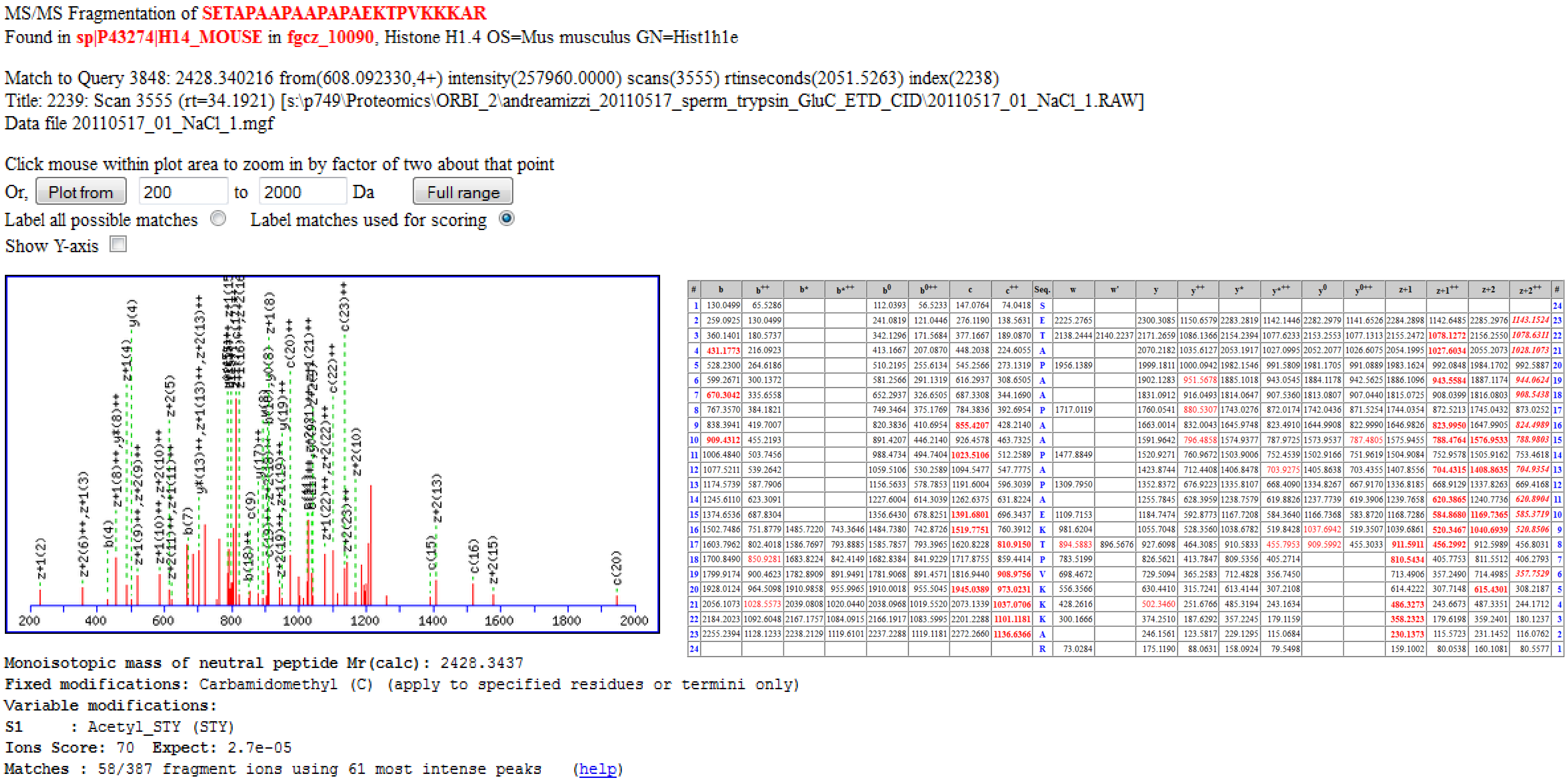
Supplementary Figure 2, Brunner et al.



MS/MS Fragmentation of SETAPAAPAAPAPAEKTPVKKKAR
Found in sp|P43274|H14_MOUSE in fgcz_10090, Histone H1.4 OS=Mus musculus GN=Hist1h1e

Match to Query 3848: 2428.340216 from(608.092330,4+) intensity(257960.0000) scans(3555) rtinseconds(2051.5263) index(2238)
Title: 2239: Scan 3555 (rt=34.1921) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

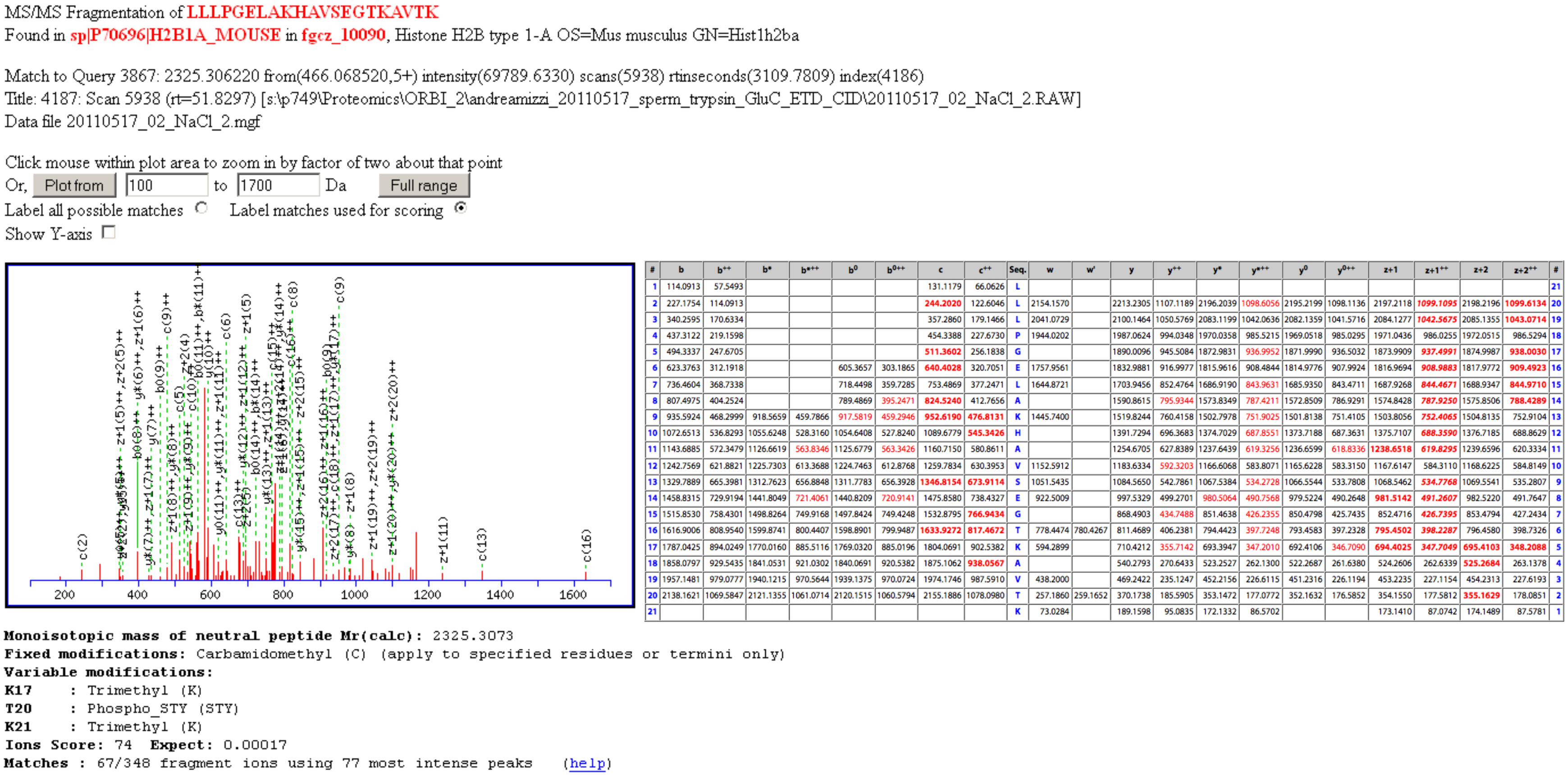
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	z+1	z+1^{++}	z+2	z+2^{++}	#
1	130.0499	65.5286			112.0393	56.5233	147.0764	74.0418	S													24
2	259.0925	130.0499			241.0819	121.0446	276.1190	138.5631	E	2225.2765		2300.3085	1150.6579	2283.2819	1142.1446	2282.2979	1141.6526	2284.2898	1142.6485	2285.2976	1143.1524	23
3	360.1401	180.5737			342.1296	171.5684	377.1667	189.0870	T	2138.2444	2140.2237	2171.2659	1086.1366	2154.2394	1077.6233	2153.2553	1077.1313	2155.2472	1078.1272	2156.2550	1078.6311	22
4	431.1773	216.0923			413.1667	207.0870	448.2038	224.6055	A			2070.2182	1035.6127	2053.1917	1027.0995	2052.2077	1026.6075	2054.1995	1027.6034	2055.2073	1028.1073	21
5	528.2300	264.6186			510.2195	255.6134	545.2566	273.1319	P	1956.1389		1999.1811	1000.0942	1982.1546	991.5809	1981.1705	991.0889	1983.1624	992.0848	1984.1702	992.5887	20
6	599.2671	300.1372			581.2566	291.1319	616.2937	308.6505	A			1902.1283	951.5678	1885.1018	943.0545	1884.1178	942.5625	1886.1096	943.5584	1887.1174	944.0624	19
7	670.3042	335.6558			652.2937	326.6505	687.3308	344.1690	A			1831.0912	916.0493	1814.0647	907.5360	1813.0807	907.0440	1815.0725	908.0399	1816.0803	908.5438	18
8	767.3570	384.1821			749.3464	375.1769	784.3836	392.6954	P	1717.0119		1760.0541	880.5307	1743.0276	872.0174	1742.0436	871.5254	1744.0354	872.5213	1745.0432	873.0252	17
9	838.3941	419.7007			820.3836	410.6954	855.4207	428.2140	A			1663.0014	832.0043	1645.9748	823.4910	1644.9908	822.9990	1646.9826	823.9950	1647.9905	824.4989	16
10	909.4312	455.2193			891.4207	446.2140	926.4578	463.7325	A			1591.9642	796.4858	1574.9377	787.9725	1573.9537	787.4805	1575.9455	788.4764	1576.9533	788.9803	15
11	1006.4840	503.7456			988.4734	494.7404	1023.5106	512.2589	P	1477.8849		1520.9271	760.9672	1503.9006	752.4539	1502.9166	751.9619	1504.9084	752.9578	1505.9162	753.4618	14
12	1077.5211	539.2642			1059.5106	530.2589	1094.5477	547.7775	A			1423.8744	712.4408	1406.8478	703.9275	1405.8638	703.4355	1407.8556	704.4315	1408.8635	704.9354	13
13	1174.5739	587.7906			1156.5633	578.7853	1191.6004	596.3039	P	1309.7950		1352.8372	676.9223	1335.8107	668.4090	1334.8267	667.9170	1336.8185	668.9129	1337.8263	669.4168	12
14	1245.6110	623.3091			1227.6004	614.3039	1262.6375	631.8224	A			1255.7845	628.3959	1238.7579	619.8826	1237.7739	619.3906	1239.7658	620.3865	1240.7736	620.8904	11
15	1374.6536	687.8304			1356.6430	678.8251	1391.6801	696.3437	E	1109.7153		1184.7474	592.8773	1167.7208	584.3640	1166.7368	583.8720	1168.7286	584.8680	1169.7365	585.3719	10
16	1502.7486	751.8779	1485.7220	743.3646	1484.7380	742.8726	1519.7751	760.3912	K	981.6204		1055.7048	528.3560	1038.6782	519.8428	1037.6942	519.3507	1039.6861	520.3467	1040.6939	520.8506	9
17	1603.7962	802.4018	1586.7697	793.8885	1585.7857	793.3965	1620.8228	810.9150	T	894.5883	896.5676	927.6098	464.3085	910.5833	455.7953	909.5992	455.3033	911.5911	456.2992	912.5989	456.8031	8
18	1700.8490	850.9281	1683.8224	842.4149	1682.8384	841.9229	1717.8755	859.4414	P	783.5199		826.5621	413.7847	809.5356	405.2714			810.5434	405.7753	811.5512	406.2793	7
19	1799.9174	900.4623	1782.8909	891.9491	1781.9068	891.4571	1816.9440	908.9756	V	698.4672		729.5094	365.2583	712.4828	356.7450			713.4906	357.2490	714.4985	357.7529	6
20	1928.0124	964.5098	1910.9858	955.9965	1910.0018	955.5045	1945.0389	973.0231	K	556.3566		630.4410	315.7241	613.4144	307.2108			614.4222	307.7148	615.4301	308.2187	5
21	2056.1073	1028.5573	2039.0808	1020.0440	2038.0968	1019.5520	2073.1339	1037.0706	K	428.2616		502.3460	251.6766	485.3194	243.1634			486.3273	243.6673	487.3351	244.1712	4
22	2184.2023	1092.6048	2167.1757	1084.0915	2166.1917	1083.5995	2201.2288	1101.1181	K	300.1666		374.2510	187.6292	357.2245	179.1159			358.2323	179.6198	359.2401	180.1237	3
23	2255.2394	1128.1233	2238.2129	1119.6101	2237.2288	1119.1181	2272.2660	1136.6366	A			246.1561	123.5817	229.1295	115.0684			230.1373	115.5723	231.1452	116.0762	2
24									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

```
Monoisotopic mass of neutral peptide Mr(calc): 2428.3437
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1      : Acetyl_STY (STY)
Ions Score: 70  Expect: 2.7e-05
Matches : 58/387 fragment ions using 61 most intense peaks   (help)
```

Mascot Search Results: Peptide View

(ac-S)ETAPAAPAAPAPAEKTPVKKKAR



MS/MS Fragmentation of LLLPGELAKHAVSEGTKAVTK
Found in sp|P70696|H2B1A_MOUSE in fgcz_10090, Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba

Match to Query 3867: 2325.306220 from(466.068520,5+) intensity(69789.6330) scans(5938) rtinseconds(3109.7809) index(4186)
Title: 4187: Scan 5938 (rt=51.8297) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_02_NaCl_2.RAW]
Data file 20110517_02_NaCl_2.mgf

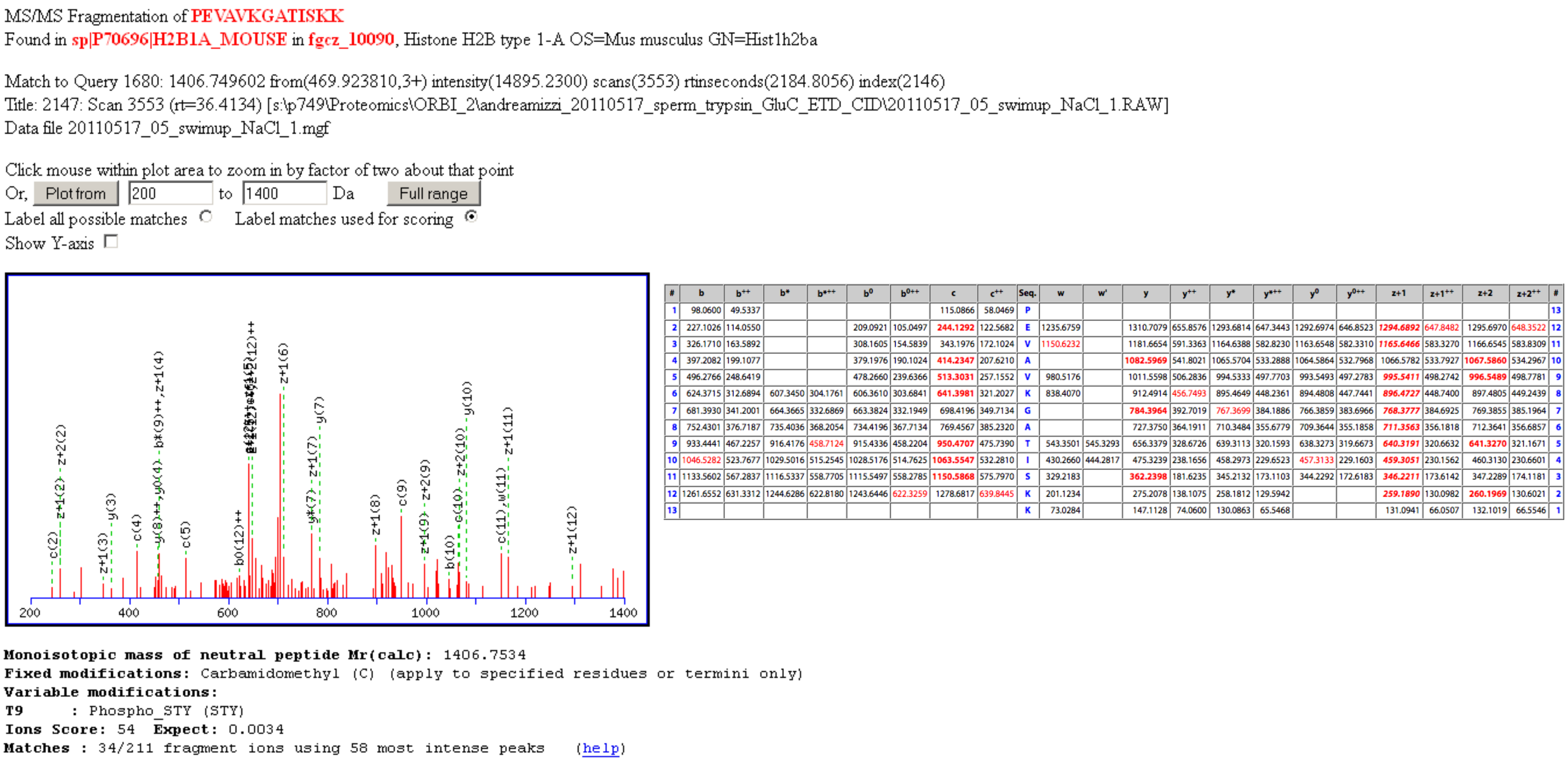
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	114.0913	57.5493					131.1179	66.0626	L													21
2	227.1754	114.0913					**244.2020**	122.6046	L	2154.1570		2213.2305	1107.1189	2196.2039	1098.6056	2195.2199	1098.1136	2197.2118	***1099.1095***	2198.2196	**1099.6134**	20
3	340.2595	170.6334					357.2860	179.1466	L	2041.0729		2100.1464	1050.5769	2083.1199	1042.0636	2082.1359	1041.5716	2084.1277	***1042.5675***	2085.1355	**1043.0714**	19
4	437.3122	219.1598					454.3388	227.6730	P	1944.0202		1987.0624	994.0348	1970.0358	985.5215	1969.0518	985.0295	1971.0436	986.0255	1972.0515	986.5294	18
5	494.3337	247.6705					**511.3602**	256.1838	G			1890.0096	945.5084	1872.9831	936.9952	1871.9990	936.5032	1873.9909	***937.4991***	1874.9987	**938.0030**	17
6	623.3763	312.1918			605.3657	303.1865	**640.4028**	320.7051	E	1757.9561		1832.9881	916.9977	1815.9616	908.4844	1814.9776	907.9924	1816.9694	***908.9883***	1817.9772	**909.4923**	16
7	736.4604	368.7338			718.4498	359.7285	753.4869	377.2471	L	1644.8721		1703.9456	852.4764	1686.9190	843.9631	1685.9350	843.4711	1687.9268	***844.4671***	1688.9347	**844.9710**	15
8	807.4975	404.2524			789.4869	395.2471	**824.5240**	412.7656	A			1590.8615	795.9344	1573.8349	787.4211	1572.8509	786.9291	1574.8428	***787.9250***	1575.8506	**788.4289**	14
9	935.5924	468.2999	918.5659	459.7866	917.5819	459.2946	**952.6190**	**476.8131**	K	1445.7400		1519.8244	760.4158	1502.7978	751.9025	1501.8138	751.4105	1503.8056	***752.4065***	1504.8135	752.9104	13
10	1072.6513	536.8293	1055.6248	528.3160	1054.6408	527.8240	1089.6779	**545.3426**	H			1391.7294	696.3683	1374.7029	687.8551	1373.7188	687.3631	1375.7107	***688.3590***	1376.7185	688.8629	12
11	1143.6885	572.3479	1126.6619	563.8346	1125.6779	563.3426	1160.7150	580.8611	A			1254.6705	627.8389	1237.6439	619.3256	1236.6599	618.8336	**1238.6518**	***619.8295***	1239.6596	620.3334	11
12	1242.7569	621.8821	1225.7303	613.3688	1224.7463	612.8768	1259.7834	630.3953	V	1152.5912		1183.6334	592.3203	1166.6068	583.8071	1165.6228	583.3150	1167.6147	584.3110	1168.6225	584.8149	10
13	1329.7889	665.3981	1312.7623	656.8848	1311.7783	656.3928	**1346.8154**	**673.9114**	S	1051.5435		1084.5650	542.7861	1067.5384	534.2728	1066.5544	533.7808	1068.5462	***534.7768***	1069.5541	535.2807	9
14	1458.8315	729.9194	1441.8049	721.4061	1440.8209	720.9141	1475.8580	738.4327	E	922.5009		997.5329	499.2701	980.5064	490.7568	979.5224	490.2648	**981.5142**	***491.2607***	982.5220	491.7647	8
15	1515.8530	758.4301	1498.8264	749.9168	1497.8424	749.4248	1532.8795	**766.9434**	G			868.4903	434.7488	851.4638	426.2355	850.4798	425.7435	852.4716	***426.7395***	853.4794	427.2434	7
16	1616.9006	808.9540	1599.8741	800.4407	1598.8901	799.9487	**1633.9272**	**817.4672**	T	778.4474	780.4267	811.4689	406.2381	794.4423	397.7248	793.4583	397.2328	**795.4502**	***398.2287***	796.4580	398.7326	6
17	1787.0425	894.0249	1770.0160	885.5116	1769.0320	885.0196	1804.0691	902.5382	K	594.2899		710.4212	355.7142	693.3947	347.2010	692.4106	346.7090	**694.4025**	***347.7049***	**695.4103**	**348.2088**	5
18	1858.0797	929.5435	1841.0531	921.0302	1840.0691	920.5382	1875.1062	**938.0567**	A			540.2793	270.6433	523.2527	262.1300	522.2687	261.6380	524.2606	262.6339	**525.2684**	263.1378	4
19	1957.1481	979.0777	1940.1215	970.5644	1939.1375	970.0724	1974.1746	987.5910	V	438.2000		469.2422	235.1247	452.2156	226.6115	451.2316	226.1194	453.2235	227.1154	454.2313	227.6193	3
20	2138.1621	1069.5847	2121.1355	1061.0714	2120.1515	1060.5794	2155.1886	1078.0980	T	257.1860	259.1652	370.1738	185.5905	353.1472	177.0772	352.1632	176.5852	354.1550	177.5812	**355.1629**	178.0851	2
21									K	73.0284		189.1598	95.0835	172.1332	86.5702			173.1410	87.0742	174.1489	87.5781	1

Monoisotopic mass of neutral peptide Mr(calc): 2325.3073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K17 : Trimethyl (K)
T20 : Phospho_STY (STY)
K21 : Trimethyl (K)
Ions Score: 74 **Expect:** 0.00017
Matches : 67/348 fragment ions using 77 most intense peaks (help)

Mascot Search Results: Peptide View

LLLPGELAKHAVSEGTKme3AVpTKme3



MS/MS Fragmentation of PEVAVKGATISKK
Found in sp|P70696|H2B1A_MOUSE in fgcz_10090, Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba

Match to Query 1680: 1406.749602 from(469.923810,3+) intensity(14895.2300) scans(3553) rtinseconds(2184.8056) index(2146)
Title: 2147: Scan 3553 (rt=36.4134) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_05_swimup_NaCl_1.RAW]
Data file 20110517_05_swimup_NaCl_1.mgf

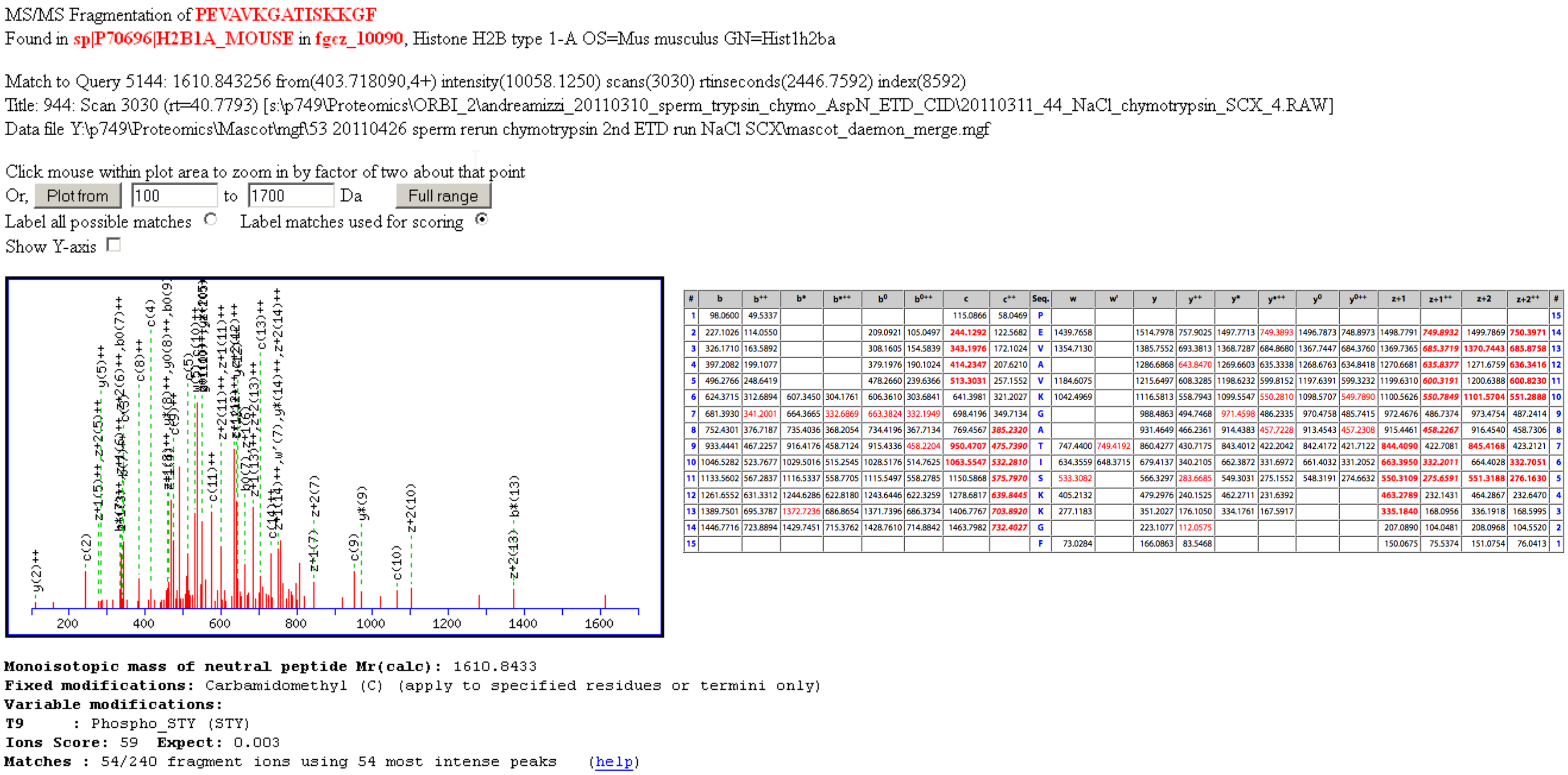
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	98.0600	49.5337					115.0866	58.0469	P													13
2	227.1026	114.0550			209.0921	105.0497	**244.1292**	122.5682	E	1235.6759		1310.7079	655.8576	1293.6814	647.3443	1292.6974	646.8523	***1294.6892***	647.8482	1295.6970	648.3522	12
3	326.1710	163.5892			308.1605	154.5839	343.1976	172.1024	V	1150.6232		1181.6654	591.3363	1164.6388	582.8230	1163.6548	582.3310	***1165.6466***	583.3270	1166.6545	583.8309	11
4	397.2082	199.1077			379.1976	190.1024	**414.2347**	207.6210	A			**1082.5969**	541.8021	1065.5704	533.2888	1064.5864	532.7968	1066.5782	533.7927	**1067.5860**	534.2967	10
5	496.2766	248.6419			478.2660	239.6366	**513.3031**	257.1552	V	980.5176		1011.5598	506.2836	994.5333	497.7703	993.5493	497.2783	***995.5411***	498.2742	**996.5489**	498.7781	9
6	624.3715	312.6894	607.3450	304.1761	606.3610	303.6841	**641.3981**	321.2027	K	838.4070		912.4914	456.7493	895.4649	448.2361	894.4808	447.7441	***896.4727***	448.7400	897.4805	449.2439	8
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	698.4196	349.7134	G			**784.3964**	392.7019	767.3699	384.1886	766.3859	383.6966	***768.3777***	384.6925	769.3855	385.1964	7
8	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	769.4567	385.2320	A			727.3750	364.1911	710.3484	355.6779	709.3644	355.1858	***711.3563***	356.1818	712.3641	356.6857	6
9	933.4441	467.2257	916.4176	458.7124	915.4336	458.2204	**950.4707**	475.7390	T	543.3501	545.3293	656.3379	328.6726	639.3113	320.1593	638.3273	319.6673	***640.3191***	320.6632	**641.3270**	321.1671	5
10	1046.5282	523.7677	1029.5016	515.2545	1028.5176	514.7625	**1063.5547**	532.2810	I	430.2660	444.2817	475.3239	238.1656	458.2973	229.6523	457.3133	229.1603	***459.3051***	230.1562	460.3130	230.6601	4
11	1133.5602	567.2837	1116.5337	558.7705	1115.5497	558.2785	**1150.5868**	575.7970	S	329.2183		**362.2398**	181.6235	345.2132	173.1103	344.2292	172.6183	***346.2211***	173.6142	347.2289	174.1181	3
12	1261.6552	631.3312	1244.6286	622.8180	1243.6446	622.3259	1278.6817	639.8445	K	201.1234		275.2078	138.1075	258.1812	129.5942			***259.1890***	130.0982	**260.1969**	130.6021	2
13									K	73.0284		147.1128	74.0600	130.0863	65.5468			131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1406.7534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho_STY (STY)
Ions Score: 54 **Expect:** 0.0034
Matches : 34/211 fragment ions using 58 most intense peaks (help)

Mascot Search Results: Peptide View

PEVAVKGApTISKK



MS/MS Fragmentation of PEVAVKGATISKKGF
Found in sp|P70696|H2B1A_MOUSE in fgcz_10090, Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba

Match to Query 5144: 1610.843256 from(403.718090,4+) intensity(10058.1250) scans(3030) rtinseconds(2446.7592) index(8592)
Title: 944: Scan 3030 (rt=40.7793) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_44_NaCl_chymotrypsin_SCX_4.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\53 20110426 sperm rerun chymotrypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

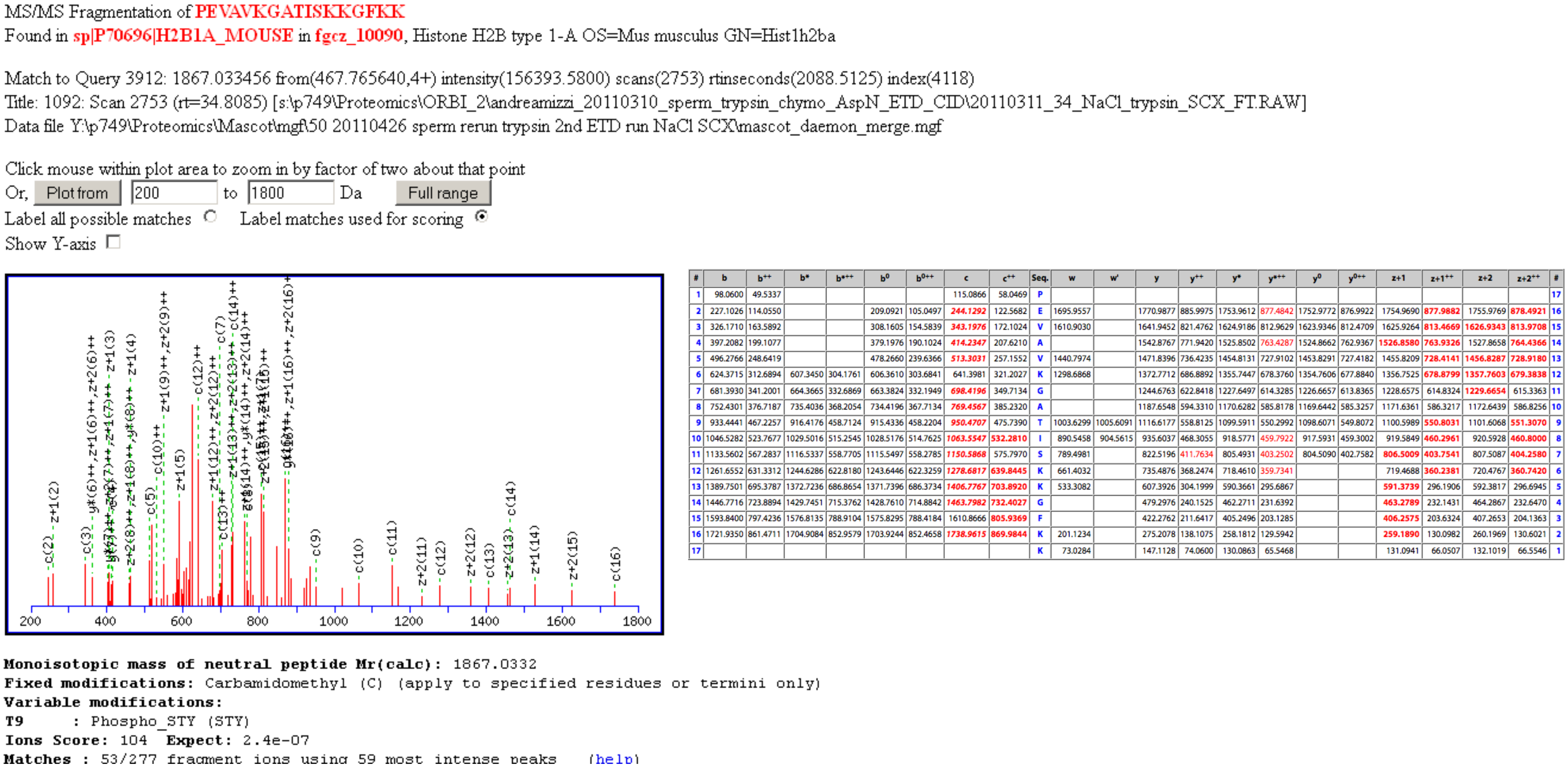
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	98.0600	49.5337					115.0866	58.0469	P													15
2	227.1026	114.0550			209.0921	105.0497	**244.1292**	122.5682	E	1439.7658		1514.7978	757.9025	1497.7713	749.3893	1496.7873	748.8973	1498.7791	***749.8932***	1499.7869	**750.3971**	14
3	326.1710	163.5892			308.1605	154.5839	**343.1976**	172.1024	V	1354.7130		1385.7552	693.3813	1368.7287	684.8680	1367.7447	684.3760	1369.7365	***685.3719***	**1370.7443**	**685.8758**	13
4	397.2082	199.1077			379.1976	190.1024	**414.2347**	207.6210	A			1286.6868	643.8470	1269.6603	635.3338	1268.6763	634.8418	1270.6681	***635.8377***	1271.6759	**636.3416**	12
5	496.2766	248.6419			478.2660	239.6366	**513.3031**	257.1552	V	1184.6075		1215.6497	608.3285	1198.6232	599.8152	1197.6391	599.3232	1199.6310	***600.3191***	1200.6388	**600.8230**	11
6	624.3715	312.6894	607.3450	304.1761	606.3610	303.6841	641.3981	321.2027	K	1042.4969		1116.5813	558.7943	1099.5547	550.2810	1098.5707	549.7890	1100.5626	***550.7849***	**1101.5704**	**551.2888**	10
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	698.4196	349.7134	G			988.4863	494.7468	971.4598	486.2335	970.4758	485.7415	972.4676	486.7374	973.4754	487.2414	9
8	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	769.4567	***385.2320***	A			931.4649	466.2361	914.4383	457.7228	913.4543	457.2308	915.4461	***458.2267***	916.4540	458.7306	8
9	933.4441	467.2257	916.4176	458.7124	915.4336	458.2204	**950.4707**	***475.7390***	T	747.4400	749.4192	860.4277	430.7175	843.4012	422.2042	842.4172	421.7122	**844.4090**	422.7081	**845.4168**	423.2121	7
10	1046.5282	523.7677	1029.5016	515.2545	1028.5176	514.7625	**1063.5547**	***532.2810***	I	634.3559	648.3715	679.4137	340.2105	662.3872	331.6972	661.4032	331.2052	**663.3950**	***332.2011***	664.4028	**332.7051**	6
11	1133.5602	567.2837	1116.5337	558.7705	1115.5497	558.2785	1150.5868	***575.7970***	S	533.3082		566.3297	283.6685	549.3031	275.1552	548.3191	274.6632	**550.3109**	***275.6591***	**551.3188**	**276.1630**	5
12	1261.6552	631.3312	1244.6286	622.8180	1243.6446	622.3259	1278.6817	***639.8445***	K	405.2132		479.2976	240.1525	462.2711	231.6392			**463.2789**	232.1431	464.2867	232.6470	4
13	1389.7501	695.3787	1372.7236	686.8654	1371.7396	686.3734	1406.7767	***703.8920***	K	277.1183		351.2027	176.1050	334.1761	167.5917			**335.1840**	168.0956	336.1918	168.5995	3
14	1446.7716	723.8894	1429.7451	715.3762	1428.7610	714.8842	1463.7982	***732.4027***	G			223.1077	112.0575					207.0890	104.0481	208.0968	104.5520	2
15									F	73.0284		166.0863	83.5468					150.0675	75.5374	151.0754	76.0413	1

Monoisotopic mass of neutral peptide Mr(calc): 1610.8433
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho_STY (STY)
Ions Score: 59 **Expect:** 0.003
Matches : 54/240 fragment ions using 54 most intense peaks (help)

Mascot Search Results: Peptide View

PEVAVKGApTISKKGF



MS/MS Fragmentation of PEVAVKGATISKKGFKK
Found in sp|P70696|H2B1A_MOUSE in fgcz_10090, Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba

Match to Query 3912: 1867.033456 from(467.765640,4+) intensity(156393.5800) scans(2753) rtinseconds(2088.5125) index(4118)
Title: 1092: Scan 2753 (rt=34.8085) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

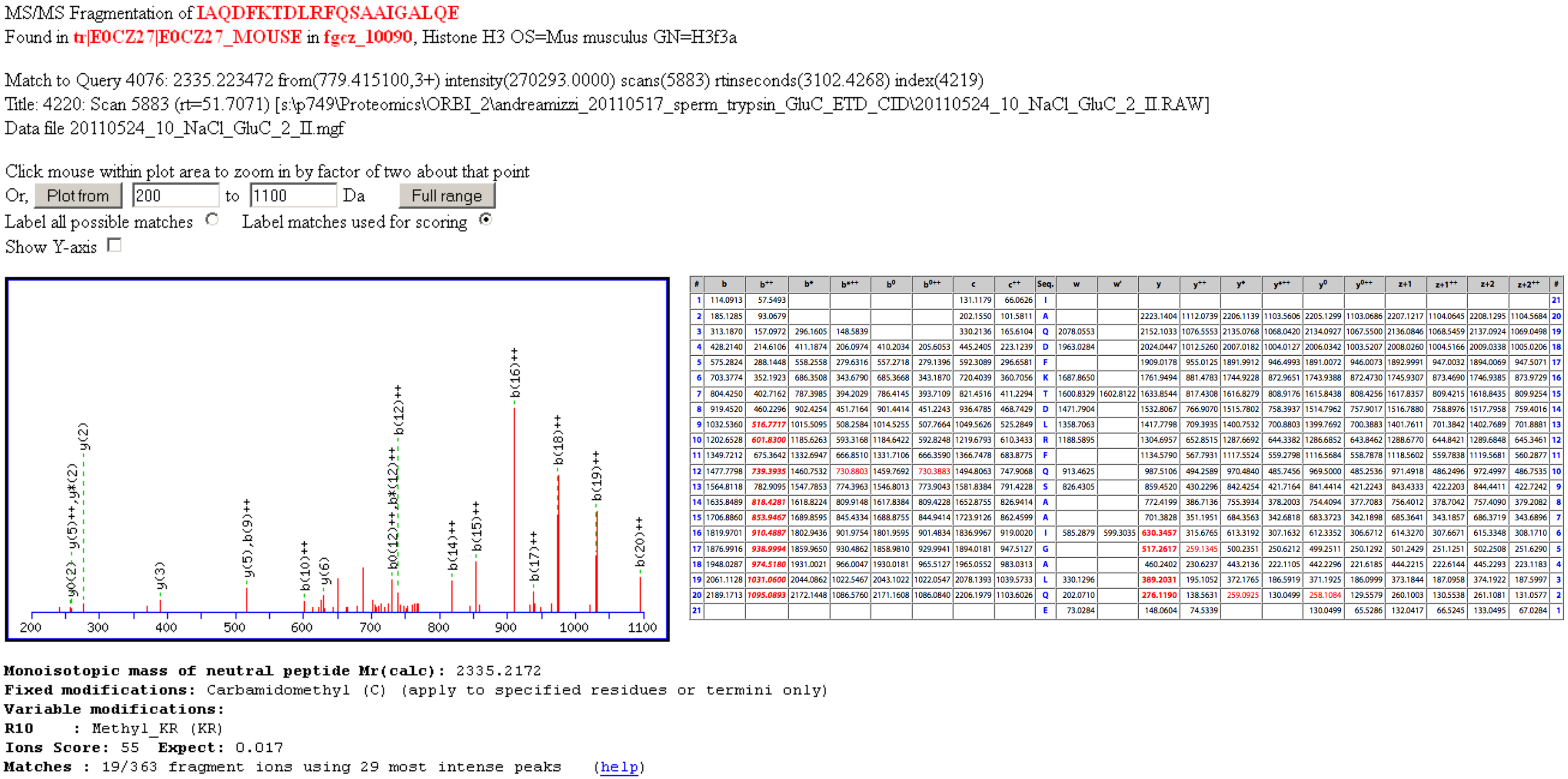
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	98.0600	49.5337					115.0866	58.0469	P													17
2	227.1026	114.0550			209.0921	105.0497	***244.1292***	122.5682	E	1695.9557		1770.9877	885.9975	1753.9612	877.4842	1752.9772	876.9922	1754.9690	**877.9882**	1755.9769	**878.4921**	16
3	326.1710	163.5892			308.1605	154.5839	***343.1976***	172.1024	V	1610.9030		1641.9452	821.4762	1624.9186	812.9629	1623.9346	812.4709	1625.9264	**813.4669**	**1626.9343**	**813.9708**	15
4	397.2082	199.1077			379.1976	190.1024	***414.2347***	207.6210	A			1542.8767	771.9420	1525.8502	763.4287	1524.8662	762.9367	**1526.8580**	**763.9326**	1527.8658	**764.4366**	14
5	496.2766	248.6419			478.2660	239.6366	***513.3031***	257.1552	V	1440.7974		1471.8396	736.4235	1454.8131	727.9102	1453.8291	727.4182	1455.8209	**728.4141**	**1456.8287**	**728.9180**	13
6	624.3715	312.6894	607.3450	304.1761	606.3610	303.6841	641.3981	321.2027	K	1298.6868		1372.7712	686.8892	1355.7447	678.3760	1354.7606	677.8840	1356.7525	**678.8799**	**1357.7603**	**679.3838**	12
7	681.3930	341.2001	664.3665	332.6869	663.3824	332.1949	***698.4196***	349.7134	G			1244.6763	622.8418	1227.6497	614.3285	1226.6657	613.8365	1228.6575	614.8324	**1229.6654**	615.3363	11
8	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	***769.4567***	385.2320	A			1187.6548	594.3310	1170.6282	585.8178	1169.6442	585.3257	1171.6361	586.3217	1172.6439	586.8256	10
9	933.4441	467.2257	916.4176	458.7124	915.4336	458.2204	***950.4707***	475.7390	T	1003.6299	1005.6091	1116.6177	558.8125	1099.5911	550.2992	1098.6071	549.8072	1100.5989	**550.8031**	1101.6068	**551.3070**	9
10	1046.5282	523.7677	1029.5016	515.2545	1028.5176	514.7625	***1063.5547***	**532.2810**	I	890.5458	904.5615	935.6037	468.3055	918.5771	459.7922	917.5931	459.3002	919.5849	**460.2961**	920.5928	**460.8000**	8
11	1133.5602	567.2837	1116.5337	558.7705	1115.5497	558.2785	***1150.5868***	575.7970	S	789.4981		822.5196	411.7634	805.4931	403.2502	804.5090	402.7582	**806.5009**	**403.7541**	807.5087	**404.2580**	7
12	1261.6552	631.3312	1244.6286	622.8180	1243.6446	622.3259	***1278.6817***	**639.8445**	K	661.4032		735.4876	368.2474	718.4610	359.7341			719.4688	**360.2381**	720.4767	**360.7420**	6
13	1389.7501	695.3787	1372.7236	686.8654	1371.7396	686.3734	***1406.7767***	**703.8920**	K	533.3082		607.3926	304.1999	590.3661	295.6867			**591.3739**	296.1906	592.3817	296.6945	5
14	1446.7716	723.8894	1429.7451	715.3762	1428.7610	714.8842	***1463.7982***	**732.4027**	G			479.2976	240.1525	462.2711	231.6392			**463.2789**	232.1431	464.2867	232.6470	4
15	1593.8400	797.4236	1576.8135	788.9104	1575.8295	788.4184	1610.8666	**805.9369**	F			422.2762	211.6417	405.2496	203.1285			**406.2575**	203.6324	407.2653	204.1363	3
16	1721.9350	861.4711	1704.9084	852.9579	1703.9244	852.4658	***1738.9615***	**869.9844**	K	201.1234		275.2078	138.1075	258.1812	129.5942			**259.1890**	130.0982	260.1969	130.6021	2
17									K	73.0284		147.1128	74.0600	130.0863	65.5468			131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1867.0332
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho_STY (STY)
Ions Score: 104 **Expect:** 2.4e-07
Matches : 53/277 fragment ions using 59 most intense peaks (help)

Mascot Search Results: Peptide View

PEVAVKGApTISKKGFKK



MS/MS Fragmentation of IAQDFKTDLRFQSAAIGALQE
Found in tr|E0CZ27|E0CZ27_MOUSE in fgcz_10090, Histone H3 OS=Mus musculus GN=H3f3a

Match to Query 4076: 2335.223472 from(779.415100,3+) intensity(270293.0000) scans(5883) rtinseconds(3102.4268) index(4219)
Title: 4220: Scan 5883 (rt=51.7071) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110524_10_NaCl_GluC_2_II.RAW]
Data file 20110524_10_NaCl_GluC_2_II.mgf

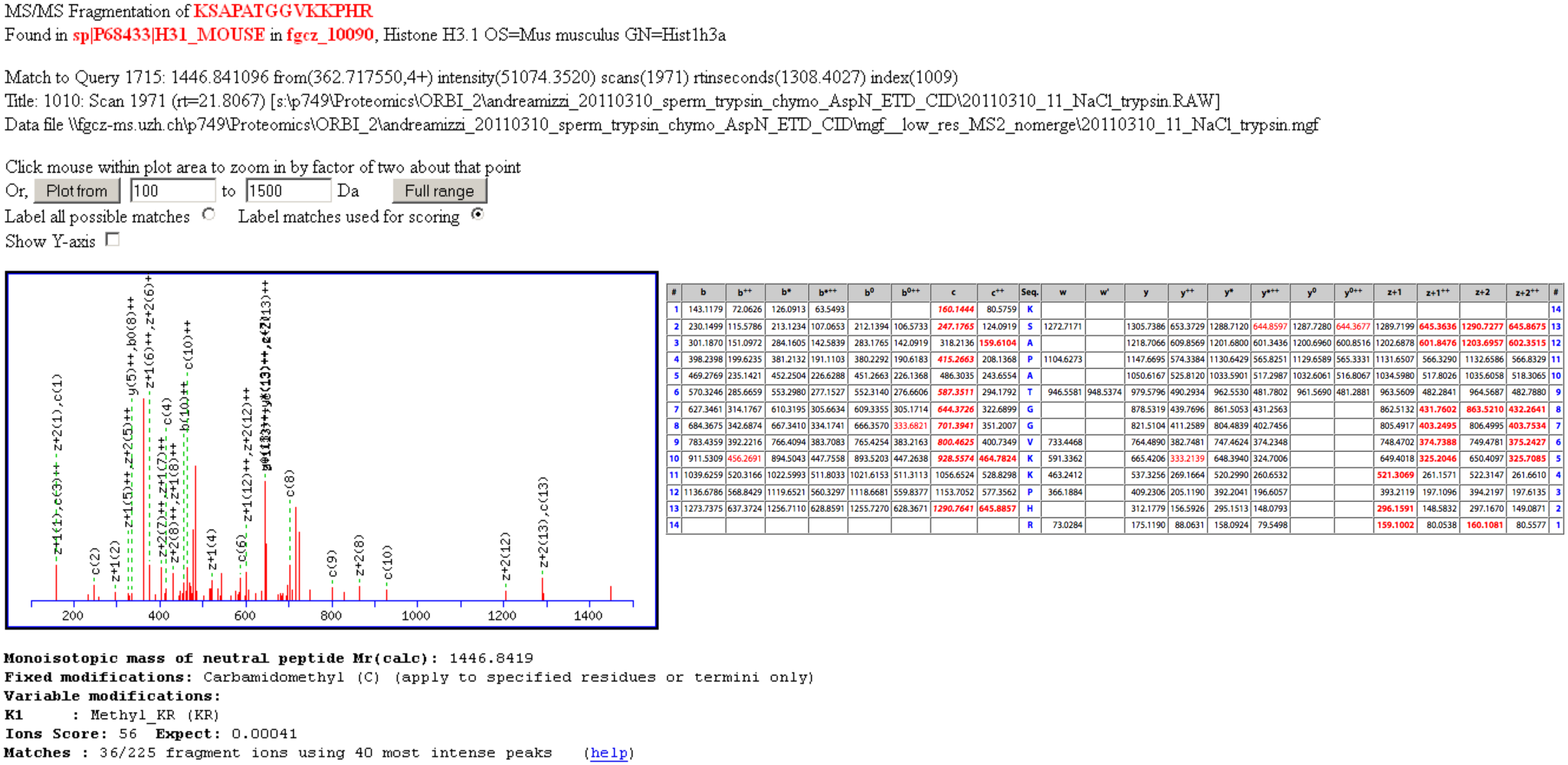
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1100 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	114.0913	57.5493					131.1179	66.0626	I													21
2	185.1285	93.0679					202.1550	101.5811	A			2223.1404	1112.0739	2206.1139	1103.5606	2205.1299	1103.0686	2207.1217	1104.0645	2208.1295	1104.5684	20
3	313.1870	157.0972	296.1605	148.5839			330.2136	165.6104	Q	2078.0553		2152.1033	1076.5553	2135.0768	1068.0420	2134.0927	1067.5500	2136.0846	1068.5459	2137.0924	1069.0498	19
4	428.2140	214.6106	411.1874	206.0974	410.2034	205.6053	445.2405	223.1239	D	1963.0284		2024.0447	1012.5260	2007.0182	1004.0127	2006.0342	1003.5207	2008.0260	1004.5166	2009.0338	1005.0206	18
5	575.2824	288.1448	558.2558	279.6316	557.2718	279.1396	592.3089	296.6581	F			1909.0178	955.0125	1891.9912	946.4993	1891.0072	946.0073	1892.9991	947.0032	1894.0069	947.5071	17
6	703.3774	352.1923	686.3508	343.6790	685.3668	343.1870	720.4039	360.7056	K	1687.8650		1761.9494	881.4783	1744.9228	872.9651	1743.9388	872.4730	1745.9307	873.4690	1746.9385	873.9729	16
7	804.4250	402.7162	787.3985	394.2029	786.4145	393.7109	821.4516	411.2294	T	1600.8329	1602.8122	1633.8544	817.4308	1616.8279	808.9176	1615.8438	808.4256	1617.8357	809.4215	1618.8435	809.9254	15
8	919.4520	460.2296	902.4254	451.7164	901.4414	451.2243	936.4785	468.7429	D	1471.7904		1532.8067	766.9070	1515.7802	758.3937	1514.7962	757.9017	1516.7880	758.8976	1517.7958	759.4016	14
9	1032.5360	***516.7717***	1015.5095	508.2584	1014.5255	507.7664	1049.5626	525.2849	L	1358.7063		1417.7798	709.3935	1400.7532	700.8803	1399.7692	700.3883	1401.7611	701.3842	1402.7689	701.8881	13
10	1202.6528	***601.8300***	1185.6263	593.3168	1184.6422	592.8248	1219.6793	610.3433	R	1188.5895		1304.6957	652.8515	1287.6692	644.3382	1286.6852	643.8462	1288.6770	644.8421	1289.6848	645.3461	12
11	1349.7212	675.3642	1332.6947	666.8510	1331.7106	666.3590	1366.7478	683.8775	F			1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	1118.5602	559.7838	1119.5681	560.2877	11
12	1477.7798	***739.3935***	1460.7532	730.8803	1459.7692	730.3883	1494.8063	747.9068	Q	913.4625		987.5106	494.2589	970.4840	485.7456	969.5000	485.2536	971.4918	486.2496	972.4997	486.7535	10
13	1564.8118	782.9095	1547.7853	774.3963	1546.8013	773.9043	1581.8384	791.4228	S	826.4305		859.4520	430.2296	842.4254	421.7164	841.4414	421.2243	843.4333	422.2203	844.4411	422.7242	9
14	1635.8489	***818.4281***	1618.8224	809.9148	1617.8384	809.4228	1652.8755	826.9414	A			772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	756.4012	378.7042	757.4090	379.2082	8
15	1706.8860	***853.9467***	1689.8595	845.4334	1688.8755	844.9414	1723.9126	862.4599	A			701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	685.3641	343.1857	686.3719	343.6896	7
16	1819.9701	***910.4887***	1802.9436	901.9754	1801.9595	901.4834	1836.9967	919.0020	I	585.2879	599.3035	**630.3457**	315.6765	613.3192	307.1632	612.3352	306.6712	614.3270	307.6671	615.3348	308.1710	6
17	1876.9916	***938.9994***	1859.9650	930.4862	1858.9810	929.9941	1894.0181	947.5127	G			**517.2617**	259.1345	500.2351	250.6212	499.2511	250.1292	501.2429	251.1251	502.2508	251.6290	5
18	1948.0287	***974.5180***	1931.0021	966.0047	1930.0181	965.5127	1965.0552	983.0313	A			460.2402	230.6237	443.2136	222.1105	442.2296	221.6185	444.2215	222.6144	445.2293	223.1183	4
19	2061.1128	***1031.0600***	2044.0862	1022.5467	2043.1022	1022.0547	2078.1393	1039.5733	L	330.1296		**389.2031**	195.1052	372.1765	186.5919	371.1925	186.0999	373.1844	187.0958	374.1922	187.5997	3
20	2189.1713	***1095.0893***	2172.1448	1086.5760	2171.1608	1086.0840	2206.1979	1103.6026	Q	202.0710		**276.1190**	138.5631	259.0925	130.0499	258.1084	129.5579	260.1003	130.5538	261.1081	131.0577	2
21									E	73.0284		148.0604	74.5339			130.0499	65.5286	132.0417	66.5245	133.0495	67.0284	1

```
Monoisotopic mass of neutral peptide Mr(calc): 2335.2172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
R10     : Methyl_KR (KR)
Ions Score: 55  Expect: 0.017
Matches : 19/363 fragment ions using 29 most intense peaks   (help)
```

Mascot Search Results: Peptide View

IAQDFKTDLRme1FQSAAIGALQE



MS/MS Fragmentation of KSAPATGGVKKPHR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 1715: 1446.841096 from(362.717550,4+) intensity(51074.3520) scans(1971) rtinseconds(1308.4027) index(1009)
Title: 1010: Scan 1971 (rt=21.8067) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_11_NaCl_trypsin.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_11_NaCl_trypsin.mgf

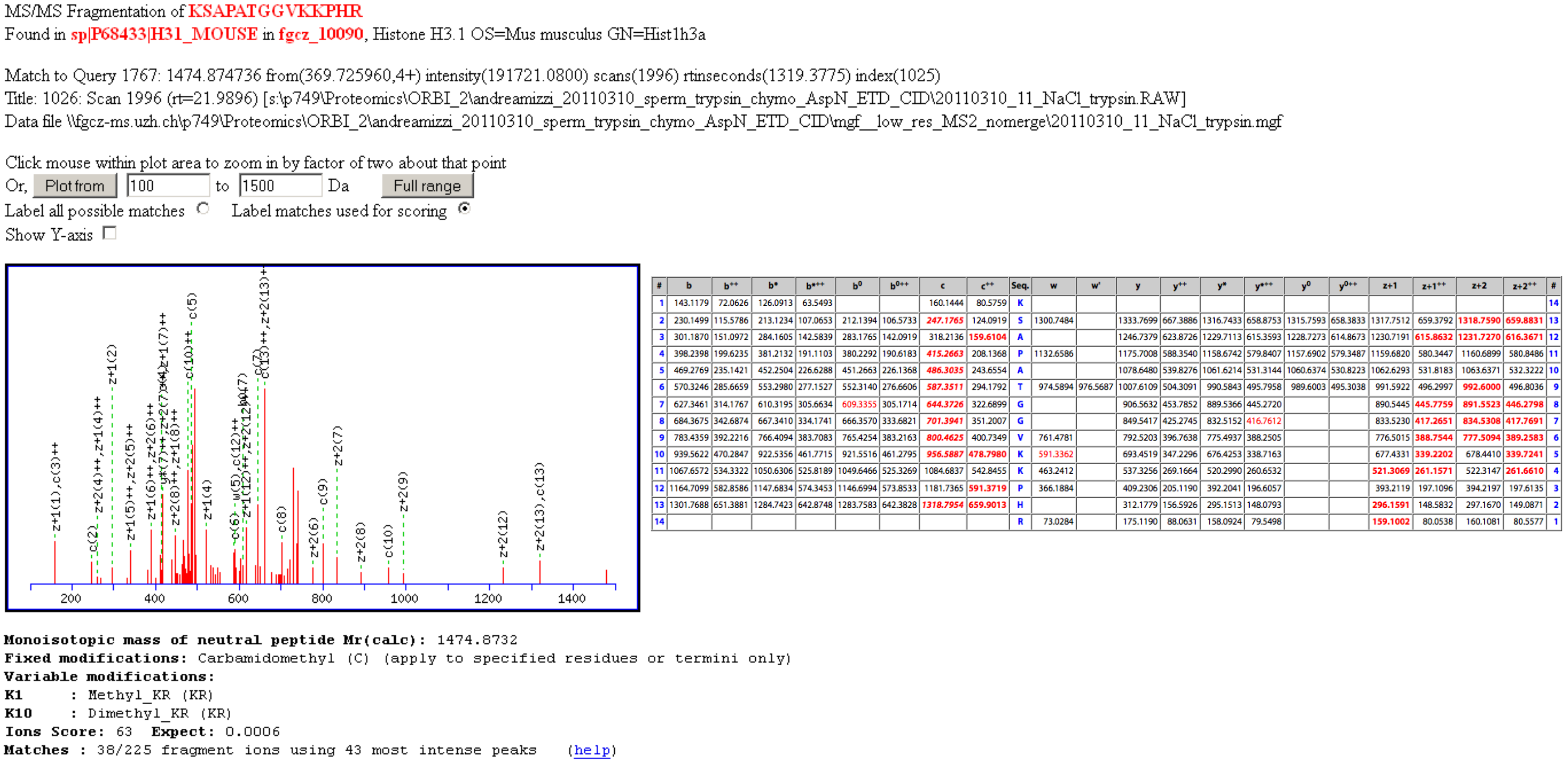
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													14
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	247.1765	124.0919	S	1272.7171		1305.7386	653.3729	1288.7120	644.8597	1287.7280	644.3677	1289.7199	645.3636	1290.7277	645.8675	13
3	301.1870	151.0972	284.1605	142.5839	283.1765	142.0919	318.2136	159.6104	A			1218.7066	609.8569	1201.6800	601.3436	1200.6960	600.8516	1202.6878	601.8476	1203.6957	602.3515	12
4	398.2398	199.6235	381.2132	191.1103	380.2292	190.6183	415.2663	208.1368	P	1104.6273		1147.6695	574.3384	1130.6429	565.8251	1129.6589	565.3331	1131.6507	566.3290	1132.6586	566.8329	11
5	469.2769	235.1421	452.2504	226.6288	451.2663	226.1368	486.3035	243.6554	A			1050.6167	525.8120	1033.5901	517.2987	1032.6061	516.8067	1034.5980	517.8026	1035.6058	518.3065	10
6	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	587.3511	294.1792	T	946.5581	948.5374	979.5796	490.2934	962.5530	481.7802	961.5690	481.2881	963.5609	482.2841	964.5687	482.7880	9
7	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	644.3726	322.6899	G			878.5319	439.7696	861.5053	431.2563			862.5132	431.7602	863.5210	432.2641	8
8	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	701.3941	351.2007	G			821.5104	411.2589	804.4839	402.7456			805.4917	403.2495	806.4995	403.7534	7
9	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	800.4625	400.7349	V	733.4468		764.4890	382.7481	747.4624	374.2348			748.4702	374.7388	749.4781	375.2427	6
10	911.5309	456.2691	894.5043	447.7558	893.5203	447.2638	928.5574	464.7824	K	591.3362		665.4206	333.2139	648.3940	324.7006			649.4018	325.2046	650.4097	325.7085	5
11	1039.6259	520.3166	1022.5993	511.8033	1021.6153	511.3113	1056.6524	528.8298	K	463.2412		537.3256	269.1664	520.2990	260.6532			521.3069	261.1571	522.3147	261.6610	4
12	1136.6786	568.8429	1119.6521	560.3297	1118.6681	559.8377	1153.7052	577.3562	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1273.7375	637.3724	1256.7110	628.8591	1255.7270	628.3671	1290.7641	645.8857	H			312.1779	156.5926	295.1513	148.0793			296.1591	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1446.8419
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
Ions Score: 56 **Expect:** 0.00041
Matches : 36/225 fragment ions using 40 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1SAPATGGVKKPHR



MS/MS Fragmentation of KSAPATGGVKKPHR

Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 1767: 1474.874736 from(369.725960,4+) intensity(191721.0800) scans(1996) rtinseconds(1319.3775) index(1025)

Title: 1026: Scan 1996 (rt=21.9896) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_11_NaCl_trypsin.RAW]

Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_11_NaCl_trypsin.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1500 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													14
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	***247.1765***	124.0919	S	1300.7484		1333.7699	667.3886	1316.7433	658.8753	1315.7593	658.3833	1317.7512	659.3792	**1318.7590**	**659.8831**	13
3	301.1870	151.0972	284.1605	142.5839	283.1765	142.0919	318.2136	**159.6104**	A			1246.7379	623.8726	1229.7113	615.3593	1228.7273	614.8673	1230.7191	**615.8632**	**1231.7270**	**616.3671**	12
4	398.2398	199.6235	381.2132	191.1103	380.2292	190.6183	***415.2663***	208.1368	P	1132.6586		1175.7008	588.3540	1158.6742	579.8407	1157.6902	579.3487	1159.6820	580.3447	1160.6899	580.8486	11
5	469.2769	235.1421	452.2504	226.6288	451.2663	226.1368	***486.3035***	243.6554	A			1078.6480	539.8276	1061.6214	531.3144	1060.6374	530.8223	1062.6293	531.8183	1063.6371	532.3222	10
6	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	***587.3511***	294.1792	T	974.5894	976.5687	1007.6109	504.3091	990.5843	495.7958	989.6003	495.3038	991.5922	496.2997	**992.6000**	496.8036	9
7	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	***644.3726***	322.6899	G			906.5632	453.7852	889.5366	445.2720			890.5445	**445.7759**	**891.5523**	**446.2798**	8
8	684.3675	342.6874	667.3410	334.1741	666.3570	333.6821	***701.3941***	351.2007	G			849.5417	425.2745	832.5152	416.7612			833.5230	**417.2651**	**834.5308**	**417.7691**	7
9	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	***800.4625***	400.7349	V	761.4781		792.5203	396.7638	775.4937	388.2505			776.5015	**388.7544**	**777.5094**	**389.2583**	6
10	939.5622	470.2847	922.5356	461.7715	921.5516	461.2795	***956.5887***	**478.7980**	K	591.3362		693.4519	347.2296	676.4253	338.7163			677.4331	**339.2202**	678.4410	**339.7241**	5
11	1067.6572	534.3322	1050.6306	525.8189	1049.6466	525.3269	1084.6837	542.8455	K	463.2412		537.3256	269.1664	520.2990	260.6532			**521.3069**	**261.1571**	522.3147	**261.6610**	4
12	1164.7099	582.8586	1147.6834	574.3453	1146.6994	573.8533	1181.7365	**591.3719**	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1301.7688	651.3881	1284.7423	642.8748	1283.7583	642.3828	***1318.7954***	**659.9013**	H			312.1779	156.5926	295.1513	148.0793			**296.1591**	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1474.8732

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

Variable modifications:

K1 : Methyl_KR (KR)

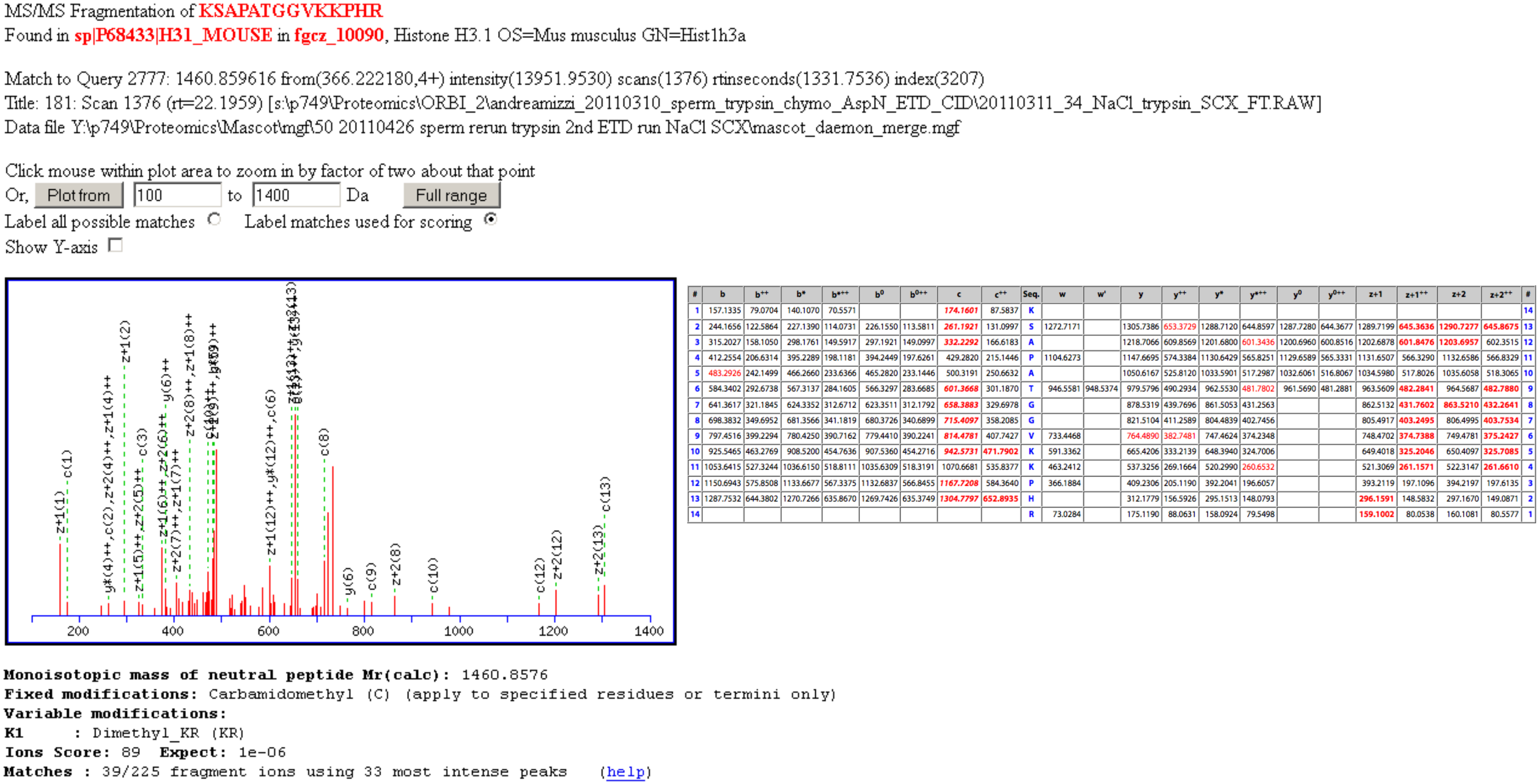
K10 : Dimethyl_KR (KR)

Ions Score: 63 **Expect:** 0.0006

Matches : 38/225 fragment ions using 43 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1SAPATGGVKme2KPHR


MS/MS Fragmentation of KSAPATGGVKKPHR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2777: 1460.859616 from(366.222180,4+) intensity(13951.9530) scans(1376) rtinseconds(1331.7536) index(3207)
Title: 181: Scan 1376 (rt=22.1959) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

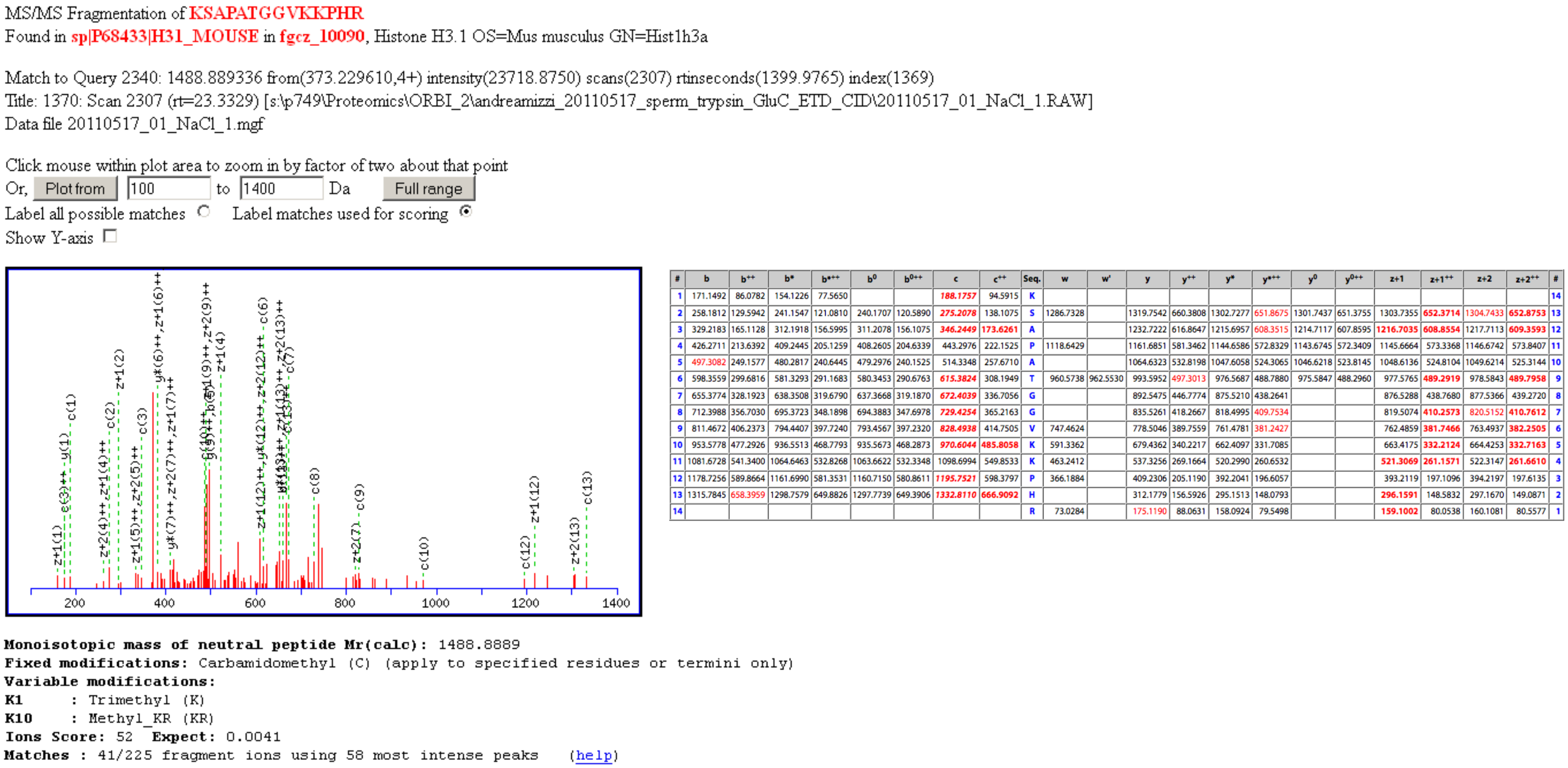
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			***174.1601***	87.5837	K													14
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	***261.1921***	131.0997	S	1272.7171		1305.7386	653.3729	1288.7120	644.8597	1287.7280	644.3677	1289.7199	**645.3636**	**1290.7277**	**645.8675**	13
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	***332.2292***	166.6183	A			1218.7066	609.8569	1201.6800	601.3436	1200.6960	600.8516	1202.6878	**601.8476**	**1203.6957**	602.3515	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	429.2820	215.1446	P	1104.6273		1147.6695	574.3384	1130.6429	565.8251	1129.6589	565.3331	1131.6507	566.3290	1132.6586	566.8329	11
5	483.2926	242.1499	466.2660	233.6366	465.2820	233.1446	500.3191	250.6632	A			1050.6167	525.8120	1033.5901	517.2987	1032.6061	516.8067	1034.5980	517.8026	1035.6058	518.3065	10
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	***601.3668***	301.1870	T	946.5581	948.5374	979.5796	490.2934	962.5530	481.7802	961.5690	481.2881	963.5609	**482.2841**	964.5687	**482.7880**	9
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	***658.3883***	329.6978	G			878.5319	439.7696	861.5053	431.2563			862.5132	**431.7602**	**863.5210**	**432.2641**	8
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	***715.4097***	358.2085	G			821.5104	411.2589	804.4839	402.7456			805.4917	**403.2495**	806.4995	**403.7534**	7
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	***814.4781***	407.7427	V	733.4468		764.4890	382.7481	747.4624	374.2348			748.4702	**374.7388**	749.4781	**375.2427**	6
10	925.5465	463.2769	908.5200	454.7636	907.5360	454.2716	***942.5731***	**471.7902**	K	591.3362		665.4206	333.2139	648.3940	324.7006			649.4018	**325.2046**	650.4097	**325.7085**	5
11	1053.6415	527.3244	1036.6150	518.8111	1035.6309	518.3191	1070.6681	535.8377	K	463.2412		537.3256	269.1664	520.2990	260.6532			521.3069	**261.1571**	522.3147	**261.6610**	4
12	1150.6943	575.8508	1133.6677	567.3375	1132.6837	566.8455	***1167.7208***	584.3640	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1287.7532	644.3802	1270.7266	635.8670	1269.7426	635.3749	***1304.7797***	**652.8935**	H			312.1779	156.5926	295.1513	148.0793			**296.1591**	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1460.8576
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 89 **Expect:** 1e-06
Matches : 39/225 fragment ions using 33 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPATGGVKKPHR



MS/MS Fragmentation of KSAPATGGVKKPHR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2340: 1488.889336 from(373.229610,4+) intensity(23718.8750) scans(2307) rtinseconds(1399.9765) index(1369)
Title: 1370: Scan 2307 (rt=23.3329) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

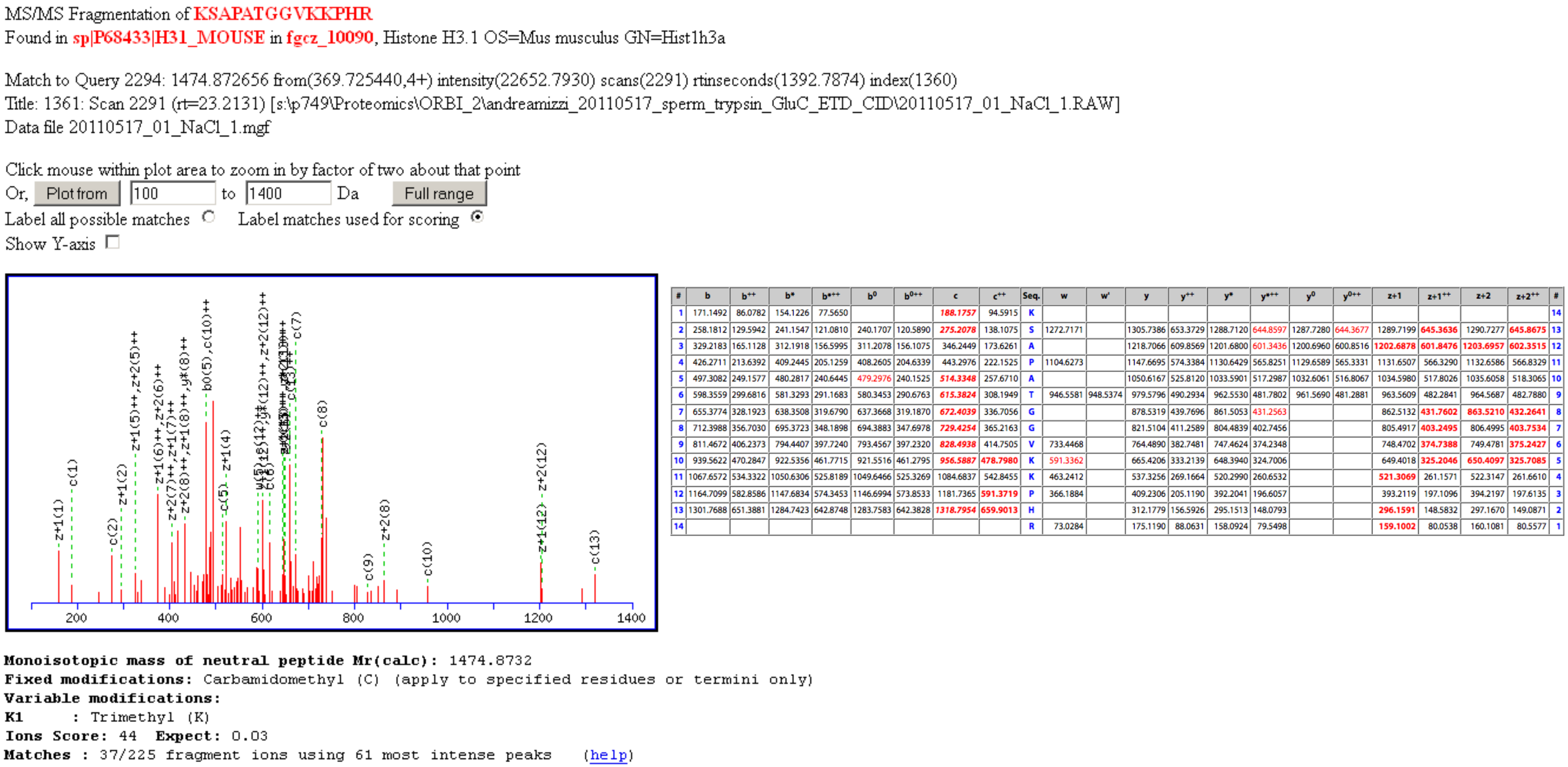
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	171.1492	86.0782	154.1226	77.5650			188.1757	94.5915	K													14
2	258.1812	129.5942	241.1547	121.0810	240.1707	120.5890	275.2078	138.1075	S	1286.7328		1319.7542	660.3808	1302.7277	651.8675	1301.7437	651.3755	1303.7355	652.3714	1304.7433	652.8753	13
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	346.2449	173.6261	A			1232.7222	616.8647	1215.6957	608.3515	1214.7117	607.8595	1216.7035	608.8554	1217.7113	609.3593	12
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	443.2976	222.1525	P	1118.6429		1161.6851	581.3462	1144.6586	572.8329	1143.6745	572.3409	1145.6664	573.3368	1146.6742	573.8407	11
5	497.3082	249.1577	480.2817	240.6445	479.2976	240.1525	514.3348	257.6710	A			1064.6323	532.8198	1047.6058	524.3065	1046.6218	523.8145	1048.6136	524.8104	1049.6214	525.3144	10
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	615.3824	308.1949	T	960.5738	962.5530	993.5952	497.3013	976.5687	488.7880	975.5847	488.2960	977.5765	489.2919	978.5843	489.7958	9
7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	672.4039	336.7056	G			892.5475	446.7774	875.5210	438.2641			876.5288	438.7680	877.5366	439.2720	8
8	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	729.4254	365.2163	G			835.5261	418.2667	818.4995	409.7534			819.5074	410.2573	820.5152	410.7612	7
9	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	828.4938	414.7505	V	747.4624		778.5046	389.7559	761.4781	381.2427			762.4859	381.7466	763.4937	382.2505	6
10	953.5778	477.2926	936.5513	468.7793	935.5673	468.2873	970.6044	485.8058	K	591.3362		679.4362	340.2217	662.4097	331.7085			663.4175	332.2124	664.4253	332.7163	5
11	1081.6728	541.3400	1064.6463	532.8268	1063.6622	532.3348	1098.6994	549.8533	K	463.2412		537.3256	269.1664	520.2990	260.6532			521.3069	261.1571	522.3147	261.6610	4
12	1178.7256	589.8664	1161.6990	581.3531	1160.7150	580.8611	1195.7521	598.3797	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1315.7845	658.3959	1298.7579	649.8826	1297.7739	649.3906	1332.8110	666.9092	H			312.1779	156.5926	295.1513	148.0793			296.1591	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1488.8889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
K10 : Methyl_KR (KR)
Ions Score: 52 **Expect:** 0.0041
Matches : 41/225 fragment ions using 58 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3SAPATGGVKme1KPHR



MS/MS Fragmentation of KSAPATGGVKKPHR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2294: 1474.872656 from(369.725440,4+) intensity(22652.7930) scans(2291) rtinseconds(1392.7874) index(1360)
Title: 1361: Scan 2291 (rt=23.2131) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

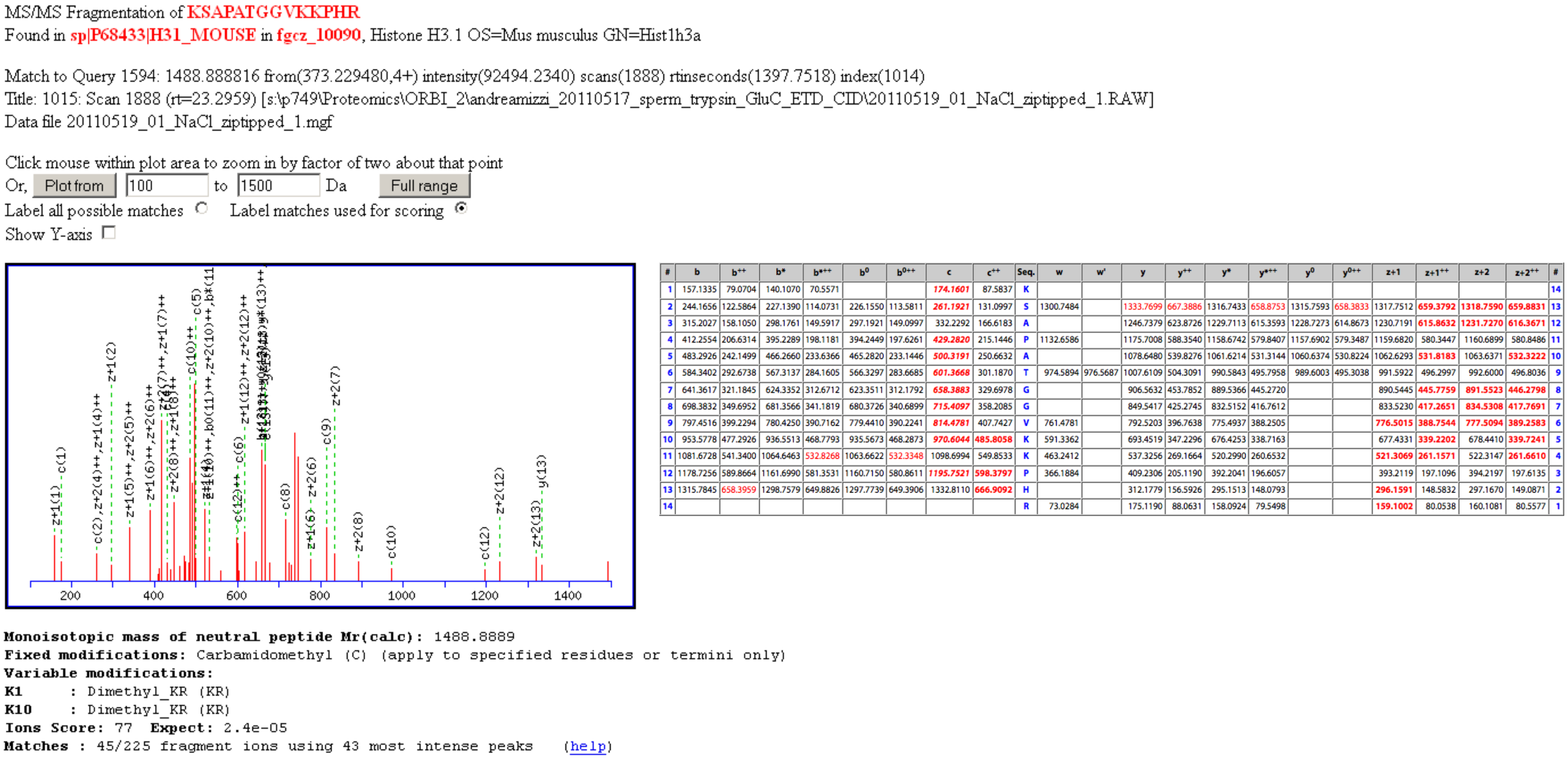
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	171.1492	86.0782	154.1226	77.5650			***188.1757***	94.5915	K													14
2	258.1812	129.5942	241.1547	121.0810	240.1707	120.5890	***275.2078***	138.1075	S	1272.7171		1305.7386	653.3729	1288.7120	644.8597	1287.7280	644.3677	1289.7199	**645.3636**	1290.7277	**645.8675**	13
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	346.2449	173.6261	A			1218.7066	609.8569	1201.6800	601.3436	1200.6960	600.8516	**1202.6878**	**601.8476**	**1203.6957**	**602.3515**	12
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	443.2976	222.1525	P	1104.6273		1147.6695	574.3384	1130.6429	565.8251	1129.6589	565.3331	1131.6507	566.3290	1132.6586	566.8329	11
5	497.3082	249.1577	480.2817	240.6445	479.2976	240.1525	***514.3348***	257.6710	A			1050.6167	525.8120	1033.5901	517.2987	1032.6061	516.8067	1034.5980	517.8026	1035.6058	518.3065	10
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	***615.3824***	308.1949	T	946.5581	948.5374	979.5796	490.2934	962.5530	481.7802	961.5690	481.2881	963.5609	482.2841	964.5687	482.7880	9
7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	***672.4039***	336.7056	G			878.5319	439.7696	861.5053	431.2563			862.5132	**431.7602**	**863.5210**	**432.2641**	8
8	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	***729.4254***	365.2163	G			821.5104	411.2589	804.4839	402.7456			805.4917	**403.2495**	806.4995	**403.7534**	7
9	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	***828.4938***	414.7505	V	733.4468		764.4890	382.7481	747.4624	374.2348			748.4702	**374.7388**	749.4781	**375.2427**	6
10	939.5622	470.2847	922.5356	461.7715	921.5516	461.2795	***956.5887***	**478.7980**	K	591.3362		665.4206	333.2139	648.3940	324.7006			649.4018	**325.2046**	**650.4097**	**325.7085**	5
11	1067.6572	534.3322	1050.6306	525.8189	1049.6466	525.3269	1084.6837	542.8455	K	463.2412		537.3256	269.1664	520.2990	260.6532			**521.3069**	261.1571	522.3147	261.6610	4
12	1164.7099	582.8586	1147.6834	574.3453	1146.6994	573.8533	1181.7365	**591.3719**	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1301.7688	651.3881	1284.7423	642.8748	1283.7583	642.3828	***1318.7954***	**659.9013**	H			312.1779	156.5926	295.1513	148.0793			**296.1591**	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1474.8732
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
Ions Score: 44 **Expect:** 0.03
Matches : 37/225 fragment ions using 61 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3SAPATGGVKKPHR



MS/MS Fragmentation of KSAPATGGVKKPHR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 1594: 1488.888816 from(373.229480,4+) intensity(92494.2340) scans(1888) rtinseconds(1397.7518) index(1014)
Title: 1015: Scan 1888 (rt=23.2959) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_01_NaCl_ziptipped_1.RAW]
Data file 20110519_01_NaCl_ziptipped_1.mgf

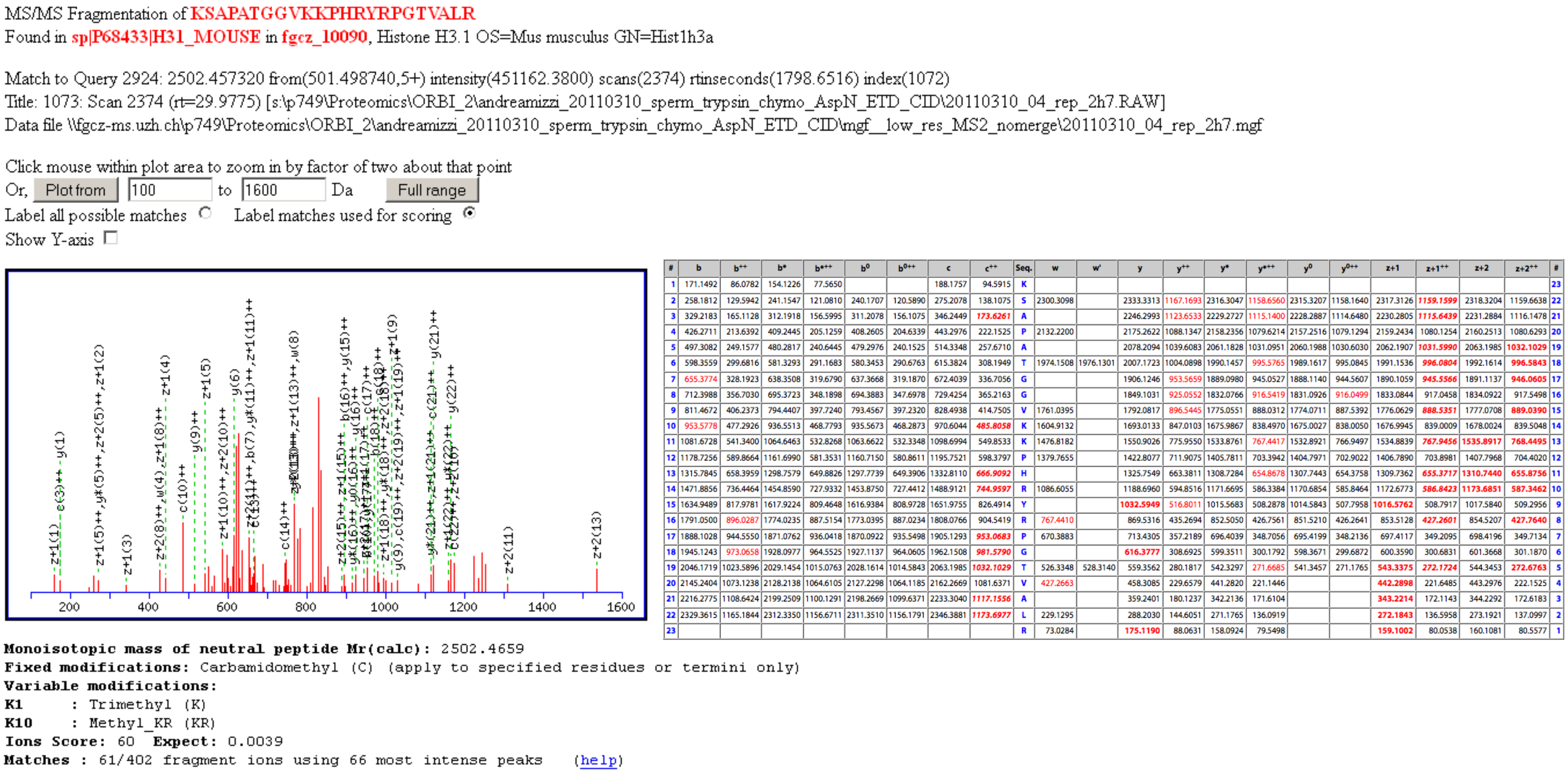
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			***174.1601***	87.5837	K													14
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	***261.1921***	131.0997	S	1300.7484		1333.7699	667.3886	1316.7433	658.8753	1315.7593	658.3833	1317.7512	**659.3792**	**1318.7590**	**659.8831**	13
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			1246.7379	623.8726	1229.7113	615.3593	1228.7273	614.8673	1230.7191	**615.8632**	**1231.7270**	**616.3671**	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	***429.2820***	215.1446	P	1132.6586		1175.7008	588.3540	1158.6742	579.8407	1157.6902	579.3487	1159.6820	580.3447	1160.6899	580.8486	11
5	483.2926	242.1499	466.2660	233.6366	465.2820	233.1446	***500.3191***	250.6632	A			1078.6480	539.8276	1061.6214	531.3144	1060.6374	530.8224	1062.6293	**531.8183**	1063.6371	**532.3222**	10
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	***601.3668***	301.1870	T	974.5894	976.5687	1007.6109	504.3091	990.5843	495.7958	989.6003	495.3038	991.5922	496.2997	992.6000	496.8036	9
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	***658.3883***	329.6978	G			906.5632	453.7852	889.5366	445.2720			890.5445	**445.7759**	**891.5523**	**446.2798**	8
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	***715.4097***	358.2085	G			849.5417	425.2745	832.5152	416.7612			833.5230	**417.2651**	**834.5308**	**417.7691**	7
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	***814.4781***	407.7427	V	761.4781		792.5203	396.7638	775.4937	388.2505			**776.5015**	**388.7544**	**777.5094**	**389.2583**	6
10	953.5778	477.2926	936.5513	468.7793	935.5673	468.2873	***970.6044***	**485.8058**	K	591.3362		693.4519	347.2296	676.4253	338.7163			677.4331	**339.2202**	678.4410	**339.7241**	5
11	1081.6728	541.3400	1064.6463	532.8268	1063.6622	532.3348	1098.6994	549.8533	K	463.2412		537.3256	269.1664	520.2990	260.6532			**521.3069**	**261.1571**	522.3147	**261.6610**	4
12	1178.7256	589.8664	1161.6990	581.3531	1160.7150	580.8611	***1195.7521***	**598.3797**	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1315.7845	658.3959	1298.7579	649.8826	1297.7739	649.3906	1332.8110	**666.9092**	H			312.1779	156.5926	295.1513	148.0793			**296.1591**	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1488.8889
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Dimethyl_KR (KR)
Ions Score: 77 **Expect:** 2.4e-05
Matches : 45/225 fragment ions using 43 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPATGGVKme2KPHR



MS/MS Fragmentation of KSAPATGGVKKPHRYRPGTVALR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2924: 2502.457320 from(501.498740,5+) intensity(451162.3800) scans(2374) rtinseconds(1798.6516) index(1072)
Title: 1073: Scan 2374 (rt=29.9775) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_04_rep_2h7.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_04_rep_2h7.mgf

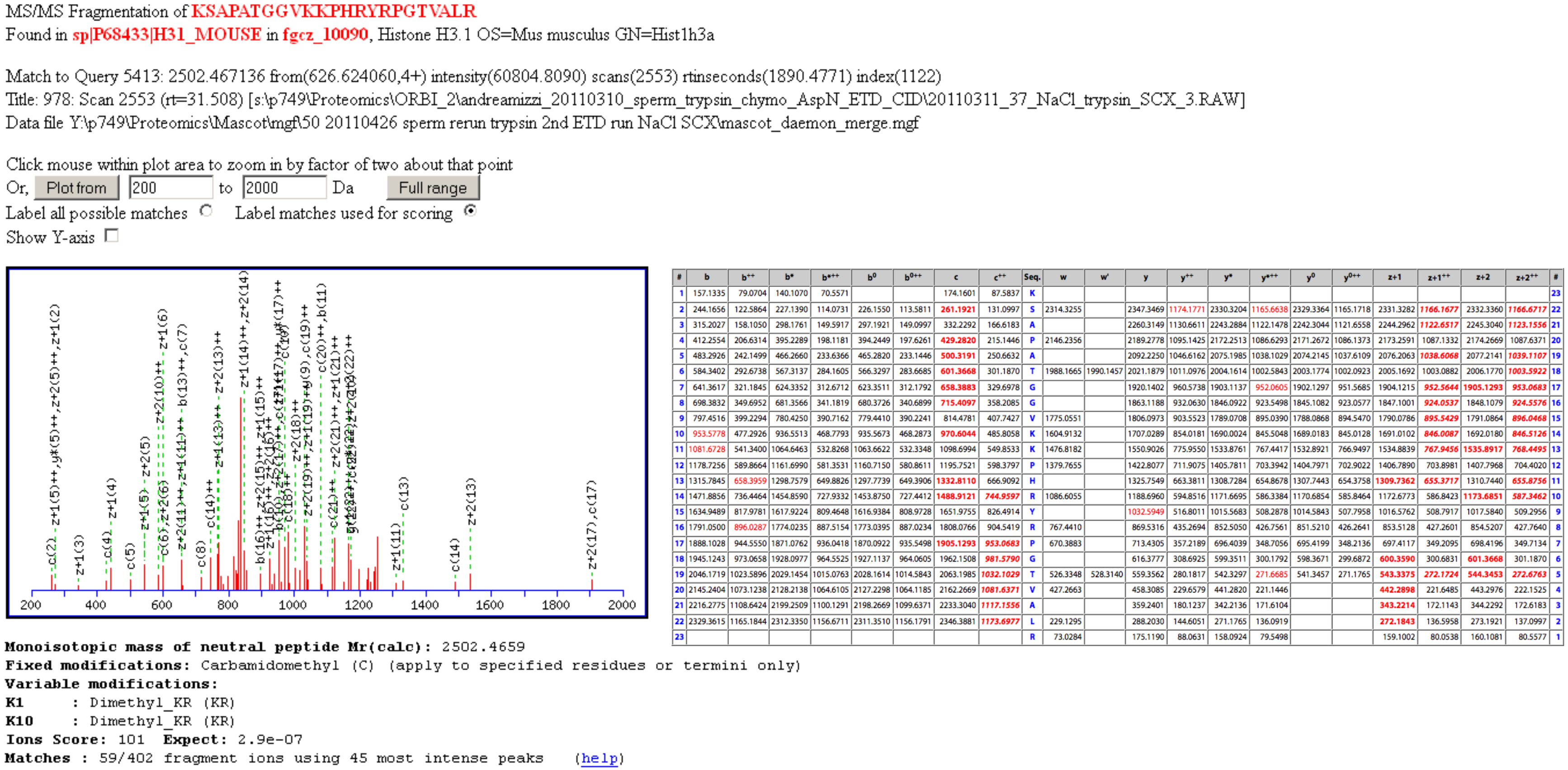
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	171.1492	86.0782	154.1226	77.5650			188.1757	94.5915	K													23
2	258.1812	129.5942	241.1547	121.0810	240.1707	120.5890	275.2078	138.1075	S	2300.3098		2333.3313	1167.1693	2316.3047	1158.6560	2315.3207	1158.1640	2317.3126	1159.1599	2318.3204	1159.6638	22
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	346.2449	173.6261	A			2246.2993	1123.6533	2229.2727	1115.1400	2228.2887	1114.6480	2230.2805	1115.6439	2231.2884	1116.1478	21
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	443.2976	222.1525	P	2132.2200		2175.2622	1088.1347	2158.2356	1079.6214	2157.2516	1079.1294	2159.2434	1080.1254	2160.2513	1080.6293	20
5	497.3082	249.1577	480.2817	240.6445	479.2976	240.1525	514.3348	257.6710	A			2078.2094	1039.6083	2061.1828	1031.0951	2060.1988	1030.6030	2062.1907	1031.5990	2063.1985	1032.1029	19
6	598.3559	299.6816	581.3293	291.1683	580.3453	290.6763	615.3824	308.1949	T	1974.1508	1976.1301	2007.1723	1004.0898	1990.1457	995.5765	1989.1617	995.0845	1991.1536	996.0804	1992.1614	996.5843	18
7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	672.4039	336.7056	G			1906.1246	953.5659	1889.0980	945.0527	1888.1140	944.5607	1890.1059	945.5566	1891.1137	946.0605	17
8	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	729.4254	365.2163	G			1849.1031	925.0552	1832.0766	916.5419	1831.0926	916.0499	1833.0844	917.0458	1834.0922	917.5498	16
9	811.4672	406.2373	794.4407	397.7240	793.4567	397.2320	828.4938	414.7505	V	1761.0395		1792.0817	896.5445	1775.0551	888.0312	1774.0711	887.5392	1776.0629	888.5351	1777.0708	889.0390	15
10	953.5778	477.2926	936.5513	468.7793	935.5673	468.2873	970.6044	485.8058	K	1604.9132		1693.0133	847.0103	1675.9867	838.4970	1675.0027	838.0050	1676.9945	839.0009	1678.0024	839.5048	14
11	1081.6728	541.3400	1064.6463	532.8268	1063.6622	532.3348	1098.6994	549.8533	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	767.9456	1535.8917	768.4495	13
12	1178.7256	589.8664	1161.6990	581.3531	1160.7150	580.8611	1195.7521	598.3797	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1315.7845	658.3959	1298.7579	649.8826	1297.7739	649.3906	1332.8110	666.9092	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	655.3717	1310.7440	655.8756	11
14	1471.8856	736.4464	1454.8590	727.9332	1453.8750	727.4412	1488.9121	744.9597	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	586.8423	1173.6851	587.3462	10
15	1634.9489	817.9781	1617.9224	809.4648	1616.9384	808.9728	1651.9755	826.4914	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1791.0500	896.0287	1774.0235	887.5154	1773.0395	887.0234	1808.0766	904.5419	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	427.2601	854.5207	427.7640	8
17	1888.1028	944.5550	1871.0762	936.0418	1870.0922	935.5498	1905.1293	953.0683	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1945.1243	973.0658	1928.0977	964.5525	1927.1137	964.0605	1962.1508	981.5790	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2046.1719	1023.5896	2029.1454	1015.0763	2028.1614	1014.5843	2063.1985	1032.1029	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	543.3375	272.1724	544.3453	272.6763	5
20	2145.2404	1073.1238	2128.2138	1064.6105	2127.2298	1064.1185	2162.2669	1081.6371	V	427.2663		458.3085	229.6579	441.2820	221.1446			442.2898	221.6485	443.2976	222.1525	4
21	2216.2775	1108.6424	2199.2509	1100.1291	2198.2669	1099.6371	2233.3040	1117.1556	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
22	2329.3615	1165.1844	2312.3350	1156.6711	2311.3510	1156.1791	2346.3881	1173.6977	L	229.1295		288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2502.4659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
K10 : Methyl_KR (KR)
Ions Score: 60 **Expect:** 0.0039
Matches : 61/402 fragment ions using 66 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3SAPATGGVKme1KPHRYRPGTVALR



MS/MS Fragmentation of KSAPATGGVKKPHRYRPGTVALR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 5413: 2502.467136 from(626.624060,4+) intensity(60804.8090) scans(2553) rtinseconds(1890.4771) index(1122)
Title: 978: Scan 2553 (rt=31.508) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

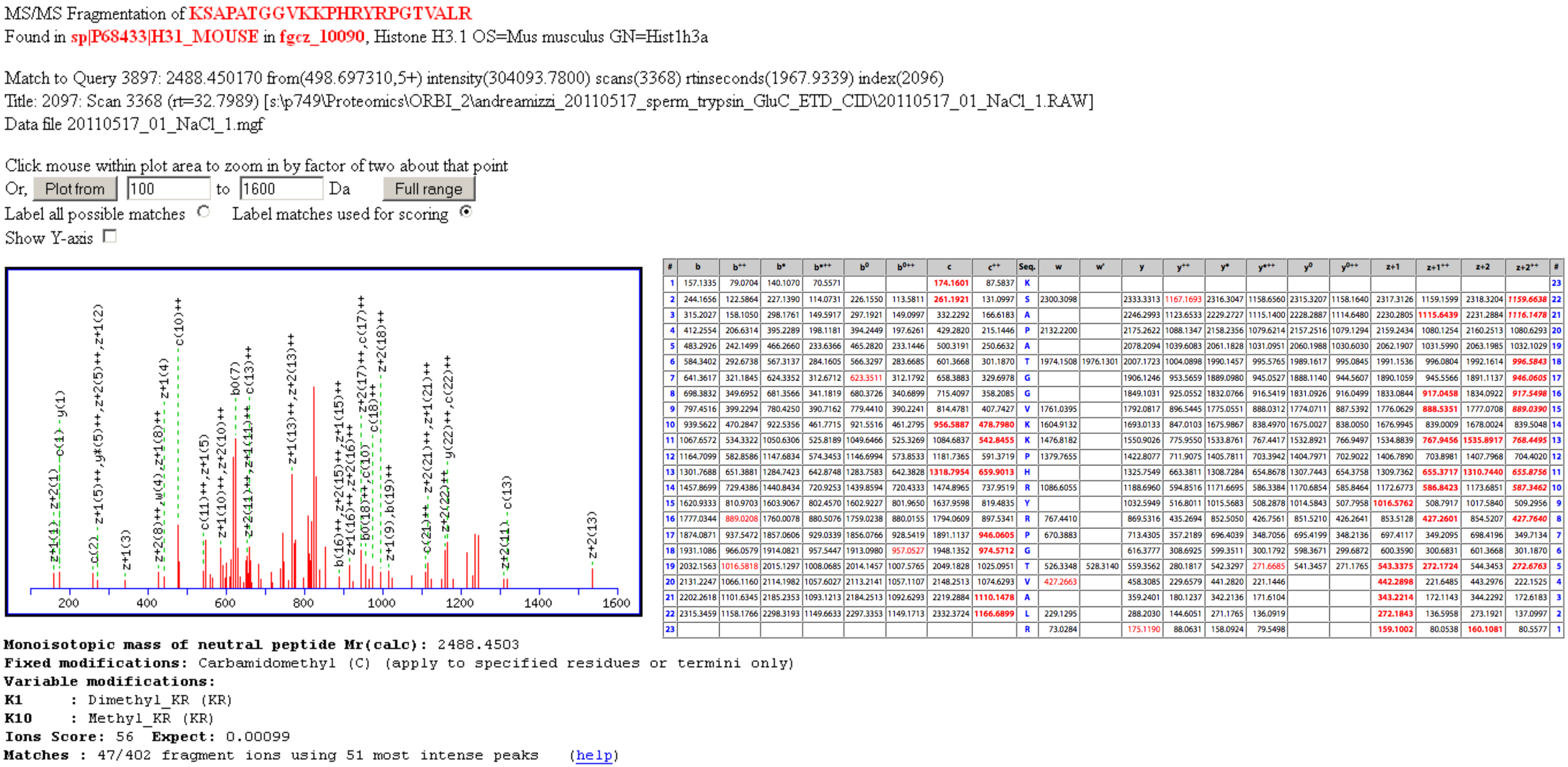
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													23
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	2314.3255		2347.3469	1174.1771	2330.3204	1165.6638	2329.3364	1165.1718	2331.3282	***1166.1677***	2332.3360	***1166.6717***	22
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			2260.3149	1130.6611	2243.2884	1122.1478	2242.3044	1121.6558	2244.2962	***1122.6517***	2245.3040	***1123.1556***	21
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	**429.2820**	215.1446	P	2146.2356		2189.2778	1095.1425	2172.2513	1086.6293	2171.2672	1086.1373	2173.2591	1087.1332	2174.2669	1087.6371	20
5	483.2926	242.1499	466.2660	233.6366	465.2820	233.1446	**500.3191**	250.6632	A			2092.2250	1046.6162	2075.1985	1038.1029	2074.2145	1037.6109	2076.2063	***1038.6068***	2077.2141	***1039.1107***	19
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	**601.3668**	301.1870	T	1988.1665	1990.1457	2021.1879	1011.0976	2004.1614	1002.5843	2003.1774	1002.0923	2005.1692	1003.0882	2006.1770	***1003.5922***	18
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	**658.3883**	329.6978	G			1920.1402	960.5738	1903.1137	952.0605	1902.1297	951.5685	1904.1215	***952.5644***	**1905.1293**	***953.0683***	17
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	**715.4097**	358.2085	G			1863.1188	932.0630	1846.0922	923.5498	1845.1082	923.0577	1847.1001	***924.0537***	1848.1079	***924.5576***	16
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	814.4781	407.7427	V	1775.0551		1806.0973	903.5523	1789.0708	895.0390	1788.0868	894.5470	1790.0786	***895.5429***	1791.0864	***896.0468***	15
10	953.5778	477.2926	936.5513	468.7793	935.5673	468.2873	**970.6044**	485.8058	K	1604.9132		1707.0289	854.0181	1690.0024	845.5048	1689.0183	845.0128	1691.0102	***846.0087***	1692.0180	***846.5126***	14
11	1081.6728	541.3400	1064.6463	532.8268	1063.6622	532.3348	1098.6994	549.8533	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	***767.9456***	**1535.8917**	***768.4495***	13
12	1178.7256	589.8664	1161.6990	581.3531	1160.7150	580.8611	1195.7521	598.3797	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1315.7845	658.3959	1298.7579	649.8826	1297.7739	649.3906	**1332.8110**	666.9092	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	**1309.7362**	***655.3717***	1310.7440	***655.8756***	11
14	1471.8856	736.4464	1454.8590	727.9332	1453.8750	727.4412	**1488.9121**	***744.9597***	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	586.8423	**1173.6851**	***587.3462***	10
15	1634.9489	817.9781	1617.9224	809.4648	1616.9384	808.9728	1651.9755	826.4914	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1791.0500	896.0287	1774.0235	887.5154	1773.0395	887.0234	1808.0766	904.5419	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	427.2601	854.5207	427.7640	8
17	1888.1028	944.5550	1871.0762	936.0418	1870.0922	935.5498	**1905.1293**	***953.0683***	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1945.1243	973.0658	1928.0977	964.5525	1927.1137	964.0605	1962.1508	***981.5790***	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	**600.3590**	300.6831	**601.3668**	301.1870	6
19	2046.1719	1023.5896	2029.1454	1015.0763	2028.1614	1014.5843	2063.1985	***1032.1029***	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	***272.1724***	**544.3453**	***272.6763***	5
20	2145.2404	1073.1238	2128.2138	1064.6105	2127.2298	1064.1185	2162.2669	***1081.6371***	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	443.2976	222.1525	4
21	2216.2775	1108.6424	2199.2509	1100.1291	2198.2669	1099.6371	2233.3040	***1117.1556***	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2329.3615	1165.1844	2312.3350	1156.6711	2311.3510	1156.1791	2346.3881	***1173.6977***	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2502.4659
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Dimethyl_KR (KR)
Ions Score: 101 **Expect:** 2.9e-07
Matches : 59/402 fragment ions using 45 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPATGGVKme2KPHRYRPGTVALR



MS/MS Fragmentation of KSAPATGGVKKPHRYRPGTVALR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 3897: 2488.450170 from(498.697310,5+) intensity(304093.7800) scans(3368) rtinseconds(1967.9339) index(2096)
Title: 2097: Scan 3368 (rt=32.7989) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

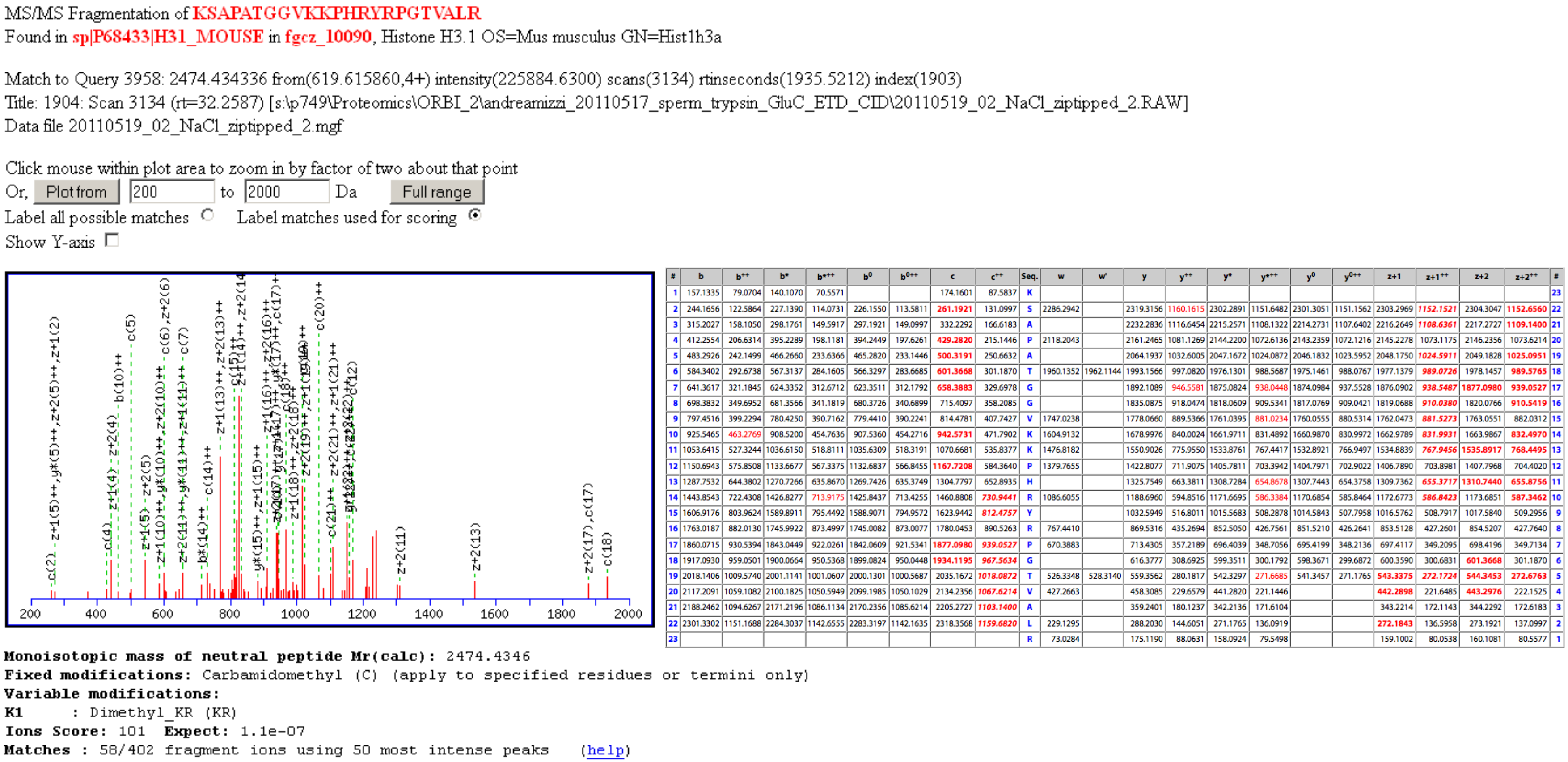
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			**174.1601**	87.5837	K													23
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	2300.3098		2333.3313	1167.1693	2316.3047	1158.6560	2315.3207	1158.1640	2317.3126	1159.1599	2318.3204	***1159.6638***	22
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			2246.2993	1123.6533	2229.2727	1115.1400	2228.2887	1114.6480	2230.2805	**1115.6439**	2231.2884	***1116.1478***	21
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	429.2820	215.1446	P	2132.2200		2175.2622	1088.1347	2158.2356	1079.6214	2157.2516	1079.1294	2159.2434	1080.1254	2160.2513	1080.6293	20
5	483.2926	242.1499	466.2660	233.6366	465.2820	233.1446	500.3191	250.6632	A			2078.2094	1039.6083	2061.1828	1031.0951	2060.1988	1030.6030	2062.1907	1031.5990	2063.1985	1032.1029	19
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	601.3668	301.1870	T	1974.1508	1976.1301	2007.1723	1004.0898	1990.1457	995.5765	1989.1617	995.0845	1991.1536	996.0804	1992.1614	***996.5843***	18
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	658.3883	329.6978	G			1906.1246	953.5659	1889.0980	945.0527	1888.1140	944.5607	1890.1059	945.5566	1891.1137	***946.0605***	17
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	715.4097	358.2085	G			1849.1031	925.0552	1832.0766	916.5419	1831.0926	916.0499	1833.0844	**917.0458**	1834.0922	***917.5498***	16
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	814.4781	407.7427	V	1761.0395		1792.0817	896.5445	1775.0551	888.0312	1774.0711	887.5392	1776.0629	**888.5351**	1777.0708	***889.0390***	15
10	939.5622	470.2847	922.5356	461.7715	921.5516	461.2795	**956.5887**	**478.7980**	K	1604.9132		1693.0133	847.0103	1675.9867	838.4970	1675.0027	838.0050	1676.9945	839.0009	1678.0024	839.5048	14
11	1067.6572	534.3322	1050.6306	525.8189	1049.6466	525.3269	1084.6837	**542.8455**	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	**767.9456**	**1535.8917**	***768.4495***	13
12	1164.7099	582.8586	1147.6834	574.3453	1146.6994	573.8533	1181.7365	591.3719	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1301.7688	651.3881	1284.7423	642.8748	1283.7583	642.3828	**1318.7954**	**659.9013**	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	**655.3717**	**1310.7440**	***655.8756***	11
14	1457.8699	729.4386	1440.8434	720.9253	1439.8594	720.4333	1474.8965	737.9519	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	**586.8423**	1173.6851	***587.3462***	10
15	1620.9333	810.9703	1603.9067	802.4570	1602.9227	801.9650	1637.9598	819.4835	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	**1016.5762**	508.7917	1017.5840	509.2956	9
16	1777.0344	889.0208	1760.0078	880.5076	1759.0238	880.0155	1794.0609	897.5341	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	**427.2601**	854.5207	***427.7640***	8
17	1874.0871	937.5472	1857.0606	929.0339	1856.0766	928.5419	1891.1137	**946.0605**	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1931.1086	966.0579	1914.0821	957.5447	1913.0980	957.0527	1948.1352	**974.5712**	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2032.1563	1016.5818	2015.1297	1008.0685	2014.1457	1007.5765	2049.1828	1025.0951	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	**272.1724**	544.3453	***272.6763***	5
20	2131.2247	1066.1160	2114.1982	1057.6027	2113.2141	1057.1107	2148.2513	1074.6293	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	443.2976	222.1525	4
21	2202.2618	1101.6345	2185.2353	1093.1213	2184.2513	1092.6293	2219.2884	**1110.1478**	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2315.3459	1158.1766	2298.3193	1149.6633	2297.3353	1149.1713	2332.3724	**1166.6899**	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	**160.1081**	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2488.4503
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Methyl_KR (KR)
Ions Score: 56 **Expect:** 0.00099
Matches : 47/402 fragment ions using 51 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPATGGVKme1KPHRYRPGTVALR



MS/MS Fragmentation of KSAPATGGVKKPHRYRPGTVALR
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 3958: 2474.434336 from(619.615860,4+) intensity(225884.6300) scans(3134) rtinseconds(1935.5212) index(1903)
Title: 1904: Scan 3134 (rt=32.2587) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_02_NaCl_ziptipped_2.RAW]
Data file 20110519_02_NaCl_ziptipped_2.mgf

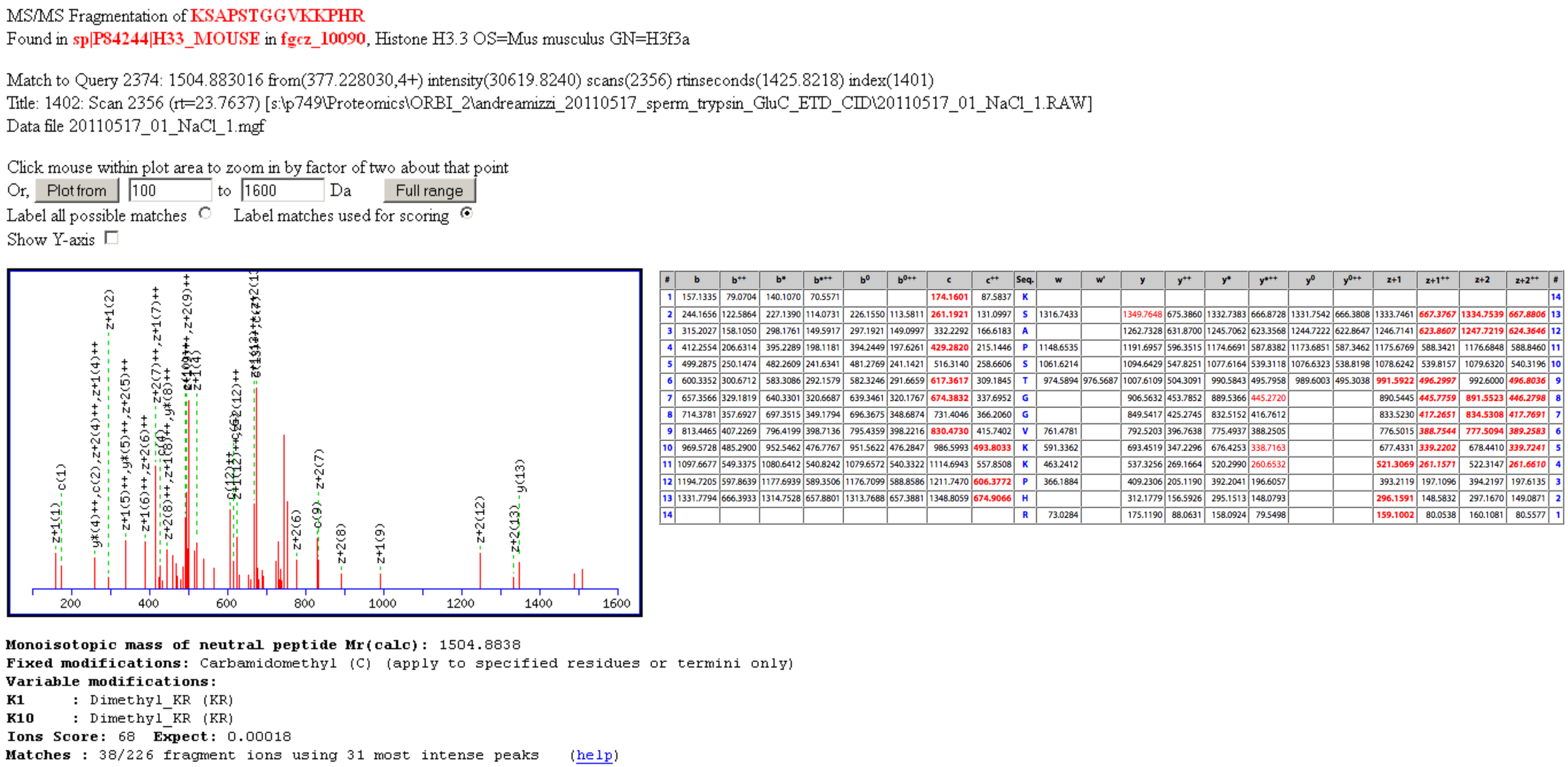
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													23
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	261.1921	131.0997	S	2286.2942		2319.3156	1160.1615	2302.2891	1151.6482	2301.3051	1151.1562	2303.2969	1152.1521	2304.3047	1152.6560	22
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			2232.2836	1116.6454	2215.2571	1108.1322	2214.2731	1107.6402	2216.2649	1108.6361	2217.2727	1109.1400	21
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	429.2820	215.1446	P	2118.2043		2161.2465	1081.1269	2144.2200	1072.6136	2143.2359	1072.1216	2145.2278	1073.1175	2146.2356	1073.6214	20
5	483.2926	242.1499	466.2660	233.6366	465.2820	233.1446	500.3191	250.6632	A			2064.1937	1032.6005	2047.1672	1024.0872	2046.1832	1023.5952	2048.1750	1024.5911	2049.1828	1025.0951	19
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	601.3668	301.1870	T	1960.1352	1962.1144	1993.1566	997.0820	1976.1301	988.5687	1975.1461	988.0767	1977.1379	989.0726	1978.1457	989.5765	18
7	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	658.3883	329.6978	G			1892.1089	946.5581	1875.0824	938.0448	1874.0984	937.5528	1876.0902	938.5487	1877.0980	939.0527	17
8	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	715.4097	358.2085	G			1835.0875	918.0474	1818.0609	909.5341	1817.0769	909.0421	1819.0688	910.0380	1820.0766	910.5419	16
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	814.4781	407.7427	V	1747.0238		1778.0660	889.5366	1761.0395	881.0234	1760.0555	880.5314	1762.0473	881.5273	1763.0551	882.0312	15
10	925.5465	463.2769	908.5200	454.7636	907.5360	454.2716	942.5731	471.7902	K	1604.9132		1678.9976	840.0024	1661.9711	831.4892	1660.9870	830.9972	1662.9789	831.9931	1663.9867	832.4970	14
11	1053.6415	527.3244	1036.6150	518.8111	1035.6309	518.3191	1070.6681	535.8377	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	767.9456	1535.8917	768.4495	13
12	1150.6943	575.8508	1133.6677	567.3375	1132.6837	566.8455	1167.7208	584.3640	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1287.7532	644.3802	1270.7266	635.8670	1269.7426	635.3749	1304.7797	652.8935	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	655.3717	1310.7440	655.8756	11
14	1443.8543	722.4308	1426.8277	713.9175	1425.8437	713.4255	1460.8808	730.9441	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	586.8423	1173.6851	587.3462	10
15	1606.9176	803.9624	1589.8911	795.4492	1588.9071	794.9572	1623.9442	812.4757	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1763.0187	882.0130	1745.9922	873.4997	1745.0082	873.0077	1780.0453	890.5263	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	427.2601	854.5207	427.7640	8
17	1860.0715	930.5394	1843.0449	922.0261	1842.0609	921.5341	1877.0980	939.0527	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1917.0930	959.0501	1900.0664	950.5368	1899.0824	950.0448	1934.1195	967.5634	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2018.1406	1009.5740	2001.1141	1001.0607	2000.1301	1000.5687	2035.1672	1018.0872	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	543.3375	272.1724	544.3453	272.6763	5
20	2117.2091	1059.1082	2100.1825	1050.5949	2099.1985	1050.1029	2134.2356	1067.6214	V	427.2663		458.3085	229.6579	441.2820	221.1446			442.2898	221.6485	443.2976	222.1525	4
21	2188.2462	1094.6267	2171.2196	1086.1134	2170.2356	1085.6214	2205.2727	1103.1400	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
22	2301.3302	1151.1688	2284.3037	1142.6555	2283.3197	1142.1635	2318.3568	1159.6820	L	229.1295		288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2474.4346
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 101 **Expect:** 1.1e-07
Matches : 58/402 fragment ions using 50 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPATGGVKKPHRYRPGTVALR



MS/MS Fragmentation of KSAPSTGGVKKPHR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 2374: 1504.883016 from(377.228030,4+) intensity(30619.8240) scans(2356) rtinseconds(1425.8218) index(1401)
Title: 1402: Scan 2356 (rt=23.7637) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

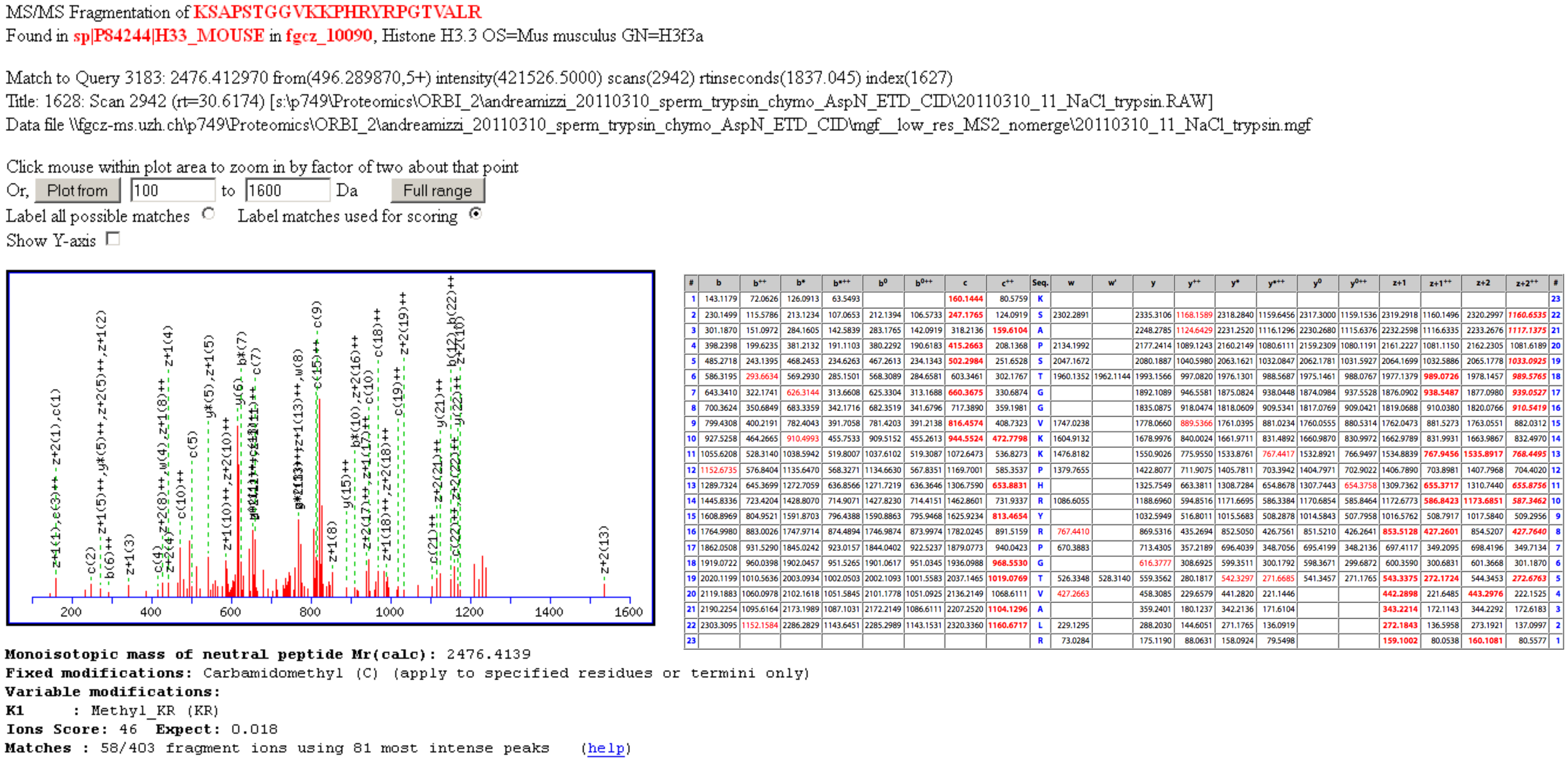
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	157.1335	79.0704	140.1070	70.5571			**174.1601**	87.5837	K													14
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	1316.7433		1349.7648	675.3860	1332.7383	666.8728	1331.7542	666.3808	1333.7461	***667.3767***	**1334.7539**	***667.8806***	13
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			1262.7328	631.8700	1245.7062	623.3568	1244.7222	622.8647	1246.7141	***623.8607***	**1247.7219**	***624.3646***	12
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	**429.2820**	215.1446	P	1148.6535		1191.6957	596.3515	1174.6691	587.8382	1173.6851	587.3462	1175.6769	588.3421	1176.6848	588.8460	11
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	516.3140	258.6606	S	1061.6214		1094.6429	547.8251	1077.6164	539.3118	1076.6323	538.8198	1078.6242	539.8157	1079.6320	540.3196	10
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	**617.3617**	309.1845	T	974.5894	976.5687	1007.6109	504.3091	990.5843	495.7958	989.6003	495.3038	**991.5922**	***496.2997***	992.6000	***496.8036***	9
7	657.3566	329.1819	640.3301	320.6687	639.3461	320.1767	**674.3832**	337.6952	G			906.5632	453.7852	889.5366	445.2720			890.5445	***445.7759***	**891.5523**	***446.2798***	8
8	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	731.4046	366.2060	G			849.5417	425.2745	832.5152	416.7612			833.5230	***417.2651***	**834.5308**	***417.7691***	7
9	813.4465	407.2269	796.4199	398.7136	795.4359	398.2216	**830.4730**	415.7402	V	761.4781		792.5203	396.7638	775.4937	388.2505			776.5015	***388.7544***	**777.5094**	***389.2583***	6
10	969.5728	485.2900	952.5462	476.7767	951.5622	476.2847	986.5993	**493.8033**	K	591.3362		693.4519	347.2296	676.4253	338.7163			677.4331	***339.2202***	678.4410	***339.7241***	5
11	1097.6677	549.3375	1080.6412	540.8242	1079.6572	540.3322	1114.6943	557.8508	K	463.2412		537.3256	269.1664	520.2990	260.6532			**521.3069**	***261.1571***	522.3147	***261.6610***	4
12	1194.7205	597.8639	1177.6939	589.3506	1176.7099	588.8586	1211.7470	**606.3772**	P	366.1884		409.2306	205.1190	392.2041	196.6057			393.2119	197.1096	394.2197	197.6135	3
13	1331.7794	666.3933	1314.7528	657.8801	1313.7688	657.3881	1348.8059	**674.9066**	H			312.1779	156.5926	295.1513	148.0793			**296.1591**	148.5832	297.1670	149.0871	2
14									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1504.8838
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Dimethyl_KR (KR)
Ions Score: 68 **Expect:** 0.00018
Matches : 38/226 fragment ions using 31 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPSTGGVKme2KPHR



MS/MS Fragmentation of KSAPSTGGVKKPHRYRPGTVALR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 3183: 2476.412970 from(496.289870,5+) intensity(421526.5000) scans(2942) rtinseconds(1837.045) index(1627)
Title: 1628: Scan 2942 (rt=30.6174) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_11_NaCl_trypsin.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_11_NaCl_trypsin.mgf

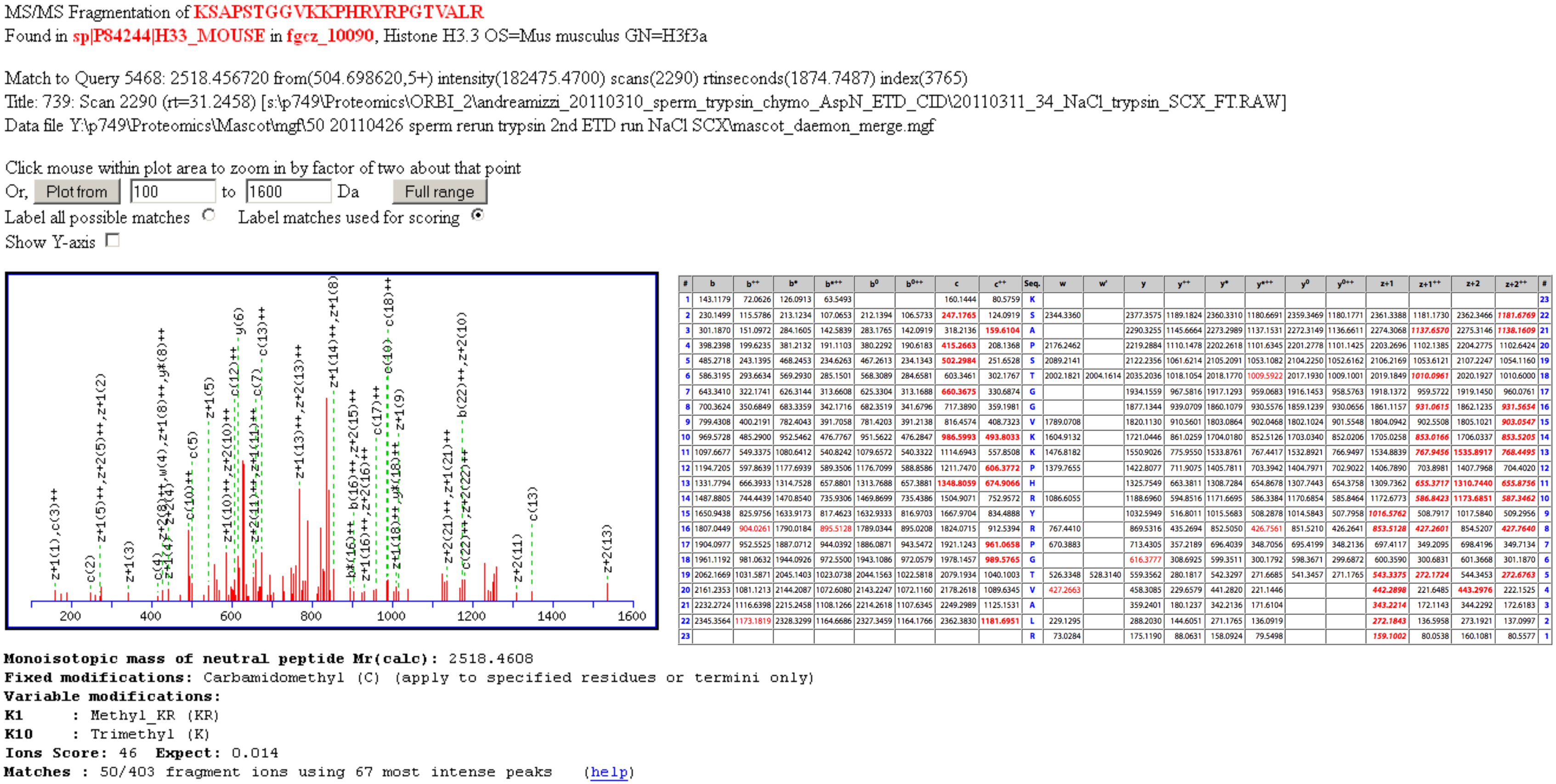
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	143.1179	72.0626	126.0913	63.5493			**160.1444**	80.5759	K													23
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	**247.1765**	124.0919	S	2302.2891		2335.3106	1168.1589	2318.2840	1159.6456	2317.3000	1159.1536	2319.2918	1160.1496	2320.2997	***1160.6535***	22
3	301.1870	151.0972	284.1605	142.5839	283.1765	142.0919	318.2136	**159.6104**	A			2248.2785	1124.6429	2231.2520	1116.1296	2230.2680	1115.6376	2232.2598	1116.6335	2233.2676	***1117.1375***	21
4	398.2398	199.6235	381.2132	191.1103	380.2292	190.6183	**415.2663**	208.1368	P	2134.1992		2177.2414	1089.1243	2160.2149	1080.6111	2159.2309	1080.1191	2161.2227	1081.1150	2162.2305	1081.6189	20
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	**502.2984**	251.6528	S	2047.1672		2080.1887	1040.5980	2063.1621	1032.0847	2062.1781	1031.5927	2064.1699	1032.5886	2065.1778	***1033.0925***	19
6	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	603.3461	302.1767	T	1960.1352	1962.1144	1993.1566	997.0820	1976.1301	988.5687	1975.1461	988.0767	1977.1379	**989.0726**	1978.1457	***989.5765***	18
7	643.3410	322.1741	626.3144	313.6608	625.3304	313.1688	**660.3675**	330.6874	G			1892.1089	946.5581	1875.0824	938.0448	1874.0984	937.5528	1876.0902	**938.5487**	1877.0980	***939.0527***	17
8	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	717.3890	359.1981	G			1835.0875	918.0474	1818.0609	909.5341	1817.0769	909.0421	1819.0688	910.0380	1820.0766	***910.5419***	16
9	799.4308	400.2191	782.4043	391.7058	781.4203	391.2138	**816.4574**	408.7323	V	1747.0238		1778.0660	889.5366	1761.0395	881.0234	1760.0555	880.5314	1762.0473	881.5273	1763.0551	882.0312	15
10	927.5258	464.2665	910.4993	455.7533	909.5152	455.2613	**944.5524**	**472.7798**	K	1604.9132		1678.9976	840.0024	1661.9711	831.4892	1660.9870	830.9972	1662.9789	831.9931	1663.9867	832.4970	14
11	1055.6208	528.3140	1038.5942	519.8007	1037.6102	519.3087	1072.6473	536.8273	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	**767.9456**	**1535.8917**	***768.4495***	13
12	1152.6735	576.8404	1135.6470	568.3271	1134.6630	567.8351	1169.7001	585.3537	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1289.7324	645.3699	1272.7059	636.8566	1271.7219	636.3646	1306.7590	**653.8831**	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	**655.3717**	1310.7440	***655.8756***	11
14	1445.8336	723.4204	1428.8070	714.9071	1427.8230	714.4151	1462.8601	731.9337	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	**586.8423**	**1173.6851**	***587.3462***	10
15	1608.8969	804.9521	1591.8703	796.4388	1590.8863	795.9468	1625.9234	**813.4654**	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1764.9980	883.0026	1747.9714	874.4894	1746.9874	873.9974	1782.0245	891.5159	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	**853.5128**	**427.2601**	854.5207	***427.7640***	8
17	1862.0508	931.5290	1845.0242	923.0157	1844.0402	922.5237	1879.0773	940.0423	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1919.0722	960.0398	1902.0457	951.5265	1901.0617	951.0345	1936.0988	**968.5530**	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2020.1199	1010.5636	2003.0934	1002.0503	2002.1093	1001.5583	2037.1465	**1019.0769**	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	**272.1724**	544.3453	***272.6763***	5
20	2119.1883	1060.0978	2102.1618	1051.5845	2101.1778	1051.0925	2136.2149	1068.6111	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	**443.2976**	222.1525	4
21	2190.2254	1095.6164	2173.1989	1087.1031	2172.2149	1086.6111	2207.2520	**1104.1296**	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2303.3095	1152.1584	2286.2829	1143.6451	2285.2989	1143.1531	2320.3360	**1160.6717**	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	**160.1081**	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2476.4139
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
Ions Score: 46 **Expect:** 0.018
Matches : 58/403 fragment ions using 81 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1SAPSTGGVKKPHRYRPGTVALR



MS/MS Fragmentation of KSAPSTGGVKKPHRYRPGTVALR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 5468: 2518.456720 from(504.698620,5+) intensity(182475.4700) scans(2290) rtinseconds(1874.7487) index(3765)
Title: 739: Scan 2290 (rt=31.2458) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

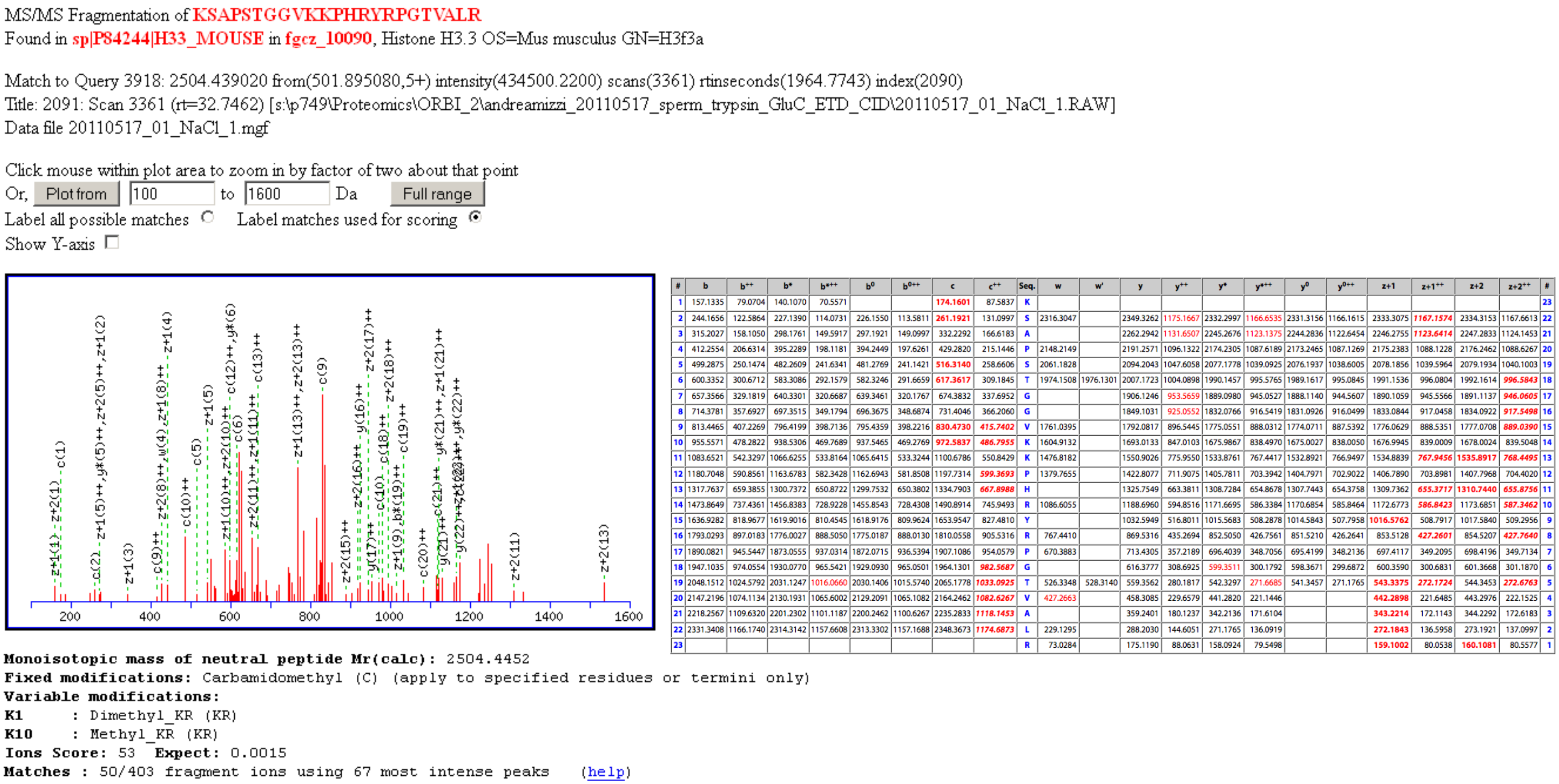
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													23
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	247.1765	124.0919	S	2344.3360		2377.3575	1189.1824	2360.3310	1180.6691	2359.3469	1180.1771	2361.3388	1181.1730	2362.3466	1181.6769	22
3	301.1870	151.0972	284.1605	142.5839	283.1765	142.0919	318.2136	159.6104	A			2290.3255	1145.6664	2273.2989	1137.1531	2272.3149	1136.6611	2274.3068	1137.6570	2275.3146	1138.1609	21
4	398.2398	199.6235	381.2132	191.1103	380.2292	190.6183	415.2663	208.1368	P	2176.2462		2219.2884	1110.1478	2202.2618	1101.6345	2201.2778	1101.1425	2203.2696	1102.1385	2204.2775	1102.6424	20
5	485.2718	243.1395	468.2453	234.6263	467.2613	234.1343	502.2984	251.6528	S	2089.2141		2122.2356	1061.6214	2105.2091	1053.1082	2104.2250	1052.6162	2106.2169	1053.6121	2107.2247	1054.1160	19
6	586.3195	293.6634	569.2930	285.1501	568.3089	284.6581	603.3461	302.1767	T	2002.1821	2004.1614	2035.2036	1018.1054	2018.1770	1009.5922	2017.1930	1009.1001	2019.1849	1010.0961	2020.1927	1010.6000	18
7	643.3410	322.1741	626.3144	313.6608	625.3304	313.1688	660.3675	330.6874	G			1934.1559	967.5816	1917.1293	959.0683	1916.1453	958.5763	1918.1372	959.5722	1919.1450	960.0761	17
8	700.3624	350.6849	683.3359	342.1716	682.3519	341.6796	717.3890	359.1981	G			1877.1344	939.0709	1860.1079	930.5576	1859.1239	930.0656	1861.1157	931.0615	1862.1235	931.5654	16
9	799.4308	400.2191	782.4043	391.7058	781.4203	391.2138	816.4574	408.7323	V	1789.0708		1820.1130	910.5601	1803.0864	902.0468	1802.1024	901.5548	1804.0942	902.5508	1805.1021	903.0547	15
10	969.5728	485.2900	952.5462	476.7767	951.5622	476.2847	986.5993	493.8033	K	1604.9132		1721.0446	861.0259	1704.0180	852.5126	1703.0340	852.0206	1705.0258	853.0166	1706.0337	853.5205	14
11	1097.6677	549.3375	1080.6412	540.8242	1079.6572	540.3322	1114.6943	557.8508	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	767.9456	1535.8917	768.4495	13
12	1194.7205	597.8639	1177.6939	589.3506	1176.7099	588.8586	1211.7470	606.3772	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1331.7794	666.3933	1314.7528	657.8801	1313.7688	657.3881	1348.8059	674.9066	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	655.3717	1310.7440	655.8756	11
14	1487.8805	744.4439	1470.8540	735.9306	1469.8699	735.4386	1504.9071	752.9572	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	586.8423	1173.6851	587.3462	10
15	1650.9438	825.9756	1633.9173	817.4623	1632.9333	816.9703	1667.9704	834.4888	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1807.0449	904.0261	1790.0184	895.5128	1789.0344	895.0208	1824.0715	912.5394	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	427.2601	854.5207	427.7640	8
17	1904.0977	952.5525	1887.0712	944.0392	1886.0871	943.5472	1921.1243	961.0658	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1961.1192	981.0632	1944.0926	972.5500	1943.1086	972.0579	1978.1457	989.5765	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2062.1669	1031.5871	2045.1403	1023.0738	2044.1563	1022.5818	2079.1934	1040.1003	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	543.3375	272.1724	544.3453	272.6763	5
20	2161.2353	1081.1213	2144.2087	1072.6080	2143.2247	1072.1160	2178.2618	1089.6345	V	427.2663		458.3085	229.6579	441.2820	221.1446			442.2898	221.6485	443.2976	222.1525	4
21	2232.2724	1116.6398	2215.2458	1108.1266	2214.2618	1107.6345	2249.2989	1125.1531	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
22	2345.3564	1173.1819	2328.3299	1164.6686	2327.3459	1164.1766	2362.3830	1181.6951	L	229.1295		288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2518.4608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
K10 : Trimethyl (K)
Ions Score: 46 **Expect:** 0.014
Matches : 50/403 fragment ions using 67 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1SAPSTGGVKme3KPHRYRPGTVALR



MS/MS Fragmentation of KSAPSTGGVKKPHRYRPGTVALR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 3918: 2504.439020 from(501.895080,5+) intensity(434500.2200) scans(3361) rtinseconds(1964.7743) index(2090)
Title: 2091: Scan 3361 (rt=32.7462) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

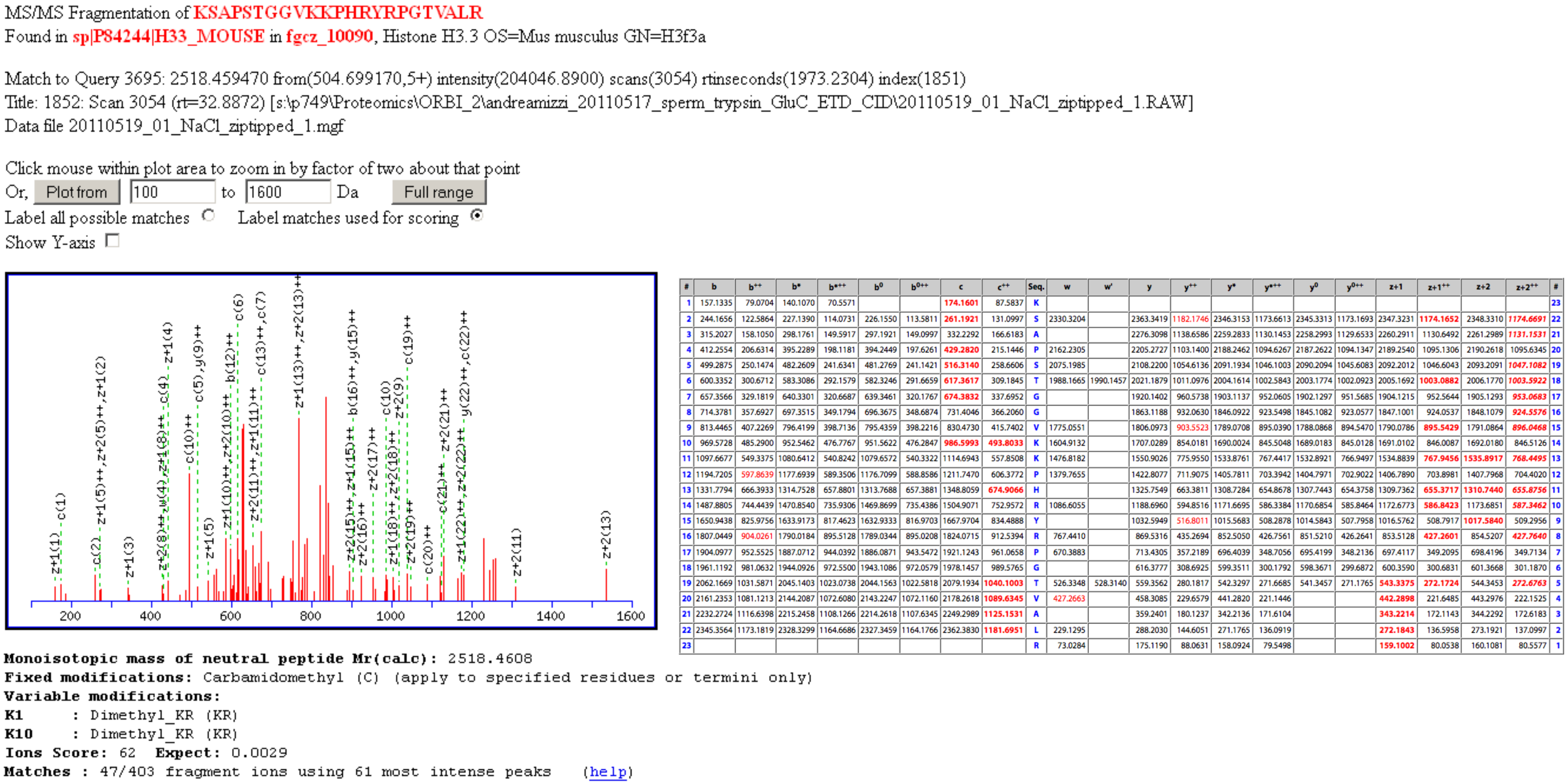
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			**174.1601**	87.5837	K													23
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	2316.3047		2349.3262	1175.1667	2332.2997	1166.6535	2331.3156	1166.1615	2333.3075	***1167.1574***	2334.3153	1167.6613	22
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			2262.2942	1131.6507	2245.2676	1123.1375	2244.2836	1122.6454	2246.2755	***1123.6414***	2247.2833	1124.1453	21
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	429.2820	215.1446	P	2148.2149		2191.2571	1096.1322	2174.2305	1087.6189	2173.2465	1087.1269	2175.2383	1088.1228	2176.2462	1088.6267	20
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	**516.3140**	258.6606	S	2061.1828		2094.2043	1047.6058	2077.1778	1039.0925	2076.1937	1038.6005	2078.1856	1039.5964	2079.1934	1040.1003	19
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	**617.3617**	309.1845	T	1974.1508	1976.1301	2007.1723	1004.0898	1990.1457	995.5765	1989.1617	995.0845	1991.1536	996.0804	1992.1614	***996.5843***	18
7	657.3566	329.1819	640.3301	320.6687	639.3461	320.1767	674.3832	337.6952	G			1906.1246	953.5659	1889.0980	945.0527	1888.1140	944.5607	1890.1059	945.5566	1891.1137	***946.0605***	17
8	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	731.4046	366.2060	G			1849.1031	925.0552	1832.0766	916.5419	1831.0926	916.0499	1833.0844	917.0458	1834.0922	***917.5498***	16
9	813.4465	407.2269	796.4199	398.7136	795.4359	398.2216	**830.4730**	***415.7402***	V	1761.0395		1792.0817	896.5445	1775.0551	888.0312	1774.0711	887.5392	1776.0629	888.5351	1777.0708	***889.0390***	15
10	955.5571	478.2822	938.5306	469.7689	937.5465	469.2769	**972.5837**	***486.7955***	K	1604.9132		1693.0133	847.0103	1675.9867	838.4970	1675.0027	838.0050	1676.9945	839.0009	1678.0024	839.5048	14
11	1083.6521	542.3297	1066.6255	533.8164	1065.6415	533.3244	1100.6786	550.8429	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	***767.9456***	**1535.8917**	***768.4495***	13
12	1180.7048	590.8561	1163.6783	582.3428	1162.6943	581.8508	1197.7314	***599.3693***	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1317.7637	659.3855	1300.7372	650.8722	1299.7532	650.3802	1334.7903	***667.8988***	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	***655.3717***	**1310.7440**	***655.8756***	11
14	1473.8649	737.4361	1456.8383	728.9228	1455.8543	728.4308	1490.8914	745.9493	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	***586.8423***	1173.6851	***587.3462***	10
15	1636.9282	818.9677	1619.9016	810.4545	1618.9176	809.9624	1653.9547	827.4810	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	**1016.5762**	508.7917	1017.5840	509.2956	9
16	1793.0293	897.0183	1776.0027	888.5050	1775.0187	888.0130	1810.0558	905.5316	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	***427.2601***	854.5207	***427.7640***	8
17	1890.0821	945.5447	1873.0555	937.0314	1872.0715	936.5394	1907.1086	954.0579	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1947.1035	974.0554	1930.0770	965.5421	1929.0930	965.0501	1964.1301	***982.5687***	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2048.1512	1024.5792	2031.1247	1016.0660	2030.1406	1015.5740	2065.1778	***1033.0925***	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	***272.1724***	544.3453	***272.6763***	5
20	2147.2196	1074.1134	2130.1931	1065.6002	2129.2091	1065.1082	2164.2462	***1082.6267***	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	443.2976	222.1525	4
21	2218.2567	1109.6320	2201.2302	1101.1187	2200.2462	1100.6267	2235.2833	***1118.1453***	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2331.3408	1166.1740	2314.3142	1157.6608	2313.3302	1157.1688	2348.3673	***1174.6873***	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	**160.1081**	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2504.4452
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Methyl_KR (KR)
Ions Score: 53 **Expect:** 0.0015
Matches : 50/403 fragment ions using 67 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPSTGGVKme1KPHRYRPGTVALR



MS/MS Fragmentation of KSAPSTGGVKKPHRYRPGTVALR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 3695: 2518.459470 from(504.699170,5+) intensity(204046.8900) scans(3054) rtinseconds(1973.2304) index(1851)
Title: 1852: Scan 3054 (rt=32.8872) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_01_NaCl_ziptipped_1.RAW]
Data file 20110519_01_NaCl_ziptipped_1.mgf

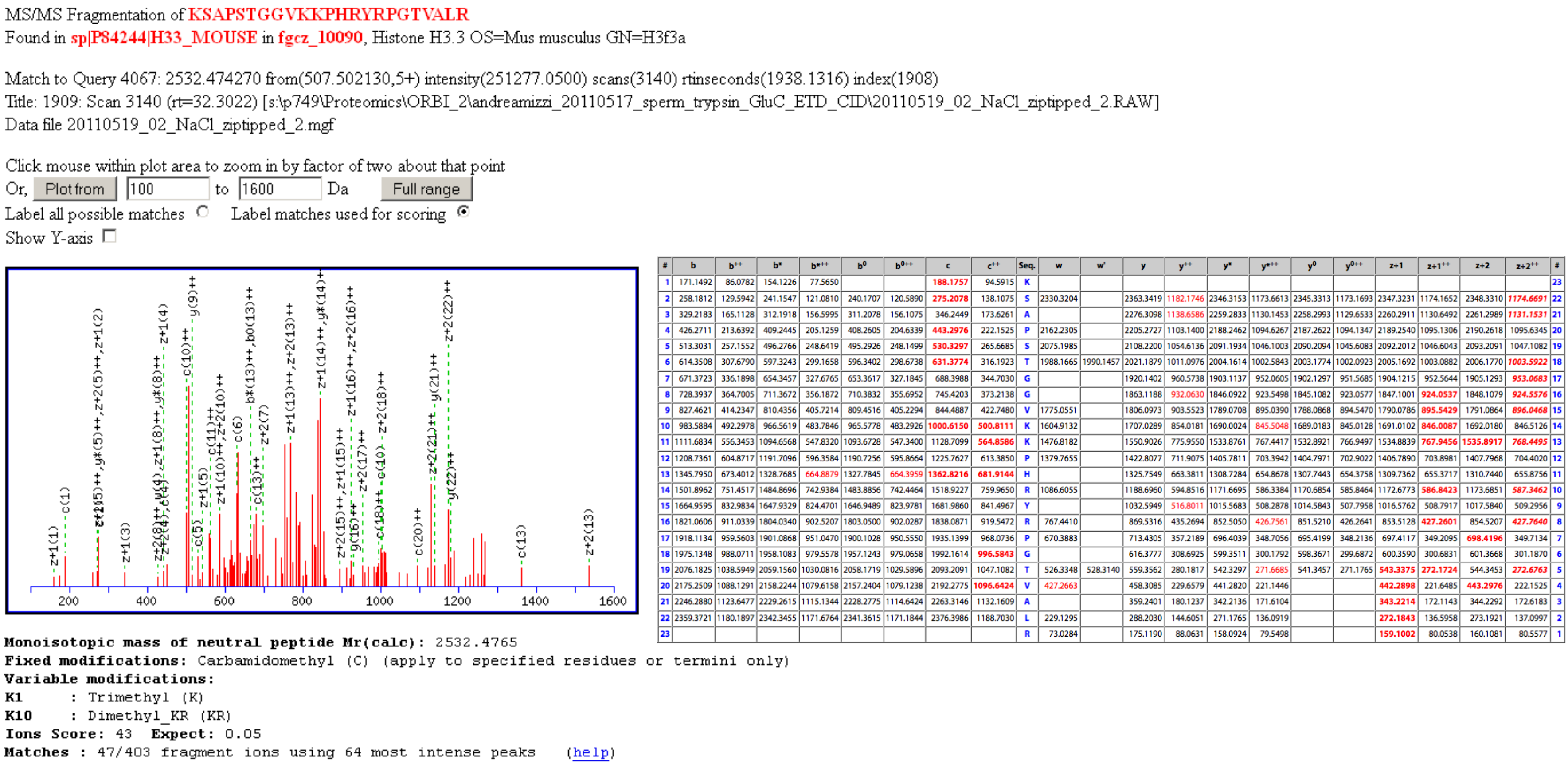
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			**174.1601**	87.5837	K													23
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	2330.3204		2363.3419	1182.1746	2346.3153	1173.6613	2345.3313	1173.1693	2347.3231	**1174.1652**	2348.3310	***1174.6691***	22
3	315.2027	158.1050	298.1761	149.5917	297.1921	149.0997	332.2292	166.6183	A			2276.3098	1138.6586	2259.2833	1130.1453	2258.2993	1129.6533	2260.2911	1130.6492	2261.2989	***1131.1531***	21
4	412.2554	206.6314	395.2289	198.1181	394.2449	197.6261	**429.2820**	215.1446	P	2162.2305		2205.2727	1103.1400	2188.2462	1094.6267	2187.2622	1094.1347	2189.2540	1095.1306	2190.2618	1095.6345	20
5	499.2875	250.1474	482.2609	241.6341	481.2769	241.1421	**516.3140**	258.6606	S	2075.1985		2108.2200	1054.6136	2091.1934	1046.1003	2090.2094	1045.6083	2092.2012	1046.6043	2093.2091	***1047.1082***	19
6	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	**617.3617**	309.1845	T	1988.1665	1990.1457	2021.1879	1011.0976	2004.1614	1002.5843	2003.1774	1002.0923	2005.1692	**1003.0882**	2006.1770	***1003.5922***	18
7	657.3566	329.1819	640.3301	320.6687	639.3461	320.1767	**674.3832**	337.6952	G			1920.1402	960.5738	1903.1137	952.0605	1902.1297	951.5685	1904.1215	952.5644	1905.1293	***953.0683***	17
8	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	731.4046	366.2060	G			1863.1188	932.0630	1846.0922	923.5498	1845.1082	923.0577	1847.1001	924.0537	1848.1079	***924.5576***	16
9	813.4465	407.2269	796.4199	398.7136	795.4359	398.2216	830.4730	415.7402	V	1775.0551		1806.0973	903.5523	1789.0708	895.0390	1788.0868	894.5470	1790.0786	**895.5429**	1791.0864	***896.0468***	15
10	969.5728	485.2900	952.5462	476.7767	951.5622	476.2847	**986.5993**	**493.8033**	K	1604.9132		1707.0289	854.0181	1690.0024	845.5048	1689.0183	845.0128	1691.0102	846.0087	1692.0180	846.5126	14
11	1097.6677	549.3375	1080.6412	540.8242	1079.6572	540.3322	1114.6943	557.8508	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	**767.9456**	**1535.8917**	***768.4495***	13
12	1194.7205	597.8639	1177.6939	589.3506	1176.7099	588.8586	1211.7470	606.3772	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1331.7794	666.3933	1314.7528	657.8801	1313.7688	657.3881	1348.8059	**674.9066**	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	**655.3717**	**1310.7440**	***655.8756***	11
14	1487.8805	744.4439	1470.8540	735.9306	1469.8699	735.4386	1504.9071	752.9572	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	**586.8423**	1173.6851	***587.3462***	10
15	1650.9438	825.9756	1633.9173	817.4623	1632.9333	816.9703	1667.9704	834.4888	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	**1017.5840**	509.2956	9
16	1807.0449	904.0261	1790.0184	895.5128	1789.0344	895.0208	1824.0715	912.5394	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	**427.2601**	854.5207	***427.7640***	8
17	1904.0977	952.5525	1887.0712	944.0392	1886.0871	943.5472	1921.1243	961.0658	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	698.4196	349.7134	7
18	1961.1192	981.0632	1944.0926	972.5500	1943.1086	972.0579	1978.1457	989.5765	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2062.1669	1031.5871	2045.1403	1023.0738	2044.1563	1022.5818	2079.1934	**1040.1003**	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	**272.1724**	544.3453	***272.6763***	5
20	2161.2353	1081.1213	2144.2087	1072.6080	2143.2247	1072.1160	2178.2618	**1089.6345**	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	443.2976	222.1525	4
21	2232.2724	1116.6398	2215.2458	1108.1266	2214.2618	1107.6345	2249.2989	**1125.1531**	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2345.3564	1173.1819	2328.3299	1164.6686	2327.3459	1164.1766	2362.3830	**1181.6951**	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2518.4608
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
K10 : Dimethyl_KR (KR)
Ions Score: 62 **Expect:** 0.0029
Matches : 47/403 fragment ions using 61 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2SAPSTGGVKme2KPHRYRPGTVALR



MS/MS Fragmentation of KSAPSTGGVKKPHRYRPGTVALR
Found in sp|P84244|H33_MOUSE in fgcz_10090, Histone H3.3 OS=Mus musculus GN=H3f3a

Match to Query 4067: 2532.474270 from(507.502130,5+) intensity(251277.0500) scans(3140) rtinseconds(1938.1316) index(1908)
Title: 1909: Scan 3140 (rt=32.3022) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_02_NaCl_ziptipped_2.RAW]
Data file 20110519_02_NaCl_ziptipped_2.mgf

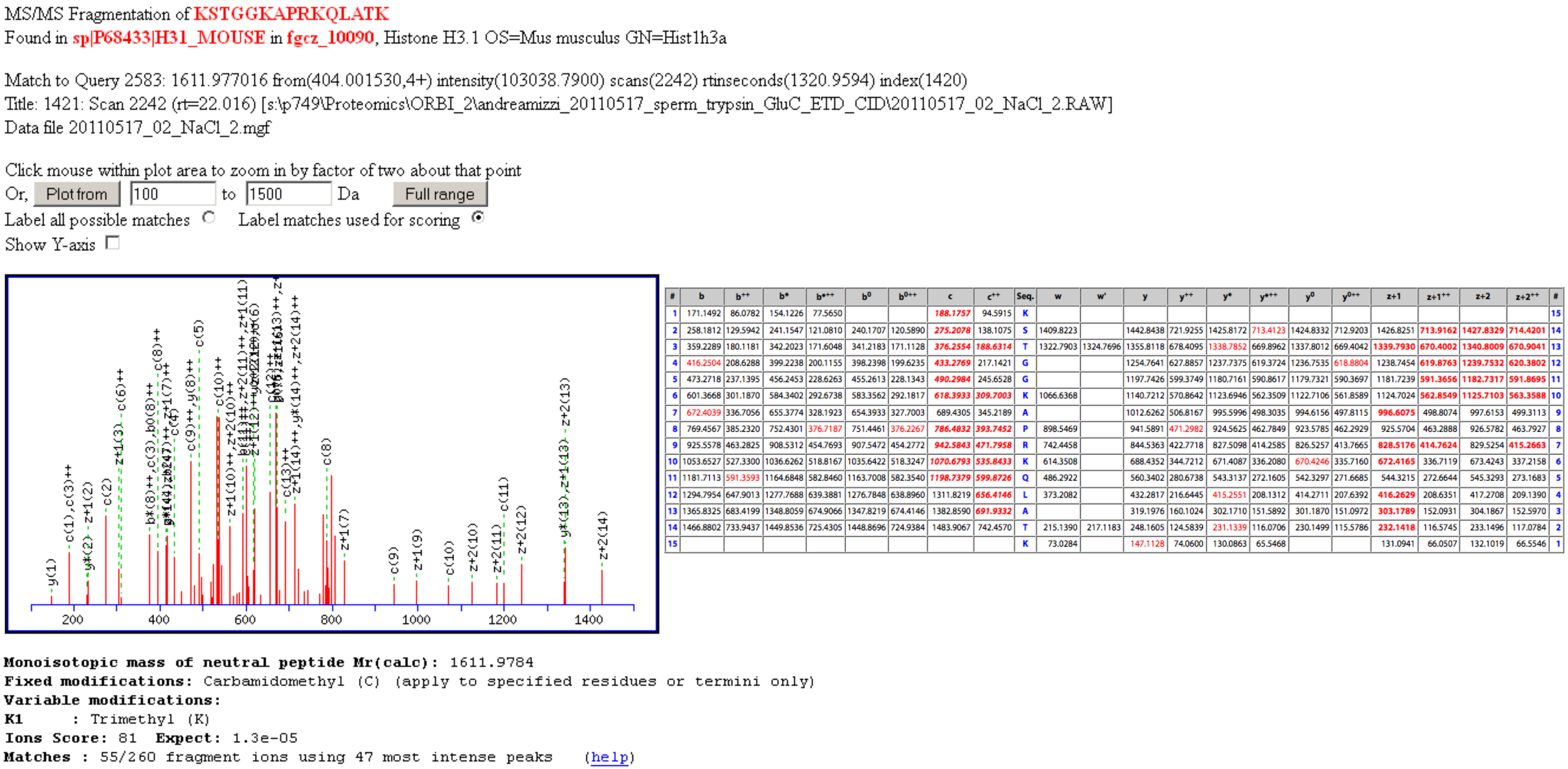
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	c	c⁺⁺	Seq.	w	w'	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	z+1	z+1⁺⁺	z+2	z+2⁺⁺	#
1	171.1492	86.0782	154.1226	77.5650			**188.1757**	94.5915	K													23
2	258.1812	129.5942	241.1547	121.0810	240.1707	120.5890	**275.2078**	138.1075	S	2330.3204		2363.3419	1182.1746	2346.3153	1173.6613	2345.3313	1173.1693	2347.3231	1174.1652	2348.3310	***1174.6691***	22
3	329.2183	165.1128	312.1918	156.5995	311.2078	156.1075	346.2449	173.6261	A			2276.3098	1138.6586	2259.2833	1130.1453	2258.2993	1129.6533	2260.2911	1130.6492	2261.2989	***1131.1531***	21
4	426.2711	213.6392	409.2445	205.1259	408.2605	204.6339	**443.2976**	222.1525	P	2162.2305		2205.2727	1103.1400	2188.2462	1094.6267	2187.2622	1094.1347	2189.2540	1095.1306	2190.2618	1095.6345	20
5	513.3031	257.1552	496.2766	248.6419	495.2926	248.1499	**530.3297**	265.6685	S	2075.1985		2108.2200	1054.6136	2091.1934	1046.1003	2090.2094	1045.6083	2092.2012	1046.6043	2093.2091	1047.1082	19
6	614.3508	307.6790	597.3243	299.1658	596.3402	298.6738	**631.3774**	316.1923	T	1988.1665	1990.1457	2021.1879	1011.0976	2004.1614	1002.5843	2003.1774	1002.0923	2005.1692	1003.0882	2006.1770	***1003.5922***	18
7	671.3723	336.1898	654.3457	327.6765	653.3617	327.1845	688.3988	344.7030	G			1920.1402	960.5738	1903.1137	952.0605	1902.1297	951.5685	1904.1215	952.5644	1905.1293	***953.0683***	17
8	728.3937	364.7005	711.3672	356.1872	710.3832	355.6952	745.4203	373.2138	G			1863.1188	932.0630	1846.0922	923.5498	1845.1082	923.0577	1847.1001	**924.0537**	1848.1079	***924.5576***	16
9	827.4621	414.2347	810.4356	405.7214	809.4516	405.2294	844.4887	422.7480	V	1775.0551		1806.0973	903.5523	1789.0708	895.0390	1788.0868	894.5470	1790.0786	**895.5429**	1791.0864	***896.0468***	15
10	983.5884	492.2978	966.5619	483.7846	965.5778	483.2926	**1000.6150**	**500.8111**	K	1604.9132		1707.0289	854.0181	1690.0024	845.5048	1689.0183	845.0128	1691.0102	**846.0087**	1692.0180	846.5126	14
11	1111.6834	556.3453	1094.6568	547.8320	1093.6728	547.3400	1128.7099	**564.8586**	K	1476.8182		1550.9026	775.9550	1533.8761	767.4417	1532.8921	766.9497	1534.8839	**767.9456**	**1535.8917**	***768.4495***	13
12	1208.7361	604.8717	1191.7096	596.3584	1190.7256	595.8664	1225.7627	613.3850	P	1379.7655		1422.8077	711.9075	1405.7811	703.3942	1404.7971	702.9022	1406.7890	703.8981	1407.7968	704.4020	12
13	1345.7950	673.4012	1328.7685	664.8879	1327.7845	664.3959	**1362.8216**	**681.9144**	H			1325.7549	663.3811	1308.7284	654.8678	1307.7443	654.3758	1309.7362	655.3717	1310.7440	655.8756	11
14	1501.8962	751.4517	1484.8696	742.9384	1483.8856	742.4464	1518.9227	759.9650	R	1086.6055		1188.6960	594.8516	1171.6695	586.3384	1170.6854	585.8464	1172.6773	**586.8423**	1173.6851	***587.3462***	10
15	1664.9595	832.9834	1647.9329	824.4701	1646.9489	823.9781	1681.9860	841.4967	Y			1032.5949	516.8011	1015.5683	508.2878	1014.5843	507.7958	1016.5762	508.7917	1017.5840	509.2956	9
16	1821.0606	911.0339	1804.0340	902.5207	1803.0500	902.0287	1838.0871	919.5472	R	767.4410		869.5316	435.2694	852.5050	426.7561	851.5210	426.2641	853.5128	**427.2601**	854.5207	***427.7640***	8
17	1918.1134	959.5603	1901.0868	951.0470	1900.1028	950.5550	1935.1399	968.0736	P	670.3883		713.4305	357.2189	696.4039	348.7056	695.4199	348.2136	697.4117	349.2095	**698.4196**	349.7134	7
18	1975.1348	988.0711	1958.1083	979.5578	1957.1243	979.0658	1992.1614	**996.5843**	G			616.3777	308.6925	599.3511	300.1792	598.3671	299.6872	600.3590	300.6831	601.3668	301.1870	6
19	2076.1825	1038.5949	2059.1560	1030.0816	2058.1719	1029.5896	2093.2091	1047.1082	T	526.3348	528.3140	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	**543.3375**	**272.1724**	544.3453	***272.6763***	5
20	2175.2509	1088.1291	2158.2244	1079.6158	2157.2404	1079.1238	2192.2775	**1096.6424**	V	427.2663		458.3085	229.6579	441.2820	221.1446			**442.2898**	221.6485	**443.2976**	222.1525	4
21	2246.2880	1123.6477	2229.2615	1115.1344	2228.2775	1114.6424	2263.3146	1132.1609	A			359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
22	2359.3721	1180.1897	2342.3455	1171.6764	2341.3615	1171.1844	2376.3986	1188.7030	L	229.1295		288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
23									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

```
Monoisotopic mass of neutral peptide Mr(calc): 2532.4765
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1      : Trimethyl (K)
K10     : Dimethyl_KR (KR)
Ions Score: 43  Expect: 0.05
Matches : 47/403 fragment ions using 64 most intense peaks   (help)
```

Mascot Search Results: Peptide View

Kme3SAPSTGGVKme2KPHRYRPGTVALR



MS/MS Fragmentation of KSTGGKAPRKQLATK
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2583: 1611.977016 from(404.001530,4+) intensity(103038.7900) scans(2242) rtinseconds(1320.9594) index(1420)
Title: 1421: Scan 2242 (rt=22.016) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_02_NaCl_2.RAW]
Data file 20110517_02_NaCl_2.mgf

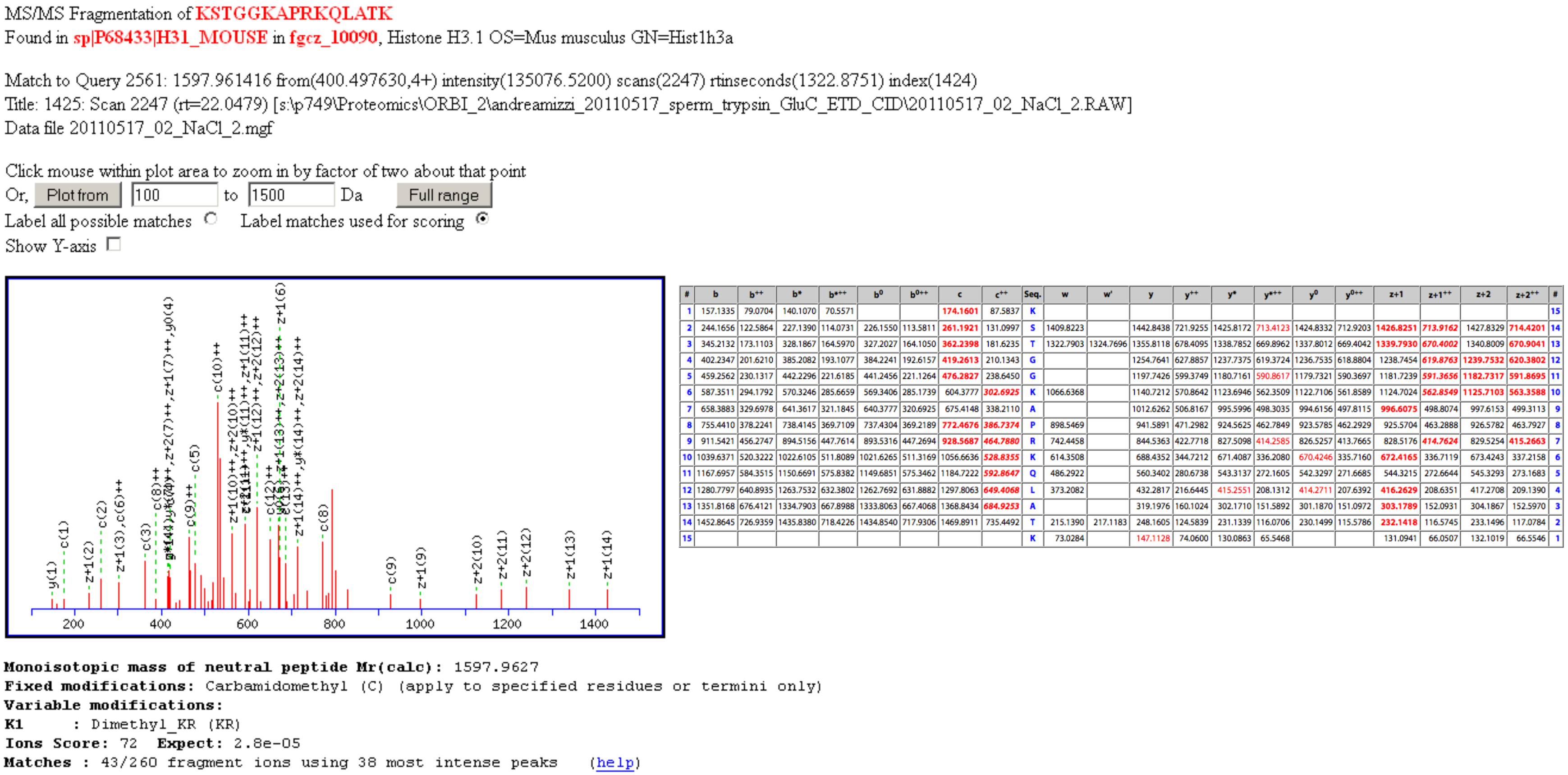
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	171.1492	86.0782	154.1226	77.5650			***188.1757***	94.5915	K													15
2	258.1812	129.5942	241.1547	121.0810	240.1707	120.5890	***275.2078***	138.1075	S	1409.8223		1442.8438	721.9255	1425.8172	713.4123	1424.8332	712.9203	1426.8251	**713.9162**	**1427.8329**	**714.4201**	14
3	359.2289	180.1181	342.2023	171.6048	341.2183	171.1128	***376.2554***	***188.6314***	T	1322.7903	1324.7696	1355.8118	678.4095	1338.7852	669.8962	1337.8012	669.4042	**1339.7930**	**670.4002**	**1340.8009**	**670.9041**	13
4	416.2504	208.6288	399.2238	200.1155	398.2398	199.6235	***433.2769***	217.1421	G			1254.7641	627.8857	1237.7375	619.3724	1236.7535	618.8804	1238.7454	**619.8763**	**1239.7532**	**620.3802**	12
5	473.2718	237.1395	456.2453	228.6263	455.2613	228.1343	***490.2984***	245.6528	G			1197.7426	599.3749	1180.7161	590.8617	1179.7321	590.3697	1181.7239	**591.3656**	**1182.7317**	**591.8695**	11
6	601.3668	301.1870	584.3402	292.6738	583.3562	292.1817	***618.3933***	***309.7003***	K	1066.6368		1140.7212	570.8642	1123.6946	562.3509	1122.7106	561.8589	1124.7024	**562.8549**	**1125.7103**	**563.3588**	10
7	672.4039	336.7056	655.3774	328.1923	654.3933	327.7003	689.4305	345.2189	A			1012.6262	506.8167	995.5996	498.3035	994.6156	497.8115	**996.6075**	498.8074	997.6153	499.3113	9
8	769.4567	385.2320	752.4301	376.7187	751.4461	376.2267	***786.4832***	***393.7452***	P	898.5469		941.5891	471.2982	924.5625	462.7849	923.5785	462.2929	925.5704	463.2888	926.5782	463.7927	8
9	925.5578	463.2825	908.5312	454.7693	907.5472	454.2772	***942.5843***	***471.7958***	R	742.4458		844.5363	422.7718	827.5098	414.2585	826.5257	413.7665	**828.5176**	**414.7624**	829.5254	**415.2663**	7
10	1053.6527	527.3300	1036.6262	518.8167	1035.6422	518.3247	***1070.6793***	***535.8433***	K	614.3508		688.4352	344.7212	671.4087	336.2080	670.4246	335.7160	**672.4165**	336.7119	673.4243	337.2158	6
11	1181.7113	591.3593	1164.6848	582.8460	1163.7008	582.3540	***1198.7379***	***599.8726***	Q	486.2922		560.3402	280.6738	543.3137	272.1605	542.3297	271.6685	544.3215	272.6644	545.3293	273.1683	5
12	1294.7954	647.9013	1277.7688	639.3881	1276.7848	638.8960	1311.8219	***656.4146***	L	373.2082		432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	**416.2629**	208.6351	417.2708	209.1390	4
13	1365.8325	683.4199	1348.8059	674.9066	1347.8219	674.4146	1382.8590	***691.9332***	A			319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**303.1789**	152.0931	304.1867	152.5970	3
14	1466.8802	733.9437	1449.8536	725.4305	1448.8696	724.9384	1483.9067	742.4570	T	215.1390	217.1183	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**232.1418**	116.5745	233.1496	117.0784	2
15									K	73.0284		147.1128	74.0600	130.0863	65.5468			131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1611.9784
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
Ions Score: 81 **Expect:** 1.3e-05
Matches : 55/260 fragment ions using 47 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3STGGKAPRKQLATK



MS/MS Fragmentation of KSTGGKAPRKQLATK
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 2561: 1597.961416 from(400.497630,4+) intensity(135076.5200) scans(2247) rtinseconds(1322.8751) index(1424)
Title: 1425: Scan 2247 (rt=22.0479) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_02_NaCl_2.RAW]
Data file 20110517_02_NaCl_2.mgf

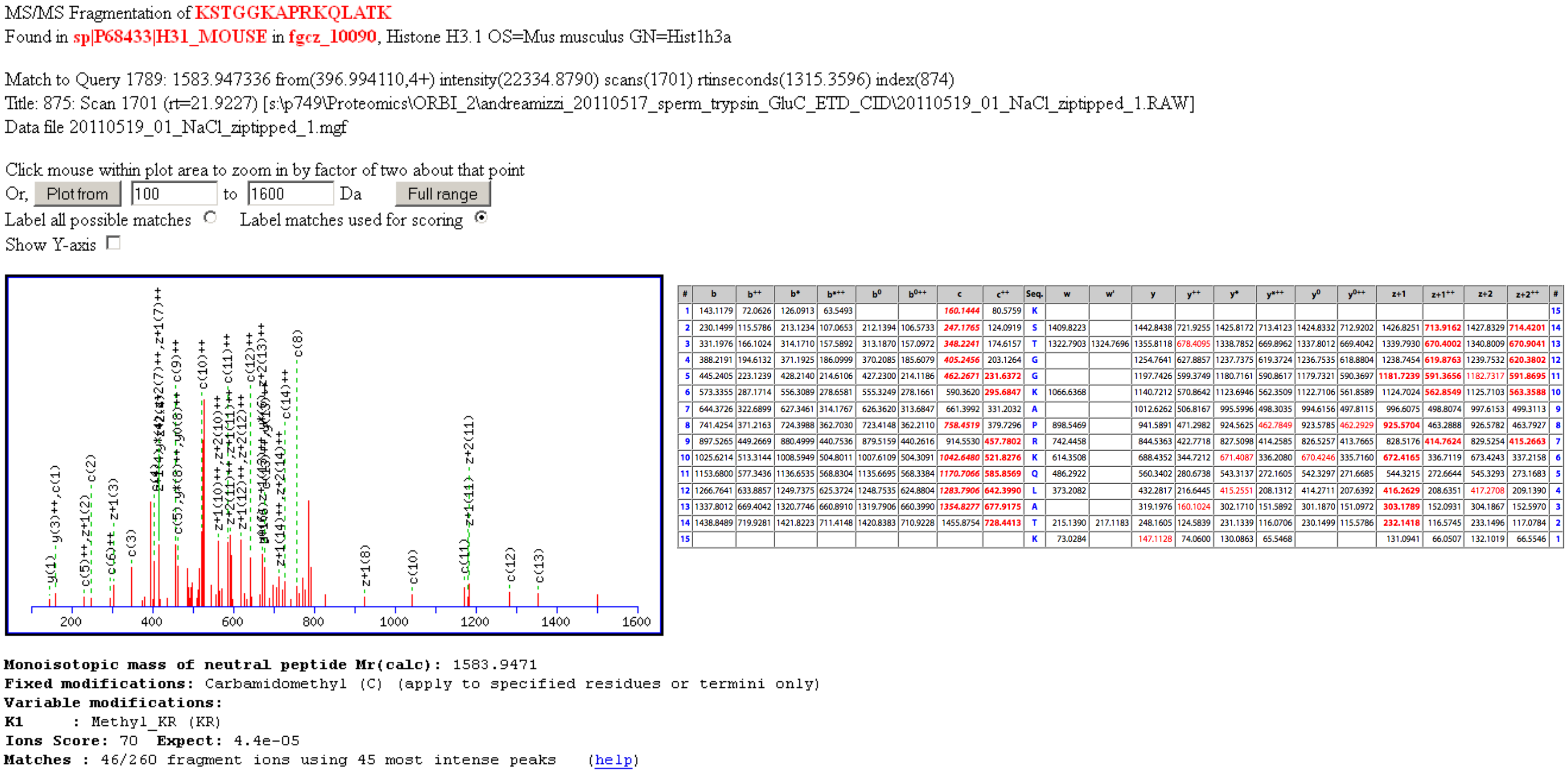
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	157.1335	79.0704	140.1070	70.5571			**174.1601**	87.5837	K													15
2	244.1656	122.5864	227.1390	114.0731	226.1550	113.5811	**261.1921**	131.0997	S	1409.8223		1442.8438	721.9255	1425.8172	713.4123	1424.8332	712.9203	**1426.8251**	***713.9162***	1427.8329	**714.4201**	14
3	345.2132	173.1103	328.1867	164.5970	327.2027	164.1050	**362.2398**	181.6235	T	1322.7903	1324.7696	1355.8118	678.4095	1338.7852	669.8962	1337.8012	669.4042	**1339.7930**	***670.4002***	1340.8009	**670.9041**	13
4	402.2347	201.6210	385.2082	193.1077	384.2241	192.6157	**419.2613**	210.1343	G			1254.7641	627.8857	1237.7375	619.3724	1236.7535	618.8804	1238.7454	***619.8763***	**1239.7532**	**620.3802**	12
5	459.2562	230.1317	442.2296	221.6185	441.2456	221.1264	**476.2827**	238.6450	G			1197.7426	599.3749	1180.7161	590.8617	1179.7321	590.3697	1181.7239	***591.3656***	**1182.7317**	**591.8695**	11
6	587.3511	294.1792	570.3246	285.6659	569.3406	285.1739	604.3777	***302.6925***	K	1066.6368		1140.7212	570.8642	1123.6946	562.3509	1122.7106	561.8589	1124.7024	***562.8549***	**1125.7103**	**563.3588**	10
7	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	675.4148	338.2110	A			1012.6262	506.8167	995.5996	498.3035	994.6156	497.8115	**996.6075**	498.8074	997.6153	499.3113	9
8	755.4410	378.2241	738.4145	369.7109	737.4304	369.2189	**772.4676**	***386.7374***	P	898.5469		941.5891	471.2982	924.5625	462.7849	923.5785	462.2929	925.5704	463.2888	926.5782	463.7927	8
9	911.5421	456.2747	894.5156	447.7614	893.5316	447.2694	**928.5687**	***464.7880***	R	742.4458		844.5363	422.7718	827.5098	414.2585	826.5257	413.7665	828.5176	***414.7624***	829.5254	**415.2663**	7
10	1039.6371	520.3222	1022.6105	511.8089	1021.6265	511.3169	1056.6636	***528.8355***	K	614.3508		688.4352	344.7212	671.4087	336.2080	670.4246	335.7160	**672.4165**	336.7119	673.4243	337.2158	6
11	1167.6957	584.3515	1150.6691	575.8382	1149.6851	575.3462	1184.7222	***592.8647***	Q	486.2922		560.3402	280.6738	543.3137	272.1605	542.3297	271.6685	544.3215	272.6644	545.3293	273.1683	5
12	1280.7797	640.8935	1263.7532	632.3802	1262.7692	631.8882	1297.8063	***649.4068***	L	373.2082		432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	**416.2629**	208.6351	417.2708	209.1390	4
13	1351.8168	676.4121	1334.7903	667.8988	1333.8063	667.4068	1368.8434	***684.9253***	A			319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**303.1789**	152.0931	304.1867	152.5970	3
14	1452.8645	726.9359	1435.8380	718.4226	1434.8540	717.9306	1469.8911	735.4492	T	215.1390	217.1183	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**232.1418**	116.5745	233.1496	117.0784	2
15									K	73.0284		147.1128	74.0600	130.0863	65.5468			131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1597.9627
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 72 **Expect:** 2.8e-05
Matches : 43/260 fragment ions using 38 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2STGGKAPRKQLATK



MS/MS Fragmentation of KSTGGKAPRKQLATK
Found in sp|P68433|H31_MOUSE in fgcz_10090, Histone H3.1 OS=Mus musculus GN=Hist1h3a

Match to Query 1789: 1583.947336 from(396.994110,4+) intensity(22334.8790) scans(1701) rtinseconds(1315.3596) index(874)
Title: 875: Scan 1701 (rt=21.9227) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_01_NaCl_ziptipped_1.RAW]
Data file 20110519_01_NaCl_ziptipped_1.mgf

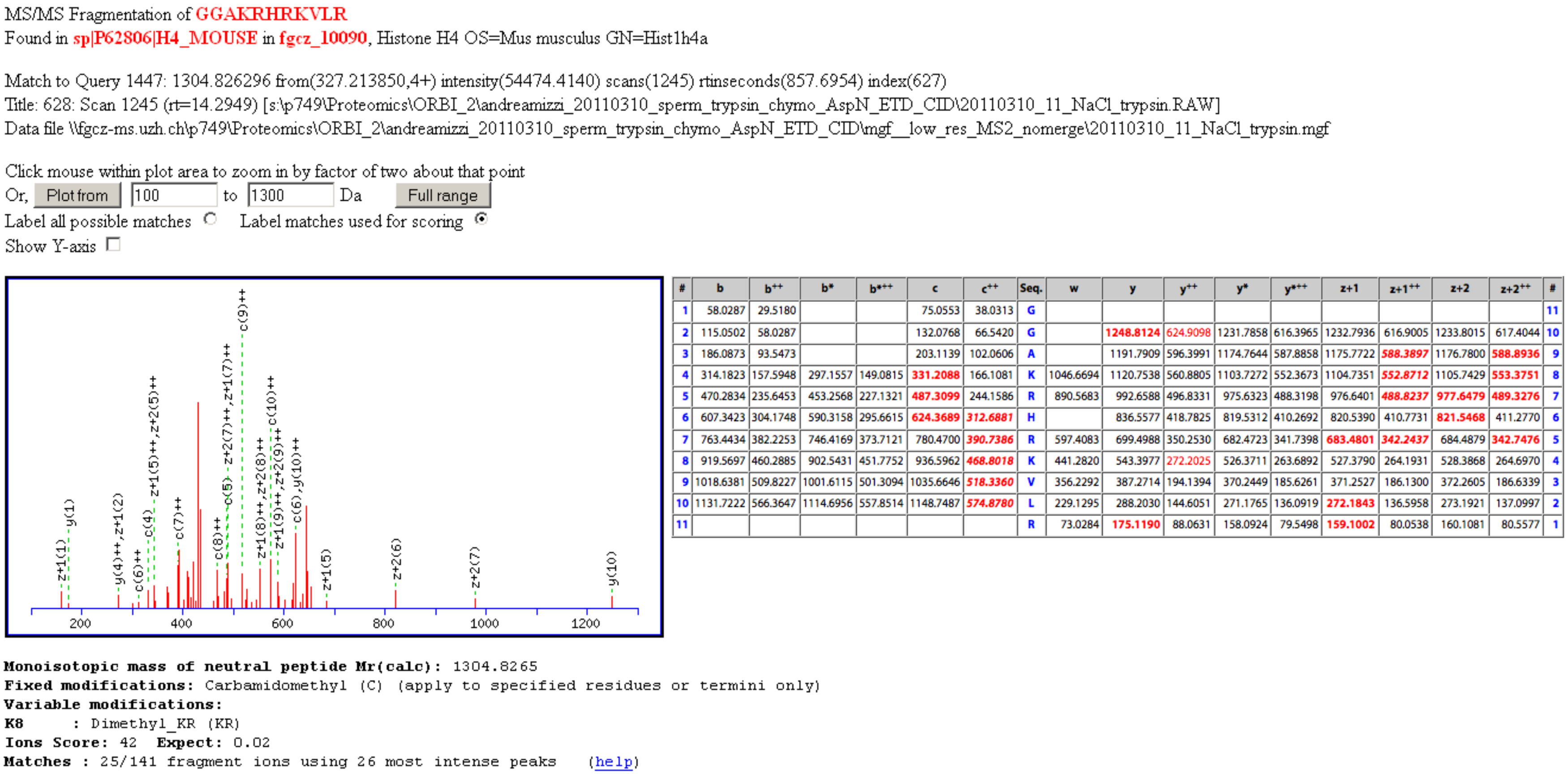
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1600 Da
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	c	c⁺⁺	Seq.	w	w'	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	z+1	z+1⁺⁺	z+2	z+2⁺⁺	#
1	143.1179	72.0626	126.0913	63.5493			***160.1444***	80.5759	K													15
2	230.1499	115.5786	213.1234	107.0653	212.1394	106.5733	***247.1765***	124.0919	S	1409.8223		1442.8438	721.9255	1425.8172	713.4123	1424.8332	712.9202	1426.8251	**713.9162**	1427.8329	**714.4201**	14
3	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	***348.2241***	174.6157	T	1322.7903	1324.7696	1355.8118	678.4095	1338.7852	669.8962	1337.8012	669.4042	1339.7930	**670.4002**	1340.8009	**670.9041**	13
4	388.2191	194.6132	371.1925	186.0999	370.2085	185.6079	***405.2456***	203.1264	G			1254.7641	627.8857	1237.7375	619.3724	1236.7535	618.8804	1238.7454	**619.8763**	1239.7532	**620.3802**	12
5	445.2405	223.1239	428.2140	214.6106	427.2300	214.1186	***462.2671***	**231.6372**	G			1197.7426	599.3749	1180.7161	590.8617	1179.7321	590.3697	**1181.7239**	**591.3656**	1182.7317	**591.8695**	11
6	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	590.3620	**295.6847**	K	1066.6368		1140.7212	570.8642	1123.6946	562.3509	1122.7106	561.8589	1124.7024	**562.8549**	1125.7103	**563.3588**	10
7	644.3726	322.6899	627.3461	314.1767	626.3620	313.6847	661.3992	331.2032	A			1012.6262	506.8167	995.5996	498.3035	994.6156	497.8115	996.6075	498.8074	997.6153	499.3113	9
8	741.4254	371.2163	724.3988	362.7030	723.4148	362.2110	***758.4519***	379.7296	P	898.5469		941.5891	471.2982	924.5625	462.7849	923.5785	462.2929	**925.5704**	463.2888	926.5782	463.7927	8
9	897.5265	449.2669	880.4999	440.7536	879.5159	440.2616	914.5530	**457.7802**	R	742.4458		844.5363	422.7718	827.5098	414.2585	826.5257	413.7665	828.5176	**414.7624**	829.5254	**415.2663**	7
10	1025.6214	513.3144	1008.5949	504.8011	1007.6109	504.3091	***1042.6480***	**521.8276**	K	614.3508		688.4352	344.7212	671.4087	336.2080	670.4246	335.7160	**672.4165**	336.7119	673.4243	337.2158	6
11	1153.6800	577.3436	1136.6535	568.8304	1135.6695	568.3384	***1170.7066***	**585.8569**	Q	486.2922		560.3402	280.6738	543.3137	272.1605	542.3297	271.6685	544.3215	272.6644	545.3293	273.1683	5
12	1266.7641	633.8857	1249.7375	625.3724	1248.7535	624.8804	***1283.7906***	**642.3990**	L	373.2082		432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	**416.2629**	208.6351	417.2708	209.1390	4
13	1337.8012	669.4042	1320.7746	660.8910	1319.7906	660.3990	***1354.8277***	**677.9175**	A			319.1976	160.1024	302.1710	151.5892	301.1870	151.0972	**303.1789**	152.0931	304.1867	152.5970	3
14	1438.8489	719.9281	1421.8223	711.4148	1420.8383	710.9228	1455.8754	**728.4413**	T	215.1390	217.1183	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	**232.1418**	116.5745	233.1496	117.0784	2
15									K	73.0284		147.1128	74.0600	130.0863	65.5468			131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1583.9471
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
Ions Score: 70 **Expect:** 4.4e-05
Matches : 46/260 fragment ions using 45 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1STGGKAPRKQLATK



MS/MS Fragmentation of GGAKRHRKVLR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 1447: 1304.826296 from(327.213850,4+) intensity(54474.4140) scans(1245) rtinseconds(857.6954) index(627)
Title: 628: Scan 1245 (rt=14.2949) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_11_NaCl_trypsin.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_11_NaCl_trypsin.mgf

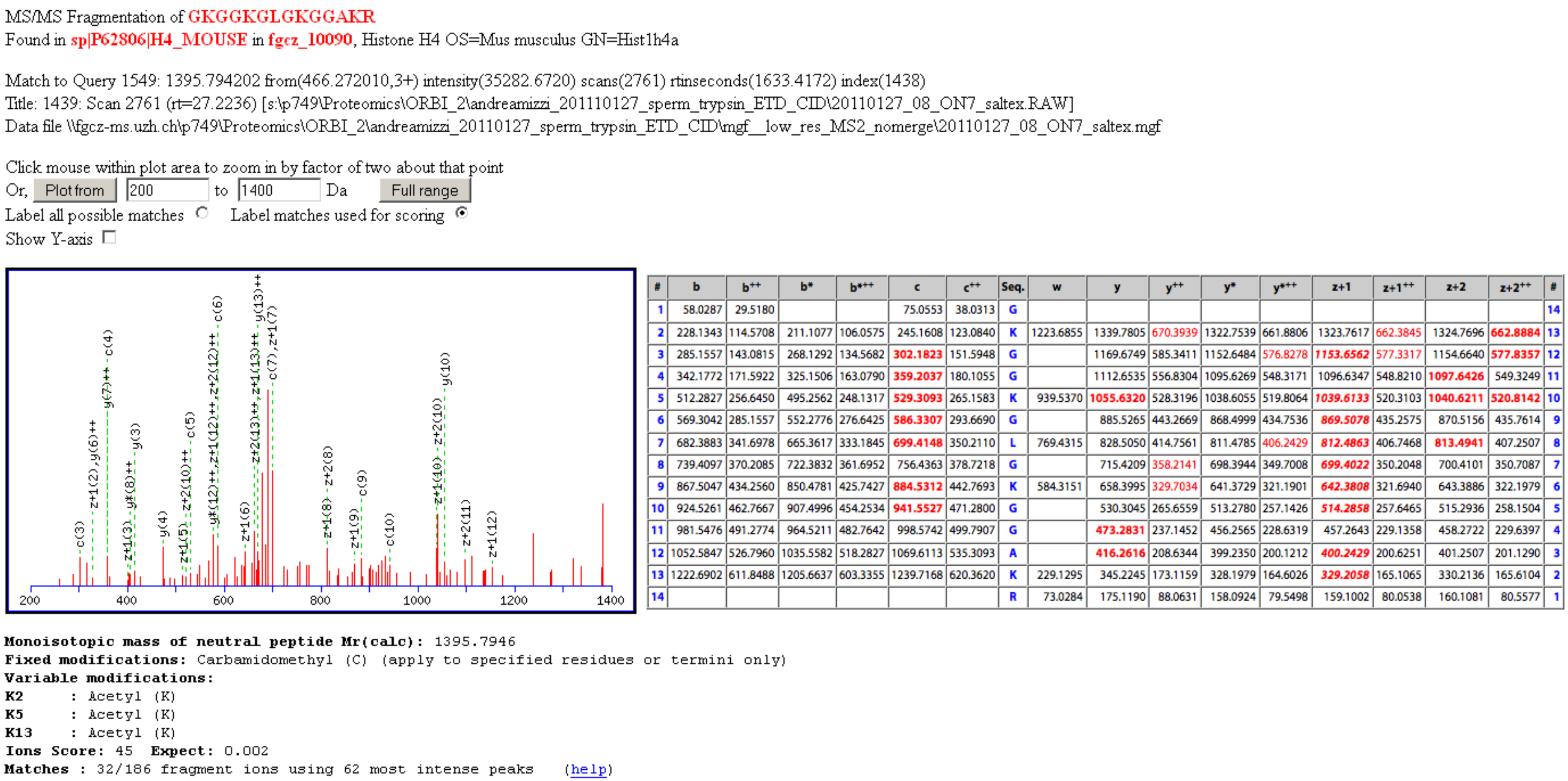
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	c	c++	Seq.	w	y	y++	y*	y*++	z+1	z+1++	z+2	z+2++	#
1	58.0287	29.5180			75.0553	38.0313	G										11
2	115.0502	58.0287			132.0768	66.5420	G		**1248.8124**	624.9098	1231.7858	616.3965	1232.7936	616.9005	1233.8015	617.4044	10
3	186.0873	93.5473			203.1139	102.0606	A		1191.7909	596.3991	1174.7644	587.8858	1175.7722	**588.3897**	1176.7800	**588.8936**	9
4	314.1823	157.5948	297.1557	149.0815	**331.2088**	166.1081	K	1046.6694	1120.7538	560.8805	1103.7272	552.3673	1104.7351	**552.8712**	1105.7429	**553.3751**	8
5	470.2834	235.6453	453.2568	227.1321	**487.3099**	244.1586	R	890.5683	992.6588	496.8331	975.6323	488.3198	976.6401	**488.8237**	**977.6479**	**489.3276**	7
6	607.3423	304.1748	590.3158	295.6615	**624.3689**	**312.6881**	H		836.5577	418.7825	819.5312	410.2692	820.5390	410.7731	**821.5468**	411.2770	6
7	763.4434	382.2253	746.4169	373.7121	780.4700	**390.7386**	R	597.4083	699.4988	350.2530	682.4723	341.7398	**683.4801**	**342.2437**	684.4879	**342.7476**	5
8	919.5697	460.2885	902.5431	451.7752	936.5962	**468.8018**	K	441.2820	543.3977	272.2025	526.3711	263.6892	527.3790	264.1931	528.3868	264.6970	4
9	1018.6381	509.8227	1001.6115	501.3094	1035.6646	**518.3360**	V	356.2292	387.2714	194.1394	370.2449	185.6261	371.2527	186.1300	372.2605	186.6339	3
10	1131.7222	566.3647	1114.6956	557.8514	1148.7487	**574.8780**	L	229.1295	288.2030	144.6051	271.1765	136.0919	**272.1843**	136.5958	273.1921	137.0997	2
11							R	73.0284	**175.1190**	88.0631	158.0924	79.5498	**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1304.8265
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K8 : Dimethyl_KR (KR)
Ions Score: 42 **Expect:** 0.02
Matches : 25/141 fragment ions using 26 most intense peaks (help)

Mascot Search Results: Peptide View

GGAKRHRKme2VLR



MS/MS Fragmentation of GKGGKGLGKGGAKR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 1549: 1395.794202 from(466.272010,3+) intensity(35282.6720) scans(2761) rtinseconds(1633.4172) index(1438)
Title: 1439: Scan 2761 (rt=27.2236) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110127_sperm_trypsin_ETD_CID\20110127_08_ON7_saltex.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110127_sperm_trypsin_ETD_CID\mgf__low_res_MS2_nomerge\20110127_08_ON7_saltex.mgf

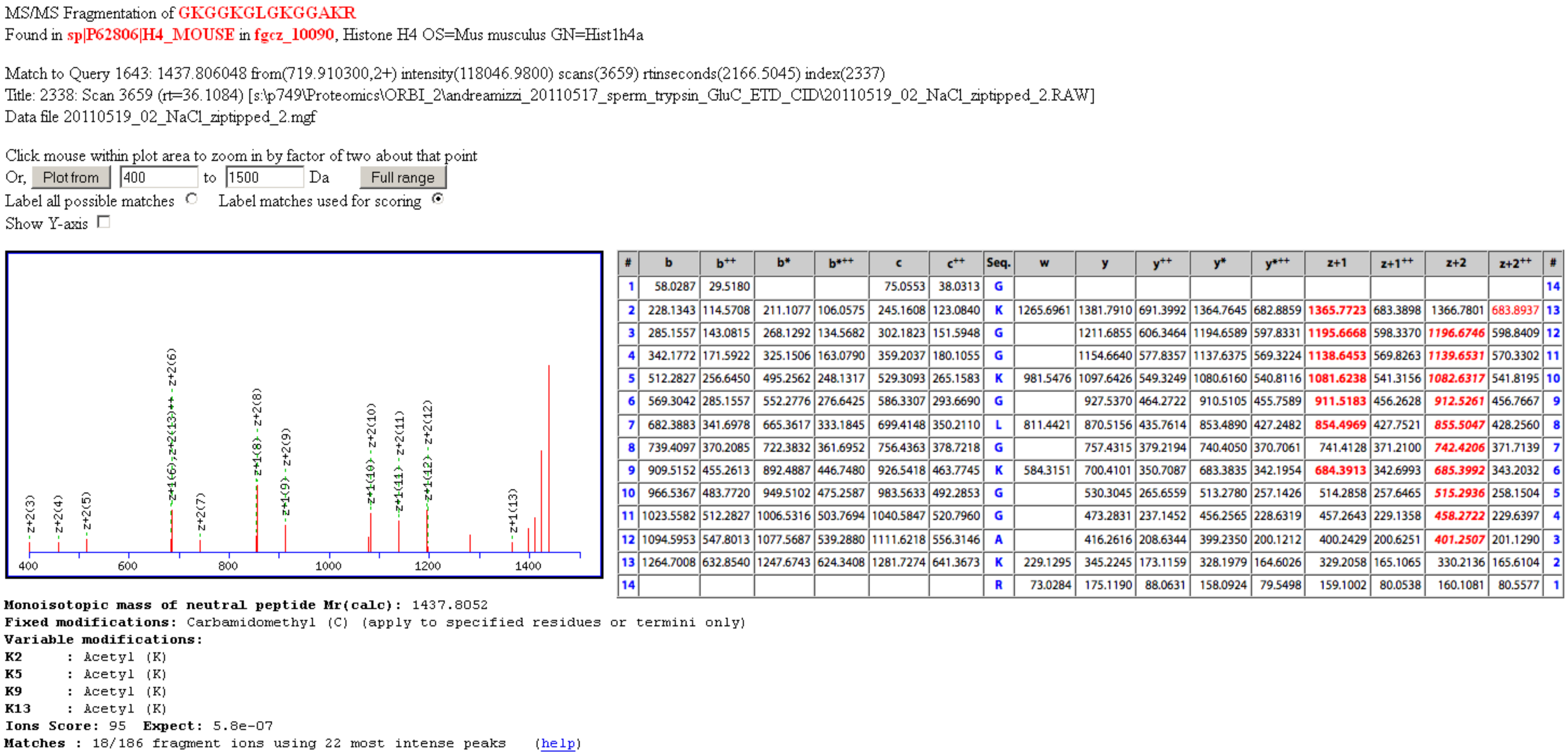
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	c	c^{++}	Seq.	w	y	y^{++}	y^{*}	y^{*++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	58.0287	29.5180			75.0553	38.0313	G										14
2	228.1343	114.5708	211.1077	106.0575	245.1608	123.0840	K	1223.6855	1339.7805	670.3939	1322.7539	661.8806	1323.7617	662.3845	1324.7696	**662.8884**	13
3	285.1557	143.0815	268.1292	134.5682	**302.1823**	151.5948	G		1169.6749	585.3411	1152.6484	576.8278	***1153.6562***	577.3317	1154.6640	**577.8357**	12
4	342.1772	171.5922	325.1506	163.0790	**359.2037**	180.1055	G		1112.6535	556.8304	1095.6269	548.3171	1096.6347	548.8210	**1097.6426**	549.3249	11
5	512.2827	256.6450	495.2562	248.1317	**529.3093**	265.1583	K	939.5370	**1055.6320**	528.3196	1038.6055	519.8064	***1039.6133***	520.3103	**1040.6211**	**520.8142**	10
6	569.3042	285.1557	552.2776	276.6425	**586.3307**	293.6690	G		885.5265	443.2669	868.4999	434.7536	***869.5078***	435.2575	870.5156	435.7614	9
7	682.3883	341.6978	665.3617	333.1845	**699.4148**	350.2110	L	769.4315	828.5050	414.7561	811.4785	406.2429	***812.4863***	406.7468	**813.4941**	407.2507	8
8	739.4097	370.2085	722.3832	361.6952	756.4363	378.7218	G		715.4209	358.2141	698.3944	349.7008	***699.4022***	350.2048	700.4101	350.7087	7
9	867.5047	434.2560	850.4781	425.7427	**884.5312**	442.7693	K	584.3151	658.3995	329.7034	641.3729	321.1901	***642.3808***	321.6940	643.3886	322.1979	6
10	924.5261	462.7667	907.4996	454.2534	**941.5527**	471.2800	G		530.3045	265.6559	513.2780	257.1426	***514.2858***	257.6465	515.2936	258.1504	5
11	981.5476	491.2774	964.5211	482.7642	998.5742	499.7907	G		**473.2831**	237.1452	456.2565	228.6319	457.2643	229.1358	458.2722	229.6397	4
12	1052.5847	526.7960	1035.5582	518.2827	1069.6113	535.3093	A		**416.2616**	208.6344	399.2350	200.1212	***400.2429***	200.6251	401.2507	201.1290	3
13	1222.6902	611.8488	1205.6637	603.3355	1239.7168	620.3620	K	229.1295	345.2245	173.1159	328.1979	164.6026	***329.2058***	165.1065	330.2136	165.6104	2
14							R	73.0284	175.1190	88.0631	158.0924	79.5498	159.1002	80.0538	160.1081	80.5577	1

```
Monoisotopic mass of neutral peptide Mr(calc): 1395.7946
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2     : Acetyl (K)
K5     : Acetyl (K)
K13    : Acetyl (K)
Ions Score: 45  Expect: 0.002
Matches : 32/186 fragment ions using 62 most intense peaks   (help)
```

Mascot Search Results: Peptide View

GKacGGKacGLGKGGAKacR



MS/MS Fragmentation of GKGGKGLGKGGAKR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 1643: 1437.806048 from(719.910300,2+) intensity(118046.9800) scans(3659) rtinseconds(2166.5045) index(2337)
Title: 2338: Scan 3659 (rt=36.1084) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_02_NaCl_ziptipped_2.RAW]
Data file 20110519_02_NaCl_ziptipped_2.mgf

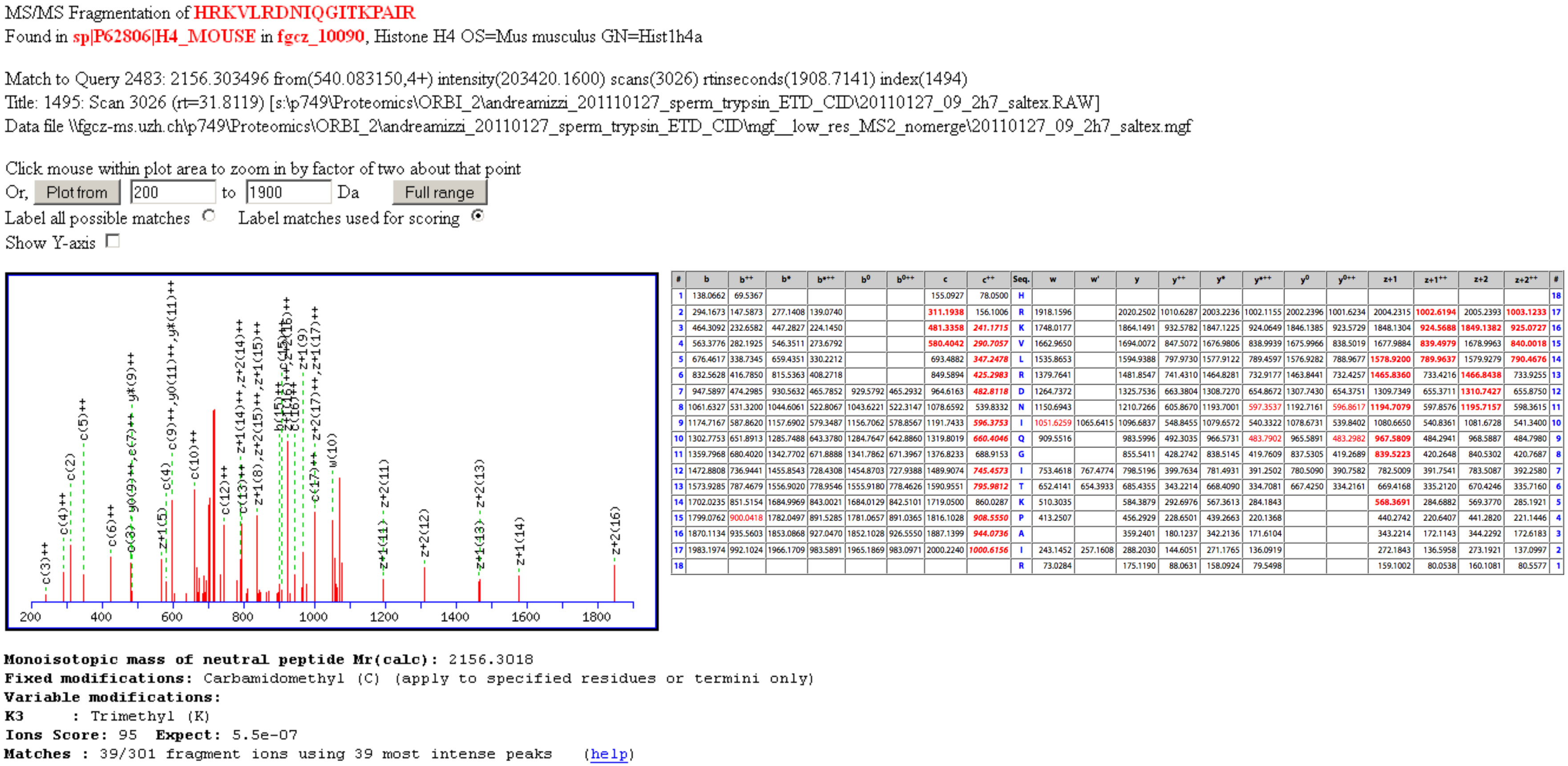
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 400 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b*	b^{*++}	c	c^{++}	Seq.	w	y	y^{++}	y*	y^{*++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	58.0287	29.5180			75.0553	38.0313	G										14
2	228.1343	114.5708	211.1077	106.0575	245.1608	123.0840	K	1265.6961	1381.7910	691.3992	1364.7645	682.8859	**1365.7723**	683.3898	1366.7801	683.8937	13
3	285.1557	143.0815	268.1292	134.5682	302.1823	151.5948	G		1211.6855	606.3464	1194.6589	597.8331	**1195.6668**	598.3370	***1196.6746***	598.8409	12
4	342.1772	171.5922	325.1506	163.0790	359.2037	180.1055	G		1154.6640	577.8357	1137.6375	569.3224	**1138.6453**	569.8263	***1139.6531***	570.3302	11
5	512.2827	256.6450	495.2562	248.1317	529.3093	265.1583	K	981.5476	1097.6426	549.3249	1080.6160	540.8116	**1081.6238**	541.3156	***1082.6317***	541.8195	10
6	569.3042	285.1557	552.2776	276.6425	586.3307	293.6690	G		927.5370	464.2722	910.5105	455.7589	**911.5183**	456.2628	***912.5261***	456.7667	9
7	682.3883	341.6978	665.3617	333.1845	699.4148	350.2110	L	811.4421	870.5156	435.7614	853.4890	427.2482	**854.4969**	427.7521	***855.5047***	428.2560	8
8	739.4097	370.2085	722.3832	361.6952	756.4363	378.7218	G		757.4315	379.2194	740.4050	370.7061	741.4128	371.2100	***742.4206***	371.7139	7
9	909.5152	455.2613	892.4887	446.7480	926.5418	463.7745	K	584.3151	700.4101	350.7087	683.3835	342.1954	**684.3913**	342.6993	***685.3992***	343.2032	6
10	966.5367	483.7720	949.5102	475.2587	983.5633	492.2853	G		530.3045	265.6559	513.2780	257.1426	514.2858	257.6465	***515.2936***	258.1504	5
11	1023.5582	512.2827	1006.5316	503.7694	1040.5847	520.7960	G		473.2831	237.1452	456.2565	228.6319	457.2643	229.1358	***458.2722***	229.6397	4
12	1094.5953	547.8013	1077.5687	539.2880	1111.6218	556.3146	A		416.2616	208.6344	399.2350	200.1212	400.2429	200.6251	***401.2507***	201.1290	3
13	1264.7008	632.8540	1247.6743	624.3408	1281.7274	641.3673	K	229.1295	345.2245	173.1159	328.1979	164.6026	329.2058	165.1065	330.2136	165.6104	2
14							R	73.0284	175.1190	88.0631	158.0924	79.5498	159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1437.8052
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K2 : Acetyl (K)
K5 : Acetyl (K)
K9 : Acetyl (K)
K13 : Acetyl (K)
Ions Score: 95 **Expect:** 5.8e-07
Matches : 18/186 fragment ions using 22 most intense peaks (help)

Mascot Search Results: Peptide View

GKacGGKacGLGKacGGAKacR



MS/MS Fragmentation of HRKVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2483: 2156.303496 from(540.083150,4+) intensity(203420.1600) scans(3026) rtinseconds(1908.7141) index(1494)
Title: 1495: Scan 3026 (rt=31.8119) [s:\p749\Proteomics\ORBI_2\andreamizzi_201110127_sperm_trypsin_ETD_CID\20110127_09_2h7_saltex.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110127_sperm_trypsin_ETD_CID\mgf__low_res_MS2_nomerge\20110127_09_2h7_saltex.mgf

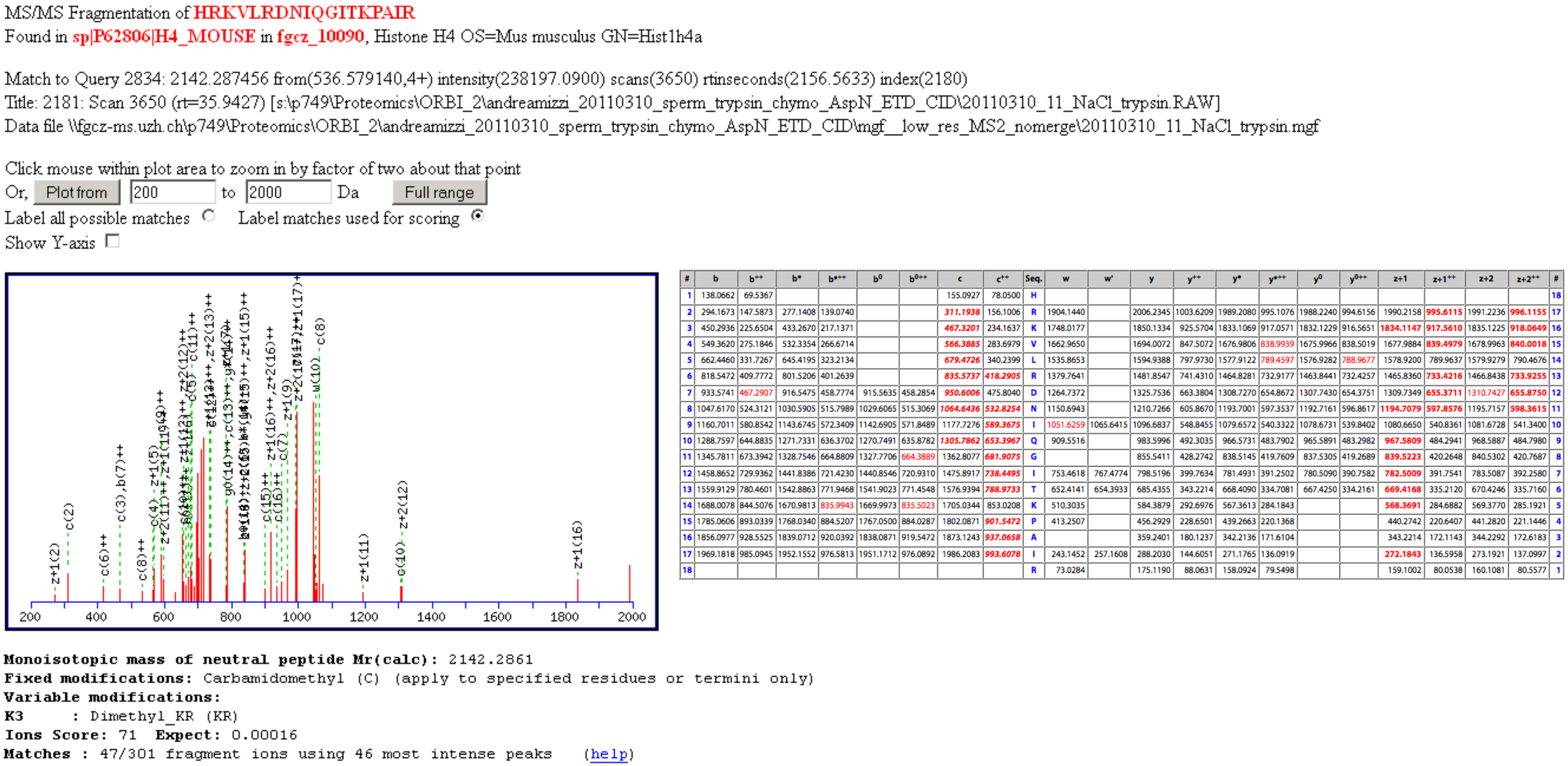
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	138.0662	69.5367					155.0927	78.0500	H													18
2	294.1673	147.5873	277.1408	139.0740			**311.1938**	156.1006	R	1918.1596		2020.2502	1010.6287	2003.2236	1002.1155	2002.2396	1001.6234	2004.2315	**1002.6194**	2005.2393	**1003.1233**	17
3	464.3092	232.6582	447.2827	224.1450			**481.3358**	***241.1715***	K	1748.0177		1864.1491	932.5782	1847.1225	924.0649	1846.1385	923.5729	1848.1304	**924.5688**	**1849.1382**	**925.0727**	16
4	563.3776	282.1925	546.3511	273.6792			**580.4042**	***290.7057***	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	1677.9884	**839.4979**	1678.9963	**840.0018**	15
5	676.4617	338.7345	659.4351	330.2212			693.4882	***347.2478***	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	**1578.9200**	**789.9637**	1579.9279	**790.4676**	14
6	832.5628	416.7850	815.5363	408.2718			849.5894	***425.2983***	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	**1465.8360**	733.4216	**1466.8438**	733.9255	13
7	947.5897	474.2985	930.5632	465.7852	929.5792	465.2932	964.6163	***482.8118***	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	**1310.7427**	655.8750	12
8	1061.6327	531.3200	1044.6061	522.8067	1043.6221	522.3147	1078.6592	539.8332	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	**1194.7079**	597.8576	**1195.7157**	598.3615	11
9	1174.7167	587.8620	1157.6902	579.3487	1156.7062	578.8567	1191.7433	***596.3753***	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
10	1302.7753	651.8913	1285.7488	643.3780	1284.7647	642.8860	1319.8019	***660.4046***	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	**967.5809**	484.2941	968.5887	484.7980	9
11	1359.7968	680.4020	1342.7702	671.8888	1341.7862	671.3967	1376.8233	688.9153	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	**839.5223**	420.2648	840.5302	420.7687	8
12	1472.8808	736.9441	1455.8543	728.4308	1454.8703	727.9388	1489.9074	***745.4573***	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
13	1573.9285	787.4679	1556.9020	778.9546	1555.9180	778.4626	1590.9551	***795.9812***	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
14	1702.0235	851.5154	1684.9969	843.0021	1684.0129	842.5101	1719.0500	860.0287	K	510.3035		584.3879	292.6976	567.3613	284.1843			**568.3691**	284.6882	569.3770	285.1921	5
15	1799.0762	900.0418	1782.0497	891.5285	1781.0657	891.0365	1816.1028	***908.5550***	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
16	1870.1134	935.5603	1853.0868	927.0470	1852.1028	926.5550	1887.1399	***944.0736***	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
17	1983.1974	992.1024	1966.1709	983.5891	1965.1869	983.0971	2000.2240	***1000.6156***	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
18									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2156.3018
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Trimethyl (K)
Ions Score: 95 **Expect:** 5.5e-07
Matches : 39/301 fragment ions using 39 most intense peaks (help)

Mascot Search Results: Peptide View

HRKme3VLRDNIQGITKPAIR



MS/MS Fragmentation of HRKVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2834: 2142.287456 from(536.579140,4+) intensity(238197.0900) scans(3650) rtinseconds(2156.5633) index(2180)
Title: 2181: Scan 3650 (rt=35.9427) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_11_NaCl_trypsin.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_11_NaCl_trypsin.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	138.0662	69.5367					155.0927	78.0500	H													18
2	294.1673	147.5873	277.1408	139.0740			**311.1938**	156.1006	R	1904.1440		2006.2345	1003.6209	1989.2080	995.1076	1988.2240	994.6156	1990.2158	**995.6115**	1991.2236	**996.1155**	17
3	450.2936	225.6504	433.2670	217.1371			**467.3201**	234.1637	K	1748.0177		1850.1334	925.5704	1833.1069	917.0571	1832.1229	916.5651	**1834.1147**	**917.5610**	1835.1225	**918.0649**	16
4	549.3620	275.1846	532.3354	266.6714			**566.3885**	283.6979	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	1677.9884	**839.4979**	1678.9963	**840.0018**	15
5	662.4460	331.7267	645.4195	323.2134			**679.4726**	340.2399	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	1578.9200	789.9637	1579.9279	790.4676	14
6	818.5472	409.7772	801.5206	401.2639			**835.5737**	**418.2905**	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	1466.8438	**733.9255**	13
7	933.5741	467.2907	916.5475	458.7774	915.5635	458.2854	**950.6006**	475.8040	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	**655.3711**	1310.7427	**655.8750**	12
8	1047.6170	524.3121	1030.5905	515.7989	1029.6065	515.3069	**1064.6436**	**532.8254**	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	**1194.7079**	**597.8576**	1195.7157	**598.3615**	11
9	1160.7011	580.8542	1143.6745	572.3409	1142.6905	571.8489	1177.7276	**589.3675**	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
10	1288.7597	644.8835	1271.7331	636.3702	1270.7491	635.8782	**1305.7862**	**653.3967**	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	**967.5809**	484.2941	968.5887	484.7980	9
11	1345.7811	673.3942	1328.7546	664.8809	1327.7706	664.3889	1362.8077	**681.9075**	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	**839.5223**	420.2648	840.5302	420.7687	8
12	1458.8652	729.9362	1441.8386	721.4230	1440.8546	720.9310	1475.8917	**738.4495**	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	**782.5009**	391.7541	783.5087	392.2580	7
13	1559.9129	780.4601	1542.8863	771.9468	1541.9023	771.4548	1576.9394	**788.9733**	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	**669.4168**	335.2120	670.4246	335.7160	6
14	1688.0078	844.5076	1670.9813	835.9943	1669.9973	835.5023	1705.0344	853.0208	K	510.3035		584.3879	292.6976	567.3613	284.1843			**568.3691**	284.6882	569.3770	285.1921	5
15	1785.0606	893.0339	1768.0340	884.5207	1767.0500	884.0287	1802.0871	**901.5472**	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
16	1856.0977	928.5525	1839.0712	920.0392	1838.0871	919.5472	1873.1243	**937.0658**	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
17	1969.1818	985.0945	1952.1552	976.5813	1951.1712	976.0892	1986.2083	**993.6078**	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
18									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2142.2861
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Dimethyl_KR (KR)
Ions Score: 71 **Expect:** 0.00016
Matches : 47/301 fragment ions using 46 most intense peaks (help)

Mascot Search Results: Peptide View

HRKme2VLRDNIQGITKPAIR

MS/MS Fragmentation of HRKVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 4484: 2128.270536 from(533.074910,4+) intensity(15082.3940) scans(3179) rtinseconds(2214.3129) index(1492)
Title: 1348: Scan 3179 (rt=36.9052) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

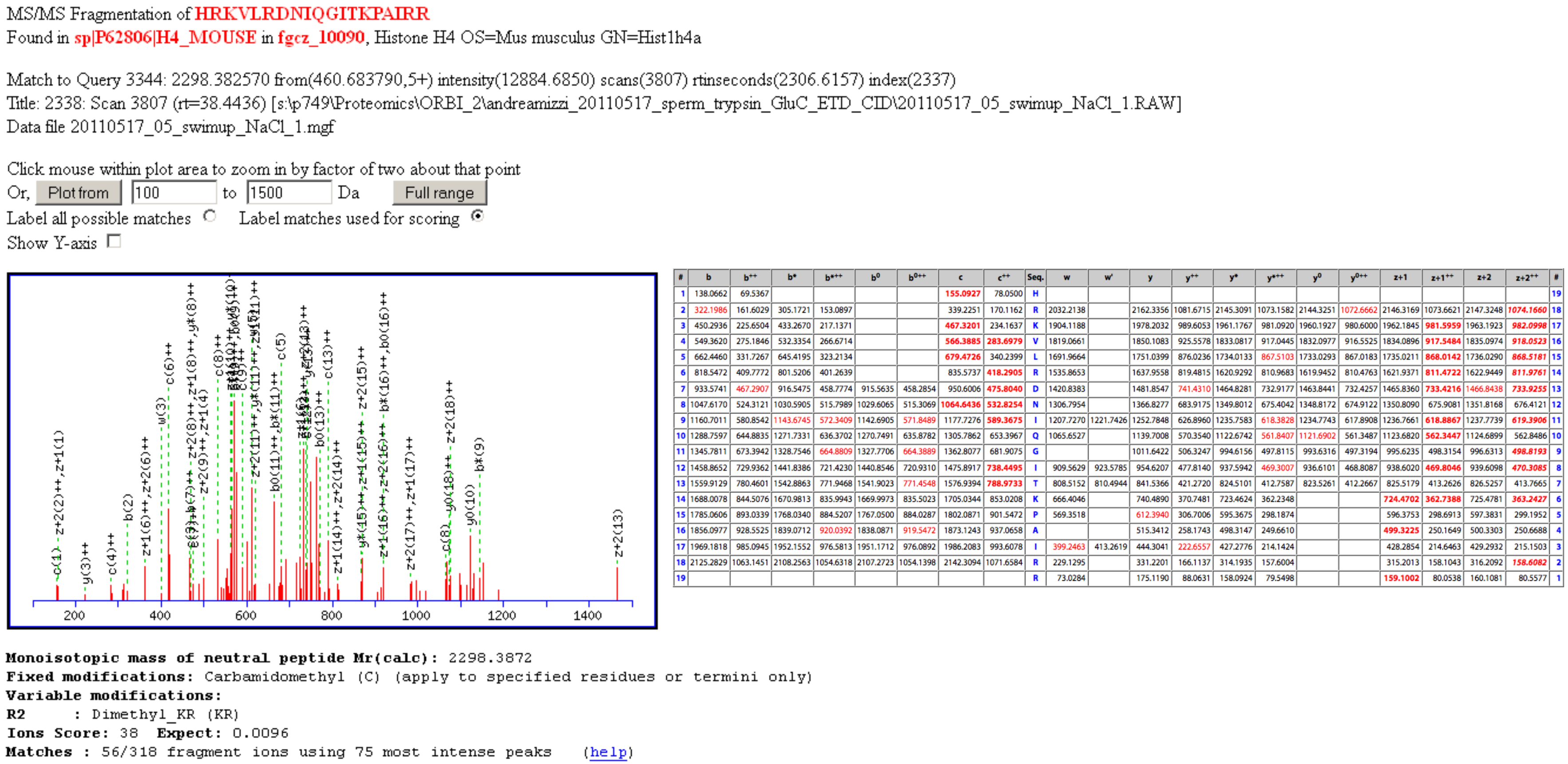
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	138.0662	69.5367					155.0927	78.0500	H													18
2	294.1673	147.5873	277.1408	139.0740			**311.1938**	156.1006	R	1890.1283		1992.2189	996.6131	1975.1923	988.0998	1974.2083	987.6078	1976.2002	**988.6037**	1977.2080	**989.1076**	17
3	436.2779	218.6426	419.2514	210.1293			**453.3045**	227.1559	K	1748.0177		1836.1178	918.5625	1819.0912	910.0493	1818.1072	909.5572	**1820.0991**	**910.5532**	1821.1069	**911.0571**	16
4	535.3463	268.1768	518.3198	259.6635			**552.3729**	276.6901	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	1677.9884	**839.4979**	1678.9963	**840.0018**	15
5	648.4304	324.7188	631.4038	316.2056			**665.4569**	333.2321	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	1578.9200	**789.9637**	1579.9279	**790.4676**	14
6	804.5315	402.7694	787.5050	394.2561			**821.5581**	**411.2827**	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	1466.8438	**733.9255**	13
7	919.5584	460.2829	902.5319	451.7696	901.5479	451.2776	**936.5850**	468.7961	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	**1309.7349**	**655.3711**	1310.7427	**655.8750**	12
8	1033.6014	517.3043	1016.5748	508.7910	1015.5908	508.2990	1050.6279	525.8176	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	**597.8576**	1195.7157	**598.3615**	11
9	1146.6854	573.8464	1129.6589	565.3331	1128.6749	564.8411	**1163.7120**	**582.3596**	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
10	1274.7440	637.8756	1257.7175	629.3624	1256.7334	628.8704	**1291.7706**	**646.3889**	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	**967.5809**	484.2941	968.5887	484.7980	9
11	1331.7655	666.3864	1314.7389	657.8731	1313.7549	657.3811	1348.7920	**674.8997**	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	**839.5223**	420.2648	840.5302	420.7687	8
12	1444.8495	722.9284	1427.8230	714.4151	1426.8390	713.9231	1461.8761	**731.4417**	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	**782.5009**	391.7541	783.5087	392.2580	7
13	1545.8972	773.4522	1528.8707	764.9390	1527.8867	764.4470	**1562.9238**	**781.9655**	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	**669.4168**	335.2120	670.4246	335.7160	6
14	1673.9922	837.4997	1656.9656	828.9865	1655.9816	828.4944	1691.0187	846.0130	K	510.3035		584.3879	292.6976	567.3613	284.1843			**568.3691**	284.6882	569.3770	285.1921	5
15	1771.0449	886.0261	1754.0184	877.5128	1753.0344	877.0208	1788.0715	**894.5394**	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
16	1842.0821	921.5447	1825.0555	913.0314	1824.0715	912.5394	1859.1086	930.0579	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
17	1955.1661	978.0867	1938.1396	969.5734	1937.1556	969.0814	1972.1927	**986.6000**	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
18									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2128.2705
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Methyl_KR (KR)
Ions Score: 58 **Expect:** 0.00025
Matches : 47/301 fragment ions using 53 most intense peaks (help)

Mascot Search Results: Peptide View

HRKme1VLRDNIQGITKPAIR



MS/MS Fragmentation of HRKVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3344: 2298.382570 from(460.683790,5+) intensity(12884.6850) scans(3807) rtinseconds(2306.6157) index(2337)
Title: 2338: Scan 3807 (rt=38.4436) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_05_swimup_NaCl_1.RAW]
Data file 20110517_05_swimup_NaCl_1.mgf

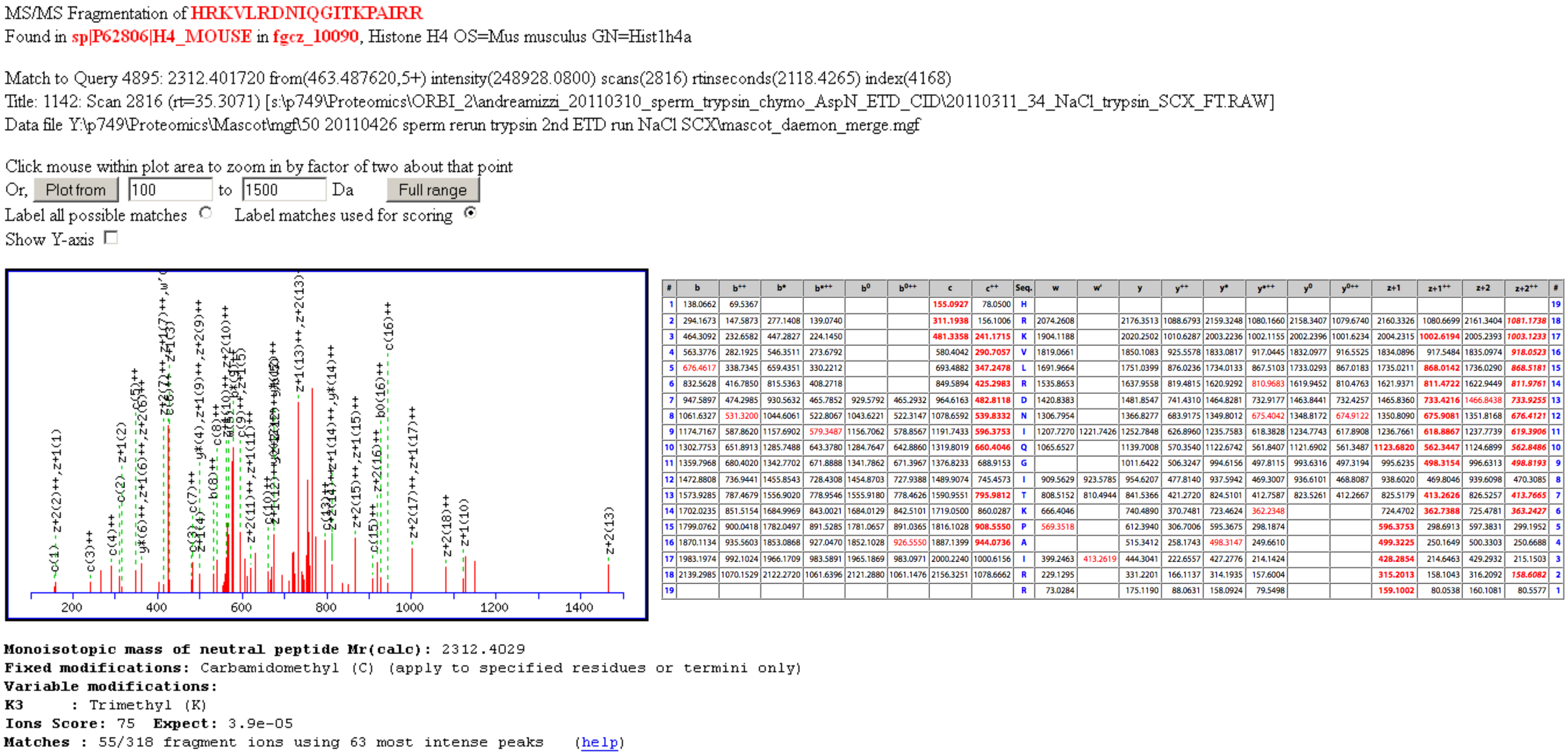
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	138.0662	69.5367					**155.0927**	78.0500	H													19
2	322.1986	161.6029	305.1721	153.0897			339.2251	170.1162	R	2032.2138		2162.3356	1081.6715	2145.3091	1073.1582	2144.3251	1072.6662	2146.3169	1073.6621	2147.3248	***1074.1660***	18
3	450.2936	225.6504	433.2670	217.1371			**467.3201**	234.1637	K	1904.1188		1978.2032	989.6053	1961.1767	981.0920	1960.1927	980.6000	1962.1845	**981.5959**	1963.1923	***982.0998***	17
4	549.3620	275.1846	532.3354	266.6714			**566.3885**	**283.6979**	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	**917.5484**	1835.0974	***918.0523***	16
5	662.4460	331.7267	645.4195	323.2134			**679.4726**	340.2399	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	**868.0142**	1736.0290	***868.5181***	15
6	818.5472	409.7772	801.5206	401.2639			835.5737	**418.2905**	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	**811.4722**	1622.9449	***811.9761***	14
7	933.5741	467.2907	916.5475	458.7774	915.5635	458.2854	950.6006	**475.8040**	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	1466.8438	***733.9255***	13
8	1047.6170	524.3121	1030.5905	515.7989	1029.6065	515.3069	**1064.6436**	**532.8254**	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	1351.8168	676.4121	12
9	1160.7011	580.8542	1143.6745	572.3409	1142.6905	571.8489	1177.7276	**589.3675**	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	**618.8867**	1237.7739	***619.3906***	11
10	1288.7597	644.8835	1271.7331	636.3702	1270.7491	635.8782	1305.7862	653.3967	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	**562.3447**	1124.6899	562.8486	10
11	1345.7811	673.3942	1328.7546	664.8809	1327.7706	664.3889	1362.8077	681.9075	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	995.6235	498.3154	996.6313	***498.8193***	9
12	1458.8652	729.9362	1441.8386	721.4230	1440.8546	720.9310	1475.8917	**738.4495**	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	**469.8046**	939.6098	***470.3085***	8
13	1559.9129	780.4601	1542.8863	771.9468	1541.9023	771.4548	1576.9394	**788.9733**	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	413.2626	826.5257	413.7665	7
14	1688.0078	844.5076	1670.9813	835.9943	1669.9973	835.5023	1705.0344	853.0208	K	666.4046		740.4890	370.7481	723.4624	362.2348			**724.4702**	**362.7388**	725.4781	***363.2427***	6
15	1785.0606	893.0339	1768.0340	884.5207	1767.0500	884.0287	1802.0871	901.5472	P	569.3518		612.3940	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
16	1856.0977	928.5525	1839.0712	920.0392	1838.0871	919.5472	1873.1243	937.0658	A			515.3412	258.1743	498.3147	249.6610			**499.3225**	250.1649	500.3303	250.6688	4
17	1969.1818	985.0945	1952.1552	976.5813	1951.1712	976.0892	1986.2083	993.6078	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			428.2854	214.6463	429.2932	215.1503	3
18	2125.2829	1063.1451	2108.2563	1054.6318	2107.2723	1054.1398	2142.3094	1071.6584	R	229.1295		331.2201	166.1137	314.1935	157.6004			315.2013	158.1043	316.2092	***158.6082***	2
19									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

```
Monoisotopic mass of neutral peptide Mr(calc): 2298.3872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
R2      : Dimethyl_KR (KR)
Ions Score: 38  Expect: 0.0096
Matches : 56/318 fragment ions using 75 most intense peaks   (help)
```

Mascot Search Results: Peptide View

HRme2KVLRDNIQGITKPAIRR



MS/MS Fragmentation of HRKVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 4895: 2312.401720 from(463.487620,5+) intensity(248928.0800) scans(2816) rtinseconds(2118.4265) index(4168)
Title: 1142: Scan 2816 (rt=35.3071) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

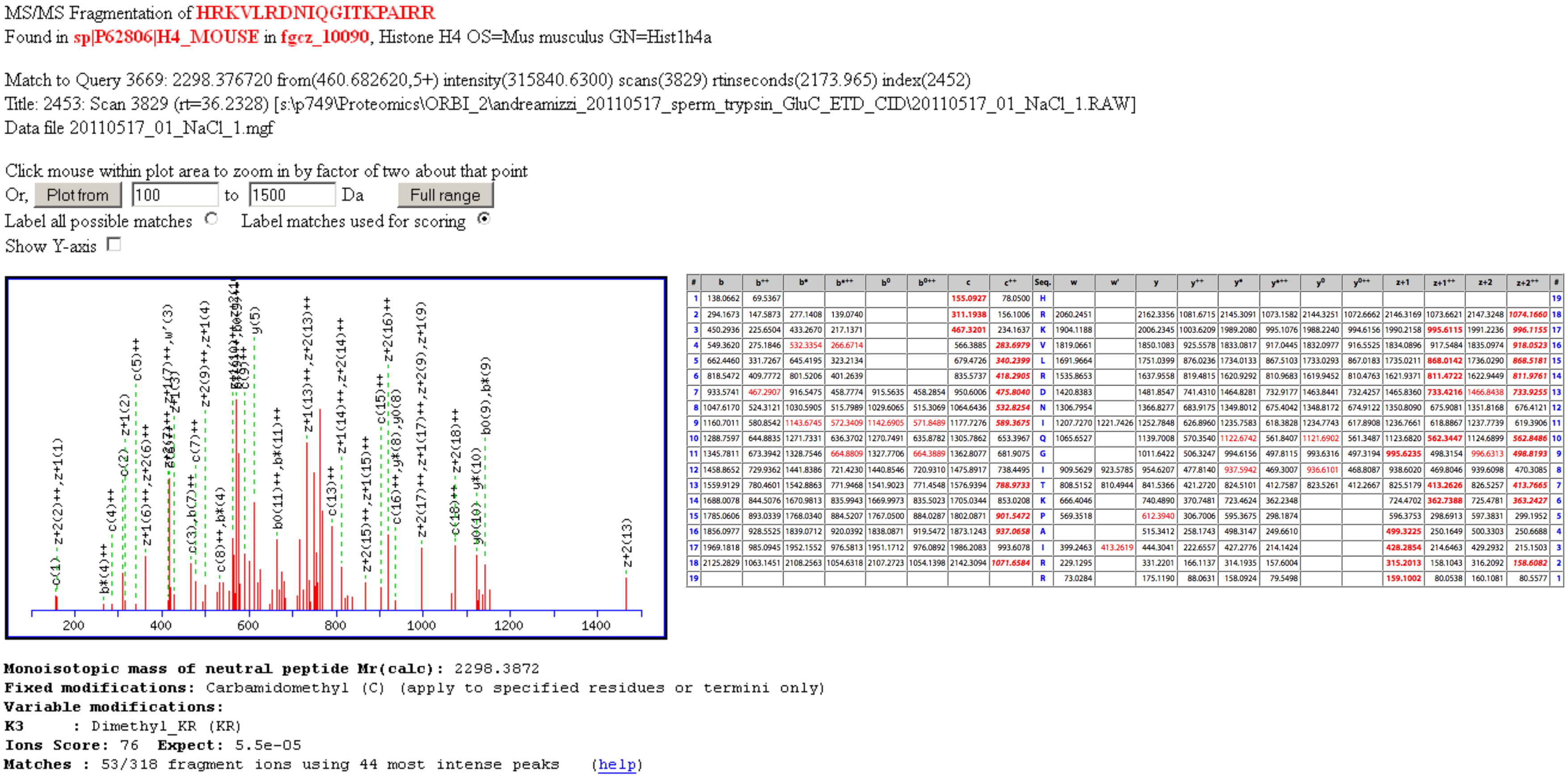
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	138.0662	69.5367					**155.0927**	78.0500	H													19
2	294.1673	147.5873	277.1408	139.0740			**311.1938**	156.1006	R	2074.2608		2176.3513	1088.6793	2159.3248	1080.1660	2158.3407	1079.6740	2160.3326	1080.6699	2161.3404	***1081.1738***	18
3	464.3092	232.6582	447.2827	224.1450			**481.3358**	**241.1715**	K	1904.1188		2020.2502	1010.6287	2003.2236	1002.1155	2002.2396	1001.6234	2004.2315	**1002.6194**	2005.2393	***1003.1233***	17
4	563.3776	282.1925	546.3511	273.6792			580.4042	**290.7057**	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	917.5484	1835.0974	***918.0523***	16
5	676.4617	338.7345	659.4351	330.2212			693.4882	**347.2478**	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	**868.0142**	1736.0290	***868.5181***	15
6	832.5628	416.7850	815.5363	408.2718			849.5894	**425.2983**	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	**811.4722**	1622.9449	***811.9761***	14
7	947.5897	474.2985	930.5632	465.7852	929.5792	465.2932	964.6163	**482.8118**	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	1466.8438	***733.9255***	13
8	1061.6327	531.3200	1044.6061	522.8067	1043.6221	522.3147	1078.6592	**539.8332**	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	**675.9081**	1351.8168	***676.4121***	12
9	1174.7167	587.8620	1157.6902	579.3487	1156.7062	578.8567	1191.7433	**596.3753**	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	**618.8867**	1237.7739	***619.3906***	11
10	1302.7753	651.8913	1285.7488	643.3780	1284.7647	642.8860	1319.8019	**660.4046**	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	**1123.6820**	**562.3447**	1124.6899	***562.8486***	10
11	1359.7968	680.4020	1342.7702	671.8888	1341.7862	671.3967	1376.8233	688.9153	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	995.6235	**498.3154**	996.6313	***498.8193***	9
12	1472.8808	736.9441	1455.8543	728.4308	1454.8703	727.9388	1489.9074	745.4573	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
13	1573.9285	787.4679	1556.9020	778.9546	1555.9180	778.4626	1590.9551	**795.9812**	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	**413.2626**	826.5257	***413.7665***	7
14	1702.0235	851.5154	1684.9969	843.0021	1684.0129	842.5101	1719.0500	860.0287	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	**362.7388**	725.4781	***363.2427***	6
15	1799.0762	900.0418	1782.0497	891.5285	1781.0657	891.0365	1816.1028	**908.5550**	P	569.3518		612.3940	306.7006	595.3675	298.1874			**596.3753**	298.6913	597.3831	299.1952	5
16	1870.1134	935.5603	1853.0868	927.0470	1852.1028	926.5550	1887.1399	**944.0736**	A			515.3412	258.1743	498.3147	249.6610			**499.3225**	250.1649	500.3303	250.6688	4
17	1983.1974	992.1024	1966.1709	983.5891	1965.1869	983.0971	2000.2240	1000.6156	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			**428.2854**	214.6463	429.2932	215.1503	3
18	2139.2985	1070.1529	2122.2720	1061.6396	2121.2880	1061.1476	2156.3251	1078.6662	R	229.1295		331.2201	166.1137	314.1935	157.6004			**315.2013**	158.1043	316.2092	***158.6082***	2
19									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2312.4029
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Trimethyl (K)
Ions Score: 75 **Expect:** 3.9e-05
Matches : 55/318 fragment ions using 63 most intense peaks (help)

Mascot Search Results: Peptide View

HRKme3VLRDNIQGITKPAIRR



MS/MS Fragmentation of HRKVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3669: 2298.376720 from(460.682620,5+) intensity(315840.6300) scans(3829) rtinseconds(2173.965) index(2452)
Title: 2453: Scan 3829 (rt=36.2328) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	138.0662	69.5367					**155.0927**	78.0500	H													19
2	294.1673	147.5873	277.1408	139.0740			**311.1938**	156.1006	R	2060.2451		2162.3356	1081.6715	2145.3091	1073.1582	2144.3251	1072.6662	2146.3169	1073.6621	2147.3248	***1074.1660***	18
3	450.2936	225.6504	433.2670	217.1371			**467.3201**	234.1637	K	1904.1188		2006.2345	1003.6209	1989.2080	995.1076	1988.2240	994.6156	1990.2158	**995.6115**	1991.2236	***996.1155***	17
4	549.3620	275.1846	532.3354	266.6714			566.3885	***283.6979***	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	917.5484	1835.0974	***918.0523***	16
5	662.4460	331.7267	645.4195	323.2134			679.4726	***340.2399***	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	**868.0142**	1736.0290	***868.5181***	15
6	818.5472	409.7772	801.5206	401.2639			835.5737	***418.2905***	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	**811.4722**	1622.9449	***811.9761***	14
7	933.5741	467.2907	916.5475	458.7774	915.5635	458.2854	950.6006	***475.8040***	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	1466.8438	***733.9255***	13
8	1047.6170	524.3121	1030.5905	515.7989	1029.6065	515.3069	1064.6436	***532.8254***	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	1351.8168	676.4121	12
9	1160.7011	580.8542	1143.6745	572.3409	1142.6905	571.8489	1177.7276	***589.3675***	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
10	1288.7597	644.8835	1271.7331	636.3702	1270.7491	635.8782	1305.7862	653.3967	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	**562.3447**	1124.6899	***562.8486***	10
11	1345.7811	673.3942	1328.7546	664.8809	1327.7706	664.3889	1362.8077	681.9075	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	**995.6235**	498.3154	996.6313	***498.8193***	9
12	1458.8652	729.9362	1441.8386	721.4230	1440.8546	720.9310	1475.8917	738.4495	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
13	1559.9129	780.4601	1542.8863	771.9468	1541.9023	771.4548	1576.9394	***788.9733***	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	**413.2626**	826.5257	***413.7665***	7
14	1688.0078	844.5076	1670.9813	835.9943	1669.9973	835.5023	1705.0344	853.0208	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	**362.7388**	725.4781	***363.2427***	6
15	1785.0606	893.0339	1768.0340	884.5207	1767.0500	884.0287	1802.0871	***901.5472***	P	569.3518		612.3940	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
16	1856.0977	928.5525	1839.0712	920.0392	1838.0871	919.5472	1873.1243	***937.0658***	A			515.3412	258.1743	498.3147	249.6610			**499.3225**	250.1649	500.3303	250.6688	4
17	1969.1818	985.0945	1952.1552	976.5813	1951.1712	976.0892	1986.2083	993.6078	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			**428.2854**	214.6463	429.2932	215.1503	3
18	2125.2829	1063.1451	2108.2563	1054.6318	2107.2723	1054.1398	2142.3094	***1071.6584***	R	229.1295		331.2201	166.1137	314.1935	157.6004			**315.2013**	158.1043	316.2092	***158.6082***	2
19									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2298.3872
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K3 : Dimethyl_KR (KR)
Ions Score: 76 **Expect:** 5.5e-05
Matches : 53/318 fragment ions using 44 most intense peaks (help)

Mascot Search Results: Peptide View

HRKme2VLRDNIQGITKPAIRR

MS/MS Fragmentation of KVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2310: 1835.109856 from(459.784740,4+) intensity(620718.1300) scans(3597) rtinseconds(2041.9003) index(1995)
Title: 1996: Scan 3597 (rt=34.0317) [s:\p749\Proteomics\ORBI_2\andreamizzi_201110127_sperm_trypsin_ETD_CID\20110127_08_ON7_saltex.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110127_sperm_trypsin_ETD_CID\mgf__low_res_MS2_nomerge\20110127_08_ON7_saltex.mgf

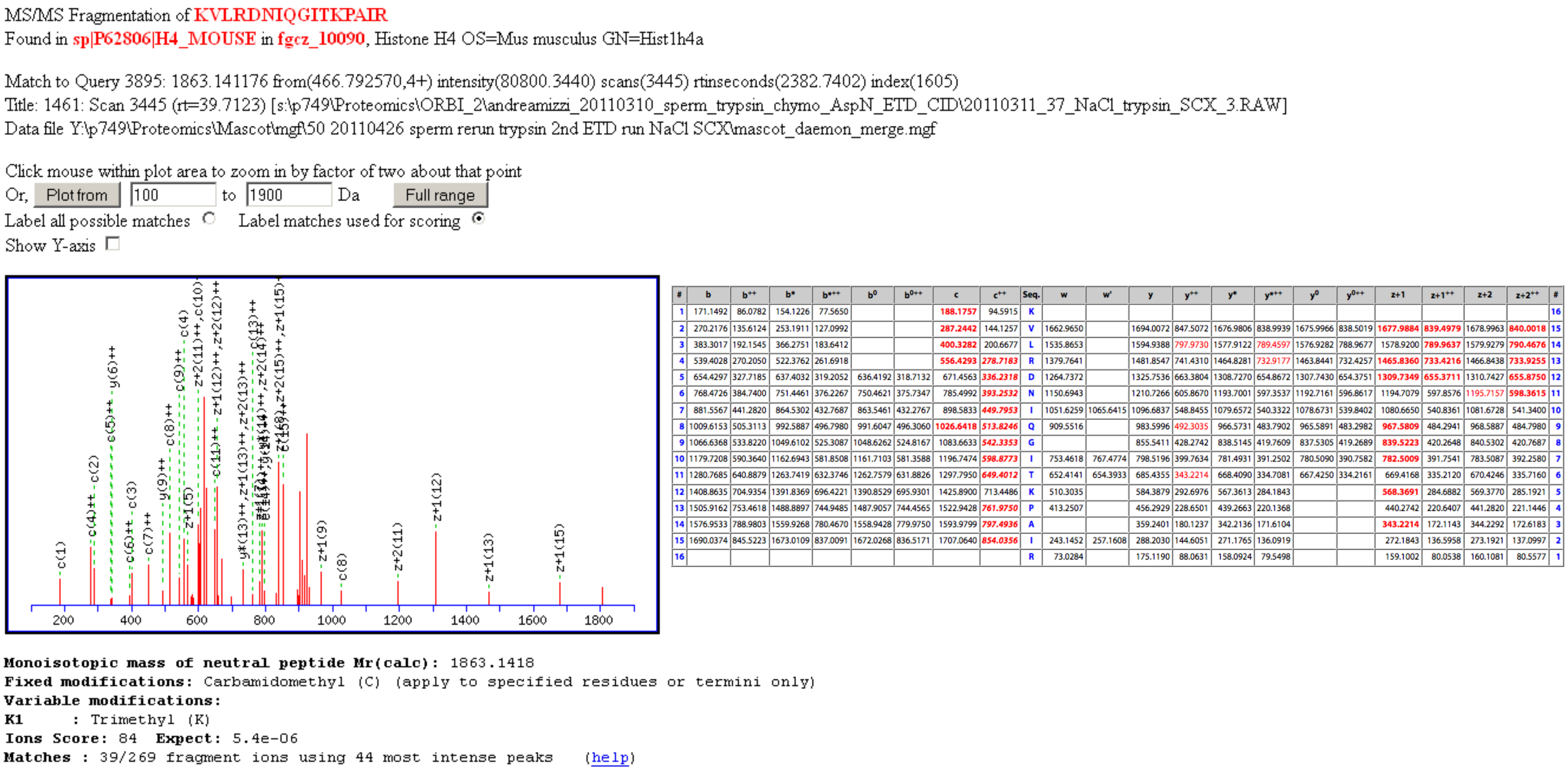
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1700 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													16
2	242.1863	121.5968	225.1598	113.0835			**259.2129**	130.1101	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	1677.9884	***839.4979***	**1678.9963**	**840.0018**	15
3	355.2704	178.1388	338.2438	169.6255			**372.2969**	186.6521	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	1578.9200	***789.9637***	1579.9279	**790.4676**	14
4	511.3715	256.1894	494.3449	247.6761			**528.3980**	264.7027	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	***733.4216***	**1466.8438**	**733.9255**	13
5	626.3984	313.7028	609.3719	305.1896	608.3879	304.6976	**643.4250**	322.2161	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	***655.3711***	**1310.7427**	**655.8750**	12
6	740.4413	370.7243	723.4148	362.2110	722.4308	361.7190	757.4679	379.2376	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	***597.8576***	**1195.7157**	**598.3615**	11
7	853.5254	427.2663	836.4989	418.7531	835.5148	418.2611	**870.5520**	***435.7796***	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	***540.8361***	1081.6728	**541.3400**	10
8	981.5840	491.2956	964.5574	482.7824	963.5734	482.2904	**998.6105**	***499.8089***	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	**967.5809**	***484.2941***	**968.5887**	**484.7980**	9
9	1038.6055	519.8064	1021.5789	511.2931	1020.5949	510.8011	**1055.6320**	***528.3196***	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	**839.5223**	***420.2648***	**840.5302**	**420.7687**	8
10	1151.6895	576.3484	1134.6630	567.8351	1133.6790	567.3431	1168.7161	***584.8617***	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	**782.5009**	***391.7541***	**783.5087**	**392.2580**	7
11	1252.7372	626.8722	1235.7106	618.3590	1234.7266	617.8670	**1269.7637**	***635.3855***	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	**669.4168**	335.2120	**670.4246**	335.7160	6
12	1380.8322	690.9197	1363.8056	682.4064	1362.8216	681.9144	1397.8587	699.4330	K	510.3035		584.3879	292.6976	567.3613	284.1843			**568.3691**	284.6882	569.3770	285.1921	5
13	1477.8849	739.4461	1460.8584	730.9328	1459.8744	730.4408	1494.9115	***747.9594***	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1548.9220	774.9647	1531.8955	766.4514	1530.9115	765.9594	1565.9486	***783.4779***	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
15	1662.0061	831.5067	1644.9796	822.9934	1643.9955	822.5014	**1679.0327**	***840.0200***	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
16									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1835.1105
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
Ions Score: 84 **Expect:** 6.7e-06
Matches : 52/269 fragment ions using 46 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1VLRDNIQGITKPAIR



MS/MS Fragmentation of KVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3895: 1863.141176 from(466.792570,4+) intensity(80800.3440) scans(3445) rtinseconds(2382.7402) index(1605)
Title: 1461: Scan 3445 (rt=39.7123) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

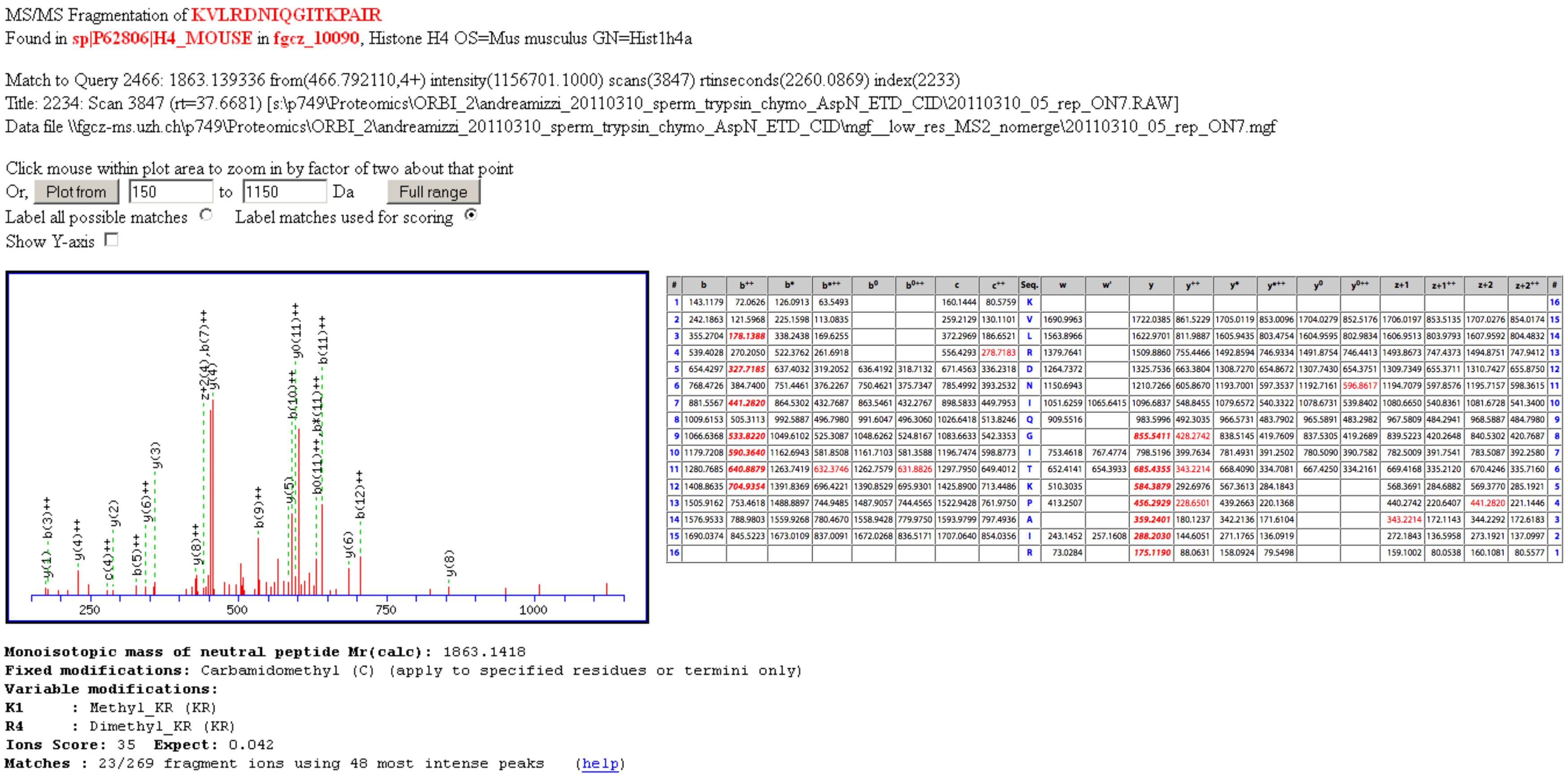
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	171.1492	86.0782	154.1226	77.5650			188.1757	94.5915	K													16
2	270.2176	135.6124	253.1911	127.0992			287.2442	144.1257	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	1677.9884	839.4979	1678.9963	840.0018	15
3	383.3017	192.1545	366.2751	183.6412			400.3282	200.6677	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	1578.9200	789.9637	1579.9279	790.4676	14
4	539.4028	270.2050	522.3762	261.6918			556.4293	278.7183	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	733.4216	1466.8438	733.9255	13
5	654.4297	327.7185	637.4032	319.2052	636.4192	318.7132	671.4563	336.2318	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	1310.7427	655.8750	12
6	768.4726	384.7400	751.4461	376.2267	750.4621	375.7347	785.4992	393.2532	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	1195.7157	598.3615	11
7	881.5567	441.2820	864.5302	432.7687	863.5461	432.2767	898.5833	449.7953	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	1026.6418	513.8246	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	967.5809	484.2941	968.5887	484.7980	9
9	1066.6368	533.8220	1049.6102	525.3087	1048.6262	524.8167	1083.6633	542.3353	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	839.5223	420.2648	840.5302	420.7687	8
10	1179.7208	590.3640	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
11	1280.7685	640.8879	1263.7419	632.3746	1262.7579	631.8826	1297.7950	649.4012	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
12	1408.8635	704.9354	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	510.3035		584.3879	292.6976	567.3613	284.1843			568.3691	284.6882	569.3770	285.1921	5
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	761.9750	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			359.2401	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
16									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1863.1418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
Ions Score: 84 **Expect:** 5.4e-06
Matches : 39/269 fragment ions using 44 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3VLRDNIQGITKPAIR



MS/MS Fragmentation of KVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2466: 1863.139336 from(466.792110,4+) intensity(1156701.1000) scans(3847) rtinseconds(2260.0869) index(2233)
Title: 2234: Scan 3847 (rt=37.6681) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_05_rep_ON7.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_05_rep_ON7.mgf

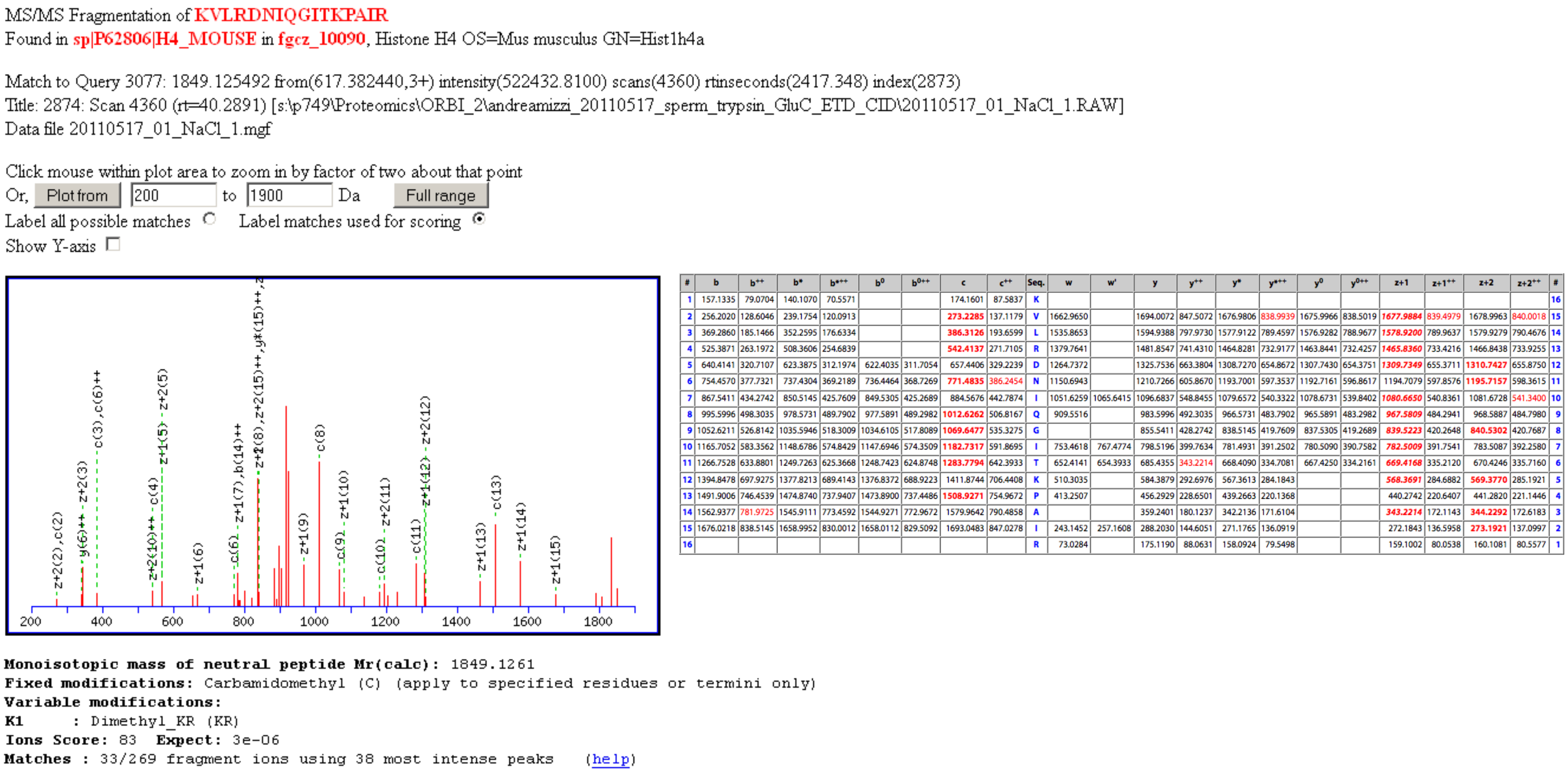
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													16
2	242.1863	121.5968	225.1598	113.0835			259.2129	130.1101	V	1690.9963		1722.0385	861.5229	1705.0119	853.0096	1704.0279	852.5176	1706.0197	853.5135	1707.0276	854.0174	15
3	355.2704	***178.1388***	338.2438	169.6255			372.2969	186.6521	L	1563.8966		1622.9701	811.9887	1605.9435	803.4754	1604.9595	802.9834	1606.9513	803.9793	1607.9592	804.4832	14
4	539.4028	270.2050	522.3762	261.6918			556.4293	278.7183	R	1379.7641		1509.8860	755.4466	1492.8594	746.9334	1491.8754	746.4413	1493.8673	747.4373	1494.8751	747.9412	13
5	654.4297	***327.7185***	637.4032	319.2052	636.4192	318.7132	671.4563	336.2318	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	1310.7427	655.8750	12
6	768.4726	384.7400	751.4461	376.2267	750.4621	375.7347	785.4992	393.2532	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	1195.7157	598.3615	11
7	881.5567	***441.2820***	864.5302	432.7687	863.5461	432.2767	898.5833	449.7953	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	1026.6418	513.8246	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	967.5809	484.2941	968.5887	484.7980	9
9	1066.6368	***533.8220***	1049.6102	525.3087	1048.6262	524.8167	1083.6633	542.3353	G			***855.5411***	428.2742	838.5145	419.7609	837.5305	419.2689	839.5223	420.2648	840.5302	420.7687	8
10	1179.7208	***590.3640***	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
11	1280.7685	***640.8879***	1263.7419	632.3746	1262.7579	631.8826	1297.7950	649.4012	T	652.4141	654.3933	***685.4355***	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
12	1408.8635	***704.9354***	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	510.3035		***584.3879***	292.6976	567.3613	284.1843			568.3691	284.6882	569.3770	285.1921	5
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	761.9750	P	413.2507		***456.2929***	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			***359.2401***	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	243.1452	257.1608	***288.2030***	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
16									R	73.0284		***175.1190***	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1863.1418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
R4 : Dimethyl_KR (KR)
Ions Score: 35 **Expect:** 0.042
Matches : 23/269 fragment ions using 48 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1VLRme2DNIQGITKPAIR



MS/MS Fragmentation of KVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3077: 1849.125492 from(617.382440,3+) intensity(522432.8100) scans(4360) rtinseconds(2417.348) index(2873)
Title: 2874: Scan 4360 (rt=40.2891) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_01_NaCl_1.RAW]
Data file 20110517_01_NaCl_1.mgf

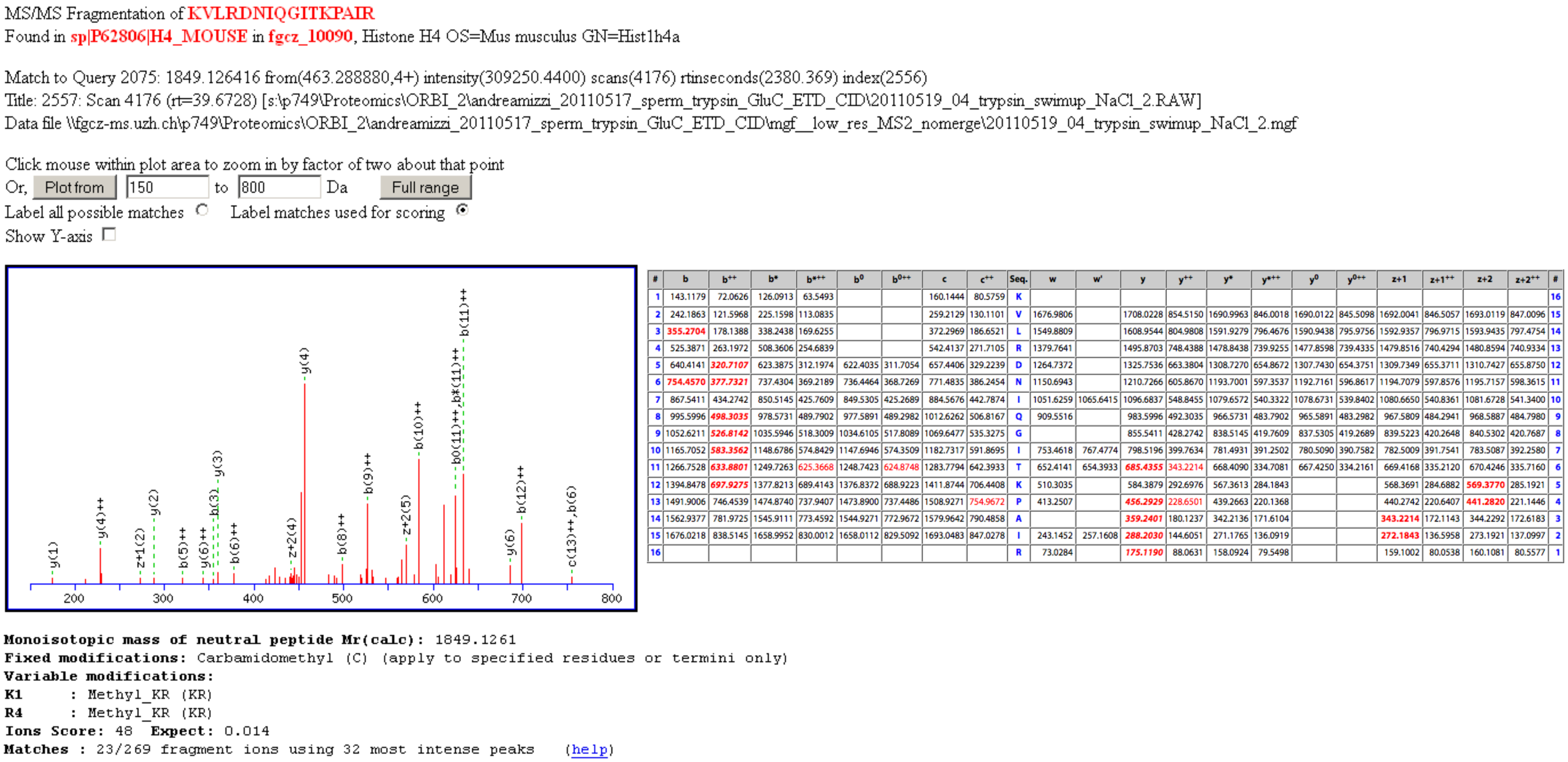
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 1900 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													16
2	256.2020	128.6046	239.1754	120.0913			**273.2285**	137.1179	V	1662.9650		1694.0072	847.5072	1676.9806	838.9939	1675.9966	838.5019	***1677.9884***	839.4979	1678.9963	840.0018	15
3	369.2860	185.1466	352.2595	176.6334			**386.3126**	193.6599	L	1535.8653		1594.9388	797.9730	1577.9122	789.4597	1576.9282	788.9677	***1578.9200***	789.9637	1579.9279	790.4676	14
4	525.3871	263.1972	508.3606	254.6839			**542.4137**	271.7105	R	1379.7641		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	***1465.8360***	733.4216	1466.8438	733.9255	13
5	640.4141	320.7107	623.3875	312.1974	622.4035	311.7054	657.4406	329.2239	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	***1309.7349***	655.3711	**1310.7427**	655.8750	12
6	754.4570	377.7321	737.4304	369.2189	736.4464	368.7269	**771.4835**	386.2454	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	**1195.7157**	598.3615	11
7	867.5411	434.2742	850.5145	425.7609	849.5305	425.2689	884.5676	442.7874	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	***1080.6650***	540.8361	1081.6728	541.3400	10
8	995.5996	498.3035	978.5731	489.7902	977.5891	489.2982	**1012.6262**	506.8167	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	***967.5809***	484.2941	968.5887	484.7980	9
9	1052.6211	526.8142	1035.5946	518.3009	1034.6105	517.8089	**1069.6477**	535.3275	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	***839.5223***	420.2648	**840.5302**	420.7687	8
10	1165.7052	583.3562	1148.6786	574.8429	1147.6946	574.3509	**1182.7317**	591.8695	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	***782.5009***	391.7541	783.5087	392.2580	7
11	1266.7528	633.8801	1249.7263	625.3668	1248.7423	624.8748	**1283.7794**	642.3933	T	652.4141	654.3933	685.4355	343.2214	668.4090	334.7081	667.4250	334.2161	***669.4168***	335.2120	670.4246	335.7160	6
12	1394.8478	697.9275	1377.8213	689.4143	1376.8372	688.9223	1411.8744	706.4408	K	510.3035		584.3879	292.6976	567.3613	284.1843			***568.3691***	284.6882	**569.3770**	285.1921	5
13	1491.9006	746.4539	1474.8740	737.9407	1473.8900	737.4486	**1508.9271**	754.9672	P	413.2507		456.2929	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1562.9377	781.9725	1545.9111	773.4592	1544.9271	772.9672	1579.9642	790.4858	A			359.2401	180.1237	342.2136	171.6104			***343.2214***	172.1143	**344.2292**	172.6183	3
15	1676.0218	838.5145	1658.9952	830.0012	1658.0112	829.5092	1693.0483	847.0278	I	243.1452	257.1608	288.2030	144.6051	271.1765	136.0919			272.1843	136.5958	**273.1921**	137.0997	2
16									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1849.1261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 83 **Expect:** 3e-06
Matches : 33/269 fragment ions using 38 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2VLRDNIQGITKPAIR



MS/MS Fragmentation of **KVLRDNIQGITKPAIR**
Found in **sp|P62806|H4_MOUSE** in **fgcz_10090**, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2075: 1849.126416 from(463.288880,4+) intensity(309250.4400) scans(4176) rtinseconds(2380.369) index(2556)
Title: 2557: Scan 4176 (rt=39.6728) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_04_trypsin_swimup_NaCl_2.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\mgf__low_res_MS2_nomerge\20110519_04_trypsin_swimup_NaCl_2.mgf

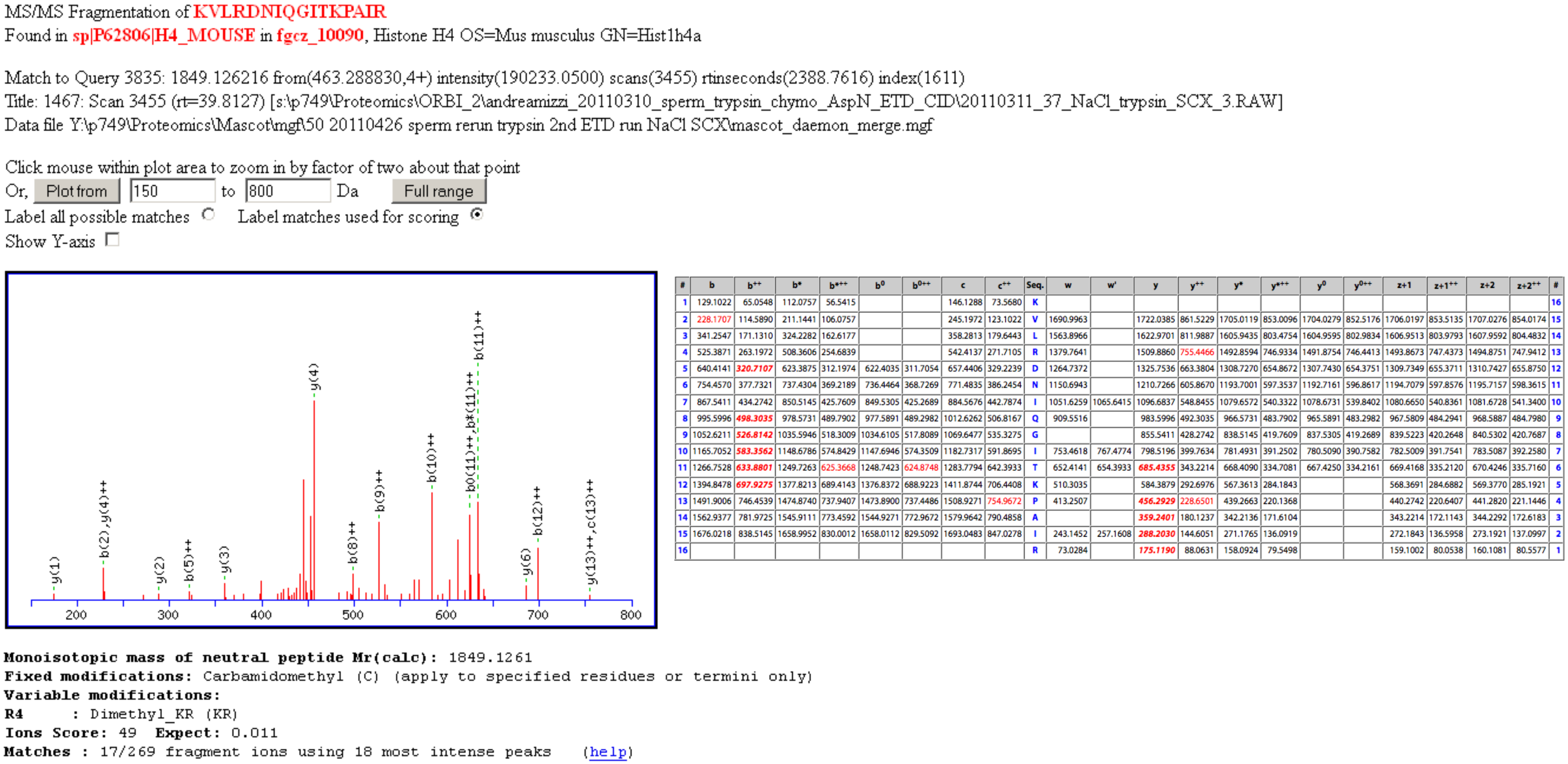
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	w'	y	y++	y*	y*++	y0	y0++	z+1	z+1++	z+2	z+2++	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													16
2	242.1863	121.5968	225.1598	113.0835			259.2129	130.1101	V	1676.9806		1708.0228	854.5150	1690.9963	846.0018	1690.0122	845.5098	1692.0041	846.5057	1693.0119	847.0096	15
3	**355.2704**	178.1388	338.2438	169.6255			372.2969	186.6521	L	1549.8809		1608.9544	804.9808	1591.9279	796.4676	1590.9438	795.9756	1592.9357	796.9715	1593.9435	797.4754	14
4	525.3871	263.1972	508.3606	254.6839			542.4137	271.7105	R	1379.7641		1495.8703	748.4388	1478.8438	739.9255	1477.8598	739.4335	1479.8516	740.4294	1480.8594	740.9334	13
5	640.4141	**320.7107**	623.3875	312.1974	622.4035	311.7054	657.4406	329.2239	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	1310.7427	655.8750	12
6	**754.4570**	**377.7321**	737.4304	369.2189	736.4464	368.7269	771.4835	386.2454	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	1195.7157	598.3615	11
7	867.5411	434.2742	850.5145	425.7609	849.5305	425.2689	884.5676	442.7874	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
8	995.5996	**498.3035**	978.5731	489.7902	977.5891	489.2982	1012.6262	506.8167	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	967.5809	484.2941	968.5887	484.7980	9
9	1052.6211	**526.8142**	1035.5946	518.3009	1034.6105	517.8089	1069.6477	535.3275	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	839.5223	420.2648	840.5302	420.7687	8
10	1165.7052	**583.3562**	1148.6786	574.8429	1147.6946	574.3509	1182.7317	591.8695	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
11	1266.7528	**633.8801**	1249.7263	625.3668	1248.7423	624.8748	1283.7794	642.3933	T	652.4141	654.3933	**685.4355**	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
12	1394.8478	**697.9275**	1377.8213	689.4143	1376.8372	688.9223	1411.8744	706.4408	K	510.3035		584.3879	292.6976	567.3613	284.1843			568.3691	284.6882	**569.3770**	285.1921	5
13	1491.9006	746.4539	1474.8740	737.9407	1473.8900	737.4486	1508.9271	754.9672	P	413.2507		**456.2929**	228.6501	439.2663	220.1368			440.2742	220.6407	**441.2820**	221.1446	4
14	1562.9377	781.9725	1545.9111	773.4592	1544.9271	772.9672	1579.9642	790.4858	A			**359.2401**	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
15	1676.0218	838.5145	1658.9952	830.0012	1658.0112	829.5092	1693.0483	847.0278	I	243.1452	257.1608	**288.2030**	144.6051	271.1765	136.0919			**272.1843**	136.5958	273.1921	137.0997	2
16									R	73.0284		**175.1190**	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1849.1261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
R4 : Methyl_KR (KR)
Ions Score: 48 **Expect:** 0.014
Matches : 23/269 fragment ions using 32 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1VLRme1DNIQGITKPAIR



MS/MS Fragmentation of **KVLRDNIQGITKPAIR**
Found in **sp|P62806|H4_MOUSE** in **fgcz_10090**, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3835: 1849.126216 from(463.288830,4+) intensity(190233.0500) scans(3455) rtinseconds(2388.7616) index(1611)
Title: 1467: Scan 3455 (rt=39.8127) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

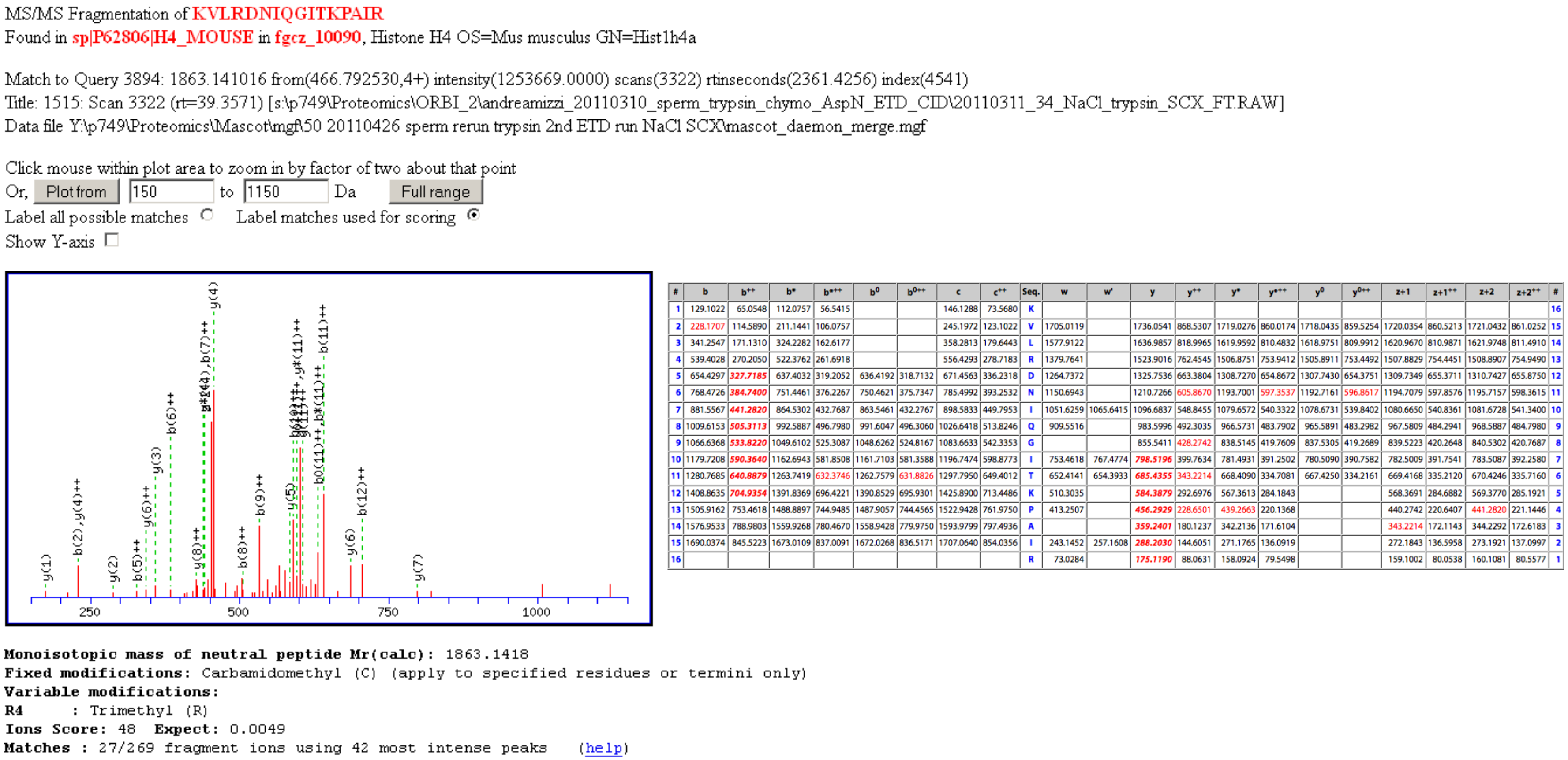
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 800 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	129.1022	65.0548	112.0757	56.5415			146.1288	73.5680	K													16
2	228.1707	114.5890	211.1441	106.0757			245.1972	123.1022	V	1690.9963		1722.0385	861.5229	1705.0119	853.0096	1704.0279	852.5176	1706.0197	853.5135	1707.0276	854.0174	15
3	341.2547	171.1310	324.2282	162.6177			358.2813	179.6443	L	1563.8966		1622.9701	811.9887	1605.9435	803.4754	1604.9595	802.9834	1606.9513	803.9793	1607.9592	804.4832	14
4	525.3871	263.1972	508.3606	254.6839			542.4137	271.7105	R	1379.7641		1509.8860	755.4466	1492.8594	746.9334	1491.8754	746.4413	1493.8673	747.4373	1494.8751	747.9412	13
5	640.4141	***320.7107***	623.3875	312.1974	622.4035	311.7054	657.4406	329.2239	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	1310.7427	655.8750	12
6	754.4570	377.7321	737.4304	369.2189	736.4464	368.7269	771.4835	386.2454	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	1195.7157	598.3615	11
7	867.5411	434.2742	850.5145	425.7609	849.5305	425.2689	884.5676	442.7874	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
8	995.5996	***498.3035***	978.5731	489.7902	977.5891	489.2982	1012.6262	506.8167	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	967.5809	484.2941	968.5887	484.7980	9
9	1052.6211	***526.8142***	1035.5946	518.3009	1034.6105	517.8089	1069.6477	535.3275	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	839.5223	420.2648	840.5302	420.7687	8
10	1165.7052	***583.3562***	1148.6786	574.8429	1147.6946	574.3509	1182.7317	591.8695	I	753.4618	767.4774	798.5196	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
11	1266.7528	***633.8801***	1249.7263	625.3668	1248.7423	624.8748	1283.7794	642.3933	T	652.4141	654.3933	***685.4355***	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
12	1394.8478	***697.9275***	1377.8213	689.4143	1376.8372	688.9223	1411.8744	706.4408	K	510.3035		584.3879	292.6976	567.3613	284.1843			568.3691	284.6882	569.3770	285.1921	5
13	1491.9006	746.4539	1474.8740	737.9407	1473.8900	737.4486	1508.9271	754.9672	P	413.2507		***456.2929***	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1562.9377	781.9725	1545.9111	773.4592	1544.9271	772.9672	1579.9642	790.4858	A			***359.2401***	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
15	1676.0218	838.5145	1658.9952	830.0012	1658.0112	829.5092	1693.0483	847.0278	I	243.1452	257.1608	***288.2030***	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
16									R	73.0284		***175.1190***	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1849.1261
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
R4 : Dimethyl_KR (KR)
Ions Score: 49 **Expect:** 0.011
Matches : 17/269 fragment ions using 18 most intense peaks (help)

Mascot Search Results: Peptide View

KVLRme2DNIQGITKPAIR



MS/MS Fragmentation of KVLRDNIQGITKPAIR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3894: 1863.141016 from(466.792530,4+) intensity(1253669.0000) scans(3322) rtinseconds(2361.4256) index(4541)
Title: 1515: Scan 3322 (rt=39.3571) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

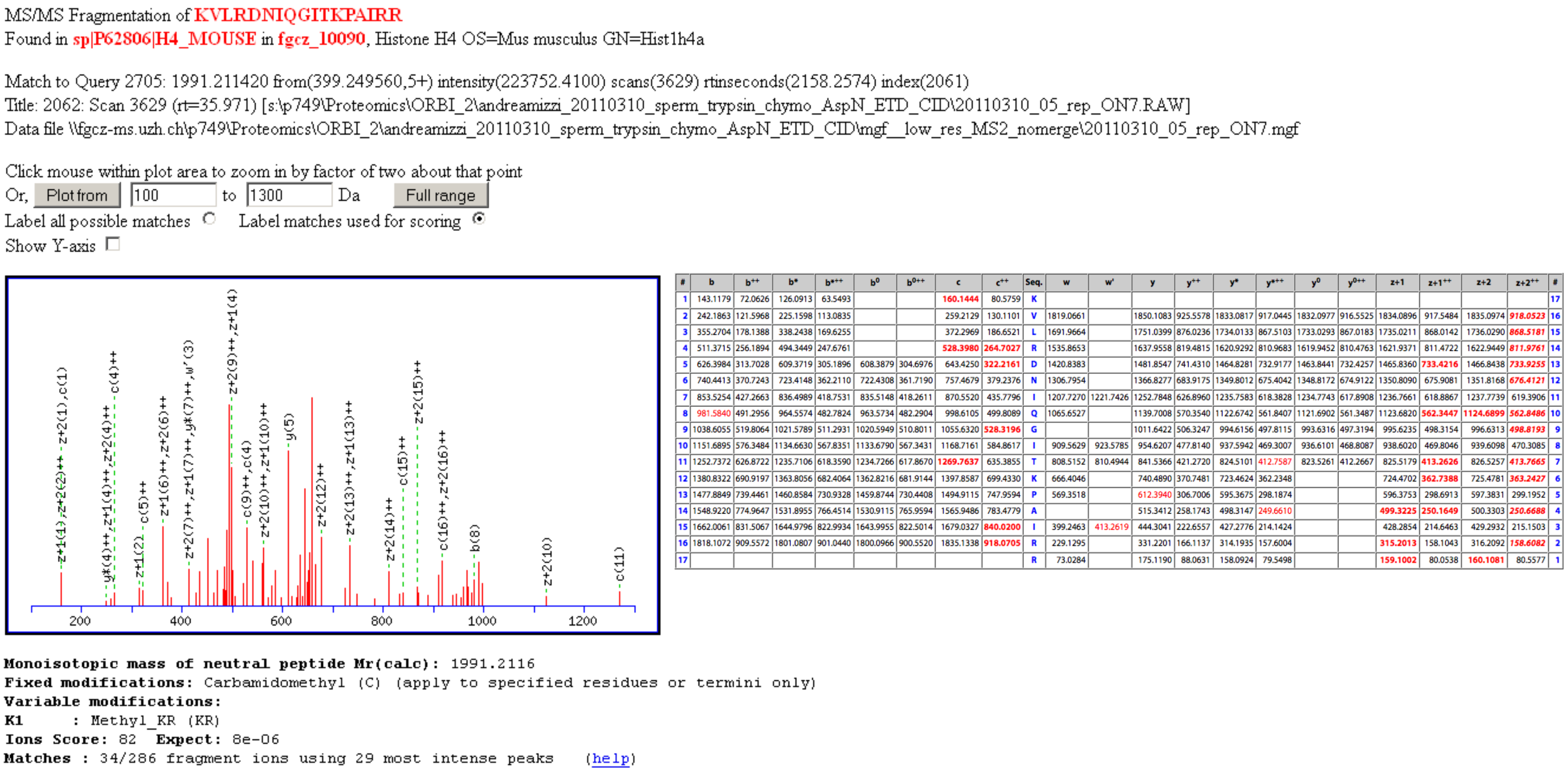
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	129.1022	65.0548	112.0757	56.5415			146.1288	73.5680	K													16
2	228.1707	114.5890	211.1441	106.0757			245.1972	123.1022	V	1705.0119		1736.0541	868.5307	1719.0276	860.0174	1718.0435	859.5254	1720.0354	860.5213	1721.0432	861.0252	15
3	341.2547	171.1310	324.2282	162.6177			358.2813	179.6443	L	1577.9122		1636.9857	818.9965	1619.9592	810.4832	1618.9751	809.9912	1620.9670	810.9871	1621.9748	811.4910	14
4	539.4028	270.2050	522.3762	261.6918			556.4293	278.7183	R	1379.7641		1523.9016	762.4545	1506.8751	753.9412	1505.8911	753.4492	1507.8829	754.4451	1508.8907	754.9490	13
5	654.4297	**327.7185**	637.4032	319.2052	636.4192	318.7132	671.4563	336.2318	D	1264.7372		1325.7536	663.3804	1308.7270	654.8672	1307.7430	654.3751	1309.7349	655.3711	1310.7427	655.8750	12
6	768.4726	**384.7400**	751.4461	376.2267	750.4621	375.7347	785.4992	393.2532	N	1150.6943		1210.7266	605.8670	1193.7001	597.3537	1192.7161	596.8617	1194.7079	597.8576	1195.7157	598.3615	11
7	881.5567	**441.2820**	864.5302	432.7687	863.5461	432.2767	898.5833	449.7953	I	1051.6259	1065.6415	1096.6837	548.8455	1079.6572	540.3322	1078.6731	539.8402	1080.6650	540.8361	1081.6728	541.3400	10
8	1009.6153	**505.3113**	992.5887	496.7980	991.6047	496.3060	1026.6418	513.8246	Q	909.5516		983.5996	492.3035	966.5731	483.7902	965.5891	483.2982	967.5809	484.2941	968.5887	484.7980	9
9	1066.6368	**533.8220**	1049.6102	525.3087	1048.6262	524.8167	1083.6633	542.3353	G			855.5411	428.2742	838.5145	419.7609	837.5305	419.2689	839.5223	420.2648	840.5302	420.7687	8
10	1179.7208	**590.3640**	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	753.4618	767.4774	**798.5196**	399.7634	781.4931	391.2502	780.5090	390.7582	782.5009	391.7541	783.5087	392.2580	7
11	1280.7685	**640.8879**	1263.7419	632.3746	1262.7579	631.8826	1297.7950	649.4012	T	652.4141	654.3933	**685.4355**	343.2214	668.4090	334.7081	667.4250	334.2161	669.4168	335.2120	670.4246	335.7160	6
12	1408.8635	**704.9354**	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	510.3035		**584.3879**	292.6976	567.3613	284.1843			568.3691	284.6882	569.3770	285.1921	5
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	761.9750	P	413.2507		**456.2929**	228.6501	439.2663	220.1368			440.2742	220.6407	441.2820	221.1446	4
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			**359.2401**	180.1237	342.2136	171.6104			343.2214	172.1143	344.2292	172.6183	3
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	243.1452	257.1608	**288.2030**	144.6051	271.1765	136.0919			272.1843	136.5958	273.1921	137.0997	2
16									R	73.0284		**175.1190**	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1863.1418
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
R4 : Trimethyl (R)
Ions Score: 48 **Expect:** 0.0049
Matches : 27/269 fragment ions using 42 most intense peaks (help)

Mascot Search Results: Peptide View

(K)VL(Rme3)DNIQGITKPAIR



MS/MS Fragmentation of KVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2705: 1991.211420 from(399.249560,5+) intensity(223752.4100) scans(3629) rtinseconds(2158.2574) index(2061)
Title: 2062: Scan 3629 (rt=35.971) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_05_rep_ON7.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_05_rep_ON7.mgf

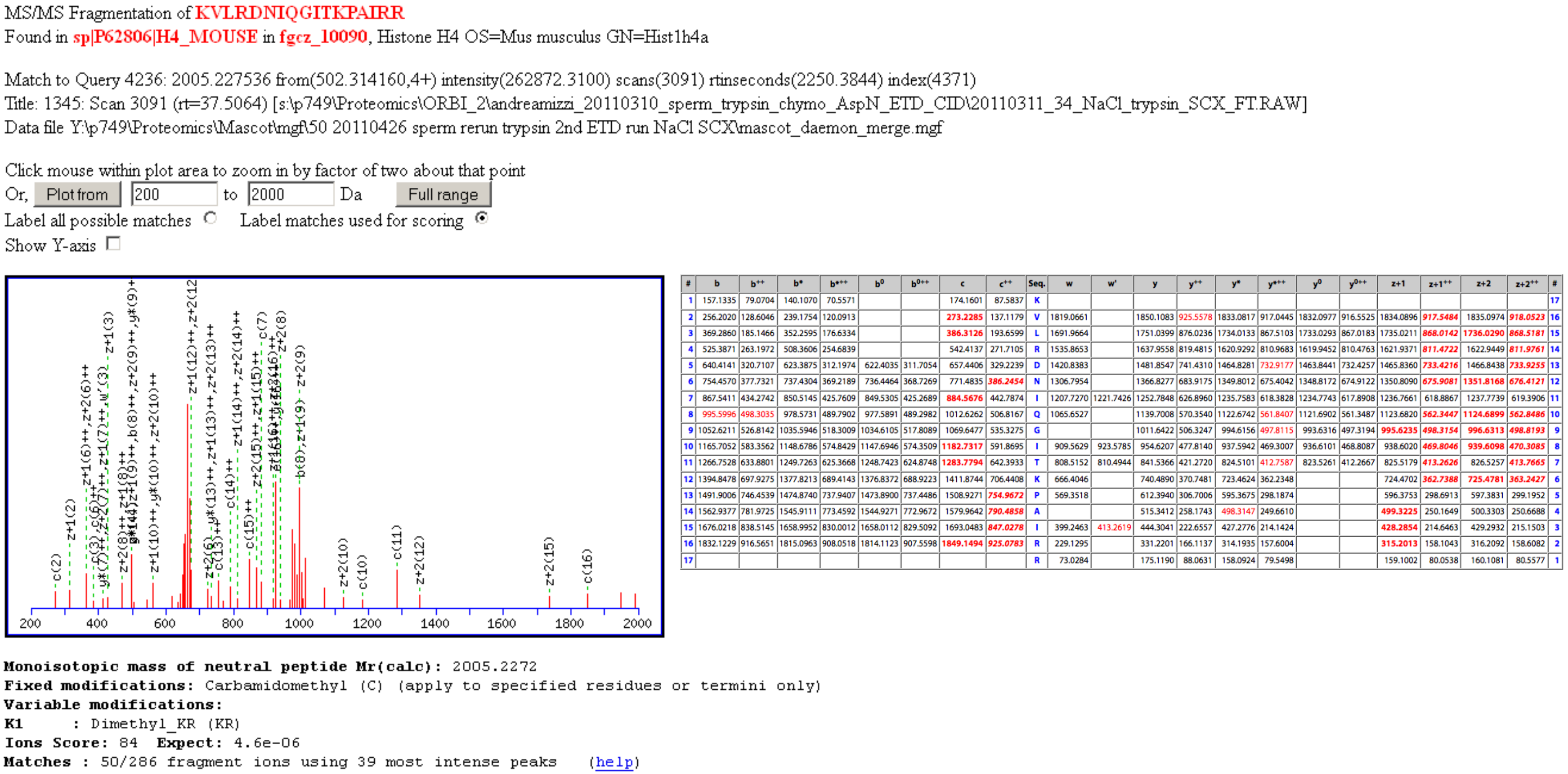
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	143.1179	72.0626	126.0913	63.5493			160.1444	80.5759	K													17
2	242.1863	121.5968	225.1598	113.0835			259.2129	130.1101	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	917.5484	1835.0974	918.0523	16
3	355.2704	178.1388	338.2438	169.6255			372.2969	186.6521	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	868.0142	1736.0290	868.5181	15
4	511.3715	256.1894	494.3449	247.6761			528.3980	264.7027	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	811.4722	1622.9449	811.9761	14
5	626.3984	313.7028	609.3719	305.1896	608.3879	304.6976	643.4250	322.2161	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	733.4216	1466.8438	733.9255	13
6	740.4413	370.7243	723.4148	362.2110	722.4308	361.7190	757.4679	379.2376	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	1351.8168	676.4121	12
7	853.5254	427.2663	836.4989	418.7531	835.5148	418.2611	870.5520	435.7796	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
8	981.5840	491.2956	964.5574	482.7824	963.5734	482.2904	998.6105	499.8089	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	562.3447	1124.6899	562.8486	10
9	1038.6055	519.8064	1021.5789	511.2931	1020.5949	510.8011	1055.6320	528.3196	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	995.6235	498.3154	996.6313	498.8193	9
10	1151.6895	576.3484	1134.6630	567.8351	1133.6790	567.3431	1168.7161	584.8617	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
11	1252.7372	626.8722	1235.7106	618.3590	1234.7266	617.8670	1269.7637	635.3855	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	413.2626	826.5257	413.7665	7
12	1380.8322	690.9197	1363.8056	682.4064	1362.8216	681.9144	1397.8587	699.4330	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	362.7388	725.4781	363.2427	6
13	1477.8849	739.4461	1460.8584	730.9328	1459.8744	730.4408	1494.9115	747.9594	P	569.3518		612.3940	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
14	1548.9220	774.9647	1531.8955	766.4514	1530.9115	765.9594	1565.9486	783.4779	A			515.3412	258.1743	498.3147	249.6610			499.3225	250.1649	500.3303	250.6688	4
15	1662.0061	831.5067	1644.9796	822.9934	1643.9955	822.5014	1679.0327	840.0200	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			428.2854	214.6463	429.2932	215.1503	3
16	1818.1072	909.5572	1801.0807	901.0440	1800.0966	900.5520	1835.1338	918.0705	R	229.1295		331.2201	166.1137	314.1935	157.6004			315.2013	158.1043	316.2092	158.6082	2
17									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 1991.2116
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Methyl_KR (KR)
Ions Score: 82 **Expect:** 8e-06
Matches : 34/286 fragment ions using 29 most intense peaks (help)

Mascot Search Results: Peptide View

Kme1VLRDNIQGITKPAIRR



MS/MS Fragmentation of KVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 4236: 2005.227536 from(502.314160,4+) intensity(262872.3100) scans(3091) rtinseconds(2250.3844) index(4371)
Title: 1345: Scan 3091 (rt=37.5064) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_34_NaCl_trypsin_SCX_FT.RAW]
Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

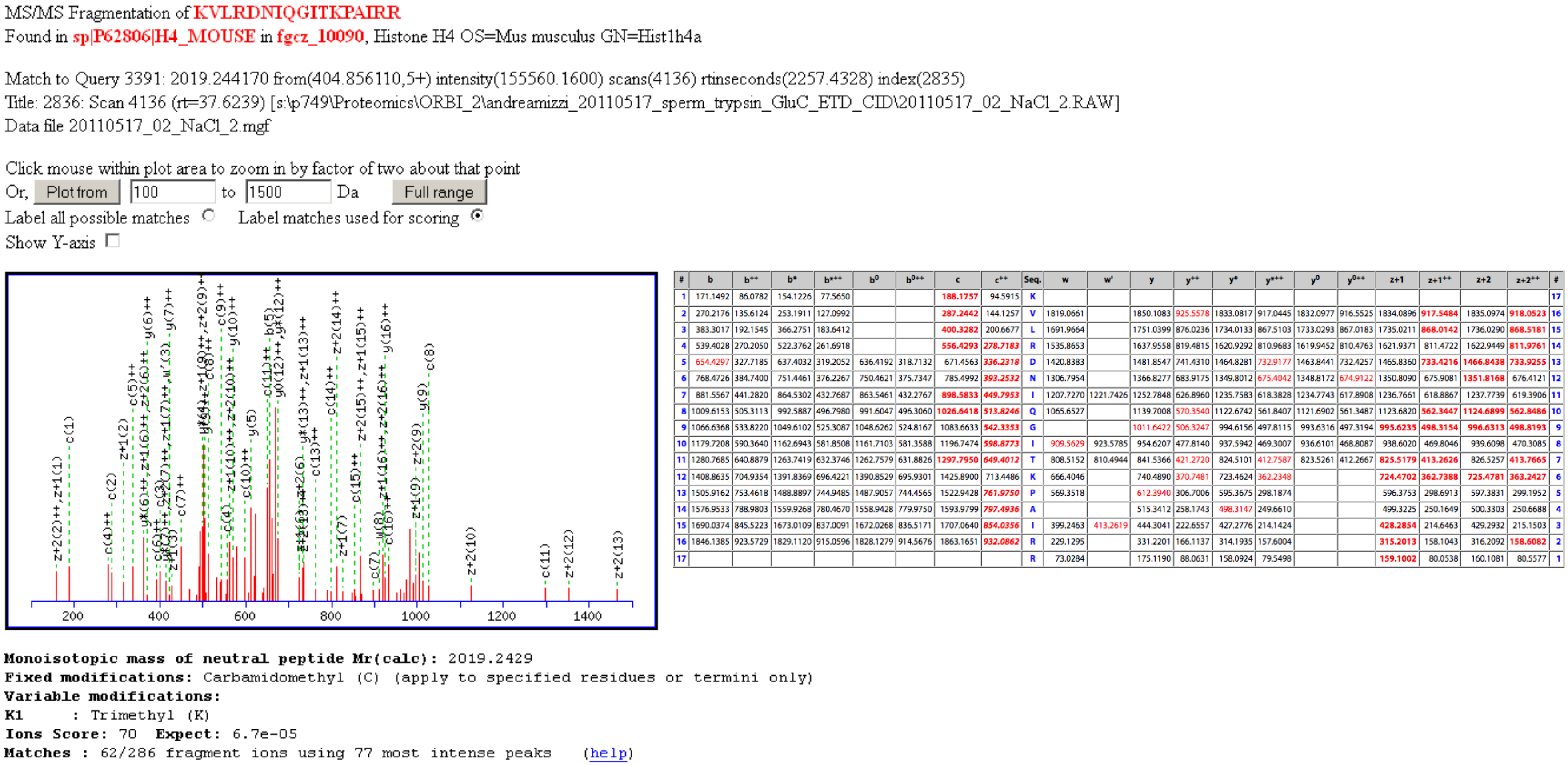
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 200 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	z+1	z+1^{++}	z+2	z+2^{++}	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													17
2	256.2020	128.6046	239.1754	120.0913			**273.2285**	137.1179	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	***917.5484***	1835.0974	***918.0523***	16
3	369.2860	185.1466	352.2595	176.6334			**386.3126**	193.6599	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	***868.0142***	**1736.0290**	***868.5181***	15
4	525.3871	263.1972	508.3606	254.6839			542.4137	271.7105	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	***811.4722***	1622.9449	***811.9761***	14
5	640.4141	320.7107	623.3875	312.1974	622.4035	311.7054	657.4406	329.2239	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	***733.4216***	1466.8438	***733.9255***	13
6	754.4570	377.7321	737.4304	369.2189	736.4464	368.7269	771.4835	***386.2454***	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	***675.9081***	**1351.8168**	***676.4121***	12
7	867.5411	434.2742	850.5145	425.7609	849.5305	425.2689	**884.5676**	442.7874	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
8	995.5996	498.3035	978.5731	489.7902	977.5891	489.2982	1012.6262	506.8167	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	***562.3447***	**1124.6899**	***562.8486***	10
9	1052.6211	526.8142	1035.5946	518.3009	1034.6105	517.8089	1069.6477	535.3275	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	**995.6235**	***498.3154***	**996.6313**	***498.8193***	9
10	1165.7052	583.3562	1148.6786	574.8429	1147.6946	574.3509	**1182.7317**	591.8695	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	***469.8046***	**939.6098**	***470.3085***	8
11	1266.7528	633.8801	1249.7263	625.3668	1248.7423	624.8748	**1283.7794**	642.3933	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	***413.2626***	826.5257	***413.7665***	7
12	1394.8478	697.9275	1377.8213	689.4143	1376.8372	688.9223	1411.8744	706.4408	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	***362.7388***	**725.4781**	***363.2427***	6
13	1491.9006	746.4539	1474.8740	737.9407	1473.8900	737.4486	1508.9271	***754.9672***	P	569.3518		612.3940	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
14	1562.9377	781.9725	1545.9111	773.4592	1544.9271	772.9672	1579.9642	***790.4858***	A			515.3412	258.1743	498.3147	249.6610			**499.3225**	250.1649	500.3303	250.6688	4
15	1676.0218	838.5145	1658.9952	830.0012	1658.0112	829.5092	1693.0483	***847.0278***	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			**428.2854**	214.6463	429.2932	215.1503	3
16	1832.1229	916.5651	1815.0963	908.0518	1814.1123	907.5598	**1849.1494**	***925.0783***	R	229.1295		331.2201	166.1137	314.1935	157.6004			**315.2013**	158.1043	316.2092	158.6082	2
17									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2005.2272
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 84 **Expect:** 4.6e-06
Matches : 50/286 fragment ions using 39 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2VLRDNIQGITKPAIRR



MS/MS Fragmentation of KVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 3391: 2019.244170 from(404.856110,5+) intensity(155560.1600) scans(4136) rtinseconds(2257.4328) index(2835)
Title: 2836: Scan 4136 (rt=37.6239) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_02_NaCl_2.RAW]
Data file 20110517_02_NaCl_2.mgf

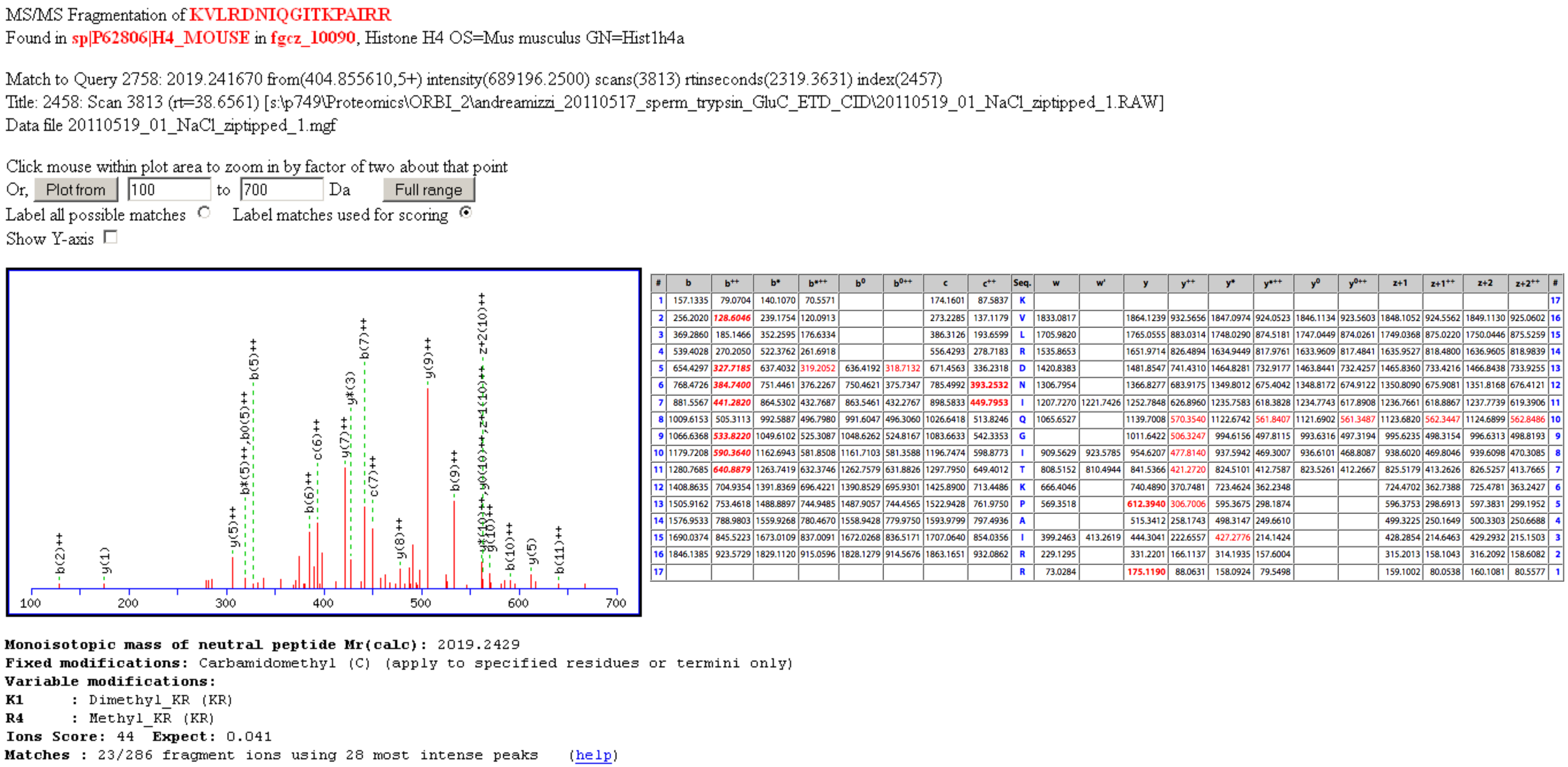
Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	c	c⁺⁺	Seq.	w	w'	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	z+1	z+1⁺⁺	z+2	z+2⁺⁺	#
1	171.1492	86.0782	154.1226	77.5650			**188.1757**	94.5915	K													17
2	270.2176	135.6124	253.1911	127.0992			**287.2442**	144.1257	V	1819.0661		1850.1083	925.5578	1833.0817	917.0445	1832.0977	916.5525	1834.0896	**917.5484**	1835.0974	**918.0523**	16
3	383.3017	192.1545	366.2751	183.6412			**400.3282**	200.6677	L	1691.9664		1751.0399	876.0236	1734.0133	867.5103	1733.0293	867.0183	1735.0211	**868.0142**	1736.0290	**868.5181**	15
4	539.4028	270.2050	522.3762	261.6918			**556.4293**	***278.7183***	R	1535.8653		1637.9558	819.4815	1620.9292	810.9683	1619.9452	810.4763	1621.9371	811.4722	1622.9449	**811.9761**	14
5	654.4297	327.7185	637.4032	319.2052	636.4192	318.7132	671.4563	***336.2318***	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	**733.4216**	**1466.8438**	**733.9255**	13
6	768.4726	384.7400	751.4461	376.2267	750.4621	375.7347	785.4992	***393.2532***	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	**1351.8168**	676.4121	12
7	881.5567	441.2820	864.5302	432.7687	863.5461	432.2767	**898.5833**	***449.7953***	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	**1026.6418**	***513.8246***	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	**562.3447**	**1124.6899**	**562.8486**	10
9	1066.6368	533.8220	1049.6102	525.3087	1048.6262	524.8167	1083.6633	***542.3353***	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	**995.6235**	**498.3154**	**996.6313**	**498.8193**	9
10	1179.7208	590.3640	1162.6943	581.8508	1161.7103	581.3588	1196.7474	***598.8773***	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
11	1280.7685	640.8879	1263.7419	632.3746	1262.7579	631.8826	**1297.7950**	***649.4012***	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	**825.5179**	**413.2626**	826.5257	**413.7665**	7
12	1408.8635	704.9354	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	666.4046		740.4890	370.7481	723.4624	362.2348			**724.4702**	**362.7388**	**725.4781**	**363.2427**	6
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	***761.9750***	P	569.3518		612.3940	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	***797.4936***	A			515.3412	258.1743	498.3147	249.6610			499.3225	250.1649	500.3303	250.6688	4
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	***854.0356***	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			**428.2854**	214.6463	429.2932	215.1503	3
16	1846.1385	923.5729	1829.1120	915.0596	1828.1279	914.5676	1863.1651	***932.0862***	R	229.1295		331.2201	166.1137	314.1935	157.6004			**315.2013**	158.1043	316.2092	**158.6082**	2
17									R	73.0284		175.1190	88.0631	158.0924	79.5498			**159.1002**	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2019.2429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
Ions Score: 70 **Expect:** 6.7e-05
Matches : 62/286 fragment ions using 77 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3VLRDNIQGITKPAIRR



MS/MS Fragmentation of KVLRDNIQGITKPAIRR

Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2758: 2019.241670 from(404.855610,5+) intensity(689196.2500) scans(3813) rtinseconds(2319.3631) index(2457)

Title: 2458: Scan 3813 (rt=38.6561) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110519_01_NaCl_ziptipped_1.RAW]

Data file 20110519_01_NaCl_ziptipped_1.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 700 Da Full range

Label all possible matches ○ Label matches used for scoring ●

Show Y-axis ☐

#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	c	c⁺⁺	Seq.	w	w'	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	z+1	z+1⁺⁺	z+2	z+2⁺⁺	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													17
2	256.2020	***128.6046***	239.1754	120.0913			273.2285	137.1179	V	1833.0817		1864.1239	932.5656	1847.0974	924.0523	1846.1134	923.5603	1848.1052	924.5562	1849.1130	925.0602	16
3	369.2860	185.1466	352.2595	176.6334			386.3126	193.6599	L	1705.9820		1765.0555	883.0314	1748.0290	874.5181	1747.0449	874.0261	1749.0368	875.0220	1750.0446	875.5259	15
4	539.4028	270.2050	522.3762	261.6918			556.4293	278.7183	R	1535.8653		1651.9714	826.4894	1634.9449	817.9761	1633.9609	817.4841	1635.9527	818.4800	1636.9605	818.9839	14
5	654.4297	***327.7185***	637.4032	319.2052	636.4192	318.7132	671.4563	336.2318	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	733.4216	1466.8438	733.9255	13
6	768.4726	***384.7400***	751.4461	376.2267	750.4621	375.7347	785.4992	**393.2532**	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	1351.8168	676.4121	12
7	881.5567	***441.2820***	864.5302	432.7687	863.5461	432.2767	898.5833	**449.7953**	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	1026.6418	513.8246	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	562.3447	1124.6899	562.8486	10
9	1066.6368	***533.8220***	1049.6102	525.3087	1048.6262	524.8167	1083.6633	542.3353	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	995.6235	498.3154	996.6313	498.8193	9
10	1179.7208	***590.3640***	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
11	1280.7685	***640.8879***	1263.7419	632.3746	1262.7579	631.8826	1297.7950	649.4012	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	413.2626	826.5257	413.7665	7
12	1408.8635	704.9354	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	362.7388	725.4781	363.2427	6
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	761.9750	P	569.3518		**612.3940**	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			515.3412	258.1743	498.3147	249.6610			499.3225	250.1649	500.3303	250.6688	4
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			428.2854	214.6463	429.2932	215.1503	3
16	1846.1385	923.5729	1829.1120	915.0596	1828.1279	914.5676	1863.1651	932.0862	R	229.1295		331.2201	166.1137	314.1935	157.6004			315.2013	158.1043	316.2092	158.6082	2
17									R	73.0284		**175.1190**	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2019.2429

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

Variable modifications:

K1 : Dimethyl_KR (KR)

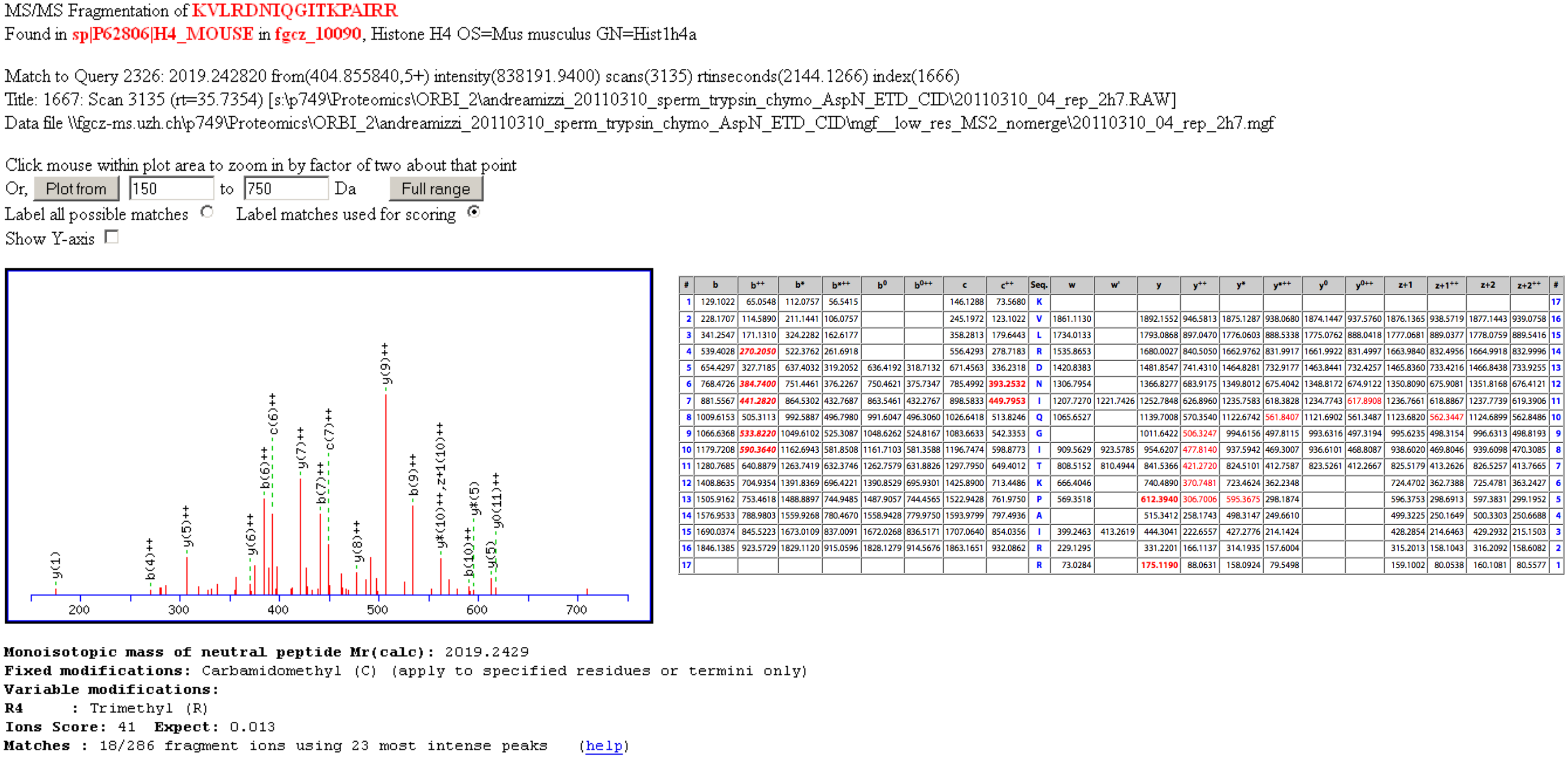
R4 : Methyl_KR (KR)

Ions Score: 44 **Expect:** 0.041

Matches : 23/286 fragment ions using 28 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2VLRme1DNIQGITKPAIRR



MS/MS Fragmentation of KVLRDNIQGITKPAIRR
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 2326: 2019.242820 from(404.855840,5+) intensity(838191.9400) scans(3135) rtinseconds(2144.1266) index(1666)
Title: 1667: Scan 3135 (rt=35.7354) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110310_04_rep_2h7.RAW]
Data file \\fgcz-ms.uzh.ch\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\mgf__low_res_MS2_nomerge\20110310_04_rep_2h7.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 150 to 750 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	129.1022	65.0548	112.0757	56.5415			146.1288	73.5680	K													17
2	228.1707	114.5890	211.1441	106.0757			245.1972	123.1022	V	1861.1130		1892.1552	946.5813	1875.1287	938.0680	1874.1447	937.5760	1876.1365	938.5719	1877.1443	939.0758	16
3	341.2547	171.1310	324.2282	162.6177			358.2813	179.6443	L	1734.0133		1793.0868	897.0470	1776.0603	888.5338	1775.0762	888.0418	1777.0681	889.0377	1778.0759	889.5416	15
4	539.4028	***270.2050***	522.3762	261.6918			556.4293	278.7183	R	1535.8653		1680.0027	840.5050	1662.9762	831.9917	1661.9922	831.4997	1663.9840	832.4956	1664.9918	832.9996	14
5	654.4297	327.7185	637.4032	319.2052	636.4192	318.7132	671.4563	336.2318	D	1420.8383		1481.8547	741.4310	1464.8281	732.9177	1463.8441	732.4257	1465.8360	733.4216	1466.8438	733.9255	13
6	768.4726	***384.7400***	751.4461	376.2267	750.4621	375.7347	785.4992	**393.2532**	N	1306.7954		1366.8277	683.9175	1349.8012	675.4042	1348.8172	674.9122	1350.8090	675.9081	1351.8168	676.4121	12
7	881.5567	***441.2820***	864.5302	432.7687	863.5461	432.2767	898.5833	**449.7953**	I	1207.7270	1221.7426	1252.7848	626.8960	1235.7583	618.3828	1234.7743	617.8908	1236.7661	618.8867	1237.7739	619.3906	11
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	1026.6418	513.8246	Q	1065.6527		1139.7008	570.3540	1122.6742	561.8407	1121.6902	561.3487	1123.6820	562.3447	1124.6899	562.8486	10
9	1066.6368	***533.8220***	1049.6102	525.3087	1048.6262	524.8167	1083.6633	542.3353	G			1011.6422	506.3247	994.6156	497.8115	993.6316	497.3194	995.6235	498.3154	996.6313	498.8193	9
10	1179.7208	***590.3640***	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	909.5629	923.5785	954.6207	477.8140	937.5942	469.3007	936.6101	468.8087	938.6020	469.8046	939.6098	470.3085	8
11	1280.7685	640.8879	1263.7419	632.3746	1262.7579	631.8826	1297.7950	649.4012	T	808.5152	810.4944	841.5366	421.2720	824.5101	412.7587	823.5261	412.2667	825.5179	413.2626	826.5257	413.7665	7
12	1408.8635	704.9354	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	666.4046		740.4890	370.7481	723.4624	362.2348			724.4702	362.7388	725.4781	363.2427	6
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	761.9750	P	569.3518		**612.3940**	306.7006	595.3675	298.1874			596.3753	298.6913	597.3831	299.1952	5
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			515.3412	258.1743	498.3147	249.6610			499.3225	250.1649	500.3303	250.6688	4
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	399.2463	413.2619	444.3041	222.6557	427.2776	214.1424			428.2854	214.6463	429.2932	215.1503	3
16	1846.1385	923.5729	1829.1120	915.0596	1828.1279	914.5676	1863.1651	932.0862	R	229.1295		331.2201	166.1137	314.1935	157.6004			315.2013	158.1043	316.2092	158.6082	2
17									R	73.0284		**175.1190**	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2019.2429
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
R4 : Trimethyl (R)
Ions Score: 41 **Expect:** 0.013
Matches : 18/286 fragment ions using 23 most intense peaks (help)

Mascot Search Results: Peptide View

(K)VL(Rme3)DNIQGITKPAIRR

MS/MS Fragmentation of KVLRDNIQGITKPAIRRLAR

Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 5013: 2345.444484 from(391.914690,6+) intensity(16222.5950) scans(3598) rtinseconds(2484.1767) index(1674)

Title: 1530: Scan 3598 (rt=41.4029) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]

Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 250 to 1200 Da Full range

Label all possible matches ○ Label matches used for scoring ●

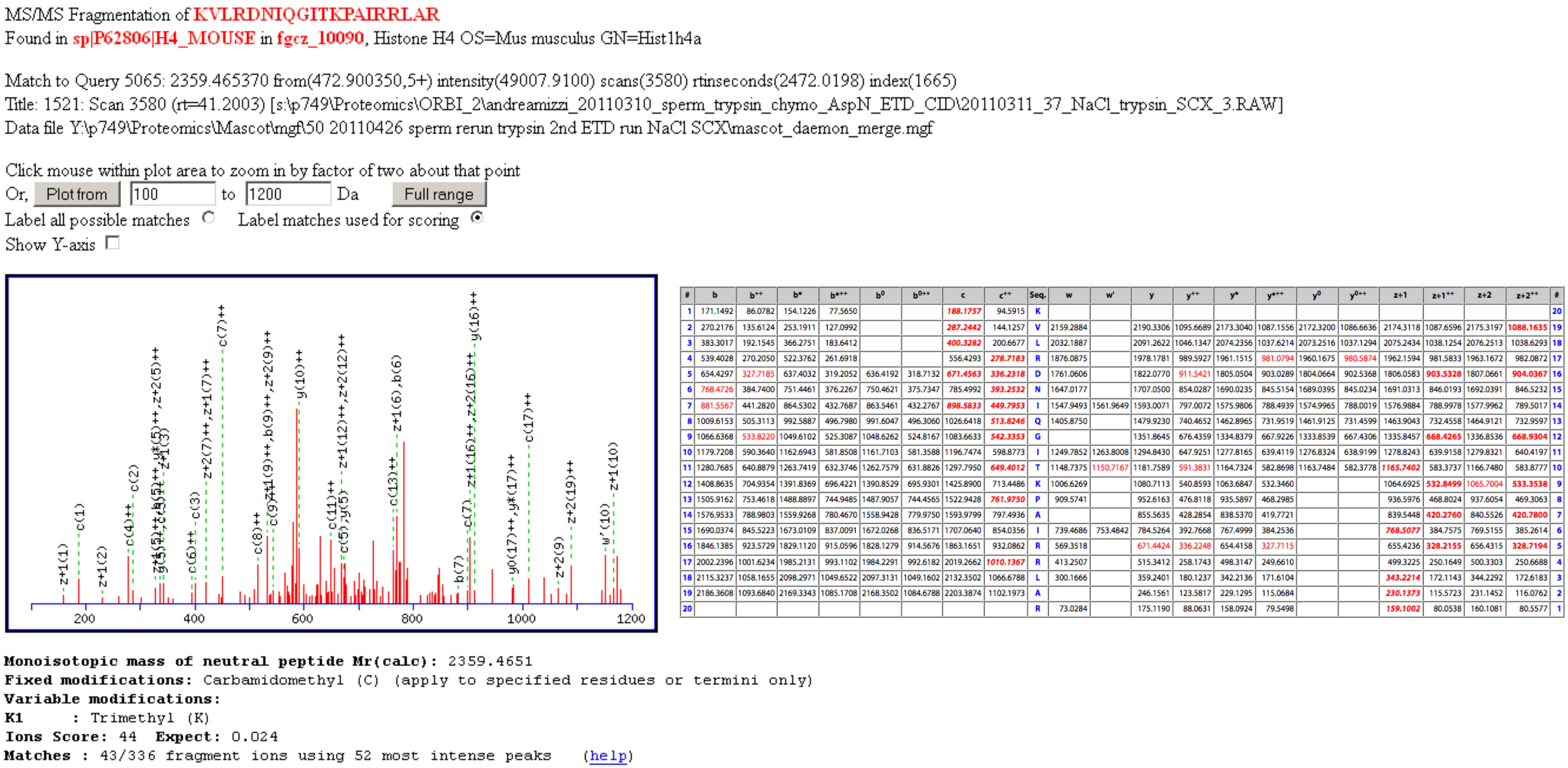
Show Y-axis ☐

#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	z+1	$z+1^{++}$	z+2	$z+2^{++}$	#
1	157.1335	79.0704	140.1070	70.5571			174.1601	87.5837	K													20
2	256.2020	128.6046	239.1754	120.0913			**273.2285**	137.1179	V	2159.2884		2190.3306	1095.6689	2173.3040	1087.1556	2172.3200	1086.6636	2174.3118	**1087.6596**	2175.3197	**1088.1635**	19
3	369.2860	185.1466	352.2595	176.6334			**386.3126**	193.6599	L	2032.1887		2091.2622	1046.1347	2074.2356	1037.6214	2073.2516	1037.1294	2075.2434	**1038.1254**	2076.2513	**1038.6293**	18
4	525.3871	263.1972	508.3606	254.6839			542.4137	***271.7105***	R	1876.0875		1978.1781	989.5927	1961.1515	981.0794	1960.1675	980.5874	1962.1594	981.5833	1963.1672	982.0872	17
5	640.4141	320.7107	623.3875	312.1974	622.4035	311.7054	657.4406	***329.2239***	D	1761.0606		1822.0770	911.5421	1805.0504	903.0289	1804.0664	902.5368	1806.0583	903.5328	1807.0661	**904.0367**	16
6	754.4570	377.7321	737.4304	369.2189	736.4464	368.7269	771.4835	***386.2454***	N	1647.0177		1707.0500	854.0287	1690.0235	845.5154	1689.0395	845.0234	1691.0313	**846.0193**	1692.0391	**846.5232**	15
7	867.5411	434.2742	850.5145	425.7609	849.5305	425.2689	**884.5676**	***442.7874***	I	1547.9493	1561.9649	1593.0071	797.0072	1575.9806	788.4939	1574.9965	788.0019	1576.9884	788.9978	1577.9962	789.5017	14
8	995.5996	498.3035	978.5731	489.7902	977.5891	489.2982	**1012.6262**	***506.8167***	Q	1405.8750		1479.9230	740.4652	1462.8965	731.9519	1461.9125	731.4599	1463.9043	732.4558	1464.9121	**732.9597**	13
9	1052.6211	526.8142	1035.5946	518.3009	1034.6105	517.8089	**1069.6477**	***535.3275***	G			1351.8645	676.4359	1334.8379	667.9226	1333.8539	667.4306	1335.8457	668.4265	1336.8536	**668.9304**	12
10	1165.7052	583.3562	1148.6786	574.8429	1147.6946	574.3509	1182.7317	591.8695	I	1249.7852	1263.8008	1294.8430	647.9251	1277.8165	639.4119	1276.8324	638.9199	1278.8243	639.9158	1279.8321	640.4197	11
11	1266.7528	633.8801	1249.7263	625.3668	1248.7423	624.8748	1283.7794	***642.3933***	T	1148.7375	1150.7167	1181.7589	591.3831	1164.7324	582.8698	1163.7484	582.3778	1165.7402	**583.3737**	1166.7480	**583.8777**	10
12	1394.8478	697.9275	1377.8213	689.4143	1376.8372	688.9223	1411.8744	706.4408	K	1006.6269		1080.7113	540.8593	1063.6847	532.3460			1064.6925	**532.8499**	1065.7004	**533.3538**	9
13	1491.9006	746.4539	1474.8740	737.9407	1473.8900	737.4486	1508.9271	***754.9672***	P	909.5741		952.6163	476.8118	935.5897	468.2985			936.5976	468.8024	937.6054	469.3063	8
14	1562.9377	781.9725	1545.9111	773.4592	1544.9271	772.9672	1579.9642	***790.4858***	A			855.5635	428.2854	838.5370	419.7721			**839.5448**	**420.2760**	840.5526	**420.7800**	7
15	1676.0218	838.5145	1658.9952	830.0012	1658.0112	829.5092	1693.0483	***847.0278***	I	739.4686	753.4842	784.5264	392.7668	767.4999	384.2536			768.5077	384.7575	769.5155	385.2614	6
16	1832.1229	916.5651	1815.0963	908.0518	1814.1123	907.5598	1849.1494	***925.0783***	R	569.3518		671.4424	336.2248	654.4158	327.7115			655.4236	**328.2155**	656.4315	**328.7194**	5
17	1988.2240	994.6156	1971.1974	986.1024	1970.2134	985.6103	2005.2505	***1003.1289***	R	413.2507		515.3412	258.1743	498.3147	249.6610			**499.3225**	250.1649	500.3303	250.6688	4
18	2101.3080	1051.1577	2084.2815	1042.6444	2083.2975	1042.1524	2118.3346	1059.6709	L	300.1666		359.2401	180.1237	342.2136	171.6104			**343.2214**	172.1143	344.2292	172.6183	3
19	2172.3452	1086.6762	2155.3186	1078.1629	2154.3346	1077.6709	2189.3717	1095.1895	A			246.1561	123.5817	229.1295	115.0684			230.1373	115.5723	231.1452	116.0762	2
20									R	73.0284		175.1190	88.0631	158.0924	79.5498			159.1002	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2345.4495
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Dimethyl_KR (KR)
Ions Score: 54 **Expect:** 0.00064
Matches : 45/336 fragment ions using 62 most intense peaks (help)

Mascot Search Results: Peptide View

Kme2VLRDNIQGITKPAIRRLAR



MS/MS Fragmentation of KVLRDNIQGITKPAIRRLAR

Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 5065: 2359.465370 from(472.900350,5+) intensity(49007.9100) scans(3580) rtinseconds(2472.0198) index(1665)

Title: 1521: Scan 3580 (rt=41.2003) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110310_sperm_trypsin_chymo_AspN_ETD_CID\20110311_37_NaCl_trypsin_SCX_3.RAW]

Data file Y:\p749\Proteomics\Mascot\mgf\50 20110426 sperm rerun trypsin 2nd ETD run NaCl SCX\mascot_daemon_merge.mgf

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 100 to 1200 Da Full range

Label all possible matches ○ Label matches used for scoring ●

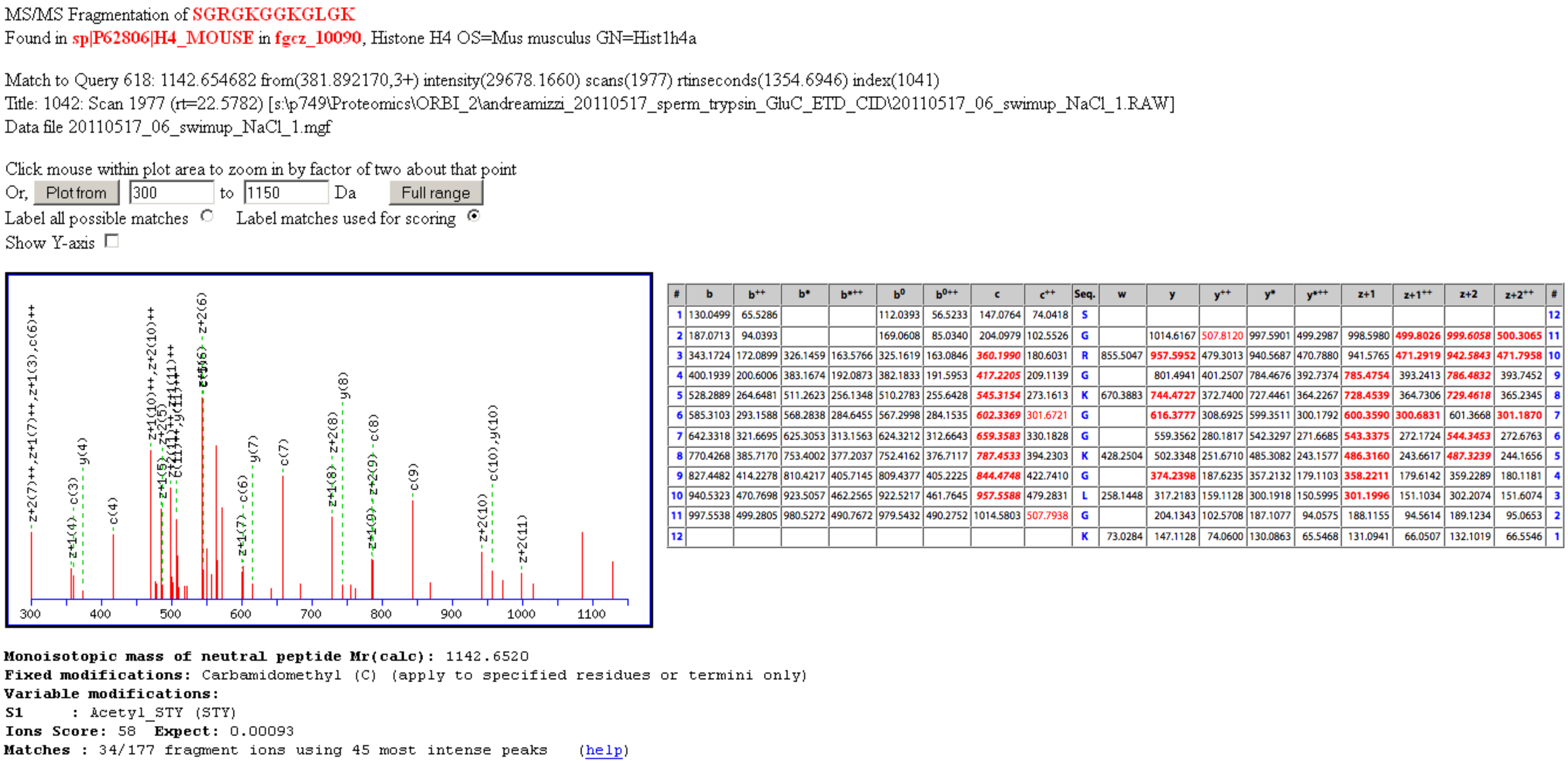
Show Y-axis ☐

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	c	c^{++}	Seq.	w	w'	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	z+1	z+1^{++}	z+2	z+2^{++}	#
1	171.1492	86.0782	154.1226	77.5650			***188.1757***	94.5915	K													20
2	270.2176	135.6124	253.1911	127.0992			***287.2442***	144.1257	V	2159.2884		2190.3306	1095.6689	2173.3040	1087.1556	2172.3200	1086.6636	2174.3118	1087.6596	2175.3197	**1088.1635**	19
3	383.3017	192.1545	366.2751	183.6412			***400.3282***	200.6677	L	2032.1887		2091.2622	1046.1347	2074.2356	1037.6214	2073.2516	1037.1294	2075.2434	1038.1254	2076.2513	1038.6293	18
4	539.4028	270.2050	522.3762	261.6918			556.4293	***278.7183***	R	1876.0875		1978.1781	989.5927	1961.1515	981.0794	1960.1675	980.5874	1962.1594	981.5833	1963.1672	982.0872	17
5	654.4297	327.7185	637.4032	319.2052	636.4192	318.7132	***671.4563***	***336.2318***	D	1761.0606		1822.0770	911.5421	1805.0504	903.0289	1804.0664	902.5368	1806.0583	**903.5328**	1807.0661	**904.0367**	16
6	768.4726	384.7400	751.4461	376.2267	750.4621	375.7347	785.4992	***393.2532***	N	1647.0177		1707.0500	854.0287	1690.0235	845.5154	1689.0395	845.0234	1691.0313	846.0193	1692.0391	846.5232	15
7	881.5567	441.2820	864.5302	432.7687	863.5461	432.2767	***898.5833***	***449.7953***	I	1547.9493	1561.9649	1593.0071	797.0072	1575.9806	788.4939	1574.9965	788.0019	1576.9884	788.9978	1577.9962	789.5017	14
8	1009.6153	505.3113	992.5887	496.7980	991.6047	496.3060	1026.6418	***513.8246***	Q	1405.8750		1479.9230	740.4652	1462.8965	731.9519	1461.9125	731.4599	1463.9043	732.4558	1464.9121	732.9597	13
9	1066.6368	533.8220	1049.6102	525.3087	1048.6262	524.8167	1083.6633	***542.3353***	G			1351.8645	676.4359	1334.8379	667.9226	1333.8539	667.4306	1335.8457	**668.4265**	1336.8536	**668.9304**	12
10	1179.7208	590.3640	1162.6943	581.8508	1161.7103	581.3588	1196.7474	598.8773	I	1249.7852	1263.8008	1294.8430	647.9251	1277.8165	639.4119	1276.8324	638.9199	1278.8243	639.9158	1279.8321	640.4197	11
11	1280.7685	640.8879	1263.7419	632.3746	1262.7579	631.8826	1297.7950	***649.4012***	T	1148.7375	1150.7167	1181.7589	591.3831	1164.7324	582.8698	1163.7484	582.3778	***1165.7402***	583.3737	1166.7480	583.8777	10
12	1408.8635	704.9354	1391.8369	696.4221	1390.8529	695.9301	1425.8900	713.4486	K	1006.6269		1080.7113	540.8593	1063.6847	532.3460			1064.6925	**532.8499**	1065.7004	**533.3538**	9
13	1505.9162	753.4618	1488.8897	744.9485	1487.9057	744.4565	1522.9428	***761.9750***	P	909.5741		952.6163	476.8118	935.5897	468.2985			936.5976	468.8024	937.6054	469.3063	8
14	1576.9533	788.9803	1559.9268	780.4670	1558.9428	779.9750	1593.9799	797.4936	A			855.5635	428.2854	838.5370	419.7721			839.5448	**420.2760**	840.5526	**420.7800**	7
15	1690.0374	845.5223	1673.0109	837.0091	1672.0268	836.5171	1707.0640	854.0356	I	739.4686	753.4842	784.5264	392.7668	767.4999	384.2536			***768.5077***	384.7575	769.5155	385.2614	6
16	1846.1385	923.5729	1829.1120	915.0596	1828.1279	914.5676	1863.1651	932.0862	R	569.3518		671.4424	336.2248	654.4158	327.7115			655.4236	**328.2155**	656.4315	**328.7194**	5
17	2002.2396	1001.6234	1985.2131	993.1102	1984.2291	992.6182	2019.2662	***1010.1367***	R	413.2507		515.3412	258.1743	498.3147	249.6610			499.3225	250.1649	500.3303	250.6688	4
18	2115.3237	1058.1655	2098.2971	1049.6522	2097.3131	1049.1602	2132.3502	1066.6788	L	300.1666		359.2401	180.1237	342.2136	171.6104			***343.2214***	172.1143	344.2292	172.6183	3
19	2186.3608	1093.6840	2169.3343	1085.1708	2168.3502	1084.6788	2203.3874	1102.1973	A			246.1561	123.5817	229.1295	115.0684			***230.1373***	115.5723	231.1452	116.0762	2
20									R	73.0284		175.1190	88.0631	158.0924	79.5498			***159.1002***	80.0538	160.1081	80.5577	1

Monoisotopic mass of neutral peptide Mr(calc): 2359.4651
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
K1 : Trimethyl (K)
Ions Score: 44 **Expect:** 0.024
Matches : 43/336 fragment ions using 52 most intense peaks (help)

Mascot Search Results: Peptide View

Kme3VLRDNIQGITKPAIRRLAR



MS/MS Fragmentation of SGRGKGGKGLGK
Found in sp|P62806|H4_MOUSE in fgcz_10090, Histone H4 OS=Mus musculus GN=Hist1h4a

Match to Query 618: 1142.654682 from(381.892170,3+) intensity(29678.1660) scans(1977) rtinseconds(1354.6946) index(1041)
Title: 1042: Scan 1977 (rt=22.5782) [s:\p749\Proteomics\ORBI_2\andreamizzi_20110517_sperm_trypsin_GluC_ETD_CID\20110517_06_swimup_NaCl_1.RAW]
Data file 20110517_06_swimup_NaCl_1.mgf

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 300 to 1150 Da Full range
Label all possible matches ○ Label matches used for scoring ●
Show Y-axis ☐

#	b	b++	b*	b*++	b0	b0++	c	c++	Seq.	w	y	y++	y*	y*++	z+1	z+1++	z+2	z+2++	#
1	130.0499	65.5286			112.0393	56.5233	147.0764	74.0418	S										12
2	187.0713	94.0393			169.0608	85.0340	204.0979	102.5526	G		1014.6167	507.8120	997.5901	499.2987	998.5980	**499.8026**	***999.6058***	**500.3065**	11
3	343.1724	172.0899	326.1459	163.5766	325.1619	163.0846	***360.1990***	180.6031	R	855.5047	**957.5952**	479.3013	940.5687	470.7880	941.5765	**471.2919**	***942.5843***	**471.7958**	10
4	400.1939	200.6006	383.1674	192.0873	382.1833	191.5953	***417.2205***	209.1139	G		801.4941	401.2507	784.4676	392.7374	**785.4754**	393.2413	***786.4832***	393.7452	9
5	528.2889	264.6481	511.2623	256.1348	510.2783	255.6428	***545.3154***	273.1613	K	670.3883	**744.4727**	372.7400	727.4461	364.2267	**728.4539**	364.7306	***729.4618***	365.2345	8
6	585.3103	293.1588	568.2838	284.6455	567.2998	284.1535	***602.3369***	301.6721	G		**616.3777**	308.6925	599.3511	300.1792	**600.3590**	**300.6831**	601.3668	**301.1870**	7
7	642.3318	321.6695	625.3053	313.1563	624.3212	312.6643	***659.3583***	330.1828	G		559.3562	280.1817	542.3297	271.6685	**543.3375**	272.1724	***544.3453***	272.6763	6
8	770.4268	385.7170	753.4002	377.2037	752.4162	376.7117	***787.4533***	394.2303	K	428.2504	502.3348	251.6710	485.3082	243.1577	**486.3160**	243.6617	***487.3239***	244.1656	5
9	827.4482	414.2278	810.4217	405.7145	809.4377	405.2225	***844.4748***	422.7410	G		**374.2398**	187.6235	357.2132	179.1103	**358.2211**	179.6142	359.2289	180.1181	4
10	940.5323	470.7698	923.5057	462.2565	922.5217	461.7645	***957.5588***	479.2831	L	258.1448	317.2183	159.1128	300.1918	150.5995	**301.1996**	151.1034	302.2074	151.6074	3
11	997.5538	499.2805	980.5272	490.7672	979.5432	490.2752	1014.5803	507.7938	G		204.1343	102.5708	187.1077	94.0575	188.1155	94.5614	189.1234	95.0653	2
12									K	73.0284	147.1128	74.0600	130.0863	65.5468	131.0941	66.0507	132.1019	66.5546	1

Monoisotopic mass of neutral peptide Mr(calc): 1142.6520
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Acetyl_STY (STY)
Ions Score: 58 **Expect:** 0.00093
Matches : 34/177 fragment ions using 45 most intense peaks (help)

Mascot Search Results: Peptide View

SacGRGKGGKGLGK