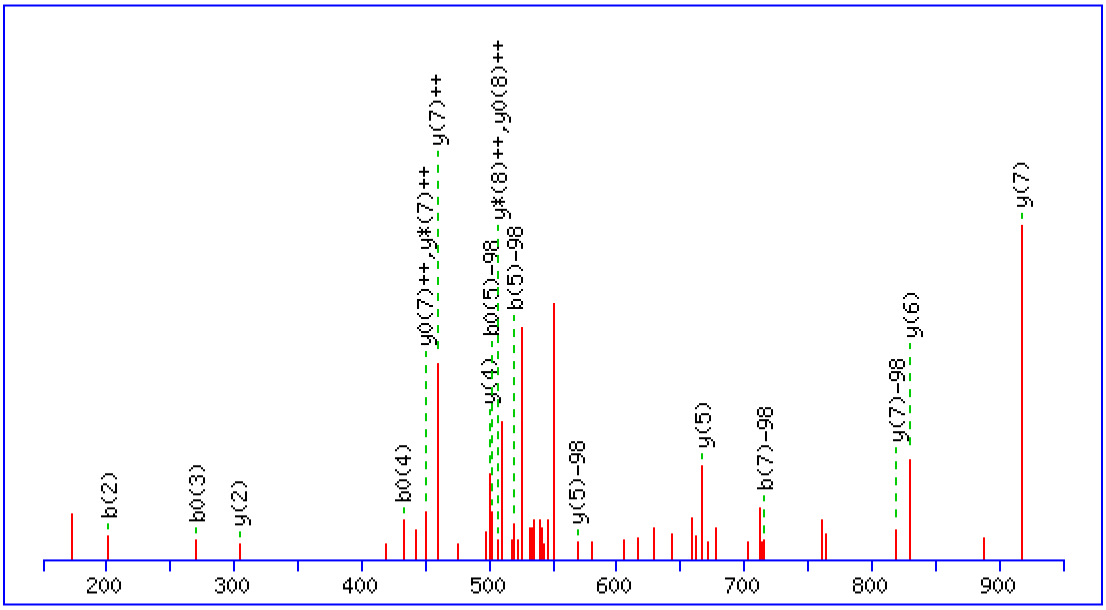
Monoisotopic mass of neutral peptide Mr(calc): 1196.4516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y4 : Phospho (Y)
Ions Score: 21 **Expect:** 0.021
Matched b ions: b(2), b(3)-98, b(3), b(5), b(7)-98, b(7), b(8)-98
Matched y ions: y(1), y(2), y(3)++, y(4), y(5), y(6), y(7)-98++, y(7)-98, y(7), y(8)++, y(8)-98++

Peptide No.937

SLSYSPVER
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SLSYSPVER**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 1085: 1116.484738 from(559.249645,2+) index(1155)
Title: Elution from: 28.467 to 28.467 scan no 2274 cid35.00 polarity:+



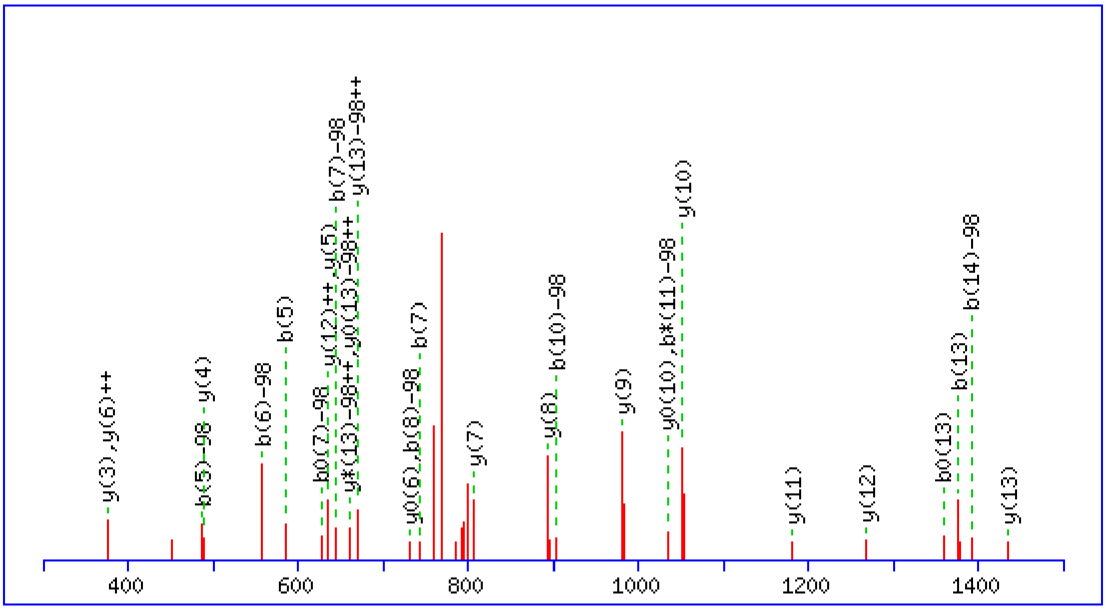
Monoisotopic mass of neutral peptide Mr(calc): 1116.4852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0078
Matched b ions: b(2), b(5)-98, b(7)-98
Matched y ions: y(2), y(4), y(5), y(5)-98, y(6), y(7)++, y(7), y(7)-98

Peptide No.938

SNSSEASSGDFLDLK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SNSSEASSGDFLDLK**
Found in **HN1_MOUSE** in **SwissProt**, Hematological and neurological expressed 1 protein OS=Mus musculus GN=Hn1 PE=1 SV=3

Match to Query 3540: 1635.666466 from(818.840509,2+) index(6603)
Title: Elution from: 46.018 to 46.018 scan no 4729 cid35.00 polarity:+:m1s



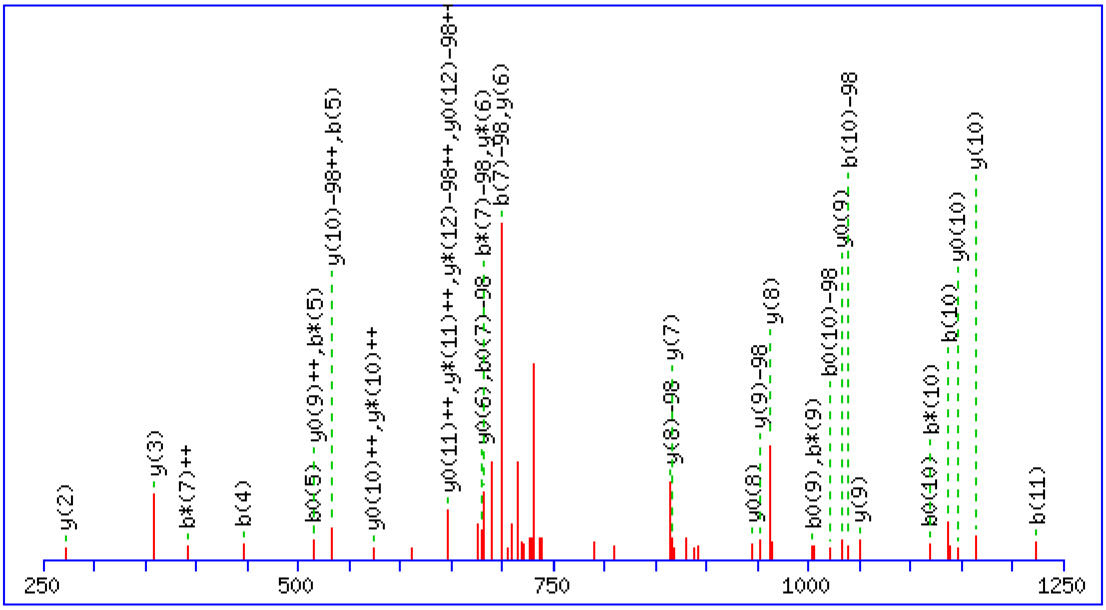
Monoisotopic mass of neutral peptide Mr(calc): 1635.6665
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 2.8e-007
Matched b ions: b(5)-98, b(5), b(6)-98, b(7), b(7)-98, b(8)-98, b(10)-98, b(13), b(14)-98
Matched y ions: y(3), y(4), y(5), y(6)++, y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)-98++, y(13)

Peptide No.939

SPFNSPSPQDSPR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SPFNSPSPQDSPR**
Found in **NFIC_MOUSE** in **SwissProt**, Nuclear factor 1 C-type OS=Mus musculus GN=Nfic PE=1 SV=1

Match to Query 2424: 1494.612638 from(748.313595,2+) index(1153)
Title: Elution from: 27.155 to 27.155 scan no 2185 cid35.00 polarity:+



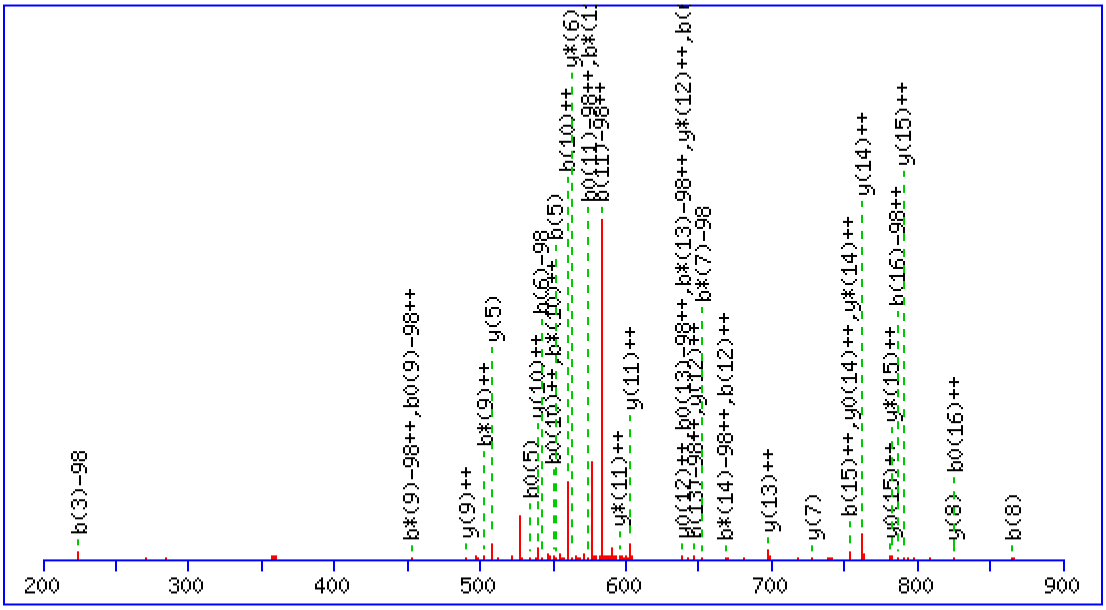
Monoisotopic mass of neutral peptide Mr(calc): 1494.6140
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 61 **Expect:** 2.5e-006
Matched b ions: b(4), b(5), b(7)-98, b(10), b(10)-98, b(11)
Matched y ions: y(2), y(3), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10)-98++, y(10)

Peptide No.940

SPGETSKPRPFAGGGYR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SPGETSKPRPFAGGGYR**
Found in **NSF1C_MOUSE** in **SwissProt**, NSFL1 cofactor p47 OS=Mus musculus GN=Nsfl1c PE=1 SV=1

Match to Query 3643: 1842.840648 from(615.287492,3+) index(3671)
Title: Elution from: 21.990 to 21.990 scan no 1486 cid35.00 polarity:+:m1s



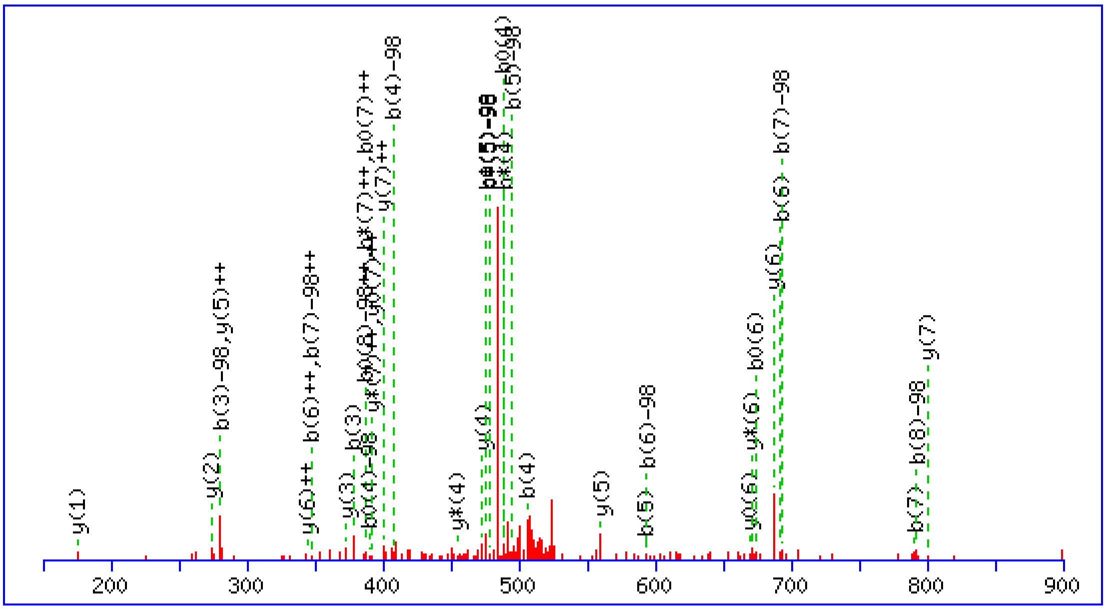
Monoisotopic mass of neutral peptide Mr(calc): 1842.8414
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.036
Matched b ions: b(3)-98, b(5), b(6), b(6)-98, b(8), b(10)++, b(11)-98++, b(12)++, b(13)-98++, b(15)++, b(16)-98++
Matched y ions: y(5), y(7), y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++

Peptide No.941

SPLQSVVVR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SPLQSVVVR**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 1473: 1063.542906 from(532.778729,2+) index(1584)
Title: Elution from: 40.269 to 40.269 scan no 3156 cid35.00 polarity:+



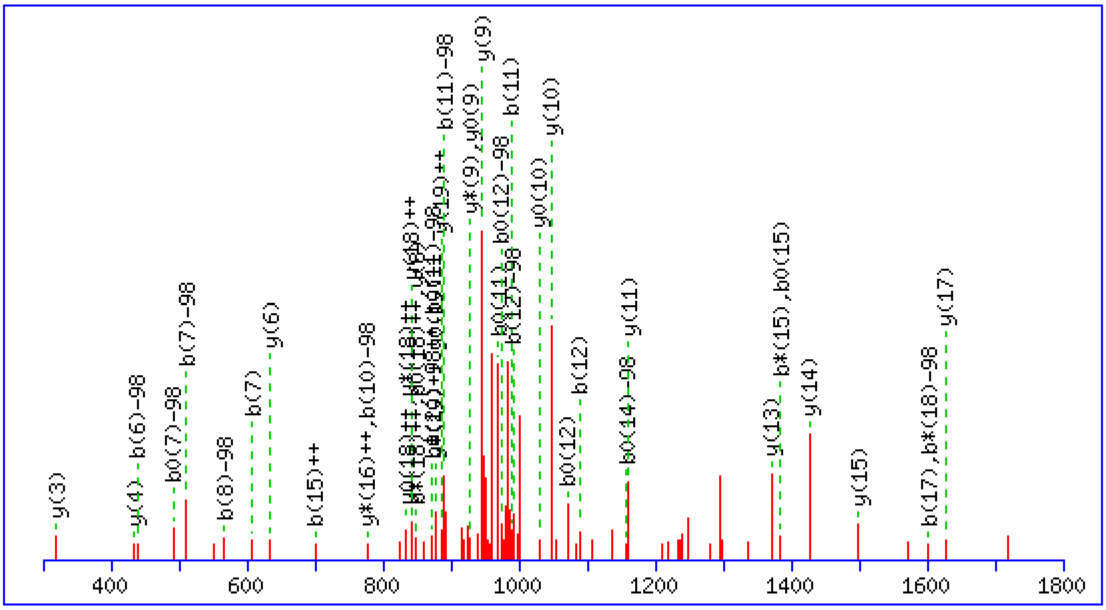
Monoisotopic mass of neutral peptide Mr(calc): 1063.5427
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.003
Matched b ions: b(3)-98, b(3), b(4), b(4)-98, b(5), b(5)-98, b(6), b(6)++, b(6)-98, b(7), b(7)-98, b(7)-98++, b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5)++, y(5), y(6), y(6)++, y(7)++, y(7)

Peptide No.942

SPSGGAAGPLLTPSQSLDGSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SPSGGAAGPLLTPSQSLDGSR**
Found in **KCD12_MOUSE** in **SwissProt**, BTB/POZ domain-containing protein KCTD12 OS=Mus musculus GN=Kctd12 PE=1 SV=1

Match to Query 4971: 2033.939152 from(1017.976852,2+) index(6221)
Title: Elution from: 42.718 to 42.718 scan no 4296 cid35.00 polarity:+:m1s



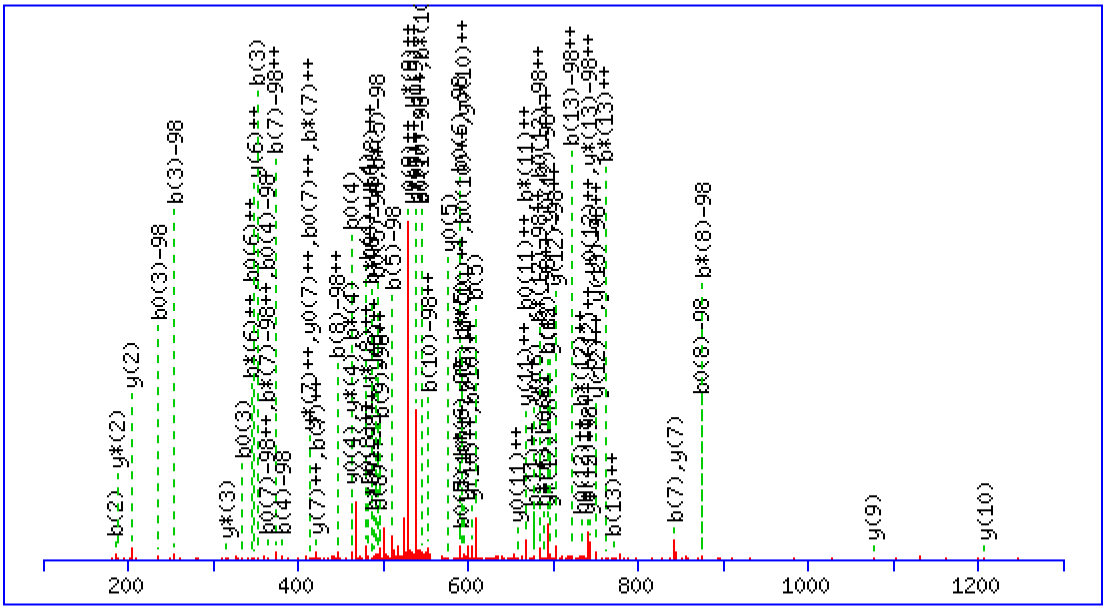
Monoisotopic mass of neutral peptide Mr(calc): 2033.9419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 7.8e-005
Matched b ions: b(6)-98, b(7)-98, b(7), b(8)-98, b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(15)++, b(17)
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11), y(13), y(14), y(15), y(17), y(18)++, y(19)++

Peptide No.943

SPSKEPHFTDFEGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SPSKEPHFTDFEGK**
Found in **S38A3_MOUSE** in **SwissProt**, Sodium-coupled neutral amino acid transporter 3 OS=Mus musculus GN=Slc38a3 PE=1 SV=1

Match to Query 4142: 1684.714041 from(562.578623,3+) index(1447)
Title: Elution from: 38.457 to 38.457 scan no 2945 cid35.00 polarity:+



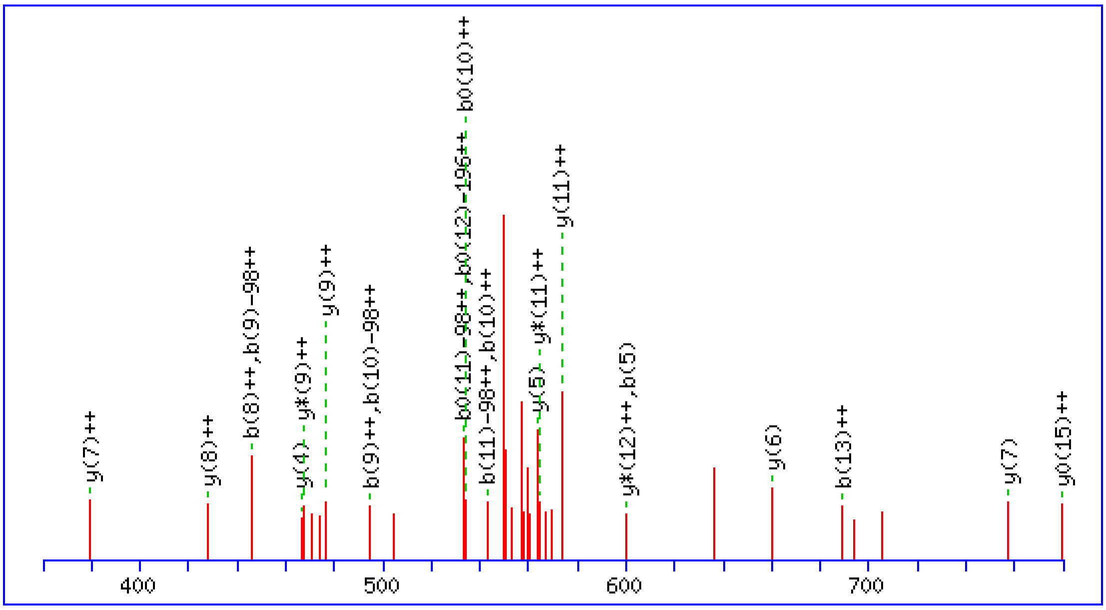
Monoisotopic mass of neutral peptide Mr(calc): 1684.7134
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0031
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5), b(5)-98, b(7)-98++, b(7), b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++
Matched y ions: y(2), y(4), y(5), y(6), y(6)++, y(7), y(7)++, y(8)++, y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++

Peptide No.944

SPSPAPPPPPPPPPPR
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of **SPSPAPPPPPPPPPPR**
Found in **SRRM1_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=2

Match to Query 3851: 1743.777642 from(582.266490,3+) index(5131)
Title: Elution from: 31.123 to 31.123 scan no 2751 cid35.00 polarity:+:m1s



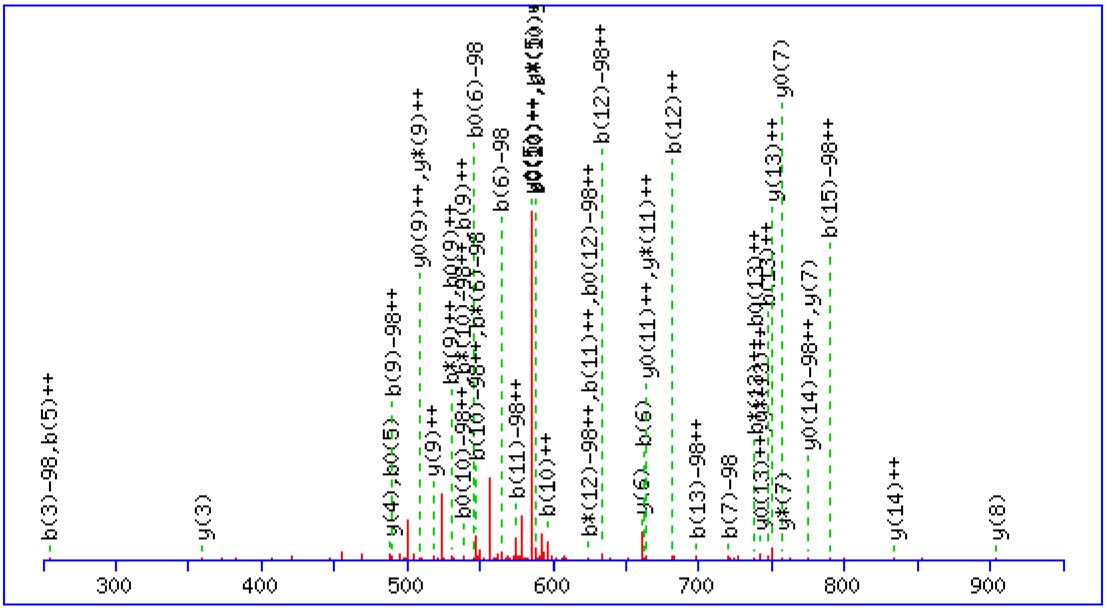
Monoisotopic mass of neutral peptide Mr(calc): 1743.7787
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.021
Matched b ions: b(5), b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(13)++
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(9)++, y(11)++

Peptide No.945

SPSPGRREEDGDELAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SPSPGRREEDGDELAR**
Found in **HEM6_MOUSE** in **SwissProt**, Coproporphyrinogen-III oxidase, mitochondrial OS=Mus musculus GN=Cpox PE=1 SV=2

Match to Query 4249: 1849.793151 from(617.604993,3+) index(318)
Title: Elution from: 19.335 to 19.335 scan no 1151 cid35.00 polarity:+



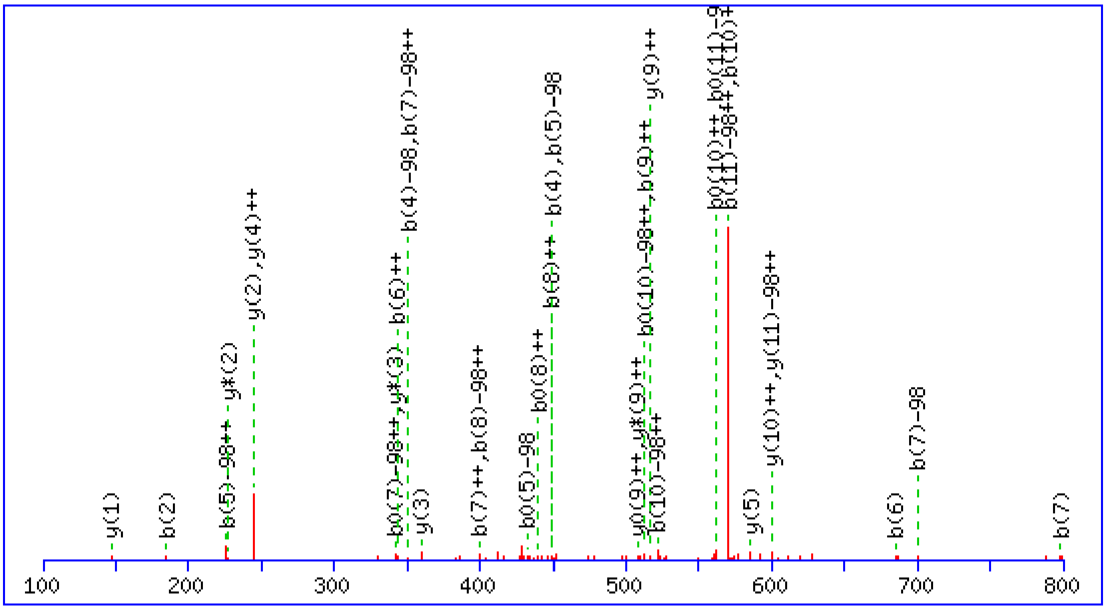
Monoisotopic mass of neutral peptide Mr(calc): 1849.7955
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.023
Matched b ions: b(3)-98, b(5)++, b(6)-98, b(6), b(7)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(15)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9)++, y(13)++, y(14)++

Peptide No.946

SPSPVHLPEDPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SPSPVHLPEDPK**
Found in **LAR4B_MOUSE** in **SwissProt**, La-related protein 4B OS=Mus musculus GN=Larp4b PE=1 SV=2

Match to Query 2452: 1381.627686 from(461.549838,3+) index(1360)
Title: Elution from: 27.858 to 27.858 scan no 2344 cid35.00 polarity:+



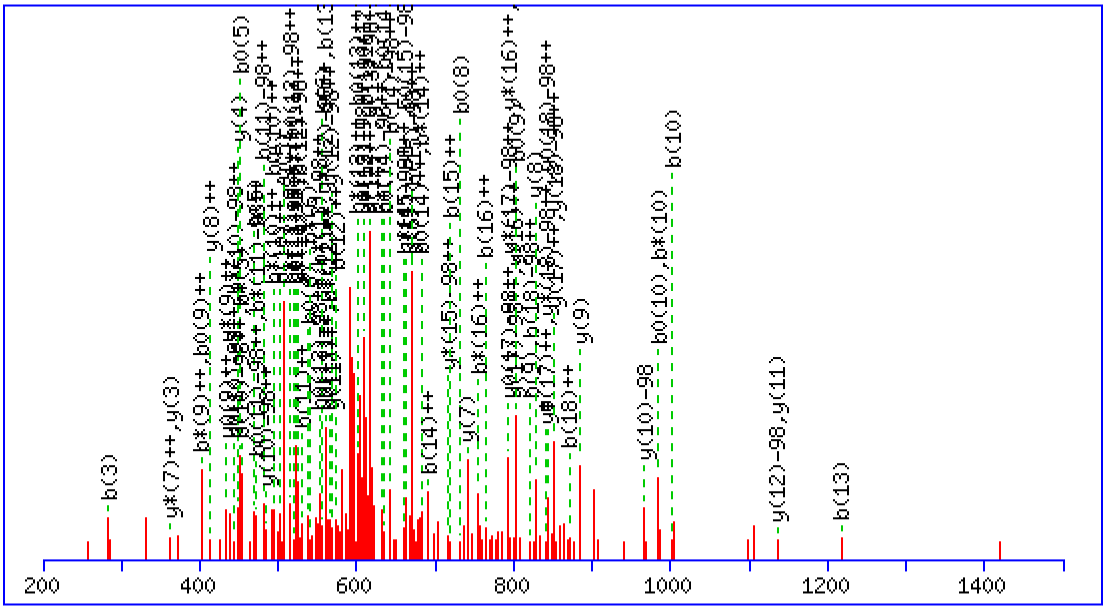
Monoisotopic mass of neutral peptide Mr(calc): 1381.6279
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.01
Matched b ions: b(2), b(4)-98, b(4), b(5)-98++, b(5)-98, b(6)++, b(6), b(7)-98, b(7), b(7)++, b(7)-98++, b(8)-98++, b(8)++, b(9)++, b(10)-98++, b(10)++, b(11)-98++
Matched y ions: y(1), y(2), y(3), y(4)++, y(5), y(9)++, y(10)++, y(11)-98++

Peptide No.947

SPVGKSPPATGSAYGSSQK
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **SPVGKSPPATGSAYGSSQK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 4749: 1884.863088 from(629.294972,3+) index(3771)
Title: Elution from: 26.819 to 26.819 scan no 1503 cid35.00 polarity:+:m1s



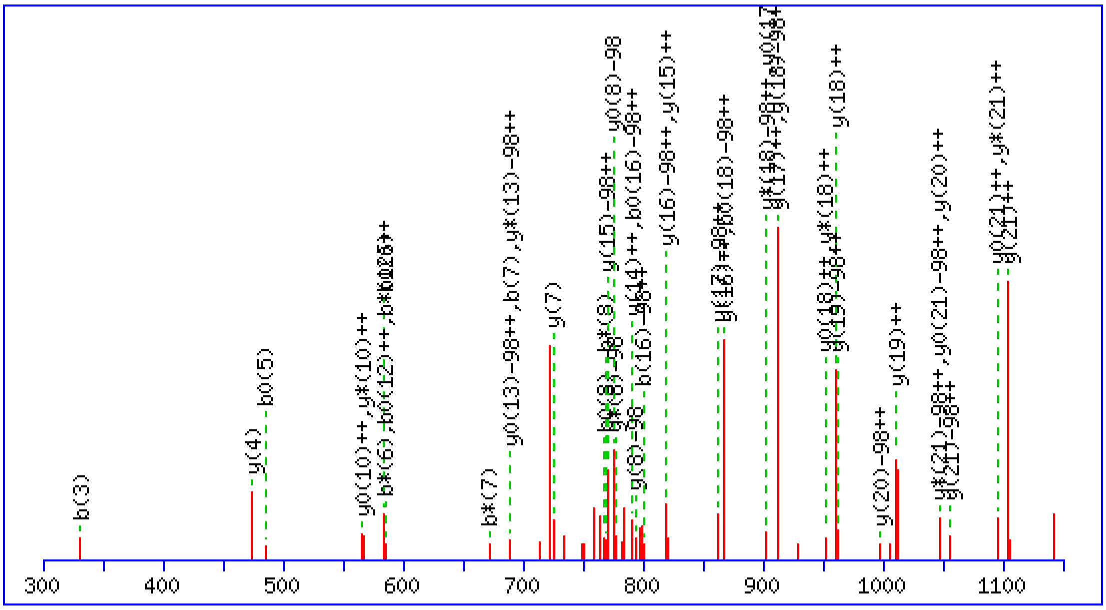
Monoisotopic mass of neutral peptide Mr(calc): 1884.8619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0029
Matched b ions: b(3), b(5), b(6), b(9), b(10)-98++, b(10), b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(10)-98, y(10)-98++, y(11), y(11)-98++, y(11)++, y(12)++, y(12)-98, y(12)-98++, y(13)-98++, y(14)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++

Peptide No.948

SQDATVSPGSEQSEKSPGPIVSR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **SQDATVSPGSEQSEKSPGPIVSR**
Found in **NIPA_MOUSE** in **SwissProt**, Nuclear-interacting partner of ALK OS=Mus musculus GN=Zc3hc1 PE=1 SV=1

Match to Query 6065: 2422.094736 from(808.372188,3+) index(4567)
Title: Elution from: 25.373 to 25.373 scan no 1968 cid35.00 polarity:+:m1s



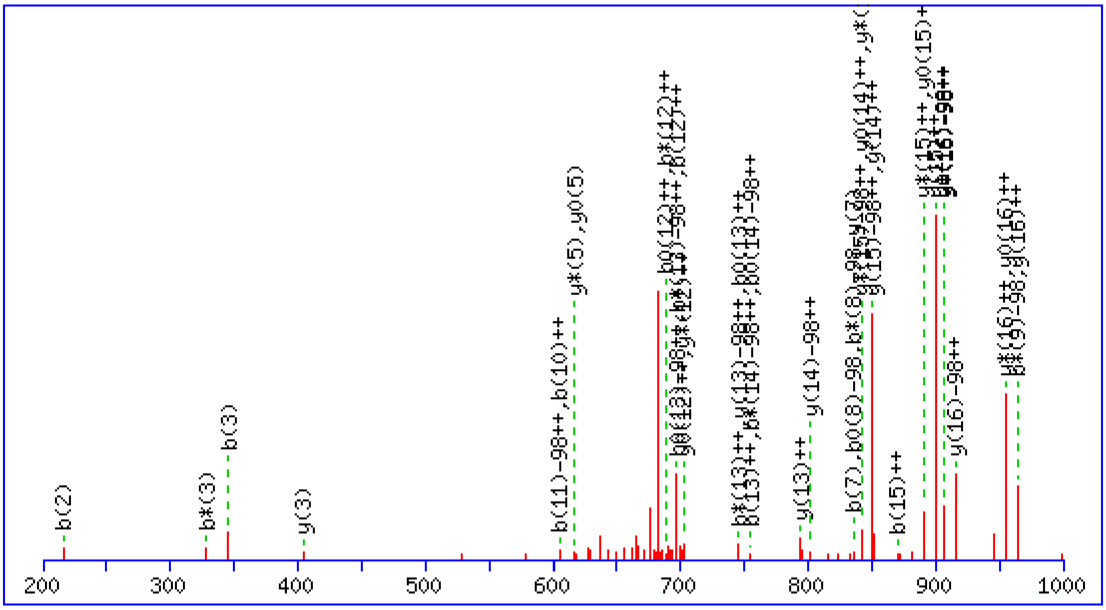
Monoisotopic mass of neutral peptide Mr(calc): 2422.1013
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0019
Matched b ions: b(3), b(7), b(16)-98++
Matched y ions: y(4), y(7), y(8)-98, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)++, y(21)-98++

Peptide No.949

SQEPISNDQKVSDDDKEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SQEPISNDQKVSDDDKEK**
Found in **LYRIC_MOUSE** in **SwissProt**, Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1

Match to Query 5537: 2140.913187 from(714.645005,3+) index(3891)
Title: Elution from: 18.198 to 18.198 scan no 1034 cid35.00 polarity:+:m1s



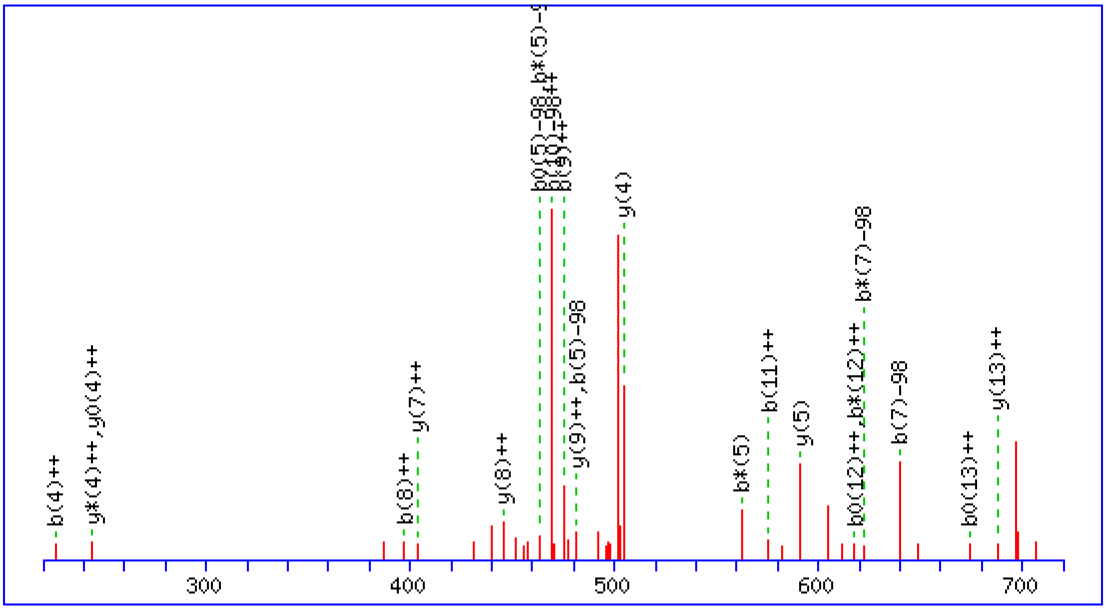
Monoisotopic mass of neutral peptide Mr(calc): 2140.9161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.026
Matched b ions: b(2), b(3), b(7), b(10)++, b(11)-98++, b(12)++, b(13)++, b(15)++
Matched y ions: y(3), y(7), y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.950

SQGPEASGRSLTDR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SQGPEASGRSLTDR**
Found in **CXA10_MOUSE** in **SwissProt**, Gap junction alpha-10 protein OS=Mus musculus GN=Gja10 PE=1 SV=2

Match to Query 2977: 1539.666390 from(514.229406,3+) index(1867)
Title: Elution from: 33.560 to 33.560 scan no 3081 cid35.00 polarity:+



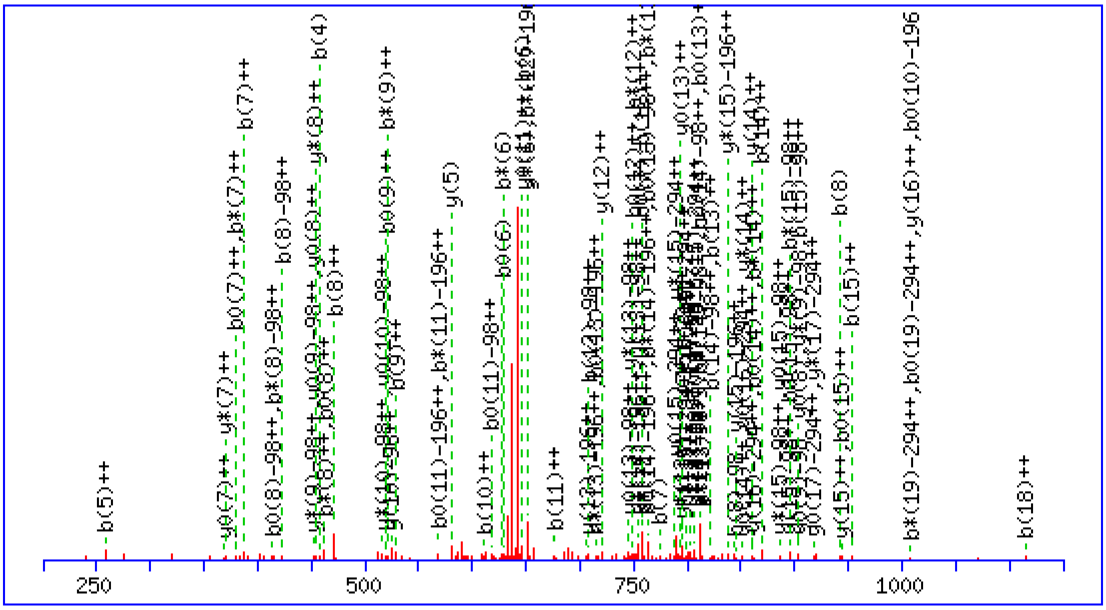
Monoisotopic mass of neutral peptide Mr(calc): 1539.6678
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.049
Matched b ions: b(4)++, b(5)-98, b(7)-98, b(8)++, b(9)++, b(10)-98++, b(11)++
Matched y ions: y(4), y(5), y(7)++, y(8)++, y(9)++, y(13)++

Peptide No.951

SQKNGMESLSKYKPSSSFTVSK
Confirmed sites: @S:8,@S:10,@S:15
Ambiguous sites:

MS/MS Fragmentation of **SQKNGMESLSKYKPSSSFTVSK**
Found in **CRLD2_MOUSE** in **SwissProt**, Cysteine-rich secretory protein LCCL domain-containing 2 OS=Mus musculus GN=Crispld2 PE=1 SV=1

Match to Query 6615: 2659.099396 from(665.782125,4+) index(3809)
Title: Elution from: 17.379 to 17.379 scan no 930 cid35.00 polarity:+:m1s



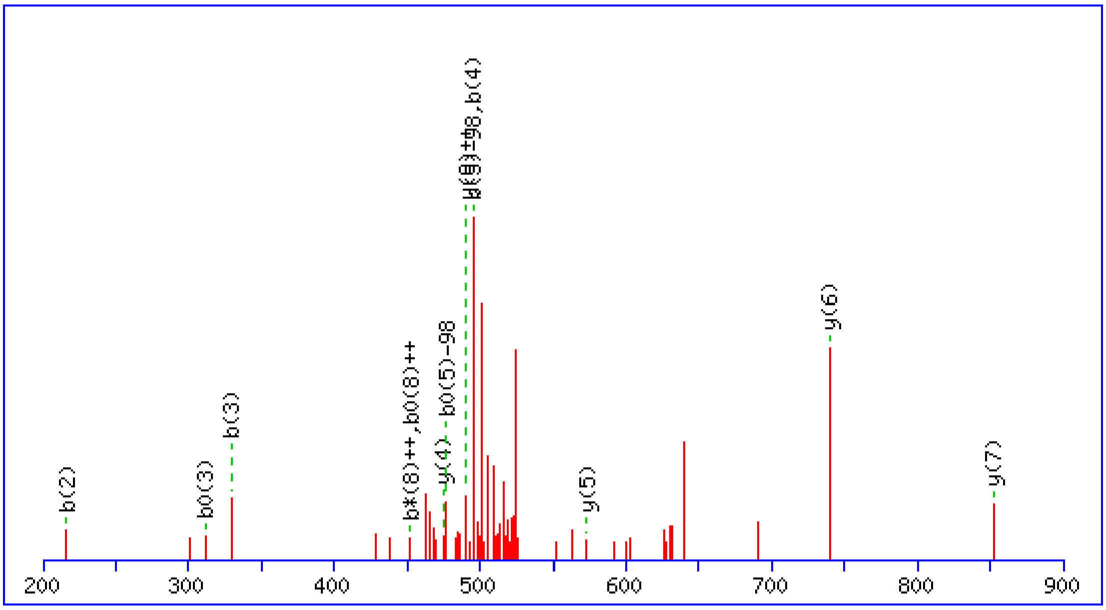
Monoisotopic mass of neutral peptide Mr(calc): 2659.1043
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0088
Matched b ions: b(4), b(5)++, b(6), b(7)++, b(7), b(8)++, b(8), b(8)-98++, b(8)-98, b(9)++, b(10)++, b(11)++, b(12)++, b(12)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-294++, b(15)-98++, b(18)++
Matched y ions: y(5), y(10)-98++, y(12)++, y(13)-98++, y(13)-196++, y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(15)-294++, y(15)-196++, y(16)++, y(16)-294++

Peptide No.952

SQLSPVKTK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SQLSPVKTK**
Found in **IF2M_MOUSE** in **SwissProt**, Translation initiation factor IF-2, mitochondrial OS=Mus musculus GN=Mtif2 PE=1 SV=2

Match to Query 1020: 1066.539730 from(534.277141,2+) index(596)
Title: Elution from: 21.624 to 21.624 scan no 1457 cid35.00 polarity:+



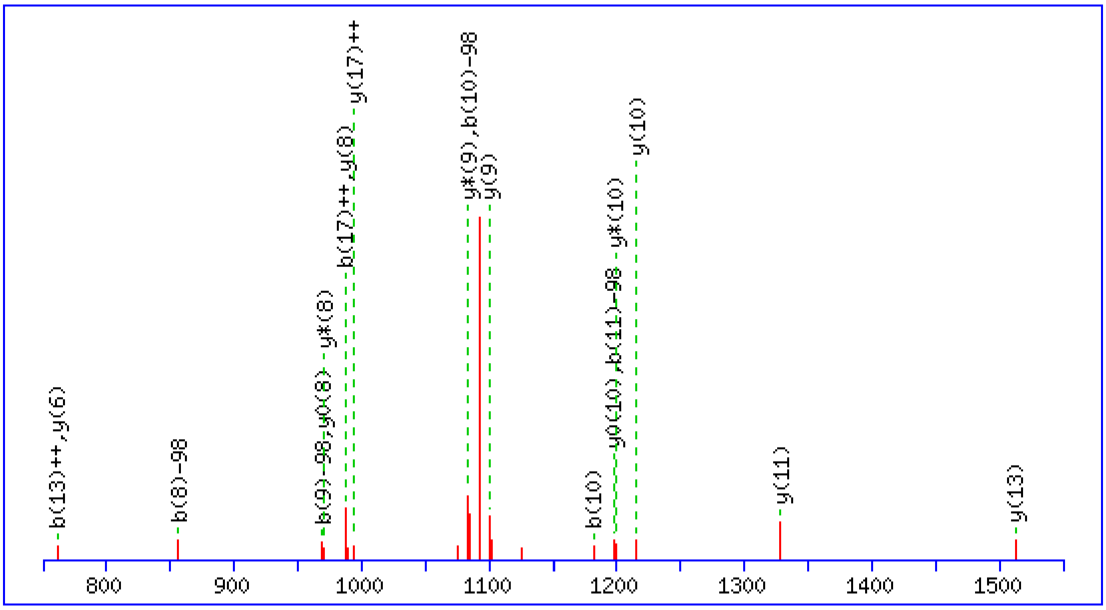
Monoisotopic mass of neutral peptide Mr(calc): 1066.5424
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 **Expect:** 0.039
Matched b ions: b(2), b(3), b(4), b(5)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8)++

Peptide No.953

SQNNFVAILDLPEGEHQYK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SQNNFVAILDLPEGEHQYK**
Found in **AAKB1_MOUSE** in **SwissProt**, 5'-AMP-activated protein kinase subunit beta-1 OS=Mus musculus GN=Prkab1 PE=1 SV=2

Match to Query 5799: 2281.038186 from(1141.526369,2+) index(6799)
Title: Elution from: 55.639 to 55.639 scan no 5719 cid35.00 polarity:+:m1s



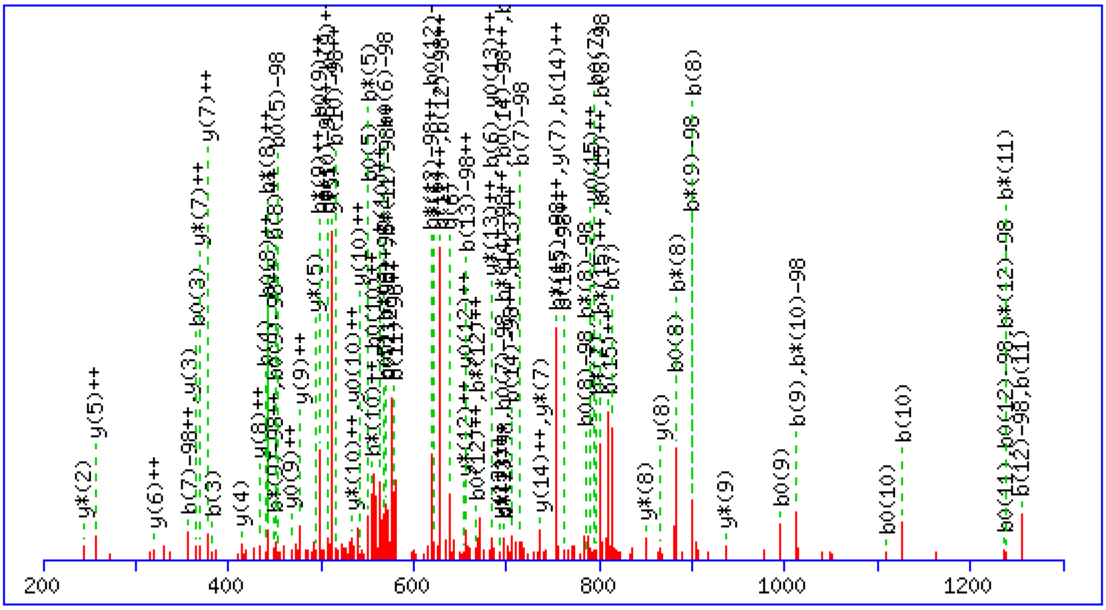
Monoisotopic mass of neutral peptide Mr(calc): 2281.0416
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00035
Matched b ions: b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(13)++, b(17)++
Matched y ions: y(6), y(8), y(9), y(10), y(11), y(13), y(17)++

Peptide No.954

SQSGEDESLNQPGPIK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SQSGEDESLNQPGPIK**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 3868: 1764.756801 from(589.259543,3+) index(1011)
Title: Elution from: 35.629 to 35.629 scan no 2477 cid35.00 polarity:+



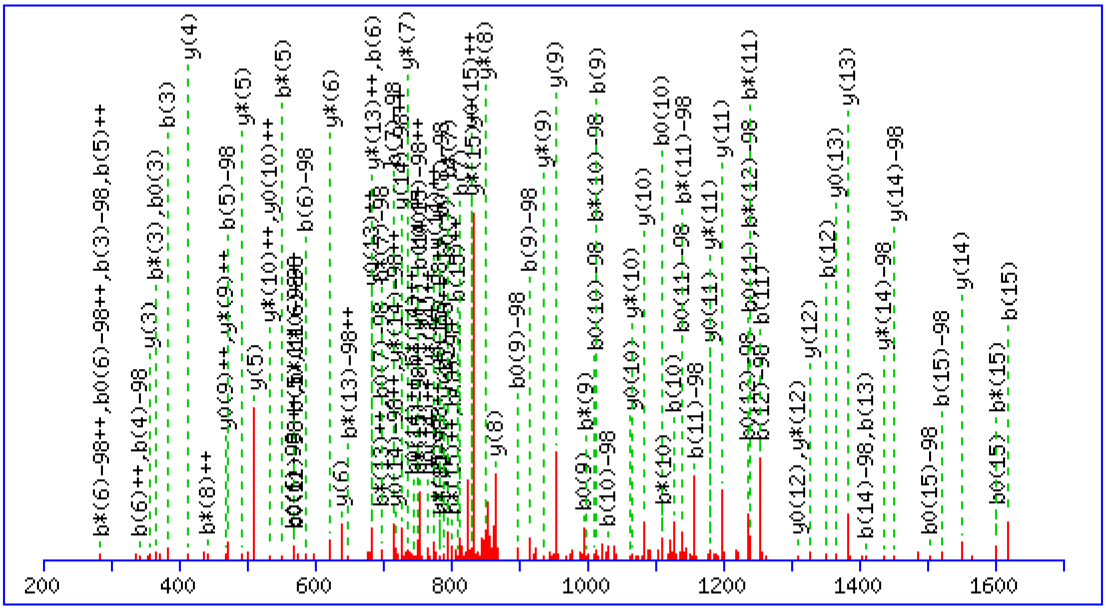
Monoisotopic mass of neutral peptide Mr(calc): 1764.7567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0016
Matched b ions: b(3), b(4), b(5), b(6), b(7)-98++, b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(9), b(9)++, b(10), b(10)++, b(10)-98++, b(11)++, b(11), b(11)-98++, b(12)-98++, b(12)-98, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(13)++, y(14)++

Peptide No.955

SQSGEDESLNQPGPIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SQSGEDESLNQPGPIK**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 4449: 1764.755462 from(883.385007,2+) index(1193)
Title: Elution from: 35.624 to 35.624 scan no 2596 cid35.00 polarity:+



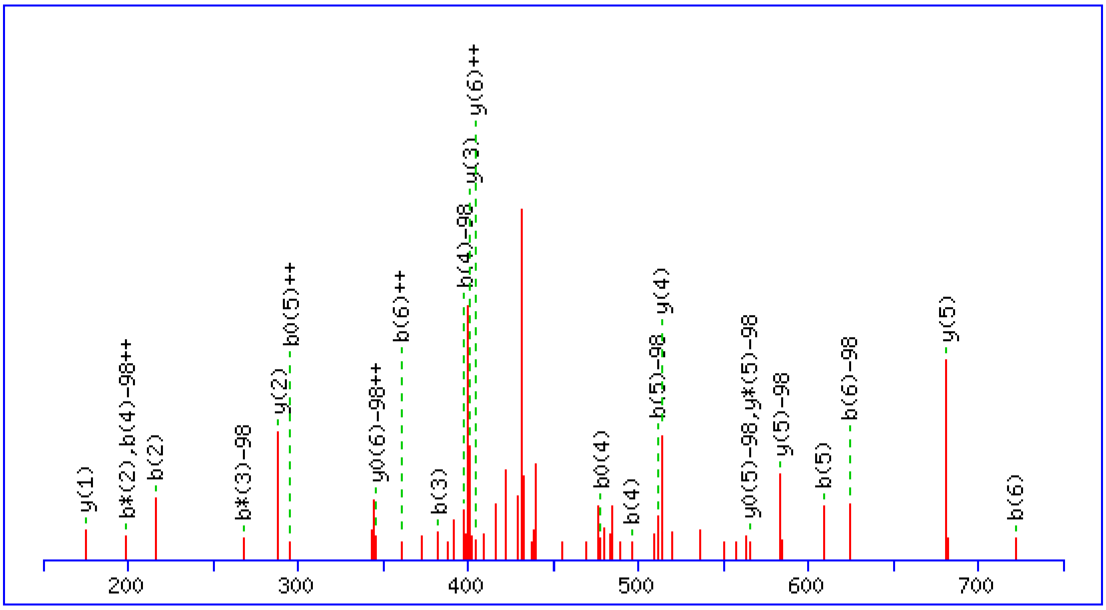
Monoisotopic mass of neutral peptide Mr(calc): 1764.7567
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 99 **Expect:** 8e-010
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)-98, b(5), b(5)++, b(6), b(6)++, b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98, b(9), b(10), b(10)-98, b(11)-98, b(11), b(12), b(12)-98, b(13), b(14)++, b(14)-98, b(15), b(15)-98, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)-98++, y(14)-98, y(14)++, y(15)-98++

Peptide No.956

SQSLIIR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SQSLIIR**
Found in **P3C2A_MOUSE** in **SwissProt**, Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Mus musculus GN=Pik3c2a PE=1 SV=2

Match to Query 578: 895.452874 from(448.733713,2+) index(1472)
Title: Elution from: 28.962 to 28.962 scan no 2495 cid35.00 polarity:+



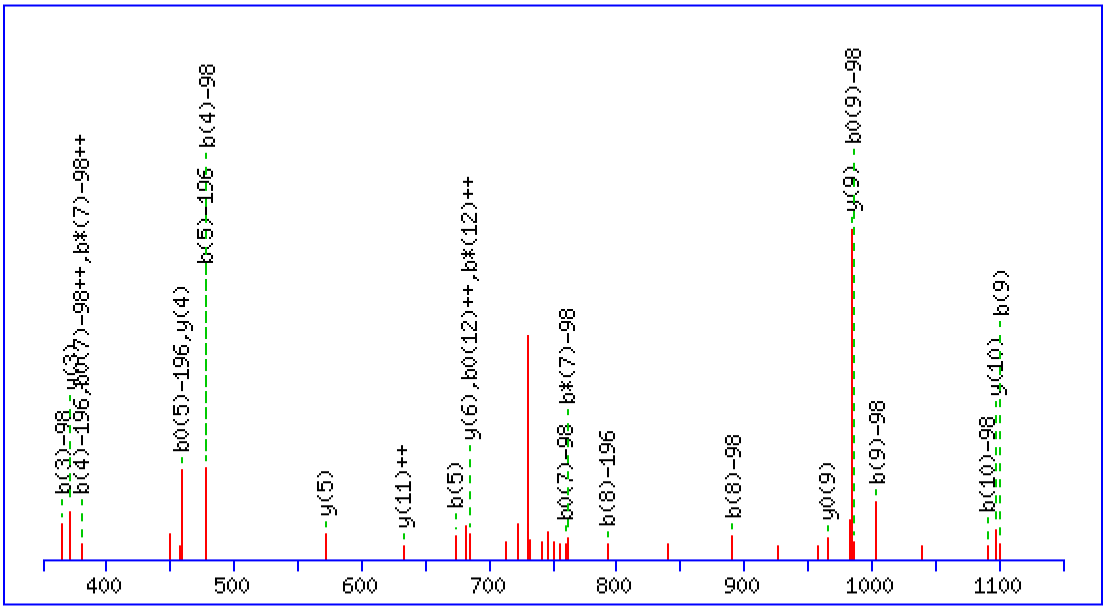
Monoisotopic mass of neutral peptide Mr(calc): 895.4528
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0031
Matched b ions: b(2), b(3), b(4)-98++, b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(6)++
Matched y ions: y(1), y(2), y(3), y(4), y(5)-98, y(5), y(6)++

Peptide No.957

SQSLPTTLLSPVR
Confirmed sites: @S:1,@S:3
Ambiguous sites:

MS/MS Fragmentation of **SQSLPTTLLSPVR**
Found in **SSFA2_MOUSE** in **SwissProt**, Sperm-specific antigen 2 homolog OS=Mus musculus GN=Ssfa2 PE=1 SV=3

Match to Query 2802: 1557.719314 from(779.866933,2+) index(2807)
Title: Elution from: 56.996 to 56.996 scan no 5592 cid35.00 polarity:+



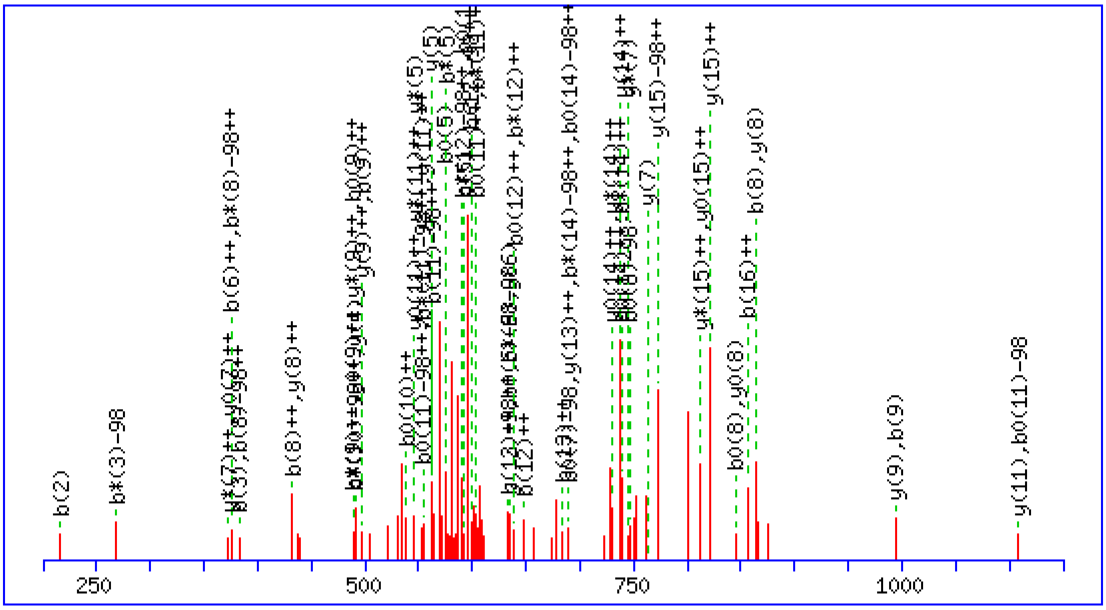
Monoisotopic mass of neutral peptide Mr(calc): 1557.7205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 **Expect:** 0.012
Matched b ions: b(3)-98, b(4)-98, b(4)-196, b(5)-196, b(5), b(8)-196, b(8)-98, b(9)-98, b(9), b(10)-98
Matched y ions: y(3), y(4), y(5), y(6), y(9), y(10), y(11)++

Peptide No.958

SQSPLRGGMTEAAQTDK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SQSPLRGGMTEAAQTDK**
Found in **BAG3_MOUSE** in **SwissProt**, BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=2

Match to Query 4284: 1855.810077 from(619.610635,3+) index(1024)
Title: Elution from: 25.270 to 25.270 scan no 1954 cid35.00 polarity:+



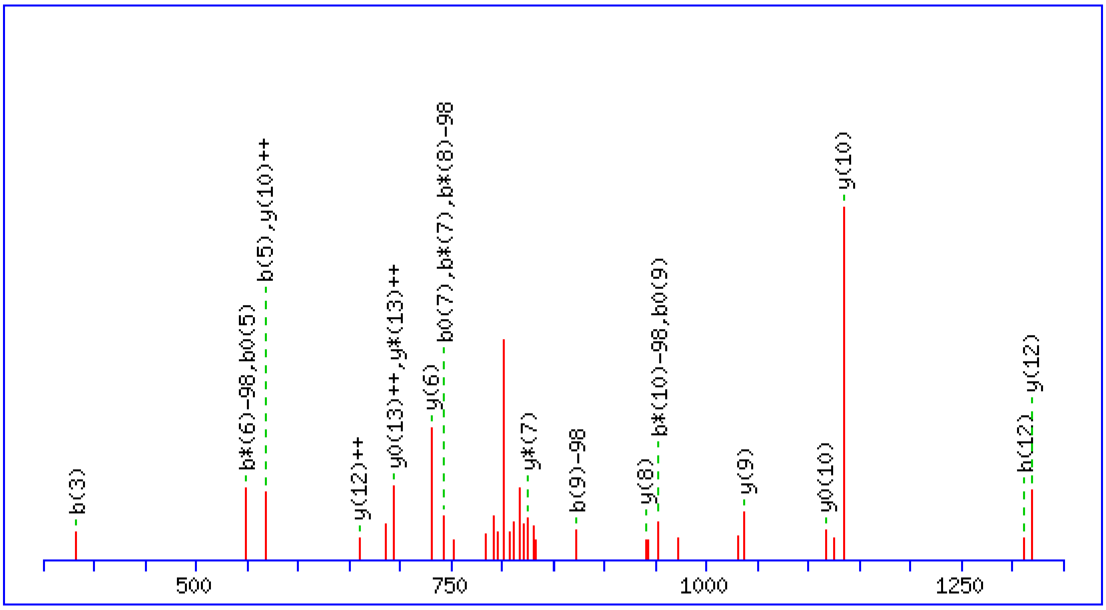
Monoisotopic mass of neutral peptide Mr(calc): 1855.8135
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.0024
Matched b ions: b(2), b(3), b(5), b(6)++, b(8)++, b(8)-98++, b(8), b(9), b(9)++, b(11)-98++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(11), y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++

Peptide No.959

SQSPSPPPLPEDLEK
Confirmed sites:
Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of **SQSPSPPPLPEDLEK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 3802: 1699.771672 from(850.893112,2+) index(2493)
Title: Elution from: 39.667 to 39.667 scan no 3923 cid35.00 polarity:+



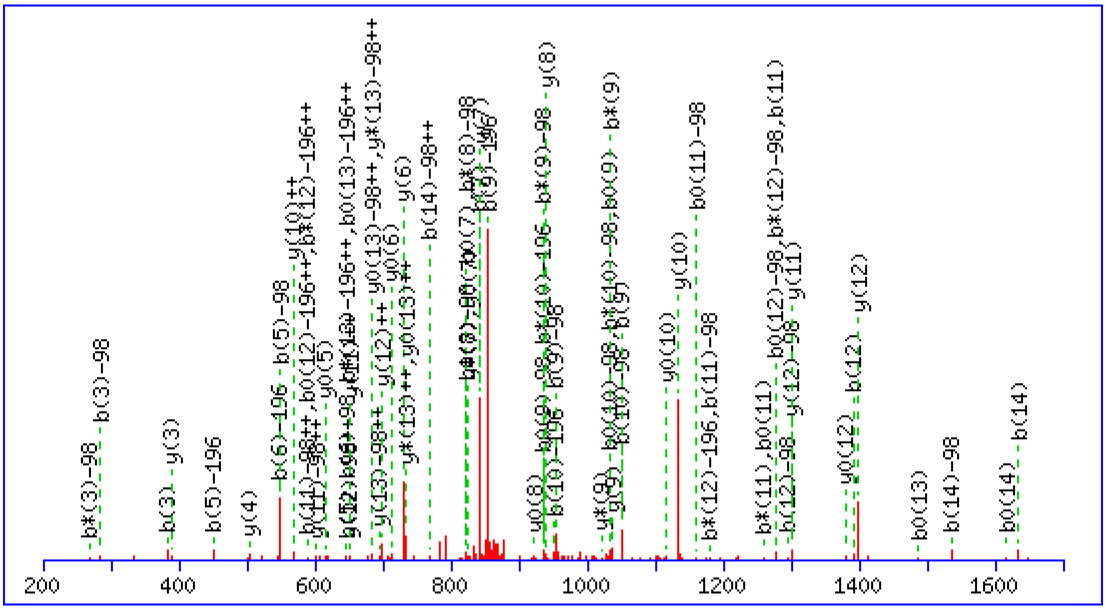
Monoisotopic mass of neutral peptide Mr(calc): 1699.7706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.012
Matched b ions: b(3), b(5), b(9)-98, b(12)
Matched y ions: y(6), y(8), y(9), y(10), y(10)++, y(12)++, y(12)

Peptide No.960

SQSPSPPPLPEDLEK
Confirmed sites: @S:1,@S:5
Ambiguous sites:

MS/MS Fragmentation of **SQSPSPPPLPEDLEK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 3883: 1779.735356 from(890.874954,2+) index(1908)
Title: Elution from: 51.594 to 51.594 scan no 4082 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1779.7369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0034
Matched b ions: b(3)-98, b(3), b(5)-196, b(5)-98, b(5), b(6)-196, b(6)-98, b(7), b(9)-196, b(9)-98, b(9), b(10)-196, b(10)-98, b(11), b(11)-98, b(11)-98++, b(12), b(12)-98, b(14)-98, b(14), b(14)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)++, y(11), y(11)-98++, y(12)-98, y(12), y(12)++, y(12)-98++, y(13)-98++

Peptide No.961

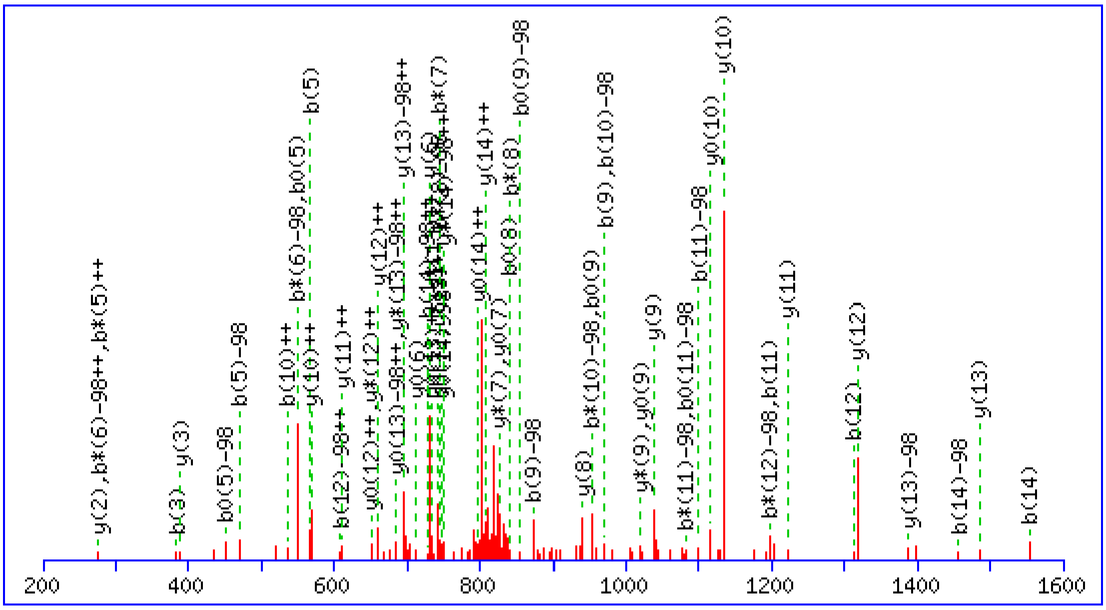
SQSPSPPPLPEDLEK

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **SQSPSPPPLPEDLEK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 3663: 1699.769862 from(850.892207,2+) index(1777)
Title: Elution from: 47.811 to 47.811 scan no 3768 cid35.00 polarity:+



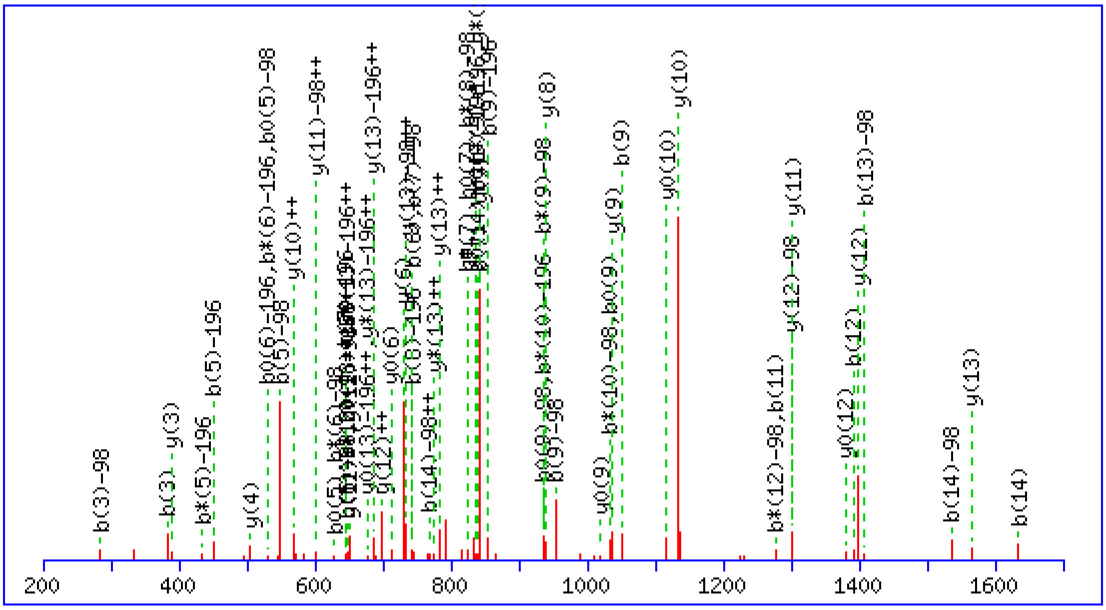
Monoisotopic mass of neutral peptide Mr(calc): 1699.7706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 6.1e-006
Matched b ions: b(3), b(5)-98, b(5), b(9), b(9)-98, b(10)-98, b(10)++, b(11), b(11)-98, b(12), b(12)-98++, b(14), b(14)-98, b(14)-98++
Matched y ions: y(2), y(3), y(6), y(8), y(9), y(10), y(10)++, y(11)++, y(11), y(12)++, y(12), y(13)-98++, y(13)-98, y(13), y(13)++, y(14)++

Peptide No.962

SQSPSPPPLPEDLEK
Confirmed sites: @S:3,@S:5
Ambiguous sites:

MS/MS Fragmentation of **SQSPSPPPLPEDLEK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 4005: 1779.736046 from(890.875299,2+) index(2858)
Title: Elution from: 45.354 to 45.354 scan no 4613 cid35.00 polarity:+



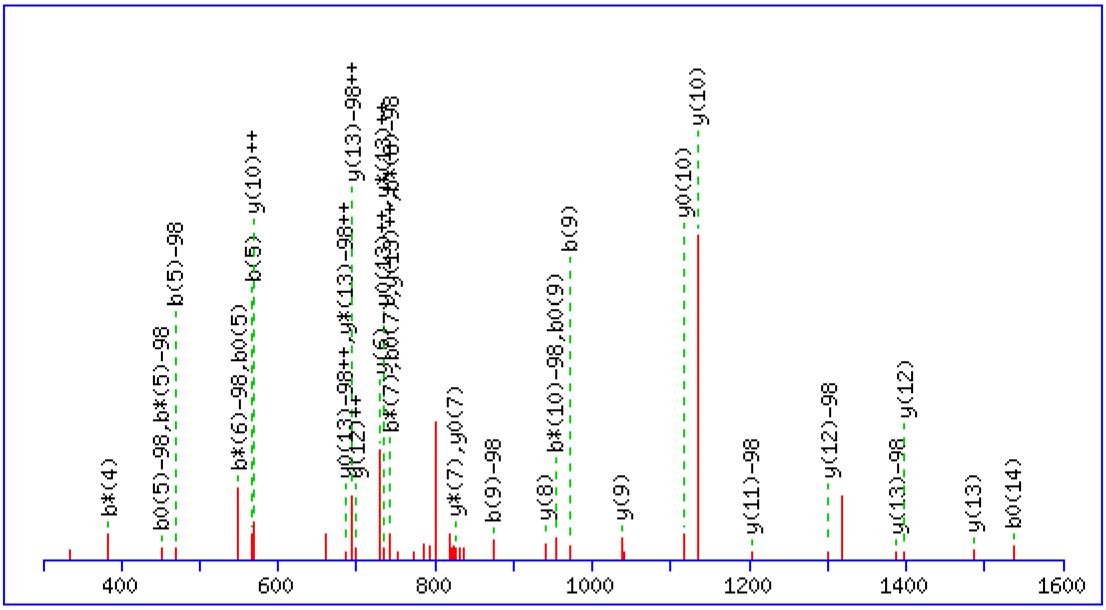
Monoisotopic mass of neutral peptide Mr(calc): 1779.7369
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 3e-005
Matched b ions: b(3), b(3)-98, b(5)-196, b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-196, b(7)-98, b(8)-196, b(9)-98, b(9), b(9)-196, b(11), b(12), b(12)-98++, b(13)-98, b(14)-98, b(14), b(14)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)++, y(11)-98++, y(11), y(12)-98++, y(12)-98, y(12), y(12)++, y(13), y(13)-98++, y(13)++, y(13)-196++

Peptide No.963

SQSPSPPPLPEDLEK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SQSPSPPPLPEDLEK**
Found in **ACINU_MOUSE** in **SwissProt**, Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=3

Match to Query 3273: 1699.768946 from(850.891749,2+) index(2107)
Title: Elution from: 39.476 to 39.476 scan no 3741 cid35.00 polarity:+



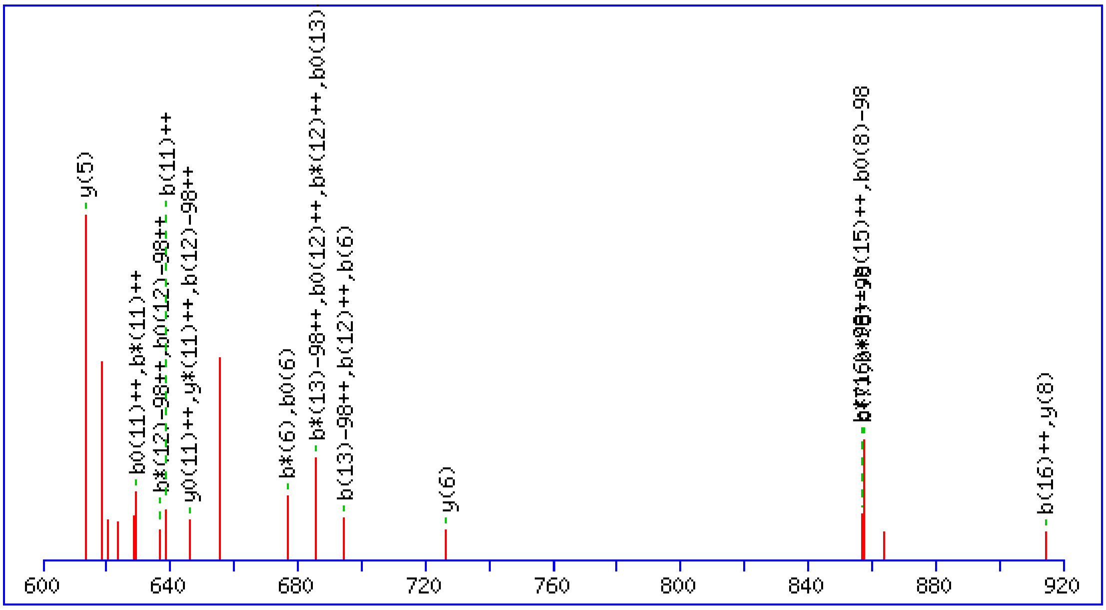
Monoisotopic mass of neutral peptide Mr(calc): 1699.7706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 3.6e-005
Matched b ions: b(5)-98, b(5), b(9)-98, b(9)
Matched y ions: y(6), y(8), y(9), y(10), y(10)++, y(11)-98, y(12)-98, y(12), y(12)++, y(13)-98, y(13), y(13)-98++, y(13)++

Peptide No.964

SQSSHSYDDSTLPLIDR
Confirmed sites:
Ambiguous sites: @S:1orS:3orS:4orS:6

MS/MS Fragmentation of **SQSSHSYDDSTLPLIDR**
Found in **CTND1_MOUSE** in **SwissProt**, Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2

Match to Query 4983: 1999.850364 from(667.624064,3+) index(6089)
Title: Elution from: 38.934 to 38.934 scan no 3828 cid35.00 polarity:+:m1s



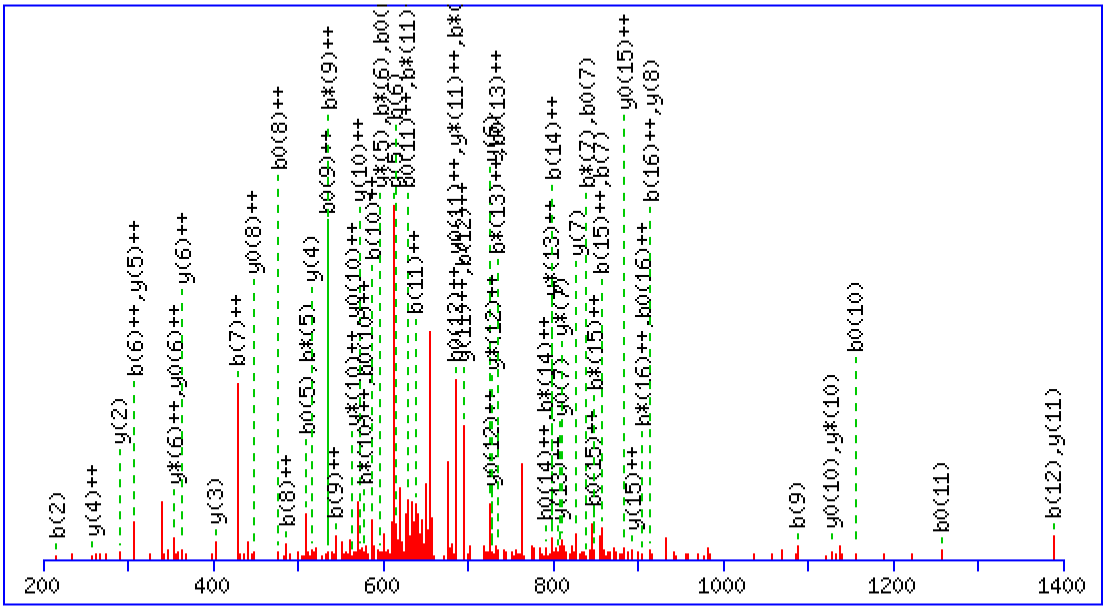
Monoisotopic mass of neutral peptide Mr(calc): 1999.8524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.015
Matched b ions: b(6), b(7), b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(15)++, b(16)++
Matched y ions: y(5), y(6), y(8)

Peptide No.965

SQSSHSYDDSTLPLIDR
Confirmed sites: @Y:7
Ambiguous sites:

MS/MS Fragmentation of **SQSSHSYDDSTLPLIDR**
Found in **CTND1_MOUSE** in **SwissProt**, Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2

Match to Query 5098: 1999.852461 from(667.624763,3+) index(2096)
Title: Elution from: 48.042 to 48.042 scan no 4006 cid35.00 polarity:+



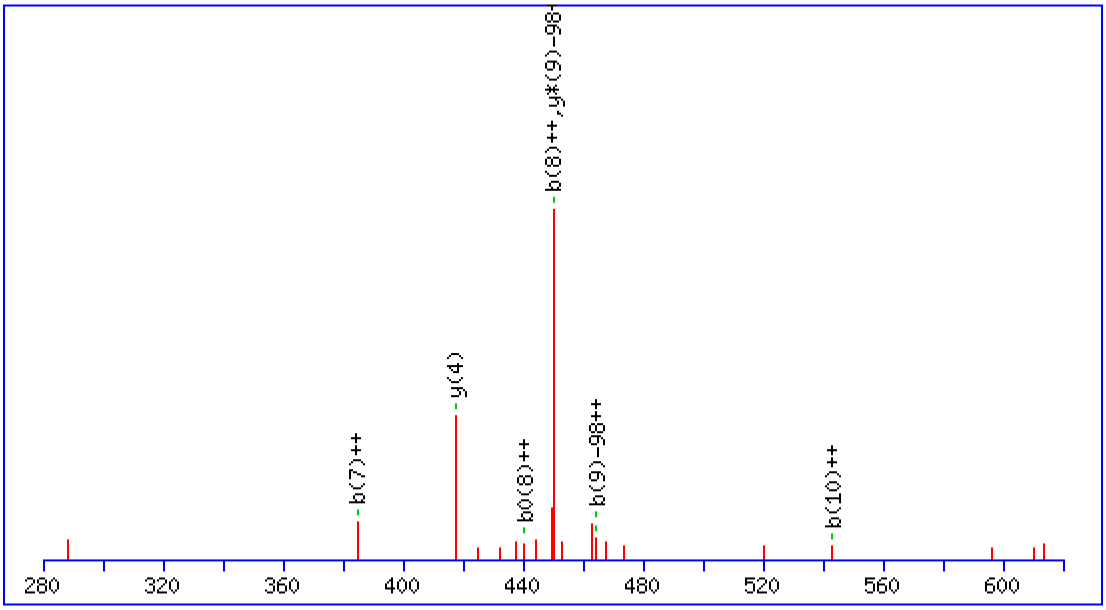
Monoisotopic mass of neutral peptide Mr(calc): 1999.8524
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y7 : Phospho (Y)
Ions Score: 27 **Expect:** 0.011
Matched b ions: b(2), b(6)++, b(6), b(7)++, b(7), b(8)++, b(9), b(9)++, b(10)++, b(11)++, b(12), b(12)++, b(14)++, b(15)++, b(16)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(6)++, y(7), y(8), y(10)++, y(11), y(11)++, y(13)++, y(15)++

Peptide No.966

SQVDNGSMKGGER
Confirmed sites:
Ambiguous sites: @S:1orS:7

MS/MS Fragmentation of **SQVDNGSMKGGER**
Found in **TTF2_MOUSE** in **SwissProt**, Transcription termination factor 2 OS=Mus musculus GN=Ttf2 PE=1 SV=2

Match to Query 2221: 1443.584196 from(482.202008,3+) index(3991)
Title: Elution from: 24.787 to 24.787 scan no 1863 cid35.00 polarity:+:m1s



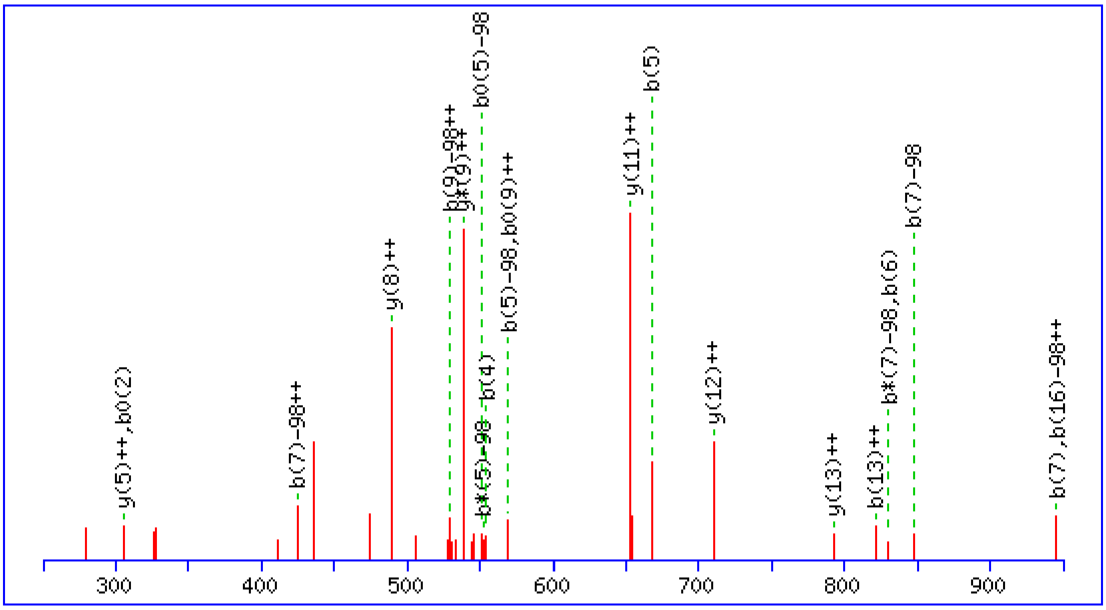
Monoisotopic mass of neutral peptide Mr(calc): 1443.5813
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.048
Matched b ions: b(7)++, b(8)++, b(9)-98++, b(10)++
Matched y ions: y(4)

Peptide No.967

SRDDLYDPDDPRDLPHSR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SRDDLYDPDDPRDLPHSR**
Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 5742: 2247.952972 from(562.995519,4+) index(5076)
Title: Elution from: 30.412 to 30.412 scan no 2656 cid35.00 polarity:+:m1s



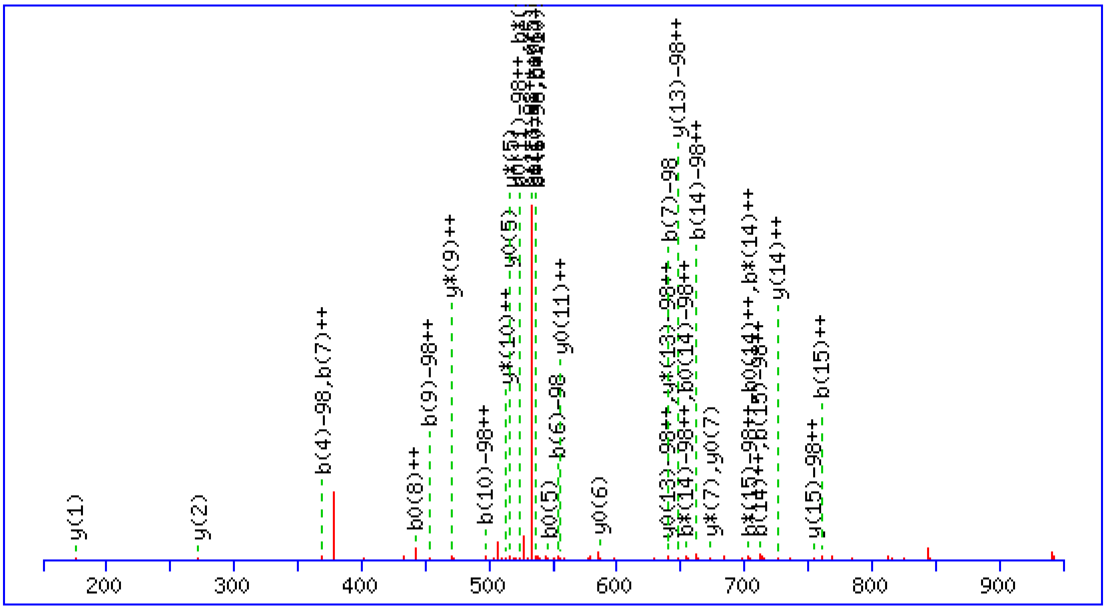
Monoisotopic mass of neutral peptide Mr(calc): 2247.9546
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(4), b(5), b(5)-98, b(6), b(7), b(7)-98++, b(7)-98, b(9)-98++, b(13)++, b(16)-98++
Matched y ions: y(5)++, y(8)++, y(11)++, y(12)++, y(13)++

Peptide No.968

SRGSPSSYTSASSSPR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SRGSPSSYTSASSSPR**
Found in **EPN3_MOUSE** in **SwissProt**, Epsin-3 OS=Mus musculus GN=Epn3 PE=2 SV=1

Match to Query 3780: 1692.709896 from(565.243908,3+) index(3944)
Title: Elution from: 18.652 to 18.652 scan no 1094 cid35.00 polarity:+:m1s



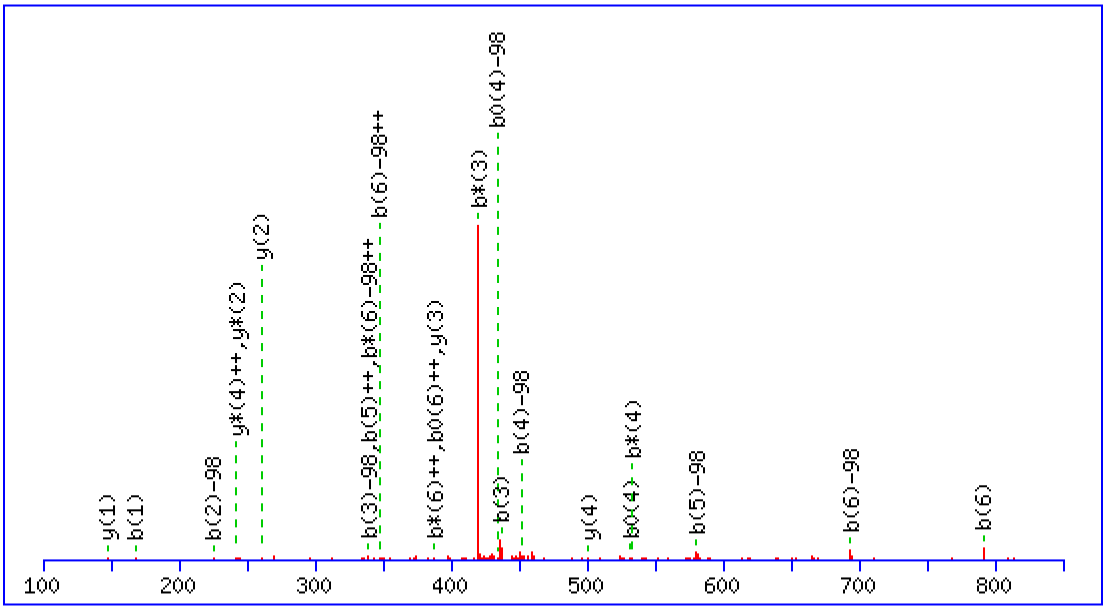
Monoisotopic mass of neutral peptide Mr(calc): 1692.7104
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 20 **Expect:** 0.054
Matched b ions: b(4)-98, b(6)-98, b(7)++, b(7)-98, b(9)-98++, b(10)-98++, b(11)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(1), y(2), y(5), y(13)-98++, y(14)++, y(15)-98++

Peptide No.969

SRLIQLK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SRLIQLK**
Found in **ASH1L_MOUSE** in **SwissProt**, Histone-lysine N-methyltransferase ASH1L OS=Mus musculus GN=Ash1l PE=1 SV=3

Match to Query 715: 936.515754 from(469.265153,2+) index(1789)
Title: Elution from: 43.227 to 43.227 scan no 3490 cid35.00 polarity:+



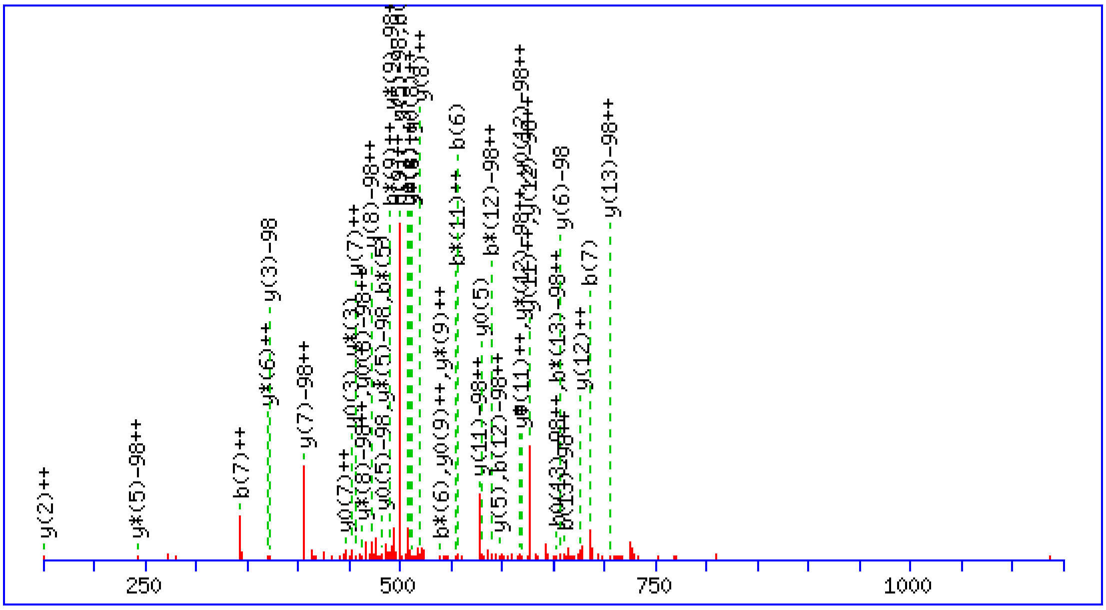
Monoisotopic mass of neutral peptide Mr(calc): 936.5157
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 **Expect:** 0.0057
Matched b ions: b(1), b(2)-98, b(3)-98, b(3), b(4)-98, b(5)++, b(5)-98, b(6)-98, b(6), b(6)-98++
Matched y ions: y(1), y(2), y(3), y(4)

Peptide No.970

SRPSAGERRAGSQR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **SRPSAGERRAGSQR**
Found in **SUV92_MOUSE** in **SwissProt**, Histone-lysine N-methyltransferase SUV39H2 OS=Mus musculus GN=Suv39h2 PE=1 SV=1

Match to Query 3314: 1593.751953 from(532.257927,3+) index(215)
Title: Elution from: 25.937 to 25.937 scan no 1357 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1593.7485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.01
Matched b ions: b(5), b(6), b(7)++, b(7), b(9)++, b(12)-98++, b(13)-98++
Matched y ions: y(2)++, y(3)-98, y(5)-98, y(5), y(6)-98, y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)-98++

Peptide No.971

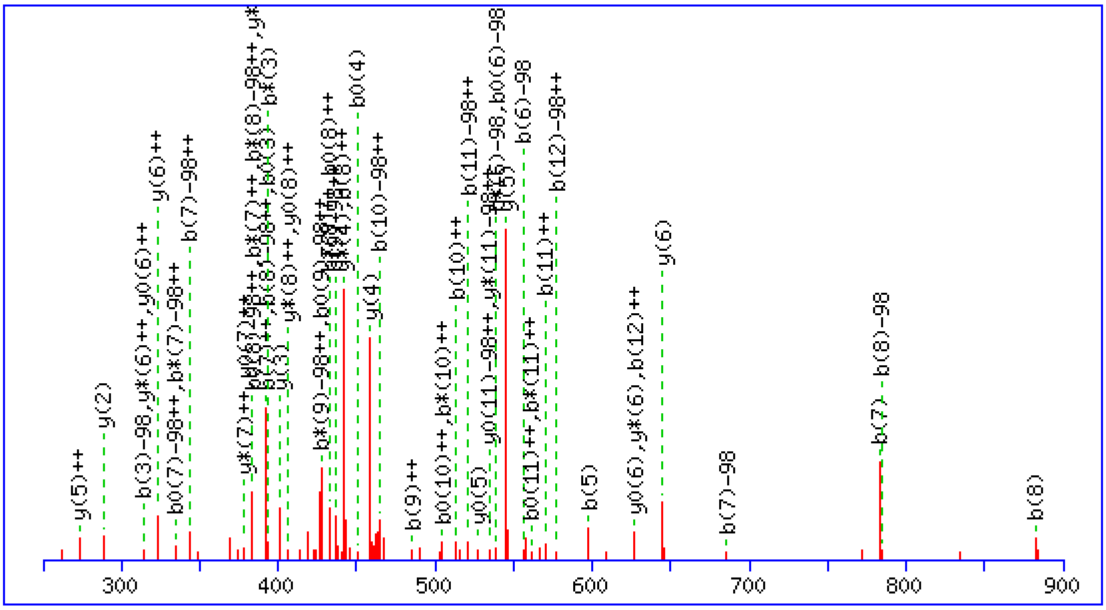
SRSGEGEVSGLLR

Confirmed sites:

Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of **SRSGEGEVSGLLR**
Found in **TIF1B_MOUSE** in **SwissProt**, Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3

Match to Query 2628: 1425.660582 from(476.227470,3+) index(1662)
Title: Elution from: 31.235 to 31.235 scan no 2800 cid35.00 polarity:+



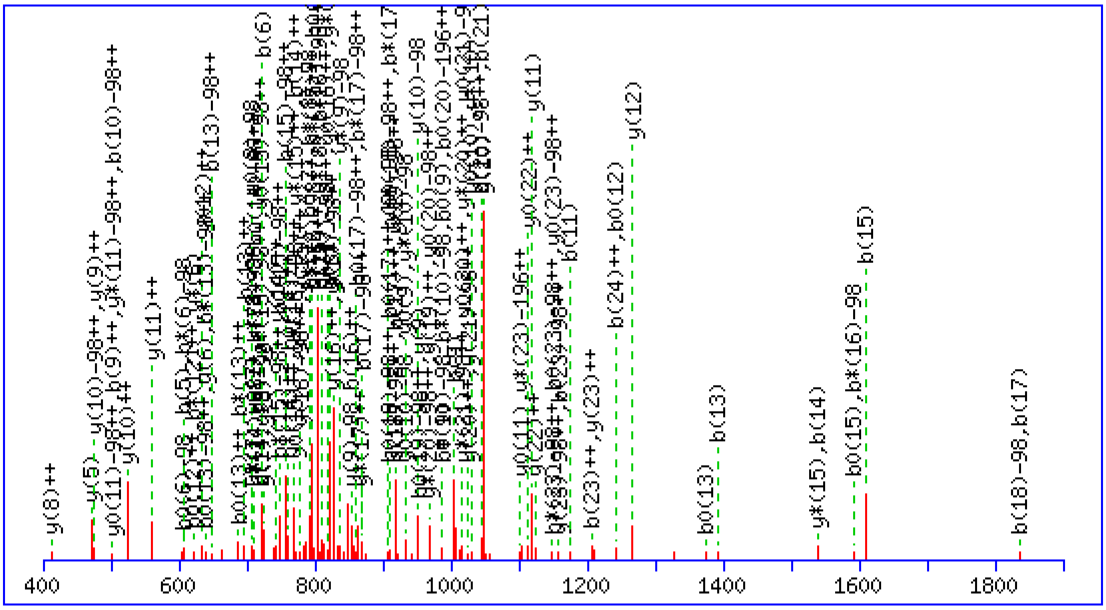
Monoisotopic mass of neutral peptide Mr(calc): 1425.6613
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 **Expect:** 0.0031
Matched b ions: b(3)-98, b(5), b(6)-98, b(7)-98, b(7), b(7)-98++, b(7)++, b(8)++, b(8), b(8)-98, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(5)++, y(6)++, y(6)

Peptide No.972

SRSPVDSPVPASMFAPEPSSPGAAR
Confirmed sites: @S:3,@S:20
Ambiguous sites:

MS/MS Fragmentation of **SRSPVDSPVPASMFAPEPSSPGAAR**
Found in **GTPB1_MOUSE** in **SwissProt**, GTP-binding protein 1 OS=Mus musculus GN=Gtpbp1 PE=1 SV=2

Match to Query 6419: 2656.136715 from(886.386181,3+) index(6515)
Title: Elution from: 47.706 to 47.706 scan no 4888 cid35.00 polarity:+:m1s



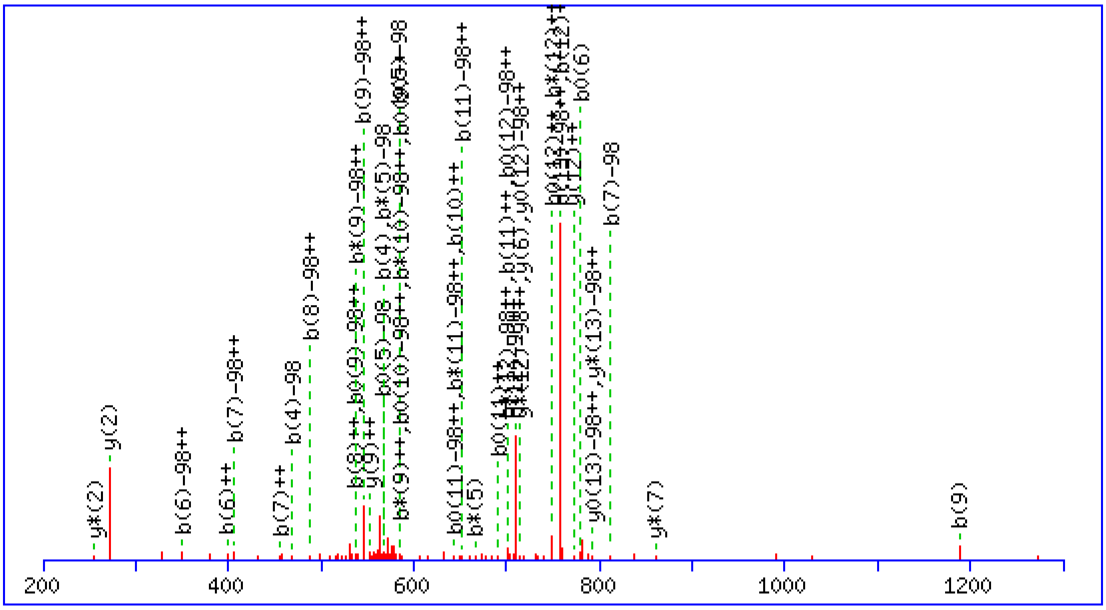
Monoisotopic mass of neutral peptide Mr(calc): 2656.1394
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 2.8e-005
Matched b ions: b(5), b(6), b(7)-98, b(7), b(9), b(9)++, b(9)-98, b(10)-98++, b(11), b(13)++, b(13), b(13)-98++, b(14), b(14)++, b(14)-98++, b(15)++, b(15), b(15)-98++, b(16)-98++, b(16)++, b(17), b(17)++, b(17)-98++, b(18)-98, b(18)-98++, b(20)-98++, b(21)-196++, b(23)++, b(23)-98++, b(24)++
Matched y ions: y(5), y(6), y(7), y(8), y(8)++, y(8)-98, y(9)++, y(9)-98, y(9), y(10)++, y(10), y(10)-98++, y(10)-98, y(11), y(11)++, y(12), y(12)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)-98++, y(19)-98++, y(19)++, y(20)++, y(21)-98++, y(22)++, y(23)++, y(23)-98++

Peptide No.973

SRSRDDLYDPDDPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SRSRDDLYDPDDPR**
Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 4021: 1785.731106 from(596.250978,3+) index(4331)
Title: Elution from: 23.367 to 23.367 scan no 1695 cid35.00 polarity:+:m1s



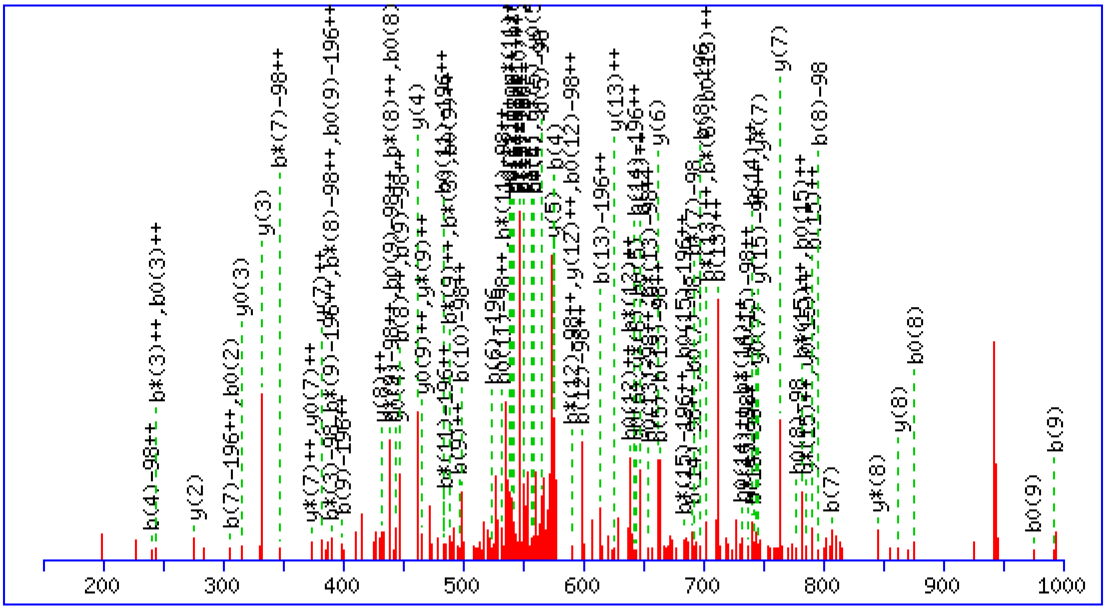
Monoisotopic mass of neutral peptide Mr(calc): 1785.7319
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 17 **Expect:** 0.052
Matched b ions: b(4), b(4)-98, b(5)-98, b(6)++, b(6)-98++, b(7)-98++, b(7)++, b(7)-98, b(8)-98++, b(8)++, b(9)-98++, b(9), b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-98++
Matched y ions: y(2), y(6), y(9)++, y(12)++

Peptide No.974

SRTASGSSVTSLEGTR
Confirmed sites: @S:1,@T:3
Ambiguous sites:

MS/MS Fragmentation of **SRTASGSSVTSLEGTR**
Found in **NDRG1_MOUSE** in **SwissProt**, Protein NDRG1 OS=Mus musculus GN=Ndrg1 PE=1 SV=1

Match to Query 3843: 1754.724009 from(585.915279,3+) index(884)
Title: Elution from: 34.294 to 34.294 scan no 2312 cid35.00 polarity:+



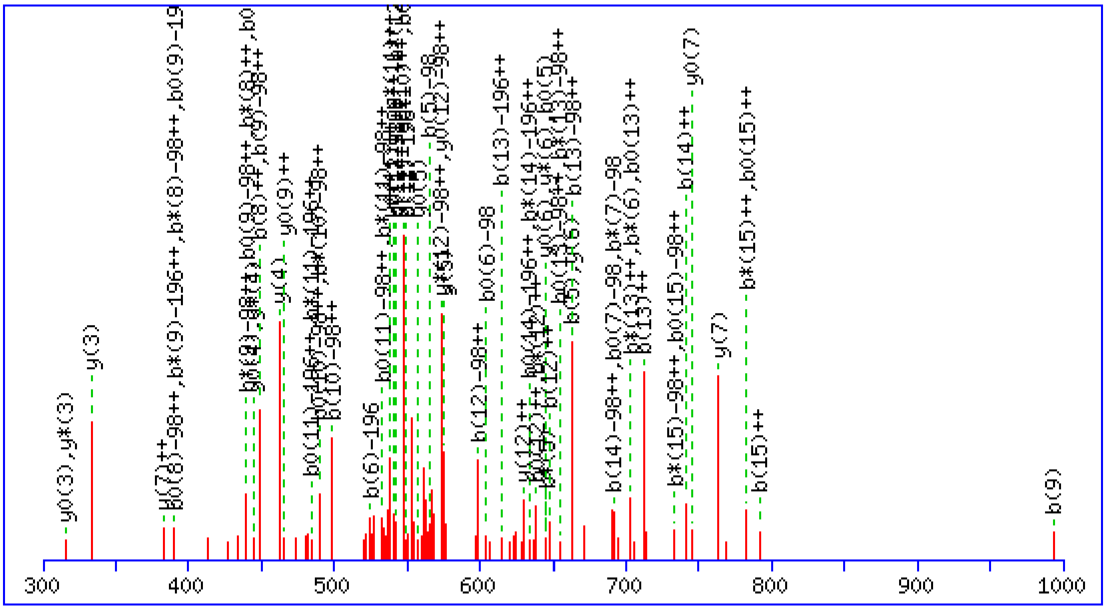
Monoisotopic mass of neutral peptide Mr(calc): 1754.7237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0044
Matched b ions: b(4), b(4)-98++, b(5), b(5)-98, b(6)-196, b(7), b(7)-196++, b(8)++, b(8)-196, b(8)-98, b(9)-98++, b(9), b(9)-196++, b(9)++, b(10)++, b(10)-98++, b(11)-98++, b(12)++, b(12)-98++, b(12)-196++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(11)++, y(12)++, y(13)++, y(15)-98++

Peptide No.975

SRTASGSSVTSLEGTR
Confirmed sites: @S:5
Ambiguous sites: @S:1orT:3

MS/MS Fragmentation of **SRTASGSSVTSLEGTR**
Found in **NDRG1_MOUSE** in **SwissProt**, Protein NDRG1 OS=Mus musculus GN=Ndrg1 PE=1 SV=1

Match to Query 3413: 1754.722530 from(585.914786,3+) index(1115)
Title: Elution from: 26.831 to 26.831 scan no 2141 cid35.00 polarity:+



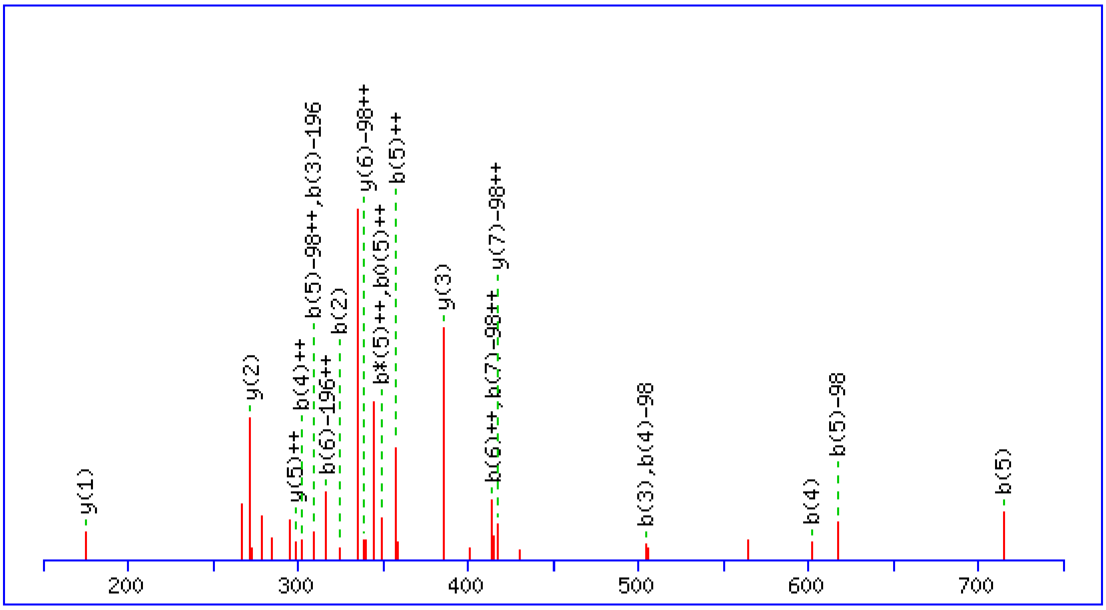
Monoisotopic mass of neutral peptide Mr(calc): 1754.7237
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0017
Matched b ions: b(5), b(5)-98, b(6)-196, b(8)++, b(9), b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(12)-98++, b(12)++, b(12)-196++, b(13)-98++, b(13)++, b(13)-196++, b(14)++, b(14)-98++, b(15)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)++, y(11)++, y(12)++

Peptide No.976

SRTPLLPR
Confirmed sites: @S:1,@T:3
Ambiguous sites:

MS/MS Fragmentation of **SRTPLLPR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 1022: 1098.498252 from(367.173360,3+) index(1228)
Title: Elution from: 27.835 to 27.835 scan no 2277 cid35.00 polarity:+



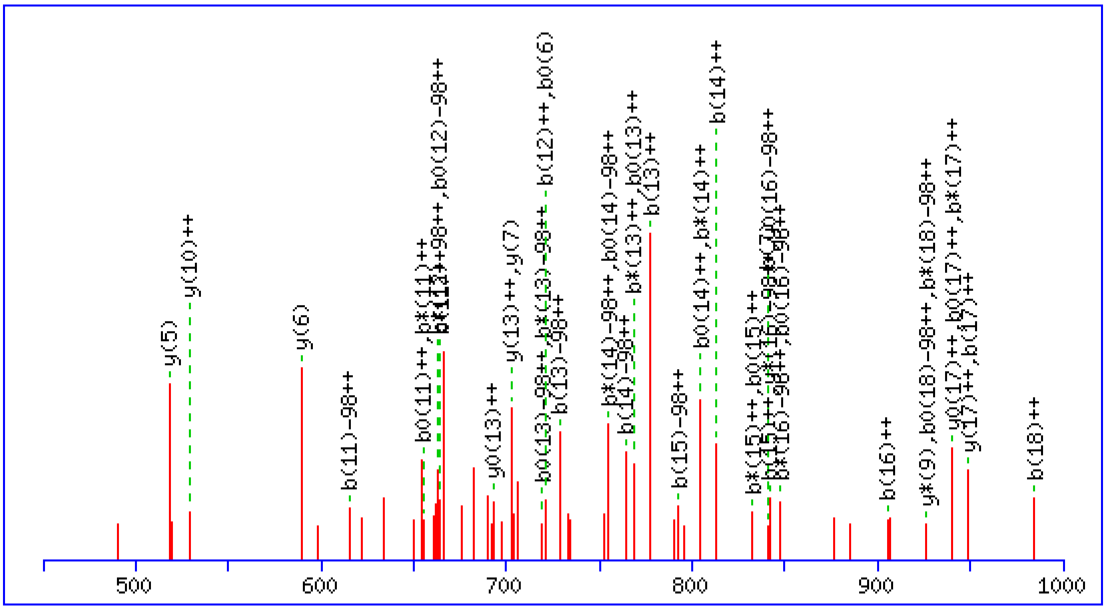
Monoisotopic mass of neutral peptide Mr(calc): 1098.4988
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.047
Matched b ions: b(2), b(3), b(3)-196, b(4)-98, b(4), b(4)++, b(5)-98, b(5), b(5)++, b(5)-98++, b(6)++, b(6)-196++, b(7)-98++
Matched y ions: y(1), y(2), y(3), y(5)++, y(6)-98++, y(7)-98++

Peptide No.977

SRTSVQTEDDQLIAGQSAR
Confirmed sites:
Ambiguous sites: @T:3orS:4

MS/MS Fragmentation of **SRTSVQTEDDQLIAGQSAR**
Found in **CTNA1_MOUSE** in **SwissProt**, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 4599: 2140.974333 from(714.665387,3+) index(4355)
Title: Elution from: 28.136 to 28.136 scan no 2318 cid35.00 polarity:+:m1s



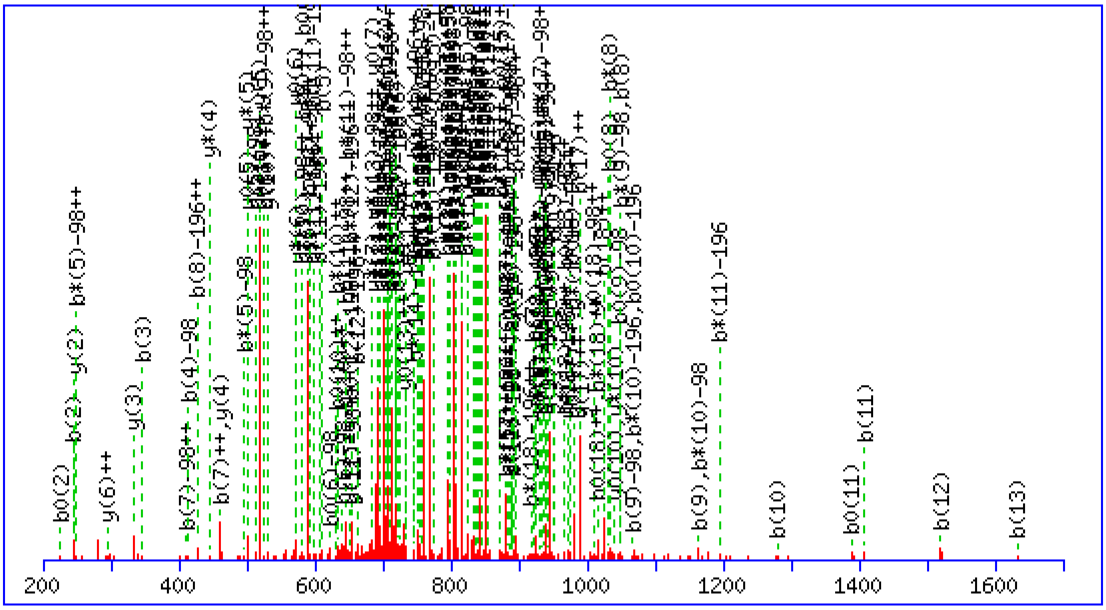
Monoisotopic mass of neutral peptide Mr(calc): 2140.9750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.006
Matched b ions: b(7), b(11)++, b(11)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(17)++, b(18)++
Matched y ions: y(5), y(6), y(7), y(10)++, y(13)++, y(17)++

Peptide No.978

SRTSVQTEDDQLIAGQSAR
Confirmed sites: @S:4,@T:7
Ambiguous sites:

MS/MS Fragmentation of **SRTSVQTEDDQLIAGQSAR**
Found in **CTNA2_MOUSE** in **SwissProt**, Catenin alpha-2 OS=Mus musculus GN=Ctnna2 PE=1 SV=3

Match to Query 5627: 2220.941724 from(741.321184,3+) index(4847)
Title: Elution from: 38.327 to 38.327 scan no 2928 cid35.00 polarity:+:m1s



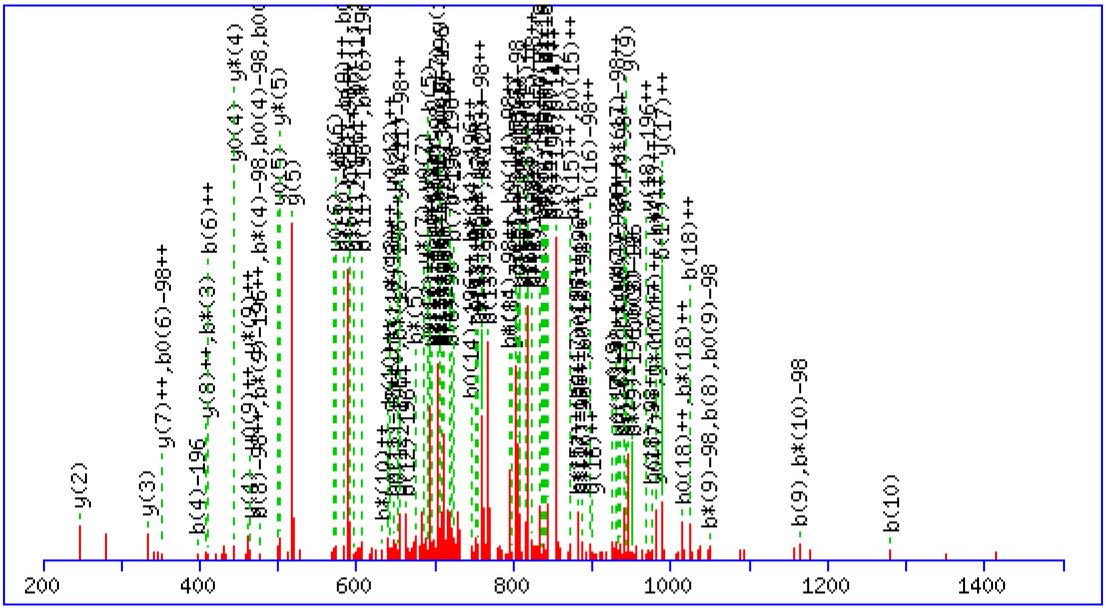
Monoisotopic mass of neutral peptide Mr(calc): 2220.9413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00018
Matched b ions: b(2), b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)++, b(7)-98++, b(7)-196, b(7), b(8)-196, b(8), b(8)-196++, b(8)++, b(9), b(9)++, b(9)-98, b(10), b(10)-98++, b(10)++, b(11), b(11)++, b(11)-98++, b(11)-196++, b(12), b(12)-98++, b(12)++, b(12)-196++, b(13), b(13)-98++, b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(16)-196++, b(17)++, b(17)-98++, b(17)-196++, b(18)++, b(18)-196++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10)++, y(12)++, y(13)-98++, y(14)-98++, y(14)++, y(15)-98++, y(15)++, y(16)++, y(16)-98++, y(17)-196++, y(17)-98++, y(17)++, y(18)-196++

Peptide No.979

SRTSVQTEDDQLIAGQSAR
Confirmed sites: @T:3,@S:4
Ambiguous sites:

MS/MS Fragmentation of **SRTSVQTEDDQLIAGQSAR**
Found in **CTNA1_MOUSE** in **SwissProt**, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 4861: 2220.943185 from(741.321671,3+) index(4171)
Title: Elution from: 38.251 to 38.251 scan no 2791 cid35.00 polarity:+:m1s



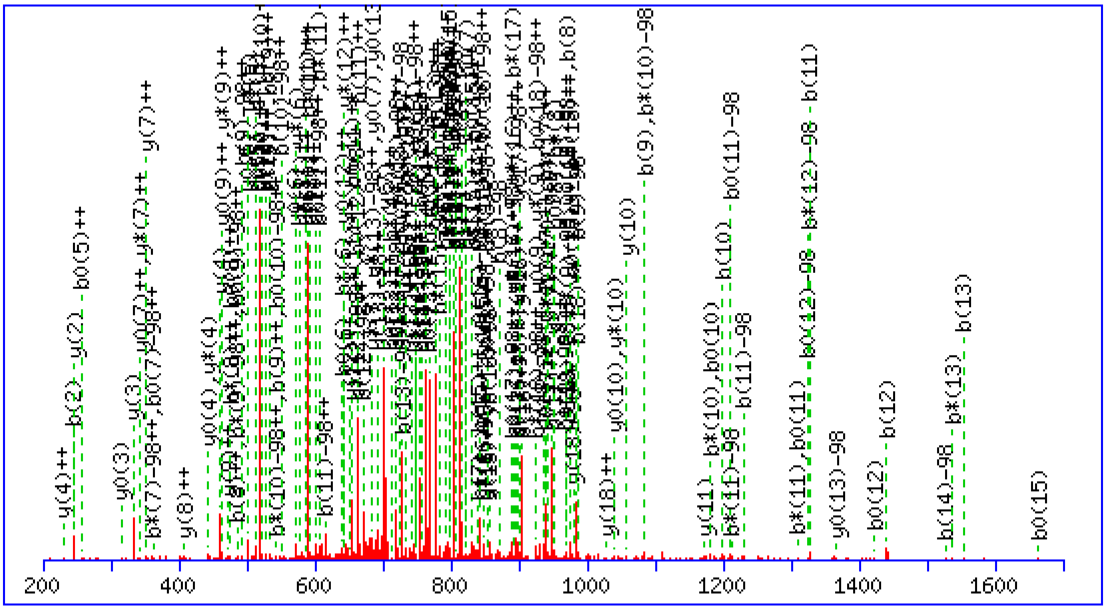
Monoisotopic mass of neutral peptide Mr(calc): 2220.9413
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00014
Matched b ions: b(4)-196, b(5), b(6)++, b(6)-98, b(6), b(7)-196, b(8)-196, b(8), b(8)-98++, b(8)-98, b(9), b(9)++, b(10), b(10)-98++, b(10)++, b(11)-196++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(12)-196++, b(13)++, b(13)-98++, b(13)-196++, b(14)++, b(14)-98++, b(14)-196++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(12)++, y(13)++, y(15)++, y(16)++, y(17)++, y(18)-196++

Peptide No.980

SRTSVQTEDDQLIAGQSAR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **SRTSVQTEDDQLIAGQSAR**
Found in **CTNA2_MOUSE** in **SwissProt**, Catenin alpha-2 OS=Mus musculus GN=Ctnna2 PE=1 SV=3

Match to Query 5439: 2140.975554 from(714.665794,3+) index(4662)
Title: Elution from: 36.227 to 36.227 scan no 2671 cid35.00 polarity:+:m1s



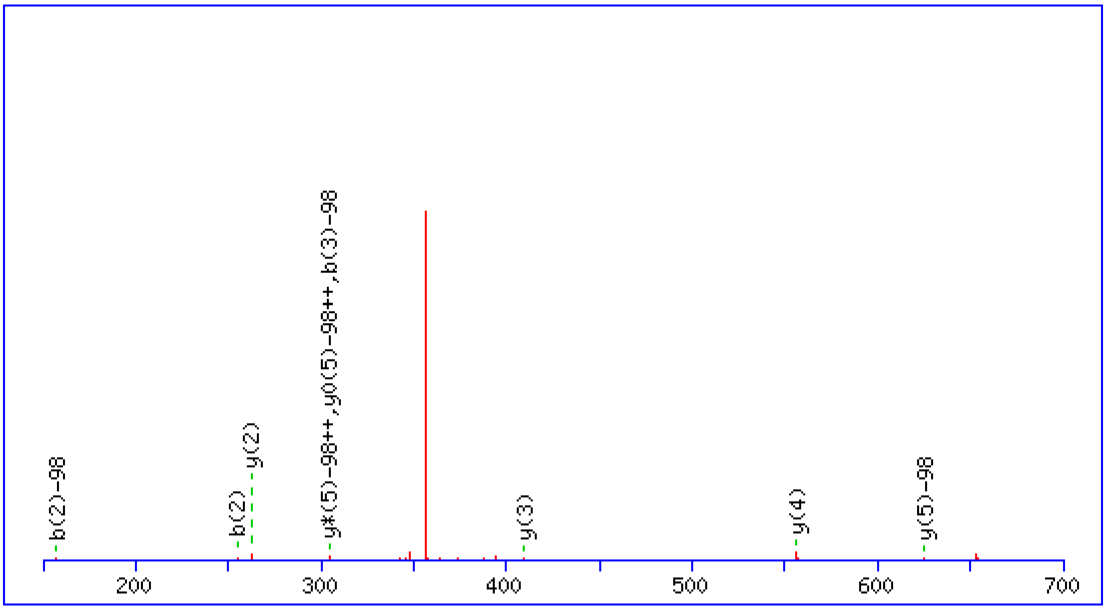
Monoisotopic mass of neutral peptide Mr(calc): 2140.9750
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 46 **Expect:** 0.00018
Matched b ions: b(2), b(7)-98, b(7), b(8)++, b(8), b(8)-98, b(9), b(9)-98++, b(9)++, b(9)-98, b(10), b(10)++, b(10)-98++, b(11)-98, b(11), b(11)++, b(11)-98++, b(12), b(12)-98++, b(12)++, b(13), b(13)++, b(13)-98++, b(14)++, b(14)-98, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++

Peptide No.981

SSFFSR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **SSFFSR**
Found in **MOT10_MOUSE** in **SwissProt**, Monocarboxylate transporter 10 OS=Mus musculus GN=Slc16a10 PE=1 SV=1

Match to Query 300: 809.311358 from(405.662955,2+) index(1287)
Title: Elution from: 30.067 to 30.067 scan no 2496 cid35.00 polarity:+



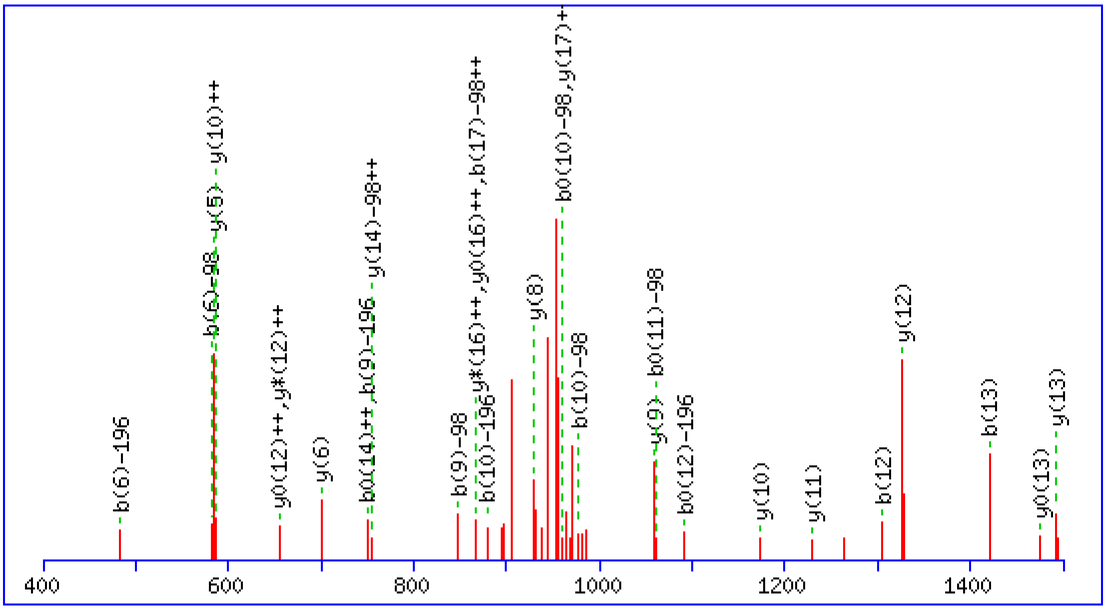
Monoisotopic mass of neutral peptide Mr(calc): 809.3109
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.0028
Matched b ions: b(2), b(2)-98, b(3)-98
Matched y ions: y(2), y(3), y(4), y(5)-98

Peptide No.982

SSGSLSPGLETEDPLEAR
Confirmed sites: @S:6
Ambiguous sites: @S:2orS:4

MS/MS Fragmentation of **SSGSLSPGLETEDPLEAR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 5005: 2003.811490 from(1002.913021,2+) index(6835)
Title: Elution from: 50.699 to 50.699 scan no 5258 cid35.00 polarity:+:m1s



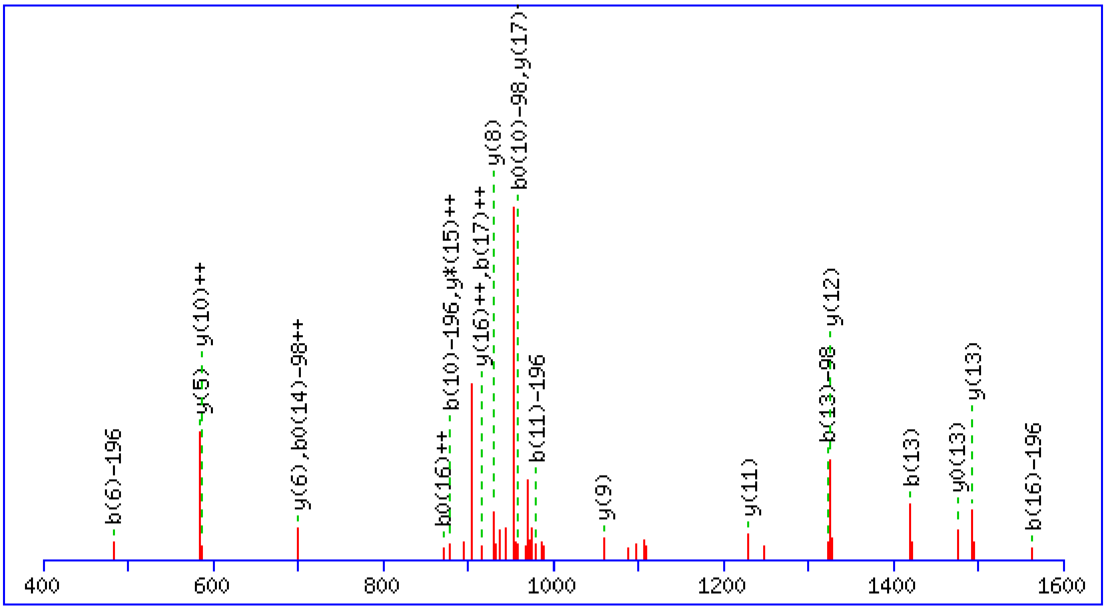
Monoisotopic mass of neutral peptide Mr(calc): 2003.8126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0042
Matched b ions: b(6)-98, b(6)-196, b(9)-98, b(9)-196, b(10)-196, b(10)-98, b(12), b(13), b(17)-98++
Matched y ions: y(5), y(6), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13), y(14)-98++, y(17)++

Peptide No.983

SSGSLSPGLETEDPLEAR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SSGSLSPGLETEDPLEAR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4180: 2003.815006 from(1002.914779,2+) index(5877)
Title: Elution from: 49.800 to 49.800 scan no 4876 cid35.00 polarity:+:m1s



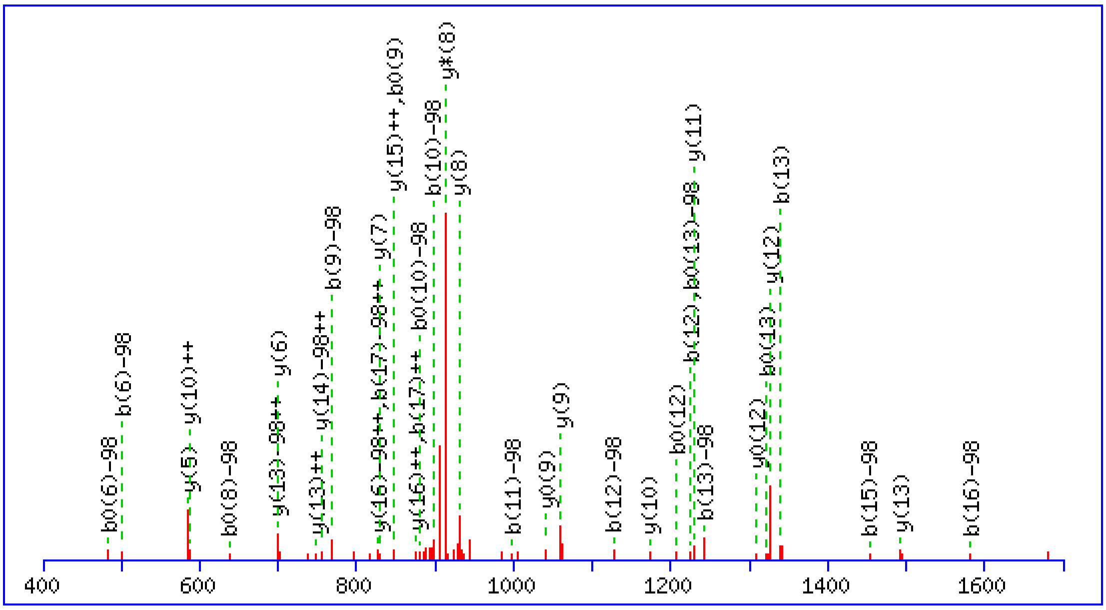
Monoisotopic mass of neutral peptide Mr(calc): 2003.8126
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0015
Matched b ions: b(6)-196, b(10)-196, b(11)-196, b(13), b(13)-98, b(16)-196, b(17)++
Matched y ions: y(5), y(6), y(8), y(9), y(10)++, y(11), y(12), y(13), y(16)++, y(17)++

Peptide No.984

SSGSLSPGLETEDPLEAR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SSGSLSPGLETEDPLEAR**
Found in **TB182_MOUSE** in **SwissProt**, 182 kDa tankyrase-1-binding protein OS=Mus musculus GN=Tnks1bp1 PE=1 SV=2

Match to Query 4709: 1923.846272 from(962.930412,2+) index(6543)
Title: Elution from: 45.268 to 45.268 scan no 4634 cid35.00 polarity:+:m1s



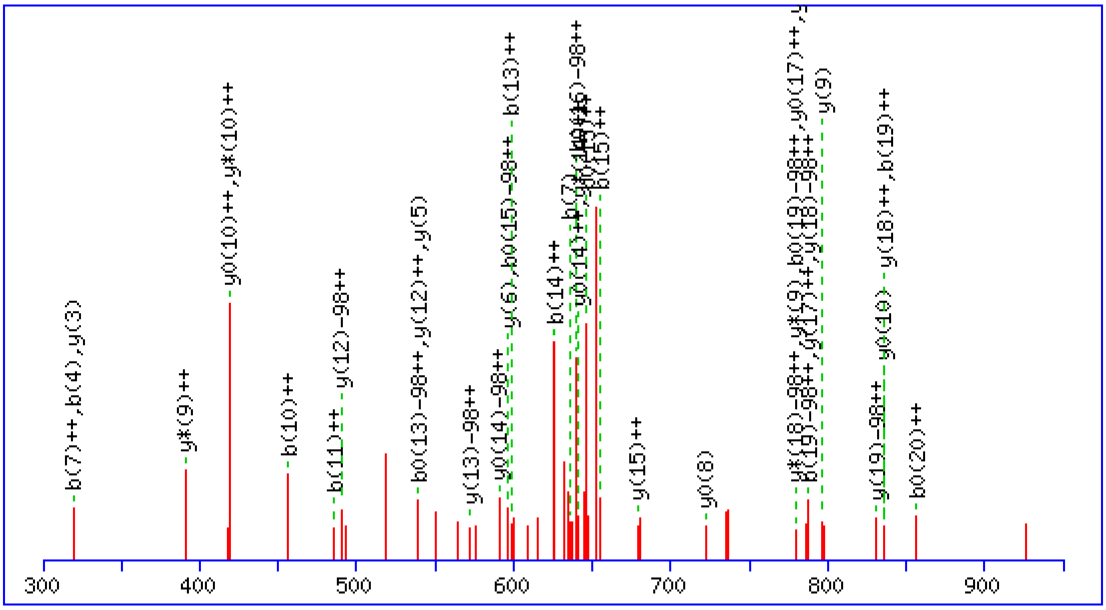
Monoisotopic mass of neutral peptide Mr(calc): 1923.8463
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 53 **Expect:** 2.6e-005
Matched b ions: b(6)-98, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(12), b(13)-98, b(13), b(15)-98, b(16)-98, b(17)-98++, b(17)++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13), y(13)-98++, y(13)++, y(14)-98++, y(15)++, y(16)-98++, y(16)++

Peptide No.985

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **SSGSPYGGGYGSGGGSGGYGSR**
Found in **ROA3_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 4198: 1989.749394 from(664.257074,3+) index(3827)
Title: Elution from: 25.623 to 25.623 scan no 1882 cid35.00 polarity:+:m1s



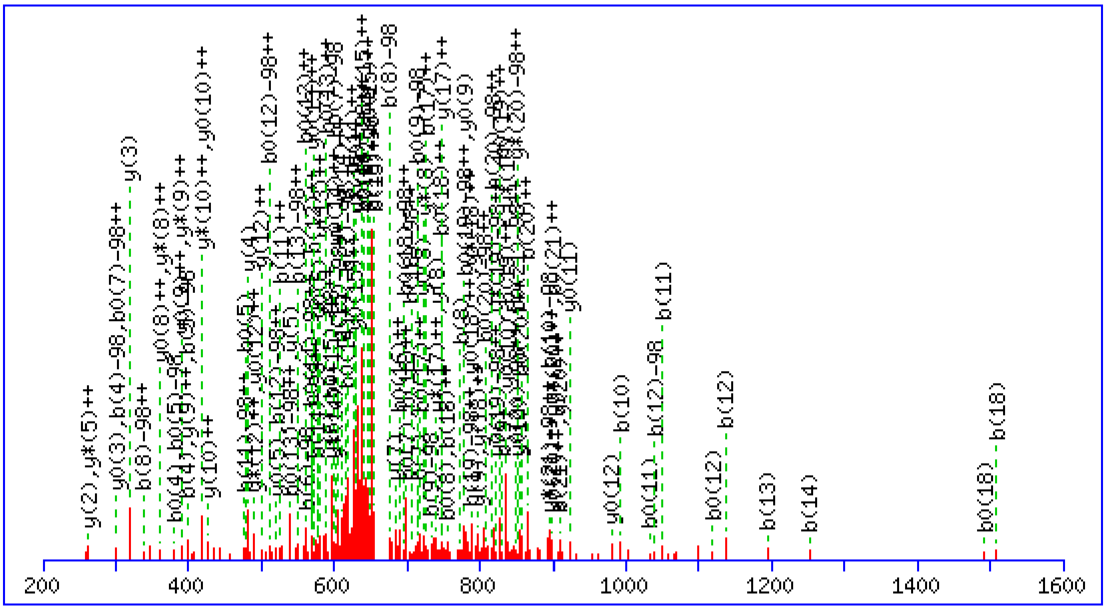
Monoisotopic mass of neutral peptide Mr(calc): 1989.7491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(4), b(7)++, b(7), b(10)++, b(11)++, b(13)++, b(14)++, b(15)++, b(19)-98++, b(19)++
Matched y ions: y(3), y(5), y(6), y(9), y(12)++, y(12)-98++, y(13)-98++, y(15)++, y(17)++, y(18)-98++, y(18)++, y(19)-98++

Peptide No.986

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SSGSPYGGGYGSGGGSGGYGSR**
Found in **ROA3_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 5086: 1989.749463 from(664.257097,3+) index(836)
Title: Elution from: 32.025 to 32.025 scan no 2139 cid35.00 polarity:+



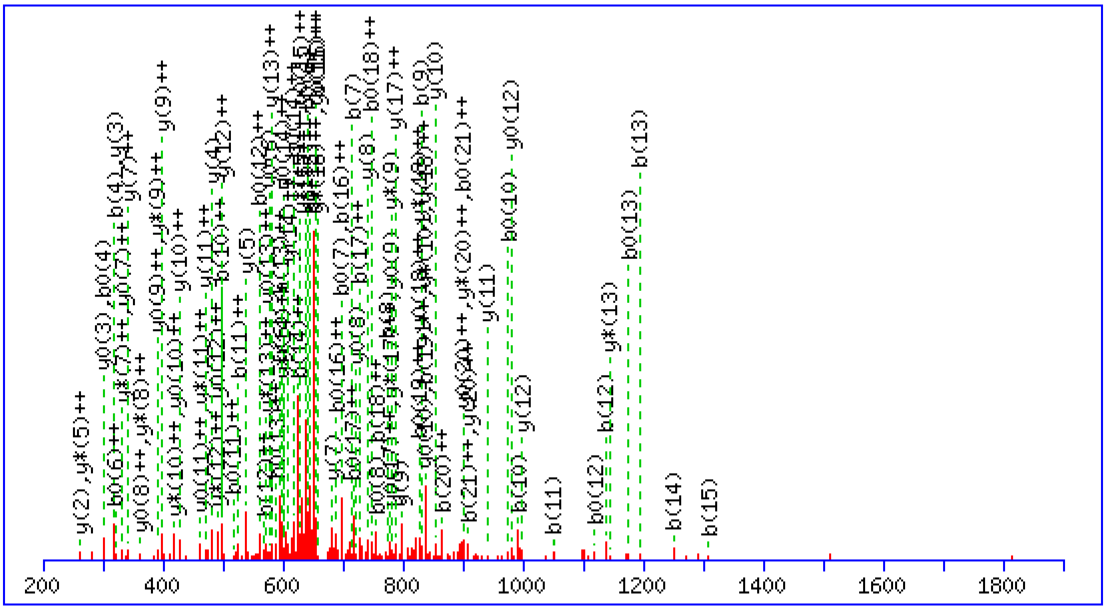
Monoisotopic mass of neutral peptide Mr(calc): 1989.7491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 2.1e-005
Matched b ions: b(4), b(4)-98, b(5)-98, b(6)-98, b(7), b(7)-98, b(8)-98++, b(8)-98, b(8), b(9)-98, b(9), b(10), b(10)-98, b(11), b(11)-98++, b(11)++, b(12), b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98++, b(14), b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(18), b(18)-98++, b(18)++, b(19)++, b(19)-98++, b(20)++, b(20)-98++, b(21)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(12)++, y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(20)++

Peptide No.987

SSGSPYGGGYGSGGGSGGYGSR
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of **SSGSPYGGGYGSGGGSGGYGSR**
Found in **ROA3_MOUSE** in **SwissProt**, Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1

Match to Query 4421: 1989.750150 from(664.257326,3+) index(3621)
Title: Elution from: 31.950 to 31.950 scan no 2034 cid35.00 polarity:+:m1s



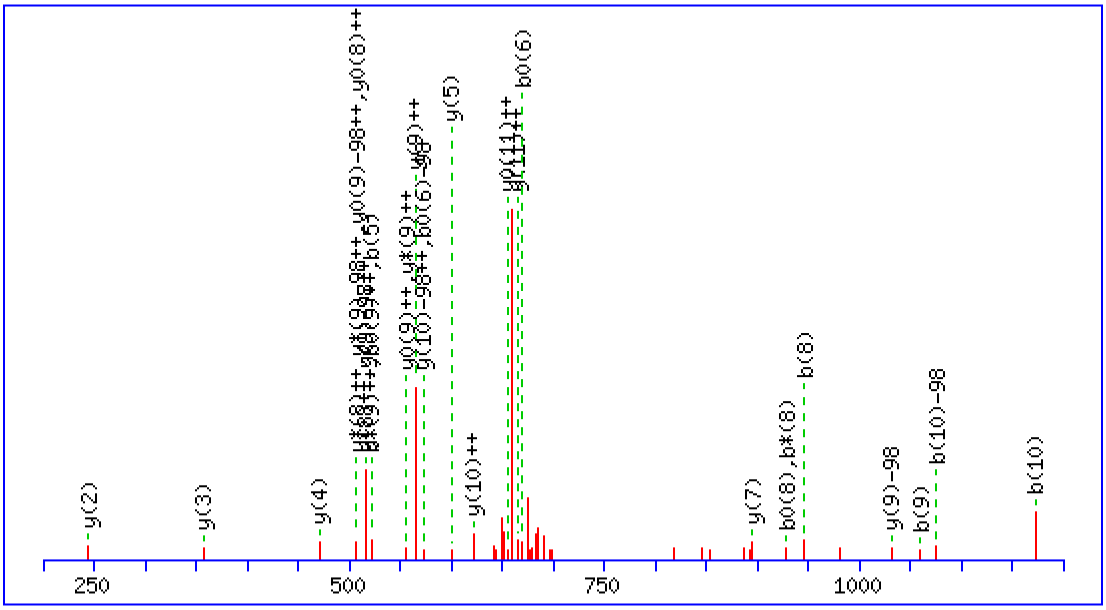
Monoisotopic mass of neutral peptide Mr(calc): 1989.7491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
Ions Score: 61 **Expect:** 3e-006
Matched b ions: b(4), b(7), b(8), b(9), b(10), b(10)++, b(11), b(11)++, b(12), b(12)++, b(13), b(13)++, b(14), b(14)++, b(15), b(15)++, b(16)++, b(17)++, b(18)++, b(19)++, b(20)++, b(21)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(14)++, y(15)++, y(17)++, y(18)++, y(20)++

Peptide No.988

SSLPHSQENLPK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **SSLPHSQENLPK**
Found in **IRF3_MOUSE** in **SwissProt**, Interferon regulatory factor 3 OS=Mus musculus GN=Irf3 PE=1 SV=1

Match to Query 2421: 1415.642140 from(708.828346,2+) index(587)
Title: Elution from: 21.550 to 21.550 scan no 1447 cid35.00 polarity:+



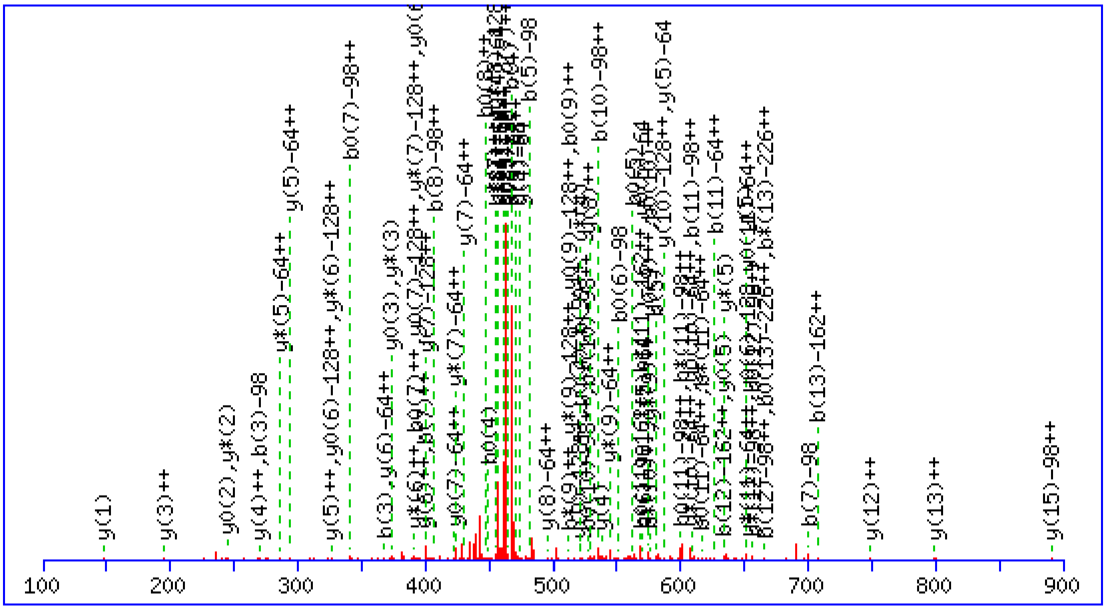
Monoisotopic mass of neutral peptide Mr(calc): 1415.6446
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0073
Matched b ions: b(5), b(8), b(9), b(10)-98, b(10)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8)++, y(9)-98++, y(9)++, y(9)-98, y(10)++, y(10)-98++, y(11)++

Peptide No.989

SSLVLSMLQQMLMEDK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **SSLVLSMLQQMLMEDK**
Found in **K1468_MOUSE** in **SwissProt**, LisH domain and HEAT repeat-containing protein KIAA1468 OS=Mus musculus GN=Kiaa1468 PE=1 SV=1

Match to Query 4715: 1963.870200 from(491.974826,4+) index(4777)
Title: Elution from: 27.394 to 27.394 scan no 2243 cid35.00 polarity:+:m1s



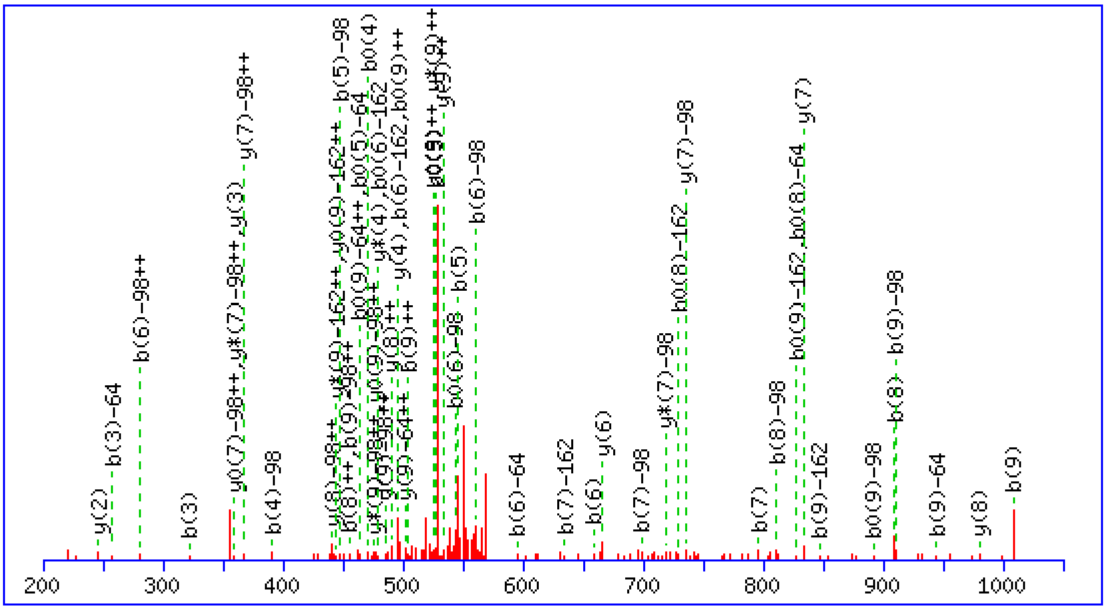
Monoisotopic mass of neutral peptide Mr(calc): 1963.8706
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M11 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 24 **Expect:** 0.028
Matched b ions: b(3)-98, b(3), b(4), b(5)-98, b(5), b(6)-98, b(7)-98, b(7)++, b(8)++, b(8)-98++, b(9)-98++, b(9)++, b(10)-98++, b(11)-98++, b(12)-98++
Matched y ions: y(1), y(3)++, y(3), y(4)++, y(4), y(5), y(5)++, y(6)++, y(7)++, y(8)++, y(12)++, y(13)++, y(15)-98++

Peptide No.990

SSMSGLHLVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SSMSGLHLVK**
Found in **ACACA_MOUSE** in **SwissProt**, Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1

Match to Query 1732: 1153.521098 from(577.767825,2+) index(739)
Title: Elution from: 32.588 to 32.588 scan no 2109 cid35.00 polarity:+



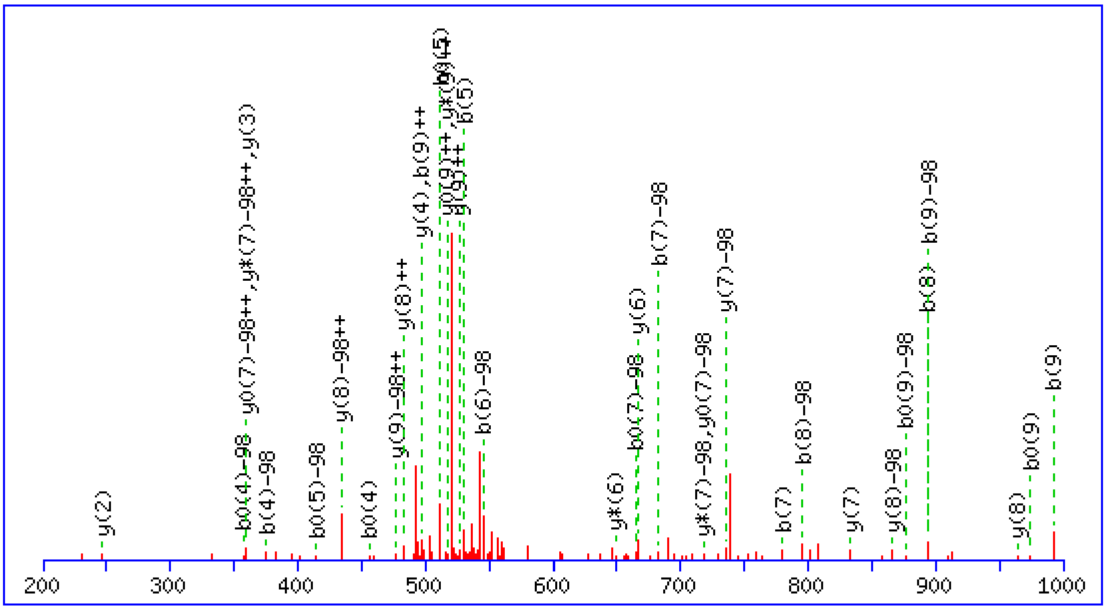
Monoisotopic mass of neutral peptide Mr(calc): 1153.5202
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6)-98++, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(8)++, b(9), b(9)-98, b(9)-98++, b(9)++
Matched y ions: y(2), y(3), y(4), y(6), y(7)-98, y(7), y(7)-98++, y(8)-98++, y(8)++, y(8), y(9)-98++, y(9)++

Peptide No.991

SSMSGLHLVK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **SSMSGLHLVK**
Found in **ACACA_MOUSE** in **SwissProt**, Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1

Match to Query 1385: 1137.524140 from(569.769346,2+) index(1644)
Title: Elution from: 31.073 to 31.073 scan no 2778 cid35.00 polarity:+



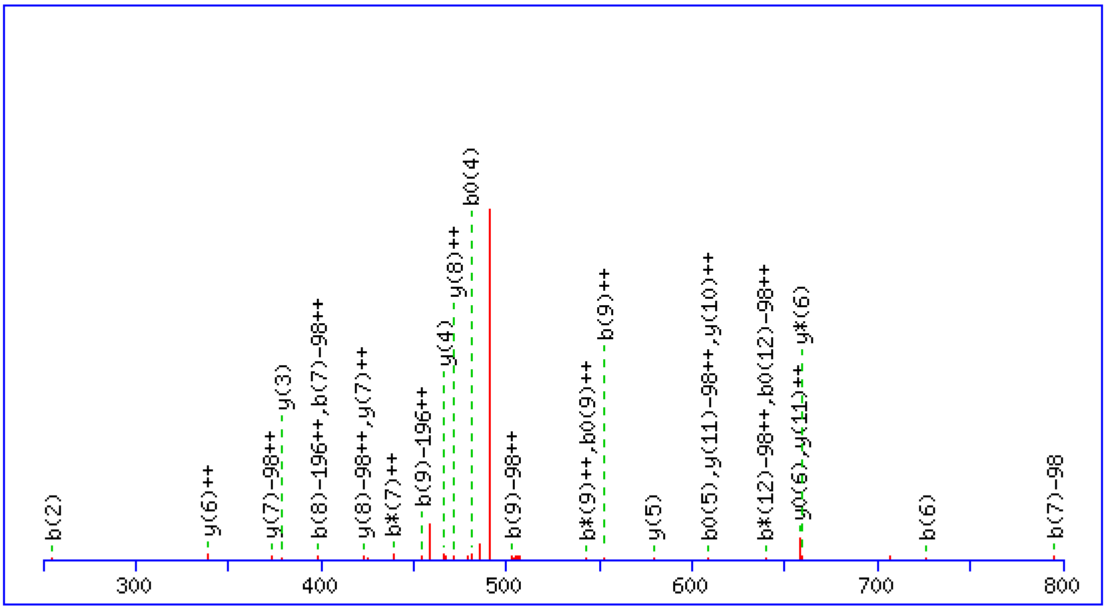
Monoisotopic mass of neutral peptide Mr(calc): 1137.5253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 **Expect:** 0.0053
Matched b ions: b(4)-98, b(5), b(6)-98, b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(9)++
Matched y ions: y(2), y(3), y(4), y(6), y(7), y(7)-98, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)-98++, y(9)++

Peptide No.992

SSPFKVSPLSFGR
Confirmed sites: @S:7
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of **SSPFKVSPLSFGR**
Found in **SDPR_MOUSE** in **SwissProt**, Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3

Match to Query 2837: 1567.685865 from(523.569231,3+) index(5689)
Title: Elution from: 51.146 to 51.146 scan no 5067 cid35.00 polarity:+:m1s



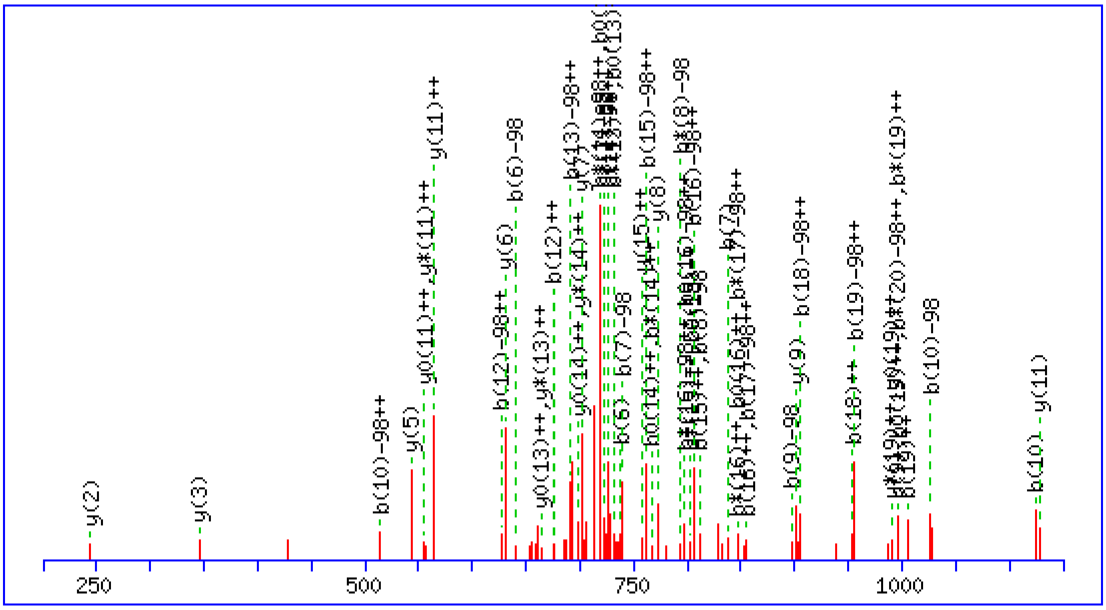
Monoisotopic mass of neutral peptide Mr(calc): 1567.6837
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(2), b(6), b(7)-98, b(7)-98++, b(8)-196++, b(9)-196++, b(9)-98++, b(9)++
Matched y ions: y(3), y(4), y(5), y(6)++, y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(10)++, y(11)-98++, y(11)++

Peptide No.993

SSPKEEVASEPEEAASPTTPK
Confirmed sites:
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of **SSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 5753: 2249.987715 from(751.003181,3+) index(4410)
Title: Elution from: 24.009 to 24.009 scan no 1783 cid35.00 polarity:+:m1s



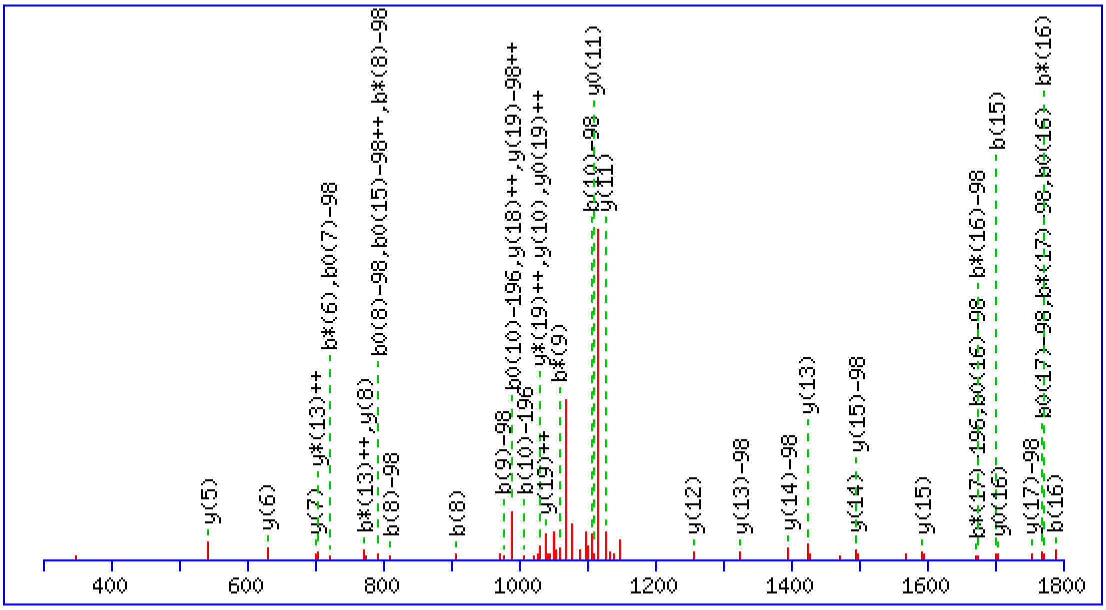
Monoisotopic mass of neutral peptide Mr(calc): 2249.9940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 **Expect:** 3.1e-006
Matched b ions: b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(9), b(9)-98, b(10), b(10)-98++, b(10)-98, b(12)-98++, b(12)++, b(13)-98++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(15)++

Peptide No.994

SSPKEEVASEPEEAASPTTPK
Confirmed sites: @S:9
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of **SSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4952: 2329.954826 from(1165.984689,2+) index(3994)
Title: Elution from: 27.198 to 27.198 scan no 2098 cid35.00 polarity:+:m1s



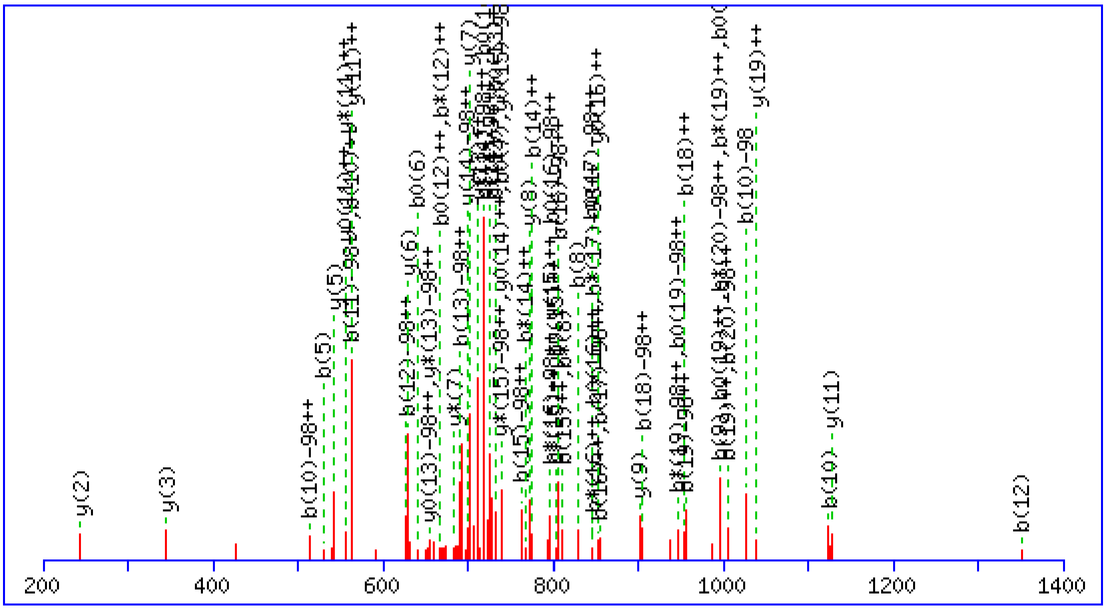
Monoisotopic mass of neutral peptide Mr(calc): 2329.9603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 8.9e-005
Matched b ions: b(8), b(8)-98, b(9)-98, b(10)-196, b(10)-98, b(15), b(16)
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(15), y(17)-98, y(18)++, y(19)-98++, y(19)++

Peptide No.995

SSPKEEVASEPEEAASPTTPK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **SSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 4860: 2249.991291 from(751.004373,3+) index(3634)
Title: Elution from: 23.982 to 23.982 scan no 1655 cid35.00 polarity:+:m1s



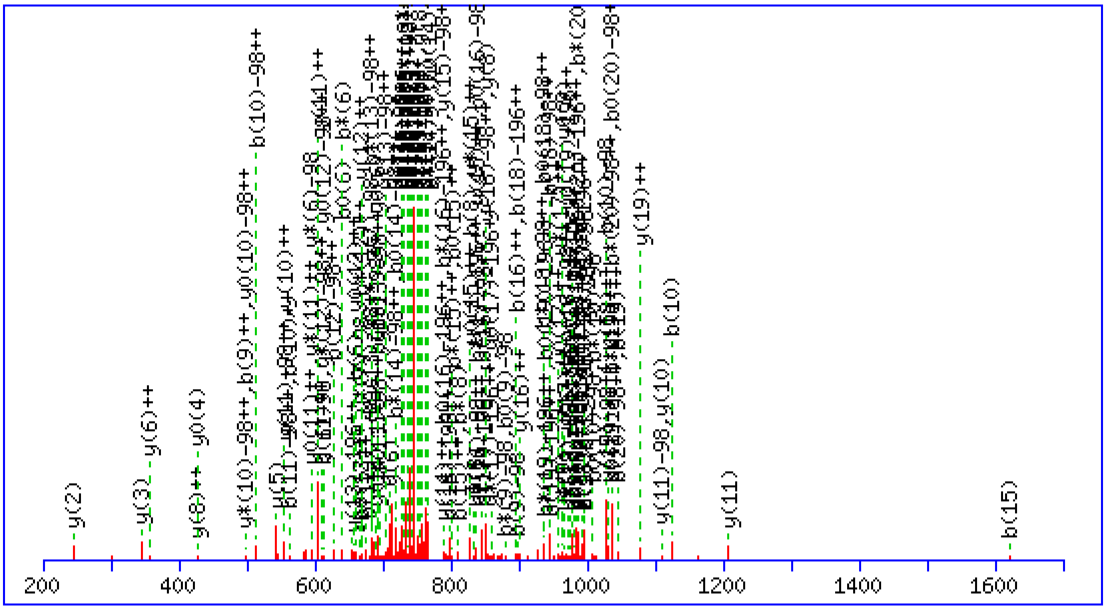
Monoisotopic mass of neutral peptide Mr(calc): 2249.9940
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 83 **Expect:** 3.8e-008
Matched b ions: b(5), b(8), b(9), b(10), b(10)-98++, b(10)-98, b(10)++, b(11)-98++, b(12), b(12)-98++, b(13)-98++, b(14)-98++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)++, b(17)-98++, b(18)-98++, b(18)++, b(19)-98++, b(19)++, b(20)-98++
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(9), y(11)++, y(11), y(13)++, y(14)-98++, y(15)++, y(19)++

Peptide No.996

SSPKEEVASEPEEAASPTTPK
Confirmed sites: @S:9,@S:16
Ambiguous sites:

MS/MS Fragmentation of **SSPKEEVASEPEEAASPTTPK**
Found in **NOP56_MOUSE** in **SwissProt**, Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2

Match to Query 5062: 2329.957218 from(777.659682,3+) index(3981)
Title: Elution from: 24.707 to 24.707 scan no 1852 cid35.00 polarity:+:m1s



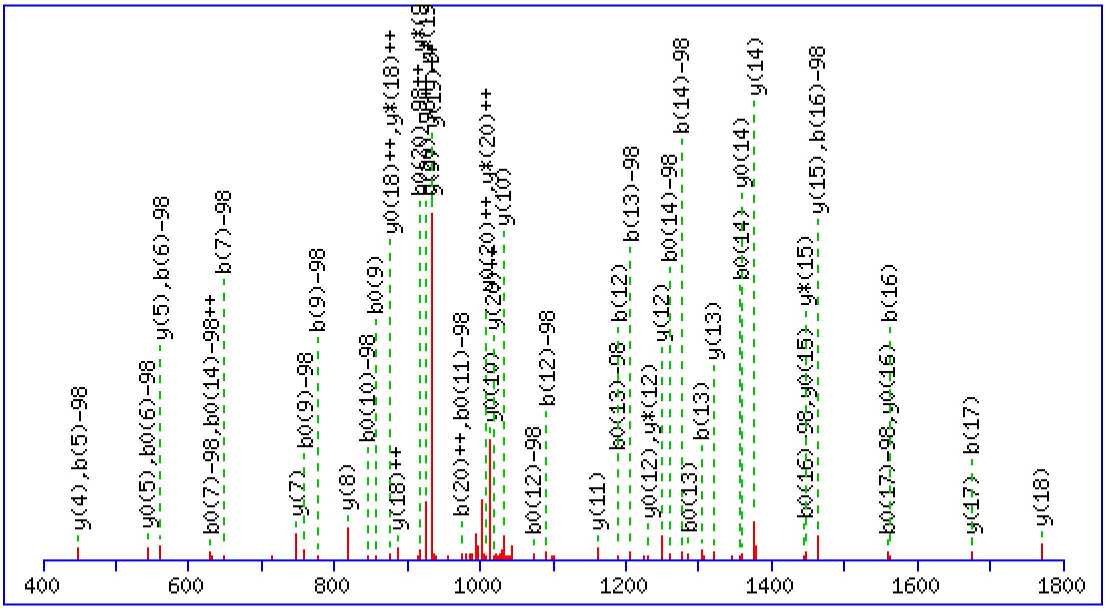
Monoisotopic mass of neutral peptide Mr(calc): 2329.9603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0016
Matched b ions: b(6), b(7), b(8), b(9)++, b(9), b(9)-98, b(10)-98, b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15), b(15)-98++, b(15)++, b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)-196++
Matched y ions: y(2), y(3), y(5), y(6)++, y(6), y(6)-98, y(7)-98, y(8), y(8)++, y(8)-98, y(9), y(10)++, y(10), y(11)++, y(11), y(11)-98++, y(11)-98, y(12)++, y(13)++, y(13)-196++, y(13)-98++, y(14)-98++, y(14)-196++, y(14)++, y(15)-196++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(19)-196++

Peptide No.997

SSPPPLSGASEVDAGELGSER
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **SSPPPLSGASEVDAGELGSER**
Found in **D19L1_MOUSE** in **SwissProt**, Protein dpy-19 homolog 1 OS=Mus musculus GN=Dpy19l1 PE=2 SV=1

Match to Query 4491: 2120.923538 from(1061.469045,2+) index(5377)
Title: Elution from: 40.316 to 40.316 scan no 3859 cid35.00 polarity:+:m1s



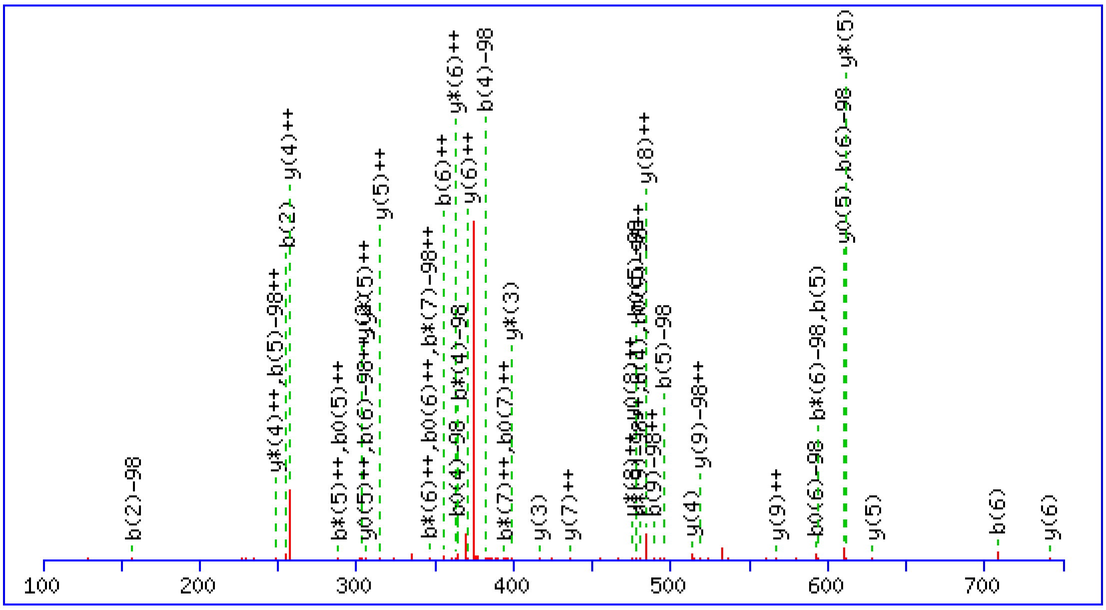
Monoisotopic mass of neutral peptide Mr(calc): 2120.9263
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 91 **Expect:** 4.3e-009
Matched b ions: b(5)-98, b(6)-98, b(7)-98, b(9)-98, b(12)-98, b(12), b(13)-98, b(13), b(14)-98, b(16)-98, b(16), b(17), b(20)-98++, b(20)++
Matched y ions: y(4), y(5), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(15), y(17), y(18), y(18)++, y(19)++, y(20)++

Peptide No.998

SSPQLDPLRK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **SSPQLDPLRK**
Found in **LS14A_MOUSE** in **SwissProt**, Protein LSM14 homolog A OS=Mus musculus GN=Lsm14a PE=1 SV=1

Match to Query 1730: 1219.596963 from(407.539597,3+) index(1241)
Title: Elution from: 26.905 to 26.905 scan no 2213 cid35.00 polarity:+



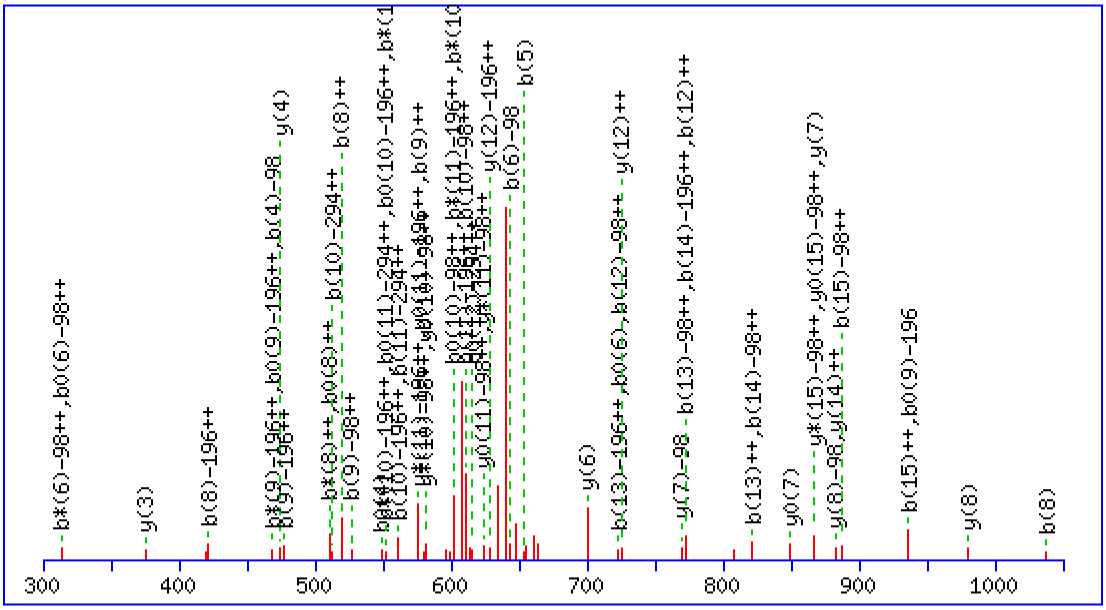
Monoisotopic mass of neutral peptide Mr(calc): 1219.5962
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0051
Matched b ions: b(2)-98, b(2), b(4), b(4)-98, b(5)-98++, b(5), b(5)-98, b(6)-98, b(6), b(6)-98++, b(6)++, b(9)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6), y(6)++, y(7)++, y(8)++, y(9)++, y(9)-98++

Peptide No.999

SSRRSSSELSPEVVEK
Confirmed sites: @S:7,@S:10
Ambiguous sites: @S:1orS:2

MS/MS Fragmentation of **SSRRSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5057: 2015.801010 from(672.940946,3+) index(4855)
Title: Elution from: 26.517 to 26.517 scan no 2160 cid35.00 polarity:+:m1s



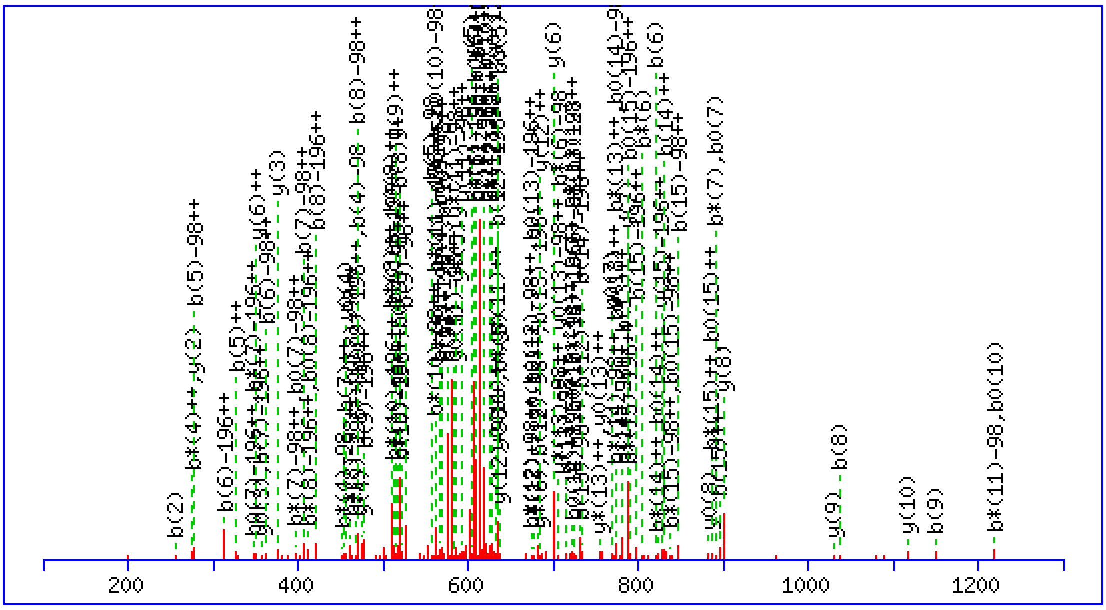
Monoisotopic mass of neutral peptide Mr(calc): 2015.8003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.016
Matched b ions: b(3)-98, b(4)-98, b(5), b(6)-98, b(8), b(8)-196++, b(8)++, b(9)-196++, b(9)++, b(9)-98++, b(10)-98++, b(10)-294++, b(10)-196++, b(11)-196++, b(11)-294++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)-196++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(6), y(7), y(7)-98, y(8), y(8)-98, y(12)++, y(12)-196++, y(14)++

Peptide No.1000

SSRRSSSELSPEVVEK
Confirmed sites: @S:2,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SSRRSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4619: 1935.831729 from(646.284519,3+) index(953)
Title: Elution from: 24.616 to 24.616 scan no 1865 cid35.00 polarity:+



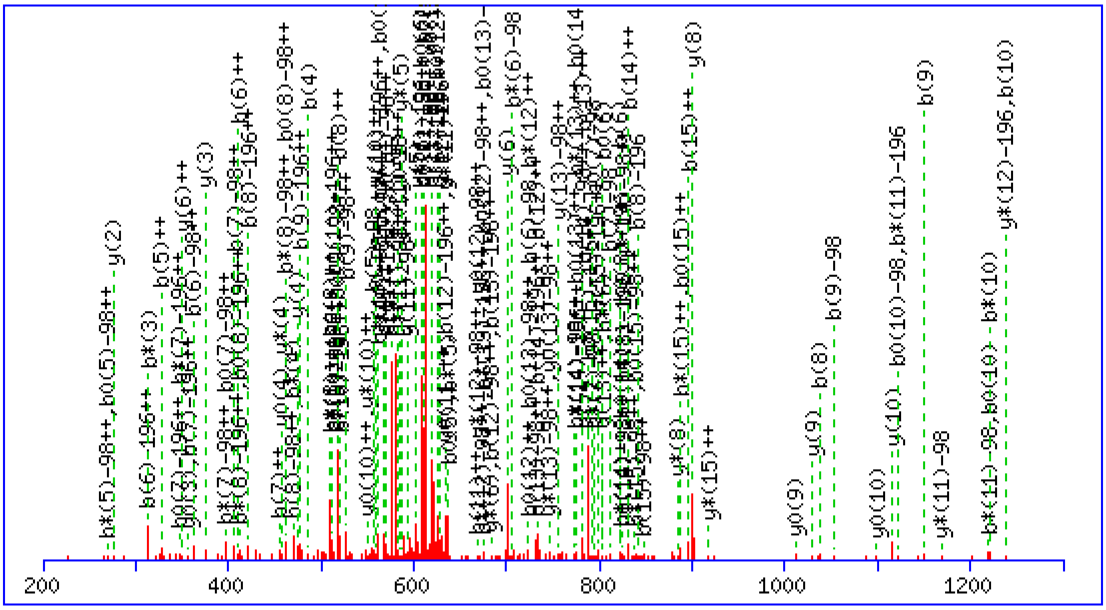
Monoisotopic mass of neutral peptide Mr(calc): 1935.8340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 44 **Expect:** 0.00025
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98++, b(5)++, b(5)-98, b(6)-196++, b(6)-98++, b(6)-98, b(6), b(7)-98++, b(7)-196++, b(7)++, b(8)-98++, b(8)++, b(8), b(8)-196++, b(9), b(9)-196++, b(9)++, b(9)-98++, b(10)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)-196++, b(12)++, b(12)-196++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)-98++, b(14)++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(9)++, y(10), y(11)-98++, y(12)-98++, y(12)++, y(13)-98++, y(15)-196++

Peptide No.1001

SSRRSSSELSPEVVEK
Confirmed sites: @S:5,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SSRRSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4262: 1935.834456 from(646.285428,3+) index(740)
Title: Elution from: 32.604 to 32.604 scan no 2111 cid35.00 polarity:+



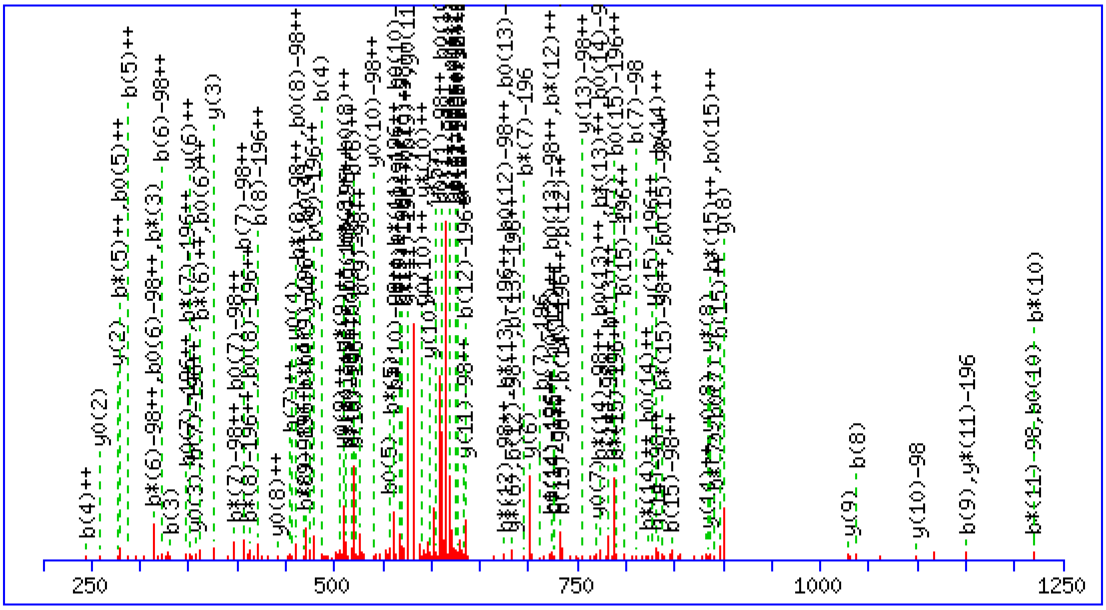
Monoisotopic mass of neutral peptide Mr(calc): 1935.8340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00032
Matched b ions: b(4), b(5)++, b(5)-98, b(6)-196++, b(6)-98++, b(6)++, b(6)-196, b(6)-98, b(6), b(7)-98++, b(7)-196++, b(7)++, b(7)-98, b(8)++, b(8), b(8)-196++, b(8)-98++, b(8)-196, b(9)-98++, b(9)++, b(9), b(9)-196++, b(9)-98, b(10), b(10)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)-196++, b(11)++, b(12)-196++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(13)-196++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(15)-196++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10), y(10)++, y(11)-98++, y(12)-196++, y(13)-98++, y(13)++

Peptide No.1002

SSRRSSSELSPEVVEK
Confirmed sites: @S:6,@S:7
Ambiguous sites:

MS/MS Fragmentation of **SSRRSSSELSPEVVEK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4765: 1935.832293 from(646.284707,3+) index(4648)
Title: Elution from: 24.569 to 24.569 scan no 1894 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1935.8340

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 30 **Expect:** 0.0064

Matched b ions: b(3), b(4)++, b(4), b(5)++, b(6)-98++, b(7)-98++, b(7)-196++, b(7)++, b(7)-196, b(7)-98, b(8)++, b(8), b(8)-196++, b(8)-98++, b(9), b(9)-98++, b(9)++, b(9)-196++, b(10)++, b(10)-196++, b(10)-98++, b(11)-98++, b(11)-196++, b(12)++, b(12)-98++, b(12)-196++, b(13)-98++, b(13)++, b(13)-196++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(15)-196++

Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(9), y(10)-98, y(10)++, y(11)-98++, y(12)-196++, y(12)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-196++

Peptide No.1003

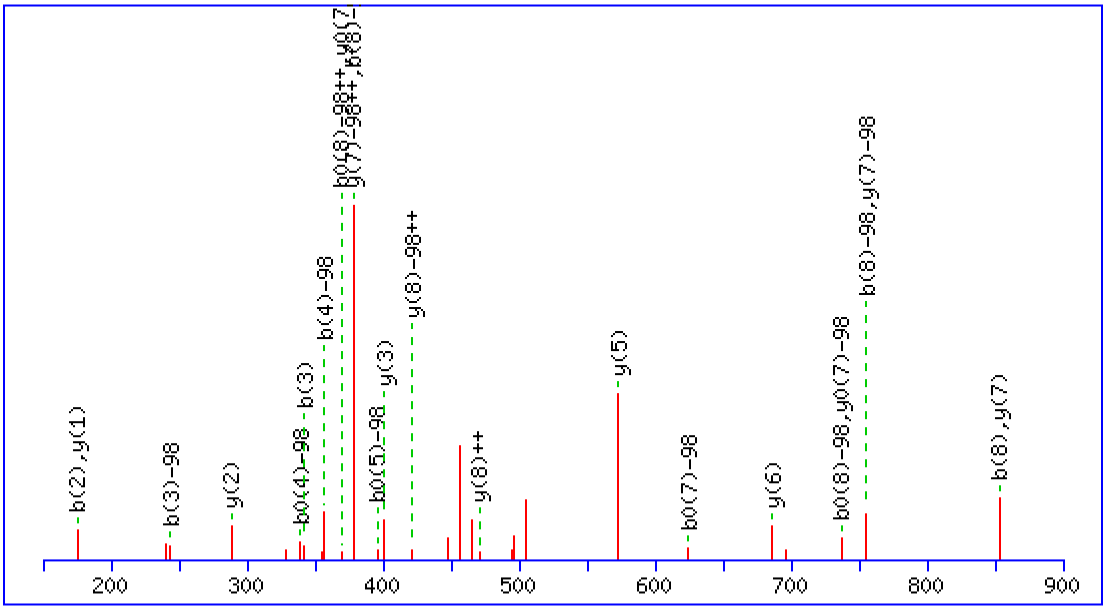
SSSLGDLLR

Confirmed sites: @S:3

Ambiguous sites:

MS/MS Fragmentation of **SSSLGDLLR**
Found in **PKHO2_MOUSE** in **SwissProt**, Pleckstrin homology domain-containing family O member 2 OS=Mus musculus GN=Plekho2 PE=1 SV=1

Match to Query 815: 1026.474204 from(514.244378,2+) index(2406)
Title: Elution from: 44.499 to 44.499 scan no 4349 cid35.00 polarity:+



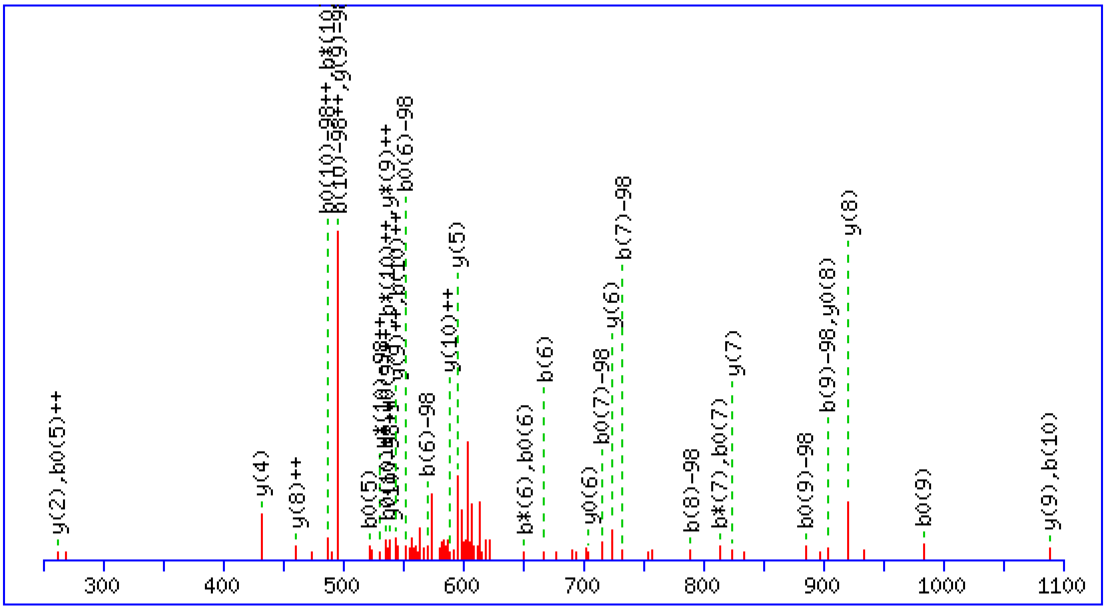
Monoisotopic mass of neutral peptide Mr(calc): 1026.4747
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 **Expect:** 2.2e-005
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(8)-98++, b(8)-98, b(8)
Matched y ions: y(1), y(2), y(3), y(5), y(6), y(7)-98++, y(7)-98, y(7), y(8)-98++, y(8)++

Peptide No.1004

SSSPTQYGLSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SSSPTQYGLSR**
Found in **MLTK_MOUSE** in **SwissProt**, Mitogen-activated protein kinase kinase kinase MLT OS=Mus musculus GN=Mltk PE=1 SV=1

Match to Query 1635: 1261.533668 from(631.774110,2+) index(962)
Title: Elution from: 25.348 to 25.348 scan no 1940 cid35.00 polarity:+



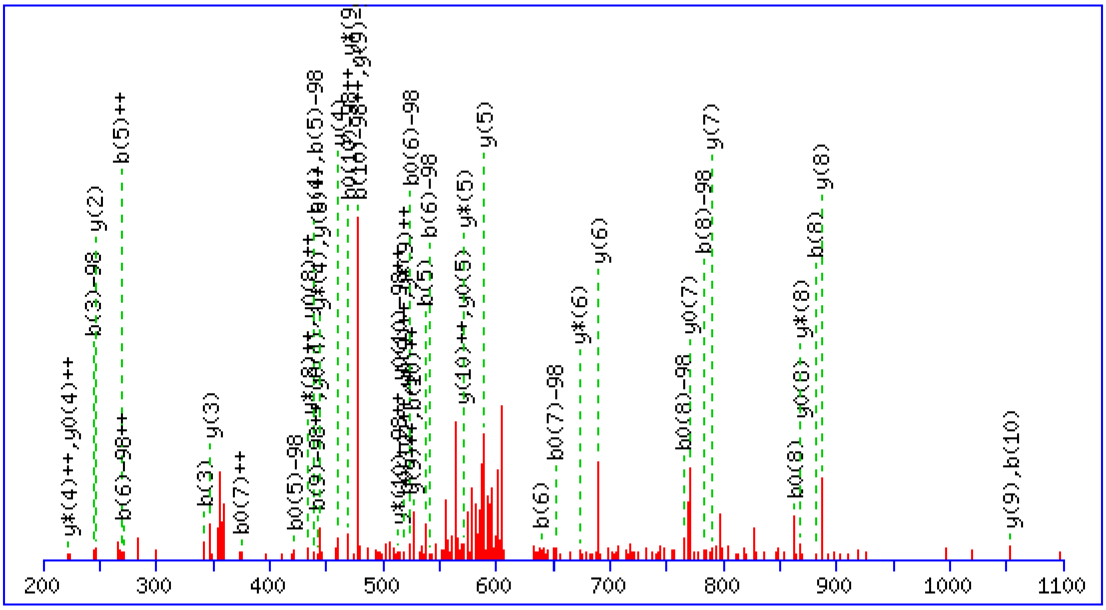
Monoisotopic mass of neutral peptide Mr(calc): 1261.5340
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 **Expect:** 0.00015
Matched b ions: b(6), b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(10)-98++, b(10), b(10)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9), y(9)++, y(10)-98++, y(10)++

Peptide No.1005

SSSPVTELTAR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SSSPVTELTAR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 2347: 1226.554390 from(614.284471,2+) index(1453)
Title: Elution from: 38.519 to 38.519 scan no 2953 cid35.00 polarity:+



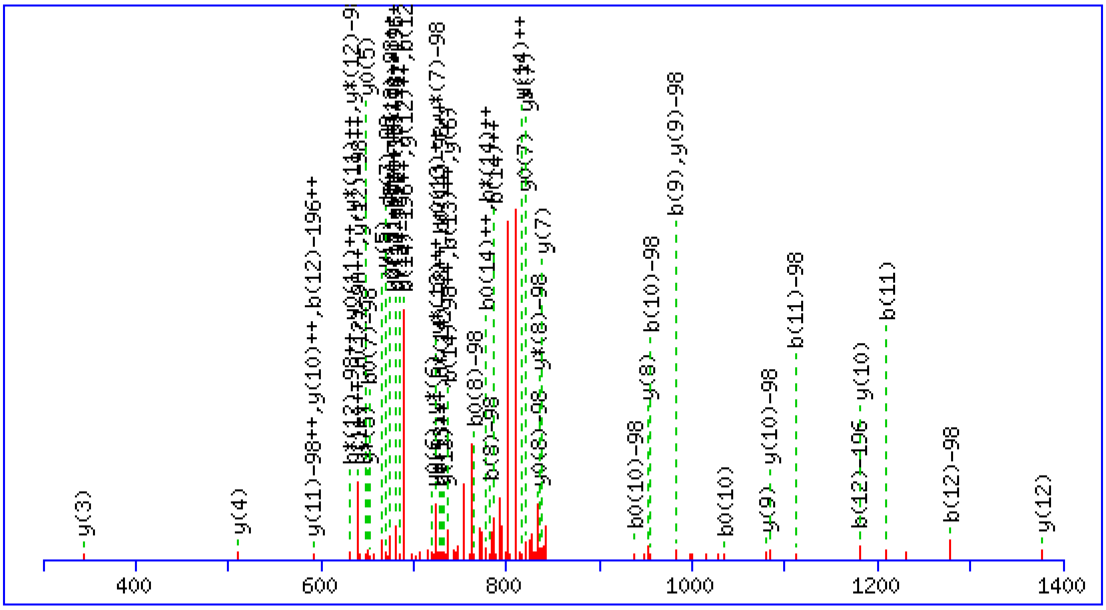
Monoisotopic mass of neutral peptide Mr(calc): 1226.5544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0094
Matched b ions: b(3)-98, b(3), b(4), b(5)++, b(5)-98, b(5), b(6)-98++, b(6)-98, b(6), b(8)-98, b(8), b(9)-98++, b(10)-98++, b(10), b(10)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)-98++, y(9), y(9)++, y(10)++

Peptide No.1006

SSSPVTELTARSPVK
Confirmed sites: @S:2,@S:12
Ambiguous sites:

MS/MS Fragmentation of **SSSPVTELTARSPVK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3696: 1717.767682 from(859.891117,2+) index(1706)
Title: Elution from: 32.071 to 32.071 scan no 2879 cid35.00 polarity:+



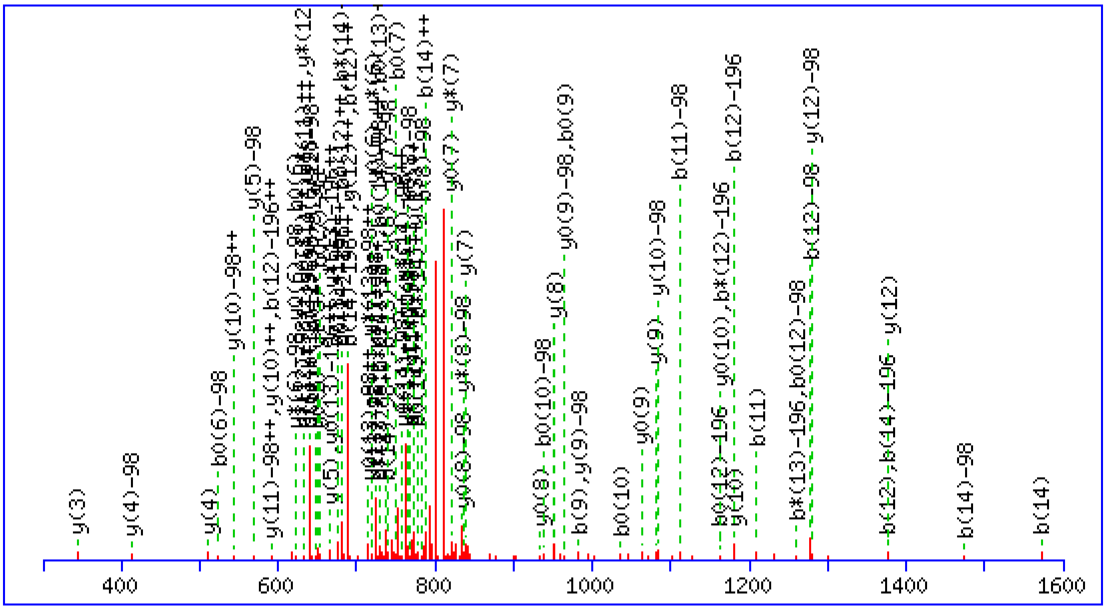
Monoisotopic mass of neutral peptide Mr(calc): 1717.7689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0014
Matched b ions: b(7)-98, b(8)-98, b(9), b(10)-98, b(11), b(11)-98, b(12)-98++, b(12)++, b(12)-98, b(12)-196++, b(12)-196, b(13)++, b(14)-196++, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(12), y(13)++, y(13)-98++, y(14)++

Peptide No.1007

SSSPVTELTARSPVK
Confirmed sites: @S:3,@S:12
Ambiguous sites:

MS/MS Fragmentation of **SSSPVTELTARSPVK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3858: 1717.767510 from(859.891031,2+) index(1751)
Title: Elution from: 32.051 to 32.051 scan no 2910 cid35.00 polarity:+



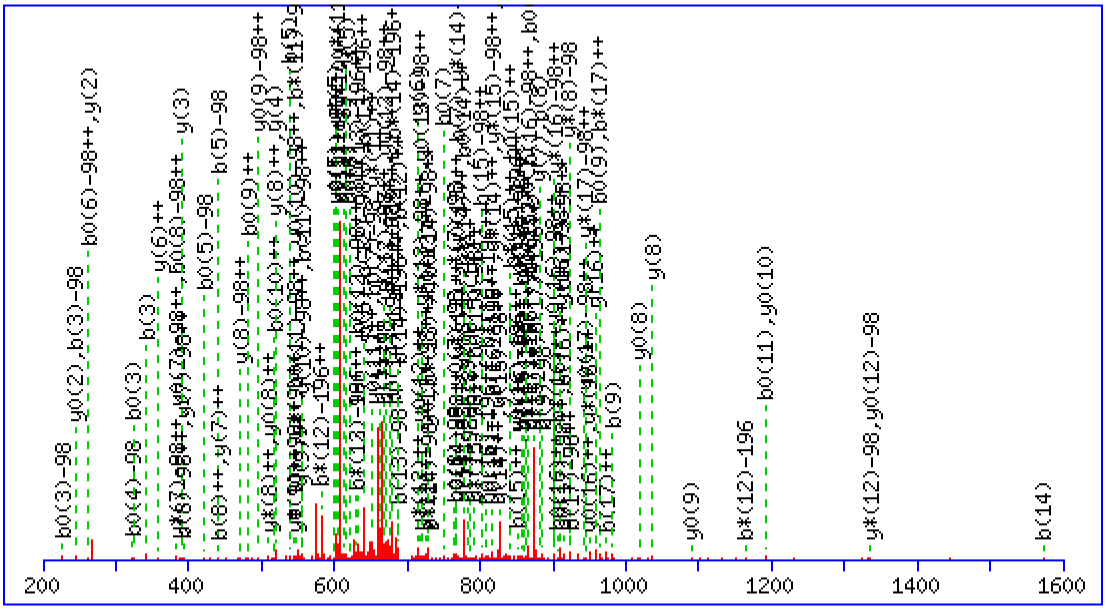
Monoisotopic mass of neutral peptide Mr(calc): 1717.7689
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.003
Matched b ions: b(6), b(7), b(8)-98, b(9), b(11), b(11)-98, b(12)-98++, b(12)++, b(12)-98, b(12), b(12)-196, b(12)-196++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98, b(14), b(14)-196, b(14)-98++, b(14)++
Matched y ions: y(3), y(4), y(4)-98, y(5)-98, y(5), y(6)-98, y(6), y(7)-98, y(7), y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(12), y(12)-98, y(13)-98++, y(13)-196++, y(13)++, y(14)-98++

Peptide No.1008

SSSPVTELTARSPVKQDK
Confirmed sites: @S:3,@S:12
Ambiguous sites:

MS/MS Fragmentation of **SSSPVTELTARSPVKQDK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5343: 2088.948897 from(697.323575,3+) index(4605)
Title: Elution from: 35.608 to 35.608 scan no 2594 cid35.00 polarity:+:m1s



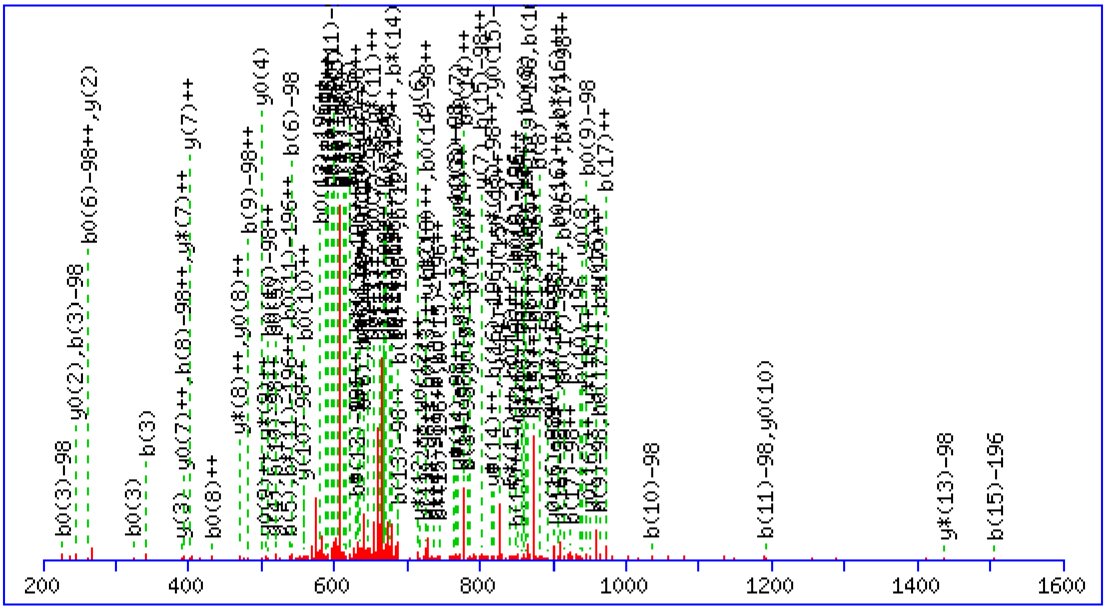
Monoisotopic mass of neutral peptide Mr(calc): 2088.9494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00014
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(6), b(7), b(7)-98, b(8)++, b(8)-98++, b(8)-98, b(8), b(9), b(9)-98, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)-196++, b(13)-98++, b(14), b(14)-196++, b(14)++, b(15)-98++, b(15)++, b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7)-98++, y(7)-98, y(7), y(8)++, y(8), y(8)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++

Peptide No.1009

SSSPVTELTARSPVKQDK
Confirmed sites: @S:3,@T:9
Ambiguous sites:

MS/MS Fragmentation of **SSSPVTELTARSPVKQDK**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4636: 2088.949809 from(697.323879,3+) index(1006)
Title: Elution from: 35.538 to 35.538 scan no 2467 cid35.00 polarity:+



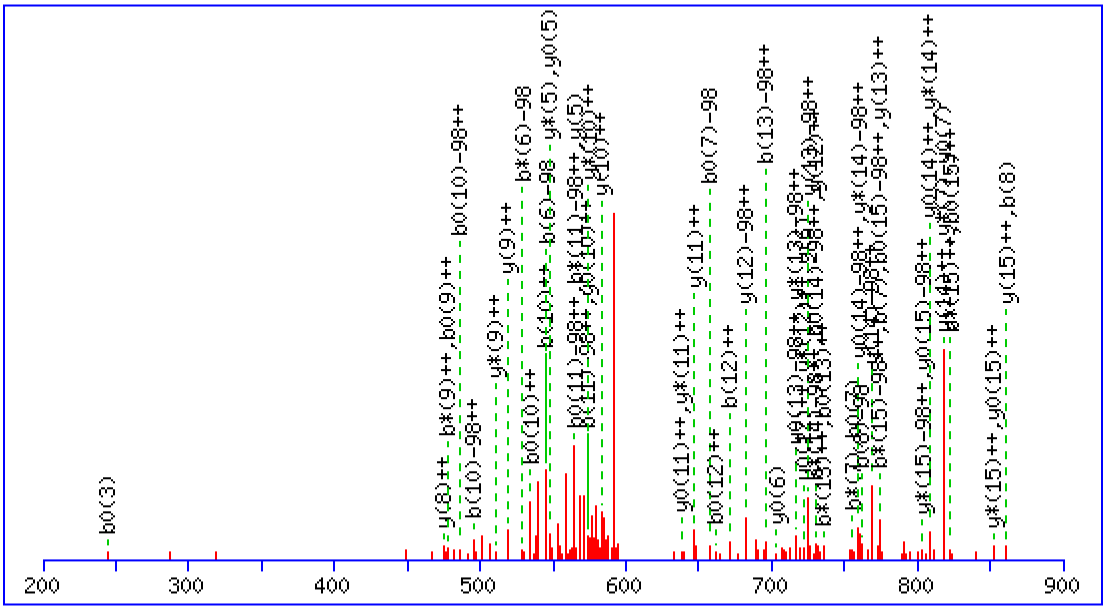
Monoisotopic mass of neutral peptide Mr(calc): 2088.9494
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.032
Matched b ions: b(3), b(3)-98, b(5), b(6), b(6)-98, b(7), b(7)-98, b(8)-98++, b(8)-98, b(8), b(9)-196, b(9)-98, b(9)-98++, b(10)-98++, b(10)-98, b(10)-196, b(11)-98, b(11)-98++, b(11)++, b(12)-98++, b(12)-196++, b(12)++, b(13)-196++, b(13)-98++, b(13)++, b(14)-196++, b(14)-98++, b(14)++, b(15)-196, b(15)-98++, b(15)++, b(16)-98++, b(16)-196++, b(16)++, b(17)-196++, b(17)++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7), y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(16)-196++

Peptide No.1010

SSSSSQESLNRPFSSK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **SSSSSQESLNRPFSSK**
Found in **CLAP2_MOUSE** in **SwissProt**, CLIP-associating protein 2 OS=Mus musculus GN=Clasp2 PE=1 SV=1

Match to Query 3623: 1806.777099 from(603.266309,3+) index(3651)
Title: Elution from: 24.148 to 24.148 scan no 1678 cid35.00 polarity:+:m1s



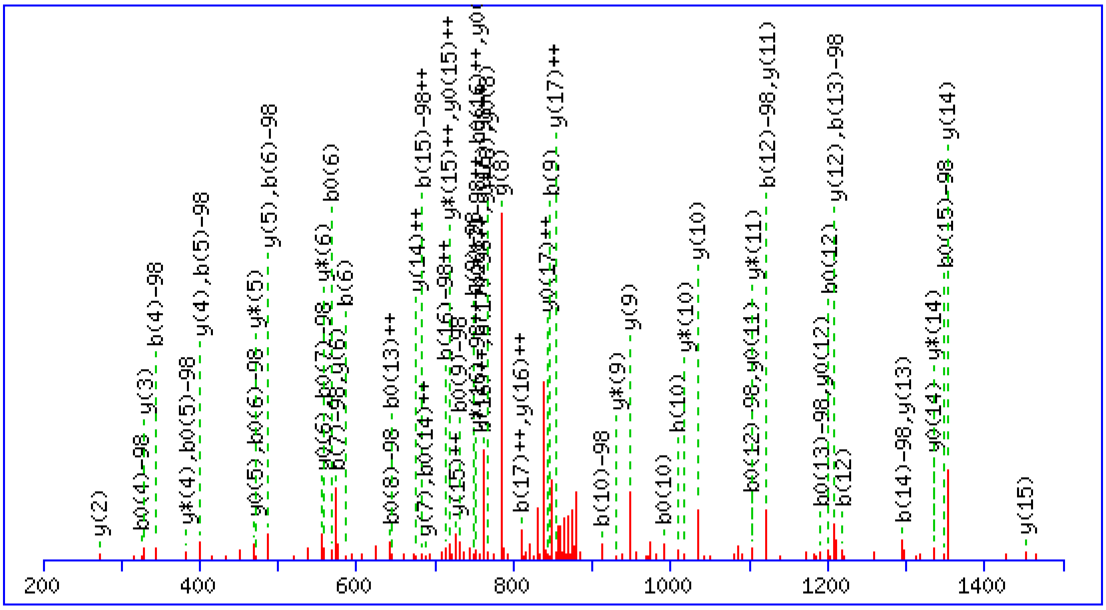
Monoisotopic mass of neutral peptide Mr(calc): 1806.7785
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.053
Matched b ions: b(6)-98, b(7), b(8), b(8)-98, b(10)-98++, b(10)++, b(11)-98++, b(12)++, b(13)-98++
Matched y ions: y(5), y(6), y(8)++, y(9)++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++

Peptide No.1011

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SSSVGSSSSYPISSAGPR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4174: 1791.765602 from(896.890077,2+) index(5232)
Title: Elution from: 30.211 to 30.211 scan no 2665 cid35.00 polarity:+:m1s



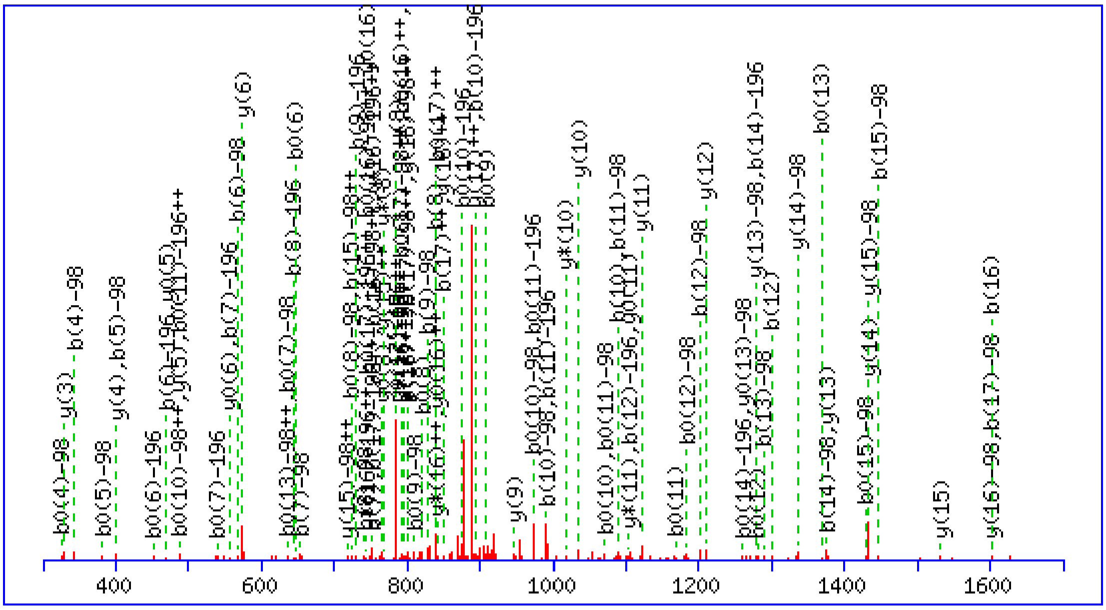
Monoisotopic mass of neutral peptide Mr(calc): 1791.7676
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 **Expect:** 2.1e-009
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(9)-98, b(9), b(10), b(10)-98, b(12)-98, b(12), b(13)-98, b(14)-98, b(15)-98++, b(16)++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13), y(14), y(14)++, y(15), y(15)++, y(16)-98++, y(16)++, y(17)++

Peptide No.1012

SSSVGSSSSYPISSAGPR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of **SSSVGSSSSYPISSAGPR**
Found in **PLEC_MOUSE** in **SwissProt**, Plectin OS=Mus musculus GN=Plec PE=1 SV=2

Match to Query 4707: 1871.736206 from(936.875379,2+) index(5075)
Title: Elution from: 41.390 to 41.390 scan no 3286 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1871.7339

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 74 **Expect:** 1.5e-007

Matched b ions: b(4)-98, b(5)-98, b(6)-196, b(6)-98, b(7)-98, b(7), b(7)-196, b(8), b(8)-196, b(8)-98, b(9)-196, b(9)-98, b(10)-98, b(10), b(10)-196, b(11)-196, b(11)-98, b(12)-98, b(12), b(12)-196, b(13)-98, b(14)-196, b(14)-98, b(15)-98, b(15)-98++, b(16), b(16)-98++, b(16)++, b(17)-196++, b(17)-98++, b(17)-98, b(17)++

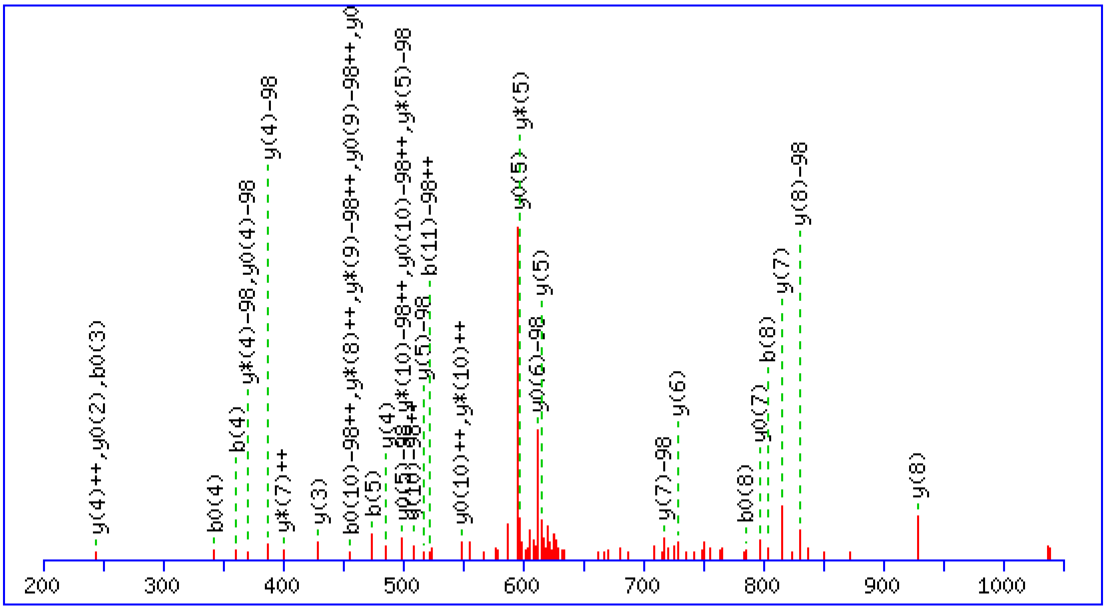
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14), y(14)-98, y(15), y(15)-98, y(15)-98++, y(15)++, y(16)-196++, y(16)-98++, y(16)-98, y(16)++, y(17)-196++, y(17)++

Peptide No.1013

SSSVLSLEGSDK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **SSSVLSLEGSDK**
Found in **PKHG3_MOUSE** in **SwissProt**, Pleckstrin homology domain-containing family G member 3 OS=Mus musculus GN=Plekhg3 PE=1 SV=2

Match to Query 1775: 1287.559644 from(644.787098,2+) index(1745)
Title: Elution from: 33.751 to 33.751 scan no 3047 cid35.00 polarity:+



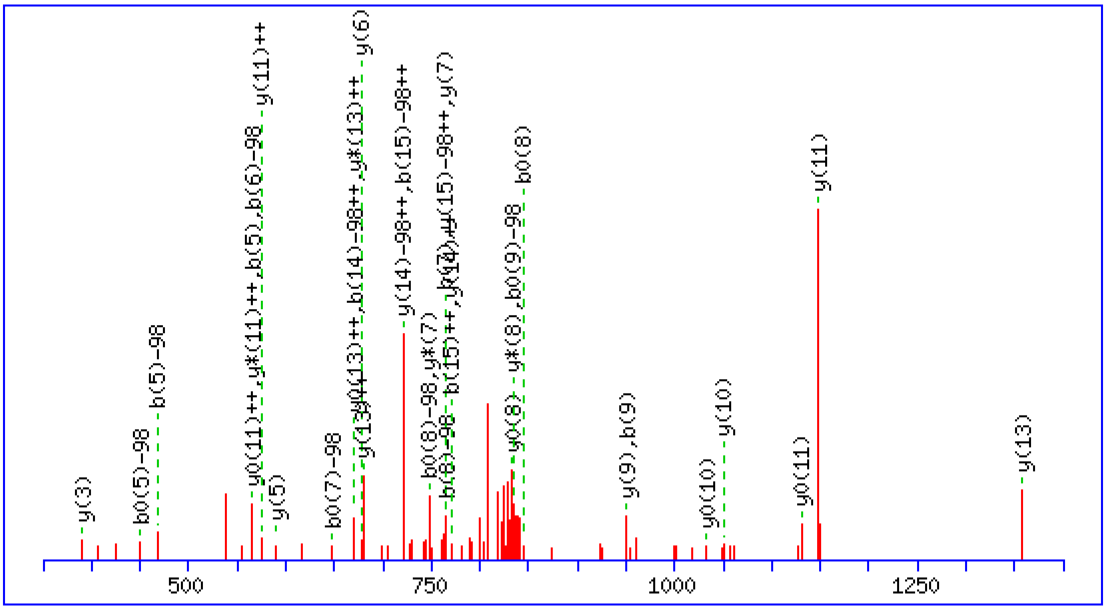
Monoisotopic mass of neutral peptide Mr(calc): 1287.5595
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.026
Matched b ions: b(4), b(5), b(8), b(11)-98++
Matched y ions: y(3), y(4)++, y(4)-98, y(4), y(5), y(5)-98, y(6), y(7)-98, y(7), y(8), y(8)-98, y(10)-98++

Peptide No.1014

SSTPLPTVSSSAENTR
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **SSTPLPTVSSSAENTR**
Found in **LAP2B_MOUSE** in **SwissProt**, Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=4

Match to Query 3225: 1712.759716 from(857.387134,2+) index(1200)
Title: Elution from: 27.582 to 27.582 scan no 2243 cid35.00 polarity:+



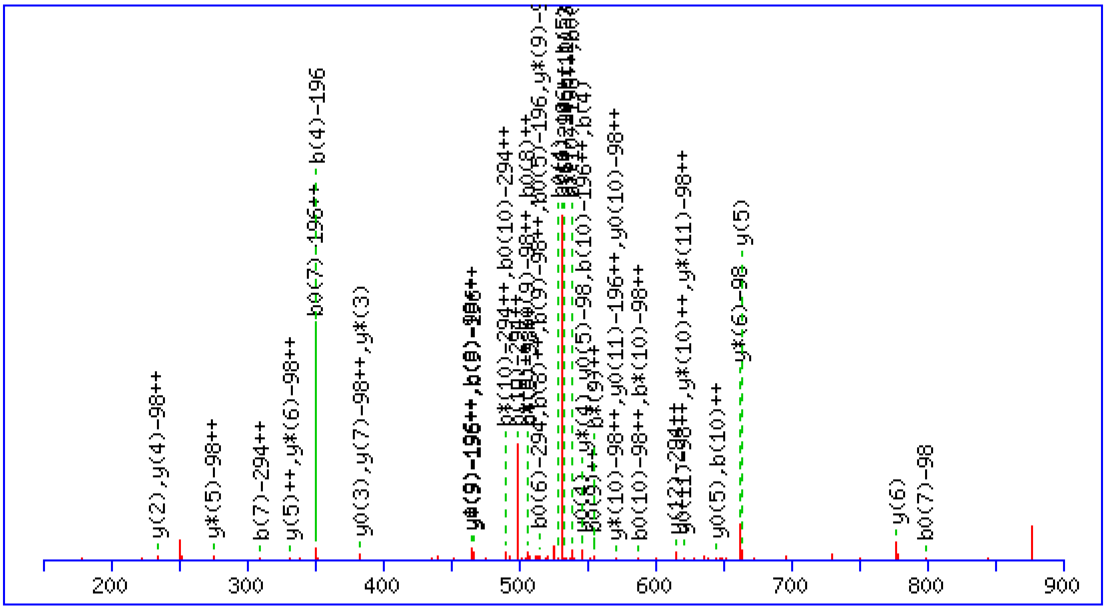
Monoisotopic mass of neutral peptide Mr(calc): 1712.7618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 **Expect:** 9.7e-005
Matched b ions: b(5)-98, b(5), b(6)-98, b(7), b(8)-98, b(9), b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(3), y(5), y(6), y(7), y(9), y(10), y(11), y(11)++, y(13)++, y(13), y(14)-98++, y(14)++, y(15)-98++

Peptide No.1015

SSVLTVSNVYSSK
Confirmed sites: @S:1,@S:2,@T:5,@S:11
Ambiguous sites:

MS/MS Fragmentation of **SSVLTVSNVYSSK**
Found in **ZN638_MOUSE** in **SwissProt**, Zinc finger protein 638 OS=Mus musculus GN=Znf638 PE=1 SV=2

Match to Query 3142: 1689.572934 from(564.198254,3+) index(1331)
Title: Elution from: 28.747 to 28.747 scan no 2401 cid35.00 polarity:+



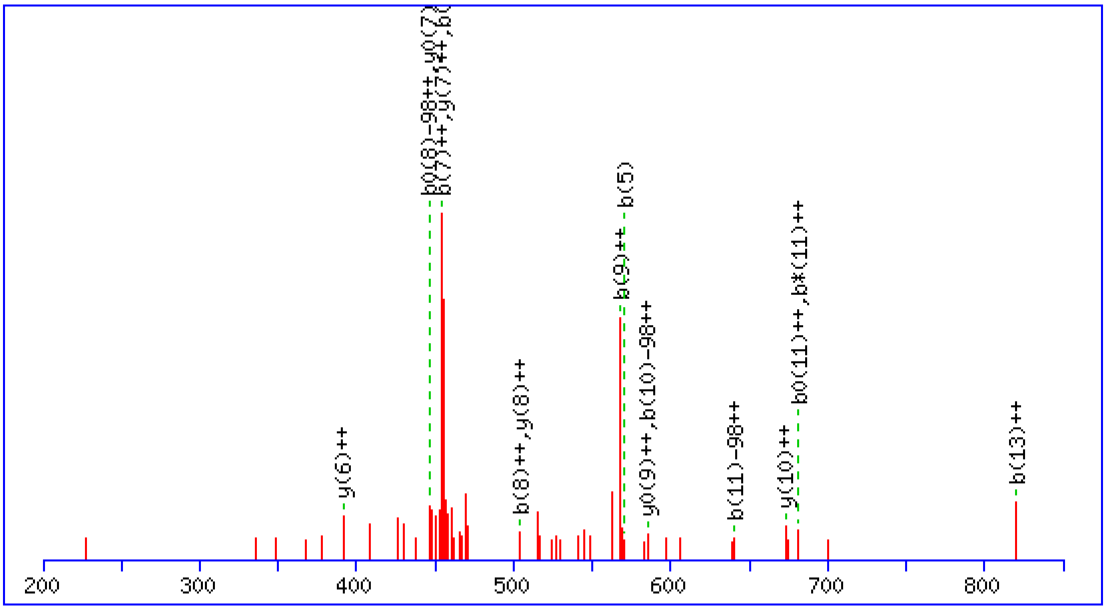
Monoisotopic mass of neutral peptide Mr(calc): 1689.5742
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 16 **Expect:** 0.033
Matched b ions: b(4)-196, b(4), b(5)-196, b(6)-294, b(7)-294++, b(8)-98++, b(8)++, b(9)-196++, b(9)-98++, b(10)-294++, b(10)-196++, b(10)++, b(11)-392++
Matched y ions: y(2), y(4)-98++, y(4)-98, y(5)++, y(5), y(6), y(7)-98++, y(10)-196++, y(12)-294++

Peptide No.1016

STPERRTVQMIMETR
Confirmed sites: @T:7
Ambiguous sites:

MS/MS Fragmentation of **STPERRTVQMIMETR**
Found in **PLCG2_MOUSE** in **SwissProt**, 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-2 OS=Mus musculus GN=Plcg2 PE=1 SV=1

Match to Query 3906: 1913.889108 from(479.479553,4+) index(396)
Title: Elution from: 20.468 to 20.468 scan no 1281 cid35.00 polarity:+



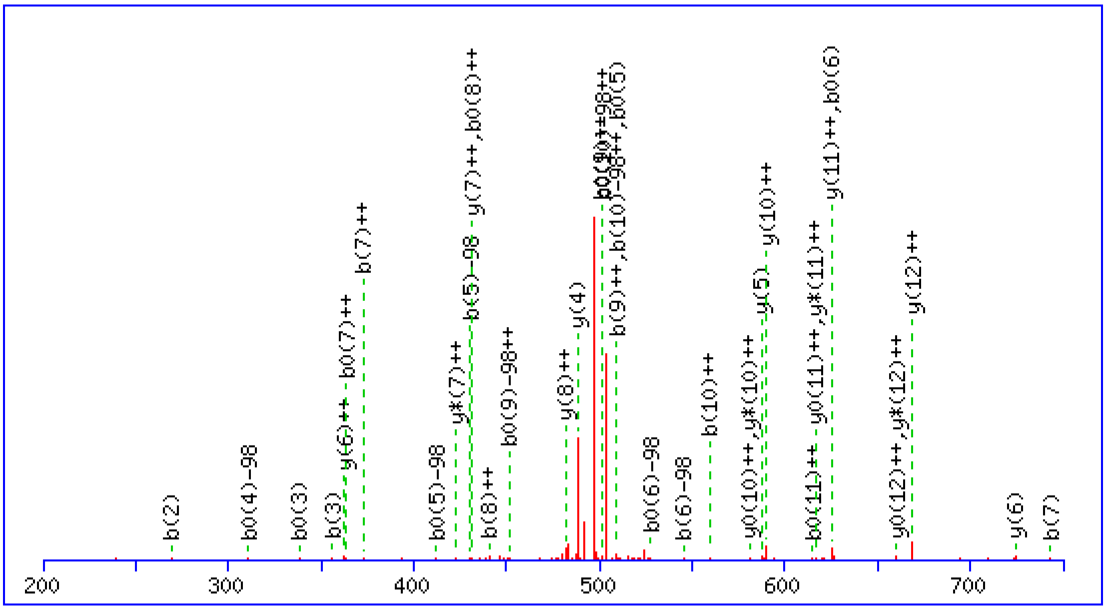
Monoisotopic mass of neutral peptide Mr(calc): 1913.8852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.03
Matched b ions: b(5), b(7)++, b(8)-98++, b(8)++, b(9)++, b(10)-98++, b(11)-98++, b(13)++
Matched y ions: y(6)++, y(7)++, y(8)++, y(10)++

Peptide No.1017

STSATDTHHVELAR
Confirmed sites:
Ambiguous sites: @S:1orT:2

MS/MS Fragmentation of **STSATDTHHVELAR**
Found in **BCKD_MOUSE** in **SwissProt**, [3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial OS=Mus musculus GN=Bckdk PE=1 SV=1

Match to Query 3242: 1603.698933 from(535.573587,3+) index(389)
Title: Elution from: 19.916 to 19.916 scan no 1228 cid35.00 polarity:+



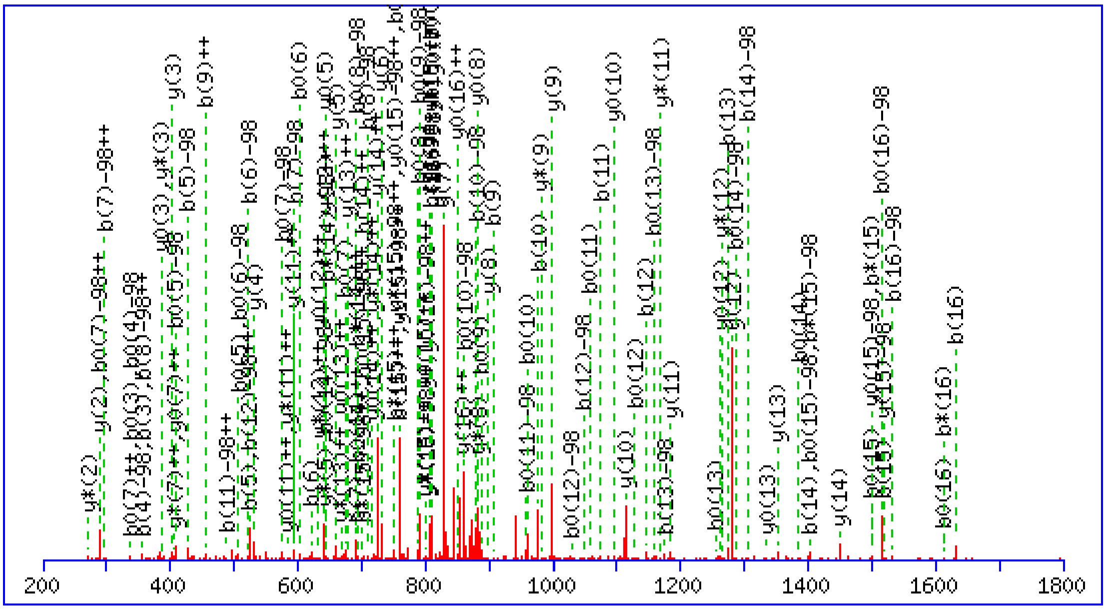
Monoisotopic mass of neutral peptide Mr(calc): 1603.6992
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0051
Matched b ions: b(2), b(3), b(5)-98, b(6)-98, b(7), b(7)++, b(8)++, b(9)++, b(10)++, b(10)-98++
Matched y ions: y(4), y(5), y(6)++, y(6), y(7)++, y(8)++, y(10)++, y(11)++, y(12)++

Peptide No.1018

STSPAPADVAPAQEDLR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **STSPAPADVAPAQEDLR**
Found in **G3BP1_MOUSE** in **SwissProt**, Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1

Match to Query 4537: 1803.803722 from(902.909137,2+) index(1487)
Title: Elution from: 38.931 to 38.931 scan no 3003 cid35.00 polarity:+



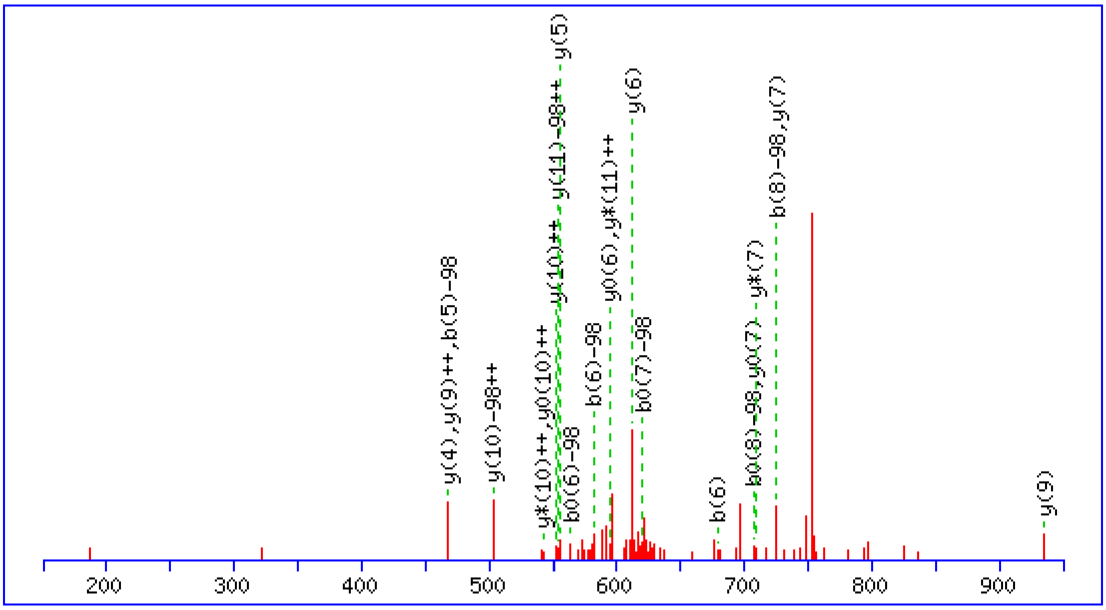
Monoisotopic mass of neutral peptide Mr(calc): 1803.8040
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 85 **Expect:** 1.8e-008
Matched b ions: b(3), b(4)-98, b(5), b(5)-98, b(6), b(6)-98, b(7)-98, b(7)-98++, b(7), b(8)-98++, b(8), b(8)-98, b(9)++, b(9)-98, b(9), b(10), b(10)-98, b(11)-98++, b(11), b(12)-98++, b(12), b(12)-98, b(13)-98, b(13), b(14), b(14)-98, b(14)++, b(15)++, b(15), b(16), b(16)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(11)++, y(12)++, y(12), y(13), y(13)++, y(14), y(14)++, y(15)-98++, y(15)++, y(15)-98, y(16)-98++, y(16)++

Peptide No.1019

STSPIIGSPPVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **STSPIIGSPPVR**
Found in **PATL1_MOUSE** in **SwissProt**, Protein PAT1 homolog 1 OS=Mus musculus GN=Patl1 PE=1 SV=2

Match to Query 1919: 1289.636846 from(645.825699,2+) index(1695)
Title: Elution from: 31.966 to 31.966 scan no 2865 cid35.00 polarity:+



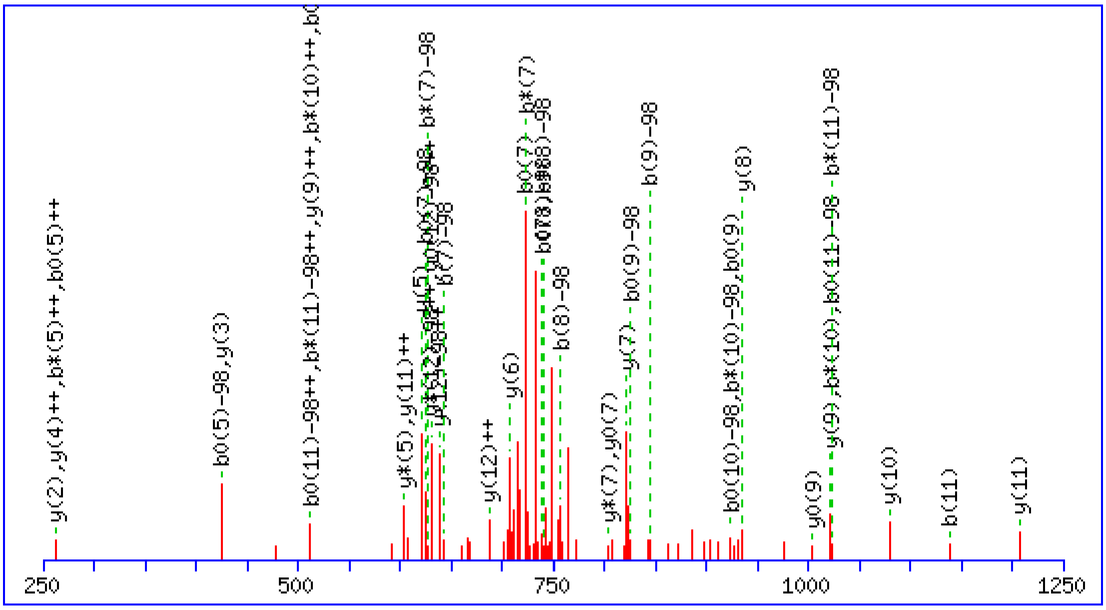
Monoisotopic mass of neutral peptide Mr(calc): 1289.6381
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.018
Matched b ions: b(5)-98, b(6)-98, b(6), b(8)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9)++, y(9), y(10)-98++, y(10)++, y(11)-98++

Peptide No.1020

STSQGSINSPVYSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **STSQGSINSPVYSR**
Found in **ABLM1_MOUSE** in **SwissProt**, Actin-binding LIM protein 1 OS=Mus musculus GN=Ablim1 PE=1 SV=1

Match to Query 3264: 1561.674864 from(781.844708,2+) index(4925)
Title: Elution from: 27.166 to 27.166 scan no 2249 cid35.00 polarity:+:m1s



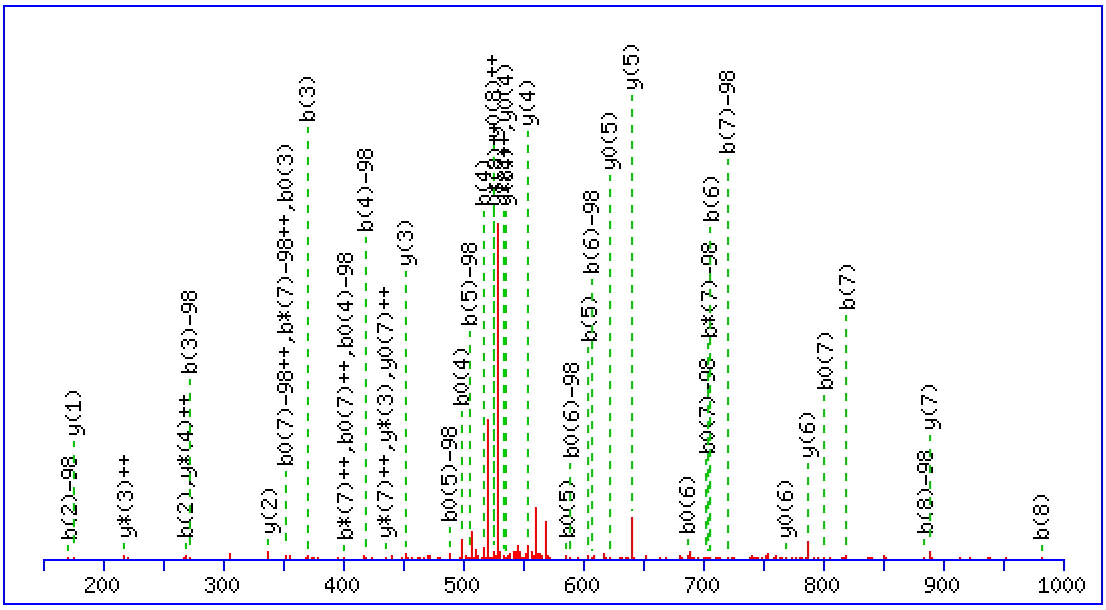
Monoisotopic mass of neutral peptide Mr(calc): 1561.6774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 **Expect:** 4.7e-006
Matched b ions: b(7)-98, b(7), b(8)-98, b(9)-98, b(11)
Matched y ions: y(2), y(3), y(4)++, y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(11)++, y(12)-98++, y(12)++

Peptide No.1021

STTFSTNYR
Confirmed sites: @T:2
Ambiguous sites:

MS/MS Fragmentation of **STTFSTNYR**
Found in **K1C18_MOUSE** in **SwissProt**, Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Match to Query 1768: 1155.460156 from(578.737354,2+) index(938)
Title: Elution from: 34.898 to 34.898 scan no 2385 cid35.00 polarity:+



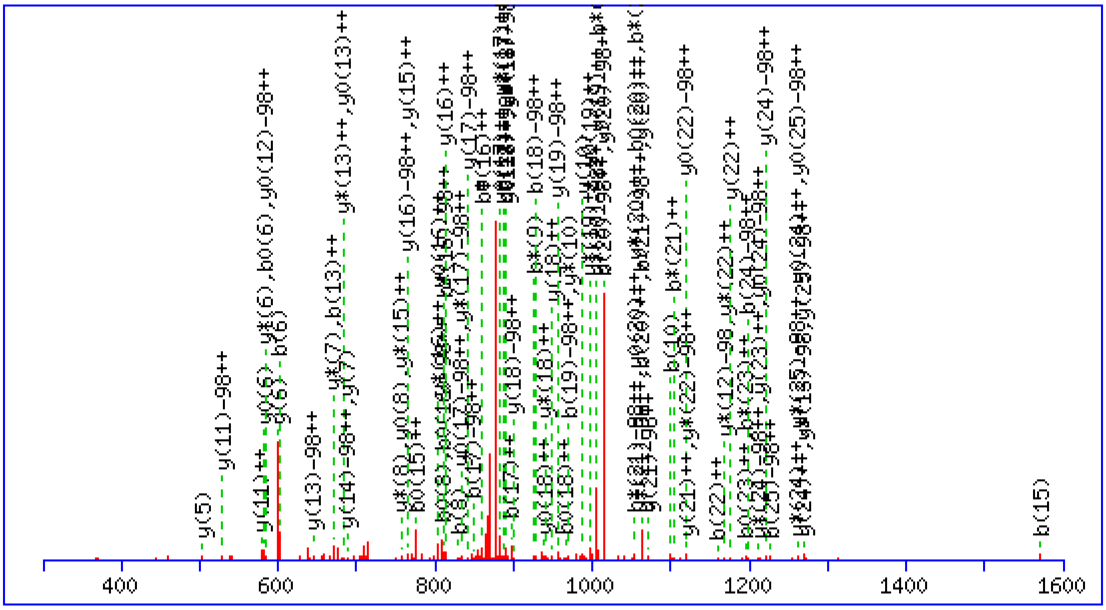
Monoisotopic mass of neutral peptide Mr(calc): 1155.4598
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.00074
Matched b ions: b(2), b(2)-98, b(3), b(3)-98, b(4), b(4)-98, b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(7), y(8)++

Peptide No.1022

SVDALDDINRPGSTESGRSSPPSSGR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **SVDALDDINRPGSTESGRSSPPSSGR**
Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 5477: 2723.209737 from(908.743855,3+) index(4268)
Title: Elution from: 29.945 to 29.945 scan no 2479 cid35.00 polarity:+:m1s



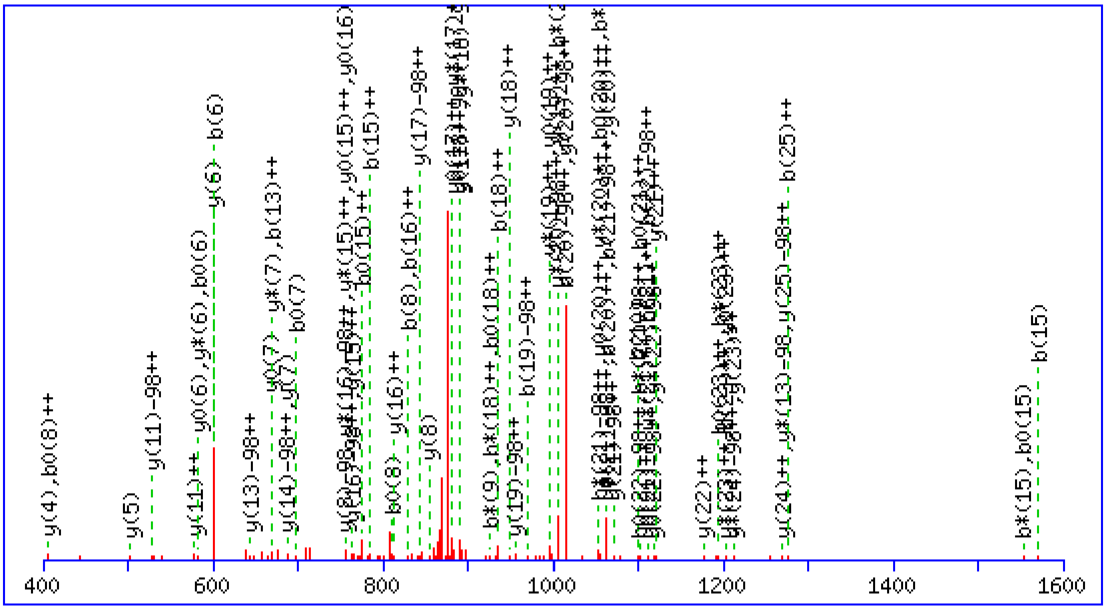
Monoisotopic mass of neutral peptide Mr(calc): 2723.2148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.049
Matched b ions: b(6), b(8), b(10), b(13)++, b(15), b(17)++, b(17)-98++, b(18)-98++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(22)++, b(24)-98++, b(25)-98++
Matched y ions: y(5), y(6), y(7), y(10), y(11)-98++, y(11)++, y(13)-98++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(24)-98++, y(24)++, y(25)-98++

Peptide No.1023

SVDALDDINRPGSTESGRSSPPSSGR
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **SVDALDDINRPGSTESGRSSPPSSGR**
Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 5651: 2723.214666 from(908.745498,3+) index(4514)
Title: Elution from: 29.764 to 29.764 scan no 2535 cid35.00 polarity:+:m1s



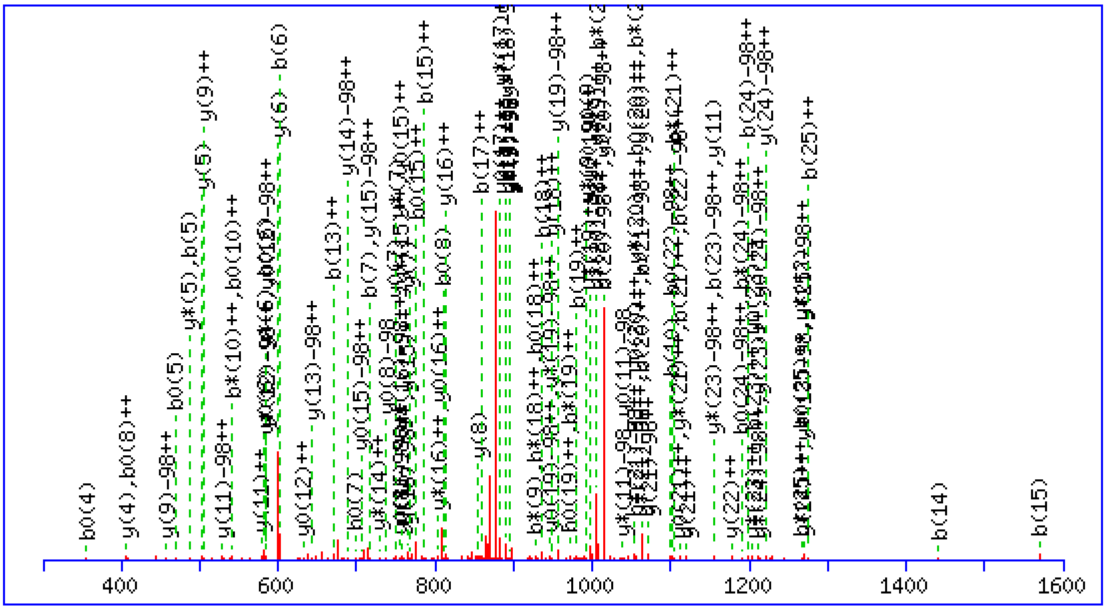
Monoisotopic mass of neutral peptide Mr(calc): 2723.2148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 48 **Expect:** 0.00017
Matched b ions: b(6), b(8), b(10), b(13)++, b(15), b(15)++, b(16)++, b(18)++, b(19)-98++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(23)++, b(25)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)-98, y(8), y(11)++, y(11)-98++, y(13)-98++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(24)++, y(25)-98++

Peptide No.1024

SVDALDDINRPGSTESGRSSPPSSGR
Confirmed sites: @S:20
Ambiguous sites:

MS/MS Fragmentation of **SVDALDDINRPGSTESGRSSPPSSGR**
Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 6687: 2723.208933 from(908.743587,3+) index(5189)
Title: Elution from: 29.807 to 29.807 scan no 2609 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2723.2148

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S20 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 45 **Expect:** 0.00027

Matched b ions: b(5), b(6), b(7), b(10), b(13)++, b(14), b(15), b(15)++, b(17)++, b(18)++, b(19)++, b(20)-98++, b(20)++, b(21)-98++, b(21)++, b(22)-98++, b(23)-98++, b(23)++, b(24)-98++, b(25)++

Matched y ions: y(4), y(5), y(6), y(7), y(8), y(8)-98, y(9)-98++, y(9)++, y(11)-98++, y(11)++, y(11), y(13)-98++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(23)++, y(24)++, y(24)-98++, y(25)-98++

Peptide No.1025

SVDALDDINRPGSTESGRSSPPSSGR

Confirmed sites: @S:24

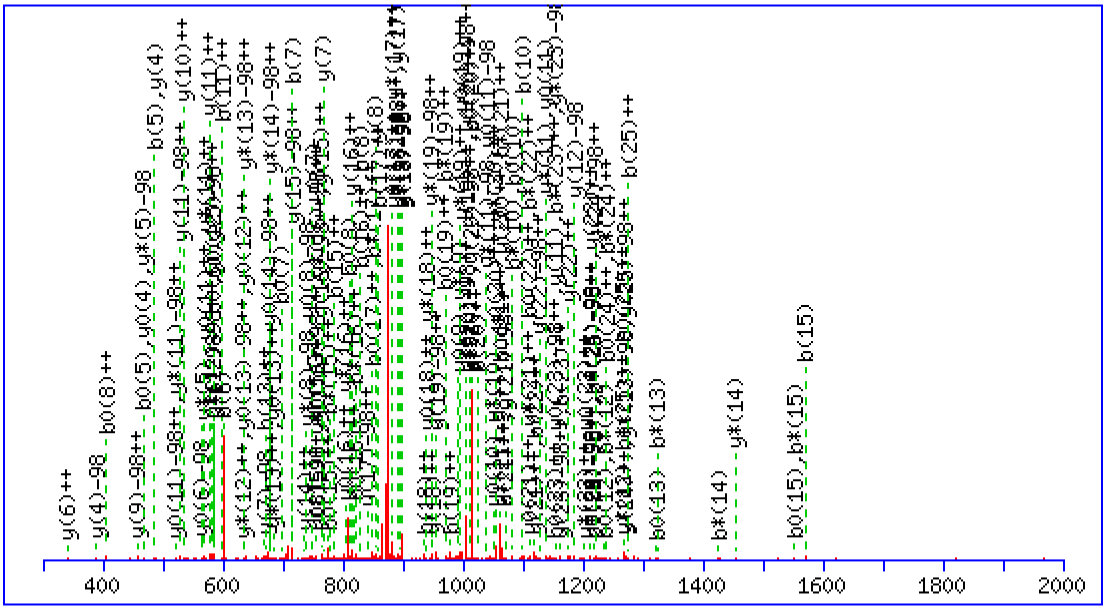
Ambiguous sites:

MS/MS Fragmentation of **SVDALDDINRPGSTESGRSSPPSSGR**

Found in **LSR_MOUSE** in **SwissProt**, Lipolysis-stimulated lipoprotein receptor OS=Mus musculus GN=Lsr PE=1 SV=1

Match to Query 6459: 2723.213961 from(908.745263,3+) index(4793)

Title: Elution from: 37.698 to 37.698 scan no 2853 cid35.00 polarity:+:m1s



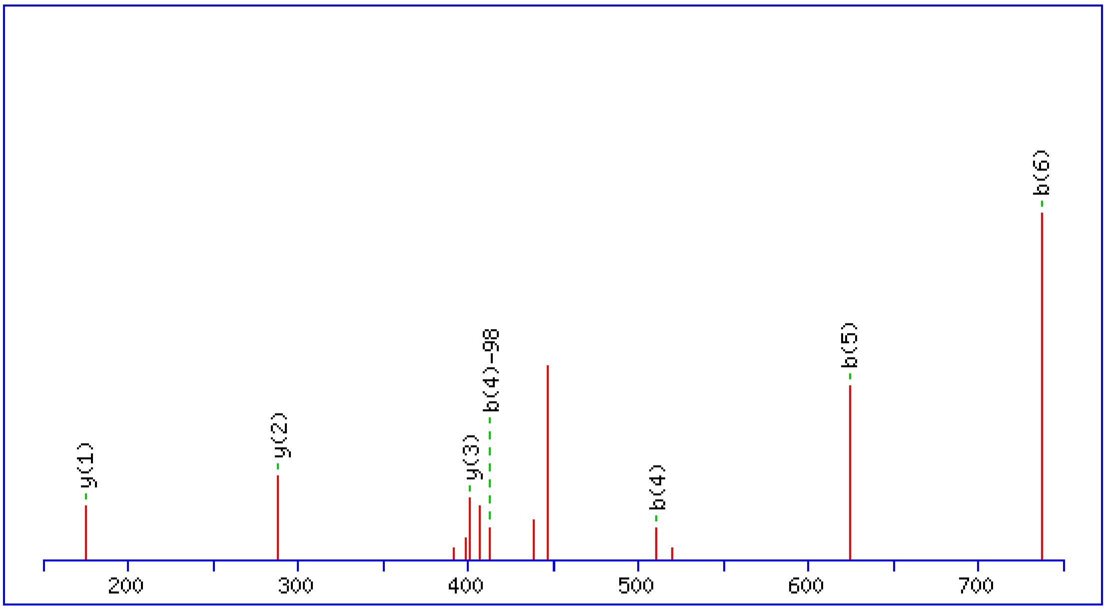
Monoisotopic mass of neutral peptide Mr(calc): 2723.2148
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S24 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00021
Matched b ions: b(5), b(6), b(7), b(8), b(10), b(11)++, b(13)++, b(15), b(15)++, b(16)++, b(17)++, b(18)++, b(19)++, b(20)++, b(21)++, b(22)++, b(23)++, b(25)++
Matched y ions: y(4)-98, y(4), y(5), y(6)++, y(6)-98, y(7)-98, y(7), y(8)-98, y(8), y(9)-98++, y(9), y(10)++, y(11)-98++, y(11)++, y(11), y(12)-98, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)++, y(24)-98++, y(25)-98++

Peptide No.1026

SVDEIIR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SVDEIIR**
Found in **PRDX1_MOUSE** in **SwissProt**, Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1

Match to Query 477: 910.416344 from(456.215448,2+) index(2144)
Title: Elution from: 38.435 to 38.435 scan no 3634 cid35.00 polarity:+



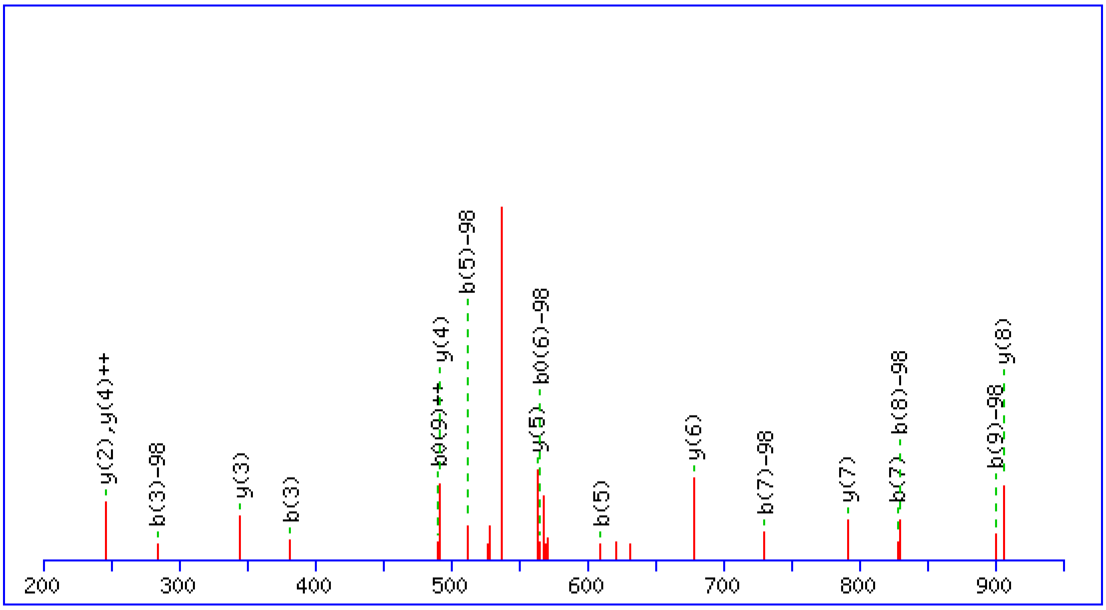
Monoisotopic mass of neutral peptide Mr(calc): 910.4161
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0096
Matched b ions: b(4), b(4)-98, b(5), b(6)
Matched y ions: y(1), y(2), y(3)

Peptide No.1027

SVDLDAFVAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SVDLDAFVAR**
Found in **CD2AP_MOUSE** in **SwissProt**, CD2-associated protein OS=Mus musculus GN=Cd2ap PE=1 SV=3

Match to Query 1334: 1171.527206 from(586.770879,2+) index(2686)
Title: Elution from: 50.556 to 50.556 scan no 5011 cid35.00 polarity:+



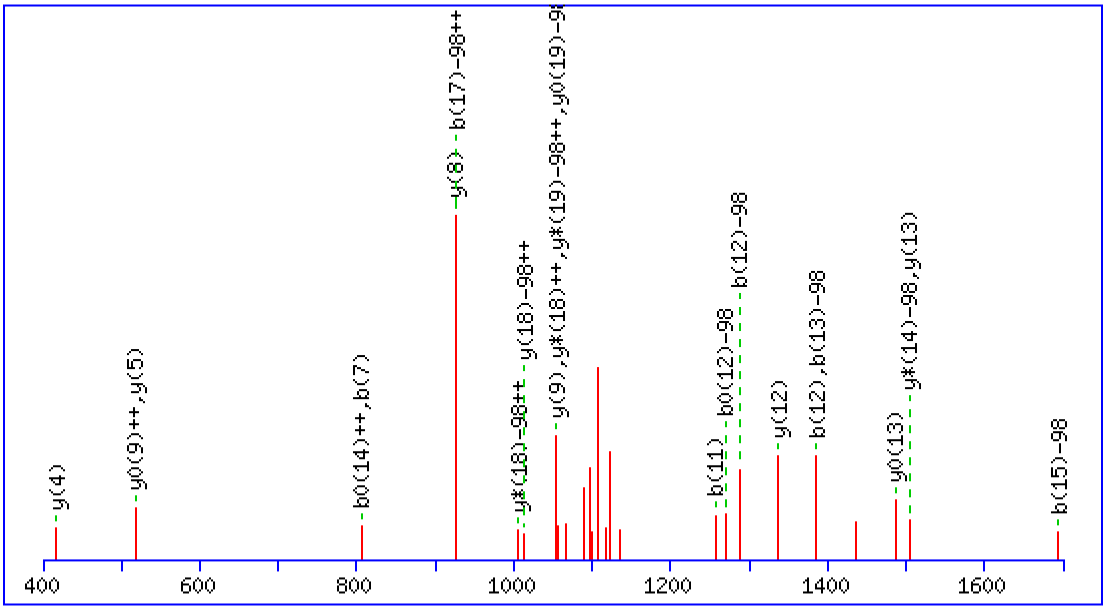
Monoisotopic mass of neutral peptide Mr(calc): 1171.5275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 9.2e-007
Matched b ions: b(3), b(3)-98, b(5)-98, b(5), b(7)-98, b(7), b(8)-98, b(9)-98
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8)

Peptide No.1028

SVEDEMDSPGEEPFYTGQGR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SVEDEMDSPGEEPFYTGQGR**
Found in **NFIA_MOUSE** in **SwissProt**, Nuclear factor 1 A-type OS=Mus musculus GN=Nfia PE=1 SV=1

Match to Query 5842: 2308.878212 from(1155.446382,2+) index(6338)
Title: Elution from: 44.703 to 44.703 scan no 4529 cid35.00 polarity:+:m1s



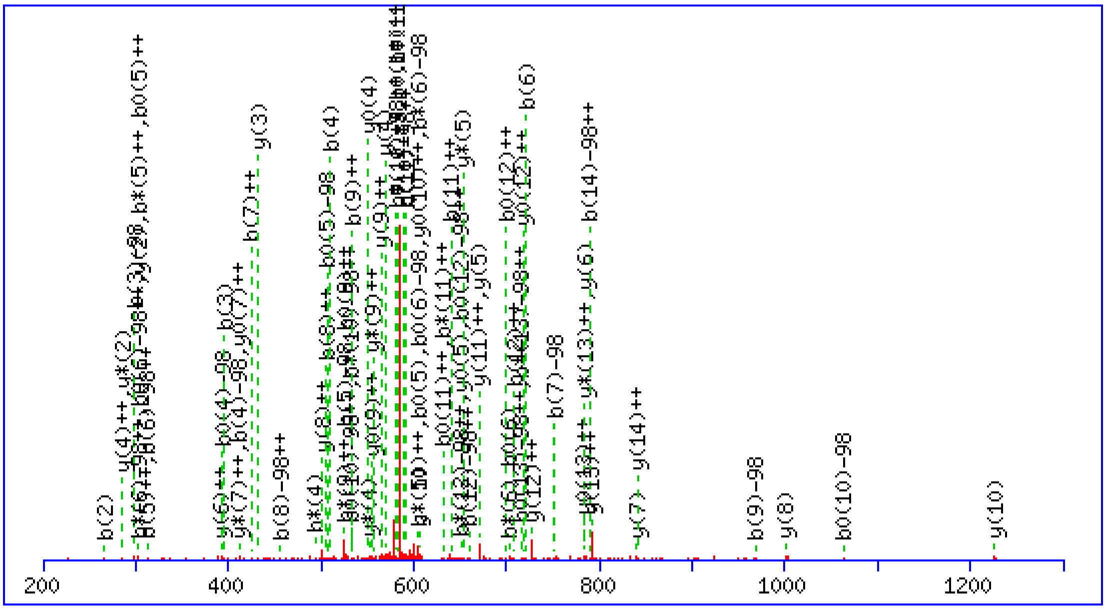
Monoisotopic mass of neutral peptide Mr(calc): 2308.8831
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 **Expect:** 0.0022
Matched b ions: b(7), b(11), b(12)-98, b(12), b(13)-98, b(15)-98, b(17)-98++
Matched y ions: y(4), y(5), y(8), y(9), y(12), y(13), y(18)-98++

Peptide No.1029

SVENLPECGITHEQR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SVENLPECGITHEQR**
Found in **PI4KB_MOUSE** in **SwissProt**, Phosphatidylinositol 4-kinase beta OS=Mus musculus GN=Pi4kb PE=1 SV=2

Match to Query 4013: 1847.787777 from(616.936535,3+) index(4136)
Title: Elution from: 37.796 to 37.796 scan no 2738 cid35.00 polarity:+:m1s



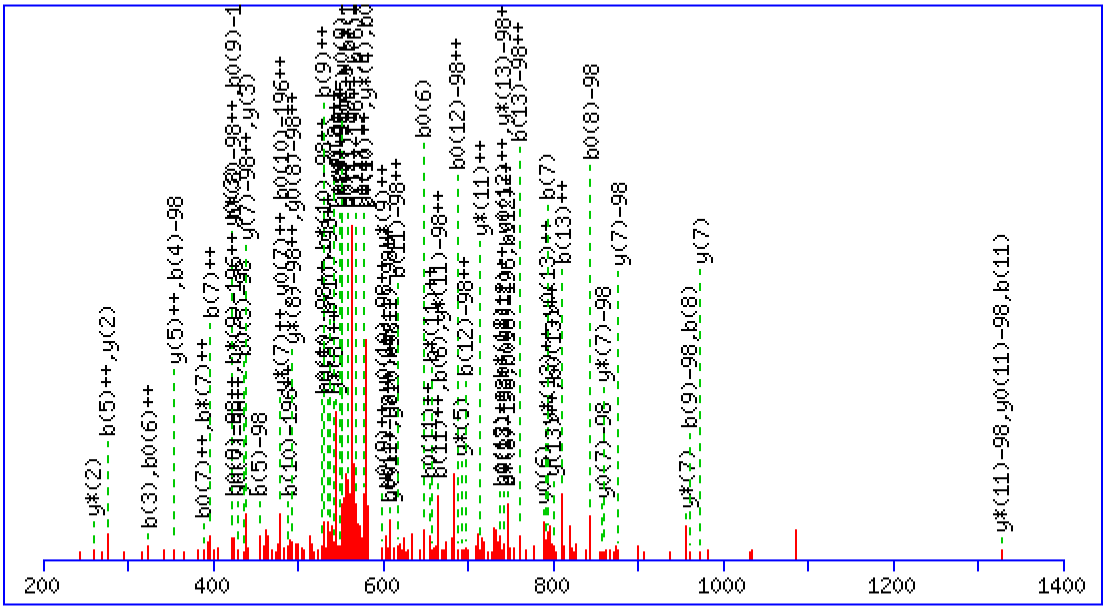
Monoisotopic mass of neutral peptide Mr(calc): 1847.7873
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 42 **Expect:** 0.00027
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5)++, b(6)-98++, b(6), b(7)-98, b(7)++, b(8)++, b(8)-98++, b(9)-98, b(9)++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(14)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7), y(8), y(8)++, y(9)++, y(10), y(11)++, y(12)++, y(13)++, y(14)++

Peptide No.1030

SVGEVLQSVLRYEK
Confirmed sites: @S:1,@S:8
Ambiguous sites:

MS/MS Fragmentation of **SVGEVLQSVLRYEK**
Found in **AKAP3_MOUSE** in **SwissProt**, A-kinase anchor protein 3 OS=Mus musculus GN=Akap3 PE=2 SV=2

Match to Query 4454: 1765.809222 from(589.610350,3+) index(5122)
Title: Elution from: 42.032 to 42.032 scan no 3361 cid35.00 polarity:+:m1s



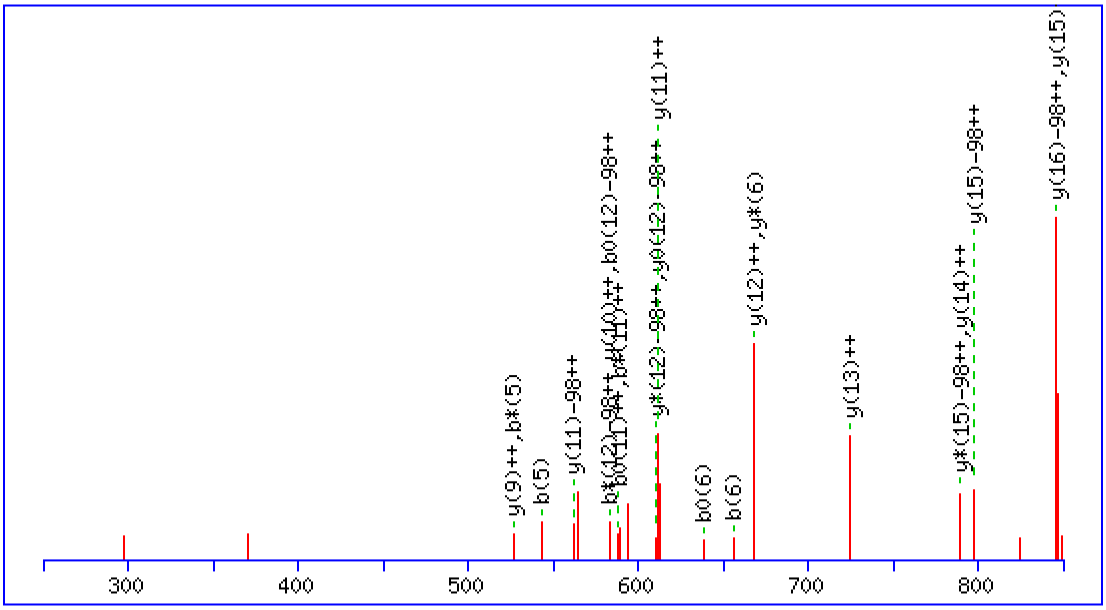
Monoisotopic mass of neutral peptide Mr(calc): 1765.8053
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.019
Matched b ions: b(3), b(4)-98, b(5)++, b(5)-98, b(5), b(6), b(6)-98, b(7)++, b(7), b(8), b(9)++, b(9)-98, b(10)-98++, b(10)-196++, b(11), b(11)++, b(11)-196++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(2), y(3), y(5)++, y(7)-98++, y(7)-98, y(7), y(8)++, y(9)-98++, y(9)++, y(10)-98++, y(13)++

Peptide No.1031

SVNEILGLAESSPKEPK
Confirmed sites:
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of **SVNEILGLAESSPKEPK**
Found in **CI082_MOUSE** in **SwissProt**, Uncharacterized protein C9orf82 homolog OS=Mus musculus PE=1 SV=2

Match to Query 4362: 1876.919358 from(626.647062,3+) index(6293)
Title: Elution from: 43.851 to 43.851 scan no 4431 cid35.00 polarity:+:m1s



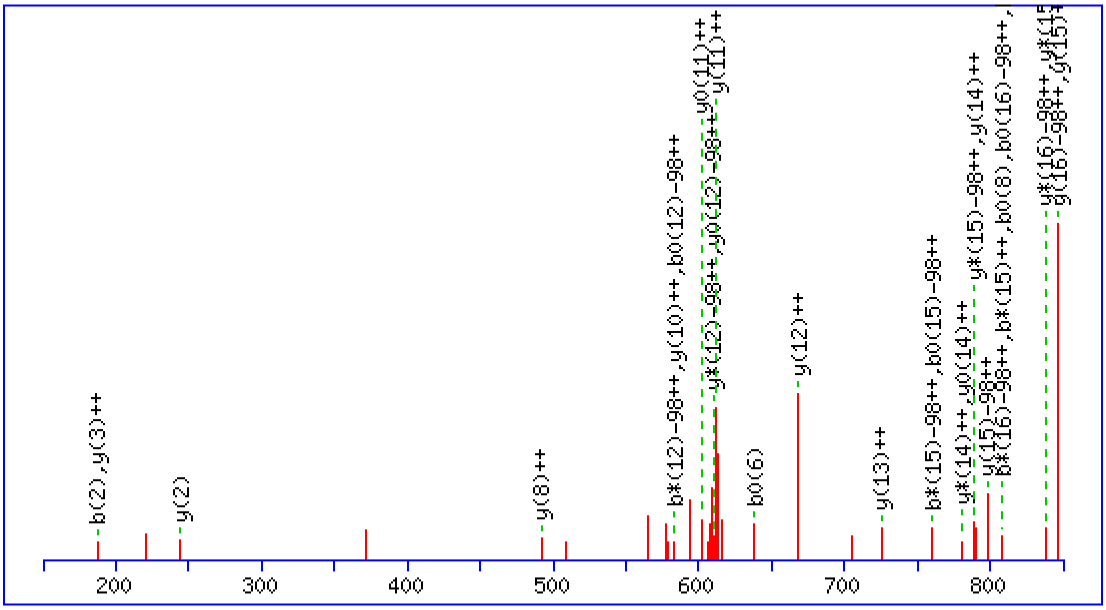
Monoisotopic mass of neutral peptide Mr(calc): 1876.9183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 40 **Expect:** 0.00046
Matched b ions: b(5), b(6)
Matched y ions: y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++

Peptide No.1032

SVNEILGLAESSPKEPK
Confirmed sites:
Ambiguous sites: @S:11orS:12

MS/MS Fragmentation of **SVNEILGLAESSPKEPK**
Found in **CI082_MOUSE** in **SwissProt**, Uncharacterized protein C9orf82 homolog OS=Mus musculus PE=1 SV=2

Match to Query 3770: 1876.916802 from(626.646210,3+) index(5587)
Title: Elution from: 43.826 to 43.826 scan no 4258 cid35.00 polarity:+:m1s



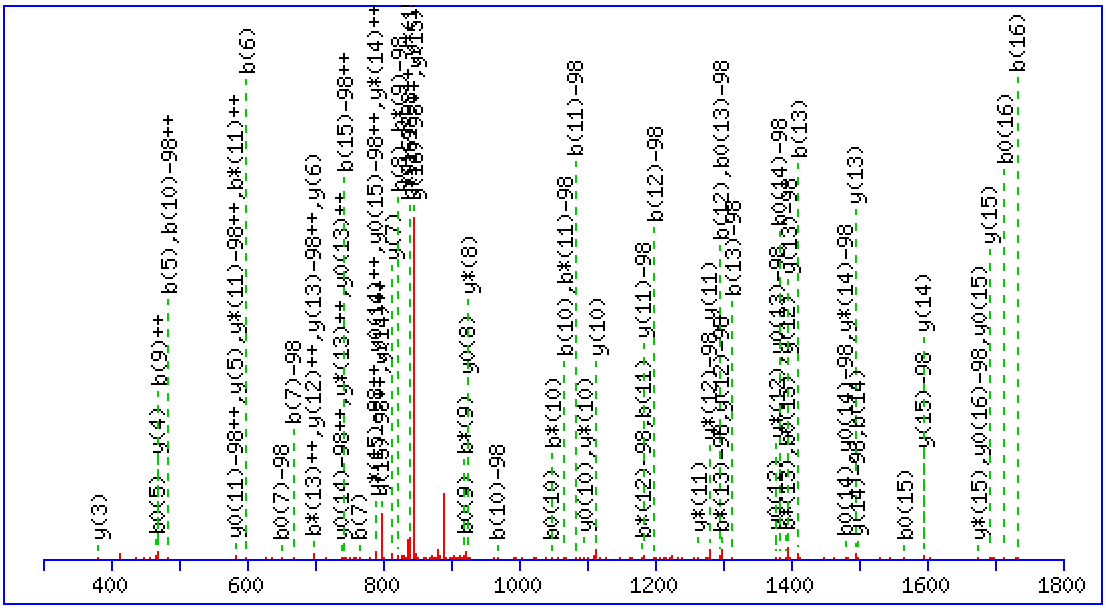
Monoisotopic mass of neutral peptide Mr(calc): 1876.9183
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00036
Matched b ions: b(2)
Matched y ions: y(2), y(3)++, y(8)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)-98++

Peptide No.1033

SVPTVDSGNEDDDSSFK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **SVPTVDSGNEDDDSSFK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4728: 1877.724522 from(939.869537,2+) index(4827)
Title: Elution from: 38.038 to 38.038 scan no 2896 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1877.7204

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 80 **Expect:** 4e-008

Matched b ions: b(5), b(6), b(7)-98, b(7), b(8), b(9)++, b(9)-98, b(10)-98++, b(10), b(10)-98, b(11), b(11)-98, b(12), b(12)-98, b(13), b(13)-98, b(14), b(15)-98++, b(16)

Matched y ions: y(3), y(4), y(5), y(6), y(7), y(10), y(11), y(11)-98, y(12)++, y(12)-98, y(12), y(13)-98++, y(13), y(13)-98, y(14), y(14)++, y(14)-98, y(15)++, y(15), y(15)-98++, y(15)-98, y(16)-98++

Peptide No.1034

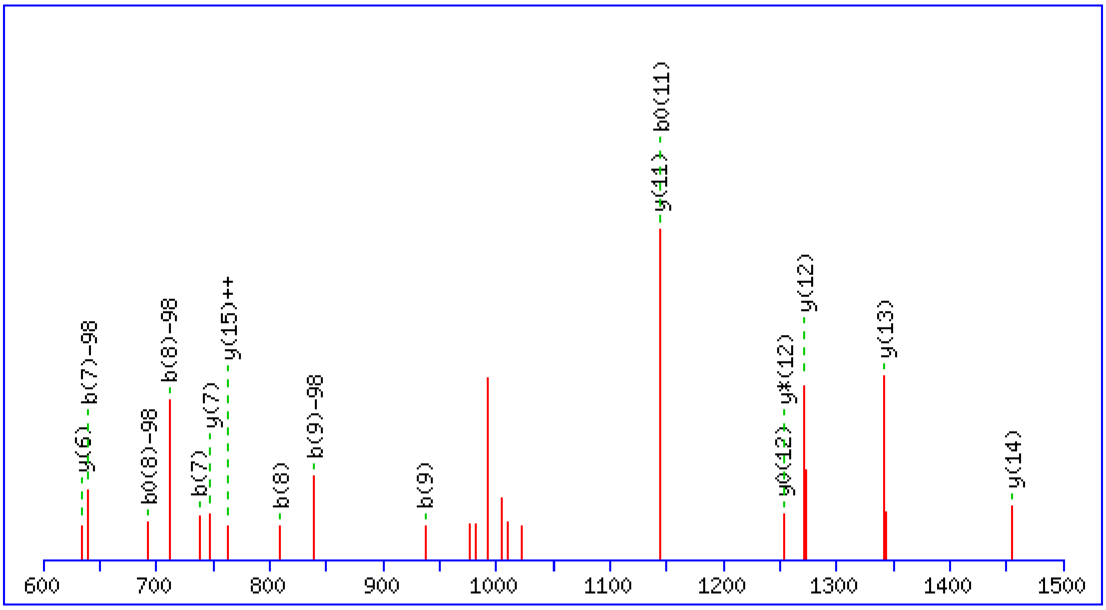
SVSEAALAQPEGLLGTDTLK

Confirmed sites:

Ambiguous sites: @S:1orS:3

MS/MS Fragmentation of **SVSEAALAQPEGLLGTDTLK**
Found in **LIPS_MOUSE** in **SwissProt**, Hormone-sensitive lipase OS=Mus musculus GN=Lipe PE=1 SV=2

Match to Query 5099: 2079.014272 from(1040.514412,2+) index(6777)
Title: Elution from: 55.071 to 55.071 scan no 5666 cid35.00 polarity:+:m1s



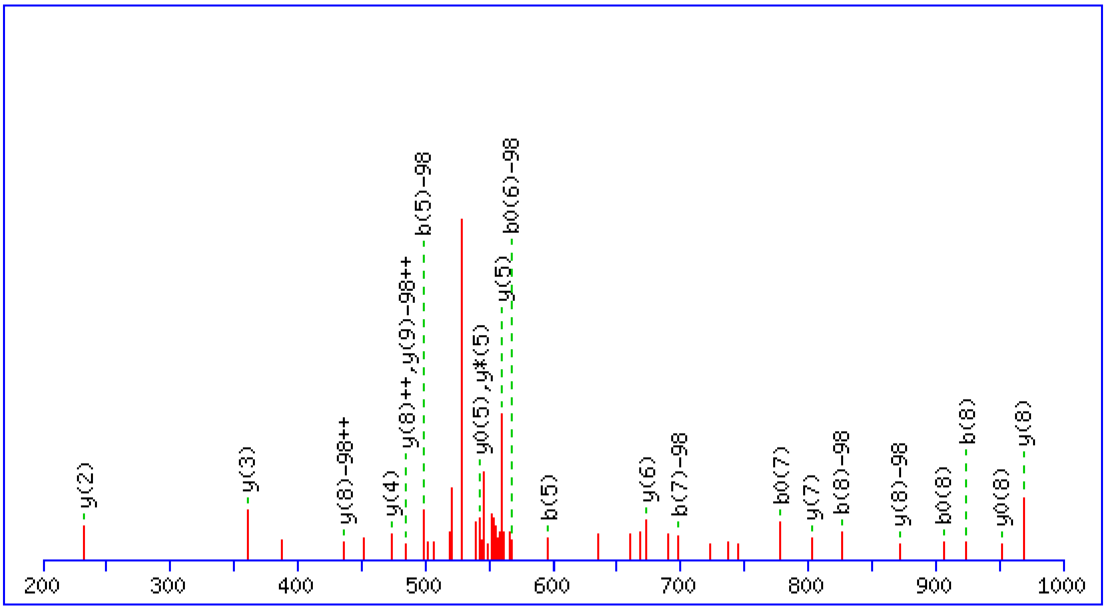
Monoisotopic mass of neutral peptide Mr(calc): 2079.0137
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.001
Matched b ions: b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9)
Matched y ions: y(6), y(7), y(11), y(12), y(13), y(14), y(15)++

Peptide No.1035

SVSELSLQGR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **SVSELSLQGR**
Found in **RAIN_MOUSE** in **SwissProt**, Ras-interacting protein 1 OS=Mus musculus GN=Rasip1 PE=1 SV=3

Match to Query 1340: 1154.531334 from(578.272943,2+) index(1869)
Title: Elution from: 33.575 to 33.575 scan no 3083 cid35.00 polarity:+



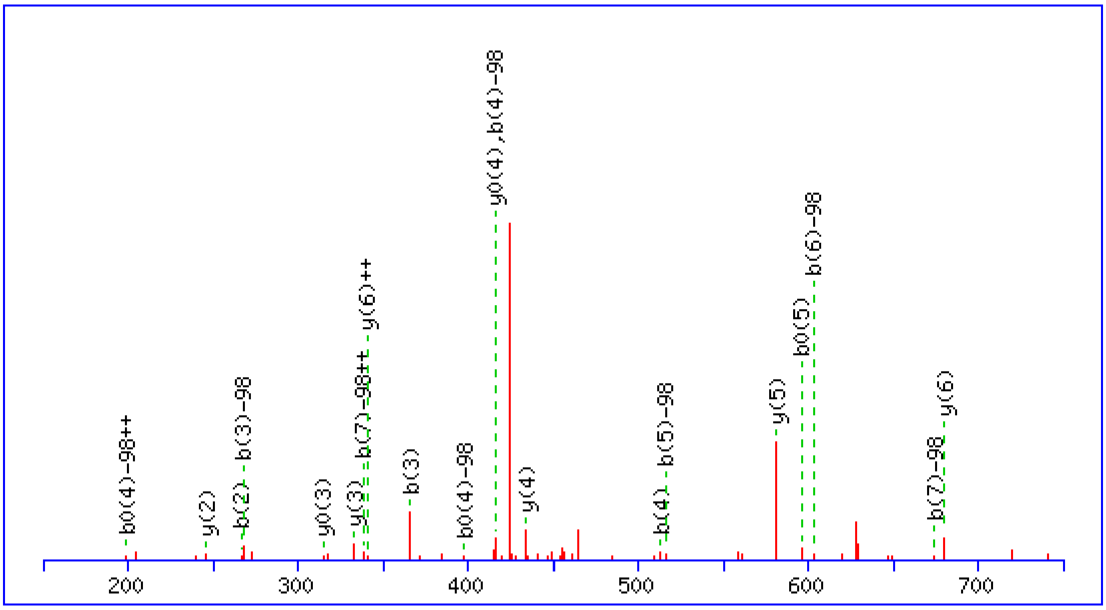
Monoisotopic mass of neutral peptide Mr(calc): 1154.5332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0007
Matched b ions: b(5)-98, b(5), b(7)-98, b(8)-98, b(8)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(8)-98++, y(8)++, y(9)-98++

Peptide No.1036

SVVFTSAR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SVVFTSAR**
Found in **CAH14_MOUSE** in **SwissProt**, Carbonic anhydrase 14 OS=Mus musculus GN=Ca14 PE=1 SV=1

Match to Query 550: 945.432156 from(473.723354,2+) index(1081)
Title: Elution from: 26.544 to 26.544 scan no 2102 cid35.00 polarity:+



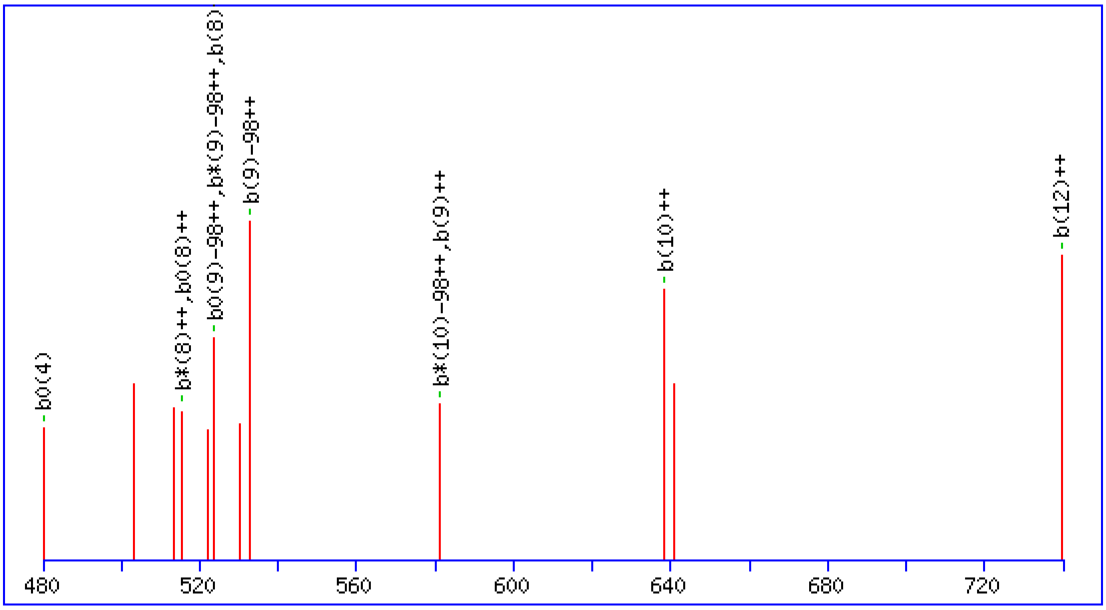
Monoisotopic mass of neutral peptide Mr(calc): 945.4321
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0085
Matched b ions: b(2), b(3)-98, b(3), b(4), b(4)-98, b(5)-98, b(6)-98, b(7)-98++, b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++

Peptide No.1037

SWHSRLSIDLSDK
Confirmed sites:
Ambiguous sites: @S:1orS:4orS:7

MS/MS Fragmentation of **SWHSRLSIDLSDK**
Found in **UN13C_MOUSE** in **SwissProt**, Protein unc-13 homolog C OS=Mus musculus GN=Unc13c PE=2 SV=3

Match to Query 3498: 1622.749284 from(541.923704,3+) index(5467)
Title: Elution from: 32.596 to 32.596 scan no 2984 cid35.00 polarity:+:m1s



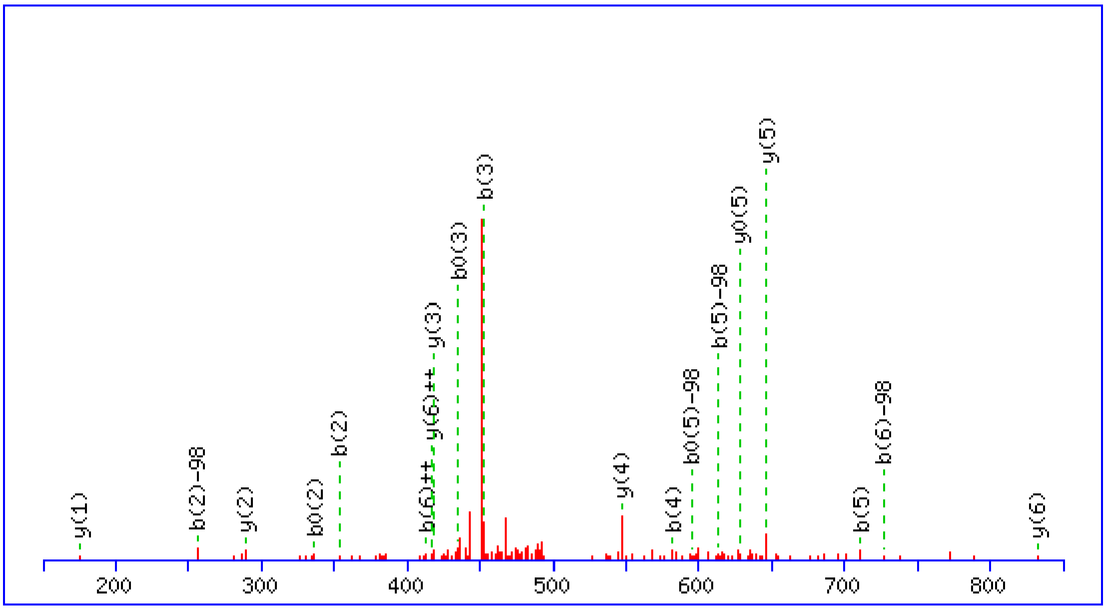
Monoisotopic mass of neutral peptide Mr(calc): 1622.7454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.044
Matched b ions: b(8)++, b(9)-98++, b(9)++, b(10)++, b(12)++
Matched y ions:

Peptide No.1038

SWVEENR
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SWVEENR**
Found in **3HAO_MOUSE** in **SwissProt**, 3-hydroxyanthranilate 3,4-dioxygenase OS=Mus musculus GN=Haao PE=1 SV=1

Match to Query 1096: 998.386034 from(500.200293,2+) index(789)
Title: Elution from: 31.508 to 31.508 scan no 2075 cid35.00 polarity:+



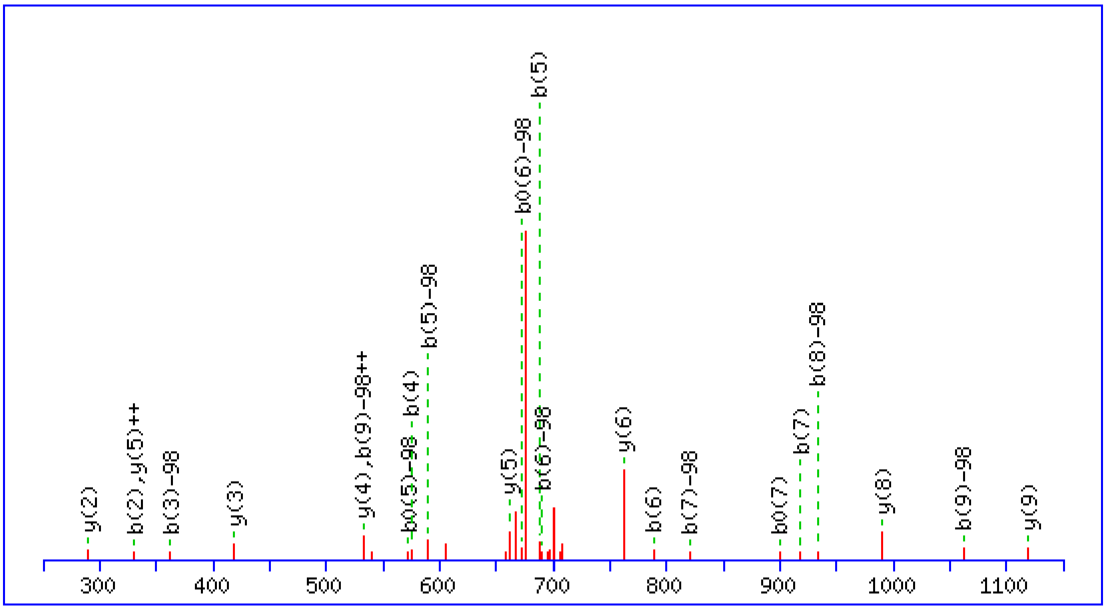
Monoisotopic mass of neutral peptide Mr(calc): 998.3858
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0022
Matched b ions: b(2)-98, b(2), b(3), b(4), b(5), b(5)-98, b(6)-98, b(6)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6), y(6)++

Peptide No.1039

SYEDLTELEDR
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of **SYEDLTELEDR**
Found in **MON1A_MOUSE** in **SwissProt**, Vacuolar fusion protein MON1 homolog A OS=Mus musculus GN=Mon1a PE=1 SV=3

Match to Query 2575: 1448.570760 from(725.292656,2+) index(2759)
Title: Elution from: 43.785 to 43.785 scan no 4424 cid35.00 polarity:+



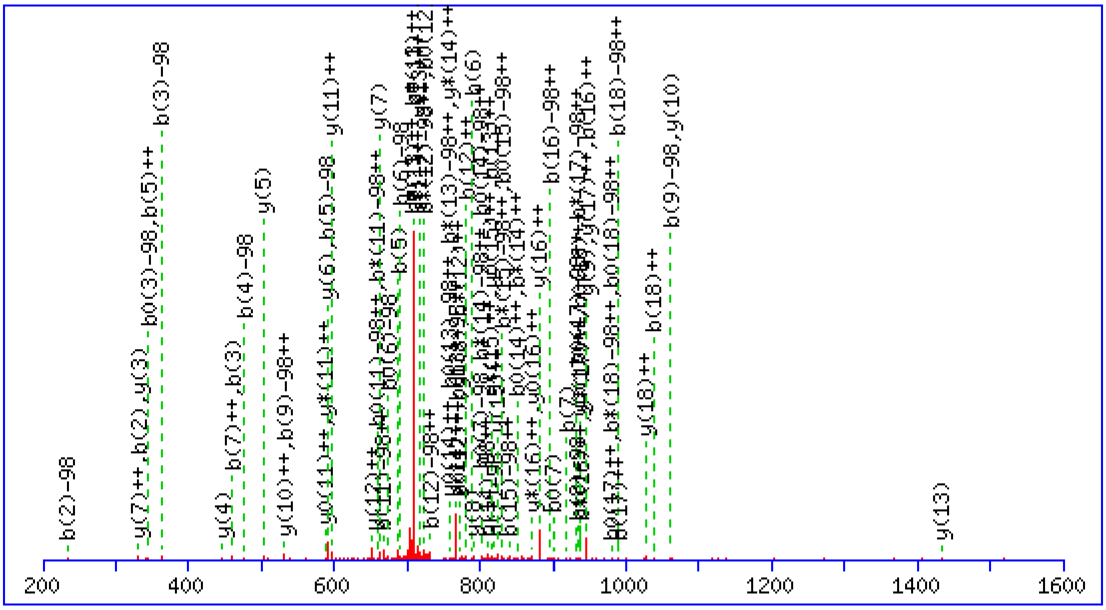
Monoisotopic mass of neutral peptide Mr(calc): 1448.5708
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 4.1e-006
Matched b ions: b(2), b(3)-98, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(7), b(8)-98, b(9)-98++, b(9)-98
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6), y(8), y(9)

Peptide No.1040

SYEDLTELEDREASGDSPK
Confirmed sites: @S:1
Ambiguous sites:

MS/MS Fragmentation of **SYEDLTELEDREASGDSPK**
Found in **MON1A_MOUSE** in **SwissProt**, Vacuolar fusion protein MON1 homolog A OS=Mus musculus GN=Mon1a PE=1 SV=3

Match to Query 5625: 2219.911686 from(740.977838,3+) index(5559)
Title: Elution from: 48.995 to 48.995 scan no 4102 cid35.00 polarity:+:m1s



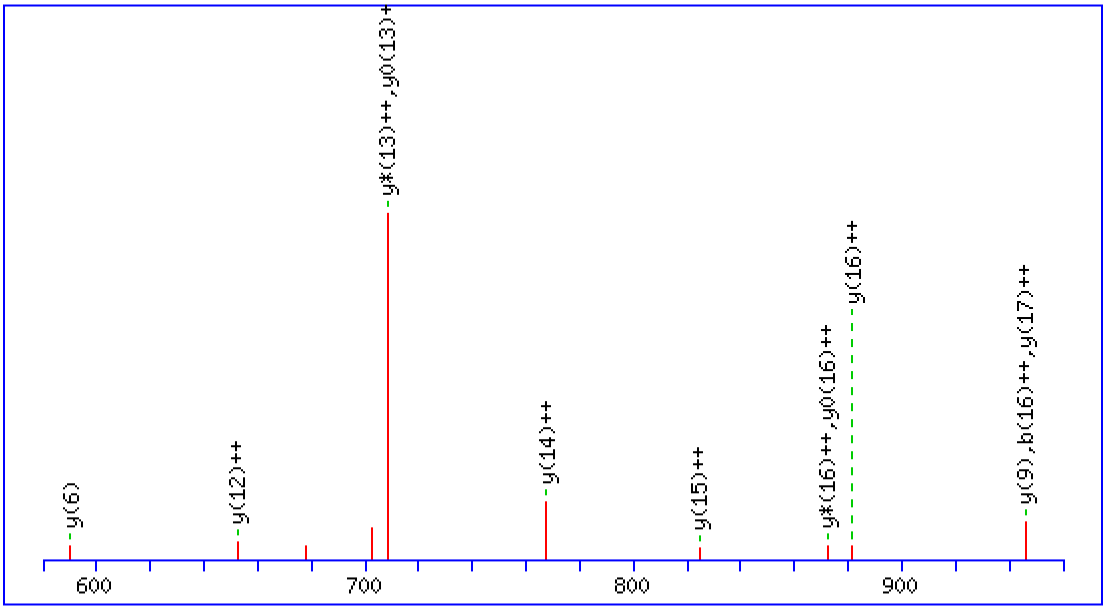
Monoisotopic mass of neutral peptide Mr(calc): 2219.9107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 **Expect:** 7.4e-005
Matched b ions: b(2), b(2)-98, b(3)-98, b(3), b(4)-98, b(5)-98, b(5)++, b(5), b(6)-98, b(6), b(7)++, b(7), b(7)-98, b(8)-98, b(9)-98++, b(9)-98, b(11)-98++, b(11)++, b(12)++, b(12)-98++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(18)++, b(18)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7)++, y(7), y(8), y(9), y(10)++, y(10), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++

Peptide No.1041

SYEDLTELEDREASGDSPK
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of **SYEDLTELEDREASGDSPK**
Found in **MON1A_MOUSE** in **SwissProt**, Vacuolar fusion protein MON1 homolog A OS=Mus musculus GN=Mon1a PE=1 SV=3

Match to Query 5808: 2219.909625 from(740.977151,3+) index(6256)
Title: Elution from: 41.249 to 41.249 scan no 4129 cid35.00 polarity:+:m1s



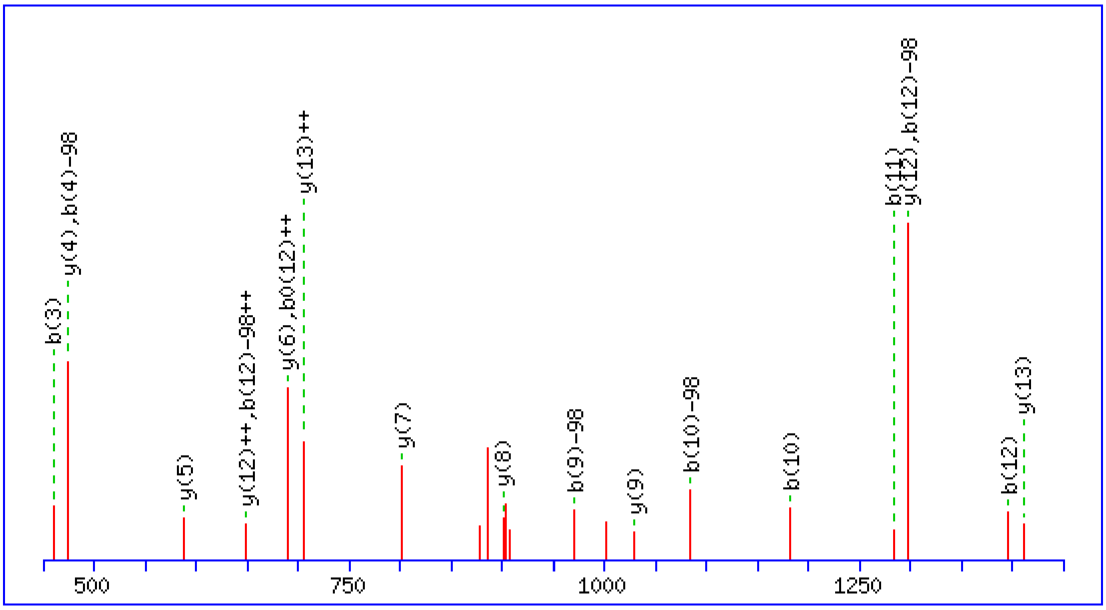
Monoisotopic mass of neutral peptide Mr(calc): 2219.9107
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y2 : Phospho (Y)
Ions Score: 36 **Expect:** 0.0015
Matched b ions: b(16)++
Matched y ions: y(6), y(9), y(12)++, y(14)++, y(15)++, y(16)++, y(17)++

Peptide No.1042

SYELPDGQVITIGNER
Confirmed sites:
Ambiguous sites: @S:1orY:2

MS/MS Fragmentation of **SYELPDGQVITIGNER**
Found in **ACTB_MOUSE** in **SwissProt**, Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1

Match to Query 4466: 1869.852092 from(935.933322,2+) index(3293)
Title: Elution from: 54.211 to 54.211 scan no 5631 cid35.00 polarity:+



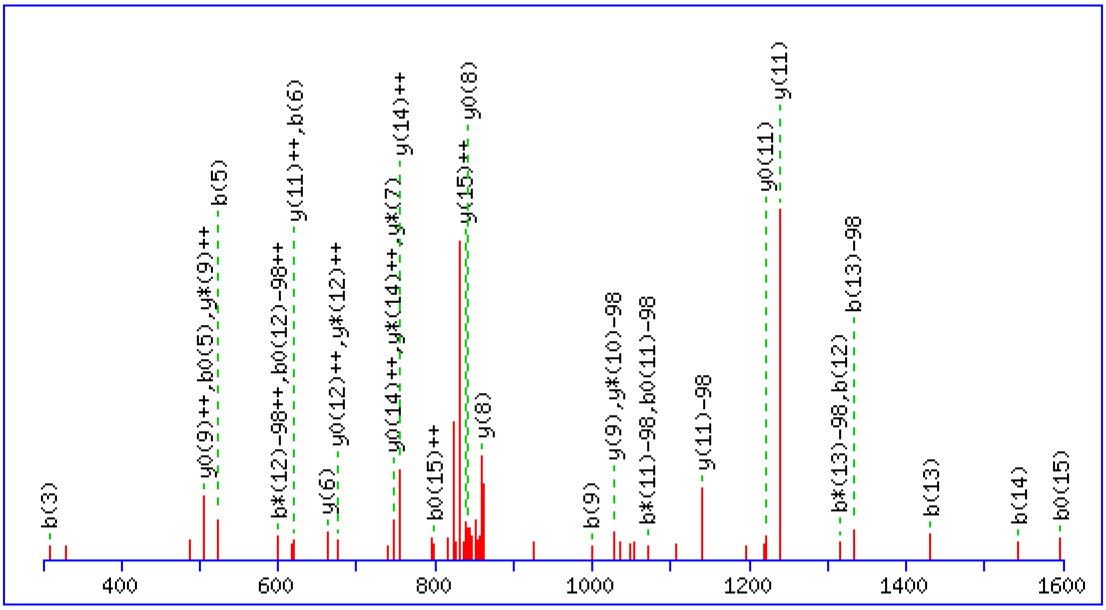
Monoisotopic mass of neutral peptide Mr(calc): 1869.8510
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 72 **Expect:** 4.3e-007
Matched b ions: b(3), b(4)-98, b(9)-98, b(10)-98, b(10), b(11), b(12)-98, b(12), b(12)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(12), y(12)++, y(13)++, y(13)

Peptide No.1043

SYGSQPNSPTSEDLAK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **SYGSQPNSPTSEDLAK**
Found in **CGNL1_MOUSE** in **SwissProt**, Cingulin-like protein 1 OS=Mus musculus GN=Cgnl1 PE=1 SV=2

Match to Query 3492: 1759.728776 from(880.871664,2+) index(774)
Title: Elution from: 25.138 to 25.138 scan no 1814 cid35.00 polarity:+



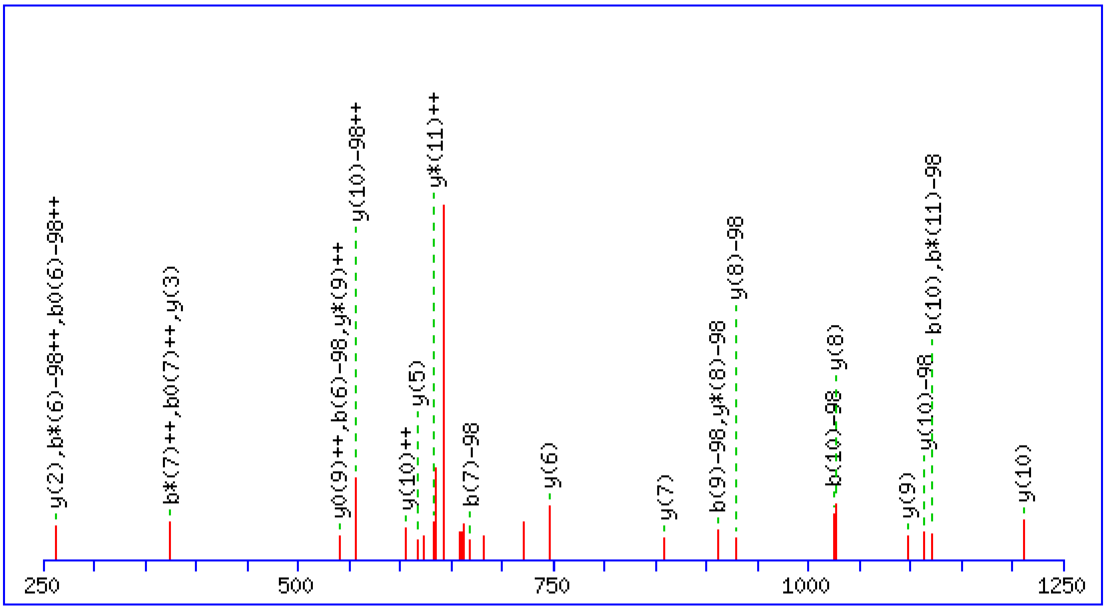
Monoisotopic mass of neutral peptide Mr(calc): 1759.7302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 **Expect:** 0.0036
Matched b ions: b(3), b(5), b(6), b(9), b(12), b(13)-98, b(13), b(14)
Matched y ions: y(6), y(8), y(9), y(11)-98, y(11), y(11)++, y(14)++, y(15)++

Peptide No.1044

TANASLEEIIDK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **TANASLEEIIDK**
Found in **VP13C_MOUSE** in **SwissProt**, Vacuolar protein sorting-associated protein 13C OS=Mus musculus GN=Vps13c PE=1 SV=2

Match to Query 2455: 1382.632632 from(692.323592,2+) index(2722)
Title: Elution from: 42.665 to 42.665 scan no 4314 cid35.00 polarity:+



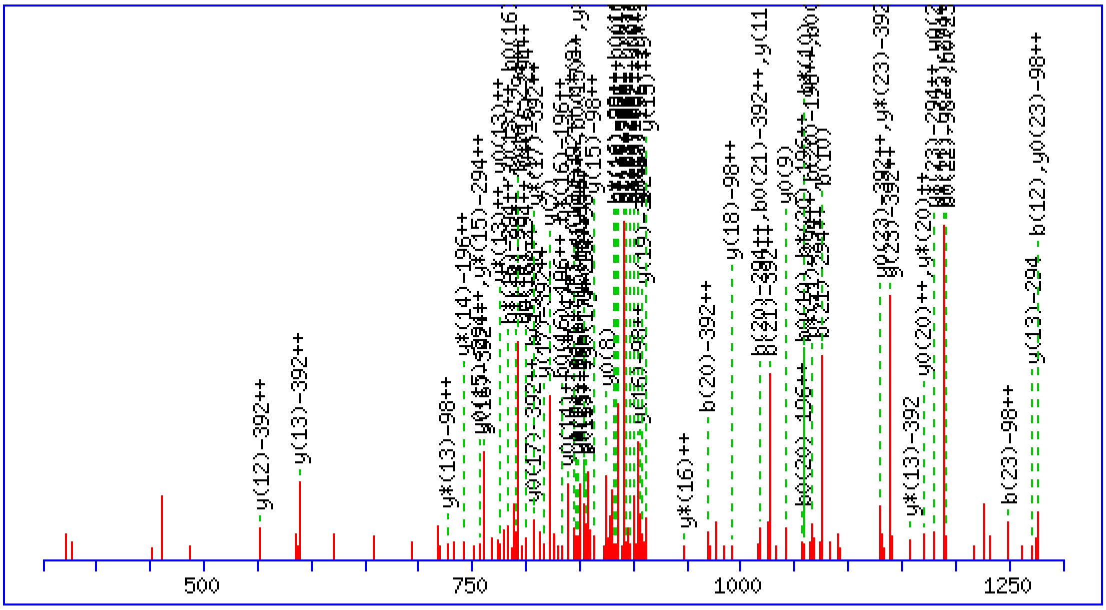
Monoisotopic mass of neutral peptide Mr(calc): 1382.6330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 52 **Expect:** 2.5e-005
Matched b ions: b(6)-98, b(7)-98, b(9)-98, b(10)-98, b(10)
Matched y ions: y(2), y(3), y(5), y(6), y(7), y(8), y(8)-98, y(9), y(10)-98++, y(10)-98, y(10), y(10)++

Peptide No.1045

TANKFEGLSQQASTSSAKTALGPR
Confirmed sites: @S:16,@T:19
Ambiguous sites: @S:13orT:14orS:15, @S:13orT:14orS:15

MS/MS Fragmentation of **TANKFEGLSQQASTSSAKTALGPR**
Found in **ASAP1_MOUSE** in **SwissProt**, Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Mus musculus GN=Asap1 PE=1 SV=1

Match to Query 5533: 2769.116517 from(924.046115,3+) index(4363)
Title: Elution from: 31.149 to 31.149 scan no 2644 cid35.00 polarity:+:m1s



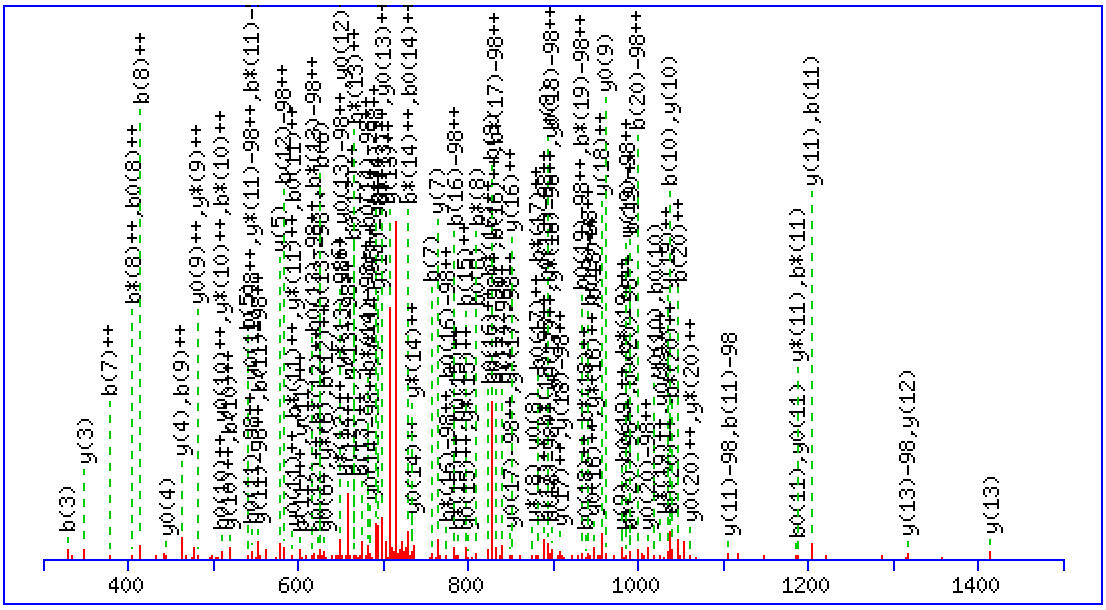
Monoisotopic mass of neutral peptide Mr(calc): 2769.1214
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.02
Matched b ions: b(10), b(12), b(15)-98++, b(15)++, b(16)-294++, b(16)-98++, b(18)-294++, b(20)-196++, b(20)-294++, b(20)-392++, b(21)-392++, b(21)-294++, b(23)-98++
Matched y ions: y(7), y(8), y(11)-392, y(12)-392++, y(13)-392++, y(13)-294, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-392++, y(16)-98++, y(17)-392++, y(18)-392++, y(18)-294++, y(18)-98++, y(19)-392++, y(23)-392++, y(23)-294++

Peptide No.1046

TARPNSEAPLSGSEDADDSNK
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **TARPNSEAPLSGSEDADDSNK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4900: 2239.919313 from(747.647047,3+) index(3530)
Title: Elution from: 20.810 to 20.810 scan no 1327 cid35.00 polarity:+:m1s



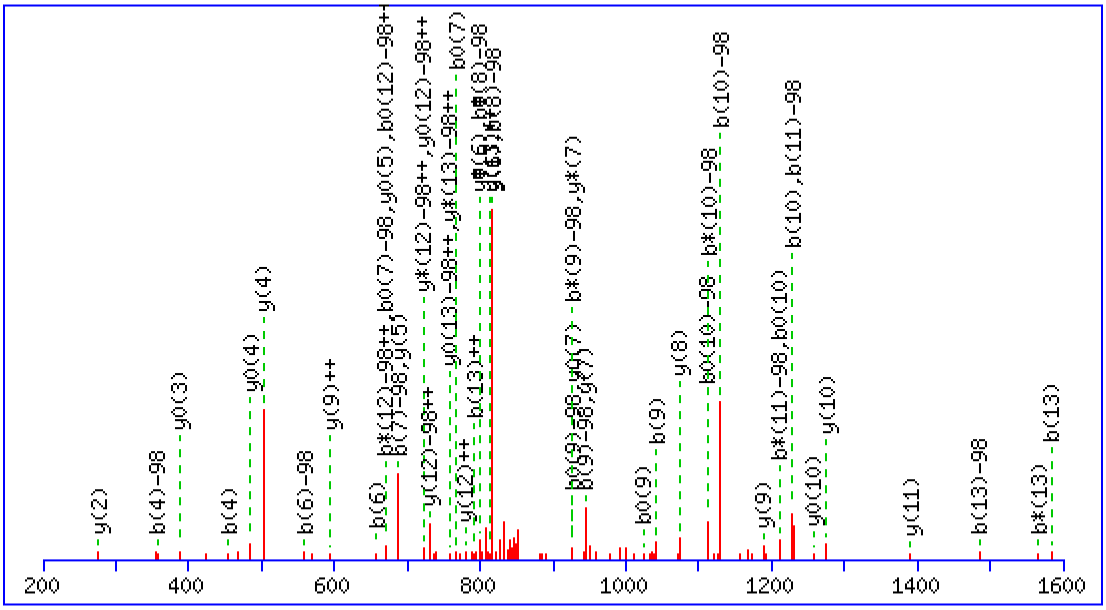
Monoisotopic mass of neutral peptide Mr(calc): 2239.9230
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 81 **Expect:** 4e-008
Matched b ions: b(3), b(5), b(6), b(7)++, b(7), b(8)++, b(8), b(9)++, b(10), b(10)++, b(11)-98++, b(11), b(11)++, b(11)-98, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)++, y(11)-98++, y(11), y(11)++, y(11)-98, y(12), y(12)++, y(13)-98, y(13), y(13)++, y(13)-98++, y(14)-98++, y(16)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++

Peptide No.1047

TASDSDEQQWPEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TASDSDEQQWPEEK**
Found in **PDS5B_MOUSE** in **SwissProt**, Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1

Match to Query 3296: 1728.648632 from(865.331592,2+) index(1223)
Title: Elution from: 27.791 to 27.791 scan no 2271 cid35.00 polarity:+



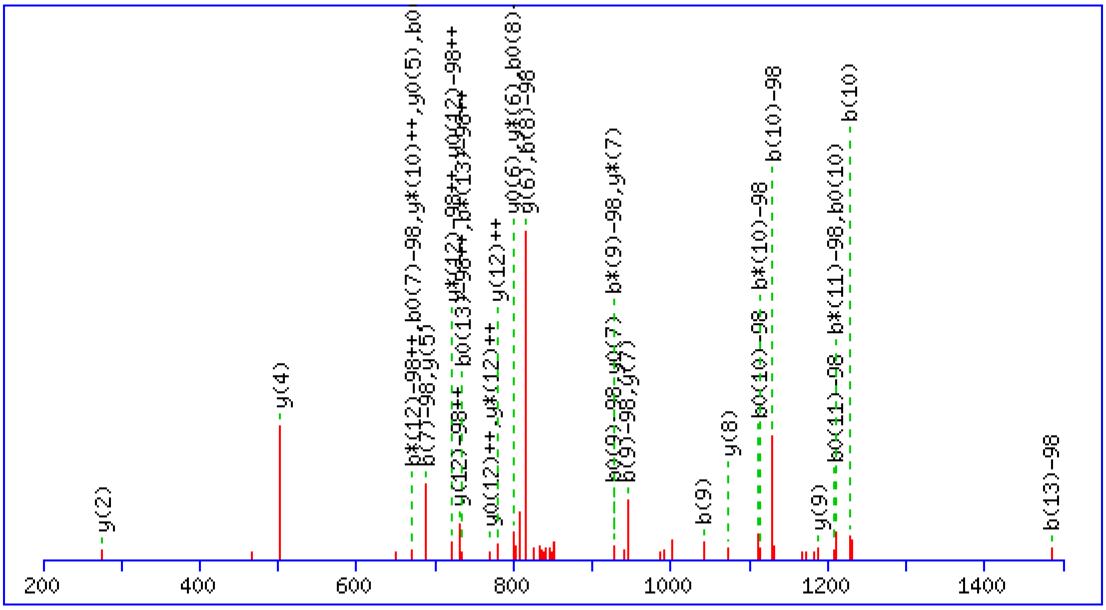
Monoisotopic mass of neutral peptide Mr(calc): 1728.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 79 **Expect:** 3.9e-008
Matched b ions: b(4)-98, b(4), b(6)-98, b(6), b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(13)-98, b(13), b(13)++
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(11), y(12)-98++, y(12)++, y(13)++

Peptide No.1048

TASDSDEQQWPEEK
Confirmed sites:
Ambiguous sites: @S:3orS:5

MS/MS Fragmentation of **TASDSDEQQWPEEK**
Found in **PDS5B_MOUSE** in **SwissProt**, Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1

Match to Query 3385: 1728.649754 from(865.332153,2+) index(1103)
Title: Elution from: 28.017 to 28.017 scan no 2212 cid35.00 polarity:+



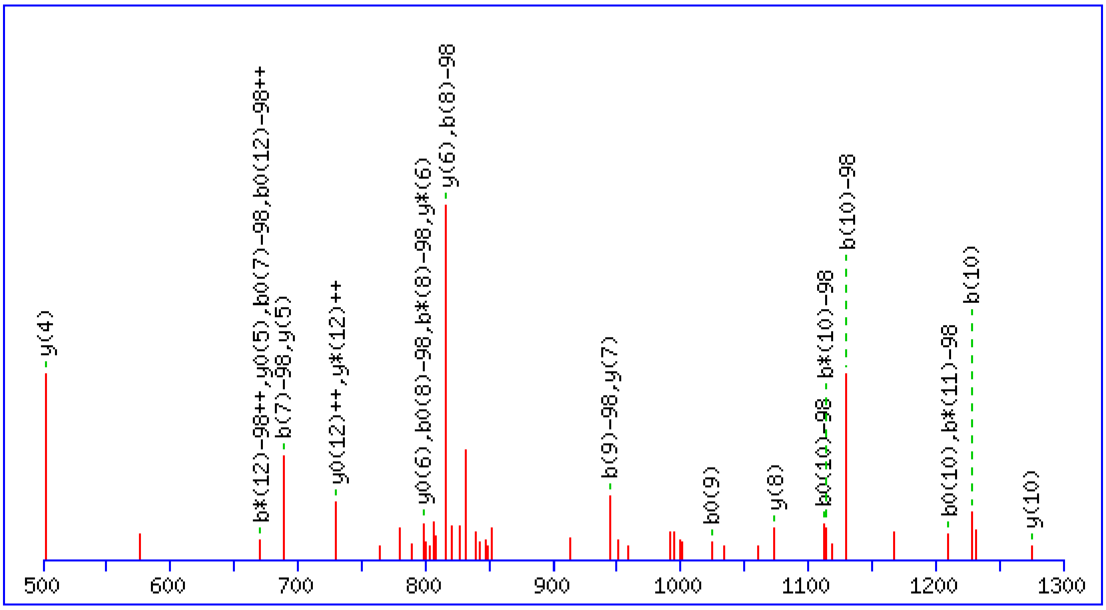
Monoisotopic mass of neutral peptide Mr(calc): 1728.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 8.3e-005
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(13)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(8), y(9), y(12)-98++, y(12)++

Peptide No.1049

TASDSDEQQWPEEK
Confirmed sites:
Ambiguous sites: @T:1orS:3

MS/MS Fragmentation of **TASDSDEQQWPEEK**
Found in **PDS5B_MOUSE** in **SwissProt**, Sister chromatid cohesion protein PDS5 homolog B OS=Mus musculus GN=Pds5b PE=1 SV=1

Match to Query 3770: 1728.650184 from(865.332368,2+) index(1337)
Title: Elution from: 28.186 to 28.186 scan no 2351 cid35.00 polarity:+



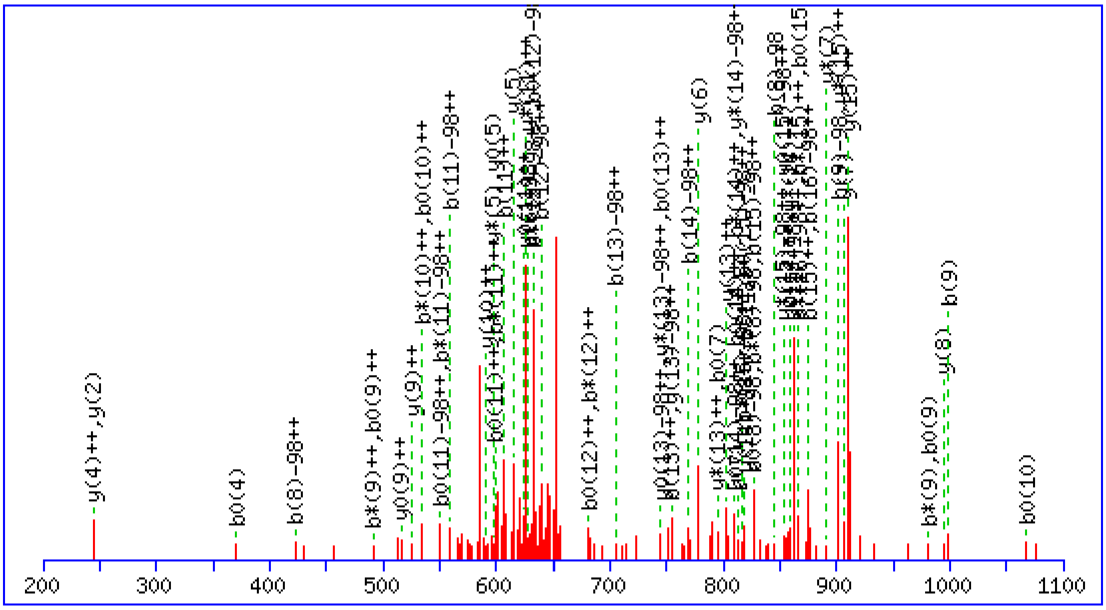
Monoisotopic mass of neutral peptide Mr(calc): 1728.6516
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 **Expect:** 6.9e-005
Matched b ions: b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(10)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10)

Peptide No.1050

TASETRSEGSEYEEIPK
Confirmed sites: @T:5
Ambiguous sites:

MS/MS Fragmentation of **TASETRSEGSEYEEIPK**
Found in **PRC2A_MOUSE** in **SwissProt**, Protein PRRC2A OS=Mus musculus GN=Prrc2a PE=1 SV=1

Match to Query 4149: 1991.833503 from(664.951777,3+) index(1102)
Title: Elution from: 26.721 to 26.721 scan no 2126 cid35.00 polarity:+



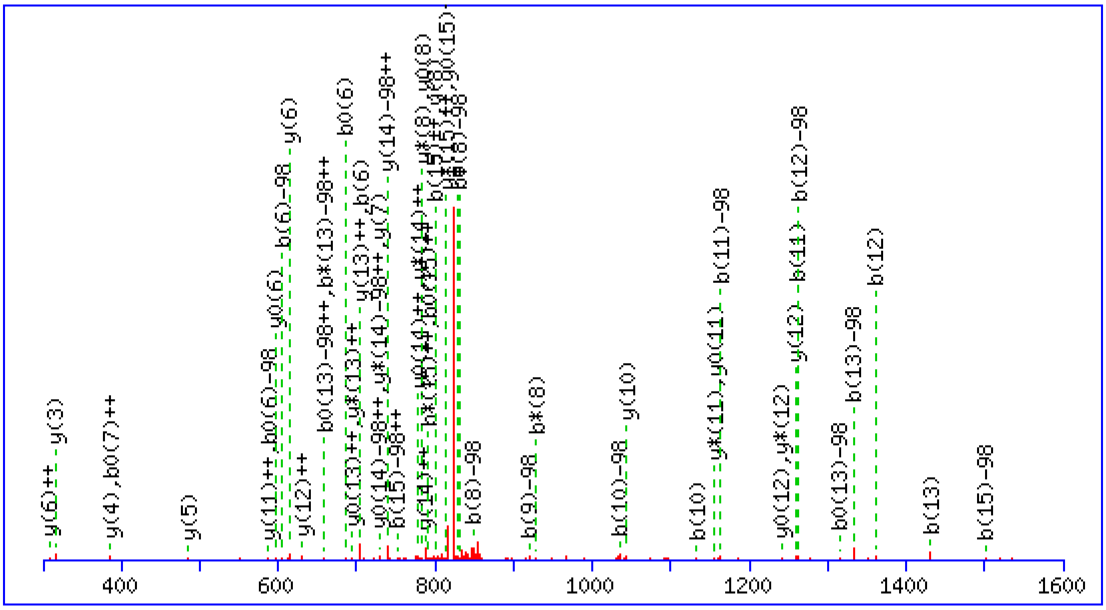
Monoisotopic mass of neutral peptide Mr(calc): 1991.8361
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0087
Matched b ions: b(6)-98, b(7), b(8)-98++, b(8)-98, b(9), b(9)-98, b(11)++, b(11)-98++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++
Matched y ions: y(2), y(4)++, y(5), y(6), y(7), y(8), y(9)++, y(10)++, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.1051

TASFSESRADEVAPAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TASFSESRADEVAPAK**
Found in **ACLY_MOUSE** in **SwissProt**, ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1

Match to Query 3371: 1744.764276 from(873.389414,2+) index(935)
Title: Elution from: 25.138 to 25.138 scan no 1911 cid35.00 polarity:+



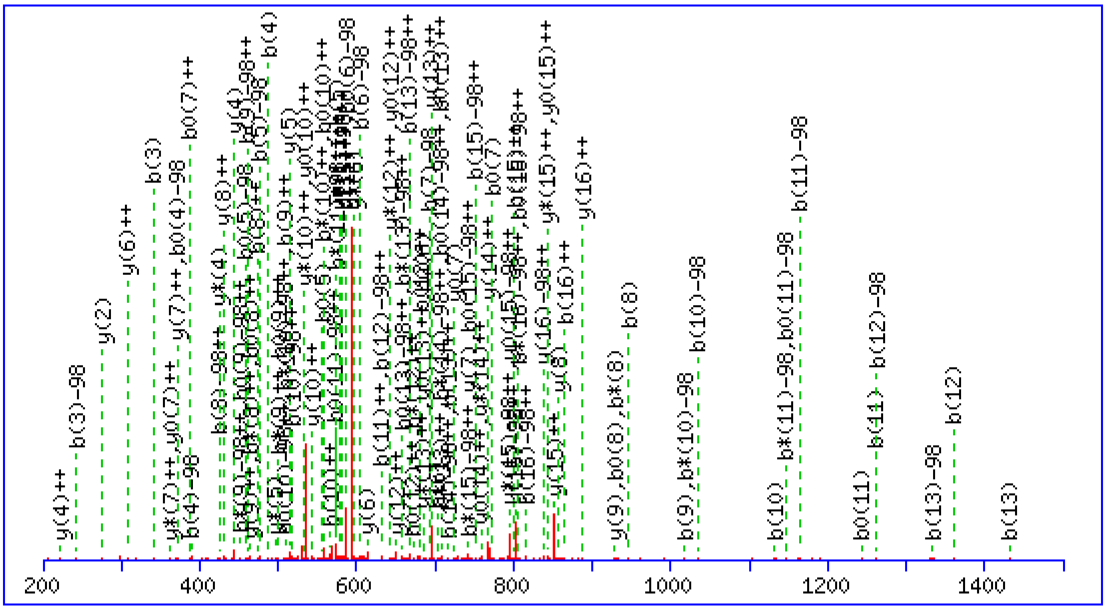
Monoisotopic mass of neutral peptide Mr(calc): 1744.7669
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 64 **Expect:** 1.5e-006
Matched b ions: b(6)-98, b(6), b(8)-98, b(9)-98, b(10)-98, b(10), b(11)-98, b(11), b(12)-98, b(12), b(13)-98, b(13), b(15)-98, b(15)++, b(15)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7), y(8), y(10), y(11)++, y(12), y(12)++, y(13)++, y(14)-98++, y(14)++

Peptide No.1052

TASFSESRADEVAPAKK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TASFSESRADEVAPAKK**
Found in **ACLY_MOUSE** in **SwissProt**, ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1

Match to Query 4483: 1872.859482 from(625.293770,3+) index(711)
Title: Elution from: 22.077 to 22.077 scan no 1555 cid35.00 polarity:+



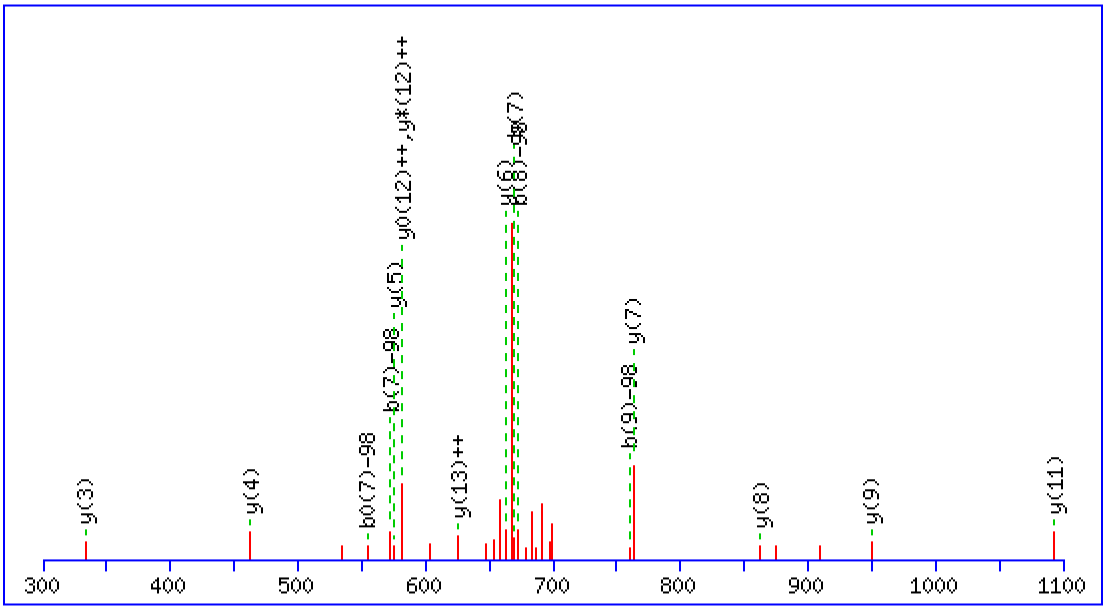
Monoisotopic mass of neutral peptide Mr(calc): 1872.8618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 1.7e-005
Matched b ions: b(3)-98, b(3), b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(8), b(8)-98++, b(8)++, b(9), b(9)-98++, b(9)++, b(10)-98, b(10), b(10)++, b(10)-98++, b(11), b(11)-98, b(11)++, b(11)-98++, b(12), b(12)-98, b(12)++, b(12)-98++, b(13), b(13)-98, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(2), y(4), y(4)++, y(5), y(6), y(6)++, y(7)++, y(7), y(8), y(8)++, y(9), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(16)++

Peptide No.1053

TASGSSVTSLEGTR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of **TASGSSVTSLEGTR**
Found in **NDRG1_MOUSE** in **SwissProt**, Protein NDRG1 OS=Mus musculus GN=Ndrg1 PE=1 SV=1

Match to Query 2323: 1431.621794 from(716.818173,2+) index(1089)
Title: Elution from: 27.894 to 27.894 scan no 2195 cid35.00 polarity:+



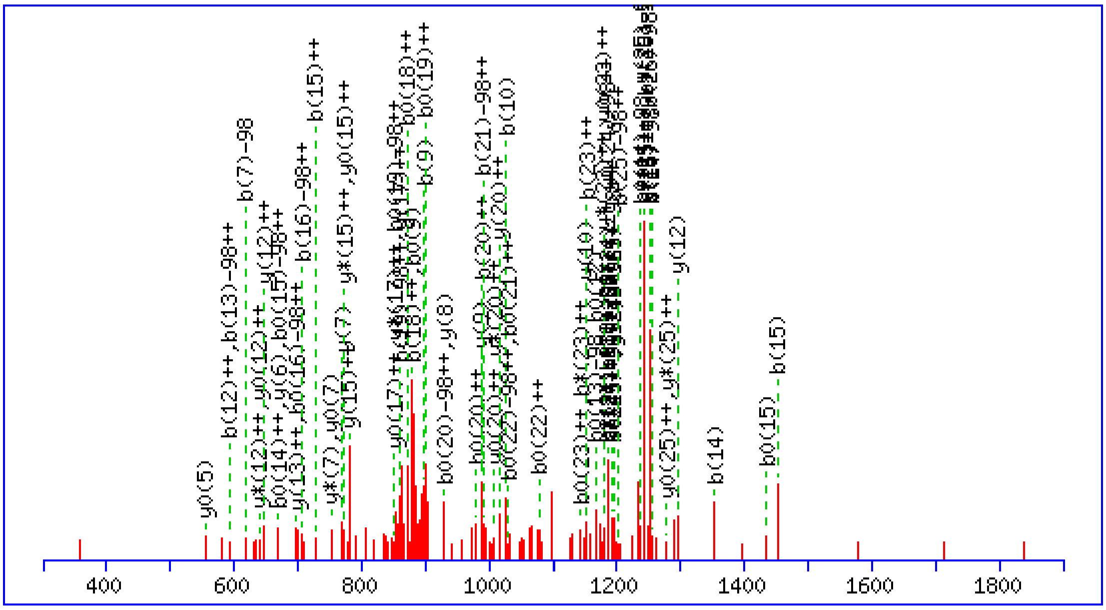
Monoisotopic mass of neutral peptide Mr(calc): 1431.6243
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 7.5e-006
Matched b ions: b(7)-98, b(7), b(8)-98, b(9)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(13)++

Peptide No.1054

TASISSSPSEGTPAVGSYGCTPQSLPK
Confirmed sites:
Ambiguous sites: @S:5orS:6orS:7

MS/MS Fragmentation of **TASISSSPSEGTPAVGSYGCTPQSLPK**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 5577: 2745.219192 from(916.080340,3+) index(4668)
Title: Elution from: 46.798 to 46.798 scan no 3674 cid35.00 polarity:+:m1s



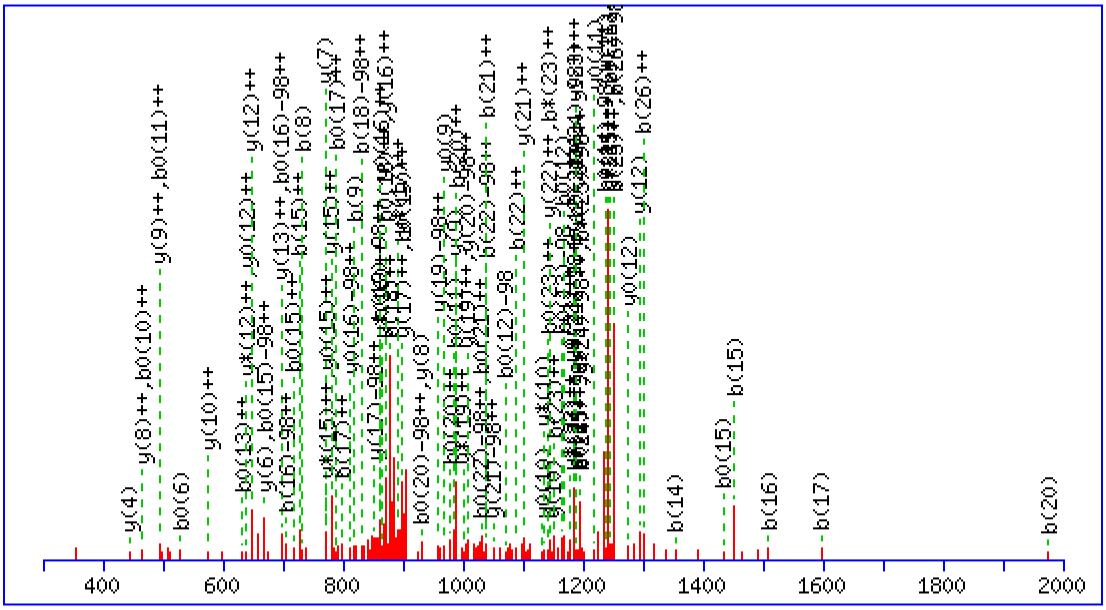
Monoisotopic mass of neutral peptide Mr(calc): 2745.2205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.05
Matched b ions: b(7)-98, b(9), b(10), b(12), b(12)++, b(13)-98, b(13)-98++, b(14), b(14)-98, b(15), b(15)++, b(16)-98++, b(18)++, b(19)-98++, b(20)++, b(21)-98++, b(23)++, b(24)++, b(25)++, b(25)-98++, b(26)-98++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(12)++, y(12), y(13)++, y(15)++, y(17)++, y(20)++, y(23)++, y(24)-98++, y(24)++, y(25)-98++

Peptide No.1055

TASISSSPSEGTPAVGSYGCTPQSLPK
Confirmed sites: @T:12
Ambiguous sites:

MS/MS Fragmentation of **TASISSSPSEGTPAVGSYGCTPQSLPK**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 6473: 2745.218298 from(916.080042,3+) index(5431)
Title: Elution from: 46.716 to 46.716 scan no 3869 cid35.00 polarity:+:m1s



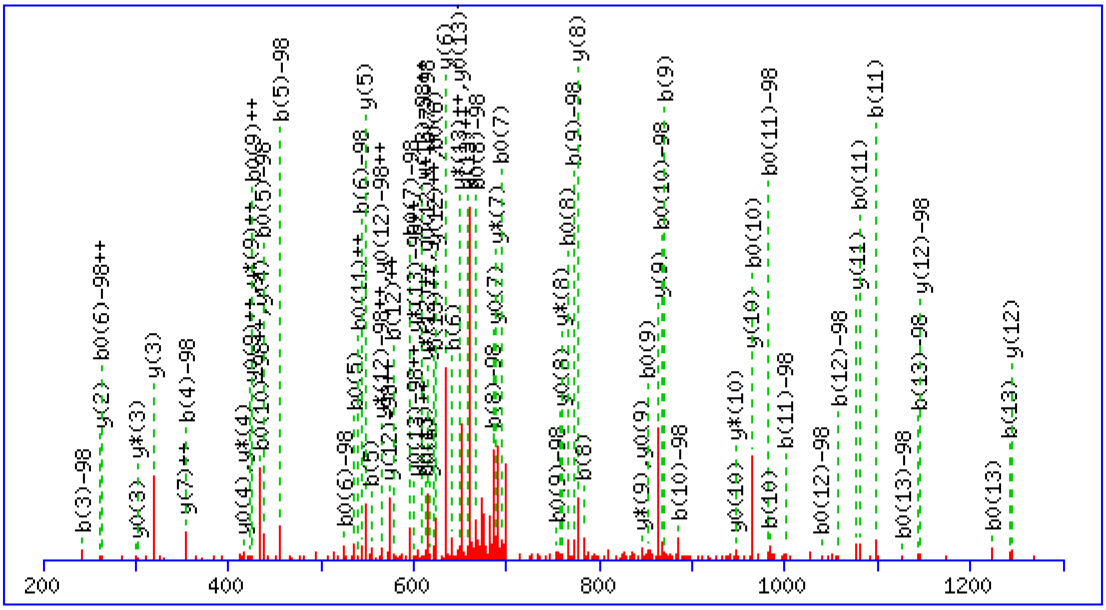
Monoisotopic mass of neutral peptide Mr(calc): 2745.2205
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 2.5e-005
Matched b ions: b(8), b(9), b(12), b(14), b(15), b(15)++, b(16), b(16)-98++, b(17), b(17)++, b(18)++, b(18)-98++, b(19)-98++, b(20), b(20)++, b(21)++, b(22)-98++, b(22)++, b(23)++, b(24)++, b(25)++, b(26)-98++, b(26)++
Matched y ions: y(4), y(6), y(7), y(8)++, y(8), y(9)++, y(9), y(10), y(10)++, y(11), y(12)++, y(12), y(13)++, y(15)++, y(16)++, y(17)++, y(17)-98++, y(19)++, y(19)-98++, y(20)-98++, y(21)++, y(21)-98++, y(22)++, y(23)++, y(24)-98++, y(24)++

Peptide No.1056

TASLTSAASIDGSR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TASLTSAASIDGSR**
Found in **NDRG2_MOUSE** in **SwissProt**, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3191: 1415.629706 from(708.822129,2+) index(1494)
Title: Elution from: 38.995 to 38.995 scan no 3012 cid35.00 polarity:+



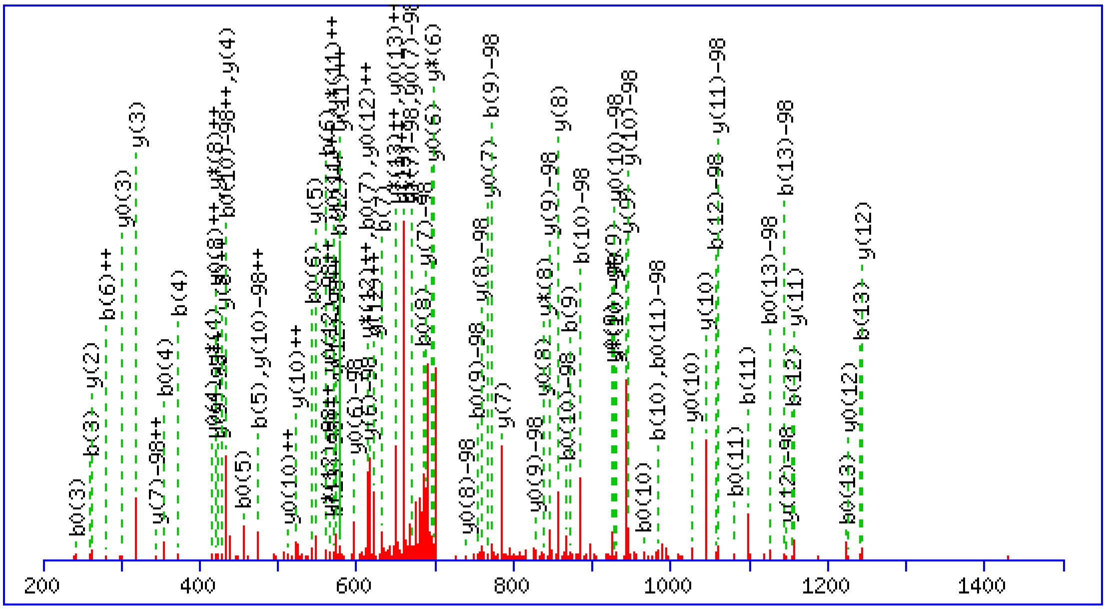
Monoisotopic mass of neutral peptide Mr(calc): 1415.6293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 76 **Expect:** 1.2e-007
Matched b ions: b(3)-98, b(4)-98, b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(8), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11), b(11)-98, b(12)-98, b(12)++, b(13)-98, b(13), b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(8), y(9), y(10), y(11), y(12), y(12)-98++, y(12)-98, y(12)++, y(13)-98++, y(13)++

Peptide No.1057

TASLTSAASIDGSR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **TASLTSAASIDGSR**
Found in **NDRG2_MOUSE** in **SwissProt**, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 3189: 1415.628696 from(708.821624,2+) index(1316)
Title: Elution from: 37.058 to 37.058 scan no 2773 cid35.00 polarity:+



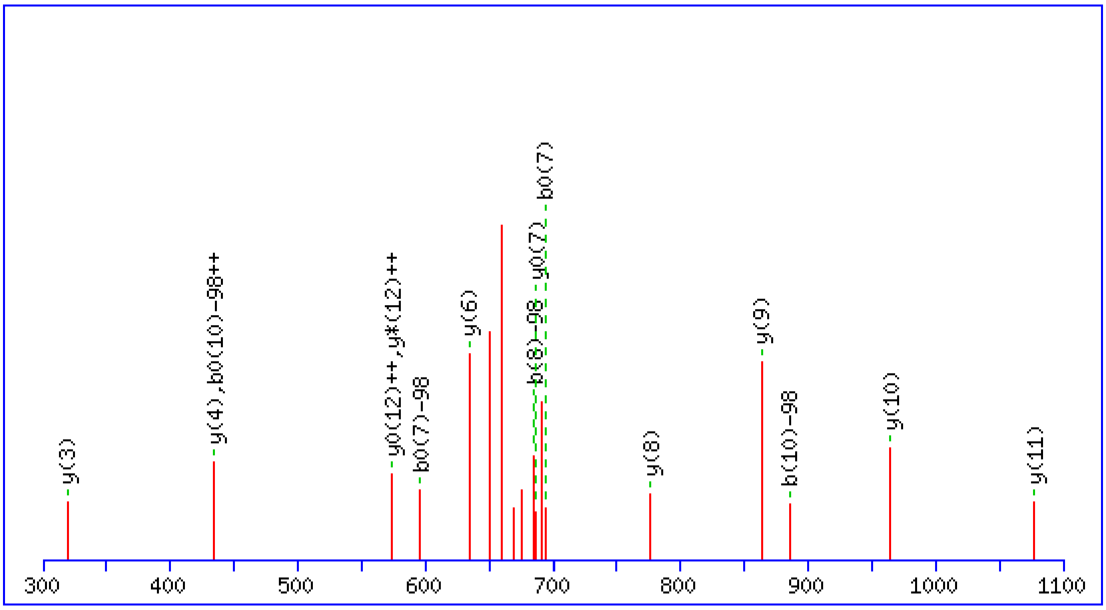
Monoisotopic mass of neutral peptide Mr(calc): 1415.6293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 78 **Expect:** 7.3e-008
Matched b ions: b(3), b(4), b(5), b(6)++, b(6), b(7), b(9)-98, b(9), b(10)-98, b(10), b(11), b(12), b(12)-98, b(12)++, b(13), b(13)-98, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(7), y(7)-98, y(7)-98++, y(8), y(8)-98, y(8)++, y(9), y(9)-98, y(9)-98++, y(10), y(10)-98++, y(10)-98, y(10)++, y(11), y(11)-98, y(11)++, y(12), y(12)++, y(12)-98++, y(12)-98, y(13)++

Peptide No.1058

TASLTSAASIDGSR
Confirmed sites:
Ambiguous sites: @T:1orS:3

MS/MS Fragmentation of **TASLTSAASIDGSR**
Found in **NDRG2_MOUSE** in **SwissProt**, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2573: 1415.628014 from(708.821283,2+) index(1679)
Title: Elution from: 31.377 to 31.377 scan no 2819 cid35.00 polarity:+



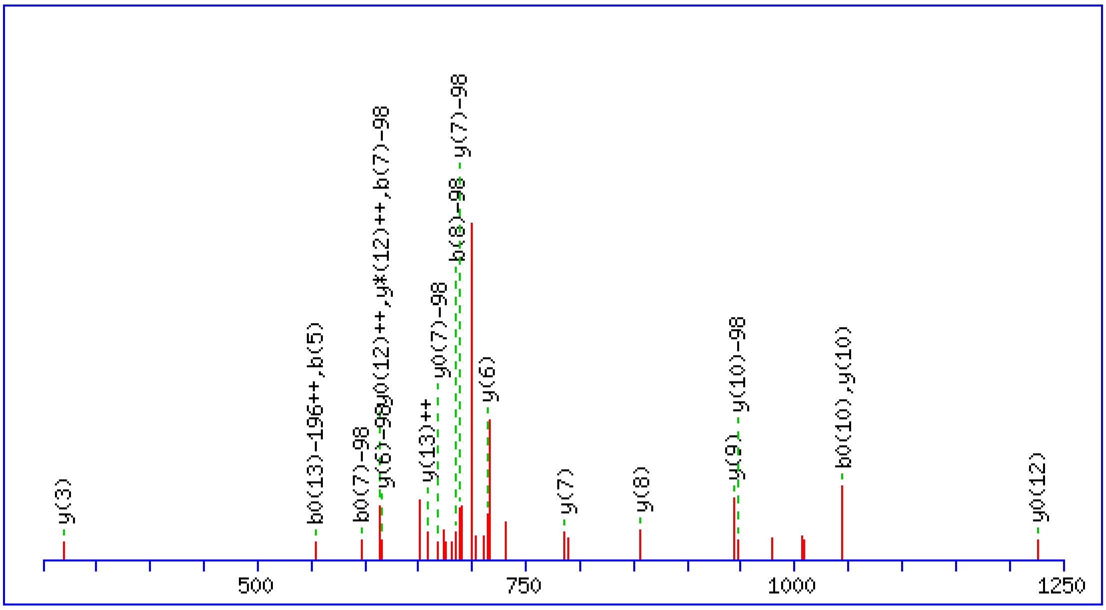
Monoisotopic mass of neutral peptide Mr(calc): 1415.6293
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 2.3e-006
Matched b ions: b(8)-98, b(10)-98
Matched y ions: y(3), y(4), y(6), y(8), y(9), y(10), y(11)

Peptide No.1059

TASLTSAASIDGSR
Confirmed sites: @T:1,@S:9
Ambiguous sites:

MS/MS Fragmentation of **TASLTSAASIDGSR**
Found in **NDRG2_MOUSE** in **SwissProt**, Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1

Match to Query 2946: 1495.594090 from(748.804321,2+) index(1856)
Title: Elution from: 32.973 to 32.973 scan no 3035 cid35.00 polarity:+



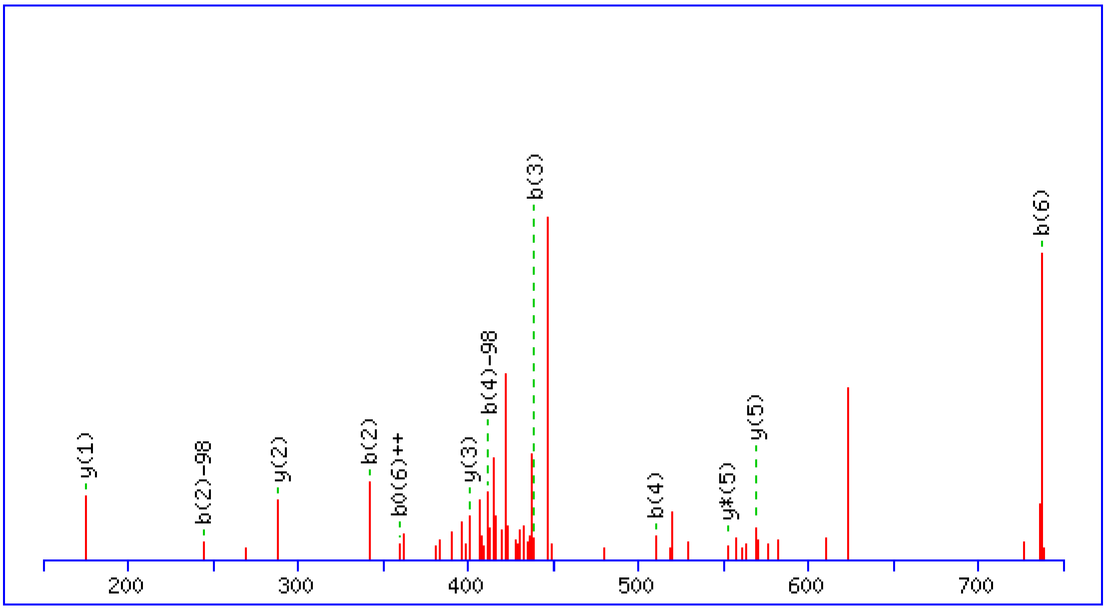
Monoisotopic mass of neutral peptide Mr(calc): 1495.5957
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.0098
Matched b ions: b(5), b(7)-98, b(8)-98
Matched y ions: y(3), y(6)-98, y(6), y(7), y(7)-98, y(8), y(9), y(10), y(10)-98, y(13)++

Peptide No.1060

TCPAIIR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of **TCPAIIR**
Found in **RASL2_MOUSE** in **SwissProt**, Ras GTPase-activating protein 4 OS=Mus musculus GN=Rasa4 PE=2 SV=1

Match to Query 545: 909.414156 from(455.714354,2+) index(4645)
Title: Elution from: 46.460 to 46.460 scan no 3636 cid35.00 polarity:+:m1s



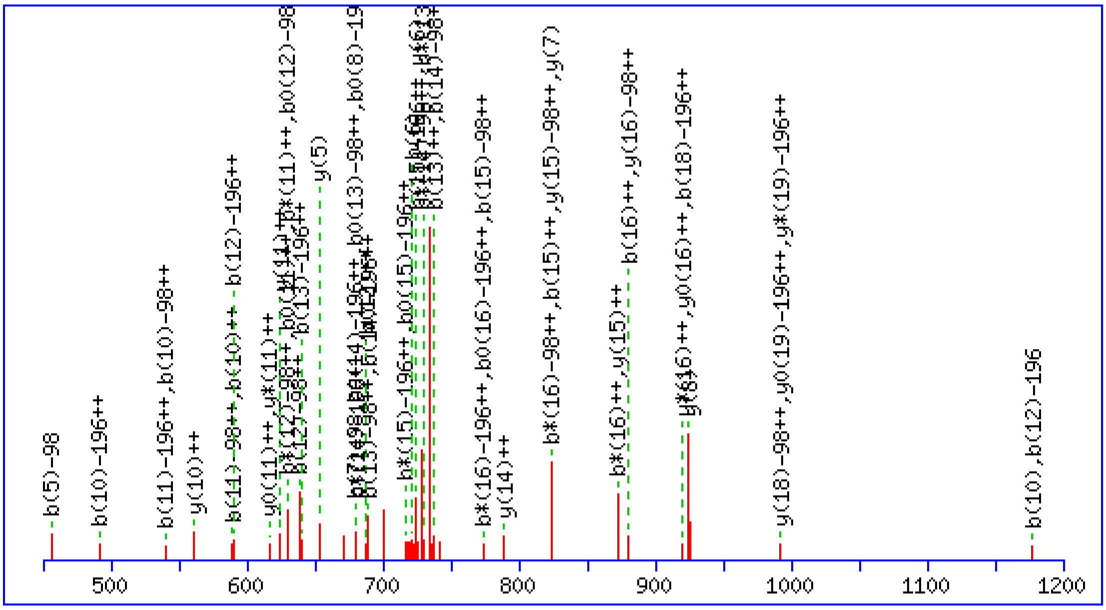
Monoisotopic mass of neutral peptide Mr(calc): 909.4143
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 15 **Expect:** 0.048
Matched b ions: b(2), b(2)-98, b(3), b(4), b(4)-98, b(6)
Matched y ions: y(1), y(2), y(3), y(5)

Peptide No.1061

TDGSISGDRQPVTVADYISR
Confirmed sites: @S:4,@S:6
Ambiguous sites:

MS/MS Fragmentation of **TDGSISGDRQPVTVADYISR**
Found in **FXR2_MOUSE** in **SwissProt**, Fragile X mental retardation syndrome-related protein 2 OS=Mus musculus GN=Fxr2 PE=1 SV=1

Match to Query 5968: 2295.977955 from(766.333261,3+) index(6654)
Title: Elution from: 47.116 to 47.116 scan no 4855 cid35.00 polarity:+:m1s



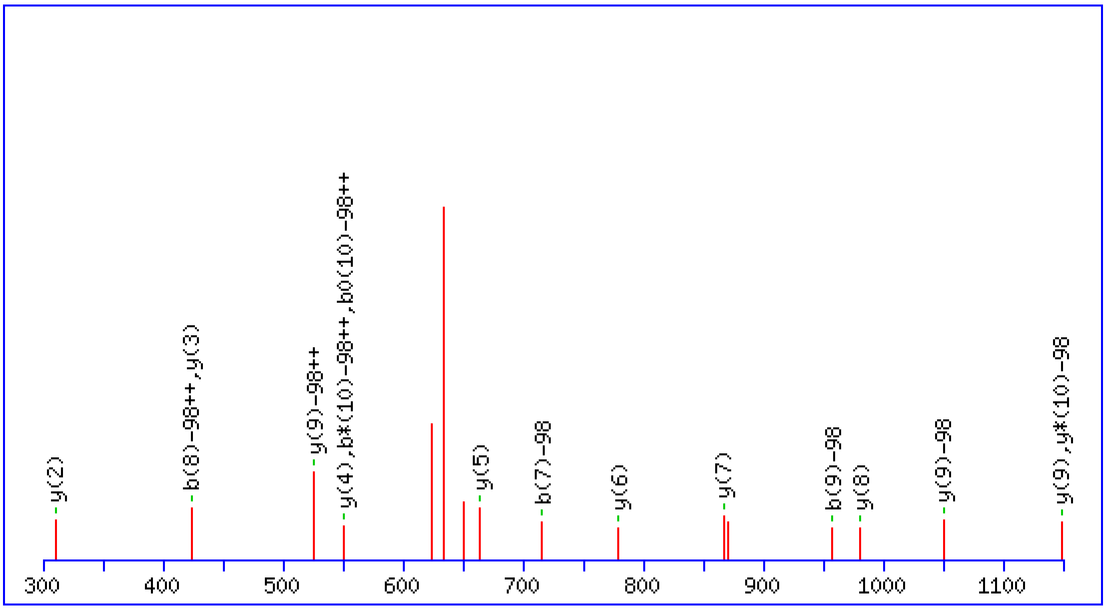
Monoisotopic mass of neutral peptide Mr(calc): 2295.9774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 40 **Expect:** 0.00072
Matched b ions: b(5)-98, b(6), b(7)-98, b(10), b(10)-196++, b(10)-98++, b(10)++, b(11)-196++, b(11)-98++, b(12)-98++, b(12)-196, b(12)-196++, b(12)++, b(13)-98++, b(13)-196++, b(13)++, b(14)-196++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(16)++, b(18)-196++
Matched y ions: y(5), y(6), y(7), y(8), y(10)++, y(11)++, y(14)++, y(15)-98++, y(15)++, y(16)-98++, y(18)-98++

Peptide No.1062

TDSDSDLQLYK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TDSDSDLQLYK**
Found in **AMPD2_MOUSE** in **SwissProt**, AMP deaminase 2 OS=Mus musculus GN=Ampd2 PE=1 SV=1

Match to Query 2117: 1363.554136 from(682.784344,2+) index(1665)
Title: Elution from: 34.429 to 34.429 scan no 3085 cid35.00 polarity:+



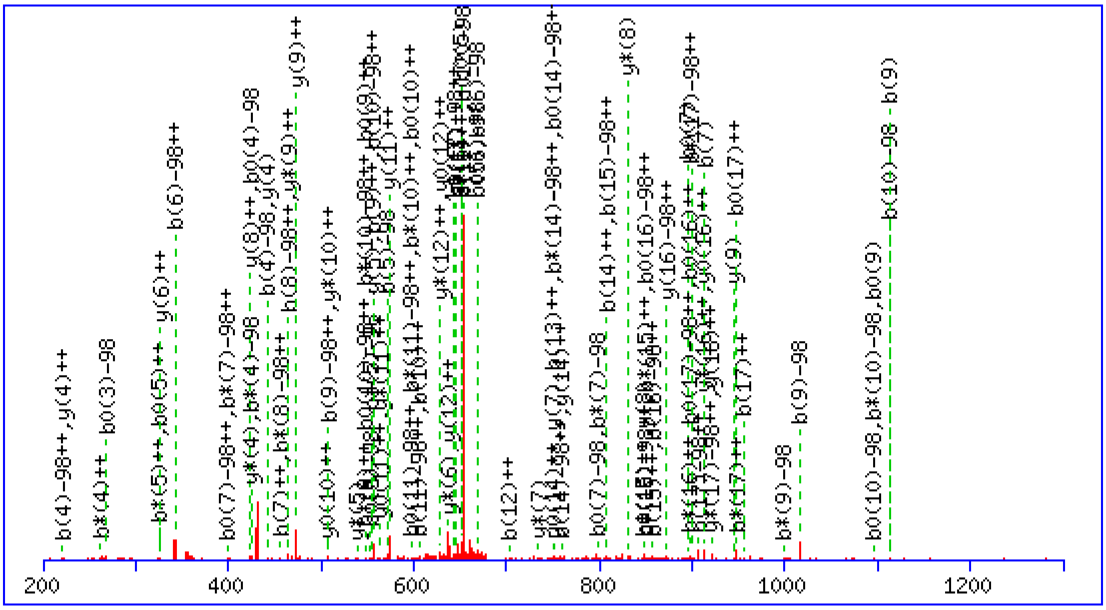
Monoisotopic mass of neutral peptide Mr(calc): 1363.5544
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 **Expect:** 4e-007
Matched b ions: b(7)-98, b(8)-98++, b(9)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9)-98++, y(9)-98, y(9)

Peptide No.1063

TDSREDEISPPPPNPVVK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TDSREDEISPPPPNPVVK**
Found in **KAP0_MOUSE** in **SwissProt**, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 5242: 2055.952575 from(686.324801,3+) index(4852)
Title: Elution from: 38.374 to 38.374 scan no 2934 cid35.00 polarity:+:m1s



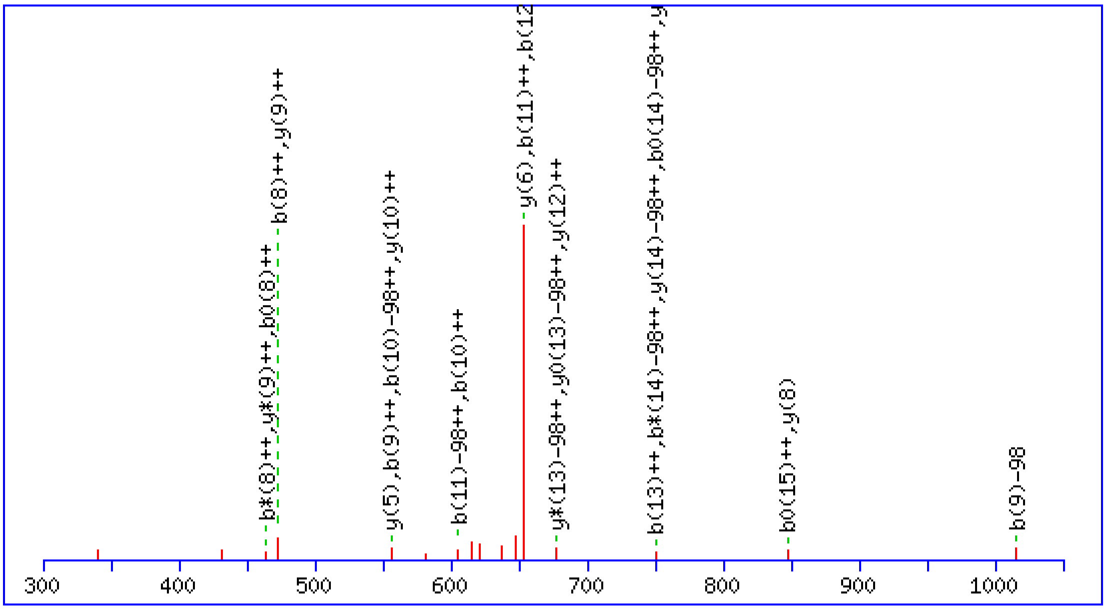
Monoisotopic mass of neutral peptide Mr(calc): 2055.9514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0009
Matched b ions: b(4)-98++, b(4)-98, b(5)-98, b(5), b(6)-98++, b(7), b(7)++, b(8)-98++, b(9)-98, b(9)++, b(9), b(9)-98++, b(10)-98++, b(10)-98, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(17)-98++, b(17)++
Matched y ions: y(4)++, y(4), y(5), y(6), y(6)++, y(7), y(8), y(8)++, y(9)++, y(9), y(11)++, y(12)++, y(14)++, y(16)++, y(16)-98++

Peptide No.1064

TDSREDEISPPPPNPVVK
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **TDSREDEISPPPPNPVVK**
Found in **KAP0_MOUSE** in **SwissProt**, cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Mus musculus GN=Prkar1a PE=1 SV=3

Match to Query 5164: 2055.951642 from(686.324490,3+) index(5229)
Title: Elution from: 30.188 to 30.188 scan no 2662 cid35.00 polarity:+:m1s



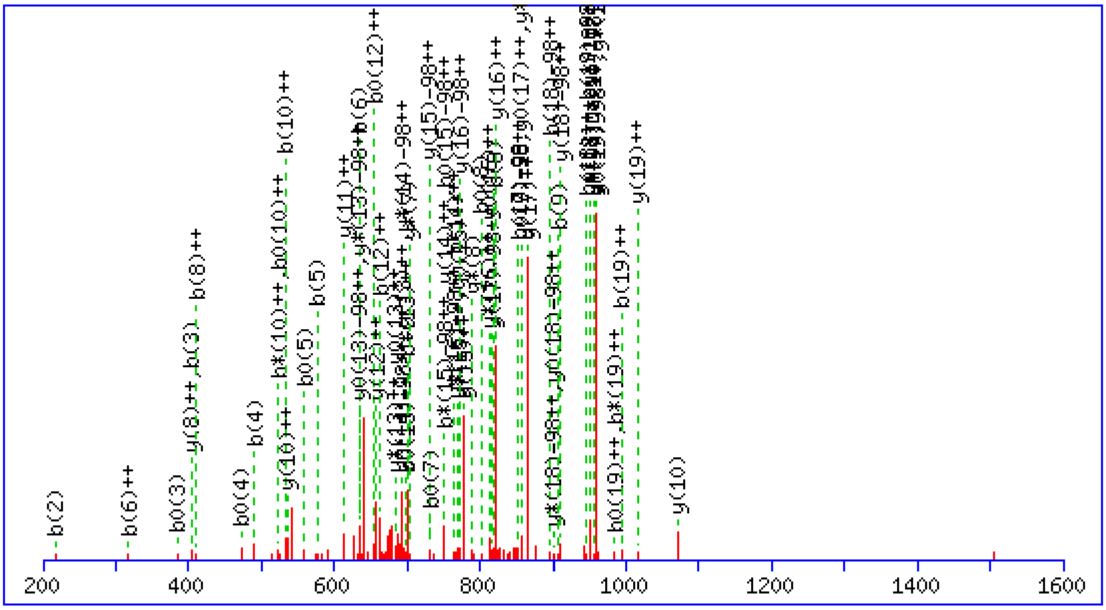
Monoisotopic mass of neutral peptide Mr(calc): 2055.9514
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.018
Matched b ions: b(8)++, b(9)-98, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(13)++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(10)++, y(12)++, y(14)-98++

Peptide No.1065

TDWSSGDASRPSSDSADSPK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **TDWSSGDASRPSSDSADSPK**
Found in **ARHGC_MOUSE** in **SwissProt**, Rho guanine nucleotide exchange factor 12 OS=Mus musculus GN=Arhgef12 PE=1 SV=2

Match to Query 5485: 2131.831299 from(711.617709,3+) index(4455)
Title: Elution from: 22.940 to 22.940 scan no 1673 cid35.00 polarity:+:m1s



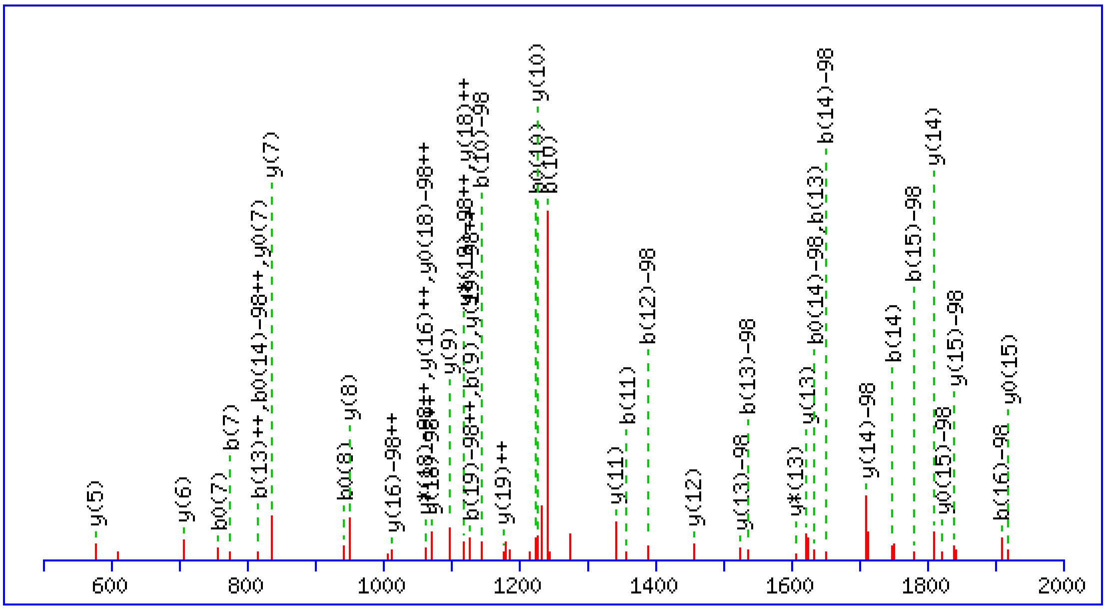
Monoisotopic mass of neutral peptide Mr(calc): 2131.8331
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 56 **Expect:** 1.3e-005
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(6), b(8)++, b(8), b(9), b(10)++, b(12)++, b(14)++, b(17)-98++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(8)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++

Peptide No.1066

TEDGGWEWSDDEFDEESEEGR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **TEDGGWEWSDDEFDEESEEGR**
Found in **OXSR1_MOUSE** in **SwissProt**, Serine/threonine-protein kinase OSR1 OS=Mus musculus GN=Oxsr1 PE=1 SV=1

Match to Query 5346: 2582.881706 from(1292.448129,2+) index(5742)
Title: Elution from: 53.987 to 53.987 scan no 5354 cid35.00 polarity:+:m1s



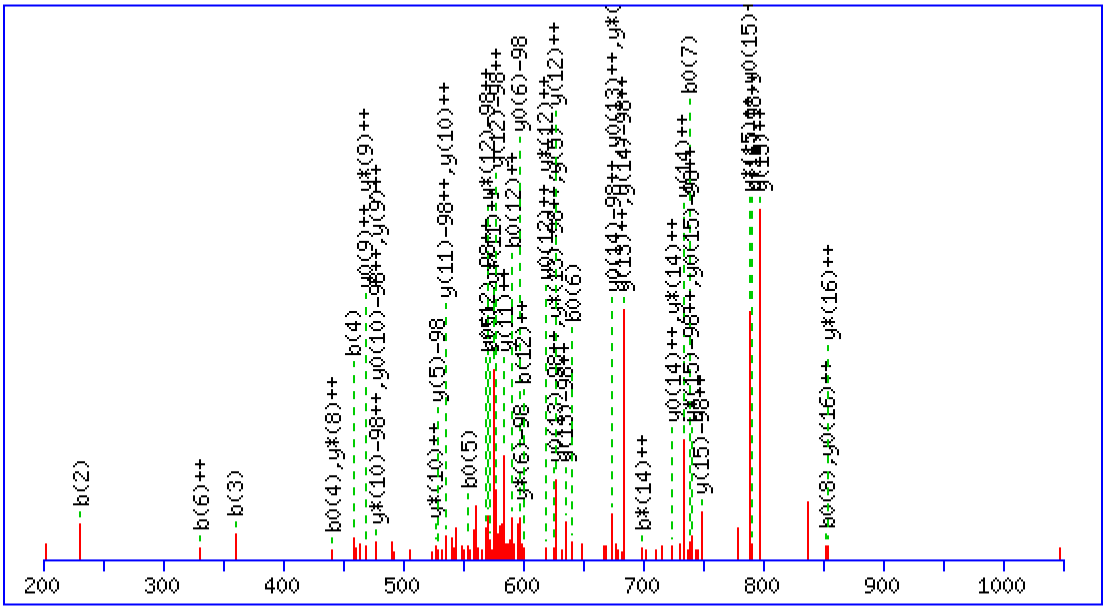
Monoisotopic mass of neutral peptide Mr(calc): 2582.8871
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 69 **Expect:** 3.1e-007
Matched b ions: b(7), b(9), b(10), b(10)-98, b(11), b(12)-98, b(13)-98, b(13)++, b(13), b(14)-98, b(14), b(15)-98, b(16)-98, b(19)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12), y(13)-98, y(13), y(14)-98, y(14), y(15)-98, y(16)++, y(16)-98++, y(18)-98++, y(18)++, y(19)-98++, y(19)++

Peptide No.1067

TEEVLSPDGSPSKSPSK
Confirmed sites:
Ambiguous sites: @S:14orS:16

MS/MS Fragmentation of **TEEVLSPDGSPSKSPSK**
Found in **ADDG_MOUSE** in **SwissProt**, Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=2

Match to Query 4176: 1823.818764 from(608.946864,3+) index(674)
Title: Elution from: 22.236 to 22.236 scan no 1541 cid35.00 polarity:+



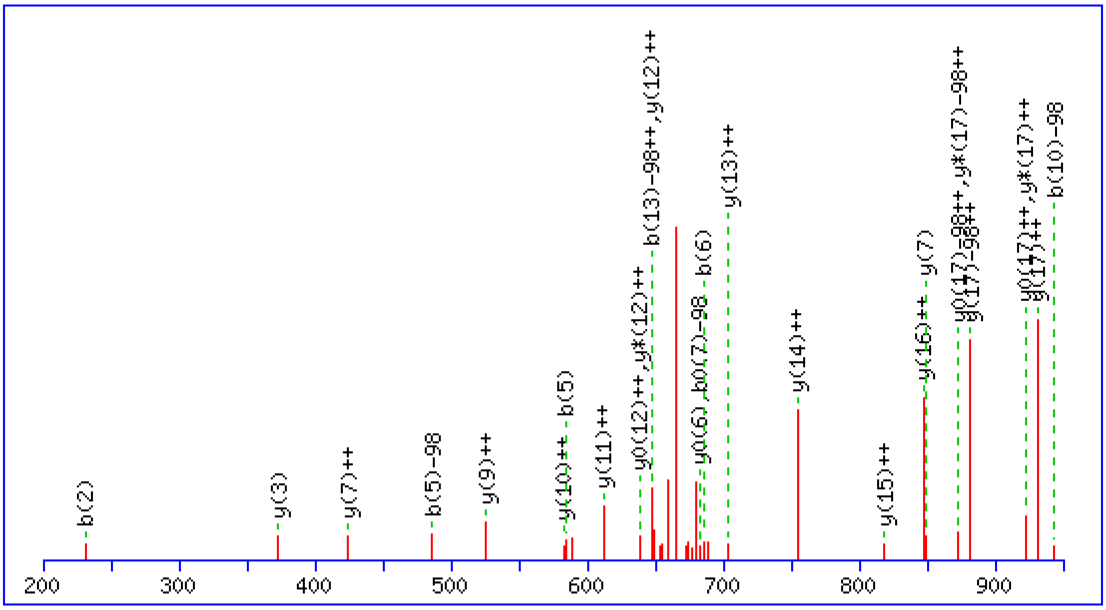
Monoisotopic mass of neutral peptide Mr(calc): 1823.8190
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0096
Matched b ions: b(2), b(3), b(4), b(5), b(6)++, b(12)++, b(16)-98++
Matched y ions: y(5), y(5)-98, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++

Peptide No.1068

TESGETLAGDSDFSLKPEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TESGETLAGDSDFSLKPEK**
Found in **TGON1_MOUSE** in **SwissProt**, Trans-Golgi network integral membrane protein 1 OS=Mus musculus GN=Tgoln1 PE=1 SV=1

Match to Query 5266: 2089.906791 from(697.642873,3+) index(6088)
Title: Elution from: 38.926 to 38.926 scan no 3827 cid35.00 polarity:+:m1s



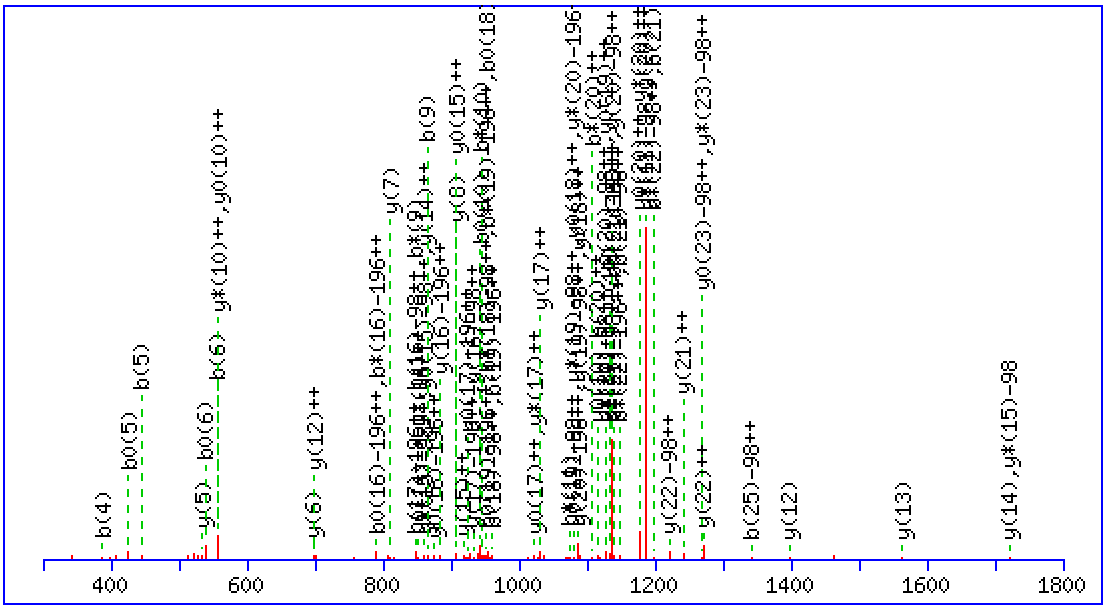
Monoisotopic mass of neutral peptide Mr(calc): 2089.9093
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 68 **Expect:** 1e-006
Matched b ions: b(2), b(5)-98, b(5), b(6), b(10)-98, b(13)-98++
Matched y ions: y(3), y(7)++, y(7), y(9)++, y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(17)-98++

Peptide No.1069

TGDLGIPPNPEDRSPSPEPIYNSEGK
Confirmed sites: @S:14,@S:16
Ambiguous sites:

MS/MS Fragmentation of **TGDLGIPPNPEDRSPSPEPIYNSEGK**
Found in **SF01_MOUSE** in **SwissProt**, Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=6

Match to Query 5822: 2925.242526 from(976.088118,3+) index(5480)
Title: Elution from: 42.093 to 42.093 scan no 4062 cid35.00 polarity:+:m1s



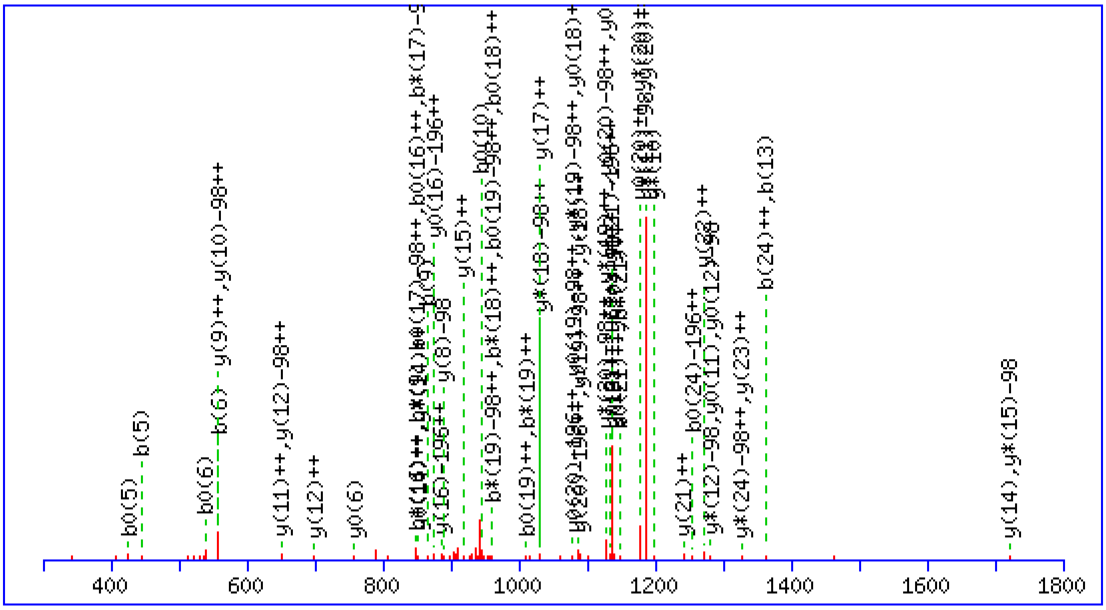
Monoisotopic mass of neutral peptide Mr(calc): 2925.2470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 1.2e-005
Matched b ions: b(4), b(5), b(6), b(9), b(16)-98++, b(17)-196++, b(18)-98++, b(19)-196++, b(20)++, b(21)-98++, b(21)++, b(25)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(10), y(12), y(12)++, y(13), y(14), y(14)++, y(15)++, y(16)-196++, y(16)-98++, y(17)++, y(17)-196++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(20)-196++, y(21)++, y(22)++, y(22)-98++

Peptide No.1070

TGDLGIPPNPEDRSPSPEPIYNSEGK
Confirmed sites: @S:14
Ambiguous sites: @Y:21orS:23

MS/MS Fragmentation of **TGDLGIPPNPEDRSPSPEPIYNSEGK**
Found in **SF01_MOUSE** in **SwissProt**, Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=6

Match to Query 6843: 2925.239718 from(976.087182,3+) index(6606)
Title: Elution from: 46.071 to 46.071 scan no 4736 cid35.00 polarity:+:m1s



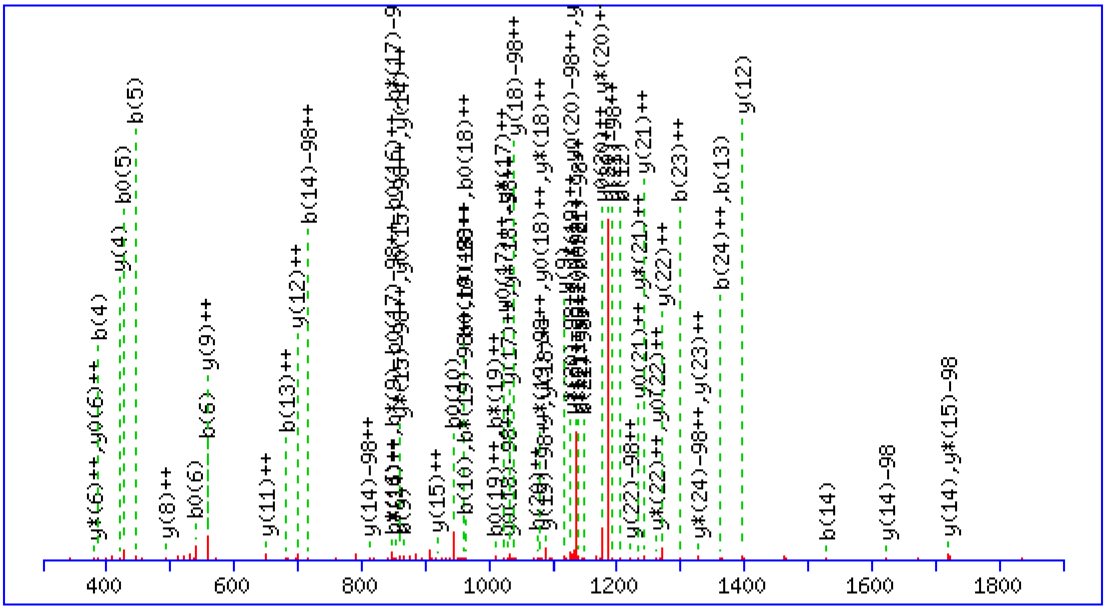
Monoisotopic mass of neutral peptide Mr(calc): 2925.2470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S23 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 3.7e-005
Matched b ions: b(5), b(6), b(9), b(13), b(24)++
Matched y ions: y(8)-98, y(9)++, y(10)-98++, y(11)++, y(12)-98++, y(12)++, y(14), y(15)++, y(16)-196++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(20)-196++, y(21)++, y(22)++, y(23)++

Peptide No.1071

TGDLGIPPNPEDRSPSPEPIYNSEGK
Confirmed sites: @S:14,@Y:21
Ambiguous sites:

MS/MS Fragmentation of **TGDLGIPPNPEDRSPSPEPIYNSEGK**
Found in **SF01_MOUSE** in **SwissProt**, Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=6

Match to Query 5649: 2925.244416 from(976.088748,3+) index(5275)
Title: Elution from: 42.296 to 42.296 scan no 4093 cid35.00 polarity:+:m1s



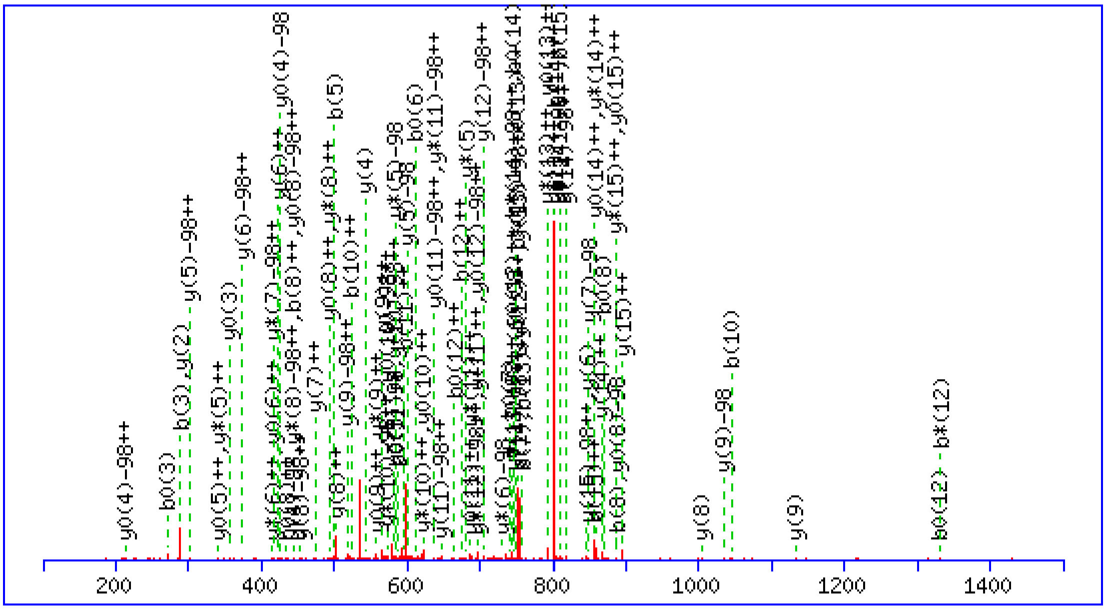
Monoisotopic mass of neutral peptide Mr(calc): 2925.2470
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y21 : Phospho (Y)
Ions Score: 57 **Expect:** 1.8e-005
Matched b ions: b(4), b(5), b(6), b(9), b(10), b(12), b(13), b(13)++, b(14), b(14)-98++, b(20)++, b(21)-98++, b(23)++, b(24)++
Matched y ions: y(4), y(8)++, y(9)++, y(9), y(11)++, y(12), y(12)++, y(14)-98, y(14), y(14)-98++, y(14)++, y(15)++, y(17)++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)++, y(21)-98++, y(22)++, y(22)-98++, y(23)++

Peptide No.1072

TGEPDEEEGTFRSSIR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4768: 1888.784877 from(630.602235,3+) index(4546)
Title: Elution from: 35.065 to 35.065 scan no 2522 cid35.00 polarity:+:m1s



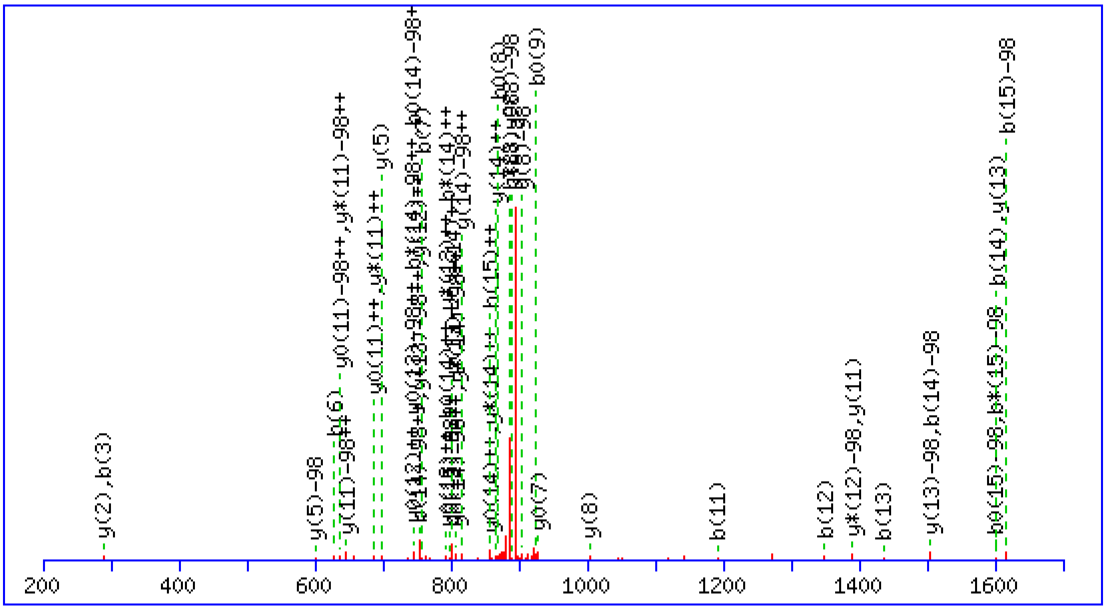
Monoisotopic mass of neutral peptide Mr(calc): 1888.7840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0094
Matched b ions: b(3), b(5), b(7), b(8), b(8)++, b(10), b(10)++, b(11)++, b(12)++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++
Matched y ions: y(2), y(4)-98, y(4), y(5)-98++, y(5)-98, y(6)-98++, y(6)++, y(6), y(6)-98, y(7)++, y(7)-98, y(8)-98++, y(8), y(8)++, y(9), y(9)++, y(9)-98++, y(9)-98, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.1073

TGEPDEEEGTFRSSIR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4403: 1888.781808 from(945.398180,2+) index(1264)
Title: Elution from: 27.535 to 27.535 scan no 2262 cid35.00 polarity:+



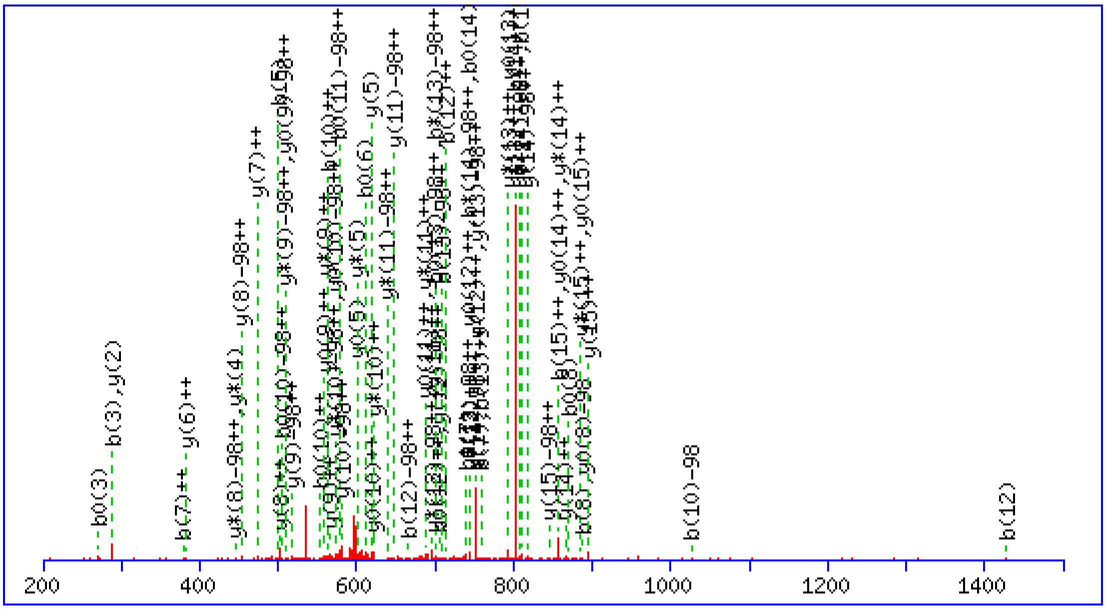
Monoisotopic mass of neutral peptide Mr(calc): 1888.7840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 8.8e-006
Matched b ions: b(3), b(6), b(7), b(8), b(11), b(12), b(13), b(14)-98++, b(14)-98, b(14), b(14)++, b(15)-98, b(15)++
Matched y ions: y(2), y(5), y(5)-98, y(8), y(8)-98, y(11)-98++, y(11), y(12)++, y(13)-98++, y(13)-98, y(13), y(13)++, y(14)-98++, y(14)++

Peptide No.1074

TGEPDEEEGTFRSSIR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4136: 1888.784835 from(630.602221,3+) index(948)
Title: Elution from: 34.988 to 34.988 scan no 2397 cid35.00 polarity:+



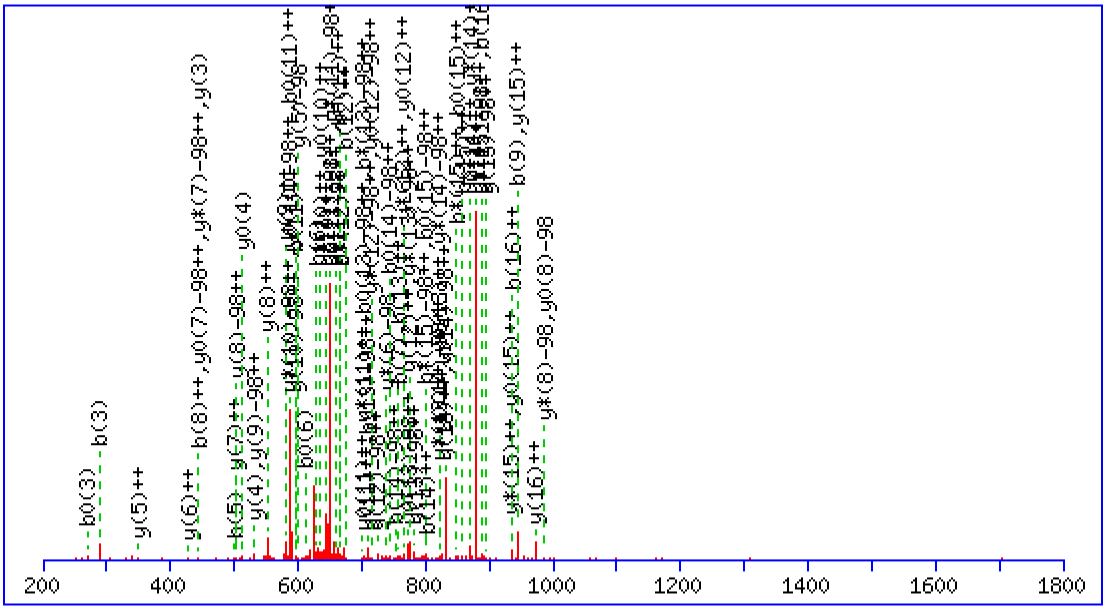
Monoisotopic mass of neutral peptide Mr(calc): 1888.7840
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.013
Matched b ions: b(3), b(5), b(7)++, b(7), b(8), b(10)-98, b(10)++, b(12), b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(15)-98++
Matched y ions: y(2), y(5), y(6)++, y(7)++, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.1075

TGEPDEEEGTFRSSIRR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIRR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 5219: 2044.886301 from(682.636043,3+) index(4182)
Title: Elution from: 31.235 to 31.235 scan no 2045 cid35.00 polarity:+:m1s



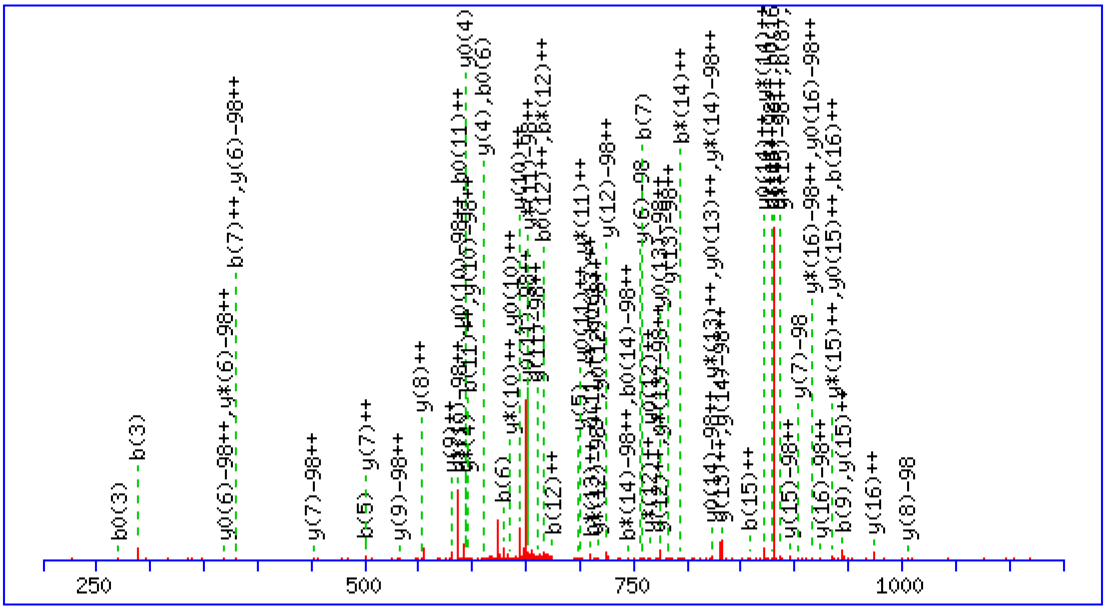
Monoisotopic mass of neutral peptide Mr(calc): 2044.8851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0017
Matched b ions: b(3), b(5), b(6), b(7), b(8)++, b(8), b(9), b(11)++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++
Matched y ions: y(3), y(4), y(5)++, y(5)-98, y(6)++, y(7)++, y(8)-98++, y(8)++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)++

Peptide No.1076

TGEPDEEEGTFRSSIRR
Confirmed sites: @S:14
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIRR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4533: 2044.886367 from(682.636065,3+) index(3557)
Title: Elution from: 31.135 to 31.135 scan no 1938 cid35.00 polarity:+:m1s



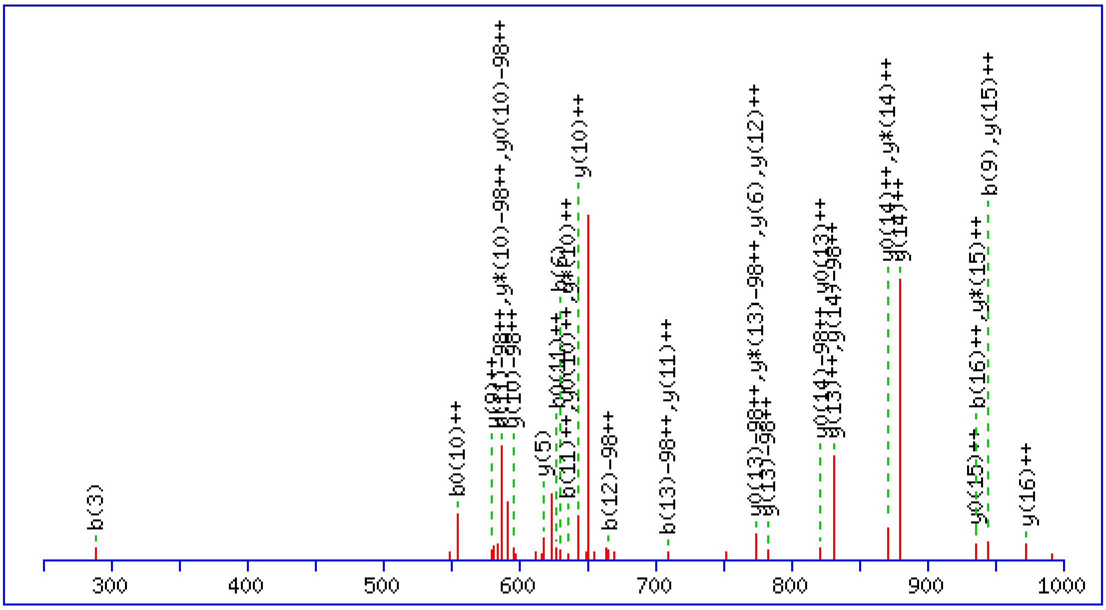
Monoisotopic mass of neutral peptide Mr(calc): 2044.8851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 **Expect:** 0.0028
Matched b ions: b(3), b(5), b(6), b(7)++, b(7), b(8), b(9), b(11)++, b(12)++, b(15)++, b(16)++
Matched y ions: y(4), y(5), y(6)-98++, y(6)-98, y(7)++, y(7)-98++, y(7)-98, y(8)-98, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++

Peptide No.1077

TGEPDEEEGTFRSSIRR
Confirmed sites: @T:10
Ambiguous sites:

MS/MS Fragmentation of **TGEPDEEEGTFRSSIRR**
Found in **PLM_MOUSE** in **SwissProt**, Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1

Match to Query 4327: 2044.882365 from(682.634731,3+) index(3627)
Title: Elution from: 23.924 to 23.924 scan no 1647 cid35.00 polarity:+:m1s



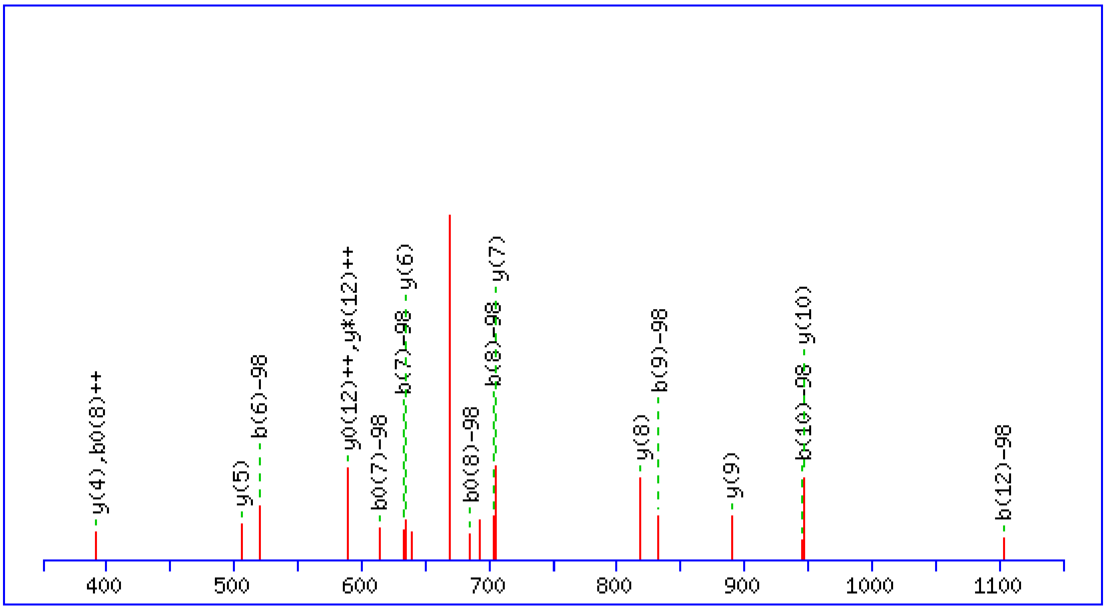
Monoisotopic mass of neutral peptide Mr(calc): 2044.8851
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 7.3e-005
Matched b ions: b(3), b(6), b(9), b(11)-98++, b(11)++, b(12)-98++, b(13)-98++, b(16)++
Matched y ions: y(5), y(6), y(9)++, y(10)++, y(10)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)++

Peptide No.1078

TGSYGALAEISASK
Confirmed sites:
Ambiguous sites: @T:1orS:3orY:4

MS/MS Fragmentation of **TGSYGALAEISASK**
Found in **MYPT1_MOUSE** in **SwissProt**, Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2

Match to Query 2666: 1433.643972 from(717.829262,2+) index(2619)
Title: Elution from: 41.389 to 41.389 scan no 4148 cid35.00 polarity:+



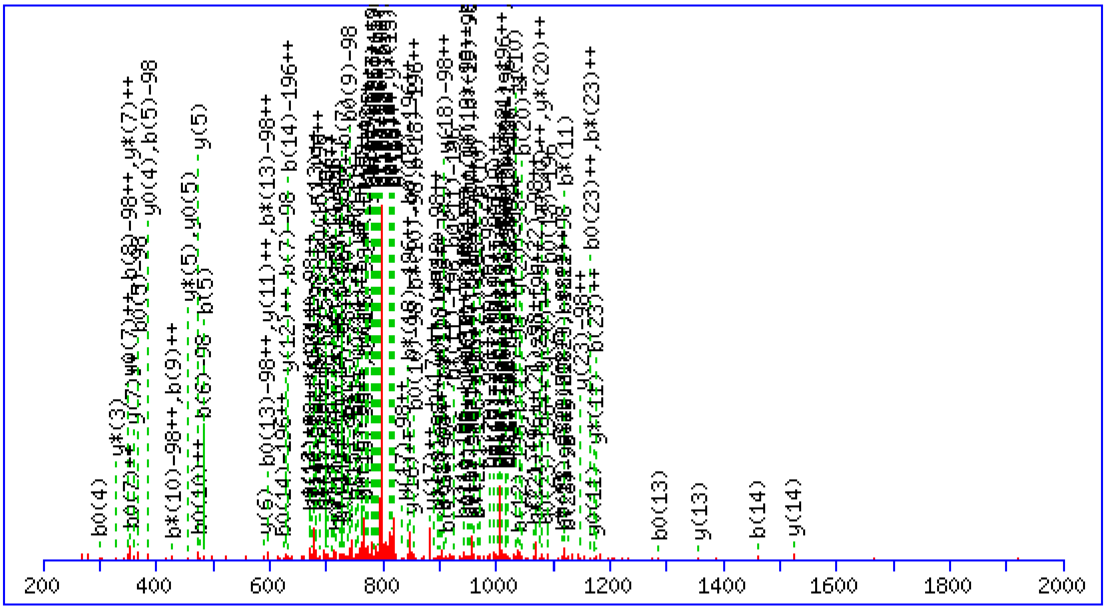
Monoisotopic mass of neutral peptide Mr(calc): 1433.6439
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 7.9e-007
Matched b ions: b(6)-98, b(7)-98, b(8)-98, b(9)-98, b(10)-98, b(12)-98
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)

Peptide No.1079

TGTGSPFAGNSPAREGEQDAGSLK
Confirmed sites: @S:5,@S:11
Ambiguous sites:

MS/MS Fragmentation of **TGTGSPFAGNSPAREGEQDAGSLK**
Found in **ZC3H4_MOUSE** in **SwissProt**, Zinc finger CCCH domain-containing protein 4 OS=Mus musculus GN=Zc3h4 PE=1 SV=2

Match to Query 5371: 2493.020091 from(832.013973,3+) index(4460)
Title: Elution from: 42.870 to 42.870 scan no 3284 cid35.00 polarity:+:m1s



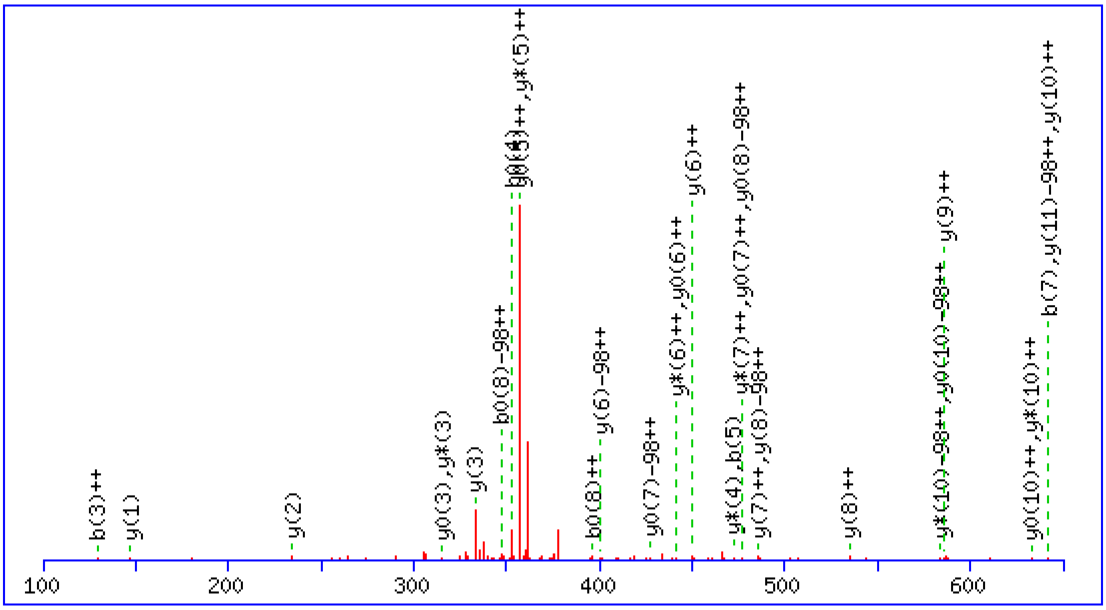
Monoisotopic mass of neutral peptide Mr(calc): 2493.0210
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 67 **Expect:** 1.5e-006
Matched b ions: b(5)-98, b(5), b(6)-98, b(7)-98, b(7), b(8), b(8)-98++, b(8)-98, b(9)++, b(10), b(11)-98, b(11)-196, b(12)-196, b(14), b(14)-196++, b(14)-98++, b(14)++, b(15)-98++, b(15)-196++, b(15)++, b(16)-196++, b(16)-98++, b(17)-196++, b(17)++, b(18)-98++, b(18)++, b(18)-196++, b(19)++, b(19)-98++, b(19)-196++, b(20)-98++, b(20)-196++, b(20)++, b(22)-98++, b(22)++, b(22)-196++, b(23)++, b(23)-98++, b(23)-196++
Matched y ions: y(5), y(6), y(7)++, y(7), y(9), y(10), y(11)++, y(12)++, y(13)++, y(13), y(14), y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(21)-196++, y(22)-196++, y(22)-98++, y(23)-98++

Peptide No.1080

TGVLTVASYRVSK
Confirmed sites: @S:8,@Y:9
Ambiguous sites:

MS/MS Fragmentation of **TGVLTVASYRVSK**
Found in **P4HA2_MOUSE** in **SwissProt**, Prolyl 4-hydroxylase subunit alpha-2 OS=Mus musculus GN=P4ha2 PE=2 SV=1

Match to Query 2596: 1539.714512 from(385.935904,4+) index(3478)
Title: Elution from: 20.379 to 20.379 scan no 1269 cid35.00 polarity:+:m1s



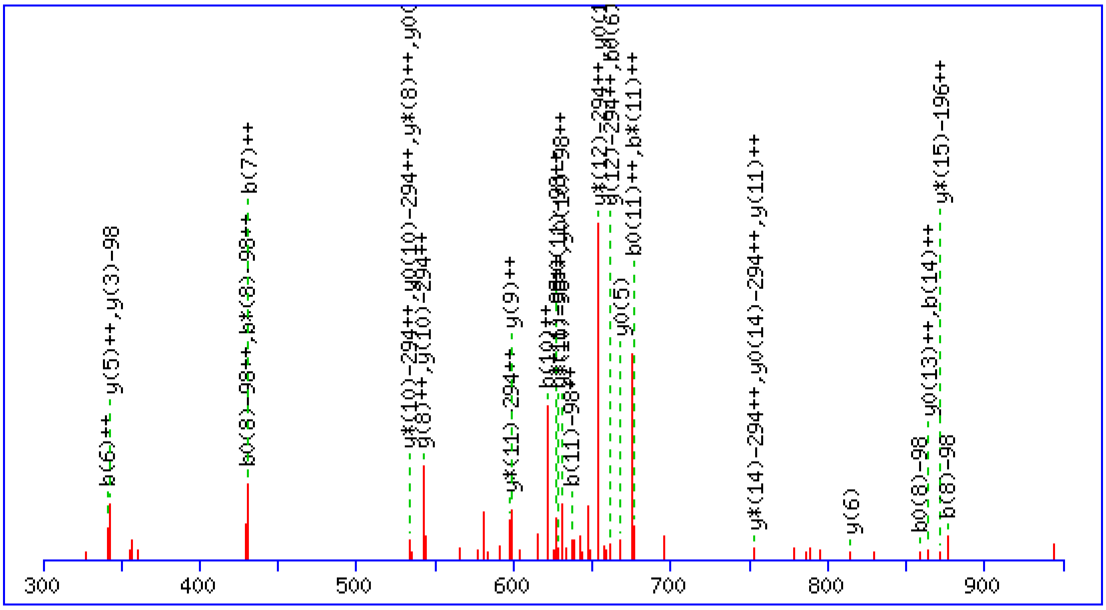
Monoisotopic mass of neutral peptide Mr(calc): 1539.7099
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y9 : Phospho (Y)
Ions Score: 21 **Expect:** 0.04
Matched b ions: b(3)++, b(5), b(7)
Matched y ions: y(1), y(2), y(3), y(6)++, y(6)-98++, y(7)++, y(8)++, y(8)-98++, y(9)++, y(10)++, y(11)-98++

Peptide No.1081

THAEIKTLSTQMNITK
Confirmed sites: @T:7,@T:15
Ambiguous sites: @S:9orT:10

MS/MS Fragmentation of **THAEIKTLSTQMNITK**
Found in **TITIN_MOUSE** in **SwissProt**, Titin OS=Mus musculus GN=Ttn PE=1 SV=1

Match to Query 4301: 2054.851275 from(685.957701,3+) index(4899)
Title: Elution from: 34.408 to 34.408 scan no 3128 cid35.00 polarity:+:m1s



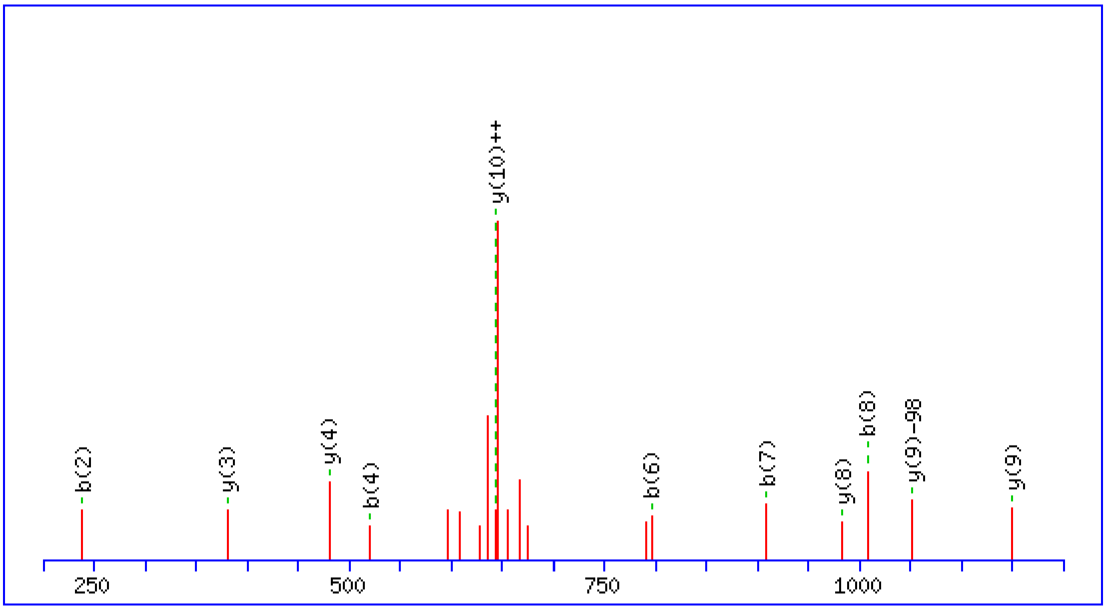
Monoisotopic mass of neutral peptide Mr(calc): 2054.8550
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.052
Matched b ions: b(6)++, b(7)++, b(8)-98, b(10)++, b(11)-98++, b(12)-196++, b(14)++
Matched y ions: y(3)-98, y(5)++, y(6), y(8)++, y(9)++, y(10)-294++, y(11)++, y(12)-294++

Peptide No.1082

THSDQFLVSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **THSDQFLVSFK**
Found in **ATPG_MOUSE** in **SwissProt**, ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1

Match to Query 2464: 1387.616270 from(694.815411,2+) index(2635)
Title: Elution from: 41.568 to 41.568 scan no 4172 cid35.00 polarity:+



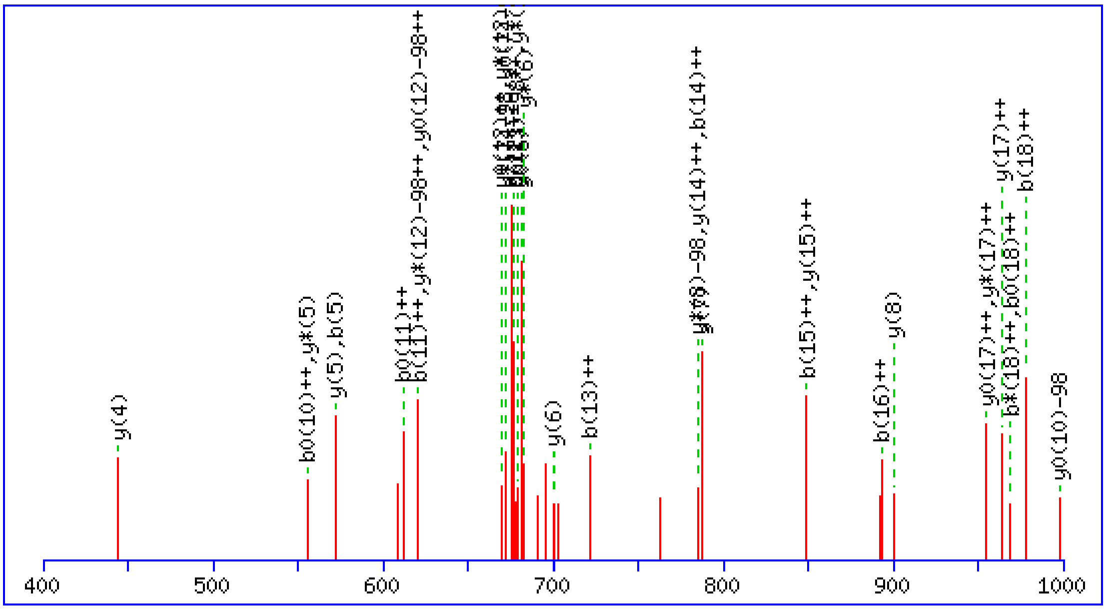
Monoisotopic mass of neutral peptide Mr(calc): 1387.6173
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0041
Matched b ions: b(2), b(4), b(6), b(7), b(8)
Matched y ions: y(3), y(4), y(8), y(9)-98, y(9), y(10)++

Peptide No.1083

TIDIEPDIETLLSQQSGNS
Confirmed sites: @S:19
Ambiguous sites:

MS/MS Fragmentation of **TIDIEPDIETLLSQQSGNS**
Found in **GPX1_MOUSE** in **SwissProt**, Glutathione peroxidase 1 OS=Mus musculus GN=Gpx1 PE=1 SV=2

Match to Query 4575: 2138.960427 from(713.994085,3+) index(5929)
Title: Elution from: 72.933 to 72.933 scan no 6585 cid35.00 polarity:+:m1s



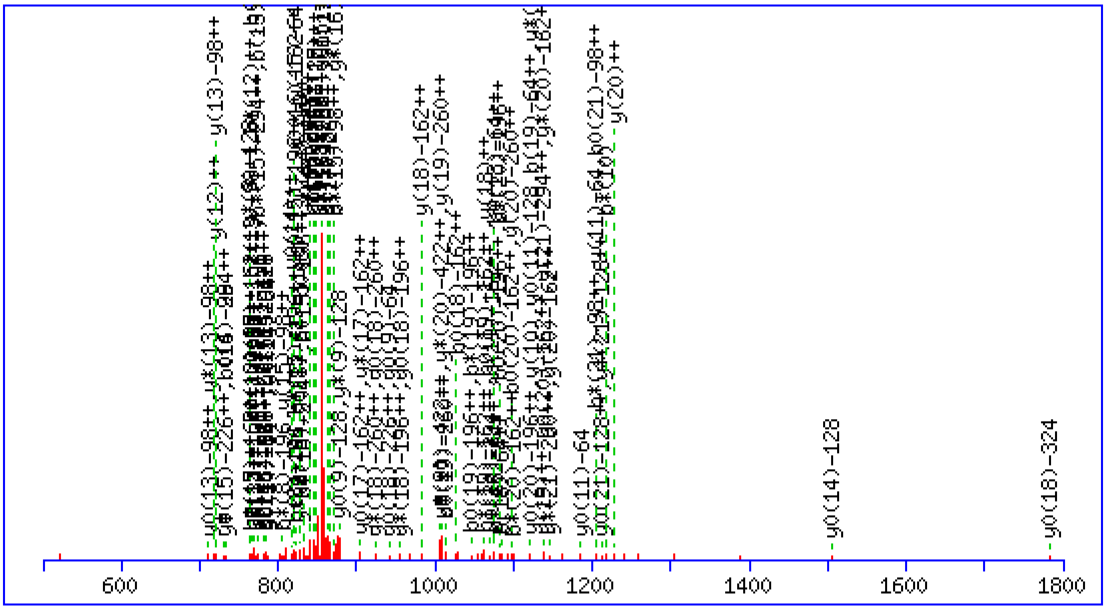
Monoisotopic mass of neutral peptide Mr(calc): 2138.9620
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 **Expect:** 0.00016
Matched b ions: b(5), b(6), b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(18)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(12)++, y(14)++, y(15)++, y(17)++

Peptide No.1084

TITFHSNGDTSFPDPDIMAAMK
Confirmed sites: @T:3,@S:6,@S:11
Ambiguous sites:

MS/MS Fragmentation of **TITFHSNGDTSFPDPDIMAAMK**
Found in **SMKZ_MOUSE** in **SwissProt**, Sperm motility kinase Z OS=Mus musculus GN=Gm4922 PE=2 SV=1

Match to Query 5526: 2666.963985 from(889.995271,3+) index(1855)
Title: Elution from: 50.092 to 50.092 scan no 3958 cid35.00 polarity:+



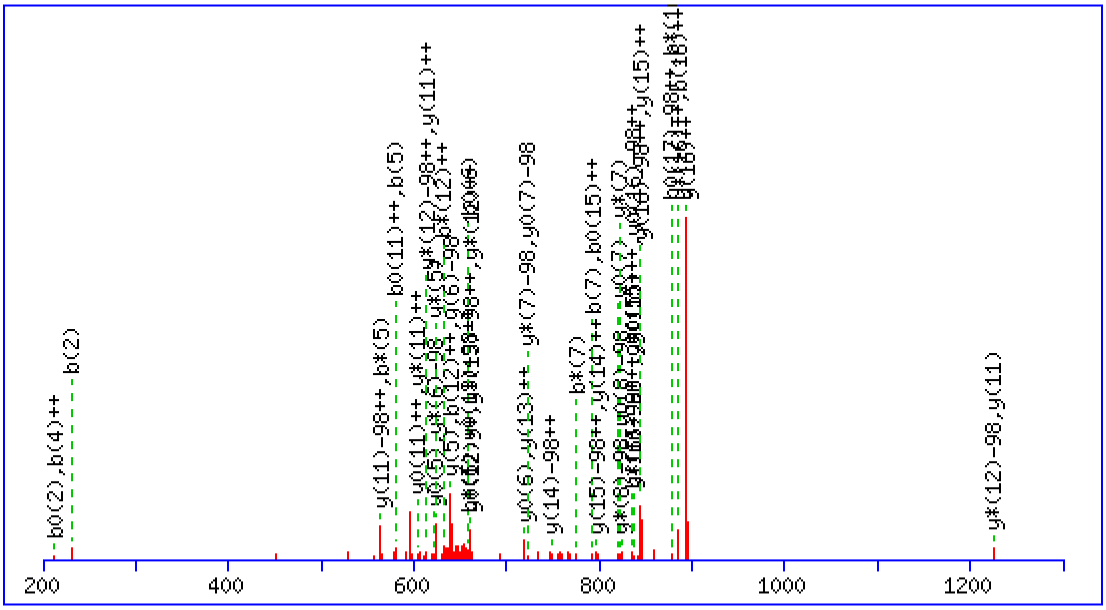
Monoisotopic mass of neutral peptide Mr(calc): 2666.9713
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M18 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M21 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 20 **Expect:** 0.032
Matched b ions: b(6), b(7)-196, b(7)-98, b(8)-196, b(13)-98++, b(14)-196++, b(14)-294++, b(14)-98++, b(15)-294++, b(15)-196++, b(16)-294++
Matched y ions: y(10), y(12)++, y(13)-98++, y(13)++, y(15)++, y(15)-98++, y(18)++, y(19)++, y(20)++, y(21)-294++

Peptide No.1085

TKPPRPDSPTTTPNISVK
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **TKPPRPDSPTTTPNISVK**
Found in **ELF1_MOUSE** in **SwissProt**, ETS-related transcription factor Elf-1 OS=Mus musculus GN=Elf1 PE=2 SV=1

Match to Query 4934: 2015.007984 from(672.676604,3+) index(4441)
Title: Elution from: 24.271 to 24.271 scan no 1819 cid35.00 polarity:+:m1s



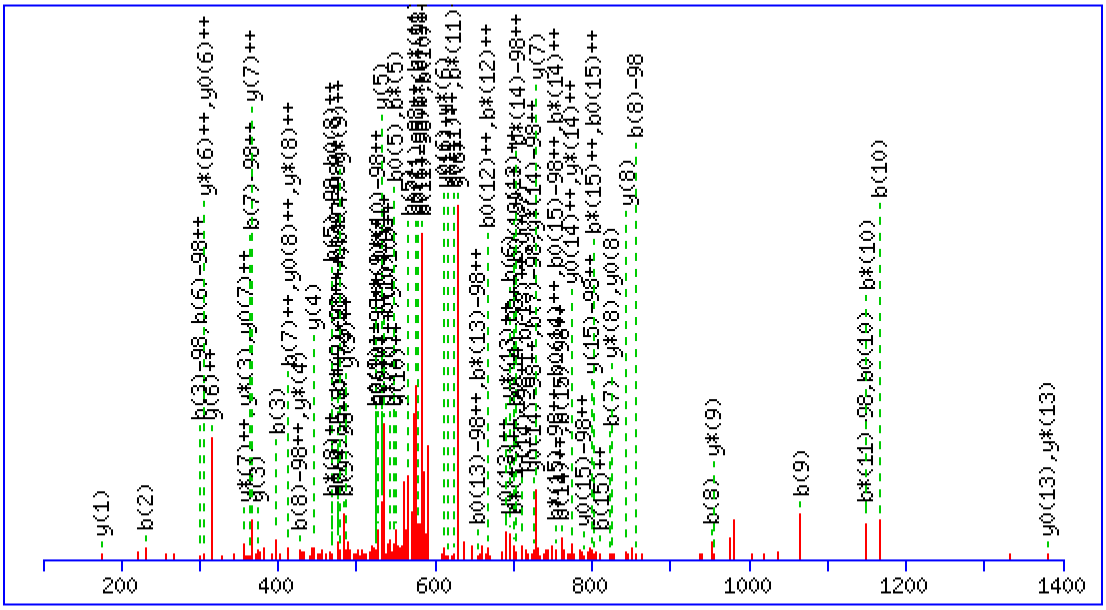
Monoisotopic mass of neutral peptide Mr(calc): 2015.0089
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 24 **Expect:** 0.019
Matched b ions: b(2), b(4)++, b(5), b(7), b(12)++, b(16)++, b(16)-98++
Matched y ions: y(5), y(6)-98, y(11), y(11)-98++, y(11)++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.1086

TKSPAEEELTPSAVVR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TKSPAEEELTPSAVVR**
Found in **PKHA6_MOUSE** in **SwissProt**, Pleckstrin homology domain-containing family A member 6 OS=Mus musculus GN=Plekha6 PE=1 SV=1

Match to Query 3899: 1792.861173 from(598.627667,3+) index(1332)
Title: Elution from: 39.720 to 39.720 scan no 2950 cid35.00 polarity:+



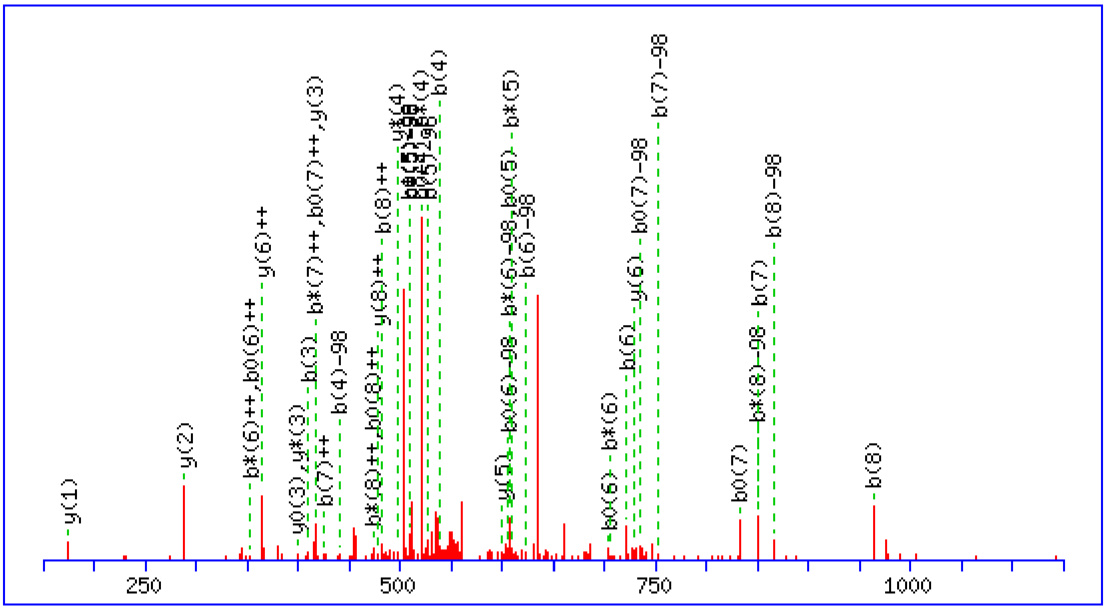
Monoisotopic mass of neutral peptide Mr(calc): 1792.8608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 **Expect:** 0.0016
Matched b ions: b(2), b(3), b(3)-98, b(5), b(5)-98, b(6), b(6)-98++, b(7)++, b(7)-98++, b(7)-98, b(7), b(8), b(8)-98++, b(8)++, b(8)-98, b(9), b(9)++, b(9)-98++, b(10), b(10)++, b(10)-98++, b(11)-98++, b(13)++, b(14)++, b(14)-98++, b(15)-98++, b(15)++
Matched y ions: y(1), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(9)++, y(10)++, y(11)++, y(13)++, y(15)-98++

Peptide No.1087

TLDQSPELR
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of **TLDQSPELR**
Found in **MTOR_MOUSE** in **SwissProt**, Serine/threonine-protein kinase mTOR OS=Mus musculus GN=Mtor PE=1 SV=2

Match to Query 1852: 1137.506790 from(569.760671,2+) index(2225)
Title: Elution from: 50.990 to 50.990 scan no 4275 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1137.5067

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 19 **Expect:** 0.044

Matched b ions: b(3), b(4)-98, b(4), b(5)-98, b(6), b(6)-98, b(7), b(7)++, b(7)-98, b(8), b(8)-98, b(8)++

Matched y ions: y(1), y(2), y(3), y(5), y(6)++, y(6), y(8)++

Peptide No.1088

TLFLGIPDENFEDHSAPPSPEEK

Confirmed sites: @S:15,@S:19

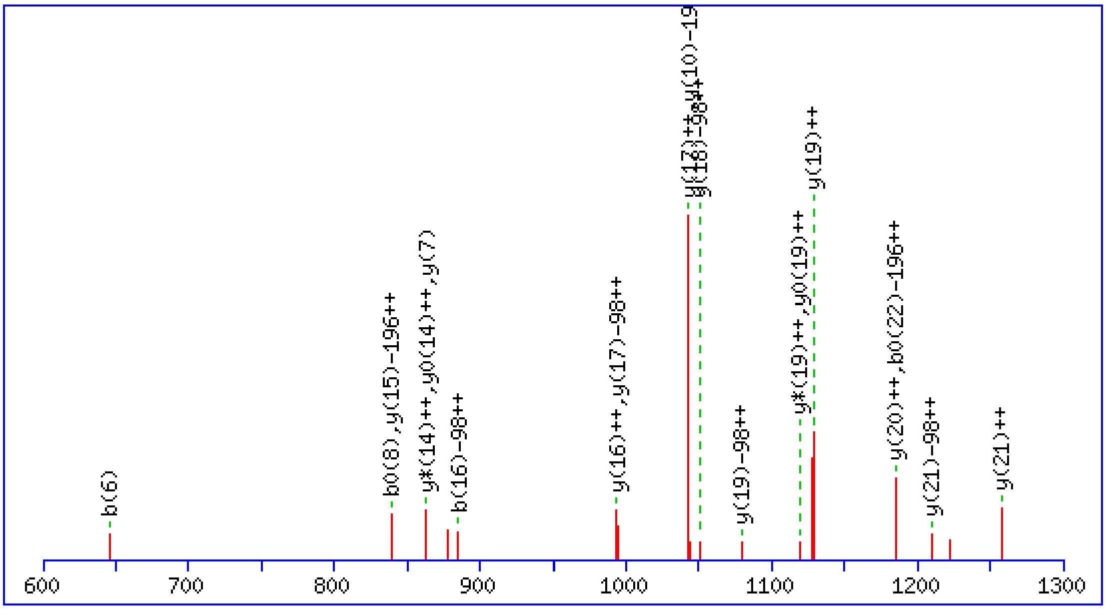
Ambiguous sites:

MS/MS Fragmentation of **TLFLGIPDENFEDHSAPPSPEEK**

Found in **M3K5_MOUSE** in **SwissProt**, Mitogen-activated protein kinase kinase kinase 5 OS=Mus musculus GN=Map3k5 PE=1 SV=3

Match to Query 6503: 2728.129647 from(910.383825,3+) index(6889)

Title: Elution from: 60.099 to 60.099 scan no 6077 cid35.00 polarity:+:m1s



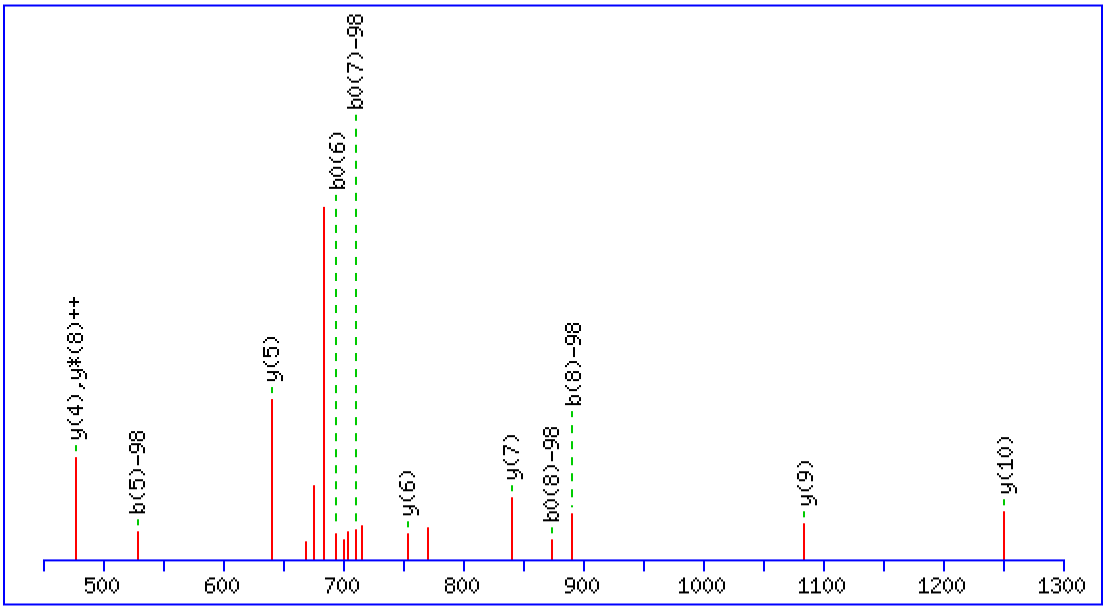
Monoisotopic mass of neutral peptide Mr(calc): 2728.1346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S19 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.018
Matched b ions: b(6), b(16)-98++
Matched y ions: y(7), y(10)-196, y(15)-196++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(19)++, y(19)-98++, y(20)++, y(21)++, y(21)-98++

Peptide No.1089

TLSDESIYSSQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TLSDESIYSSQR**
Found in **SI1L1_MOUSE** in **SwissProt**, Signal-induced proliferation-associated 1-like protein 1 OS=Mus musculus GN=Sipa1l1 PE=1 SV=2

Match to Query 2676: 1464.612330 from(733.313441,2+) index(1717)
Title: Elution from: 32.174 to 32.174 scan no 2893 cid35.00 polarity:+



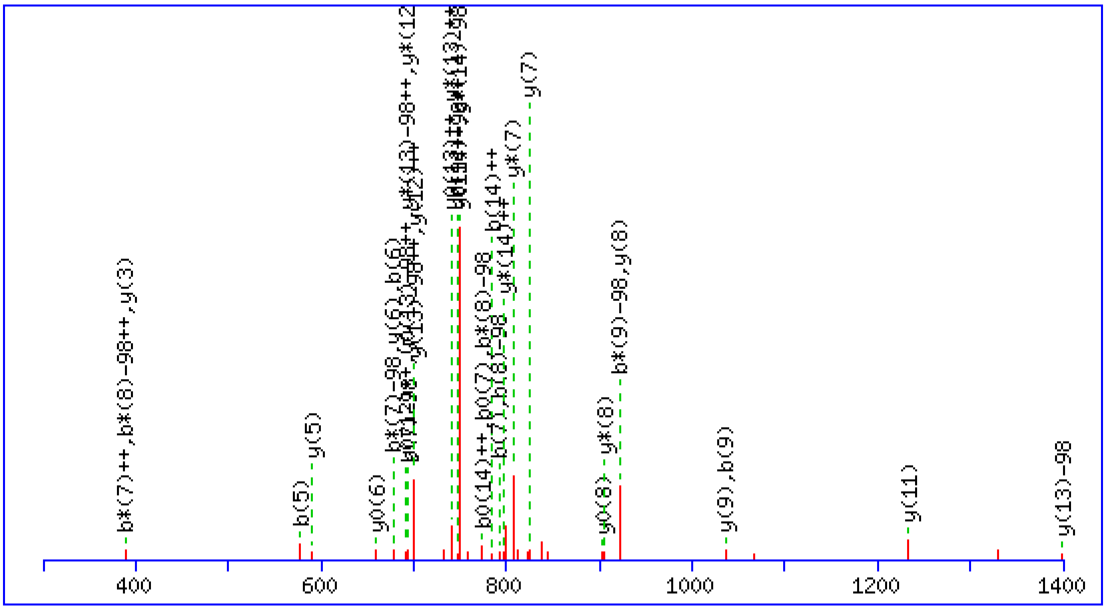
Monoisotopic mass of neutral peptide Mr(calc): 1464.6133
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 **Expect:** 0.0018
Matched b ions: b(5)-98, b(8)-98
Matched y ions: y(4), y(5), y(6), y(7), y(9), y(10)

Peptide No.1090

TNPSPTNPFSSDLQK
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **TNPSPTNPFSSDLQK**
Found in **NUMB_MOUSE** in **SwissProt**, Protein numb homolog OS=Mus musculus GN=Numb PE=1 SV=1

Match to Query 3840: 1711.744116 from(856.879334,2+) index(2501)
Title: Elution from: 39.772 to 39.772 scan no 3937 cid35.00 polarity:+



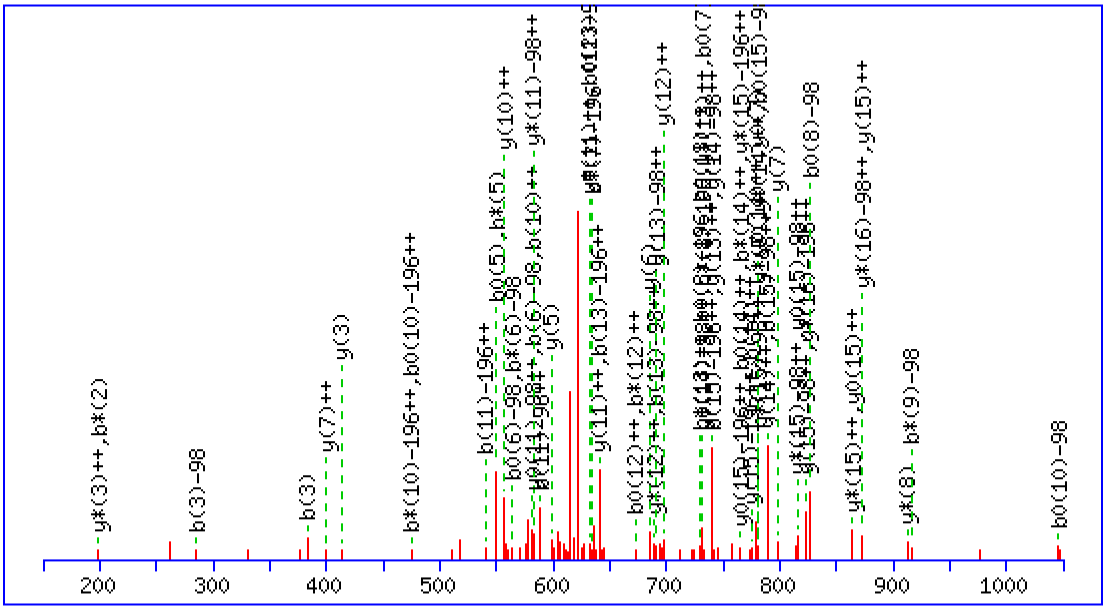
Monoisotopic mass of neutral peptide Mr(calc): 1711.7454
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 **Expect:** 5.6e-006
Matched b ions: b(5), b(6), b(7)-98, b(7), b(8)-98, b(9), b(14)++
Matched y ions: y(3), y(5), y(6), y(7), y(8), y(9), y(11), y(12)++, y(13)++, y(13)-98, y(13)-98++

Peptide No.1091

TNSPSISPSMLSNAEHK
Confirmed sites: @S:3,@S:7
Ambiguous sites:

MS/MS Fragmentation of **TNSPSISPSMLSNAEHK**
Found in **ATX2_MOUSE** in **SwissProt**, Ataxin-2 OS=Mus musculus GN=Atxn2 PE=1 SV=1

Match to Query 4839: 1958.787543 from(653.936457,3+) index(6172)
Title: Elution from: 40.056 to 40.056 scan no 3972 cid35.00 polarity:+:m1s



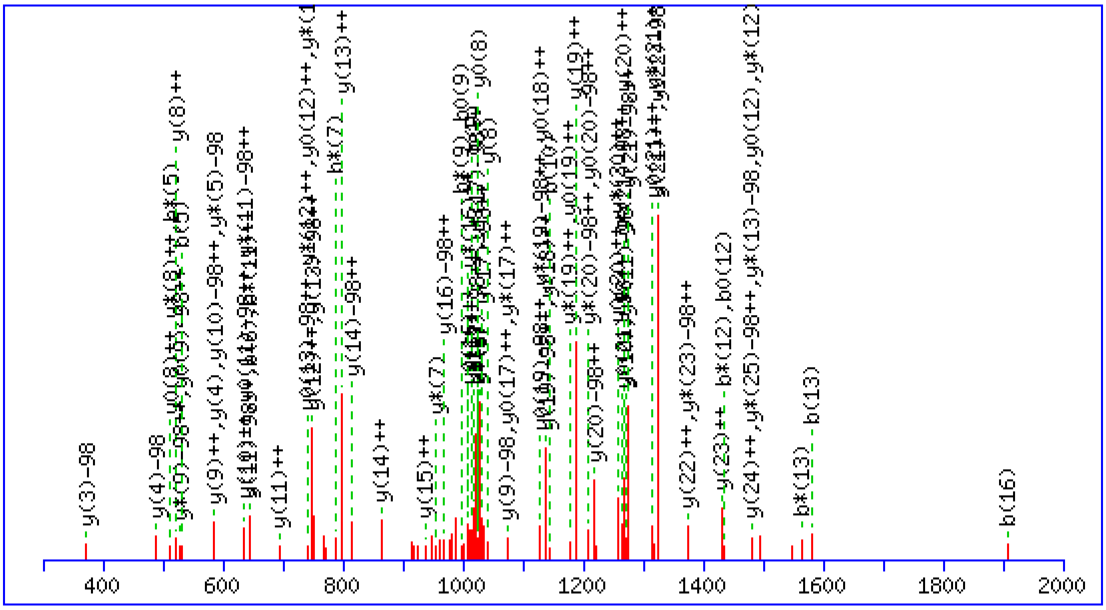
Monoisotopic mass of neutral peptide Mr(calc): 1958.7846
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.025
Matched b ions: b(3), b(3)-98, b(6)-98, b(10)++, b(11)-98++, b(11)-196++, b(12)-98++, b(13)-196++, b(13)-98++, b(14)++, b(15)-98++, b(15)-196++
Matched y ions: y(3), y(5), y(6), y(7)++, y(7), y(10)++, y(11)++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(15)-196++

Peptide No.1092

TNTNVNCPIECFMPLDVQADRDDSRE
Confirmed sites: @S:24
Ambiguous sites:

MS/MS Fragmentation of **TNTNVNCPIECFMPLDVQADRDDSRE**
Found in **FINC_MOUSE** in **SwissProt**, Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=3

Match to Query 7001: 3175.297236 from(1059.439688,3+) index(7028)
Title: Elution from: 56.714 to 56.714 scan no 5868 cid35.00 polarity:+:m1s



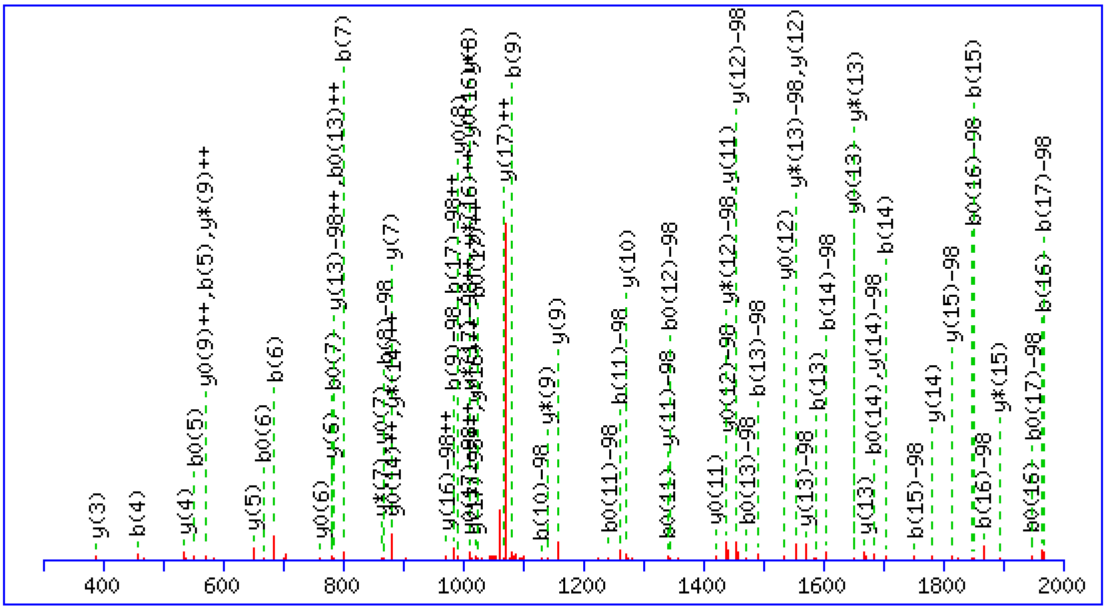
Monoisotopic mass of neutral peptide Mr(calc): 3175.3046
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S24 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 93 **Expect:** 4e-009
Matched b ions: b(5), b(6), b(9), b(10), b(13), b(16)
Matched y ions: y(3)-98, y(4)-98, y(4), y(8)++, y(8), y(9)++, y(9)-98, y(10)-98++, y(10)++, y(10), y(11)-98++, y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(20)-98++, y(21)++, y(21)-98++, y(22)-98++, y(22)++, y(23)++, y(24)++

Peptide No.1093

TPEELDDSDFETEDFDVR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **TPEELDDSDFETEDFDVR**
Found in **CTNA1_MOUSE** in **SwissProt**, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 5847: 2237.848000 from(1119.931276,2+) index(6831)
Title: Elution from: 50.624 to 50.624 scan no 5248 cid35.00 polarity:+:m1s



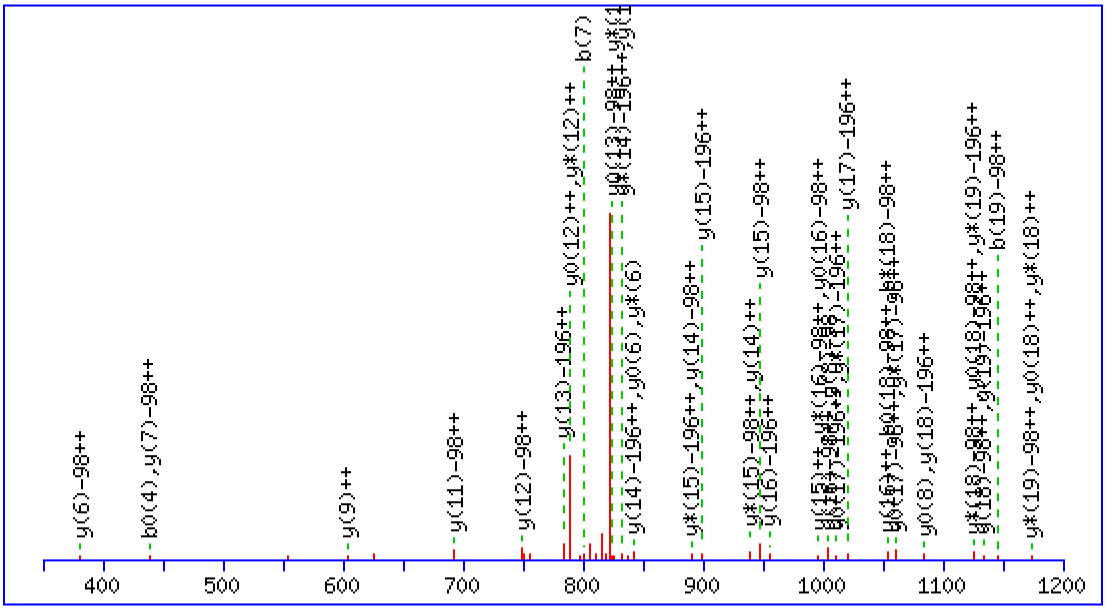
Monoisotopic mass of neutral peptide Mr(calc): 2237.8526
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 **Expect:** 1.5e-009
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98, b(9)-98, b(9), b(10)-98, b(11)-98, b(13)-98, b(13), b(14)-98, b(14), b(15)-98, b(15), b(16)-98, b(16), b(17)-98++, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98, y(11), y(12)-98, y(12), y(13), y(13)-98, y(13)-98++, y(14)-98, y(14), y(15)-98, y(16)-98++, y(16)++, y(17)-98++, y(17)++

Peptide No.1094

TPEELDDSDFETEDFDVRSR
Confirmed sites: @S:8,@S:19
Ambiguous sites:

MS/MS Fragmentation of **TPEELDDSDFETEDFDVRSR**
Found in **CTNA1_MOUSE** in **SwissProt**, Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1

Match to Query 6310: 2560.948407 from(854.656745,3+) index(6661)
Title: Elution from: 50.775 to 50.775 scan no 5221 cid35.00 polarity:+:m1s



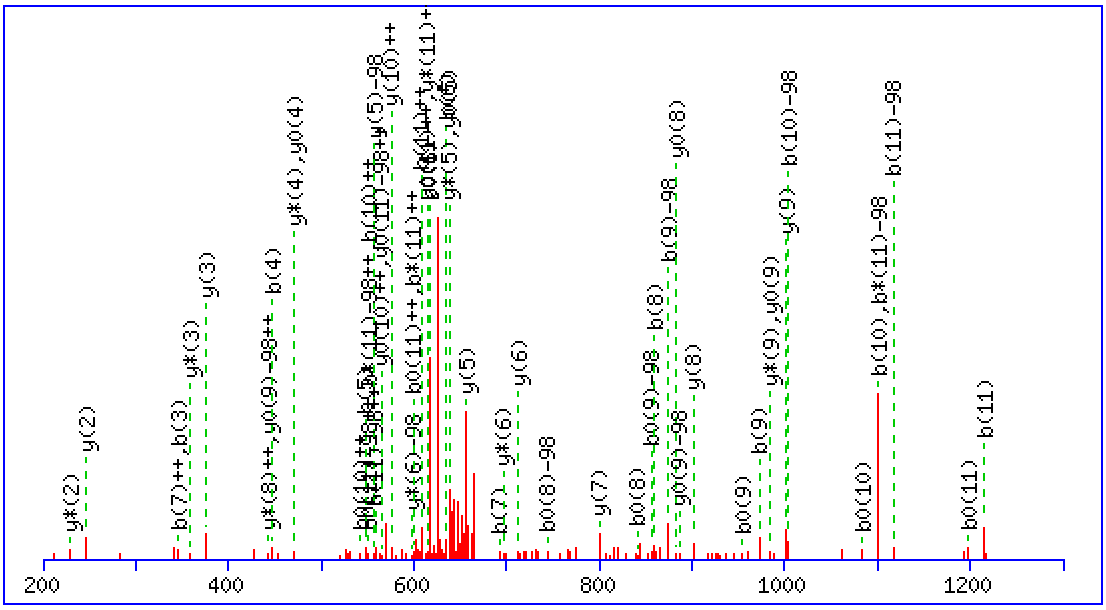
Monoisotopic mass of neutral peptide Mr(calc): 2560.9520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S19 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00038
Matched b ions: b(7), b(19)-98++
Matched y ions: y(6)-98++, y(7)-98++, y(8)-98, y(9)++, y(11)-98++, y(12)-98++, y(13)-196++, y(13)-98++, y(14)++, y(14)-98++, y(14)-196++, y(15)-98++, y(15)-196++, y(15)++, y(16)-98++, y(16)-196++, y(16)++, y(17)-196++, y(18)-196++, y(18)-98++, y(19)-196++

Peptide No.1095

TPFTTSGSLENN
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **TPFTTSGSLENN**
Found in **CDO1_MOUSE** in **SwissProt**, Cysteine dioxygenase type 1 OS=Mus musculus GN=Cdo1 PE=1 SV=1

Match to Query 2619: 1346.539890 from(674.277221,2+) index(1530)
Title: Elution from: 42.931 to 42.931 scan no 3292 cid35.00 polarity:+



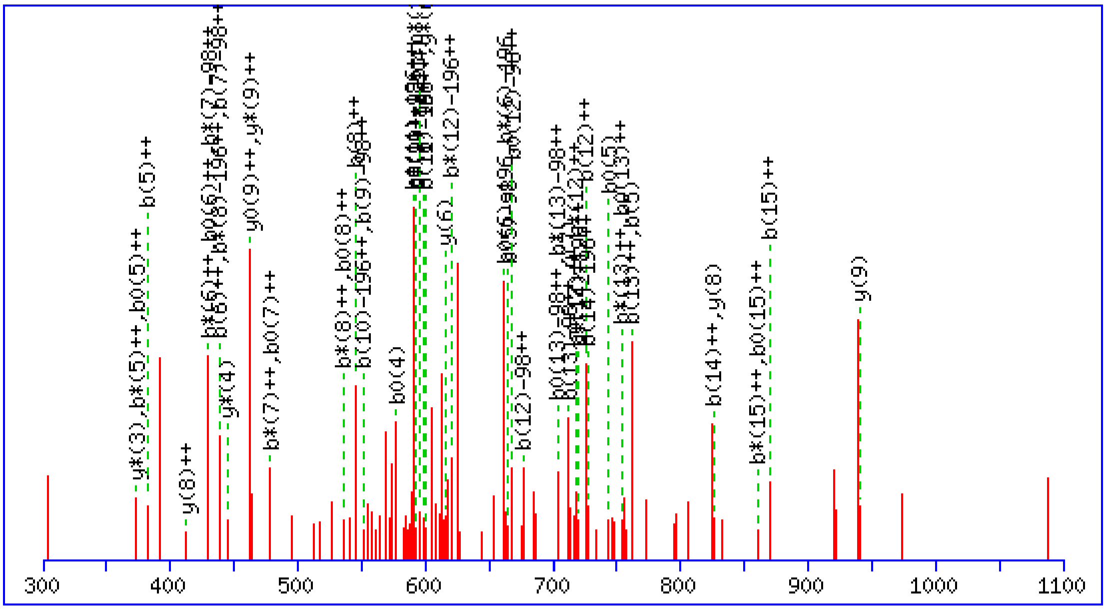
Monoisotopic mass of neutral peptide Mr(calc): 1346.5391
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 34 **Expect:** 0.00086
Matched b ions: b(3), b(4), b(5), b(6), b(7)++, b(7), b(8), b(9)-98, b(9), b(10), b(10)-98, b(10)++, b(11), b(11)++, b(11)-98, b(11)-98++
Matched y ions: y(2), y(3), y(5), y(5)-98, y(6)-98, y(6), y(7), y(8), y(9), y(10)++

Peptide No.1096

TPRCSLPDLPPGAQSR
Confirmed sites: @T:1,@S:5
Ambiguous sites:

MS/MS Fragmentation of **TPRCSLPDLPPGAQSR**
Found in **MMP17_MOUSE** in **SwissProt**, Matrix metalloproteinase-17 OS=Mus musculus GN=Mmp17 PE=1 SV=3

Match to Query 4642: 1910.816685 from(637.946171,3+) index(5468)
Title: Elution from: 32.611 to 32.611 scan no 2986 cid35.00 polarity:+:m1s



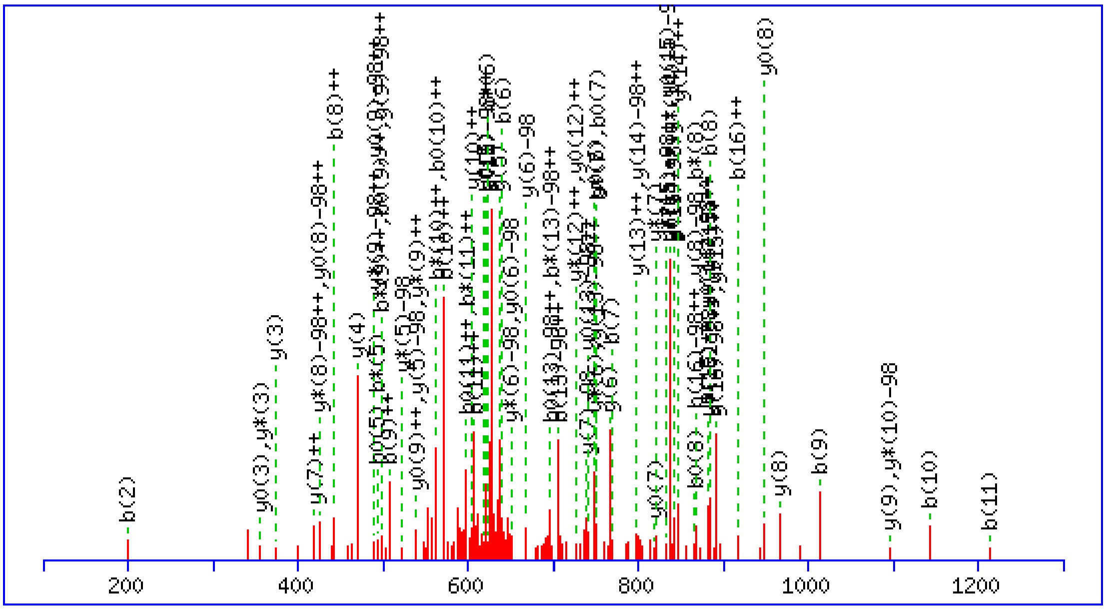
Monoisotopic mass of neutral peptide Mr(calc): 1910.8111
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.014
Matched b ions: b(4), b(5), b(5)++, b(5)-98, b(6)++, b(7)-98++, b(8)++, b(9)-98++, b(10)-196++, b(10)-98++, b(11)-196++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-196++, b(15)++
Matched y ions: y(6), y(7), y(8), y(8)++, y(9)

Peptide No.1097

TPSPKEEDEEAESPPEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **TPSPKEEDEEAESPPEK**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 4925: 1977.805533 from(660.275787,3+) index(4090)
Title: Elution from: 19.840 to 19.840 scan no 1253 cid35.00 polarity:+:m1s



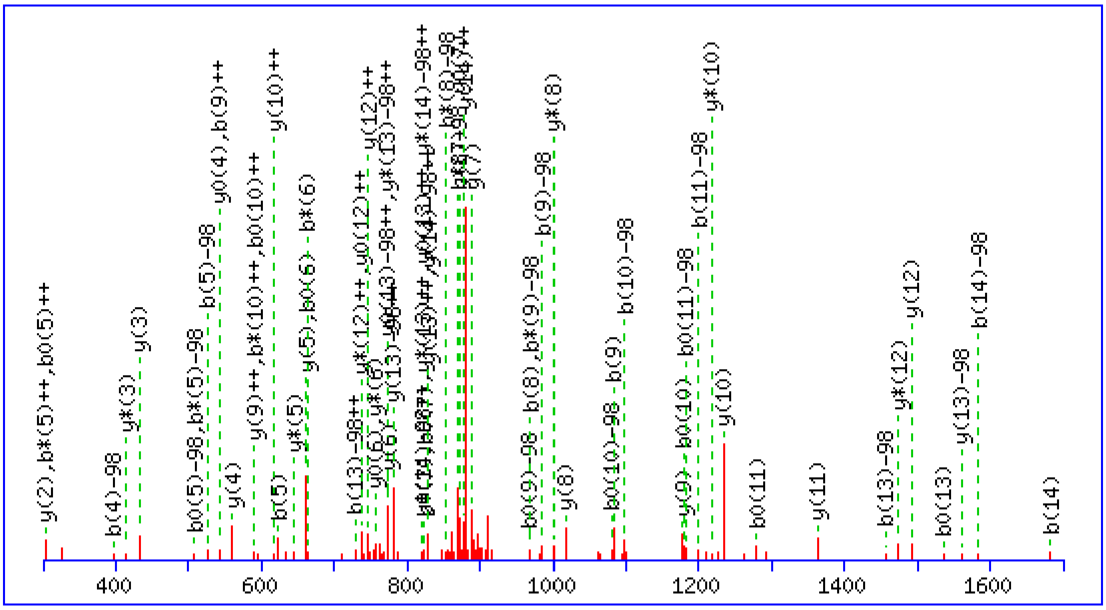
Monoisotopic mass of neutral peptide Mr(calc): 1977.8092
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 6.6e-005
Matched b ions: b(2), b(6), b(7), b(8)++, b(8), b(9), b(9)++, b(10)++, b(10), b(11), b(11)++, b(13)-98++, b(16)++, b(16)-98++
Matched y ions: y(3), y(4), y(5), y(5)-98, y(6), y(6)-98, y(7), y(7)++, y(7)-98, y(8), y(8)-98, y(9), y(9)-98++, y(10)++, y(11)-98++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++, y(16)-98++

Peptide No.1098

TPSQEGCQDLTQEQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TPSQEGCQDLTQEQR**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 4418: 1855.737714 from(928.876133,2+) index(1031)
Title: Elution from: 24.870 to 24.870 scan no 1935 cid35.00 polarity:+



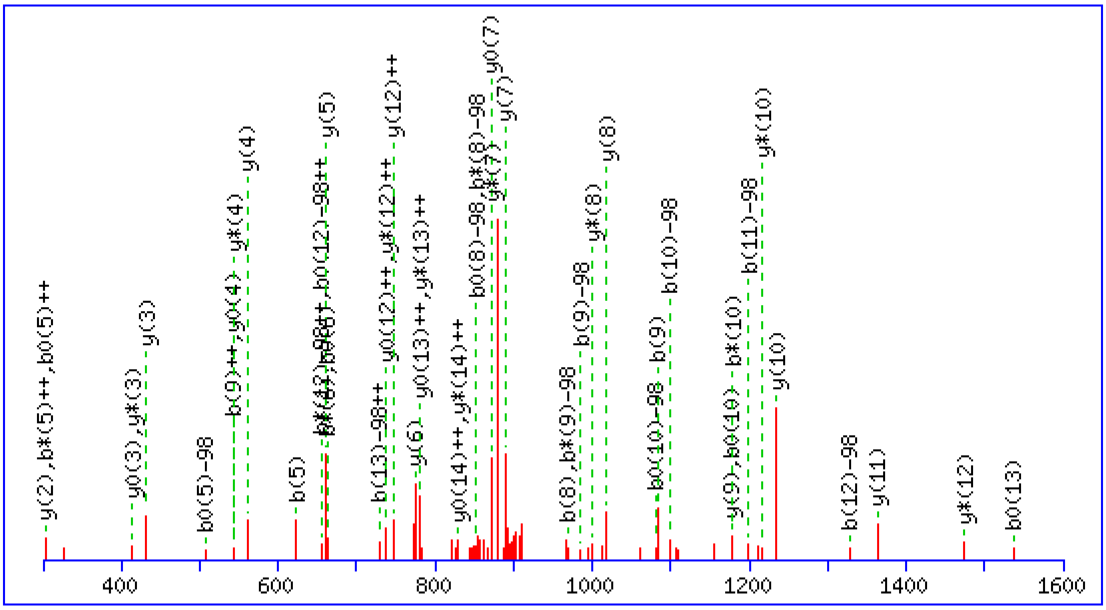
Monoisotopic mass of neutral peptide Mr(calc): 1855.7408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 94 **Expect:** 2.4e-009
Matched b ions: b(4)-98, b(5)-98, b(5), b(8)-98, b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(11)-98, b(13)-98, b(13)-98++, b(14)-98, b(14)
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(9)++, y(10), y(10)++, y(11), y(12), y(12)++, y(13)-98++, y(13)-98, y(13)++, y(14)++, y(14)-98++

Peptide No.1099

TPSQEGCQDLTQEQR
Confirmed sites:
Ambiguous sites: @T:1orS:3

MS/MS Fragmentation of **TPSQEGCQDLTQEQR**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 3701: 1855.737186 from(928.875869,2+) index(848)
Title: Elution from: 24.361 to 24.361 scan no 1805 cid35.00 polarity:+



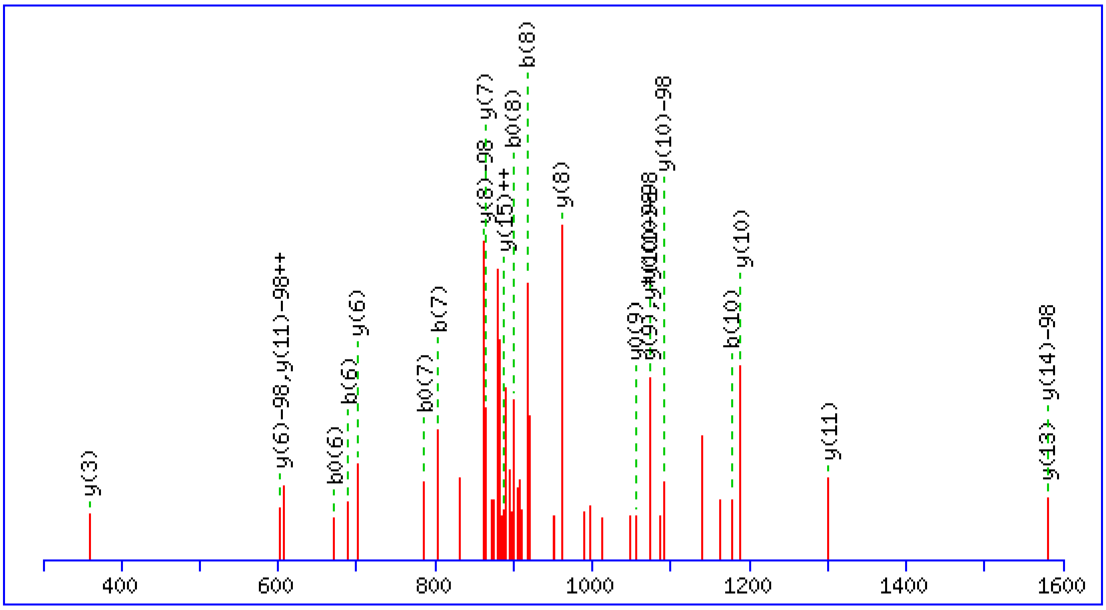
Monoisotopic mass of neutral peptide Mr(calc): 1855.7408
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 **Expect:** 2.9e-008
Matched b ions: b(5), b(8), b(9), b(9)++, b(9)-98, b(10)-98, b(11)-98, b(12)-98, b(13)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(12)++

Peptide No.1100

TPVDYIDLPYSSSPSR
Confirmed sites:
Ambiguous sites: @S:11orS:12orS:13

MS/MS Fragmentation of **TPVDYIDLPYSSSPSR**
Found in **SRBS1_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2

Match to Query 3762: 1875.828474 from(938.921513,2+) index(5900)
Title: Elution from: 50.605 to 50.605 scan no 4951 cid35.00 polarity:+:m1s



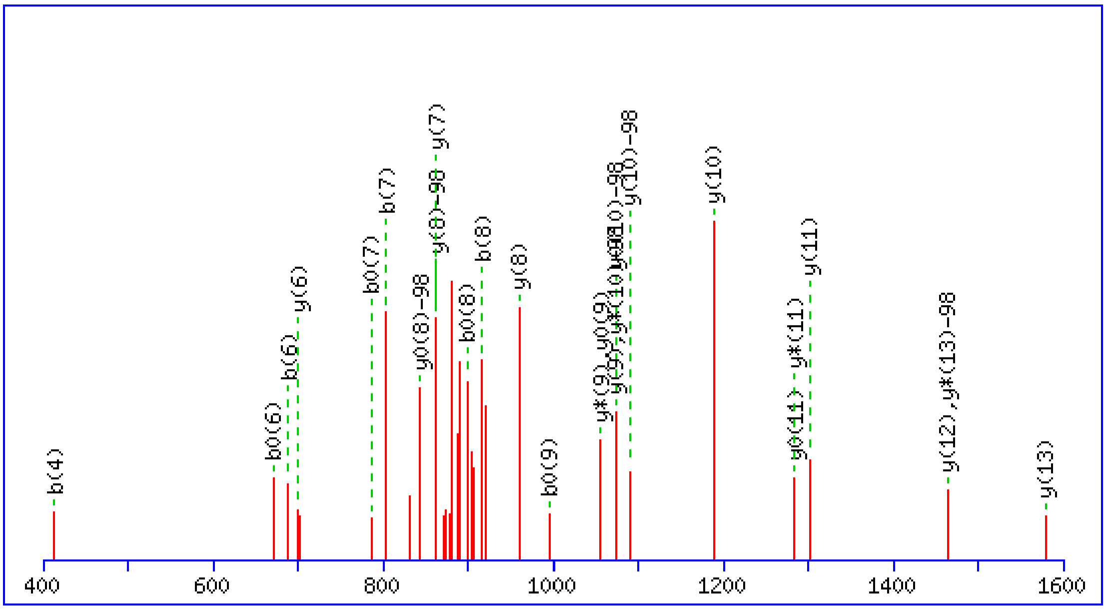
Monoisotopic mass of neutral peptide Mr(calc): 1875.8292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 **Expect:** 7.5e-005
Matched b ions: b(6), b(7), b(8), b(10)
Matched y ions: y(3), y(6), y(6)-98, y(7), y(8)-98, y(8), y(9), y(10), y(10)-98, y(11), y(11)-98++, y(13), y(14)-98, y(15)++

Peptide No.1101

TPVDYIDLPYSSSPSR
Confirmed sites:
Ambiguous sites: @S:11orS:12orS:13orS:15

MS/MS Fragmentation of **TPVDYIDLPYSSSPSR**
Found in **SRBS1_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2

Match to Query 4354: 1875.830816 from(938.922684,2+) index(3149)
Title: Elution from: 51.289 to 51.289 scan no 5276 cid35.00 polarity:+



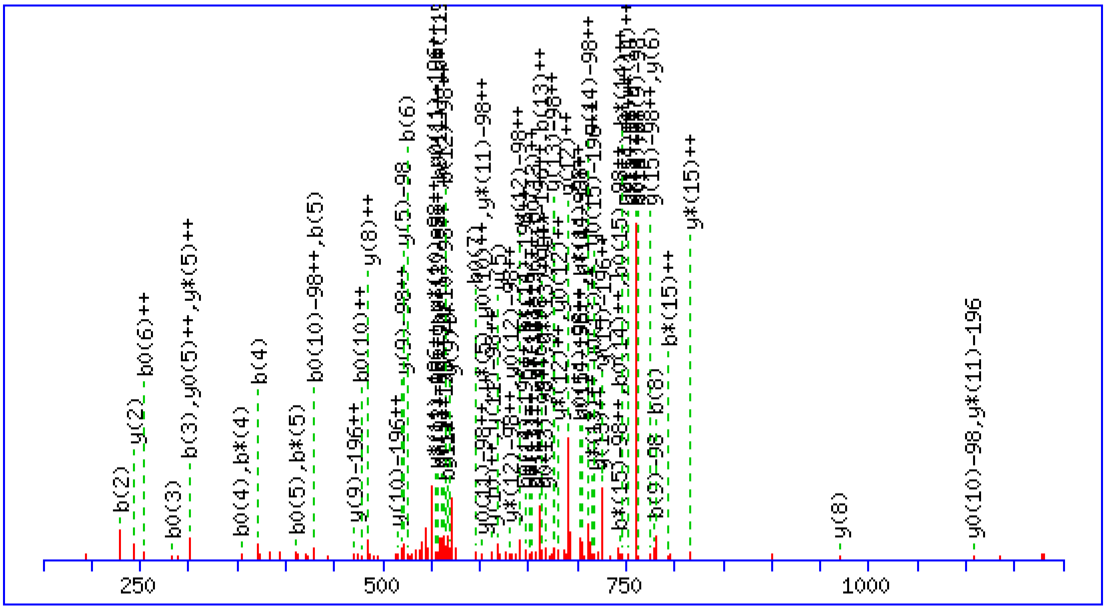
Monoisotopic mass of neutral peptide Mr(calc): 1875.8292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 53 **Expect:** 2.6e-005
Matched b ions: b(4), b(6), b(7), b(8)
Matched y ions: y(6), y(7), y(8), y(8)-98, y(9), y(10), y(10)-98, y(11), y(12), y(13)

Peptide No.1102

TQAAGPSSPPRPPTPK
Confirmed sites: @S:8,@T:14
Ambiguous sites:

MS/MS Fragmentation of **TQAAGPSSPPRPPTPK**
Found in **XRCC1_MOUSE** in **SwissProt**, DNA repair protein XRCC1 OS=Mus musculus GN=Xrcc1 PE=1 SV=2

Match to Query 3380: 1747.768878 from(583.596902,3+) index(3893)
Title: Elution from: 23.929 to 23.929 scan no 1746 cid35.00 polarity:+:m1s



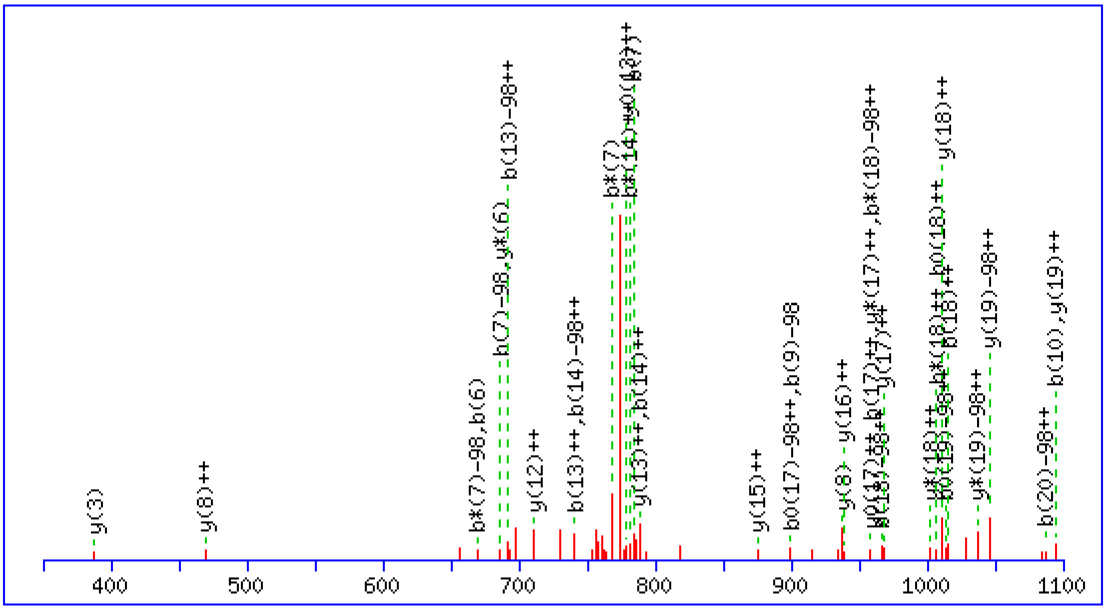
Monoisotopic mass of neutral peptide Mr(calc): 1747.7695
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.011
Matched b ions: b(2), b(3), b(4), b(5), b(6), b(8), b(9)-98, b(11)++, b(12)-98++, b(13)++, b(14)-98++, b(15)-196++, b(15)-98++
Matched y ions: y(2), y(5), y(5)-98, y(6), y(8)++, y(8), y(9)-196++, y(9)-98++, y(9)++, y(10)-98++, y(10)-196++, y(10)++, y(11)++, y(11)-196++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(14)-196++, y(15)-196++, y(15)-98++

Peptide No.1103

TQSSGQDGRPQEEPHAEDLQK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TQSSGQDGRPQEEPHAEDLQK**
Found in **PI51C_MOUSE** in **SwissProt**, Phosphatidylinositol-4-phosphate 5-kinase type-1 gamma OS=Mus musculus GN=Pip5k1c PE=1 SV=2

Match to Query 6055: 2416.024692 from(806.348840,3+) index(3964)
Title: Elution from: 20.309 to 20.309 scan no 1280 cid35.00 polarity:+:m1s



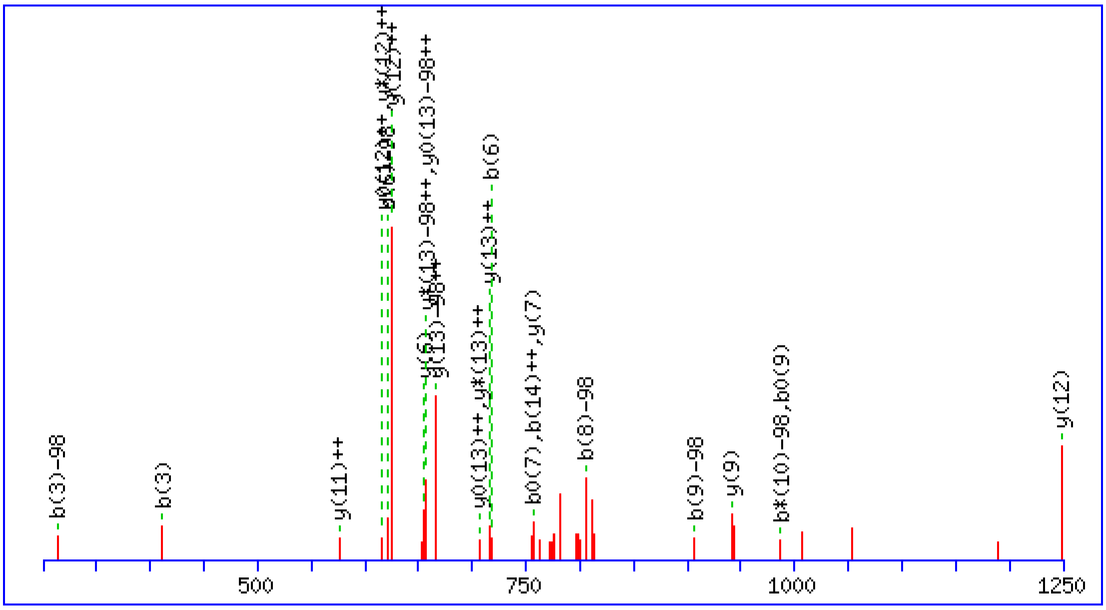
Monoisotopic mass of neutral peptide Mr(calc): 2416.0292
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.02
Matched b ions: b(6), b(7)-98, b(7), b(9)-98, b(10), b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(17)++, b(18)-98++, b(18)++, b(20)-98++
Matched y ions: y(3), y(8)++, y(8), y(12)++, y(13)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(19)++

Peptide No.1104

TQTPPLGQTPQLGLK
Confirmed sites: @T:3
Ambiguous sites:

MS/MS Fragmentation of **TQTPPLGQTPQLGLK**
Found in **IF4G2_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 4 gamma 2 OS=Mus musculus GN=Eif4g2 PE=1 SV=2

Match to Query 3638: 1657.844354 from(829.929453,2+) index(6312)
Title: Elution from: 41.847 to 41.847 scan no 4209 cid35.00 polarity:+:m1s



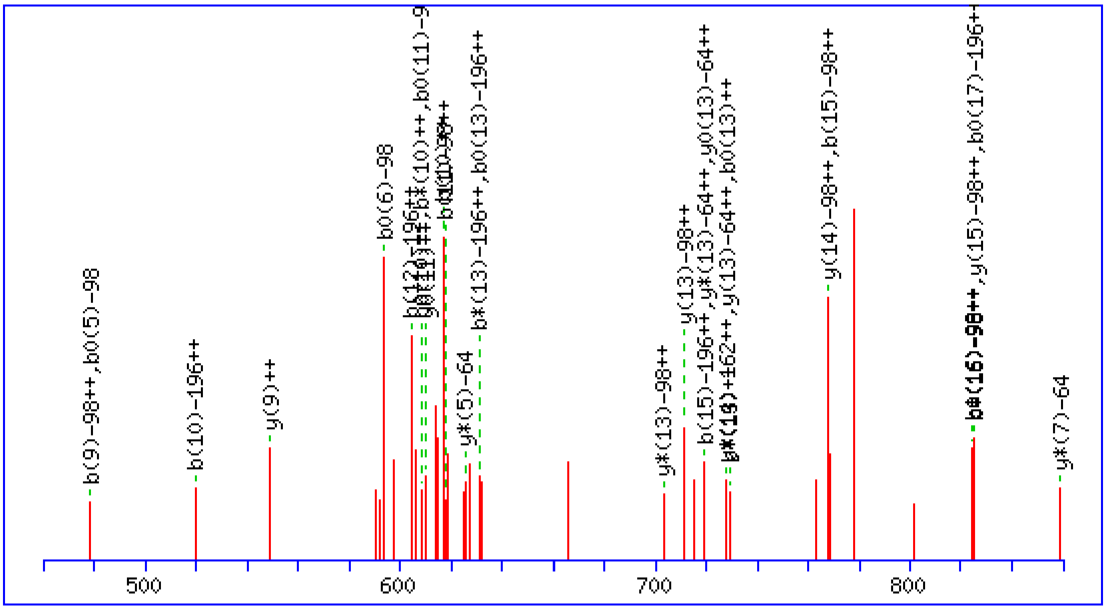
Monoisotopic mass of neutral peptide Mr(calc): 1657.8440
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0072
Matched b ions: b(3), b(3)-98, b(6)-98, b(6), b(8)-98, b(9)-98, b(11)++, b(14)++
Matched y ions: y(6), y(7), y(9), y(11)++, y(12)++, y(12), y(13)-98++, y(13)++

Peptide No.1105

TRGAEDDLNTVAAGTMTGMLYK
Confirmed sites: @T:1,@T:10
Ambiguous sites: @T:17orY:21

MS/MS Fragmentation of **TRGAEDDLNTVAAGTMTGMLYK**
Found in **TIM23_MOUSE** in **SwissProt**, Mitochondrial import inner membrane translocase subunit Tim23 OS=Mus musculus GN=Timm23 PE=2 SV=1

Match to Query 5474: 2569.990812 from(643.504979,4+) index(2150)
Title: Elution from: 38.495 to 38.495 scan no 3642 cid35.00 polarity:+



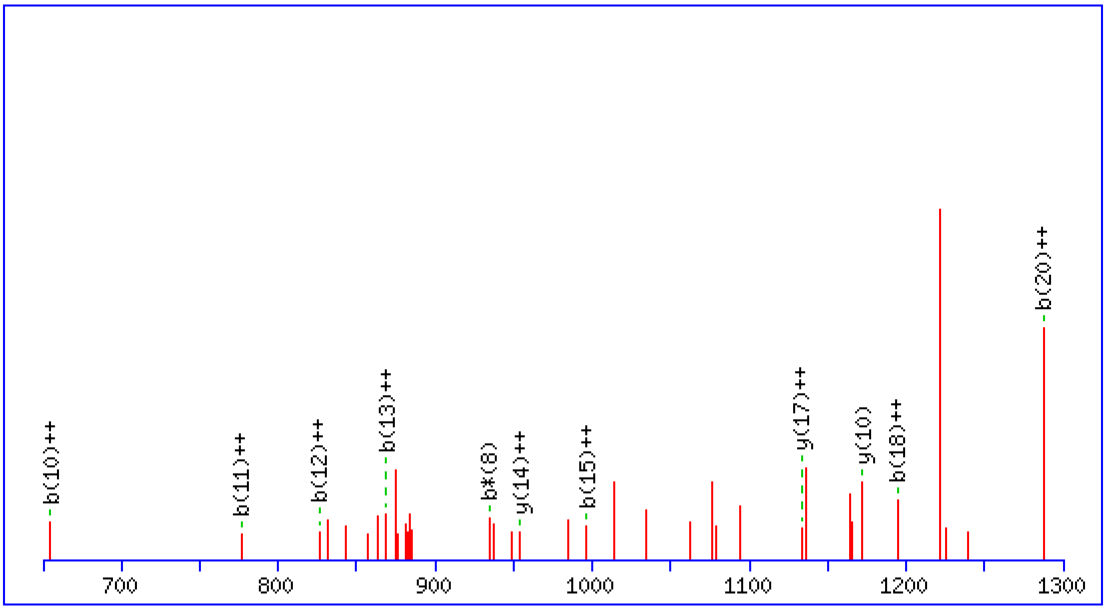
Monoisotopic mass of neutral peptide Mr(calc): 2569.9872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M19 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y21 : Phospho (Y)
Ions Score: 23 **Expect:** 0.027
Matched b ions: b(7), b(9)-98++, b(10)++, b(10)-196++, b(11)-98++, b(12)-196++, b(15)-98++, b(15)-196++
Matched y ions: y(9)++, y(13)-98++, y(14)-98++, y(15)-98++

Peptide No.1106

TRVVEDNHNYYVSRVYGPGEK
Confirmed sites: @Y:10,@Y:11,@Y:16
Ambiguous sites:

MS/MS Fragmentation of **TRVVEDNHNYYVSRVYGPGEK**
Found in **PLDX1_MOUSE** in **SwissProt**, Plexin domain-containing protein 1 OS=Mus musculus GN=Plxdc1 PE=1 SV=2

Match to Query 6492: 2721.100890 from(908.040906,3+) index(3330)
Title: Elution from: 58.532 to 58.532 scan no 5945 cid35.00 polarity:+



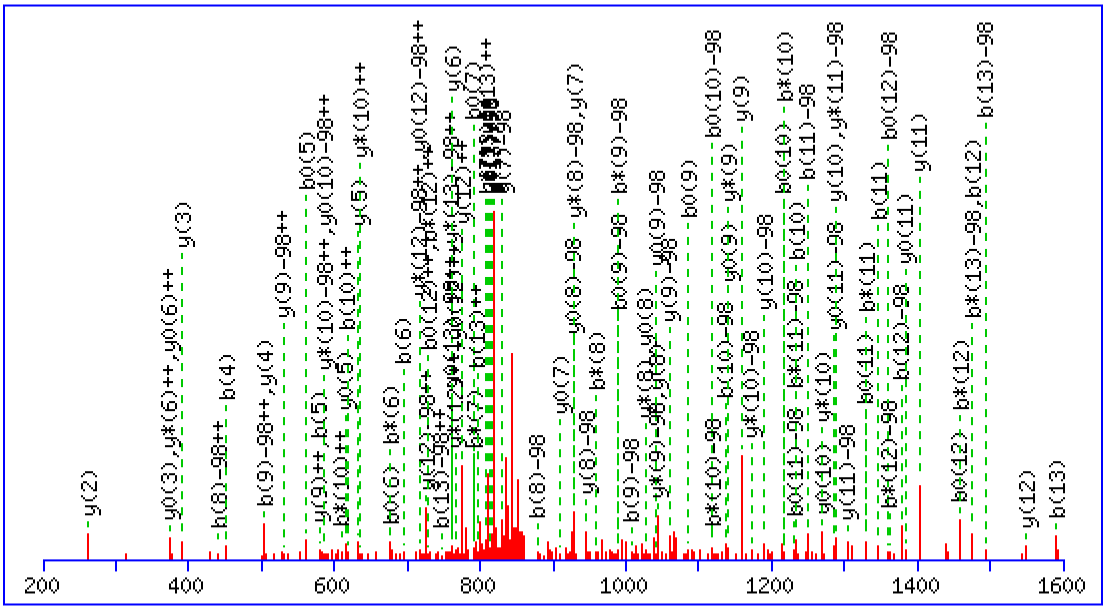
Monoisotopic mass of neutral peptide Mr(calc): 2721.1026
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y10 : Phospho (Y)
Y11 : Phospho (Y)
Y16 : Phospho (Y)
Ions Score: 22 **Expect:** 0.042
Matched b ions: b(10)++, b(11)++, b(12)++, b(13)++, b(15)++, b(18)++, b(20)++
Matched y ions: y(10), y(14)++, y(17)++

Peptide No.1107

TSFDENDSEELEDK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **TSFDENDSEELEDK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4358: 1736.629518 from(869.322035,2+) index(1421)
Title: Elution from: 38.114 to 38.114 scan no 2906 cid35.00 polarity:+



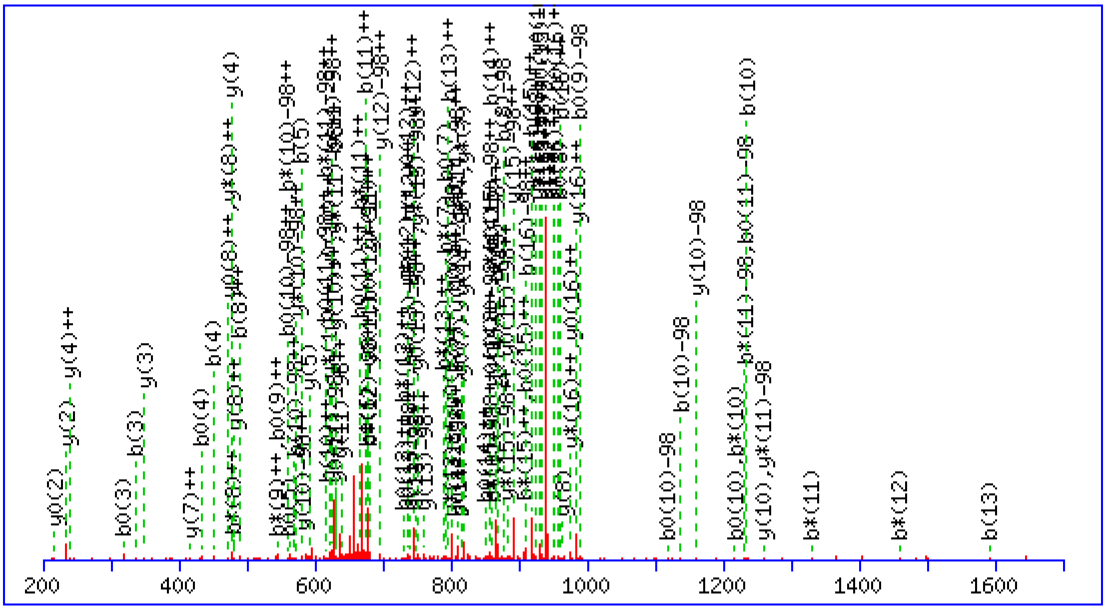
Monoisotopic mass of neutral peptide Mr(calc): 1736.6302
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 74 **Expect:** 9.6e-008
Matched b ions: b(4), b(5), b(6), b(7), b(8)-98++, b(8)-98, b(9)-98++, b(9)-98, b(10), b(10)-98, b(10)++, b(11)-98, b(11), b(12), b(12)-98, b(13), b(13)-98, b(13)-98++, b(13)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(8)-98, y(9), y(9)-98, y(9)++, y(9)-98++, y(10), y(10)-98, y(11), y(11)-98, y(12)-98++, y(12), y(12)++, y(13)++

Peptide No.1108

TSFDENDSEELEDKDSK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **TSFDENDSEELEDKDSK**
Found in **IF2P_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2

Match to Query 4581: 2066.786043 from(689.935957,3+) index(3731)
Title: Elution from: 33.343 to 33.343 scan no 2195 cid35.00 polarity:+:m1s



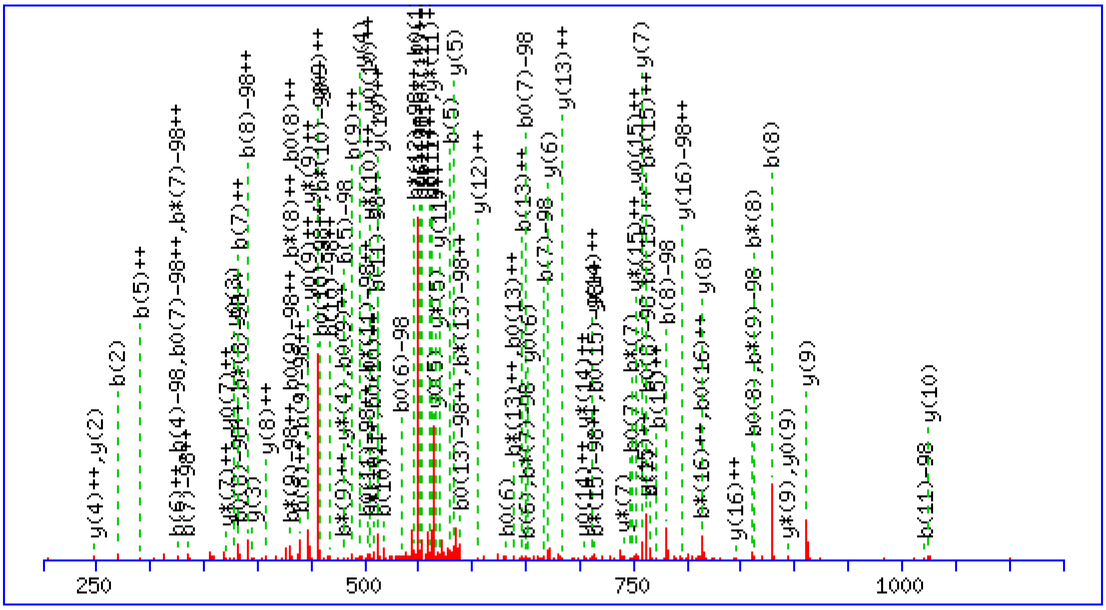
Monoisotopic mass of neutral peptide Mr(calc): 2066.7841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.02
Matched b ions: b(3), b(4), b(5), b(7), b(8)++, b(8)-98, b(10), b(10)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(13), b(13)-98++, b(13)++, b(14)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(7)++, y(8)++, y(8), y(10)-98, y(10), y(10)-98++, y(10)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.1109

TSPGRADLPGSSSTFTK
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **TSPGRADLPGSSSTFTK**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 4489: 1787.810298 from(596.944042,3+) index(4703)
Title: Elution from: 36.783 to 36.783 scan no 2736 cid35.00 polarity:+:m1s



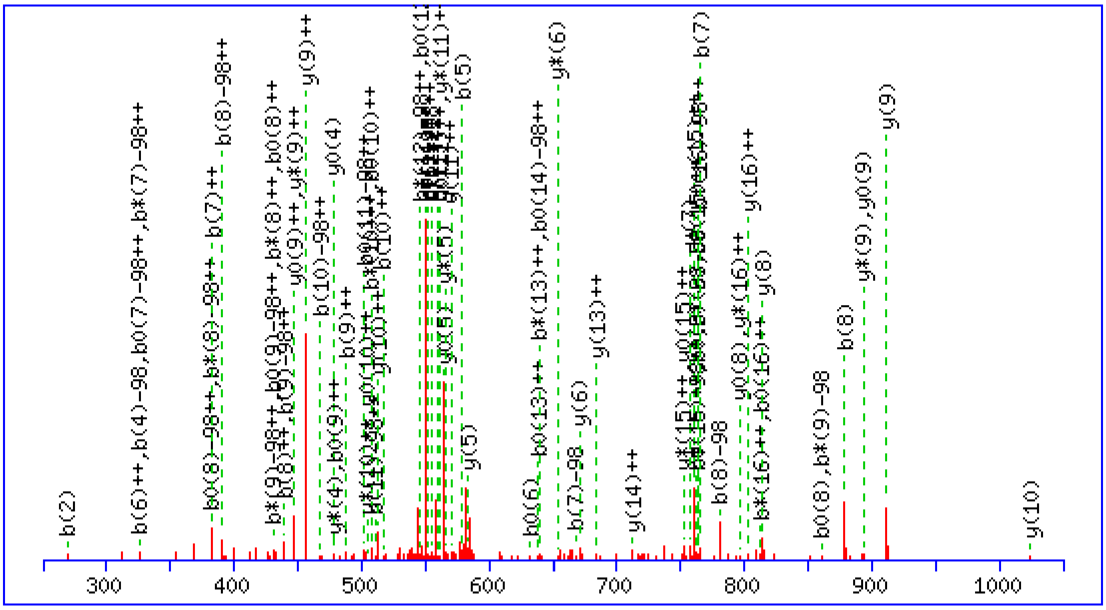
Monoisotopic mass of neutral peptide Mr(calc): 1787.8091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.019
Matched b ions: b(2), b(4)-98, b(5)++, b(5)-98, b(5), b(6), b(6)++, b(6)-98, b(7)++, b(7), b(7)-98++, b(7)-98, b(8)-98++, b(8), b(8)++, b(8)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98, b(11)-98++, b(11)++, b(13)++, b(15)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(8), y(8)++, y(9)++, y(9), y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++

Peptide No.1110

TSPGRADLPGSSSTFTK
Confirmed sites: @T:1
Ambiguous sites:

MS/MS Fragmentation of **TSPGRADLPGSSSTFTK**
Found in **SRBS2_MOUSE** in **SwissProt**, Sorbin and SH3 domain-containing protein 2 OS=Mus musculus GN=Sorbs2 PE=1 SV=2

Match to Query 4026: 1787.809050 from(596.943626,3+) index(4920)
Title: Elution from: 28.700 to 28.700 scan no 2422 cid35.00 polarity:+:m1s



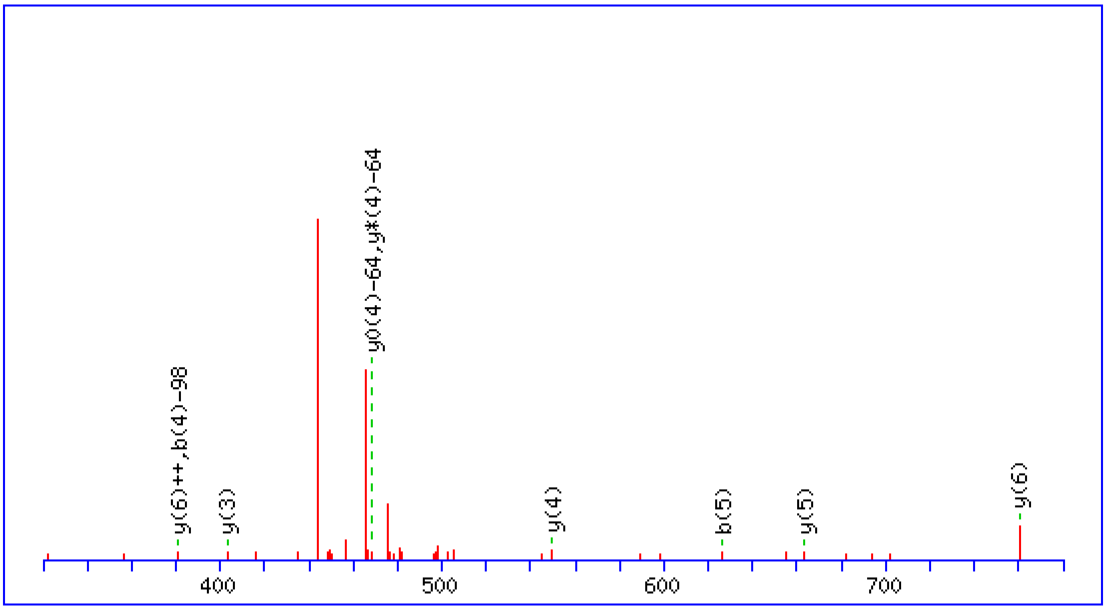
Monoisotopic mass of neutral peptide Mr(calc): 1787.8091
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.042
Matched b ions: b(2), b(4)-98, b(5), b(6)++, b(6)-98, b(7), b(7)++, b(7)-98, b(8)-98, b(8), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++
Matched y ions: y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)++, y(11)++, y(13)++, y(14)++, y(15)++, y(16)++

Peptide No.1111

TSPLMLDR
Confirmed sites:
Ambiguous sites: @T:1orS:2

MS/MS Fragmentation of **TSPLMLDR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 805: 1027.440386 from(514.727469,2+) index(1273)
Title: Elution from: 28.257 to 28.257 scan no 2334 cid35.00 polarity:+



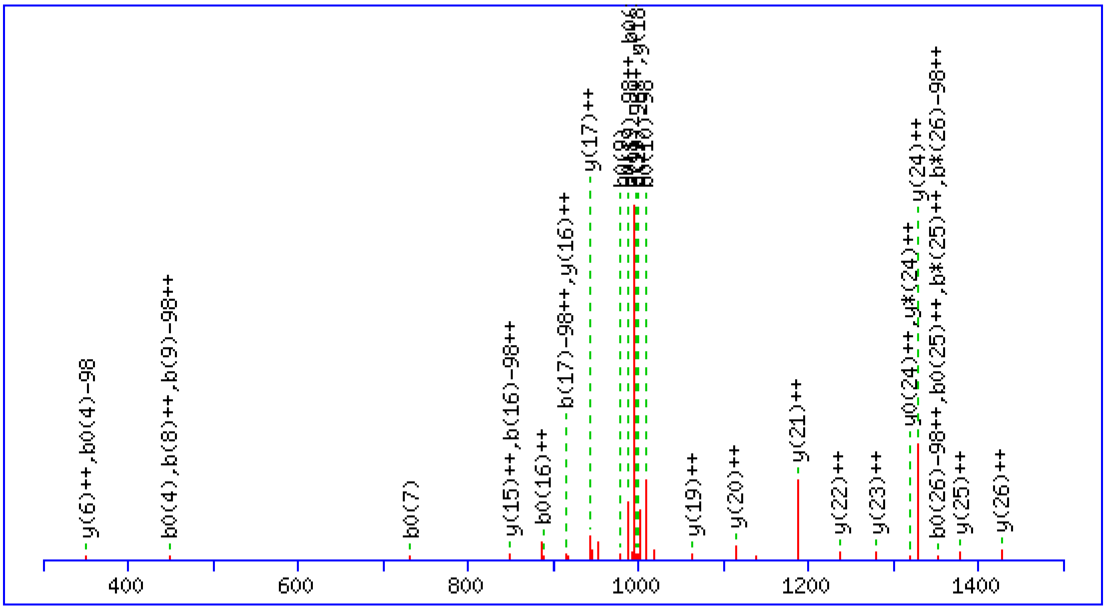
Monoisotopic mass of neutral peptide Mr(calc): 1027.4409
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 19 **Expect:** 0.039
Matched b ions: b(4)-98, b(5)
Matched y ions: y(3), y(4), y(5), y(6)++, y(6)

Peptide No.1112

TSPTPSVFVELGEEELEAVTARPEAVER
Confirmed sites:
Ambiguous sites: @T:1orS:2

MS/MS Fragmentation of **TSPTPSVFVELGEEELEAVTARPEAVER**
Found in **B2L13_MOUSE** in **SwissProt**, Bcl-2-like protein 13 OS=Mus musculus GN=Bcl2l13 PE=1 SV=2

Match to Query 5733: 3121.487130 from(1041.502986,3+) index(5931)
Title: Elution from: 74.782 to 74.782 scan no 6684 cid35.00 polarity:+:m1s



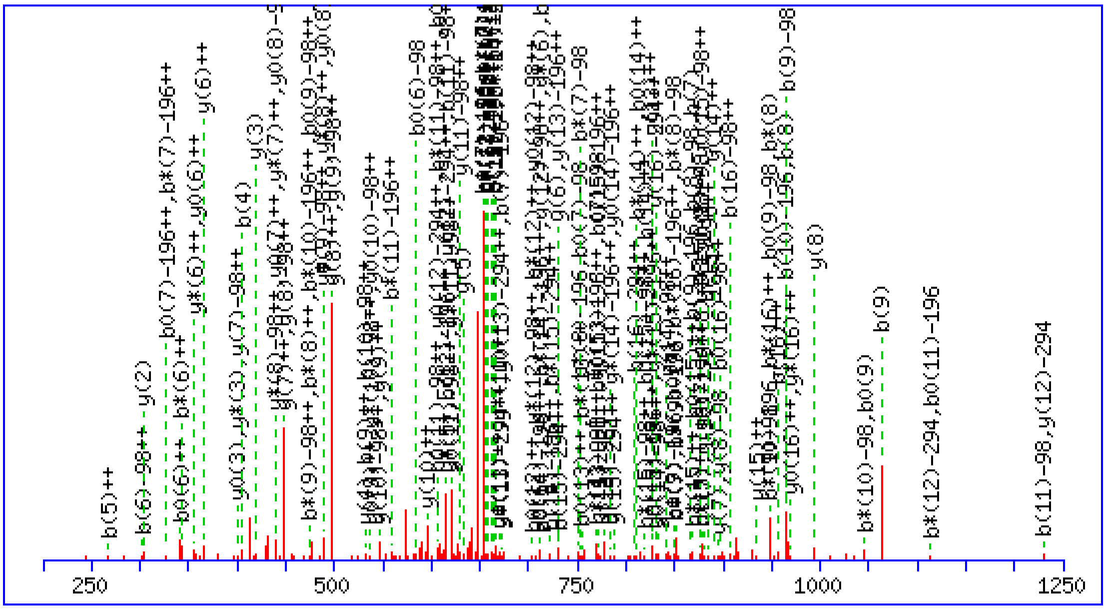
Monoisotopic mass of neutral peptide Mr(calc): 3121.4856
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 67 **Expect:** 1.4e-006
Matched b ions: b(8)++, b(9)-98++, b(9), b(16)-98++, b(17)-98++, b(19)-98++
Matched y ions: y(6)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)++, y(21)++, y(22)++, y(23)++, y(24)++, y(25)++, y(26)++

Peptide No.1113

TSSKESSPVPSPTLDRK
Confirmed sites: @S:6,@S:7,@S:11
Ambiguous sites:

MS/MS Fragmentation of **TSSKESSPVPSPTLDRK**
Found in **SPTB2_MOUSE** in **SwissProt**, Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2

Match to Query 4345: 2054.835741 from(685.952523,3+) index(3640)
Title: Elution from: 24.040 to 24.040 scan no 1663 cid35.00 polarity:+:m1s



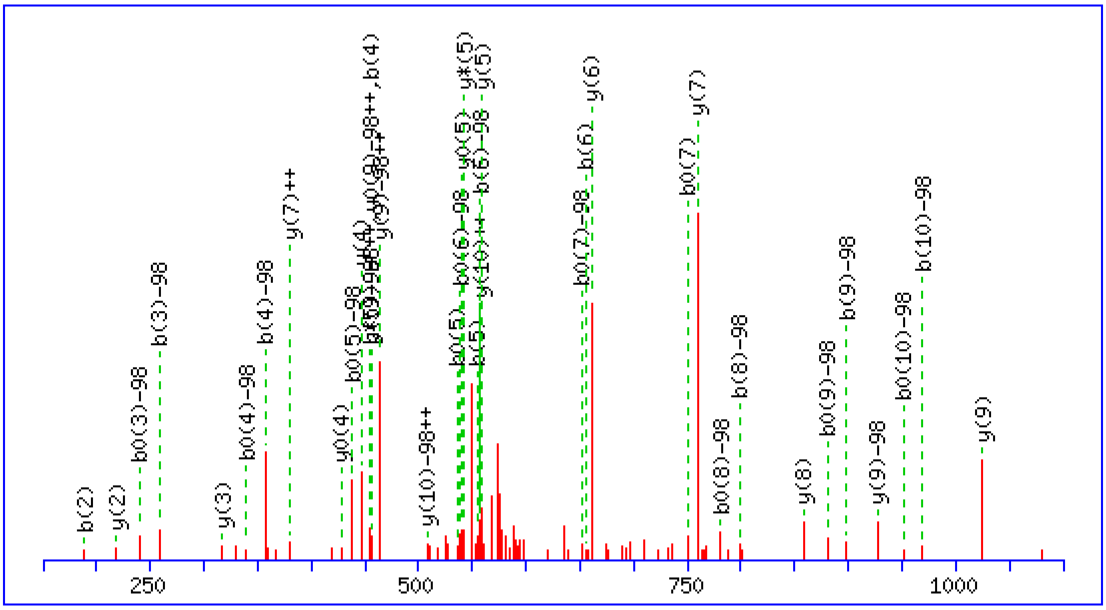
Monoisotopic mass of neutral peptide Mr(calc): 2054.8364
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.038
Matched b ions: b(4), b(5)++, b(6)-98++, b(7)-98, b(7), b(7)-196, b(8)-98, b(8), b(9)-98, b(9), b(9)++, b(9)-196, b(10)-98++, b(10)-196, b(11)-98, b(11)-98++, b(11)++, b(12)-196++, b(12)++, b(12)-98++, b(13)-196++, b(14)-196++, b(14)-98++, b(14)++, b(15)++, b(15)-294++, b(16)++, b(16)-98++, b(16)-294++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7)++, y(7)-98++, y(7), y(8)++, y(8)-98++, y(8), y(8)-98, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)-98++, y(12)-294, y(12)-294++, y(12)-98++, y(12)-196++, y(13)-98++, y(13)++, y(13)-196++, y(14)-98++, y(14)++, y(15)-294++, y(15)-98++, y(15)++, y(16)-294++, y(16)-196++

Peptide No.1114

TSSVVTLEVAK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TSSVVTLEVAK**
Found in **AFAD_MOUSE** in **SwissProt**, Afadin OS=Mus musculus GN=Mllt4 PE=1 SV=3

Match to Query 1450: 1212.599744 from(607.307148,2+) index(1689)
Title: Elution from: 33.058 to 33.058 scan no 2959 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1212.6003
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 5.3e-006
Matched b ions: b(2), b(3)-98, b(4)-98, b(4), b(5)-98, b(5), b(6)-98, b(6), b(8)-98, b(9)-98, b(10)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(7)++, y(8), y(9)-98++, y(9)-98, y(9), y(10)-98++, y(10)++

Peptide No.1115

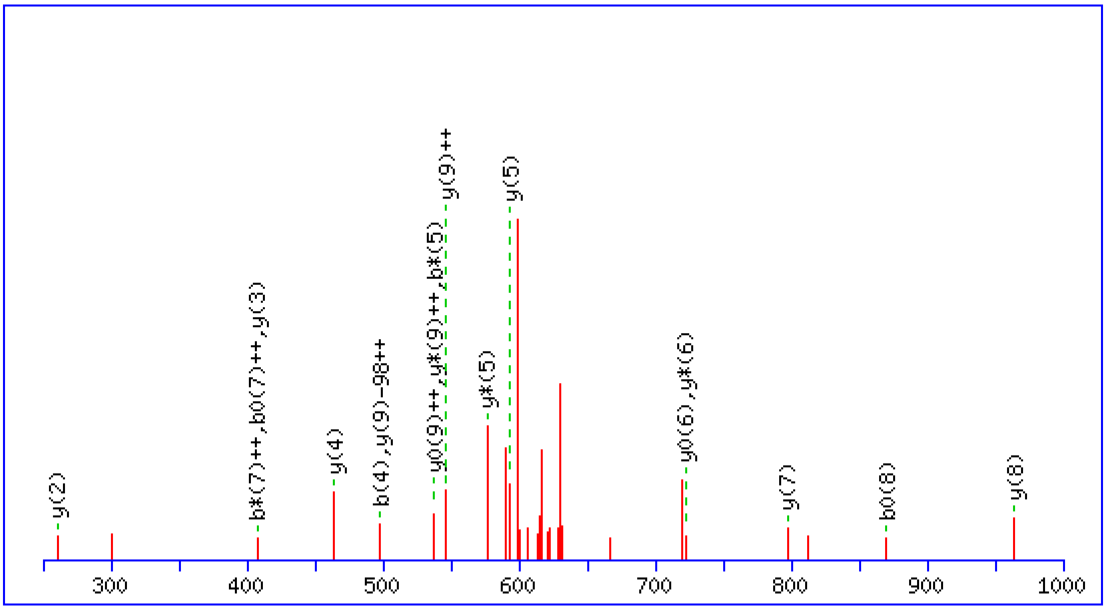
TTQSGFEGFLK

Confirmed sites: @S:4

Ambiguous sites:

MS/MS Fragmentation of **TTQSGFEGFLK**
Found in **URIC_MOUSE** in **SwissProt**, Uricase OS=Mus musculus GN=Uox PE=1 SV=2

Match to Query 1914: 1293.563802 from(647.789177,2+) index(2579)
Title: Elution from: 47.692 to 47.692 scan no 4714 cid35.00 polarity:+



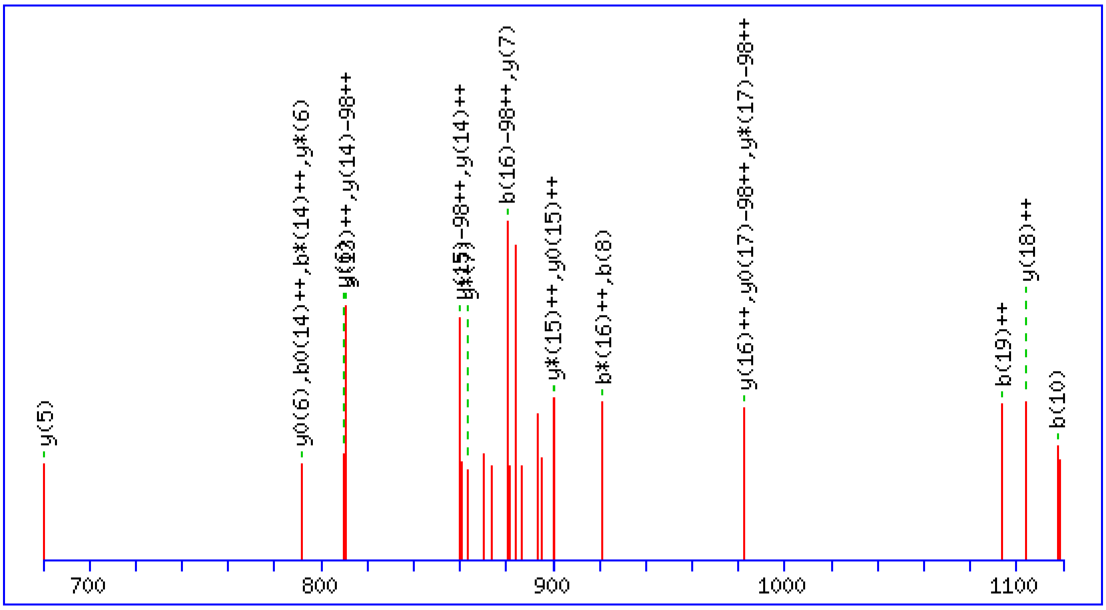
Monoisotopic mass of neutral peptide Mr(calc): 1293.5642
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0043
Matched b ions: b(4)
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(8), y(9)++, y(9)-98++

Peptide No.1116

TTQSLQDFPVADSEEEAEEEFQK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **TTQSLQDFPVADSEEEAEEEFQK**
Found in **TFP11_MOUSE** in **SwissProt**, Tuftelin-interacting protein 11 OS=Mus musculus GN=Tfip11 PE=1 SV=1

Match to Query 5675: 2736.130032 from(913.050620,3+) index(5834)
Title: Elution from: 48.478 to 48.478 scan no 4761 cid35.00 polarity:+:m1s



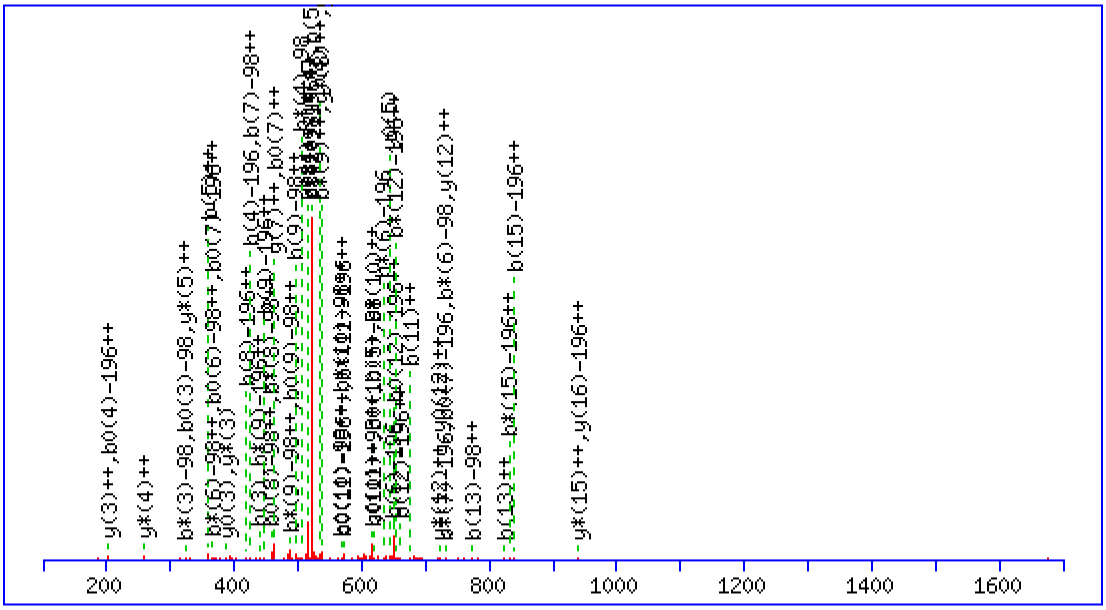
Monoisotopic mass of neutral peptide Mr(calc): 2736.1327
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 **Expect:** 0.0091
Matched b ions: b(8), b(10), b(16)-98++, b(19)++
Matched y ions: y(5), y(6), y(7), y(13)++, y(14)-98++, y(14)++, y(15)-98++, y(16)++, y(18)++

Peptide No.1117

TTRTPEVSGYTYEKTER
Confirmed sites: @T:2,@T:4
Ambiguous sites:

MS/MS Fragmentation of **TTRTPEVSGYTYEKTER**
Found in **MAP1B_MOUSE** in **SwissProt**, Microtubule-associated protein 1B OS=Mus musculus GN=Map1b PE=1 SV=2

Match to Query 4786: 2176.903592 from(545.233174,4+) index(44)
Title: Elution from: 22.428 to 22.428 scan no 1048 cid35.00 polarity:+



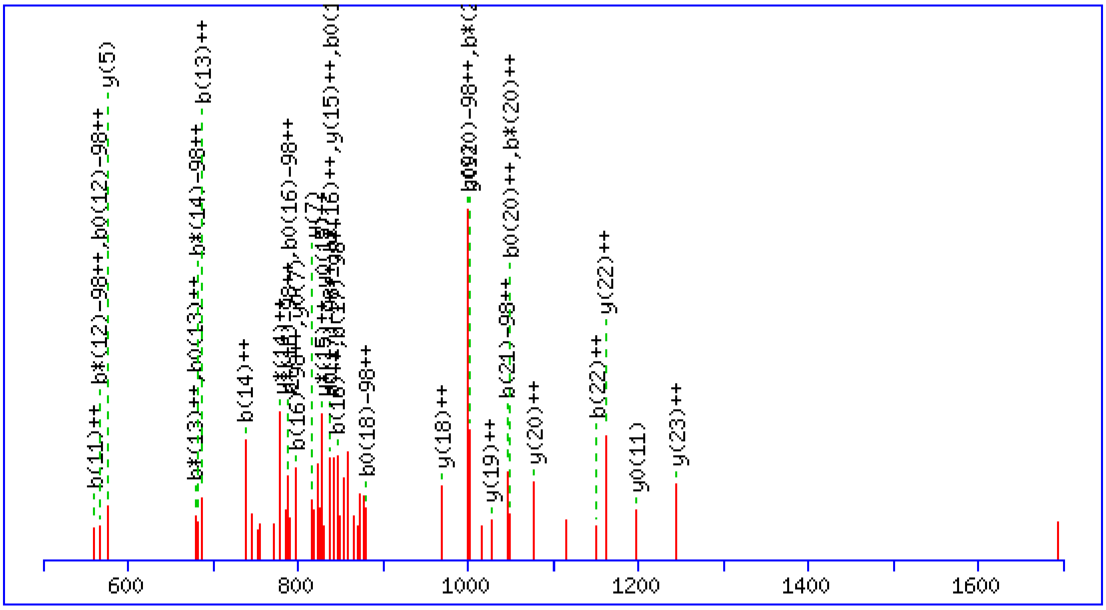
Monoisotopic mass of neutral peptide Mr(calc): 2176.9079
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.027
Matched b ions: b(3), b(4)-98, b(4)-196, b(5)++, b(5)-196, b(5)-98, b(6)-196, b(7)-98++, b(8)++, b(8)-196++, b(9)-196++, b(9)-98++, b(11)++, b(12)-196++, b(13)++, b(13)-98++, b(15)-196++
Matched y ions: y(3)++, y(4), y(7)++, y(10)++, y(12)++, y(16)-196++

Peptide No.1118

TTSPATDAGHVQETSEPSLQALESR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TTSPATDAGHVQETSEPSLQALESR**
Found in **AIMP2_MOUSE** in **SwissProt**, Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Mus musculus GN=Aimp2 PE=1 SV=2

Match to Query 6654: 2691.203214 from(898.075014,3+) index(6177)
Title: Elution from: 40.116 to 40.116 scan no 3980 cid35.00 polarity:+:m1s



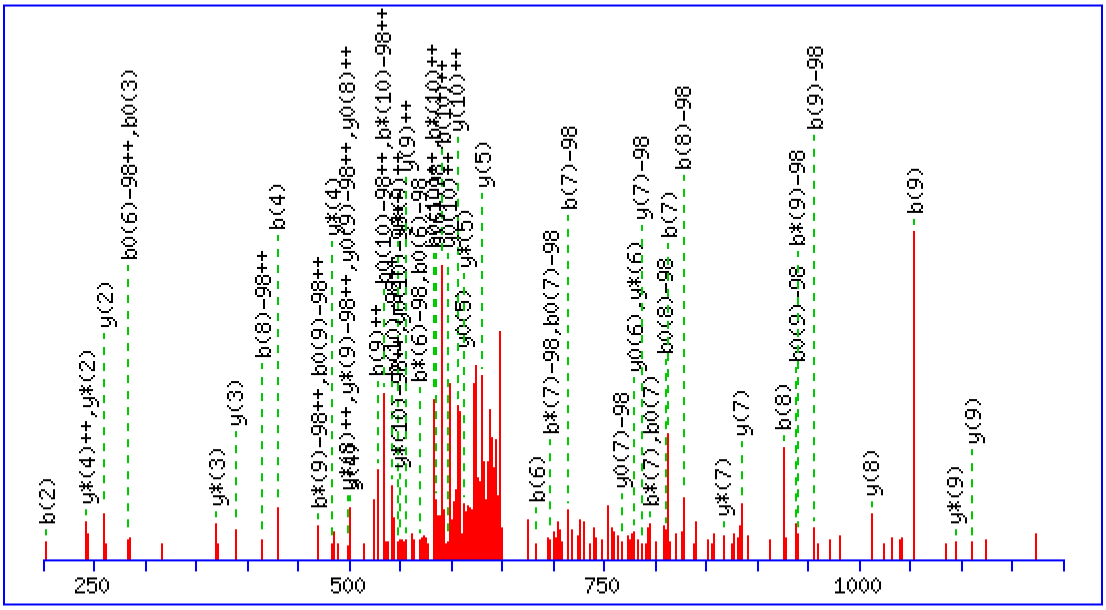
Monoisotopic mass of neutral peptide Mr(calc): 2691.2025
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.023
Matched b ions: b(11)++, b(13)++, b(14)++, b(16)++, b(16)-98++, b(17)-98++, b(21)-98++, b(22)++
Matched y ions: y(5), y(7), y(9), y(15)++, y(18)++, y(19)++, y(20)++, y(22)++, y(23)++

Peptide No.1119

TTVKSSELQQL
Confirmed sites:
Ambiguous sites: @S:5orS:6

MS/MS Fragmentation of **TTVKSSELQQL**
Found in **SO2B1_MOUSE** in **SwissProt**, Solute carrier organic anion transporter family member 2B1 OS=Mus musculus GN=Slco2b1 PE=1 SV=1

Match to Query 2887: 1312.627570 from(657.321061,2+) index(1739)
Title: Elution from: 42.627 to 42.627 scan no 3420 cid35.00 polarity:+



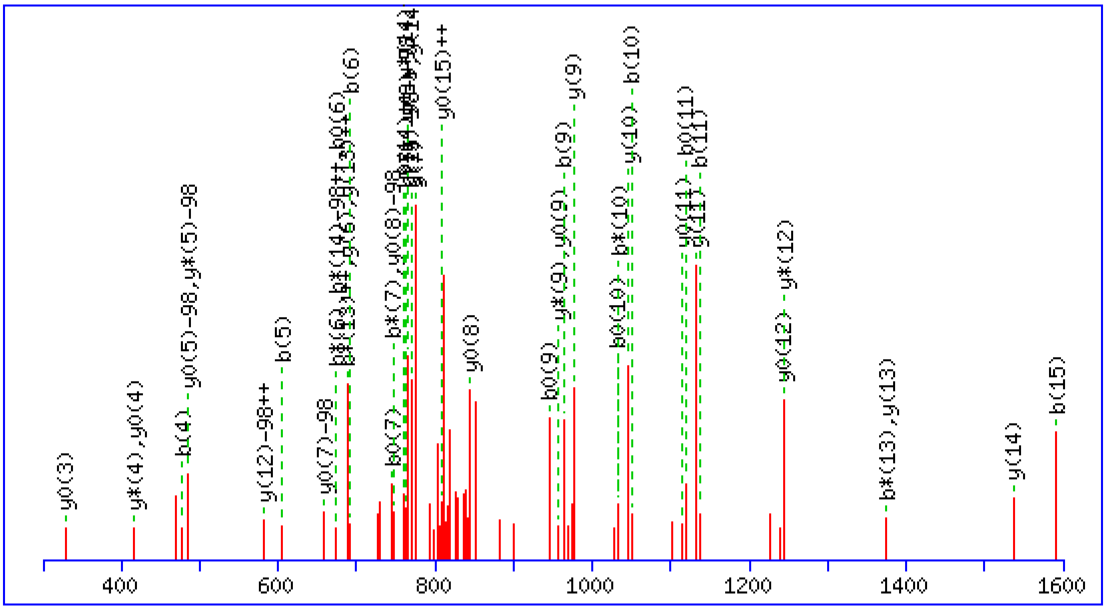
Monoisotopic mass of neutral peptide Mr(calc): 1312.6275
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 **Expect:** 0.0042
Matched b ions: b(2), b(4), b(6)-98, b(6), b(7), b(7)-98, b(8), b(8)-98, b(8)-98++, b(9), b(9)-98, b(9)++, b(10)++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(7), y(7)-98, y(8), y(9), y(9)++, y(10)++

Peptide No.1120

TVYLQSALSSSSSAEK
Confirmed sites:
Ambiguous sites: @S:12orS:13

MS/MS Fragmentation of **TVYLQSALSSSSSAEK**
Found in **EI24_MOUSE** in **SwissProt**, Etoposide-induced protein 2.4 OS=Mus musculus GN=Ei24 PE=1 SV=3

Match to Query 3981: 1736.786028 from(869.400290,2+) index(2301)
Title: Elution from: 37.545 to 37.545 scan no 3643 cid35.00 polarity:+



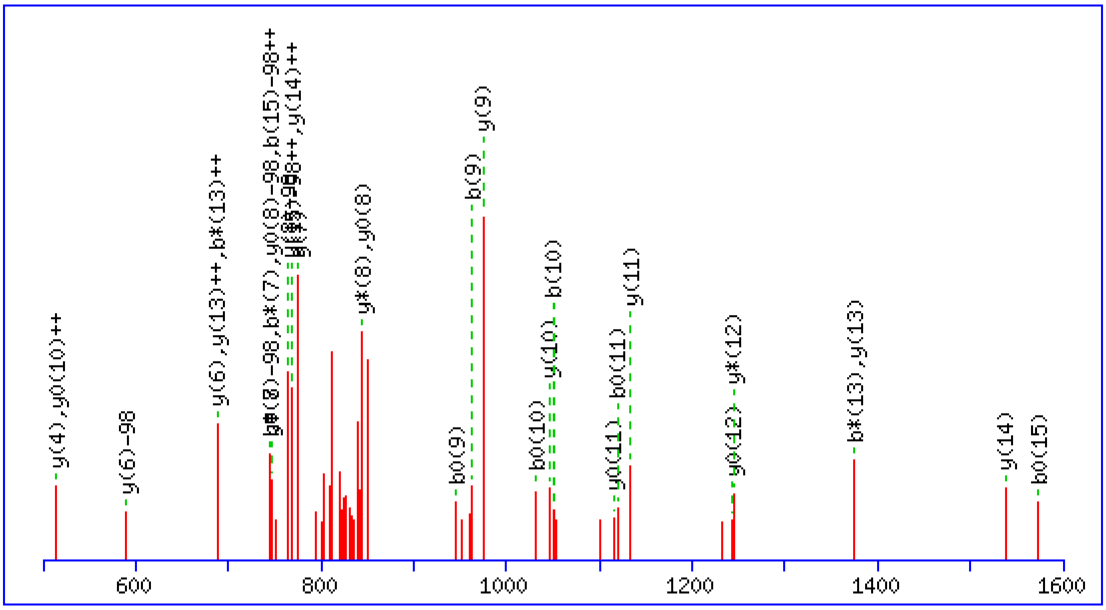
Monoisotopic mass of neutral peptide Mr(calc): 1736.7869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 3.2e-005
Matched b ions: b(4), b(5), b(6), b(7), b(9), b(10), b(11), b(15)
Matched y ions: y(6), y(7), y(8)-98, y(9), y(10), y(11), y(12)-98++, y(13)++, y(13), y(14), y(14)++, y(15)-98++

Peptide No.1121

TVYLQSALSSSSSAEK
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **TVYLQSALSSSSSAEK**
Found in **EI24_MOUSE** in **SwissProt**, Etoposide-induced protein 2.4 OS=Mus musculus GN=Ei24 PE=1 SV=3

Match to Query 3825: 1736.784128 from(869.399340,2+) index(2266)
Title: Elution from: 37.584 to 37.584 scan no 3620 cid35.00 polarity:+



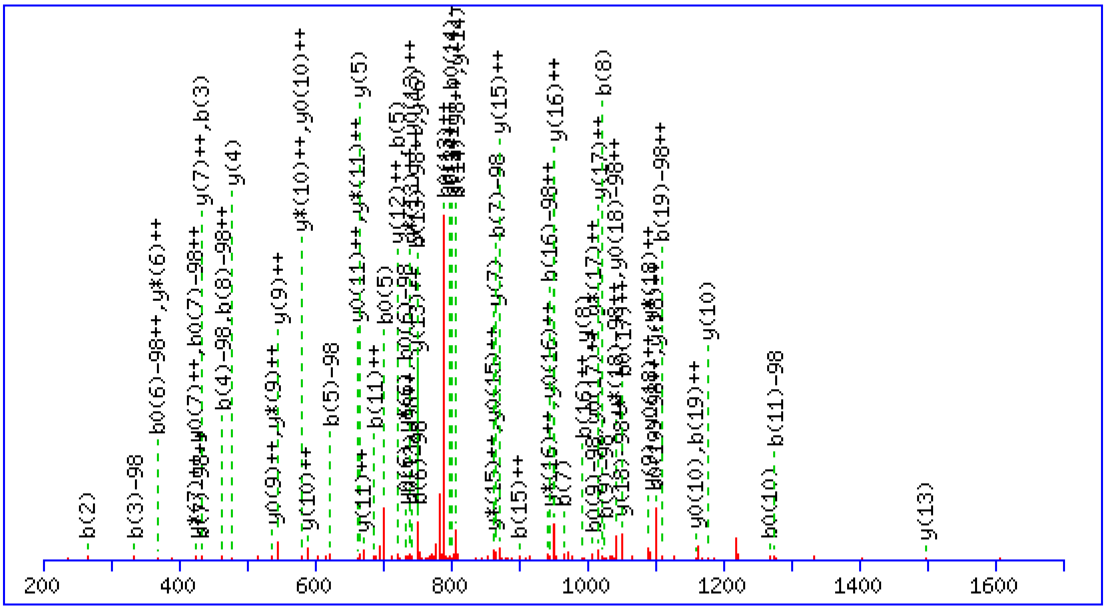
Monoisotopic mass of neutral peptide Mr(calc): 1736.7869
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 **Expect:** 6.2e-008
Matched b ions: b(9), b(10), b(15)-98++
Matched y ions: y(4), y(6), y(6)-98, y(7), y(8)-98, y(9), y(10), y(11), y(13)++, y(13), y(14), y(14)++, y(15)-98++

Peptide No.1122

TYSECEDGTYSPEISWHHGK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **TYSECEDGTYSPEISWHHGK**
Found in **PTSS1_MOUSE** in **SwissProt**, Phosphatidylserine synthase 1 OS=Mus musculus GN=Ptdss1 PE=2 SV=1

Match to Query 6307: 2461.950537 from(821.657455,3+) index(5675)
Title: Elution from: 34.617 to 34.617 scan no 3255 cid35.00 polarity:+:m1s



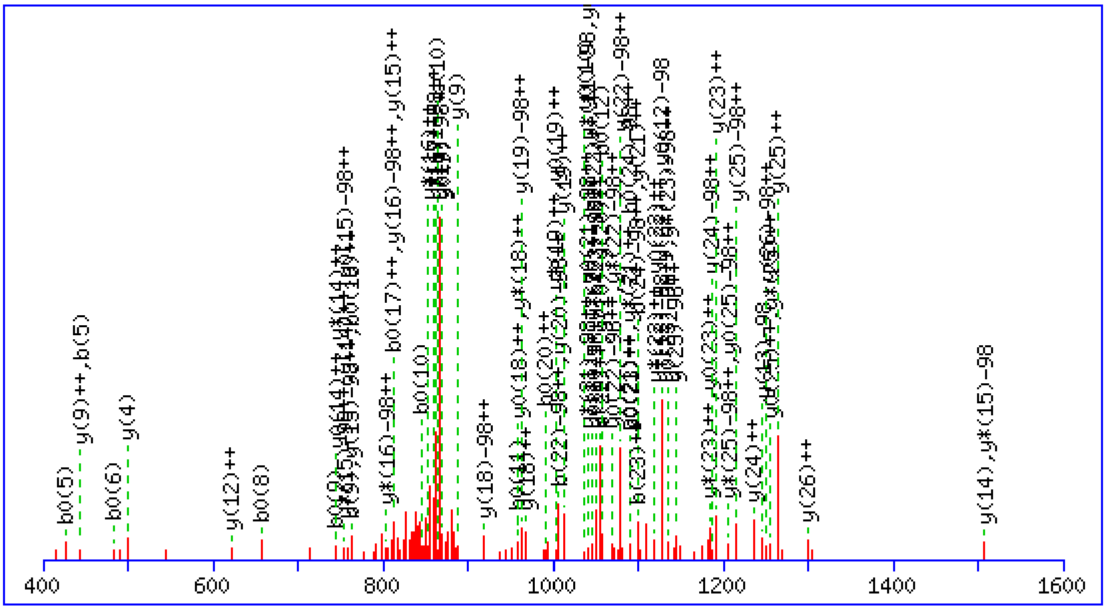
Monoisotopic mass of neutral peptide Mr(calc): 2461.9522
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 62 **Expect:** 3.2e-006
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5)-98, b(5), b(6)-98, b(7)-98++, b(7)-98, b(7), b(8)-98++, b(8), b(9)-98, b(11)-98, b(11)++, b(13)-98++, b(13)++, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(19)++, b(19)-98++
Matched y ions: y(4), y(5), y(6), y(7)++, y(7), y(8), y(9)++, y(9), y(10)++, y(10), y(11)++, y(12)++, y(13), y(13)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(18)-98++

Peptide No.1123

VAGSEGSSSTLVDYTSTSSTGGSPVRK
Confirmed sites: @S:18
Ambiguous sites:

MS/MS Fragmentation of **VAGSEGSSSTLVDYTSTSSTGGSPVRK**
Found in **RBBP6_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase RBBP6 OS=Mus musculus GN=Rbbp6 PE=1 SV=5

Match to Query 5455: 2696.213811 from(899.745213,3+) index(4362)
Title: Elution from: 31.142 to 31.142 scan no 2643 cid35.00 polarity:+:m1s



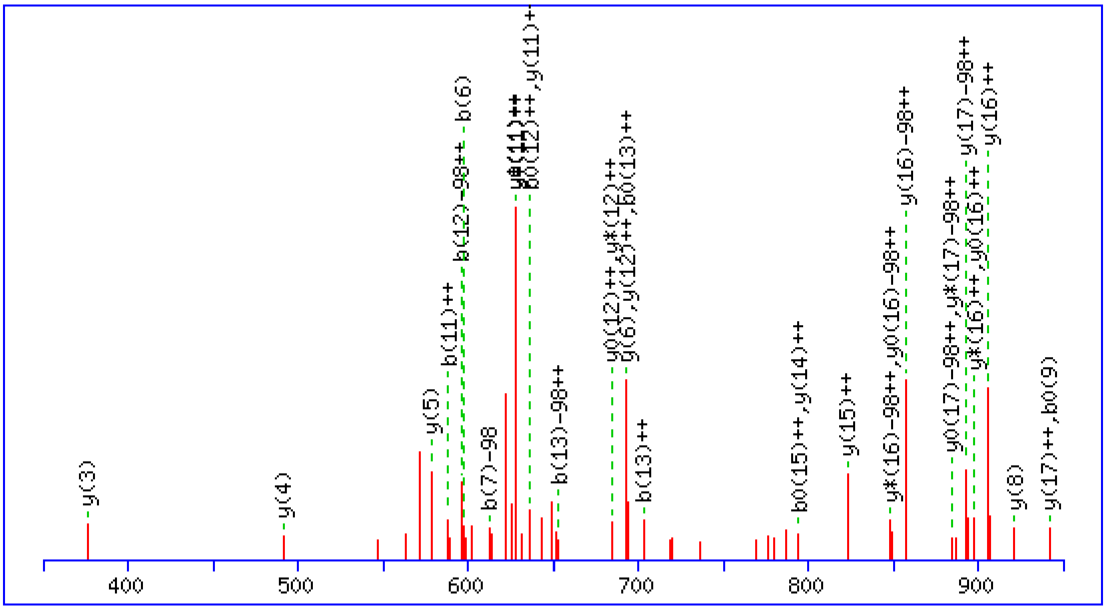
Monoisotopic mass of neutral peptide Mr(calc): 2696.2178
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 **Expect:** 1e-006
Matched b ions: b(5), b(9), b(10), b(22)-98++, b(22)++, b(23)-98++, b(23)++, b(24)-98++
Matched y ions: y(4), y(9)++, y(9), y(10), y(12)++, y(13)-98, y(14), y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-98++, y(18)++, y(18)-98++, y(19)++, y(19)-98++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)++, y(24)-98++, y(25)++, y(25)-98++, y(26)++, y(26)-98++

Peptide No.1124

VASGSDLHLTDIDSDSNR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **VASGSDLHLTDIDSDSNR**
Found in **MY18A_MOUSE** in **SwissProt**, Myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2

Match to Query 4177: 1980.843672 from(661.288500,3+) index(4911)
Title: Elution from: 37.101 to 37.101 scan no 3439 cid35.00 polarity:+:m1s



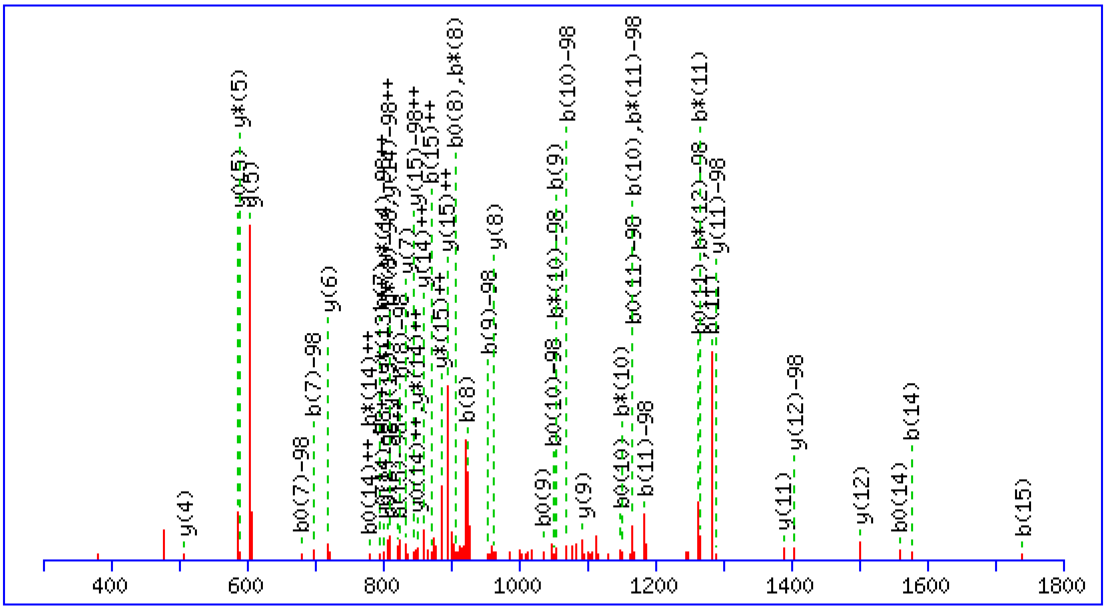
Monoisotopic mass of neutral peptide Mr(calc): 1980.8426
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0024
Matched b ions: b(6), b(7)-98, b(11)++, b(12)-98++, b(13)++, b(13)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(8), y(11)++, y(12)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++

Peptide No.1125

VATLNSEEENDPPTYK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **VATLNSEEENDPPTYK**
Found in **VIGLN_MOUSE** in **SwissProt**, Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1

Match to Query 3871: 1885.796468 from(943.905510,2+) index(4270)
Title: Elution from: 29.967 to 29.967 scan no 2482 cid35.00 polarity:+:m1s



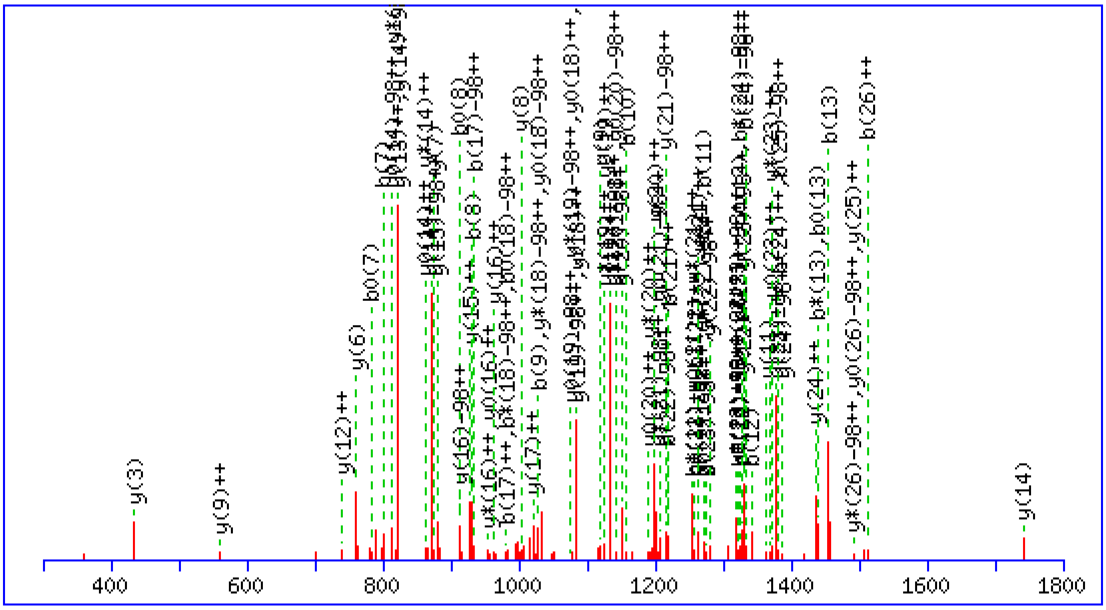
Monoisotopic mass of neutral peptide Mr(calc): 1885.7982
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00048
Matched b ions: b(7)-98, b(7), b(8), b(8)-98, b(9), b(9)-98, b(10), b(10)-98, b(11), b(11)-98, b(14), b(15), b(15)-98++, b(15)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(11), y(11)-98, y(12), y(12)-98, y(13)++, y(14)++, y(14)-98++, y(15)++, y(15)-98++

Peptide No.1126

VDIITEEMPENALPSDEDDKDPNDPYR
Confirmed sites: @S:15
Ambiguous sites:

MS/MS Fragmentation of **VDIITEEMPENALPSDEDDKDPNDPYR**
Found in **AP3D1_MOUSE** in **SwissProt**, AP-3 complex subunit delta-1 OS=Mus musculus GN=Ap3d1 PE=1 SV=1

Match to Query 7015: 3196.338825 from(1066.453551,3+) index(6824)
Title: Elution from: 50.533 to 50.533 scan no 5236 cid35.00 polarity:+:m1s



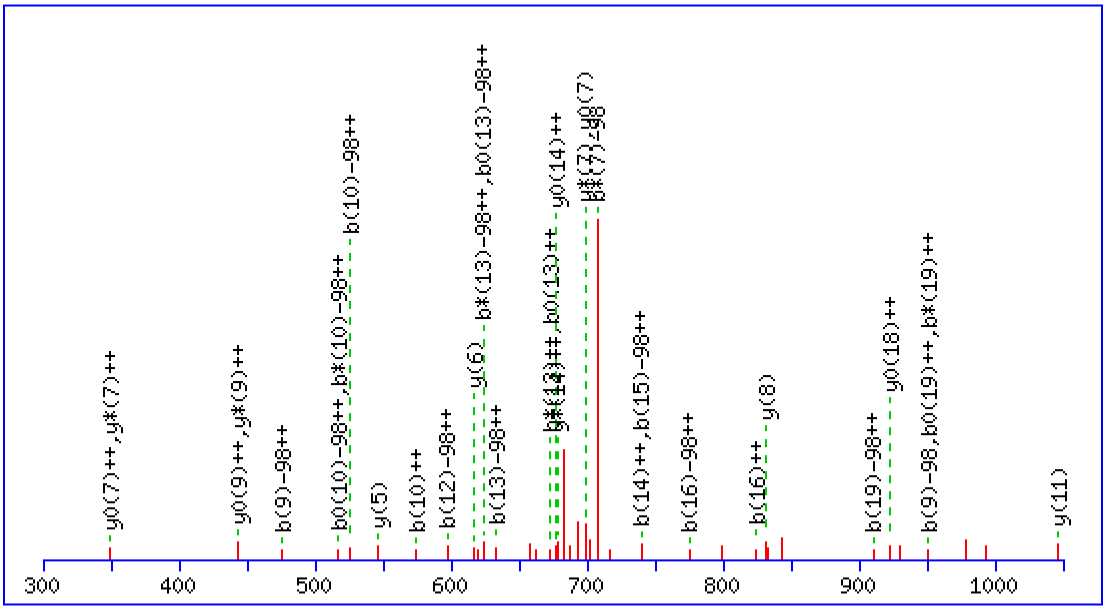
Monoisotopic mass of neutral peptide Mr(calc): 3196.3431
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 96 **Expect:** 1.9e-009
Matched b ions: b(7), b(8), b(9), b(10), b(11), b(12), b(13), b(17)-98++, b(17)++, b(21)++, b(22)-98++, b(23)++, b(23)-98++, b(24)-98++, b(24)++, b(25)-98++, b(26)++
Matched y ions: y(3), y(6), y(7), y(8), y(9)++, y(9), y(11), y(12)++, y(13)++, y(14)-98++, y(14)++, y(14), y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(18)++, y(19)++, y(19)-98++, y(20)++, y(20)-98++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)-98++, y(23)++, y(24)++, y(24)-98++, y(25)++

Peptide No.1127

VDNARVSPEVGSADVASIAQK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **VDNARVSPEVGSADVASIAQK**
Found in **FAM21_MOUSE** in **SwissProt**, WASH complex subunit FAM21 OS=Mus musculus GN=Fam21 PE=1 SV=1

Match to Query 5564: 2192.045535 from(731.689121,3+) index(5662)
Title: Elution from: 36.138 to 36.138 scan no 3429 cid35.00 polarity:+:m1s



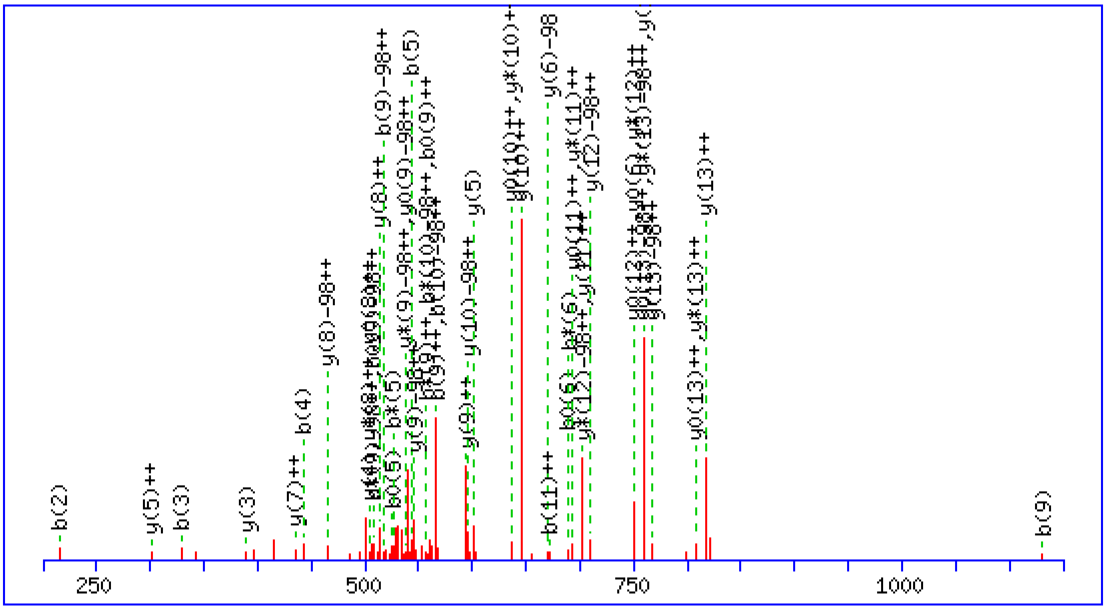
Monoisotopic mass of neutral peptide Mr(calc): 2192.0474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.034
Matched b ions: b(9)-98++, b(9)-98, b(10)-98++, b(10)++, b(12)-98++, b(13)-98++, b(14)++, b(15)-98++, b(16)++, b(16)-98++, b(19)-98++
Matched y ions: y(5), y(6), y(8), y(11)

Peptide No.1128

VDNLTYRTSPDTLR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **VDNLTYRTSPDTLR**
Found in **SRSF2_MOUSE** in **SwissProt**, Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4

Match to Query 3781: 1729.803012 from(577.608280,3+) index(5091)
Title: Elution from: 30.583 to 30.583 scan no 2679 cid35.00 polarity:+:m1s



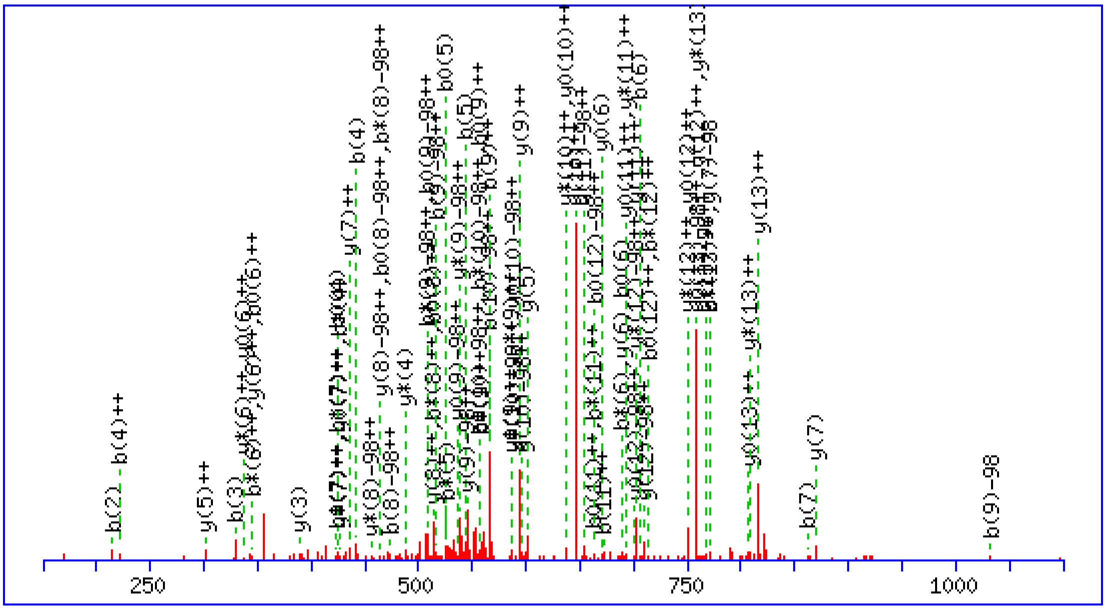
Monoisotopic mass of neutral peptide Mr(calc): 1729.8036
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 55 **Expect:** 1.7e-005
Matched b ions: b(2), b(3), b(4), b(5), b(9)++, b(9), b(9)-98++, b(10)-98++, b(11)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(6)-98, y(7)++, y(8)++, y(8)-98++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.1129

VDNLTYRTSPDTLR
Confirmed sites: @T:8
Ambiguous sites:

MS/MS Fragmentation of **VDNLTYRTSPDTLR**
Found in **SRSF2_MOUSE** in **SwissProt**, Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4

Match to Query 3752: 1729.804599 from(577.608809,3+) index(1264)
Title: Elution from: 38.621 to 38.621 scan no 2835 cid35.00 polarity:+



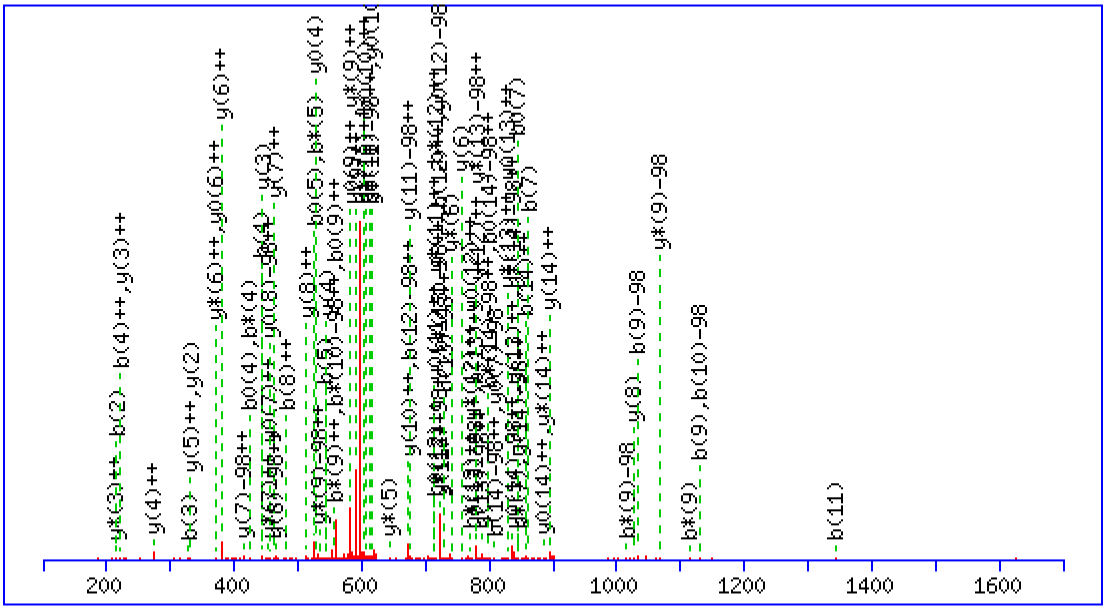
Monoisotopic mass of neutral peptide Mr(calc): 1729.8036
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.00028
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6), b(7), b(8)-98++, b(9)++, b(9)-98, b(9)-98++, b(10)-98++, b(11)++
Matched y ions: y(3), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(7)-98, y(8)++, y(8)-98++, y(9)-98++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.1130

VDNLTYRTSPDTLRR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **VDNLTYRTSPDTLRR**
Found in **SRSF2_MOUSE** in **SwissProt**, Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4

Match to Query 4121: 1885.906107 from(629.642645,3+) index(3859)
Title: Elution from: 34.758 to 34.758 scan no 2367 cid35.00 polarity:+:m1s



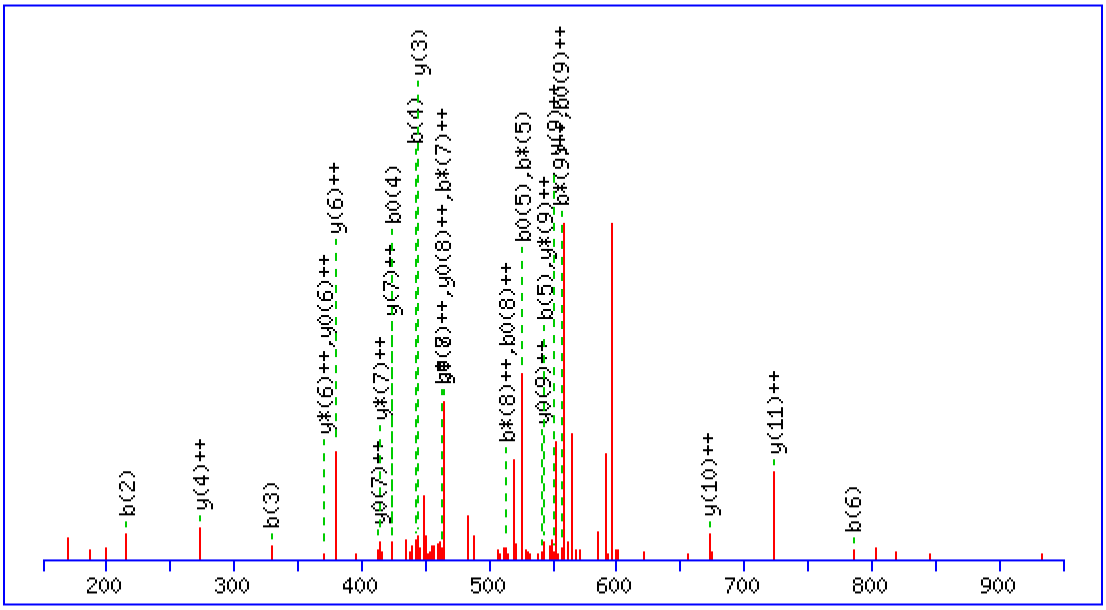
Monoisotopic mass of neutral peptide Mr(calc): 1885.9047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 43 **Expect:** 0.0003
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(7), b(8)++, b(9)-98, b(9), b(10)-98, b(10)++, b(11), b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)++, b(14)-98++
Matched y ions: y(2), y(3)++, y(3), y(4)++, y(4), y(5)++, y(6)++, y(6), y(7)-98++, y(7)++, y(8)-98++, y(8), y(8)++, y(9)++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(13)++, y(13)-98++, y(14)++, y(14)-98++

Peptide No.1131

VDNLTYRTSPDTLRR
Confirmed sites: @Y:6
Ambiguous sites:

MS/MS Fragmentation of **VDNLTYRTSPDTLRR**
Found in **SRSF2_MOUSE** in **SwissProt**, Serine/arginine-rich splicing factor 2 OS=Mus musculus GN=Srsf2 PE=1 SV=4

Match to Query 4537: 1885.904132 from(472.483309,4+) index(1257)
Title: Elution from: 27.021 to 27.021 scan no 2229 cid35.00 polarity:+



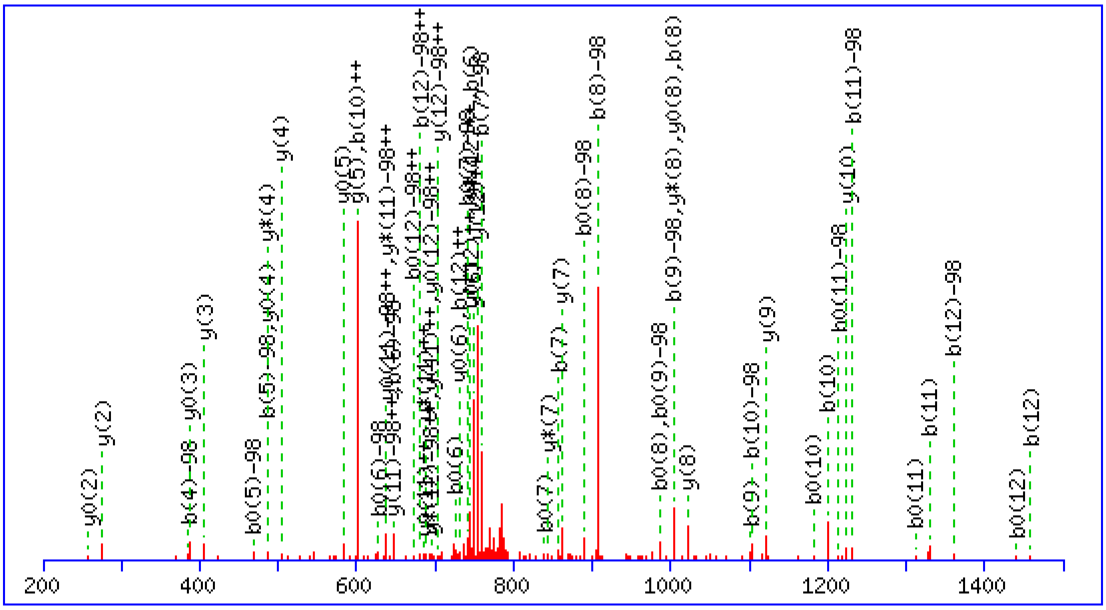
Monoisotopic mass of neutral peptide Mr(calc): 1885.9047
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y6 : Phospho (Y)
Ions Score: 23 **Expect:** 0.037
Matched b ions: b(2), b(3), b(4), b(5), b(6)
Matched y ions: y(3), y(4)++, y(6)++, y(7)++, y(9)++, y(10)++, y(11)++

Peptide No.1132

VDSTTCLFPVEEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **VDSTTCLFPVEEK**
Found in **GFPT1_MOUSE** in **SwissProt**, Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 PE=1 SV=3

Match to Query 3352: 1603.684360 from(802.849456,2+) index(1993)
Title: Elution from: 54.699 to 54.699 scan no 4321 cid35.00 polarity:+



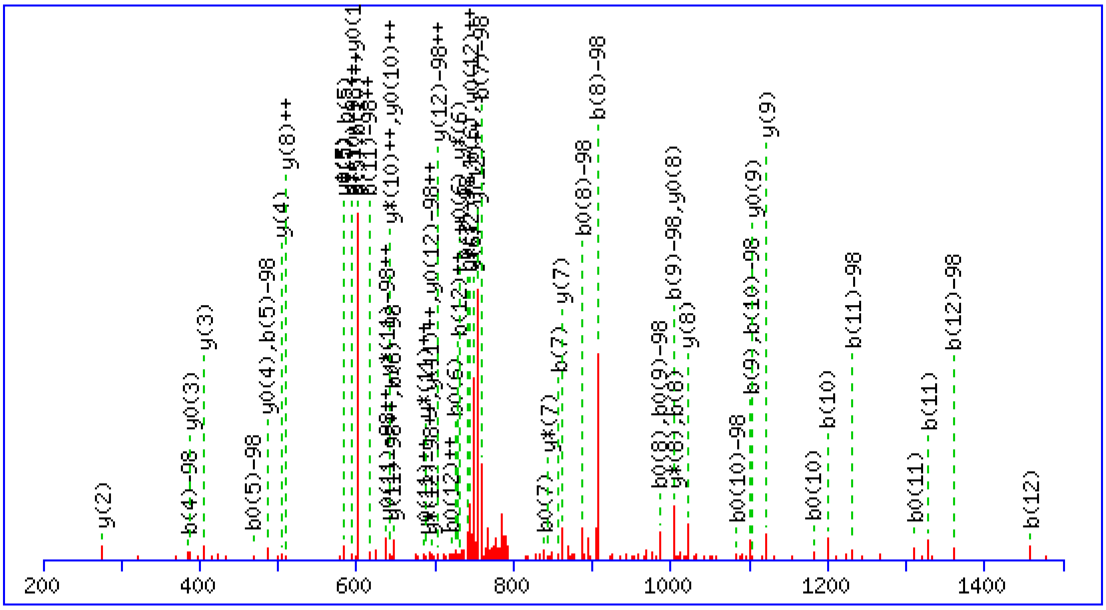
Monoisotopic mass of neutral peptide Mr(calc): 1603.6841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 **Expect:** 4e-008
Matched b ions: b(4)-98, b(5)-98, b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9)-98, b(9), b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(12)-98, b(12), b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11)-98++, y(11)++, y(12)++, y(12)-98++

Peptide No.1133

VDSTTCLFPVEEK
Confirmed sites:
Ambiguous sites: @S:3orT:4

MS/MS Fragmentation of **VDSTTCLFPVEEK**
Found in **GFPT1_MOUSE** in **SwissProt**, Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Mus musculus GN=Gfpt1 PE=1 SV=3

Match to Query 3858: 1603.684238 from(802.849395,2+) index(2364)
Title: Elution from: 54.641 to 54.641 scan no 4592 cid35.00 polarity:+



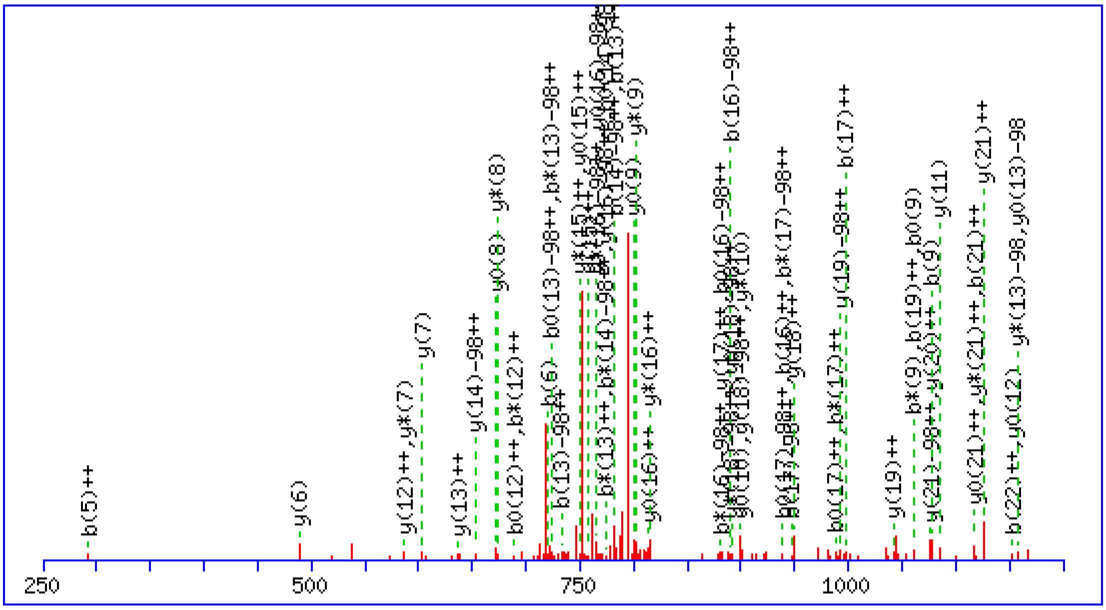
Monoisotopic mass of neutral peptide Mr(calc): 1603.6841
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 **Expect:** 5e-007
Matched b ions: b(4)-98, b(5)-98, b(5), b(6)-98, b(6), b(7)-98, b(7), b(8)-98, b(8), b(9), b(9)-98, b(10)++, b(10), b(10)-98, b(11), b(11)-98, b(11)-98++, b(12), b(12)-98, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)++, y(9), y(11)-98++, y(11)++, y(12)++, y(12)-98++

Peptide No.1134

VEPAWHDQDETSSVKSDGAGGAR
Confirmed sites: @S:13
Ambiguous sites:

MS/MS Fragmentation of **VEPAWHDQDETSSVKSDGAGGAR**
Found in **LARP1_MOUSE** in **SwissProt**, La-related protein 1 OS=Mus musculus GN=Larp1 PE=1 SV=2

Match to Query 6164: 2478.042060 from(827.021296,3+) index(4492)
Title: Elution from: 24.690 to 24.690 scan no 1875 cid35.00 polarity:+:m1s



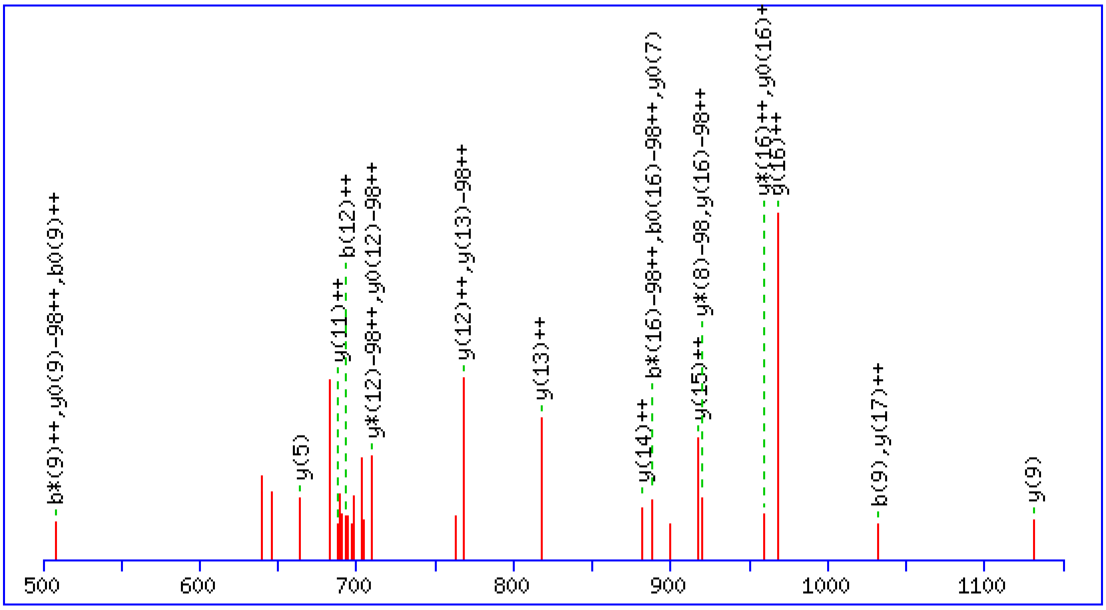
Monoisotopic mass of neutral peptide Mr(calc): 2478.0449
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0037
Matched b ions: b(5)++, b(6), b(9), b(13)++, b(13)-98++, b(14)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(19)++, b(21)++, b(22)++
Matched y ions: y(6), y(7), y(11), y(12)++, y(13)++, y(14)-98++, y(15)++, y(16)-98++, y(17)++, y(18)-98++, y(18)++, y(19)-98++, y(19)++, y(20)++, y(21)++, y(21)-98++

Peptide No.1135

VETAEVCSRPQELPQSPR
Confirmed sites: @S:16
Ambiguous sites:

MS/MS Fragmentation of **VETAEVCSRPQELPQSPR**
Found in **FA63A_MOUSE** in **SwissProt**, Protein FAM63A OS=Mus musculus GN=Fam63a PE=1 SV=1

Match to Query 5588: 2161.980447 from(721.667425,3+) index(5017)
Title: Elution from: 27.907 to 27.907 scan no 2351 cid35.00 polarity:+:m1s



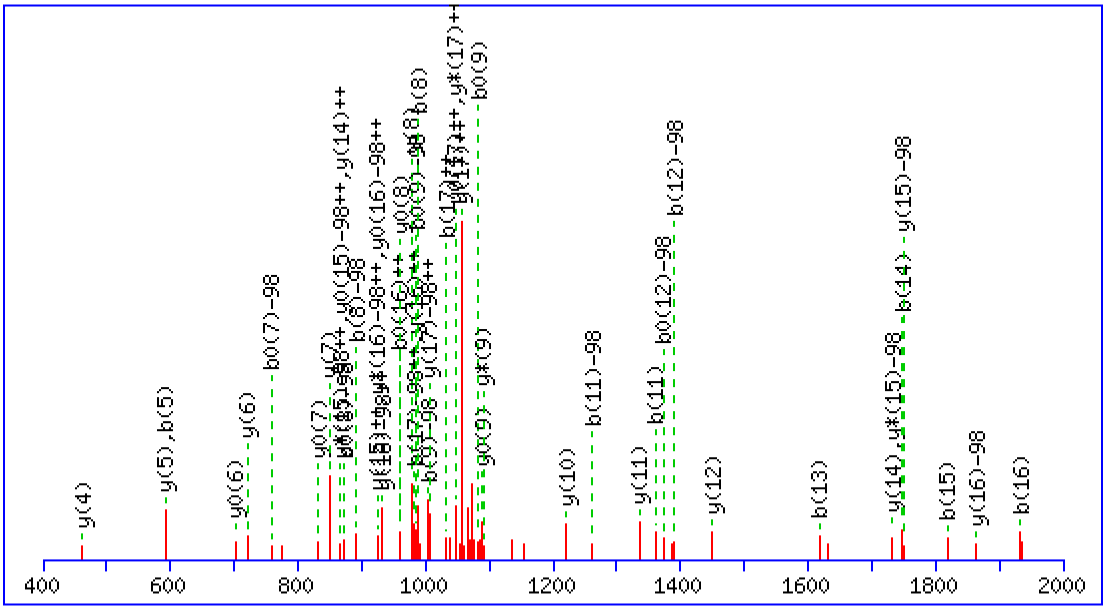
Monoisotopic mass of neutral peptide Mr(calc): 2161.9827
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.016
Matched b ions: b(9), b(12)++
Matched y ions: y(5), y(9), y(11)++, y(12)++, y(13)-98++, y(13)++, y(14)++, y(15)++, y(16)++, y(16)-98++, y(17)++

Peptide No.1136

VFDDDSDDIEEEEEADEK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **VFDDDSDDIEEEEEADEK**
Found in **HTSF1_MOUSE** in **SwissProt**, HIV Tat-specific factor 1 homolog OS=Mus musculus GN=Htatsf1 PE=1 SV=1

Match to Query 5769: 2207.772610 from(1104.893581,2+) index(6046)
Title: Elution from: 38.532 to 38.532 scan no 3774 cid35.00 polarity:+:m1s



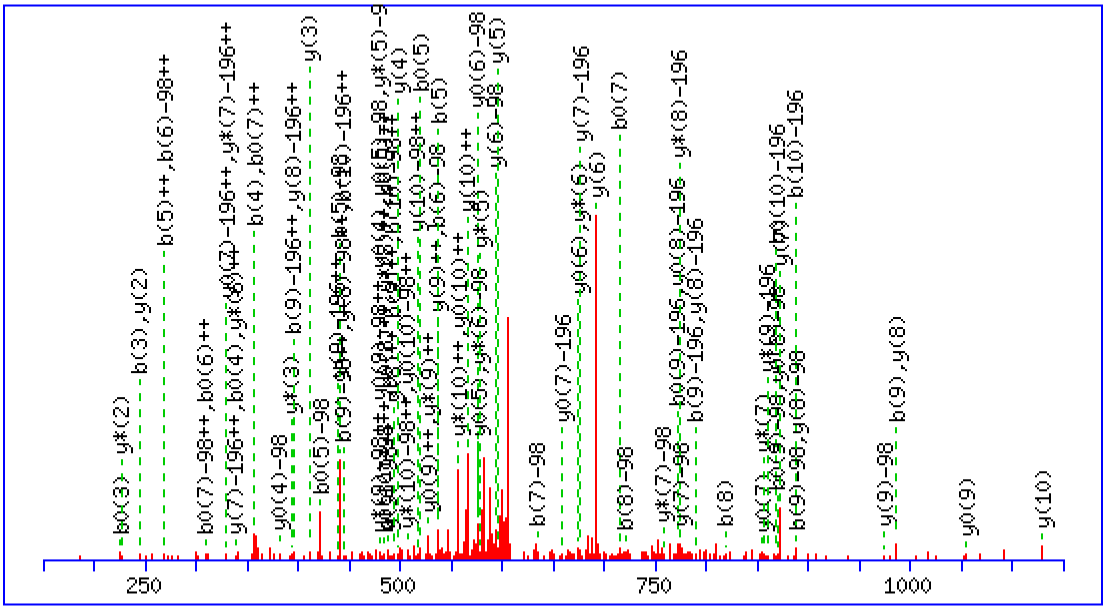
Monoisotopic mass of neutral peptide Mr(calc): 2207.7791
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 1.7e-007
Matched b ions: b(5), b(8)-98, b(8), b(9)-98, b(11), b(11)-98, b(12)-98, b(13), b(14), b(15), b(16), b(17)-98++, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(10), y(11), y(12), y(14), y(14)++, y(15)-98, y(15)++, y(16)-98++, y(16)-98, y(16)++, y(17)++, y(17)-98++

Peptide No.1137

VGSLTPPSSPK
Confirmed sites: @T:5,@S:9
Ambiguous sites:

MS/MS Fragmentation of **VGSLTPPSSPK**
Found in **AAK1_MOUSE** in **SwissProt**, AP2-associated protein kinase 1 OS=Mus musculus GN=Aak1 PE=1 SV=2

Match to Query 2360: 1228.514866 from(615.264709,2+) index(1000)
Title: Elution from: 33.817 to 33.817 scan no 2357 cid35.00 polarity:+



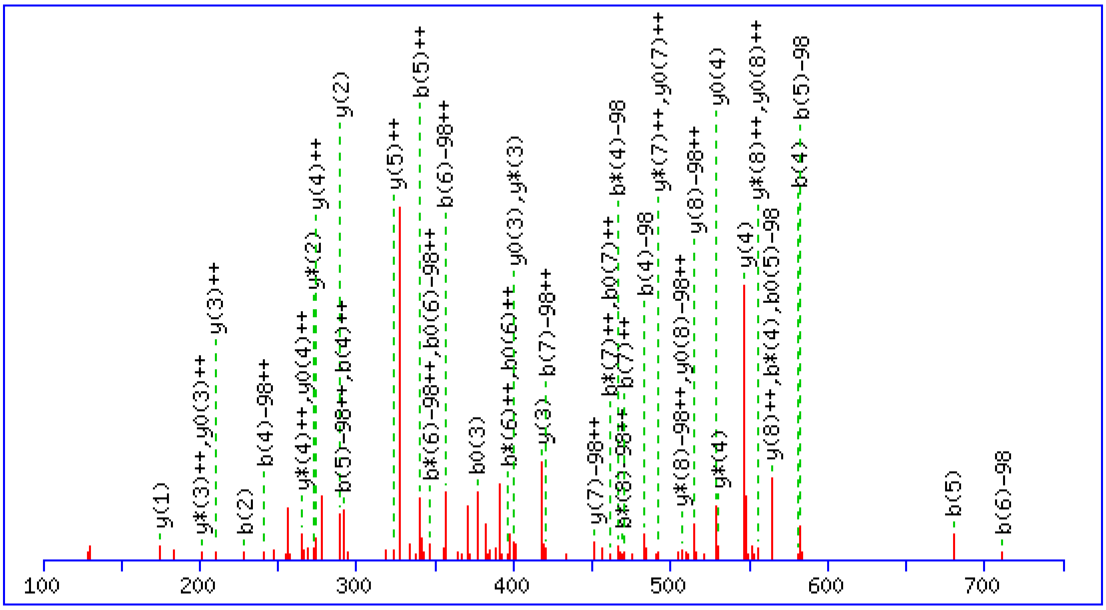
Monoisotopic mass of neutral peptide Mr(calc): 1228.5142
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.0075
Matched b ions: b(3), b(4), b(5)-98, b(5)++, b(5), b(6)-98++, b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(9)-196++, b(9)-98++, b(9)++, b(9)-196, b(10)-196, b(10)-196++, b(10)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)-98, y(7), y(7)-98, y(7)-196++, y(7)-196, y(8)-98, y(8), y(8)-196++, y(8)-98++, y(8)++, y(8)-196, y(9)-98, y(9)++, y(9)-196++, y(9)-98++, y(10)++, y(10), y(10)-98++

Peptide No.1138

VKSWVEENR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **VKSWVEENR**
Found in **3HAO_MOUSE** in **SwissProt**, 3-hydroxyanthranilate 3,4-dioxygenase OS=Mus musculus GN=Haao PE=1 SV=1

Match to Query 1494: 1225.549371 from(409.523733,3+) index(727)
Title: Elution from: 23.320 to 23.320 scan no 1663 cid35.00 polarity:+



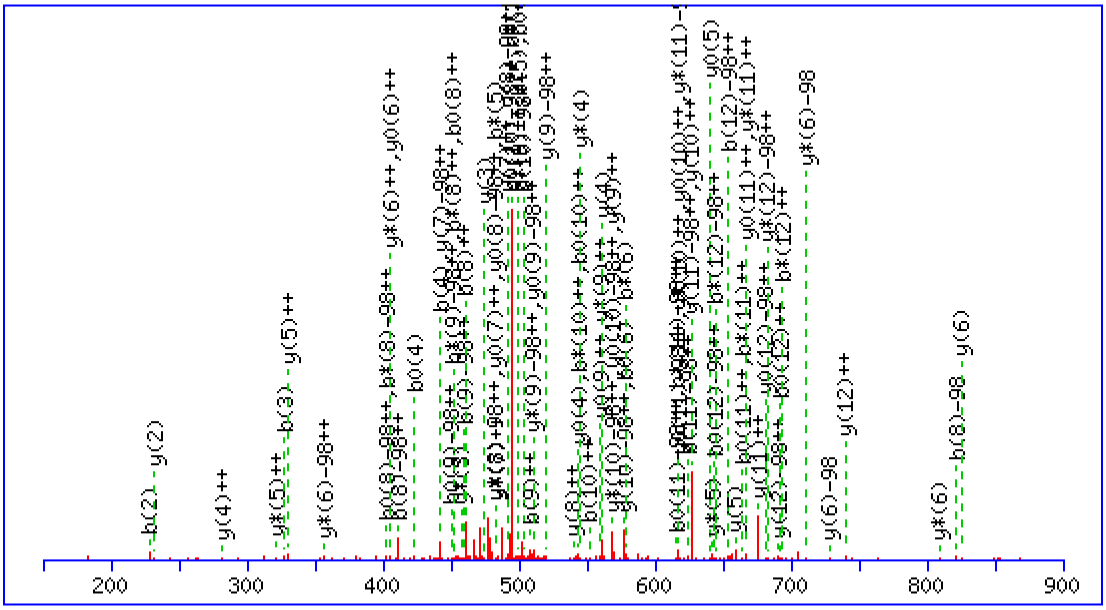
Monoisotopic mass of neutral peptide Mr(calc): 1225.5492
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.014
Matched b ions: b(2), b(4)-98, b(4)++, b(4)-98++, b(4), b(5), b(5)-98++, b(5)++, b(5)-98, b(6)-98, b(6)-98++, b(7)-98++, b(7)++
Matched y ions: y(1), y(2), y(3), y(3)++, y(4), y(4)++, y(5)++, y(7)-98++, y(8)-98++, y(8)++

Peptide No.1139

VKVDGPRSPSYGR
Confirmed sites: @S:8,@Y:11
Ambiguous sites:

MS/MS Fragmentation of **VKVDGPRSPSYGR**
Found in **SRSF1_MOUSE** in **SwissProt**, Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3

Match to Query 2739: 1576.679472 from(526.567100,3+) index(384)
Title: Elution from: 20.386 to 20.386 scan no 1270 cid35.00 polarity:+



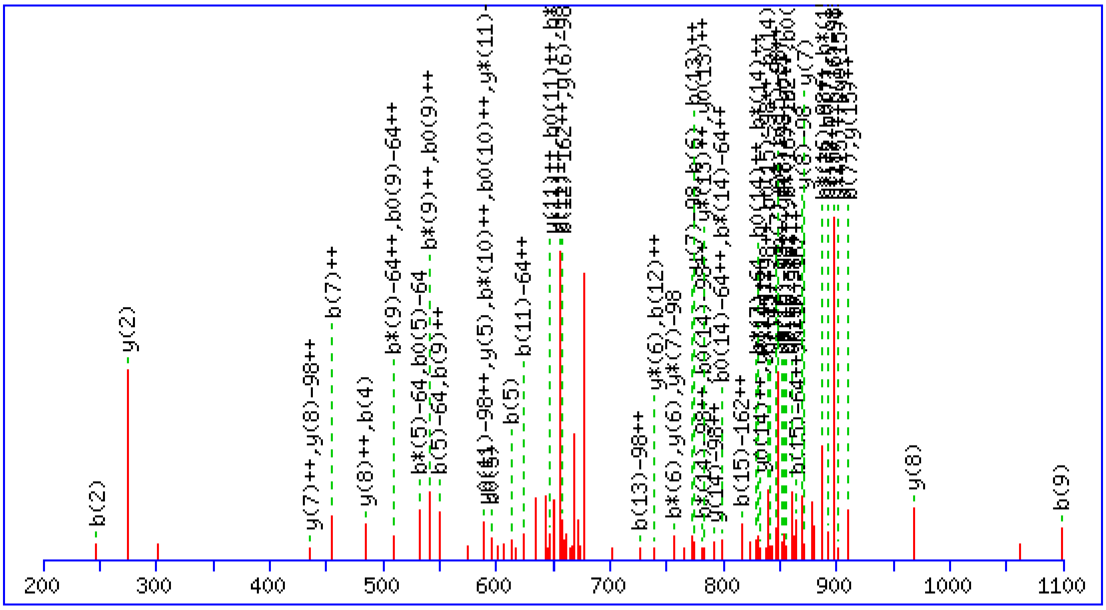
Monoisotopic mass of neutral peptide Mr(calc): 1576.6800
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y11 : Phospho (Y)
Ions Score: 22 **Expect:** 0.025
Matched b ions: b(2), b(3), b(4), b(5), b(8)-98, b(8)-98++, b(8)++, b(9)++, b(9)-98++, b(10)-98++, b(10)++, b(11)-98++, b(12)-98++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5)++, y(5), y(6)-98, y(6), y(7)-98++, y(7)++, y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(12)++

Peptide No.1140

VMHTQCHSTPDSAEDVR
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **VMHTQCHSTPDSAEDVR**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5195: 2064.800382 from(689.274070,3+) index(145)
Title: Elution from: 17.234 to 17.234 scan no 914 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 2064.8031

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 32 **Expect:** 0.0027

Matched b ions: b(2), b(4), b(5), b(6), b(7)++, b(7), b(9), b(9)++, b(11)++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++

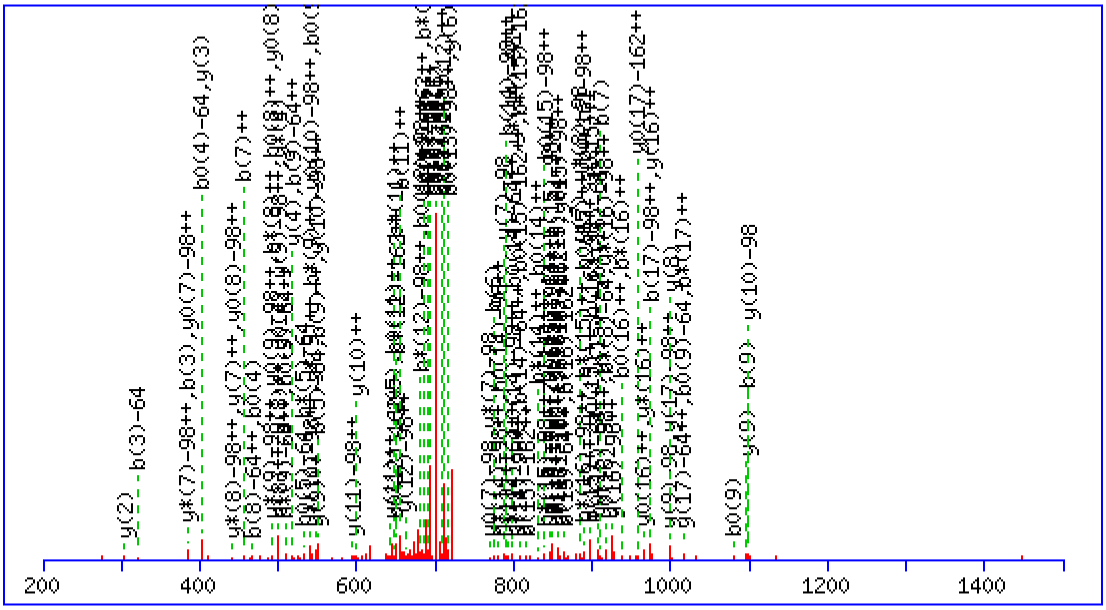
Matched y ions: y(2), y(5), y(6), y(6)-98, y(7)++, y(7)-98, y(7), y(8)-98++, y(8), y(8)++, y(8)-98, y(11)++, y(14)-98++, y(14)++, y(15)-98++, y(15)++

Peptide No.1141

VMHTQCHSTPDSAEDVRK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **VMHTQCHSTPDSAEDVRK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4782: 2192.894847 from(731.972225,3+) index(3118)
Title: Elution from: 14.244 to 14.244 scan no 693 cid35.00 polarity:+:m1s



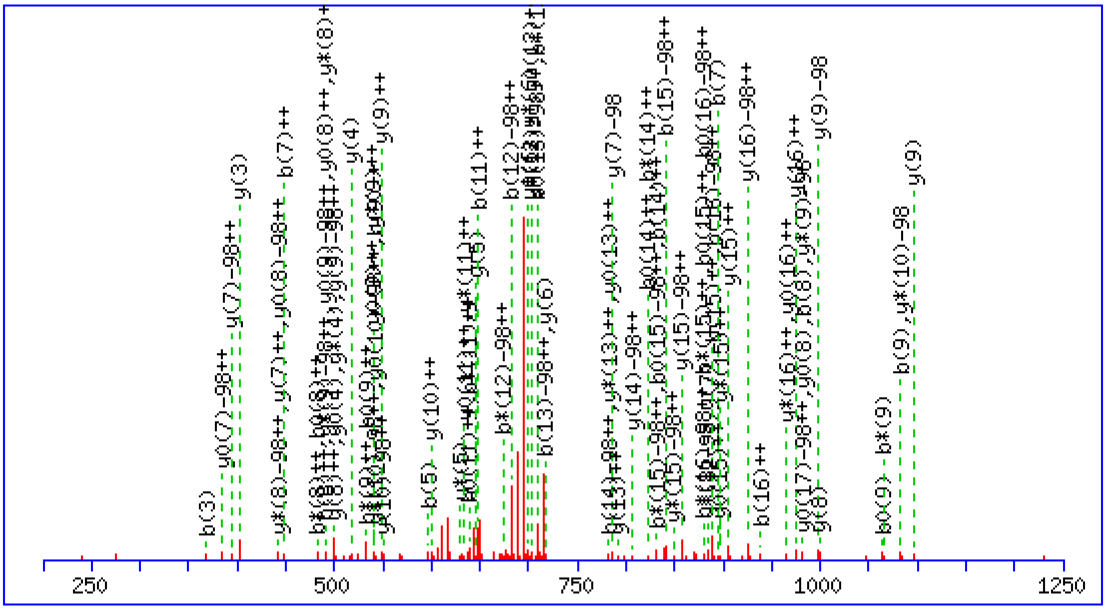
Monoisotopic mass of neutral peptide Mr(calc): 2192.8980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 45 **Expect:** 0.00016
Matched b ions: b(3), b(6), b(7)++, b(7), b(8)++, b(9)++, b(9), b(11)++, b(12)-98++, b(14)++, b(14)-98++, b(15)-98++, b(15)++, b(16)-98++, b(17)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)++, y(7)-98, y(7), y(8)++, y(8), y(9)-98++, y(9), y(9)-98, y(9)++, y(10)-98++, y(10)-98, y(10)++, y(11)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++, y(16)-98++, y(16)++, y(17)-98++

Peptide No.1142

VMHTQCHSTPDSAEDVRK
Confirmed sites: @S:12
Ambiguous sites:

MS/MS Fragmentation of **VMHTQCHSTPDSAEDVRK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 5646: 2176.899309 from(726.640379,3+) index(3799)
Title: Elution from: 17.266 to 17.266 scan no 918 cid35.00 polarity:+:m1s



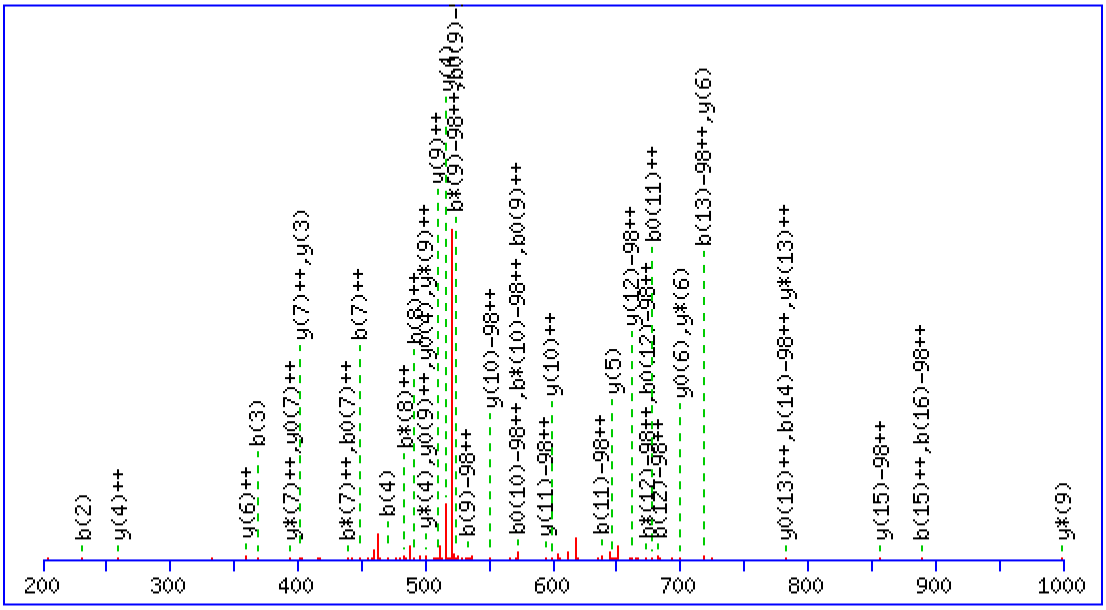
Monoisotopic mass of neutral peptide Mr(calc): 2176.9031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0015
Matched b ions: b(3), b(5), b(7)++, b(7), b(8)++, b(8), b(9), b(9)++, b(11)++, b(12)-98++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++
Matched y ions: y(3), y(4), y(5), y(6), y(7)-98, y(7)-98++, y(7)++, y(7), y(8)++, y(8), y(9)-98++, y(9)-98, y(9), y(9)++, y(10)++, y(10)-98++, y(13)++, y(14)-98++, y(15)-98++, y(15)++, y(16)++, y(16)-98++

Peptide No.1143

VMHTQCHSTPDSAEDVRK
Confirmed sites: @T:9
Ambiguous sites:

MS/MS Fragmentation of **VMHTQCHSTPDSAEDVRK**
Found in **FETUA_MOUSE** in **SwissProt**, Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1

Match to Query 4704: 2176.900640 from(545.232436,4+) index(3166)
Title: Elution from: 17.241 to 17.241 scan no 884 cid35.00 polarity:+:m1s



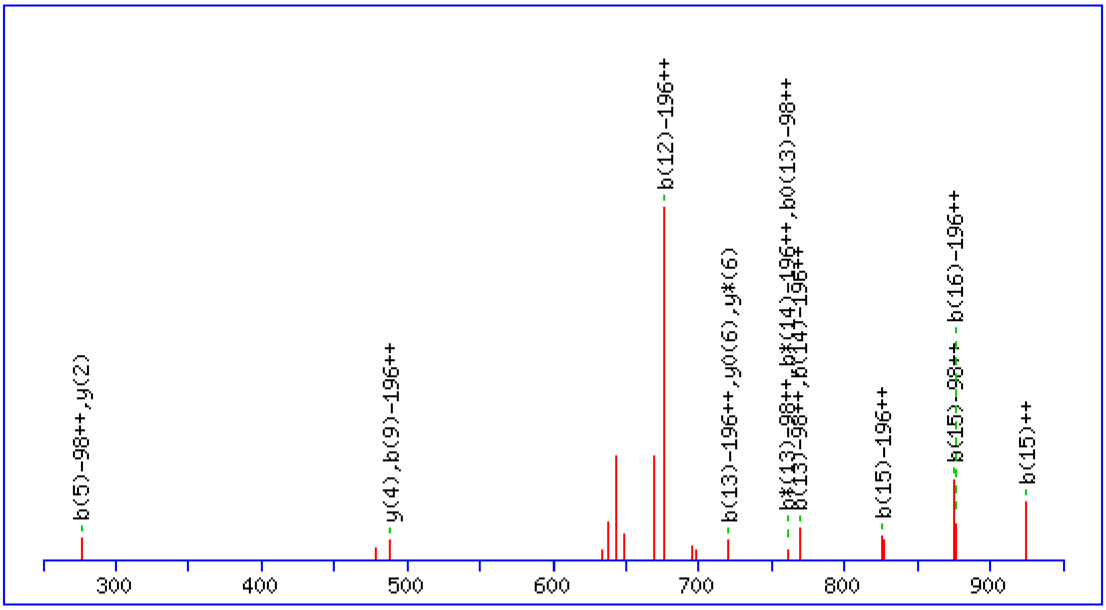
Monoisotopic mass of neutral peptide Mr(calc): 2176.9031
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.026
Matched b ions: b(2), b(3), b(4), b(7)++, b(8)++, b(9)-98++, b(11)-98++, b(12)-98++, b(13)-98++, b(14)-98++, b(15)++, b(16)-98++
Matched y ions: y(3), y(4)++, y(4), y(5), y(6)++, y(6), y(7)++, y(9)++, y(10)-98++, y(10)++, y(11)-98++, y(12)-98++, y(15)-98++

Peptide No.1144

VPSRQSLEDRGYSPDTR
Confirmed sites: @S:3,@S:6
Ambiguous sites:

MS/MS Fragmentation of **VPSRQSLEDRGYSPDTR**
Found in **ZO3_MOUSE** in **SwissProt**, Tight junction protein ZO-3 OS=Mus musculus GN=Tjp3 PE=1 SV=1

Match to Query 4498: 2121.887163 from(708.302997,3+) index(4111)
Title: Elution from: 25.847 to 25.847 scan no 2006 cid35.00 polarity:+:m1s



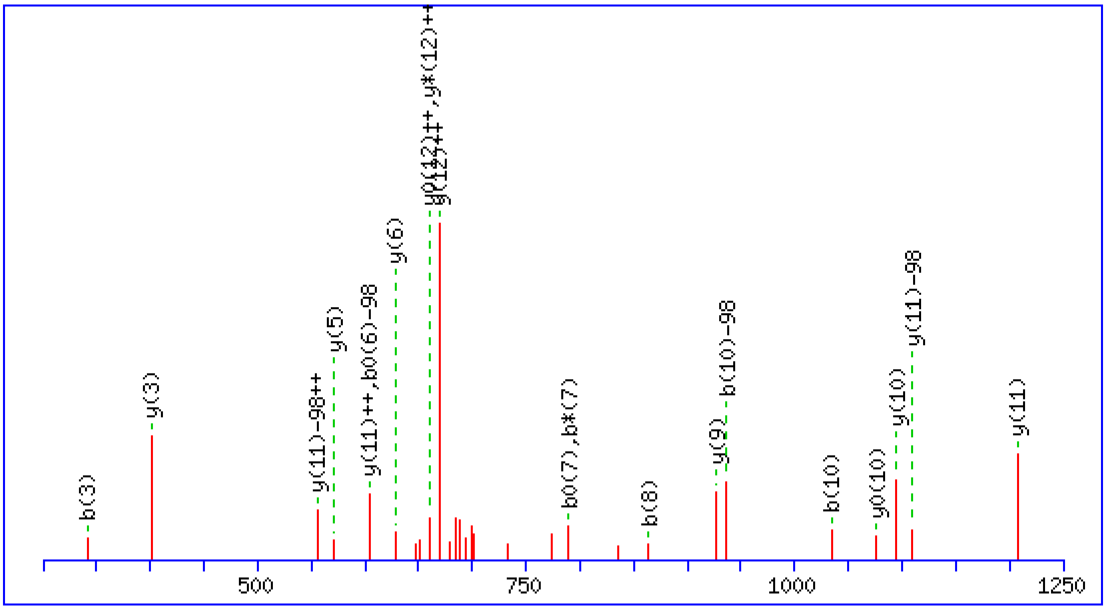
Monoisotopic mass of neutral peptide Mr(calc): 2121.8882
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 **Expect:** 0.0017
Matched b ions: b(5)-98++, b(9)-196++, b(12)-196++, b(13)-98++, b(13)-196++, b(14)-196++, b(15)-98++, b(15)++, b(15)-196++, b(16)-196++
Matched y ions: y(2), y(4)

Peptide No.1145

VQISPDSGGLPER
Confirmed sites: @S:4
Ambiguous sites:

MS/MS Fragmentation of **VQISPDSGGLPER**
Found in **FUBP2_MOUSE** in **SwissProt**, Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=2

Match to Query 2326: 1433.654556 from(717.834554,2+) index(1448)
Title: Elution from: 32.028 to 32.028 scan no 2762 cid35.00 polarity:+



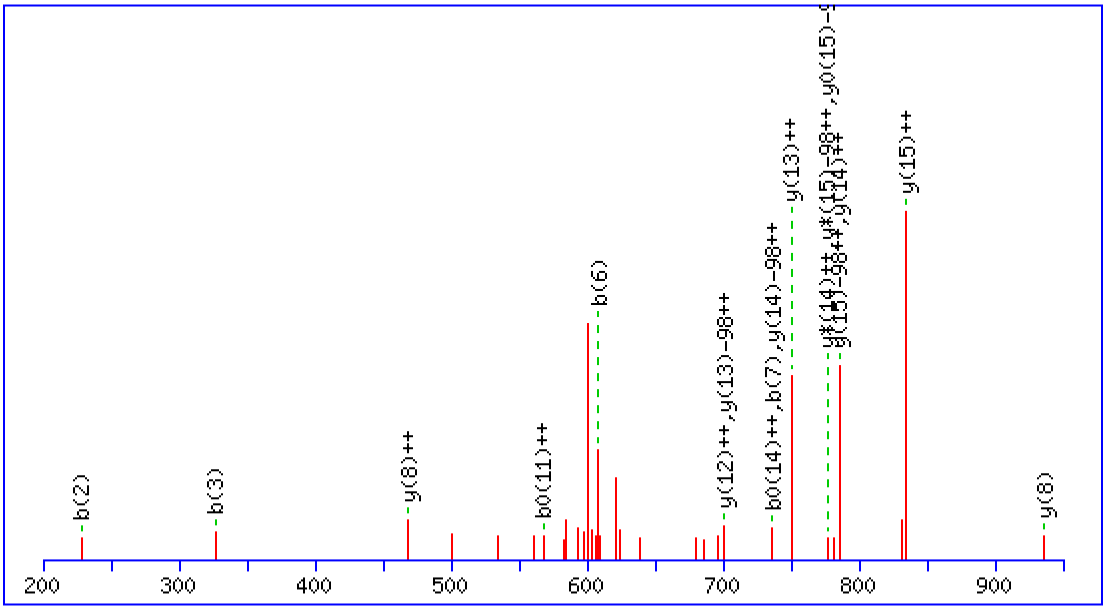
Monoisotopic mass of neutral peptide Mr(calc): 1433.6552
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 **Expect:** 0.00041
Matched b ions: b(3), b(8), b(10)-98, b(10)
Matched y ions: y(3), y(5), y(6), y(9), y(10), y(11)++, y(11), y(11)-98++, y(11)-98, y(12)++

Peptide No.1146

VQVAPLQGSPPLSHDDR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **VQVAPLQGSPPLSHDDR**
Found in **ZO2_MOUSE** in **SwissProt**, Tight junction protein ZO-2 OS=Mus musculus GN=Tjp2 PE=1 SV=2

Match to Query 4571: 1894.894764 from(632.638864,3+) index(5674)
Title: Elution from: 34.601 to 34.601 scan no 3253 cid35.00 polarity:+:m1s



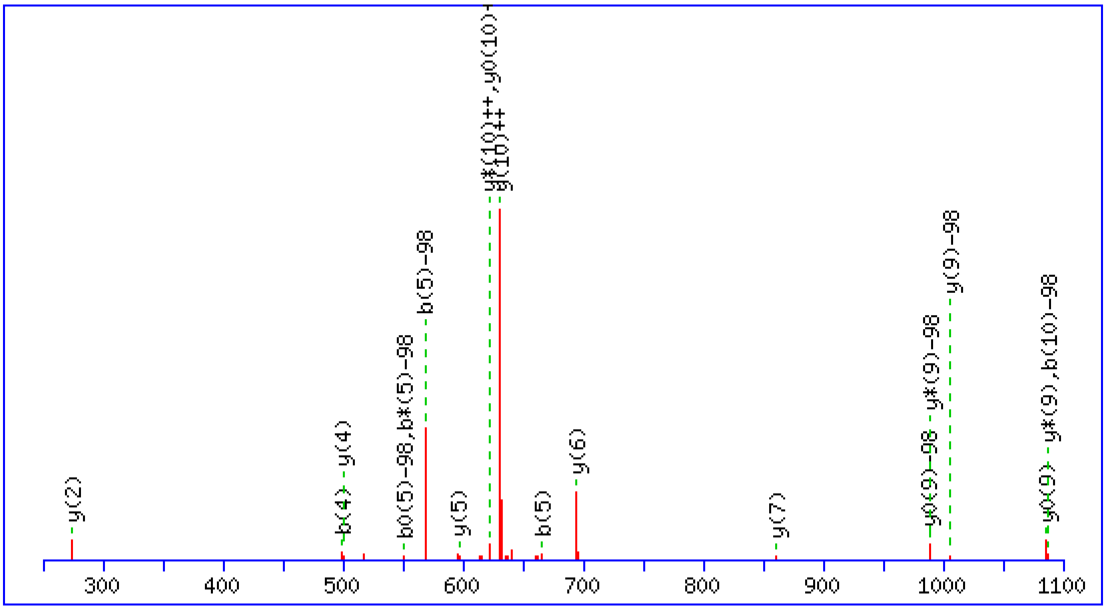
Monoisotopic mass of neutral peptide Mr(calc): 1894.8938
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0067
Matched b ions: b(2), b(3), b(6), b(7)
Matched y ions: y(8)++, y(8), y(12)++, y(13)-98++, y(13)++, y(14)++, y(14)-98++, y(15)-98++, y(15)++

Peptide No.1147

VRGWSPPPEVR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **VRGWSPPPEVR**
Found in **ACSA_MOUSE** in **SwissProt**, Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2

Match to Query 2192: 1358.648292 from(680.331422,2+) index(1711)
Title: Elution from: 32.129 to 32.129 scan no 2887 cid35.00 polarity:+



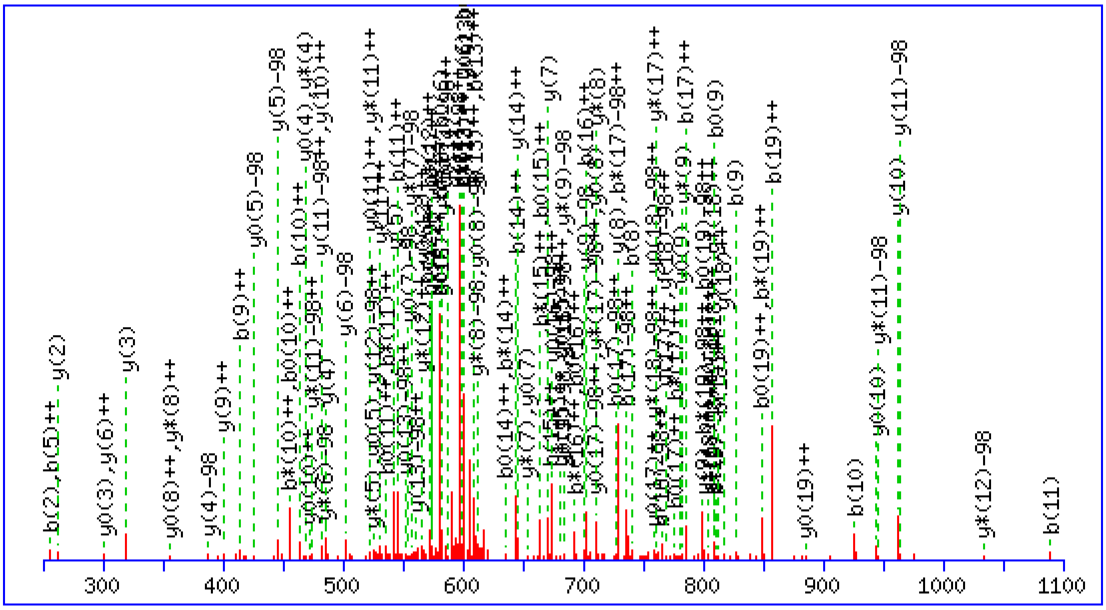
Monoisotopic mass of neutral peptide Mr(calc): 1358.6496
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00065
Matched b ions: b(4), b(5)-98, b(5), b(9)-98, b(9), b(10)-98
Matched y ions: y(2), y(4), y(5), y(6), y(7), y(9)-98, y(10)++

Peptide No.1148

VRPASSAASVYAGAGGSGSR
Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **VRPASSAASVYAGAGGSGSR**
Found in **K1C18_MOUSE** in **SwissProt**, Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Match to Query 3807: 1886.862195 from(629.961341,3+) index(3805)
Title: Elution from: 23.171 to 23.171 scan no 1643 cid35.00 polarity:+:m1s



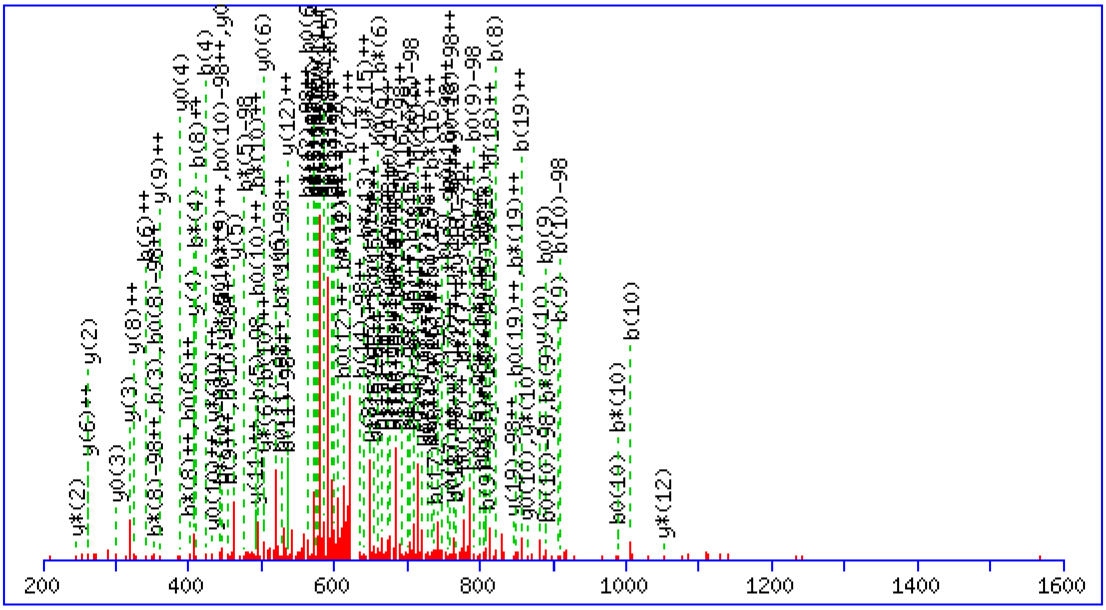
Monoisotopic mass of neutral peptide Mr(calc): 1886.8636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 89 **Expect:** 9.5e-009
Matched b ions: b(2), b(5)++, b(6), b(8), b(9)++, b(9), b(10), b(10)++, b(11)++, b(11), b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)-98++, b(17)++, b(18)-98++, b(18)++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(4)-98, y(5)-98, y(5), y(6), y(6)++, y(6)-98, y(7), y(7)-98, y(8), y(9), y(9)++, y(9)-98, y(10), y(10)++, y(11)-98, y(11)++, y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(16)-98++, y(17)++, y(18)-98++, y(18)++

Peptide No.1149

VRPASSAASVYAGAGGSGSR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **VRPASSAASVYAGAGGSGSR**
Found in **K1C18_MOUSE** in **SwissProt**, Keratin, type I cytoskeletal 18 OS=Mus musculus GN=Krt18 PE=1 SV=5

Match to Query 4123: 1886.862345 from(629.961391,3+) index(3567)
Title: Elution from: 31.280 to 31.280 scan no 1955 cid35.00 polarity:+:m1s



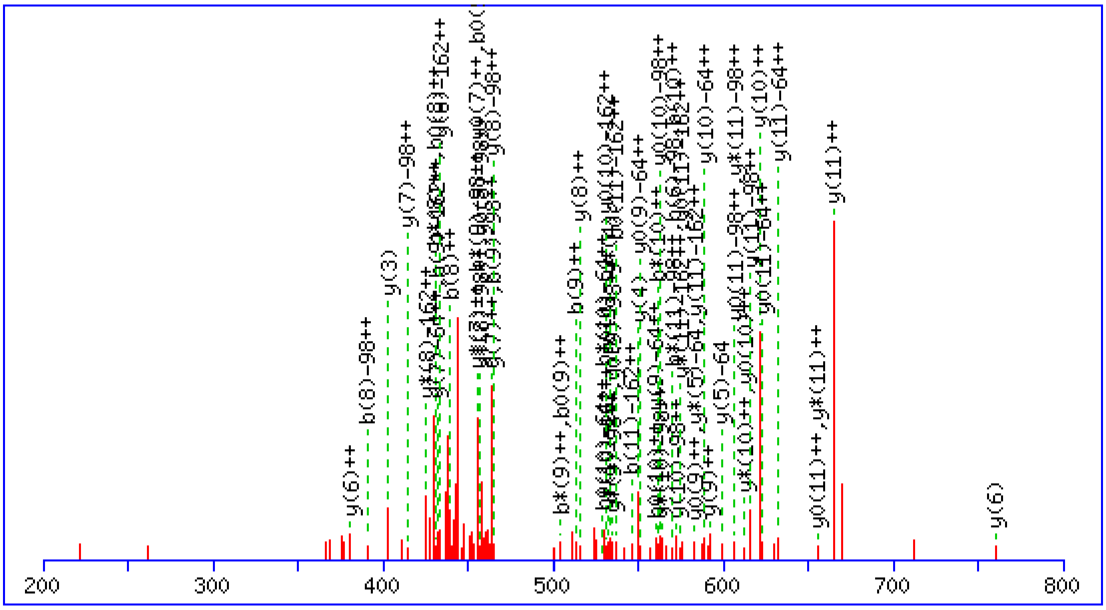
Monoisotopic mass of neutral peptide Mr(calc): 1886.8636
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.4e-005
Matched b ions: b(3), b(4), b(5), b(5)-98, b(6)-98, b(6)++, b(7), b(8), b(8)++, b(9)-98, b(9)++, b(9), b(10), b(10)++, b(10)-98++, b(10)-98, b(11)++, b(11)-98++, b(12)++, b(12)-98++, b(13)++, b(13)-98++, b(14)++, b(14)-98++, b(15)++, b(15)-98++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(10), y(10)++, y(11)++, y(12)++, y(13)++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(19)-98++

Peptide No.1150

VSGRTSPLMLDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **VSGRTSPLMLDR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 2634: 1426.662861 from(476.561563,3+) index(1037)
Title: Elution from: 24.914 to 24.914 scan no 1941 cid35.00 polarity:+



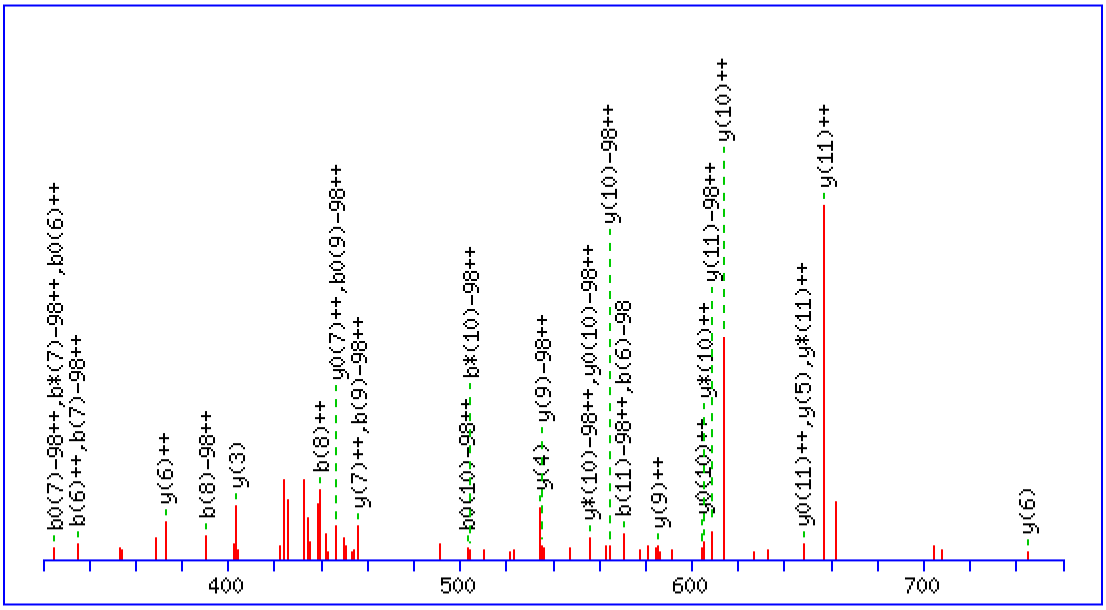
Monoisotopic mass of neutral peptide Mr(calc): 1426.6640
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 27 **Expect:** 0.0097
Matched b ions: b(6)-98, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)++
Matched y ions: y(3), y(4), y(6), y(6)++, y(7)++, y(7)-98++, y(8)-98++, y(8)++, y(9)++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.1151

VSGRTSPLMLDR
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **VSGRTSPLMLDR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 2392: 1410.668256 from(471.230028,3+) index(1266)
Title: Elution from: 27.550 to 27.550 scan no 2264 cid35.00 polarity:+



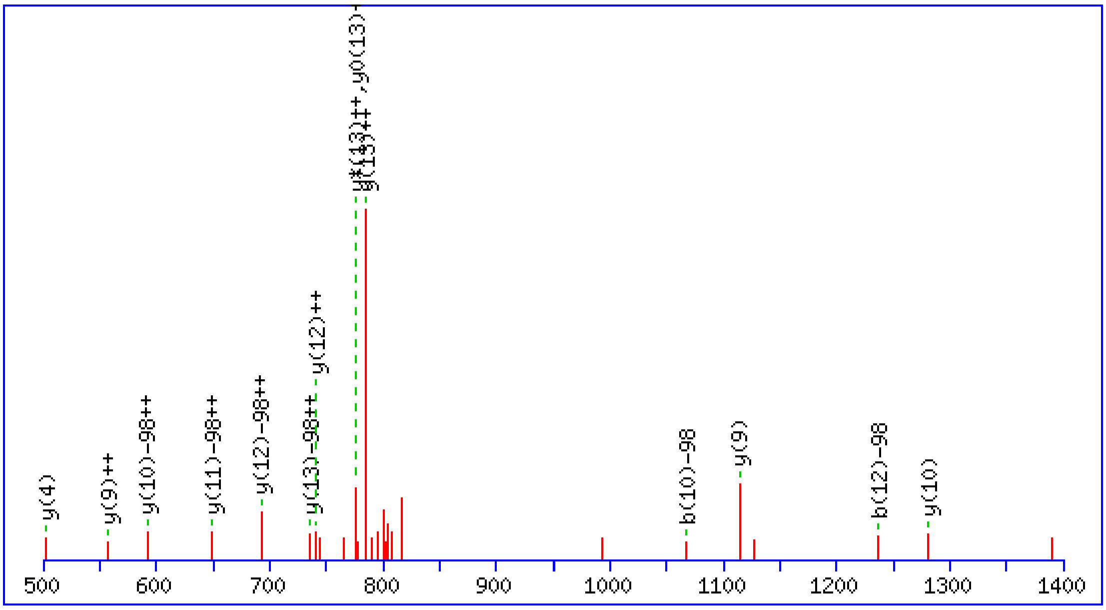
Monoisotopic mass of neutral peptide Mr(calc): 1410.6690
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 **Expect:** 0.01
Matched b ions: b(6)-98, b(6)++, b(7)-98++, b(8)++, b(8)-98++, b(9)-98++, b(11)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(6)++, y(7)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.1152

VSSLSPEQEQGLWK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **VSSLSPEQEQGLWK**
Found in **FA76B_MOUSE** in **SwissProt**, Protein FAM76B OS=Mus musculus GN=Fam76b PE=2 SV=1

Match to Query 3498: 1666.758946 from(834.386749,2+) index(2679)
Title: Elution from: 42.554 to 42.554 scan no 4278 cid35.00 polarity:+



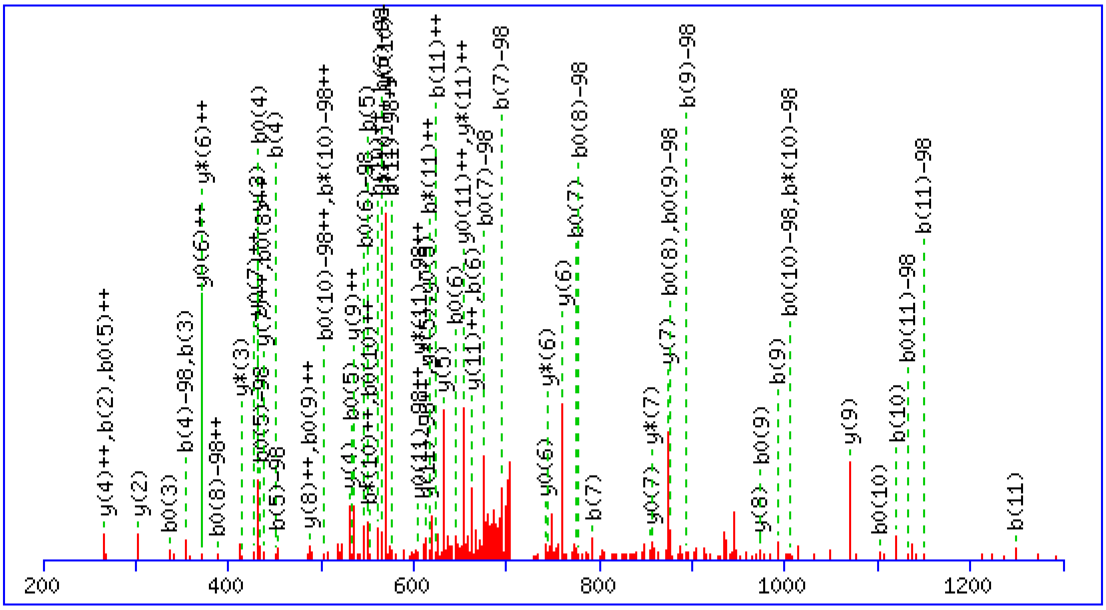
Monoisotopic mass of neutral peptide Mr(calc): 1666.7603
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.013
Matched b ions: b(10)-98, b(12)-98
Matched y ions: y(4), y(9), y(9)++, y(10)-98++, y(10), y(11)-98++, y(12)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.1153

VSSPVLETVQQR
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **VSSPVLETVQQR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 2824: 1421.691196 from(711.852874,2+) index(1262)
Title: Elution from: 38.599 to 38.599 scan no 2832 cid35.00 polarity:+



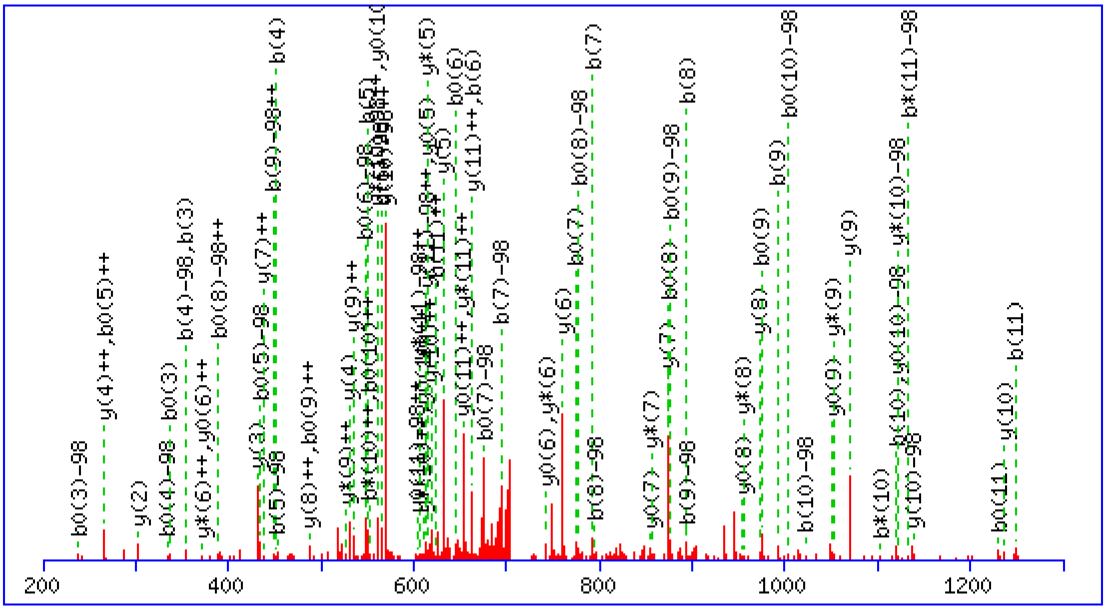
Monoisotopic mass of neutral peptide Mr(calc): 1421.6916
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 52 **Expect:** 2.5e-005
Matched b ions: b(2), b(3), b(4)-98, b(4), b(5), b(5)-98, b(6), b(6)-98, b(7), b(7)-98, b(9), b(9)-98, b(10), b(10)++, b(11), b(11)-98, b(11)-98++, b(11)++
Matched y ions: y(2), y(3), y(4), y(4)++, y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(11)++, y(11)-98++

Peptide No.1154

VSSPVLETVQQR
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **VSSPVLETVQQR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 3213: 1421.691080 from(711.852816,2+) index(1458)
Title: Elution from: 38.595 to 38.595 scan no 2961 cid35.00 polarity:+



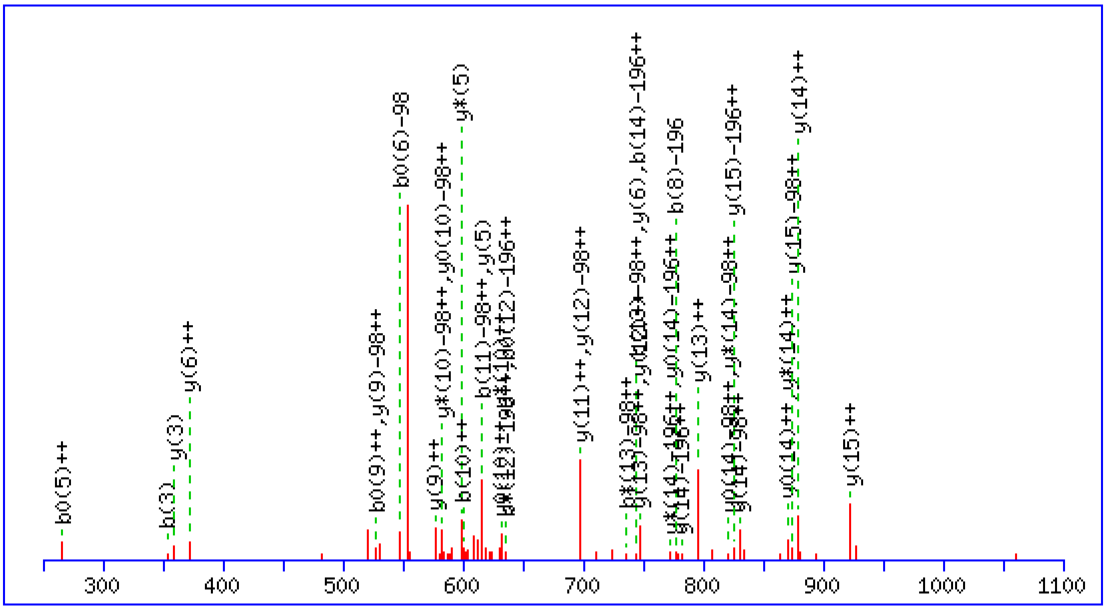
Monoisotopic mass of neutral peptide Mr(calc): 1421.6916
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 6.8e-005
Matched b ions: b(3), b(4)-98, b(4), b(5), b(5)-98, b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(9)-98, b(9), b(9)-98++, b(10), b(10)++, b(10)-98, b(11), b(11)++
Matched y ions: y(2), y(3), y(4)++, y(4), y(5), y(6), y(7), y(7)++, y(8)++, y(8), y(9), y(9)++, y(10)-98++, y(10), y(10)-98, y(10)++, y(11)++, y(11)-98++

Peptide No.1155

VSSPVLETVQQRTPSR
Confirmed sites: @S:3,@T:8
Ambiguous sites:

MS/MS Fragmentation of **VSSPVLETVQQRTPSR**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4782: 1942.891131 from(648.637653,3+) index(1590)
Title: Elution from: 30.307 to 30.307 scan no 2678 cid35.00 polarity:+



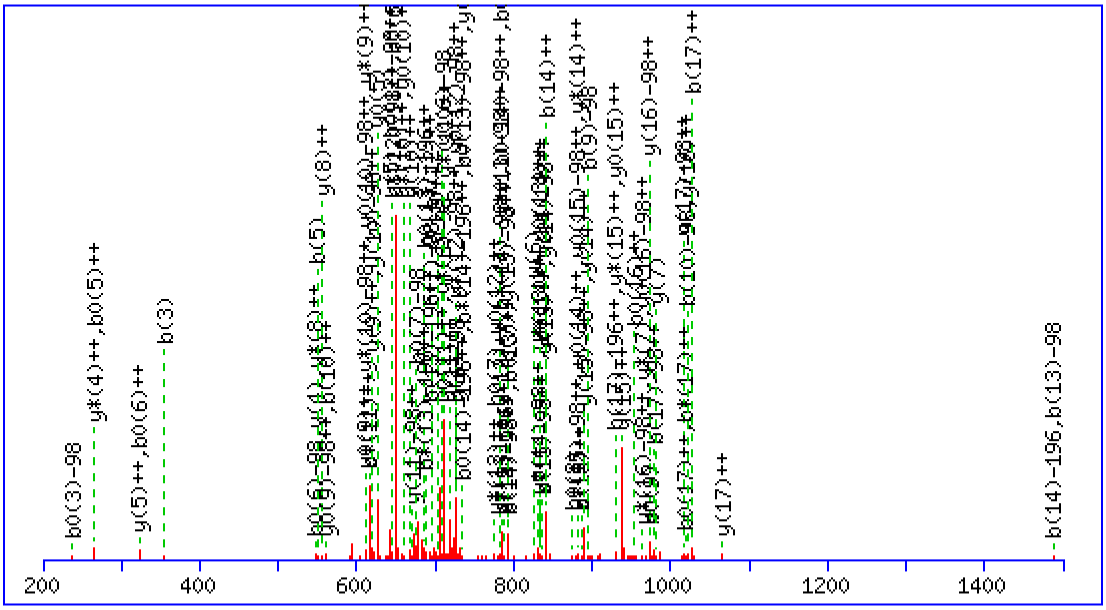
Monoisotopic mass of neutral peptide Mr(calc): 1942.8915
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 42 **Expect:** 0.00041
Matched b ions: b(3), b(8)-196, b(10)++, b(11)-98++, b(13)-98++, b(14)-196++
Matched y ions: y(3), y(5), y(6)++, y(6), y(9)++, y(9)-98++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(14)-196++, y(15)++, y(15)-196++, y(15)-98++

Peptide No.1156

VSSPVLETVQQRTPSRER
Confirmed sites: @S:3,@T:13
Ambiguous sites:

MS/MS Fragmentation of **VSSPVLETVQQRTPSRER**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 4871: 2228.031702 from(743.684510,3+) index(4224)
Title: Elution from: 26.948 to 26.948 scan no 2157 cid35.00 polarity:+:m1s



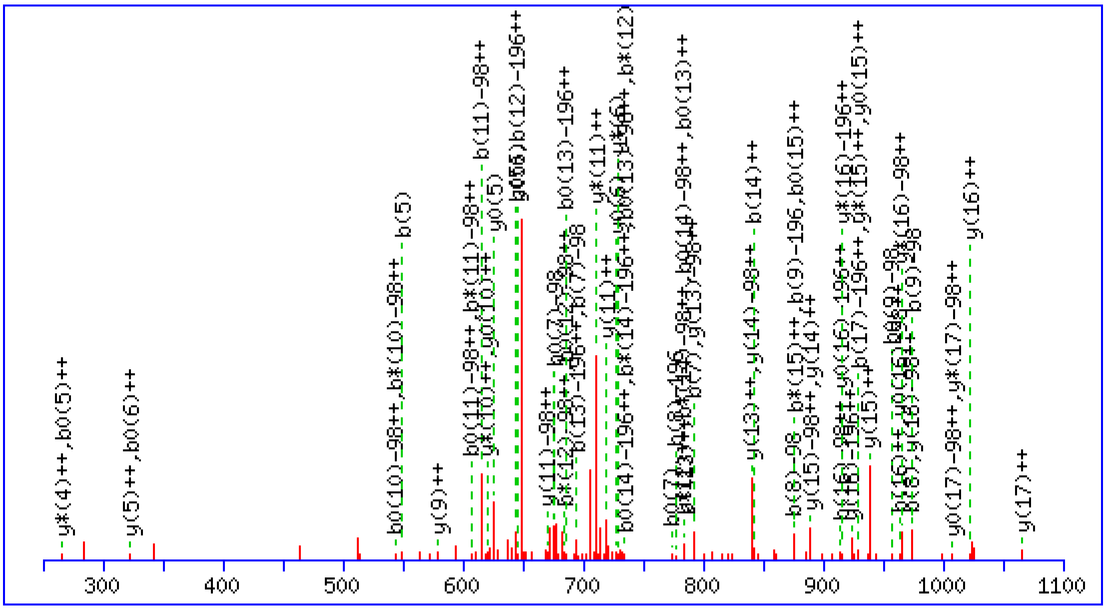
Monoisotopic mass of neutral peptide Mr(calc): 2228.0352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0036
Matched b ions: b(3), b(5), b(7), b(7)-98, b(9)-98, b(10)-98, b(10)++, b(12)++, b(13)-98, b(13)++, b(13)-196++, b(14)-196, b(14)++, b(14)-98++, b(15)++, b(15)-196++, b(15)-98++, b(17)++, b(17)-196++, b(17)-98++
Matched y ions: y(4), y(5)++, y(5), y(6)-98, y(6), y(7), y(8)++, y(9)++, y(10)-98++, y(10)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)++, y(17)-98++

Peptide No.1157

VSSPVLETVQQRTPSRER
Confirmed sites: @S:3,@T:8
Ambiguous sites:

MS/MS Fragmentation of **VSSPVLETVQQRTPSRER**
Found in **SRRM2_MOUSE** in **SwissProt**, Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=3

Match to Query 5673: 2228.030151 from(743.683993,3+) index(4754)
Title: Elution from: 27.212 to 27.212 scan no 2218 cid35.00 polarity:+:m1s



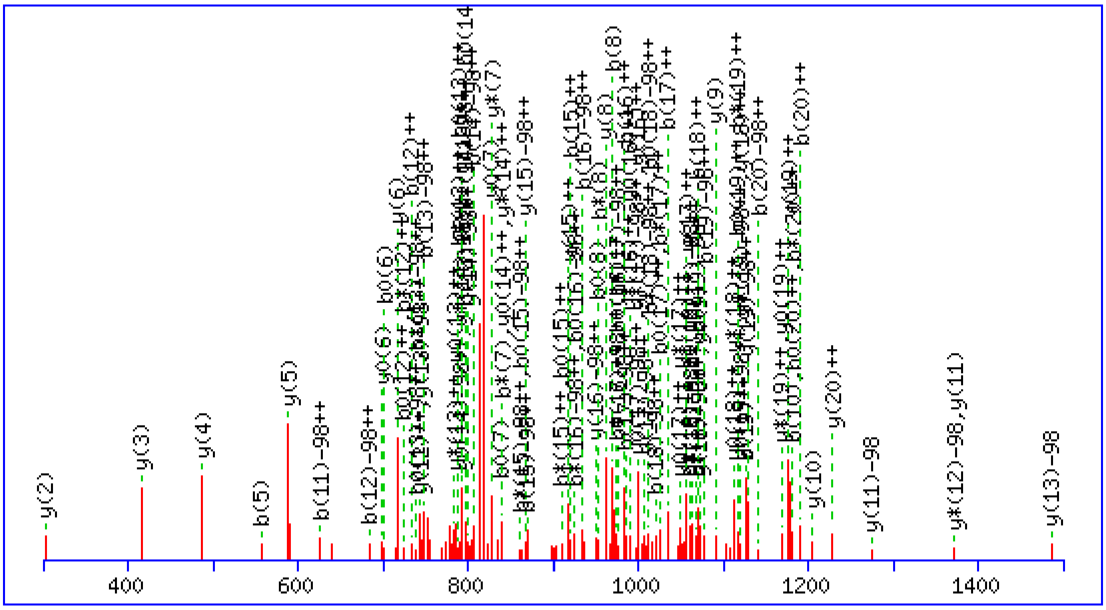
Monoisotopic mass of neutral peptide Mr(calc): 2228.0352
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
T8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 **Expect:** 0.044
Matched b ions: b(5), b(7), b(7)-98, b(8), b(8)-98, b(8)-196, b(9)-98, b(9)-196, b(11)-98++, b(12)-196++, b(13)-196++, b(14)++, b(16)-98++, b(16)++, b(17)-196++
Matched y ions: y(5)++, y(5), y(9)++, y(11)++, y(11)-98++, y(12)++, y(12)-98++, y(13)++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(15)-98++, y(16)-98++, y(16)-196++, y(16)++, y(17)++

Peptide No.1158

VTLQDYHLPDSDEDEETAIQR
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **VTLQDYHLPDSDEDEETAIQR**
Found in **ZFY19_MOUSE** in **SwissProt**, Zinc finger FYVE domain-containing protein 19 OS=Mus musculus GN=Zfyve19 PE=1 SV=2

Match to Query 6475: 2553.091185 from(852.037671,3+) index(6507)
Title: Elution from: 44.819 to 44.819 scan no 4576 cid35.00 polarity:+:m1s



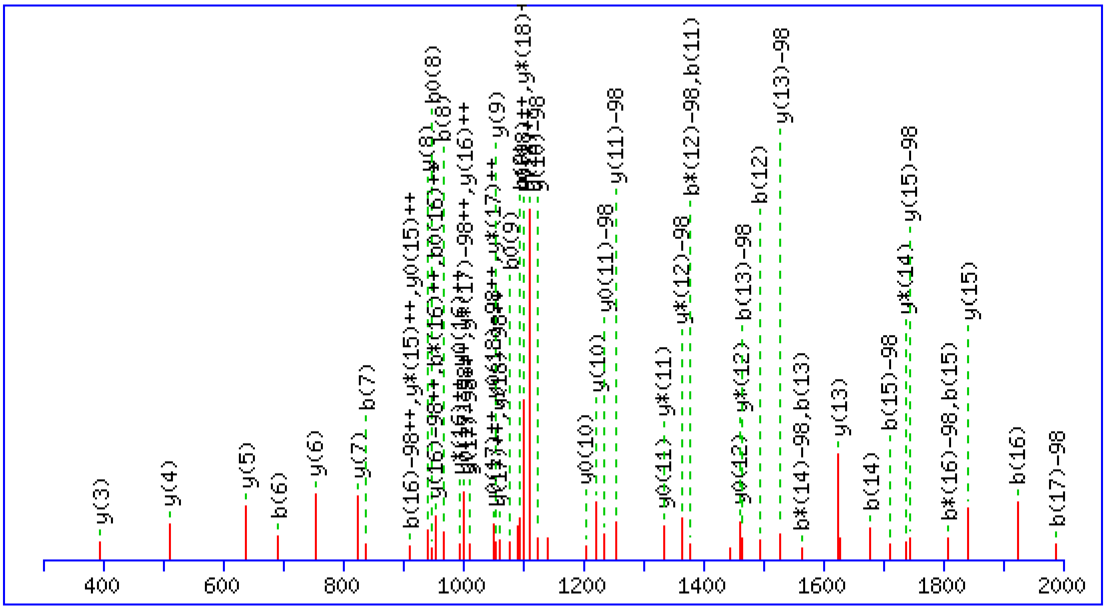
Monoisotopic mass of neutral peptide Mr(calc): 2553.0908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 59 **Expect:** 1e-005
Matched b ions: b(5), b(8), b(10), b(11)-98++, b(12)-98++, b(12)++, b(13)-98++, b(13)++, b(14)-98++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)++, b(17)-98++, b(18)++, b(18)-98++, b(19)++, b(19)-98++, b(20)++, b(20)-98++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(8), y(9), y(10), y(11), y(11)-98, y(12)++, y(13)-98, y(13)++, y(13)-98++, y(14)-98++, y(15)++, y(15)-98++, y(16)++, y(16)-98++, y(17)++, y(17)-98++, y(18)-98++, y(18)++, y(19)++, y(19)-98++, y(20)++

Peptide No.1159

VVDYSQFQESDDADEDYGR
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **VVDYSQFQESDDADEDYGR**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 6015: 2316.864130 from(1159.439341,2+) index(6175)
Title: Elution from: 40.100 to 40.100 scan no 3978 cid35.00 polarity:+:m1s



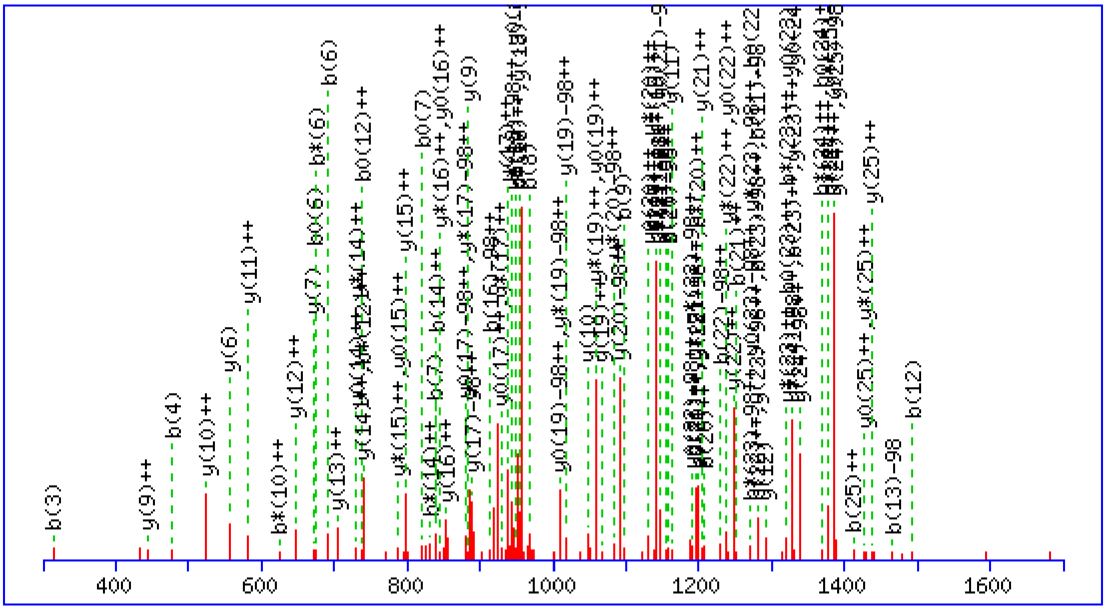
Monoisotopic mass of neutral peptide Mr(calc): 2316.8696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 77 **Expect:** 7.9e-008
Matched b ions: b(6), b(7), b(8), b(9), b(11), b(12), b(13)-98, b(13), b(14), b(15), b(15)-98, b(16), b(16)-98++, b(17)-98
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(10)-98, y(11)-98, y(13)-98, y(13), y(15)-98, y(15), y(16)-98++, y(16)++, y(17)++, y(17)-98++, y(18)++, y(18)-98++

Peptide No.1160

VVDYSQFQESDDADEDYGRDSGPPAK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **VVDYSQFQESDDADEDYGRDSGPPAK**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 5685: 2969.181654 from(990.734494,3+) index(4798)
Title: Elution from: 35.998 to 35.998 scan no 3289 cid35.00 polarity:+:m1s



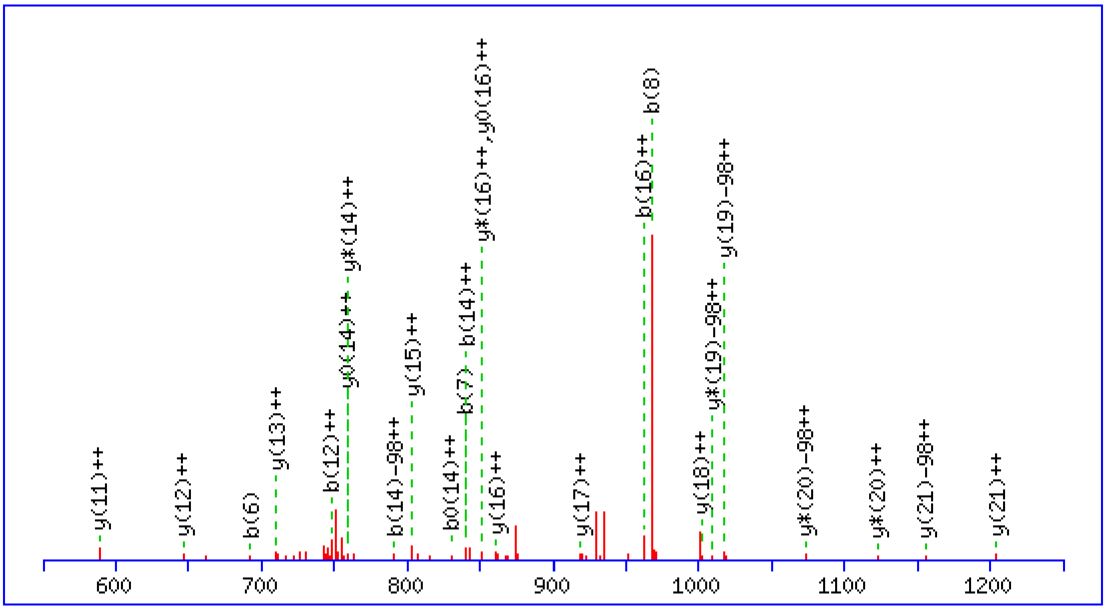
Monoisotopic mass of neutral peptide Mr(calc): 2969.1876
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 95 **Expect:** 2.4e-009
Matched b ions: b(3), b(4), b(6), b(7), b(8), b(9), b(11)-98, b(11), b(12), b(13)-98, b(14)++, b(16)-98++, b(20)-98++, b(20)++, b(21)++, b(22)++, b(22)-98++, b(23)++, b(23)-98++, b(24)++, b(25)++
Matched y ions: y(6), y(7), y(9)++, y(9), y(10)++, y(10), y(11)++, y(11), y(12)++, y(12), y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++, y(21)-98++, y(21)++, y(22)++, y(22)-98++, y(23)++, y(23)-98++, y(24)++, y(24)-98++, y(25)-98++, y(25)++

Peptide No.1161

VVDYSQFQESDDADEDYGRDSGPPAKK
Confirmed sites: @S:10
Ambiguous sites:

MS/MS Fragmentation of **VVDYSQFQESDDADEDYGRDSGPPAKK**
Found in **NUCKS_MOUSE** in **SwissProt**, Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Mus musculus GN=Nucks1 PE=1 SV=1

Match to Query 5912: 3097.278988 from(775.327023,4+) index(4722)
Title: Elution from: 32.393 to 32.393 scan no 2872 cid35.00 polarity:+:m1s



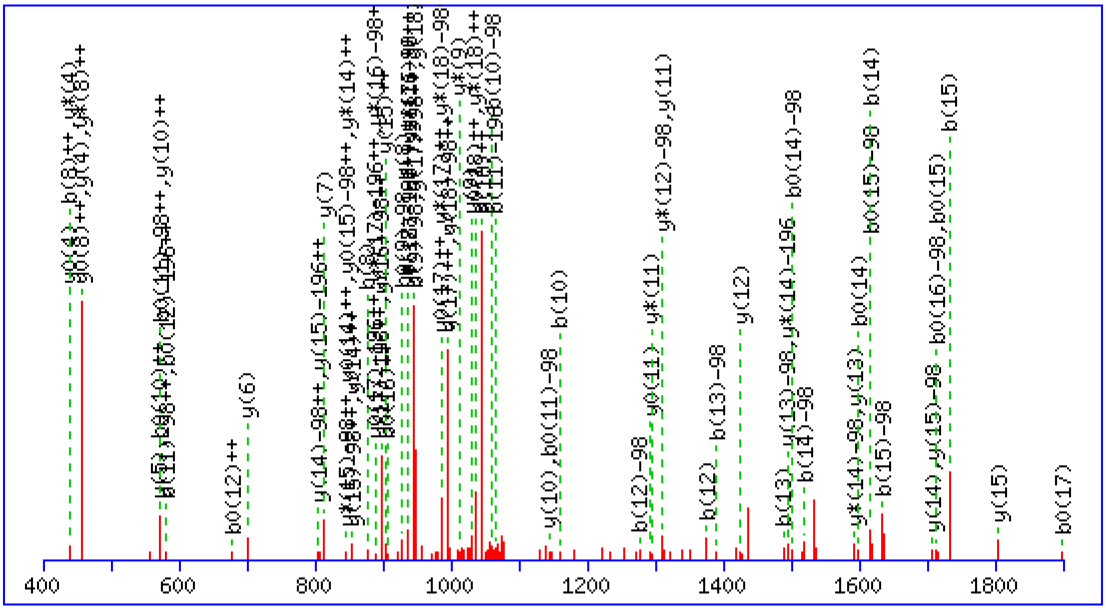
Monoisotopic mass of neutral peptide Mr(calc): 3097.2826
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.037
Matched b ions: b(6), b(7), b(8), b(12)++, b(14)++, b(14)-98++, b(16)++
Matched y ions: y(11)++, y(12)++, y(13)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)-98++, y(21)-98++, y(21)++

Peptide No.1162

VVPSPDSDSDTDLEDPSPR
Confirmed sites: @S:7,@S:9
Ambiguous sites:

MS/MS Fragmentation of **VVPSPDSDSDTDLEDPSPR**
Found in **MLXPL_MOUSE** in **SwissProt**, Carbohydrate-responsive element-binding protein OS=Mus musculus GN=Mlxipl PE=1 SV=1

Match to Query 5548: 2186.825206 from(1094.419879,2+) index(5765)
Title: Elution from: 37.262 to 37.262 scan no 3577 cid35.00 polarity:+:m1s



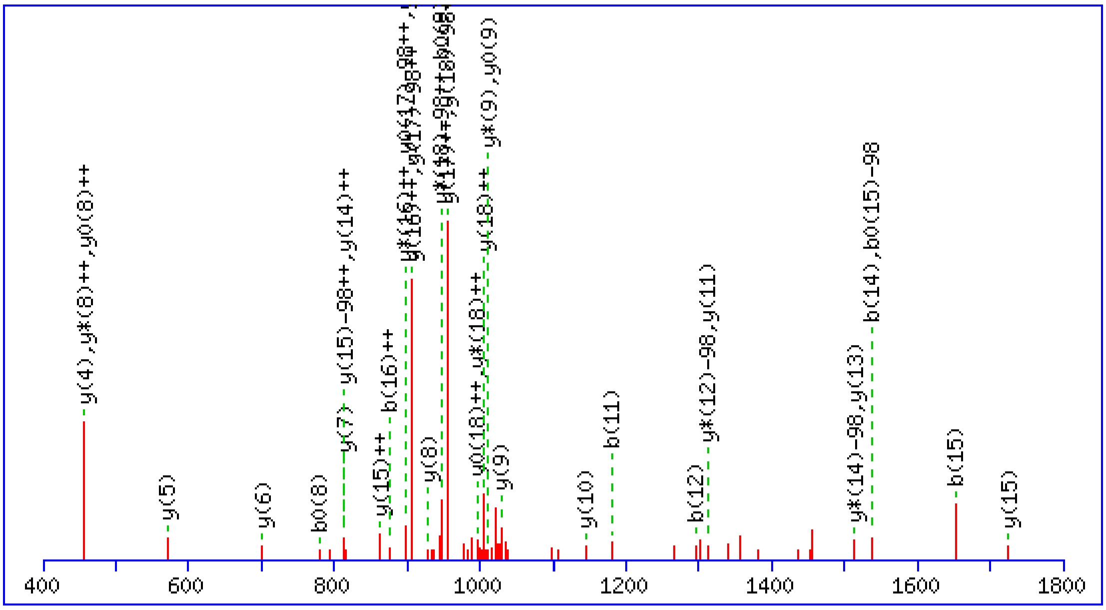
Monoisotopic mass of neutral peptide Mr(calc): 2186.8294
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 **Expect:** 4.2e-006
Matched b ions: b(8)++, b(8), b(9)-98, b(10), b(10)-98, b(11)-98++, b(11)-196, b(12), b(12)-98, b(13), b(13)-98, b(14)-98, b(14), b(15)-98, b(15)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)++, y(10), y(11), y(12), y(13)-98, y(13), y(14)-98++, y(14), y(14)++, y(15), y(15)-196++, y(15)-98, y(15)++, y(15)-98++, y(16)-98++, y(16)++, y(17)-196++, y(17)-98++, y(17)++, y(18)-196++, y(18)++, y(18)-98++

Peptide No.1163

VVPSPDSDSDTDLEDPSPR
Confirmed sites: @S:9
Ambiguous sites:

MS/MS Fragmentation of **VVPSPDSDSDTDLEDPSPR**
Found in **MLXPL_MOUSE** in **SwissProt**, Carbohydrate-responsive element-binding protein OS=Mus musculus GN=Mlxipl PE=1 SV=1

Match to Query 5321: 2106.858178 from(1054.436365,2+) index(5591)
Title: Elution from: 33.782 to 33.782 scan no 3145 cid35.00 polarity:+:m1s



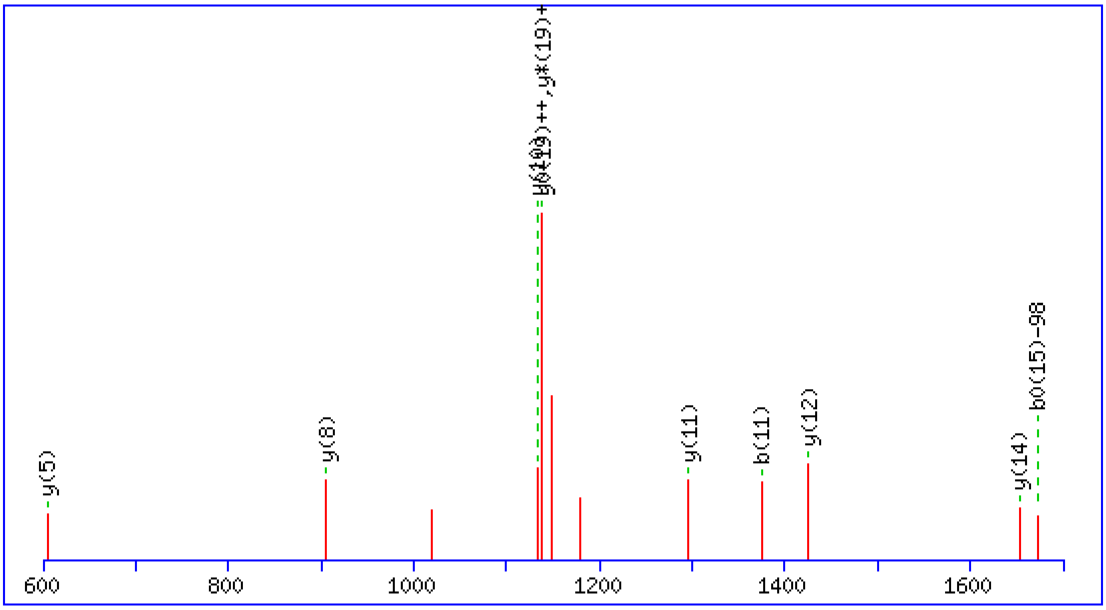
Monoisotopic mass of neutral peptide Mr(calc): 2106.8631
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 57 **Expect:** 1.1e-005
Matched b ions: b(11), b(12), b(14), b(15), b(16)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(14)++, y(15)-98++, y(15), y(15)++, y(16)++, y(17)++, y(17)-98++, y(18)-98++, y(18)++

Peptide No.1164

VWTSGQVEEYDLDADDINSR
Confirmed sites:
Ambiguous sites: @T:3orS:4

MS/MS Fragmentation of **VWTSGQVEEYDLDADDINSR**
Found in **AQP1_MOUSE** in **SwissProt**, Aquaporin-1 OS=Mus musculus GN=Aqp1 PE=1 SV=3

Match to Query 5171: 2390.992172 from(1196.503362,2+) index(5861)
Title: Elution from: 49.093 to 49.093 scan no 4824 cid35.00 polarity:+:m1s



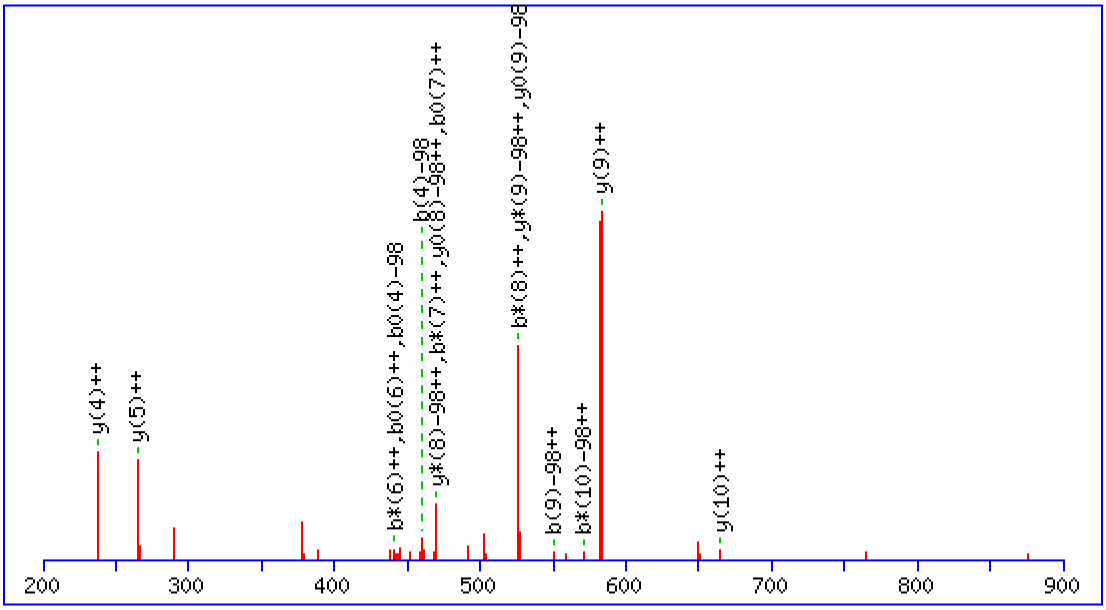
Monoisotopic mass of neutral peptide Mr(calc): 2390.9904
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 38 **Expect:** 0.0011
Matched b ions: b(11)
Matched y ions: y(5), y(8), y(10), y(11), y(12), y(14)

Peptide No.1165

VYLTRWGIQGR
Confirmed sites: @T:4
Ambiguous sites:

MS/MS Fragmentation of **VYLTRWGIQGR**
Found in **K1644_MOUSE** in **SwissProt**, Uncharacterized protein KIAA1644 OS=Mus musculus GN=Kiaa1644 PE=2 SV=1

Match to Query 2491: 1427.705013 from(476.908947,3+) index(5508)
Title: Elution from: 34.628 to 34.628 scan no 3225 cid35.00 polarity:+:m1s



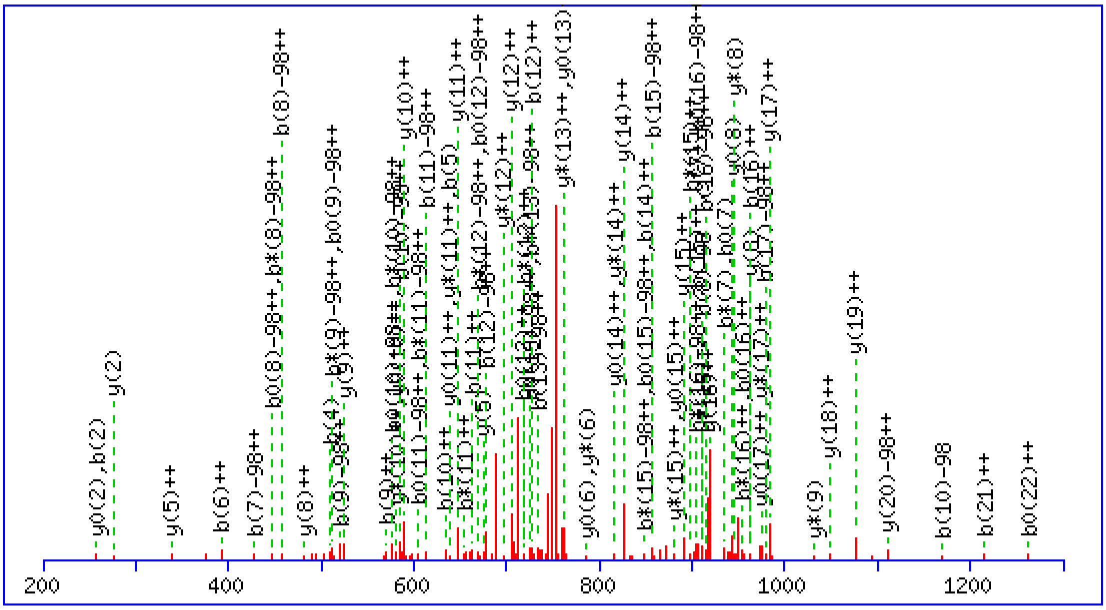
Monoisotopic mass of neutral peptide Mr(calc): 1427.7075
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.013
Matched b ions: b(4)-98, b(9)-98++
Matched y ions: y(4)++, y(5)++, y(8)++, y(9)++, y(10)++

Peptide No.1166

WAHDKFSGEEGEIEDDESGTENREEK
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **WAHDKFSGEEGEIEDDESGTENREEK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 6771: 3102.235388 from(776.566123,4+) index(5221)
Title: Elution from: 31.936 to 31.936 scan no 2861 cid35.00 polarity:+:m1s



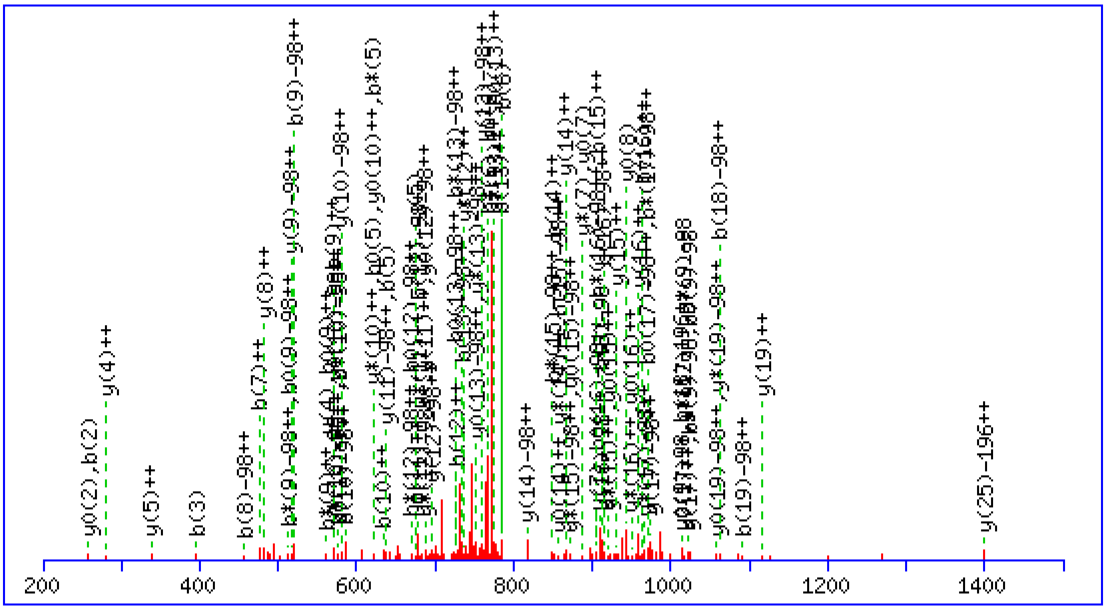
Monoisotopic mass of neutral peptide Mr(calc): 3102.2363
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 56 **Expect:** 1.7e-005
Matched b ions: b(2), b(4), b(5), b(6)++, b(7)-98++, b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(10)-98, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)-98++, b(14)++, b(15)-98++, b(15)++, b(16)++, b(16)-98++, b(17)-98++, b(21)++
Matched y ions: y(2), y(5)++, y(5), y(7), y(8)++, y(8), y(9)++, y(10)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(17)++, y(18)++, y(19)++, y(20)-98++

Peptide No.1167

WAHDKFSGEEGEIEDDESGTENREEK
Confirmed sites: @S:7,@S:18
Ambiguous sites:

MS/MS Fragmentation of **WAHDKFSGEEGEIEDDESGTENREEK**
Found in **TR150_MOUSE** in **SwissProt**, Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1

Match to Query 6809: 3182.199160 from(796.557066,4+) index(5251)
Title: Elution from: 32.226 to 32.226 scan no 2900 cid35.00 polarity:+:m1s



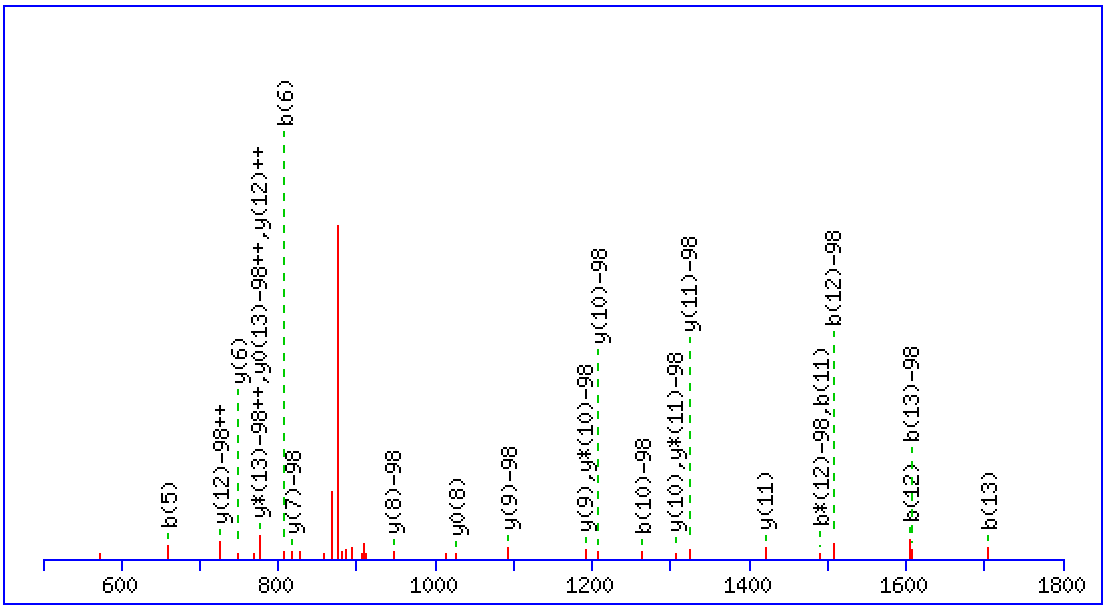
Monoisotopic mass of neutral peptide Mr(calc): 3182.2027
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
S18 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 37 **Expect:** 0.0011
Matched b ions: b(2), b(3), b(5), b(6), b(7)++, b(8)-98++, b(8)-98, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(18)-98++, b(18)-196++, b(19)-98++
Matched y ions: y(4)++, y(4), y(5)++, y(5), y(7), y(8)++, y(9)-98++, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(13)-98++, y(14)-98++, y(14)++, y(15)++, y(16)-98++, y(16)++, y(17)-98++, y(17)++, y(19)++, y(25)-196++

Peptide No.1168

WDKDDFESEEEDVK
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **WDKDDFESEEEDVK**
Found in **RBBP6_MOUSE** in **SwissProt**, E3 ubiquitin-protein ligase RBBP6 OS=Mus musculus GN=Rbbp6 PE=1 SV=5

Match to Query 4244: 1849.689278 from(925.851915,2+) index(2149)
Title: Elution from: 36.295 to 36.295 scan no 3450 cid35.00 polarity:+



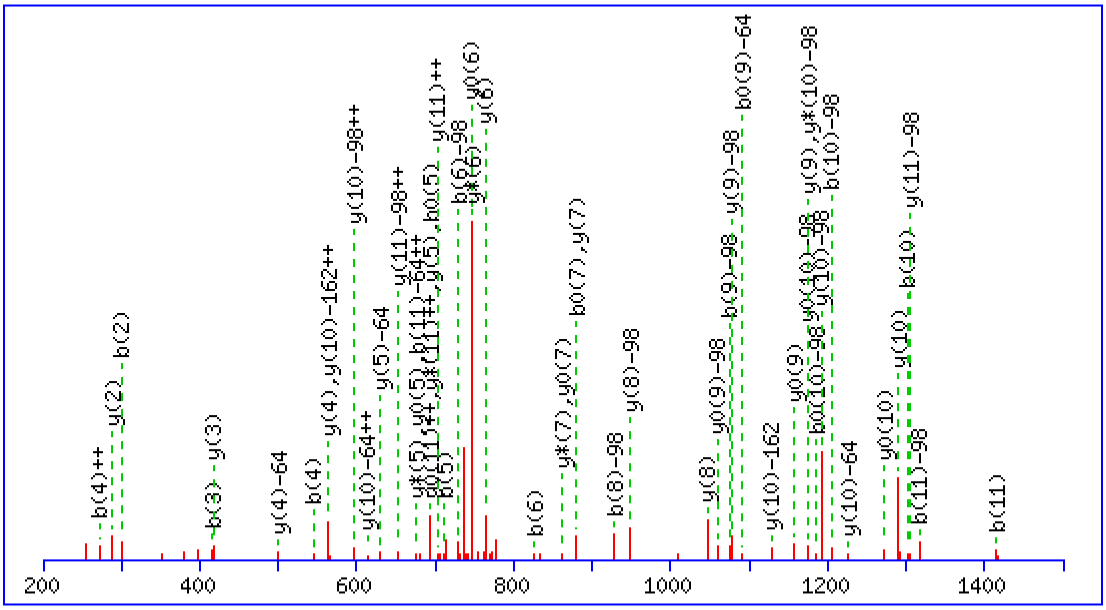
Monoisotopic mass of neutral peptide Mr(calc): 1849.6931
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 43 **Expect:** 0.00015
Matched b ions: b(5), b(6), b(10)-98, b(11), b(12)-98, b(12), b(13), b(13)-98
Matched y ions: y(6), y(7)-98, y(8)-98, y(9)-98, y(9), y(10)-98, y(10), y(11)-98, y(11), y(12)-98++, y(12)++

Peptide No.1169

WLDESDAEMELR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **WLDESDAEMELR**
Found in **HACD3_MOUSE** in **SwissProt**, 3-hydroxyacyl-CoA dehydratase 3 OS=Mus musculus GN=ptplad1 PE=1 SV=2

Match to Query 3374: 1588.610918 from(795.312735,2+) index(3046)
Title: Elution from: 47.834 to 47.834 scan no 4939 cid35.00 polarity:+



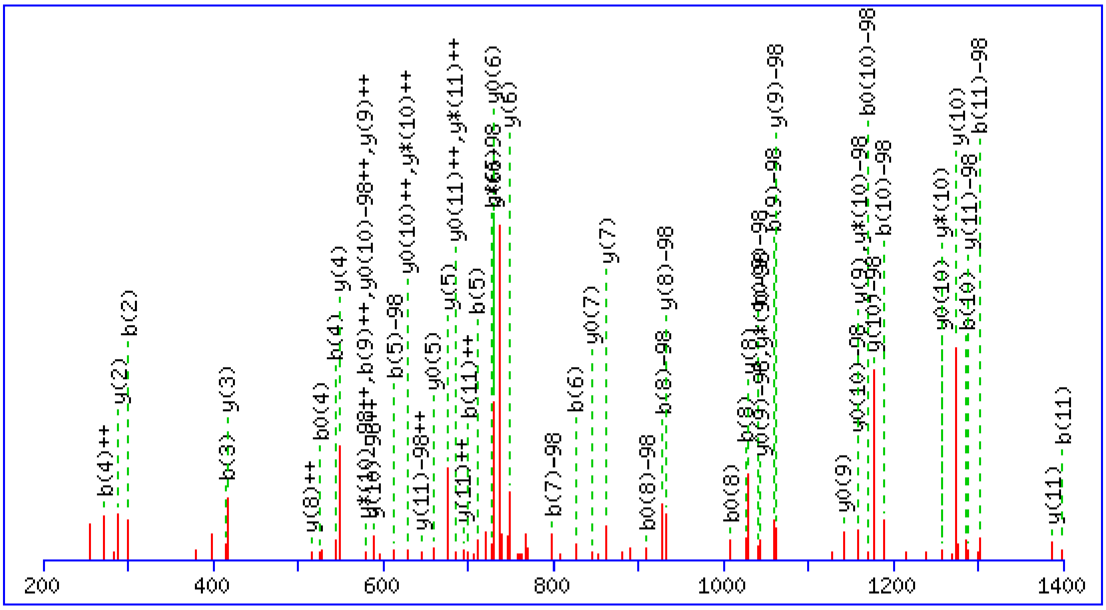
Monoisotopic mass of neutral peptide Mr(calc): 1588.6116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M9 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 61 **Expect:** 2.8e-006
Matched b ions: b(2), b(3), b(4), b(4)++, b(5), b(6)-98, b(6), b(8)-98, b(9)-98, b(10)-98, b(10), b(11), b(11)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9)-98, y(9), y(10)-98, y(10), y(10)-98++, y(11)-98++, y(11)-98, y(11)++

Peptide No.1170

WLDESDAEMELR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **WLDESDAEMELR**
Found in **HACD3_MOUSE** in **SwissProt**, 3-hydroxyacyl-CoA dehydratase 3 OS=Mus musculus GN=ptplad1 PE=1 SV=2

Match to Query 3126: 1572.616266 from(787.315409,2+) index(3150)
Title: Elution from: 51.356 to 51.356 scan no 5283 cid35.00 polarity:+



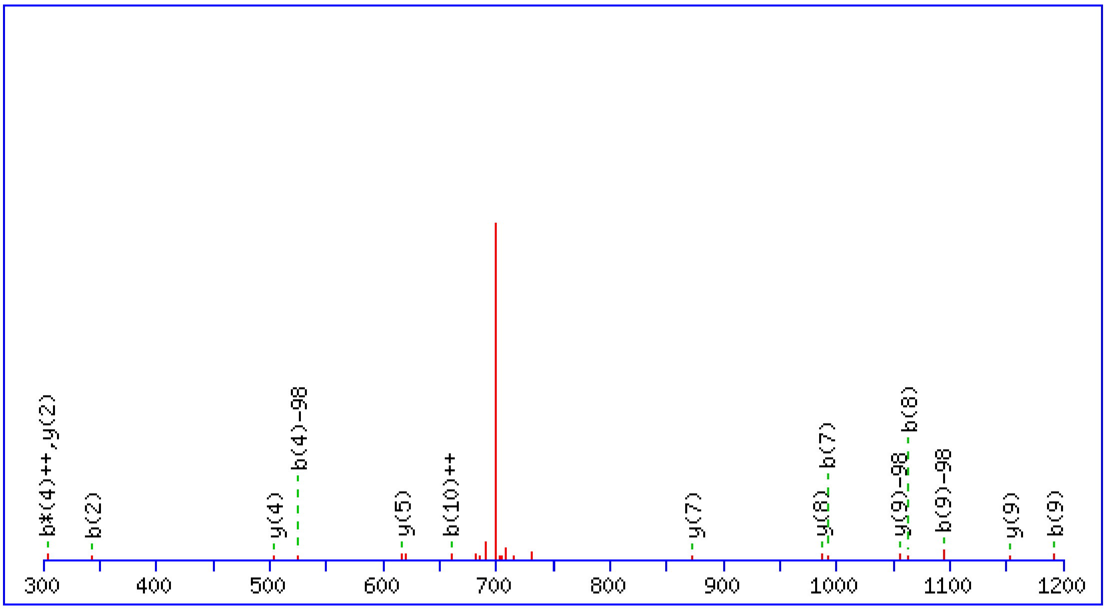
Monoisotopic mass of neutral peptide Mr(calc): 1572.6167
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 71 **Expect:** 2.8e-007
Matched b ions: b(2), b(3), b(4)++, b(4), b(5)-98, b(5), b(6), b(6)-98, b(7)-98, b(8)-98, b(8), b(9)-98, b(9)++, b(10)-98, b(10), b(11)-98, b(11), b(11)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7), y(8), y(8)-98, y(8)++, y(9)-98, y(9), y(9)++, y(10)-98++, y(10)-98, y(10), y(11), y(11)-98++, y(11)-98, y(11)++

Peptide No.1171

WRSLQQLAEER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **WRSLQQLAEER**
Found in **SPTA2_MOUSE** in **SwissProt**, Spectrin alpha chain, brain OS=Mus musculus GN=Sptan1 PE=1 SV=4

Match to Query 2788: 1494.697400 from(748.355976,2+) index(2417)
Title: Elution from: 39.210 to 39.210 scan no 3836 cid35.00 polarity:+



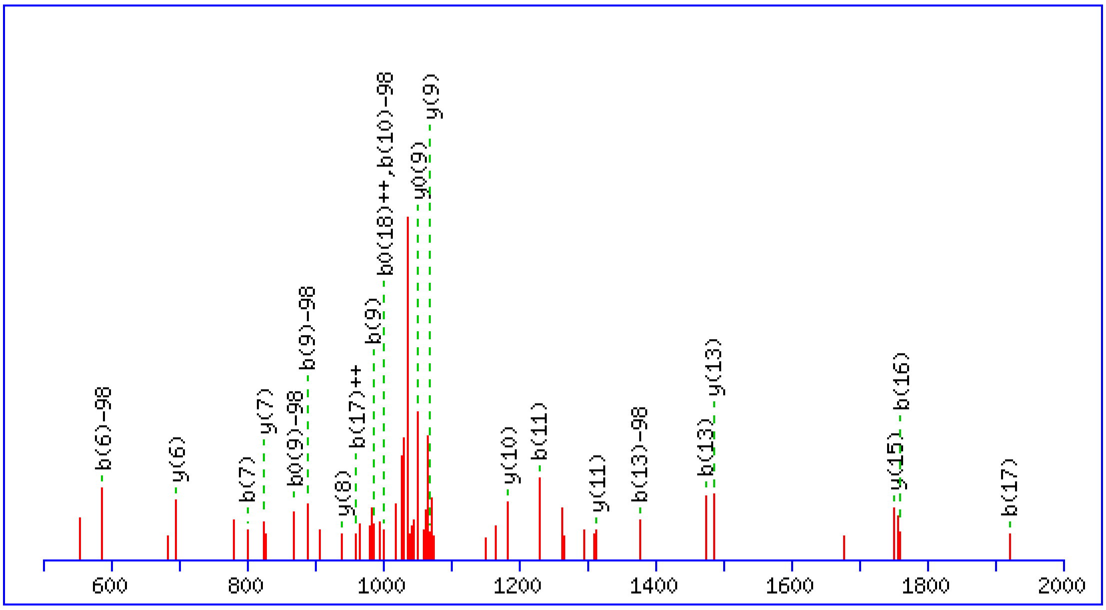
Monoisotopic mass of neutral peptide Mr(calc): 1494.6980
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 **Expect:** 0.00038
Matched b ions: b(2), b(4)-98, b(7), b(8), b(9)-98, b(9), b(10)++
Matched y ions: y(2), y(4), y(5), y(7), y(8), y(9)-98, y(9)

Peptide No.1172

YAALSVDGEDEDEGDDCTE
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YAALSVDGEDEDEGDDCTE**
Found in **IF4B_MOUSE** in **SwissProt**, Eukaryotic translation initiation factor 4B OS=Mus musculus GN=Eif4b PE=1 SV=1

Match to Query 4674: 2168.726528 from(1085.370540,2+) index(5355)
Title: Elution from: 40.022 to 40.022 scan no 3822 cid35.00 polarity:+:m1s



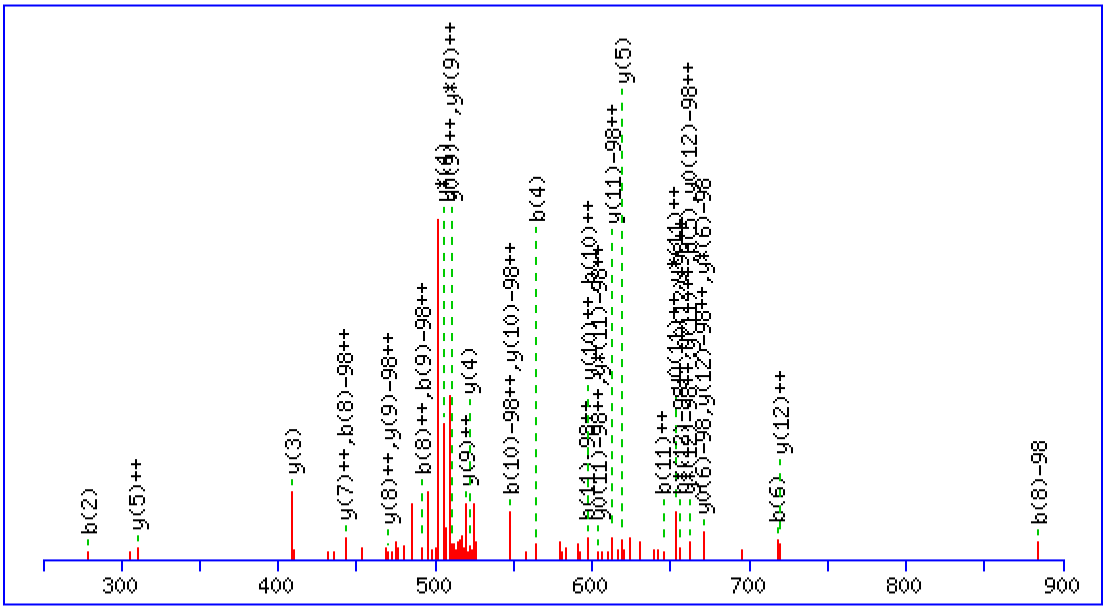
Monoisotopic mass of neutral peptide Mr(calc): 2168.7253
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0015
Matched b ions: b(6)-98, b(7), b(9)-98, b(9), b(10)-98, b(11), b(13)-98, b(13), b(16), b(17), b(17)++
Matched y ions: y(6), y(7), y(8), y(9), y(10), y(11), y(13), y(15)

Peptide No.1173

YDERPGPSPLPHR
Confirmed sites: @S:8
Ambiguous sites:

MS/MS Fragmentation of **YDERPGPSPLPHR**
Found in **RU17_MOUSE** in **SwissProt**, U1 small nuclear ribonucleoprotein 70 kDa OS=Mus musculus GN=Snrnp70 PE=1 SV=2

Match to Query 2958: 1599.719952 from(534.247260,3+) index(406)
Title: Elution from: 21.910 to 21.910 scan no 1375 cid35.00 polarity:+



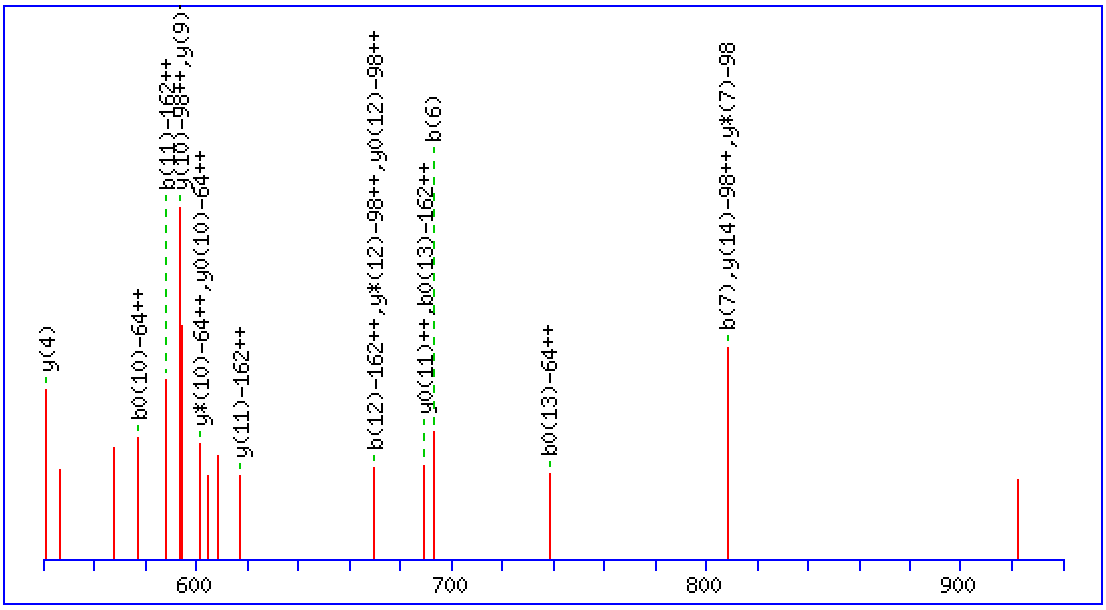
Monoisotopic mass of neutral peptide Mr(calc): 1599.7195
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 **Expect:** 0.031
Matched b ions: b(2), b(4), b(5), b(6), b(8)-98, b(8)-98++, b(8)++, b(9)-98++, b(10)++, b(10)-98++, b(11)-98++, b(11)++
Matched y ions: y(3), y(4), y(5)++, y(5), y(7)++, y(8)++, y(9)++, y(9)-98++, y(10)++, y(10)-98++, y(11)-98++, y(11)++, y(12)-98++, y(12)++

Peptide No.1174

YFLGLVDMTTVYGFR
Confirmed sites:
Ambiguous sites: @T:9orT:10

MS/MS Fragmentation of **YFLGLVDMTTVYGFR**
Found in **PI5L1_MOUSE** in **SwissProt**, Phosphatidylinositol-4-phosphate 5-kinase-like protein 1 OS=Mus musculus GN=Pip5kl1 PE=1 SV=1

Match to Query 4497: 1876.843281 from(626.621703,3+) index(1562)
Title: Elution from: 30.044 to 30.044 scan no 2642 cid35.00 polarity:+



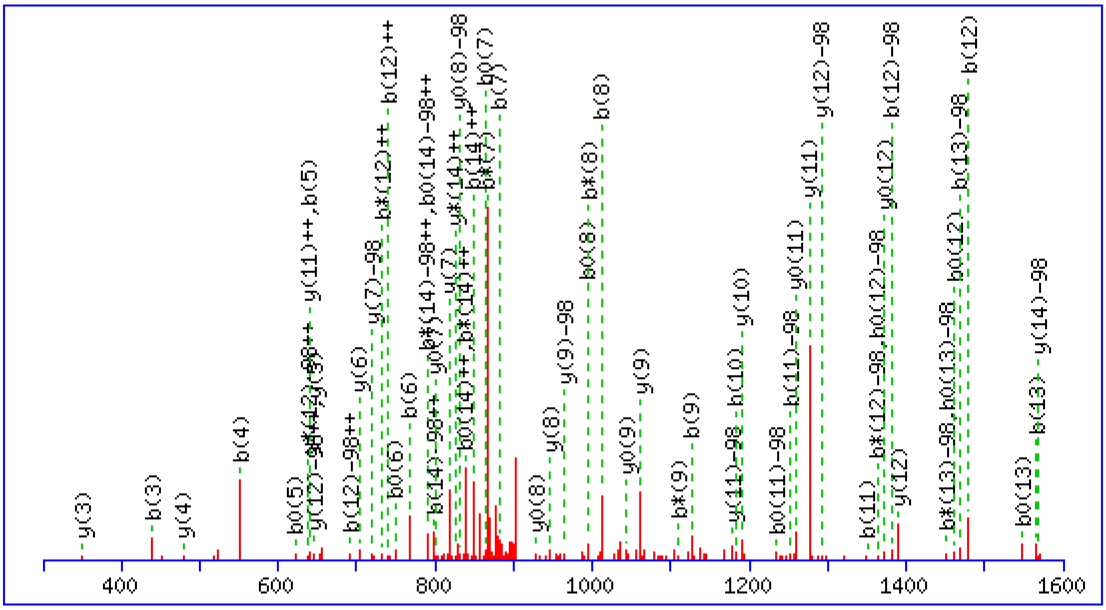
Monoisotopic mass of neutral peptide Mr(calc): 1876.8471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M8 : Oxidation (M), with neutral losses 63.9983(shown in table), 0.0000
T10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.022
Matched b ions: b(5), b(6), b(7)
Matched y ions: y(4), y(9)++, y(10)-98++, y(14)-98++

Peptide No.1175

YFQISQDEDGSESED
Confirmed sites: @S:11
Ambiguous sites:

MS/MS Fragmentation of **YFQISQDEDGSESED**
Found in **RL22L_MOUSE** in **SwissProt**, 60S ribosomal protein L22-like 1 OS=Mus musculus GN=Rpl22l1 PE=1 SV=1

Match to Query 3987: 1827.636416 from(914.825484,2+) index(4778)
Title: Elution from: 49.787 to 49.787 scan no 3932 cid35.00 polarity:+:m1s



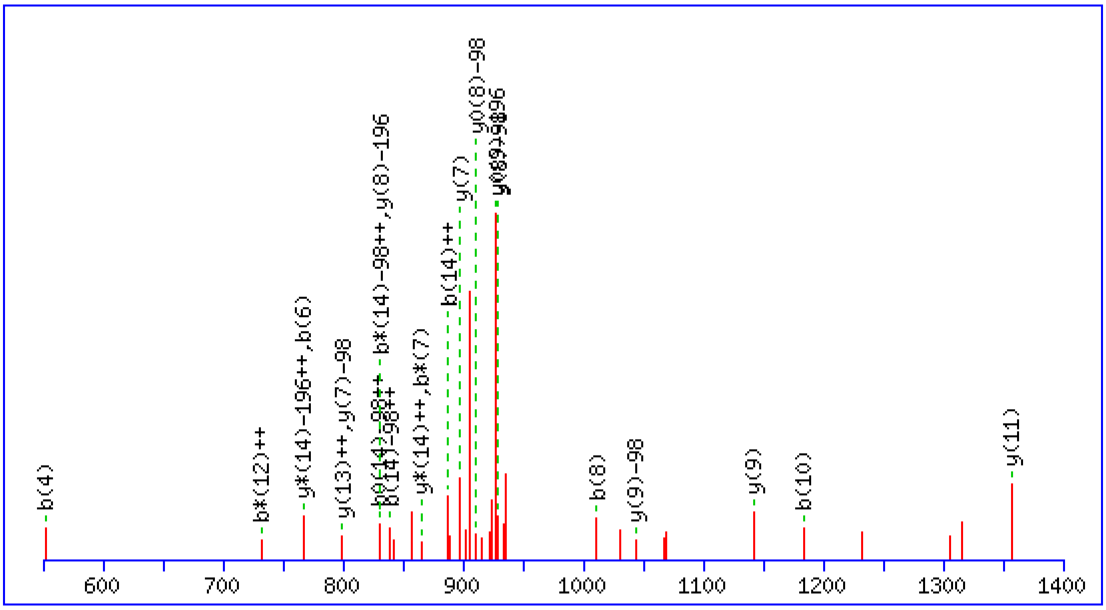
Monoisotopic mass of neutral peptide Mr(calc): 1827.6360
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 **Expect:** 5.1e-006
Matched b ions: b(3), b(4), b(5), b(6), b(7), b(8), b(9), b(10), b(11)-98, b(11), b(12), b(12)-98, b(12)-98++, b(12)++, b(13), b(13)-98, b(14)++, b(14)-98++
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(7)-98, y(8), y(9), y(9)-98, y(10), y(11), y(11)++, y(11)-98, y(12), y(12)-98++, y(12)-98, y(14)-98

Peptide No.1176

YFQISQDEDGSESED
Confirmed sites: @S:11,@S:13
Ambiguous sites:

MS/MS Fragmentation of **YFQISQDEDGSESED**
Found in **RL22L_MOUSE** in **SwissProt**, 60S ribosomal protein L22-like 1 OS=Mus musculus GN=Rpl22l1 PE=1 SV=1

Match to Query 3877: 1907.599226 from(954.806889,2+) index(5894)
Title: Elution from: 50.215 to 50.215 scan no 4918 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1907.6023
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 20 **Expect:** 0.014
Matched b ions: b(4), b(6), b(8), b(10), b(14)-98++, b(14)++
Matched y ions: y(7)-98, y(7), y(8)-196, y(8)-98, y(9), y(9)-98, y(11), y(13)++

Peptide No.1177

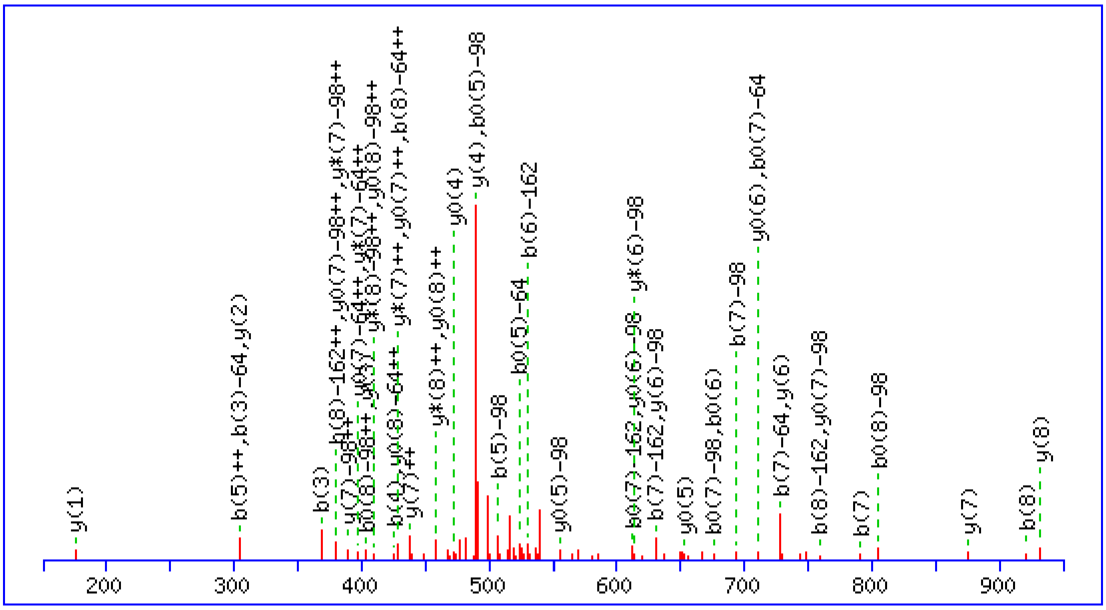
YGMGTSVER

Confirmed sites: @T:5

Ambiguous sites:

MS/MS Fragmentation of **YGMGTSVER**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 1229: 1094.409494 from(548.212023,2+) index(291)
Title: Elution from: 18.638 to 18.638 scan no 1092 cid35.00 polarity:+



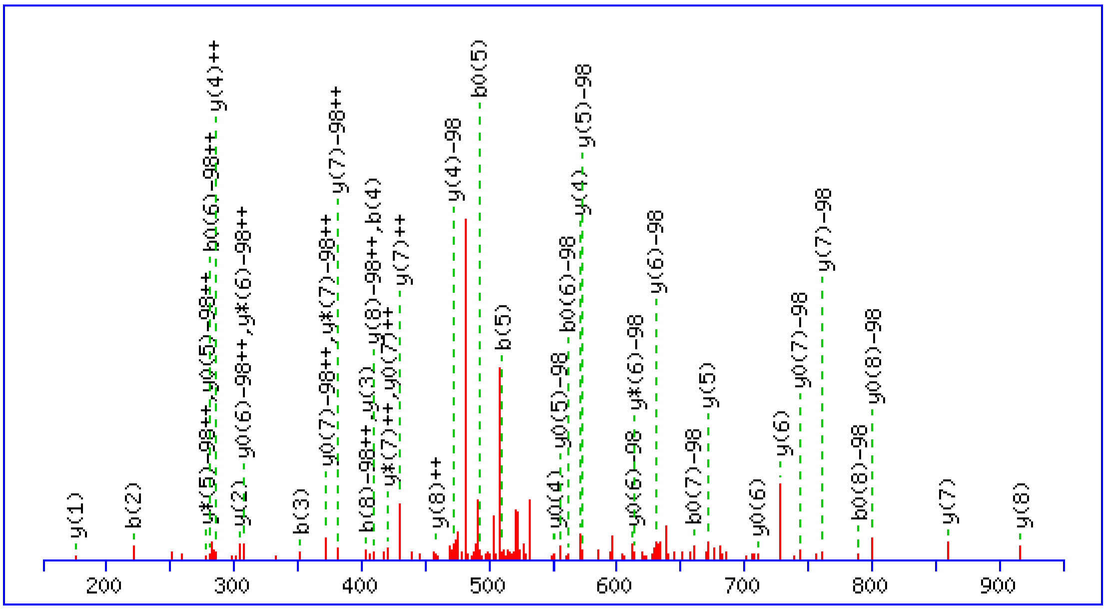
Monoisotopic mass of neutral peptide Mr(calc): 1094.4104
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 50 **Expect:** 2.2e-005
Matched b ions: b(3), b(4), b(5)++, b(5)-98, b(7)-98, b(7), b(8)
Matched y ions: y(1), y(2), y(3), y(4), y(6)-98, y(6), y(7)++, y(7), y(7)-98++, y(8)

Peptide No.1178

YGMGTSVER
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **YGMGTSVER**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 1043: 1078.414764 from(540.214658,2+) index(897)
Title: Elution from: 24.154 to 24.154 scan no 1803 cid35.00 polarity:+



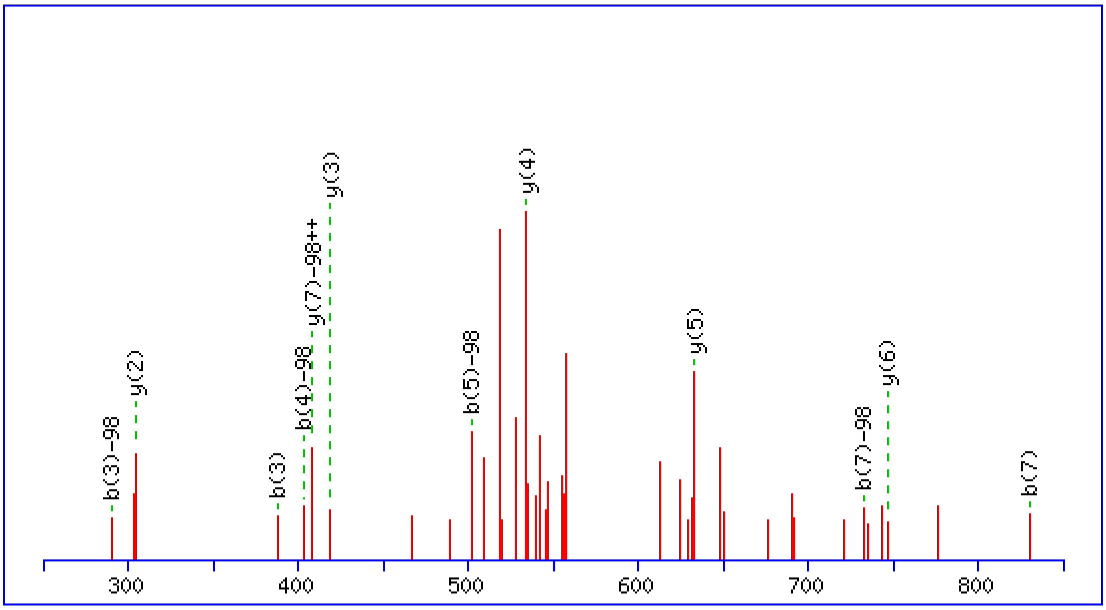
Monoisotopic mass of neutral peptide Mr(calc): 1078.4155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.0031
Matched b ions: b(2), b(3), b(4), b(5), b(8)-98++
Matched y ions: y(1), y(2), y(3), y(4)-98, y(4)++, y(4), y(5), y(5)-98, y(6), y(6)-98, y(7)++, y(7), y(7)-98++, y(7)-98, y(8), y(8)-98++, y(8)++

Peptide No.1179

YGSIVDDER
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **YGSIVDDER**
Found in **IQGA2_MOUSE** in **SwissProt**, Ras GTPase-activating-like protein IQGAP2 OS=Mus musculus GN=Iqgap2 PE=1 SV=2

Match to Query 1353: 1132.443046 from(567.228799,2+) index(1322)
Title: Elution from: 27.545 to 27.545 scan no 2301 cid35.00 polarity:+



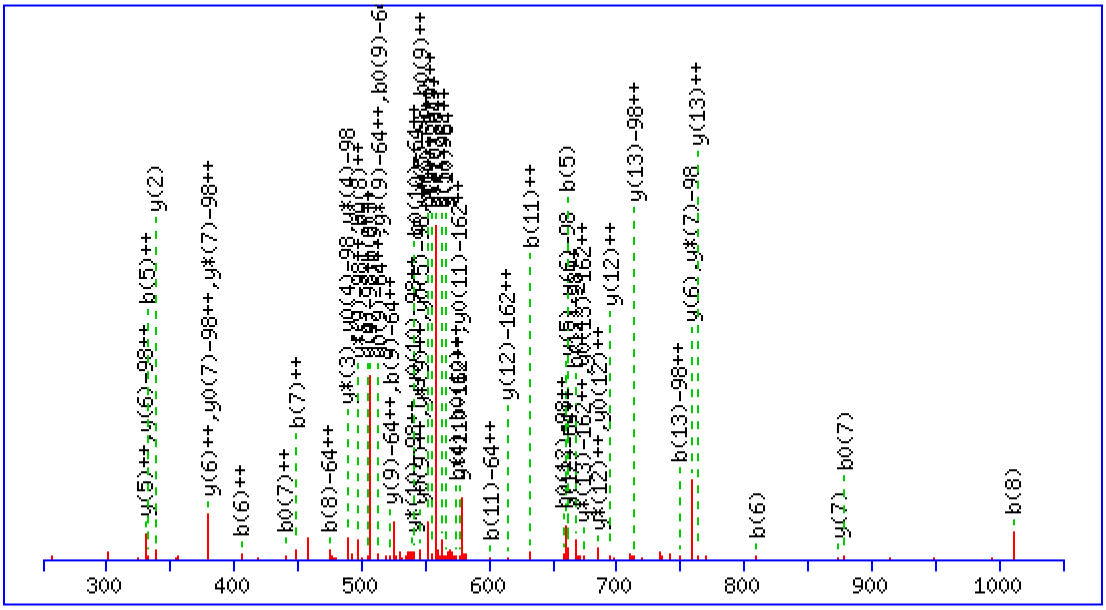
Monoisotopic mass of neutral peptide Mr(calc): 1132.4438
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 **Expect:** 0.014
Matched b ions: b(3), b(3)-98, b(4)-98, b(5)-98, b(7), b(7)-98
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(7)-98++

Peptide No.1180

YHGHSMSDPGVSYR
Confirmed sites: @Y:1,@S:12
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3872: 1767.612162 from(590.211330,3+) index(223)
Title: Elution from: 26.069 to 26.069 scan no 1370 cid35.00 polarity:+



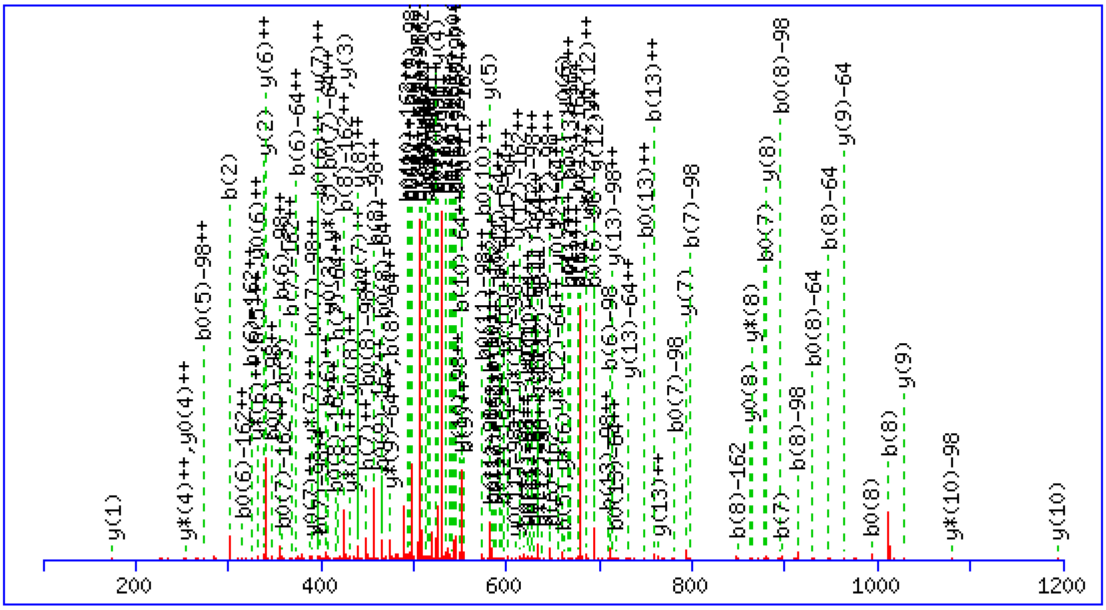
Monoisotopic mass of neutral peptide Mr(calc): 1767.6113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y1 : Phospho (Y)
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.0053
Matched b ions: b(4), b(5), b(5)++, b(6)++, b(6), b(7)++, b(8)++, b(8), b(9)++, b(11)++, b(12)-98++, b(13)-98++
Matched y ions: y(2), y(3), y(4)-98, y(5)++, y(5), y(5)-98, y(6)-98++, y(6)++, y(6)-98, y(6), y(7), y(9)-98++, y(9)++, y(12)++, y(13)++, y(13)-98++

Peptide No.1181

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3754: 1687.644777 from(563.555535,3+) index(309)
Title: Elution from: 18.791 to 18.791 scan no 1112 cid35.00 polarity:+



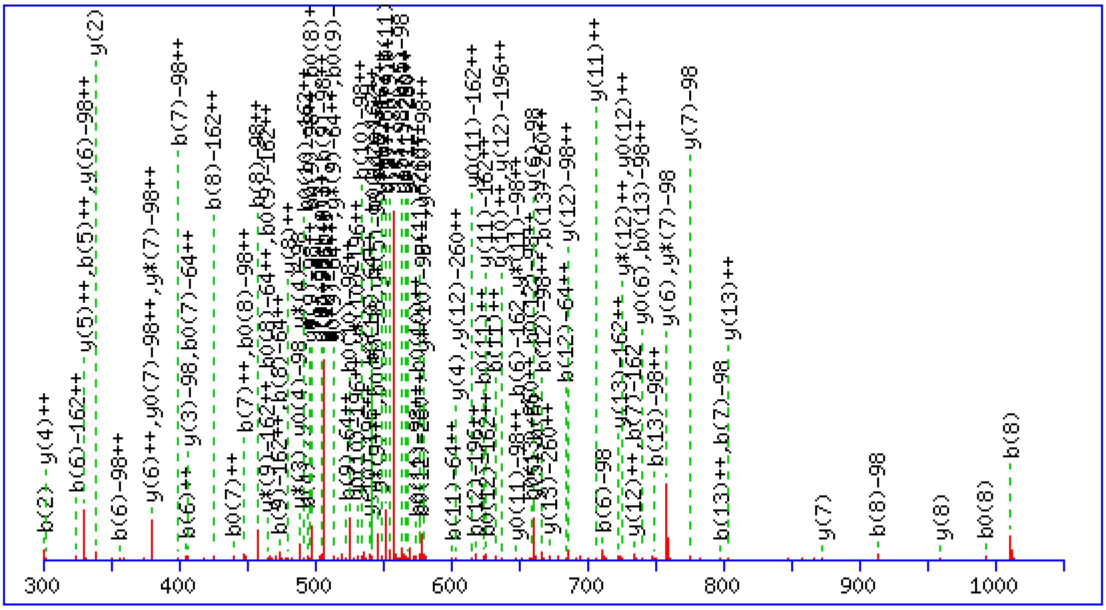
Monoisotopic mass of neutral peptide Mr(calc): 1687.6450
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 39 **Expect:** 0.0004
Matched b ions: b(2), b(3), b(4), b(5)++, b(5), b(6)-98++, b(6)-98, b(6)++, b(7)++, b(7), b(7)-98, b(7)-98++, b(8)-98++, b(8)-98, b(8), b(8)++, b(9)-98++, b(9)++, b(10)++, b(10)-98++, b(11)++, b(11)-98++, b(12)-98++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(10), y(10)-98++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(13)++, y(13)-98++

Peptide No.1182

YHGHSMSDPGVSYR
Confirmed sites: @S:5,@S:12
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 4107: 1767.610059 from(590.210629,3+) index(4119)
Title: Elution from: 20.089 to 20.089 scan no 1286 cid35.00 polarity:+:m1s



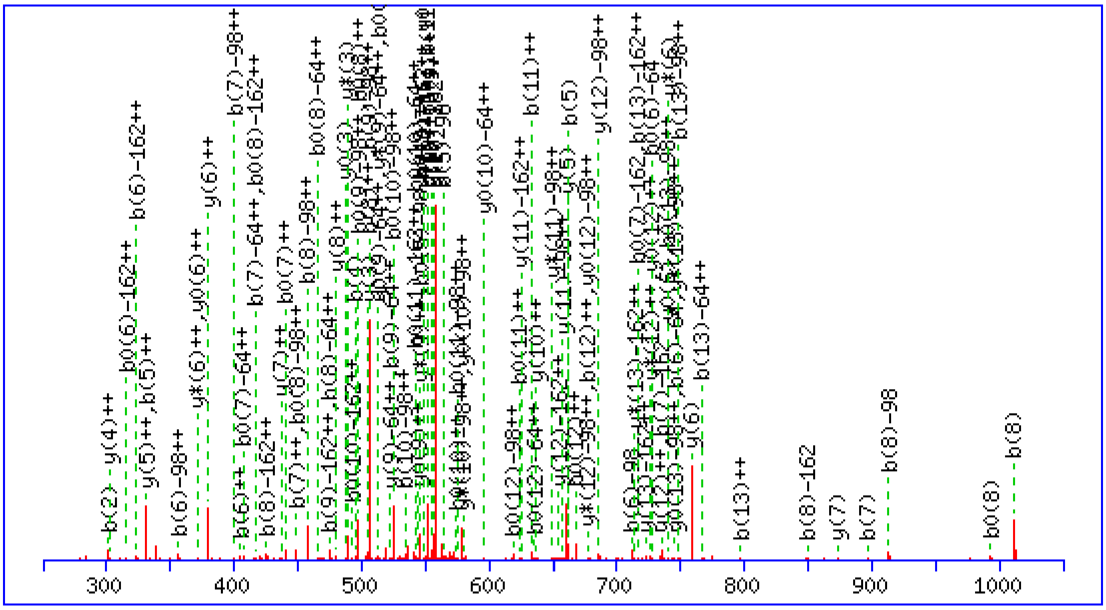
Monoisotopic mass of neutral peptide Mr(calc): 1767.6113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 **Expect:** 0.0055
Matched b ions: b(2), b(4), b(5)++, b(5), b(5)-98, b(6)-98, b(6)-98++, b(6)++, b(7)++, b(7)-98++, b(7)-98, b(8)-98, b(8), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(11)++, b(12)-98++, b(12)-196++, b(13)-98++, b(13)++
Matched y ions: y(2), y(3)-98, y(3), y(4)-98, y(4)++, y(4), y(5)++, y(5), y(5)-98, y(6)-98++, y(6)-98, y(6), y(6)++, y(7), y(7)-98, y(8), y(8)++, y(9)++, y(9)-98++, y(10)-196++, y(10)++, y(11)++, y(12)-98++, y(12)++, y(12)-196++, y(13)++

Peptide No.1183

YHGHSMSDPGVSYR
Confirmed sites: @S:5,@Y:13
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3973: 1767.609411 from(590.210413,3+) index(414)
Title: Elution from: 20.144 to 20.144 scan no 1258 cid35.00 polarity:+



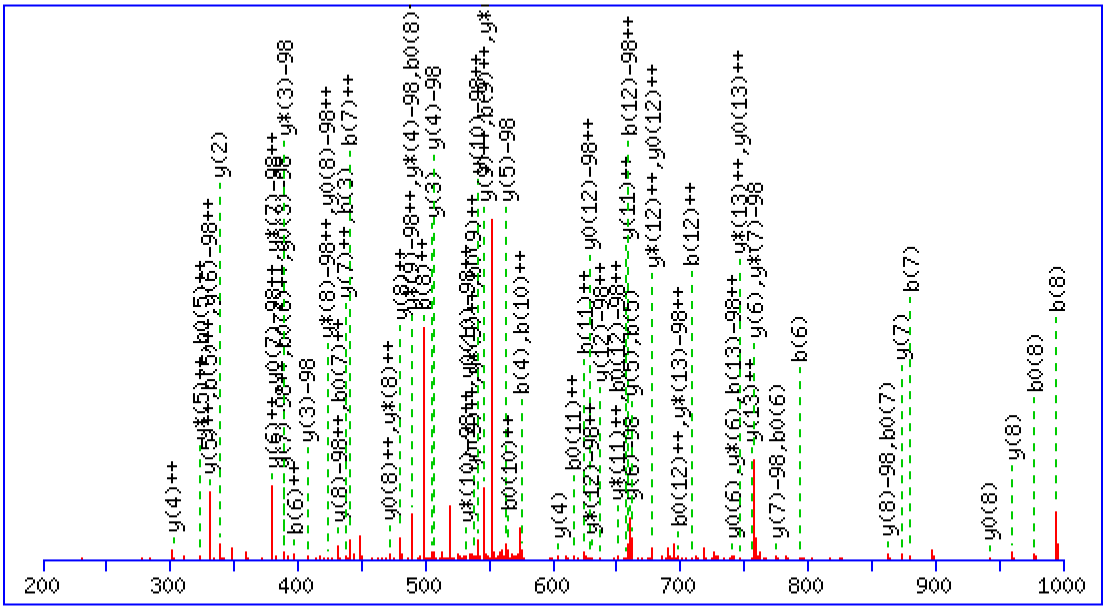
Monoisotopic mass of neutral peptide Mr(calc): 1767.6113
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Y13 : Phospho (Y)
Ions Score: 25 **Expect:** 0.0066
Matched b ions: b(2), b(4), b(5)++, b(5), b(5)-98, b(6)-98, b(6)-98++, b(6)++, b(7)++, b(7), b(7)-98++, b(8)-98, b(8), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(11)++, b(12)++, b(13)++, b(13)-98++
Matched y ions: y(3), y(4)++, y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(9)++, y(10)++, y(11)-98++, y(12)++, y(12)-98++

Peptide No.1184

YHGHSMSDPGVSYR
Confirmed sites: @Y:1,@S:12
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3907: 1751.615334 from(584.879054,3+) index(4383)
Title: Elution from: 23.796 to 23.796 scan no 1754 cid35.00 polarity:+:m1s



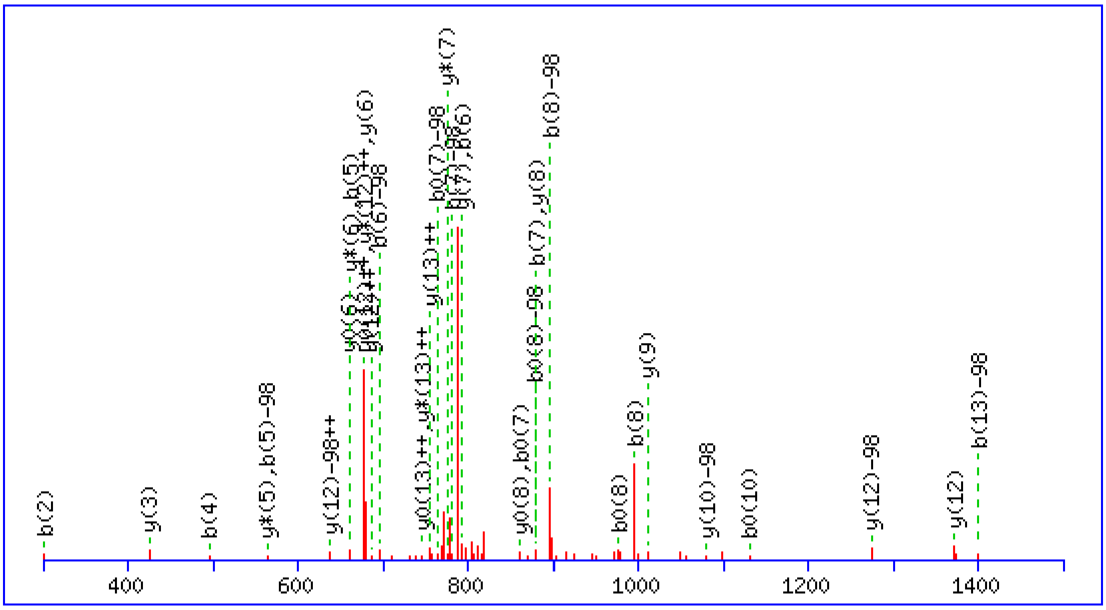
Monoisotopic mass of neutral peptide Mr(calc): 1751.6164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y1 : Phospho (Y)
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 39 **Expect:** 0.00036
Matched b ions: b(3), b(4), b(5)++, b(5), b(6)++, b(6), b(7), b(7)++, b(8)++, b(8), b(9)++, b(10)++, b(11)++, b(12)-98++, b(12)++, b(13)-98++
Matched y ions: y(2), y(3)-98, y(3), y(4)++, y(4)-98, y(4), y(5)++, y(5), y(5)-98, y(6)++, y(6)-98, y(6), y(6)-98++, y(7), y(7)-98, y(7)-98++, y(7)++, y(8)-98, y(8), y(8)++, y(8)-98++, y(9)++, y(10)-98++, y(11)++, y(12)-98++, y(13)++

Peptide No.1185

YHGHSMSDPGVSYR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3509: 1671.646164 from(836.830358,2+) index(4157)
Title: Elution from: 21.869 to 21.869 scan no 1491 cid35.00 polarity:+:m1s



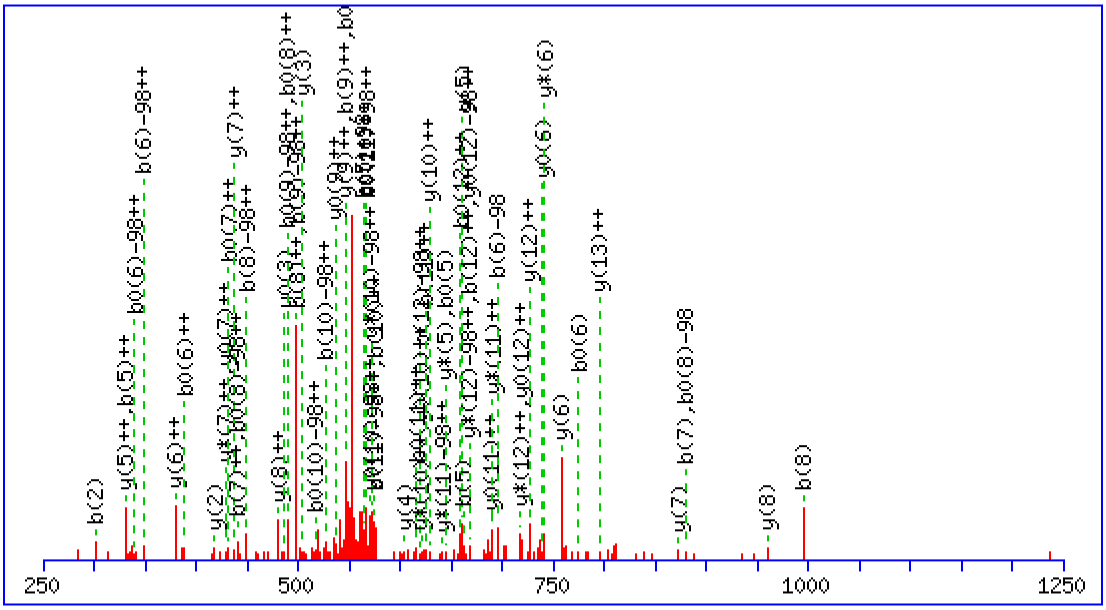
Monoisotopic mass of neutral peptide Mr(calc): 1671.6501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 **Expect:** 0.0016
Matched b ions: b(2), b(4), b(5)-98, b(5), b(6)-98, b(6), b(7), b(7)-98, b(8)-98, b(8), b(13)-98
Matched y ions: y(3), y(6), y(7), y(8), y(9), y(10)-98, y(12)-98, y(12), y(12)-98++, y(12)++, y(13)++

Peptide No.1186

YHGHSMSDPGVSYR
Confirmed sites: @S:5,@Y:13
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3830: 1751.617665 from(584.879831,3+) index(620)
Title: Elution from: 31.112 to 31.112 scan no 1935 cid35.00 polarity:+



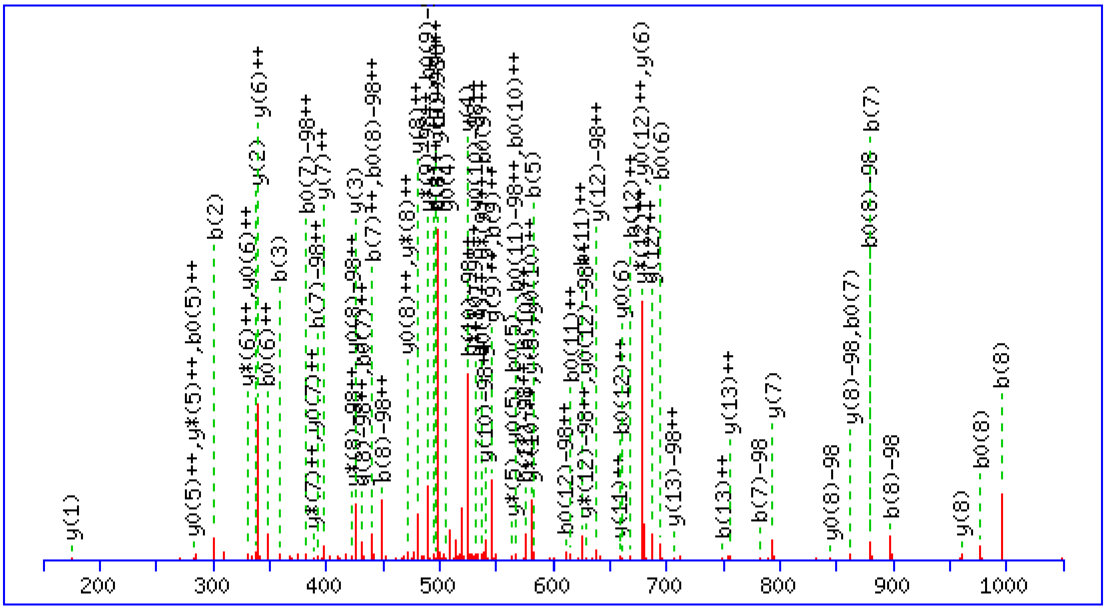
Monoisotopic mass of neutral peptide Mr(calc): 1751.6164
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Y13 : Phospho (Y)
Ions Score: 27 **Expect:** 0.0049
Matched b ions: b(2), b(5)++, b(5), b(5)-98, b(6)-98, b(6)-98++, b(7)++, b(7), b(8), b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)++, b(12)-98++
Matched y ions: y(2), y(3), y(4), y(5)++, y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(10)++, y(12)++, y(13)++

Peptide No.1187

YHGHSMSDPGVSYR
Confirmed sites: @S:7
Ambiguous sites:

MS/MS Fragmentation of **YHGHSMSDPGVSYR**
Found in **ODPA_MOUSE** in **SwissProt**, Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1

Match to Query 3687: 1671.648795 from(558.223541,3+) index(679)
Title: Elution from: 21.819 to 21.819 scan no 1520 cid35.00 polarity:+



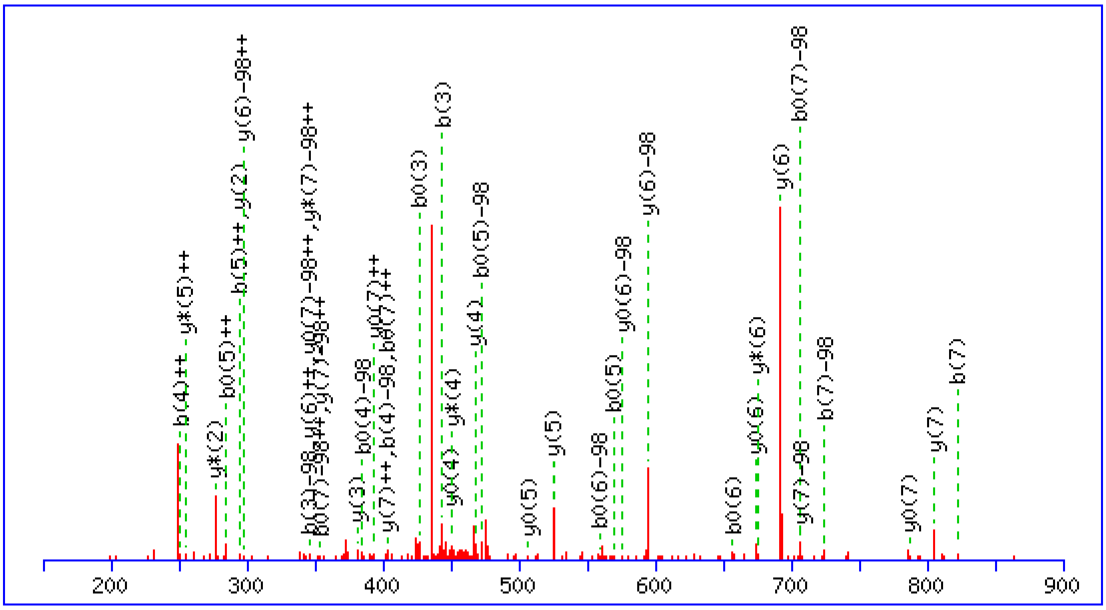
Monoisotopic mass of neutral peptide Mr(calc): 1671.6501
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 **Expect:** 6e-005
Matched b ions: b(2), b(3), b(4), b(5), b(7), b(7)++, b(7)-98, b(7)-98++, b(8)-98++, b(8)++, b(8)-98, b(8), b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)++, b(13)++
Matched y ions: y(1), y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)-98, y(8), y(8)-98++, y(8)++, y(9)++, y(9)-98++, y(10)-98++, y(11)++, y(12)++, y(12)-98++, y(13)++, y(13)-98++

Peptide No.1188

YISGSSFK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **YISGSSFK**
Found in **DHB5_MOUSE** in **SwissProt**, Estradiol 17 beta-dehydrogenase 5 OS=Mus musculus GN=Akr1c6 PE=1 SV=1

Match to Query 898: 967.405264 from(484.709908,2+) index(1230)
Title: Elution from: 36.020 to 36.020 scan no 2646 cid35.00 polarity:+



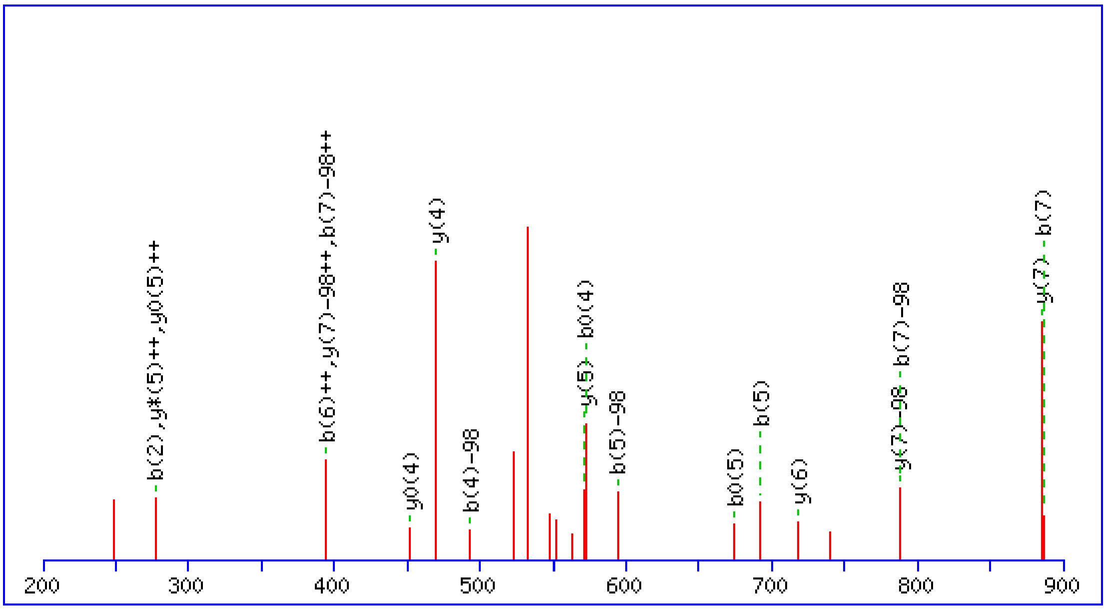
Monoisotopic mass of neutral peptide Mr(calc): 967.4052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 **Expect:** 0.0025
Matched b ions: b(2), b(3), b(3)-98, b(4)++, b(4)-98, b(5)++, b(6), b(7)-98, b(7)
Matched y ions: y(2), y(3), y(4), y(5), y(6)-98, y(6), y(6)++, y(6)-98++, y(7)-98, y(7), y(7)-98++, y(7)++

Peptide No.1189

YLSFTPPEK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **YLSFTPPEK**
Found in **PAK2_MOUSE** in **SwissProt**, Serine/threonine-protein kinase PAK 2 OS=Mus musculus GN=Pak2 PE=1 SV=1

Match to Query 1371: 1160.516790 from(581.265671,2+) index(6084)
Title: Elution from: 40.954 to 40.954 scan no 4067 cid35.00 polarity:+:m1s



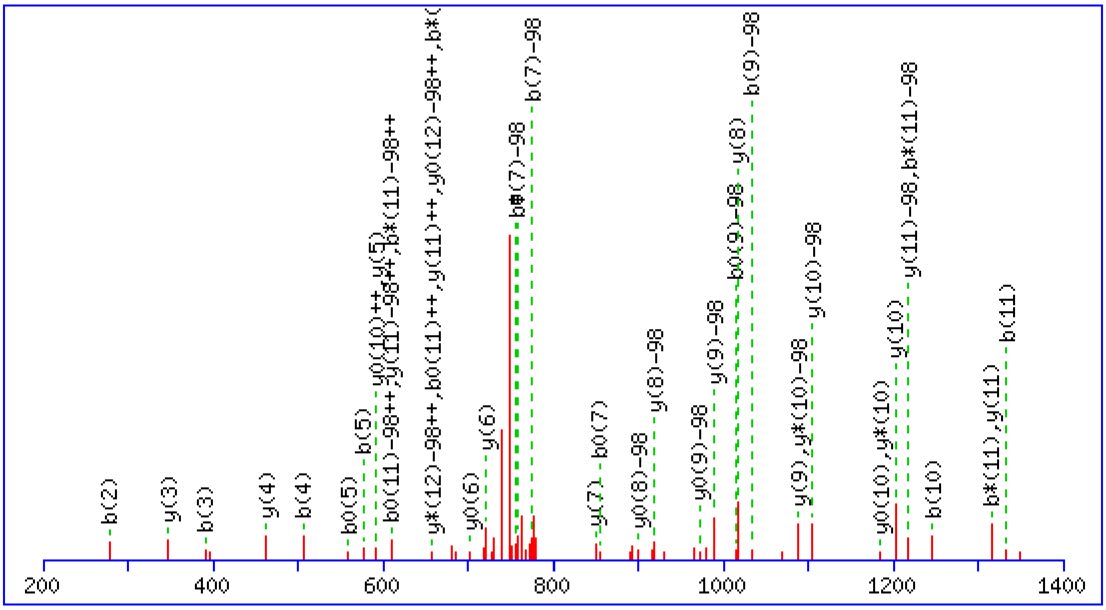
Monoisotopic mass of neutral peptide Mr(calc): 1160.5155
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 **Expect:** 0.0018
Matched b ions: b(2), b(4)-98, b(5), b(5)-98, b(6)++, b(7)-98++, b(7)-98, b(7)
Matched y ions: y(4), y(5), y(6), y(7)-98++, y(7)-98, y(7)

Peptide No.1190

YNLDASEEEDSNK
Confirmed sites: @S:6
Ambiguous sites:

MS/MS Fragmentation of **YNLDASEEEDSNK**
Found in **ZRAB2_MOUSE** in **SwissProt**, Zinc finger Ran-binding domain-containing protein 2 OS=Mus musculus GN=Zranb2 PE=1 SV=2

Match to Query 2928: 1592.585254 from(797.299903,2+) index(872)
Title: Elution from: 25.957 to 25.957 scan no 1928 cid35.00 polarity:+



Monoisotopic mass of neutral peptide Mr(calc): 1592.5879
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 59 **Expect:** 3.1e-006
Matched b ions: b(2), b(3), b(4), b(5), b(7)-98, b(9)-98, b(10), b(11)
Matched y ions: y(3), y(4), y(5), y(6), y(7), y(8)-98, y(8), y(9), y(9)-98, y(10), y(10)-98, y(11)-98++, y(11), y(11)++, y(11)-98

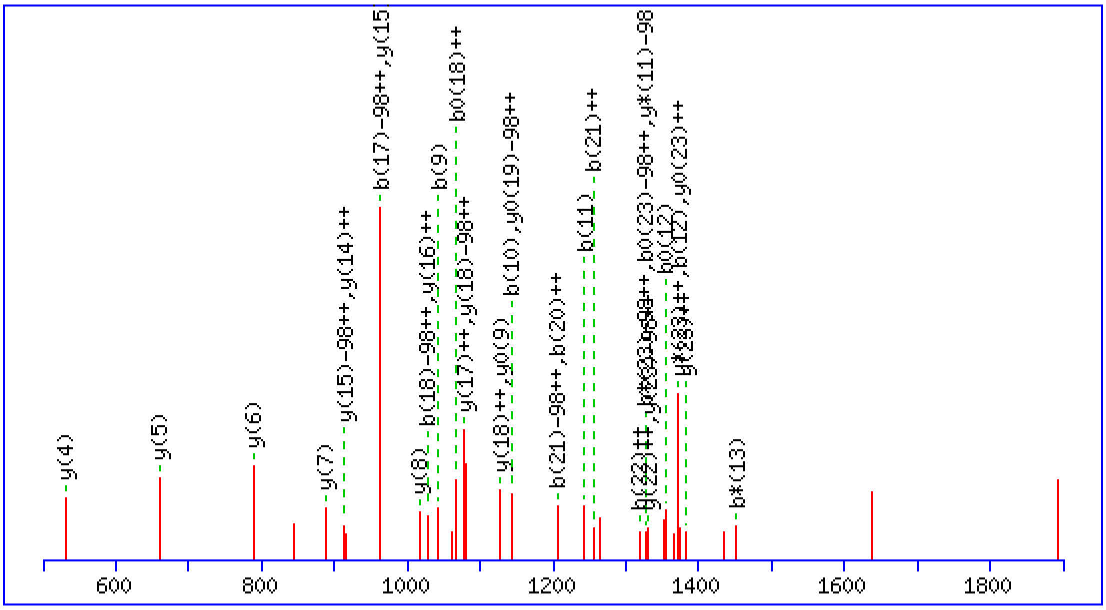
Peptide No.1191

YQDEVFGGFVTEPQEESEEEVEEPEER

Confirmed sites: @S:17
Ambiguous sites:

MS/MS Fragmentation of **YQDEVFGGFVTEPQEESEEEVEEPEER**
Found in **G3BP1_MOUSE** in **SwissProt**, Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1

Match to Query 7069: 3295.317489 from(1099.446439,3+) index(7009)
Title: Elution from: 56.058 to 56.058 scan no 5810 cid35.00 polarity:+:m1s



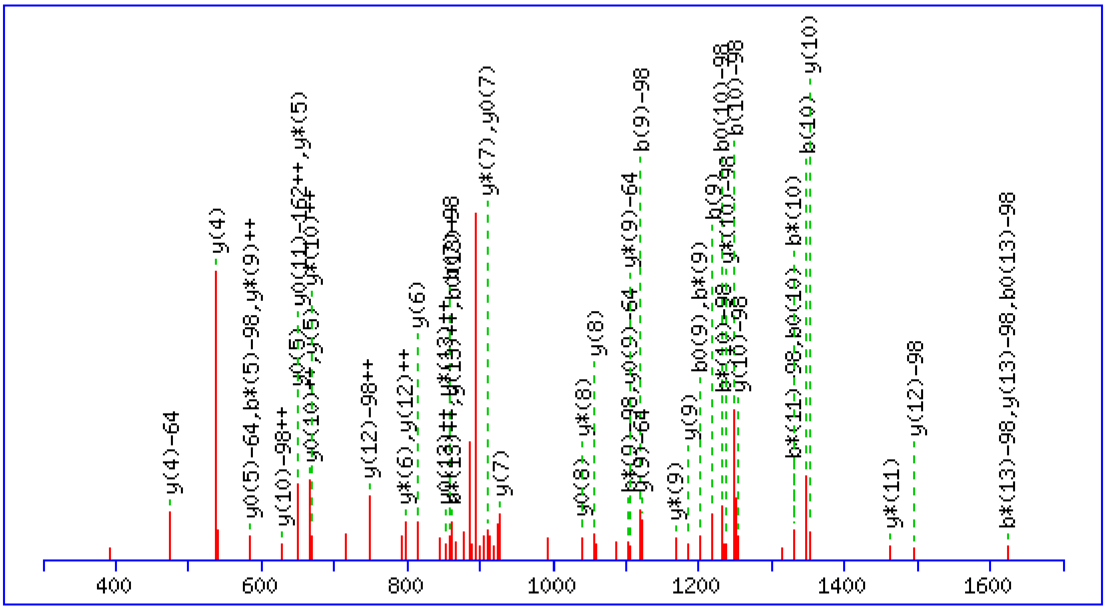
Monoisotopic mass of neutral peptide Mr(calc): 3295.3242
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 **Expect:** 0.00026
Matched b ions: b(9), b(10), b(11), b(12), b(17)-98++, b(18)-98++, b(20)++, b(21)-98++, b(21)++, b(22)++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(14)++, y(15)++, y(15)-98++, y(16)++, y(17)++, y(18)-98++, y(18)++, y(22)++, y(23)-98++, y(23)++

Peptide No.1192

YQLQSQENFEPFMK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YQLQSQENFEPFMK**
Found in **FABPL_MOUSE** in **SwissProt**, Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2

Match to Query 4386: 1883.778450 from(942.896501,2+) index(6426)
Title: Elution from: 45.835 to 45.835 scan no 4674 cid35.00 polarity:+:m1s



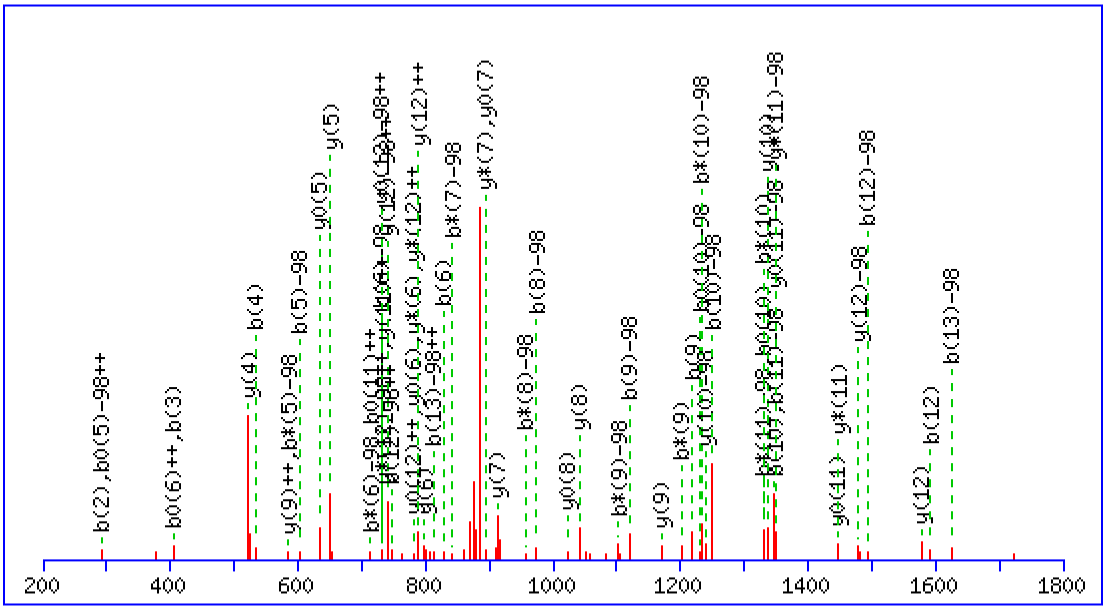
Monoisotopic mass of neutral peptide Mr(calc): 1883.7801
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
M13 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 45 **Expect:** 0.00013
Matched b ions: b(7)-98, b(9)-98, b(9), b(10)-98, b(10)
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9), y(10)-98++, y(10), y(10)-98, y(12)-98++, y(12)-98, y(12)++, y(13)-98, y(13)++

Peptide No.1193

YQLQSQENFEPFMK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YQLQSQENFEPFMK**
Found in **FABPL_MOUSE** in **SwissProt**, Fatty acid-binding protein, liver OS=Mus musculus GN=Fabp1 PE=1 SV=2

Match to Query 4325: 1867.783016 from(934.898784,2+) index(6690)
Title: Elution from: 51.682 to 51.682 scan no 5313 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 1867.7852
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 **Expect:** 5.9e-007
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98, b(6), b(8)-98, b(9)-98, b(9), b(10)-98, b(10), b(11)-98, b(12), b(12)-98, b(12)-98++, b(13)-98, b(13)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(8), y(9)++, y(9), y(10), y(10)-98, y(11)++, y(12)-98++, y(12), y(12)++, y(12)-98

Peptide No.1194

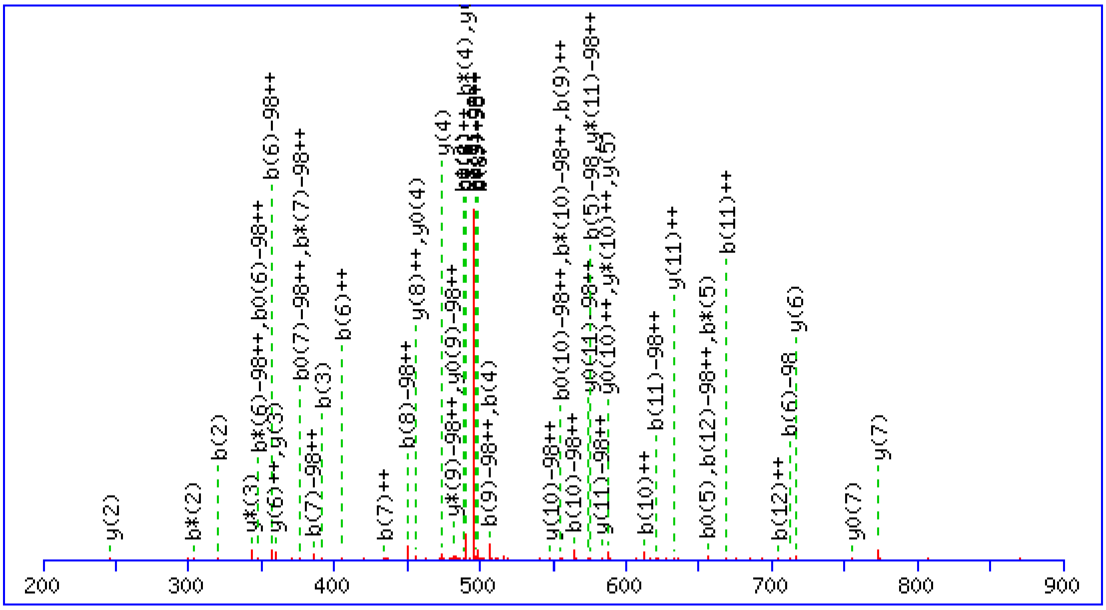
YRADSHGELDLAR

Confirmed sites: @S:5

Ambiguous sites:

MS/MS Fragmentation of **YRADSHGELDLAR**
Found in **ACOT1_MOUSE** in **SwissProt**, Acyl-coenzyme A thioesterase 1 OS=Mus musculus GN=Acot1 PE=1 SV=1

Match to Query 3345: 1581.693051 from(528.238293,3+) index(1141)
Title: Elution from: 25.842 to 25.842 scan no 2067 cid35.00 polarity:+



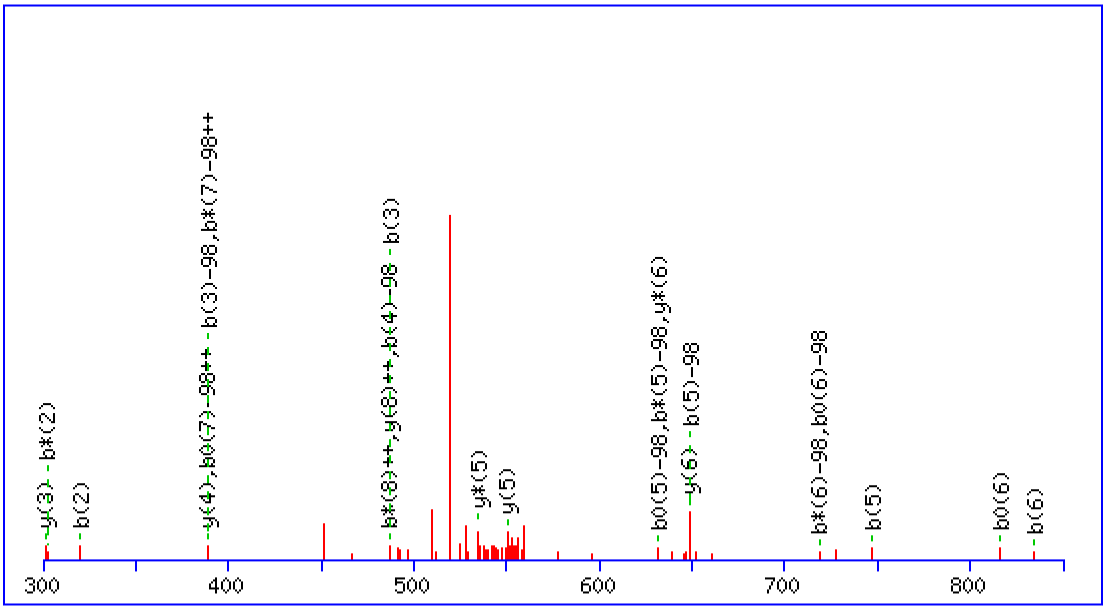
Monoisotopic mass of neutral peptide Mr(calc): 1581.6936
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 50 **Expect:** 3.6e-005
Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)-98++, b(6)++, b(6)-98, b(7)-98++, b(7)++, b(8)-98++, b(8)++, b(9)-98++, b(9)++, b(10)-98++, b(10)++, b(11)++, b(11)-98++, b(12)-98++, b(12)++
Matched y ions: y(2), y(3), y(4), y(5), y(6), y(6)++, y(7), y(8)++, y(9)-98++, y(10)-98++, y(11)++, y(11)-98++

Peptide No.1195

YRSPYSGPK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **YRSPYSGPK**
Found in **RBM39_MOUSE** in **SwissProt**, RNA-binding protein 39 OS=Mus musculus GN=Rbm39 PE=1 SV=2

Match to Query 1361: 1133.489128 from(567.751840,2+) index(246)
Title: Elution from: 18.251 to 18.251 scan no 1041 cid35.00 polarity:+



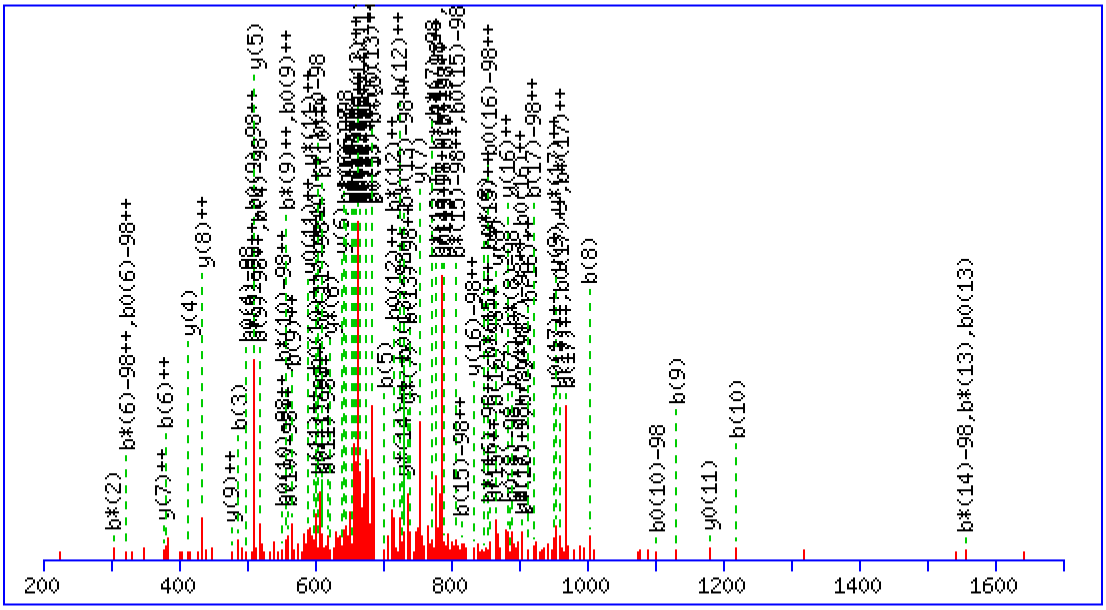
Monoisotopic mass of neutral peptide Mr(calc): 1133.4906
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 24 **Expect:** 0.014
Matched b ions: b(2), b(3)-98, b(3), b(4)-98, b(5), b(5)-98, b(6)
Matched y ions: y(3), y(4), y(5), y(6), y(8)++

Peptide No.1196

YRSQSGEDESLNQPGPIK
Confirmed sites: @S:3
Ambiguous sites:

MS/MS Fragmentation of **YRSQSGEDESLNQPGPIK**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 4602: 2083.921776 from(695.647868,3+) index(794)
Title: Elution from: 33.319 to 33.319 scan no 2192 cid35.00 polarity:+



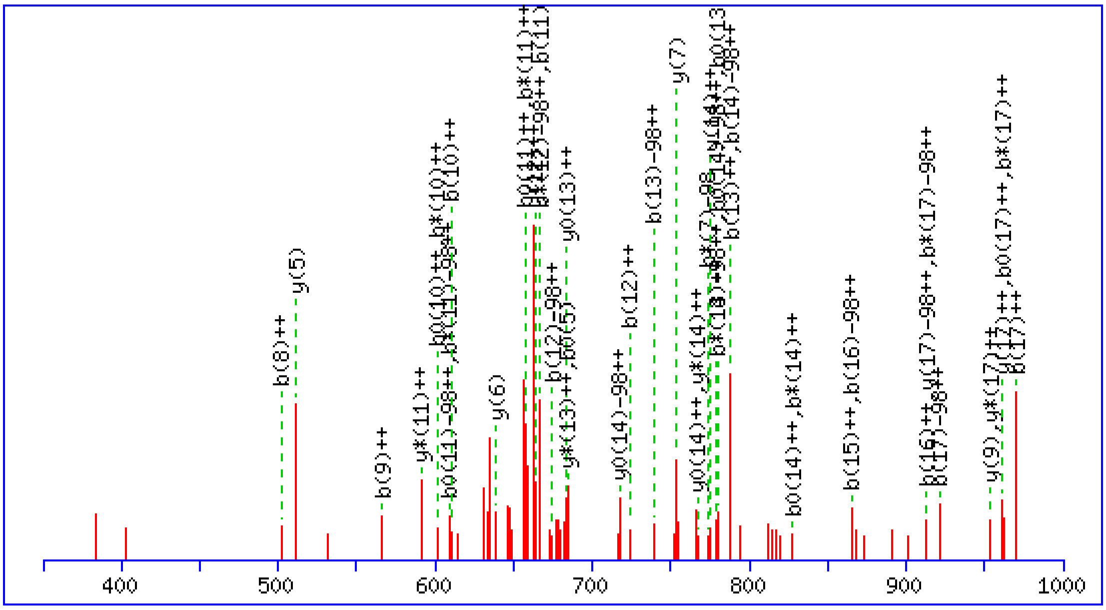
Monoisotopic mass of neutral peptide Mr(calc): 2083.9211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 **Expect:** 0.024
Matched b ions: b(3), b(4)-98, b(5)-98, b(5), b(6)++, b(6)-98, b(7), b(7)-98, b(8)-98, b(8), b(9)-98++, b(9)++, b(9), b(10), b(10)-98++, b(10)++, b(11)-98++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(15)++, b(15)-98++, b(16)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(4), y(5), y(6), y(7), y(7)++, y(8), y(8)++, y(9), y(9)++, y(11)++, y(12)++, y(16)++, y(16)-98++, y(17)++

Peptide No.1197

YRSQSGEDESLNQPGPIK
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YRSQSGEDESLNQPGPIK**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 4421: 2083.918764 from(695.646864,3+) index(3852)
Title: Elution from: 25.862 to 25.862 scan no 1915 cid35.00 polarity:+:m1s



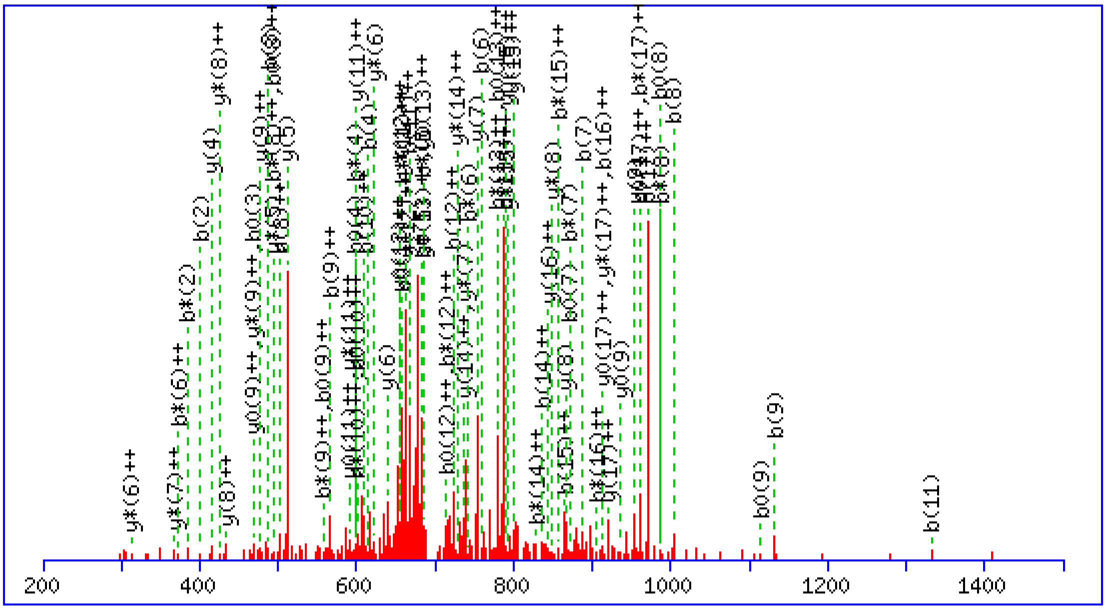
Monoisotopic mass of neutral peptide Mr(calc): 2083.9211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 32 **Expect:** 0.0052
Matched b ions: b(8)++, b(9)++, b(10)++, b(11)++, b(12)-98++, b(12)++, b(13)++, b(13)-98++, b(14)-98++, b(15)++, b(16)-98++, b(16)++, b(17)++, b(17)-98++
Matched y ions: y(5), y(6), y(7), y(9), y(12)++, y(14)++, y(17)++, y(17)-98++

Peptide No.1198

YRSQSGEDESLNQPGPIK
Confirmed sites: @Y:1
Ambiguous sites:

MS/MS Fragmentation of **YRSQSGEDESLNQPGPIK**
Found in **PEX1_MOUSE** in **SwissProt**, Peroxisome biogenesis factor 1 OS=Mus musculus GN=Pex1 PE=1 SV=2

Match to Query 5301: 2083.920498 from(695.647442,3+) index(4370)
Title: Elution from: 33.356 to 33.356 scan no 2300 cid35.00 polarity:+:m1s



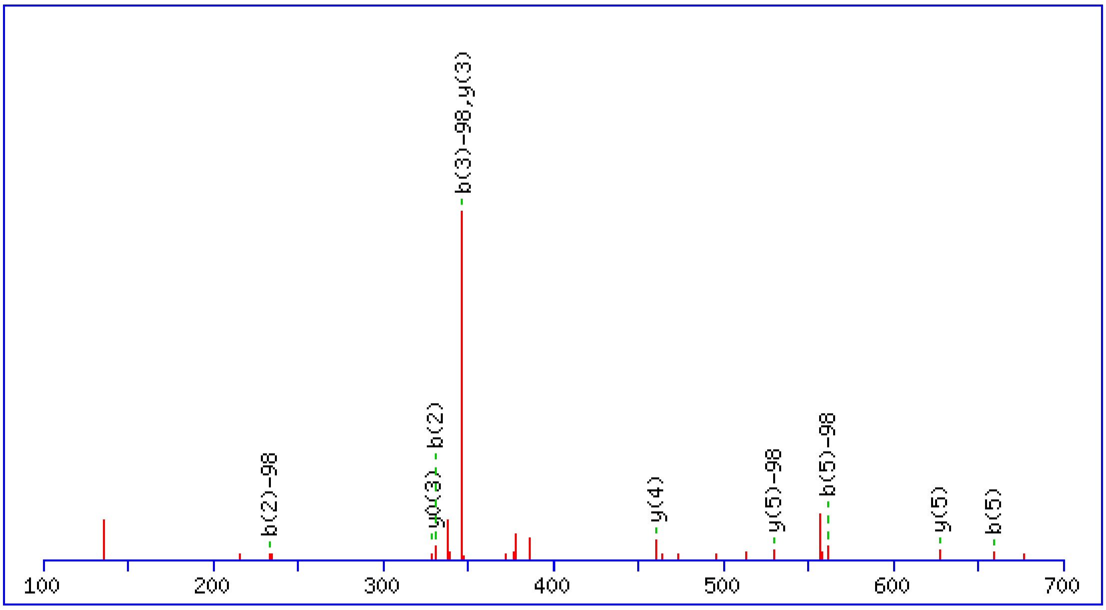
Monoisotopic mass of neutral peptide Mr(calc): 2083.9211
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y1 : Phospho (Y)
Ions Score: 28 **Expect:** 0.012
Matched b ions: b(2), b(3), b(4), b(6), b(7), b(8), b(8)++, b(9), b(9)++, b(10)++, b(11), b(11)++, b(12)++, b(13)++, b(14)++, b(15)++, b(16)++, b(17)++
Matched y ions: y(4), y(5), y(6), y(7), y(8)++, y(8), y(9), y(9)++, y(11)++, y(12)++, y(14)++, y(15)++, y(16)++, y(17)++

Peptide No.1199

YSLSKL
Confirmed sites: @S:2
Ambiguous sites:

MS/MS Fragmentation of **YSLSKL**
Found in **NUDT7_MOUSE** in **SwissProt**, Peroxisomal coenzyme A diphosphatase NUDT7 OS=Mus musculus GN=Nudt7 PE=1 SV=2

Match to Query 264: 789.367722 from(395.691137,2+) index(1882)
Title: Elution from: 36.712 to 36.712 scan no 3386 cid35.00 polarity:+



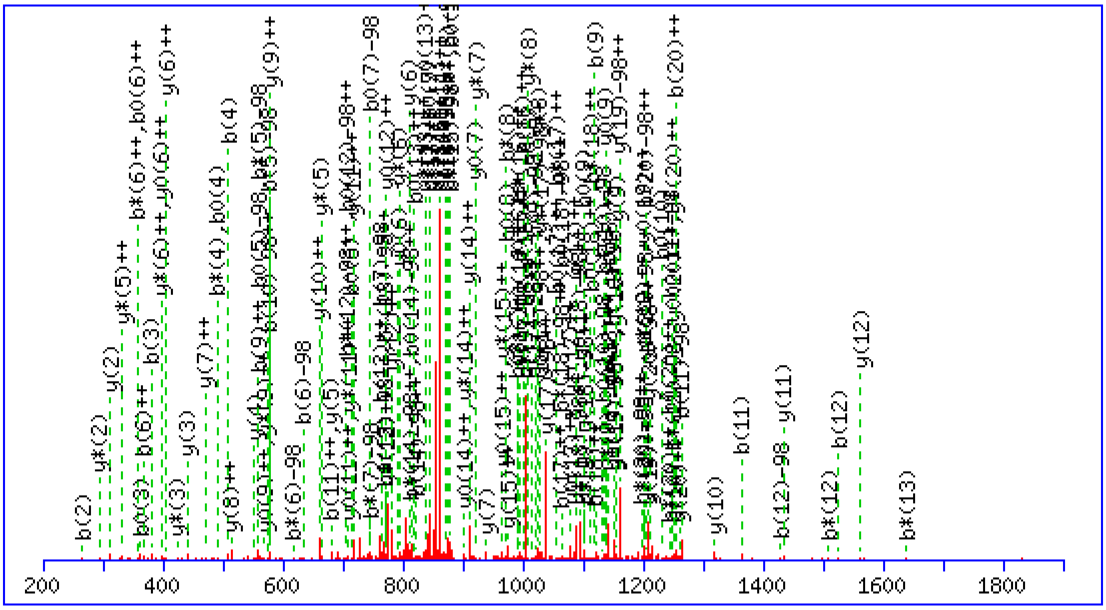
Monoisotopic mass of neutral peptide Mr(calc): 789.3673
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 **Expect:** 0.009
Matched b ions: b(2), b(2)-98, b(3)-98, b(5), b(5)-98
Matched y ions: y(3), y(4), y(5)-98, y(5)

Peptide No.1200

YTDQSGEEEEDYESEEQLQHR
Confirmed sites: @S:5
Ambiguous sites:

MS/MS Fragmentation of **YTDQSGEEEEDYESEEQLQHR**
Found in **COQ9_MOUSE** in **SwissProt**, Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Mus musculus GN=Coq9 PE=1 SV=1

Match to Query 5617: 2680.007256 from(894.343028,3+) index(4513)
Title: Elution from: 29.758 to 29.758 scan no 2534 cid35.00 polarity:+:m1s



Monoisotopic mass of neutral peptide Mr(calc): 2680.0086

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 74 **Expect:** 1.6e-007

Matched b ions: b(2), b(3), b(4), b(5)-98, b(6)++, b(6)-98, b(7), b(7)-98, b(8), b(9)++, b(9)-98, b(9), b(10)-98, b(10)-98++, b(10), b(11), b(11)-98, b(11)++, b(12), b(12)-98, b(12)++, b(14)++, b(14)-98++, b(16)++, b(17)-98++, b(17)++, b(18)++, b(20)-98++, b(20)++

Matched y ions: y(2), y(3), y(4), y(5), y(6)++, y(6), y(7), y(7)++, y(8)++, y(8), y(9)++, y(9), y(10)++, y(10), y(11), y(11)++, y(12), y(12)++, y(13)++, y(14)++, y(15)++, y(16)++, y(17)-98++, y(17)++, y(18)++, y(18)-98++, y(19)-98++, y(19)++, y(20)-98++, y(20)++