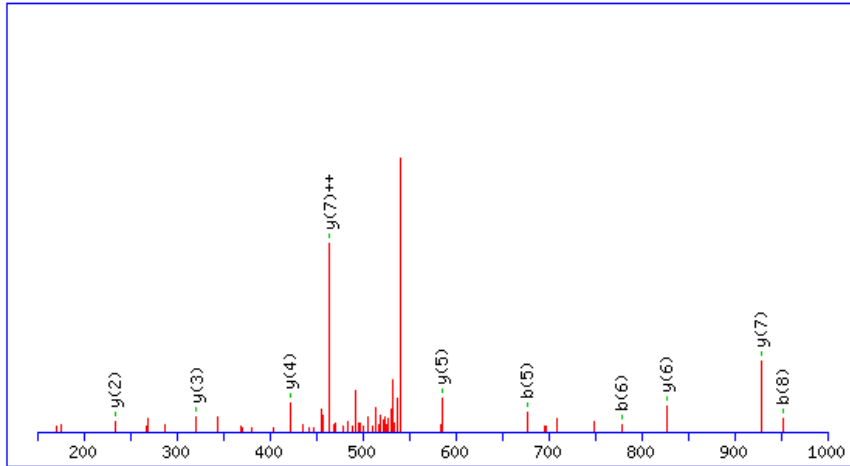


MS/MS Fragmentation of **AVTKYTSSK**

Found in **IPI00111957**, Histone H2B type 1-A (Mus musculus)

Match to Query 15067: 1097.572048 from (549.793300, 2+) intensity (1858.7252)



Monoisotopic mass of neutral peptide Mr(calc): 1097.5717

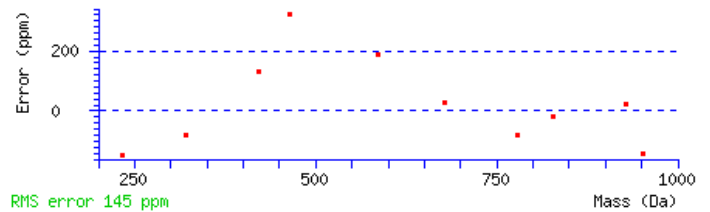
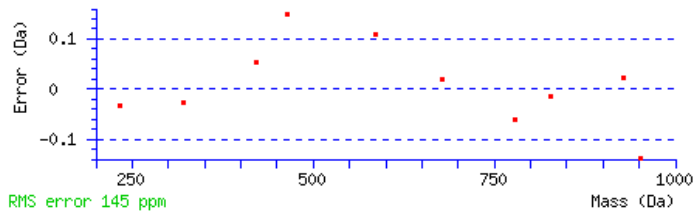
Variable modifications:

K4 : GlyGly (K)

Ions Score: 47 Expect: 0.002

Matches : 10/84 fragment ions using 16 most intense peaks

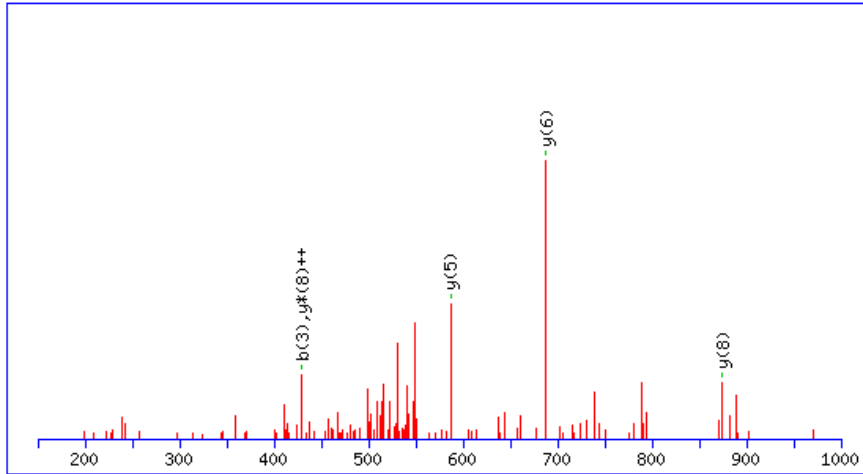
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							9
2	171.1128	86.0600					V	1027.5419	514.2746	1010.5153	505.7613	1009.5313	505.2693	8
3	272.1605	136.5839			254.1499	127.5786	T	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	7
4	514.2984	257.6528	497.2718	249.1396	496.2878	248.6475	K	827.4258	414.2165	810.3992	405.7032	809.4152	405.2112	6
5	677.3617	339.1845	660.3352	330.6712	659.3511	330.1792	Y	585.2879	293.1476	568.2613	284.6343	567.2773	284.1423	5
6	778.4094	389.7083	761.3828	381.1951	760.3988	380.7030	T	422.2245	211.6159	405.1980	203.1026	404.2140	202.6106	4
7	865.4414	433.2243	848.4149	424.7111	847.4308	424.2191	S	321.1769	161.0921	304.1503	152.5788	303.1663	152.0868	3
8	952.4734	476.7404	935.4469	468.2271	934.4629	467.7351	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
9							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **KSVTEGSSK**

Found in **IPI00119808**, ATP-dependent Clp protease ATP-binding subunit clpX-like mitochondrial (Mus musculus)

Match to Query 16051: 1115.491648 from (558.753100, 2+) intensity (3090.5637)



Monoisotopic mass of neutral peptide Mr(calc): 1115.4860

Variable modifications:

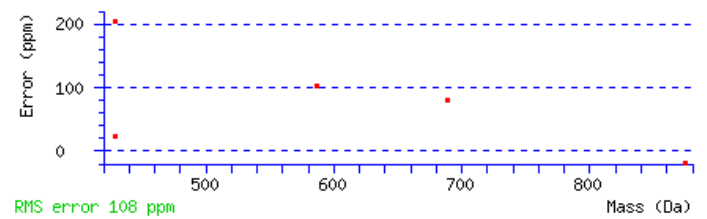
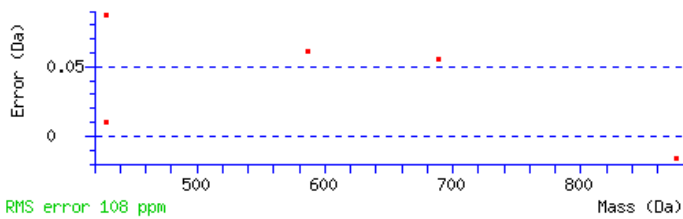
K1 : GlyGly (K)

S8 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 12 Expect: 10

Matches : 5/140 fragment ions using 8 most intense peaks

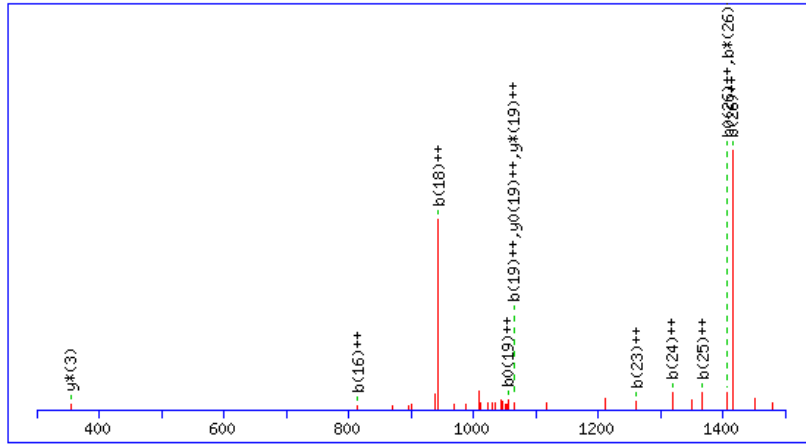
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							9
2	330.1772	165.5922	313.1506	157.0790	312.1666	156.5870	S	874.3554	437.6813	857.3288	429.1680	856.3448	428.6760	8
3	429.2456	215.1264	412.2191	206.6132	411.2350	206.1212	V	787.3233	394.1653	770.2968	385.6520	769.3128	385.1600	7
4	530.2933	265.6503	513.2667	257.1370	512.2827	256.6450	T	688.2549	344.6311	671.2284	336.1178	670.2444	335.6258	6
5	659.3359	330.1716	642.3093	321.6583	641.3253	321.1663	E	587.2072	294.1073	570.1807	285.5940	569.1967	285.1020	5
6	716.3573	358.6823	699.3308	350.1690	698.3468	349.6770	G	458.1647	229.5860	441.1381	221.0727	440.1541	220.5807	4
7	803.3894	402.1983	786.3628	393.6850	785.3788	393.1930	S	401.1432	201.0752	384.1166	192.5620	383.1326	192.0700	3
8	970.3877	485.6975	953.3612	477.1842	952.3772	476.6922	S	314.1112	157.5592	297.0846	149.0459	296.1006	148.5539	2
9							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **MDNPSSDPLPSTLSGEEKPLALLPPVPR**

Found in **IPI00121173**, Zinc finger protein 524 (Mus musculus)

Match to Query 73205: 3200.583372 from (1067.868400, 3+) intensity (1185.8872)



Monoisotopic mass of neutral peptide Mr(calc): 3200.5911

Variable modifications:

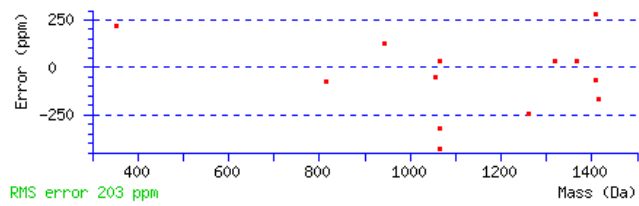
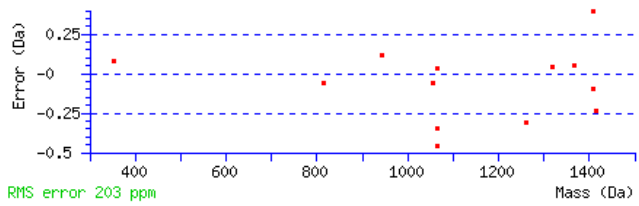
N3 : Deamidated (NQ)

K19 : GlyGly (K)

Ions Score: 28 Expect: 0.48

Matches : 13/308 fragment ions using 19 most intense peaks

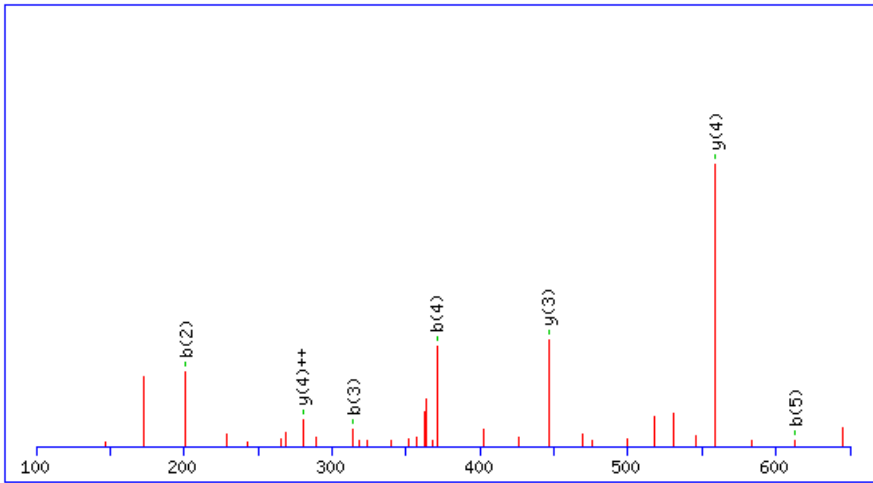
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275					M							29
2	247.0747	124.0410			229.0641	115.0357	D	3070.5579	1535.7826	3053.5314	1527.2693	3052.5473	1526.7773	28
3	362.1016	181.5545	345.0751	173.0412	344.0911	172.5492	N	2955.5310	1478.2691	2938.5044	1469.7558	2937.5204	1469.2638	27
4	459.1544	230.0808	442.1279	221.5676	441.1438	221.0756	P	2840.5040	1420.7556	2823.4775	1412.2424	2822.4934	1411.7504	26
5	546.1864	273.5969	529.1599	265.0836	528.1759	264.5916	S	2743.4513	1372.2293	2726.4247	1363.7160	2725.4407	1363.2240	25
6	633.2185	317.1129	616.1919	308.5996	615.2079	308.1076	S	2656.4192	1328.7132	2639.3927	1320.2000	2638.4087	1319.7080	24
7	748.2454	374.6263	731.2189	366.1131	730.2348	365.6211	D	2569.3872	1285.1972	2552.3606	1276.6840	2551.3766	1276.1920	23
8	845.2982	423.1527	828.2716	414.6395	827.2876	414.1474	P	2454.3603	1227.6838	2437.3337	1219.1705	2436.3497	1218.6785	22
9	958.3822	479.6948	941.3557	471.1815	940.3717	470.6895	L	2357.3075	1179.1574	2340.2809	1170.6441	2339.2969	1170.1521	21
10	1055.4350	528.2211	1038.4085	519.7079	1037.4244	519.2159	P	2244.2234	1122.6154	2227.1969	1114.1021	2226.2129	1113.6101	20
11	1142.4670	571.7372	1125.4405	563.2239	1124.4565	562.7319	S	2147.1707	1074.0890	2130.1441	1065.5757	2129.1601	1065.0837	19
12	1243.5147	622.2610	1226.4882	613.7477	1225.5041	613.2557	T	2060.1386	1030.5730	2043.1121	1022.0597	2042.1281	1021.5677	18
13	1356.5988	678.8030	1339.5722	670.2898	1338.5882	669.7977	L	1959.0910	980.0491	1942.0644	971.5358	1941.0804	971.0438	17
14	1443.6308	722.3190	1426.6043	713.8058	1425.6202	713.3138	S	1846.0069	923.5071	1828.9803	914.9938	1827.9963	914.5018	16
15	1500.6523	750.8298	1483.6257	742.3165	1482.6417	741.8245	G	1758.9749	879.9911	1741.9483	871.4778	1740.9643	870.9858	15
16	1629.6949	815.3511	1612.6683	806.8378	1611.6843	806.3458	E	1701.9534	851.4803	1684.9268	842.9671	1683.9428	842.4751	14
17	1758.7375	879.8724	1741.7109	871.3591	1740.7269	870.8671	E	1572.9108	786.9590	1555.8843	778.4458	1554.9002	777.9538	13
18	1887.7800	944.3937	1870.7535	935.8804	1869.7695	935.3884	E	1443.8682	722.4377	1426.8417	713.9245	1425.8576	713.4325	12
19	2129.9179	1065.4626	2112.8914	1056.9493	2111.9074	1056.4573	K	1314.8256	657.9164	1297.7991	649.4032			11
20	2226.9707	1113.9890	2209.9441	1105.4757	2208.9601	1104.9837	P	1072.6877	536.8475	1055.6612	528.3342			10
21	2340.0548	1170.5310	2323.0282	1162.0177	2322.0442	1161.5257	L	975.6350	488.3211	958.6084	479.8078			9
22	2411.0919	1206.0496	2394.0653	1197.5363	2393.0813	1197.0443	A	862.5509	431.7791	845.5244	423.2658			8
23	2524.1759	1262.5916	2507.1494	1254.0783	2506.1654	1253.5863	L	791.5138	396.2605	774.4872	387.7473			7
24	2637.2600	1319.1336	2620.2335	1310.6204	2619.2494	1310.1284	L	678.4297	339.7185	661.4032	331.2052			6
25	2734.3128	1367.6600	2717.2862	1359.1467	2716.3022	1358.6547	P	565.3457	283.1765	548.3191	274.6632			5
26	2831.3655	1416.1864	2814.3390	1407.6731	2813.3550	1407.1811	P	468.2929	234.6501	451.2663	226.1368			4
27	2930.4339	1465.7206	2913.4074	1457.2073	2912.4234	1456.7153	V	371.2401	186.1237	354.2136	177.6104			3
28	3027.4867	1514.2470	3010.4602	1505.7337	3009.4761	1505.2417	P	272.1717	136.5895	255.1452	128.0762			2
29							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **SLIGKK**

Found in **IPI00124049**, Four and a half LIM domains protein 5 (Mus musculus)

Match to Query 1571: 758.466868 from (380.240710, 2+) intensity (2867.9771)



Monoisotopic mass of neutral peptide Mr(calc): 758.4650

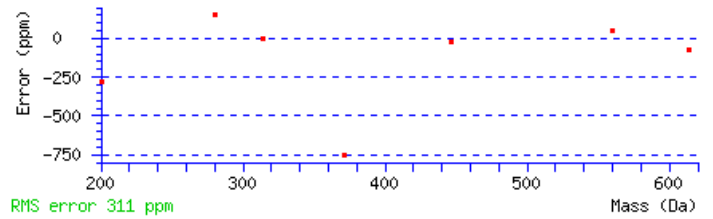
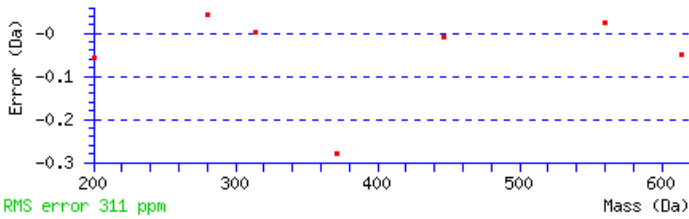
Variable modifications:

K5 : GlyGly (K)

Ions Score: 24 Expect: 0.25

Matches : 7/42 fragment ions using 15 most intense peaks

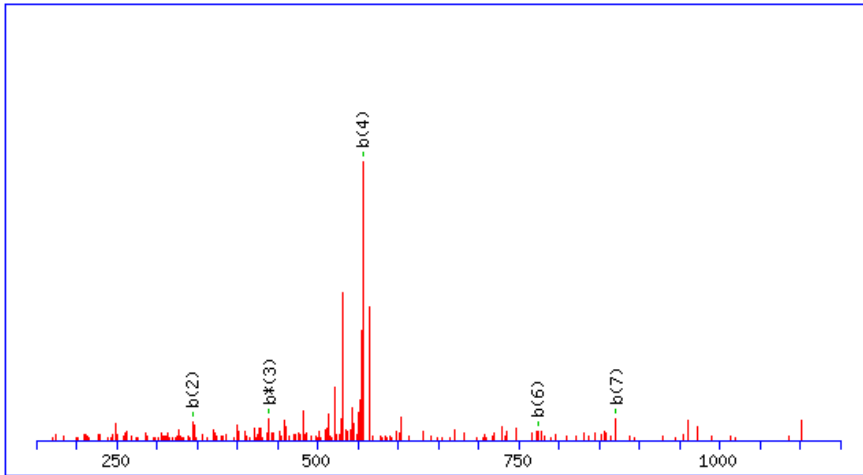
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S					6
2	201.1234	101.0653			183.1128	92.0600	L	672.4403	336.7238	655.4137	328.2105	5
3	314.2074	157.6074			296.1969	148.6021	I	559.3562	280.1817	542.3297	271.6685	4
4	371.2289	186.1181			353.2183	177.1128	G	446.2722	223.6397	429.2456	215.1264	3
5	613.3668	307.1870	596.3402	298.6738	595.3562	298.1817	K	389.2507	195.1290	372.2241	186.6157	2
6							K	147.1128	74.0600	130.0863	65.5468	1



MS/MS Fragmentation of **KTLVAFPQK**

Found in **IPI00128285**, Putative uncharacterized protein (Mus musculus)

Match to Query 18041: 1145.648928 from (573.831740, 2+) intensity (2066.5100)



Monoisotopic mass of neutral peptide Mr(calc): 1145.6444

Variable modifications:

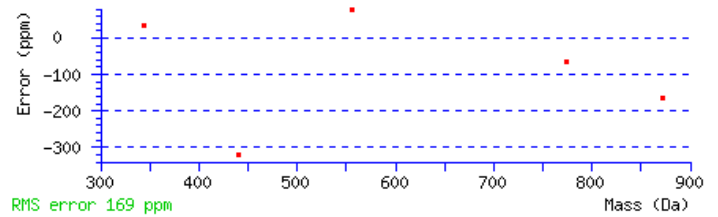
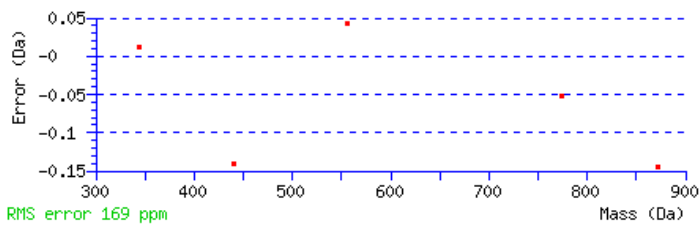
K1 : GlyGly (K)

Q8 : Deamidated (NQ)

Ions Score: 18 Expect: 0.84

Matches : 5/80 fragment ions using 10 most intense peaks

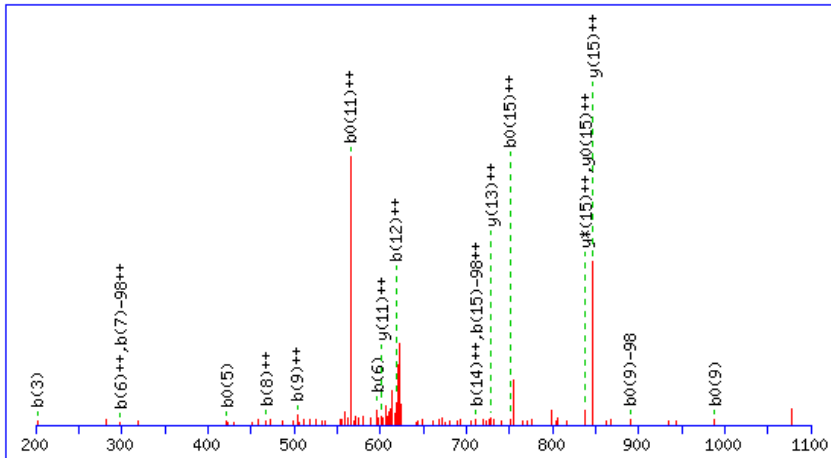
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							9
2	344.1928	172.6001	327.1663	164.0868	326.1823	163.5948	T	904.5138	452.7606	887.4873	444.2473	886.5033	443.7553	8
3	457.2769	229.1421	440.2504	220.6288	439.2663	220.1368	L	803.4662	402.2367	786.4396	393.7234			7
4	556.3453	278.6763	539.3188	270.1630	538.3348	269.6710	V	690.3821	345.6947	673.3556	337.1814			6
5	627.3824	314.1949	610.3559	305.6816	609.3719	305.1896	A	591.3137	296.1605	574.2871	287.6472			5
6	774.4509	387.7291	757.4243	379.2158	756.4403	378.7238	F	520.2766	260.6419	503.2500	252.1287			4
7	871.5036	436.2554	854.4771	427.7422	853.4931	427.2502	P	373.2082	187.1077	356.1816	178.5944			3
8	1000.5462	500.7767	983.5197	492.2635	982.5356	491.7715	Q	276.1554	138.5813	259.1288	130.0681			2
9							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **GSSTGRP KAAASEGVQVK**

Found in **IPI00131063**, Isoform A of Methyl-CpG-binding protein 2 (Mus musculus)

Match to Query 55994: 1893.901092 from (632.307640, 3+) intensity (4713.4600)



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1893.8945

Variable modifications:

T4 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

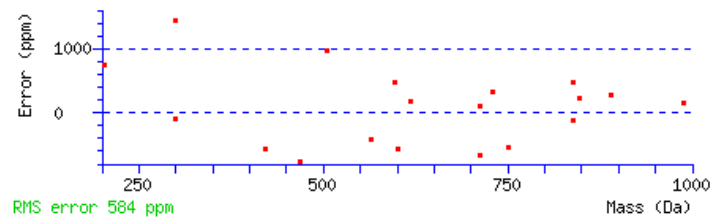
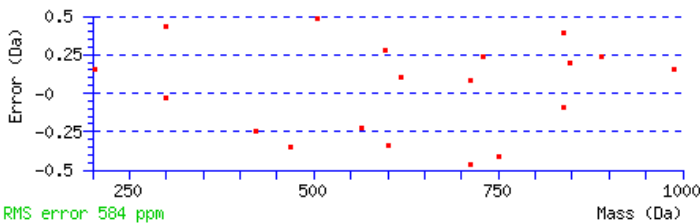
K8 : GlyGly (K)

Q16 : Deamidated (NQ)

Ions Score: 19 Expect: 4.2

Matches : 19/280 fragment ions using 33 most intense peaks

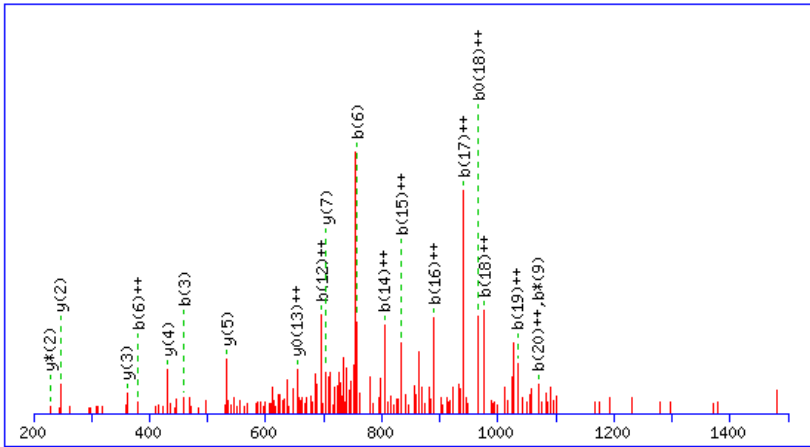
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							18
2	145.0608	73.0340			127.0502	64.0287	S	1837.8804	919.4438	1820.8538	910.9306	1819.8698	910.4385	17
3	202.0822	101.5448			184.0717	92.5395	G	1750.8484	875.9278	1733.8218	867.4145	1732.8378	866.9225	16
4	383.0962	192.0518			365.0857	183.0465	T	1693.8269	847.4171	1676.8003	838.9038	1675.8163	838.4118	15
5	440.1177	220.5625			422.1071	211.5572	G	1512.8129	756.9101	1495.7863	748.3968	1494.8023	747.9048	14
6	596.2188	298.6130	579.1923	290.0998	578.2083	289.6078	R	1455.7914	728.3993	1438.7649	719.8861	1437.7809	719.3941	13
7	693.2716	347.1394	676.2450	338.6262	675.2610	338.1341	P	1299.6903	650.3488	1282.6638	641.8355	1281.6797	641.3435	12
8	935.4095	468.2084	918.3829	459.6951	917.3989	459.2031	K	1202.6375	601.8224	1185.6110	593.3091	1184.6270	592.8171	11
9	1006.4466	503.7269	989.4200	495.2137	988.4360	494.7216	A	960.4997	480.7535	943.4731	472.2402	942.4891	471.7482	10
10	1077.4837	539.2455	1060.4572	530.7322	1059.4731	530.2402	A	889.4625	445.2349	872.4360	436.7216	871.4520	436.2296	9
11	1148.5208	574.7640	1131.4943	566.2508	1130.5102	565.7588	A	818.4254	409.7164	801.3989	401.2031	800.4149	400.7111	8
12	1235.5528	618.2801	1218.5263	609.7668	1217.5423	609.2748	S	747.3883	374.1978	730.3618	365.6845	729.3777	365.1925	7
13	1364.5954	682.8014	1347.5689	674.2881	1346.5849	673.7961	E	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
14	1421.6169	711.3121	1404.5903	702.7988	1403.6063	702.3068	G	531.3137	266.1605	514.2871	257.6472			5
15	1520.6853	760.8463	1503.6588	752.3330	1502.6747	751.8410	V	474.2922	237.6498	457.2657	229.1365			4
16	1649.7279	825.3676	1632.7014	816.8543	1631.7173	816.3623	Q	375.2238	188.1155	358.1973	179.6023			3
17	1748.7963	874.9018	1731.7698	866.3885	1730.7858	865.8965	V	246.1812	123.5942	229.1547	115.0810			2
18							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **KICALDDNVCMAFAGLTADAR**

Found in **IPI00131406**, Proteasome subunit alpha type-7 (Mus musculus)

Match to Query 66300: 2311.079772 from (771.367200, 3+) intensity (1362.4364)



Monoisotopic mass of neutral peptide Mr(calc): 2311.0759

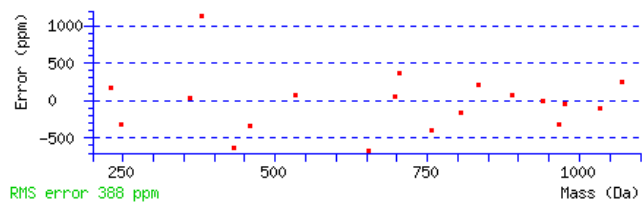
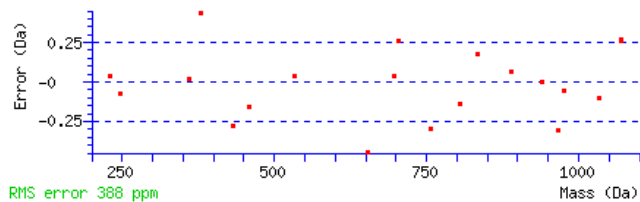
Variable modifications:

K1 : GlyGly (K)

Ions Score: 45 Expect: 0.015

Matches : 20/226 fragment ions using 36 most intense peaks

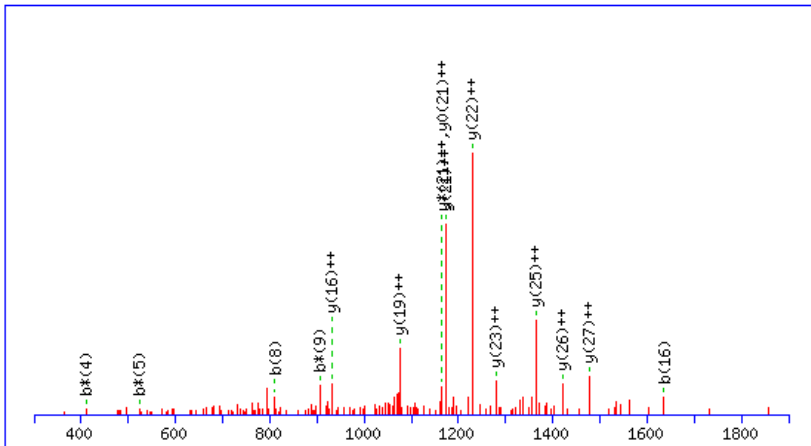
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							21
2	356.2292	178.6183	339.2027	170.1050			I	2069.9453	1035.4763	2052.9187	1026.9630	2051.9347	1026.4710	20
3	459.2384	230.1228	442.2119	221.6096			C	1956.8612	978.9343	1939.8347	970.4210	1938.8507	969.9290	19
4	530.2755	265.6414	513.2490	257.1281			A	1853.8520	927.4297	1836.8255	918.9164	1835.8415	918.4244	18
5	643.3596	322.1834	626.3330	313.6702			L	1782.8149	891.9111	1765.7884	883.3978	1764.8044	882.9058	17
6	758.3865	379.6969	741.3600	371.1836	740.3760	370.6916	D	1669.7309	835.3691	1652.7043	826.8558	1651.7203	826.3638	16
7	873.4135	437.2104	856.3869	428.6971	855.4029	428.2051	D	1554.7039	777.8556	1537.6774	769.3423	1536.6934	768.8503	15
8	987.4564	494.2318	970.4299	485.7186	969.4458	485.2266	N	1439.6770	720.3421	1422.6504	711.8289	1421.6664	711.3368	14
9	1086.5248	543.7660	1069.4983	535.2528	1068.5143	534.7608	V	1325.6341	663.3207	1308.6075	654.8074	1307.6235	654.3154	13
10	1189.5340	595.2706	1172.5075	586.7574	1171.5234	586.2654	C	1226.5656	613.7865	1209.5391	605.2732	1208.5551	604.7812	12
11	1320.5745	660.7909	1303.5479	652.2776	1302.5639	651.7856	M	1123.5565	562.2819	1106.5299	553.7686	1105.5459	553.2766	11
12	1391.6116	696.3094	1374.5851	687.7962	1373.6010	687.3042	A	992.5160	496.7616	975.4894	488.2483	974.5054	487.7563	10
13	1538.6800	769.8436	1521.6535	761.3304	1520.6695	760.8384	F	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	9
14	1609.7171	805.3622	1592.6906	796.8489	1591.7066	796.3569	A	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	8
15	1666.7386	833.8729	1649.7120	825.3597	1648.7280	824.8677	G	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	7
16	1779.8227	890.4150	1762.7961	881.9017	1761.8121	881.4097	L	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
17	1880.8703	940.9388	1863.8438	932.4255	1862.8598	931.9335	T	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	5
18	1951.9075	976.4574	1934.8809	967.9441	1933.8969	967.4521	A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
19	2066.9344	1033.9708	2049.9078	1025.4576	2048.9238	1024.9656	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
20	2137.9715	1069.4894	2120.9450	1060.9761	2119.9609	1060.4841	A	246.1561	123.5817	229.1295	115.0684			2
21							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **AQLNIGNVLPVGTMPGEGTIVCCLEEKPGDR**

Found in **IPI00137787**, 60S ribosomal protein L8 (Mus musculus)

Match to Query 73359: 3266.611572 from (1089.877800, 3+) intensity (1493.0007)



Monoisotopic mass of neutral peptide Mr(calc): 3266.6097

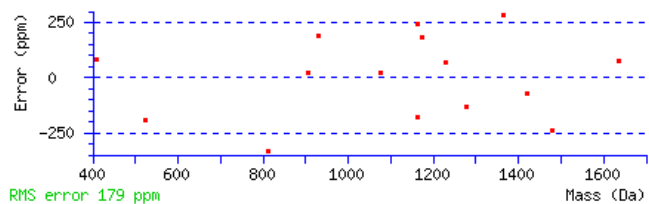
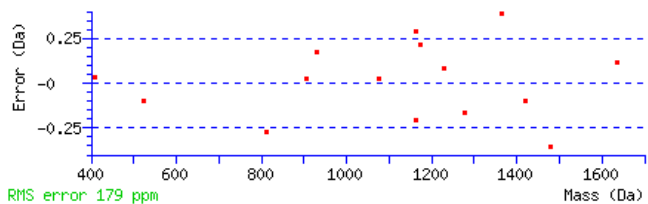
Variable modifications:

K26 : GlyGly (K)

Ions Score: 32 Expect: 0.18

Matches : 15/320 fragment ions using 28 most intense peaks

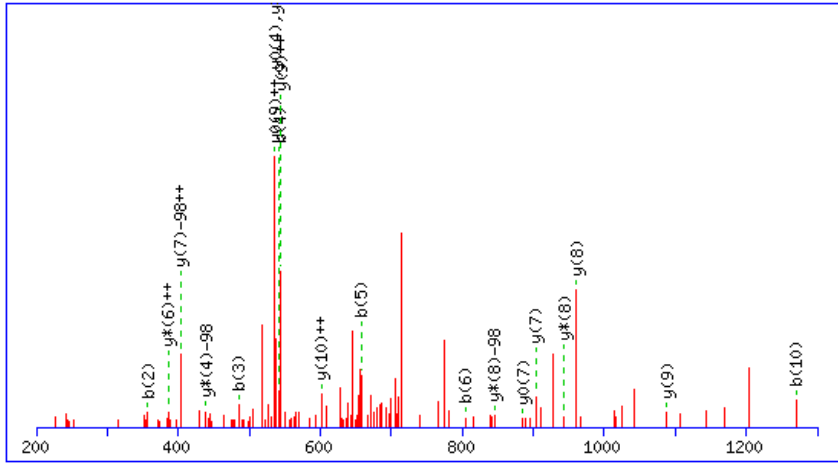
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							30
2	200.1030	100.5551	183.0764	92.0418			Q	3196.5799	1598.7936	3179.5534	1590.2803	3178.5694	1589.7883	29
3	313.1870	157.0972	296.1605	148.5839			L	3068.5213	1534.7643	3051.4948	1526.2510	3050.5108	1525.7590	28
4	427.2300	214.1186	410.2034	205.6053			N	2955.4373	1478.2223	2938.4107	1469.7090	2937.4267	1469.2170	27
5	540.3140	270.6606	523.2875	262.1474			I	2841.3943	1421.2008	2824.3678	1412.6875	2823.3838	1412.1955	26
6	597.3355	299.1714	580.3089	290.6581			G	2728.3103	1364.6588	2711.2837	1356.1455	2710.2997	1355.6535	25
7	711.3784	356.1928	694.3519	347.6796			N	2671.2888	1336.1480	2654.2623	1327.6348	2653.2783	1327.1428	24
8	810.4468	405.7271	793.4203	397.2138			V	2557.2459	1279.1266	2540.2193	1270.6133	2539.2353	1270.1213	23
9	923.5309	462.2691	906.5043	453.7558			L	2458.1775	1229.5924	2441.1509	1221.0791	2440.1669	1220.5871	22
10	1020.5837	510.7955	1003.5571	502.2822			P	2345.0934	1173.0503	2328.0669	1164.5371	2327.0829	1164.0451	21
11	1119.6521	560.3297	1102.6255	551.8164			V	2248.0407	1124.5240	2231.0141	1116.0107	2230.0301	1115.5187	20
12	1176.6735	588.8404	1159.6470	580.3271			G	2148.9722	1074.9898	2131.9457	1066.4765	2130.9617	1065.9845	19
13	1277.7212	639.3642	1260.6947	630.8510	1259.7106	630.3590	T	2091.9508	1046.4790	2074.9242	1037.9658	2073.9402	1037.4737	18
14	1408.7617	704.8845	1391.7351	696.3712	1390.7511	695.8792	M	1990.9031	995.9552	1973.8765	987.4419	1972.8925	986.9499	17
15	1505.8145	753.4109	1488.7879	744.8976	1487.8039	744.4056	P	1859.8626	930.4349	1842.8361	921.9217	1841.8520	921.4297	16
16	1634.8571	817.9322	1617.8305	809.4189	1616.8465	808.9269	E	1762.8098	881.9086	1745.7833	873.3953	1744.7993	872.9033	15
17	1691.8785	846.4429	1674.8520	837.9296	1673.8680	837.4376	G	1633.7673	817.3873	1616.7407	808.8740	1615.7567	808.3820	14
18	1792.9262	896.9667	1775.8996	888.4535	1774.9156	887.9615	T	1576.7458	788.8765	1559.7192	780.3633	1558.7352	779.8713	13
19	1906.0103	953.5088	1888.9837	944.9955	1887.9997	944.5035	I	1475.6981	738.3527	1458.6716	729.8394	1457.6875	729.3474	12
20	2005.0787	1003.0430	1988.0521	994.5297	1987.0681	994.0377	V	1362.6140	681.8107	1345.5875	673.2974	1344.6035	672.8054	11
21	2108.0879	1054.5476	2091.0613	1046.0343	2090.0773	1045.5423	C	1263.5456	632.2765	1246.5191	623.7632	1245.5351	623.2712	10
22	2211.0970	1106.0522	2194.0705	1097.5389	2193.0865	1097.0469	C	1160.5364	580.7719	1143.5099	572.2586	1142.5259	571.7666	9
23	2324.1811	1162.5942	2307.1546	1154.0809	2306.1705	1153.5889	L	1057.5273	529.2673	1040.5007	520.7540	1039.5167	520.2620	8
24	2453.2237	1227.1155	2436.1972	1218.6022	2435.2131	1218.1102	E	944.4432	472.7252	927.4167	464.2120	926.4326	463.7200	7
25	2582.2663	1291.6368	2565.2397	1283.1235	2564.2557	1282.6315	E	815.4006	408.2039	798.3741	399.6907	797.3900	399.1987	6
26	2824.4042	1412.7057	2807.3776	1404.1925	2806.3936	1403.7004	K	686.3580	343.6826	669.3315	335.1694	668.3474	334.6774	5
27	2921.4570	1461.2321	2904.4304	1452.7188	2903.4464	1452.2268	P	444.2201	222.6137	427.1936	214.1004	426.2096	213.6084	4
28	2978.4784	1489.7428	2961.4519	1481.2296	2960.4678	1480.7376	G	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
29	3093.5054	1547.2563	3076.4788	1538.7430	3075.4948	1538.2510	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
30							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KNQGDFLSVR**

Found in **IPI00225419**, Isoform 2 of Tyrosine-protein phosphatase non-receptor type 6 (Mus musculus)

Match to Query 35135: 1443.640128 from (722.827340, 2+) intensity (988.7264)



Monoisotopic mass of neutral peptide Mr(calc): 1443.6507

Variable modifications:

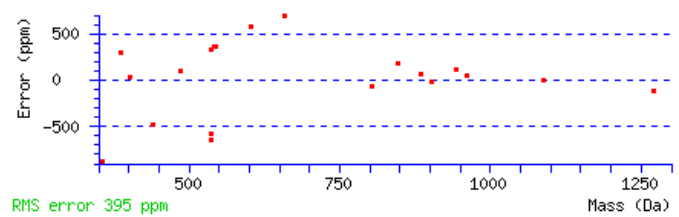
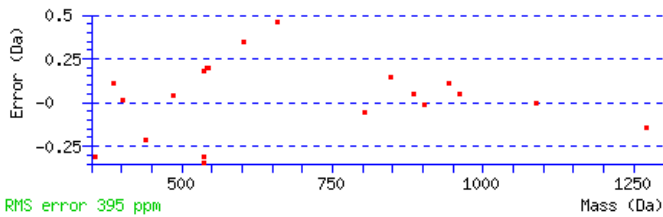
K1 : GlyGly (K)

S9 : Phospho (ST), with neutral losses 0.0000 (shown in table), 97.9769

Ions Score: 16 Expect: 7.5

Matches : 20/168 fragment ions using 55 most intense peaks

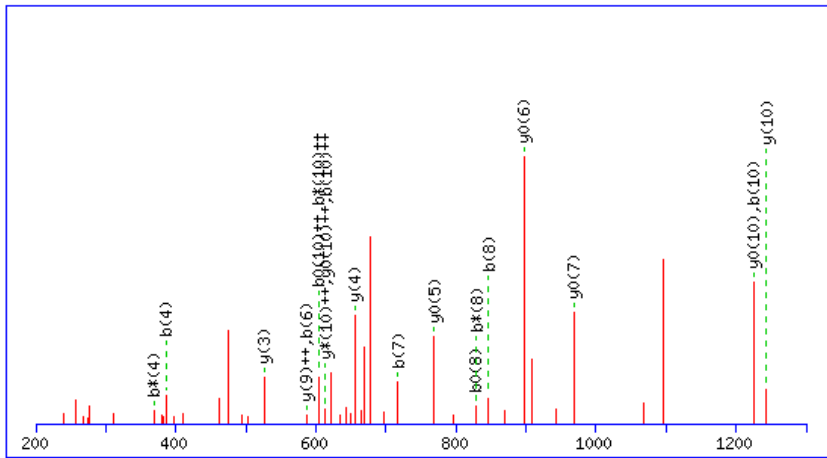
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							11
2	357.1881	179.0977	340.1615	170.5844			N	1202.5201	601.7637	1185.4936	593.2504	1184.5096	592.7584	10
3	485.2467	243.1270	468.2201	234.6137			Q	1088.4772	544.7422	1071.4507	536.2290	1070.4667	535.7370	9
4	542.2681	271.6377	525.2416	263.1244			G	960.4186	480.7130	943.3921	472.1997	942.4081	471.7077	8
5	657.2951	329.1512	640.2685	320.6379	639.2845	320.1459	D	903.3972	452.2022	886.3706	443.6890	885.3866	443.1969	7
6	804.3635	402.6854	787.3369	394.1721	786.3529	393.6801	F	788.3702	394.6888	771.3437	386.1755	770.3597	385.6835	6
7	891.3955	446.2014	874.3690	437.6881	873.3850	437.1961	S	641.3018	321.1545	624.2753	312.6413	623.2913	312.1493	5
8	1004.4796	502.7434	987.4530	494.2302	986.4690	493.7381	L	554.2698	277.6385	537.2432	269.1253	536.2592	268.6333	4
9	1171.4779	586.2426	1154.4514	577.7293	1153.4674	577.2373	S	441.1857	221.0965	424.1592	212.5832	423.1752	212.0912	3
10	1270.5464	635.7768	1253.5198	627.2635	1252.5358	626.7715	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **QAADAEMEKHK**

Found in **IPI00229509**, Isoform PLEC-1I of Plectin-1 (Mus musculus)

Match to Query 31225: 1370.629008 from (686.321780, 2+) intensity (3835.4539)



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1370.6248

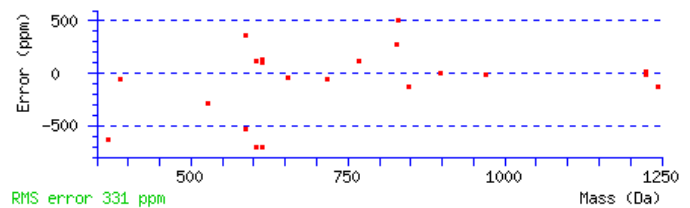
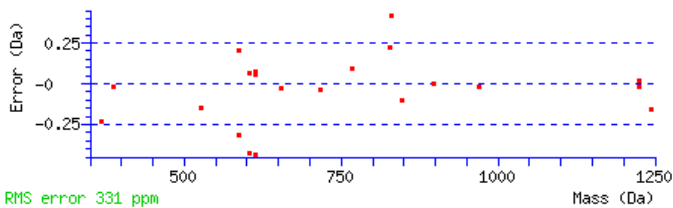
Variable modifications:

K9 : GlyGly (K)

Ions Score: 21 Expect: 1.9

Matches : 21/108 fragment ions using 34 most intense peaks

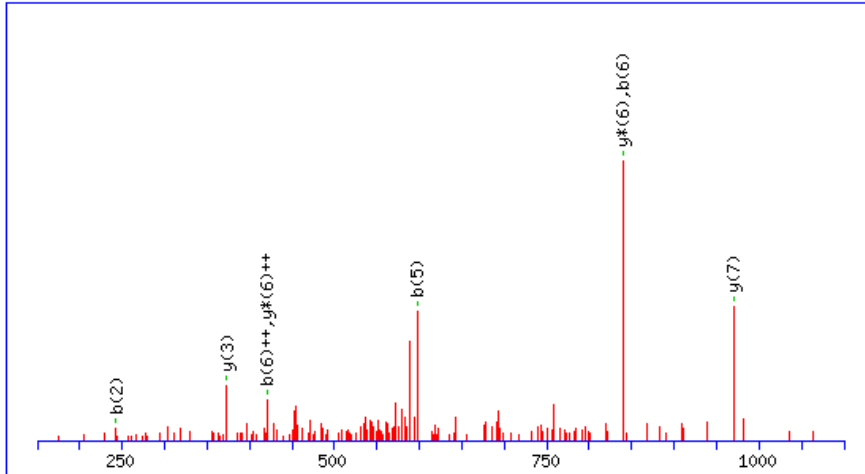
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							11
2	200.1030	100.5551	183.0764	92.0418			A	1243.5736	622.2904	1226.5470	613.7771	1225.5630	613.2851	10
3	271.1401	136.0737	254.1135	127.5604			A	1172.5364	586.7719	1155.5099	578.2586	1154.5259	577.7666	9
4	386.1670	193.5872	369.1405	185.0739	368.1565	184.5819	D	1101.4993	551.2533	1084.4728	542.7400	1083.4888	542.2480	8
5	457.2041	229.1057	440.1776	220.5924	439.1936	220.1004	A	986.4724	493.7398	969.4458	485.2266	968.4618	484.7346	7
6	586.2467	293.6270	569.2202	285.1137	568.2362	284.6217	E	915.4353	458.2213	898.4087	449.7080	897.4247	449.2160	6
7	717.2872	359.1472	700.2607	350.6340	699.2767	350.1420	M	786.3927	393.7000	769.3661	385.1867	768.3821	384.6947	5
8	846.3298	423.6685	829.3033	415.1553	828.3192	414.6633	E	655.3522	328.1797	638.3257	319.6665	637.3416	319.1745	4
9	1088.4677	544.7375	1071.4412	536.2242	1070.4571	535.7322	K	526.3096	263.6584	509.2831	255.1452			3
10	1225.5266	613.2669	1208.5001	604.7537	1207.5160	604.2617	H	284.1717	142.5895	267.1452	134.0762			2
11							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **QINLQKQPK**

Found in **IPI00229884**, Serine/threonine-protein kinase PAK 2 (Mus musculus)

Match to Query 22095: 1210.673988 from (606.344270, 2+) intensity (2281.3484)



Monoisotopic mass of neutral peptide Mr(calc): 1210.6669

Variable modifications:

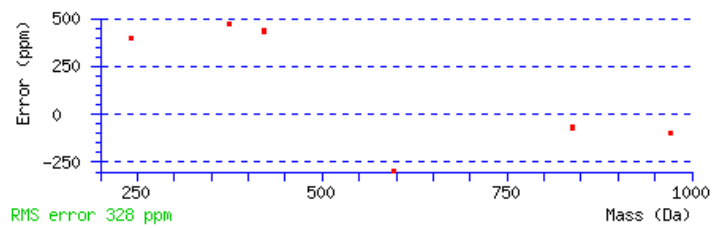
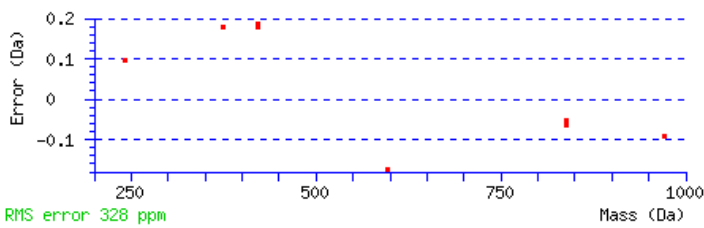
K6 : GlyGly (K)

Q7 : Deamidated (NQ)

Ions Score: 16 Expect: 1.5

Matches : 8/64 fragment ions using 9 most intense peaks

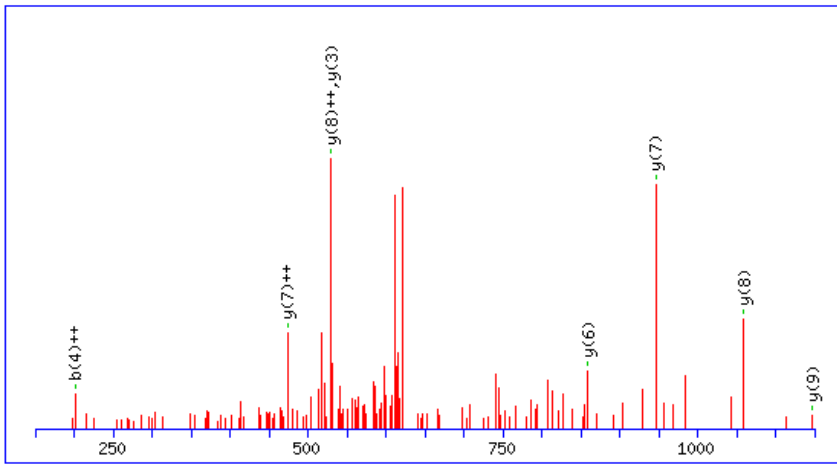
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233	Q					9
2	242.1499	121.5786	225.1234	113.0653	I	1083.6157	542.3115	1066.5891	533.7982	8
3	356.1928	178.6001	339.1663	170.0868	N	970.5316	485.7694	953.5051	477.2562	7
4	469.2769	235.1421	452.2504	226.6288	L	856.4887	428.7480	839.4621	420.2347	6
5	597.3355	299.1714	580.3089	290.6581	Q	743.4046	372.2060	726.3781	363.6927	5
6	839.4734	420.2403	822.4468	411.7271	K	615.3461	308.1767	598.3195	299.6634	4
7	968.5160	484.7616	951.4894	476.2483	Q	373.2082	187.1077	356.1816	178.5944	3
8	1065.5687	533.2880	1048.5422	524.7747	P	244.1656	122.5864	227.1390	114.0731	2
9					K	147.1128	74.0600	130.0863	65.5468	1



MS/MS Fragmentation of **L₁S₁L₁S₁Q₁K₁L₁R**

Found in **IPI00331223**, Isoform 1 of Striated muscle-specific serine/threonine-protein kinase (Mus musculus)

Match to Query 24976: 1258.713108 from (630.363830, 2+) intensity (1462.8279)



Monoisotopic mass of neutral peptide Mr(calc): 1258.7245

Variable modifications:

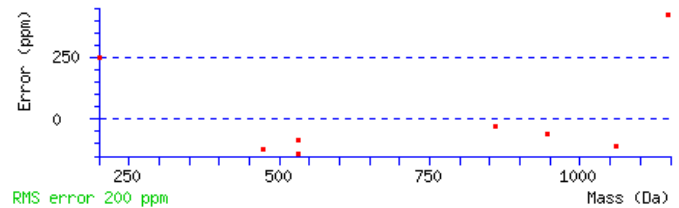
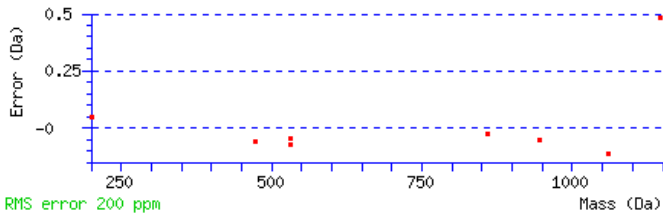
Q7 : Deamidated (NQ)

K8 : GlyGly (K)

Ions Score: 34 Expect: 0.019

Matches : 9/86 fragment ions using 10 most intense peaks

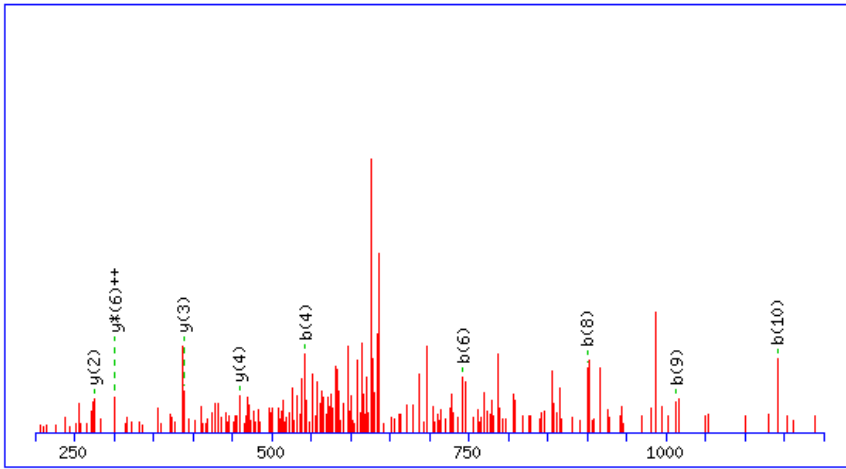
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							10
2	201.1234	101.0653			183.1128	92.0600	S	1146.6477	573.8275	1129.6212	565.3142	1128.6371	564.8222	9
3	314.2074	157.6074			296.1969	148.6021	L	1059.6157	530.3115	1042.5891	521.7982	1041.6051	521.3062	8
4	401.2395	201.1234			383.2289	192.1181	S	946.5316	473.7694	929.5051	465.2562	928.5211	464.7642	7
5	514.3235	257.6654			496.3130	248.6601	L	859.4996	430.2534	842.4730	421.7402	841.4890	421.2482	6
6	601.3556	301.1814			583.3450	292.1761	S	746.4155	373.7114	729.3890	365.1981	728.4050	364.7061	5
7	730.3981	365.7027	713.3716	357.1894	712.3876	356.6974	Q	659.3835	330.1954	642.3570	321.6821			4
8	972.5360	486.7717	955.5095	478.2584	954.5255	477.7664	K	530.3409	265.6741	513.3144	257.1608			3
9	1085.6201	543.3137	1068.5936	534.8004	1067.6095	534.3084	L	288.2030	144.6051	271.1765	136.0919			2
10							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KPDSEASALKK**

Found in **IPI00345676**, Isoform 1 of Chromodomain-helicase-DNA-binding protein 7 (Mus musculus)

Match to Query 26568: 1286.695288 from (644.354920, 2+) intensity (1686.8608)



Monoisotopic mass of neutral peptide Mr(calc): 1286.6830

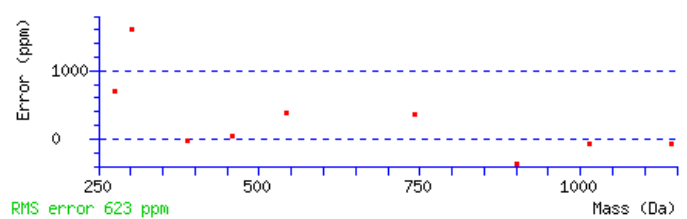
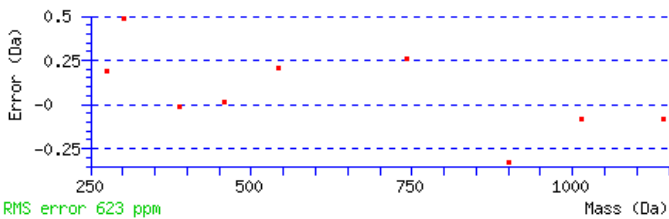
Variable modifications:

K1 : GlyGly (K)

Ions Score: 23 Expect: 0.73

Matches : 9/108 fragment ions using 20 most intense peaks

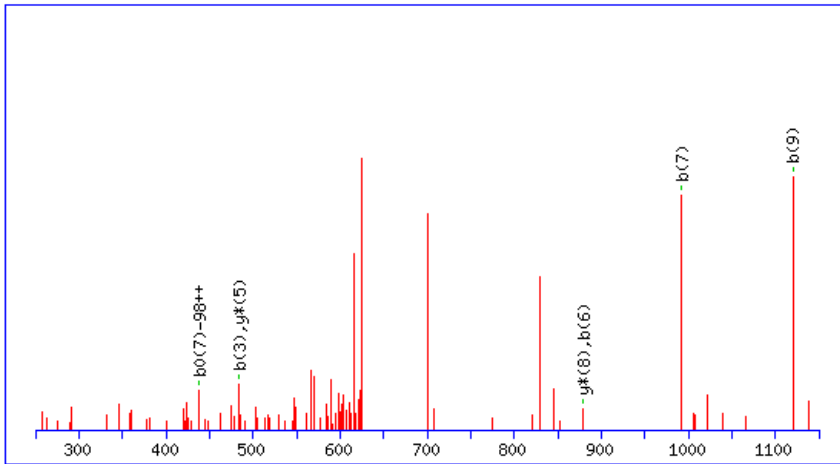
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							11
2	340.1979	170.6026	323.1714	162.0893			P	1045.5524	523.2798	1028.5259	514.7666	1027.5419	514.2746	10
3	455.2249	228.1161	438.1983	219.6028	437.2143	219.1108	D	948.4997	474.7535	931.4731	466.2402	930.4891	465.7482	9
4	542.2569	271.6321	525.2304	263.1188	524.2463	262.6268	S	833.4727	417.2400	816.4462	408.7267	815.4621	408.2347	8
5	671.2995	336.1534	654.2729	327.6401	653.2889	327.1481	E	746.4407	373.7240	729.4141	365.2107	728.4301	364.7187	7
6	742.3366	371.6719	725.3101	363.1587	724.3260	362.6667	A	617.3981	309.2027	600.3715	300.6894	599.3875	300.1974	6
7	829.3686	415.1880	812.3421	406.6747	811.3581	406.1827	S	546.3610	273.6841	529.3344	265.1709	528.3504	264.6788	5
8	900.4058	450.7065	883.3792	442.1932	882.3952	441.7012	A	459.3289	230.1681	442.3024	221.6548			4
9	1013.4898	507.2485	996.4633	498.7353	995.4792	498.2433	L	388.2918	194.6496	371.2653	186.1363			3
10	1141.5848	571.2960	1124.5582	562.7828	1123.5742	562.2907	K	275.2078	138.1075	258.1812	129.5942			2
11							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **KQLDSLLGAK**

Found in **IPI00346834**, Putative uncharacterized protein (Mus musculus)

Match to Query 25363: 1265.627548 from (633.821050, 2+) intensity (1787.2828)



Monoisotopic mass of neutral peptide Mr(calc): 1265.6380

Variable modifications:

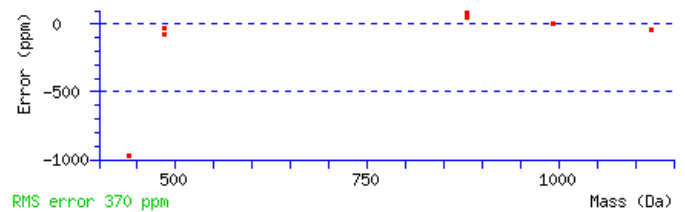
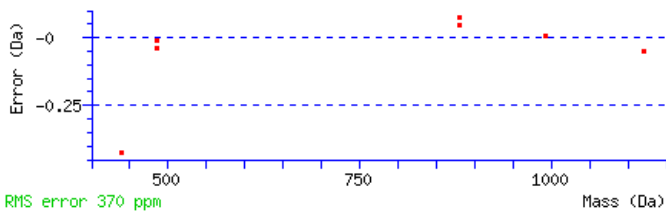
K1 : GlyGly (K)

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

Ions Score: 21 Expect: 1.4

Matches : 7/146 fragment ions using 9 most intense peaks

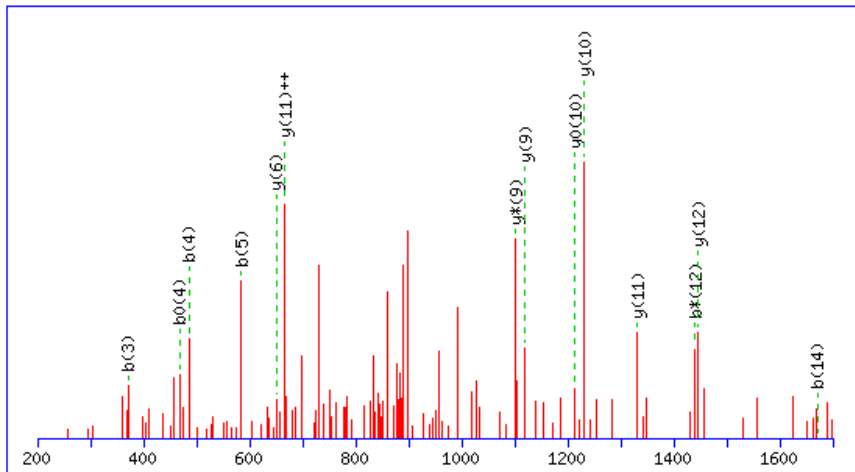
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							10
2	371.2037	186.1055	354.1772	177.5922			Q	1024.5075	512.7574	1007.4809	504.2441	1006.4969	503.7521	9
3	484.2878	242.6475	467.2613	234.1343			L	896.4489	448.7281	879.4223	440.2148	878.4383	439.7228	8
4	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	D	783.3648	392.1860	766.3383	383.6728	765.3542	383.1808	7
5	766.3131	383.6602	749.2866	375.1469	748.3025	374.6549	S	668.3379	334.6726	651.3113	326.1593	650.3273	325.6673	6
6	879.3972	440.2022	862.3706	431.6890	861.3866	431.1969	L	501.3395	251.1734	484.3130	242.6601			5
7	992.4812	496.7443	975.4547	488.2310	974.4707	487.7390	L	388.2554	194.6314	371.2289	186.1181			4
8	1049.5027	525.2550	1032.4762	516.7417	1031.4921	516.2497	G	275.1714	138.0893	258.1448	129.5761			3
9	1120.5398	560.7735	1103.5133	552.2603	1102.5293	551.7683	A	218.1499	109.5786	201.1234	101.0653			2
10							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **LCPDVLLKNTSTVDK**

Found in **IPI00354163**, Isoform 1 of Uncharacterized protein C12orf35 homolog (Mus musculus)

Match to Query 53045: 1815.932888 from (908.973720, 2+) intensity (505.8741)



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1815.9400

Variable modifications:

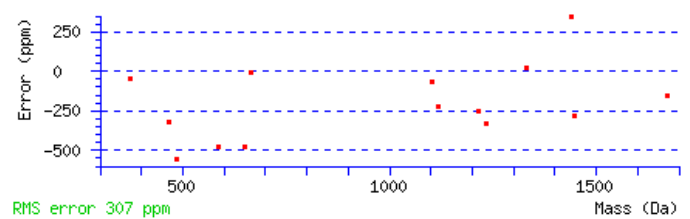
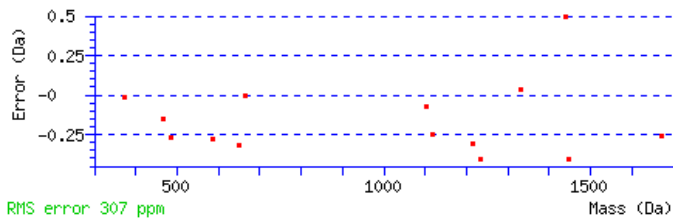
C2 : Carbamidomethyl (C)

K8 : GlyGly (K)

Ions Score: 19 Expect: 2.3

Matches : 14/146 fragment ions using 30 most intense peaks

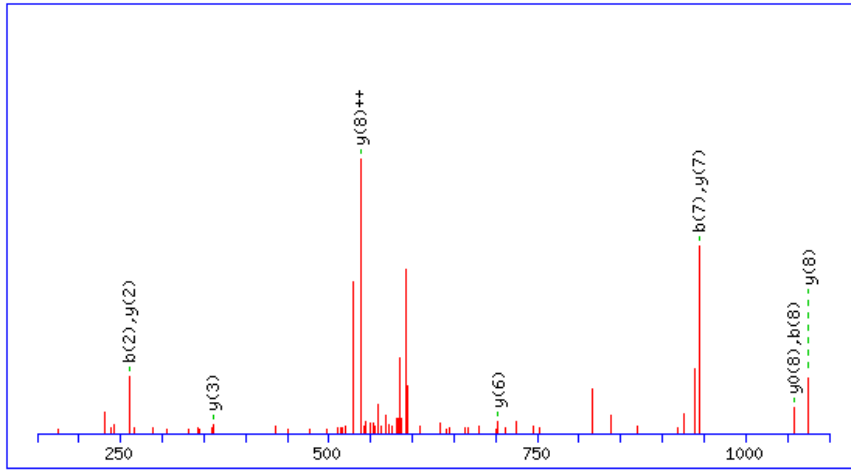
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							15
2	274.1220	137.5646					C	1703.8633	852.4353	1686.8367	843.9220	1685.8527	843.4300	14
3	371.1748	186.0910					P	1543.8326	772.4199	1526.8061	763.9067	1525.8220	763.4147	13
4	486.2017	243.6045			468.1911	234.5992	D	1446.7798	723.8936	1429.7533	715.3803	1428.7693	714.8883	12
5	585.2701	293.1387			567.2595	284.1334	V	1331.7529	666.3801	1314.7264	657.8668	1313.7423	657.3748	11
6	698.3542	349.6807			680.3436	340.6754	L	1232.6845	616.8459	1215.6579	608.3326	1214.6739	607.8406	10
7	811.4382	406.2228			793.4277	397.2175	L	1119.6004	560.3039	1102.5739	551.7906	1101.5899	551.2986	9
8	1053.5761	527.2917	1036.5496	518.7784	1035.5656	518.2864	K	1006.5164	503.7618	989.4898	495.2485	988.5058	494.7565	8
9	1167.6191	584.3132	1150.5925	575.7999	1149.6085	575.3079	N	764.3785	382.6929	747.3519	374.1796	746.3679	373.6876	7
10	1268.6667	634.8370	1251.6402	626.3237	1250.6562	625.8317	T	650.3355	325.6714	633.3090	317.1581	632.3250	316.6661	6
11	1355.6988	678.3530	1338.6722	669.8397	1337.6882	669.3477	S	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
12	1456.7464	728.8769	1439.7199	720.3636	1438.7359	719.8716	T	462.2558	231.6316	445.2293	223.1183	444.2453	222.6263	4
13	1555.8149	778.4111	1538.7883	769.8978	1537.8043	769.4058	V	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
14	1670.8418	835.9245	1653.8152	827.4113	1652.8312	826.9193	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **QMKNLLTLK**

Found in **IPI00380440**, Novel protein (Mus musculus)

Match to Query 21668: 1202.66688 from (602.340620, 2+) intensity (2720.2737)



Monoisotopic mass of neutral peptide Mr(calc): 1202.6692

Variable modifications:

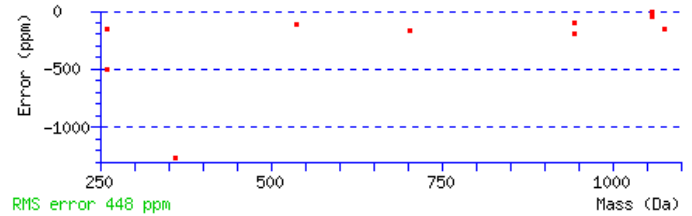
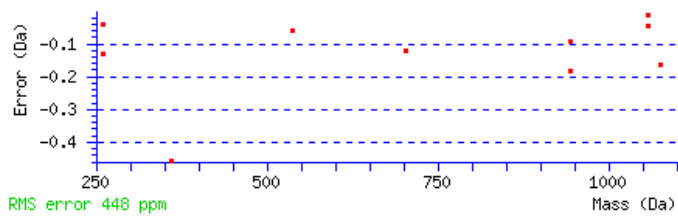
K3 : GlyGly (K)

N4 : Deamidated (NQ)

Ions Score: 37 Expect: 0.016

Matches : 10/80 fragment ions using 10 most intense peaks

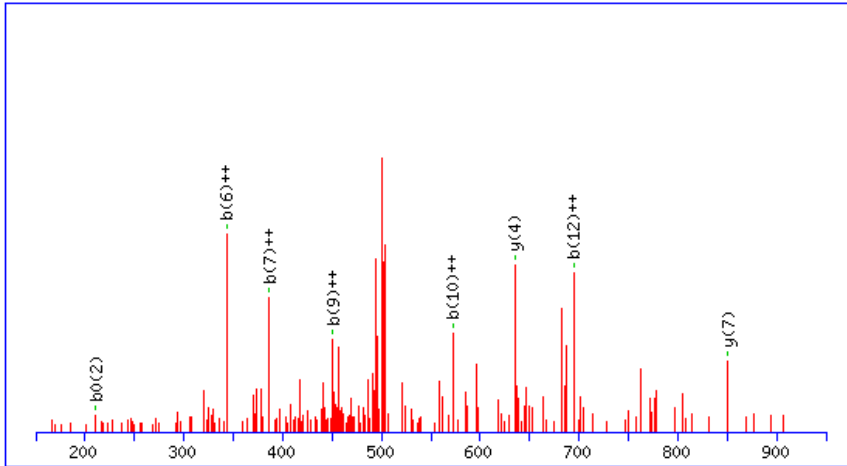
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							9
2	260.1063	130.5568	243.0798	122.0435			M	1075.6180	538.3126	1058.5914	529.7994	1057.6074	529.3074	8
3	502.2442	251.6258	485.2177	243.1125			K	944.5775	472.7924	927.5510	464.2791	926.5669	463.7871	7
4	617.2712	309.1392	600.2446	300.6259			N	702.4396	351.7234	685.4131	343.2102	684.4291	342.7182	6
5	730.3552	365.6813	713.3287	357.1680			L	587.4127	294.2100	570.3861	285.6967	569.4021	285.2047	5
6	843.4393	422.2233	826.4128	413.7100			L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
7	944.4870	472.7471	927.4604	464.2339	926.4764	463.7418	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
8	1057.5710	529.2892	1040.5445	520.7759	1039.5605	520.2839	L	260.1969	130.6021	243.1703	122.0888			2
9							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **DIDILNSAGKMDK**

Found in **IPI00396739**, SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 (*Mus musculus*)

Match to Query 40212: 1533.745122 from (512.255650, 3+) intensity (2175.5291)



Monoisotopic mass of neutral peptide Mr(calc): 1533.7344

Variable modifications:

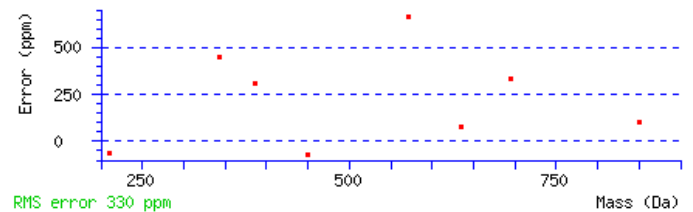
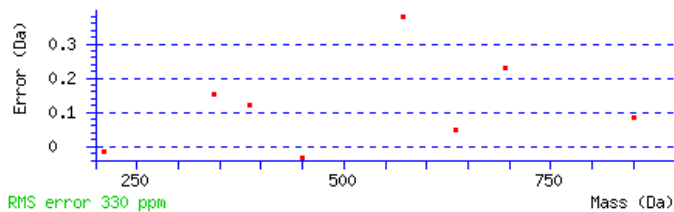
N6 : Deamidated (NQ)

K10 : GlyGly (K)

Ions Score: 20 Expect: 2.6

Matches : 8/132 fragment ions using 16 most intense peaks

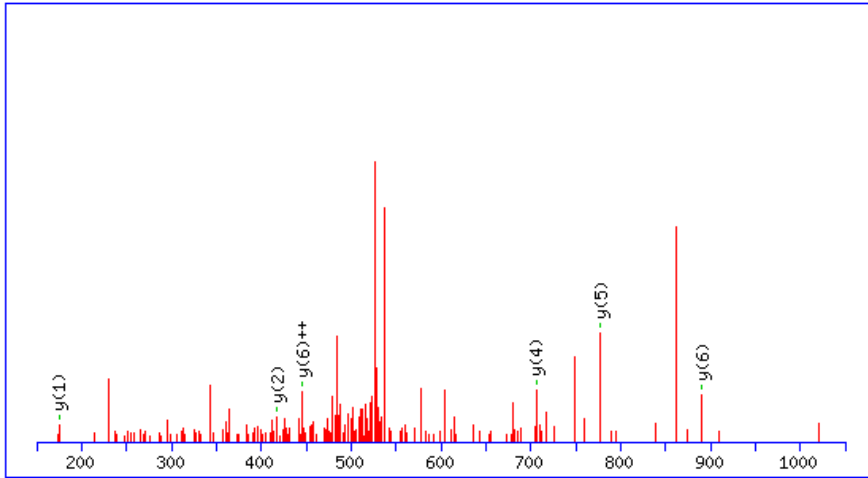
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207			98.0237	49.5155	D							13
2	229.1183	115.0628			211.1077	106.0575	I	1419.7148	710.3610	1402.6883	701.8478	1401.7042	701.3558	12
3	344.1452	172.5763			326.1347	163.5710	D	1306.6307	653.8190	1289.6042	645.3057	1288.6202	644.8137	11
4	457.2293	229.1183			439.2187	220.1130	I	1191.6038	596.3055	1174.5773	587.7923	1173.5932	587.3003	10
5	570.3134	285.6603			552.3028	276.6550	L	1078.5197	539.7635	1061.4932	531.2502	1060.5092	530.7582	9
6	685.3403	343.1738	668.3137	334.6605	667.3297	334.1685	N	965.4357	483.2215	948.4091	474.7082	947.4251	474.2162	8
7	772.3723	386.6898	755.3458	378.1765	754.3618	377.6845	S	850.4087	425.7080	833.3822	417.1947	832.3982	416.7027	7
8	843.4094	422.2084	826.3829	413.6951	825.3989	413.2031	A	763.3767	382.1920	746.3502	373.6787	745.3661	373.1867	6
9	900.4309	450.7191	883.4044	442.2058	882.4203	441.7138	G	692.3396	346.6734	675.3130	338.1602	674.3290	337.6681	5
10	1142.5688	571.7880	1125.5422	563.2748	1124.5582	562.7828	K	635.3181	318.1627	618.2916	309.6494	617.3076	309.1574	4
11	1273.6093	637.3083	1256.5827	628.7950	1255.5987	628.3030	M	393.1802	197.0938	376.1537	188.5805	375.1697	188.0885	3
12	1388.6362	694.8217	1371.6097	686.3085	1370.6257	685.8165	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
13							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **ISIAWCKR**

Found in **IPI00454114**, DNA topoisomerase 1 mitochondrial (Mus musculus)

Match to Query 14592: 1089.577588 from (545.796070, 2+) intensity (1719.6333)



Monoisotopic mass of neutral peptide Mr(calc) : 1089.5753

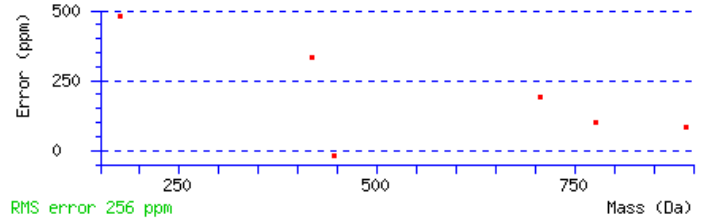
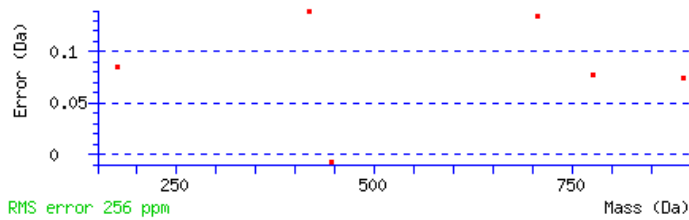
Variable modifications:

K7 : GlyGly (K)

Ions Score: 19 Expect: 1.5

Matches : 6/58 fragment ions using 17 most intense peaks

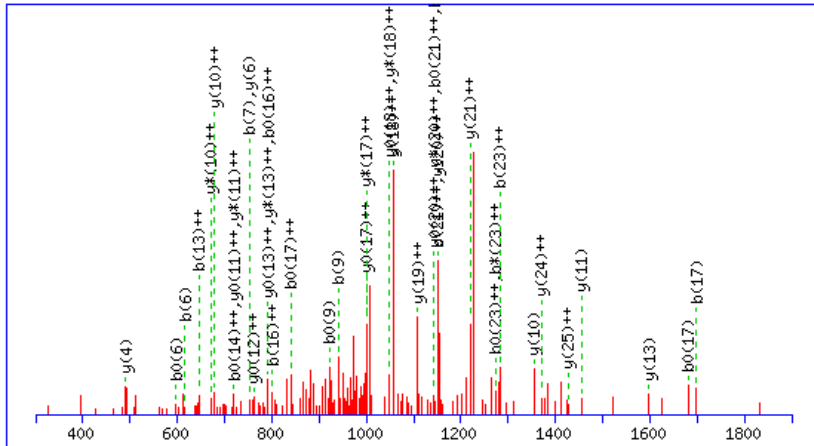
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							8
2	201.1234	101.0653			183.1128	92.0600	S	977.4985	489.2529	960.4720	480.7396	959.4880	480.2476	7
3	314.2074	157.6074			296.1969	148.6021	I	890.4665	445.7369	873.4400	437.2236			6
4	385.2445	193.1259			367.2340	184.1206	A	777.3825	389.1949	760.3559	380.6816			5
5	571.3239	286.1656			553.3133	277.1603	W	706.3453	353.6763	689.3188	345.1630			4
6	674.3330	337.6702			656.3225	328.6649	C	520.2660	260.6367	503.2395	252.1234			3
7	916.4709	458.7391	899.4444	450.2258	898.4604	449.7338	K	417.2568	209.1321	400.2303	200.6188			2
8							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LSLEGDHSTPPSAYGSVKPYTNFDAER**

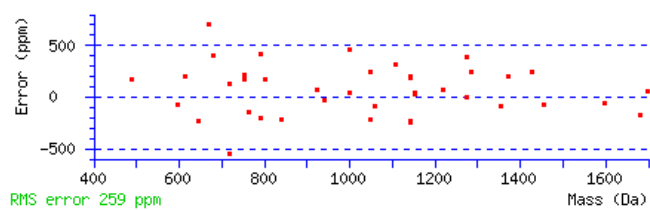
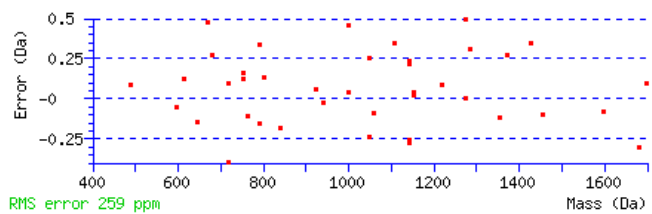
Found in **IPI00468203**, Annexin A2 (Mus musculus)

Match to Query 72730: 3052.408572 from (1018.476800, 3+) intensity (4254.1299)



Monoisotopic mass of neutral peptide Mr(calc): 3052.4050
 Variable modifications:
 K18 : GlyGly (K)
 N22 : Deamidated (NQ)
 Ions Score: 21 Expect: 4.7
 Matches : 42/274 fragment ions using 70 most intense peaks

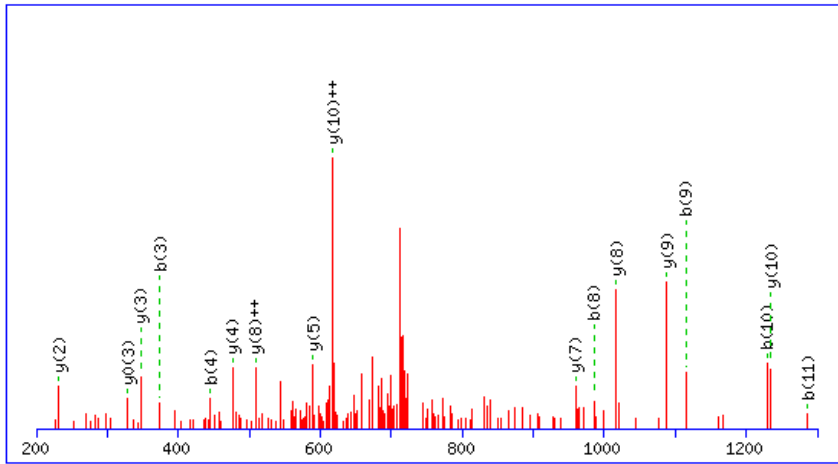
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							27
2	201.1234	101.0653			183.1128	92.0600	S	2940.3282	1470.6678	2923.3017	1462.1545	2922.3177	1461.6625	26
3	314.2074	157.6074			296.1969	148.6021	L	2853.2962	1427.1517	2836.2697	1418.6385	2835.2856	1418.1465	25
4	443.2500	222.1287			425.2395	213.1234	E	2740.2121	1370.6097	2723.1856	1362.0964	2722.2016	1361.6044	24
5	500.2715	250.6394			482.2609	241.6341	G	2611.1696	1306.0884	2594.1430	1297.5751	2593.1590	1297.0831	23
6	615.2984	308.1529			597.2879	299.1476	D	2554.1481	1277.5777	2537.1215	1269.0644	2536.1375	1268.5724	22
7	752.3573	376.6823			734.3468	367.6770	H	2439.1211	1220.0642	2422.0946	1211.5509	2421.1106	1211.0589	21
8	839.3894	420.1983			821.3788	411.1930	S	2302.0622	1151.5348	2285.0357	1143.0215	2284.0517	1142.5295	20
9	940.4371	470.7222			922.4265	461.7169	T	2215.0302	1108.0187	2198.0037	1099.5055	2197.0196	1099.0135	19
10	1037.4898	519.2485			1019.4792	510.2433	P	2113.9825	1057.4949	2096.9560	1048.9816	2095.9720	1048.4896	18
11	1134.5426	567.7749			1116.5320	558.7696	P	2016.9298	1008.9685	1999.9032	1000.4552	1998.9192	999.9632	17
12	1221.5746	611.2909			1203.5640	602.2857	S	1919.8770	960.4421	1902.8504	951.9289	1901.8664	951.4369	16
13	1292.6117	646.8095			1274.6012	637.8042	A	1832.8450	916.9261	1815.8184	908.4128	1814.8344	907.9208	15
14	1455.6751	728.3412			1437.6645	719.3359	Y	1761.8079	881.4076	1744.7813	872.8943	1743.7973	872.4023	14
15	1512.6965	756.8519			1494.6859	747.8466	G	1598.7445	799.8759	1581.7180	791.3626	1580.7340	790.8706	13
16	1599.7285	800.3679			1581.7180	791.3626	S	1541.7231	771.3652	1524.6965	762.8519	1523.7125	762.3599	12
17	1698.7970	849.9021			1680.7864	840.8968	V	1454.6910	727.8492	1437.6645	719.3359	1436.6805	718.8439	11
18	1940.9348	970.9711	1923.9083	962.4578	1922.9243	961.9658	K	1355.6226	678.3149	1338.5961	669.8017	1337.6121	669.3097	10
19	2037.9876	1019.4974	2020.9611	1010.9842	2019.9770	1010.4922	P	1113.4847	557.2460	1096.4582	548.7327	1095.4742	548.2407	9
20	2201.0509	1101.0291	2184.0244	1092.5158	2183.0404	1092.0238	Y	1016.4320	508.7196	999.4054	500.2063	998.4214	499.7143	8
21	2302.0986	1151.5529	2285.0721	1143.0397	2284.0881	1142.5477	T	853.3686	427.1880	836.3421	418.6747	835.3581	418.1827	7
22	2417.1256	1209.0664	2400.0990	1200.5531	2399.1150	1200.0611	N	752.3210	376.6641	735.2944	368.1508	734.3104	367.6588	6
23	2564.1940	1282.6006	2547.1674	1274.0874	2546.1834	1273.5953	F	637.2940	319.1506	620.2675	310.6374	619.2835	310.1454	5
24	2679.2209	1340.1141	2662.1944	1331.6008	2661.2104	1331.1088	D	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
25	2750.2580	1375.6327	2733.2315	1367.1194	2732.2475	1366.6274	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
26	2879.3006	1440.1540	2862.2741	1431.6407	2861.2901	1431.1487	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
27							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **LIFAGKQLEDGR**

Found in **IPI00470152**, ribosomal protein S27a (Mus musculus)

Match to Query 36141: 1459.779548 from (730.897050, 2+) intensity (1477.7528)



Monoisotopic mass of neutral peptide Mr(calc): 1459.7783

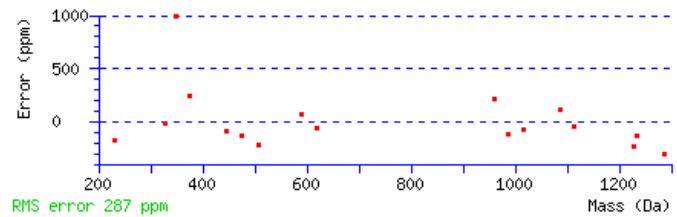
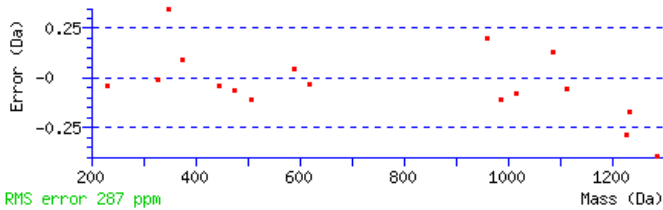
Variable modifications:

K6 : GlyGly (K)

Ions Score: 48 Expect: 0.0023

Matches : 17/102 fragment ions using 32 most intense peaks

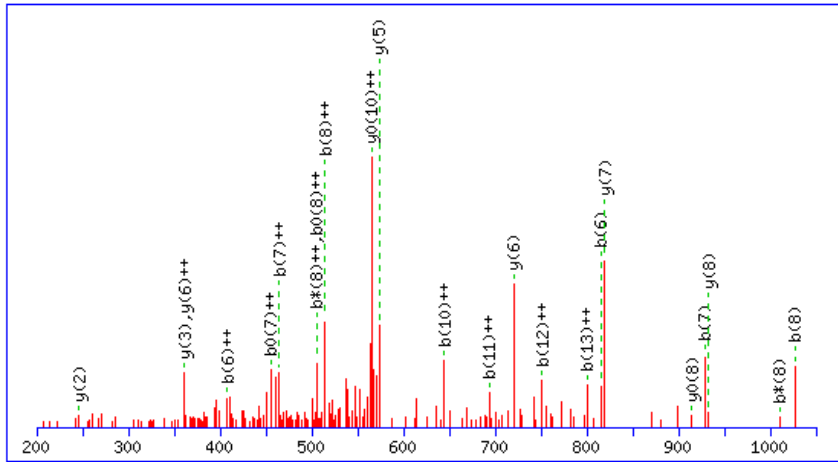
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							12
2	227.1754	114.0913					I	1347.7015	674.3544	1330.6750	665.8411	1329.6910	665.3491	11
3	374.2438	187.6255					F	1234.6175	617.8124	1217.5909	609.2991	1216.6069	608.8071	10
4	445.2809	223.1441					A	1087.5491	544.2782	1070.5225	535.7649	1069.5385	535.2729	9
5	502.3024	251.6548					G	1016.5119	508.7596	999.4854	500.2463	998.5014	499.7543	8
6	744.4403	372.7238	727.4137	364.2105			K	959.4905	480.2489	942.4639	471.7356	941.4799	471.2436	7
7	872.4989	436.7531	855.4723	428.2398			Q	717.3526	359.1799	700.3260	350.6667	699.3420	350.1747	6
8	985.5829	493.2951	968.5564	484.7818			L	589.2940	295.1506	572.2675	286.6374	571.2835	286.1454	5
9	1114.6255	557.8164	1097.5990	549.3031	1096.6150	548.8111	E	476.2100	238.6086	459.1834	230.0953	458.1994	229.6033	4
10	1229.6525	615.3299	1212.6259	606.8166	1211.6419	606.3246	D	347.1674	174.0873	330.1408	165.5740	329.1568	165.0820	3
11	1286.6739	643.8406	1269.6474	635.3273	1268.6634	634.8353	G	232.1404	116.5738	215.1139	108.0606			2
12							R	175.1190	88.0631	158.0924	79.5498			1



MS/MS Fragmentation of **KIEDNTLVFIVDVK**

Found in **IPI00623004**, similar to ribosomal protein L23a (Mus musculus)

Match to Query 50142: 1745.95642 from (582.992790, 3+) intensity (3518.8088)



Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 1745.9563

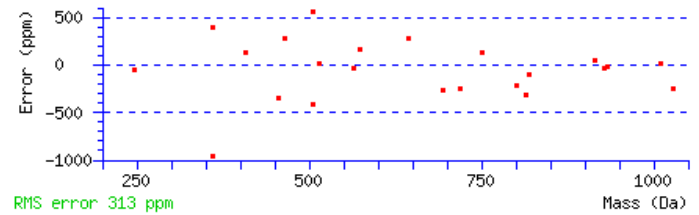
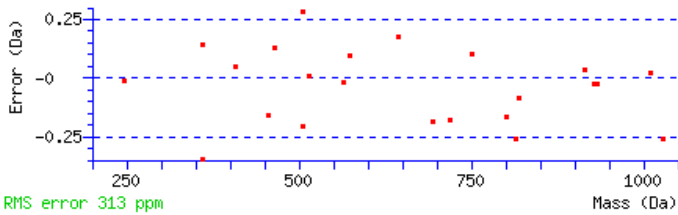
Variable modifications:

K1 : GlyGly (K)

Ions Score: 55 Expect: 0.00016

Matches : 23/148 fragment ions using 26 most intense peaks

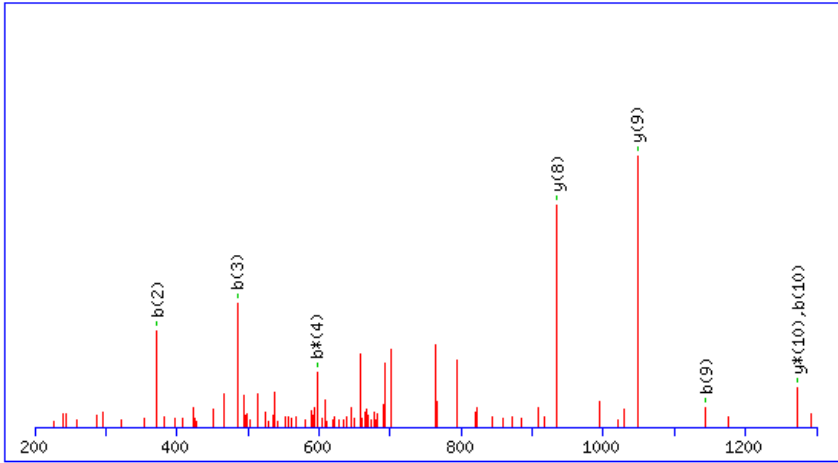
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							14
2	356.2292	178.6183	339.2027	170.1050			I	1504.8257	752.9165	1487.7992	744.4032	1486.8152	743.9112	13
3	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	E	1391.7417	696.3745	1374.7151	687.8612	1373.7311	687.3692	12
4	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	D	1262.6991	631.8532	1245.6725	623.3399	1244.6885	622.8479	11
5	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	N	1147.6721	574.3397	1130.6456	565.8264	1129.6616	565.3344	10
6	815.3894	408.1983	798.3628	399.6850	797.3788	399.1930	T	1033.6292	517.3182	1016.6027	508.8050	1015.6186	508.3130	9
7	928.4734	464.7404	911.4469	456.2271	910.4629	455.7351	L	932.5815	466.7944	915.5550	458.2811	914.5710	457.7891	8
8	1027.5419	514.2746	1010.5153	505.7613	1009.5313	505.2693	V	819.4975	410.2524	802.4709	401.7391	801.4869	401.2471	7
9	1174.6103	587.8088	1157.5837	579.2955	1156.5997	578.8035	F	720.4291	360.7182	703.4025	352.2049	702.4185	351.7129	6
10	1287.6943	644.3508	1270.6678	635.8375	1269.6838	635.3455	I	573.3606	287.1840	556.3341	278.6707	555.3501	278.1787	5
11	1386.7627	693.8850	1369.7362	685.3717	1368.7522	684.8797	V	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
12	1501.7897	751.3985	1484.7631	742.8852	1483.7791	742.3932	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
13	1600.8581	800.9327	1583.8316	792.4194	1582.8475	791.9274	V	246.1812	123.5942	229.1547	115.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **EKLEVQCQAEK**

Found in **IPI00623749**, A kinase (PRKA) anchor protein (yotiao) 9 (Mus musculus)

Match to Query 33829: 1418.680448 from (710.347500, 2+) intensity (1236.1418)



Monoisotopic mass of neutral peptide Mr(calc): 1418.6711

Variable modifications:

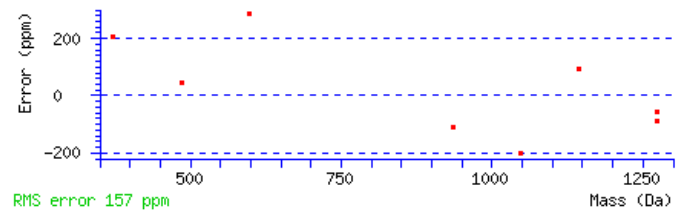
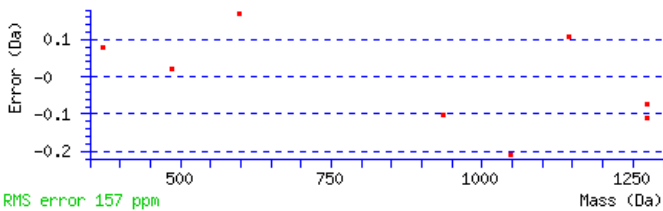
K2 : GlyGly (K)

Q8 : Deamidated (NQ)

Ions Score: 25 Expect: 0.75

Matches : 8/116 fragment ions using 11 most intense peaks

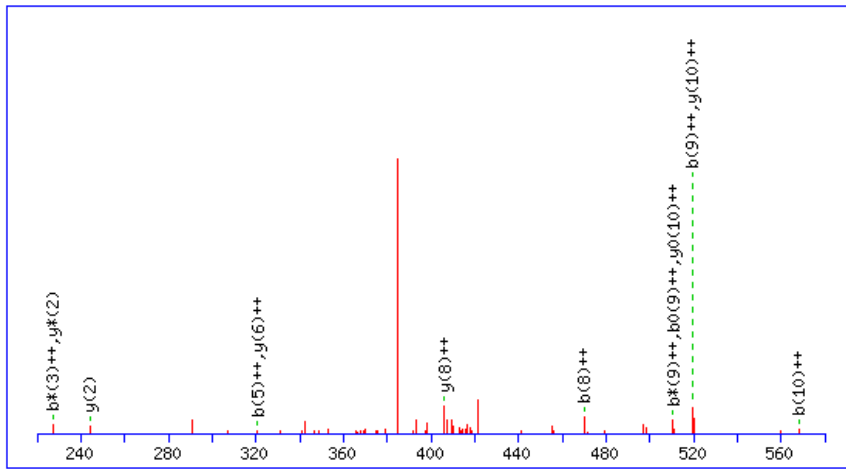
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	K	1290.6358	645.8216	1273.6093	637.3083	1272.6253	636.8163	10
3	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	L	1048.4979	524.7526	1031.4714	516.2393	1030.4874	515.7473	9
4	614.3144	307.6608	597.2879	299.1476	596.3039	298.6556	E	935.4139	468.2106	918.3873	459.6973	917.4033	459.2053	8
5	713.3828	357.1951	696.3563	348.6818	695.3723	348.1898	V	806.3713	403.6893	789.3447	395.1760	788.3607	394.6840	7
6	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	Q	707.3029	354.1551	690.2763	345.6418	689.2923	345.1498	6
7	944.4506	472.7289	927.4240	464.2157	926.4400	463.7237	C	579.2443	290.1258	562.2177	281.6125	561.2337	281.1205	5
8	1073.4932	537.2502	1056.4666	528.7370	1055.4826	528.2449	Q	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	4
9	1144.5303	572.7688	1127.5038	564.2555	1126.5197	563.7635	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
10	1273.5729	637.2901	1256.5463	628.7768	1255.5623	628.2848	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **KPEATTVPVK**

Found in **IPI00756257**, Isoform 1 of Titin (Mus musculus)

Match to Query 26172: 1279.710762 from (427.577530, 3+) intensity (3471.4924)



Monoisotopic mass of neutral peptide Mr(calc): 1279.7136

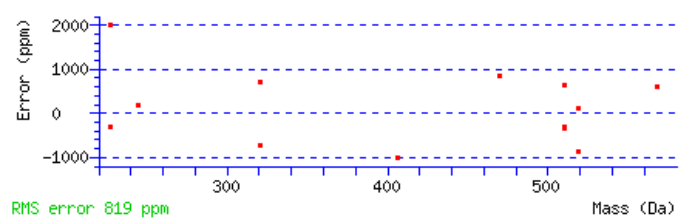
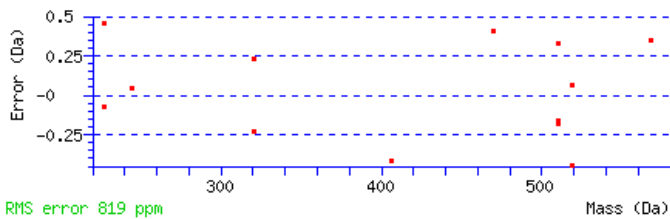
Variable modifications:

K1 : GlyGly (K)

Ions Score: 16 Expect: 1.1

Matches : 13/106 fragment ions using 17 most intense peaks

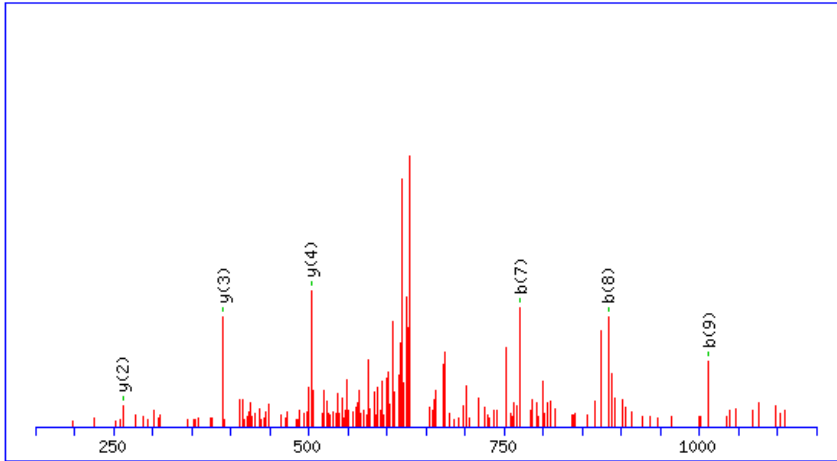
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							11
2	340.1979	170.6026	323.1714	162.0893			P	1038.5830	519.7951	1021.5564	511.2819	1020.5724	510.7899	10
3	469.2405	235.1239	452.2140	226.6106	451.2300	226.1186	E	941.5302	471.2688	924.5037	462.7555	923.5197	462.2635	9
4	540.2776	270.6425	523.2511	262.1292	522.2671	261.6372	A	812.4876	406.7475	795.4611	398.2342	794.4771	397.7422	8
5	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	T	741.4505	371.2289	724.4240	362.7156	723.4400	362.2236	7
6	742.3730	371.6901	725.3464	363.1769	724.3624	362.6849	T	640.4028	320.7051	623.3763	312.1918	622.3923	311.6998	6
7	841.4414	421.2243	824.4149	412.7111	823.4308	412.2191	V	539.3552	270.1812	522.3286	261.6679			5
8	938.4942	469.7507	921.4676	461.2375	920.4836	460.7454	P	440.2867	220.6470	423.2602	212.1337			4
9	1037.5626	519.2849	1020.5360	510.7717	1019.5520	510.2796	V	343.2340	172.1206	326.2074	163.6074			3
10	1134.6154	567.8113	1117.5888	559.2980	1116.6048	558.8060	P	244.1656	122.5864	227.1390	114.0731			2
11							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **KTASVLGIQDK**

Found in **IPI00875801**, Alpha-protein kinase 3 (Mus musculus)

Match to Query 25815: 1272.707128 from (637.360840, 2+) intensity (2097.3022)



Monoisotopic mass of neutral peptide Mr(calc): 1272.7038

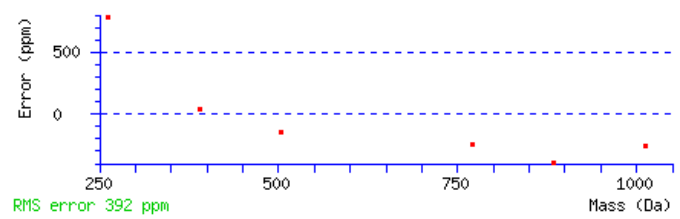
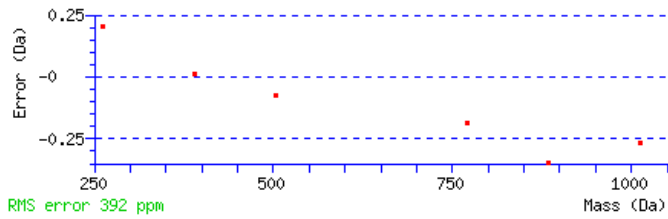
Variable modifications:

K1 : GlyGly (K)

Ions Score: 16 Expect: 1.9

Matches : 6/116 fragment ions using 10 most intense peaks

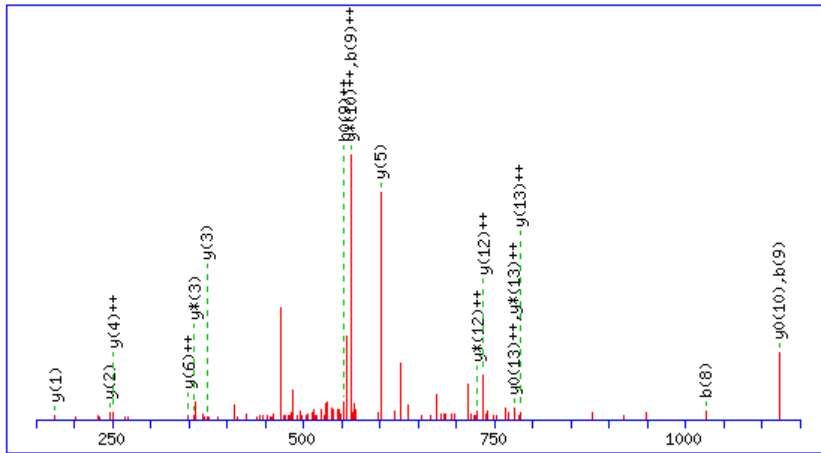
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	243.1452	122.0762	226.1186	113.5629			K							11
2	344.1928	172.6001	327.1663	164.0868	326.1823	163.5948	T	1031.5732	516.2902	1014.5466	507.7769	1013.5626	507.2849	10
3	415.2300	208.1186	398.2034	199.6053	397.2194	199.1133	A	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	9
4	502.2620	251.6346	485.2354	243.1214	484.2514	242.6293	S	859.4884	430.2478	842.4618	421.7345	841.4778	421.2425	8
5	601.3304	301.1688	584.3039	292.6556	583.3198	292.1636	V	772.4563	386.7318	755.4298	378.2185	754.4458	377.7265	7
6	714.4145	357.7109	697.3879	349.1976	696.4039	348.7056	L	673.3879	337.1976	656.3614	328.6843	655.3774	328.1923	6
7	771.4359	386.2216	754.4094	377.7083	753.4254	377.2163	G	560.3039	280.6556	543.2773	272.1423	542.2933	271.6503	5
8	884.5200	442.7636	867.4934	434.2504	866.5094	433.7584	I	503.2824	252.1448	486.2558	243.6316	485.2718	243.1395	4
9	1012.5786	506.7929	995.5520	498.2796	994.5680	497.7876	Q	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
10	1127.6055	564.3064	1110.5790	555.7931	1109.5949	555.3011	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
11							K	147.1128	74.0600	130.0863	65.5468			1



MS/MS Fragmentation of **RPKSSQNIPVQQAR**

Found in **IPI00876033**, Putative uncharacterized protein (Mus musculus)

Match to Query 49192: 1722.926022 from (575.315950, 3+) intensity (6088.6660)



Monoisotopic mass of neutral peptide Mr(calc): 1722.9125

Variable modifications:

K3 : GlyGly (K)

N7 : Deamidated (NQ)

Ions Score: 19 Expect: 1

Matches : 20/132 fragment ions using 38 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							14
2	254.1612	127.5842	237.1346	119.0709			P	1567.8187	784.4130	1550.7921	775.8997	1549.8081	775.4077	13
3	496.2990	248.6532	479.2725	240.1399			K	1470.7659	735.8866	1453.7394	727.3733	1452.7554	726.8813	12
4	583.3311	292.1692	566.3045	283.6559	565.3205	283.1639	S	1228.6280	614.8177	1211.6015	606.3044	1210.6175	605.8124	11
5	670.3631	335.6852	653.3365	327.1719	652.3525	326.6799	S	1141.5960	571.3016	1124.5695	562.7884	1123.5854	562.2964	10
6	798.4217	399.7145	781.3951	391.2012	780.4111	390.7092	Q	1054.5640	527.7856	1037.5374	519.2724			9
7	913.4486	457.2279	896.4221	448.7147	895.4381	448.2227	N	926.5054	463.7563	909.4789	455.2431			8
8	1026.5327	513.7700	1009.5061	505.2567	1008.5221	504.7647	I	811.4785	406.2429	794.4519	397.7296			7
9	1123.5854	562.2964	1106.5589	553.7831	1105.5749	553.2911	P	698.3944	349.7008	681.3679	341.1876			6
10	1222.6539	611.8306	1205.6273	603.3173	1204.6433	602.8253	V	601.3416	301.1745	584.3151	292.6612			5
11	1350.7124	675.8599	1333.6859	667.3466	1332.7019	666.8546	Q	502.2732	251.6402	485.2467	243.1270			4
12	1478.7710	739.8891	1461.7445	731.3759	1460.7605	730.8839	Q	374.2146	187.6110	357.1881	179.0977			3
13	1549.8081	775.4077	1532.7816	766.8944	1531.7976	766.4024	A	246.1561	123.5817	229.1295	115.0684			2
14							R	175.1190	88.0631	158.0924	79.5498			1

