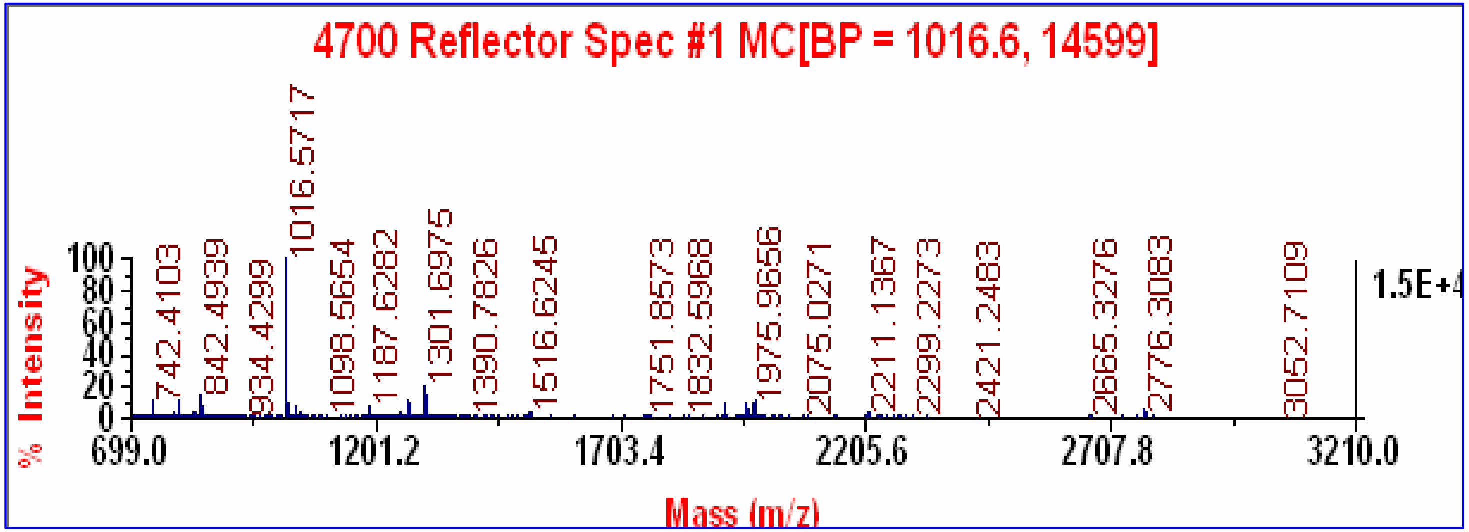
Supplemental materials

Figure S1 MS and MS/MS spectra of the 27 identified protein

This incudes the MALDI-TOF spectrum and confirming MALDI-TOF/TOF spectrum of 27 differentially expressed protein spots in RV-infected Neuroblastoma cells. The MALDI-TOF spectra were given by annotating with masses (blue), and their peptide assignments were tabulated with masses. In tables, the peptides with statistically significant ion score (confidence interval, C.I% >95%) (red and bold) or ion score above 21 (green) was considered to be confidently identified by MALDI-TOF/TOF, and their MS/MS spectra were shown with masses detected and fragment

Spot No.0442 gi|70724981

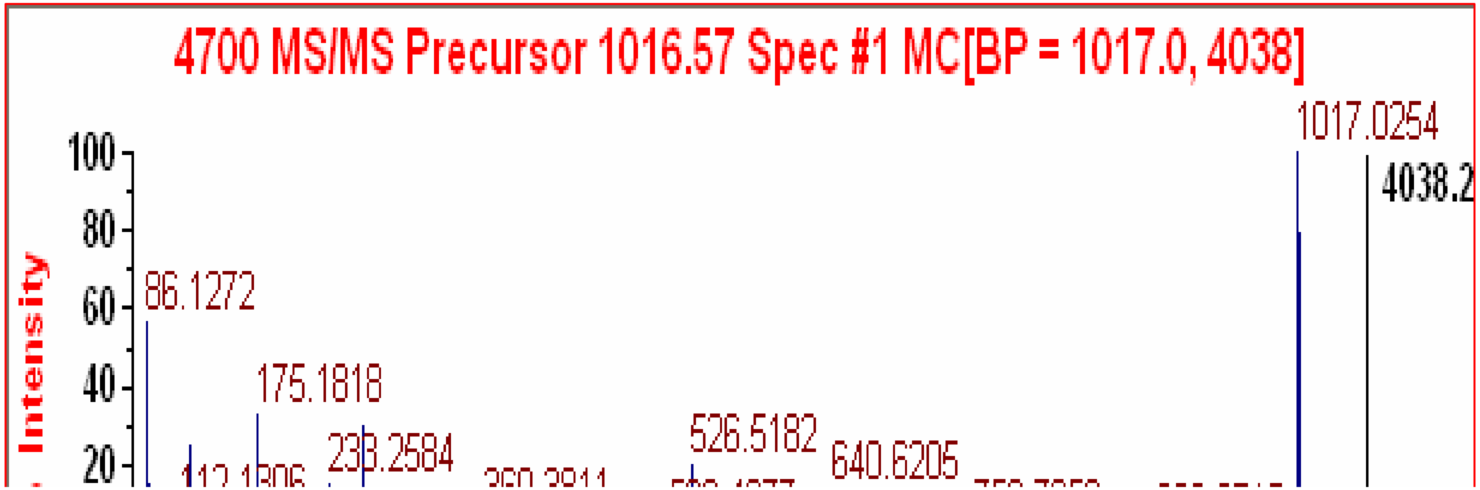
phosphoprotein [rabies virus]

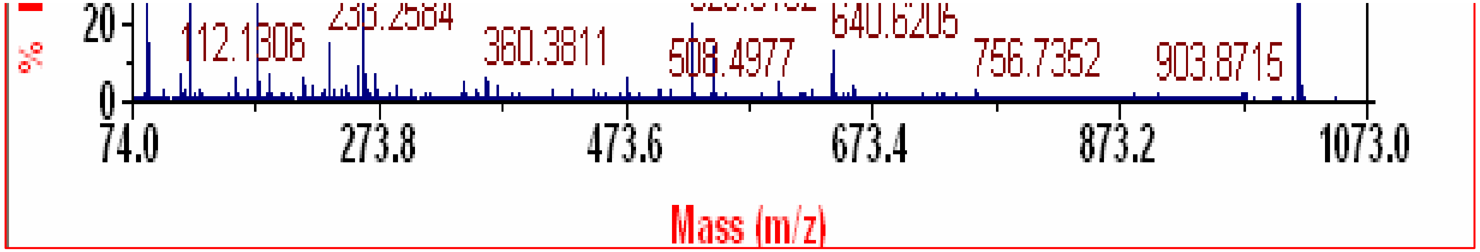


Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
742.4206	**742.4103**	-0.0103	-14	243	249	NVPGVTR		
750.374	**750.3625**	-0.0115	-15	145	151	STQTTGR		

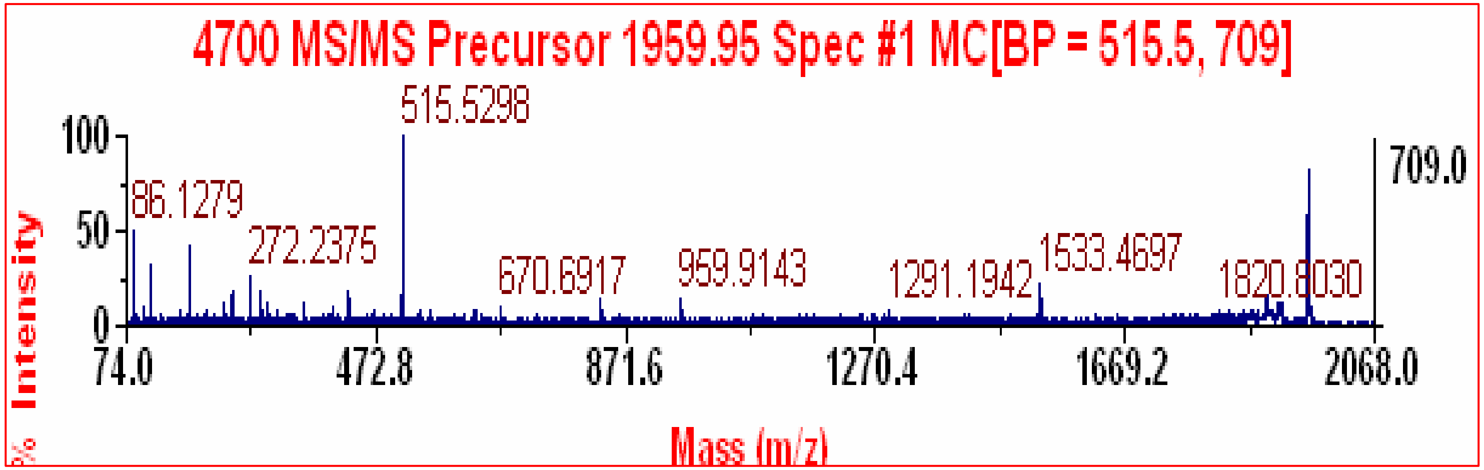
797.4304	**797.4183**	-0.0121	-15	213	218	YKFPSR		
870.4468	**870.5228**	0.076	87	110	116	SGERFFK		
1016.5887	**1016.5715**	**-0.0172**	**-17**	**4**	**12**	**IFVNPSAIR**	**54**	**99.143**
1016.5887	**1016.5715**	-0.0172	-17	4	12	IFVNPSAIR		
1016.5887	**1016.5715**	-0.0172	-17	4	12	IFVNPSAIR		
1034.5299	**1034.5298**	-0.0001	0	63	71	LSNLGEMVR		
1190.678	**1190.6438**	-0.0342	-29	273	282	KFQLIVEADK		
1296.6027	**1296.5942**	-0.0085	-7	140	151	SSEDKSTQTTGR		
1349.673	**1349.67**	-0.003	-2	283	293	LSKIMQDDLDR		
1390.7941	**1390.7822**	-0.0119	-9	274	285	FQLIVEADKLSK		
1504.7788	**1504.801**	0.0222	15	63	76	LSNLGEMVRVGEGK		
1959.9691	**1959.9473**	**-0.0218**	**-11**	**13**	**30**	**AGLADLEMAEETVDLINR**	**105**	**100**
1959.9691	**1959.9473**	-0.0218	-11	13	30	AGLADLEMAEETVDLINR		
1959.9691	**1959.9473**	-0.0218	-11	13	30	AGLADLEMAEETVDLINR		
1975.9641	**1975.9653**	**0.0012**	**1**	**13**	**30**	**AGLADLEMAEETVDLINR**	**47**	**96.126**
1975.9641	**1975.9653**	0.0012	1	13	30	AGLADLEMAEETVDLINR		
1975.9641	**1975.9653**	0.0012	1	13	30	AGLADLEMAEETVDLINR		
2030.9963	**2030.9792**	-0.0171	-8	55	71	QFHLDDEKLSNLGEMVR		
2046.9913	**2047.0293**	0.038	19	55	71	QFHLDDEKLSNLGEMVR		
2776.2842	**2776.3069**	**0.0227**	**8**	**31**	**54**	**NIEDNQAHLQGEPIEVDNLPEDM**	**64**	**99.925**
2776.2842	**2776.3069**	0.0227	8	31	54	NIEDNQAHLQGEPIEVDNLPEDMR		
2776.2842	**2776.3069**	0.0227	8	31	54	NIEDNQAHLQGEPIEVDNLPEDMR		

MS/MS Fragmentation of IFVNPSAIR (1016.5715,1+)

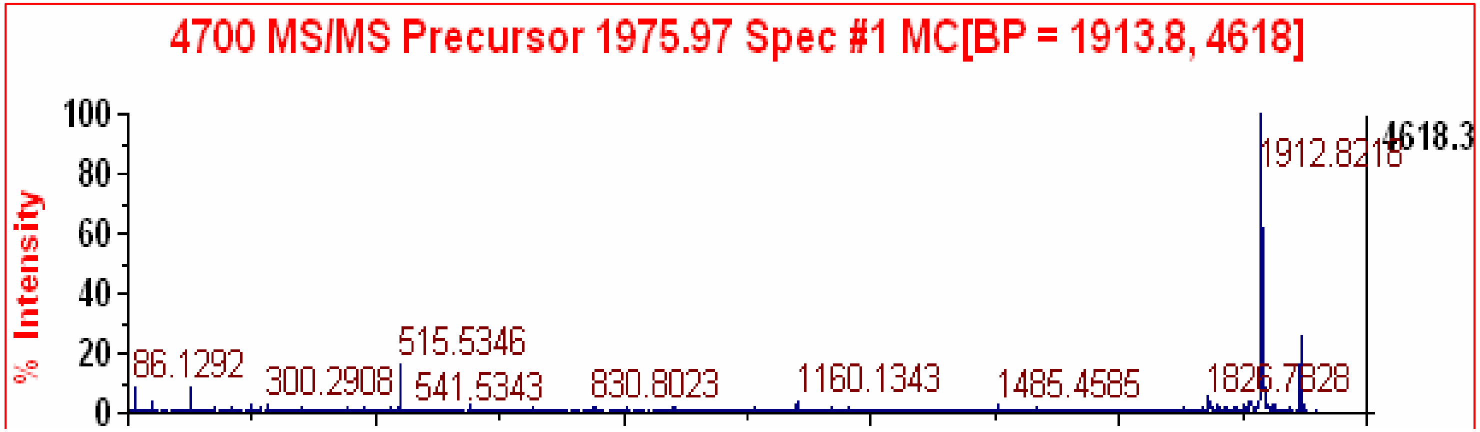


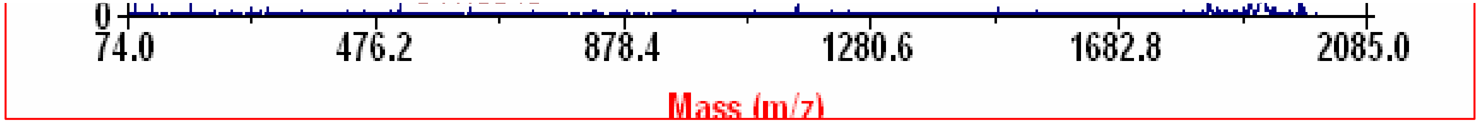


MS/MS Fragmentation of AGLADLEMAEETVDLINR(1959.9473,1+)

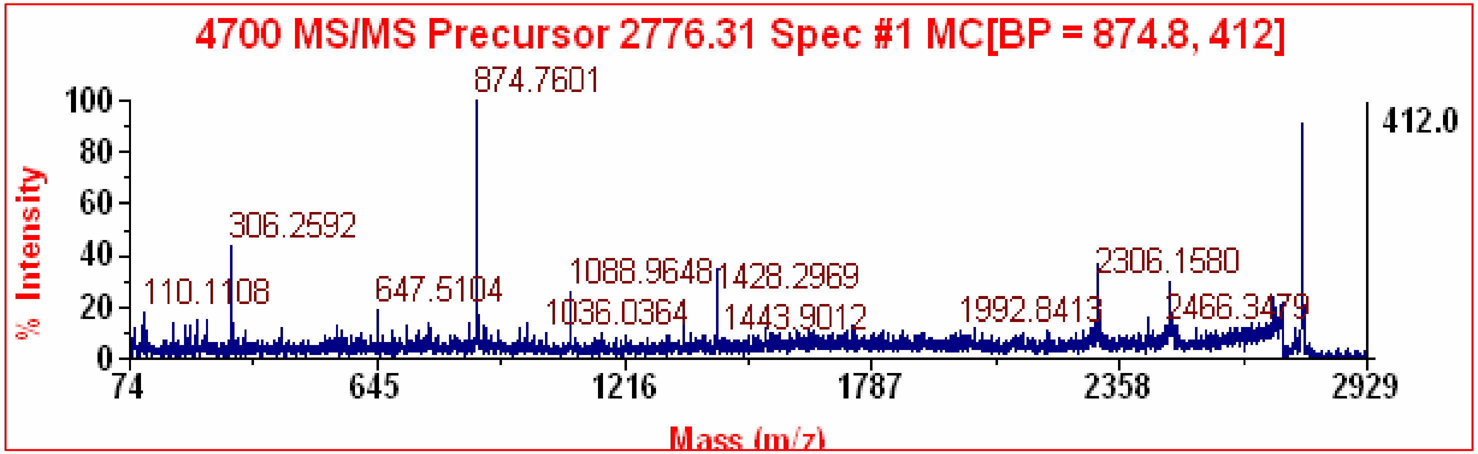


MS/MS Fragmentation of AGLADLEMAEETVDLINR (1975.9653,1+)



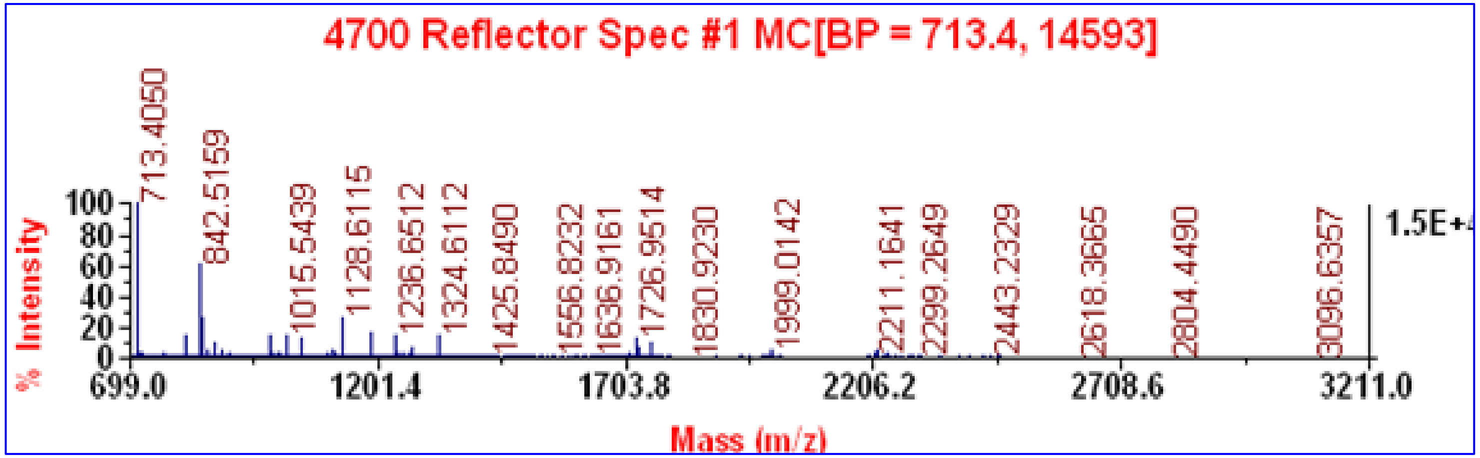


MS/MS Fragmentation of NIEDNQAHLQGEPIEVDNLPEDMR(2776.3069,1+)



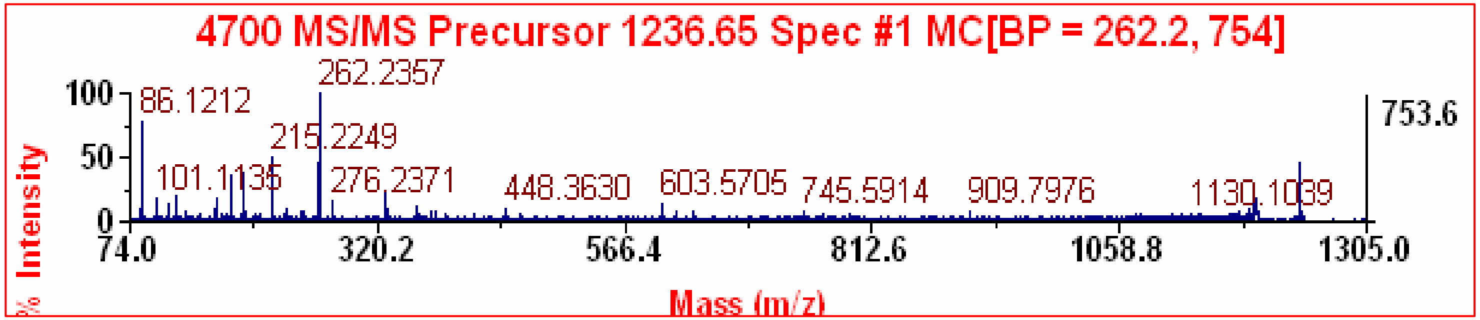
Spot No.3135 gi|9627200

M2 protein [rabies virus]



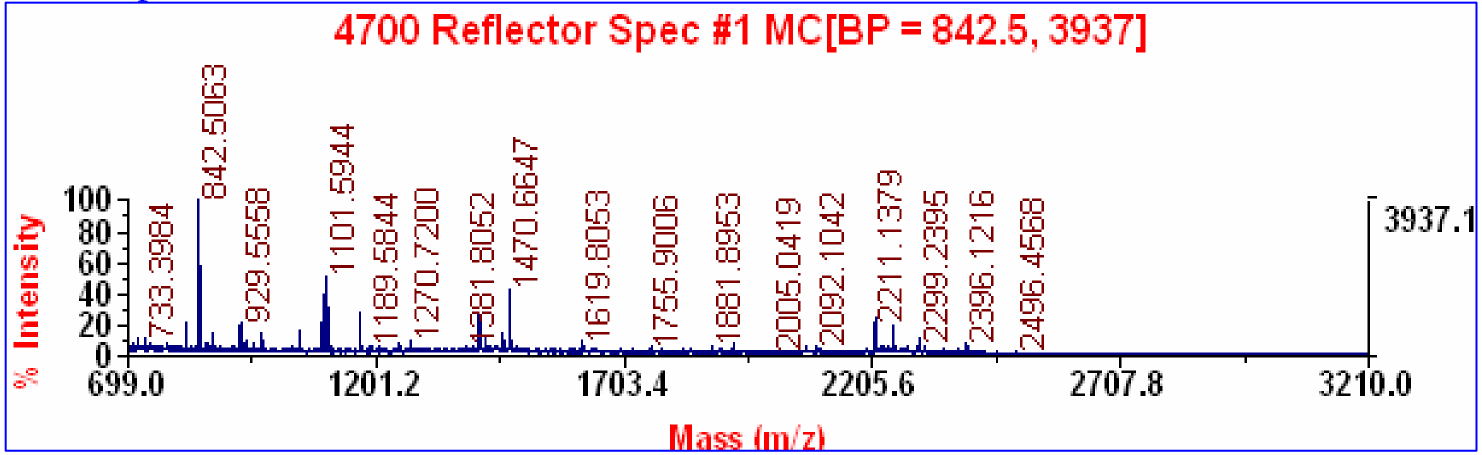
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1236.6372	**1236.6494**	**0.0122**	**10**	**119**	**128**	**TLIFQWADSR**	**55**	**99.684**
1236.6372	**1236.6494**	0.0122	10	119	128	TLIFQWADSR		
1324.5917	**1324.6112**	0.0195	15	78	88	SFDEIYSGNHR	30	9.311
1324.5917	**1324.6112**	0.0195	15	78	88	SFDEIYSGNHR		
1349.6565	**1349.7142**	0.0577	43	166	176	GRIWCINMNSR		
1392.7383	**1392.7472**	0.0089	6	118	128	RTLIFQWADSR		
1636.7748	**1636.9153**	0.1405	86	177	190	AGQLWSDMSLQTQR		
2225.0139	**2225.1982**	0.1843	83	177	195	AGQLWSDMSLQTQRSEEDK		

MS/MS Fragmentation of TLIFQWADSR (1236.6494, 1+)



Spot No.5679 **gi|18478987**

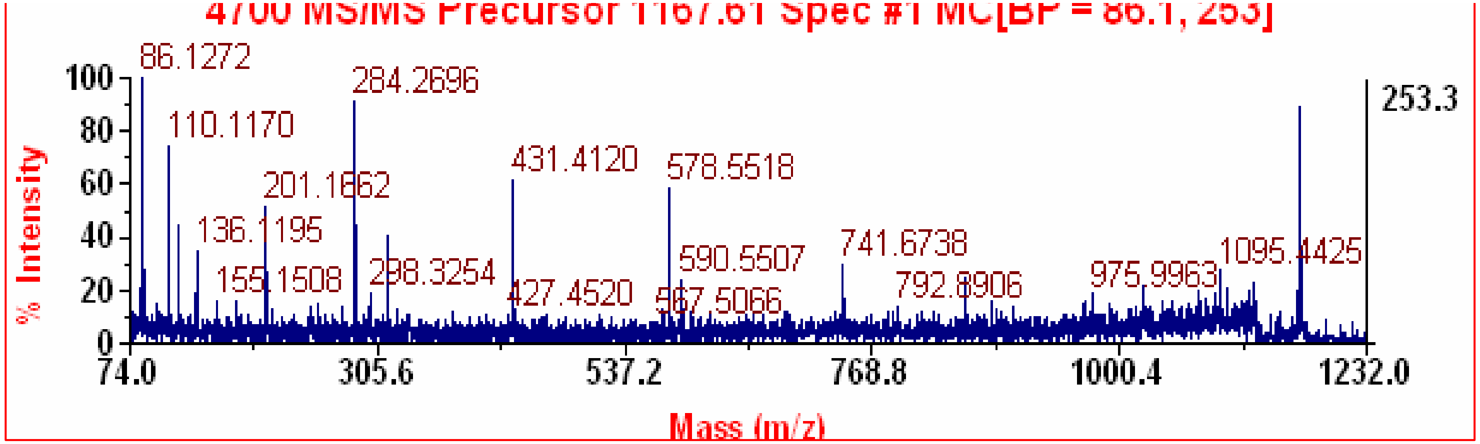
Nucleoprotein [rabies virus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
778.3698	**778.3656**	-0.0042	-5	409	415	IMMNGGR		
794.3647	**794.3458**	-0.0189	-24	409	415	IMMNGGR		
815.4733	**815.4678**	-0.0055	-7	248	254	QINLTAR		
841.4202	**841.4213**	0.0011	1	359	364	FFRDEK		
922.4628	**922.4625**	-0.0003	0	401	408	SPEAVYTR		
936.4421	**936.4403**	-0.0018	-2	264	270	NFEEEIR		
1092.5432	**1092.5344**	-0.0088	-8	264	271	NFEEEIRR		
1099.6357	**1099.6027**	-0.033	-30	103	112	ITPNSLVDIK		
1101.6051	**1101.594**	-0.0111	-10	217	225	IEHLYSAIR	17	0
1101.6051	**1101.594**	-0.0111	-10	217	225	IEHLYSAIR	17	0
1101.6051	**1101.594**	-0.0111	-10	217	225	IEHLYSAIR		
1167.6198	**1167.6062**	**-0.0136**	**-12**	**255**	**263**	**EALLYFFHK**	**47**	**96.853**
1167.6198	**1167.6062**	-0.0136	-12	255	263	EALLYFFHK		
1167.6198	**1167.6062**	-0.0136	-12	255	263	EALLYFFHK		
1339.7039	**1339.7214**	0.0175	13	52	64	AYKSVLSGMNAAK		
1409.7383	**1409.6499**	-0.0884	-63	150	162	LSKISGQNTGNYK		
1409.7383	**1409.6499**	-0.0884	-63	150	162	LSKISGQNTGNYK		
1409.7383	**1409.6499**	-0.0884	-63	150	162	LSKISGQNTGNYK		
1421.7675	**1421.7631**	-0.0044	-3	169	180	IEQIFETAPFVK		
1454.6772	**1454.6688**	-0.0084	-6	205	216	FLAGTYDMFFSR	5	0
1454.6772	**1454.6688**	-0.0084	-6	205	216	FLAGTYDMFFSR	5	0
1454.6772	**1454.6688**	-0.0084	-6	205	216	FLAGTYDMFFSR		
1470.6722	**1470.6644**	-0.0078	-5	205	216	FLAGTYDMFFSR		
1470.6722	**1470.6644**	-0.0078	-5	205	216	FLAGTYDMFFSR		
1470.6722	**1470.6644**	-0.0078	-5	205	216	FLAGTYDMFFSR		
1923.0474	**1923.0842**	0.0368	19	14	29	VVSLKPEIIVDQYEYK		
2004.9919	**2005.0596**	0.0677	34	113	130	RTNVEGNWALTGGMELTR		
2070.123	**2070.1257**	0.0027	1	131	149	DPTVSEHASLVGLLLSLYR		
2092.1074	**2092.1035**	-0.0039	-2	163	180	TNIADRIEQIFETAPFVK		
2293.1421	**2293.1704**	0.0283	12	226	247	VGTVVTAYEDCSGLVSFTGFIK		
2309.0808	**2309.1472**	0.0664	29	272	290	MFEPGQETAVPHSYFIHFR		
2395.179	**2395.2205**	0.0415	17	424	444	YVSVSSNHQARPNSFAEFLNK		

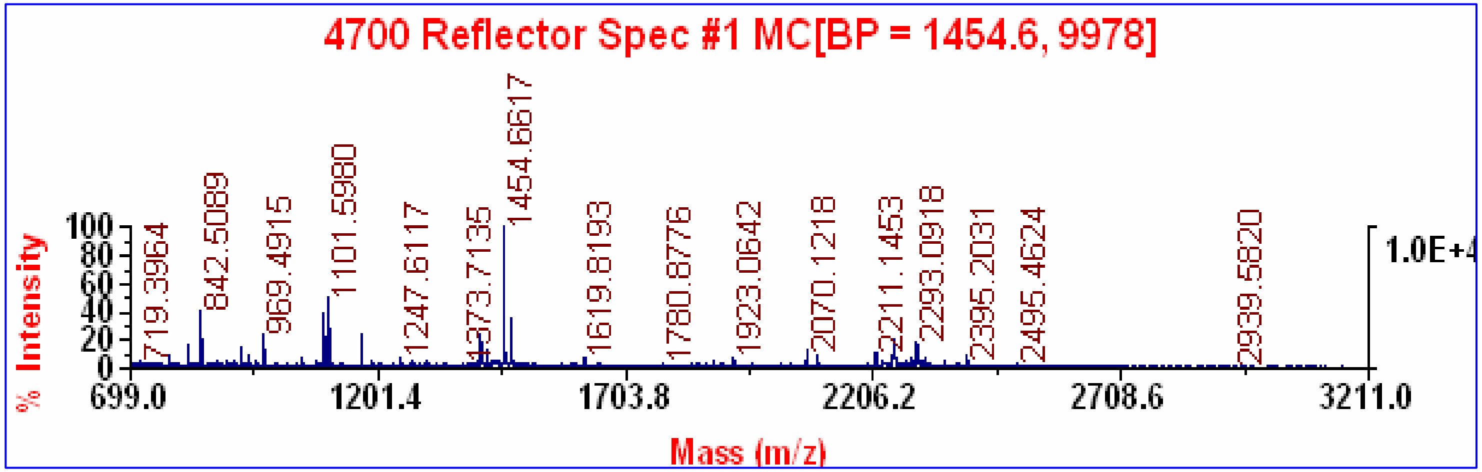
MS/MS Fragmentation of EALLYFFHK (1167.6062, 1+)

4700 MS/MS Precursor 1167.61 Spec #1 MC[BP = 86.1, 253]



Spot No.5683 **gi|39930275**

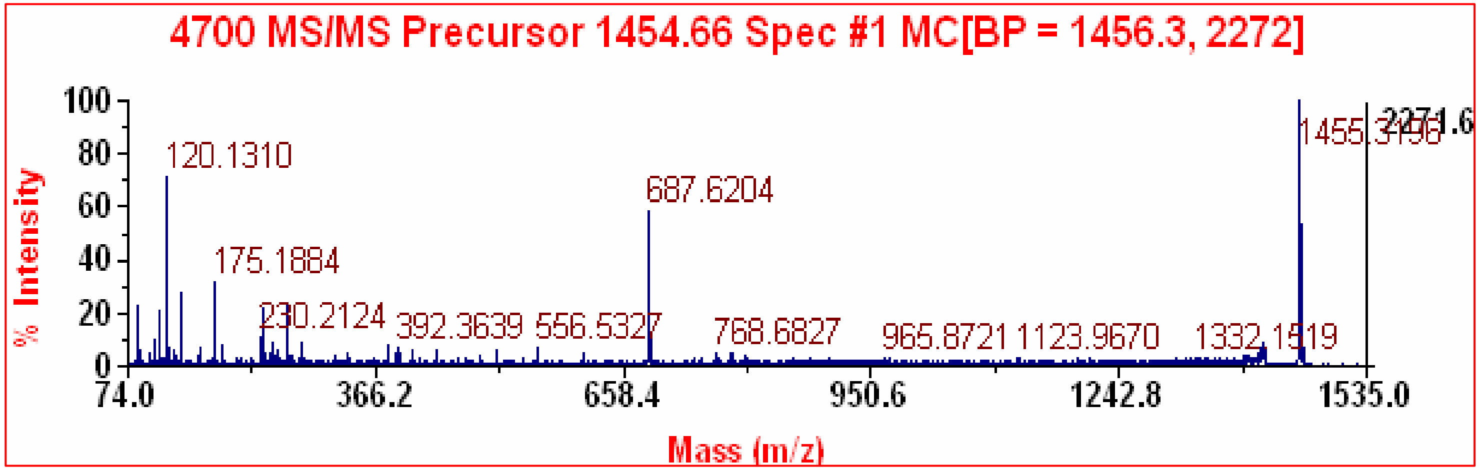
Nucleoprotein [rabies virus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
778.3698	**778.3687**	-0.0011	-1	396	402	IMMNGGR		
815.4733	**815.4728**	-0.0005	-1	235	241	QINLTAR		
841.4202	**841.4284**	0.0082	10	346	351	FFRDEK		
912.4421	**912.4698**	0.0277	30	388	395	SSEAVYTR		
936.4421	**936.4421**	0	0	251	257	NFEEEIR		
1021.5095	**1021.5024**	-0.0071	-7	42	51	SVLSGMNAAR		

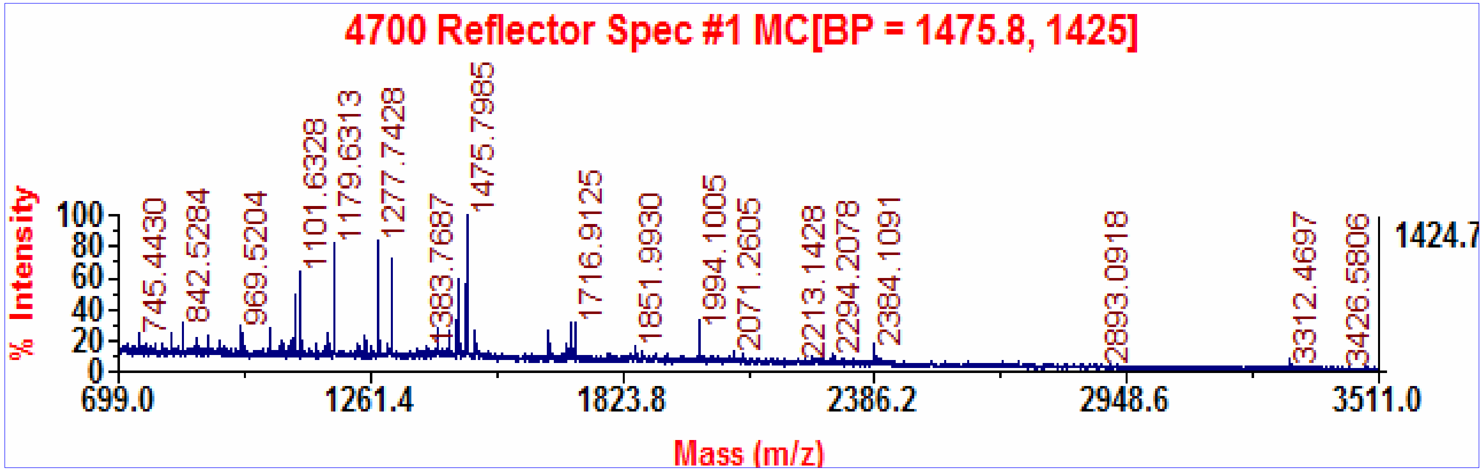
1092.5432	**1092.5388**	-0.0044	-4	251	258	NFEEEIRR		
1101.6051	**1101.5977**	-0.0074	-7	204	212	IEHLYSAIR	36	78.937
1101.6051	**1101.5977**	-0.0074	-7	204	212	IEHLYSAIR		
1167.6198	**1167.6108**	-0.009	-8	242	250	EAILYFFHK		
1270.7366	**1270.7206**	-0.016	-13	90	100	ITPDSLVEIKR		
1409.7383	**1409.6428**	-0.0955	-68	137	149	LSKISGQNTGNYK		
1409.7383	**1409.6428**	-0.0955	-68	137	149	LSKISGQNTGNYK		
1421.7675	**1421.7594**	-0.0081	-6	156	167	IEQIFETAPFVK		
1454.6772	**1454.662**	**-0.0152**	**-10**	**192**	**203**	**FLAGTYDMFFSR**	**52**	**99.471**
1454.6772	**1454.662**	-0.0152	-10	192	203	FLAGTYDMFFSR		
1470.6722	**1470.6589**	-0.0133	-9	192	203	FLAGTYDMFFSR	17	0
1470.6722	**1470.6589**	-0.0133	-9	192	203	FLAGTYDMFFSR		
1864.9109	**1864.8771**	-0.0338	-18	101	117	TDVEGSWALTGVMELTR		
1923.0474	**1923.0635**	0.0161	8	1	16	VVSLKPEIIVDQYEYK		
2070.123	**2070.1223**	-0.0007	0	118	136	DPTVSEHASLVGLLLSLYR		
2092.1074	**2092.1072**	-0.0002	0	150	167	TNIADRIEQIFETAPFVK		
2293.0859	**2293.0935**	0.0076	3	259	277	MFEPGQETAVPHSYFIHFR	33	57.584
2293.0859	**2293.0935**	0.0076	3	259	277	MFEPGQETAVPHSYFIHFR		
2309.0808	**2309.1248**	0.044	19	259	277	MFEPGQETAVPHSYFIHFR		
2395.179	**2395.2043**	0.0253	11	411	431	YVSVSSNHQARPNSFAEFLNK		

MS/MS Fragmentation of FLAGTYDMFFSR (1454.662, 1+)



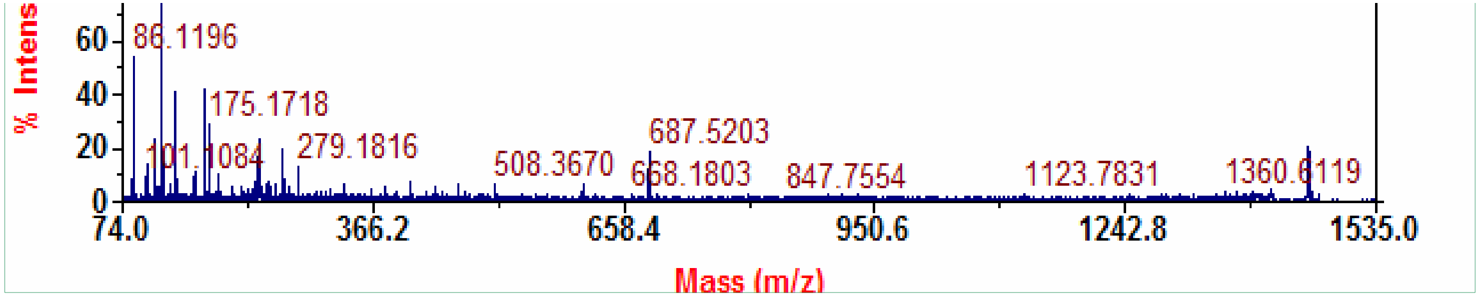
Spot No.6680 gi|38017865

Nucleoprotein [rabies virus]



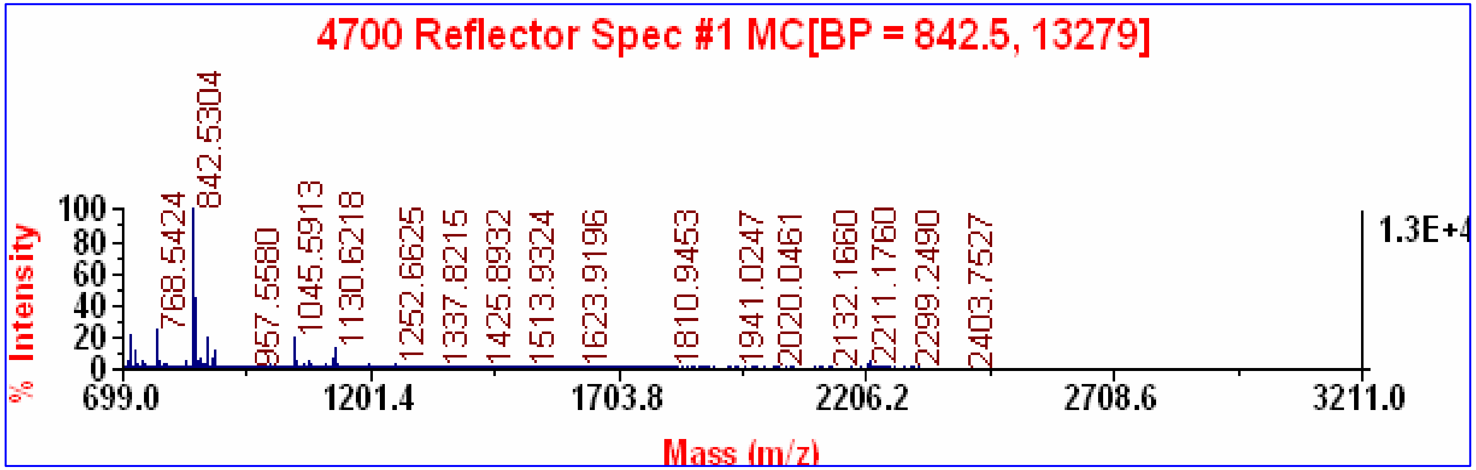
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
815.4733	**815.4953**	0.0220	27	209	215	QINLTAR		
1092.5432	**1092.5631**	0.0199	18	225	232	NFEEEIRR		
1101.6051	**1101.6326**	0.0275	25	178	186	IEHLYSAIR		
1101.6051	**1101.6326**	0.0275	25	178	186	IEHLYSAIR	19	0
1167.6198	**1167.6403**	0.0205	18	216	224	EAILYFFHK		
1409.7383	**1409.6761**	-0.0622	-44	111	123	LSKISGQNTGNYK		
1434.8354	**1434.8120**	-0.0234	-16	130	141	IKQIFETAPFIK		
1454.6772	**1454.7185**	0.0413	28	166	177	FLAGTYDMFFSR	26	0
1454.677	**1454.7185**	0.0413	28	166	177	FLAGTYDMFFSR		
1470.6722	**1470.7504**	0.0782	53	166	177	FLAGTYDMFFSR		

MS/MS Fragmentation of FLAGTYDMFFSR (1454.7185, 1+)



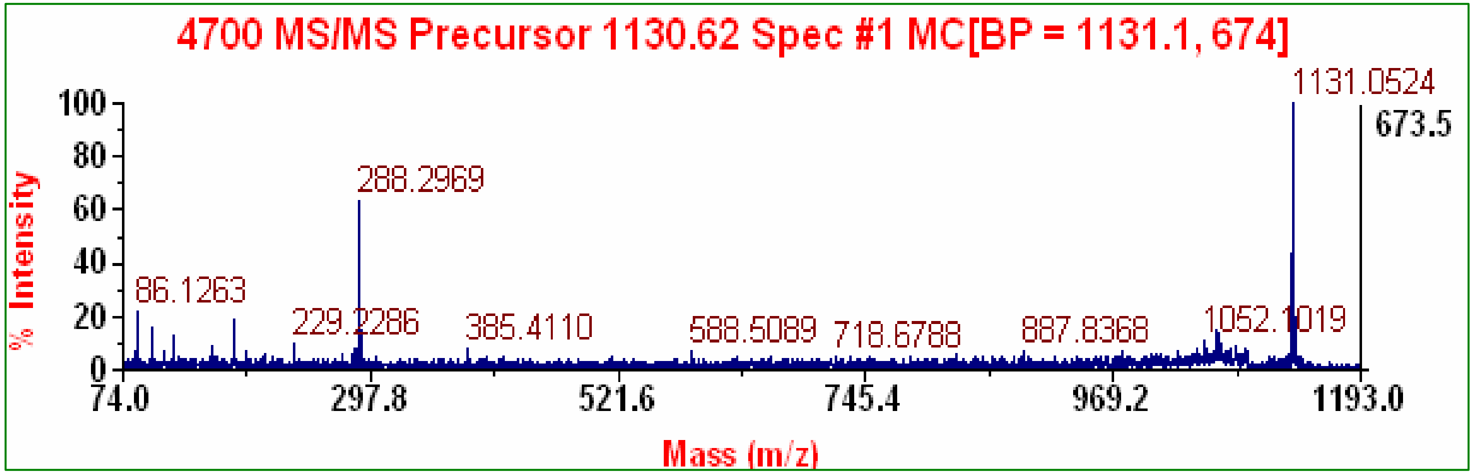
Spot No.3261 gi|26355849

Unnamed protein product [Mus musculus]



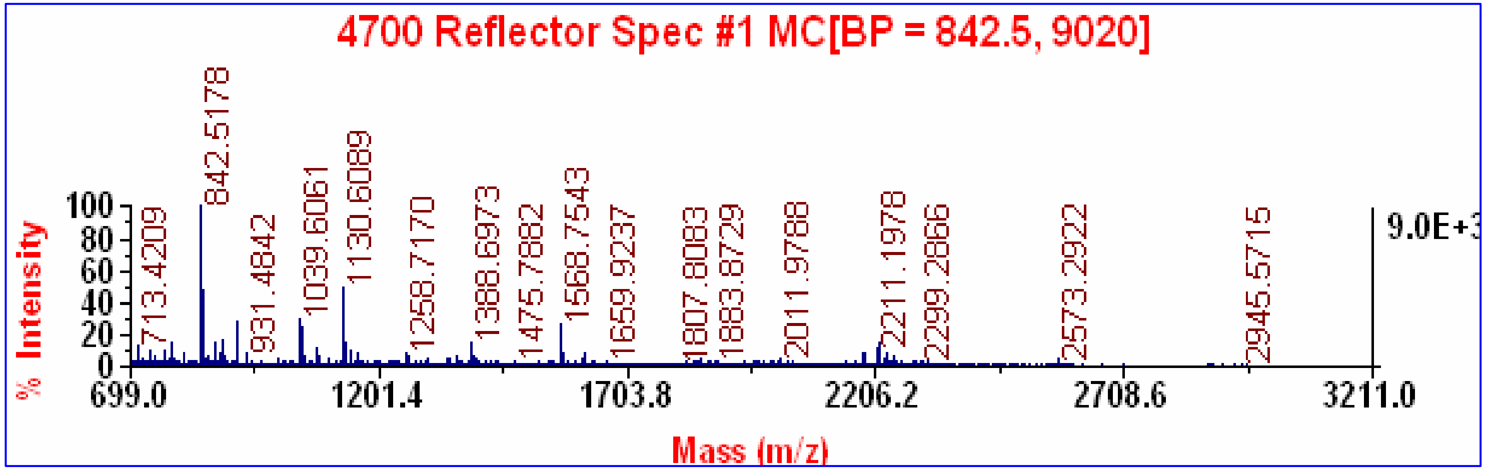
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
709.3483	**709.3671**	0.0188	27	277	282	GRMSMK		
738.3529	**738.3729**	0.02	27	235	240	GSQQYR		
1077.5323	**1077.5634**	0.0311	29	113	120	IREEYPDR		
1077.5323	**1077.5634**	0.0311	29	113	120	IREEYPDR		
1130.5953	**1130.6217**	**0.0264**	**23**	**200**	**209**	**FPGQLNADLR**	**23**	**0**
1130.5953	**1130.6217**	0.0264	23	200	209	FPGQLNADLR		
1159.6293	**1159.6482**	0.0189	16	211	220	LAVNMVPFPR		
1252.7161	**1252.6619**	-0.0542	-43	268	278	YLTVAAVFRGR		
1252.7161	**1252.6619**	-0.0542	-43	268	278	YLTVAAVFRGR		
1258.6902	**1258.717**	0.0268	21	200	210	FPGQLNADLRK		

MS/MS Fragmentation of FPGQLNADLR (1130.6217,1+)



Spot No.3432 gi|7106439

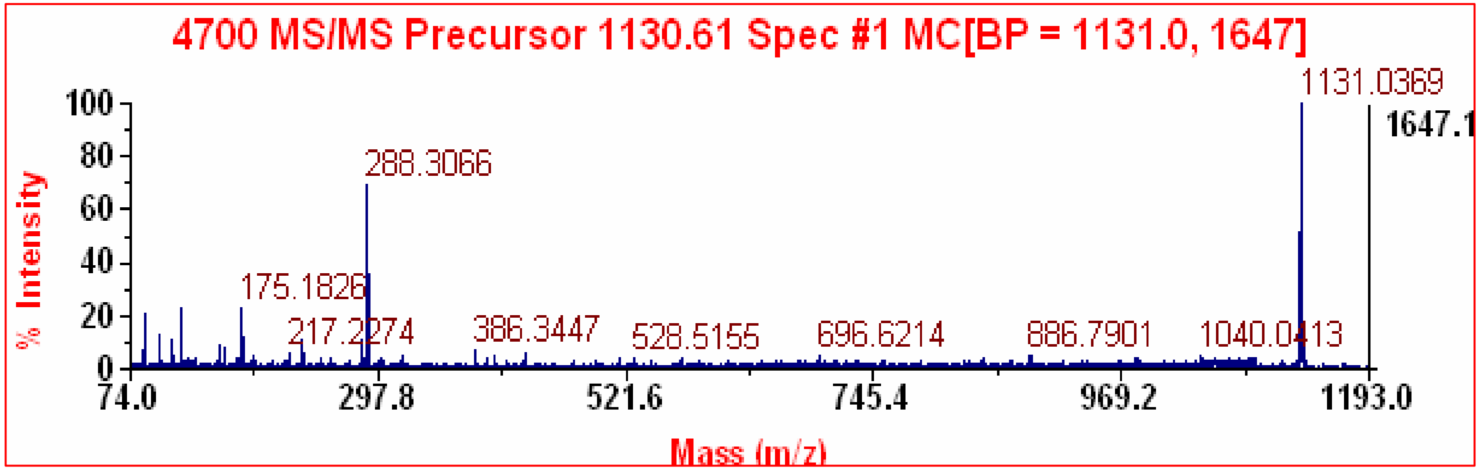
Tubulin, beta 5 [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
709.3483	**709.3511**	0.0028	4	319	324	GRMSMK		
738.3529	**738.3593**	0.0064	9	277	282	GSQQYR		

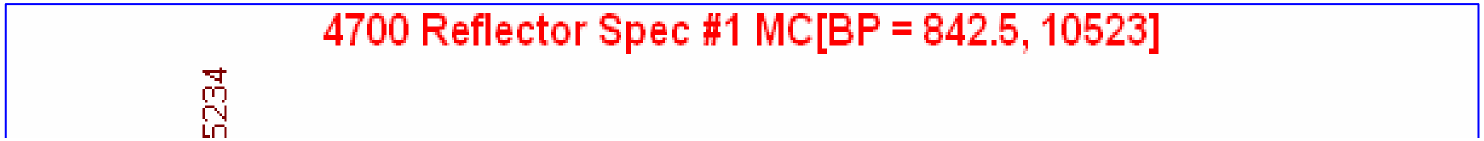
1039.5935	**1039.6058**	0.0123	12	310	318	YLTVAAVFR	31	83.03
1039.5935	**1039.6058**	0.0123	12	310	318	YLTVAAVFR		
1077.5323	**1077.5496**	0.0173	16	155	162	IREEYPDR		
1130.5953	**1130.6085**	**0.0132**	**12**	**242**	**251**	**FPGQLNADLR**	**44**	**99.16**
1130.5953	**1130.6085**	0.0132	12	242	251	FPGQLNADLR		
1143.6343	**1143.6475**	0.0132	12	253	262	LAVNMVPFPR		
1159.6293	**1159.6404**	0.0111	10	253	262	LAVNMVPFPR		
1258.6902	**1258.7173**	0.0271	22	242	252	FPGQLNADLRK		
1301.6372	**1301.6819**	0.0447	34	47	58	ISVYYNEATGGK		
1615.8359	**1615.8591**	0.0232	14	63	77	AILVDLEPGTMDSVR		
1631.8309	**1631.8546**	0.0237	15	63	77	AILVDLEPGTMDSVR		
1636.8304	**1636.8665**	0.0361	22	263	276	LHFFMPGFAPLTSR		
1659.8953	**1659.9293**	0.034	20	283	297	ALTVPELTQQVFDAK		
1958.9818	**1959.0319**	0.0501	26	104	121	GHYTEGAELVDSVLDVVR		

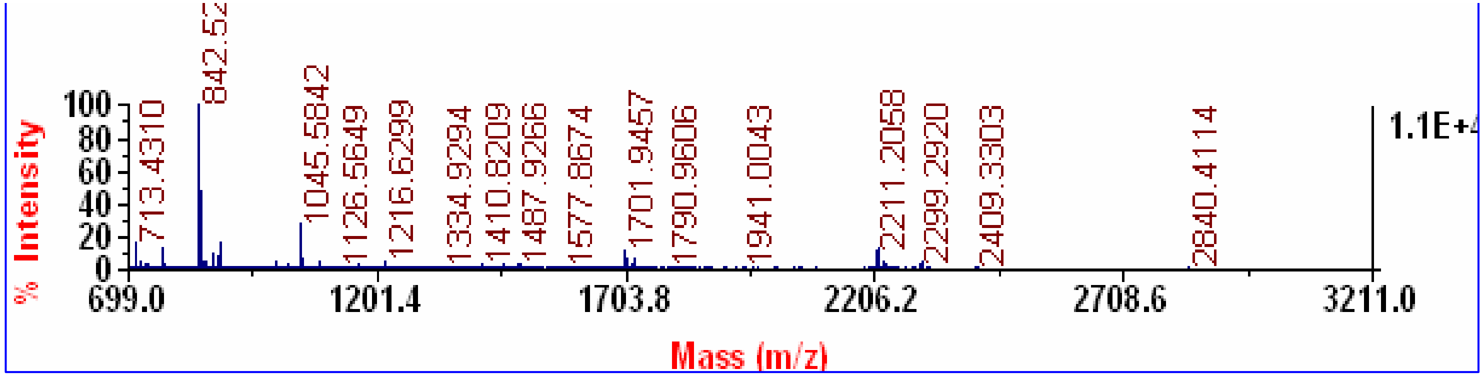
MS/MS Fragmentation of FPGQLNADLR (1130.6085,1+)



Spot No.3447 gi|202210

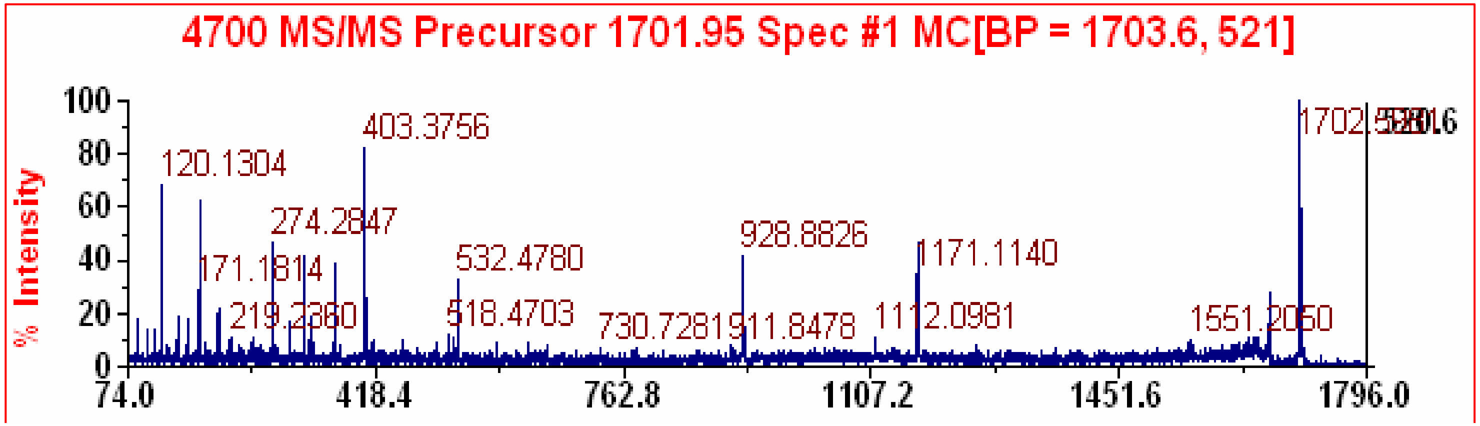
Alpha-tubulin isotype M-alpha-2 [Mus musculus]





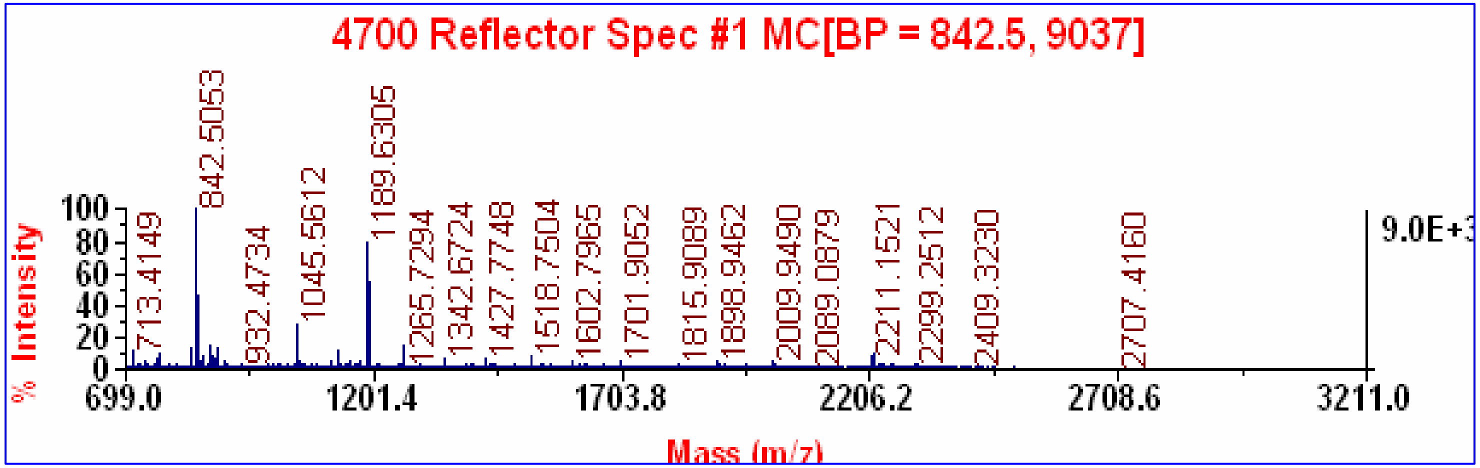
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1023.449	**1023.4754**	0.0264	26	97	105	EDAANNYAR		
1085.6201	**1085.6433**	0.0232	21	113	121	EIIDLVLDR		
1410.774	**1410.8201**	0.0461	33	85	96	QLFHPEQLITGK	28	51.27
1410.774	**1410.8201**	0.0461	33	85	96	QLFHPEQLITGK		
1487.8792	**1487.9265**	0.0473	32	230	243	LISQIVSSITASLR	18	0
1487.8792	**1487.9265**	0.0473	32	230	243	LISQIVSSITASLR		
1701.9058	**1701.9457**	**0.0399**	**23**	**65**	**79**	**AVFVDLEPTVIDEVR**	**50**	**99.703**
1701.9058	**1701.9457**	0.0399	23	65	79	AVFVDLEPTVIDEVR		
1718.8821	**1718.9323**	0.0502	29	216	229	NLDIERPTYTNLNR	13	0
1718.8821	**1718.9323**	0.0502	29	216	229	NLDIERPTYTNLNR		
1756.9633	**1757.0457**	0.0824	47	265	280	IHFPLATYAPVISAEK		
2409.2085	**2409.333**	0.1245	52	244	264	FDGALNVDLTEFQTNLVPYPR		

MS/MS Fragmentation of AVFVDLEPTVIDEVR(1701.9457, 1+)



Spot No.1649 gi|2253159

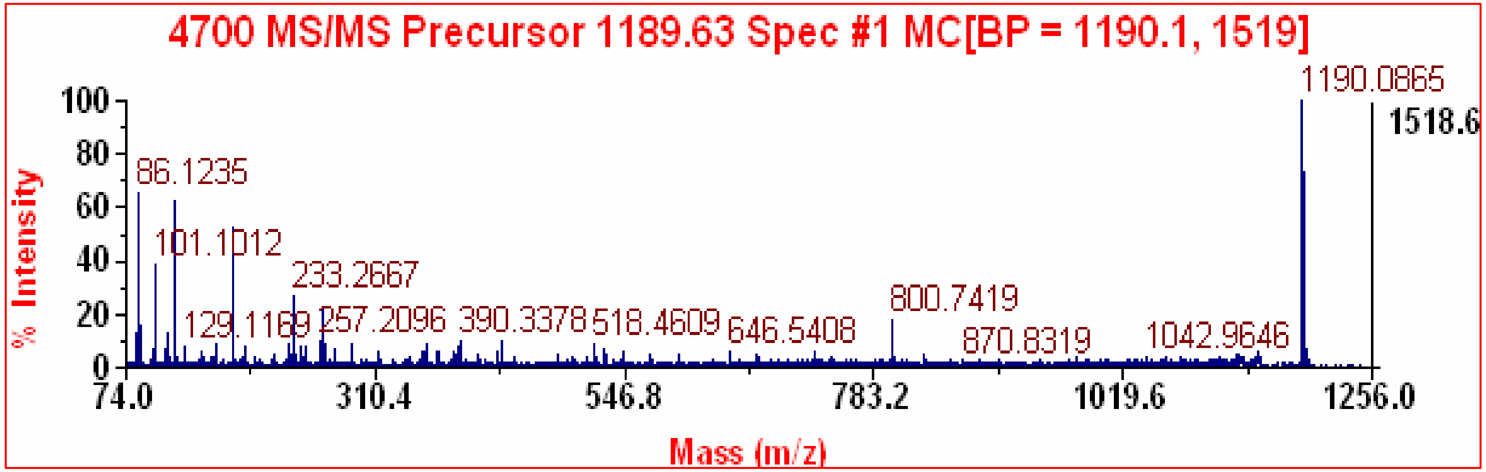
Peripherin [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
739.3845	**739.3815**	-0.003	-4	305	310	NHEALR		
760.3948	**760.3889**	-0.0059	-8	131	137	GELSQAR		
788.4148	**788.4263**	0.0115	15	365	370	LEEELR		
829.4777	**829.476**	-0.0017	-2	158	164	ELELLGR		
868.4562	**868.4961**	0.0399	46	112	118	FANFIEK		
873.4788	**873.4772**	-0.0016	-2	335	342	GTNEALLR		
901.485	**901.485**	0	0	167	173	DRVQVER		
932.4683	**932.4734**	0.0051	5	403	410	LLEGEESR		
985.5789	**985.5742**	-0.0047	-5	157	164	RELELLGR		
1053.5687	**1053.556**	-0.0127	-12	234	241	KLHEEELR		
1060.5382	**1060.5424**	0.0042	4	185	192	QRLEEETR		
1114.6215	**1114.6134**	-0.0081	-7	158	166	ELELLGRER		
1143.5753	**1143.6277**	0.0524	46	17	26	SSISSTSYRR		
1189.6324	**1189.63**	**-0.0024**	**-2**	**121**	**130**	**FLEQQNAALR**	**38**	**95.681**
1189.6324	**1189.63**	-0.0024	-2	121	130	FLEQQNAALR		

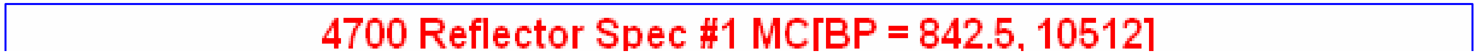
1295.6664	**1295.6566**	-0.0098	-8	391	401	MALDIEIATYR		
1342.675	**1342.6725**	-0.0025	-2	195	205	EDAEHNLVLFR		
1399.7539	**1399.7606**	0.0067	5	174	186	DGLAEDLAALKQR		
1444.8019	**1444.7516**	-0.0503	-35	119	130	VRFLEQQNAALR		
1484.8472	**1484.842**	-0.0052	-4	411	424	ISVPVHSFASLSLK		
1541.8435	**1541.8345**	-0.009	-6	379	390	HLREYQELLNVK		
1601.8064	**1601.8245**	0.0181	11	144	156	ADQLCQQELRELR		
1602.7719	**1602.7928**	0.0209	13	99	111	SNEKQELQELNDR		
1631.8235	**1631.8165**	-0.007	-4	207	220	DVDDATLSRLELER		
1815.8733	**1815.913**	0.0397	22	295	310	YADLSDAANRNHEALR		
1955.9531	**1955.9534**	0.0003	0	82	98	LDFSMAEALNQEFLATR		
1971.948	**1971.98**	0.032	16	82	98	LDFSMAEALNQEFLATR		
2009.9563	**2009.9465**	-0.0098	-5	346	364	ELEEQFALEAGGYQAGAAR	15	0
2009.9563	**2009.9465**	-0.0098	-5	346	364	ELEEQFALEAGGYQAGAAR		
2298.1038	**2298.1909**	0.0871	38	274	292	AQYENIAAKNLQEAEEWYK		
2407.2	**2407.2092**	0.0092	4	343	364	QLRELEEQFALEAGGYQAGAAR		

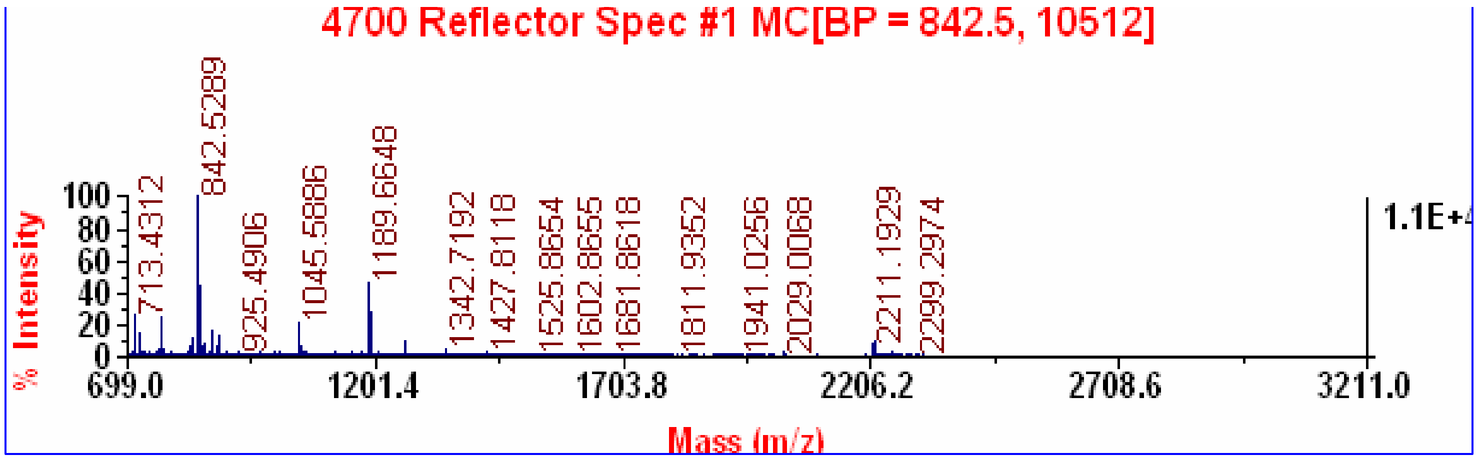
MS/MS Fragmentation of FLEQQNAALR (1189.63,1+)



Spot No.3272 gi|2253159

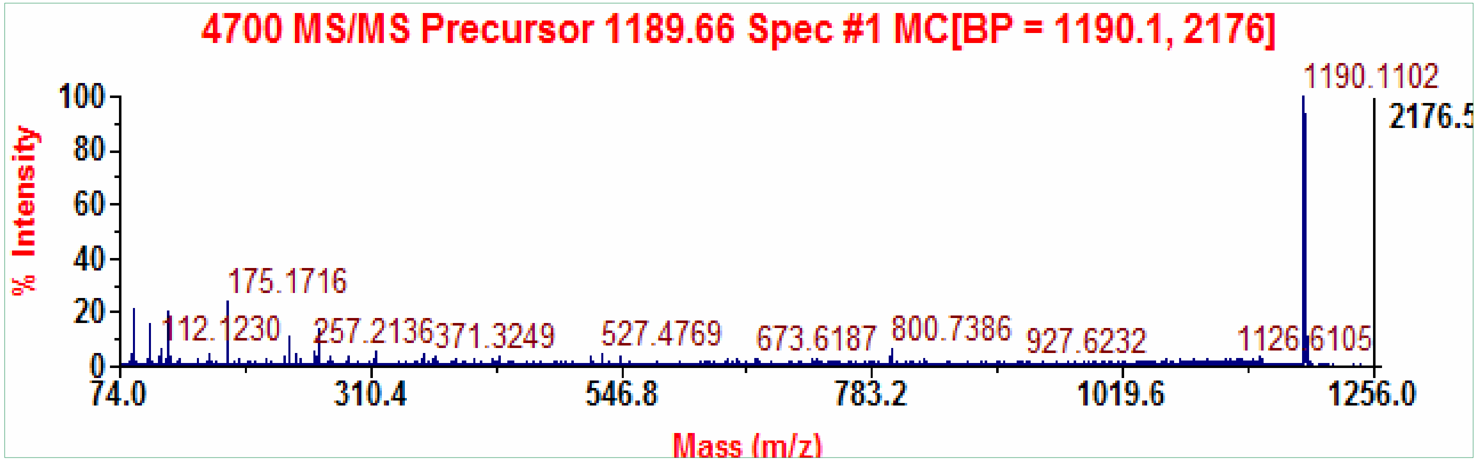
Peripherin [Mus musculus]





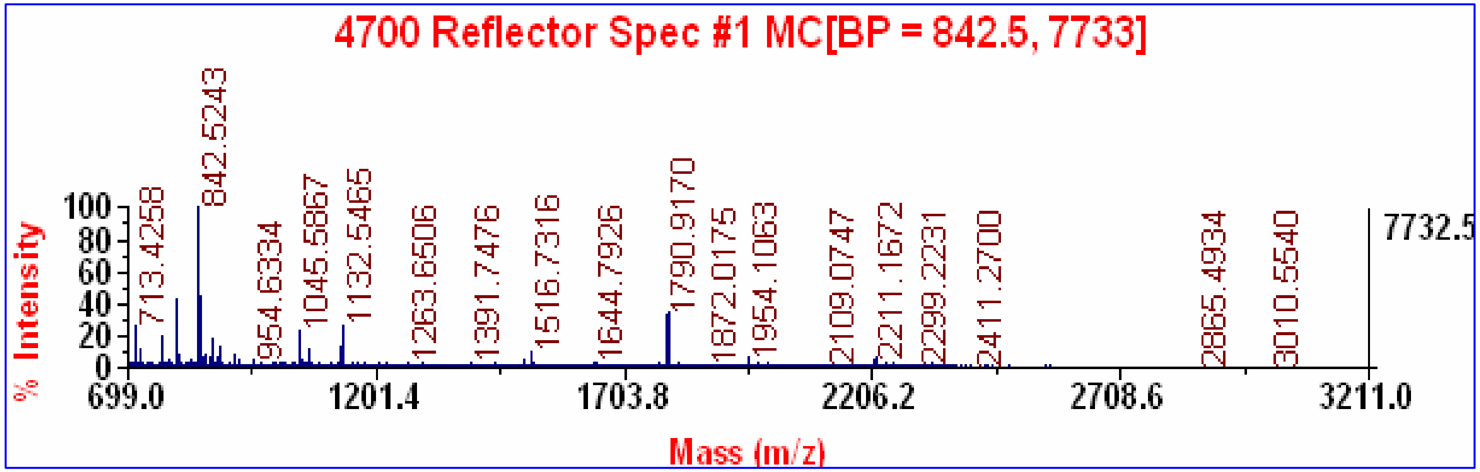
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
760.3948	**760.4161**	0.0213	28	131	137	GELSQAR		
787.4672	**787.4589**	-0.0083	-11	216	221	LELERK		
811.4896	**811.4924**	0.0028	3	69	76	APRAGALR		
829.4777	**829.4946**	0.0169	20	158	164	ELELLGR		
901.485	**901.509**	0.024	27	167	173	DRVQVER		
925.4737	**925.4906**	0.0169	18	235	241	LHEEELR		
1053.5687	**1053.5972**	0.0285	27	234	241	KLHEEELR		
1053.5687	**1053.5972**	0.0285	27	234	241	KLHEEELR		
1060.5382	**1060.5453**	0.0071	7	185	192	QRLEEETR		
1118.5801	**1118.6107**	0.0306	27	52	63	LLGSGSPSSSAR		
1189.6324	**1189.6644**	0.032	27	121	130	FLEQQNAALR	36	93.087
1189.6324	**1189.6644**	0.032	27	121	130	FLEQQNAALR		
1203.5786	**1203.6403**	0.0617	51	144	153	ADQLCQQELR		
1342.675	**1342.717**	0.042	31	195	205	EDAEHNLVLFR	12	0
1342.675	**1342.717**	0.042	31	195	205	EDAEHNLVLFR		
1498.7761	**1498.8153**	0.0392	26	194	205	REDAEHNLVLFR		
1541.8435	**1541.8104**	-0.0331	-21	379	390	HLREYQELLNVK		
1602.7719	**1602.8657**	0.0938	59	99	111	SNEKQELQELNDR		
1955.9531	**1956.0193**	0.0662	34	82	98	LDFSMAEALNQEFLATR		
1971.948	**1972.0549**	0.1069	54	82	98	LDFSMAEALNQEFLATR		
2028.9662	**2029.0042**	0.038	19	27	46	TFGPPPSLSPGAFSYSSSSR		
2028.9662	**2029.0042**	0.038	19	27	46	TFGPPPSLSPGAFSYSSSSR		
2298.1038	**2298.2969**	0.1931	84	274	292	AQYENIAAKNLQEAEEWYK		

MS/MS Fragmentation of FLEQQNAALR (1189.6644, 1+)



Spot No.3375 gi|49868

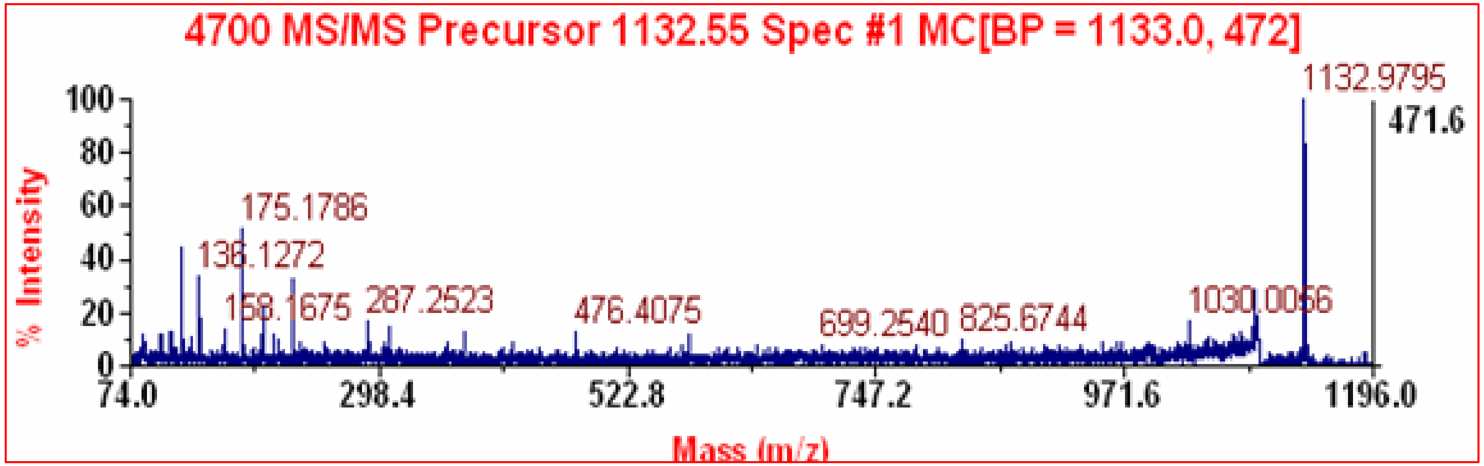
put. beta-actin (aa 27-375) [Mus musculus]



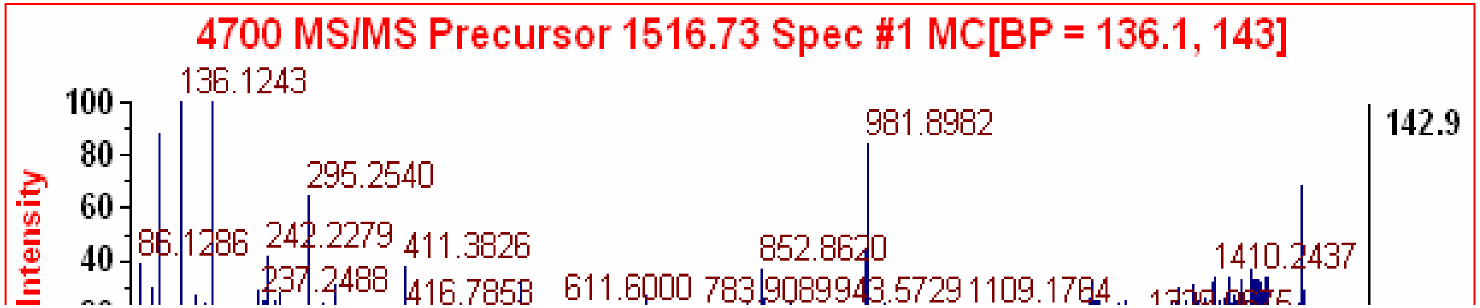
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
795.4723	**795.4829**	0.0106	13	303	309	IIAPPER		
800.5352	**800.5449**	0.0097	12	36	42	RGILTLK		
923.5672	**923.5899**	0.0227	25	303	310	IIAPPERK		

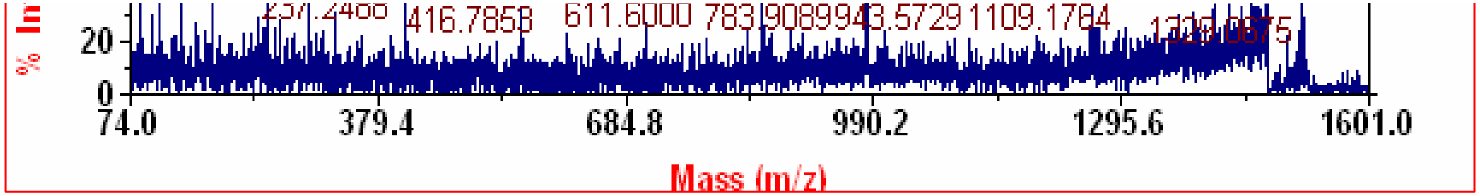
1132.527	**1132.5461**	**0.0191**	**17**	**171**	**180**	**GYSFTTTAER**	**39**	**96.195**
1132.527	**1132.5461**	0.0191	17	171	180	GYSFTTTAER		
1516.7026	**1516.7313**	**0.0287**	**19**	**334**	**346**	**QEYDESGPSIVHR**	**48**	**99.53**
1516.7026	**1516.7313**	0.0287	19	334	346	QEYDESGPSIVHR		
1644.7976	**1644.7889**	-0.0087	-5	334	347	QEYDESGPSIVHRK		
1790.892	**1790.9172**	**0.0252**	**14**	**213**	**228**	**SYELPDGQVITIGNER**	**47**	**99.454**
1790.892	**1790.9172**	0.0252	14	213	228	SYELPDGQVITIGNER		
1954.0645	**1954.1057**	**0.0412**	**21**	**70**	**87**	**VAPEEHPVLLTEAPLNPK**	**70**	**99.997**
1954.0645	**1954.1057**	0.0412	21	70	87	VAPEEHPVLLTEAPLNPK		
2215.0698	**2215.145**	0.0752	34	266	286	DLYANTVLSGGTTMYPGIADR		
2231.0649	**2231.1848**	0.1199	54	266	286	DLYANTVLSGGTTMYPGIADR		

MS/MS Fragmentation of GYSFTTTAER (1132.5461, 1+)

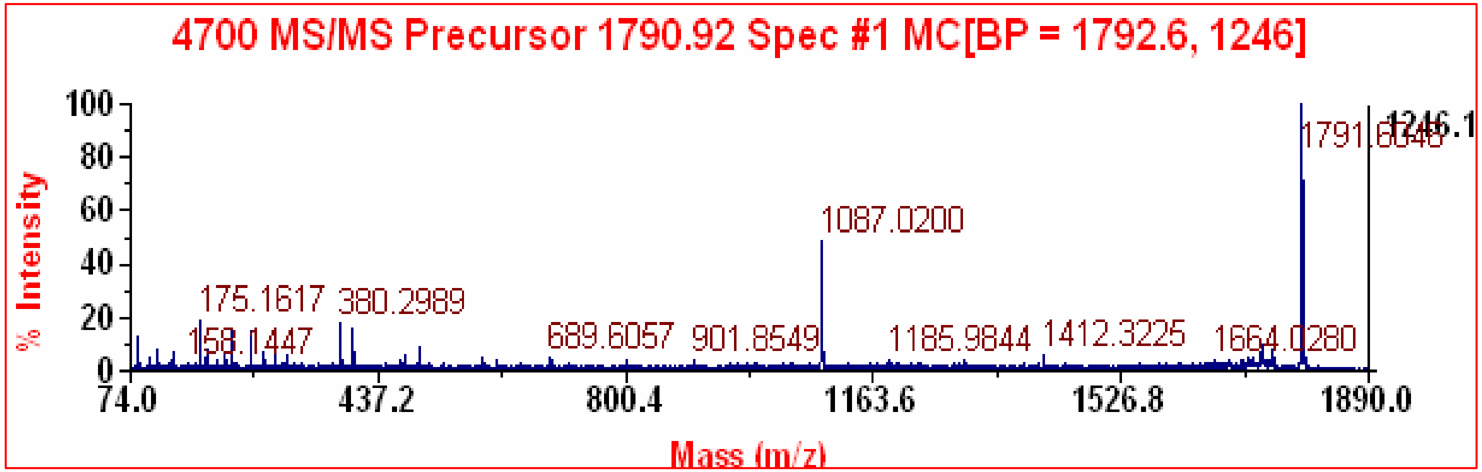


MS/MS Fragmentation of QEYDESGPSIVHR (1516.7313, 1+)

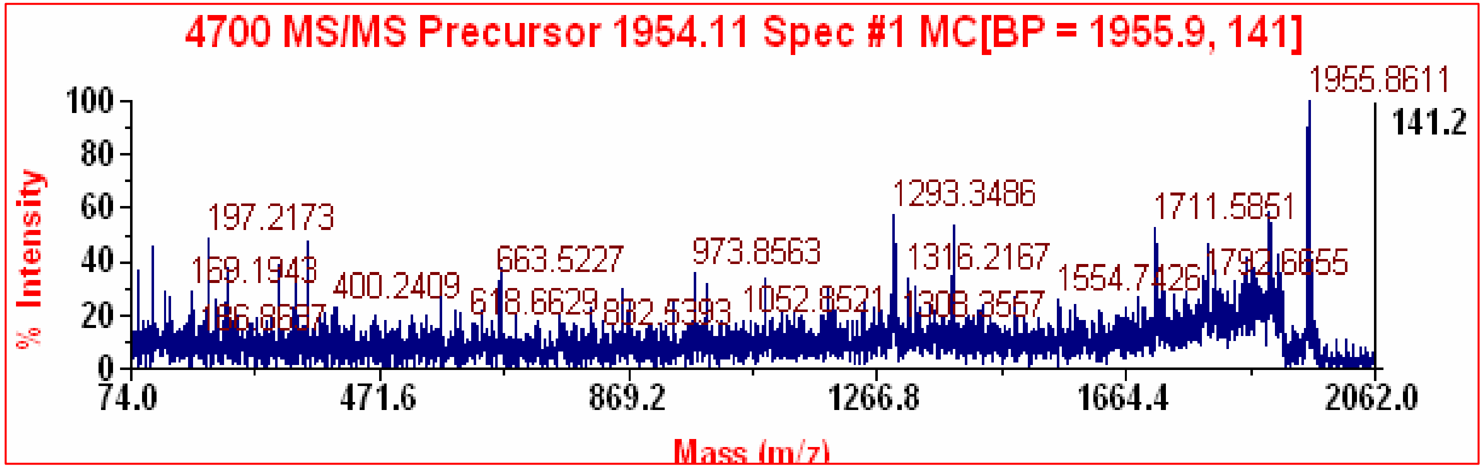




MS/MS Fragmentation of SYELPDGQVITIGNER (1790.9172, 1+)

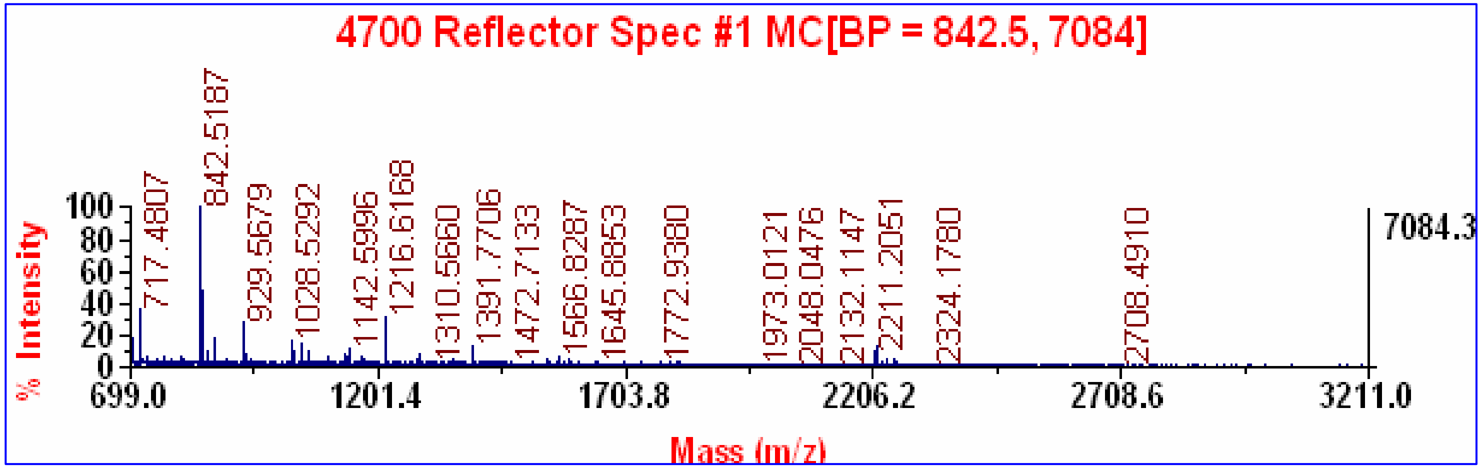


MS/MS Fragmentation of VAPEEHPVLLTEAPLNPK (1954.1057, 1+)



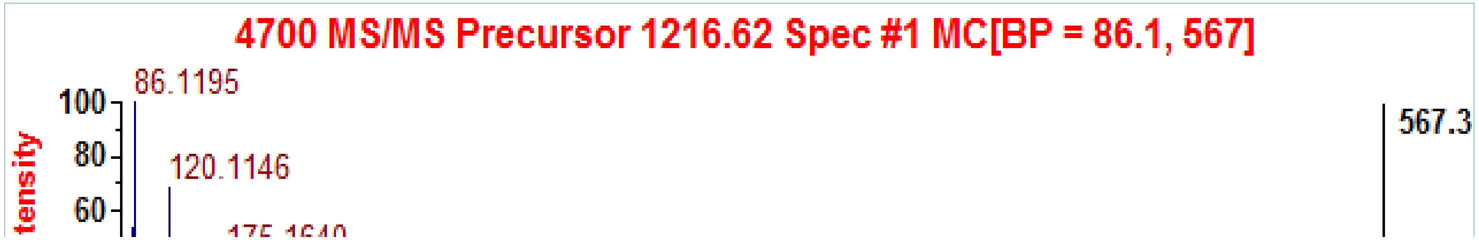
Spot No.3461 gi|148693874

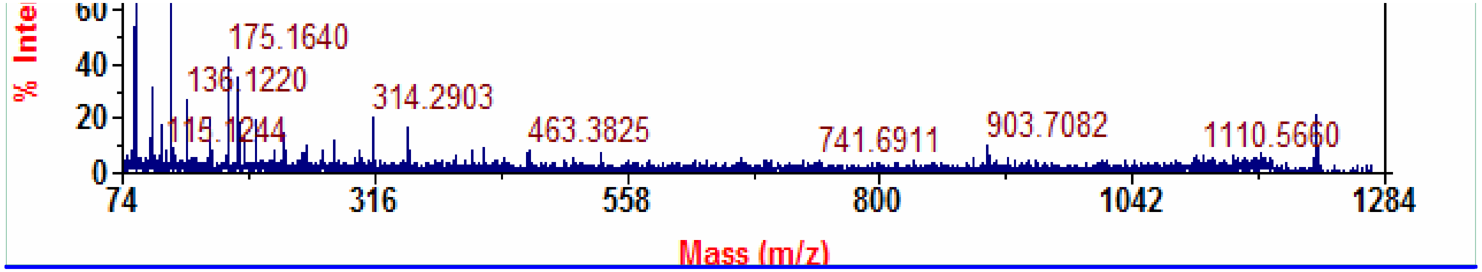
Isocitrate dehydrogenase 3 (NAD+) alpha, isoform CRA_d [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1028.516	**1028.5288**	0.0128	12	56	63	APIQWEER	11	0
1028.516	**1028.5288**	0.0128	12	56	63	APIQWEER		
1142.5411	**1142.5978**	0.0567	50	314	323	HMGLFDHAAK		
1216.5997	**1216.6163**	0.0166	14	176	185	IAEFAFEYAR	31	57.1
1216.5997	**1216.6163**	0.0166	14	176	185	IAEFAFEYAR		
1353.7896	**1353.6729**	-0.1167	-86	2	14	RMRPGVAAVAAVR		
1391.7529	**1391.7712**	0.0183	13	132	143	TPYTDVNIVTIR	5	0
1391.7529	**1391.7712**	0.0183	13	132	143	TPYTDVNIVTIR		
1590.8784	**1590.8972**	0.0188	12	98	112	TPIAAGHPSMNLLLR		
1606.8734	**1606.9371**	0.0637	40	98	112	TPIAAGHPSMNLLLR		

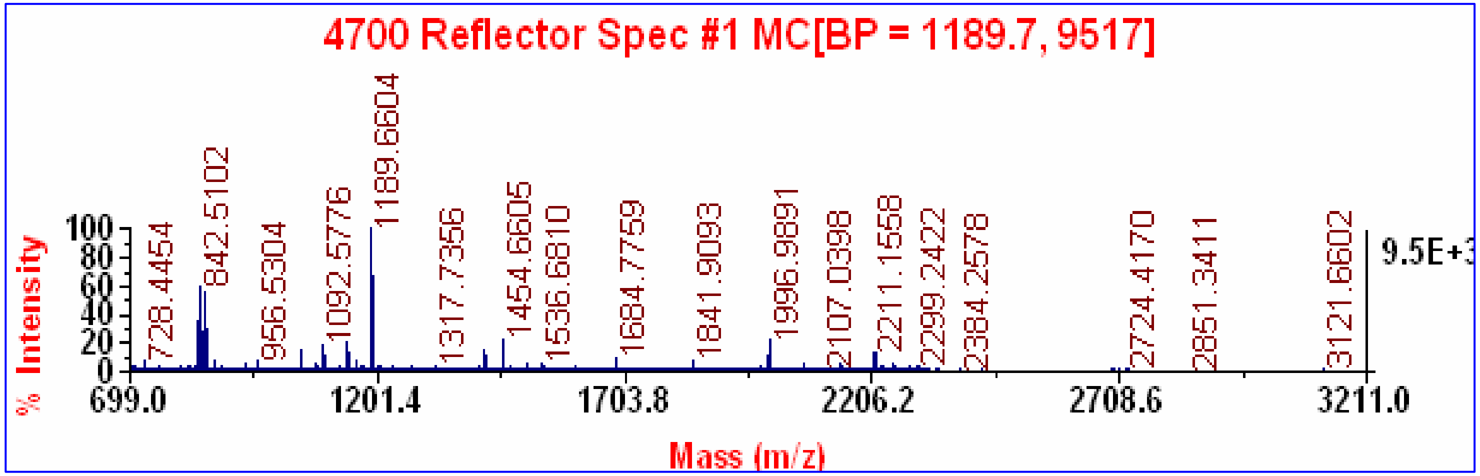
MS/MS Fragmentation of IAEFAFEYAR (1216.6163, 1+)





Spot No.5674 gi|21313536

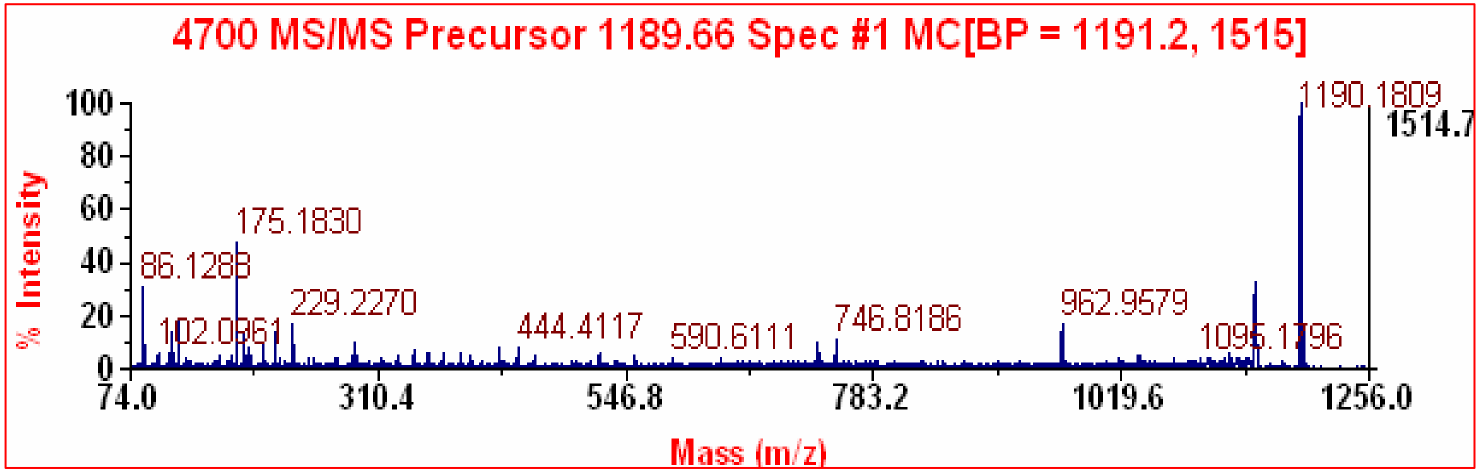
Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Mus musculus]



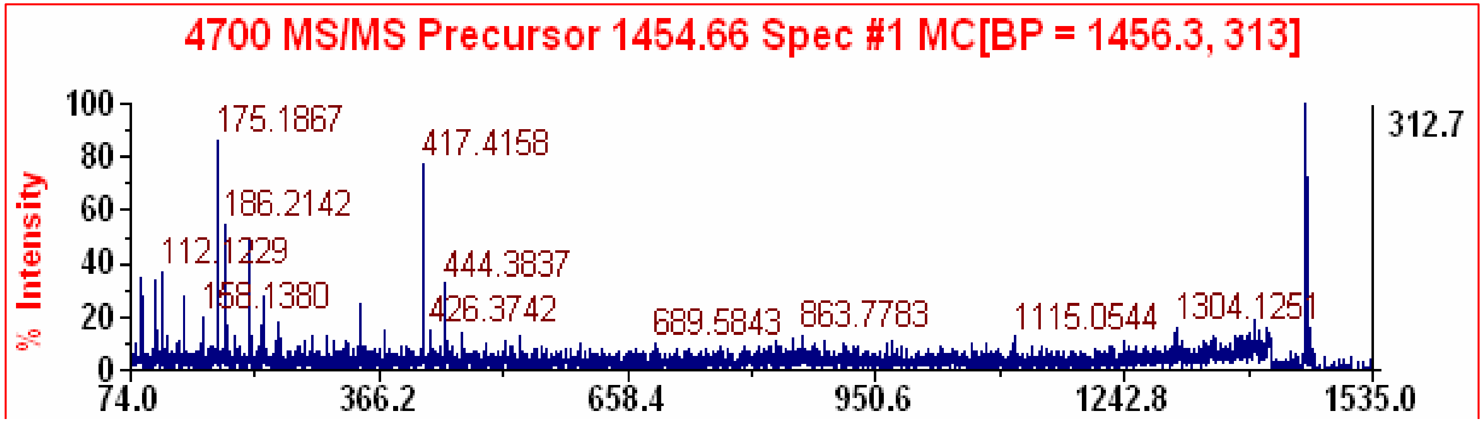
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
728.4777	728.4453	-0.0324	-44	235	240	IAQRLK		
757.3839	757.3898	0.0059	8	442	448	AAVEDPR		
835.4672	835.467	-0.0002	0	432	438	EAVTFLR		
852.5665	852.5658	-0.0007	-1	327	334	GLVVPVIR		
931.5029	931.5099	0.007	8	30	38	SLPGVSLCR		
1189.6576	**1189.66**	**0.0024**	**2**	**135**	**145**	**VEGGTPLFTLR**	**42**	**98.596**
1189.6576	1189.66	0.0024	2	135	145	VEGGTPLFTLR		
1317.7524	1317.7358	-0.0166	-13	135	146	VEGGTPLFTLRK		
1389.7849	1389.8219	0.037	27	427	438	LIDGREAVTFLR		
1419.7478	1419.748	0.0002	0	314	326	DYIDISVAVATPR	30	78.007
1419.7478	1419.748	0.0002	0	314	326	DYIDISVAVATPR		

1454.6581	**1454.6604**	**0.0023**	**2**	**335**	**346**	**NVETMNYADIER**	**38**	**96.053**
1454.6581	**1454.6604**	0.0023	2	335	346	NVETMNYADIER		
1470.653	**1470.6538**	0.0008	1	335	346	NVETMNYADIER		
1979.983	**1979.9774**	-0.0056	-3	411	426	VEVRPMMYVALTYDHR		
1995.9779	**1995.9795**	0.0016	1	411	426	VEVRPMMYVALTYDHR		
2066.0916	**2066.1436**	0.052	25	309	326	EVVYRDYIDISVAVATPR		
2187.1292	**2187.1724**	0.0432	20	288	308	ASAFALQEQPVVNAVIDDATK		
2248.1091	**2248.1492**	0.0401	18	69	89	NDVITVQTPAFAESVTEGDVR		

MS/MS Fragmentation of VEGGTPLFTLR (1189.66, 1+)

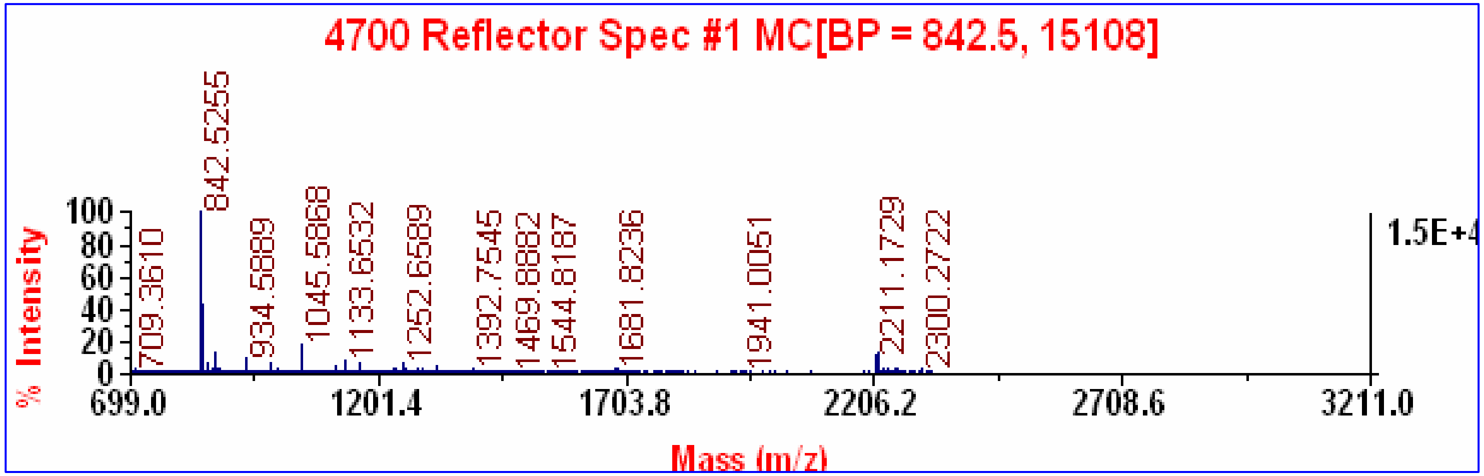


MS/MS Fragmentation of NVETMNYADIER (1454.6604, 1+)



Spot No.6415 **gi|148686116**

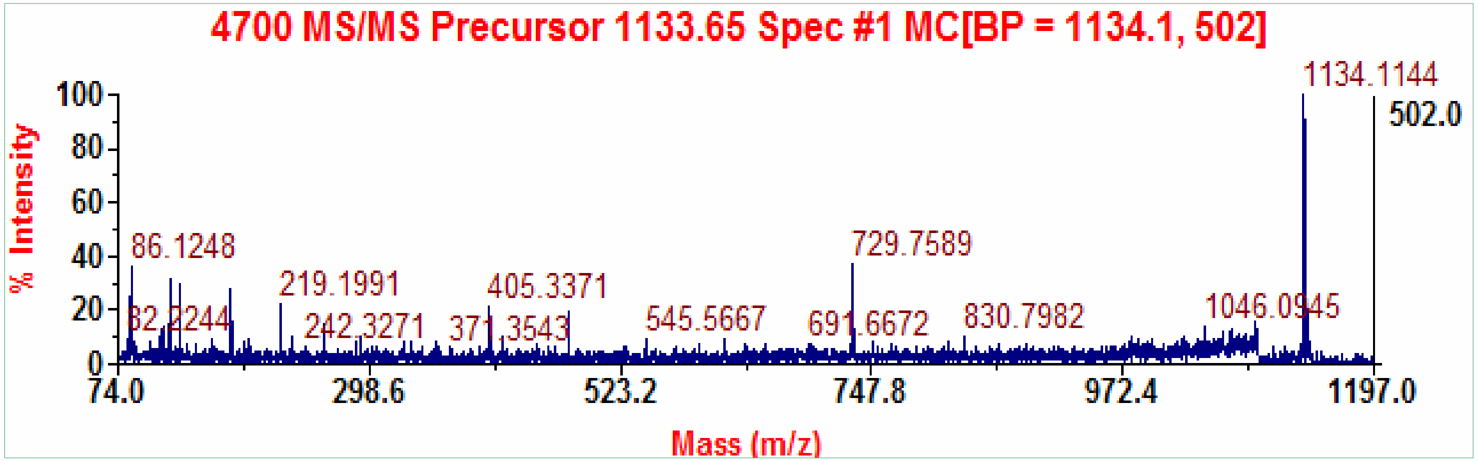
transaldolase 1, isoform CRA_e [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
785.5131	**785.525**	0.0119	15	205	211	LLGELLK		
863.4297	**863.4567**	0.027	31	166	171	IYNYYK		
876.4421	**876.4656**	0.0235	27	49	56	VSTEVDAR		
934.572	**934.5889**	0.0169	18	70	76	RLIELYK		
934.572	**934.5889**	0.0169	18	70	76	RLIELYK		
981.5186	**981.5409**	0.0223	23	177	185	TIVMGASFR	9	0
981.5186	**981.5409**	0.0223	23	177	185	TIVMGASFR		
997.5135	**997.5303**	0.0168	17	177	185	TIVMGASFR		
1133.6313	**1133.6521**	0.0208	18	261	270	FAADAIKLER	23	0
1133.6313	**1133.6521**	0.0208	18	261	270	FAADAIKLER		
1242.7052	**1242.6991**	-0.0061	-5	212	223	DNSKLAPALSVK		
1252.6355	**1252.6576**	0.0221	18	57	67	LSFDKDAMVAR	18	0
1252.6355	**1252.6576**	0.0221	18	57	67	LSFDKDAMVAR		
1276.6532	**1276.6569**	0.0037	3	89	100	LSSTWEGIQAGK		
1311.6692	**1311.7523**	0.0831	63	139	149	ILDWHVANTDK		
1439.7642	**1439.7778**	0.0136	9	139	150	ILDWHVANTDKK		

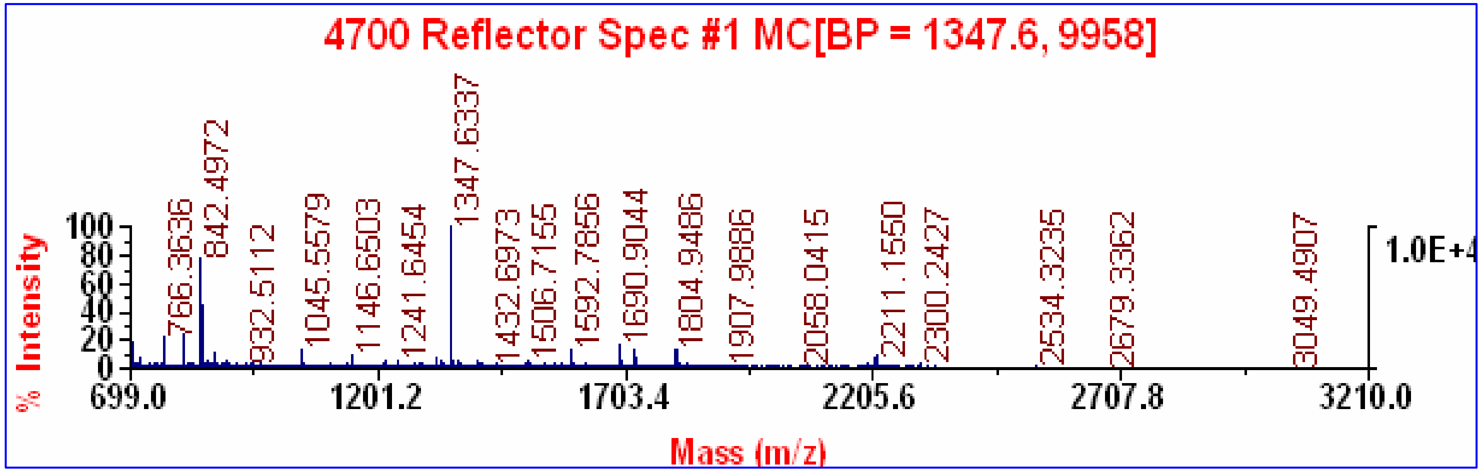
1680.8479	**1680.8379**	-0.01	-6	2	16	PAYQELVEEAIAYGK		

MS/MS Fragmentation of FAADAIKLER (1133.6521, 1+)



Spot No.6574 gi|70794816

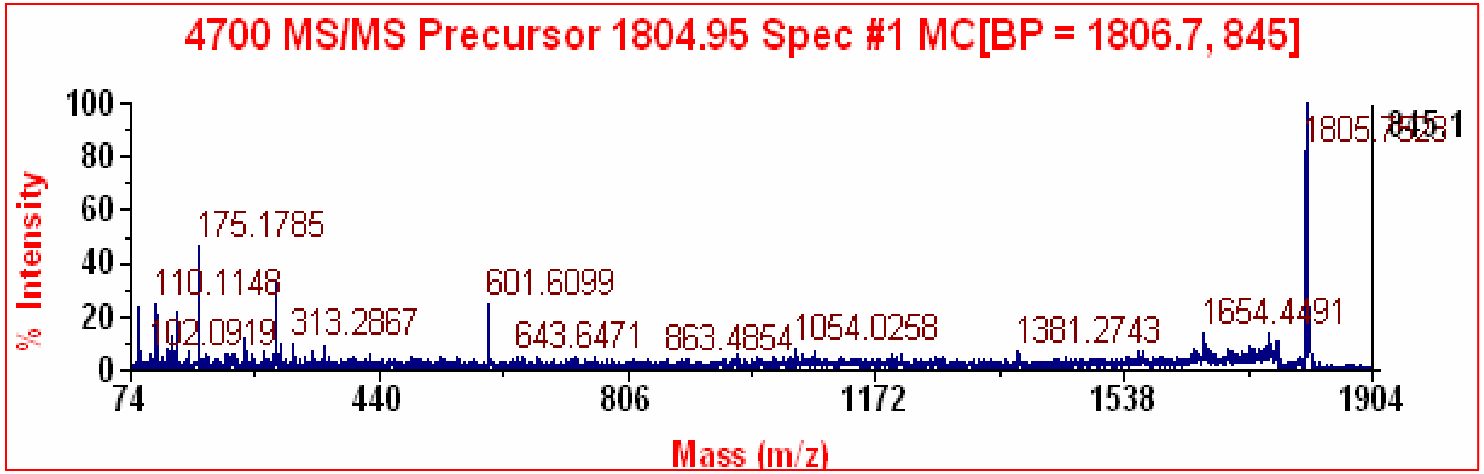
Hypothetical protein LOC433182 [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
704.4089	**704.4256**	0.0167	24	127	132	GVPLYR		

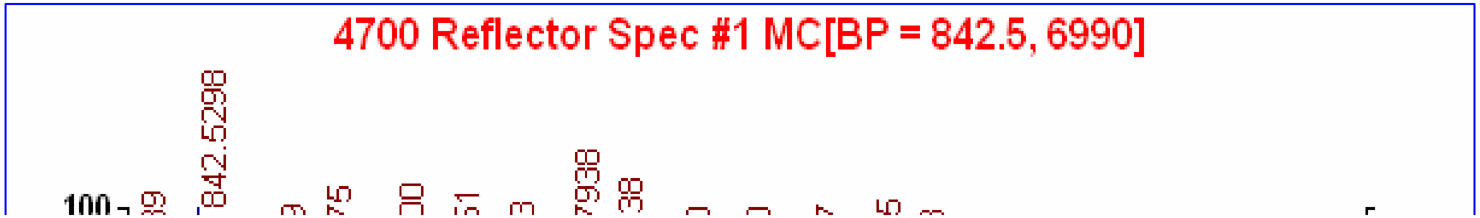
766.3729	**766.3636**	######	-12	10	15	EIFDSR		
806.4519	**806.44**	######	-15	407	412	YNQILR		
932.5312	**932.5112**	-0.02	-21	427	434	SFRNPLAK		
1439.7417	**1439.7354**	######	-4	270	281	YITPDQLADLYK		
1557.759	**1557.8121**	0.0531	34	359	372	LAQSNGWGVMVSHR		
1804.944	**1804.9489**	**0.0049**	**3**	**33**	**50**	**AAVPSGASTGIYEALELR**	**49**	**#####**
1804.944	**1804.9489**	0.0049	3	33	50	AAVPSGASTGIYEALELR		
2192.0327	**2192.0659**	0.0332	15	234	253	AGYTDQVVIGMDVAASEFYR	30	#####
2192.0327	**2192.0659**	0.0332	15	234	253	AGYTDQVVIGMDVAASEFYR		
2208.0278	**2208.0671**	0.0393	18	234	253	AGYTDQVVIGMDVAASEFYR		
2277.1357	**2277.1111**	######	-11	33	54	AAVPSGASTGIYEALELRDNDK		

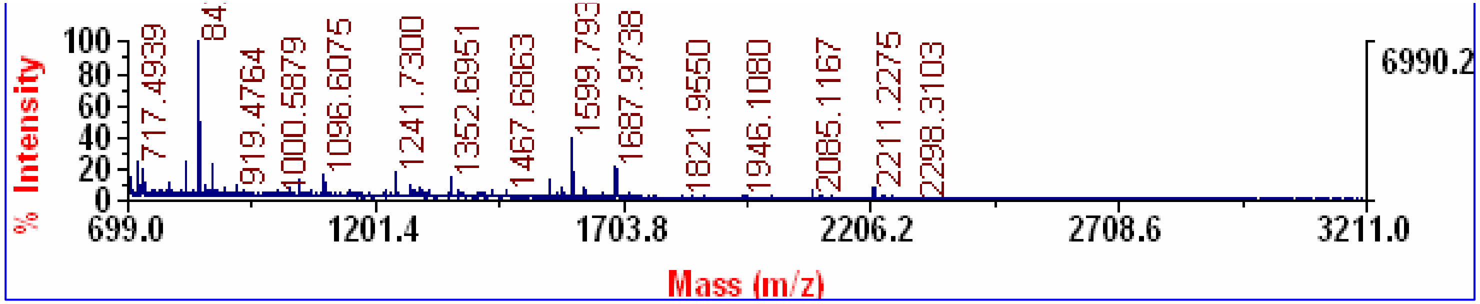
MS/MS Fragmentation of AAVPSGASTGIYEALELR (1804.9489, 1+)



Spot No.8657 gi|148677504

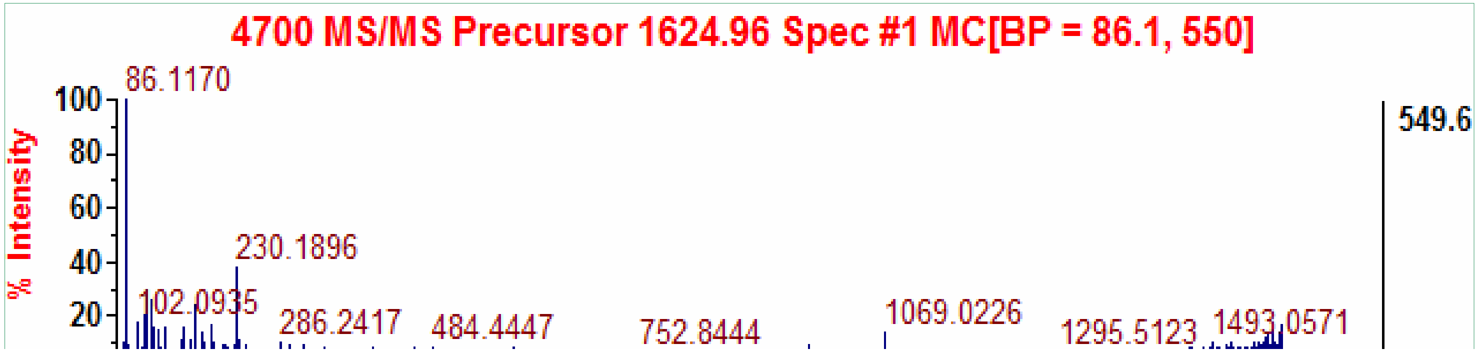
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, isoform CRA_h

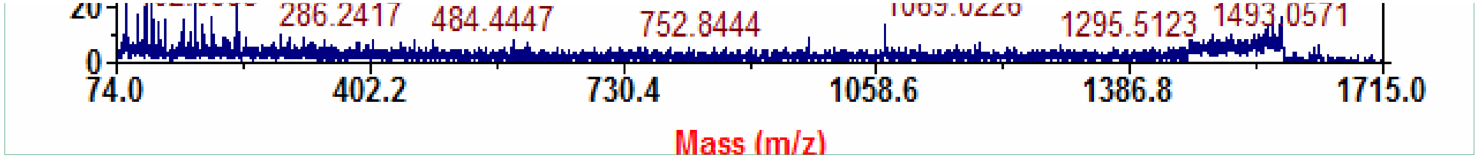




Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
723.4511	**723.4763**	0.0252	35	129	135	APGIIPR		
730.457	**730.4213**	-0.0357	-49	17	23	RAGLVSK		
815.4733	**815.5284**	0.0551	68	115	122	GPIGSKTR		
860.5022	**860.5187**	0.0165	19	276	282	QMSLLLR		
876.4971	**876.5211**	0.024	27	276	282	QMSLLLR		
892.4886	**892.5123**	0.0237	27	388	394	LELAQYR		
919.4553	**919.4764**	0.0211	23	140	147	EPMQTGIK		
1026.5942	**1026.6212**	0.027	26	148	157	AVDSLVPIGR		
1094.6793	**1094.5911**	-0.0882	-81	6	16	VAAAVARALPR		
1096.549	**1096.6069**	0.0579	53	378	387	AMKQVAGTMK		
1306.6749	**1306.6991**	0.0242	19	24	36	NALGSSFVDGIAR		
1553.7383	**1553.7957**	0.0574	37	288	300	EAYPGDVFYLHSR	12	0
1553.7383	**1553.7957**	0.0574	37	288	300	EAYPGDVFYLHSR		
1577.8573	**1577.8484**	-0.0089	-6	493	506	LKEIVTNFLAGFEP		
1624.8904	**1624.9558**	0.0654	40	87	102	TGAIVDVPVGEELLGR	24	0
1624.8904	**1624.9558**	0.0654	40	87	102	TGAIVDVPVGEELLGR		

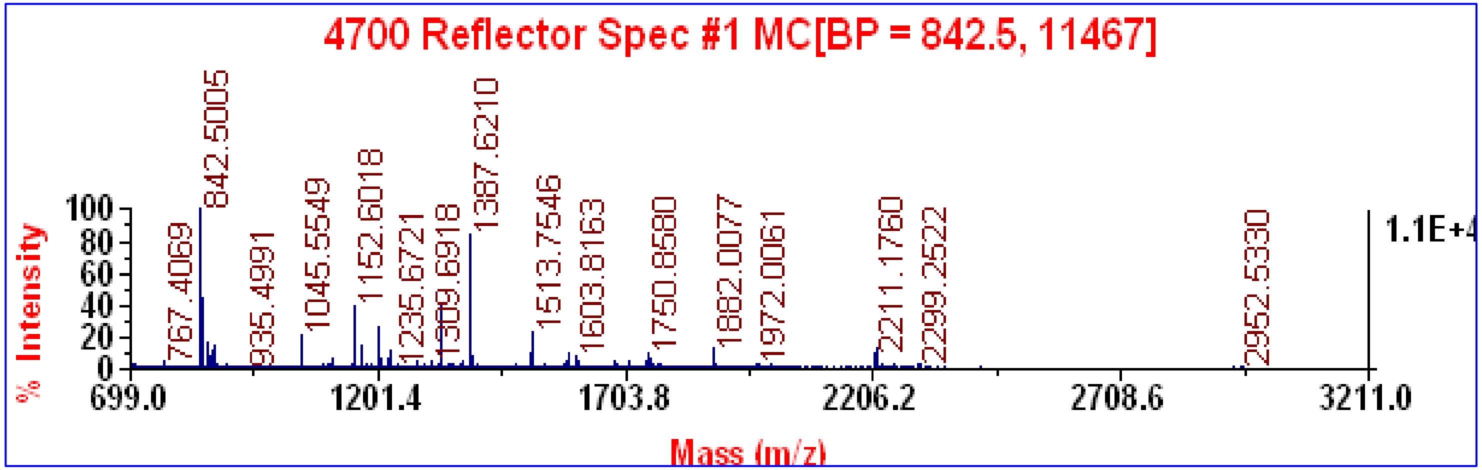
MS/MS Fragmentation of TGAIVDVPVGEELLGR (1624.9558, 1+)





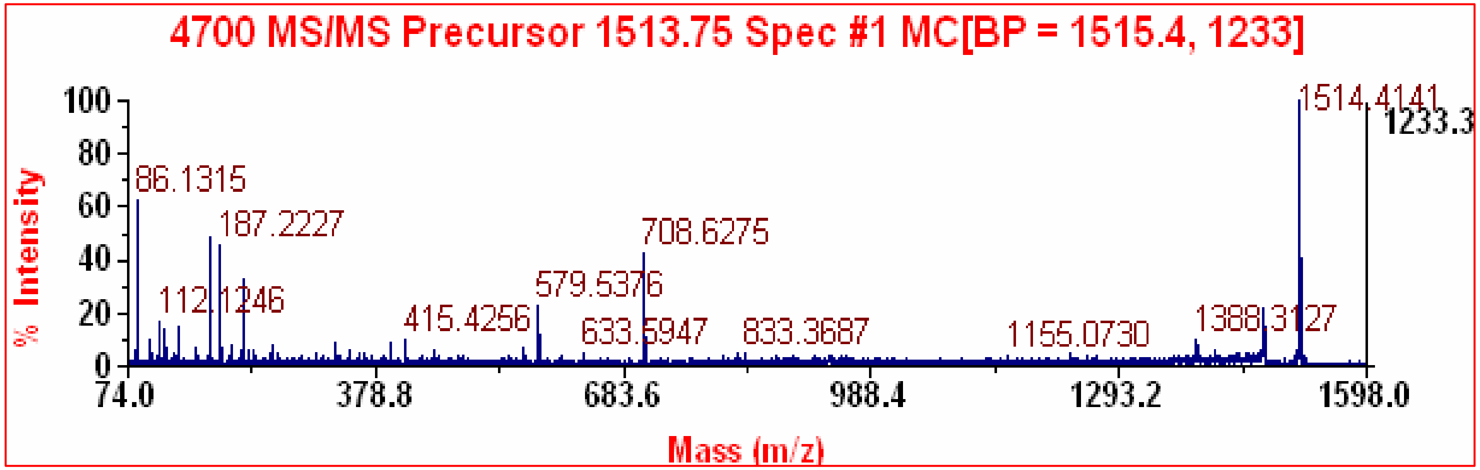
Spot No.6477 gi|228480253

Septin 2 b [Mus musculus]

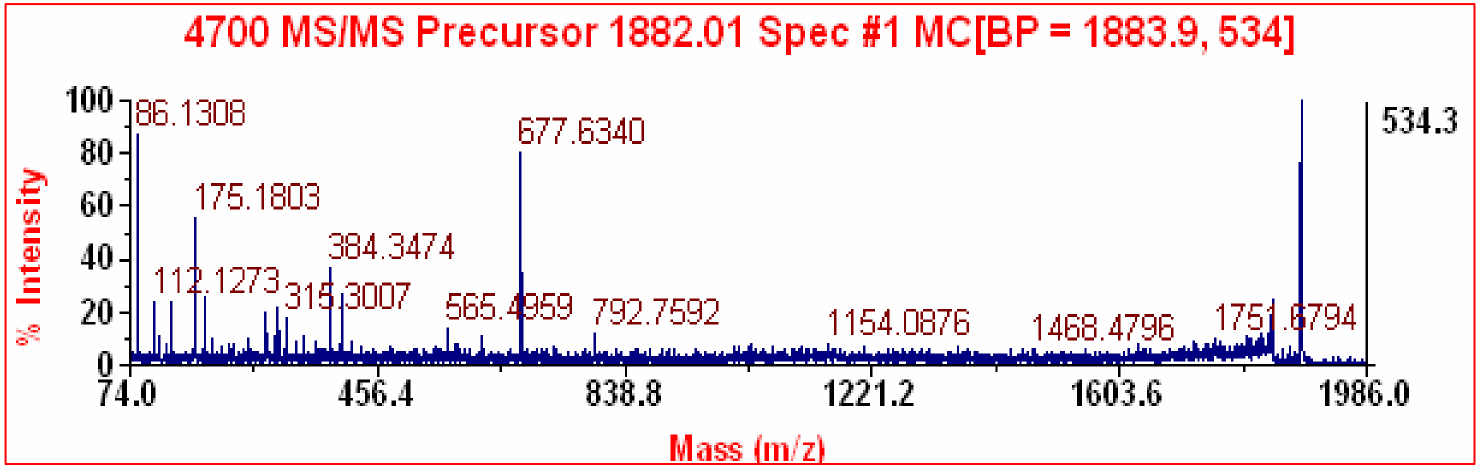


Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
767.4158	**767.4069**	-0.0089	-12	100	105	HIIDNR		
773.4264	**773.3781**	-0.0483	-62	286	291	EAELRR		
978.4196	**978.4753**	0.0557	57	271	278	VENEDMNK		
1203.5753	**1203.5677**	-0.0076	-6	89	98	YLHDESGLNR	32	86.608
1203.5753	**1203.5677**	-0.0076	-6	89	98	YLHDESGLNR		
1325.6947	**1325.6788**	-0.0159	-12	159	169	ILDEIEEHSIK		
1359.6764	**1359.6653**	-0.0111	-8	89	99	YLHDESGLNRR		
1481.7958	**1481.7928**	-0.003	-2	158	169	RILDEIEEHSIK		
1513.7533	**1513.7528**	**-0.0005**	**0**	**77**	**88**	**TIISYIDEQFER**	**41**	**98.271**
1513.7533	**1513.7528**	-0.0005	0	77	88	TIISYIDEQFER		
1603.8174	**1603.8159**	-0.0015	-1	38	51	TVQIEASTVEIEER		
1759.9589	**1759.9924**	0.0335	19	193	209	ASIPFSVVGSNQLIEAK		
1881.9956	**1882.0082**	**0.0126**	**7**	**11**	**26**	**STLINSLFLTDLYPER**	**51**	**99.829**
1881.9956	**1882.0082**	0.0126	7	11	26	STLINSLFLTDLYPER		

MS/MS Fragmentation of TIISYIDEQFER (1513.7528, 1+)

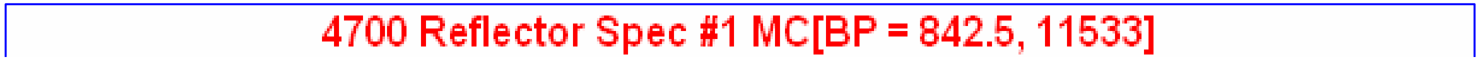


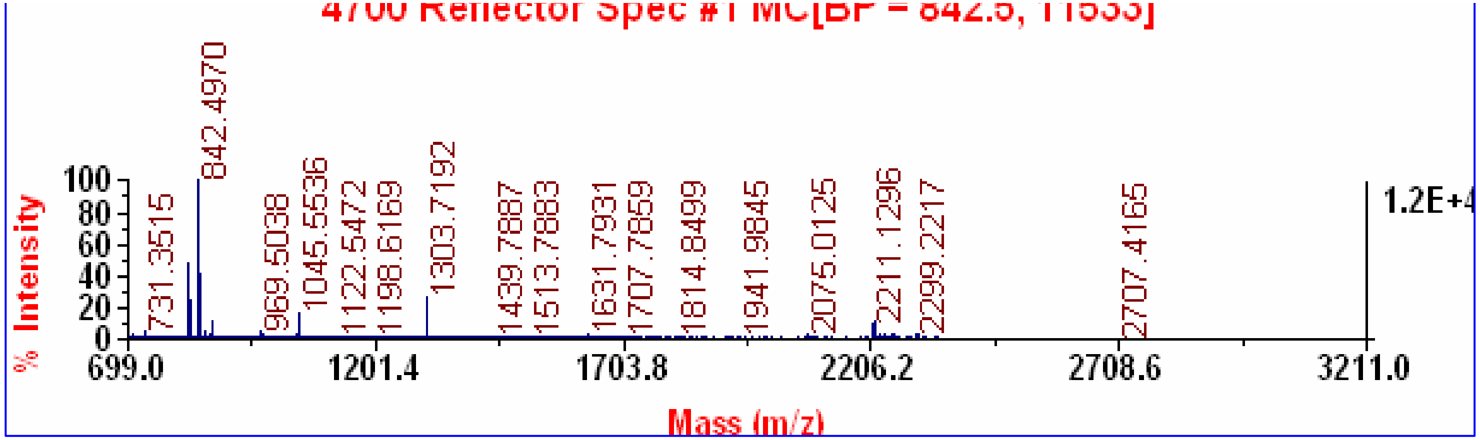
MS/MS Fragmentation of STLINSLFLTDLYPER (1882.0082, 1+)



Spot No.5454 gi|52696229

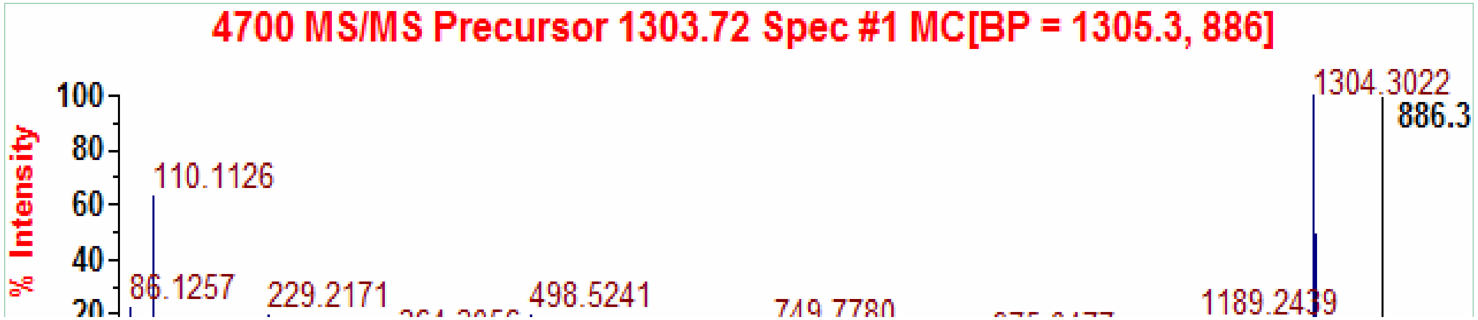
Chain A, Crystal Structure Of Mrna Decapping Enzyme(Dcps) From Mus Musculus At 1.83 A Resol

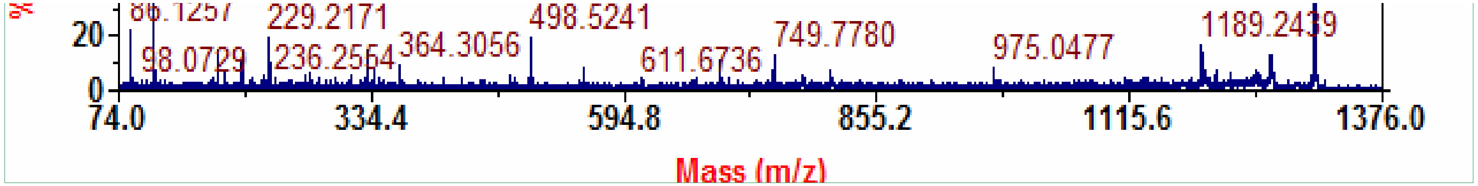




Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
731.3583	**731.3515**	-0.0068	-9	322	326	HYQQR		
821.4879	**821.4748**	-0.0131	-16	327	333	TLTFALR		
823.446	**823.4343**	-0.0117	-14	53	59	LPFSGFR		
1043.5844	**1043.5535**	-0.0309	-30	258	266	EGQEAILKR		
1283.7206	**1283.6982**	-0.0224	-17	334	344	TDDPLLQLLQK		
1303.7369	**1303.7191**	-0.0178	-14	243	253	DLTPEHLPLLR	33	88.082
1303.7369	**1303.7191**	-0.0178	-14	243	253	DLTPEHLPLLR		
1659.9541	**1659.9103**	-0.0438	-26	240	253	SLRDLTPEHLPLLR		
1800.0491	**1799.9492**	-0.0999	-55	243	257	DLTPEHLPLLRNILR		
2075.0232	**2075.0105**	-0.0127	-6	117	133	LQFSNDIYSTYNLFPPR	14	0
2075.0232	**2075.0105**	-0.0127	-6	117	133	LQFSNDIYSTYNLFPPR		
2094.123	**2094.0967**	-0.0263	-13	98	116	TPFQVEHVAQLLTGSPELK		
2313.1055	**2313.2239**	0.1184	51	2	21	GSDKIHHHHHHMADTAPQLK		

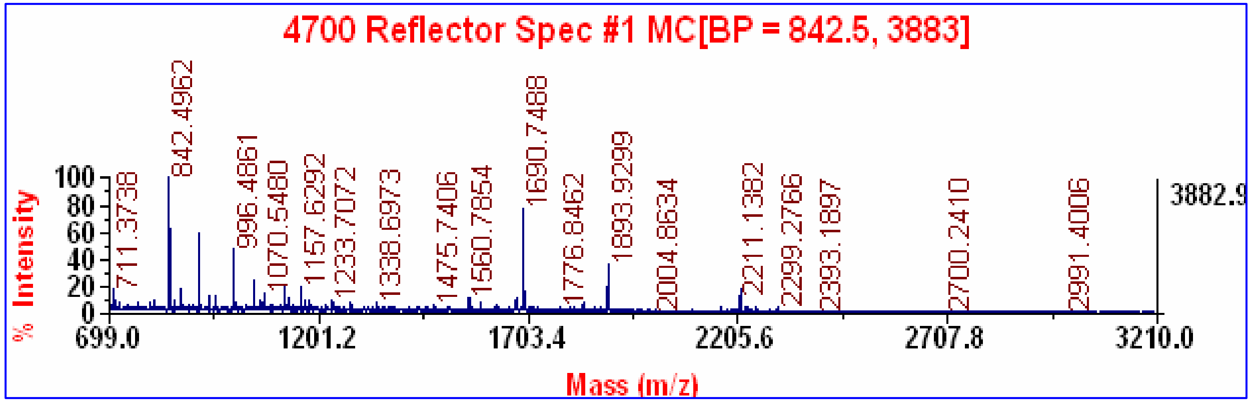
MS/MS Fragmentation of DLTPEHLPLLR (1303.7191, 1+)





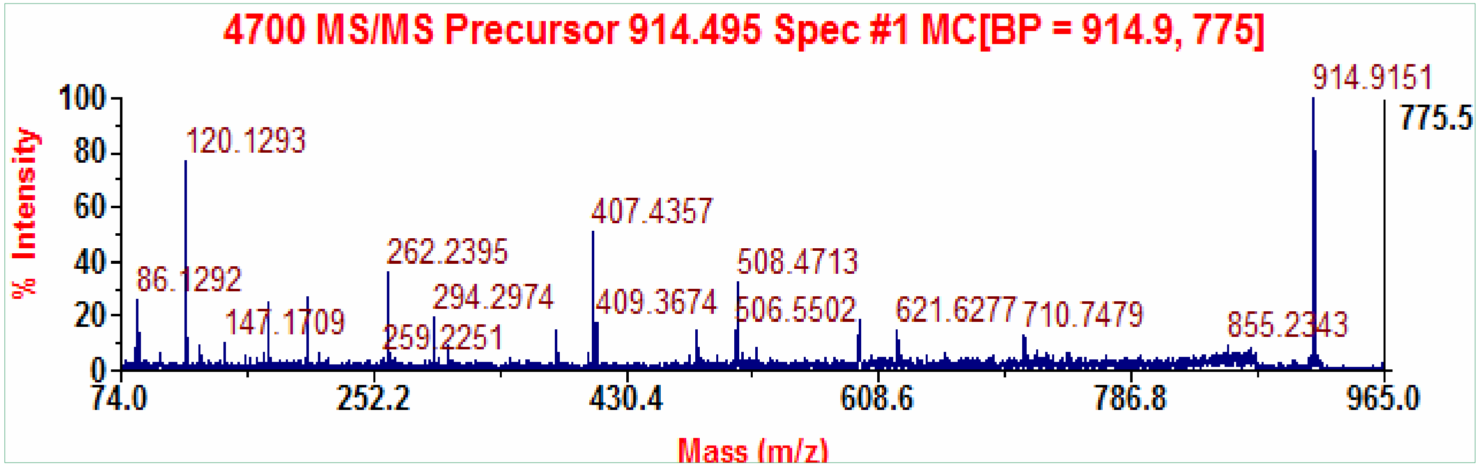
Spot No.7328 gi|81917948

Heterogeneous nuclear ribonucleoprotein D-like [Mus musculus]

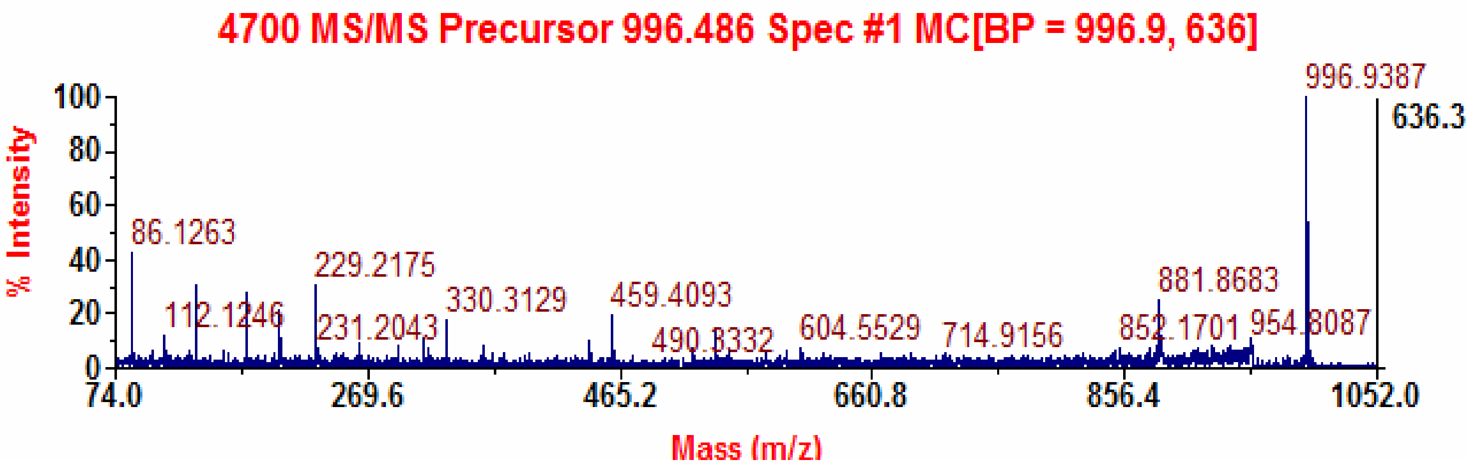


Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
745.3839	**745.383**	-0.0009	-1	62	68	TDPVTGR		
889.4526	**889.4468**	-0.0058	-7	176	183	YHQIGSGK		
914.5134	**914.4954**	-0.018	-20	71	78	GFGFVLFK	32	86.402
914.5134	**914.4954**	-0.018	-20	71	78	GFGFVLFK		
996.4996	**996.4861**	-0.0135	-14	44	51	DLTEYLSR	30	79.036
996.4996	**996.4861**	-0.0135	-14	44	51	DLTEYLSR		
1089.6051	**1089.5742**	-0.0309	-28	188	196	VAQPKEVYR		
1110.5499	**1110.5188**	-0.0311	-28	52	61	FGEVVDCTIK		
1157.6466	**1157.6273**	-0.0193	-17	69	78	SRGFGFVLFK		
1462.7397	**1462.7214**	-0.0183	-13	193	203	EVYRQQQQQK		
1705.8643	**1705.8495**	-0.0148	-9	116	131	VFVGGLSPDTSEEQIK		
1776.8513	**1776.8466**	-0.0047	-3	156	170	GFCFITYTDEEPVKK		
1833.9592	**1833.882**	-0.0772	-42	115	131	KVFVGGLSPDTSEEQIK		
1836.916	**1836.8979**	-0.0181	-10	52	68	FGEVVDCTIKTDPVTGR		

MS/MS Fragmentation of GFGFVLFK (914.4954, 1+)

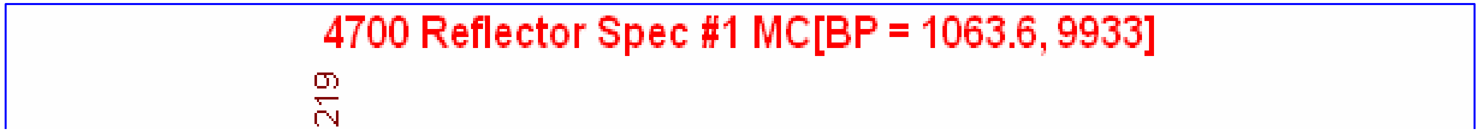


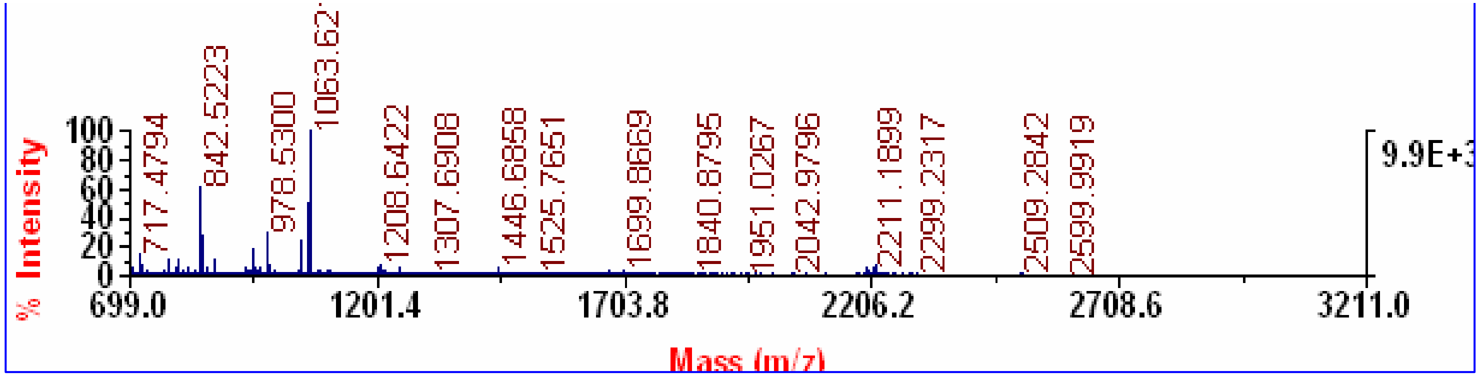
MS/MS Fragmentation of DLTEYLSR (996.4861, 1+)



Spot No.2155 gi|123295280

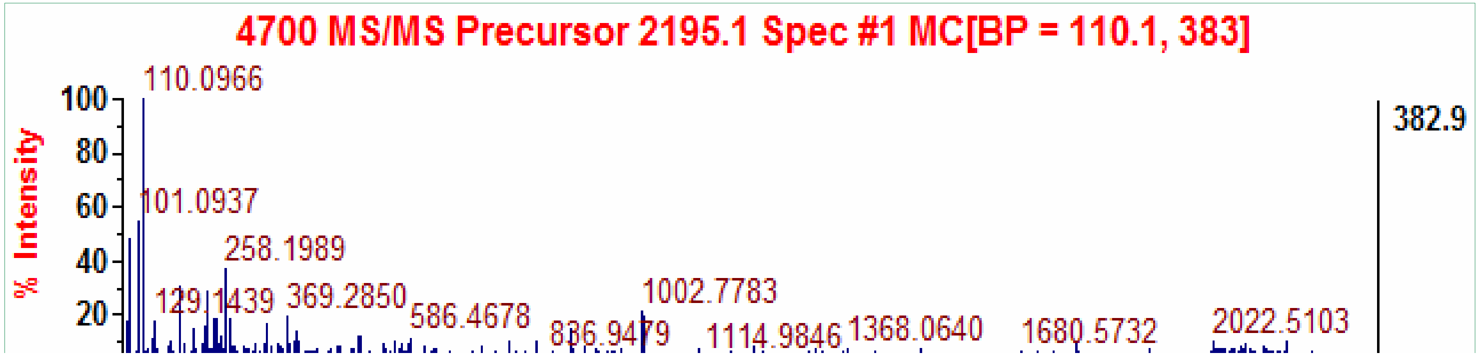
SET translocation [Mus musculus]

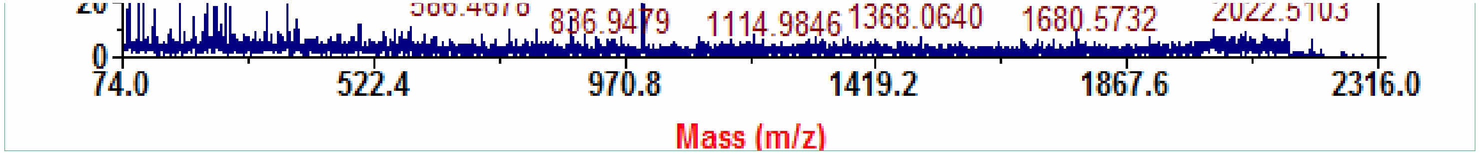




Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
794.4195	**794.4289**	0.0094	12	77	82	QPFFQK		
816.4937	**816.4398**	-0.0539	-66	83	89	RSELIAK		
935.5785	**935.5252**	-0.0533	-57	15	23	KPRPAAAPK		
948.4857	**948.4987**	0.013	14	181	188	RSSQTQNK		
1063.6047	**1063.6218**	0.0171	16	75	82	LRQPFFQK	17	0
1063.6047	**1063.6218**	0.0171	16	75	82	LRQPFFQK		
1208.6045	**1208.6416**	0.0371	31	122	131	VEVTEFEDIK		
1446.6495	**1446.6864**	0.0369	26	154	166	EFHLNESGDPSSK		
1671.8224	**1671.8698**	0.0474	28	122	135	VEVTEFEDIKSGYR		
1757.928	**1758.0021**	0.0741	42	57	71	LNEQASEEILKVEQK		
1840.8064	**1840.8784**	0.072	39	136	149	IDFYFDENPYFENK		
2195.021	**2195.0999**	0.0789	36	39	56	EQQEAIEHIDEVQNEIDR	24	0
2195.021	**2195.0999**	0.0789	36	39	56	EQQEAIEHIDEVQNEIDR		
2509.1802	**2509.2856**	0.1054	42	36	56	GIDERKEQQEAIEHIDEVQNE		

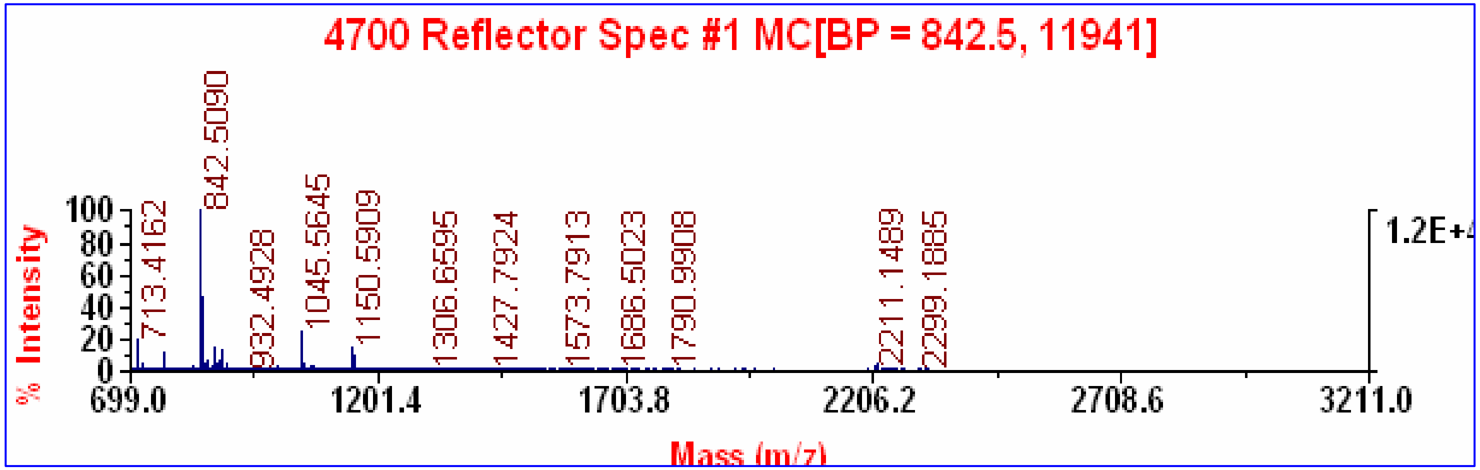
MS/MS Fragmentation of EQQEAIEHIDEVQNEIDR (2195.0999, 1+)





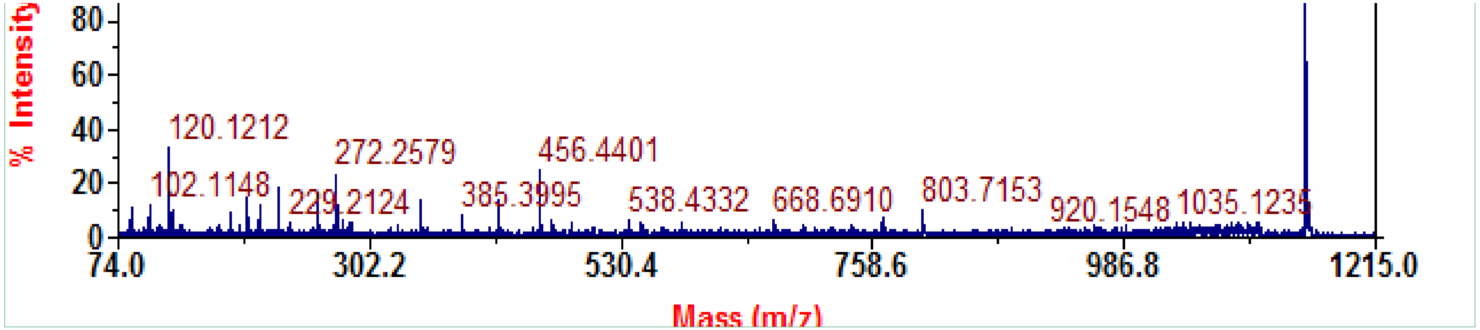
Spot No.2381 gi|50510319

mKIAA0002 protein [Mus musculus]



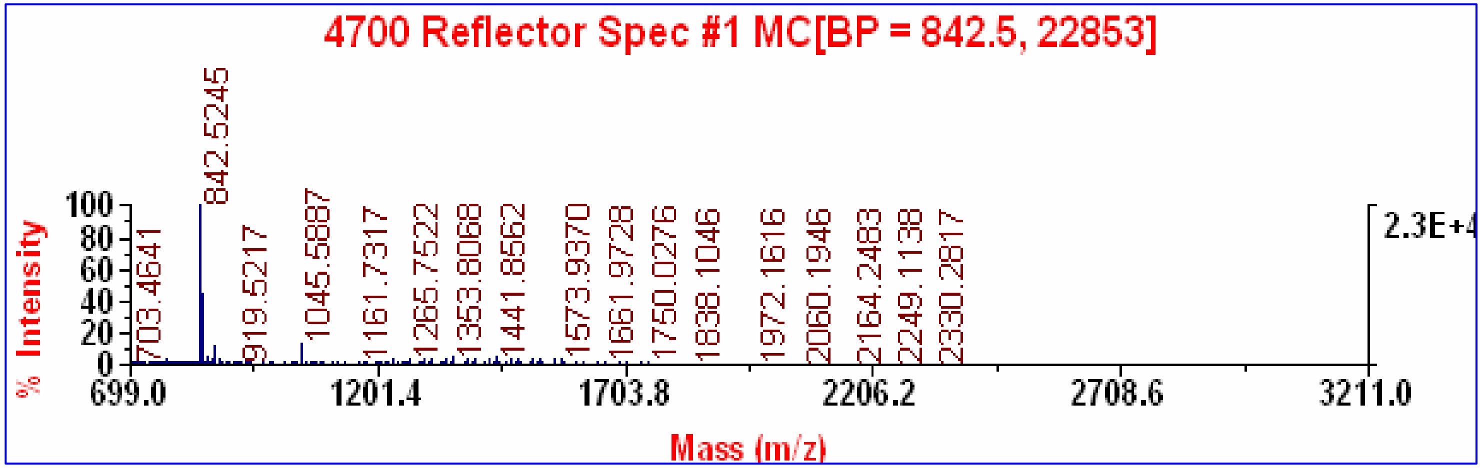
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
882.4866	**882.5624**	0.0758	86	7	14	AMALHVPK		
1128.6736	**1128.6497**	-0.0239	-21	517	527	LATNAAVTVLR		
1150.5891	**1150.5905**	0.0014	1	448	457	FAEAFEAIPR	32	69.54
1150.5891	**1150.5905**	0.0014	1	448	457	FAEAFEAIPR		
1278.6841	**1278.6866**	0.0025	2	447	457	KFAEAFEAIPR		
1681.8148	**1681.7928**	-0.022	-13	52	66	TAYGPNGMNKMVINR		
2225.1821	**2225.1775**	-0.0046	-2	211	231	VCKILGSGIYSSSVLHGMVFK		

MS/MS Fragmentation of FAEAFEAIPR (1150.5905, 1+)



Spot No.4255 gi|13752262

HSP90 [grapevine leafroll-associated virus 5]

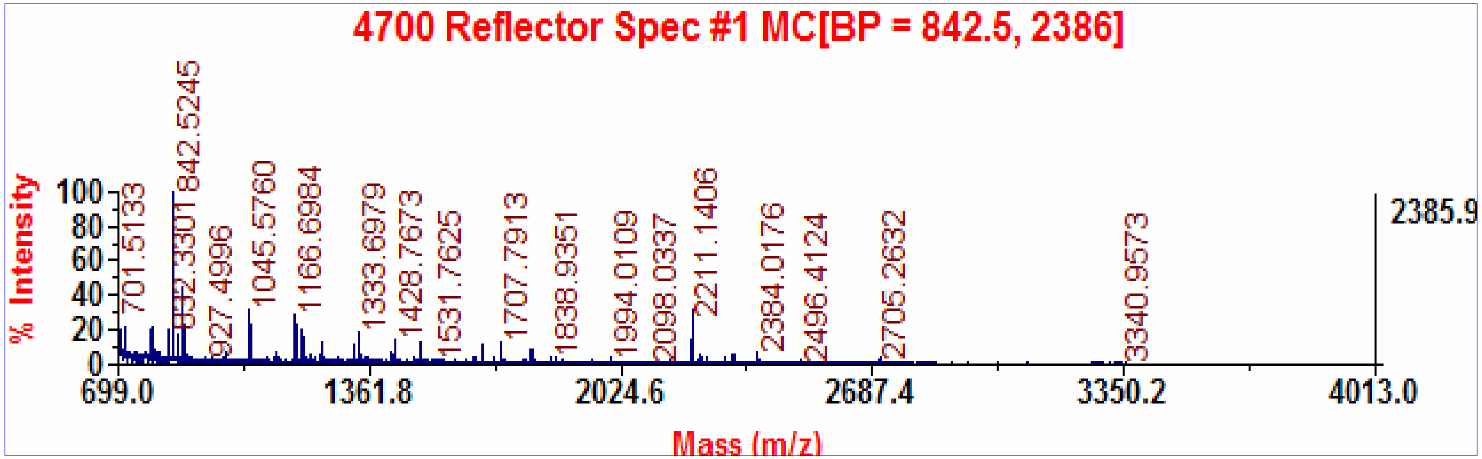


Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
703.3984	**703.4645**	0.0661	94	142	147	VEAEKK		
737.394	**737.3932**	-0.0008	-1	47	53	FSAISGR		
800.4988	**800.5008**	0.002	2	209	215	LATLNLR		
880.5039	**880.4903**	-0.0136	-15	135	141	FPFKVSR		
983.636	**983.5814**	-0.0546	-56	359	367	KLVGALLNR		
1045.5889	**1045.5872**	-0.0017	-2	125	134	VGKPVTETSK		
1199.6089	**1199.6869**	0.078	65	1	11	MALSATSTYVR		
1215.6039	**1215.6503**	0.0464	38	1	11	MALSATSTYVR		
1252.6605	**1252.7804**	0.1199	96	403	412	LDYMIKNEVK		

1353.6719	**1353.8064**	0.1345	99	109	121	SAVATPMSVFTDK		
1353.6719	**1353.8064**	0.1345	99	109	121	SAVATPMSVFTDK		
1391.7423	**1391.757**	0.0147	11	335	347	NTTGGLLMRIGSR		
1463.7853	**1463.8678**	0.0825	56	12	24	VSKSDEGFVNLLR		
1479.759	**1479.8146**	0.0556	38	220	232	QGDPVEGVFFKTR		
1513.8043	**1513.9304**	0.1261	83	1	14	MALSATSTYVRVSK		
1529.7992	**1529.9098**	0.1106	72	1	14	MALSATSTYVRVSK		
1661.8341	**1661.9713**	0.1372	83	192	207	GSLLLDVGSDVTSNER		
1749.8741	**1750.0256**	0.1515	87	157	171	HTQDLIFCIGNYLGR		
2249.166	**2249.1121**	-0.0539	-24	302	322	EDIDLDAALSSGTLLKGEVFR		

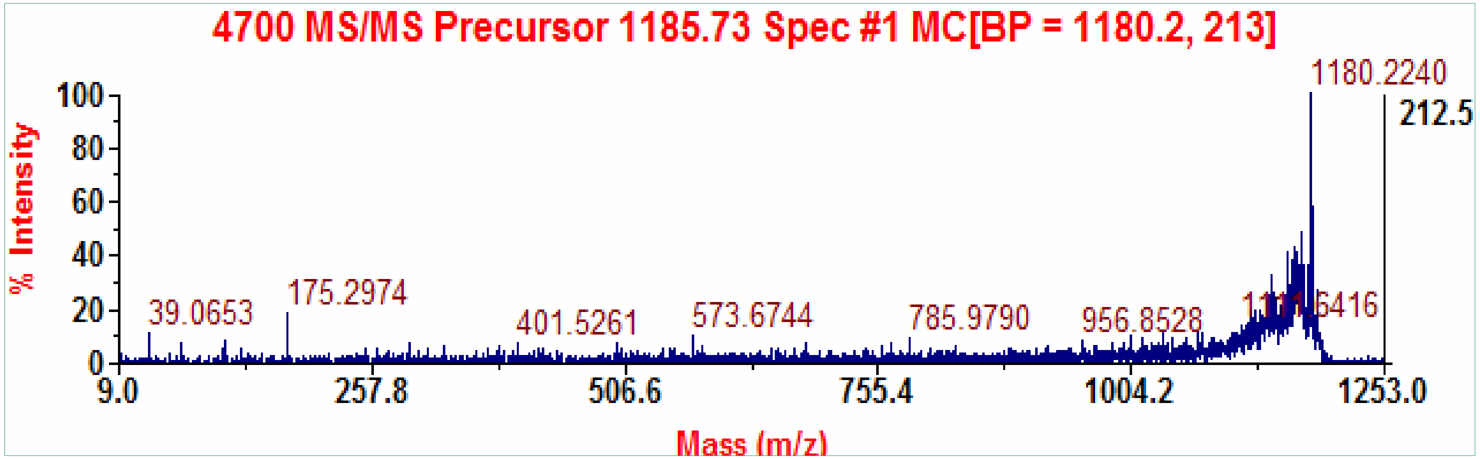
Spot No.7466 gi|6753320

Chaperonin containing Tcp1, subunit 3 (gamma) [Mus musculus]



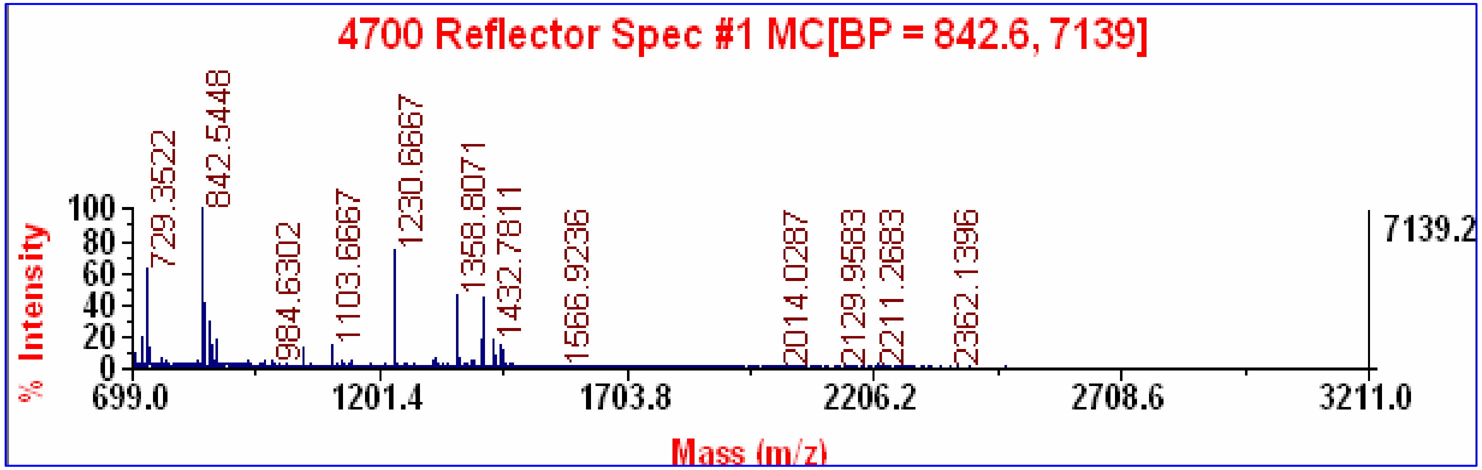
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
832.391	**832.33**	-0.0607	-73	529.00	535	KGDDQNR		
1166.689	**1166.699**	0.0098	8	439.00	449	AVAQALEVIPR	20	0
1166.689	**1166.699**	0.0098	8	439.00	449	AVAQALEVIPR		
1185.720	**1185.7288**	0.0086	7	508.00	518	TAVETAVLLLR	21	0
1185.720	**1185.7288**	0.0086	7	508.00	518	TAVETAVLLLR		
1207.607	**1207.6157**	0.0091	8	182.00	191	TVQFEENGRK		
1419.705	**1419.7102**	0.0052	4	295.00	306	GISDLAQHYLMR		

MS/MS Fragmentation of TAVETAVLLLR (1185.7288, 1+)



Spot No.6159 gi|159031195

putative oligoadenylate synthetase 1b [Mus musculus]

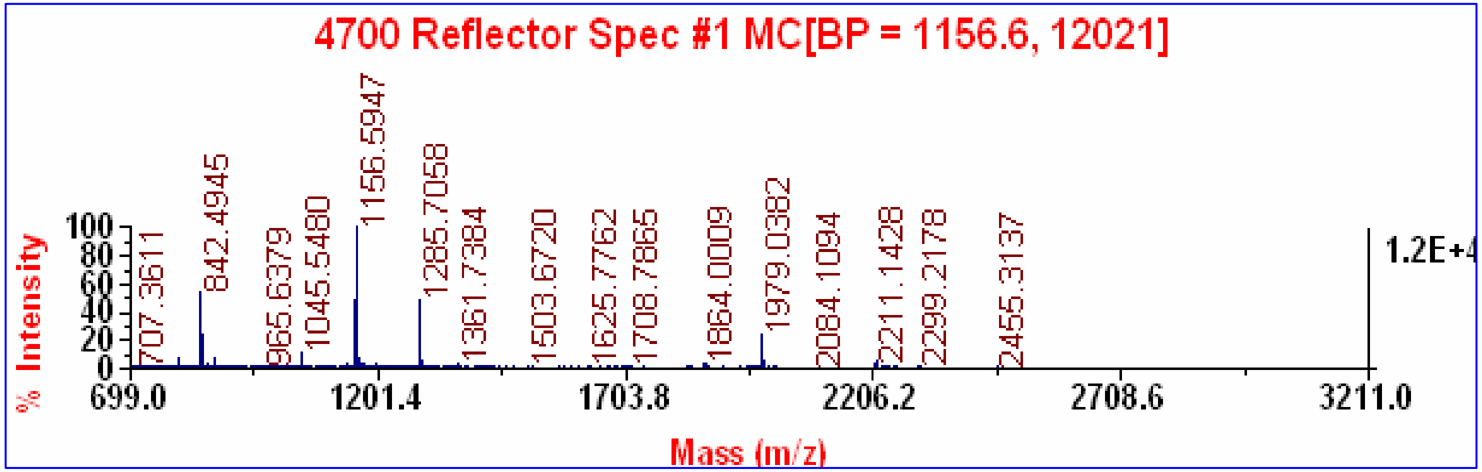


Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
833.3821	**833.4748**	0.0927	111	1	6	MEQDLR		
856.5138	**856.569**	0.0552	64	132	139	LSAPDLLK		
1141.5823	**1141.655**	0.0727	64	192	200	YFLNCRPTK		

1212.7198	1212.6625	-0.0573	-47	132	142	LSAPDLLKEVK		
1268.6746	1268.6616	-0.013	-10	243	253	VTKFNTAQGFR		
1311.6587	1311.7391	0.0804	61	101	110	QLCEIQHERR		
1311.6587	1311.7391	0.0804	61	101	110	QLCEIQHERR		
1358.6079	1358.8055	0.1976	145	179	190	EGELSTCFMGLR		
1358.6079	1358.8055	0.1976	145	179	190	EGELSTCFMGLR		
1432.7101	1432.7805	0.0704	49	1	12	MEQDLRSIPASK		
1448.822	1448.7627	-0.0593	-41	291	303	VRPVILDPADPTR		
1458.7985	1458.8243	0.0258	18	32	44	EVIDALCALLKDR		
1470.7079	1470.7495	0.0416	28	179	191	EGELSTCFMGLRK		

Spot No.6237 gi|6755198

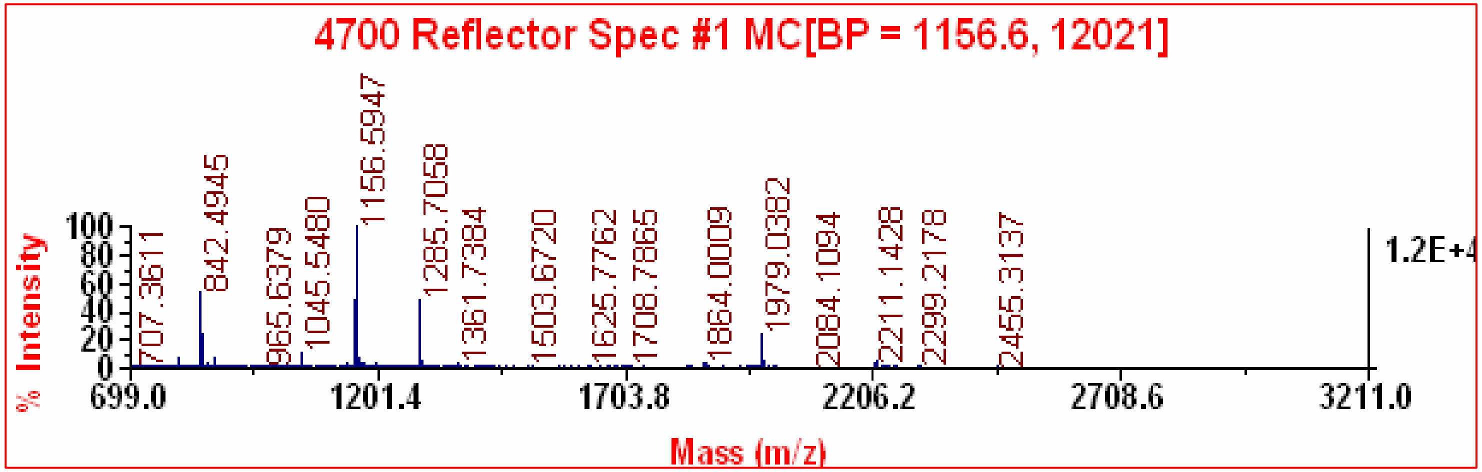
proteasome alpha 6 subunit [Mus musculus]



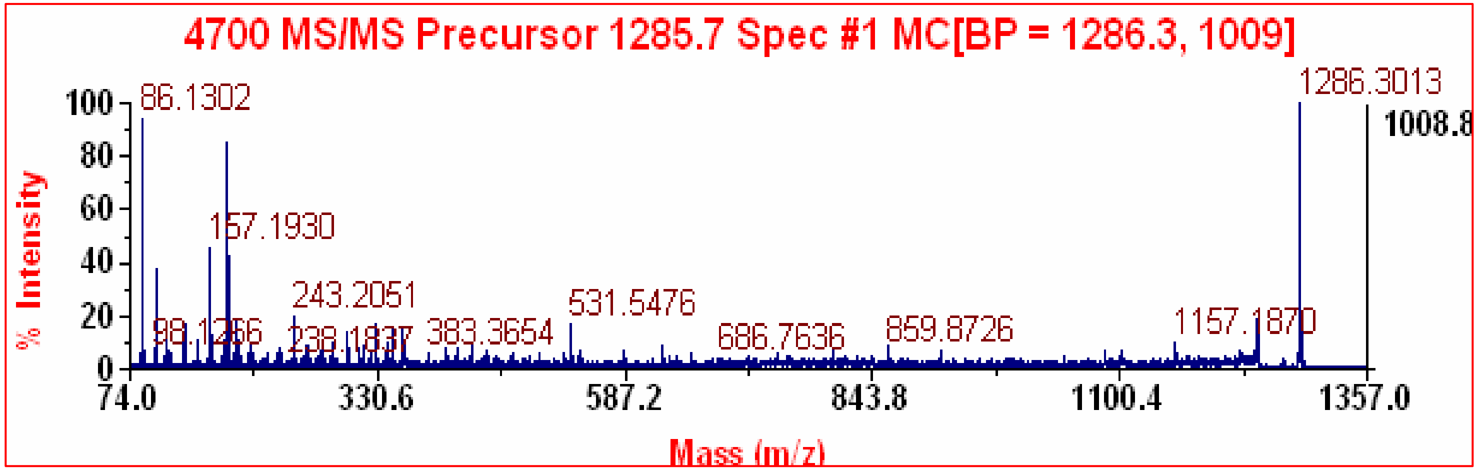
Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
796.3583	796.3398	-0.0185	-23	4	11	GSSAGFDR		
1108.5535	1108.5613	0.0078	7	94	102	ARYEAANWK		
1156.611	**1156.5944**	**-0.0166**	**-14**	**12**	**21**	**HITIFSPEGR**	**47**	**99.528**
1156.611	1156.5944	-0.0166	-14	12	21	HITIFSPEGR		
1160.5986	1160.5873	-0.0113	-10	22	30	LYQVEYAFK		
1172.5735	1172.5925	0.019	16	96	104	YEAANWKYK		
1285.7223	**1285.7036**	**-0.0187**	**-15**	**31**	**43**	**AINQGGLTSVAVR**	**68**	**99.996**
1285.7223	1285.7036	-0.0187	-15	31	43	AINQGGLTSVAVR		

1360.7471	**1360.7335**	-0.0136	-10	60	71	LLDSSTVTHLFK	11	0
1360.7471	**1360.7335**	-0.0136	-10	60	71	LLDSSTVTHLFK		
1864.0175	**1863.9991**	-0.0184	-10	229	245	ILTEAEIDAHLVALAER	13	0
1864.0175	**1863.9991**	-0.0184	-10	229	245	ILTEAEIDAHLVALAER		
1979.0444	**1979.0386**	**-0.0058**	**-3**	**229**	**246**	**ILTEAEIDAHLVALAERD**	**72**	**99.999**
1979.0444	**1979.0386**	-0.0058	-3	229	246	ILTEAEIDAHLVALAERD		

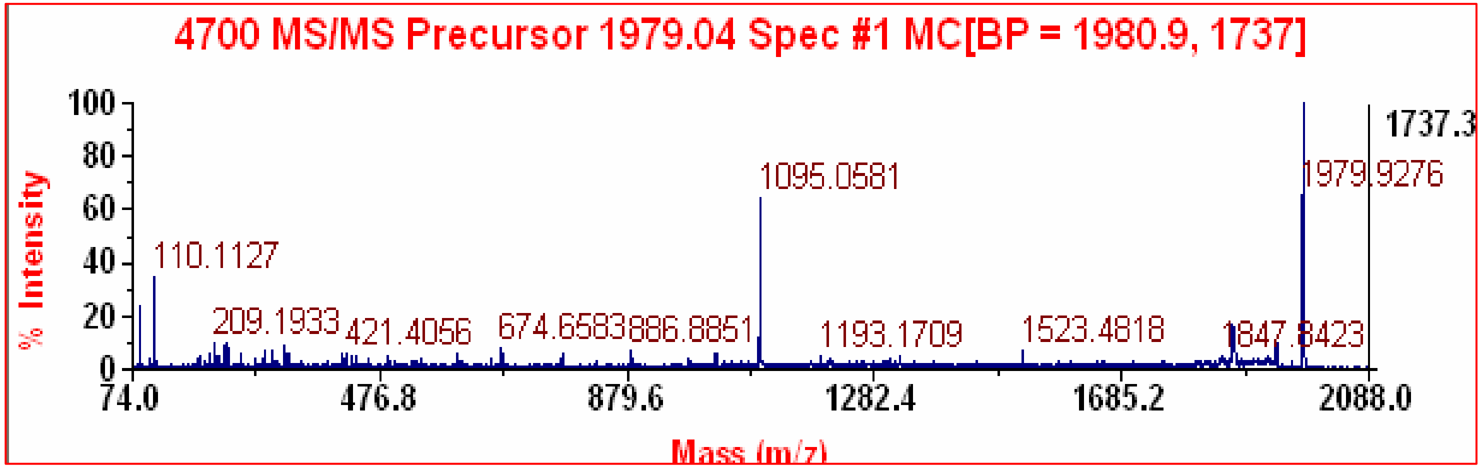
MS/MS Fragmentation of HITIFSPEGR (1156.5944, 1+)



MS/MS Fragmentation of AINQGGLTSVAVR (1285.7036, 1+)

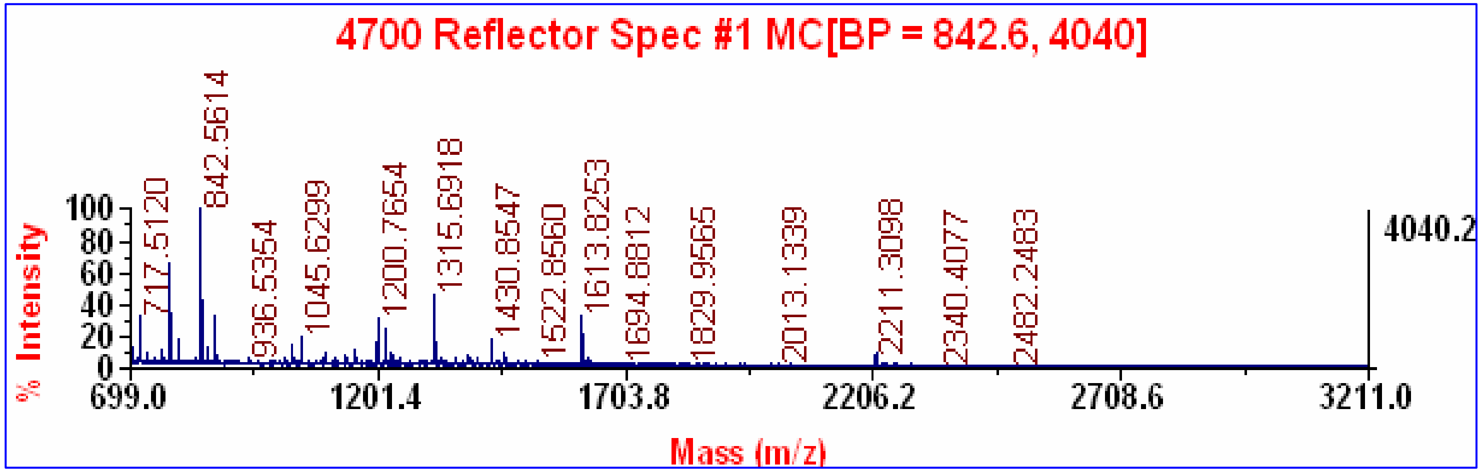


MS/MS Fragmentation of ILTEAEIDAHLVALAERD (1979.0386, 1+)



Spot No.4518 gi|14149756

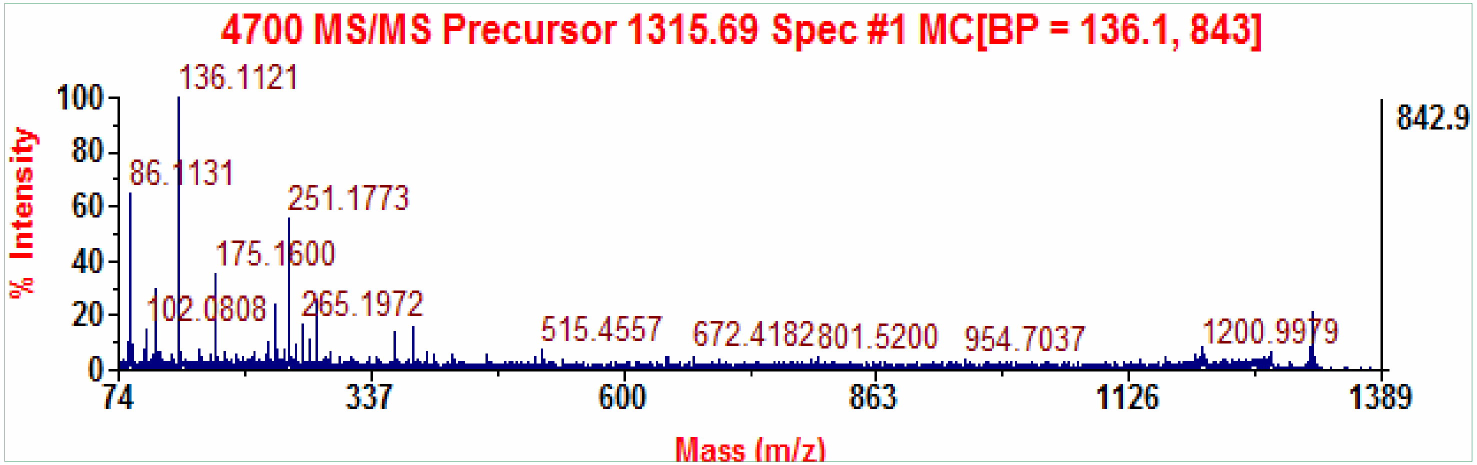
eukaryotic translation initiation factor 2, subunit 2 (beta) [Mus musculus]



Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
763.4209	**763.471**	0.0501	66	258	263	GRFQQK		

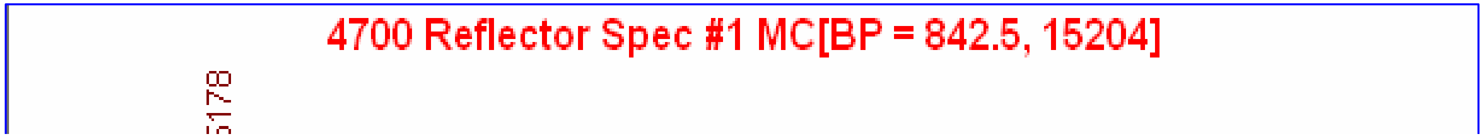
779.4232	**779.4687**	0.0455	58	181	186 VFNIMR		
795.4181	**795.4642**	0.0461	58	181	186 VFNIMR		
871.4995	**871.5662**	0.0667	77	264	270 QIENVLR		
1027.6007	**1027.6696**	0.0689	67	264	271 QIENVLRR		
1116.5466	**1116.6945**	0.1479	132	189	198 NPDMVAGEKR		
1200.6921	**1200.7651**	0.073	61	200	209 FVMKPPQVVR		
1200.6921	**1200.7651**	0.073	61	200	209 FVMKPPQVVR		
1216.6871	**1216.7666**	0.0795	65	200	209 FVMKPPQVVR	0	0
1216.6871	**1216.7666**	0.0795	65	200	209 FVMKPPQVVR		
1315.6165	**1315.691**	0.0745	57	171	180 DYTYEELLNR	28	21.73
1315.6165	**1315.691**	0.0745	57	171	180 DYTYEELLNR		
1328.7871	**1328.8787**	0.0916	69	199	209 KFVMKPPQVVR		
1457.6287	**1457.8627**	0.234	161	2	14 SGDEMIFDPTMSK		
1499.677	**1499.7325**	0.0555	37	295	306 LYFLQCETCHSR		

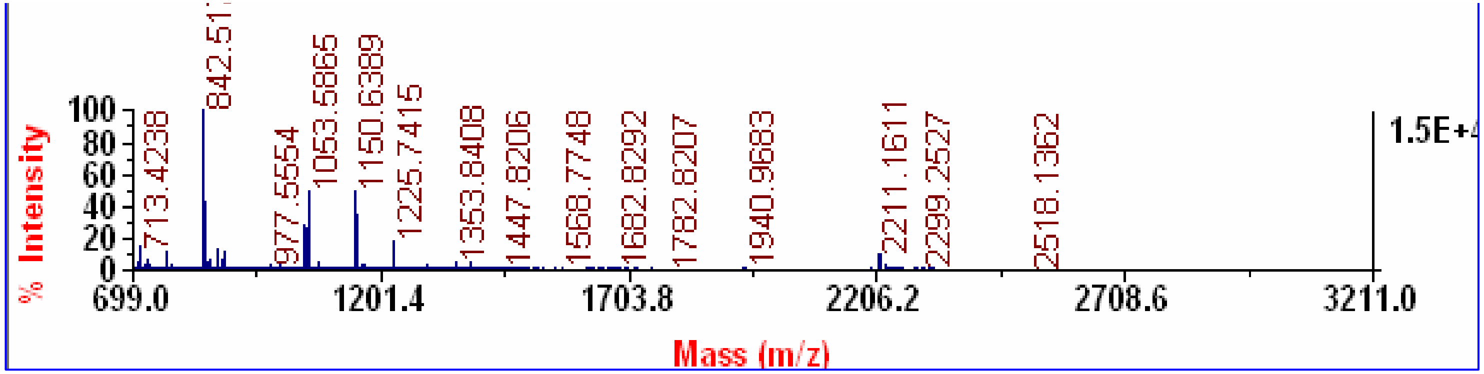
MS/MS Fragmentation of DYTYEELLNR (1315.691, 1+)



Spot No.3379 gi|6678131

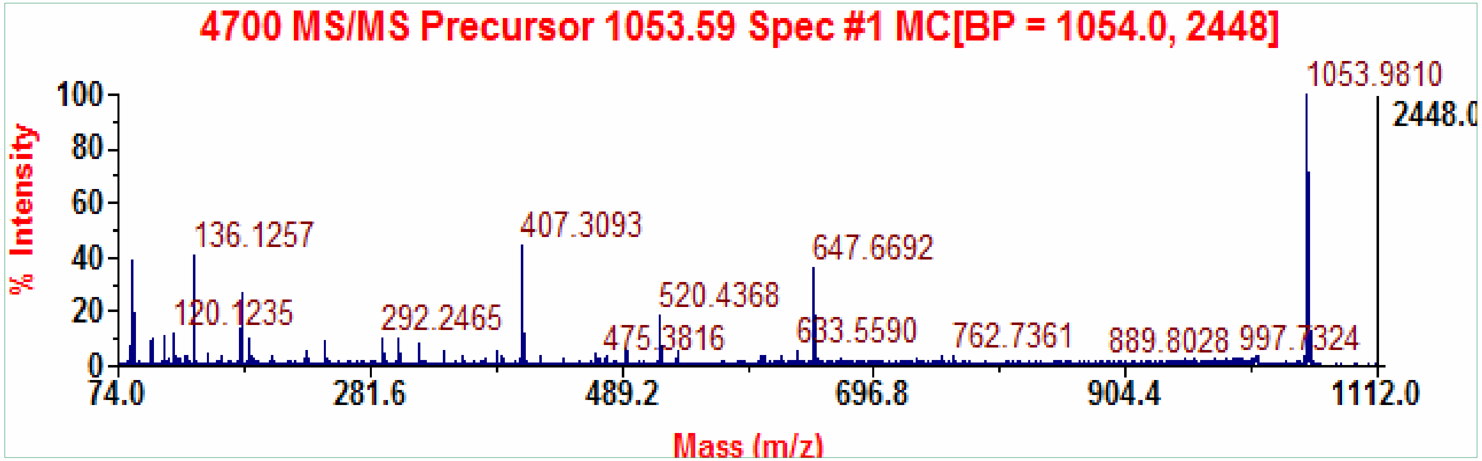
spermidine synthase [Mus musculus]

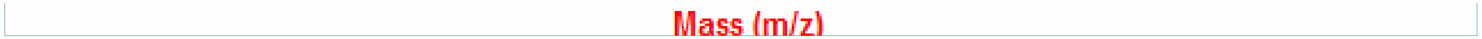




Calc. Mass	Obsrv.Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %
1053.5728	**1053.5862**	0.0134	13	48	55	YQDILVFR	27	42.017
1053.5728	**1053.5862**	0.0134	13	48	55	YQDILVFR		
1150.6255	**1150.6385**	0.013	11	286	295	AAFVLPEFTR	19	0
1150.6255	**1150.6385**	0.013	11	286	295	AAFVLPEFTR		
1225.7262	**1225.7413**	0.0151	12	97	109	VLIIGGGDGGVLR	31	79.895
1225.7262	**1225.7413**	0.0151	12	97	109	VLIIGGGDGGVLR		
1296.7059	**1296.7186**	0.0127	10	46	55	SRYQDILVFR		
1343.6664	**1343.7051**	0.0387	29	136	148	FLPGMAVGFSSSK		
1353.8212	**1353.8406**	0.0194	14	96	109	KVLIIGGGDGGVLR	5	0
1353.8212	**1353.8406**	0.0194	14	96	109	KVLIIGGGDGGVLR		
2233.0496	**2233.1653**	0.1157	52	278	295	YYNSDMHRAAFVLPEFTR		

MS/MS Fragmentation of YQDILVFR (1053.5862, 1+)





MS/MS Fragmentation of VLIIGGGDGGVLR (1225.7413, 1+)